>TCRU_0 Histone-like transcription factor (CBF/NF-Y) and archaeal histone, putative
MLQDLTRLAAAEAERQRRRTVTYADIARVVHHFDRFSFLSDIIPPVSVVAGGAKAVAVGS
ATSLAAESKTSRSAAREGAVRAQLKSTETGGGGASMRQTTLRF*
>TCRU_1 hypothetical protein, conserved
MDEPLQQWRDQRETGERHRKPTICFLVRFDAAPLEAADGVFRGAQAFRSPSEIVVPLKMA
LEEASLTALQSDFMSRTFRRFPQLSNRTVEAFFVSAEEHFMASSTGLSRPYLLRLDACMN
GDDTLDSFFTPVATNAPIVYEVIAHWAPEKLTDTVSSHITLEGEEEEENGDTLPSDTVLE
DTIPAPVVYPFAHRCTYARLIPIQPETPVTDGSTIDEVKAEAPPILNAMRRKEAARMARR
EMEFVEGTERRKLLEEERSARGTVAELEEESRIQTVTLLRLMYDEVPECGVNYIQSIAPR
QRYPVDTLPLAPFPSSVYMKGLSKCAEETARLSHVFATTAISGSAAAPTKHEDTLVAPVP
ADKLNNEKIQEETQEAIPCSDSGEELVRHYADLRRDLLLWERTTFRALTTEMRRILEKQK
KIDEEIVQKAFLEEVENASILDFDSYVHHYSHEHLLEGRSDTPDTVTNYIPGECKRSSHA
ASLVFRRPTESPKFPAAQKEVETTVGAEVGATPTTLSLPGAIRTPSPSLPRPRSPRSLLA
EEKQFREALERSKARAKAALEAIALVDRHWHEPVAFKLAKHRLLLDEKGSRNAILAEEME
SWENHVKEVKKVEIGWVMKAISARKHLFGPVIGEEEKFRADLDEQQERHFAMLLSLYYLG
MER*
>TCRU_2 asparaginyl-tRNA synthetase, putative
MAFRLIFERRLAPLSNSCRRCCRTMFSGPTPRITSVTRSGLRGYVLWQSPPHGSCICPAL
SSSRAFIHLPERTTMASSEELLESLQRIVGLDEKNSKDLSTKPERVQDLLGFFANQNMTP
ESPREQKMMLFNLWAKVKLPKHRDLLADYVKRKKLDSTQKVDAAIRFVDGMKEDALFDAA
KFEKECGVDVVVSKDDTLRLVKTALAEEDLKALKTSWVKNPNMLLGKMKRVPGLQWADFT
LVKTILEELVPPMIKDVVIDEAEPKTEEKTATPPRTKGAEVAATQKCPRNADWKCVVDLH
SLHRIGDLSSMQEGTKVRVVGWAHRVRHQSRLSFVVLRDGSGYIQAVFNGETEPFHRETS
LAIRGTLKYEPKAATELQPPYELHVDEYAIIGNSDGSIENAITPESSPDKLLDDRHLVLR
GTYGSTTIKVRHELIRAFREYCWSVNMFEVTPPTLVQAECEGGSTLFDVIYYGTTAHLTQ
SSQLYLETCTSSVGDVYCILPSYRAEKSKTRRHLSEYTHLEVEYSICDFELFLSKLEDLI
VGAFNRTIERAGDLIAFMNPEQLVDPKANPCDPNNWKFAPKKPFRRLKYADAIKLCNDNG
ILNPETNAPFQFGDDITDQPERAMVAILGEMVFMTHFPAVMKSFYMARDPEDPTLTESVD
VLAPGIGEIVGGSMRMWDHEELIEAYRRKDLDPSVYYWYTEQRKYGSTPHGGFGLGVERF
LVWLLNLDSVREACLFPRYMGRCKP*
>TCRU_3 Clathrin adaptor complex small chain, putative
MGKTRLAKFYVPCDDAEREKTKREVHALINGRDARMSNYAVCGSLKLVYRRYAGLFFCFG
IEKDDNELFYMEFIHLMVEVLDMFFRDVCELDLVFNFHKVYLIIDEMILAGEVEEVSRAV
IMDRLRTLDITNT*
>TCRU_4 hypothetical protein, conserved
MLSWDRFIFPAGLLLLAHSVYLALCIREQLQEHHHSGGGGSVTSAYFPMSSYPTGVMAHM
NASTLPIFVELLVGVVVAIVGFVKQSTFKRARLIDKNCHQRYDDTIFTGVGFMHFNHRGS
VMGNHSGGAVNGDASVSTSKKKV*
>TCRU_5 hypothetical protein, conserved
MDLIFAEGTRTPSAKPFAIPSEVKSRLRARNPAEREHVGGTEEAGKRKEGEFSGAVAARG
LPGSLVKYIQRCIEYGQNSTHLEEELQAANGLTDSTRRLAALQSALSILCHIAAMDKSYC
FISSRSTAPRKQPLARTSRNRSQTTKVISDPFFSLTDIYTTVRSLKLEYEDVLKQQKSGI
GKQEHMSVNSVAASVSTIEARVDASLALLEFTVLQMLLNFDRARDISVGYVADMLRTMPQ
IFATEKRPLTVLQGDDGKNRERKRFRDGGNVVDDVANAANSIVLKALQALKSKDCLRTLS
RANSGNTVRASDGSLPVSFDGMMTNALDGTYRGRGIYGALHDMKMLLYGLYATAPSEQEE
HIALARLQFEHSLREEYDLFLRKTGLRGEVEDPLLPERTMFDVNPLFADADSTSCTDTQL
KSLKLLDLIREVDNENWFEYPVFDMANIELSSIEKWVRGSIFGMKTNREAFLALRDVLEQ
MVDNCVLSYGPTSPFSQVITLMRQRLVDAAREVGLL*
>TCRU_6 twinfilin, putative
MLTVHFRLDSTLQEAFATFREANAPFRALLVTVEDEVMRLHGKMLESSANMDNDLAKVRE
NITTEKLEAAFIIVKISEGEFALVSFCLDSLKPRVRMLYASGAGHLADVSGLNYILKEHA
MRVEEITPSLFSRENSASRTELMTEKEKLYAAIEKMEIAPMQMTMPGVTMPITEEGVNLL
KELCRGDLNAISFAVDTDKIVVDKVLEASEDLLSSFSLSEFVETVKVLLPEDHPRFVLLR

FPSNETANIIMVYVSPSASKPRERMIYASSKSSFVLQAEQHGINFLRRSEVGSVDELQEV
VADAFGMEQKEGSEE*
>TCRU_7 hypothetical protein, conserved
MYFRRVIHPRRHLLFSAAVLSCMRCVSSGSASAKPLSPVNVDSFTLNEEVVKKDMEALQR
WNELSQMIERSRAEKKNESILAAVEKGLAMLSEMGAVNAPIQCETLLLLEASQAHYNLQQ
FEAALKSAQKAKNMLLETPSAVRDAALLAEVNQLMAYVLLESGKTEEATNAFTEILRWID
VDSKAAMPMQAVAAVNMRRSVVTGIGFCYQKRAEKEAATGGDGKELYGKALDLLIEALNA
HIDENDYDLVKKTLSGVLRCFEGVNDISQAISTGEKYVSWCRRHSDEAGVAQGTAWLKEL
QEKHGKGGDTIL*
>TCRU_8 hypothetical protein, conserved
MDEEDEKCVDLRHAWRTFMVPHSNKKEGPPCSRFDGKYTLLRSYRLVGTDTDDQPLFFLS
LISPNRELISTTAHLFVQFNGQFRDCVAENENRMMAMRALHERQLADLVEAENRDTRDMV
VGSELTRNFVLKHQRELEELQRECREREISVELEVRQSLLAFLKTSAPDALTALAREAGR
EKLRADTAQLTRITDMAHFVATPVPVRAVELPNPLCHEKVGAHSRDVSLRPVVVDVSPTT
SLQACLTSLYSAERETAPAVAEHLLRLSQQTHAVLLLIGSQAEAESLLSTPAAELFLKNS
FYSGGSPHFVPLKRHCHLKMMLSTRFWGANIIFLWTPPKQEGHPSGWPLVVEDALQLAFS
WNADMFSVAVMKSSSYWQGTSYRSSIEQAQDVSMAVLRQLQRGVARLAHEAAGVKLSTTW
GMPEAPDTHTLPQPQRWEDGYVVKSPASVGKPQVKFNTHIAIRAFFPFSVSQTEEEEGLS
LRDSAPVINSFSSATVAADNSTDRGRRTGRRRRSMSTASLSSGGSFSSELAVSHKRSSRL
QQPMSFKKLLVYTFGNAVVVH*
>TCRU_9 sarcoplasmic reticulum glycoprotein, putative
MSSKQIASPQVNLTPRSADESWDKHIDAVLSELRRIYFERVRPVETKFQYDVFRPSWFAE
SIVQKRPFVTFLGPFSSGKSTFINYLLQTNYLLTGPQPLTDKFTVIMHGDEFQQIPGRVL
MADSSQPFRGLSQFGETFAEVFQGLIVPHPLLQSVSLIDSPGVLEAAGDIHSRRYDYVKV
CRWFVEKSDLVFFLFDPTKLDAGTELRMVFKHALRGHESKIRIVLNKADSVGPQELLRVY
GALFWNLSGLISTTEPPRVYISSFWDQPYQKDTDHCLFTDEKSDLLYDLTELVPLQSLDQ
RVSSVMLRAKHVLIFALVCASFKSRMPWLFGKEKARAEFFAQLPQISEDLANTFRLGLTD
FPTREEMSDFLSRVQTDDFYGMDHLRKKGWPQLLKRTIEEDLPALLNPIKHTEVVDPRDR
KHAIMMQRNYIKQMSNQLAGQRGIQGGLGQQQAPGHRVQTMPNAASLNTGLNFPTQQTQQ
TFLSQMPADQMSMMMQMMQNMMLQSQQQQPQLLQLEQAPTQQLTPDQMSMMMQMMQNMAS
NNSS*
>TCRU_10 RNA helicase Prp43
MARLEGVNNANTVSVESEINPLTNKPFSKQYYEIRALRATLPVYEKAELLKRYVRDHQVV
LLVGETGSGKTTQVPQFIAEMGYAGIIACTQPRRIAATSVAARVATEMDVKLGEEVGYHV
RFQSMMGEKTRVLYMTDGILLREAFSDHNLSRFSVVIVDEAHERTIDTDVLLGTLRLLME
RRSEFRLIVMSATLEMQKFQAYFSQAPLLQVTGRKYEVQVKYTTQPVKDYVETSVQRVYD
IHMNEPPGDVLCFLTGEAEIEKAVTWTKMKLDALLVRDSEATHDSRQGPMWVQVLPLYGS
LSMEEQKRVFASPGPHTRKVIFATNIAETSLTIDGIVYVVDCGYHKQSLYNSEVRVDYLL
PALISKASAEQRKGRAGRTRPGKCFRLFSPQDFATFPDQTHPEVLRSSLVNTVLLLLKLE
VENPYQFSFIDPPSQQSIMDAYYQLSFFGAVDEDLHLTEFGRLMAEFPVDACLARMLIRS
AEHRCGADAAVIAAMLEAGNVYVRPSGRGNEADQQHTTFQHPDGDHLTLFNVFHAFWRNN
QSPQYCFDHFLRYHALLQATRVYAQLTKLMGKKSIPVVSTYDDKTRLFDSVALRKTVLEG
FFTQVAYKPPSAEHYKTVKDSQWVVLHNQSVLSKKKRPPWIVYDRLEVHGKEGTFIRFAS
VVEPEWLLVVSDFFTDPAELSDGEICHILQRLKNNDELNLSSAHP*
>TCRU_11 Kelch motif/Galactose oxidase, central domain containing
protein, putative
MELQQNGDGKIELEVVRKDGRPIVCRPIDVNELLSKQGHTIDLGDGVRVRLEEYSSDTFS
SSEEGTEETDSEASASDSRTSDRTNVPPGRRRLTGDGAAFDLHGGEEKAKTQKLSFHDPE
RNKGMATQHGTISGSNVSEKVLHSRRDIWASFAPPIDPERNHNWLQSTSIIPGATSRRFR
LPPLMLHATSSYLGPSDQGQRILVYGGITNFGKKVEKELYEFSVLTGHWRRVEGKHFFFP
GNYGHAAVVVERLQRLVVIGGMSPGGQPVQGERYSDEFSKLRSRILFPCQDKTKTKRPPS
VRMEFKESEKPTLWSLAMRAEEEPPIGFMPVLFEMNLKTLRWRVVQTSPEIPVALHTAVA
TSNTIYLFGGVTNRLLVSAQLIGIHAENNSISLIRSSAVSPKARYLHSAAIYGNWMIVYG
GFDAYNEPLADVWAFDLVNERWEQLECHGTPARGAHASCILGSSLIVIGGFEGAITTETK

PTSSIYELQLVPTSTGQYLWKKITVRPAIPPLAFSAACHCADDVSFIVYGGCTVTGIKAK
KRPPDSKRVGQLAFTKSRDARNISRHDSDGNVYNDNFWQGLVPLDDGFAFTFPLKKNDAT
GSHGDGSGASIHVNELGVVTDPEELTPEFKAFVRRQEEFILKKNASRSQAMKRTILDELE
NMEPNLYLTSEEIELLLEKSNLLCESLTGYNMEAMPHNIPEREQRLQHTEKCISLSRQIR
DVLMSMKGYAPGVTAVKSKTHRIKSGEKFEDHSVAKPFRRVIVMGLVREIKTELKRIHNL
NIVLKTVEWPEKKEYLDAVETMQERKTEFVQAVKDILEKYIERRVESLISAADRQKDNMR
RLAEIVAKIRHEKIFQTEGPDPQRERVRQMWSKGEGQETPQTDTKRSVSRSHHHHRRSRS
TGAGYYKDEAKAFISLQPKELQKLLKKIHLVHKVATSFSSYCQSKKSDVQKSSSEMPPPP
SPSTAPPALSNPESSSLAVPAALAIVETVPPSNVSPATHTADADFGTASPSELVIRQSDA
IREEAIEIATSVGQSVCAFAKELETSFEADTKPNSQTDVNKDEKKPTLLFLSSLRPLLSC
KMQLAQLREKISRIRVNRWAVDDVAGAPQDVEAQKRCEKLSKCLAALVQRLTASFLSKAG
ARPPRLTFRRAHSSGALKPPSSSLASPPRSSPSLFSSSSSPATDKHRRVLQAISTVDSSD
VAALEKGDDSSPQAQEETAEQEPEKQSTCVFGPLSTPLMLLDTPPLLKAAAMPEIPRTIC
LTSNEAQSLVPPFCTTSSICNEGAIIPSVRDTKVISNTHQEASTWSNKDSSIMVPHKEFF
TAVTCKDSSQSPPPRIFVSKGPQTTTAAAAMAIPAELPPFGESLSAIHIRSNTDGDKNTS
SCMVSLSPGCFHGSSTSGVAVDPINRVDPQQEALCLEEDYFLFGRRYAAEPVASPCVVED
ARNRQVLVAKDSPLVVRSMHAVKVSPPVGTPAAPTVTAPRKRVVNSIFRKHFTSASQPGA
PEDVSAKPLKKGLFSGKLTPGEMHIIQARERLRTSSSRR*
>TCRU_12 Glycosyl hydrolase family 65 central catalytic domain/
Haloacid dehalogenase-like hydrolase, putative
MPFWRRSPLAREYEVTKRPIFLLDGWNIVQGTDAAAYVSGSVTDGVMYGTNGYLGVRHRS
ECETVGFESNVFVNGVYHNVPVDRQIDSEALPYEMQMGATVCTVNLDCLIDGDCGTLRSV
PPRRLDLRNATYHSECRDVMSGDGGLMFDGDYRRVVSMKELDLWGADIVYSNFTFGSSPY
DLYLGESPNIFYANNMNSTNPDASPSYLLEFVVTITVDLREWAILRGDSVDDILLQSRTS
GVVESIVTQSTCAVDYENSSVKITPEHQLLCETGDHGLMEQNFSAAALSCPSDSESDPGF
GGRIISSFENQKKKTLSFKKRFILSITPDTLPTRVTVTYLARHHSGGIPSARLFPTISEI
MEDQRLILNEFWDHFFIDLQQQEELTPDRLRLSLLFNAFRLFCVSHNLHNGLPRGGCSAT
KTSLLYDLHQYLYHGIFYTLTSPPRALALLRGLYSLLPQARVNAHLISLKHGAIFPRSTI
KGTECEQHNTVSQARLHVNAEIGYIINFFFAAVETVDQKDRLWLLELMLETARVWPQLGE
WVESEGVFRLDNIAGPDEYNSTASGNFYIHLSAKMHMRYVLDLYEQQLALLGEEAMTNLL
KQIDMDKSELENFRATSDGIVIRRNDHLGVYLVHDYFHTLKEWKGERPKHPLSMNYHPLA
IFSHMLVDIPEVLLGMLLYQEEFEKKDLVRNLAHYEALCTYDSPESLAIVAAVDFQSNGS
FAHGLPLLRSLMSLDVDNVIYTADEGLHFGVMSSSWIAIVSGIGRLKLGKRTLYLDPCFP
AGLSIVKFTICWRGSTLSTTVDKDYVTYELIAGDSIRFVHGDGHRIHLHTGFHRYTAKRQ
VSVPRLIRSGEGEFDGAVFLCETLFDEITDIHYMAWYKTLESLFENYRALHLREIQPLTT
EEFFEKVIYQAEEREIAFSGIHNVLLDRGIDLELGTPDDAEIVETRYGLANAKVAEMAEI
LSRMTPRVNAGMHALLKDLSNSGIALAVVTYSRSLKTLMHYNPEVMPLFLAHIDGEEAYD
RHIKSRPHVDIFLRAAEKIHVNPARCVVFSMYLDRGFKASSLANFRMFFDVEGIFATKRM
SQQTQPYPTLSNDAAAAVGRDGVPLILRLSRENLPTTIDALEDMLYGRCNAVDEQHVASY
TK*
>TCRU_13 hypothetical protein, conserved
MSVTDTLGPLFTFLIIINVIGTALPLLRHRFVLYPLAFVLFGFAGLFLILAVIFLLGDAT
VSVYNVNAKGQVKVQANVPFDLPAFFRLNLTMTTWMLSSVLAMVTWLCYQSRKGWHVYIV
PMLQDLNTLETSCWSNTLDLRNRVAPNTM*
>TCRU_14 Endonuclease/Exonuclease/phosphatase family, putative
MARQPNTVIVLHPVNSAIITLDICLQLDDSLSSIWRKNMARSEDEVAMRTIERLQILLVQ
QKEGKNSRRMKREDLLKDSQPIHVFGLEIDEHEAEGQATAPTSNTLKPLDTSITNKLFWK
RAKEMLIGSTVVNIKYNVPTITSIVPPSALYVGLPALCCGITTLFTSEVGILYEWCLCST
DSREHTNISVISTDAVFTPLEEHLGKTLVLRVSPEGDSGLWTQVDLPPVRAALTPVDRWK
HTLAPAEAPAFRVVTYNVLHDEFCSTSAAKRRIYPFATDDILSLEYRQVRILQELLAYRA
DVICLQECGEKVYRQFFERILHHSGYDGRYTNKNGGVKEGCACFWKRTRFCMNETLVFPL
NWTTLQEDHPDLVARVSLYPEFREALEKVTSIGALVLLKDLQTKEELIVGNTHLFYHANA
CHIRLLQVYMLLYKLKIFAVSQPSVVLCGDFNFTPTTGGYRLVTRGQTEAEHHSWKKGEL
FYWGCDRMLGVGTEEMEGVEEAAEEGASSSVPVTQPDKRQPPFGAFRETLSAPLQLRDAY

SETGQELPWTNYAMTFREVIDYIFFSPTRLSVLRTVPIPPESELSENVALPNKQYPSDHL
ALIADLVYTSSSSSSSSSC*
>TCRU_15 SET domain containing protein, putative
MLSITRRRADFGKELYGKLSTLPGDFYEACRSHFGITLHQDTFIGVRSSQVRGLFLSTSS
TPLEANKPIATIPLTSLYTVSNIQSKPNTLRHVTLDGVRNAVREEEFKMMSPQFYLGLQF
SAIISSIPDITHARDAEEVERITQILRGGAMPWARLIDDEDFNEQFIFGMYGMALDMWQR
KSYEEMTKLFHHNITAIHEKFQPPFSVDTFRRIARLVLARVEHMPPPDYYDGSAVWRRVR
HYMRQWIKKPDPSEVCMVPLLDLVNHSNRPNCGLRVGPSSVVGGKGAITLYSIARINPGQ
EICRHYNFAINRPNALFRYGFLPFDLISIVEHDAIDEYLVKNQHMLREESEEVRMKQQKE
REEIQKLEKIFQHARSGR*
>TCRU_16 hypothetical protein, conserved
MQLLDVQPYETALQRLLRAGVCSEDQLHDYHLSQAFRSLAYAVNRASLSVAALLPSHGPP
ISNEAPLSPPSSGLTSSSTTNADATGSAVVLCRMCTCALASQASLRTLIYVSTRLLCDEA
SAFGEGNERPCCTTAWVEALCSPGVRRSFLHKQMGVHRRLTLGYLLLLSGTVRAVTHGCA
KGKRLHSHFVQFAQQLLADVVPYVALIADTREATTLADAAFVDGDDASLRDGTKKELLVP
SLMTVEANNTLLHLFHGIALDVLEVHQHDEKQTTTSRRAVLDRDAPSRIWSVVSILQRAL
LRALEWVQSEIIWEMSSINSADPSTKTQAVNETFAVVRIALEDGFAQLIKKQETLECSRR
AVEKQFGQNSKDYHAISGMMWTNTLRLFFFCRSLSNAWTYIYGGLGEMGVQHTDEQILAL
IASFVSSVPSFEGEEKEHDVFLATTMLLSGALAAVAAAPAPSMQAALWFSELNLTQQIHN
TIVQRGLRYRDENVQKLSALLSRLILYSSSNNSAFRIIADSPDQLLELLSNGRDGASQCV
IGVMIRAAVERPHFILPSLFRLLQHGDTNTRRNVLDVLSALPKASDDSAYGGAIAPERMR
PVLRLLSEELLLRIQDEELQIRLQSSKLFAKVWPEDVCRSLLKLATQRDRSVKRKSSAQQ
ALRLVVEAHTSDGSVVLLLIKESLTLLGENVTSICATPSTPADILAFATLHCGTLQDTVE
SQQVTNSSTEEEGNINERIMRLVALLGRHWAEGVINWTKACILPLLQRAMEARAPLEQEL
LVRVMSQIAYVCGATNEGLVALSLSCLHIMKPTEEGTSNSTVWLENLTGPSTALSSDASI
YQIIAPLLFLRGCPRRIFATFVTVTQMPPPVAEIWEFLWSVLLNPNYREELSLDAQRLIL
ELVCKYNASVMMEQLRHLGSRYMKEGFFSLVDGSIAFFICRVGFFCIGFLLSQNQALFCP
KDMKSNLGLNEHEAEEREMVGMVATAEKEREEEMEFTELVSGAQMVGRWAEDVVLPWLLS
EDDAGICDVPFPVDFQRLSRSAVECLAIVMIAALNRQAFSDTVTPFVMLPLTQLAQHCRE
RVNFWKENCSATDALVEWSPSPHLLGRFEFAIHIHQRALNLLRAHPSGGTTIGLYFKHYM
PPLIELANAICTAVLRLGKKDIAQVAVESCHALFLAVMASTGASPGLSGGETPKGRAEAS
KSVLMFLDVTDRNALVTFAVGSARYSDLPQVQSEGVKLLSALLGAAPEIFVTEANMDEAP
LGEALTVLGSVALMHPDAKTRVIAEQVLGILQAN*
>TCRU_17 hypothetical protein, conserved
MGEAFELLRFAALSSAVHADAVECLVDDTRSVLSRIAMDTERLEALEEQLAGLLEEQRRI
HAVRDVLSRSRSTRNTTEPTKRGKHPTEIRSKLDTRSPGASPPGTSRLGTENVLRFASRA
VPEEDVPTMSRAPRREHVATVEILTDDLREEKATEGEKCIDEMVERVKSEIRSLESMSVK
TKLRELEALKRRIKGLDANAIIERYVEPFRFGDEVERLWDAPDAILDNTNMDLFISRACQ
RFSGRYEDALGAISDFSSYEDGDAAQVFGSLMYLEALTSSSNYDAAAVRTLQGLSKESLL
EYYREKRRAATVSTTVRRSRVETVLGPEEFGFLPEDWWSSRALFIPAGIQLPPARHILTA
RFSFADAHELNTLQSVRVDFQRSVVDAFIRMPKALAELREQIEFQSKHDEERDVSASLLR
LLVENEKGGGGDIWTTIARCS*
>TCRU_18 eukaryotic translation initiation factor 2-alpha kinase, putative
MPDASIRIGLLILCILTLGLSFGVGSTTLLSVSGDQAHAQDANLLKNVETESAGDEISAS
RPDNKELVPSYRLHPSNRLLLLHKDGKISSYGLDNGVPMWTVDTGGDMLRVEIEKHPTER
VIRQDPLALPFLLEGGMLFTRRCVAPFGCKKQMPERCFDRKGIEVETRPEARPGEAKTRS
GSGDSCEIPFSSTHPRCFMNLSTLIEKKHVQVGETDIFVTTSAHIMDVDSNDGKPVPETN
SLFSYLHVVRYDFTVHVRRPGEYSWHMSIAQYKLSEKSPLQSSEENLSDHDPLFVSRVLQ
SLLQKGDCGDNEYVPSTNEENTVDKVNIEPVVEEGSHNDIRNKQLMIREVDRNTYVLWSK
LKHAPVWSSVVNPLSTVMSAFVWFSDRGKVHSLPVYRLETPKSIADTVEILEPENTDSLY
LPSSLNSDQHRSKMSFNLHGFPNTWEFDIVADELELRELQNLYQQCSWIHGCDGSSGNIP
NHSPNQRNPGMSSQMSLVSRFPLSHTDTGNTLLLLFNVSCYVVSFLSAFLAVLFRWYLWN
TTGVGPDAFVDRISNSSRPGSIKMNPLDPKISASQSVKSIDSAYKELKASHATEGGRSFD

SITPLAEAEMLPPSTVNVVGTKSMHHVDSWWRYSGDDEFSISDKPSSECRIQPNSTVSSQ
LFQQQFQKPEKIGSGAEGSVFRVKHQFTGVSYAVKAIRIPDDNEIYIQEAVLHSTFDSVN
VVRFFNAWIERVPRNFAETLGILHRDDTMDNISAETLESFHETPFTESASSDACYTVLFI
QTEWFERGTLADHFVRRKGFTRLENLKHLLQISEGLQYLHSQCVVHCDLKPRNIFMSDSG
IMKIGDFGLSRKNRKRPHKLRGDADGFTSNSEAGDEGHAIAAFTPLYCSPEQKRGDAATT
ASDIYSLGLIALEFYCVFTTQHERFCTLGEARQGVFPKEFADTYPVERALFQKMLSEDES
CRPLMKDIVKALRQGIKEEEEVMDGLIMRSKTLSPIDEYESSNPASPLEKFKEKGKLTRV
APKFTRLSLSSLESTEFTQNT*
>TCRU_19 hypothetical protein
MHSGGVQKAAAGAPQLPPTAAFWEEMEMQKKESQELQAKIEAFCSLFCPEQMHLAPFLSV
EFCGREEELEGILSAMYGHSLSKMPRAKGDEEKEKGAHSTGGAVTDSDNDFMAQAVALSS
FFGLGRHFVPAVYAQTKRTRNRRRMSWGAWLPKDEEELGAVEGVGKEEERHIKQTVLFEV
IAALFPDFLCTVLEEGDQRTAFVAKRLAAFLSFHEPESDVKKYLVSHGGRTYLGRSFRNV
FMKHYFSFLKECSGTNLSLDDLDEVGSLSSSSVVTIESAGGGEDTTSRRRKTKAVLREWT
TAYGLRAHSTPMPSRSCPELHNVAVDTEELSAMERMRAIKLRLSRTEMGTMTQSQPPAFG
FDSTKPATRRFYGTGTPFWGGAHNEIHAAAARWKQKWLQNPEEHILPNPSIVLETNSCQK
CLFLEAQLAETKAAFQRASRKFVANEEQQYYNEASCYVKQKEILYPFDLSEANGSSSKKI
MPQHFVQPSHGCLMCQDLRQRIKCLEQRLRESYDNCRELIVKLRRSQLPLPPHMCVISSS
VNEAKKRDVSTMTELTGQQLDECIGYMILESL*
>TCRU_20 multidrug resistance-associated protein, putative
MSRKEQESVTTTVYAVRLVHAVVLWLAVVFFGISVVFLKRRLPRATPISFYFCCLLGIGG
VFVSALYQLAGPRSARGGGGGIFWVTWAGLVCWLLLLMRSVRHANLPDVLFVFLLLALVG
MECTGIVLQFISTRSRIADILMDAFIAVPHMLVFVTLVGWDWLMVNDIALVFRENTPIEG
GRYEGNNKDDDDDDDGGLGHVHDKNPHAFFLLPPSQDIFIQSSAASSLFGESLRFDGHTS
IIRTIVRHWGPTYFLLALVRLLYDFGGLLPAYFLRQLVDNLMQAKTSGKKGKDGGADIHM
SIISVLLIVIITLTCTFLRVHYNMKLQKMSLYNRNLLTIELFHSAVRCRRHQLGNQREGE
IMNYLSVDVQRVADAVQTINDLWALPLQLAFALYLLYVQVSFAFVAGVVVTIILIPVNMQ
LAKRIKHVQTSLMRENDERVLTITEIMNNILCVKMCGLSHIVQRWVEIPRSRYMKHLCWL
KFLDAFCVFFWAVTPTLVSLLTFITFIWMGGKLTPGKAVTALALFGSLILPLNAYPWVIN
GFVEAYVSWQRLKPFFSSSKDQGCFFDGTTSVIPGADDEVVLCDVRENIINTNLLEEEQK
SLHMPGENQPLLQATNQLMCGVHPVEQHQLNSPKQRQEISSDVLVDIQQGDLILAASSGD
DVLEQLFTLRISRFQALRGQLIAVVGHSGSGKSAFLSSLAGELIMTPTFSLTVARSSMAF
VEQAPFLMTGTIRENILFGLAFDSARYESVIRAVALDEDLRHNFAPDLDRTFVGDRGRKL
SGGQKVRVALARALYANKDLYLVDDFMGCLDTTVAHHIVQEVFVTAAQQGKCVIVVTHNE
ELIHYADAVYECAGGWLAITERSKATSASSPTWMPREMDHKGQTEEGIGKKTEIDSIEDA
KPSFRALEVSEHGVIAWSTMNCYLRRVGWGLTVFIVISVAAMQVARNASDQYVVVWSKDG
DGDTAAFIHVLSALAVINSLLAFIRGFSFAIGGLRAAHRIHNELLHHVMSATFHFFSNTP
PGRIINRLSSDIYTIDDSLPFIINILLAQTFLLMGSMMIIILNSTGIILLTLIPLSLLYY
RVQLPYRIVSRELRRLEAAARAPVLDTMREVLLGGVVIRTFGVSVARFYMHRVNEQVGVL
LRTQYNALMLNSWFALRLELVGILLLILVGVLAIYYHGNSHAPMLGLALAYVQPLTSYVN
GVIGAFSSTERDLISVERVLQYFYLEREDVMDRDVPLLFFDSWPTRGKIDFVGVSMQYDD
SGPKVLQRLTFHVEAGEKLAILGRTGAGKSSIFLALLRLVKLTEGYIAIDDIDICQLPLD
VIRTRLNVIPQNPVIFHGTLRKNVDPLGLHSDDEIRAALACVNLADLSLDSNIVDGGNVC
GGKQHQIAVARVLLKRSSLLLLDEPTSQLNSEAESLLWHVLGTHLKETTLLCITHKLSHI
DFFDRVIVIDKGRVVNSGSPSILRRDGAWPFA*
>TCRU_21 NAD dependent deacetylase, putative
MKPRRQMVTILTGAGISAESGLSTFRDKNGLWENHRVEEVACQYAFFRNPLLVQRFYNER
RRALFSDCVAPNPAHLALAKLQREYRGGRVVLVTQNVDNLHERAGSVSVLHMHGELLKVR
CTATEEVFDWTQDVVHGTSRCKCCNAVDTLRPHIVWFGEMPLHMDEINAAMDETDLFVAV
GTSGNVYPAAGFVTRAREKGARTLELNLDSGTNFSEFDESIYGKASVIVPAWVDRLLQDA
V*
>TCRU_22 ubiquitin, putative
MLVKVKTVSNKVIEVASLNEENTIAELKEKLEESEGIPGKMIRLVYQGKQLEDGKRIKEY
PIAAGATLHMVVALRAGT*

>TCRU_23 hypothetical protein, conserved
MSFWPFRTGNDDRFQVSSKEETIYDAIKGEMPPHRYETEVSNYLEWRWRRGLIQSVFPVT
CYSAVLGLSLGFRQARLEGRYIGRYRVLWRYSSTFAAVGLLTTAFHHLLVVRNKYNDRMH
YPMIAGASGAVVLTMASQMGTISQGMLAGSFIGVLYTAGCYGMTYYHKRRLKIFLSQQQL
QQVPIHRVSPELQPMYRAYLYDNRPLEEEDFLKRQAVVLSLGEEDVGLDAKRIVSNMVPE
IVDWVNFPDWWPLKFPTQTEEERMILERKRHEEVERRKRLILESEDGALLKRVNRAKNYR
DA*
>TCRU_24 cardiolipin synthetase, putative
MPTSGCKFRVALQRLNIERLLPPPLREKRGSNTVGRINNNSGGVELRESVNKDFKDVCSA
VGNGARGVYCNGLSFHVRWDRIQRNLAVLGRVSNGNTVVPYRDSAEAFRVMWKAVDEAKR
SVLWQTYICKDDLIGQMTVEKIAAAQRRGCQSELLYDCGGNITGRRRLIDKLKQSGANVI
EHRPVLHHVLPYLFGGMKWERSPAIRNHRKILIVDDKIGFCGGLNIGNEYCGRSQGGTGR
FRDTHCSVVGPAVAHLREAYEDTKAPKPWQWSWTRWRKIASTTMARRYKQGRNATDDLLG
PMTKSVQQRGKLYLQQQMERAEEKRVRFMERIRWKRQRERLELFMRWYPKKAAKLLPQNL
VHVDVEDGTKFPTERAVDTGASTVMKQRMEHYRMRALNRAKAALERRLAERPLSKAPLSD
ADPVPGAEEYGKIRSNATQIICCNPHTRDWSIPYAFWQVSQKAHRRLWVTTPYYLPHRKL
LRAILYAARRGVDVRILAGSNCTTDPWFMWHASNYITERLLAAGVRIYEYKGDQIMHAKT
VVVDSIWCSVGSYNWDMMSNKNMEVCLCHLGYEMAREMEGHFLKDLQTSIEVKYEEYQRR
SFWLRFTSWFFYVGLQIAEKLTFRTFWDADLSSKVDDLD*
>TCRU_25 hypothetical protein, conserved
MQEQDLLISIRDVFVGRLGLQIKQNAAFCSNNARTLRLISSANHIDVNVTVDRTEAVEAS
AVLQELLNDSKSAHPVIIFMKVILKQFNVHSSQLTPYVLTLMVVAFSRFCSYMSPLFSFN
YYPHTRETVEPGYLLFSFLSFFSPLPRGQFDPTQMCLVPIHPHGVVYETNEGDHLSQLGK
NVGGIYWRVMEPTRRGDNAAASCVLIDKCRDLFERILVVLLHHYTGVVFTCPVFVDDAHA
QILGAEEVPKTEKIPIDNHLISLLLRDWWLKKQSEFF*
>TCRU_26 hypothetical protein, conserved
MWKIRVWSAFSHRTLTLALQRLDVVSAASAHCFYPAWHVARRECTTGSEGHPLQSLKDAD
APPQTTTTTTKISTTASTKSNDIDWDDNTVVEEIRSILTLELLPRKGSCDEGGDNTVPLY
ALFRALGPTLRSQLQNSSFGALSKAVKSRPDWFIISADGARVGLTDAAYSCRATNHDAIE
SNKKGIDGLRQDKSCRASTAASGNVMQTPCLEKRAITRSKSYVLVRGCFGSTPLDVLKPP
LTSAEIEEWKLTRILLPVTLYFLMDKEPITLFPYGEKPRRLSPDLEEAESLYVSKGLFPP
SEVAAAFVHITPTFFVETRHVLAAMSPDVAQCFESHISKDRVVDLFFKKYPMIFKIKTGK
FQKTAVKLNLDFSFIQNYPGCGRADRLLRRHNQEYRATVGGVVSRQITSPSREQEKQGRS
GESHVDVKIFEILLRNLPRFPSDKSLSGAELEERRCAPIPLVKWIDGFPQEDLDVLNSVP
QRRVLTLLTRYSHIFQLVCRGEDSNLFAEHMYLNSSKNSNTPRRAQQDDGSKNSFVRPLD
STSVCELNEIPHADESTVEEEKADKLEADTPLPPETEMKRREANIAAALRDDLIGVDDIL
SSDAESVPTLTDEGEDTELGDKLNTDEDEVYSAEGEEGGEFFDANEVKEEEEDVDGGESQ
RNLEERGGDGVKKDPPLTDMSYADDESDGPYIPSQYDIIYVRRLPRRIAPRSLSDYNAAN
SPEPELLQHIASFLNPPPSLREAKQQIMQSNRKARKVPLFTSGSAVGPWRWVPIQRIYAS
LSKEQKRLLRPFKGLVHFMRLHGEIFEISMDFLHVIAHDPEGQIAPFVPTQLVFHSEDRV
LLPQKFDDDEKSKASLIADLERNKFKSILGASQIPTDRPQLLLLDPLNPVLNHEILCEEV
SLFMPDHPVPLHQLINRLPPILKAALSLRHKNNFKTSKHLKVWNEGNRTMLQKSQLAVPE
SALMGEETISVEDAIESVREVIPDEGVMIGHLHRMLPYAAKKTLNTHFGNVYNAILGYPQ
YFYIDKVEENRSNSTVFLVERLQEEIQC*
>TCRU_27 hypothetical protein
MDEVLDEEVGVPYLTPGQVPLQAAAVLPFLTPPAGAPTFPRLYAASLGEEYIDTAECVEY
ASSNDAGFMVKSCFVLVGYGGVLCGCLADSLEPNEPTAQRSFTELLEAKINETRNTDYSL
DTITFIPFFPDDTLDPALGSLLGIFSVVEDPTWCLFVSHAKREENGSDCILHVKILRIPI
VEEADRLHRALNSLVLHHCGGPNGNSICRSLMSVEELFATARKYSDCVVAGPAWDRLFSL
RLTNEEIFCIAKKMILSQPTFLMDVNGTKLEEIPPLAVAVRIEAFTNVPKSEGESGGVEK
AVALEEKGTAAQQREVLRELASVRAQYRAVLREGNDLMACIDEEEHRWNKIEMHREEEQR
KRKEHPAAPPSEHDEHIRKNVCALETLQQKREKEEGEEESAQATARAFVAEKKRKKTGKG
SRGGGGSDKKFASTSNFTSKEAEIRNVRAHNTALRRLLEKLAHELKEEEQTMENLSIDLR
GFMSDINKLEKAKLLLTVEHSMLMNTTARLQQSLRDQKEKLRQEQEAAAAEQREISRRLL

VQKERTKKSLHVKNGTTELLHRLKTNLSK*
>TCRU_28 hypothetical protein, conserved
MKRDLNPNAGEFHPTGGRLTPKPSLNEGGSRSSSLQGGSAPAAASSSQQNNANPNDRTPF
QVSEGLVEACYFVPATRFLMDCRAAFYEHPETTKCKHMEFERLLRRCFFGAHEANELSIS
LASASGQNRPFWVSYSAAYFRMAHDVVQEVELGTPCPSTQLLPPAAAGASLAMPMIPPNL
TSFTNNSTEEERQRESLREVYLSRLRPVVPYSIRKQLAFRAKRPGVDLQEDVTRAMTYAL
DIFFFFTRLQFLRFLDASSGLSYSACVQFLTRLRERLMKLEVADSFLSVALVLMLVSTAH
ITFAPRAVEVALNETNSSKLKAQWLFCRYFSALVVAFLSGSSLQSVEELRHSFVSTKQDD
SLPVLRACPGALAAIREVISYNNKTAMLWSITLSEVVKYALRHLGQTDRTKRPNRAVPFF
LSESTTLDDHLHVKFPTVLAALLGSTNTVAEEKESQHVTQQKGGVSSRSKEFHALATKAA
STSGGSEYETVYFSLLALTNMGCFSPTGLSWLFKALEDSYNSDSHPSALDAFLSSTVCAT
VSPTARELLDVLRTLMRVGHKPLQLQALIEFKGILERQQNALPSDGTPTKQPTKP*
>TCRU_29 Protein tyrosine kinase/Protein kinase domain containing
protein, putative
MPPKLSPLPRKPTVQPSFLSADDDIWLGNIHVGPGGVEFTGEGDLHVPCQDLSLDSLDCV
KCLGKGTQGKVSKCINQKDGAVYAVKRLLIPRTTDRMNKSTVAGELRNIFSQGTNAYTVE
LYNAFYRDGTLSLVMEYMDWGNLEELIAICPTIPEPACAYIASQILHALQILHTKANHPT
ETDQKGRRQIHRDIKPANVMLSKNGVVKLTDFGIAASTETIGVNSFVGTATYMSPERIQG
RTYSTPSDIWSVGVLTAQLLLGHFPFSAAEGGFMALLRQVTECCSLSLVDQCACSQKAEN
FINHCICRNPDDRSTATELLQHEWIVQNASNGKDVLTELLGTVGEPVASAEYGNS*
>TCRU_30 hypothetical protein, conserved
MHQKKRFFETFALEVEDKDVNAITSQLEKKGGCGTLSPDSGKHKKLNTTSSFTGGTHVSS
PFMQQNDSNVIEPLRMLHNCIRHFASHPETYGSNLHALVDREICHVMRVKASEAALLTPG
MVPVASYPLPAINNTKARNNKYQHPAMNKCASLMFCPRSIEDAVSAGTVAGVDGMFGFGA
TTFVEGTPGFFSLLDKASRLRTLHEEPNALEIADTAGDVSALASSATDLVTLGKDSSLQD
GTPQQESTRVRFVAFSDGFSGNTPSSSALRTGAGPKLLVDGTSYEVSFLRSQLQQVEAAY
NAKCISHHELQQENAQLKSELSKTEKKLQQYTTKNQEMRVQLESLKRELDAWKQRSSEFN
LAGHAGNSHTSSEGSRRVQAMQLGHAKRELSHMSRLWRETEKSLQETKRTLESAEKETQL
SHRYLDDAFFLIERLERRVLRRDHYIEIQQRRQSSLEEKYEKLMWCFEELRTMNGGSSYV
DFLLSQDNGWSLFLFVRLQRRSMGYAQMEEPFPANPGPLFFRRTPFGGRFCDMYSPNLVL
KLVTDYTQRKLGNTEGMTEMAWGVSIPRWRGNYIIDYTPPSVGGNGEGINTENVMTSWEG
LYRSFPVLSLASVLLPQPSTALTGNVPIEEDIPNSAQYDQATIRLIIYCFWSERLLQYKK
EMERRVRVFKSSRREPNSGQLQGEAKGEGDVTDRPIYPSTFLAALVDFVQRTFPLNTKVA
EENAEEETKRLVVRGVVGKNEKAVDSVRMLFSTIFYIMKDGKEVPVVLSSQARELLFSLY
YYAEEYKEVDADFRLFYLVAHQQVPELVAINFWASLEALRKDCEELLCHHIGPSSSFRSS
LSKMHDSDTAFCKKTPQEELIHDTPFNALKRAVEVIDTAPLVEQSTSIEPDSDGEGYGLI
LPGSNVSSSEKTSSHDRAAEPARSDFYTLKHNIHEYLFRFKEESAVSSAVPEKPEKGDTP
FKDVAKDKSAEKKEIPTAWRTLDERIGAVLGPHASFLEAFKANQGPDISKKQRIKRQSFN
KETTSFSASRGLLPLDEVLELMYKHCFATYAVSCCGAARFSLVETLTRTGDSSTVDGILN
SLEHLTKVGWLPPTETQMRRLRFAISMDQPSTLVRFTDLFDVDSRYGLPSHFHDEYLQLT
LDAYMEHQEAWMNTILNFVIPVDDGYGVRNSDEIDMLVPFPIIRRAVLNVFHQLLQKPEQ
GNTLAKHFLLYCNLLREDENVRLGQFTDAPFFINALPLSPAEAESKFAKIEKRRWPVEEE
SASCSLLHLSLAIRMTHIIWGSSSTPSARLAGLVLSSTASEQARGVELPGGHGTPSKGMR
DGAFLNNVKEEFSDALLRVKTGVMQHNVLRHLAAEFTGAMREMEETPSPLDLTVDSKSAL
EASFHIRRLYAPWDDDQRRALPSRGSVPRGGRRSYTPRRMTSAFSGLNLQPETTVDRHYT
PEVASLTRFLRLSRIGKSRGDKKRKSKSPRGFQETETIFLAPCASYETAYMSHQARLVRR
LVEAASTPQPLPAVSAEETSAGPQLRTDSETAIASSCFAPAADRFNSIDSNIVEAAVAGA
ANISSMSTTDDSNIALPDVILDENGSTQKGKETIGGRNAVYQRHVSVRQLHAGCATLSLM
*
>TCRU_31 FtsX-like permease family, putative
MAQTMDRGAVSDPNSILNVELEAKSESWMAFMRRLCAERKRIFPMTAVFMKNALMNAKAH
KVSYCISFFSVFLVVFLCVILMSTIFNLPIVFLRLGEVHNGKNDLAITTGGELHSASSLN
YSIVEEIFPLTDPLRGYHSPRIRFGGYILKYSTCSGITKPQDLWYDKKKELCLPACLSEY
CDGTETPTVIFAINEERETRMGFGISWKGRKLKKGEVILSIGVAVAANNTRVGDKVLLLA

SLGNPLHEFFKSYPSLIRNTRTIVPLKVVEIVVPDRSKFDSDDFVVLDYDTFVSMVSEGL
FPKHDQEDVKKFGESNPKSCATSIHFNLGPSERTNTYKTTDYATVRLRISSWVSSIAEPL
GFNQITVNTPILNFLYTVRFFSLFVELIVSIILLSLAFLSIMLIYSLLNLSIENQVYELG
VRRMIGFSRGTLVFMLFVNAYAFTIPAWILGLIAGQVVFLGLRSVLRDIIGVNLPYIVPG
QAFGWATLLGLLLPLFGALLPVINLLRQNLPEALNASRGRNVGVIYKIERGGYSRSVNYM
VFGIGTAFAVFGFLLHYFFPIGLMHMRLGLLFYIFFGILIGMLAGMVLLSLNFERTLQTV
SSYIFFFWESAAVFRAFQNCLVAHRKRNRKTTLMYAFSLGFIIFITIAFQVQLRSFQYGI
RRSMGAEVVVDFEGLDLFTFSRMSHFIKAALPQVSAVTYLSHTVTADFNIQNVSLYSPGR
YQGVFINSLVAISPNYLDALNKDFLLVKKYNKESRKYSISGAVYTEKRNQIIVSSSVFST
LQSSSLEDPEMLVTAIMTDAKERSVENVRHAVKPSAVLDAAPQVSMTKFREMDGVVLTSY
PSLTRFSGVEYLSVRSIKISTVSLRVPDSRYVNYVSRVIEKYLRRRRITKTSVRDDGRTA
QYLGIADRTLGFFFIFVQVVTLAICFFSLLSSMTANISESTKEIGIYRCIGMTRFQIYRI
FIWESFVVVIASGIVGIIVGLTIGYSMQLQNYLFTQLEIPFALPYTQLLIVLFMAIGAAL
LASYPPVAFLLHLPSITHILRRTT*
>TCRU_32 radial spoke protein RSP10, putative
MSKQKKEVVINLDEVDEQTGYKSAELFVWLKFDETYLQKPEDDREADVDAWVDAFCEQME
EEGMNYDRNFVRSVCVLGIYAGARDEFQQRMGSGKAVYPNGDRYDGEFFEGKKHGTGRYC
FVSRGKSECDRIVEKEMQKLGGAVPDEQFITNVAEKYKISRQIVSWIIEYGVYPCYHGDY
VRGVRTGQGLMKNKDGTVYKGDFLANKRHGQGMFYYLNGDIFSGTWRNGLKHGYGTYHFA
GGSEYRGSWVDGVFTQGQWIFPDGTYYEGLFNKKNRPCDDAASMHFPSIKMAQTGVFRRG
VWAPSSALQVCEETPVDGMSWID*
>TCRU_33 hypothetical protein, conserved
MVYTRWKCDRLPVFQLKLFSQEYPLHTTVGILCMMFLWKHMGHCSEETERKHGWWAGYPY
WRDPIARRNEAKYKQLINKNDVDITDPKWTGCSFEQLEKLKKLI*
>TCRU_34 hypothetical protein
MIQTESEQPLISRANEGGRFPCCITLEDISVDVCTNFTSALSSCVETPCWDEMRVVFFRD
GVTQTTRWLSPAVAMHQMMSASAKRIGIDKGSSERLPGITEVKWSPINAAAYTVYFRFLD
KDADHSLDPGYERPVFSTNLKYLDSYNTDDADRLRSKVSPKVIHPFYFSIECRNPNRAFV
YTGGEGERPTSAKVEAMSAYYSRCVSKISTVFRKASIKLSSGSTEGSRSVEGEAADRPQT
KGHGHCSNYSSSFYVCDKYGVDPSEAYNAPGGRRCISLPLIPSHSKLPQNKTGVPLTLHL
TMVAHLNDPLMRPVRDYHSMVVLVDQVILDVMNVEAETGGKDASSARRVEAYGFGLTSNT
SQTAELRFSSPFLAPPDIPLNQEGGVRLVDFSVLHPSQNERELTALDLAKNPTSICIVSS
GCKVGNKRRIGNRPVLVSRFKTGVDGLCKSSYKSRLVMGLIRRYNTGEVEVERCSHPVDL
ASILNQEEYSDKIGAMIFSRGEYMSFRLRRRCFAEPERYRTELLMPYDYDNSGVEISDVV
DDDDIVMFSAQGARILPEENASKSGGGDDVPNGDGGRPDESRMTPQAATPTGTTGQLVEK
PMPSVTDSVMTSYSHEYQSYVPAQKNEKEAATGSSNRFIIGKPQRDGDSPVVKTSRDIHA
EDSESLRGKGNAEGAESNADGRVSSRDVSLLRETGMAVETGQTNPFEKTTSNFLFDSDAP
KEGAAHESLSLVTFELNAMGGINGNDDTQFALQVEPYISETIDAPRATENPRVYWWES*
>TCRU_35 hypothetical protein, conserved
MFRGILGGAGRQWRSERRLATVMNATSRNPAQKSTYRISRTNLAKQSAVRMKEDAKRRQK
SAVAQSVSRGDLSHADAEFLRHQQDEALAEHDARVRAFTKDTGSAHHHRHAPNPPRHLEY
DSVDANSGHSIIQQRFDALVHDAVLKYGPPLPAEFVSENDIVSPFGSRGDFNASSPFQEE
NPNAHYFYDEVQIRPQELFGIIRKLDPSFSVRTHADGVPFSLLIKNCLYFRVWGGKVHFM
RCLKRVPLRTGEAGEDDEEMRGEVTTTLSKYKMRESPSFDGLRQGPQPWLYNYRMM*
>TCRU_36 hypothetical protein
MKEEGKGATCTLNVNARHVVEGISALLKPALGVEHISRSVLLQQQRLLREIESLNDELEN
NRTHFETLNEAQREKLDIISAKIARCRSSAALLFRRLSEIKERLLRVHDVILQRRLKKPL
EKVAPEEEPVTTPSEQGNVAVVLFATEEVEASRQLNRHPEDVDNQHEEAVLPAEGEAHDE
*
>TCRU_37 Got1/Sft2-like family, putative
MHQAWNLVRDEPPEEVEVMEMPRENGIMGDLQEMSSLTYHQRFVGFFATLGMGLCFIAIA
TVFAPSVAVFPKKFAFFLTAGNLFCLGSTTFLVGIQQQIRSIFDAKRMEAAVMYAVSVIL
TLVSVLHWKSSVLAIVFAVAQVCCLLWYALSYVPFARRTIGIVWSYAWYIIWPVFCAVSQ
ALRRCCGLLISSVK*

>TCRU_38 brix domain containing protein, putative
MGKSKVMPGTVDTAEADKATPKSIIIYRGEVGNNVRALMHDWRAVFLPWSSRNLHGKNSS
LKDFLAIASTFSVSHLQLFTAPLHGTSLRIMRFANGPTLYFRVLSFTLRHEIVATQRRPI
SLNQAVWEAAPIVVLNNFTHPDARRRPEVPLLEATFRGMFPTVNIQLVKNSDIQRVCLFH
YDHVEHLVEVRHYFINAKAVGVSKTVKKLLERRCPTKLGTLESIDDVLHREDVWSDTDGE
GEEVPLAQPFRQHREQCRIKLHEIGPRLTLQLVKVTNGFAGGEVLFHRFESKTPTEVAEN
AVKVRARRSEKAKRKAEQDENVRRKQNMKEERLRAKRLRREETMRQQAENPLEVVDSGYG
ADAE*
>TCRU_39 TFIIF-stimulated CTD phosphatase, putative
MWPTRGHMKRLVKSVVPCIVCFFQDAVLDCVVAWKNIHKTLYVLFCFFTGRSHLAYPHPL
VQLRKKKAELALHRSRSTNPTVSHASSSSCTTLERLGSSWDDASPRESSGKEGNSLLMGR
KPALSMAEGDTAENECWIQRHVRRGHKGELSERVLKTRASPLVSPAYHLCHSESLHRLVS
NIIGPIQQPTVSALPTRHTAPQWPPHSSGRSLARHDGRGDDFSITTDEYSSTTSSQCHPL
RSVGVQSNTTSGSVDARSNSSFRAVPSVVYRRESSKQVQFDRSKGSRMPLQPIASITSHH
VLSYQATRQKVLIMDLDETLCFVSTKSTSSCSPPTFSEVIPTASGAELFYVWERPHVRLF
IGTLAKLFNLALFTSATKPYADSILRRLDPERLIRRRYYRHHCRQIPRSACGVSPGGRSL
AESVGSSTKTAAQNVTSLTGQTERSCGTAANDVVAGRMGDTVPPSCVHEGARKSDGGEGV
SGTVLVKDLRILKVPPELMIMVDNTEESVLANRENALVVPPFFPPAVMGTGDNAASDDVL
LSLIPLLEALLVVPDVRSVLRHGRVYWPNLNEK*
>TCRU_40 hypothetical protein, conserved
MLFRLGRHVVSRVALVALVPGGSVRLLSNSALQLAPKRRTKTSEPGKAAALGASASPTQK
NDPPPRRRQRKTKGDGHDTEVLNPRGSLASLPRAKKTKGVQSVAKEVRGPTPTTSDETSE
SATPSFTVDVLRVVEEWGAACANVQPEDVESGETQVENKNAASHVAVAAGTKGKPQLGAT
ALAALLVRAVKLPEEYPTLHGVLQVYQQTPLSRSGVVVLHAIELVRNVDHLSTLVAFLRV
YRTSAFSSTPVYEAVMEELVRATTMWWHQDQNSTKRGERDEIVMRTTLMWILLEFRRNYF
EMNATSTRISDASKGNKKKVGDKRGASIEHSKWLEETTQKLLADAAVPAADHIAQEAGDR
KLQTLTEGVVNMALFLLSSAMATELQMYSSHKETWERGTSQVQTAIDVYLSHNSSEDSLN
ASMKHLRAHGFDLLDALRLLSMLDTALSPLLRERLKRTASECFLKLCGAVGARPTLFTEV
LCTPEMAQRVRALTSNDIGDYVKAALFTGAALFCERADDAAVNRIAQQLQAVKRVSAKKE
GDLCVDADEKEEDDAEVTSPRSRRATIAYGLFSAGFDPEAVLSSGLCVGHNAMEVLELLQ
AAALFSRSFALSPLPARLSMLLTTEVAALIEARIRAENRAGVTPTDCIEGPRPLAELLEN
FSPVEKNTSGKKDGLVPLEVIFHLAFGTAVELLVRGEEKKLSSQLVRLLTLLEWEGSYKY
LVDGLSLLIDGFVERFRTAGRCQHDRHQQKSSMTTSTEVEQSLSEVTAFFVPRVVEAVQR
RLAKTKRASAMSDAEEKEAAQLLQLVLHFTVYVAACGMNATTAKQLVGLHTMVVKGLTSG
GSDTHLASLSETVIRMNILVSYLTAKQREFGVARHPESPGLRHCSIFLNDVVAVHLKPIA
AVVRRGGTIVVAQERYQVLSLVSLLFRLVSEYTVEAEPAELRAFRTDVLDPTLTRVLQEQ
NNGDVQCNETLDLDALSEITVVMCVPHTIHHLSSQLLDQLAAAVVVAAPKQLQLARTEDQ
RRHSSKTATRLLVSAAAVCQLRQDKLTARYLSLVQALGPLLLPAEVSAVLCSFVAFNVPS
DTDAVVELRNRLTEEAVSTNSSLSVPETISSLQVLCELEDTTRLAHAAILRRIIYSGHRL
TPGEVGILVRITTRLQQLNGTLPEDDLKFLQDLPFSLAEEVLRVRQHCSASDLPLVLQGY
SQLEEDRYGELNDRVMKAYILRTIQVRPLLGPKEVVECLESYAAARVSHQYLFGVLLARV
ADVKLKFSLPLAVRLVRCGVNASWDKNIQTACITAAQPVFIGLVRHLLQNDPASLPSVSS
NAVVVLQCLTEAFPNDPTSDLLLQNMASHHTALSLSTMMAVLELIARRSSTEYNILRCMT
EHAASALFPQTSPSAFAELTRLFVRCGVRSRVLFTALSRRFKEISNKCDGNVLATLAEAF
AVAHVDLEEGIITTFIERIVALSEGKQLLLQLNHCISILKLFSHIDAEKVEQATNLLLES
ARKSLEAKEMVHDGVKIQQAQEINILLSASLRTAPLRHRALAKQCADALLGIVGAEGVGE
EKNCGAWQTDLMLIVQLASNIVRLGLRNHPVVPYLFDALYEKRSALMRRRLLLQITAETI
QIAGEHTHKQLYALLVQGKLVA*
>TCRU_41 leucine-rich repeat protein (LRRP), putative
MGREQSADFEKAFADLLLAGLRRQGEVHGDERVRSIMRRVLVERGGDGREETGTVASAVF
SLAGAGLGDKGAIAVAEALLKLGSPQMVKSHGVRRWTVLLNDNGLTDRFSAHVSLLVSRC
APPVVLLDARGNAMTPAAIQRIEEARELSPAPCALRLPPTAGTAGVAAAASLRESASSAS
TAGGWRRGLDAEALRKRRSALFASGAASSTAVGSELGGRGRPRSRQSEGEAPHDVAAVEV
AARAPSSASGPAPEERSRRMEASGRRHSAGAGKSEKREEEAPPRGGDCGEPLDVTANLSP

LLAVVLDLSNAVPTGRLQALYGTDDIWSVVASSGEAVSHAFPPKQTPFLRAGIKSMVSFH
SLTVLCIRKNRLESLKILPPSLLRLDVSENELRELTGVGQCRMLTLLNARRNRLQSIRGL
ERNLALSHLFLAYNEIAFVEGIAHLLLLETLDLAHNRLKTQASIRPLSLARGLRHLLLRG
NPVVKCIKGSYRPVLRNLCPSLLSIDGERLTFSRFAAKAQQECSDIRIPYAPGDSIGGIN
VSLISAEDGKATKVTQCANFMHLLTRGTAVGAGSGYSDAARAVRTAKALQARGAANDKKG
KEQRRPAYLADGEPLRKELLKRLAQESRKYLESMLGERLSNIQASHVYDNLPGSGESRDG
NNESEGLSNDTSAQRESSGQGSGPHLFSGDRNRKAPEFTQGLFPVEVASEENIEKHRTIP
LEKKMPAVHRDATLDHEQWLRLRECRIRRSAPFGDTPQRISPSPKTPDISYTKSEEKEVY
ISPIRKDHDECQAASINVTEILPDMEMLDSRFRADGKVSGEPNGRPRLVKSDLGRPMLLS
PSAECSPVKAHRVYSSLQSQKGNKPILSSSATPLHGVKAANEPVIFSPPPPLLSPCSLHS
NARSYAVKKWVNQLREDAEAVQEALETLVSILDSRWWSKAAITGKPSFIPPEVLEERKRC
VDILTESGMLLDTEIPLDVVEYYHFTPDELRHTGEEDYGEEGDCAANPLSVVTACDSCRE
KREILHCIRVIGDGKTCLRYLVLLIEEMKEEELQQYVKELQLLTTCE*
>TCRU_42 hypothetical protein, conserved
MKITDFSAKLQGPPETETLLNCLVGVLLGVTRRKATEGPTRKGISTSPDGNSEAGVISSL
RSVNPSSEDDSFAQDVYLNELCSYLSSGTSSRETGETPGASPPIPLPLPKIGSFQKARTL
FTRLAKSHYWRRRFLIPLLRRWWREEGHSVFGFLLLQSITDAVARELVCIQSDSGEAVMG
NEGQETCHDDGMGNNKKLLCPGAMQDLEELLKSTGSFRGLCIGVDAIIRNNLSNLLRCVR
KLLAGGACKDEKDALTGSARAEMECLVDGSTKSVLKDLFAFFFGTMNDVEKAFRESVWTF
LVALLSAYTGALILLKRDTNSDAQDNLFFLEAQRMFIGKMQEHLRGYLTVRLSSDSVAMG
NSPVTVHNVVCRQSFFWRASMEVEIAMESLPPAFISNSLVVSWARKLVAAAWGNAFCLVQ
SLVRAQEATEEVPGTVETTDSIISAIRRRHRELSEEHLERLVSAELRCFSGTKRPRMLET
DAVGDKTKGGSRTVPTTEETPAFGFSSYATEYFLRTYHPSCFAVLSLVEQDTLVLLLRQL
YAVIVNKEREAIRRSLLTVTVPDGSNVTDTQKSLLQWHLHHVHTQVVQALGEDALLLMCL
LHAVFIFLERIGKTNLNVCDVLSDTLLPILAMLCSERHGGFAEHEDGEQYYEIQQCIMML
LASGFLVLPWCLRGIRIRQVLYNYIWANLRDSFSAEEAFTEVSHIFVQYADVLNPAEDAA
AALCGDLSDDPFLRMLASEGEAATTTMEVMDDLLRLETPVQFPAPCGALLLISIFRTLSL
NFSRLFAEWEQQKQHVREGAMDYLGREATFCTIRDIGVFRVLIQLAHRMVLGFQLQPVGL
LRLWLSFLTHLFTHFVPHLTEDDEIVLMTLHTKDGSRSRAEEEPPRRAYKRSPNETSQGE
LRAILGELLADLALMPLVDAEAVMQCPVAVPHRPGSAQWIQKQSERSQDVLILQRVLPVL
VLEELCFALRIPIEDLDEREADQAFVRQVGKTVEQSFLGVLGVFAFCQRMELFVVPGTFT
DKRFAELLQTLWLAVEAGSMVMAPT*
>TCRU_43 hypothetical protein, conserved
MRTGSVQLGRLFSPSLIGRNRYCTPHLQQANYLLPFVAGACCSVEDARRLFARCCGCYHH
YRAEGEDESHGGDNSTDTESVMEESVMSLQRLGLISHTHEEQAVRGELQVRRIYREPIIT
INLHSINVTSLQRGEKETEALFQMLHGVIIPLMFSRLASSSATSPTNCSPHFEEEVSAQL
CFSLLQQSRGTCSKVNDTTCRFMVDLVNEALLLGVRERVLFPCGGGLFRLHREMTQRVSP
CLLTFQWWWWRRVDSFLRHVVASRAAGKDVASEAMIDAAQERVRYWIKRRDEYLPHFFLH
ASMDDTMALVADAVRCWGVPQSPVQGQKAFSVPKWRLQLSDEAKASLALETLNSIRSCLV
RRPAGISVDELSTLIAWSTISSLLQKKSILKTLNSFPSNFVVKTVQGVTVAQLQLCLGET
NTINATEARTWVLGRRNESSDTTVSFLQEVDFVIRSVLFLRKRHLLEKRVTFEDLRAVLL
PEKDMESTDAFLEVLRRYDVVTGFEAEKPVSWLSLQQERVFLSSRESVALKAIEASRKRK
GSKYQLYAEAISPFLSRCSEEATAAGISDASMPIALLERWLQSDRLLLNRADLFKMLREC
SLPFVMDEKAQSIYLGRGKMADLSQCAVPPSPVDPMPSTLPPPPPPLPTPVTPLQKLTFD
SQLSRALKGQHPDALFRFAEATIHAVFGLILPLVSVPSGMRLQNLIRRVRWGSVAATLGV
LPSFLEAFDGLFFDLFADTSGPMEDMVVTAYRGHVGAWLLYARLISRLFPTDVNIPLRLV
AEGLSWGVWFAPRFGDLPTLLRRVGRSCREGYLLAKNECTVVPSAEDDAALWEILENVRR
EEKDEQKPHKVLTEIRSYLLVKPTCLIRYMRGNKETDSSGDDMWMQYAETAIRRFPLFFQ
WNTALQGATPLLRIALKCAPAPDGLAALVEEYVCPLLRQRPQDGTSIAELDDRLGWSRGN
FDTHPASSRALGVVASGTSLYGILQRYVEAVDPPRILLQRGSTRATEHESVMVRPNTCIY
RSPEDMLLEVNGLEYMTNENATLRPSGRPVSLFELLAEEQELQGGENVPSLPRTEQWRVS
LQCNGEKAAEWEVELANGRVDVLVWCES*
>TCRU_44 hypothetical protein, conserved
MGGGDETIERIESIGDTCHTAVGVDEHATHGGEEAFLVENNSTSSHSSKAVHPTEKAVEL

QERRKGTSSTGTARREGDTFPEYSLSTMLENTAAASVDPYETDGRMVKENPALTAVEITT
VSSPSSCSHSVSATTGLNELSDGDANGDNCINDGEDCGGESYMSPIVVQANAFQETRRNT
VDAYYPPLNYMRPTMSWRRQHEGLEWPTRLRPSQGRSRSVTSNYSLRSGNERNWKENTLV
HLIRIPFEEGPGVWGDVEMPRRPFGYDALGNKAYEMTNAVCCRAPVTTTISSSARRRDAA
CRFMAEGSTSRSPSRARSSISCHANGTPTAEKENQEFFEDPTTLENLCGIVGRKFVAPQH
RITATNADRISTTRRLRSMTPSYVDAFYKLDREVAGRKRFLASLRRGATLRESSRRAATT
PCRQHSQHPYRRSDGGNISGRGLTLSPGTSCMNFSSSPWSPKPKPWR*
>TCRU_45 hypothetical protein, conserved
MSPGEKLCDGCGNPAFSFQCPLCQAEIATDRGFFCGQECFAKNWRNHRNTFHKKGVVRAK
QPPGPASVEAAGDCQKRLTGGTKEAGGSIKKRRKLEKEVGVKTKCPGAVPWLPPPRGSPA
TAEVTPPLPPETPRAVVGCPSADRRIAFWSAAVAASHHIAAAFSQGEGVAPFSVLVVTSS
PLAAHAMAWAARCAGLAGVMRLVVSAPSEAVGANLLKHTSDERRVIITTQEIVRCVADGS
VAVWLPRAESLLVTLPGVVDACDLQAVHLRAVFFVGRTAGSDSTEDNWCVEEEIVHHVSP
PLSPPAALLHQVDVFSIPTEDSSATGNKEATDTTPKLKLLRFDNDVSTSLSRGDLSGALQ
HLVRLYSASRGMFEEVFLSTFLSALGAASVTHAHHMLAYAARYLVDHSARFAGPPGGTLK
EMTLRAVTKVVRLFPPIKEAEEGKVATKKKGDAVTTDATGNGDLSEFLTQPSAIEKRKFL
NYYETLPNLQLQATICYLYEHAPPGTVDAFGAAWGVDKVVPGLEALKLADRKREDAVQRL
RNRYGSKLSSAFANYLVVLMHFIYDAVAGYSLAVEELERRTLWSLTLEPEVGSLRSFLSN
CFLLQKEDTSCAESKRGETARLSSRKVSNKPPSRTEILRSFPVRTSVFEEPLFLSWLTLP
LVGKRQRDMERLQRQAVEEILMAMPRNPRPMYIGDVGNLIGKWNHFNARFEGALGVSLME
FLMQHPEHFRVVGNLVTRRSAGVSEQVRMRFDNDDSGDDDDNGKESDQERKAKDRALLTG
VKGSGGRGLNAKDLPARARKKATVKAFNKARFNRNYKPMDPAAKVPGYVKHGPRKVKGRG
RKVNKRVTKRGG*
>TCRU_46 hypothetical protein, conserved
MRASPRLSASFSSSAISSTPTAVAAAASSSSLDGTLHEVERCFLRHVIPMRVQGAGSAAA
LYRHAFLHQESLIQRVLGALESVPLPALPRMLLAEGFQRMLDGETPQRDIRALFEEAENE
ARRVLIQAEFHSSLNSQHCDGHFYAAIKTNPLMRLLAYELRAACGYYAQIMSIRSQPEDG
AAMLLRTLIAADIRTDPFLVDVMLKFAALRRNVDTGERLEACPSPVEEFVKECLLLERDA
FGRFRFDARGDNRHLLHCIKLSDITRAPRDFAVLLDPVLRQYGNFCIQSTSVHQGRWMEH
RLSCAEESHRVDPHLPLLETVEVPSNKESELSVGDAVGVAHGVSGRPPLVFFVRYNDPMC
RRHKETTREKGAEKDHLEVFELAVEDKSRTFWEKWFMDR*
>TCRU_47 choline/ethanolamine phosphotransferase (CEPT)
MNNSQKPENVRGNASLRIDQVSFGSYLPENAEERMRAYVYRGTDKSLLYKYVWRPLCARI
VTYLPVWLSANMITFAALIFVCSTHVLLAFYIPKFSVASGGNGVGGFCEIGEEGNEFMKE
NFPPPPSFVFILCALSLMAYTFLDNLDGHQARRTRMASPLGLIIDHGCDSFNSIILSLSI
SASTLAGPTWKTWTFLLCMMTGFFMNTWEEYYLGELLLPLINGANEGVMAAVGVYLFTAW
MGGPQWWFMNGVELPERLIPTVLTLSPPVATVTIEASVLRTVCPCISVPYFYVPNSTLSL
LPLLFGLNCSDAYISAPPIPINAANQTSHAVYIGHNTLQNTILGLYDPSHPNLFWVRFNT
VVVLFFACSTLVTVLGNIIRVYRALHRHNDMSISTSGSIVCRIYFVHALTRLMPLVSIMF
FATLWLFTSPSNIFRRHPRIFCWTFGLLFAKSSIHLMIAHICNVKFHPLHRTFWPFFFLA
IHLTLTYCRNVVEWIQHYNHGDTLALLSARNVWGVALDEEQALWCLFVVCVWNYIHLVCT
VVRDTAKRLGIPVFTVPRSNQVTLRRQIEEERAANEKAGEKILGATHLLKDDGTPMDEGG
RGKKKGSVSGE*
>TCRU_48 hypothetical protein, conserved
MLQTARIRTEKPPVFRRRHRQGVSSTTTTPFPGFIPGASFDATAPSRREALQQFHRLEMM
LEVEERLRAEDGLVHSDTGGGSEDGRSEWGDKTGDKSRLESAAKAALHDAREELAGRTLH
ADPYCVENVWSEAQRECQVEEGHRMGEDEAMFSARKGIDFEPSNLLEADTHAAIMEDLEK
LHSRIQQARAQKSRHSSPLGGDAEGASSTSESSIHLSEEVEFDPERFVAPLLRHSDVIDG
AELWTPQFGIDGGGVVCFRTAHDIFSDTTTVQEALQLLQYSVHSNRPDVVACVQRCQEHQ
RQHQPITTIPKLPTGETVNPPRRKRKVVIPATNVGKQHEEEAKLYRPLPSESPPSAEELA
AILSKTLPAIPDELRNELIDQRRLLERLAAAQEASFRQLAREQQESARRRIMAPRADTTM
PLLAPSKLQYSEPFEIAETLQNLQADPKRPLPPVITISTVRPQPTKILPPSPPLLPPHYI
EEELRRLHRHYEKILRDERRAWTDIMQKQKATFEMEKNAAVQTLRSAAEQRQNENTEEIK
RAIALQEIKRRRWQYASESKQRIEFQKMLYKTFPLGDVGHGHGGGKIGVAARITPGIRQR

QTDIAEGAKFFSSNKQIHSPEAEREEEDEKKKKKNEKKRDLKRPFVRGPFSVVLPEEPG
VEPTATAHDASLERVDEVVMLSDGEEKNGIQQARGEASVGSRALTDKLRIGFSSPAGKQR
RVLGPQRSPYAVSSKPSVLRGTAKTSSGGGVKSAAAAASGIKHARAPSHSRGARPQHRLL
SKGSQEKSPHAFAVHDARIGDERNFYNTTETVLTESVHSLDATLTPPPVVGGTSHLHENT
LDIGGSIAGRAVFPRSILLLSDPLTSEEMERQHSLNCAFNALLPPPPRATSKEGSGQIQR
PCDIYYFGEEHGALTPRRRAKLRAAEAQTRIEARRRLEHIKALSLTSKGQKLGEPVPHFP
ESQLFEARSEQRLADLLANETIHSIIGGAAEESLFADLFKELEDELVSAELRRLAFNNLK
QRDESGQEQKLMEEEYEGDTKPPDMVSMERAVASAKIFDAPINEEIFLEETVLRLLEESL
LHFLLQEKSDEKEEEKTIDNENIEGGEATMVSSQRGQTVLMSDGAYETETGPLWVREVVS
ATTDPLWHGAEEEVNPPRESSIQATTMVSSEEHAPVLSAPPLSAPPTSKKAPLTPASTAQ
MGVVITMEGARGNVVPDTAGTVRIVLDIAPVMEHLTAIAPLDAVQPTRPAQVDAILREDP
RLPCAKEEELISCEVVDAPTITGTQRLTVSTEVKRDEMQEVRPPLLVSDIQLGESHPPAL
TKEEKTNVPQPSPLPLQGYVTVTEVPKARQSQHIEIERQKECARLCDNELIQRQMLEEQE
DTLRASWHMMWDWQQMNVAMLIQHQYQKNPFDVASQPFSAAVPFTETQTVNKVEPSGNNV
LPPAPLDSTIRDPITRFIFEWMHDYDEKKKEETARKRLVELPHEASCVPEGKTLQEGSSG
TCTTGTEVRRRLLFDIDNAESSSWLSSTHLSSFAEDGFPRFANRPQPRVVRPQRKYRRSG
DENFSSETTETTRYTNSSSILWLAQEAWSRGVSPPPVFPTAAVGNATSTTVTTSSSSRTW
PSTSSSEKPHLRETMLRHLRRIQSSDPYQQGEQESQREEYPSVEELRKEVERVQASEQRA
ATHDASRLEGADQESRHTENFVALLPLLQRPQSW*
>TCRU_49 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase
MNSVTGARGSSETAPQAADDDSGDATASGNTNGNVASGNSAQAKATSEQAVETEITTTTT
TTKTPAAAAAVGVHHRGCPGNSRGGECGFCLFEEVVVEASPPSSSYLFPQNASASPGVDS
LQQCRPLDSFLDTACGKASGHLSSSTRICPSETESTATFVNGVVQSDRNLKESRRIWATS
FPSSEFFSAAETEKALQHQMQHETAASFPLSDKPAPERRHALPLLQVPAQDTNADSVIKK
QNIAALICVLERQKFALQRQLKEIRKELSAQNIFSLVRASNASQLQYLLENKICDVNKRD
YNGCTPLHVAALEGNEVIVRVLISFGADLMAVDNTGRTPLDWAAANRHSSVCHYLMNVIQ
RLMLTQEQKKPQIQRNNDAESVESTEKNVQRNTSFGVSSTNNSMMQSTHLTSALRESTCS
LPTPSLPLDSEIGNEQQNEHGLLSSFLTCLPPDMISLMRSRSALSANPIEAPLHEDESEF
EEQGTLSNFSSYTTISGTVPLVVCMVGLPGRGKSFIAQRISRYLNWKGVPCRVFNAGNYR
RRLLGVEGTSDAGFYDPNNANGKQMREKMAEFACEDLVEFISRHRIAVGVFDATNTTKAR
REHLVEFFNKAFKQRHMESRVMFIESICNDDTIITENILRAKCDNDDFKNVGDTSKVIAS
FRSRISEYEKVYEPLDRADDLSFIRIIDVKRHVVMKNIPCGLASSIAFFLMNLHPVAHPI
YISLPGETEGEKNHMYGGDEHLTPLGNKFALALKRFILERHFPHMIVLHGTNHSVLNTLK
PLAQSLQEDSGDGADKVEEEENSAFSGITCQEELLCPLPGLDSINYGLFSGRTVQWVRKR
YAKLSRLLYVASPVCGDESALNLYNSKKLYAVDVDDKKKGIIETHEYPKKQDQGEKDARK
QHFDKSARATSRFLHVPNGTDPRLSYCVQFPNGESCRQVNVRLEPALMAVMRVQGPVFVV
ATSVPAQGVLAFFTDTMPEVSPTLRLPQHAVVEIGVKGEITVHQLVEPVDHVPQPGSIRE
GR*
>TCRU_50 AGC/RSK family serine/threonine kinase, putative
MSETKMVNKSKNGIREKLHSAIAWLFTPGHKSIEYCKNQGEGDHQVSAAVDGSSSLAGDG
CPLTTPRSNLNVKINREGLQQAAVSAATSQHAGELSTRAAGNNLDLDLDATSIDHSEFFS
FLEDVIGGKHVEMLKELNQLHESNSNSNVEANAVDSPSSAPVESGEGFRESVLRASSFLA
PCVEAQGQSERISEVKQDTLANKKERDGASSAARSLKGYELIAYLGKGAFAEVTLARHKA
TQKLFALKKISKRKVREEGCVQRTFTERQLLASLKHPYLVKLYQAFQSLTHLYLVLEFAQ
GGDMYFFLESKPWLREMRRKVQKLRRLSFCSDTACPFPGGAQDESDPTSNHSCPPKHLIS
TVSSFSSTIQLAPDQSRAPIRLVAFYAIELALVLQYLHDHGFVYRDLKPENVLIARDGNL
MLTDFGVAKYYGGTKLKKSGAERTNSFTGTTPYMSPEMLLGEPQDARMDWWSFGCILFEM
ATGRRPFEGESQYAVVQSIVERDVEVCQDDFLLTSLEIERRVMQLQERYEAYLVRVVEQI
KKCKENGSMTEEERTQFSGSLEDAQLTFTVDAASALHDTSSCGSKNLLGDGTRSSLGEAF
CRTFGSETLNAKSSMTIENQSLFMNFAVGELDEACDLLKDLICSLLERRTDRRLSGPAVL
EHPFFSCPYVCSQIYYKHDARVDPGDISGFYVPTKWRNSFSSGGHFAEDEKKNENGEKND
GHDAEDDDGGTTELQKHLGAARFLAQSPTQRPDNWRELFLEGVVSSLYVPRLLSADDLRY
FPHAVTATGDSVVTQQRALREQIRRKHGALHPRGGEGDHQASPLSVTQKGGHPLHQENQM
SEEDEDVETLPQSASQRSSLVESLRGSKHAAFAHEEPLFMGETVSSLAFPHHDNFSVYSV

SSLEVSPAKYPSFLAKSYGRSYNKECCNEIGKETVTEPMEESSNRLKLSALDLSYSTSAE
AAKATAKTPEATLGGVLAEVAPSLISHSFPLQLGESQTAAHQELHPDLGRAYTAPSEIFT
STPTKSRDALPSFNLSTGNLGAREVLSSDTSYVTTEDEDSTGNAFDDIKGQTQGTLHGIA
YDVDDYFPSCTKQKRLLLKSKTGIPTQRPSKTNRSIFSVQRLRRSLLDKRATKFSRQLVA
SARASPTVPQQLPMCASYETFAFKSPKKNSHKTDSEYDNRRCSEDMEGRRLSLLSVYSPM
LYTATVSPRSPKKTEFLNSDSLVHETNILPGLCSTSRTGANSDSVEERPNSPTMESSSHP
GNGGAGTSVQHYLGFTFDSRAGNAFLLGNTSNGGSNDKWCF*
>TCRU_51 hypothetical protein, conserved
MHQPAATSHSQRVCHEHGEAETELAGHNLQHAAAIHRNVPKHTRTFVEANARRTPRAVLY
GEHGAAADTQVRRKGVHHVRLRQDSAVVHVEDAGQVRHEVALHKDRSARAPATHQRRPRH
DKPRRQKPDTVQDKRGAVPGPRMATGRRHVLRPANRRAQR*
>TCRU_52 hypothetical protein, conserved
MQHNRALQRRHIRHVDEGVRNQARRALAEAANPQLRAAHKHTVAQRHVQRVSGQVHRAQV
HRHSDRPAEHHRVEARRRTPAANRHGLRQRHATHAVLRTAAAGPRRRHVERQARVAHTAG
AAAAHAVGERRRQRIEARQRCRTAVARHHAHGGQAGHAVVAAALQHAAARTVALHGHSAA
RDRQPGDKRRAGGSAASNRHGAAAQRHTRQRRHRRRLAHRPHVAQLQPPADTDRPTVAAH
QRRRDRPLDAHEAQHRIKHREALAKHNAAAAAHYRHVRHGEHRVAPQTETRRGRHMHRGR
GRTARRLQQHAVKHHRARQQVHTAANVHRRPARLQRPQHSAAHTQLRLQQRRRVQHKRRR
HRVRRPAQLGVAHRSRRHNRRVTDRHVRACRQVVHKHERAVAPRLPAHAHLQAPVTRRLA
AVAPHVDLRTAVAHAVPHFDAQRAGKHRRNVEHHSHAVRDAHAVHQHRVHGAANRDGSVH
RAAPQSQHHRMRRGHPRRRRNQRQRHKQRHTHSRNGPAPHTVPAARTRTFRRPHPPTQTG
TNRAVVACRTRTVNRNSCLTNPLSSDGEYRYTIPIYRYPTNSAIPNTAINN*
>TCRU_of Trypanosoma cruzi region 4, putative Dispersed gene family protein.1
MDGTVALGGAGGKFVVGCLTLSGQALQPMDYRSAGIIGEFRPVACGVCDADVRCFAAATR
AMSGSCGCRCAEDGYGHDCLPVYLPHVDGCNRTLAPPLLSHTAAPTETLTPTPTWTPGMS
ATHYSPTETLQVTETVALSPTRTPTASVSSTLWWSDVACPTLAVTTRRLVGA*
>TCRU_54 hypothetical protein
MPARCCSRATEHRRRRLVRARRECGCGGERRFRDVGGVLRVCDLCGGRRGGRGLDVGERA
QRDAGELHACGRSEPVRCRVAVRPDCWPACRCVDQRARVALRRRRGCGEPLPAGLARHCG
GLGADCREARCVPRRLRPWRCVRVPCGAQRESDGERADHCAHAGGGGVRRRCWRVGCWRH
GAVVARCAVLGRAVGADGAGAVRVGGGRCRGQRRLRGGVC*
>TCRU_55 hypothetical protein, conserved
MWSAVGACPHSRHRVRHRAIATVRVALLVLLALVAAAAWMPAVHAVALRLRGGTVDRAIT
VGRAVDTVLMDGVCITNGVAVVFDVAAMLPGALRIELRNCVCDGGAQIYVRGYSGEPASD
RSLEVSVSGLSGSYCSLVFVHNLPARTNVTVRDSAIVTPGPMRYSQLSGPADAVASPLVL
HATSLLQTQLRVSSTVLRSSRAGGSAVHVGGGVDLLSSAMVLDGVLLEASGGPTASAMHV
SSSSRLSLRSHSVFSLTNVSVVSSGGGIVLGERLAVFESVLRFVGVEGSVASSLVRCDGG
TVGVGGWLELRDVWAVGEASSVASLSGVTLSGGAVSIARCAATGATLVSGLTITSGAVSV
QCNRAGGRVLQSSGDYRMAGLISVSVVPCDGCAAALACFDALTASFSECVCSCRAGGVGD
ACLPFDVPPARAGGGGDTAQDCVSGVTLTESVTVGGGRATACLDSVVFSGPITVAVDLRS
MDLSADALKVTLRHCVLAGGAQLRIGGLSESTARLVPHALVNMTNVTSLEGTIVLHGTMP
LHSSVLLANSTLRATVGGSRYVPTTPDHEESRYGPALVLDGVRLLSTRFVMTRSTLVCGG
GSCAAILVEHGLGVHLSSVFYMDNCAVNSQTHVMYALASDLRVSGGSVFSIQNSSWSAPS
TEYYKGALVFGDVAVDGGSVLQVVSSEFRLGFAMLMATTLTVTGGGWLVHRDNEFRTAYV
VHVDKYDGVAFRDQSVWSILYNNFTYGSYSSTTAYMTSFWSAQDDTSPTIYGTCNELRGS
PVTDYDEDLYIRTPVTALDCGTCTVGAVCFAARTSSIRGCECVCAAGGYGDTCLPAAVPD
GLGPFPLSDAKDTEVRCVYGDRISSVDYPDPGVRGLCFVNVTFTAAILLDLSYFNAPEQT
LNITLLQCVLMGLSIRGSGACVHVNVTSSMLDSGALEFEGDFGASSQMLVAGSKLVTNLG
YAIHFPRFTLGANSALLLLDNNMEGDIYAVYFPVAVVVDGGGIIMKGNTLRSKKKDYGSA
SAVYVHTVDLKNCGYFDVENNTMSAAIGIYFYGDTTVSSAGLLRVADCTFTGSTEALNSA
LLYLYGSVALQDGAQWRVEGNNVSAASVFIMPYSWHSIELSGSGTIVSLAHNRQADSSKA
FARIASSNTFLASPARFVVGCNLQDDEEVLYDGVFPGEVEVFRCGTCNDDAACYMPGTES
VDRGSCLCSCKDGWHGASCLPFEVPDTVVPPAPERAVDGDTSCVVNQTLTNLTLNMWKTH

HCYVGVTFSGVGAALTFFLNSMPLHLPINITLTGCTFRDGAALQFVGGTEVAESAGVLIR
VSQTVMRSSVVLFRRALPQHCDIAVTEVDAVQSSDIQLSGTASSRLSVVMLDDVVLTASS
LLVSNVKARLLDHGGYGLYSTGTLTLVGGSSLYTRYCSFDKYTYMLYMHRLIASDRSVFA
LLNNTMATGTSFLFQYHDFTVSNHSVLRVVGNSGSVSYAIYAYDSWTVRNSSWLDWRDND
AGAGAMFYYFSFYASVNIDGSSVVTLTGCKMGSTGLSESPLSRIDAGYGFVAGCLTVAGR
VLTTAAELELNGITDVTTVAACGECTRDGDCFAPLTTAVSDCKCQCAAGGHGDVCLPAPV
PAGPPPPPMPLPPPPPPVGGCISDVVYPEVTQAVGSGLSWLCYRNVTFSGGGMILTVLIG
GMTGDVANITFDGCTWRDGAVLLLLGNTYAAVESLNIVVTGNTFDDALLSPEGVFPPHTN
ITISGNRFTVTRLISRPGLDVDSPSCVAMNGLAISNDSAVVFSGNVFQTVTASSSAIHVV
GSPLRVSWRSLFAVMGNTFHMDGGDSTLMHLGGSFQSSSLDVLNNSAVVIRDNVVSRPVQ
YFMLFLRALRVESLSAVVFEGNDMQRSVAVFFTNYYTYVYYNSWLQLSGNLCRDSLSNAF
VHLSPRVNLRDSTVSVSGNQLMSNTGTCHIADLQRLMHPCGVVLPRVHDDGLE*
>TCRU_56 retrotransposon hot spot protein, RHS3, putative
MQASGHYLGMKRAVKGEVTFGEDIRGLCDRGFNNLPGWSLAAAGVKATVHNSSKHFLDAA
AEEARNPTTTSAPEKLEGVYESVHNARWSHAEELPDGVERKKTVTGMGVHEGRPEQSWSY
RKADDAIEENDAVQQSGAAPPVLMVLTSEKGWPYSWHTIQDLPKDVFVNCEVERVWQIVK
GDVTAWFSPHGGTDFTPKRRVLIGTPGIGKSMAAGSYLLYRLLHCDAEKIQVVVHCFGGG
GAYVSDKTTRAVTRCSDEDMCISELRSLRERGRNVYIIHGVAKEGTPPPRHFAPTFGWGM
IAVPFPKVTNYDEWAKQLQAARIIVNCPDETDVKAMCVDNA*
>TCRU_57 retrotransposon hot spot protein, RHS3, putative
MYLLGPIPRHVFDEEAFTERCGAVKFALQSINEVTAKEHFSRGGELPWYSEDPSHKLVKV
VREIYASGVILFNAPISACLEERTLERLPSVAE*
>TCRU_58 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily, putative
MEDGTLVFPMMAKSEEEDVYSMIIYSKDNGSAWALSEDMSPAECLNPRITEWEGSLLMIV
DCEDGQRVYESRDMGTAWTEAVGTLSAVWVKSRSFLWDLSLHVEALITATIEGRKVMLYI
QRGNFSGKNKANALYLWVTDNNRTFFVGPVGMDNAANWMLASSLLYSDGSLHLLQRSING
EGSVISLSRLTEELKTIKSTLSTWSQNDVFFSSLSIPTAGLVGFLSNTSSGGDTWIDDYR
CVNASVTKAAKAHDGSKFTGPGSGAIWPVNSREDNNQHRFVNHRFTLVATVTIHQVAKGS
TPLLGAGLDAPVSTNFIGLSYSMNKTWETVFDGKKTTSNTTWELGREYQVALMLQDGNKG
SVYVDGKIVGSPEKIPTLETQGHEITHLYFGGEGDINSSVTVTNVFLYNRPLSVGEIKMV
KKSDAKKGKR*
>TCRU_59 hypothetical protein, conserved
MVCQCGETQVQMTFIDGNQLSDETLTVAPSATGLCLFHGPVSKAWQDSTLVGHIANLRAP
QIPNFETHVLLPAMGVARELGHQQGLITAERERLNFDCANAVADVRNRNAYLNSRAQEAH
HNLSVRESTIAGAGNQVLELQQQLEAAHAQLREREFNLGVLNAQLQEREARHNAQQPARD
AETAGRDESPATRHVANDGVTTLPHQTDILMAGGVPSSAARRSSAAYRRPHGNVGRPHFH
PSTPLPSRTSPLDAQLPMEEDRGFCAFDVTTWPSRIWNEGASGVVIDLRCAYQCWQQDDE
QVKLAFDNLVEWIGALED*
>TCRU_60 RNA triphosphatase
MLSDRQGISRHEVVSMGNAEQRAVAKALFDAVNKHLSNPFIEVEMRLGQFKVGEDALREN
TGDQNGAQTNGLRIVDANFTACVSTEDYERIKTYLMTEMGNSSMTRSVTHDVSLRGWRHT
YATDEDGNPTCCVSIVRKKRILVKNIVVPLGAYNLRFAVSTETPGDLRFSGAGPRAGHTR
LKDRLSITDGMFRYDMTQVTEKGVLMHEVEIEGVFSSHETQLTESWLEELLSRAMRLATL
RTNSTHGVALN*
>TCRU_61 syntaxin, putative
MQGIMKRLQLINGTSENTKGAPLLPLREELHMQPQKTMTPYEKAQLEVASRIRRIRELVT
QLDGLSADASRKFRVEVSQQIRKEELQAKVEMQNARRVAQSEGRMQDFELLSRHFNDTLD
IVRERYGGGLPVAKPGGSTFEREPLPFTDLEYAVNQSAFLASNSGNVVPKPGNAYNLHED
VEFLQFFYETQKNDEVIDKSLDCIYVGVQRLNQNATVITSELCTQEQMLDETEKKMDDVH
GRLGKLNVKLKKALERMDRPMMAVYLICCLILLSIIVIIYFMAKK*
>TCRU_62 kinetoplastid-specific phospho-protein phosphatase,
putative
MGRKYAQLETLHNVNGRVVIVGDIHGCLAQLEDILSVTDFVRGRDQLITAGDMVNKGPDS

FGVVRLLKSLGARGVIGNHDAKLLKLRKKIRKHGTLHGKNSQSSLAPLAMSLPQDVEEYL
LQLPHILHIPAHNILVVHAGLHVQHPLERQLVKEVTTMRNLILQDDGLYRASEDTTDGVP
WASLWQGPETVVFGHDARRGLQRYPHAIGLDTRCVYGGELTALVCPGEHLVSVPGWTSNR
SKV*
>TCRU_63 Domain of unknown function (DUF4498), putative
MGPQTRFSFEPLTHRRLEIVLTDPAYKEAQRRWGLHSQTRVCALRFEQENNSRIAQEGAS
HGGGVGNGAVVAGAMRFSGFHKGVLQEFLVSLFDSTAVRDALALSPALRLTRDAVEYTEL
HCSWTTLEPFTRLVKAGVVRHVEVQGDVCHDEAEAAIFDGCVRLPVVRRPDFYLPHDIAV
TDELRALFLLAHNRAICHEGDEYAEEEAWDAINYGSGAGLSLAALRRVFTEAERSEFLYH
ILWRLVAGGGSNNQWDDDLGVYLDVARAWYKGLVAIRAVQKNEAPSAGGGMDEPDHAAYV
DGTVLTPEVVSTVVSVQAVSGFSLFTRTDDAEPSNLNYCYVCIDPVEAEVVVWYHCL*
>TCRU_64 emp24/gp25L/p24 family/GOLD, putative
MPNLRERLRGQQSSPPQLSFLLFLLSTALLSLTVCLIGVEAATTTVGSGEKLCLREVVPP
QSRVTFQFQVVGGGNHDIRASVADQEGHILKEWGETSDGLYEVLAQSGTKAIVACLDNTY
AHYTPKLVVFHFRYHVDYTSVAKQSELDPVERKVEHISSLMRQVESLQMLLRTQQKEHRA
TVEESSERLLIWSVFQVLTLVIMSCFQLYFLKRFLERKSFV*
>TCRU_65 monoglyceride lipase, putative
MGSCCSCCDASHALKFSKPSRVPPDPELFPRYFQNKQGLWLRFAEWEPPREVPAVRAVLF
LVSGVAEHTARYDPVALTFAREGYHVFCMDNQGAGGSEGKRLHVEHFYDFVDDFLLFKKI
ILSRYPGYAVLPHFLLGHSMGGLIAAHVAFRDPGAWAAVVLSGPALELDPKLTTPLLRRI
APMVSRHFPKLAVRSLDIDLISGNRPVVELAKQDPFRVSVPLTARYGAEMMRAIDDVWKN
MERSTFPLLIVHGSKDLLCAVGGSRRFMELAVSTDKRLIEYEGLMHEVLTEVTWRRVLSD
IQGFLDGHCLSR*
>TCRU_66 hypothetical protein, conserved
MQRGSGRTARRLQQHAVKHHRARQQVHTAANVHRRPARLQRPQHSVAHTQLRLQQRRRMQ
HKRRRHRIRQPAQLGVAHRSRRHNRRVTDRHVRVCRQVVHKHKRAVAAGQPAHAHLQAPV
TRRLAAVAPHVDLRTAVAHAVPQFDAQRAGKHRRHVEHHSHAVRDVHAVHQHRIHSAANR
DGSVHRAAPQSQHHRMHRGHPRSSSNQRQHNEQRHTHSRNGPALHTVPAARTRTHRRPHP
PTQTSTNKAIVVCRTRPVDHNSCLANPFLQIANPVTRFRQIVILILLILILQVIPNALKR
*
>TCRU_67 hypothetical protein, conserved
MSMAKPRRKVLDTICSTLPPATTTSSNTHAALPYSVLGALHELFCMENTEPPPTRRSDAR
AYITCICELTAQLSMKKTLDRFTPRPRSTRIAAHEPPPHTSVDRVMTSRVDRSRTPSRAS
VGPYRDPAWPVVVGTYCDLPTVARSVEFASSTLECSGIAPRSTIVPSSEVTFVMLTRAWG
IRRAVLSLRPPIRSCAPPTSTQWRSVTFSASANASIERRSTATVIGPLNTTESKHAVARP
PPTVTDSVSITPLTQSSAPPPLPPGLATGTSNGRHASPTPPSRQPHTQSENDAVSASKHA
SAAAQPSHGTTLTEDRPAKR*
>TCRU_68 hypothetical protein, conserved
MALKNQLTRIQHRGDHVHVHACTTPLDRQAHEDALQQCDVECLLWCVKIRQVQHNRGSEG
HVDKAQTTHTGIRNVHGADAATVHAADLRVLRVGGRKRPKAVRNRSWQTRVTIAASSTYA
LTAADAARPRCEAHGAHGARAAVQHHHGCSNIEVDSVIRHRRAPCRVAHAVDDRVRVGWW
*
>TCRU_69 hypothetical protein, conserved
MQHNRALQRRHIRHVDEGVRHQARRALAEATNPQLRATRKHAVAQRHVQRVSERIHQAQV
HRHSDRPAEHHRVKARRRTPAANRHRLRQRHATHAVLRTTTAAGPRNRHVERQARVAHAA
GTAAAHAVGERRRQRIKARQRSRTAVARHHAHGGQAGHAVVAAALQHPAAGTVALHRHGT
ARDRRPGDKRRAGGRAVHNRHGAAAQRHPRQRCHRRRLAHRPHVAQLHPPADTDRPTVAA
HQRGRSRPLDAHEAQHRINHRETLAKHKATAAAHNRHARHGEHRVAPQTETRRGRHMHRG
RGRTARRLQRHAVKHHRAQQQVHAAANVHRRPARLQRPQHSVAHTQLRLQQRHRVQHKRR
RHRVRQPAQLGVAHRPRRHNRRVTDRHVRVCRQVVHKHERAVVAGQPAHAHLQVPVTRRL
AAVAPHVELRTAVAHAVPQFDAQRAGKLRRHVEHHSHAVRDGHAVHQHRVYGAANRDGSV
HRAAPQSQHHSMHRGHPHSSSSNQRQHNKQRHTHSRNGPVPHTVPAVRTRTHRRPHPPSQ
TRTNRAVVACRTRPVDHNSCLANPFLQLANPTTLFRQIVIPLLNLILQVTPNTLKR*
>TCRU_70 Trans-sialidase of Trypanosoma hydrophobic C-terminal,

putative
MPPAGKPSEAPGEQATLQQPPEERETQENTTVGESASTQQVPANRSQGSVGSAAALNSHA
VGGATGDGGTVRGSGLLPSLLPLLLGLWGFAAL*
>TCRU_71 hypothetical protein, conserved
MEIELSDDTAQATRISGRSVSFPDVTCKAYFVSPTVRPPVYMDSDHHLQSHTAGTEDGIP
RLAGMLPQRKHVAFVLRDADWNASTSACGTPLASVTTWLGMRKYTIPCGCRDRPEESRRT
EWSRPSVLQRQPAPS*
>TCRU_72 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MGVRESTSLQEEVPPHPGTEVIPKADVERPIHEEEATSPEGATERQTQETTAPLVENEDS
EDVGTASGNTSTLPGETKIPSGSNATAPSGTGILLENGHFEELAGMALFAESTMHGCVSR
VLLLMLLGLWGTAALC*
>TCRU_73 Protein of unknown function (DUF1253), putative
MGKAGGFFKRLKAKQKRSASRRRRGTKGASKEERRVKHNERVDYYAAKREAEALAAISSS
SSDDDNDAVLSDSEMEARRQEHALLRLRRLIGVAGGSKRSRMDDSTNKPNGNGHNSRKYQ
DDKCTDATEMAEQLSEDDDWKAYLSEEDEEEQEEEEEDETDGDEEMSLDEMPGDDGDDDE
YEPEEEEEEEGEDAEKEDEYEDDESVVDYSDDDDDVEKEGGKQRQQRMEEAVQLLPQFRP
GTTGVTALRHVVTANDPWFVKYHQDKHGGIDKTPMQSREEHWRQQQAAGDGKMEDVSRVA
NIAVAASAHAVRHFLHPPFVFGKKQQQKPPYMHETLWAKWLEYCAAESRNPMTAEERGLL
DLLQGYPDVMDCCRSWENADARREIFILHALNHWFKARSVVLAHDALLQERRKNKKGRQK
KRKIQSSKKNRGEKEQEEGDDDADVDQDEEEYEFRDRGFGKTRVLIMLPMRNIAHRYVTT
LVKLLRATPDECAKLSTFNEDFTELAEAVDPTFKRRPRDYQRQFAGNIDDSFCVGVRLEP
SRVRVYAHPLNSDLIICSPLGLRRRLERSGDVLVSLASIEVCIVDEAHVLLMQNWQHMTE
VLRLLNKRPKDTTHGLSDLRRVYAWALAGHSGRHRQTIMSTNLTNATLLATFRSCVNNSG
RVLLQHREEAGVLAQVMVPVRQHFLRFDPGTSLEKCDDTRFDFFTREVYAKKISPLVERD
VRTIIFVPSYFDFVRLRNYMIREHRDSFAAICEYTSLQHQRKALGQFTDLERPLLLVTER
FYFFKRYFVKLAEVMVFYSPPLFPAFYTSLVGRLVATSPNAFALTLFCRFDTHELHRIIG
TRRTRQLLEREADAFSFVTN*
>TCRU_74 hypothetical protein, conserved
MSEERLDSLFDTALEAVAELERRRSLLHSLLQAAHFLYSDVQWEMDRAGLVLGLAAVPAL
EGAVCPQLGVAWRAKSTEEMDKEGGEGSHDRYELSVVKMAAGEGKDPARWFASVPSKRLR
ACQQQFREVLNACVQVVQAQERALAAAENYRVAAL*
>TCRU_75 hypothetical protein, conserved
MLSLTRSFRRRIVNPSVRESTIAGAGNQVLELQKQLEADRAQLREREFNMGRLTAQLQER
EARNNAQQPARDAETAGRDEASATQHAANDGVTTIPHQTDILMAGGEPSSAARRSSAAYR
RPHGNVGRPHFHPSTPLPSRTSPLDAQLPMEEDRSFCALDVTTWDPRAYGMRAPPESLST
SGAHTNAGNRTTSRLNLPLTIWSSGSARWKTGRIPLIES*
>TCRU_76 hypothetical protein, conserved
MQVWRLVERSSFPPSSSGKAREGSRRIPTADARLLNEAGIIEDASSTITGGWIIPFSVVE
EKTTGSRRRWIAWPRDKSRDDPYEANVPLLHISHYLPPVMAEAASCLDLKASFIVSLPRE
TRHPFRCRVEDGTLAELTRLPVGYKAGPEILQIIITSAIAVVTTVAHRLWAAPPLVRADV
WIDNIRIAGSKSDVTLWEAQVLRNADSCRASMGEDRESGATQYTFLGVHFDHTQRAVSLS
ERFVCSVRAMPALNSSTIAEMEATVSRFLYLAAILGTRLCDCYFFIKAVRRRLSALHRGI
VLETSPANLPPSAVGLDERLQHIIENIIVGESSSPRKGICRHHHERIAPWMGSRFHSRLR
RR*
>TCRU_77 hypothetical protein, conserved
MVAPLMLDLMDFRRMMCNISVPIRLLVLVQNGREAMLSLCLQELGRVYGWSGRLIVSRHP
ENIGYSAAVNIGLRLALSLPREEVPFVFVTNSDVKFLPDLLPNLLRDVHEMTRHGAARMD
ELAVEAANEPSEYSFVLRRGLRVLRSTVNDNRLSTSALLPDRIRYASAKEREKAFSKHYG
HFCAYCKSSCFVSVMLTRLAISTVGYFDENFYPAYVEDVDYSLRLRLLGFRGRNVLYGKF
VHRGSSNIRLSEQLELPDALWYRRVKSLMTNQPYAVMKWNGLKACCDGCKGPYDGMVPLD
VWVKDEARIQRIRVYGHDEEQGVPKVDYDRTLLYPVRTKGR*
>TCRU_78 BNR repeat-like domain containing protein, putative
MDILTSDISLLCMQHGDTAANNFGTTELLRPTTLVLGDSVYVLLGNYSHTGPQVGGTNER

GLLLLKGTLTDEGGRKKIKWNETHVVEPQGRGDSRSLTELVGGGGSGAVLRDGTLVFPMQ
AKDKDGTSVLLSMRLSNSENKWKLSSETPGNGCRDPTLVKWEEKKDDERLFMMAHCAGDY
YDVYMSTPHGVNWYTSGQPITRVWGNSHNRKGTASRADPPPQSLREGR*
>TCRU_79 Protein of unknown function (DUF3676)/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MSSGSYAEEMPEEEGEADGRSGGSTSSVGASSDMDTATETVDSERQLQQSTELSAENEGL
RSTGTGTTGAEQSLGLEAGDRNSERTMGSDSSLTPSGIDAEPTFAEDTDDVSRTEGTEVS
FEDGKEVPQTVDTKPENTNTTPGGEGIPSTKGAARHSDNDTFTGEIAELLSMGLSRDSTV
HVCVFRVLLLLLLPGLWGIVAL*
>TCRU_80 hypothetical protein, conserved
MQHDRALQRRHIRHVDESVRHQARRALAEAANPQLRAARKHAVAQRHVQRVSERVHQAQV
HRHDDRPAEHHRVEARRRTPAANRHRLRQRHATHAARRTATTATGPRRRHVERQTRLAHT
AGTAAAHAVGERRRQRIKARQRGRTAVARHHAHRGQAGHAVVAAALQHPAAGTVALHRHD
AARDRRHGDKRRASGSAARNRHGTAAQRHPRQRRHRRRLAHRPHAVQVQPPAGTDRPTVA
AHQRRRDRPLDAHEAQHRIKHRETLSKHNAAAAAHNRHTRHGEHRVAPQTENRRGRHTHR
GRGRTARRLQRHAVKHHRARQQVHVAANVHRRPARLQRPQHSVAHTQLRLQQRRRVQHKR
RRHRVRQSAQLRVAHRPRRHNRRVTDRHVRVCRQVVRKHKRAVAPGQPAHAHLQAPVTRR
LAAVAPHVDLRTAVAHAVPQLNAQRAGKHHLHVEHHSHAVRDVHAVQQHRVHGVANRDGS
VHRAAPQSQHHRMHRGHPRRRRNQRQHDEQRHTNSRNGTVPHTVPAARTRTHRTPHPPTQ
TRISRAVVVCRSRPVDHSSRLINPFLQMANPDTRFRQIVIPIILILILRVIPNTLKR*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MFHYSLITTVNVDGSSVVTLTGCTMGSTGLSVPLLSQAAAGYRFVAGCLTVAGREVTTAA
ELALNGITNVTTVAACGECTKEGDCFAPLTTAVIDCNCRCAAGGHGDVCVPAPVPAGPPP
PPLRPPPTPSPPPVGECISDMVYPEVAQAVGGGLSWLCYRNVTFSGGGMSLKVLVGAMTG
DVANVTFDECTWRDGAVLLLLGNAYAAVGSLNIFVTGNRFSDALLSPEGVFPPHTNITIS
GNRFTLTWLVPRSGLDIRRPSCVAMNGLVISNDSAVVLSGNVFQSVTTSSSAIRVSRSAL
RVSWHSVFAVVGNTFHMAGGDGTLIHLEGPRYSSSLSVLNNSAVVIRGNLVTRPMKCFVL
FIRTLDVESFSAVVFQGNDMQRSSVVFISGDSSNIYYNSWLQLSGNLCRESPSEAFAFLY
PKVNLRDSTVSVSGNQFVSSSVTPTVLRIPQSSRDLTNGAIVAACNTVNGEEGAYYAIPS
VYNATIMTCSDPCTLAASCFPAYTTTVSSEGSACRCAEGGHGDACLPVAVPEPPGTDGTD
LCVRDVRVEVEVNVSFGTSVACYVGVTFAADVVVDVESMSGSVRNVTLVNCLLVGGASLY
VVGWRSDPPAGERADVLISGLESCSGGGVLVANRFPPGSRVTVVDSVLIAEARVAYRGAY
GLGDASACLVLHNVNLTGSVLTIARTHVAAVFRDAVGVLFVGGVALSSRGALYVDELLVQ
TALGLCVSVEGGVAASGGSVVAFVDSDFLLCKHAVSVRGAVSVSGSAVAFVRSEFLSTED
YAVAFYSTVSLDGGSMLLAKGNVHDGASREMLYAAGAVTAAGSTLSFVRNRALLPRMLSL
SLSLAAGAHVRVACNDAGDRVLSTAEEYAAAGFGDAGSIDVAGCDACDRDTHCYAPGTAS
ASMRNGVCACLCGSGGHGEACVPVGAPALPPAVGTASSVFVREGVTVRSVFVVPAGASEV
TLRHVVLDGVSPVLYVPWMARDGVRIVVQNVSLLNGAVLYVMGGGALRGAVSAGSDEGGP
VELSVCNVEALNGALVLTGTFPAGSVLTVTDSLLVAARPTPLVYLPGSQSSPYAPVLVLS
GLRLVRSVLIVSGVALVTVMTGGRTVVVDGAVLELVGGGVALDAAVFGGEYALYASARVV
ASWGAVLRVSGSQVYAAHGLVFGSGVEANASAVVVNDNAGALTDGALLVLRGSASFASGS
WLSVRGNSISGRLLSVPPYPRRAELVQSTLTLHGNAGSGPVVMDGTVALGGAGRKFVVGC
LTLNGQALQPMDYRSAGIIGEFRPVACGVCDADVRCFAAATRTMSGSCGCRCADGGYGRD
CLPVYLPHVDGCNRTPAPPPLSHTATLTETRSPTTTWTATPTPSLSTAHYSPPWYGPTET
LQVTETVALPPTRTPTASVSSTLWWSDVACPTLAVTTTSAGGSLTQNDIRGGGSAVPTRL
MVALPPPFRWARDPQLGTHLSFVPVSTAQPSGFGGPWGAMLSNATWVRNATNPSTVLELA
VPVHRGYFIAADETIVIRCDAAAVSGGCKGVLLGSFTIRSDTLPAAASALSAITGVVACA
TAVAVVVTGGLGSVLEMQALGVFARMSCASAQERASTVALPYFLSVFAALDPLWMVVGNA
LLAAAFGCVHCGVTAAFQRWRGVDAASAWAAMRFPSLTYVVAHAMHLGIFFGSVLALAMP
GARVLHRVIGVVGVLYGVVFPAGVCYLIARHAGASFTRYWQFSRKPLHERLLYPVGYWHP
AAQQRMYGGMLTNVRGSRVYWCVFQLSVLCVVGLIAAVHPPVGGCHVQYFCMAAVLPAGA
GVVAFTNMMRSSFLTVMHAASFVLLAALCVVSAANHLAPSDGGARAYAAIVLLLATVVLA
VTVYSMVVWYAEDRHWQELREPRRGGLEALLRDGEESDEETQKPHEVTTFSYVSGATAAS

SYRPPAPP*
>TCRU_82 Mucin-like glycoprotein, putative
MPVQEGEKKGTTEDENDTTAPKSQSKGSTVEQGEADVGGGKSLTAPKRQSGDVIDTVHEE
DGSTTGPQSRTTKSAEQTDRETKDAAATTTTTTTTEAPSTTTTEAPAVSTTRAPSRLREI
DGSLSSSAWMCAPLVLAASALAYTTVG*
>TCRU_83 hypothetical protein, conserved
MLAFALSPAVISAPCIEADPFTVEFTQQLSSGCAAGPALALSHVFQRCLADDLMCVFRAA
ASSFLFVPNKKHFALRWVFICVAVDARDDAQRVCLLFSGHEGDFGVCQQHRGSLRRRIEA
KIREVCPLHLSRQLRGAPDAQSEWMDAAQLGRPVVFSALRCQGNRESTASLPAAFYCWGS
TVLKLPV*
>TCRU_84 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MSRRVITSAVLLLLVMMCCGTGGAAQAAEPTIPEAPVPKSSFGWRDTTGDETVSSLRGPS
LVEVNGKVFAVAEAQCKNGETTVLTGIASRLLTMEKGNEPKDVLKEAKVKTQVLEEGGSG
KGKKKVDVSRPTTVVEGSDIHMLVGKHSHEDLANCQVTTETINSGILLVKGEVVEDGNKV
NWNDTDGVPCTLGPKHESLSQLIVGGGSGLKLKDGTLVFPVEATKKKNEEDKDVKAVSLI
IYSLKDATNWTLSKGMSDDGCSDPSVVEWEKDKLMMMTACDDGRRRVYESGDKGESWTEA
LGTLSRVWASKQKGKVEIVGSGFITAALGDGDDKRNVMLVTLPVYSKEEGNGKGVLHLWL
TDNTHIVDIGSVSGKEDDVAASSLLYKSGDNEKELIALYEKKGGEQPSPGMVSVRLTEQL
QRVKEVLTTWKKVDDRVSKLCPTENAEHDSSTDDACSTTDKITAGLVGFLSGNFSDGTWR
DEYLGVNATVNENVGAEPADNGVKFTGHGAGAEWPVGKQGDNQLYHFANYNFTLVATVSI
DEALKSGSHITLIGAKMDDNEKSVLVGLSYNNKEKKWILLCDGGENKEHSSHLETENSEH
VVILLRNGNQGSVYVDGQRVGDAQLDLKDIKDKKISHFYIGGDEGSAEGQEGQEGVSVTV
SNVLLYNRPWTSEEIAGLAKNKITISKPEGPKTSMDTQSSATSGSPVQGAVSLSNSARQL
PSEQETLKENIGADGVSGAASVTTPSADANTPASNGEGKVEPAVKKEMSVSSGEDAETVG
GTDVQEGIHPQAGEVNATALNSSLGHLSQGNNSDGGTVRGSGLLPSLLLLLGLWGFAAL*
>TCRU_85 hypothetical protein, conserved
MALPGWVRRFEVYAICMVWPIATIVGLVSTYKVFMWSYGGRDCFRYVAIQEPFKEQWYQA
NPKTAIGLDTPLAHVPKYLSTPGHSTGGEEHLHHRNY*
>TCRU_86 aminopeptidase, putative
MSTAYKRQRTKSAYEEHNVSAFVESCIHFRTNLTFHTAAEGMQLANEALQNHPQEPNIVL
LLGNQKQLQEKKALSTFFPYYSKAVESAINVAASGKNYLAEITPHARVLVGMVSSKASRH
NCPLRPDMISTLVKDAVHQARTGDCEKSVLRSVDIYCCESQNVLCVATAIARAANRSFSA
KRGRAEEGYWERGLPVRVVFAANTTKPGAAVDGDGFACGSRRALEVAVTVVQLCQRLVDA
PTNLLDTITFTEIAAGHVEKLKGEGRDVSIGIIAGEELREKGYGGMYGVGKAAEFPPHLV
TLSYQPSNGIKPQEKLAFVGKGIVYDTGGLSIKTLGGMCAMKHDMGGAAAVFCGFLGLAM
IEAPQQVSTVLCLADNAVGPRSQRNDDIIRMKSGHTVEINNTDAEGRLVLGDGVYHASAL
LPYTPDIIVDMGTLTGTQGVATGRFHAALYANNEEIENRLLKASRICGDLCFPILHCPEF
HSLEFNSSVADSRNSVTNRGNASSSCAAYFIGTHIDPKYQGSWAHIDMAAPVSRDEATGF
GVTLLLQTFAMSIYNPA*
>TCRU_87 Unc104-like kinesin, putative
MPQSAQSEEGRITVCVRARPLNEREKRLKSPSCLTFHEGKKVQIFRKGFAADGVEGLDES
FVGKVFAFDHAYDTDVPQSSLYEDLGLPVLDSSFKGFNTCIFAYGQTGSGKSYSMMGPSG
GRDVFVDPGIIPRLSKGLFAMLRERQAKNQSDREAARANAVEEHALPPEVNVIVLVSYLE
IYQERVNCLLNSKLDNLKVREHPVLGVYVEGLREVKVSSEEEIMQIMERGNQCRHTAATK
MNDRSSRSHAIFAISLIQERKSITKDGKVTSTMLRAKINLVDLAGSERAKSTGAEGDTLR
EGANINRSLTVLGQVISALAQASKQKSDAAGLKHVPYRDSTLTFILKESLGGNSKTFMLS
TLSPAAANYDETLSTLRYADRAKAIVTRAVINESAGDKKIRELEDEVRLLREKMRHYEEM
IARGEVMSQMSISGSPQLRDKIGKDGESKAIVEDDMVYANAKTPRQAGDAAVLERELHRA
ENLVQNLVANKGISLESFIMPAFHRNTSTIRVNGNDPFILNLDGAGDWVVEYIVARITYL
GVEASATGNDARYIVVSGSQTAGIAPQHCCFVRQDGGQVLLRPLGGNRTYIDDDPDPVDG
DTPMKSGTVLCLGDEYVQFKFIDPSAPQSAVRRRTVRNSESIPMQSLSIDAKSSSSNSNH
SLKSSPLLTGAGSGNAGHPPVPALKLKEALQRMQSNSARTKKAHRDPMTPTGTSLTSAPH

GISVVGITPRTTRTAGKVVISPSDELTVIYRHTFLFLGACNSGKSALRENLQKPDRWYSM
FANDKLHVRPTFGVDSSLIETFAGNQPVQMNLMELSGNRCFSFFESLLPTRHVSYVLCFS
LRELPTLETLQPLLEFILCRTFNRDATVILIGTHLDEISLDEIKLAHLFAIIETEINNYF
FLVQAIPEKRPSILGRFAVDNIGRVVVSPGFSKFKKFPELLSWFSDQALQRCRNDVEFPN
AQVPLRAVALSKKIREINREGQWYLTSANYKAIAKAVDARYGLSRHDLHRHTQLLVGWGV
LHHHFRHLTMKKYVVIDVQWVFRVVAVLACCTYSRGYGTENNSLLQPLPLLFCRKTMEDM
QNVIPFDVKTVMASDLCCVFNQGVVSMKTAMSLFRGVLGEKGLDSCHLTSILELLRGYDL
IIMGSRLKFSSFMGELRENKSHGMMDTSVLRGNDPVENDDDVDDEEEEEEEEEETAGASV
LSSEFFMLIPACFTCQPPSAFNLHLPSFLFGPFYRFTLNIVPHNFFARVMSRVAHFAEKI
YIGPVSARLVPVENLVSVDCSNITIRGSICHAFGDHDSRNVSVGTMEGRRAGTSQEKTSM
VGKSHFWGSTAWIISSARSRALIRMVHHSLLITFHDLDDDEEFYNGLRHVVRNLVYESPG
VKCEESILCSRDFMEEGEKASEVHGDKVYWHDVDENLNSLEKIRQREQFALMTARSSTSR
TLSGGAEGRSNIDALMEEEDDNMVIPFVRNRTECVDVEASVRRVCEDSLLTDDVLHGVRE
ALHAMNKARRRGSGAGQCRAMDRLVDVLAQA*
>TCRU_88 hypothetical protein, conserved
MNVAQFLTGRVEELAAFSALLFRKRPRHENERAFSRTARSVVHYRRPSSANVPLSDVMRL
ANFRSRRSKRFVRLLAAEEPPPATPKTVEEEKGRVQKKKRPLTYRAWCLLLRRRRRFLLR
RRATTRRRIRRRIIALRYGKTQLPLCSCGPPAAAPQPSLPQCLSTQAFSSGGGRTAVLWL
PTHWRFCRRFHYSVLKTRINGCSSSPDDDFSSRLVTVRIAVPTTSQRKQHRVLQRWAARL
PSCCALGKPPRRLKSKPMAVPPPLCFAAERSHMCVWAIQPRENGHPLTTEEVMNILMIQT
CKAPPVTLHTRDLATMAETPVNSLPYETCWRRTESGVFYGYMWSLGKAISKAKWLLRGGV
ELFDTDTTPIVVPVILLRNEDVDGGTYHLVAPTPVHIGARARRGLEMRLVSHWNPCGAPK
PMCSMFELWCCADAVSVKGADMSSTRDGSFILEWIRGRVHATVGRWCRVNKISSFAQQEG
YETNNNSSSLIKRTTVCVFPSIPPNLETIDHTSFPVHRCVMSILVFSKESFPQLDTTGSA
VRRDRMCHFQFARKLFASLTDATATAWRTMRHDDEKIAWAFRLCQSLGYRRNVRIIGEEE
RETLLSLIGCPAFTDVSGKNASFQISRMARLRCSPSNAHQRVLLKFAARGGREHQREGSA
LFVLKPGSPAGLFHVGAVTSAPFFSMRFGTRMAYAWVWDDAGWELVKYYTRFSLRNVFRE
GTEVFHEGPKRGGATEHSGAGSGSNICFFLAAAEKVSFLVPFLKNSPIRIPGCSASSCPV
EGEVSRQRWHHRHGTKRLRTGDPVVSAKMKSWRAMETMLCDGDTCLPVEVVLLGTAGARR
VGLSSRHSCDSDVTRTTTV*
>TCRU_89 hypothetical protein, conserved
MEAGHLLLWARCRRFVGDVCAGRDATHGLAHMETVTGNALLILHMEHGAASCPSLTISRV
ILVAMLHDVADHKYDAAGRLIQQVREFLGAEKGAITAAGMDGEEAFSHALTTIEAISFSK
EKKQCMRWFEAKLPSDWVFVRDVVSDADKLEAIGEEGLRRCLVYTMHTLLIREGRQGWDA
VLQQRCLQGVKEHFVEKLSRLSKEFIVTTAGKFLAAPRHAAMERALQEWESQGLPSFF*
>TCRU_90 SET domain containing protein, putative
MEDASCLVLRWAKRLEGACGDSGNSVNGGQTRGLGQQRQAQTQAAVAEAASVGMALLKLL
LQMEQKEDEMADDDKDAKEGTETALPHQRLTQLLVEVVLAILDSCIQWTGTKNAVQAVCC
ELMAASSREKGQEDLAEKLCDWWDHEEVAEQAWRWCEAHLTLLPADEAAWRYGASHGVAT
PTDWWWRPDAMTSANSNSLSETTAAAARSLFQEVYATVSQQCIAESPRTELATAKELLHN
LFTLPASFFFYRIAVSRGVLQRLFTMKATALLHQAHLLTCLAFLKNAAQPRYTEKSRKTS
GGGSSHELLWVSRECLSLAWKNLISSITAVQVATIHFGASCGGLRQQVRRALFGVKEVAS
ETDGTFSSCEDFFYVHPSVEPSENACRVTHGVGLVATGKISEGSVMLQERSLLFHSSPDQ
TAAKTEMQNNEMSTVTGAALELFRRGGMTFISDAVTSQVVESLQSGAFFGEPTQAGEMWN
ALHLIATMQPADRNSIGTEDGFARDIADLVRCWTERAIPFCPVEEFRIELEGAPGEGKGL
YPFAGFINHSCSPNALFVFGEEEGACCSSRGGVLRVVALCDIEPGEEITVTYLSSLLLSR
ELKRERNGFYCCCTFCLSYAALLEGVVCPTCQQLVYDDHNDKEEVSSKAVDVVSSVRANN
TANGRVKPYAHLPGCAYAGYSSYKDLAGPMKSGFKKIIDNIHCELLGKSITDAVHEHGNC
MQEGFGAGETEKYKEEEDDDDKKYAQRAQKAVRQLMDLDTLVSGLPSTHHYRLQARMECL
ATSLNAIMTPNDVTRLMQLCEKLLEDLEVLLPRNYPLLTGIRLHYALARSRYLIATTDIN
DPAADGYPEGCCGSVREQAEMMRLPFMRDAIIRECVVRSFQEHYVYTGWRFAEANDEEIL
QSFLRRYEAELFACGVEELSHFNMLSLMFDAAEGGSG*
>TCRU_91 hypothetical protein
MEVIGTLSAAVALSKTTNTLNPATESSGSYVLASISHLRSDFVRPNGLRVCVHSGEMLMR

THILSDPTPHLEKRQQEEEGSDHQTHQGEGSGAMPNGEVFGRLLSRVGSGSDMSNLGSRH
EVTSAVFSWRWLVERNDVAPFNHELKSTISSGKRTDDRILTPPGPIHTPRCAGSGRMDDE
ALIAIDMLRDWGEKEKEELFLRHPRLEAYATRELHTPLSAVLTGFPLAGTSMNDRNARPV
AMLAPLPNLPSQGMTTTNKRHALASHPSSTDLGLLLNPRVSTERNYTPQLGKLLSGFAQE
GRQVPLEVASVSHTDDIPEEDDLLSRGLCGRGDPILGDRGRVWPWRKGGRIDKRSLPLND
VLLECHFFGVTDILEVLRYDCEGDGSDDVLLTNFQDNSELSRSVIGRVVALADRSLRRHA
GEDEYGEISTNTDVHFSTAGMQERRNDALQASRILVDSYQSAEDELGYVVDLWRMAAECA
EPSSSLTPSTETEVIT*
>TCRU_92 SEP domain containing protein, putative
MPKNEDDEVATLIAFMPWLQREEALKLLKNYGGDAESVMRFLEEAASSQGEPQASPSPAD
QRKKTGAKKAEGKKMTEKYFVGGGSSSGQEVIGGDGGVDNVIESLFDKARQQLGEEGAEA
QFFFGRGRRLGHTTSESPFIESTLKPRREIVLTVYRDSYRVDDGPRMPKESEEGMAFFKA
LEAGVVPEGIAAIYPNTSISVRLVDCTQQDAPPTFLPFAGEGHRLDSNTSTTAPAASSVA
KTGADATPVNMSDNFELHEDEEVTKLAIVNLIGERKEFRVNPNRHTVGDVFFLAARHAQP
GALAFQLIARDVPPRPLTDRSLTIDVANLRNATVIMRRT*
>TCRU_93 carnitine O-palmitoyltransferase II, putative
MLRRSFVLCIATAPIAVPKDIHDWSRLRQYLEGFTVGACTDTGVLDASIIPTRHLQRSLF
RLPIPKLKSTCSRYLDAVKPLVTPKQFDTTSKIVKDFESGEGLSLHEELVRTDKANKHTS
YISADWFDLYLLDRKPLPVNTNPCLITRRDPDKGDMLTRATFWITSSVAFYRMYLENTLK
PDIFNFGSRDHYSRKDWFERTVALSPRSISAKVCVFGSNFHAFPLDMSQYANLMNSTRIP
GLIKDEVRGFGFAPHIIVQFRGHQYVVTVADSECRPLPEEQIYARLKAIIDLNPMPPRVD
IGVFTSTDRTTWHSVRTEMLRDSENQKSFELLDSAMFVLNLDDDVEVDFLTSRGAVETIR
VMLVRNVNRWWDKSLSVIVTKDGFLGINFEHSWGDGVAVLRYTQDVFNHSIMRSRRSMRH
DAAPTEGVRQLKWCLTPKLEQEGAKAKRRIDADIRRMDCCSCLVNEIGSSDPVFRKGPIK
VDPFLQLAMQLAWWRLYKSTVSTYESASTAAYLHGRTECIRSATIESQAFTILMDNPRAT
TNEKFEALLKAAKKHLQISKNAKMGEGLDRHLFALQNVALRRNPNSIPDLFLDPSYKTLG
SNMMSTSTLRSDALVGGGFGPVSPGYGIGYASERKCLCFNVSCWKEFGPRYSADEFTHAL
YSAVVDMYNIMLSVKQNE*
>TCRU_94 hypothetical protein, conserved
MAPKKKNASAAAAAKEETEECAPAEVTTTTPPTSPQTESLPSACNAVELYATLQAAVSED
PVKLNDFVRELLQALSDAECPDAPLLVRVRTLEFISKYGQHVRDGNALKKIVTSLVKILS
GSEDTPQLLVAAVQGLSSLGPVSVLDKKWEYLSREGADVLMQVMLDEEGFAESVRQAASK
ALDSLIQTAFRPVVTKLLHWISDNRETEDEDQLKKERRMALTRLRKLAHTPSLQCQWTEE
VQEHVLSLIVRVLPTVTVQEFVQLTSIAASLPIVRAEAGVPFLKAFLAQNAINTDRVLES
LSIIGEHIGATPYDIVPVLEDAGLLTTPVEKNTARGMWHAKVLLLAARLATPDNIDKLYN
AVLEQLAHVMHDGSALPENMTTLEVLLFAVMAAGQKKPVEMLKYLNDDAFVAKCMGLAEL
VAQMEPLLIYAVKKRMQKSSAGQKDAEVIGCCHNVRVILSAFSAKHMPTGTLTESWLHKN
KLPSVKHARDPAATAKATETTAGIAGAAAGQLGVLPPPPGTEEHAKKRSRGQESGYNKNV
NRNKGGWNGNGRYKRARRGGVY*
>TCRU_95 hypothetical protein
MVRHHKRKPIGVVAKCQTLLKGPPKMLQKAANAFIPQISWHVMRFSHIPTGVIDKMQAQL
ARGGVNLWLKLRTKSWKFNGHDIRQSRRILLVQALLVIFERWLLR*
>TCRU_96 cystathionine beta-synthase, putative
MAQNPSAVNNKKEVPDRRTCILDTVLDAIGSTPCIRLNHVPKKHGVCCDVVAKCEFLNPG
GSVKDRIARQMILDAEASGRLRPNQTIIEATSGNTGIGLSLVAAVKKYPMIITMPKKMSH
EKEVTLQALGAEVIRTETALPWDHPDSLIGMARRLEKEKGYVLLDQYRNPSNPKAHYEGT
AQEIYDQCGGKVDMAVFTTGTGGTMAGVARRLKELLPNIVIVGVDPYGSILADPSVPLDP
KPYLVEGIGYDFVPDVCERKYVDRWVKSADKESFALASEVHREEALLVGGSSGAAMWGVL
QAAKDLRPDQRCVVVFPDGIRNYMTKFPDKNWLVENGLEEGEVTRPTYGSLEAQLEEAKK
KLSEYEAKCGGSVEEGKRCCEKAK*
>TCRU_97 zinc finger protein family member, putative
MWRNAECPAADEGSVLLQKIFPPADGVATAKRKRKKKRRRVLYDQYLADSGSECSTGSSE
GGGEVLNAYEFEEFEPGMDINVLIQQTVQNVAQSVSLEDYDGLSQFGDYDLICFAAAVKH
NSSILSLQIRYLDVSDVSLVPLCRALEGHPCIRALDLSGTRGGNATIKAVFRLVCTNPNI

LFVRLDDTMVASHDAGEIELATRYNALGCPDPTNNPFHLGLLRKIGDMEEEKQKYKEQLS
AHSWLFSDHTGGAANQATKRTKKFLFAEKVAKSRIGADVCAQFMSGRCNYGSRCRYIHPD
KTAALQNAITLSQYKISKELEGDVNSLRTCAALLSSGSKMRLQSRLRPAKFALKEHACSR
IVAEPKDVDSCSEVDDFSTPNVVWAHAVWIFSVTVVVCSVVVAVNY*
>TCRU_98 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MSRRVFTSAVLLLLVVMMCCGSGGATATDNGGSTPRTSPEKHFVWRDKNGEETVSSLHVP
SLVEVDGGVFTVAEAQLKEGEGDFFTGIASELLEWTDKESKELDATKLKTQVLEECPAGN
NSCASPKRAREASASQSRTKVRVRRPTTVVNGSRIYMVAGNYSFEVTDRAAGNTAAAAKW
GLLGAVGRVTNDGSSGKKKIYWKDAFVISLTDFEKHESLTRLIGGGGSGVKMKDGTIVFP
VEGTKKDGNAVSLIIYIATEDGKLSKGMTDGGCSDPSVVEWREGKLMMMTACDDGRRRVY
ESGDKGGSWTEALGTLSRVWGNKHKGNEKGVGSGFSTATIDNRDVMLVTLPVYSNRRGNG
KGELHLWLTDNTHIADIGPVSGNDDVTASSLLYKSAGSGDNNNEKLVALYEKKGDGKPSL
GMVSVRLTAQLKRVREVLATWKEVDDRVSKLCPSTAARNPSTGNDCSAGKITDGLVGFLS
KNFSGGTWRDEYLGVNATVKKGTNGVATGYADGVTFRGAWAEWPVGSQGENQLYHFANHN
FTLVATVSVHGGPKGDNPIPLMGATMNDKNTVLLGLSYNKEGKWQVLCGGKTTKELRSNS
EPGTTHQVAIVLRNGEQGSAYVDGQRVGDASCTLKNADSKGISHFYIGGDGGSTGRKEDV
PVTATNVLLYNRPLDDNEIRVLNANKISIPKLTDLRTVAAGATGVGTARHFGANGDGSAV
CGGGLLPLFLLLGLWGIAAS*
>TCRU_99 hypothetical protein, conserved
MNCGGVNFSPDGTIHPPARSGDADRTGIRQLPPPREGRDDTKSGGTTAPQVNAEPSHQNA
DWRQSAAADGPNTVDPSPASNTESNTSETKPELAYV*
>TCRU_100 hypothetical protein, conserved
MDTVLELCAVCAVEDGPAGTLIESVLSFIVQKTARVALPHMSAMERGALTLQLISAGGLQ
HDVCRQFLFKELSPPYSTTAIVRQSHELYIRPAERMARIDDNENTTMLSRRKKCSLPFLS
LLRKSGEMERNQPPVDFHGEDAEQLLAALLQSWNSSNAASLPHSLSLRELPPGLATYLTL
HYPARTLQLLRTTIVGPSVPQTWRDLWRQIFFFAADANAAADTMHMLLSQGACANFWPSA
LRALVHPLTGTVGDTEPEAKLLANFEGPSTFLTHALLCLWLSESRHDYDMGRMEALSGNA
ELRKETSSFLVAPLVSSKSSSFLSMTTDEVHPLWRRTLIHGLRLVEKDEAYGSHEEPQRG
RAAVVQAAYALLLSLYHGHSMASQYVRSALDHPDVTLFVPSFEDLNGELSEGAQWGGDEG
ICSISAFLAALALRIPAAQLYIAERVWRHLETMLAPGEVEARERQTAELDARLRILLNSF
AFSDVPLVVAHGGRGTSVPPVHTTVATLGEGSQKREDGPRLTLRLKRPRADGQIPQTADD
GRKDTVKSKSQTRMVPTSSDISLAASLLRNALIDFATEEIVQPSTLVHSSAPGSTFTATS
DGQLSRNKTRLMLLIPPHMKSFLGCFSAFSSSSPCSLMVCNVCCVIMSVFLYRQCYALQR
WLLHEAKSGLKAAVVGRFVWRVRRWLRFLAPLGVFCYAPVSDVLLPECLREMEKQKEKTV
DDGSGATATAILKELCGVLMSAI*
>TCRU_101 aminopeptidase, putative
MNRPPATDSGASEFVRSCVNFKTNVEFTDVDAYKKTHTAGLASTFVVILGTHAQLREDAL
KELPFYCPAVAEAIQRVKKGETYAVLAEGVKNEANERFVRVLVGEVPSEASRTNCSARPD
VVASLLSAALEEIKGPETKVDVFVRSTAALAIAVAAARSAKRNFTAKEGLAARGYCDNCV
RLTVVFPEAPNPSPSELAVVATSTQLCQRLVDAPTNLLNTATFAEVAQSYAKELGCAVDV
ICGEELRERGYGGIYSVGKCAVEAPRLVTLSYKPKDETRKKVALVGKGIVYDSGGLSLKP
TNFMTGMKRDMGGAAAVFCGFLTAVRLQMPIELSCTLCLAENAIGPDAYRNDDILTLKSG
KTVEVNNTDAEGRLVLGDGVFHATHEISFKPDVLVDMATLTGAQGIATGHRHAGIFVNDE
EEEFSFLKAGRVSGETCFPVLYCPEYHVTEFRSPVADMRNSVKQVNNASVSCAGHFVANH
LSPDFKGKHIHVDMAFPAFENDKATGFGPALLMEYLRNLR*
>TCRU_102 hypothetical protein, conserved
MDRHGFWYAENMEQYLRLKEYCESVRRLPQQIRHFQTDGLPCMPLVVELSRSVNAASVTS
LPAPPSFDEVAPIATMERNRMKLRHRTCLK*
>TCRU_103 conserved protein, unknown function
MGGVPSRDAYPTFFSLRYGSHEIALIPLLRRYFCNENKELRKQFVRMRNDPSVRYNFMRS
PKYSMKELPPASYTEKDLDTFLDVIEETLYDSLKEMVEDEDAPLRPVPCAVCFVYVNGRE
GTDCFLFYGRRINVIGQFGCHRYEDKKDDEPCLYLQKAILKAAGDRTLERVVTLAAMALK

EEFFRAVTTVNREANAKEMFLRRISRLPLVSSTFWNSYPVLKFLYDTAAWSWSVGNVQEH
NDAPSFRFYEVPESGESGLVMEMPGSLLLRFIFWACSSINPSAVRGMWEQYGMDDTAMHK
KEKMIANWLETSPDVNMFVGGVEFTSRVKKHLETLLSEVVRARETPTEDLSVWSAEQECS
HDGKIYRIFDSPLCGPFLTTVKVKRDKKNGTTSGAEGNRSNQTLDPLLNIAEEHKKRDDI
PPVSRVRVGGASQPHATRPPPEYEEAVNSMMPSPFLPSGPSTICPVSLPATVLPHGNVSI
TAPQNSSVMMLPQSLNPASSSFSLPASSASVGPTFIPLYSEPPKPAPLPMQSFGIPYVVL
TPSGPAVPQQNIVPLNSGASTTTTTTSPNLTTMESSKNDGVSGNAGNITTENGATSTLFP
SIPSTPFVPTGATFTGVLNGPMGLQSRSVQPIGNYVLLPDGNIGVLNSVPVTPINYWNT*
>TCRU_104 conserved protein, unknown function
MGAFPSHDTPELFYTTFVPRPSTETQVEVCLVPLLPRFFNDTHKKAKRKLNDILSRRGND
PPPAAATPSGTTTPGSATASANSRRTETTSGGPIVDCIIASNDPFFLVKVKDAIISSDAL
LGNKPHIKKKLTTPDLPSASAAGSATEMNTSHHHQQQSTSHSSPVPLLRPVPFAVCILDP
INPSNESSSATSKSHSHLNRAQQNIAANSGNVLIIKGHRLQIVGFISCCLGRPVHLINPA
TFTKTQALGGGGSSAYSSHTGIGDSKKPSIPVVLDVIFDDVEAHGYLTESVVLLASLAFR
KQFVNSSALYYPAEDRDVEASFDYYMERLQLRIILQHNNYRELRMFYSQYALLDMIKELR
MHETAPPHFSMYENHLGEYGLEVTFSNKFLGLWLRYVENKMRVDSVKGQHIRCNTIDFLQ
ERQRLMQERHDSGAFLEEEEEDERLYGGSLLASTLKQWLLKGSQSALQQQAQLAAAQQMI
MYPPTSGTATTAANFWSHMPTMFMGAPPGWPTNVMPFNAAATSIPLMPGQQQQFMFPGSR
PQLQYASPQTTLPGASPFSSPPGLHVLSPATSSYGVAAARGVPPQQILYVLPGGPIAQSS
AMPHAPTATAAYPPGAAPPMYFAQPPTYGVPYSSYMFSQPPATAPAPPE*
>TCRU_105 Overproducer of inositol protein 10 homolog, putative
MAVAPNVLPPFAAILPGLPLVTEFNCLDGVRWIAPLGNAPESIVVFLTSPAPLAPGICLG
IYLAREDDGAFLYVGHLSNMRPSTILRVPPVLLNVDFPVRLLIGISQEKEEDVANLGATQ
EQPLQQEQAATRLAMAERIVEDLFNFVMSYGRVLSADPTDAQSEETVYLPASFVSRWRER
VLTKMRKDASFWN*
>TCRU_106 serine/threonine protein phosphatase 2A regulatory
subunit, putative
MTEHFDSVKSMINNLRSEDPEERLTSMRGIHLIASTLGPERTRDELLPYLTDYLDENEVV
LRVFANALGTMLQEVGGADHLQSILTPLELLSSLDEITVRDEAVTSLQTIGGQVFRETGE
AAAQAQRDFLDLVHRLGKATTQCRSSASYLIATAYPHVSTAIKGQLMSLFIELCNDKEIM
VRRAACISLGKHMVHVLGNRSTELINALTAFSQDKFDAVRLQTVEAAAALLKALPYELHA
NVFSSIKALMSDYSWRVRHMAADRLGKLAEAMSPAEVKNILPFFRSLSQDAEAEIRASAV
FSMASLLAVFRDPSAKRELLTAGCRLVNDENAHVRMCLASAVLRSVAHVAKELWATTIVP
TCTQLLKDQEADVRLALVSGFSSMGNTPEAREMAPKLVPVVVALAGDPNWRIREVVISQV
PFLITSLGKNAEDVVELCVQHLVDRVATIREAAVRSCCTLVAENGTAWSRASLFPRLSSM
ASTNNYLHRVALAHFYASLASVQSLDCGTASQHILPMLRLFAQDSVPNVRLNCAKALLAL
KKGRRLLDSDTEPLISRLRKDADVDVRFVASED*
>TCRU_107 rRNA biogenesis protein, putative
MLFRDYRVHHAAPDGIVVQLPGNGGFGRLTVETLGGDLLAEKLLKRLASREQVRAVARRT
RDAQQYRILSIQLRELWSDVATYPPPVATLLPNLFRKNVLIGLGTTTMARVVKASPERGA
VLSIAGGLTALAALEHVDAHAGAVEVRLLNYDVQTGVANVTARTEVVERTPSDVIAMQTI
FSGLQAGDVVPATVLLSLTDDHCAIVEVPCGASSLIGYYVYNWHGTAASGEPPVVGASMQ
LVIEFVPHGSLLQEVLPFLVLSSNRTVFTLPHWRRAPLPPGMKGLLGLFPWRDRKRQHSL
EGKQQQRQQRHPETESDENDSIDDNDGTTDKNGGREQKLRKRKIEEAIDAYERSMETTVP
SSPDEFRRLLLAAPNNSYLWVQWMAHHVALQQQEEARLVAEKALSTIGVRETQERLNVWV
AYMNLENIHGTVESLSAVFKRALQRAPDQLVVYERLADIFSATRKPNQLLALCRNMVSKF
RNEQRTWERLGKVLIDQKKRDQLRRMVKDMGGALRRDAYSLTVVRLAVHEYKSGSVENGR
ALFEGLVVRMPKKSDVWSAYLDQEMALLVRRDESAAVPLVRALLERAVATNFSAKVMQQF
LTRFMSFERAYGSPADVEKVKTRARSYVEAKIHASVGDGADGIVTAVHVSAKNNNGNKTK
KKDSGVTDETDE*
>TCRU_108 hypothetical protein
MNGDGVKTPVDQNTTGDGAVANSKKGTSGQQRKQHPPKRGAEKQRTEDDVRSPVGKGLNT
QDTARTVTSSGLRRLSHKKDVKRSCSPDPITEIQCEAGVATRNRTRRVNPPDSLCTLVSI
GGTKFNEGKPDEKKKAGHNFSNDAKSENWTAAAATNTKGFNGKSLPSKVESPPSLSPAWI

LHRGGIDPKQFQQQRRQQTGKSLLTEDELSVFAGLVILDGNDGCGDDNDDDGSVEYEDES
VVVCPFRLVGSCVKGQHTEREMLSSDTIHSHLMSLAGLVHELRTEQRITEKECQKLHVRL
ESQKITIERLERYILAQCPASGKLLQTEATSPHEIGPEAPRTDAGKNPKGNILPGSILKP
AQDRSVPMKPEMNSLSNSKLHFGGESFSERVRSKTSVETLAFEPCNAVATKKGEFVGYEG
DRHGSVKYMAEELGTPVDLSRAALDLSQVSATGGASRKGANRHASGKQRHQKQEMPDWRG
HKGKAQDDRYGGAVGVVDDSRGDVLSPIPTVVGLQDNDMSSNDDVVVAVASSVHPSGDAV
QLPDLGERCTASSKVLLGKNNGRQNGTREKAKKRTIQGNSHSFGSSNEKTKRQGKNLRCV
DSALEEAHLSILRPNPKTFVECEQLRLRYHKACCFILYLFFIVIIFFIWSYFFGVFA*
>TCRU_109 Quinonprotein alcohol dehydrogenase-like protein, putative
MSVGIYSLKAETNASSTGGSRGLNRMRRLPAIQLDSWEFRKHAREGSVMPNALVASDVDG
DGVEEIVVGTTEGQILVVKPDHRMPIFSRTLAATISIVLYSATYRRLVLVTLEGTCEVTE
GFLSGGCKVPPSASSNALQSKGQCDWGLPPSLEPSNHMNHGWGGHDEGKKSNPPSTSSHV
FCIVPNCTCGDITAEVGGTTIFLGAHNCIYVYSITTDGECLGSLLLQAPVTSMKCFTVPF
ATEGHLRIINAPLFPCRNAAATPQTTFDGSTPRNDAVFIGSSTQTVAGATLLLVSCGERL
VLLNASSQDVKEWGGSGNLRCVATQECPLGDFPLTGGPNIHTAYSSSFYTTDVLNPYEVT
GTRRTPLQPLWQCSMSRTSEMQQRQRWPLKSSMDEGHTQSGFFDLSTVSLPVSSPDTCNV
VPREELLLSPRRQQLQRGVCDTAAAGALLNYKEDSETALDLLENDLPVSFAVDVAVSKNK
LQFAIVSEDGRWLILEMSPACGEGSMGAVPRTLSTKQHENGNEYPPNKWFSATIVCLASG
CLKPQWFLSCVCNFCVRQDEFCTVFLSTEGNCYLVGSNSEISESRLGADASSFTILKGGF
MGNSVHPAWASSNCATTVMPTGVSSALVRDFTEFPQEQQQPSLLRASSGRGVCLVCVTLD
EIVISSVGSELFLSAQQSSVPLAVSRGLNFAGGDGIHGWNETRSSFGITAEGGAHFVDEM
DEREEELMLQLGTALLEAEGYADPTALFSPEERRFAARMLCAAGYTEREWELLWQMDAEL
SE*
>TCRU_110 Mitochondrial Editosome-like Complex TUTase
MALMVLQELGLLPVFSKPTGDFGELTLPDVQLQLESFKLPAIYDSLQGDDEKLGEAVFFC
LQRFAEYYSKYDFRSGTVSLIHPRRHRSVYEKVVKQYLERLGVKKRIEWEKHLAEHKEDG
AFDENDFSAAMQNEATQRPCTSPFVVEDFVNYVNCGRRVQATRVQHVQQEFNRLHEMLVD
KEEELDFEEVFRESDVVPRFHGFEGVGARDPRVKTFRAR*
>TCRU_111 SET domain containing protein, putative
MPVYENRHLLRLLLTPQEQARQFVEYCRAHQVITRGLCRIGTTKRGGLRGLIANKEIKKD
ENVVMLSVRASLHPGTALRDKQFFDLLPLREREMYFLRRPFIENSRLADRSIIRHNQFLL
ATYMSYLILRNDVNEGSQALKYVNFMPRNEGDFEQLMCNMSGALDSVEVCQVCQSALASF
FKVTQAEVRPLLLWSLSMIFSRMAPIDHRWTLRHAFSGTPFVDAFDITGPDDDENLVKEP
IVFLCPVIDMCNHSDHENVALMVPEKTPTAHEPVICLRSLRDIENGEELTMTYGGSPTEL
KVIWGMQHVL*
>TCRU_112 ribosomal RNA methyltransferase, putative
MLHGNWKYLRQGGRQWMEKQARDPFVLEARRRGYVARSAFKLLEMDDKFGLFARNHTRVV
VDIGCSPGGWLQVARERCGDRCALFGVDLLHVSPTVTGAVCIQGDFTDMAIQQQLLSRME
NVHANGLVDVVMSDMCLNRGSGGTDDRQKQTQLNMEALAFATSQLRTGGNFVCKVLGTPT
AFEELRGELQRWFVRSTLCKPFSSRRGSDEAFMVCLAKRETPRPRGCNIAEGETRDFGLD
DWPGFLRRPRQQR*
>TCRU_113 hypothetical protein, conserved
MWLIIFVILTAVLPGCAEASAHYMYDGEYDVLRVGEVRFNDTMAFPASMATEVRRRYVLT
GVELGTRYLVHLSHLGSPSIEYRIHVGRVHRSAIKGKIWPAKELAPGRRKLADVIMLHFK
THVDELLFEYIDGDGDVDNGDIEYGVKNDELVVLEIRGTRNAFPVQPDKWRKFSYNLRVE
AIGSGSGINRLIMWHAMLVITAVAVVVVLVPRLIGNTIACDAPMPTRPRYDFLIFLVNKR
TKTKA*
>TCRU_114 acetyl-CoA synthetase, putative
MENLTVEEARHRHDKDVVQPYKANSAKSYVGKSISDRQALYAESKKDPVLFWSKIAADNF
YWKNLWPSEKPAMEFNFHKSKGKVFVKWFDGARTNICYNALDRHLAQHKDRVCYYWEGNA
EGETSSVTYGNMHEAVLQLAAVLRHQYGVRKGQVVTLYLPMIPFTVQLMLAAARIGAVVS
VVFAGFSGKALASRIIDSASELVITADSSFRGEKPIPLKEVVDVAIAECESEGHHIQCLV
YERHGRENIPMKSGRDRWYGDVVAAMTASQLADCPIEWVDAEDPLFMLYTSGSTGKPKAI
LHTVGGYMVFAGTTFKYSFDYHEDDVYFCTADIGWVTGHSYVVYGPMLNAATSVLFEGTP

TYPTPSRWWELVDRYGVTVFYTAPTAIRSLMQYDDEPVKRTSRATLRVLGSVGEPINVEA
WRWYYGVVGEGHVDISDTWWQTETGGHLITPLPGCTPLKPGSATLPFFGIEPALLDPMTN
AEIDGPGEGLLVIKSPWPGQARTIFGDSERYEQMYFPVDGYYMTGDGARRDEDGYYWITG
RVDDVLNVSGHRIGTSEVEDAVNTHPLVVESAVVGIPHNTKGEGIYVYVTFHQNTIIDKD
LLNAVRATVRKVIGPLATPDHIHPAQCGLPKTRSGKILRRILRKIAAGIFDGLGDISTLA
DQTIVAKLIEERNGVSI*
>TCRU_115 Domain of unknown function (DUF4200), putative
MAGTLESITAATQLRRAVMEVQKELDKKRELYMVRMARVREVEDVIAADRSRLQDKLVQY
YKFIQENEIRRGRAVRKAATEERIKREREEQIVELTAKLDSLNKRREELRQQYDAYAKYQ
QYLEGVLQRNDCDEYQSPRDIIQRWNTLQDNTKVLQRRKTQLEEELLRNKNSLNLKRQKK
NNESVELQNQLNELQATYETMQKSIKIKQDELERCINQRSSTSRTVSHVRMACKNLYDRC
IAWTAPYSGRGKFDVREADVLFQLHVIGDCLRDFRDVIAAHHNSQQQQQQQQQIAASRA
EKEEEDE*
>TCRU_116 nucleoporin 48
MYQPLLELPSEAAAVFVAGDRLLGEAAGSLYGSSKRVSFEAQGGAVYPLWKLANRNVLGR
RAGREKPSSLSSSVFSLSWWKKQQTFGVVRWLLRPLVSVMPLLRFVFPFVVPASANCAPR
LLNAADCPECVTAVAFHPDRMVLAAAVDEGAGCSRVVVYDVAEGKETCVLTHAFQRHVRC
VAWKPLSRDVLAVGCDGGALVWSLSFGVSPVVTVYGRSNNGHSEKGLGAGEEDDVDRKAH
CLFYRCTTHVPTTCISFSCRDGRYLACGSTEHIALHFHDIRLPPSNSSLRKNVSVEGATE
DVLFADDDTFAVKLVCGASVVVMIAFPSCVESVVPTAAAVLKMTKAQALGPNHFFLQCAH
VEGVVIAHANPFIGVQVIALVSTGIAGGIGGNVRRMACSDRRLYIALETGHLLVCHYGRR
GGAFTLIPVGVAELDAAHLAVFDGFTRGSLLAAVEASDQSVIFMPSYHS*
>TCRU_117 N-acetyltransferase subunit ARD1
MQIRRATMEDMYQMQHCNLRCLPENYNLRYYFYHILSWPQLLYVQEDYNRNIVGYVLAKM
EDEEKPANIHGHITSIAVLRTHRRLGIASRVMRASMKEMEKEYDANYCSLHVRKTNDAAL
HLYQETLGFRCANVEKGYYVDEEDAFHMKKFFKGPNPGLYVAANRQLVRQQNSAAAAVTG
MAALQRNGGTAPPPPPPSSSSVGGQRGENDTADLEKEQLKLVAELLEESNKESGKGRQQK
QKQQQQSKGGNKRGKTKK*
>TCRU_118 hypothetical protein, conserved
MFREILECVLEFVGSHSEQYGCSGKELLSFVSKDALPYHGLVDHASLRQMVLDLLLSESS
EVSVKRDGNPVVPSELLNGTVPYEQCTFYPSMALQEKALGVSLRFKNTRIAVNYACDNLV
TGVRRFQNSAAGEEERRPSEAGLGGGIRRLLREQWLRVFYVCVDEGAPVVPHLFPHFATP
PPPNQPKQHLRPLEAYLARRRGELQPPLIVIDPLVARQIVLSSPERRLVFEDAIHAIFAA
HGHEVPVINGRRMYLALRRMLRAGGLRIAIAPIFIRKSKRNARVVVANSSPDASDADADD
DDDDNDNDNDNDGEDDDGNMSGASNSSDEDDSDADEGNDDSKEHGGGAAADLNANAKRNK
ESFGVDPSYPLSLQLVKEAERRPLVVESVLPRVTLYDLRATGNELLRFARQFEERWETIE
STNVLSAHSKAFTRLLRPKGWGDDRHGSADKMSSMEGKELDLVKGVSSWAVNKVMEALHV
APLQALLLNDLLRIVDRRTLGRVIPFLRDKGLVATTGLSTPKGRRLGVVTIAGVELTAEL
RAKLMHSHLDGASVRGQKRKRSTALIKHLPDPKKGDEDDSAAAAVATKPCSRSVRMVAKV
TMVRNGYSRIGLFRLSRLHLELWRLWLALRQTPSTPMTVERVLHEMSFSSFCIIVGVADV
DVGEYVGGRSMESCLWGTPICRLPPSLQTRCRRSGVQPLLHSLAGLQSKGLLVCERSLVA
YLDVPLAEVSIALVSTALDERRRRHIFCDGTDMTPQDTCRAVLNFWSESWTTAAVTHEPF
RAMELISEVVATEPNLSNAQLIALSRLLRIDPVILAEHVLQRQGVVRARKRTLRDVIQVE
ESNKRRGEGHRASCTRRRIEVNGVTMAEALGAILQSEQPYFGLANLQRLVRGYSKELCSS
RYDPQRKRVHGSIQTLIQVLMNVIERQQQSGMPPAVHSVMTSVLSPNFSLAPDDGEQRAS
EQEDGAPTGPAIQENSAMDASHGVPCEALQDVLRMILLTDEAHYDAIAAKALLAQFPEEE
QLRCIDWLFKFPSFRTRSGGSGRIPRIELSPIFTFVPATLATTVTHCQSRASNFLQEITT
SLLFTSPPNCQRWCVPPFAVTENTTGRDSLCQAPRLVEQPSMNLDSFAEEIREQKGLRVL
RLPRFAWPSHPAAAPKTTLPPGVAAANAAVIPEAVSAATLTRTKTEPYPARALLRPWRHL
NHLELRDIPVDSAPSVEQVIMARSASATPKNEGLPLPRFPSIFHHVDGSFHEFVWRSFLF
ALYSLVHHFPGITKEQLVQRLKVSGLVSDASCHVALEFLKASLVIVARHVLVPCDGEVQS
PFSSSGSACKYSECYFCTVSRDGPWRIMEL*
>TCRU_119 hypothetical protein, conserved
MSLSAATVLYNLAEKVNQIDNVQELTLILQQQFVELFRGGEMPSSPSKPKVSSLASTEEE

KLLVVRAVEAFHSVGLQRHGVFFQSDSYHTNAAFFIHELLASLSGSRRIWFQKLQKASLH
ACVAVVKAIGCRNTRLCLPGIVSACVHYIDRAHHGTDAVAVRTGAVELLRVSLKASLVSQ
GDDTQWLQSTVGHLGHSMTRLLDPSRLALGAKTLPFAQSLLHLTTDLLLLPSLGTFLDTP
FMREVIVGWFVLSNVNFILSGGVFGGATDSTTQIPSGFFQERAVVELLQAQLKKLRGVEL
LHFSSALLRCKDTRATAFPVEDHNQHLMQRVLQRCIQVVGTEMSVEDLYSAKVSRSYPCI
VGDTFIECAAYAVTATTTTTTTSEDPAGCVTVGEQVLKDFMAECEATLADWDLYMLHPPT
IYVLTRLVLWQFRTPAWVTEEEEKGRPAEEFILSDTFEQLWSIVAQPHLWNITEDENLCS
YQQLRHRQTVAATILCFLETAAGLLRDEPVIHRAKRKRAVQRLNLLVLYIVLEKATGPTF
VRDAAMGVMKALGEAGFYPDTLAFFLSQSGYIVDEAARAFTEEDLRVSAASVLRGGVSFL
QSKLLSVPGKEEFTAITSRQWVDVPRGRNPAAVVLVTSAVPKVSDFVSSAVKVASDGCRR
STLQEETTGALASVALLLDCFSVSAALNRSVPQLGIHEDQDCMTTAAEPRVQILQLAVLE
AVQMLLAYCTRNDAVAPLAISAVTRGLTVFLTTPRAETWINETESNGDQPPPVFEWEDNT
PAVLPRNHLRTVYQVYLSFLAILAEPVSGFTTTSNSKRLSAQERRVLEAVQPTPAVIAAM
EGLKALFALATDFLSRRVVEEVLPVVFTWHERGALPRIPTKTDERLQTAAKKFLQDACVI
DPSLEKQLHAECAFLLPPLASVSAAITEEA*
>TCRU_120 long-chain-fatty-acid-CoA ligase, putative
MQNVRLFLRILTFTGCVGGTNSRCGGFAFQLSYRFGTSVAGTYYSESDVASGGSMNNDMR
LGLVIKPQSTLVELWEQAVKVWPLRRFLGTKMWVRGQLGYVWATYESIEAEMAAMRTLLH
KMGIDKGSRVVVISENRYEWVVVHFATLQLGGHFVVLPTNVNPMEAQQVLKSTQARVLFV
ESTSSYATVKGWIGEVGELQHVICFEDQIGEGSYAVAINIASDVPEKIPPRNDITAEDTA
MIMFTAGTTGPPKGVMLSHRNLVANISSIYAHFGGALTHTDLFMSLCSWCVAGAITVELY
QAICKGACICIPPEQLEGFQDLPLVQPSVITSVALPFQRAYANMVDDIMNRGSLTKDITR
FTLGRITENRLMLQKPGQMLRVASHVLLGKFKEQFGKELRIAFIIGSQLTRDQMELLADL
DVFTVSTYGCLEAGGLIATDIDVPLRLKALPGIEVRVVNEKNEIVAPGDIGELLVEAPHA
MQGYFDIHIDPDEAKNSLVAYGGRTFVRTSDYGSVTGGWISIKGNKDVLITLANGAVVDP
LEVEGTLIKSPFIRQIFVHGENRPYLTALVVPNAKAIASHLRKVERRDGVPIVSEREKAD
CIRAELRRVSQGLPSRSHVRRFVFIEECTLANGFITCKYGFARRRIEKHYVHYFNAMYDE
TPKFFGHAVDDYDDLF*
>TCRU_121 radial spoke protein RSP4/6, putative
MSVRPLVEDVEEMFGRTKAYLMNANKDGVSVYDQLTRLMEQLLDENPHDIAADPSRFNEI
FTLLQQSSFVNGQSTPACNEPCSVPPSELARLADNERLFDRPPPETLTTIEQPDPYTTVT
TTRIKPHTAPPYDSVAQHNLYWAWAGCGVTEEEAFLLDRSITMLAMEKKLRDVRFFGKIF
GTKADYYVVSSQRYVQDGEKVYKEVNTMPRPARRKLEVPVQPEPGFVGVNRLSFWVTSHP
AAEWKLLPDVTPQQILAGRRIKRLFTGDLNAAVIASPPFEWNEAVYLRVQLSRIASGTYI
SPMGALEEPEEEVDEEEEAEDDEGNAAKKPREAKYRPLTQPVKGFASEEDSDVTQWAKLD
QWVHSEGYIYANGRQTKVPEKQEDEEDEEAEELQQQQQQEEEEEEEEGEEEEEERELFTP
INLDFLYAVINIPEPPKVDEEDEEEEEEDDDPAEDAAEAEKDFDDMPPKPVTDADVPDDD
PMKVKIAAWTVRVVNNNSKKHRVVVVRSLRWPGAVAFAAEGGKKWGCVYFGNGLNKTDFS
FTPTLAPPVLPECGDITEVDDPTPATEKLVRRGEDPPEPDSEDEVEEEEEEAEGDM*
>TCRU_122 serine/threonine protein kinase, putative
MENYLIVELIGEGSFGKVYKARRKGTGQVVAMKFIVKKGKNDKELLNLRSEIEIMTKLDH
DNIITLFEAFETQQEFVVVMEYAQGELFEILEDDKKLPEDVVQRISKQLVQALYYLHSNR
IMHRDMKPQNILIGQNGSVKLADFGFARSMSYNTMVLTSIKGTPLYMAPELVQEQPYNHC
ADLWSLGCILYQLYYGKPPFCTNHLYKLINQIVNDPVKFEEPISPDFKSLLKGLLTKSFS
ARLNWPHLLNHPFVAFGEEDGKWQKKIKEHEMVMKEHMDRLECFRLCAQPSRFQPNSSGH
TPRSTGVSRQSSLGSKESCLFSASSIEIISSSKNSQEIIETFKGLAKAADTLTSSPSQST
ILLERIPQMGILGPTLRRINNGQTIDIVRYALEFIRILVFPENGSVFPFPSQYPSETIMS
ALQSRSELPPFDFLIRQQVALELMEKPQETLDFMMNEFIENRKNLREDCVKVIFQCVKWG
TGFGAALIKMRIFPIFWASLLDSVKESTVRNGSHFQFYAAVAFHTVSALVPHIKLSSPDQ
INAHKVSEFVSTGLTAVCYYDPSASGDIAALNCAAAAALLVAFVHREMKDTIVFEPDSIL
MDGLCAIVEGVRRISDQLMVSRALGTSYGFADYGFLDGVTHMLSVVFSDPKSIVYQQNSD
SLNRNFLDNDKWGSLRTVIGLLRDSDSKVELSPNGVLAALRCVQQALQNQQEGMQSMSLL
IESVEPYYGDGGGPISVIAIVCRQLRKNYLKQLRLWPEYRGGGTVGVNAHLTIVVQILLV
TFQPAKQGSRSDDDTIAAVQQILYKEGVMEMLIAALDYTEVAFWGSPFTVIIKLVMGSPL

FAKAFVEGDGLHPERIRKVLDSRKASIGLVSDGLNVLSQLARISRDFYPPIHSANLYESF
LDLMRNRDAGIRSKMCNLLGNLCKHSPYFYEPLAKHKLIEALVERCSDEDPTTQKFAAFA
AGNAAFHNDFLYEILRPSIPVIVKLLSSSDEKTRQNAAGAVSNFVRNGGSLTSALMGNSV
VEALLRILRKDKVGLRKIALITIGSFCAYEECKKKFLWLGLEDALTQLEQSDAIEAEPSI
AKYVTRIKQRIGSS*
>TCRU_123 ALBA-Domain Protein
MSAENAERPKNAVRVGFHGSKFLYVDITKHLLHDGEKEVSISALGKAINEAVSVVEMLKD
QQMVLVKKISTSRGGGEGARNNTVDKIEIVVTKAPGFNEKYEEQQKVREAKKLEKGNENV
AK*
>TCRU_124 ALBA-Domain Protein
MSCDAEEPSGPIQVRVGVDRRNFAYVDFTKHRLHEGKPEVIITGLGRAISDAVAVVEILK
NQGLVTVKKITTSRGNVKSSSTSVIDKIEILVVKSKEFDSIYEEQQKRKDESAEKGQ*
>TCRU_(Ubiquitin related modifier), putative Ur.1
MSSYRRITVQFAGGCELLFDKQTQLQLEGIVPHGTTINGLVQMLKVNHIKERPDLFVDQS
GTTLRPGILVLVNACDAEVVGGLDYVLTDGDTIEFISTLHGG*
>TCRU_126 selenocysteine-tRNA-specific elongation factor, putative
MTGEETLLANINVGILGHVDSGKTSLAKALSSTASTAAFDKSPESQRRGITLDLGFSACC
ISSAVVAPPLHAAGIEQIQCTFVDCPGHASLIRTILAGAQIIDIMILVIDACKGVQTQTA
ECIVIGEVLCKPLVVVINKIDAVQGSTPEEKRVTLDKLRKRLQRTFERTRWPSVQMVEVA
AAPRRDEATSGEVSHPINMEEVISAVLGLVDSTALKDQLTTPLRSEDFVMMFDHCFVLKG
QGTVFTGTVICGQVSVGDNILIPDSHVVKKVKGLQAFRKPLQHARRGDRVGLCVVQFDAE
GVERGILCSAQHQRGNAISNVPLLFESTSVIVAEVNRVRFHQLLCDAHTKFHITIGHSTV
MGTMKYFSRPTTIAPEEKEASFDIWQESMYVEELTEDAFLTFHSTEGQPQSGQPVAVKRG
PLTYYAIILLERPIMAAVGTPLIATRLDMERDNMCRIAISGSVRAFLSSGTSADASIISW
RELPIVRFKSRALVVERVVNEKTCIASGVVGFEAPETRGSSINQKSKEKDTLHAEVKKFI
GMRVHFRPTGEEVNDATILTGVKEGIIDSAFGKTGKVKLVFKDPIFAENEPSTTGRTKRG
GVTFLTDGVVELTLKKYPLAVHCQLQQ*
>TCRU_127 Bacterial transferase hexapeptide (six repeats), putative
MNRLEVIRKSISYVGLDPAMFKPYPFNVSSSALSELMDCMSYIVFPEFSEPPMNPVTVPE
QRLGGSALLQWTLTRMADIINSQIYSALMLQGHTKCSKDEAGIPHSLNAESGSNDDGFIP
QNETHAFGEVSSFHLEAKKKAEEITEAFLMRKLRNIRWLLRTDAESILNNDIASNSLSEV
VLCYPGLRCMKHQRTAHALHELGAPSNFTRLLTEMAHSTTGIDIHPATSIGHHFFIDHGT
GIVIGSTAIIGNHVSIYHGVTLGTRSFPVVAKTGERVRNLARHPIIEDRVTIYANAMVLG
RIRIGKDSVIGSYCLVLKDVPPKSMIRRTPNAKLPTPYITI*
>TCRU_128 hypothetical protein, conserved
MFSASALWLRGQYKTRLKKRMVGFIPKVIPRKIKNNMVALRSEANTGHMEGYMKTEAERL
DATGRKVQKVLWDPVLQRHCLFKETKIRGPFMTKANIVKKMDFPIGAAGTASLK*
>TCRU_129 hypothetical protein
MPLQKSRVAAVVDGEDDSDDGELPHTANAERVPFVEELKQNVTLLYQRAAVQSSSQQATP
PRNDPHVVELPPPPPAPSRELQVRESDGSLSALQRQLTALQSVLKSSQERFQVRDDATAR
RSLPIVTASQFKRPISEDFLHELRECRLTQSGGDENTAHLKEGFSCHCENNLRTAYNRWR
GILAEIHANALKRTSTIASKLDSEIKGQKQFLEEARQRIKGTILLTSTLSDAITCFTRYS
PEHYGALQENRKTPI*
>TCRU_130 ribosomal protein L3, putative
MSHCKFEHPRHGHLGFLPRKRSRQIRGRVRSFPKDDPSQKPHLTSFMVFKAGMTHIVRDV
DRPGSKVNKKEVVEPVTILEAPPMVVVGIVGYRQTPVGHKTIGTVWAHHTSVEFRRRFYK
NWKQSAQLAFTKRKQFARTTEGRLAEARTLKAFAKKADIIRVVAHTQLRKLRNNRVGVKK
AHVSEIQINGGTIAEKIELAKSLLEKEVRIDSIFQQSETCDVCAVTKGHGFTGVVKRWGV
ACLPRKTHRGLRKVACIGAWHPARVMYTVARAGQHGYHHRTHLNKKIYQLGRAVSMEPNQ
ATTTYDLTAKSITPMGGFVGYGTVRNDYIMLKGSVAGPRRRVITLRRPMAPQTSRKLTEQ
ITLKFIDTSSKIGHGRFQTKKEKSQWFGPLKKDRIRREERLRKERVARAAERKAKGVAVA
AAPKKAKK*
>TCRU_131 Patatin-like phospholipase, putative
MSRGSANDDSKVFDLTFGFAAGGWFGMYHFGACQAIVDSGIIDRLTAEGKRVRFAGSSAG

ALVALCMVLKNYRFKEMRDFLMGCAEHYRYSWLNLFRIDRYLDDALDQFGGHLRELEMKQ
ELFDTLNDGALEIFVTTLPKMKSKIFTEFHSHEDVVEAVKASCCAAPFVGVPFRLRGTGE
WVCDGGLSIVTPHNGEPRTITVSPFYCSTATVHPTIFVPFWWGLRPPGKVALRNLFALGY
NDMIEGLVVNGYITPEKGESLLRPEVQFLNGGGMFRRYGLYLLDFLAFIFVRPVIVLCIY
VELAFMSFFYFLRGLFCLDNRPIRRMYDNLRNIVSIRTLGRLIFGENVPHNVERLEKSSR
VYRVFNPILLGGKNTTERAVMSPTGVFSGVMPTLSSKTRKRATSAAQEKSEKIYRRL*
>TCRU_132 hypothetical protein, conserved
MGMASTVFQEPGRLPFAKGLWIIVPSVPRATGRDGAGIHSTCRRGQGLSQAKSRGWSRQV
HTAGKADPFPSHQEPKECSEQQQQYKAVWHVKPHKMTDKQICLLPRQGAYAAKFSAEHNR
FQRMRMRVRRRHAVKISPPRAG*
>TCRU_133 hypothetical protein, conserved
MHSRTALPETTRLNWSTTRQRPGTQLFLHCVDDLPRRMDNIYSASALMCADEHILVASGA
GIHACAAAMQPALSPITTWAAEHNLKINVDKSEAALFHISTHTLSDEEMVDLLLGNRNLR
IQSRPVRLLDTTFDRLLNSGPHASTAAKQTTPRRYQLRPVAQAGAFHHNTQSFSIGYGHG
VSLYSGEAIVPCLAPTYLHNTELLYRNSCKTHLGISAPTEDTSF*
>TCRU_134 hypothetical protein, conserved
MEQAEPAAEAAHKAHTSPRQETACFEPNSSKKWRTKIKHYAVASLCFWKPARKKLGPHPA
RAGDISAAWRRRTLIPWNRWCSALNFGLRSASATGKSAPPSFCAGLTCHITLYCCCCRRT
PLLSGDREMGRPLTPYELDVAIRDSSLGSAPGHDNMLNEFLHRLGPVARGTLRTMIHNSF
ADGGLPGSWNTVDTIPIPQPGKGPCRPESCRPTTLLSVLLNRKNDSPPSVSV*
>TCRU_135 hypothetical protein, conserved
MKSHLFAVLGLWLRIGTPLLCIAASTTETKTTPPLEKVPRHARCGEVNRSACRLSGKTAR
PFRCGHSVDVTRGGDVRKNSGTEEDGYITNWQLNIAGLSSAKKIASAARLEQRPPDIVLL
QETNTRIATAAKLTGHNSFLQAALGAVVAVSLWCATLCRASA*
>TCRU_136 retrotransposon hot spot protein, RHS3, putative
MLAAGRLLVKDYNVTMEVFVQDPDDYVHDQRPLEEILNLTAHQALEAITRPLHEGVLSLS
GNVGTMKEKHTITPLARRTPNGVLTQVLTEARREAEERLRRTQEMKFAISTNIEEVLFKG
RARVNEMRLNDFLTRELDGRGVAETNRDVMLEEFFRDPTRYIRDKGALNEMQASGRYLGM
KRAVKGEVVFDEDTRRLCDKGVNNLPGRSLAAADVKAAVHNSTKRFLDAAAEEARNPTTT
SAPEKLEGVCKSVHNARRSHAVELPDDDERIKTGTGMGVHEGKPEQSWSYREVGNAFEKD
DAVQQCGSAPPVLMVLASEKGWPYSWHTIQDLPKDVFVNCEVERVWQTVKGDVTAWSSSH
RGTDFKPKRRVLIGTPGIGKSVNAGSYLLYQLLHCDATKLQVVVHCFGEEMRTCLTRPAG
R*
>TCRU_137 hypothetical protein, conserved
MNSHIVAVLGLWLHIRTPQQGVAASTTETKTTSPLERVPRHARCGEVRRSACRLSGKSVR
PFRSGHSVDITRCGDVHKNSGTEEDGYITVRRLSIAGLSSVKRLLLLRDGSDIKLTPFFC
RK*
>TCRU_138 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGASVAVLSADGAGGGDGSAGEYLPLQWRTRFLTECAEEVG
RRTGGRANASSVEECVRQVMESLHAAVDGRSRWRRQLSAVAVAAAAEGGGKENPNTVEDE
KTSETLATSGKASTGKKTAVASEQTSVNPAPAIVPPARETLVQGKHNETNAKEEKEEEGG
EKDDSEEEEENHKEDDEQEDAEEGEKAEEREEDKKGEESEKNTKEEEAKYGVEEDEEDKE
KDDDNTSEGMPAVSQEKRNSTSGPEGAPNKTNTEGTQTPGDIDGSTAVSHTTSPLLLLVV
VSAAAAVVAA*
>TCRU_139 retrotransposon hot spot protein, RHS3, putative
MKGYIIYDVETQGTQPDPGFAPSTGWGMILVSSPEVSNYDGWEEQLKVSRIIMNCPDETD
VKAMCAWMKRDETKKKQAECWRMVEERMEKVGPIIRHIFDADEHGKRTKDVMRALEWINI
GDRGKYFTQGGENEWHSEDPSQKLLKVVRVREHGPIEDFANAPICEYLGVLTVSRLAKVL
SPHDILFLVLGMKNAIQSADLKKYALNAFLNEDFVTSMVKDLKELPPPSPSKPRPSVLTL
NPHGYPTEAAAITELNLIDGLQKLKRRLLYIPTSPTFPLVDCFFFMESPRRTLVGLRMTT
ASAHHTTASTVRQFTERLAAYFEGWEEFSQGLSWEMIYVQHADSTPMNDWQRCDCVNPNN
KIDAEKKIVAFWDGKVHQYRVMLKGKFPEEIKFSDDSLPEGDKKNRKI*
>TCRU_140 hypothetical protein, conserved
MGVARELGHQQWLITAERERLNFDYANAVADVQNRNAQLNSQVEEAHINPSVRESTIAGA

GNQVLELQKQLEADRAQLRERE FNMGRLTAQLQEREARHNAQQPARDAETAGRDEASATQ
HAANDGVTTIPHQTDILMAGGEPSSAARRSSAAYRRPHGNVGRPHFHSSTPLPSRTSPLD
AQLPMEEDRSFCALDVTTWDPRAYGMRAPPESLSTSGAHTNAGNRTTSRLNLPLTIWSSG
PARWKSCRIPPLES*
>TCRU_141 hypothetical protein, conserved
MRGQPSLSWIGEKPNALCDANVVISLDTRHLHAMCAPEGINYNTGVLQKTAEGCRTPLMN
TDDGSSIHSTTSHQSSQAAHRTADAPPDLSNCPTQSSRRAMGLVCQRRSTVVRRNTDIPA
LGQLYEESERGRSRDLGAGNVGAENVPSGAIHNLLPHARTADERGELCGLFDGNRSRAID
PTAAHQDAVDHVGNESNPAGHGDSGVTKIAARSETRQVRSSTKEGMNQLIRSRTDWKERV
VLRLAWITANRWSEIAALTPKNFKLRTDGTLILDWPVAPKTARADPHRASRFVRIRGQDA
LDTTKSSRILRLPKSNEPWFLGMPRRIPQNAVR*
>TCRU_142 hypothetical protein, conserved
MQVWGLVGRSSFPPSSSGKAREGSRRIPTADARLLNEAGIIEDASSTITGGWIIPFSVVE
EKTTALRRRWIAWPRDKSRDDPYEANVPLLHISHYLPPVMAEAVSCLDLKASFFQVFLPR
ETRHLFRCRVEDGTLAELTRLPMGYKASPEILQIIITSAIAVVTTVAHRLWAAPPVVRAD
VWIDNIRIAGSKSDVTLWESQVLRNADSCRASMGEDRESGATQYTFLGVHFDHTQRAVSL
SDKFVCSVRAMPALNSSTIAEMEATVSRFLYLAAILVRRLCDCYFFIKAVRRRLSALHRG
IVLETSPANLPPSAVGLDERLQHIIENIIVGESSSPRKGICRHHHGRIAPWMGSRFYSRL
RRR*
>TCRU_143 hypothetical protein, conserved
MAAEGGPVAGGSGRRENVNSEDNSNQEDEGGGGNTVGEDPNPTSAGALTAPTRQDQSSSD
PLRSGTCNPSGTGSASAARMRASGPESLGGGQAAGTTSPRSDASQQAAGGVHAVGGRTSQ
GSQASEQTVTGQSQVPGTAKEAPRGDEGGEPGAQHEADQTTKMTVVTSCAKTAVEEESRQ
RDRKMHHVSIVAGMLIIIIFPCFYRHV*
>TCRU_144 RNase H, putative
MQPHDGVPCTAPGHGKAECPSYPAQAKTLLVVTDSHSLLAAVTKGPHSQTDWTEDQIWQR
VLSLMRAGWSVQLQFCYGHCGVHVNKPADQHATQNTAIGQHTEHGIAPIRHTDLLSCINT
QLTNKWRSTMHQDTHHYLLGGARPSDPGGKHIITQEALDQQERINTARQGAGNPSSGADY
TGP*
>TCRU_145 hypothetical protein, conserved
MLLQQRVSSARAVRTKVASIPSCGLGQSHTVAVPVPNDEGIPAVDEAESPVVRRGSAARG
VRDEAVAEEPGPSRVPAVVLPACLACWHAWQLRWRPAREAPVKKTVAPLRHPHGRPSQTI
ITPG*
>TCRU_146 hypothetical protein, conserved
MQHNRALQRRHIRHVDESVRHQARRALAEAANPQLRAARKHAVAQRHVQCVSERVHRAQV
HRHNDRSAEHHRVEARRRTPAANRHRLRQRHATHAILRTVATTTGPRRRHVERQARLAHT
AGTAAAHAFGERRRQRIKARQRSRTAVARHHAHGGQAGHAVVAAALQHPAAGTVALHRHD
AARDRQPGDKRRAGGSAARNRHGAAAQRHPRQRRHGRRLAHRPHVAQVQPPAGTDRPTVA
AHQRRRNRPLDAHEAQHRIKHREALSKHNAAAAAHNRHVRHGEHRVVTQTEARRGRHMHR
GRGRTARRLQRHAVKHHRARQQVHVAANVHRRPARLQRPQHSVAHTQLRLQQRRRVQHKR
RRHRVRQPAQLRVAHRPRRHNRRVTDRHVRVCRQVVHKHKRAVAPGQPAHAHHQAPVTRR
LAAVAPHVDLRTAVAHAVPQFDAQRAGKHRRHVEHHSHAVRDVHAVHQHRVHGAANRDGS
VHRAAPQSQHHRMHRGHPRSSCCQHQRHKQRHTHSQNGPAPHTLPAARTRTHSRPHPPTQ
TRISRAVALCRSRPVDHSSCLSNPFLQMANPVTRFRQIDIPVLPILILRVIPNTLKR*
>TCRU_147 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MGAKVNDGDKNAVLLGLSYNREKRWELLHSGEKTLEHSSHWEPGTTYQVAIVLQNGIQGS
VYVDGQRVCESVQSNLENTKSKGISHFFIGGDGGNAENTGGEEGVSVAVTNVLLYNRPLS
SEEITGLAKNKINIPTPVAARTSSPAVSRPKRSSESLAGGAAGVGTARHFGANGDGSTVC
GSGLLPLILLLGLWGFAAL*
>TCRU_148 hypothetical protein, conserved
MGRNDVVQLLCEKMKLGPLAVQVTSSCLVNAILNAARRAKRRQILLYGIMASTDPIPKAK
LHSSCILLELTVATWGVGVRAVVMFTVPTDTPPQKKRIFFFWKRSDVTNLQRNVADSMMA
KRSGRREGATHPATTPRWDHHRSNFAVQHAAFGAAAVTDRPTTAQHATEVDLTL*

>TCRU_149 hypothetical protein, conserved
MGENCKFVHADVDYSTLEGQPIHVNYIWRDEKLCIYERLPPGDVLEVLLPNCKHPAVMIS
SEYVLATRGARSFSKGRPQTLSHCAHYYFNYLCSRGEDCSFIHAIYVDPTISEVCKRAAG
RSHRQRVPGALRSSVESADSDSQLQCSRQRKKCGVPPEIPVTIDARNSRGDGVMAPTVNA
EGLNSWAGLNGPSEASSEGPRHSSSGEEGTLEPLVGLKCREPNGVQMIGSACGRAAMRRA
RVYRHDPYGIF*
>TCRU_150 hypothetical protein
MCTPNGNGFYGDAMYQTHFCIRNKRENGLIGVTKSRFFGSYGDSASCNSIGNSVSLLPYG
YMGSTNNGGSPTSTANQDIVPATSFPLAVNTASVSIATPTAVIPPASHGSTNTVATSLSQ
RLQRQAVLLVKLADGQPISCMPVQQLVLARPGPLNPASLLTSEDFQGSKRCSSGVSSPAE
GGPRDAGEGVISPLKSTSFLDEQAINTSRATVFSVMSPVTHVSSRPLSFAYHPSATPLAQ
NGNNVLPPGPDSIRKSDFYRRNPTTTNNKGTISIKNQGDFAGDGLRVDVYSSDFSCIISL
SPSAIFHKPHPSLGVSRLVLCRKYFPGRPDSCWKGAMCKFVHADTTGAPRYSIHVNYSWR
SAECCTYPRLPAGEMIHVLAPNGRQPLETFPSERILVTRGSINWKNHIGPLSRCAHYYFN
CLCNRGEKCNFIHTVYVDLSVEGVFKRAPASRTIPPTKKRASRAKLFASSRSDVAANGCA
SVSKKKPVLMQPSRGHNNILSEDFDIDGDTVPTANQNLDLAIPKHVTDSFSHTLLSVRDG
SARSSTSGETRPIEWTFVDNSEDSILSDGVSALQLS*
>TCRU_151 hypothetical protein, conserved
MLTKSGGVEAKLEALQSKLEAMHADIKKIVPHSVSFLNEDNSVTRSTPVQSFTNGAAVME
MPTIPIGRGSRLNAASPAAEASPNTTPSSFFLPVISGGGSPKRVGFQEKGHGAETTNSLN
TRRKADAARQKLQDFVKPMILSPGEENVAELRSAPCAWLLSIALACSYVSGESITIEDIL
RQNRLGLHYVSFPSVTLAELFDVTNEFLTDHPKLREMRVHCEVATFDSETVDELGEVMGT
GERLPIMTLSQFRKDLSNCDPNSICVLNFDPYLIEQHEIRMRLNYMELNETDYPMETIVP
RWPAKNQGTFGLILNFSPALHTVTVGTPILLENGRIVIQEHTVPVQVLYKALCVKDNYCN
RSRGFVRVFISDQPVETVPSIFPLNVLDGSLTGGLLTTALDTSISPHILGLSIMHHLVTN
VLLDDTERQRQNATNFCDVMLRGIPVTLVCQQLGLGIATIVGGSNKASVPSAFSWYRVLL
KKLKIEDAIALGIVLVERRGGAEDGPVNISDDTFMRHIELAVESGSVMLMGFDVNVALNV
KVDNRPEPCHFAIVIGMDQERGIVRLADVNVKKYRKTWHLPVTRLYSAVIGYGYIVAAKS
RKTIEKLNATGFEQSVLSEARYALPPTQRLLRFEYPKKNYVVTILADAFARLGFKADVES
VVNFSGFHLSFMLSEHLPLENAATVARNYSHTHAEDGVSVATRHMDKGATGSTLQGLLQQ
IRFALQFPESRCLIVNFQTSIIHANKAVWNGSNGGSYAIVLHFDESSSLVTLSDSNHGSF
YRTWVCPLDVLFDAISAVDSIALRARGTLMLTTTSQRDMYLDCYGYDMRHSIVHHPFKPS
VWPAFHCLALVASEMSRGDSTTGQSVQFSAEDFLYSLSSFSVHNVLRNELESEHIAALAN
TAFERLEIPLEANAVDVTISGSFIKACCDETVNGKPVTMTLLGYDTRPIHRVAGFSVAAI
NRVRGTEKEGFVQLVEGNGCTFGSVWERPAQELQFAVTAMVRIRRR*
>TCRU_152 acetyltransferase, putative
MSGSEIVRLPPRGGVPIEIKLRWGIQKEDLTALGVLHDAAFPVKYESEYYDWMLTDSCLA
LLAFATENCILSLLKAAEHQQNTETERDEENSFGDVEDDGSSSLYSVMVGFCIGQIAYGQ
RRDGRIDASPTGYLGSFAVDSRMQRCGVGGALLDRFLSYMFFTVSVPPHLFLDYSPPYLG
CEGLWGLVSSAYPTLFDWMSRWWFGRDRKGTNHVPQETLKDKKLCDSVNPTVDSQSGRIQ
YGVGEVWLHCIAADTKLLLYYMKRGFSRVLVAPNFYFFGGRYHEGALLVCRKDGAVIDLH
DLNSARATGKKLEDGAGQETFIAKGLSHGFRLRSGNAVFPATVSEEDSGEGEIVDLLLMT
DLAGLRRKWRSSVGKTAFFSDLLAS*
>TCRU_153 mitochondrial carrier protein
MSTDKKIRRDAPLPKSWTIGIAGFSGMFGWVFTHPFEMWKNTVMMAPPGNSHLDVLRKVR
ERGAFKGLSAGLLRQVVYAPARLGCYPIFRDALIMLKGASPETAPSIADRALAGALSGAF
ASVLSSPVEVCLVLQTTSPMKVSILNAATQVYTASGITGYWRGVGALASRAALVGVCQVA
VHDQMLTFLRRHNKCRAEQKGVSPYGDNLVVNTASIFTALFYAFCTMPVEMARVRMSAEA
RKGKLPSGQAAELKYKNVLQAISRIAREEGVLTIYDSFIPYFCRCATHTVVCFFVIECLT
RNAKLWRSSRQTKENSFGSRRVDVPA*
>TCRU_154 ttaggg binding factor
MSYTQCPVSTSPPPMDFTVLHEIMRDHIRRGNHFAVLGILALTVVHEDPAFWQTCTYHDG
IASAVIANYVGNDRVKTHPPQESRCQTEEIAPNLNQEFLTENELYLMLRRVCGKDPLLCR
VIHQLEMDPVKENNASNGRSKELDAAVSVPSEAMRVNLDELFAVLHERFCSLDERRSQSQ

GTTIPSATIGPQALKRARESDGSEENLGVIATESAAVAPPKSRYLEPVDGVDGAGCSDAL
EVLAHIHALPGTTCALNSFDAVAGLVDDGERGGLESHSSRQQGLEPKGTSRSDIAPVGLR
PKQRRHKFTPEEDEAILQGVARFAKGPGRFESILYAYRGVWHRDRTATQLHDHWRGTLRQ
RAVLQQGGYRGKNSIATRGGKSEME*
>TCRU_155 pre-RNA processing PIH1/Nop17, putative
MPLETINLSGKDAQDGEKFTPTPEELRTIQEKMKDPKFVELFQSYMKSMEDPETRREEEA
YLKQVEHQAKAGGDYSFDFVFPKPGFVVELLEPSTSYQVTHPSLKAESKKKKHVPRVYVN
MCSSEKIDPFSEQSTGDREKSNWLVPVSVSKPRTELFSEEAATSGKTGEKQTHESGEGTN
PVVVYDAVFHPNTLQLTDRSDRFCCFLVNIAVEHINSGYGDCHGFEFRRLPSRIQSVGTP
QNQTISREKGKSPFAAAMNEQTLTHPTKVLPPLTSTSEKGRTTPCNKGKETSGVQAKKET
DAEAGDKVEKKEHIPHFTIAHQGHIDLTDTWGWKIVDRRVGVPEALVVKMDFTGVQSAAD
LNIEVESTYVIIAKSSSHPYYGSVTLPFSVESTPLEAKFERRKSRLTLVLRVVPPAPTGI
TAEDMRQELLSAGNPPDSVTEHAEDVVTERKNNDSAQDSATAGCVANDETSTVSDLLPAE
ARPTAVELPKKTPSVPQFSCVGDPDRVRIVMEKVQAARLEREKAAAAAEEQETSFAKTGS
DPQEKENDDDPAKEPAGNPEHEPQREVVTGSTALEGAASTSTFTLTEVSATAGADGAVHV
GDGTETAEDAAGLELLRQRQDAWQREIHRRTEARHDEDREKALIADREARREAERLRRRA
EAARLQEAAAVKLAERMAELPLRNRHIFTVD*
>TCRU_156 hypothetical protein, conserved
MGVTDNPACFLCFSRREMDSGEKETAADALQSTSFPLSELNKFMHNALSWPATDLTPDSS
LPALQKFSSGQPMRLCLSPGTYACKIIENTASCLVAGASSVRDTVVSLTDREGESGFVGK
DGFSSMAVFQQPMKIYSRASLVFHRVWFMNFVEVVGGGPVFFSQCFFGASTCGGNVVGLP
GSSQFASVHLAMDGDCFFFDCDFDYRCGVAGWEGNNEVPAVTASGLTKLHILNSSFSGPG
VVSTALALFDTARLEADYISVVRCGGHSLVLRDKSSAIVSHALFDRNDSGVWVKDNGKLD
IRESSLELVRHGRSGLVLSDGGHCLAHKCIFSAWAAGPQSIGRCIVVAGDNSYVSLSLCE
LFWRNGEDSINSQELIKGPDPVPDSDTCEKMKDFGLCHVLLGGRSEATISRCVFRLPLTV
ESNGQSSVIGVLLRSVPKRDSITFYAVENTIVFGWSMEGDDVRRARLPERGKSSHTWGLV
LPYVSGRSEEKRLKQLATMWMTDNCFLESNEEPLKDASLVYSSYEGYCRGTGVSLVFPDV
AKNKDEDDANAVCSSTVSFMTSDFVNSPPVQDLENHSVNVHWTPRKSVTSLLSGGAALTP
TSLCEDSPPWREHTCPEQGYLSLVEEESSDSTSLTSYSGSEKEGRGITVAKRASLSLPEV
GNSPYACAQNNVGILRSPSEFPSLNGVHFHTKRCRKISGVAAIGLPDRKQEIVLEPFPQM
TVASTEAPRPLSVSFATDEETPTSRPGLKEGGRQFCIFAGGRRRGVCQRRQLLMKQEVID
CQRKLRSLMSRRSKGTIVSSSHTGTAQAQKVRNSLATKKSNTRIFSELFPYQSELGPRRR
PLLAGRESPSERLVEKGNVSSKEVWPWEVPTLRRFLMEKLGMYSSIEAQKRAFCGRGKDE
EREEGEDLVWSPQRKRAPANRVNVGSLNGNTRRMCSTSPRRETRLRSPSLVSTPADSFCA
RRPSPGKAGYVPLRLYEKFWKKWCKTHFVRETSDQPQRDQREGECRSRGVMEHQAPRLHS
SGSTDKKWGPATRVAGSARNYAFQQRDATQPSKIRELTAEVRQPSSAVVVNQTLHDFSDT
EEEKAEENDAGHGATVIPPRMPLFRPPLTAARVEGRNRFAFKRRNPAYSSV*
>TCRU_157 SET domain containing protein, putative
MSHSVPSLLLRNLHCSLPAIAQLYKEAAGVGTGGVVEGDRGIPSCSSLPLTVSTTNDGEA
VLDFFCRELGMGASSLRHWRSGLTKAAHRRWWRGGKLPSQNAADASLFTDTDDVLFMQSA
IWDLKAVVSPFLTLTKPRRKSAVRGSSFMATRRLLPGVYLLSLPVEAIFFASPPPATDPI
TSFFMYVEELVGQLVVAGDDVSENDWRPSHAGYVNYLKKSVIPSNNLPFLEREEIARILQ
SDKTKPLLGAIGESHTVSNKSPALELWEYFHNDMQGLPLSAYLRQRLSKEEYAWWVSLVL
SRRAGAATLIPLVDKLNHHPEPNCYYTMATEETFCGIDVFDNLLAGVPSDLLYEPFLHTF
SIREIQEGEELTLCYASPTINPNDRDSRSAGGMSVTSQEGRAAWQLQWGFFPENDSPYSS
TDLKEVAAIVAERRVNLRRQYFPPDG*
>TCRU_158 hypothetical protein
MEKEVVFSKRIQQLCRRIDRARPVFEQHASGELRVLSEAQSRQVEMYPLWLEDLEHLRQG
RPPPLRPSKLPNASIKAPDGATSQEELPARDTAVVVGTESRNELELADDVAAQRSEEGSA
TVEKNGNEEEEVMDERGSSQQQSRCTETNKRGNAKKQVVANGFVGNFESEKERVVEHLRS
LPPAARETFICKYLRKINDADELRILKKRFESANNLRQKMISGDVSCPSKSQLEIIKGLP
ELRRTLSRLKRHAKMEGRRAMKFFLQLLEEIKEEEEWGKQPASIVLLENEDEKRDDENGA
TETSANGETAPDNSTVEEITETHVEMQLPIVNTLAAEQTDSAIKLEGNFALIRRGVVDSS
GNENSTSVQTEFKSEGEANIDPSLSGHTSLCGNNAVRGVVVSPRATHEVGPSSTGDRERD

RIYNPLVDCSNFNFSKNGSRPEIKALHFNQVNKKEEQEQQQQKQRENDGKKSEGLIRSDD
ESAFIGTDQKTREMAKQKVLEMPSHITREELGFIQLHIPIFYRCKASEGREQSAHMEELE
PRTAAVLRRVEKELQYILQHPIPNVTVINSQLRLEKGKCSHAKIEAESESITLARWNVYV
SPSDGPLAGQLLHIVVDFSQHYPFVPPLIYSTLFLPLTTMMVSESGQPNTIRLFSTCAPA
VAHDGKRLANKKCTIWCPESGMHEVFSRLPSFFDSGAFAASREALGKELYGSSVAEARLA
CGRSAVEFLMGNGKVKVPTPTTIEMVNGPFLVYAPAAGDAKGEKKKYGNSKIKGKKGAFG
SETVQYYEDGDRGVIQGPFRGCWGHLLQMQLPFARARRNQKRRSKKISRGLNGPVVTARV
WARAGEVFPELELVAISEQSAISKELHWAESVLGTPRTEGPNGEKNQQPSGSLAVIAHCK
VKLTALEDRKGAVVRFFVEEEEGVTRDNDENGKRNLPRCENGDQAGVTHVYLPRSCASLS
PEGEETSLSWAIVIYVGDGCSATVAFSVPALGSNVEDVRNAVEAGTHVSDVALDLVAGTV
SDSAERTFARRISSCYDPASLFCVASLAAGREAGILGVLCKVIYPSPSTHSFVPENVVVF
PRLILSENAFDAHFLCGMKKLFFTSSPFSPCTFFLPLTAPHETLPHAVQNRLKLSLTQVQ
RNPDASTAYAPPFKEKWALRFFVLALRSLGDQAKDVHDTGEAKDETRESFLHSVYKHTAY
SFTQLVRGEAGLQKLCHFIAAGDFPLDRPSATRTSHKRDAEELEALEWLLASWSIRTGLV
AFEAENNTNFIASSATTSKNTILQPTREDWHATTNKLMASLNESKKKDLLSQIQLHANFL
YDATSK*
>TCRU_159 bifunctional aminoacyl-tRNA synthetase, putative
MSASDCRGESEMLKILRALGMDLPTISHEEKHTVEEANKELGRFGVPCTGTKNIFLKSKK
EDLVLVTALHTTRTNMKVIQDALSLKDLRFAPEDVLRTHLGVVQGGVTPLALVNNESKNI
KLVLDKALVESTVPVVLHPCRNDKSCLMTPKQLQDFLRKLEYPFVVVDFSAEATGGTPSG
DNTRAKSSTSLKETGKKTSQPAAAATTGGANVTGETKLGILVKREENFPQWYVEVITKAE
MIEYYDVSGCYIIRPWAFFIWSRIQKFFGARIERMGIEDCYFPMFVSKSCLEREKDHVEG
FAPEVAWVTKAGETDLEVPVAIRPTSETVMYPYYAKWIRSHRDLPVRLNMWNNVIRWEFS
HPTPFIRTREFLWQEGHCAWQTEEECSQEVLEILDHYAAVYEELLAVPVVKGRKTEKEKF
AGGYYTTTVETYIAAIGRGCQGGTSHNLGQNFGKMFNISFQDPEKNDGSTLIPWQNSWGL
STRVIGVMTMVHGDDSGIVLPPRVASVQVVIIPVGITKNTTDKERKSLLEGCKTLEKVLV
SGGIRAKADLRDNYSPGWRFNHWEVKGVPVRVELGPRELASLKISLVLRHDGSRRSLLWD
KELPTAMTLLMDEIHNSMFAKAKRERQENTKKLTEWSDFTPALNRKCLVLAPWCGEMSCE
EQVKKDSAEESKAMQSEEMKDDARAPSMGAKTLCIPFDQPESVEGKTCICKSCSRPAKHW
VLFGRSY*
>TCRU_protein (LYR family), putative Complex.1
MVNLSFCLRHKLRDAAGNAHNFAFDIMTKVYREAVYAKDARYAGNPMYPERQTSATAAGI
ARSPPASASTVAELGKIQKGDQTGASTSASSEMPRSQRRSGVQVDILNLYRDMLRALQRL
EDPRTRKDLRKFIRSEFDSNRDIPRRCITRIEWHLHHGKNKLEELRTMRPDTKFFLVK*
>TCRU_161 hypothetical protein, conserved
MRRAAWWCLHLIGVVAPFSSTGGGRCVHLPADGDSADGSRCTESRPSGPSKTTARLTLNA
LSTDVRRLLENSATRFWETPGSVDTVLTILLGHQRGSHGGNSDILHPLLGVEILKGLGFA
VWKGGTIGGGGGWARRSGISKEDLGKVARCVLQPLLPHVIGHPRVRSLLPVIVEWLVCIS
DIPLSEWLPQLSLYLDDFAALKTNGRCFMGPSPGFFLQYMTPKLLHEAVDTQREVSLDLR
QVLDRMVQLLATGDGVALTPEKTLSDGSRSVSTSNDLIDCIFWQGEIPLILRNNFVREAY
VRLCHSTRCEANEYFPHAGFVGKESQTFLILPVVDDDVFRRLLLRLMPTSFCSAASETAA
ISLDYLVLVKPLLKLEDPSIIFRFITPLSEFVSVVLDGVFSSPLRLSFNGIRALIYSIIG
ELQQLQKRPPPSCFSLLPHKPRIHLLKALCDRLLCDAERKLKVSGADATFPGVPLQDQVN
ILRSFSHAARRLVRAVQTEKTASLLEEGPEGSALQAGGVVVKHNDVTTILRNTAFRVLET
SLFRYYDALEKWSSLSTGGDARNNDHVADALTEIEHHAGGRSTFFTARHLLQHPSRHDVT
AVIEALRIVAIQALLLRLPECREWLRANFATAIAVAFFDVWHRTMKKSLSCNMRGLNQEE
ESFSVFMESENLVSWRLLWTMLLLHQSCCSCDASMKSQLGINVGSASICAVFRSLLDLLT
LHGTCTEFSSFGSSLPLQDVEVLSTAEAEAMPEVKEEKRDETPKSLPKCVAYSAMGGFSI
GGSTTRWELQEELLSLGSGVGRGLWRWLGTPRAVWEVVSAGANNTTTVTGTMPAGSGGHY
AGYLLPWTTVAHSRHSLRLYDESGQSAAAASAFDANLSALFQLEDRPVVRVVGLTEEAAL
FREMAFTPELLLGSGVSVVHPEACRRSRGRDFLMEMEVDDDDGLD*
>TCRU_162 hypothetical protein
MEQQTEIFGNSLDALLMETLEAVKKAHENHLTQAEWRNTASPERRRGVRKERDLNQRAQD
ESLDALRSELKSVRVELAEKESAIRTLLRLQMRQGEKLHQELRNEPVPKTPGSLGNSPAS

FSRVRTSSTSLGGEKFGDDTSNGPVLDSPKTAPRSGGALCATEDGVQHFHSADRTGMIRG
TLSSFVPATVSGHGKPNQPRHHRSHSQHMPRTQFRSLLPSGEIVSSSSSSSGRFSNSLPR
EATDEHHSCSNRVQRGVMRKHQEVWMRQAEMMGILTDVSQYGASSYRTTSLQTEN*
>TCRU_163 hypothetical protein, conserved
MQHKRRRHRIRQPTQLGVAHRSRRHNRRVTDRHVRVCRQVVHKHKRAVAAGQPAHAHLQA
PVTRRLAAVAPHVDLRTAVAHAVPQFDAQRAGKHRRHVERHSHAVRDVHAVHQHRVHGAA
NRDGSVHRAAPQSQHHRMHRGHPRRSSKQRQHHKQRHTHSRNGPALHTVPAARTRTHRRP
HPPTQTSINRAVVVCRTRPVDHNSSFQNPFLQIANPVTQFRQIVILILQVIPNTAINP*
>TCRU_164 hypothetical protein, conserved
MDTVLNKLIANALLYSDGALHLVGARDNEEKSSLFPAPLTEELQMITSILRNWADVDASF
SASPVSTVGLVGYLSNAGTANTWIDECRCVIATVTNGKNVTNGPQFAGQHCPVNRWEDNN
HCGFVNYDFALVATVAICETHAGVKSIPLIGVK*
>TCRU_165 hypothetical protein, conserved
MAIAAMRVALLFLLALAAAAAWMPAVHAVVLRLRGGTVDRAITVGRAVDTVLIDGVSITN
GVAVVFDVPAMLPGALRIELRNCVCDGGAQIYVRGYSGEPASDRSLEVSVSGLSGDYCSL
AFVHNLPAHTNVTVRDSTIVTPGPMRYSQLSGLTDAVASPLVLHATSLLQSQLRVSNTVL
RSLHAGGSAVHVGGGVDLLSSAVVLDGVSLEASGGPTASAMRVASSSRLSLRSHSVFSVT
NVSVVSSGGGIVLGERLAVFDSVLRFVRVEGSVASSLVRCGGGTVGSGGWLELRDVWAVG
EASSVASLSGVTLGGGAVSIARCVATGATLVSGLTITSGAVSVQCNRAGGRVLQSSGDYR
MAGLPSVSVVPCDGCAAALTCFDALTASFSDCVCGCRAGGVGEACLPFDVPPARAGDGGG
GAQGCVSGVTLTESVTVGGGRATACFDSVVFSGPITVAVDLRSMDAFADALNVTLRHCVL
AGGAQLRIGGLSESTAYLMPHALVNMTNVTSLEGTIVLHGAMPLHSSVLLANSTLRATVG
GSQYVPTTPGYARFRRGPALVLDGVRLLSTRFVMTRSTLVCGGDLCAAILVERGLGVNLS
SVFYMDNCVVMSRAHVMYALASDLRVSGGSVFSIQNSSWIASSIEIYEGACVFRDVALDG
GSVLQVVSSNFRLGFAMLIAETLTVTGGSWLVHRDNEFRAAYVVYVANENGVVFHDRSVW
SILHNNSLTARTRQPL*
>TCRU_166 Metallopeptidase family M24, putative
MGRGYSNSRSKSARPTLRMKRRRSLSLQQLRGSVRPAHTTRQKVAAVPKPEAQTPTVDAG
HKTSAKRAPTPQRGGSARVRSASTIRQKLALMEKELEGELEPAERVAETIVKPDVRTKYK
SAGRALDEVMDILTAACVPGATTKQLCDRGDEELLQRVRAMFSKAKDADGNRILRGLSYP
TNVSVNYVLCNHAPLVEEEAVVLRGGDVVTIHMGCHIDGYPVTAARTVFVPHDVTAANEE
VRQLTQGASNAVEAARVALHGMIHLLQPGMLNADITDFIHRVGNYFEVQGLEGVLSNRTK
RWVPDGMECIITRRVSAEDPHQDVADCTIGANQVWTLDVAFTDHPSYKVSPADGVTTIYR
RNEVEFQSDARVRSVLASLQEITEKHQCFPFSLKHLENPLKARMAVAMLRRQGVIDPLSV
LRIKGDRHITARFSATVAVSERRVTVLCGLPPAEPLVVPDDVRPPPLPDDIAAVLSEPLV
FAKGGEKQQEKKADKEEKKKGLHAAADFNANEKEQQKE*
>TCRU_167 hypothetical protein, conserved
MRYSQLSGLTDAVASPLVLHAMSLLQTQLRVSNTVLRSLQAGGTAVHVGGGVDLLSSAVV
LDGVSLEALGGSTASAMHVASSSRLSLRSHSVFSVTNVSVVSSGGGLVLGEHLAVVDSVL
RFVGVEGSVASSLVRCDGGTVGTGGWLDLHDVWAVGEASSVASLSGVTLNGGAVSIARCA
ATGATLVSGLAITSGVVSVQCNRAGGRVLQSSGDYRLAGLPSVSVVPCDDCAAALACFDA
LTASFSDCVCSCRAGGVGEACLPFDVPPARAGGGGDGAEGCVSGVTLTESVTVGGGRATA
CFDSVVFSGPITVAVDLRLMDAFALVLNVTLRHCVLAGGAQLRIGGLSEITARLMPHAFV
NMTNVTSLEGTIVLNGAMPPNSRVLLANSTLRATVGGSHYVPATPGHAGSRYGPALVLDG
VRLLSTRFVMTRSTLVCGGGSCATILVERGLDVNLSSVFYMDNCAVMSRTHVMYALASDL
RVADGSVFSIQNSSWSAPSIGVYEGACVFGDVAVAGGSVLQVVSSTFRLGFAMLITNVLT
VTGGSWLLHRDNEFRTAYVVYVVHENGVAFRDRSVWSILYNNFTYGFYSSTIASMTSSWS
LPSDSRPTIYGVCNEARGSPVTDYQEDLNIGTPVTVLDCGACTMDAVCFATRTSSISGCE
CVCAAGGYGGTCLPAAVPDGLGPLPLPDARDTEVRCVHGGSISSVDDPDPGVRGLCFVNV
TFTAAIVLDLWSFDAPQQTLNITLLQCVLMGLSIKGSGARVHVSVTSSMLDSGALEFEGA
KPRSRVYDHHPLF*
>TCRU_168 hypothetical protein, conserved
MRAELRVACPTKRRRQRHHQQRRDNAPTAADVVLRQAPSSRRRRHGERRARHVAPPQRAA
HRRRRGPRGRQRHRLRHLQRLRRPVLRRTVVRRPRWRHRRAARLRQRRRATQQRHAGRAV

APVHVRQVHRQAVAPVPALSTAAAARPRHRPRRSSKAAHVGVAHATRHGAEFPDDAGGPV
VHRPQCLPIERQAPHNELPAGAPERNGAVHHDEPAAGVPVERQCALREIRTARVRRHRQE
PAADVVAAHRQPRPGHERRRPPQHQQRAIGQRTGVVVHYDGGRAGLHTAAKHQPVRGVHL
APRQAQHSAPRRNHARTSVQRIFATEHSRVQRNTATDKLQHGAVHHHRPPTSHHGHEGHA
GHNQHGTHKPQARQHKHRCVRRGLRAGKIHKRRRPRGDQQGVRHRQHGPRRERAGQHKRT
VQRLHIAHRQLHRPALVAPRRTRTAQRPAAHHAQHGTVQQRHVLHNDPHAVPRHPRHVEQ
RTHAVQHNVAQRHLACAGRHNEH*
>TCRU_169 hypothetical protein
MTMAVDSHDPSVRYLFFEEQRQQQQQVPVDGTSSGRLPLLYSARPACHPVNDVRSAVALR
RITEGFLNLDQQMKMWRRHLHRKLGNLESRLSRCESVLLLKKTPVPQPAVVEAPTTTYND
IYDGVEDEFKRLHLTVTALREKAAECCRDGQSFFPPNRQGKKGRGKPAGKHAMCDDEDVS
IEGGEVFDSHCEHVGVAKRMSPTADTAAVESGESVGLTPDGAEMPSACLFLGETVVDGDW
QHVEGMQPREASCCLYKLQNQSSFQPTPSFSTMTPVSEQKYFAMDSTCRHDWSPFIHEPC
RPEKGIIRGGKPATTDKTPPNVPDLRMGSTATTTQEKCCEINESPPLQASSLERRLIYSP
ETPKRMQGQLSPVPSDAARSASSSTKRGMEIPLSNADSVEHLHNLAEPALPSKPVTNGQK
GPDVTPSSQHGGAFVDAFASAVAGVPSSSPLYVLPQQIYSGRGDSCDRRSEWDNTEDEEK
ASENSNEEVLSAVALSMPTVGTVWQRVVSLAHAEQYYDQLSRLNHPSLSMLSSDILEISE
LTVQET*
>TCRU_170 Sperm-tail PG-rich repeat, putative
MVLIGGFTEWAHLRLRDHRPGPMSYIPVRNDVPERSILKKYPARPAEATVGPGEYQIPST
VGQCRSTVFGPASGPESAADAKAGSEKSSKENLRKKKGRKLSPLPKQYSLALSPDTPAYS
IYGRLRDRPLGSGVGPGEYVISSSFDSSGKGPHFGERTKLLTTRDIVPGPGAYQLPRFGD
DTSKRKEYITSVRRVPERENGPGPGNYDDPTTIAARLAPKKLRLYEGPLFGGRHSKSNCS
LSTGPGPAEYGDVSRIMRKSIRCTPKFHPPVQTVPPHKTVRGTMELSQGPYTYYLPSDFD
RDYNKGVSLGARVFYQPKTAASDAVGPGLYDLGKPPMTSNGFRFAAQPYDAIALAEMEEK
AAAAASNAASGPNMYYPNLDAVRPSRYRAVAGFGLGERFLVQNAGGPLCYDVKPPEATRA
TVFYRGDYRRSKNLHGLGDGGPSYVVENDTIADSTRKGKGFTFGIRYPARATHQVCKPYD
ATTNINCEYPDETTWMTKLK*
>TCRU_171 oxidoreductase, putative
MSKITSKGWCYARCGPISRVLKHVTFEVVPKKEEVIVDVLQAPLHRTDAAVVNGTALGRR
RFSSAGFPRVGGCEGVGKVVEAGASQNVKDGDTVWVAPLHGTWATRVAVDHKMVHKIDPK
HVSLAVNASNYVVAQHLLNGFASLRKGQVIVQNGGSSPTSLAVAALAKPLGVKVFTACTP
GERFKGAKERHAKYSSEVFEYNGKGARAMRQAIGNVGATLYLNGVGGRHFDTFLGLVGCG
GHVVSYGAQNGVGLMISGSNLIYNEVTIQGLFLPSYLAGISYSERQTQLDFVLQQLSSMG
FSYPTSVAASLEQLPNVWDDAFVHGGKKGVVIVGK*
>TCRU_172 hypothetical protein, conserved
MYVVNLCSLPRQLLTLSLCEHHSSLGPAAVICDLNSHHELRDGCSPSTTAGEDLAATSTG
MEIELSDDPAQATWISGRSVSFPDVTAQRVLRVSHWTSTRLHGLGPPSAIPHCRDGGRHP
ATGRHAATTENMTPLSCVKLNVMLPPRRVEHLWPL*
>TCRU_173 hypothetical protein, conserved
MLRSMLEMNRTPLGMAILGLQKIAARSETKQARPLTKEEMNQVIRSRTDWKERVVFRLAC
ITASRWSEIAALTPNNFTMEADGALILYWSVAPKTATTDPHRASRFVRIRGQDAFDTIKL
CRTLQEKEKLTNITNVKVERALAPWNATTHSIKRGALRHAAQIVEALNLNPHVISQLAKH
VDPFDLPQNTVRYLWRYTTLLTQVASLVALM*
>TCRU_174 hypothetical protein
MGGACLPASGRGRAGVVGGGHGGEGRGPTESLPPGLLFWNAVRGSAEKTAAAGRRPPYGD
AFLATMEAGGSRTSGEPAGRGAVVALLLPRAEEQHEARAVFASYFAAAEGQRTRRAGENA
LGRRRGARV*
>TCRU_175 Glycosyltransferase family 10 (fucosyltransferase), putative
MHTRSRHRRGIIFLFCTIAIFSLWNAGGGDVDSFAANVEGVLSPQSSDGHPRHVRTFNGV
NDVLVVPTRPGTYLCEYMSNATLLPEGCVQSCGNDGQENGKDFNCYVHSRHRVAEFRRAD
IAINHNGPVPSCPFGQRRPHLTLFYTGESNHTDKKRSTEAYQRLYDVVISFHHHRPYYFT
WAHRQQQQFLKILHGNNQPLANKDAFDWGKWQQRHSAVAVFVSRCKARRAEFIRRLSEHY

PVHSFGACARNRAIPSECARRTGRYPQKLCVFQKYKYAMALENSNETDYVTEKVYHALLS
GAIPLYWGAPNVEDFLPSGRGSIVELERLLPGQVGDDARATANAKDAFRGFGEKLRRLEE
DEASVRRLLRWRRAKRAAEWGNSFLGNLYHPDPFCAVCAEARLKRSKDGKEK*
>TCRU_176 CorA-like Mg2+ transporter protein, putative
MREGEKGAKVHGLAMDAQEVGSAAVGIVQPMQRCLVVHTATAVPFSTNVFCNPDRVVDDL
RKRMQDGEVSPDGPCVWVDMQGCTDEQNRNVLQLLFPDLQQSQIEWMIRCDTYDTVELQP
VKGEYLIGSLACPPNRGPSLSAPAASEVEKENTVVCTFACNDRFLVTMHAAPFVGLAELL
RHVEVEGSGGHRGGASAAPNTASPQMQRSIAPAPSLRGITSAAILSLLVCFTCEAFLPDP
TSLLAEVGNIDEMVLLISPGEQDQRDLLRRVALLRRRISNFRTGLYLKEKLLQELIAPTM
RLSFVAKEPDTVRDYKETLEKVRQVSERLDDARDMLNQANLNFVTGVSMRMAQASAGLDF
KMSLLNQLAAICLPIHLVISVFGMNCKVPFNRDEYPTLVPFWIICAAFVFWALLCASPLL
RIAIQGLRATPVTSYE*
>TCRU_177 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MLQGNKASVYVDGKLLGEEETMLTGETPLGLVRFCFGACEIHNFPVTVKNVFLYSRPLNP
TEMRAIKERRHIPRIEGVRAKAPAGSGLLPLLLLLGLWVFAAL*
>TCRU_178 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGVGCGFADKVVEAAAGVVASNRTDEENLILNWYVLTQGEC
ANESTTGGKLNVTAERICMHKVMKEVCDAFYNKTSGVTHDRDVEFICTYYATIPEEPVEP
PTPQGPPSHSAVSNATSDEGTPKNAPESDVAGRGEGKEDDKEHGNTKQKAVETAAVESIT
RSTDSEVSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>TCRU_179 DHH1
MSSEDDWKKNLLAPKKDTRKKTEDVESRRNVTFEEYGLRRELQMGIFEKGFERPSPVQEE
AIPVALQGKDVLARAKNGTGKTASFVIPVLEKVDTREPHIQALLMVPTRELALQTAQVTK
ELGKHISGLEVMVTTGGTTLRDDILRLQNPVHVLVATPGRVVDLASKRTAKLDRCRIIVL
DEADKLLSQEFTELIEDLYTYLPADRQSLLFSATFPVTVKDFADRYLRNPYEINLMEELT
LRGVTQYYVFVEERQKIHCLNTLFNRLQINQSIIFCNSVNRVELLAKKITQLGYSCYYIH
ARMQQQHRNRVFHDFREGHCRNLVCSDLITRGIDIQAVNVVINFDFPKYAETYLHRIGRS
GRFGHLGLAINFVTYDDRYNVYRIEKELDTVINAIPGEIDPELYAA*
>TCRU_180 methylglutaconyl-CoA hydratase, mitochondrial precursor,
putative
MRRTMWLHTTAAHLLLDGECRLTRMTDHVGVLTLNRPSRKNAIGQTLLRELSECIRMCRD
PANAIHCLLLESQVDGIFSAGADLKERRTMSLEASRAFVKDLRDTFTAFEDLPMPTIAAV
EGKALGGGCELALCADMRVAGAAAMFGLPETSLAIIPGAGGTYRAPMAMGLSRALYFILT
AEQLTAERALQFGLVNEVVPEGGAAAAALSLAERIARNGPVALAAAKAAVRHGFGRPREE
ALRGEEAQYDVVLQTEDRVEGLRAFAEKRPPKYMGK*
>TCRU_181 hypothetical protein, conserved
MSTAVLAARACARTILWQSLRLSAFQGAVPHVLLVVDRLPCTLQKVLLEGYMQELDAINM
GSSNPVEGPPRLDLDLLATTPSYSNGLDKDWKVTYGVLPFSAGSFLEDVQTLQAFLRQCG
APVDTEEGRIGGQWSEEKMKGVLDSLAPILSPYRADDNADGSVEWKDALLHTLRAGQPRE
LLGCILIQRNAFQNELEKYRLRLDLFKMGLRVAEHNHLECMSRTADTLASGKDGGSRERC
LEEEEIIYYMQSCSLQPHVAESMGRAIADSIDALSWSRRTVAADGSDGVKLDVVPPASFY
ESLSNADLLSVYNAGVLRWEGSCYEKNTVTGMDPSAASWNISGPGAPLRIICQDGQVLSF
EGGLEECLLNTGYYAAAHAPERNCVQGHRQRFPVRDAGEANKVEEGAEEKEEGDIASMRK
ASDAEKRGRLKKKEYLAMLKRTGKKNTAGRTSSPSDENDDGVRRRGNDCGACVGSSIGGT
FPVGEVISESFDLSKLNGSCSVFAYPSLFKEVTMSDLNPVTMRIENGIVTDIGPNAPEEL
VELVSLVRQAEGACYVRELGIGLSPHVGRGRIVSDVTAFERQFGVHVSLGQRHPLFVKQP
AKRNADGSVAVQVDGPVLKRKAGKYHIDVFLDAARLEMGAFVVDFTKGVCSFSSAAAAAV
SCA*
>TCRU_182 hypothetical protein, conserved
MPYFVNSLSGRACGLLAGAATAVLFAFGGFSDGEAGWLRRARRQDTVPLFDASAIERVEE
YARYPCQAFPGYSVVVSNYYTRVQKDDVHRNGDGGETLLKRLLSLFSNDTHTAADRGDSS
ADENLLHLVREVVGDSRAPLPDTDTSTTAVNSPFVASSTWPLGTAKYAAMTMEPSSSFSA
AGEPVDVMRRLADRTTNQSLIRCDPFASPSMNCVADASYLGAPYLRMMLSAFLLLPSPLP

RLRVAVLGVGGGSLPSFLQQHFSRDIMRLDLVDAEPQCFRAAVEDLGLRETMRGGAMSCH
VSDAAAFLKGAVTGLSEDAAAVFYSGASPPFVKEAPVVVKGRQRAQRYDVLFVDLFVGST
PPAFLASSSFLQLCHGVLSSVGVAAFNLPAPDPEFMVRCRRVFGRGNVFQIPVPASANVV
VIARRVVGSEMVDGVPISRRHFYRRAEALQKSHALPYDLAGHYPFWWRFW*
>TCRU_183 3-keto-dihydrosphingosine reductase
MLLSLLVTIGFALVVAVAVLAAWSVQHVPPFNIKSCRALVTGGSAGIGLETARQLVRQGA
KVVVISARRVDLLRAAAEELRREVGKTGTQVFYVEMDVSNEASVAHAVEEIETTMTGGAG
LDLVVCNAGFSIPARFVDTSSEDVRKMMEVNFFGCVHVVRVVLPAMLERHYGRIVLVSSL
ASRCAIAGYSSYAASKAAVRAFAHSLDMENSCLGVRCQVVCPPDIETPGLQSENLLKSPE
CKAISSFGGNVPYTAEAMAKCIVKNIKRYRFEVSLGMDAVLLGLGSAGIEPATSLLELTL
QFFFSGWLRLVMAAYSKVHYEIVRRVRGRESTTVHKKDT*
>TCRU_184 serine palmitoyltransferase, putative
MPSYVTTETLIDVKGEVEQITAKTDIWMGSPSETCNKESTTTPPLSPQETDDARQEEQEV
VKTCQQAEQPLQEPRKNGEEMESCSLLFKIGVYMSFGMLTLFSLFYEFYYRLFQKEKERD
GYAPLLKGFDRYWQKYFYQRIRDCFNYPIDSRPSRVIGVMERVSYDYNENFSLTGNILPC
VNLSSYNYLGFASDIPSITRQVLDSIDRYGIASCSPPQLAGQHQPVVQLERAIADFLSKD
DAIVCGMGFGTNFRGLPALFGRESLVISDSLNHSSLVNGIRMSGARTKVFKHDDFQQLET
ILREAVVLGQNPRGEYLPWTRIIIIIEGIYSMEGEIANLPRVVALKKKYGALLFVDEAHS
IGAIGRTGRGVTEHCGVDPKDVDILMGTFTKSFGAIGGYIAGEQRVIDYLRIHSSISLHC
DTIAPPCAQQVLAALEVISGRDGTDIGRKRIHQLKENSQFLRRGLIAQGLIVLGDDSSPV
IPVMLYRTGAMPVMARECMRRGLAIVIVGYPATPLLGGRIRFCVSAAHTRDDLQLVLDVI
KDMSKHVQLQLRPIPKSLQE*
>TCRU_185 hypothetical protein, conserved
MNMNDLLFQAATQTIDALSFTQSHVIDEDFRAHSKATINSVRSLQREQRSRIEQNYGPRA
VSSDAIAAQLRATYRGETTSLELMKEANERGVPPAFMANMSHSKCQVFKKEMKRRIHEWE
RAFREEHGVAVTAHDKASLHHVYELYKAAKNRLKETESPRKTVFEPKVEDTSELHQPQYY
EKKHEPYQPQQAVYEGGGNNGDAGRDERGGTVGVQPSQIRGSQMDIAGSKQFTAPASVTS
SINVPRQNSPARPIRKGKPASQMSDDDLATEKRYLKYILHRFESDFEQKNGRPPTKNDRR
VWTAEYTRYGELKNEILRRSANGNQGEASNVEGGAHTRVSAGPVTIPENF*
>TCRU_186 hypothetical protein, conserved
MQGSSLSRRVRVGGVEPEDAVLRAELFRTFASYGVIEEACFEEDRAFHSGAAIIQFQRIS
ASEKLQNDVEETGRRWFLSFLPPIVHVGAELLVTSPKAIDTSYLRSLVGEGVKIEEKLLS
FPGAKRIGSTTAEEGAVDYGSKNAGARDVFIKALSSVRAHAIGRFAVLMQFATVHDANEF
LTTHQMPFLTSNEMYVVHVGPDAALQHALKHILLTRRSTKDVARGSVLRGFVLPQHESGN
IGGSGGGGGGGNRMIKCEVDAGLIRKGRPVFLQTQTNFVKVSPWDIVEVRLTSADGEASE
NLEAELRGVVNAAADTAEAQKPTVLFQRLRQAGVSSSSSSSISTAASSKKALAGKLYQAL
HARKTEPDNAGEQLHSFPQGLHAFSVVSVCIQRVGDDGLYARTILPPHATSNTPSREWPV
FVPSIFVPCEGGMGWKDFAVPGERMTVTLLYATAVGGSEAALRLVASKREADMRRASAFF
VSAATPGAKDGAGGGFNDTKTLSVGTSFSGIRAVWLPRTPSTENPVYILLPSSSSPSVLF
TITVLKHATESPTDHQTPETMTMDAGLHPFVIASIVNSDRLGHYAVAVEEAVYRQMEAER
RAAEIQKESEQDAMLQRIMTEVFSNGASVPAGDGDNSAQGRKRPRYSQEE*
>TCRU_187 60S ribosomal protein L30
MAKKNKTKVDTINTKIQLVMKSGKYVLGTKQTLKTLRQGRSKLVVISSNCPPIRKAEIEY
YCTLSKTPMHHYAGNNLDLGTACGRHFRSCVFSITDVGDSDITSA*
>TCRU_188 60S ribosomal protein L30
MAKKNKTKVDTINTKIQLVMKSGKYVLGTKQTLKTLRQGRSKLVVISSNCPPIRKAEIEY
YCTLSKTPMHHYAGNNLDLGTACGRHFRSCVLSITDVGDSDITSA*
>TCRU_189 DnaJ domain containing protein, putative
MSLSFIESGFVPSDGMRRGVEAADTSAAAELLHLAVPPLMNAGGKTRVCVAFYEAAQCPF
DSRCEHAHHFSELNGYTQNKLLETVPVESIPKHFVAPLNSNSSSGNNKNDRTFYATDGNA
ANYTATAAVDGGVAHRSLGGEHVEKEKTSTNRRSKRTARLYDISGSNTNLCDNSLSSLAS
STDTLLLLGSVHDSKDVSPQKGTRRDEGMEAFRIRLPPRCRYPHRNTRGTYYDVLGIQRT
ATQEEIIASYRRWQKEYKSMKQVDPQGADAHDTIVVEARNVLGHPVLRSEYDRTVSAFWS
SNISCSKDLTRGTATLSSANSSRSINMEATTNTMRIANGPSSADMMSLTQSGLPEDSIW*

>TCRU_190 NDUFA5/B13 subunit, putative
MRGSHSLRAALRRTAALFTISDEYIPRAFPVKSTTGLAGVAVEPLWKPKLLAAAAELQAF
LTTSDIPPESTYYNIAMTLVKRINHGIKECQDDWCTLEKRYFWGWPVEYILQVTWRELET
AQKWNEWRFWELDPEQVKKVAREDQNIGREGLGYNSPWEQVVREDFDKRKKALTQEEMAE
LKRMDTERMARETAAYKERKDRIRDDLEKARGDMLKKFLNKRFAVDKDLQRMQPGKRYSG
KTSEDLIAELKSSVQNNPQKQDPKK*
>TCRU_191 tubulin gamma chain
MPREIITLQAGQCGNQVGSEFWRLLCAEHGIRHDGIVEPFASAGDDRKDVFFYQADDDHY
IPRALLIDMEPRVINAIQRGSMQRLFNPENVYIHSEGGGAGNNWAHGYEMGDSVQETLFD
MIEREAENSDSLEGFVLTHSIAGGTGSGMGSYLLEHLNDRFPKKLIQTYSVFPNQSRGGD
SDVIVQPYNSLLAIKRLTLHADCVVVLDNTALNRIATDNLHISSPTVEQMNGLVSTVMAA
STATLRYPGYMNNDLMSMLASLIPTPRCHFICTGYTPTTLDTSNIQSSVQKTSVHDVMRR
LLMPKNMMVSTSMKSGCYISLLNLIQGDVDPAQVHRSLERIRERSPNFIPWGPASIQVIL
SKKSPYLDTRHRVSGLVMANHTSINSLFQRTLKQFDLLFNRGVFLEQYKRYGPMKENLDE
FKHSREVLESLVSEYKACESSDYIRNF*
>TCRU_192 Ankyrin repeats (3 copies), putative
MASRVEEILLAVEHGNVEFLSKNLTPQNVNYVDTERRMSLLMWAVALRKHSIAEMLLNLG
ASMYPRDMFQFNVFHYAAWSSDVKMLEILYYSTSCSGCKSADLNCLCLAHLKNRQFRPGS
RSLVDLPHPYTGRTPLMLAAVRGDVEMVEFLIKKAGCSLSVRDFRGSTALDLAACCGHKA
VVILFLSNGDDSADFVFESTRRQAEANCENAMTLQQLEVKKDLNLLLCREWLPQSLVAIS
*
>TCRU_193 hypothetical protein, conserved
MLLLDTTAESLLRDPQYLLRLYHKVIQYLVKCDPSSFARSLSSSFNQIDTRYRVRSREQA
IEVWSLKGILRQILPVSVMSDRELSIILAMLPLEDYGGNGTGNGGDDVLVSPVVLLLCLR
KMCPVQASLVLEMLRRIDTRPKRPHPYESACGKALLVSARDGRGDACVFERAAILDYLTE
SYDMTLSEAFFLTDYCSMGLPPSSSTVAIDGSYLYAFLYQRPLPSDVKYPLLMSVFAEAI
CDPNIGAPLGTLALIEGLHRLSPKPNHGMHREEVFDVNIDTGGELEHYSLTRKSFEDLCR
YLRVGLLLEEVHQLFYYLRGESSEELLSAHTLLCEFKRHFVPVSESLFQIVEEAVRRYLV
KSGGMLALPRLHLALHGGPLSVARFIDVLRVAGVPEAVSDVELEWLRFKGWDRERLVSLL
SGRFPANREALVRQLFDQLKNVKGLTMKQDHVEVERVLALFHPEKVEGTLIGSSDDWRFV
MTQCFDGNISKTLTYDQFFYFWRAVSAACSDDSVFTMILWRSFNMHTSR*
>TCRU_194 kinesin, putative
MNGTNSFEETYTHLMKEVETLRRRVCTLQEEVNIEKQRSALVSKDDSLNKTPAKAANRCK
ADDNSVLVEENPEAARMRRHVLELERQCAVFQSILRDRENELNAFESRGDIAEKVRRELQ
QQAREREEAQRALEEAAPQLETSELLRKVTDTIVWMQEQLDGVCQQKKFMMKAMEGMRCE
QHRIMTDLLEARKNVLQLENAQEESFRKFNDVFAENTKLKGIIDELNLKLLREYAERAIR
EETMSWFKALTERDEQCERLRAAFEDQRNLCDVLQSRLNSTEQELDRSSKHQGALLQEMR
KKDEAFRTIWLFLTPQQKARFMSFGDQSEGANGTPSSSLHQGHENVQLRSQIRTVKRQLE
EEFLRNKELEYRIEDLEKENELLKKRLQNCEDEYKSLVSLEQDYREEREHMEQQIAYLFT
YIEEHNAKQQVSERQLCELKSEWERLNEEHRNAQREVVELTAKLEQAKGEIWAQGVDNNK
LKDRLKEVKKQDALLAGLHRQLTATQHIGDEASRRLGIADRMQQHVASEANIYNHHGDII
KRKAIRRNSDTLLKALMQRVDSAQRVRGAAVQPLPLNNRVQRLRNEVSQQFRLCGPSSLS
FNGTARTREESFGSSHTHHSGSRRRKRTMLHKPHDLRSKPLFRSSNFVVAEIPSFIIDRT
RRRNM*
>TCRU_195 electron transfer flavoprotein-ubiquinone oxidoreductase,
putative
MFRRSCRIFCAPVERMVEEFDVVIVGGGPAGLSAAIRLKQLAGDAKDDFRVGLVEKGSEI
GAHTLSGACIETHSLDELLPDWRKATDLPTMTAVKNDALYLLRDKERSMKSPLLPPTLHN
RHSYIVSLGSVCKWLGERATELGVEIYPGFAAAQPVYDGSGEALEGVQLNDVGINKKGEK
TPQYEPGMIFKAKQTIFAEGCRGSCTKQLEKKFGLRGEGNFQTYGLGIKEVWEVPAEAHR
PGTVMHTIGWPLTDKGHHNTYGGSFMYHYGDGLISLGFVIGLDYSNPHIRPYMEMQKWKT
HKLISSQLKDGKPLLYGARTLVEGGYVSLPKLHFPGGLLVGDCAGFLNLPKIKGTHTAMK
SGILAAEAVYDDAFASGKEKRDGVECRSYDDRFRNSWLHKELYAVRNVRQVFARNFFQGV
LYTGITTTITRGWEPWTLSHHKPDHEALKVAADCEPIEYPKPDGKLTFDLLTNHSRSGTA

HNADQPAHLKLKDSSVPEKVNLAVYEGPEGKYCPAKVYEFVDGKLVINAQNCLHCKACDI
KDPTQNINWSVPEGGGGPNYSAQM*
>TCRU_repeat, putative Se.1
MSGLFLPQLRLLRPQGSVTPVFLVLIISLFFLPSTALSSSSSPSSSSGPSSSVSTASGDS
EEDPRDAVKTATERAALPVKEYPELQRENEISAASEKLTQSKKDALGIKEADRSVVEPSD
SLALAHVMEEKQEKNPLQASEEKRHEKRRNDAMREFALVVQQEDDGVMPIVNDVDTLTTS
VSAAEYSVNDRDVDETNHHMNRDNAVDAAAEFGIEEIYSKEFPTTETETEGADAYSFVPS
QLSNVEPSELYQNVVRSIYNGNLSSTFELIKEGTLHGHGRLHWLLGVLHANGIGVPQSDA
KAVLHYTFAALEKVFEAHMALGRRYTDGLGVAKSCQDALEHYREAADVVVTNYEGMPNPT
ERFSRQFSADALKHGGHSNSKMVQMLMFRADEGSTDAIISLGYAYFKGIYGLRRNWHQAR
LYFLDALAKGDVAAYGALGRLYATGDSTANPAIGRDLATAATYFSQGAEKKDAVSLNGMG
YLHAIGFFNDGNSSAAKGRKPNFEKAAKFFAESVDRGSVEGTHNLGVLLLHGRGVPYDPA
AAIKQFGLAAMRGNVLSIWQLARHEQRKGNCEQAMQLYSRVAGFDSIFDHSNDVPYFALS
DGSSSSSSLYSSSFASSADNIFPQLLEMLAMAETGHAASRYQVAQLLDKLPIIEETDDEL
EDGVFAKSGRPPERALRMDGGVVWLQWYHNSMRPVPTGEASIIPLADARLLSQREALNML
RLRMYGLSALSGSAEANLRLGDFYYYGESQLVGVSMSRALLHYEAAAAKQDPKAYFNLGF
MYQLGLGVSGRDQVSSVSDALYRIVTNTLLEEETEGGGKSGSEANFSRTTSTKNIKDALL
AEEMRLYLAKRYYDRAMEFGSGGSGYAVKLALMTLNLQWWWLYFSHQQFGFSWMLRLPMP
MARGGGGGDGGSGAENETEKASMAPELHEQQQQQQRRQEHQGPKQLLSTGSETLPDVVS
HEWRWDDYTFAASATTLFLLLLLRHHVA*
>TCRU_197 Molybdopterin guanine dinucleotide synthesis protein B,
putative
MRRTRRLLFTGTTEVSAGAEETTTRGGGIPLVHPWAPSDAVTALPEGGNRDDMDTAPPVK
RLKLPDKVLTRLGKTPPASGMGNVEGDSAAKGVAEVIHSKKLAAAKHHASASDIEAGDDL
RALVSVRRIPRPQPRQGEGQQRSGELNPPAEHFANSNDEFIRFAATGRAENSDSSSLISS
WSDEKLQDDDGNADARTEKQRRVIDRHFAGYESENIESLSEEEEEEEEEEETSGSESSEN
DDGGEDDKDNNVPPKNEGDRAGFGLLERRRHQQREQQSQKGKMGAVKDEGGVDAATNHTS
DRRYRYTSMFFEMHIAREAMRPCHHTLICLSGPVTVQGPCGIIGFGIGEVAVGGFFLGKK
QINLYSEADRVVLTPVQRLKSKNAGLESLPVPVPFSFKAKNDPVTVVPPTIRESYEDAAD
DNDVEIFGAIDWVWVETTIGSWRGRFANKMPSIVLVVQPYDPYGLPPTRRHRLKGKGKKL
TDAFMEVPRFVARGNDVGIDAVLLPEVIPAIVKQGTGVVVVLGSQNIGKSTLARFIANAL
FSQHGVCYWLDLDLGQPEFSPPGVFSLYCVQQPLLRPRDTRKVKLVKGFFLGGSRPRCPV
ATAIAIEQLCAIVGPLQRRFPVVVNTHGWVLSTGRRMTVEAIRRLQPKHIVHLVKEGETR
WARDSELLMCPTKGLNSEVLHKRFFVRRAELENTKRKVNDVIGRLPYPHSVMNRPEYATT
AEWSGRVHTVNVTRSEGSLQQGIQPKASAIRSAIWQQHLAPIFCYYETLDEKRRKNGGNE
LQLTEADESTTLFRGQLRHFESIVLAGVDDARDMTDDMVCAALEHSVVALSFSLVPSSSP
LACVTQRQEASNGPLGNYRSLMDMPKGFSFSCFGFVESTEAEMRVSKEVKIRLPYHRDVV
RGMLSKEDDTKMIRVSLACTLAACTDTAALEAYFYGDDGGGK*
>TCRU_198 cleavage and polyadenylation specificity factor 30 kDa
subunit, putative
MFTDSAAHTSLAFEDALPDEPHATVKRREICQPFQHGKCRHGTACPERHVISQFKTMRLE
VCKHWLRGACVNGENCLYLHEYDDRYVPLCAFYQRLGECTNPECPFQHVIQVEKQPECAA
YRRGFCPLGPKCHLRHVFRPSCPFYMAGFCPLGPKCTMGHPVQELYNRNSVSERLRQRML
IERVDDPTFNKNATCYRCFDPGHLSPNCPGVQSGLLRRMLMAVQEPGEQLYFQSDGRSAR
KCCFFCGDESHEVRDCPKKPKNHQWHTHRRA*
>TCRU_199 hypothetical protein, conserved
MRFSRVICGRLRRRTHGNVPVMQQQKQQCAWEREETLATLPLSNAERTASALAFQLLERH
RRRHASDLHGRAAVGIDGTAEVGSHPTQEEIQEGPLNNSRTRPSHLPAVDAFTGYGKTAV
TTNLAHMADPWVVDTRNLLESTDREWEALTARSKMSATLTDTGDRPTMRAWVRYSRGNAS
AHLPEKFGEKIITPFDAVMRRYNSVVTNHRFRVVTVDAFCSWRVNMPASLTQRGTMRCVL
ARKEQLDRQNEWRKLRKSQLPLGSDIGDGKFDKERRNVEKLSSSRDFSSMPFASPVFRRY
CLQFGSHTLRRVAFLTDPTLYFVLCNWRSTGNESLMEVRQQAECLSHRYMSMAYLP*
>TCRU_subunit, putative N-acetyltransferase complex AR.1
MTTYRDFKLTDIMEFNFVNLDQLTETYSTSFYGEYLTHWPEYQRICVHPTTGICMAYALG

KAEGKGEDFHGHVSAVTVAPIFRRLGLGAALMKELEATTSLVHNAYFVDLFVRQSNKVAQ
EMYHKLGYIVYRRVLGYYRGDGPKGTFKDDEDALDMRKAMLRDRERGRSSVIPLAKPIKP
EELEWN*
>TCRU_201 ATP-dependent DEAD/H RNA helicase, putative
MSLAEMDAQQHLAVLGLSKCSENDTLDRLLAGAERGPSVDLNDWGDGCDLCVDAPSQPSP
AARAAPVMEDKSEPKRLKRKRTSTLDAEEDEFRSKATAESRAFRGQFPAFADAPLKNKNI
PPSSSLSTVFEADKACVDAESLPPLNELVHSKLLRPLTECLHITSLTCIQKQSWTPMVDR
TRDVLLRSETGSGKTLAYALPLLHQLLCECDARPIQRQIGSIIIVLCPTRELVVQVTDVL
SVLTRCALFLTVGGIHGGENRHKEKARLRKGVPLLIATPGRLLDHLRATVSFCVASTQTI
VLDEADRLLDMGFERAIKEIMGLLLEKTENSACSCDEIFTETREKYTLKRVLVSATITAE
VERLSHFALRSNVVRVGETEDTFSIPSSLRQHYALVPIKHRLSTLIGFLRSQIDAGAQRI
IVFVSTADSAEFHYRLLSRLQSPFCDRRKEVLFKGASKQNARQYGVKRRVEEANRHVQNQ
SEAIVTFEDDSGSEDDNDEGQTLSGRNALLDVNILKLHGNMSQVDRASVFKAFKHVGGAA
RRSLKGVLFCTDVAARGLDMPRVDWIVHYDPPTDPACYVHRIGRTARIGNVGDSLLFLMP
HEAGYVPYLSKFIAKESGSSFTGNEAAAVVATMEKRNYESFLYYLAKLDPKSNHIWMQST
ATLERAISRLVMNREEPVNELPAGDASRNDDLTRLALFAYQSYIRAYAGHSRELKTRFFN
LDMLHLGHIAHSFGLDKRPSEVRAQLQNLIMEDRKIAREASSLNTQERVRGCDGSRVRRR
LQVEVRHDDRYRSMIVQKQRKVTRDWFQGKKDGVPKNKTLQFTEFDA*
>TCRU_202 ATP-dependent RNA and DNA helicase, mitochondrial,
putative
MRRIQVAFLKKLRQRRNCGSFNERALVQRTCEHIYCSSSAREQLRQLIHESSVENALRHL
GEFSNDASVLKGSAWLGQLSKAPDVVGRIAVILPQFEKWYVARKAPEKVTMHEPWDWYPK
ARFMRRRFVFHYGPTNSGKTHAALETLVKAKSGVYCAPLKALAAQVWKRIDASVPCDLLI
GDERRFGGGAEHVSCTVEMTPIDYQIDVGVIDEVQMIADRDRGWAWTRALLGLPAREIHL
CGEERAIPLIRKVLYKTHELQRLEVVPHKRLVPLEVSPSLDGDLRRIENGDTLVCFSRRA
IFDMKKKLENISGMAPHCIYGSMPFSVREAQADAFNNGTRDVIEGKSGKKHVLISTDAIA
YGLNMSIERIIFTSMRKFDGKQMVTLPQATILQVAGRAGRFGVLRSHKFGRCTTLDSNDF
AVLCEAVNSRLPSLQKAGLLPTAEVLELYIRLREAEEGGRVTENNLASFYQRMREFSECC
QASDLFFPCDLSRSLLQVAKELEAVTDLSLSDRILFCYVPLNDRGKETYDLLRAFGHDHA
AGRHVVLRIDEEFERLVKQCDLVCSGDTRRAHQVLTRMEHLYRVAEMYCWLAWRFGKTFV
HLETATALKERAALKMEEILQHL*
>TCRU_203 haloacid dehalogenase-like hydrolase/Putative hydrolase of
sodium-potassium ATPase alpha subunit, putative
MGFMGVLCFWRSKKRGKDDEIRIVHAGRPSMEYCDNTVKSSKYTLLTFLPANLFEQFHRP
INLYFLLLTALQFTPSVAPVSPFTSLVPLTIAFLITAIKEGIDDWYRHKLDDECNSRWYS
IIDMETLNVERVQCRDIRVGAVLLLLPMEVVPCDVVLLLSSGENGEVVISTEALDGETVC
KKRYAILSDMYAQRPTTSVATVDSMQEDETNIRVAAEFIRDTECVIESEGPKPFLNSFTG
VARVQVPHDTEEEVTIGVNAENVALNSSVLRNTRFALGVAVFTGNETRVSMTRTTPPTKW
SLIDQRFNQMVIVVFVIQFILVTVYVGLSDAALEKDQHALWYLGMYEEKIALKEYVILLP
LRFFLLVSPMVPLSFKVMVDASKAFISILIKWDEEMSDENIKTEVHNSSLMEDLGQVEYL
MTEKTGTLTRNTLTLKSVVATSGKIFNPGTPHEASVVRREMRQDESLLQLMRVLVYCNTV
ESTRGITLNVAQTSAPKSPPSSAWVSPSPDEVALVEGATFLGVKLLERKRRRAFVMFGNN
VESATVLKFLPFTPERRRSSILLQIDGDTQFLLLTKGSDESVLPRCIKTSYNRQRVLHRL
SCLSSEGLRTLVSAYRYLTDEEAEIWLADVRRKEAIVTAAARAVNVGEAYESLEKDLIYC
GITAVEDQLQDDVCRTITQLRSAGIRVWMLTGDKSQTAKQTAIASGLVGPDDRVIALTPE
DVESLSVQEHFEYVERRVNYVLRKRKFQEAEKKHNIHRSWYVRSGLRDFVGEFFHHESIL
SLLYHPSSKSFSQDCDEYFTREDVAENEQEDLLSNSVTIQSGGYVILFSGKTIEFLKECG
NKELFVNFKRVLLHASTVICSRMAPEQKSFVVRTVKKAGHVTLAIGDGGNDVSMIQSAHV
GIGMRGREGTQATAASDVVVSQFCFLSRLLLFHGHTAYQRSAIIVQQSFWKTVALAWMQL
LFNIYTKFSGVSFWDSFSLMMYNSLFTVPVTFLCALNIPLSASVLLNNPQLYILCQRGRY
LNMVTFYGYVFRGFLHGTIIFFLAFGFLNDSSSGVMRFGHPMDRACDFYVSCFALVTLHS
CIILLETHYITFFHWLALIWSVMALFLCLSLYGLLSENHSLLQLLRNASFYLQWNIVVAV
PFISLSVYSAIKLFFFPDVLQLQRLIIHKMSKVPFLSGLWPFWVDENPSRFWGSFSVRHW
CHDKSLTPCGSQSVGGITSLDMQAQINAEDHCGEPHIVKMALDRVRDSTALSEPFIKRV*

>TCRU_204 arginine N-methyltransferase
MTTTETPAPTKAPVAGSATGDYYFDSYSHYGIHMEMLKDYHRTTSYRDAIWRNAYLFKGK
VVLDVGCGTGILSMFAAKAGARKVIGVDCSSVTVQARQIVKDNGFEDVITIIQGKMEDLQ
LDEKVDIIISEWMGYFLLYESMLNTVLYARDRWGTPDVKLFPDRANMYACGISDQQYKEE
RFDVWDDVQGFDFSYFKRLSYIEPLIDTVDRNQILTNMSNFFSFNINTVQEAELAFTTEF
ELIAERSGCVDAISVHFDTPFAAGHEVVVLTTTPLEAPTHWRQTVLYLFNSIHMNKGEKA
KFRMSCCPNKGNPRDLDIALHVDFDGKLQSSHYDQDFRLR*
>TCRU_205 hypothetical protein, conserved
MEGQSELVERVVRMQLTSPDFAEYCVAHVTDPKHRFLFSRNEDEAERRLYVRLLEGRGHQ
KRAETPAVVAPAFAPERTSSLMTHGGTAVLWMSLLDYFSSTPGVRGPHMPHMFRTEADLT
AFVDMLDGAQREHVSLEDVVQFMLRRLPMTEVFLYVLCYMCDVRIHEVRRETRRRSSGAC
VTDSADGASDEKTLQAAGTLLFIANMLLLQHDALERPLRYLSVFEFYMQRMVEALAGTVP
KNSPVDAFLRETVMVWSEGHVFGEEALDCMKRAIGCSLG*
>TCRU_206 hypothetical protein
MRRGGSCLTVEGKALGPLGSRSPVFIMLAILFTLFTNSSEFGPSDEVGTIITSCPRPTLL
QQLVSFAAMRDVAEEEQLDWGVPATLGRQNTYRLQVKPAEQSEGDHAGENPHGNAASSAS
STGNDVNSANAPSQSRRRPHRRQRRKKKTESESLGEDVGTPVSLGTCGTKSLNGASSSGG
SNLYSSDVGEHAETVFTTSQRLWAQLHMVEVAFSCGDNNLLHITERFLRCGNMYPIIYRC
HLSQVQAAHEQALLDAPNTGLQKSCFWSCRSCGKAHDLVCESCMRCKRQSGPYKKLIFDQ
LLPETDYATSVLRLLHATHPEVTIHRIETQPHVDGGGRSSVAVYVSADAAPELVEKLNGN
VFFDMDDDDDDERTGGGVRVHYVYGSQRPWLWAFINMRKAQCKDPNKLPWGALVVVMETS
KEKISGGTATRAFRPTRTKRNLFLMSN*
>TCRU_207 hypothetical protein, conserved
MMASASAITLRGTPQCHGEHLKPTVRTRSTSESGTVQISSVTSSCAASEPRRSASIAERE
SVAAGTRVGDRDAAAMRGTENCLWPSSVAGHSARQEHARLPAAAR*
>TCRU_208 hypothetical protein, conserved
MSSDRVASVGEATACHVARIVSRLEGRSFDSTHRDEGGTGECGPFMQRLLPVVEETRVDR
RLDDVFRRAHSIFEPLSQATVAAGDDAEALMADVASRASRLVVEEVLQPCDSTKSSPSSF
SESPLRTQQAAWCRTGQLSLGIIRESTCGFYFAPSTGANSAPQRVPVLLQRRIPWRCKAN
DGSGSHDAVGRDCDADSGREEGDAPMLSGVTLQWGAVLGFLQLLSRAVGLTTSVDGEYTA
VSSLTEGEHSLLHIVADSIIVMMERNHALLQEARDMNQLGMAAEVLIIAANNFAWIRQRC
QRIPMANAREVEEILTQSLAGVLQDIIDGFVEEIQYILSMYMTSSGGGGGGRQRVVTYSF
LATRVTAICRLSNGLVHLLPRQEVMSIVLEQSLRPVVEQLLVGDKQNEVERGGITTGVLK
RVGDIFLPADAFLRHDAAHVESGVDENGSGTLAQRLSEVLQILESEEAFGAAICQRSPPF
RTLRRLLPTMTF*
>TCRU_209 hypothetical protein, conserved
MSRERRDAASSDAGDDVTPAKFNFSEGTGTPLAELPAVRAVGNRGAAWKQLETRLEPLHR
MVFGRPGRTGERRRALESFCGFPEAMGEVVLQSVQKLRKDKLRELIQALGMPVQFTITHA
RMADGVAAFLMQPHVAGTRVSSSGKTPQPQKKAVKRERATTVSESGGAAKTPKREVDPAS
TGAEKVKESLRRMKNEVPVAESSSAVQPPSDDTIRVAVYKRVLATSRAERSHLTTKALRL
ELERQFSDLEGRKVVIREAASECLAALIAAEEAAIISASLGNAAAVASLNGGDRTVEPSP
APHPPQFTEPPTVNASRSQAPPPVTPDGSVALNSSVPTFPAHPPTTLPTVSNPPQLPPGA
PMF*
>TCRU_210 hypothetical protein, conserved
MPGDEPSLWFLDTLSTNTTDARNPEETHLNAVAHAALRCLGMQVHLEVTEKGNVRWSHAR
TERRLRGPLDPALGETLFAVTTRRCARYPPPAAAYFRWFRGTARREHVEQDGFTGIY*
>TCRU_family, putative Se.1
MAKVPHRDAHIFALGCTPHRRLQQLVRARIAPKAMRLKDIMLDFVATEVLVFHPSMQNGF
PQLLSPLSPPTRESVLNVAESLIVAAIHTMNNGVPVIRHQNRGSICHGFARTFFEGFSGS
ATTSRISLRGADSRGNPVRIIVDWGCVTVAPLMHQRTCQCLLDELMPLEKKVYEQTCRNR
LGVGSKRQ*
>TCRU_212 hypothetical protein, conserved
MGLSPDPHRRRMPWTAAKECVPGVVRSSKEKMVLDGAQRVDVECVDRASQVYPLEALRAA
VATCEYNIFRGKNIFNWSLRWNPMCSGNALRQGVAGGDARRGRHSHRHLFPSPRDHNAVR

ANTPCGFSEAACAVLFVATVPPSPSVGAEVPVDATSYRLRTHPLIDAAGTAPSSWCSGTG
DENTADQVQSDGAGSPVSVSPTTAASTEIDGKGEESNDCQENNCLLTSLPVKQPEE*
>TCRU_213 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSVCAAETEEITVDLEAEDEVDGRDNRQSPHAPGIPMNQNQT
QAESPEAAPSLPPPPSVAQSQGTGQPGSSSNGAAAKHGNNAGDTGTLPGPHSQSSGAHNT
VQREGTEDKSGEKSGASTSTEQAIKKVDDSAETTMTTTTTTTKAPTTTTTTTTTEAPTTT
TTRAPSRLREVDGSLSSSAWVCAPLLLAASALAYTAVG*
>TCRU_214 RNase H, putative
MTMGASRNTKLLGMDLDPRLTLNVAATKKCAATSQRISQLRCIAHKEAGPSPHDLRTFVI
GYGASKLRYGSELIWAVATDSAKNETQKTYATLARIVSGVPSTVDPESALLEANMPPLHV
LCLRARLSIFENTRACQMDWMRRPPPEPPPRAGFRISPLSRDELYAFVDAYTKDYGITES
SPREERFFRSSIPPWFAASARRATIGVELPIDHSITDEEELIQEKHRVSEEALALHSHRS
WILATDGGVDVPKSAGVGILLSSLNSSEIIEKASINCGARPCSYRTESRALLLALEKLMI
PLIRHRRKTLLVVTDSQSLLAALNKGPLSQTDWTEDQIWQRLLTLTRAGWSVHLQFCYGH
CGVHVNELADQYATQTMESGQYTEQGIAPLWHTDLLTCFTTQLTNKWRSTIRQDTHRHLL
CGTRPSDLSGKDLITQEVLHRQELVHLARARCGESELWGRRYWAVRDCTNQCRFRNISPE
QSAYMCSNNDPSAPGTDTVPPSAREEDVSPVRRRTLTRRRKEKCPHCDSTLTGFSGLVSH
CRSFHPEHPPPLPELKCDFCDMVFPTRRSTAQHRSRCAHNPDATRHRNSSARR*
>TCRU_215 hypothetical protein, conserved
MAVELVVDAACERLYEVITIALRKMFLDAKCIHAREDHNIIPSTVFVNNDSTTSLLLLLI
TLDDWMLMVRHNCVCNYLKVVYDASNCPVYVVILGQLTGHRQSRFWEEVSCLCADDSFLS
ILVGFDIVSSVEQLAEVAVAHGLKAIKQQNLEGDPIVRSEGRRKCDPTDFHALYLDMLLE
ISSVSERRASTIAGTFPSMFHLLEFIDSGAHNRVQAEEYYEKRGTSVLDPYIAEVLSTDY
NTTEAQEMMNGLFDASAGIFS*
>TCRU_216 gamma-glutamylcysteine synthetase
MGLLTTGGKPMRWGTDENNRAIPHVSSHGIQQFLTMRAGKKEEKNFPFYWGEEVEHQLVR
VEGGKVKLSLNAADVIEQLTKSSQKDNAVWHHEYGSFMVESVPGVPYTLEVDSLCSVEGN
IRRRCELLDSVAGENTFSLTLVTFPLMGVGDFITSDSKEVPYSRSLFVPDVCINQSHPRF
TNLTRNIRLRRGHKVCIQVPIYIDTYTMEKTVDPRLNIDRTPHNIDIDCSSTEVTKAKGE
KFTINDSVISKEKENNSSNNNNNKDSNISSKYPSAEEMTHFYTPATHYYYAQYFKKSQME
LVKQRYDACPCPVPSVSHPCIYMDCMAFGMGCNCLQVTMQLENETQARHVYDQLGVLCPL
FLAMSSSTPFQKGILCDSDVRWLTIAASVDDRKREEVPHIIKSRYDSFSVFVSLTLPNLE
EFNDEEFVINDTYLEVLKSAGVDTRLAKHVAHLFIRDPLVVYDQMIDIDDTTHTEHFENI
QSTNWQSVRLKPPSLDGNTGWRVEFRIMDVMPTPFENAAFSVFVPLLARAIIKYNPLFYT
KMSIVDENMGYAHNRSPCRQKYVMRRDIFAKNISTDPSENSEFTVNEVFNGKDGEYYGLI
PLVRRYMEEENMLSSTLEGYLCFLSMRAAGEIPTAAEYLRNFVMQHPDYGHDSRLTERIA
YDLVLHVRKLASGEVKDDLFLPMNKFMPKRSRE*
>TCRU_217 chaperone protein DNAj, putative
MNGEDVRNYPARVLLAHDDRLVQFLDASVCQDWNAAVEEWQMKKQEEIAFQKKARIPTCV
DVPSTSKTGLFSDEEFFFLTKQLENITAALSAHSATKAGVHYGENDFVYSPNEVPDLFLL
DPAMHLLPLDGEKRRKCQEASEAYQRGSYGKAAEIFSSVIDSCLPNMLNAALISNRAACY
LRVENYKLSLRDAIRSYEMDNDYILGVCRALRSLICCGRVAEARQTIEKFRRNKCGYNFE
REMTDISLYEKYGAFLEGNEHSTALMHLNELLERVPCATFEVLKVQLLAIEEGNEVALAH
VNNTLRIYTDFPELLYWRAQLCFLESASMAELQAVLPFCSVTGSTDSTGRLRQVLQRVQY
CVDLCREMESLVSKSEWMRLIELCSKSVKTLFIGDRLRAGILAKRARGFYEIKHYYECMD
DIDAAIRNITSGNVRAELLLLKALSEEKLLRWSDAIRSAELAMREHRTIETVEAWKRLCD
RKKEYEWRKQQKQRFHSGYQDGEEGEEGKDSKDGSAPERNGFPRTHASGSGENERRKQHT
RGPDHHVVTQLYAQLSLPTGASAERVKKSYRALAMRWHPDKWCSASDQQRKEAEEKFKIL
KAAYEELMCIVGG*
>TCRU_218 hypothetical protein
MEKNLIINVTCNPPVISILGPVKESTIEKLNDVLPGACTTTNTGKVHFAFVRKEEPPHWY
GELQTHFASEDIGQSQLFVSLLDAVEEEGMWKLCGSNANVHDYDKATHKFFFVRA*
>TCRU_219 hypothetical protein, conserved
MEERARRPPSVLTSEVYNEAETIFTMLENKEKLVSFLDCMTLLRGMGMNPTQTDMDYLRE

RMADPVLRLEQWRREEELRREKERRREELREKRKSSSAYSQKKPRKSTVERAMQVGATEG
QVPQQNVKIVPVEEIKNIDWNIFISCAEEIYRDAATEQKEVLGALKVFDKEGAGEMTVDD
LVRIVTTNGETVLNPVEVQQLRSIIPPRCSLVELAARLQGTYIPPTKEELERKALEEIER
RRQQEVSEKRFSDDAMLLP*
>TCRU_220 membrane transporter protein, putative
MNPQHRWENDDDNACMLSGNADGRVSIHALVCRTIKVALPTDFSSVLWMASQMVTMIFVG
HCLGEDGLSQYSAGILVFNVTAMSIISGLNSAIDTISSQAFGRNPRSSVIGETLQRALII
NMVLWIIMSVAFLNSKPIMVYVFGEAVGDGAARFLRMCPLYLLTQILTGIISKTLYAQCL
SSLVVYSNAAAALTSPVANYFLIFMGIEGAALSQGLTGMMCAVTDVLLCLFHPEVVVREA
QWPSPALCHKSGWIHFLKVGIPSLIAVCSEWWAFEVQALFAIAISPLALAVFGVAMNIIS
VMFSIALGLSVSASTIIGNALGGQRPLFASQYARFILICDVMIGICTAVAMGYFGGHIAR
LYTNVPEMASAVESVMPFVILCHIGDSLQYCLQGVFRGAGRQEQAARGVVFTLWLVGLPA
SALYVFVFNWGVRGVLGGLLTGFCFEIPLLYYLMSQWDWRVLAQEAQVLSSLQDFVVLES
VFQNDESSEHDSDVSVKKEVELEAVVYNRTDSQYKVR*
>TCRU_221 hypothetical protein, conserved
MEIQLGEKVALLTTHKTYRDDLEGGVRAVASYLPFCKYVATCAEHGPVPSTFIIRSIRRV
AQRIVGLIMEVECVTRSGKIVQTVDICDSNPVIIFPVATVNGIRYAILVRKRQVSVGCNF
IVEALCGVENNDGSFTIPNDELLIPLGVDLQKTHALSSKRYTIGNEGTTPYKVHSVTLEM
TPESLQKLQNTPKDLENSLIALPLDEVLSTVGDVKASLAASLLLVS*
>TCRU_homologue predicted S. cerevisiae Go.1
MDSLYKWNDSTKIGVALTGLGALFTFLGVIMLLDSALLTMGNILFVAGVALVMGPKRFQS
FFFSRRRASGCFFLGMLLIISGFCFVGLLLQGFGALNLFGNFFPMIARVLESVPLLGPIM
LSKPVQRLLTLLGLQDHRSRNV*
>TCRU_223 Noc2p family, putative
MTTKDKKSFKKYAKKHLATVIENRRKSAKAKKEKLERVERKKMREVKEVQREEREHQEQL
DHLKEIDPEFYSYLEEEDPTLLQFGEEEMEVVDDGVGSDAETEMDGEDEDNNDDDEYKAR
DCYLEKSAKCFSSSRITRKEIEHLVKGRSIEACVDIFVSAVRELGYNVKENPKISSTRKF
DDPSLVKESVFRIARAIGSNLSHFITGKGSFKSYKTRFLMRRLLISLVTIVSEGGNVDAV
LTAGLLHALTPFVPILHYIKGITKSVLRASLSLCSASEESVRIAAYVVVRAVATRATGTR
SMYQSAAFKGIFLTLVKKAYHYNIHNASLIAFLINCVVDLYGTDMEAAYQHTFVYLRQLA
IYLRSALHQQTQSNVRAVVNWQYLNALRTWGAVVSKYSEPSQLGPLIHPIVQIALGLMDL
FSSPRMFPMHLQVIEVLNHISLRADGVFIPVAPYLLRMLTSPSIALNRPTQGEGEKFERV
DLQFTIRMKKAQSRSSSYHQNIFFECLYLLTEHLATHSHTLGFPEAFWVVETTLKRLRSE
VKIPKIHSQLTILLRHMQTTTQRIIARRDQAGNGPCDLAAVKQLEDELKAAGNPLSTYHQ
MLRQQRVEVFATKQKNANGGERTTLEAIMEGGRERKSRKRSVRAFEV*
>TCRU_224 kinesin, putative
MGRRVQLVIRLRPGEGGASCVSVGVNKKEITVVDLSGTHASSTPREFHVDQVVQEDCGNE
ELFRSLVLGRIRSSVDEPDTSCFLAYGHTSSGKTHSIAGTDKEPGLLTLSAEALLHTYGV
AEVAMLEVYGESVHDLLAQGERRMIRRRAGPDGTVIMVENLTSCSLTSMEEWKALSEFGM
LARRTAPTERNSRSSRSHAIFTIKTRGMRLCLVDLAGSERQTTYSPQLNKESIAINKSLS
RLSTVLEALSSARLKSDGSTSYVNFRDTTLTVLLQRYLSGASMTVFLACIHPDTAFYYET
MSTMRYTQRLKCINTKNAPKKPNEDMSLFQLGENQKLLEELMILRRIVGRQHEQREEYHY
YDGEFRKVSEETVIGRLPKDHCSDSLFQNHESALQESSPMISASIVGHRQRLLRYKDAMR
VAGWLLSRILSELPELSVGFDDYFDTYLPSQVQVVGYISLMTCMAPRDVNEAMGGLAFLD
VGDIAMGLSMLDAGIPACVGLHRLTCGESNTWEAHEYDGVNRVFVLAFFEINEHLVEIMG
DTHDAFECCGGLLTLEPLVPLAIVLCTPLDSSDELKENVLQHLVTLQGEQDGALESSIGG
SSSLSQLTPMHTGIDGAMENPKLNLLKAMTQWRDDYVKEVTSSSDTESFSAAPLAEEIER
QALNKLQVCSPFQESASVNSGEAFSNEKPTIIHLDHKLHVIYASSSSFSSESSSDSSVIL
GSKLSLLSPAVADEGQCQEISRTHMSSECPSETECDAEKGVGMPQSIDREVHGANQFGVS
VSPADVHVDMYNRPYLPHAPQTNCYSIEEFPAYAVIARERSKSDKKDDCADCSATASVSP
PEKKRIYEKNEKKKKKKNLHRKRKPVLQGCHNCVVL*
>TCRU_225 SNARE domain-containing protein, putative
MLFFTLIVRQRDALALAADTDTSSAELEQCKVAAKTLLRKLAAEHSNPSLCVPPLLTIVW
KNYVFHILSESAVSFLTMCDTAMPAGIAVAFLEDVAREFLQQYGSQVEAVTRPYCFIKFD

LYLQRTKKVFATANSSRSMNVSRVGRTAPVRRTFEDVMAGIDSKTGSSMSSRGGGVRDTE
KTRRFLIICFIAAVTLLLFCGIFYYAALA*
>TCRU_226 60S ribosomal protein L17, putative
MVHYSRKPQVSSKSAKAKVSDLRCHFKNTFETANVINGMPLRKAQQLYRQVLAKTRCIPF
KRYNGKIGRTAQAKEWGQTKGRWPRKSVVAMLSLLKNAEANAIEKGLDPNKMVIKHVQVD
QAARMRRRTYRAHGRITPYMCSPCHVQLFMTQPQERVPVPKSKPKK*
>TCRU_227 hypothetical protein, conserved
MRSLRLNRLITVAALARSQSGSGSGRYQQREQQQQQQQQQQRFGGPRDGRPLRGRPPQN
FQQGGYRNSLNEPQLVAKLLELYPSGKSWMPINKWASSIPEEIQEALVAFGGLAQFTASQ
SNFFIVRKENGTVVVSLSTMASELCAKREKNIKKREEKAAAFSARRRDDSRRQRGRD*
>TCRU_228 CutC family, putative
MILKEFCAEGYERIPEAIASGAQRVEICARLDVGGVTPSADTIQKTVEYCHSRNAMVMVI
IRCREGNFYYSDEEFQVMLKSVILARRLGADGVVFGAIDVLGNVDPRIGILLSAAKGMSL
TFHMAFDEIPTEKQFQAIDALTAYGFHRILTHGGSASTNIEENLDWLKELVLYAKNRISI
MPGGGVTSLNAEKIARDLGVTEVHGTRVVRFV*
>TCRU_229 clathrin coat assembly protein, putative
MNVKDSNELKRGAGYLKEKAIIGLARVTGDELDRAIMKVTSHMLKAPKEKHMQRLLATTY
GHYKNDTRDGKSICGHIVAELEKRMHTHNWIVVLKTLVTLHRLMTDGSNEFNACIKRNRS
IFCARNLKDLSESVEGAAQALFIRQYLSYLEERAISQEAIGVDNRLESVDFSSYLRSMDV
DSLTPFFGALLGQLAALVAVEYQEAIVDNFCTLEAYQRLVCDGKMLYQLLSNRVIFVLDG
FDDFSLPLKKVWLELYRQYSVVVEKLRLLFDSILRSSKVFMQPPPQLKPLPDSFLGQLED
DVRLSSIPREDVTETLGKLGICGSEIKSPPRETVEKKSPPLSPSVNAQPRSGKESPPIPP
VATEKKEAAFSMDELFVSAPAAESGPAVPSAPADPLVDNQHFPLFSPQSEENIGPENLGD
HYAALNTVIDDGWSTGAPVSWEGTPSVQYSTAAPVADGMSHTVWGGTYSSATDAIPKQGN
ENVFKELYNEEQKGWHANNI*
>TCRU_230 hypothetical protein
MSTTPVGGKIEFSSHREIAHVRQDLAVTKEILAIVKEENERLCSVAEERAVEVARLNKDL
EEAKRQFQNQKHAHEMEIARFQSGRTSLEGELAEALAERKRLSDLLHSLRGQVDGRLTKL
VEELQRKDETIHGLDYRNREYEREIERLNRMVKTDSLTASELEETQGKYSKALAEVLLLK
EQVAQYQLELSSTRERVQQLSDNSVDDSQKSFLREAVSLLMLYRQWLVEFNVSLWDIEDR
IETSLNSGIDALAQMTNPGVPYRPPTMERERLKEMKKFERERKNFDSMVYPDKNETCENA
FAFSVHVIRDTWDSSRHSLEKVKVISKQLLETLKSVVQVSEDLHTKTVLASPSEIVTNAK
VLRYECDQSRLVDTLKENFEMQLQLREEEQRKKEAEITNLKSMISTLEGEKDLLSNELLK
TKQDVINASLSSTSKLNELECKLRETVRSTEDMNAKTLSVLKLEQEKERKEMAEANSRLK
KTLEEEGANIESMKKMLLESKRRRLILKDENTALRKQLQKTEDLVNALRLELLGAKQTIE
LLYAELHFAENNHERQPNSSSSKAFLSFKKGIQKSSLEAKAVYLPRAL*
>TCRU_231 endosomal integral membrane protein, putative
MARWGHFALLSLLLLFAAPGVSCALLDHLSSPTIYQAGTEIPITVNSLTSKRGLLPYNFY
SVKTCQPDERRMRDERIHENLGEILLGNRILPSMYSVKVGENITCREVCFVAYSESEMKR
LQKLIEQQYCAHMFLDGVPLLERPLNASTEQHLRVGYQLGVPAASDESTKTTIHNYLHFK
VTYTNAEQGGFSITGFYVVPSSVNVLTGCPDPETTEGGSIQPATPESMDVKYFYSVSWEL
DTEKIEFVATRWDVYARAGHPASKRGHLMAIMNSLALLSFLGIIVMVILTRTVRKDLLSY
ADADLAEENSEESGWKLVRGDVFRAPPNALLFTSLVATGCQVVFMAGVVVIAAVLGVVHP
*
>TCRU_232 60S ribosomal protein L21e, putative
MVHSHGYKCGTRHLFAKKFRKHGVPSVSTILTNFKVGDYVDVVADSAVRAGMPHKYYHGR
TGIVWNVTPRGVGVIVNKPVRNRTVRKRICVRFEHVRKSRCQEAFKQKQKDFLTFQAAKK
AGKPLPPLKRSSRNGGIVRAKRVELLARRAAEYEAMIPY*
>TCRU_233 hypothetical protein, conserved
MLLPRTDSHDPDANDADPRSTSSAPSVSAPVLSFTTTADALAITPLSNTNPCAAYTWLPD
TRSTAPSDATTRALAYNATSPPSTAASSATPPPTSSSTAPSTTTVRPPVITVTRATPDTT
STDRTSRRPDSTSTGAYGEDREPRRYTSGVGLAETSRESVTVSTDPAGNLPVSTSAPFSA
STSHTDSSTGPLSSLPAATAPRNASPPITYSTAPFSSDTFCTTIRTPSRAIHGT*
>TCRU_234 hypothetical protein, conserved

MLPSRKRQAHRDHPRQQRSVAHKAQRAPSSGHGASRVEHLPRDAVVHVALRQQHRPASQA
HSRIKRHRVVLRRQKVAPHKRHSGARHAHSPTHRHRVLAQQEVAVNKRHHGAAAGRNTAL
HRHAQPQRRLHKKPVHVQRTARMQRHTVNQQHASSVTEHRRHLRARDGQHTPRQIHVVHH
EARGRVAKVVVAAVRNTRLCNQHRVHHCDARARRKSVRHQHAAAGARLKPADQHINALAS
RRVGPPPNNVQARSAQKRAVRQRHVAHTPRHRRHVHNDIRRKGHTNVARHRRPETGVHLH
THTHVPHAQVGVVGARWLGNSNGQARIAVAALRARAGAAITQGCRRVRGEARRRKGAWVA
AGQNGGIVHGRNGVFRLLLAVQSVARSHNRSVCEILGPCEYPKYLRHSCAGDESVAGHRH
RGVAEIHRRIKKEESFRWGFTAEVVAQLQPGVVVDVGEVA*
>TCRU_235 hypothetical protein, conserved
MMRRCLCYAARCKWGQRTWSPTASSGGAAPTNGVSAQEALQIVYRPMPLPQTVEYEEDFG
HNLMIHREFVSKRHRDQLSFELGALAYSEVELRRGRQHLAGVMNRERRGVAIGAAGAPSD
QLHMQTDVDPDTREVLTARYLFDEKRMQFCDRFQNFLQSRLEGHAAQSSDGGKGGEDKHY
LFSLMEACAVIYGCETHAAREVYFRMFLSLDLESLEAEQEALRHRIAEGKLVRQALEQSE
EKEGEGNAVLPVSRGNSSTTLDDDAAFIASIPELSLFEDTPEVDEGGSVKNETHPPALAD
KEFLPAGVVDDSGSLRNSSHSAIELPEEFEEYAPLYKAYLAHAKGESGIASYDVSTLGST
GITAERRRWRNLMDKIVREEYHTMTETEQMDALILNEQLHTVKFFDLKVGDTVREILQLL
QRETGCGSSAHRDEPLCISPHHPERRI*
>TCRU_236 Thioesterase-like superfamily/Thioesterase superfamily, putative
MVFLTLLRTAAYFIYGAYQRRRMLSTNPQAVIEPMKKHYTCVYAGIRMADIFGHVNNSKY
LEICELARWHYGGYVGMMKILWELRASFVVASVNVQYVREILPCRRYLVTTEVLRFEDAG
SSSDKPISGKDESGVARNLPPAGRMVIMHEIWSMDKKTLYAGILLRAALVGDAKSPLAIP
SGGKRRGRYALLDCRAVYAAIRGADGANELANENMRNFYNRLGFQPNQEDFNGDPWIEAS
MRLEKEWRSKLQSVREP*
>TCRU_237 hypothetical protein
MAALAPKNGSFLHALQLENDALRRQLRRAHEDMERVLQQLQRESKGGRGTAEGGSHGGRH
EGGGDAWHVERLERRCELLATRLVGIVRDRQLSECAEIHFLLRTQEEERRFLHDALVTLL
ERQKGSSGGDEYGAQTEKEIHPGMLSALIMRVAENMQSSRSQLKLEQTERIMLLGQTIDL
ILDIQKAIEKAARWVYGYHCDFLHAGSLQELTLWREAQNSGIVGLRSLAEVTPDVPPRTS
FRKRSSNHSERRWREEVDCSIEFPSSSVHQTEAAANFSSRRGDLLEACDVLRACHQALTG
VRTLLGDAMSNVTSSCSSRKGKPTSVEELLKGFHRDLQEMVRSNERCRETLARRLEAEIE
AHRRTVQKFEARLKLAERELIDHLTSSHKFQKPLGSNDADAPSFSNYPSKVKAYHGETGA
TTPPTPTGTTATGNRRTVRVNNNTRFQFAPEKTVPLSPRRDLPFVLEGQNDKKQKRRGDT
RPGTPHKGSACDVVSFFPPSLPSFAALAGPLPETRGRQHEDLQSFSSRDNFEDGTRSNST
GEGSVAHSSPPLPASRRERHPSSGKIQEGREAVSSQRCVRWPRGAVLLSPSAF*
>TCRU_238 zinc finger protein, putative
MPPSHHGPSAISSPSFSQQNYSQSVSKTDYLECFPSCSGPRGGDPTSHSSDASREDGNSK
VSLASSMAEIMNSIPNEEGLEEVKVVAQNHLRATEEGGGKEEMLRPPSPFVVLGYGERGG
DLTTNGVADVSIVDLETELANLRKELLKLRREEEKRRQQLYEVWRQKNPKVTRGLSSPLC
TSRGRKNRNRKAASTVDDVTVVKSNGSDVTSSVICNTKAICNGILTPPAEDEGAHDGEKD
TGNAAVLDQPFHGHNNDNNFLFSGRRPRATRNGMVADPSDPFGKCTSLGNDGGSLASRFN
PPNLYDFPKAGKCWLGGRRARKSTYTVVAAADGHGNDDAPTGDNRGEEETSLPCVDKKSG
VNGWKTHDGELDFSYYSLSLVQTGSAGMLEFVFDEDDAVKRRAFRDAENQLMLAEQRILL
QMETLRHGRSQAGRHYWQSNESVTHCTRCGKLFSITVRKHHCRRCGILLCNDCCSQVGRD
MYALQHDKVSEQEEDEEDVVVVDDNGEIQATVAVESTNNQKKEYDWMFDTYELTDGTNWR
QEEGDEDKLFSQRSKVATSHTTRGSGRGRGGLKVRSAPWCRICNCCYLICLRARIERNYS
DVLSDGRRRFHVLRDDEQAFTNLNMAWEARVAQLDVLKHLIVERATSAAQGQMGHFAGLF
KEWMRSLGRRTEQNHIESNSDRSNCGSESQ*
>TCRU_239 Der1-like family, putative
MDFEFFRTIPLVTRSFLLLSVASVMLVSFGVVHPVEVVFSPLLVFQERQYWRLITNFFYF
GHLDLNSILELHWLCVVSSGIELQYFRRRKVDYCITLFAGMSLLLLFRCLRVVDTPYLSF
SLCNALAYLFSRLMPEQEANIFLLVTIPVRLLPLFFLAIAIIFDMQRSIRLIVVENLVGH
ILWYFLEIFPCITRVHPLRLQEMFMQ*
>TCRU_240 SAM domain (Sterile alpha motif), putative

MNTLSVWCERQTASFTKAFKKRYVTFDPESRKISYAENEQKPPKGVIIVTKIVRCCQVME
VKTSDLFTLMVDGSHEDGKEDQWTLRMPNRQVFEEWTEVIGNVCAAAGLMQPLNFGLPSI
DPRTNLPFAQVPLEYLFKFAVLEKAVIHFFGTVTLVTSTTGKDNHPARHNLVVGDKAIYI
FTQNATILYCSLISHIRRIYHGPEATFFAVHVKSPAPDIVVKDFSEGAQVAFILARLFHV
TTGKSLSVMPINVPTAEVLVESQQLRLNGDEGYKLHVVSPTTKLRLRQVIDTNKDGRSLS
GSVNMNANGGGQKQGVDKALAVEPTVVVPTDPLTTLLHKIGLPEYAPKLLSQHVDLDVLQ
CMDVSDLMTFGVSNKSHCQMILDAALSSDTADPENVDDDALDAFDPKTGYPSGKPVGGVT
LSDDEDDEIDLFVPPQRTVTLDEDSDEELLPSRTPAVNVSKPPAIVIDDDDL*
>TCRU_241 conserved protein
MTEYKKLCAILAQLREEVTSLVRAFEGGEGRDTVALHSLSTSIQTLVTNAQPRLLKILRK
ATETDPNRQIYNEAMCAAIKQLFDDFCELLGCLFGVPMKEMVLSEGKINFEDSPSISWTE
DVHNNYLLHLAQTEAWKKRIAANIADLVFFEEETRAVYFAEERKARETLLQTKRNEKTNI
LHMLKEREAAKWEAEVRRRNDEHKGLMNASSFYGVQNIATVLLRVPEPFRKLLAGNMAQL
VRALRTTPEDPNIRRIRCNNRRVMMDYSHIVFCVECETCRILVAAAEILWYIMGYRVEYS
TAPTSSLRTVIDNNPPILLPCGRYASEHAIAVIGFEEYSERFFTLHEPDPMRDSDEWMVW
YATLEALIARLEDCLV*
>TCRU_242 dual-specificity protein kinase, putative
MYGTSKIQGGGLRGSLHYCTQQRFLPSANRSPGFVNARGKVTASKAATSSEYHAAYLTEY
EKSEIRGYKDVYYVGQNCERKIQAPVEGGYNCGYDDERGDYTIMLHDHIAYRYEVLGTLG
SGSFGQVVKVADHQNGTTVALKIIRNKKRFMSQAKIEVQILSHLRRGDPNGIYGIVQMLD
SFTFRSHVCITYELLSINLYEHLKQRNFHPLSLSAVRKIGAGVLVSLSYIWRENIIHCDL
KPENILLKTPDRATVKVIDFGSSCFENARIYTYIQSRFYRAPEVILGCSYNKHIDLWSYG
CVLCELATGVPIFPGESEQDQLGCIMEYLGAPPHELILQSSRKQELFDVNNGYAPKLVPN
SRRKIRYPGTRSLAAFLGLPQDDGFVSFVRQFLCWIPEERVSPRRAMRHPWIADIFEGPP
PPLSQVSKTQTNLAVRAAISNAHRITGQALKVPHLPKIGEH*
>TCRU_243 hypothetical protein, conserved
MVGRADQAQRRKEHKARSVHHRQEGRAHHVREGNNARARNQHSRHAEVLDVAASHGRLHS
RNQAHHTQHRQLEHAPVHVAAPHVRQHAAVHPLLRRGVPIPDRVQQALVQRLPRKLPVPR
EARARVAGNQVAHASRKRRTVQHANDTNHAVPHAGTGHRQ*
>TCRU_244 hypothetical protein, conserved
MHRVRHDVRQAREAHRRPRSRRVHAAPPLEGRRHTAVHAPEHSGEQRVAHHHPQRVKGSE
HRQEVRQRNGARTLLRQGAWHPRKHAERLHLQDGAQPAGHHHGNSRRTRNNAGDRREGAG
GGGQRVGPDREGPKQHTPAAAGHCRSVAANEYRLVGSNEVTAVHGNSQLQDGGRIRRVAH
PRRVAQHRSPRTAKPARLRRRHRHEAQVRAELRVACPAERRRQRHHQPCRDGAPTAANVV
LRQAPTSRRRRHSERRARQVAPPQRAAHRRRRGPRGRQRHRLRHL*
>TCRU_245 hypothetical protein, conserved
MMPADLYSIGCSVFPLSVRHPTTNLRPAPPSTTVPSITTGPLPAFPWSVSVLCARSALRG
YGGTDRSLPRMLLPRTDSHDPDANDADPRSSSSAPSVSAPALSFTTTADALASTPRSNTN
PCAAYTWLPDTRSTAPPDATTRALAYNAYSPPSTAASSATPPPTSSSTAPSTTTVRPPVI
TVTRATPDTTSTDRTSRRPDSTSTGAYGDDCEPGRYTSGVGLVATSRESVTVSTDPAGNV
PVSTSAPFSASTSHTDSSTGPPSSLPAATAPRSPPPPITYSTAPFSSDTFCTTIRTPSRA
IHGT*
>TCRU_246 Mucin-like glycoprotein, putative
MMMTCRLLCALLVLALCFCSSVFASESETAQVEDIVSGIYSPSHVPGGPPGVSEPLPPIT
LSTARGAPMTVIGQSMSSGEVSGLVPRKGGGRRADVADALQKKDRIDMTAPETSDTSPAD
GLLGNQDREGLEPSTKEQTVLGTGEGGTTVSQSRTRQPAEETIESVGGLAKTTKTTKIKS
PEGASQGDLPAKATHLTPSPPVEGPLPNADKAPVPQPEEDSVSMKPNKDLAEEDIATTVD
TDQNETSSGRATSTTTTTLVASNNANNEADRSTGEDIPNNTPDSDVSGTEERRDENKYNN
TKKTPVQVADIKSVTVASGNSDSSTAVSHTSPLLLLLVVAAAAVVAA*
>TCRU_247 hypothetical protein, conserved
MTLHLVAVLGLWLRIGTPQQGVAASTTETKVTSPPEKVPRHARCGEVRRSACRLSVRTAR
PFRSGHSVDIARGGDFHKNPATEEDGYINVWQLNIAGLSSVKNIAFAARLEQRPPDTVLL
QEISNRGEAATKLCGHNDYLQASLGAVLPLWCATLYRASACRSLALTSWRPLLSVYFHRA
VAAFAWRISAILPQQLVNNPHLSISFVACARRDYRG*

>TCRU_248 hypothetical protein, conserved
MRNGTRRCRNSFNMSSGPGAEPSKESRMVTSSTYGGKGRSISQPPGTKGVQRAAAAVQGG
MARETAQNDGQADLPVAEAGRIRGQVQCGAQPIPEDEGAAPPCREDIATSGWVRLQVFSR
GLPEAQRSNGVRLDFVPPFFRVHSAQTRQSPGEAMCVLRVLLRRRTRPVPFRVSISFWSC
HGCRAGCGAQLLVRCLREDPTMWTRWQGGFHTTWWKQANPLYAG*
>TCRU_249 NADH dehydrogenase subunit NI2M, putative
MMRRSCFLLSAGMVEYHEWHLHEPLLQNYEGWRILDNPRYESKSEAYIYDFIGSVRHLDP
IIDDPRLTHKQRVCRLYRWALKELQMWLVQLNAHKFNLAYKVVRRRFEMYRYVTDPAMCD
MMVRETQKYLRENANFYFLRRNNTSPWSTHTLANPMFHPDGSQVYDHWTHPEVMWYDDAK
LHRWTGHHPMYAGAGEMSDRFGDMDVSPHLRIFTIAIFGCISLWSICSFLAVFDRDVDPH
FEKWCESFDDNLKGALYAAERNSRSRTSMLGWDWDRIMGKVQHQSGYHLYNVQRFQ*
>TCRU_250 superoxide dismutase, putative
MRRSAFSTGVVPAIAAILSPAALQASRRGGLVMHTPKSDIVLGRFSFMDQYNEFRNRSGR
APDYYVEKYRDTYWRVDEYIRRAEHYIQSQGFFYLPTLEFPWYRGCLPLFSSYQIRLHYG
RHHRGYVEKLNQLIEGTPLYGSNLDEIILRTHDDVMLTGVYNNAAQHYNHCFFWKCIQPY
GSNIPPDLKAAVEKQYGSVEEFERIFTDAALNLFGSGWVYWVYDTRLGQFDILSLSNAGC
PLTNTHVVPLLCVDVWEHTYYVDYENNRAAFLAKYFNVVDWHWAERHWKRATGQEYYEMK
FW*
>TCRU_251 WW domain containing protein, putative
MQDEAVRAALESGVWREKKDPKSGKTYYANVQTRVSVWNLAKELARLQQQQKSTEEMELR
KQKKLQSLAEERQAQAKKWQEEEETLMQRMAELEREKARLESEITILQGPTEVEAASLQE
EQSRLLDAKQSLELIVSEELRKRRESAAELQQLQARLEALRQERQEELGMFESLRKRLEQ
LRQEHAEALGDLQREEAVEESLREELQREERQLEDALHEEVRLKELLKMREDEVDHMKAE
LKAVCQRKAELQQQHQRLVEEVAESAMGAAEDTLQEPPSSSSLLLSHLQREVANRKKSLR
HLMQQQRLAKEAEWMEAESAELRRFTALAEREAQRLAQFSRELSDQVRAVTPLLEAVKHD
VQQLEEEMEELR*
>TCRU_252 variant surface glycoprotein (VSG), putative
MEAKLEAVVAALHGRFDKNGSFSHPSHAYGIAWELVNALAATERRCQLQRLLLLFEGNRD
DYTVGQIVSAGSLVRACGLLLEHDVWRWERAMHSILVSHPPFSRDVVSSVCFCVAQMAVC
GDSVALIGVAGASLQNTALGESLPEEVASELLAECTDVLVRRHREEEEEKEEGDTNEGKD
PRGKSSSRRAALRDALIGYALDALSCKRGAEALSSLLSCRVLIPLLLSGGHQSLESHHPR
VQSLLQSISKETARQGEVVVLVTALFEYLFRFTDGDKDRDYRCSPHLWNTLYAAFWDALT
CDADAGRRGNMQLRVEYLLKRIVDLTHGQETHEKWEKTVFFHEQFVWVPAASHNQWGLFF
LVLEATNEFGLHIVQPALLKLDVLVDSLTCDAVAWAAIKDGGNTEAAVSGPSLVGSLHPA
WVELLLLKVLLHPNTAVRKTGLRRLWSLSTSVLRLFSSVFLFTSAVEASLDSRLCADVDR
TPHATHLSMFKGFEGAEVRALEGMAGPMADQLERFYACIFRDVLCTAHKRKEAMCRLLHG
VVERPSVYGVTMLLCILHGVAETLSLDTEARSREATLEMITDPNVLQELLLLLRDAAHDG
VPFWLDVRLSAVAFSALLHFARIDPTLVHQCDGLWKLLCVCGPLGNSCGGNASAIDSVGH
IGALGTCIHPRFLNEQLIRMSIATPIGGSNFRFARILLRTDRLLEDVRQFLRFASFDEAR
VKQLFFLCGALDIAESEDRRLLADVAQEIGTTLLSFAKRPYSPSESFLAALAAFVEFHRS
VGAVACKRYYSLATVVDLREALHTVALSALRQVFRAMTQVNSFDDFSTDVWALQHTSEWD
VVVAAVLSAGQIAVAHDSTGGNTWFQTRQHVIDVLQLLLLDADGTFAAASVGDTTKVTRH
FAKMVVFRNASRLLQSVLSGVITLGTPGNTLEGLNAAEITCRLRIENADLLHWLRSLMRF
PSLRLLTCDVPCPLTSLSWATLLAQYYGGVYNAVFVLCSCVDPQQSPDLVLEVQDYALDH
VERCWGTNLASVYDILAWVANSGTFTENNAVREKCVDHRAIINAMFGHLKDVGARDHGRV
SVLAFNVLRCGAVEHEELLKSHISRALLDEADSERSVYLAAVTVATEVLRDPLANWPRLK
DLLLHVAVLYNSGRDEEASEMMVAATEPLILLFPEALRVQYPPTVRLSAVGRALAISTIL
WCCRLRNDWATEISLELLDWNTTHAAVKHEPCMPNSRPHRCRIRLWQLLCALLPMLDDAA
AQQSILGRVIKTCLPLTNMGSVRRLMELYALKILERQPALYTLLDAAMTDYNLRPQVCGS
YVLIMAHMMLQQLRGEVERVDGLFHVLLHRLFQQSTSHQHLLRVICHIGLHQIHETCTKQ
GVKFLPTEEMVFDYIARAPEHVKFREKHAEELFFNLAEACTPRQLFCVKRKEGNNILTES
IPAAAFDRMRFLDHEFRCLIGALSPVEMLRVRIISDRFESRRILEPFKSFPYIPHTESHT
TYCVDYTAEAMALLTADNNNNNNTNNRMIDGDENIQRKVTPWWNGLVYNELHPRALKQEKR
QPLIVLSSLLQNPVNVAGLFRCGEIFAIEKVVVSDQAVFAHPHFVAAARSAELWMPWDAV

MAKNLPEYLGSLRQDGYTLIGIEQTAGSVSIASYRFPERAAILLGAEGHGVPAELLPVLD
VCVEIPQFGLIRSLNVHVTGALVMYEYTRQHLMENK*
>TCRU_253 hypothetical protein
MSLCYNSRGLLFKSVFVLVAVYFCFFVLWPGHNANKQGKRSTQIHQAAHGLGAQINGSQG
FQLGWSGRTCGPGARLIHKSLLSRCRTFANRRGSVSLAFCDRILRPGPPPCGFFVGGKFK
QPLRLLGLSELKQLRGDGRFEACASRRMYDGVQSNSTLHAVDVGNGSSFAFEVRPALCPS
YRYVSPLEALSILHHASIGRNGHGIIVTGDSMLRQLLLRLMFFLRGEEVFAEHEFHRDAL
YVVYEDRDELILSFTCVHAALIETYFPGYQGHMKNKTSCAHFLQSERVVAIFLYLWDPLV
NDFREDAFRIRSPPVHLASFMYWWQRGEERLGGLTRYFHRLRSRMVFDKKAFGVPATKYV
FFTTPRTEALPSFLFPDDLRLERNAFAWESLQSMEEELDTGGFGTAMMSLVDFAALADLR
RISRTDDLIHFMCTWRPKSPRKVSSMKTAHVTCQDPVNLAVVQWTLHLLWTGL*
>TCRU_254 hypothetical protein, conserved
MEELSAIDSVLSTWAPKDIFFSSLSIPTVGLVAVFFDAVSDDTWNDEYLCLNATVRNATK
DSDGLQLTGLESRAIWPVNTRSDKVRHVSLSHDSTLVASVTIEVTPSGNTPLLTAMLADT
ASNHTVGLSCSHNTKWETAFEGKTKARSSNREPKEEYQVGLMLQCNKTSVHIDGESLWEE
EVLLAGERPPEVLRFCFGACGGHESRLTVTDVFPYSRPLNSTAMRAPKDRVPAPTREAAP
TPPERIRVVDSVSEHVAGNIGEEK*
>TCRU_255 hypothetical protein, conserved
MLSRVAAVKAPRTQYRRSESRTITESNTSETRPEFAFVRNTKVAPTPPEKRSKPVTEPKE
DPVDDAMSGSINVELLQGVDLFVPQTTLVQSEDGIVPVTTRDSFASPSPVSAGGVIAAFA
EGHTDAEYQGGQLSEPFSSDVVAGCIDSAWNWSTLVGEVNKRYMEGTRCAWCSGGKGEFG
CCAPPHNNYEGPRSVSSCGRL*
>TCRU_256 hypothetical protein, conserved
MPFPTYEGNFPDDVLRHPHLFYLTTRRNAGLVLSDESPPSRLEPKRRAHEETCCSRPVDA
WPVRCLSATVEHLICLIAAPSTNCTVLVLLSNADKGGLHDGVLLLEGSVRRKNVFFLFLD
ETNLSFDSSTNALLQFLLAVGGFGVCSNQWLSLAIPRPNIDWCRRSWAHVAWPINYLCNW
TTKFSVGVDHVLQNMTTAAAERAGVCCVLHDSDDVLADFTLLRVSNVTSVPLRVAEA*
>TCRU_257 hypothetical protein, conserved
MLLPRTDIHDPDTNDADPRSTSSAPSVSTPALSFTTTADALASTPLSNTNPCAAYTWLPD
TRSTAPPDATTRALAYNATSPPNTAASSATPPPTSSSTAPSTTTVRPPVITVTRATPDTT
STDRTSRRPDSTSTGAYGEECEPERYTSGVGLVATSRESVTVSTDPAGNVPVSTSAPFSA
STSHTDSSTGLPSSPTAAIAPRNAPPPITYSTAPFSSDTFCTTIRTPSRAIHGT*
>TCRU_258 hypothetical protein, conserved
MEQPRDRKTVPADRDVCVRWKHTLRAEQRVNKCVAGDDDVQRPHSGVRVAQQQQHGAVPP
RASIERDIRHVARHPPNQHRQAHDTPAERHVAVAQPRQPAAHRLRNLGVHHVADALTNRR
RWRWWRWRWRASRHRRRDALIAVPSSSALALAAADRRRQRSKAVAVLRALPARGNRRHVG
DAVQRQFSRRRHLPSRDRQTPSNETVAGVSPR*
>TCRU_259 hypothetical protein
MLRLGVVQRTDHCGGGPALDGRVRRRAERDAAPLRACGRRAAADWRPQREHGAPDAARFR
QHDECDVAGGHDCAAWRDAAALECAAGELNAARDGWRVAVRADDSWLRRVSVRPRACPGR
RPASVDAVCHDAVDAGVWRGLVRCDPRGARPRREPVQRLLHGQLRY*
>TCRU_260 hypothetical protein, conserved
MAMMMAGRVLLVCALCVLWCGAGGRCDGDEVSSSALSGPRGGVDGPQSSSKSVAGVSEDA
RQLLYAQNGKNENQGRGSVIEPSLDDVYEEEKGEETETRETPPPAGGGIKAPSASAGPGV
IPTSGSSSLSGVDSSSRIGGGTGPTVSTSSNTVGKASKEDMALQEKESQHTQLGDGEAAG
THNNGSQQNSSAPPPTGGQNDNDAVTLSADGLRTLGVQIAVKGDLEASRSEEPSDGPSTN
LPESGRAPPESSQAAAAPEHTPQHKVMTSVKEETERMNMNASANLPGAPKRSNEDPASTA
TTMQSTSTGGQEGEATPSSNGIPKIQEEKLTGNNTTENVQPSDTAETEIRQSVNTSKVGD
SDGSTAVSHTTSPLLLLLLVVACAAAAVVVAA*
>TCRU_261 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MSRHLFYSAVLLLFLVMICCGTGSASSKEKSPVQIPPPKTYFDWRDVKVEETVSSLRVPS
LLKVNGDVFAVAEALCTGKKDTGEGSFTGIASEVLELTGENPKEELGKNKLKTQVLEECT

FEGGNCPSQNAAEEGGSRSQTTVHVSRPTTVVEGSDIYMLAGSYSWTLTADDQAGGWGLM
LVKGNVSTVDSKKRIYWSDTYGLPWSYKVKQNEPLMRLVGSGGSGVQLEDGTLVFPLEGT
KKLNGAAEDGKTTTVSLIIHSVKDIASWKLSEGMSADGCGVPSVVEWEKDKLMMMTACDG
GRRRVYESGDKGESWTEALGTLSRVWGNKKREKVELVGSGFITATIDKKKVMLVTLPVYS
SKDGNGKGVLHLWLMDNTHIVDIGPVSEKDDDEVTASSLLYKSVEGKKDELIALYEKKKG
VEETSSGMASVLLTAQLEKVKEVLATWKEVDERVSQLCTSESVGRDTLPGTACSADIKIT
DGLVGFLSGNFSENTWRDEYLGVNATLDNEGVEQVETGVKFKGRGAGAEWPVGSQGENQL
YHFANYNFTLVATVSIDGEPTEGNIPLLGVLLDGEKKTTLMELSYDREKKWILLCGGETH
KKHSSTWDPETTKKHHVVILLRNGNQSSAYVDGKRVGEDVPCALGNTDSKEISHFYIGGD
GKSAVSTGNGEDVSVTVTNVLLYNRPLTSEEITALNTNQLSIPKLEDLKTEARDAPPPAG
TEPHTLGAVSSTIHGGHQDTEEKLLKISNDAGGGASNSAKTTMTTHSVGGQSAEQLASG
GSHDVNKNVNVDSSSNGNPAVGTVGGDTKQGNGSPQIPVGISDTADANTPTTEGEGQYGP
TVNPEAGVSSGENGETVKGTNGQEEEEIHPQDGELNATALSSSLGNVSQGNNSDAGTVRE
RRLLPSLLLLGLWGFAAL*
>TCRU_262 hypothetical protein, conserved
MDLAEKRRQLDEIRAAREAKQRSVQQQLQQQQKKGSQHHVSSSSLARSGTPQSPMASSVG
GDPLNRVASTLSAVSVREEQQTGDSRTTSAAASRRPPVTLSTRISSGDLRSKVNRRGTGS
GTTEAVGGEGSAWKVEVGVGAFALKPTVEEGESDHSVRDGMMAASVVGALSALEVEDASA
CATERTQNCEASGQQRVVPPPDVAMQLAHSLRAESFCNCKDRCVLDVVMLDPKISGGNTG
VSDDCSGFLVAFALSEPHQADEQSDSAPKLHSGRGIDAQSLLPLPLSTSTATTAAAVAEV
LGELRGLVLLWCISRGKTGDASYSVIPLCFDSEIRVLTYTRHRQHLLFGGAANGCVVGWR
IDHALQGHSCAVIANGLERFSVAPSLMPLPAGGVAAVEPSERSFPSPHTHQSRVIGMAVH
GDVNYHHLYTISQDGRVCMWAPPQLGLPTSSRDGMVLGQPIGCVGSCAAFVDKAADAMSK
VVVGCLDGRVLEGRTKSSSLVEMSPINAMPAFSITNGVLPRSNSTQRTSVDGPAHHATVV
AVAPHPLHADPRISDTVLTAAADGSCILWLGSRRIAIDGFTSQVNCLRWSPTHPAVFVAG
ESNGRVAAWDLSRNSFSPVAVVYLRAVPSAAGWASTPSATSAVSAGSYRSAAVTNLAFSD
DGAWLSCGTAAGEIHLLHLRSDLTVENAATTAAKEVKAGPLSRARNEEVAFKDGCDDATV
TAAAVGRHATSSWIDARFGF*
>TCRU_263 'Cold-shock' DNA-binding domain containing protein,
putative
MFRLAGWRLAAVASMTPLLQKASISKKTEENATAQPAKRRIGTVVSFMHRRGYGFIRELE
SSPGKEKKTHKAAAVAPADADAPGSSAASNFFFPRSSLDGGFYVAEGQTVAFDVRLTEQS
KNINAHLAEANISSSAASASSTPLRTDGTDEEVDGEQSKKLTFAHRIRLYDARGGKEKPV
TPIMLVGYVESWDQLAGKGVIAELDLSGRLNEDAPRFTVGLEDLDLAGHSELRRGRYVRF
CLESGDRTAARRVIIDRGAERKRAAQLSAAAEDQVDGNDGRQYGTVREIVEGRFGFILLD
ETGESVFFHMSNAEGGVVKQGDTVSFIMREVTQGKHAGKRTCLRVRRCAARNSTSSAGAA
AGNGQKSRAAQDFDDDDEFELLE*
>TCRU_264 BNR repeat-like domain containing protein, putative
MTCCGIGGGASAGGSNVRKAVDALMGIGWEKLDNWEDFSDAGGKYGSLRGPSLVDLQGHV
FAIAEAHCKDGGDCSDVGFTGIASKYLDLSGVADPTEILTADASIFGADLLKEGSEVISA
RNGITRPTTLVLGDSVYVLPGNYSHTGPQVGGTNERAFYF*
>TCRU_265 BNR repeat-like domain containing protein, putative
MQAKDKDGTSVLLSMRFPKSENKWELSFETPGNGCRDPTLVKWEEDEDDERLFMMAHCAG
DYYDVYMSTPHGVNWYTSGQPITRVWGNSHNRKGTASGVDPPPQSLGKEGDAHHRAGVSE
GGK*
>TCRU_266 Protein of unknown function (DUF3676)/Trans-sialidase of
Trypanosoma hydrophobic C-terminal, putative
MSSGSYDEEMPEEEGEADGRSGGSTSSVGASSDMDTATETVDSERQLQQSTELSTENEGL
RSTGTGTTGAEQSLGLEAGDRNSERTMGSDSSLTPSGIDAEPTFAENTDDVSRTDGAQFS
FEDGKEVPQTVDTKPENTNATPGGEGIPSTKGAARHSDNDTFTGEIAELLSMGLSRDSTV
HVCVFRVLLLLLLPGLWGIVAL*
>TCRU_267 hypothetical protein, conserved
MQRRRGVLHARDGVGGPRLVLVQLQGRMAWRVVSSLRGARHGCAARGGESRRRRHELRGE
PDADEPHAEHVEDAPLLRRCDVQRRGCRADVFPRQYAAASPHQHHAH*

>TCRU_268 hypothetical protein, conserved
MAAGYFFILSLQTQPVWFKETALVPYTASEWCDIGARLWDLVRQRGDIEVQITFINGTEM
SDETLTVAPSSTGLCLILGNVTKPWEDSSLTGHIANLRAFQVPNFENQLILPIMGAAREL
GRVARARHC*
>TCRU_269 hypothetical protein, conserved
MRSGGVCLCLTALQLFALERRRTTTSYKYFEDTASIRAAFFRLTDAERELLEQSAMALRH
DVALTSVRGEEGCLEVATDDIAVQIDDPSGCAVDAAGDPAEEGGAGEICL*
>TCRU_270 hypothetical protein, conserved
MGSTVCITGATFSPENEAILWTHAMARGYAASVWVPQSLVERLQLTERGHTTAVPVGVNA
ANGRRFFYNVSQLECTEEEVRGRVSKMSVPATRRPAACESDFDASHPLNTNGEPLPPVFV
EEVHARFGRHHSAGHSRYWATVDEAELIFDSPFDPLFLNRENAVTLRASNGSSCVTYYNV
CGTRRPEVFNSDNCRRYQPVNFCGRRYSPGIATQMKASAISYGCMDSFIWLTTRRARKNG
IGVRRGVTPLTVCAEGIFHLVNIAMTNDPARLLSLALSRRLPGSMDDLSLTVSG*
>TCRU_271 hypothetical protein, conserved
MPGEPLGTYGGNYQAPAALDAMQHVASVCLSDGALYEGPLVEGKPEGRGVCVFPSGVICA
GRFSHGHLDGNAEVLLPTGALFSGSFKSSAAHGSGLYVQDGRLTRGRWHEGFMVEQAEDN
LGGGARAQLFTRIAFLLCDELQKLTAVTRAPNWQHLYVNSRISEPKVRLCRECSPEKNTM
LSNSEKPEYFIVNCSSTRIPSRAIISRSFVDRQASLSDTEESLTAATTQRQTAHAEIQMQ
EKPATKNALAMGASAYAIFACAAPASNEFFSFSHYVKYCLIFLFPFLSLPQFPFSPIRKA
RLEMEREFIVSGASLLRKYDPPFLSLHFVTLAMCCSFSAVVIAASKVNLGAVSDGRLTLA
EIVIPCVFWVLQSLFYAAYNSYMRVAHALERFERRLTPRLSAFTAGLVDTKAKVCIYTWD
EKGRGMVTNKHYRYRWLACSVVVGIVMGLAAPLTRVGFRHPFFGTGTYDMAAAVLVFISN
MLFSTILAYYVLKMTDMQRQILEQMRVISRLAYLEGRSLMRPSEYLNQRFNFDEPLNPHD
VFRGVAGWCVVRSLVFYASTCSNHAARSSAMSVYLAFALFGFLATILDIVHILLAGYLHS
GMHFSTGHSYAIVLCTLWGLMLLRYLYICVETVKEHKVHLYLLDVASLYHRMRQGPGGEG
SEVIARCREMIKEHEELPSVFSVQISPHILAAMAFIHVLALAVLVLNIYIAIHNRQSHRM
*
>TCRU_272 hypothetical protein
MHGRPEVQQLVGGGIARQEARWPQSQLGLDDVPDACGGGAFHELAEAAAQRYRSVGSRGW
MPFSPDWAGVAQPRVANSVGRPLHVGGYQTARGRHASPYDLDGAVPLNVFRRVRAPVPRA
TAVWCGRALPYLLGEVHRIRRDRWRRVGLWVPCCFRRLQLHEVADLQVSAEHWAIEIHGW
RAQGTRGLSTGVLPAACCRPCPRARSGVCASGFRMLRAAPPCDGGPAADRLLRGVRRQRR
GKISPAMEPRMAIAGGSSPGLLP*
>TCRU_273 Endonuclease/Exonuclease/phosphatase family/Endonuclease-reverse transcriptase, putative
MLEPFTWLPAERYFHPLLNSIGAYQRYTYRLRAVCDAQRQKPLLSGDIEQNPGPIAVLQM
NFSCLTPSKLATLMAQGADIIAIQETWKSSEQIASMHTGECVLYAQSRIGKGGGVAVLVR
KTLRSKRIPLTIPQHDTSHEVVVVQVALEQNRDIIVAGAYMRPTPQVTQSFRRLVNCLPA
SSPLLLCGDFNMHHPQWEPFLETSPSEVAAEFLELCTDAGLTLVNTPGEITYARGTRERS
CIDLTWSKHLTVSNWSASVSPLSDHHMLTFTLHQAFKDTIPSAPPSAPKFFYSWGKCKWD
LFIKDFDAQLPAYDYKKQSTGIKAFTRALITSYRRHCPAACTRTVPGFGKTLSWRRSGLP
RTARPAIYSYRRPTVRQKCNGQGVNSFSCSESAWATRIHTASAS*
>TCRU_274 hypothetical protein, conserved
MESGQYTEHGIAPLWHTDLLTCSTTQLTNKWRSTIRQDTHRYLLCGTRPSDLSGKDLITQ
EVLHRQELVHLARARCPESELWGRLYWAVRDCTNQCRFCNISPEQSAYMRSNNDPTAPGT
DTVPSSAREEDVSPVRRRTLTRRRKEKCPHCDSTLTGFSGLVSHCRLFRQEHPPPLPELK
CDFCDMVFPTRRSTAQHRSRCAHNPDATRHRNSSARRRSLLPQDQPASTSTPIGPQETLH
HLLPECYSTLAVRQRLGIEQDLRLGKFSQWQLLHSRKLLSLLDHLFGTQMTLYS*
>TCRU_275 BNR repeat-like domain/Concanavalin A-like lectin/glucanases superfamily/Protein of unknown function (DUF3676)/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MRDGTIVFPMQAKNSDEERILLSMSFTPSDKKWELSHTATGKGCRDPTLVKWKEDEYGAE
LFMMAHCAGGYYDVYSSTSDGYGWNTLGEPINRVWGNSHNRKGYGVQSGFTNAIIEDKEV
MLITAPVYAKDNEGGKGRLHLWLTDKARVYDVGPISREADDAAASSLLIKDENRELISLY

ENKKSDGSYNLVAVRLTGKLERIKEVVKKWRDLDSALRTCRSGSSGTVDLPTKGMCNGPV
PTDGLVGFLSGNFSENTWRDEYLGVNAIVHGPAEKRIVVPNGLTFKGSEAGAVWPVGDMG
QTVPYYFANNEFTLVATVSIHEVPQSGSPIPLIGVRMNDTSGTVLFGLSYTHDKKWLAIP
GDGEYFDDWEPNRAYQVVLRMDYYYWTVFVDGEEIHHTEYNTSLFDSHRISHFYIGGDSK
DQSATGGRVTVTNVMLYNEELSEDDLNELPDSKVTIPSLSVEEQPTGQAASTDDSVASGS
RSKESATAEKLTEGDRDKQDEESVLNLVPVAPPSTVVAGSSVPKPATAAESAGASLPDDN
IQLSGGENSPQTTMNEAKESMQRDSDVQTQDLQSAESTEFNDVEGSSESNDTEQTVEEGE
ANDKSGGTTSSVAVSSDIDTVAAPADGEHQVQQSVELSSENNDVRSTGTGTTGAEQSFSL
EARDGNSERTMSSDSSLTPSKSGAETTSAENADDVSRTEGTEFSSEKGKEVPQTVDIAPG
NTNTTPGETKIPSKSNATAPSDAGILLENGHLGELAGMALFAESTVHGFVSRVLLLMLLG
LWGTAALC*
>TCRU_276 retrotransposon hot spot protein, RHS3, putative
MGMEVYEGKPKQSWTYKAVGELFEKDDVLEQSGAPRPRMVMLTSDKGWPYSGIVGKYIHD
CHVNCEVERAWQIFKGDITEWLSSDRGTEFTPKRRVLIGTPGIGNSMAAGSYPLYQLLHH
DAEQLQVVAHCLGGTAYVFDRTISTVSVYMSEPRMIKFVKELSLSRVKAYIIYDVGCTWK
ILSPCLPPGEWGMLVVTAPETTSYIHWVGMKREPREP*
>TCRU_277 retrotransposon hot spot protein, RHS3, putative
MHKLGPILRYIFDERDYNYWIGNCHNLVDRTPSWGSESYFVFGTSKLWEGNNALEYIARI
VRVRGERNGESPFNAPITAHLASKTLCMLAKLMPQADFNLFVSRVRDYLISENFGKCAMF
AFLNGAFVGAIRRKLKELRPPARRPSHRCAPEVYSQEGSTRHDFLPSVEHRYQKTDVECG
VLYTSWATNFPLVDVFFFVKSNPKTLVGLRMATAGEHNTTAGTVR*
>TCRU_278 hypothetical protein, conserved
MVCVRCRCWAAAICDCAVAVRGVAAVSLLLLPLYVDVLLVCAEGCRQVTGVMAMMMTGRV
LLVCALCVLWCGAGGADASNLDNDAVGGCMASWVLNTNKSYTPSGCDKTALTLPLRSVLS
ITAVAASTDPLVTGTAENKSDLAPSSGADFGGAGSPPGRGGEGGGGRDDGAGGPGGVGGA
SGSQARGSKASGGGGGGSNGGSKARVDGSLKSPASDVKSPSPVLGDGGSSPGAPTGSVGS
DGSKGFILGSFSSGGRSQPDVGSPGGDASLSAPVAGGNSPPSITDESDALEKTGAAASTK
GGKPQEAGEQSGANRARSELPELSAPAESTPEAQEDSPSKQEKPESEAAGRAATGDEKRR
SDAEAQGPSTVMSTASASNGRRRTTNSGGSSGRRKPNGTNRLANFDRRKDKNATVTKQKG
A*
>TCRU_279 hypothetical protein, conserved
MPVGSPVTRNQVLSNEALSLQSPPSPKPSAPELQDLPEGPPVSGGSQGGEADNAVGVGPS
GSSSGSGVKSMVSASFSAGTLSPPNPVDGDVLQGGKGTTATLSMDSSEKSVKSQSAEPPA
PAQPNLDRQEASTSNAENHSPIKPHTAGNQVVNGGATGKENTQRAAVTGGPSSDTRSTTL
QAAPQEQPKTELIIVPAGKERATDPRTREKEERDSKKAPPPPASSAGGTPAAKDKFQRRK
CTKRHRQKPKSSFWDKKPLQRMTRKIKTLRAQQHRIR*
>TCRU_280 hypothetical protein, conserved
MVSASFSACTLSPPNPVDGDVLQGGKGTTATLSMDSSEKSVKPQSAEPPAPAQPNLDRQE
ASTSNAQNHSSIKPHTAGNEVVNGGATGKENTQRAAVTGGPSSDTRSTTLQAAPQEQPKT
ELIIVPAGKELQISTEEMHQTSPSEAQKLLLGQETPSKDDAEDQNTEGTAASDSVKDEAA
SSLVETTAPPISTSGGADTKSVASEDADNAQQPNHKEAHKDPEPQNTSPAFTATEALPQT
AIPLTTAPTNDNTTPGDSDSSTAVSHTTSPPLLLLVVACAAAAVVAA*
>TCRU_281 oligopeptidase b
MKSGPIAAPKDHEVVFGYVEGENRGNNAMNPPRRRNDPLFWLRDDSRKNPEVIAHLKLEQ
AYFEERTADIKDFSETIFKEYISHIKETDISAPYRYDGYTYYTREVEGLSYKIHCRVPLG
MTPGKSEDEQVILDENKLAEGKSFCMVHEVKPAPPDHNLVAYSVDYVGNEMYTIRFTDNA
VTDVVEGTNGQILWGPNASCFFYITKDAAERNYKIWRHIIGRPQSEDVCLYTENDLLFST
AMAISGDGNTLIIGSGSFETTESHLLDLRKGNGHTTLEMVRPREKGVRYDVELHGTETLL
ILTNKDNCMNGKVVSATRNTPSDWENVIVPHSEDVFIGEIGVFAKFVVLSGRRGGLTRVW
AMPVGSDGLFRSGAFVQEVSFDEPVFTAFPVFSHMKMYDTETLRVSYTSMSTPTTWFDLH
VVNGTRTIVKVREVLGNFDAKNYTCRRLFATAPDRTKIPLSIVHDVSLDMSKPHPTVLYA
YGSYGACVEPEFSVKYLPYLDRGVIYVIAHVRGGGEMGRAWYEVGAKYLTKRNTFSDFIA
CAEYLIEIGLTTPSQLACEGRSAGGLLIGAVLNMRPDLFRVALAGVPFVDVMTTMCDPSI
PLTTGEWEEWGNPNEYKFFDYMNSYSPVDNVRAQDYPHLMIQAGLHDPRVAYWEPAKWAS

KLRALKTDSNEVLLKMDLESGHFSASDRYRYWREMSFQQAFVLKHLNARTLLRR*
>TCRU_282 cAMP response protein, putative
MSLAAQADNDLFNRNVLDFGSYEEYLDQQVTPEDLFYLGNQDAARQIVELGYKGKDFLSR
EEFEAACQLALEGPSRREETVDVICSAGKKLDDAPLLSALAKREELVRNGKLSTIIFLRD
IVRGQEVSAYIDYGHRLKTEDFTEYFTKRKKLTPKRTDLSYYNWKTHTLFYNNSFTFQVL
ADNEMGLLMKHKRDRKTINVDPKAPTPGDNSNRTVIQTSDYVQVTIYDHVTRRKN*
>TCRU_283 conserved protein
MPRKGSKRRGRGTEQTNPPQPPVKSNIPFNDPTGSLKEREPQLLSPQTLIASEFLENPIS
SSTHCSEIGTPSSSVPTLAMVKYLLQQVAEDEESDNTAGRMILIREESALRSIIENDASM
EHHAMMKAFYGRSPLSSVCGSVNSWSASSRRVHGVESETRAMKPCGLWRQQEDTEVPLAK
TAALPMSASNCGVQVTSPLQDLQEEEEEEKKKGSEQVLSRRFHLVPSYGTMEGLQGDANS
HLGHVNSREVSSNPLFFNFVTGEEDRTIAWVLYENELPVFKIVDDSDFDVTVEIEKEMKG
LLRVDVNFRDFFRAMARQVLFLILSMGIFFPSMAQSGLFASMDLLTNVEGSVTRRNMMKL
TLLFVDAAAIFILMPLIAFCFHGGNSIRFIILFTATITTVGSGICLMRGYTSGSFALMMI
SQLLHAVGFVLSVMMMLFINCAKMGAFLGTISLMFVTIYLWLMSIAAGIFIFLITLRLSE
GEVLEVLRGFVYLTCVGPIFALAICLLPPPPPTDCQGTTRISHSAIDAGTMFATLRRVEV
CFLLRCIACGCLLAVLFLIIEFESLFSSKLFAFTSPSFLAYFLLFTVIVALPLCLLPRFG
SFVRLCEFGLLTSLAAVSLFGLMFTNIPSEVATSIIPFSLPWMPAMTAILCASSFAAALA
GLMRSLASVKRALPLVVVPALSLTTLLSLCVALATGVAAVVLEFRLQSGNKKEGMTRSGA
NDTGETQAGQAVCVGRVAFGMCVGALFLQFITAARTFFAPNFQ*
>TCRU_284 hypothetical protein
MERQLQERDDALAALRDRLEEYGREKSALESRSSESVDALAAMERQLQERDDALAALRDR
LEEYGREKSALESRSSESVDALAAMERQLQERDDALAALRDRLEEYGREKSALESRSSES
VDALAAMERQLQERDDALAALRDRLEEYGREKSALESRSSESVDALAAMERQLQERGNAF
NIFDGPVNEICMEKPSLGVRLKTGTDMFVVFLRRLRGLGEGEYGVSFQDGLCTFHHAKDS
YFVSFLWGVFKSLRSLRNFVFGWNWNGNCRNEDWWDALGHVQLEFGCVEAELHEFSELLR
KLEEDCKDTEPTRRLQELIDIHAGYGENEDAALNLEENFEVLIRELRHRVCEMKTMLVGQ
SVRERLIQARIDALSSGIHRVANLSFVVNGEVDKDKRRRALEELHEKHDSLSEELSSLGR
GLLVLYALQQGREETFLRPLHEYSPFLAAKCLRNAGFLTDTIETGVFSLTSGVLMVAVIV
TLMYKRYSLI*
>TCRU_285 prefoldin subunit, putative
MSTEDGIYGPPSSFDAETGRMARLEHFLDAVLRQSLEKVLRERDTVYTMASECCQLRELF
QEMRALSSTHSFITDGDAPSLPATMAAGEGEKEDEEKRPQRNQIMVDIGNYFFVQCSVKD
GSQVWVNLGCGVVLPMSTAEADVFLQKKEKLLRERAARLSKEALRIKYRIRLVMEAISQL
YDRATGQRK*
>TCRU_286 hypothetical protein
MFLRLATVGAFVTVLVAFTLLHGDELWGFGPQRRRGNSPCECLTGVIGDSALLGALHRKS
LFLGLHWRATPAHVMAYLDPWQLKYANCISFHRLELSGIKNDTSAVDVLRERLEEDAAND
TSGSWMIRDRGLMASRQRHRQHGRLKTSAAEPTCHVWILPETARIPLTVWVALKGLLQEG
TIADVPVRLSARETKWSMYQPLGVLLWADPADRETLKHVVPPRTVMMFTTISR*
>TCRU_287 DEAD-box helicase, putative
MALWPSVGVLSAGMRCTVASGCRSFGGVVSNRNRTALLTPARGIIVPQQLKAYGGTFSRS
IGERSDHLVGNFVLQSLSPSRTAHSPLLAKNVKTKTVTSFEDMLLAPELRKALTQSLHVD
TPSPIQQTAIEVILQGKDTVVAAPHGEGKTLAYLLPLYQNMMKDRDVYKIPLRERRPRMI
LLAPTKELIAQLQHICATLDAATGLRSISFTSRKRAKYHLSRLLKNTLADVVIMDPKVVL
RLIRSRRLFLDDIRYVAVDEADVMLSSQHDHDAVHLLMKVQKRMMFKYLWPVQTQTVFAT
AYITRKLEFVIGKKFPNAVTCLQRQRMHRPPDTLSHRFFAIQREQEKMDVLQHLLKKHGN
HPRVIATDVDEVQAHTQTHYLSGTLEEFMERRRNTAPPSPQPNYQQRQQQQSDELPEFEE
EVVQEQEESHHYEGESNGSVNSLDCSSSPSYSLSLDVERDVNEEARRILEQVRPLRWEHL
TTVAAPFTCHIPRTVFGEGQRIIVFTRGIDSATAVYHHLRGRGFTCSLLHAALPWDVRRR
MFADFASGRTNILCATDLAARGLDVHVDVVVNFHMPTNALVYLSRAGRTARQGRLGRVYS
LYTKHQGVIVSAVRAFLKKNIPLEGVSNSKSHMMNPRYAEWRTHKMNAIARSYVSLITQK
TIPAHLERTYLHHNATWRPLFHPQTTGIHAGVPPRQQQRVMDAVTEQAVWFRRGQLARRK
GGRAKFGGRDAERGVWNSIGGIATSWVANAAQSANPGGPDFGPPQGPPK*

>TCRU_288 Uncharacterised protein family (UPF0160), putative
MPRRFVAEYVTKHLCGVRVLESFAETSTATGVIGTHNGSFHCDEAMACGLLRCSQNFGQS
NILRSRDPNALERCNIVVDVGSVYDEATLRFDHHQPSFHDTMKTPKAVYQTRLSSAGLVY
KHFGREIIQGYVESALASPYRVKLLDATKWGTDKKKLSEQELDTLFDIVYKNFVEHIDGI
DNGVNAYGPAGTEGEEGAVPVSSSSPSCVRKYNVSTTLSARIGNLMPWWNEEGNGKVENE
NAAFLQAMELATSEFFDSVHYHVFAWMPARGIVRAAFLEAMNVHPSGRIVVFKDCFCPWK
EHLLELEEEHGKVGHVLYVLFADKKGWRVQAVPKEASGFENRKSLPWRGLRDEELSQASG
IEGGIFVHVSGFIGGNKTYEGALQMAVKALTVVN*
>TCRU_289 ras-like small GTPase, putative
MSAKTNISFSASSSSLIKGTEPRIKIISIGSSGVGKSCVIKRYCEGRFVSKYIPTIGIDY
GVKRVSLRAPAHMSPAPPNFFVRVNFWDMAGRDEFLEIRNEFYYAVEGVLLFYDVTDASS
FAALDEWLKEMQTYVNAPRNTGGETLGVNPVKKPAIVVVCANKVDNEVDGGKKRVVSEAD
GRRWAEAHGYKYFETSACTGLHVTEMLETLFNDVVAAFM*
>TCRU_290 hypothetical protein, conserved
MNSYARFFCGDQSGLSWIGWNRLRDKQLFFGSLFFATSIYAAVHYSEEKERRRRHVSIEN
DIERERWRAKELGLEEPRDDGFADAYMKKLRGRQ*
>TCRU_291 hypothetical protein, conserved
MKTGSERNPSPRIRVHNAELYTDVMNASDWSRMIEREQQRERIAARRQHEAEEWQLQEQM
KLEEVRLQAARDTEAAKARQERRAREDTQEQELADFMRRFTAFVEEHENFNARCACQTRR
EERHLRRVVEKLHRAWKEDVFLPVQAFIDAQLQDVEGEEHRTLLRHNMLTAFLKECNRTD
RFGGRHAVYRDIIDEVRYDPLGQLQTCTIRYPAPPRRETAVDAQRRAAEEVQRKYAQLAI
DFHGLERESTTGVLTDPPLNDTSQIPATNLPITGVVSTGKEFHFASRTWSSDPREVATTA
TGIESNATLSTTGWTAKHCTSTAGRTTRRTVLPPLQHPPPPKDFRHLSYGINVNAVDSLA
KWTKERRMPRPREADLPVTMWGRFPETIHGWMATADGDVKPSSRRRVDAARKAQHSDVMF
DHYNFPRGLDGPLHTGKRVL*
>TCRU_292 hypothetical protein, conserved
MLTAFIRQTATLRAAYLPLAAAYTSSSSSTSNPLAVVATTGNATPITATGMTNATERVRS
LPGGGVGAGNDTMPLVGDPRVSIWRDEEALLRASLGRLEAERELARMRRRCEDELQSLRE
GLKVREGQVARIVRRVITRTPAKSRRGRHAHVVANNINSTHDTAISCVESGGEEVVAATD
ECEGHGATVMTQDEAHTEEICRPAHPGRANKKEKAHRLTLGNAGAMEVEVEELDGKGRVK
DDNNEVEAVNDAERSEGSNSFSGDDAADNADGDETGTTVPSGMELKMSLPGTRRGGLAGG
TVHVGSNATVTSTAGGKRQAATASTNGELTKDAVGRRGRRRAGTTKKGTGSSNNNNSSSS
STKNKNKKRETGRSPAKNKKAVMKTLTKQRINSKGRTVSHNAPSSKKKVQPKPRVKTGHP
TPKRKTSSSMRKQPKKQDHKNNKSKQSSLNKKGNDHTKKATNTRQRR*
>TCRU_293 hypothetical protein
MHSVGKRSGVNEDSGRVQDDTTCMVGQELNNGVGQREEESANVQLSLSFSEMRVGTHTEC
VDSLMRNPTPTLSVFGGGTTLGVSTDTENGAGNKDAAYQPLRLQIAWDGDICMSQVDGVC
VMLSAEEAQAEDVHSAAPHANSIDSELCPLGCDENSSATSWMLRQRRLQNRAEQWRRHEE
ELWRRRYEQSISQTCAATIVKFPPLTETTALQSHDDVHLGTDENGDVDGDAGGCDDSTEP
QTKRFSTANGRRLRRYRPEPIKSEDDDVAMPLWQKSTCRRNP*
>TCRU_294 Concanavalin A-like lectin/glucanases superfamily, putative
MCTGPVPTKGLVAFLSGSSTETEWRDEYLGVGAIIKNTAAAVNGVTLKGAGAGAQWPVDM
NGPTVPHHFANREFTLAAAVSIHEVPESGNVPLVGVGVSDPNSTVLIGLSYTHEKNWSFM
TPSDANPDEPALFDWKPNTTYQVTFEMNTDGCYVFVDGRGLYMKKADEESFATLLEKHRI
SYLFIGWGSARGTESSRMTVTNVILYNHTVYGEGLEQLNASTVPIPQSGVAKQQRKHEGD
PSSGNSTVHLSVSPVLLLPALVLQLWGMTALC*
>TCRU_295 BNR repeat-like domain containing protein, putative
MSSCGDGQHQLCVSDGHGTSWYPNRVSINRVWGNSHDRKGYGVQSGSTTAVIAGEKVMLA
ALPAYSKDNEKGRLHLWVTSIVRVHGVGPISREGDDAAASSLLVKGNNDELLSLYENKER
SEDGSDGHVAVRVAAGLERVKDVAKKWTDLESALQ*
>TCRU_296 hypothetical protein, conserved
MWSAVDACPRSRHRVQRSAIAAMRAALLFALALVAAAAWMPAVHAVVLRLRGGTVDRAIT
VGRAVDTVLMDGVSITNGVAVVFDVAAMLPGALRIELRNCVCDGGAQIYVRGYSGEPASD

RSLEVSVIGLSGSYCSLVFVHNLPAQTNVTVRDSTIVTAGPMRYSQLSGLTDAVASPLVL
HATSLLQSQLRVSNTVLRSLHAGESAVYVGGGVDLLSSAVVLDGVSLEASGGLTASAMRV
ASSSRLSLRSHSVFSVTNVSVVSSGGGLVLGERLEVVDSVLRFVGVEGSVASSLVRCDGG
TIGGGGWLDLRDVWAVGETSSVASLSGVTLSGGTVSIARCAATGATLVAGPAITSGVVTV
QCPWLSRPPQRGARV*
>TCRU_297 Polyadenylate-binding protein 2 (Poly(A)-binding protein 2) (Poly(A)-binding protein II) (PABII) (Polyadenylate-binding nuclear protein 1) (Nuclear poly(A)-binding protein 1) (PABP2), putative
MSNFPAASPSIWVGGLDPNLNEQKLYDHFVRLGPVASVRVCVDSVTQKSLGYGYVNFQNP
ADAEKALDQAGVKLGSKHIRIAKIQRDPSKRRSGVTNIVVKKLPPSVDTYALKEMFSKYG
RLTAIGLATNENGESRGYARISYEKEESAIQAVQEVNGMVIDDCAITVERYQPHHREEQL
KQFTNLYVKNLDPSVNDEKLKEVFSAFGEVTSAKVRDLGANQTVGFAYVAYATHEAAAKA
VEELDEKESPLAKEGMKLSVCRFRSRDERQRERERLRRERQQQHSKYPNLYVKNFDDTVT
SERLKELFERCGETVSVSVMMDRATRVSRCFGFVSFKEQSAASRAIQELHGSTALGPRPL
FVTYALRKDARRQTLEDMRNKQPRMRQPPMGSLMGGMMGPQLGFMGPQAMFNGVPFVNPR
MSMMPTPMGMGGQLRPMGPTPMNQVRARPMPQRPPMQPIMAPPPQPQSLASQGQNLSTVL
ANLTPEQQKNVLGERLYNHIVAINPAAAAKVTGMLLEMDNGEILNLLDTPGLLDAKVQEA
LEVLNRHMNV*
>TCRU_298 retrotransposon hot spot protein, RHS3, putative
MRLPHEWGMAMVTTPNEGNFKEWYNQETAVRTVMNYPEEKDVKALCVWMKRDQPFGKQAE
HWREVKGCMDKVGLLLCYTFDKL*
>TCRU_299 retrotransposon hot spot protein, RHS3, putative
MEVKEGEPPQSWTYKAVGKTLEKDDGVQQSGAARPRLMVLTSDKGWPYSWEEDGSTRVCH
VNCEVERVWQIVKGDVTEWFNSRPEEHFTPHPRVLIAKLGIGRSVNAGPYLIYQPPHYDA
EQLQVVFHCLGDMT*
>TCRU_300 hypothetical protein, conserved
MESGQYTEQGIAPLWHTDLPTCFTTQLTNKWRSTIRQDTHRYLLCGTRPSDLSGKDLITQ
EVLHRQELVHLARARCGESELWGRRYWAMRDCTNQCRFCNISPEQSAYMRSNNDPTAPGT
DTVPPSAREEDVSPVRGQTVTRRRKEKCPHCDSTLTGFSGLVSHCRSFHPEHPPPLPELK
CDFCDMVFPTRRSTAQHRSRCAHNPDATRHRNSSARRRSLLPQDQPASTSTPIGPQETLH
HLLLECPGTLAVRQRLGIEQDLRLGKFSQWQLLHSRKLLSLLDHLFGTQMALYS*
>TCRU_301 Endonuclease-reverse transcriptase/Reverse transcriptase (RNA-dependent DNA polymerase), putative
MHHPQWEPFLESSPSEVAAEFLELCTDAGLTLVNTPGEITYARGTRERSCIDLTWSKHLT
VSDWSASVSPLSDHYMLTFTLHQAFKDTIPSAPPSAPKFFYSWGKCKWDLSIKDFDAQLP
AYDYKKQSTGIKAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERIATDSKARYLQLP
TPDREAEMQRTRSQFFLLLRERLRNTYLRRISKLNPGEPLAWKYISGRKKASLPSPTSML
LGDGQHTYKTARRAANALNRIFLPFHPSHKAVRFSKGINRQSASLNINASFLFGQQNNSE
SAASFTSFSSTSSSSEPQNNNESAATFTSGSSLSSSSEPQDKNEAATTSGLVAHLHSPLD
APFNRTELLAALRNTPYGKAPGPDEVCSEALRHISLKGLRFLLRCINHSWTTGTIPVEWR
RATIVPLLKPGKSPEMLESYRPISLTSIVSKVAEKMVLKRLLWVWTPHPHQYAYRSMRTT
TMQLAHLIHEVEHNRNHYFQVSLPKKSGIGNQLHYRPHRTLLVLVDFSKAFDSIDHRVLS
RLLANIPGVNCRRWLRNFLCGRYAKTRVGHRHSDRRPMLRGVPQGSVLGPYLFSLYVHPL
LNLLNSFAGVTADMYADDLSIIVRGQSREDAIPTANMVLKKLHAWSQENGLAINPSKCEA
AWFTLSPHTESDYDREGRWPLVVAGCQIPVMTMGASRTTKLLGMDLDPRLTLNVAATKQC
AATSQRISQLRCIAHKEAGPSPHDLRTFVIGYGASKLRYGSELIWAVATDSAKNEMQKTY
ATLARIVSGVPSTVDPESALLEANMPPLHVLCLRARLSMFENTRACQMDWMRRPPPEPPP
RAGFRISPLSRDELYAFVDAYTKDYGITESSPREERFFRSSIPPWFAASAHRVTIGVELP
IDHSITDEEELIREKRRVSEEALALHSHRSWILATDGGVDVPKSAGVGILLSSLNSYGDN
RKGQYKLRHTPIQLQDGIPCAASSPREADDPSYPPQA*
>TCRU_302 hypothetical protein, conserved
MDTVLNKPIANALLYSDGALHLVGARHNEEKSSLFPAPLTEELQMITSILRNWADVDVSF
FASSISTVGLVGYLSNAGTANTWIDECRCVIATVTNEKNVTNRL*

>TCRU_303 electron transfer protein, putative
MLRKITTPYKISVRRTTSTAPEATSKKAILRLIRFDPTTNRQRIESYEYDKQHEYMVLDL
ITAVKAHQDPTLAFRASCCEGVCGSCAMNINGINSLACITFSQQVTTVGPLPNFPVIKDF
VVDLRHFFRQYAQIRPFVRNTNLDRSRVENIIERYDTLRKVIYGVSPHGIPTDSDVPRGG
NAETEVVGLLRLLDAISEAGNVTHLVSTLEELEAKGVQLDQAKVKELIETTLRKHGERTK
*
>TCRU_304 Ran-binding protein, putative
MTEGRVVELFGGAIRCLLPVTTVDVSEFRQVPDTQEVYTEAETGMCIIVELLARQSEVSD
RECGVFFFKDLAHANECRDGDYTLNAQEPLAPSDYPKVAQLPPGAAPGSGQECAYGCLIS
GTQRISKYKNERGKENEVFVAIGVLRFLPSISSDVLLSISAPQWIHPESSEARVVRQLRR
KEEVLAVLRRMLISFEVRDWSLFVPEG*
>TCRU_305 DNA polymerase theta (helicase domain only), putative
MRKTFVCRGGFHAPRKVTTAHDLPFAEVSQEKGAGDDISAVSLETAAIKRPRVESSPRDT
PPVTVARPLESSLPPNTTAPPPHGRSANGTAVETPPLENEEELQREVEEDQRLSTDLPFT
PSKTAAGLGTPPFVFSQPLLEEEQDDTKENANTAGVVAFHNNSDAVPVTSQPNNIDLSVQ
PRDIASSSSEVVLVDGGGVFYDLPQSAQNFFLNRRGIKKLYPWQHEVLMRDDVRGGGSLV
YSLPTSGGKTLVAEISLLRCLLNRKKSCFFVLPFVSLAEEKAVGLRPFGDALGFAVDGHY
GTQGRLPLPKRTAVFVCTIEKANSLLNHMLEEGLTEELGAVVVDELHMLGESHRGATLEL
FLSKLLCLPHQVQIIGMSATIPNLPNIAKWLRASCYLGQYRPIPLRQYAVVDGMVMEDGE
RNERNLVAAGYATETEQLLLLATEIQGASVLIFCASRQQCVDTARLIARNRKGMKDGFHS
ASTSTLGALQNELSSFGADVNVLSQLLPHGVAFHHGGLLGEERELIERAYRQREINILCC
TSTLAAGVNLPARRVIFKTPYVGRDFLTKSRYLQMCGRAGRAGLDEFGESFLLLSRRDCH
RGRELMRQEVEMCSSQMLSQASAFERALLECVAVGVIGSPSAAQAWMANLMCHHAAGPFD
PVYDVASRPLPVALEGILQSSMDQLIRSGLVQRVSLRRESDEGGDAATMQPAGNDDEQVS
LSATPFGACSVRSCFSIEEALLVRGELENLQRTGLILADDLHLCYFLTPLREIGECNWSA
YCEVLSQMSENRQRIANMVGVDEFFVHQRSMGLGDPYGGSGSRTFATRRFFVALMLADLL
SEVPMSVVERRYQCNRGQLQSLMRSASMFSSSITSFCRAMEWFSLEAVLSSYVKRLGFGV
KPDIVPLMEIRGLQPARARALWAAGFKDPAAIAASNPGELLQRVKNANAPENKSVKFFTL
RAAVALIREANLLLQHHIREKKGELIELTLRSRASPLP*
>TCRU_306 predicted WD40 repeat protein
MSILFDSNALLTASDDGVVKMTSLDTGVHLRTFFTSGSEQHSAVHDFAVNTQLRLLVTVG
PERYGIVWDFSHDAPLAILDAHNSPCRCCAVHIRQRQIFTVGIDGTIFIFDTHGYRLTQV
IHVHHLHPQCVVYDEKKLRLLCLASHPYYHGKQLSAAFACSNKYQGNMASMVGMIYNKTY
DLIVTIDLEGFVMTWKRSNGAPVFAFQLKDFSDSVVMNAARLSSFALDGLGRRLLTGFQN
GAVAVWNLVNGQTTNVITAATESFATTTLRPEVTSLESLTRDGTTFFFFAAAGHLFSTRE
SGTFTIASANKWEVPAVYGEILSMLPVSLQILVCGTSSGALIFYHFLAERQVGSALWVTE
PTESMHRSISFSSEKRRSDVQASVLTSRIIAIFPLHAVGPHILMSVHADGTVALWHTLRR
LLMDSVSLRSAFPAGRGETGLAHVAIDECNQCFVFADDRGDIHVCNLQLQAVNDPGSMRP
ARTPPLKGDAERPMAHWPGSPFRNYEFVGKSPRSKAKGQNDVAGQPNENQQQKGLEQEVD
VEKTLYVFLRFCQEYVFHCGFPSVSGVSIVKEPTRRDPRGVTTASTATETPLPIAKGAEV
GEQACGSLSEGEAEHFIGNYGPTSDAGFYLDLTSSTASAGIIVVSSGSDNFTRVFTLTGT
IIGECGMNIWTLGKESTYEFLGVKPTRRLPARGCSVQAVDFLQETPKGEKSHPVGSRGLR
LTRGTSKVGKILRDSFSGSELSTCHPMADTTELWTSPTTRFPPSAPPSGATPEINPLEYP
SMQPTGAEVREFGNRKKKDSHAKDRLLRRFLPKATTPFEEAGVLSTHIHSRRLKEENIQG
LVKSEFISRLRGLPVNGSDEDSAAHRTPLAFERNPRGGVYAEPSSESFLSASGVNNHNSI
NTNNHSGLTNVTAVVNSLPEETFTPLDTRNHVPPVFVVGGLSHSGRMAKAQAGAVAWKWD
LPAANDIEVTQTPVSCALRQNALSALTASPVEDEAQRQDLIQEHMEAQRRMLLALGRKDS
VLGTALSCRSSRHSSVSPAEKMGKTTGTQLLETLRIQSLGMMETRDRIARITARLHLAPV
SPIAPPSVIREREGDSPLKDGRKNTHSAALR*
>TCRU_307 nicotinate phosphoribosyltransferase, putative
MVDVARPIITSLLDTDAYKLHMQQAVFHLYPSVCTAFDFCCRDRDEHFGDAADAIREEVH
LMQNLALTDDEYKYLASKRYLRKDYLDWLRKYRFNPQQVTVRAVPSDDGNVDLAININGP
WVETILWEVPLLAIVSEVVHRRRTPNLGVAEALAHLEKKLEAFFAQTTEESIETFCVSEF
GTRRRYSFGVQEAVVKALHSHPKFGRYFCGTSNYLLAKNLGLPAVGTQAHEWFQAHQQLT

PILRDSQRVALTQWLKEYPHDLRIALTDCISMDSFLCDLTKDLADAYTGLRHDSGDPIEW
GQKAVKHYRKLGIDPKTKTLVFSDSLDLEKAAMLHRTFSNEINVMCGIGTQLSCSIPGAR
GINIVVKMTDCEGKPVAKLSDDPGKTICRDRDFVSELRRAFGLPMMAVALVTAVASVPNE
GICGLQA*
>TCRU_308 Mucin-like glycoprotein, putative
MMTMCRLLCALLVLALCCYPSLCASETQQNQAQADGNDSRTLPPPPEPSTTTTTGDPKPP
VSESARGDTGHSGSSSSGPVNEPETPTIGEKSSKSTVMQSVETKKTAKTDGTAETQSLTH
PSPHKAGQNAEASAQTTTSTTQAPTTTTTTTTAPEAPTTTTTEAPTTTTTRAPSRLREID
GSLSSSAWVCAPLLLAVSALAYTAVV*
>TCRU_309 hypothetical protein, conserved
MVDNEDDGTDKEKEERDKAQEGAPDGQTQEEEEVSPPPSPLSPAPLQSPPPPAASDGTQP
GGGPGADSSGGGSNGSGSSIGGGGSNLETLALNGGSQSAFGSLGYGGETGSFSGGAGKGG
VDIGSPRGDFSDSSLSADGTFLSPALDAPSSQDTQSSENVERSKTMPAGLPLPNVNALKG
PESKAGSLPPNTQEKSKFSDASGGAAGNKAKQSDVETDDPSSSFANTGDQTVEKTLLLPQ
TPAVLLPVPSAELSPEVPPVTPVQANPDKEV*
>TCRU_310 hypothetical protein, conserved
MTGRVLLVCALCVLWCGVSVVAADGAGGGDGGADEYFVLRWHAQLRKGCAEAFGSRSEGR
KDVFAVDDCVPLWMAVLSGDASVLR*
>TCRU_311 Zinc-finger double-stranded RNA-binding, putative
MTRRWDAPPGPAARVTGDSTRLISSDLLCPSEESAQRQRRYVAPGHAIPDGAGQAGSQNQ
QPHFRQSCPRPVTQNLVPPAPHVAPSTGRHQDLPHDHPSHSRGNYGVEENRRHVCIRMFL
PPSFPDTNARGEKKNRELRSWRDLPANPLNGLPGLATQVMPVDREECNFYCDACQKGFLS
QERYDGHMMDHVWCTMPGCRFTCLKGKEWKMEMHMETLHNRPDAPNLADVGAYLSQRRQR
FPTQDTVKSKVEELFYKASRGVIIPDERRRWLRQHGVLVKKNPRTEETYIDSDALRRPAN
AATNKAVEGHQGQKEKQQQQQQQQQNDEESGEKEENTEMNVPPVSIKNPHEEGITVKENP
AVAAPNPSAHGRPKRIIPLGPNGTLTRGQKVQLIRDRYRDAKTVPRFYVCHRCGEKGNHW
VDECPKRDDENFGRQTVWGEERLEPARQKHRTEGEKEEEKAKTKNINENEGQMEDIPSPP
GGGGRNTKGSTTAFCEGKDLVEDDGTLEIVEDDGNPPAESSARRDDAAGDSTNPTTEVSR
MLAPVAAATLTEKKGKAQQRVSSRSRTRPPPPPTLYERLVESRKANEQGLLLQAFRFFVM
RRFFEPL*
>TCRU_312 ABC transporter, putative
MASLWFIQFRAFLWKVFLQRWRAPVSTLAELLLPCVFTLLLALGYWFSTTTKVPVTDYSG
TQPMDMSSLLPAFFCQNMSSPRPFGRRLHVGPCGPAGPSTMCFPFVRDGALCVRDRGTFS
KVMFGVYYASGPIKVPTLDAYLALSAFVSHESRRTGSTFFSRSAQASLSHYGDLLVAGKD
GDTSFASGFVKYCSDVSALCAEVVHKDRVFPTLAEAEKFALKHDDRVWAIVELPTPLPGS
PAAAGVEGTIFSISMNYTATPWTFESKMQFFKGLGDNDYMLYVASGFMTLQNVVQQFYAR
YRLDKAPPPPPSGANATGIFEFVNLQGPPLIPMPAPPYVDNSFYSRWAYFMPLVAMLAAL
FPVTKLVSWIVEEKSLRIREAMQIMGLRWSCMALGWFISAFLMDFVASLLAAMVFRLSFF
SYVNFGVLFFLYFSFMQQNTALSLFLSSLFTNPRIAGAVGALCIFLCSMPYYSFPDGMSM
LRLVTMSFVPCVAYAKAFDELAKYASFGYKFTWKNTRVGDYNVAMAIGLMWASSGIMWIF
WIYLDQVLPSSIGRRRHPLFFLSWVRKLFPCCFCCCDREGSELSEKDLQNTRKFSNGLAS
ASVGTLPPHDGKPVDEEVNSHAVVFRKLHKVYETGGIIGWLYLFLTGLRRDGDRREAVRD
VSFNMDFGKINALLGPNGSGKTTLMGIATGMVTPTSGDVYICGHNAAYKLHKCREHIGYC
PQSDIVWNRLTVEEHLTFYARMKVNGGWDVREQVDAIVASMQLEEKRHCIAKSLSSGQRR
RLCVGIALIGKPDLLFLDEPTAGMDMRGRKAVYDALQKGRDTRAVMVSTHLLDEADRIGD
KILLMHEGALCGAGSSLFLKSKMDVGYVVTCVVESCSSEMEENICISRLTEFVREKSYPG
HSRNMSTELHSISTKCKLLGIERRGREISFRFPLSLLSASGSAIIRALEEEREALCLRSI
GLSLTTLQDVMEYLTKRQPSTMATAPSNEPLTDKATEHGISIQIEGMGSNQGSCFGTAVG
CEMNRDNSSMSLLNETRNLHDESEYYNPHRQSLARHFAVLFMKRVHCAKRDLRLVVFQIL
LPVVFLSLALLTDLMSPPKQPALTLDASLYPGYDTQPYSEVMWTVSSKFPDVFDVERSNM
STAFGPYYTPIRAKCDVENCSQPLSAELIPDIRTHPATRYIALALTSAQGKKGTPTSILM
HNVSARHSAPQSLNALYNVVNHQLFGQGSMTTARNVPMHVGPFEQKMVSAFRRVIFGIFI
LLPFTFIPSNTVSFMVRERQSGSRHLQWLAGANVVAFWLSSMLFDFCCYLVTEALAMIIF
VIFKRTEFIGEPKTVVASLTLFTVFGISSVPFSYVVSFFFSSPFVAQGVVLIANFVLGFL

WVMGEQIIGGIKELETFVTRTTHVLRVIPSVSFGEGIFTLSGVELANMMFPERKRPNLFD
KLEFVEGKFRGGIGTALIYMSCTLVVSLLLLALLEYARIQRVKWFFTRMSCSKRKNKKSS
NQNADAPPSAPCICHQREANMSIDASVAREEEEVCRNETGRIEDCITLQHITKKYGGTHR
PALDDLSLGVHKGEIMALLGLNGAGKTTAVGILAGEVVPTSGSAYINHLSVLRSASRSYV
GYCPQKDALIDHLSPGEHLRLYAGLRGATDKYIRKEIPKLLDALGLTSQKNTPAYSLSVG
NKRRLSLAVALVGGTTSVLLDEPTAGMDATARRQTCAVVRRLTRAKSVILTTHLLDETEA
LADRVAFISKGKLRCVGTPQELRTHYTNDSVYTVRVVFADGCGAIDATGDVMKRLRELFR
TSSSTEGEECVLEGVVGRTVTLLVQQSLSQICSVASEIREGGLEGLPPVVQVSATQATLE
DILLSI*
>TCRU_313 Golgi vesicular membrane trafficking protein, putative
MQPQSSVFRHRARLHEEAENSRANAGVISEATEEENNEIMRALLGDVRSVRHKFTAMGEE
VRRQNTLLESLDAVFARTRVRLGRTLRQLDVAGVTSVTHMWVLFVFVIVVFMLIYFMLKF
G*
>TCRU_314 Scavenger mRNA decapping enzyme C-term binding, putative
MMLLGVTAPRLAGAIRRTAGDAAAAGGPRTQLPFLRKVVRDALRSPNTHQSTTPFRPYPP
LGAGEEKQRRSGVIYKDTQCIVVNDAFPKSRLHCLVLPLDLSLHSLSALRIQHVPLLRHL
MDVADRYVQFLRKDASGSDFASLSFATGFHSLPSLPHLHMHLISLDFDSPYLKKKKHYNS
FATPFFLPADSVVEDLERNKCITLNQDVVGLKRMEEKELSCLWCGRVEAGMPQLKAHLRT
CPKSRAFLNSTDAK*
>TCRU_315 flagellar radial spoke protein-like, putative
MTGLTENEIRESPLWQHMKKVLLQVVQQQPSSALDAIIPSSFVLQTGSTVPPHATTIYAD
HRPRVINAVPSDALENLRWASSFGNVLAPPKPRRKPTEEDEEMPQEEAEENEEEVLLGDV
SNVVGEQAIFNSVGEGLQPEEAFRLVVGMKQLVKTEPLATARFWGKILGSGADYYIVETK
IDPERLPEDEEDIGMANDEEEEGIPIDNVADVLYSYGAKKQADTEVEPAGSGLNEWVYYA
AQTADPTSWTRLPDVTPNQVIVARHIRRGFTGDLESSVDTHPHFPGKEMNYLRAQIARIS
CACRVAPRDMYTSEGAVPEEEDEEGNVLPPPESVRAYTTLPPLTPQEVPDEEDTEAIEPI
KSWFYGYRDDELLQGKYWVHIAPTLLKTGRTVAREQEEEDTGFDHSEKIHPFLCEVSRDD
PLTYASHSRSQLPAWSFRKAFHNESSKTRTYVARSATWPGAFTYAVVELGQPGSQYQSVY
IGTGLKSLQGMNYAPKLPPRCLVEYPETELVLQRDATADDELEYAPPPPKADAADEEDEE
A*
>TCRU_316 hypothetical protein, conserved
MPPVTGRPIGKTPSPHPIIRRTRSWRGIMQVRFNDTRADRNKIVKNALFWAPMRIFGIGF
LTTTAMYFTIGHDRFMHTLFGYESEMHYEARVNPDASVVIGDTLLDKDRGWKSPLRELEM
PLHPKRQFDVMRDPNST*
>TCRU_317 Triple RNA binding domain protein 3
MNSRGKEPIGFRGGRGASGVSVAARGFGRSGGNGGRDFAHGRGRGRGGHLLRAGAERPES
SAVMSHEDSGSDDDEKGVMQGENVHLATGKCSTALHKQRHVKTMLTEEGTELPKKLNNKV
FIDGLPYEHKATPGSSTLEEELMQFVAAWKVGKPVRLIKREGQGFGFLVFHSPHSVDVAV
RVLNGRKFLGRKLRVEVPKPKDMTTNDVDIGLDAGKSSFARQVLLSDLAKITQPEIVREI
LRDVAPQLEKRLESIKMTSRNRKAFLTFLSADDVEPAVRFLDGFSMLGRRITAARAAAPG
SLPYTKSPGHVLSHKRSGASADEESHGEAMHAGILHGDADEEECGQPVLPLGVVNPPAAQ
QEARRAGRNVAKELKPSNITGVTEKYNLLEEGPAEVFVGNLGEEITEEQLRCHFSVCGRI
LSCDLLVNKSTSLPTGIARILFALPAYASYAQKHLHGSCLHGHVIRVDRGEEPSAPLASD
LAPHDGEDVVDEDGYMAHYGVKDKAAYFKGTSLEERRDGRNKSKRARETAVDTKKKRRKT
KDEAFKSSGFISAGGNDDDDEEEERFHDVDKVIVPVTASSGRREPKKRLIAVKRRAKRVK
KAFE*
>TCRU_318 NADH-ubiquinone oxidoreductase complex I subunit, putative
MLAFYARARGAPAAASAALLLQRRRVEYWGSSVTGRTQPFAQGDMLPRLDNTRNAINKSS
SAAASITGNHLGIAYDGNNIFSVEEYSRLEKEHYQPLRGVSRYKVEPINEGDGLTTQRLM
LELEEDTVVGIDAAWWGAVFKDFPSLKKPCTSEFKAEFADFYKQALGVAHDEAAVTALAV
PFVRRQMQTKFISFPMFWRIAEKLADALLTAAAGRRHEMRVSRIAVERVTKIALNTIEDE
PWAHQDTTSPLLFDVSNFRAWHEAGNW*
>TCRU_319 hypothetical protein, conserved
MDPLEVSQPRPPPPEEQQLISFLLHAPVHHATFFSLTLVEELLRHARRVDQEVSFLSLPL

PRSRESTRVLSRIVQENRYEEYWPNEHPALDEARQSAPSASYLLRIGVLRALGFNTTGVD
DFVDDVSLALGRRIVSAAPLPEDTASVPLRYREAAQEELRHVALGEWCEDLIHFTAYRGF
SAEQVRCVLLTAMHLMNVVADLSPDATDVEAEKRCTQLLEELLIEQACGLPRKVVETHKS
WRTVTSEIPDPEFVAEMETAISQEKNKKRRTALKEKLENAPRINYTRQELQKERFLTEIV
VGPYFTLQEVAQILDYFSSSVVRHWRLFRAFLAEPQPVETHDEVQVQWDIHSFCVPPLEE
FVRDDMYEIEQERRDLMSACEDAIESAFEEEFIQPLLALQREKDELLECLKERERQAEED
NIRNALDGPGYMQVTRGFILRLNKCIERNERVGKLELNEKPPDSTPPSPEPFSSQMSPSL
SLANKSRRSVTTRQGLGLAGVAGSHKLAAAAPPSSHSENPADAVFSLEEVEARLEKLENA
MRETRWSSHDRGRKKQTGG*
>TCRU_320 intergrin alpha chain protein, putative
MIAAPDIQLVRREVTTVASRSPRCMVVYPLGKKSRQRIGVADKNGIMSVFSLRKAMERVA
VFETPPQNRPVSCATIYEDQLFFVHGSTLEAYSRKGRRFFSFDTNVTDVIHTLFVSTPFI
ICCGNFMATGFREASELGFYMAPDRINAMAVFAVSSVANLEERNFDDYRCILGCNDRTVR
MLRSHKSIDDIRCEAPVTSLGVSDGMRRVYYGTSAGSLGCLDIGSGDSFLSRVFSFVPDD
HQAAVTALAVYDINMDEREELLVGRQDGSVQIFYVYAEEWADSGHPVCMWSGNTDESVLS
MAAGFITDSRRPGVLVHSFSGRITTFTLKEEEHAAPKEMEAVDAVLECTDAQINEAREEI
EGLKRSIEARTRELAAYSGVKKGDTPLLAVSSTFKTKVTLSQQKDSPALRLIVEVDTPLD
CVVLQSELHLHFLEESAEVIVQEEIPRNNPLTKTIAIVHPLETRNYSCSVAFWVEDGQWG
LLKVTALAAPAPRTAQVKMVQLRPLPLYARVGRVDKAVTEGNASPVLSTMEVRGNFSARD
MHSWIFRLLPGTPEMYQEKMSTLSYEDTFFQNPLEVKYGDGSALFTTELLQVLMVTERFI
RYCASERSLEVSFSVGIHSEAVRSNLSRIVPRIAACNKGLTSFRLLEALQELQGGQQTDM
VCFPKEYQRILSQADETKKEHAQAMVTRGYLQKAFVSLCSSVVEIVPKKPKMSLVTKEAL
AALTDCSDASEMMSRLDSLLLCDEGGEGLKSTVDEGGGDDTHNVRDRDGGRE*
>TCRU_321 Elongation factor Ts, mitochondrial, putative
MLCLTRLRANVNKVAFMEMVKDLRFRTEAPIAECGAALKETHGDVEKAMEVLRKKGAARA
MKKRSRVTEHGSVVACVGGLFGAAVITVCSETDFAARSAQFQNTCARVKDALQRKIIDSK
GDVLTNPMEAHRSLVEATAEDIRSSIAVLGENVTIKSVESLRLAPHVAEHISIGSYTHGS
LDVPDVGRIAGVVAVSRLDPTREVQASTLTDVARHFVASSGAEGNYAHQNFFGTEETVGQ
WLKHHGLCFSSSLVVDFGKEPITHTASQPRNAVKHPEG*
>TCRU_322 hypothetical protein, conserved
MPSTIRRKWLATALVFSVQDRRNRARALREVRERKAALLALSTNDVAQRLRAMRPPDDIM
DSRGDGIGEKTQKAGQNSKFTTSDDAATPFRPPMSYEQWQEEGFPVGCWRPLLLTELYHP
LEAEKNYLGKKYSLAPKDTERRGTAASRKRR*
>TCRU_323 peroxisomal targeting signal 2 receptor, putative
MPSFNFHPGFAGHGMRCNPWQPTQYILTAAEHFGVVGSGKVYIVNTAPGVPPGSPVSLLG
CWGTSDGAFDACFSEVDQNIVAVACGDGVKLYNVQQSLNLDGAPPLVHIMEHQGEVAGVT
WNRDNFLSCSWDGSVKIYQAANPNASCMTFQEHMKEVYEVACSTRNPASFLSCSGDGTWK
LWDARTPRSVLTQVGHNHQIVLSIDWNKYDGCLFASGGVDRTVRLWDLRRPTQPLASLPG
HENACRRVRFSPHSRVLLASAGYDCRVCIWDLNQPQRPLVGRYAHHREFVVGLDWSLAVP
NALASASWDGRVFFWVSGQQVTPSPPLPQLPAAVPPPRVRVPRNKVLPGLPPAPPAIPVQ
Q*
>TCRU_324 hypothetical protein
MAVRLVPQLPVRVLSPTEFATRLRRIRGDQSTSWVADSHAVVSRVLGSSNDSQFDAPEST
TAASPSPLRQNVEFVIGESPARDTSGTPWSLPDSDVQLLSPWSGNPCPSSASGDKKRSAS
PDLLPAGNTVTSKAKKAKKPTTAGNKRRRTIEEFFSRQR*
>TCRU_325 U3 small nucleolar ribonucleoprotein protein MPP10,
putative
MATTKKDAALPRKLKGSVGTLQQALDNGLDHFFSSRKAGEETSRQCLSSLFVLASSLHTP
RLPYYKKSLETSAARHVTVEQIWGQLSMLLRPVLRRLQDNVRRLQKTVNASSASQKRGST
RVQTKRPRDDVNVDDSDALEEGKDVLSTRNSQLSESDLDEEIAQLLVEQQQQRRKLAKPA
STNGHNGDDLWRYALGKGDGDGNDENGDADVDGEGDDDEDSNSDLARIRRRHARAMAGAD
DDDDNEEEEEDERAVEELAAMKEMYGEDFVPDEDDDDGAEDDDDDPHFEEDLAWDDPTAV
FKESDGMYFGNEDILAGDGAQEEHQQHERGDAVGENDDDDAELNDPSLTMLQRERQRERR
LVERLEQERLYSTQWAMSGETSGNQRPRDALLDEELDFEHAMKAVPVITEAVTAKLEDRI

RRRILCANYDDVQRRTSLSAPGDLVTTRRDATIDSEKSKLSLMDLYEKEYLERARALEEA
SGDAAQSAEPLTEIERDELRAIQMWRRLAQHLDALSNFYYTPKPIQEELAARVRAVDGQA
PAIALETVGNFATTREAALAPQDLYRSADRKYADVGINELVPRERRALRRAKKEQAKAAS
DRKEKRAAQAKKKKQQLPEPQ*
>TCRU_326 heat shock protein 90, putative
MARHPIIQAILIALIVLGVAVTGVTVKDDGSVEKGRPISFQAEVSKMLDILINSLYTNRA
VFLRELISNGSDALDKIRMLYLTAPKEPKNKDGEVPALEMRVIIDNERKTLTLRDGGIGM
TKAELEEHLGSLGTSGTKRFMEKLKETKDDSLIGQFGVGFYSAFLVADRVRVASKSDDSD
VQWVWESAGDGQYYIYEDERGNTLGRGTEITLEMKPDALEFLSTDNVRDIVHQYSEFVHF
PIYMQKGEKWEVVNENKPIWTRKPSEVTEEEYHKFYKSLTHDYRNPMYYSHFNVEGEVEF
SSVLFIPQEASQDIFVNNEDTRDNIKLYVRRIFITDEFRQLLPRYLSFVRGIVDSNDLPL
NVSREVLQESRILRVIKKKLVRKALSMISEIAEKDARLKEGLEKEKSGEDGEAKDENTTG
KKSGDDKAKEPLYPKFWAQFGKHIRLGVLEDANNRGRLAKLLRYTSTKSNGTLVSLQEYT
DRMKPEQKHIYFLTGDSVKKMRQSPHIEEALERDVEVLFMTDAIDEYVVSQVQDFGNKRL
INLAKDNARLDEPTERDKAIEKERKKKYEPLTERLLTLFGKSQVRKVILTRRQSSEAFIL
STQENDMTPRMVNVMNQQAISSLHTMRYSRVLELNHRHPLVRDLLTRFEADANDQTAIDV
AWVLFGTANLQAGFPVSNQAMYAKRVNRLLRGRVGLAADDTILPPDDDEYDISDVKPDTT
GTDEGLLLPVDNDGDESSDKEDAEPTAAEMKPTKTEDDAGDL*
>TCRU_327 hypothetical protein, conserved
MSAVPGGGGRSGGHAEDGDGGFGGNPKDHVRAAAEMSSWMRNAVDEARRDPSKEVGISAE
ELQQRRKMASNPRAFVSEQTSRAFEVKSSARAQQIMNKGLLDRQRETRNKEVLKKMTILR
RIQVGTFFLGIGVAWWMGVEYLLPHYAAVQERNRLLQLRCEMAQRKREEVEAQRRQQQ*
>TCRU_328 U-box domain containing protein, putative
MATIQKLAERLESDVPLRVDEMTFWSRESEIGRAQVFYGPSLEEAKRCAQRISDKLVTKY
LNNPNTNEVPLDHKSRVCLILNNLALHKPIRGCIFDVLDKLEGIFEESIREDGTLPFNPD
LGRMTEHVAVLLMRVTGYKLKAVNVLEFTDGNAQFSVQLMLAILLKEPAYEFGLRGNCIT
IILGFTQPQAFFDSSKGVEEASCLLFTEKVDSLLALMLRLRAVQVISDVLTEQLDSTNVM
TPLLHVATCSVMRCVMNIFRFSSTKSTQWRQHILLSTTLLDHSVTLYLLMQCEALQKSLE
GASPDLSIEMLRGMSLGFKFASLCTFRMHRHARRVRLFCPYLHDMLQFSIRHVRQDNPAS
GVLMRLYVDMFHLMANIDALGGEKDLSIEEIPQQLLSEALLKTTEAFLQREIAPGGLAWA
RAWHTALKTVEADTLVDRSTHTFTTLEKLFGDLEARVAAHQPLPSPAPVAAGGRHRILGE
MPPLRSKTAEVKVPVESAAAPVDMKQYIEVVRKDVIEGVDPILLCALTGNVMKRPVVSPY
GHTFEQEAILAWLEQNGSVCPITGKTLTADSLRPNKEVAALIMKRVIQQSMSTYNQENEA
DLYDF*
>TCRU_329 stomatin-like protein, putative
MSCCFCVSTSSLGIVESCGKFQRIANPGCQCLIPCVETVRGRVTLKLQYASVNVETKTKD
NALVLITACLHYRVLPEEATNAFYRFANPEQQIGSFAANVIRGEVPKYTLDEVFVASRNI
KHAVEEELKERLSQYGFALEATLVTQIEPSTELQQAIAQTQLNAYRRTAAEHQAELEKIV
KIKDAEAEFEEKRLAGVGLAEERRAIMEGLQSSIESFVDGVPGVGARDVVQLLLMNQYFD
SLKEVGSTGRNKVVLLPPSGGQSVLTDLLAAQMNNKSMV*
>TCRU_330 hypothetical protein, conserved
MTMGRLAFSTSCLRRRATGGLTVKSLDRFESDVPIVLQRLPPPPPSSSAAEMPQGGTYKT
FRRSAYAVLRNRNTSPGVCAKNLLSPKEILSTPNRNRCCCAALLYRVTEQEPENSSFAVS
RSEEDRERDDFVFALKLADVEQPLRELVGEAKYEALVGPALAQAQQVGLCECLPQLEEAE
GVGKREGLWVARLLLTPEEDNRVKWLREDGELSSAAFARVPSFRSMYVAHHAGEKHRLEL
RQFESIEARMVENGVDWGMCDAAAVYSFAIYSRELRPYLFHVLRDVLVEYRKDSSNSEVE
KLTKVNLRHVLGAILLLQCLKQLKREADEVGGHVVTPPTYLFVAAEKLFSLATALPKTDD
LAHVLNFLAGICRQSVLSLAATYIVPADSPELTEFTLWLLKEVPNSSVCHDHFRRVVQHS
QADAIILLEKGGLLSAKFTDLRVVMTIILPLLDSSGHEEFFFLVIREVLMGMEERLRRGA
HSFSKVELGFVAALGARLFETQQQKNIPLHHGTGSCESMARGQLEELQVMDGSPWALVTF
SYRSLKEILRALVRDHRRLKRQVQAQMRNIVEAVTYDAPNDDNRGYSPREGDKAAPASAS
PPTTFSSAEEGRNAAATTATAAAVDRGNFNSDCGGGTMRPLRLSTPAPIRERFLAFVEEL
IKALVDETGANQQSCKVVSDELFAFVEKHVPLPNIHDEYRRKLFLLVNVFTEGKFGKEES
NAGNDSDGDTGENSDEIPAELRLLVTSLPLTLSPWASVMILREVLSESAGNNPRYTYVLN

AAIDLQLPISTTRSRIATTLNMWRFLSSQADKLTFKEQVRMKQRCFFNLPLSYILSSYWS
LLTWLSLLAIFGLNVVGMDFESQYVATRLFKEFAPPDEVLPPVTEAWNKEGAEELASMYL
DDSGPGGNGIHHQKRRRSSSELLLSSASYIFLGEDDQRRPMTIVSISSRGTQSAVERATE
ELACASAVLREMSLQLPFPFFLQVEKELPVELIISRVAERIRRVSFNNAWFVSRVIFRTF
PLGRYHTEYTLVSHTCAQANLTRRRMTFLLYVNQGVTLSPQLLFRLRESVLAQKGNLVVV
AHEDSLKKGGATPEVISELTDGGSVRFIPYNRQWATLAVHGAPPPRTIEKYFTEISSRWR
EMVSKCAADVFLLLRMLNRHVAQNGIREWRPTLHVGQAVFPHALQGEEEEEERGQD*
>TCRU_331 Nucleoporin
MLKPGQASAGTGFAAAPAATAGKSASSGFGGFGANTATTGGFGANSTVGFSGFGAAKGFG
TAAAIGGQAQVPSYKGIKGPGFSTDWARSVNFSTFRDDVLFEELPPPLQQHLMELHNFIQ
AEHDAKRFVESFLTDSMGTSAGDYSSYMELQKKLVQLTAGDNAVDAIRVDCFEREVQGQH
LGMLLENCEEEVVQYSKHVWEPLAEQDFTQRLGGNRAELPSEPFQCCLSEVQTRMEEMSA
VLTELELAVLPNAQRHKRTTNNDKNTSNTTNAEPSASHFSRYTAEMKPLDTATGLRPTIA
SHPVVQMNTTLSNELATLLNLAAWTSRLHARADAARDLFAHLYGSSEAEVLLAQQQRQMP
VGPKRPFPLCSAEASSFSEPNHDTIGDIHRRSVGLDRLAALSNGERRMQYDVLLERQRQD
SAPASVGTNNTGFGAPVAPAAAIAATASAVPTVAATTAGTTTTTASTAAAGFGASAPSAT
GTGGTTAFGAPLGTASSTRTANKKGRG*
>TCRU_332 hypothetical protein, conserved
MFFDDDNEVNDGSEGARSPSSGASSVCDVPLPPLPPPAPPSSIYGMATDEIYSIIKELRR
QIDDPATHQDIKAMLKKEPSVLLAVARVLHESALLRRTVVNVDGRVEEQLVPLPEAPTPP
LPSGWSSWA*
>TCRU_333 hypothetical protein, conserved
MLAVLFGTFAAPQRLKALLPLCQRWSVPVPSGDGEGCDQDVCRLAMERLAAKVCGVIKKS
VSGDSIEGGLRTMSLSEGAVIWSDGALRLRRFSVERAGLLGELHRRSGFCQASLSTAEEV
WWMEEDPVATIQVRRRV*
>TCRU_334 hypothetical protein, conserved
MGCTNTKEKKDANSCGGKEQLAAGVEEFGKLAKENPVAAKLKEEWSAFVCSLSLPTPLEA
PREVWANTVDNPLTHRTVDKVGKLFLLYVKNDLTLREWGGNFDYTVVGLENQGFLKATAS
VDASSSTGRSKEAMWEVKVHYHSTAKTS*
>TCRU_335 hypothetical protein, conserved
MVVPLMLDLMDFRRMMCNISVPIRLLVLVQNGREAMLSLCLQELEKVYGWSGRLAVSRHP
ENIGYSADVNIGSRLALSLPREEVPFVFVANSDVMFSPDLLPNPLRDVHEMTRHDAARMD
ELSAEVANEPSEYSPVLRRGLRVLRSTVSDDRLSTSALLPDRVRYASVKEREKAFSKHYG
HFCAYCKSSCFASVMLTRLAIGTVGYFGENFYPDYVEDVEYSLRLRLLGFQERNVLCGKF
VHRGSSNIRLSEQLELPDALWYRRVKYLMTNQPYAMMKWNRLKACCNGYKEPYDGMVPLD
VWVKDEARIQRIRAYGHDEIRRVPSIDYDRRLLYPVRTKGR*
>TCRU_336 Nodulin-like/Major Facilitator Superfamily, putative
MVLGFNDRLEAPNSINESQRFGFMVCSMFCAIASGAVYSFSLISGKMTDDYGFTQNDITT
VSTVGIVLGYFTLPFGFILDYIGPKPLFAIGIFAYGLGAALFALTFSGRIGASVGSLAVI
NAIMNTGCAMFDMGPILSVISWFPVDRGLLVAAVKSMIGLASSVIATIYNTYFSGNHSTF
MFFLLAVFVAIGFWAFIFIQIPPYHMTGHRIKHYTEEEHAIARRVEHMYLIKKAPRRRFL
ILFVIVLSLLIVITVQSIVFVFVEGEVPFKTKNPPAIIMIVLCFSLFLVVLPFNCLDKPL
RGSRKSTSGSNEPLEESNKKNDSKVNTSAGDAKNEIMDGAFEGEERLVSNDDKNFPQYQT
GFFHNVLHSIPLWCFWLNAVIVSGGVHIVMLNSRQLFVAISEDPSSEQLPALYVALTSIG
NAISRLGVSFFEAWNASRPLEKRTPITITYCIPSLMMCLSCIFFLIVPARALIVPMLLGG
FANGSYAATLVLTVRTIFSIDVAKHYNSIFFFDLIGVIVFNRFMFGELMTRNSVRASDGR
VHCLGRSKCVRTSFTVLACLCALAFTASLLMHFVYMRFVRSRRAQEEAGRNVPLEMAGVT
SEEVQ*
>TCRU_337 Galactose oxidase, central domain/Domain of unknown
function (DUF4110), putative
MGKGRDKRKKHEDPLKAVKRASRQAQKRAKGIYKGDAGDDEVKGFNNEEAPEVTLNRIRK
QEGKMRTTLVEENVPAPSPRANVVFTAHPERDHELMLFGGEYWDGEKTVAYNDLYFYNIK
RDFWSRLVTALNPPPRSSSQGVLYKHFLLICGGEFVSQSQSQFLHFKDVWRFDTKKFEWE
ELKGLKGGPSSRSGHRICIWRRNAVLFGGFYDNAQECHYFNDLWVLSHLDGSGKWTAVKT

APYAELPHPRSGHSMAVWNDTLFVYGGFSSEKFNRFKKSQATVHHDLWSLKLPQGIGAAD
NNNAECEFTLWTKIRLGGIPPPIRCGVGSAFKDNKMYLFGGVVDIESPGGKVVSSFCSDL
FVFHMDTKRFYPIVLRARRKTTVSESKGGDLQSELKALHLQNLKDASKFSSDEESDEEDE
EEAESHGNVEEDDKEEMKESFEVNKRGQIYPHRRMNASMLVLGNTLYIFGGQFESGLREI
TMSDLFSFNLHTCDTYRVLLSQDLSRLVWLGKAAEESDAGSWESGSTVVSAAFDMEYDED
DDEEAEGAEEAAVDGGVDFSRIPRSLECGDNDDEPPQVIPAELDTAVTPARDIVDGITTV
KGKKGLKVHKEQLLAQLGSGSAVPTPLREETPVLFFERTSAFWVSIATESFADAGGNMRQ
SEKRIYRRAMRFAFLRYHEAKKLLEQLRLVEEREEEETRFFKERRQQKEKEWEEHERKIG
EQEEDDDKSA*
>TCRU_338 peroxisome assembly protein, putative
MIRSMEADSVELAVQLELCILRAVTPKDYQCVLERNGKMDGNTVRLLQAIMQQDDKVHLG
QTILLSEHFPVALMVVDLAPATAGVLCDTTTLIVLPPCVSNGATDVCLAAHTTEENPKEE
EEEEEEGDIDEDQCTVVLDDSLSGSIAVSSERFFLRTLLMDGAVVCVGDAEYTTAFSICM
KAHGEDGADSVPTLHTSPGVFRNIRAAILLESLSSVEATRVQYSDQRLNTSLSVFRPALD
SACMPLTLGLSKNGFSELQMSCAVLVPAWPLAMLNAVLGDTYEKMLVLAINASKEMLSGR
MVSEGDVLIFHFTPQLFLERQLDYTDVTEAVLRHVAHLVQGDAAETTMRLRQNFDGTIAV
PLRVAEVTTSSGKPYGLLELDGQGTEVVLSIRSKLPCVDVTPLYPPLCSSGTVYLNLSFT
LAIREALGSFFLPLHSAGTHVFVVRAMPENFPYECITTALAMNGVAALIVDLDQWRTEDV
QRLVSEYMQGRGEVALVIKNAQILPDNPHLLHLFDTDDTISDTCLGVRIIFLVCEGMEAP
PPTVAARARNVEGVLNCANPSDTDRRIIAETLFQEAQRSFGVCKSLLLSFDSVASWTVGL
SAADVVAYMQECLSVLRCMRLPEGVRPVLSESLCGSVLQKYQKTHGYSLVSTKLHPVRWK
DVGGLEEAKRELRETIQLPLLHPELFLTGTKRRAGILFYGPPGCGKTLLAKAVATEMNMN
FMAVKGPELINQYVGESEKNIRLLFQRARDNSPCIIFFDELDALAPARGAKGDAGGAMDR
VVAQLLVEVDGVGHTRTDGSTTAQVFVIGATNRPDLLDPSLLRPGRFDRLCYLGLPATRE
EQLVALRALTRKFNLADDVDFDALLEPLSMDYTGADFFALCSDAMMFAVESMLQRTAAER
GDDTQSVRRHAEEAPSFFVQMRDFVRARDQLKPSVSKEELQRYESLRSKFTTW*
>TCRU_339 Glyceraldehyde 3-phosphate dehydrogenase, C-terminal
domain containing protein, putative
MAWKIVPSVTGAAKAVGKVIPAQDGRLTGMAFRVPTPGVSVVDLTARLEKPATYEHSRAA
IKAASEGEPRGILCQTEDEVVPSKTQLVRALVLMPSAPRQQRRPREGNIAGSWLPPTIRS
N*
>TCRU_340 hypothetical protein, conserved
MRRLILYRRELCGREACVSLRRFLRRRGTPKKEEVESVDSVDVPSLRVGGMMAAPDTSLD
DIRTEILRMRSEHVRREEKLNENAASSVKEGSTMNDAWNDDIEKLRSNEVYVKGHDVLER
VKAKDRAVRKQLFLDAEEVLRKSNKEDTLRYLQLVYGRIGSYHREEVMESVKALVQLVEE
ETQKIKGRIQENLIDRDPLAELDAAISSDEVKQMAWVNALTNMSDEDLKKLWKWGILDFD
TIESLACMDMDNETRVVDMNLQENSETEKFFVSTTGQRQEGEDDSLLDPTIPQLSIAENT
EALQNVGEIPEFTATLYESLFLGFPNIDLAPVIQKVQEKRYESISESELRLLEHYEESKQ
SINLSAPSTITPSLNKTEKSEEKEVVKQGALGERFSKDTHFLDTKTLPCKMSLTEAMMDR
AFSPSNRFLHAVARCDPALRSSLEVMERIKRHALLDPVFQAAVEEAHAWEETSIQKHLQN
GGVSAKGETRKQRRLRRAEGSATPILGGPLAKPQHAADIPYYYGNIRSFVPPQGRYNMPA
PRLSREEAAQLRNQERKQKKSRMRFSQ*
>TCRU_341 hypothetical protein, conserved
MTSKKAAKEKDEYTPQERLTAAALEYKKLEGHNQSSIERMYGALSSPFRVSNKPCEVPRA
AVLRCFEEILGKTNSGENGSTDNLTETTVVGRSISGGNNADGRVLLSSDSRFPSVHRCYD
AVLQYESCVVEKTLAQHHSLLAEFEARQLQEVESTNEVPKAVASGA*
>TCRU_342 hypothetical protein
MAPRKKNAPKKELTAEDMRRLGMSEEDIARILAERGKSAEERRQEQEAAEARRRETEQRQ
KRMKELEKQKEELVRLEGGPRVAIRDEEDAEWEQLEETLTVEKKRRLRECAEKMVQQRFA
EARRKREAEAAAYQETLGHLTPEEREAFVAAQIAAEHARSEAEMQAKEQQQKREERRLAR
ERAARRAQRQRRRQDGEEDVDEEDADDIATVGGGAKASYERIKSIDELSADLHDKYD*
>TCRU_343 BNR repeat-like domain containing protein, putative
MSRRVFASAVLLLFVVLVCCGISGATPANEEEVKNELINIQNLQRVDLFVPQKTLVLPKG
GTGSVTTRDSFFAPSLVNAGGVIAAFAEGHMNAEYQGGQLTKPSSDVVAEYIDSAWEWST

LVGEVSESTWKAHTVLGATDGTNRVGVVLRPTTTMKGNKMFLLVGSSAVFYESGGNWS*
>TCRU_344 syntaxin binding protein 1, putative
MPRPVRLRLLLLLVTASSTDELTEAKKQQLIRDGGLTPDAHLFANFEHVARRAGSVQRYS
TASAQGGRSTSASASNAATDEDPLLKQACMMMETGRNRTLRVGLSLASVQRDRAMGPNGA
SGGQNSGEA*
>TCRU_family, putative Se.1
MLDVVHGLSKVFYCDAHAAAVLNCSLRLHDLMEHGVTLLEDLMTPRQPIMSSSARYFFAV
EDASVSRVVEDWMAKVPYRDLHVFALGCAPHRSPEQLARARIAPRAMRSKDIMLDFAAPE
VLVFHLSMQNGFPQLLSPPN*
>TCRU_346 hypothetical protein, conserved
MDVFLLGFQFWVQAAQEEAQSPRSATPTTPQIDRVLPRRRQRQTEEAADRDKQQQQCHHR
ESGTGLLAVRLAASILAAERRFSRSVGASWPDPLLLWRRMLLGNSRVDILWWCAATGLNA
LRNGDGCP*
>TCRU_347 hypothetical protein
MKTNVSESHDALSGVGQREESTVNGSKGKAQMLMAPVTVGRLELVPQRERALPSSDGSRA
TGSRENESAQDEKLKVAESSGAVGQREEPSPQHSLPLGGEKDHYQQNQPQYRANK*
>TCRU_348 hypothetical protein, conserved
MRVDRAVPCRSRQAFPLLVRDVLVRAGVAVLLGETKINDVDVVPLLPGAHQEIVRLHVTV
DDALAVDKLDARNHLLRQHQRCLQRQLPITEAEKVLERGSQQVHHHHVELALHAKKKNVG
DAHDPAACVENAVESDLKGKLWMARLRLLQLDGHGLARLYVCAAEDLAERPRPNLLAEAE
AVTHSKL*
>TCRU_349 hypothetical protein, conserved
MRVDRAVPCRSRQAFPLLVRDVLVRAGVAVLLGETKINDVDVVPLLPGAHQEIVRLHVTV
DDALAVDKLDARNHLLRQHQRCLQRQLPITEAEKVLERGSQQVHHHHVELALHAIKKNVG
DAHDPAACVENAVESGLKGKLWMARLRLLQLDGHGLARLHVCAAEDLAERPRPNLLAEAE
AVTHSKL*
>TCRU_350 Reverse transcriptase (RNA-dependent DNA polymerase),
putative
MVLKRLLWVWTPHPHQYAYRSVRTTTMQLAHLTHEVEHNRNHYFQVNLPKKSGIGNQLHY
RPHRTLLVLVDFSKAFDSIDHQVLIRLLANIPGVNCRRWLRNFRCGRHAKTRVGHRHSDR
RPMLRGVPQGSVLGPYLFSLYVHPLLSLLNSFAGVTADMYADDLSIIVKGQSREDAIPTA
NMVLQKLHAWSQENGLAINP*
>TCRU_351 hypothetical protein, conserved
MDGDAPRHRTSGSRDIPTGICTDGMEQAECVAAAACHELKCSANGRTAIMPSAVASPCCQ
RSVRNSLVPSRSQACDAPRHGGATSLPSGIGCAAVLLGPRLCSASAGTSSRREHHHSSPT
SERLIDVLLPTPRQTGTRPADHKQPFVSVVLLLLTLKGQDRPDLLRNLHLACPRHLLVER
RAADQRRPAQAAAASSRPSTI*
>TCRU_352 p21-C-terminal region-binding protein, putative
MPKRHREPENLLPFAVEDYGDGVAEQESCGSDEFHSSEMGNDGNVSSPAGTPKDDADDSS
SVMMGSSNDDGDGENASLINVEFGVFEMRRDVNAVMHLIDQLCPDKMNEVDRDELGAALH
ESPFTCVVKIGDDDDDDEGEEEGEEEIYGMASVLDAVHDTRLESLLHTLRENVWRTVAPG
ILPTEILKSIDDATGRAKCVLLVGEYVRNVPLELTSQILHDMMERVETAFNARSSMSNKA
CEDAPSTVQAIFPCMFAMLSKIQRAVDAPLKTPTPMNARQDPLPKKRRGQNAAQPEEFDL
CRYLFWREEDSIIYEYRDKRIATLAYRCRPQYDGQPENDIPISILYVVPYGGLMQAVAEI
RKRESTQVNVVRY*
>TCRU_353 DnaJ domain containing protein, putative
MTAPSELSGEALVFYVMRTNGNPVRLFGADGVTAESALKRVYKALALRLHPDKNGHPRAH
EAFQLLQQSFEATLESLQSKAPEEKKTRPNFPPPCPSSSPPPPPPPPPPSFAFAKSTLP
GVRKEEQKQRQHAFAGNSLFEIPLPPDVFGAFAAPDSSEPPVASVSTGCPGTKPPAKRTR
PLPALDLSSDDEEHVDEAGGLQASRRDDEQEHASQKRNAERKAVQKEKRSTGRRTLMQLF
AEFNISDDEEEMAPVNHPTGKETGHHWEPTSCHETNRRQQSGAGKPATTLASSSVACPCC
GAGEFSAHIMRGVVCQSCRAQFVPAAIGMMAAERHAAGRKKDRASRGELCACGKAKKGLC
FLCD*
>TCRU_354 palmitoyl acyltransferase 4, putative

MGPIRVERAPVVGREYSVICPVCSNNVTFDCLSRSVYGIQCHFCRTLIDLRNPSVPLPPN
DTGVLAEDVNGGFFFSPEVEESGRGSATTQLSMVLADFAEQQQKEMPTTMGGEARQAFSA
RRIQALSERFSFLYPLVYVIEYIVFGSKPVARIGHVRIFRKRLLFFWPVNIPVTKTSVSY
SAPLTVAILLYLMTTFYTKSLDDEWMWCMHRFVTFFLVLFMVLLVCCVYTDPGFVRPAYL
ETNGSHMGELTLKEIEAKQRESRWEMVNGQPEERKWCSTCEIYRPVRAAHCYLCGLCVHD
HDHHCSVIGVCVGRRNVRVFFFFVITTALLALLPGLSLLVKLFLDANSLTARQLGIGLLL
IAVLLGFGLVVGFLGLTMLYSLAVETTTRERLQNTYANKKNPFNRGLLRNIFWHMCHRSL
PSLFDDDFVQLCATQV*
>TCRU_355 AARP2CN (NUC121) domain/Protein of unknown function
(DUF663), putative
MDGDKEQRNKSHKGRQAGSKAAKKEEFRKKKAGIELEPNRGKNRKAFQGPTAGSRKGQKL
LRSLEKRETALHVPTVDKTLRHIVAEPPLLVAVVGPPGVGKSTLIRSMVKFYSNRNVQTV
RGPITVVAGRSRRVTFIECPNTLTAMCDIAKVADLILLMVDGSFGFEMETFEFLNISQVH
GFPRMFGVVSHLDQLRTGKALKKRKKFLRHRFWHEVAAGAKLMCLAPMVRGMYRSTDVLK
LHRLLICVEPKLQSWRNTHSCVLIDRYEDITAPQNIVEDENCNRTIAFYGYTRGKPLKPQ
QVVHIPGLADFPIAHISQQEDPCAIDDHQGSGNSQGHKMRHLSMKQKRIYAPHCNVSGVM
YDDDAIYIQEDAEKGMIERSGEGLQYIRELQRAKPMDAAATDLDVVRRPVVFRDEDAMEL
DMDEVEAPSDEEDEGSSSSSSSRNDDLEDRMPRNDLSLYGPQEVDEWEDQEAAAGDEGLA
PRGRNAPDAIRENVVRHDWSETALLRRLKNLCVTGDWNCSADAAETSGEDRLGSEASKGY
ESEDEEFDAIVRGERPLTTTSARAQSDDDHEDQFNGDTEGEERREKERHGRQRVDALAAV
GNEFSSSSTWGAFRPADTRHHRGDWGEKKRGHDAYDDGIDGSDYDILAEDDAAVCKSAFA
DAELDDLVSTFLAPRQATTKGTTTTMAAASVSGAVSSLRNDGDEDAIQFYDPHHSRVGED
NGRNNGDGDNNDNSNNNDDLEEAAAIVSGKTLTEEQERRLQKKMAKKKAFDESYDMGDRS
NTYAHYHQLTRVVEEKKQRLDAALQEMGEDVAKKIQLVGYFSGLYVRFVLENVPVEFVRL
FDPTIPLIAGGVNAGEDQFQIVHARLKRHRWYPKILKAQDPLLLSMGWRRFQTQPIFATE
DPNGRVRYLKYTPQHMHCIAAFYAPVVPTNTGFIAIPVKEQRSPNFRVSCTGYTLGNDHA
TNIVKKLKLTGTPHKIMKTTVFVRGMFNSDMEATKFVGAKLKSVSGIRGIVKAAIKGKDG
LIRATFEDKLLPSDIVFCRAWKTVHPPKYCSMQRNLVDANWMGMRNMRELRWEHNAPLVT
KGDSEYKEIKRRQRDDEDYAAADATKVLLSRNQKLQLPFNMKEEFIPLERTTALQQRLAG
AVTVAPEPRDMRRTALLDVFASKADAMLKKKAEAKKRTRLRHQRESTAEEEEYLRQLKKA
KKETARLREFRSQHKTRK*
>TCRU_356 hypothetical protein
MNDHRTYRNAGTEGRYNGNRIYFHATKEPLVKSYPPNKVDGRLLREWEMPGFVASRSFLQ
PYSAIMTVYRGRVLGHSLDSGTLTGVAAGFSSTSATEKSREWVDFLEHAVQIDQPLLCRI
RQRILRHSFGLRRCCVFYGNLHSTSPSLNNTMGRRLMYE*
>TCRU_357 Putative methyltransferase, putative
MQHASLGPHPPTSLLLFLQSAPPQETFEAFKDDCKLFGMPWYCLQAQQLCVVLLVRHPLV
QKYPPRKSNVRAFLKHFITQLELTWATPHVKEALNDEVIDSQLIEAYICYSLRADSDSQT
SMCYKTFYAPGARETFLSVRLAAEQFANVGLALWPAAFVLVQLLLAECSSPTPVILPHEG
ALRILELGAGVGLTPVMLHQYSCYKKRVQGSVLTDYQPELVENILFNLRSHIMSGERPHE
SLSDTEETGAPHVAELLDWTEHERNREKLREWGCNVILAADCIYEVDLIDSFVTTLHQAL
SVSEAAVAIVVQTHRQNKTMKCFFDAVRKAAMCVSSYRLAKSSSQPSENLMLLHSSLCQD
DAIAGSAVVCDEIDADGSFKGCQAGSCVRGWVGPFFLHSEAAVGIHVLRLG*
>TCRU_358 Domain of unknown function (DUF4586), putative
MVFSIPSFLGLGDRYKHAVDERAQGVNFVTCYPKTGHNPDALFDKEFKYMYNGDRRSDPE
TMARREQMEKRKKDMTATGFAYVGPPQKGEGLGSYYGLIQREPYPHIPDNPMPRGPQPFP
KSMPRQILTSPGKLGSYGTPGLALSEIGNEYIATIYDQPRINAKKERDAWRRRMPAVPFI
PVGRRGYTFDESPFAGVSTCYVMTKPFMPKLVQPSFKHFVVDKPWRPAGYVEDKPTAMDY
REDPYNAFDPREDPKSRVKKPSDAVFRTGYRCDNFCYTQSIVFRRL*
>TCRU_359 C-terminal motor kinesin, putative
MQQRAKKRQRQSDESNTRPAHNRNDGQPPGRRLPLTSSVASVTPGGDAFPSSSLHAPLTA
IDLVWQRKTAAVQKQLLQLANLYAQKAQENEAVLDAIERMIASHELELAAVAAESESHTC
QHLELIAELHRREDATLAEKQSAMDEIKTLQERHVQLEQARERLQEDIVIQSDALEQLQK
TLEAERQVTDEEQRKLNDVLERERVMQDATYGLSGEVREMVAEMEQIRKAKEAAERASRE

TEIVRRQLYSQCEELKGTIRVYCRVKGSGNNTNGEVLLVPESSREASISSHSTISLSTEG
LHNLAAAGGRGAEGKRQKIHGGQQKTLHGRFEFPQAEDGVQRTLCVCQSRNNATSTGTQE
SKETFTYDCVFDGNATQEAVYANVEPLVNCAVDGYRVCIFAYGQTGSGKTYSMEGEVLDE
QKCGITPRALRTIFRRQEELSSDGWKYSLSCYFIEIYNDVIRDLQQEPSVYEPGGAAASQ
PNYHVIKHQNESGSTSITNVVERRIRSFEDFQRHYKTAMKNRSTAKTLLNDHSSRSHCVF
VLRIEGENALIRQRSEGTLCLVDLAGSERMSESGTRQGQHLKETININRSLLDLGKCISA
LNNSGSVAPWRNGKLTYLLQNYLGAKGGKMLMLVTVSDKEEHMAESLNSLRFASRVNQTV
VGPSVRRVTDY*
>TCRU_360 replication factor A, 51kDa subunit, putative
MQHPSNQQIQPIDSLTPFLGGKWWIRARVTDKSDVRTWNKPTSQGKLFSFTLIDESASIR
ATVFNDAVDLFNPLIVNGQVYYLSGGQVKNANRKFSNVNNDYELTFDSSSQISLARDPSS
ATIPLQRYNFVPIAILKQREVGSLVDVLAVVLSVEELSSITQKSTGRELIKRNVKVGDIT
AAVEVTLWNDQAKEWAYSPGTVLAMRQLKVGSFDGVTLSATFQSAFDVNPNIPDVKKLAE
WYISTGGRDVSSLSSLGVGAGNNAGGENYRGRKYFDDISAEGLGRGPKADFIDVRCVPVY
LKQDAQWYDACPQCNKKVTLEGAQGERYRCEKCDRQVVPTQRYLVSIQASDNVSQKWLTL
FNEAGVEFFGMPATELKKQQEADPMFVTKIAQLRMNRPVQMRLRVKEESSSSAAGGEESD
RVRLTVMRLNEFMPLDTVSEEKRQAMAAQLKTECEEMVRCIEAYL*
>TCRU_361 ATPase-like protein, putative
MEEVSVVPVEVRCRPPRVNRTELSKVITSFIRQRHAFIHPGEILSLDTASDLIASTVELL
RVCDVYCPQLGIPAEEADYAMVMYTLYTDESCGDSLNSVGPDEDAGAGLAPCSVLSLPSV
SLEGLWETLFYGETRSDSVRLKRDLLQYMRTAMVFSRAGVDPHIVAWNRLILLYGPPGTG
KTSLCKALAQKLSIRLNDMFPFAQLVEINAHSLFSRWFSESGKQVMLLFKQIHEMADKPN
SLLCVLLDEVETLAATRQSALRGNEPSDAIRVVNALLTQLDSLQRRHNVVVFATSNITGA
IDVAFIDRADKKIFIGAPGFQARLELLKSSTQEMIRRGLVILEASSCGEFINEETWPPVV
SRDMELGQSELLQLESIARQCEAFSGRTLKKLPFLAYSEYAMGGCGVASHLISFSTFMNG
LQMAVRAEVSARETMMSS*
>TCRU_362 DNA topoisomerase III, putative
MGRTVLMVAEKPSLAESIAFHLSNGQAAKRSRALPVYEYSGYFFNTPAYFKVTSTTGHVF
SCDFTPQHQSWDRTEEEDLFSAPVVWKDEAGKVSRHLAHEAEGCDTLVLWLDCDREGENI
CFEVMQVVRRSIHDMRDIWRAKFSAITREEITHAFLHLGKPNKNVSDAVTCRQELDLKVG
VAFTRYQTKYFQGKYGDLDSSVVSYGPCQTPTLAFCVQRHDEILNFKPENYWKLVPVSNR
FGSLMTFDWARGRVFDELMARLLHQKVSHHRAAKVTDVSVGVDTRARPTALNTVELMKVA
SKALGMGPHHAMQIAENLYIGGYISYPRTESTAYPSSFNFMAALTAQERSPIWGNYVQEL
LAHGHTRPKAGKDAGDHPPITPMRLATPQELSGDSWRLYEYIARHFIASLSPDCKLTWTK
LLIEIGGELFSFTGKVVEDPGFTTVLPQFAVKDDKVPTNIQVGSDFPISDVRLQAGQTQP
PGYLTEADLIGLMEKHGIGTDASISQHVNNIVERGYCAVKPGRVMEPTKLGVVLIHGIKS
IDPELVLPLVRSKVEEYVTYIADGRASLDEVLSYSLDLFFGKFRFFKQNIERFDALMGAS
FSSLSASGKPITRCGNCMRYLKHLEARPQRLYCAYCEVTYELPQGGTIKQYSSFKCPLDN
FELVICHVDGGKSFPICPNCYNNPPFEDIQKQRGGRQHMACDECRHPVCYHSLATNYVAD
CVDERCDGCMAFVPRTSGKWKICCNHCTMMILLPPTAQRVYVSPEECSECGAMMMDLQFP
EGKSPLPNRKDRIVACVFCDPTLNSNVTEVRGRLGNFSRRGGRGGGGGGGARGRGRGRGR
GGRGRGGSRGRY*
>TCRU_363 protein kinase, putative
MGNQLAAASSVNVADVSSTLALVAPLGREHRYYFRSFHCAKLAGAATSTTETLRSRHIFT
STNDGRAKDMSLRHPFQRAGSTDVVVKVFVRTFGDNQQKQLVEFCYEKLLEIDGRMRNTQ
SAASNSTFMNGGNNTAVGNHHHSPAAPPAPCNVLFYSGMVVHNDRFCMLQRSYVAYSLSE
RLATRPYWKMGERLFAGYQLLQGLAQLHDKWETVHGDLKTDNVLVDKAGWIYVTDVCPFK
PGLLPANNPALFDYYYDTNETRICFLAPEKFLDETVLFNPSNVNANAHTKAMDIFSAACV
LAYIFTEEPLFSLSDTLSLRLMQTQEERESSVQKILIERGVPPNVRRMLLDMLCNPPATR
PTARQLLETFTPSVFPSYFGFIYGEILPPLLARPPDLKVQLLHSRLTDIMDEVTQRFGKN
EDATSHLAVIQDAKQLSVQLLLPVILNAGLHLITDDAFCRLISILQKILPYCSSEVQKDI
LLPYVLHYLKLECHPVIARIIALRTLSMICHSIPFSASDATIFDDLVLPCIEQLFLKTDT
TDVALLAEVADQLPRILLRARAFLEHCQALASANAWQSGFGEQLNSLLDRGWDAFRLLYK
HHHTTVAVVTLRRTADVVAFLGEERAQDDLIPFLTTAIASAIDIQRELYPQAIMCHLHLQ

TPKLKTLRFFVEEGLKQTDVTCLERTIESITVIVEKECFAVWDIMPLVHQALPYIMSSNK
WVSSAASRMVEKVACTHRVSDVWMYLECAVRPLLRHPVPLFRMASFPSAVKLELSNNIYV
VEQLMRNMNLETRFLGGDAAFYERILRSSTIYDSPYFNSFGIAKRSLQGIVSRATSVDVT
FDSSMLKPEVSSTEKAEGTLSDGSRNNKWELFFRPTKREQKRLLLRQKPLRDDGGFNAIP
SLFQERQQSVGSLHTTRGGSGGSRRSGNEVAGSPTLSMTQVTWEEKELKPIAAPWFTRTS
HLGGIYCSSAAKGGTLVTAGGRGEAILWSLGSEGVDYSHRIQTNASLMSTFLFAGFMREG
LSPLLCMGGTDGDFCVFDVACNNIVLRRLLDGSTLTSFCLIGNFTTLVSTALGGVFAIDV
RVGKDVWQTKLPPSVGPPSGLLPLFFDTQAYGASVVTLTGGVALFDLRFQLMVQEYRLGK
DDGNSHESGRVSWPGTHAMDNPNAILCVSPDTTCTTLDRTDGPGLFLGTQAGTVHWMDLS
TGENRVVLEPATIGKPTRALLVQPKHSVVMTAGNDMWIRKWCLTAPNQSKTLVCPPYTSP
AYHGTTRGGIAEAQSQNQFVSARPFNSNEPCLTTNGFVCDGAVPRHHEDAILTLCAVSNG
NASYLASGSRDGTLTVWLNSE*
>TCRU_364 methyltransferase domain containing protein, putative
MTIQRDAADEGCGDLLRAVEERIPCEIRCHFTGMASYRQLRDGNEGESTFVSHPMKRFRE
FTCEKEVCVESCISHVLSCTACQILKGYCVLWAESLVNVVMYEPFVSRTERRRRGDAKTQ
TTTTNKEIRGRHQLIFHTLHIVDKAAYKHPLQHSFALQSVCQPGRVLQLECYPYHMIHFG
LLIYALWRSPDEVFSAIRNMPRQKKVNTPLEKGACMTETATMSLTPLHLPLLATTEDASV
LILGLGGNVIGNCLDSALPVDVSIDVVEVEPAVFETCQKHGQVPPCSEVRTKKENGTTRV
WVVRKGRQRHPNYRFIIGDARVVLQEDKTHQKADSEGPLHDRCYSLVFLDCYDPEKERMM
HDGSLIDVCQSRLCPGGALIVNAHILPTREALEEQFLSRGFASVQVLRVAGCVQSIVVCL
ARDKASAKSPNEEKSNKREGGQQQIGRLDRFCVRHARHLASYIQCASRADPGMCRLFRSG
FSLDANWLRSSRSVEGASCNTRVWEHYD*
>TCRU_365 proteasome regulatory non-ATP-ase subunit 2
MVVGLSSSKGILALLNETDADVIQFALKRLLELVDTYWYEISPDLPLIEELHESCDLSEE
TRMLAALVASNVHFHLGAYNDSVHFALEAGTAFNYMERSLFTDTILSCCIDQFVQYQEQP
EETRGKLDPRLDSLFTALTNKWILQEGTPVRELVGFTIRARCLDFLEKVLRQDIALTKSA
AILNYTFDLASVMLRDIGFRGKILRLLADLYAQGGLSTIDYFSRAQCLLFLGDSESTTRL
ITDLMQANDKATAYQLAFDLYEYGNQEFLSAVVAALEREAAEIPHPGLTSSPPENEGEET
STKEVDTSNLSDVHQKLLAVLTGETSASFYLKFLYAQCNADIHILNHIKQSIDAKKSVPH
NATVIAHALMYSGTTIDAFLRGNMEWLARANYWAKFVVTASIGAIHRGHIDEGLAVVDPY
LPKEGVGLLPYQEAGALYALGLIHAPVGVTRNRKTIDYLKNVLRKYSTSEQMIHGASLGI
GLAAMGLKDEELFDSLFACVSGCDAVASEGAALGIGLLMMGSGNRGAIQSMRALASEDNQ
KEKTIRGISMAMALMMLGREDECWAVANELLDDSDPWVRLGGCFMLGLGYAGAENTKVLE
RLLSVAVKDTSDDVRRNATTMIGFLTIKDPALCLELTRVLVDSYNPHIRYGVGMALAVAA
AGTGDSSVIEVLWTLKDDLVDFVRQGAYIALAIVMVQLTEAEEPRVKELREIFSKKIAGR
KEDMCSKFGSIIATGLLDAGGRNCTFSLHRQRHRLDKAVAGMFVFLQHWYWFPYLLMITL
AMRPTCFIGLNDNLDVPEYTFKSNAPASRFALPKSVLAEKKEAKAASVKAVVLSTTKKEE
QFHRLKRMSGSGRAHDAAEAVAASKNAAAAEPALTPLGAETEKKEPEPSFELLKNPTRVT
SRQFAVISHDVDGRYVPLKPYPTGICLLRDTKPSDGKQKIVSEVGWNSADDAPPPEPFTW
P*
>TCRU_366 hypothetical protein, conserved
MILQFNWDRLDVMAAEAIRALVNAKLEEDLRRRTAFSGGVDAPAVGGSTRAESLCVTGIE
WGIAPPFIEILELDDAQDLSRANFTPHDTIHSRQEAASHCNLFRLSSSVSSQYGGEHGSE
VDSSPGGCPSASVTKRMPGAWMGSSIPQSGSPVVPSKDTLAPFVGLGGLYILLHVTYGGQ
MRLSVSCVLRHDIPLGSISLPVRMPLTLLVSKMDMDFYLSINLHQNKCRVWMEPGKLSTS
PITRMNIKAVFGERRTYSSQLLDNWTGIPPVCEDADTSDAWTHVASSHLGSEEEDDAVFT
EENVISRFVLSEIRAILQEKIIYPHFVEVPLFL*
>TCRU_367 hypothetical protein, conserved
MSASSESLAVNSTQTTPSRLLQRGMRRREVSVSILSSGIDPTPSQQGSGGKPESYANTVT
IPLFMTQSNEDLLFLPVCSRNKRVLSQATTRSSSASSYTESPFQRQLNSVRMKLGLAEAI
VQNASITAKVPMAPEKRRRQMLQLEVAKLILFVARQHNIREELQQVAGNSLDVSDEIMYH
RRSIESKISFLAREPPPDLSLKELKRATFEMEKHLEKMKDKKSNAPSVSAHGATSNLSEF
LWLIESIELETLDPQDVYLGEEAASFIAPSTSANTSTPLEALQRQHELPQKKRPELFPPL
LHSTPSLQNEGESFSTLLRSPGLYLLEYPPHLSTDKTTTKAENETEEEELVGFSVDVESP

GCRAVEAAGLKLLQFMYDAVDAKDKGLKLTNGSEEEIAAMFRAERTMQYGNEIMRSLNTE
EADAAEPKECLLGSDGTMRNFDATRQTQSARNRATGTLSNAQEEELSNQSKTSSISALGE
DSFFFSGHPAGFEPSLVNSWIRPVQSTVEVHPLRTGIIDILKRLYGDFNYKHYFEHCKPP
KADKVPKTKEDYYQELERRVARRKSEKQQRIVSDQNEEDSMLLRWKGRSSSSKSLTVGKR
DSNIKIQEEITDDQLESMATGTAETPPLETPSVVTAPPTETTVDTHGEGIVLVVELEEGI
HFLLKGRRDERAGQQSASGSMNSFKKGKDLTKGGSIENKKAVSERGNAAQSESLEPDFDS
YTLYAVNQSDMPRQATVETNRTKLKNLRLKALLKYFGKKRNAIAVDLPPRGTQLVLVMKP
IKKGRKVVFDEALKFYEGPPKEEAPKTTYAIAKQSPPQVQSTTTPPRSAPLAEPEVLRDS
GGTGAEAQAKGESVSQAEYSENKTSTKAGKTSLEVADATEPSVHGNEEEDQGKAAALSGA
RVPSMQTFKPLLLRNTGGYTEDFSSEAYSFDGSSLSGNDVSAKGVNDWGVSVLPLGEDLE
DQQEEGWRQKGDMGVPRKRPKESDNKAARTRFMGEKGTKRGSETRIGSSKGSQFEADRAS
GEATRVHQWGVPLTNDDDEAFENNCVVLSVLQASEWQSGSKVPRRSLGSKSAVHSVEGGE
PKEMNVKDGGMDDATGKATEGGILMESSLRTTSERYPSARFRATSIDTKEEDIVTAALYP
AGDGDALKTEEIVSSFLQRIAEAEQLNLEEQIDNEDISCPKGGEETPLPAGSAALWRRQL
VSQSQQDPHSIGSQEESKQLLSSLTPGVETEFPLGSDREICKVQGSTSLAALRAESEEHE
KGSTLRASSSHMFSSEQLTANATVVQRPSVTLEGGSSAQRMKIYGLPQSSVTMNESVTPV
HLDENYTSTSYPQQPSVATKVDGGEIGDDVSTPVETTSGLGTTSRTADKRSVSIEPLQGN
RYASPTMERPAFNLDLLLKSVKKAEKKEAPLPGLSTRIVKDEYALPEQVMPASPSRQHAY
AEARPDGRFAIFAPEEMNVKGAAHTSDRMDKKKMSTRLSGVVENAAVFAEEIRTTFHAFA
RQATSQRRQTFARSEIHGKATVGRNVSVDVMRHATLPALSMVYSPETAQDVEDMEAAEEE
AKALFLQDPARYDCVIDELTKRAIARVYEEEEREKERRDSAAHGTAGRKLKEGLIVVPGR
MQNRSVAFRQFSVVGSQMGGFQAMNISSTGSMVQLNGDPVHFTHGGSFLKGRHPSLLLGK
SHRDKVRHDTKSELDQLLDEQRRAKKIVAYILMEMRRMWRRRCLESNLALRSAVDRFIKR
SVLFSWHFERRRVLNLHKLIHLLDRKTGRVGGWLPFYMKDRVMEDRFVWEPAPLHLSRPL
RVVHRAMCLARQQRMFPIRLVRQQAFRRKNSQHILYGYKRTIMEPFRSPAVRLRHGRRSR
YAAPFQNPTMRFSPQVEWMDGTPKK*
>TCRU_368 hypothetical protein, conserved
MPEPSIGNAAALSMMQDVSVGKKNSSTTSPTPPEPPDDNPSSDLANPPPNSTFLIAANNS
VTSTTGMTHSPTTSLTVSPTPSLEDVPDNMYTRAESCDIPIVNKCVERFCNCISRGQLQN
ANRSWYIKNGVYQCHEFANANCYYNLYCARERVSCLWSASFLYKAYRPQGNTLATSYELS
QKNSQGSMPCVGLEDIQGNFSQLTKNTNYYDSLFYSECVDYVTFILQRTGDGICAASIVP
MYVCGDSLFPVPPTRQIHYTPLSEGARRLVISIVARIVGNFTPIFNLERAKYNEKYQMNI
ENQLSNAMYSCFFDAIGIKGVFSVKHEDECLVVRYEVGVGEADPWVGDVVTANALSLMVR
SASWMDPAQRVIGNITDSVKLSAPIVVYYVSFESGTAQPEAKLCDAGCSVAISLVLFLTL
IAFAFSCVFCCRLSRRPYFMFDDDHDFEEMEIVKGRRAIVPNRK*
>TCRU_369 hypothetical protein, conserved
MGCRHSGPRMPPLEQQQGHSLDRRKERDVVDMMPGDGVDAKSAHVAGLSGATSVDGAQGK
PSRRDDVYSPMPPQVPSNSWYAREFTEVTRMSLTEFHMKKRGNVVFSNAYIPVGASELEK
LPGRAPPMPATLEIGRDLVYGMAYLHNTPLFTEHQWRLRVAHHAKWRQDEGKKHEGSEER
RSICRREWAKTIYDRPGIDTLVGIRVFVENKLVPDEYPTTRSIPNCTATIDASEAFNNWI
CIPIVLVGYLNNFLLGTITLYRFLSLNFAGYMLRQPINLSGVEAAAAGYDGDGEGADDCS
DDHASRKFEIYVEVVYGCSSEFNFCTDYISKGSVEVIMTRRSKLALKTYKERLHKLIQGS
LLSREQVVPMDRLEMVAQQQSSRNCLFCGSPLRYTCTICGAQLCGTLMCVWRPFAGYPSG
CSVHKAQVIM*
>TCRU_370 differentiation inhibitory kinase
MISKLFRLDPQRREKHEINPHDIKALRGMAATHNITSVAVPQYRVRENYVEYVIECSKRS
VKWQVFRRYQQFRALDQKLKQLCSMGSQYHCEYGVLPVLTGSHWAEVTNQSIDLVEKRRR
YLEIYLEQLLVPKNLFYVAKTALYKFLHEGEVPVRCRTNVLRPLIGFAAVEPSRRPEKSE
DDATTVEESPNPLDISAAGGNLPVTTTCHTTPERGVSNSVESSSTNRSSGMEEYDDVPSR
EDTDNEDIHMPPASPLCLQCNAEFSSMLYPHRCFLCKQRFCRNCLRNVELEEEVVRVCLQ
CYENHERHSKKKQTAKDATPETPLSQFKGVTAAPEILQLHEGNQLRTDVSLSDFELVTTL
GRGTFGKVLKVIFRENGQVYAMKILNKCIIHKRRMVEYIKEEKDIMASLPFHPYVVTCHF
AFQTDYHLFFVLDFLPGGELYSHIYPKCTLSPVDVRLIIAEVVLALEHLHRYDVVHRDLK
PENIVFAADGHLKLTDFGLARMNFSRHRRYSFVGSPEYLAPETIRGECQSRALDWWSVGV

MMYEMLMGSTPFHAANNNDVCNNVLNRTLDLTAPCFTPEAASLIRQLLQRQPKQRLRDAE
QIKAHPYFASLNWSALENKSLPPPIRLNLEGNDTKYFKREFTAEWAVIARPQEVSRATLD
MLKKQFSNFVHVPDVGAGVSLPSPSSGKRASLPQSVKADADEVLTVQRLVGIWRLVRVEM
TTDDGKIAYPWGSEVCGLLAYFPNGIFTMQFTLSRRPHTGSHFPEQATVDELVEMCNSYV
ASFGRYQLKAESNAIVHCPNGSLFPNPSWNQQKFFVEVSSEKSVGGVAALKLCTPQYNLQ
EEQLLARTVLTWERADGF*
>TCRU_371 protein tyrosine kinase, putative
MIRKRVLGVGASSATMLVQDTEANGVLRVLKRINVSSWNAADVTETLEMYKTIARAKISY
VAEVHMTMLQGYFLSLVITYYAGGDLESYLEDGSGSPFEESKVVQWLLVMARVVEQVQGL
TGGYFYGLSPDRVFFADGEPGICVGLPMPRYLYFKWLMDREALGVAVEREYPPEVVNERK
YKPMVSDVWHLGLLGMKMLSAHTSYSSRSSEIRSIISAMVEQSVEYRLTIAGVVRRLTEI
VDGQNAPRPFATQRSPTQSLGPEKLTSYGAGLYATAPSTEGSTGDENNGSNGNSINCNIP
AKNEVAPALNTSQRVSRMRLQESWHRRAMEQFEELQRLNASSPVGRSRGCSPTARSRRSR
SAGVGLSQSTSAMDMASTAPSPQDIRTSGQFQARSPRSFSAKVTKGQTNLTSVVQNALKQ
HMEEQRRRDAIWQGQETRRLRKQEKERALQNFHQNHVEKLRKIRSKRDEETKNEIRMHIK
QWRDQPRVLADENVIVNREGDVSVFVPKNGRPPPAAATTAPPPPISSVGTLGRKDREKDP
LAVRAGESKEVKEVEGIPVLALPHRATSVPVGSRTTPPSVGPPRFAALYRESGVSPRVPQ
TRAKVVSTPPPVGTIRGTKGILSISSPRSANGRSLSFFAGVEAIEMPPPLLDPESILDTS
VARETEEVDPFSSSNSGPRDETSLFFSLNGSIKALNESLSSLLANHHKHREVIVAMDKFL
MRSEAERCNPRLNAVFMSTLRGILNDEQLFLAAAPLFVQLMALRGLLKKNSLAKKRDLKM
E*
>TCRU_372 hypothetical protein
MGAVPSRESLLRGLIRVTPNRESTDHTAATSRRSAWGSAQEMVLVPLIPDYFPSAEEPSF
LLLFNVYKEASLCCDCVHEEDYLMNMKHVGTERELYEHYMHISKQRLFETDSELIAVHRA
GRVFSAVPCAVAFVQECGSLISSSSSSPAPCRRSPLGQTIPTVQLHGLHLYIVGFIGDTS
LCPPSIPQNKAKDNPFRMLLLLSKSVGGNQRMLVTSLAAYTLITQLRRIGIVDDPMMFAY
LHSAYNGIGEQQQLGLNSLQLKEGTASEGQEVDKKWSWKSMNISGHVIFRPLEFTVALSD
IPWMCYVREFRARLSESTLDVPPTIGNEKELLLSADTLTKHSLKTFVESNSLCGTMDAGP
FKKCVEWACWHHETRFQSLVGAQATEFRAALAKENLKCVLEGNVFVDSGEPTAAQRGDVW
IVGSDSYTRDRIHAAYTPVTRGSVMSHDGSQWCLQPDRFAEEILLSVFCDECKRARTADP
DDPHWMRGTDGSLLCSETGLYCWKFVRHGLTLVYSTVPGFAKQRSRKKMHATLTHGNGGI
VSDKPVDSVGAKKKECGRSPSLNHSGPFLAVGRSSVVGLSRNSLSFENAFVGSHYESPSQ
WGAASYGEGGDVSCAHLSSEQDLKNPIRSFNSCELRNAVLSPPGPVSHPVDVRVPTIFSS
QSTQLSVTAPSIASRQQKSCLGSFSQAASFQADAPKIIKQTEHCLEAHGKGTDGSTSGGG
LRAYDREGKYRWEWGRRFK*
>TCRU_373 hypothetical protein, conserved
MQIVDGQHFSGGVQRSEALEDSATALKHSMQMGRFFAYYTHPHRLPLSQSAEEPMCEKLP
RDEAMLAPGDFAFLPNPTYCGRTTVDKVLYKHCLSLDILL*
>TCRU_374 Mucin-like glycoprotein, putative
MTTCRLLCALLVLALCCCPSVCVTATGEGSDKDNSSLSPAQSEGAGGSGAKNTSTTSSST
GPTDVLPRPQKQDSEGQASDETTDTGKGTGGVDVTSGITGDSAEQPRIDNHTQQGTSSEK
DTVKKKGEEETSGTTRDTVQETGKGPAPPETPDKATPEHIPKEGAGASDGSGSSGGSVSP
AAASSSVTAPVPAQIQKESAPTTTTTTTTKAPTTTTTTTTEAPTTTTTTRAPSLLRESDG
SPSSSAWVCAPLLLAVSALAYTTLG*
>TCRU_375 hypothetical protein, conserved
MVCVRCRCWAAAICDCAVAVRGVAAVSLLLLPLCVDGELVCAEGCRQVTGVMAMMMTGRV
LLVCALCVLWCGAGGGGCDETTQASPSGSGGGTVVGTGGGPSGGADNGLVASEPNGESEG
DRLEGTDLGQINSSPRGGTVGLDNKLAVMPVGSPVTRNQVLSNEALSLQSPPSPKPSAPE
LQDLPEGPPVSGGSQGGEADNAVGGVGPSGSSSGSGVKSMVSASFSACTLSPPNPVDWDV
LQGGKGTTATLSMDSSEKSVKSQSAEPPAPAQPNLDRQEASTSNAEDHSPVKPHTAGNQV
VNGGATGKENTQRAAVTGGPSSDTRSTTLQAAPQEQPKTELIIVPAGKERATDPRTREKE
ERDSKKAPPPPPASSAGGTPAAKELQISVEEMHQTSPSEAQKLLLGQETPSKDDAEDQNT
EGTATSDSVKDEAASSLVETTAPPISTSGGADTKSVASEDADNAQQPNHKEAHKDPEPQN
TSPAFTATEALPQTAIPLTTAPTNDTTTPGDSDGSTAVSHTTSPPLLLLVVACAAAAAVV

AA*
>TCRU_376 hypothetical protein, conserved
MLDDYVAKKNEKLHDAETKEHHLSSLVDQVLNYLRNGVRMTKISSKGNARRRLYFLSEDC
KRIHSCELDHQGFPLNRKRPPVTIWIRDIRKVLIGLYTTSFVNYSGEAQLAKTRQEAVSD
NGTYRHDPTQNITPSNLGINNYRAFALLLRGGKSLEVVCETDSDCEAWLVALKRLLHLRT
PAERLLEERRGT*
>TCRU_377 hypothetical protein, conserved
MRERHSIEAVRRTVREERCRQRRQWTHQIKEMNAKFPEPVRPLAEERKKKREQAKAKEDA
AERALAADIKMIEEYLPKLISLEDIPVNPEETGIIRRQFDEVFTQ*
>TCRU_378 conserved protein
MHVEAEDEVEGGGVSSTMHSTLASTEGDDFIKRDLEVLDALIKEGYSVTGAVQARFINNY
DPMYDKPYTHYELNTGRYLNEELSQLLEDDRRKNTKHHLQTDKIEKFYMLALLAHSAILR
H*
>TCRU_379 glutaminyl-tRNA synthetase, putative
MTAPSTTAASTAVPFLEVKKDLRLLQTGRPVAGYSNTPELLEKHHALTGGKPYFRFPPEP
NGFLHIGHAKSMNLNFGCAVAHGGKCYLRYDDTNPETEEQVYIDAIQEMVRWMGWKPDWI
TFSSDYFQQLYEFAIQLIKAGKAYVDHSTADEIKKQRESREESPWRNRSIEENLLHFEYM
RQGRYAEGEATLRVKIDMKSDNPNMRDFIAYRVKFSAHPHAKDKWCIYPSYDYTHCLVDS
LEDIDYSLCTLEFETRRESYFWLLEQLNLWRPFVWEFSRLNVTGSLLSKRKINVLVKKGI
VRGFDDPRLLTLAGMRRRGYTPEAINRFCDHVGITRSMNVIQSSMLEHILRDDLDERTER
RLMIVDPVKVVIDNWDGEMEVMCPNHPRKPDLQSRKVMFTKTFYIDRSDFRTEDNNSKFY
GLAPGPRPVGLKYSGNIICRGYECDAAGRPSLIHVEVDFGRTTKPKTNITWVSEKYAIPV
EFRLYGDLLKDDRAAIDPEFLKYINSDSEQVQQGYAEPEIQNAKVFESVQAERFGYFVVD
PDTRPGHLVMNRVLTLKEDKEKGAMAPCPQK*
>TCRU_380 proliferative cell nuclear antigen (PCNA), putative
MLEAQVQQANLWKRLIECISGLVNEANFDCNPGGLSIQAMDTSHVALVHLLLRDDCFTKY
QCERNSILGLNLASLSKVLKIVEGSDSLTLHHEDDSDVVVLTSENVEKSRKCEYQLKLLE
IEGEAMGIPEMEYGSTVTLSSQEFAKIVRDMSVFGETVTIEIRKEGVKFSSSGDVGEGYA
FLRAAGGAGRTVRTAPEVKKEEDDDTPISRANASGTKNSHTAIGVEVRTDEPVTLSFALR
FMNVFAKGSTLSDRVSLKFAPDSPCMVEFNIDQVGYLRYFLAPKMDDVM*
>TCRU_381 phosphomevalonate kinase protein, putative
MDTAIATTRASSSGKVLILGGYLIVEAPNVGISVGTTARFETRLLKTRDAAKGKCCVRIH
SPQFGKEFAFECTVESTPEPAVCVAQIEGTHSPFLRYSVLYTVAAAISQGGNVFKELTLE
LLADNDFYSQRNYLESQGKEVTAANLRLLPPHLPLVGDVSKTGLGSSAAMTTSMVACLYR
SLTAQSTSDNNKNNNAAKTDTSAEKEIVHRVAQVAHSVAQGKIGSGFDVYTAAYGTCAYR
RFPAKFVESVMSTNESPSNVVVSTLADCVNMEKEWVKRVPFHLPLGLKLLLGDVHQGGSG
TPGMVSKVMAWRNSVADNPYNLWEQLRENNEKYVASLKALILQAEEKTVEHVNSVDVLKH
VVLAQHIPQNDAERLWVEAATYASKSRRYLREMGQAASVEIEPNKLTALLDATCAIPGVF
AVGCPGAGGYDAVFALVFGDETCTSVESFWEEYTAMRVCPLLVREDAAGLLFSEEK*
>TCRU_382 hypothetical protein
MATQCVAECTGYRSLRADCARDPCLAEGMCKLLDAGITDCAEWCCVSRGGYVFFIVFFFS
AGTCALLSMYYLWRLHRANVAAGAVTEMGEKIEAAQASDAHATAEKLRKKRQVTVDPELF
RAIGLPPPGEERSGVGGFR*
>TCRU_383 ribosomal protein S6, putative
MTAEISEKAFPLAGDRLTQTILDLVQEASNAKMIKKGANEATKALNRGIADLIVLAGDTN
PIEILLHLPLLCEDKNVPYVFVPSKTALGRAAQVSRNAVALAILQSENSPVSAKVQAVKL
EIERLL*
>TCRU_384 hypothetical protein, conserved
MLRLLPLRLASKVTAGNAKNQAGHPRRKAKLFHVIPGTPVTPMEKLKEQRRRYGQDRHSR
LPEYRPGKNVRLDPNTFTLYATTKGVMTIRESRINPGYKWLDVEPDIQKVYRSSQMRRAL
AARGMTSQMVEKNAHYRSEMDLLLEPHWRQRVMGVPKAAERFKDPNLFVRGVITELTPMD
RYCYE*
>TCRU_385 nucleobase/nucleoside transporter 8.1, putative
MALGFSSWAEFYVYTTCITLGVSMLMPMNALTSAPRYMVDYYRYVSGDPHAKANVPIFWA

NIFTFYNVVSLVTQIIFGPTVLTHLARKFSLSNRFIFALTCMMLEVIVVLLLPTGKVSQN
SAIVAFIIVSIVAGAGKSYLEATCYALAGTMPPKFMSAIMFGCGFSGLVASTMQCIIKAT
MENTYDSVLAQAYIYFSLALGIMFAALLMALSLRYNSFAQKHVAEYRMLKRATDGETPSA
EATAYGNVEPIDKAVEKDADSGKAAGENLSCRNENGAPVIVQSEMTTSEQLLTTPVFPVI
KKIYPMQIACFCVFLSLIIFPSLVIPIDRDDEWFATIAILCYNGGDALGRFLTSFRKLWI
SRRKTLYLSFVRFLYIPLIFLCVFHQIPGHVAPCIFMFTIGLTNYLGALTMVYGPGTPEL
KTDGERVMAGQLMGIALLGGASFASLIAIVVVLFLP*
>TCRU_386 40S ribosomal protein S4, putative
MTKKHLKRLYAPKDWMLSKLTGVFAPRPRAGPHKLRECMTLMIIIRNRLKYALNAAEAQM
ILRQGLVCVDGKPRKDTKYPVGFMDVVEIPRTGDRFRILYDVKGRFALVKVGEAEGNIKL
LKVENVYTSTGRIPVAMTHDGHRIRYPDPRTHRGDTLVYNLKEKKVVDLIKSSNGKVVMV
TGGANRGRIGEIMSIERHPGAFDIARLKDAAGHEFATRASNIFVIGKDMQSVPVTLPKQQ
GLRINVIQEREEKLIAAEARKNMQTRGVRKARK*
>TCRU_binding domain containing protein, putative Thiamin
pyrophosphokinase, vitamin .1
MSRMAGVWKRKVVQHDFYDAAGQVAAVVLMNSPSNGRWEYEEYLRLLRVRRFNNQQPESS
VGRCYFLCADGAFSRLQAYIEEERKHRPELRPFSHVPFCDAVIGDMDSCKNPPHNYGTHG
SVDGAGFSLSAPTEGYATVDDIPTSVLDQIHDRYTFTVAEFTRMSTSMEGASLAEWDKLD
AKGRDELLSLPFWLYVRCQSTTDFMKALLLLNRLREKHKEDIVPITPHVLRTESGKRLLE
TGGAIIPNAGSIGLDLDPARERELCAEACKEEAVLLPTYVCMGALGGRFDHEMASISVML
SASTRAHVVLINSNNTIFACQFNGWTQLVRNARCEGVTCGLINYGTMKECETSGLQWNIA
VGRGKPSESKDLVLGFGKLISACNSIRREVVTIDLRRQLLSTRSQGGSNTKQAPANERDD
EVDEDHNPPTIFSIERCDGDENKFGHSC*
>TCRU_388 aminopeptidase, putative
MAKIRNVLPDDPTPRHYKIIILPDFDAFLFTGHVDIQITAKNLQNSITLNYNELSFVKVT
LALAGNSSVVETIPIESIILDAVEMKATFPLQKPFIGEAVLSIDYKGEINDKLAGFYRSK
YIVKGKECYMGTTQFEAVDARRAIPCWDEPAVKAVFEMVITAPSNMMVLSNMPHLYKEEV
NGQTSWAFAPTPKMSTYLLAWTIGEFECIEQSIKKTHGVRNGQPEDTLVRVFTTEGNKSK
ASFALDVACKVLPLYEEFFESSYILPKVDLLAIPDFAAGAMENWGLITFRETALLCDENS
AASHRQHVALVVAHELAHQWFGNLVTMQWWKELWLNESFATYMEYWSVNKLFPGWHVFTQ
FVHDEIARAFELDSLRSSHPVEVDVQNAKEIDDIFDAISYSKGGGIVRMVVNFIGEDVFQ
KGMASYLKHFAYGNATTEDLWKFLGKAAGKPLAPILEFWTGKQGYPFLTVSSLRDKQSLL
ITQHRFLATGDAGEGEDETVWKIPLLITTPENGVQREVLEERKNSVPVPHPSWVKVNNDQ
SAFCRVLYEDEELLQNLLSALSTKKLSNIDRFSIFSDYHAFTRAGYCSAVKVLKLLSYYK
DEDDLTVWLSIVDFETKLKVIVASQGEEAINAHNAYFRTLYSNAIKRLGYAFESVDDHNV
IQLRAALFARLVAAEDEETIAYALKLYAERQKTPIPSDLRAAVFTAFVKRNGRAAFDEVK
ALAETASDAMERTHYLRALAFSGVDGLVAELFEYAVSGKVRSQDTFYVLSSLACNTKTFK
AYAMELRRMWPILAMRLPGLILGRALKLLEYGAEETVANEMEVFWNELNEKEQMGMSRSF
RQGVEGMRNNAAWASRDARDVTEFYSKAWV*
>TCRU_389 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily, putative
MNGEVFAVAEAWCEKDSVIFPCIASQFMKLDDKTPKALEATEVRTEVLEECPTDGGNCAS
KTEDKDDSQGGTRVHVSRPTTVVKGNDIYMLTGVCMSKGLSNCQVGVAGVAQWGLLLVKG
NVSGVDESTKRIYWNDTISILCNAIGDNDDTLTGHIGGGGSGAKMEDGTLVFATEAVKEN
RVNGTAEDGGNNNVSLLISSSDAANWTLSKGMSDGGCSDPSVVGWKDKTLIMMTACDDGR
RRVYEIGDNGRPWTEALGTLSRVWGSNRKPHEKGVGSGFITATIENRDVMLVALPVYSEK
LEKGGAQKGELHLWLTDNTHIVDIGPVSGEGDDAAASSLLYKGGKSGEANNNEELIALYE
KKKGAGGKPSPGVVSVLLTEQLQRVKEVVATWNKVDQSVSQLCPPSAEKDRPTENDCSGV
KITDGLVGFLSGNFSENTWRDEYLGVNATVSNNEGAAKATLHAGGVTFKGAWVEWPVGSQ
GENQLYHFANHNLTLVATVSIDKVPTTEGPIPLMGVKMSDAENPVLLGLSYNNEMKWKLL
QSGGKTEELSGTWEADAKYQVAIVLQNGTQGSIYVNGKLVWGCAM*
>TCRU_390 Leishmanolysin, putative
MLTWCCAWQSAVGGGALDDCRGGCEEPRDSDDIDGMELQDGDGDGRTLESHWSQRHARDE
WMAPIGSAGCRTELTLAAPADLGCMRVKWEMAEPMRW*

>TCRU_391 hypothetical protein, conserved
MRDSFAAPSLVRAGGVTIAFAEGHAEYKGSHYRLNVRPSDIVAGYINAAETWPLIAAENN
KDKWRVRTLFSTVSEEDLFGVACNPTAIAKDNKVLLLVGSYNM*
>TCRU_392 BNR repeat-like domain containing protein, putative
MEGGTLVFTLRARNGENRSFSRITYSTDNGNTWVFPEGISPANCTDPRITEWEGSLLMIV
DCENDQRVYESRDMGTTWTTAAGKLPGVWTKSKSEDYPEGVLRVEAPITANIEGVKVMLY
TWKGYFSGEKKGKCVPSLGHGQQPLVFCWTGCHG*
>TCRU_393 hypothetical protein, conserved
MINYVLKSWAQLDSSFSESFTPTAGLVGFLSNASSGGDTWIDDYLCVNAIVTRNAMKAKD
GLKFTGLGPGQYGP*
>TCRU_394 hypothetical protein, conserved
MQRRSRRQQHAARQRMPPPPRVRPEGTLQLLRSEGSLRVAQRRAHNPLADSAHYTGHWPR
SVCVVEDTAAESLFLSGGRTPVFTLFPTQVDGCAMAPQQNEAAVFTMEGQYLWCYALGM*
>TCRU_395 p-nitrophenylphosphatase, putative
MSTRTILTAGEAAEVLASVRYVLLDVDGVLWAGKHVLPNIPETLSYLRLREKQIRFLTNN
ASISRAGLVREFQRRGIQGVREGEVYNSGFAAALRLQSLFTANKSTGSGRPLVERNIFVI
GEEGLHEELRRVLAPGYIAYGMELHDAEKCGGYDAHVVASAWKQRVLPAPLQSSATSCGI
AATGHAAGGISISDLSPAAVVVGLDMHFNMLKLAYASLCLQERPAAQTAGTSSSTPTYFI
ATNEDPQIPVGEDFLLLPGAGGMVSALRTVSGRSPDFVCGKPHVDMAKVLFEAEGITDPQ
QCLMVGDRLTTDIAFGNAAGCKTMLVLSGAEKMDRVRQAERDGHVSLLPDFIAPSLAIFL
PPA*
>TCRU_396 aminopeptidase, putative
MQYWHPTHCTLQLNFVQSASQRDDGRALLLAGDVYSGRSTIRYVRRSFSSATMHEEFPAL
RVENKDGLHFHAITASTHAFPKARPLVLHSIKVHQQYNDAETLKVLQVVESEFNKDDNGG
AESGEQHSVTSKGGNPRGKKAKSKVHDANETERQGSHDSYDKQQGRSDPGSKHVFFEGAE
SMPAGSIVTLEIAFTGSIQGWDQGGIYVNDNPEIVKAAAANYGVLLTHFEVALARLAFPC
PDDSQCYRLIWHLQSLQLPSSYSVVVSNTAKQSEKAMGQKGTQHTFFPVGPLPAYVLAFA
AFSGSVQVVEETLFLRGPLTPGAEGRNSRLNTVEKMVPLRVLAATLSGVTLDTLRQIADT
VREAVNLLEDFFASPLPLQQMPFSNEFEWQEDVLTIVVAPTMPYISGMEHHCCIFLNEAI
YRSFSRDGTVRGTVRRPMTEANGTHEVSRVMLIVHELAHHWVGNTLGMPFVLKEGICLLL
EQCFGDVIVGKPMRSIKPSGDKMMSDTAVPSRRVVSRIKKASTPPVIVVDTEKGKEFTEY
SYQKALNTLRDVVSGMGFNDFKERMRRIYQTEVMGCKENIGMIDGRDCGDLFLAPYITTK
QFLKYMEASRVTV*
>TCRU_397 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor,
putative
MRRVIASCLCAQRLAQCATTSTAVLAFSASIRRQGTRQGAPTGVPPELRAPPQGSRPSHH
EHQQTEMNAAPEENFEPPQKPAEPPKMLKIDTNEKGITTVQLSRAPVNSLSLELFEELNK
WMLWLGSDEECKSVILTSSIPTVFSAGLDINEMFNPQPERLRRFWQAFQETWLILNSFPK
PIIAAINGNSPAAGCILSLGSDFRVMARHPSGKPDRLYRIGMNETKLGITAPAWVIPAYA
YVVGSRNAERMLQLGETPTADEALRIGLVDAVVEEEQLREAAVREAERFMAIPQQSRWMS
RDMMRREFLQHIATDEDREYDTQFVVELMMNPEVQKGLGAYLARLKGQHVKK*
>TCRU_398 hypothetical protein, conserved
MPTGNETSILSFLRAGTLAGCPYVEQVASTVRKVTVPPAESATSLSSPLSPSLSSSSCLW
PLAFCNFENCRQEKTLLWATALRHKAITAEAKKLGLDALQRGEVRRRAKLFFHVEGRHKC
GPNDTASDAEKHTLADILREEVDGCRAWTDVANGTRFQMSFLLGGGDMVGVAKEMSALEA
TMSGHGDTSQANRIRLLVCAVAVVSAMLNHFCPLRWVITASTGVPHVWDQAIALVEQLLN
DEAIVSFFMAEALASAIMSISSSDVTMRRYDVLLKEKRKRMLACILPLQHVLGGGEAAPL
SIAGVAKNTLHLRTETQLLDLKRGLQKELRERLAIASNLDQRSVDRARQFKEACELCRAT
VKENQTDGRHPILQKKGLTALSRTDILPGRCVQLSDVPGENKLRTETKRKLSCETDTSTH
EAKVTSSCWERTVLEVWRARREAVLGVLREYWIVDNGSLRRKGIEKKTETKEKAGPLWMT
DALLGTLSRQLLALIGVQGQNLISLLDTLWRWIGCQRDALDEGMYTALAVELVVFLLVAK
YYSSRADNLLSELMAILKHLAGIRVRDDFSSPLLQKVPDALAVVLFDAVFFSISTGISCF
SEGNSDGSRDRRLSSPVSTLLWEIQSSVTLRHAVSILQGGSSRQLPTGSGGVNPLSLTPS
LGDTEEMTLLTDVARHGRCGGFALNVSPRHDVCFLVTLTELLGTSVFAHLKEIPIRTKRP

PPRFLSEALWNALLPLTSGLLHHIQRMHIENGSKAVRRFLEFSRALVEELTPRWEYNIVP
TRRLQKKGVAIFNYTAVEQEYEANHVVEDRVVKFTSLLEWLLMGASEFFPELLTDGHSFS
RMCNAVGLILYDVDGRTGHKIMTHLLRLVPPKEKMDIEAYIAAIRCLSSMRHGCTLWEEA
VKYYREAVHFMEDDANAKDAMNSHRRPHVPADLSTARVLRCIGSSPLPHVPRCTLTLQIV
AFARASGVPLSLQSYSSCLLNFTLRKNPPTKAFFVAPWCDALEWYDDVMSRSEQVPLPKQ
DPLCFQVACLQSLLAQGDWPEALFSLPLADIVRQHDDDAAELNLSQFSGKVSFLLRLCAS
DRTRSCAHAAKSLLYVFQTLPSLKPGTQAANLEDMQKLCHVANTYLPVVSEPKLTNGAPL
FRHETPLIPRISLELEFEWARSLEPFGFSFCHFYHIQDSLMEKLEAAILSRLHRRKSDTD
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YASVMLPLRRLERIRAEKRRGMRRRDPSLRQDRGGRRETGRNE*
>TCRU_399 hypothetical protein, conserved
MMRFSRCLGAPVFCRIIDVMRQNEPYARPGILYPIRVELGNNVEKCTSRELQEIIDNMLS
RSQRFATVKTGMVYNSDQSVATEIKAYGRYVVTGNMRGGYIKGDHRFGPRLTGYGGATTK
PGLRWNGDDL*
>TCRU_400 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MPVSGEHFPPNIDLPLMGQVDTADEDSPRIGNTDDQAPHSVSPDVSESVGTNSGPDSFSS
TNVSGGADAAPAPPSTAPGETKIPSESNATIPSDHDILLEFRELAAMALIGDSTVHVCVS
RVLLLLLGLWGTAALC*
>TCRU_401 RNase H, putative
MQKTYATLARIVSGVPSTVDPESALLEANMPPLHVLCLRARLSIFENTRACQTDWMRRPP
PEPPPRADFRISPLSRDELYAFVDAYTKDYGITESSPREERFFRSSIPPWFAASAHRVTI
GVELPIDFSITDVEELIREQRGVSEEALALHSHRSWILATDGGVDVPKSAGVGILLSSLN
SSEIIEKASVNCGARPCSYRTESRALLLALEKLMIPRIRHRRKTLLVVTDSQSLLAALNK
GPLSQTDWTEDQIWQRLLTLTRAGWSVHLQFCYGHCGVHATEIADQHATQTMESGQYTEQ
GIAPLWHTDLLTCFTTQLTNKWRSTIRQDTHRYLLCGTRPSDLSGKDLITQEVLHRQELV
HLARARCGESELWGRLCWAVRDCTNQCRFCNISPEQSAYMRSNKDPTAPGTDTVPPTARD
EDVSPVRRRTLTRRRKEKCPHCDSTLTGFSGLVSHCRSFHPEHPPPLPELKCDFCNMVFP
TRRSTAQHRSRCTHNPDATRHRNSSARRRSLLPQDQPASTSTPIGPQETLHHLLLECPGT
LAVRQRLGIEQDLRLGKFSQWQLLHSRKLLSLLDHLFGTQMALYS*
>TCRU_402 retrotransposon hot spot protein, RHS3, putative
MNEKDTITPPARGKPNGVLTQVPTEARREAEERLRQTQEMKFSISTNIEEVLFKGRVRVN
EMKLNDFLTKEPDGRGVVDTNRDVLLEEFFKDPTKYVRDKGALNEMQASGHYLGMKRAVK
GEVIFDEDIRRLCDRVSTIYRGGHWLLRR*
>TCRU_403 retrotransposon hot spot protein, RHS3, putative
MTVVGLRMATAGGRHTTASTVRRFTECLAAYFNGWEELSRDMSWEIIYVQQTDSTPRNGW
QRCDVENSNNVSDESREIRRFGRKRCASTKCQYRTETFEETKLSEVCKK*
>TCRU_404 Mitochondrial carrier protein, putative
MKCGAGGISATIAGVAVYPGEVVRLRLMSGERQFNGIFNTIRCIYAETHSLRNFYRGLGA
SLMQRVPDILVSFAVYETMKYRLIEKDFLSSHPSYKNIVSTVAGGGAAALASILVAFPLD
VAKRRIGMSGKGKSGVVYAGVRDCLRQVYAQEGIRGLYAGARVEAIRCVPQVVLMWFFIE
GFQSFLTGHCVH*
>TCRU_405 proteasome regulatory non-ATP-ase subunit 9
MEAKAQAYLEKLSNSLQAAGRTATADVLKRAKEEFERSLWCEMTDDLLLAVRDPLVLESA
YELHENVLKVTRMDMSPTAYVKLLHYICFCPNSTLQKALDLLNGAVVALSTSSEQGENMA
NCIRALLLLDSYNDKSSPAGTAASEASRILDKVESFIHSKQMHEVEPVLAALHCQARGKD
YEIRQQYTKYYSNAFETVKSAERAEMPIIESDLLSLAYKAALSALLSEEIYNFGKFLNER
HFTERLADSVQHAWILEWLRLCNDGKVEEFEQYAVAHKAEMAASPILSESFPSITKKVRL
MALLHLVFYTPFNERTFTFDVIARRCAVDEERVEPLLLAALAQGIIMGKIDGLTQEVHIT
WVEPRVLSLQEVKELAVHVSRWKEKTLGLMQCMKEAAQETHN*
>TCRU_406 SPRY domain/Ankyrin repeats (3 copies), putative
MAAEPGSQIPRFRVGNATISNKRWLENFAALKEETFTTTLPTTTNDDPNFFLETLDVFSC
TEEEFLNGLAIIKEFALRSKMKIMKRQLKKGYARRKMEAMQEELLFYRIAVVRACTTLRE
VIDRVKRRLCELRRDEALLHEYYQALDTDIERGEREVLPKEGSYHLRQRELRRVAPRQRY

REDRTFVEARHEKLNALLHELEEEEIAIQRVNEENGATDLDREYGICDPKRGKLEDIYDT
TAGTEAEAGSSNLELRLRIRPLLEKVRELRIVPPLSPRSVQSRLRKELLLPFSARVLALK
IDDDNNAGERFVEWYVNAAIDPLAMAQLVELVPREYLVTTTVRLVNACDTYLPLRQTQAL
PDVLHVLLQAIAEGRFDDLASLVLSPSDSYLHALESREHAGIIFYAALITGQMEVLRHLM
SVGFYNTNALIVWLFLNPNRHDPNYMAYVTEMRSNIKKYMRSVAHQAQDNTNAESLRGEL
EEDYMDPTLVTDSMQNNENFLSVNRDLCETLRRFLQERMRWKKQVVSRTDKVTMDTDKNE
KGKLSAENPPVTKLELEEDEDAQAATRVGSSSAASGVSFSLILGKKRLDRLQISSVKCAV
LPAVTTSFMRRVDRWGYTPLKATDSHFLLVGDTSTANAHVIQLPPRHADLWPDDDPTVSP
HVRWQRERKEAAAKAHGLTFYYEVHVSLNFLLSGVPVSTSVFNGFSASLERTPETMPGLQ
TSTVFVGWCSEECTSAADGRSTHPPLGSDRNSIGISFDILHRSKVNQLVEEVIIRPMKHE
RGRNAVYQVLDEDAQEKKEVEDKERDSVDLPFPLLRILLENNNEGNDVGFVSPTNGPFSS
PIYEASASAQTNETLEEAHMLSAAYAAKESIVPTVEVLRKKGNGSTSDSEESNSIHWNLA
FSGNSVVLRGVPVYNSQSLVVGCHVDFGAHSASFTVNGKSLGIAFTTLPSPVGLRPAVSL
QASNRITEVLQRVKPSAGVIVRFVFDESHLLASQTVTTEMRNTFLLNSSPATRVGTPDES
VETCREFIPGVFPLKLPLLFDENMMHCALIRLVTCGESALLSGHDSHELIQAERETLSLG
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LTQRQRVAAYRIAVHPFTDFVSQDDASKRQRRMALLGSATLGYTEVLYALLERMSISETL
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LNVTLDGLTPLLLAVTFGSQEAALKLLECCDAVSNVSNYKNSSTRTIQHRSPKRETFHED
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LQVAIMNRNEHLALELLEYAKDKLRRGSNVLDISAIEKNGNTALHLAAREGMLQVIEYII
FQFSDEEITRISCIHKFLKRPDAVNIVEKNRQGMTPLLVAIHAHQEAAAQLIASLMPESL
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EDGAPAKVEGIKSVLYHDGEKRRQQKRKAREIQESRRRTRYQKKTSVSSALLWRTSLTPE
SYAGKLGDQTGTQKAPPSRRRSTLHTRISRTGRHRRRSTFVQMLLAKGGSGFTTLASIRI
LEQGFPLEEVYVMADIISTETTHSSQTVSAMQHVETLISFLREYGGVRIATGDAVVFSRQ
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FRLALRSADVDTVSVFLSLGLRLGSIQEILEHKELPKAEELQQTAIQELICQPVDTLPAG
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EEEMDLLLAILRHLPAASTKFSFLSMVYSNLHPIVALRVAVLYANDVKHILMQPEAINAF
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SLEGTKSLNLSLRQGGTPFETTPPPLPPRYFAYYLCDWALHTTLLLHAPRPSSRTIDTLL
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TRYFLAAALFYFTYYQYDPPSTMPPNFALIDMPKLPQKTLSPELRGAMKTGDVDALDDDE
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SFYSVPRILLVSMNFIELHDEGIPKPRNHIAELLAKEVADATLVRNQAASQRTTRTAFLP
PLLSGNVSLLHLGLCSADDELVLQHINEKRRQQLRILLLSQMPRTSPTPYMMTQMSTSTL
GYQRQDKLVHSSVSGTKDLNGQKSSTTRGKDEKELSKALKLVDTLCDCGFVLFPLVLPLD
VEASQIIEEDAVNEGTAILLTMTPMALAVSAGVVKKDEHSQSSSPMMKRSLKSPDIFRRA
SKDGTAAVPPRFTPAPGKNRLPADTLDAWVASRRLARSNASGKDPHMHLLVRAIGSGLVG

RTIHHLGLSTAPSYESHK*
>TCRU_407 WD domain, G-beta repeat, putative
MSGEAEGKNGASEETATPHHTNTVDHSNAVTRKRPRVACLRQNFSRQLYQMMIRQLHHDG
YLGAAAAVADATGVVVPRLEKDSQRLSKLVSMGLAHEASNITEMENFMTYEVVERYLGAS
KLYVPLHLTESSTVGQMAYRMRERFTTSSLGGVVRRVNISPDGSLAACGGNNGLCVVFSL
KTMEDLMALEEVRQENQFRGLDGSGGSGNVGVRNASNKITELAEARRFHEHTQSVEAMHF
HPSRPLLLTGGREGDLYLRDYSQPNNKVLHKLHDTFPIRSAVFHPSGEYILYATDHTAPR
LLNLRTWKLMTPNTVSGNENNAAATNIITGRSGMSNRGGFYRRGTDDSHTAALCDVDFSL
DGRLLASCSLDGSLIVYDGVSSRPVAKVNNAHSSVPVTSVKFSRTGNFILSAGMDSVARL
WDLRRSDGGCGTAEVMSFGEPGKCNHRSIHAAFSCNESHVLLQDTSLFAIHSYCVYSSDK
SYSLVVPNHMQRGFAVAPFCNVVVSGGDDCRVRLWTPAWAAA*
>TCRU_408 hypothetical protein, conserved
MAGLTSDNISIASARQYGFSRERDLCVYCGKNSKPPPTDPFAPVFVFFSLVDCRHYVCQP
CALVNCDNAGRYIRCPTCHSISRLAQTGKKRTGPDELRVTIDDGVSSAASHASRRSVRVS
ADNVPARSALAKADRSKKRSASVQFSANPTTSVVPPPEDSENKKRRDASVTSPLTRDAVG
NLPKDPSYRQRERMKEVVTRSNTRETVAVNLYTIKSSSVTRRRSSGSRASSVPLPPTEHR
YLAPPIPFAPPPPLRIRTVEEEEEEVGEKDVQQDVHVSLSAIAAEIEESLLAAVAKEAQE
RSTISMAEEYRRNAMSKQREIREKDMLAAQVDITSVLDLGVSPRTPLDVSEGQVSATSDD
ETPASLLKRHPVAPLLYDEEEKQPVSVIASDTTIQPEGTQTTEVVLQKLEDTENSIAHEK
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LHSSRVQAEVEISAFEAQRLSANRAAQAATNYIAYISKEFDEYASSEMEHRTFIEDMQRS
DWSTLERDFHASLKRFFEVELLRLTEKHQMELTRASITLTTEETKARMWLEQNALDDLTR
LHMNSIEALAECRRQLQMKEMQRGVSRIVAVQQLYMQHLYDLAVEEDNKRWKILEEEQRD
RHAEWTSFITTVPTLRTATASPSSVTSASVRGALSSSHAPEYSRTAATASLSVASQYFAA
LVEEAELEALQLQHMERHERHALINLFLAQSQRLKVCEAPMDTTYSDTPLSQRAIANSWR
RLELREEERRIELQQRSWASFRSIVKKATEEHEQIDRMERMLRSIAERSRSVLNRCFGEV
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VARLRDKMGECESVEEQRRIGVQREEASAWATLVREQIRDAANAYKKEGQRRIEETRRER
YADRSQRCRRALEELLQDEDDDRHYIFEDEREARRRLRRQALQLSCDILEKKKIEENIPS
QPVLASQGIGHGPVNDPSAVTVDEEKIRQKRLKELAREEELIEAQTRLREAELRIAEEAE
LRARSEEEKRAALAESVRLLREAEQRAEERIRRARQEAERYVEQEVSRLRDANERQATHA
AALRAIEEEEKSAVVEAKLRAAEHALREAERRAADDVRRAKAEAEAFAAAEAQRVALEAK
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RVERAAAVDAAKVSVRAAQQRMREFEESRESTPQQPPLAWPVETAASTAEAATAAVLKGP
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VFAAKSKQKKAERRCSPPVRRARANRHMSAAAAEELQQLQRRFPRNGLKEHLAAAHNNQK
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CHNAGSSKIRRPTPCSHDPCITVHLFPDTRIPTTAAGPMKMTRGGSSRRNTSRTDRRSTL
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>TCRU_409 hypothetical protein, conserved
MLGLSGVQQQQPYHQHPSQQQFLRAKGRRCLYCQQQGCPGLQNCWWPRLRSLGSRPQRKV
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KPVKGVGCVDFSHPEGKVATGVADVSASPPLQGDPESKDVEGLDHLLRELTAQNVALCRR
LAEMKIVLEQRDTLLQSILAEKLKLNATHASSSVQAFASAQLTGQPKELFSHLQEAQEEV

AHLREETRQLKKALKGCKANLEENNAETEELRRQIRPPTLFSKDSNTIAATPPILSTDGN
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QQE*
>TCRU_410 hypothetical protein, conserved
MSTASPVSSRSTYDEEMEFLMNPVAAASQAEETPRQKSTELMSQEQSQTHYAVNRAVTEA
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REDSISDFDDDNNVGGCLRQVPQRVLMERHSEDGRFLQRHSWNSAVSEEATRRHTEHKRT
WAKLFDCDDLHQEELTGHEDRTTMLPAEKCTRASRTSTKSSRPSASSFKDLWTESEGGPR
QTTVSRTSLATLLNEAEAKDDETYAQSMAAAFSASNSDGKSCRFTDVLANEEAEEGRMPS
CHLVGKPMFSTRLPTHGNSPSVPTAFAVLHGSTRRVGSRGGTSAVLKQLSENPISARVVA
YLTRSFEDWKLDAALIRRANEEDEPHNLSFSGPSLLETSGVQLKLLVKVVESAFSLYCIR
CEVVWADAQASKELFFDAHTADSMISMQKEHEGEGGGNEAGVGHKMKKPPVTWTVVLTAA
TFRAIPIVVGSHLYLARPFFCYPSIRVIVASLNITSDAAVQRLQPTARRQRRPRDADSSE
PKTGGRAQSGEFCGEELSFGATTPERRNRPSASLTGVSPFRAYDPFVNPPTNLFCKNSVA
LGPSNPVSERILRRSASMPRKTTMNLESDACGQLLASRSQMVAHDVIGAQFPRGPGEEWD
VPLEVLVALCPPRKRTSSGEPEAHRRRTNNLSLTPQRTCNEKYSPLSSLSSIDVEEPSPL
AETQARGGVPL*
>TCRU_411 CHCH domain containing protein, putative
MANGVTANSMRVNVKAPDLGAFPLDHYSECKSQVEAYYRCLKSNEYVTPLCRDQMREYLQ
CRMDRGLMKPADLDGFGIPKTEFVPTRQHRIDLKQQWLRQKMNQVTVVWEENYRRDDLQV
PDGYEREKGGGDGGGGNPKPVGEKVNT*
>TCRU_412 actin related protein 2, putative
MSTEKRPVVLDNGSGFIKCGYAGANFPTAVFQTALGRPVLRSTKKRSHGSGGGEEGHTHV
DPMMRDIVFGDECSGVRHLLDMTYPIRNGIIQNMDEMCHLWDYTFGEMLQINPSEHRLLL
SEVPLFSSKHRCHLYEVMFEKYNFMAIQSAVQGTLSLFSNGLQTGVAVESGEGISHCTPI
FEGYALPKANRRVDLGGRNITEFLIRLMQRRGYSFNQSSDYETVRRMKERFCYAAVDSKL
EKQLALETTVLEQAFLLPDGSSCSIGQERFEATEALFQPHLIDVECDGLSTQLWNCIQAA
EIDVRAQLYSHVVLSGGSTMFPGLPSRIEKDMRAMFLEKALKGDRSRLGHFKLQIEDPPR
RKYMVFLGGATLAALTVDQPEMWLTQAEWQEGGVSAVRARFGA*
>TCRU_413 Fcf1, putative
MGRKKRVASHAIKSILMKEKSLAQKKKREMDGYQDTPEPVLSQVKDEAAVRFQRNQLTVA
APMQTNMFLSFNKSLGPPFHIWLDTNFINFSMQNKIEIVEGLMDCMLAKVIPCVCDCVMA
ELEKLGKKFRIALKIARDKRFRRLTCDGKYADDCVVRTVTRHPIYIVATCDQELKRRLRK
IPGVPIMYISKHRYTIERLPEVYGAPG*
>TCRU_414 hypothetical protein, conserved
MLIKTRRVRCPLGPATNIGTVRRCLTTIAAGASVLGAPSLKSTSVALSPSQWMRSSLQEQ
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SVVFSAERTIAKLREDAARYDGIAQRIYNRPDKAFMRNWRPTSTGWSEDACGMDEEPEEF
FGGRWKERRKRPEHAAIRQYYQQQQQSNGGGVGVPK*
>TCRU_415 Kinesin motor domain containing protein, putative
MSHRPDSTGGGEDRGGAAAPSRTGVGTRQRETAGLDHTPISNVVSLQSAIQKEGLTEKIF
FVVIDVTDGRRYKVFLRPDDISRLKVSKIRKTLSSTSGKPPFSFVLWLGDEPLIDKEDVN
CAALGITPRTVMRMCPTKEEMPHPIGGSEGNGGVDRKREARDALDNRKSSVSIADKIMEQ
ILDDPLETLCLVELNQRQRELQFQLYKEAKRCHIFSKDDAVAGIGRHRDDENDDALDALL
SPPQTAKNPQMCSVSSARIPGEPICEDDSLMGFIEEILNEGPKRQDGPRPTPPSVECCPA
MPDERQSCAAAAAAAKQPSLTPIGSNNNISASEIISHGMRLNEMYSLEDTGEFVEPPRFL
NRDASSERKNSGENDKGKNDALPIKFGAAIAVPIATQGEEREVTRLVEDLRDDVNNLLAL
HVRNETAKRALQRELSSSQQLVRRLEKKEAVTRQQLDALLLRLRHAQEANGIQGFSEEEV
RVALRNMAALRQNELLQRENAALEQRLAEEVRRRREMVLALEDMKGHIRVLVRVRPPFRL
LHEQYVGMEGNNPMSVRDTVDESRMTADERRNTITITDSRGESKQFNFYRVFSESSTQAE

VFVEVLPLVQLACDGVNVSVLAYGQTGSGKTYTILGGDGNQSNTEAKGDEGNKENDDDGI
VPRSLRMLFQHLQVEAATEAVVMPREDDNCNDDERASSTYEVSCSLLELYNDKVRDLLAP
PQVIIPNFQLRKSNVSEQRGKTQVTPQCNLKIGSDGLTHVVGLTQHVVCDAGEALRTLRE
GASRRQVHATQQNCHSSRSHLIFTVYLTQKRRIPFRNDASTTRASSTFLRQMESKLVFVD
LAGSERISKSQSVGDRLLEARHINKSLAALGDVVATLSNATISNTAAVHVPYRNSTLTGL
LQDVIGNRSKTVLLACVGPSDPPYENNTAETVTTLKFASRVRCVRNFAPLFPTTGATGDG
DTMKGPGTDNLEPDVDPSHISSSLGRGAKKLWMRPTKLSKQRTNIAARFRLVSANEAEKT
EDGGRTRTPAPSWPPKGNNPHAEQRPRMRF*
>TCRU_416 hypothetical protein, conserved
MLRCASRVCRAASLLGYPLRRAAAMEMLYGGVRVQHLAQSPFSLRKTRSEALPSPSLQRE
RDDLELEVKDSANNVMGLRLFPINIGMRARNEAVRLRSEDCYKRLLAQRQCAEVGEALKF
PVPSSLSAGEHKDATASRQLYATHFHPPSSRLSILTRPVDCSDCKVKTTPSDVALYHPRA
WRPLQMLKPMPHNWSPTLRSSGVRGPHMQLMQERLDGKGFGWKRKSRFLWQQDIDTAGFR
PKRFF*
>TCRU_417 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)/
RNA recognition motif (a.k.a. RRM, RBD, or RNP domain), putative
MNANLFYTQQRPEHQHHGPQQQQQQPAGSGFLLPAAPFTAAGPGATNVFAGFCMPPSAPC
PQQQQQQRQEQGQTLESNVAAANGLLLATQLEAKDGRRGTASFSGAIPDVSNSIWATQEP
NSSTTTALQSLNASNSINYPPFGIKYMVSPTNASASTQETPNQTYLYPVSMQSEEAAPAL
MLLPTGSKDGSSSMSPAYYVLVNSPQASGAIHYTNGTMQPPHPTSFILGANSSTKTTTTN
SFNAAQQPSPFRMPVGQQTQGVSSNLGISWPPQFASNMATTTTGVFPGLIENPRPPQVDS
AAFPSHGQRAYYTSAVFTQSLNSTPSPTLCGHRRPPSGSGPAEGGTMRSRSSRNSGTSIN
SIGAGGSGGQEMERRGGLPFEEDPIPIDTTKTQLIVNFLPQFLTDDGFRELFTPFGEIHT
KPTKIIYDRGARRGKGYGFVYYKDGRSTEAAIKTINGLSLGGRRLKVRYADQQRGKIDCD
SCVDEEEKE*
>TCRU_418 hypothetical protein, conserved
MVSQLTSMLSLRHLSGKSNVANCTETREPKRLSEREEEERTAGFDVGLPYAHVLAAERAT
LSAASVCLCGPSTRLLVSLMKGAAISHAARVGSAIHITDAGVTLTHLTVHQRHRCAMALT
KVLEVLKASFVAVSAQEEEKRKEDDESSLRQIRSAWNKSNQVFFLLLCGAAAMSEEKDEL
TAISMFKNALQQVRRYFGPTSGVASEPLYLLAMAYNESERMELHPSEVSTPVSEGGNEYL
LASANGATDSAQQTFSVAWQVASQARRLALLHCVLALQEGGSKENHRHIVGEWNMEVHRV
CLLMRRELMEVVSL*
>TCRU_419 peroxisome assembly protein, putative
MFESNLLSLINTASPLPTFVEVDFVNSLNNSLSKAFQFAHVLLAEKSDIAAMCLPWDAEI
WLVLHSLLEHRLLFHANTTFSEMLFGLRRGCIASPSKPSGSQGRLSWWVRGPLPAPSLEE
KALQAPDAAASPAALGAISESPLPQRNGELTAAEMQAAQGASYGHLRFIPITNRQRYITL
FLITVMPYLRERAAKWYTHRMDSSPEANSMRIAYATRYPTRARIKELLTRLYPLVYTALR
SLRFFYQILFLLELTPYTTPLHRLFGIVLRRLTRADQIAASNPRAQRALMLARVLVLLIF
LGFRLLELTGAGNAAGGSTALTLTGSGGEDLATPPPPVWGVDVVIPPGTKVPQPGICPVC
ERRVTNAAVCTASGVVGCYPCLLGYARTNGACPLTKCRTTVDCIRRIYEC*
>TCRU_420 hypothetical protein, conserved
MASIRGGVGGFLIRRAAVKSVRQKYQTGPQFNKRKFFQFPKGYHRLHLRIGGVQLGSPTQ
QREHTRFSHLPGDTRTRPQYDFTFGERRADGALYAWRKRGNLQLYQMGGKPETFVCYRCG
YPVRSQLVAIKGDNWDYRMCYKCYTTTVHHGMENDT*
>TCRU_421 RNA binding protein, putative
MSYAGGTYYANQEADSYYYDQQQQMAEEENTIDFRPPDITEHQDKIIQLVAKYVVFSCDG
ARYQHLLIRRTKFNSYFAFVASPEHKYHEYYQYLIRSYIVWRDMAAATSAGEGNTDEGYA
FYTEQLRQQEQQQQQQQYQANIYYTASTDYSTQYTDPTAAAAMTTTGGYYDANTAYSLQQ
KQNQNTSVLGESSAVVETSRGDDVSRKRARSATPQESSDEEDDAGRELVFVMENGVARAL
PK*
>TCRU_422 protein kinase, putative
MLRAPASNDPFGDRLLPAPVQETVYSVDWSHITSPHGIIYIGSGAFSTVRLAWLQERRKC
YKRILTSNGEKTRTTVFLGACAAVAVKRVMIPRANDGSCKYRRLLLLRELQVMERIRMYP
HPNIVQCWGFLFGKGEEEQTFESWNPSGDGTENSTDGKVLTSLNKEGHRMAFNEENNDGD

ERTDQQIPEGTSYVDLCLSLCTGGTLRNYVALKASEVPHAATAGTECSASESQMVNVAMA
FEKVSFDHFSGAQGITGSTNEDTSPYGCEDYDAYHSYPKQILGEGKKIANASSNLPHASV
SISAHLAVPERDIVAIVYALVHALRHTHETLKTLHRDIKPSNVLIFSGVGKAPEYALQPS
SLPIPASGGEPSQERDKTCSSQAKPLSLRVDSEIRSTLGDSDETVEFALFPQCPATTHGS
TGALRQSAGGNLATPTATAGGMSKLNDEPPTTLVVPLGLGYYRLPCTATDSSRRVYIDCL
PQAEGWRIQLADFGVATGVDRLAGSGRCGTPPFMAPEVARHADQGVPEQYTTKADIYSLG
VTLQHTILYLVIEGEEGSPRTCRYADALGAQWIDEDDTATQSRLAFGTGLESNSTETDLK
PNFIVPNAWRCDKELVEGEYIRCGSLETEFPKRGVDDEKEHESKPKGFVVPRAWRCRDEL
LERQYIRRELSPRRNDTDIHAHLLTSLPNELNDFKENSAARERRGSRCSSCGKIHRNLIE
LLNAMTVKKPSQRPNLSTVLQSTAIIERGTFLEKGRQFSYPNNAAWDVGAEDHGNQPSMD
TNSLERGAAAQRFSRARRWAEERNRVRSPPTGFRFDMTEPRQKSSQGKNRGGEDDTTVLL
WRPPSLSFLRASRHKMEAHNR*
>TCRU_423 Pre-rRNA-processing protein PNO1, putative
MSSNVVSAPGAGKEKSASAFVRETRSVKVPHHRFPPLKKVWLEVYTPIVEQCKLEIRMNL
KSRCVELRTCPATMEAAGHGGDSSKVLLQKAEDFVKAVVAGFEVKDAIALLRMDDVYIEG
FEVKDVRANLHGDNLSRCIGRMSGSHGKTKYTIENVTRTRIVIADTHIWLMGTTQNIRVA
RDALCDLIRGSPAAKVYTRLRAVMNRVNDTF*
>TCRU_424 structural maintenance of chromosome 1, putative
MLSHIDRVELYNFKSYAGNVTIGPLKDFTCIVGPNGAGKSNLMDALCFVLSPSATTTLRG
KDATDLIHRGAQRKECAVTAVFCHTTPISPAATATTTAAGQGRDTEISFTRAVDQRGRIT
HKINGEPVDDRKYLAAMSKFNVGTRVNNFLVFQHEVEAIAQKKARELTDLLEQVSGSAEL
REEYNRCKKAHELANQELTTASAEKRDAVVALNQMRLHKKEAEKYEEVLRRIGEERRDEA
LVQLFYVESNLERQKQELHTFTEKLTALEKSIASDEDIRKMKREYAEKHKTYLEELKKIR
KEADTLREKHNTLERIKVSLNHLKRQHEVKRHGLDNLMKTEKVQSREVQRIEEQLQQQKA
ILMAFDERCKKEDEEHMTLSGSLTAEQLSEYRQLRKEAECETVVLRQQMERIKRQQHSLV
EGQKQCTIAIENVRSQKQELQQGVQRSNERVAELKNRMNDLQDTVQELTSNISQKRADLS
QKEKRNREREVELARIQEQLHELRFMKENDKHGSRMAGALQALRALYGVRGRLVDLCTIP
NDKYRHAVTVALGKNLEAVVVDTMETAISCVRYLKEQRLPPMTFLPLDSVKGKEVNDRLR
TFGGTCKPVVDVIRYDTAIETAVQYALGQTLVCNGMAEAKHVAYGSEDGERFKVVTVDGS
VLMRNGAVQGGLASIQSRARKWDEKKYEDLRAARDRLLNDAAGGSEAEMARTQCELRDME
ARLEFTHGRIKVIAAELQATEQKVSNMNREMKNQENEERTIEKRHSTYESELRRCLHELQ
EKHGSIMQVEERIFSEFQRRVNIPNILELESHEAQILRERAEKRQQMQLLVHKLEISLEA
EHKRIGMQSIDDLRGACVRLEEEIQRCEQDLAAYSEIVKTAEKKQSQSRDSVSEAKVQLD
SLEADIRQQSRTSEQELGKLAQARRGVTALQAACDTLRLQRMNILRRCQMEEIMLPLKPV
EARGVKRSRAAESGALTQSEPFVLPEDAPAAAPTKQSQPSQSQRSAATREAQVVVDFSDL
PEPLKEAASDRTHLAAYKQRTETLLENLQRAAESLAPNLKAASRFAGSEDRLGSSSAHLE
EAREKVSKAYSEFSKVKELRTQRFMETFEKIAENVDRVYRELTLSTRAHAVHGSAYLSLE
DVEEPYLAGTRYHATPPLKRYMPMELLSGGERTMAALALLFAVHAVSPTPFFVLDEVDAA
LDAGNVEKLANYMRKNCNTTQFIVISLKDQLYHVADLLVGVLKNKQKETSSILTMDLRGY
PF*
>TCRU_425 hypothetical protein
MSWDALPSVPVRPVALHHALTHDGYFLVDESGLQEDKERTGRSGDRNSTLPIPASLNAIS
DMLLPVTLEEFELAEEVLNACESGHAPSL*
>TCRU_426 hypothetical protein
MLLIAYVRCRGDKADEVMDAKEAFDEIRAHFAMRSQFSEAGNRLSAMVRRFQESLQRQDG
SDIQGVKGARHVQQRPSKSSMQKLPPPIFRPAAVEALLHYASPLPVRTEEGKNVRGGAFI
LYNDKENDMRSNRIGDDYLSHKCVAQPCASGEGAFQGKRDSFSSTPVAFLSSGRNQDQPV
DVGAKFSHNDGFRSRYTHEASAARSSQCILRKEQDMFPFVNGDSDGGTQKPNGCCEERDD
ALHSLGEFDGETMVDCVCHAMQKNKCQKSEIEEEKEKSEEENKKNDELRAKGMEEAPADT
ARKTTRSILADLDELEKTHHDAVAVMLMRTPLRPRPQKEQKLVTSDGGQRLDQHGAPHGI
QHHVHPEQRATAVNLDLDVLSGSQALRCRPPNGPIDLSVSNSGTRVLSNLGQGNVKNVPY
FVKGSSSVLNFSSTSSSDAYDAKDKWLNVSFL*
>TCRU_427 hypothetical protein, conserved
MMRCSRGCRRQLRPYYNLPSKSDHGRKMTGFLTPYRHWMWKQNELWRNVHEAQFEHLRKV

YKRQWLESFRVNADEYIYKYNITKAAQLAQWEYEMQAQEKKRLEAKQMTEGRQALKKKHL
DLLREFHERQFFFWYERASERLQSMNLIQYIPQSGVQEHIERELDKYVAGKIEAYPLNFV
GQMPLVEDREGNIVEVPESLLTNHVSEHPDSTAKPHQPHESTSVSVEEQLLRTMASAREE
SLEEWLEDDSRALSETIDDISREEEQRDEDTRVARSMEETDNEREISRRMYIDRGKTGSK
AISRRPALSETDGGSASGSVGGVTAPPADTSAPMRRRKKGKLDKAHALQEQQDAMIARMS
AKSLKDGESSISIVKRGEIATSRGRIRDKAAIPTQEVLMQKPELAAGSVPNARISFKDKV
DQLYHRGKYKQKKEDDNNPNEDL*
>TCRU_428 hypothetical protein
MGGLAPGSIDDVTDGDFPLGRLHIDGGGTTGSSCYSTAFGEETASIYVDEEPPFPLRSYS
CDGGDFLHIFRPPNQPETGSIHCYSPWTVRGDDEFSLVAHVEVEDEEKGFTLGICGATES
VVGTFLQYFSAGQTMHPMGTQEVRRLCICPWHRRAVLLALLDDRIISCVYLPSAEFCLSR
SGRGREEAGLTQESPTALFEPTPIDVDAWRVVVEHKGRGFVRFYTVERRKGSCYCDAPLS
QLS*
>TCRU_429 acyl transferase-like protein
MKRALVFSGQGAHRQGMSMEYLRVPAVARLWEKMKDQMMQKYGISLQEVMTVNPQKIHVR
DDALDVSVICKRGSLEDRNVAESAPRKKFFSSQEGVMSLTFLTQPCMLAAHMLALEYLRS
TRGYSVESALVIAGHSLGEFSALCALGIFSPEVAVDLVYKRGVLMDYALEQFSANRDDYV
MYACHPGRAKLCEEDLDVAVDQFHVLVELVARALSATTSFVEVVNYNIDHEQYVVAGDRV
GLSALGKCLDPQFRASVCGPSSSLDHIARTAVSSVWQDKKDGVTMHPNKGPLPDFVTSSV
KKYGVRSTFRRFLRGPDDGYTPSLEELTHLTLQEDGRSGLKKKSWFVPLPVNVPFHSSRL
RRAMDLFLPVVQDAMPEEDVLRSMLGVATKPLEESNSASATSAIEKRPVWLTNLTGSAFR
PLDPEFQRQALEMMQSMNVGEVRHHGRYQTDLVEKAFNDGVKHNSVREMCAAVLAAQLAH
PVQWIDLMDAAVIHAGIREVHEISPVRTTADMFKRTAFCEAGEAGVALEMVIRCLPAEER
FL*
>TCRU_430 peroxidase, putative
MFRLRTVGFGCAGPLCVSGARLLWWGYKEHDLHRLARQRPWWENAAIFAGLLCFIQVTSM
CYYFGNRMYQAWRPSGNTLYVNKAMDTKVFARPDLSVAAVRMVIHYVLSGTQTPFGAPMV
YPEYMRPEAEELMKFIFDLHSEQPMFSIPDLWAMLSAKALARLGGPNISVRRGRPDPPGH
LAVEQLLVETPSLVPEGKRDVLKMKRLLAGQGFSVEEIVGMIGGIRTIGFHDSSGFHTKE
EVKPQMRRHPSLMGPQEDVFHLPETMEKCTLDPYVFGGEYFDLLLDYNWRQRSLIGWRSG
PFRCDEKDRKREITLLDPFSEQAVMRERKRLQAQEQAREAVERAAQKRAQITVPEEERAE
SEMGRVGEAQFIPGVEMQESVDDDTTEAVGSLVVPEFKSPCSSVSMREMDMMLLDDALLT
GWLHRFSTNEIRFYTVFGEVMEKIQNRGYNLNSLYVPT*
>TCRU_431 DNA-repair protein, putative
MNESKQEGKTRNVAAAAAANVDGYLRNASRRVRIPSASGGRGTRRKLAMVTAASVEQAPR
SVVNTNASDAVDLDDEWDEVVLPNANAAAVKKDEGKLKEESSQKPKMDVPVANSCAGSIK
AEALEVEDGEVVRGDEDPSAQSLMEGTRPPLTGTSIQRWRRNEHFQERMPEQQQILAAQR
RSERIRRAAEGMSVLIFALQRCKTLVRESRHPQLLRKLLRVCTVEENGSKSFPFIQAVQR
AREEYQRALDPTVKNPALSPCWVTVGKDTVRNYTSNSIMALLSGITTVFTLEDKVDASIL
SNWAAPISFGHLSNLLSRSHQFLISPDAKLRLPHSLYFSIIFLSVANILDMSCRLVMAIK
KERERQNPVANENGNVSEKPAQMTIFLPRVKRQRKEGTNEEDKLPQKLPSSCFWVEVWCP
QRESFISVNPCKGCTALWGAPYTFSVGGDVAMDVTPRYTTKYSSAFTYRWGRCDSYRFFW
KHLDWNDTREASEVILDAFRKDMTRNTCIQLARERRQLHSLTYAEEIPKTLTALHKHPLF
VLENELARHEGVYPKDNTTIVGSVKGHTVYKRSAVVNLRSRDGWLRVGRCVVSEYEAPYK
VVPPPASRPFGSSSGFFGVWQTKPFEPSPLRSDGSLPLHGKTRWYVLLGKPVPEGLAYIQ
RPNIARVARLVDVEFGHAVMGFQRRRLDERRFSHWEAVLDGIVVREADAANLLHAYDEWR
QLTEEQEATKRRQRANRWWLHFVQRMLAMQRVRQQYLDGASHGYLPLH*
>TCRU_432 replication factor A protein 3, putative
MRSTPYLGGGARATTNNLPPFTGVSPRVSSRSVAMHRGEYVSIVLKPTALNTQRGSLEAL
CVATDEPVEVMGLPSGAEVAQVNEFVCYVNPSSGELEYFQHGTYNDEYDVETYRKLLDLC
PKFPQLF*
>TCRU_433 hypothetical protein, conserved
MESTLQTFLEAYPFRHPENPYEQTRAIWSKLVGWEGESAAGPSPSLCVQPIPLALLQKWK
RYFAFCSRVIFYEMDWRDVFVYMGDVPKAATLSVPRDHVGSDRKAEVGVDADRGEGNGEK

QLETTAGAYHRSTTALIHTLANGCERRFGAYPLRFHYQWLVRWTKMLAQCIEWRLLDISK
RGGSVPLEELQRYRLVFASRARELVGAAAYIRTVLELLEIEEEKELCNTDISLKGLPSLS
LSQNFPLTLTLSMRFTLSRATSVSIEQCFSAHSARVLDSLWADVLCIPWDVLDPNSMPEK
VRRKLLASLNNAEGDTDEIYVLCGNGGCRMRSATLKFILENETLERAGIANNPLLGIVRL
TTAPLEFIEPHQLPNVKHLLETVGYVMLTKIRCHFVEKCYYTLPFLADFVAAGVLLKKAL
VSFSRVSADPTLSKAEESKVVLGMGLTPMLLRGLLEATEDFYASCVDSLLHDYSKRAMKH
FVEFCGGSATVVVSQVTLKLLEVVVEPTLEVLFMLLSHASSSKEECIFIYFIADMLKFVL
NEKMREARRECKIGSRVLLQCRMDLLLLMSYIDEHPLMRRRASLM*
>TCRU_434 LEM3 (ligand-effect modulator 3) family / CDC50 family, putative
MPQGGRGPMVLLKQQRLPAWQPILTPPHVALAFFLLSILFIPLGVFVTLMNKQAKEVTVR
YDHIHRCTITHNTGAFMYEGNNMTFKTGCMTEVSFDITEKLKAPVYLYYELTRFYQNHRR
YSISRNDEQLAGKAVRYLPDTSPLTIPGDIYGISGTPIKYVDGSDLRYKDFLYVPAGLIA
WSIFNDTFTLYTEATDGGTPRKLICNATDFSKGNNLPLNGSESENMCVKKGIAWDTDVEY
KFKAPDLEAKNRFWTAAKELYTGKVPTPELSNDDFFNKGWYAGELGHAIPVTTDEDFMVW
MRPASLPSFRKLHRVINVDLPPGKYVMVIGEHFDVSSFGGTKSFALATLSFLGGKNVWLE
ALYFSLGGFSVVFAVVLLLVHRFSGDRASKAIDELMQK*
>TCRU_435 hypothetical protein, conserved
MKGETAEATDLVKTLLKADEECRELRDKVATLEKTCRVRERDVRAIGATPSDGNGASKKI
KCRTITLPIEVFGELNSKAGDVTLLLREQKKLLKEKKKLEEILRSSAAATEEANGLNTDL
KQRIGYTDGETLLHLKDASDTVAYKNGLKHDILQSLRDRETIQTTLKRQTQHMRGLLADL
VKSKELDEQRERAAQQLEEKRNELEGIREEVYSMRRLLERKEKQLEKEKPVDELLLAQRA
ENERRTVVHKLEREEETLRQNEISIRHRATQIAKLERRIEMIGDALGSEENADEERVDAE
LVEQLRKEILSLCRIHQKCEARQELLDADIADLDRRSTGLIRTAANMRKEMQRIEKAHQK
FTDAQKKELEMEQMAAEQEIGDIEREIEMLRRINSRRKQKAQRA*
>TCRU_436 hypothetical protein, conserved
MGAARSRPAREAPVRYVAKQIPRADRIPVEQQFKKPEFTAQGINRRLEDVNTEPLMYVET
SKDASSTELTDHTAPRWYLNTYMEMVDNQRTDQVIISGNLPLSWERDKFEPYALVRGRID
DEDLKWVLAAEQRKKGVDELLPSTKLERNVLQDILDTVELPRLQYRNYKGKLHKTIEDAN
THIAARKEQIERAREAEILRKIGYTEQEVLQEEQYLTNRSRGVKSLDDLGASLREKKRRE
RAAQTNEMEDLLEERRTQELEAGEAVFTEEELLEKPEVLGIKPKPYGTRRQVYKHVYAAD
FGKDDRNQAKFQWWLDRTRRIKRAVDTIHGVPVYNERLSANEEQTRKQMREAAEFNFALS
QAQGAKGFTDPRGHYDEFVSVLRKNKDLNDDSRVEVHEDDVLKNDIFRFPHTKGHGPKPP
PRRFTDKGEKPEKVCTDVNRLHSVEEAAQAAQQGVRAAEEVVRQYGLGKEEIEKPVNENM
GDITSPDSDPSSSKGN*
>TCRU_437 TPR repeat/Tetratricopeptide repeat, putative
MLHTVEKRLVTVPVDGELVSQEVYVDASTELDVDPQTGVFRTRAETEELIKEVYRIARDA
LPKELERYNNWMRSGSRSDVSHTPLQHKSLHVVRSGTAASVPQKTEKAEEYRARGNDAMK
QGNLRKAVRCYSEALKYEPSSSTLWSNRAAAMIQLDRGDDALSDAKRAISLDPMNVKAYY
RKASALYLLGARTAAACCVKESVKRFGTNAAWESLGDRIGTMARAVLVDHRWICNDDVEE
GEELCTLKPIKLPCADPSEVLHLWAKAGVPSAILAEEAAYYAARGSEPLVEPYHGVREAQ
KVYDMCADADSEFSLMSRSTDILRWSCLLLGFADTRIPMGRGPWLETIFGDGFIFLGASL
FSSPTHEANVSLCFDQASHDLRVVARRKIGRYETLSSLSALCR*
>TCRU_438 Vesicle coat protein involved in Golgi to plasma membrane transport, putative
MPRAFWSVPMVTLGEFDALEGAKATCVSEYYAYQEVDIFGPHLLRLSAVCGKTFLSARVI
SGPLCPEYKERMKAVVARVLASNESNEESVLMLDPLAGGIAGMSFCLEDILARGEKRRFC
IILTHPQSAELVRQWPLVSLFLNILLEEWSTATKKRLALEYSIFPDLERCREEARKRSMR
SLMCLISQNTESEEEAFKRVHSFFERFFPALFGVEPLRVTDSVLEPTSVNDIKQRLEVEL
PLVNIVGIDLDSPPGEKGCIAVGNGRILAVGEKFVVKPLAVWLLEFMQKHIGGLQETEML
LSALLSGIQILVYGCDSVQCANLALSLSQILPRPLRRLAVFAEEYLMPYENRIISFSERL
CQRQQLDHKNEIENELSVTDTVCVNVSSEGYILSVHEYDERVHAFAGTRRYSSQNKEEVP
IPSIVTRIVELFYLELSSETNLRTFRLLQFQIECLVNEYVMRGQVYSRLFREHEIRCNQG
LLGIGNMNVNNDSLLNTLSRSVRQFVGGSSLRRWYLEPSASSSSSERRRISKGDTSLFLN

SLGRIYLNAWVTTSSDHNVLLFLGSVSGVM*
>TCRU_439 Tob55, putative
MNNQENASVFSQEVNITEKDIEKVMDLPIRTHVRIRGIQRIHPRVISRDVEAIKRSRTIT
EITNNMSEAKSRWVQMGVFNSVNFNLEPTYDGEANDVCVHIDVEESKPKKSFGIFTTETV
VPELTISLENILGGRYTLSGNYIPPTSRTHAASFSILSNVPFLGQVGEYYIGKRTENKIY
HPASSERIEEIRATAKNEKRGFFSEFSVGFQRRLLVAKGKEHLNSDLLNDFSTTFKGYMR
HELALSNTGYHADPFLSNMYPLPIQGNQISIKNELAGGPFGGQFTFLKTEIQAAKYWPLG
PFCSFQWNTKLAGIWSYRQARIPLNDRLFLSNCHVRGFKSVGPSTLDIIQKEGGRFAATG
GNALWATSISVNFPFIFFPHNGLAAMHLFANLGNLKMIRYQSEFLDIYQWLRSSAASVGF
GVVVTRIPLFGVAPSGRFELNFSIPVGIDRSGNVTWRNGNKNLFEHVKFGLTWSSAFSL*
>TCRU_440 dihydrolipoamide dehydrogenase, putative
MLHRSHFWGLKKVDVCVIGGGPAGIATALRAVDYKKKACIVEANRIGGADLWNGALQSKT
LWEMSKFVRLMTGQTASRFMKPLMPLPPIDSSNAQKAIKNASELRYAQIVHQLKIVDIDV
IEGYGSFMSPQSVDVQLASGGTERVEADYFVIACGAQPRKHVSVTWDGKVVFTSDDIMNR
AFPKSIVIIGAGVIGCEFASIFANFGMTKVNVIEKSNRILPMEDDDVAEFVQKLLENKGV
TFHHHSALESNKVKNGQFHYTLRNLIDNKLTTHIVDNALVSIGREPNLSGLGLENIGVGI
QRGKLERDQFNRVKPHKHIYACGDVATKFALVNVGELEGRSCIDHIYHPHPEGEFVQRLD
NLSTIMFLDQEVAAVGLNEQQCRKQNIAYKMARYGYEFVARAVAMGNTRGFVKLIVTNDR
EMQVLGVRAIGPHASSVIELASLAIHNKETLYNLSELRTAYPTVTQGFQECVNMLLGTSL
LKPNVFPQLVLQEWSPPNFDRGRAYQGDRI*
>TCRU_441 N-terminal glutamine amidase, putative
MTHALPSLETVRRDVGSGDKSTRSRLEDVFNRLTRDRVPYASHYCEENTYKLIEILYAEY
AVPDDAVFAVFVSNERKQTPVWMQRLAEADGRDPVLWDYHVIALMTDTSGNWWVWDHDTV
LSYPCSAKRYIMESFRPEMQMREEYRQWFRVISGRKYLASFSSDRSHMKTSGVPPPPWPI
IQGSLAATTMQLPLYWNMAKQDDKKANMDGSMGDAYGNVVNIEGMMALVSND*
>TCRU_442 ATP-dependent DEAD/H RNA helicase, putative
MSEETGVGSAPATRKKRVRHHRPKRKGSTAVEAVDDSHRSLEEDAEDVAVEKTTEVPAAA
TKEEGAGRRVKKARPELPSQQEENAEEEKQERSVNPDDATRAPKQRERAPCVSDYKALNL
NPHIVTALENDFKFGELTGIQGRCVPAALSGRDLLAEAKTGSGKTLAFLIPIVEIISRAG
FRPKNGTAAVIIGPTRELCLQIEGVLLKLLKHFNGSITFLCCIGGQSRNQEAFKLVNGMM
IVIASPGRLLDHLKLTTDWLTKNLLVLAVDEADRVLDNGFEEDMREIVSLLPKKRQTFLF
SATQTTRVEQLARISFYRPPLLISMKRREEKATVDTLEQGYVMCPSEQRLLVLYHFVKRN
LKKKMIVFFSSRNAVSFHCELFNYIDVPCVAFHGKQKQHQRSATYMQFCNAPSGVLFTTD
VAARGLDIPHVDWIVQFDPPDDPVKYVHRVGRTARAGRCGNALMFLLPQEKLFLKYLYDD
AHVTVSEYTFDLSKVKQGVCEQLEQLVSTNYYLRTSARQAYEGYLLSYSSSQLKNVFDIH
NLDLAAVAKGFALSEPPPLKLDLSQSAAHMSKKSRREFRHMKETKDKRRRAVNEETLKKR
KSNISGEW*
>TCRU_443 hypothetical protein, conserved
MKRARSRRGEADQSVSSPRRRVEAHASEDVSEGQSKHRQRDDDTGLLTAAQRESRGFAYV
RDASENTSLPMETPGAMEGEPTAPLPSVKGAVPSNADEEGEEFVSPFGARSLTRGFSHLR
ESISFALPRLRGSEHRVSISRGGSVLLPLSTPPHESASGSSISSSHSLRVSRGNNQHAQQ
RQQQQQQQHHQQQQQRRRKYHNHRVNGSDQSFLSTRSAIEYLNSTGSLGGVLSSRESRRS
SQATGSHHSHSKSTLGPIDLSPILKERKRQRRRAAPRGGVEANALNGGNNNSGGGGDFST
RRPPLNGLPIEVPAAMMNPADIEVRNSRSLALEAFHHSMARYSRATNVFLITCLFVFLWG
LLAAPLLIQQTGPEDVFVRHYVDSVSELHFIYEVPYMSLSFHEARRLYLRVLSETLERLE
RATSHMRPPDTDVKAQILYYKQMIRAYLALRHRARLYARSRDRSRLNQFVFNPLRDVWYY
GILRNGFKMTLYELILEPSFSLFLARVKDIALCLRQDEKLPCPTLAYLEEREKKQRQWEG
VGETQPDILTDDAVKDSSLFHEEKAVEELRRLNRTLNYVKESCRQSNREYNHLYTIDNTQ
SMLW*
>TCRU_444 ras-like small GTPase, putative
MEVTPCNLVLLGSEGVGKSAILQQFLKKTFRPDYVPTTLETCVHVVSVDGNTYRLHFCDC
SGSRGFSVHRAPYIVEAHGVMLVYSTTSRNSLVHLLGCANEVFCTRRQHGVKGKIPFILV
GTRADIVGRRVVTINDANRVAQGCLLALGLKIFKEKKKIGYKGGCNNGGMEVDPINDLPV
LEISGANTHEVSQVVYTMIRMVRYFRATSRLPRFSLICPGVVPRRYVVVETNLDAHSGGA

SSSTSPDGRFTPALSDNSQATSHRHAFHMSPVGSDEWSASYSPRSVGVTQSVRSSGVEED
RAIVHPYLQQVEDREVIFSLPPRISSDASVNVSASTKTQLSSFALDGPSERRAPKVGPTD
RQCPRCHFM*
>TCRU_445 MORN repeat containing protein
MLTVTEDKIPVPLIPDTELCDVRIGATDPALFFCINLDSPCQVKIEFQEFNTAARCVLLL
SSTDPRPSIHTAVWKCLSPEQKKTVTLLPADPSYRVGPLYLAVRYVEKSGNTFVRLNLTL
QEQYEAEWYSQSNGALYYGMWSGFCYHGRGRCIYGVEPELMEKGTLKWTGRSLRQQSNSL
SWQFDSTPPIEDGKLAINRKDLGWSILPLPSPKLELYDGEWVHGKKEGLGAYQWADRAYW
GMWKGGGREGLGVLCTRDGYRYEGEWLNDKRDGVGNAFYPDGTQYMGGWKKDKRSGEGLF
NYTNGIVIRGTWEEDVLCPTVTATYADGSSYVGEWAHDCRHGKGRHIDAIGNVFDGMWDM
DKRTGNGTLQFINNVICVALWEEDVRKDGTFNFPNGEAYVGDWNDEKYIREGQGKCTYPN
GDFYVGSWKNDKRHGFGKFVYSGEKCVYEGVLCTRDGYRYEGEWLNDKRDGVGNAFYPDG
TQYMGGWKKDKRSGEGLFNYTNGIVIRGTWEEDVLCPTVTATYADGSSYVGEWAHDCRHG
KGRHIDAIGNVFDGMWDMDKRTGNGTLQFINNVICVALWEEDVRKDGTFNFPNGEAYVGD
WNDEKYIREGQGKCTYPNGDVYEGSWKNDKRHGFGKFVYSGEKCVYEGEWKEGKRHGIGT
QETEEGTYQGEFQDDMRYGHGLHLGRAGSMHRGIWRDNGCIGPGVRFDSKKGIMYDGLFL
LGKLQSVGTSRTENDIYEGTWCDGERHGVGLVSLPNGDVVRHLWHRGVPQDGHVIYMYRD
GDKYEGEWKDGRRCGKGTQWYADGSVYVGEWLDDKRHGSGSYTDVRGETLVGEWCGGERM
DVKGSLRFLDGTVYEGEMRLGKPHGNGRLKYPDGTVFEGRFSNGVYLL*
>TCRU_446 hypothetical protein
MDDAGLARGMDGDVVFARRDCVSSAALRGVAAAVPAGEDGGIGASGTLNSDAGQPPVGDA
GSGTEAQRQWGCTNGFIFCCRYRRCQQYSCLGCWWWCWPKQQPAFVSGVQDDLPAGGSVA
GEREEAGSACCGEEPSMSSVCSQPPQFSAGSATLTVEERDGKKGSASVTNIQSEWTQQER
EGPHVLRTGESARRTPAPAPAEGQTAHATQPSEDSAEHAAAPSSGLTRGASNGDSQEQTP
QLQTATDAEQSVSVVQGVPEWAQEDQGMW*
>TCRU_gamma, conserved domain containing protein, putative
Elongation factor.1
MQFMTANLIGLWLQRMEHVRQYALGVAFMIGEERRHDIVALWVLRGRGMPTIVRDVEDTE
LFDWEEVTDFAAQWERMTDCVCWRGAC*
>TCRU_448 hypothetical protein, conserved
MKKLRIATDPKENVAPTPPKGKPSIAMSRNIEMDLNAFVTKTAPASALRKAVGSKDARKS
ETVDGSGEHVPGKIAGGMNGHNVPGTPKRHQEM*
>TCRU_449 paraflagellar rod component, putative
MTTMQKVDATLARFDRKSPRAAYAQVCEEMGIHPQKSLSLLLSDAPRDWDKHRVLECKNF
ILGPKGCMALVPVLLCSRSLRRVSLPGCHVTDEFVAQLAETLQDHQCIRSVDLSDNPLVT
VYSADPIIKLLRVNKNIVRFSLEGTHIGTNVANLINDLCDKNHEEVANYFADDYFRMKNI
FNYLDGDGSGWVSLRGLVLNAPFPVLQEQLIERVALRRPRKRSDGTISVNTFLELVYYNY
KTDVEIAKRAKEADTEYYNIIVNWKRLLDAMEGDGKKEMNELKKQRRNEEDDDEEDEEES
MTDVPLPGKLPVLPPEDLFRLRIRSHELRPSEAREIVLAAMKLQIDADARCLAEAEEEEA
EAARAAGSDDKKENTEDAASGEQRVVRLSIPCLRRAYRSVLQPEPLPRRFRFLQEHEEDY
IPPMMRAGSRLISISKLSFLDSFRSSGGGSFVSQDESLGINPDETQTRWWGLPPAVVRLA
TKFFNKQVAKMPKRRQSKLVISPRTQRDNAMQKTAIPVTAFLGAKFVTDLETIHPRLLAD
KFLQYSIPIDVSTITLQEIVNCLNEYYVEVSVDKVFTLDQIRNMPVPTVQDIQSSTGNGK
TEMSILDEI*
>TCRU_450 hypothetical protein, conserved
MAAAFAESLQREVDTAIREAASHRGGLRRRVAAACDRIRQQQALARAEALTPLFRADLLR
RGRAIQKNRARLMQALKRFARVLPSGDLCESSGLSNVVVVFRVAQEALRVEEELAYWRQP
LPCEEAWCAVCTAVREGGYRADAPLQLPAATEQQQHRRKERQEAALEHLLFPVCTNVGSG
EEEETSAAAAAAPAIPWIALPCFCTVTHFCRHEQVPVVAAAAKGNSGSQPVNPGASGEED
DAMHDEMAEAERGVSSDGRVTQMVLDATAAHLGRLGVRAGDCSSSGEDEEAAESALEEVR
LRVSLEVAARVTACRHAVESLAAGEDGMLLDGVTTVTAAAPLAVPVMALVLPPTEQLFFC
IAYTIGAAILRDEQNERRAAATTSGTAIVVDDDDDDGGGWKGEWGRWMRQESCIGGADNA
PVGPRLLRYLLEYVFCPAECESQRKGAAALVRPSTVRRWLELALGSVPDKDGAMDAMMTL
YMNRR*

>TCRU_451 clathrin assembly sigma-adaptin protein 3, putative
MIKAVIIINTAGKIRLLNVYEKDIPLGVQQELVRRIHRLISRRSADLCNFVDNFRDWPTP
DTRVVYRHYATLCFVFIVDSSESQLAILDLIQVLVEALDRTFENVCELDLIFHSDRVQLL
LMEMVMGGMVLETSREEILRANTEMQRIGSSKAGTGAAAVTGYH*
>TCRU_452 hypothetical protein
MPPCSACTTHDPTVLHPPTVLTFLRPVLQQTADSLVLFPAPQQQQRVVHPAIDQEVLGAT
PMPSQVEPVLLAQHPAVDLMGVDYLLRMCEESNARTPLRPSVGANSNAAVHDHVNRAGGA
EIITVDSGDDDEGR*
>TCRU_453 hypothetical protein, conserved
MDAAVNKPIANVLLYSDGALYLVGARHNEVKSSLFPVPLTEELQMITSILRNWADVDASF
SASPVSTVGLVGYLSNAGAANTWIDECRCMIATLTNDNNVTNGPQFAGQHCPVNRWEDNN
HCGFVNYDFALVATVAIRETHAGVKSIPLIGAKEAGRTVHFWLSHSHERSLGVMLNANRH
TGFWELNKQ*
>TCRU_454 hypothetical protein, conserved
MAMMMTGRVLLLCALCVLWCGASGRCDVEVVRVADSPANSESGSVAPDKDTDHTVHGGEG
VVSGEQSQKQKVGGQPLVAPQLQAVLQPESTVQQTLFDTEPTDSLSHSQSLQEERQGGSP
DGSLGRLAASHSQEDRKNESIGDQQRKDPPSPAINNDVVSRKSEELTEDTPRRTEIIDAA
RSEERQEPENVTPSLEQTRETSTAAPAITTQTISMQPPEENASSTVKMSEASPQSTGTAN
TNHTTTPGDIDSSTAVSHATPPLLLLLVVACAAAVVAA*
>TCRU_455 hypothetical protein, conserved
MLWSVKIRQFQQNRGGEGHVDKAQTTHTGIRIVHGADAATVHAADLRIVCIGERERSKAV
RNRSWQTRVTVSASSAHTPTAADAARPRCKAHGVHGAISTVQHRHGRHNIELTSVILHGR
PLYLVARAVDDRACIVSYKPKACHVCSDRRIGAVPKVVVKYRPHTPIAERHAVVSSHVQN
VGSAERVVAVHQPAAASHSQRGCHEHGEAETELAGHNLQHAAAIHHNVPKHTRAFVVFGT
RRTPRAVLYGEHGAAANTQVRRNSIHHVHLRHDSAVVHVEDAGQVHDKAALHKYRSARTP
ATHQSRPRHDKPRRQKTDAVQDKRGAVPGFLVARSRRHVLRPANRRAQGRVRQQHTRVQR
HRAMQHDRALQRRHIRHVDEDVRHQVRCALAEATNPQLRAAHKHAVAKRHVQRVSERIHR
AQVHRHSDRSAEHHRVEARRRLPAANRHGLRQRHATHAVLPTATTGTRRRHVERQARLAH
AAGTAAAHAVGERRRQRIEARQRSRTAVARHHAHGGQAGQAVVAAALQHAAAGTVALHGH
SAARDRRPGGKRRAGGSAASNRHGAAAQRHP*
>TCRU_456 hypothetical protein, conserved
MQRRRGVLHARDGVGGPQLMLVQLQERMAWRVVSSLRGARHGCAALAGESRGRRHELRGE
PDADEPRAEHVEDAPLLRGCDIQRRGCCAHVPPQSYAAASPHQHHAHWVHIP*
>TCRU_457 hypothetical protein, conserved
MGYKAGPEILQIITSAIAGVTTVVHPLWAAPPSVRFDVWIDNIRIAGSKSNVTLWEAQVL
RNADRRHATIGEGRESGATQCTFLGVHFDHTQRAVSLSDEFVRSVRAMPALNSLTIAEME
VMASRFLYAAAILCTR*
>TCRU_458 hypothetical protein, conserved
MAMMMAGRVLLVCALCVLWCGAGRCQETLLVSQSEVPGAIEGDRGQPQGSSGFKTPESHA
PGSEASVREVQQEQDPSPPREETQLGTKGGNKVEKAKEKGAAKDAGKEGEVDGKTIELKK
PEDKLTSVEGQQLNNNEGLQPTTLNGPHGVETTTPSREILSVREDQQDLSSSLLPPLHNT
SPGGTPPSTPAAGRADTKSHENDIGKKNSQQSVVGEIGQNNDTGEKAVDSTGEEEGSRLS
VATAEEMSETTTKSDSGGTATTTAVGTDIGTEETPPTNHPSKPSTEGATPPGTTSDGEAA
STNKYDTVSQNAGSTTAATTNATTGDTAKRGDSDSSTAVSHTTSPLLLLVVVACAAAAAT
VVAA*
>TCRU_459 hypothetical protein, conserved
MHAAVVTNVGLVVDAVIVERCVDEKELLCDPAAPKSYFAYGNSQQNSSSQTNSSYPTPRR
FSIASGVSVPVTPIGENSPRSYALFQSVLNDNVHYECHATKRPLQQRYFHMFDVLPFGME
SPSSVFGVTGRHTSRGLVVGVASSGLFVVRPYCSGAPLQLIQYGPDRQRVRKEDVELIAK
VSNSPVVTEGIAAFMDIAKRWKEAVKKAFPLDGEKDAFRQGHAEAGDSSSSNEDVVNLLE
GMELWSLKDLQLPPQLALHDPISPLCVGSRVLARRFCSDVSLHIARVLAVNYDVTYTLEY
ESDGGIDERVLHNDIHLLDASDAEQCSVRDKVTVALHKQLPAVIIVCLGDEEYRIILAQN
PNRSLTITRRQIVFIAPLLKEALYADPLILQWFRDLNPSCSGVVPWKEVRYLILSWESYG
KNLSFQKLGEVQRDLCIHVGRMEPQLLRKVPVQEEDLLLNYAEFEYVILRARNLL*

>TCRU_460 hypothetical protein, conserved
MQRPKNKNTFGESYARQNDVPVTGQNPVSAAFFPQEDAGATGDVFCSRRCHRCKRVFQVK
LIAVIFKYTCWRCGCPVCQNCRTPRPHAADMWACTSCVRPISFIWLFQTTYHGVGLLLRV
LEFCDTRSTRIVKFLFPAAALQCMARRETPAKQTASRCETPKRRLFLVKASDGAGAATGS
SGAQRRVLVEHSPRRLPLRQHPTQRMARAKTAIKRYSPLQEQQQQQVRGYRARTPNGISS
YSPPKRFSLSDYKLSTTTTPSATSNNKKDGAFFAEFQAPTKFAVTAHVERHELSAEVRRP
MDEGSGNRFLRIDATKKVGGRVDIPRIDGTQPSPTPSVSGSRSDSPPPRFPSFSQFLGDR
GSALLLEEQHSPQPQQQDSSGVERKTGGRPHNTSKVFEMREKEVEVVELGACRESRISTW
TVSPNPITPRPSKMGGTTVTGGSSTKKKGICSPPPHLGMISLNASLSMSQRRHLTNGGKP
SAATPVATTAVNNATTARTIMANHSITPVNHGIHSLYPIASHRRTKATTDKIMISNTPMH
FKLHASRGPTTGSSIPARVTTPRPFASVSSTFGGIVPLTERHVGAASFGNHSTTAHYPRT
RMSINFKTDTFRLQRMTSNITSPRFARKPTVHTPTTSGGVPISARAPPSSQVGTRSMITS
PRTARPPEQKKSKIRGNNPPSCSQTPLMRKTSPPNARNVTPRGSHARTPLQRIASSRLLP
SGEAARRYLPTQADACGRELQMKSPPVLMIHLTRQRGTVVPNLTEEKTPRPACIPQPMGK
EQPEQQCHAQPEKPRKE*
>TCRU_461 hypothetical protein, conserved
MFGRSALCLAKRFRYNTKYPSLVSYNKLPWEILNHETPEFHMHVAPHYEQIMTLAASTHV
PHIVGKKHLEMPPEHRLRLLPGMFYMLDGDSIPEGFTANRVLDPTALQYYGRLESLVATV
QAVRMLISDDLRIVCTSVTLQGPLRLPVASYASLASLEAVTNKASASFTLFHFVRPNRPP
SELQLEKYYIHAPRAMALAEFNSTSNTSWEPKLQAPKRSKRVTPLPAYRPPQSYLMGLAE
RLAVVPGSSFGRRSLMWGHWF*
>TCRU_462 hypothetical protein, conserved
MTTETDNFLHATPSSAKSYPTYTPPPPLPSRNSVRTSSTATRRTFHDECDEVIRLIREDT
LAASPSERAIGGVCVSRVSAHEKYRAILDEVEHLNRLLEVTVEERVDVQGELQGKLTQME
ISLRARERELRQRDEELLHLRGAVEALRTQLEALHRTRQTETQTTRAVSGSDSLRDAVVH
RDGGDGVPSAATDAATRKETSTKTTKYIAQRSLRWLKFLLKRCFFIDEGANGKLTQLMNL
LNELEEYTVEPRREAHAMRSLCTQVSNRLVDVVLRGANGRRLLDPDVSDLQTSTERHFSH
DQEEFLRRLVAELKVERDTLKQEAVAIAEENLQLMSELRSREIAAPRTPSPSARVEQLEA
QNAILLAERNRQAVHIDELEQKVRALEDEKNAMHLNLVQQRELLKRHEHVLHFISRHEWG
VRSDSSGGEGSGSGRVHTTVAK*
>TCRU_463 kinetoplastid-specific dual specificity phosphatase,
putative
MNAQPFTAASDLPPPPPPSPLPPPPAFARGGYHSNGVRGSGKLKHNRRHHRFSDKNVVDL
CRLDRSSSSTNDNNTRSNRNSNSHSISRNSNRKNGGDGTPRGCIRAPHSSQPPTPAQKEQ
QQCPSTHGSSSSLLSSCTTVPPYSSLGKISSFSTCGREPPTKILDFLYIGGVRDATNAEF
LRRENIVTILNVSREEYWSVDRSIVIHPFAVDDTTEANIQQFFRPTHVLLEQVRKAYYDA
KQRGASVCPRALVHCQRGKSRSVTIVLAYLIYRNGWTVAEALQYVTRRRPRVEPNLGFID
ALRAYQESMDVEERTRRCSSLGLAVRNLPRDTASSFVHKFFEDHVGCVQEVMMHSSRPNQ
NRNIAVPNTNGVDQGKRGNDDNDPPASFGLSGRRDGNSSSSISVKTCGNDADGNTLCLVF
FSAAECVRLAKLLYMRRPELFNVLGVVDGKELRLTIPSKLIRLSRTAHAHCDDGDNTRSK
KSSQGEEDTPKGDAEKNDAGT*
>TCRU_464 adaptor complex protein (AP) 3 delta subunit 1, putative
MAEATRVASQILFQNSLAEVVRKLRSAKKSEAEVIEQCIAETRKEITSTVQSVKVTAVLK
AVYFSMLGYSAAYGAFNIIEVMADRSFAHKRIGYMAACITFTPKTDVLPLLTALLKRDLA
SANQYEVGFALYCISSICTKDIARDLVVDVVNLLNHPRNYVRKKAVLSLYRIFFEYPDAL
RPTYPRLKEKLDDHSERCDNDPAVRGAVVCILCELARRNPANFLGLAVPFFSMLSTVHSN
WTLIKIVKVFGYFAPHEPRLGKKLVEPIANLICATGAKSVQYECILSVANGMSKVPSLTK
LAAEKIKLFVEDADQNLKYLGLDAMSRMMRENPKLIIDQREVILACLNDMDATIRRKALE
ILQGIVTKKNIVSTINSMMERRVRSPPDEEWSNRVIATVIEVAQTDDYTLLQDFEWYFSI
LLDISLVNLTAYQHGALVQRELVTVLTRVNAVRQFGVQAVSELLCNSTLLNCDATRSTQW
QIIKAAAFLCGEYPYWLLDKRLTCERLLSDRIAAMHPEAQVACVAAVGKIAAFVHQPCPR
HVTLSHGEEELKLPDDPVTDAELRAVILPQQDSEKEKDVGDDDKGKEKYSGLELFRHSIY
PDVQERAHLVFYHVDTNPDIGPTFYVEELLSVAVGAQDAVKPPDDLDLGEPFCTHLPPLL
QPSDSDDDENMDGDEDEFDFLGGDAVELQRRKEEERRGEVAAFYIKDTTLTREELPVDVR

LEKVTAASLHLHGAGLHVPRKTHSINRELLRPSNYVAANPARRRNEEVEEDEATKKFRNV
DVTRALTADEKLPEPIPYTQSLQLRASVGSGKEEARAAEAAAEAAVFDPVVLLEERHLRV
TANVVSCHVHKECTLLTLEVEVSNLASSSSAYDVQLCIKYDEDNFTEQSVQLESLDFSDT
NNSNSNNVHKNDDKKKKRENIDDSNQQQQQKKKGEEKEEEEKGNGGSGVTGVCLAERIKG
SKSVCRKIGIRFISQLPSSLVKPLTFILAYTRGKKPAATTLQLPLFYPYFSKIPKDVPPA
EFSQTILGKFLLAAPMVSGFVDVNLTHVPLAMPLIQQKLRLKPVEIFKDVASFYGVLHAR
KSTAEKAHVAVLLRKDTVEGDKKGITIMVKAHQSCLAESLVQEIASLMIQEAF*
>TCRU_465 Putative zinc finger motif, C2HC5-type/ASCH domain containing protein, putative
MPPKRWNAPSMMSPAETIKEALVRYIKKEIEDNNFLGLVGEELDNMANMLATCGSKREVF
DWCETLMIGEAVAAEVTKRRVDQGPPFDETPAAPTMSAPEGRSADGNRGKGRQLAATGRK
AGKRKGTLLSKAADKSGAAALKPGFVECGCFATTHAFRGNCANCGRIICEQESNETCYFC
GLDPSTCVTYEIKVQEGLIGAAAVAKNQEEYEASVRKRDELLHYAETRAKRTKVIDDQTA
VFLSPKNAWMSPKERQKADEDEALAERRRKVAAMHRAKGAYRVHLDIMNQNVSLGCPEGP
AVESNSLASSESYVSCCAEEGDDGEYNVEEARALPLPSLMQKIWYSLDGSVEKPSTASST
GVTNREESPVKKPTGRRVVELSRRVQVNYYEDDAHLFLEAQKERQEEHSQVESDGLDAAH
DGADAEESTIDETNVAPTGETAVVADISTGVSTRFTPSLTMRINDDGICLSMHQPWAGLL
VSGIKFHEGRVWHTDYRGRLWIHAASTQPHDIKEVEEHYSKFMKPTQQFPKHYPTRVLLG
YVYLVECLDRDTYREMFTEEEIQVDSPFTFICAEAKALPFPLPMNGDHKLFRMDHKVHTA
ARKQLLEIM*
>TCRU_466 phosphoglycerate mutase protein, putative
MAVVHICRHGQDEDNFEGLLNGRRDRPLTQLGREQATALSQKLKERGMTYDIILTSPLQR
ANETARIIGEALSVNVETENELVEREFGVLTGKPMEQIRTHAGENVVQGDRVLYFLSVDG
AETFDECYDRAARVLQRVDANFAGKRVLLVCHGDIGKMLLAVRRKITWREGIMLPYFANT
DVLET*
>TCRU_467 hypothetical protein, conserved
MGSYENVGWKFVEEAVIRDKGYDEEIVLASILQSYFIRQGFVESLTALNEELRELQTMTR
IGTTPMAEASATTETKEVTGRRVRRNGKGIFVNQEELRNDVVSHDDGRKNSNGSGKNSGI
IHVSNDNKNNNTNNNNSVDCKGVETVLESMKKRKRLQLLCLNEQYEDAAASLPQGSVFIV
KLLAMEAMKRARGDQSAALLFLCEKVSPLIADMSDAAMAHQIYVETLATITGTDATGCSE
ASPCRIAREVNESLLDDHEPSALHVLLSWSEWQAMAKAKEGGEGGRQFPFLVGMERP*
>TCRU_468 vesicle-associated membrane protein, putative
MPIKYSCINDGTVLLAEYPPGEQPKLAETMQKVIATVPGKEYRRKTIEDKEGGVNYHYIS
NGEGRIVACVTTNEMRMRTVFAFLEAVEPLVRGNVGPPGTELRNGKKLLQQKMDFYNNPQ
NDKITALNDDINQVVDVMMDNMDKVLARGDRVDTLHEKSNTLADQAEQFKQRSTQLKRSM
CLKNIKLTLMIIGTVGVVILIIVVIACKPNFSNCK*
>TCRU_469 Transmembrane amino acid transporter protein/Tryptophan/tyrosine permease family, putative
MADKVEYLPQANHGAYEKDGDLNSRIQETSENPKEPNCIVKTTRRLIPDGGILSGVCNLA
GSSLGAGILALASAFNSSGIVAGTIYLIAIYLLTVFSMYLLAVTSLKTGIRSYEGMARQL
FGRGGDIFTAVVMFVKCFGACVAYVISVGDVIEAFLSDDSVTGYWRTKSFVRVVNCIVFF
LFMLPLSLPKRINSVRYVSFFAVSFIIYFVIVGILHSVRNGLKHGLRDDLVLFRGGNEGI
RGLGKLMFAYLCQSNMFEVWNEMKPKSTAFRMTLETAISMFLCTVLYWLTGFFGYADFGS
DVTSSILKMFKPMRDAMMFVAYIGIVIKLCVAFSLHILPCRDSLHHLLGWKLDTVAWWKN
AVLCSGVCLVALIAGLFIPNVNIVFGLLGSLTGGFIAFVFPAFFFIYSGGFTYAETGFFL
YTFTYLLLFAGIVVICFGTISTIYGVVK*
>TCRU_470 queuine tRNA-ribosyltransferase, putative
MAKEYPILVVPCKRGGIPCLTPDQARAILNEEERVISVSIFDASEFVDPCKKANQGFAEF
CGLGEFRTILTVRSPHIGMHASAPATDAGLCANHEKGRISLGMDKWKEMVLPLRPEIAIP
PYDSVSINEPQKKRRRTAMTRSAKWATSADSLQGNGNCKLMKPLCAAENNGEFVFLEELC
QNETLQQYTYHVKEAINKGQVMSTAISLPSLLICLKYNVCFIESAIPWILAEKGIGLVFD
FNPVSGVSPARYETQIDLNDDCFTKDIRPLSPDCNCYTCKRHMRAYIHHLLTVQEMNSKT
LLVIHNLTRLIQLVRLYRILDAEDREALLNWLFAQF*
>TCRU_471 structural maintenance of chromosome 3 , putative

MHIKNILISGFRSYRDQSFQVDLSPKNNVIVGKNGSGKSNFFAAVQFVLSEKYTTLTAAE
RKELFHAGSGRPALSIFVEIIFDNSDGRLIIPGRAEEKEVRIRRTLGLKQDEFRVNDRRF
TATEVRQLLESAGFSSSNPYYIVEQGKIVNMANMSDEERCQLIKDVAGTRVYESRRKESE
EILEETSGKYRKIEDSIDQLQKRLTELEAETAELKSLQEIERERKCVEYSIFFLELANAK
ECLQKLDEERSKYVSSLNEQRDAENNTNSSIEIEEKNIRNCAQRIAHLEGEMQTLEREAT
KLNSKKAIAQLDVVDAKNSISRNERERLALQKEVENLEKNAEKVKKDLELSRNNLNQHQR
TTDHKSNELASLEKKLEALLAKRGRRKLFKNKKERDVWLAGEIERNRNTIETHRKEITRI
KKSIEDIDNRIHEEDKNQKEKEAATKKVETKLADHETRRGRAITVRNTLNMERRSLWQKV
NEQEIIVQRLQDEWSRSRHQLERAVRHDTRQGIQSLREVLHELADEKLTNAVHGQLIELI
DVGKGYETAVEVTAGNALFNVVIDSFDVGALILDQINLKKKPGRISFFPLDTCKSEPIRF
DGKEGCSSLMEHISCNPRFKGVVAEVFGKTAIVSSMEEGSKFVKEYNCDAVTMEGDQISR
KGGITGGYLESRNSRLLSFNNEKKLSERLANEKTLLEKLCQEVAVVEQKITDAMNEIESL
RGEASRAENDADADLRDARLHDERKVRLEKHREQLLETRKSLEKGMADANSSLELLQQEA
REDFVSSWGEKEESHLESVITEVDKTREDLSALQLQRVQITTEVQLLEDTLQNITRRLNI
ARDRIRELLWVNTNNQTLTREQGNVDAEISLVSARIETVRQSIAETTNEKMASEEKLEVL
KNKQFASARAVQERRDNDEKKQIQRTLLVQRRDDAMEKIRKLGIVPKDASKYSGQSLGML
MYRLKENNEKLKKYSHVNRKAVDQYSSLMETKNELVGQKEILQNELKSIHDLMEHLDKKK
DEAVERTFKQMQYQFEVVFKEIVATEDCHGELQLVRSAAKKNAGEDPYIGARICVSFGLG
NAITDLGQLSGGQKSLVALALIFAIQRCDPAPFYLFDEIDAALDAEYRSSVAKLILKDSE
NCQFITSTFKTEMLEAADRVLGVFFHNKTSRIQAISLEEGVKLLKQAAFEERKRTREIEE
*
>TCRU_472 hypothetical protein, conserved
MPESYIVRFKVLKVESAALVDGRQYTISYRRGETSRSTPCYIAEGGAVDFSTMPEGAAIV
HFKSGGARFLPKWITFRLEEYIRGRPRKMIGETQLDCAELLGLHSITASARRRVIFSVYG
ASAQMVVALLVYPANHPALSFGDIASTTGSDGQRSKTKNGEFKRMTRGEAMTLLISLEAM
LERRRKEEPKGKEPSNLERCLAELEERRRSLTGVDGMATAVVKKRAEDVVAAQFLALSRK
YRANYAGEVAAYLRQLAVTSGLPLTADISEEASPDAEGARERLQRINARIDTLSGQVRKL
EEEQLSLGRQQNRTDMKDELCGITNKMEALQSQIQLLLKTRTALEETIRGKGHDGTPIGR
EVHDIRQRLRVLTEEEAKLREQVRRMMNVASMHVLKWARSKNPPLEDIQTDLAALFAADA
PSQEAKQEKSTPKVLSSEERGQLVEALSNVAKVSAPPVRSEVSSEMEGPPSRQPQQQVDL
FGATGLPSVGDFGGSATKKGRNESTTFSKTDKDAEKHVDPFISDLKSDMFAPSAVSEHKK
DTSKVHEFNFGATAEEDTGAVGVGGSSEYATFFKDVHDAAMDLGTPPVVDLVSIENDPMY
DFHPPPEAVSTKPFTIEFEESPLYHGLDGDAATNPPAFTFEPEGHQSTNSNTHALPTYSF
GPDSATKNSRTANAPRLPTYDFGS*
>TCRU_473 Leishmanolysin, putative
MSHWGRRNAKDELMASFVVSGYYTAITMALFTDLGYYKANFEMAEPMSWGSGAGCALLTD
KCVTDGATLYPDMFCTDSSDATLRCTSDRQSLGTCAIYQDDNIPPEFQYFATKQGSRRGA
MMEYCPFIAPMNGTGCMDGDEAIMPGSVVGPSSRCLTGENLRMGSTVVGDVCVQLRCGEG
TLSVRYRGSEEWHPCAPGQTLTPPAPFTAGSIRCPSFSDVCLTMLKHSDASSTDVESHPK
HLAMVRNNDGSALAVTSAPLLLLLIVIGTVIVAP*
>TCRU_474 Thioredoxin, putative
MHSTEKRGREETEVAAVPTVHETEGVVVVGKGDDDVRKKKKRPHLENDANNNNNNSTTNN
NNNDVTDTLDAHKKFAGLREERPQQNEPLQHPPSVNEVSVDGRGETDGSEVGANDVDVEE
PTLFFGPTHAARDEKRSDGSGVDLRCVASGGQNQRPDAAHDGCRAPHTVGAVTTLYSLRQ
LEELIGSAPLPIAHAGVLNVTPSSSSSAPPSLRLRAGETVLIMLHRCKGEAGVLPQHTTE
QLSNCRIFLLDLGELPPCEYEEKSNVACPNGHDERGVATGFLQLPPTDTLLSLASQGAHD
MEHVMRRASSLLCVDEVLNANDADSSKSQTSEKGGGDENASADATHSCKREELALPALVM
WRAEGGLADEYCYPKEKGKNDSHANNHDNPQPPLAGRYHHGRPLVVKQLTSLDQLHSFSL
LTPVYTVTHFLRTVCEKALFPDDPAAGASGTRSLIYFGASWCPPCMRIVHALPTMMKEDF
PSNMTCSVKADMDLATPLFEFFGVEIIPTFVILDNESLRTAGDWKALRSCSISEEALSQI
YEGLRRSELGRIQNSQRVTVRTFIERHSGMLKFDEDF*
>TCRU_475 hypothetical protein, conserved
MLGKRIAAHALAASTPRHRWKAAVTPQCTHPNTAASSALPTTIHSGSRAANTDRKYGSAT
VLARSCAEAHGILANTPSTCISRMEPSPPVTTTATAAAPATTPVIAERVLAAAGSVFDLI

VKDPSSTPLQPPDTATASQRMTSVSSAAMK*
>TCRU_476 hypothetical protein, conserved
MNELAISNDSAVVLSGNVFQSVRASSSAVHVVRSALRVSWHSVFAVLGNVFHMTGGEGTL
IHLEGYTEFFSLCVLNNSAVVIRGNAVTRPVQYFMLFLWVFCVESRSAVVFRDNDMQGSS
AVFFSSHSSYIYYNSWLQLSGNLCRVSPVVAFAVFNPTVNLRDSTVSVSGNQFISSTFTP
TMLQIPLFSSDLTNGAIVAACNTVNGEEREGIVKRRSRCQICAEGVVALRVCCVGQRVSY
DWRRGYADTS*
>TCRU_477 hypothetical protein, conserved
MYPSKLQYRAYSELPPTSVSVPNEYKPKPPYLKACALTLLTSSEEAVNTTSCSNNTLHML
FTVSGKWTAEDCTTSTSVTAMSQCCGKASAKATTEDRITVWLTRIRTPAESAASSPPTNC
SAAPPRNVHSLSVMLMGRCSGILSNENVSTAPTPLNVTPS*
>TCRU_478 hypothetical protein, conserved
MTTCRLLCALLVLALCCCPFFCTKAVVAETGVPNEPLTQSQVQSTGDSSSGLNPDTIKKP
DSAGASHKPVSAVAGGGSGGLSNTQDGAITSGLPGPGVGDADSPGSTGNSEELVVKTTTK
HDPAVPVPNGEVAEKAHNATNTTPTIKTPPLPISAVLQPKASPAVTVPETGKGSAARNLS
QLSREKNKENTASQTKALSEALKRHPGDAEAEQQEQESDTSNLVEIADNGKHTETTSSSI
SINDSDDAQGTGAENNDNDPRPNPTETNDHKVDNTNLASAPTETAPETVNTATAERNETL
KSEGSDGSTAVSHTTSPLFLLLVVACAAAAAVVAA*
>TCRU_479 hypothetical protein, conserved
MEGCPGGKGRRAHRVTGARRCGEDSIPGVGPDIVPRVAALRTGAMRHPPTLRQACTRPAD
HKAPPVSVVPFLPHCGDRPASASAGTSSRREHRNSLPTSERRIDFLLPNLRQSALFRPQY
EGTRRTCSAWRSDSLRGPHMWMPQWCQRLINRRLKRRSPPKLPIMPAGKTRRKHKCGHSR
WTRLFRHRLITDATGC*
>TCRU_480 hypothetical protein, conserved
MRVGRAMQCSCRRAALPGRGGEWEPDTERLPRRCGAKRYVDAPNQKVSRGVPGRPSLCTQ
PQLMAAWHGPHRSNGDVHTKIEVSINRIAEQTHRVGLDALVPIAQTMVGCVLVRLSV*
>TCRU_481 hypothetical protein, conserved
MVCVRCRCWAAAICDCAVAVRGVAAVSLLLLPLCVDGELVCAEGCTQVTGVMAMMMTGRV
LLVCALCVLWCGFSGIAADGAGGVPDGSAGECLFSRWRAQLRRECAEEFSRRTGGRANAS
AVEECMRQRMDGVLAVVDGRRRWRRQRPAVAAAAENADELGTENTSSERNVLSGGNGSGS
EDAHVRGGIYFLNHVTVLYDQKVQHRRN*
>TCRU_482 hypothetical protein, conserved
MQRRRGVLHARDGVGGPRLVLVQLQGRMAWRVVSSLRGARHGCAARAGESRRRRHELRGE
PDADEPHAEHVEVAPLLRGCDIQRRGCSADVFPRQYAAASPHQHHVHWVHVPWRCRAAVC
WGCWCGRVIRRPDPREPDGDAVLCCCVYECPPAALRHRRHGG*
>TCRU_483 hypothetical protein, conserved
MHRGRGRTARRLQQHAVKHHSARQQVHAAANVHRRPARLQRPQHSVAHTQLRLQQRRRVQ
HKRRRHRVRQHFQLGVAHRPRRHNRRVTDRHVSVCRQVVHKHKRAVAPGQPAHAHLQAPV
TRRLAAVAPHVDLRTAVAHAVPQFDAQHAGKHRRHVEHNSHAVRDVHAVHQHRVHGAANR
DGSVHRAAPQSQHHRMHCGHPRRRRNQRQQNEQRRTHSRNGPAPHTVPAARTRSHRRPHP
PTHTGTNRAVALCRTRPVDHNSCLANPFLQMANPATQFRQIVISLLIILLLQVKPNTLKR
*
>TCRU_484 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGVCGGGLAETTQGLLDTASEESESPKKNKDTGGSAGTDGPT
AETKAPQAADRGSKEQEGTVEQAAASVPGVTGAGAGMETAPQPGREATESAKGTRGNKEE
TKKEEESEKELEEGEEEEEEKKEEEREKEKKEEDVTDAKKGISAESQEQRSLPSGAEGAS
NQTKPKSAQTTDVNDPAAEGAGKRKEKQNENKEANPKKTPVEATAMKTTTATPGDSDSST
AVSHTTTPLLLLLVFACAAAAAVVAA*
>TCRU_485 Dephospho-CoA kinase, putative
MLNSSRRLFLVAFLPRVVILGVTGGIGSGKSVRCTHLLRLAQSRARQPIYSFTAHTISAD
KIGHDIYSPGKPCYYDVIDAFGKGILHDAKSEEMSGTSHSSHSEPFIDRKKLGGRVFSEP
HSEELRKLDNMCWPHIHEAVEKEIEFMSRDAISKNKSVLLIILEAALLTESSLLSLCDDV
WIMTCAKGVAVRRVMDRNDLTEAQAEARVESQGSVEKKLDFLKNIKFKGEVLVFDTTNDS
LEEGLKRVTIAFDEYWCRKLEPLQKDPDEESSPW*

>TCRU_486 Nuclear transport factor 2 (NTF2) domain containing protein, putative
MTVGNERQQRVAASFARQYYTLMVQMPERLPSFYTQNASFNHMGHKATDIMEIEDAVSKL
YPMQADASVKIQSLTTQTDGDGHIHVMIKGSITTPPGMSQEFIHLVELMEHESHPGSFGI
VSDKRENTFSEEAPRRWALETPPMFAKEPAHGIMEQIEQPVSTTELAKIENATTKKDLEK
LERAESLASAKVASPVPAAGTTVSTTSQSQASKDVEKTTDKADPSVPATTTEVKKPKSFA
EAIMMSKRVGPSQGQTTLLTVLARESREPTALTPAKEKKKAVTRPVEKNGTKTVPKNGVN
KRTAGTSVPANDGKKNGKTLATGSNRKSNNSSEVNNKRKDADGRALSRFVVFYDIIVKGL
PTDATEQTVRDIVDPTAPTKLIKVLSRTDKKDPNVMRTFAFVQLDHNAIKEAGDDVKAAV
AKVLAAHKGKKSVAGHRIQIDEVREKYTAAPNDVAVDVSA*
>TCRU_487 hypothetical protein, conserved
MSSRFFQKYFLRCGHCQSIQRHAKGYRPIPNPILFDADAHCRSYHREQRECTGMSGYVVT
CRCEKCHRIHSSWEVVDFQELLDAKGSMSPEKRKALLWPLAGTSSATKMLK*
>TCRU_488 chaperone protein DNAj, putative
MWHGSRALLVGGAHRTLASSFSTQAAAGATAMLFQARFASASTNPYAVLGIKQGATKEEI
KKAYRVLARKHHPDAPGGSHEKFQEIQEAYDQVKSGIWIRRDADGGSTDARGGSDGGNRY
SNFRFTTRQHKSKVSYDEFYEEMHTGKVKKRPFEDDDDAEEAASKDPRRNPFAGNEALVQ
AWFRVIILWSVVFVSLRTTLFLTFPPKYESVRRAPMPERPRKPPPPKPLMNNSLVA*
>TCRU_489 Domain of unknown function (DUF4475), putative
MRRSAARGSAAEVVGPCRSRPQQQLTATPSHGTVVRSAPESYGMVVDSHEVHEEIRDLSK
RVKGVIEGNFQKNATSEGQVLQGIRRFGPSAQSKKILNRENEAAMLALKTGVYAVWRCEE
PKLSGANTDFCARIGYQHRCFCGHSLEEHATLKPSRGCVPAPRCQACACGGFNYVPNEPE
EIGEGWLSRRRSWDPLKWSAKCRCGHGHKQHDPQKRHCKECGCGGFTSHFLCAVCDRDGE
THSTVFELEQDRLKKGLPVREAFFPLMALDWSARELVFDDPTGGGALTAPPRNPALETNE
PSSCDKRNALQRIPLPKLRPTSEPTPLLPQHCTGCGAIFRSAQVKFCSKCGKHRQQNAQ*
>TCRU_490 ATP12 chaperone protein, putative
MRKFVVPRFSSLPYFLSVLLSGTRCCSSLSSSGNSGCSSNNGTASGPTIAPKKTKRRISC
NIDASSLLDRVPRDPGAHAELSTAELERKLEEWSNMNPRQLQELYDRLEKQEEEESRVLT
EDSLYQMDVSMRDRSRAAVRVFWKDVNVGPLDGHEGWYTVLVDGRKVKAFESTHVLAIPN
EAMAYCCAQEYAEQSGYLNKLLMPMTDMCSGALTVSPQMIAPRVDYLMSFYQNDNIYFRA
APIAEEQDRVIGPIADWFSRAFNVEVPRIVGIGHPHIPIGATLKVRDALLAMSMNPYQIV
ALCVAAQFTSSLLLPLAMFNSVVDLPTALSINSSEERHNTSTEGAIQGYHDIRDADVVTK
LCACAVTWQLMKGISLSKCLEVARINVENEAL*
>TCRU_491 GPI-anchor transamidase subunit 8 (GPI8)
MKRQMGVLWCCCILFFLLTTVDTVIASSNKTKTNLWAVILSSSRYFFNIRHTSNALTIYH
LCRKHGIDDDHIILLVGDSYACDPRNPYPAAIYSTLSGPDRINLYGCSVEIDYAGYDVDV
RRFLGVLQGRYDAYTPPSRRLNTDENSHILIYAAGHAAESFFKFQDSEFLSSMDIADTLM
MMWEQRRYRKVVFMLDTCRALSMCLEIKAPNVICLTSSDATLESYSHHLDPLTGLTVISR
WSLESLKLLEHAKCEVGPNETTALQMSWYNFNYGEERARLPPPRSVPSHFDAVNDPKAIH
KWKLEEFFCDRKQDPVPVDVQYDLL*
>TCRU_492 tubulin tyrosine ligase protein, putative
MPSGERRGRVGPVRFRTFLRNTVLDVMRSRGWLETDSDLGWDLFWADVGWIREVHDHVRL
DDVQRINHFRNHFELTRKDFMVKNLKRMRKSLEREGRVEEATEFDFFPVTFSLPQDYGMF
ETEFRRQPNAIWIMKPPAKAQGKGIFLFSKISQIAEWRKDYKQRQVGAVGEKAGGPYGAE
QVEPYLAQRYIENPHLVGGKKYDLRVYVLVTCYSPLTVWLHRTGFARFCHQRFSLRDIEN
TFIHVTNVAVQKTNPKYTPSSGCKYGLRNLRQYITASRGVETAQKLFDDIQNMILRSLHA
VQKIIVQDKHCFELYGYDIMVDNDLHPWLIETNASPSLSAETPADYHLKFNMLEDMFSVI
DIEKRRTGDEIRVGGFDLIWKNGPVGPACRGDAKGGGVTQSFLGCANELEIPISHMRMPP
RLQQMDSSERLLT*
>TCRU_493 hypothetical protein, conserved
MDIDVLAKLAEEALTSPDKAVRDRAAARLRFMNRYEHWEEVKRLLPLCQSNYLRFIVCKA
MQFMASNELGPNERKKIQQYVLDYLTMMRERGEELPLYIKNEVYSIYACALYVDWRLQIL
STDQVPGPIGIYISELTSRFPLSDVLDCILEVLTYFAQKEANDGLDRMRVNFVEGFIPRV
LTFVVFQFSYCLKSALELCCIIMEIMSTRSPAPITVKNKMDGSIFLEKGEKWFPALSLLV

DGCIQILLTYQSLDLRGKCVRFLRMASSIICVDPEWLQSQNKLSDSFLELFSRLPSMYKS
SGLPQLLQLGCAVLVNVSDRDEGRVSNYLLNRPYLIEQWEEAVIGVLERWEDGEEELRQE
LMHLFFLLGDRVIPCLAGEGENTREMPIMRSIMQVSRCYFDNVVAKAHLAEDSYEARSDL
GIMLHNEKTLLPIAEMLFCEKIDIYGIVAQRLRSTIEQYELCVRIRETGDSDGMGDLLLS
LAVNVQAVFPTLTALDAPLFLMHVCLSRLSVIISTVAIAVLNNAAHQSDELVGILARFAR
ELLSVDGTLTSALLTSLSLVDVEDDDSQLSSTTGGGKVHLGILRALFFFCVCLYESFSEP
SSEFYEIMISLLCYVYLHHSEKACLTHDANLLLNRVLMQGVCGFFLSSEKMFSILMAMKE
ERIELLRITSDKLTDEGRKARSRMLSTLTSFTECRHYAGFPTLDLISCIVTRSLDVDRLT
ADPHSVFYDLCAIADGINQVESLYCLLDALLKRSQEIEDLLRALPANAPLLLRLCAKLCN
LATRLFVEDNKCETRWGLVGFAFRAVHGVMHTLGLSGSNWKGPIEEIPPGVVSEIYVYDV
ADIIYSMISGEWCNLGVALFYSKDFIFLYGGFLSLLFSVSAELVMAHKNSRERVFDALMK
SFLSSGNLGIELKEFLDTHFVWKRLLKYFLNCLRYSFLPVIMLAVDAVFTSLGNTSVHGS
SFLEDRTIGDLFEELAVHITIAPHMERNEVELCFKLLTNCMQFCGIVCTERMEKLLDFCT
AYHRVRLRHLFTVICSGKEDAPASYTTVFGRESKVQTLSAW*
>TCRU_494 hypothetical protein, conserved
MHLDSDDARSALRRRLRNVMRVIDETLLLHGRYASLSFLCGSANDAMEASGTFSPVPHAS
VEAGSFLEQQRRELRAEREDAQRRLAILKRARERRGKRLDVKSDRLDTSGPLTLPSHSGE
LDSQPQPQPSLTPASLSTPAALDIGVNRERREREGEMRRSPPRGAETHVAVMEETLRTHL
SERRAEEESWLKELRTVRRSAMAARQKALAEAQAQIKRTESERVAKLIQIESEMKRAVAE
TQQLCVLTEEEVRAIEVHEEALAVLRACTGIKAENKSPVRPPPPLPPPVVALLASSDVSS
PSNGGASPKKIRSPSVDRDSFATLSSTPLLANLLASPVEPVGTSPPPPFTSRNTVASSSK
IDISGNLSVAAEGIPENRISSSLFPVSHSEISSPLTFNNGKKELPRTCALTRLSRARPLL
SPSVTLSPTKQLSLDPPVNSLLPSQALAVLHKRGILADVLPSEGRKIPALVQLSKDRREV
LLLVERIIRDLNGLARKSSGREFQASVTSMPSHDKQGVQQFQTEMGPTQKKQQQQQQQLE
NREVDRGSTRRVREIHHFSLMDGLLLYPLGTIGSGSTGNISCILCGAHARQLLMEFSCTL
FAHDDASSYCIFFISQSPPHHTNGALGLPLSHRRRPIDPNGAAVLVLRFRCRRDWIAFLI
AVTDATMQLRQTSPLSYGRALWMLAARLWLKHRSDFFVSPPTKHHKIPPFSALSFPPALK
GKSVSSAGAASGARERGKSLRTASGRFAVPLSCDSYDTNGDVIEIGHVGGNKFFGGDGVL
QNVHSHRFGVRPVADSNGSFSRHCSLSATCIGGAH*
>TCRU_495 UDP-galactose transporter
MPTLQWASPAAVSLLVLVLQNSLLVVMTRYSRANVPPERQYHASTLVLNQEIVKMLFCII
IFTVENYLCGVPLLELGKSSTAQSGVPQLLWGVIFQKETLKLAVPAALFTMQNYLTFIGL
SELDALSFQVWSQTKLISAGVFSLILLGRRLSMMQWLSLLVLTLGVLLAQLQNGGGKRPN
KLLLKEQRPQRPLLGVTSCVLSGLSSSYAGVYFEKVVKTTAPSLAVRNIHLSLFGIPFAA
LSVFLLDFLPTLPAEGKHGQAFHFWRGYDQWLTIGLVFIHALGGLLVAIVVKYTDNIVKG
FATGVAVAVSGFMSFIIWGHMPSVMFVLGCVLITAATVMYHFFDLHVPTH*
>TCRU_496 hypothetical protein, conserved
MQRTWLSSLEFSSNVAAGFFIVARRLFVQGGPPPPKLHEGIEPMKKLHSHRAEMDARYAA
EREAEREFYARTPHIPSPLPHNSHEKGKYGMRRRLKIHQAEDDISVESLSEAVETGNHAM
RKG*
>TCRU_497 hypothetical protein
MNEIRPQSPRVQFAKVHNAVVKGNAERLHKDPGIQMLGHHVLPVFPPGEVLPRSVNENDK
NHGDEDRVRRGCLGVAWRLADAGVVKDKRTAVWPYEDADECPDKSKDDTSNVIKHPPPPY
KVHFA*
>TCRU_498 hypothetical protein, conserved
MSDSESIVFREQTANNSLQSENMQDALIQSSQMPSASPALDKPPLHHTNQRGSRTITQPR
PEAKHTKKSFAAGERSHDDAVSEHSQSIHFSFDGAEHNASIASRASVRRANGLQPPPKRG
GGHLELRSTHLRRSGSQRTDSEDESIQFALETSNSHARPKTTVHSEASPNDSIFFHVVDD
TRTDGANSRASGNPQHDASTDGIEFTVLNETEGAAEGSLGKSVQTRTDAEKGRGFELPVE
KKRLKKTVLSNRLRHPPTVLLRSGRVSNPPATKRSNGRKLTENIPPATLSPAETGPLDAP
AIPKPKPLEATEARLESNRMPPTAVSMSFKDDQCTSKATPNELGNILFPTRRSPSTGFTD
PIGIKNASTAAAKKSTEGSPPRISIEVPSPYPRPQSEVMQPSHSDTLDEWIFQAKLCTEH
WRLFNDFQREEILRLIERIAKARQPDSFLQFIDTGVKERKPTQAAPGGFANLYKQRVFAA
QNAAFCRGKSNTVPSTIKLAFKVPPRARSATSHGISTCRSPLSGRTQDHRPPVARPPKTA

EAGQLTAAPQRPPHAPSRRSAGGRCLSLFQDASSSDGVAKLAQTLGVVWPPWSPDALFFV
SGARLTPQQRDEFYKAAELQKAAFAKLHAELQHSSAAQKRETKGARQKKVTLSRTSILRK
AFDLMDVDTRGIIHTADLPALQHLLEAERQELETKAADGVAASSFLTRARGEQRILKGTI
DSKRPATKPEDDATSIAKKIMLHGFVLEVIFPLIRASNLVVVDFASLGLLVFGSLCLSQK
GASASFVKWFQAALHYFEALA*
>TCRU_499 Protein kinase domain containing protein, putative
MRTPYSSATSLADRAVSPSQCLYPRTTARQIRPLVLSPMTPVDPKTMSPHCPESPQSLQS
GSPESEGIGRTEPQSLLPTFLAADFDVVDVSARLENEFFSAAQSAELNGSRSRHLQETIN
SHENCSSAEKLLHRNGSCCRVDVTEEMTQVFQEPMTPLREASSLIEENREGQDDAEADRA
SNSPFSVHTPPENIIRSSLMLTPPWTPVLATPRKSAKRPSPQTFTPSAHRRGVSSHNLSM
ESREVFGVLPHITHADYLPPNRNPCSPYLEYADERQLLVQLRMEEEEEEEEMDGGLISIT
DGMLQRADAFAILLEQTVPIASAVRTERCWSPLLHKAGKGGGGANTFPNEVREENDITGL
SPVLVEMDSAMRRNASTAVETGDVSSGNHFLDFCGFSDDGTSLGTMQNETPHRLSREAGD
VACDASTRNLTDGQTSFETLPNKLLCTRVFYDRRGQVGEQTSPPSNSPCILHNAAQWDRT
VGMHFSRNRIHETGLSFQPSLLSSSLSIRGDSQTCFSADNSGDLPSQLQFRNCLSVHFPV
KFDFPTAGYPVSDAEDEIPRGHVNSKEEEEEEEEEEDEEFEPGDRFCNHHRYQFLHWLHW
RKAYDFVPNHLDRNGVVWLVTHRVDGLPYAVKEIPGTQQNTLQTELECLTLGNASVNALQ
QQAADYITRYFSVSPYSVVSCDSHESMAFLLQTEYFPMGNVMEWALDPHRLRGKEFRVPP
EDFWSCVLQHGLLAMESLHAAHIIHGNPLPFNLFIYSPRHYKLGNFGSAVKFPSTYPVGS
PNVFLPSNMADGSPWTPYEMDIFLFAHSMLQLWNHCIDKRKLVSNAVQTFDHDSEGTLCD
IFMKDAMCISFSGFQEDRVKGYHEISDHLWNVLQAALRRTPISTLLRMLEAPSRLQWTLF
SLFDTEEFYLLRRKRRLKRMLEERLQRKAQEKVKRQSLPSTSVNYVDDPVILLPPAEWSC
QERTAHCCSDVQIRGSMSTAAPPLPFQLPLASNTFASLGNGVALSPGRGKNESCNHRDAA
CNRHGRRLFNGPKRVKEDTPLSSCDTSVASYSPHILHATKKFSLLKDKNCSFNYLPEEDM
DNKSMLKCAHGGRPPYIRRRVDANISFANRDRLDANLLWTIRQIMAVMNWEDALKGIALH
FDEDVPARGFFSLSRYAVRPLTSWE*
>TCRU_500 hypothetical protein, conserved
MNTDDGSSIQYATSYQSSQAAHRAADAPPDLSNCPTKSSGRAMELIRKRRSTVLRRNTDS
SALGQLYEESKRGRSRDVGAVNVGAWNVPSGAIHNLLPHARTADERGELCGLFDGNRSGA
IDPTAVRQDSAVYVGNGSNPAGNDDSGVTKKVAARSETKKEMNQLIRSRTDWKERVVVRL
AWITVSRLFEIAVLTPNNFTLKADGALILDWSVAPKTARADPHRASRFFRIRWQDAFDTI
KLCRTLQENEKLTNLTTAQVERALAPWNATVHSIKRGVLRHAAQIVEAHDLDPHVISQLA
KHVDPFDLPQNTV*
>TCRU_501 hypothetical protein, conserved
MDAAVNKPIANALLYSDGVLHLVGAMENEEKSSLFPAPLTEELQMITSIPRNWADVDASF
SASPVSTVGLVGYLSNAGTANTCIDECRCVIATVTNGKNVTNGLQFAGQCYP*
>TCRU_502 UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase,
putative
MLVLYVLGRHPSHGYGYSAALLEEAAQWNDVVALPMNEGRVLPEKKVGVGGDSGIEASIG
MTRKTYMWFDLAHRLFPNARYIAKGDDDIFLRVPLFVAHLRLLPRRGIYMGVHAGDSFLV
KKCFLHVAFIVGYCYTLSRDVAEALVSYEPLRRLAYLPYSKERDDEFALLGFLYEDVMVG
LVLEKEVKYKPMLYVKVLGCHFHDARNGTGHSQVVPTSMCVHHVREDDYAALMARFGNDT
SPVARVERVSDDVVYPSCD*
>TCRU_503 hypothetical protein, conserved
MSPATGRGGAGGRYDDATVVPEAYDDDVISWGFCVSSLSSSSRSSASSPPRRGSRSSCQW
RSSAYHTTTLYTVTASSTVVSSSTMAAYALAPPSLGTRWLAALTTHSAASSTKLAVRITV
RKDERIMFVKATTPAPASSTAAMQKYWTWQPPTGGCTAAIRHTTHSTDSWNTHQYTWLPL
MFVSMPPYIRCCAAGCQYPTGYSRRSCSGFLENCQYLVKLAPVWRAMK*
>TCRU_504 hypothetical protein, conserved
MPRCIVCATTYVRLGKRIAAHALAASTPRHRWKAAVTPQCTQPNTAASSALPTTIHSGSR
AANTDRKYGSATVLARSCAEAHDILANTPSACISRTEPSPPVTTTATAAAPATTPVIAER
ALAAAGSVSDLIVKDPSSTPLQPLDTAAASQRMTIVSSAPMK*
>TCRU_505 hypothetical protein, conserved
MSLCVRLPPAAVVVTASVGHATSLHHSVLLTDAVGVRVGNSATVSVTCSVSVGPYCVLLR

LGVGVHVEVRLRVSVSVAVWLSSGIAGVRLHPSTCGRYTGRQSRPYPPSAQRQTHDPDID
IVAEAKQRTSASHTLHATGRNFPMMPADLYSIGCSACPLSVRHPTTNFRPAPTSATVPSI
TTGPLPAFP*
>TCRU_506 hypothetical protein, conserved
MLLPRTDSHDPDKNDADPRSSSSAPSVSAPALSFTTTADALATTPLSNTNPCVAYTWLPD
TRSTAPPDATTRALAYNAYSPPSTAASSATPPPTSSSTAPSTTTVRPPVTTVTRATPDTT
STDRTSRRPDSTSTGAYGEDCEPGRYTSGVGLVATSRESATVSTDPAGNVPVSTSAPFSA
STSHTDSSTGPPSSLPAVPAPRSAPPPITYSTAPLRNDTFCTTIRTPSRAIHGT*
>TCRU_507 hypothetical protein, conserved
MKRVAHHRKQGVPQHPQRRSNKVNGARRCRHALKHIAAQHHRGVIADRQLIHRNTRRAVN
VQTLPRDQPRDREAVPADRDVRVRWKHTLRSEQRVTERVAGDDNVQRPHSGVRVAQQQQH
GAVPPRASIKPDIRHVARHRSNQHRQAHAAPAERHVAVAQPRQPAAHSLRNLGVHHVADA
LTNRRRRWWEQHWRWRRASRHRRRDAHIAVPSSSALAPAVNNRRRQRSKAVALLRALSAR
GNSRHVGDAVKLQFCRRSQHTSRDRQAPSNEKVAGLYQRSQRLRQPHQAHRAACQRHHTA
AVNDKKSGFGFVKHRTRSHVVVTPIQPA*
>TCRU_508 hypothetical protein, conserved
MPSGKATALAAATLLALLVVAPAVASAQRSLDCQKVWDGPSIDNDVLKCLSNTDRIKGQW
RYLVYPGVCALLFVVTLLSFPLVFLSVACCHSCCQPKPGRSSDASRCFLWMWVIYVVLWS
AAMAVLVILGAKLLATSAPSIIDNTLDGPLQYFNNTAERIIDFTSNWSSGKREPIPSIDL
DITAFTNISTNVTDLLMDAKHKISKYIGWVPIVSYCVGGVGVVLMLLVVLLACCRCGIPC
TTYLFSCIYWLFGVVFALLAVVVTVLTYLSWAACGEVELQQQRQPGVFQWYLVPYCEQTF
DFSDINRKADDAERRFSEDACKKLLKSCDNKPNLFKPLLCGNNITSEDQCPNFGTMASVL
SATRVKAFTMACPVAGESCTLFECAANCTNTDVKAVASVILQLAAQASNASIALSYARPL
LDCNFVVDKLLGAMSDCNELKAGTLMLGTGFFVGGLMFGLAIYIMFRGSCIWDARSIKQG
RSPRGLNGSGSVNAAQSS*
>TCRU_509 DNA repair protein, putative
MRHHCVTHNELLARHMERTWPGRFSEFCTAVRRYPLPVTSGAAATVLHGCSTDAVRAVGA
YCCDVQQRCQAPECAGAELDLLSPPPSPSWADDHAVAMHSPFRCFKLRRLESSVSHGAGD
PSPLPWLFGTGAEDGECFLLTPPDLSHSPRREICAGCPLPPITRRDADAQPTAEKLSLRE
LRSRCASRGLLTTGTKNVLLTRLRQHGVSQPTGPVPWSERDGEGQAEQPVESGECGGALP
GRFMSTHEEQLEHSQRLRTPFRSPSTSRPSSPRPRDQPRIRRLVGTPQEFVAAPRQEAKR
EDRVGGSLAHVASEEKVSRYQWRILVDNRERIHGAHGRVIEAFTTAGVPTASCTLPCGDF
MIGIDMPGDSCGSHASPPTARELDSLGATHSVPAAGECGDAPAQRLFSVVVERKTVKDLC
ASIATSRYYEQRRLLSVSPFRSVVWVVEGTTELLRPDERRRVLSACASLAAVPRFRVIRT
RHLKDTVSWLRSLGVAHVTALANAARSGARPPQLADCATCLNVTARIKRALRARTTFARM
LICVRGCSSGFATQLACKYGSFLQLWRRLRCCGREACDADMDVRRLSSTQRDVYVRLTEF
LLAEEYC*
>TCRU_510 hypothetical protein, conserved
MMVPNASKKRPSFANGPRILVASNASGIMSVTCGGREHVAADNTDEVNERSATGHKTLVL
ENTVAGSGFVAEGDADGLTQRNASGHDSKPQLREFTAQ*
>TCRU_511 hypothetical protein, conserved
MMRRVFCVVLALTLLCCCLCVFAAEEEVEEEVLPVDAVCAGDGENVGRWQLRGRPLWYNC
TAEASGLGKMICGMGAGNCAPEDVKKRVEGNAKDGVFEIKFHTPTPGRVKSWWESNVEPK
PATAASGPAKPAEERPPVDREEEAPRDTTTISSGSSPAGVGGSAGALSLPPTTPRDAGAN
AAAGAAGKTDPSPPATLQAQNPAPSGELQGAAHSASAASESPPDPEPTESGEHSSHDPPA
GRQEETVDAPPTRLSQTGEDGGAAEGAEEDTANTTDAATSEGNATAAGMPGPLSSAPTTR
ALENSAGNDACFHDPRLHTRLLLVLAALTYGTLG*
>TCRU_gamma, conserved domain containing protein, putative
Elongation factor.1
MASSGDDSRCAPGTHPHTIPCVSLRELDELKIDYSHTDTRTVAAPYFFQHCDAAGCTTLW
YNKYNKMQCMTANLIRVWLQRMEHVGQYALGAALMFVEQRRHDIVALCVLGGRACRRF*
>TCRU_513 Rieske-like [2Fe-2S] domain containing protein, putative
MATTGRFYVGPAASFKEKSRQLVKCDKRNIAVYRYKDRFYALDNACYHHGGPLLEGDIEE
MGSHPCVVCPWHEYRITLDTGEGLYWALQMTPEGVPDKKAPQKVCSKGMKQRTHIVTVED

GEVFVTLNNSGPRLASDNYAEMVIANMQGAMISPLEDSRRTHRSMNGLGAGIHSGVRSGH
VFAGMVTGNRLQRFSYLNHPILTCVAVEPVCDDTQEYYFRLSEGELDTSSLVPGQFVDLK
LPIAAPPGRHFVRRWTMVELNKEGCDFTLIIKTAEHSNGGTAWMSNNALRQRFSLLHYGG
SFTLTHHMSRLREVGGRVVMLSAGIAMTAPYSSLRQEFEGKRMQGIPKLRIIHLHVERRV
SCVAKLEDFVRWHHSKTEHLEYQFHCYLTKQQELSAKAAGDESLWSLFTCGRRPAEKDIQ
SFVGDFLGPSSSVLAMVCGPPPFVRMAKEVLLACGVLPSDVLTDEDDDYNSL*
>TCRU_514 translation elongation factor EF-2, putative
MSLETTAYLQRLSEKPERTRNFCMVAHVDHGKTTLSDYLVASNGILSPQLAGEVRLLDSR
PDEQERCITMKASSIALRHVHKGVEHLLNLVDSPGHIDFSCEVSTAMRLCDGAVIIVDVV
DGVTQQTSSMLRHAYREGLSMCLVLNKVDLLVMVQQITPEEAYYRMRSIVESCNAALAAF
ANQLKIQEGEESFMHQDRGDPSDDVWFCPTKGNVLFCSCYDGWAFTTNFFASLYESKLDI
ANLHASLWGEYYLDAKTKAIDITPRRAGQQPLAVQLMLEPIWQLYRTFLGEKDNVEVQLR
MAAKLGVPERLWNNPRRDQRGKLKALLSSWLPLANCVLSVICDKLDSPVVAQRRRLPLLI
PRFDEASSQVKDALINCSNSPDAPCILYVCRLIDTQFLVGKTIGQEKDRDDAFIGFARVY
SGRLIPGQRVHVHSDEKVVEVNVGKVFLFRGTGLDEATEACSGTLCGVGGLTSYITKYAT
LSTMEGVPPFKPLVLQSTSILRASVYPKDPKDHLQLVKGLQLLFRVDPQVEVSILPTGEH
VIGTAGEVHLERCLKDLVDTFARVEVLASEPIVSFRETLAAGGASMKPKLHTGTTADGAF
SITLHARCMPPDVFDIIKDDCMNHGSSMQVQRQVETALMANKRWAAEMQKGIVASGPTKL
RFLGALLLLQFGDDETSLEKLRLFEDWKDSIIAGFQAAAESGPMAQEPLLNIAFIITDIS
VDTSSGLTGGMVLPCVRDACRAAMELHPRRLVEPVYECTVYSFGATQGKIYGSLSRRRAE
IIEEVPNEGSDLFYIRCLLPAVEAFGLQDELRVITQGASTAQLQMSLWSIVDADPYFTPT
TKEEIEEYGNEVVMKNIAGQLLERVRRRKGLHRERVVENAEKQKFSLKGA*
>TCRU_515 hypothetical protein, conserved
MMRKTPMFAVAATRKALVGNGPTFSTGGECMNTCDIQNAFPMNERGVRSSSPFQEPNTAI
YDTYMSWTYFQPIDVNIEKLPAPEAKYYQRHTKRPWDISTTELIEIQSRKKYFQVWGYLI
AFIYLYFLMPKEKSFSGLHGPDGHWIMLPKSRPELF*
>TCRU_516 Snapin/Pallidin, putative
MDEQPDDAMEKQRVEGSHVSEATALAENEESHGAWTPPQETSLVPEQLLVALRDGVFGSI
FELLRGMQTQQNATLQTIEEVKAELNETQEQMRQAGEIFEKLQAYTQKLHVMRDNMKVLD
ENMAKTKRMARGIQERLEKTAEWHGE*
>TCRU_517 hypothetical protein, conserved
MGKGGMRVLEDEKVLLAELGKLFHMARANAREQRNTHRAERRRRKATVTTTTPTTTRGTK
TTGAKKDLKEGRPPRTGSKRSRKTSTRGGSVWVVLKGGFAHVPTSEKTNKIAHNTVFRGR
LSERRRVQALEEAERYIQTAWQQAQEAGLLLDDGSGPNGDEGLQYLCEQYEVAAGMLRRE
PVGAFLKQIVDQTIPSGAPMSLTTPAPTFSSVDNAATSTKLSRDEWVGVIARENVILKRF
APRASKQEEEKEEAEGHGESVLHEADQLPSLYYFPIAEPLASLEAASAVTGMGLRETSGD
ARGGEQARDVLPTKCIVRIRGSGRQKHTAILTSTKSVNYFKSNFMQVIRRELSGSKLPRG
EDAVEGKQQHQPVSNSAGAEHAAAGSSKRNSKRRHK*
>TCRU_518 hypothetical protein
MEGYDANTDSRDLRFDDDEREVEKYNTTLRPNEVNASMDQVGFNDLSMEEMREGQQVASK
ASPGVSPRSASEGFFDPEGTCDYPTTMASRKTSQGNPTHPQELNQATNAQQPIDWNLLEQ
MMMMDPFKEVMCPPSCTFSVYDAEIQNHYNIDSTQIVATHGSVEYLKMNEARGAQSRFRF
QLCKRYLNKRCTRGANCQYIHTHLVPPPTSVHVNENVISAAVVEGLEMPPEVLRGGNNKH
GYPTMPSGVIFRVFPPNQGKSVPQLIPSEMILRTAGASNVYSVFAYPGTGKARDMLTTET
ADTSGSESGNLTNVKARHCAHFQFNKMCNLGESCNFIHSLVPYVQRLSMSSQGPLYNSIV
TQRPLLMPSTSMAHFSRFSNGNNNNGVVSSYPMEFMQPSMFHVPPQTQQQPQQQKQQKQQ
KQQKQLHQQPQHAMPPTTVSHLIPSPQPSEHLMYQSNMSMMSLPMYMSSPVSSTWDGVRY
GANYQ*
>TCRU_519 amino acid permease, putative
MEGLPQISREGEQSSDSAYVVSIERKKERASAVNGALSPQQECGKSIAGCLALLLGAVIP
HGGLLSNSFSLASASLGAGVITLPWAFHACGILMGTLYLILMTVFTVYTITILGYVMEKT
GYRAFEQMSRGTLGKGADYLMAAVMGTSCFGAAVAYVIAVGSLITPIAQHSTATPEFFKL
KKGIRLLVCLVWLLGMLPLVIPKEVNTLRYFSAVGVGFVVYFVILVVIHACQNGLPKRSE
VQIVSTGNIGMEGLGTFVFAYLCHAVAFQVYFEMKARSTTQLLLSATLSMTVCSVLYWLV

GVFGYMEFGREVKESVLYMFDPVGEPLMMVAYVGLIIKLCVSYALNMIPCRNTLYYIIGW
DINNISYWKHIACVTLVSTIVLVAGLFVPRISTAFDLAGALCGGFIGFIYPALIYMYSGG
WTLKRVGWFQYIMTYTSLFVGVICVVFGTGATIYSNFG*
>TCRU_520 KIAA1430 homologue, putative
MPVQPKPTATTLWLEQQRQREYMQHRRRVEEQTSCIDNKPPHALSLSNKRALMEQERCKR
IEEENRRIVHNMTIIMKRGGGIDNKEPWRSANAARDAERRRRREQQRIEEENLRILKRLQ
KTKPAYSVEKWESDRIQNEEYIARLSRYTYEPMGSRRSERE*
>TCRU_521 hypothetical protein, conserved
MNRTDLNFVPLLNSTRRDSVACNKMKRLTLLPLQHSVITFGSPRRAPNFVPFSTVVEGNR
TGEVRLSDSRGIRRSQEEDVATEQKRVQQLSLELQRALDKLRVKNKEERKLRRKAAVAEL
KLGEEVERRTSTIDDLLELMQIHTDFMRGTNAELRRLLQQAAEEHDKTVIKLREEQEARL
GQEEVQQRVSILQAENKVLRQQLEEAQRAKVGLEELCKRLQEEKDKDEFSFLKVKQQLEL
DLMRTQAQLQGVNRELAEAQNSITASDTLMQQVRLFMQMVCQPDFYVVKDRSLQPVDKNR
PEPTGFVLVPLSILLQGYTLLLPGDRQDLIESYRARL*
>TCRU_522 hypothetical protein
MTIVALSMTDLKELPALLERALSSENSVRFQAEKEIDRLTLFQGFLSQLSHYAYLNLETV
PRSHRLLVLTVLRRKVSLIAIEECFEVSKILMDLFPLEEDRPVANLSAAVISIIVSRMES
IKTENMVVSGSLHFFVKWLSDEFFKFNSNRHELNFMILLSELINHLPIGSITRNEIFSLT
PRLFQIVVSNTPREASYLAVNLLRELILPAISIREFFLSGLIKKTWENFFPALSGALLTP
FFSSKGEPEYLVRNRLTLGITALFNDMLQVDKWTRKRMTANIFCGLLTRIEADNNVYMET
LENDENDDDSILVIQQIAAKRWELLGFMVHLKTLRSDLGKAIINNLSSFLNVVLSHTMLC
DKEAEEWLIEANDFLRKEEEREDEVLWNVRDTAADFCRICVSLLGDGGEIVRALLEFLIS
AEESWKKRESILFVLEVLLRRCPRETILRGVGCHSQLLQVLLEKDIKGPAILSSRALSLL
GILLSMMKRERIGAESLCASLIPQAVVSLSSSVPLLRAAACKLFHRLIPLAHVDDALTFF
SKGQEALFSLLLNESTSGELLYVCLEVHTEWIARCHSKRRDVASSESYNNLFLCWRNHIR
DPNMGELVVSLFGELITEYSGDEFLTGHFSWLADVLNSCCGTAEYCVVPFVVQILTCIFE
KGSDEVARKGAEFFTGALCRLLLGTEESSIISSASNCLAALLQRSPQVGAMKVLVAIPSM
EKPFSVLNGEKLSCSDLVEIPTLQRDELKPHPLSSVLVTIAMKMLGEEIKEALLMNVGGV
LVAIAQNTSVFQDDEIEILITTIVRRLMRVRTDTVTQELVFPLAVLMKLHMHAFINVLWS
SGILIEMFSVWLPKMSVFTVKGALFHSCDALLDLLIQCPLDERLCGQLLAWIEEDCKRGT
LPLDVALFVAVGKGLLNLATPVSLDYEEGEENEEMEVSEEEGENEPEEDQENKVVEQDAV
TGEVSHELRYLLQKIYPLVTNYGPAASVCFSRSELKNLSDLLDAVTASS*
>TCRU_523 phosphomannomutase, putative
MKKVLLLFDIDGTLTPPRLSQPDEVREVIRRAKSVGFTVGTVGGSDLAKQIEQLGEDVFQ
QFDYVFAENGLLAYKHGKEIHRQNLLKELGNERIVKFVRRALRLLSELDIPVQRGTFIEY
RNGMINVCPIGRNCTQSERDEFEVYDKEHHVREKLIKELQNSFPDYGLKYSIGGQISFDV
FPVGWDKSYCLRFVENDFDEIHFFGDKTHAGGNDYEIYTDKRIIGHAVKSYKDTVDEVNK
LISSK*
>TCRU_524 TLD, putative
MGQRQPVEGQGEKAEVHGEEHEEMPTIIHAFSSSIVSNDRCSPVNSTACVAPRILGFAHG
EELHRILPESLSLIIFNALPTSCWPVSPQQPQWYLLYSSRIHGRSFQKLVQGLVDKGPTL
IVIKACESSNVFGGFCGDPWQTVAAREKQERSRSAAARRATREGQGAQGITCRPANQNSA
FFGGENCFLFTNRDGGLIYQSKPSINSNFMYLFDSHPLVDKNGVGMGGQPGHFGWFIDRW
LEKGKCCGVCCATFCNPRLTDTEEWTIDGVEAYALHPETVESLSKAPRKGTERNSCLQNP
ANDADKLLLGLHGIYDFDSQEQPEC*
>TCRU_525 Guanine nucleotide exchange factor in Golgi transport N-terminal/Sec7 domain/Domain of unknown function (DUF1981), putative
MSKSVLQVIARIASLCKGRHAYLREVCLYTPGALEQTGGAGAAVNLLFYPLLIASYVSNE
EQMFLPLALEGILCLLRLHIVSERTMYGPPEVPLPEKKRKGLFATTDVTAPGEGLSFNSA
SATKSTPLTDVILDTVKRHRHSVLEEVSFLVLQCLTELMLNCEWIKGSKLVDCFQSAFEA
QLEVRPMSGSGVSNSLLPHVLSRILAGHRGANSVEQKRPSMDTTLSCSVDSTMGSNEKQS
TLDKCNSLINSMNITIAASSTDIVANRQHSAGEEEDEEDQQQKQQLTLSDHQDCYALLVR
ICDLSIKVVESRTPADSMEWRRKRLSTRLLAHFINGVNDEFARSDFFRSALHEKVTLSLL
HNCALEDPVLHGVALKTLYQLVMRYRNLLKSKVVIFILGLLLPIVNSKNTSYEQKATILT

FFEHTLRDPQLLMDWFTNFDCVQGMPNLCEQLVSGLSKMSKMSHMSSWVNAKQDALLRLQ
CIKALGTFVRSLEGIAKEFPMGGGITPRSQERELESRENQEMKLVAAENEKGETGAHSKN
NVNSGSLSECGVEQLLRGKKAFDAVVDKFNSGDHAAAIAMALNVHLLSSAAPEAVARFLL
QKELDPVGVGEYLGKDNEERKAILRAFIGLNDFSGLPIDDAMRLFLGKFKLPGEAQVVDR
AMELFAREYCAQNPSSFFGPGPAFILAFSIMLLNTDAHSSHVTDKMTLEQFVRNNSGIDD
GKDLPRSLLEGVYQRITAREIVLEARGAVPSNGLRKWSYGTKDMHPLSSSSSLSSLGARR
RNHRSSRHMEQAYLLETSVEQITRDVSSEPYTSINSSELVGALMESTWTALLAAFSIPME
EMENIELIDASLEGIESAIKVCCKFSCRTQRKAFISALLAFTHLTNFREIEYKSLKSIIA
LTRVALEEGDHLETSWYEVLRCISLLSKLHILAESPWTSLLNDRNGNHAAPKAPNTSLEG
QGRSSLQPQWERAKLERQNAEIIAKYIDEVEVHRLFSRSNYLKDAAVVSLVEALCLVSAE
ELAENPPRIFSLQKLVEVTDTNIGRLRYVWSKMWTNVSRHFVKVALSSNELEPMYVVDHL
RQLATKFLARGELGDFNFQKGVLQPFEAIASRTQSTKLKELLVASLGQMVEAQAQNLRSG
WGTVIEALAHCVQHDTNPDVVSSSAFVLQNITLCHLHLLTTSDLVKIVRAWAVVARSAFS
DDFAHSAVWFVRYVTIALALQADSNSSCEGVQHSHASQCGTSSNGEKEIHVDESHSHAIK
ENNKSHSLLLKEEIKVLALRAAFPVDGDDNNKVERGRDRTKENMQLFPVAVGALASLLVH
RSISGEAMEAMLFVMTDHRAVFTPEEWWHTVGSGVAPALDFLLQQCRFSNEAERDVWLSL
FKRAVTNVVQFVGYNLDGNPLPVDHVLFLFRVFVGRACCGSHDKATELGLQGARQMLELF
KEHAVVDELLWNGMVEYIQEIGDILLGALDSIWRYPMDPTQQDTLTPTLLALLQYVKWNR
DAALTPQLTTLCRTKAVKVLLKTLQRFMCLMRTSISFRDSVTEKKDVFDLALFIALECSL
CNAILDAERRYGEILENESNTLWMLIIGQFLAVTGKSSNVSREEASSLRGIIRELLDAML
EAPQRVMMARCRVCMPFLCQLIALSDDVFAESLANLFLRYHTATVQNI*
>TCRU_526 LicD family, putative
MAVKKGKGVARASRFTRALLICIAAFLLVTLFLLRSLESWDGHASSSSAAAAEGGLSQPT
PHARPPGSVTSGENAPDHAKMSRPAGTEAMDDDGTLVPLRDIPPSPYYAFGPRTMPRAFL
RILQNSSRRINKNWIRSKFNRYDKANISDCDVVTPECGLHKYLIKRTGDDLNARPYRKCC
VEHKALLETNVWVVRKLNSANITYFLSTGTALGVRRHAGSIIPWDTDVDISVYPGDEKKV
EQLLQNNGEHYFRRDWKGRFMFWVYHSKDGKPQTGPHVEIFYDPVYTRFPHLLLPLEDCL
FYSEPVKCPNIKQFQEWFPSGWTVYSGAHYHSPEKCIIYVNGMRRVTKRC*
>TCRU_527 DNA mismatch repair protein MSH6, putative
MDDALVDCADVYRMEYTYSFLAGIDPMRPPSSITIPAKELDAMAGMERQYWEIKAKYFDV
LILFKKGKFYELYDQDAAIAHREFGLKLVFSATNRGKMRLAGVPEQSFSEWARLFVFRGY
KVGRVEQMKEETDNSPIKTARTKVLQRELVEVLTPGTLTDPAMLSGSGPVFILALCPLQE
NVVDGLAVDLSRHVVYHCPCGVGRNDVLRKEETLLMVCALLQQLRPREIIFPLCFVPNAA
QADRKASFAKRLLDWIEGEGFRVELVDVSSLSFSKGNSDGVDKILDAHKFLAHYFQTLKL
YHAVPILSEAEPYTFHLPYASSNTTIARKHEGEVSNSSSILWHERRVDRGLVLDATTVSN
LELVSNLRDGGERGSLNQLFNRCCTNGGKRLMRSWILRPSASSRVILARQEAIRFIIEHK
LDELWGEGGEPETTLGIAAASPTLRAETPREHEPICVVKRERPVGSKFETRFSSLVDVDF
ERNLSRLTDLKNNSDAQVAFVDPLVQYKKQLQIIVTTVQALEDMVAWSHDIQKGITSSPP
LLKELWAQIDAAAPAVTSIGNCFDRHAALASGVIVPSQGASSVYDEASGTLDAIEGKLQG
ELRRLQEEVFDGTAINYSVVGHEQFLVEVPISAVPKTPLRGFVERSRSGKSVKYVVASLE
PLVESHKKAKKEKSNALLLVLQNVASHMCHYFPLLYGATEALSYFDCLLSLASLRKCGVT
TAWPIVKDDAVGASLEARELTHPFLNRDSVPNDISLDAAHGRILLLTGPNMAGKSTLMRT
VAVNVIIAQMGGPIFGAFMRLATVSRIFTRIGARDASHKGQSTLYVELSETADILRHADP
WSLCLVDELGRGTSTHDGYAIAHATLHSLKERLPVSPLLLFSTHYHALAQEQLGGDAVNV
SSLAPDHGSVVQLGYMDFAISDTKKDGVSAITFLYRLVSGICTRSYGVEVALLAGIPSSL
VHMAAIKSHELASWNDRQKDIHTIRQFLHGPNAATLFKKKKS*
>TCRU_528 hypothetical protein, conserved
MSGPLLTLAWVDNHLKRRGLPSKYASESRACTGAISEAHFDGPHVAPSSSTDSVPPVEEL
LAAVGHRQMPGGKRESVQSIGDGLQNTGVDDSRDAKSGDSLIQSQRSTPQRVASGVASFV
EQQAGRTGTLNGPTQACLVLHTVLTACVRHALRYSRIDQSYDAASSVFFPSSPSAATTDV
TSGALGDATLEHGATLEEVAASSQIRFPWSARVASEHLLEVIQDAAIQRGLRSFLWKVVD
KEHKCIMRNAAALCLNEAALLADIGVEEAEVRRLFSIPSDVLSSAREALAFSSSAATSSV
RMSWLNQQPLSFLGEHHFVYTTSSPRLAALLKEGTSELKPIELERTNARVRVGAGVSSPD
GFARQLNLLFLEMTRVRMALVLILQFEILMRRYAAFGKQQPGGVTTAFLPSSSPSSLAHE

LCALAIAAGSRALETSQHRKRFVTQFRVLARKPEQRQHTNSNLDDAPHCSLKSVFAALSQ
AAKANAATERAAVDGVSASSVPLSTAASSLSAPATGSEDPLEHDPVLHAVMSWKPLKLEK
ATDRNGATHACESLKASSAEGSTDPPVRKKKKQKQARAGAEPLPEEQENQAGLTWHFRCC
GGELGAEFNAVDALPCGETDAKVQLLRPSIRVPWPFVLEVVAAGKNKKKDAMTISPSRLG
ALEKFTRPLPSAAMRMRYNPAWMTGDEKITPLDARHTTQLQRLLRLRSDRLLMINGCPAE
KLKSVMRIAERSVRLVVRFR*
>TCRU_529 hypothetical protein, conserved
MGNGASVGENRHSQLFQQGYKSLQEGRYTYAEIYYDQAIERHEGHSFWTRLDDLIEWERR
DKAGQKGTDAKQKTAYRDGGQEEAAFPEVRKDSLKEENEVNVEMGEAAGVGGSGKIEIPL
DSRLADVVDYLVLRADIAESYMAEGRYEEATPHMDFLSSHTRVMLKFLQIARMTKAEESA
NSSNPLEGSTADAGADNAGGGNRRAHQGFMMVSDVERDSILDCFEQFLRMHWVSAMANSV
FIVSERFKKGKSEKKHKKELDTAVVACAKIQEELYNVAKRRARSLSNSVVLSFLEGIMEE
LDAESSTTSITNERMGTANGKTRTNTLFEEQNNRSTGNRSANEIDMLTDRDECPIKVHLQ
MVYDRRSLCREVPAPQQAPTLRYITWIDDEIRRVVPGTNYNLEIQCGMVDEKRKKQLQKR
SLKFAAQRNCNYNDRVLLGKSFDEENALLLFPVFLIQADVQFELGAATKGINALDIVDKL
STQLYGVGSLERQSIMRSVMESRKRGGSLFMMFED*
>TCRU_530 hypothetical protein, conserved
MTASVTNAVKVENGFQFTRPGSGATWPVNSRERTGLYTSVSRDFTLVATVVIQNFPRLST
SLLGAVLTSPVSTTIIGLSHSTEGKWEIVFDGNKTAHGRTWEPGKEYQAALMVQGGNKEL
RVRGWPACGELGNETNT*
>TCRU_531 hypothetical protein, conserved
MSRHLFYSAVLVLLVVLVCCGSGAAHAVGSVSWCVRLLQCAEIFVLQETPVKPKDGSESN
VKDCFVSPSLVGAGGVMTVLAEGALARCPTKQVYPADFVAGYANPAWGFSSLVAEAIKDA
*
>TCRU_532 hypothetical protein, conserved
MASFTSCARILYNTTNVDRTMHTIVHCSDGKYVEVPKAVADKCPFIEKVKEEMIPEFEYP
AAVLENLVCWTEHYGIDGFAESEIVRPCIYRNILHVLKNKWDNGFFVSRLTSELNIGHYL
QTVNAAEKFNMKGLHCFLCVGLSCKFRSEDDAELIHKIMGLPSNVQPNQEDIENVTTRYP
WLNEAIEPVVRK*
>TCRU_533 GTP-binding protein, putative
MGKPGKKAGKGLLPPTNVNRRVDANKTSLRDQRTIKRLKMYKSKLLRDEKGNIVKGSVLQ
ASDRVEQQMVRVAPDRRWFGNTRVIGQEALQNFLKEMGAKYRDPYSIVIKQSKLPLSLLE
SSGMNEGSVRQQMEWEKTFGAKANRKRVRLDTIDMEGFANRAVSKGEEYLTEKKGVDRNL
INKEENLRDDRSKNRILFKKGQSNRIWNELYKVIDSSDVVLYVLDARDPLGTRSSFLEEY
MRKEKKYKHFIFVLNKCDLVPLWATARWLQVLSKDYPTVAFHASINHPFGKGSLISLLRQ
FAKLQNVTHRGSKRTKTPISVGVIGYPNVGKSSLINTLRRKSVCKVAPIPGETKVWQYVA
LTKTIFLIDCPGVIYDRETNNDVQAVLKGVVRVERLGNVDKTDVVNTVLEIVKPKDIVAT
YGVSDWRDVNDFLEKLAKLRGKLVSGGQPDTEAASRMVLYDWQRGRIPWFSAPPFDSNKQ
YRDALELPEAKQMKLIEHYGTFNIVEDAMDHNEKSDEETLQNTCDYSGADSSNEKQIQKS
KKETNIHATVASYMSEQIILKKKEQRKRSMSEPAIKIPRAKETNNNYNDDDLWNRFLAAA
KK*
>TCRU_534 hypothetical protein, conserved
MQDTSRKRKAHEYYNGPGGTSPGSLGCHGAFHKTRCIEARCSNRGDIQFGSTRDLAVGEA
RQSVRPSPEHCSIFEDVYHNADPGAVAGRIDVKGETAEGQEPWLRAAERFSMIFITIILL
LK*
>TCRU_535 hypothetical protein, conserved
MELICQRRSTVVRRITDIPALDKLHEESERGDSRNVCAVNVGAEDVPSGAIHDFLPHART
ADERGELCGLFGGNIGCGAIHPTAARQDAAVHVGNGSNPAGHGDSGATKTSGAIGDETDA
PLDK*
>TCRU_536 hypothetical protein, conserved
MEGCPGGKGGRTHRVTGACRCGEDSIPGVGPDIGPRVAALRTGAMRRLPTLRQACTRPAD
HKEPSVSVAPSLPHCGGRPASASAGTSSRREHRNSLSTSERRIDVLLPNLRQSALVRPQY
EGTCRTCSAWRYNSLRGPPMRMPQWRHRLLNRRLARRSPPKLPSMPAGKTRRRHHRGYSR
WTRLFRHRLITDATGC*

>TCRU_537 DNA-directed RNA polymerase subunit, putative
MSDRDGDDDRLSLNFGEEQEESTLRSDDEQSEGDGADVVLSGRAASGSAVRRDGKDRVTA
PVLTKYERARILGTRALQISMNAPVLVALEGETDPLIIAQKELREGVIPLIVRRVLPDNT
YEDWRICELDIDFDRPADERYTNI*
>TCRU_538 Amastin surface glycoprotein, putative
MSKISHNRQGGNNFSCRVTVLIFTILAIGCAVCANIFPVFKKESNTKKIKQTLWYSQTTV
PGGVGTKVDVSDSLCGQYKLFFQVSEGAAVAAAGIGLVVLGLAIAQLILEEKSSRFTCCA
ASLISLAFAACGACVALIVYGYMKGYCQSDAVLSSQYGPLKDQGYKFSEAFYLICAACGL
FLLSSFFQCCA*
>TCRU_539 DNA-directed RNA polymerase subunit, putative
MSDRDGDDDRLSLNFGEEQEESTLRSDDEQSEGDGADVVLSGRAASGSAVRRDGKDRVTA
PVLTKYERARILGTRALQISMNAPVLVALEGETDPLIIAQKELREGVIPLIVRRVLPDNT
YEDWRICELDIDFDRPADERYTNI*
>TCRU_540 DNA-directed RNA polymerase subunit, putative
MSDRDGDDDRLSLNFGEEQEESTLRSDDEQSEGDGADVVLSGRAASGSAVRRDGKDRVTA
PVLTKYERARILGTRALQISMNAPVLVALEGETDPLIIAQKELREGVIPLIVRRVLPDNT
YEDWRICELDIDFDRPADERYTNI*
>TCRU_541 Amastin surface glycoprotein, putative
MSKISHNRQGGNNFSCRVTVLIFTILAIGCAACANIFPVFKKESNTKKIKQTLWYSQTTV
PGGVGTKVDVSDSLCGQYKLFFQVSEGAAVAAAGIGLVVLGLAIAQLILEEKSSRFTCCA
ASLISLAFAACGACVALIVYGYMKGYCQSDAVLSSQYGPLKDQGYKFSEAFYLICAACGL
FLLSSFFQCCA*
>TCRU_542 hypothetical protein, conserved
MESIEWIHISENRLWAENLMKQLMEKDAEEIKPPKLNIWGNIHDDSVSFESYWCTLLSQK
FRHPAYVAFRTSLFSALPLMYIGDRYPDIFPMHTLLALFGVAYSKDTVGEQICMISTMIP
VLLWMMLWGSLMHLFNLLAHQTAWWCAVFFGAFGIGLIGDVRGRKLAILMTLIVMEVERA
QLMVEKGALLPLLVGRDAFLALGFACFQSFIPPFTMCKRVDEAMAEAWVYIGEVVHNSVK
ACWSENPIDAAVALSKTSSEPLHKIFTTVPFELSFVHYEPWESPLRLQLRSERIKVIGGI
MPMLHALVGVVRALHAAQRSRSPLDNDQYAVSPGVGVIRGRLEEALEPYLQALRVTLKQL
GCVLNPREVVATVPFDDLQSATSSLQSTIDKIHYDMMKGRFGNVDSVWYMQIVFSHLMMV
LIGEELLRYAELMRNFDCSRYTSTSRRILDFFFLEHWRDFWTELPKRLTLATPNDVRLAK
DAFKLACGYTLACVYTLCIDFDSVYYFGMTILIGVGLQATGDSLVAGLQRVAGLVFAAAL
AYVIRRHHKSDLEAYPIALVLIAVALFTSSFPAYFNCSFYCALLIPSMMHMVAMPLMMFS
RVISNSLTVMTYYAIVVFVFPVDTIRVLHNSEVWVMDGISDYLSSLIRLLQAPVDDQEPD
VMQEIHALKACSSGLWRAVRQLPPKIKTASLEPTIRGKPYPVHEQDEFHPVLRRLLSSLD
IMLLGLTILHRARLGPVADELVEMLTSSRQLLKNINLYSVYAMQDFVDAVQRPKTWSCAK
TVDHFSTLLRLNAELKKMFSMAHGKMLSAIRGKANELHLNNLKLSMVIDNSSLLSLMPWR
RENSSVPHGNASICPYGEEEEGDEREELTAPRNASFMLRPEEFTINHDMNMSIAIFVGID
LFCSELVKTMRTMFYINQFELSRRN*
>TCRU_543 RNase H, putative
MQPHDGIQCTAPGHGKAECPSYPAQAKTLLVVTDSQSLLAAVTKGPHSHTDWTEDQIWQR
LLSLTRAGWSVQLQFCYEHCGVHVNEPADQYATQTTATGQYTEHGIAPIRHTDLLSCINT
QLTNKWRSTMHQDTHHYLLGGARPSDPGGKHLITQEALD*
>TCRU_544 hypothetical protein, conserved
MHQDTHHYLLGGARPSDPGGKHLITQEVLHRQELVHLARARCGESELWGRLYWTVRDCTN
QRRLRNISPEHSAYMRSNNDPTAPGTDTVPPTTREADAPPVERRPSTRRRKRKCPHCDAT
LVGHTNHIGHCRCFHPERPPPRLLRHGPPHTKKGTAQHRSRRAHNPDATRHRSSSARRQS
LLPQDQPASTSATISPQKTLHHLLPECADALAVRQRLGIKKDLRTESFSQWQLPRSRKLM
SLLDHLLGILVTSCG*
>TCRU_545 Glycine cleavage system P-protein, putative
MSQGTPPVILRKVIENPAWYTPYTPFQAEISQGRLESLLNIQSMIIDLTAVNLANASLLD
QATACAEAMYLAFHHGRKERMTFYYFIEGCLAILRRDGKNKG*
>TCRU_546 phosphoacetylglucosamine mutase, putative
MPLPLLFAQAVQECVSKFPLRHDARTAPLLYGTSGFRTLGVLLPPVAARVAFVAVLRVWW

AVVSRSEPAGCSVGCMITASHNPATDNGLKLIDVDGGMLEVSWEKVCTAVANATTAEELM
SELEEWVVRNNISVSSFSMDQLVARCPFSVLHLARDTRPSGMEILSAVQTSLQSLQLPFR
DHGITTTPQLHYLVQRANQPSMATGVTNVFEFGTALYRQDILSSLGALLNTLTEPTPNRR
GRRKIVLDASNGVGAIAIHSLLEAARQMSSQNFLEELFDITVLHDDVKNDGALNHLCGAD
FTQKTRSPSGKMKEWAADYGKQHCNEPREEREEVHYYSLDGDADRVVAFFHDCDGGDTWH
LLDGDRVAILYAMLLRQCLGQNALQVLDIGVVQTAYANGASTDYLQRQLGLRVYTTATGV
KNLHPVAHARDIGVYFEANGHGTVLLNKDSIASKVSSLADPRAQVILQHLPVLLSQVCGD
GIADLFACEFALLALQMDFNAWYHIYTDLPSRQTKVTVPNPRVITNTPDERRALTPPGLQ
EAIDAAVAATALASNSVARAFVRPSGTEPLVRVYAETGSEALCNSLCEVVEGLVIRYCDP
LKKDALPHVE*
>TCRU_547 RNA-binding protein 33 (RNA-binding motif protein 33)
MQVSDPTAASVEDTSSSVKDYRYFIGGIQRHITQQDIERYFAAFGDFEGFTMKRDSAGNS
RGYGWISYRSPPLGIARQDPHVLKGVVLTVEQARSRGPHEGNRSEKRSYVNEGASLRRRR
SRSPSSSSSSSVASRRGNYRRFTSSRQENVNSTSRLPAIAVGNSRLPPLSTQMYSSAPPA
QSSTSTTSHGNVVSTNNCDDGNTMTETYLCIPITLCPSEYLSDPRTFCARLDQNRVGSLN
IVPTPLVSTNAASVSVPPPPPPPPPSTRNLSQYGLIGERDSRSNAGLPQSVSSSTTRVAM
QRGLTH*
>TCRU_548 hypothetical protein, conserved
MSFKQVFLRDNEECHAFPWDALTHPSQSAGEEQRTIHHQLAWSAVCEREEADMGTQPARN
VSELTSVSFSFQPPFARPRRKTGRSSLGRRHDRPLYAAGSAGPRCGEKPTLFVGAAEADF
CEDMGWRQRSSSPVSSVEHNAEDDGEDFDVEPVVLKKSLSEKDRRKRLHLSEMSARLCHA
FAMKPFRLACGLGSDECDGGVGMENQSGWGAGEEAAVPLREKDDDDDTTPARQTAPISET
KRGNTALNFTDNDLSVVRAIALALMEEEEKKRRQEMRRKTN*
>TCRU_549 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase,
putative
MSVDANDHTEVNEWAIHSSVEPSDTPIAPADTHPLATAAADEARKSAADEDERESRLLEL
IKGPIRPFKEWSWRESAYFKELREAENVEECRTNAKPEMTVEDTSVQSPENCGNPPISAK
CSLARGRIHTALSCEAVQTVLSSSQSSRPSAIDSTLNVLTPLLDNYTIPITRQGPEHFSS
DAQESVASLCIIMVGLPARGKTFLAQRICRNLGWHGYRAKVLNIQVAWRRLLLEYKRCHS
GLDAPNMLPVDDASSSAKCTPAKSEGTSKKSPTVTCSNSERDTEITAKQKDISDPVVSSL
PEYSLPMMGNSQKKNYVCAEQFRALTCDPDSVERRLYRRVLERYAVDAKSFYASGGDVLV
VNDDFITEELRDEAEALFSPLASQTFFMEVIRSNERNQKFNELKLHDKSEYPHDVNASEA
QRDFARRIEYLTEVYSTLSSTCQSPGEPSEDEVTLGDVSREKDKVPGKTTRRKQRGRRYM
KLWNSVEIEVHGVTGYTASRIVSYVMNLTQDKIQHPIFFVRHGESIYNAENRIGGDSVLS
ADGEKGANEILGFLASLKRYYCADTKKTADGEGHVNNDDDKAGGFCSSDCSAQCEKPVKV
EVWTSQLRRAIQTVENSEPLLGIKNVRWSSLNEIHAGICEDLTIEEVRTQHPMIDHFRKV
NKYTFRYPEGESYQDLVLRLEPVIMELENADRIVVVVAHQAVLRTLLAYFGSTSAESCVR
LELPHRTIWRCTYDSKGISSLAEMKFGLQ*
>TCRU_550 AAA domain containing protein, putative
MGGVAFFAVPTPLLAAASLVLGVAIGATAALTYINRTNRREFSPRRRSLRHAGFASFFSN
DDGKDGAASSSKRHLQQEEIIGGQKRRVSRRLNSGVDLHPGLFSMKSYAAQRIGQNSRSS
SISLILKSCLGAESLGTESQEDRDEGDAEERKEENDSEFPISAVGSEEEGTRAFLPSTKG
SGKKKGGNVQNVFFTSGEAEFSSLSTLEGLFSEDDASSQDNNEEEGQQEEQHSNNPKQNE
DACTTKQEETATGCLGRSGRSYSVNCILDRTAFSGLDFPGGSKRLGASQNDAVFSKRHFY
HTHSGAIITRLPSVAAVRCRSILQLLHPPSSTRKDESTEEDGNLSQLTQSIRSTRSLMDD
PIYRVVITGGPCSGKTSCLSYLRRVFEKLNFNVFCVPEVATLLHSGGVNLILSTSEERIT
QQRVILQMMMMLEDAFYELASMRSRPSLILYDRGTMDGSAYCSDEEWDAILKITGYTNEE
LSDARYDAVVHLVTAAIGAEQFYTIENNAARSEGLEDARRLDAMTLNAWRGHYLVSVVHN
EDTDFEKKMLRVAEFIGFVTGVSTLEENATESVVPKKTARSAGETTITTATPEALSSAAQ
TTKSPSLTTPFFLQQLTTVLSPHDQKGGDERDGEDDVAHMAFLATGTRAFANSASMATVS
AHSLCNNNTNNNTNDNSICSPLTPPDFVTQCGGGELGRTSAPSSPSLAFAMDMHAERGGL
QRHFFVNRVDLAQIPADAVVANVVTITLVPLRANYRTEVIIRLSRANDSHPLYLRRVEYQ
NPEQTTLPPDGCEHELKGHRPGRHLTRVKITKSAFLELARRRNPSEPVIQKSTKRFFYNM
RHFTLVTFQHPRELRGVCRLVAPADTTEEDIGSLADVEPFSLLMREGVM*

>TCRU_551 hypothetical protein
MLREGSLTASPQGLSGPSPVLLSASRQLLLHYSPNEMDSPAKKLETASSLHSSITEFMRS
PMLVIQNPDFMKTTEKSPTTHGDENLLHDVEELRRLVGTTQEEVCALRRAVAELEAEIHT
NKKELLMRLYSDLSTPPPTGLEDKDAGGAGVEVDQLLASLRNQLLSQVRELEEQATLCRL
NNTAKEEALRSLYASILAEEKNNEARKTEIQAGESVCHTLRLKLQEAQRRVWDYRRREAF
VSAAEKKYLEQMEKIHTLREEVRACGLHLPVFGAGGDKTGSVIPTCNRFCWERRCVGRQN
AVKPPLLLEAGGVSSDRTGRDWNEGREEGDPNAIVSRVFAFPPGVLYALQLAMSGDKGDR
STEKEGADDNEYVSHREMSLTGGGGRGLRHRARALGLSLEYQQHLEVNPYPPHSPEEQRG
TEREKGSSATRDGVKVIIRGRRWAVHQFQKELEAAMATLELSDGTKVYFFDSTSPDGV*
>TCRU_552 retrotransposon hot spot protein, RHS3, putative
MPGNQASAVPQGDIRRRARPESEGDTDQPAATRGRVEKVRRLMWALDSRVEGRTLWEDYE
SVYNARWHHVMEVPGGEGTGMEVHEGEPPRSWTYKAVGRTLEKNDGVEPSGAPRLRLMVL
TLGKKWDFLGGNASTDCYVNCEVDRVWQIVKGDLTEWFSSRPEDHFTPHPRLLTGTPGIG
KSMAAGSYLLYQLLHYDAELLPVVVFVVSGREAYVFNKTAETVTRYMDKSMMIKAVKELS
RRGMKGYIIYDVVYSLDIPSPFLPPGGWGMLVVATPETTSYIHWANEKRAVRIIMNCPDE
SDVKAMCVWKKRNQPPPQQAEYWREVKGRMDKLGPILRYIFEEGRYKYWIGDCHKLVDGT
TSWGIQSYSVFGTSKLWEGNKVLEYLARIVRARGERNGESPLNAPITAHLASKTLCKLAQ
LMTQAEFNLFVSRIRDCLMHANFGKCAMFAFLNVAFMAAIRRKLKELKPPTRRPSHRCAP
DVHSQEGPTSHYFLPSAERIGKKTCINHRLLYIPEVENFPLVDGFFFMDSNPMTLVGLRM
ATAGGRHTTASTVRQFTECLAAYFNGWEELSRDMSWEIIYVQHADSTPLNDWQRCDVVNS
DNVSDDESREIAAFWEEKVRQYQVSIPSRDA*
>TCRU_553 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGAGGVYARDIDNGAFGGCMASGLLGTNWCHMPSGCKKTEIT
LPLRSALSITAAEASTDGEEATVTIRHSPGFNPSSVTPPIKQSESLAPTISSEVPPPPPP
EKESKEPLSSRPPVPGDSDTGGGNSDRDSGAGGTGGVVDGVGGIDGLSEVPSSGVPSSSS
SDPNGNDPSKTLSNTPSIQNRESSEKGEPSGKKSPGPVSPSGQTGEVSKLEEKSRASDTQ
EEAETSVAGKDTTKAEGTQSDMKTDGSSNTLSTAGKSKVQPPPPVKPPTAEELQPNRAPK
DPRTATEEKHEMPTSATKTNPDTPKTSLKDGMADRHGHDATTPVLVKNAATGNSAERKSP
SISTNDSDDAQSTGDENNDDDPRPKHKETGDHKAANTKVASTPSETAPQTVKTETFTVAQ
KNDTATSGDSDGSTAVSHTASPLLLLLVVACAAAAAVVAA*
>TCRU_gamma, conserved domain containing protein, putative
Elongation factor.1
MQCMTANLIGMCLQRMEHVRQYLLGVALMIVEERRHDVLALCVLRGRGLPAIVWDVEYTE
LFDWGGGGGRCGAAGVHDGLPLLGGARVEVSVACL*
>TCRU_555 hypothetical protein, conserved
MDGVRAVVDGRSRWRRQHSAVVAAVDSDDKSGEGSDGTLKGLSSSDQMPQAGQGGEEGQE
HTGSLEVTNKLEGNEDSQITGERNVSSDADRPKQTGSQVPAGGQPEDEEGTKSPQPPPPP
PPAESLPQIPRQPPPGTNTLQSEETHPPITAEKHSKPQDGGHSHETKMPQTKGSTKHEEG
ASSLQSPESVSHLIRESTTPLSTSTGSSGVAASTVENSGANNPTPPAASVTQHDSEGDTG
PAALPASKSELQSEEIPNAGIIATTYDDDNDSSRAAPTAERTTAGTRSTQTSGDASDLER
ANNDDVNDDVAHNGKTAEFEGASGDRNTEADNDERYTTVPETATNKTINTEIPADSDGIT
AVSHTTSPLLLLLVACAAAAAAVAA*
>TCRU_556 Regulator of chromosome condensation (RCC1) repeat,
putative
MFFWGSYNFQTPNLVEHEKRPALRYPLYVPPTLAMVGDGGSHVHNVYEADDAEGERLRLI
DARRIVGKLLACGQRHLVAVLASVEHSYDVAAGAAMPSPLVSCAQDNMNWFVYGMGSNHC
GQLGHRVPEYTTTLTKLHFEELLSAGNTVTGLACGNKHTIICTSAGTVFAAGDNSFDQLG
VTAKVTGFAPVAGLAHITAVYAAGNASFALSNKGQLYSWGEAQYGHLCHGDDGARMDART
LQTVKTNVKIPALVQWFVRHHVVILEVAAARGHVVCRSSDEVYTCGEGSYGKLGLGGLAS
SFIPQRVRFPERSHPERLCGIAAGDDHTLVLRESSAVGAVVYHFGKMGNGDGQLTPIIIA
APATINRIGAGRGTMSTALTSDGLLYVWGKHSHNKVSNGTNADAKRNDPQMVTALRSFFV
TDVIIGGTFVVALANFQRGFIEGTQTAPEMNAINERNNCHRHTWDVVVPQDARVRARDAE
VADYTYETAVQAFLAQYLGPKLGPMYVAEMPEAPPLTDHNANAFVRIGAHALTTGQKVRL
WMTNVYALGTVVAVLTSPQAESNIDPIAMRNEEEEAGKSKENSPATDVKRETKNSTEAPV

EKKYGCRLRIEWQRDDWHDEVITLYSDDETLDTHNPNRWQPLWFLPDPENSGDFLLDR*
>TCRU_557 Serine/threonine-protein phosphatase PGAM5, mitochondrial, putative
MFVKVFFGGVVGVFFSSFSSCWCEGPSQRGISPDGLRNYTLESLPPPTKEELEYVKTWGV
PWVSDWDRPGVRGIRADRHRSFQRQIILIRHGQYQNESSNDDRIRTLTLLGEVQARRTGE
YLWKAFVQSGNKMVRAKDCAADYLASDASSSGGVAGAALGENHMGGFLIATEPKFIHVSD
MTRAQQTAKLILEAFPSHVRRRLATDAALRERFPCDPEPVFRNKYASYKDMRAVEGVFEK
YFHRPTADESSVEIIVGHANVIRYLVCRALQLPPEAWLRISLSHCSITSIIISGNGHVRL
SCLGSAGHLPVDQITTRNVS*
>TCRU_558 IQ calmodulin-binding motif containing protein, putative
MNTCAYLQPLRPQLVASLMEAMAHASSLQHVELSAAITIQSFYRMWRDRRSYRVLRSAVV
CLQRMYRGHMHRKRVAELREEAEASHERAVYEYYATRIQACFRGYYVRCHIDDFYARKFY
IEQTVRASSHVQETANKMLQDRLQEELERRQSKQKQNYKEATEKLHHLISTTCVSGIYRR
PVIPCSTVTVYGTSVENDIRINSGAALRSQHGRRMREKLKKTVNDGRKDGMVATTITDGD
FKKSHLNCAGDKNEEEKNVWKFSTLRGAWNRSGVEQVSLPPIKTPVGSGTKYLGKVVSHS
CIDEFEPMYDTDTAALKRFVDAKEIEALHGKKPFVSSFSSGM*
>TCRU_559 hypothetical protein, conserved
MSVPLAFLSKRVESIGLSESALPAALTSEQMQKIITNLEGLSSAENRPCGRNFFGRDSVC
AEASSFLVSQGCPSQSLVESSFVAAGEHSELGQMLQWFARAVVALFVDGVKSGTKFPQAW
EESMRRHPTLASHTFELQGVGALFSFLMCQLAAVESAMSKCGVSGEIGAMRKVELRSDQR
KAKKRNGFDTVSGQRDGTQEHVLRKNVPTQKNSNEAAVPKDTSITNTAAAGATTTTTTTA
TATAQGDNVDRQTVITSATKPRLSLRTLKMKSVQPLWNASGTTDVSAPLKPPIPCPPLTS
LSCNKSQEAHSGSFLSPMQPRQQVACSGALAPGVGGLDHLSHYSKWPDENIVPPLACTHA
LTIRSLSARNNREPVDSDGDACDGTSNFPKLRGHLSGTASTTEEPKVEKKQPFNSQFKHL
RLEDIEQQSRVQELRKQYGVKNIINYARQEVEDFKTEMQKMRDILDAEFNRTEDAA*
>TCRU_560 hypothetical protein, conserved
MDAAVNKLIANAMLYSDGVLHLVGARHNEEKSSLFPAPLTEELQMITSIPRNWADVDASF
SASPVSTVGLVGYLSNAGSANTWIDECRCVIATVKNGKNVTNGLQFAGQCYP*
>TCRU_561 hypothetical protein, conserved
MQHDRALKRRHIRHVDEGVGQQARRALAEAANPQVRAARKHAVAQRHVQRVSERVHRAQV
HRHSDRPAEHHRVEARRRTPAANRHRLRQRHATHAVLRIATTAGPRRRHVERQARLAHTA
SAAAAHAVGERRRQRIEARQSGRTAVARHHTHGGQAGHAVVAAAPQHPAAGTVALHRHDA
ARDCQPGDKRSASGSAARNRHGAAAQRHTRQRRHRRRLAHRPHVVQVQPPAATDRPTVAA
HQRRRNRPLDAHEAQHRVGHREALAKHKAAAAAQYRHVRHREHRVAPQTETRRGRHMQRG
RGRTTRRLQQHAVKHHRADAIKSVTPLLSHCPHSPTQPPCQVAWSRQNKHDHWRS*
>TCRU_562 retrotransposon hot spot protein, RHS3, putative
MIVVPSPNVGNYDEWMKQEGAARIIVNCPDEMDVKAMCAWMKRGMDPDKKAECWRMVKER
MEKVGPIPRHILDANEFIAHSAAIEDALDAINSLDGEKHFTHGE*
>TCRU_563 hypothetical protein, conserved
MTLVASCGGIYFPETPVENILTLTWQVKEGSEAAVPYGCVVFKVKSSSPKSFYVHPRYGA
LLVSDGLGLPRDPCSTQVTFGLRPAATEVLSEAAATTAPRSATSIGVGNGYHERIVIEYI
HFSGDRAIYDRLSQGLAANSRLSEVVRGVWDLMTAGTLHATRGTPITLKVYTECVTRESG
KKGDGVVVVVPPTAKLVTPALREQLLSRMSTAHAREISTSSNALSASEKHTRGAGTCELR
ALKLGIDALRNEPEVATTTAPVATDDTYNSSSKNVPRLQADHTETDILMRMPKLDSATTK
GSKDGVPLFMVLAAMLFTYVITMLLLRTI*
>TCRU_564 cdc2-related kinase 2
MNPAAGGVVYDTLSSQPQRIMPQPHYAALEANERYFRQEKVGEGSYGVVYKCLDRQTGRI
VAVKRISLKLKDEGVPATAVREVSLLRELNHPYVVQLLDVSLQDSKLLLIFEYMEKDLQG
LLKQRNTPLVGGKLQRIMFQLLLGLHACHSRRFVHRDIKPSNILISRDESVVKLADFGLG
RAFRVPLQTYTTEVMTLWYRAPEVLLGDNHYLPAIDVWSMGCVMAELAKGTPLFAADTAI
SQLFAIFQVLGTPSESTWRGVSSLSHHNVDFPQWRPTSLSSVIPTLEPEGIDLLQRMLLY
DPRQRITAYDALRHSWFDDVRHDMSEEAAL*
>TCRU_565 hypothetical protein, conserved
MVKEDELSCFQECVFNVCEALLIEWLVEAADLVNSEGGSAITTGTLDVTGRTCPPDIKAH

DSDRSDSLGVLGGKSSKASPLQARETSAVERVQYGESVENTAGDSLLVSGDPTPVLHKED
AQSVVTVPISAAVVKADIIRKQLLSGDQVNIALGPAVTGEVWSCPTPGVKKGGGSNAAMT
EAVTVYIVEQAGVAVEAIGDAGDLSYATVEATLWRGLIGATSAAVASTDEVTEEWRAGLR
ALAERIASDYVYFASKQKLRKLDEYLWHAEAFLTPEEITARSIAAVTPRRFFNGLQRSDV
RFLIHHHVELARKGTLNEDIYTEARLRENLFERQHDDVASPLLSQQTSGTTTKKNNASGR
TILAVNRRRAGLTQLVLGHALENLLEETVAETSKWIASLVAN*
>TCRU_566 hypothetical protein, conserved
MLWSDTNNPREDCVFLRVKCALRRGGGPKSVVEALRQFFELEEEQRARGEKGVTHKLFID
LLRDFGMRFREGETEYLCAAFDDDQDGYITSDRFVRHLTGLNTRRHKAVLRAWEVLPKNE
RGEVSRDELHERYALSGTRGDLSDTFASPPYTQGGVEGTAAASAEAHASGGVRLEEFVAF
FSAVSPEFPLDEQFELYMLREWDADAPARPTMNETQREWDSNGDPLAISKSMFVQDALNT
ALGMSSKSYNFSHMQRSHPHVEPLPPLERDYMSVMKRDFCYFPKDKILTANTLCYR*
>TCRU_567 actin, putative
MQIAEGTAKILSNIPLPDEVAVVHRQAAIVDIGSYTTRIGFAGDDKPRVDEPTCVVKGTG
KESSSLCLKKAYNCRATTEVSRVIENGEVDWEAMEQLLSYLDELLQLNSKEVQTPLLLTE
KVLVPRTQRQKLAEILMEKHGVTAVHFAQSPVLALYAAGICSGTSVEMGYNACHVVPVFQ
GYPLFHATHMLNVGGDLCTRQMMSTGPELPAMVHPNHRIDVWSHLKEKYCETCPEGAVFR
QAREEEAANKVAISSGNSDGITSKYAVRHRLPDGTIITLDSNRFVPAEMLIDPSLVSSDV
LSGDQFFIDNVERLRTSTEPHGLPRLILGSLNVCDRDISPLLERSIHLSGGCSMIRGFPE
RLDSELNAFIPHTFHVTARTERRHAAFVGGSILASLPTFQEFWVTKLDYEEFGPSAVLRR
CF*
>TCRU_568 Eukaryotic translation initiation factor 4 gamma type 2
MEPLRAASVEKPRRTSSVPGSLTRASHRRSIPQSLVDALCAARESFERYGVISLLETAVR
APVDGVREATLTVLKDDRGENPQQQQQQMELSTSLPGVSPAPPTTVSSGETKMEACAAST
ERVIGETVEGEMSTTTAVTNKPTSIVSDPPKEKLTASFTCLSYDATVTREAMKRLKHVVE
YCPGRTAAFLEQLREIVATTVPEIPAAPPIAVSRLKSNSSAYHTARQLEALSELWGNRRD
APVSVSSTLGRKRGLFGEVERKELHHLVISILNRVSNDTEKYREVKNELLRLPIPEANDA
MLAKIVDVFFLKAVREQHFSNLYADLVSALCKVPGGQRIVGDKQQSLEYRMRQQLLHRCQ
MEFRQLEEQSIERAERGGEDRASQGAEESFKERRDRVCGIVRFVGELFLRHIVTEKVIGN
ILVTACTGLYGREGLCVPPPYTPTESQMDETITLLGIVDATFFRTPLGSSMLVECAQFLQ
HWSLRHPVSRIRFLLMSAVERLQKLVEERNAAIAASQEQLQLQQQQQQTTQTADDPQQVQ
QSVQDGKRLTNGSVILPQPLSPSNEESYFNSTGSRSTSAMANDMSVKSKQLVFVGGKPIP
APRSAASRQCSVMSITSSNCFTNFSVQLTKQLATSENVAQHMQNVTLATRSLEEVVEEIM
KSFADYIAVVGVWTERCLTVVKAVKDRSLYGAFLSSLNRYHKGTSKQELRKVAMSTFANA
VCQRLHEDLGIFKYWAAMILSDTMREVLDEDLLNEALHYLLVNDPAAVKVYLRDVAKHMQ
AASSSPRTPSDETTNFTRYRPLQVVHRHNTHRKREYELNVVNFPDVRLASMEIHVFCALI
TGTPSKEALFDAVRSSSYLRCPLMAPEIFSAILHAELCSNTTAYLEDNLDLLSLVVDGQD
REIRELLLVAELYVVLKEGSTESLRPLSAGAHVMAKLGDSIISDETRLRAQKYFESRDDC
AHHYIGAQSAQLQARHVPSSGSSSVVNNSSSTNSNNNNMNTNSVVRRPAIQRR*
>TCRU_569 hypothetical protein
MSLSVSPPANGNGADVNESLPSHAPAMGETSADDASPRPREEKQQQQDESTAQDDARGTA
TPIHSAMKGKSGRDRSTDMKPRFNPEVSVIETPSYFLVMNNEESGDEAEELAVFNRLYEE
AKSRLERSKAAATAGKDGEVEDPEAKECTFSPVVSDYAKQLGRYTKFAEFLQTQEERRKV
SAMHFEKKKERVLGEDCVPLFEDMPRKHSLRIISYLEKERNYKGPIKGWRERFRAYMNKL
QEQDRELNPNKPKTNASTPSVHSGITRDDAVFDRLYDEARVRAVSQRVVAMTQLERESRE
LYRPKTNESEYRGSDGHSSQVSPSKGRSNSRCSSSSQRLSSRGGHLASVNSDSMSSVFEE
LYAMGEEYRRRREIRAMEAIENQEEFTFKPATNPESSKIIMERAIARAKGELPERAARKQ
RLDAADENDGNETNARERKRNIRFNPDIFCSRLQRKEFERLKRLAELRHQLRMDEASECT
FRPSISRNSQIMAMQKGYGQITFAPSLHSSPRHSRQHTAGSGEGGQEHHDARNGDGDDDN
AFQRDVYRHHQQRRQEMAGRGNSKGNADDSVRRSSSGSSGGGGVNEPAGRLFDAEEVTEG
YISALSSEIQGVLSQWTEAAERAKAAI*
>TCRU_570 hypothetical protein, conserved
MQPVHTVRTSDENDTYVLDGCVCNDGSSLCLSVSDHTIRCYDTHTATFLFTLTGHTCAIK
DVTTPASQATVLYSSQEDTGVMISDMRQVNPAHFLSEFCGTGATGGTVGVTPNGRFLGVA

VNGDTHIVDTRMWHTTHVIANMHLDEITRLRFLDDTVYCSAGEDQMINFIDSASEVAEND
MLLQAISCGEVVTKMTAFSHLGVLGLVGSCENAYLFPFDLQEKEVRYPRPDQATYLVEMC
VLAGQPYLVRGVRDDDGNVGPLSLMNWATRDVTQLAPVHRETCRMAIGVGDCLVTGGEDG
LVAFWHTNDTAGAVTATTLTDAAALGRGVMKSRHHVTRPLRSMPYAK*
>TCRU_571 hypothetical protein, conserved
MLRMCEAYQVNITVPQPPELFDSFLRALEEHQLVTSFLVEAISDWREPLSRPFPFVVSGE
NYLYRIMDDCSLLDASLLGSLIGLRLTEYPLGSRNDRVAESKRKRGGFVRGVGGLMCVEC
EEKPVVMQGWPSLWRRKKLQRWIHEIDATSKRRCPLGRKFKCSPADLQRGEAVIKGEGIL
QRNLMDELSMKAEQGLFVTLLATPDIVRGASDGLPLLEGCSALWYERAVGGKFIHRHYSD
NNNNNDNDNK*
>TCRU_572 hypothetical protein, conserved
MNDDEELSSMTSVSSRSLEDMTPMLNRFGRHAEEDVSKSRRELKPSGLSVVGRKLTAPWC
PADVVEAAPLQGGDDGGRATEPNCIVPPASHDAQALRAAADTLSGRSITFTAEDKAACIA
TVAAVLQGILVQTRRVLPCYYCGEGQPLSSYRLHLDFCKIRTEALYARYGLNPLRFMMSV
PVLPIPALTATDAEKSAFAKACYRSVKESILPCPGCDMSFRIHELPEHQNVCNNSSKSNR
IGGDLPLKEKK*
>TCRU_573 conserved protein
MSSIPDGLFGRWLLTKFNGLDLRNEVRRFRMRFSRAQNDVEVRALVVNVMSGFMEYRDGK
LTGGMASTLSLAPPFFMGMENFLRNGFAAGMDVRLEGDVLTLIHGEDVLVLTAE*
>TCRU_574 hypothetical protein, conserved
MAEAASCLDVKSSFIVSLPRETRHLFRCRVEDGTLEEPTQLPMGYKASPEILQMITLAIA
RVTTVAHRLWAAPPLVRVEVWIGNIRSAGSRSDATLWEAQVLRNADRRHATMGEDRESGA
TQYTFLAVLFDHTHRAVSLSDRFVWSVRAMPSLKYLTIAEMEVTASRFLPAAAILRTRLC
EYHFFIKAVRRRLSALNRGLC*
>TCRU_575 Solute carrier (proton/amino acid symporter), TRAMD3 or
PAT1, putative
MYYAQKQRQPTSVLGAHGFTTEVAGRDRVRFFRRPVEARSIPTLYADIDNVRFAKSEPNT
PTPTGSQLAAALFPQRTASASGQKTRPHHLPAIKKRVHHAGAGTSRTFTTPMDGAGVSRD
VGMQTVYRENEAQTVPYTPEYYIPEGGDPNPEVLGIRQLKWNDGLPAGMEEVELIQRLRR
RRAVEASLPPETDAKSAEERYRTLYELEKQERKECEDHMAKIRQRRLDSIRDALMERERA
REEANLLRLENVKAQKLAELRRTIERTEVKRILKGQRLLEDEASKTAPSVACGMYAVDPI
DSHKPKKDLIEFHSKNGMFATTPQVTHGRSMSPVMKEPSDHFRHYDVRPTMLTLEEGVKE
LEETKVPRIQRIRADAFLAPENYAINSLPTLYQRREATRVVDALEYVNAKIHKQDSPEEK
MRIMELYRATPRLQRPDTPELELEDDEGEELEEACILLQRLLRGRAVQNDFFDGKERCRG
LIEELQAASNAKYAERSPEEKEMDERAKRFEAIAEGLGDAAQGDVIVETLDYLFHELERQ
RDLSRLEELRREAEAVRAEREAKEAELRAQQRILHDKEAVQYAAYIRAIEDVVECYSHQL
YTTSAEECAMEEAIAAECSRLERPPTPAREFLDADATENLVCDMLDSFVLPAVVDMVCLR
QEELERKAPAAAALEEANGTIPPKETDEKPT*
>TCRU_576 hypothetical protein, conserved
MIRIQRLWTQRSPFGRSNVALRFSVFHRVVSIASSCCSHSGTIFLAVRCVQYEQTSATLR
GINKKKRALSAPWITKSTKDYMSEADAKATAVNPIKEKLLQNSKERKERFVRIAEETDRV
FDSEMDRMRDYNVRRWRKGINFFKAQGLGFTLLYIFAYLGCLVALYVGFATGILKKETAY
EFMFFLLGGYVDKEWFYMRVEAWGTYVDFGFAFLINEMLELFRFPFMIYTFYTFRPYLTG
VNRRVKASIFRWNAAES*
>TCRU_577 Protein of unknown function (DUF3773), putative
MWRRVLFFSASLTVALRHTHRLTVTRTTTSTKNSSPGTATLWCDVAVAAQQVPLATVEEM
FGRMEGDDYDEKGDESAPHPATASLRDGRDAVEEEFFEWLDDENNTAAAGTGDLSLDAVM
NAALAEPDPGGERNASDEIGGNSDTKSSDSVRASHGNGAGGGEGRAVSRMDDILAEEAVD
DYDGVVAAGGPDVLFDDNGGNDEREDHVDDVEDDDASAIPAEEEEEDQVEQLIRATQTAE
SAAALFFKDKQRVVKATVATPSFDDAAAEGAELEIVGEVMPSPQRF*
>TCRU_578 hypothetical protein, conserved
MNLSVQKKSTSSLLPSTYSASTDGWANGLSADTSFANPKTVEDRFIGIVDYKEFLHNPHD
MCAHAAGSVAEARYRKTLESRMGLGGSGLMLFHAGDLASNFPRLDLNGGDYYPFSAGCAN
RGDGITTMDGQLQLPSFNADLMTEVAQEPNDGFCTPPSTPIKNRIEGAQISFPSSQRTAS

TFSSPKPTFTAHVQLNNGCHTPLAVSKNWGMGNQETRSSGMNGGFISGSPYSYSQRCDTH
RTTPALSTNGFPSPLRGSRSGDVVSTLATSPHPGRNATLHSCASPQLRTPVRHENDLLCT
PTQGGHGGNITVSQGASPVSRRSVLYSQHATPRRQGETCDRVLSAEGLSVCDDQGRPNFT
PLSWGHMGVVVALQRSVYLWQESGKTYFLFETPTAATLVSAVASSMRPTEMGDVFLAVGM
NNGFITVLKYYVGGGDSIGCDASQFTPTGILLEKTTQSSFMGTTSHVSTLYLVGHFLFSG
CMDGILTVRNLRDGSVIWHSSGAYAQIDLSSYASRLADYSVDVGAPIYKIEATPDGEHIA
VGTNDSLFVYQTNCMGPENRTRRRVVFSGAPRPVRAFCWWSFPFSSSNGRAVDAHHGSGS
GSRFDFLHTVLLYGGGSDGSVLSVYFVGSRCHKTTYRMSAPILGIVSSEASEEIFVSLDI
AGGEVENVSNAEEIGVPPVVDGNVHRVADNITVGGFGGPEDWASSGSSSEEEGLPQAPSV
GQHLPIGVSGRGGHNRMNGNGAGGMTLGLSPALARRFIHRIEATRARPPLPHMTLFREST
RGAGLLQLFQLKDGGARLERLSGFVGPHIASLYMALSPDNSLLATAGSEMKLRIWRAFKL
KSPVRGVRCELR*
>TCRU_579 hypothetical protein, conserved
MGKFSLCIESNLREVNSLLAFHNVHPQVRADVQRRLQRLTYRVYDHIGTLVPGRSEPAED
VCAAVVQELVENTIQKALPGVELAAEERRSAAFQQRTRDLELELSKSEQQCRELGERLDR
FRKAHNFMLRCYFREVLLLRYQLQDAMWRRRRSHNSQAQGGHFGENFKDSTSRGLLAVIP
ETKTPKSEYALPTIQASSNLSLSEAVQNNSTSSGSAEAIMDSEPQLSTTSELGKNNAPSS
PSTTGAVAKQSNAVVKVSSLTTMPTGEVPAKHVTPIPAVLAVAGVSSLSQPAEVPHSSPL
ISGVARPRPAPRKVETNFVTVNAASVKGVVQLRTASTQTIPLMGDDSVGAIFDYERYIRQ
LNRPRRGSALSVEAEISKSPQPKVLLEEQRRRKAKRLQLMKQKFAQYQENAANATLSPSG
KKSGMLQAFILGRKKSAAMEGRKTLLEEFNEIYLGVRGLREQHFKDMVRLKKEMDSIESS
VALLLGFFGTYAEEVSRLAAVLSCEEGAASSTMNVTMKKEDDPYRRRAVMDYFSAAASVG
AKPVLSSEKRENEEMKEFITLEQQEQRKRQILFWENNPVTLRAKAAFFELQAAAAKLREE
SSFRKGQKGAMDLLPTVVGYDAFSSALFKDLIRGKSEQEEEEGNRALLLLSREEKLKTLV
QLRMKRISHRARHRTQLRQLADGAKKGKKGEYLQKILLRASLHEKTVERLTRMINKLLRD
LGLSGEDLEAQRAFFTKNLASSPYLCESGGNLREDEESGVVYVPLPVSTRHAGDLCAALS
SNPAGYIIFNDEVIPIANVTYSVRTGLPDNVEQLRGQRSAAAAEAGGRGTRRVLPFHGTV
VDYYPGVQLGIPLGDNHGPMYVFWGSDEGSFFLVEDGLDAERTASQRAPPLTARQGHQQQ
LGQKRNVNLSTILLSPPLPEPERMRPFVTHSSGAFVTSPRDASGIETSPVVTYALERVTP
APSLTLQEERGKLPSCSPPAPPTIRPFRPMIVGPNREERDLMRIESLSARRGAGGANKVT
SLSYGADTALARLKGAQRERQQKTVASSKQTPTNGKTQGRTPNDHFFRMRLPYKRSTLPP
VFE*
>TCRU_580 magnesium-dependent phosphatase-1/HAD phosphatase, family
IIIC, putative
MTEESVPLVIVFDLDGTLWAPEMYELWGGGGAPFRADPSDPNGAFDRAGTNVRLLGETRE
LLQKLSTDPKWSSTSLAISSTCDEPRWAMELLQLFQFTDSSGRRVPMLSLFGDLVEIYSA
NKASHHRTILRKLREKEIDVKEDFSQFVFFDNQTNNIESVSSIGVTSVYCPRGMVSGVFE
RGIQQWREKVKRSVL*
>TCRU_581 hypothetical protein, conserved
MSHGRGNLLEATADEFLRSISVEPDCQIKAYPNGAEAGIAQKLPFDARIVEVDGQAVTDR
GELREILLSGDASRQVSVVYEKTNEPSERVKIEESVRCDGCVSGVAQQPLLETVLNKIAD
EDLSLPVSQETPVQSSLSKLSSQTAFLLDTGSCASQSAAMKDGEEDKTSVASSDLTAETT
GSAPCHSMGTGYLNKVNSVPELLEFEKIDTPARTEDSFHVNLRRPSENSMRRRLMRAVEM
VAVGRCIVCVCYDVNPIAEIELVAKTLNMHIVTIDLGVKLRLRPKAEVFVEQFKAAMYDG
AWFVLVNAHKSIASCRILEELLKESESRNFQGFSSNARVIICLEPHPHFPRFLLKEAEIT
RIQSCLSASVSELSMATSMSCNRLVTAESWYSRRTSGWGVPTTSDTVVGTTGDKPRVRIN
ASVDVVDIAPREVVSAPRERPLNIHGAVVLRSAFTGVPGDKFLCVVSDAVEGRFAVGSSM
GNVYFVDELGNSLMQAHTHEAAIWDISFKERYQFATGCEDGNAVEWSFEMGGIDGAALSP
TSSTSLGNDVYCVSYVHGQTVPPLLIGGLSRSIVLCSNDRPVQHLTISSNAQVMDCIPTG
SVVLVGGSDGSITVVDVASNSILTSFKGHSRKLPALTVRDNNQFFTGSFDSTILSWDYRV
PYRPTGKPIIDGLPSANFTHTLQLKDYVTGLHVDDVHLAASVGENLYLWDVRKLTEVLGG
FPQAWKGLSRGVWVSSISRCVVTASQDGYVRFWTFV*
>TCRU_582 kinesin, putative
MSIEVHVRLRPHVPNGVWSSAETVLYSTHNPNTRYVYNKVHHIGTSNQSIFQGMEALVHA

GFDGKNVTVMAYGQTGSGKTYSMNGCEADPGIVPRTAKLLLDLRTKFPGTQIVIYFTEIY
NESVKDLLEPQRGELGLHDAPDGGVYFDKKSVPIETIDDFVRLQNLAERNRKYGVTNLND
HSSRSHIILTFEIHRTYRQVSTINLVDLAGSESASRANTDGLSLREGGFINKSLLTLGNV
VDAIVEKRSYVPYRDAKLTRILRNCLGGSGMTFILCCINPSHENFEQTVASLRFTQRAMK
IKNDPVMVLNMPPLFTHQYEAGAMGLVQGFRELCDAYYQRGIRDAFMYTSSTVSSIVTHF
DGQVSDSLHAMANAQRLLIAHDHAIAVDQVGRLYNQLHEVTRQSLQSKEIEEHERKRQRE
TEEEVEIRRAKIARLEADVKEKDADVDTELAGWEYQLYEARQRRVTPLELLLSSERSKRC
RLQYEWAVCMERIAARCVPTIISLGPVTPPVADKNTALQQLRQQLQQSQRELADLTVAHD
MIKGDLPELRRKAEENSCVSTISPAASLSPQPRPHGVSIATEATDEEIDQRIRELEGEEK
ALMSRAVHVARCESTRRLRETLKPPRSRTPPTMRSAVRHDNFSPPKEQQTPMADMYSGNT
RGDCGRHVSPVQQRSPTPRTARTIFPIAEESSGVETFLVSEKSASPKNEQLTDGVRRALG
LLRDVRSKLMNHTRGRQRRAEAADRPTASPPVDAAENYANFPASVNARSSSRRCRRVGSH
APQDENMTLAEMYMQRDEGKGHEAVVGIAARRRIEKAPLRPNAERALWRMSISPTSPFVE
MKSRSRSNRG*
>TCRU_583 hypothetical protein, conserved
MMTMTGRVLLVCALCVLWCGTAGAAADGSDERADVSGMGGGSLPELKGIGNSPEGPQGKK
DEAGDVKGKKHPASSEDKEEDDADGDEEDYDVVVDDVEQEEREEETLDPAETEIPNDPTK
EEASSPPQSKHKKGPAPAEGIPTTQSPATPVQPTPQGQPPTAPPSPEDSPVPAASTATVT
PAVTPSEQGNIPAPARKKDEKQSEDIDPAQESEQPDPHDVVLVQHSQGVHESKESNNNPR
NPVSASATANQRDATFNGRGEPAQTTSSTESVKQSNDDNSGTEEGISSDDPTADGAGTKD
TKNSQNKHGNTKETPVEATAVKATTATTGDSDGSTAVSHTTSPLLLLVLVACAAAAAVVA
A*
>TCRU_584 hypothetical protein, conserved
MEGSSKTPRQPQENSQKSTGQPPKLQVPPAKSPSQASDLGEADAGPVGIEGTGRNVIGGS
LDKNKDPKGREGHISGPPSGGASSSPISNNGDASQMNGGALPTQDTTSLKNNEQSGPTTS
SGNAPLNRETAERSTPDAKQHSSDTQENETSQVADGDANYSAAGQNAMGMKGSSGVSTTA
SNAPTTPQPQLPAPPVPPTATVTGAPAEKPTAERSPPPADSTTGGNLAATTTAPTNDTTT
KPGDSDSNTAVSHTTSPLLLLLVVVACAAAAAVVAA*
>TCRU_585 hypothetical protein, conserved
MNQVIRSRTDWKERVVLRLAWITASRWSEIAALTAKNFTLEPDGTLILDWPVAPKTARAD
PHRAFRFFRTRGQDALDTIKLCRTLQENEKLTNLTAAHVERALAPWDATAHSIKRGALRH
AAQIVETYNLNPHVISQLAKHFDPFDLPQNTVRYLGRYTTMLTQVSSLIALM*
>TCRU_586 retrotransposon hot spot protein, RHS3, putative
MNAGSYLLYQLLHCDAEKIKVVVHCFGEGEAYVFDKTAKKVTKYVGSKASRSVFSSFPQC
GMKGYIIYDAPTNGSQLPIIFTPPIGWGTIVLASPKVRDIYEFLRQRDSRRITMNCPDEM
DVKAMCAWMKRDGTPQEQEKYWWMVCRQMAFLGPILRYIFDAKDFSKRYNELDRVLRSVK
SRDDAKRITHGGMTAWFTGNPFCKLMCVKREREKKGAEDFKTELLSRHLAGRAASFVIKI
IPLNEICSLQ*
>TCRU_587 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MPDTMLQSSAKPQPSEQETLTTNIGGVGGVLSRAASTATTPSSDFAQEAATRSGDTMLGN
GSPQTPEVGVSSGANEETTEGRDGQKEGIHAQHGEVNATALSRSLGNVSQGNNSDAGTVR
GSGLLPSLLLLLLGLWGFAAL*
>TCRU_588 hypothetical protein, conserved
MLTSEDPAEHAGQAGQAIRPPPSPESDGTRPSDSSRGDSSVSPLSTAGISSSSALDAPLV
QSTQPSEKGLRSETMSLGTALPNDQPKERSESKAKQGSSTSEEAAESPDDSGDAVEKKKK
KGDVGLKATKSLSSTTSNPPVTQTTPRSSAEPSPTETELQAGEETSTENVTITMRNATAN
TGDSDGSTAVSHATSPLLLLLLVVACAAAVVAA*
>TCRU_589 hypothetical protein, conserved
MFYHGSHPEHPLRTLKNPKAGVLCSICKACAHPSMAEWCFCMQAGCGYILCCKCSEIEEQ
LFDIPQVITRNPVLPHEDMSVCLRTRPRSNAHVLCPLYPGRLMIAVSSAKGTLNANETYY
RLRKGGWVNAAHVVRVLPSQQLIEELAKTHLRAEEHHSHEFMALEEILLCIDESFRLMDE
RSPYGTVMASLTFFPLLQYSSSLHLISSEERTVVVRASLGFIHYLFHFVLEEVSQWMNNV
DHRVKTTALTLYVELLGKSLLVARDVAESQIVALPSELGPLITRTAAVVLEILPIVECGT

APFGGATVSLRAPSIATRQVDLAEEQARLFVCCCNMVETTGWLLLHTPTFTYDLKCLRPL
RVAVSIVPNSESLERMLCQVVNNALEKMPSLRRRVHDLDVIEVAISLAGRATCAESQMAV
FRLISAIAHNSPRNISQSASLVIAPLIQLAMKAWNTVVANAAFDCFAELAYNDPRVDGFR
SDSQSEELMLPVCSAALHPQEAPYQMANVYEVGDHLQALCEYCSHSHPLINGVLVREPQF
AYFRCQCESCAHVQLARPLPPPNIPTTPAIQEMLKENIARVVLFWLKCSESAVANAVGRL
SLKISLPVEVTLTLYRALLKQNLVGYADAALAIAAQSHLPAVQEMRREYPCAAISQYLSC
QPAFRAAAFSKETPGKDSQNEDPDGLSPSPDVTTKKTEMFASLPCGVSPPLVDLFTGPQK
MYLDEVL*
>TCRU_590 Sperm tail/Sperm tail C-terminal domain containing protein, putative
MVAFADDERDERIAERRIRVRRRLKELCDSERSTQTVVGAENNVSDGNGASGAIGLGEES
VRQARCEMAEIVSTAHSAVTSWEVNVGKNENERREREERLVDERRQKRREELKANEIKQG
AIELRFESIYKLNAPHELKKSLEEQEQQCKELIAAKDRLIELLREQLEEREEEFVAILQR
NAADVNNLVAEMRGQTEKYLDAYTSQLREVEATYENERKEYLTRCNEEIQQLMKLRRTRE
TEYRKKREDEIMEAQRKMDDKHRGNCEEYNEIKREHLQEIHALMEELERCKAEFLLNGER
LSYNLQILRERVKENKSAQALHKRKLGRLQDTLSYLVARYAESEKKYQRTNKDLTAQLHR
VANQYRDLQKKFQKFERSDKEKYRQLWDMHEEKNIQLVHKSLQADRVLFEEILGVPWNPP
QLKYWLDDEAADAVEDNEVDVSSSDDEIELSEEALMLLAILHKQAPFIADENVYAAIRQV
QDATEDRAMVESILATLQIRKNEEMDDLLQYFIVDGPEETTALIRPQDAIRALSTFLTEK
QREKKQKEEGQKESAKRNKEMAKMKLEERRRAAEKEYWLRMARSVPKEHQRVWGALEKGL
KLYIAQLQQRKNLIVDTDSLRAQNAELRALLTQYLQSDVNYQLYIPPKLLLQSRAAS*
>TCRU_591 hypothetical protein, conserved
MPGGAQGHSTILQGLGPTSFNWHGSIPTNQADTHFEPNFRQFDFFLDTQAMPDESLAERV
YKVPEGESHWNLRTFWGQNLRCMPVVFTSLAGAAFVNFFYTRFLNRTGASIRWSFLKCYA
AIFAWNNFTKFVARERYFQRDFQRNQLYSFDEMRDQRDRQRVREALYEKQFVKNPIAEYR
VKAWQVAERFA*
>TCRU_592 protein-L-isoaspartate, putative
MAWTCSALSNASMIQNLERAALLSTPAIIASLQRVDRGWFVPDGMRSSAYRDEPLSIGYG
ATISAPHMHAIMLELLSPFLLGTPGSLPKAVLDIGSGSGYLTAILADICGDGSRVVGVEH
VEELQERSLKVVLQHFPSWVNEGRITFINGDGRDISKLFHPHTTMFDVIHVGAAAASVPK
DYLEAIKPGGCLVIPVGNENEVQHLHLYTKDEKGTITKKTHGGVSFVPLTSLRHQKTRS*
>TCRU_593 hypothetical protein, conserved
MDRPFASYELEVAVRDSSLGPTPGPDDMLNEFLHRLRYVARGTLRTMIHNSFANGSLPGS
WKMGDAISIPKPGKDPCRPESYRPITLLSVLLQLTGGMIHRRLSALLPHHPRQFRICTSA
FYVGRGGTCYRQITRGLNEFGIVEHERPGDDAPHDALVAIARSFD*
>TCRU_594 hypothetical protein, conserved
MKSSWSPSCSQKRPAAKFLKATRAPAPRQGPTSSLGTVDTGNGWRCRHSQFSRDWHTALI
PAFLGNNREGQYQRRHTPMQPHDGVPCTAPGHGKAECPSYPAQTQTLLVVTESHSLLAAL
NKGPHSHTDWTEDRLWQRLLTLTCAGWSVQLQLATNIAEYTLTSLQISMRRRPRQPGNTR
SME*
>TCRU_595 retrotransposon hot spot protein, RHS3, putative
MKGYVIYDVTEKGMPASWFSPFNEWGMIVVSSPEVSNYDKWERQKGAARIIMNCPAEMDV
KAMCAWMKRDETAEKKAECWKEVKERMDNVGPIPRYIFDANEFVAHSAAVEDALDGINSR
DGEKHFIPRGVRLWYSENASQKLVRVARARGEVGAEVFLNAPISVCLGRRIPHYFGERDE
*
>TCRU_596 retrotransposon hot spot protein, RHS3, putative
MTTAGGHHTITSTVRQFTECLAEYFNGWEELSRDMSWEIIYVQHADSTPMNGWRRCDVVN
SDNVSEEESQKIAAFWEEEVRQYQVSISSRDFRSDEALRSVEEPSK*
>TCRU_597 hypothetical protein
MHVCLPRRFGVLDPYFTLFGAAEVDGEVVLSRAARAWWTPLRDPVDDPSKSKCTMRFGST
RKEETLGGLGELQCTRLQKMTCIIEFTLTTTWGPFLEVVNPS*
>TCRU_598 retrotransposon hot spot protein, RHS3, putative
MKFTISTNIEDVLFKGRVRVNEMKLNDFLTREPDGRGVVYTNRDLLLEEFFKDPAKYIRD
KGALNEIQASGHYLGMKRAVKGEVIFDEDVRRLCDKGVNNLPGRSLAAAEVKATVHNSSK

HFLDAAAEEARNPTTTSTPEKLEGLYESAHNARRSHAVELPDGVERKKTVTGMGVHEGRP
EQSWSYRKADDAIEENDAVQQFGAAPPVLMLLASEKGWPYSWHTIQDLPKDVL*
>TCRU_599 retrotransposon hot spot protein, RHS3, putative
MYLLGPIPRHVFDEEAFNERCGAVKFALQSINEVTMKEYFSRGGESPWYSEDPSHRPVEV
VREIYAGDVILFNAPISACLEERTLERLPSVAE*
>TCRU_600 Leishmanolysin, putative
MAVPSLAPCTLTVSFISRTPRHPHRCAPVGPCYRVHLPAHGKPQHGEECCWCVWQGAVGG
GRLDDCRDFCEEPRDSDDINGMELQDGDGDGRTLESHWSQRHARDEWMAPIGCAGCCTEL
TLAAPADLGCMRVRWEMAEPMRW*
>TCRU_601 Thioredoxin-like/Protein of unknown function (DUF3638)/
Protein of unknown function (DUF3645), putative
MSAVQEALMTSTEELQKCIAALSTLSAADAADVRELTESVLHLANDIFAPIKKEGDNEIT
HTGHTANEVDDFVETRVQEYRLQRMQGCRSAVPLEWLLGALLSSDMASDLRAVNPFHGDI
ERLKAELVLLMLLANRSYMAEQAKQSVRQIVLFLELCARIRGASSDDGDDCSRRDFWSPR
PNPESSRSRLQELLQCFSIGVDVDALERGGRQPTSGGDANKSSEGSSKGSQGLRVLSDDM
VAVLEGRMLQLENESIELLNAKRHYATVGGGGDGERVSLDPRYLLFEFIHNILLRARQVE
MVRWFVDNTRAGVSRVQQMIMGQGKTTVVGPLLALILADGSQLVTQVMPTALLEQTRGIL
RRCFSVVVPKQIYTLQFDRAFDDTDTNNIALLEQKIAAAAKTRAILISAPECIKSVFLKA
IEQMHLLETTPTEELDAVQNSADERVSAQARGILRRTQQRSAMADAITPIIQLWQRGVLI
MDEVDVLLHPLRSELNFPIGLKHPIDLSGPRWTLPIHLLDAVFFYQRGRISCGAVSGTKL
FDVTPTSEVRQDDVGQFSPEEDGTSEERQTLQMTLLNTIRDAIGKGYEMQALQREPHLVL
LDHTYYKHLLLPALLPWVQLWLFHEIQCVSRHEFHVTTASFAASLNWQSFIESTTDFLLH
PERPSRESAVGSAINANFSPFAIQLLCLAHDWIHRLLPHVLAKIDRVSFGLLQPQDMEAV
TVEERERMPMSRRMMAIPFVAKDVPSRSSEFAHPDVVIGLTILAFRYEGMRFTDVKALLQ
QLKQDFARQSGPKEHRPAARLYHHWLRLSMSFDAQGEPHASCNMLTLPSPSAAAGVGAKL
PLHNMTGGVKTHDRSGIPLSQLQVTDEVAVHALHYRLRYLPEVVHYYLCSHVFPRTMNFQ
GMKISACGHELGSSMLFTSRIGFSGTPSNLLPLDLGDCFYEPGSDGRVLSVLTNPSVVTT
EVLPLDWTPLRVLDRIATSHPPYHALIDAGALITNMENEDVARYLLGKLSPALFDGVVFL
DSKDRQMILQRSNGLKVPVAQSGIALTRRFTFFDQVHTTGTDVKQAASVTAVVTLGKDLV
FRDYAQGAYRMRGVGKGQRLRLYLIPEVLSRIHATLGSATTGNSLLDVPAWLLLNSMQME
SLQFIKLSVQELANVWRKKALQYLLRDSIHFHEHSDLYTDMARCRRFHMQRPFVIEMEGE
PPLPDVSLLRSAIQEFREPVAYPVDSVIDTPLPFLQRLMDHMRERPQELIVGDAASQQLL
HDLMHRLASSLAIRGPELTTATNTDGSMNLDSEIVHEQEAEEEQEQEAEQEEQRISVASR
DDELHIPWRVETLQTHGKDHPTEGSCFYPLRRLRVRPQQPFICVDPVVQVSDNYYREFWH
GAGERRLKNVFLSLEWIPRQSNENAAHVIHSGLITLAEGESLRWMMHHQTPLTRLIGMAL
RVVSSGRYMDFTEPFVAAVPRVRAERVLTDPLTQRVSLISPLVSSVERDGALLLYRFFNN
DMFFLPEELAVLEVVMRDVPHTDRLQFFTDCLRARRRHRNHWDDAPVASLFVPVERPEAM
RPLAILTALRGRFENLYERALRAPPTAKLMTQLRFFHERFAMACKEQRSEVHPMGTSIVF
LPIDMMGRILHDVFPSVIKPFTPHDLEHALRYLSQQDAAGLDTPTPADMSNFYRVPLHRV
MEAFPVLQEEFFHTHLETMQASEKSQQEPWYCEVCTLLNNSTVRRCVACDSARPSAAADG
ECAATSMDMLDEPWPCPQCTFINGSRRQLVCSICLAANPTPLQEPKNGAGGVDADTSVVW
GCPAGCWVCSVEHGGCSKFNPNHFFYCQVCDKARPDLATLRF*
>TCRU_602 Leishmanolysin, putative
MADTAWSVRVAAHEIAHALGFSQECMEEKSLVKKRERSVRGTHRRMVAGKHVRDKAKAHF
GCDSLEGMVLEDEDGPPEKKSLTGRDATRGTS*
>TCRU_603 hypothetical protein, conserved
MFCGAKDAETPRCTSDRRHVGTCTATIVEDKESLVDKDVCPVVSLEFHEISSGTTYRTCS
DENVDYLRGSLTGGGLWCLDAELLETTDGDGHKSVRGVCAQVSCEGGTVRVRHLGSSGFQ
P*
>TCRU_604 hypothetical protein, conserved
MENIRKGNQVDSTGNTRNKEHDSATETLELLTASINTRHSGAPVNESNTTLLSGTLRSST
AGTEEQAKAGSMPLRQPKPPEEKLISEELPPTATEVEAPGGPSAPPPKSLPQSALPSSKK
VPDTTQSTEDPQSKGIEPTTDARQNAVTEGHAETTSPSSPVDDAAANDADKSNVEIANDG
SAVNAGVPEEEPHQEQVDGSEKQTSFTSTAKKHNATIGDSDSSTAVSHTTSPLLLLLLVV

ACATAAAVVAA*
>TCRU_605 BNR repeat-like domain/Concanavalin A-like lectin/glucanases superfamily, putative
MQLVAGGGSGVQTDDGTLVLPVEGTTKGESEKGGKSVSLFIYSLDDSCWTLSKGMSDCGC
GDPSVVEWEKDKLMMMTACDGGRRRVYESGDRGDSWTEALGTLSRVWGNKYEEQTKRVAS
GCTTATFENGDANKKVMLVTLPVHSKEKRSEKKEKSELHLWLTDNTRIVDIGPVSEKDED
EVAASSLPYKSAGGEDNNNEDRLIALYEKKKKGLDETPHSLLSVRLTEQLQRVKEVPATW
KKVDEHVSQPCPTSGAAKSALTDNACSAVKIADGLVGILSGSFSSDTWRDEYLGVNATVM
KGTKGVATGYAEGATFQGARAEWPVGEQGENQPYHFANHKFTLVATVSTDKAPKEEDNST
PFLGVRLGTEGGSKLMELSYNSEKKWKLFCAAETNREHSSTWEPEAAHQVAIVLQNGNQG
SVYVDGQRVGGE*
>TCRU_606 queuine tRNA-ribosyltransferase, putative
MTVDTTLFCFETNRGPRTRHDHDGDHCHHARRQQARSGLFHLPHGPLRTPIFMPVATQAA
LKGVTVEQLEELDVEIILGNTYHLGLRPGEDVLNEVTRLKNVQESAAKGNEANEPQPLRI
RNNMDGIHFLQGWRRNILTDSGGFQMVSLLRLAKITEEGVRFQSTHGGNGGGVQMVQNNN
NNNTNNSGNNNNNVAFNRTEECMEYTLMLRPEDSIRIQNAIGGDIMMQLDDVVHVLTTGP
RVEEASKRTVRWLDRCLSANMNPDKQGIFGIVQGGLDATLRAECIAEMVKRTACKGYAIG
GLSGGEAKDDFWRVVAQCCKGLPYDKPRYCMGVGYPEDIIVCIALGVDMFDCVYACRTAR
FGSALTSTGKIQLTKKAFANDMRPLDPACNCRTCNSFTRAYLHLIATKESLGSTLLSYHN
LAYLINLTRRARAAIEDGSFTEYVQNFFVSYYPKRNYPQWAVDALDSVGIELL*
>TCRU_607 Hydin
MYPSQTAASGVGGDGDGSTVIAAHGRLPKILTFEVNPQEICFREFEPHKTYESPLHLKNM
TKETQFVRVRQPQSRVLKLRPPRRNVTSVKVAPGLTVTYKVLFTPEESRNYSCDLVVTTE
REEFTVPLHAIASRGQLTLPESFTVAPCPVKSTGTTSLFIRNTGKLECQWRAEASLPFTV
TPSSGVLSPGGGVFPVSVGFAPTRLQQYESTICFLLGPEGDVVQKLPVVGNAVEVEVVLE
QNTLEFPVTFVTLESQALVRVRNDSGYTVHFSWKSDRSFAEERRAIEQSLLGQTEAVTHA
VLTSSKNEATRRRLREERRETLAGGGRVFDDDVFTLEPVSGTIYAKGSQEFIVTFNPQLA
MDYVATAYLDIGGRRQRLPLQVKGTGIGPQCELEYTRLDIGEVFVGAVHEYQVDIINKGC
IEARYAVLPQNTIMGRKFVFQPSEGVLAPGTQETLFIQLQTDLVGLISETFHIHLHGSLD
ELTIRIRGSVTGPALRFEVEELDFGNVSYNCLHSRVTQMVNVGQVPITFRLRVPESSLLH
GLITVSPSEGIILPKQQEEIHVSLVSDIVGNCETMLLVDVEGVGDGVDSIPIKAACLVPT
LCLSTERLQYGTCFVGHEYVMNLEVVNKTALLGKYNLVLLNEEGVRAANAIVVIDSPEGS
QAPKVIEPHSRSQVPVKLTPLAVGGLQMTLYVRVLGSNEPPLPVLLTATARGPVVTAEPK
SLAFGTLVLLQPSEREFVLTNTSPIPALFFANFPETSKHNSISTAFCIEPSKGEIPPHRS
TTVKVTARLDDARLFSEQIQIIVRHAEEDPLFVSVNASGKGYALVPIGPIEKIDFGDVFT
STMAEKNILLRNEGRRDVEVLWSGARARAGGLSPVFRIFPETVVIGAGSSCTFTVQGLVD
EAGVFTEEFLLKDKKEFRLIFTTCVTGNFVLPVIAYSKKRIVFDYVYGAEGETGNTVIMK
TFTMKNTTTQSLDVTLKCVEKSGEAASPFTLVSPKSFTLMSGETQIVAVNCDACYRHDNV
AHTAKGRILVAFANHPFSEYVSLLANIAFPSIRIEPEDRQVKFGSILTNTEGRSELTLTN
LSPVVPAEFCWSIEYRSEVPSEQPQRDQKRFDFVPFRGVIPPGGKRVVEAVFYGTRGRHD
ATATCTLKGGPSYNVSLIGWSDVTVRFESTSLDFGVMHYLERANKTISIFSPSRVAVPFT
VNTIALKQPGSIVVKPMKGVVSNKVVLTVSFCPMVPDEVVETFFVQVGHLDPQLITVRGF
GQAHTIMLSTSDKNVKLNRIEDSQYLRCMEELKDKEWVPYLEKSGFPCAAPNVLPVVLEA
ERQAYCRNLLLAAKNLTAGASVTEHIEEFRADTSKRERGVLARYVIDFGHMTRLDVRTIN
VSLVNTSIYPVGVILDKQVMESGPLCVEPRKIPTISPFSGTNIALTLFFGDTGNVTNGAN
QLEFFLDIHKGPRILVEVRCFVATPALTPCETVLDFGDMLLGRVKNLPLHFYNKEDIPCT
WRMTLTEPKQKPGAKNETDTANPVNPPLVVASRRQFKVHKERGTLPPQCGMSIMVSFMSF
TLGPAKTKLRLRYASNPEEQYVVLKGNVVGVNVELSPSQLVFPTVFPCQTVKHCFTIKNN
EDRSVEVFSKNFDEKHRVCVGILQRALATQKLNSGGEGEIHLPIREAGDSLPEPFLDFFF
TELQREERALEYRDENGLEIDFQRELRTGSCLSSRRRRASQARSELQTPLARTPEIPAGD
VPPTQPISKAKPQIVVITGPPFSGKTTQIRRLVEKLNVSQLDLDAMVRAEAEFDTAEGEL
IRTILSEREENRTPRVVEDVARSPSPVVAVDRIVKSNEVKILHALLLRHLSTLSSVTDVV
IDDFRSILTEDREAVLIAIERAASVTGRTLQVLSLGVSEATTGLRRSLDVQKKCREIAEA
AITLPLTEEEYETLDEEGRDAYNRRLLHYNACKRALTEASNEVSRYEAELENNPQLTVQE

HAEQNIIALEEQEALIRSASRSKKNVSEPRRRPQWEEISELEQYKELYTQLRRIGGVTHI
VVSGEAEEKDVNKAIVEQFFSGDNVMHSSPPSPIPFSLMEDKNESLSFLPNVGRSGMWEL
ITEETMGRTNTRVEQFCFFTVTRREALVKKTAKGSPAQTTLAMEETARWIVPPKSSVEVT
VVFCSDGLGQINIPFSFGITGTTQEITLPVFACTAYPEICRDYKKIFPFTKPRAIAGKRP
IRVFVMSRKTYEFGPLIVPGGVVSAQSSSFKKNRQLNESLSTFTRSTVPSNKESGAQVTM
TFTNTGIFPAEVSLSFGKEKEPNFSVTPNKFTLIVGETANVVLRATPETIGEVFSTLVVT
VRDNPTPLFVNVSCVGTRPAVTLNGKKELLVQYGRCLIKREVGKVINIANDSLMPVCWRI
AGVEKVPMEFKLSSTGGVLDVNGMYPLEIVFKPTRPGVHNISLRVEVTDAEETLFESIPL
TVKAEAHDVVIEWSNHVDFKLMHVGETKKENVLILNKSPYDVGYLLRLPKCLQNLISLNP
SEGVMRGLVGFKDAFLLNVEVTIRFDKEGEIPASLGVIEASFFDPVKNELLFPVQSIPVS
GEAWYNRFTIKPACIDFGFCVVNQSKKCSFELQNTGHFPINFRLFNYKNGPALLQQEDEE
GVGKKQRKSAKPDTGFQLGVFTVSPSSGTVAVGETFSFQVLTVQKTRSNNRETLGIYVDH
CDPETEAKGIPFELVASTTTPGIVSDLTSLVDVETIFEEQQVVSSYSQRNKTLRAYARDT
RTFYFGTTLVGSRVEERFRIANSSPLMCTVKLQLLPQYPREGKEKERDKKEREPLLEVDG
FQLSIDGEPEKINTLQLPSFESRFVTVSFAPSTLQSSRARFEAVVVGIPDPKASALEFEL
AGEGVLPSVEYILPPRLQTPFAVSLTTTMKKGSRVRGKEPRKIAAHQMAEFATENIVSDT
IQLPVTLVGNASSRTFTVRNTGELDAHIRVSAPDEFTSDISVSKLREVLSLPPGCAESFT
VNFAPTSIEKHRVRLRVAVTENPYEDRELWILAESYFNAISFENIDPGSEDQLTLGQCYV
SQPVEHVMLLRNNSPHAIRFEWSCSSSILQCTPQLGHMSPGSTKQLTLRLYTDTVSGETI
SSVFRVKSITTMEGDDWDNTQTKSRWAVLSPAEDSDAVENSTSSESNTRKNLRKVLEAVP
EPSYEVTGDISLQKTLYVSYATEFASYKITLPMSGDMEISDNLTFPLTKIFQRRIATLRV
KNTGLNVLPFSFEIHDPQRQSGREGGMPGVFTVEPASGKIDPRAYQDVSVIFAPKSIEST
SQVLVGSFPHSLEPKLYISLQGTAECPLVHFNVPASDYLVSRVDGEAGTNLDPNTIPLMF
YSCGLNSKCSVRFKVINPSTNTYRFEWISDPLSRRISPFRCLTPSGSIAAGKQYEMAFDY
LSNSIGIREAKWSFFISGHMSVSFLLVGKTDEPNVFLHVSRVHFGGVTVGNKDERIIELE
NRENTSFPFEFDRTMLNSEDCCVGVKPLSGTIPPKSIMPLTVSFAPKDEVSVNVRLLCRV
KRMSDPLTINVKGEGLRIHPSLTIEDDDDDDLAEPVFVPQLQMFHCFLGRVQPNTVVKKR
FVLTNDGQCSMDYVMLVPEHRFLKLSPLSGTVGPKQRAVMSLVYFPTEEEILRNFKIQCR
IDKVPVYNIRLGAVAYVPKVQLSFMNHDFGPCFITEFSSDSVVTKTLSMMNTEAKESVAL
DCILSKNGIFELDGTSFVLSPGEMRNLVISFAPPEVGDFTSELQITFNGSYSIYIPLKGE
GIIPRIEVPIRFIKLGGARIGERRVADLRLDCRSRAVTPISFVNCVDEALREKGISIFPN
EPFLMRPREVRTVTVSFKPTARMPEFQRELRMLVCGREMPLVVVSAFCEDAEVHLDVQNI
LFNDVVVGTTAFRRIVIMNSGDISQRFRWDPTLSTESEMRIVPPTGLVRAHSEQVCEFVY
TPKDAGNVFRRNVRVEFDDAPAATVNVEAHATERPKAEAVLTFSCCAKATTTKTVPVDNP
TDGTWTIKPVIDSRLWTAPKSFQINPRSTALLPVTYAPMFVSGEKDTATLFIPFHNGAAR
VIELEGVASHPMEEGKVAVKTIEAGTPHLENFEVYNGTTQPLRFQVNAQWTPELEKGMVS
VKAPASIDVPAKQMKICAITFVLLKEGDFRGTVQFCCPEREDHTQLFDLALRVVPKKVSS
RTELVAKVRNAAIHLMPVKNPLGKNAHANIRVENGSDVIFVDSSINIPPKGTVDVPIRFF
PLVHKEYPVATVTATSVEIGTVSCQLLLRSKPPEPEKVTRVSCPLGQTTVFPLRFTHYCK
SNCEFTVRFGSRVTPFSKVGSSSNVKMPGTTRPEGQEVSMEIQYEPTVVGEIKESIEVFS
PQAGLYIFPVLASCLPPQRQGPFLLRLGQVTSIPFRNVFLEPLTLTLSTDSPSFLVLKTT
ETVAAKKTINIQVTCKPEEGGSVSQTGKLTVSGVNNGETLQWVYYLKCGVVDAGPSVAKA
SFRGRE*

>TCRU_608 splicing factor 3a, putative

MFGGVLEKIRLFEADIEHHIDNIVQQKLLADVSNRRHQILRDHFILQEAEAIAPIADKLL
DLYLDQDDIVAVQEAPSEGEDVLSAALKEFEAQIADIREYHRTFRDLPPVKTDLDHPDAA
AMEQLFSVGERYGSCLDLEPHYHRYSNFMLTTSKRAQEEGDAVGSAWEGRVGYFAFVPAI
SSIILHDIDAHRKLYGFLQYKEFVDELLAYLIGFHDRAKVMEKDVLLSSLARCDTDAEEY
WSKLMEHKKAVVKSGSGNSDVSSADKTASSLIVPPPLRKYTKAFALWPITHLESMIVEGM
KAVSPSLAEVKTVIHAEGKIVMLLQTLLFDTLKETEKVLLRDYSKTAEELEWERKHLQEE
FLQSVEEARKKSATTVEGSVAQAAQYDVMATLNSKDVENDPKENTAVADDTSGQLLDRDG
KPVARWLIHLQQLHKKFYCEVCGGTVYVGPKAFKDHFGAERHAEGLRRLGVTVHLREYAG
ISSIRKVIEMREKVISNTASIRKRLHEDQEGEEMQDAQGNVITAGAYKRFQISRKGI*

>TCRU_609 hypothetical protein, conserved

MGSRRRAKRPSSAATEVAEKKVDEEANTKEAETTTLSPKVSEHPASESNVEQPPALPLPA
AEEPEAPAPKPSRRALQRLRGWEPVIKPPEGMAALPASPVVPTADVVWLDNSRRVTLIPN
SGGGVHTRRGAANLAAVSPPTSYFVCTRDPLIKLVRAGTQSVHVITSLPPGGDPCSILDN
VPSVGSFTQRSGEAVTRRSNVTSSFSSSSCFSRPREGLNGDSEGEGGEETGMGDEEELEE
ANGTNADAHAASCRKQPPNKVDTSTNSVEYGGTEADVGKGKKNATLKKSGNATPAATTAA
TAPPTRIGVLSPAQAMLPPPYRRMRRLKRKLHITEETPAFAIHSELRDKMPQLFPKAPFS
TEEDVLRSTIDWCDDMTLMYTRLLWEFAPDEFLKRALQNQQQHDNEDTKKPKLTENLLPL
HSLEEEEA*
>TCRU_610 hypothetical protein, conserved
MPLGEPQFATVSFLLGDAVEGTFRVPITDETTVRRLAKDAMHRLIARSNTGRHVIPRDKI
SVSEVFVKSGTDKAEIFAQDLVNQVVLVKEEVLYMRLRIRETVTAGMREEFLTATTSTVG
ATTSNIDKNGRMNSTTVQTVDVHSSTGEPPQEKASKGKKNSVATEKPVEHTSSSFLSSGA
AAGEKCEAQNGKRAKQEGGEETEVKKEDARTVAGGGKGKGTGRGLGWGPEAHKCFADNYI
TSPNRLMQKSRAKRKATAKKATTPVTKLKGKRELPEKEPSPEVDAVTQPKRRLGWGPEAE
KYFPDNYVASPDRIARLKRQGKRMQEKKKKEEEEAARQEREKKEKEEGEEEEAKMRKKNA
ASSAPTFSSIVQSLEKRLNENQHRDTSPDCTSTVTTRNIKGGTSEGGREPRTAPTALAVA
STPHPNHGNACRRSTGSNLSRKRRLGEIGEDGSALFPIVVERQLSFEAAEETSTTHTPKE
QSTRQLLEGGTAAGEPQQKAPPEGWGKEATRYFDVETYFDDPSKARLSAEILARPIRARR
DVVLPYYFSAIAK*
>TCRU_611 hypothetical protein, conserved
MLSRKGYIGRQLRPSQLASELLPADQTWCATCHLAVLKKNWPDHRVSRSHRLASAKMQKM
KRLSLDMWARHRAAPLEEESAHEESIEAEFERFRTEQRRRERMVQLSSWKR*
>TCRU_612 AAA domain containing protein, putative
MLQSPKGINILITGTPGTGKTSLAELLAQELGDFKHVEVGKIVKENHFYSEYDNALDTHI
VEEDDEDRLLDFMEPMMVNEGNHVVDYHSSELFPRRWFHLVIVLRASTEVLFERLTARRY
SGQKRDENMEAEIQGLCEEEARGAYDDSIVIVRENNTLEEMAATVDLIRLRVESLRGNAA
*
>TCRU_613 RNA pseudouridylate synthase, putative
MGRRIRYSRPKAALPEKLLEFLCSRFSYLSRDEWIKHLAAGHLSVVSASDSNAVTTSGEY
VLRQNDEIYFNPPRELEPDVDEYIHVVHDDDDVIVCVKNGNLPVAEGGRYSGNTLVGLLE
RRDAVSFVSEKYSAARQKRDRTREEDGDAGVSVHKMPASYYPIHRLDKETTGLVVLAKQL
AAARALSTQFEKQSERITAQVSKRTDPAGDGLSAAVFEKLLAEEKVVTKVYVAVLAGAAP
EGADFVMCDRIGLLFDSLWNEGDTEDAKKHNKLKKLKMACFPVNLKENPKRHGRPAASRV
RILSSDKKLGVSVARVDILTGRTHQIRIHCAQLGYPVLGDKLYETTTPGVAGGCCAVPDD
TYIARAKGNEGLVSAAAPRLRVKRHLLHAAVLSFLHPVSGERLMYFADPREWFLRDVMEE
EGAEGDAVRTTAGGSRSALEALRQLLDRAVGALGL*
>TCRU_614 hypothetical protein
MASGPTEPLIDEERFLLTVEVLLANIPSLVSDLSSAKYALLSFSDKFRNEVRQKSSLIPA
VSDAYREFLETRGSLQEEQRKLNELETQLVRSSPPNFLSVEEVHFEDTGGALLVDEPRRS
DGADAQEESLIEENLVKPHAASAGSTVSTAEGLVNIYETHKNSTLSEDASQTALVLSADD
IKRVRESESLLEEEREKLACLARETNVLEDQLELDRSQCEEMSEHVRSIRRNYQAILAEL
TAVESERRQYATLREEWEGRKGIYSEARRDMEEIFVLCRNEELAIISVVLEGVNEHVISI
ERELNEKKRSQEVELAVYQIAYKEQQAVVDELRDAVSYLQRHQWELELMAKRQEIEKYKR
KSIRRLLMASLSASLNTGEALKQELSEEYIKEAKEDHRAVSLVSARIGALEARRGVLAAE
LLRISSTEKDTTRMNCALRRMREILMDEITIDESMLQNEDELTPWYNRELLPPYS*
>TCRU_615 hypothetical protein, conserved
MQYSICVATDCDGEKANLRFLFDSYGPSVAQLLNRSIVAFNNLFRLRSVPRTFAVSAAVV
FNDVHSTWDRLERSTQLLHNSQVYLFQPDILDLPAEIPEPFEGHPLLGDEGSWPQCDASN
SPRAVGPSHYDPRPALTIESPRGLPMWSGHPKKSLLYGYGSRSRHGNHDYDVRGDGTNDR
YRRAAYATPKRGDNLDSIEKGQTSLLRRTLRYSSLSPPIRKPREPIFRSYSDGRRSILRE
EREKIEYQMRLPIDEMRRHLREETRQLERSISPMQRQLMNGSSQCSNSGEGRNLEMTKTY
KANSEGGYVY*
>TCRU_616 Endonuclease/Exonuclease/phosphatase family/Endonuclease-
reverse transcriptase, putative

MEPFTWLPAERYFYPLLNSIGAYQRYTYRLRAVRDVQRQKLLLSGDIEQNPGPIAVLQMN
VSCLTPSKLATLMAQGADIVAIQETWKSSEQIASMHTGDYVLYAQSRIGKGGGVAVLVRK
TLRSKRIPLTIPQHDTSLEVVVVQVALDQNRDLIVASAYVRPPPQVTQSFRRLVNCLPAS
SPLLLCGDFNMHHPQWEPFLETSPSEVAAEFLELCTDAGLTLVNTPGEITYARGTRERSC
IDLTWSKHLTVSDWSASVSPLSDHYMLTFTLHQAFKDTIPSAPKFFYSWGKCKWDLFIKD
FDAQLPAYDYKKQSTGIKAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERIATDSKA
RHLQSPTPDREAEMQRTRSQLFLLLRERLRNTYLRRISKLNPGEPLAWKYISGRKKASLP
SPTSILLGGGQHTYKTARRAANALNRIFLPFHPSHKAVRISKGINRQSASLNINASFLFG
QQNNNESAATFTSGSSLSSSSEPQDKNEAATTSGLVAHLHSPLDAPFNRTELLAAPRNTP
YGKAPDRMKSTVRHCDMFRQRASDSFFVALTTVGRPVRSRLSGDALPSFHS*
>TCRU_617 hypothetical protein, conserved
MPGISVSSSAATTAVRSEASTEGSRTISDLSPSSSEDDARPKNTPDGDDAPHIAEDVVSP
SAGTPMPQRTAAQTDATATPGDSDGSITVSHTTFPLLLLLVVAFAAAGTAAVVAA*
>TCRU_618 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGSGGGFAEDESPAVGASADVGGRQPKPPQLETTPPNVQGP
KIPSADVGLPMLEVADTSLEGTDGDDVEEDDGEEEEQSAGKGNEGIRAQEQHGEHDRQND
QHVGKRNEMPMIQNQEKKEKRLEKTQRQREACSQLPRTAHRHIYRMMLEEAMRRSPEMRV
RQEMMIVDKIH*
>TCRU_gamma, conserved domain containing protein, putative
Elongation factor.1
MTANLIRVWLQRMERVRQYALGVAPIIGKDRRHDIVALCVLRGWGMLAIVEDVEDTELFD
WGRRWWRTLWRGGSA*
>TCRU_620 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MLNASKVSIPNPGEEFLTEKEEETPSSPEEGKAEQEVGEALPRPQSSVEAPEGSDAAAVS
SGIRGSHGKREEETETDGSGELASPPALSSVGTSAHSGDDGMGVREGTTLQEEVPPPLGT
EDIPKADVERPIYEEEATSPEWATERQTQETTAPLVENGDSEDVGTAPGNASTTPGETKI
PSESNATSLSDHGILPEHGHYSELAGMALFAESTVHGCVSRVLLLLLLGLWGIVALC*
>TCRU_621 hypothetical protein, conserved
MPRGGRHAGGAHTAPNGIQGRPRNSPDYYLGNCGGDDGGSLLWAALPSVRVDVWIDNIRI
AGSKSGATLWEAQVLRNADSCHASMGEGRESGATQYTFLGARFDHTHRAVSLSEKFVRSV
CAVPSLNSSTIAEMEVVASRFLYAASILGTRLCDYYFFMAVRRRLSALYRGLCGRHPR*
>TCRU_622 hypothetical protein, conserved
MVSMRLNDLDRARHGAAGDVFSLHAALIPVYFLLGSFLFSTLMIFCFVCFFLLTEDGEAS
NSPHGDAATEGNDEQQGSEAHSGGEKGVEGGHDDDGKPSRKHSFFQESRRNRDVRDMPQG
APDTPTGSNGEMFLPQRPRQRLSDID*
>TCRU_623 DnaJ domain containing protein, putative
MTDYYQSLELPRDATQEQIRRNYRQLALRFHPDRAGPEGAERFKEVQSAYEVLLNPQKRK
IYDRFGASFVDNPVSDVLILQLGGRSILCIMACIPFVAASLVVIFTAFLVAYVAGRLVAR
DAHSVNDHSQAYWNYVKVFSPLFIVDIIIGIPTLVVFLCRCARYV*
>TCRU_624 Leishmanolysin, putative
MLTWCCAWQSAVGGGALDDCRDGCEEHHDCDDIDGMELQDGDGDGRTLESHWSQRQAKDE
WMAPMGSAGCRTELTLAALADLGCMRVRWEMAEPMRW*
>TCRU_625 ADP-ribosylglycohydrolase, putative
MVATLNHNSVPRTTNFYENSLKQLSDIQQKQTGLLIGAVVADAAARGLDGCSADEIAEFA
RAQAKFNSGGGEEEAEEELLVFVRAGPQRRSSGPSLTGALQHHSYTCLLLRQLLRAMASA
RGEFPVSYVKDHWVSIARAHPQWFAAEHASLLNVLGVVLPLPVIYPWADDTTLRSYATQF
IDFLTEPPVGQAAAEKTRSAVKSYTFSALGVALRCLQSNPDPSRNAAIMAVPGTADLFPE
DLALLCPARTHKELLSQLIDANSTGCAAGGAAATPISMCGGSSSCGAGSPSLPVSARPFA
RDVCVAREALVVARHARSFADGVRAAIRLGGPVCQRSLIVGGLLGARMGVRCISPSWLSA
THDHSPLATLAIEVAQWSWNPPHH*
>TCRU_626 hypothetical protein
MRAGNPGLELGLMENTASSLGGVAARSFLNDSITAVVLMEISDFSPDFGWLLLPELDMTL
LCMGERSRDVGVRFLPGVGTRFVPGERCRPFLIGGRKPSLQEASGPRRDINWDM*

>TCRU_627 hypothetical protein, conserved
MDAEPEHGSLQSDAVQADGDPAGDGDGGAAAHADPDGVGERHAVVERGGVPDTRRDDDGG
WWEPDAERHPRRWERRPDAADGGAAAAVSVGTRPAARHAPELCAGVDGAAARVWRSVGSD
AAQRDVGAQRDESVHRPGAGCARAPRLLHCCRRDDSHSLRRCGGVRRLQGCAAWVLHDQV
RHAARRRQRPLGDHRRCCGCGGCCGGGDRRAGLRPGDAGARRVCEDAMRLGAGACEHRCA
AVLPVGVRCP*
>TCRU_628 hypothetical protein, conserved
MVGRADHTQRRKQHKARRVHHRQEGRAHHVREGNHARARKQHSRHAEVLDVAASHGRVHS
RNQAHHTQHRQLEHAPAHVAAPHVRQQSAVHPLLRRGVPIPDGVQQALVQRLPRKLPVPR
EARAHVAGNQVAHTSRERHTVQHANNTNHAVMPAGARHRQCKHGAEEYA*
>TCRU_629 retrotransposon hot spot protein, RHS3, putative
MVPTLQLDMWRGVEETQRTEWTMSSTVEDILLEGSTLRTDMKLNDFLRNYVGGRGVEEFN
ENVYMEDFLISSNEFIQDELFLRTIEASPPYQEQKKEREEFYMLLEASNKLSHERIFTLR
QCRDYERKGYDHSSCKGKTKRSTHAGTDRSEAGGRGKARTNAGNEIYHLH*
>TCRU_630 hypothetical protein, conserved
MHSWVTHALEERYIEALQGLDGTEGVYCMAWEHEWYEDGIVMDWSALHRGLVASVCFPPV
AAQMDDLTRFGCCVRDDTLLVTSIDIRAPWRMIPLSDQAQRLSAFLLPPAANACGNGARV
AVEELRGYRFVKGPPGQRSVRDDVYALLQTVNRQLTRAGVKTYVFFSNVIVASKNFAQLM
HHTAAVFRALREAGFAINGNGSSFEPRRVFTVVPGRYWNTLTLDSLRREEDILAFLVDMF
YRWLEDCYVWLCETPPRSLLLSAGDDDKKLQLFSDFYTRLVYPRHDYIHFLAVKGMTLAD
VLRLAGPRLAKKMPCVGPQKWSTLELRLCLSALDAYNNFPCK*
>TCRU_631 translationally controlled tumor protein (TCTP), putative
MRIFKDILTNAEVVCDNDRPMDVEDEIVYVVKGSYIEVGGEDYGIAANVDEDAGEGAKGE
VDDSRQRVVDVVHNNRYTETSYDKNSYMAHIRGYMKQLLERIEDEEEKKKFQANAAAFVK
RVIKEIDEYQFFIPEGNEEDPDNGMIVLCKWDGEVPYFYYWKDGVKGERV*
>TCRU_632 START domain containing protein, putative
MAYLVRKTEFSSSPLGFASHKRGVPDNDDGLYREAVNFIDVERLLLADAPATGFKLIAQD
EDCGISLHSRPVEDCPMHLMRAEVELPCRPAEVLAYLNVSTRRRWDDYIAELRSVRILPR
PGGVLGESNVVDVDSVAELQLRPGQRRVALYYMAIHTPILLVQNRDFEMVVAEEVRHDGT
VWVKAFSTPLGYVEPLDPRQSKYVRALMLFSGILARPVINAKGNMESHVSYVALVHPMGL
VPSVLVNVVLGAQLNALKRLQRFIQQNPLSTLATEMAGKNSEHRSGAEYSGKAVIADRVR
QAAGSQSTDQSAANVAVSKKGKNRNDGGNMKNKEAARGGINPQIRRQFASLMGRVMGFMR
SKL*
>TCRU_633 hypothetical protein, conserved
MEEPKNEVTLGVRLATRYVPNQVLPSTLSWGFFMGVEDFMRLERCFAERSITHDGDPAIT
KEWLVHYMMQFLGDHLNLPASGVGTEEATVCGVQLLDEEKMQFYKEEVLRWASSFSIGVS
VHDPLWDACEVSNAELARAEHSMNSSTYASSFNKGASSSNKSGGYSATTTASSHEGAPRG
GRFGRTRSVVRMLLRYNRPAGHAQTQRKEPARHEIVRWSDLTTNLVRDYERFHQVDEKEL
SFTRVRTELTSGNSSLLRSVAGKEGLDADWSRVTEGRGDTETDVFTGSELHAQSADHILV
STVMDCVVTASKDGVVKLWNGKTGIFMRNLYNAGNAWVIGMFLLHDEEYILIATTKSQLT
VLDFPEGNVLQKYVGCISLQTALYEVVQLSANNIQRYGMKPGECGRHRVELRKDETAEHY
HARRRESQNCVFSKVLPAKPVVGFDAPTASWFDKYSGIFFFGTATGAVGAFDISADVRPS
ALLAGANSKPVCLLFLTEVHAGAVVGVFYTSYVTSVFTAGADGCIYRTPLGPTGKPSGES
RLVAQQARAIRSMQWWPPSKFYVTIHVDRRVVLWVIGRYGDPLHQFPSETQEVVSAALHP
RRQRLAVLLSDKTIKVYETHGNKSLATIAQPTPDSNFTATDATRQMMERSAVDEDGVVAW
HPYNSSIICCLRATVVYEPSKNQLQTESVGETEINFPEDERGAFSNRDVRDIAEDVKPKQ
RNLSAVGVVESRRVESHRSGVVAMAVQRQALRLHTFDEEGWRMWDLDTGVIIRQVNVPRV
ARMEHMPLKRATVASCSWTTSLQVRLVTGGQDASILTWDPVTCLPLAAEMLVHDVSEQLD
SDVNLMSHRNKLIAWSARLCRITTFNTGSILPSGIEESKSVLLRVPSLASITACCVVRDA
YLCVGTGDARIFFFSLRGGAPTHDCVLREKTEEGKGAVVHLIFLNEQNQNLLLVILDIGI
LFVYSYVKQAVVYRICLGRRFECRIRKALYIPEDGTVVYGDSLGRIRVVDVRGCTSLSVE
FRQAFILKSTFQGATDEITSLESFYSSGRRYLLVGSLDRMARLFYFDDTDWLHAPFSNVA
MQQNSVAAVKFVGAFGRDTWRLSDPTTFSEEPPTALRVPANNTAEEEMLLETILHPETRP
ESVRSLMDSLLDDDFSVSRARSRRGTKAITPLSASGSPRGMLTRPFFLTDISHPQEEVTQ

VPSLSFLSSTESARQPPVAQATQSTHEKQGPSIPSGDEEGGAPSTSQGIDRVSSMAPATG
RRPQFRPRPGEKFSNRCSVSLFTEPRPQLPSLDRQTEGPSEGGNPYQGFLAGSLSPPKKR
MALLTMTRRLEAVLPRKFANGEFFKYANELLMADAQLGLRRTKSGRARQEKVDLQLALEN
RRQLAERVEEYKKKQEKRRCDKRNTLMPFAARHELIPVVFPQPSVLSNEGNISFAWMLNA
SSMGLPQKPFAHASNTM*
>TCRU_634 hypothetical protein, conserved
MAWRPALRAAAGGGATTASFNSPSPISLLGRGVAVQLCRLTLFCPQRFKSTSTTATTGGW
SYEQVDTRTGRTPLDTLYEERLQRIRAVFESPLPPMPRDGNVSPDFLVGFAHYEYRLRDQ
YRAVLARALDLPVAAVRLSVAWSGRFDVARFNRVQKVCGVCVASGNTPHMAELQERIRRV
VRAINERQSESFLASHLVQASGAITEVEFAATERDAIVAERVHRWLCEHILRPHLVVVVY
GANNDARDGPNSNGVQKNGEFARQRAFIEEKWLKAFYHRRVVPHVLSFSRLKELFQDAVR
RGEVKGVALLQPKANPDEEARHAKKSLEAEAKSGPTASATAAPAEESGTPVKLLALDDEA
AWYTLLRSAVFRRCDNRVAFPLLFIHGDSVGGVEEMRYLLHNREALDAVLLHPNDVAFKK
KFMSRFRSSHSRLHMAEEMSV*
>TCRU_635 radial spoke protein RSP9, putative
MSSVAGDADGLLFVGRALSTAERAALQSSIPLLSARYETPVRFWGKILGYKGDYLVTQAV
PEGVFGKRFSFFSVDGGTSWRLLDPLTEDEVAFCDQLRGVYMGDPTFMYKVRRDIPPEPE
PTAAMPDADELLTAAREKYGAEKTGQEGEEEEEEQEQEEAEEEEEEEEDEDEEEHEEQPK
KKRPKFMIIAVPETVRLAHFIQLHDAACTLVVRGQYVFTPSGSGVSKNTMFAGQPVRHAM
KPSCYLRAFHPGNEERNRILYGPTYSSVTDRLSPITDDEPQGVWVVKYDPTASIVTVQNL
FYNGSLFWYRPGTNDCGQVYFGNGERDLETCFLL*
>TCRU_636 Domain of unknown function (DUF3437), putative
MLQGTRKGEGEAMMEPRDGNETIRTTTNSRTTRVFYEDPLLPYSLQCIHPRLRDAVEVKG
RAELLRGAQLLIEHGTPEDVARHISLKVRERESIVDQSSSPEEEDNLCAGIPLQPAFTSP
NSEYNSFYEADEELQHRCHYFLSTFTDEHESYNVPYDVQRRVVPLLYAWIVDWDFLRRNT
DCWVCVTQCFCRVVQSRRRRFSVRPDFSLPWRPLVEILISLFFQSDGVMDLNVFQGMRKA
AGRHLERLCELAALHFGADAWPGLWETFAPYFSADREEAPIMLCLLSHLFPIHHLSDDAT
GEPLPITERIVKFLLEDSLYWQQLSQNWLVYSLKILFKMSLHHVGVVDFDRYAEPLFSMV
LYELHLPIAEDMAVPKGPVGFGVLSKVSLFRIGENEMSAAEGFIGSMLPRRTDSPLWNHL
QRFVNATSVFLRPNATDKVVLRRVFAFYSSLVAVIHRRIKKQRSYQFMRATKKTKFEGRI
IREAYLWDRDTIDWFVELVAPVLRLLLHHRLEDAPRIVGLLASLSPQIVQRLFLPYVDAG
LRGHLGSPTQRGLALRLLAKCLFPLSECPATREECWLFLAEVLPLLLQWVNPGELSLSTL
VMNLILIACSMTKLRDLLGGQDAECSFALTLVERIFDCSAHVKFGKGCAFDLLMHVMNAL
SLNLSDETFSCCVSRVLKESEVQGGISKAHAVSCLLEPFARRAPERMMRWAIQTFAPPLK
NVSTPLNELQWCAHLLAGCIRGAGLAGFSYRHELLHCVQCQVSFITREEQILAAAALYNA
LFTAFTEFICTEAKAEPFSHSKVGDMAFCDTDELVYDKKQDEFEVSMCFCRSSAVQLTWR
EASEFHIAYVVDVYKRFVEDSVDIIRNIEQVLPPAEGERGEGLRSLLHIPLDKSADTKSD
DGVGKLGDAASATASVEADVDAFTPKNVLRGVLLWLRLVIEINQEFHADVFCAAQTFNMV
PWWAQDPKSTLQLLPQSLGSPLLSAVPEKIHNVLIEYAFRRVSGMTAAESITAKAFYPDR
SLVMQGRPRLHSTQVDEMDPRGLHLVLTILAELCNITPMTPLQYDHCYIYSQGPDVFANN
VVETPKGRLYLPAMYWRMKAESFTQKRRSLLTRVVSPKRLSELLRIAHTLLFSPYQLIQD
NCSHILTGCVPMMSRKATSQFLSEHLSVLEEISNLWSQENDVTEQHSHDHDPGNTTSPSF
RGDDDCETDYPADGPDGVKATTLKGSGRRRKHDDCKKKIAVDDESGYGDGDAPAPAPAAD
AAVVVCCCGGDGDGDGDDDKYEDMKGAMPHFSSQLRRIISSALSLMSAGFNSSYFYYDDD
LIYRTCELLVQFPDQLVVRRIISRVLTQSSYDLGCLSAIEGARAVRLCDKLLLLAMKFAH
TAPDRTLGCLLKIVALYRPSQIALLSPQSVPLLFRLAVNCHAKVRETSFHILQTLVLSLR
EPHPKAYVLTRRGPLEASENAAFFRSRYELLKRECPSFYGLRDLGLAFLPKAIRVDAEHV
SPDMFHDGEVAAVPAETVKLCKNYTEEKRDYFIDAAQGEAKQQEQRLAQEELKRIIGCLS
GILDDELNPSTDGEANMDDAARAKLRDGWIWKVMQLRHDQKTFSESRMRVWKSMGKLVGV
EPSVRFFTRVVRLWVNDFVELARSGSATAKESQQSLFSCLFDVLVAAIRISKRHPVAREE
AMRCYMDALRLVCTSALVPHEVLDSFLRSISALHDTLKVNEVWLIYEFLFAELKPFLRAP
LATDASTVKNETESGMTCCTSWCSGRTQEIVRVLNVMVHLICVFAQEINVELLPQLCKQV
LQNKELFLCSTSSSIQGCSAFMISEIMRLSLYQSEYIASNSAVLNEILSFVDCIEQLVEL
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RCTKPFGNLATVKTFVMCWCRPLPPLLNARVKSVLNVLVRALDIALPEMDALNLRVEAAL
QRIAYVRLPRNTIHDMLQMLCGILKEEQPYGKSRPAKVAVSRMLSRVLLTNLHRIGKFAT
MQNVASAALASIGHGDGRVRSEGRLLLAVLTRVASVEQIERIIRDCFMELRGLSSVAASM
TGGHLQSPHTLHENVRKRRRIALLLALCSILCATPGVVPPYVPRLMERLAAHAHDPAPEV
QRAVKRTFEEWWRSHREGWELEHKPRFVAANIQIDAMLPLLTAPAYLV*
>TCRU_637 hypothetical protein, conserved
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QSGKSTLIDFILQRRHAQTKLDSGATAVSKAEECDKSEHSLRKILSPRPMNSSSTSLESH
SVNRISDCSTSFSKLGGLPCQKPNGMNGMDEHEELEGILCSSTSNASIFVPSERGNKPDT
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VTGMDKNSPHGSMVVISGRFDITIVDRIRRKKGDAAHLLREGEKKLCDQANGIHSPTTNS
GVSGSRQTNAPSASAGSVGAGVRLFNPCRAPFWLLQENVGGGVRWEGEGTTAVQLSDSLC
AEAFFFTLPCEVVGTHRMVAIMNEFFEPFATLTEGDRCKDGGGEHVTSPSNQQQRHCSQE
KKGCAHDEKGDDYQSICQLISDITFYVLTFSDAIVLRSEGVQTTDKQLVNRSPPMANSLP
ELVAMFQREMLRLFDIHVDSWQVIPFSGPMSRVTRDVLTEIYEARLARMDLLDADDGPPP
TFSALEPLFSLNVSTLFPITSGVVNTEGKLQVAITEFCDVMYGQRFKESRGSFSPGQMEE
LVLQHALRDVWKDSGACQLLHIVRCFDWNSPHHTVSQIALSLVIWCRQMHLVLLQAQKIL
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HHIPFVAQNARELKLTMRKELSLLLARLNTEVINYFMAELANAFPALVKMCEVQRKIAKG
KLLQLVTTVNSRETYDSAERRLLRSMLSEIPRLRLLEMRPDQELEAFVTGLRSSLCQDQL
VLYVKHLDDGWNGQYAGCAAKTLAYLLKAEWESDARQLRSVDYIQPQNATLLQQLREYQD
VFWAPMEMTEMTPLPSDRGGNLACIGLGDQPSINGATGKAKEAAGTHVDNGSSVSKELPQ
EGEKGSLMGSNDILVSKRNPIGFFLAVWQEVFSSMSFRPWLLLHNVRYASLLNNITLIFL
RGQARLESVLKERSCETEAVLRSVRHEMHLLGVELPSSLKRLSSRAIATAHNMKKLNAET
IISLSS*
>TCRU_638 hypothetical protein, conserved
MADTVTAPTFRDYTATFSAAMPPVLSSQSASFSALLKPTPTALTKVPSIGIDCFPQRFGE
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AMLAEERQRMLDLAKEIEMERAKRTEEQQKRLLAQERELEEWKHERAKEMEEQRRRRVEE
EDRLRARQHEREMLLMREEAELRLQAQKSVDDHKKSIETSVNSAAEAVMARLREEFRAIE
GQWTSRLERLQLEHINETASLRQEIERERQLVAHGESQLSETRNQLAKMTSQLEELCRQR
EGDAHSRGTETFMGEIHQKAIERLQRAFEEDKQSTKQWFVEEQQRILNSHERTLHEIQDS
HRAQVRRLEETLDASNRQLREMEIEVQQYKTKLAGAALKPSSASADELRLREELRTIRKQ
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LTSAREAHAEELQQVRKNQRKSESAVTRDAAKEFETTLRRMNERHEETRRALELEKGQLV
RQLREAEQRCEDKQRRLEIELEKSEAARRDGERIQQKHDEKERALAELQESVEELKRKDC
SVADLSSRNRKLQQELEQLRHNHETATRAKDSELQELRHDLAETRRRVVGLQDELTAARR
MQEEVEVRMKSYVSDAELKEKQLRRSLEEATQSVQSWKDSYTQLQSQSASAAPKMQGLLS
EKETELSRLQETLDALKRDKNSLEKRTQELQTISATREKEMLDQASVVKGLNAEIVSLRE
QLSTAMRPDKEMSTQYLSRALDYSQSPRTPTVGGATDARPAQPKSTVEASKSSNLSLTAT
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EGVPLPTGRQSIPTVRPSLPGVFPPGVGTFNSGTHLPVGFSPLASAQANTSASASRSPSV
TVPAPSTSPTAPGHFSAQSVVPVPVPVHVPTPDPAVGHPVSSSTFPQTSQQINPSSGLLG
VSSGVSISQQLVPPPAPAAAATSNTASLVPSGVSSTISVPVPLSIPNPAAGNPRPQSVPL
TSAPVPVPIPLPIAPMATAPFSRK*
>TCRU_639 nucleolar RNA-binding protein, putative
MQEFHAFEVQPGKEHALTLPPLHGFHLSVVSIPHAGKGRSTLYVTVDGKSYAIATLDASQ
GILQNATDLIFNEAQKVIFRVKGNAPLHCCGYRQELDVDFHDANDRDGSVDDGPNAVPMN
GGKDKEEEEEDEEEDEEEDEEDYEEEDEEEDKEDDIVLHDPTQAPQNGYQGDKSEDYDTD
HEEEEDEDEEEMDDDEVQPMKRAKPEENSQSQKKPQQAQSPQNRPSNQQKPQQAQSPQGR
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PQNRPSNQQKPQQAQSPQNRPSNQQKPQQAQSPQNRPSNQQKPQQAQSPQGRPSNQQKRG
RE*
>TCRU_640 Domain of unknown function DUF59, putative
MTELVNPNPTVFRDALQHQPQRSAEELLQEQDESFRDPIDSLEVFHHIRSIRDPEHPNTL
EELKVVEPELIRVDEVKQTVRVQFTPTVPHCSMTTLIGLCISLKLQRSLPRGTKVDVYVT
PGSHEQEEQVNKQLNDKERVAAALENKNLLNVVESCLNEFE*
>TCRU_641 RNA-binding protein, putative
MKEAGGFFTVSCTDRGGVGSSQASSSVGKADNSPTSGQFSTPTDSSKGSEKQMHPGSVLP
AAGTSGGVFIAEKNTGFSVVAGNVPPSNWQTGSNAHWPQSSGKSTLFKSTLNPDAKEFQL
PSGQGNDALALTHASMFNPSLTHGVKSSTFMPLFAMPSTTTPWKTGSAVSSEAIFVSGIR
ADAMKWPQVSVHTRPFASRDAAGPPPSLLTPRTITRQVMEEYAEVCCSKGYHIVTVFNLE
PRTTQEELLAIFFPMCAQSAELLPIHCSPRSNRRSGVVFFLSKAIALMAVEKLDGFVPNK
QHQPLTVLYSGPDTSETGTRESSILSANSPQSVKSAHQQAQLLPQPAPETVTSGSPQMWR
HPTAVQMDQLHKEMWQFVKSTASSSSSGVMKHVVAVHGLTPENAQSVLLWNFINKGAERY
ELWPMNASGLSSATMPFKGISALVWFSQEAAAKEVVAWFEQQRREGGQALQIDAVYLNKL
DFAHENSSVGNAQLRNGVHDANNNGQLTAVASPSHMAIIENIDAFFFREYDDPKLYLVAV
HNLSPNTDKKALFSLFSPHGALDAEVYPGIVEFAGELRRSGVAFFDNEFMARKAAEKLNS
FVPFKQPNPLVARYLKKVWNSRMMTPLDCASSSSGMAESVAVAASGIKLNDMVVSVKKML
YAPVLDGERLMEKMLLVITHPDTTREVVEQLASVIVEALTAMSHHAGALSTPLVNALMSL
HEKLNIPQNVVKDSNVNEAVKNSELKKYMAYMQLIAHTVINLFMDKTKPHESRKVAAVLS
AYLFQFSYLVKTPYELSVLLMKKHEAALNRAREYMMKRHANIKPMAFLGDGEEEEHRPWL
TLMECLEQLTSLWRQNNKSRAKKDPFRKEYEQRVNEFSQGEISLKGGGSSLNTSTRPTPR
RVVAKVTPGTGSGGGGGSSSSPGLTHGSSNSSRIDPRTLGENNIMSHEISRESNASPVVV
LPVFCANDPNPSGAMRTDENVSMIASKLSQYQSQPQQTLPPQISRRDMPVRSGLSEGLCM
SEATKPTLGGSRISGGPVQSVYTHAELMERTVYITKLPSFLRRAQFRRILLHFGEFNKVR
LCRDDNQIQAKNEAFISASTSAVSAASSSVQGAEPSVILYFSFVEFAEQSSAKAMIEYFR
NIVTNPQPFSFLLDNSVVWPESSYFTPQNIQALLSVRTSPARNPIHDQLPMDAVLVPTAN
TPRHVLRNRPCVFGIDGGEKTLDATADANSSSSFSAGVLANPSAVCGSSGVGASGRKVAS
VVATASESLPLRPSSTSALQTERFHGDAAGEGLDLNAIVSAVAPAVMTNTWVSETVELPG
HNDHVFNPIQGSWLTDVTASTLGGDPLAGVTFSEENAHPTTAPAPDACTAEADGKDIWPP
CVPSCFHQFFDSESDADDDDDGKNN*
>TCRU_642 Integral peroxisomal membrane peroxin/Rab-GTPase-TBC
domain containing protein, putative
MSDPLRVTVECWENQRYHPLRGWGFHRLPMDRSTWSNKKGDAVICRDSFLTPVGWVWSSD
WEVAPNGNESDGWFYAADFSIPTRFCSAIPNAMSYVRRRRWVRTRMQVAADTGVDSVLLD
ALSLSSSFQADPRLVWLNTSFYGFVGASVKEQRENQRLQHISCYHLHRLLDISCSETSVD
NNDDDDDLCGEEKNGRGSPSPCRHRSVTTEVLRCVYRYGLPQCLRSALWLEWSGGSTLLR
ESPRMYDELLERSDRVHGQPLQDILQDVVRTAPRHPFFAKKGGGAEDLRNVLLALELACV
LPSYHQAFSYIVATVLLNLPAREAFWVVTALFSGFLPSGYHEHYTLQYDLQVYNEIVAHK
FPDVHVHFASKSIDVSVFASGWLQGLFCAHFPFCTAARVLDVLLAEGDSSTLVRFLVAFT
GKFRSEILTMDSSGSLGYFANEWARNCFNIEDVVRAMEKDGLRSVVLSRREELTGATVAS
*
>TCRU_643 DNA repair and recombination helicase protein PIF7
MWTGALKAHQHLRTMRRWNEARVGVGQDGMVCNERRCEGGEDSDRTTHATSHAHISIECD
RGVMKRSRDVATESDGNDSGSQLTPLLVGFTGSASVTEERGMMEEGGDDGAAHNAVEMVS
HSTEVAVCEVIVLDDDSQGAEKSNVLSSKNSTPASYSGKLEQLLNSEKSALVSSTPSGES
PPSMKLSAEQHHVFDLVVKYGRSVFLTGGAGTGKSHLLRAIIEALPRSSTFVTATTGIAA
LNLGGSTLHSFAGCGIVDFQTHSAEDVCDTVRGKSRAKRNWRFCKVLVVDEVSMMDAWFF
DVLEYVARKIRGDNSPFGGIQLVLAGDFLQLPPVVKHSGQDPRFCFESEAWCRVNPRVCI
LSERFRQNDEGFFRMLNEIRCGVLTAASLALLASLSSTTTVRFVQEATRDVRAEGVIEGT
LGTSPPSLLTARDVVDSRGRTRAERYDGFSILRARRAEVDAVNSERFNELKTEIFSYQGF
HWGEGKYPADLPAVVSVRIGCRVMLLKNLDVFVGLVNGSVGTVESFIDIRKVRDFSNKTT
PVDLRNMAKHTFLPVVRFDTCKDNGSKDSACGRLVMVEPHRWSVLQGDREVSYSVQIPLQ
LAYAITIHKSQGMSLSRVNVDFRGIFEEGQAYVALSRCTDLNSLVIENFDAHRVNPNAKA

LAYYKALADAVEAEEKAEKKMLHARLRHPWGYNDMDDNDNDDDDGDQEDNQSHSRIHSEA
ARKRRNMADVVEEVRQRITPSYILWSSLRQRVLSTAELASSVHGALLVMDATSLLALGSS
HNSTALYEKVFVKNQNMMRVPRLVKEELLRTASVSGVEVRVTPTVCLSFSSLRSNSPGGN
FVHEAAELAAGTLCLMEDAKSDFVLDEQRAGESRPLPPSVPEWEGFFSRCDWSDCELNNT
CVGPYSHPHQQHIELLEFSCYLLEQYSSHQAVLVCTESIELAARALAVGLRVCSMMYLCP
VDWARILDEGGKSK*
>TCRU_644 PPIase, putative
MVKGDCIRAAHLLIKFDGSRNCVSHRTGKSTADLTYDAALAELKQWAKRIADGEITFEDA
ARQRSDCGSYNSGGDLGFFGPGVMMKPFEDAARSLNVGEVSGVVRTESGLHIIKRLA*
>TCRU_645 hypothetical protein
MAHAGLAEEEIAAIRRELDTLKLQISTTSPDSSPSSLDGATSTPKRGGDDASPQRSVDSL
FERLTQEQQRTRQLEKELQALRMSQKQMNTESLDEISAKKEELDKLMRERDELRDWLQRG
VNECRRVAEEASRLKRDLEERTRRCQSLETVKEELQGKINKVQQLLIESQSQIERLQEKQ
RLLEASAGEHVIAEKKLMEVNEEMQKQYEALVAEAESHRLHAEKLEDAEVCVQLLTERLR
QLLTHVERLGQAVRKGCVEDVAVDEFFSRENVAEPQHPLDELVARAKSLPHTIAIGIQQL
QENIVAFVAEQRRLRAEQEATQRDHLEALHLEKQTVLHRYEKERETMTQEIAQLRGELLR
VLSKNAVDDDESPDRQRARIIEIEELLRSNKQQAEENERLRNENEELRQKLRRMKIDWRK
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GYIE*
>TCRU_646 KREPA5
MFTSTWRSLAPRPLNRVTLLGAMHDVQRGFLGQSSVFQFTLTCLLFEPPKRDQAEKKPVA
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QLFPTILVEQGRWSHVALLHSLRRQRRDWQLQNALTETRNLKQP*
>TCRU_repeat, putative Se.1
MNPSTASTRPNAVACTTHMFHVAKPSVPPKGRGVRRTKEAIPTRAAAVVAPLRRSELEER
LQYLLQAEEELASAVGPNDVMQVLEELRRRRQDRKAVALPRKRLSESLHFICPHVATLVR
ACESTSDEAVVQILREFYQSHYAAGGNEKGRSLVSTALAEVLLKRRANENDISEALSMLD
DAVANGHTGAMLLVGLCLRDGIGVPKDLEAALVWVERSADAGYAPAMFELGVMYEDGVED
CGESTLPADWGEAAEWYKGAADRGHTMAQLNLGKLLWKAAALARDAKPDNCDESTIVNLQ
TKSRAWLEMAASSGSEEAVRLLRRR*
>TCRU_648 cation-transporting ATPase, putative
MIPKNNIISEVRLLQRRHWSTWVTVWPFVVLYAVSFALYMDPELVWDRMTYLVHSTYIDF
FHAICTPVLLFLHGFLSLFTIWSVRFRSMILFKTLTREHMESATHILVCTHEHKGESEIV
PLMQASEDHPIHFVFQERKWKLDAKKGGFVKPHFPVKEPLSHYLDWQGLSGSAMCAEQLD
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GTCIVNEATLTGESTPQLKEAPDRMELSLVMKKHGRHLLYSGTELLLSNGPHGKSDTERG
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VIALAMRPLQEEERLKASVHNLQREDCEKNLKFVGLAVYECPLKKDAKSTIVMLQNGSHR
CVIITGDSVRTAISVGQDVGILQCRRQLVASGVGDGSGAVEWCDALTGERISLDQRAILE
KTFVRTRKHMSPLDDEWDLCVSAENLSPSSMTALIAAYNEQIAVWARCAPTQKEDIVTDL
KKKDHTVLMAGDGTNDVGALKQAHAGIAVLNAAAVAPQKTDGKVVNNSPQSHNEPDVPAE
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GRSTLVTTLQMYKILALNCLTSAYSMSVLHTDGVRLGEKQMILSGVILSVCFLCMSRSQP
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KPTLLNSAMFLLTTLIGGVTFAVNYRGEPFMQSMRKNKPMFYALIVLTLVVIYFASETDP
EGNALFEIVAFPSQEFRHRFIQLLLTDAGGCFAIEYACLFFLTDYM*
>TCRU_649 Dpy-30 motif containing protein, putative

MLGGDEGSATVAPPSEEPVRLLSVPEYLESTVMAVLTEGLEDLCRQRPANPIDHLALFLL
RRSKSNTVTEVPAKDAIPAEPPKKYE*
>TCRU_650 lipoate-protein ligase, putative
MMRRMGWCLCPTTTLFSFLTRHATATHSERQLTEARASVALVSNSRCIFENLAVEEALLR
GVILPPGQQLLFSYVNRPCVVIGRNQNYLQEVAVSAARRDGVPIARRSSGGGAVYHDTGN
VCFSFFTHRSAYHPERTIEIIRLFLCCAFDICPERLTTTFRHDLFLDRKKITGSAMRVQR
DIACHHCTLLVKSCSERLSAYLQPEGQYVFFTTSSIGSVRSSVTTLQMAGVLPEGYCSDE
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SGSLDEQSALLLFMRAVLSVWRVKNVFIPVISQ*
>TCRU_651 KREPA3
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GGATDDAVKSTTGVHYVHSQESVLPQAPQYHLDVAPNAPEEGDVAAHWRCVNYCVVLGPV
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TGRLRMIPQYDSAMKKYYHYPVIQVHPGCGSVVKV*
>TCRU_652 hypothetical protein, conserved
MTSVVRSGESSKRPSGMEPVESFKCEARCCCVAGNDVWVTELKGGIAVCDAQRGNVLERI
AVGGTDTRVQFKCMVLVHGDEVWAGSINGAIHIFDVPTKRWKQSMTILGVEARAPILSLF
FDGFSVLGGSETGRIVQWNPFTKEQVKVFVALAPVTAITVTGGFVVNGGRDGVVQFWDSR
SGEVICEHTQDKSAVTSILVDSTTSTLWVGRTNGTVSVYTLSVPMSFNCRLSVGNGAVTS
MLAVSGKVLATSYDRSVVVFAAKTREEVSRSRTAHNAFIHYAARVYAAEMARIWTIGNDG
VIYVWDVAGYFLPCRSSPTISPYDQAAVVHDARGALTVENAQLSSRVAESLSRVVDVKEE
LRKVRDEAHEMRLRLISFENVLKEKEMEIASRTARMKELEEDVNRLQKSVTDSNARVDAA
QRETNVLRADHNTAVQDASQTKAQLSAKISENANLKQQLSATCTEKSHLEIRLRDRDAEL
TQLRAENARLHGAMGQISSSQSAEREMYKKMLANTEGAMRQELNELRRRSQILGSLVVSM
EYTIRRKEEEERDMTALMNAFRRRVAERVTDPHLAALLNFTMLRNPDRFDMDCDEHTKEL
LCDRNGPFIQFLHLLRDRDPDSYGQLLEYLQHPDAGSQFSQLFDKILSLAQKEGNASGDD
DIVTFKKSLPALLDSLNAMKAASNRTEDAGGSVGNISKPGASVANANYLLPPNTAASSNQ
TGGVAGNVGLGSGASGVYSNGGNAATFSGTATLQPQTSSQQQAGAGAVEAGGALSMNVDD
FKTFLRSMNISIEQPDLVGQAPLGLTEDTYVKQLKSTFEFILQTRRDLVQQMGILFKRIV
KGRQVVDALTRNAREGLSPTHRSSGSLGGGSGRQNLGSIATSILEELHRFVLNLLAVYFT
AAEKQRLGLGA*
>TCRU_653 Bucentaur or craniofacial development, putative
MAHLRSLSISHDDENNNSSSGSSGESEELSSGRGELSSSSCSLTSDSSHVRGNPGKGCCD
ALAKERMERQQRLRRLLSQRNLGHAVALDDGKHVEPFISRKGALDADDSVILSIFSNSLL
FSRLLAVLNSSQNPAHLQNFDEVLSAASPHFYRSFKAPLEDSTRQPARVGALTRRECAAL
ERSGIVVRRRKRDRPASKVGSTFFAGKVRRGRAADNGQMTHGSSATSGIIANSLRNWEQH
LTEELKAEGVTIETFRQQRHGNSYLEERRFLQESQWADYQRELRLEEKRKEQEAKRAIRR
GEENKN*
>TCRU_654 hypothetical protein, conserved
MGRSAKITRGGDKTRVNQGRQEAKLRAQGAKSHATSVKEAVEARRVQKKRSQAIATELRS
KTQAQAAPIVKMAPKIKKPQE*
>TCRU_655 proteasome regulatory non-ATP-ase subunit 10
MPEACFLCLDSTEFMRNGDQFPSRFLGVQEAASLLSNAKIQMNAENTVGFLTLGGNACTV
FETLTLDVERVMCSLANISIRGKRCHFSQGLQIASLALSHRTNPRAEKRIVAFIGTPLSE
TDEELEKLARKLRKDDVAVDIVGICVEANVPRLSAFVEKLNKNGNSRFLNIPAGANLTDS
LMSSSILLGADSGGGANETQDTYQGFGVDPSNDPDLAMAIRMSLEEEQQRQAAAATIAAS
QSTAPVSTATRTDVPPPSAEPENLENMSEEEMLARALKMSLEEAQKAANTAVKSEEESSL
HEAEKEPERPKPTEKSFQSAEEDELHENEEKSSGEKQPRNKK*

>TCRU_656 hypothetical protein, conserved
MVLATIRVLVCGAEFHRVESALGSSVENTNFAWNRRYEISCTSSTGVSEADGRLLSMCHL
VVLTRGASPPLEVKSYCGKPTVSLESAPEGVVGMLRNCDFYYGVHALEKLRSLVVDIGLS
PPHVIWDGVLRTFTRNGELSIRRAFWLLDKDGDGVLNEEELLAWQRSVTSACFSKSDLAE
LCTHCSLNNFPPSINGETFMKMQENFLMNGDAKKVWATLHLTGVCPDGLPYSWRDIHAVR
VSKESNTYLSHTAIQFFRNLYKLRRFSDLNNMWDVTPGCPWKHVHGFLTTEIPLDRFIEY
WKYMALTNRSVVVQYARYWGYKGDTILLFLLRHARPYREVGEAVPNTIQVLVVGSAGCGR
RSLMFTLTALDEEVYKEDTSASQEMYVRTTTFPVRHGEGEALQTVVYVTVPIENLTKVLE
DDTLEKQLDVVILCYDGSHIEETTLPIMRAYLEAKALPLRCRNLPFVVVMTKAEASASTE
APTNESQVMERFCREHQLLWPPVVTSVETPEESDIAALNEYMYAVAKEPEIAVGNAPLTL
QRILRRVAIVTFFALAVGSVTRYFFRRMRGRRQ*
>TCRU_657 peptide methionine sulfoxide reductase, putative
MASGAPATFAAGCFWGTERFFVKKFGDALLSHEVGYMGGAESDEVVTYSAVKKGTTGHAE
VLHVKYNPEKVTYQQLLDFFFRIHNPTTVNRQGVDVGTQYRSAIFYHDDQQLKEAKDYIS
RLNGADPALREGFVKAFGDAQVATSLEKASRLHVAEDYHQMYLKKNPDRVCSHRIHW*
>TCRU_658 N-terminal region of Chorein, a TM vesicle-mediated sorter, putative
MLQQAVSYVISSLAKIGDIDACNVESSLRERTLRIRDMSLRQDTLNTFLPFPIQCGKVGD
LRVKIPWPASNEPLLLCCEGMAFTLNGETSQSCTKEMTREEIRGGITEESILGTVVTPSV
PVNSHEEQRSAAPLASEENSEERETSWSAALEDDDYMSCQSVSNTSFASCDSQEDLTSLP
QNGKVFFCFLSIPPVVLCRGS*
>TCRU_659 N-terminal region of Chorein, a TM vesicle-mediated sorter, putative
MVKTEPTLEAGAELMKVIVITFSGVAVCANAAKEQTQKIVEIDHLSIRITSVYSSAGILC
RKNVAIVFDGVSSLFFDEDALRSLTRCAVSHGIMKEVPEYCRPFYKLRSLSSRWSHAKSC
VFAFIRDRRRRYNFNSSHLHFYAEARTSYLALLDYCHRTRDIAEKREQLADIEGDIRYRD
VVLFLRRKVQERYSTTVLAGSTGAGVTPPPTQPSDARQFVVVSSLHVDAKITCVRLPAET
TVWLRDVAFVKRHGESNFSVGNVTLVAGGKSQLLRAPDSGEPFFSLQQTESNGMTFVRTT
LEALRFITTSNWMLQLVQPIMVAMPHVLRAIPETNCNAPETKLSNRCEKTTSFVFPLIDF
HVDDLRFHLKQLSLTHIERTSGDSRVGLLMKELSVRFGEETDVLSPMKVEMTEEEDILVS
AVTLNVSNALWEYLYHVRTEWNDALLRVSNMPGFVSRVQSTTGNTQIKKSFAEVCCEAEL
KEEFNSALKLQRTYLLGVVITFEPLNLSMQLGTMNMWRGAQTCGFPSVHANISSFEFSTD
HVEGGVLTVTCPSGILYSKTSSTSDASRVNVSIGVLESVWKASSTRNLLHIDAMQFHVYG
DATHCSAETLRSWML*
>TCRU_660 BNR repeat-like domain containing protein, putative
MSRRVFTSAVLLLLVVMMCSSGGASNAATSNSGNVQLPHTVDLFLPNQTLVVSKDGRSQG
TKRDAFVSPSLVSAGGVIAAFAEGRMETEYQGGPSIKPSSDVVAEYIDAAWNWSTLVEKV
NKGTWKAHTVVCAAEEEESLGVVLRPTTITKGNKVFHPAGGSDVSYEGVCWREGGLELKL
FVGDVTNSTPGDPGERIKWGDPRPLFDSKYSLNHKSKLNTLFPSGGSGVLMEDGTLVFSL
MARKENPNEAFYTIVYSKNGGKK*
>TCRU_661 BNR repeat-like domain containing protein, putative
MSPPNCYNPRVTEWEGSLLMIVDCENDQRVYDSRDMGTTWTGTIGTLPGVWVNSQSEDYP
DGGLHVDALITSTIGGRKVMLYTQRGNYWKGQTERTNALCLWVTDNIRSFYVGPVGMGNA
GEKELASNLLYSDGYLHLLQRRGNGEDSAISLSRLTEELSAINSVLSNSAQKDVFFSNLT
IPTAGLVAVLSNAASDDTWNDEYLCLNATVTTNAKKLRDGFQLTEPDSRVSLPVNTRANN
VRHVSLSHNFTVVASVTIEEAPSGNTPLLTAALGDAGPEYFMRLSYTADNK*
>TCRU_662 hypothetical protein, conserved
MAKGFLRVNWRACGGWLILQWQRPLPGTTERVAVSVLANGTTPLVAGLGSKACQRVRVPY
GRDSMFRVLSGCHGLRRMLSRRLISMHSTMSVTKLPVHGPAGTHQCQETLPDPVLVEGR*
>TCRU_663 hypothetical protein, conserved
MTMGASRTAKLLDMDLDPQLTLNMAAASQRISQPRRIAHKEAGPSPHDPRTFIIGYGASK
LRYGSELIWAVATDSAKNEMQETYAGLARIVSGVPSTVDQ*
>TCRU_664 hypothetical protein, conserved
MCSQYGPLRNSSQRGRPIAVSVANSCLRVAATQKFSKPPSAVHPRNIGRQATEDSMSNEL

KGLAGVYQHQRSPMGSAVELASSTALLGKVRLEVIGSVMLHFVYQVCQLHRRGTHTTARM
LVGTRRPQPKQSPQCHFLSSLTHDGRRADGSI*
>TCRU_665 hypothetical protein, conserved
MPHGELSAPPAALCPARGERRTGPPPPVSAAGTPPTVSAAGTPRRQPRLTPRRTVSDVVT
PVRDKTARGLSERIAVECGRCRGGVPRCTLTVAALSQSRPASRLRSAPLTMGECWLCPAG
SRACAVEPNTGCAATWEAAALG*
>TCRU_666 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MGSSGVNGGGASPSAVPTVSTPSAGKDSLQQVASGKSSDGTQTVDGGSFSDGEPTVETGE
GGADGREKEEIHAQNGDVNAAALSNSLGNVSQGNNTDAGTMRENGLLPSLLLLLGLWGFA
AL*
>TCRU_667 Concanavalin A-like lectin/glucanases superfamily/Protein of unknown function (DUF3676)/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MEGRVPWRECNCDEWGEKGSQWRNIQGPGAGAEWPVGDMGQTVPYYFANNKFTLSATVTI
HEVPQSGSSPVPLIGVRMNDTSSTVLFGLSYTHEKKWLAIAGNRATSKLVDGWEPNKTYQ
VLLQMDYDEWTVFVDGKEIHNKRYDKKLFNSHRISHFYIGGDSKHQGATGGHVTVTNVML
YNEELWGNDLHKLHASKVTIPSLGVEEQPTEQVASTGALVAPESRSEESTASHELTEGDT
DKQGENSVDDLLLAAPPSTVVAGSSVPEPATATESAENSRSDDNAQSSGDETFQQFTLNK
SNESMQRDSDVQPQELLSAESTGVTDVEGSTETNDIEQPEEEGEANDRSGESTPSVAVSS
DMDTVAAPADSEHQVQQSVELSAENNEVRSTGTGITGAKRSLILEARGSNSERTMNSGSS
LTPSKSDAETKSAENTDDVSRTEGDEVSSENGEEVPQTVDTAPENTNTTPGETAIPSDSN
ATTPSDTEILLEKEHLGELAGMYLIGDSTVHGCVSRVLLLLLLGLWGAAALC*
>TCRU_668 RNA-binding protein
MPAKKKGGRGKTINLVDFNDEYIPEDNLDWAVEVPREKSRDELAGEKIAKRDYSRTANNA
LMEKGGFRDSPSEPVNRTKGINDLQPPFVAHFGNLRNGTTEEEFLRNFHEDCIVTSRLIS
QDGKSFAFVEFKTAQALAIALAMDQTMVKGRKLYVDLATQKQVERLHGHNGISRQNPGQS
QQGAGLQQLNLTRDAFGSTQMTEREMGHRSGFCSRNDLHMLADLSRDTLGTATRSSESAA
SPVGQPDFSSWRNEGPVAQPEFHTGLPENRRSDAELDRRGGMGGGRNSKRQSPVSAGCLA
NWRDEPMTQPPPPPPLPPPGSGSGGDNSKNNGEDGRKGGWASDGAGRGNHRGPPKSQAAP
RDDSKWEALRR*
>TCRU_669 hypothetical protein, conserved
MMEIRQCESVSGANSSVLVPPLVPKSRGPSLPDGRRTPGGPPRTTPTRTASRYYCRRWHS
VGERLPSSEEPQVVRLIPKAANGGSTAWGEKSSIADSPSSFNIETVSEPATLHGDRASIV
FELEPGMDSGSKRLHMSAPTGSEDHLRGTPDAMKATPLPGVLTPRTIQRSAMPNPATATT
RSSPSRSPPSLRFHLVDHPVMYGDDDDADSLPSALPPPKPYPIVEVAAASQYGVNGTKLR
LYGNVMNNTLVSPRGRSNMRGTPNMYTEGTVEKGVKPYTTSIEVGAPSQTLVSAPSPPPY
MLNTPVQSLLNEVNAWVDVIHSVEDKNCYKIYLGSTEKALHDTQGEMKALATKHKLVNKE
LYAAKARHVERLDGNQARKKPVAQVKDAENKANTAWKRQNEEEEEVGEEKEMTREEEEWR
LEKGLLLAEKALLLQKRKELCYHLRRGTNIKNVAALALSGRSSWSRSDGSANDTVSENTA
PSVSDLETIQLRLELKEAQVQLMKLVDSHRILQGAQRTRTKEFEDEFVVLYRSANLAKQE
TEGHRGTLEATLRKAEQLLEKCQQKNEESLLLLLEQRVEEARAALRPRDDKLLTNDGFRS
RMPSIGRCSSTGSTARRVSGASVSPAFVTPKTTAKAEQNSLRAKMQ*
>TCRU_670 hypothetical protein, conserved
MGTARKLGHQQGLITAERELLNAEHANAIADVQNRNAELNWQVEEAHHNVSIHESNIAGA
SNQVREPQQQLEATRTQLQERKFQLGELSAQL*
>TCRU_671 hypothetical protein, conserved
MARTRRAPPSHSRTSAAPPPARPTSPSHNQQQHHTHQTASTPQQQPQVTNVYLQRGGGGT
GILGTMASVAAGSVLGHGISNMLFNREQPPTQPAQAQEMAQRVGDGACAPQIKSYSKCLE
ANAEHPENCKWAWDYFIQCQDEQQQGQ*
>TCRU_672 ubiquitin-conjugating enzyme E2, putative
MALTTRIIKETEKLQREHQEGIEARPSPSNPRYFHVKIRGPPQSSYEGGIFHLELFLPEE
YPMVPPKVRFLTRIYHPNVDKLGRICLDIIKDKWSPALQIIKVLLSIQLLMASPNPDDPL
DNEVAESWKRDEVAAMRTAREWTQKYASPQA*

>TCRU_673 hypothetical protein, conserved
MWRLSLLRRAAAAGGRVNSSGSASLPYRRVLKMLQAEGEGLPAAGGVFEQFRAFYRQVMA
DKAASERAVKPIEEFCGASEDVEPFALVMMKVLCDLQKMEDLRFLFAQCLLELHSPSIEL
FNVYLLAISLTDSFNQYEIENVVEVMRARAIHPDVVTRLSLFILYIRLGQDYSVWWPEIR
DEVLKIAKSGQRGQYPLLEVRLQHCFQTILRLHHDVTMIHECFDLLKLVDQKRISSRLLL
PYMLLSANNAAAPPATTVQIVELLEATRKLEDNTSEGASLRAVSEDAETERTNVGSTDPV
LNNELTALKLLAKCAKWGDVASAVSVREYLRKHPGIISPTSQPAVSLLFLEAASRGAMLK
EALTVLEDEVPETHCQPGPRPKFFLESRKVTLLNADPIMTLARLVAFGEASVEKGLAILE
ERREAGGEVSHKSLNVLMEAAALLKDEGKAAMVFAAFESLGAVRTSRTFLLLLLSMPDAA
SSTARIPEVLAEMSDLGIEVSSDFLRGALELAIDAQDVFTAMQMVGYHEKRSISIESKLS
IRLMRLLCLVVDVDSVRRLIAALKATESPVDSRTVSLCVATFKKWAIPCDDLKAV*
>TCRU_674 S-adenosylmethionine decarboxylase proenzyme, putative
MLSNKDPLSLMAMWGSVKGYDPNQGASFEGPEKRLEVIMRITDETHSEGLHALGDGVWKG
VVGSLNAQIVSKESNEYIRSYVLTESSLFVMRDRIILITCGTTTLLNAVPFVLEAVSDVR
GEVEWVSFMHKNYSFPWEQKGPHLSMAEEFNTLRTYFPSGKPFIFGPVDSDHYFLFVYDD
VIRPCETENDTQLSMTMYGLDRTQTKHWFSDRFISTGTETAAIRKATKLNKVADDSWKLH
DLQFEPCGYSINTIRGAEYQTIHITPEDHCSFASYETNTPAVNYSERINTVLGVFAPIRF
SVIVFIDPDSDVGRLYQKGQNVGVEAEYYPKYELQNRTVNEFAPGYVVMKMNYAMRAEVA
EKDSTDTVEE*
>TCRU_675 prozyme
MLESTWAAAREEVPESVHALMAMWGGFDGPRNANDCGIEKRLELDFRGVIVPSEVSVLDL
ESVMSHAGELLERHSAEKGLISLVFGNSLMQLTQRHVIVTSSSSVLLHEILGPLLDLLRS
HGIDIEWASFMRMNTTSPWSSLCEMSEIMAQEYAQLKSVFPSGHPYLTGPLDSDHFFYFV
YDAIERNVLGAPPEDDVQINVYMYNVKTDGSGDDDDALKSVQQVVPLSETEYEMLRVSTD
NMAHPFAAFETNSMIAATKKRELVRGLLEKFCPDRFTMVVLQDRCSPLAQKGSIFDEMEG
YTIMNRATNHFGQGYAFHQTSYIRAE*
>TCRU_676 valyl-tRNA synthetase, putative
MKRLTPQMAAAYTPKDVESEWYEWWEKSGFFRPASDLGRKHNGNTFVIVSPPPNVTGYLH
LGHSLTGAVQDTLIRFHRMKGDNTLYVPGTDHAGIATQVVVEKRLLRESGKTRHDLGREE
FLKRVWDFKENHAHVITRQLRQIGLSLDWTRERFTMDDHCAGAVLEAFVKLHEDGLVRRS
TRLVNWCCALQSAISDLEVEFADVPKNAKIAIPGYDKKVDMGVLTHVAYRFEDSDDEIVI
ATTRPETILGDTAVAVHPDDERYKKYHGKRLKCPFRDETIPLILDPVLVDVGFGTGAVKI
TPSHDPNDFEAGVRHNLPQLTMMDLNGRITIDGPFKGMHRFDCRREIVKELEKMGLLRDV
VPYEYRVGRCSRTGDIVEPLLMPQWFVDCSEMARKSVEAVRNKELRLYPSSHEAVWFHWL
ENIKPWCVSRQLWWGHRIPAYKCSGVVPSNHEDPWVVARNIAEARSKARAKFNLTDAEVE
QLVLDQDPDVLDTWFSSAMWPYSTLGWPGDTDDMHKFFPGNLMETGHDILFFWVARMVMT
SLHFTGKLPFSEVFLHAMVRDKNGEKMSKSKGNVIDPLFIINGITLEGLHSTVTNGNLDE
KEVPRALKLQKETFPNGITECGSDALRFGLLSYTQSGRSVNLDIDRIVAYRQFCNKLWNA
VRYVLYHALGTEYKPGLTVIDVLRAESYPLECRWILSRLDVAVEECTRGFSEGSYDFALT
TNAAYRFWLYELCDVFLELTKFSIHAGGDRKQLVQDVLLHVVEVALRLLHPMMPFLTEEL
WHRLPNYNTFGVESIMLAPYPAVTGWKNETVEEKMRIMMDTVRNVRSTKASYSLTNKHKP
DVWITAQTAEVKQLLMDHSYMVISLGVVGNVSVISPEEVEANVPKGCGFSVVNKEVGVNM
MLLGFIDVQKEVAKLDKQLVGLQKQIEGLKKKMSIPNYDMKVPADVRTANSEKLDTLTAQ
EKQILEGLEKMKSIL*
>TCRU_677 UNC119
MAANIQVTPEQVLQFSAPTSEFLCPFTANTYNIEFYRFTIRDMETGKVMFDVERNPEDYP
SIPTIAQLPEEVHRTMRTIYYNFPPSMLRRRAIGAKLVFGINSDFPVRNFRMIERHYFRD
TLIKSFDFTFGFCIPHSTNTWEAIYDMPALSEDWIRAIIDNPNETVSDSFYFVENKLVMH
NKAFYAYDAPEENAVI*
>TCRU_678 hypothetical protein
MRSRGSAPSSAPGEQHCTLRIRNPAADVVYHLVFEGNIRKLTGAQLRLHLEAICLIPAEQ
QVLTFNGVPVENTSTGASLGLHNKAVLELHTAGEASRIPSSRRGDWGDRRRGGRQTHPAE
EHLNQSDRIEFSHGLNTSATTASQCTPVPRPRQQRADRERAGERQRYPCDKHDCGGPRAA
TGTCAVAPLERTPSAQTLSPVDVIIEEDAIDGLGTAMIPFYDADVEDARLEQREYVWMME

QMRFETERMNRERELLRQREELEHEAEILEREKCIVKRRTLQERRKLVELHQWICEEMAM
EAQILNLNGHENDYNNCANDDGDGGDFIERGK*
>TCRU_679 mitochondrial carrier protein
MSTPQTHPATLVDARYNGRRFFFYHLVFGPTGAATLAGLCEILIFHPFDTTAKRLMSHQH
IVFDPTSLSNTWRVFLRVVFAGIEHDKPLGARITSLDRVRHMYPGSTYAMLYKVLQRVIK
FAGQSYMRDFLESRFGHIFLGDAQEQSKQQKQHTHRRNNHGAMALEATAGCLVGVFEVIL
LPIDRMKVLNQTNKGAIKNRSFFRILRQEGVMRMYAGIGTTAVRNAPGSFLLFGGVAWTK
EYVFHLEDYSDATVVQNLVSSTVGGFLGVWFTNPIDVVKTRIQNKRFEDGRVTGWSVMTE
TFRREGVTAFYKGMLPKLLTSAPRLVFSYTMTQFFIRCFRGEKPKPLRESK*
>TCRU_680 hypothetical protein, conserved
MSTKAIGSCNPSGTARHTDSEGPGQMSQSSPGRSEDDTVAHRGGPCPEKVTVNTQLADAA
TAEEERRRENTDATRKTFMEVSGQHRRPPPEQMLRQLLATVTAAPRSPSPLPHFASCLCC
CCRDGDCACMKWRVLRAREGQRKLHCPFDEYCLQLPRNMNSRGVRGLLFSCFIAFLLLWA
PRLHFCVKAVCERCGHDRRSRHVQYMWWGLVCRPCWSLPPPSVCCSRCMTVCVCVCLLPR
IGVCVVRGVRRTVHAWLLLSRLVWYALCVRLPHLSSLLLSIFLTVQISPTPLNDHTHDDD
DVPSAMRPVGARRVLLPVRERDSEW*
>TCRU_681 hypothetical protein
MMAMSKGESDGEFLKADWRLIAPLRLLGTVVSAEAKNDEERDGCGGKEGAFRDICGKPLS
SASLDVLGVGVRGDADSHLPPRALSAGGSSPPTGWVMLTTVVTHPQVSLGTQRILLMAAG
TRRGKLGA*
>TCRU_682 metallo-peptidase, Clan ME, Family M16
MLRCCLPRRGIVQTVKKDNYVLSRLSNGLRVLTCDDGNGITGMGLFMLNGTKFEDEKNTG
AAAVFESLPLRSNQIFTGREISEALGSLGNAFKVTNNKEAMSVMLMMPRYHQKDGLELLN
AMCLHPTRDEMEFQIAKEKTGERAGLHHRDATSVCLELVHEAGWNGRGLGQPLDPKKEDL
DKLTLEKFTAFHRTYTRPERTVLAATGVADHKQFAAEAELILSFDSETAPLGAPRKHPYT
GGSRLVQRTEAPESMNKFQEKNLSHVALFCQGVPMNHPDYYNISVIQTLLGGGTSFSSGG
PGKGMQTKIFREVLNREGFLHGLECITAWYSDGGLIGLYGSAPHEYVYALLKVMIYQAAS
ICQRVSPLHLEMAKNQLRSQLILLGEGREQLLSDMGFNMVVHDHIITASETTEGTKHITI
DELKRVCDEMVQRPLTFVVYGETTKMPSHEKLEETVRKTYERLN*
>TCRU_683 enoyl-CoA hydratase/Enoyl-CoA isomerase/3-hydroxyacyl-CoA
dehydrogenase, putative
MRRVDTILSHVGHRRYCHWERSGDAAILILHHEPSNNLTPKMRAAIQHYFREAEADPAVR
RIILTGEGRAFSCGVDLADFSASASQMEYDGVLIPSLATLTNMVENSVKIVVAAINGLTF
SGGLELAVAAHYRVASPSSEFSFPEVKLGIVPCGGGTQRLPRLIGVRAAVDMITTSKKLT
AREALRMGLVDHLASCTKKHDKDRNDGDNAVSNKDGDHLRGNNDHLVAVAIQLSTYWKTP
RHLSCDNRRLGNSIVNRALFRWMQREIDKNAPKGVKAPMRCLEAIRASTTVASFSEGLQV
EMKLFFESLESPEAHAMQYLLRAANAAFCGNLASLPRGASDGLNIRHFAVIGCGTIGTGV
VLLMLRSQIPVTVVELNEEQCLRARLFVQEELDREVENGRLLPELCEQRLSMLSLVPYHA
DLVQALKEVDMVLECVGENPALKKQVFTRLSEVCPPHCILATSASTTSIGELAKVTRRPE
KVIGLHFIPPSDVTPLLEIVQGSCTDQFTILQALRVGHLFHKAVILTRDVGACLTTRLFS
AGLYQAFSMLEEGAFPVEVDRALRRFGFRLGVFALEDLAGLDFTAEIRTRLQKNNTTFSS
QADVYTIPRQLVEEGRLGQKRGLGWYNYEKGTFFNSIVTKLRGAKRAENEGVAALGVWRK
GGASLKRVPRPDRAVELLILDVCRKKDILRRDISEREIVERIIFAIINEAAKLLGEGAVL
SSADVDVAMTFGYGFPAWKGGVCYYADKFGIANIVHRMRIYNRAFGDAVFPLPCDVLASM
VTSQQTFRSMWQ*
>TCRU_684 hypothetical protein, conserved
MRKRERSASASPVMGATSQVEPPGQRVWLRQQVLFDVLRRTSLAEQKDREIVEWLTDAAE
WLQDSEYEKLGAGSQAELRFLVLGVLHTMPWWRVVEAVDPKRVHVASRGAQSATRAITRW
HEKIQLAFERVCMLLIEQSPHAVRGVLEVAMKPFQMRPPVADGARRLIPADSIMRIMNAV
STKYPSALVLDVLEQTMRSLVPKRRWAEERHHRACIALFLHLALEAHVPLFPTHTYGQIE
PFGNGASDPFCSTSHVISVQGSEDSATDAAASSSSNRYHQLHPLEMTCPVMSASDADFSD
ASMNISSTASGHFFPTRLTDFTMQNNKMLAYRNELIRFVLQQLLDMELSLQNSDNESLQE
LTSPSSSFYSIGPTDATRVPWRPLIGRFKERSADKPFVDILRGCTSIVFHRLAEDLVRQR
AAGVCGNAEWWRELLAFHLNFVIKMECPIFLLYLAPSLALLGGEEEAIDMMHKLVSLVTK

GYLPVQQSARRVTAAGPARVRMAPPCVGPLMIPMTHRVRAAVYIYPLFRFLRDRLGSGEG
TRKRLQKWVVQELKGTAIVSASLIVQVLFAQCAAMSQLLEADFVEEMNSQLPGSIALRSL
WEQYLFPEGMTSRACNGDNEGMSSVSTNNSYNGTNTTTNDTVDVGAQKRRMDLLKMEAQG
FLHPKLMDDCPWDWRRCQTERALE*
>TCRU_685 hypothetical protein, conserved
MKSVASQFLDTPYKEEGTVGTRQNGMTMGVRSDDAARCVNHPPLFSSVLAPRPVLIGPLL
RSPRISETVVLLDGVPCGAVCFSGRVVRCEGPQRHGGVSASRAYTALLISDNTGLISVMQ
PHTARVNVDVGAAWEGVTPCLTGGVAELAGNATDEMVHENDYVFVVGWLAFADTSREVRL
LLQGVVDFVTGGDGTKPDENCFCVRGTVRQIHDMNELHFWALAALETNVRLLAKAGDFPS
VFPTRRKNV*
>TCRU_686 hypothetical protein, conserved
MAGCPADELREIYQELTQPCKHDNTYVTVQPSWLRSAALRSTSGRTHPTAVGFSSRNGRP
VAAGYTSLPVNCREACEGASGSSEHTSTSGQNAMRKSPVSLGLVDTPSGSAGKGNRPTRV
NQSHRTGLESNICLPEAMTSKVPDAGGMNTRHSGLFLSTPTEHRWSCWLCETPCARPGWL
NAPELYLGEEEGADMDDYYQHHKHHLPVTLLTLCSRCSAACSLPADASHASVLRKAGATR
VLVQRTEVFVQFLRGFKRLLESLAAKIEEKMVSDARVYAGGTRPSLWDFHPDFQSSVMHQ
LIDMLASTLEADLLQSRRQQVDVLSAHERLLLEGERVWLQRQLSTIEENGPSPMWLLRTA
VVPLSTAENGIMSHDVSHAPQRGLQDERRKLHANLRPCFLSAKTEPGGWWHDQRNRVVQG
GEGSNEALQNMMERALTARWHQLGDESASSANVTDTPATKDDKRDNQQLHSPTFVSLPKD
AGGGGARLIHEDPDNILLHYFEGRLEDLPKFKLLSVDAARGGGNNECLPQPFRHVPGTHR
SSCGDLSNVSSDVVLVAADDAAAVSMDTEGLLKHLREEQKRREESEAALRESHQKIAALE
KATDHISGLALELEYVLGEQLARMWRFLRNATQGCVDVMMQKSLLFSDEMAALMRQAQRQ
AYGVSGMFPPNHAGRAVEARRDLPSPAPMKSPNGALAESNFERLRSCANSPASCAARIGP
THAL*
>TCRU_687 protein kinase, putative
MSLSKGEHLKLYEGDLIDSRFRVLRELGAGNFSKVYCCHDITRQRDVKRALVAVKIVKRE
YMEDAYFERDMLDVFRRKRAEGPMVCRMMEFFEWRKCPVIVMSIHGPSLRTRRLGFKNGV
VTRAKLVQLAYSLLTTLRYVHFDCQMVHTDMKPDNILLADLDAPKHSLGSQWVVCDFGSA
SLWRMDQLDADLITTRPYRAPEVVLGNQWFYAADMWSMGCILFEVATGQRLFDVRDDVTH
LQLMEKRLGPLPDLFTRNAKHSAKYFTSSGSFIAESESIRAGKVSMRKLKDVFSDDPELY
ELISAMLIYDPMKRLTAKEGLQHSIFDGIHLLSKKTDAIDNNGHNLNGNSIAFSPSVLHS
HIEGKLDTGSKQLEILSGVGGKIVTRRGSSVPAISIDNNTSLNPHPPKRLGLKFVGKAPR
VGGTTSRAFIFQKARPQDSSVVNVEPPRCLTPERGEKTSPDNSHPSGSFASSHGNDQTHK
MRRFPVVYASPIDMSTENETLVEGISKLCEKSVFASSSNTSEGDSLVRNPPGPFPIVIPT
PEKVLSSADCFSEYTNPHRERDQPPLKVSDISQSEKSLGVSQVDDTAGAGSPLGPLTHGI
NMNGLVLPTECESEVNVGNVLRPFPSHPLSCFSATLNSLDLNAAKGGSDWKDSTRKSGLH
ALATREMKGGCNSLTLHPAHTNVSELSWLSNSILRPSTSSLPPSHAPTTGKQSLPFNLAD
VISSPKTAQTRNLLKEGNVRVRVFPNGAQGAVMPRVIIKKSFEGTATNSTQHQLPSPTVR
NAGQQGLSGAMNSLAGLPRAGSSQSMSLRASTIKVRRRSDTHVHVLKTVNTVRSKTNHPN
SQEISFQKSNYPLKNGSTVAGRGVLMDMGTVSSETSSMFAPKLTASTGVVSTKISSFNSV
NPTVLGVPQKRRPSVDIRPTHSQLIQRNVVSSGKPCVCVNNPPGQEYLNQSDVSRAMQSN
GGADDDTFVSGVTAGMDGNATQHVGALMSTVEDASCEMRAPHMTRHFPTVQAPE*
>TCRU_688 glycosomal phosphoenolpyruvate carboxykinase
MPPTIHRNLLSPELVQWALKIEKDSRLTARGALAVMSYAKTGRSPLDKRIVDTDDVRENV
DWGKVNMKLSEESFARVKKIAKEFLDTREHLFVVDCFAGHDERYRLKVRVLTTRPYHALF
MRDMLIVPTPEELATFGEPDYVIYNAGECKADPSIPGLTSTTCVALNFKTREQVILGTEY
AGEMKKGILTVMFELMPQMNHLCMHASANVGKQGDVTVFFGLSGTGKTTLSADPHRNLIG
DDEHVWTDRGVFNIEGGCYAKAIGLNPKTEKDIYDAVRFGAVAENCVLDKRTGEIDFYDE
SICKNTRVAYPLSHIEGALSKAIAGHPKNVIFLTNDAFGVMPPVARLTSAQAMFWFVMGY
TANVPGVEAGGTRTARPIFSSCFGGPFLVRHATFYGEQLAEKMQKHNSRVWLLNTGYAGG
RADRGAKRMPLRVTRAIIDAIHDGTLDRTEYEEYPGWGLHIPKYVAKVPEHLLNPRKAWK
DVRQFNETSKELVAMFQESFSARFAAKASQEMKSAVPRYVEFARL*
>TCRU_protein, putative NUP.1
MRKVEEVNAELMKAQRDYRALERLLRSSGRLSISRVENNDGEEHEREMSFTPTFLRNTEG

AELAQFLQISSLQADLMLSRSTCHRLEARQLELQTALEQCEWRLASLPPGVEESHAELLR
VRGQLENHQLEYHRLEGRYKALKRQRAEEVEQLQRQNERLVQQLREKRDKIGSLSRQMRD
SEVAAKQQAEELAQAFNLLETQMQALREEVEGGQPRGRQARRQGVEETTEAEGKMLRGRI
TFLEHTLRQKETEMHRLQEELGRNEAQLDQFEDQVTVATQRLENTARRSTHLEQKVHELK
RTNQELREELGAVRACVVVQAERRSPQRAPSTDVLREALHGGRASSLASTPTQGEREGRA
ASALPRAATKRPRAIDASS*
>TCRU_690 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MGAILKDAENPVLLGLSYNNKEKKWTLLCGDGQKKEHSSTWETQTDRTRYQVAIVLRNGT
QGSAYVDGQRVGEPCKVENKNSKGISHFYIGGDGSNKGSQEGVSVTVKNVLLYNRPLDGN
EITALNAIKPPITPPKDPNAQEVVLPSPGRTPQAGQEPLNGGEGADGLGVPKAASIASTS
IPVGQTVQQLASETSPDGNADVDVSSSSSGNPTVGEGSADTIQGDGPHTPSVGNTAAAAD
TNVLTAEGEGHDGPALTRDVSVSSGADGETAGGTDGQEGIHPQDRDVKSAALSSSLGNLS
QGNNTDAGTVCERRALPLLLLLLGLWGFAAQ*
>TCRU_691 hypothetical protein, conserved
MAVRQSRVRSAACFLRANQRDTLDARVCLANSHRRHKREFVIHKATVIIILPTVHGAKLP
CELKPICDILAIRHRCNHATALVDPCVGSACVGKISNQTHRTYGRREEGSVHVRPITGDG
SDHPQLLRQGGRKQAAFLFIVPRSHKVQHTIRVQQGVGNRLIQSSVHESRSNTKHAVAVS
HPNVERMGLTLPPRGAHFRAYSMTLLPPTVAVTMAPTRKLFFQRPDCELVQTPAIAPGTS
THIAPLSRDSCTLQYRLP*
>TCRU_692 retrotransposon hot spot protein, RHS3, putative
MPPKRNRVQGGNARSRASAVPQGGQRRARPESEDVTDQPAATQIRVEARRPEWTMSSTVE
DILLEGRTLSTNMKLNDFLRNYFGGRGVEEFNENVYMKDFLSSPNDFIQDEVLLSTIKAL
PSYQELKKGREEFYALSGASNKLGDERLLTLSHWRDFERKDTVIPLARAQISTAYSHVVR
VEAEGRGKARTTRTGN*
>TCRU_693 retrotransposon hot spot protein, RHS3, putative
MDNLLRWLVAAAEVKASVHEITKSLLDAAAEEARNPAKTSAPRYLEGYYESVYNARWSHV
VEVSDGEGMGMEAKEGNHRSHGITRKLTTLSKRMMVWSNPVHRVPGCWCSPRTRDGRTRG
I*
>TCRU_694 hypothetical protein, conserved
MDAQVQLVFDGLVLCRRALEIDRDPTDQLMDFGRTLLRTFRMRIMMASDPSITLSKLRDR
LHMAVHVADTFAKAALPLV*
>TCRU_695 hypothetical protein, conserved
MESTHPVEYCRLVVSGSKDPVEYFVRAKGDGRAVMPAQTETRTGWLMCPVTLRARLRHWM
RAEQVALRCLLASRPTRWPLLKGIQEHLSSEGVSVVWPAHCSTRSIWLFLCWEDGLLHFL
DPCGGRVMGQDAHRFGVGAPRACSRVTQEA*
>TCRU_696 hypothetical protein, conserved
MAMMMTGRELLVCALCVLWCVAADGDVVGPVTSGDPGGGGQSPLADGSHGGSGCSKADIS
HESKSEPLVAASGEESPAIHLDPNGVSSLSEEHLRPEKREPPKENGKSHNHRLKMHRRLK
*
>TCRU_697 hypothetical protein, conserved
MLAWLTDRRGRTFRTGCYSVWALLPCGAPQGSVLGPWPFEVFLDDLGHSFHPTHLPAAIV
TPIVHFPIIDHTITADIVAYACDVIVRATVPGITHLDVAMQPLFNAILEWTRAKALPLSD
RTYFMAIRIAGHHNSPVPDFFGINGRRCPCKR*
>TCRU_698 retrotransposon hot spot protein, RHS3, putative
MGAGSHLLYQLLHCGAEQLPVVAYFIAEQTFLFDNTTKTMSEDVVEPDTLNIVDGLLDRG
FKGCLIYDVAMKGCQPSTALSCKGWGMIFVTSPHAS*
>TCRU_699 SET domain containing protein, putative
MPLLGGNHFLFHMPITCGYRSAFQRMTLRFNLEKAMVLSTIETGARYFARVSPVQGKIDP
PKGGFVTDDVKIDMNANIGGAYARGVFACREIGYGREIMNLPAYAMYIGDSEEQTLREQV
LILTKEVFTKLVLGSPEEKLYIKHRVMTLMSGGFSYFTRERDVFEFVEDVRAPGAEGVLK
NGANYLLSGEFSSYDLQKLPLIIEFNRYDVEYNGRRGICLFPEAQYFNHQCEPNVEVTIT
YNSLKGRFFLSARTVRPVREGEELFINYMPGNTLPLSRLALAMKKRWGFECTCVRCKSRG
IGAVTMLFVVVLLPMTAYLRSVNVRRTQEKQRGV*

>TCRU_700 hypothetical protein, conserved
MSGNMFAIDDWRRELTAEDHVQRQHLAKTSLQRNFRGDAQRRVTSSTASSNMAVIDCCWA
RGHRTGGASSSFSTVLSNYLFCALSGGVVCILNTTNFMKMYLFEHDSSRRSRRDERAQKK
DVSRQHDSRREGVAAIDTVLFPRRGKRESSVSITTSGTALEGEGFLSLVCASAEGSLCLF
TVESEASSHTRSVSIKTGAVHKAVELPSDDAVPAKGRWEKAYIRFSPKGGRVVAVFSSTV
PCGATTVETNSFFLTGEIVEYVTLFCVLKWKEGESIETFTVETPWTRIRSPSNAASAELQ
YVGWWDDDESVFLTAWSDGAVSLMGVHLETLAHTSIFCTPAERMAGRVSMVTAVPPIPQK
KGSGRAFTYYQSGLVAMVLDGNIVTVFTVHDSQQHYGTASEDGPPLKFAKLETTKGHTEP
VREFTLRPGHHTYCSEDIPVSDIALFDNFLPYTLAVLLRSGALIALDTVTMEILYHRPLQ
RIFPSKGGKAASSINEKREAAIVGDGGNSSGNGGCVSEGMSYFMRPKERPMTMCVVEHNT
VLLLRPS*
>TCRU_701 hypothetical protein, conserved
MALRGVPIRLGVHRVGYTHPSTLPVPCAQRWDLRLARARIFQEYIEEKAPGAWQLEDERS
MSPEFKTFTGYPMREMRPGYGQNLPDFIMKKRLPNNTHYELFARRDIPNEDNAMYGKYLY
DMTVHGTSLPSTYRMHKDINKAQRNDRKLSGNRFRVLCSSGAKKPPSGWEPIPDATEEEE
*
>TCRU_702 proteasome alpha 7 subunit
MSGTEHDQSTDIFSADGRVFQVEYACKAVDNGSTAVAACCTDGVVVAVEKILTSRMLEER
SNDRIHAVDRQAGVCICGMLPDGRAVVSRARAEAENSRDVFATPIPGSVLASRIGEFMHV
YTTHYAYRPFGCSVIIASYADDGPQLFVSDPSGTVAGYYGIALGKGKTVAKTELEKLNFK
SLTCDEAVVKLTKILHDVHDKSKDKLYELEVAWVCNKSNCVFQHVPNDMIPKPPASQ*
>TCRU_703 zinc finger CCCH domain-containing protein 6, putative
MAERRQPRVLGAKRTVSDALGANALEGGGLAAVVRCVVAGTVDDSVTLGQLENVVAFYAN
HNSEYTRPGEDDIHVLMSEILNNFIRSVMLFSDFSSAFTDVEVYSISVAVQYNLSLEAIT
MNGVNVSDEAISMLCEALTKSRVSFIDLSNTPLEDEAGRSLAALAHVNPYLRTVVLDDTL
IAEEVLDEIDVACQFNQSNFEANDGAVEIGNPAELARLRHRLQHIIRAKHRKTYYCVAHL
LGMCPNGDLCLYSHSLMTTGAPDANANLHERLANLFASGGNWQDKLPSPPQAGASWKDPN
EADGQTLRLNLERCKAGASKVAAKGRGRNGVQHPTDGWRGSYRVVGATVALAAVVLVAGL
WSSRRK*
>TCRU_704 hypothetical protein
MKILLQEVSVGLIDEFCILCNVWLAGDVSQHTHGEKHLRWSEAAQAVFRQTAPAACVLAA
TLLRRVVEGEVRDHYCGRCSQHVGGKFRQAIHHLDSRRHHRKEEKQISLVSTVIKEASLH
SDGFVQGVFCSMCLCVVSVQQEKHLLSKRHQRNLRAAMSSASQTEAAEARQEMWVELLQP
LHGNICCSCAAYVPAEDIIQHFTSERHKRAHSFAQGIKDKDGDKGLRDFLENAEEHAADR
YCSVCDVTLRASMRTQHAQGKRHNMELLKAYRDPEGHIKLWRERFIANLAKERGQFPNVD
NTMPTVEVPSAPPDSLTSVAPTSATPEKCPQEPSGTCLLADMPLLFFFINGLCILCDCVV
APQSTGLVATPVGKEHCRTPKHKEALDAFVFQQHEMGQVDVATAWAARWYKDAFGALREE
CASWRECAERLSLYTSDDFMKLLQDDLRVDAFVEAVSLLRTAS*
>TCRU_705 alpha-tubulin N-acetyltransferase, putative
MSSTSQVALLPKLSLPDGVTVWDGTALEYERRCNNVDEHAVHLMQTINILGIRSKEAQCL
NTVLTSVARLRENRQARVYLLCQDGYGVGILKMGVKKLFVTHPSYSSLVEIDPLCVLDFF
VDTSFQRKGFGKTLFDAMLLNEGLNPGEVAIDRPSVKFLAFLQKYYGLVEYTPQSNNFVV
FHRYFDKWQPQRGKGHWGGNAVPTRSLVRPQNCLRVYPKYQSTTGPNNNFEEDATHRTPP
PPPLPPPLVPQGSVTSPGVGKKTAYELQYEEYLREQAYRRRQGGDPRLQPVPNPVSSSEI
VAASCGARRRMSPTRSGVQYNIISGTPEH*
>TCRU_706 ATP synthase subunit beta, mitochondrial
MLTRLRSAALRGAAGTRAASGMPTADHKGRVGYVSQVIGAVVDVHFAEGVPPVLTALDVV
EKLGRDEPLTLEIVQHLDAHTGRCIAMQTTDLLKLKSKVVSSGGNISVPVGRETLGRIFN
VLGDAIDQRGPVGEKQRMPIHAVAPKLADQAAEDTILTTGIKVIDLILPYCKGGKIGLFG
GAGVGKTVIIMELINNVAKGHGGFSVFAGVGERTREGTDLYLEMMQSKVIDLKGDSKCVL
VYGQMNEPPGARARVAQSALTMAEYFRDVEGQDVLLFIDNIFRFTQANSEVSALLGRIPA
AVGYQPTLAEDLGQLQERITSTTKGSITSVQAVYVPADDITDPAPATTFSHLDATTVLDR
AVAESGIYPAVNPLECASRIMDPDVISVDHYNVAQDVVQMLTKYKELQDIIAVLGIDELS
EEDKLIVDRARKVTKFLSQPFQVAEVFTGMTGHYVQLEETIESFSGLLMGTYDQVPEMAF

YMVGGITSVLEKGKKMAEEAAELEKLRRARAAQAGQKE*
>TCRU_707 BNR repeat-like domain/Concanavalin A-like lectin/ glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MPNMSRHLFTSAVLLLLVTTMCCGSGAASTVEGNSEGTIIFKGEESFSDSENKSLVQAFD
SFRAPSLVYVNGVVVATVEAHYTNSTDSKSCVSIAAKSMEIDGRTWTKGSAIVFDHYDVR
IDRLLRPTAIVKKGGYEVSALLGGYHTSGAPLKEVGDGYWTPRMAEGEVSGEEDGKKEFE
WNQVASTTNLQGVLNDYNTNIKRFKQFLGGGGAGIMLEDNSYVLPIQALKDDGKEVSLVI
LAKGTHYGWEFSNDTSRDGCIQPAVLEWEDRELVMMTSCEDGSRRVYRSSTMGKMWTVGY
GTLSRVWGNSRNRTGHGVQGGFVSATIDGQKVILVSRPVYTEKNGKETGRLHLWLTDMQR
IYDVGPISAENENVAASTLLYATVEAQSLEEGEPNKEKEKLYCSYEVAAEGDKYSIAFLD
LTEKLEDVRRVLATWKENDAYIEKEYSCGNEKNNWSSDCDDKDLNKWLVGFLSNTSTGNT
WSDEYLCVNATVKNGVPGADGGLTFQGSGAGAEWPVGKMGQNVPYYFANEEFTLMATVSI
HKVPTEGSSSPIPLMGVKLSETDSTLIFGLSYTHDKKWRVAFNGSFRDPTHDGDLSWEPN
TKYHVALHMDSDDGLIVYVDGLVIYDSEEDYEEDNGFAEAFRSLMSSHSISHFYIGGDSE
RDSDNINVTVSNVLLYSRAFNKAQLKPLMKTNTVGTPDAEVPAPNVATQTIVASQSSGQP
ADEPVVTNEAQPSGNANGPAVSRETSFPSVLGVSTSAAAGEVKGEAPSSSVELLSALSPT
PSAGVRREVLETEESVSGVHMEGDQEYSPTNGTASTMEQAGRADEVSSQNVSTNDSMQHS
IDREEDTDVLTAEGTNSSTDPATVHRNDNVSGGASAAPTHLSTAHGEAKIPSEFNATIPS
GHELLLEHGQFRDLSAMALIGDSTVHGCASRVLLLLLGLWGTAALC*
>TCRU_708 hypothetical protein, conserved
MPSAGFSADRTYAKDACVRRESNNLYIRCSSHVIAFDFELPLFAAPRSEVLSTQTSMMDG
KMAEKADKAKRTARASACMIRKGFLPHSPPGSFNVDKVWDENWSPSMERCVRDDGDRRLF
RGLDDSLTIIPDDVSQSLAQTNRCRRTVRRGCLQHNPLVKCG*
>TCRU_709 hypothetical protein, conserved
MVPNASKKAPSFANGPRILVVLNASGIMSVTCGGREHVAADNTDEVSEPDATGHKSLVLE
NGVAVSGFVGEGDAGGLSQRNAFGHENPNYENSPRSIPGAV*
>TCRU_710 hypothetical protein, conserved
MAMMAGRVLLVCAFCVLWCGAGGGCDEEVVEAAAGGLLGTAGKGTVETSGTSTPGPDGSD
LPKGLPKVNQSTETSTGKSLEVNKVNVDQQDVAPGVGDEEDGSPSDHLEEPLKDDPEKGK
TKPELKNKGQEGREPPQLQVTVPQQPQPPLQQSQPPSAPQPQPSASEKGEGAGKNNKGGE
GQLSLGVEHKGNAAPEAPRKEDLLEGSGKESENSEQVQTTVPNKVTPEHKTQNGMLTPEQ
KTNESQSTDTSMNLPELQKENKEYSASTEGTAQSTSTGSQEQETEPSTSEEPSPFEEEHS
TGTKTSEDARTPDAAATEKRQTGDNEKVSDSDSSTAVSHTTSPLLLLLLVACAAAAAVVA
A*
>TCRU_711 retrotransposon hot spot protein, RHS3, putative
MDEVGPTPRYIFDERKYNNWVQRCHKTVDEATFSVIAQYSGLGCGASWDRTKVLYWLARV
VRERGEEFGYEFFSNLPVSAHLGNKTLFKSAKLMQQHYFNLLISWLRDYLISENFGRCTV
FAFLNGSFVSAIERRLRELRPSPQRRSHRCALAVYSQERSTRHHVLPPLEHFSERIDVEC
GVLYVTEVENFPLVDAFFFSESNPMTVVGLRMTTASEHHDNQHCEAVH*
>TCRU_712 MSP-B, putative
MRHTMLLLVLLLCCVSGSVAVAEHHCISDEIEKKVGSRTTAVVLELPTRESGMMRALTAS
DPDWAPVRFQLFTEDLNDPSRYCTAEGQIRPDFTGGTVECKERDIFTEEKKSIILNSLIP
RALKMHTDRLLVEPLMGRVIVPEFLSGACAQFTIPSSHHTEGVFGADMYLYVSAAPIKGS
TLAWAVACSALPDGRPVVGVVNYGPRSVTDSEYGVRALVHEIAHALGFTLEIMEERNMLK
EFLNVRGKASVLQVSSPKTVEKTREHFNCVTATGMELEDEGGERTASSHWKRRNAKDELM
AGLSGIGYYTALTMAAFEDTGFYRANWGKEEPMSWGNNSGCALLTEKCVMNGVTKYPEMF
CTAESRLLSCTSDRLALGYCALKLYDAPLPPQFQYFSNPKLGGSPDLLMDFCPYIEEYAN
AGCSDGNATDMRGSRVGPRSKCLKGDGLADFMGFIGDVCAEVSCDKGEVSVRYLGDDAWH
KCPEGSSITPTGLFMKGRILCPKYDDVCIVIDTINGTGDVSSLLSAFPPIPLIMLVLIFI
SMF*
>TCRU_713 Reverse transcriptase (RNA-dependent DNA polymerase), putative
MLRGVPQGSVLGPYLFSLYVHPLLNLLNSFAGVTADMYADDLSIIVKGQSREDAIPTANM

VLQRLHAWSQENGLAINPSMREAAWSTSSPHTESDYDREGKWPLVVAGCQIPVMTMGASR
TTKLLGMDLDPRLTLNVAATKQCAATSQRISQLRCIAHKEAGPSPHDLRTFVIGYGASKL
RYGSELIWAVATDSAKNEMQKTYATLARIVSGVPSTVDPESALLEANMPPLHVLCLRARL
SIFENTRACQMDWMRRPPPEPPPRAGLRISPLSRDELYAFVDAYTKDYGITESSPREERF
FRSSIPPWFAASAHRVTIGVGLPMDLSITDEEELIREKR*
>TCRU_714 Endonuclease/Exonuclease/phosphatase family/Endonuclease-reverse transcriptase, putative
MEPFTWLPAERYFYRLLNSIGAYQRYTYRLRAVCDAQRQKLLLSGDIEQNPGPIAVLQMN
VSCLTPSKLATLMAQGVDIIAIQETWKSSKQIASMHTGDYVLYAQSRIGKGGGVAVLVRK
TLRSKRIPLTIPQHDTSLEVVVVQVALEQNRDLIVASAYMRAPPQVTQSFRRLVNCLPAS
SPLLLCGDFNMHHSQWEPFLESSPSEVAAEFLELCTDAGLTLVNTPGGITYARGTRERSC
IDLTWSKHLTVSDWSASVSPLSDHYMLTFTLHQAFKDNIPSAPPSAPKFFYSWGKCKWDL
FIKDFDAQLPAYDYKKQSTGIKAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERIAT
DSKARYLQLPTPDREAEMQRTRSQFFLLLRERLRNTYLRRISKLNPGEPLAWKYISGRKK
ASLPSPTSILLGGGQHTYKTARRAANALNRIFFHFTPLTRQLGFPKASTDRVHL*
>TCRU_715 NADPH--cytochrome P450 reductase, putative
MLRRWIAVAAVVAGISGVVLVARVWRSRHVAYVYDASFVSKYTALLGKQTELPSEQSDED
ARILVFYGTTSGNAEAYAKGLVADLRERGVAVALIDPSCWDYLGQYKSHQDHGQHPFRLG
TSGESPILVFVVSTTGEGEVPGNFLCLYSEMQSVLEGALKNGTKPFDGLMYAVFSLGDSS
YKYYCRGGLEVKTLLRRGGGTEVVPAGFGDARNPLRDDVFEEWEEKLMEAFERRCGVVFT
ADSNLPPKPQLVFRFAPEKHVGASPYPPPPSLLEPSMQFPAEFRVQAKTPRTERREDGSF
ILHLVLNIEGYTMSYQAGDHLAIYPANPPNVVEAYRSILKITEEEWLTPVELCASTNARA
RASLKNSLPACVALRTVFERYLDLCGRPRKSLLRVLSKYCSDPAEKSLFTELLHRGVKEN
GKDGENTMPTSLLMPSQTYFSSSHCHTLLDYLKKFPSCCCIPVGHFVEMMPRMQPRLYSI
ASDMMTHPTTVEAFIRIIPEGLASQYLGRIAVGEKVTAFIRKSKFHLPAKCGGRPILMIG
SGTGVAPMVGFCYRREALMKRHPGAAHGTMILFFGAQRRATEYFVRKEMECWCLHEEGKI
QTPDALPSSLLCLLDLAFSRDQSEKYYVTHLIEKHKDHLVQLLTSTEKGGCLLYLSGDAS
RMARSVEQALLKVLQCAGMTRSAASEFLRKMEQDRRYMKDVY*
>TCRU_716 Double RNA binding domain protein 9
MSLTEELFGLPGPSSAAGIKNERDVPEGMPLSFAPAKKAAFDLFALAPQVKKPTRKEKQR
LRLQKTFADKDGTQGSEGSDRQEAGGDPFKTVLLTEDLGVGKAAEKKGIKSNKHLRHALH
ENKEEESRTVFVGNLVNDVKRRIVEKVFKNCGAIECVRIRAQALEGGGEEGRRNENRHKS
VGRAIRVLRGEIKKGDQYSAVAYVLFKDEGSVTKALEMNGVVVDGRHIVVTTMDAKSREY
APETSVFIGNIAYDTNEEMVWNFFLEKGVTDVRRVRLVRDRDTGSCKGFGYVEFRSPASV
SRAIAVRGSHLNGREMRIVHVQKSRVVSATKTSRREKRKREAQAAAGRGQNDEKKTKKLR
AEEKGTKRHANAEGEFSWMGVVTSPRKKIPKDLRPLVEGKRGRPASGLRASVRRKMRNPE
K*
>TCRU_717 hypothetical protein
MSADRVFLEGSGAPSLELHVGGAPLAEVLADMMRLIRSQQKELESVRRDAEERIYRNECG
LKKHDGVLESFAEDLQIHVRPINYNGQPPMPTMADAVANVECRLWRVEREKKFYAAARLS
EVTRKKLMAAFYSQWWLLRKLRAKSHFLLKETQREIWRRYMRKWSRSLALRRRQAAWRRH
LMGLTAAHGRRIMMCYWCKWVQVVAFKSQARANRRISAYDISDTMLHITCRGIARRYLYA
WAQFVAAARDARCRAREALWLEQKTARILARRYFERWLDAHRWCRLPLMRLKALDALRVK
LSRGLARSFLRAWQDFVRNRCERRRVLRLIPHLHHANLAALARRYFSRLYAFRFVCRDAR
VVETLEQRLKTLSERADGLQRQLDMGLHTLAHTNSVLARVVDTVMVAGEPRDALQAFLQG
DTMISVPTVPSVEEKRSQQGASAPSLSPNSRRHEESASSTGRERQPTDEHRCVSASEMLQ
NLRVRLEKTYKMAGGEP*
>TCRU_718 hypothetical protein, conserved
MTLRQTKQRSDMMSGIDYSKWEKFCDSDESDGSDETPGNEPRITRLRYPSRVTVGPNGVH
MENTPPIATTSPFKEGIDATINKNTAAAATTTTNTASVMGPHSKQNTRKDVRGVEEAEED
EMMYHNLTRNGGREGQSHLWSQTRDTASVSFILPSMNTRAKEIMNFRLYSEEQPDRTSVC
VLTFGVKGVEGDRRCVFRYPIKVDNDVVEGCWQLHSLHSKSLRLMVVQLVKESVAVGMAL
WWDRCFVTDQTTVDTRTLVDRSSSEALRGEQFQRAWNEAHEEFKKRVNKGRGRQPATGEE
EEEFIE*

>TCRU_719 Yos1-like, putative
MKDSGIMGFSVASILQALLLCLNAMAILSERRFLSKYGLATTPLTEHGGDAGYVPQSFGT
GDEFVRARQPSPWKAQLASVLSGVRTLLRLPLIIVNTAVIIFTLVFG*
>TCRU_720 hypothetical protein, conserved
MDGSRFGTESLTPLVGDCELVLQRSTSYEPPMYLFPELLPKVPEDTAPFSVSDAVSGAVD
VEASSLNIAELFHLPQMEQRDDTGGSQGGDADGTTPATNPASAAPMTTLASLLAADRLQV
AGLSAEMLQRGKFSSGSIIEELIKLKDRAELNDNEAKAIMSNHFINVLAWRTLIEANNKA
LSDVKGENTLHGCRSFARPREAETAEVDIGALRPSDDPWGTHVDLQPGVFVSAAEQNVEK
RIELIETLSALYRRPWQTLQSRGIQTEKFTPGSINETAPHVDPIKLPAAMLDPEEDLGWK
QSAVEDASNNHWELRVTSSSTAASELIPVRGRFMHFGRSAGVTSAAHGTVTNVHVGLSAF
TNHPEFLSPHHFSLAVLSAKPPWSASDAGAAVKHEVDGNGENGDEGQFIWLMNYGRNGVR
VIGKQWALGDMVRLDPGDVLQPTDDIRIVIGGCAQKTEGDSSNAKSEVLMED*
>TCRU_721 hypothetical protein, conserved
MSFLVKALLGSNVVHPVEHEGSESPSLQQGDAEEEKQRVPTRTLILRVQSCTVAQDRRDA
LKELQACPDLPYVMAAKEVSYLCNVLRIFPDDNDVVESSLAVLSGITELTSYPSSSSNYA
VSEKEKRRIRDSFLHELVPEVPLFLNHVQAGSFWCRFHAVQILQRLQEHDPSAVHKLLLS
SHGIGMLLDILNDNRHCGALRSEGLLLITSITATDTELQTILAFDNAFEMLFAVIKEEGG
LDGGVIVCDCLTIAHNMLRNNKATQKLFCEMGCARLVCNLLEAVPERLRAAMHRSASLKN
QGGDTGENMEAIFTPLSDMQNDVIFKAVSILSCVLRGAEAHQEGPAAQEAFLQSGALGPL
SSLALGGVIADDASRVEALRTLAVLLQDRRVGIERFIQLQVTTLVSCEFSLWVEEWSALR
GILHVLLEIEDRVMQSAAAQVFHALLSVSVCEGDVAEKLLEGFAPSLSSLAPAAPAATAS
RGVLPARCGAALANTLFRPIPCSRSSQKYYSALLLDRLLCVSGVMRQLLGTNQREMASSL
SLGKPITPSETNGVFLAYVQYVIKCLRGQGEMDLNTLSACFRSLLRWVIGCEEAVQVFLS
DGKYYKSLLQRAGQDDGPVHVRFWSAVLCAALCVAAPSGLPKTAQEPPRAGGNGRMRECE
GGADGVPSSPSLNRRQLLELFLNYLGGPSIFDSFLFDVKASSPMWSEPPKNAFLRPTPAL
YDEKMKHTLLGVIKEFNEICPSRGKMQPTAMEESDLSVAPASTAAATRVTNTAFATVVDD
VDFFSEGPLLLREDLNENLGAVGTTAPKQQNLSQVEGCLKNAEDEACNALRNVYELRVKG
LLEKNAALERELQVMRGQLHADAESREVEKKPEKRHLEEVKGLRENVRLLEEALSAEEEE
HRLLAQSLNMLEEQLREARANRSNTAEVLQLRREIEKLTEERDRLLVLVAELDEENLPMN
YTGLGKTYPSPSPPPLPPPSAPYSFFSSTKAPQAICGEVNLLPATNYAGFAEGEQITPAE
PSHSLFEATGPNGFQTSPSPSVRPPQEQQQQSDLQPARRPFERTLGITNGLQEPVEKLAS
MERNLFSDEHPDGCVRGNELEARHMESASPAGAARRSAPLKSNPFANMVGPHDELSGGPW
*
>TCRU_722 Nop53 (60S ribosomal biogenesis), putative
MGKLRDLWHGDSERAVNAPQPVRVAPGWNVQPEALPAKPLAPRRRKYVHVRPNNRDAVAL
PHPGQSYNPLHDDHQDALRVAVRKLERKKTADEKFVAMMTNGRDVPITGNFSADKTWEEE
VQERPQKTQKKEKSTEKEECKKKKKKDKKKAKKTSVQAARRALPHRRHPKHEIALKEA
DALDDIIVEHQQREKRREAARERCRAAKREKMQVKSFGRYHHTPLALDVAPTDKLVGSLR
HLNGGYIHPLTERMKSLEERNLVPARMRHTYNKRKVLKPKGEVRVKRETFGVMPETTF*
>TCRU_723 hypothetical protein, conserved
MAKKKSGTNALLPELTVNRRYIKKMKFIVKRREAAAAAARRGKAGEKKKKGGARNKAGDA
AKGSGRGKLSHHSAAKKSPGVSAKKKKTAANGGPAKNRRRNINDAKSGAASQQQKQLSRE
EIEQQMIARAIRGDEGTRNASLSAGALDGVDVDDLVQYPYLPFLEDYAEQKRSEVVSAET
LLSNAHAYFKDLGRKESAMRRAAARRLKELKNINRRGGDKDGFRYVVPRNVKEVVRQMMQ
NAEGADASGVDKTHLTSTFGGDEAQDTFERPMHRKRRKNSCYSDFYQFQVSKRWTCNAES
FLNRGRAYKSMVEASRPQRSIKKF*
>TCRU_724 ubiquitin-protein ligase, putative
MSVRSEVQTENSKQQLKAVQSQRNDPDKVLEPLEKLCISLVMGVEPYLRSFDAATAIPIL
LCMTEKEFFSFCGDTMTMLLRALALIMEYVPSAYESVHLYHKRLMKSVCQVLSRTLLAKM
KYNNTDNVMLLEESLRLIQFITKDEGNISVLRFGVTDVIRIAASENTLLARQAFDVLVTI
CSKIILPSDVEKLNIIGLSSFLICGRKKKSKKGCLESLDSHGKIRVYAVENVIVPFLHST
LQQYSASLETFPEAWTFLELTIHCLGMLMRRSMLSHRPSTTRKIVTRDMCRTLFRLLLFN
DTNVAIDQSVRSERILLCETVLDAAMAADSLVASEFLLAEEAVSFYKLLLGEQESGIITQ
LDDPFPVSGASSRSTQRRDKNNIVSIAAIRLFVLACPRVLSEAFGPKPKVLLPVHQWYWE

DELRNSNSISEEGCVALETSFCRLCKETPFRMHMKSLRANFQSMKLSGGFGSGERNISRK
IVPFVFHFVDEADLRLVKSAKEAIMLCNPTPKCRRELGVINASEAAAISKGLGELFIINR
DSVVPPLYMSIAEMFLESLCSFVVSVSGQMAMQLGTSACASLLQAAICTEENQRLAGLLS
KIIRPLCEMLREALVSGDKATKSVSLTMMVWLLCHPQASAWNFSETALRCGVVNQLEILL
SGGAVVSSKKTKPHKGLTKVGPEVKQTRTAYLAASALAVLRAINKQLSKTQSPRSERSLS
TMDVMVVRKAVNELKICAATPGLHQGVVARILELMEKSANTVTAYEFSTLGIADAVLKYL
LVEHYKDYCRDAVTMVGTATPSVATGSTEVKEESFVGGFGQELTEGDLLAFAGTRTANGL
HQRCQKERLQCFLESAMQRPRGVKALIENLVSALPLHSTFPLVESLLGPSRATCRPPTKA
VLVGSHISPIVSLCSKPDAESDAAKRWEFERKNSKTLIKRSKSCPVSMPMQPDAGLFSGG
GVEVVHSRDNCPRGHRLLAISEGHSLGLCDMCEEEIHTGFCCHRCEFYICKDCYTDPKVQ
YSNANSGASPSSGAAAGGILGFVAQSQQQQQQQTSQERQRQQYSRPIIRAHLFSSIGDIE
RYFRTGSYSTRNTDVAPAPQSVLQNIDYFVERAKSFLARKRLNCSDEILRKEVHRILSSF
LLNGPTIDPEATAEDVTDVHPLGPKELQELRRLLRDAMEERYVLYTAPGGRCAYQETLIG
NFLRRAIHEGNLGVVEQLETCLLSIEGYCESSNGVQEIHRNESLLLRQDEVGLPPSWTDV
PERSSNARTYMFHHFEKDEDTRCLCGKASRAELNSMYPPKLVRKPSRLSQNPDTLLLILL
QKLLSPLIKQGAMDIDAGLFVSAPFTTLVVKSLAASALRVALLPPRLAVPRWADFVITEA
NFLLPLNVRERVARFFAYGARRALHGHLKASPLSRSNRSINVYPAEWGRWANHKYRVSRE
SLLHDAYTVLQKSADSRLPISIEFDGDVGVGQGPTAHFYTLIAEEVKKAKLRLWRTGAPA
TKTKDGSTHGDMSSGDARVVPPAEGLYPFVSAMKDQCRLFQVSSWQQPGGATMLTDRFAF
VGDYAEFDRERARCYYLIGSALGRAFTDELVFPLDLSPALSIFLSRGAPAPCVFFSGDAI
ANKGIERPIDFMGLSLDDVDLMDRSVATSLRSLLSLSGATLKSLAVPFTLPGHDNFEMIT
GGSEKLLTKDSVAQYIRRVSSGLLYESAVLPIQFLIRGFRDIVPCEALASLGEQEMMSLL
CGCRANDKKPLWTLAEIKSILVAEHGYQTDSPQMTMLQNILANRLTPAEQRSFLLFCTGC
PRLPVGGVGALGAITVVKRSDFTMFHGSSGRNSGGSDGIGGADRKEQNPKQPGEWNSLPN
ETDWPLPSVNTCFRYLKLPPYPTEDLMYKKLRLSIMQGGETFQLS*
>TCRU_725 Fumarylacetoacetate (FAA) hydrolase family, putative
MKSSLAFSVRHAVVPVMGCNLLFPVRRVYCVGQNYADHAKEMGGQVSKSNPFFFTKPPDA
VVSGETNHTAAMDVNIRYPPQTNNYQYEVELVVAIGESHGGREKYRAISPLEAHTVIYGY
AVGLDMTRRDLQLAAKKNGKPWDLAKGADESAPLSAIVPVKLIREKASALFYATDANYRE
AMNAKAQGGPTVLRRGDIELRVNGERRQKGNLSSFVTPIDELLSILSHSIELAPGDLIFT
GTPAGVSAVKPGDEVRATIEGVGEITARLH*
>TCRU_726 hypothetical protein
MRVYGLLLLMCTLLGTTTATGRLGTKSPEFTSVAPESRGIESFRVVIYLNATACSASEEI
PQTFFVAFEEDLLGGILPEISSMCGASSASPSLSCLAVCSIHSPSQELAFTEHFGGAGAS
FFQHPTIVCEWKADGSVQMPMGFYPTCRKRVQDLYAMENALEVIKAKKSHKKRNRYTFGR
SSEVYYKMTGDARHLVAVGGDCYLTDFSAESARKMCGRVTCLEASMIVLTAVIALMVVVA
VMYLCRRQLFVHFFNFGLRDGESSTSSQLIVHLPDKNESHSSTAYEAWKKSTEPHTPPAS
RLPVSFGDSNASPSRSPGSNEVDFTKMDKVLANASPRTEQSGGFSDRRQCLTISRTSSQS
HFLTPWRYRQPRVGSNDVAVSEGKKIDGLAASHQEKALPEACEVDISKEEREQLQRQRSW
LREHVIGLDAI*
>TCRU_727 Autophagy-related protein 24
MGETVFEFKVLDPEQRRGTGALDLAYWTYRIRASTTLSTYAQKDLEVVRRYSDFEWFRAQ
LCEAYPYCIVPPIPEKDVQGTLDKIVGSGSQSASRLRDYRQRALRKFLVRLGAHPRLHTS
HLLKDFLEMNEDEWERKMKAFAKNSEGFFTSSLGEGVNHAFTRQWNTSGAVAEAGAAYTR
VVTNTNTTPQVWEETRLYIQQLEDSIKMLRERLQLLVDRRRNTSNALHEFGVAFEKVGEI
ERGIESTPLSNALIAVGQHSEQLFFIYSDYANEEMKQVVETLNYYCGMCAAVRETLRRVH
NRSHYVESLRQHAAEVVAQKERALEKGGQAGRVARLESELAGLEDRLSTAKRELEAGETI
LKDELRRFHQEKQYDVKAILKNFAELQLKYAARMKETWESLRPTVEAVQFEGEGGGQGNA
LR*
>TCRU_728 cysteine peptidase, Clan CA, family C19, putative
MSAPAIRHGGPSGRLPTRQGHHFMLTAEPPGRSFATSATTPNVPKTTLPSYPGMHRLYSR
PFRGEPQFLGVSSSSHILPSTLHGQEDRRWNSMRSHSHRPPLLSLRGRPPQLQPLLAPSA
PAIGFARQASSTSEMQMPRTSEHQSPIPLRNFGNTCYMNATIQCILHSPWLFSSLAEANA
WSKRRLATSALLELGAARVDAPGQLLLTVKGEAAKFNAEFQDNGQSDAHEFLRTFLFVVH

SEINTSGGHNTPYEELKEVENESEEEAMRRWQEHYLRVDNSIIYDLFGGVMRSRCVCSSC
GKVSLTFDPFLDLSLPMIPGARKAATIESMLKISFDEAEEKLRGGNQLLCARCRRLRNGT
RSVKIIRWPKILVLHLKRFDDTGKKNSEPVVFPESFMTHDNSPMQYQLYGVVCHSGSENW
GHYTSYVRTLSGRWYHCNDAVISLSTVTEAMQALTTAYILFYSVK*
>TCRU_729 Flagellar Member 5
MASARSPVLPHLDFRPQSAEGRAPGVTDQAAYNELVANYTTLRAKVNAMLAKNVDIIRHS
PVVDLTRNYVGAAGLQAMTSLLAKNDNLQELRLPGSGLNNDAVVFFCRAMVKHPRLTSLD
FSCNNISLAAGLALISLLQQNKNVVHIDMSETQVPGAVMKKIQLGLQRNKLLAARAAAAS
PDAADDTTSVTRSTEGGFCSTIRETVRKVEWERREEEALHRLREITHSAAAETGNDRRFV
PLPDRESGWRLIEVAILSPPFLFESELSLLIKKVFPRLNEELRSSKVHLLPLLDPPDGPA
GTYLKHLRFAIAADVLRNVEKSRMVTIELIGDRAGEYQQLPSNEIMKRPQLLQSMRRQDG
AAKLIPAESKWAPPLSPVLQSAHELATALSNWIIVATRKETRRTGVPPSLAPLLTEEPNV
EHPDYLQSQIRRTVTVGSDVVCGTQTIECDASLKAKKWHEHQIFRENLLETAPVQELVIR
NYNATFDFCSEDGQVHFKNLDEFVEAIYKRILLIMIAHFPPCHDSHPAHYQGYNVEKFAA
KKLGLYQKRLHDLLRACVEHSFVKKSITDRLNLYIITPPSRNVFVLHGSEPVPVTALIGS
FTSRLLAKEEQKFRIAFHTTHATSLTEEPNELHEIICHVILQLFPEQEIYRRAIAEVDIV
RLQQMFLDLLTDKIKSTETFKRGGGGGGENQITVVILDGMDSVLPTVCPCNALRLSEDTG
KDIWGTPAPPAQQSARYGYIPVCLSRNLRLVLGCATNSDMHHQLGSRGPDSAELLSMGPI
TPNDFDEMLHPDMLSKIGATLSDDDFIVIRKKEEALCPEYIMLVLDTLRSLNEVPGIETH
SVVTSLPGTVKGMIQLKYNNLQQTFGTALVRKCTRLLLSSRWGIYEPQLRLMLQLPQRRF
NQLVRMMRPLLGYGTLFSLGIKEGNALLSRICIRSREFRALLEQEDLQEEGNEEDQKLWH
EMLARFYLNVVHDVIGREKTPPIFGLSSTNPYERISVKELPYHAVKAHAWHILFRFILSM
SFLMIVYRNRLGYHLVRELIVAFNTLYEMYELGEFPEENGATHGEKPSALLRLREYIYFL
REYNARLTEFPHLVIQTAVESAARYNFVGSDAKEYVTRKMSHHAPIVQRRTVFFEIIAGA
KTVIHHGAITTCLFSPKGNRITTGSVDRSVCRVSPVTGAVAAQLRQAPTRVEEILYCETG
AYHAVICHDRTLLIYDSAQMKLLSRCDGGIFGAPLSSVAFSARGRFYLVATEDLHLRVFE
TEKGRLLLHVDQRQFLHGYCDGVDINLLRGYSCVIPHRIEDDVFHSTCHNVLIKWQFSPT
RDEFASETRLGVSFTVSSGKAVLIGTHLLLHPIPFPAPTSGRRAPPRFVHLHSLLTGREM
AVLTSPCSQLFYQLSANERLLASALDDGSVAIHQLCWTSLQKEDGDMIAIPPVMELAAYR
ESPVATVRALRFRGDCKALFALGNSFEMKFWALPQRLLDGGGDNVSDADVSYPVEVDDAS
REEEKELVEGVADGEFILEPADVASWDVVQVPNTKDAEVIFGDSSGRLTMLRMWSPLM*
>TCRU_730 Spt4/RpoE2 zinc finger, putative
MVEEPPPQLPIGDRGYLACRQCRLILTETQFIRDGCSVCGTGPVSRDELHDVTTADFSNF
VGLIAPEKSWVARMIGRTGCPNGVFAAMLNDEDEEEIDSNDDGDDGAVEEDDKEEEVEVG
DEHTDGGGGHRDDTPPSSRPASPVMTDEEFLATEK*
>TCRU_731 Eukaryotic protein of unknown function (DUF1764), putative
MMRRAKKQQFDGTNSKAATVVGVASATAGCRGGRVVVEPKGESEIADIFAAMREKLHRDG
CRSRSGGDSIQRRKDVKTASQCVSDGLYHAPEKTLELSDPAFFDVASHRQQKKKKANAST
ATKFPEEVLRREGVDRIVTLEELRGITSSNPKAGTTANCPFDCDCCF*
>TCRU_732 aminopeptidase P, putative
MHSEECYVVEQNTPTKTTMASNNKQNGHKDNACTAYPFKVKREMYREQRQRLAAALLSSK
DATHAAFLQGGSEVPVNSSDINYLFWQESYFAYLFGCDIPDSFGAVLADGRGLLFIPRYP
VSYAVWMGELPTPESVKLATGLEEVYYTDEIEAALTSKGVQTVEVLDGVNSDSGLHVLTA
KLPEGSKVKISNKWLFGVLTQQRCHKTDLEAELLQYVCRVSSEAHIHVMQHCKPGMSQHH
LESTFLHYVYYHGGCRKVAYTCICGTGHHGAVLHYPNNDAPVEDGSMALLDMGGHYMGYA
SDITCSFPVNGKFTEDQRIIYNAVLDAHDSVMRQLKPGVNWVDMHKLALRVMCEHLVRAG
ILLGDVDTIMRKRVMGLFQPHGLGHLMGMDVHDVGGYLEGCPPRPEESDCCKLRMARVLE
KGFCLTVEPGCYINRTLLTDAFQNPEFKPHLNEAKLRSLWNFGGVRIESDVLITETGAIN
MTLVPRTVEEVEKTMAGAPFSREPEVFTH*
>TCRU_733 Poly(A)-specific ribonuclease PARN-3
MTSDITFITRQNFTEIFPHFVRDLSEANFTAVDLEFTGIDRESNSDFLRLPEEAFLQKMA
AARLFSPLQIGFSMFRGDTDLEGNSGGNSPGAGVNSQSYRDAMGWEAKSFCPCGLMGPML
KQIIESWVSKGQVDPNELAELEKRRREAENICGSVAEFNSVYERLRAHQTLNEINTVIAM
AQRWKGYAERKKRHVAVRNYSCYLFPAPEKDEGDRTVTLSSETAVFLLKNAMDLNKWVTE

GLFFVSFDEYAKAQQGALCIPFAADRLIEQGGRVAALYRWINALPPAELRGQLSAEFKNI
LSFLKQAEVGDSVELNIPFMKAPWFAEFENHMRVLGLHFSRRTITRVPSSGDEGVPIEKD
PRYFGTRLLETLVTATRCWKKILVIHNGLSDLAFLCAAMHQPPPETLGEFKRTIREMFPF
FFDTRTLTCAPSLQNIGILTATLKKTYFTLLKRNKRIQLHCPSSFEVAEQSEMKEHDAVI
DAFMTGSLFLFAQEELAQVGSDFRRLRGITPIYGCVFSVNFEDEVADCIVHPPSAPIYLV
HRPSHMSLNMETLRNKLSAVAEGVAFIFNGDYCLVKICDKTVKKGVKEHIEVVIRQWCES
LSMGFKPLDVASCVRAHNISYVSEIEGPLLVPH*
>TCRU_734 Importin 1
MSDVRQAILDALGAAADANPDIRHHGEAQLQRLKESPDIFFSSCAELFTDARVPTRGRQL
VGYLLKNHLAHPSCLQNKTLQVAVMESAVVDPECGIRAVACAIISAAVREAYWPVQPVVS
SLTGVFSTRSGELHAVHGAMRALSQIVDDTVQLLDMRQLTGVVVSAVLPYLRAQFGGREG
LEVQLKALDTVSVVLEQAGFDCSSFSYSSMRPYVLNVIESCFMNLQNPSSAQLSTKSVKC
LVLSLGYHDLISDELFHKITNLMSMATASPDGTDEDLRIEATEFWRGVLCFPRFASLVES
TLENIIPILIRSMVYSEMEISMLQASAEDWNVPDKIDDIRPRHYQARVNDTGANDADDDS
DDDDGEVEEWNLRRVSALTLDSIAEYYGERIIFTVLTVIEGMMQPNNSWKELEAAILALG
AIMDGCFDSMTPYLPEISTRLLQLLGDPSVHFLVWNISLWTMTQIGKHIVSVPEKLKGFI
TCILQKMESPSKLVQEGATAALQKTIVLCDEGQLDNEIPFIIDCMARCLRGYQLKNRVLL
LETLETFCEAMGEQLRVRPDSVELLMAPLGEIWGSTPNDSPLLFSLFKCISGVCRALGAA
VQPELAKNLFERSYCLLVMHVQARTEARRTNQDPPEYEFLVTAADLLSGLFDALGTGLGP
LVMQCHPPLVYTVLEALRDEDAEVRQSGFSLLGDLSKVCPVTVQGELERVVKAALENLAV
LDENTYGVISNIGWCMCNLLENQMDIDNLSTLDAANGMPQLFAAMARILGTVSHAADMRN
MAENLCICLGLMLYADPGVESQSGCQVSLFADAFCSYMRNVKDVPHKEQAVSGFLMAVRQ
QLPFVVLRLHLFFDLALSLASCRADVKRAMGELLQAARAHAGARWTQQMAEYSEQLRTRL
YHVYGIQ*
>TCRU_735 hypothetical protein, conserved
MRRAFALFRPTAVVRCVQPAAFRPTRVLHIPPQLVRLIVAGGLLVFQAFVVAHNREAQRL
REEADGTATGEGCSTALMSSSEALHILGMDANLRVPLEEKKDREEARRRFDHLFAIAKNN
NNAYLQGKFSAAYRLCVDANWDADENSCSNRGIDSSGSGGEQG*
>TCRU_736 hypothetical protein, conserved
MRRLAAVSCGGCLPLLLFYCPNLSAGTLFSSVQGKPGHSDDDALGAEDSFKAVEAALKDK
QTSKDQALPDEIDPVASAVNQRRNRRKRSVDSIFGDVLHDALRLRDMGHKPDADFVYKRA
QERMYEEEYGHKPPSAKDHAAKYVPFPPDLGLNRLIPLEHIIGDDPWPARSITAQNPVWT
RQQVEEDRVKHGGAQLKEWEKKMFGPREGFDPCGEFIDAMEELAYWEERFVKFIREAPLP
QRRTLPLLHEVYRYITHRLVRAERRYLGTRDAALKKARASSSVYKMTEANIERIRSLYSE
THRSLSSPNYDPVRMKKSLTGPLLQMSESEFEEWKNVRKHQRNRLVAEIV*
>TCRU_737 hypothetical protein, conserved
MLVFVTQALAESLTVTSDACCNMSINGVRGRRRKTRDPSLCPFEERLFKAFQRGFSSCPR
KPHALLHTFSLSPSAAKACAYLQRQTSPSMLERGYYVVDLDHIYMEAPTFFDEAHRCWKY
STRGLRMQKKTSISRHPELLMIVLSPPETAAVRGPGTMFPTLVCRCADNADGTEEGIYAR
LCGFPPSAKFSVLSEQLQQLSLSYPNKALITEGDGWNWLMAHLQSRDVSCDWCRASLISS
DFVKQSLFFLEWCVPEDFAWLPCPKTTVGWGSDVLGKLLRGISEQLVFAGGADSEPASKR
CRAEHEEAFLDMFIPTGLDAVASSMEALEEAKREVDMRFVEKIHSAVFRPRQGLLLKTLL
GQLEMVEEFFSGYNLYPCDESLVNAADMNFSPLPAGAPTGRVAQLLNEWERIQKSHRCSS
FPSSDTPHSRTRHGDAEVELPGEDAAAPFLEMMRRHFINHGSQGGVPFRLTGDGETLLEA
PCVAETTLREPPEEMVELADVAELLTALSASADIDFRLAVGDCGLDNQLPRGPLKSIMEA
SVAAYISLAFGAKTLAVGTAACGHDVVDSSREGDGDCRSTPSTAPLEVLGDVFFKFMNEM
DGGRNERSSELHDVLNEVMKLMCHVKADEAEAAGGYIILSPKGSGENNMDSDAAFPITSI
ATRLVDAARTAMRQAASGLTEVEAKSRGIRWLRHIAFLFSHASVPVGASSPIFLPAPMMS
KETEGDQVRRVVRGLEAHLFFLDAALCAVDEAIVRRWEDAHEALGKGIA*
>TCRU_738 hypothetical protein
MLYLEDCYNNFLEEGLRKLQGERGGSNSRGLGSLFQTKLLQTLLSPGLCVQPFAPQKKSS
NTNSHGEEYVNPLAMASRERSVVSTTPSVGRKLWTWVVDRIIVGVYGMPTRNKMERGTCW
KYGDSA*
>TCRU_739 hypothetical protein, conserved

MSSGAGRGGGFGTPTQLGVQYSSEEERSIYKKVATIDGYTFEVPPVNRFHSKAAESKFVQ
LTGSMNPKFDAERFDALRERLQQADKKGKDSHLQAIAVLYAESLGNNFLRAKNVDLAELE
RCFYPSHIPSYAAALRTVGLKKPLWWRQGPFVRLEDISRLPLSRCDVNKQTVMSFEEWYC
LFWNYYTPFNTLAYLLMVTAQSTFPTRELIDGTAEYLAYRHSLIEDPRARKAPILFLGSR
TGKLGGLLNQTGKIPVPVIHVHEKPNMNPYLLVIPPNKQDEFKPHPIIKMKDQVALEKYE
PAIVLISDMIMNNDPTSMIRRIGSVREYIYFGIPNSYIEGHPWDTWGNPRYREKGTDHIP
SYIRENWLKVSLPHLSRWMIYKTDSEMQMGNGAVTTWMRRPLKPSAKAILSWRLARYKPF
Y*
>TCRU_740 DNA excision repair protein, putative
MADDLSQLGVSWVEESALRDEVVAEVDAQVVAEAAMDEAELRRRWEALGEMEHVVAELQS
LAAQSQKGSASSRGVAEVLGGKNDKVGRREEENTAAVLQFRLAKAQREVENRAKLLRRWQ
VEMEGRQRKRLEEAKKQRQLAGKEEEEAAAERGKSNVSGNTAVASAGLHGVMDTTSITAV
MNVSGLQVASSFSSLISAASPLKAADDTRREPKIPLKTRVVSNDAATAVHSRTATQPQRC
HRSGSHPSVAMTASEYAGGAILPSLYRVTLTRSDLRSKSIKYADDGDLDVFHARQQKRRR
LEEVAATMAASHLALSHSGTVKLEAAGNTGSMEVKQENDEKGESGNTRKEAIDVDALMEK
VDDDDDKNVMRQLLMNSGGGCDNNSTVHSMNRREHETSVSIVPGISLLANIYNRLLEHQR
DGIKWLLRLHTQRMGGILGDEMGLGKTIQVASMLNALHHSQQLRDPCLIVSPLTVLRQWV
AEMHRWAPYIRTCVMHESSATNMSREKLIQSIRSTPAVLLTTYAAVRQHCHLLHTARFQY
VILDEGHKISNPEATVTLAAKSFPTPHRIILSGTPIQNTLKELWCLFDFVRPGLLGTMTK
FVEEFEEPINASKDVRASPLALATAVECAQALRERIAPYLLRRLKRQVMSDTLPQKYERV
IRCPLSDDQLEAYVELLTSSRVQRLLSSTLTSSQLMGGLNCDGRDANGCLHIAGRRFQLF
QRQYHGGIRLEAFRVLNELRQICNHVDIFRLRRAAKENGAEYFDDNEEDETDGVDGKTKR
RRGSHMSLRSNRLVNYSGSGKLQTLQKLLTVWQRGGQRVLVFSQTRMALDIIENMCEQEG
FKYIRMDGSTSGHHRQELMDRFNEDDSIVAALLTTRVGGVGVNLVGANRVVLFDPDWNPV
TDEQARERAWRIGQTRDVGVYRLIASGTLEEAILRRQLAKTYVTEKVLHNPALQRFFHQQ
ESLTETFYLGAEYDSRVPVGKKHILATQEISPLLEAEEDDDGREQDDGAKVMQEKGAAAV
YRVRATTMTNKLNASSTPSTSTAASASRAETALLQDLVDGQEVRVSGGDAIARRLARLSA
AQTMQRVTNTTRTIEQQQAEMRMRALREVKGENGN*
>TCRU_741 calpain-like cysteine peptidase, putative
MTEIKYENGQPTFEGPTVVKCFKDNGNGLLFRIVNEEKKQWAFYNDTKEYNMNVKAAFGK
DSKVEPLGSTKMEKDEATGEFKCEVQVPPLATVLFVEGEPNGYKLNFEANPVAK*
>TCRU_742 calpain-like cysteine peptidase, putative
MTEIKYENGQPTFEGPTVVKCFKDNGNGLLFRIVNEEKRQWAFYNDTKEYNMNVKAAFGK
DSKVEPLGSTKMEKDEATGEFKCEVQVPPLATVLFVEGEPNGYKLNFEANPVAK*
>TCRU_743 hypothetical protein, conserved
MLLPRTDSHDPETNDADPRSTSSAPSVSAPALSFTTTADALATTPRSNTSPCAAYTWLPD
TRSTAPPDATTRALAYNATSPPSTAASSATPPPTSSSTAPSTTTVRPPVITVTRATPDTT
STDRTSRRPDSTSTGAYGEDCEPGRYGSGVGLAATSRESVTVSTDPAGNVPVSTSAPFSA
STSHADSSTGPPSSLPAATAPRNAPPPITYSTAPFSSDTFCTTIRTPSRAIHGT*
>TCRU_744 hypothetical protein, conserved
MPRCIACATTYVRLGKRIAAHALAASTPRHRWKAAVTPQCTHPNTAASSTLPTTIHSGSR
AANTDRKYGSAAVLARSCAEAHDILANTPSACISRTEPSPPVTTTATAAAPATTPVIAER
ALAAAGSVSNLIVKKPSSTPLQPPDTAAASQRMTIVSSAAMK*
>TCRU_745 hypothetical protein
MSSISVLFPRLRLARHRGNNLLLGNCGGVLLPGDEVAPSRGAGALPEYKNIAAGGRCERD
GDHDDVIFADSRRISKTILSWFTVSKAWAWSTKTASVRCCGALQCMAALRCSNWSREELL
GRRPDGCGDNWDSMMSRLRAARIRYMSDPRQLLSATGRCEWVF*
>TCRU_746 hypothetical protein, conserved
MTEGCAGGKGRRAHRVTGACRCGEDSIPGVDPDIGPRVAALRTGAMRLLPTLRQACTRPA
DHKEPSMSVVPSLPHCGDRPASASAGTSSRREHRNFLPTSERRIDVLLPNRRQSALVRPQ
YEGTCPTCSAWRYNSLRGPPMRMPQWRHRLLNRCLARRSPPKLPSMPAGKTRRKHKRGYS
RWTRLFRHRLITDATGC*
>TCRU_747 hypothetical protein, conserved
MTEAASCLDLKASFFQVSLPRETRHLFRCRVEDGTLVELTRLRMGYKASSDILQIIITSA

IARMTTVAHRLWAAPPSVRDDVWIDNIRIAGSKSDATLWKAQVLRNAEGFHATIGRIANR
VLRSTPSWGCSLITLTPGGITE*
>TCRU_748 hypothetical protein, conserved
MNQVIRSRTDWKESFVFRLAWITASRWFEIAALTPNNFTMEPDGTVILDWSVAPKTARAD
PHRALRFVRIRGQHAFDIIKLCRTLQRNEKLTNITSAKVERTLAPWNATAHSIERGALRH
AAQIVETYNLDPHVIPELAKHVDPFDLPQNTV*
>TCRU_749 hypothetical protein, conserved
MAMAPCTATEWSFSGSRMLDLVRQQGNIQAQLAYMDEHRPLDVVVTVAATMAVRRWISGD
IAKYWGDPTLMGHFANLRAPQLPIFETQLLPQFVADVRNRNAQLYLQVEEAHNYLLACES
HIAVAGGLFAGRGDAVSTGSVHLSERAAR*
>TCRU_750 Concanavalin A-like lectin/glucanases superfamily,
putative
MKVLLYTQKVGYPPRERNDKALYLWVADSNHTVYFGPLSVETGAKRAFANTLLYYGDALY
LLQGMGNGKTDGVFLFRIIEELGKIKSIVRNWIEVDAFFSGLSTPTNGLVGVLSDSSDAG
KWNDMYRCVDATVLGAIRIEGGFKFTGHGAGGIWPVNSRGDNKQYTFVDFTFTLVATVVI
EKMPSGGSSVPLLGAMLEDGMGTKFLGLACAENRMWETVFDGQTGQGDFWVPKKEYQVAL
MLNGNEGYFYLDAELLGTSDTMRRREERAYDVLGFYFGGDESGRDSSASVKNVFLYNRKL
TPDELKMVKKTGSPKHESSSSEASGSDSSAHECVYFVPLVSLGLWALAVFYGV*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MTGSVRNVTLANCTFLGGASLYVLGWRSDPPAGERAEVLISGLESRSGGGVLVAKRYPPG
SRVTVVDSVLIAEKRVAYRGDHGLGDASACLVVHSVNLTGSVLTIARTHVAAVFRDAVGV
LVVGGVALSSRGALYVDGLSAQTALGLCVSVEGGVAASGGSVVAFVDSDFLLCKHAVSVR
GAVSVSSSIVAFLWSDFFSTEDYAVAFYSTVSLGGGSMLLAKDNVHDGASREMLYAAGAV
TAAGSTLSFVRNRAVLPRMLSLSLSLSAGAHLRVACNDAGGRVLSTAEEYAAAGFGDAGS
IDVFGCDACDRNTHCYAPGTASASMRDGVCVCACGSGGYGEACVPVGAPALPPAVGTASS
VFVREGVTVQSVFVVPAGASEVTLRHVVLDGVSPVLYVPWMARDGVRIVVQNVSLLNGAV
LYVMGGGALRGAGAAGSDEGGPVELSVCDVEALNGALVLTGTFPAGSVLTVADSLLVAAR
PTPLVYLPGSQSSPYAPVLVLSGLRLVRSVLVVSGVALVTVMTGGRTVMVDGAVLELVGG
GVALDAAVLGGEYALYASARVVASGGAVLRVSGSQVYAAHGLVFDSGVEANASAVVVNDN
VGALTDGALLVLRGSASFLSGSWLSVRGNSIRGRLLSVPSYPRSVDLVQSTLTLYGNAGS
GPVVMDGTVALGGTGRRFVVGCLTLNGQALQPMEYRSAGIIGKFHPVACSVCDADVSCFA
ASTRAMSGSCGCRCGEGGYGRDCLPVYLPRVDGCNRTSGMPLLSHTATLTETRSPTPTWT
STWTPSLGRTQYGPTETLQVKETVELSPTRTPTASVSSTLWWSEVACPTLAVTTTTAGGG
LTQNDIRGGGSAVPTRLMVALPPPFRWARDPQLGTHLSFVPVSTAQPRGFGGPWGAMLSN
ATWVRNATNPSTVLELAVPVHRGYFIAADETIVIRCDAAAVSGGCKGVLLGSFTIRSDTL
PAAANALSAITGVVAGAAAVAVVVTGGLGSVLEMQALGVFARMPCASAQERASTVALPYF
LSVFAARDSLWMVVGNALLAAVFGCVHCGVTVVFQRWRGVDAATAWAAMRFPSLTYVVAH
AMHLGIFFGSVLALAMPGARVQHRVIGVVGVLYGAAFPAGVCYFIARHVGASFTRYWQFS
RKPLHERLLYPVGYWHPAAQQWMYGGMLANMRGSHVYWCVFQLSVLCVVGLIAAVHPPVG
GCHVQYFCMAAVLLAGAGVVAFTNMLRSAFLTVMHTASFVLLAVLCVVSAANHLAPSDGG
ARAYAAIVLLLTTVLLAVAVYGVVVWYAEDCHWQELREPQRCGLEALLRDDEESDDESQK
PHDVTSSSYASGTTVALSYRPPAPPRLVAGDIRSDALSLFDRASSASCSINYVPLDR*
>TCRU_752 hypothetical protein, conserved
MDAPHLPLAIESSEIPITSSIYHKKPVGDAFKGKSAVYKEKIQQIESFLSVNCARHVAEP
QRGNNIRKALDDLSRLEPSISGILLSVRRYLNEWLTTTESTQESLRSEIRHVEERTFKKC
EEIFENRFLQLLKDKRKAEATIKSLRDEVLKLRIERDVTLMKAKEDVMIRLNDCERKEDE
FRSFRKLISSVFKTNEGLVNRVEDLEALLRKHRIEIPRVNDDLYAYNKPRGEAKSSKRDS
DGVKKIGDQVSLEFMYASREEMNLARLSLQRELLNSAFDDRTAYRLQVNGLRHENSDLQT
QIDALQNQIIGLERYIHEKRFLFSTTDGDEAPLTPRPRDVPFTIQTDLGIDLRNSTARIV
VELAALGTNLKHQLNSAVMTLRQLSSAVDWMEDETMLKIADEANVRGALPTFPTSAWANI
PHFLRTHVEPDVPNLRWSETDIAFLLFGLFSNYSSLKAACRTTRDSKMLAPRQYKLFERC
ENPMVRLDASLNELQRDENSVPFGYVVSYFVSNVLLVNVADSPYSSLIQPGTLNPSFSID
GKNASVEMELTKYSYNIWYAAQRYKEQQPLCRLFADVVDGRLPVEIFDVMKHVLRIVEAR

IRKFDTDGSGSFTYNKLVSSVLKLVADMDVQVGRCAILAVMETFKANQTPLVGGRIFLPS
IFADESAPKKKDAPRNTSNRSAVSTRSTRSYIDREPQGASVFTRFWRRLVIQRYERVYSL
MERILGPLVLESKVVIGLFLLPIPSAFQAVRDFDTQCGNMTEEEFNLKYPLLSEKTTSVG
GKSLLTSGVKGDVSRCTDEYEKLLTRNKTTLRYIISLEEVLNTTLGSVSLLSRSMHFPAH
EEERSEPEEKSTDVPVLEKPINSPVNTAGLKKEFSPKRKRGKTKVNAKSKAKVGTPYGKK
EPVQEKSVLEEPVRDIIPSEMTVRSDKEMAEWYGFCATLRQSVLKFPEAIFSDGIFQGER
VHFSGRSTDVSGSFDEELSADKSS*
>TCRU_753 40S ribosomal protein S15, putative
MTSNITQERYEQLKKERTFHKFTYRGLEIDPLLALSEEEFKTLVHARARRHMNRHANRRA
PVLLKRLREAKKDVKAGEKPRAVKTHLRDVVITPEMVGSVVGIYNGRQFNAVEIKGEMIG
HYLGEFSMTYKPVIHGRPGVGATHSSRFIPLK*
>TCRU_754 hypothetical protein, conserved
MMMTGRVLLVCALCVLWCCAGGGGCSEAAPVVPGTGVTGNGNNPESKNNTTDGVGGDGQT
GQKAVTQPAAGSVQKVPGTEAESAPKPGAQVSGTAEETIEKKDTTKKEDEVDKEMKGEEE
EDEDEEEGKDEDKEEGEEDDGGEEKKEKEEDDTSTTEGKSAIGQEEPISPSGTVKASNKT
QPQSTQTTGDKDQAADGAGTQEEKKNENKEANPKETTVEAAAMKTTTATTGDSDGSTAVS
HTKSPLLLLLVVACAAAAAVVAA*
>TCRU_755 hypothetical protein
MCHDGNGVLLPSDTAGAPQEAERESDLPDIDYVAADGVASVVGQSLGDEAVSDKAGGGAT
TTGPKDPDAADDAQGAVDPPPREDDAAVVRGVGRQT*
>TCRU_756 hypothetical protein, conserved
MKRIRVSLNLSSTLGSREFGMKASLEFYLKSGAHAISGAEGMLAPKSPLAFLVLWMRALR
LRGEPGKQFMDLGGIVPLAFRMRIVIKFDPSIPIQKLPARLHTVFHEDDTFARVAQSLMD
RRELDRNNNDRCYANCALFMDTRHLLATCVQKGVSRTTSERQKTAKGQPAAY*
>TCRU_757 WW domain containing protein, putative
MSVVLDCVPDASYEPSEAELLEYGKWLGMKFPEDKPFLWIAREGLKAPLPENWKACRSEK
GDLYYFNFKTGESNWDHPLDKQFKELLQSEKENPSPQSIAKGAKRLTIEIDNAAETVTEQ
TEAKESCISSSRGKSRTQKLKTLKLKKELPDNLRLKPIARVNSGYDTSERGSEPVGVGKR
TGSKACSILKQNIETLSTERSEGSLSSEKVTFEADLNDELRRFQSEKLREHQAAKDEYEM
KLKDSWKRYQKLQTEEYEKKMNSYKDELEKKLFEEKNNLEENYSTSVQKFGKEVAARVEL
EAKRMRDYLSEKYEEEKSDIEKGWQEELENFRRSKDLELDRLRASNFQSVAELKQVTDEL
WENALYFVETYKKAQDAFVEELTNTKIIFSKFGEHALSKLIENARELYNSELNEIKDSFH
SELEKIRCQFLEEIVAFQRKQKLLLEEKEKYDEENETLLNRVNKISDCTNLKPCMTHITQ
RQEKDPQENTRIQGVIEKRGDFASGIKGDCAQFDEDTMGVRSEKELFESVVTYMKEVQRK
ELEAVKRDLKQRAEEELKATLDEVVRDRLHLGFEPLPEEKDEIFSFHGSEKALPEIKTEE
KESEKERLSTALSDTIKKDDLTDFLTEALRRVFAGSPFIISSPKSGDAATVSTTAIFGAV
NGANGKQTYNAEGISVPCRTEVNTLDGFPVSFQEQKMLLAGEHQRVAEGKRFVENQRFGL
EERRQQLKMARHQWKQDVRTAKEEGVRASSKRGKLLNKLRIALENQARGLERDESILRDS
ERWLLMKEQSVYQMEKHIKELEEGKGRDTSINSIDTVGLVTDFFKPTMPSSGFYSPNHDA
MQGVVRKRDLDPIYTKTLDKIARRLEEVTSMMNIQKQKRGSSLPYENLPRRRSAQKPTKG
A*
>TCRU_758 BNR repeat-like domain containing protein, putative
MRPTTVASGDSVYMLLRNQGVTPSVDKLANARDWGLLLVKGSVSGGNEITWKETHAVTFG
NDEYVAKFSTQLVSGGGSGIKTKDGTLMFPMQATEKGTTSLLSMRFDNSENKWKLSRKTV
GDGCRDPTIVEWGEENRLLMMASCEQGYRDVYASTGNGVDWYTYGETLTRVWGNSHDRKG
HGVQNAFIKVTIEDKDVMLVTLPVYPKDDNKQKGRLHLWLTDNTRVYDVGPVSRETDDAA
ASSLLMKSGNEKLISVYENKKGDGSYSLVALSLREQLERIKSMVKTWKDLDSALRTCRSG
SSATVDPRKKGMCNDTVPTDGLVGFLSGNFSDNTWKDEYLCVNATVNNGERRVPNGLTFK
GSGAVAVWPVGDMGQTVPYYFANNKFTLVATVSIHEVPKESSSPIPLMGVRMNDAQGTVL
FGLSYTHEKKVGVHTSQRRL*
>TCRU_759 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MLYTHKRYRTLEKKEKALYLWITDNSRSFYLGPIYVESLLSETVSNTLLHSDGALYITRL
TYTRAGRVISLARLTEELKTIRSTLSTWKKLDASFSESSTPTAGLVGFLSDEASGDTWID

GYRCVNANVTRATKVHNGFKFTGPGSKATWPVNTWEENTYYGFVNHDFTAVATVVIHQVP
KGSTPLLGAGLGDGAGTRFIGLSYDANGKWETVFNGTTTASGSTWELGREYQVALMLQGG
NNGSVYVDGELVGSSETLPTPETRGAEITHFYIGGDEGDSDSSVTVTNFFLYNRPLSDDE
LKMVKKIDGSVRGDVSRVLMLLLLGLCGIAALY*
>TCRU_760 mitochondrial DNA polymerase beta
MFRRTFWRFNPDSRENIIRIFKEMADLNNALGEKYKVQSYIRALNSLKTNLDLPLRTVED
LERFPGFGSKLLKKAEEIIMTGKLEELEKKTKPKLKAIQELTQVHGFGPRAAAALFDREG
IFTVEELIEKADRIQLTDQQRVGVKYFHDINEKIPMHESVLHENFLRESVQARLTSDYEI
QVCGSYRRRHPFSGDVDAILARTLSAPPLDYPVTNTGVLGTLVDYLQERNYLEATMAQGP
LKYMGMGRLPPRTTNGTTKHYKARRVDIRLIEARSVPTALLTFTGSKNFNVIMRQAAISK
GYLLNEYGLFKLGSPEEVKALQERVRANKIAGTKNSPTDAASDPTVEEGVDPVVSVISGH
SAKMETLGLTKEELEVKRVHVTCEKDVFDVLGMPFAKPENRDP*
>TCRU_761 mitochondrial DNA polymerase beta-PAK
MMLLRATRLLRVSKRTVASAGAQGAVKRATTTAAAPVAESTTLREARAAAATKAAGQRKP
LHHSRGGSGDSTRPVTSLQASAQLKGVRTISKASSFVPDHREKVLQIFQRLAEINNALQE
RYKAQSYQIAVDNLKRDDFIFVHLPPNILPPGVDDAKRTEQLNAVSATPVVGEKLKAKIV
EILSMGDLAELHSLQAKPIIRAIQELTQVHGVGPRTAVTFYKKYGIKSVAELQQRVKDHE
AEKGIGDGDRVGSNCGNSGGAKKGSKKTSAGDDDPVLHLTEAQRLGLKYHRDIMQRIPYE
EVRLHEAFLKLRLRKYLGKGYELSICGSYRRRQPTSGDIDVLITRKMNGKGPAIRRTKSK
KGGHHHSDEQVLAPQEVLAAFVEALKRERYIEATLAQGATKFMGVSRLRSYNYNAGATSP
KLYPARRLDIRFVEPECFPAALLYFTGSKHFNVVMRAEAIKQNFVLNEYGLFHNDAATTV
AAAAEDNAVDDSSSCSSGSSGGNSKNKPNNNNSNNGGGGNTARGRWNAEAFQKLVRAQYY
SAKSPAFMGEDDGHGEEDDDGEDGADGAGEDTRSKKHGKKVSAARQRQQQQELAALWREV
ESRRVKVKHERDIFDALGMTYVQPEQREM*
>TCRU_762 Beta-lactamase superfamily domain containing protein, putative
MAAEYIQLVGTDVPGSYGSCCFSGQVQHEALRCPTQPLALSSPSPTPSTGVATAANGDGQ
LLFFNCPEGTQRFSSEANMRLVRTRGFFFTRWAVSAVMGMPGLLFTINDAGVRHANFFGP
SSHSLTVEGGDGAQTQQPPFSAGLEGMLGALRLHYFWYRTMSFQQLRVGAVLRQLPTALP
WNYVCEVPLHPLEEGEGGTSADPHDMSSSSSSASSFFVLALLLSSTSALLGFRVSRKAST
PSEETYGYAILHAPKACFDPKRAKAFGVPPGPMYGQLKQGNGVWIDDEQSPPCVAHSAEK
SRRFIHPRSVKQATVGSRCMYVSLVLDGDDSGEVAEALESLFGRDASYRGDQQEEGVNAD
AESERLRGGELRRFLVQWQPFLLFCDDDHAASGEATVTAHPPMERTLVLRHVVHVQCSDF
FSSFAAGATGSVEAHYVTSIFTRVQREVREQAVESFRHDRYDGDSVVATGAKTGTMHHFC
AAVQQQFSAFPTALAHRYHLNCIANAQFPITLPSAGEKEHERMKEDTGRIWPYAVKHLLI
PPEAAGHIPHNTYNLAMKGPAFHVATFSSLVPGSKQQKRKGGNSKKEDVSGLLRYPTARS
AVDMLSKEFRSIASRAHEQMQGVLLSPSSFSSVFHHSHGDTHDNFHGICGHKDSGNTWHL
DGGGALTFLGTGSAMPSKYRNVSGTYLEVMYQARSSTTLSRAVVVLDFGEGNAGQLAIFW
GNGFAQALFQFFNDLVFVFISHAHADHHLGLMTLLELRHRVRLQVEKQDSIDSGNLNEPL
LVVCPQEVHEFLQDTWGRCTAYRQWLEEEVVYDVFPAERHRVGGAPATSVLLPRLNAVCA
RLDEKTAATNHSERHGASPTVWGAEVFPVHHPANAHALLLRFPAPMGATTASRVFLFSGD
TRPSPLLIERCRRFTRWTCRLHEQREEEPKEEGDDGPGVFLCLHEATFGEDCGEEAVEKC
HSTLPEALQVAAAIRAEHVVLNHFSQRYPKLPGLMKSQLNGRDVDLHCKRRKPRPPDALT
ALTESSPFEEAVKSLEDVQRGDTPKRKPLDTPNSGELKMCFGFDFMRLSFASLESQQTAQ
LTPLFVQLLEEYESWGVGTTKRLRG*
>TCRU_763 protein kinase, putative
MNALDELNLRLGIGPTRPHLPITLQRSGYSAVRKLGKGSFGNAYLVYHAGRKQQYVVKHV
NMASMTARQRRDAHQEIVVLQQLEYPNIIRYVEFCEEHPHLYIVMEYADGGDVYTHLKNL
KSSVWALGGGSGGVGDGVSSTGGLTEEQVISLFVQTTMAVKYMHDRRLLHRDIKSQNVFL
TQNHVVKLGDFGISTVLMSTVAMAQTMCGTPCYFSPELCQGKPYNNKSDVWALGVLLYEL
CTTGRLPFEATTMNRLMGEICKKEPRRIPSRFSDELWNLILWMLKKDPRQRPDAGQILRS
PVLLRYIPNIIKKLSATDGHPEDEFRRVLTGDATPPTPIRPAMDLQLKQLGKETARDGPA
PSTGAIPVASAAAAAAAAAAAAGRQGFAQKRHDQYPFKRVNDDNAIKDRVGGILGMLAQQ
RQQIQKMKEEEEAMKRAPPANQPPLAEPLNYVPVLLQRNQKLTKNGEKVDVNSKFNKNDN

CNRNDNDAGGNTPKKEKNIFARTPLRPPKNVDGGNLKRENGVPHVDASKEQEQRKKAINH
LPLQDLFLLYDESKKRILNEKEQRLGPARQPMNYQPAVAAPARMRPAVVELQVGGETKKR
PLSPVLPNHPIHGSTKAFPYGTPSMAEEKSIPIPPIALPTGAKSSALTSLEMLDHDKNTK
DDGNRASGKIPAKNEPTGDLALVLKEMTNHLESMRSSAARAESNTEAEGPKGTPGTNSLS
AVSAFFGVDAVGNSPFPASEMNVDQVGEEFSDAMGTTLNVQELQRQRSASSFSHEEVNDG
AAGEFLPLCISRYNGVWSSRGSRVAPAGMTATPGTAKETSEGRETQPFNDIQPSKPGISF
PALNTGPNAVSPQLVEAVAAAQENEGGGGASLFTGGCLCDGVHFTGLASAIFGSFVCNCF
VCSRCSGALMGVEWLHLPDVPFEDLFADGFPSEAASPSTLPKMPIASPVDETSAGSGVSA
EQSALKADPSSALRDGARKASNAEIVEEEEERRDKEEFVRLPELLKKFVVQVPVVNEDGV
ETLGEYTVYFCGRCGSTVGMNHDDVAGGLVAKAMLSEASLGMLELFQKTMPLHNSEALTP
RKIR*
>TCRU_764 hypothetical protein, conserved
MRFSPLTACFYSGARRQTPLQSWCRYHGQDACRQQRFYTLGEYLQRLPRGIRDLLLWSPA
IAAAYFMLYKQAVYFLPSMGRQLLRRPITPATEPSNRSTDRAQGSGELRAVKVRMDDACG
SVVDGLLLPLVDREEEAAVASSSLSPPIPPFSTGAMMDAMPLRAVRDVDTGKVSGYTRL*
>TCRU_765 hypothetical protein, conserved
MLRRWLLMPLTAGLPATLLSSSDSVSRGSCVRCVGSWQQSAKQSRRFSKEAMMEGRKRHH
WQKEVAALRQHINEEHGLQQRQRAQLRQRCDRAATALIHGASRGSSASAANALATARHLL
TLQEATRKAMKSEKSRRKAMFVSGKKWRG*
>TCRU_766 radial spoke protein RSP2, putative
MTESAYLKSSVGPVLAKAVAETVLAQPSNPQEYLALYLLHVLQEEERRGADAERKKKAEI
QRQMWASERALREKRAADTIQRFYRQCRRKLQLRREEEEALWSKYEEAEGEAEELLDEEE
TAAAAGKSTDEVDKMDDKDGAAAAGGVDGNNEEEMIEDAASAVEEARRDFYKAQRFMLHI
RKALIGALKKELTDQREQIRVGQDRMYDLLDLAEVERREKEEAEFVAAVTAGAIPSSAAI
TELVKKSEIPRHERISTSMILYRVMRCWCYLFFDSTPKQTDTPAKVAALVKPFTFMQLLR
AFNPVASYQRNRPLRIGLEGKHEEGEGDADDMLQDGGDEPLPQPKPRQARRVSRVLRVLM
HDAEYVCAVNPADYLDEEEEEGAAKNSTAPERGAALATASERGAALATLVETAAKKHSVM
LYALLRMLRTASAYRDARDRWVSLLQQNGQDAPPNEEMPEDDDADSKNEEGLRDDDGEVD
EAAVRRLLLVIGTDTDEALAKLWADQDEMQRKKWQAMAAARRGEEEEEVATNDEGDDDAG
DD*
>TCRU_767 Protein of unknown function (DUF2453), putative
MTAGFLTVVCPVTFITSKKQLTQVAQSPSAKTGTSHCSDGDICAIGDDGQSMTKHSVECR
AISGMDHTVVDVSSGKCSDAFGSQMVDSNEALLEAVNRVRDVLQRCQGTHNSPDTISSLQ
SPPLTPFLAHQEKEMEGREEMLTAIAALLEKDTAFGPRFLSSLSGDALRSLLVIGTTQEY
FGQDAVEAQLRAVDKDQDDNISSQDYDAWVNTAVRERVAMRFELPRATAHVQDTTTSKAS
ISPNTTVAAAGYIPWGLWHRIALSSAVPFMAFGMLDNTIFITAGDAIDKRFAEAFGMSTM
AAAALGGVVSGTAGIQMHGLAERMAQRSRLARPPTLTPSQSASASNGSATRVGSTLGMIL
GLLFGMTPLLLLSVPVSRSEREQPAKG*
>TCRU_768 hypothetical protein
MHVPGGNKATSPPLHQQQLQQQWPAASLRRRAVQQRQQQSPGIRRAANSTTAPSSSESSP
TPLIMTYELENSSEDDSEEYSETTYTPSNVPHFLSMPFGPTGDGTASLIWGMSSTSSYCA
DVFSSQGTEIGVGSKTLSPYRILRQISLCDTHSNKSGIPQMPVIVSERNSPVHGEENQEL
RPSNLTRTNLMNAAISTQLPQIVGSEARIQHTQKPMVNLEPPHNESTSRVATLPPAPGKI
CTRPSKECVSPITARPSTPAAPAASCRGARSAVGGSGVSNVSRDSRTLLDDDAKRGVKAL
REEVEGEATPRLILNVAPPAHSSAETPVVAVVPAEEKVGTSRGNFATNLHEIQSSVTATT
ASPASQCVCVNATNGTTQLTRQAMTAATRRVKPKEVPCGSERRRIVSGSDAYYKLPSLFS
STNSVLPRVEKRQKFFAESLQNHPQQNQQQQQLSELAIVPRRLGDRGPLVQERIQRQRIR
RWETAERVAILNKIMEMKQIPNIPHAFRSKDVASCAQSPPQLLSQLKGCEANESDEVTGK
ILRSVNPIENWGSQHNATPQGLGTGLGSAKATDDPTRHFPENTKTGVKGLCPPRCQRMES
ARRRVRNQQMDMLPSIGGSRIKLTESSQILPGHEGNMT*
>TCRU_769 chaperone protein DNAj, putative
MGGEEEQAEEIRRLLHCAASKADAFAILGLDAQSCALSDINRNFRKIVLKVHPDKCTLAK
AADAFHVAENAHKLLSNEAVLVRLKIAHKKKQEREEEEAARRQATASAVGGGGTVGTVDE
ANLSKEERVRLRRREQLVEQQLEAARLAEEAARKKQRVERETRERAELAAELERQRKEWK

DLNLF*
>TCRU_770 AAA domain (dynein-related subfamily)/von Willebrand factor type A domain containing protein, putative
MLRYRAQPLFAMLTRYTEAKAKTPFFNTQLCAQGRHGSTDGLLLTIGDITVPVPENLSHP
ENVKWLLPGIVGCGADTDKPDNSDDNSTGNMVEKGFQLHGGNAFFQLNDSTTRSYLRWMC
QKEQLRQDMCLVGEPGPAMRWLVQMYSYLVRREMQCVSLNRDTTESDLGQRREIRNGTLV
YDDQCVVVAAREGQLLLLEGLEKVERNVLPVINNLLENREMHLENGMMLIHPERYDRLLQ
ELLSAKKRRYEHGSSDIKNGEKMSSHDAMTHAAAHEELRRMGFIRVSEHFRVVGITVPVP
PYDGNPLDPPLRSRFQCLYVSIPLPGLAAAKNMTAPASVREGYATGAAESLLKLRTIIDE
VNASTKDFIMGGKQAGNSGEPSNHHHNDNSSGIGGVTSTVRGLQTIGSYELAVVSRQRQL
FPDISLGEILPRAFPWMLYAQQTATSGVAHIEEAARCRREYERLLGACHIGVPLYECRHS
SIDEDGDVIGNNHEDGVYAGEEDATNSRAPVGILSTRGHARMSQTLREKLAAQRRRSSRG
GSEKSTEEPEVSRRPEDFNDVLSIENIRVAETNCGAVVGDACIASREKGGIYRLPICMGE
TAMHTANGETTNSFLVAARCPTPCNVFTTAHHHVLQSMLQLHIAGQHILLLGPTGCGKTT
LLREFAQLIGYRMETMYLYADMTNRDLFQRRTTDSSTGDTTWENSALVEAALRGRIAVLD
GIDKLPHGMLASLQHLLVDGNSSLYDGTILKSQREYEILKQKLMATDLEMKARRIFPVHP
AFRVVATARSTSSAASSGGGGKANQSRWRVTHEVTSLFGLVMMPATTQTILHAVLSRAAS
TELETWRNEMSSLTESDGGAMAERSLETIKRDVDRLLGLRDALERLQETEPKVPQLSLRQ
LLHLIRFRVRHPDDFTPGVESTLLLPLMNTLTAEQVRQAMHSCGFHGVSDHEEKQKQQQR
HYGTRKGTETVADLSEGRRGKRHDVLTEVSALKNTNAITECQGCGFMRVFAVHGRPVFCS
SRVYSEEERAMVPYVPYFHSNPVHESIIAWLAKQYAVGNNILLIGNQGVGKNKVVDAFLA
RIGVPRQYIQLHRDTTVGTLTINPTVEGGRVIWSDSPLVKAVQRGHCLVVDEIDKAPVEV
VQVLKGLVEDHEMRLRDGRQIRGPRARVVAADSDPKVEANVIALHPDFRIIVLANPPGFP
FHGNDFYRECGDLFASYVMGNPDALSQLRVLKAYGPNLPDTLLVRLISAFQTLQKSFEEG
HLTYPFSLRELIAVVKHMAAFPHDGIYDALNNVFNFDARNENTLHLVRQVMHLHLHPLVS
AGGMRRLLPLRAGQSLPLHFSPQSLQVPATASLKLSTTPSVSDATLLPVRFVTDADCDKP
YIAQSVPTWCEQYKESEFAAVVPNVESEGFTEWLAAPNIPFLRSGDVVVGIAPVEADVDM
GALITLAVLFLREEATNDTSNNNSSRIKRLLLAMVAPPSVASFGMVTMRRSHLSLGQIQF
FDLTRFFPDADFSSSSSALAPSLHAFNAEPHSSFLVTETQAGWLNDAFGAPIPLVAVVDA
QSGLVLLINTAAAAVQSCDVSPRQQGEEEECTRGAVLPVRIAPPSCEPSLCLCSLRPLSG
IVAMTRPRSPELFVWMNGQRIVVTLPAASIHKLQFVTDNLAMVSLRVGEMVSNCLLKMAV
SADGQAKASLLHLPDGISGDIVGFAGNQATALPSDHALLQPLKLEELKGAVVVPSFSETN
RGDVVYMTLDEYSPEKRMWSVRLFTDADAAAAVGTGSLRVSHPNHQLLATEWSSAEHRGR
IVAVDFQQHMVRRFAPPPTASSSSSSQDPGMPLFALNEGTGVALWYDNTAQRLLVADVVE
ERVQKRYRNWSTLLEGSVKQIGNVASTTRQPLSMTYSKPRAKPSGTLKHGKEDDEEHHGG
NTYAGGTGGTDTAGLGGIVGPYRLDKGWPVHQVSPEEKQRVPPHIIEEAKRMGKAALEER
LREIGMSAKEYEQYRALQERVQAPVALLRSVLSGLKAAEGERTWLRGQTDGIWDDSKIVE
GIVGERNIYKRREESTETNPFQSKHKKRLLFVLDVSASMYRFEGMDHRLSKLLESTVMVM
EAFAGFEEKIDYAMVGHNGDSACIELVSFGHSPANQKARMEVCQRMVAHAQYCWSGDNTV
EAMRQSIDLVTAEKGDAYLVFVISDANLPRYGIQPSELSAIMRSHKEVQMFCIFIATLGE
QASNLQAEMPPGHGFECLDTQALPHILKQIFFSVNLL*
>TCRU_771 hypothetical protein
MSGRGIVPILERHGDVYITGSTVVRHKVGSNGDELDLFPSGYDLQLVLSAKNLYKLRQRH
PPPRLLSRKPGDNRKEGKEEDELQQKKQWSLGEKSHAPLPPPPPPPEMMWRESLGLIRAL
VPLHNHPSRMWAAGRHELGANCYGFAIEYFSTKKGPKPSAQRTVLQRYMKEIQCRCVNDV
FTDVKLVALDGTPGGLRVREFHVGLMRPPQSGSEPARTLYASSEGSPFLEQEWCCVFREA
QMNYWHERLEDKLIEDPELFQYQIYAMEFPNTTTASTAAGRATQKHEKQPLLCQLVLSTE
RLYVVPRHDAKLLAVELPLHHSEMHLRWFTVAALQSISFDPYTGVIVCVGRQQHEGKQPK
SSLARQSLTHAGSAADSSKEVRFTLGFFSVAEAEEAVLEIQRVWELTHRHEDFPLA*
>TCRU_772 histone deacetylase 4
MKKRGPQRMGGFGAKLDGDVTVRRFLAPQLRTTTAIRRGEMLEPIGEVAMRVGVDAATVE
GLVDAQGLALFGKLQHGAEVFLAGAVAERSDKHNSNCDDSGGMLSLQPPDASVIWAYDSR
MLLHVPPIDRIPETPYRLQRAIELLRSAPRAGELLPEELLCPDKGKVDTMTGATRGDVND
TSLSGVIPPSYWLPPRLATLEEIALCHNVSRYREFVEQGTALPPPLKSDVYCNDMTSSVA

TRLAVGAVIDAARRALSGAPSFAFCLVRPPGHHCTSDTPGGFCLANNVAIAARQLLKDWR
DNNNGSGGSDGGPPPRIAIVDLDVHHGEGTQSFVEEEPPPHGGTSVSPLLYLSLHRYDHG
NFYPYDPRGDTAYIGRYRNVCNVAVHTAANDPACCEEVVSDAVFERVVDDIFVPRLKRFS
PDVVLLSLGFDAAHGDPLGRMAVEGGFTYAVRALKRFCRTQQQSSRGLHAGLVVVLEGGY
SPEAVAQGVVAVAHALRYPANDAEVVRYAARQLPKTWQELRRRMARQQYEMERQQQEVEG
DEGNAEASYEPVPVSPTQGTGAIISLPEDDVLLERHERWCDRLISRVLAIHEESNKRQ*
>TCRU_773 hypothetical protein
MGGGISNTNQRENAQDDNVNEKRQCRVDEGKRKFITSTVNSANKEYTEGMSDPLVARGIP
DPVESTTPRSKLTFVKGNSENPTSGAASAGNIGKGAGNSSSMNTMRNMRNASLAVQEDSE
NPTSGAAASSILVKGAGNSSSMNTMRNMRNASLAVQEDSENPTSGAASAGNIGKGAGNSS
SMNTMRNMRNASLAVQEDSENPTSGAAASSILVKGAGNSSSMNTMRNMRNASLAVQEDSE
NPTSGAAASSILVKGAGNSSSMNTMRNMRNASLAVQEDSENPTSGAAASSILVKGAGNSS
SMNTMRKMRNAFVAIVGDGASETVESEKSNLEVEPGATTSQGSVMNVAGPFICQSYNNAV
EKTKGLGRAPAPGFFRSVVGPSPVVSNLTRKKVTSFLRPCVATGSEEKISLDVAFDPPAM
PFVTPSTGSGSARGPLRMRLRIKQGNEGNPVARADTPEKGSLQKSGAKNKTVPPSAPYNL
DFDW*
>TCRU_774 Sperm-tail PG-rich repeat, putative
MEQTGSSHAVLVADDFQTQVDVLYAQILASVDSSIDNNLESACGAKSVTQRPVRKRGASV
ACSAPVVKDVAVGEKVCCFCADDVVDVSTTTASTILMSDVNRVCGCSCHSPCAARGLHPE
QQQQQQNSVNTSSECLGAMPRSVSSPQKTAGGAYGAYGRSKTGGLVPPRQRQPPSTFGSG
RSGMCDSIKKTSAPGPGSYFRGDDEAMRYSMATRSQSKNPPVGGGGGAVGNCGPLGTRHA
RRSAEDAARALQRQFTLLCQCYWKQFPELGISTNAAAHARNCPCHSIHTASPGGTDSHSS
SSSRSSCNDASFRVGAKKTSGRRPVVPLTLSPFRVVSPSTKRGAVFGTSPCRVPPTEKQQ
QQQRSTHTESVENGPRKGRGPLVRDNTPSRGRPMELASTPGPGAYNVASAFDAASARGKT
RSVSIGKAARRLHTPTESPGPGTYDTESKGQTGAQLKNNYFLTTSSRQLQWMAKHDGECS
PGPGEYSTENATRTDARHKNSPAFSFGRAKLPVDAKRLVDPSVMGKPDEVPGPGTYDVPM
MLPDGATVIGGRSAVITTARRDDNMWRGVYYPPDDVPGPGHYVILKETTGPQWTFSTRGL
PSILEEPSPGPGDYSIPIFDVRRGRSATSFFPTAPRLLHEEANRAANLPGPGTYDVEDVA
GVTRSAFIGTTQRFFKPESQEEGVPGPGAYVVKHTARERRMAVPILASTAPRFYGFDSVD
STNLIPGPGHYDVVDNMRTLHERGAIIGTASRALTLDTAVATAATDAGPGAYDITLPKHG
PSFSMRQRLMDRTVNGDPTPGPGKYDPRELSQGPSAVVGIAARFQSADEEMLCNSVPGPG
AYEAALPEKLSTTTFFGTSPRFVNNGAVMDEKMGGGLGPGVYDPREARSNIAGAAWGTSP
RFFKEEYRDIPGPGAYEVASPSPMRGAVFGNADDKSDWIIPADAANLPGPGSYLPQDAPD
RMASAVVFGSSPKNALSPEEREAFMQRHIGPGSYDAVLQVPHAFHATFGGADTKRLGEGK
PSDTTPGPGQYATTAESQAFVPRGVVFGTASRVPPLQDAAGTPGPGAYVPTMQPNDGSVT
GPVSFPTAPRFHGGSEGFGDGNTYDTPGPGSYVLDNAGNQLGGRGAVVFGTEPRIPDYEQ
RERALFPGPGQYECVQDATTTNGPAYSFGKNPRISMHGNNDDGGFVGGGQAGDVPGPGSY
DVVIPTLTAPTTRFGTSNRTVGPLLLSEVPGPGTYDVTKTTTVAAASAPAYRFSTAPRES
HVDASDTPGPGQYGDLAADGSMWRRFTGVSFPTESRFTTGKETDVILPGPGQYSPQHPQW
NASQVYSFPSGKKEFFVGNDELPGPGTYNPTISPAGNGIRFGTAERGGEQSGQDGDVPGP
GTYDVTLNRQEGSAFSMHRTAPRGPTLVEVEKSYIPGPGTYTLPPAFPATEGAGTGVSFL
KAERFKAFDTVVDNVDCVGSLTAPGPGYYDPQLPQSTTGVFIARAPRLAEVGDATAGVTD
LPGPGHYEVRRGDPLLTTPLDGGVAMRFTAARFPLRDEATASEMPGPASYSPVAPQNTTS
GASFPHAPRFVLNETQERAEQPGPGEYSLPSAWCPSQDVGYSFGTSKKIENAYTTQDIPG
PGSYDTNRYATRYLTGPAFTVQGKSTYKDGHAGAEYPGPGAYSPQPVETARTTTFAPPST
VDPDVVFAARVNATPGPATYAIPATLSSQTVGFGTAPRTLEKTDDLPGPGAYLTSGPIVI
PSQPAFSFGHAPRPDIVPQTQKNAPGPGEYHHPIDPGPPVPAFTFAGAERFVEAQSVSTT
VPGQYYHPVPASQPRGPSFGFPNTISTMTTTAAAAAAGVRAGAGSGLGPGVYFHPSHWDL
RERGPSFPVTLGHYPPALGADTPGPGAYHVEPRQNTPLAAMTAQIGVLNTK*
>TCRU_775 CYC2-like cyclin, putative
MYTSSALAAGVAAASHFAPSRPRDGDGGGQGYSTGGHHATNFAGVGTATTVAVENVEGGM
VDTGAMGTEDNNGEADDEGMKRTSSSNDEPTPETCTDTTPRTVIDEVFAQPHEGQQQNHH
HHQEEEEQQQQQQHQEGDALQGQQQGCNFSQDAPPLSCNSREDACKSEVSNEDGKDVDVT
GATEEAEACEMCAFSPVVVSARKPLQSQIDLVTARVAVTLFLENLSEDNKAEPVLTSDFH

SHRLPQMPIEAYLDRVVRHSGVSGETLIASLMLLLKYSHFINHPVSVYNVHRLTITSLLL
GAKLRDDQYYSNEYYSRIGGISNAEINKLELRFCGCLEWDMWLDEAEYETLENLLLQLVT
VFASNMEEIDEVTRRRFQRQFWVEELRPWKERFDVSSSQRRERIRRCAAEDFSSEQAKIQ
CLSPSGSLFPQNPLVYPGTGMPGVSLDQIILPAVYRQTSGGTVSNAHTTALVTVIAQNAA
GSTTSKPTHYYHSYHPIYQPPPRQQMQYGCGVYDANINNNTNSNVGNIGSGRSTNAGAGF
GILERAVSLSPTTPTTRTTTTTGLHHSGISIHAKPYHYKSRGSSTKKFFNKPHRYHYASS
QQMDSCHAGDIAMMDATTATYCSSSSRQNSIHNNNYNNNNDMEFASITSTVWRPSGTNNN
NNNNSSGRRPATSDSVTMERHSGGGGGSAVRGSGPLVFPSQPQPCTDAANEEVAERRNRR
KRPKPDHYRDYR*
>TCRU_776 kinetoplastid-specific dual specificity phosphatase, putative
MSLMPADGGEGVGPPGDGNQQQQQQPPRPQQQRCCNKQKNREEEGENCEEEETCPLEAF
GSAPASNTSTDVSGAQGLTACKEEGSGDMTATTKTTTTTKTAAVVKVVDTNAGRSQQNGI
VAPARSGVTEYTCSGRSSSSSVGSSAHVSPSRFVVGSTRHISLTTKPPAPGNGARVSSGS
LSNSQMQAVIKFVSCRASGDKKQNVTQTSVPVGQSPLQTPGNDTSANTARASVDVTPMPT
ISLPLQGQSSKGQMASLSAIDLPLPHVSLRQCTSTPLVPNTVGTQPHSCYEKEEERDYFL
QKVTPQLHRMLPLWRKNFGNEMVTEEGMTVTTTTTTTEAETEAECQQEQWQEKILSENDV
SDRRLRQRLPEASSRLHIRLPASPMCNAANSAYNPGSSDFDVSVSSSSSSSRTLSTLQAS
SHHFVRSVCHVLTGTPTFSSCNVGPEENETEKTFGTSKAQTTTTTTTTTTTTTKATTMTI
DGGGGSNSSNSRSDGFVLTSHEQNDCICGVQAIGIDAPVEFVQENSTRQFLTKNGNQSGV
FTPSPLPPLPPLSHGACNSYSLDAAMVLPGLFLGSYSDALKIDALAAHGISLVINVAEEC
VMMETMIYNDYDIKFIKFPLKDHSDENITRYFGPITRIIHRQLHRRERALRSSRKAATGN
IRSYDDEEVMSISNKSVGGGVLVHCRMGVSRSAAIILAYLMIYGETLWVDDNCSIQNQHI
EEESFTPIFTPPNVSPISTLLLDGSDVEKENHSTNGKCCECCCCLAIQNPHITCNTDGVY
KPSVVKSYRDAFEFLKKRKKDINPNIGFVLALRELDDREGK*
>TCRU_777 hypothetical protein, conserved
MNVVCERRIKRLEQQLRCYRHAYDAQRKVLFELNAKLQAAETVEGAALNSGETTAPPAPT
RSEENGMQMSAVVPTVEWDEAFRQRLLQVLRDPLEQQQAVTFPTVASHDTCSDDANPLHG
DREIRMRSLGPPRHDASIRNGDGGSNTEDDGDSPPATRLPSARHGSKAMESEQLTASLVI
ASTDAATRFLEMMRRLWSAYFAHMHSQVQGVLRRMDDNFARFDASPSEETLVEFLEAHQR
LRPHLSGIFGMPEGEEKEEKEGQPRGAALPSGNPLEQEGVFVQQLSLCIAEAVSPLFALA
LRSGNNGTQVVEESHDEKKTRSSRQRRHDGHRTRTAAAAAASPVCSAPFSPSRSHSMSTV
FTDAEESVTESLKPNRDASQEELLDSHNGNRTRSSGESTTDSSEGRNSRALDVTGMGPKG
THPPSPVCPNPVRNDHKTDAGTPRLNEEDAENYPPQRRWRRDNDSLQVEAVLYSRGSSAS
MRSPLNGPAATSTAHRAIGEEEEVEVGGATTWQNPHTRLRRLRMQEERLSFTLIDIVAQR
HDYSSEAKCYAVNKRLARVRSAIIRTEREVNELRRIQEEKEAIRKERAARQRRLLYI*
>TCRU_like, putative Vt.1
MTSSSSLTVNVPDHWVATLRPYLQRADEFDKVQPAISYFLRTHVAHLAMKQRKKDDPVGT
QYLRQLLQVLEAEKQRLGQEVTEVDGRTVLTKTALTLFSKADDAERSGAPAEMGLVRLFF
TASILLDATAQFSENGELDPIAAKRRDYARYIAVRMKKAIESGTPYESPNAPETSGGLDE
MFSEDVNDDKRTQEQQPGFPASMYHPMMTPEQPPPPPPPPYQPPNPSPPPQPPAPAVPMM
VPNTGSVADGPSMDAMISAQKCAKQAVSALQFYDHATARKQLLTALKFLDGK*
>TCRU_779 Flavodoxin/Radical SAM superfamily/Wyosine base formation, putative
MTESVSEALWWVLLGALIPLVTLTLTTLLDRWVSRRRKRQMEVARAQAAKEGKTTWMEPN
VHNSTGKTNGNGSTIHDAAKGSKGGVDVKKILIAYATQSNTACKLAHKLFSTLSTALHES
RDEMQGGSSSCVCSEGPSSCCATSHTARHLPKLKVLQLTEEGRQCGVEHLLESQAYGLVI
LIASTYTDGTAPESSQVFANLLQDAYTDFRVPRDTLAKKKFAIFGLGDIAYGEKHFNRFA
KNLYMWCKGLGATFVVPPVYASEANTIPLFNVFAASLVKWVGRVTFTADGVTILKRQQKQ
LKEKKEKGQLKLCNDVELQGHATCNSEEDEEDEEREEEDEENGRKKRNHNSEGDVEDVVT
DDEDEGEDVNGQSGSVDHAVQALSSEPPELLYPRLRQNLQRQGYHLVGSHSGVKLCRWTK
AMLRGRGGCYKHTFYNIVSHQCMEMTPSLACANKCVFCWRHHTNPVSRSFRWKVDPPQLL
IAEGIAGHQKMMKQMRGVPGVTPERLEEGMHVRHCALSLVGEPIMYPEINTFVDLLHERG
ISSFMVTNAQFPEQLHALKPVTQLYLSIDAPTPEELKRVDRPLFEDYWERCLACVRELRR

KPQRTVFRLTLVNQYNTENVAAYADLVRLGWPDFIEVKGVTYCGTSAASTLTMKENVPRH
EEVVRFCAALCEALASDTAPRDKRTWQGTEPETGPLQRDLNCDEKRMSVNNMENNNRRCN
RKDEEEGVGINFSGPYGIACEHEHSCCVLIALRRFLVNGVWHTWIDYEKFNALARSGRTD
FTAAEYAAPTPSWAVFRSNEKGFDPTQVRVYRKSGNTTVVTSGC*
>TCRU_780 ubiquitin-protein ligase, putative
MNSAEVSVRLASRDDSAALVGELKSSLLVFKRGKSEDAFQRLLMALNRICVAFCFGDEEF
IRRLDVERYASVLVSTLRSVSRNEFSRLRSVTVQALALLADLVPRGGLAIAAAKGIRPLF
CIMKDVKLQGNETFLEELLKCISHVSAEAKASLVHEYAVSFITVLETRVETHHLRMLCLK
CLCHLFEAARLKDWNKYFLVPCNTLVVRFSQQVKRVFGESKDQPLERLSKENEAYMLRLT
ECVALIYDRILRTRELILKNGSILENSLPAFVNMLIRTASMGTQGSTFRDAVCSPLLTLF
FADPPISLRMFLKYHVLQSICGVLDTVLERTTKRISYSGVAFAEAFLSNDVSAIPFMAEE
KQIIHLLEFFLVIFPTALVARESDYYVTLPHFVWQCEDDFHNRTDCTDSLSKQMEGEYKR
QRRLSAFKPYEVCNASRTLKIDFDNMQYMSNELSSYPHSLGRHAFLSGYFHSRVMYCNCG
DKLLLDATDEKFISKQHGEYSSESPKRTYRHQYNPLMANSTEGSGAVNEDIFSTITARST
DAAYSHRIAHAGGLRGAAINRRLVDGNECGSWCAYIAGLVRQGERQTGRQRSGNKTVQRK
DLLLCEFFRNSREGILNYSIIRLHFLHDSMIQLILSWCLPVLTTMVRKTVSPIIARHCSI
LILRCVDLSVEFFRDDGNRFRPKVMEELRQRFNIVCSQLGPVLSYLATANTNHTITAFVQ
PFKEFQNDHSFLQALMAVGLKPNSRLPAMTLRCEIQMSALSSVLILQHACRSTMSIFNGN
QKLILCRMLENLKVRVSRHQGVLRSSIYGGTGIILCPFHVTAEKIEEVHAKLIEQAILVI
SLDLGKVYKGHGGTFLSTSFKLTSTSSSSNRDHANSSLARTAILVEPKKFNIPESCIISD
IMVRANMHSDLPTGVQKVFAIHEYMLECETNLSSLVYGHPEFLEELAGELQNSTIEPALN
KELAEAFSHVRKGLLSVINKNIGLVNAEDAPPIERQSVRPAHRLRRNKITLAMANHIWTP
LRVKLESLDFTETDEHSPSSVGIIIIADERYTVLDLSLERETVSILPTMPLSHLAKHIVL
QLNQKYMDAGKCKAGVRLGRRHTAPDAMEVQSLYSTNSPFLPKLERVEGDLGQSFLSRSY
SILDPHVSNEPESAESSFSNGSLVSWENNYESERRHSAASVRVQSTYDREESAEGFSIER
QTLPDPNDDASWNILPSNIVFFYNGKPVVDLSVSLLELFWDSATVLASGRAATTEKEKAG
EQLAATGMQRMLAMWLTTQTIHYLVVKEPFMQSLDGVTEDRAYGTRISSPKKVFTHLLSC
SETQSSLKVAAKLLNEMRRVLLSVKATLGSSEGRLCSALIYGFHNHIGIFMLPSVVWLPL
LCSSLNEQQDQHLASYILWNYPQIFSLDVRRALIQLIFSVRRVPIVMLAKLKESARLTGY
VAPVHGLEWVTPDVDMRSTKKVIVQRDNLLESGSNVLRTHAMCPLPLSVEFENENGVGAG
PAVEFYNLFSAQLQEQRLNMWRTEEFTDSSGALTKRVQLPLFPAVCQTAKSLSYFELLGL
LVGRVLLEGRVVDLPLHHCFIQGILGNLEKNRLRDIDPELDYHLSRLSSLSEEEFIACDL
TFVLPRPDAATAGEEIELTPNGSMKRVTGVNVSEYVTAVRQYYCRAVLTGPLMHFRQGLR
YAIIPSYLELFSVEELQLLISGPDGKIWERPEDLERIIILSHGYDKDSPVVNFLLEVVSS
WDAPLQRAFLRFVTGSSRLPLGGMRPPITVVRRTLGVTGEEGGNASFSAAPSFGEESRKM
QLLMDASLPTVNTCAHYLKLPSYSSKALLEEKLRTAVTEGQESFLLT*
>TCRU_781 Regulatory particle triple-A ATPase subunit 6
MKTAVNTSRSTHDPVSTYFLQKIQELRAQEKRLLDNYLRLESQRNELNRRVRQLKEEVQM
LQESGSTVADVVQVLGKNKVLVNVSSNQGKLIVDVEKTIDVAELTRNTRVALRNATYAIH
YILPTKVDPLVSLMKVEKAGSDSTYDEIGGLSRQVKEIKEVIELPVKHPELFEALGIAQP
KGVLLYGPPGTGKTLLARAVAHHTDCTFIRVSGAELVQKYIGEGARLVRELFVMAREHSP
SIIFMDEIDSIGSSRLENTGRGGDSEVQRTMLELLNQLDGFESTQSIKVIMATNRIDILD
EALLRPGRIDRKIEFPAPDEAARLEILKIHSRKMNLTRGINLKSVAEKTNHCSGAELKAV
CTEAGMFALRERRVHITQEDFELAVAKIMHKDQDKNVSLKMMWK*
>TCRU_782 hypothetical protein, conserved
MHGRNGELGAVCHVAHAVHTCGNCAASCAAEEEGATVASTMNVTTHKYAGPYELWWRQFS
PDGTIHPPARSGDADRTGICQLPPPREGRDDTKSGGTTAPQVNAEPSRQHEDWRRSAAAD
GPNTVDRSPASNTATNTSETRPEFASNPNEVMFPNASKKRPSFANGPRILVASNASGIMS
VTYGGRENVAADNTDEVSERSATGHKSLVL*
>TCRU_783 Glutathione S-transferase, N-terminal domain/Glutathione
S-transferase, C-terminal domain containing protein, putative
MSLTLWSGVNAGNTRTHRLLAAATLANVAVTPKTCEYGRENETAECCRNCSPCGRYPVLQ
TEEGCVFESNAILRHIARLDRSGGFLYGRTPLEGSQVDMWLDFSATELDAAPAPFVQHAF
RGGQRLANAMDCVHEVLRALEAWLETRTFLVDERVAVAFAPQWHYRPSGAEGEALTRKYR

NAYRLYNTVVQQPKTVEVLPPSRLCWTR*
>TCRU_784 hypothetical protein, conserved
MKVAPTPPKRKPSIAMSRNIEMDPNAFVTKTALANALRKAVGSRDARKTEAVDGSGEHVP
GKIAGGMNGQNVPGKPKRHQEM*
>TCRU_785 hypothetical protein, conserved
MARGRRHVLRPANRRAQRRVRQQHTRVQWHRAMQHDRALQRRHIRHVDEGVGHQARRDLA
EAANPQLRTARKHAVAQRHVQRVSGQVHRAQVHRQSDWSAEHHRVEARRRPPAANRHRLR
QRHATHAARRTATTVAGPRGRHVERQARVAQAAGTAAAHAVGERRSQRIKARQHSRTAVA
RHHAHGGQAGHAVVAAAPQHPAAGTVALHRHDAARDRQPGDKRRAGGSAARNRHGAAAQR
HTRQQRHRRRLAHRPHVVQVQPPAGTDRPTVAAHH*
>TCRU_786 hypothetical protein, conserved
MRLDVAHQQRRRTQQNVFQQHQYAKLSLPSVKQLDLEKLHRGNLRNGDVAVLREGAHKCN
KRGPHHRLAYTDQDACRLGRLSTPKKLQRGTATECAPGKRDVDGEMQRHTVEKERQHSTH
AAKCHAHVAVVRLPHVQREARQRLVHHTARVAVHGSLRQGRQKSVGHLEGKTRRAMPSVL
AAARARAAVHRLRPGHVARRAVVARATPEHLHFLRKHAAVRHLLTALQVAPNHKPRG*
>TCRU_787 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGAGGRCDEVGTAGHGVQPGVSASGGSGAPDNASGQTASGVA
GKPSAEQTQLEKVEDSAPGSPQLQADLQNQLPTIFTLR*
>TCRU_788 BNR repeat-like domain containing protein, putative
MIICSTDGGRSWVLSRGILPADCIDLLIAEWEQGQLLVITHCYGSRYCRVHESRDEGTMW
VEVPGAIAGVWANSQSVRWDMSLRVGAIVTATVGGKSVML*
>TCRU_789 retrotransposon hot spot protein, RHS3, putative
MQASGHYLSMKRAVKGEVTFDEDIRRLCDRGFNNLPGWSLAAAGVKATVHNSTKHFLDAA
AEEARNPTTTSAPEKLEGVYESVHNARWSHAEELPDGVERKKTVTGMGVHEGRPEQSWSY
RKADDAIEENDAVQQSGAAPPVLMVLTSEKGWPYSWNTIQDLPKDVFVNCAVERVWQIVK
GDVTAWFSPHGGTDFTPKRRVLIGTPGIGKSMAAGSYLLYRLLHCDAEKIQVVVHCFGGG
GACVSDKTTRAVTRCSDEDMCISELRSLRERGGNVYIIHGVAKEGTPPPRHFAPTFGWGM
IAVSSPKVTNYDEWAKQLQAARIIVNCPNETDVKAMCAWMTRDETKEKQAECWKEVKKHM
YLLGPIPRHVFDEEAFNERCGAVKFALQSINEGTVKEYFSRGGESPRYSEDPSHKPVEVV
REIYAGGVIIFNAPISACLEERTLERLPSVTE*
>TCRU_790 hypothetical protein, conserved
MHFLALEVTIWAPRVWNEGISEVFVNPRSAYSYKCLRQADAQVQPAFDGLVSCRRALEIE
RDPADRFIDLFRALLQTFQLQMMTTESSVPISELRAGPRTQQQRSLRCRLCRIYGRDAST
CNVGDATRGSYSQRRWPSKNGKRADRRL*
>TCRU_791 retrotransposon hot spot protein, RHS3, putative
MDHWVLYKPWATNFPLVDAFFFVDSNPKTLVGLRMTTAGGYHTTTSTVRQFNECLAAYFE
GWEELSRDMSWEMIYVQHADSTPMNGWRRCDVVDSNNMSRAENREIAAFWEEEVHQYIAA
VSSADARRGEALRGEE*
>TCRU_792 Mucin-like glycoprotein, putative
MMTTCRLLCALLVLALCCCPSVCVTASDEDQGGSKEVKIPTPSPRVPEEVKVVETEQKLG
TSGEPGERSQNIVDQTPGTTDTEEPLNQVITPHTEEGAPATAGERLTTNSEQATTGETET
AQKTEERTLKPEVTDHSDVQELTGRIPQMKVSDIENTAKNKITTTTTTTKAPTTTATTTT
EAPTTTTTTTRAPSLLREVDGSLSSSAWVCAPLVLAVSALAYTTLG*
>TCRU_793 hypothetical protein, conserved
MAAPSLAGSECDNANDGKESDEYYGDDLHREADYLRVLAHESQEGLDALPTIPGLAEPLA
FALSPAVISAPCVEADPFTVEFTQQLSSVCAAGPSLALSHVSQRCLACDLLCVVQAAASR
FLLVPNKKHFALRWVFICVAVDARDDAQRVCLLFSGHEGDFGVCQQHRGSLRRRIDAKIR
EVCPLHLSRQLRGTPDAQSEWMDAAQLGRPVVFSALRCQGNR*
>TCRU_794 hypothetical protein
MRVIVRNSTALLCGAVVHIFFFFIFILLSGSGTAHVHAEVTGAVTWKSDESPAGNTNGLS
IPVLSADGKITGFAEVLPIQGVFLLRDTKGKIVSKITDNSLLDCTDPTGTSLINDGPAVM
IFCGGKSSFLYVMLSGGMGSMRVVEVSTETTFYPSSSLPPTPLVRIRGSSPDSRKDAVFA
VSKQGELDCIGQYAFEESVSLCDKDSILDFYFQKWVPITSDESNPEGFIITERKSAEGLK
IDSYYLPDFGFSAAPNASVTLEFVGSSKAVHTNVNDISQSEPLIAYVQGTAAETFKLAVV

VLDANSLVRKHSGSIDAGIAVSESTLVTGAYMVSTARGALLMVQTSALLMAVNYTILSEV
NAPLWTAKASSTAGVLFLPFRAMENSFKEYYRRMLSPSFTDYNPYHIIKATEVQFLESAK
NVTKLNILDGSLKSSFEVPWTGASFCSEADRLAAITVFEEPMVYLGCEKSGHYCLVDPIA
SKPHYSITFPSMGPAEDVTFGYLLDDPSVVLCNGSRSAGLALHPLLLYSESVLIPQRDAP
VGAYDRGRMSIVTNNFTDPGEMLFYFYVHDTAGNSGGRDPLPPSNGPVSLIKNASSAKPF
TTFFGDGNNYVAVATTPGIVSIFSAANGEPVMDLLLVGCVPSGGNPDSGVITFMKSVQHF
GNKEDYYVLLGGTDTCLFEVNDSLVVRVTSLQGYQSGVVVGTTRYSGYKFVPATRTLQAF
TSFFGPSSMPVYTEAGIDYYVVGSNVFIYVKDDEIICRSVRSDITVWKYKFSEKFQGPVV
HMTYYNNTVFVVSQREFFRFDVQYYEDEDRYSRLLFQNGLTEEDEKYLGAAVNQGIVFLY
SGQKVYCHDAVNGKLIWKTEPRIQYEAKDAKVEAVIYSPSDTGGVSTDDIGTAYIEVRMT
VSQGNNKARFTHADMYAQASGELLKSVLDAPNDLTGPVIWGNKYVTFSTLTKGLVTFRAL
NISQVDIPEQAKRPEDPMTDVYVPGEKPIEPPPPPLPRGDNFMAASPPMKFSVAGRAALI
STDRKRAVVGKVEHKNGMYEYKIRCFNVDDPQGNPIREWAFPPAPVPLETKFMEFNKDHF
AIFLPSNVQFYSWSNCKEVGKSISLTGIVEGLPSYISLGYQNQWLFLNSDQVTCLEPSTG
NEKWRRNVRGCITIRRVDNYIICDGGSNLVVLNAGSGAILFEDAIEGGITTMGLDFGGVV
RIPRGYEAAFYTTSGKVFQSSIAIPWSAGKVMGAIPGTLDKNVVVFFENLAASIMFDTSA
KKASLLWTSDLNGERARPGAAAYAGARGVNIVVGTENGIIMLNSSSGKGFLNISLPKRYE
EDTDEVQVLKMVAVKENTLYGISWNGYAVLLRVTPGMEEALFAFGLGRVRASQISFEDDF
LVISGGGSAGTVPIDATYWGAPLSCVGMSFSASTNFMAGWDQTNDTAVNLVVVTAGRTWS
SSHIPHERAILSSMSAASAVVFFGKRTISTIGGLEGIGVEFTIPRECEETKLKEVSVGGS
TTGASLVWYTGEVRDCIFVLGAGGAPPSFLAGLSGKYAAVVNVRYGTSFGLFTSTHLSLL
GYDGTRIDSIDVNNPIYVSSLSSPDTGDGIFLVVSADNQLICLQINGLFHVWNYTLSSPS
RAPATYYNEGVFISTEAGPYFFTLAEISYPCHDRAIFRVPRVPTEGRSNFHTEVVVNEEY
AIGFVTTFETFYAFDALTGEVLWQRPDLFAVSHATVLREGMLLVVSTKSSGVVFLNPFTG
VSLLYFANIVEESSEIFLSPDGTTVGFGGSMATAINVIEYAHYFDVVKANRPKQQTPPAF
RPYNYGPTDNPNDCSEPSGDGEPIHVQLSPEWVSGSKYGPSNPKQTTVAMSHGEKSGWAA
SLEKQKLYIARAVDGAFEETALFQPKESGCDLLNLYSLSAKKAYVGVRCGKKTHFYNASG
VEQGTLGRAAKNAICAVIKSNGYFVNTDGYFDAVNLNKIKPLPSSPSKARCKAKFDIVPA
NRLERLLFVCAGTGIRILNHATLAQIGSTITGGVSRPDFTMYEADDNLRVGIACGKNGTN
VYMVAFSLETAKTILMHNESVQGTPLCGIRYPDYPSRNGPLFVFAYPNGYRTWEVQGGKP
KTTQEAANTFPAAITSHGVIYHNTGNDYYFRSYGFPTSSLIVSSKSPATGSMMVKGPDGV
QVSPLVIIYGNAFTLAVDTSTVNLRIFWSGNGLITFTPEARFVSNLPFVYTTVGNSLVAF
MLAGDSFALEEVLRINTALIDQEQRVFLSQRGTIGCVDKDGKVLWNIGFSNSGTPQILFA
PIVLDNLDFALVSGGVRVAAIINKRTGVVARSVQFERCSISPDSTEADVVVNGTIVYVAI
RGWSCVHVVDLNLKNKSGKITGPEVKALEIENTSTGILGGYPMVAMVEFANHLVFALQPE
NGDMRRPTFVVYRVDDMSKSLWTQLWKKRLRADLGKISTYGYFLYTAVDSVLNVYDLLTG
RYVWGYIFEKSITGPVLGADRTLYVTTVNGIQSLRSTLSLSWSLRLMGNITLPNRMVTPS
DVTIGPVRTPYGHIIVSNSVGTFAVEHEREGSVSKLVWYTEKSISRFGVYDVDSKVKVGL
FDASDGTGIMDLTSGKMLWLGGVYPTDGKTNGVASPSFPFFVCFFVLYVPTCRLVPEKYL
MPSRNLPLYKYDTEPTEKTPDEWDPIYPGGGGSVPLHPSPRCQSMMHAYIPPFTECINKA
LRLIYPRGRGTRLVCPASLYIIGICQDSLKELADACPDVGVLLVESWKAQTMDKLSPLGL
CEAEEASARCQTKNGTVLNATCSVVSMTFVLNDYENPMGYELGYELPIFDFPSIRSAKSV
GAILGGVMAVLVVIAIGAAVGVHFYRKKKKVRDSRFFDDDVNASLLGSEGQDLPMQIIKN
ESHKLMSGEGSLANMDAVSSRVQENPPPELENGFSPSQGETNGVTHTAAAPAAIAGPKKM
PPKMPMKMPGKMPPGKGLGPKMPPPSRPVRKPANENPILDDDL*

>TCRU_795 hypothetical protein, conserved

MSLAASTFPPTRARVDRRRKLGLANAVAQGRPLYRVGIISESEIADIRRLANADEGAFDA
YRREEDARRREASKARTDLWPDTMQAKQEAFLRRRKDDKAEEERRANIILELDAQQQEEE
RRQRQAQLALKYLKEDPRGRNVRSLLMLDEAIKDREAQIAFKKELKRQEAENEKEKQELL
QREQGENRLTEEQEKLARRSRNVEEKNSHLQQMLFQIAERKRMKAEKKEMLAEVNRGAEE
EKQENQEELMMQKEKMVAVHAYNRSIAKPPLSKHDRLRRRIQQEEGDDAARELQEKKIEA
MKRVPMERLKKKQELFENRKEQSWRMFEEENKAMRHKERTQDVFEQCGTSIIDSMAAREE
RRKQEALEERRRRQEEFLRVTNGEVEEPPEGVRRAATHRAGFMDDEEARQYQKEMRTHPA
RVLAEQQAEAAKRREEAELLQHIHRLQAAEKKENERREAEELVEARRRQREAMETDDEHY

RTYVKSQLPSDMDPYLYAKAMKLHC*
>TCRU_796 RNA polymerases N / 8 kDa subunit, putative
MIIPVRCFTCGNVIADKYLLYLDLVAEGVSEEAALDAFNLQRFCCRRMFLTHVDFSDLLL
KFNPADTNAAIYPTGVH*
>TCRU_797 Uncharacterised ACR, YagE family COG1723, putative
MTDSESDVGAIQLRNRLLELVYTSGAVFTISQLALILAVDKARIVHELRRSDFRGIVYDQ
DEETVHMRPQHRMSPSDTILSGKMPTSRGIRRSPGIVETRYANYGSDGYHHYRRSTLGGG
RVVSTKSTYRKTKYRLPFDADVVSGDNTESALPKGRVGYVCVADEFHLRELEAHYSAQGY
DTKFDFDVLHIRFSDREMSAKGTRTSVLAAKSLTNFTNPTSAGCGTHGTNTTEGSNNENN
SNNNNNNTGGEKPSDRSSLPSAKNLCKTGFDLFVFEYGAIVWWGFDQRFFKIVENDFMLP
NSAISRYMENRYMTQLISENYPVWCTYTLERKDTLEPDEHFRERLRFDHFIIPFGRGDMD
TSNVSMLCASHALAQSAKIDYLELKVQELAENCSPLPRELREKGQVSITERRLLQLRGEV
LSYRLMLKSGSNLMDEPDFFWENAYLKPVFQATKECFEISERVEALDNKLDAANEILSML
AEEFSQRHGARLEWIVIWLVLAEVLIGILELLIDLKPWFYRGL*
>TCRU_798 Alpha/beta hydrolase family, putative
MKNLAYKTVRGGAWGKTSSRVVIAHGLLGNSSNWATVSRRLAEHDLLRSKLHEIDMLDMR
NHGNSPHASPHTNAVLASDLEVFTLQRQAVASPPDDGGVVLIGHSMGGLALMATLLRRAN
ESSLLLPSMEELQMRLARGDYYGWEDEQGFAQEMRSVNESMGFPAQQPLDALFGCKEAVS
PASSRHSPQKEEKRGPRVNAAIVVDIAPTSRVGSQSAREQSVAVTLDAMARADLSRMTSI
RDATEELERVGVREKAMRDFLLTNLILDSKTRKSKWRCNLPVLCTDYNRMELGLLDWFLN
APVEGGCSDGGMVAPTRCAIPTLFVFGSESPYNRPEDRLLIDRFFSNVTQAEVVGAGHFV
HYEKMQEFVETVAPFLARYLLNTEKGGN*
>TCRU_799 calmodulin, putative
MDHSISQKELDEFREMFDLVDTNHSGRITRGELRKLLKTLQLRPTEQELEQMFSDAEANE
SANEINFDEFVALMSRRVQSDYTLEQLRNAFKLFETEDMPPGYVSREVLEHALVSYGTEK
LTHDEATRLLAAVDPEGTGRINYIEFVSLVGGGDP*
>TCRU_800 hypothetical protein, conserved
MIVRRLRCASILLPGNDTLRRRRRAGLRHGSSVMDAFALTAADREHGSLHDNRGGLSPHD
TQPADDIYGSRHEESSETMLPFTDGAYCGGDEAEGGQHCVVEGKRSVGEKDETQSLRLSA
RTLRDAAEREIKAEIERDSRDGVAAIPPLPPSGWKVQHPAGSNYFVMTRTLRGGAKSAEQ
QTRRYQSVHDVFLKALKENQRQKVLRDTKRREEKEEEQQQGIQGQMQEQARNVMDDIASS
SSLQSRGSFKKMVVDYTGQDQHRAVLREMTASNDAEHVDRMDVCLTVFAPFRVYDPSFHD
PTVNICEWSSFDVLVRKKMAAEKQGSRGRTNNALNSLAHLVHDRALCMFVRLASVNSEMR
IRFIQFLSINEAQALEEHACFGRGEPGFLELMRRRRQMRARTRPFRSLRRYDEPLTLLHE
APDTQDASSTSPLAIGSQQGSRGSAYELLTECFDSTGEYSRTLCYSGPYLSELSKEMMGA
LQDYLQGDLALSQELCEYVCQMQFFLEQEEYMAWLGRLRHVATVASERSHK*
>TCRU_801 adenylosuccinate synthetase, putative
MDKQAERGQSAGPVKTPQGTQPPAHNYTYHTNAAQRAVYDYLKNVKPIPELAEPKTYKTY
EEASVEAVLYPIIEKHQVIMVAGAFFGDEGKGKTVNAVANHPGCTCIARVNSGENAGHTV
YDDAGRKFVFNLAPSGLLSKGKRNYVGPECVMDPISFMENEVKQLIEANVPYKEQLFIGN
VSIVTPYHKLLDLLSSAPNSSTLKGMAPIHASKVTKRGIRLDHIFNDQSVLRSRLTKDID
TYFGFLKVKGLSDADVLRRCEEENGDGVVRVPHYVMEFVQAEDKVEYLVKLYVDRVRNNK
NFPARCDVAHELRSALSRGEKVMLEGPQSYWLSNAREKFWESTTSADTTASGLLATAQYN
FQRYSSVVINVHKAPGSSRVGVGANPSSFVAQDYFSATGVKTLRDLPENMCVDFDSIQKL
FFTKAFHPETKEYNGIWEPLEFEDSTGKYNIGVAMAVASSRQHGECGAVTKKPRVCGFFD
CVLQYEVNAVQGPYLSISALDRGDDYDKLGVTIAYVYYNGKNDEVLNINGREYKNGDIIK
AGEAVPGEVALYYCHPIVKLINGWKQTPIAASKRKPGDPLPRGVCEFLSTVEYFTKAKII
SIGNGPRGKDIIYIKQ*
>TCRU_802 hypothetical protein
MPVQGQGGMQRQPSFGGYDGMPVQGQGGMQRRPSFGGRGGMPVQGQGGMQRQPSFGGYDG
MPVQGQGGMQRRPSFGGRGGMPVQGQGGMQRQPSFGGYDGMPVQGQGGMQRQPSFGGMPQ
SSAQRRVMQGRQM*
>TCRU_803 D-tyrosyl-tRNA deacylase, putative
MKVVVQRVLSGSVTVGDEVVGAVGRGIVALVGMHRDDTVDDVNYVARKLLGLRIWPSEDG

KKTWERCVKQIDGGVLLISQFTLMHVLKGNKPDFHLAMDPEHALEMFDCLRDTLKREYME
ERIATGQFRSYMNINLVNDGPVTILLDSHSRQ*
>TCRU_804 Glu/Leu/Phe/Val dehydrogenase, dimerisation domain/
Glutamate/Leucine/Phenylalanine/Valine dehydrogenase, putative
MKYTSVDDFINKCVKKRDPNQPEFEQAVHEVMTSLWPFLEKHPEYCQDSLLERLVEPERV
VQFRVSWVDDKGEVQVNRAWRVQFNSSIGPYKGGMRFHPSVNLSILKFLGFEQTFKNSLT
TLPMGGGKGGSDFDPKGKSDREVMRFCQALVTELYRHIGPDTDVPAGDIGVGAREVGYMA
GMTQKLTNNKACRFTGKGISFQGSQMRPEATGYGVVYFLDALLKKHNQELKGKTVVVSGS
GNVAQYAVEKCLQLGAKVLSVSDSRGCVHDAEGFTPEKLKVLMDIKNVKHGTVEEYAKGL
GLQYYAGKRPWHIKADIALPCATQNELELEDAKALIKNGVTVVAEGANMPTTTDATMEFI
NAGVLFAPGKAANAGGVAISGLEMSQNAARLSWTAEEVEQKLRDIMNSIHDACVKYGTVG
GKTNYVNGANIAGFVKVAEAMKGLGVV*
>TCRU_805 Centrosomal spindle body, CEP44, putative
MLSATFSLLHRRLSSLGFDGWDAVTEEDVYSGAPHCYAELMRAILFSFPHDTAALMRKYP
WLCIEGEDSALAHSVLRLLSLEGSRRIVIKATQFGEKKYAAAKMNVCIELFDLLSRLSWL
RENTQGTRAAARRAALARAIPFYPAACDASAFFLKARLGELNGRRKALDHHLDRE*
>TCRU_806 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MLKDDKKPTTESGTWELKKEHQVALMLQGNKASVYVDGKSLGEEEALLTSGTPPELFAFC
FGACDFGDDGVGDDDEESSPKKIGKKPRVTVTNVSLYNRPLNSTEMRAIKDRIPVSTRAP
EPQVKIAPKPVAPAAPAVPGPRELPAAPGRTTVGRTANTQHAPAGRLTSAGNEGTAREKG
DGGANGDAGSAYGRELLPLLLLLGLWGLATA*
>TCRU_807 hypothetical protein, conserved
MWPQRCPEGIERPQGTAFAFIRGSVTRKMRAFRLLASRCLLTPYSVSLWVLSDVPAFYWM
IGAAEMWRTFAAPSFGMFVARRVRDGCRLPHCMGCCKAMHYATRLCCGCHAVEIFDVVEV
PLDGWSGDPPARVITDGFTRPFEFSVSSLYVHELTADIAEYI*
>TCRU_808 BNR repeat-like domain containing protein, putative
MEVVGKAVDPFQGTTPVPYKRQEMTGSEAAAGSLRVSSLAEVVGGVFAVAEAQCSERDGA
CGHAAIASTHIETGGGGSKAISAMDAGVSLIEPVDAASGTIRAREKMQPTTIVSGDSVYM
ALGDYEKKTSGGQVADADGWRLLLTRGTLTEDGGQRKIMWGDIRAVDPVAIGLTQFLKRV
IGGGGSGVVTKNGYPVLPMQAVEKDGRSVVLSMRFNTRMEAWELSSGTTGINCKEPSIAN
LEGNLILITSCAAGYYEVFRSIDSGIRWDMSGRPITRVWGNSYGRKGYGVRCGLTTVTIE
GREVLLVTTPVYLEEKKGRGRLHLWVREGARVHDAGPISDAADDAAASSLLYSSGGDLIS
LYENRSEGSCGLVAVHVATQLERIKTVVKRWQELDEALRTCRPTATIDPVKRGMCIRPIL
TDGLVGYLSGLSAGSEWMDEYLCVNATFHGTVRGFSNGVTFEGPGAGAGWPVARSGQNQP
YHFVHKRFTLVVMAVIHDEPKKRTPIPLIRVVMDDGDRTVLFGVFSPMMGGG*
>TCRU_809 Peptidase family M20/M25/M40/Peptidase dimerisation domain
containing protein, putative
MPLDSVEWLRRLIAFDTTSRNSNLELIACIRAYLVDECGLEKVLVQRAADDVHANLWATL
PGEGGVTEGGIILSGHTDVVPVDGQKWDSDPFTLTERDGKLYGRGTCDMKGFIAVCMSMT
PELLKMKRAKPIHFAWTYNEETDFAGIRQLVADAGIPVGAAAGCIIGEPTDFNFVVGHKG
IRSSIVHLRGKAMHSSLVPYACNAIEHGAEIVRFLRDLGREFRDSGPFEREYDVPYTTVC
PAMVEGGNARNTVPADCYITYEFRNIPGHSGKEIQKRIDDFVAATAQKMKEEDGSCGTES
SCLDEQEAFKGRSDSRVCEALKAASEESCKVVLAPFCTEAPNYQMCGVDTIVWGPGGLCA
HQPNEFVEAADLKKTERILLRALAQLTGSAVGSRL*
>TCRU_810 lysyl-tRNA synthetase, putative
MSSTNETRAQIDDLAATIARVKKEKGAASEECKALVAKMTELRKQLPAKKVEKAPELSYF
DTRLAMVKELGLLGAAYPHKFDRQYTIPAFKARFAPQLSEKGQRVEEVVAIAGRIVNKRS
SGSKLNFLTLQGDADTVQVISAISDYVDDTFAAVHGRIRRGDIIGVKGVASLSKTGEFSM
NAFEITLLSTCYHMLPDGWYGLSSIEQRFRQRYLDFIVNRENIQTFVTRSKVIRYIRNFF
EDLDFLEVETPVLNQIAGGAAARPFITHHNELNQRMYLRIAPELYLKELVVGGMDRVYEL
GKQFRNEGIDLTHNPEFTSVEAYWAYADYNDWMRTTEDLFYGLAMHIHGTPFVKYAPKDS
EGNQLPEVVFNFNKPFKRLYIIPELEKRTNVKFPTEFESDSSNAFLQELCSKHGVECIPP
LTTARLLDALISHYLEPECQNPTFVCDHPRVMSPLAKWHRNDPQLTERFELFLNKKELCN

AYTELNNPIVQREEFMKQLRNKEKGDDEAMDIDEGFVQALEHALPPTGGWGLGIDRLVMF
LTSQANIKEVLLFPAMKPETSSSLTYPPGTLLNGQGVPLL*
>TCRU_811 hypothetical protein, conserved
MAMMVTGRELLVCALCVLWCVAADGDVVGPVTSGDPGGGGQSPLADGSHGGSECSKADIS
HESKSEPLVAASGEESPAIHLDPNGVSSLSEEHLRPEKREPPKENGKSHNHRLKMHRRLK
*
>TCRU_812 hypothetical protein, conserved
MESTHPVEYCRLVVSGSKDPVEYFVRAKGDGRAVVPAQTETRTGWLMCPATLRARLRHWM
RAEQVSLRCLLASRPTRWPLLKGIQEHLSSEGVSAVWSAHCSVRSIGPFLCWEDGLLHFL
DPCGGRVMGQHAHRFGVGAPRTCGRVTQEA*
>TCRU_813 dihydrolipoamide dehydrogenase, point mutation
MLRRALLLWGGKPPLVRWRPVELSHFDVCVIGAGPAGIAAALRAVDYKKRVCLVEAKRVG
GCDLWNGALQSKVMWEMSNFFAKANGSGALRVYSTVISSFMEPDEEKMRESLVQASEVRE
KQIIEALRAANVSLMYGRAFFASPHQVEVRNRETKEYHAVTADYFIIATGSTPKEHPYVK
TDQKRVVTSDELMMMPLPKSMVIVGGGVLGSEFATIYARLGKTKVYLIDKEKCIMPKEDD
DIVERIQQSMENHGVVIHQDSVLYDMQSWEEDDAEMQAHPEDPTQRSGVRYSIMNRRTRE
IETYEVERALIAIGRKPNYIGLGLYNAGCKVREGALVLNPFGKCVDRDHIYAIGDAANDS
KLVSVGEAKGRLVVDHIFGVQQTSPLRHDFTRLIFLTIAVASVGMNEKECQRQRISYVMA
KYGFELCSRAVAADNTDGFVKILATNDSKKTLLGVRALGMNASTIIELASAAIRRNQSAY
QLSELLTAYPSVSQAFLECLRVILGSSTLKPGTFPGLVCQTWTPPDYERGRAYTSSSAAQ
NPPRGDATSP*
>TCRU_814 dihydrolipoamide dehydrogenase, putative
MLRRSWAWRKMPVEVTRNTSKLPHFDVCVIGGGPAGVAAALRAVDYRKRVCLVEASRVGG
VDLWDGTLQSKTLWEMAKYASRLSGPAAQRLFEEDAVAGVKNKISDARVLQALQDVSGVR
EQQLLDALRTAGVEIVFGKGMFSSPNELDVHSTGSGVYNVVRADYFIIATGGVPRTQFHM
EADGRRIVTTETIMRLPIPSSLVIIGAGAIGCEFASIYANLGRTKVSLVDRTPRILQVED
EDISQFVQDQLVRLGVTIHSNCTLFDLESWGDNEEEGGCIYSVRKNDIDVVSPVETYEAE
RALISVGRVPNVSGLGLENTSCKVTDGRLVVDAFNRCLPHKHIYAIGDVCARRALVNLGE
AQGRGAIDHIYSEKPEKSINAEALTNLSTILFLDEELACVGLNEQQCRARSLGYIVARYG
YGHLSRALAMGNTTGFCKVIVTSDSEKRLLGVRAFGVHAGSIIEVASLSIRRLESAYELL
KLTPSYPSAVQGLVECIRMILGRSALKPNTTPDATLKVWHPPHFRRGREYIDETGYEESV
MNSDDVKIART*
>TCRU_815 protein phosphatase 1
MAKGQEMAINLDDIIERLLLHPSHNGAAALASASIENPVGRQCKYSRQSRLTAFKNAQAM
DSYRQLNEMSSLKELSEVEVRYLVIQARMIFMSQPMLVEVTAPVRICGDVHGQYHDLLRL
FDLGGYPPEANYLFLGDYVDRGDQSIETICLLLAYKLRFPESFFLLRGNHESSSINRIYG
FFDECKRRYSVRLWKQFTDTFNCMPVAGLVEDRILCMHGGLSPELKQLDQIRCILRPTDV
PDSGLICDLLWADPGECSGWGENDRGVSWTFGEDILQATLKQFDLDLICRAHQVVDAGYE
FFSARRLVTVFSAPNYCGEFDNAGAFMIVDENLTCSFAQIEPTNIMLQYSF*
>TCRU_816 hypothetical protein, conserved
MLESGREGRLGKLWQRLLSSVCSEEALAEATRGPRVAWNPYRPARGEHLLQGILNSEVYE
WRSAVAVNSLRLHGTALSTDGLPQSPLNTVHNIKFFHLEANVSGITTNGLSSDRTAAQCS
ERTGPSCEIESETIEGMCNENNRENILRSTEPQDVIDDIFEVLWRTFAVPWIIERHASGH
QLRREKREPETHDNSTAILSFYCADPVRRFAGKPNRNNDLVPNRRRPTTGPAMRRGGTER
RAAPALPDEKKTPLLLLHTEASLKKEFVDVAREEGHPVAVARQGVQFLNEVGHSPKQKRV
SSFRLSVLASSGNAEAERRRSLLLGKPTIGRPTLHCKGDHPFSSVLHPRDNSSPDRRHSP
KGKKNNVFAKKLDRGAQNVRALSGCRGCKLAPLPRKARVCSPTIIKHQNEEV*
>TCRU_817 TIGR00269 family protein, putative
MPPRRLCIHCCEEKAAVKRPRNGQLLCQKCFFHLFEEEVHETIMAEKLFTSGDVVACGAS
GGKDSTVLMHLMKLLNERHGYDVQILLLSIDEGITGYRDDSLKTVHRNSAEYELPLRVIS
YKELYGWTMDEVVRLSGLRNSCTFCGVFRRQALDRGAALLGATKIVTGHNADDLAETILM
NILRADLPRLSRCTSAITAGDGLIPRVKPLKYAYEKEIVLYAHLKKLDYFTTECSYSREA
FRSEARTLLKEVEKLQPRCILDTIRSGERLRVKERESVPENPQGFCVRCGYVTSQKLCRA
CVLLQALGSRDPMTAVRGQHQKTQSEMDV*

>TCRU_818 centrin, putative
MGNNDFLRSTAQRLPPDLSDSQKDEIAEAFRIMDVDGTETITPNDLKVVLRALGYEPQKD
VIKKLVAEMDKSGVSSNLILPEFEAIMKGKFFAEDSEEVLLSFRHFTKGNSDYITLEDLK
RVVEEVGEEMPEDVLKAMIEEADVLDHDNRVSKEEFLRMLLPHKEK*
>TCRU_819 CCR4-NOT transcription complex subunit 10, putative
MADDAIKEQLENARKAFEAQNYQACEVILQKMPQEDLKAQHNLAIVRLLQNHADMEQTIA
ALADNSTEGLPMLSEREGEAKNSVSLLYEGHETAHFNRALLLARSGLLNEAAGILRGLLG
THNSITPAVLGRALCLLQTITRIPTKAHHRQRSDDELIQKVITENMSKFSKDPALLSMVK
GAFADSSTIHEMPHNSDADWAVYFNNLGVLTMGDSKMNVASLCFAKAEKAAAQCNTPLMR
HPIVYNAGLCALLRGEYDSAITCFLSVQEFMKKSPLFWVRFAEAAVGKLQTETRKRDMEE
YERMQNHFSEQLRNGKMLPNYEYLILPGAVICQGPLADPKDSSVSTALETLVCSTIHNAL
ILLLPQGHTAASAMEAFPHNVQLIQFALFYWCALEIFRNNYTVVVNVGYDLLSLHERRPL
SPNLHAALLSYTVEALIHLNEPERALKVLRRSSLSSLVVGSSLEPLDSHQQGRVEALFIN
LAITHIANGLWNQASSVVESLLAKVYEGRAAKEKEGAGSISSGSSTASNQGVILAYHMLV
IFLELAQGNQEKAQEALLRVSWVA*
>TCRU_820 hypothetical protein, conserved
MPHRESCRPLPLLSVLLGVRKGLVRRRLSALLAHHRRQPGSTPRRTASELVTPVSDETAR
GLSGCIAVECERRRGVIPRCTVAVAALSPSRLASRLRSTPLAMGECWLCSAGSRAYAVAP
NAGSAITCEAAALG*
>TCRU_821 hypothetical protein, conserved
MDSDHHLPSHTARTEDGIPRQAGLLPRRKHAALALRAADWNDSATACATPLAAVTTWLEM
HRGTVRAARRNIPHVSGRTEWSSPSVLQRQHGTRTQLHPEAACPELKLSANGRTVIMPSA
VVSPCCWRSVQSSLVPSRAQACDTPRHGGTTFLLSGIGCAVVLLGLCLCSASAAGKFARP
SHCPSLTCCDPHSCLHSLCLRAPC*
>TCRU_822 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MVSVLLTAQLQRVKEVLATWKKADKLVSELCPSSAEKDASPGDACSPTVKITDGLVGFLS
GNFSGNTWMDEYLGVNATVKGNDDGGKKATLHAGGVKFTGAWAEWPVGSQGENQLYHFAN
YNFTLVATVSIDGEPKEGSPISLMGVKMNDGDNPVLLGLSYNGGGKWELPCGGGPIKEHS
SAWEKDTTHQVVLMLRNGTQGSAYVDGQPVGGDEACALGNKDSRAVSHFYTHFYIGGGER
SAGDAGSEEDVSVTVTNVLLYNRPLSTAEIAALNPNKDSMPPAVPDNAQETLSQSSSGGK
SPSGSKLLNGNEGAGGGITSPSAPSTVTNSREESVKQLALRVSPGGSKHVDVASSSDGDP
AVGAEAGGAVQGDTPPQTPVDTPDTADANTLTATNVAQVDPAATTGVAASSGANEETAER
RDGQEEDDIHAQHSEVKAAALSSSLGNVSQGNNTDAGTVRGSGLLPSLLLLGLWVFAAL*
>TCRU_823 hypothetical protein
MLRKGKYLFRYTLQPLFVNGLRAVRSDVASFSLLNGAVVREGVPKESDAQLSRTGAFPQR
VRQGLPCIVGGSAAGGGCSRGVAEGLRLSLELAEVRCSSFAR*
>TCRU_824 hypothetical protein, conserved
MLGYALVNSTPGNNSPQTEHQKAASRDPTLLHCVDDVLHRLGNSYPAAAFMYTDNLKIVA
SGADIHACAAAMQPVLSLTTTWAAEHNLKINVDKSEAALFYNSTHTRSDKEMVDLHPGNR
NLRIQSRPVRLLDTTFDRLLNSGPHASTAAKQTTPRRYQLRPVARAGAFHHNTQSFSIGY
VHGV*
>TCRU_825 hypothetical protein, conserved
MVLVNITATGDINGVAAAKRPCSFARQSAGRPFHLPAPGMAWNLLEEWSRLGLRCARRNA
PQRSSYMQPEPQHRDKVRLHRWGLPNVVKDLI*
>TCRU_826 hypothetical protein, conserved
MLDDYVAKKNGKLHDAEATERHLSSVVDQVLNYLRNGVRVTKIPSKGSARRRLCFLSEDC
KRIHSCDLDRQGFPLNRKRPPVTMWIRDIEKVLIGLSTTSFGNYSGEAQLAKTSQEAVSD
NGTRRHDPTQNITPSNLGTNNHRAFALLLRDGKSLEVFVRLTATARLGLFLSSVLCI*
>TCRU_827 hypothetical protein, conserved
MRVDGNTVQFNCPQPLRDAGFAVAGASFDVDVALDRPDASTLFRKLCATAAPNFTQERQN
MVAFSYGVRSSPKRQLMYGSAAGEGYAARVITEVIRLEAKKGIFALSCRFIGPTEHRADL
LDADNELGVIVGSVKEGPRVRMVARIRVPLAGDVRGAMDTIVKDYEKYFSSVLCEKQPTP
ELEAMPSYLPDTVVLQLYRDDGEAESAYYMDANSLTFVALGDAERPALCGIDAAAQLHHE

GVQRALVSAAGIVSGIRRRRLRIPFGNSELSQLLRRAYNTEKGNRNNSLTGSTETALLAH
AFLDAVCAEESFHCLSTTRRVGNILVSTGIGSATRDPAVDKWRPDQDIMELRDELMIART
AYDYRPCIYESNRPISNIKEEEMKRINAIESNREKARERQLSVVRERAKHEAEKMTKELE
RRGGATLDEIERTLEAKKRESGALQADRESRIWEYEHTLEKIRTRKQTEESASERLRQAM
QQPEQGLSLRQSAIETKEQQLEIFQLDGAKGREAIMRERRSIEAA*
>TCRU_828 retrotransposon hot spot protein, RHS3, putative
MTGMGVHEGRPEQSWSYKKADDAIEKNDAVQQFGAPPPVLMVLASDKGWPYSWEEDESTH
DCHVNCEVDRAWQIVERDLTEWFSTHGGTDFKPRRRVLIGTPGIGKSLAAGSYLLYQLLH
CDVEKIQVLVHCFVGGDAYVSDKTTRAVTRCGDEDMCISELRSLRGHGRNVYIIYDVAKE
GTPPPRHFAPTSGWGMIAVSFPKVTKYDEWGKQLQAARIFVNCPDEMDVKAMCACMLRDE
TAEKQAECWKGVKKQMYLLRPIPRHVFDEEAFKERCGAVKFALRSINEVTVREHFSRGGE
SPWYSEGPSHKPVEVVREIYAGGVILFNAPISACLEERTLERLPSVAE*
>TCRU_829 retrotransposon hot spot protein, RHS3, putative
MLAAGRPLMKDYNVTMEMFVQEPDDYVQDQRLLEEILNLTAHQKRWRPLLSLFTKVCSLS
GNVETMKGKDTITPIARRNLNGVLIGRGKAERNAVTEARREAEERLRRTQEMKFTISTNI
EDVLFKGRARVNEMRLSDFLTRELDGRDIVDTNRDVLPEEFFKDPTKYIRNKGALNEMQA
SLAQPAASTWCQGLVLLLERKLSACCSCFKPDE*
>TCRU_of Trypanosoma cruzi region 5/Dispersed gene family protein.1
Dispersed gene family protein.1
MTGVNGTLIYLEGSMHSSSLSVLNNSAVVIRGNVVTRPVQYAIFFRWGLIVESFSAVVFQ
GNDMQGSLVVFYSSYSSNIYYNSWLQLSGNLCRVSPVDAFAFLLPKLNLRDSTVSVSGNR
FISSTVTLDVLLISIGSSDLTNGVILFECNTVNGEEGVQYIIPSVYNVTILTCSDPCALA
ASCFPAYTTTASSDGCACRCAEGGHGDACLPVAVPEPPSTDGADLCVRDVRVDVELNAGL
GTSVACFVGVTFAADFVVDVESMSGSVRNVTLANCTFVGGASLYIVGWRSDPPAGERADV
LISGLESRSGGGVVVANRFPPGSRVTVVDSVLIAEKRVAYCDAYGLGDASACLVVHNVNL
TGSVLTIARTHVAAVFRDAVGVLVVGGVALSSRGALYVDGLLAQAALGLCVSVEGGVAAS
GGSVVAFVDSDFLLCKHAVSVRGAVSVSGSAVALVRSEFLSTEDHAVAFYSTVSLAGGSM
LLAKGNVHDGASREMLHAAGAVTAAGSTLSFVRNRALLPRMLSVSLSLSAGAHLRVACND
AGGRVLSTAEEYAAAGFGDAGSIDVAGCDVCDRDTYCYAPGTASASMKDGVCVCVCGSGR
YGEACLPVGAPALPPAVGTASRVFVREGVAVRSVFVVPAGASEVTLRHFVLDGVSPVLYL
PWMARDGVRIVVQNVSLLNGAVLYVMGGRSLRGAGSAGSDEGGPVELSVCDVEALNGALV
LTGTFPAGSVLTVTDSLLVAARSTPLVYLPGSQSSPYAPVLVLLGLRLVRSVLVVSGVAL
VTVVTGGRTVVVDGAVLELIGGGVALDAAVFGGDVALYASARVAASGGAVLRVSGSQVYA
AHGLVFDSGVEANASAVVVNDNAGALTDGALLELRGLASFVSGSWLSVRGNSISGRLLSL
PSYPRRAEVMQSTLTLHGNAGSGPVVMDGTVALVGAGRKFVVGCLTLNGRALRPMDYRSA
GIIGEFRPVACGVCDADVRCFAAATRAMSGSCCCRCAAGGYGRDCLPVYLPRVDGCNRTP
ATTASVSSTLWWSDVACPTLAVTTTAAGGSLTQNDIRGGGSAVPTWLMVALPPPFRWARD
PQIGTHLSFVPVSTAQPRGFGGPWGAMLSNATWVRNATNPSTVLELAVPLHRGYFIAADE
TLVIRCDAVAVFGGCKGVLLGSFTIRSDTLPAAANALSAITGVVAGAAAVAVLVTGGLGS
ILEMQALGVFARMPCASAHERASTVALPYFLSVFAALDPLWMVVGNALLAAVFGCVHCGV
TASFQRWRGVDAASAWAAMRFPSLTYVVAHAMHLGIFFGSVLALAMPGARVQHRVVGVVG
VLYGVAFPAGVCYLIARHVDASFTKYWQFSRKPLHERLLYPVGYWHPVAQQRMYGGMLTN
MRGSHVYWCVFQLSVLCVVCLIAAVQSPVGGCHVQYFCMAAVLLAGAGVVAFTNMMRSSF
LTVMHTASFVLLAALCLVSAANHLAPSDGGARAYAAIVLLLTTLLLAVTVYSMVVWYAED
RHWQELREPQRGGLEALLRDDEESDEDTQKLHDMTSSSYASGTTVASSYRPPAQLQFMTG
DTRSDVLSLLDRVSSASCSINYALLDR*
>TCRU_831 hypothetical protein
MPPPLLTTETFVTENTEWLRRLRRDEDATRIADAVGPPDASSDTPSNTTALDSRSTPPPT
YTADPPACEDLSTVLLTRSRVCNSDVACSTSGDATASVSPLSWE*
>TCRU_832 BNR repeat-like domain containing protein, putative
MGRRGRSPWGHSIARLWANWHDGQGKGVLSGFITAAIGEGNVLRVTLPVCHKASEKEKGR
LSLWLADNVHIVGIWLASRNVYAAADSSLFYEGGEGEDDDELILLCGKRDDGEWARSHLS
VCLTAKLKRVKNLVRALKELYICVSQFCPYSNVKKNLLSVEGCDTFMPPAGLVGCLSGKL
FENKWKEEGLGAERYGDGWGSCGRRAFQWIGFQGRWFLGVAVRWQSGEESDVVPCNERVH

LLWRRFLFTSCHRLAAASF*
>TCRU_833 phospholipid-transporting ATPase, putative
MVSGADREEMEGNCSTTTSDSSVSASFVEINLLREDLNATRDYPDNSIRTAKYTWLSCFP
LSLLYQFQKVANIYFLIVTVLSLVPGASPVNPFSTILPLCIVLGAAIIKDLWEDGKRRQS
DDCANNTLAFVLRGEKFVSVPACSVHVGDVMLCRLGEEVLADVVMLNSSHPGGVAYIETV
NLDGETNAKTRRAKPQTIEALGTIEDIIESCLPDPAIQAYFMERGTTASWNAAAARDTFD
VVTPVNSSLVQKNRSGMRDERTWGANGQSGAREFPGRRREPFMPYPLGRRASLDSRLGKF
THVRSHTYGSWGRKPPETPVYHKRHLTFDERFAVGREMPVPSKILEMSRRYDEKHMGHHR
QRRRSCPFFADNEMMHLPNGEDDPDNFDGAEENSNQNCKSTGGIVILGAPPCSELYSWIG
QMRMRDGEIVPLGIEQLLPRGCVVRNTEWILTAVTYTGRNTKMLLNQRPKSVKFSVVARR
INILNCFLLLVHQSFLFFLCGLAVRWRNERLEAPEGTRSGYSTWYIQWNLSRYTAKEFFG
WRYLTNFVLLSYLIPLSLYVTMEFNKAIQMVLISRDRRMANFDEFIGELRYTRPKTSELN
CQLAHVRYIFTDKTGTLTENIMTYVGGCTATKTHNEQERPGGLGEEFIQLIQNYPNRSGT
RSVIQGNCFFRGRRRKFDFDESMMESEPLFQYLRALALCHSVVCFDRSSVDQAAIISSLS
CTHVSYGHEAENAHFRMQTGEQQELQALDPAITGTFNSSGAQVSGFHTSTASGVGKFLQG
HNGSSSWYVTRYNDMQTDQRSATMPRIVNELKDESKIYEAQSLDEIALVTASRDNLFALQ
RRSATHMFIKVVNKIMCYEIIAELEFTPQRKLMSILLCRSPTHDDEAFEQPETTISYHRL
NTATAFIPVPRELECEENGIVDIIPPSEDPSATRKREERAIDNVDMNVNATHGNTERSLD
NAEERPYLLLVKGADSSMMTILNKNNPRNAELWPTFQRELEAMAQQGLRTLVMGQRYLSE
REVREWLPSFHEAQCSMHNRMERLHRVYAMLEKDVDLVGTTAVEDRLQDGVPETIKFFLE
AEIVVWMLTGDKRETAVTIAGTSGLIDPQFEDCVIHLDVAEASLQFTSVTEAAADATLWE
SLQEQIREAVRKCNTSDEIYGSTRTVVLVVDGRTLDIIFTDVACTREFFEIGIRCRSAVC
CRMTPLQKAKVVRMFQKNTSSVALAVGDGANDVSMIQESHIGVGIMGLEGSQAELASDYA
IPKFRFLKRLLVVHGRFALYRDAHCITFSLYKNVVLCTGLATYAFFCGFSGMILVESWLL
AMFNLFFCSLQPLALGIFDKDVDDELAESTPSLYPALAREHMFFSWSYILKWLCDGVLDG
LALFFVIFYTVAKWDELYPYRSASLEDYGTLFFMMVLLLLNLRIAAVMTCYTAISVAVIA
FGFIAIPTLTMVYSAVPHILGSNWGVNIAMELMGTNKFWMLMFFSVGVFVVYGMAVNTYI
ALFWPWANGGAAMRAAWRSPYRLEYKERMKQRG*
>TCRU_834 Ubiquitin-2 like Rad60 SUMO-like/Ubiquitin family/
Ubiquitin-like domain/Ribosomal L40e family, putative
MQIFVKTLTGKTIALEVESSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLADYN
IQKESTLHLVLRLRGGVMEPTLEALAKKYNWEKKVCRRCYARLPVRASNCRKKACGHCSN
LRMKKKLR*
>TCRU_835 DnaJ domain containing protein, putative
MRRTLVANRGALSLLGLDERLHYTEEEVKSAYRRQVKRFHPDAGGSAERFRELHDAYVFL
LGDRKATDTPAESCDSSSFYNNAHSRWSAGRYEGAGCGAAFARDASSGYARGDYEYDLGV
EWDGERRYANRSTRDFYRPYTSNPFAHGFTDEEVLETERLNRLRVLWAVLKHGLIFGGLV
YLLFVCWRDNRIQRAIEARNNGYVDASYWEKLKEDQQRGLTPTPRRHWADLQNEEFMQAW
NKRLEEQRRRGSPCGGGGGYACRPVAVTFQGRPFTATGVRGARSGVPKNTATYEGDEHCE
LDDAEGD*
>TCRU_836 hypothetical protein, conserved
MRGEGVERDEWLVGLQLFMDVRLRTVPFHVASRNRPGVSVPLPIPNTQYIMDGIMWSVRD
YIAWAPNAWLTIQNHLQSCSQRYTQLAERLSESHAHNNFQDGAEVERERLYSSHAYVQDL
YVAFCAVDAFLRHVAEASQSTAREAVEKELPRLVADHMPIWQLARSQYMHDAVEDYRLLF
LDVLRSWTVTKLLRPDTHRRIEEYVRYKLKTLRDNSTTHEGDQNVGRRSSEAISAGLRVL
LAGAGPSQSSTSSLSSSSPSAPATIDVVRRNMREFVVAIFPSHRSDSGRKRCAHCGAIFR
TLAAKIAHYRYHFYNRSYLTGEKIVRLPYPTLEDYISHEVTSRVTGDFVRVTENLLDVLR
VPEKRTVHVRKEKQEKNPS*
>TCRU_837 Kinesin-13 4b, putative
MLGNDQEKGLYLLAAAELFAQLTPEHEVYVSLYEIYCNSLFDLLMNRTPVVVREDHNHRV
NICGLSWHNVSSAEELFLLISSGTDQRRTGSTSANERSSRSHVVLTIRVFCRKDTSFCGT
LNFVDLAGSERASETSTNDKQTRQEGAEINKSLLALKECIRALDEKKKHVPFRGSKLTEI
LRDSFTGNSRTVMIANISASSCSYDHTVNTLRYAFRVKGLSIANIVPSKARNAPRPMRQA
VSEVPPLLNFSNIAAADAPAGKAKTPPTGTNGRRALSTQRGRSYTPKTGNLNVQRGNMNP

IHQSTIGDTHADKFSTYLRAVTHEKLLDLLPPAKLREMLNKDTSNRDGGASTSESSTVSL
EEKQLLAEMVSHVVEKLKVELGSDLTQNIKKRDRLIRKLRDENGALRKAIVTLEKRVGEC
PRCRQRARSNSIS*
>TCRU_838 hypothetical protein
MKCAVLRGLSVKEWELACLFPHGLPEDLKSVSERLDNLSNSALLPNNTLIDSLWSHCYAS
TDNSICSESLDVVTCDTIDMDCFCAARLDGEKCVGAELPPVGRSLSVGKRDFIDDYVEQF
VLLESFFRGSIAETAEREWLSILQREVLARSTLSDAEQNMGKNTALFRRLPVPLRLIARG
CLWLALMVMSFYFLIGSVFGTLFLSCFMNFLFFSMFIEPYKAFPYGCALLVTGCHCALFC
SRGIELARRTYNGELVDAFRFIGPRALLMQALACVAALIAFFVVFCVMASQYDVVSGIQY
SMATGWIVAVCIILLYHFLYAFGVTGYYKSLRKESAAVATLYFFLDVDMDANQTTMRGTA
TIEVTMASIVAMAAFAFGLSYVLDGSIFFLCATVTTTFLIGLFVVLFLNTGRDSSTDGLL
TVVAFYSGLTWLTIVFTTAAHGWQGRWGTSLGALLALALVTDTVVLLYTFLPVRNRVARR
WMFRALWMWIIAQFIAFLALAFISDYRLGVITIILGVHLMLHGMRVGGGCSNYGLSIVVF
IFLSALLFCIVGGWSTAQSVYKTPASTWLLPNYTWHGGNTPVTGVSLPQSLSFLPVCLVR
FSSTVDIVGMALFAKLSDAGSLDVTLADLHRWFPNFRYVYNDTFLPLSFLQTKIFTSSLK
GHNTTIVTLGTTDQMYPVMESMTIWINVVALSLLALITPSGWFVQLVSLISAADELSALL
WNSSIDRARDILSAYVKSIVSPTHDVYFVGHGLAGAAAAFFVSDLPENVHSVTFASPLSA
VAWRRGHNWMSDELSSRVLSVVSSSSLFSLRWMWGGLSYMIPCNLPEGECHNIDSMARLL
DALCGLNTKSDGN*
>TCRU_839 hypothetical protein, conserved
MFRGFWHDVTRRGRRFISIGGRHTRGGFSQPLGKHPQVKQGIAEGVPRRIPGTTKVTYTN
KKGRTFNFSIPVAEITHPQVELTNSSGNWREIDTSFSDLGDMEDDMPSAVDECLQMSPDA
TSLRSLYEAFVSFCKEYVLMDTTGMKNMPFYGELNVGPGYEHYDRRLKRKRHWLAIRHRF
EDVRYIIWPDDEAEVEELSPDAQLSVRQMLDALRWLEAASTFCVRKMHPADMTNEEEFLP
LDLHREVAVVARRARNDATLFSSLSTESDLFVACATLCLNHKVPFHLFFAAGDRNSTKGV
TAGDGSCILVNMPFVHTTLGAIRIMSVIGGDSTAYAFSNLAGAVERWDVLEGLSRLMSVE
AFGEKDALENVGEDEICIIMRFCVEVREKNAAFFSCDSTENVEDVSFRAKYRQVSHLALS
RCKYLLYRLDGPRTRVMSEGGYVPLVDLQKHAERTNKDTLVHYNLGIRSAQGLRRVTLGA
QSSAQLAELVDRLEAPNARVNGNTLLVDLVQHLSCKAAASKISLTLKEVNTLLPLLARMR
AETATGELDSRFDRLLNVMETAIGTAMQQNRSVEEIVDLLEGLAACNFVPSSFKQVEMVL
MRLMMARSCRMSHVTRVLASLSSLFNSEVSQVLLQTAASHAMFCTKKGTISGREVDELVE
LLEALASCRYAALPGLIAHCREECFSDEVLFSLKQRCGYASLLASAASGMRHQDESFSQQ
LANDSRHHFIEYIRNREEEKDLACFVDCITGLTTVGFGDAAENEEYYSTLVSFLRSPCLS
LERCATMSTMALATLLEGVLLWCTTLRVPPEGVVAPIEGTLLARICSFNDPGSTLDSSEE
LAESVCRLVGLQRASEDLRRAAAQALGKIILHAEAVAEAWIPTAQQNLSFEVVALANAER
ESKHMNTVLRYCAALQQSGMLHLVEGLKMQ*
>TCRU_840 retrotransposon hot spot protein, RHS3, putative
MKGHEPSTGLPCEGWGMIVVTSPDKNNYESWAEQMGAERIIINCPDESDVKAMCVWKKHN
RRLAEERAEEEAEEEAEEEEADYWKKVKGRIDKVGPIIRFIFNEQKSDARFNECKDAVND
ITPPMLQYYAGIGTGESCNGNHVSRKLVGVVRVRRGNNIEWPLNVPISPHFERETLSKI*
>TCRU_WW domain containing protein, putative Phosphorylated CTD
interacting factor.1
MQVRTRREGVDDCFGADESLADIARVCLVPSGAGRKAAYVLSCDSIQYNIRLGSRSAFLL
RGLTPRLGRSLVTGQTPEDAADARNDTKNTDGGVRRKGGVDTISCAEEEVLAARISADDE
LDRHDAFLDLSRALEEAFCWHGAFTAIDDTAGRGRLLMAPQAARELPARWVMQSLNETTG
VRANRDTVTLLDRGETVRLRHVHDATLYTVVDVANMAGGQYWVEIAPTEPSTMDSRRVDR
EDIILEPPRPVYFDPLLPADEFNNIRGTSTCLFVAATLALRGIRLPREKTMVTANKMKEF
SKNVTVRMGHYVRGLRKKLSERCLARRSCCDEPGMTLSGLVEVRMTQDCVTLRYGGRAVE
VLQRTVERLSLLWDARLQREREGTAVNGRGVESARNVWQCAVTQQRTSVSDGLHVFMTSE
PFFLRVFTMLLRYRSLFGEMGYNQGPHAAVPPLVMRQLCEAFDVQCEAFASPINAQLSHF
GSLFPDTDYYFGSLGSFFDLSLVAGHYEVNPPFVTAVLQRLQTCLLQDALACHDGEDDPS
LLFVIVLPSHDLDDAEVALHDSPTPPQHRHTVREKVGNIDNNRDGGGGDGHDGISRKRGR
PDSAGETMSVERALRESSFCLAHALCAAAESAYVDGHQHLLRAPLFCIGTPTRLIVLGNR
AARRRYDNAAERLAAVKDTWCRYTLEFKLEKRRA*

>TCRU_842 3'5'-cyclic nucleotide phosphodiesterase, putative
MKAPAAHVPVKRIADSRPNERLMALFIAQLRKRLAESTSLDEFNNWMNEQYQALEASLLE
PQSLRPLVDAVGEAVLTPTSQETLTECGDEYTEHGVYWAPETQGNPCTTFSSTTESFRVN
TPASIGKLNRASPRAANAAETNTQNLLQHEMNRLLLSPRSTGPGEDVKTEKEALSVLQLS
SVWAPSIFHRGIAKPLGRGKPYRGSETNPLGFGDSHGSENQSYSILPDSIHGASTVSHRT
GAPPLRNGVSILDIGSNGDFGEGMPAFSLDGRLTNQGPIFSRSSSRHSPVFRPIDQVQEA
LRSVGVPFLGDVNSSNVDILHYRQCYGPKAYVYTCLNVLLRYNFSVRFGFNVRRLYCFYN
TAVNYIFPGNPFHNAYHASDIVLAANQFLSEPHVAENFSDEELFSFLFASTVMKLGHVGM
TNAFLIKIHHPYAALYGFFSPQQSVSLALGLTLLDTPECRFPTVASSQESDHDSTPSVWT
HEKGVELYEMTAQLIISTDERRHQVLLNQLQQILREGAGNVVRESHLMIILQNVLHAADF
CYVFRLSSVYRIAAACAVAEVYQQNQTRIWLTERGLRQWPWNGPHAATAGEKRAKESNNN
ILGGFFSCEGSFYGMGECREPEKVPSMYSDLTEGLTPSNPSLTPSVGHIGEASGFSPLHH
AKVLQTAVLETVFLPFIFTLSPFVPDYWLTNAQSNLVWLGEFSADAFEADVMGLLRHPET
GGLRLRSIGANGFERRVLRRIVDPLFQQHTEETK*
>TCRU_843 hypothetical protein, conserved
MLLSQRIAALQRVELQLRRILKEEAIQRSPSLFHPGVDVRQNGEAQRRAAVKDKLLFRHV
PVAVSLLERSFLSLTSGKKTAAQKRPKEHETQPPRERSTKLVPPPSQSHSGVGPASPENF
KTDLQQGTILTASTALKSQGHFMRQPEYALRLLSSLHFMEQERRKLYRHHMSRLESRLQN
TEHALHTVRKRREDTVALNAARDAVTEAKADVTLLQGSLLSRPYISARLWRLLLREEIWV
TAVRDFRKQNGVNGVGTASSVIVMLLSLTRLGFGALQDSLKGHALNTRAPRFVASLPSRR
MRRRKLARLGLKGEKGLTVPASVLVPVNSNGDSKDPAMLMMMEMMKTTSETAKEEPPPSS
ASKATVEVSISETNSTGDSMKRIPPLRWLPPSSCEVSSLVLETLAMCSHVLPLLDVTAII
TCCGEAQELFDLLLVLQASASSLLVLYANEGNGEATMHQTLRRLEDAMMKCGENAKGALV
TQMNEMSLVLPPVKAARLLFGLESMKLIQTEEHVSQKLLMQLVKCMFPQLSTGTQRALLE
KSRQNSLFAFATRSQRAKLRREHGKQGTESAFLNSVRARVRLQQRQMQAALRMKHLEEVN
SQSVGQLAEELSPHSLLILFDLLVRAARDAPRRGMEVQSCFITAALFVVEAVCVARARTP
SSNSGTTLQPDDLPSLLFTLSVLWPLVTERYQMFRNAPNDRQYNQNHGYIPRRYRGQQGS
GVGDSVAKSELMIVTYVTDMVFSAVNAAMAERVQRAESVTEPNSERELGHTLSLKDVMRI
VDALFEWGKNSLTNKNSMSLETTARLIKRLLVTDLQLWDELRQLNETRREQFFCRLSDVL
LRLNMMDTTVTQVLFSVC*
>TCRU_844 L-2-hydroxyglutarate dehydrogenase, mitochondrial,
putative
MTSKISTWAVRLGGVGFVGGVGAAVNYKYKYEYITTDAAATKHAVSIFSKDARREFYDVA
VVGGGIVGLAVVREIRKQFPNKRVILLEKEADVAQHQSSHNSGVVHAGMYYPSNSLMARL
CPRGHDLMMEYCKRNNLPYDRVGKIIVAANELEIPAVQRLYKQGIENGVRDLKILANEEE
IKKVEPNVCGVYALYSPDTGIADFSAVARHMLKELYEGSKGLFNAQFRFEAMDFVGLSFE
EEEKKAPSEMVLIRGREEGQLGPEKTIAAKNVITCTGLSNDITAKRSGPILSRIGKKVTQ
TFSFRGRYYQLKPEARDLVKMNVYPAPDETRGLSVGVHFTPTVDERRGRQVIVGPGSAVA
THRYGYSPYWFDAEYCWHSVTSRGGWVNFVKHFDTVIRTFCVDASRTVFLHEARKLVPSL
KDSDVEESFCGVMGLAIAENGALESDLCIELSRPRTVLSATLKPKKVIEVVENANTDGSS
TKGQNNPLILNLRNAPSPSATACMSIAESIVAVVKESFNW*
>TCRU_845 hypothetical protein, conserved
MPQLVGRYTHVSIRHRYLARVKVHGSSKWTTIIQQDAQSRPRPYTRSRKNIGVENHVGTN
HTHRVVLVWDGEVIAHPQTGSRNEDGARHGPHGETLRVQLNGGGESLPQNNAPPLLRQHV
VRPACYCAAVVVNAQIPRRSAVPQRVVHVLRGHLDADRSPAIVPILAGGGVRLHGALSPA
RHLTHHRSRQPAVFLHHRVKPTAVLHGGIRGNANTGATHHHHEPRQQWQWRGVAWLAHGF
GTVCLFLRCGQQQWY*
>TCRU_846 Leishmanolysin, putative
MRQPRHTALLPLLPWLMMVVCCAGVCVAADRSVKHRCGFDAMMKKYGRLPTAVVREVPRR
GQGAVQAYTAASEDGDDGWAPIRIKVSAEDMHDPLRHCTAAGDLRIDHDGRAITCGADDV
LTEERRSIILRQTLPAAIQLHAERLSVRPVTRPVLIPRTGLGMCDNFTIPDKHHTVGVVG
TDMILYANIFPTSGVRSWAALCVLLDDGRPFAAAVNFDPSQIAVSIGDVRAAAHELGHAI
GFDVSYFVTLHMISEVPNVRGMSKVLVISTPKTKAMARQYHNCPTLEGIELEDEGDYGTA
LSHWRKRNMRDELMTSDMGVGLYSALTLAAFEDMGVYVANYSAAELLWWGNNSGCGLLEK

KCLTDGISEYPDLFCNQFDKNVKFFCTYDRLSLGSCDLKRHEEALPEEYRYFADPRVGGD
DPYMSRCPYVEAYSNGGCTNGNPSLMPGSVVGPNSRCVKGQELQFDDEYIGDVCVDTRCG
DGTLSVRFLRDDAWHECQEGETVTPPSGPWRGSIVCPQYADVCTAFPNISSHPIPVVDPP
LADDPTSAEDAEGDEGEVPRKRPRRL*
>TCRU_847 syntaxin binding protein 1, putative
MPRPVRLRLLLLLVTASSTDELTEANKQQLIRDSGLTPEAHLFANLEHLTRRAGSVQRYS
TASAQGGRSTSSSASNAATDEDPFLKQNCMMMETAGRNRTLRVELSLASVQRDHAMRPNG
ASGGQNSGAAGTTPRHFKGVVAKRKIIQICVAVMLGRLPSQLLSA*
>TCRU_848 hypothetical protein, conserved
MGLSPDPHRRRMPWTAEKECVPGVVRSSKEKMVLDGAQRVDVECVDRASQVYPLEALRAA
VATCEYNTFRGKNIFNWSLRWNPMCSGNALLQGVAGGDARRGRHSHRHLFPSPRDHNAAR
ANTPCGFSEAACAVLFAATVPPSPSVGAEVPVDASSCRLRTHPLIDAAGTAPSSWCSGTG
DEIAAQQFQSDGAGSPVSVSPTTAASTEIDGTGKESNDCQGNNCLLTSLPVKQPEE*
>TCRU_849 Mucin-like glycoprotein, putative
MMCRLLCALLVLALCCCPFVCAAESTHTEVQVSDVTLAPTGLSSSSTEEGQVKGQSGPPA
PPVTEAAEKPGENAGAGQSLTGTPGLQIDTNKSAGETDQDAEASAQTTTTTTTRAPTTTT
TTTTTTTAPEAQRTTSTETPTTTTTHAPSRLREIDGSLSSSAWVCAPLLLAVSALAYTAV
G*
>TCRU_850 BNR repeat-like domain containing protein, putative
MSRRVFNSAVLLLVAMMYCGTGGAASSQDTSGKGSSPKTQFVWEDGKKGETVSSLRVPGL
VEMNGEVFAVAEAQLKDESGFNGISSELLKLNDEKSKELVTAQVKTQVLVECPSNKTNCA
SQADVSAGSQSEKKVRVSRPTTVVQGSDIYMLAGSYSFEVTHQTSSEAQWGLLLARGNVS
TDASRGNRICWSEAYVIPWIHFEKQHESFTGLIGSGGSGVRMKDGTLVLPVEGTKKEVPS
GRHEKGWKGRFADHTLLGC*
>TCRU_851 hypothetical protein
MSLVEELRRLQREAESNDGRIQRLLNELRLLDVKLEAKRNAKKRYAAEAQEEISRLEKDI
ASFKELWRSVTTAAAKHLVSSPSASLSTFHYSPTMSRDRSENTGNDLERQCEQLAELRAQ
RQGLEELLRRATVCYPHYRITDLFDVNNDLERVALARLTNTT*
>TCRU_852 kinetoplastid kinetochore protein 4
MARHHHQQKQQQQQQRDATNNVESKFVAQYGAAVLPPAPSLPSPPPLPLPTTTKTSLATA
SRTPRQRRPPHAPLQQQHSRSGQRSGTSSVVGGPTRSPSPVNPKRGAEQPRCFVVTSLTE
EERARVKAAVAAIGQHGVVLESDYEDPPPFTATHIVVRGPPRSMKALCGVVGSKWLVQPE
YVYASRDAGFWLDEYEEGGLRCFPPPLKCQRFLLTMPEGIVKEKLEQVIEYGGGEVVRPA
RDGRSYDQGVVVIASGDDLLHFATRIE*
>TCRU_853 THT2A - glucose transporter, putative
MSTDCSMYKKEVACNRVLNAECSWNGTRGECGWNGFTCFWGHGKDKTPCLDDSRCKWVYS
DEECKNPTGYSSSYNGIFAGAMIVGAMIGSIYAGQFAARFGHKVSFLIVGIVGVVSSVMY
HVSSATNEFWVLCVGRLLIGVVLGLVNVACPMYVDQNAHPKFLHVDGVLFQVFTTFGIMF
AAAMGLAIGQSVNFDKDTKMDARMQGYCAFSTLLSVLMVALGIFLGESKTKFTSGKHEDD
GTALDPNEYSYLQMLGPLAMGLVTSGTLQLTGINAVMNYAPKIMGNLGMVPLVGNFVVMA
WNFVTTLVSIPLARVLTMRQLFLGASLVASVSCLLLCGVPVYPGVADKNVKNGVAITGIA
IFIAAFEIGLGPCFFVLAQELFPRSFRPRGSSFVLLTNFIFNVIINVCYPIATEGISGGP
SGNQDKGQAVAFIFFGCIGLVCFVLQVFFLYPWEESTPQNHGDTNEESALPEQQSPIEVA
TPGNRQAA*
>TCRU_854 40S ribosomal protein S12, putative
MADETRVEKQGEEPTVTQQFDVEPENLRDAIRIVVRKSLEVNGLVRGLSEVARALDRRTA
HMCLLAADCEDEEYKKLIKALASQANIDFVEVESREELAEWAGLQKQKSDGSVKTFKCSC
VAIRDFGERTRALNMLLGQLAG*
>TCRU_855 target of rapamycin (TOR) kinase 1
MESCVHPLIGQLQPIFNELHSSTAATLPSVILKLEYIIGDEGDTFFQGSAGGEFRASHSG
LSTWVNTQIKDLFSKSETQLAGILCTKALLGTDYIGSNSLLQFFLQLLEGSVRSSDVVVS
EKSAEVWGLLLNNSGSFAEGTAQTRLKTCIKDLRMTGDAVDKVAASLFLCQLLKHTPSTV
VPYLHLVFEGIRVALRDLSERVRVNAACVLQYALSVMYTSMGSSTVIKLLDSFLGDSLNG
LESKKKDLQHGAILCFNAVLFSITNGISSYGAAVILSSASISYLHEIWQCVNAKIVNPSL

LPEIRRELLNSLILLASYDTVKFRERSIPVVLAAASTVFRAAACREEHSMMFLAMGKLAA
ILRDHVTLFLDRMMPHIQAALGQKSKDDRCLEAVTCFATLAEVSPKAARPYLRQILALLF
SFPPTVGFTRDIARICEAFPELRSTCLSKILEATKQQLLNAHHRLSISTGENDADAVLSL
ECLSALSSLDFSGYSTLPFLCDAVICYVSFPHEELRRAAINLCFKLLLSGCTGSQLPCRR
TPEGVVVHHGRDHTRLINTIVSKLVNAAVSDPESDIRLHTLESFTEEYDHALALQHVVSS
LFPALHDKHQNRLAVVRLLGRVSRRNPAHIYPMLRKIMVQCLTEIQFFEHAKKQEQAFSL
LGAIVESTPDFSKPYVPSLLNSCVKRLREPSQTAAVLTALLSCIGKLVRYAEGDDVRVAA
EIRPVVVQHILDSSHLPKKREALRALGDIIRTTRDVNIFEVHPELLSVLLQALHGGFKET
WPVRNDVLQLMGIIGAVDPIRVKEILRNSHVNDSNTEMVPSFGLRGEDSIAQTVVRSVLQ
ILSLPSLTDEQSVGAVNVIVKIISLREVSSSGLIPYHAEIISLILKHARLQVRKREDILI
CLTSFVSHIKEYVRPYLDELTLAVASFISASDISVLNQTLALVKQLRRCFREEFRPYLSS
LLIPILNLVEESPHTAGENVFGFLSEMGSLLDDHLDNVLPVVCDVIVNASFSNTSRVAAV
ETLRSFAQQLPSLRFHASRCVHCLCRVLKEQGGVKATARGSLGSAAITALLAIAQNLGKT
FENFTPIVFPVVAGHYGEMDGEYKRFCGILRDTINTRKNPEMQRCQEENNSGGTIASRSG
TNSDKLPAERPSDPFETLRHVLRNWVRSNDEDWNHWLTQLAVILLRSSPSPSHGCALTLA
ELHDPFARQMLYSAFATCYSEMNESTRKDVVGLLSEVLRGPRVPSEVLQELLNLSEYMER
LEIRQNAHGNGCGNASQDFRLFDLPTLMESSERCNLYSKALHYVEIEFFETIREYERSVF
RGIPRPLPSGVWQNLLQLCEKSIYLCNLLGQRESANAVLKFIQQNYSMLTGQEVTELFQM
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SKKEVVELAPMGAHAAWLLRCWDDMENITSFMSEDSYIGTTAVFYRAVLATRKRQFREAD
RLIKLCRKRLDSNLSALVAESYDRAYELFVGIQQLSELEELAMAARDVRNVGRWQELWEK
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SAVANQMLQPAVALGAFQHLYETNRKKKAIEMLEQYVEKVEQMGTQHANRTREELAICHA
KLAEWLTHRKKSHSFAETLRSALHHLRCATDLDNKNGTIWHTWARLHHEAAMKNVSGKVS
PSVEDHIVCAIDGYLRSVCLSQELEDTLGFLSLWFMHASLPSIQGSSTIKAGIHQVSPTV
WLKVIPQIIARIYSRDAVIAEYAYHLMVIIAKSHPQAILYSLNVANTSHQMKVSSECVER
QKGTQRVLARIAEFHHNGKTMVNDAALACRELVRCAVLWPELWFDELERVWFQWGKDKNA
NNVLSALNPLLEQLKMPETMAESHFAMEFGQLLTEAFGYVEKSALLDSEGCMEEAWSRFK
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SKQRPRRIYINGSDGNLYKFLLKGHEDLRLDERVMQLLGFANKILEKHLVTKRRGCLIQT
YSVTPLSDNAGLVGWVDHCDTLHQIIKEYRIHPKYLSTELNLMRSMSDELHHLTVIQHVE
PFELALERTEGDDLVRSLWMKAPSAETWLERRTTYVCSLATMSMVGHILGLGDRHPSNLM
IHAFSGRVVHIDFGDCFEVAQQRSNYPEKVPFRLTRMLVKAMEMGGIEGLFRHGCIMVMG
VLREEGSSLLALLEAFVHDPLVSWWRDEGGNDRCTNNKDNAKQSTSMTGSLRASHEEYDV
GSVHGTQRSLHRRGAISRVCIQGEEIALQQTRKAQSVVNRIKEKLEGFDFFHDRPSRGDD
GLTVEEQVSRLIQEATSNENLCVHFSGWCPFW*
>TCRU_856 hypothetical protein, conserved
MMGEEGIIVPFCASVDAYIKKGAGIDLIMKSVAGLSRLVSLYSQNEETSRNYAKFGQAII
NCRMLANHFRYAESLNFAIVKFKKRDGRPLLSWLCLVGSFFFRSLEQVFGDLNYYQSVFM
HHWSRTFLSLGYWFFKSLSLTCGFFYELMSLRATIASPEWRTKSAQGRSKILRAGCISLL
RYIFDMVVYYQWVPWYNPYKTVQYASAAAAGILGIYVSWKETQAARVAGAKKAPELRTAM
NGKEGNEIAELKTVVPAE*
>TCRU_857 legume-like lectin, putative
MNAFLLSTILLLPLALVREVSGGDQIQVHSVFPPILQNYWENGMRFWSFGLSTVVTDKYI
RLTGGSPNAKGYLWNKHANRMEAFELNVTLQIRGRQITGRDDVRDGGMGIWYTTSAMPAT
NTDVGFFGFHKRFYGVGVILGHSDEISLVSNDNTFELEPSSLLSRRHGYCSVPSLGELHI
TITILYKEGNISVLYVYHEGDEPRLEDYDRAVFCTTAPSTSFLGIHHFGVTAVNSATFQA
THEIHSVIMTPLSDITHHKEEENKAFQFRLFEEEENETRKELLDDLNEKQ*
>TCRU_858 Concanavalin A-like lectin/glucanases superfamily/SPRY
domain/HECT-domain (ubiquitin-transferase), putative
MEEDLSDWGLLSIADILDFDFLRKNEALSSIVITLKDCEIPLLPCEPSYVVKYVQMLIKN
SKYNAENRHSNFEEMDRFRSIKLKRSLAASELIRERLLGAIESFALTVQKETHKPSFLQS
VVHLGSIVCPAIGSFCDALIEGAEAMALRGVSSKKDIGSCVEVLQLFRSRIDISVLTEEQ
KRRLFFAEFSLALRSERLGVVVNCLLQKSTKDALRGKYCPPLLEHRVSFVKAKTDGFLTR

TCELPFPIHSAQVNCFPSDEKLVVCSGNRGCVFDQLGMMGTRFKLREEFEVSIEKNTRII
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SILSCLVCSESSRISNSKCHLIQKDLDIIFSVDNHQFHVTSQCVLTRGQGLWHSTKKCYY
FSKGNALSIGRVTLKENFHPFTLEMWVYPCNALENQSVLSLGDKSLDEVLIEIEPTPEGV
LWRGGSRTPHLGASFVTFSVPGKLAFCQRWWHVALLFKGNSWELWVNDAIVSRAPALVSP
EALIDVECVLGKSFVGCLAEVRIWNCCRTPVQLARDSRRSLTTIEPTLFGYFPLDESEGD
VIADYASNGSHALLHHGQATWLLVDHFPIFPLNIVRCIDDFAPIAWRESSGILFLSSCPG
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PKRLLIWELHQQHYFPFLRKDAYDNILECERDLLTQCAMYAKRLVGAERCLVDQLSWSVQ
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RSEKLPYELGVALTSALCRIGCSLLVSSDVVTSEVELKYLHLLWGGIRKSGSERDAIIKN
LQQGVGSISRVVDELHKDDPGALIVLRDDRLVKLERLLMAAFCALLIPTESLRHATKQTL
APMFRYIHNMRALVLSKRQEDQESLEVLEERAKLLARFEPICGVRTEEPPQIKNSTRDTS
PQRKWKRFFQTWKALRVLKTKMPQQRETESGEPGAVILQFLWDKNLERESVERLVVQQTQ
RAHYRLSGMLLLRQLIEETRASDTLARIVLPVLAKTFTGWHYSDDVQCCSKGDFLRLHGA
FFQLLELVVFNVKSGVRDVWADVFLSLLTSELRVIDFRRVRSDVTTTLCFLWKFENRKTT
GIPHLNGSIPESMRNTLLSPSGAAPTLVIGRSGFTMKGLGGRGTCVVSSEWSLGKKNVPY
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CIGDVMGCGWNTETREIYWTKNGKDIVASVEVLQHQLHPLIGMCGKGLIKVNFGAERFLF
DKVPGIKSIRRPLGENAWDVFRVFSLRASLGLVESCSGLRTHSADSIEGLRAVVEQCIEC
SCAEMERTLFLSMSESFVISLSSHLITLAKVLVSAKDDELTPCVQRVVMVLQRITHHTLQ
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ESRPAVEAWTALAFLQYMNSDDPPHRWREELHKWIMQNLEGTKDKVNTSLALRILFGAPR
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VTWFEHSEVGGRPNDFCQHEIDFTTQNGEDGIFTVDTANESSSFTTLWRRRKDQRKDHLL
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FDSRCSSSSVLVTLYSDHTLSSIIAQTPGYALNTLLIRAPRFFFDVRMDATTPQWGYKVA
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NILRVTNVRSENLRVSINRLKARANKNSWMSSVFGQTFSLLADQHPRIFRTNKRFWGVVF
LGEGSEDVGGPFREHIGEMCRELMSTALPLFVPTANNVHNTGTYRDAFVPAASAIGTAEL
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NRAGSGDMFDEVFDAETFTTRLSDGSVKELIPGGSNTRVTLERCEEYADALSSARIGEYT
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LWQALEEATPLQRRLFLRFVSGRDRLPVKLRVLPLSSPGDADSVLPRAATCFFALELPDY
SSVEVLKAKLYYSIENCADIDTDFNPREVDESESPQLMVGLEDTRQEEVDSTTLSD*
>TCRU_859 hypothetical protein, conserved
MEISSISETDKNAITRLLSSDLSRTVARHAIIVLHYFRTISDEDLPIDVLLGGCVLYAVK
QRQASNANYFLRECLERVKESDIVGFELLLVQVVRHNVLLIETCLRSVFHEVLLENPVAG
LDRERTIKVCLHLISFLYRTSWCLFPESAARGAFLVASEKCEVKLGKLSSAFDGPMVKHI
AKYLRDQFWN*
>TCRU_860 hypothetical protein, conserved
MRKKLVLPLSIGRGFSSWDDGSDGHEWKSRALAEKRLLALTYLGDVNKRVQIHDAIRLRG
EVNKQAIRACELPTFFQTKETNEAENLQEIDYHSLLSMIEGEFEVDTLAHIAPSDANFLK
TEFLQCDDSAEVKLLGQWSNLRRDTADYNNYASIPDGERNAWSAWYLRNVRPGKTEND*
>TCRU_861 hypothetical protein, conserved
MDFDLSTSSVTEALGDLQMKLQSVQEDAELYSNLEKKARSSFERHRAELTLLLQKERAIH
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LQEQVKATRTEADLAQEEKTWHEMQLREVLGRQRGLNDELQRLRQDVEGQHTREAAEAQR
QDRCSRRQGVYCGLEKVFLPSGPPDRCHTTSPSSHHIAAIVSTVERQNYYKPRLYYRRRG
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AKTRTPSRAVTKSGRHLEAVCRSLLREILSLRREYQDCSVALNDPVADSVEVSRRMRSIM
NELDRKVHQLRSLRQQQAKVEDKLRLHDMMMEIAAENNYCENIYSDLLELIRS*
>TCRU_862 DNA topoisomerase II beta, putative
MANRTVEEIYQKKTQHEHILSRPDMYIGTIEPVTEDMWLYDEAENIMKLRKCTWTPGLYK
IFDEILVNAADNKVRDPLGQTAIKVWIDAERGMVRVYNNGEGIPVQRHREHNLWVPEMIF
GYLLTSSNYDDTEAKVTGGRNGFGAKLTNVFSTRFEVETVHSRSRKKFFMRWRNNMLESE
EPVITPSEGPDYTVVTFYPDFAKFNLQGFGEDMVHMMRRRVYDVAGCTDKSLRCYLNDTK
IACSSFLEYVDLYPMMGEERKAASYARVNGRWEVCVRVSNIGFQQVSFVNSIATTRGGTH
VRYITDQVIAKVTEQAKRKSKTEVKPHMIRPHLFVFINCLVENPGFDSQTKETLNTPKNR
FGSTCDLPPSMIDCILKSSIVERAVEMANSKLTREIASKLRNADRKQILGIPKLDDANEA
GGKYSHRCTLILTEGDSAKALCTAGLAVKDRDYFGVFPLRGKPLNVRDATLKKVMACAEF
QAVSKIMGLDIRQKYSGVERLRYGHLMIMSDQDHDGSHIKGLIINMIHHYWPDLIKTPGF
LQQFITPIVKARKKGRSDGDDRAISFFSMPDYFEWKNAIGDGIRNYEIRYYKGLGTSGAK
EGREYFENIDRHRLDFVHEDATDDARIVMAFAKDKVEERKHWITQFKANTNVNESMNYNV
RTVRYSEFVDKELILFSVADCERSIPSVIDGLKPGQRKIIFSSFKRRLTRSIKVVQLAGY
VSEHAAYHHGEQSLVQTIVGLAQNFVGSNNVPLLQQDGQFGTRLQGGKDHAAGRYIFTRL
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EVIDNLMRLLRGEEVQPMKPWYFGFTGTIEEKEKGKFVSTGCANVRPDGVVQITELPIGT
WTQGYKKFLEELREKEVVVQYREHNTDVTVDFEVFLHPEVLHHWVAQGCVEERLQLREYI
HATNIIAFDREGQITKYRDAEAVLKEFYLVRLEYYAKRRDFLIGDLRSVASKLENMVRFV
TEVVDGRLIVTRRRKKELLEELRQRGYAPFPLQQKKKVSSTTIQQGEEEEGAADATHATA
EDVFLVLQPAVDEGGDEDNQETPEMRRAARDYDYLLGMRLWNLTAEMIARLQSQLQKARD
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ADDDLFMSDASGGGGGGGWRPGDEEGDGGSDGVVLDDDGPGNNAGGGAKKPQPKRPTAKR
APRKPKEEGLKRVKKEAAKKVVVTDDFDIDEFGIEALTRTAPKFNNKNTTTTAKTTTAAF
TPPPQSTRVASVIDTDTDDDLALLGISSVDKKTLAPVPPPKRSPQRPKSQPKKSQGSRKR
RRSSSSDEDSFFDDDDDDDEDDDDEASSGSSSYDFSD*
>TCRU_863 retrotransposon hot spot protein, RHS3, putative
MKFTISTNIEDVLFKGRVRVNEMRLNDFVTREADGRGVADTNRDVLLEEFFKDPTRYIRD
EGALNEIQASDRYLSMKRAVKGEVIFDEDIRRLCDKGVNNLPGWSLAAAEVKATVHKFTK
HFLDAAAEEARNPTTTSAPEKLEGCYESLHNARWSHAVEIPDGVERKKTGTGMGVHEGKP
EQSWSYKKADDDIEENDAVQQFGAAPPVLMVLASEKGWPYSWNTIQDLPKDVFVNCEVDR
VWQIVKGDVTAWFSPHGGTDFTPERRVLIGTPGIGKSVAAGSYLLYQLPHCDAKKLQVVV
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TSGWGMIAVSSPKVTNYDEWAKQLQAARIIVNCPDEVDVKAMCAWRTCDETKEKQAECWK
EVKNTCIFWDRFHFTSLMRRRLRNAVER*
>TCRU_864 protein kinase, putative
MRRQGKNTTKRSMLLRVGSFSLDAERTDGSTVMAGLSPTSGGIITPRRIVRSLNVSPAVT
QLVPLDAVAQRPLSTETSATVLSEEVLDDLISESVSATYVPEGSLPVLGVHNGPTEGMTA
SFDPGNQKSMSYSLTRMTDKDSLCSSSLSGGSSTHSFSHEYTLAFDVESVYSCSLSCVGD
AKHGTRSVSRQMASPAATAAAVSAAVAAATPNNSVPDCGDTITRDPEAGIVQLIATGDGS
NAVEVGRGRRIVNVRREERIGRGGYGDIFRAVDLDTGLPLAIKEILVTADISKDVEKQLR
ALEREIRVMRKLNHKHIVSYYSARRDESCSALLIYMEYVGGGTIAQKLRTNGPFSEDETR
HYTRQLLEGLDYLHQRRIVHRDLKGDNLFLTEDGVLKVGDFGTSKELQTTLVTDSVAGTP
NFMAPEVIACSGHTCMADIWSVGCCVLEMLTAHPPFWNLDNHMAVMFAIMKGRLEEQVPH
QISGDAKDFIRACLRNDPKERPTAAQLKQHRWLLCKEENEDLGSRVQSCLSLSSLGFSNG
DGKHREGQCATQEGSLTARKDAFKSSTAPVVAIIPDGNDTSGGSPVNSSKGGNKKTGKRK
RILDPPAPSKAAKSPSGSAPNLMPPLATPLSNGQLTNHTKQTTTRSVPHANGVKHGKRST
KVGIGSTRNGGVSGGHGEPKRGGLTSEGCVVTKTTKGGRLTTPRLEATTCSTR*
>TCRU_865 hypothetical protein, conserved
MRPSRKQQAQRQHPRQQRSVAHKAQRAPSSGHGASGVEHLPRDAVVHVAPREQHRPAGQT
HRRIKCHRVVLRRRKFAPHKRHSGARHAHSPTHRHRVLAQQEAAVNKRHHGAAAGSNTAL
HRHAQPQRRLHRQPVHVQRTARRQRHAANHQHANSVAEHRRHMRARNGQHAPRQIHAVQH
EARGGGAKVVGVMVRNALLCDQHRVHHSDARARRVSVRHQRTAARTRLKPADQHIGTLAS
RRVGTPPDNVQARSAHKRAVRQRHVAHAP*
>TCRU_866 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCSAYCRCTEEESASLSRSGIGNSRTGSGVSGENRVKTDKTR
TMRTASEGDSHPSERDVSDGGSFDQAPPDKSMCKEKNDGSTVKPLTTDGEVLVDSQETVA
THLKGTDTDLADPNINQNHKNPKAIDGIDTQLPDAPAAPKAQPSPPTVPTANKTVNSKEE
LTAEETPEHSRATRNPNEGSETKNPTDQALKPDAGGIDTLASEDASSPSIDDAATSEATA
NTARVGSPIASLNNTDGKNEGSGDGESPTPSPSAAEPETITTAKPTTHDVSHPNKNGTVT
FTGEKNAPTTNPKSATEGKETADVESDSSTAVSHTTSPLLLLLLVVACAAAAAVVAA*
>TCRU_867 C-terminal, D2-small domain, of ClpB protein, putative
MTSNLGSEHLVHVGNSPKGLEATREKVWQVVRSYFRPEFLNRLDDIVLFRRLGFGELHEI
IDLIVAEVNGRLRSQDILLEVTDEAKNFVLENAFDAEMGARPLRRWVEKYITTEVSRMIL
AQQLPPNSTVRVLLDSSQGKLAFSVKRSFVSE*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MSVSGNQFMFGTGTPTLIKIPKRSSDLTNGAIVAACNTGSDEEEANYVIPSVYNATILTC
SDPCTLAASCFPAYTTTASSDGCACACAEGGHGDACLPVAVPEPPSTDGADLCVREVRVG
VEVIAGLGTSVVCYVGVTFAADVVVDVESMSGSVRNVTLVNCTFVGGASLYVVGWRSDPT
AGERADALISGLESRSGGGVLVANRFPPGSRVTLVDSVLIAEARVAYRGAYDLGDLSACL
VVHSVNLTGSVLTIARTHVAAVFRDAVGVLFFGGVALSSRGALYVDGLLVQTVLGLCVSV
EDGVAASGGSVVAFVDSDFLLCKHAVSVRGAVGVSGSAVAFMRSEFLSTEDYAVAFYSTL
SLADGSMLLAKGNVHDGVSREMIYAAGAVTAAGSTLSFVRNRALLPRMLSLSLSLAAGAH
LRVACNDAGGRVLSTAEEYAAAGFGDAGRIDVAGCDDCDRDTHCYAPGTASATMRNGVCV
CACGSGGYGEACVPVGAPALPPAVGTASSLFFREGVTVRSVFVVPAGASEVTLRHVVLDG
VSPVLYVPWMARDGVRIVVQSVSLRNGAVLYVMGGGALRGAVAAVSDESGPVELSVCDVE
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VVSGVALVTVMTGGRTVVVDGAVLELVGGGVALDAAVLGGEYALYASARVVALEGAVLRV
SGSQVYAAHGLVFDSGVMANASTVVVNDNAGVLTDGALLELRGSASFVSGSWLSVRGNSI
SGRLLSVPSYPRSADLVQSTLTFHGNAGSGTVVMDGTVALGGAGRRFVVGCLTLNGQALR
PIDYRSAGIIGEFRPVACGVCDAEVRCFAAATRAMTVSCRCRCAEGGYGRDCLPVYLPHV
DGCNCTPGMPLLSHTATLTETRSPTPTWTPSPTPSMSATHYSPTQYGPTKTLQMTETVAL
SPTRTPTASVSSTLWWSDVACPTLTVTTTAAGGSLTQNDIRGGGSAVPTRLMVALPPPFR
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VADETIVIRCGAAAVSGGCKGALLGSFTIRSNTPSALSAITGVVAGAAAVAVVVTGGLGS
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MRGSRVYWCVFQLSVLCVVGLIAAVHPPVGGCHVQYFCMATLLLAGAGVVAFTNMMRSAF
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RHWQDLREPQRCGLEALLRDDEDSDEETQKLHDMTSLSYASETTGASSYRPPAPP*
>TCRU_869 succinyl-coA:3-ketoacid-coenzyme A transferase, mitochondrial precursor, putative
MLQGRHTDVTPLDALQVTATGEIARLYGVEKVLFAETVTMQTLCGGGRGLVLLEHVDRDG
KPRIFEQRDMPVTWRGRVGTIILDLAVFGVVYMGDSACRLLLGELAGYFTVEELQYKTGG
PISFNCRIE*
>TCRU_870 hypothetical protein, conserved
MCSASSVADARCEESLPSRLAGASPATDAVTHATAESETIAYLLRHCRFPVECWWISLNL
LERWRLLQSETMSLGSFRKRTSFFPADMSPASCAHLMRNLSYTCVAWVDVLRLYELATRD
VAAPEAARRQRETTDRAGDEPRASRRVSLRWMRHTALTSLLQANQWKESLQFYRHMLYQG
DTPSHVSAGHLVQRLGKVGAWEAVFRIFELHLKLIAATPTYSTARQGNDGVEHLSARVAS
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SFPSELDRVNVLRRAHASGQLDHFKIIRGLVHHGKWLEAIAVFADGLATQQLHRRDIGRS
RLNILHASSGDSVQAVLYCLQRLTRRPENSLRVNDAEVECVLSKVPSMLPTSSGASFASM
AHWRFCLQVLSENYASFATSGGRGVMPGIEGRRPTQRMVSLLLRHSMPWNVALRIFELSC
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EFVPLEFFSSNRGVPERKPLMVEDKVLYHFVETTMNWERALTLLHLVEDQRAGAVTGNVK
PLQVISASVHCATLKMLRRCCAAHGELWLHSLQYFQHAVSGLHLLDCHTHPRRLAQQHGD
TDVNTILYCVLYETLLNLLEEPSGASIVLREKNCFSLMECVTARCGGRIPTHMLLPNQMD
RLLPRLGVGEPTVPNVEERTRVSMKLIMCVLVGLLGSTGKEGLKSPHMTPPDTVMFYELQ
KLVCRVAEYRHYLMRLHETGQSLSNSASPRKTAATEKRVVPQPFQMGLLWQTSLELLGCQ
CRACGVDSMMPGTLKLVYRSCATSGGQWEAALHATQYLLQHPGAVEGEHCAMYCSLFGWE
RALAVWCRHFPQQMLREVSGHAKGLEYCMQSLECALE*
>TCRU_871 hypothetical protein
MIHDAVRICQNLLRAAGRRTDKHARKIATTATETVVPEEGKVVRSNKATSTYVYVCGVAL
ARAQADASTPYAPRGLRCPVALVNVDMPAHSWSVEASWRQSMLPHTKSYEWTTFAMVPPK
DPVEPLIRLVTWQRGSYVTVAATTGNSPTAASISKEL*
>TCRU_872 potassium voltage-gated channel, putative
MRRRAVINAGGRVFETQFSTLLRYPNTPFAKMFPLPAGGRKKCEYFVDVTPEVFESVLGF
LRTSQLHLPKENEQLRAEIVHCLNIWGLLEHVFPAAPDDTSGSDIVELPGICVVQICDHM
QHDQGVKRHALTITFGADGFHLRRLTQRIRRDLEGLISSTYWQCCQTNERAVFFVTTKVA
NGTADLLTTSVNQQVIEHTEAMGYSLASSYVTLSPDVVHTSVRMLVHNFTFRRVRRTALE
VGDELALSGEGDGKEEEVIETHENILSMRVGPQKKSLYEERSLPPNSTRASDIWRAH*
>TCRU_873 protein kinase, putative
MDEEDAERTEAPTVRVLCDNNWEERVLVRRGKHSRFYRVHWAKGGVWLGLKEEECVDPLA
TVRNVLPIQRLHSKFILHHYDICVDANRDNLLLVLTELMDYSLSDVMHRHCSRGHLTECQ
ARAIAFLTLHALVDLHDRIGMVHGDLSPSNILLRATGELKLGDLSSAMPVNAAVDCFSGT
VLYTAVEVLRDRQWASSPSSDVWALGVTLHECVNGSHPFSGNSDENFWEFLSLMEAAMRA
QHQPLCPPCFSRDFHDILSAMLCWDPARRPTVRSLLEHAWFSQYSVAAAQRVLCLIAQ*
>TCRU_874 ATP-dependent zinc metallopeptidase, putative
MDPLSREEDASKSTSFYRGFYDAQQRRPTKNVNPTVSQAVGGAIFTALPFVILGYFFMRR
RVNVASSAFGAKRGNFLSNAMDMLQKQMNPLGDKNFRVEVRDTKFRDVVGVPEALEEVQQ
YVNFLKTPERFTRLGGRLPKGCILTGEPGTGKTLLAKAVAGEASVPFFTCSGADFIEVYA
GSGPKRVRELFAAAKREAPSVIFVDEIDAVGSRSNGQGALGLSSEENRTVNQLLAELDGL
QANEAVVVFAATNFPDNLDKALLREGRFDRKVEIPMPDQRAREELFAHYLNRIVVSDATT
NAQRLARLTPGVSPATIATIVNEAALAAAVQGDDKVTERTLLPAIDDVLVGKKHRSRMSE
ATARRVALHESGHTLIAWLLPRQSDVIKVSITPRGPAAGFTQQVGKETFDMPTDVSLFTD
ICVMLAGRLAEATRHAELTTGAQDDYRRATKTAIHAFLAFGMSPHVGFLACEPQRLDEGR
IYQKHSEKIQAVAEEEAARLVGTAQQYTNTLIAEHKELLHRLADALFTRKELLKEDLEAI
LGPRGAARLSLEAEKALTAFVQKSEKHGTTVRSTSG*

>TCRU_875 inosine-5'-monophosphate dehydrogenase
MVNVDLRTKTIRDGVTAEELFQSDGLTYSDFVILPGFIDFGASDVQVSGQFTKKIRLHIP
IVSSPMDTVTESEMARTMALMGGIGVLHNNCTVQHQVQMVRSVKMFRNGFIMKPKSVGPD
TPISVIHEINADKGISGILVTENGRHDGKLLGIVCSKDIDFVKDVSLPVSQFMTKRESMT
VERYPIRLEEAMDVLNRSRHGYLPVLNDKGEVMCLCSRRDAVRARVYPNSSLDRNGHLLC
AAATSTREEDKARVAALAGAGVDVLLLDSSQGNTIYQVSFIKWAKKTFPHLEVVAGNVVT
QDQAKNLIDAGADAIRIGMGSGSICITQEVLACGRPQATAVYKVCRYAASRGVPCIADGG
LRSVGDICKALAIGANTAMLGSMLAGTSETPGRYFFKEGLRLKTYRGMGSLEAMSQGKES
GKRYLSEKETVQVAQGVSGTVLDKGSVTKLLAYIHKGLQQSAQDIGEISFDAVREKMYGG
QVLFNRRSPIAQMEGGVHSLHSFEKNLFTSKL*
>TCRU_876 WD domain, G-beta repeat, putative
MSYLTEEEEKERKREEQRRFSRQQIIEHVKKNLPYTAFDVKWVPRGASFAVVGQYPNNKG
AISVLQLNKGELSVQCEIKGKVPIKCSTFGHNTSNWQSNITLCTGDFAGGLSLWDIERLD
ADPLFLVPHAHENIINAVDGAQHSGPPEIATCGRDGCVKVWDVRQSNKPVVALNPANPAH
ARDCWTVRFGNSFDPDERVVAAGYDNGDVKLFDLRIQKMLHEFNVNNGVCDLEFDRPDIN
MNKLIVSSLEGRVRVYDMRTLHPNLGYAYVEERVSNGTVWCTRALPQNREVFMSGGGGEL
TLCRYRYPPERMLRDPEGVAKGVAGSVEELNRAKLGDQPIHALDWNRAKEGLLVCASFDQ
SIRVVLVTKLSLLQ*
>TCRU_877 Protein kinase domain/Protein tyrosine kinase, putative
MQPESGTRGATGHILVPGFLGCSGSTDSKYTYVRYLAHGSSWETWKVLDVSDGKPYALKI
TSLKNYREPKLLRVRTEVRCLESIDHFACIRLHEKPETESHFFFVMEYCDAGDLRYQMRD
GGKLLEHQIVHILLKLVLALHYLHTKKKILHRDLKPANVLLKTTGLLKLGDFGFSNAYDT
ISGDVGLTICGTPAYVAPELWRNERYGAAADIWSLGVILYEAMTGRRPFEGTKYEELRHK
VLHEEVLPIKTSHSVDLKRTVYALLRKSSVERPDTTQLLREPLLVAALSNFPEVLRVSDV
EDSLLQRVLHDISPEQLLPRPRLDHSVLFSGMVWKLKPTQDYQERYMELADGQLSLLLRP
GGRVGFRGCIPLLRVEQVACIDPNHFALKIEGADWCFFQTPQAAVWEEQLRAALGI*
>TCRU_878 Choline/Carnitine o-acyltransferase, putative
MEPKSLEEESMMYLCGNGHNRWCDKSFNVIVTEGGHCGVHAEHSWGDALTLANVVEYSHA
SDEFKELYTEDGHVKKLPEDEVALTEGKFKVFVPNRIRFTTDAVMKRAVQGAQERCIREI
KDVDIRVCRFADYGKGFPKKQRCSPDAWVQMAMQLAYFRDQGHFDQSYEAASMRMYRKGR
TETIRTVSEESCAFVRAMEQPSLSAEAKLKLLRVACERHQKTSPDAIAGCGIDRHLFGLY
CASTGFEVASEFLQAAMQSKWKLSTSQLLTRQLPAKFYPPSDEPFETPNGGFGPVQDDGY
GVCYCLYGESLFYFTITSKHSCKSTSSTRLAEHIKRALRDMAALTGWN*
>TCRU_879 Choline/Carnitine o-acyltransferase, putative
MAEARFAVRPTAALHHVGFEVDTSRKQTQLYVSRRGLVLYVPHPYFIIKNMRRSFWHGVD
KVQFALYPIPLSVVTAFSFGVFLWVLNSPADAWIRVNCVSDILWRLDERNFISARIPSRY
RMPALCANVAFGAVTLFTALQRFVLRKLLSYNRWIYEGQGKLTRKTMLWGFILKTFFMHN
LKRTGAYGSCLPSQPLPDLKITVQRFMKSMVPFYEGKTAEWEHLKKLSEDFLRNEGPQLQ
RYLWLKYLLADNYMTDWWIKYVYLAQRESLCINSNWFGVAFAKYLPTPLQASSAAALVHN
LVKVKKSLDRRTFSPQFSGLVPLDMNQYRYVFNTTRIPGREMDVLVQHEGIKHIVVIHKG
RFYQLEVLHPLTNHQLTPYQLEMALESILHSEDETDPVEALIPAFTTAPRA*
>TCRU_880 hypothetical protein, conserved
MRRATNTARIHWAEQLRMYRTPLGGTYFEQPLPSSLGASRAKGKEISTAHITMRRRGPRK
EKKPLSVPLTAEGLRGKMRQIGEAMAVFKQRRADGGEVRIAGDSHHEMRQRAFHNTEENE
FTPMRIATELSPVILVDQDDMVLAETGEEEVEGKNTILPGSSVLGSDLDRLEREMMRDYH
QRGKELPHFDRVYAAFGSGRRSKKPYHVLAEEYRQQMAVRINTTVSGAAGRGVNFCRGFE
QRSEDKDEGEEDAMLPPEANPHFPVAMEFGAVSAVAATDMQLTENAASFEPSSPSSPPHD
ASSSARLAHGRLPELRGAEFWDDAVNRERLQQRLDHAAEGHTHEMLAEGAVDTGEIGYSA
NRVRRETLLYFQAHPINEMIQEPFVRIRSILPSDGQAEVHFPAGDADTDVDLPTSQARRM
ARELGLDLIRVGAIHTDRSDRRVVALCKIADHREQMRDMLRFKLQKLGVQPPPTKECIEV
PFRGGTHPHAIRFKSIGIAKHLLRRHVVRINLTEFGTPKEGFPVFRTILDEVKKQTLQLR
AYHTAGTVRANYNEVYCYLFPSTGRSPKTTVTHPTQAQLDAVRDQRILEDEREIYFDDLN
NKKTARERLAYIKKLEKGTAWADKDEGLSLQRQREIKVMLGYLPKGNRELYAARGDVDIP
PPFRASHPTSVERWTHPPETNLEQASRGAAVLGKRLAMTVSEMHDRQETADNPTLLDRFY

YRLQGPALEAGELKEALGLKRNRKSVPRHASGWGTLGMPKNAPGEPGYAAK*
>TCRU_881 UAA transporter family/Triose-phosphate Transporter family/EamA-like transporter family, putative
MFVTPHRFLIPFFLALNAFSSIAIVFCNKLIFEDHDFRASTTLTLIHFVMTFLGLVFCLA
GGIFKFKRLSLMKVMPLSVSFCGFVVLTNMSLMYNSVGFYQLMKVLTTPLLVLMETVIYD
KQFSKKIKLSLLLICFGVSVATVTDSEVNLVGTLVALSALFVTCQYQIWVGTKQKDLGCD
SFQLLLYQAPLSSVLLLPIAYFTELRRLHYPCNDTLSVILLSGFVAFIVNLSIFLVIGKT
SPVTYNVLGHFKLCVILLIGHVFFDGPMGSKRFLGVLLTLVGVFWYTHLKTAKHSGVEVI
ISTEEFKGKDEDSDGV*
>TCRU_882 eukaryotic translation initiation factor 4E, putative
MQTRLKSRPDEPKLAVHPTSCITPLWGVWEMWCVLPDPVGGAVGNNTGVRGSAVKKGCAV
HKEGNRATWLDQVRSIGLFDNAEGFWGIATCTLPPSQLPPGITYYMLRRNIAPMWEHEAN
RRGGRWVVRFQDQQHRQQRKGENEEEITEDRSSRVDEAWESLCIALIGEQLPCPETEVCG
VALRRAERRREWKLSLWTRTAADRETQLCIGRFMKTLLNLEDDVLQYLSHRELMQASKEG
CWKVPPKYEL*
>TCRU_883 hypothetical protein, conserved
MSGDTYFRRAIDWMYGDTAYLQRMPSPEIGEKHINELLGRHPFHPFDPEMKPDHPCYNAN
AIFYNCMTADHVEGYELHMKHVSCYFPYKTDLMKCLSGEKRRARAAARQGVTE*
>TCRU_884 oxidoreductase-protein, putative
MNGRAPKRPREPGPSDCCGSGCSRCVWDVYFDDLAKYEEFVKDLSGQGKETGGDEDDEFG
SSSHDDDDDDDDGEAHDFVGSVVIKYVDAPTNEERVITPLVAVSKKLERFLPIHDVQLVS
SSSSHEFDGNTLKEGQGQAVQIVDVLLENSCELKRPMNFITPSPGDVVEVFIPNDYDMHN
SGYSGEVEKLCDRLNLNPSQWCEIHRSPFVPPTHFPPWLPFQSQIQIRTLLAYFVDISSC
GYLLRPTFFQTLWRLATLSKTTQLPTVAEKGVGTMELLETCASKEMAPFIYGIVMNGGSS
LCYPRLIDMLNVFPFVKIPIERLLEVSGPLRPRRFSVSDYTLDDSSAEKRLRSIQLCLRR
VEVVGVTSDKVGNDEVNAARILAEKLRAAALHRGTMNGGNCNGTTPFLFKGHVSHPLCTF
GSRPHPLPMFVGTKMFGTTLFARGLKEAIMPFMTQTAASTTLPLLILVGAGTGIAPLVCA
VHELVRYRQGGVGCKTQIPNCWVVYGARNFAELVYHRKLQEALELNAISRYDVSISRSSS
EGYLKYVTDVLDAHSEELRGALLERGARLFACGPAALLKSLRLRLANNILRSNDDDESVR
EQRVLLLEKRGQLMFDVWSAVNIFE*
>TCRU_885 mitogen activated protein kinase 4, putative
MDKPQEVATLAEGRRLYLVQGQRFEVAKSYKLIKLVGCGAYGSVCSAIDEGSGDRVAIKK
VSRVFADIKEGKRILREMDILTTLHHTNLIRLRNFIRPYGKDDFDDIYMVMDLYDTDLHR
IIRSRQKLTNEHYQYFMIQAFRGLCYLHGAKVMHRDLKPSNLLVNADCALAICDFGLARD
DQWTVSDALTEYVVTRWYRPPEVLGMGSHQYTNAVDVWSLGLIFAELMVGKTLLPGPDYI
RQLIMILHLLGTPTVEDMEFLSDEARNFLCAQPPQKTRPFTEIFPMATPEAADLLSKLLV
FHPAKRLTAKEVVEHPYFAKFRNSTEEPAPNEPYVWRHNEELTPESLRDEMWRIIVTHSP
EP*
>TCRU_886 hypothetical protein, conserved
MAEAVSCLDFKASFFQVSLLRETRHFFRCRVEDGTLVELTRLPMGCKAGPEILQIIITSA
IAVVTTVVRPLWAAPPSVRVDVWIDNIRIAGSKSDVTLREAQVLRNADSCRASLGRTANR
ALRSAPFWGCSLIALTVRCP*
>TCRU_887 Protein of unknown function (DUF3682), putative
MAMMMAGRVLLVCALCVLWCGAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAI
TVLLRSILPITVVEASDGKAGALATKNDSNSSEASDAGVNGSGSAAVPGAGDSDVGERAP
AAADGGGSGTSTGNHGTGSVSSGSSEGPSDPPAAPGVDSSAGSSDGKAGSPGTNPSNTTG
DSPTGNQTPAAAEANDTSPPERLAGKTSGTEQKGKEKEEEEENEKQQQSDETQVQQHQQH
EHPAENGEESAKDKTALRTNATANTGDSDGSTAVSHTTSPLLPLLLVVACAAAAAVVAA*
>TCRU_888 retrotransposon hot spot protein, RHS3, putative
MVEHTGLKYQFFTFVACVDWDARDRESMAAGLCPLYQLLHCDVEKLQFVVYCFGEGEAYM
FEKAIQTVTKYVDEEKCIMAVRSLRQRETKGHIIYDVAKKETQPAQFFFLLSYAWGMIAV
SFPKVTNYDKWEKQKGAARIIMNCPAEMDVKAMCAWMKRGLDPDEQTKYWKMVETHMEKV
GPIPRYIFDANKFLAHFAATEDALDGINPRDGESHFTHGGVRLWYSEDPSHKLVRVVRTR
GEVGAEVFLNAPISVCLGRRIPLYFWKRDE*

>TCRU_889 retrotransposon hot spot protein, RHS3, putative
MPGGQNGLQGGNAESLVSAVPQGDGLGRARQGFESETDEPAATRGREEERQRPQWTISST
VKEILLEGNTGMAKMWLSEFLRSNLDEEWVVDTNENVTMQEFVLRIPRVISAMREYWAKY
RHQIIT*
>TCRU_890 DNA-directed RNA polymerase II subunit 2, putative
MPLPTRGSDDAAYNTRKLALLPALIGMKGLLNHHIASFDHLINVELKRILLNESNREIKS
SIDPDFSIRYTNIRVCQPREIVGKGQLPKVVSPHECRTRDLTYRGDMIVDVEYTSRDRNK
RPCTETDIKIGTIPIMLKSSSCNLFGKTREELVAMRECPLDPGGYFIIKGVEKVCLVQEQ
QSKNRVIIEADDNGNIVAHVQSKTHYSISKCSVTFKKGRIVMVHRSFKEDIPIVVMLKAL
GMESDQQIAQHIGTTPAFESVLFACFEQAAALGVKTQDDALHFIGERRKETSWEVDDAQQ
RHIQKSKADNAAEFLGNVLLCHIREGQVQRDWNFRHKALYVCFMVRRMIEASVDSSLLDE
RDFYGNKRFETTGTLMGLLFEDLLKQFNRVVKTAMDQQLSKKDTTKPFNVKQLMESKLEV
IQSGMRVALSSGRWELKRFNMSRQGITQVLSRLSYIACIGMMTRLASSFEKSRKISGPRS
LQPSQWGMVCPCDTPEGESCGLVKNFGILSQVTLDMDDSFVRAAAHNLGVEEVDSISSRE
FLNYYTVFLNGTLIGIHRYPNRLCRGVRALRRSGRLHPHVSIAINDRQKSVQIGCDGGRI
VRLYIVVNHAKPAVTSAHLDQLSAGQCSINDFLAEGLVEFIDVNEANDCLIAVYPRDIET
YTTHLEVEPLSLLGVVAGIIPFPHHNQSARNTFQSAMGKQALGTIAYNQYIRTDTVLMLG
AYPQRPLCRTKAMDLTHYEKLGAGINAMVCVMSYSGYDIEDAQVYNRCSLDRGYGRCVVL
RKHEVDLERLPNGEYEIILPPDSNAGKCKALNSDGIASKGAIVRQFDILVNKYTPVASLE
PRPNPLVYKYPQPAVVDHVVILPPGDSERSMDVEQKIKVITREVRVPEPGDKFSSRHGQK
GVVGLITDGVNMPFNEKGISPDMIMNPHGFPSRMTVGKLLELVSSKVSALTGTFGDGTAF
GGDNAEDLGMHLLRNGFNYHGKDVFYSGITGEIMQAYVFFGPIYYQRLKHMVTDKMHARA
TGPRSMLTRQPTEGRSRSGGLRVGEMERDCMVGYGASNLLNERLLLSSDLFTVDTCRSCG
FLGYCGYCPYCNTKNTVSHVNVPYAFKLLLQELQGMGISTRLSLDFIGQH*
>TCRU_891 hypothetical protein, conserved
MHKDGPRLWDDTLMEAERMATDSKARYLQLPTPDREAEMQRTRSQFFLLLRERLRNTYLR
RISKLNPGEPLAWKYISGRKKASLPSLTSMLLGGGQHTYKTARRAANALNRIFFPFHPSH
KAVRFSKGINRQSASLNVGSSCISEPQNNNESAATSTSGSSLSSSSEPQDKNEAATTSGL
VAHLHSPLDAPFNRTELLAALRNTPYGKAPGPDEVYSEALRHISSKGLRFLLRCINHSWT
TGTIPVEWRRATIVPLLKPGKSPELLESYRPISLTSIVSKVAEKMVLKRLLWVWTPHPHQ
YASS*
>TCRU_892 Reverse transcriptase (RNA-dependent DNA polymerase),
putative
MQLAHLIHEVEHNRNHYFQVNLPKKSGIGNQLHYRPHRTLLVLVDFSKAFDSIDHRVLSR
LLANIPGVDCRRWLRNFLCGRYAKTRVGHRHSDRRPMLRGAPQGSVLGPYLFSLYVHPLL
NLLNSFAGVTADMYADDLSIIVKGQSREDAIPTANMVLQKLHAWSQENGLAINPSKCEAA
WFTLSTHTESDYDREGKRPLVVAGCQIPVMAIGVSRTTKLLGMDLVPRLTLNVAATKQCA
ATSQRISQLRCIAHKEAGPSPHDLRTFVIGYGASKLRYGSELIWAVATDSARNEMQKTYA
TLARIVSGVPSTVDPESALLEANMPPLHVLCLRARLSIFENTRACQMDWMRRPPPEPPPR
AGFRISSLSRDEPYAFVDAYTKDYGITESSPREERFFRSSIPPWFAASAHRATIGVELPI
DHSIADEEELIREKRRVSEEALALHSHRS*
>TCRU_893 hypothetical protein, conserved
MATGQYTEQGIAPLWHTDLLTCFTTQLTNKWRGTIRQDTHRYLLCGTRPSDLSGKDLITQ
EVLHRQELVHLARARCGESELWGRLYWAVRDCTNQCRFCNIPPEQSAYMRSNNDPNAPGT
DTVPPSAREEDVSPVSRRTLTRRRKEKCPHCDSTLTGFSGLVSHCRSFHPEHPPPPPELK
CDFCDMVFPTRRSTAPHRSRCAHNPDATRHRNSRARRRSLLPQDQPASTSTPIGPQETLH
HLLLECPGTLAVCQRLGIEQDLRLGKFSQWQLLHSRKLLSLLDHLDE*
>TCRU_894 hypothetical protein
MDSIPVEASSTPLLDRLLLKQGSTAKQPFTVSSAPADILRDTDTYGISLIASLGTLARAR
QNPSVLLWLDGVARRQFRWRKKDATAQRLFRWASRQIERREALKSHLDPAKGLSFQPTIN
GNFVIKRHGPHVAHEDLVQWEQRRFKQLEEKNCSQPRQMSPGPQKILQLRGTVEDGEEGS
RRKGEHNDDVSTPQNTKSNSRRITKDYPPLLERMQDDIAVRRQRAAEREDYARRESAALR
LSPRQVATQISRLSQHADTKRELFFDEDVTFTTKTNGEIFSPPDKPPGVSVAIASSFQLR
RQGDTGPSSAPRRCPPPEMPTARAATSPIQIKAFCERQRLWETRRRDRLRCIGEEINARR

EEKEMAECTFHPTVNVSPLIHTPSFEETRSLSMRIPFGALEYKSPTHRRPLDYEDINELR
LRQPRLRKTPASANKSNAHAQGRRNASLYGRAASCTPSRRAGTRTYVELHTPRREDSKRT
DRSNVMEKSSVTRRASQSQKDIGSGALDLDEQTLLDLSIWWKDLLMQELQVSCGTCKKRE
DDALDLRLQDWALETPFTCTLAPKTVIQAIQELIYLSAGESNAMALERIFGNESSWIQTI
LQQGGRVTFAQFIEIYKKLLHTK*
>TCRU_895 hypothetical protein, conserved
MHQPAAAGHGQPFYHEHGEAETESAGHNLQHAAAIHHNVPKHTRTFVVFDARRTPRAVLY
GEHGAANNMQIRRKGVHHVRLRNDSAVVHVEDAGQVHAKAALHEDRSARAPATNQHRPRH
DKPRRQKPDTVQDKRGAVPKPFVATGRRHVLRPANRRAQRRVRQQHTRVRRHRAMQHNHA
LQRRHIRHVDESVGHQARRALAEAANPQLRAARKHAVAQRHVQRVSERVHRAQVHRHSDR
SAEHHRVEARRRTPAANRHGLRQRHATHAAL*
>TCRU_896 hypothetical protein, conserved
MHRGRGRTARRLQQQAVKHHRARQQVHVAAKVHRRPARLQRPQHSAAHTQLRPQQRRRVQ
HKRRRHRVRQPAKLREAHRPRRHNRRVTDSHARVCRQVVHKHERAVAPGQPAHAHLQAPV
TRRLAAVAPHVDLRTAVAHAVPQFDAQRAGKHRRHVEHHGHAVRDGHAVHKHRVHGAANR
DGSVHRTAPQSQHHRMHSRHPRRRRNQRQHKKKRHTHSRNGTAPHTVPAARTRIHRRPHP
PTQTDINRAVVVCRTRPVDHNSCLANPFLQMGSPEIQSR*
>TCRU_897 hypothetical protein
MGRHQAEKVERRTAIEDGMRTQGMAEPHGATGGRLGAQHLMAHNSGHPQDNATNPTRPRE
QQEGIHGDAVSSPRRRTLLIRRSTLPSSSKTKRSRTRCVTIRRAMEGRASQLATSTWGPF
S*
>TCRU_898 hypothetical protein, conserved
MRPSRKRQAQRQHPWQQRSVAHEAQRAPSSSHSTSGVEHLPRDTVVHVALRQQHRPVIQA
HRRIKRHRVVLRRHKFAPHKRHSRARHAHSSTHRHRVLAQQEAVVNKRHHGAATGRNTAL
HRHAQPQRRLHRQPVHVQRAARRQRHAANQQHANSVAKHRRHVRARNGQHTPSQIHAVHH
EARGGVAKAVGAAVRNTPLRNQHRVHHGDARARRKSVRHHHAAARARLKPTDQHIGALAS
RRVGTPPNNVQARSAQKRAVRQRHVAHAP*
>TCRU_899 hypothetical protein, conserved
MDRCPITDPALDVGDIDAVILRGEYLSAMPGDEPSSWCLDTLPTNTTDARDPEETHFSAV
MHAALGCLGM*
>TCRU_900 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGTAGAAADGSEERADLSGIGGGSLPELKEIGKSPEGPQGK
KDEAGDVKEKKSPASSEDEEDDDADGDEKDYGVDDDLEEEEQEETVDPAETEIPNDPTKE
EASSPTQSKHEKGPTAAVPAEGVPTAQSPATAVQTTTQGQPPKAAPSPEDSPVPAASAAT
VTPAVASSEQGNIAAPARKKDEKQSEDIDPAQENEQPGPQDFVLVQHSQGIHESKESNSN
PRNPASASATANQRDATFNGHGEPAQATSSTKSGFESNDANSGTEEGISSDDPTADGAGT
NDTKNSQNKHGNTKETPVEATAMKGATATTGDSDSSTAVSHTTSPLLLLLVVACPAAAVV
AA*
>TCRU_901 5'-3' exoribonuclease D
MGIAGFYLWLQRWYGDCVEDVPEEVVKAALDGQPLPASSDTTQRFDNFYLDMNGLIHPCC
HDTAPLPEPESEEEMFERIFAQVDLLYKIVRPRKCLVLCIDGVAPQSKMNQQRSRRFRAA
EERIESEVFSAQCAEDVVKKGLPLPQTRSRWDHNVITPSTPFMERVGLAIEWFIMKKINE
DPAWRHIAVIFSDAHVPGEGEHKIMHYIRELRAQLGYNPQTSHVIHGMDADLICLGLSTH
EEHVTILRNQLTETFQPDHNRFCYFSLYKYRLRLREDFGGIGQMDFERVLDDFIFLCFFV
GNDFLPHVPLISIKTKGIELLLDHYVRGFKDHSYLTHGGEVNYGNLAKFLRFFVVGYMEK
LKQEYGGVLRAKQRAKAKVEERVKELERELEEQLNSLQKDRKNAQQVSNAAHKLLLSIMR
ERARLVVDKEPLGFSYVNDDHRDKYYEKKFGWDPADREAFEKKIQLCCAEYLRGTQWVMR
YYTTGCPSWDWYYPFYYAPLLQDLAHFPGKVKVKMTLGAPRHPVLQLLAVLPRLSVEALP
EELHDAVKDPESVLGVFYPEKVDVDFSEAHFSYQGVLRLPFVNNSHLQSACQKLVRLEPD
FGFTLLLCHESSRLSRALESLLADKDGEKVMKPIPKVLAAKVPIGGKVGPHEMEWPRHAR
LHCPDDGIASETSYGAPIKSNAACCYRYELNTQSLYRPVLLRELRKTMRGAPAPASTADN
LVKNPAVRKSSAPADSLRSSEKKLIRGAKHGREEPQEQNTEVEVVVNKKDTSTAKRRRVE
NTVREPTLKAEPPKKAVMRKSKTRRNN*
>TCRU_902 RNA polymerase IIA largest subunit, putative

MSGGAPLPPSQMDLQKVVEVQFEMFKEKQIKDYAVCLVEHAKSYERGQPVRGGINDLRMG
TTDFEFACETCHRKHPECPGHFGYIDLAEPVFNIGVFDIVLQVLKCVCKSCGALLMDTND
PQVHKKLQHLTGVNRLRQVVKMCGMKCRMSTDATTPEEAVVARGCGATQPRIGRYLGIYP
TLIIKATLEEQDMVWHADTARQVLDRVSDEDARVMGFDALRCHPRDLVLTVLPVPPPQVR
PAISFGSLKSDDELTHQIMSIVKRNNQLRKDKESDVQVAVDRSRALLQEHVAAYFNNASM
YYKPTKVNDTKKLKSLTERLKGKYGRLRGNLMGKRVDFSARTVITGDPNIDVDEVGVPFS
IAMTLTFPERVSAVNKKRLTEFVRRPVYPSANYIHHPNGTTTKLALRRDRSKVTLNIGDV
VERHVINGDVVLFNRQPTLHRMSMMGHRVRVLNYNTFRLNLSCTTPYNADFDGDEMNLHV
PQSLLTKAELIEMMMVPKNFVSPNKSAPCMGIVQDSLLGSYRLTDKDTFLDKYFVQSVAL
WLDLWQLPVPAVLKPRPLWTGKQVFSLILPEVNHPATPQERPPFPHNDSSIMIRRGQLLC
GPITKGIVGAAPGSLIHVIFNERGSDEVARFINGVQRITTFFLINFGFSVGVQDTVADAD
TLRQMNEVLVKTRENVEKIGAAANNRTLNRKAGMTLLQSFEADVNSALNKCREEAAKKAL
SNVRRTNSFKVMIEAGSKGTDLNICQIAVFVGQQNVAGSRIPFGFRRRTLPHFMLDDYGE
TSRGMANRGYVEGLKPHEFFFHTMAGREGLIDTAVKTSDTGYLQRKLIKALEDVHAAYDG
TVRNANQELIQFMYGEDGLDGARIEGGQLFPLPFRDNKEMESTYKYEYDETGAFNEKVGG
AYMDPHVKKMLRADPENVRKLQSEFDQLMADRDWARQMMDLEEREKLKLNLPVNIGRLIQ
NARSTMGKRSQVSNLSPVTIIDHVRKLQEDMLKLFPCYHKGVDGRIHNLLSRQRIENALT
LFSVHLRQLLASKRVLREYKLNDKAFEYLLKEIRTKYLQSLVSPGENIGAIAAQSCGEPA
TQMTLNTFHNAGISSKNVTLGVPRLLELLNVSRHQKHASMNVSLYPPWDKKRTAQQAQHL
IEYCTLESVTKRIQFIYDPDPRETVVEADRAILELEWSVMDESDERARLQEVENGSPWIA
RLELDADMFVDKALNMKDVKQAILRVDDGYVIETGMANDTKERTIRMRPKKNDGVDSIPR
LKHAIPELLARVHLRGIPGVRKALLKDRTTFTVDPATGKMKGEKTWLIDTDGTALRRAFI
GIVDEKGNNIINATRTSSNKVPEVCSLLGIEAARYKMLHELREAYLAYGLNINYRHYTIL
VDTICQRGYLMAVSRVGINRSEMSGPLMRCSFEETVKVLMAAAAFGERDPVRGVSANLVL
GNQARIGTGLFDLVLNMAALQQAVPQEDAVAPGKEVNVYHGLASTQNLPSSMPYRAKDHE
ATPFVNDASLFFREGVGGSSSAAPLTASTLYGGMHEASAVHFSQAYPAMGMLDQRVRASS
VSQPYSVMSSASVYNPASMQVPSALPSSVDYSEASSFHIQSSMAMLSVPSSPQFEAPQAF
GGGRFGGLSPAYVPSVMSSVATQPYQCVGDSESQQSASYVPTLSPAYSAYTARRSVVASR
ASASRVDQQSQQQKEDDSASYLPKSPGLHGLPPPVGEFSLTEDPEEEEERHQ*
>TCRU_903 hypothetical protein
MSRDEDVASSDAILTVLQRLRGNPVLRQYLHGHEGSCGCDGMTLSALRAKGAVTAEGTLP
RREDRESLVAFQARWSREEEDRLQNSIQAQRAFQQALQSLATCREVPGAVTEGRKRTVVP
SSFSAASVGRVVFSFEPQDATRAEEKTSVDDIQDAALTMQEKLAFRDHTIQRLQKELEET
RARYEADIASMRAAHMQSKQETGREMAELKMRLAQLALAGNSATNACENSGEFLEALEFK
ERLLQEMHDAFEHASEEWKSDTMCTLASLRLAAEDEVRGIVSRAEQLVGDLQRALDALTT
PRNDTAASFTAGVARRLLQDEEGLLLSMETKLREHVRMTVKNAVRSRVKDILRPLVERQL
LSHSELHDPRRLSPLHIVFSVRTARGALSPTPLALSTLPSPIPAEGRSGEAPAIFQPMTS
RQEQRAPSQRRELSAGGAAAPAVLDELSRGVKAHDINRPSDGISRPSWLNRFCH*
>TCRU_904 calreticulin, putative
MRAAIFFCALLGLATLSAVHGTVYFHEEFKSMEHWTTSKHRDDFGKVEISAGKFYADAEK
SKGLRLTEDARFYALSTAFPTPINNEKKSLVVSFSVKHEQDLKCGGGYIKLLPSMDPEKF
HGETKYWLMFGPDRCGSQNRVHIILHYNGENREWSKRIRFPEDKLTHVYTLHIAADNSYE
FFLDGESKAKGQLEEDWSLLLPREIVDETDKKPEDWVDEETMDDPEDKKPEDWDNEPAMI
PDADAKKPDDWDDAEDGPWEAPMIPNPKSKGTWKPRQIPNPAYKGVWEPRKIPNPDFVED
SELHKVPEPLTHVGIDVWQVESGSIFKDIVIGDDLKEVLDLVEKTYGGLKKAEADALKVM
EDMEKEKRKKEEEEEREKEKAEEEKDEEELEEKGDGDKEDL*
>TCRU_905 hypothetical protein, conserved
MSLAGQFTTFCRTHEQPINEESWAVFLVAILDVAPSTRQQHARMLRSMFEMNRTPLDMMI
LGLQKIAARPETKQARPLTKEAETKQARPLTEEERDEFIRGRVDWKQRVVF*
>TCRU_906 RNase H, putative
MIPRIRHRRKTLLVVTDGQSLLAALSKGPLSQTDWTEDRIWQRLLTLTRAGWSVHLQFCY
GHCGVHANELADQHATQTMESGQYTEQGIAPLWHTDLLTCFTTQLTNKWRSTIRQGTHRY
LLCGTRPSDLSGKDLITQEVLHRQELVHLARARCGGSELWGRLYWAVRDCTNQCRFCNIS
PEQSAYMRSNNDPTAPGTDTVPPSAREEDVSPVRRRTVTRRRKEKCPHCDSTLTGFSGLV

SHCRLFHPEHPPPLPELKCDFCNMVFPTRRSTAQHRSRCAHNPDATRHRNSSARRRSLLP
QDQPASTSTPIGPQETLHHLLLECPGTLAVRQRLGIEQDLRLGKFSQWQLLHSRKLLSLL
DHLFGTQMALYSQTRW*
>TCRU_907 dephospho-CoA kinase, putative
MLLIGLTGGIACGKSTVSTMLEKQHHLTVIDADRVVRELQRPSMPCTRKIARRWPGCVNS
QTGEIDRAALGEIIFRDPQARRELARIMNFPIFSKVMLLLVRFWWESMKQRMRGEGPLLV
VLDAPLLYESNIYTWFIDRVVVVGCKEEEQLARLEKRNGFTREQAMQRVRAQMPIEEKCR
RADYVIHNSGTLTELFFSVKDSVEWMRQQSGFKMNTIVFVSAAGGTVCLVAVVHLLCHLP
WWQ*
>TCRU_908 alanyl-tRNA synthetase, putative
MTEWPVNRVRQEFLKFFEQRGHKFVPSSPVVPNNDPTLLFINAGMNQFKNLFLGTADPNT
EFGRLTRAANSQLCIRAGGKHNDLDDVGRDTYHHTFFEMLGSWSFGDYFKRDAIRWAWEL
LTEVYKLPKDRLYVTYFEGDPENGIAADEEAKQLWLELVKPEHVISGNAKDNFWEMGDIG
PCGPCSEVHFDRLGGRNAAELVNKEDPMVIEIWNLVFMQFERHEDGVLVPLPKMHVDTGM
GLERLTSIMQDVHSNYDTDAWTPLFEAIQAVTGYEKSYAEIRDQNDSDATVAYRVIADHI
RCLSVSLADGAMPDSVGRGFVLRRIIRRAVRYGLQFLGAKVGFFSELVDAVVASLGPFFT
HMQDPRTVQRIKTVLADEEASFAKTWDVGLKHFNKAVADAVDNTISGDNAFILHDRYGFP
VDLTCLLAEKAGLRVDMNGFHAAMKANQLSAGRVAAAKTFLDVHQLEELKQMGIAPTEDA
AKYIWKNRTAEVKAIFNKKTGTFVDMLMPGEEGEEDIGLIMDVTNFYAESGGQIYDTGRI
VAAADAVFEVKKVYNLGGYVVHLGRMMTTNSTAVPIPVTSSVDLQVDYKRRIAIAANHSM
THVLNWCLRRVLEDEAPENYMEVQQKGSLVTEEMLRFDFSYNSRVSQEDLAKIEKALNEK
IQQGLVVYRKEVELEKAKHIVGLRQMFGEKYPDPVSVISVGVPVDDLLAKPESAEWRAYA
VEFCGGTHLSNIKEAEVAVILSEEALMKGVRRIVVATRDAAREARARGELLEKEYRDIVA
GGMTDSTAKSLSVLNKKVGDSLIPLTVKNSLREEIDGSVRAAIANVKAMAAQLREKATVA
GRAEAEAYDAVENPFFVKRLSDFGAEREALQAYADGFTNAVQGDVGVFLFGTDANKALAL
VTLPKAFTAKKLSAVDWAKAAIGKGGGKPHAAQSGLTAADVDVAMEKALAEAAKMKTAM*
>TCRU_909 hypothetical protein
MSADEAKDGKSPPPVEKEEAAMERDENDIGLQPAPIALVLRHQWAAEALTAMKEEESVDR
LSLVRSYYSGFLAIVSQSIHTLHLDSIALSRVQAQQQLITGLRCMPVPMNSKKRVSDSAA
SRARRRRAVDLSDGDTEQGNDKESSKGFLQRLRLNSFRRMNQELIERQRQVEAFAAGELR
RSAATRKQEELLSARRCSNEYKYSMAKSMAVRDMRARQRTEKYEDQQNTVQARQSSLQES
RNRKPCDSAAEHKEMQLILNKRRILFEKAMKELQKVVDWINERHHGGCVGDTAFMASVAS
SIESSFPTAFYQAPKSRCKKRNTTPIREEEYARLCGLKGAAIRSVVAFSQELSPTAAAPN
NSIARELQHLCISPILWH*
>TCRU_910 hypothetical protein, conserved
MRWLTRGVDLQRATAHVGGLHFFSTWNVALAPKRAVGGRGRTHTAAVHGKTSSLESPPPP
AALGSARSRNSAALSVGDNRFGTNRSGGKSPKEAAAANKNSEDVDVEEEERLLAEGDTRL
AMRLLMQHHFLYQHNVRRPEERRLEEEREMLREKHRARMERIEEKTRNAMQLGPDVSVDG
ILPLYGRGNSAAAALASKPSASWMRLNPVEAETGDNDGDDGESRSITGALLTKPDMSVYS
VEHDHRIRSSEVLDEEQRRRREELKSGDATKKLWSQEELEMGGGLTPQRVMESQMLEDED
QDFAVEAYSNDYDE*
>TCRU_911 ribosomal RNA processing protein 45
MMAHRCAFQTIASPALTQREVEFTKSAWIAGLRPDQRGAQQLREVNVDFPLLSRDVSCVR
CGGTIVTAAIACELVEPFPCRPKHGIIDFSVRQPYTERDSSAKTAELKKLTAFLERLIKG
GGVVDTEGLCVLPGRRVWSISVDVTVLNDEGNVTDVAVWATVAVLLHYRRPELTIRGDSV
ILHPTHERDPVPLSIHHTPLSFSFAITMAPGDRNKLARGRRDSQEALEVVVDPTFAEATA
ASSSVVVAVNAEGQVCSVSKSEGSCIHLNEVNHCMETASLLAPHILSLIRDAMAAHDKRR
QEVLKRMFLWAQKRSGVTREVTEPESAKKLKTET*
>TCRU_912 hypothetical protein, conserved
MDASHIQDEELGASEVLWSPDLDARWHLLRRHITPFEKDRMAYHSAKYQKPVFVHMNPII
WRRLVEKQGAYRAVDLMLMLGFAPAPEGAANLVEWIEREAAVAARGTAGMSVATTASSSS
SPVSNGGGLLPGRRSLALPTVVGDEPRTNGGIRFWVLNHEDSRPSSFGSPVNQYISPHST
APGACTSSPAHGLTVAPVSLPASASAPAQATAVVGPQTEAEASASRIRNLEAEVRELTRQ
IRLLKSRDSDRDGSVLSDVTSQNEMPQPHIIVSPDRPFIASTNCHALVCLPVNYLDPDCA

PYVVSLGVSTGRTLLACSIVEHRYVIFLAPPHRRGSMAVVLLCTRDGTLRPYTRAVWLEY
RAEDPPNTLTHHAVNQLLQEIPLPSSATVVDPNPSEVEQTKSESAFEDDNTFCDTDTAVS
TSDQGLESEPRLPLTKEMLQLIPNGIITGPRVSNAAKSGQANTNGTNLSVVGSESSLCGG
DREGRARAGRLWNDNDEMKPGSASMSTGQPTSYQRGPQSGFSDEETTQLAFNCMTNRTEM
SSSRATSVISIESAVPNGGGGFAGIMASRGWVRRYLQGSPRSSQCFGTNGNAGSLSATAT
ILDEQLQCAESQPSWPRGGSVTSQ*
>TCRU_913 kinetoplastid-specific phospho-protein phosphatase, putative
MDTQSAVLSQLRLLKLSNGARVVDSVQRPESTPTTSVAAALKDVMGGRGLFNAVPQQADT
IKAGNSGRGSNTTSPMTLVTGSAGSSSHPSTSELKLVRGNQGSATATATATGGGGGKTT
RNMRPTPRSLQQPMLNQEKEKEAVTPAQSPNNALKQLLQAVSSTTISTSRDAGSSSFPVA
IALTNVEPSAVRMSTLVAGTAADPRLLEPIDNFNAQKPIIRTAPPCEHRYIVVGDVHGCP
EQLEQLMLKVNYQKGKDCLILAGDLVNKGPDSIGAVRVAQKLGAIGVLGNHDSTLLNCIA
RCRKPKLTVQEELDPVMQLALSFPQGCQDYLRSLPHILRIPKYNVIVVHAGLNLNNSIEN
QDVFEIMHMRRLEKIGGSEDKKARTITKAKWKAVVKGTRGEPWAEHWKGPEFVVFGHDAR
SGLQEHPFAYGIDTGCVYGSELTCVVYGPDSPKGTLFSVPGLPKFTNEERGLPPPAAPVY
EQYIEDMERQILRPTSRATPSVVTNDYKPTFLSVPPTTSSPATSSTFLGASGGCANGKTI
SKQCGVERATLLSLSQAGELTAVNTLMSLPIYEAAWMSMLNNEAEDCTITFWIPFVQGIV
TKLLNVSAEFPMDCVDDVLQLALEVCDELETVRKIVAPQLHVLLTREGSGAISLSKATMK
LLRLITMTQQ*
>TCRU_914 hypothetical protein, conserved
MAAPSITDSECDNTNDGKNNDEDDDDLHRRADYLRVFVHESREGLNAVLTILGLAEILGF
ALLPAVISAPCVEADPFTVDFTQQLSKGCAAIPALALSHVFQRCLACDLLCVLSRPPPPV
FFWCPIRSTLRCGGYLIAWPSTHVTMLNGCVFCLAGTRETSVCADNSAKVFVDGSGRK*
>TCRU_915 Mucin-like glycoprotein, putative
MKTCRLLCALLVLALCCCPSVCVAQDTEKVEESAKTTTTTTTTMQPPDPKTNPKAGAQAN
LGVTISSSSSTEGIEGKDQPSPHAPPVNKPAEKPGEDAVAGKSLTGTTELQSDTNKSADH
TDKEDEEPAKTTTTTTAPVAPSTTTTEAPTTTTTRAPSRLRETDGSLSSSAWLCAPLLLA
ACALAYTAVG*
>TCRU_916 Concanavalin A-like lectin/glucanases superfamily, putative
MINYVLKSWAQLDSSFSESFTPTAGLVVFLSNALSGGDTWIDDYLCVNAIVTKNAMRAKD
GFEFTGLGSGAIWPMSIREHNGPHTFVSCDFTIVARVMIQNFSKLSTPLPGACLDAPVST
NFIGLLINADSRWETVFYGIKTASGSTWEPGKEYQVALMLQDGHRGCVYVNGELVGSYAT
IRTPETRGLESHSSKLGEAREAAAAVRR*
>TCRU_917 hypothetical protein, conserved
MRDSFAAPSLVRAGGVTIAFAEGHTEYKGSHYRLNVRPSDIVAGYINAAETWPLIAAENN
KDKWMVRTLFSTVNEEDLFGAACNPTAIEKENKVLLLVGSYNM*
>TCRU_918 hypothetical protein, conserved
MTKHVDRSRTPSRTSAGPYRNLSRPRVVGTYCDPPTVARSVEFASSTLERGGIAPCSTIT
PSTDVTFVMLTKACGIRRAVLSLRPPIRSCAPPASTQWRSVTFSASANASIERRSTATVI
GPLNTTESKHAVARPPPAVTDSVSVTPLTQPSAVSPPPLALAGGTSNGRHASPTPPARQL
HTQSENDAVSASKHASAAAQPSHGTTLTEGRPAVR*
>TCRU_919 hypothetical protein, conserved
MEQPRDRKTVPADRDVCVRWKHTLRAEQRVNKRVSGDDDVQRPHSGVHVAQQQQHGAVPP
RAAIERDIRHVARHPPNQHRQAHAAPAERHVAVAQPRQAAAHCLRNLGVHHVADALTNRR
RWWRWRWRWRWRWRWWRASRHRRRDAHIAVPSSSALALAVNDRRRQRSKAVALLRALPAR
GNRRHVGDAVERQFSRRRRLPSRDRQAPSKKPVAGVSPR*
>TCRU_920 hypothetical protein
MGRHASPWPPSAHVQAQPSLEAVVVYAGKHDAAIVHGSLQVKMAALYTDGMMYSTPSSPF
TVLHAAKIAPFVISRDPLGIHSTVGVPVLEINWLPDTDTVESRRFTVE*
>TCRU_921 tRNA synthetases class I (W and Y), putative
MGDMYPTVVQVQRMLTLSAVKNTFGLKDSDNVGKAAFPAVHAAPCFSSAFPRVLRRLAGD
PPLKCIFPCAIDQDAFFLLARNVAPRMKCCAPALLHTKFLPALKGAQFKMSSSAEGNGVI

TLHDTEQEVRKKVRKAFSGGGGTLEDMRAEGVNLHADVAYQLIRFFCPDDNLLAEVTSKY
SRGEMNSAEVKELAADVVVRHVLSGWQARRAGVTDADVEHFSGIRSILL*
>TCRU_922 Fungal tRNA ligase phosphodiesterase domain containing protein, putative
MLDGKKVQKAFHVTTLYLRRDACKDPVLLRQLVGLLGESIELTLTSVASDPKGTAIAVRN
EGEVPCENVHPHITIANAPGVPPAHSNELLDDSHADDPCRTVDSLPAGTRVTGTFVFRWP
*
>TCRU_923 retrotransposon hot spot protein, RHS3, putative
MLASKDNILPIFFGWFALKSFTESAFVRAMATKLTEFEPPTGRQAKPCVLKLAPELHPKG
DEGLLPSEYEKTIRKIKYGVLCKPWATNLPLVDGFFFVESNPMTLVGLRMATAGGHHTTA
STVRPFTECLAAYFNGWEELSRDMSWDIMYTTLRQHADG*
>TCRU_924 UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase, putative
MAKTKLLTLRQKLKRVTVLLILFIVATTVLTLRFDTAADDEVPGPNNLRHSHATAAEDAA
LAYIPRSIVDKWSRREYLIVLGVPSIDEEARRTQRNLQRTTCWRFPGVATRANDFTGAML
VLYVLGRHPSHGYDYSAALLEEVAQWNDVVALPMNEGLVTTNKTVGHYGFFGAEANVGLS
RKVYMWFDLALRLFPTTRYIAKGDDDIFLRVPLFVAHLRLLPRRGIYMGVHIGVAQFANK
RFPGNTFMFGWCYTLSRDVAEALVSYKPLRHLAYLPYSEERDHEFALLQFHNDDAMVGWV
LEKELNYKPMVYVKMLPCHFHDARNETGHWQVVPTSMCVHHVRGDDYAALMARFGNDTSP
VGRVERVSEDVIYPCCD*
>TCRU_925 hypothetical protein, conserved
MGDDNLMGDDNLMGDDNHLMGDDNLMGDDNLMGDDNLMGDDNLMGDDNLMGDDNLMGDDN
LMGDDNLMGDDNLMGDDNLMGDDNLMGDDNLMGDDNLMGDDNLMGDDNLMGDDNLMGDDN
LMGDDNHLMGDDNLMGDDNLMGDDNLMGDDNLMGDDNLMGDDNLMGDDNLMGDDNLMGDD
NLMGDDNLMGDDNLMGDDNLMGDDNLMGDDNLMGDDNLMRDDNLMGDDNLMRDD
NLMGDDNLMGDDNLMGDDNLMGDDNLMGDDNLMGDDNVHSEMRMTHDRFSRKLSSPLVTL
LLVGVLLLVRLKMYYREPKCH*
>TCRU_926 hypothetical protein, conserved
MLAHGPLSKAWKDSTLVGRIANLRAPRIPNFKTQVLLPAMGAARELGHQQGLITAERERL
NIDCANAVADVRNRNAQLNSQVEEAHINLSVRESTIAGAGNQVLELQQQLENTRAQLRER
EFNLGRLTGQLQEREALHNAQQPARDAETAGRDDAPATRYAANDGVSTLPHQTDLLMAGG
VPSSAARHSSAAYRRPHGNAARPHFHPSTPLPYRASLLDAQLPMEEDRSFCAFDVTTWPS
RIWNEGASGVIIDLRCAYQCWQQDNEKVELAFDNLVEWIGVLDGGQDPTDRLMNLGRSLL
NTFRMQLMMASNPGIRLSKVRARPYTAVHQMDAYARAAQLLVDRRETQRTVRCQRCHTYG
HEASTCNVRPRGNYLQHRRPSTNGRGAAARRS*
>TCRU_927 hypothetical protein, conserved
MQDTLRKQKAYGSYDCPSLTHSGSLECHGAFHKTGCVKTRCSSREDVQFGSTRDLAVGET
RRTGRPSPGHSSIFVEVHHTADPGVVAGRIDVKEETAAGQELWLRAEERFFHDFCHNHAA
TITRLATRTRLATPQDEHAIPLQQVNVPVLNLEWIKSRLRPAALERLMQVWGLVGRSPLP
PSSSGKPREGSRRIPTTDAHLLQTAGIIEDDSSTITGGWMIPFSVVEEKTTGSRRRWIAW
PRDKNRDDPYEANVPLLHISHYLPPVMAEAASCLDVKASFFQVSLPRETRHLFRCRVEDG
TLVELTRLPVGYKAGPEILQIISSAIAVVTAVVHRLWAASSLVRIDVWIGNIRIAGSKSD
VTLWEAQVLRNADSCHASLGEDRESGATQYTFLEVQFNHTHRAVSLSDKFVLFVCAMPAP
NYLTIAEMEVVASRFLYAAANLCTRLCDYYSFIKAVRRRLSELNQGTVQ*
>TCRU_928 hypothetical protein, conserved
MISMTFANGLRLCGFQCGMEPRLTEASWRRPDILIVGLDTYAITDVTVTYAGRVTAYVSE
ESMEEADALRAARDRLTQKRQKYRYWALANGLDFEPFVMLTNGAIHPASRRWLRRILGAR
VLAYAGAQWVAERQ*
>TCRU_929 Endonuclease-reverse transcriptase/Reverse transcriptase (RNA-dependent DNA polymerase), putative
MHHPQWEPFLETSPSEVAAEFLELCTDAGLTLVNTPGEITYARGTRERSCIDLTWSKHLT
VSDWSASVSPLSDHYMLTFTPHQAFKDTIPSAPPSAPKFFYSWGKCKWDLFIKDFDAQLP
AYDYKKQSTGIKAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERIATDSKARHLQLP
TPDREAEMQRTRSQFFLLRERLRYTYLRRISKLNPGEPLAWKYISGRNKASLPSPTSMLL

GDGQHTYKTARRAANALNRIFLPFHPSHKAVRFSKGINRQSASLNINASFLFGQQNNNES
AATSTSGSSLSSSSKPQDKNEAATTSGLVAHLHSPLDAPFNRTELLAALRNAPYGKAPGP
DEVYSEALRHISLKGLRFLLRCINHSWTTGTIPAEWRRATIVPLLNPGKSPELLESYRPI
SPISIVSKVAEKMALKRLLWVWTPHPHQYAYRSMRTTTMQLAHLIHEVEHNRNHYFQVSL
PKKSGIGNQLHYRPHRTLLVLVDFSKAFDSIDHRVLSRLLANIPGVDCRRWLRNFRCVRY
AKTRVGHRHSDRRPMLRGVPQGSVLGPYLFSLYAHPLLNLLNSFAGVTADMYADDLSIIV
KGQSREDAIPTANMVLQKLHTWSQENGLAINPSKCEAAWFTLSTHTESDYDREGKWPLVV
AGCQIPVMTMGASRTTKFLDMDLDPRLTLNVATTKQCAATSQRISQLRCIAHKEAGPSPH
DLRTFVIGYGASKLRYGSELIWAVATDSAKNEMQKTYATLARIVSGVPSTVDPESALLEA
NMPPLHVLCLRARLSIFENTRMSDGLDAETPA*
>TCRU_930 hypothetical protein, conserved
MLKSFQDTYIEYLKSTLHEIEVDVSIVGETLASLGLDERSISDILGGSLHACATGASSVS
SVSSDRDWDRRLRKGPEECSTISSTSKKSLLTPQREGMLRVDIGKFDREQMGGAALPASS
SSSLSVIESPRAGRGNFLHRGHDASCNVEEEDEEALTSPATAWDDPIVTPDRRDSYKEHL
EALEKLLGVVWRPVAGGGDDSVPLEVRSFLCRERVQNLLLSQFKARGIALPASPPKRNTP
HQRFKVRHEEKKQPEGSRNNSRRGRVKHSQCIRHFGSLLETKKSPQVGFRWQCEFCARLD
DKPILPSVSDHPRQPQVTPAAMGNACGVKMRPQAVNTVGSGRICTKLLATTLLYREDRVK
KALAYRDGWNASGCAER*
>TCRU_931 hypothetical protein
MSGVGDSGGGGGVKVVTHLDAAVSCYLSSPGVTPLEVYLTKVEDAAISLTQEFGSLVFSY
EEHASRAGRATLECSTALLQGTVFLEERLREAMALANGVVEGMTGIAAAVKGMEDLLSEA
RKVAQDVSLVEDAIKAAEAARGRDANS*
>TCRU_932 hypothetical protein, conserved
MFAKVSQDPGGRLGIIYFASVALSSAFVAWIAQKWWKRQHGTTGDEGIFDDVEESPLFDP
NFVFPAKLGVKRASDAGRDLECVGPLSMAEREGALRMARGLMRQLGGGAYNEEGENNNKN
EEEEAESSSSGDETNVSLNYHIATELEKEARDSLVEAVIHSELLKMEAQGKRIDPSECAN
ILAKLVEYFDISNEREKLRERRIAMRPNETTNNGFLWANSDGYNDRIAQQMAKINEAYAG
FFSRETEMDQRLRAFNKDGAEERFEMDWDGADDDDEEADLMNYLDQDDAAGYGSRMELRM
KAMGRDSLRMMDVDGEMNYRDDDDDDDDDGECEEEEESDDIYEKTGFERMLLDKLHQLA
ASLGEKTTSSLGTGAAELPRSNGTVAACDAEREKEKEEGSSQNEWETESDDDDDEDEETK
EK*
>TCRU_933 high mobility group protein, putative
MSTELKSGPLPADVEEVIANIMREEGVSFLTSKILRLRLEARYRMEFTSHKAAIEGIITK
LMQLPEFKKQLENAVKEEKAASSIGGKKKKRSASAAADERNAKVNKKEKKPDDYPKAALS
PYILFGNDHRDKVKEQNPGMKNTEILQSLGKMWAEASDAVKEKYKKLAEDDKKRFDRELS
EYKKSGGTEYKRGGGKVKAKDENAPKRSMSAYFFFVSDFRKKHPDLSVTETSKAAGAAWK
ALSDDMKKPYEAMAQKDKERYQREMAARAS*
>TCRU_934 hypothetical protein
MGDGDRDGENFIDFFLDDFCCLVSRFLKISCRTRVGLVPAPPPASPPSSSPSFIKPVTDA
THVEEQLDAADSMLRLMSDAKPRVKTSEKKADFPTESAVFLLRLRSLLERQLNQDQQSDV
LPSTSKTTRSTRGESPSGGESKFSLTCSDAPCRRVRKHVHRFPNAMVEDIRGTSTLNRRI
ATEDAQCQTEFSEMLSMGREPSSLGQGVAVHLRRRVSSLSDAHGRLALILQQHTISSILA
LGHVLAEANRNPTKMQECDLRIQTRYVEGIQGVLEREQVRLNKECSNWNGIKEHEQLHFS
EIVQVLERLEMAVASVDFRAFVVEEVDEGIKGCDVHDKPVSIEGSSVTHLVDFFGKSCAG
FVSKLVVYCLQCFSSALTSASGSPLRWSYLEKVLFLTDSESPVPTVPMEMSRTPSRGSGD
MDVDKTPTQERSESVRACDVDELPKRRNTDTPWQEGENQLLRLMQKFRPCHEYEEVRQLE
IPV*
>TCRU_935 U2 small nuclear ribonucleoprotein B, putative
MGEPKQTLYIRGLPDKVSEKEMRRALYLYCTQFGPVLEVSYRKSRDMYGQAFVVFSDVAT
ATSARRELNERQFYGRLVQAFYAKRQSFSADPGERRRRDLRRERESAAKRLREF*
>TCRU_936 guanine deaminase, putative
MTVFCGTAFHVPERHKLEVLQDVLIVVSDTEGIIERILRPSDCDYHKVKEEAREAGNLVT
LRPRQYLIPGLIDLHVHAPQWPQAGKALHLPLEEWLQENTFPLEAKYKDVKFAEKVYNSL
VETLLANGTTTAAYYATIHVESSLELARICLQKGQRAVIGCVAMDIPGACPDFYRDRSAV

DSIDKTAVFVEAVKALKGNERALVLPSVCPRFIPTCSTESLRGLGELVKKYNCHVQTHCS
ESDWEHNHVIERFKKHDAFALDGFGLVTRHTILAHSNFLSTEDMDLVLSRGAAVAHCPLS
NFYFSNAVFPLKKALDKNLHVGLGTDVSGGNSPSILDNCRYAVAASRALEDGVDPKKDAK
ERSGWKGARINFIEAFWLATTQGGVSLDLNIGKFEPGYAFDSLVIDVDARSSNVKVFDSE
DSLEHIFQKIVYQSTSANITQTWVGGRLVHQL*
>TCRU_937 cytochrome b5, putative
MLKGLLQIIGLKKEWPVFTLDEVRQHNDRSSIWIVAGNSVYDVTHILDTHPGGLNALLRR
GGGVKDCTEDFYFHSRAARRTWNSLKIGELDLGEAMGIGTLAVSLTDSRDGSSAPEASPV
SHACASWECDGGKNCCCTSTVETHGSTSEPVPERLCSECLHRHSAWR*
>TCRU_938 hypothetical protein, conserved
MFYADTIFRAALASHRPVLASSISARSVVRRLLGDRGYRVPNVGAMDSVVTKTKGRGLPG
TACVVGRAALYVHHGNPEAAIAEINRVLPEIQEADLKRHAIGIRLRAKNDLLDIKEAALK
VDGGTTELDVCTLRSAIREDYEALKSASSGCWLVEMAAAEYALYEAKAEEAYKVFCDVAE
KTESFIASLEGLHISSEVASAENTQSFSLLSFLLKRAHDAEGVNPSASKIVEEGIKNILN
DDSVKGSLATFKKELGVSLTDEEAVEVACVLDAAHVRHHFHDFFPLEGEYNDWRSEGAKE
AKNEIVQVFTPQAVVISNELLENVKKSVPYKPFYAPEDQLRKFLSSGHKNYLAELRATFG
PSPACVLAKSDEAYFEAMNILKQGPPSADTAGDLSYPQKQNEICRKLARQLLYRTKVNTA
VALTQLDHLNEAVEILDKVIAANEFVYMWRAFLARGEAKKRLGFISNSDKDFRQLSEQKK
TFRRKM*
>TCRU_939 ADP-ribosylation factor-like protein 3, putative
MGLLTLLRKLKRNDTEPRILILGLDNAGKTSILRKLSDEDPTTTQATQGFNIKSINCEGF
KLNMWDIGGQKAIRVYWPNYFDEVDCLIYVVDSADRRRLDETASELENLLQEEKLREVPF
LVFANKCDLATALSPEDVSTALNLQSLRDRTWSIQKCSAKTGEGLHAGLEWAVKNLKK*
>TCRU_940 hypothetical protein, conserved
MTVARDASSMPIVAHFELHTSKVGHDDACMHWLKGRYFREGNIGVTQQKKTVEDTDILLS
RMENDLAACATHRWAHFSQRSPVYEATSPRTDNTQLNKVEVRIEECNATGKDGEFIVSVQ
DPHSRRVLGIREDKMLAEPSRHIFTEAVRKRNQTRLAMEIEAAGRLHDVTNVRRPYFGGY
FLPPHSVGPTRFLLFPQWMHDVHLDATQPQELPYFLRGTIDRKSGCTSDEGAEMSEDKRG
PLHKFLKSIIFNASFARKFPETMPRWGIFNGVDALRLELYANNENSERLFSSCANAEASK
NTQVKHKSRPLTLNFCDSGARLAFFFRDPRYSLTVSNAYRVAQHSSKSSAKQRAIASLTV
SDNYDSAVQRFSTPLLHRWFPSARYQLQWSAGPGVEYVSVGKPWTVFGKLGTEWWVELPF
FKRALFYIRNQSALVQPLSLRRTKEVDERNDDAHNSAASPEDNRSSAHSYFWATQGPRWN
PSLVRGFKDDYPSLHYASRWYTLISAELASDRRQRDKGSKTWQVPTWMIYANACFTDSFA
TPPRASVGFAFSGTPRGTTDAFNVFTPSSFECSFNWWLKFYQGRPSLVSGIVSGQRAEES
TLRLSPFETFRHFRCGLTWKA*
>TCRU_subunit mitochondrial RNA binding complex.1
MYRFCCRGAVWRPINRSHVLSGLAWCASQGVPPADDGKPRKAARHVAPSDEDVAEMLTAD
REVPTSRTGSKLSDAAMEFTRVDSVDDTGGRKHAEHFRDATDFDGEEDDDDDEDIDDVRR
RPSHVHGHGERRTAEDVLTDENELPHESDATASSPPIDILLGAEDEAAEPSVLHPIAERQ
AVARTMSAVELVEMLVLYLRATENPRLVSAEEEHVLFPVVMERLNELHLGQMLDIVECHW
ARSTLVRYGITFKDMVRDRIAMLASVAGKDAAQKPKRASRVDKGFGEDDDATNDVDDDVD
DDADAGEVYAHEVKTPTLDPILLQARDEMNAEGVLRCIIVMGMSAGRRKRDLQFFQAMGM
FLVHHVNHYKDPHDLVRVLTAFARAKIVPPKGFLALLGRRFAVLNKRKPLGALPSYRAFV
NLYKMGHDQMNNFRFLANCIYEFMDANVKSEKKRQRLLELQKKSGTTDAASADATKTTAQ
SESTESNEDGSTMERMMMAGDLDPQLLQFIKARERFKRLTELKPSMFTKLLLVLARFGAP
HQQYLRPTIVPLILPTLRCFPPPSFSRLLRALYLFRTTDLELIEPIIDYLADDLGVQSVI
PEDVLEMIRIVSPAEAPVPRNLSKILLLCESVYAGVDAAPVRLILPTDMCSVAAALLRIQ
MKEDVPLDALDPLTRLMEVFADRLYSLLQLHVVSLTHVDIFADLCRQQQHPDVSGKIARL
IQERRRLSSTEGDDDYYSRLDIDVRETFHKIMVVNDFKTYGQYRPTPGVLQVDFKQALTE
VSAFDVLEATHLFAQAFPNTLRPTVVRHLSRSIIAKLGDSGEEVITEDNTMVLRPPRELL
LTKEDLLKFVELVQATPLKRVKESPVVWRFIEEKARRLRMSELLKTVEQQAVVATA*
>TCRU_942 mitochondrial RNA binding protein 1, putative
MRRFALATRRVTAVTSPVRLCFRAASVPASNPVAAPETTTVREPQPRQKENVLKVPSMTL
AQLLTSVVGEMQKKSLTPTAHENVSQNKTEGSSEEAAKDASKEAKAGLLPYKLSPEKFIM

AVSTYIRREEEMALMSRSNFVAMRRQYLMLRAKQPRLSSSQRDILLHEASCIVEKREVPL
NVAARLLRPRWPNYFMDVVGVRHHAFLAQSLRGWTVELIRDGKLTAKEARRFLMQCPRLF
FGQVSLMGSVVECALSDLNTIDDPELLIKLMWSVNNAKTHAPDHFWRRIVDKLAMLNRSM
RDQVGDAIRIEKGKDEKKSEEEVTEANSVMVGHVFSGLTTRQLFRILRVLRKERWCGDVP
VIFDFMDKALKNIVFEVEATQVADTNSSEGPPSRRTVVQRVKKASDLSPVELLSLLSIAG
ELGADFHVSLARLSEYLLSPMTRYLDRDHLLLLTTCVRRTRCDSAQLVQTIVDTIVRRGV
TYSSSLALTKAVLRTILQKPALLSHLTLAPFMDHIFYLCDTHKRHLRAPQILAWVELLYA
LSRLYAPSSSVGVRVRAAVESFADPLIAMLAVEVVPTSIVSRMLEYTVILGMRKQPQYPL
TAKLWEDRNTLVNGRRAHADSLGSGDENDTAPPDHGPEEDVTSDTMEMEEVPKGEVTKSV
KRVYDDLISVYERQTVMQMPLLKGEKERVCETFQRVGLYSIFMGADIMKQLHLRDAASTS
SASTLRHRAPSSRPLSTWIERNVASIVDTRIRSAKISPESTDNDVLRLFGHRQCDAAKVR
RFQVLLMSSPLLLARESRSLWEYTSELARRFGGAQEKSLAEEMLRKALH*
>TCRU_943 rRNA methyltransferase, putative
MYRCRSAHKLLELDAAYHIFAWPCRTVVDLAAAPGGFAQVALQRMACTSLPTSTEDVRPV
VIAFDQRPIEPMEGLFSVTCDVNDHPRVMAQTARLLRTLRGENETQRKDVHVVLHDGVSV
VKGQSLFSVTYGQNQMALGALRLAGSFFALHTHHTFARRLACGDVKHHDDNNRSTSKFIT
KAMHSSHFNTLLEACQLYFYDVHVHKPSECKPESLETYIVARGFSARRWLLEEKRAKDLH
PHLSLPPRREDVVSGRQMMWRCWGCREVRLGTSPCPLCSAGH*
>TCRU_944 hypothetical protein, conserved
MEGCPGGKGRRAHRVTGACRCGEDSVPGVDPDIGPRVAALRTGAMRLLPTLRQACTRPAD
HKEPSVSVVPSPPHCGDRPASASAGTSSRREHRDSLSTSERRIDVLLPNLRLSALVRPQY
EGTCRTCSAWRYNSLRGPPMRMPQWRHRLLNRCLARRSPPKLPSMPAGETLRKHKRGYSR
WTRLFRHRLITDATGC*
>TCRU_945 hypothetical protein, conserved
MSVHVSCSRTDGRLGWRLPNETGWRKCANKPAEGGGGEDECALVCIAAGYVYKDAENPRL
CAPGGRPSVVWTGIGMFLSENVKNCSSAAAPTAAVVGQAQSGVGSPPGEAAEAPQKKSPE
HTDEGGSYPSLSENFAVSLLTSTDTNEHVASAPEASSQTPSSPSGGTATGMRDPGGADSS
DAATVWVRTSLLLVTALICAAVR*
>TCRU_946 hypothetical protein, conserved
MFKGKTTTRSSTWEPRKEHQVTLMLQGNKASVHTDGRSLGEEEVPLAGEKPPEVLRFFFG
ACGGHESRLTVTNVFLCSRPLNTTAMRALRERVPAPTREAAPTPPEKIRVVDSVREHVAG
NITEEK*
>TCRU_947 hypothetical protein, conserved
MDAEYQGGQLSKLFSSDVVAGCIDSAWNWSTLVGEVKKDTWRAHTVPGAAEGEEGLGVVL
RPTTITKGHGVFHPAGGSDVSYEGVRWREGGLEPKLVVGDVTNPTGGRQSGSNGATPNHS
RN*
>TCRU_948 N-terminal conserved domain of Nudc./CS domain containing
protein, putative
MSADERFDTMLLAIAQQHDGIDSILDTFFSFLGRKTDFFTQPQKARESVQRALERHLVRA
EERLQKKQTEEALRKQKDAASRVEVLEDEEEAASKAAAKAAAEAAKRKAEMEKAANAVAN
AKEDEDGMKPKGLPPTAGNGFDYEHYMFSQTLQEVEVRVPLPIANAKGRDLDIVLQQRHM
RVGMKGKTPIVNGDLYAAVKAEECMWTIEDGSTVVITLTKMNQMEWWKTVIAGDAEIDLQ
KVVPENSKLDDLDSETRQTVEKMMYDQRQKAMGLPTSEEQQKRDMLAKFMAAHPEMDFSQ
AKIC*
>TCRU_949 F-box domain containing protein, putative
MPHLFSDSSVSFLKRFQFIQRGRHGEVARQGTIPTDTLSLMDVLLHTNSTFTLFFHLKHA
LDAAQRSENANDGTSSARRTDDLANASHHLQEDMTEFDGGLAEEILGPILLSFLNFYLDR
SIDMMSIRRTLCTLFETTPYLREMHDDEDKNQPLSSNIALLLLNLSRALLHCQAKGEMSL
RKKNRVVQQHALPLLPWLRSCARNATQKPTWYWWASQNSRTLSILTNGAFVYRSTTCEAA
ADEDAILVSYAAQPAPRKRGRGVDDDDVMEAAVEKNRRISSTSQTHLNGGKFSLGVVPIP
YAVQGIILEYLSPRALSTACLVCKAWWSLIDQSLTLRFYLFASQAVTRVFIQFFEDDWGK
AWVRLNELTTFRRLSLQRMYICLVQNHLHRQRASAASIGDFVLRLYNEFGKKSPQWEMLE
GLWNAMEVEMKIMPFLALRDVTFSSPLQNGTTPCCCNDISRAAALVQMKQVLRLLQSSDY
PFFSLFNELLRRWSVLLSAVHSPPAAMS*

>TCRU_950 pyridine nucleotide-disulphide oxidoreductase, putative
MLWRLFLGSVVGGVVSACRSNIRTTLAATAPTLELILDPSKDVVPVRCVIVGGGYTGSKL
AYMFDSMFDVTLIDEKNYFELTNDIIPIVANPWSELNEEACRRLFILHRYYLKRSNVLTG
TVDGVDEEAVTLRDGRRVSYDLLFIAPGERKPFPFATKQRTIAGRVQELRHFNQFLGTCK
KVAVLGGGPVGTSLAMDLARNRPEMQVHLYHSKSELIPALPTTSRKYAVNALQKCKNLSL
HLCTRVTDVDGCDSNGKRIDLNSSSLLTRLLGFGRPPAEPARFMVRYDKLHFEPAPQQSI
VSQAYFGRREPHLTGDKVESSGEEEFDYVFSTIGDVPRCIQAGKGKCNILQEHEAPDGHY
RVSTLMQLYKRPNIWAPGRCNNLPWVRSYGSSDVQVRTIFRGLNSVVYNPTERFLSSRDG
VQPQRMAIPRLLVRLGNNDAVGATPWSGGMVGLSAFHEFMQDRNHLVKEFQQPIFYKQQD
PAKVKQRISNWASHETTDIVDFSHL*
>TCRU_951 mRNA capping enzyme, beta chain, putative
MLHRIPAYRDPLLQVLSDALKRALDVYRREMSAGMSIEFECRLGTFSASKHTYAHPFPTH
TLTPALLDGQSTTPFFFFAGVAQPSFIAAHETLKTIGASMPPRSSTVLSVRTVGKDRLEY
AMNEACNSGHLLAIVEKERIFSHDVRCPGWGADFRVSVSREKTIDRETWNQAKWESFTPN
ISRLRQRKSVRIDPFLSVDMAMVRSFTDHSRFVRPWSPELQVPFISAPHISFDVELEVNM
PALHRVVKQTRLVESILGRTALDLLTVLQFLAAKRE*
>TCRU_952 hypothetical protein, conserved
MCDFDYEKLFSLRQDDDLELLRITEDLQRQMMVIDDDDDEDMNKKSLAAANSPILGSAVG
NATDDNNKSSANELRSGQGAKGLSNATITPPRNPPRTSRVMEPIEGQSFSSSHSRGHPQL
TSSGPQTPTQTSNENSNPRLPVLTVAPSPPSELSVLKMAPALVQDAIPKPLPPYSHQEEF
PPPYGWVGGVPAKQPPGVTSMPQNHQTVPAQNLRPGPTAHSIPQLPYATYGSNAQILPPN
GFPAGLQSRPMVLQPQSQPQPQQQMQPQLQLQPQLQPQPQPQPQPQQQPQLQLQTQPVAN
GAMVQPLNVNQQPPVLPQSLSHSLESSVQQDQHQSQSQTQHVTGTLPPGYAQVLVPVRTA
DGTTGYQLMMLSTQHISQGASSFSPTLVQAQMEQQQLQQQPRPHPQPQPQQSQQAQQQQQ
QQQQQQQQQQQQLQAMMQYMWQSPSQAQSQHQYVSQQPQPQPQPQQQQQQQPGSIPQQF
LTPQYANIASAPQRYALVSANGQQQYLMALTLNPLQQVHQQQQNQQQQHLQQQAQQQAQQ
QQIQQQSHQFQQQLHSARPVYLTSQQPQQVFTTSMISSGMPPGYRFN*
>TCRU_953 ubiquitin-conjugating enzyme E2, putative
MSTALKRLSKELREASLNPDSDMDLHLLHAGSLFTWEAVLRGPPDTPFEGGEYRLLLRIP
QDYPMLPPTANFVTKVFHPNVNFDTGAVCLDILKSRWSPAWTLNSVCRAILNLLAEPEPD
SPYNCDAGNLLRAGDMEGYASLVRMYAIMDAGAPPFPELA*
>TCRU_954 Protein of unknown function (DUF3608), putative
MKAVGLRWRPRNSAKQSAKGQNDTPVTVVFRAHTDTVAKVPFLYSPKNYNRPMPTEEEGF
TEAIIELCVPNGMNIIGSSTAAGAGGGECSGNKNESKIGSTSPGCWQRHSGMGGCALSPG
AAAISPSLMEMGHRGAASPASEGAGLMGAARPAIFAGDAVLNSDALRRRRQQQQQEQQQK
HTDPSTSSAGVSFFKYDSWVCRAYCFGEKDAIYANGAISVHQSLANKSQFINNIAKGKAL
ARVVPTYDEVRERFGLSHLELSFENQFVTRADMFLISEALRDRILYEGEEVTLCGFTMKV
NEMLRALQPVAAAESAAGGALQQGDGVKTNNTAALDVDGEHRGAAENSWTSLKTLGSQRV
PVQPHFSHPSLTLPSPQHQQDGKEESRYRRVQSGLVTKETLVNFRSLSPVHYILIEISKE
MWNPTVDGRITLCWVMKNFLREYLMQQVHKHKASPLIHILMVGRLYPKYAINGNVDVLHV
MKIPHDYRSTSLVEEVELQCEEFLRRVLQEVKKTFKKEKAPVSTEAAGETTCTPGEEVPF
VSQADVADTLTEQSLFVHAKNTCTVETINLVLEECIKGRWDTNTGYIISVVSAGKGLYQV
TNELSQTTCTRLFSIGIEKINIICMGRPPLHITPLFEYFSEDETLRSQYHLHVGQRSQRF
YERPEWARCFFYHPTVDASSCGLLAFDLLTREEWMQRHRAVPGSKSQFFSGLGLPMAPVG
EVLLPVMETRRKEQALSNSVRVADADSLVSPMPSSALSAVPEDSGTQFYPTLFRHSFEVR
EKAQPPLRLTGTRNKHEGITRGERFGMPGRTSGTTQPDGDAKSSPTPGHSRPLVFASWYC
HRGCAFSSQQTFSREYLYDFIIHQSHEHSGDGHTRNVAMEPEANGIVSCGLNILDSDLQS
GYVFLRLRIDSSALPEACWSPKILTDVDMWAVLMGAFSGEDNRLSEEEKKHFVSRFRALD
IFCRTFSAILEDGLTLILASHSSKLTFSTPEEIVFTFRQPLIVASSEVTPFSTTIAHLQI
RNSILFAIKPISPYRPTTESEIASSASRNITADVILRRRWQFAYPELPSSGAQKSPWATL
CHCKILPIYGTKSPYQRDCFFGVPTHQYAVSIRDNMQLLEYVLQRLQQQYQIVVVGSSPA
GIQWPREEPTRNARVELSIGHQIHELKIGEAGQSISVTRILHGGMYSNASVTHIISHSYL
LLNYLKPGFDLRTVHLETQIGEKLAFQWESLDSYLRDRHRANIFIPRGPDLSLREGKLCV
ALLPEAFEAPSVSYAEFSAFINHRFSVHFKMTDAAESEEEKVGMTTNFSETLNGSDGITA

RTVTLIHDNPLTLEPYCLMDHKTGRTLCLEAPTRNRMLSMEVSIPATYSPNCHCLLEISW
LVCITPIIADWIRSIFAGAARFRLRAVPLPCFSPSTKSGFFAVSYTVRARKEEEEPLFRS
RLLSLLTNSTYRYFPDVTVMSRICRLLHFSGLCYVTLHWGGTALARWFENSMLRTGQPEH
QQLLREFTEAVQIVRDEIEVS*
>TCRU_955 NAD+ synthase, putative
MSPVIALHEDLQKRLEEYRSTRGFSPVKWIEQKCAALNEYMASHGLKVCVTSVSGGIDSA
VVLALCSRAMRMPNSPIVRNVGICQPICSSAWALARGRENIQSCGALEVIVDQTELYKQL
SRIVETAVGIDGQNFARGQLRSYMRTPVAYYVAQLYSQEGNAAIVMGTGNMDEDGYLAYF
CKAGDGVVDVQLISDLHKSEVFRVARELGVPANTLQASPSADLWEGQTDEEELGFPYDFV
ELYTGWCLQLSDEERQSFLHSLSSDARQQYEKYKDACENTHRRNAHKLRGPINL*
>TCRU_956 Paraflagellar Rod Proteome Component 9, putative
MTDGTAAAAGALSELFIDEDKVHRSLIPDDVVIRDYLSCINDDTWVRHAELVQLSDLKET
PHEELVKKEVLRTFIEERRRSGVEMPRDLIMEGILWQERFMEEYKREQRSQDKKEASNYK
QSLMSKFRTKRTGVSDVTDSASRGTRAIEYKESQASAPEYPTENTDARDTYHELPNGNAS
AAQQDPNNDVPKKEEEEKIEPAAANEFDHEIDIAAEPCPVEDHTEPEQQADEALQQGHSG
ESKNEYPTEDEFPAGQQSAVAEPAGQAAVPGDVTQAAAEYPSEEGISAEKPSHEGEATAP
DTEAPDGTEYPVEDAKTPPNEPAADLADQPATDANADTDAEEM*
>TCRU_957 coatomer subunit epsilon
MADPFYDARNALAIGNYHQALAEASGAKTTLRKPDDLAIFNTEREALLSLAQIGLGQGES
VVTQLASASHPTLLAVKNWAQFSLAIKNKSPDGALNQTAASALTQLTEAAEEVDPARIQG
AVLAASALLASGDNAGAISLAKRWIGELPTPEGASNIRQQMELRAVVVEALLRMRRSEMA
RNEVKGMEQLDDESVLTVLCSGIVSLHEGIKSRDAYERAIQRFKELSMRCGQSVLVHNLI
ALAQMELGDFTSAERSLLDALAMRSNDVDTTANLAVVSSYLGKAADSTNRYTQQAVAIAG
TWSHQYAAMNARLEEAALQFSKTA*
>TCRU_958 Mitochondrial carrier protein, putative
MTDFLAGWMGGIAVLLVGHPFDTIKVWQQSRHAVDVALSIPAPRGSSFTAAMELYRSNGV
RAFYKGLCAPMCAVGFANSALFGTYGVIVNFFIRNESSQYYYDDDHHVTVMYTSRQINGN
HASGNTYQKQDLSEHFRTGGGLSAFENFIASTGGGVAHATIMNPFELVKIRLQTEHLFPH
RRYLGTVHCVRRLYENGGIKYFFKGFSATLIRDIPGAGVYLFSYSSLIQLLGSEKNYSIP
HILIAGGCAGLAQWIVIFPLDTIKTRMQVAKQGEMLGWTRCARQLYKIHGFTGLYRGMAP
ALVRAFAANGAAFAGVEATLQFFRTTGLEDIEVCDS*
>TCRU_959 hypothetical protein, conserved
MGVGSHKRSQGGAAFTQTSHAPPLPALLRPQFQVFGEDNLNAIDRRLRRGEAERVEEKKI
QERCARVRERRNAELQRNIEMIQKRTARHASAAGLVEERRLRAEFRQLCRW*
>TCRU_960 hypothetical protein, conserved
MSEHKNPARVDQYDSGTYTRKGQTTRVVVREKPFIKSRSQRFFEFLRPSTRTGFNVVQGF
ELAKVMVCIVFPIFMLLYWKRMQKRLPDQWESQFAGLQHRKLKEDVLQEQETDYFTIIET
FKERREKALQKKQKEAREANQQFRQ*
>TCRU_961 Ring finger domain containing protein, putative
MEDNNGPKRARSEAMEDTSSRSTTPLQVDQSTTPEATPARDPLLEEQMDQLGVDEDFKAS
LRCMSPNTRRDVMNDIIRGQQQERTTMATPFGLFSILGETSILPLFSGVDVRLSVEEDSE
DEQRGSDGSRAHSSSRRMSPSSGADDRSENSRMETPALREQVLRSQMLYLLHIMRGSHIA
NTISEAIAQRSLGITQDIDDMSYEQLLELQERIGFVSKGITREQMQQCMQDVPWPKEGSC
VVCQSEWQDGTEGNERSVELKVCHHIFHQRCIEQWLGSNKTCPVCKKDVV*
>TCRU_962 Vesicle transport v-SNARE protein N-terminus, putative
MSSGLFALYEDDFNESSRQVRAAAAALQESLKQDSSTYEPPPTTGPQSRGHHCEVMQQGL
AHMRELVTSMLYESNDVESGELRNEVRRRVEDYKQMVTVLEGELFRLRQDSKNADRMDLI
SGGNDTLDEANQEARAFMLENTQRLRQGTTTLERAERALHGASDLGTSTLNTLRTQTETV
RHFHATVHDVDSQVMESRRLVNQMQRTAMKHKLWLIGIIVGLFVCIILGIYVRR*
>TCRU_963 Vesicle transport v-SNARE protein N-terminus/Snare region
anchored in the vesicle membrane C-terminus/Sec20, putative
MSTLFQSYEEEYRDVVKSVREGLDGLRATLNREADGYNAPPATGPASRLQRGAQLVKLTT
QLKELLNNMEYECNDVPVVHRPALRERLAECRRGARELEEEIAKTRGECATADRLDLMGA
PEKKGSAPVDARGLGLDDETARHRLQMMHNTEKVKQASGTLNRAERLLNETEETGAAVMK

NLRTQTETIQRINATTTGVNEEISEVSKILTKMHRTMVKHKSMLIGIILVLVVLIFVALY
VSFLKHKKETPVQPSQTPTDAPELPKWGPDSGGGLPVD*
>TCRU_964 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MSRRVFTSAVLLLLVVMMCCSGGASNAVTSNSGNAQLPQGVDLFVPQMTLVVPKGGTSQE
TIRNSFISPSLVSAGGVIAAFAEGQVYTVNGAGQNEKTSSDVVAEYIDSSWDWSALVGKV
KKEEWKASTVLGTTNGTDNRADFFYHPTTTTKGNKVFLLAGSLYEYRQTVGKQTYSGFKS
RIELVVGDVSEPTSSEPTERIKWGEIRSLLNESTITAHKGKLTWFLAAGGSGVLMEDGTL
VFPLMAESGNGGYYSMIIYSKDNGSTWALSTGVSPANCTDPRITEWDGSLLMIVNCNYSR
RVYESRDMGKTWTEAIGTLPGVWVNSRLYFWDLSLRVEALITATIEERKVMLYTQRGYAL
GENANTLYLWVTDNNRSFYVGPVATDAAGNWEFASSLMYSDGNLHLLQQRGSSEHSVISL
SRLTEELSAIESVLSTWAQKDIFFSSFSIPTAGLVAALSDAASDDTWNDEYLCVNATVTN
AKKVKNGFQLTGHSSGVLWSVNTRGDGIRHVSLSHSFTLVASVTIEEAPSEKTPLLDAML
GDTNSNHTMGLSYTADNKWETMFGGKVTTESRPWEPKKEHQVALMLQSQKVSVYIDGQSL
GEEELPLKGESTLELVRFCFGACGEDAGQKTKVTVTNVFLYNRPLNSTEMRAIKDRIPVP
TRGPETQVEGMATTEHLAAVHDPREVPAALGRTTVERATATEHAAAVSFTSAGSGLLPLL
FLLGLWGFVAA*
>TCRU_965 root hair defective 3 GTP-binding protein (RHD3), putative
MVAFAGGARTEDAHLIDDEGQLLPVNGIEEYLFTALGASRGGDALHRVGITYHVVGVLGG
QSSGKSTLLNCLFGTKFQTMDETKRRGQTTKGAFISRANFEVLCGDDGEMDAGASALMES
YAGKSLPLFVVDFEGTDGFERGEDQSFERQLSLFALSVADVLLINMWAVDVGRFNAANMS
LLRTIFEVNLQLFSHDSYTKEEKPTLLVVLRDFTEVETRTHFETVRKSFDKIWDNIVKPE
AFKNSTIDTLFDLRYHVLPHFKLQRAAFDKETAKFRQWFYLSTCDEYLFHTRGMFRGVPL
DGIPSYLSSCWEMIRKSKDLDIPTQREMLARHRCLEVKKQILQLFTEFCSNYTERLQRGE
LVTHLTSLLEHDVDDKLRDFHQQTRLYRIDIVRKTEAELEEELLKVELKLVGEYAKFISS
KVLEELETAVSGTVDGALRWLLHQAQSIPFLSAEAGDAGGGTEYMSHLKSVERASSNDVY
ITDNEACNVLVHSFWKRLCRALQAEIELLYCDYSQQHQRQRESQTLNLYDRYASLVAEDP
ALQEAIAHFVSDAVFQKVSRRFASMAENAAETIHQAFEGVLNRNQDGTVRFFHTTKALQR
IEPQARQAGLVLLGCLLYYRVKVVADRVVYKLEDTDGLSRAAVHLLGERRKLIVRENSEE
QKFFLHYATISEAPRYPIGAPVAETDSADTSDNVVDRDCVLLSQQAVQRAFDLYTQKCEF
TMQLQLRSIESEKQNLPAWVLPVLLLLGWNEIWYVLSSPVLLVVVVIIAAVFLRGFLLTQ
WAIFEETGPTCVVVGVRVVVQQIRNIYKALVPMMPDDVKSNVARHRDPGSFSDVTASAVG
TSWPYAAAEPTVLPPSTTSATLTRRLKKEEEVPTQKE*
>TCRU_966 hypothetical protein, conserved
MSVKVPYGSVEYQSHHHCQCDFCDSRRKVGAKKFALSSAIAKQKAQQNQHNCCCPGHDAS
AKQPLSGNGAPSFELDDPEHHVNQTELNAKMGRTGLPDGNQYTTAVGGTRGLRGAGESGT
AKAKKREEMEEEKMEELDRLERLLILEHKARAKATADAEILSLRQSTGRGPCPKPLEAVP
PLPVEDGMDQTMQGTGAYQAGTARETHENAHESFVASPPHGETSQLPQQTVRDGHELARE
SMNQQQNNAAFGRSSQIGGVGGTTTRQVNSLQADASAAKGAGNSTVKRPWDYFGPRPEGA
GVVWRKIQPSIPEDTTTGVGGLGNVDNRHLWKKTLLKGSSAKENTANANSKKTAVAAPDP
SIMSPGALAALSLQKQQENDHQARDAVGSPVPTVCNADDTPI*
>TCRU_967 hypothetical protein, conserved
MPIKAKPIDPGRARLAALGQWNRQRRTTSTGPNSAKRRGSGSWANSTGSSTSTSSSEGSR
TGRRGRRRLCNQNGKREGNGNGGTPAFLTSSRTVDSDSGTSNSDPELYRAARERTERFLY
PNGRSGINVSSSNHGAVMEARGEAASNAENISLDASLPMAPVAPVFSGLQSQNQKKESDN
KGSDANLESSRKFSPPSPAVVPLVVQEALRGLQGTKDSASEREFARLMDLFAADVQKERE
KEKELQQEKELEVDTMDTISSMMAKNQNQKPAQGPWDETYKLYTSPPHTFDELQERALLQ
LYAANEENKDSGYFIATDHMAEAFTLATLEATRNEFPGESDAASGASGALNDNNEKFRPI
GAPPSLMEIVAIERARRNARAAFQKRREGEEGVTIDRNTEALLSMDTEVLAATAEENLNR
FLLAVRCIENAVRNRRVTDALGRFLFAHHKPFLRTTRGAGSSADAIREFPHEAFAVYERY
GHYVGKFITELLNRNVPKFNMEEFVLSLFDVNMNGEENNNASDAEDVSMDVLSYPAWRLL
QSISSFNEFCTFMDDFIAEEYGVEKVVAHENESTNGDAGVKASRYDGDGVVVVAGARGVR
ALLTKSKAKLPSARASSTCDASQQMRVPNEGAHESNDDFLFLPSEGGATETPLSSPPRES

QAHGDCSAAEFSTRTDSAPTVLSNSHPALSGSSRPPFGNSLTPPPAASLQGPRPSKNSLS
TANSIPQLPHGSRRIEAVRGRNLPPLSAAGGKEAETMFFTAPLKLSLGSEANVVPPGGFK
AEPVTTERTVRGTDSSGKIDKVSGRQAPSSSIGISYGHKKKSKDSRSRSGARTGAETTTT
TTKPRGKKLKSPQDA*
>TCRU_968 hypothetical protein
MSAAEKPSSPSSPESSAGKDVAASAWSRFVAPIDSIFRFPKKMWACTADGLSRLPYVFSL
WQQFGVGDVLLLSGPRQALFFAFTAARAVSNYVQRFLTEELLPFYCDVSAWLVLRPGETA
HTVGIKSVEGLRWVYIYFGFLSRNTTSPSRGRIICTGITAVTTAPPSSSSLTTSAVNSAA
PTNRSRRWKIKSGIPNWLRASFTFLFSPKRKASASPPPPSRSVEGGSGLCGMSRGAAPPA
KGSRVSQEPKPSAKEASQRETMPNTQRGLLEKAFLFLKWLTCGFSFVVSKPSGKSFGQKI
EMADKKSWIPKKAGVEIHSSSLEPLDLPGRSSFFSFKASEHAAEATLKSSKEKSISLTRA
ASPDDNNDKAIVHTVTPRIVTVHHFGFAVYVTGKPPHKFEEKIEGEFSLQVVQGTFIRDV
AHLFSSAFSIPIDNVNVRRHGSLYHVGFDVLQLPGGNFWKKREIDTHENEELPKSTSETK
SQSEHEEVLESEVEQLREYHAQRGMRVSGDFAPDLEHIIVSGENFQDHRAAFCEKTGSAG
SSVVACVVSLNSFLSAFYVHRHFCLKLVVLDLKGRCIFATGDKLVVFDCRWPIVSMRSIS
EPAEADGISEEYLKLNEVHDTIVMDDSPGLSERKLLAAAHVLSSDQHCAEIRTVVPSSAH
VMNWMDTSVVISGIVCTAVSIGFCVLAVQRSLLHRRGDGEWLMKRWQLARSELLLKALNE
RFSVLLEALPAHFGVPREEMFFLRRVVQAYFISCESHYIDLVRSIGMREQMVLQRREAAA
KYIQHVFDLKWLFQLYEVMLLEEQHRLRLCVEEGRNANRLLEQMMAVSNVQLEYFMGREG
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>TCRU_983 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MVPKASKKRPSFANGPRILVASNASGIVSVTYGGREHVAADNTDEVSERSATGHKTLLSE
NGVAGSGFFGEGDAGGLTQRNASGNEKTQLREFTAQYSGNGVSLHDCFALLNDAKLTLRE
LTVGSTVRVCVYWVLLLLLGLCGVVAVL*
>TCRU_984 RNase H, putative
MTMGASRTTKLLGMDLDPRLTLNAAATKQCAATSQRISQLRCIAHKEAGPSPHDLRTFII
GYGASKLRYGSELIWAVATDSAKNEMQKTYATLARIVSGVPSTVDPESALLEANMPPLHV
LCLRVRLSIFENTRAFQMDWMRRPPPEPPPRAVLRISPLSRDELYAFVDAYTKEYGITES

SPREERFFRSSIPPWFAASAHRVTIAVELPIDLSITDEEELIREKRRVSEEALAPHRHRS
WILATDGGVDVPKSAGVGKLLSSLNSSEIIEKASINCGARPCSYRTESRALLLALEKLMI
PRIQYRRKTLLVVTDSQSLLAALNKGPLSQTDWTEDQIWQRLLTLACAGWSVHLQFCYGH
CGVHANEPADQYATQTMESGHYTEQGTAPLWHTDLLTCFTTQLTNKWRGTIRQDTHRYLL
CGTRPSDLSGKDLITQEVLHRQELVHLARARCGESELWGRLYWAVRDCTNQCRFCNISPE
QSAYMRSNNDPTAPGTDTVPPSAREEDVSPVRRRTLTRRRKEKCPHCDSTLTGFSNLVSH
CRSFRPEHPPPLPELKCDFCDMVFPTRRSTAQHRSRCAHNPDATRHRNSSARRRSLLPQD
QPASTSMPIGPQETLHHLLLGCPGTLAVRRRLGIEQDLRLGKFSQWQLLYSRKLILLLDH
LFGTQMALYS*
>TCRU_985 Reverse transcriptase (RNA-dependent DNA polymerase), putative
MHKDGPRLWDDTLMEAERIAADSKARYLQLPTPDREAEMQRTRSQFFLLLRERLRNTYPR
RISKLNPGEPLAWKYISGRKKAPLPSPTSILLGDGQHTYETARRAANALNRIFLPLHPSH
KAVRPSKGINRRSASLSINASFIFGPQNSNESISTFTSGFCHCPLDAPFNSTELLAALRN
TPYGKAPGPDEVHSEALRHISSKGLRFLLRRINHSWTTGTIPAEWRSATIVPLLKTGKSP
ELLESYRPISLTSIVSKVAEKMVLKRLLWVWTPHPHQYAYRSVRTTTMQLAHLIHEVEHN
RNHYFQVSLPEKSGIGNQLHYRPHRTLLVLVDFSKAFDPIDHRVLSRLLANIPGVNCRRW
LRKFLCGRYARTRVGHRHSDRRPMLRGVPQGSVLGPYLFSLYAHPLLNLLNSFAGATADM
YADDLSIIVRGSPGNTPFPLPTWFLKSCMRGVRKMAWPSTRQSVKLLGSHSPRTRSQIMI
VKEGGPW*
>TCRU_986 conserved protein
MSSIPDELFGNWLLTTFNGLDLSDQGGPFLMTLEPAGGLVYLDIQITNILSGLLEYREGR
LYGHLVSTRMLGPPLHMQIEQAFGAGFEAGMNVLMEEAGMIFSQGGNTFFFVAQTDSSQQ
*
>TCRU_987 hypothetical protein
MDEEDAYWRSYRHYFLARCVEELLVALKKLHAYHPGLGAGRRAEGQSCGVEQSGAGSAGA
SGEAGQTVAAHRHLREACGTVPGEATGGCVGSGAKHYRRAQALYDKPQQHAAPGEGCRNA
PAGATASSPVAFGCEQQRRVDGGQEAAADPRRRTDARRPFVCDPRACDEEGRERATIQHG
VGAQRTENECFRRQRRDGRGSVSESGLHDYGDGEQEEDAAGWAFVGVDSARSCDEAKWRE
LCPKQWSSRK*
>TCRU_988 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCVAGGVYARDVDNSAVGGCMASGVLGTRRLYMPRCNKTAVT
LPLRHVFPVSAVGASTDGQVSGTIDGGLLPIPAPPLSPAPNIPKAPEAPTSHGVSQPAVG
VHSGDGTPSLHIPNVDSSVGGGSGQSGNSSGSVLSVVEPPSTVVVISPSSISPGVGGLQN
KDGPPSNPKLGSPAVIVESGKILVGHNGETEKDSTPDDGSESSRIQQETESRATTEEARG
SEAGQSGVGTNGPPNVLSTESQQQHRETTVTETKPPPPSPGKQIPAVSLPPGVDAPAALS
PGPQASSPEPSRAAEDPEEEKRILPATTASHNSKGETHKASSLRTETVSAAPKTPSPDVV
LEQSSEGTVTKDAMKTDAYTDGLAATSESSISTSDSGVAQDKTEEEDDNEQRREAKGPHN
DPYAGNTNDAPTASDTAAETVKTITTPKSATSKSGDSDGSTAVSHTTSPLLPLLLVACAA
AVVAA*
>TCRU_989 hypothetical protein, conserved
MYARFRTRSKFYKRPERVLRAYNVSPNILRRPNVKPGLIRGVYSDEKVDLRDRERLELLE
SIRHPRERDFYQDHTYHNQWIRRDLEKHQKMQLSSRYRYFAPDYVITPWIWYPGDVVEVV
SGEGIGQRGAIIAVVKYKNEIIVQNINVQDVVIPASETRPEQVLQREHPISVTRVRHVDP
STNELCNLDLVKVRNKETGALEEKRMSLETGVLLPIPPLDSGMEVGDPLKDTPIQDADEA
TYDREAEMAVLVQRRLHAMEEYFVRSLRKSYEFHEPLRTKNAEDLKAFQSDVVDAASTAL
AEKLLPVDGTTPSTWWKDALAPYVESIEAEMRARAEEEEAEAAVAEGETLATQVAEEDEF
LDEEEDEINMEKDASSL*
>TCRU_990 MSP-B, putative
MRHTLLFQVLLLCCVSGSVAVAEHHCISDEVENKVGPRTTAVVLELPTRGGGMMRALTAS
APEWAPIRFQVFTEDLNDPSKHCTAEKQIRPDFIGRNLECNKRDILTKEKRSIILNSLLP
RAFRMHTDRLLVRPLTGRVIVPRYSSGVCAQFTIPSSHQTEGVSGADMYLYVSAGPTQGS
TLAWATTCLKLPDGRPVVGVVNYGPRSVTDSENSVRVSAHEVAHALGFAVWLLQERNMLK
EVLNVRGKAKVLQVSSPKTVEKTREHFNCVNATGMELEDEGGEGTASSHWERRNTKDELM

AGISGIGYYTSLTMAALEDTGFYKANWGMEEPMSWGNNSGCALLTEKCLMNGVNKYSEMF
CTAETTLISCTSDRLALGYCTIYLYTAELPQQYQYFSNLKLGGSNSSLMDLCPYVQPYSN
TRCSNGEASIMHGSRVGPRSKCLKGDGLVDFMGRIGDVCAEVSCEKGEVSVRYLGDDTWR
QCPEGSSITPTGLFTGGKILCPKYDDVCIIFDPLRGGGDVSSLLSVFPSISVILLVFIFI
SIY*
>TCRU_991 hypothetical protein, conserved
MQKLLIAINGTTTLRPSAPSKARHKSPPPLPREFGVRPMQQRGLGDPAWKGEPHDAPGEV
ELLLGLRGTQGLMREIRGWQGFARRIAVAPFGGVLECMLDATPGHSSWMRLGSLFRRRLR
QTPACRQRWEERGTLGVRQSRGIDVHGNSPVDRATAYTQSHGSSGQQKRILER*
>TCRU_992 hypothetical protein, conserved
MDRRAPFAAVLDKSSGRRWRSIAWPKPRNAQEDAEATFRHFTFHSVLARCETKPPLYWIC
MRLFTGGSLGGYARTSFRCRVGFLDLVESTLLHTGHECIPEVPRAAARVLAEDPEMVRPQ
SVAPRAVSTPVWICGIRTSGPRRSVVRRYQCAVKKWCQQENRWSLPRGVNLLAYPSSARR
RAPP*
>TCRU_993 Reverse transcriptase (RNA-dependent DNA polymerase),
putative
MLRGVPQGVVLGTCLFFLYVHPLITLLNGFSGVTADMYADGLFIVIKGRSWEDAIPTAKM
VPKKLHAWSQENGLAINPSKCEAAWFTLSTHTESDHDREGKRPLVLFGCTIPVMAMEASQ
TTNLLGIGLDPRVTLDLAATKQCAATSQRVSQLRCIAHKEAEPSPHDPRTLIIGYGASNL
LHGSKLI*
>TCRU_994 hypothetical protein, conserved
MCRVFCVVLVLALLCCCSCVFAAEEGEEQEQEVLQVNAECAGKDKLGRWQLYGNSLWYNC
TVADGGVGKEICGMGDGNCTSEDVESRAKGVTKDGIFTINVTSPTPSAVKSWWESNVKSK
AVTVAIVPAKPPAAEPLGSREHKASGGTSTTNSESSDVEDSADVSPPPQTATPGSAVANS
AAGAAASQASDSAPAGGFQGPSHSTSAASAAPESLPDPKPTEGGGHSSHDHPLELQEETA
AAPPTQLSQTGEDGGAAGGAEEDTATTTDTASGEGNSTAASMPAPLSSAPKTNAPEKSVG
TDACFYDTRPLNRLLLFLAALTYGTLG*
>TCRU_995 hypothetical protein, conserved
MAMMVTGRVLLVCALCVLWCGAGGRCDEGEAAGHGVQPDVSASGTEGGLGGTKNAGPAPD
SQIQSSGEEQQHKSREGRPALPEGSLEEEEEEETVENKNLDEVTERGEEGRREDGQDANE
PDGSQTSGVLTKQKETLPPSTPAAPAGEGNQNASPQAPSVDSHGGGRTDRIEDSILGAPS
SGVALQHAGNASTNQKNNSLETGKHAENTITGGPVPSQAKTPKEPINDAEIHSVTGEDTA
SNQVVGRGTAEYEAQQRALATQDRSSVSFTESETKWQPTPHETPGTQVPPSATEPSSREG
QPPTAKTDSQTPNAQEHKKLLLPKKEYIAPERPSEDIVAEQQGQATATENLTENAPATNQ
AETTASSNSTSGSGEARIMADENTANAQRPNPNESHDDLEGSDTHPLPQTLRQHHKQQ*
>TCRU_996 X-Pro dipeptidyl-peptidase (S15 family)/Alpha/beta
hydrolase family/Prolyl oligopeptidase family/X-Pro dipeptidyl-
peptidase C-terminal non-catalytic domain containing protein,
putative
MQKVVVSTLPNKVKTIENVFIELRDATRLSCRLWLPADDVPRPAILEYIPYRKRDGTRGR
DEPMHGYFAGHGYAAVRVDMRGSGESDGLMHDEYLQQEQDDAMEVIEWISRQKWCNGNVG
MMGKSWGGFNSLQVAVRRPPALKAIITVGFTDNRFTDGIHWQGGCLLNDNFWWGSIVLAY
QARPIDPEIVGDRWKEMWLQRLENMPVNIADWAEHQKYDDYWKHGSVCENYDSIQIPVMA
VDGWADGYTNAVFNLLSNLKVPRKGFVGPWAHVYPQDGVPQPAMGFLQEAVKWWDHWLKG
TENNVMDGPMIQVWMEHEMKPSVHRPVSEGHWVGVEAWPSKDVTEETMRLECGRIVDFAH
AVRQEPASVLLRTPLNHGLLAGEWMGAGVSGETPADQRMDDGMAMVFDAAELQHELEILG
RPILEVELTCDKPKAMLFAQLSDVSPDGAVSRISFGVKNVTQAAGDQRIEYLQEGKRVRV
RVLLNYCAHRFTKGHRIRLSLANSQWPMFWVSPEINTLSLDLSTATLRLPTYRGPAIAGP
NPQPETAAPTPLTVLRAGFVDRSITYDIVKDEWTCITDGVGGVFGDGVYRFDEIGTAVEH
NLRRELRLSNKDPLSARYDIKQKMKMGRPGWEADIDIDTRQTCDANYLYVTAEIQAKMND
EIVFEKNWSRRVYREGM*
>TCRU_997 cation transporter, putative
MQSTSHGDHHEDHHHVGHHHGGCSATTGPYSLGLHVGAIFILLFASFLGTVIPLAGKYVP
GLRLSPFLFVLGKCAATGVVLAVSLLTMIHHSMHSFAEDCIPKGLHADTYDAFALLFAMI

SAMLMQLLDVLLDGMLQSWSACDAGAQTSTTVGEPGNEQKQDGRCAGSCGMEGCGDQPGP
SCEMGGCCQNRGALSAAHLNSARRVAAAILMEFGLASHSVFLGLSVGIASDKDMRTLLVA
LSFHQLLEGIALGSRLVEASMSIMLEVVMTMIFSVSVPLGIAIGVITMKGTHTSMTGPAF
VALQGVVNAVGGGMLLYIAFSLIFNDFPADMRSVAGPTVAHCGWRRCAMFAAFWGGTGAM
AVLANWH*
>TCRU_998 ZIP Zinc transporter, putative
MNNAESSDAHLPSRVLQQAGAESQQSQASTAQMYARPELACTETKGEYSVALHIVAIFVL
LVASLIGTMLPLAGKYVSFLQLQPFLVVIGKCISSGVVMAVAMVHMMNHGVLGFMKDCVP
ESLQQSFDAFSLLFAMIAAMLMHALDVLMDLLLESWAKNNASEATSQIEQAQLPEMETTT
TGQEMPGAGCHNHGGIYTARLDSAKRIIAAVFMEFGLALHSVFLGLSVGVANDSQTRSLL
VALTFHQLFEGLALGSRLSEASINFRLELLMTFIYAVSVPLGTVAGLVTLKTSDISMTGT
GFVTTQAVLDSVCGGILLYLGFTLILNDFMSDLRQYAGVNAAHRGWKRLAMFVALWGGGA
VMTLLGKWA*
>TCRU_999 hypothetical protein
MTALKCGVHLESHVHKSFVELKLILLVGNVGNKLHRLLHAFHVVHNDSKALLLLSHPRKQ
ENHLLQELVFFAQCIYLLQLGKVCGILMQERKQTRRLVLNKKRRKELRMRLRQRGVHCLV
SGLQRLQVCPQITTLRPFQSLHDGRGCEKRSQQQRLCCFFLIHNSASHVNVFQEELDGPV
LVPGEQRRQGLQCFRKEFLFPYKTEELITLIHP*
>TCRU_1000 hypothetical protein
MADAAKKAAVLLLVRHLLAREGVDTGVETKPLPEKYEDLRDGAILYRILARISPQTFPEA
DEMTKQAPSSRQNWVVRKGNLVALVRHMNDYAHQFLGAPETLNLTLLISPTEIANLPELS
EESETPLELEKGMECLMELTDIFVVMVVLSGDPAVLQAVKSLPHAEQVVLSNAAKACITK
HALRPRRRHGTLALEDSLKSGLHRSVTAGCAESSSHAAHLSYSLVGEEALNHQILQLRRG
LDDANAKVVELDSKLHLALTERQEWESKYKNLLAEAELRRMTAAGEDHLRQLLAKKEEIV
QKLTATIEDQKKRISAFKEATAAQETALGSFRRKIKHTEEELMKKNVERREALDKLSVAE
RSLAAQMNIRAELERQLEDLRTELALANAQTHNGMENSEACLNRSFGSVNSVDRVVQLEN
ELDEARSQKEAAERLLQVLQRQVAALPSEGFGSSAAMGALKAQLRQAEKEKEELRNQLAA
TIARLEDAQGYWRRRGSTSFVDNETESPLLEGKIGGENADSPSGREETDASGQQHRPCEK
QDGVSRERTLLGSTLLLLGYRNLMLQQQLTMTSGGKFTASGDGEKENNGGFAGNTGSFLT
RHRYEVEQGLLRSVLSRGG*
>TCRU_1001 hypothetical protein, conserved
MPVPLKSFTKSKWLAFFAELTAKLAHHNVMVVMEGCEVIKRLLVSRVSVAAFLEEGELLT
HLVDIIAGEMLSSERRSGRPPLFMAEKLLFTQLETLSLFIDMMLALHADKNPYYCLLVLA
RAGAILMTLVKLLQRQHPRFFGIIGTMVKLLLSLPLGREVRGLPLNESQSVAFTCHLQQL
QAAVAQHEEILQETFETLQTLCFATDGPMRYCSHSLLNMAVHRLRRLKKRSKQGSSAGEA
SSSRHEVGLNRTEYIPADNFMESSLRSHDATCLAADETKISINTAMDGEDAILEEVADVS
IPEEEYTDCFDRLSKAGSHEEFLFVMNRLWCITVAAGDQLQRRFTSLNFSRAFKRFLETM
PSNQQDQVVFTSVLLWLSHMISGFHLRSETRDSIASVAGSSLIKIVLQDLNARDMLLPQR
DASDLSTIDTSTHAASAVSTSRVNMSASSPMRCERPGGLVERPSISLVVLSFLLIAERAC
GPQEMGQWIRDAGLFALIESLIRNVERTKSALIDTPTTVDGALSDEVYLACAMASTRTEH
TTLAALACKLLSSVIWNHYMVLNKLLAPETLQMLRSTIPLLMTIGIHNPTLTSAIESVSG
SAIHHLPSCQRASRHTSLGECSLVALDACFWLMEFSRMDAVCLRDVIPTLPAVSRATRHS
IHPPLRASVYRCLSRLCTSSAELMTILHEMPSVLSAAVNSVLEYTKTAPQWEAAAAAEWL
AHVIRIASSDAKVEQNFDFIQTALPVKLLELASSNGITYATAAMLSLMTSLFGQQGRLAE
FHQNTFSNVLLPYGKRSLECWLKLLLVATQTNEKLEHVSETPIPAATTTKDALSRFLSGI
EGISVQFSFVCSLAQGLLFLFASNTVVREQISDDVICDFIISVFALPLPDDIFDMLSSRF
GVRVEQHRTLEDSYEVMLQWVMEFFSLWFTPASRAEKNPLSLSSTFFTHVCKVIRNNRLS
QRIRAHVCSFVSGIVLVRCDALYEVLAASSGDLFVASLLVHPASSVCGMQCRLLSLFALA
NDKAHEVGWVAAKVTELDGQVQALKKNGGMVGGDEMNSLVMALSFVSSALAFSECRALSR
DVRQSFCSSFRILLGYETTQRAAFQASAALARSNEGRRCLLHEVCSTGDPLSRSCFGRIL
GVTLGVLQSGEHLQLQKENNDAMKHVPLGEREALRAAVVISGFDICATACGKGGVPFTHA
VMKLKGVEHIESLFLKHERQRVPTPLGLFRLLAAISFQLEAQLAIVRRAELMTILIETAG
STNHTGTLSLLTLRNLCFNSTLKTQICQDSRILLTFKAALMAIPSPQTGTHENSSPKPKD
CMKIVLSSPNEVGEKRASLQTFLEQRMSWQSRNSECVSSIDDSLGDLDIFRRQELAVTAF

WSLMYDNQRGKSYVRGVFNQSPTVNINKLLTTCSGLTVCAPDFAKYSEKMSEAIGNIKFL
GKGAI*
>TCRU_1002 hypothetical protein, conserved
MTADLVFCEVKKEQDGGRHSAVVEALEKWCFLPYPESTRSRLEQVNIFFVASCRTPATDT
TEGAEDVSSAMVGVVGVVWVPLAPGAQVEGYIQLVLVLPTHRRRHIAQQLLRRALRLVEG
GDPSRKIVRWRLHTMTPSQQTTAYLRRVLPDGDDSASREQLLEEMERLVAAVPRVYETLG
FDIRRNMYAYYDNSADAVEMVKVVQGARKRF*
>TCRU_1003 pyridoxal kinase
MSEEKTILSIQSHVTHGYVGNKAASFPLQLHGFDVDGVNTVSLSNHSGYPIIRGHRMDLQ
EYETLMEGMRANNFLPSYRYIITGYINNADIVRSIRDTVKEIRTLREKEGKKLTFFCDPV
MGDDGIMYCKQEVLEAYRELIQCADVATPNYYEASLLSGVNVTDMTTALQAADWFHAQGT
QNVIIKSFRMKEDPQNLHFLFSTMATGGKTPQRFTGVVPYHEGRYTGTGDLFAASLLAFS
HQHPMEVAVGIAMGVLQDVILATRNEGGDGTSSLMNRELRVTKSVQSLLNPATVAEVKPM
*
>TCRU_1004 calcium-binding protein, putative
MDTTLYSEVNRLERGDFLLFHCVQLSQHERDVQRYFFGCYFPRWRGFYLEEVRDMPGPLG
YKVQRHFPAYPFDVYLKDNGEHFLTDDFQEGSIFTLGASQNQRDGDSKRYKVVHCDDSRL
RTRTGTTLADIGNDITTKLNQTHRVPGEVIDLLREIRDAYVVYAGNGIPEIGIKAMGRHF
RHVSEDGKRWMSLENIGKLVRDSRAFSTTLSFEDTQKTNSTISNNARSIHEAFPQNEEGC
IDYDLFMDYVRGPMSQKRKDAVWEIFRKLDFDGDGYLNILDIQARYNAQQHPVVAVERLF
SADKLLKGFLTVWDENKQYGLIPYAEFIDYYNGVSAVIADDYIFFDILRNQWKVMRDWGG
TVGTRRGKCEVPTM*
>TCRU_1005 Zinc finger, C3HC4 type (RING finger) containing protein,
putative
MENGAEGLVPIECLICAATCEALAVFKCGHYVCYVCGLHIHSIDHGVCPVCREKGETVIV
TCTPPGENDDEDKFSAELIRTMEDVSGFDSHLQCFVHGKALANELRKMYEYVCPVPKCWC
RGVQEPFCEMYPLHEHLKTDHGLGYCTICLQHRSVFLCEHQVYSKENLRLHMDGVCPHDS
PSFLGHPFCRFCPKTRFYDEDHLLEHMKQHHFTCDICNRGEFLFRYYENRKKLLQHFERE
HELCDHPACASLDPMMRVFVSDLELALHKQRVHGVRSRLALFTTDASSTNPSSSPPTSTT
PATGFNANVISITFDYVHKQETVKLMQACAQRGSGGGFKGKRKGGGNNHMDWVRGDAPGL
PVHFRTRGVLKPLMRKVRERDVALQATSHPRAFGLSESAETYNTKNRVPLNPTELRGALD
AVLQEELPDLHRMEGFRECTADFMSGKMLTMRYYNCLRTEFFPSESAFQKVFPLVVATVP
LPERRDALVQIEKMRNSPEVQHAQRMQEEEEKKKKDSEKWKKQTEYLERIQQGSKRQKGN
NSGGRNVWLERGSAALINQAHGKQSETQEKEQPRQQQGSQRTLWGKDNKHASQKSGNERS
LSGDATSARPTAWGAAQERQQPRLSLLPIGAAGYYPNPEDFPALPTRNPSRALGLPQAKR
TSRPNAWYRK*
>TCRU_1006 AAA domain containing protein, putative
MGCGVSRQPFSTELRPLRATRECAPGGFDCAAGCGGHPKQITGESHENGISSERPSPDGG
SATKSDSPPPRFSAAETVVGGNSHRDDSRDEVKFSVEWNRSVSPVPGLSEYATLPLRHVH
KKLKHNHRVFRICLTGGPCGGKSTLLTQLQAKMPQRTGYKVFCVPEAATLLVTGGMVWNS
DLIEEQQLALLRVQIGLEDQFYNVAMASGAPSIVISDRGTMDGRAFCSEEIFERLLRRLN
VTLETLRDRYDAVIHLVTAASGAKEYYNLDNPSRYENVEEAVESDKKLRQVYVGHPMLRI
IDNSTTFEEKMERGLSLVGQVIGQRFSMQNTSYYLVRHCPKELPVQSVTSTLTITLLCNS
QINDVRLLIRREHPSGECMYFFNSIRCAGKGNSFGHKDGSEGSVTRDASPVRHAEIQAVQ
SAFMGTMESGQRVKTEQRISSREYATLICNRDAQRHDVVLNAVQFIHDDARYEVTTIVEP
PWAAGKQALTLECDDQENATFPSFVKVDREVPIDSLSTAFLISHTEMGPLYTSLVYAPVF
TRGILTRGTRADADGSCATSDSGHRTPRASKRDVEDEADEKKKLMKRKKKKRVKHTAVTD
EDESLPLQKAEKKADFTATVVEAVDAREIPPNLPSQSNLGPTDDTPNSPPVPSASTTPPL
PSGPPTANPRGAMTGMH*
>TCRU_1007 small nuclear ribonucleoprotein Sm-E
MSATTKQMVKPTSIVHRYMTEGQRVCVWLVHDTKMKIEGVILGYDEFMNVVLGDASEVHH
KTKEVVHVGKILLRSDNIGVIHPIGV*
>TCRU_1008 ubiquitin carboxyl-terminal hydrolase, putative
MLCSCTERVDPQRLRVKFANAWLKEGVLTSEPLTMYCTLCEQRGLMSGKTKSKTKLHGFN

IFRKTRDEADGSGENALDDLFLCFTCTMCFCAAHAKIHEEEQRRAAMAGNNNRGKRHFLF
FAVPFWAKTMGNYTPSGKNKTLFPTFHVDDLEHIRESGPLTLEKEAAIVFRPSSDSHGWV
YNVWCTHCSEKPAPLRFSEFQESDPIHVQIKLLGDIIARLRFLFYEGIRIELPAEWSALN
QGNFHTGESSSYPRACGDIYANRNTLHDLDVHASGTSSMGTSSFALRGSKGDAEALVLAH
VAGIENHRNTCYFNSVLQCVLKCRFFTRPLLSLEVGALPGPLSYRIYAMARHLSEQTLVD
VQTRAVYPFARAVLRCLCELAPLFAEDDQQDSQELFLCMINGVADEFDKGKSEEEKKKGP
RLSFEGVMRTEVVCTQCESRFPREELFMALSVPVEDSIESGLRKLFRPMHLREKDQYACE
RCFKGLTKAEQERHNAAIRAENERKEKAKKKASAEEKRSLNCVYSDAVVSTSISRLGGTL
ALHLLRFQSDGRDFQKVTRSVAFPMSLDLAPFVSKDVLREYEMARGLSALQARFPHVQRD
RLLRFFEHANGDLQRAERMLIGMEEKGALNGEDDALLEFKAGQGTSDGSIPGITTGRSSG
HTSCDVSPAGFSPVSSVIKTNGILGEGQEPLPALKRELVGIVAHRGSLHGGHYIAYVRDD
SRPNSWFRCDDEDVERVDKEYVLRCQSEVYMLFYE*
>TCRU_1009 RNA decapping enzyme
MTLTTHDAFSAVAGRHQTQIPVLECTSDDEVVVVAFDGLRYRRSVCVVIMNDQGQFLGCR
RCDNRQILQFVQGGAKSHETVQQTAEREVFEEIGLPAKHLRFVAEILPKTVGRELRAAFR
YRSKTWRKKDIIGQELYPLLYLAEAGVVDLLHFKAVPGVRQEFCEAKWMTLEELMQNCPP
SKAAVMANICIAVASFARGGLGNGSELNICGGNAPQLVGIVQGTDVRNEGTASGRGNTGG
GGGHRNRRGRKPRVQQE*
>TCRU_1010 hypothetical protein, conserved
MPLAEQRGLLPRGVAELNAHFLSSRGDIFTRGTLTVEFAPMMSSGLSGNGMTRDEGINNR
HAAILLTLSPLHEIGEVSVRLERRGEDAGDSMGECHQLPLNNLKLCETKRRVVRINDGWR
PAVASPDILAVDSASSVAVEHKLGLVEAEEKNEPKIDEDNGAEEVLELVFGSSDSENDTK
AGEYDDADDYANENCESVAEEDPLHSAFLEESGNDNTVQQFVLKLWPFPANGKDTMEDGA
WFISRCCIEVRLLPPSQLASLSYPRLTVSSAAGKTHSKQEEVWEFGSENYLLLVGQRFYD
YFICPRVAYAESGPDAAIFEAVDVYVTALRPFSDAIATSWEILPMCSFPVLPEDLVCAFV
RPQQGEDASLVAEETHAGVRWRVQHHSAYTVLSSIDEEDAIDGKDLYFFNCDHVLSDSLF
PLIRLAEEAWEEKNSRAAVRVDASFCRRKTTWVVTGCSNTLLSLRRGTLCTRGAVVLVAD
VLRTVRKTMTLSTPLFQVNLLRAKAAVLSSALEMLWRMSAGNGVAPEFEFTPSSSALTRG
WALCLLCNEFGWTELLCQERRIALTHISASSQLHPWWLTQRYVQETHETLMFLSSAFVVA
SIRQRRLFPWQFFEKHRKYKPSVEMLGESNVMVSSGMHLLLVQQMLTQRRHEGGGGGIPS
QPVVFHGSLYYEGIKQHATCCDINLRLNCVKANATNRLRMHGMRLSQSIWGIDVPFTVVF
FAVDASEASQMAPEGVRKEKRLQCRVTHVLPCCWRVSGLKWARGVDQQASFSFLGTVAEN
FERDFVRKNETMEKEESEEGNDEPLFMKIPMLVLNLKIVPAALSISVQHDWFWLNLISPL
DALARQAILQRIMEESVREGENKVEETDLIFTPLMNQLLEGVVGDHCCPSAKSEGNLPAT
LFLSALQTVDLDFTAIGSRIRPGLYTRFTRLVLKLNLTASVATDPAGALRRSCGDDERFR
LPGVVMGVEEKMLSNLRTVEAYDASLPRPNPRRRQRKEEENEGQGKQLGPRLVLSLRRRS
VVQQAEEEKGHQEMRAKNKLEMTPLDNPADLAAMVGRIITKGAESNVADDTFLAARSAAL
SLVLPLWLLLHSRPDMSEAQQAALCDGAEDIYESLRDSAVANDLDPVLLKGYECLAQKAE
SRMGQRDCSGHP*
>TCRU_1011 MA3 domain containing protein, putative
MQASSRRHGRDEGNDEEFDKRRDRKQRRRGDREARKEARIMAHEKWVEQRRIMREEMRKA
REMKRQNRKETHRKRLATSDASAFPPRRATNVAKSMKTVSGHGKTLADTLDAGDARSPLR
AFASQKGPSPPHEEEHSPMALAKTTTSASAAEVTTIASATETNSAKYIPPTLRGKRTREK
NATLDEITRRIINKLTVHNVVDLTRETSELFGGAVKGSSRASVLRSLSEHINCMCMLDTG
PLTPIASLSFAGLIRGLQLLHGNVVGSELIESLCFALQEHLKKYNETSASNGAMVLAHLY
VLNAVDSLLISSFIRSALQMKGHQGVCAAACTLTLLRACGEKLLKEAPGQMEQALTEAKS
YKRQQECNVRYSTLLSYIADILSGHTRSAKRTVDEEEVPVELLLNDMTTLLPSGGKPSNK
RVLYRIMSTTSVLTGVTWARMMRTDKPSRWFVLGAWDDVDGNENSSVLPKTNAEAIFFAD
SGSENTDDEEDEVEVKAERIRQLRQQEKAISGQRFNTENKREVFQALTNASDDLEAFTLL
IHRDPSFSRLHDTFAVLLQCAYQEKVYNPYYAQVIQRFCSAKESCKNTLQFALWDMFKLV
RVEPVDVTGYFNLSCLLAHLIEAGVFTLAVLRGLDLDCTNRTIGLFTRILLLRLIFQLPP
ARLAEVFFGGDGFRAHDVKIDTSVLRSNLSKVVERYFVDEREAGKWIPHFYDVVSRGTFF
DVHRRDGAEGIGGDEGVMDDETRLQLFMKRIQVVFKALRGGIS*
>TCRU_1012 hypothetical protein, conserved

MQRPQHSAAHTQLRLQQRRRVQHKRRRHRVRQSAQLRVAHRPRRHNRRVTDRHVRVCRQV
VHKHKRAVAPGQPAHAHLQAPVTRRLAAVAPHVDLRTAVAHAVPQFDAQRAGKHRRNVEH
HSHAVRDGHAVHQHRVHGAAHRDGSVHRTAPQSHHHRMHSRQPRRRRNQRQHNKQRRTYS
RNGPAPHTVPAARTRTHRRPHPQTQTSTNKAVVVCRTRPVDHNSCPTNPFL*
>TCRU_1013 hypothetical protein, conserved
MPSRTSSLDAHSGTEDQVLHFIAFGVATWALRIWNEGVSVVIAYLLSAYGYYWHQADAQA
QLAFGSPLSWTRALDMDRDFADRFKDFGMALLQAFRTQTMITSGPASRFLNFAPAFARNN
SDCCDANCAIFVDETRPHATCAA*
>TCRU_1014 hypothetical protein, conserved
MGDAVVRAGLSCSATSFPEGCSTALDSVSVSDGNFSFFSSFEFCATFGALRLPSPAEKLG
AVDFFSDGAGADRPGDGTAGDGANSGVGCCTGGLLAADNDLEGIPVSTVFCTFFFPVVTS
SVSGLSSVSCSVEDCSSAFGCVIAGACDLGSEGARGVVPECTPVSEKLFF*
>TCRU_1015 hypothetical protein, conserved
MGTVCVDGKTLGSSATTVTRGPQLLDVSCFYVGGDGCSGSYCSQVTLTHVCLCSRPLTRQ
ELQMPLLRGKQTEADCREGKATPRPGNFAAKLPQDLGVDAAAREVLPVPAKGELGLGNST
TDVNGSTVLLFPKGIGDGAVHGCVPWAFSGFTSGSAWGRGIFMSRRVRLCVF*
>TCRU_1016 hypothetical protein, conserved
MPRRTASDVVTPVSDEAARGLSERIAVDCGRGRGGVPRCAVAVGAFSWSRSASRLRSTPL
AMGECWLCSAGSRAWAVAPNAGSAIICEAAVFG*
>TCRU_subunit mitochondrial RNA binding complex.1
MRRILQPPTYGVSGLFAMAIKNATGLRSGTGACLASRPMTLHVSVRAQGGFGGGRPARGQ
RGGGGGGNEGRGRGGGGGGGSGGGAAQSKGGAARRTVINKTGDGELSDFTRIVMRDDSHI
LKNIVKHIPQNGAISVKSLHAQLSPDVQEAIAEKYDGLKNFLEQRKQLFVVKTNPADGVL
YAAATPLAMQKLVAREKQRETMQEMLGINSPAGSGKRGGRGGNRGGGGGGNRGGGGNRNN
RGDGGGGGGGRGGFGGGGGRGGFGGGDGGGGGERFHRGRGGGGGGGRGGFDGDGGGGGGG
GRGGFGGGGGRGGFDGGGGGGGGRGGFRGRGNGGRIGGESRSFGTQGRR*
>TCRU_1018 hypothetical protein, conserved
MFVVGRGALRWKAVLQLLTHAGRGGTTTRGVTAFVRGTWPPSFVCHVSGAVVTQRRLHAT
SSGDGESTEKGASTSGSSDAPAASSTVSHQEAMERLLEEIQVVLSRPVPIGSLFRALSPT
SRKTLVKNKEPLEQLLMRYPEHFALYQQGNAKNKIIYCAPPHLVPSTARRMVFEEPPVVA
AVSSSSAQSKDGKGINERILQHDPVAERQKRINTVLQYIPNEWAAFTDLNIPEEVRVKCM
GKPSLRAFHYFEKYPQYFEVRQQGITDHSFYVRRSLALQRKTEKPP*
>TCRU_1019 hypothetical protein, conserved
MSRRVFASAVLLLFVVLVCCGISGATPANEEEVKNELINILNLERVDLFVPQKTQVLAKK
GTDSSGRDAFVSPSLVSACGVIAAFAEGHMNAQYTADGKVIKPISCDVVAEYIDSAWEWP
TLVGEVNESTWKAHTVLGKADGTNRVGVVLRPTTIMNGNKMFLLVGSFAVFYESGGNWS*
>TCRU_1020 CLN3 protein, putative
MIPVSVKKLEESVHVKHRIRNAFSLWWLGMINNFHYTLVLAGSDGIAEGYGMKKYVALIT
FANVFFGIISNFLNAFVIQRLSYNIRVTAASLMTTVAILLVSFAWGIGGHNNVAAFIVML
IGVTFVGVSSNYGSSVFLGYMERMPSWQISSWSSGTGLSGVSASLIFLGLSSAGMTSPQI
FLTSTVFVVVYWAMYFFGLKLPYCVPVKSSSTTMRNNGRSEVFRGEEEEVEYVCKAMVNW
KGTPWTSIVPAKPEFKPECLREMERARRASDFADSEHEEVANECEACGDAHLSGWARWKR
DVWPLIKVMHRATLWNNFNLALVYVAEYAVQFMAPFSFPRQVKESKNFWLKNSFVITQFC
YQFGVLISRSSLLCVRIRYVWIMSVIQVINAIAWFLQAKVKYMSDPNNMDRELKFAFVLF
AWMIFVGLMGGASYVNVFHNILEETRLMQEKELNEAMVFLASRQKNGGDAGGAHAERGEQ
ERNVVDGESKELCEAAHYITTVWKEKRDLAMNIGSIYSTIGITLGSLLDLLFTLVVLKGE
AEA*
>TCRU_1021 GPR1/FUN34/yaaH family, putative
MSNSNFDELQGEQFDGRHSNSRKTNDPLANRLLAALTADEEKSELMLTVLQNILNSNDLA
LVKKVALPKKRVNLSSLGMLGFGISTILLQSRNAGIFELGSVIPAMGLVMGGGMQLFVGL
LEYFDGNAFSAISFLSYGAFWLSLVGTWLLPHTEENALVVKTEGSLMGLYSLLWGFHTVC
MGFVAFLRSHRVMQFLFTSMAFLFFLLAAGDFSGKKEVTQAAGYVGIACGSSGLYIAFAE
ALEESLGYPVLPLFHVKRN*
>TCRU_1022 hypothetical protein, conserved

MRCCCVLQDKSMFAAKRRVIVPIHPTPNYPAHFIKASFTTDPLKEKQKARFSSGGEAMRE
VQMIPKNLEGERSRRELMSRGDTEFEALVEFIQGASYDQLISGRRFKKVYDKLSENDDTF
VWLCHTAMSVLNPGDVRSRLVYNHLRTLAEAVANGEMTLRTAFRFYESAVRSPAYREIAK
RQMEGGAATRLAGISAAADVMRRMGLTRRPMASYFELYQRIVERSEAMTPWGFPPLFQFE
ERLSLEPRLKFFSRASQQALERRRRGHIMSAYTTLQGRRIFWIPPTWNRAGRFLGPHVTL
YPGMTPD*
>TCRU_1023 protein kinase, putative
MNSCAPLIFDVPPVFKVESIIGQGSYGAVCKAVYGTDQIAIKKIPNYVKSEETLRRVLRE
IEILQNLQFCEQVVGCRLLFRPTSREKDVYVVMDYIPSDLSLVVKSKSIALSENIIRYIT
CQLLLALRAMHRCNVLHRDFSTRNILINYNSQVFVCDFGLSRFFDPDEQLSFGVVTQWYR
APEIILDAEYDAANDLWSVGVIVCELLLRRHLFPGKCNDSADQLNLIFHLVGTPPATVFN
EGQPFARASVNAKNYALSVIEKRPRKSMLRELLLRTPILQGKDAEKSLIIDLAENLLSFN
PRDRPTADKALQHAWFEPCRTFINEMIAAQDEQCTSPQFSSISSLSMEELMEKIEELVPM
FSEELLASEDAS*
>TCRU_1024 hypothetical protein
MSRRKDNKSHLKEFLRRLRDQGRQGTPQASAGRGRARTGEGSGRYALSFSGRSVVATAPT
RGRSYLPRSRKDNEDDSMPLTVANAALSSTDDARDQGREHQRRHRDEETRTSEESSRRRP
SRSTESDPHEVVLSESRASVLPSTSTGSRASGSTDPVSEHAARRADAGRGIGRRRGGDSE
KSLKRPRTGGP*
>TCRU_1025 delta-1-pyrroline-5-carboxylate dehydrogenase, putative
MLRRTLQFAFAYAKCPTIVNEPMDTFEAGSVSANGTLEACRRMRESVTDCPIVIGGKEYR
TDNVIRRTIPSDHKKHLATSYNATPELAQKAIDTALQASREWSQTSFRDRAAIFLHAAHL
ISTKYRHELRAATMLGQSKSPFQAEIDVIAESCDFLRFSVHYAENLYRDQPLSPSSGAVW
NSLDYRPLEGFVSTIAPFNFAAIAANLVACPALMGNVVLWKPSPHAVLSNYLLYKVFEEA
GLPAGVVNFLPCEPDVMTNFVNSHRDLAGVAFTGSTKVFMSINKQIYARLEEYRNIPRIS
GETGGKDFHLVHPSADLKLAAALTVRGAFEFQGQKCSATSRLYAPKSRWEELKNYMLGVH
EQLKMGQPDDFKSFMCAVIDETAFERNKKYIDIAKSSPSTYSVIAGGGCDKTEGWFVQPT
IIESKDSQAQLMHEEIFGPILTVHVYDDSKPGFWSDVCDVVNRSTKYALTGSIFAQDRQA
IRDATTKHLRYAAGNYYINDKCTGAVVGQQPFGGARASGSNDKPGSPLFLTRWVSARTIK
ENFDHSTQVSYPHQLPDRLFV*
>TCRU_1026 U2 splicing auxiliary factor, putative
MYQDRCIFFSKMGACRHGDHCTKVHVRPTSSPTVLFPMMYPNPMAIEHIQDRQWDFHFDR
KYLKRHFEHFYKETWRTFMELGRIAELRVVSNLGDHLLGNVYIRFEEAADASHIARELKA
KKLNEIILLPELSPVTNFADACCKEDLEGKCGRGAQCNYLHIIKVSRKLMEKLEKEQAKY
WKKKEKHSRGSDRKRERSKDRGRERSRSPRPHPSDLCHICGKSGHISRDCPLK*
>TCRU_1027 zinc-finger of acetyl-transferase ESCO, putative
MKRQRSLLEYFSKGREEALDVASASPTADPWAHGATKGVNDGLPLALETSAAASSSLAAT
TSKMPLRHCASDVAFHAAAPQIDDKENVGDGAPSRPPTFLRCAEKTRRMRNGARSPQAAV
QTSLDFGQNNAGGVLKCGLCGMLFNFTVKEDIRIHERCCSALSSGSVSATMIGRQFADGL
DMWIASEQLGKALEGVAQPKRRSQAVRDSTRKCTPEEFCTRVQETSDSELVLYVFDCSKK
DCVEDAVFRRLVESLQFSDVLSCASAYCLVSVVHRHAGCLLCAVAGRPFTRQQDPVLLLR
DSGDSTVTHCYTRSCMTFCDVPYVWCQSVAVLESTARDWWLTKTVTAIQSTRLAIQDFFY
PTRRNDNTQQRLHALLESALRCAVTTLGRHVSYGHTLCPRSEFSYDCSALSIDVLSRVDS
VTACIDSEGPLYTHNNGCDALVDSESSLSVVSYGD*
>TCRU_1028 ABC transporter, putative
MDLLQVKAVLDARHPDVVRVFQDNVPEVGLRQLDECVLEYLLKMLEGQMNPASYLPEETI
RHTLKLYLAEFAVCPSEDALNKAVDAICSEMETRGLAQKPKEDVSRLVNAVSIGRQYEEN
LKKATMINNVGKVTMINTNADWTWETKRNAAKETRRKRKEEEKKSMMAEEYEEFLRKRGI
ANATAIVKLHHKNEGGSYSSDIRCENIHIHMGKNVLLDNTDLNILTGHKYGLVGRNGTGK
TTLLRALTERELEGVSPFVQILHVEQEVVAGNETPLQVILAADVEREQLLREEQDLLKCN
DDEASTRLKEVYERLDAIEAHSAEARASSILNGLSFTREMMSSPTKNLSGGWRMRVALAR
ALYVEPDVLLLDEPTNHLDLFAVLWLEQFLKDWRRTLVVVSHSRSFLNNVCQEIIHLDDK
QLRYYTGNYEQFEVTRVEQLRQQQKNHEAQERQRAHIQKFIDRFRYNANRAKMAQSRIKM
LERMEVVAAIKYDPQFTFKFPEPEPVPGAYLQMVECEFGYKAGQTLFRDVNFGLDENSRV

GLLGANGVGKSTFMNLCYGKLEPRQGHVVRNKKIRVAHFAQHHLEFLSPQLSSIEFMRSK
FPHVEDQMLRAHLGSLGLTGDKALQPIYTLSGGQKSRVVLAWITFTRPHLLLLDEPTNHL
DIDSLDALIEALLEFKGGLLVISHDEHFITSLCDEMYVCANNTIKRFDGDFSEYREIVLK
QLR*
>TCRU_1029 hypothetical protein, conserved
MRYYPSGKDRDSHISGVRPGGKFGALHDVNKRRDILPEHVFATIRDQVIQEERLRLLDEE
ARAHVKLLLASGKNGKRMAGGAAGDERRELERVEKVEAIHARHRALLELYSLEKEQWRAE
LEHRGLSMDT*
>TCRU_1030 N-acetyltransferase, putative
MVAANNAAVNQSRYVGPELRPVEGLQIRTLDDPRVVERIRILDQYCLAVKYSDSYYDTYL
RPCGHQYNQIALYYDMLVGSCTCRLESTTNENEYRLYVMTIAVLAPYRRLGIGSHLLDTI
LRNVAKETKLCIREVTLHVQVGSGAMEFYKSFGFEVVEKVPKYYTGLEECDAFKLRKVVP
QIGTASTQSQRAKSGGVKNGKKK*
>TCRU_1031 leucine-rich repeat protein (LRRP), putative
MYSVIQPAASATEMHVSGQSRNIKEIDLAAVFLTRQDREILALITSFDLSHNNIEQLHQL
DALTALTRLNVSYNKIARIGFLPVTITELDLSHNSLPSLEGIGSLPHLRDLNVSYNCLKN
LMGLSRSQPLQVLRAGGNRIVSTIGLESMAQLRLLSLDHNLIDNANELHFLSSTTCLEML
SLRENPVANMNGYRTLVARLQLSVLSLDGVPLLRAETACPSTPKEVQKLTLAPVSLDTSR
KSPPPMSDAVTHATFPPATPMEGTLAGNNCLQEQAARGTEVPAPSKKVRPKCYSTRGEAA
PETAAGDMPALSECGQKNHIHDHNLPKYGSLQSQRQKIPEKTNQKFSQELLLASFNVEKS
GREPQTKKTTAVEKSKNLAILPSHTVERKLHEAELLLEDMRKENEYLRTRNKTIGDQLKE
ARRVITSQLDEINRLRLQLNSAEENEKKLKGRLDKMKRGARVVDMHTHNTVDAMAIEQER
LKAVYGAQIADLRQQLRCAHRQLATAVTAKITQPSGMIKEKSPPLSSRSVQGEADANDAS
VEIQAVIVDDTRAAPTSGDHNDTSLFTTNGETEEQTPGRIARLRAADIGKLAGELKNWLY
SEMAEDARRAEEERVLDKIRQSLDQDTTLKKE*
>TCRU_1032 myotubularin-associated protein, putative
MSVLIGRRELFAFAERYSSCRLKDYTDLADGVVLCNLFNLVFPEMRIRTASPQTHTLSQR
TQINWAALRSALDEVGIPQNLLDQGAIHEGDAKEGFSALVLFYFLYHLTKRTDFSAEFAA
DVSDVLTEFLQSIDSIAALFAGGALPLDAVPLQLQEQLSKATMARKRRTVSKHVQKGEGS
MAAASLFTSVEDNGARFERQLSFDSEVTSVGQFVLDDEAVRAKHVSNVPMMDTAHSGQPH
YHDKRRKSNKEKTASGKVPERNRSVSISSRSSQMTRGEKNLMDTDAVKREAELQQALIAK
SEECEKLKMQKMELPSKMEKMGEEKSVNVFSAMPDGKDATKQKLEEEQRRVAILEEELMY
LRRILQKTREERCNQIPLTGSFAEELLKDVVDTETGEVVNVHETATSLHGVILDALRDSP
RRRREAQRWLWLIVSAYHVIETRLVTACDVAAMEWQRLEKKIVDGNHHSHSGGADIGSNC
NSASEATAELPSTPGTIAKKLRGFQRVSPSSFSPGVAASTACVDLSKLETEMERRQQQFE
KQLADLHTNEKKLRQRVHQLEMRLRRLAKKTIERELNWKSLCASIHEAERTSFAIAEAES
AEEVEQLLTRRQLWYARADEESAVLVQQGADDTFDIESEPTGLHDVCEAMQTLVLSVTQD
RDRLQREIVELRKEMQTSVQLPETAAHTSALKDEIQNRLMEQKEYEQDEVWFVRAESRPP
YTLSCPSTKRASVTPQTTSRSVVQDGATPFARNLSVLLASVTPA*
>TCRU_1033 cytochrome c oxidase assembly protein, putative
MLCRSWALRCAAKGAGGKPRRIRIESGYEREGKKHYEERGQFFSAFASMSIMSLGCTFLF
VPLYRIYCAPTGRGADPKFYTPQAQREREEMDKSYPIAKKLLKVRFLSDVGNTMPIAFVP
LQKEVEVLIGEPALAFYSAYNRSNRTLLGVSSYTIAPPEATNYLNKIQCFCFEEQRFKPQ
ELVEMPVFFYIDRDFLNDPLVNWLDEVIVNYTFFNLEKTRDIIFRSNLA*
>TCRU_1034 DNA primase large subunit, putative
MQAIITTAKSFAGEEKRPRDVKAAAAAPVLDWATMYTRRPAGTSTLFTLEAMVAKRMELL
AWIDQLMNSPNVRSFSVVLDEIGARLPIERRKHVTQHAADHVVVLGRDDSPAADDADSFR
TPRLSVSRSSGSAALNAFVFEGDEDLISHLLARFAFCMSEQWRKWFVKTEEALLRARLKL
QMAKYETDFLPSLMRDNGLPCDPLSDEQWQDPLLQEYIVYFAVFQGKQQSRSREDYFSVP
MTLATRLIKTRSVLCLKGHAILHRDQAQEVFVTVFRSKLNKGLHEAYLARMRLTSNEDDE
ERETVMRMLDAFLEYFVSDPTSAIQEAVSGAVSAGEVRRIAQTHFPLCMRQVDEHLRREG
HLKHHGRFTYGLFLKAIGLSLQDSMTLFSSLMTVKGVAGNSEAFAKTAYGYNIRHNYGME
GKKTSYSSMSCATLLALPPVVDRFDCHGCPFRFKDEGAFRSMLLKEQLNPLGKEHPPLRP
SASDIEEIVQDCKGQHYTRACYKYFVATHPGVKRDTLFRSPFEYYTLSREVGERPEEILS

EQTTPARRLMTGDSLKRSMFTPTLKEDVIRERKSPP*
>TCRU_1035 glycerol-3-phosphate acyltransferase, putative
MRESAEKNVSSSKLEGVIDNGTHMKPHELHETQAVPTGDKDAEKAGKKQRKDQVSASVKT
GAGDAEMGEAARSSSLQRRRNSVKDRIEVTKHNKFVRCTVCGDDIPIGEWPDHRDRLRSV
RLLSLRVSKFHEFVVSLFIDFFMWVLMNIYFREVTVVNKEMVPKTGAVVFYGNHQNQFID
AMIIRANCGRPVRFIMAEKSFHRPIVGQFARMMHTVPVVRPQDVPIMPGEGFLLRMNGAI
VHGEGTKFHTSLANGDVIMWGKGTNNCTAQVHCIISDTELELTMPVLASNVVTQPTAFRV
SRRIDHSTMYASVYQTLQKNQCIGIFPEGGSHDRTSLLPLKAGVALFSLGAAERGISVKV
VPCGLTYFYGHKFRSRAHIEFGEPITPSEDLVELFSRDKRKATGIFLEHLNAELRGFTIN
VPNWSALNFLHGFRHLYQPPNCTLATRDYLRLARRLNAIMEAQKNNPEFIDFRNRVENYQ
DYCNALLVRDSQAATLGKLGTTEAQQLQLLFRRSFTLFLMGVILVPFFVVGLPIGFLASH
LSQRHRKKALSESSVKVVGADVEGSYKLLVGFFSVPVVFTFVSLVMFFYTDLRTALTVFF
SLPMAMYVSLLILQEAVIELRAALPLFMSVVSKHKQFRKLYERRQALVALTNELVAKWDP
ELAEEVQTYVRESKDDMKRREPSLFSLRHSGLRRLADRMS*
>TCRU_1036 hypothetical protein, conserved
MKSSEVQKDSIRAAILMECVKNKSLDVVYQRSVLYQRLTSQETRNLVYECCLELVEDPQR
RRDVGQLILNCISSFPPSQATLQAIANKCKPYATSRTPYSGIYQELKTVIDTYLHHKPLS
YMLGRTLPRGKEGLIFRQSELSRNPDYIQKCTLQPPIAQHTEKGKRIVPLSSWSNEELAV
TAGEKNRARSGLWTVKYHVVGCKDYVNQLPLECTEAVIDQQVRVLNSFWEKYTTNPALLR
ATSFLIKLMCDAYVSKIPLQSNYSFFRSVSICYLPTLFDLMGSTYACVRNHVYDILLTLG
IHFQLVDTQGIFPGCSKALEEELIWMLLTVLRKQSLHESSDEMVWTAAAKCALAIIPPHK
LYLIDVRALYQFLSLPVIVAYHPHLYTTFAEAFAKRILRWDPAGDATEEMLVLDEEEFKK
LGHQPVAKLLYLYRQSMTLGARLAFFQVLFTHAVTVLQSRSSLSRLYPRVLRRCYIELVK
VGFHWHLHSLLFYQSHQVFRELPGHITYDMDVKEMREYKTEAVAIVECILQIVEEDARLP
DVIMNAFRNTLGSRTEERADLATVLTDCLSMIPAMLKEDTDGDLYNIGWRMAFYCMRLSK
ENLGNERSTAIIETLATNLVSFSGSTDRLELAKIRSVCPDVLASLMFLGRKHANQAVEPF
STLILRFLLDTEVVDIQTVMRLYYRLIGSMSIQNGPLNKSAEADISQMLCSEQLVTAQSI
VDDIGARVLWALYRSLYPVQMFSVCRARHVLASFLDELEPVGGSSQAHSWKAVMADPYPP
VALIGAQKILQMYGRSAYDRFDEAMSIPQKSEKGDSVYALAVKVAQLAESRKE*
>TCRU_1037 methionine biosynthetic protein, putative
MEKVRLVPRKVDLFVQKAQEQGAAATEMADIVRLFPRRFELLGHVVVVKLNPGVTQEEFV
CYAKAFAESFSPRVVDVVLLDTEGITGELRLPKLVTLWAKEATLITMPRESLKYALKQFK
EQSYILSEDLKQFEAYADSPTFTTHVENGIRYSFDVCKVMFCSGNGTERMHFATIEARDE
VVVDMFAGIGYFALPLAVFGFVKVIHALEKNATSAGFLKYNTLQNRVGHLIRTHCGDNRE
VASELCGQCDRVLMGYIPSCTAFLPRAISFLKQSSHGDPVGTIHYHFLSDKKTAEETAKQ
HIRSELGEHVTSLMHIVALRTVKSYAPKIFHHVADIRFEAS*
>TCRU_1038 Dual specificity phosphatase, catalytic domain/Tyrosine phosphatase family, putative
MGLCCIAARRAVSLKKRRIKYKNAPGGTVDLDLVQIHRRIVCMGFPALGIESFYRNRYKD
VLRYLDHMYGTDYMVYNLCAEPKYRYDLTFFHGRVREFPFPDHWACPLIMIPRFVEDAVR
YITSVDHAREAVVVVHCKAGKGRTGLLTCCLLMEIEPSIGGLAKNAISYYGIQRTFDGRG
LTLPSQLRYVEYYERLRNEYGGEVPAEVPVVDIHQFHIRGIQAKVTITSCKWYTCERVCV
ISLNSSRCCNAQVIKSSPHFTTVNVANNDFFKKLSQDIRVEFLNGCGIVGVLTFHTLFIE
REYVYRGLDKICVLKLPESAGISFDFTSSLEK*
>TCRU_1039 Myosin head (motor domain)/IQ calmodulin-binding motif containing protein, putative
MPAGRIGTLAVYFTPAHHWVVGKITNYDPRRDTYSFSATQPEFINVDNLPRDSSKLWFPK
EDALNDDFDDLLNLVELHEASVLFCLKKRYLRDVVYTNIGPILVALNPFNYFIPAYVEDK
MEDYLSEGSVIEKNLPHPWATAHNAYRELRESGRNQTILISGESGAGKTEAAKIVLKYLA
ALSTKNGTPEDRELSIQINKRVLASSPILESFGNAKTIRNDNSSRFGKFLRVQFDKHGIL
VGCHATKYLLEKSRIIGAATGERVYHSFYQLVQGPLAKEFSLRNPKVYRILNAGECINID
GVDDAVEYASTRQAMGDVGITEEEQMSIWSVVAGVVFLQNTDFVESEERAGLIARMDSNL
LPVLARACQLWGINEEEFMKELISTCIVTQKEQTVKPLNKVKALDMRDSVCKSLYVWLFD
WLVLKINQTTNREAVTTHWIGLLDIFGFENFQKNSFEQLCINLANEALQGHYNQHIFTLD

MQECQNEGIDTTHVTFADNNECVELLMGKVGVFTLLDEECAVSGNETSYLHKLMEKFAPT
KGKSGNAHFLRATGRAVDNHFIIRHYAADVQYNVEGFLDKNRDTLKERMKQIFMQSKVAL
IPEIIPKEEVKTNLKGTVGGLFIKQLLQLLAVINQTNPHWIRCVKPNAEKQCRQFSDGLV
LQQLRSAGVLETVRIRKAGYPIRFKYDDFLKRYRVLFKNGVHGKVASREIVQNCDIDPAQ
VQFGETKIFMKHEAYFKLNHRREQAICRFSFLFQAVGRGSLARGQLFRDYALLHRRRIME
ERRIREEALRMQREEEEKRRVREQAERERRESLLKERRHKAAVSIQKVVRGFLSRHKFLM
VYLSTLRAREEHSRDDEQQKYRLYEANRHRKMCVLEARRDGQHGPTNTHRRELLRERRER
TMRLLEEKRLLHASKLEKEVAQEKAQRAKERVQRRKQMLEMWKGTKTSQKESMDLSGASQ
IVEKRFFGEMIRKLQGHAKDSNESPTEFSQNVGGDSRYQDSTFDIVKKQWEEKERWKDER
ERILGPRHEAHGSALTPRQRHLEGQYRIRTVSNVLWQLESKAAALSFQKQQR*
>TCRU_1040 hypothetical protein, conserved
MAQELLKEGTDGGGASTTALSTVTTSPAGKESVDLLASGTSPDGTQAVDGVSSSDGNQTV
DTADGGKTQEDEPHKTPADNANAADAKAPNSEGGLQDGFAVGPERTSGEDGETAGGTDGQ
EEEGIQPRIREVNATALSSSLGNVCRRGITAMPAPCVSADCCHRFFCWDCGGLPLCEE*
>TCRU_1041 hypothetical protein, conserved
MYVVNLCSLTLAISHVAHFASTILRLCPAAVICDLNSHHELRDGRSPSTTAGEDLAATPS
GMDSELSDDSARATRISGRSVSFPEVTAQLVLRVFHWTSTRLHGLGPPSGIADCGDGGRH
PATGRHAATTETCCLFPA*
>TCRU_1042 hypothetical protein, conserved
MRCASSAVVLTPSVSWCVRCCWGAAICCCAWCSGCVSLCFLVLSQVGSAALGDSTVCDDD
WPCALRPVSSCSDAQLLVRVSEGCCDGVRLRPAGDGAVTAGHARGVMAAEGGPVAGGSGR
KGNVNSEDNSNQEDEEGGGSIAGEDHNPTSGGSLTAPTRQEQSSSDPLRSGTCNPSGTGS
VSAARMRASGPESLGGGHVAGTTSPRSDASQQAAGGVHAGGGSTSQGSQASEQTVTGQSQ
VPGTAKEAPQGDEGGEPGAQHEADQTTKMTVVTSCAKTAVEEESRQRDRRMHRVSIVAGM
LIIIILSCSYRHV*
>TCRU_1043 hypothetical protein, conserved
MLAGLFYTRAAKRQATETKEKGGDLEGDSATNANKREVPFFLPQHSVVANDFPPASDLGT
PDPRQRISDEFISSADIFGIGEPSATLAANENYIRQPILDEQASLEKIKPVLLGWLVRKR
LRSLLGRALVAQIVGMKNSNGVENKLGSLIEHKESQRSQFISRLVSFLENGVITNKEEYW
QKKIDKTSKNVPKESGRRAKKESGEAGINRQLIIQLYSSDESKKTEEELLGSLQEAVGMK
NIHRDKLLRDITPVFLFERRSAFLRTIFALEDFEERFPQVPRLTVGNGQNMLSSDRSFIS
TFGGEYFQLIDNVNHICGNLR*
>TCRU_1044 kinetoplast poly(A) polymerase 1
MRRFLKIYSAREGARRWIALPWKSSIPPINDRCWEGIGSFVVQQALTSDTGRLAFEECSV
ARQQLENIVQAAGYDANVFVFGGLVVLGLLEVGGDVDFVGVMDVEPGVGEAGEIVSRLSR
EMRRLGMKSSALSKARVPVIKVDRVSKLLPGTPLHHLSACGLFQFTRQLNDNETQSFKKR
MQENYAATRVDWNNNQQFATIEFNSTTALVSALTQVRRHEGIDIPFRLPVDPRNGPELYR
LPFDFCFSSIGLRNSYLLSNTLSHYEFSRHLLLLIKKWGRRSGVINSMDGLLASYALTVM
CAHFLIKVGKLPKVSTLRSTDEPQLLPFFPEYRPLNDGKGLDVAELGFLTAAFFEYYGHI
FDYEKNVVCTTNMNLLKKTMRWEKSPGLETGRPPFFEFAIKDPYGLDNIGRNLDREATEY
VKDAHIVALKYILDERNDPEFTINNITQSPPRPQWKDRTLASRGIASSNCSPDQLEAHHM
LKRMEFHERRKAMERFGQRTVRSTEQQRVVSSVANDVLGWIRSDDSQQ*
>TCRU_1045 kinetoplastid-specific dual specificity phosphatase,
putative
MCDVLKKIQWSPQQRIVSSVETTSTETDISWLKLSNIFEGLFVTCEETICNRFFAQENGI
SLILTLNGSDYVAPYRVYEYSSDLQRCVYNKLSSFDAFVTQIDHYISKEIPEEIQLRKVF
IRSVSAEDSPAYDISRHFSELCTLIELVMLSRTKFKNCPSSLHAVVVHCLVGVSRSVSVV
MAYIMKRTGCSKNEALLLVKNARPMANPNPGFHSQLLYWEEGGFYRVVDSLTASLTANEL
RQDGALETYMEKYFPLLIRVNRFVCDREFFALVIAEAGLGEDSIRYVLEKVYSYIAFAIA
DELYVDIPAFFDNICETNASFARFLPTLFVHTEERTGYYFDDLLYYEFCKNLASVGDTGK
SFIIVKAFCSFFEAIGSKHFLNNPGGRPQTLDSFGKVVGTPYEELSLTFPFLPFLAPFAA
GFVPQQQLEALGKEKWTTQVMERNLSDLLSLFQENFLLTTFKTGISPDTFSAVGRWHANS
RLLFLESDMEVKVLESVERGSTLSDAVSPYLHLDHLDQNSCLTWMRKVTGAVIGTRFFYD
AVDRYFNAQFRDSISDDTAYLMADKFAPWEEIFKIIQSAGELYAKKCGGESPALLAWIRE

ELRPLVSIGVVSIPSP*
>TCRU_1046 calmodulin, putative
MASAFDEITRQFLKRNYDVFDRDKIGRVPLSDLITLLQVCGATPSELDVESWKKEADPDG
RGSMNFEGFCRVMMIAFQNMKTSRDLKAAFEGLDPEGKGLLSQTELRYYLTTYGDRLSTE
EMNEFIEEMRSEMDMEGNFVVTDLVYKMTPEMFR*
>TCRU_1047 RNA polymerase B subunit RPB8, putative
MVAVPVILEDTFTVTALNPDGVVYIKVSRIQCKNERGNITITSDINTEEFPVSLDDRLTI
MLANSIELSGQSGAKHYDQSVYHRETRLQDCDYAMHGRVYGHEVDESSLDVKVHISCGGL
LTQVIGTPQSLRDIHYNSDVYILIKRVGK*
>TCRU_1048 hypothetical protein, conserved
MRRSRNAVFISLDGVFLHHQRCSNRDAREPYRRRSSDPKTIREKGNFQRDMKFSKQRPLP
TAPWLQDKKRTYMDDAERLYGRKETWCNVKDEALREKLASLLQDYLKDMIDATRLDIRDA
KKYMRLCEQMDAEYRSYVAAATFSSPHLLRSWALTVCQKDEKESRMLSALGDSQEGSLSR
EDDVMDPLREEEEGDGANEEEHQETRLTRKRFLESRRRQGEEATLENTPATMDLLSGERQ
SAPYSAFPFLRQRAMENETTLDPSLVDWTAKYFPEDDDRTFSSPPKLHGDAEEGEPVLGS
SSTQVSSAGNNDFSSPKPSARRRLQRSLRLHQDMHRPTFDAEGVFYRVRRQGNDDDRASK
PREVRGSDACIDRDSEMVKVPWETVVKAKEQGYSVDILRAKERLMRLSRGEDPKTIP*
>TCRU_1049 Leishmanolysin, putative
MPAREHHDCDDIDGMELQDGDGDGRTLESHWSQRHARDEWMAPIGCAGCCTELTLAAPAD
LGCMRVKWVMAEPMRW*
>TCRU_1050 hypothetical protein
MTGNRLHSFGLLRGGFPLSLRGGGRGSATCVRMRRHAAWDFGFTWTLRSAKMPYSHEFHG
GHIRNPYVEQRLCAWRQLTSKVTESATSSCGVGVAGPTNFRPLFHLLTAKTRSALEESAE
NFIQGERRRLYAIYRPSPSGDDSLMPSPYDYVCVLQRLSACGMGVTSKIVYLILVELLKK
PLHPSQAGTEWDLPEEATVNVQARALEAVMSGLEGRDALEFAQSCLMPPLSSTTGTDGSR
HSGEMVLIHAIHRQLKGSGVNPTPVGVNGRIIDGRLIVTPFVVAAVAAALIRCNTNTKKQ
QAFELLQLASIARLRGLNLFDENVAERCAEAAALIGDAETVTRIIFILYRARGVLGQSVS
SENAAGENADDGVINSKGKGGGSLWDRVFLGLGLPASAEKRTEGDGDAAFRRATVRLLKS
VIHAALRRPNATDSREESLTAIREAVRLFGSLRMGCDWDGTASMAVELLTQMGVETRRYL
DHEPHDGDMEPLFYLHREALRVVIVLWDALPSRPSAYQHSVYAACAALAMKCYLVEVSIS
TENGMTVPVLAVPFFSSRIKQLDYLFAAITATLDLFDSMSPECQVQQMHLAVTFSAAAVA
ISSVRPNDGSVIEHIFSRLKELFFRTGLLTTNPTDMMSRFSSLGDQGTVCGALWLYMVLS
AGLLPVLLGEGEKMHAGEVLGEGMDKWVASALPSQRRLLWELLSSPVFHAYFSLMPSLLT
VMVSAVELALDTARTSPERRSEAVAMLRFLYSQRWCDSVADATARAIADRLLSSLLRFGV
TTASATDIAEKCSSDLETNFASEEVILVIGASGIQNARGTKRDLLELLREMASSCETAGV
SLHVGSSGAFTRRLILTLDAVILLVELSLRIDDGKCINEGALEVLSWLQQCPPLDPLFHQ
VLIMTPNSRVASLSVEMTRERRCSVWSQRFRDGVGESCAIALALADRITNPAQASRVAVF
LWDNDDEDDADDGAGRHTGAKTRYALLSRHGVRPLSRRRAQVQRAKADVMEILRASFPPE
SFTARHRRDQKKLCVKSSFERRGVVSPSSHIP*
>TCRU_1051 hypothetical protein
MNIWPSQSKAAERRKAAGHSPVDEMQRFRMLVCCMFCGICTSLIYAFDLFTTDFSNRFNL
SAGDQSTISTVGLVFCYFTIPYGFLYDYGGPFPLLIVCVLTAGVGALCLGLTFDGVITGN
LASISVFYALMNISSGVIDVAYIVTLAETFPRNLGPIIALAKVMVGLGSSVLASISVNLF
RGNISGFIYFIMVYSVVVCSVAAFVVVLPPYFINGWRRRGKTEEQIAALKSLEPAYRRQS
VPIRRLAVGYAVVALLLVFLSVQSPVVSYTRVSNGVSTAFGAITIVLVLSFFLMLLPVRW
LGGMDDRAGDESMRAIVSEEAVDRSEEISFTRADAAVTNAPDKEQCPLPEMTSDTADAAS
EIPQDPRYGGTLWDNLKRPDLWLIFLMFICQSALGVIVVYNASTISVALTGRKRSQQTSA
LYTAFFGVANSVGRVCMGMFEAFVQHQSPNKRRYLVTLALPLSPFLAAVAGTLLLTIPGE
AILLPYIIIYFEEGVFAAVTALIFPSLFASHHGVYYNVGFLTTVISVIGFNRFLFGFVVD
AKHDSLGFGPKEECSVAECVRLPLIVATCVETVGTVMAVIVHIRYSRFVREALRGRFAAG
AGRTVPLRVRCEDE*
>TCRU_1052 RNase H, putative
MTMGASRTTKLLGMDIDPRLTLNVAASRQCAATSQRISQLRGIAHKEAGPSPHDPRTFVI
GYGASKLRYGSELIWGVATDSAKNEMQKTYATLARIVSGVPSTVDPESALLEANMPPLHV

LCLRARLSIFENTRACQMDWMRRPPPEPPPRAGFRISPLSRDELYAFVDAYTKGYGITES
SPREERFFRSSIPPWFAASAHRVTIGVELPIDHSITDEEELIREKRRVSEEALALHSHRS
WILATDGGVDVPKSAGVGILLSSLNSSEIIEKASIYCGARPCSYRTESRALLLALEKLMI
PRIRHRRKTLLVVTDSQSLLAALNKGPLSQTDWTEDQIWQRLLTLTCAGWSVRLQFCYGH
CGVHANEPADQYATQTMESGQHTEQGIAPLWHTDLPTCFTTQLTNKWRSTSRQDTHRYLL
CGTRPSDLSGKDLITQEVLHRQELVHLARARCGESELWGRIYWAVRDCTNQCRFCNISPE
QSAYMRSNNDPTAPGTDTVPPSAREEDVSPVRRRTVTRCRKEKCPHCDSTLTGFSGLVSH
CRLFHPEHPPPLPELKCDFCDMVFPTRRSTAPHKIRCAHNPDATRHRNSSARRRSLLPQD
QPAFTSTPIGPQETLHHLLLECPGTLAVRQRLGIEQDLRLGKFSQWQSLHSRKLLSLLDH
LFGTQMASYS*
>TCRU_1053 hypothetical protein, conserved
MLLGTCIRWSKRTPGYVFWRQNTLVELEKTKRNYLLTERPVPIADIARRMVRVKSRYLDT
KDFHEQNLLRGEYKYFSGKLCDVRHARTEDMVAYVECGSFFGFWDTAQMNRVMDELLLKL
NELGSVELVHLFTSLPSLRKQSSNLYEYVARALVAVVPELSLDECIRVAVACDDGVPEEL
IYNLMRAIEPEVSRGGLSAVRAVELIDAFGTCLPSVQREFDSLFDNMKRTAVAGMMELSV
MDIAVLCTSLKLREELDASTETNAVRVFLSRLEETCARSTSMMFTAVSGTLAFAQAMEER
VVFLATDFTPSELLSVFSVYMDNYTSMYIVTSGDDGVVAPATKKSSSQSCIGELHFAQHR
QTTFLLVLRELMDQMILQMESATAYFLPAVQLQYLEVFSKAVENIGSNVSHLTSAVPVLG
RCLELLSSRVIASLQRYTYMELVALLQLCAPLGKLVADAAVGAAVQELIQREVGTSKEES
MELYSMLQRVSGLRAEHQRHIENFLLPKLRERSGWAG*
>TCRU_1054 hypothetical protein, conserved
MLRRVRLLHSPIDELTITGSCWSRLLARALPKTPPAPSPIKSTPFITLIPTLHVASVEFY
DKVLDYMVRAVQERENVVILLEGICDTEESEAQQMGEYFSIARNEELKAAMLQKADQNTL
YDDETVKTICEELAVNYKVLLKQQATVRLQECYLKPKMAALVGSYLRNGADLNMSEVKAI
LAEEGNGSGGTFFPFSHLGANPAVRQSRERKVARAAQLRCVEWIQRGCEGEVILPWGFYH
AEGIKHNIFATNAHDETVVFLESDDKLCRLPFGITKELLA*
>TCRU_1055 hypothetical protein, conserved
MGLCCGRSALPVVDDTGRQHRTLRPKVFVTPVPTLEFDIVAPEGSPSLALNMTRVSGGGG
IGSIIGGAACMDQSLHTVSEYSVSSPDPQGQSLSGTLRDEANRSFVTNGLNEVLSGNIDQ
FVTGVLEMTTSEPVNILEESLYAASTSTLSRTRNSRGIRQGLVTHSLSREQVRYLDAACD
MTERMARLVELEQMSRQEIFGAWRMNSALMILAMKRIMPTIRRFRGTPRTRRQKSAQEVL
IIHARDIELQMDEEKVKENGVARPGKLNRRHESSEQGPLFSPREEQDMSKRGQPVAEHYQ
MLALTAREISMTASVQAQVVNDTWDFLSLPEAANHLNTGNVLFRFLCAPVMKLGRDSLFL
IDTFINLSSFADEVQENNVPKIDIFSLEEQEKYVTILVKAMYLLPGVRLSNLTVDLLASL
DYQRNCQPGINKFEVSDVPNTFRTIKTVIRFVFSVTIQMKVSEINDPEVLNSFKDVDGMV
PAKVLLLERTKKNIHKIDSTVKVRSVLLYYPVNDGVLVTNQTILLNSSLPVVVSSLMQTF
GSQGATEAAQTAKLTRRYLIRRFGDCRS*
>TCRU_1056 hypothetical protein, conserved
MSVFVRKGAAGRVNADRLYAFNKTLKKDVLRERSYWEVSKDSHPVNRWSYRRWKRRKEEL
SIFEERLDKVPVDQKFKIKKLLTVANISVVGPIVLFFYFLFCYWRHRLWGITPIDGASAI
ARGVQNLPRPPGY*
>TCRU_1057 helicase-like protein
MTNRTRIFNCAYGFYIAMHPWLKGSGYVKVGYTANLSRRLEMASFTTCFTPEWSYFAVFE
LESIKEAFLLEQAVLFLFKDRRVSNRELIQGSATEVLEGARRVCLALNLNALVNMQPNYS
STESPVRGRSGRELFPDNVSSTHNALRPNTLGRYMEALEKLYDSVRKPALCDKITVDRGE
KFAENEEEEEYDLDVLETYKEESFSLTTLRPYQQEAVTRCREELESHGATICQMACRCGK
TPVAFKIIEYYLKNKRDTRVLYLVPGLTLLRQTVRKLYSYGLREIKYLLIGSYPTSVSLG
DGNSLMMTTDEGVIENVFKGSSSQMVVISTYQSSHIVSKLSVFDLTIFDECHRVCGSASI
TNFNSVLFQPRSGNRLFLTATPAYDTPIKMDNTHLFGGIAYRYYLREGIDAGYVNAFSLR
IVLGEEMDDMNPYFYEAMRIVDKMIVYCRSIEHAIQLTESLKCPFPDDTVPFNVMLAHSR
MGCRVVTDVLRDFSASKRCILFNVRLFQEGVEIPDLNAVFFAAPRYSSRDIVQSICRPLN
KMENKPKSYVFLPATIDKNLPETHPVNLQKFSTLIPFTDALMDEDPILFEYLIDPQKVSY
DIDVVGLRSLKLSSERLRKFVLPAIRRGVRYTSQNTDRLHRAARIPWKSAFGELRRIVLE
CNRYPKTNDAWVIGKKSVSMALFYRYARKGYRQYMNHEPSYLKVYQIRDLESLPLWQSYG

MQGPYPWEECLRTLRNYLSMHAHVPPLDVHKGGYIGLDATPFERLSGALMHINQCDAHDK
LRLDLSKQKDLDDLCGAYGLKWRKRRDASGKVIPGETTFINESYERFKKLYGSCHRNQFQ
KYIDQHFPGYPEKHERMEDPRNLKKGRVPPRHVSRDERNKMHSAGRVMCRVCRRHIAVKA
WERHLKSHPHLANLQQITL*
>TCRU_1058 methyltransferase domain containing protein, putative
MEVIRKSTRNCGGGKFSDPEAIQLHANDFSWEEKMEELSDDERKLVQNYLYNCEQKLLEL
NMKSITVHLPTPARKADAWDSHYRTNKRHFPLKNYIVLAFPLIKEMCSSSTQSKCLYVLE
CGCGTGSTLLPLMRQFGENVHFIGFDVSDNAVSVLLDHPLSKEFIEGQRLTVFTHDILCA
RERPVDGPEKSRVRKESGGLKSVILKRVSDCTHGVDLVLLVFVISSLPSLESMVYALKEI
AEVLKPNGFLLFRDYAVPDHNLFRFTRQGNEVVNDLAFRKGDGTLQMFFEANFIRKLFAL
AGFKEVDGHGLQYHCNRIVNRKNSKKMDKVFINGAFCLPPT*
>TCRU_1059 RING-H2 zinc finger, putative
MQEGCCEAVSPPEGNEGQRRFELKRWNAVALWSWDIQVETCAICRNHVMDLCIECQANQS
LSPTDCNVSWGACNHAFHTHCISRWLKTRNVCPLDNKEWSYQKLGA*
>TCRU_1060 hypothetical protein
MDRLKLSTKALLGMATRTVDQDHGMRHTCVKSLFQAVVQYEFAISKLVAALSTLSDSLEG
VEKAYKNVISNEKQVSVFDGLNEVTNHLEKCRTTVISGSIETFRANVAPSLSALKEHCEL
CERLHNERAKAVDLYDYHRDVVEKKEVQYASKGKLLDDSKRYKEEISKRDAAHDAYLAKH
SEYNKAYDEFMCKKSELTTLSGRLFFHELLDIAEKLKNEVSSMCDVVDQIPLNPVGYKET
SAPLGGGVDAETNVIEYTINRDSSEAKDADAAVLHESTDEQSPAEICGESKNNAENTTGP
AEE*
>TCRU_1061 syntaxin, putative
MPMSRDPFDESVSDVSELVAKAKSVQESFRAKGIVDRVLIEEVRRTLDAADEELELLKNV
LQVIEQRNGRVGDQVFSVNEVLRRQGVVRNLETELKGLRTFSDAVEVRVVEAEKRLIMNS
NEIQVNDSFLLGQEQIQRKEHMEQDIILDRLSHGLQELKETGVNVNDELQQQEILLVEAQ
QDMEGVQARLRVLNTKIDKLLSSMSNRKKICTILILLVTLVFLASIVFG*
>TCRU_1062 hypothetical protein, conserved
MEDAVTLSATLRRASPLTRRRALVILFALRGVAKKSDMTLSLTSITTALEFSMAGRPARF
LFATGGHASVLRSHDRGGTWRIAYRVKGTSNDHMEEGVPPSDKMVTMEDIAKFLPSSESA
KGQKWYLASECSATELKTQISHVTALDSMLAVCGSRAFLAVSVDRGMSFFCVKEEDIHSF
MKDEPSASCESWQIDGVAFLSDQLLMFFSKNSLFSIELIHHHHKQQQQQFGVVAFGRVRL
VKKFAVPVGCLKTFSQSGKFMCELFVSTKGFLHYSSDGGQSFLTFPHKIGIIRAIEPLDI
VLRRREVPQLPNLLLTHMQSAATEETKSIKTGKYIYRAISRRDSVEEKDDGKQNVVDSGN
WVTTGAFPYCSENVHYRVFLVGGIGTSILPYDYTALLFIAATLNDSNGRIGLLGSLAESV
DYIPYVRSGAAEPISIALCRRPGSKGCVFARSNASGVSLSSDMGRSWTTPTQAYTVAVIA
MDGGEFVCCNRRNVVSNIHGDSREVHSIPADLRVPYLTDAAVML*
>TCRU_1063 WD domain, G-beta repeat, putative
MSSVPYLKPTQFQSFAGLFGSGTAALTLRSCEDSNMPHHLIVGGEDGNLVLVDYELGTTT
RRWYGAHGRDVNSLTRPLSSGVFASASRDKIAKVWNLHSGEALCELHGHTANVTSVTMGA
EHNFLVSGSRDNTVRLWDLERAEEVQCCEIKQNIVQFTQWVPQLHCVAQGGEDLTVRLWD
VRMNANGKKALGLSLATTLACIEYHPICCELIPGEETCGLLTGHNGFNGHGAYVVEWDLR
MPKCLRIFHGHAGTVRSIRTLPRQDPANHGEFVSAGDDGAMIFFSMGPSSHETDVAYDPR
SIFKLNEGRVTCLDVCANGDIFSSMWDGAVSVLRCTSPKKGVKGTFKRFRCFGAEELPK*
>TCRU_1064 hypothetical protein, conserved
MVVHEIAAQPASKVADVARSLAVKGDRVEAVYIAHEILEENLAKLPVMIAETRRPASSYL
DPWKSISETMESLCQDVELCLQLFSMGANIQRFKGLRTVASLYDQKKPAADRLRGFFLIV
SLSFTVDDAVTPMPARILRKFAQAICIFDAIQAAEWLSVGVQNMLDAGRLSQLSDSFLVS
RSLICISVFGGEKTAPGCGKAKGTKASLMTAILTLLIRCRADAGVTRMEVHEREHELRGF
LEDDKLKSLLHFESVCATAMAEKKQRIQEKMARRTADKRATAATKKDGADSKEMNADAHG
DKTSYRRYLNSSLEYFLGSEWRQRPSRIVLVVAGVILLLLMIRQVASIVARGLRKMKSLP
HGARKTLTL*
>TCRU_1065 cysteine peptidase, Clan CA, family C2, putative
MTTLEDLYASYCRRRGCRPNSFLSRYLQEEFTRHSQQRVLESVDLSDNYVGAKGIIPVLD
LVKNVKTVRRLDVRKNMLEHEQLEHLVYCLALHPSIEEVDVSGNALDDGSVDIILKLLQA

NESITVFRVDGNHFASSSLSLINDHLERNKERKAERQKEMPPVYTGKWFRAQVRGSLTEE
TSGGHVHFSTWWKNQQYIMRVSRRAQVRVVMDVDDPKAARQAGFFVFYSDGTRKVIVADA
DHIAAESNVDHSHCFVTLLVEEHAAYSIMPFTFHPERSMSFTLMVELCQESLKSSEGWVT
LEPVDSALDWLVYVMHGEWTSASAGGSPTQHLWCRNPMIHVQYAGSIQSYRMASPATVFV
QLSKSIDADENDDRHIGFDVVTLDTTGNNKPPICCKEESRKCTCPHEHRTTVTASFVIMC
AALDLFIVPSTAIPGELGSYTVTVFSSVPLRLTTSAFPHGWNYRAVKGVWDEDNCGGSRE
RSMSWKCNPSLALHFDAHQSPPDLTLFLEESLPRPKSPVRRGSADSCGNLMDSLSAVEET
QKKKELKEFLHRHQLSHLEGCISLVEACPPMYRLLYSSEYSRGSVVSLVVPAVSEEFFLL
AATRHAGQLGNFILHIFSSRPFVTDELKTLALREREYQLLQCAQESQARQAANSVLAKKR
SGPKDSEDAVLAQNEILLRCMVTGEKYVDRDFPRGGSSLWIDPAKKTPAWCGKEIYWKRP
TELVEEVTFLREWKCDCPFPFSRREWFASVTYAIATKPLWLQNLTAGYNVTEGLAQFRFF
KSGQWTLVTIDDYLPFDSTMELCMGRPSRDNTDFFFPLLEKAYAKHHRCYEALELKVTPE
LSIVDVMCHGLMDLSGCAPVHFPLRGSVEMSAEQQNILWMKLKNAIQQDVLFTFLLRGDS
AEAAERISLGILSDHLYPALDARFVEGQRLVKLRHWGQVGEVRWGGKWRAMSTRWTTILR
DLLKFDEDDRETFWMSLDEVFFYFTDLIMTAGTKHTSWVSADFADCPKECGTPVMEGAQF
TLRLGDFPPDLNKTQISLGLHQPDARARVIRQKNALAAYRTAIGLAVVATEDNTVWLKEV
READVVKCLEPCKCRDVMCSLNIDMDNVKGSKRLTLIAFREDQKAANVPFLLSAWSDNCE
VALTPITRDIKTTVSGEWPIGYPVGSPSSSFWRDCPQYFVFPSESTEFLFVLRQDLPVGE
LPKPIGFTVHREMTCRSYLEYNPDTVVLYVQAVASACVEGTVRLLGMKERRGMPYIIVPF
CTEATPGGKFWIDAIANRSSRFCCIDPRLDWYRDRKSVSFTLADGSFGGSPRFSSWRSSP
QLALNFPVGGQGRLFVVVRNDDLSDNRTELGMMLLRGDNQWENGLRRKLFISSGDIVARS
EEKIGETVIDCNVDVQPECTLILVVYASMPYREAAVTVALYSASAVEVEPVKEWAQVAVA
EGSWELGYTAGGGSDQFGSWINNPFVALNTYRRTQIVALLLQYPQGPDKPLVKRAGKKKA
FLPPIIINPNNRMMIALDLNVQNSELTPIASTPYTYNSEVTLVAHVPAADSLPFLFIPHT
KLPEGNGEFKLFVYADSPIELYTLEKKRLPYV*
>TCRU_1066 DNA topoisomerase IA, putative
MMRRTLAALEKLVIVESPNKVIKVEGLLSDPNVVPDWSFKQEHLRRLGVGAEKAVAMATT
GHFMAMKEIQWTPRAISFPEVRGAGEEPFPPNGTVAEYTLEWQLLPGRRIQETLERYIQE
KLNNVTEIILATDPDREGELIAVHALQTIKRLYPKLKVPYSRAYMHSITEDGIRKAMRER
LVDKCDYDLANAAETRHAMDRIFGFLGSSVVRAANSQMRSIGRVQTPALILIHEREEKIA
AFLEKNKTNYIVDVMCQFPGPHGTTFSQVVTINPDVKGEASHWATEAEARRCLHGWKLNN
CSGFTVPLEPLIVPSEVPPPQPFTMATAIAKANRHLKMSSETVSGCLQDLFQLGHITYPR
TDSTRIDESALTDIYATIKKEFGKEFLYRLEDRTVSAPEGKKSKRTGKKNSTKQSKGADQ
PVGNVEDAHEAIRPTNIYADGESLSLPPMTRAVYDLVRRNTLASFMIPMKSEKIAATVKF
TSGSGDKLQVVLEGKRVAEPGWTRAFQKTDFTAAAAGAASSTNNTTDSSVNDKNTTGVAE
EVTEDITEKEGAPVIRSLSQEEFRAIANLRSALASLKQSRFFELRSPSVRENRPVPPLLH
SEGTLIEELKNNGVGRPSTYPMIVKTLLTRGYIAVNPKGRCETTPIGRLLVSTAKSTFPS
IVDIGFTATFEKKLDLIAKPNPAKRPTILRGTNVSQADYFLSMFLSTFLNYVAEATRAQR
ASIVERSMRLKHEQEEGSGKDDAEFEESVANAKKKVALATGDLMALPKTCHNFTALQRGL
HDYLRRHFPPSRLGSFATAPANADGNNMMMEGTSPHMISTKHKLEKSSEV*
>TCRU_1067 protein kinase, putative
MPWSARGQQNSATGAGVQLTTLPALGTVGASTAASNLYSGDLGKQMAAAEVSNKISSRAL
LNTTALRTARSISCMEVMNNESSPDLSSKEMGSIHAMLLDASPRQGRKDFKAADAGTSGK
ETTPILVKRCSDSSPSTPLGLNGLRIEETGEQNTVTLEEMLREASEVHGISLKWILYGVM
LVTVLIFLMLLGEVHLFVKDNIIIPEEELVGISSATAMNQLEWLQYGVTNMLHNFELIRG
DPHDTSTNYTLGILCRSIGGAPLVFARYGPLGTPLLESYACPSATTKPVVPPTSIGTQHK
LPTGFPRMAVYRSDFIIAMMTLRAGSEVLTVILHKEPVGRLLLANSIPTYSSLALKHSAT
SFFLPDFSSLKIVVALHSLDAEYTRYDVAQPTPLGHVLKNVFNGICAAGKFHTWHTVVRP
DTNPLPMRENDMNASHNALPGAYVAYRGLWGSVSRVVICGVLCSESEKNECSSDNPTRVW
FIVDDEPLRRETEIALTAVSIISSIAIFLVLVALVIAYLSISAPVQHLKSLVFNTVGDKW
KKTKQQQWVFHHTRNCWPGDLQALVRSFQVLSFCFRFNKKYVPQHVLEQQVVALRKRKDY
LWRTIVEEIESDDDEEYDGEEEDMVPGVNDRMDMEAFVKTVAIPDGVAAMGRFNGPEGMF
QRELSWCGLISPDVEILEASGNNFLGHSNIDLAGGGMTLVEGATVLVVRLCAVELAYFTN
YRAALKPHRRIMNLLLGRIRRYRGELFERSGDCIAAAWNAFESRTDHAQRAAACALSIAK

MLSCYREAGFRVGIVLHQGPFVCGVVEDNKEAFTTVFGTVPRQAIALAELASSLPYFRVL
VSEPVKQSLASLYECIMVDVIKYHEEDNPIVMFELYEERRLPLVKGALLSSSTFAEEHAR
VFFDFRNHDFARAMMGIEQLRLRFPGIGRRLLTRIEILCKYYMYHENELPMPYFRPFPIW
PNFEAIANTECSSDIGVQSTKEDSFLDPPRYLRPTKSIYEDEAVNFRQELHDKVLASKRT
QNQSPTLKAANDAPSKDAEANNAQSPHSLIMLSQTQNMLRSTPSLEPETGEGDDAASKEH
QSKPLLRVAVVSPHEEHAEQCVEADKKRCSGASAGKEEVNREEFAPSIREPTANACATAA
VSATGSDEKGDPGDEENDGAGRQRFSLTNRMGLAFPDCRSCSFFCGTDSLDSINSETVVT
APTFSLCNIDGSLTKVASEIPTEIVAKNGITYQRSSRILGKGSFGCVYLGMDILSGRMVA
IKFLPLPSEEEEIANVEREVVTMQKVKSNQVVEFISYAFKSNLIIIVMECMMAGSLQGMI
SAFGSIPGTTARLFIRDVLRGLHKLHSLGVIHRDVKPQNVLLTLAGNCKISDFGASAFLQ
ELVRRRMEGKGLQIQGTPVYLAPESARGTPEEKSDIWSCGIMFIQLVTGKLPYAKPFLEM
SPQILVYQIGSGAAKPIIPESLDEFDAEFVCNCLKDDPNERLSAQRLLELPLFAL*
>TCRU_1068 hypothetical protein, conserved
MYLRLQRLLTSSTEGRIFARGRSGFLSYPMNGRGLHLSGPRLSIGSGSGSFFAETGFEEE
QLQQQWASDTVNTASEISGDGVTRHTPTSGGEKGALNAQEVCGLTAASILREAVPLTSSE
DIKDLLKGCKNAKELRHVLDTVLYRNPLCHDVLNGHGYRVAVLQALTAVAPRTQCLHEWF
DCVDNFRRLGFVLTRTFAAEGFTVIREWLSHHFNYEGRSPLLVTEGISHIRELVQFCKED
RLVFDHVLYTRIVFLLTMIVGFFDRQNIYRSAFPENFTKRDGVVVEWVISCERCVDFDEC
VLQCDAVLEEVLEMLRQDIPSRPNFSIMYRLIDYYFATDNVEKMIAVMEDTESYGIDIAE
SSTAKLMQLACALNYPNVPELFMRWRVSLPQCVLATPDMSRLMFYYSRSGGGRPCPLCNE
PYNHRNVSVYVWQKTPEHQRNCQALMDARRRKGELDENTTLPQNQDWSEMAFGLWQLSQS
RAIEWGAVEWRGFLLCCMFSPRALEAKGLLDKFFDHTKMDDFLRATYVRLLRHHAPELVF
SALSDWREKGQRLSPIVLQESLMGSVMINEANERQRAVKHIWKALLEKDSYVMPFTKRLL
QRRLEELRARTTGGITSEETALFLEIIGMQPRHLSLLDMKDSTSDFVVGISKKNYYAPHT
SSAGAKIESGRQRRRA*
>TCRU_1069 serine/threonine-protein kinase, putative
MRELALPGYTHVQHICSGASHETLVAQSDDTKELVLIRVYALDYLRKHPSLRRRIERRAL
ASRVAHHPNIVKGLPAFVSDVDLFLVEEHCVGGELLIALDEYYRSTAAPSANDTGRQPAQ
QPFRCLSLSFIRRTMQDLMSGLHYLHSVCGLVHRNIKLESIFLDSSNRAKLGRLEMCAAI
PSFEVKDGMLQLCCASKHYAAPELVMGCPYRGELIDVWSAGVVLFVMLTGRFPFEEEKEV
VDGGDSLLFQRICTADEVLQIHPALGMVPDPLAVGLVRNMLRVNPECRLTVEEALQHPFL
LTS*
>TCRU_1070 leucine-rich repeat protein (LRRP), putative
MRRVAKHANAAISTMRWLWTLHDVAACPSIDVLRLHMCQRAQQETEWDLDFALLSSLNKS
HAPNEVLRCCCAAMSSAAHSVERIAVAVTSAAVGGALARVLCSAQVESLRTLHLTLHEAA
FLRDDLSLATLLRSTAHFTSNLNSLCITMVACDMQHGLQWNQKSLRALAANIPSLALRVL
SLEYINLKGANENDLMVLCEAIAHCHLLTHLSLRGTRGLLPRVPLLRFAVAQMRKLEVLD
LSSTLLGDVVMEQLVDTLRMSIGGWYRLRQLNLLETNVSVWGLRRLLRDVGETSHGETAK
IELLNFSSNSMDDEGAFVLASVCMHCGMLRELHLRHNRLTKKGAADIGSALIAAASLRRL
NLHSNPLSDEGLFALLQYANYWPELRSLDFTRCRLTARCLPALCAALPLFDRLEEISLDR
NDLRVVDAGDASTTEDKRETPEGDLPLFAYDPKFMQGGSRGDWKVSTSFELDRRDAIEGR
RRFKGTESFQTPLSSRESIGGVVSFEQLGLALSGCRELGRLSLSSCSLTDDCFLAMAGAL
VVRRLTHLDLSANPLFTRMESLEALAKLLRRASASMQKLDLSCTGLGSVGASLLVDGSPT
DDTNGDADEAVSALRSLTALTELRFSSCRIGAEGFEAIADAFPAMTLLERVFLDGNAVKK
LDTILYLLSALEALPSLRFVGLYGSVPPHLAATVGASREYAALQSKGVVVHL*
>TCRU_1071 hypothetical protein, conserved
MKGPKKRYRGDGDDHQSYHHHHQQQQQQPRVRYADLAPEVKLQRRREERQVKKEMERTL
SYFKSVQRALEEQASGAGDASTLASIVDGFFVELIKLLKADSTLHLLRNGLVCRVIESAL
ANSLLLHSKSLLYVLLGHVFDTVTSPTASYTMETLLASLAQALSALADDEVESFEAEMTD
GGPGVHAGSGVPSAATLITYVVEELSERAEEIIVHEVAARAVRSIVLVLGGFTIRGAPAL
EHVVKFTQPLGALGVALMRGLEATFRDHNSRHAADVWLNIANTPTASFILQSLLRVCEAG
TEVDVAVRQRLESINDDDGVALLRHLLMDPMGCHIFQAYIKVPVPLELLEACDVLSNRRA
RAAAELTSAKGRRLQEILRETADNVTDEEERVVALRAQEKTCWDKALDVVMEVLEDIFDP
AAEQMNPVHYVLQDLVLFAPTAVHLECVWERLLKPRIRMFVSLPAPMHVLAAFARKCAFS

GSLGPRDGGNNGNNYNDIAVAGAVESSSDALPKDIDQLLRTDMARGVRYFTVSVNFQETV
IKTLCSAINEECKKGAAQFLLVDGNAHEKGAELARYILHFQPLASAMFVHAMDKLSLKDM
EFLIRHGKGSLVVQQYLRAAAVVQTLPHAQGNKGEEKKLDKTGPMRFLRRIASLLHDLVG
DTYAAYVVEVLYEVGSLEVKEELVKLLVPIYSSLQHGHEKASKVEDRDESREVEEDGNAT
AANRPQMRDFIARKVMTKCCVELYMHRPDDWTKLARRQCQVMRLLQRMSAVSS*
>TCRU_1072 hypothetical protein
MANSRKELRAVQDRLEYVERREKEREQDLYGQLKSMQLELSQMRGNFTSAENECRQEMSR
LQREWQKATAAAKEAQKKAENIWRDLILEERERLATEHQQRERERFDSLHHVVESLANEL
ARLSDIVAATRTWNSQLSSHVEQELERHRSWLKRHKREESEFLKLFEETCTQLQDALLHE
RRAREESMNRIEKLLTRRGVDSAASPVSNLHRF*
>TCRU_1073 CHAT domain containing protein, putative
MGGKTNLCELYRTYCAEEGCRVNSAVLQYIESRGAMCPLEKLELGSNYLGARGLRPIIRL
VEYSQTLTSLVLDGNGADNETVDRLCEVLEKHLSIQYLSLRKNPITVTGGKRLLALVKQN
PRIVGVDLQDTDVFDALIYKITKVTESNHGRGMRERPQLTATELDGTQMSRGHIGAAATR
PSAERPTLSTLPAISRDAAGKEALSKVIGPLPHRSSVAPVITKIRTRPLEPALASKECGR
LPDLQRQELQRRYKEKAILSREINSSQASRAADRAREELMLLEKTAKSSSSRKKCGAKTT
TAVSLPENTKNRKSPLSHHAQTTDFTEMASPKINVDASLLPQQQKDKDNGMQGPEELDAA
ASISNSTGELIVKGKSGDNNEAGADATPLPDADAHVVAPAEQTDAEDAIVKKKTESELVA
TNNSDDIPLDILRDTPQWMMLDSNEQFQRLFDGGCRAYVRHDFDEAYTTWNEAMNIAASK
KNREWMAVLSSNLKRLSYEILVREGVEELKQDHLEEADLIFQRAQEVAQEARNAKWEADM
HKARKDVQHAVFQRCHEAALKVFERAQQVHEHKLTEDDYFVVPGTDVMVQHTETYVNVWP
RMLLVKEAVEMWAASRRVTQRIGGTESRVLQNVVNEALDTVACFLAKRCFDTEDTQSLSW
MRTSLYSYHECVMLSSLWTDMASCDVFAEHHKLFAALAAAQIGNFYLATNQLSEAQAQFD
TLEWLAGELDDPLLRAAGHTFSAIVNWQRSRYAAAEPLLRAAVLEWGALRDASSSQRKKE
NGGDDTADSNEDKTCGSKLLASVPTDYFSIMESVSFKYLVSSIASTYRYSEALEVLEHSL
VCKYRDLLFDKMRVNFGAQPTLERIVATSSLIRSPFIYQVATHRYDWSVDERCYVVDEKL
LMWVVLQRNEMRFVEVGVTKDFKVPSINGLIETLRRGLLLDPLSSSGNTETEITLSLPKR
AWVEPLQTLYAIFVDPVVEFLRALDPLFLSKNGVITMIPTEQLWLVPFNALIARNGNFLV
EDFAVQLAFCATQCAFSVLSAKRVLQRDLQRDVVLVQREIDAPALHLLSHVAFPFDSLRS
RKEGDLIVRTLAENKRSVLQSTRTTDSVCVTTSSETLVEDLDAFRELLPKSRTVFIATST
TSATRNDDNSAGAICMAVSHEEIDLLRSSEISRMRLFAELVVISNTNMSNARVAGTHDDV
QGLIRGFFSSGVPCVIVGQWCTPDMTPSELFSKFFQLLSEANNKPRRFSCSHEVATTAIA
TAKTTTSDAELKHPVRANDEDEVGGHDAACFYRHKALLLAWAIRALLEDNFFRFAPRTWA
GYCCVGYGSHQ*
>TCRU_1074 hypothetical protein, conserved
MADHQVLFFGCVAVTLTEVRVKDAVFPTKMQNNNGVNFFVRMAILPKEGNETEERMGEYV
DSSMHPLKSAEMAEELLIPVMLERALPVSAVAGGLSLSYETPKQNNEKDHIADDNGTAVR
GDNGHGMSVELHLEVAVARGTLQATIAHRKVIIESLLNIAHEKCGVVAAHVSADALRQCA
VWGKGFSLPTTDKSCVLEETHEDDENDDDGVCSGMEVEFIVRALDMSEPLRFMLAAECEA
RNLLHMPKREIQTTFLLPALRLPYGALPLFLLHQHYRRFYEHFFNKTLNPSDQVAKLLSV
DDGNIGACRWCALSVVDMRRNILGEEALAPLLATLYHCPSLSSLVLDQNSLGDFTCYWIA
ALFHKHRLLREVSLYRNNIHECGAEQLLRLTRRNKILTQLNVIGNPCSPQILQRIQRVTE
VNQAALKKDPFNVISSLYDYAVSPNSFSPDIVKKALILWAMLSSSSLKAADSTLESKQPS
LIPQCALAPLLNEVMRTVALEMSFLIQDHFIRMVFVDIETHWRATPSLQDEDGKPALEED
DGGRETGHGELRVWEGNDDEGEHVFPPVDVEELYSYSFLRVIVVTMRSMLREGDWAESKT
VLQAIGRSQQAIGVTPEDYRVALKVFIRALTIVCGGEHADAENSAAFLQLLALGVRTTLG
VQCHDCNK*
>TCRU_1075 major vault protein, putative
MDPRVVRLEPYEYVHILDNNTCKVTLLEGPCCITLLDHLVNLHKNAQHHIVIPPNHYCEV
QNPVVLSPDGGEPTYRMGHREVRLSQPPFPLYPGEVASDLKPMRILTSKEAIIVRALEDH
TTTEELTGKTVQRIAGEQWLVKGPGAYVPRVDEEVLRGVAPLLLSANEYIQLCAMADFKD
PDGTARRVGEKWNLLTQGVFFPGPYTKQEPVKKGITLSPTLALHVRAVHSFYDTRFGIQR
CLGDRWLVTHDEVALFLPTEDEDPETTVPLTIVGQQQYCILLRTVQDGAVHDGKRKLLKG
PCSFFLKPGESLQDNEVKDAYLIGDHEALLVEAVSSFAEEDDTWREVSSRWLVSGPCSYI

PPLDVCVLERRERLLLTGSQGVYVRNVRTGMVRAVHGQAIMLAADEILWEKPISPLVHRL
LQADTFSVYDAGALKSASEKEPYASHKVVFYKVPHNALVRLYDSSTNTSRVEEGPAALFL
APNEEFTPISLSGGRPKASNRIHSLCLFLGPDFMADVIEVETLDHARLMLHLAYNWEFDT
TDMERIKKIAFELPDFVGKACNTLANRIRAAIASESFEEFHRNSSSLIRQAIFRSHLGTT
EMREDGLYFPVNGLLITNVDVQSVEPVEPNTRDALKKSVQLAVEIITQSQENEASHQAML
LEQEARGTLELQIMKDKASEEAERVTLLQVTAENTAIELSGSSRAQTLAESEARLVELQA
ELDVTPNRCRALEFMTDAELDLQRERMEIEISHRRAMNDLAVQKAKALADFEATKVEKIF
SALGRGTVTAIARAGPELKAKLLQALGLKGFLVTDGTSPINLLGMANCMVHDPRGKRA*
>TCRU_1076 hypothetical protein
MAAPLREVVIGTHDSANSHNDNGASLTMPPWDDHLPELPELAEVEAHVASLRALVTNGGA
PIEPTHLQLIDTIVDRLDQVYYWAVEEGTTLLSEPSQLAQCKVPQLTVLCIRTKRPRIVL
AALRIMRHLLRHGQTGPQLVAAVAEKKEEKNISTVNADDEELFGMLASVMEQHAGLSDLQ
AEAAAVAAEAALIDIEGLLESPVISHVLAALERHGLSTAMQREGVLLFSTLVDIHRGGTP
RENAANDVRPTPVAILLSHVGVVVRFVVSVAKAHVGSVDVKRNAVHFFLRCASYPENLDV
LLREGVYPVLVGALPSAVRVPELFAELTEAIAHFIPLLDPLQQRSLVLVVRRVLLETTSP
ILVSLCAALLVRMLQVEPRRGDPMPCQSMQPGLSQEAALNLCVRGGERTLSDTIHLGEGD
IRVFMSSNFIPQLLCCAADTIGEDDAILRRVVAEAIELLSPYRWR*
>TCRU_1077 EF hand/EF-hand domain/EF-hand domain pair, putative
MPLSETQRERFSLQFLIFDKDSDGRITTEQLGPLLRIWGFCPSEAEVQAAVRLLDPDNTG
VLTKAQAFDAAESMPNQMITEVDVREALRVLDADGDGFLTTAELRHVLLNLGVRLSLEEA
DEVIADAYADEDQQVNTDDFARMLFSDASEGKMDI*
>TCRU_1078 Acyl-CoA dehydrogenase, N-terminal domain/Acyl-CoA
dehydrogenase, middle domain/Acyl-CoA dehydrogenase, C-terminal
domain containing protein, putative
MLCRFFCARRTAIAVRCHGGVLDCARRCGSFNYAEYNDGDPLLLQEQLTDSEVEIRRVVR
EFCKKTLLPRVTDAYRNEREDRKIFRELGALGVLGPTIEGYGCAGISSVAAGLISREIEA
IDSGYRSAWSVQSSLVMHPIYAFGSDAQKQRFLPKLATGELIGCFGLTEPNAGSDPMSMT
TRARKVAGGYSLSGCKTWITSAPLADIAVVWAKLHDTNKIAGFIVERDFKGFATERIEGK
LSLRTSCTGMIVLDNCIVPEENVLPHATGLKAPFNCLSSARYGIAWGVVGAAETCFNIAR
DYSLERKQFGKSIASMQLVQAKLADAVTEITLAMQSCLRAGRLKDEGKLSHQVISMLKRN
NTRKAIEIARAMRDILGGNGISDEYHVMRHVCNLETVLTYEGTYDIHGLILGRSITGMSA
F*
>TCRU_1079 actin-like protein, putative
MSGDRPVLIIDNGGYTLKALYIPDPSNTALQPPRQAVVPNCVGAASFAGRGIVGEQLFKM
PHFHGFMLRRPVDRGFVVDATLQSYIWEYLLQYFAIADESDVELVLTVPFAAPKQVGELL
HYLVAQRFKFRALTVVSATFLALVADASRDWLHRNVHESCREDDEAGGGCGMVVDFGFSA
TTVVPYVDFLPIRESAVRVDVGGKLLSNRLKELISFTQVNMTEDGWLVNHIMERCCHVAL
QPKASLRAAQRQKQRGKSSSSSSISDGGGGICYGNGNAAGLRYYLPTIPPLMPLGCREEE
LHAVLGGDGSGVERHELQHLLFHHEAFLIPELLFHPVDVGIQQMGVVDAIARGTGSRGML
RDAPTLHAALLHHIVVFGGTANFPQLRERLQEELRKEFTACSTSASLQPPVERLRMAPHA
IDVDDTAIGYSAHDSELQPLYGALALFTCPSRQPQLRLLRSRCHVDLTTLRKNKTGVGRA
QASVALKTQKTLLDAMQHLP*
>TCRU_1080 hexokinase, putative
MSARLNNLLQHIAVKDKDSDTMRHLKQRMALASLANQFTVGKDHLKQLMLYMVHEMIEGL
EGRESTLRMLPSYVYKTDPSKATGVFYALDLGGTNFRVLRVTCKEGRVADRVDAKFVIPQ
QALQGTAEDLFGFIAQSVKKMMEQKAPEDLNRTVPLGFTFSFPTEQKGVDHGFLIKWTKG
FSTRGVEGKDVVELLQKALKRMEVKVKVVALCNDTVGTLITNYFFDPDTQVGVIIGTGSN
ACYFEDAYAVTKEPSVAARGTTQTPINMECGNFDSKYKFVLPVTAYDEAMDAVTPNRNYQ
TQEKMVSGMYLGEISRRMIAHLAELHCLPSALASKMAKPWSFETKFMGMISADRMPGLQF
TRQVFQELFHVDVTDVADLHVIRDVCCLVRGRAAQISAMFCSAPLVKTRKEGRATVAIDG
SVFEKTPSFRRLLQQNMNAILGPGCDVTTALARDGSGIGAAFISALVVNDK*
>TCRU_1081 Pentatricopeptide repeat domain containing protein,
putative
MRRFLRSVLCRVTPWRLSPVLCAPVHQVHHTSSVVGNSSPLAHVMELMEAKNYDGVVQFY

EASYRADRMSLQEFSGGAFQARDMAVCLMRTFTALGRMDRVREVFAAGLRDLAGNGQGKD
SGRTVSLLNANFFNAYLEVLTQRKNFATEEVLYILKEMKAANVVPDTLTYHYLIELHIRM
GVDPVGLWNDMRRGSELQPLPCTVQALLLQVVPSSPDASFVVDVTREALRHGGNVLDKRL
LAGLMEQWLHNAQEYPPEYVLWLMFELEIRCVLDKASFVQFVQKQHMAELLQRCAKCADA
VTAGKALALMDRHVMTKTADVLSLVVWCWAQALELEKAFDLLELMARKGHLELTDPFKKY
TVDCLRQVMDRHFMMALADAISTTALLDRVLRHLRERRRRGQIVSAHSLDLVVLAAAKLG
EDRRAMLLVSEYIADWGIQPRTNTYNCLLVGLSSRRGASLQRTIYDAMLENGVMPNAFTF
RVLIRQAVLADNIDEAIEFLQRVTSHVGLRVEVEMVLPILERAARAGDAETVNRVSKFAL
ECDIGIDSVVLNGVIKMLTEAGQDVEVIKGHQPLHDALRSRSKTGRQRPRSEIAA*
>TCRU_1082 hypothetical protein, conserved
MENGVVFASPRAAGFRALRAARQTFAHLFLREMKERQSTSAAAEPIAVLDVSEADCAFSR
VAVHVGVEGGLELERDFHVSYVPLSEVAAAAPEEKDANITSLLRLVAHPGGRLEKEPLRA
LQSRYFVLGCYTAHSGRQRRAKGESVGIELAHVISKLHRGSTLLVNLLGGQQQQQEQEVV
GERRDISLLKREVTAMVSEALSRSGRWGVISDEVLPASDCYDAAVSVVVSLD*
>TCRU_1083 hypothetical protein, conserved
MMRRWILWEHTLLAVFFLLLLSGWGVDAWNVGEIIPVTLHMRLKRVAPTVTVGRNDMEEL
EDMQESGQGEQFLRPLPPDFCPRFGINRRVHQPAKRLFEHAHKQTKASGRSLSDVAVRFQ
LERGLSKSTAWLPLLKTTVRPSMSNRGQNASVRDENMLYLAAVTFSFGYQESTFNKITTF
YAEPVYAPVHHEEIELQYHWEERRAYNPHKALSACAFISVFATIAVLYMIIFSSRSLSKE
IKNKTFTLRSHRE*
>TCRU_1084 elongation factor 1-alpha, putative
MGKDKVHMNLVVVGHVDAGKSTATGHLIYKCGGIDKRTIEKFEKEAAEIGKSSFKYAWVL
DKLKAERERGITIDIALWKFESPKSVFTIIDAPGHRDFIKNMITGTSQADAAVLVIASSQ
GEFEAGISKDGQTREHALLAFTLGVKQMVVCCNKMDDKSVNFAQERYDEIVKEVSAYLKK
VGYNVEKVRFIPISGWQGDNMIDKSENMPWYKGPTLLEALDMLEPPVRPSDKPLRLPLQD
VYKIGGIGTVPVGRVETGTMKPGDVVTFAPANVTTEVKSIEMHHEQLAEATPGDNVGFNV
KNVSVKDIRRGNVCGNSKNDPPKEAADFTAQVIILNHPGQIGNGYAPVLDCHTCHIACKF
AEIESKIDRRSGKELEKNPKSIKSGDAAMVRMVPQKPMCVEVFNDYAPLGRFAVRDMRQT
VAVGIIKAVTKKEGGAGKVTKAAAKASKK*
>TCRU_1085 elongation factor 1-alpha, putative
MGKDKVHMNLVVVGHVDAGKSTATGHLIYKCGGIDKRTIEKFEKEAAEIGKSSFKYAWVL
DKLKAERERGITIDIALWKFESPKSVFTIIDAPGHRDFIKNMITGTSQADAAVLVIASSQ
GEFEAGISKDGQTREHALLAFTLGVKQMVVCCNKMDDKSVNFAQERYDEIVKEVSAYLKK
VGYNVEKVRFIPISGWQGDNMIDKSENMPWYKGPTLLEALDMLEPPVRPSDKPLRLPLQD
VYKIGGIGTVPVGRVETGTMKPGDVVTFAPANVTTEVKSIEMHHEQLAEATPGDNVGFNV
KNVSVKDIRRGNVCGNSKNDPPKEAADFTAQVIILNHPGQIGNGYAPVLDCHTCHIACKF
AEIESKIDRRSGKELEKNPKSIKSGDAAMVRMVPQKPMCVEVFNDYAPLGRFAVRDMRQT
VAVGIIKAVTKKEGGAGKVTKAAAKASKK*
>TCRU_small nuclear ribonucleoprotein C, putative .1
MEGSSELSQERRRRQRRRRLAAKSPETRRRRLQYSRRHNEKDGRLLYCDYCDLFVSSAQR
TWMQHLRGVRHMEAMEAYYAMVEARDPAWVKAFREDVVRAHVEERIRQQQLALGKGASVP
MPAMTLGYVGHQGIVVGGTQQPGGTHTRVGGGNNNSTSPQCGSPSVRVGGLLVAAATPPV
VKIDGKALPMPRSNQTTHQP*
>TCRU_1087 Vps51/Vps67, putative
MSAGNTERRRRIREQLREFYGDPTASRERHPVDSGKSAIPPEMDLDSEFFNVSKYVTDLL
RRESLKELVETDTQLLRNVRQLDGELQELVYRNYAKFISATDTIREMRDNITEMDAKLQA
LSSNVENIDKVSKSITDKLQSHRSRIEEMVLNNRMLRKVQFLVELADTMRRLIERQEYSA
CVRYWIVGDNFLAKHMNLSRITKIRADCMVLAEQLYKKLQETVVTTSLDDPEAMDVIRCV
VEDMRLMRATSLFANGAVKGTSTTAVADCSSPASFETEILNTLMKNVSGGFADGIQSVNG
AIRAALAVPDFASMDRTRWAEVMENARLQEALAQLKSLCALFHSNSERVYTLFHREGDAT
VSLRIVEEVQPVLIDIMSPITAQFSELLIAVIDAFCSDGEGALANPSIVKSGLSAMFTTL
AKRLKYYSGTLKTLGVNYLDNAHSQQSRQYAALVDQSVLEIFQRFLGALEAKLTEGINVP
DTIRSNVTAKDPAYQKPLQFCMTRFLFAHAANAADLDGITSLIDTETLKQTDVAGLQRQC
SCVMRAFLHRGIVLLGQLHLQWVAAASCPADAVDPTSTAAVNFGVSRSLYELVGQLGNIY

TLLRRGILPVNAAAGEAVKERRSVDGATGSSRLYMSTGSGRSSGMAASRKLVVTFARQTD
NALQLSVDRIFSKESQRNAELRTFPREIRPSSIVAAVTVYVLKGMIEYVRKQTFTRTGFQ
CVQITCTFLLHALTPFVPPASPGATTAGSDKCASPLSGEWLCECKDDSMMKSVPQLLNEC
CTCAYERCREKAPLTSVVVDKLVKSAIENMRGPSPPP*
>TCRU_1088 Protein of unknown function, DUF607, putative
MFASFLEVRVRFQCRFVCPRRYLRGVAAMELVRRECSSRSVDKKRRVECGGGLEEMETCI
NAVSTVPGNSLFTLEGLCNYRESHLRPLLIQKRHALQQMTEIKTRCEAVALRYANYYAAG
LFVLLTAQAVTLFYWVYFLFDWNLVEPMTYLLGYGGVWVAIACYATTQRDFTYEACMEMI
AAYYISRLYRQNNFDLQLWQRLTAEVKLLEERLRGLEGF*
>TCRU_1089 hypothetical protein, conserved
MNVEEYWHMKACEAVEEHRSLIQQQRDEIERLQRRCNDLLHERSMMRAATAEDVRQFCVE
YQRNQLQQHFAATAASSTISAGRLSAVSSVDSIPIYLLLQFLHQYSAGMVPMTENIRRKR
SRETMNSVCGPKTVGQQRLVQRVVARRRLRMREDDTIEELQQEHGQQYDQCPCADVAR*
>TCRU_1090 Rtr1/RPAP2 family, putative
MTSSGGAWEVVVDKAVLELSKYLAVTTDPFLPDSRTAQWMLTLIDKSTLRDVLVERNYGN
HCGMIGCSGCCRTARRRQGEISNERVSSSAGGGGNNNNANEEHNREEEEDEEGEEWEKDA
ADAFRQYERYREQRTQNAVGEPSIELGATMADRFCSPACAEEFLALMTKVPSSLVYERSD
VIHAVGGLFPNMSLAALHRLAGAESTSLGNISERNIQQEGGERQQPPSYLPNSIPVHSTA
VQEALSCIQAEGNTWSRDMRCAQVTESQVGQRRHMPLPLMVYDWCMTISTARTKVIFAVL
CHKSSLHSHVWKDSEGLAGRNRSVYVKCVLPIRMACVQRAEQELLSLGGEELGGEDPPCV
DPQLQQQRLALFATHVFSADTTAALSRLLLYDEGTLRQAWGVWQSSALLTSLQFPFALPG
AFVAGGVAPHVLFLALVLLAATGLCEPTVWAEWLRQDEDGSNALDELMEALGVTAEDLAA
CVRALVLE*
>TCRU_1091 Protein of unknown function (DUF667), putative
MFHNSYQSGFLSILYSIGSRPLQIWDTKVRNGHVKRITDEDIQSSVLEVVGSNVSTCYIT
CPADPKKTLGIKLPFLVMIIKNLKRYFSFEVTILDDKGIRRRFRASNYQSTTRVKPFTCT
MPMRLDEGWNQIQFNLADFTRRAYGTNYLETLRVQLHANCRVRRLYFSDRLYSEEELPPE
FKLFLPISQQQQQQQQQQQQQQQQQHAQQQQQQAPQQQSQPQPQEAPASAQQQPQQQSV
EAV*
>TCRU_1092 NLI interacting factor-like phosphatase, putative
METAPHNIQTERFEADQYVRVQLSTGRSEIGVILSIDESGGTAVVATRHGYDITVRLSSV
RRAFLLVLDLNGVLVSRGRGSFFDRPGVCEFINFVMNNFVVAVWTSGLERTSNPIIDKVF
DGFQDRLLFKLYRDSCTVWPTPEKPYRTIKNLQRIFDSYPKSFNAVNTIIVDDSPDKCSH
PDIALCPVPFTDPVKQMDDNGLVLAMEVLKEVLRTESHAPLIRASEERLVALAAQEEQGK
KEEEDALAGGPSAGDANDVKSVELPVTFLWAARLCCDYISGGCAREDCRFVHSFDDGKRP
CSRKGACRRGHARRWIDEPLAEAEAPSTTTSLKTPGTSGPFNVPSVFSLFSTNPDRQKEH
QQHDYAWSGNAHSKQEWTKDTKHQLQQKQQQKGQQQTKQQQNKWQKEAKFVGRQKDPKDV
FFGQKDINRGVSNIAQFLGSHHGAPRNAHSLDSVAPGPKSMRFTGDRKDGNALLRQLQES
LSIAKEGRPANTRPIRGKDRGC*
>TCRU_1093 hypothetical protein, conserved
MMPRKCVSVFFVLLEILLVLCFVALPVAGAYCVTPTEIPANVCPSFTLTDQLSALFGRDT
AVASCYCGRVCQTSWDARQELSLRWEMERWIRANRTAGMFPEEYEFVMDELMRLTTPLRG
DEPWHVRQEKEVYAKRANATLRDMPWLLVSNGTFKRAQDFYHRNVRQRHIVRSFHLSREK
SRPGIIRFYLQEVAGWWAEAEKHVSRDLRVAAPLLPWISLEQLIGPPMTPAEIPQPEMAG
RPAAAATKVPAPMQRRSFRFAPARLRAPTAMVYYYSDDCVLCEALGVAFDVLPLIYRRLC
EYGHRSIVSCSPLFLFFRASAELSGFRTPAIALHGVELGVEPTWMPPMSILYDIDELVNP
ADAFGFLTLSVPVNTSLQETLVSLIRPLVALHVINLRYLSSDEITELGRLAYKIMKQKKR
QQQQNASAENSSDTKDAILSEDDEGKDEASEERNRDLAWQQGRVITREDYLHEVVVFHMR
ELWGNSTAEVESNEFPLWSQLEPPWIMVVSSVLSVLWLLILICVPKGFRF*
>TCRU_1094 hypothetical protein, conserved
MDVTRGDTGRHYRFTFFMPAPDPFCGGEKDKATGAVKYRNAVVRELLNQVSLEAALTADR
EWDVVFHGKNVLFESGAESLMSALLSDSCQRIPLALFYGLETE*
>TCRU_1095 rieske iron-sulfur protein, mitochondrial precursor
MFRRSCISAVRRTRLNHVSLVFKQLEGSNPLTVKDKPVNSWSDEFLKPPVSKEMMNKHGK

YAKYSDPALCTVDTSSEVVLNTYPDGAPQGRIETTAGVALKDYDASMWDEEFFRKFILKP
KLPEELEDRARVTDYALNSALLGFVILMARYAVLPLWYVGQPAMSMVGQMNIEAEVGELE
DRQCKTIVWRGRPVFVYKRSARQMKELQETPLSALKHPEADEARFPDHREKAVVIAICTH
LGCIPIPNEGLYNGFFCPCHGSHYDASGRTRQGPAPLNLEVPPYKWIDDNTIYIGKL*
>TCRU_1096 hypothetical protein, conserved
MDGRVKDLLRKSCSAGAPWEVAVQVVSSLFQSKNGSHHDVCLIYAVVGECMRLCIMHQKT
ADALRIYELFSRSGYVLGQSRHARLRSLPVLLSVESLRGLSADELALVALRQHPHRVHQS
RIVAQMIAAEDADLDDVRNTPVMTERPLASKAPPFRDGVQTFVNMDGGFAETFNVPFLGV
TEVTEAEQFRILLQQNMQLLRETRYFQQRLGLHYLLSQMRHVVDNKRLSSEVEMVPLVHV
GRAVLEHPFIFAKPSTETARQQLLFEEFGSLPVHKGLSEVQQTKLMALETTVEPLRPLCR
EPLKFMDSLASSWDALFVRRAALTLVLPREAHDVLPRSRTRGRGGGSINVSGGGGDCGRG
ERHLENSLTASTWTDASSELFGGVEARDAASRVELLINRRLHHNIVVPDTTFLLQNTNQL
LQLARHREVVIPHSVFLDLVNSASDDQGRRRFHSRRVLLLLMHATTTKKTVRDTHGSLDS
YSVHMKRSQGGVTLLGLQDEVVLLENSHERFFLADALAGQEQEGPSIGRSSLASVLVAKQ
LGKMVSSTPGYVTCRDASTNASEVDHLVAGVIASMKDESETQGDHGALVCIRGKPAPLFK
SRSRSFWARTPVVLATTSDVTRRVAFMVGLPMFPPVSAV*
>TCRU_1097 chaperone protein DNAj, putative
MESSRIDWIIANERNYYGILGIPRDADERDVRRSYLTLALQLHPDKNINNKRAGEAFRAV
GKAYAVLKDKRMRMIYDEGGVDRVHGLDAEDLSIKNLMAALSKLVAAKVLCIVARRAHAV
EILRQRHGWVDAFTSWGPADDFACLQKSPREAARRIVRKVFISVFMFFLCVSVGHTFLQF
IRRTPNEGSSEEPYRRLSRYNSNDTGATFTIRVLRGGKMTDTVIWRPSSISENDARALVL
QWIHEMCPTEKLLSWASRERYNRTATLRVGRKLRAAPSPNRALRRKWAPKGWKVKFQEFF
PITSAEDLYVPLPLCEGVG*
>TCRU_1098 hypothetical protein, conserved
MQECYNPQHRILPVGSGESAGAFVPRWTLCVTCLLNHFERLPTNAAVQALQDTEFLLQQS
FSPLFPNQGVGIGGEKPSVGSATPSVSPESLWESFMSFQDVLAQLAEMLCASSSLHLQAQ
LYRASLTLLSLLFTLLREAERQISKMNGTAYILEGDNLELGDRGTGKGGASICLVTLPVL
ARRMCDAVRMGLSKEGDSPAGLLLLTDLAEMSPTFLRVLSEHCVLSVCALLTSLSNAYRV
ELTLYLLHQVFETCAIHPTWLESLAVVLSGNMICDALGDSFLDFLAGTLDTFRDDEPVVV
NALSLARFLVTYETTRTALLFSKLTNTTRAGKGDFAQIVPLRLLRHLTLLLLDLDADIIV
AASETMREIIVATQPPGGECTNIADYVIESLRTASVYSAVVLVSLLNALPTEVVPAGPVL
RVIFELAGNNEIAFEEAVRGPHFLASVKGHLSNINYVAQSVAHAAECGGRTSLHCFLLQI
RALEAACGGINAGTCTIIPETVSVIANTLLQLVTKERGPALTEDELTDGQWLFNNRFFTL
TNEPLWDLIFGVAFLLPAVQGAFLPLATEIIAEALRRFSEFDFVSFDGRSLLFDGPTGNV
LLVLSAAVLEHMSADGDEGNTADRLVKRQVRQLFEKDLLTFLLRVSGDSFSHRGRILYHF
MRLVESNRNGRSADLPAATVLDGSSSPRALLEKSFRHHPHWAASLLLALAMTGCPQPVEV
QELEEFLFKQISILPWFLRDAKRALTADGAEDLCSTPMGNEDCAIAALTALKASAAYHKW
RGELPHREFFQVDSVLATGRVCDVPEELSFIFFQLFRSEERSWLEALKSCSWGTGLLAVL
VSSSIMHMKRDFPKESVKEAYDYLFSDGASQNSDVEMALCRLVVTLAPTCHLFLSQLFGI
VRRSVADNLSLGCCVICFLCQCVSLAVGEEVPNSTAFIRTLLEQHVTPCLLFRENPALTG
YVARLVVLTLARIPVAMASCCDHTLFRWSMQHVTHPKAQVYTWHVVFLLLERVHGNEFAL
RYESELEMKLRADGGEKLPPFFAAALATVKWMVCGAMRRRGACRMNPVVTMPLKEWSQDL
SQHVLLRAFIISTVERETRGNFPDASLLNVSPMLLSWANEMFARRYATVATARVFYTLVK
ISPKLGASLEALGLFLQMTNETETGASPTAESSQPSLIEQRAWVFAALVLSWPPWGVSAG
LREAVDAFLTTLEMPPRACKGKKRPREQEVDIFHTQEAGVRRAMEALVEACECRSEDHGT
FPLNRPKDFFLLRHAAQPDANVTHEVMFKAVHEGCELFIPS*
>TCRU_1099 methyltransferase domain containing protein, putative
MWLRRLPPTHSGAACSVTVLARWCSTQSGRGPEGKESSSKETTTTEGKSEDLSLTNTNSS
VEKKGGFLQPSDDVVLEYARHALEREGRDKKPEAVIWQWDTTYSPILSKGKQNFYDYTDD
IPKHVKPFWHHEYYQQREYFRLQREKRPLREQLKTWGIVVACLSVAGAALTLIRVWVEQP
REIRELREELLQQTYGKVLELAAGHGQNIGAYPYAVHEVIMCDSNAQQLQALRYRLPRTS
YPKYDVRRVRSENLDIFADGEFDCVVDMFGLCHLHDPVKALRQMQRVVKPSGLILLLEHG
SSPYPPVNWFLSYFEQRHKVNTHGCKWNLPIREFLRESRLEVKELRNMHYGTTYYVVAYP
EVLEAFKDRGAASASALATA*

>TCRU_1100 metacaspase 5, putative
MDLLLGVLSSGILQNALPFVAGVGRVKRPKRVKLEEAFREAHLCRPVIPYRAPTPYTGGR
VKALFVGINYTGTRNKLSGCVNDVRQMLGTLQRIQFPISECCILVDDMRFPNFTALPTRE
NIIKHMAWLVHDVRPGDVLFFHYSGHGTETKAERDSEELYDQCLVPLDFQVQGAILDDDL
FELLVKGLPAGVRMTAVFDCCHSASLLDLPFAFVGNNNFYSGGRHEMRKVRANNFSMGDV
VVFSGCDDSGTSADVSNVSSFGSGLVASGGAATQALTWALVNTSQLSYADIFIRTREILR
QKGYKQVPQLSSSKPVDLYRPFSLFGPITVNTSLIHYVPQQYLQPWGPPQPYYPPPQPQQ
PYYPPPQPQQPYYPSSQLPTQYNNLAPTAGIPLMTSSSELPPGQYPQALSGDQNGGVPPQ
YPSDQSTYYSSAQYLSGVGKPL*
>TCRU_1101 hypothetical protein, conserved
MKERSAELRFHPVMLAMLMVMVMIGFALGYHHGVKAWEKDFVNKYEQSHGRELHAGSMLG
VCGDELFLLSNNVSSKNQTIHAVQNENAGIEQEMKKLSQEFKSVTDLVDKCRAEITIIGE
EGSRRDGDPHLELKAIEDELRVLRELLSNLTEGEGMHRVHIHGLLGSMREKHKHFCGRLP
GCTLLSDESILRRWKEVLYNSSQRRMLKEADRMRRMKWRYDKQTPQERESIYFSEREEGG
KVPTYFGRTGNSSLLLAQGQMSQVVVSTALERVLLLQRFALCAYRTNNPNITFPSIFQWS
ASSENTVADLRDLVETPLLTFCMDCAEVEITSDIAQLCLKAPEGENGYGKRDFWAMRSML
LPHSGVVHDAKNFYTAHALTNRKVLAVVAHNSVRDCLAHFDDPRGDHFLYLLANFPEGRT
RFENHVSNNTLHQCSPTAAQLAKRITQVLEEGKLDGVNSSFDAVYMSVSSEIWKELRGIE
KKLPWWGMALFRQGEIASAHDELVDLTIIGRAHGILVSPFLAPSQYVLESFLLSHGLQPM
GRVWFF*
>TCRU_1102 Nucleoporin
MRSTASEFPPTLVAAVRSGFDAFVQLQRVRLGKCTDELPRSLAEGFGSCEPVATPAPITN
TAATAAVCTVNGSHNHHNDKSTTAFPQTLCGWSDLLLSRLKAINDVSVVDPTAEVVWELV
SVVIAILENGGDDGVIASGPYLEWYRSRFVSMDAIYGLRSTLNAVPPRATLSSAAEEDLF
EGLLGPYMISIQRAFLAGLFPVAAELISSLVDYLRSCEIDPFDAEDESALADVIRLFLET
PRNSTEHREWTSTANLLIVDCKRVFTRAGDESNLIVQAAQQLKSLCLDLLLMVSGDAALI
LDTCHLLELDVMDYVAAVCAVCKPYIALRQLHHLYQSALDTWGGSVKGPWYVGVVERLLA
SRCMADVVCAMELVGRAVRCKEYLPKPPSEDSNVVSSPPANSVEEEDDVSGVEITSEAPA
DPKLLRRFALLFMAAHLADICAPPLGAPVEQIEVTFVRNELVEDFVALFRHHPLLWRTAA
MYVVYSPLMNPAILYRIVTERAGNAVSDRYTFLACHTFIYSSWEETSAFQVALRRLLREK
YPLSETLDKWIASVDYYRRKAIEVLHEKIINERWACGETAPAVWLAVECQQSKSLQIRFE
RILRSPGALESVEVYVVGQAVNNNFISVDTSSNLRMLNVLRVCAAVSEYRRAIGSLQGLD
GQKDPVRSPDTIHWVLRAAEKALCCTASFRMHPSTVLALVEQTVDVALRLPEEQRPRKFI
PLLSHALELVLAYHSEKRSQHAAHASAIREKIMRLL*
>TCRU_1103 Concanavalin A-like lectin/glucanases superfamily,
putative
MKHTLSKEQLADFAQQAVISIRRFMSSSQEIMTLTQQDLISTSKSIEESWRKRRIVPDIT
VVELWAMSFQEELLSQLEVYSSNRDSNSNSQLLTEKDGAPNVSLAGPSSGRKSATRKFIG
ESSLLACTEVLKILLRTNGEKSAEVFTRFHLATHLTKYLMRAPMSKKMRDAFASVLLEIA
GYNSLLLEEFLSVSHELLVFPEGSGSGNVVTPQQVQLAWLLSSVFRRVDVNNVSADSARI
QCGRDGFLSGIIRTCSLLSGGTAEGGNEGMRFTAFLVYFGLVNCMVRGCAANKALCRGEL
RDELVRLWVIAASNVSKVELSLPIPTNVPGKDASLAVEGTQAWASELIEFLVEVATSDSF
SLRRQALHDDSMNNGGGRNMLNNTGFPPLSPSPLSSPGISRASGGYELLPAHWDTLLTGG
SAYAWHLALLLFNCVLSREGCDFIAEALLRIDTLNAVSEFIYRGVIATLMLLCVATPRNA
ELLAESPIIEALIALITCSQASVFAHEVIILEKLCTPCRALNAYAIQTTMAFMSLLSSLC
VAERTLPNLLHAVEEMCLQQTCVADADVIDSLLHVFTCSELPRGVLFFSGCGSVVCMVDR
FPTTRFNGYGFAAWIHPKCVWLEGCHLFSFTDGSSGTSVALIVVANGRSCSLMMRTRHST
DVTLSSIPDTSFPADAWSHVAFTHNMTGFLLFINGRKTENSLSISFPKTPTKKDRLQFAF
GGYRDEPSFFGFIASIELFDGSLSEKDVQRMYQAGPRSSREVPISCHPLLSVESQMVSGT
TQLCVSVNGGLAGKNKGVSVHSVMACSPLNVQEMFLHEDVVNWALRTLVKAKNSSTNFVM
IAKLCVQFVCTAMKLTTTEEELNRMVGEHVIGQLREDMLKWENIPIEVPAILIASTIPRG
GGKVMRAHSTTQDILSLLLDVIHEQGVHPTVILCILRELSDALLLSENVAIFRAVPGRFE
RILSLSLELPPECVESVITLVERLFKESREMEQTLRFLLSASNSKMADFVKTEMLRMMFD
IALTNTAMCDLIGGAFGNSGLSFLIGLVGGINHSSEAIRVFALRIISLMHHTNKRFREHF

MKYHGYEMLGAVMTDTSSSVPIRLPTFNCLFQMAFDAFQPTENEETTLLHLQQSSSSKMK
RRTTRHSEHSHISMASVGKSGPLQGYMPGLLSPELRVTRREYSFDFSHDLQCVSDIRPLL
DDTHRCPRSRANIHLVLQVPQAIQAVLFLLERLLRSVGVGTPPVLSVTGDSRLSSEVASD
ANVAVHEDRGANNAADSVSRVSVISPTQEDSKEIITLRVLGHIEKIVDRPENAKILLPFP
WLIWLWGAVGPVLDPASNSSTEPLSKMSKKHMVAIQQQFRNIVRRLAILDVICNTKAGIV
RTLRQTEQPPFLIRLVLEEIVAHFTKFRCEISSRSDATNIIKNLDFLFHGIEDLLRPFPL
PLGLEIVNAISAIAVNNNSWVRTKMKNSSRLFETRRNLSLALLISTKRFSKLESPALTQL
LGANGYEPNTIRVLLRRLISATSICDVDEVEQLLALTRQFLSGDPNHCQAILSIIGMEYR
SFAELLCGNAGNRKVNSLTCPERSLPGSTASSIRTEEQVTVDELPAAEVIRWSLEDKVRW
ETVRQRVYAATNSLGTVHGGGGSEDVTVSPLPRSKRIEERQQSIQHKVAAEVCRIKREVN
YYLNMNGSSVASHLPNTSFMKTSTPVDSAMTEIQRNISF*
>TCRU_1104 hypothetical protein, conserved
MNLVALPSAAEEMAEDVFFTFRLLSPGGEAYIPPCFIMTAAREMGYYPTSQCLRNCLSEV
IGRGKRLTFPLFLKLCSSLEATRTLNTGAIEECKRVFDVRNSGTLNRGEFRTILTSSAAA
EMTSGEVEAIVELLDPAHTDAIQLCAVQMILMRCLSKDARAIDDFFYTPRSARKEVSQPV
AGGDDHHLQLLPLNFVEGDRKDLSRDSKNLRANNKEAVRPLKAIEVNGRCASRPSRGCVN
TVQRKRQKSPVPTAPDDASDDTAEESLIYLHPPKTTAPSPCTSGPVTRATSLQQVPPLRE
EPLSRLETPTPPSEVAAPASLPIGDVEKSFMRGSHCSMPPSQTSHTVVPSAAERGKTTRE
QDGRTTLVASKSRFLGSGTRRTLPEPPLEELREVSLGDSCVLGNTSDVVHLHEDVAAADA
TVEGSRVLQSTHGSQGAANENASGRNQVRKKKAWVHNCCIQS*
>TCRU_1105 hypothetical protein
MAQRVAIPDDCVYEGYGNLYRGDAEVTPPQPIVGARGGNGVLYGTIDSEEALRQLRTALR
VDVHPQLKALVQEKKLDEVASSPASLPWLVCRPNAPQLRTLPSSFSSGTRYEIERMKSQC
RFLRDWLMCHETPEERVEAREFLRTAQRLLQKESVEELLGRTENLLQQLENWPAVVEKAR
PHIAEWNDDKSLTELREFVGDVLGTDEVCARLSKLTCRFSLLAPLLEEAAFRSAALEEME
QWSSEATVSSLRSLRASIHDWEVGVAKDQQNVLDSSQLLLERIAAVRNKRRESAGNLT*
>TCRU_1106 Thiopurine S-methyltransferase (TPMT), putative
MNMHLGTHNVKEFWTTVWRTQNTGWKLGERSAPFTRILFAFLKGAGILSAEELKKDPYDA
VLCFLAGKTVFAPLCGDSAIISYMVGCRVKHVVGVDLSEQALSLQCQVNFPNVSFQTTRL
DPVEGTAGDFVVHEATVGDSRVTLFQGDLMQLPCFKAYSELKVEFMYDRASMMAIPPDIR
GAYVQAVTRVFRANTTVAYERMVRVLPEERHWGPPFMVDMDEVLQMYRESTGREYRATRV
LADEMESTLCPEWYAIVPHNWMSSVHLIL*
>TCRU_1107 hypothetical protein, conserved
METAPRATGGAASSSVCSDLRELNEAKVANILSYLDEAVATRPQLAAPFAQNDEMLPESY
VSEGIPLSSSAAPNRLLLNKPPLAAPPPQLTQRQQQQQQQMSSSASASCLTSYVIGGTLD
PYVGVYHGIKSKIEALRFSNDELRAENEELKARLSTARQRETENVEKLQAAARSEVDSLR
KGFQESEKEHNRVTQLLQREKAQLTKAVESLTTQLRQEMSRREEEVAKLESANAAAIAQL
KTRWQAQEKAAREKWKISEAKRIKESTLQSLEPDIVLLLNRHKAEKARLREEFENELRQR
DEVIALKEAEVEEVKAKLARDAEAMMTREQKEFRDRLREEIERVNRQLEDERRVARQKTE
NTEAFFEEQKSVMQREISRLQKELFALKEAAATEKATFHDAVAREVAGITANSNRIVSDL
KEQLMWEFSQREKETRAQNAQYLAAKEEELRRKYEAERDAAVAAATQRLEQEHIKSLTES
YNNDGVLRDRFAQMSRENERLRVEAELLQEQLKSALEAMNRKEEEIVRLREAAELTEQRV
KAIEDRIRGECETRLHVLDTEWQRKLRQFEIRHVEEVGGMQHELEKATIELEAAKNAAAL
EQRNIEQKHNAELTSINERVLVALATKDNTLKAQTEQISLLQEALRMRDEHIARHRELL*
>TCRU_1108 mismatch repair protein PMS1, putative
MIKRLDAASARKLSAGQVITDLSSVLKELVENSLDAGAHTVTVRIENYGLDKIVVNDDGS
GLALGDLLTCEGTVREDASLPLLACRATTKNLLEEADASVAQFRDSLGFRGEALHCLANL
SEVSIQTMSAESQPATLCITYDVKTHRTSVNVTQERKHPGTTIVVEGLFRSLPVRHREFN
KNRKKQILAATLLMKQYALSHPHVRLLMTHCLSPQSAPATLVSLTGTNDVHRALAEAYGG
RYLAEMNRVEWEFSFGTITGFVSKVTSGRLSADMQVLALDGRLVDLPIISKAVTDAYAEC
QPNAAQRAYPVFFLHLSCGNHVPYDVNLAPNKRKVLFTEESKYAEEVHSRALMEFRASTD
GIDVDRHIHIERTRRVDWKATQDFKLTRTPVSATSFTQFTYRRTDPLLTPSSTDDVLASG
LVEMSKIRSSIYYTQTEATILSTGTTVDIESKRISSGSSSASSRCSSTAERSCNEDAPST
RILKRESPVDSPCTPTQKMGGDESNSPVFLTDEANHPRPAGPRTGMRFPPLTELSMQPLS

HGPNECKSIPFKRTRKERQTFTSLTEQTENQLATYLDKSSFKEMIIHGQFNHGFILASLG
DDMFVIDQHAADEKFNYECLLSQYTARPQPLLAAVSVSMDPHDVDLAVLHSEELRQHGFI
VKRGEDANKLLVYSVPVLQYEAVGPHDIVELVQQIALYGNITKPLRSLWHSMATKACRSS
IMIGTALSEKTMRSVVSRLGELEQPWNCPHGRPTLRHVACVSSLMRSMKEASAD*
>TCRU_1109 retrotransposon hot spot protein, RHS3, putative
MDATAIVTNCPEENDVRAMRIWMKRNWPLQEQAEYWREVRGRMNNVGPILRSIFGKQACD
DRIKACQQAVDGSTASELERNLGIGCCYSSNDSDLSRKLVRVVRVRRGNSIESPLNLLVS
SHLERETLSRLEDEMKQSDFIFFVLRFWDYVPPYLIEKCAVSAFLNEDFLRAIRLKIKEL
WPPGRREPRSCALKEHSDTSFTRKEVLPPQERLSNPVAMDHWVLYEPKVQNFPLVDAFFF
VDSNPKTLVGLRMATARGHHITASTVRQFTECLAAYFNGWEELSRDMSWEIIYVQHADE*
>TCRU_1110 hypothetical protein, conserved
MRKGRVQAVREFVVKYRPHTPIAERHAVLLGHVHNVGGAELVVAVRQPAAASHGQRFCNE
HGEAETEITGHNLQHATAIQNNIPEHTRTFVDFNARRNPRAVLYGEHGAAADTQVRRKSV
HHVCPRHNSAVVHVEDAGQVHDEAALHKDRSAQAPATKQRRPRHDKPRRQQPDAVQDKRG
AVPGSCVARSHRHVLRPANLRAQRRVRQQHTRVQRHRAMQHNRALQRRHIRHVD*
>TCRU_1111 hypothetical protein, conserved
MDGVRAVVDGRSRWRRQHSAVVAAVDSDDKIGEGSDGTLKGLSSSDQMPQAGQGGEEGQE
HTGSLEVTNKLGGNEDSQITGERNVSSDADRPKQTGSQVPAGGQPEDEEGTKSPQPPPPP
PAEPLPQLPRQPPPGTNTLQSEETHPAITAEKHPKPQDGGHSHETKMPQTKGSTKHGEGA
SSLQSPESVSHLSRESTTPLSTSTDSSGDAGSTVENSGANNPTPPAASVTQHDSEGDTGP
AALPASNTELQSEEIPNAGIIATTHDDVNDSSRAAPTAERTTAGTRSTQTSGDAGDLERA
NNDDVNDDVARNGKTAEFEAASGDRNTEADNDERYTTVPENATNKTINTEITADSDGITA
VSHTTSPLFLLLVACAAAAAVVAA*
>TCRU_1112 hypothetical protein, conserved
MISSLETPPSVGGIPPNSLSEEGDGSQSLGDTLNSEDEVSSEVIGPSVQTKTPGQSDSPI
VKAPEKSGPETKTHISDKQGEAGSTEANEDATENEKGQSEVVKRDASSAPQSPPTPPVPA
FPTKETPLAPAELRNSVEEKLNTPPSQTKTDLEAPEPSLEDAEAEKHGEGATTSDSMKDA
AKGRSGDSTPSSISTSDSVDAQRKAEEEDGNEMEALNPNEDSILPLVNKNGQGKVIPSFP
AEQHEQKGQPLGKSSAGGASALSTVTSSSAGKESVKHLASGTSPDGHQNVDGGSTADGYQ
TATTGYGDKTQEDGALKTPTGNLANAEDANGPTTMGVGQDGTTVTPEVGASSAEDEETAG
ENKQEEIHPQNREVNATTLNSSLGNLSQGNNSDGGTMRGSGLLPSLLFCWDCGGLRLCEE
*
>TCRU_1113 hypothetical protein, conserved
MTVVVFSAHTSTHSPPCLSVGVIAAGAWSTAAAVGAAERDEAPRNKRANLLDEITMADES
CFVAFASCIAKNATCRRLTGCLHSAPFEALFCFIQCNATIIMAAPSLTGSECDNTNDGKE
SDEDYGDDLHRGADYLRVFVHNSQEGLDAVPTIPGLAEPLAFALSPAVISAPCVGADPFT
VEFTQQLSSVCAAGPALALSHVSQRCLADDLMSVLSRPLPPVFFWCPMRNTLRCGGYLLA
WLSTHVTMLNGCVFYLAGTRETSVCADASAKVFVDGWRLK*
>TCRU_1114 hypothetical protein, conserved
MLRRCTSPVFHGDELSRCRGNFRRSKPNLHHLLLTQSPLLREHDAEAGTPAEHRVVARIS
IIGGVTAAPSNQLDSDILLRLMGHFIAMAERPSDSLDDIMAWRVGVSLPLYPTEPALPRC
CCVDDDAVTEGTAVVYSR*
>TCRU_1115 Mucin-like glycoprotein, putative
MPLTVQISSTPLNDHTHIDDVPSAVRPVGARPVLPPFRVCGTTVDGEDQDVAGSDTLAPK
ATVETEQTSGTPDNLKGGSQKYAGQTSNPTNDKEQTLEFHSAPQTHDGAPVTAVGQITTN
PEQPPTGGTESANKAKERPLSLEVTGQVDAQQPTNVTAVMKVSGSDATASTTTTTTTTT
APEALLNTAINTEAPTTTTTRAPSRLRESDGSLSSSAWVCAPLLLAASALAYTAVG*
>TCRU_1116 hypothetical protein, conserved
MMRSLPWSVGDQQPVASVMRRWRKSLFHIGFPRLCFLHVRSAGMLGNIGGDLCARRLLGG
RWRHCGVRMRGVLRTSEHKAENALILWTDEKTLPQIGQENVNPPLVGQQRFAVLTRGGGS
GGRGGPISSVREGRRYRHKGLPVICRACAILPKSGQESHRSCARSCGSWHNIWPDTSNGV
FAIPTIAGSGVVCAFLFLLDFLPA*
>TCRU_1117 Reverse transcriptase (RNA-dependent DNA polymerase),
putative

MVCAREQHSRKQLISAGGPQGSVLPPQLFLHCVYDLLRRLEDMYSASALMYADDLALVAS
GAGTHACAAAMRLALSLVSTWTAEHSLKINVGKSEATLFRTSSDTRSDEDMANLHLGNGR
LRIQSCPVRFPGTTMDQLLNFGTHASTAAKRTMPRRYKLRLIAQIGAPHHTMQSFLFGYL
HSVSLYCGDAIVPCLVPTYLHNMEVRYRKGCKTSLGISAPTEDASVYLKANPPRSGRHSG
LLRSHNTNAIYASMITRICVLLSTRNPCLRPCIMKRRHQSRSRETPLLMNYDAYVTLLGH
PTTTIVLLLPNIELFPGTLCVAIKRDFISHLLSKDASDDFRRTAFDSIYSSLVL*
>TCRU_1118 polyubiquitin, putative
MQIFVKTLTGKTIALEVESSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLADYN
IQKESTLHLVLRLRGGMQIFVKTLTGKTIALEVESSDTIENVKAKIQDKEGIPPDQQRLI
FAGKQLEDGRTLADYNIQKESTLHLVLRLRGGMQIFVKTLTGKTIALEVESSDTIENVKA
KIQDKEGIPPDQQRLIFAGKQLEDGRTLADYNIQKESTLHLVLRLRGGMQIFVKTLTGKT
IALEVESSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLADYNIQKESTLHLVLR
LRGGMQIFVKTLTGKTIALEVESSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTL
ADYNIQKESTLHLVLRLRGGMQIFVKTLTGKTIALEVESSDTIENVKAKIQDKEGIPPDQ
QRLIFAGKQLEDGRTLADYNIQKESTLHLVLRLRGGMQIFVKTLTGKTIALEVESSDTIE
NVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLADYNIQKESTLHLVLRLRGGMQIFVKTL
TGKTIALEVESSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLADYNIQKESTLH
LVLRLRGGVMEPTLEALAKKYNWEKKVCRRCYARLPVRASNCRKKACGHCSNLRMKKKLR
*
>TCRU_1119 Ubiquitin-2 like Rad60 SUMO-like/Ubiquitin family/
Ubiquitin-like domain/Ribosomal L40e family, putative
MQIFVKTLTGKTIALEVESSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLADYN
IQKESTLHLVLRLRGGVMEPTLEALAKKYNWEKKVCRRCYARLPVRASNCRKKACGHCSN
LRMKKKLR*
>TCRU_1120 hypothetical protein, conserved
MQARGTVKVQGDANVDGKMSTGQHPHHQHLNSTQANATTTALEYRAMNRPLYRGPISHNI
ISEMAEGFYVLSGGYKKLFIPSKDVYALMQNVGMHLTEEEFHDALRVIGQSEPQNADELS
FSDFLLLMTREVDDTMADELRSAFFHYDKHKTGYVTRKQFTELFATLGERSTPEELEELL
AVAEVDETDDKIDYNRFVNELTSRVNCM*
>TCRU_1121 hypothetical protein, conserved
MMIVWLQKTPARSETQQARPLTKEEMNQYIRSRTDWRERVVFRVAWITASRWSEIAALTA
KNFTMEADGNLILYWPVASRTAKADPHRALRFVRIRGQDAFEIIKLCRTLQHNEKPTNLT
TAQVERALANWNATAHSIERGALRHAAQVVETHDLDPHVILQLAKHVDPFDLPQNTVRYL
SRYNTMLTQVLPLVALM*
>TCRU_1122 hypothetical protein, conserved
MPALNSSTIAGMEVTASRFLYATAILGTRLCGYYSSIKAVRRLSALNRGIALETSLANLP
PAAVGLGERLRHTIENNRKRIIKPTEKASTAIITDASLHGWEPFLFQTPATLKLPEGKWE
RKPFLIMQAEARAVRLALSAFSAILPSAMDVWVDNTLLQGAANKGSSKSHAIRVPMAVGQ
NYLFIINFAFTANPF*
>TCRU_1123 Leishmanolysin, putative
MNGALSSAHGNAVAEEVVPAAVKPHADRLLVQPLEGSLVVPSLATGSVCSRFTVPAEHCS
AGAANSDTVQYVAAAPGGVWALPCATLEDGRPVAGAMNIARPPYFTDASPPASPRT*
>TCRU_1124 Leishmanolysin, putative
MAGRGMVRNAACVRGGALLVVVHSTTAAMAAREHHDCDDVDGMELQDGDGDGRTLESHRS
RCHARDEWMAAIGVPATARS*
>TCRU_1125 Pyridoxal-phosphate dependent enzyme, putative
MARRLEKEKGYVFLDQYRNPSNPKAHYEGTAQEIYDQCGGKVDMAVVPTGTGGTMTGVAK
RLKELLPNIVIVGVDPYGSILADPSVPLDPKPYLVEGIGYDFVPDVCERKYVDRWVKSAD
KESFALASEVHREEALLVGGSSGAAMWGVLQAAKDLRPDQRCVVVFPDGIRNYMTKFPDK
NWLVENGLEEGEVTRPTYGSLEAQLEEAKKKLSEYEAKCGGSVEEGKRCCEKGK*
>TCRU_1126 hypothetical protein, conserved
MSCDIRRGLFCRLSRRWAARRSGIGRLFGCVACHRVPSWRVCFFPPGGLHPTAVLLRPQT
IKPNPAHTPSGKFDRSFEKLSGEIENRMPFRQQQILFGSKYDHNFGEENQDAMRQAAKDD
VYGREPERAAARQARSYFTGDDLSPTALHVKSPRLKVSQQQHRQKYDRNILKTSQESAEY

YYHRESTSERNVRRGMMTACGAVGLAGTWWGLRLLCQYMLE*
>TCRU_1127 kinesin, putative
MASETSAVCVAVRVRPLNARESPLECTVTVLNDHTITLTDVSNATMGASSSNTGQQHVFA
FDKIFWSVPPHVLPLFPSAVAPPTFTPRSSIGETATSTNVSRSASLFGAPSACSRTNSYI
GSLHEPISATTSRVPFSGLPCFANVPAYDDQASVYAFIGPRMYESVMTGYNSCLFAYGQT
GSGKTHSLLGPPEYVSLRSEERGIMPRLCEDLFELMRKEREEDESISYNVECSFLEIYCE
RVHDLLFHGGGGGRDTAAAAGGAGAAPLQSPSASSQSSLRIRQHPSRGPYVEGLSLVKVR
DAEGVMKQLMSGLRERATAETRMNEYSSRSHAILQLHITRVAVVREEAAVVTKTRVCKVN
MVDLAGSERVSQSGVTGDRFEEARNINLSLTTLGRVILQLSEKQSGKHVIPAYRDSVLTW
LLSDSLGGNSKTIMLATIAPSAYCYQQTINTLRFAGVTKKVINVATVNEDHHFQKLIAAM
RQQIVKLTLQLEKGKAAEVHREEIQAFRRERDELEAQIDSMRATMSTMVPATEVATLQRR
ITDLEEDNAQLQKEKNQVQRQLVSTTTALREELAQKRGEIMKLHEALLRKDGELQESLRR
YREETVRRETSSQQLEQQQHVASSSVVDTREGVGPSQSPPAAWKENVGSSGFEAPPPLVI
AGRSLRHEEELERRVGVLTKEVKAQQERAEEAEKAKSSLQEKMKMLQQEQDAMAQLLEET
QQRFAEKAHALDMAQSDLAATRTMLRAERGANSAAEGKNGLFAQLENVRAEYLSEKKTNI
DLLMRVSRVEQQLSKLKKDSATKTRDINELEQLLLEETETSERYYIWLRYSQDVLSILSS
FLRRTLSARGKRITALKGKMNSSVGSHAGDSVDLAGILWEQAVWDCARGEAYSRALLEQE
RLNAMIEMLGQKKVLYEISSGAAKDELMTLRALAAEAAEEPQRLRRKVKSLELLIEKASE
ERLNMQVTIQNSESARERLSRQVEELTNQLEQLQQNNNSLIEKIVEEHSSRNMLGTCSVV
SGGGSTSQEDELQEAEDTGKRQFQQLQRRLEKQVAQYQEELGLLHAQLEKERHDKAEKRH
SMQRERDEFTQELRRVRNECKASISESAQIVRDYEIRIKELQEMITTLRSALEEECNNAD
KAKDEMLRAGMEKRETLMELRRVIASRDALEMRRNDDEKRFNELRTQVRELQLAYYKLEQ
QLAGVKTHTPDVYITIDRSFGTDDGENSWMLKAQREKEVLERQKRSVQRINNELLATVRQ
RNESLRAVHRQITKIQRGGVSPDMAEMEIGDDNSPLGAQLKFE*
>TCRU_1128 Nitrogen permease regulator 2, putative
MFSLHSVLLIALDVVKGPYLHCHAPLNPFLPVAQEPTSSTPANTTTHSRDNNKNSHEKEN
MICPGDSGSKRKMRHDSSCKCDASSYRTTSADRLGGFSDVFVPRSEFCRRVMYLMEAESG
LLYLFYPEEIAGLHYQRKTLRYTLCFVFRVDVELVTPSLSLTERLIQPYSVVLTGIMEEL
RKTEVAYGYISMGLARVTSHHPSVVLPRHFSREREPSTTMAMTMTTDDSETQPPRVDVHA
ASGENVAAAASVNTTGVPATVAQVASSSVTNEDSVHTSSKGTSRVNVFLTPLQDPASLQW
TPLEEMIATLYACLSREERQETPRIRRTPRKGETPGAHENGLHTTIKDEEEQQQQQQQQE
EELCPPVEERKVTVRLSQTHSYHVCRMIQPYVLRYHTLDEVPIPIVEYTAEMLEWADLAI
QDVYKAVDGYRTIASIVQLLAVGHEPPGEETQKESRVLSPLSSPHPPASSLAAAAWALSP
RVKNAAGCSFASPNLRGTSAALPSVIGILSSTHGTETRVPSPLSQESRSGMSPVVTVSKG
PTSSVTFLVPHERSADEVGIGSHEGGQHWYGELEFIVLEALQHLELHNYVRIVRPCQLNS
KYNTTRAFYSVVSNWKHASRRIIGQRMLLVEEEFYRLRKKQPHTQQERQLMHRRRQHESK
SGVSSGFGDSPSETYALTLPAVLLAKAALDWQEKKRDEDEKEEKEEGDTGPAHLAAVEQS
PNTFSWSGVVPTPNDTLKETTIELEDAPAIGMAHSESDINAAAAAALCAIGKFTNNTVAN
VQWEMRRIPGWSTAFASWEEMCCKALVEIALLNDWLVEVGRPPTSYS*
>TCRU_1129 hypothetical protein, conserved
MSTSAPAAHYTIDTLRGVGLLPMQLALSRQPRLRPHVRHLKGLVYPLPYYAMWRGNHNKY
MYNQSTVSRWGEGETRHMYHQHYSHAKCPTDYGRGGREFEYLSVKRGRLVKKPLPQVQYV
SKGSKPTWLFKSWHTPLSSPTMWEREVQYAEHVPEHLGAKRPLAVVAPRTMHRYLFLMHM
EKITITISPFLFGYGHTLQKAVMDFYRRAISARAPFPKDKVFLFYAIDHITPRIEVTWLN
GKTYVPPLLEGTSSHDLIQMVMEEAWLAADRMGAEGRVLNPLAIDDYKWEQLIVFKKVRD
KEAAKGGGKKK*
>TCRU_1130 WD domain, G-beta repeat, putative
MDVFRSGLSGAFNGGGIEHLLQQQQQQQQLTSATTTGTTVAGTAPSRMVGSGNVSAHTT
VHVTTSTEVDPFDEKRIDEIRRTLRMLEDIGHGRHIINWTELVDPSQPVESAKKISAALA
RPTTVPGAISSVAECITTPAHLSIVALLDPPFLAKVRDAVLQDLLNALTMVHESNPMPVC
SEMLVEMVKLNLVVLRGVASTLEALLSDPNSRRAAIAALGKLADQKRGNEVFLGAMQNLE
PLVRMIDEPEYEYDCLAISRLLGWGGAHKTASLVPVKRMDHSSPVTAMTYFRQRDELASA
TFDGTVTIWGTPHPSTGDVKAAVALDLPQYCVPVAMDGPPRGNYLLIAGMPFPAVNVQTM
ELERGSINSNVMNNSFNSSGKKRSSFATVPRGPIVRLLTCNESTGAWTSGETVTRKETVT

LTTAAALASFVVCTAESGPSDKLSESGLQHDLVLLNGHTSQFLRRFERVHDDYTTIIRAA
EDGDRILFTGSRDSVVKVWDIRSGNNRAGLTTAATMSALATPLHRLKGNHTDTITAILPH
RKALLTASLDGSFLVWDARRMTAPMHEVRLKDPILDLALADSGYVVISTARGLKLFSLES
LKAHDIIPNVAYTQLKANNDGSIIFAAGNSGVSIYALHR*
>TCRU_1131 hypothetical protein, conserved
MMRARRVVVALSPHAQLCVHVQWRLYTPIWQPDPAVDHVAPLRESDENRTLWASSAPIAN
VSDAIAAWIRFGNDPVLHTALPVIHVGQNERTRADGSSASLSLSSLPSPSSTSPFATVED
YMGTNMVFGSPEHVKDSAAVWASYFERRYLSQLRHSRRTAANHVGLVNAPDVFTDEADRP
ETKWSQDTRFRERAYMAEKFLKEKVVNLQQLEQALKQAKPAEYIAFHDALQQQTLTLIPL
PSPSVWHYGGARRTQWAERFLPLSHEAQQFFTTVLAEDLKRAGGAPEKVLQKVAAVFAEV
GKILLQRHRRCLGGREWSALAPHEKDEFCMKEVERWKQQVEVGEFDPPLDGDDDPTSTEW
QSEHDAIMQLMTATIDGLSFSALEFWTHTIRCEEMETEHIHTEKRVRAISAAARRAMYDT
TSYEAVLQGIVDAVAKGQLDMKAAGFKPHMNDIWCQLNYAKFGASTVTQHTTTARRQLNY
FHAGLLKEVAATAALYYATKPLSSSLDYASPYKFRRSLVGLFSTYGVEMVYAVQRPLLFS
AANLAKAEDLIRGVVKNVARPFGERRRAKLKQLRAKHRRLATPVQGVVVSAVVSDLLESG
ADVSEAKKAEKTQESVTFWPLGARRVVSYDWPTPHFDALKRRVAAAGSAVTAQSTKEIQE
IKRNAFVEVSLWRRVTAEETKQRHDAVEEETRRVADVVRTIPPLAQVQQYATSLYQRIED
AVPFPAATDTNAKSEQEDDESSWEFVVMLDDRVVLNANQAAELYLPYTDASGVPIPQGEC
RVRVRGFDVDVNPTLNPAFCSEAFSTPFQVFDAIPQLVQQFFGTAKPSVAEVSDISSSKF
IQFCAFLREAGLDVPVQCEFEAGQALNAEGDVFMEYFLNLLRSDRFHRSCAQAGLTGMQR
VIESSCRAHWEVHHPGANEAEWAEARRRVLDRAMEKEREWWFPNEMLDVMNMSPGSNHGL
RLPMYPATVRYGRELCTLLAAEGQFDNNSGLSATCAVNGTGAAESITFSTGDHISSTFSM
EEALAVAKGALRNAHDRQNTLAAFRLGPLSKHSQVLLFCGINATEFGGKYARTYTYAFEK
AKKELAETFVSGRVVPGVDEDELLRVSDKEGVDRFASSTHPEQRKTQFVPRVGPGGTPIE
DPTADQKTQWGR*
>TCRU_1132 hypothetical protein, conserved
MLPFLQRHWEAGLEGPLIEEMISSAFSDFAPYAGAEQQQLRFVRRQMDGTTSSFMYDDEG
DWAVNVENRNIGAVAFSTRREVLCDLRARVPLRLGSVENDNHNDKPGGNADRTEISHAVS
SQTRDSQRRFISSAVLPSRGRPGTIGVLEVLFSPAVERYGIGLRAGPFSLRTTTGPARSE
EKESPNSTQTDTARRTPIFIDGSWCVPVGPMLPDFLATALPSSLHLSVALQHPMGSAEGD
TLASLCFHSKPHERYEDTFHFLVVQTLISSNRLSHSANEIARSRSTLFSGDVSWRDLGTL
IGVSKSFGNGLFRLSASSMMHDGEMDYEAAMMLDATPAFANQTQFKVGINKVGCIGIGIA
TKIFEGLQLTLGVHHLRRSGTRFGLEIAI*
>TCRU_1133 UAA transporter family, putative
MKSTNGASSNKPGADMQQKNTPEKPKREASGSRKGASPPLSVIFVMLQIVFCVSGIYVCF
GLWSIKQERVVTKPYRAVRADGEHAEMAKLSTVFVLGLVQAIAGTLVGALLLLVEKMYSM
YVAHSAGTGSVGKMSKAGRLAAFRMTAVMGFTNAFGSSLSYAAMRRLPYPVVLATKMSKM
VPVMLVGFFWHGTRYSFSKCAACAITTGGVFCFYLLGEKHSRHEETQQHDGAALSSWLGF
LLLFFSLLTDGFTNSTQDVLVKRLGWGGNRLMFYTNLATGTWLLLVLLALEALHPLAVVI
LEAEELTSTALSSTSAIASALLSLDTGLRWYLREVAPLKDLSRTWHFFQRYPEALKDVLE
MSFLNATGQVFIFRVISFFGSLTLTAITLLRKSGSVLLSVVVHGHQVAIGQWIALLAAFA
GVVWEALMHVRKAPSARRSSPGAGNKKPAGSHGKEESDMPAPASATQGNTTRRRGREKNA
KAEA*
>TCRU_1134 hypothetical protein, conserved
MVGAPSSLTFAEKMQRLLQHRAERQPLPEGYMRCPLNPVHQVPIAAIVTHLERAHQQDAL
ALSPSAMYGSGTHRRRREFLEKQFHRHNRADHRQPQSGRHHHKRGRHRRSRRSSRDSSSS
SASSQNSLPQVNSHRSRRRYRSENQESHVRNSGPPAANYNGVGATSLPPHLSAASAAQCG
SYHPAVAAVPSPAPPTRALMGRYSIGFSIDKRSLMEYLLQFGSVLRCDVQPRSATFTVLY
DTLEAASRCFTQSYPSVIIDGVAVELCPTAGEAEVAAAPDTGMAVSGISPVAPMYSRECH
VTPPLSTESTSQHPCTLSWAQDAPPVITVAGKPVGVAMLSNVDDCTKINTIRGRNSKIEP
PKCVFIATLKKSEDGDKKKADERHIWEEFARFGDVSNILLVGPRVVVEYASHDGVEKITQ
ALQKGQEVFTCCTPLQ*
>TCRU_1135 Galactose oxidase, central domain containing protein,
putative

MRDSVDASEIKALLQELEGVVGTPTTNKGENERPFSPKKRGSSNVDVAVSRYAGHLGQSK
FSTYANTTNDSRRAVVPLWERLPPMNTVDITGDASCPVKSPVTASQKTFLRPKLVGGVVG
ASLQRMPLEGKVNNASPLKNDEQGLQQTKLTSQKQIQEEEKEPPTTSFSKEPVAQGEGED
REREVNFLPIMCARYINPAGITPRARWGHTLTPMQDQKLLLFGGMEIEEGETASLFEYDT
HHISWDPVCVSGGVTPTPRTNHAACASGGRWLYISGGTTDRGTRVLGDLYCYDIFTQEWT
CLWEYGGSSTRSKHEPTPRFGHSMVSWEDRLYIFGGKTPKRDQGDSQSTQHVTVASTDVY
VFSLTSRKWKRRIHAGKTMGVNGDGKNILNNRKTEETPLPAASSVTQLTNVFSERPANRF
FHAACALGDCMYINGGTGDGGVILSDTWFLDLRKQHWVLLHNGRTADSFPREKHHLFACG
EALLVVGGCSASSHSTRITLKYHNFVAVLPFEGNDSPCWIPVAMGNVSIVAPNRKSFGAA
FAGGFVHVFGGVSGSEPASNSMVRFLAADGYFETDSRSWAKSNADALTSMMRHIREASIS
TMFDTYAIPRSWDGETGIDTLSNRPYGVHRGFLQQRAPKFWEDLKRCRMEHVKPAGTGIA
MPSLDLTDPLKEAFTPSPVFPTTGGVATTSTAAGETHPSHAVAYFTEGNSRIQGLSVSLS
AEQLQCLLDYIYWGDVRHRILLEQEEEEYTMDANVSGQGDAMQEEAKVLQALRHAADVYE
LHPLMDICDALLARSRKKLKQAHERSTRQLQADLLSLLESSNSATATVLFVDPHTKQKSV
YSLHPFILMAASSFFNDLLRPLVSGEKTTFQVGPVAAKMRSAGRGSSQTRRDILVGPVSV
PYLAVKPLLRFLYTQMLTVPREAVFATLLGSHLLDVAPLQAYCESILAREEVNYDTAGHF
YSLGRKYHAPLLQETALLTAVLGYAEVCRSPAYKALSEKEAREIDAVAHELGATSWIAPP
QTVSEVKPAAVYQLRWNASSPLSK*
>TCRU_1136 hypothetical protein, conserved
MQRVSRPLWLSSGINSGRLRLAEQFATMQGWQAGEDVSFDAYVKEKRLKERYEAFDQRVE
RGYAAAAKLHRAEIQNAVKRRLKSTGTKFTAATLREMKVALEERMAWLRDVWTQIDADYR
SGDTARQETAAREISAALRGEPSDYMRWVYDKKRELRFAGPIKRGEMQGELQSAELPDVS
DEEVNRYHALRLNMMEVEYNVKSKYGLAGQQHWAELQATKDDEYVKKLDDAAEVYKQLLD
QNARLDESRRTELQRSHVERVHQAQVRFRAAMEMEKERERLIDAHREMKKERDLREKEQR
RALLQEAAEMRAKGKTSAEVLAALKERQIEADAQRQAEYELKEREDILRRKSQLINMIAQ
FKHDVEEREGRELLQRQKRTANRPTNVFGFSDDDAIDGSELSVDSTGNTESAPFAHSTKG
SAITATDGDSSRSSHSVRRPLAHPNKNELWKAINEDTYEDPFRTVHQARLDAAKTYDPTY
ARTFPLNLVLGRKYSRQGAGEMAAGNETDRQILQKGNAVALSFQWGIGNGTVHDLDAEGS
TDYFMDGNFHVRDKKTGDIDWRYEKKKGGVILKGPKFYRLGAQREAMDPGEHPMDPMPFT
KLPREHRWRSS*
>TCRU_1137 small nuclear ribonucleoprotein SmD1
MPAAESSTLIGFLQQLRGTLVEIELLNSSIVSGEITFVEPSMNTHMRHVKITAKGKNPVQ
AETYVVRGNSIRFVILPEAMNTDDVLNKATAAQKKTKK*
>TCRU_1138 hypothetical protein
MRHVRPVLLWSIANARRSAFGWGNSKGNSSSSSSGGDNSNNNTTNNTTNYNGSNTVGGGY
MQLTEFVGKAAALKRRHRGRGQYEFARREAEKFLQEEVPRTGTNVWMENGTNALALSQLL
SFFEIEPEPSLLALITNKLLRLLDDPNIDSHTRLQVAIALSSRSELYMERIFATVDDVLK
QATRDVAYNDNSGDFGDITHKWNVIELSAKVLQRNGKHAPSVLNESLTQMVIAQLERTPT
NELPILQSSLLRVYSWMVRTGKVAEANHLLVALVEHTGEFHSYDFATLMSSCLRHHQLSP
LPLPLLHRMARVGLMYSTLANGRDVAAILASIARMLGSLEAGKNGVTQRDVGELGGRMSM
LLEEYEPRVLRFLDSNDDLYWKHCDDITSIAFAYEMGGRLRYRHVFLAYQSYVAQNVTCF
EPQQLAIASGILRRSHLLSRELAMKLGERIETVLGEFSLSEISHICSTFAPISPSWMPEA
KAVATRLLVTNCSSYTKLTLSMAFPDDEALQSQINYKEISGRQLVDAMTLAKGIKFEGII
VAELTARLNAAQERFSPDDLRMVQASGRQELLAACMMYLSSRFAEAEWTADTLYSLPLAS
GIPHARDPVKALAAAKAVSISPEQFVSLVEILTSVFGEDSDEAMVNFVVTGGEELVSEEK
VQLRTVLRYLEAVRPIRKLHPRSEWLAIFNEKMLRFMRSLGTREMRSLLWSLQEVYGNVA
QQPLLQQTLTEIVTHAYGRITQPDEEAAKFTLLIAHIQYGMPNPPLTASTPLAVSVKSNA
ATYPAEVRDAVMNMSLPQEAQTKQVGRFTLRAVRALATPMPTPPTEPQSHDVNAALDADP
FATPLRATASDATTTGTTTLSPSQQQQQQQQSQPLSQCNVGTMPAFGAKDVSPAQMTKTT
GSQPAATTEAYENATRNHTNGKQEQTNDSASAPPSATHSGNTASASSGMRRWNLFGTAPD
TSMKPREPVMSAPPVAPQQQPPEESRTADSHTRSSYMKLFDPSRLSNAWHEVSQQELHGG
DMINQSNSNTIDEQLRPRRTGLPRVDKHGSSTGIHTPPAAKSSFGYDSPQFSYDGWNTSP
NAARTNAPPTSGWASPWSVPRPSMASAQGNHMGGQNATWLSPQMQPPARAFGGNGNSFGV
NTQHQQPMQQQQQQQQQQQQQQTQQKMPQPPPMNTSMMQQHSQQHQQQHEQEPQQQQQQ

QPQQHQQQQGAPSAYRMAPRGGVASPGNHLFIDPASSSRPRPVITKKNSSSKAQQSVPSS
SLDEDINQMYAKNAEGPNEGVSNFMKKAGLTKITGYNMGSTDGETTRGDQKGFWADLINQ
SVRRTKGESRRTNKKPNRLSEWLDAPPTRAVTAARKGRVATPSAPAAKGKSKPKEKRGNG
KEHTPLATAPTLSAKPTTAARGKGANAKASLPKAARGTSAKAPAAKVASKVAAKSTSKAA
VAKPKKQPENNNHNNININNNKKVVKKKNEKKPVMKKAAPVPSSVAANAKNKTPKKTKSS
SNRKK*
>TCRU_1139 hypothetical protein, conserved
MLTRLAISTVGYFDENFYPACVEDVDYSLRLRLLGFQERNVFYGKFVHRGSSSIRLSNEV
EPPDALWYRRVKSLSANDAYAMMKWNRPRACSGGYKEPYDGMVPADVWVKDEGRIQRIRA
YGHDEEQGVPRVEYDRTLLYPVRTKGR*
>TCRU_1140 hypothetical protein, conserved
MDRTPPDMMIVRLQKIAARSETKQARPSTRKAVDKCIRSRTDWKERVVLRLAWITASRWS
EIAALTAKNSTLEADGNIILDWSVAPKTARADPHRASRFVRIRGQDAFDIIKLCRTLQEN
KKLTNITTAQVERALAPWNATTHSIKRGALRCAAPIVETYNLDPHVISQLAKHVDPFDLP
QNTVRYLWKYTTMLTQVSSLVVLMRGEAAEGQEPWLKAEERFFMIFILTPPQLQDARQGR
VWPLHKRSEPSR*
>TCRU_1141 Endonuclease/Exonuclease/phosphatase family/Endonuclease-
reverse transcriptase, putative
MCIWLPAERYFYPLLNSIGAYQRYTYRLRAVCDAQRQKLLLSGDIEQNPGPIAVLQMNVS
CLTPSKLATLMAQGADIIAIQETWKSSEQIASMHTGDYLLYAQSRIGKGGGVAVLVRTTL
RSKRIPHTIPQHDTSLEVVVVQVALDQNRDLIVASAYVRPPPQVTQSFRRLVNCLPASTP
LLLCGDFNMHHPQWEPFLETSPSEVAAEFLELCTDAGLVLVNIPGAITYARGTRERSCID
LTWSKHLTVSDWSASVSPLSDRYMLTFTLHQAFMDTIPSAPKFFYSWGKCKWDLFIKDFD
AQLPAYDYKKQSTGIKAFTRALITSYRRHCPRGMHKDGPRLWDETLMEAERIATDSKARY
LQLPTPDREAEMQRTRSQFFLLLRERLRNTYPRRISKLNPGEPLAWKYISGRKKASLPYP
TSMLLGDGQHTYKTARRAANALNRIFFPFHPSHKAVRFSKGINRPSASLNINASFLFGQQ
NNSESAASFTSFSSTSSSSEPQNNNESAATSTSGSSLSSSSEPQDKNEAATTSGLVAHLH
SPLDAPFNRTELLAALRNTPYGKAPDRMKSTVRHCDIFRQRLFDSFFVALTTVGRPVRSR
LSGDALPSFHS*
>TCRU_1142 hypothetical protein, conserved
MGTTTVSLLEKVPRSVGCRGARRFACSLTARTAQSVHCGRSVGITRCGGVRKSRSAHEDG
LVVVWQLRTLEFLPFRIALAARLAQQPPGMVLLHECWQQSAPATRLIGCGDFQQACSERA
AGVAILLLHTLP*
>TCRU_1143 hypothetical protein, conserved
MCALHAAAAVDSACSIPSVVIPLEPSRLPHGIARLAARTVPQCTSNHVARNVACAEVEAF
QSASRREKTACFHSGSMPACRGMPSSVPAVCDGRWWSDCMQRLDVKWETRSARCAVTSGN
ETLRPLIRAACAGSSESSDSMPVGVVARSSPAVVDAERPSRSSWCEFR*
>TCRU_1144 hypothetical protein, conserved
MLSDRTLRSAGACKATSGCAVRLHRQRGCPGSQAAARIQMHAERETTSRPSSGLRHTAQG
GAGRFKGRSSDTVQGVVGVPWLEDARPAAAHSVADENSVLSMRGADVVREDPHVAADASQ
FLEDGISRQRNGRRCLPKY*
>TCRU_1145 hypothetical protein, conserved
MAPRSPTQRESGRGHRHGTIPPAGLRQCLARGLSHCSQATLLEGCAGGTGRRAHRVTGAF
RCGEDSIPGVDLDIGPRVTASRTGAMRHLPTLRQACTRPADHKEPFMSVVPPLPHCGERP
ATASARTSSRREHRNSLSTGERRIDVLLPNLQQSALVRPQYEGTCPTCSAWRSDSLRGPH
MRMPQWRHRLLNRRLARRSPPKLPSMPAGKTRRKHKCGYSIWNRLFRHRFITDATGCWSH
GGPREGLPRPLRECPRRWELGLRLFVTAPARTTARMRRNTCLLSADSPFATHTFFPQDAT
KKLVNCFFDEYWPHLPWNNNPRGVRGSLIFECYFAFVFLWALDPLACVCAHPP*
>TCRU_1146 RNA-binding protein, putative
MDPLTVLAFCPTGEFARIERVIREWSGVEAVGSLRIKERKKDITNVFIKFNSEDIARSAS
LQIDEVPGLYLTDEKKGEKQKGAKRNATKGRSKTVEIELMNFGTYNQEKVALEQQRKKGF
ERNRQDRESRGRRTQRGFRGFINNRGSKLRPFIFPSAQVNVAFVDNIPFNMTNDQLTEVF
SPFGRVLDINRYELMAMIFYDSPESVLRCIQQLNGKTVRGNIISVSSGSVRIPGPVALQM
GI*

>TCRU_1147 hypothetical protein, conserved
MHRWDAFKPLVSSLCKKKPSWETAIAHYQRSLVEVGSSLELEHAQRIALLFLKQNGVPGQ
LSSWARLFSFEDIPTCSLMLKALVRHDLWRSAINLWVWNPNDATGEALIDELAFCNMWKQ
SIYVLQQLIMNEKFYSDSKKTITGDIIEEKHIDSDVALALNDAFRLANDPTFIPPEERRR
RGTIPHLVNTAFPLKSQWQRAISLLVRLSERDISSDTRKELLDVAAARLAYQAGKMEDTF
FWIKETEYFRGSRSLQRTFFRSAISIQRYEEAISILEILSNHGIEEIPSGSLQDLCKCFV
REYNAGKYVELLDRFSTVVLKCSSRIYSKETRDELRHFFQCNAVDTTALDFVGSLERTRG
STFIFGDRSHLEGIVTSATDIDKAASALLHKGYWKASLELLKRLLEVKPLDENEEVLIEA
ARVSLGSWKTAILFIA*
>TCRU_1148 paraflagellar rod component, putative
MVQNLVINLLFNSPEIRIMGPVKEQTIDKLNEVIPNATSTARSTRVAPSRFQYISNPNHW
YMKLDGQFCDEDGISYLMVLLLDALEEEGLWKLVSSTALRTPVGQSSKDYTETHVLFMNK
LVGDEI*
>TCRU_1149 intraflagellar transport protein 57/55
MSQEEILQQTTGPSVPGKGVIVDDGTMEDLIDKLRILRYEKDFCPRVKPPFKPLSKYYFS
GPSSIDNPNAQFHYFTSLCSWLMGLAGHNFEPPGQFDDPNATSTNILGELRAMNISAPNL
APNRIRQGNGEAVLTILSVLSDHALLKKGFTVRSVDYKNVEKYDELDGVTDADDDNGIGE
EVEDNVMIESDDEEELYVRATGERLVKEDAGVPLESEINAEEWNLEVERVGPLLQVRSDA
LQDWRSRIESAGVLLRAVEKMYPEVRQMLQHVADDLEKSRDRIQKREQTLAQQFSDQVED
YRVKLRELNTSQDSANMASQSVEQLSAELNQLSGLLDQVKRGIEDREAKISDTTPLMQVK
DAVTKVRAEIKQMSLRIGVLQHAVLHYVMKQTKAKREGLENGLGLDDWEEIESM*
>TCRU_1150 hypothetical protein
MLSNLFGSSLDGIGKLCSSSSTVEEIIAREDLSSYIQSQRKNGKGMLPLVEFIEHSIPEI
VKAALQPICEEECVGSVGKEGDADGHGPKKKTPGKKQVLFNENATELITFYLDVSQEAEV
FIRRIVAAAFLVLGIAAPLTPLVAQCFRRIILGAFDVSSVTTTEAIAAVLDEEMVLAIIR
HMSTSFIISDTLAFLFEPNLPTTEIVFFQPRPLIFTEACIRLRFAKHLASHMAAALRTVS
CQPYFNVWKELINHGCSQAAGPIVDELLKYDLLSVYFMDILLGCEEARKNPSAVPLAAQG
VELYHDIIALVRTSLIPPDVREMYFMNLMLIAPIKLLKMYTERFCDLIFSSETVITSCVD
SMRIELCAMFVEILRFHLRDTDSIIVESFFLEKLVAICAKYPDCHRLCLLLQQAVLSIFS
CEIKEKDNVVLQHLTVEDTSGKPGFLLECLGFCLDEGIRHTALSVIMVETWRTLATKTPV
VDLCGALRHTMELFLTNPNVQSRIQNMERRITGQGFVEVGSGCQEKVQHRPTINYITQQS
LGSDNSSFSSSEPTPSSAGEGSPNRGVNHTSAYIMEPLSEPEENLEAISPDGETTRDALF
TAPEALLYDAEDTVTMDLEWAEEAMLAEASPQARAYPKFADVRISFEVREEFPSDNPTEY
GADLFLRRRRSTDEHEDEDAWINGRRPRPRP*
>TCRU_1151 hypothetical protein
MNRNSATGNDEDATTRRVFLEVQIHGEEPHRFLQLEPHVNFKNVLKSIRRAGDLVWNGLL
LRPMETPKSVGMPRGLANVVFLRLFTRGPVTFSQKEGGRDNTPQALPLFVVPEPAGKARW
NGAPAEASQTHVFAGDHTATDVAGSDETRAPERSREVIGALEIRLRELRLELEEERGKRE
ALEREFCRLKWERRQPLHRSTAEEIHRWQMEELRRQRGVTWRTQSPRVVTSN*
>TCRU_1152 hypothetical protein, conserved
MRNSFFPVLCERQPTPELEAMPSYLPDTVVLQLHRHDGEAEFADYMDANSLTFVALGDAE
RPALCGIDATAQLHYEGAQRALVSAAGIVSSIRCSRLRIPFGMSELSELLRRAYNTEKGN
RNNTLNGCTETVLLVHAFSDAVWAEESFHSLSLHESSCWQCCLDRDWIRHKGSCR*
>TCRU_1153 hypothetical protein, conserved
MRTRCRRRIFHVCVFLARTAVGADAVVRLASNEGTGCCGVSTVAVEVAVSLSAPSLFRLR
HCALLRRERRLHDAVSRYLGPGVYLDSRWGSPELSDRVWRAMARNGFATMRCCRCVTGVR
RPNCSGPRNGTAEYFLLGDLVRSRRHVRSTLFGGNKCCGYQRETGA*
>TCRU_1154 casein kinase I, putative
MSSVKITLFQGKFRLDRLLGKGGFGEVYAGVQVSTGEPVAVKLERNKGRCFLFHEARVMQ
DIQNSMPGRTTPGIPELKYFGQEGDFRILIMSLLGPSLEDLHAKLGRFSLKTTVMLADEM
LSRLEFIHSVGYIHRDLKPDNYLLGVGRNVRHLYLIDLGLSVRYRSTNGEHREMATGKSF
VGTSRYASLRTHKGFSQSRRDDMEQLSYILIYLYRGHLPWSGLRMKDREAKEKAIGEIKQ
KLTTAQICSKCPSQFEDLLNYSRKLEFAESPQYEMCRILIASVLDTIGPNVKHDFQYDWV
NVRKRDNSPPPPPPCIVTHERRATENKINLKKGNENGEKDAATIGSKIFCFFPGLSSSAS

QEMVLVNEK*
>TCRU_1155 hypothetical protein
MQAELVAHREMRNARINERLSHPELCDSASPQMPPPNTEVPVAPEIVRSEPLYSVTIDEL
NKTTTLNEQLTRALAQREADNEKLAEDLAQREADNEKLAEDLAQREADNEKLAEDLAQRE
ADNEKLAEDLAQREADNEKLAEELAQREADIEKLTDELAQREADNEKLAEDLAQREADNE
KLAEDLAQREADNEKLAEDLAQREADNEKLAEDLAQREADNEKLAEDLAQREADNEKLTD
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NEKLTEDLAQREADNEKLAEELAQREADNEKLAEDLAQREADNEKLVEELAQREADNEKL
AEELAQREADNEKLAEDLAQREADNEKLAEELAQREAVIEGAEADASKTIEGVYSRCREL
EELAARRELAATGDVDILERELADALVQLKALEGENAALAALLAAKKAEMVEASDAAGRS
VRELESRLSAAVSEASHERAMAEKLISTTRGALTAMVEENQKQVEQLRADHDQARATMQA
ELVAHREMRNARINERLSHPELCDSASPQMPPPNTEVPVAPEIVRSEPLYSVTIDELNKT
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EKLAEELAQREADIEKLTDELAQREADNEKLAEDLAQREADNEKLVEELAQREADIEKLT
DELAQREADNEKLAEELAQREADIEKLTDELAQREADNEKLAEDLAQREADNEKLAEDLA
QREADNEKLAEDLAQREADNEKLAEDLAQREADNEKLAEDLAQREADNEKLAEDLAQREA
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RCRELEELAARRELAATGDVDILERELADALVQLKALEGENAALAALLAAKKAEMVEASD
AAGRSVRELESRLSAAVSEASHERAMAEKLISTTRGALTAMVEENQKQVEQLRADHDQAR
ATMQAELVAHREMRNARINERLSHPELCDSASPQMPPPNTEVPVAPEIVRSEPLYSVTID
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ELESRLSAAVSEASHERAMAEKLISTTRGALTAMVEENQKQVEQLRADHDQARATMQAEL
VAHREMRNARINERLSHPELCDSASPQMPPPNTEVPVAPEIVRSEPLYSVTIDELNKTTT
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LAQREADNEKLAEDLAQREADNEKLVEELAQREADNEKLTDELAQREADNEKLAEDLAQR
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RRELAATGDVDILERELADALVQLKALEGENAALAALLAAKKAEMVEASDAAGRSVRELE
SRLSAAVSEASHERAMAEKLISTTRGALTAMVEENQKQVEQLRADHDQARATMQAELVAH
REMRNARINERLSHPELCDSASPQMPPPNTEVPVAPEIVRSEPLYSVTIDELNKTTTLNE
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HVFSSGDGGVIEMLEGYMERASLVSGAEKDALERLSLSNKELAMLRSDFLAERDLMSREI
ELEKAEKARLLGELEVTQRNLETLKNAPVVASGENELSVLRQKICDLEEVVDVKNAHLES
LNERLEGLVEELHDKREELFHVIGQLDDFVVKFEKAREGEKVAVEKLAARDQELFELERM
HRELQTEHEQIVSHLQKQVEELRAQQSDDAIALEDLKSDIKGLRGSLQEVQGALREKNDE
INRLKEEILAQQEEAQALIDELAEERDQKSLEVSDSLKKLEEFVELMEDARKCEEEALQR
SADAERSLCRTQEELERLRTRQVEGRDNPKASELDTLRAALDEACDVKEHAEEENKKLKL
CVRLLTDALSKNQSRFTASSGVLEEACDALSNMQEG*
>TCRU_1156 hypothetical protein
MRRLGHRRGQTGLQLPHAPPCCIASFHHLGLLCSEQRSQGSVLPLQRLQLDESVRQFALQ
DIHITRSSKFPSRSKLLKFTTAAIHTLNCLTRVRLCTLNYRLPLCKILCELLDVSLPLRK
ILCELLIVSLPLRKILCELLIVSLPLCEVLCELLIVSLPLRNFLCELLIVSLPLRKFLCE
LLIVSLPLCKFLCELLIVSLPLRKFLCELLIVSLPLRKFICQLLDVSLPLRKILCELLIV
SLPLRKGARQLFVECCCLVELVDGDAVERFAAHYFRGHWHFSIWRWHLR*
>TCRU_1157 hypothetical protein
MSRETHNTWGHGGRLLQTVKLITETFGPGTTVIHLMDADRHLPRGADTTLHPGVGTDLVV
LVYTRVAFIIGAGLGAPLADDAPFHIKETALRVLQPDIHTI*
>TCRU_1158 hypothetical protein
MRRVERSSRGEGEDALATGEANVRKDTTVDVLRQASRHAQGAIETSWMTTRRLQVQGEQL
EEIDRALDKMEHDLGVGDDALRRMTWTGRVKRWFTSRRKQPSDGVESSTSSSVPSPSLPI
KPQGLREKNQQREGTRGSKREDVIGCGSSTSHLAMEEEKLLDALLNDVHAMREQATLQGA
MLTEHNCRLDVIATKTDAVHNHVNRTKQKVEKML*
>TCRU_1159 hypothetical protein, conserved
MLTRAWGIRRAVLSLRPPIRSCAPPASTQWRSVTFSASPNASIERRSTATVIGPLNTTES
RHAVARPPPTVTDPVSVTPLTQPGAPPLPPDLAGGTSNGRHASPTPPARQPHTQSEKDAV
SASKHASAAAQPSHGTTLTEGRPTMR*
>TCRU_1160 hypothetical protein, conserved
MTADPKRAREGTGKTIEEELATLLSGGHGGIMTAEEERDTTVLSPPCSDLVGKLLRNVAS
LPFSFFHVHVHLPSSALFLTPSTTKKNTATHEARVLFDKREEDRTEKSVVARLAGGLEPA
VPFAVGSPLVVRCGVTCGSSAGYEGVVADGMPFGHIQCLLRVCTRGGRSDGSEEPEEAAT
IPKACSEPPESLMHESKAFPVATNDRESNKRENVNDCHGTPNGILESWKLGVSLDPKIPF
YVRTMTEKRPAAACTGSTFDDVLSPSRSCGYTLLGRRDCETYILPQRELLFSFYAPAEVV
TMCAQQNEERMRRQAALGYSGPTHAFAEGPRTASRLLQGAHCNHVAAEEAAVAAASKYGT
NCGATPQNGPVVYEVRALPGDVVFVPRGWRYSVERIVGTAIMNAAATSTPTEGVVTRKKT
GSDVLPYGEMRTAFMHKKPSTLASLLGKVRKVSIKTESQLRCMEAAEICGVEVEAFLLCY
KPYPVLSAEQAAAYVPSNYVRRGVEEFYAKGGNDVFHKYV*
>TCRU_1161 hypothetical protein, conserved
MRVDRAVPCRSRQAFPLLVRDVLVRAGVAVLLGETKINDVDVVPLLPGAHQEIVRLHVTV
DDALAVDKLDARNHLLRQHQRRLQRQLSTTEAEKVLERGSQQVHHHHVELALHAIKKNVG
DAHDPAACVENAVESGLKGKLWMARLRLLQLDGHGLARLHVCAAEDLAERPRPNLLTNAI
PVCNH*
>TCRU_1162 hypothetical protein, conserved
MLSPRTDSHDPDTNDTDPRSTSSAPSVSAPALSFTTTADALATTPLPNTNPCAAYTWLPD
TRSTAPSDATTRALAYNAYSPPNTAASSATPPPTSSSTIAAVKATLTKHRPRIPGSGWST
ELMLPPCTQRTSVPFASESGSGPRPSGTAVGKHVSPWPPAAHTHTWPLMLLVLAAKRAAS
TVHAPQSNAVTGAPILRSTR*
>TCRU_1163 hypothetical protein, conserved
MRVWGLVRRSPFPQSSSGKAREVSRRIPTADALKVTLRHCVLVGGARLRIGGLSESTARL
MPHALVNMTNVTSLEGTIVLHGAMPLHSSVLLANSTLRATVGGSQYTPTTRGHEGFRCGP
ALVLDGVRLLSTWFVMTRSTLVCGGGSCAAILVERGLGANLSSVFYMDNCVVVSRTHVMY
ALASDLRVGGGSVFSIQNSSRSAPSTEYGEGACVFGDVVLAGGSVLQIVSSTFRLGFAML
MANTLTVTDGSWLVHRDNEFCTAYVVHVDKENGVAFRDRSVWSIIDNNFTYGSFSSFACM
TSK*
>TCRU_1164 hypothetical protein, conserved
MLRSMSQMDRTPLEIVILGLQKIAAQSETKQARPSTKEEMNQVIRSRTDWKERVVFRLAW

ITASRWPEIAALTPNNFTLEPDGALILDWSVAQKTARADPHRASRFVEIRGQDAFDIIKL
CRTLRHNEKLTNLTTALVERALANWNATAHSIEWGALRHAAQIVETYNLDPHVVSQLAEH
VDPFDLPQNTVRYLWRYTTILTQVSSLVALM*
>TCRU_1165 ribonucleoprotein p18, mitochondrial precursor, putative
MRRVSRQLIHATTVAAATRFAATSGAKKYDLFGYEVDTNTAPWIEKIKKCKYYDEAGEVL
VNMNVSNCPPDIATYNAALQRIYEAPSKQAQPVENESKFCAMLDLLEEMNHRNKMKPNEE
SWMWVMRECVKSGQFRLGYCIQKVMEAEFKSCPADLVKQNEANAERAKAEGKEHPSYLSL
QVGLFDVKIE*
>TCRU_1166 replication Factor A 28 kDa subunit, putative
MNLNAYGFSGQTASNAGNGAVGAAAGSNQPQRRMHPIRPVTIKQLLEAQRVGEGVMVVDG
REVTQATVVGRVIGYEDDTTNRVTGALTAKHYGYRITDGTGLVVVRQWMDADHQEEPLPV
QCYVRASGTVKVWQNAPIVTGTVRLVSDCNELNYHYLDVILTHLRLTRGDKHAKEEGAVP
AVSNTASTLGVQNMLPGGGGKVFATDVLLNAIKQNARGDAGLSMDELAAAARQYGFSVND
VRVALRTLAAEGSVYQTHDNRFNI*
>TCRU_1167 hypothetical protein, conserved
MESYKDVILSQAPAMYDKMGNSAGISMENYKGILLCARPANLPHGPSVQLRGENASAGPL
LTRGGEPAPAFVPGGATETQAGLGPSVEDRATMERNHRKQIENAIARRNRAFTVLTRHRR
WLRSFAEQVRKMKEEEIQREIQLARRAEQNRQRQAQKRAEAVSGGFSPVADPTHTAREQQ
QEQQERAATEAERAEAEKKKKKAASKKKKKPKWALTEDEALEDELADADELLDFAKKLDY
EKFINDYEVAGALAIMRERVEEIARENNWSKEVVERAASESVAEDLEGEGDADAGEGNTA
AKVGGPRGDDQTPQQTVCTAAARKAAPCNIALHKEGWNKSTSVGGVLRRAIFRDTLLLAE
RILASSMSMQKIHTKYSLARLLQRCVLNGDNALEAMQKPSMGGSKGLDVEPRVVKVNPEA
TKQESGGGDTDLGSQRILVAMQRSKERTQGLPYLYRCPAI*
>TCRU_1168 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGGGGCTEKLAASAEITVDSASGGVVPQLRRNCAEEVSR
RTGGRANASAVEECMRQRMDGVLAVVDGRRRWRRQRPAVAAAAAENADELGKENTSSERK
VLSGGNGSGSEDAHVRGGDLHSESRDGVVRPEGATSEELNVNSNSHTEALPTKEIRQVIP
ESISPVSSPDSKEVEEDTAGKDDKTQEILVSGEQQALQSSSSLGGNSPASDQGAELTAAE
NPQNDKKGEAEKEKNLSDKNVPTGINPSATNSNDNAPTKLQAETLYRHLPMRIFLPHITP
TRVLRRRFWTPLLFLLPQ*
>TCRU_1169 hypothetical protein, conserved
MKDVEGREFAEALQSGNTLLVEGHSGHRLRLYYDSLSSVAAKAGSGGERAPVPLLISSLK
CLSNYLRKLDFSRRYVFFVNRDLCVPCEVRHVLCQHYGAAARLQTMSLRQLHHSCGETLK
LLEALEQKCVAKLAAVNFRYSLADVSRHPLIIPEEYGMSGFASRSQNSTDATLSTGLVDV
HSYCSKWMPDLDKNLWTDTFVFERTWPSDPCGDFLPIFRGVVEALINREVVLIDVSDPRE
SVERVALCVALSSREKHRAKEFVERIVTGTRDMGWVLVAQIATPSSFDMPQRRIYLWCGA
RVVFRDGRMGTVKGFDKTSLCRSGKADWPFVMLDSGSASTVVLPSITFLQRPLNLRVSEL
PLRYADTMTVEELFLTPRVSLGKRFFVLRPSLFVGRLSHLRCAFASLPSLSCLALTGPLP
WKLLVTAENS*
>TCRU_1170 Repressor of differentiation kinase 1
MEEKVSEKTPEAAEVVQMAASKASESRHSAEYSMQNPLGSIFGKSAPIHPMPSFSLYNEG
HGLEEPEGEEARNATEDSVETDYEVKKSGFVISTVLAVALVISFGVIAVGLIGFLPGHMI
GFRAVSGTAEIIQVEAVRGVIIIMRSTILQLPDFAHTITANYMRNQTSAYTVNAFPKNSQ
SLLYSLLSVLSTFKDTISFFNFMDRRGLYGFASEILWPNESGSMLLLGAHNSTTGISPVM
TYNATILDVVSPDPLAYWNISDELSQEQGRFELIVDPWVKNKSITQRWFPSALNRTGLYF
DFIIPFEIDGFAGYCEVGMPTHRLLRESRPLIAALRKHGRVMLFDDKRDIVILTSWGENS
TWWAGDSYLSFGYLTLDGIKDPLAAAVARQVKSNRKQMSDVVNGTTELVFPFENSAVRAS
FARVTDKNGLNVMLSVAVLRSDFFSGIVQARTIIIVVVVAVVTMSAITAFVGACYLVKPL
THLVNALKKASNLELPGSDSKVMKPSRILEVGEIQADYVKLFRQLLMLRKFVPEAILARI
NLGDMSTLTASVDVNENADDRDSSFSSNTSRSQVVGNEIGVKRDVRLNSDVFREQLNLFS
PRHCTVVAVEFHASQLWDDSKKYMTLFIATATELSGCVEVLGPDKIVVSFGAHTTIPLHS
IEGCRFAFEFLSKLSPYEQGAVTIVVECNEFLVGTCGAHLRNARVLLGTDYLFDLTRAMS
GAPYHIAATSGVASQIQGYQAFPVDCVLIPSTSLPVVLYELRLLTTGEEQTQNVTKLFRL
GFSAMRQGNYKQAISHFQRVEKSDPQAQRLIRLCAQRRLAKDTTPYVRCVNNSYDIANNT

FQYSSGEIWNEVPEKRELINKTPVSLKRENSNLSREESMALFELCQSSSSSSESFQALED
GCNSADDLPLLLTDMNHRVWTRSLKKISEGAFSAVFLGMSEDGGQVAIKCIPRRRRDIMQ
ESLEAEMNVASKLRHPNIVQYVSCSVVQSHLAIIMEYVPGGSLHAVIKNFGRMSSLVARR
FTVDILNGLSYLHGLGIVHCDVKPHNMLLGMDGVCKLSDFGSTISEAADMARTMADEVML
RGTALYMAPEVAAGGRCTSQSDIFSLGISLLEMLLGRLPWKWSSKAPEGSDATSLQALFN
RDLLFVQSLARDYLEPEIPDFLDFEVAHFVRSCCHPNPAMRPSASALLSYSFVL*
>TCRU_1171 hypothetical protein, conserved
MADAEWEISALSFPTEVENEEGIQHLTVISPQLNTAAKCDANSGDSSRKQPDDFGVPPLC
PIPSGGGSSANAEVAQERHLVELLHKASQVIKEERARSATLQQELNELRQSSSAQLVTQQ
LQNENRELKRELLSLHNQMDKAQAYDLQPRRQVGKKKDQRSVRSGSLPSMERGTDSVTSR
PSASRTPFTPLTANTDAGGSYSSAQHRKRQAVSLQRRQLLAPSESSRERGSSGSQKIQEP
PSSPKKQQEEERNQKTKQQYVAKKRASSSSSNLPFVPQKQLPNAKEEEVLVLPQSLLKSP
AADEIWQANASYNRETAYSLGMITRLRRAMAPPPTKEQLGEVIHAMVQEIVRDARRRGIG
LKLTRQAPCVYLFELRGAASKKGKGDTARVVHLSIDSGRLSVKVGGGHENLLEYIERYHS
LSSV*
>TCRU_1172 hypothetical protein, conserved
MPDYTQFVKYFNEYPNIPASETSAYSRLADTTWRLLTASEKENAGGKGSSANGATCPSIV
IGRLLVSTEDRWRIQAHMRREEVKAGAGRKEYNKKVTRAAKNTKGPAQGEGFPPGRGRPV
*
>TCRU_1173 exosome complex exonuclease RRP40
MDQVSPTTAMIKGVRELAPLRSHVCLPGDPVLLLDPTAVVTLGNGLRPLPHAPPHGNTTS
GSAGGGNTVVVAELCGPVECSVESNHVRRYTLDAPAARRYMYSPRDPVVAIVVRKTSSYY
YCYTGAAMLAVLDVLGFDGATKSSRPRLQEGDVVYAFVKPKPSGAQPASGDACVESAGDE
VELSCMAGDVGLVAKDWTSAEAVFGPLTDGTVVRVPISYARSLLASDGASRLLSLLGERV
PFEVCVGVNGFVWVRGQTSDVDAAAAARRTVAVASCILESQDDATPEEMESRVKSYFPSE
*
>TCRU_1174 hypothetical protein, conserved
MPDASACARAAAAELQGWVYVTNQLLLESARNTVAQVEEPSRRASLNAEYVEGLTKLFYS
HAAAVTSLLFLSAAKSTSSAVVLDEEHEKKWEIERERVVAEVQELTRQKQALEQEVERLQ
KEEQRVGKAVSVARADADALRREVEREQKALETLRREMQEESVRQREEHEHQMFNARQEL
RQTQEEFAAEGRRLQKVRQQLRSLADVLAELRDGDGDGDERVLHEEPSESLRQLLEEFVA
YAEVTQRTQQELQEELVALREQMAAEEPVASRSRAQTLYQRILPPPAVNPVALTLQSVRE
QVRELRPQAAGTPCGVVDTPRIQNRQWQQHSCRSHIKGETSFTASPVSQCQTPQTWLPNG
VSSNLIAWREKMALLKAELHDLRREIEN*
>TCRU_1175 hypothetical protein, conserved
MDLVFVRVVLCLWLLFLPTCKGAWSLWVKSSSRSDPVKEGGAAATSVSGHSDDRVQIPDL
FTLRQKKDAGQDRQAAHLLNELEKKGRISSCWKRAVDALKEGCSSLQSDDGARSRLALTM
ASCDGEADGGRRAWSYCAFDTDVRKCVDHLDDAQYLMYVQYRLHADVLCLYIQEEAFQER
TEMAVQALYASALAASETLQALRSSSSELHSSVRKTVEQQASNLVETSKLNDQLRDLRSG
QSLAFESLRSSTEGMARSLTDARLSLNELHTALYESTAQAAAAVREVAREATAFQKRTED
HANTMVRVLERIEVFQQGLLEKTIGLSEMIRAAVILVILLLLTIPTRTAAARRPCIGVVA
LAYALRPLFLPYPRSGLGNNFFFATVILISGIILVFFAYTHRSPEYTLRMMLRSELRHVV
EYARPLFLESVRQVVIEGVTFVLHSLDYEKEAAQPRTPKDTALLLASEEARAEETCTPPT
VAKPQRKATHRRTLSRLR*
>TCRU_1176 hypothetical protein
MPTAQPQYCEFILPSRFAAERPRTWHLVMDDAGRSLAARYGGDVPLRNLPDEAALRSRDR
RMRDEVSRRRMGLASGARNSGTLDTHKFSRADANLLSLQHHRREEGLRTAAASFLSGRIA
AVQRNAPPRLQRTTPDDVIPREVPVSLSQ*
>TCRU_1177 hypothetical protein, conserved
MLPSAREVEELVVATLRGGNWARAVMLFAGALKLPCVPTSRTYAEVVAAVATRSTWEVTV
QVLDRLQTSPLSARAVYHTAADAILARNDGVLPEKLLAVILSARRRRVILDARHYMQCSR
LLLDSGDWHGALLVCSHERLIQHAPFLAQPTMLAAAAGHHWVAGLKIMSSLLALGNIPSA
AITESFIRCFSPTSPWWRALAVASVLTCRDAPEVKQRAHDLREEVTHHAKSPEINAKEGR
RRVLLRVTNGGPMPEDLTMGEAKEVLAMMKDRQWERALDLFCAFPALLELTPRPPALLLP

MTVLGNVARRLRYWEALWQAVSRTLIAAPMDNVISAASLFLAYMRIEEQGADAQEKAKEV
ARAKDAVIAFVNDRRMHEGRALEPAALHSFVHSTCTRGCWEDALSFTERPAMVFAEVVER
SNWQAAIAIYGTMLPSAQERAGPQLEHLFISMGLWIPALRYAQSYLPDDTFALRSLAIPL
CAALGQWRRALHMLFSHVPLPTAAEALLKRYCFLRHTEETIYEASESGDWMKALQAWNAV
RQIPYDRTILARRGGEGKTDEDAHPCISPHAVKCTAKLLLEHQRYDDCCLVLSSHNPTAS
DPLLLRFLLMFYYIRLSPLSYGRVLQKYREAHAPYRVVLDGYAVLALSVSGNYSGAFWIL
RSLSSTREAELENAIARGFDEVPHLKQMFSSLLLKGTKSSQVVDLEAVMGMLIPCVRSFE
EVNLFNEPLTAFWGSDSDALRECALSISTRLAQHMMAKELPVPWVVLRIVAGGIDRPAEC
STAHLLYEAVRQQGVLGTTEEVERVGDEKSGFWRPSKEERDIFFRRCAQAFIRMGHWSRA
LEAMQDCETTDEMTLFRTAVLLKEEKDCRMRMAHRVILEATSNDDKNTSEDNSSLVLGRQ
AEEALFALTQLHAWKAALVVFNGVVAGGRHWSRGSGGSLSSGVVNALLSSVASSGHWELA
LQILKTVQKEFSNVIAFIDKGITDVLRSVRRHGGAIMCSKLLLFFVEEMGGVPTPLQYEV
LLGSVLGSQLTAVERDVCAGNLKRLSQSLNEKQVIDLILAITISGRSWEEEDSDGAIVLP
FAGTERRQRMASSNHPRPTCWIPVERPPLSVEEFHQLCHLAPRIVLATSRGLETLSQEAF
SGRFRPFELKLLLQHYRMEVLARVRDTGDGALTLDTQLVEYCRESKLLHILLLPHERVWR
RTLPPVGTESAAAFIERLTSAVFHGFASPQTVAAVWEMCHPFVTQLAEKRWPWLCEYELL
RAVRRRGGKPPASLLTRPDASRVEITSYWATYGRAIWPELFFSGPELCQLAVYVPLVEPL
LGNEEELSELLAGIQLTHFSVEAIPQGEELLRQPRSVRAIRAVFKLAFKTLKRLHTQLDT
DARGGRFYYHHHPDASLWKRYSSEANMKERLPRWALALRIIHHYRRFTANTLPPRMLAAL
FSACASDAAEATCVSKKKAKQPKKLSFWELAIQCAQAVEPKFTPTLWYHAMQLACLQMPF
KGAHARASDEYCLEDMHDTSLQATSRVLLSHAKKRDGKIPFAESLLLIDQTKELMDEMHS
REYAQDECTQGEDVLTLWALLQNHGCLERMEPPHAVLLRRLFLEGNPSSEVL*
>TCRU_1178 methyltransferase domain containing protein, putative
MEPDDVAEYSLQRYWEKRYSKEEQYNWFPSIHQTSVQALCEELLNVFVQRKAQRAFCPGG
CHDASPVLRVLHLGTGNSSLCMDLHNAVQAHRLPFVLEQVAMDYASNVIENMRAKYPPEV
LPNMKWMVGDVRRLEEFCSLGPFDVVIDKGTMDALEADKNSPNMEKDIWAMLYGVNELLK
HAKGYGAFMQITWVVPYIRLYYTKRDAFAWGDQVRHALLGESDMYRLFVYTVKQ*
>TCRU_1179 hypothetical protein, conserved
MQHHVAESDTVLSESSSWNDSENSVIDDMFDRLAVAVQGLLATMRDEQRPYTGSLCTRRL
QDRIQRAFPVEYRAVVDGIYQGSWEQYLKEKAVVFCFTQKRDIKRPNIEWMIGLGAMRCY
FLSEDIELVNDNDELLGCLVRDHCRGSLENNCRTILMELFSALIGTEPVEEEDDKTSSVA
EYELGSLVLWRPVLRKLWLHPIKGRRVPLRDLERPCQQLGFHIRLRCRWATYVGNNLLLK
YIHICVLRVLLNVVGPPLQPSKGNQQEDTEGTLMVGFSESLGNYIVSLEKTDMWGRIPPI
PRNSLRRGRIFS*
>TCRU_1180 retrotransposon hot spot protein, RHS3, putative
MNCPDESDVKAMCVWEQRSKPPQQQAEYWREVKGRMDKVGPILRHILDEQSYDDRIEKCH
ETVEETISPETQYYTGLGNSTMWGGNSVFHWLAKVVRIREEACKGEFSLNLPISDHLCNK
TLCMLAKLMQQDDFNSLIETQA*
>TCRU_1181 retrotransposon hot spot protein, RHS3, putative
MERGDAWLRSRLMVLASDKAWPYSWGACEFNRDCYVNCEVKRAWQIVKGGLTEWFSGHGE
TEFSPHRHLLIGTPGIGKSMAAGSYLLYQLLHYDAERLPAVACFICN*
>TCRU_1182 hypothetical protein, conserved
MSPSRWSYDAVQRLHGSGLGLDGAVCGGGAIGVPSLALVLDKLVGGYSGSLGKLTFHSAR
ERAMPRELKPCVTTLTRQLQCLPHTGRYAGASDRGGVGSTGRLRSFRAKFFACLRWGIRD
AATACARDGELQWPQQPSVFVRNPAAEADQCGLFPLVRWSPCAWLPSRLSRWCGEVRA*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MSGSVRNVTLSNCTLVGGASLYVVGWLSDPPAGERADVLISGLESRSGGGVVVANRYPPG
SRVTVVDSVLIAEKRVAYRGAYGLGDASACLVLHSVNLTGSVLTIARTHVAAVFRDAVGV
LLVGGVALSSRGALYVDGLLVQTALGLCVSVEGGVAASGGSVVAFVDSDFLLCKHALSVR
GAVSVSGSAVAFLRSEFVLTADYAVAFYSTMRLADGSMLLAKGNVHDGVSREMLYTAGAV
TAAGSTLSFVRNRALLPRMLSLSLSLSAGAHLRVACNDAGGRVLSTAEEYAAAGFGDAGS
IDVVGCDACDRDTHCYAPGTASASMRNGACVCDCGGGYGEACVPVGAPALPSAAGTASSV
FLREGVTVRSVFVVPAGASEVALRHVVLDGVSPVLYVPWMARDGVRIVVQNVSLLNGAVL

YVMGGGALRGAVAAGSDESGPVELSVCDVEALDGALVLTGTYPAGSVLTVADSLLVAARP
TPLVYLPGSQSSPYAPVLVLSGLRLVRSVLVVSGVALVTVVTGGRTVVMDGAVLELVGGG
VALDAAVLGGEYALYASARVVASGGAVLRVSGSQVYAAHGLVFESGVEANASAVVLNDNA
GALTDGALLVLRGSASFASGSWLSVRGNSISGRLLSVPSYPRSADFVQSTLTLHGNAGSG
PVVMDGTVALGGAGRRFVVGCLTLNGRALQPMDYRSAGIIGEFRPVTCGVCNADVRCFGA
ATRAMSGSCGCRCAEGGYGRDCLPVYLPHVDGCNRTPAPPPLSHTATLTETRSPTPTWTP
SLSVTRYSPTQYGPTETLQMTETVALPPTRTSTASVSGRLWWSDVACPTLAVTTTAAGGS
LTQNDIRGGGSAVPTRLMVALPPPFRWERDPQLGTHLSFVPVSTAQPRGFGGPWGAMLSN
ATWVRNATNPSTVLELAVPVHRGYFIVADETIFIRCDAAAVFGGCRGVLFGSFTIRSDTL
PAAASALSAITGVVAGATAVAVVVTGGLGSILEMQALGVLARMPCASAQERASTVALPYF
LSVFAALDPLWMVVGNALLAAVFGCVHYGVTAAFQRWRGVDAASAWAAMRFPSLTYVVAH
AMHLGIFFGSVFALAMPDARVQHYVIGVVGVLYGVAFPAGVCYLIARHVGASFTRYWQFS
RKPLHERLLYPVGYWHPAAQQRMYGGMLTNMKGSHVYWCVFQLSVLCVVGLIAAVHPPVG
GCHVQYFCMATVLLAGAGVVAFTNMMRSAFLTVMHTAGFVLLAVLCLVSAANHLAPSDGG
ARAYAAIVLLLTTVLLAVIVYSVVVWYMEDRHWQELREPRRGVLEALLRDDEDGDEDAQK
PHDRTSSSYASGTTVASSYRPPAMP*
>TCRU_1184 hypothetical protein, conserved
MWSAVGACPRSRHRVRRRAIAAVRVALLVALLLVAAAAWMTAVHAVVLRLRGGTVDRAIT
VGHAVDTVLMDGVYVTNGVAVVFDVPAMLPGALRIELRNCVCDGGAQIYVRGYSGEPASD
RSLEVSVNRLSGGYCSLVFVHNLPARTNVTVRDSTIVTAGPMRYSQLSGLMDAVASPLVL
HATSLLQTQLRVSNTVLRSLQAGGSAVHVGGGVDLLSSAVVLDGVSLEASGDSTALALHV
PSSSRLSLRSHSVFSVTNMSVVSSGGGFVLGERLAVSDSVLRFVGVEGSVASSLVRCDGG
TVGAGGWLELHDVWAVGEASSVASLSGVTLSGGTVSIARCAATGATLVSGLTITSGVVSV
QCNRAGGRVLQSSGDYRMAGLPSVSVVPCDGCAAALACFDALTASFSDCVCGCRAGGVGE
ACLPFDVPPARSGGGGGAARDCVSGVTLTESVTVGGGRATACFDSVVFRGPITVAVDLRL
MDAFADALNVTLRHCVLAGGAQLRIGGLSEITAHLMPHALVNMTNVTSLEGTIVLHGAMP
PNSSVLLANSTLRATVGGSRYVPTTPGHERFRYGPALVLDGVRLLSTRFVMTRSTLVCGG
SSCAAILVEHSLCAKLSSVFYMDNCAVKSREHVIYSLSSDLRVGGGSVFSIQNSSWSAPS
TEYYKGACVFRGVVVAGGSVLQIVSSTFRLGFAMLMAATLTVTGGSWLVHRNNEFHSAYV
VYVANENGVAFCDRSVWSILDNNFTYGSYSSTIAHMTTNWSPPSDTHPIIYGMCNEARGS
PVTDYGEELNIVAPVTVLDCGACTMNAVCFAARTSSISGCECVCAAGGYGDTCLPAAVPD
GLGPLPLPDAKDTEVRCVHGGSISSVDYPDPGVRGLCLVNVTFTAPIVLDLSSFDVPQQT
LNVTLLQCVLMGLSIKGSGARVHVSVTSSLLDSGALDFEGDFGASSQILVVGSTIVATSG
HAIYFVKFTLSANMTLLLLDNYIEANRYAVYFFNGVVVDGGGIIVKGNTLSTTKDDDGVE
SSVCVNGVAVKNGGYFDVENNTMSSVNGVIFFGDTTVSSAGLLRVADCTFGGSEVFDSAL
LHLSGSVTLEGGAQWRVEGNSVVAASVLIISYSWHKIQLSGSGTTVVLAHNRQVNDSYPF
ADLALPSMVKKPPARLVVGCNLQGDEEASYDYVFPEGVVVFRCGTCNDDAACYMPGTELV
DRGSCSCSCKDGWHGASCLPFEVPNTVVPPLAERAVDGDASCVVNQTLTNLTLNMWKIHH
CYVDVTFSGVGAVLTFSLNSMPLHLPINITFTGCTFRDGAVLKFVGGAEAAESTGVLIRV
SQTVMRSSVVVFALAFPQHCDIAVTEVDAVQSSEVHLPDARRNKLSVLLLMNVVLSASSL
LVSNVKAHALRYDAFGLYSTGTLTLVGGSSLYVRYCSFEGYEYLFHVYRLSVSDHSVFAL
LNNTMFSGVSLLYQHHGVSVSEHSVLRLVGNSGSARYAICNDGLWTVQRSSWLDWRDNDV
EVGAMFYDAGSAFVSIDGSSVVTLTGCKMGSTGLSVSLLKRADAGYRFVAGCLTVAGREV
TTAAELVLHGITNVTTVAVCGECTKEGDCFAPLTTAVIDCRCQCAAGGHGDVCVPAPVPA
GPPPPPTPPVPPTPPPPPVGECISDMVYPEVAQAVGGGLSWLCYRNVTFSGGRMILTVLI
GAMTGEVVNVTFDGCTWRDGAVLVLLGNVNAAVGSLNIVVTGNTFRDALLSPEGVFPPHT
NITISRNRFTVTRLVLRSGLDIWIPSCVVMNGLAISNDSAVVLSGNVFQSVTASSSAIYV
VGSALRVSWHSLFAVVGNTFHMAGGDSTLINLEGSGQSSSLSVLNNSAVVIRGNLVSRPV
RYFLLVILALRVESLSAVVFQGNDMQGSLAVFFPRYSSNIYYNSWLQLSGNLCRESPSEA
FLFFNPTVNLRDSTVSVSGNRFMSSTVTPKTVLIPKRSRDLTNGAIVAACNTVNGGGERF
MS*
>TCRU_1185 WD domain, G-beta repeat, putative
MSKAKLKLSIEGKTVVYEGRPESRKKDLLDILVKMKVDPSVAVKAFRENIEDAARYTDEN
IQQQFLDAQRAYAEKKKRKMGEVISEEQQKEKPERITLSFKGKQFSYEGLPSSKQYAVIE

LLIKQDATRELVVETFRVNLPESSASDEEIMSMFTAAMDAKNARKAAKKKDTAGELAAQS
SSRSIEQPPPPPPPPPQQQQQIMNTSSTSGVDAIEEITGMSVEERDSISNFIKQVLEQPE
MDLTARMREESNTFSTVGAMTRNTGPGAGAEDDALTMTLRSTRGKIAIYCQEENSMANKV
LYISPNTTFEEFCAMVEKKFGRKMVMSFNEGEDLIDMDDDDVFCMFLEMSQNHTQEGKRM
KLICAPPETRKKVSDDKLTDTKGGDVFKIKAFSNGKLDVREERSYTGHASAVYCCSFSPK
GERFCTASRDRSVRLWNTVTGSSSVMKGGHNGFVLSCDFSPRGNRIVSSSDDRTIKVWNT
TTCAKVYTLKGHDDKVYCVQYNSTGDYIVSASCDHTVRIWNADSGTKMLTLRSHSLAVFS
CCFSNTDCGKYVVSGGDDRLIKVWDWAKDDEYCSMAGHTDTVWSCKFSHDDARIVTASMN
HELRVWDWKNRNCILSWKGHQVPIHHAAFSTNNKYIYSCARDWTVMVWDAATGELFETIT
GHHSTVYHLDVVGNKLLTSSLDDTLKLWTINEK*
>TCRU_1186 PH domain containing protein, putative
MRKYNPGKLGTIDGILKAYKGREEQMFEALVRKYGPEPSRDEPHLLEQKKPPPSGVKDVK
RLHSEGISTRNVIEKVLRVAEVSYEEVLLALWCQKRYLFDAISELPTTASKELRAESFSP
SSQSTASRERLSRFFTMYAPEKLSGMDALIEAAGAEGMNKLIDSLVAMYGPEPAGDYETE
DSRSAGNENTKKRFVSDGGDNNDCEERQLFANWLVGTGRGAENIFYTLMPEEQLLDFVGA
TFGDYENRLRRLFVRYSPARLQEVNSLVADHLGHEEELIERLTRELGPEPARSAPTALTR
LFIRRRIDADRSHIEEEKWSDNGDTNGGDNDRVNAAEHLPMTLVNGRALIDEYASNESAE
FSGDEAAAYPRDEEYWYRLFVHSCEDATNNDDDTDDEYEDNSLRTHCDSAKNDGLSTDCA
KTATLSSTTITGEHRSLDSPTTAELRKIRGGKQRIRVMLGNKFGQAIGTLCTACGESIVQ
SFEALWQPVGPQYLQLFSETVVKDGYLEKLSPDTRRMGVKWQKRYFRVNDKGMHYYETSA
TSEKPKGYKVFTRNSVIISGVDASTHPNCIDRRYHYFAVTVNESNDVFYLRTPSDEEKRQ
WVSFLQLALARMRLTTVGHDQNPSRWRARMTGTREANIALIELAQASANVLQSLEQKHNE
LHERIRSERAQRELMETQMSEMQKQQDFLAQRINEAKAQARLAEEDAEVKCLELAERAAS
IKQRRLDMKDNLEEARSSIDGITHSVLKLQRDIVDMENECRSREAQLRQVYNKWQRCEER
RAYEKGGEYRKFSS*
>TCRU_1187 39S mitochondrial ribosomal protein L46, putative
MRLMTLQPRLSGRSFHSQHRTPIIPQIPGGDTVPGSNTGVLVGYLLHRHPVLKHTPHPLE
MEMGFLLEREHQRYCRHEASESATHFMGQRGFSIDVMNRTDPRETKGNFFGLDLYQDAMR
VVLQRYKPERRVTPQDLWNPSELSATTPPPRHSIHRKMDDYLYLIIQDAASSKWTVPYTA
LKDRETLRMGVDRAIAKHNSDTLDCYVWSNAPQATVSNNVDNTCLFMYAATYLMGRPRFS
EFEPTLKDHAWVTRHEMLQYKQEFQSAELLEALLDISADGIFES*
>TCRU_1188 hypothetical protein, conserved
MDGTVKCSWRVHRHDCPPPNLMFCEDAQSARMHAEAVAASRADGNANTTAVVLDDENEAA
AAPWMTLQLQNPLRHLVVLSNARVLEVHVGESAIYTHKGVAVAAGLFLHDTECNAVAGQT
LKLKFFARKAKHVIDLVALSLVFDFVGPDDKSGGHDGHVADAASTVESRLRQLEMLLHTS
MKSVVLRLKELEARIGALESRGCDEQQC*
>TCRU_1189 pumilio/PUF RNA binding protein 5
MVMAASNDPNDHVAFSGPYLKQVLPPRTSTDINCSATTQGSAITAGRIRRYTHNPYASQS
ATTSCSSTNTSRQLNSSNNTSCDSSIQVYNNCFAREASGAELVLLSSNLLEQFFAVVGNI
PRTACTVTGRHLLVSVLRLQHTEKVQIIIDELLPQLNIVALDQQGCHVVRALIELISTEL
LETILPHFAPKTIIELAVSSQHTRRVVQSIFERHKSEALTPIVTTIAQSGQQLAVSQQGC
IAVIRTIENSLPHQRRSVISMLLPVLPSLTMNCYGNYVVQCLLQHMDHASLVSVVCHNFA
GHWLTLSCNKFASNVIEKVVWQLDGVARKEVVDELVMDASNLRCLMQDGFGNFVLQAIID
SSNDLEEFSEVSSRVRPLLHTSPYGHKIGNRLHGGLVRSLQVTPAPQVGGSAAPLMDE*
>TCRU_1190 hypothetical protein, conserved
MNDGVENAGPSTDTGAELSIKTIMEQQRVIDTLREMVTAMKSRLSTLEAAASNEVANPSA
TATVNCDRDASLHQKENLRLSRLVEQLASERDAAKAKCAELEAAVEKGDCRMAEALKCCR
QLKQMEGELRTTRCLLNFTESRYRETELDCRRLKEEMEALSFERSRWKALAMTITNRLDT
VTRERALMHISSLEREQSMRTAERRAVSPNSNPNTAAAAIASDNVTSLPTFDAMKLISAW
GTQQTAPLPPLPRGVANGGTRHSSPALPSRSITPRRKGGRYLVPL*
>TCRU_1191 hypothetical protein, conserved
MCNSPVPVYVLGRHMLDAYFFEMEGTADLDFVICDVAKNSTSDRERIVDYSWLEFAKKPC
FSPADSISSRVRALVRWIERSYTEKCTRELPEALRAHSKTMGFEYDVYLSSIVSHDGRRV
EGVVQAVDGCVYITLAIPLLLEERARVRRNLSNVVELYSKVLQLRLDTVPQFSRVEISLI

ISCCANSRDAPVDVLSERISMDLGEPNNSTEVSFMSFITSCVKFRRMPRYSSTLQRGASF
MDYIPLLERALFVSLREPLHFLELVCMMSSVFGRPISVNVATNYPGECGNAGDVSVRCAT
FCVVDDATQFGFCICVRYHNGWTLPSVGIIANQYADGTSQGSPLQGKLQYSEDVRQLEKR
CSNEEFLDVVALCEAIERGSFEVMAFLIAVCR*
>TCRU_1192 hypothetical protein, conserved
MRLSYSDQLIGLDQQRRAKAYGREAKRFHLKLVIFASALSYLAARVAAWIYPKSVSHTWV
DDVLVEVVEDDGLERVCSIFGCVFTASLFFFLFLTIRADVRRNFFPPSRGSRAAGERGRR
VKGWSESFSSLAVPASTIFGALPKADGPTATAVGSAQHLRLNQYHLPQQQQSIRTEAQLN
QFLSSKESSSENGGGAPLATVTAAAAASFPTATPSAPAVTSSAPCAGSVFNGPLVGGGIA
AGPSDGIRVQYLGGAEKQSAAQPVDTEWAGLGILSAERSILKARRWLSDLCQELMEETAA
CDRWFAERQISSFDTTHCLHETIPGPRPSNSAGVGVGLPTLLSSTTPAVLRKLDALLNER
QKLAGQAQNVQNFDVILHLDQRLSLEAKLDPSGTFPTASPLSVAEQQAQRQYVIKRLRAF
ASQKTLASYRHNHGDADVWREGFPTDAHLLIHIVRVCVDGFANYVKFLHQPMNPQQDLAI
FVGDTGEPYFYVRYRSGPDDKTYATHQGVNSLFEALLIFAAIVRAYHNDSYGGIWGVMDL
SQTGLLNLL*
>TCRU_1193 cyclophilin-type peptidyl-prolyl cis-trans isomerase, putative
MRYLLLSKVTQLLLLLLLMLSAAVSARADPVVTDKVYFDITIGDEPVGRVVIGLFGNDVP
KTVENFKQLASGENGFGYKGSIFHRVIRNFMIQGGDFTNFDGTGGKSIYGTRFDDENLKI
KHFVGAVSMANAGPNSNGSQFFVTTAPTPWLDGRHVVFGKVVEGMDVVKKVENTKTGLND
KPKKAVKINDCGVL*
>TCRU_1194 Domain of unknown function (DUF1768), putative
MNKGVVRFHDVHEVPYGVFSPLSPHPIVIRHKQYPSVHHYFLTERFRDAPVTAALQSATS
VWELDRLVKEAERTGSQREDWNRVRVDVMLLGNYMKFKQNEAVRSLLLETGDKLIIDHTT
SDDFWGDRGDGSGKNLLGVILMAVRDRLRREMATKAREK*
>TCRU_1195 proteasome beta 6 subunit
MIEDHMEYGHHFPRKLADSTLSLPRQGVKEQQWSPYADNGGTIAAIAGKNYVILGGDTRL
NGDFCIHARDDRTKLFHLTEHTFLASTGMQADRLQLQQMLKYRIQWYQYNNGGKLPSTKA
IAKLTSTMLYQRRFFPYYTFNMVVGLDEKGAGVCYSYDPVGSTEPFRYGTSGSASSFVEP
LMDCLLTRQHMVQQAPAELSMTETLEMLKNAFTGAAERDIFTGDAVCFHIITADGIRSEL
FELRKD*
>TCRU_1196 hypothetical protein, conserved
MWVELPGAIAGVWANSQSDLWEKVLACGSLCHFDRWRKERHAVGSEVSSPWWESEAHALY
VWVTDSNRVFCVGPAYMDAALNKSIANALLCSDGALYLVGARDNEEKSSLFPASPDGGAA
DDHFHPP*
>TCRU_1197 hypothetical protein, conserved
MLYTQRGHASVKKRATALCLWVTDSNRTLSAGPVAVDNAANWTLASNLLYSDGSLHLLQR
RGNGECRVISLSRLMEELSAVRSVLSNWAQKDIFFSSLSIPTAGLVAVLSGAA*
>TCRU_1198 BNR repeat-like domain containing protein, putative
MWLRGASTLRGIGPLLLARSIKDTWRAHTVVGAAEGKESLGVVLRRTTITKGHRVFSLAG
GSDVSYEGGCWREGGLEPKLFVGDVTDPTGGKRSGRIEWGDPKPFPKLISSASHEGEWTE
FIASVGSGVVMEDGTLVFPLTAKDEAEDVYSMIISSTDNGSIWTLSEDISPAQCLNPCVT
GWEGSLLMIVDCENGRRVYESRDMGTAWTEAIGAL*
>TCRU_1199 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MTALNTESVTIPKLDHAKPEPRGTPSTPAGQQPSELGHLVGSSKVASGGVEGADSQIRGV
NATALSSNLVNVSQENNSDAGTMRGSGLLPSLLLLLLGLWWFAAL*
>TCRU_gamma, conserved domain containing protein, putative
Elongation factor.1
MASSGDDSRCAPGTHPHTIPCVSLRELDELKIDYSHTDTRTVAAPYFFQHCDAAGYTTLW
YNKYNKYNKMQCMTANLIRVWLQRMEHVGQYALGAALMFVEQRRHDIVALCVLGGRACRR
F*
>TCRU_1201 hypothetical protein, conserved
MQLICQRRSTVAQRNTDIPALGQLYEESERVGSTDVGAVNVGAWNVPSGAIHNLLPHART

ADERGELCGLFDVNRSGAIDPTAALQDAAVHVGNESNPAGHDDSGVAKNCGAIGGEAGAP
LDKERDRGMYPQPDRLEGTCCRTTCVYNGESLVRNCGLDTQQFHNGAGRGHNFGLFRGSK
SVGAGLRRAPLPDRIRGQDAFDIINLRGTPRRSARLTNITNAKVERALAPWDATAHSIKR
GALRHAAQIVETLNLNPHH*
>TCRU_1202 hypothetical protein, conserved
MEEANDYFSTRASSAAVADGLARRESAFAGRERHLETTPETRGTPQCLGRVDKSGQLEVP
SSTRGTPDAPAHEAEDGVATTLRHERLAEGCAPVSAISDPFPRESDGG*
>TCRU_1203 hypothetical protein, conserved
MGTTTASPLEKAPRSVGCGAARRFACSLTDRTAQSFQCGHSVGITRCGGVRKSRSPDEDG
LVVVWWLRTSGPVLLFFSAARLAQHHPGMVLLRESRHESAPATRLVGCGDFHQACGGRAG
GVAFLVRHTLPCERL*
>TCRU_1204 hypothetical protein, conserved
MCQLIHVTPRSAVLLELLVVMMLVMCCASGCFAASLTCSCPSDKAMRADRAKSIPAVVRD
VPFGSEGASQKCSVIRRNGWAPTRIDVSTRDVDGTRKYCSSER*
>TCRU_1205 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGAGGGGAEMNDETLVDSQHLSGVCEKAPKGLPESGERGPDS
AGHSLDKNNGINSNLQGGTGTGTTTERVGKKKEEDVGDDDGLEEEEEEAETDDDDDEEEE
KEKSKEKEDTPQAGKSESSSKEVAATIPTASGLSGVGGGSPSGVDDGGSNGSPKGIEDLN
LEVPGPVVNSPSPLPNAAAGGLQNPDGALPSQKNNFSETGVHSGKTLPTPSLPKPQAPAI
TQPKAEEQSSTEQGTEDSPETEEVTTGKENVQNTVETVRPSSSLSAASKPPVQQPTPLLT
QSPAAPSPERLAAATSEEKSIAPSFSAGEGSRRAPNVARNSKEEKNEKLPSENETESKAV
EQPSGNDEAEQDSPARTTASPIPASGGADDQRNEDADNSNARVLKSEGTHKNSETGYTNL
ASTAGDAETQTEKALADAKTNDTTRGDGDGSTAVSHTTSPLLLLLLVACAAAAAVVAA*
>TCRU_1206 hypothetical protein, conserved
MMVPNASKKRPSFANGPRILVASNASGIMSVTYGGREHVAADNTDELSEHDATGHKTLVL
ENGVAGSGPAAEGDAGGLSQRNASGHENPNYENSPRGIPGVAGVYTTALPCSTTRN*
>TCRU_1207 BNR repeat-like domain containing protein, putative
MSRRVFNSALLLLLLLVIMCCNTGGVEADAPAQGPRSLPENHFVWRDKNGGEKVSSLYAP
SLLEVNGKVFAVAEAQCTENDKVFTGIASGLLTLDKKQTKGELDASKVKTQVLEECPSDK
AECASQPEEKDVSQSETKVHVNRPATVVKENEIYMLVGKYSPTAVVVPPKNDAEDCGLLL
VKGKVGGGSSDSIIWGDTAGVPCVSTVEKEKIGSTRLIGGGGSGVKMHDDTLVFPVEGTK
KEGEAQKAVSLLIYTLKDTNTWKLSKEVPADGCSDPSVVEWGEKEKKLMMMTACDDDRRR
VYESGDKGESWTEALGTLSRVGQQKGRRSEGR*
>TCRU_1208 BNR repeat-like domain containing protein, putative
MLVTLPVYSSKNEVNRKGKLHLWLTDNTHIVDIGPVSGNDDDAAASSLLYKSGKDGDNKK
GEELIALYEKMKGDGKQSHSLWSVPLTAQLQRVKDVLATWKKADNLVSRLCPSESSVEST
SPKDACSPTVKITDGLVGFLSGNFSENTWSDEYLGVNATVKKENGAEPAENGVTFKGRGA
WAEWPVGSQGENQLYHFANYNFTLVATVSIDGEPTSGSVPVMGVRLSREGEKKTFELSYD
KEKKWQVLCDVESPEDQSRTLATDTTHHVVILLRNGTQGSA*
>TCRU_1209 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MSHDGTAVTAELGAHSGASGETVGGTDGQKREDIHARDGEVKAAALSSSLGNLSQGNNSD
AGTVCWSGLLPLLLLLGLWVLAAL*
>TCRU_1210 LisH, putative
MNQSRSGMSDENFDPSLIDDNRTNEAAGSYDNDQHDTEEISDDEEEMLMESPSTDLVKDI
MKRLLKVQKQIKSLTHKIENVLNVNSLDLHPLGVNNENDIEGTILLLIKYDELHLFLWGR
MAKLLHEEHQQCADVYTDTLNLHDRVPFESLTYTIHHNTVFCEYMGELINITIDHTANHS
DVEGEHLRQNWAKHIRSMEKSQILATYTALLVVEGSRESFLDPFSTYDLCKIIVEEKIRR
KRLLALSLLFSMLEQDDQAMGETLNQQLPQILLQRVRHLVHRIFGYPEKQNVMFSREHRG
SPFRDYSTLIHSNSNSPFSSRRASPEIVNRNLVNDTRGTPLLSSALASLHNGTSSSHAAD
NQGITSAEAQMRELPIINMEFEKPLFQRVKHTRDNQESELTSRPAKAIKLEINERGPECQ
ESNENWEPQKGEKVGRGPAWSFENQAEACDIGEVLGVTTTEEILVSWVRNVDSAVDNDAE
SRVFRYKYKKPHEQVVSWQRFLSIKSMKSEDIDFKMEEFMLNCAVIGAICHQREAVLPAL
QFQVIESMIHVLNSIDLTDAATMAKNAEKSTEMRERTLLRMEEEDRAVDEDKLEIRLRWD

AKLYITKEHYRRVREIVARVGWVLNGLLSHKKLAFLFLELGGLRQIMTLINANLEVSTTY
GCCMVLSQLARSAVLEKLLRNHGDYFEPIMKFVLHHWKNAPSHDVQSSAGGFLFQALSFP
CVISFFDIHEGPQSTMATIERLLNNSEERFDVIYPGLTLAALKCFYVYLVSHLMLYTRVV
FRKHRFLSTLVTNSSQGVSLPRDPATVEWILSFLSSTSASIPDVTIETVHSLLTRERLVV
FRSLIENDFHRLLLRCTQFYFNQGRWELLAASLNVLCVLSVVPFVRPLIADAQYPESGIV
HLIMILSDLPSASRNGNTSRESHLIPCVATALQILLHLAVPPVDKSDEASVATFNQVCGM
IRANDGVRTLLEVLKIRKDAAMSAKLHFFPVVARALQLMVTLRRYADTRLLFDALDVNSV
ARELLKQYDDVQKEYISMMGSRYTAGDVHATGRFMENVKCFLFDKENKENLTVSVDPVEL
ERRQAIIAHSYINYSRESLLELIYRYLDSEGLQNAASVLRRDANLSSDFSQLQQSTHVNT
DVTAFSTIGAPTLDGIIRSYLRQQHEKCTNPISTLPQFDLRKSHVYYPLPAPVEYTRNTF
NRGLAQKMGIDFSLRMRNNENHFLYRYPGHLFGITGVGDEMQGDTIAFCDNGDTLIVGTS
DGTIALFDTFPDDSSVEKLLEQHLVFDDDGVSGVFVSDDGDMFAVVSTDCKVAVMRRDSL
PVVKYSVEGSRAARFSNSNKFLLTTCDERHTCRLYDISAQQEVRHFSDPSWVGENLDNVA
TFDAFSQLILSDAVLWDIRCGDKPIYRFDRLNESFCNAFHPSNLLVLIDEKIWDLRTLTM
LQTVPAFKKTSSFHINLFGQVIYSFREASSLGNSASSVLSVVESHTFETVFSTEIRPPFR
AFAIDPSDRYCAAIIDQDMGAVVRVFSTSSGPLPGQQTFPFPQSNGDNASETDLGENEDA
DEDELDHDSSSSSSDEDSDDDRSSDTVDEEGSEWDHTEVVSGADSEEVSDAFENGTLTTT
GDETSGGDESGETAEEMEEVSDESMSST*
>TCRU_1211 retrotransposon hot spot protein, RHS3, putative
MWRCWGWLDIALLRGRWASAASPTGVAVRLRGAPTTEPCECHAQRHWDCGTKQPRLSFGA
SGTCWPQLGGASGMLHHTGVVMAHRRGSCDGSGAAARHVAGSKVWPQWTMSSTNMRLSDF
LWNYVGGRAAVDERLQCDDGDVFSGAG*
>TCRU_1212 kinesin, putative
MCGSVRVVVRCRPLLSGEEGDACSRVHFEAEGGNVLVDGKAQKGTRCFTFDRALPPNSTQ
EDVMQEVSPMIEHVLKGIHATVFAYGQTGSGKTYTVEGIDYLRHGSGNPRPSLKTDPRQH
GIIPRAIQLVFDRAREMQLEDGNLRFQFCCSFYQIYNERVMDLLNPSTTHSPNTGLKVGW
CRGDVFAVENLFICNCDEPEKMRRCFFSGTKEKFMGSHAMNQQSSRSHCVFTIYVARCDA
DSPETPIRAELSIVDLAGSERVAMLSRSPSSSMLKDSPDINASLLTLGRVITALTANGTR
AKKGKPADRSHIPYRESKLTMLLKHALGGNSLTTMIACISPSDRYVDETLSTLLYAGRAR
NITNIPRVNEDAKSALIRQLRAEVASMKRELKYYTELLARLGVPHREQLNWGPPSLNVG*
>TCRU_1213 ATP dependent DEAD-box helicase
MRRVHQLSGTPWRDRHLFSVFVVIRCVIQSSQSNGLRSPLDQYEDFRLVQQLRKNRQGNY
YRYQQRLWPSTEALERSMTERLYSPTERSPLALLPQPKRTSPNRTLVLEGNGATALLEAA
ESTLAQNGQTTANEATTPSAPLSDMEEMLAEHLRVELQGPIGSKIITEADLEGTILESAR
ERARHVIEEDLLVNDLVSSSSSSASSAVLSLRRKVPSAKDEGGVAWISLGLDPVLSERAL
AKYGPAPTRLQCRLLPALLHEDHNDVLFNGVTGSGKTSVFLLALLQSVRSEAAGLNVFVA
KDGLTALHAYSQLRALCGPLGGTVVDRPRDDWSWLYLGSYREGYEKYYRALRRSLHSDHG
PVRIFITTADTMCELLFEKKMEFESFGYLRRVYIDDIGVQIPMIPPNAPVAEMRKRLRNP
LACELLLGTLHQLPGPHIRSILQLGLVSADMDERLKDHLKALCVKLERHTIVLSSVRVPS
TIHCLFSFHLFHEDLYEYLVKLIWNARDTIPGRAVIFIRQEDNLLQVRTKLRGLGMNAKL
FSEVCHDGEFCGKWKFLLLRESEAFGIEIPLVSHVFITFCPRTACSFQHMCGRTGRLGNL
GWVYTVTDKRDARSVREIATQLDVDFCNHVINVQLAQAPPKDMDHQTKEYELYGLDPQYA
VRQHYIVQTENPSMAYRSREFFSKPAKKQFQMEQYTPISVLHRRFVNSKKLAADINRDPS
VAVSLQKQGLLDQSLKPTKRLKFLLNKKSQKHGVSLYGGKNGIHDGR*
>TCRU_1214 ubiquitin-conjugating enzyme E2, putative
MKNISNKRIIKDLKLLLEEVDANNEANSSGSPHSAAIFSVHTDTIYNWILKVKAPADSVY
GGAGNTYQLSVLFSEDYPHEPPTVRFVTPVYSPLVTEEGGICDRMVNDVWTPDQRASDVI
KLVLDRVFSQYKNHSDDDVNPEARHHLEKFPQEFAARVRRGG*
>TCRU_1215 Hydroxymethylglutaryl-CoA lyase, mitochondrial, putative
MFSSRFFLAPIRLVECPRDAMQGLSHFIPTAQKILYLNALLKCGFYSIDCASFVSPRAVP
QMRDSAEVLAGCNHALLTGEDAPKLSVVVASLSGLKRALETPIVSTIGFPLSCSERFQQL
NTKKSIAEALNELTEMQKAVVDTNAALSSSNGMSLELNKKKELLVYLSMSFGNPYGEPCG
PEVAEQLVSNLVSMGVRTISLADTIGVSEPQKIHDLFTRLQKKFPDVFFGAHFHSNTATS
KEKIIAALKAGCQMIDSALGGMGGCPFAKENDLVGNVATETVLQAIDELNLLPSSIDRKQ

INECVLLKQHIFGVTVKDMLLSQSLRDEKRFFQLCQEHFKLYDVNDTGMLDYEGFRSSML
RVFEELGCDPPSEEKICSSFHKVDVQKLGCITLDAYTMGARRLLMKRLGFFANVKSGETG
GSRRIATA*
>TCRU_1216 hypothetical protein, conserved
MPTYYERLDNLFAVYAPEKRPLVAGILQKYSGREEEVLQSLVRKFGPEPSEVPNHTKGGN
SYRERLVCFYTKYAPGKLVTVDATLARCAGREEELFSALVEKYGPEPAISCGDEDSRSVE
KISDTQSDLSRTTSSMSLVPYNVHDFRWRLARILMEHAPGKLAILDQMMEKYAGREEEML
AGCVARYGPEPLPPDIQSPRSRLLRFIEHYVPRKASSVDVMLKKYDGRTEALFAALVHKL
GPEPPAPSPGNELSKPTYRQRLIRFYEFYARERLADVDTILRRYNGDEESMFRILVERYG
PEPDPAFDSDAPIEPATDYHTRLTRLFTKYAPERVDSVPYLLAKYKGSESNIIKALIKKL
GPEPPFDASGTQSAMVHLGNVNEGPGNGVPPGTSEFRDDDGKEGSEFHSKAEKPEEWLRH
LSLPLSAYRRYAVNRLGEARVSALEILFGVPRLLFNENGGDEKDEKRWVIVKAGMASGKK
FDAAQESEELKEPMIAECISANFACLVLILETVKFPLPAVYDEGKVFSLYPFCTLLGDRD
RFTLRICAAIMDLRKRVEAEVASLLHEEEVCRGLIQRMDGWKQQHIIRLKAKEAYKERLV
QKSIELLPEFEEKERQDIITVEQIEIKGKAFWFYEGLQTPMNTCEDLQVPYGRQRLGNEK
KMAVGGKHVGSPPPPAGCRGFSQLIFSHLLRGQNRENYGLRSLQSYKSSAEDTMDVSLVG
GQKMGSPATVTTPVSWGPKHSTQEENSPCNLLEASPPPRKPRGAVEPTVRVLRFSGERIR
VNGQVTHAGNKVDITGRDKWGPSKDGRISQIAAVPCRDTREAILLGEDPGKFCKSGNNWL
V*
>TCRU_1217 Regulator of chromosome condensation (RCC1) repeat,
putative
MIRDAEFWMEARRKHSGGDAIFTAMLPMLHARQIVLDSGIEVDENEIGREDSAIFSFPSK
FVRKEPFEDNKVIHLPKSNASGKKVSSLVLRVLQQIMMFAVPLYSLQYNIPAMSMSWRTS
CVVDRTTKQLITFGAGDGVKVPKQLLCRGCVATDEFFAILTDQGEVWVSGGLSVLSLENG
KWTAGPLGKAESLSTVAEKALLIVGHGTRLACVTRAFVVRPLSILSNPVKSVIPSRHVRF
LDLGYGEDYYMVGIDSVLYKTLASKRTLGTPRRVMALSRTPVSRVSCGMGFCLIIDQNGH
LYTLGRNKKGQLGNGQQQNARRKPYLQKSLCHHFFVMVAAGDAHSLALTSSGVVYAAGSN
ENGQLGLGKSVDTMLYFTPISLPSKCVGIAAGPAGSMFACEDGRVYVCGLNDQKQLGLDT
SARIVYTPSFIPVIATGVEAYTMDFGAYQKPLITTRNSVQSSFQPNDSSAAVTNPEETIP
QLIPSELLQTSVVSDTNRHKQFEQTPLPRKEKNGKCVKCCATM*
>TCRU_1218 IQ calmodulin-binding motif containing protein, putative
MQGVTYPRFEEKRLQKPVVGSVQLPPVKMSRQPPTEVQKRQGISSSDVSPSPKMKKNHSG
NKKRRNTVRNVTGSATSVETVMEMNKKAMALMKDGKMKASYDVLQTALTAAEAGVRRFPS
LPMGSNSENQEKRDAWLLAFAATLSNLGCLQRRGNQPYEAIRYLQDARNVELQVFGRPSC
STMVNLSAVLLELGSTEEAFFIARDCALASEESDPMLHIIALHNYGVALSQHDSEEMRQL
AAPVLMKALREAEIHLGEEHPTTILIRQHCGMDLKKTTDGTDTCSSNNSGAITQLRETPE
NSIQPLPPGGRLPPLAPVPAHLMKAKEALQVLNYGGMPSMAQNYDSPVPDSIKALNRPES
ASNDGEALLSPTVAPVLRAVEIMIATSKRRCTSNEPAAPSVEEGVEATLARQGSSLVGTL
TAPLVPLQEPPNEEEEEMDEKKESEEMCEDDYGNKSNTLGAAVETLEEGRAESLIDCCVT
DPGKEGQEDTGVNKDAPGGALYDDDDESPMRTEEKRIDPAAVSNTFEETKRPAKNTIPGE
YFLIGAQGNRSEPSFYRFAPTDVSVTMNMYGGEQNVAAMKAPETTIEKETPLIDFDYEEE
EEEDDYDYGHGYHELRPFEQKRRQEEEKKRLDTAEKVIEKKREVFFKIIGANPTLRRQAR
IQQERLEEEVLCARIRKEAEEKAKKEYFESTIEAIIFRTRDRAARKIQTTWCMWWYSVGK
RRRELLVKRAEEKARRERSRQALFEHERRVEQERRRRKSNKGGFEVGTIPSVTSCGKKWL
EKTLCVRYLARCGISHKDQKEDFFVSKVSKIQAIWRSYRTRGKMREAASYRAQTWVLKRQ
MEREVYAAMVIQMFTRRCFARRAREKKFLERYRPPTIKIQRWFRSVMPCRRALGVDRVSK
WRRQYSARLIQRAWRAYLSRLAYFMERLRYKLDEDRRHERVASSLLQRVGRGFLSRSYVA
RRWAKSSNLRRTMYALEWGEKGMDANKGGMLTVAAPVGNYVPTPIEEVNAVAELEREKYH
IGLFVDVVAERHRAEWKEALRLRPFEVLRRRAHEDHLCELELNASRRDRAAVKIQREFRR
WLRIRDAPFSDKTLLLIARGNYQVLEYGRKIDFMRHACEQDAGRVIFGEQVALMREARAA
AQAELQAVRPLVRTQVPHHEVRTREERYEVEKELQRDEHLLKKQLLTDTLRERRESFMRR
AAEAGIVGSAIGRTKKQLTQ*
>TCRU_1219 ATP-dependent DEAD/H RNA helicase, putative
MLTGLGTWESAVDSVEAQDQQPKKKRGGGFQSFGLDKPVLDGVLRLGYNVPTPIQRKAIP

PMTQGSDVVAMARTGSGKTAAFLIPMLNLLKSHSKTVGIRGLVLAPTRELSLQILRFGIQ
LNKFLDLRFAALVGGNSLEQQFELLGSNPDIVVATPGRLLHIMEEASLKLSMVKCLVLDE
ADRLFELGLQPQIVAVMQKVPDACQRALFSATMPSVLAEFTSAGLHNPVVIRLDAEMKLS
DKLKQSAFVVRNDEKVAALIVLLKKVIGVAAGDTNDGTAQQALIFVESKFHVDYLQMIME
AYLISCSAVHGQMDQEARRNAVQAFSRRETHVMIVTDVAARGLDLPLLDNVVNFSFPSTP
KLFVHRVGRVARAGRSGAAYSFLTFEDFPYYVDLMAFIDRPLQCRRTEGDLLFTADDGCF
GRMPEEDLQLELDFLRRLALEDVEVRNMAKVVDNAHKKFTRTKKKATHDGIQEARQEKYQ
FDNTPLHPIFVERLEAKRIAADEARFDLKRFKAKESVLEMIHGEKMFQIMKPVTIQTLWK
EQREQAEEDDAVTGKGAAEEEPQKSDRAKITKRDVTVPEKKLSLGEKLLLKAQERKKRER
QEMDGATNEEDAVTVCPTRSMHRFESEYGGGSGKYRDQDYFMDTTKRSTMEDAHYSVKDA
TFDVGAESAQEAQQQRQVYAWSKKKNRFVRMNVNDAKAMLRGVKNEAGKAVNFKSKLEAY
SRWMKKSNMRIQDVGEEEDLGPLHRARAAQEQGTGGYNHDGDDDDDTVDISDPNQGKKLR
VGRKQRRLPKDGHIRTFEEMAHIKRKAEKERARLSRKKQKRKSK*
>TCRU_1220 Glycosyl transferase family 8, putative
MHRSKRFRPGLRHRRCWRCSWTSLLLTLFFLVLNSLVWLYGFRRIPSLTPFPFPTDREEP
AVVGPGAKEPRRAGHNSSQAPNFVLSGSDNERHENIILPKGFGHEIECVTSQRENSSLLY
VRFTDRKRVLTLKDIIKKVHHNLNKNDSNNHYHDVNVSICPPLPEDVKIPINDSFEIGMI
REFVGGMYHPLYCKQWKRHNSNRTENGNIEKDEVGGEYAASICSAETQHKLTEAINHPPK
YAYVMMVSNHRYLDGAIVLADSIREHSLLSRNHEADIVLIINENIKKEMFPLLQVVFDRV
QIFRGMQKWAPKSIFKATFDKMYLYMLEDYTGGILFLDADSLITDNPDFLLQMQEKIAAI
VKSEDPGYWTAARRAALSYPLKESEWKRLMSTQKMPFLFAVGDEEYFQTGLMILRPSLNM
FLKLYLEFRLGSYGYNRVGARDGVLFRTCFTTIGELVRRPHGVYHFTGTPKPWFNLERLD
HTLRPIQVKMRKQLPLSWKDCKLRYDWWTRYERLHLEHFQRIELETRACCGPAQDAELIR
WRNKYGDKIRQIPSDLHITKYGGAMLLRKRTRDLRLPLGINSLKEAIHASPKSYMWLMRF
SKDVEYLHPVREHMAKLRTYDAPLASMHELNSLLSAFNSFSTTMHYPKRIAYAFAAHPHG
KEGNTQDGLWSDCDFQCARLGLRCNASLLIDTRIADCQYSEPPSSMANGLIRCKRCLSYY
KAGAPFVIFKKNERNTLWIREAEVCFFNAWTRFAVPSCNATEPQIYEYELQHGEFLAPVC
ACQ*
>TCRU_1221 hypothetical protein, conserved
MQAVVHYGEQFVEVPDASVTLRDICGSFGMTGDLAGVCIKHRATGRVVATLPFECLPAAN
DAQGEEEKIYDVCAPSEVGVEESTPTTDDMTDILRQLVRLGATSLLSTESEQNRSLDPYD
PRMSPGLLMRTIYPPSLYSPYRHRGDPLNMQGRFANSPITGQMTGPPYVSAVEPYTVEAP
TELTLQLRPDLVPQSEEEARDILQGLVAAATRVKAMVAMADEEEKRHAPSDVKPNVALMQ
MN*
>TCRU_1222 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MAMMMTGRVLLVCALCVLWCGAVFVSAAGDGDGDGRGVSEKAPMGLSEPGERGANNAGHS
SNKNNEINSNLQGGTGTGTTTDRVVKEEEEEEEEAETDDDDDDDDDDDEKDKSNEKEDTP
QAGKSESSSKEVAATIPTASGLSGAGGGSPSGDVGSSGSPDGSEDLNLEASGPVVNSSPP
LSNAAAGGLQNADGALSTQKNNFSETGVHSGTTPPTPSLPKSQAPAITQPKAEEQSPTEQ
DTEDSPDTEEVHPQDGEVNGTALNSSLGHLSQMNNSDAGTMRGSGSGLLPLLLLLGLWVF
AAL*
>TCRU_1223 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MNGDGNNVLLGVSYDSGKKWHVLCGDGKTEELSSTWETETQYQVAIVLKNGTQGSVYVDG
QRVGNEECALRNDESNEISHFYIGGDGENAANKEVSVTVTNVLLYNRPWDEAEITALNPN
KDPTPPVTPNAQETGASSALDGSQLTERGQSMGSSGAGSGGASPSAVPTVSTPSAGKDSL
QQVASGKSSDGTQTVGGGSFSDGEPTVETREGGTDRQKEEGIHAQNGDVKAAALNGSLGN
VSQGNNTDAGTMRESGPLPSLLLLGLWGLTAL*
>TCRU_1224 40S ribosomal protein SA, putative
MTSVESGAKVLRMKEGDVQKLVAMHCHLGTKNRSNAMKKYIHSRTKEGTNIIDLHMTWEK
LILAARVIAAVENPQDVTVCSTRLFGQRAIFKFSQLVGTSFLAGRFIPGTFTNQIQKKFM
QPRVLLVTDPRTDHQALREASLVNIPVIAFCDTDAPLEFVDIAIPCNNRGRYSISMMYWL
LAREVLRLRGTIPRSVPWDVKVDLFFYRDPEEALKHEEVNQAAAPVAEVDEGFGWVERDN

NAWEQ*
>TCRU_1225 Domain of unknown function (DUF4496), putative
MVLSSAPKSGGEKVGMMQGGLEEKRDPLINSAGCYACYGEIASIVASTQGLYYHQTRGNG
GTDLLNRIWRSMGELLEEQLLLKRSCIVTDFFHASVKVQNIQYYDGKHVFYKLQLVLLPD
FTSKFHLQNVLTIADAQYHASVPHIISYSKIADRSGTDRFVVEAAIIDSTREIGKYLMRN
AKSVLRIDIGIAFLEFRGREYRIKWTEEFLQRFRKAVGPRSVVSPYDPPLMSPAATGCRF
QTACLSEDSLHKSLINTVQREGRPAVVEMNSSGGGSWF*
>TCRU_1226 ARM-like helical domain-containing protein
MKSAAPKTSSKALKGKTATPNKAVEKAPKKLSKCEKFLHELEDLNQSQRWKKVVEMGRAA
HAGGEASSELALLLQLSQSGVPYERVLGAMGLCQTNCSSEIGRLLRDPCDRVATLAMMPA
AVHLSDNDLCELFKELPRRRLSFLCERLDHKKRLPAVADKYIATLPPLVRSSSAHALLCW
ASEAHLSRQNPLALRHFSRSEWYTVVKRLPDFALAFAEKGLKDAATLESASERIHVILNA
FRRFYPSVGLKLLTSAMNHFCVPDDCIVAYSNIFPEAVAELVVKHKRLCVFDVWRPPKNL
RHETFLALIDSGGMQHTHVTDFFLLAPPKLRSFLYNSRNDMFRNANGSMNVDVLFYVTDP
AERRREGMRALTEIAELRTDPIEWLKYLFVLPFPEALELAGRYLQVSCVNTRAAACASLV
KTGSFHPEHLHDILDFCVKRGKENDIVRHNFLSEISGIPPHLWKEDHYPKLVKIIQGAFD
SRDASTATFSSIMSLIRGTVRFNTVLADKFLLNILNRGFQFLLSNTKQIPRAVMEHLWKF
MLPWLKERVDKKAFSTVNYILEEVGPSLHFVAESSVPFMKTLLKSSESCAAINAFKVLFR
FFRPTAMELLPGLLEESLEWIGVDEVRHVVSLHLQGHWLDRYLVPIQTNGRLGTRKGQWL
VVFRNGHCWTAAKQEKYAKSISRNLSCANYSREFILGNLAALRKLYSANVTEALAPFIKE
EHTDPFLWSNAIELLGKLDDAASLKVLKDAFNDERVRVAVYAIRRRICNLPTAQIIEELD
VPLHSKLVAVQKVALRHVCDAGDDVAYAYLSQLRHGEKMHPNLEAVWLSAMFQFLEKREV
WDIFMDVAKGKEYILAKTLVDVPDDTLVEDWQLVNLDKLLAVLLSCEELTVVLAVLERLK
KRSLRRDEEVVRTMLHILKTTTINEIMNLTVGALCISSAEKQEVASAFLSLRPESRLWRV
ADTLIQLRHTACDRFKEIAVAYMKLLLENCCQTAVACQLICYLPVKDLLRHLNDVLQRGL
LHAGAVNSMLRSLKCTAEIVNEFEAVENQLRQHEHPHMQRIGLAMLESAASTGKWDEKRR
KALEVYRNASNGWVSDDAKMVDLPRE*
>TCRU_1227 hypothetical protein, conserved
MDSLSRTEALRVVPLAVRGYVTEESWIMLLSLIQRGHSVEFMFSPSHCGIPRNEAADDEA
MIARSLPQEGGPIWHVDFLTAVRRRNWRDAQKKGRARTPHERRLSVWQGLYSWHDQKIVP
RVAALRKGTVRFLPTPRHACACPSYQK*
>TCRU_1228 hypothetical protein, conserved
MAEAVSCLDLKASFFQVSLPRETRHLFRCRVEDGTLVELTRLPMGYKASPEILQIITSAI
AGMTTVVHPLWAAPPSVRVDVWIDNIRIAGSKSDVTLWEAQVLRNADGRHATMGEDRESG
ATQYTFLGVQFDHTHRAVSLSDKFVRSVRAMPALNSLTIAEMEVMASLFLYAAAILGTRL
CQYYFFIKAVRRRLSALNRGIVLETSPANVPPSAVGLGERLRHTIENNRKRIIKPTERAS
AAIITDASLHGWGAVFIPDSGEVKIAGGKWERKPFLIMQAEARAVRLALSAFSAILPSTM
DVWVDNTSLQGAANKGSSKSHAMTWELQRIYEFLDSRGIQATFAYVRSAENPADGISRGR
VFTLRKLRRGSAGSCGWRTPKSATS*
>TCRU_1229 hypothetical protein, conserved
MGYKASPEILQIITSAIAGMTTVVHPLWAAPPSVRVDVWIDNIRIAGSKSDVTLWEAQVL
RNADGRHATMEEERESGATQYTFLGVQFDHTHRAVSLSDKFVRSVRAMPALNSLTIAEME
VMASRFLYAAAILCTRLCDHYFFIKAVRRRLSALNRGIVLETSPANLPPAAVGLGERLRH
IIGNNRKRIIKPTERHRPPSSRMHRSMVGEPFLFSRLRRS*
>TCRU_1230 hypothetical protein, conserved
MGEEAFSYHAAEVRAVHLALSAFSAILPSTMDVWVDNTSLQGAENKGSSKSHAMTWELQR
IYEFLDSRGIQATFAYVRSADSPADGISRGRVFTLQDLAKRSGGVLWLEDPKVCHFVSNN
I*
>TCRU_1231 hypothetical protein, conserved
MIAVLPFAVHFSSGQAAAATHSACYIPSVQIHVGMSRLPLVRCLGASPTMRSQRPETFHT
PRWKHHGQLHAGQWRHFSVVAACLPVAGCRPPSLQCGMADGGPSPCERVDVQWETRSTRC
AVTSGNETLRPLIHVACAGSSDSSISMSIGVAAKSSHAVVDGERPSRSS*
>TCRU_1232 oligomeric golgi complex component 8, putative
MEVRMSDEEGVRRSIVEATVEHYSLLAETQEVNAKVASASGNALSCVRRLNDSLGRLQTL

SQEMIRVGKQWRREKQIALGTVSQHQKLLAFLEAPAVLEDCIRNEMYHEALMVLEHINRS
AQTMATVALFRRVEMEARCNLERALSEIVLPRLAEQLTVASAVKVTTFFRRLGVGEGQVR
QLFLWKRAEYVDGLLREAEESGVPYSRIFRYVTAFKVHVTETILQYAACFSPTIENGSCS
ELAAWCHERAYVFLEGFRASLEKITNGSELASVIEECNSCCATTTLLQMDVSGLINESLI
SRARALFAEQIVLAMQSYSASMLAFSWRPSNGLQCASSQKRVEAAPSSSNGIMSPPLSLV
QWLPLAYALNGVLTAFNTIRKCVVPGVELFCAAKLEGLLQTIAKDLSRDKDLLMAMEGGE
KQFYLLFVEAFVNDFYPHVLACMRELLGEDAQRLLINGVRESIESLRSLLFMESSTKQSG
APQQQMTDAAGTPADIQGDRITPNVVGA*
>TCRU_1233 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MSRRVFASAVLLLLFALTCAAVGPVQAQSFGTRVCDSYGGHSSEQSPGEYRAANTAAAGH
IFRNPHLVNVDGKLLVIAGAQFNESAGSGSASMQLMARISNDDGVNWSPYSRPGDLDAFA
ARLHQMLFTTPFRLFGPLFAFVEGYDLRKGVRPHYANWWGGSGVESVIHFLGTGPGRSGG
FSMSSVSMSIRLPYPYKSDGLIGFLNDASTPITKMTDGTLVFPVQFLTMGGSTASTIMYL
NPRQQHWTFANSATHAGCTNPIILEWEAGKIIMITSCEYGHRRVYESTDKGNTWTEALGT
LSRVWSNSLAGLGLHIQSGFITATIGGKKVILLTQLEYSRHDSKGEIRLWLTDANRIYNV
GLLATGYGATSSSLLYADDRLYCLYEASGGSDSGAFFLDLTSELQRIRHALDTWAAKDNA
LGKCSSIASDAALSRGDCSVPFPTAGLVGHLADRFSGHKWEDEYLGVNAVVRGATKKVPS
GLTFEGQGAGAEWPVGKQWPTRPLHFANYGFTLAATVSIHEVPKGITPLMGLKKMGTTTL
LGLSYDKNMEWRVVNDLFPKHFTAWEVDKTYHVVLKMHDGMGSVYVDGTLLWNMRLKNSF
NEGLDTVSHFYFGAYDEQLSSGKIHATVANVFLYNRPLNETEIGALNASKVTIPPPEREP
VPAAAATSPSVESASDTVATNTQPTVPSPAAAGPQPTDQKSLSASSVPSGGALSEPAASR
PEEPEPAESRPEEPEPAREGTADQPASVTSSDAASTDVGASSSDDAQTVGTEGGDMMQAD
QPAQFSVGTPDAANAATHNAEGKGQDGLHPQVNEAEAATLSSSLLNSSQWDNSVAGTMRE
SGLLPLLLLLGLWGFAAA*
>TCRU_1234 Complex1 LYR-like, putative
MSMNVYKRQEKLRLYRALLKGANRFPLRSRREIVAEEVRGAFRHPLNDSLTTKEVDYKLL
LGWERAAAIQTYAENMYWFHSRDEVSREMMHHSLERDRQRIREMERCNAVGNAEIKTPEV
TEFKSSMYHVHPDYHGKIGQMPLTHSRDIWRARGQYGSDVGGPRQKFYVRRFKALFPQGW
*
>TCRU_1235 hypothetical protein, conserved
MAEAASCLDVKSSFIVSLPRETRHLFRCRVEDGTLEELTQLPMGYKAGPEILQMITLAIA
RVTTVVHSLWAAPPLVRVDVWIGNIRSAGSRSDATLWEAQVLRNADSCHATMGEDRESGA
TQHTFLAVLFDHTHRAVSLSDKFVWSVRAMPSLKYLTIAEMEVTASRFLPAAAILRTRLC
EYYFFIKAVRRRLSALNRGLC*
>TCRU_1236 Elongation factor G 2, mitochondrial, putative
MLRQNVGCHWRQVTPLWQCNSALRVRRITQCAPLKNARAVTMSSGSKADALESSIARMRN
IGVVAHIDAGKTTTTERMLFYAGALKRIGDVDSGTTTTDFMKEEMERGITIQSAAVSFSW
RNHSIHLIDTPGHVDFIVEVERAMRVVDGVVALFDASAGVQAQSYTVLRQSRKFGIPVIG
FLNKMDKYNADFKKSVESIREKLEVEPLLLQIPLQSEDGAFEGVIDIVEMTACRFGGTHG
LDVEVKDLRLLDSEPVHIVQAALIARHELISTLTKLDDPLSDAVIALLDQTDGDEKRAED
LIPSDLLRAAIRRRTLRQGVPRPAVPLLCGASRRDKGVQPLLDAITYYLPSPRDRPLTGY
ARDGKIVPLPPATSAPSVPVVALAFKVTHATSPKGRRQPLVFFRVYSGKITPNMTLVNNN
CNRHENLEKLYVIHANRQLEVPHLVAGEIGAAFMQSTKTGATLFRAPQQVHLDADHTKNE
IFTLEGIQPPPPVISFSVEAATKQQIPLLEAALQELSFEDPSLCVHKNDFGQMVLSGMGE
LHLEIVMSRLEHDYKLKCRLLRAIVEYREVVLEAVELLHGIGMYNELPYVECSLRLQPLL
EEDGFCDPGQCCSFVLDETLTEKYLAGAAGSRNDRRRRMEDHHRNVKEELRIITDVFSRA
VTDCSHMGPLAGLPLHGVRVALLEFKKLGGTQLSEGPLQQAARSLVLELFRSVSKANLAT
MEPMMEVEVHLSEAAYIGGVVSSLSERKAIAVDIQDDGRSVKAIVPMRNIVRYTMELRKA
VKGHASLYARLHHYRVIEEKAVLSRIMKNLGIYEGH*
>TCRU_1237 ribose 5-phosphate isomerase, putative
MTRRVAIGTDHPAFAIHENLILYVKEAGDEFVPVYCGPKTAESVDYPDFASRVAEMVARK
EVEFGVLACGSGIGMSIAANKVPGVRAALCYDHYTAAISRIHNDANIVCVGERTTGVEVI

REIIITFLQTPFSGEERHARRIEKIRAIEASHAGNKGVK*
>TCRU_1238 leucine rich repeat
MNRVQSDAAAVYVEACNREHAECALELVQAFENNEREANLSDRSVQLNDVDLSCIAEALC
STAHSIRVLNLEGNAFGMAGLQALLEAVEKNPGILRELRLGRNKLKDQAAVVIGHALSRD
GCGLKVLDLSENDITKLGVIPIAAAIGDGSCDVVELSFHNNKIEADAATYLGQAIRHAGK
LRHLHLGYNAIRDAGAAQLAQCIPVTVSLSTLDLTANRIGPSGGKELARALMTNSCNMQR
LNLRHNLFDSETIEMYAEVIKTNTSLIQLFLGFMNPTPHSAALVLSALCANRSLLLLDIY
GWKLHVEDAWKIIDSIQRTNGTIAAIVTDACQSIAKRIDEGNDEREDHGQHPIYVGPDDR
DAYIATKSLRRFSRAQSRRQSRASSRGAMSSRGAMSSRTGSPSHRRAVERSHSYKDSSVH
TPHSTRAHQEILYQSTQGMSVAAKEELQHYRRTASGINDPVTIPSRENTLSQLEYQSGDA
MRQTVEQLRRELFEQKQIQRALEFRVAALESRLEGMCCNKTFDSVDRTHVSRAAGGSSHG
RGTLNRFNDGYKKNGSSYRSSSHNDAYRFSENIPYSHMAASVGVSHRKESIERSKSAEAI
SFELRQNGIAASGAAGGGGMAAAHSPSSGASGGPAEFPHISVARTERSEPPAEPLELPKE
RRPAEAMLQTSTRVVGNHQPQLAPSPSKDKDPPRRKGSIRSA*
>TCRU_1239 protein lipid droplet kinase (LDK)
MSMGKILGDRRYRIGCPIAKGAFSTVYRCVDLTTGKAYAVKVVSRALVEANKMQCAVVCE
INAMEVMPRSKYLVNLVDKLVSTRNYYLIMDLVEGGTLSDLIRSSPLMLSTQWCRRIFRQ
LLKGLSALHGSNIVHCDIKPENLLLNEEHTQLIISDFGFACYAPPGRLLHRACGTLKYCA
PELLQCDPRYDGREVDVWAAGVTLYVMLFNTYPFQGDEKCPDTLVQAVMAGKYTFPSPVS
PSLEHLFSVMLQPVPAKRWSVERLLRHTWVVGVDPPVAKASSRTAISLGDIVPNNHCCGH
ASEEFLVQSSLAKALEDDDLCGLSRRSRSCPLSSRKLSGDEVLGHTGLKGEVNGGAPKYI
SGIGNKRGRKGNANISTRASDASGEGEKCTELGGGGGGLSTDLDVVSNDSYNDNNSHIFR
TMSFVINSSGGSPTSLSTSSKVSRDGSPVSYTRDFILTLKAIVNFFLFCTALVVIGGMRL
LLDVDFNDLPIPSFLRAMVERLIKPPEDVISQHVEPQRNRNQTRGERLRQMFASAERAIS
ASNPRRRVVPT*
>TCRU_1240 D123, putative
MDLRVPLSYVLDTPLAQRHAIPHRTLFLDATHPFIQYLNSDDTRLPQHPTLTVEARPVDE
YETYVGEDDWRREKAVDSDNTDPAPRFDDVVQWVSETLNEIGGNGDGVVLCGRRVVADDC
GWAVFSRTPTLLSSRDVFIAMRNSSKFLRDLHHQLQGVALAGAEGPVKVEVTLAKALSGN
NAREFRAFLPYRLHTSAGDGCVEAWAGHMYAGISQRATDVCFPSLMAWDEATHDENYAIV
MRHIEHAKLLERALENDALLRTALFRQANKPSVADPAPKKKSPVVLLAVDVLFESPSLPV
YLLSAAVRCFHHDDVEDPACAFPFILDDDAKLGRGNDGNTTTTTTNIANNNNNNNNNNSK
ADGWSGESEDDDDDLLSDSVSFFRLFRDAANWNRHVEVWRRRGSTAGVGERSDTTRTQKE
RRFFVVASERGDLASTKEYMAKRGLPLEFFRPDLFKGDGNFLREWRERLMQRISMAEQSR
GD*
>TCRU_1241 hypothetical protein, conserved
MEPDADFGSVTAAFRGTEEYAAAFDLELWKAQQQARLRSELNEEKKRLKKEVAAEVRKKE
EQRLGDLDTVRQDLEQVARRLQIREETLQKRISQFEAREAVFEARRVKVAEQHEQHLLSV
EGRTRRQLEEAVVRQGVLQAQLREREDTITRLEEKLRAAESEHDALQRCMARHVAEDEDK
ARITRLEEELASANAAVTTLQLKLKERESELVVARKERDQFQEASKLSRDQLGQLARRYS
ELQKQWQQRERMLLDEEKRRLEEDKRRHQLVTLQAGSETKGVYRHDVLGHQFAEGIVSRE
VRDRVLKRGNAGDDSSTFLRELMAEVAQGLRELRVKEKKKGKKVKVRIADSSEPRLVYAE
VPPRHQDENSLHVRGGWRAVSSEEFVEQKRHQPRDFTQTTTACEDVANSTLSSLTQRESE
GRRELTEPYYSPLAEKPPAVKEEEEEADVDVSSSYCYADVESWIAEREDRRVLPREEAVG
KDVMESHLPTFPSAADAPPRPTPPSPEDFLQASRAAPPSASRESTREEMVEFVKKLRMNK
KRLLESGVYTEDDTLLKEMTDKIALYEDFLMRHF*
>TCRU_1242 NADH dehydrogenase subunit NB6M, putative
MLQRSIPRLVRDPVPTDTKAFYSWFSGQAYRQERVIPGGYPAVRVYPVYGKRWFTGRTVM
AMIAGFSLFGAWFRPEKERYNMEMMIEWSERQAAHLPYQKAEVNLRCLITSYKRHRYEQE
NLIDKGFVGLTSEFRKFFYHDDVWRPPLHDVLMHPYAKFGGPLFSYNWTIGYF*
>TCRU_1243 DPCD protein family, putative
MAERLAEPKSSVIVNGRKRITSKFVDGSEMVEEYDVITDELLLRKRRVKNTLGNFGDWQV
EVGSEVKTRNLEKELLIEANGSPEIVKQDTPEYHVFRIRNLPYAKDVFSVTVEHREPGDV
GEIVVRTSNKKYFKRLSIPELQRHHIQLDPGHLLYDVQHNTLIIRYKKHLAVLAADAAAK

KERAALPARRIDGADGNASDGCAQQ*
>TCRU_1244 DNA-dependent RNA polymerases, putative
MAFHPRDAFILHQEQIQRYNEGDEVDTSAEQKVQIELQRLTDSESTVTIAFSHEDHTLGN
PLRHVLMQNREVTSAGYAIPHPLEAKMLLHVQSTDYAVEAVAEGLERLASICDETLQSFE
DCMHRMRCEGAKQE*
>TCRU_1245 tRNA threonylcarbamoyl adenosine modification protein,
Sua5/YciO/YrdC/YwlC family, putative
MARIISASELEKAADALARGNLVAIPTETVYGLGGNALNKEAVEKIFIVKGRPLTDPLIC
HVSDVEKAMDLWDVHADPEAVELARVLGTAIWPGPLTIVLRANPLLPNSVTGGSGFVGAR
IPRHEITLRLLQLVNFPVAAPSANTFGHVSPTTADHVLKDLGPKDSSLLIVDGGPCDIGI
ESTVVKVNNVESVEILRRGGVTLTEVLRALGDKFHPLITIRDTRLRHLSPEMAMDGPGQL
LTHYSPNVPSRLLTPSSFTTNLPMDPEGALVEFSSNSSVAAPTEVLLRHTVIIDFGGKLQ
CLKPGCLAYRDLSVNAQVREACFAVFDALRWTETIPGAEVVLFPLVSGWPHASVDTDLLA
AVEDRLFRAASGKVARIRMQSRSV*
>TCRU_1246 CEP76 C2 domain containing protein, putative
MPGDPSHVNAERLKELRVAVHKFLQDSNVYSKIRDIVDSYVAENPGDSSNPASSADVMKI
IREKGLVQDLLNRLRGEKSPGIVQTPNKALSWKLLPGEYYLHLRLAGGKAFVDNLDLTPS
FAKDYQMYVAVHFGSQRYRSNLEDVSLDPPFRDEFLIDLDYKSFGSCAADLIEVSTPLHI
AVFREERLLTFSKMVGENIVDWRKVLRTGYLGLTVELCGDNPGIPAGILELQLELLPNKA
PRFSEEDVASRIDLQRSAITSADREFLLYARRWWMEFQDIRPTHKQRKIKVFASTSNGRM
VPTTHFISVVRPDKGIDTPLEAARFVSLIAVTDEENLTQEFLLGGLGNGKSANCWSSMFT
FLSQRRGEPCNHAALLCSLLLGFGLDAYCAVGTNKKGKTAMFVVSRKRLSAGVFDVMLWE
PTTGGRFALTDAHPWETLGSVFNHRSFYANIQPSDIITTISFDLDNEGLWKPLNPLKLRM
VPKYPNPSLLWISSDTKSLEEELLTLLIRQLTEYRDIRGITTRFNENLAYVLRQALSAYE
SHRRNGAPEDLSFFENCVKGVIGEGKTFKGVPVNVTHLNSRKILATFEGSASGKEILELT
ADSLTLAVQVKIYSFPEGVLSVWVMLAAAYAFSSV*
>TCRU_1247 glycerophosphoryl diester phosphodiesterase, putative
MVSCGVCAILFLGGYIMGAGIMVRVFPLRPAGERELLKERFPYPVTKIAHRGGSLIGPEN
TIYTFGRAISVGNADMLELDVRQSRDGEIVVSHDAALLRTCGSFHEEKNVFDIVVDGNPN
KTLPQSLREIPIHFESPQRGGCYKATDSVPVDETTRLCLLSEVFDAFPDVPLHIDIKSEG
AEITKKVLKLIERYGRETKTLVGTSNWRNRKHIYDYFVSGHLSESERLLKKRKRFRIFAG
PMDCFVVYVAYFLGVLPLVPLAFDVFSIPVFTKCKLKALGSCFTRFIAYFVNSPVLWKHL
QRRGILVLGWVLNDDEEFEEASNWPINGIISDDPIALDAFFKSREMPTAMNIL*
>TCRU_1248 RNase H, putative
MNPRIRHRRKTLLVVTDSQSLLAALNKGPLSQTDWTEDQIWQRLLTLTRAGWSVHLQFCY
GHCGVHANELADQYATQTMATGQYTEQGIAPLWHTDLLTCFTTQLTNKWRSTIRQDTHRY
LLCGTRPPDLSGKDLITQEVLHRQELVHLERARCGESELWGRPYWAVRDCTNQCRFCNIS
PEQSAYMRSNNDPTAPGTDTVPPSAREEDVSPVRRRTLTRRRKEKCPHCDSTLTGFSGLV
SHCRSFHPEHPPPLPELKCDFCDMVFPTRRSTAQHRSRCAHNPDATRHLNSSARRRSLLP
QDQPASTSATISPQETLHHLLLECPGTLTVRRRLGIEQGLRIGKFSQWQLLHSRKLLSLL
DHLFGTQMALYS*
>TCRU_1249 Protein-tyrosine phosphatase/Dual specificity
phosphatase, catalytic domain containing protein, putative
MEANGTLVECKRGESDAVVFRFLIIDAPSPSSVPAYMKLLQRHNVRHIVRACGPTYNAEV
FERQGIVVHGWNFDDGAPPTQTVIDNWLNLLEQEKNKSPPETIAVHCVSGLGRAPILVAL
ALVEYGGMPPLDAVGYVRGRRKGAINQVQLNWLMRYKPRHQEGNEGSLICARCTLM*
>TCRU_1250 phosphatase of regenerating liver-type phosphatase,
putative
MDVNCTLIECKDRRDVSRTLFNLLILDAPSPSNFPTYIKALQRRHVRHLVRVCGLTYDAT
QLEKNGIDVHSWPFDDGAAPPKSVVESWFQLLDKEKEKLLSGASTQPASIAIHCVAGLGR
APILVALALVEYGGMEPLDAITLVREKRRGAINQTQMQWLAKYKGRSAAGGGSSGGCIVM
*
>TCRU_1251 mitochondrial carrier protein
MAEEYFHTFVAGTFSGVVGVLLEYPLDTIKVRLQAYGSLYRGYWDCAAMLLKNEGMLSFY

HGVSTRFVGSGFEHAVVFSFYKWTLRRVGADEYHPLAWQIFLGGVGGGVASTVFLTPLEL
VKCHLQVANMLPAGQREYHGVTDCTVKILRRGGVTALYKGGVAMLAREVPGTAAYCGTYD
KMKEFLTPLGGSTAELSPWRLMFAGGCSGVAFWTVFFPADVVKTRMQVDPVFSRWSFGKA
LRVLYAEGGMRALYCGWSLTAVRSFPSNAAIFATYDLTMRAFTNQQRNTNSAAGAV*
>TCRU_1252 Las1-like, putative
MPKNTARKRSRAWQNSPNEKRKRGTCIKIGLGELGDLDAVAPTGTSGRIRADVSNTKAVG
SASAEGEFAFSTAPFLSFSRLAPSVFGHGWDEWKRVKQMLFDPQDGTGLTEARRKALNRI
QLVWKARERKNRQLPAYAEATALLMEAFSLDEGDQLSSSGAVSFYGAAISRAVHLMTGSF
ARGAADTYRKRARLIGFPEEAVEVRQRVAHGALPLLSELRWVCGLVLQFLFHHYWVEQER
HVHLMEEETEGEEDNTTSGHGVQQSAPSTTVEEMRQILEDLSDVGEDVTDYSNDRVEFLQ
DGWQLC*
>TCRU_1253 SMP-30/Gluconolaconase/LRE-like region, putative
MELVAELPGRLLTGLALDANDDVFAVCACSGELLRLNKTNGTMIPIMATETSPHALAIDP
RNGDVYLTDRSENAILKLEAVPNAKGHAEKDEKCDNDRGEVDYTVVRYLNSFENRQFVGP
TALAVAPDGELFFTDAGAEGDSSFADPVGAVFRTLQGHSQVVPLCRRGLIRPTGIAVTSD
KSVYVCEQGTNRVLRFVLRGTYYIGSVFAQLQGGMGPSAIAVRKSDGSIFVTQYDMKGSS
SSSSPNEGAGGIITVIGRDGEVSGIVRTTCPSLCAIALDSREETIYAVEADEASGGSRLL
RFRLSPAAQQVTE*
>TCRU_1254 SRP40, C-terminal domain containing protein, putative
MRPAPKKAAIPDSSSDDDDAPLRKPAQKAKASPAMRPAPKKTPRSECCGEQEPVKKSVRT
EVVSAGPGGKEWEDNNVNNTRKSNGNGGTALRRFQRIDPTKVVFVKDELRDNRPGGEHMA
FRQNQEMMRVKGKNFNKLKQKNKAKFYAAGVDTSVRSFQFDDSD*
>TCRU_1255 WD-repeat containing protein
MPLFPASASGNGNNTGVAEEKPLNLPFDPPPLLRVDPVAVLEGHEDRVWCVSWCPTANVL
ASSSADKTVKLWSCLQHAKAVDEQHQQYPQKGLSWECIHTLAGEHSRTVRHISWSPSGEY
IACASFDRTATVWKRASDDVNRFDFELEAILDGHESEVKCVAWLTDSTLATCSRDRTVWV
WDRVDVGEFECAGVLAGHAQDVKACAWIPPIDGGAKPLLLSCSYDNTVKVWAESHIRDDW
HCFQTLTRHDETVWSVAVQPVEQSIETLRAEEEEEGGEAQPACQPIICCCSDDKSVTFWK
RNAEGKFHVIVTATGFAERSIYTVGWAPSNCGAIVACGSGDNKITLLGLYQSRGYNEVHV
TVLAELPSAHEADVNSVAFCSIVNGALDDSKEVVNDNNNNSSSSSALLLASGGDDNMVRV
WRVARA*
>TCRU_C-terminal conserved region, putative PS.1
MLIAPLSDCTAGVIQEANKANNVACSELRKAIRRRHTHNPYLQAILTPVVTSCNFNDKKR
HEPNPNAPAFVPAEIPWNTYAPCVYNENSCVNETAYDYAVYGSSYYYSQRISPSFAKTTQ
MTYQLPAVPTESINTSSVADKTMNLSNNSTSCGNTGTSVVSTPVKRSNNLYKMYVDGRPK
VVRGVMYAEVKVKLRLGSEVFIVNDVPQVFGLIVNPEELVGRYVIVEGDRGEDMGIISAI
ERSEQEPVKQVEKAEEGDNSHPRVLREALAEEVESFHGLDRLEEEALRFCKAAINSLKIR
TPLQVKRAVFQFDRKKLTFTYSSDSYVEFKVLLRALNRQYQCRIWMHQLNWEANCKQRRQ
SSDTEGSRKSRRDPRKCGGTKKDGKRSQEADE*
>TCRU_1257 dihydroorotase, putative
MARVELPTLVDCHVHFREPGLEQKGDMRSESEAAYAGGIGVVCDMPNTKPPTQTITAFAE
KVRRAKAVEKLCDIRLFFGATAHEHLQELETLWTQPQHAALKARCAGLKLYLDNSTGNLK
SSADVTEAAFELCGKLDIPLVAHCEHATHNDEACSANPYTGPPSHSLRRPVHSESASIVY
GIELARRHGTRLHVAHLSTGEGLELVRQARAEGLHVTTEVTPHHLFLTTGDYGCCGARVK
VNPPVRPPEHHERLWEGVLDGTVDCIGTDHAPHTLEEKSDATNPPSGMPSIEVVVPLLLT
VCAGRWPHPTAAMPKALEARRLTIGDIVRLMHTNPNRIFGLGLSEKSQRFFDLSMEWVVK
ESQLKSKCGWSPYANWHLVGKAV*
>TCRU_1258 glutamine hydrolysing (not ammonia-dependent) carbomoyl
phosphate synthase, putative
MFEEKVKASLVLHGGECFEGYSFGYEESVAGEVVFATGMVGYPEAMTDPSYQGQILVLTS
PMIGNYGIPPIETDHFGLTKYFESMGGEIHVSAVVVSEYCDEPAHWQMWETLGQWLRRNN
IPGIMMVDTRHIVLKLREMGTALGKVVVNDKDVPFVDPNMRHLVAEVSTKTRSTYGHGTL
VILVIDMGVKLNSLRCLLKYDVTLIVVPHDWDITKETYDGLFISNGPGNPQMCTKTIEHV
RWAITQDKPIFGICMGNQILALAAGGSTYKMKYGHRGQNQPSTCRSDGHVFITTQNHGFA

VDFKSVSQDEWEECFYNPNDDSNEGLRHRTKPFFSVQFHPEGRCGPQDTEYLFGEFIAHV
KESKVKEASKYKPRKVLVLGAGGIVIAQAGEFDYSGSQCLKALSEEGIETVLVNPNIATV
QTDDEMADQIYFVPITAEAVERVIEKERPDGIMLAWGGQTALNCGLEMDRLGILKKYNVQ
VLGTPISTITVTEDRDLFRNALLQINEHVAKSLAVTSIEEAVGASKEIGFPLMLRAAYCL
GGQGSGIVYNEEELRHKVGVALAVSPQVLLEESVAGWKEVEYEVVRDIYDNCITVCNMEN
FDPMGIHTGESIVVAPSQTLTNDEYHMLRSASIKIIRHLGIVGECNIQYGLDPSSHRYVV
IEVNARLSRSSALASKATGYPLALVAAKIALGKGLFEIANGVTKTTMACFEPSLDYIVVK
VPRWDLSKFNMVSQNIGSMMKSVGEVMAIGRTFEEALQKALRMVDPSHTGFDVPPRLEAK
KNWDYMQDLKVPTPDRIFAICRALHEGVSVETIHEMTRINLFFLNKLHKLILLQNHMLQQ
YKGKMNTMPRDYLLKMKANGFSDAQIAKYFLCTADDVRERRMELKITPKVKQIDTVAGEI
PASQCGFLYTSYNAYHDDVEFTERMYAVLGCGVYRIGNSVEFDYGGVLVARELRRLGKKV
ILINYNPETVSTDYDECDRLYFEEVSEETVIDILLKERIQGVVISLGGQIVQNMALRLKQ
HGLPILGTDPVNVDKAENRHKFSKMCDELGVLQPEWILSTSVEQVHEFCKQVGFPTLVRP
SYVLSGSAMAVIASAADINRYLEEAALVSGEHPVVVSKYYEGAMEYDVDIVAHHGRVLCY
AICEHVENAGVHSGDATMFLPPQNTEKEVMKRIYNTTALIAEELDVVGPMNIQFLLTKDK
QLRVIEANIRSSRSVPFVSKTLGISFPAVMVSAFLSQHDSNLVPIKRARMTHIGCKASVF
SFNRLAGADPILGVEMASTGEIGVFGRDKKEVFLKAMLCQNFRYPQRGVFISCDVDAMAE
DLCPYFECIAHRFPVFTSKQTSRVLADYGIPHTVLTQRHEDSEPTFDTAVAVKEKFDLVI
QLRDKRQDFMLRRCTQENATPDYWIRRLAVDYNHSLLTEPNVVRMFCETLDMDVKEIEIE
PFRHYVPRVYNKMENDNYTMLHRHKVGLCITSTNDSKVLAISLREEKIALTCFHACLGGI
KNNSEEIAEQFRSIGVPVELIDLRTEMAELGFDMVMAMVDDDTNNWHLQKLSLHVMGLYL
LKAMRMRHMTVVAQSSSRGKKDLNFERYVRTFFPQMGVYNPWRDPSLLDQFPSEAHKIAF
LRMHGVEARIAQAESHSSVCGITYSFSDTRSMPTPQMVRPLRDCLSVPEFCSLTFRSARC
TNINRKEVTPLQALQMANEIAGRNGIGLVRTREGVMYETPGMTMLSKALRFLYDVCFDRG
AADMFRLYSGHLASQLATQGLMERHTQSALEAIRYLTSEVDGVVEVELNQGEVIFLKVSH
VRKPAKKRVAKLMTEEELEDVFQPGNGSFSDVQW*
>TCRU_1259 hypothetical protein
MGYISVSSPGSFSVAAGASGELHGFTVQLLENSRGRLRARSITLGKATVVILRVGELDDM
LRFMEESRREGETSTAPSPFSAQQHSHVYRYPLHEQENNVHEESLNALFVAVGSDAGYSA
VTLLRIAALVSELCLFLNIDPHRGGPNAPVLKQILLYMNSRLMQHDVSLLCQTIERLVRP
AIIATGFASDGASSLLDDLARQSLQQDATGCRLPNYIAVLLGHKLVLETSPRWSEETAKA
GGVEHVKLHDSDRYLAHLVTCAFFSTPLLHGCYEVSPQEQRLQALERRLRRFGIHRHNVS
RLAARRAIQTYAQALKKGDVNESRRAFFFENAYNELLATMNRQKPTCGTNKSPTARSPSV
AFNEYHQKDMDFNAVEGRTFELDNICFRNSDFVGFMQLRWIPAAGPHQQDSGDLEDENPL
MEKCPHGYGVFLLYLPPQSAREQESWRRSPTTADRPVFAQFTRDVLGSMETSFNCFQWLL
SPPVDAYEIPGLIHFVVVERRRNGGVVASFHRMMHQRPANVQDAVVTLRRLVALNISRAH
SFLQAGYSEGLWGHLGMQFFYSVCNFHDSPGKVVNSPLQTPQAPRLVKRRPFFFFGGESS
TSTSSYVPTRATSTVSSQQAAMSFDDSTASVKGADSLWGSLDGRLKLPAATLPHLALRPM
LIPDFTCDEPAGVCVMEVYAVFVGAMSPADVCREVEKLLRSRVVPL*
>TCRU_1260 CrcB-like protein, putative
MGEESHLQEEMDDGGLQEETAAEQGEMAFAGGQPPQPNKSILDDVWLTHVGAIIGVACWS
LAGTALRLAIEQTFVRNAVLTTYTTYGPNCIGCYLMGFIASLASSKSQNAIFPWIFRSLL
VGFCGSLTTFSNWMLDTVRQERVALCFGELVSGLTMPFVFFLWGRDTAFLLRAFIMPSLG
CIIGTSASRYELGGRQMRLVNVIFLFVSVVAAVAVPVAIEASVHRHLLNVSFINRRSVVI
SPLGAVPRYLLAQLLNGSSRFWNFPIGTFAANMIAVLLMGLLDHFYRTGGNVWCKIAMDG
LCGSLSTVSSFVNEMIGFYSSDNRRLMYIYAIISVAVGAALMSVCRHVF*
>TCRU_1261 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily, putative
MLVTLPVYSKEKGSENKEKSELHLWLTDNTRIADIGLVSEKDEDEVAASSLLYESAEGEG
NNKEEDNLIGLYEKKKKGDEKPSHSLWSVRLTEQLKRVREVLATWKKVDEAVSKLCPTAS
AAKSALTENDCSAGEITAGLVGFLSDNFSGNTWRDEYLGVNATVNHNGGAEKAKDGVNFR
GAWAEWPVGRQGENQLYHFANCNFTLVATVSIDKAPEGDNPIPLMGVRAGSKGETKLMEL
SYNSGKKWKLFCGGDTTNELSSHWEAGTAHQVAIVLQNGTQGSAYVDGKRVGAAPCELEN
ADSEEISHFYIGGDGDSAEVREVVSVTVKNVFLYNRPLTFSGGDADLEEAPHLPPANPQP

TEAVPQSVEGDQKAMPPAGKPSEAPGEQATLQQPPEERETQKKIRRWGNLPPHSKCRRID
RREVWGVRRL*
>TCRU_1262 hypothetical protein, conserved
MRSRLPIGGSLVHIPHNCRVPALAVSLHHQQRRHLYQRQQQDEHQKEEHLCASESNGGDT
PVGNPRCPASTYAGVRVGSYILSPVFEEYHSLWQWRTVMWREKLHAVPFLLYCAPGVPLR
HPFLHGTLVESITTPAAKGRLREAATASKTTEFGVKQRYMPLAVPSPIGMLYPTTSGTSA
CHPAAKWVDELFHFLEQGAAQTAGVPNSFSSTYTDVFKSGDATISSLRGQTSWKKQHDQS
RNTATATDLKETSGSDNNVHHSTQRVLHSNWSVPLKNRNVIGCGLAEVVLAIDRYAAMLA
RREITYSKACWAVLVDSKADVQPYLRSSAVAIEKELIAATAAHEAVTAAVGDPARRPLLK
LADYPALARW*
>TCRU_1263 RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)/
RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain), putative
MPQSKPRARLFVGQLNFGATEDDIRAIFDFYGHVLSVNLLHDKSKNRSKGSAFVEYGSTG
EADCAIRSLHNRYYMERDKPLQVSYCERSELISPFGWQQALQLHQENSANPPPPDRSLPT
PAKRLL*
>TCRU_1264 RNA-binding protein, putative
MVLGQARLFVGQLNFDATEEDVCALFDFYGKVLHVNVLRDRTTNRSKGSAFVEYGSTEEA
DCAIMALHNRYNMEREKPLQVSYCGKSEVISEYGREHALRLHRENSANPAPPERTVPQ*
>TCRU_1265 RNA-binding protein, putative
MVLGQARLFVGQLNFDATEEDVCALFDFYGKVLHVNVLRDRTTNRSKGSAFVEYGSTEEA
DCAIMALHNRYNMEREKPLQVSYCGKSEVISEYGREHALRLHRENSANPAPPERTVPQ*
>TCRU_1266 trypanothione reductase
MMSKIFDLVVIGAGSGGLEAAWNAATLYKKRVAVIDVQMVHGPPFFSALGGTCVNVGCVP
KKLMVTGAQYMEHLRESAGFGWEFDRTTLRAEWKKLIAVKDEAVLNINKSYEEMFRDTEG
LEFFLGWGSLESKNVVNVRESADPASAVKERLETEHILLASGSWPHMPNIPGIEHCISSN
EAFYLPEPPRRVLTVGGGFISVEFAGIFNAYKPKDGQVTLCYRGEMILRGFDHTLREELT
KQLTANGIQILTKENPAKVELNADGSKSVTFESGKKMDFDLVMMAIGRSPRTKDLQLQNA
GVMIKNGGVQVDEYSRTNVSNIYAIGDVTNRVMLTPVAINEAAALVDTIFGTTPRKTDHT
RVASAVFSIPPIGTCGLIEEVASKRYEVVAVYLSSFTPLMHKVSGSKYKTFVAKIITNHS
DGTVLGVHLLGDNAPEIIQGVGICLKLNAKISDFYNTIGVHPTSAEELCSMRTPSYYYVK
GEKMEKPSEASL*
>TCRU_1267 ATP-dependent DEAD/H RNA helicase, putative
MSEFEQLGIHQWLSKQCAYMALQHPTPIQKLCIPAILAGKCVVGGAATGSGKTAAFALPV
LQILAEDLYGVFALVLTPSRELAYQIVDQFVALGAPLHIRTAIIIGGLPHEQQLDALKAR
PHVVVATPGRLKFMLEKFPEARKAFLHLRFLVLDEADRLTSDDIETDVEEVVRLLPPARP
ERRVLLFTATLEQRLTRVEEGGWLVRLGVTPAAQHLEVFATNTVTTVADDNGATTESYAV
ADSLKQRYLFIPNMVKLAYLVASIRAAGTEQSTIVFTNSCMRCEVVRLTLQLLGFPVCSL
NSVISQKHRVDNLATFKLGIARILVATDIASRGLDIPAVGLVLHYDLPKQVSTYLHRVGR
TARAGREGLSVAFVTEYDVNLVRRLERKMDCTMTLWKAKGVNEKEVLKLLDEVSAAKVQA
KIQVEDQFGRRVNTLKVHAAEKRARQREEQQQQQQQETTARVCRVASKEDNTSKAALLHP
MPDQDPVKLQSEKKREKSLKKRRRADA*
>TCRU_1268 hypothetical protein, conserved
MVRHVNNDRSPPFFDNHYGNGVLIENWQEGRIYDACGRKFTLAMDNSVGPKRSTYTSDYT
NPGRTLLQPMMRRRGLGKALMFGEGNSTVFKSEPTSTTYGETQRHLIDSRYGTSHRAKDR
LNNTMGGLSKQNFKGTTMPKTLKPTADEELYGNFSSTKAAMDLPIECFHFQRQMAYNKVP
C*
>TCRU_1269 hypothetical protein, conserved
MVTGELPKLTNGIYPDRSNALLYDAFLPYEFLERHNFKRSGDRQRPDKFLFSFIQGHSRV
GLYEETTLVSNTTSEWSDIRARLLDLSRQRCDNRAQLVIMDGNETRNAKLTVADPSTDPL
SISGSNAEP*
>TCRU_1270 hypothetical protein, conserved
MGYKASPEILQIFITSAIAVVTTVVRPLWAAPPLVRVEVWIDNIRIAGSIGDVTRWEAQV
LRNADGRRATMGEDRESGAAQYTFLGCSLITLTVRYP*
>TCRU_1271 PRP3, putative

MASKKPRHRPISIDDDADIDFSAVTKKAAPARPAVPPTLLQCTVTDTAQKQKETAVVLQA
VDPRLNSQTHRVAARRRVGFGGAPAIPPVFNSTAPLAATGMTASGVTSNNSGGTDDAKRS
KELLDAFWREDAARKEEESCQTRRETYEQRLRALWHGEVITSEETLNAGRVDAAPLQKYF
LLDQFFEDGVPDVEPWDLWALSMPRYGAANLAAGPLDRVHHPVLPGTHYSQHYQHRAEER
PVEVKLMKTREELRAERRERLRKEKEVRDYAKKVAHQEQRNEAQFGGELTAASLGSTAKD
RLTNNNLRLNLFSDSVMNPLSTENKVFSQYQERFLEHQRRNHERHVAAIPQQVEKRKRDL
KRHSEERPVFRVYRIYPIFTPAHLGKLRNFANDGLLRGFILWVCRCDALVVLTGGEVAVR
HLERWILEKMRWESSETVAVRLVTCPLQDATTFSFVSEKSRKRGSHPARTREKEEEGKEG
DKKRMNRDEKKREDGTEHVYMNFVDSVQEGESFMRSMPTEGPWRDLSHIWRAALAPGVGR
NTNLS*
>TCRU_1272 hypothetical protein, conserved
MSRRCFMVYPLPSVADESFLNVIFDGGVCRSVFAGFGPRRFALVELRDDACAEAVTSALG
PTPSPHVNTHTSASSLLKDKDDDCGLEKLGSAPVAAASNSRRKGNAAGRKKDGDDPTGGA
DSDGCTGTSGIAYIGRLRFRNTPIQVLPSPITLDEIYRCGGQLPQRCSGRKKESDKPQGR
VGRGPLERKRQRPPATEETTTESENAAMAGGGKTTASNGDAYRRCKSAEHFTRQCSAELS
TEDADGKRCGAAGAATGSGPRGTSPRKRTAKHVFPADCCQKCGSSLHFTRHCDADVHSAG
ESARPQDHTGLDNAAAAHAVVPKKQDKAGHHEPPNKKKEKPQQKQEQRHVALCTSKDHCK
HCGSDAHFSRHCPSK*
>TCRU_1273 hypothetical protein, conserved
MAPRSENGAAKPACESARRLDFYLPPPDDRAYRRGRIQRLRDQITAWRRQPRRGGAQAYT
RAASAGTEQRGLVVDIPLWKASTVSPTRRNVSRHEKVFMLSQVSRSPPNAKHIFSSATQG
GELREKTPLRSSNYTNTKNSFNHKAQTTGRVMEVPYFHDQTIFCLPRDGRVPMTAATVDA
AAALSDAMDDGEGQQTDSNAGFCYGVTSNSEEMTRHSEHLRHERKADRDGKPLPEKTTFG
SDRFEGAPSVFLSLQSKGGRAASVPKSTESKGLTIDSTFAAMTRSVELATAVHAECTHRR
TAMQRSRSDSFRQRVLEQTMEIPVDWREFERVTPCGNASCLTTFPDEQCSAASMGRTHCT
ANFGSCSVGRGPMRLYSIRLRKRLLNSEGSMEKASSFPRLGTRVILSKSWV*
>TCRU_1274 hypothetical protein, conserved
MTDPTAAALLHNTATRVTLGNTPLHAVPVTVAKQLKPLLESSTSLTVLTVHTQFTPPESL
RLILLGASRCRSLQHMRLVGGISVLQSKMIMSAFMQFTFARRTSRTTSAVRPFSDPAGRC
PHTPLSKRPSPAQRIRRNVVVSDAKMTTGGCQTGGYGRLNSPALRNMEVSKSPSPRFSWL
NGVQMVLDLHHLDDVVAGFLLKGLERSERIIGLDLHIAPTSQAATRAAVRMLSHANVIVA
RNARRVRYLLSQNPPVDAAFFRGADKRDKTDFSLCSPLPEDVSRAEQREQVREGGEKEKE
EWGREATTMRQGLSTFDLNTLPPRRYSPPRLLSGAPPDPSLRPMQPHVVSASPRIFDNGE
LEMGHMSRRGEQKQMEEEASHENECFVCSGGSLYTPEKIQASKIPPNTINRCAGERREDG
SCAWPAPKDPLETTQPSPSFSRHTPCSPPSPRGQFVQHIRYLHGCMREINGVVVRYQMES
RDSIQRLVAEMHVLEEQLTERVTSKLTDVLLSLSELEKQVE*
>TCRU_1275 poly(A) polymerase, putative
MPPTALVVGQSVMKAFQHLSTQDLHTRRVEEAYRVVVECITAVDPAMRLYMFGSTAVYGV
HEKGSDVDFVALSKTDVEDGKGEDAGTQVAKGLQAEFLGKLARVVRQKHLSWNVEEVRRT
RVPVIRVKGGSSVDFDITVNRRNGVRNSALLRAYFEQDPPCRWLSMGVKRWSKRAGLNAS
VVGGSITSYGFNLMVVYYLLQRGALRFIEPHAIDVANVAPVPPYLPLEPPRNDGAELGEQ
VLDFLAFYMHEFDAARHVVSLSRPGITTKEQLNWTKNAEDLARMNGEKINYQWCIEDPYE
LNLNVGRNVTPLKRDFLRKHLEKARETALLTSTE*
>TCRU_subunit mitochondrial RNA binding complex.1
MRRWSGLPLAPLWGLIGRRRVSGDDRSGDSSAFLSDDEALRGELASALETEGEAAPLDIM
QHHPLEAATMSSSTSTIYLEKIARPPARFDLLTNSFVYKWQTKAALARKVSGPMREWAAE
LKYRTGVHMELEPTFPERIPDEESKTGEGDTYETADDVDITVYLFGSERGIFNCHKLMET
AIQQDPVYVRLGVFRRLHGSNEVEWLMLRRINREMRPPDIPPISLKLPGKWTLLYERYKE
AAIRTLWEETGITVDPTSVFPTAQLYQTSPKYYWRVPVRYFVAEVPHDVRVEGPQVVPTQ
YMRNWDVRLLRQSPDPIDRAWAQLADPITGCAWMKAPMIDELQKPLRGEKYMATRYTPPP
YSNLQEVVGLGDGDQDTQNKETEAADPNA*
>TCRU_1277 NOL1/NOP2/sun family, putative
MPPKRRQGARGGALGAKRSAGFEEFYAGVYGTRWPALRKALTAASPKKVLLWNRFCQLPF
AKVMANMKRMDEESLLQVFRCQDGCEVAPPASDAFNVKAYYPLDYASALVVEQLEVGAFD

RVLDVCAAFGGNSIGIAQFLSADGALTVNEPNHERSARLRRNIREYIPSNYVPVTITQRN
AETWYAPSMYHRVLVDAPCSAERYFLQRDGGAPVSPKMWTEQTSLELSRRGCVLLLRALE
TCRPGGRVVYSTRSLSPLENDGVVEDALRRTRCQVEVHPTTLCNMGEKTRYGHIVLPDTA
GGFGPLFCCVIHKVSDRREEVDSNEEGEECEYDDENGDS*
>TCRU_1278 hypothetical protein, conserved
MRHWSPWRCVGAAAATGALIHRRQFIADGLYDCRAGAAGKDDTSKYRLPLRRALHFVEKG
RQLAGAVVEREGGGGEALPSNREGSLLHEDAARYAAYHCHHMLTSFRAERRQWTKLKEFS
FDEFTRVMEYLFFAALLLHLTALYETADKYCEALIDVAMSCTIFLSKDADGLHHADMLRQ
GRSKSTDAKVAYLSNGEEFEARDEPWNSLHWAIVHFSRGVFAWGLLDHTELLFDMKRTMK
PYSGMVRTFAKIICERLAGMSLSAEDLAFLSCLSTEEGAGKWLGTANISAVSSTDVFARA
DKNIVEATLHFAQQRRLQILPLMWMALLTRHSAIIGAPRCFQPARHALLNAIPLFQEEAE
ADTALKLLAQCCYFPSSSLLKASSVEVGVLLSQMERHGVFSSSEFMLVELLQAWMRVEAP
EELSPSVKSAYGAYMAFRNIPRCALRVVGKPYTAKSDGEAFVHELLFHALVQWSSCLSVR
APFHREVEELLISARYVASLFDSIRQHGKDRDSVGAAVLVVEATFRAFAVRVADICTRGR
LVESMSPSDLAEFDRLVDHVLREGTEGSVGGCVPQLYEENRQLWIYSTRRNGS*
>TCRU_1279 hypothetical protein, conserved
MYARAQRASSVRESAGVGEHRLPRGFEKMPASPEARVACEREAELERLHQSVEAAAELVF
QQRLAIHRMKRSAFVSEIKRRPFYNSGSGGDAYSDALKQLVDLEDNLSQESSRCIRVSNV
TALHLLNEKQYSRTLQILLRVEALAQKGAGMWFPLFFSTECGMVGAGEFVHFAGDRRSGD
EEGVREIFVPFFTTRHEKMRQLVLAVIDNNIGLYHFKIAEYELAVRRMSRALHLEELLGV
ETIGVTYFNLAQAQYECGSLEDAFSAITLAEEAIEKRVHEYQSQNNHLRCTVDCSGSGVN
NIPGLERRRLDVYIGWREGVCLLSRVLEAHGRWLQSSNAYKPAINCYEQSDRWLSSVKRL
SAEENNWRQELRQRIQECRRFQRHSCCFPKSTVLFSSPAPGVPSGSPRSIVVTTTLPRKI
EITACATPFDNGQKGTGKEGSKGIDQRQTRQRKTKHKEHSGKSHYRDVYELSATTTSTSN
AAVTTGHHRSRTAPRRPEWDAGTQVVNPDTTRVRPATTATTSSVAHANSEARNSSRLTSV
AGTPLSRGSKHERGSSGKPDLSSETGLTSSDVRRTQASAPVAQCTTPFRAQASSNAMANR
AWNINISDKSLPLTRFTSSSTKLCPLSLMRCIHILQAFARSRVSLFEKEWRKLPCEAGFV
SPQSHSHSSFSVSLPSSWSGRHLYETDGASRLMCGDDSFLKNGGLFVGTPSAHATISLNS
CEILLAFLAARRSASLVCQRSIEQRYTKVMEGILRQHASCAGSPSTTVKMRVLRDSARSR
SLEETEPRRTISGGAAFSPHRTESFPNRNGELCHRISEGVSSGEGKKNGFYISEGRLHRR
YNSLLRMVPQGRETPDTCLDAVKANNRFNGDLASDTAGAMGSQLYSSMPVTPPLSEDSGS
RNSRADEIPTSTWRARRWSDFPYTRQSEKNPQKVKNHPQIVPQQRNGTMGAVNCEDFDAP
NGKVYGNGVQNGLPPRHPIIRRTPLLTCENHDDIAHTTAVIIRQRLLREEAAIIIQGAWH
KWRERRQLGAVRRVGYR*
>TCRU_1280 histone deacetylase 2
MAFTDAVAGKTSLPPPVAIIVGHNIDASAMPLTYERNRLVIDMLQHYACPVFSHKKSGDA
MNTVSSDVFEWVLEPLPVVGVEDMTAFHDRAYLNYLSIREALSEVDERASTVKRSRAEGI
QPPVSRRSSAQNQPPLRVLPDLVPIPTDEEYGLVNENMPFVGMWRTIQATVSGTLLAARL
LAQPGRFAAIHWFGGRHHAKQSTAGGFCFANDVVLGVLELKKLLSSDKKGILVVDVDAHH
GDGTQSAFLHDNSVLTLSMHAHGVGIFPGSGGIEEIGAGLGRGFTMNVPLPEGATDILAV
TLMYRSIHFAFKKLGEGLAAIVIVCGSDALSGDPLGALNLTVGGMQSIIRLLLKEAARRS
LKVLLLGGGGYVDTSCARLAGVVTKDVLSCAAAMRLGKTEYFGDSANLGDNLGVAVPEGC
EYFTRYGPSFLMHGLPPARVSKLYRLPYGSPLFMRMQRAATKEALRRRRNQEQDEEEDAE
DEEEEEEEEEEEEEEEEEVEEEEGEGEEEA*
>TCRU_1281 hypothetical protein, conserved
MTIRVGVSFDLLGTLVDVHRSSGYQYAIDFCRFVEKKGFDSPPINVDVLEENSKKSLKAE
IAKDRAEWTAKNLGVAEEMPFGGVTKESVVKFWCRVVNSTYDREGAFCGHDPKTISIMQQ
AQNSSEWDDFIVSVVQRFATPEPYSWLPETLPTLHSLKRWRELQLPLGIQCDPPRVLTNA
DYRLVSVIREMVQREGDEELLGPVFSADVVGVGKPSPCGIEVARKAACVPSASQWIHVGD
GGADRVAAERAGCHFLPCLQTKGVVWEELREKLEQVCRLAQEAAPCE*
>TCRU_1282 hypothetical protein, conserved
MSSILLLIPTVAEEGAVARARPLDAPVHTLRHERTGAAKTGQGISTSWYSGLDVRSVGFK
RSYIDGDEDADEGDAWSTFSDDALNNARQGGRKNREGKEEQRVVKRNKVETNEDTAANTN
GIEGTKGVKKYSDDVQQATNDGAPVSLLPTSAFSTLEGATQRVDKVDFSGINVEDLESLT

ASLLQQWASAGKAAMPFSEVTKVVLKSHPKYTEMKAKHQSPQGRQEALEWFRVSQKAVRS
YVLHLGYTIDSTNNVYLSRPSNT*
>TCRU_1283 Major intrinsic protein, putative
MPKSDSSPALEKPRSTTPQPAEPEASNKNKYTDPLDLEDNEIETVEMSTKTQAAVHLPPR
TLQQESPEACTAHGANTVHALAAGVPAYSGGEENDQNPFHKGKREISTTSQLTTSASAIQ
DSATEPDGKKFFISVEVTSDGVTRLEELDPRELARLYAQQQAALRSISGEFDILYVPDWV
RLHPLLGSYVAEAFGTFACVLTLSLVSVRNQSLFDRSNDTNMTALPIGFMFMCMVFTFGY
ISGGHFNPAVTMAVFLVRKLDFVRAVGYTICQTGASLGAGLVAMAIQGGTDIFVPYVDKA
YVSSGIFSELIFTFAIATVVLNVAYSRQSGNFFYGFAIGMTVAAGSASVGRISGGAFNPA
AATGLQLALCLTGNCEPLASFWIYWMAPLVGSALAALLYANLSQPENTRALTDAAVLRAD
SAANGVAPVQ*
>TCRU_1284 Major intrinsic protein, putative
MTEEVLAVEERSYLARKLPLVKLSAYQAKFICEGIGSFVFVMTVSLAEMNCGITSINGKD
RTRNLAPIAEGFMLCVLVFAFGYISGGHFNPAVTFSAMLIRAMRLEEAVAYWIAQVIGGV
LGALFGIVVNGFPRHLPAPQVYQNLPAYIFTGFLAEALFTGFLVTVVLHVAYSRQRNSHY
YGLAIGMCLLTARYSVGSVSGGAFNPAVATGLQLTKCIAAGYCIPLMHLWLYWAAPAAGA
LGASLLFKMTHPAPQETEEENQRKALQRSARHLYGS*
>TCRU_1285 hypothetical protein, conserved
MSEDDDESCGVTNKTNSSSIALFSSLPDVLSFTENSGTWISRLVCIFFARLASGEELLPL
IQYVRTELLLPTQAPLGARAIPVATLEASVANTTTDVPGTMLQGSNPRMEAMDGVSDQDK
LFLYRAAKVALLLSAEGEKAQDEATRLLCEPVVAQALRLAANQGDAVALPLPRKYDFFLS
SRVAVCCAKRWAREGRWDVGLRLLERAVATPMTKAAAVELLSNAGRWEMAVRCLGQLPPT
LWTEIEVSAAVRSLYRAVEGRRRNGMKVGDTPNAGLWRIALHILTLVRDNKVKLSAPSAV
NDALGLLGADGQQWVMACRLVKTMLLNLEKEGRTGESSGTVRPNMVSIYHMFRALRQHWH
LALQHASLMMREGDVCISDDREVTDRLLKACVVGYRWVEALRTVQKSLESNPSEEGRDFI
HTDVFLRVLGMLHERQKGFLATQLFQQPQLSRHFSKDTTGKAYNVMLRYCNTVSEARVWL
QTMGTKNILVENESYEHLMILYSREGVWQQALSLFNALLTDPQRQRLYIPCAKAHDAVQY
ALERVLPPGPSWEVSMTLFTRMCELNVPISEVAFQSVVKKCFSQGKADEAQSLFRFVVRH
GVRR*
>TCRU_1286 Endonuclease/Exonuclease/phosphatase family/Endonuclease-reverse transcriptase/Reverse transcriptase (RNA-dependent DNA polymerase), putative
MEPFTWLPAERYFYPLLNSIGAYQRYTYRLRAVCDAQRQKLLLSGDIEQNPGPIAVLQMN
VSCLTPSKLATLMAQGADIIAIQETWKSSEQIASMHTGDYVLYAQSRIGKGGGVAVLVRK
TLRSKRIPLTIPQHDTSLEVVVVRVALDQNRGLIVASAYMRPPPQVTQSFRRLVNCLPAS
SPLLLCGDFNMHHPQWEPFLETSPSEVAAEFLELCTDAGLTLVNTPGEITYARGTRERSC
IDLTWSKHLTVSDWSASVSPLSDHYMLTFTLHQAFKDTIPSAPRIFYSWGKCKWDLFIRD
FDAQLPAYDYKKQSTGIKAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERMATDSKA
RYLQSPTPDREAEMQRTRSQFFLLLRERLRNTYLRRISKLNPGEPLAWKYISGRKKASLP
SPTSILLGDGQHTYKTARRAANALNRIFLPFHPSHKAVRFSRGINRQSTSLNINASFLFG
QQNNSESAASFTSGSSLSSSSEPQDKNEAATTSGLVAHLHSPLDAPFNRTELLAALRNTP
YGKAPGPDEVYSEALRHISSKGLRFLLRCINHSWTTGTIPVEWRRATIVPLLKPGKSPEL
LESYRPISLTSIVSKVAEKMVLKRLLWVWTPHPHQYAYRSMRTTTMRLAHLIHEVEHNRN
HYFQVSLPKKSGIGNQLHYRPHRTLLVLVDFSKAFDSIDHRVLSRLLANIPGVNCRRWLR
NFLCGRYAKTRVGHRHGDRRPMLRGVPQGSVLGPYLFSLYVHPLLNLLNSFAGATADMYA
DDLSIIVKGQSREDAIPTANMVLQKLHAWSQENGLAINPSKCEAAWFTLSTHTESDYDRE
GKWPLVVAGCQIPVMTMGASRTTKLLGMDLDPRLTLNVAASKQCAATSQRISLHSAQRGG
TIST*
>TCRU_1287 hypothetical protein, conserved
MLPPGGELGTVCGHARWQDAPLGRSMQVCQQLRGEAPQGARSSGESSGSAADPEAFSARD
NEPCVQRPASYGPREAQAASTADRLTPSRASLSVPWPEDAHRVAARSVQVTIRCSA*
>TCRU_1288 hypothetical protein, conserved
MVGLSVTADNKREVAFDGEAGEVQHGKSGLERNYRVAVVLQNGMGTVCVDGKTLGSSATT
VTRGPQLLDVSCFYVGGDGRSGSYCS*

>TCRU_1289 hypothetical protein, conserved
MGEDRELGATQYTFLWVLFDHTHQAVSLSDEFVRSVRAMPALNSLTITEMEVTASRFLYA
AAILGTRLCDYYFFIKAVRRRLSAVNRGIVQESSLKNVPPAAVGLGERLRHMIGNNHRRI
IKPTEKASAAIIADASLQGWGAVFIPDSGDVKIAGEKWERKPFLIMQAEVRAVRLALSAF
PAILPPTMDVWVDNTSLRIKAAQNHTP*
>TCRU_1290 hypothetical protein, conserved
MQEDYPVNLRVEMTPDGSSVVLPGSITITRTTVSVFKLCEASDEEPLFVGVCSVPLIRFA
RVPSTVLTSADSLVLTGASGHLFINAALSAGIAPAKDGSVVSARTASTSLFPGSSREEPT
GDELQRLDNPARWGNLRLDFPSDEDCDRCVEALLARHAEDITAEYMRSTRLVGNKTQTAD
KISKKILSVRAADESIASNRSTNQRSRNTQDYTVTKGDLSEFMQSCRSSPMDLESPRGDS
YLVQASKIPASRPSESFKELGTPQSELRTPHESQHGRILPNRSHPTASQRELPTPHASLN
GSNFMQGSQNAKGLPVRSNPTNSRRELGTPSELRTPHESQHGRILPNRSHPTASQREPPT
PHASLNGSNFMQGSQNAKGLPVRSNPTNSRRELGTPSELRTPQGSRIDSVRELPPDAVLM
PKSLNNNSVYAKTPHSTSSLRTGDDFGRTRHPGSVGRPTSLGPNAIPSTPGSSHAMHVAP
ASGQNDDPVGKFPYQSPSDLTVTQRSSRARTEHQRFLRNVMKFMHHRLHLMQYLHKELVH
EAYLVEEAKLFGGRGRGSRSASMSRSLSHSISRPTSVSPRSSRRAALSTIAEESSRLREI
EARLRSVEKLQREAEQDRQEALRLRNEAEKKLEAASQELANAPRHSFSSRNMLEPQKNDI
PVRSQSPILRGGQQHPLQKNDSTDVLHAPYPEKHRGSELSRMSRPSTVLTGSGQLAFASS
QQLHHFQPAGALTEVEYSNTILDRYIYGDEWHLLYPAREEDVRFCALIDTCLILKLPRRL
VTITNVSLDQPGMRITAEIHHSRDHLPRETIERRFTTQPFLFLKRLYEIRHCFPESPAAL
GQFYRGNRHGSRGTSRAVTPRGNHTNSLSYLRVADEEMDSVEDGEITTEGSMTGMNGRMR
ELERITQERVQQREQERIRERERKQKFFQQERLRQQLGQLERDEDSRRSRIVLSEAQERQ
DAGCKTDWNHKKPIAVSQNALEVEEQVQRAEVEAGYARQLQVLARAQNRNFTFVRMFTQE
RERRWRVADQEREDRLVLDLMMNPRVLVGVSSQTEVDERCCRQRLIEAEAKQRRQIYANM
RSFLIDVLQDRVEAIVGDERTARMILAADEMKEWLDIVCKGKTPTSGGVPRAAFFSPQAW
QALFAEEVAERTHLFSDEERRRRLFRREFIFTTEDAARNEIELKELDEHVFMLESIMHCN
RAMLERRRQERKDMTNLSNEEQYYRKGVLSEEQDEWEVLVELFDSGLNDVLVEEAARLAA
EAAMADLESPQRRRRVTGTPRQAKPFHYMTFVPEDMDHPPSANLAIEGILGCSINKNLEV
TSIERPLPRVEEDDLQFQAGDMILDVAGYSLHSLSHLREVLSNRTMQIQHEAREEFVDLP
EEELTVNPALQKYVDVLCEHHNFLVQVLRGCDIFQIIVKS*
>TCRU_1291 retrotransposon hot spot protein, RHS3, putative
MEYHTNNSIKHPLLCIPAVGNFPLVDGFFFVEPNPTTLVGLRMATAGGHHTTVRTVKQFT
ECLAAYFDGWEELSRDMSWEIIYVQHADSTPMNDWQRCDVVNSDSVSKREKQKIAAFWNE
KVRKCQVLISSGDLRGDEALRSVEEPRK*
>TCRU_1292 retrotransposon hot spot protein, RHS3, putative
MVDASKSRADQCEVLDEMDVKAMCAWMKRDGTTHGRAQYWKMVKERMDKVGPIPCYIFDA
NEFIAHSAAVEDALDGINSRDGGKHFTHGGVRL*
>TCRU_1293 hypothetical protein, conserved
MMTGRVLLVCALCVLWCGAGGSCEEDAGAPVSGGVPPPAAKELETAGQGTKNLKVGSPDI
DGKVIPAPSPPTEEAGDEDSDEEEETAEETKKDKKGEKEKNKLHPQTHESQNNEGAPPPP
PTIPSGGPAPSSTAGEGGPLPDQENLHNVTKAKKENTPSRSKTDSEAPEPPPGDATQGQH
NHDTDTKDSTKNAATGSPAETTTTSSTSTSGSGDHAQNKADEVDAQSSEEQHESLEIGNS
NVVPPLSETAPKTARTTTDAQTNGTVTKVGESDGSTAVSHTTSPLLLLLLVACAAAAVAA
*
>TCRU_1294 retrotransposon hot spot protein, RHS3, putative
MDHWVLYEPKVQNFPLVDAFFFVDSNPKTLVGLRMTTTRGHHITASTVRQFTECLAAYFN
GWEELSRDMSWEIIYVQHADRTPMNGWQRCDVVNSDSVSDDESREIAGFREEEVRQYQVS
ISSGALEETQLSEVRNSHGNGKRNWGGKGEVLISGKK*
>TCRU_1295 retrotransposon hot spot protein, RHS3, putative
MDATAIVTNCPEENDVRAMCIWMKRNWPLQEQAEYWREVSGRMNNVGPILRFIFGKQAYD
DRIKACQQAVDGSTASELERNLGIGCCYSSNDSDLSRKLVRVVRVRRGNNIESPLNLLIS
PHLERETLSRLENEMKQSDFIFFFY*
>TCRU_1296 Nucleoporin
MARSLKSGSRILRENFKPSSSAPEIRLVMQNDLKDDVSKTVKQLILNKMFAKRSDKVMGV

DQWIEKCPVYDEHLTAALQKFRAHYVQKVAEDSDVFQALYNECHESMEKELNRIVELRKA
VVQQQLRCIEGIMEQLKEGKMAEKKTFRLLKYYPANDVMRFRPFGKVSGISEMGESADVC
EPPAPVLVNPFNTAHSANSP*
>TCRU_1297 Golgi reassembly stacking protein (GRASP homologue), putative
MGQEGSKVKETLKGICGLQVARVLPRSPAHNVGLVPFFDIITAVDDCLLVDEDVAVMQFR
SFVSQRKNSQLLLKVYNLHVRAYRELVCFPSTSWGGAGLLGCSIEWCRAKDCLRRSWHVV
GILPGSPAAHCEELRAERDFIIGMQRPEEPVVTLLKDEDDFYGRVDLWRSLQRVAIQRLN
RNSMALPAGADGKAASSADIGRLLLLVYDALENEVKEVVLDVGPDVDAPLGLNLAAGLLH
SLIISSPMEERRSISGSNDSKDGNENDNDGGCATNRRLSLPVMTTFLTSLGVVERSLPAT
PLQTPFRKNVGMHSHDELPDPVPTMPPTPTPYRTLAPPDFCEITMPSSKPLIGREGVIQR
QECLATPGAVDMSRTLPAAGEVELGELRIPSVLHPDCKTIPAISQGSLTNTVGSGLEGLT
NPCTVSQEAASNALPPVITENGNKPLQPTAQRGEQHVGTSSSGMQRHGPVAHGASWNTFL
SANKNFNSPPQLTLLKIPPPLHFPIIRPTTPTSWK*
>TCRU_1298 heat shock protein 84, putative
MRRVYQRICRDALSHSTPSGRAAFAAAISTLSAAYDGSRGGNKMRAALATPMRFCSTSSD
AATKKPVDITDEDVVIDPTPAAKDGSTGADGASPSSSSSAKPNEDSERVVGESEEMGFKT
ETRQLLDIVACSLYTEKEVFIRELVSNSSDALEKRHLLEISKPEEYPREEDDEAPFIAIS
CNQSKSRFVIRDTGVGMTREELAENLGTIAGSGSKEFVRELQSAASGAQAAEKIIGQFGV
GFYASFMVAKHVKVYSRSAKKGSKGYLWESDGTGTFKITECEGVDKGTKIVLDVKDTELS
FCTPQVCERVLKKYSNFVSYEITLNGGKVNTVEALWMKDKNAVSNEEHIDFYKFISGAYD
SPMFRLHYVVDAPLSIRALLYVPQSHTEKYGGGRMESGVNLYCRRVLIQSKAKGVLPEWL
RFIKGAVDSESIPLNVSREHTQDGSMMRRLSTVLTKRIIRWLEEEAKQDRQKYERFIQEY
GPFLKEGVCTDQVHKMELAKLLRFETTKSDIDYPLVSLEEYRDRMLANQTHIYYINAPSK
EMALQSPYYEQYKEHEIEVLVCTEPIDDFVMQHLDTYAKHKLQNIEMFDASLDGSVQHKK
KLEGEKEDVKVEKQLTEAQVKGLSDFIAKRLVGRVGVVKSTSRLRDSPAVIADHESAQLR
KIYRVTGQMAGPPPKYNFHFNPKHPIVRKLYTLSISPTAEEVETAGLLVEQLFDNAVISA
GLLEDPRSIVSRLNNIMSRMVENVPEPTADK*
>TCRU_1299 hypothetical protein, conserved
MTRAFPQWMKRSLPWFVGGSAAHGVCDEAVAEVPGPSRVPAFVLPACLACWHAWRLRWRP
AREAPVRMTVKQSRHPHVRLSQTIGTPGRARRACAVILWTEESTLTKIRHVDFNPPLAGR
QGVAVLTSGRSSGRGGQAGHSPQRERAAPPTQRVPCDPQGACRPAEERAGVASRLGGDPP
LRDRCPGQHQEWSSATPRSACHAMCAPSFSSWNFFQYGRLTAVRRPT*
>TCRU_1300 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MLLPGGELGSVCGHAQWQDTPLGRSMQGCQQLRGEAPQGAPLSGESSGSAADPDDAQRDT
TSRPPPTQFPASNNTLATNRARMPALPWARIAAPIHSATVIIDNVSGGADAAQDYLRTTS
EKPEIPSEHDAASLVSNGFCEHGHFTDFLAMAEICDSTVHGCVSRVLLLLFLGL*
>TCRU_1301 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGGGFANDEKSGPGNRAELPLASQGPETAPQDSQGSQNR
APGEEENLTSVLGEEADGDDVDREKKAEEEEITERQGSEGGTAAVGSDSRETNLSDSEQE
TGQPIVPAGSISPSNSQESNANLTQTEVEGKKEPDKNTTTVEGALTTVNGEHTLPAGIAE
GNLPPPTEDSVDSREQDGEDATSEGKKNASSPETAATPQRDREKGSEGTGGDTKATTVTA
NTTDTTSTQNSDGSTGEFCNRTDSICFVVCAAAAAVVAA*
>TCRU_1302 protein phosphatase with EF-Hand domains (PPEF)
MGCTNTKESSERGGGNASELGKGGRVGLTGVLAANGLHGGGSANDQVHWPTCHFCGKRIP
EKEYNAHTVMCDEREVTCWNSWCRQIVKQGMLHNHLEECAKKQRALCYKCGADLLATELQ
AHRDGCQPQKCTSCGELCITRIMKWCPDNFITRVPIMHGPFATEVLLARYVKGGAQNKSG
GAAPVALVSYNVARMQLLWRWTKAKSYLEEAIFRLTSKEMNLKKEGFAIFKALDKVSDSH
VLEPRRSRSILQTPVVAPAISSHYFPTRMAEPITIEVVQRLINDLTDHVLLPYPAAWRVF
TDAMSHLNTMPNVVRLSPPVGARVSNGRINQGSKVVVVGDLHGQLADLLHILKECGMPNE
GTYYIFNGDFVDRGANGVEVLLILFSLMLACPKYVTLNRGNHECDYMNDEYGFDVEVSTK
YDRNVFRLVQRCFCALPLATIIGKKVFVVHGGLPRRKGVNIEDISRIQRFRQIPMPDYSQ
PEEDEIFQDLLWSDPVEDLQGWRESPRGAGVVFGADVTQEFLQNNGLELVIRSHEECLRG

YEEHHDGKLLTVFSASNYDGPETNFGSFAVFVGDNPEPSFHTYQVAEDDVEVQTLVDLGE
TFTPTLGRVSSFATLSQSKLLLRRRARDDVLRVLRERIYQRRHRLLAYFAKLDRTRKGSV
WKIEWVEAMRNVLNLDLPWFFLRGYLVADDENTRVWYSHFLVKFHNFFQPLWLNDWIQSA
CYHLTQQQRANHRSQYVAKAFNKEQVSYNEFCSVIRAIDYTMSEAQLFQLFVYLDEGGTG
HIDGPKFVNMLSEMAAYPLSDTLRWDLGAMEQLQSVVIQGRSQLPYLFKVTSKDRALPKE
KFMLGLAQLGRGMRKQLTQQQKEKIYEFLAERAPPSGVMFEHFLFMTAVFDVQAMPRSPA
VVLADVNLFGNYLKNSSFSSMCK*
>TCRU_1303 hypothetical protein, conserved
MSDDNNSNRSARGDEQPGGQADNSRRPKSGAVSMDAITSLTVREQVDALAQALLREFMHR
RGYTKTLQKFDCECPRDERTIASRQLMRQLLEIPSHAFPSRLSGEGGTHNTAVIIASGER
EANNEEKKSKKKKKKPAPTYMEELCSYRLQKREVKQRRQHEEEKKKETGEGTETTTIIDP
SDAEMEEWRAAAVEKERRIAEARERHEQLLRERRERKQRKREKRKKKQEKKEKKQKEGEG
SRHHTHEEDEGDGGDATVNFHNSVPHRYGKRRSHLDDVSDSDDEVLLRPMSGKAVAVPHK
SHRNGGGDSVDEGVEGAGARGGLAEPEFLLGRMEKRREQRPTGHTVGSHWIPCGGNVTEL
LGPGRAALFGPDTPMPSPSVTDSLSPSVNSERPPAFLLGEGMSFMSERMQAAKRLSALED
CRLPLSSPPPPAPSTSPLRKPASTIWGSRTMRGGAGFTSSPASNVWSRSSSREGSPGSAM
PIFHYTTAGQHMMSLSSSGRAHSPPLSLDGSVSVTLPPPPPTSSILKTSSLYSSGNRGFD
GKAQPASSAMRKDDTNTTDKNGDGASGEKKDSEREQSSGRKNRKVTILVD*
>TCRU_1304 primase 2
MLQLSRLLQCVRIASSSSSSSSLFASLRAFSNGRRVGKKALASATSGEAREVGGDEDTDD
SADMRHDTMSELGRTRPNIDFASFEADVNDGGMMPLPLRGRLQLPPSQHQKRQPRRLGLS
PPSSLSSLSALPEEVLQATNASDPIDAARRERRVRGAREEEEEEGEGEGEGDDDEEAGME
NEHDPVDAPAAFPNGYTNHHHNHNKHNNEYDVDIGKDTLSTTINSHNSNNNNNNYHTNIA
GLTNPFLGLHEHITRSYRLDQLLAVARPEDILMGRQEAKSGAFSFIRFESGPQFLASNAK
SSTTPRSEETPHNDCALVVAERLMAFPPHMRHFHSICGRENVPCDFFADVDLPNETPASG
EKLLLEMLNYLEVRLEGIGFHQPSFLVLANEVPSPDKVSYHVHARSMGAMDEKTTADDEE
GDDDANEHENEDEEADLAGTKGSPRGKKRNNNNNNNNKKAAKAKKGQKQKKIIAFQDYRVV
RLLADEVNTTLGRTVVDEQCYRANGMLRCAFSSKIAPSPNGGVVRQKGKRLVPMLKAQDT
ALQRRLNEMSAYLNTLSEAEVLERTFGTRFAPITGSQKADTVKDSTRQFKLLRARNVLGP
KEAQAVEFDAYGNAVSLYLTEGAKWRRFKMVIEKLRRMPPRSAESYDIWVRVGLALHNFS
NEDHVFEEWVRFSLKCPQKYSRESCRKKWQQFERNPDALNWRRGFNYLNTTVWRSVYRE*
>TCRU_1305 alanine aminotransferase
MSGSRKEIRINPRVVAAEYAVRGMLPMRADEIRAALATPEGKAKYPFSSIVYCNIGNPQA
LEQKPLTFFRQVMSLIDAPFLLENEKVTSQFPADAVARAREYLRHIGDRTGAYTDSAGYA
FVRDIVARQINERDHEIKPLVDASSIFLTDGASSGVRLLLQVLVGDASDAVMVPIPQYPL
YTAQLTLLGGTPAMYYLCEKDNWALNVEELASVYDECVAKNNATPRVLVVINPGNPTGGV
LDRDVMEAVAKFCCDRGIVLMADEVYQENVYAAGKRFLSFREVVLGLPAPYNTDTVLASL
HSTSKGIIGECGRRGGYFCLTNFPAPVREQVVKMCSMVPCSSVNGQLMTALMCSPPRPGD
ASYESYWAEYNGIFASLKKRALLLAKELGTIRGFSCQPVEGAMYAFPTIELPEKYFQHNA
ELNAKEGRKLGPDTRWALELLESSGVVVVPGSGFGQRPNTLHFRTTILPPEQQMERMVKA
MRTFQEGIWAKYG*
>TCRU_1306 alanine aminotransferase
MLRKTLFGFRAIRINPRVVAAEYAVRGMLPMRADEIRAALATPEGKAKYPFSSIVYCNIG
NPQALEQKPLTFFRQVMSLIDAPFLLENEKVTSQFPADAVARAREYLRHIGDRTGAYTDS
AGYAFARDIVARQINERDHEIKPLVDASSIFLTDGASSGVRLLLQVLVGDASDAVMVPIP
QYPLYTAQLTLLGGTPAMYYLCEKDNWALNVEELASVYDECVAKNNATPRVLVVINPGNP
TGGVLDRDVMEAVAKFCCDRGIVLMADEVYQENVYAAGKRFLSFREVVLGLPAPYNTDTV
LASLHSTSKGIIGECGRRGGYFCLTNFPAPVREQVVKMCSMVPCSSVNGQLMTALMCSPP
RPGDASYESYWAEYNGIFASLKKRALLLAKELGTIRGFSCQPVEGAMYAFPTIELPEKYF
QHNAELNAKEGRKLGPDTRWALELLESSGVVVVPGSGFGQRPNTLHFRTTILPPEQQMER
MVKAMRTFQEGIWAKYG*
>TCRU_1307 hypothetical protein, conserved
MATPPVAEAAATTASLTACASCHRLCEVLDEVARKDSALQQFRALFEKMGRDYEVEQRNA
AQAKLELAALTTRHETQQQELIAVKAKSAMQESRIKEEDDAWERRTRQLRQELAAAVDER

DALAGEREVQWQQIRALRSRLEGQQRQLTVMEDAWKCRLEETRREAEEKVRTGMREREEL
LRLREVELQRSTSQLEGRLADMAAEVRRQHDASEALMLRIENLQRSLRRQEAMTQRAQDA
LSVEQKEKAQLGEYMALERQTYRQRQEQTETSYKAQLQEIERVCDQHVRERERLESEIAL
CQRESQKEAKRTREVWMQEKQQLEATIESLRGELIREHMRFDKAHESHQRVEALLVRTRR
ELEASQHQEVVLQETIASLQKAAAKRDATHLRLEGEITRLSASVAEREREAERWRSAMDR
MEWQSRLETARDARERERMHPEALPPPPLLPLYTSSAPRRDTTRRSAWVTPNKRWEQAES
IEHTPLTGSPSMKGAENPPRGGEDRDADMLRSIVQEVLQECVTRTEPSSSLTHASDSAAL
HPAAVATGDRHLRTPRRRKTSSRARRHAKNGDSHLGEDSLRNGMPCASPITRSTPPRDVP
TTKIRASMALAPTRISAPTPSMATSTNSSILQAAAPLFTSTSNNSYLDSSTVSQPQRNLP
LRDCDHGDVASHFSVGSPLAVPVERRSADADKAAATAALIQKYTLEREENEQRMRQTLRD
LEQRQQQLLYSVESGAEATNNTDAPPTRKEGRNGDGVKVHDISHASSAAASSSSLATGHI
SSHSSSARASTAAPAPPSRLLLLQERFATMPIIQ*
>TCRU_1308 TPR repeat, putative
MHRQESVSSGGGNATGRGSLTTAEVLDRAMNQCMQRGLFDTASWLGQLALNATDSVLRDS
ISATSPAVAALQDPPLTGRAHRYLVVALSLMQKGEYIRCHHELNIALKEFSAESKPEESE
KCARDNPPMSRGSGRSTPLPPPSSSSMLPPPQLQFLCLYSLYMAGECIKSTSSNPRKSSN
PHLRTLRGRLLTLLEQQRRSLSSSPASIKSSMRPAPLSSASMAVGAPAYGDPFLCWLHGV
VLRELGMKQESATYFLAALCNHPMLWCAWEDLCTLVSRENQIEEIEAIIASLEPRFMSEI
FLASVKAALNVAPMSLVPPSLSTAAAAAMAQRSTSPHCGSLPRQPTSALENQEQHYRPQH
HQRRGESGVSPRLVNSWEALLERFPNNLFLLANLAGYYYNVKKDLEKAQSLYKRLHEMNP
YRLESMDDYSIVLFLRGDRIGLSSLAQQVYQIDPFRAESNYVVGNYYVLMGAHDRGVLHF
RRAVAADPTFLAAWTLLGHAYLETKNSAAAVEAYRAAVDLDPRDYRGWYNLGQIYELLQF
YHHALYYYWHTTTLRPTDPRMWSAVANCLDREGRTGEAVLCLERAEAYESSSSDYYPPLV
HRLGLHYLGIRRLDRAVIYLEKLVFSEARRREDVLFAIPHVVPYYLQQARQLLDIPSRSP
SYEPQPHHSTTAGGGDGQLPQTMASAIGATNASTGGNVYRSSLADQWLTADAAARRNIET
RWEQATLCLTSSERHLENFASVLGIPVASAADNGARKSTEYGDTGVSGSGGVAGVTMDEG
RSQHTLQLACLYRELNKIRQYLTSQQEQVETAMRMRGEETHRK*
>TCRU_1309 hypothetical protein
MRFDPQQQQKHQGNKDAPLSNGHSQPFKASKLSLDFTGTNDSAPMKAATVQEIVDQQDAD
ADVVRAGRCCTVVFLPFIVVALLLGTILGVSFTNGRALDVEGVPRAVLFIIEGFKGTTFN
ELLEGQRLPHIRQMLLEQHGVYAACASLEDVRCARAVLVEDDVTGEAFISAGAGIATILT
GVSPRRNGVRNDTWISYAALSSTSVQFPSVALRVTLAKKRAAALGGPHLLNGLDARTGQC
NVPGVLDAECVTPPVSVNSVDANEFNRTQPAATLTDGVDHFDIPPMMTCLHLKSCNLFKR
ALTLSSGRDGREEREFTRGLIDLFGGLSREGQEAGNSYDNSLLIFNLNALALRAGEENLP
DFTYDRGSLEYAAQAFLIDSLVGQVLAFVQDRARSRKENWLVVGTSNHGGVGKSFGNFGD
EDEVVPFFLATYTSNRRGYRRLRPLTRPVTHMDAAPTILKWLGIAPYDEDDEEEEKQNYL
EGGDNTDRREETGWQHNDHDQSKPAASKTRNSPSNTGDQRTLLDGVPQGICGSGLRTKDC
AVVGEE*
>TCRU_1310 BNR repeat-like domain/BNR/Asp-box repeat/Concanavalin A-like lectin/glucanases superfamily, putative
MKGNKVFLLAGRLYKHKQIVGNWTYSGFKTQLELVVGDVTNPTGGEPSKRIKWGEIQSPL
NESAIAAHKGNLTRFLAAGGAGVVMEDGTIVFPLMAKSGNGGYYSMIIYSTDNGSTWSLS
EGISPANCTDPRITEWDGSLLMIVNCKSSQRVYESRDMGTTWTEAIGTLPGVWVNSRLYF
WDLSLRVEALITATIEGRKVMLCTQRGDFSGEKRERALYLWVTDNNRSFFVGPVGIDTSV
EEEFASALMYSDGRLHLLQQRDNGEDSALSLSRLTDEVSTINSVLKSWAQKDAFFSKLTI
PTAGLVAVLSNAASDDTWNDEYLCLNATVTNAKKVRYGFQLTEPDSGVMWPVNTRDNNVR
HISLSHNFTLVASATIEEAPSGNTPLLGAMLGDTNSNHTMGILYTADNKWETMFKGKITK
SGTWEPKKGYQVALMLQGNKASVYIDGESLGEEEVPLTGEAPLELLRFCFGTCGEDAGRK
TKVTVKNVFLYNRPLNSTEMAAIKDKAHTSNGPGEALAGWAALEGAAAREHAAVVGLTSA
GSGLLPLLLLLVLWGFAAA*
>TCRU_1311 syntaxin binding protein 1, putative
MPRPVRLCLLLLLVTASNTDELTEAKKQQLIRDGGLTPDAHLFANLEHVTRRAGSVQRYS
TASAHSGRSTSASASNAATDEDPFLKHACMMMETADRNRTLRVGLSLTSVQRDHAMGPNG
ASGGQNSGAAGKNAGIFQGCGGKWGIILIWVAVVVGRLPSQLLSAFCCLFWVVWPAARGA

RSMRYPKGMAVRWSLGSLAAAS*
>TCRU_1312 Tryptophan/tyrosine permease family/Transmembrane amino acid transporter protein, putative
MTNAPIGEQIDDPLNDGVELVEDLQGQAGLPTGDRMDVAKIRIEKLNQERQERVARRRDP
QSCLKRGLHRIIPYGGIISSGCNLASSSLGAGILALPYAFNTSGLAMALVYLVVVGLLTI
YSFTLLGIAGKRTGLRNYEQVTRALLGKGADYFLAFLLWLLSFGAEVSYVISMGDVVEAF
VQNSPSSSEYLKSSSGRRLLTSMVWLVAMLPLCLPKEICI*
>TCRU_1313 amino acid transporter, putative
MSPSLPVVVSVADGVAESSGFYDEVFFTEQEPANTDETTCENLVKTTRVTSTLSPAEQRI
QELNAMRAERVARRRNPDNIFLKAMHVVMPYGGILSSAFNLASSTLGAGIVALPAAFKMS
GIAMSILYLFIVASMAVYSFVLLTVVGERTGLRSYEKVTRLLLGRGADYLLAVLMWILCF
GGDVTYVISMLGIIKGFVNNAESTPEFLKTLPGNRLLTSIVWLFFMLPLCLPKEINSLRI
VSTIAVFFIVFFAICIVVHAAQNGLKNGIRDDIVYIQSGNQAITGLSIYLFAYVSQVNCY
EVYEELYKPSVGRMTKSAALGTSLCTVLYFVAGVFGYLEFGPAVTDSVLLLYNPVQDKMM
GVAYAGIIVKLCVGYGLHMIPCRDALYHILHIDARLIAWWKNSLICATMAFLSLIVGLFV
PRITTVFGLVGSVCGGSIGYVFPALMFMYCGNFNARSVGWGHFIGAYVLLIVGVIAIVFG
TAAAIYSELQNG*
>TCRU_1314 hypothetical protein, conserved
MQLVLGHCGVPRNEACDAESEKASDLSQLTDTWSTGIVALAERIIRARQLRTEARRSTAA
GDWEATHTDFILTRGEEAALARLRS*
>TCRU_1315 MSP-B, putative
MRHTMLLLELLLCCVSGSVAVAEHHCISDEIKKKFGSRTTAVVLELPTRGGGMMRAMTAS
APDWAPIRFQFFTEDLNDPSRYCTAEGQIRPDFTGKTVECKSEDILTEEKKSIILNSLLP
RALKMHTDRLLVEPLTVNVTVPKFHLGLCAQFTIPSSHHTEGVFGADMYLYVSAGPIKDS
TLAWALACLELATGRPVVGVVNYGPSFVTDSEYSVRITAHEIAHALGFSFCMLIERKMLK
EVEGVRGKARVFQVSSPKTVEKTREHFNCMSATGMELEDEGGLSAALSHWKRRNAKDELM
AGHSGIGYYTALTMAAFEDTGFYKANWGKEEPMSWGNNSGCALLTEKCVINGVTNYPEMF
CTARSSLLSCTSDRLALGRCTIHLYGFSLPPQFQYFSNPELGGLPDRFMDFCPYIEKYVN
TWCSNGNATVMRGSRVGPTSKCLKGDGLADSEGLVGDVCAEVSCDKGEVSVRYLGDDAWH
KCPEGSSITPTGLFTGGRILCPKYDDVCIVIDTINGTGDVSSLLSAFSPIPLIMLVLIFI
SMC*
>TCRU_1316 NAD(P)-binding Rossmann-like domain/Flavin containing amine oxidoreductase, putative
MVELLTPKIVIIGAGPTGLGAAVRLTELGYKNWHLYECNDTPGGLSRSFLDENGFTWDLG
GHVIFSHYQYFDDVMDWAVQGWNVLQRESWVWVRGRWVPYPFQNNIHRLPEQDRKRCLDE
LVRSHARKYTEPPNNFEESFTRQFGEGIADIFMRPYNFKVWALPPCLMSTEWVGERVAPV
DLERIRQNIQENRDDLGWGPNATFRFPQRGGTGIIYHAIKAKLPSEKLTFNSGFQAIAID
ADAKTITFSNGEVVSYDYLISTVPFDDLLRMTKGTGFKGYDEWPAIADKMVYSSTNVIGI
GVKGTPPPHLKTACWLYFPEDTSPFYRATVFSNYSKYNAPEGHWSLMLEVSESKYKPVNH
SALIEDCIVGCLASNLLRPKDLLVSKWHYRIEKGYPTPFIGRNNLLEKAQPELMSRCIYS
RGRFGAWRYEVGNQDHSFMQGVEAIDHVLGLATEETTVANPGRVNGTRATTRFGLLQKDM
*
>TCRU_1317 hypothetical protein, conserved
MKASSKSGARAISGAEGTLAPESPLAFLVLWMRALQWHREPKKQFMDLGRIIPRAFRMRI
VIKFDPSIPIQKLPARLHTAFHGDDTFARVAQPFKDRRGTRSRQQRSLRCQLCLIYGHDA
STCKVRPKRVFPNYKRKLKNGRRAAARRSLMPATAAAPNLPPPAIPHRHRTAPLTPHPVV
RAADEIGERGGRDGLRNVGDVKLGAENAPGGANLKIWLHARTGNQQGELRGLFGGNRSGA
IDPTAVRQDAAVHVGNGSNSAGYGASGVAKVCGAIKGEASAPPDKGRGESSNPQPDRLEG
TCCLTICVDNGEPLVRDCGLDPNNFTMERDGTLILYWPVAPKTAKADPHRASRFVKIRGQ
DAFDTIKLCRTLQKNKGKLTNLTTAQEERALAPWKVTAHSIKQGALRHAAPIVETQNLDP
HVISQLAKHVNPFDLPQNTV*
>TCRU_1318 clathrin coat assembly protein ap19, putative
MIKYLLLISRQGKLRLAKWYVAYPKKEKAKLVREACQLALGRSARFSNVVEHRGSKYICR
RYASLYFVASIDKDDNELIVLEVIHHFVEVLDRYFGNVCELDLIFNFHRAYFVLDEVILG

GELEDSSKRTILKYIQVHDGASEEIEQAGSNGAAAAIAATVGALKIA*
>TCRU_1319 Degradation arginine-rich protein for mis-folding, putative
MPPRRYLRNGAAPLPWLLVLLWMAFMVTAAAAELTEADFKRMKIRELRDFLEDRGLTCPD
CQEKADFARYAYQNRDKKPTSEQGKREVPNASFWEVWRDIAKEVCEEAVKKRGLDVSAEP
QSEVCSALAYVTESFFLQHGKRTAGKLRKKPEALLKTSFKAVYYDAGRVLLGRLADHCLA
SAGNQNTCSSMSKLMALAEESKIADLAKWMTNVGIENTNPMYEFIDQRDDL*
>TCRU_1320 BNR repeat-like domain containing protein, putative
MSRRVFASAVLLLFVVLVCCGIGGATPANEEEVKNELINIQNLERVDLFVPQKTLVLPKG
GTGSVTTRDSFFAPSLVNAGGVIAAFAEGHMNAEYQGGQLTKPSSDVVAEYIDSAWEWST
LVGEVSESTWKAHTVLGTTDGTNRVGVVLRPTTTMKGNKVFLLVGSSAVFYESGGNWS*
>TCRU_family, putative ribosomal protein L4/.1
MRRVPLAVCLPSACARRAIIFSTRYDWRTSGVHDIAPRDEGDFVYEGAQQVLPGAHPLPL
YHPHNTVTRPLISPYLPSPQRSHPYFTEPLPELPHLNTTKPVVYTCGTMKERIIVPVFNL
KNEVTHTRELDPFVFGMYPETEELSKNLTYWLVRCQNYASKWDYETREIWRKAKKNWPNT
GMGMPRVSNRKNHQYPWGGRTKPSKPWNMLMPTMDVKTWSKSNRMMLTLKMLQGRLQVVE
RLTLSEPTQECYLGLCRTMSWDVRHTGGGVLFMDGGSRITPSIEFDRSFFFGSFFNGRNK
VVRPTLLCDEQYDYNKTASKQRMKGPKGPKNPIPINRFNVFDAMQHERLVITEGAIMQLE
EEMYEHKLHLLPPHIRNQLPERGYLDSETLGDCVPSLRTIQMEAAARTEEMESGMYQKFA
DNPYQLWTDEAHASYSVDAADGTIQQFIGGKKSSWSMLS*
>TCRU_1322 tRNA pseudouridine synthase D (TruD), putative
MKLASKGPISRWSPRNPMTGAFFSRNDWRSGRDLSREERDSGLLLRLRDVGGRLSDATLP
VAVVKAQSTDFQVNEIDANGRVAALEKAPKGKWRKISRQKTVLIEDNAEISFGDPTKTFS
PRVQSYGEYVRILGKLPREFPILRFVVYRDSYSLLSVEKRMGYVLSLQPGSTFLRESSGG
SFGCISQYGVCVGMTREFLPHASRQFNLHPLIFNPQTYHTQDDFQDLLRRPAGHYYRLVL
RCVDGDPDTINRRLKMLVEGGFVNYFGIEAFGVGSNRLFEVASFAAHGYFRQAMGALLQC
VAECDGVHHDYYIKYLNADPSTVLGVSQLWADAAKHMRSQKWLVDLLKGVAKYHEDGEKE
EHLRILWDSLPIRDRIQGSAAEFVWNAMASQRLLSKGLDVVEGDVVRVPIPDSHFAVGSC
SSYQYKLVTAEDTRLGIYAITDVVLPVPYGNDALNNCLFPQIAPLDRELYGEFAAKHGLS
FLFEEPIEPCAFPREYYRPLVVRPGDFQASVIKDPNSFTCLKSDLSMMQERKPIHSKDMD
YVSRVREPCVYNVSERFVEKMGPIKKTHTGCYSVVLFCRLPEGTSPFVMLRESFSLRYAA
FHDMYGVL*
>TCRU_1323 conserved protein
MRVCQATHDYINGGRHYLPLCREDVLFILEEHPSGWWTAQNVKGEKGIVPSTFLREFVIC
PPFEVLLHEHSLILTAKRFSVDLSSHAPAPLNKGEVLLQWETPCEKTALTELERGIGDLL
VQRETVRQVLRESLKDLDRNTREPFNDEGNCKKNAVFLETKLATLRQRMNLLEAHRKQLK
SALRSLRDNVLLTKCRAPVRLIGRVREFLGEEPVPTSRIPPYLNSLHDQLERLHGDVRAG
EERLFLLSKNIHELECSCQEAKELLSYRISLRNSKIRAFLKFWSEKAEVAKEKYLHRKLQ
SLHLESLHQEEELRLRQLMQKRRAKYMEAEDECRHWKEKTKQTQFFLEEKATLDQLNQAI
QQVTEEERVWRKKLLSTRINVQEPNTRGEEEGKD*
>TCRU_1324 phosphoinositide-specific phospholipase C, putative
MGLCTSKCNVEDKMCRYAPAAKRLVDDFFAQDNEVLGDAGAFFACMWGASRDILLCSGEE
ATAFLRRACFSNPKSEEALNLYLSSSNFGRALWDLNRAKFMMIWMKYDADNSGDISLREL
GKLVKGLNFPADLSKQLIAAVKAAGGIVNYAFLEKEYFLLTRLKELEYVFTGVAGPGRET
MTRDEFKSFLRNYQGEELNGERVKEILDYVCCMTTGEVYFTNFLKFLEDNRFCSIVDEEK
VGKVYQDMNQPICNYFINSSHNTYLTGDQLTSNSSADMYRKALLDGCRCVELDCWDGFAG
EPIVYHGHTRTSKISFLSCIKVIKEYAFKASEYPVILSIEVHTSSAQADRMAEIMCDTFG
DMLFQSPWAPAEPTTFLFSPENLKRKILVKSKRVATSSAISDAEITENEEEEENDEEEET
EGEEKELTTSGPNPLYRQFKEEKKKEKKKKIKVALEKLSRVVSIESAGFKGTSDTSYLEK
RQPYQCTSFVESKAKKIAVSHAMEFKLINQHCLSRIYPAGSRVGSSNYNPQLFWNCGCQI
VALNWQSTHTYAWRLNKGFFSDNGNCGYVLKPESVRSSAASRNGSQVRSLNLEIISGFCL
PKPKRSNKGEIVDPFITCFIEGPDGNSDRKTSGTIRNNGFHPVWRGKGLGSEFSWDVKDW
DLSTLVVQVYDEDKKTRDDFLAECILPLRVLKAGIRQIPLHDINGNSIFGSFLTCSLTFS
*

>TCRU_1325 hypothetical protein, conserved
MASTYALIVSAFLAVANAVAAEDNQTSTKENKKEFPLVWVCLGVTIVGIGMALYIAYRRP
DELHLPGSTVMVSTEMEEASGNNEPTMRTKLNDDLEKV*
>TCRU_1326 hypothetical protein, conserved
MLDLVRQHGDAQVQLTFIDEHGPLDAVVAAAATMTGLRLVSGDIAMQLEGSTVAGHLANR
RAFQVPNFDVQVLLPIVWGRPGSWGASKGSSLRRGRY*
>TCRU_1327 Protein of unknown function (DUF3682), putative
MAMMMTGRVLLVCALCVLWCVAGGVHARDVDTNALGGCMASGVLGENGSHMPDGCNKTAI
TVPLRSVLPITAVEASAGKGGSAGATGASGGPGPGDAGGSGGTQKNSISSETSDAGGIQN
NSHSMKTSDTGVPRGGDSDGGSAAGEKGGSGGGGSGTSTDGHGTGSVSSGPSAVPAPAPA
APPSAPGHSGGPSAPTDATGVDSSPSGSDGEAGSSGTNSSNTTGESPTGDQTPAAAEAHN
STPAEGLAGTTSGNGHKGQEKEEEEEKEEENENQQQSDEAQVQQQEHEHPAESGEESAKD
KNALRTNATANT*
>TCRU_1328 EF-hand domain containing protein, putative
MQRESVVLQDLVPDVRKQQLQLQPRNTDTFSKPGRPLTEDEVLRLAQRYFISPAVAKEAY
EVFGRYTAMEEQRRGRMNGSTMPYGRLTLTATKLPMMTLPEVTERCLSGNLEVPEEKDPA
VAKEKEKKDGGENDGVTLWEPDTVSMKSTLCGEGKGQQQQQHQQKKEEEDKREGAQNNES
EKESKEVMEERLGIEGLQQFFNDLGIRMSALEVSDMVHDLNDEPIDYVLRLRAMEAAAAE
SQAVAAGSSSAGQGQTRGSPLSAKAGSSRRRGNSKVDLSSGKETELSAPLFKDSSMEGVT
FSQFLFTLSHMRLEREESAEMKECEMRDLFHLLDTDGDGAITVRDIQTVVQRLIDEEVLA
DDRDIQQLSEMNTIELEAALMECDVDDDGYFTLEDMYGVLQP*
>TCRU_1329 exoribonuclease 2, putative
MGVPLLLTWLKRRFAPCFLSSSSCPAADCLYIDVNGLVYQAAALATASEASAVDIDAAIL
RKLFDIIDDIVLRLVRPRFLVYLAVDGISPMGKLAQQRSRRRRRSGGGSRGRNAVEWDSN
SISVGTPFMSRLTEALHFYCASRAERINGERLRDELQQVARGNTTGGDVPVTPITFIVDD
VWRPGEGESKIADAIRRFRSQSTYDPNTSHVICSSDTDVTVCSLILHEPRIHVLRYECSP
SHHSGGASRGGDSGSWRNQVGDAWASTFFSIHAFREELRNKLRLQTSRKDSAEEAERRNR
QFERALHDVVFVLLLFGNDFLPSVGCRIEEGFLDDLLELLATDFISRDRSIIDPVTNTIQ
FDSARYALDSLAEMRRERACGDGLCVDNGKEGATDWGFVDDTFRKQRQLKEETELAPKCY
AYWTMLQWSLQNSAGVVEHWGCYYPYGTAPPLHLLRKYCGMLSYDALMELAKKRSHSRHR
GATSDSNAVETTDKLWDDGPGDVLVQLLVLLPARSTALLPSAVRNAYGEIEHMVLAPVEQ
MNFAAISAWCEEKKAMFTEEERTRFRAYALAARPHMLAQEVHGAPIHGSEMVFVADWDAE
AFAMEVQQAKSARLSEITTAEGLKKSENGATAPAVSTSSLFVSSFFDTRPARKASSAAAA
ALIAASKKADASDRNNRNEKSACSNESHTNDVPLTPAVTVQETRPRLSEEVEMRQGRGFT
LVTAPTEVLGDVAMIKNVGSVVGDTFVCGQHTSPPLSRNPRTMRVRLRWRVASKPLLTSA
TFVPDLLPGYITPPSLPSAPSSSSHETNKAVVKRPASAMNVSDSNSGSSDNGDYVDKKGE
VEEGKGDFSTCNVISELEKKKEAVRRRLEALQSRVGGNAL*
>TCRU_1330 hypothetical protein, conserved
MLISRKGVEITSNPSVCSTVGEVEFSKAEEINSARSFQVSFDSPKDRRMIDFSVYDITNR
RHTSKLTGFEIPLAGMCSILAGESMCEKKSISFRIDGKPGRLEVVFRMHPASAPPPPLKT
ASAGGANDSAAASGKGGETQSSKPSGRLPVRAVGALTKAGIFPSETEVVEMDNDLAQEIA
ARTALLFPEERDLQEKVRTLEREIAQLEYDTQYAAKDKVISGSAALTALRDELKHWQNIS
DEIDAKSAHEAGIAPILPAVRTAPTIQTKALIAEVEDQLAAAQAKMRKLEALQIHRDVSN
DVIPLLDEIESLEAVLIDLKKNTEEGSLEKKQDSGTEKYVDQWEQLAGMLYDKESVVEQL
KHTVLALNRLQFEPYPAGIEAGFAEEAPKELPFIRDNKRRMVAEQSLDAALFGNDSPPRK
TPQLPAANSGRHVDLLDDLFGGPPPPQPPTAQPSEQAALTTTGAELLSVQPSQDPVETYH
PPVAATVVPVWAQPPQPPSEQQQQQEQREQQSAPEPLTLESAAASNVMNTERVPGSENKQ
SAPSSPSATGSTKQIVQPGGPQNGDTSASADISATPAATVSGEQWPIPQRSGEGDLPALA
ASPLESQPQQTASEPYSPIQQAQGQSAQQSPQNYASLQAQGQSAQQSPQNYASLQAQGQS
AQQSPQNYASLQAQGQSAQQSPQNYASRQVGQPQQQVAPSEAPVPPFVRRPATLEEIPYT
NFYNIPLMGRACPLDIYLDGKTPTRGTELSILNNSDYDFIIGGVELKQEDMLSPSPDSTR
TVPTRRWPQQLCVPGGGSRATCIIALHPSFPRASSLLMLVVVYIFSNGRYTPYAARFAV*
>TCRU_1331 Oxidoreductase family, NAD-binding Rossmann fold,
putative

MAPSPKTRIRVGVLGAAKVLRETWIAIHEAKHEITIVGCRDKLRGEKFVDELNAFIPFAK
KPLLGDYETVVASSNVDVVYIPIPVTARHKWVLECAKHRKHVVCEKPTAVSSLVLQEWLR
HFAAKRLLFVDGTMLSHGRRVQDVRLALREIGKLRRMEAHFAFLASEEFLQSDIRLNPAQ
EPMGALGDVGWYCVRYFLHMVDFVLPDAVMGRVAQCSGPKNGISAFSGELLFTVEGEPVV
ATFFCTYHAAYEQLVRIKGDDGIITVYGAIKPTDEDVPTFSIERNSFEGSEGTLSFHRNV
EKRRCDEDYTFQMVQLWRDVGLALMRIDPEEPSVVVPEKSEQWARMAFTTQYVCDKLMES
ARKSAELASSLSLVDNNNGNNTGRKETAPTQTPAASEEVHA*
>TCRU_1332 hypothetical protein, conserved
MAEEAMDASTKPSSGVALFLCDEDAHTPAFAPIQLHGDITLKELAEEYCITSVLECDSTG
CVQPRAVALDSPLDTLRGGKYYIARRDLPRVGCSPRVTFRGKITVEEFEADHVLGRQQQG
KEKENYGPVALSASTTTAANSIAPIKSATRKRLRHDEESNDDYDEDEYEKGTNMDGDDTD
DDGVNMSDVMDVARCEFVPFVGDLYGDGREAMIRLEDAKRLCENVESDELMFAARHAEAE
EILAEAKRVLLELTPCGNTGGSVGINLC*
>TCRU_1333 WW domain containing protein, putative
MDVAVSSPLLESLYSECVPLIDIMQRHLRRSNGDHRNGGDVMNRYDGDEEIAFLSSVQAP
SELCLALACVSWRREAARRSERGPLLVFVPFHEPKDEVFVEVPVAAFGDSRRQRGLQLLS
LNEYSSLFANIKDGLPPRKGFFVTFRTREAQQRFREAMNHLIRAYSRGGPLEDRNRLLRA
MGSSPNVRANHKEGKFSEGGGENVPEAIQPSHDAVFMPRSSREAIRAASIIDSLLAERDR
RREEYISSIHSSPPRNGQNHKDIRFSNNPSGQQQKVNRGVWSMIAGTPERQVAEAGPRVG
EHNGTMITQSEPWQQRNAYSFSHSLPSRVDQEVLLNELRSALETYDNMNSAQGSGEMSLM
DASRRFLRQHQDYLRQIQQGDCAPDQSSSAARQDYTENSLHLVAATTQRPITMDGSSDEA
PQPPRVVIPQQQQQSMQQTTPVTPNLVKEAAETSVQKLPVPSQLEKPTLEPTEAQSEPQS
RLRDELQRALEIESRILSSVHNMAPKPLADKRIFGRAPKASLLSSSSLGIDEEVKKEDGG
GGSDDKKSGNTTLAFETFNVQPSLAQVEVQGDDASRKQEEGAAKEVEVKAPTCGAGWKSV
RDPASGKSYFVHIATKKTTWKIEDTFKDVSQEASVKEIPACGAEWRAVTDPNSGRTYYVH
RKTKATTWKLEDTLKENGGSFSADLTDLQQKKEKNATEWAERKDPSTGKVYYYNKKTKKT
TWKRSETDLDPL*
>TCRU_1334 hypothetical protein, conserved
MNILHRVLVVEFSRLSEPLDEKGTPLLLSWQSLRFRLTIAFSNVNGELDREGAALMAAMG
ESDFHLMWRKLFHTVRIVPVILGSAASSSAGKTQNLPEPESRATTASGLQHGVGCFFSFG
VPQFWENRAPAEKNAPFLASSVMATAGKILTVAAEQCDEAVVAPAEVLKAEMPKPYLKGA
VPSHLHCTYTFSYALPELEDFHGPLTLGFVLLLSFPNGSGKGGTDREGDDDFNDDVLLRA
LVPVEDQRMAWYRPSYVVLGTCYYRAHVSKLLCCSSEARRVSRYRVLVNVNVVNIAGISV
RVQQVFFDIFSTWIGNSLGSLSSVPLWSEQRAGPRSGDLKYIELLRRVVTVTPVVVHEFC
APVMLEPEESMNFQFAIQLLPHLCYLFEPNSLESVYGKFLRGYMEDVAEEEIKTVLSSPS
GPMHISSQRITTSSTSVGSLKPVAVATGATDEISCEELLQLMSFTFTSHVYVYYEAISPT
SKACSEEANRSINGDGIYASLQLRHPVHWSMGLP*
>TCRU_1335 Poly(A)-specific ribonuclease PARN-1
MQVTRDKFPAVLPKFVELLKSCDFYAFDEEMTGISTAELPESITDTPEESYRAKRTVASR
YNIIQVGICLFHRENTAADSTLAHYVARPFNFVLFPHNSDEFNANERSRDVVLSPSSLAF
LRRHDMNFQSWVYQGMAYCDANQEEALRQRHEEKYRELDSIRNEGNQEVEGVSLLTEEEK
KWYDNAVTLAKTFSERIQATLEQAKVKNAGQTAGMAEVSAALDLIQSGGREVFLPPQRSK
SAREALERHVEQHFHNLLLTFRRQGAVHMGMLRAVFPEERNRLREKEQVFREGELMNMLG
FRLVFNALVESRKPCVGHNCLADLLFLLASLDGPLPDSLPKFKRRMNELFPIVFDTKYIA
SRQQFFPLERFGARYLSGLFGEYGFRSANAHVTLPLGFESYDPLAVGGGERHHSSGANAG
GPTHEAGYDALLTGTLLLNLLAEMGGYDVATAPECVVNRVAVFRSLFALNLGAPDEDEYL
PESGVLELRHEKRVKLHHIDSCFTALSLQNIELHPVDETRTLAVLPSTWSKMESVEERNP
GWLSTHMTSRFPQFFEASVYQPTRACLGANGAFHTTSRALMRIILRSAMR*
>TCRU_1336 hypothetical protein, conserved
MQDTSTQREAHETYDCTGDTSSGSLDATAHSIKRGALRHAAPIVETHDLDPHVISQLAVH
VDPFDLPQSTVRYLGSYTTMLTQVLPLVALM*
>TCRU_1337 retrotransposon hot spot protein, RHS3, putative
MPSERNRVQGGNTKGQASVVPQGDSQRRARSDLEGDTDQPAATCIRVEEAQLRWTMCSYV
SDILLDGETDISDMKLNDFLREHFGSRAAVEEEQNVGMWDFLRSPDAYIKDQQLLEEISN

LKGYQLLTDRRKLEEGNVHNLEDWIEFKKKDTVTPPTRKKITDALTQIRKEVARWKAEER
AKQREEDVMQDTEEKTTKLEGFYESVYGAKWGHVLGFYDNKICEDRMEIHEGKPPQSWTY
KTEDSIFEKDDGVEQFRAPRPRLMVLTSEKGWPYSWRENKPIVDCYVNCEVERVWRIVKD
DLKDSSSPEQRVLVGTPGIGKSMNAGSYLLYQLLHCDAKKIKVVVHCFGEDKAYVFDKTA
KMVTKYVGSKASRSVVSSFPQCGMKGYIIYDVPTNEAQLPISFTPPTGWGTTVLASPKVR
DIYEFLRQRDSRRIIMNCPDEMDVKAMCAWMKRDETPQEQEKYWWMVHRQMLFLGPILRY
IFDAKDFSKRYDELDCVLRSVKSRDDIVCVKHEGMTAWCTENPFYKLMCVKREKGEFGAE
AFKTDLLSHHVGRRAYPFVEKIIPLKEIFGF*
>TCRU_1338 folate transporter, putative
MATDDSAPPRFMSAEETVPARSVHIDARALFSALPCLRRAPIFGTSVEAFGPKCVLSMGL
SEFLCKGVADFLIRCSLFPMFRRRYGVDAMTYQRMANLASMGWSMKPITAMFSDIFSFFG
YTKRWYLAVSCVVGAAFALAFALLPPAKASAAPAAAFVFLTSFTKANVDILTQGHYSRLI
RRIPLAGSSLVSWVWWWVLLGSLVASVIAGPLADASLEWIGVIVAATLQFVTTFFFVMNW
YGENKNRVNRAEDAKFMRAKLLEERRDSSKRLREDDDTAVAEMGNHSMLVLSDEVCAGVP
GEEVDEVPPLPTCCCGVFEVNKEVARRSWRIVLYCLLVAAGSVVMAIVTVLGDIWSLLYA
CIAVSVAVCVFGFFALPLVIAKANLYTFLSMASYIQLPGALDSFYMARPDCLPDGPHFSF
FFYNTVASIIGNIGGIVGILLFRYVFSKKSYRITFVFTTLVMVVASIFDLIIVERWNRPR
VSDHVVYVLGDQVVYQVCYMLHFMPGIILLSRLCPRGTESMVYALLAGFANFGQAVSNTV
GSLLMEFKWPVETDPAVGCDFSNVKWLLIVGHLLCPLVCIPLVFLLIPAARICDNIDVDG
RVVRPQEPPGDCKVEGSRESLSAQEPVLK*
>TCRU_family, putative Se.1
MEHGVTLLEDPMTPRQPIMSGPAPYFFAVEDASVSRVAEDWMATVPHRNAHIFALGCTPH
RSPQQLAWSRIAPRAMRFKDIMLDFAAPEVLVFHLSMQNGFPQLLLPPN*
>TCRU_1340 syntaxin binding protein 1, putative
MPRPVRLRLLLLLVTASSTDELTEAKKQQLIRDGGLTPDAHLFAILEHVTRRAGRVQRYS
TASAQSGRSTSSSASSTATDEDPFLKHACMMMETGRNRTLRVELSLTSVQRDHVTGPNGE
SGGQNSGAAGKNAGPFQGCGGKEKNHPDLGGGGGGGTIALTTPQRIVLLVLCGVACSERR
SVHEISKRYGREVVIGEPRCRVLSLLCAGTWHPTAL*
>TCRU_1341 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSARATAGEVKTGEEVNVQVIVSEVLNKLGGEHNSDTDVDAL
RTGKAASGAGQNDNGTPSSNSELLVPIIDTLKSESPKDVQEQALDGVTETAKEGKEKPLN
PEVTDTSDAQQSTSLTAVRKVSENETTAANTTTTTTTNAPTTTTTTAPQATTTTNAEAP
TTTTTRAPSHIREIDGSLSSSAWVCSPLVLAVSALAYTAVG*
>TCRU_1342 hypothetical protein
MQIAIRVQQVAGEHPIRSIVHDNRSNRKRAVVVRDPKAERSGPFLPRGVPSLSVQCDSPF
LNGRGHEGIHTQAFVPGSSWSCVDPHDLGCPDGLRPRRPHATRLVHPLAIVSMKNHEK*
>TCRU_1343 hypothetical protein, conserved
MPVQRQAPHDKLSAGTPERNGAVHHDGSAASVLVKRQRALHELRTARVRRQRQEPAADAV
AAHRQPRPGHERRRPPQHQQRAIGQRTGVVVHHDGGRVGLHTALEQQSMRGVHLAPRHAQ
HSALRRNHARTRVQRIVATEHSRVQRDTATDKLQHGAVHHHRPPTSHHRHEGNAGHNQHG
PHEPQTRQHQHRCVRRGPRAGKIHKRRRPRGNQQGVRHRQHGPRGERAGQHKRTVQRLHI
AHRQLHRPALVAPRRHRTAQASTAHHVQHGAVQQRHVLHNNPHAVPRHPRHVEHRTHAVQ
HNVAQRHLARAGRHNEHRPHRHALTDKQTRRSAHSGRQRGSTHRHACLAVPAAAAHALAH
TVLHAGRRRPGRVAVRVPVAGVAPSNVDAPSVAKSSSSVLLRRRQDTSTRVVARHPHMRP
SRKRQAQRQHPRQQRSVAHKAQRAPSSGHGASGVEHLPRDAVVHVALRQQHRPAIQAHRR
IKRHRVVLRQRKVAPHKRHGGARHAHSPTHTHRVLAQQEVAVNKRHNGAAAGRNTALHRH
AQPQRRLHRQSVHVQRTT*
>TCRU_1344 Leishmanolysin, putative
MAAREHHDCDDIDGMELQDGDGDGRTLDSHWSQRHANDEWMAPISCVVCRTELTLAAPAD
LGCMRVKWEMVEPMRWWRNSCCALLQRKCSAPNMSEYSQMFSEAGVHAGRCTLDRYSSCW
CVDELSMKGQQNVRWTVAPSLVPHWM*
>TCRU_1345 hypothetical protein, conserved
MAAPYPHPLESVVLRADIDRICALSRQKANLLVRHFVRVSRATSPYAATVRRAPLLPGDR
EMDRPLTPYEIDVTIRDSSLGSAAGPDNMLDEFLHRLGPVACGTQLER*

>TCRU_1346 hypothetical protein, conserved
MRQLVHGNPWLAALLVMFVIRLSSGGVAVTLTHSCSFLDDVVRADGAWATPVVVRDVPLT
AQDASRVCSVVWKKQWALVRKKASTKIPDDSRRHCGFSWAPAMNSHIVAVLGLWLHTRTP
QQGVAASTTETKTTSPLERVPRHARCGELKRSLR*
>TCRU_1347 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGACGGFGEAPTVSVPDLPTADTVAQGITDMTGDAGNGGPQ
DGKEKLQGETKPEVNVNNSENPAGTPSGVNAEEEEDDKEETEEEEEIREDEHNVETEPRK
DQGEEAEDGPGVPNVRPVASAQQHLQPAPSTGSNSPSGSLETTLQATQTGLQQSADTPNN
LPTGNNTINKETGRKTASDKIAEETSPSSLREGVVDIQKDAEGNKEKSENNPHLPATAAT
VQVHQQDGKLDTINETILSGETNNKENMQQNDSSSTSVEAVQSDAGTEGNPTANELSRPS
IEDATPISKTHDFNKDSDSTENVASETAGSVTAPNTDSKPGGTAMPGNSDSSTAVSHTTF
PLLLLLVVVVVAVLAA*
>TCRU_1348 paraflagellar rod component, putative
MPALSERDLSGVEKFSNAMKAALGRQSRQVNLKDTDSQRILSSNPSASDITEMILSERRL
WAEAAVAFWRLASRQQIHLLSHVSTGALRELHRFCEGLLDHIRITFLSLAPTATPLQVLD
CVSSLGTDHILFLLDTFCSPKGCISMEGGEETRGRELHTHVCRVLAEQDHLYWMTRVVRA
FCDESWRVCSEKDEMSRASVSAIHGMLRCLHHCCATSAACAHALIYTEPRPLVAQLLYGL
RLRISSSTLIRPVVRDDPTRLGVALSSTPSLPTPTMRLPATKSALAEYLTSGRTNAFDEI
SREALNVAVAAVKRVAAHETPEVVIGLCHIVDVSSRSIVPSPKDEKKPSISTQIAMYENV
LMALEALFQLLQVKDDEPWSQELVLRQEIVLQQILNHDLARAVERLLRHCPTILDADSTL
FQSIGTLCTPPFTSSRRRRRQSTVSRVENSTQHVPGNGDSLSGSMCSRNASMVSLTSSIH
VSRPALPEGSVARASNLARSLWMSVWPGASRGSGVAGLTHAHAASRPAPSDDEPIGSFFQ
RGTSDMIFDHAPSPTCLSLDFDGEEWWYSNKTYVNLLLSLTQLLNAMFSDATTPLSIRLS
ICKLLTQISMRSSSAFAASEGRLVMRSFLTTLRAHDQGLCTPSVEIHDVPHVEEEKNKKE
ISHEIHLQTHEQSSEKYPCTSIEDDMLYAALAQKIVAGLWHVYHVLHMIPLSGETVDIIE
LPLLSLRWRGEVKEAEEEKVEEGATKSFGGIHKAVLSLFGPVVRVWYTALMSNDDEDLNK
RSQEVFMEVLVRLLKLGGVPLTTMDFLRASTVSIPSTPPTINFNWVASHSENSSFASMEK
DASRAEPSDTIKSMRSVFVILLQRDPGFLSFELLKVLFALLWANDAQLSELGRKCIASSL
DFGEVYPTYAKVIGNADSSLLIQLLLIFSAGLVSSEVSMDAKHERRAWLFQHGCVNAVIA
VLERVLRAPHDVQSFPSLIRQLFCFLSLSESAQGRGPKLEDTRLVHVFTESLHFLEGAEY
LILITQSVLDAATSKYDQYRSRTRRINTHGHFTLPIPNCSVEKPIFIDLVPPLLCYAHEH
AMNVENDLLSALHLVLKMTTNVRSDALLKWALQRKHTALLPYLDLDAAVADRVLPYFGNR
SDIESFWTPILQEAPERTELRFSCTGGIAVTLGRWPEKGFSVSAYFRFEEIYSDIQLFEF
IDGEVLSPSLASIRIAGGDSVNIMHDGKRVPVNEGHALPDLEPQRWAHFIVVMSMAHTVS
VYLNADKVGTCSLPYFRSHSEVVMNIGFVNTTVHDSLFSIGEVVLWDEELTTPQVEAYVA
TTGYKPNVCKILECEIPRELSETHEKLPIEDRIAVFSPYETRDSMLVDVLQKESRGYPIL
AKLTGTYAEAPKNWIDYRTLFLNRGGLVYMLEWIAASTSAEELERYMALTCNCIRGTTSG
GTMDVQTYALLDFHLRCLAHLITPAVCDSLLHLATAKMSVNDEFHPFIINRLVFDHIFRD
IELFADMPLDAALYLIEGVERLFTVASCRFARRNAYYIIPFRFVDSVLNGLVYANVSLPF
VLRGRVISCLKHIMIATDFEPNIVHVIASTAAVLTPVEMEATSRHQPALRVKIPKARFSQ
ISVTLHGAFETTCLILRSLVECCCNGKFAAAFGIIVDLNWYAACVSRFADVACVVYATRL
FFEAMRFNMDLRNEVMHHPAVIVHTLSPHCLNEDLLLLLLSLSVGAVKRIDVLSSKHPML
QQLVGILDSMTPELDAVVLPIFSKLLTLYLTAASSTPACFRPSDISSAMQRRLYCSYRLH
KYFSLARVCSILMLQIYARRLPPQAKKTGHLVSVSTGGRSIPLSLKKDASKEDVTAGNKK
TPVQFGRYRRAFAALRVCLYLWKAIQRRRYRRVRQQNVSGHTPLMVSDVEPEKALFILRT
LQSLPLKPGLFVPCTLSPYQIEVLAFFGTFLKREAVSARFEEKLGLHEGEDLPFTASTTS
LHRLIKENTTGSDFFPPHVKIFDESHLLPVLHDTVNEEETKHDDDGDGDEGDDDSTVEKK
EQGGKWQHGVHQQNKWVEREEKFRVKSEKYFENQLHMPLTASAPRELHVRQTSSCTPNSF
LHGDGDVPKSPPLAATPVSTEVASLPEDDDAPAASGSGSRVDQMTDAATSSEEDRHLSSG
LEQLFLPVEETTLRSEMGGSMSADVSMGSFAPFAKLQSFNAKSLQECAVGVLCNTVLASL
LNLPVTEGWVGGQTYGSCGALLFQLILITGAMCSTEEVTLTLTQFFIDQLLVCVDLSERF
VEPNTSVVSSPKGSGFENSARSFTSLPGSVSDVFIFNICRLNDLLVQFISFDVMRLSSLS
PYFVWLLGWASSSWPQRSQQQLRSQIVKSCIAVLNKPSPNGVTHEQMEIVYMLLQRVLCR
QWIMKDMLECLLRVLFRVYASLPPTSINEAEEARRKELVILTLRLLMRTYEGCKELHKAL

SASALRQRISLYKEFAATLLIEDEAISVVAFETYCKENMTTIHSFISGRPKTKTDMAYKS
MLKERCEYVKRINTFKEAYSKTINIRDKYRPPELVQAYTARFSSCVDPISPLKVSQLHWL
VKQQCSLQQNDPRVRVLNYLDLRGNYTTVISNHVSKDAASTVLGTDNCEQQHNHISTLVQ
PFAICCRPYILHTGTPFVDISCCVTPSALSLLRYLLEPNEVLRFISNGFRIHGIHATPCL
ILLTDSSLKLIGFSRITVEGDIILCQRENDEREEPVLPVHISTTKSSKNKWGSQLTASSF
AASMTNKLQRFLTDGGGKKRRRIETEKLHDGTKIAHSVRQASGDSYRDLFWVYFLQNIRS
VRMAYYMHQDTAILFELMYDDGPMLSLVDTHQSMNTSARDKFLAVLKDVLGTQRCEFFDH
SQRTASIRSMLIRWAAGSVSTYDYITFLNSVAGRTRRDFNQYPIYPWVLADYKSSELDMD
SPKTYRDLSLPMGAQTEERRQKVMQVYQQMVEVQKADPDFEGVQPFHHGTHYSTSGGVLH
FLIRVEPFTTFARIFQGGEFDVATRLFDSIDASFQSCVHGPTDCKELMPEFFFDGMFLVN
ANHCEFGEKSDGTVVNDVRLPPWAKGSTQVFISVMRYALESNFVLQNIHRWIDLIFGVRR
CGKLAVESYNVFQRMTYGEEVLQALKKCDNPHDIDVIIAEVDNFGQTPIQLFQERHPAQR
ELKPCHPMLSTGGTGGAHCTTGGNVLCSGNTYTTAFQEQLPKVLSMVMHALDSPQTWYTL
EDPAPGSFQAMPKSVSDAFQIHESPVLDFVTTRSGMNMCCYKYSLPVDDTDHIICWNHSE
HMLMRFDNTRGHFLSSVRCKSVLRIPASVSAFCVSCRETLILIGSNSGTVYCFSHSRTDG
VLVLSSTLCNHTNPIAGFALSIKYGRIISFTTSGIDCPTVWCVQHCHTVKLHALDLSRLL
PLTTPGDLIVVAAAIDPINANSIIVTRRHLLLFDRNGEPYGVGTLPNADKTAPHLEDEAG
QVGFAVDDSKNFIASMTAVTTYETLEWASGIQLLITGHQDGSLSLWRAVRLPPERMEHGR
IVLVEHHGFLFTGSQTPRLGAITALRQERPDVPVFFVGYHSGAVKVLRFENRTADMTKMT
TS*
>TCRU_1349 GTP-binding elongation factor Tu family, putative
MQGGGGDGDTPPCFCLVLAEPETLELAEWVRDVVAERLTPPVTGVVLRNVGASSGDEYRF
HAAALLSLGQVAADIIRPTGGTRNETAVTASKTVKAVCLVIAVFWDGQSESVKAEFTRLR
ELSDVKKSTDANEDKNKNAEKENDDSQLSQLQLSETQFILQALSAKKGEHTLKENSEALV
SSLRKKLTFSTAVRYVDPQNSESLALSRHMSGTSCNGKGTVIGREDFSESSIAASITEGQ
GECFFLVSGRSMEEFQQRVAQFQESVRSLGVGCMPLVEGPRGIQETGSNDVNSNSPIRSN
HGSGGVGNGAGNKRTKIIAQEFLVRQSESETHIDLRLAMCGNVDSGKSTLTSVLTRGCRD
DGRGSARAFVFKHKHEATTGRTSSISENFLGLSSTGEVVNYTIPALKRLGGGGGISAGQL
AQEVVAQSAKVLTLYDLAGHERYLKTTVLGMTRNMPDYACIVISANNGIQRMTKEHIALC
LALRIPFFVVITRIDSTPENVRQETLKSINKLLKIPTVRKLPYPVRRIEDVVLSAKNLRI
DRIVPIFEVSNVTGDGIQDLIRFLNLLPLRKDWRKARMQPREMVIDSTFFVTGVGTVVGG
IVTQGIFHVNDAVLLGPDSFGAYRTVHIKSIHVKGMEQQEAVAGCNAAFCLKKEKRNAIR
KGNILADPHHPVAAYWQFEADVTILYHSTTILVNYEPVIHSATVRQSARIVYVAQEVLRT
GDRSLVRFHFLYRPEFMKVGQQLIFREGRTKGIGTVTKVIVDRMESLLAKRRPR*
>TCRU_1350 hypothetical protein, conserved
MSSSKTVTRGRFLAPFCKVACKIEKRSARKLNAVDACIAKTIAEHNASGTDAAVSSTKRY
IYEQKQLFHYRVVRFFDECRYLASGEYFRTYSFKDFVWDIRFFTKFLLLFILGTLFGRQS
IFPPIDPDSPLALALETKVNPNY*
>TCRU_1351 transcription elongation factor s-II, putative
MVPYPVYEPFDRVWVKMEGYDWWPARIVSDEELRANGQSRAEGCDITVYFYEGTTTPASL
EHFKSATTSITFFETSSEKAVTADADLLAAIRRAETDETANPLKYEFAAGDRGGGNKTGD
GVAAGAAAVVTATGASVSSTDGMRRGTGNAAANQRPVSKRSRAAELEERHVAAPALNLLR
DEKLIEIAGRINEAVSICDLPSLRIELCDLDTVSVTVRQLETTKIGVAVGSILGRKELEK
LWPLSRAIVSSWARAMPVETIEAIKRHQQYRLGKRQDDANKSSTMELSMMSPLAAGAPSF
ADVNDVSGPLALRSVENGERVRMRFVHRVQKLLDNPTDPPIPGVTSSDLEAVAEELCRDV
VEPEDRKHLQEQLEKPGMTQLRRSLATRAMSGKEFLKLPRSALMTEDERRMEEARITKMI
EDQEKLKLANVSVTSLFKCPNCGKNRCSYYEQQTRSADEPTTKFVTCLECKYVWTTE*
>TCRU_1352 transcription elongation factor s-II, putative
MAFPLNTLVWLKQPGYPWWPGMVLDPAALEMVLPAGYDTCVLCLPSVSSSVAFANSSNAE
ELLRFDPETDAELIEAGKQDADCAAAIEEALNVYEQQAQQAQLEEEGEKNEHEDGGGRKG
THTRKKHMPHKADKHERKRRKRHERNGSTPVDRRYRHEKKKNERRKYMDSDDLESGTTED
LSDNSDDRRRGKRTGKKSGKAGSLDAVDQYEEEAGFLPTHQEDDAAYLERMLRENRHTVS
DSTLATIRHKLETLTEACNHGGVISVSEAAEEELLEVLSPLSLVNVTLDQLRRLKIGVTV
GKFLLRDYPVRVVSLASAILTYWFRQLPPATQQLLSKKSALDMASNDTTIGSERQEVSLG

PLGVQLEACFTDEEVCDTINDPVIVAGNIEKELEAVDDEDVSMEVLAALRDGSNTALRCG
LLDGSITAKDFVANPTNPDLLLKRSDNDGDKTSGVSPVEPESPLEEGSDLTNFTTLYVCP
GCGAREAVANEYSVQAHDNMAVFVRCLKCDETWNVEA*
>TCRU_1353 cysteine peptidase, Clan CA, family C51, putative
MGTLRENNAGFGDEKTDHSNNSIRVSTPRMQPGEAELVNSLDLNGPTNEFAGEQVEMQSN
DSQDTFKKRMSRINAILTSVVIWSFLLLTLLFLASIVFGIVYSGIHYHGPGWHDASSAKS
ACVSPYGAILGAAGDVFAYSNCIRNYDSKSRNNVSSQNKESGLKWDCMEFARRYWMLRGT
PVRATFDSVVGAADIWALNFVRLLDGSKTPLLKYPNGLPRRDGGSAPRAGDLLIYPRQRE
DFPFGHVAVVVGVTKNSVLVAEQNWDNKMWPGPYHNHSREIRMLYSPIHDAYNITEEENI
IIDGWMRYTT*
>TCRU_1354 hypothetical protein
MQELQGHRNCVQHKLISAVDPIFLRCRRRDPFIVYLLQFCGVGPVQPLDVRLAFVLVALG
LRENNFKLFYVRDGGDTAVSNSAEYYGLVEEERGDGGGIGGSSRRVSFSREMETRGAEAT
LLLPTTIRRFVRAMEGTTDMPVACILRVTDGSRLVDGRFSTIMPEERCTLGVFETTGLRP
IEDVEGCAAVAFLFCVFLQLCSCRGGVDGMWCGCGVGGVIHTLF*
>TCRU_1355 hypothetical protein, conserved
MAASSFTDSECDNTNDGKNSDEDGDDLHPGANYLRVLAHESREGLNAVLTIPGLAEPLAF
APSPAVISAHALRLIRLPWSSRSSSRVVVLLIPRWPFRMYFSVAWRVI*
>TCRU_1356 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MSRRVFTSAVLLLVVMMCCGNGGAAATEDTSSASGFSPDKSFVWRDKNGGETVSSLRVPV
LVEMDGDVFAVAEAQLKEGESNFTGIASELLEWTDEESKGELDATKLKTQVLEECPSDKK
NCASHSEAQDASQGRTKVRVSRPTTVVKESDIYMFAGTYSFEVTDKAAAGSKAAATKWEL
LVAVGNVSNDESSGKKKICWKDTSVIPWTGFEKEHESLTGLIGGGGSGIQMEDGTLVFPV
EGTKNGKTVSLIYSSATESGKLSKGMSADGCGDPSVVEWKDKLIMMTACDDGRRRVYESG
DKGDSWTEALGTLSRVWGNKKGVRSGFITAKIDNRNVMLVTLPVYAKKEEKENVEKGELH
LWLTDNTHIVDVGPASVEGDDVAASSLLYKSGDNNELIALYEKKKGGGDTPSPGMVSVRL
TAQLNRVKEVLTTWKKVDERVSQLCTTLLAQKDPSAYTACTDKITDGLVGLLSGSFSEDT
WRDEYLGVNATVEGGAAKATKTSDGVTFHGAWAEWPVGAQGENQLYHFANYNFTLVATVS
IDKVPEEGDTPIPLMGVKMNDGKTVLLGLSYNNKEKKWQLLCGGGTKSEGLSSTGEPGTK
SHVVILLRNGNQSSAYVDGQRVGVGAQCELGSTESQEISHFYIGGDGGSAVSAGSREDIS
VTVTNVLLYNRPLSSAEMTALNTESVTIPKLDHAKPEPRGTPSTPAGQQPSELGHLVGSS
KVASGGVEGADPQIRGVNATALSSSLVNVSQENNSDAGTMRGSGLLPSLLLLGLWGLAA
Q*
>TCRU_1357 hypothetical protein, conserved
MTASASAVTLRGAPQCHGENVEPTARPRSTSECGIMQIFSVTPSCTASEPRRSDSIAERE
SVAAGTRVGDRDAAARRGTVCGHAQWQDTPLGRSMQGCQQLRGEAPQGARLSWESNGSAA
DPDARTARDDEPFVKRPASYSSGEARAASRAIV*
>TCRU_1358 bromodomain factor 2 protein, putative
MRKRGREGTLDKPRCLAFVHQLWDKDKLKMFHHPISAAELPDYHKVINYPVDLSTIRQGI
ESGKYDSDADVQNAVAQMIANALEYNAKGTEWHQQALSFRNIYLDVARQCGLSVDDDAAY
IPSAAFKDDESTLRKAEKKIAENLDVVLKDLEEEKAVPLEELKAKYKRAKKKKGGKNADG
SDSDDSDDSDESEESEESDEIADDSDDDSDDDSDDSDDSDEEKFYYDDESDDE*
>TCRU_1359 MTR4
MSGSDEPTAKRPRREVTPAMTFPYELDSFQKLSIDALEDGDSVLVSAHTSAGKTTVALYA
IAKALREKRRVIYTSPIKALSNQKFREFSEKFDSVGLMTGDTTIKADSDCLVMTTEILRS
MLYRGTEMLREVGCVIFDEVHYMRDKSRGVVWEETITLLPEGCQYVFLSATIPNAREFAD
WVESIHPGTKVHVIHTDYRPVPLQHYLYPCGADGIFLIVDEQGKFRDDNFRRAMSSMGAM
DAEAGGANGADVSKAATSTRGKRKPPRKGTQPIMEIIKLAMDHNMYPIIVFSFSRAECER
NALALSKLNFNNMEEDALVTEVFSNAMECLAEDDRQLPAIEHLLPLLKRGVGIHHSGLLP
ILKEVVEILFQAGLVKVLFSTETFSMGLNMPARTVVFTSVKKFDGEKNRYLTGGEYIQMS
GRAGRRGLDRVGVVIAMVDEAVEPETLKQLTGGGADVLNSSFHLTYNMVLNLLRVEDVDP
EFMMRRSFAQFQRLRNRPVLEKRAEALTEEIESIHVEHEEVFRQFTLCQELLANRRKQMA

DILKQPTFLKRFTHSGRLLRIRRAADDVLFNWGICRAFHAKVPNADPKSPSEFSVDVAVI
CLKANAANPTSLLPCHVNDFTTSTADLYTLTFDFTDIESVARFRVNLPAEPDTESGRAQM
VQTLSKLHRQYDEKVPLLTAEEMGVDDPQFEKLRVQVERLEAQLAENEFVQNPTTELESD
FERFTHRTKLEKELNDIREELNQASRAIFSEELKQMMRVLRRLDYIDKDNVILRKARVAC
EITTTDENEILLTELLFKGVLNSMETEMIVALMSCLVNVHRTPDGFSLPEEFQQPLKELN
EIVSRIATVSIESGVLQEGGVSVERTMPSLMEVTYMWAKGAKFVDIMSKTSAYEGEIVRM
MRRLEEQLRQMAGAARSPAIGSMELHDKFLKGIQLIKRDIVFVSSLYL*
>TCRU_1360 exosome complex exonuclease RRP41A
MSEKKEYISPAGLRLDGRRPQESRRMTLEFGKVLGCDGCCTVMSGLATVCASVYGPREVT
NRLESKYNECIITCEVAIAAFAGEKRRAPQRRSKLSEEMSAAVLEVARSVVLLSQYPNSQ
IHICVEVLRQDGSDKAACINAACLALVDASVAMRDIVYAQTVGLINAVDVVDLTTEEMRS
QCPTICIAVKGHDPSSIVWMESNCRVTSEVISRLVTVAQKSSEGVFESALRGPLEEHAAA
ILKLQGNLGNSD*
>TCRU_1361 Adaptor complexes medium subunit family, putative
MIGVLMFLNSRGDVALSRTFRDGFSVRGLAESFRNRLISTSEVERSPINILDDLCYVHVR
YRDVYVVLVSDGNTNCFACFQYLLQLLGVCQAYLDTISEETLKDNFVALQQIIDETMDFG
YPQTMEAELLKTFIGVKGINIALMKKPEQSERVTARLTGKMPWRKRDLFYRVNEIFIDVS
EELYVLVSQRGQVLESNVVGSVMVKNFLSGMPECQIELNDDFNLNDASYHPCVSLQADRT
ISFVPLDGKFLLMRYRAALASSPPLKVLHTHVREVSKTRTEIDFGLKCDIKEGMRCDDVE
IRIPCPENTADVKLSVARGRVQFDGVQHAVIWKLPSVSQNDEELLLTAEIVLLAPTIATS
EQVWSRPPIKISFTTPSHVLSGFRVKELRVEEPLLRYSASKWVRYLTTTGQYEWRL*
>TCRU_1362 RNA-binding protein, putative
MPDERILLVTGIPSKLCRGEELYKVFGSYGAIQQLRLGDDASTKGCAIVVYELCEAASAA
LEALNDFRVDKDRYLRVSVYDEVRDRKALERRKRRREMKAEYKQNIASEFGVTEEKS*
>TCRU_1363 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MVSVLLTEQLQRVKDVLATWKKVDERVSKLCPSKSAESASPENACNTVKITDGLVGFLSD
NFSNDTWRDEYLGVNATVKNKDGGETEDTRETGATKTSDGVKFHGAWAEWPVGSQGENQL
YHFANYNFTLVATVSIDGVPAGDTPIPLIGVKLNDSGKTVLLGLSYNGGGKWELSCGGGT
PKELSSALEPGKTRQLAIVLKNGSQGSAYVDGRRVLGDAECDLKNTKDKKISHFYIGGDG
SAKADSDVQDVSVTVTNVLLYNRPLNDSEITALNKKLSIPKAKDAKTVKGTPPEAMKQAT
TEAGTPSILGGQQRTEQDSLRTSENAGSGGLSTSAVSIATTSPAAKESEKQSASGTSPSG
NKNVDVDSSSEGVQTVDAEAGDTVQGDGTQQPSAGTPATADTNAPTAETMAPDGTAVTPE
VGRHSGEDGETVGETDGQKREGEVNAAALSSSLGNISQGNNSDGGTARGSGLLPLLLLLG
LWGFAAL*
>TCRU_1364 hypothetical protein, conserved
MATVMTGRVLLVCALCVLWCGGTVLVLAAGDGDGDGRGVDSEPLLESAESAALLPSSPES
RVELKVVSNPPPKHVEEVHTPAKESSAEEEEAGEEEVTVKSEEGQQEDENSLQVNRRKTP
ELLINENETPQAREGEGSLTAGALEESPTTPGPQAPTLQVPPPPAASGVGEADGGPVGIE
GTGRNVSGGGSRVVAVDTSRVTGEAIKDPKGSEGPISGPPSGGASSSTTSNDGDASGNNG
GAPSTQDTTSLKNNEQSGPTTSSGNAPLNRETPERSTPDAKRHSSETQENETSQVADGDA
NYSAGGQSAVGTKGSSGVSTAASNAPTTPQPQLPAPPVPTTATVTGAPAEKPTTERSPPP
ADSTTEENLTETTTAKRNDTTSPGDSDGSTAVSHTTSPLLLLVVVACAAAAAVVAA*
>TCRU_1365 Leishmanolysin, putative
MNSSNGNCECEDEVVSSAHGIILENEVVPAAVKLHADCLPVQPLEGPLIVPPFVTGSVCS
RFTHPHMASRSTVRHITGAWQSAVGGGALDDCRGGCEGHHDRDDIDGMELQYGDGDGRTL
ESHWSQRHAKDEWMAPIGCAGCCTELTLAAPADLGCMRVKWEMAEPMRW*
>TCRU_1366 hypothetical protein, conserved
MPVDIGLSLLHPLLSVATAAAATSRRSNGKGQAAAALLLPWIGGGAFFMSAYQPPHPTAS
SSLGGGSTAPCAVSAASGLLGPVAVAPPPALSLAASSPNDCPKTDATPSAATSSMSGRSL
SFSASCGAPAVSLGKSTPLPSWHLRRLPSPLATDASGEQPCPHTSVVCHGRSQCFLDRGR
MPVAKLVQ*
>TCRU_1367 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-

terminal, putative
MSRLVFASTVLLLLLVMMMCCGGAAAVEHAGAAVDPFKGTMPISFANWREFKDGGSKITS
LRVPGLVKVGDDVFSVAEAQCGEKEGTGSCPGIVSKHLDIKDDPMDILTSDISLFCMQLV
DTAASSFGITEVLRPTTVVIGNSVYMLVGKYGRTEPQVEGTNERGLLLVKGTVTVDGEKK
KIKWNETHLVNPQGKGDSHSLTELIGGGGSGAVMGDGTIVFPMQAKDSNGTSVLLSMHFP
KSGNKWELSYETPGKGCRDPSIVEWGENEGDERLFMMAHCAGGYYDVYMSTENGDNWYGH
FQPITRVWGNSHNRSGDGVQSGSTTAIIEEKKVMLITAPVYANDNGKGRLHLWVTDKARV
YDVGPVSREEDDAAASSLLIKDKNKELVSLYENKKSDGSYNLVAVRLTEKLERIKEVVKT
WKDLDSALHSCRSGSSTTVGLPTKGMCNGPVPTDGLVGFLSGSSTGTEWRDEYLGVNAIV
HGPAEKRIGVPNGVTFKGPEAGAEWPVGNMGQTVPYYFTNNEFTLAATVSIHEVPKSGSS
PVPLIGVRMNDTKGTVLFGLSYTHDKTWLAISEDPATSKLVDGWEPNKTYQVVLRMDHHE
WTVIVDREKICHTKYNESLFDFHRISHFYIGGDSKDQSATGGYVTVTNVMLYNEKLWGND
LDELHASKVNIPSLGVEEQPTGQVTGTGLSVASESKSEETTAPLVENGDSEDVGTAPVNA
STTPGGTKIPSESNATTPSNTGILLEHGKFGDLPAISLTGDSTVHGCVSRVLLLLLLGLW
GTAALC*
>TCRU_1368 hypothetical protein, conserved
MEADGTLILDCSVARKTARAHPHRAPRFVRIRGQDALDTITLCRTLQENEKLTNLTAAHV
ERALVPWKATAHSTKRGALRRAAQIVGTHDLDLTRDLAVGEARQSVRISPEYCSIFGEVH
HNADPGVVAGRIDVKGEAAEGQ*
>TCRU_1369 hypothetical protein, conserved
MGMRTRSATRNAVRWMVLFLLLQYLGSHPSFTAAGEEEEGHVVIEIVRYFNYPNSIFFQN
YAGDVSYFSSDDVCHLGGGVLSADQTPAAHVAIADELRKTAVHNYDTSHAYLGGDADHAA
TPTTDPKKSCGRGLNLPTLNCIFKWNQGAFADSSADGLGVAFFRGTLYTLVGVGPMNGYK
AYWPYHYPHHGKTFLMLRLKTRENSEQATWYDWYPAPKTHIDTPYRSFGVVCETQKGYVV
STTTLPPAVVVPWLQKNWYVVLIVVLLPVVVAVALITVCFYRCRGVDDESKWVAHMVLRE
INDNPLYAIDRNDGIHNKDSQMKQDSTLGDGMPTTVPSEHENAEVPTVIASQESTVYDLG
DIL*
>TCRU_1370 hypothetical protein, conserved
MSLAGQFISFCRTHAQPIDEKSCPVILMAIGDVAPSIRPQHARMLRSMSQMYRTPPEMVV
LGLPKIAARSETKQAHPLTTEKMNQFVRSRTDWKQCVVLRPAWMTASCWSDIAVLTPKKF
YTGVGRDHNFVSVRGAKDGEGGSPPHLVVRPDTRAGRVQHYKVMRDTLTQRRTHESYDCP
SETSSGFLECHGAFHKTGCTPQIVESHNLDPHVISQLAVHVDPFGLPQGTVRYLGNCNTV
LTQVSSLVALV*
>TCRU_1371 hypothetical protein, conserved
MADLVRQQGDIQEQLAYMDEKGQSESMMTVSATISGLRWISGNTAKHWKDSTLTGHIADL
RAPQAPNFASQLLLPIMRAARELGARQGLTIAEGRRSKPHYAAADVQNRSAQLQHRMEEA
NNHFSARASNTAVANGLLARRERHLETTPGTKGTHRCLGSAACSLGCGDSPGQRGVSSSR
RGPPDAPAHGYEDSATTPPHHERLMARDAAAPTIPQPSFTGERRRVNTLASLGTVGDRVS
LTP*
>TCRU_1372 hypothetical protein, conserved
MTVGSLYAFGRGVLLPLCGFATGWVAYRAVEERGLIDESYLRRIRLGNLTLQLYLQQHVL
PVAFTENYGYPEEFLKTMIERLGRGDDADNEVERQTFEQILRECDLNGQIAWLEEHVLYD
IPYFYIADIFDGWCALHRSLFTTADEGEGKESNLTRRGDNSDAFASEVLCRGVVEKTLNG
IFPYDVAVRVLCVLAVGHTSNARLLSQLISPTVIVERYEAYLNDLEQRNMMAGDKIPNKE
VTAATLELLRALNTASVHRRWWYFWGRASTGPYPIAAQLNGEMWCRCLGDLPAGTREICP
DGALLFADTLSESFKCGSGNRQLGVSGAGRS*
>TCRU_1373 hypothetical protein
MPALTRPWENASDSSPSTSAVTDTNALVRRNSAVEVGLSSPPNTLTKPPATATAVQSPAD
GSQQVVSSNNTTNTVNRYASGYNSGAGYSGLGMGSMYGGLGMGGMYGGLGMGGMYGGLGM
GGMYGGYGLGMGMGMGMSEDIQRSQMTFMLLGRLLEMCGMFAGVIQMTFGNALQFMGNYI
GMSQQYNQLKSGMYMDESGKWVQLPRRCVTDVDSLKKSHKRKFVNRKRQGRAWVAILRRV
VFLLLAVFMTRRLMGRAAAKELSRLQF*
>TCRU_1374 zinc finger protein family member, putative
MSSSEKEREAAENGVPTSDAAEEREVKQTASNGTGAEGSTATAATAAPLSQQKQQLSGDS

APAEEESQDHRPATLAHIQQNFGVMSRVLEREVFRRGLINSSVEEMYSAFFVISGVLIEI
LKSETDQRLLHMQLLEMLLTILEPTYGIDHARMLVAIMDQSVSDLYLFQALLSSSSLEAL
VQRAEEFMNPPTRSVGAGMSGGIPGNYSGVQNENMRGVQPAYNSVSATARPSYAEFNKDR
RVEPSAEPAMSRGANTYTEGGGAPASSQPEDDAMPAVASGWAAVQRKHTDLDRDVTVHHH
HHHQQQQQQQPQQQQHIQHRVPFNQYLHQQRNQAPNVAHHHQVVVGTGPMGLQQQQQQQQ
QQQQQQESPQTDSFPRAPVPQGQQKRMVERLPPGTQESDEPHVRGPLWRVPPAPSGTQQE
TVTVPQPSYHAQNPSSTPTPHSNQHQAASPNSPTHPRFLIHHRHATTHFVPPGPVGKQAS
PQPATQISPQKPPHSATMTTTTTATTAATASASITNSQRVMIPHHHHHHHLHHHDIPPPQ
LMMPRVSPPSQSVHAVKQEPVSPPETKPVVHNAETAVPQLRPHHFHHIPPTQQKVLRQPQ
SVSVSASLGGGAGGGISTGSGGGGGGGGGFNGGGSEAPSHGVMIPTHHHMIHHFQQIRP
SVPPPQQQYRQPTTSAPGPMSIDALSNDEINWASSQSAMLSGPQELRYFLRERGVAETVI
NILAKIFFSLDELMAASREAFEERIKKEIVSVNNRQYIWTILHPSEKLPSEKDVPEMNEL
RNFIHNNAIHNNMSQDGEDDTTTLKPGRPNKNILQVPQPRTSQGKQQQQQQQSGKVGECK
GVIWLSSVRSWQIQSAVEELSKYGKVLQHGASSQRPDLIYFKLGDHKSELQMMRKIGSAV
VEDYYRVSPGDVDDGAPPTPTGRPEGADDNGPSKILSQKAGSGMHAYHQHHQQPSANRGG
YGVVDEEDMDGDETRNFRKGTGVKHARGRGRGGHHNYHHHRHPEGGTQMVCRFFSKGTCK
YGEHCQYFHPPKNASRS*
>TCRU_1375 zinc finger protein family member, putative
MTQIITENLRSSVPPAAPKSQRVCRHFARGRCTWGSSCRFSHDVERAAADETQISQTFIG
LQQLQLQKERHVILKAALDGEFEIKPYSVAEEYQRHIVHLRFSSSTIILPRLLTEESLQQ
QLIELEENEQLRIGGLLFLVGEPAVFWSMMQLYRLRRTTTSSKWDTLLENAKRGYVECMF
FRSAVGCLSSDCPFSHTAPPAVKLSTPLQNMATNNALLTPLLGFGLTAPAPATTAASTVA
SVTKTHTNGFRPPADPVRHVGVSPLTVGKMEESVAFRDSVWGACVIPELKPTHEPQESLS
FMWGGGLRSVQDVEW*
>TCRU_1376 hypothetical protein, conserved
MVEKTSPANRPPAAVGLGERLRHIIGNNRKRNLKPTEKSSVAIITDASLHGWGAVFIPDS
GDVKIAGGEWERKPFLIMQAEARAVRLALSVFSAILPPTTDVWVDNTSPQGAANKGSSKS
HAMTWELRRICLFLDSRGIQTSFT*
>TCRU_1377 hypothetical protein, conserved
MDNTLSVVVEKPAGLRRQWIAWPRGKSRDDPYEAIVPLLHISHYLPPVMAEAASCLDVKA
SFFPSLFTAGDSASLSMPRGGRHAGGADTTFNGIQGRPRNSPDYYYLGNCGGDDGGSPLW
AAPPMVRIEVWIDNIRIAGLKSDVTLWEAQVLRNADSCHAYLGGTANRALRNTPFWGYNL
IKLTVRYP*
>TCRU_1378 hypothetical protein, conserved
MDFRKHCQHWEDSTLTGHIADLRAPQAPNFASQLLLPIMRAARELGARQGLTIAEWRRSK
PHYAAADVQNRSAQLQHRMEEANNHFSARASNTAVADGLLAGRERHLETTPGTKGTHRCL
GSAACSLGCRFARTARSFLFQERAARCTRARVRG*
>TCRU_1379 hypothetical protein
MVDPQSTSLEQHLKDERAAYASLALLNIQSSALLDRFYREWFALDSKRQTLMKELEHHSR
AIREHRRQLELTLFPPEVRGWMQSVLPEMEILEEGGSKMNALYEPFSDTPCSRLPATGKT
RAAFEEAITRQVVRWEEGNKGACSEYKEQPAPSRLSRVTPQPGILLGSCFLPYRDPQTAE
LRRRAVGGDVIVMKSPELSVGRVLVSMHMVCRGDLIMVETPLFTSPTSGNEANHEGLLPP
AVRNAMNSVLRQSEVFAVQGWDTRLIRPFYEWLTELAFGEKQEEFLQRWDELGCPVEDAD
PTLLSKLSDLAHFVWMSLPSSLSSIVGSEERVLLFFITLITNAMNYGGGTWADEDVFYSA
ENGVCLGMLETGIGVFGGISLIEHSCHPNAIVVFRHGCTPESIVFAELRATRPIGIGERI
TIAYVPTFIPKEERQKRLRAKFFFSCACVHCTAGYDTTRLMFVSCESLDERVVMCPKGRG
SEWTLWSLKLRPCVYGLKEVGKSYRYDDTYVLDATRDEMLFRQDMNNNELNGDDTLVPAL
RREVKQLTDVLHGEAKSHVSPLHHLFLLRALQVAAITKSRFSRLDAAMIEAVLMLMCELL
KELIGIIFLLPDWFATELLLNERHTGALSDDLGDRLLNDSSNRGNGARQPWQECLTMHPL
LHPHGNLLVSLLEYYAILREESGNIEAAMNAWTACVFLLRYGMCQGGSERCIRAQLRALH
CRHQQQKQH*
>TCRU_1380 hypothetical protein, conserved
MLDYFVAIGVALLGLLVVYFMFHSIKKSEFVAFNASKERKSRPRKTPKAPRRDDSRLDRE
MEALIAQEVAHHTTSMRADIRVVQPVLLENMQRKVAAEKNKAASMKYSSAASEQALIDKE

MGFQKVVNQSKPRKSLSPPPPQRPQQANTDEELSRKLGQFFSNNRKDKKGLKVNLKEEQT
ANTKGNGVHVVVRKDISNARTWSLVA*
>TCRU_1381 tubulin tyrosine ligase protein, putative
MAGKILPPPHNLPTFYPQSLGFLQRDGRDDMDVMTADTTYILHRHQRLVVGKFVPDINNE
DPSNPRYVVQATGRLRPSRMPPLSRSLNGNRLSNASSVEETSSDTAIREELARTNRVATE
KIHYTVVEPLYPFSAPSLFFPIRHSSRAGGKAGDIRSPRQINLAYHGRDRTHYRLEALTV
QKNNLNRMCLYKLGPGAVAFKVVIDAFEAAGMRYTPSNELFNVMWAKRATNYTLAHLGSY
QKVNHFPGTWGIGRKDCLAMNVDKMQRYFGVDAFNIVPTSFLIPKQWKELEEYVKRQPDT
TDDPLILIVKPSASSCGRGIHLFRGMPPMPTGTRQLVCQRYLGNPMLIYGRKFDLRLYCV
VTAFDPLRIFLFDEGLVRFAAQKYPGMDKDLENIHVHLTNYSVNKTAELNRASRGKEYHS
DDPLDIKWCLSDLRDFLIKKNKDGGLAWERIMRGCEDVVIKTFLSIEHDVVQRIRRECSD
KTGRGCFELYGLDLMVDNQCNVRLIEVNIMPSLATGTPLDKAVKSRMLAHLLTLIRVIPH
QRNAPGHTPPNFGEPSSDRHNICYRFGRHPHGDAELVRKPLLSRFNDPRDSDSVLSPSEY
LLLVEAEEELACAGGFRRIFPTAENVLTYLPYFTHGVLRNNYLLASAVRMQAKARN*
>TCRU_1382 Protein kinase domain/Protein tyrosine kinase/Kinase-
like/PH domain containing protein, putative
MPNNDSHDAQLLRHYAQFFPNVLFTSEEEMEKYCQDARPDAVKKVLDLPEGEEVPEDAMN
DPRAHLYILKHIVGRNATTAAFVALRGSDKQKVVAKFIMLNDEKQAAYARSEVHCLAACD
HFGIVKHYDDLKSEDKLLLIMEYGSGGDLNKQIKQRLKERLPFKEHEAGLLFYQIVLALD
EVHSRKMMHRDLKSANIFLMPTGIIKLGDFGFSKQYTDSVSLDVGSSFCGTPYYLAPELW
ERKRYSKKADMWSLGVILYELLTLHRPFKGPSQREIMQQVLYGNYDPFPCGVSDGMKAVM
EPLLSKDPALRPTTTQLLHTELMKYVANIFEEIVRNSEVIEKHDKERILRQLAESRAKAP
PPNSIQAGAVSNDVVREGYLLKYSSDMKWKKRYFSIKNGQLRISLTDNPEKDGVSPKSAS
LETVNDVFPVPEAYCRSNPHQLVIWFTNGQKIIAMAKSAEERDQWISDFQRACGM*
>TCRU_1383 DNA replication licensing factor MCM9, putative
MTGEALVGEKLLQKLRPFFLDCCKPPQCLTPASSTESLTTRSLWTQEIDCMRLLAVLPEL
GDLLFCQTMTLIDALRQVCAEMCKSAGRSLNPADLSPRLTHLPTVGAPPPSMPSSRGVLV
SLCGTIVRMNAKRVVPFVHKLKCAKCGDTVEMASSPFDRGSKPKGRCGRKECGGGELKPV
GQVWMDYAECRLQQRSNLSGRLPRTLLVTLEDELTMKCTVGQFVEVIGISFPKWRALYPN
SRPIIEPTVWALNINSVESYREGGSGSMAAVPRRKAVGSMEGSAFTPESFFYSFCKDKLR
RSTALVTSVCPHLFGLFAPRMALLLAVVGGTSTTGKARMHIRSTIHCLLVGDPSTGKSQL
LRFAALIAPRSTSTTGTGSTSAGLTVAAAKENGEWVLEPGALVLSDGGICVIDELRTVSS
ADRASLHEAMEQQTISVAKAGMVTKLRTSCSVISACNPPPTRHGGTEIGVGGPLLSRFDF
IFLLWDKPSMEVDSRVATHILTCSQAGKQPSSVLSQEDISRYLRWVHSHYAQNDGPLLSD
QAAELIRTYYELQNRRGASPLLADCVPVTIRLLESLVRITQAHAKLHLENVCTEEDAALA
IFLMEQSAHSLKCPLESLGPDVYTNSKSLEECFLDPTPEGVQRQRAVLRAIVDVFSNCGN
AHHSSDDTATATWLDKMKFPSEETSLPSQQCGKRGREVSLPSDAVLRSARRLEAEISSPF
SSVQTVVQYTPSSMSQTPIKKSCRRREVDEIMKSLVFRS*
>TCRU_1384 hypothetical protein, conserved
MRQTSVKLLHSKRLEIKQRMLQRNEARRSQLRHAELDRFRAQSTEGGDPEQDAYEFIGRE
FHCDVGDPAVLDLLLSIEEEIRNEQLVSLYEESQNEDWEKYFQHLA*
>TCRU_1385 hypothetical protein
MPLSIPKAIETVRRYVADQRDDATGSVGNTTCLHSSAVEVCEDPQRRILPAFRETWRGGP
NIIASNDGSYFVAADCLWHDRNRILAEEIKDYASLKETPWAGGKLASTISSCARCKIDAT
SAIFSNWPREQVTENLVKQSILDRAKLYRSCRINYIHGALGLQESPYGHAGEVYGDIHQK
LSRARARAICPVKRQAKHTGDSLFGSIPLRQTLCVRRKGGVEPKDHLFGSLHVEEKKYL*
>TCRU_1386 meiotic recombination protein DMC1, putative
MQHAGTRANKSDTAKDAAHCSDTTSFQEDAAHVIMEVDRLTEQGVATADIAKLRQAGIFT
VAGIHMQCRKDLALIKGLSDAKVEKIIEAARKLFDCGFTNGVTYLQQRGKVTRMTTGSTA
LDQLLGGGIESMSITEAFGEFRTGKTQIAHTLCVTCQLPTSMGGGNGKVIYVDTESTFRP
ERIKPIAARFGLDADAVLNNILVARAYTHEHQMHLLSMVAAKMAEDQFGLLVVDSITALF
RVDFSGRGELAERQQKLAKMMSHLIKLAEEFNVAVYITNQVVADPGGASMFVADPKKPVG
GHILAHASTTRLSLRKGRGDQRVCKIYDSPSLPEVECVFSISEQGIVDARE*
>TCRU_1387 TPR repeat/Tetratricopeptide repeat, putative

MSTVEELRQSGNAAFSAGRYQEALAFYEQALALDAENVDLLNNAAAASHSLKKYDDAIAY
ARRSLSVRDNFKAHTRVGAALWALNRLPEAAMEYERAAVLSPGNPSVEESRQTLLRLLQQ
SFGSGGVVLPLCSTGKLGVCLDVAVVTLSLLTMFFLFFMPALAKKTWNFLMATAVVQQAM
IARRQGLLKASKEVLLKWSDHRCTLELLLCSIALIGAVEPQMLLVSALGIYSAVSLASNL
PTLSNISPFLHRLCAPYLQRILANQSMVANYAATLEAIMLFTVMFSGGAIFTLVYIQYVK
NLYLIDNNTRVAFTGIRMNLSRLTRHPYMPLFVDTYMQKFCELIYTIAQRGI*
>TCRU_1388 hypothetical protein, conserved
MNRRHSGGGDTHYKMCKKIAQLTKVIYQLNTQNEDYDERNAEMRRRHEEELRTICSEAER
RVEGLRKAFREEEEKRNGAVEAMKRGYMAELQEAKDVYARKSASMVDELSASKKKFEEVI
AEVRGKALEEAAKKSAANEAETAALCAAKDEETARLRASKEQEISNLVREYNERYKAMLA
EQMDARDALEEKLNLLQSQLDAATAAHAEELQKWEQKLHDSNDVATSMSAELSRWKEDCR
CREAEVSRLQQECDTLHRRLDAESNSLGVSRDVEATLRQDAELLRTHLKEVQEGRDKLER
ALSEKTTGLTKASAEITDLENQKSLLETQQGRLLHDLNDAKKENQQLLSRVEALDRRVLE
LEEAKKAAEQEIGRRSRAERLLEERCDELGQNASELVKKHQEEINALQAKHENALFDIHL
ASQKSNDVFVTQLRREKEELISHHTQELRRQKEQHDQQIEKLTREHEKVLLDLRGQLSSA
DSVGGDLRVTIAQLRETVVKLEEELNTAKNEIQVLVTQKNELAAKCEAMRGDHARRIAEM
EARMNAEREVQIGKRDALEAEIASLRNKLQADAEASERNWESKIRAQAEGYESRLRQIRE
EHNNRLRHLTELNNSANAQLEARHQEQIRNLMEAAKLQKEAERKESNSERKEFAKQLQRG
EEELQRAKDQMDAMRQSAKEHATRFYDEIQSQRQYIEKFTADYELLREELQKSNVELNGL
REEYAQLEKEMRLWKGRECDARQALERLEEASSRSMKEVEALHRDYVSSMEEKFSQKTQA
ALAELRATLTAERDAVQLRADGVIAAARQKCADLQEEVKSLNLKLDASVHDIRKRTEELE
REKSRKEAVHREFTATLEAMRRDFEDEKESQRRDTENQLKEISTNHKMIIDDLMEQHDEE
RTTQNNVIRKLQAALDELRYRYEYRESREEDVAMINRLMREIKQKDQALEKTIRDMKMYK
MELINREENYNKVFGRRPLVEPGPPADKAPRLLQGMRENRDRTERRATQQ*
>TCRU_1389 Archaic translocase outer mitochondrial membrane 40
MLMEWLRGKSEEVSAAPEKTVRRKLLDVDPETPLEPSPAEAASQREEKFRRKLAASAKEG
PTSPAKLVSYESMFRGAQRLLMEGNFGEINEGLTLNVARNAQNVMISSKCVLLSPQMSHW
EVSFQMNGFSDIVAASYNTLSRWSLMYQRVSSTGALLLAQCMAQRQQGMTQGTVVGMLQY
PWVQGGCTAVQYVKNQSFTLSHAQRIIRGLHVGSSLSWDPMTKGTSLSHGFTAVNSLKKG
SLSGDWTPSKGEWKLAITKKDWAHDAEFAMQLDHTQKDQDMTSQLSFGLKKQFIGGSSMS
AVLNGFSVVKAAVGLPFGGERIGLNQMHCRYNVHYNIRSGALKHGLVFTA*
>TCRU_subunit, putative proteasome alpha.1
MSRTGFDKYITVFSPEGSLYQVEYAFKAVTYAGLLTVAIRCKDAVLVFTQHNVPDRLMRP
DTITSLHNINKDIGTCITGRAPDGKSLVQKARQEASEYKYRYGSPIPVSVLAKRVADMAQ
VRTQHAGLRLMGVVMTFLGMEQNDADGSWVPQIYCVDPAGWCGSYHACAIGKKQIEANAF
LEKKQKNAPFHTLSQKDAAMIALAALQSALGASLKATDVEVGRCSVEDHCFRRVPDEDVE
EWLTALAEAD*
>TCRU_1391 hypothetical protein, conserved
MGCVLSNQKLLQNSNRQCSSIVRGKPRVQTDPVSEAVIHDSRGKVINEYDALAFFSDAAA
NSNLVALTDYRGVQVYVTNLVLSKVNSICRWVDSILEVRERNGGYFIDPKSEASSMNRWE
NQTDVEECSATIVQESNSSFQHRFDVSTCGHGASTTFRQTEKSPFSPKQAEYSPASSRNV
EGAPSGEKLHYAEKLCMPEGPMKVEKFSPLDKLQTTPKIDVK*
>TCRU_1392 hypothetical protein, conserved
MTTALLRIARPPVSRLLVAGAHYHTVSDALTEEERRHLEQELPPRELLSELRTKDQPPDG
EGDDDVKVPGDSFGIMRNRVVFYRPIPREVHPGALGELFPEGCHPMRSVNAATLRRLCGR
FGVSLEEAAAAMLEAELEINVAVDLLVRRKGIKAPFGSFGLVGFETYAPETFCMVNFILP
SFEATRDDDVLDAIHELTLSAAELPLDIPKEELLNKFLNHWTIEDGRNCREVMNSFDITA
QSIVMLPYGEYSVQGFYIFNPVKEDVPNIGTGAAACCLDLRTGIHNRFRFHVERVADSVS
EHVLRELVHYGQNIHLLRQAYWFKPEYSVEEYIRFKESLLQPSASIFEMRYAVLTAAPYG
LEGYRNLVEMEKLKVAQHKYEKHYEDFISPGKWLTSDNAQLQTVAGGSGDAPGSILHMQT
NSPSISKTAMETRTAPLRHVLEKSIQAHGDRVFDRFYRMNYH*
>TCRU_1393 Histidine phosphatase superfamily (branch 1), putative
MFLFMVFALVIAVFIAVSPAAQALRMKIGSYISGVQFMMVADDLPKSFTGSNHMQMKAPA
TEGSKRVIRVVFIRHGQSVWNSLFNSFGALWPLRLVKAFVRETIYLFMDPFNSVIIDSPL

SSKGNLEAEELAQFIRTSKGKISFDTNTSLVVCSNLRRAMETAVVGMRPRISSTRERIVV
DSSLQEGSRNIDAQTLSTERGKLVPCKMGKLNFSEQLGTVFDAHLNAGNKTSKINVYGRM
DEFIRHLFDGSQPDSYTPATSSALGNAELKEVIVIGHSSYFRCFFCRFLPSSSQHIAKKK
KLRNCGVVVFDLLRNEFTNEIFIDESSITVLYKGF*
>TCRU_1394 hypothetical protein, conserved
MSGVVDPVDATITRDSWTCPICTVEVSRQNAFCQVCLRSRPMDRCGVPQIFAGCRIHFNG
VIPRTIKHPSHSVEWRMAERHGATCIVDFDVSQVNVLVYRPGYERSDKVRRCVEGGISNV
FVVPITWMLDCLLQSRQIHVGLYRLTSIPAVAQPTGKGPVLPHHQHPYYLMNVEEYAIPT
SFSQNRQKEANGSPNNVLVNANANLPPCFEVPELQYTNVDVFEAVCNAQKGKASVEDDQE
NYEDARETRKRAANIGIFSCEQRHNRVDSFLFSGMKFLLTPSLESNPHLTRALKLCGAQI
VSSSEGSLGKLLRTAVTHVLYDHGEKKCDVMIEAANVKKELPGLTLAKVNWAEDCLILGE
LVPPCGHYVPTEKLLATLSKKFARR*
>TCRU_1395 adenosine monophosphate deaminase, putative
MSRATSFRLDSTNEYGEEDHLQHSAAGENRRLSRHKITISHGNAKFLKYQLQESHMFKVV
IDGDDGGVDMRKVHERIEAALRMRPRYKKVNGRIQMPPLPSRVRISQENGVYKLSDHDVS
PMYSLQSWSTFASDVQHLRLTVGNTTCIKACSHRLNIMQERSRMFFLLNADIEEKHNFRK
AGGVFSKATKVDNSVLLSRSTDAQETLDFILDWYSRYPDAPLRLRDGTNSTLREIFEVYE
VKDPSKLTVEGLGWRPTPGSVENADFALDSAPLSSELRYSFLHLRGSCAPRFLQKRLQRA
EQQVRYVQATEYSIPLYATYPNELADIAMVLNKNNIGPYGRNMWILQVCFMRNPPFGVNY
PVSCNTIQDQLDFIFLPLFKATLYPTVPNYATLAWFLEQVGGFVIRPPANVLEADFDEKS
PVPSEMPYGTKPNELYYLYYMYANLTVLNSLRKRKGLNTFQLRCSGGNRTSMDGLLAGYL
LGDVITRATEIMDYPVLQYLCGLHGVGLTVSPLHDHIQGIVHYQNHPLPNFLHRCLNVAI
ATEAPLLYHHGSSPLFEEYGTAMKICGLSFLDLTELARNSVMISSFPLETKKEWLGENFN
RGVEGNAFELSQVTNVRLAFREESWDLERGMLKDLYINRSLPREAIGSSRWHYISNVKEV
EYHTVLDTRVRFPRTVLNGPHKEVKWAVSAARGIARAMDLRFKYIWEPPNPWEVTQQRSV
EADFQRKTDSFNEDDWTYAANDAVFISFPKNVVHAWPRQLPTVEKFRNDLKELQDICASS
DVKDFSQKRLENLEHRFRLHLALNHANEAGTTEDRVSSNRDIYQAVKVDTHIHMAAGMTG
RQLLSFVVKKLMYSGDDIATKRGDLIHTLGHFFKKNGITKNLTVDQLNVQADHTLFERFD
NFNNKYNPMENPELRSLLLKTDNFMKGRYFAELIQDVFAQYSRDRHTYAENRVSIYGINI
REWDNLALWFSTHGMSSKHNKWVIQVPRVYKVFRAQNLIGSFGQYLQNIFQPLWEASLHP
SEHPLIHHFLNHMSGFDSVDNEATLDLPFLPVSPWAWTSVENPPYNYYLYYLYANIRTLN
EFRASRGFSTFALRPHCGESGSAEHLYGAFLCANSICHGINLRDDFPMQYLFYLSQIGLH
VSPLSNNALFLRFLKNPFPEFFRRGLNVSLSTDDPLMFHQTQEPLIEEYSIAARVWGLSP
NDLCEIARNSVLQSGFDYVFKRDAIGDQWYMSSSLGNDSLRTHLSDIRVAFRFETYHTEM
DILELCSGRPIKRCMLTTNQEEEINEKNFDVEPEKVILSTHDQAIEIMLREVETGREQLR
VSRVKVDALRRQQKSLVDKLTELAIHQQEMQEEAERCNRAEALRYERRPPTPPDAAFMTS
ERATVQRLLRWRPKPLDVLNHTTESSVPLRNPRRLPSLNAPSIGVRRTI*
>TCRU_1396 peptidyl-prolyl cis-trans isomerase (cyclophilin- 40), putative
MGKLCWLQVSIGGKPAKEKILLELFDDITPKTCANFRALCTGNEGKLTDETQIPMTYKGS
TFHRIIAGFMIQGGDFTKHNGTGGVSIYGERFDDENFDVPCDKAGLLAMANAGPNTNGSQ
FFITVNPAQHLTGRHVVFGKVVRGMNTVRALEHTETGANDKPVKPCVIVDCGVTDTLPEP
EPQVGGDTFPDYPEDCTPSLTDAELFDVGEEIRQIGNKLFKASDFENAIQKYEKAARFVK
TINKTTANDVAVNEKLIACYNNTAACAIKLGQWSEARNAASRVLELDNSNAKALFRRGFA
SLSAGDSESAVADFTKAQKLDPDNTEIVTVLQQAKEAEKVRTAKLAAGLKKMFS*
>TCRU_1397 hypothetical protein, conserved
MTLSALICEAIMRMDPWTILLAALVQQLFSMVWFGLIVKTVADYYLAADKGVRRVEHIVY
RYSPVFCCITTFAAGAARAVAVHTIITVCNGKGLCDYQTAGVVVALLTCINQHQFFSCQR
PLPLLLTECGYEFAAALLASVCCLGMQTFVL*
>TCRU_1398 Regulator of chromosome condensation (RCC1) repeat, putative
MPVLATAGSNHHAQLGREGDSSSFEVLSIEGDFVQISCGAHYTLALTRSGSVYGWGRNES
GQLALAAPTVNYPTLINTCFDDRVVKVSCGESHSLFLTSSGQIYGCGEGSCGQRGDGTYH
GECYEPRRVLLDETARDVFCGARTSFAITDAGDLFGWGETTTGMLGPKVWHTPTLAVPTR

LSVGSSRTRIALVVASVNFAILVTTTGDILGAGSNSDGQLGIADCCTYTWRPIRDVGRVS
LVACGRRHTLCYQVERKRCIVLSNKIESFKLSKPTGLAAGDDNVFAWTDGGSSLFVYGRN
GDGQLGVGIIPYVERLTKVPLPIKANVVTVSCGRKHTCLLLSAEEVQRGNYMVFMEDSFA
ADGTYFWETFRESDWKKPSFGWVCTATSFAALITGVLIARFYVCHR*
>TCRU_1399 hypothetical protein
MSRVEEARLYSWNADLEKRAAAVRSARSKLEEKKAACIQLEASLVELANENDASERILFQ
KEQYVASRKAVLEQANAERSSQRSLLDRERKKTTMDAERVENALDNEWRGLEEEEKAAEL
GHHQRMIRFQQQLEELGKQETELIEKLRQLQNAELNVSNILRQLKQKDEQLRSLSEARLQ
HMRAELREREAFLNQ*
>TCRU_1400 lipoic acid containing carrier protein, putative
MRRVFQLSSTLFLASARLYGTRYFTDSHEWVEHDGGVATIGITAHAQESLGDVVYVALPN
VGDQLNAKEVFGEVESVKATSCMYSPINGVVDAVNDRVKDEPALINRSPEGDGWLIKVKC
SELPQGLMTEEEYKKFID*
>TCRU_1401 Kinesin-13 6, putative
MPSIPLLAELGAKAAEFQRLLDSTEAPETVKKKLRPIMEPEELFVSQDSRIFVRCRPIIP
FDQEDMHSESMIRKVEGRRDLVLMVPKVSLAGQCLLDPHTVNLDGVFDGMDDTSRVYRES
CYPLVNLSVEGASTCVLCYGQTGSGKTYTTAGILQLVSRDLASYFTSHDIFITVIEIQAN
KNIDLLTGTEVQVVEDVSGELKIRGADAFECSNEEILWAVFEEAASQRMTKATGRNEASS
RSHMVTCIRIVSKNSKWARPGELFMVDLAGSENTADSATHDKERQMEAKFINTSLMTLKE
CIRTRVLAATSTNHLHIPFRRSPLTLLLRDCFEIAVKRPTKTVMIACVSPLLRDARHTIN
TLRYASLLAVSPPARVVADDPEDPNGFDRKQALEFLVRCSRGRVTEPESILPEGDGRTLV
HIPEAEFIRRILESHSNITEKGAKQIYTSIWQKVVDARTRGRKVMTAARGASFTKKCACT
RK*
>TCRU_1402 protein kinase, putative
MPSGDAMIPRVCRTFSDAFASDEATAKEQGKKYWISRVLGSGATGTVLCAKRRSDGQSFA
VKVVEMEGMSEADKNRAQAEVQCLLNCDFFSILKCHEDFAKKDPADEENVLMVALVLDYA
NAGDLRQEIKNRAKAARAFREHEAGLLFIQVLLAIHHVHSRHMIHRDIKTANILLCSNGL
VKLGDFGFSKMYSATVSGDVGKTFCGTPYYVAPEIWRRKPYSKKADIFSLGVLLYELLTL
KRPFDGENMQEVMQKALAGRYDPLPPTISPEMTEVVTSLLCGDPHARPSSSKLLNMPICK
LFVSGLLEIVQTQPSFAGPLRDTISTHIQSVKQSLKEERRVTVRQMEESQSAAAASTTIL
EGATPMGSVGDLTLYEGIVKKQSGDLAWKRRYLCIRGALEEGERLDVGRMPKFKSLDLVL
AVSKETMRQQCITTPFSELEDVFPVASKYTGSNAQHVFAVAFKTGRRLLFQARGDPERDA
WMQKIQQTLGIDEAD*
>TCRU_1403 Protein tyrosine kinase/Protein kinase domain containing protein, putative
MLNLREVLLNSRQCVSSQQRMERCVLLFPFYAVSPAYSTKTGTPSPKAEEEICERGSRDA
FQLIGSLNDKTVPAGLEDSFVSQVQLVRALNSSAFSTIFLATRGSTQRSDIQKEGSQLPP
LHMNSEVGVSSSSRPCSVSSAAITSPPLRQQQCIVVKFIELGKEDKKLRELANREIQCHQ
SCNFFSIPQFYGVYTRRLCPEAPPHPVKNPITAHVLEMEYANNGDLSQEIRLRVKNDYKL
FSERNALLIFEQVLLAVDYLHDKGIIHRDIKAGNVFLCSNGLVKLGDFGLSKFTPGDVNE
KRNGSFVGTASYITPEMWERKPYGGKADIFSLGVLLYEIFTLRKPFVGKDKNEVRQNILK
QEPKIPSHVSPEIASIVLAMLQKEPDLRPSAMDVLLLPLMRNTLASFLKSVIMDGMNDTL
RRGREIGNGSVSDNFADSTRQSGEKATVYCRLLSCEREKVLLDLSWVYRRILYKAVTLSS
RASQIRLQLSKLNALTRKTSQVLIEGEILKENSGCWKLRHLCLRWATDSTDMSPQQESAH
SGVIELILSLKKDSAESTRTCVSSFIDCFEVLERYAMDGAKYVFALLSRTGKTIFFQASS
EEERQRWISFCLASIQHNNGLA*
>TCRU_1404 engulfment and cell motility domain 2, putative
MLRPSIVSTLSTNAVLLEYRKHHKPHSSGGNTSRSSSVISQRPPDGAIVVLENEENASDE
FSVREAMSPAIMSASDETRIVNTKKNGGLEKSNAQQRIAVDWDWVNHETEQQRVNSNISS
VPCINDQQENISFLDAVRLLKNDRYTWEPYVSAHRFSENKKSNCLISLIERLRDIFCWCR
HSYSRDGIVSSDPDSILHHDTEFTLTLPFVPFDHSYSIHRRLLITIYHNLFRQTKNGSIN
GGTRPGAIDWEVLGFQGSDPATDLRFTGILGLLQLVYLIEYYRDFAMLLWNTCTNGGSGL
LVYEELPFVLVGFNFSAVILDMLKDSGFYTEITRRAQALFYNKTRASRLPIISDSEKALG
REFPLLFICCEYHVGCLFLFWECWHDLKMQRDGKQPTIGDFGVVKAKLCTKLKKNGPQYA

FDACAKAGDPFNTAFHAESAVMPGAMQLSKDDVAIGTNWPQPQEGREGEELWRSEGK*
>TCRU_1405 leucine-rich repeat protein (LRRP), putative
MDAEENPLAADVMMASLDVLTHNEMGHLVYARSNLSSLRLTSIELLGAYKHLQRISLDDN
MLDSLTPLRELRSLVYLSAANNNLTDEVFDDLAPSGTTLERLNLSRNRLASLRGLRLLPF
LIDFYAEENQVTELRNEDFSMLHSLTRLNLMSNQIQRVQLDTFAGFFTVRFLNLSHNALE
KVQFVMHLANNLESLDLEHNNIKSLHGFDILRELVYLRLANNGIESWEELETLSGLINLR
HLTIAGNPILRRPASSSLTKSIPEYSEFQVSADIDFSAGKRSVLFDSLTGAEASNKLVSS
MVVPSARNLVKDVTMLSRRLEEWDVDGFRELERLPLIEQHRFRVISILRQLLTIDSVPVS
SEEIPRALRLFKKKRGTWNFVGGNILPAGSAARAVESQRAKNGSGMP*
>TCRU_1406 hypothetical protein, conserved
MTLTIVAPSPSLVRNPRCWSESWEELRETAVKSRDQIVLTCDSASPLNSDNFQARLVCYV
RTLPRLNDVKSALRRLNTLHELGHSYVRRADDPVSPNRQYDGETQGHRVPRPTIWKVENS
VEGGITVIDALSGAKLMCILEPKQGVMVASMLHAPFRGFINRRLEVIPIENPQDILLVRE
SSLINTDYVWVGFMDGSIRLFPADSRWVREQDRSVLLARGQLADLVYELPRQHKGAVIAI
TRSPCHDDSGTTDLVTANRLSSSIFELTAATSRGCREDREHLSLVCTASEDSCVVVWDVR
KIYRRLEAMRALSQNTRMGGFGVEPSLVSLGGDVVTFNVQPTTDQHGYTVRSTYALVKVR
PLLRLKGGVGGLRTLNWVSSAVTTVGYQKGRDVVAMTRDPKEDTASELIKNRRAIQQTTR
WEKREEHRVMLRLSEENMREVEKELEQLMPPLAPEPNQRRRVNLIIAGDVHGTVHFWNLD
EELERETSEIHSMCSTSRTASASRDSRAGQSPLRSLDLSLNSSRRHPAEPAVTSARGSVE
RRNDGGKLTSRRREFSPRVHTERDTKGKRPNKDAGSEAAGKEQQSSSVPSPRTPGDVKKH
VKARNTAADKGVKTPTRRVSKPPSLNKPGVQLGKQSNITTLRAPHLSPMSSVTADRVKKG
NTLAAPVRMGGRGLSSAKGVRQGNNCFRTSPQAKNSLCQSVRSPRSNLTPLATGRRTPRT
TEKQLLRRTSKCPRQRPSRGLEGVSDVKKTRTGDSGYFSTACMNKSLNMHPCESSANRSP
FRVPRGMPEIETNWTVQWNSPRISNSGSSPSSGRRSPTRHPSPYDATHSARADKEAEFKE
WIGGHRYINDMYSRNAKFHISLIDGVTVTGIAVDLPPIITVTMRRLPDPPEPHYSLLEQP
TKEEIRRRELANSFYSLTEERALFCVFERIQFYVSVERTLMNMQCSPKARVDVLEQRVGP
GRLEEEGVIVGRTPFNFDIVFRRHVLEMHSQPIVRLFIDHPRRQLWVARNHGLLSVFSTE
TKSIITRVKGPSADEAIGPPNAAEWKRTQREMALFGRRPIYLDSHKSFRKHRPGYFTGFR
PISLLQQFELMRTSLVHELDSERELSTPASETVRVHLTIIEGKDALDKHAKNREIGLSVL
LEKLRACRQHALTVRQAQRDHYNALFNGASFRIGSLIGRCATFGVLHAARKIFWSWAHHR
EYFPRQYVLRQLRQRGMKQLSKVTNAVSLNFEMRLRGEYFTKWRVSVQKRRTCRLETWFA
RCLQAQVRTSLRERFANFMGDRNRRQRYWFMWRSLLAPTARPPSLPALCRSVSPLNSTGV
TKIFSPSSVQSMRRSSTSRPRVPERNGVFLDMYAIIRQIYGLRQELISFRGDVGSDSVLD
LEDPWFDAIEAASEEAEAQTAYALKLAVFKFALVPFLESLLSTAEGVLPYIRESPVTEEV
RSMLRGCLLCVDYLYADAEDLTSTAATRRSGRASTGSHLSKNGRASLLLDITTRREQEMR
QLFDDAMEQREFQISIESIAAQRDTIAEFLRVCSGQ*
>TCRU_1407 STAG domain containing protein, putative
MAGKRKTKKAATPGATATAAAAPTDTDAARGSGVPDAAEPVLLQEEGSSLGESLYKALVE
GASADHVVKDLVRIYSDGGKETVCCAILNLVGKASGAAQVELDGNALKDDADVTTLLEEM
YARTQQNASAYPFVRKETKYRVFRTAYRRFFARLVEFCYNANILLDGLLLSTLLRWLIAM
SESKARCFRHTSIVALLALVGALNGLIRDLNHRLPSRGRGKKQQLSALQESIQTMVELRN
HVISQAIHQRPRDVAPEIRLLVFEQLEKWILNYDEEFAENKYFRYFGMALYDKRPEIRAE
ALTMIQKCLVATPESGNRMFLFLQFFAGRLVEMCGDVNMRCAELAIRVMVLILRVYGEEA
EGKEILDNEMIDRVLLTLFDERPSIRHEAGVLLRAFIDSRVPKDASNGVAYQKAAMELLC
AFSATLRSQYGEVMPERYLIDALYNPLQELPPFLENYGSMLDFVLSDDALEVVVGLGFVA
ALLEKLRCKLYLGPLPKEDRRQGIVKKLPPNKQEVIDALVTSLSRDVGVLLDGVLEKHRG
DVAILSGVSAVIAAMEFKAFTSLEQVARINALMTLMRKATAALPRCEEAHLNQITCAWLG
FVVEDHPLKSAAKGQIQELLKQVLKQLSALQKGKKRSESQLEEKELFHVWGRMSILSSIV
SLVDQWDLLKASILRYTNSSTSPELLRLILSTCMRCVLWQLKVEQEAADSLEAATTASQM
IGELVTCIFKVWEMDSQRQTENFTLLPVDGMVYLCDLCALRCYTMSQMEQDVFLGKFSEL
SSVLSKEMHEAKEKLKNAGELFREGGALSEVARSRREVSRLEASQLRVATGVARLLMLNR
LSEDVAPRVFLQWLHAPTKSVSDVFRFLFRSLRDRCNDSFTLEKSILIAAYHHSSDALYQ
MGMKLSSMHWPLPDKYYAACVNMVRFGIEFATTTDPAMLQAVVAYCPKLLKMDALSLAHA
LAANETLAKSTDQNAQLFISAIRRAARLEEAEGATTPVRRAKRVREEEMSEIMEASGEHT

LQPRKSQREATEEGKEEENMFTSPSKVNSRSRSGRRTAGKAPVASRRVLTEDGWRVRPDK
EEVVPSMASSISESMEATRARPTRGLERSHAKAAAATEAAPPTATQETVLSSLAADFDND
EVFIATQEYD*
>TCRU_1408 hypothetical protein, conserved
MPRKETKKRKRASSSTKESVSSTDEQGKRGGALSKFKEFDVSELLQKPQEVPEIQPVVEE
QPCSPCDEVVADPPPLTATDTVEATSEEPAAPIPQLIPPEPLKDLPPDEEFVPLPTIQVV
PMMNRALEAQSGLLKEPAPPASIQRVTQPGALPPAMPTALMELLSG*
>TCRU_1409 Proteasome subunit A N-terminal signature/Proteasome subunit, putative
MFKNQYDTNTTTWSPTGRLFQVEYANEAVNNGSAAVGAKNKDFVVLTALKRSPVAQFSSY
QEKVFKLDDHVGMAIAGLVADGRMLARFVRTECMNYRYMHDSDNPLPLIAEIVGEKYQRH
IQFAGKRPFGVGLLIAGYDSTGPHLYHTVPSGDVFDFKATAMGLRSQAARTYLEKHFESF
PDCGLDELIMHALKALAAATSGGAELNIKNTTIAIVGKGTPFMVLTEEAARKYLDGFKMR
PEDIPPAPEAEEEETLQERSLDVEE*
>TCRU_1410 BNR repeat-like domain containing protein, putative
MRDPRVTEWWQGQIIMIAHCDGSRYCRVYESLDMGTMWKEAVRRLPGIWVNAPSGAYQKE
SLRVEALITATIEGRKVMLYTHKTSHPLEASEPNALYLWVTDNNRTLHIGPVSVDGVVNK
TFDNTLLYSDGALHLLQAKGDHESTDISLARLTDELKTIRFVLSTWARLDTFFSKSSIST
AGLVAALSNAAGDDTWIDD*
>TCRU_1411 Concanavalin A-like lectin/glucanases superfamily, putative
MNKTWETVFDGTKTTPSSTWEPGREYQVALMLQDGKGCMYVDGVLVGGSATIPTPETLGH
EITQFYFGGGEGDINSDVTVTSVFLYNRPLSVGELKMVKKSDDKKGNGGGKKGNGDGSMR
GGRLSGAAVRHCGPLLRNRGEDFLPPAGTYASGHALF*
>TCRU_E3 ubiquitin ligase, putative BR.1
MAETPYESPSDVSEMDPESAVLVPIQQRIEAQLRKHLQEVSQQLYDVKNELVTVQKEREK
YGVELYNAQQHLAKLQETLEKQHEKHVSVQRQYEEKLQEREEISTQADSLRKEIEDYQRQ
HERQQADLAKLTETIVKVQQFNDQLKKEVQVERRAAYKTEEDITNLEREKLKQDNMIDVL
EKRVILVEEEVTTVNTQIESQQKETKRAREILAEALAEMEAINFEKKQLVQQWKSTLIGM
QRRHEAMKKTEEALQQQKDDLQALENEITGCRKDIQGVQTETSKLMEFMSRVDNEVTVLE
KQIDALVERKEKSAQSYAMLKNNLEQTDAETKKLEYEARTHASEVTNIDRKIQKCARDVR
SMENDIVEALSKQSTLKQEGSGTLQEIEKIKGSIRVKELQVTQMENELARIRVDTLQAQS
HNETLKSTLGELEKELQSRGVLIERMQMDIRRRHDEIDRKQKQLDQLNHQYEGLLAAQVS
DKGEHVGPLEATINSLSRAITEKVNENEGLQQEWIKLQTELVNCKNNANEVNEAILELQA
EATVLMQKRERLLANIANEKKEITNLENKANAMHIEMKKVNTQLSKNSEDQKNIANEAFL
LENDLIRRLQEKKREAIELELKVEETRQAKTDLLEQIMNCERDILFWERKMQIAKETEMA
LDPTVGRAEVEKMRKEIGIMEKRMNDLQREQRFLVEEMQRSIDHREIIRTKGQAIQNATK
KNGRGATRLDVDKESARMFKELNEKREEAQLKERLIRESLVEIEKKSKEIETIQREVENL
DEQVTELQAQLLSAQKECDRLEDEKRIKNTTLQRLRDAENGAYNLAVSPEELNEEVTHLE
EKRKMLVEIIDDLTNRYPELEEELSDILSAL*
>TCRU_1413 hypothetical protein, conserved
MNAANALAPWSVQQIFPSLEVSVKYRADLLATASRLPDVASRTLLCPLFHHRLLHHFAQS
SVFGVLSSMCSHALTQQRLHEETTGNGFNGAKNNGYATEDEVKFAATITSSLLEDSMINL
DAALLPIIGNSQGHLLTILKKRLRETEESSLGVKFHEKPTLSMSTQRKITFVPRRKTMEK
VLDQANLPRRHIFSKKLASLTNVAQSADACERRELLGNLGDTPVPFQVRSREEVRQQLRG
QKAFETSMTVVLSDHAVPLPLWKRRRNEVEEITENEGFTAPPTAASSTALNSPQESFVNA
TWVKEGELLLVNGCLIHRDTKRIVEPSAKKEKICALERGEIGSMETPETTTSVKKKTTAE
SERKKRTAKVVCGSFASGRIGTVNTQGVPLMSREEILALVNSLQISDALRAAFLIGLNGD
DNSKIKK*
>TCRU_1414 Ras-induced vulval development antagonist, putative
MATDGFWFPASEPTGEELETTIFLTFLQNIFSTQNVPANREAAQMERKRSRLFQPKRKRD
RHEESAESDQKERGGNLFHIISCIVHAAGIPYEPPLEEQGVAASGFVSMAAETTTITNTP
QPEKDVSFEGDYAAPNKLVQQPRSALASLVEIARLKERLQKTENSERKTRAFIAVSADPL
RSNNEGANIMLERHKSPTASEQSGDDFGVALPLGSFISDDTNDPSKKFEIPVAKHPSQMS

QEEFLRQFKRAPRRGEIGYDAESVAAAEAVGYVMSGTRNKEKQHYVDNIQRKLHEKEARK
LRLQFRKVEDERTDNTMIQGIIAVVNEKTPHEGL*
>TCRU_1415 hypothetical protein, conserved
MQAQLEEKVRQNMETRYALHAALKAESLKWQLSNAQKEKDVDDERGGDDESHENRFGLTN
GEEREKILHAPRGLDSGSGGAHLKKKHMKVRTSFVRFDLVTSHISPHRPQATAVGQPAEN
ATTSACLEIERLQEALYALDQQEEYQEKRAEEQRLQQDAVQLLHQQGLRVVHLRR*
>TCRU_1416 Endonuclease/Exonuclease/phosphatase family/Endonuclease-reverse transcriptase/Reverse transcriptase (RNA-dependent DNA polymerase)/RNase H, putative
MEPSKWLPAERYFYPLLNSIGAYQRYAYRLRAVCDAQRQKLLLSGDIEQNPGPIAVLQMN
VSCLTPSKLATLMAQGADTIAIQETWKSSEQIASMHTGDYVLYAQSRIGKGGGVAVLARK
TLRSKRIPLTIPQHDTSLEVVVVQVALDQNRDLIVASAYMRPPPQVTQSFRRLVNCLPAS
SPLLLCGDFNMHHPQWEPFLETSPSEVAAEFLELCTDAGLTLVNTPGEITYSRGTRERSC
IDLTWSKHLTVSDWSASVSPLSDHYMLTFTLHQAFKDTIPSAPKFFYSWGKCKWDLFIKD
FDAQLPAYDCKKQSTGIRAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERIATDSEA
RYLQLPTPDREAEMQRTRSQFFLLLRERLRNTYLRRISKLNPGEPLAWKYISGRKKASLP
SPTSILLGDGQHTYKTARRAANALNRIFLPFHPSHKAVGFSKGINRQSASLNINASFLFG
QQNNSESAATFTSGSSLSSSSEPQDKNEAATTSGLVAHLHSPLDAPFNRTELLAALRNTP
YGKAPGPDEVYSEALRHISSKGLRFLLPCVNRSWSTGTILVEWRRATIVPLLKPGKSPEL
LESYRPISLTSIVSKVAEKMVLKRLLWVWTPHPHQYAYRSMRTTTMQLAHLIHEVEHNRN
HYFQVNLPKKSGIGNQLHYRPHRTLLVLVDFSKAFDSIDHRVLSRLLANIPGVNCRRWLR
NFLCGCYARTRVGHRHSDRRPMLRGVPQGSVLGPYLFSLYVHPLLNLLNSFAGVTADIYA
DDLSIIVKGQSREDAIPTANMVLQKLHAWSQENGLAINPSKCEAAWFTLSTHTESDDDRE
GRWPLVVAGCPIPVMTMGASRTTKLLDMDLDPRLTLNVAATKQCAATSQRISQPRCIAHK
EAGPSPHDLRTFVIGYGASKLRYGSELIWAVATDSAKNEMQKTHATLARTVSGVPSTVDP
ESALLEANMPPLHVLCLRARLSMFENTRACQMDWMRRPPPEPPPRAGFRISPLSRDELYA
SVDAYTKDYGITESSPREERFFRTSIPPWFAASAHRATIGVELPIDHSITDEEELIREKR
RVSEEALALHSHRTWILATDGGVDVPKSAGVGILLSSLNSSKIIEKASINCGARPCSYRT
ESRALLLALEKLMIPRIRHRRKTLLVVTDSQSLLAALNKGPLSQTDWTEDQIWQRLLTLT
RAGWSVHLQFCYGHCGVHVNELADQYAAQTMATGQYTEQGIAPLWHTDLLTCFTTQLTNK
WRSTIRQDTHRYLLCGTRPSDLSGKDLITQEVLHRQELVHLARARCGGSELWGRLYWAVR
DCTNQCRFCNISPERSAYMRSNNDPTAPGTGTVPPSAREEDVSPVRRRTLTRRRKEKCPH
CDSTLTGFSGLVSHCRSFHPEHPPPLPELKCDFCDMVFPTRRSTAQHRSRCAHNPDATRH
RNSSARRRSLLPQDQPASTSTPIGPQETLHHLLLECPGTLAVRQRLGIEQDLRLGKSSQW
QLLHSRKLLSLLDHLLST*
>TCRU_1417 hypothetical protein, conserved
MCVILLLCCVSAALLRCEAAVVRYDVHTVRAKVAALPDDHWARYDETVFERGRGSFVSGY
DDAPYFEPMNISSPFFSRDSVPWHVSSDGFLAPTPSPLCAFFCSDSAPDTLFGQYQFGDA
IYGGGGDWPMIGLYVADLNPSAARLSPSVRVHGVTGADGGPGYERVTVEYRDVPLPACVA
PRDTLTAQVEVWANGTIVMRYRQIPACGRASVGLVLSKGERVVATATPRPNGIAAIRYDP
VVDVCAAFLSHSACVNAADLCGWCAATGACVATSLASSCCPRGSFRTAPPPSPVGGDFYV
VAVEQGAELVRLAALRGHVRVVPAGQSLQLDMGFDFPFYTRDQASHVTNTTHLLSSGLIS
VFSSTQRCGPIWNVCPDGNYTFAAMPFVTAGLWGPGTSITYARLPERTGADVLCERPRCP
PGFVVEVANTSSFASFARSSTYQVYLDASGAVEFRYGLPVATSIASSPVLGFFAFPPPFV
GLFRYRVEDPATVTVPPSLIRTGTRVRFDPTGRCNDCGRHGTCDPASARCVCETGFSGDG
CERCVAGYYGPECLPCRRCRNGGVCDDGVNGTGVCRCREPFSGVDCAVRCEGPFDCSHCN
PRGGYCECGECRCDAASGWGGADCDVADDPCWRHSFDGCEVCNKDTRNGCAFCFDDMCYS
TLLKDTPNGHACSYPAPSGDASRCVPAVQVEVHWFDWGYVAAAGLCLSVVLSVLALLVLA
PFAVRARGVHDIHHAGAAGGAPDRRRGRRRREVVQAVLVQQGAHRGERTHVLGVPLRQVP
LAKLYESQRHGPS*
>TCRU_1418 hypothetical protein
MEQNGLDKNNYYSILGEPSKEQQQLYVQGKLGAVKNTQMRRDNEEANHFRFYELGLSQES
PRFFLLPAISSIVSPEFDNKRNEVIHNWCEFLPRGVPNETTFQKSVSRRLDEILERACEV
FDGQVEKKGKKLRIQPSAVVLHDNANSSGKLHIEKKCISLQKEECVFTSLDRTSNAVTSL

EDLPGVSGLLMDLTSRFQKGQNVTLLTADATIGKHHLALTMLLDFVRLALKRKPNETYIT
FSFVFVRNGRFVYDLLADQETLMASKLSFKCNRLLGPMIQDGVRWHDVQHAHEMDAIIKQ
IEQTLSVLLVRCVSKEDMQSTFIMLTAVAKTVEPHDVVFSSFVGFFVWNEVNLYDFLLRS
QEQEKQVNSAEKEAMRSILLSAVRDRSSFVRTCFVYHTAMPETCAQRFLMVQNRLCGCFS
NEPHKGTLASMTRRQKAKVTGKTTGWRRLLGRGSVKMGEDKSRMVNQLKYFEMILADTYK
AVLLVEGMESKPPSTESPENGGETGKDE*
>TCRU_1419 DIGIT
MPSPPAPPRMIDRRHVFGVCEKVKDGFQYLDDTNVVWVSGKSLVILDTQLGTQQLISCTP
TCQSVTALAISYNHRLLAVAESSKFPCIVIYVCDPSGNPKLRRKKVLQVPDLGSTEYISL
GFSLDGRHLISLGGYPEWNLVYWNVERAKIMATCAVLDENELGSRDKRLLNQCSICPNDF
SLVCVSGHGIVRFLLLRDNQLRRASGGLREPVTNYMAHIWIPSENRLILSTENGDLILME
NNEYKYPLPMSPSDGVSINTLIAYSKGFICGGDLGLIYIFERTDNKEMYRKVRTFKFNND
AENMGPPSELIPVILSLALSPPPAEEYVSFMTSTKQLYSINLPNADFFKSDERVFEPIGQ
PFHSGAVIAVDVSVQRPHAVTAGRDRCIFLWNLITGVVEFRKRFSSDIHSIAMHPSGLHL
LVGLTDGLRMMNLFHNDVREFKNIGIRSCMECRFSTGGQFFAAAHATTIHVYYTYTCELL
GHLRGHSGKVKTIFFVPPDDTRLVSVGLDGAVHEFNLCDFHKVNDNVLKAMTYNCGLADV
GTVWTAGNDQKLRQFDRTKLQPVAEYDLQNASLYSMVISPRLKLLIGGAEDGTVRVFNTY
LGEKLSGMERERENGGEIMIESHNAHSGIVTRLALTFDESLVVSVGEDGAVIFWDVVAPY
RGPHKEVEYSRELFMANSDLEASTKTVSALEAEVNELKQRMQQQQIKRDRVHEEQLLKLE
QEYADEQARRLAQYEALKADKNEQAIQFTDFMAEMETKEKEALKRTKEDYSLKIQSLRDR
ADRLRQLIDELQHEQDAHLAEVREVAAKKRAEDSERQRKVLKELEEENHQLLMERDEDTK
RTENYCALIEDETDVEVTLLKEDVEKRRKEQEEEVATLQANNDLLLSRENIIKAELEAVK
ADVREKLRQQSTLESQIEAAKRDIGALTQEFKDRGETIAEKERRVLDLKKKNQELEKFKF
VLEYKIKELKLQIDPRDEEIRQAKSRLSEMGKEADNYTHSNEHLVLQIRNLRHKKAGQQK
ELDKLAEIMRGFAEYLSRLWTELSCLREETNPRKLKECAKMLFDKYTSTKAVAANKTLAS
RTAADEVREYNRERDHLERNLAGLKNKVNKDAENNRTDKNRITTENVILIREINDLRKEA
RRLAEKAGAWRKTEKCGASLQQEETKRELAMQRAELKRLRALARKLAEEAREKGITLTLP
SLTEGRPGS*
>TCRU_1420 hypothetical protein, conserved
MWRRRPDRSAPGCRGAHVADEPNHAGHGVSGVAKNCGVTRDVAGAPPDKGRSGSVYPQPD
RWKERVVLRLAWMPASCLSEIAALTPNNVTLGPDGAIVLDWPAAPKTARADLRRASRFVR
IRGQDAPDTTKLCGALRHNEKLMNPRTARVERAVAPWNATAHSIERGVLRHAARIVGTYN
SDPHVITQSAGHGGSFGLPQDTVRYFGRRTTTLTQVSSLAAQVRRETPRKDRNPG*
>TCRU_1421 hypothetical protein, conserved
MALVPYTVSEWCDIGARLWDPVRQRGEAQVQITFINGTEMSDETLTVAPSSTGLCLILGN
VTRPWEDSSLTGHIANLRAFQVPNFENQLILPIMGAARELGRVARAHHCRKEALEHEKRP
CRRGRAESKRSASFAAGRGAQQPIGARI*
>TCRU_1422 BNR repeat-like domain containing protein, putative
MIVDCENGRRVYESRDMGTAWTEAIGTLSAVWVNSGSGDSQKESLRVDAPIAATIEGRKV
MLCTQRGYASVENRANPLCLWVTDSNRSFYAGPVAVDNAANWMLTSNLLRSDGSLRLLQG
RGNGECRAISLSRVTEELSAVRSVLSAWTQKETFFSSFSIPTA*
>TCRU_1423 Endonuclease/Exonuclease/phosphatase family/Endonuclease-
reverse transcriptase, putative
MSVLTNGTVPPARPATSTWCQGLVLFAREEAKRLLPIRCARRGSRRRTNGSEGHLMEPFT
WLLAERYFHPLLNSIGAYQRYAYRLRAVCDAQRQKLLLSGDIEQNPGPIAVLQMNVSCLT
PSKLATLMAQGADIVAIQETWKSSEQIASMHTGDYVLYAQSRIGKGGGVAVLVRKTPRSK
RIPLTIPQHDTSLEVVVVQVALDQNRDLIVASAYMRPPPQVTQSFRRLVNCLPASSPLLL
CGDFNMHHPQWEPFLESSPSEVASEFLELCTDAGLTLVNTPGEITYARGTGERSCIDLTW
SKHLTVSDWSASVSSLSDHYMLTFTLHQAFKDTIPSAPKFFYSWGKRKWDLFIKDLDAQL
PTYDYKKQSTGIKAFTRALITSYRRHCPAECKRTVPGFGTTLSWRQSGLLPTARPAIYSH
RRPTVRQKCNGQGVNSSSYSESACATRIHAASAG*
>TCRU_1424 hypothetical protein, conserved
MRRPPPEPPPRAGFRISPLSRDELYAFVDAYTKDYGITESLPREERFFRSSIPPWFAASA
HRVTIGVELPIDHSITDEEELIREKRRVSEEALALHSHRSWTLATDGGVDVPKSAGVGIL

LSSLNSSEIIEKASMNCGARHAATGRNPVRCF*
>TCRU_1425 RNase H, putative
MIPRIRRRRKTLLVVTDSQSLLAALNKGPLSQTDWTEDQIWQRLLTLTCAGWSVRLQFCY
GHCGVHANELADQYATQTMESGQYTEQGIAPLWHTDLLTCFTTQLTNKWRSTIRQDTHRH
LLRGTRPSDLSGKDLITQEVLHRQELVHLARARRGESELWGRLYWAVRDCTNQCRFRNIS
PEQSAYMRSNNDPTAPGTDTVPPSAREEDVSPVRRRTLTRRRKEKCPHCDSTLTGFSGLV
SHCRLFHPEHPPPLPELKCDFCDMVFPTRRSTAQHRSRCAHNPDATRHRNSSARRRSLLP
QDQPASTSTPIGPQETLHHLLLGCPGALAVRQRLGNEKDLRLGKFSQWQLLHSRKLLSLL
DHLFGTLAAPYS*
>TCRU_1426 hypothetical protein, conserved
MAEVRFAVRPTAALHHVGFEVETSRKQTQLYVSRRGLVLYVPHPYFIIKNMRRSFWHGVD
KVQFALYPIPLSVVTAFGFGVFLWVLNSPADAWIRVSCVSDILWRLERNFISARIPSRYR
TPALCANVAFGAVTLFTTLQRFVLRKLLSYNRWIYEGQGKLTRKKMLWGFILKTFFMHNL
KRTGAYGSCLPSQPLPDLKITVQRFMKSMVPFYEGKTAE*
>TCRU_1427 Choline/Carnitine o-acyltransferase, putative
MTDWWIKYVYLAQRESLCINSNWFGVAFAKYLPTPLQASSAAALVHNLVKVKKSLDRRTF
SPQFSGLVPLDMNQYRYVFNTTRIPGREMDVLVQHEGIKHIVVIHKGRFYQLEVLHPLTN
HQLTPYQLEMALESILHSEDETDPVEALIPAFTTAPRA*
>TCRU_1428 Choline/Carnitine o-acyltransferase, putative
MEPKSLEEESMMYLCGNGHNRWCDKSFNVIVTEGGHCGVHAEHSWGDALTLANVVEYSHA
SDEFKELYTEDGHVKKLPEDEVALTEGKFKVFVPNRIRFTTDAVMKRAVQGAQERCIREI
KDVDIRVCRFADDGKGFPKKQRCIPDAWVQMAMQLAYFRDQGHFDQSYEAASMRMYRKGR
TETIRTVSEESCAFVRAMEQPSLSAEAKLKLLRVACERHQKTSPDAIAGCGIDRHLFGLY
CASTGFEVASEFLQAAMQSKWKLSTSQLLTRQLPAKFYPPSDEPFETPNGGFGPVQDDGY
GVCYCLYGESLFYFTITSKHSCKSTSSTRLAEHIRRALRDMAALTGWN*
>TCRU_1429 Protein kinase domain/Protein tyrosine kinase, putative
MQPESGTRGATGHILVPGFLGCSGSTDSKYTYVRYLAHGSSWETWKVLDVSDGKPYALKI
TSLKNYREPKLLRVRTEVRCLESIDHFACIRLHEKPETESHFFFVMEYCDAGDLRYQMRD
GGKLLEHQIVHILLKLVLALHYLHTKKKILHRDLKPANVLLKTTGLLKLGDFGFSNAYDT
ISGDVGLTICGTPAYVAPELWRNERYGAAADIWSLGVILYEAMTGRRPFEGTKYEELRHK
VLHEEVLPIKTSHSVDLKRTVYALLRKSSVERPDTTQLLREPLLVAALSNFPEVLRVSDV
EDSLLQRVLHDISPEQLLPRPRLDHSVLFSGMVWKLKPTQDYQERYMELADGQLSLLLRP
GGRVGFRGCIPLLRVEQVACIDPNHFALKIEGADWCFFQTPQAAVWEEQLRAALGI*
>TCRU_1430 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MAKHRNTDQFGPHRISHFFFGAGNKEDEGNTPVTVADVLLYNRILYRDDLRNLNARTVPI
RHPAAEELDTAVKFTATGEEKQKATQLTTSLADVEDPRIAQPTNSQSVRVLAGSESSAEN
VTDGLSPRTAAKNDTSVPETSHSASDGRMSSEDRLALITDAKLILHDLSGDSTARVCVSR
VLLLLLGLCALVAVL*
>TCRU_1431 hypothetical protein, conserved
MRSAVGACPRSRHRERHRAIAAVRAVLFVVLVLASAAAWMPAVHAVVLRLRGGTVDRAIT
VGHAVDTVLMDGVSITNGVAVVFDVPAMLPGVLRIELRNCVCDGGAQLYVRGYSGEPASD
RSLEVSVSGLSGGYCSLLFVHNLPAHTNVTVRDSTMVTAGPMRYSQLSGLTDAVASPLVL
HATSLLQTQLRVSNTVLRSLHAGGSAVHVGGGVDLLSSAVVLDGVSLEASGGPTASAMRV
ASSSRLSLRSHSVFSVTNVSVVSSGGGLALGERLAVSDSVLRFVGVEGSAASSLVRCDGG
TVGRWVLAGGWTCTTCGRWARRACRSTCRLRGPVVVRGTARVA*
>TCRU_1432 methyltransferase domain containing protein, putative
MKRVVIDLRPKESYAEGHIEGAFNFPWESIRADACGLPPRDVALIAICDGQMDLDIVEAY
LNRFHFASLEVRRLSKNDELVCELPKGTCWSPNPFLSEVITEIEVKNGGPSFALDVGSGT
GRDMVYLASRGWSVVGIENRFRLIEQGVALSKKHNVDCRTLYIHCELKKFFPVKFEGPDL
LHVCRFLHRSSLEMLLKLPRRGGFLVYSHFLDGCQKTEVGHPSSIDGFFLCGELRQILFG
AGYTVIIERETTLPDKRPLVHIFAQRTR*
>TCRU_1433 leucine-rich repeat protein (LRRP), putative,
MSGVGVLGVLPSLCVLDVSKTSLTDEGLDGLSVNNSLRKIILDDCARLTNVSELSSIISL

RDVRLRGCNKMTGISGLGSLPELDSLDLSMTAVTSRSLSGLGVSPSLSKIFLEDCWNLTS
VHTLSSILTLEEIYLRGCIRVTDVGALGTLPVLCLLDVSKTSVTDEGLDGLSASPTLKRI
LLEDCTRITTIAALTSIHTISEVNVCGCSGVKSFLSTP*
>TCRU_1434 hypothetical protein, conserved
MRKADNAQQKTAILQLPVAIAITKIVKRFPPERFSLHVEHLLDEVILKLRTKSDKHRESA
RKILSAMLCETGPGKLAFVITKLRDHLVHGYQLHVLGYTVVTLLYNLYEPQHAMSYRRKK
HVMGAEGAAAAAAIAAKGTPMEHAGAAFHQGDNDNDNDDDKEKVEQQSQTEARQKETTRE
EEEDAEAEEEEEDLVRQLIPASNKFDWAYGVECLTSCLDNLMSIFLDDYLGEVGEQKEQV
ELMSTMVEVKRNRALQGFTLIASHCEASRVIEVFLEKITWLLTPPSMADTVDVSTLRGSA
RAAALLLQELKTKYSTVSKNAAADFVFVQKVRLLAVRFARALIKNATMEVESSFLTVRDL
LRRHNEVREEKIKTFEAKDGTRRIRGNVHLTIQRAPTATRKDQLDSNFLVDQLPERVDVD
FSAHTVLATQQRQKLRAYRGRYGKEVQQAAKNFYREDPATAVVLDTLDEFLLKYLLSVLK
HVLGIGKERKYTTAAVRLDLLRAQRKKNKNRKGENSCQDEDDDDDDLPEELRERGGKEEN
EEEEEEEKGGDSSSDEEGEEEGTDTLLLLDPQPLDDERGDALDRFATAAQQENEEWDKNA
GEVSEQLQPMTTKKEKAKRHVQEVEKKNKTRRPMADLTTSFTRHHQQLLESLLPVVLTTL
QGEGCDAVVGHALDCMLALVSLRPPLHAVGALHTTLYETVTAFFERGGAIKQRAMRVAAA
VVAHQRFILTEEKAAQLLQLCRTELVDRNEFLPMALSLFHAVLGKHIHVVEVYDLIGVVT
ELMMHTSAKRLLRQRCIAVLARFLTEYRITPEKFRSHMDLFCRNLDYPEVTGRIAILELL
GVLVYRLPTAVLRQEAPLLLIPLAVTLAVSEFYEARQKAGDVLQSLVKNAGVDVIVPTLS
QWLASGQTRPRRAMALQTWAVMIPAVAASYDMSVDEDACEFEACWSWSLQALLDAATFDQ
VATFGTKRKYEELTAAFKRKLELKSWTYVFFGLRCLEGIAMVAPMQVWHNMSVAPHLVPF
LSGRLVLHSHPWIQSVALRLLRMYCHDGVERRCGYLRGIDWVAAGYLVVTSKKNHKKGKR
RKSGMGGNFHATQRASSPVVSHSHEDDKDDGCIPPYVVYFHESLGPPDTVHRALNVLDQM
AAAMRTLLQFIALSDVPNEKYNAHRAMQQPSRTDAVNVALYISRAMFVVSMVLLKVAVFC
AGSEMSYVQDIIAQHFTSLRHQLHSLVKPLIKNGGVANVMVRTTSLVQYFGGFLAALPTD
AETDNTINGRKEEEGDDRNEPDGKVTSREASGATGPVKRAVCWLARNAVGLRFVRDTIVP
TLTVAMHCGERSEKLSSLAAQASTMVREQLERHHVHFGGDFKTTTTTTTTKRKRLEKNKT
RRDEANVWGKETAATTTTGDVDGDAVTVDEVLFTLTAAMTAVRTARKEKTTRRDTIQTVR
KRSHSGGDDAAPLKARRRREK*
>TCRU_1435 Endonuclease/Exonuclease/phosphatase family/Endonuclease-
reverse transcriptase, putative
MEPFTWLPAERYFYPLLNSIGAYQRYTYRLRAVCDAQRQKLLLSGDIEQHPGPIAVLQMN
VSCLTPSKLATLMAQGADIIAIQETWKSSEQIASMHTGDYVLYAQSRIGKGGGVAVLVRK
TLRSKRIPLTIPQHDTSLEVVVVQVALDQNRDLIVASAYMRPPPQVTQSFRRLVNCLPAS
SPLLLCGDFNMHHPQWEPFLETSPSEVAAEFLELCTGAGLTLVNTPGEITYARGARERSR
IDLTWSKHLTVSDWSASVSSLSDNYVSTFTLN*
>TCRU_1436 hypothetical protein, conserved
MVPNASMKRPSFANGPRILVASNASGIMSVTCGGREHIAADNTDEVSEHDATGHKSLFLE
NGVAGSGFVAEGDAGGLTQRNASGHEYKPQLREFTAQYSVSGVSPDDCFALATTRN*
>TCRU_1437 Leishmanolysin, putative
MLTWCVWQSAVGGGALDDCRGGCEEPRDCDDIDGMELQDGDGDGRTLESHWSQRHAKDEW
MSPIGCAGCRTELTLTAPADLGCMRVRWEMAEPIRW*
>TCRU_family, putative Se.1
MEHGVTLLENPLTPRQPIMSSPARYFFAVEDASVGRVVEDWMAKVPCRDAHIFALGYTPH
RSPQQLVWVRIAPRAMRSKVIMLDFTAPEVLVFHLSMQNGFPQLLSPLSPPN*
>TCRU_1439 hypothetical protein, conserved
MGVGRQSTVSDQLLLLGLRQLVGAARSHKQQKTQTHWQGHCGIPRQSPHAIQVFPEGFVP
NGDVLFHLPHLRQSLLPVLCHKPRANIDVQRQSGLPLPKLRRSPHRTAQLRKIGLRLHAM
RQSRVIRVEFFQRHRKLLHALRKESMTVGAPVHIFLIHQLLPLRVHTQTIPTGLLIQVIL
QRHQVIKQTPTCALLHQRRHRDTAPINDDPHRVAAAVGAPK*
>TCRU_1440 hypothetical protein, conserved
MMTGRVLLVCALCVLWCGFSLVSADTGDDREHSGQGVVGSVGQPSSPVGGHGDNGVVTDG
SSLSSGSHLPGSAPTGGKPSLPGVGECVGLTKSKDALTLAKEGHEFVRDQHELVPQVSHH
TDAGTGGKSDLSAPEQSPNAKTELENGGGVCGDDAAAAEGEVITTVNEEQLGGSSTSDSH

PPAADRGAKEQEGTVEQAASTAALTPVVGRETTPKGDTEEDSPEDKATTGAGITQDIPAA
GQQQTHSSSTSTTGNGPTSTLGKGRAAEDISNNNERSGKALLREGAEHETVAGSQSQAIP
AATARNTLGTTLPGGSDNSTTITTAVRSDTGTEGTPTSNHPNRQSIEGATSPGMNSDGEA
ASAKNYDTVPQNAGIPTTKAIATAKTNDAASHGDSDGSTAVSHTTSPLLLLLLLVACAAA
AVVAA*
>TCRU_1441 retrotransposon hot spot protein, RHS3, putative
MKGYVIYDVTEKGKPASWLAPCGEWGMIVVASPKVGNYDKWETQARAERIIMNCPDEMDV
KAMCAWMKRDETKEKKAECWKMVEERMEKVGPIPRYIFDANKFIAHSAAIEDALDGIKSR
DGEKHFIPRGVRLWDSENPSQKLVRVVRGRGEVGTDGFLNAPISFCLWRRIPHYFGKRDE
*
>TCRU_1442 Protein of unknown function (DUF1619), putative
MHVLRYIILYNIVLLALFWANAENPVSYPIDWEGSSSTFPDSRNLESSFLGECVCDMTWG
VCDPNCCCDTDCTVEEKQKFLFCLQETVGSSSMDYCYEKQQDEKVTRSSRRYLDRANVGS
SAVCIVRSNNLEDLNSFFVLPKEVPKPREKKSIDWSERKESNGYEVNGDLLLMKRIEVGE
SLYEMRSMGLFRIPTGSRGGYCNPEGRRVRFMNPIDTTSCVLPGERVCTLFSTSTYANLF
FVSPGYSSSKIFTPIQLRIFNHTSGKLLAEVDSNSSIPEVYSSVVNGDSCQNGVVRVQTV
LFYKSNDNGLSLINATTNLYINNINREAIFPMSFQIKFFRSVAAIKLNYFSGTPGYFEGS
RLRAGTLVEKSGKTAILERVSGFSVPSGGRSCYKNKYRTVGFLYDILSSGCTIDFSELEL
RDICSGGGTTKILRSILSINVEHSTDFDGQTKPIEYVARTNDALTNDTTSWIKIDGMNFS
DITPDPYDPVKRKCSNIYVGLHYSFVLSKVGAESNPQDIIVAAFADPIIGSWRIRNTRNF
GENAKSTQHFLFSVSFKWIDSDLQKKRRRRVIAPPILPRLDETVLYPFKAPG*
>TCRU_1443 WD domain, G-beta repeat, putative
MQELYDTVSRYTGRGTPSHFSARVHPRKAASQFVGSSIFHGRLNSFCAALVARFMASNEV
LVVVSRDAVQSISCDGYALQPRSSTPGPTAGEITGVVTSDGFTTVGYSAGVTRYSPSLQL
ERELLFDGYSNSILSIAVTPDGTCIATGGGNATVTVWTRDMNPMHYLSGHTDWVRFVKFT
KGKSQRLQLFSTGDDGLILHWDPIAGVMLSRLDYSHGESVHAFEVSWRTGFMAIACDSPV
ITLYKPRENGMIMPCHPEMSTVENIGQITDAHRLVPTAVRFSEDSQWVISAGEDETLAVS
SVRKLKRVFVCTEFITRRHCMAFMNTFTSLCILASPPETSVLIIAACATDGTVVQWVVNP
ATSRSSYTKKLQLHLGALVAMDIMRDGTGS*
>TCRU_1444 EF-hand domain pair, putative
MQRSLIAGHNNNRHLNYEELENNIGGLPITENKLQELFDSLDTEHNGYLAIEDVKAFYKG
LEHYGLDPTDAEVANEIRKYAKSDDNFMTFDEFCCLMLNFAQR*
>TCRU_1445 hypothetical protein, conserved
MQRGRGQTARRLQRHAVKHHRTRQQVHAAANVHRRPARVQRPQHSVAHTQLRLQQRRRVQ
QKRRRHRVRQSTQLRVAHRSRRHNRRVTDRHVRVCRQVVHKHKRAVAAGQPAHAQLQAPV
TRRLAAVAPHVDLRTAVAHAVPQFNAQRAGKHRRHVEHHSHAVRDGHAVHQHRVHGAANR
DGSVHRAAPQSQHHRMHCGHTRSSCQHQHDEQRHTHSRNGPALHTVPAARTRTHRRPHPP
TQTRTNRAVVVCRTRPVDHNSCPTNPFLQMANSVTQFCQIVIPVLPILILQLIPNTLKR*
>TCRU_1446 retrotransposon hot spot protein, RHS3, putative
MGESSIVKVVKGLSRRGVKGCIVYDAAETDNRLSTCLPPLEWGMLVVTPPEAKMHGHWAS
ERRAARIVMDCPDESDAGAMCIWIWRDQPVQQQAE*
>TCRU_1447 hypothetical protein, conserved
MWNPRNDGNGTRRDGSNAVSSLPLLSSQRLYLLAAALSIPPGRLLRYITEVQRRGPHPLH
HQQREAHCDVIRADVTARSATDTAAVADAFGASQSGHHYHHPRKSKDRLDASTTDGTESV
QEFPLLLHGILSVLVLPFLKLEGSSGAPSASSSQMAAAESVVTQLKDDGGKRLTLHKSGG
SRRVQVTGATSAASKDFISGRPIRVNMQEHFALLKGVIVSQHVSRPSQESLSGAGSNFSS
SRHSSSSSSSRGKMNSTSDDDGDASVSSGSAARGVNEEGDVSVTNKKSKSLKSHVYNLCE
IPPFQREASIVRLLSELAEPFLAERHHVIGNISSSGGGGGGGGGPGNSNDVESQTDLQQC
MRLVPRELHTAAGVARISELYPPFMPLLIEALLKESVHGDAFGLTARRVVVRLIELSAPT
FVSKFFKWGNGASVEASKREEEMYHSMMLHATKRLATTAVSLLEVIEDPVWALNISGSLI
ASQLLHPNAVRALLRHRTVELAKKPLLWSPTVALAYCLVTQHSLRTSVRTEKEQCVLNQQ
TEALPVLNETIDPLDTTGVGILSLISPNSMGKGSILAAASYSMHEFPEHSQEEQQTPPHR
DPFHLSQTQPTPTSAEAASGMPFNLGLSAALMGRAASLTSSLRFSPLQLSTAPEVEHPFP
LRWPLPEKVPPTVTMPNVIVMTCMVLGAGTLGQHTVVALGQWCLRSLTVLPATPCAVGLT

HLMLKYPQFLQKASLRISPGTFSSSTATSSFAATAAAAAAAAAASNNIGGTYGNGQATTP
FCIAVFREGCRLANTVMLRQAKLRTDGRLAMVWQRDKAFASARNEVNSSDFEETPFVSED
NALHELYEVQCYLVMMLQALVMRHGVQLAADAQEELFSLFLTTTRIRIAVGTPKGFEGAI
LPDDADDDGGGYQIPKRTLSQLVVKLVDESFRAVARAVDILLHDYDAGCPRQLCESLMSL
LPPNNSLFSELDRVGAWEKHLDCLETVQAAAEAYREACRSKLSGVQSQEEEGMDMAPSSS
WPSRHNYQRDPLQTHVSLLELQQELELRAKQAAGAVRSRAEVMFGSLISVLPSSGEPLCL
SATPSSGLTAAQQLWWVEHTIAYLVEEWWRSRASTPVRFRLGVDDKDEIEKDIPRLREVQ
KSFIQCCPHPI*
>TCRU_1448 hypothetical protein, conserved
MFDGDPLVQKKKQSVIDVGQRTQLDLVNGEIRRNKETLTNLRLENTKLQVAMRQAVRGQH
QGKDEDYFRREEEQLQNKLYLLKRSLNSVTGKKEELAREIERTMEETNFIMKEGGPVVDE
NSTVGQKIRALENRLDKCLIKHNEVNAIRRTYETLLERLQQEQSGFDTQLAAMEKTLQCK
EKDLADLNSVAADATKGRDAAKAELQRLKSQITKERRVQKKDIAERRVFVMSKREQLQKR
AQTLRDKIEKGEERRLRARLAISNSQKKRLRVNAQKKLQPEEVEQQKRQRELYNRLKEIT
MSNNVTDVIYKLQERRDANAQLLLTVKEADSAEASLKEERKKLQDEWEEIQQQNGGTSRA
LMQQHSQRDHFGMDADDIGKGGRGGSPEKGDTSLAHVVEQRAIARRRVLEEFDDHLSNRQ
NELEEAQRLQDSLGKMLLDVDAGVHHLAEKIACGETLGSITGTASTARPSVDTTVSPRSS
SCVGRGEAIVNLLRSCGLKLQRMLDAMRESELETTAKLVARWHGSLPQSNIRVPLERTAS
PDEKQAHDDMEDPGGAGFFLGSTEKGRSVSDEGEPVIGSHKWLGAAVGRGAIADDFPENE
IHDRNELKMMSITTVERERKKAKKQMQQRSKEEKP*
>TCRU_1449 hypothetical protein, conserved
MPSNPARDVKNNISFVPLVSKGGGTAYSEPHPSNGNEPFLCSLSGACRTRPTSPLPGAVV
GRQTEPSNSSHDLGTEDCEEKKNACSSTAWQCEHSESGLPCHAVDGEGEEINGSRDARGH
KANEGKLSKDEKRTMPQRDNCETSPTSSVSGRRGTSPLLSLAGKPAGGEPVRRIPLQGRS
NTPISLDEKVIPTLSPLFDRLPPAVSMPSPHHWSVFYPDGIDSQPPLLLHYLSLGGWRTV
AGGWDYFSHRRLQDGEVIGHDVRWLHSARPRDRFVFLISPVEPKADDESVGRWHKFRDQI
YGPPPCFAYRKGKLFKRPPFGPSESVLPKLGESASVLGPVSNSYEFSTSATESFSFNAEG
GKHRPCKPHIGRGEKRDHRLGATMNTHSTHNSTAGVCGKATAVGVEVIEVRHEDITATDY
SPRLSSSRFAIESKAVYAYYFSTLEGALTYYDCLDDLRLMEEQTLRGVTNRMPCRPKRDP
YKPSQSLGSATIENGYKGDGLAPATTMNTTPRMGVVGMGKETPLPSRKEMTTELLDLTIT
DRNDVSLGEQTELLPLWNEGQTSLSSLPESPNLSRNTRQVKQRHQYDRSIQHLIPVNTAA
ECAYGPHGEPHHPSYRDVMTPFSTQRSPSRDHAIASEPSIRPRLLPTLTTAHFDTIITVY
SEDPNFNAVLREVLMPEPGTHPYTVSLKEQRRMLSMYETGMPAWTIFLASTGLPYRRVFR
LIFVGLVNIWPLISLFVGLYDLYKHLPRMKTFVATTLAPLLEWIEEHVTFRLSMLTTYII
SVGVTVAASFTSFFSQFYLLELFISPLRILGRLLQTPFSLVFELLWSIMFIIGSFLRLLL
VTLKMIFVGPFLLVTHLSSWEFSSTPVLPAAVEGTSLTMKWWRAWQEFWVTVASPVKNLA
KAWYDSVVHVAVSAARREASIRRWYTPRLRYCVALVAKVREICAVNLAIFWQLCGPGWGL
WLLYSVLFTCTAYLLITGERGGLLDPHAMFGVIPSVVNGEGGGEGFIGASASAAAATESE
GLLKERPSEFPGTATTPMVRSSQAPLFRRHEQEIEDNNGNGFDALFFAWETLIAVWVQLP
W*
>TCRU_1450 ecotin family (I11), putative
MSTAPKTLADYQAPYPEATPNQKRYVIFLEEKDYDSELEEYKLQLIPGRVMKVDPVNRCF
IAGSVKEKTIPGWGYNYYVVEMGPMATTLMAVSPGSPPLRKFVPMAERPFIPYNSKLPVV
VYMPKEGELRYRVWTPTKPKEEIAGER*
>TCRU_1451 metalloprotease, putative
MFACLRSIYEEQTAPPSKPGLIPSPSTERRLRRAVFAAVSSSERRLTQLHEERERKSEGG
VVAAEDRNSIERRLTQFIAHTVQDHLRAVKLESTLVAHSCKQQRNNEDGGDESAARDQAA
LLCSAEELAQLLWMNRTMALGATISIIEGKCPANEALLEAVRQPAERRAPDVRETILCVR
NSSPALRAVLLDGPMIAAGTHVEGGKGKDVIPMEHEDGDAETAPDHHLHPNPQSEAGVKR
LRTDTEETSGLKGWRLGKRQPFALKVDGGLLRSFQDDPALPTVSPSWGNPISNNTIQQKQ
QPLETQREPEAALQGDINLQATSQANCQMKLGLDCGGKLSFAQAPAISSLHTSGVASGPS
PFTVGSEAPRLQPSFTSQPTAPPLFAIEQRPHPLPEGWLTDESVEKAAAEGVKRGINARE
PRGGIRAVISKRRVDETGEAHAKVGGQNNGGFVTAGEQLVADVRAGRTAPSSLSLQRRTP
ALGLRRSSFTPPFQQQRQSTPPPKSDALSATTGVSSATFVGEVLSSIHKNSTKGSHDSTT

RGVRGGHGTAEDRDDSDSECSEFPASLLLPDGSVPPILKPLDPKLVTQVAMEILEHGAGA
ANVGWDDIAGLEHAKRSVEEAIVWPLRRPDLFVGLRDPPRGLLLFGPPGTGKTMIARAIA
NRAQCTFLNISASSLMSKWMGDGEKLVRCLFAVAVVKQPSVIFIDEIDSLLSMRGEGEMD
SVRRIKTEFLVQLDGVATDRGDRVLLIGATNRPDELDEAARRRMEKRLYIPLPDGPARIE
LVKRLLHTMEAQQQQQQEQENHSEKGKVEEHTGYVVHALAEKDIAEVAASTAGYSGADLK
QVCREAAMGPLREVTVRLTDVSLHDLRPIQRKDFVQALKRIRPSVGASEVMRYVDWNRQF
GSFASQTDEATEEEANEPVTTMQ*
>TCRU_1452 hypothetical protein, conserved
MLNGRLGSGKSVDSPGVLTLRERIKLRVDELRASYDRAEREVANELQSLRREFPTCIRDA
NPALRSDDVLCIMERTRQEALAADDADVRAVELIENEQLNRSVFFINDERCVFAALEAYS
IADEELKKACDAKCSRQHIKGLSSERDVAQYKHRLWRARQNRRRLHLKFFTHYREGDEEV
TVSDEETLFAAKAASTLSAEDSYYLYLQQCKTRKLLGAPSPAVRCLTEMMKGRVLQLNTD
VTQAQLAENRVESELQKKYFYLHVPFGDLSHSRIPFEQDADFMRLVAERQELLTPPKELL
QRFPFLSKTINGTSIAQLGLMGDPIFTKLAAEREELLGPLRTASQAVNVKEKQIRERWDA
LVSNAINEENELRAQWPHLMHLPFDVALRELHLESNPEFVALLAKHAALCEDPDRAGGAE
AKRLERAMRDLAKRIAEDVVEARRRALVETENLHEKHPCLPEEPAPGVAIVEVGLVEDPV
FRALSHELDGLRADPTKNAEQIAATERAVRARAMELGSAKLQATEEEQRNYPFLPRRVDD
VLMSDLRLAEDGVFQELVARRDALVAAGPGSNPELLTATERQLRGRASELAAAKKAVDAF
RTDEDEAVRARNPFLESNEVKLVPLRFLNLMDDAKFRDYYKKRLATLGVEEIDLERLRMF
DELLCGRAEIIAERQLKRYDSIWSSMRKRGLSPDLQAAFPFVLLMGSDAMEKALDSLGTG
DDLDVIVRRMGETQALAERGIATELNVLRAQYPMCVRDLNPAVAFDTKFQRLETKRLSLL
QEYTEVELIESLEEEERNRGVELLLDERYVVASQKACEKSKNKGICEMTAEELTSLWRHQ
LLARRSSHRAVSFLEVTNEDWEDAQRPSVRQRRKRSNSCTSASTTSFIDVPDNTPIEIME
ENELLHFPPCSNRTSRIFSSGTSRAEFPVGVDENKNLAVSSNERKRVLMLRRLRNRRASR
YVALDGIEDIDAADILESGAASQSAAESGGSGNGMVDVHASALRWRGPVSQAAKQTKQAQ
MRKETKYVVRRRMKLRHGHKTSFTHLAVSSIPDLPAGELVETGTENLNEGSNVSRNLPKH
ALKQQPEKPRLSNKCVSGSGKEKLSFHSFPRKQRRKSASTSTVMFPAPEEEGVMLLNEGA
PEAPPPHPSDTVPRRKDSAREAYPLVSPVRDQEKSREPNFPHLAMESRPSPGCTLTARVS
MTDVRLHSLSVSDVSIPTPPLRLPKIYPVPSGKSVAEESVAKGASTSHLAKRPSERKRRL
RMKQNNNKSSLVFLHLEEDTYGEIRDTMKDEFPSAGRGFLDSNFRPPFQGSERSARRLRT
ISQHRPSSIEQLDQGDLLSVQDDVTASPTKTRRRRLCSFGFSKAFPSDRREARELERERR
LISEVLLNAQQYLSRSVTAEEIECDSAAMALVFKYDEISQAFAMRRAAIVDAFLKEIFSS
AVQRVIDMSKEPNLPGLVHLPPSTRQQRRQKIVRGAETLGGVSKEEMDSGAFPVTNPRCV
PQPWAHISNEELAQDRRLYEMLNARPKESGENIVHYLREWSERKEAENEEIFGKYPFLSP
LPHGVPLSELRLYEDAEFQREAAEYEMRREDVKLETVLRGIVDRLAKQQAVLRGRENPQH
LSLLERLRAACGDASPSAAIRTDARVELEVVAPYKRSTFREESLRLQFIAQCKRDSVCLL
RRLMVRMKNERTADIPLSIEDIETFRFFFDGVDCGNFGVLDRGDFVDFVMLTICDELSMS
RREVENLAFPTAQKEPLPCVVDFSDFSMFYKSLALREVKRQDSRFCEETGPSPVRGRYLP
PAKEPQKILGAVSKISRGVKMSVNTTALSVILPSLCSQSTCVDTAGGMPLQRRPLTSARR
ELEPQKEMSLPVILPTVRGNMTQGTQAWVKNSCFSLTEGISDTQKSCLAGREWKNEKEKT
K*
>TCRU_1453 retrotransposon hot spot protein, RHS3, putative
MSGRPESVQGGNVEIRVPTVPQGDCRKRTRPESYTDTYHPAATCGGVGKRQQTKWTLDSR
VEDVLLGGKDRITSMGLNEFLCNFLGGRGVVDANEDVSMEMFLTNPMLFSNGETLSCTLA
EFPLCRAMKMLLEAAYTLKGEGVFLLAQWRDFEGKDTVTPIAKGALDAALLLWREEAERE
AEKRARRKAKERTRQKQQIKITLSTNIEDVLLRGRVRAKNMKLNDFLTVELGGRGVVDAN
RNVLLEEFVRDPERYIGDEGLLNEIKTLYNYVRMEIAVRKEMTFCEDLRSLCDKGVDNLL
KWSEAAAEVKASVNGITKHTLDAALVDVRNPKTTSAPIYLEGLYESVYNARWHHVVEVPG
GEGTGLEVREGEPAQPWTYKAVGDTFENNNGVEQSGAAPSRLMVLTSDKGWPYSWKWEEH
KFIHDCYVNSEVDRVWQIVKGDLTEWFSSHGRTEFTPKKRVLIGTPGIGKSMAASSYLLY
QLLHYDIKKLQVVVHCFGATAYVFNKTIQTVTKCEGNEISKIVLYGLWQRGIKGYIIYDV
TWQETPPASYFASFREWGMIVVSSPNLDNYDGWATQVRAERIIMNCPDEMDVKAMCAWMK
RDETKKKQAECWKMVEERMEKVGPLPQHIFRAEDFKARFGAVENALEAINSRYADSRFIL
PGRGLWYSKDPSEKLVRIVRIRGEVGLERFRNAPICYFLGSRSANILAKAMSEKGFLLLV

LGSRKTISSACTDRFCLHALILDGFVSAMAEELKELRPPAHDIQDTVMKANPVAHPTEIC
EIPGVEEINEKQNINYQVLYVPVARDFPLVDCFFFVESPRRTLVGLRMTTAGEHHTTTST
VRQFTQYLSEFFNGWGEFAQGLSWEIIYVQHADSTPMNDWQRCDVVDPPSVGDVDHERIA
EFWETTHQYQFALTECFLRRML*
>TCRU_1454 hypothetical protein, conserved
MLSDPVNRLEELQAELLSRQNALSSRIQSILSETGEKELPELQVLSEDRVQLIKEIQHTK
DEGDALLLQVEGNGEAASMYRVAARVQRFEEFANRANEYVKNVLPEEIERVADADRHHSD
DEVAAYIKELQAKREEELRKIGMLKERTTKRANDLRNGPRVENGELNALCRVTRAKEEEL
DKETKETQEYVDEARLKKADLIAKIKELRQAKSKIQVELLDTKHKNEKKVNEMKARIRHA
ELANKRDIRVCQQLNTTNAALTTNAQTLLGQLNVEHYGIEGAPSEKALITMRKEEERRAA
AALANGRGNNNNGSHPAGNETDGLCPRRDTGNFNGDASAPSSRRQSNQQNPALAVMQRTA
SQRSRDASQKADLDQRRQSGQLSQASRHSATSKDHQAGRTNSRGSSAH*
>TCRU_1455 diphthamide biosynthesis enzyme Dph1/Dph2 domain
containing protein, putative
MFHDSTITPVVTVRRRQKQRPAVRSHYKLDEVAAFILAGASSSPASRTPFQRIALQFPDD
LLEDAIAVTETLKALLAEDPRRADVVGDSARGVEGDLMKTEGVKIDDKKIRLFVVADNTF
GSCCPDEITAQHYGSDCIIHFGDACMSRSTRIPVFYVQDDFRFAAFSTYPQEKERVISVR
VVIRAVKLLRCRLNKLCRVLEENDISAAVSLIVLGSHRSRSLVSASACHWDDKERTAAST
DNKVLVEWCSFDHVQAAPDRSNASFSSFTEGSSWVLNGVRFSRAGSGMLQYFLFVGGSNA
PLLIHLLNVHQYNLFHYPEELRETAFTSDNPHVLTILDEDFGRGSDAGTLGDAESKDGHN
DDDDSVRRMDAALEAHFDRNKGKLIAIQTTLNKRIRQRAFNLELIRCSSAVGIIVASLAI
EGYYETTSLLHQLLRAHGKRAYIIYIGHLNKYKIANFVDTVDCFVSIACPNSREGHFPSK
EDDFPKTVVSPIEVLVALRTEDGDSPLFGHPAFYNTTLDTVLPLLREAMHAVECERAERK
TAVIAVPMGSGSGASLIRASAGVVATQGANGALHRLYERSFVGLDPKKGQTPVQEGILEG
RHGIARGYASEREQQEGNLY*
>TCRU_1456 hypothetical protein, conserved
MDLGQTQRPRSSPGTFNDFEPRRKCAFCCGVRCAAVAGAAVFAITFPCNLVVLGGRMCEG
RGMKGFLDRHLLLPLPVFLIIFTHQTIQSEALWSKNKKTLWKLNWQSAGLNVFLWTFMTL
IGTIISRRYATHWSRQYRLLMWEYQRKRRSCGNKYMPTVLGKITEDLDWYNILWTLSLYH
IVWGMITIMEEREIGAHYAMFYRDCPYSRWCSPRWREWRELEVLKHVNKEHLVGSSRWGS
FLLNDRWRSSGI*
>TCRU_1457 SNARE protein, putative
MDTSESGTSAEKQLRQAKSNVAVLSRLVAEAEKGGSIPYEDVQERMESARVALLALSEGR
LDVNPSNGAVTSQAVWEMSNVHARAAGTQAVTDLQRRVAQQLLAELNLIDTSLQRSRRKA
LQRQTHISEVEKLLGTMRSGGGQDDLSSLKHLENERKSLHYARARVRAMLDESNSVMKAL
RDQGGRLEGTGSKVADVLESLGVANSTILQIMRRNKVDAWLVYGGILLTMLLLYFVW*
>TCRU_1458 hypothetical protein, conserved
MNQSQATLSAVTDGRQREKDAVSDPPHPLEGETETPTENYDPNHQQSYYYYEPSDGNYYY
YSPQDGIANEAVQNSGEIPVTAENLIRSYEFEDWEPQSYNWFADIVLGIFMSLEFRLYFF
FLLYCAGSLLFVLSLNWTFEVLFRMHVSSSGTQFDPSFLLGFFIMFLFLSFTLVTFFCTW
MDMLRGLKQVGREDILFWGMSHYSGKRPPYVIYFVIVIATTLLPFLWGVIASASAGQSIL
FFAQLYSFISIIVSMFLILLCYVWFYWCALKCKCMAFKRRMERDEFILWEKASKHNGLRT
VTKRWYHASTVLEEFGLDGESLRWNAIVFTFGYVPLLSLYMAQALRSYIGNSQVTWGAIF
SITLTCVYVVSWMTLLRRKAQWYVYVSLFLVSILVLVGVVCGGLLASKELVLVIIVLFIT
SHGMLARKRPHKLTRKEQCALFQLPLDPEIQHDAQRRSFDTHLLCCRDAILGCLKCFDVK
TFFGYRHPDIVRAERQYASYNVSILTDQKVLLYWWLIVMFSLAFVIALGNAMVYRFIGNI
AMKSNPIVGENSTLLLCNIRYNKNGSAPLGIYDLSLLAALSYTVAGYGDADFVSWFSQYP
ELIRRYPVRLQPNWDYATSGVTIPFSDYTDLQSDYHFVTLNSNNRGLSLMRNVDEWGTSM
AVQLAGAISPFISIWPEAYRAKFVYGADFLSRWFPSIDALKDVSEYIDGLIADGKKDRIL
LIGDQFNGGYAKILSSRLGLPFVAFNPPGVKYKLPSVVEGVQIFFTHGILSYVDSLEDTL
TTLCLECDADYSSIRCSRIETTIEVISKLCGDPYGRRMK*
>TCRU_1459 serine/threonine-protein kinase, putative
MRLEASRQDARSPSCGSPLYNRTYSHQGLKSPLATPSLQHRVESRGSPTSHHYMPPPPIT
SKAGRVNTVDLDLVTQGSSPVPNLNNAIPCSPSPLAEARYPCLGEPWRPASAVGTRPYGE

LDPIKSCSSPQRAASAVIAPPRTKATYHDGCGIIVEERDSLTREVISRYRCGSLLGTGGF
AQVYEFKDLKTNVQYAGKIIDKRNLTRRGSESKLLMEIDIHRRVKHPNIVQFVKAFQDES
YHYIILEQCSKKSLMDLSKERGVFATEEIQYIMIQIVSAVEYMHRNLIIHRDLKLGNIMI
DAYGNMKIGDFGFASELASASEKKNTTCGTPNYIAPEVLACDKTGLGYGLEADIWSLGVI
LYALAFGTPPFETKDITATYNRIRRVYYIFPRGIAVPESCKELIRWMLQKQPQHRPTPAE
ILRHSFLCIPQPPRTAPRSLVPPQAPRSTSPNARGSPLWASPIAINSPFIDCDRFPVDYQ
KTSLRKEENKKGTEHELQMTLHEFLKENDCISETTSEVRHLRSCGKPVLPKPPLPSIVLK
SSVFCNKYGYGFLSYQCGKQYPVVFLNDKTKLIYDIDSDTVFYYGRARMQAVAPGSGNRS
PLLSEELAAKGFRDELVVFPAASTRLAHRNEGEDATSLFEASAAKKLAITKFFLPFLERG
TRDKRMVAMTCALREWCSSWEKDLFVACGSGDEQVDIVYVKDAVLETLYELTGEHRDTDV
QLLVARMSDYSFQVSVRCNGAPQASFRPKYNVLEASENSLPWCLDVLVYAGFRAVMAMET
AQSSLAFSFWDIRRDAKTVKDGRVYFAARSTTQLKSMMLPTALLRTIAILLRKVRCCNDI
VDCFC*
>TCRU_1460 hypothetical protein, conserved
MVEESFSIMQAEARAARLALSAFSAVLPRTMDVWEDNTSLRGAASKGSLKSHALTWELRR
IYEFLDSRGIQATFVYVRSAENPTDGISRGRVFALQDLAKGWNLRRGAAVSFGCRTPKSA
T*
>TCRU_1461 hypothetical protein, conserved
MVAPLMLDLMDFRRMMCNISVPIRLLFLVQNGREAMLSLCLQELERVHGWSGRLVVSRHP
ENIGYSAAANIGSRLALSLPREEVPFVFVTNSDVKFSPDLLPILLRDVHEMTRHDAARMD
ELAAEAANGPSESSPVLRRGLRVLRSTVDDDRLSTSALLPDRIRYASVREREKAFSKHYG
HFCA*
>TCRU_1462 protein phosphatase 2C, putative
MKGDVNGEEGGITSVPPSQPSSGVTQSLWRMFEYGVTSEQGTRKTMEDQHAMVPEAIPFF
AVYDGHGGTQCAEFLRDNLHTLILSHPDVMTNPEKALRDGIANAEAEFLKKCANGKCESG
STCAVAIIVDDTLVTGNVGDTEIVLCRAGSPLVLSTKHSLQSNGAENERVKACGGRIISN
RVGHPKFNPQVLSLGITRAIGDAGFKLDEYTDGKPSGIIAEAETRTTKLTDDDEFFVIGC
DGLWDVMSYDRVVQFCSRLAAEGVPPQDITDRLCQEALRQGSTDNVTCIYINIKAKRPNS
SDWRPQSAASTSQKNA*
>TCRU_1463 hypothetical protein, conserved
MVCVRCRCWAAAICDCAVAVRGVAAVSLLLLPLCVDGELVCAEGCRQVTGVMAMMMTGRV
LLVCALCVLWCGAGGADASNLGNNAVGGCMASWVLNANKSYTPSGCDKTALTLPLRSVLS
ITAVAASTDPLVTGAAENKSDLAPSSGADFGGAGSPPGRGGEGGGGRDDGAGGPGGVGGA
SGSQARGSKASGGGGGGSNGGSKARVGGSLKSPASDVKSPSPVLGDGGSSPGAPTGSVGS
DGSKGFILGSFSSGGRSQPDVGSPGGDASLSAPVAGGNSPPSITDESDALEKTGAAASTK
GGKPQEAGEQSGANRARNELPELSAPAESTPEAQEDSPSKQEKPESEAAGRAATGEEKRR
SDAEAQGPCTVMSTASTSNGRRRTTNSGGSSGRRKPNGTNRLANFDRRKDKNVTVTKQKG
A*
>TCRU_1464 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MVVDGDNTREQEGVPVTVRNVLLYNRPLTSQEIGSLKPNKAPISPSEDLTAAMVVDTPST
AVGGPVAQKTVSVSTPGGSTVNHESSASSGEDEGTVGETNAQKEEVHPDAGEVNATALNS
SPGNFSQVNNSDGGTMRGSGLLPSLLLLLLGLWGYAAL*
>TCRU_of Trypanosoma cruzi region 5/Dispersed gene family protein.1
Dispersed gene family protein.1
MLPAAASVLSAITGVVAGAAAVAVVVTGGLGSILEMQALGVFARMSCTSAQERASTVALP
YFLSVFAALDPLWMVVGNALLAAVFGCVHCGVTAAFQRWRGVDAASAWAAMRFPSLTYVV
AHAMHLGIFFGSVLALAMPDARVQHRVIGVVGVLYGAAFPAGVCYFIARHVGASFTRYWQ
FSRKPLHERLLYPVGYWHPAAQQRMYGGMLTNMRGSRVYWCVFQLLVLCVVCLIAAVHPP
VGGCHVQYFCMAAVLVAGAGAVAFTNMMRSAFLTVMHTAGFALLALLCLVSAANHLAPSD
GGARAYAAIVLLLTTVLLAVAVYSVVVWYAEDRHWQELREPRRGGLEALLRDDEESGDET
QKPHEMTSSSYASGTTVASSYRPPAPPRPVAGDIRSDALSLFDRASSASCSINYVPLDR*
>TCRU_1466 Leucine Rich repeat, putative
MHFVSTSAAAWQQQQKLQHNIDFNAVLAYCCRPAPYALACVSPWFRRRMEQLNWIGLVEK

IITANYPELLDNTVAKLILGDGNVFREGVAVPRRHLHRMAPGHDHHCAMLLDQLWHKGIL
DSHDTEAVLYLKGTNNNVLVVEDMSSTCHAFISHDAPPPTEDLLYWLSRPQHDKNWWSDT
RNRMPLAVDEMARDTTESSHLLSAQPDNVRVFSRARGLALHITERHLAWLATSLVGELPQ
LQELYLSLDEGRMPPPREMWWWIKCMLAGIPALRVLCLLPRPALLLGQSRKRFDDDDVLA
PYVEEVDCIKTDMRVLGRLQKIHFQTGEQNILSSENVKNYKEGRGPSDTESSFVPPPGAA
VYNENSKLITPTENSFNVSHLLDKTDMEGLEQLSSLEVLYICPSAMESLPFLAHQPSRMK
ELYLLSNPRLETSGIYGLESLPQLEVLWIEGTSIRQLSALNVSTSLRELHVALDSAFSAS
SLQGIEQIPTLEVLHLERVTVDALSFVGKCLSLRELILHACRIYSGNALQGVEKAHLEHV
SLAHSSGIREVKFLSECKTLRVLLLTRCNGISTASIMGLETLPHLEFLELEFTRVDSTSL
LAESPSLRHLRLNNCKRVLRGSIRNLDRCATLQYLSLQDTNVINVEAIYGSCSLVELDLS
RCKHLEQEGVEGVVRISTLKILRLSYTPIISVAFLRTSISLEELYIDNCANITNEGLYGI
EEIPTLRVLSMVNCQASDIGFFGSCPCLEVLHIASMERLRTPGINNIGDCSRLCHLNMAF
CGVDSVSCLANGCPNLRYLNLRGCQRLTTEGLQGLEKLPTLTDLVLDDLDLVCDINSLAE
STSLQRLSAARCTSLTLYGVRDLLLRKPPISLRL*
>TCRU_1467 hypothetical protein, conserved
MEEREEVTATSFRVMVSEAEPYGFQTCAAQQLQSSVRITHITFTPPSSDELEAYMQHKDK
LASATPPSKTDTSICPATFARLRTLCASGELESHTVACFPWSQHDETTTALMATHGNDES
NKNKSINSKNKKGESHLLQSTTTAAAHPLEQVQLAGLFDVVLPRQTDICSNVDLRFDVDG
SVWLEVVGPGSVTFFGEQNSSLIPEWLSHRFFTVSDDDEETGGEEEEEEEEEEEEEGDI
AAMYGLVH*
>TCRU_1468 HIRA-interacting protein 5, putative
MWDVACWVPRRAFLIRFQETPNEACYKFFVNDVAFLPAGHAGTLRFDLDNCFQSPLAEKI
LHGLPMVEEVTIGPHFVTVRRVDDADADAAARYFAHKMGSRTDTPKEAARRSAALQQRVV
DAMLEGDADGVQPPPTSSSSSNDHGEQCVTNSNGESSLHREDASQLKREKLSEKETEEEV
GTGEHVDEATLRDLLLSTHWSELKLHVSALLTDHLFSGRPHVDPDAPHPHPDTLPQEGDS
EVVLILKELISTTIRPQLQLDGGDIRFVSLEGGVMYVEMLGACRRCKSSKTTLSDLIERT
TRHWVPEVHEVREAEQRKPPHNNFPRRGETKCINQEKKETETRTTVACDAE*
>TCRU_1469 hypothetical protein, conserved
MPASFVSFGAKRSRDEGGENDNLRTPQFSASSSSHAAIIEITHGMSRSAAAEYDKQSVGP
TVPWKDTDALLNSPSFREKTCRFLTLRADGVRPDGPVEMGVIQLLANDGKTLLFTSDAIK
PVNISTADGKRVCIGDLVLFQRFTSDAQEGNGNTFVPAMVEFVALDSSALTDEADWSHAV
SWNAVTMANWMHQLLSVPPGLAQLTCIMDSFWGDVGASVTVADAWLRSLQLPVFIQQLKN
LDGVELRKIQQVKKLVFSMLRLYVAILGNAEAIITLSSTVEGVVYQFLGSPLFVEGLSSV
LPQLAGNVSESTWASAQQAMLEAMKFALRYVCREVVEEEGKVQREAREHAERGFLTVLHR
ISALWLTHEKRAPQPGIQAVMKLVEEMARIGVFRRAAQWMRHKERLAETVSLVDKVHRPP
TLKDIKDLHGLKLSSLREMMMAMNQTYTPYLRQETLRFVECAMLAAYAELYGPVACAVSS
YMESVDKTRAGDGDQGSMMKPLHVTQVSQSSLRLELSEYSLEEVRLHALFGLPLFVTLRV
TSEMSVSSRYLLETHSCFGFILVMLNGKTFVFPVVLCGVVDKTEKESAIISIAYVLRDRD
ILPSLVAASAASSSEHQGIPEAWLFFDSCHVEKESGDDDDDDDALPVDHLGSKTPRFLPM
GTSAVSYFLYILHLQKLRAQMRQEELNSLTAVGRAKGGQGKGDLANKGGVLWWGSDGSGV
AGDMFTQTSSLTGENEMLQRCLSEIAAATLLTASQVECLHTLTTAGPGLRTLVGAVGCGK
TTLMHASSLSRGRMQEALRKHHQPLWHATIKHSAQTLYTRLGELAAAEEMEDLFKASDGS
SARDLPEEVTNAALGHIQEHVHLSEKLRHCHTPMLLRPRAFKQTIPFHSARVLQEENIAQ
HFCSIETLMKQSHQRSLNAPLAAVLNARLKRLKRLGDLLDTIALSLEEIVVPEEGEWKLF
IEFLPWIMSKKERMDTFTEALRKGKTWEAYLSEDLWDASTLVRSTDFDYTPQKTVWKSMG
PAGSAFHAVTLPNASRSLCEYSQAEAAGWRAVFWEKQRDLLSFLQQEIMDEGRHIFLLFL
DLIQAVAATSQTSKATVVTATGGTLLREISFLRKWQPHYLVVDDYDQICDSLYLTLSSVT
SAIVSHQAESSFQHEQRLPVVILRALQRELQGTPLLSTVVLSESFRSTNPDIHKAAQLCR
NASVAFSTALPLGVAGIKEGANNFVVVEGAVGGGVGNDNGDDQTMRKHAAIAGFSSPCSV
EFWTHAVALSAAVACDGVAAAFVRNRLREIEASMTVTVYCGFVKDKAVILEGMMSGSDVD
ATEIMGPVCTIPFDSEAFVERDEECDVAVLCLSGIARRLRRFSSVGRHQAWERLGAERSF
VEQLEWWLWRTVSYVRRGVILVGSREVFSFIEPLHRLERFVLQMREKRQFWLPPEAKGAA
LALRCPDHENFRQLALIAYSDYGGCQVRVMGEKTCRSLCLAPYENCTNPSHACLRICHVS
GRESGALAMEDDEDPSHSNCPFPCMRVLPCGHMCVRRCGELCLPCEFVGLQELSCGQRVV

SGISDVGPVQTLVHHFQRISCGESPRLCEERVTLRCSRCGVKNPMLCHEVVARGGMERAN
LTELECAGCVALYNRVAREHEAAEIASTVPPTAGDLPLKSLPKAAQTRLQELQSITAKKA
QLMLQKEALETMQGRQNSEFYQQQEIYNRMQKQQEEEVRAHRQRVQENIQKWKKILKQKY
AVQMTVNEAMDTEVPLMISEAIAEEEKQRSHLFV*
>TCRU_1470 Ubiquitin-like modifier-activating enzyme ATG7, putative
MTSTATTPAGSRLKFKEYSPHIEVSFWYELERRKLHEWRLQEPVVPLTLFGTVNSAYTAT
PANIVSARRESLGNDTDAIVAGLPQNPLVGVAAATDTNAPFPIPVLLSGELQNFNTLEQL
CKLPRREAIWRVLKEKLLIPLFSGKGSKTIDVNEDRKAAEILVDKVWEGINFALAALFTY
ADLKSHRFHYMMAFPVLDLGSPVDVKHRVNGGYAALATDHGVSYFSSRKAVDRIHAHLLD
QLRRHPERGPNPFIVTCQASGHGENEEVIFYPFTFSTINKMKELSFLVVMADVSTMEEFP
GWPARNVIGALRLARPSITAFALYCIRHNEVERSVVFECTCDPLSYTFEDVMTEGTEGKQ
NAFARAVGWTERKSADSPVSCIDLGAMMDPERLAESSARLNLSLMKWRMLPELSLDGLAS
CRALVLGSGTLGCNVARHLLMWGVTKITLVDRGNVSFSNPVRQTLFEMSDVINPRLEERN
KAVAAAKALKRILPTVEAHGVPLTIHMPGHRIDKQRESEVIAEVERLDTLIQEHDVVFLL
TDSRESRWLPTLMATTHNKPLINAALGFDTYVVMRHGLEPKEGSGGSRLGCYFCSDVVAP
RDSMTARSLDQQCTVTRPGLSAIASATAVELLAQLYNHPLGFACPPYTETEMQEVHLQQP
GDSKATNPTDTNGAVCVLGKIPHQIRGSVLTHYIYTLYGYRYESCTACSDSVVGAYRRER
QSFVLRCVNDPLYIEEVCGVKAFKESFNLEDLDEWDVDSHSD*
>TCRU_1471 tRNA-splicing ligase RtcB, putative
MRRLARERLFIVAAATVKQRCGCADASGQGLLPYDVLRGEGSNVEVRAWIKGVEVERSAH
EQLIQLSRMGEIIRHPIAVMPDVHTGHGATVGTVIPTTRALIPASVGVDIGCGMIAVKTT
LTPEDLPGSLVGLRLAIEIAVPHGRTHNGRSGLDAGSWRGELPKNVVDIWNLHLRKGFEE
ICAMQKSIEASNHISHLGTLGGGNHFIEICIDDDIKNDAQRPHVWVMLHSGSRGVGNRIG
TVFIELAKKDMGNHITQLPSAELAYLREGSPHFDQYVKAVDWAQRYAKWNREIMLQNVLQ
AMRSYLPQPFGVDATAINCHHNYIERVELSPQNSVWLTRKGATSARGGEMAVIPGSMGTK
SYIVRGKGSPLSYSSCSHGAGRLYSRGETKRRFTLEDHEAATADVECRKDTDVLDETPLA
YKKIDDVMRAQGDLVEVVCALKQILCVKG*
>TCRU_1472 hypothetical protein, conserved
MGQLLSFNATHEEVPEDVKEKVEPIEYTPASEENRPQDDRFCANCGEPYFYYFTPSTNCN
WCGGQFCTRCCPNRHLLGGKPGCPECTRRAYLIKRKELLDDHLASLRKKGERPAEVNFAL
EC*
>TCRU_1473 hypothetical protein
MGTIVALHRTDEAEAAVFVGVVPIGRKELEKLPHPTSCPDCGRPFDERTRSRRCRICGEA
LCKQCCRRCRNWKRRPLCDYCMDSCLHDYYRRINGESFAAAHQHEHHLRQRVKKKTASGG
FLRGFFLAALDGEDFLHASKPQGRVERNISLGT*
>TCRU_1474 hypothetical protein, conserved
MLVAGSGGAYGYTLSVASMRDGCAVVLGITTKIILAISSEAGEEVLRVNDGQVVRGVALL
RAPNGAICVAAGGDGKRINVYRANTMKTLLAPDARANDVGAGEMKLLFSFGPHTKRITHI
ATCDGNSILFADKFGEVFRLVIVWGVSDSLTMAQGDAAAPIFLLQHFSVMSALFLSAPIR
QGTPDMKETRRLFTCDKDCHVRVSCYPETFRIEQFLWTESPQSVVTSIAEVTDSSEKKGY
SYFVTGNYEGKVHLWAADNTLTNVLPTEPFTIVGSICAPEQVDMDEEGAAAVVSVVYVTS
SSHGGFDRHAARGFLHGVLIAYANAKDVVFVPLMESVDDHRLLFALEGITRTRLDSPLLA
MVGLATNSALVLGRNGRVHVLQIVGEAGEAVPVSLVESRQVAIETAIGEVERENGGNLFE
KMDIFSQWHYDAVDPRTRKTVGTRNDSEEDEDEKNDDDNKDGGEDVTHNTAVGEKLIGNK
RKRTECRSDA*
>TCRU_1475 procyclic form surface phosphoprotein
MCLFGIVDAVEDFFKSVVACACCLIIGGPALIIAGSILLNQKDLRKAFRDAVNEFDPTPM
NDWTGTINGVPITVRRESLNVKGVDGATSVFAEAVIPASQRSSSRLQVSVNVRTVTPFIR
MAPFNIMRNSTYFCSSSDCKDEKDCQCKRDVRSFGEKCTARGGRYNQAPTWCKAGNICGE
CLETLYLRKLYLVVREVSKGKYAEDTNLRSAMYAFGDLDNDYQPGVPSTVTVRLYSSKDP
YIALQRLTKGTNDLGLNPRTVGIVLIVLGCLFLLLEIGVCTALICYWMRRKKTSSGAPPY
LAPASQGISTPGASGNAAPNFYAQPAQQTGQGYTYGQAVPPGYTYGQPPQGQPIPPGYTY
GQPPQGQPAPPGYTYGQPPQGQPAPPGYTYGQPPQGYAYGP*
>TCRU_1476 hypothetical protein, conserved

MLAFSIISDELRDESSIPTPADLGTSTPPSVASIHERWLCSARASSLTLRFSRTSSSSSV
IEWSIGSSTPMVTRRAEAANQGGMELRKNRSSRGELSVMP*
>TCRU_1477 hypothetical protein, conserved
MSRNIEMDPNAFETNNAPATALTKAVGSKDARKIEAVDGSGERVPGKISGGMNGHNVPGT
PKTHQEM*
>TCRU_1478 hypothetical protein, conserved
MLQGKKASVHIDGRSLGEEEVLLTGQRPPEVLRVRFDACGGHESHVTVTNVFPYSRPLNS
TAMRAPKDSVPAPTREAAPTPPEKIRVVGTVREHVAGNIGEGK*
>TCRU_1479 BNR repeat-like domain containing protein, putative
MGTSWTEAIGTLSAVWVNARSGVSQKESLRVDALITATIEEGRKVMPCTQRGHASGKGRA
TALCLWVTDSNRTFSVGPVAVDNAADWMLASTLLHSDGNLHLLQGRGSGEGRVISLSRLT
EELSAIKSVLSTWVQKDIFFSSLSTPTACLVAVLSDAASDDTWDDEYLCLHAMVEERSEG
QR*
>TCRU_1480 hypothetical protein, conserved
MNVTTHKCAGPYELWWRQFSPDGTIHPPARSGDADRTGIRQLPPPREGKDDTKSGGTTAP
PVNAEPSRQNEDWRQSAAADAPNTVDPSPASNTATNISETKPEFAFVRNTKVDPTPPERR
PTLVTEPKEDPVDDAMSGSINVELPRGVDLFVPRTTLV*
>TCRU_1481 Reverse transcriptase (RNA-dependent DNA polymerase)/
RNase H, putative
MLTFTLHQAFKDTIPSAPPSAPKFFYSWGKCKWDLFIKDFDAQLPAYDYKKQSTGIKAFT
RALITSYRRHCPRGMHKDGPRLWDDTLMEAERIATDSKARYLQLPTPDREAEMQRTRSQF
FLLLRERLRNTYLRRISKLNPGEPLAWKYISGRKRASLPSPTSMLLGDGQHTYKTARRAA
NALNRIFLPFHPSHKAVRFSKGINRQSASLNINASFLFGQQNNSESAASFTSFSSISSTS
EPQNNSESAATFTSGSSTSSSSEPQDKNEAATKSGLVAHLHSPLDAPFNRTELLAALRNT
PYGKAPGPDEVYSEALRHISSKGLRFLLRCINHSWTTGTIPVEWRRATIVPLLKPGKSPE
LLESYRPISLTSIVSKVAEKMVLKRLLWVWTPHPHQYAYRSMRSTTMQLAHLIHEVEHNR
NHYFQVSLPKKSGIGNQLHYRPHRTLLVLVVFSKAFDSIDHRVLSRLLANIPGVNCRRWL
RNFLCGRYAKTRVGHRHSDRRPMLRGVPQGSVLGPYLFSLYVHPLLNLLNSFAGVTADMY
ADDLSIIVKGQSREDAIPTANMVLEKLHAWSQENGLAINPSKCEAAWFALSTHTESDYDR
EGRWPLAVAGCQIPVMTMGASRTTKLLGMDLDPRLTLNVAATKQCAATSQRISQLRCIAH
KEAGPSPHDLRTFVIGYGASKLRYGSELIWAVATDAARNEMQKTYATLARIVSGVPSTVD
PESALLEANMPPLHVLCLRARLSIFENTRACQMDWMRRPPPEPPPRAGFRISPLSRDELY
AFVDAYTKDYGITESSPREERFFRSSIPPWFAASAHRVTIGVELPIDLSITDEEELIREK
RRVSEEALALHSHRSWILATDGGVDVPKSAGVGILLSSLHSSKIIEKVSTNGGARPCSRT
TESRALHLALEKLMIPRIRHRRKTLLVVTDSQSLLAAVTKGPLSHTHWTEDRIWQRLLSL
THAGWSVQLQFCYGHCGVHANEPADQHATQTMATGQHTEHGIAHIWHTDMLTCINTQLTN
KWRSTIRQDTHRYLLGGARPSDPGGKDLITQEPLDQQERIQTARKGCGESELWGRLYWTV
RDCTNQRRFRNISPEHSALMRSNDDPTAPGRTLFPRRQGRPTHRLWRDGPPHSVGRRNAR
TVTPHWWDTRTTSVTVGAFIRNTLHRFPTSTAIATTQSSPHKKGTAQHRNRCAQNPDTTR
HRSSSARRQSLLPQDQPASTSATISPQKTLHHLLPECTDALAVRQRLGIKKDLRTESFSQ
WQLPHSRKLMSLLDHLLGTLMTSCG*
>TCRU_1482 hypothetical protein, conserved
MAISEKKCLFIRVALYLLFIAAYAAGVVVFIISFSNYWAAAGFFLACIFIAITTVLYVVP
DKRLTARLPPGSLSRIIFQSTILIGTLGLFAVALYLLAQGIMLKQRWTGSSYFCSFIAFM
MAAKWCYFIGYRVHGLRNDTRTIGKADPEEIKKFFEEVPDAWSNEKNADIM*
>TCRU_1483 Torsin, putative
MGPCTRSVCGLALLVFFVAALSSRVAYIELDLGEADDCSPRPLCSSHPTLVKRLLCFFFC
YPVNVDGSDYKKHVLDRLRRLTQRNLKGQPHVVEGVIRSIAAKLENPDKPLVLHFAGDNG
VGKTTLAQIISLSLGLRCHDTACETGDSTLVLSGVSYDGYSVQEFRRVVIPKVVQHIIRF
PKNGVIIINDLGALHPDLVRVLLPLLGRATSFPEAPGVFLSRLFVIVTTDFGRQGRTQGK
SLTEMRRIVEDDFKGLYSQLSSSMIETFPFLSAALDTAKEIVWLTIMNYKCRHREAIREL
LVSEDAILWLVDFVRDDLPMENGRCVANAVSALVGPGILRHLLENPSTPVTLRVDINDNG
SVTVLPVRTD*
>TCRU_1484 60S ribosomal protein L12, putative

MPPKFDPNQELIVIVRAVGGEVPATASLAPKVGPLGLNAKKIGEDIAKSTKDWKGLKVTC
ELRVKNRVATVRVTPSVASRLIRALKEPPRDRKKVKNIKHSGNIPFSEILKIAKEAAPNS
MGANMKSVVMEVLGTALSVGCTIDGENPREIQDRVRNGKLKVPN*
>TCRU_1485 hypothetical protein, conserved
MHGRNGELGAVCHVVNAVHTCSNCDASCARKEEGATVAFTVNVTTHKYAGPYELWWRQFP
PDGTIHPPARSSDADRTGISQLPPPREEKDETKSGGTTAPQVNAEPSRQHEDWRRYAAAD
APNTVDRSPASNTATNTSETRPEFATNPSEVMVPNASKKRPSFAKGPRILVALNASEIMS
VTCGGREHVAADNTDEVSERSATGHKTPFFRKWRCGQWICC*
>TCRU_1486 UEV domain/Zinc finger, C3HC4 type (RING finger), putative
MNEIITRFFSSSSHCKPEVLGRILHDVENLCNTFHFYCRDATWGVTQQEKLCIYGGLPIT
IKKSNSDHTSLTPDSREQAPPHRYVLPLQIWLTHLYPIEPPLVFLLSAEQGCRIASNHKY
VDATGRCHTPELAAWHPVSSSLCDVVKKLCQLLSAEGSIPLCFGEEGVSSPSKGHATAVS
QRLRHGLENGDDDKQTDEHERCVVCFSPKETVLVPCGHYCLCDACATNVTHCPLCRGSVK
FRQRVFS*
>TCRU_1487 Mucin-like glycoprotein, putative
MMTCRLLCTLLVLALCCCPCVCGTASGEAQVSTTGHPPPLPQGQTRETMSSGSKAPTPPK
ANTSDEVDLPVTVDAEGGSDVSSTTQDGIILPGKPGSDGGIKSQPGLIDNPDQSVVKSQA
QEAGESKGNKDFTVKTKNTKNTTPITTTTTTTTTTTAAPEAPSTTTTEAPTTTTTHAASR
LREIDGSPSSSAWVSTPPVLAAFALAYTTLG*
>TCRU_1488 syntaxin binding protein 1, putative
MPRPVRLRLLLLLVAASSTDELTEAKKQQLIRYGGLTPDAHLFASLEHVTRRAGSVQQYS
TASAQSGRSTSASASNAATDEDTFLKHACMIMETGRKRKLRVELSLASMGRDHAMGPNGA
SGGQNSGAAGKNAGPFQGCGGKEENHPDLGGGGTIALTTPQRIVLLVLCGVACSERRSVH
EISKRYGREVVIGEPRCRVLRCVCAGTWHPTAV*
>TCRU_family, putative Se.1
MWGGLVRSRPTEAGQPREPSNGVCGCVRDYIFHQMLDAVRGLFKVFFCDAHAASALSSSL
RLHDLMEHGVTLLENPMTPRQPIMSSPAPYFLPWSDASVSRVVEDWTAKVPYRDVHIFAL
GCTPHRSLQQLQWARMAPRAMRSKDIMLDFAAPEVLVFHLSMQNGFFQLLLPLSPPN*
>TCRU_1490 hypothetical protein
MQSHEAARPRGGCPLDDDDGKKFVGLIDADETNTKVNLSSMWMDECEEGVDAAASKLTTD
RLLSRILLFSAMRVLKRNSAKGVQARIPCNTFFPSDAHCPDRGRSLKLNCVRGDSPLDID
EYELYDSSATPFLVFAPSVSFSAEKSECTAHVSTTFVSLIVDVDLPETPRFATPHYTPAV
VQWSSIQL*
>TCRU_1491 tubulin-specific chaperone, putative
MSVVRVSITHSSSGIRVPEKRYELSQTIASIKSNIFTHFATPPEQMQLQLIDDRGVKVES
SMADDKQLGYYQCRDDFVIHVVDLRPTQQIANFEDVSQVQKYEITEEAYSKREDNARAFR
QLMMARQREEAEKAGNPLPKELDADSYKETAEKIHVDDRCQCQPGDRLGTVRFVGRVASL
KPGYWIGVEFDEPVGKGDGSVKGTRVFECQPKYGGFLRPDQVTVGDFPPEEF*
>TCRU_1492 uracil-DNA glycosylase, putative
MVQRTLLDFVRKKDPSPNVINVDVESDEQDEAASRKRRMQGVREPALAFTKPRTENKDDI
CCSNNFSALITDSGWRAFLQPLTSTTNFRNIEQFIEGEKAKGKVILPPSDLIFSAFNSTP
LDRLKVVLLGQDPYHNIGQAHGLCFSVLPGVRPPPSLLNMYKELTTDISGFKSPPHGYLQ
CWAEQGVLMLNATLTVEAHQANSHAKCGWQAFTDGVIRLLSEKHQRPIVFLLWGGFARKK
ITLIDQKRHLVIENAHPSPLSAAKWWGSRPFSKCNAALTQLGHSPIDWSIPMSVERRH*
>TCRU_1493 hypothetical protein, conserved
MPPLTLEQVLARSMRLPRKHMKHTATPMASNPAIGISTPPDNSLGRGDKSVAKLFSLIEK
DEESTAAGRPFIHQSNNLIRNSHDLLTYLHTAKRMRAWEDALRSFAEVTKMLLINQTEEG
DGVSLTLREGAEGAEGVTASVSHLALLLDTCASAKQWHLVEQIGEIFRSQSRQTLIDAVA
VLANTKKETIGEGLYGWERALHFLQTRIPPEEQPVEAYNACIAACETALEWEGALAIVRS
MGPNPLQNLDSKVFSGTTGIGVASAGSTVGGVSSSLGTEAREESVLATFPPPAPDVVTYA
TLISVLEQSGKDALASEVLQRLPPVEKEEITASYAALIHVWSEQKYRNHRRRF*
>TCRU_1494 hypothetical protein
MVGSTGLSLDDDIVRFISCPSNSSCCSFAATESHVFFGHTSGEMTVCRLEHHSKGLETVA

SVTTLLPAELNGAKGENLRNKRTMSLAIDCLCVCPYASISGTLISSLHRGYFVTFVTFDA
MSSRSGDGGIKIGRSLELFADETSLQYTNRVTAHCWLDDDTFLVGCLNGTVLAVSASVND
SHRVMLREESPIIQMVWDAETSVLVISSVRRSIVVTYANGSMTFKPIGNKPREEGLFGAC
IWPINHAVYAARHNARVFEYLPSKGEVSRTYRMESDVALGVLKPLRLSSFLAGSSQGDEN
LDGGKEQVFLPILLWSEGPRFISFLLLSATDTHHITRRFDDVAIVSSVILSSIALVLCSD
GRLMYIPLGINPLCLQDDRVDNAREILARPESEQTHDAAITKKRVHRIKVVKRIVRVVRR
RELLGQRVSPELPGRVAPFSDCADSIESSSFTTDDKAHSCDSPVSLKRPLSLHRNNSFTD
EADAEGMAQNDDLGESRTLQEGSGHANNCLFSNLSDAVTTVPIVDGDIPFGESSTTNRMN
FVRKEHEMQEEKSVWKSKRFFLELDRIIRLFNVHALHLGEHEQLYTAVKEFLPLLEERMI
ECGLLTKSFHSVLSQVRVISCGANSPATCDSNREDTSSFIEEEATVNALRNVLKSALAWS
IKDKTGDKENPWVQTLFILYLLLAVPWPAPLFLPRRHATERYVGELESWRSRGIEEEWCL
EEASVIEKTVKRSGADGRYLPLVLALSTSFVSSMTKTQSGRNTRSRLLGVINGHEQCISL
VLQLQVDRRSLMESECPLPMEFHLEQLIVEQSPQIVDAMEASPYPFCFFYVYFPYIFATY
PSKAIVLSMRHYPGTSLAFFEWALSSSVQGAAFQQLRKMGSEVERLSLEDVADGLADLVL
ALFEASGPSICDSPADYLACLRILLQRRFALLWARIKMGQMRLKQMTCGADARETVQLHH
AEEGSSTILRTQRKLQRVERGVLGLLQLMQSVIITIGVGNSVQKEEFKQDVLSLLEEHDF
PEGVVELCWIREYIDYCIKKGCLERLLSLFQIPGATSQKEWAFLFKRAHEENKLEIAMLF
CLSVEKLPDRVQQLLENAFPKRFVSVEDAHDDEQLERVALKLSMLL*
>TCRU_1495 aconitase
MFRSTSASRTGNPQLNPFIKYVATMAADGGEAKYFKLHEIDPRYETLPFSIRVLLESAVR
NCDEFDITSKMVDNIFNWKETCHKNIEIPFKPARVVLQDFTGVPCVVDLAAMREATKRLG
GDLNKINPQIPVELVVDHSVQVDKAGTPTAVKENQDMEMQRNRERFEFLRWGSKAFDNLL
IVPPGSGIVHQVNLEYLARVVFNNKGLLYPDSVVGTDSHTTMVNGVGVVGWGVGGIEAEA
GMLGQSLSMVLPQVLGYRFTGKLAEGCTATDLVLTVAKNLRKFGVVGKFVEFYGPGVDNL
SLPDRATLANMAPEYGATTGFFPIDRETINYLRCTNRSVEQLERIEAYARAVKMFRTGDE
KIEYSHHLELDLSTVEPCVAGPKRPQDHVPLKNMKEDFAACLQAKSGFKGFGIPAKDVNK
TKNYMVDGQEAVMRHGSVVIAAITSCTNTSNPHVLVAAGLVAKKALEKGLKVPPGIKTSL
SPGSHVVTRYLEAAGLQSSLDALGFNTTGYGCMTCIGNSGDIHAEVSKCISENNFVAAAV
LSGNRNFEARIHPLTAANYLASPPLVVAYALSGRVDIDFNEEPIAKGVFLRDIWPRNEEV
QEIVSRYVTPELFKSVYSNITTINEQWNALQVNEGKLYEWQPNSTYIHHPPYFESMTMEP
TPNTVIKDAACLALFGDSITTDHISPAGTIAKDSPAAKFLQDHGVERKDFNTYGSRRGND
LVMVRGTFANTRLGNRLVGEGQTGPFTIYFPTNEKMYIFDAAMKYQQENIPLVIIAGKEY
GSGSSRDWAAKGPFMQGIKVVIAESFERIHRSNLVGMGIVPLQFKPGESAQSLGLTGKER
YSFDFSGGLRPGQETTVQKGDGSSFSTILRIDTEMEVKYVENGGILQYVLREKIRGAL*
>TCRU_1496 hypothetical protein
MDQSSEETHVENAGGNCVIVTTLMSSATDTSNRHHIPIFFQPDVQKAFDPGNRWPPLLPL
APRSNPSAHLENNYAGAFTKTDPCSSSCRVISCENGLSEKRQSENHWRSSSASVSLDPQA
LVPMDANMTSSSWAVKRTAQLGPLVVVKRSKKPNALEHITPLSEVEMMSLQREVDNLRIQ
LKRSNEKLEEARSEAGQQFLERTRELEESHREEERRRRQQFQEALSGLRAENEELASRVR
CMQDNAGLAAVREREKLQTEWSNRLSENENQWRQRLAVAQQHWEECVDEQVQEKHEALRQ
VHELAGVVKELEMTLQQVTREKCWVEQELETLLSKQNQGKDRCVCAKGETIDVGTRGALE
GEAMELRRMLKELEGREAALLVQLEMCGKERVVQEEKLEKQLQQVRQELEIERRRGSDVV
KLYSSQIESLHQQLSDALRRNKQLTKELARFQ*
>TCRU_1497 tubulin cofactor C domain-containing protein RP2
MTDQVTEKLIRARLESSGELGKMWAMVVDAALRSISEDSKMLSNLFMPSPTLTAAKKATE
GKQALAIVMDYLEHLGLNYTLNVLKREAGLTENAFEDKGAIMRALNVPDTTGPILMTLIQ
GVCNEDGGDKPKVENTTMGSTTISPSSSKVTVVPKKADNGEDTKYFISNWTGKTFYRCGG
QVSGQQVQLEYLNNCTVYILDPLDSITVDDCENGELIIAACEGSVFLRNCKKMTVYVACK
QLRTRDCEHIALHLFASTDPVIESSHHMTFKPFNLRLPELKSCFESARLDPKVNRFVHVY
DFTEDDQELQRPHFNVLYPNHGLHMTDRCKEKGKPECPPEIEDLLEGRIAPASSSESGKN
KSYNIKTGAHIWKEASPDSIDNADVGRTPVVILPTSTNKRPPQSAPMANPTFSNQINPAL
AGRRGGSDDSYSSFDDDDNGDEGTDDDDIDVDEDSDDF*
>TCRU_1498 hypothetical protein, conserved
MSASLSEYHVISGKRDQLFSKGLLRRTTVAALQNALCAAVGRILIGILKRIGKVGLHSTV

LKQIVKEFFSLDPLKWASIFAALACFPLLKQIILKLGRCCRITEKVAAAISGSVCAVPVL
VMNKETRTDLCLYIFVRALNSFAVRHIIPLLPESLQQFQYYDILVMCLSASQILYSVVFA
PFSLPPSYQQFLSKASMLDNRLVRGHAGLARYQLTPELVELCIERGVKIPQSPREHFRIG
CMLTHPGMTCNHFFISFIGRNMIQVGLPLYIPLKLGAILLYQRKELRRRPFKLIQKTFFS
VLSSALFLALYSASTVRFACVFAQWNIRGGVFFAIFCSFAGIATLLEPKGKRMDLALYCL
MHALRSFVMTQHRLGWIPYPKHILVCLLYIFSVGYLIFQFDQEPDKLNPRLRAFFSKLLP
VEEEEKAEGIVSRMEE*
>TCRU_1499 hypothetical protein, conserved
MLYAFIALFLGVLAMSHSEAFEILPTRVTHVNADHGVWQPSGAVVLKEGVACARAHQDSC
PQCSQEATAVCTSDGARSFLVQQTSYPFCGNRGVVVNNSLFCPSNLKQINSSVINFTVVS
YEWVDSLVETPREDLVMSFHYWPGEEIKDINFKGNSLFFPGENLYIMNAVVVRENSTTDH
VLFYSSDGQVWNAQSKIPLDVVDKTALSQSGKYQIAVSAYTKGEHKIIYSFYKGTRWSTP
KYLNTSLPPTALIVGTGIMIQTGLSNHTTSLELGGSVEGSSKKKLFHIVDLYKNRTEHNE
LPQDFTTECIEESSCLTSSHVALMSLQPGYVTVLFDFVSGESQRKTIAAVTMEVDDSEEK
EEIIQAQKKAEESARLMEELKRKVAQERAERKRKEREEKRRKERERRQRFMEADFVNIEA
AKSRIIEDGEMIVVREVIDEMIDMEKSTFFW*
>TCRU_1500 Leishmanolysin, putative
MAASEHHDCDDIDGMELQDGDGDGRTLESHWSQRHAKDEWMAPIGCAVCRTELTLAALAD
LGCMGVKWDMAEPMRW*
>TCRU_1501 hypothetical protein, conserved
MVDGASATHHDSPVGTCLGRWMWSVVGACPRSRHRVRRRAIVAVRVALLFVLALVAAAAW
MPAVHAVVLRLRGGTVDRAITVGRAVDTVLMDGVYITNGVAVVFDVPAMLPGALRIELRN
CVCDGGAQIYVRGYSGEPASDRSLEVSVSGLSGSYCSLVFVHNLPAHTNVTVRDSTIATA
GPMRFSQLSGLTDAVASPLVLHATSLLRTQLRVSSTVLRSLQAGGSAVYVGGDVDLLSSA
VVLDGLLLEASGGPTASVMRVASSSILSLRSHSVFSVTNVSVVSGGGGIVLGERLAVFDS
VLRFVRVEGSAASSLVRCGGGTIGAGGWLELRDVWAVGEASSVASLSGVTLSGGTVSIAR
CAATGATLVSGPAITSGVVSVQCNRAGGRVLQSSGDYRMAGLPSVSVVPCDGCAAALACF
DALTASFSECVCGCRAGGVGEACLPFDVPPARAGGGGGGSQGCVSGVTLTESVTVGGGRA
TACFDSVVFSGPITVTVDLRSMDAFADALNVTLRHCVLAGGAQLRIGGLSESTARLMPHA
LVNMTNVTSLEGVIVLHGAMPLHSSVLLANSTLRATVGGSQYVTTTRGYEGFRYGPALVL
DGVRLLSTRFVMTRSMLVCGGGSCAAILVERGLGVNLSSVFYMDNCAVLSQSHVMHALAS
DLHVVSGSVFSIQNSSWSAPSVEYYEGACMFGDVAVDGGSVLQVVSSTFRLGFAMLMVNT
LTVTGGSWLVHRDNEFRTAYVVYVDDVDSVAFRDRSVWSIIDNSFKYGFYSALTYMTSNW
SPPSDTHPTIYGMCNEARGSPVTGYQDDLNIGAPVTALDCGACTMDAVCFAARTSSISGC
ECVCAAGGYGDTCLPAAVPDGLGPLPLPDAKDTGVRCVHGGRISSVDYPDPGVRGLCFVN
VTFTVAIALDLLYFDAPQQTLNITLLQCILIGLSIRGSGARVHVSVVSLMMDSGALEFEG
DFGASSLILVVGSTLLMRSRHAIQFQRFSLGANSTLLLLDNLIEGESYAVRLSFVVVDGG
GIVMKGNTLRGAEEEFPLESAVFFESAILKNGGYFDVEDNTMCAVSGIYFYGDIIVSSAG
LLRVADCTFAGITLFFEPALVHLDGLVTLEDGAQWRVEGNNVGAASVMGMPKSLYKMRLL
GSGTTVVLAHNRLVDDSCPFVKMALSNTIVVSPARFVVGCNLQDGREVSYDVVLPEGVVV
FGCGTCNDDAACYMPGTESVDRSSCSCSCKDGWHGASCLPFEVPDTVVPPVAERAVDGDT
SCVVDQTLTDLTLNMWKTHHCYVGVTFSGMGAALTFSLNSMPLHLPINITLTGCTFREGA
ALQFVGGAEAAESSGILIRVSRAVMRSSVVVFALALPLHCDIAVTEVDAMQSSAVQLPES
VNNMLSVMMLRDVVLSASSLLVSNVKACAFGYGSFGLYSTGTLKLVGGSSLYARYCSFDG
YTHLLHMNILIVRNHSVFALLNNRMDSGISLLSQQQDFSVSEHSVLRVVGNSGSVSYAIY
AYNSWTVQQSSWLDWRDNDVGVGAIFKVWDSAFVSIDGSSVVTLTGCKMGSTGLSVSLLS
RADAGYRFVAGCLTVAGREVTTAAELELHGITNVTTVAACGECTKDGDCFAPLTTAVIDC
KCRCAAGGHGDVCVPAPVPAGPPPPLPSPPSPPRTPPLPPVGECISDMVYPEVAQAVGGG
LSWLCYRNVTFSGGGMSLTVLVGAMTGDVANVTFDGCTWRDGAVLVLLGNAYAALGSLNI
VVTGNSFSDALLSPEGVFPPHTNITISGNRFTVTRLIPRSGLVLWGPSCVAMNGLAISND
SAVVLSGNVFQAVTASSSAIHVVESALRVLWRSLFAVLGNTFHMDGGGATLIYLEGSSES
SSLDVLNNSAVVVRDNVVSSQVQHVIFLRWALIVESFSAVVFQGNDMQRSLAVFYSKFLS
YIYYNSWLQLSGNLCRESPSKAFVYIDYTVNIRDSTVSVSGNRFISSAGTPTVLWIPTIP
RELTNGAIVAVCNTVNGEERVQYVIPSVYNAAILSCSGPCTIAASCFPAYTTTASSDGCA

CTCAEGGYGEACLPVAVPEPPSTDGADLCVRDVSVDVEVNVSFGTSVACYVGLTFAADVV
VDVASMSGSVRNVTLANCTFLDGASLYVFGWRSDPPAGERVDVLVSGLESRSGGGVVVAN
LFPPGSRVTVVDSLLIAERRVAYRGAYGLGDASACLVLHNVNLTGSVLTIARTHVAAVFG
DAVGVLVVGGVALSSRGALYVDGLLVQTALGLCVSVEGGVAASGGSVVAFVDSDFLLCKH
AVSVRGAVSVSGSAAALVRNEFSSTEDYAVAFYSTVSLDGGSMLLAKGNVHDGASREMLY
AAGAVTAAGSTLSFVHNRALLPRMLSAGLSLAAGAHLRVACNDAGGRVLSTAEEYAAAGL
LACCTVWRSLLACAT*
>TCRU_1502 pyruvate dehydrogenase (lipoamide) kinase, putative
MFRRCFRFSIPHLQDLIHRLDYFEKEIIELRTFRQMVEAASPEMALAAEAIAKERQRAKG
DIDVVMEYPLTSEEFVELNQFYALQKEKRLPLRNMMHIRNVEDLYVHAKIIHREYLVRLA
QRARALTLAPMGLSQMPSIQELRRSYEWSFHGVNSTKPPIDLESAQEFDSLMRCVFLRHY
NVSSLLSEGMYELGQREMWSERDFSDKSLVETFEELQVFFDEFCTGRVRLRFLVGNYMYL
STHILNVEPKESEKLTTSLFFDHDPDSFTGMICRKCSLENVLKCAIRAANDLYDESDIEL
RVAGDPNLTFVGIPYIMYDTLSAMIDDAIQANMIRQEKYGVACTPVVVTLSQRDENEQIC
VRVSDTAGGMPLEEVKHALKYSSSFKVSEQETKTANTWIHSPIRMPYAYCAARVIGGDIS
VVSIEGYGTDRILYFPRSGIRDIHI*
>TCRU_1503 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MAAFNPNKAPTPSLVDGSVEGGAIQSSGGGRPEEQRQSLGSSGVNGVSAPTVSSAKTSSG
GEGSATQLVSEKSSDGHKTVDGAFFSDGEPTVETREGGTNGREEEIHAQNGDVKAAALSN
SLGNVSQGNNSDAGTKRGSGLLPSLLLLLGLWGFAAL*
>TCRU_1504 hypothetical protein, conserved
MRTMTICTERRIICVSWHTNPRRFECRPHNSRPCGTVGFCAVTRRNYCPCVEADPFAVEF
TQQLSSVCAAHPALAHSHVSERCLACDLLCVVEAAASRFLLVPNKKHFALRWIFTCVAVD
ARDDAQRVCLLFGGHEGEFGVCRQRREILRRRIEAKLTEACPLHLSWQLRGTPSAQSGWM
DAAQLGRPVFFSALRCPGKIDNPQRHCQLHFTAGDRLC*
>TCRU_1505 BNR repeat-like domain containing protein, putative
MLAGVCMSKGLSDCQVGVAGVAQWGLLLVKGNVSGVDESTKRIYWNDTISILCNAIGDND
DTLTGHIGGGGSGVKMEDGTLVFATEAVKENKVNGTAEDGGNNNVSLLISSSDAANWTLS
KGMSDGGCSDPSVVGWKDKKLIMMTACADGRRRVYEIGDKGRPWAEALGTLSRVWGSNRK
RHEKGVGSGFITATIENRDVMLVALPAYSEKLEKGGAQKGELHLWLTDNTHIVDIGPVSG
EGTMLPPAPCCTTVVEVVKLIIMKS*
>TCRU_1506 ubiquitin carboxyl-terminal hydrolase, putative
MSCFQLDCECDYKEFKRTIYYHAEDFTIPDCSPASHFSVCERVYEKAVKELKARNFDLAA
FYFARCMSIIERANLRPQVSGAKKLMWNCLEALERLDKNELLEHHSKLLQKVRQHEEERK
RIVEQQLLPDEGEQESLEDRHLRRQQELLLNENTVVDDALKRIRNVQIPTPYSQTNKDVQ
PYWHKPSVEQLEIKKNQIAPPRRIPTISPNAYLVWKFNVGSFSVSTPRRGMVNLGNTCYL
NSVTQMLSVTSLGAYFLRDDYTKDIVGADKGEVRLVNSFTYILRELHRTDFATPASPSHF
KDSIGGLYTSFLGYSQQDANEFLRLLLDGIHNSLNDRKRLNNNISEVDTTNGSDVEISGR
TWSQYKQKNNSVIVDECAFQERSSIVCPSCHQISRTFTPSLGLEVPIPSSSGRVSIEDCL
KAYCKEEVLDSESLYTCPSCKQRVNASKQLLIYSLPRILFLTMKRFRSYGDFSNKVLEPV
VFQKELNMSSFMCSPGKNTNYTLVGVVNHRGNIHGGHYTADCLGADGIWFSFSDERVSRA
DSPDFQLAYILCYRRSD*
>TCRU_1507 hypothetical protein, conserved
MRRSCFLFSQIVDVVSALTEKRNYSVKLCKVLLFPSPPLRSLSFAPPPKWTSELSRRLQK
QFPEIKRQHHVLYLRAFIHPSFTTSDAMNSTMNATTSIGEALLASVGECLIVNAFRDLKR
DEVLLLMSFLLSDATLSSVLRYHWEMEDMVLTDASVQLFQGKTLRSTAGLMQWLSSSGKQ
QTPDPYCAGCVKSMIGAVYLDRGLEEAAAFIYKHVLQNIS*
>TCRU_1508 leucine-rich repeat protein (LRRP), putative
MASSITSIGTQESEELCFLEAYEEVAPTKTKEQLIEEQLQDLYNYQFTVPELPEDDPSGK
LAYLDACEKLHKESFMKFPTRSVARRICDGKESLDLSFFGLKKKGSIALSAALRVNLSIK
TLSLVGNHITPAGAMEIARSLSESRTVTLLDFGQNKLGARDPGETVRGGAVVAELLRAGN
VLKTLSLRDNGLSDQHIAEFVEVAIDNTELNSLDLSFNKIGYLGAIDVAQILSRNGDLRE
INLEWNQFQTMGSCHILKEGLLMNNTIKRFNLSSDGLDDNCAQLVGRIIGENAIEEIIIA

HNRIGPIGAEAIAKGLLATSALTTLILDDNPLQTEGCSALIRVAAEASSLKHLSMQQCRC
IVDLLLDAERLTKEARQDIVILISEDCCAKEGM*
>TCRU_1509 hypothetical protein, conserved
MIDDIEATLNRMLAFPSGASSLDAAIKLKNIALALELAEQIPLLTETCMSLCVELAENTP
PQVATVHSVLSLLARFCMREENRGLATRFGVFSLCVLILQDHKSLPEDTIFAVFDLISTL
CMNDGNVRRMLRPSIPYIIEIMNDNTSSLQLAFGGAVALATLTMLDADNATLAVERGSVQ
LLISSFIRAYDRKKEIDCQHICHVSRCKKEEEQQLCEKVMRWSRDALQKLVQSPSHAVDE
KLEEADFGKYGSRVEVDELKWMLKFQRRKVSVIHP*
>TCRU_1510 zinc finger protein family member, putative
MNSAVDSLLMRLKLSDLIPKFKEMKLDRIVNLRKLSEEELREAVPDDEQRNLIIHAISNR
GTHEKRQQSQAANINPPRNADDGGRVGMSFPRGSTRGGMGRGVSRGGRGGGSINNNSNSE
TNTSFPGRQRACNHFFSGECKFGDRCRYSHDKEIYDREMAENGPRRPNDSVSKPKDYSEV
CEIPTHRIKFLLAKKAERLKQIHIQNHTHNEPFKRVDSNVEKFELVVYGPDPQSVLQSKK
MILSYVGVTKQEEQKSRLQYTINELSSNQHAAKLLAACNIKNEGTARELSEETLKSIISF
FRFEKQQDVRHFYLNVNHDRVKLDKVAKIVAQLRGVQAIMFSDQKRVMEMSKVASKIARF
FNGVTPLFLHREIPKEERMRILQEFKDGEENESGIRERLLITNEDYAKLARKTLIPYVNL
VINYVVPRTEEYYLLQSLVAGRSDTVGVSILCVSPYDQSTFHELQQKIVFTAIEEESDFM
ETAVQLVYDTTANPLTDEDADPPRDWKEKLEKKNASA*
>TCRU_1511 arginyl-tRNA synthetase, putative
MARICTGANVELALKDIVRHAMEKAFPTISTPEVLISLGKVTEYQCNNAMGLAKLLSKAT
PPMKMSPINVGEELRKNLEENDLIEMFEPTPQGFINIAIKQEWAATMVSRLLKMGIQPPI
LPPKKVLVDFSSPNIAKEMHVGHLRSTIIGETICRLFEFCGFEVHRVNHVGDWGTAFGML
ILYLKRQHPNFLTEMPDITDLTKFYREAKKCFDEDPKFKEEARLQVVKLQALENESIQAW
KIICDISRKEFSLIYDRLGTRIEERGESFYNPIIPRVLSLLQEAGKLEESSGAKLVISKE
KKLISSLNAKDMAKLIVPHLIQIWRDNTVEFHVNMITVLREVGILTGEEGNETIMLSKKE
TKPLSKFDARTDIDKIVPKLEPYYKNQLSPLFREVFEAAGITDGDTIAVPRFNFPLILQK
SDGGFTYDTTDVTSMYHRFVMEKMDRVVYCTDVGQYEHFRMCAQLAKDMGWMGDATWDHA
GFGLVTGADGKKIKTRSGETAKLKDLLDEAVERSLAILEEREGGERRQGHTKEEMETLSK
IIGIGAIKYFDLKQSRVNDYAFSYDKMLDMSGNTAVFLLYQYARLCSIKRKANVSEDEFM
KAEVVINTPQEKRLALCAFRMESVLLKTVEDLFPHHLTDFAYELVSCFSDFFQNCKVVGD
PMQNSRLCLVELTRITLKKVFDILNIEATERI*
>TCRU_1512 Cupin-like domain containing protein, putative
MTQSWFRPHPLGIYPRGNARKAELLSAPRFGTLSVFQFAAKGWMRKSAIVKESTEEAFVE
LLLHLLSFFSVDDLCRLSATCTGWYCFIHASESFRQNCSLVSSKCLRFRGSWKETAIRIF
LLEATDTASFSVTKRHRTECDTSAANGFQFKHRPVAVSRAFFNDYLFQVWMCTILPCHYH
LLPGVKDDAGASANHGAAWTCEGNLPQQRSSFRSLLKDVPRRSGLSPREFREQFEEPSLP
VILTDVATDWPFFKILQGRFENLAEKKEELFRPGVSPDVSMRCEHTTMTVSDYVRYAKEQ
TDERPIYMFDAEFGTSMAIESLYSVPEHFVCDDFFKVLGDARPKYRWIIAGPRRSGSNFH
VDPNYTNAWNANLAGRKRWILFPPGCTPAGVFPAEDMSEVTTSVSPSEWLLNYYDASVER
WRGFGYECICEPGDIMFIPCGWWHFVINLEDSVAITQNYVSESNLLRVMKFLFAMKSSIS
GIDEDAEDVTSEVVEDRRAHFAEEFAAAMRASFPDLMQRVEVEIKKETEQRRQKKQECVA
LPLLDAGSEGFTFNF*
>TCRU_1513 hypothetical protein, conserved
MGFLTDYYDKLAKEGRLDALLIFGMYDERVYEVVDRHHLANEILNMLPSPRAAVFLSRGM
VYNCISEVVIRDFIKICMMLSRYRSVEEGASLAELIGSCGIPEQYRMNMFNFSETYRHMI
LSRSYFPQRSVLRLLSYIFCDDVLSDAVAQLQYKSDILNHVNKVYVDTPDFVSWRFSVRV
MSLAGGYNEDRSDVEYTEALTRVVTRTIPEFFMYFTVTFFYAMFRHYPRRVRGITPRWLA
RHRALFSAIYGAVLGVYVNSFLEYRIYKHRVLYELRKSQEYRRRRGAARRGIEYPENKYF
NNLEGVTRRIYSMQCTAYSVTVGALLLSMLPLTPVKFPKWMGDVAWRHPFVPRLFPTLLG
MHTASRCMVPFVFAPFVTLTIARFNGWGATLYDRYVECRMRMWYRKVEVAFDTSTDVADV
DITRDSHQKTI*
>TCRU_1514 hypothetical protein, conserved
MLVEGVLLRVKLGKPARDAVDLLQISTEIKSAEAVLKSTRNVLEKARRTASTEGTTENHE
CEQAALCYAAKKRAGMEAFFISEDVFHAFQRVFLDLVEEERVARCRLDDLHADTKKRAAK

ARSAEYFMGTKCVFERFAVEEEAREKKVRLFQEYSGFLSALRFAEEEERQEAISRARARR
RVSLQQSVAQPMPLSSFGQPGVMSPPVGLQQTARPQGPPQFAHQQPPYTAQTQPYGLPHN
FFGRVQQMYQPQPQQMQASGYYAAAPVGRGGYHYGAPSAPPFQAPAQNIFPAQYQAFQQQ
HPPNSGWSGHSQAARGRTHYYGL*
>TCRU_1515 LicD family, putative
MRRPRRWRLYPVRSAVAFIICLCFIYLFVSIESIGALQGQVSFLKVVVRSSAISGANLSL
RVTNETSALASSGIFSAVGSSRLSLLYNADAMIDLAAQREFNQTLCPTEPREKEDPKFVE
FLEFFTKVFKEKYNNIPWWLDEGSLIGVGRAGAIVNADDDFDFFVLLPNATSPCRPGSLE
CTREEFNLLIHQFLLPLWEAGACIRRFNPDISKFDSERRLMYSFQIRKPNELRDPMHCFN
PRAPFAHMHFGMLNADGELETNKWVGPNSHPKDKLPLDLMLPVRRCRLGPSDAPCPFDIV
GYLTLRNRGEYVRRSREGSCLLVKKKWSKARRVNQVKKVQLLHDCGYNSMIRLVKRFADS
DYDTC*
>TCRU_1516 hypothetical protein, conserved
MPQAGQGGEEGQEHTGSLEVTNKLAGNEDSQITGEQNVSSDADPPKQTGSQVPAGGQPED
EEGTKSPQPPPPPPPAEPLPQLPRQPPPGTNTLQSEETHPAITVEKHPKPQDGGHSHETK
MPQTKGSTKHEEGASSLQSPESVSHLSRESTTPLSTSTDSSGVAGSTVENSGANNPTPPA
ASVTQHDFEGNTGPAALPASNTELQSEEIPNAGIIATTNDDVNDSSRAAPTAERPTAGTR
STQTSGDAGDLERANNDNVNDDVARNGKTAEFEAASGDRNTEADNDERYTTVPETATNKT
INTEIPADSAGITAVSHTTSPLLLLLVACAAAAVVAA*
>TCRU_1517 UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase, putative
MVAWVLEKEVKYNPMVYVKVLGCHFHDARNGTGHSQVVPTSMCVHHVQEDDYAALMARFG
NDTSPVARVERASEDVIYPLCD*
>TCRU_1518 hypothetical protein
MLGYNASAPEERSRKQVAIMDLVRQHLRLPENPRSRQATRTNHDKQHKADWRIGHFNTTT
VGWGATETTEDGEGLAGDENEHSDPTAHQTERILTASDINKAIRAETLCTLQATGRAAAL
LAAAEAEPVVFSPKLVKSLDDLYPQEDTSLYPEPAVSALLVTFDSKDVAKMIGSRLARGA
APGLDGWARELLYPLTKDKALLMAITAILTDMANGNVAPEVAHRLRATNLTMLRKPNKKF
RPTGAECVWQRLYHSWRWTRSCQPSQPALRTCSMVSATT*
>TCRU_1519 hypothetical protein
MKPAVAGHTTAPGHGGAGGLLRKGTTGPLVEVDAGSAPGHGAATSPLLHRHHRHPPPTGK
QLPQRQLHGVPGRRHGGGTTGHAWEGMQGDLPGVACPWHRDKQGQDGGPQSREPVDMPAE
YIRPFARVLGAGIANDPKSELITQFVQRKAEETDRLFRAIVELNLQSTRSGGSCRRCHA*
>TCRU_1520 hypothetical protein
MRSPASEGDCGVRLRVSWREGKQRALTDELDAKHQSDPYETLQTSDRKVFVSNTAAGAGR
LLTDPQVHADDKGFSTYLRERLLVRVLPEGQKCVCGADASNEHVHTCTRLQQNPRTTRHE
MINMTFANGLRLCGFQCGMEPRLTEASRRRPDILIVGLDTYAITDVTVTYAGRVTAYVSE
ESMEEADPLRAARDRLTQKRQKYRHWALANGLDFEPFVMLTNGAIHPASRRWLRRILGAR
VLAYAGAQWVAERQ*
>TCRU_1521 BNR repeat-like domain/Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MGESWTEALGTLSRVWGNNKQGVSGVRSGFITATVGNGDNKKVMLVTLPVYAEKDKEKGK
LHLWLTDNTHIVDIGPVSGEDDDAAASSLLYNSGETGDNKKKDELIALYEKKKGNDVKPS
PGMVSVLLTEKLKRVKDVLATWKEVDGRVSHLCTSLIAEKDRASTDDVCSADKITAGLVG
FLSGNFSGNTWRDEYLGVNATVNNKAGEAASAVTSTKNGVKFTGRGAGAEWPVGKQGENQ
LYHFANYNFTLVATVSIDNVPKEGNTPIPLVGVRAGSNGEKTKLMELSYNSEKKWHVLCS
DKTTKEPSSGWETETQYQVAIVLQNGTQGSVYVDGQRVGNEECALGNGESKEISHFYIGG
DGENAANKEGVSVTVTNVLLYNRPWDEAEITALNPNKDPTPPVTPNAQENGTSSALDGSH
LTERRQSMGSSGAGSGGASPSAVPTVSTPSAVKDSLQQVASGKSSDGSQTVGGGSFSDGD
PTVETREGTDGQKEGIHAQNGDVKAAALSSNLGNVSQGNNSDAGTMRESGPLPSLLLLGL
WGFAAL*
>TCRU_1522 hypothetical protein, conserved
MHDFGRTERQTEAGEDLKHLQEPLATSASVMPINASFTAVGGGTSTSPTPCLMRQFLHFL

GDCYNHIDAPLDSALQQSVELARFVESTQCQDFLPRQQQQVRWGLWELLRDEKAREVSLL
EMEKQVRLYGGSTRLGRKREFGSYVNPSREALGNAVGSSGGLGQGGVVNVVFGSAWHELN
EVDEDALLETLRARGRYHARLPRHASHCQRRIGCRKNSSFSQSSSASQLTSSLPPRPNDS
RFMTVMGVMKNNTPQTESSSGSNTFAEVNMTESDDPCVVLGTVETLTPGCSLCIAQGLIQ
GCWVSLHLLQLVNVVSTAHLCAAPLLVPNEALSTSPQEALCVGYHVAQQQLKVAVGFLFS
VSASTSASIQSTSAIQREQAKNSTVDDEKKHHAKVVRVMELLARQGLDVCVHLLAALRLL
EPENAYVVLLHAAVLSFCDRNGVHKAKQLLRRFIASSPAFSERKTMEKGDFDMYDMWLQF
EAALGEKDVMRSDSERIMLLLEQVVTGILFSVFLELLEMKERPLVIMRIPYASGDDTIAK
KTVESSIAMCLRARDVLDKIVQPRLFKLCDAADGAIGTRARQSQSLCWLLRGTLCHILTA
LSLAPGTASMFSHTYAADEALACTREAVKRSDAAREFVGHPLAPAWVEQMLNGPNKGEGR
GEATHGGNNAPFLHAEEIGGNTFYEWRLRVEGDAGAANTTKEANEICSVYAHSADDADNN
DDNDNGGVDVLPAHERVTDVALLPPPAMRLWFVLAQTLFRSTSADLVIARSRDSDGAEKR
DGDTCRESLEASAVPSMCQTGATLASHTGDVASLAPQHRKMKPKKGLAAQRAVMAERENV
RKVMEARRLTEQSPLGFWWRWQEAMTHYCLLSVKTDTTQTSLLRRYRHLLTSVAGEGATL
TTFMRALAITHPILPSESWTFVATHFFPYSLLPSKQTPMREEGSKHAGPSLEIVDVRLRE
AWQRYELQCVQPAIAATTVPTDEENTRHTTTSSAVQPNDDRPFQQRTKQEVSVKAATLPR
PTRGMAQLTNAIAKPTSLQTSSLSQLKTTEEPQRKSFPRQRQQRRL*
>TCRU_family, putative Se.1
MEHGVTLLGDPMTPRQPIMSSTAPYFFVVEDASVSRVAEDWIAKVPYRDAHIFALGCTPH
RHPQQLAWARIAPRAMCSKDIMLDFAAPEVLVFHLSMQNGFLSCCRLRIDGPFWTLRRHV
LWRLFTP*
>TCRU_1524 hypothetical protein, conserved
MGVWCPSTVLDQLLLLGLRQLVGAPRSHKQREKTQTHWPGHRGILCQAPHAIQVFPEGFA
PNGDVLFRLPHLRQSLLPVLCHKPRAKNRPAATVWFASPETPAEPAPHWSTPQDWPSAPR
HAPIPGDTRGVFSAPPKAPSRTAQENNDGTSAGTHLPHQLLPLRVLTQKIPTGPLIQFLL
QRHQVIKQKLRCALVHQRRHRGTAPINDDPHRVAAAVGAPK*
>TCRU_1525 sphingomyelin/ceramide phosphorylethanolamine synthase, bifunctional
MVLMGPHSALRLLPLKTQAIRFLLLFLLSVLILGVALLVTNARMPDPKVVRPLPDIGFEV
FPKVGWLEHVTDVCIFILNFLSLLVAFKLYLLHRQNEGLDELQPFSCCPLIGKIIFGVWD
RGRQSGIEKRDAHLIVWIRYFTTYFIVMLFRAIVVVMTSYPATDNHCQNPVKITNPVKNV
IMTLVTFGSGFTHCGDLMFSGHTVPITLSLLVQWIYGSMLHWVFRPASVLLVLLSFYSII
ASRSHYTDDILVSFYITVTTFLVLRHSPEGAPWQLQLLIGWWPCCVSNEETEDSDRHPTF
VAVEVFLPHGDYQCAERISEEKTTVGPACGNFGHW*
>TCRU_1526 protein kinase, putative
MQKYRILGKKGEGTFSEVLKAQDIETKRFVAIKCMKRLFKSKEQVNRLREIQAVRRLQPH
PNIVQLIEVMFDRSTGRLALVFEYMEMNLYELIKGRRQYLGEEQIMSFMYQLLKGLDHAH
RTGLFHRDVKPENLLVNEDGTLKVADFGSCKGVYSRQPLTEYVSTRWYRAPECLLTDGYY
TYKMDLWSAGCVFFEIMTHFPLFPGNNELDQIYKIHNIIGTPPPEFLNKLKKYGTRMEFE
FPRKNGTGLAKLLPNASPEALDLLTKLLTYDDEQRGTARDALRHPYFKTLRESEKKARRM
RLENEKSKMMESKTGGNMFPQLSNTCSQVLTHTASKTLLILGTGDATGNQTTVNRASLLP
KLCE*
>TCRU_1527 hypothetical protein, conserved
MTNRVDRSRTPSRTSTGPYRDPAWPRVVGTYCDPPTVARSVEFASSTLEFGGIAPCSTIV
PSSDVTFVMLTRAWGIRRAVISLRPPIRSCAPPASTQWRSVTFSASANASNKRRSTATVI
SPLNTTESRHAVARPPPTVTDSVSVTPLTQSCPPPPPPPALASGTSNGRHASPKPPTRQP
HTQSVNEAVSASKHASAAAQPSHGTTLTEDRPAMR*
>TCRU_1528 ATP-grasp domain containing protein, putative
MEGKVVVLLRTSSVARAPIYKHLREMGVIFVVVHPVRPADAFDGVFHYHLQHDTNEVDAL
EPILRRFLTQHELLPDAIISFDEYGIYPAAVLSQRMGYRPIPLPPEKLRRTCVKSLLRED
CAREGIASPKAGVLTRPQTASVELVVHIQETLKAAGVTFPLVLKPSPGAGSILAKLCYGV
EDVRDHALLMWDAFASHSDMKHLTAVLNPAEGMERVEILFEEYIGGQEVDLDCCVENGNV
VFCSISDNFEVRPPYFLEEGGLCPTALPMYEQRELMRLLDKFVVLHGKDLHGVLHFEAKY
DFERRQAYVIEVNCRLGSAETNSMLRTCYRGLQLGESLVRCALGLSVREQLFLLYPEKLE

EVGSNENEAKDALFPPSCYCASVNIYPFQEGSLVRLEVPVSGKGLVDYGVAAVPGALVAP
PPNSFTFLAWMVAQGTTAEEATMAIANLRENFVQEISAAQ*
>TCRU_1529 hypothetical protein, conserved
MDAAAEAAAAVAPRVVRFITTMKATCQYVFCVLLPGEDRQGIKGFWQTLQQGDNGASSGD
ALLSSRSYRLVLHRLLHRTGYYNVHVGGIMLLVQPVTASTSRSEDAFHDVFENHGGRGCS
AGISAIEIYELAPGSSGEGGSSDMEGGRLILTTKQNVENYSERRYRIAIVARTTYPLTLA
ESRQYSVNMLKDQDHVTAVVMEHVLVKTSGAVLLAELDAGIFKRLGTFWARLQHIIGAIP
GTGRSFSEKQQQRGRQQQQQQQQAAELSVLSSPSFVPLSRVSREESDRLERPLGEGQFTQ
LPLEQLTGEGCGGYSPEMQVTTPYVLLRFFTLQLEGLTLEMKFSSSKMPDPDYYGPLTKR
LWEHLRSEAEASFPTTDHSKFSGVDGPYLPLTMSLYLKSLDVSLGSEGVLEVFLGEGQLT
LHDYKERVQSNIMHFVLDPDSKEPCIVVRQRQSRSCDTAWSVARKAHAPFTDAYEKEEIQ
AESNSLISVVVNIRQVHAQLHQDEYLLAVFYLDQVLEMVDTMRTVINSPQKHSENKEYAS
LEEIAGDFNFAISGASNVSEGHLHYGSTEYDPITTSISVRLKVEKGALSVWAPRLSSAGC
TIGDPLWRCIPQGERCGIDKEHLYHLYDVMFSKVSVFVFHQASARLEKTALHGKASDFFL
RERLCKAKLTYVDFPWPAEHASSPNWGGVVTLLQSYSALYNRSHNIRVRPPCASSTESSR
NRHAVGVSLCRHRNVEDHVEAYDVALQFDRISVSHQTAHEGDHWLFVLLNYFSDISGEGL
SSAVAEKEATADTHVTEENDAHSDDGVAIATSADVKITLIDVFVEYRPFGRSSMLVFLAP
RLNVTVSVPSLLKETTTVKVHLDKENLSVFLHDNFQQYLLEYDQEAGLGSLFGSSERGVA
TDLKNIGFVLVLDVAQSAGGKNSGTDDEKDIVTSRSDVSNITLFINPTAEKPVFLEVQKL
RASMFFAYDSLYHFRTVISHFLGCNDLAYLPSPHLLVERSGSRFECIIQSNYVNKGKHAA
VACHRVPDYVPRLHQLLETSVLNIGLASSVVAAGGEVASKAGLPKRSLATNSLEDFDIIE
TAELEASIAPVWETFENDSINLIGRSKYTNFLSIYGAWCSASSEYAQNRRCVPRPLPPNN
LVSMEIHLYDCDVIAHLYGGEDFIHFDVPQSYLHTIQRFGNMEEEVQEPSVLWSGMDSDV
ELHQGRREGRRSGFLGVGRRQDEYVVGRFTGIRLQVDLFVPGKANLLQVYLSVRDGEVVD
CIEKSSVRTLFMASLPPSLRDHDGDLFEMKWTTVVPRSSSMNAGMVVVGKPEEQLIVRLQ
PVTVAVHRRAMNLLSKFIEDPETLSNESIASDDVQSQTLFFSKIVVFPVQLILYVYFEGH
DTSRATRMDMFELCNFLLPSIERAQIKVPLILVTACPLHRVGDRILDLMREQILNFHGLF
MLLCGVQPLQLASNVGTAGVEILFAPLNEYRRNRRFFSALSAALRKFLFTLVSQSLNSAV
AVSRRAHNTTSSVITSVLPVSELSPVSRGSQPVSLLEGLKRGFAELLQGLRLASNVAAYC
LGPHGSPMRLPLAASLVFDGFMRGALEVMCGIRNVVAPELYGQEKKIFKGKRRKIT*
>TCRU_1530 hypothetical protein, conserved
MVAIAEGLFEYKVQEHKLFVVRFPDIVAGYIKAAEKWQSIVAEVNAGKWKARTVLGSRNG
DNLLRVLHRPTAVARVSEAFLLVGSDTVGYDSSDGI*
>TCRU_1531 hypothetical protein, conserved
MKDGMNWLFASNLLYSDGALHLLKERANEKGRAISLARQTEELKTIKSVLSTWAQLDDYF
FKSSTPTACLVGFLSNAASGDTWIDNYRCVNASVTKASKVKNGFKFTGPGSMATWPVNGR
EDNNQYGFANHDFTLVATVTDHKVPKISTTLLGSVLANPSARSSLGCRTARTVSGRQCLM
GRKQHRAARGSWGENTMWRSCCRTATRAPCTWMV*
>TCRU_1532 hypothetical protein, conserved
MTNRVDSSRTPSRTSAGPYRDLSWPGVVGTYCDPPTVARSVEFASSTLEFGGIAPCSTIV
PSSDVTFVMLTRAYGIRRAVLSLRPPIRSSAPPASMQWRSVTFSASANASIKRRSTATVI
GPLNTTESKHAVARPPPTVTDSVSVTPLTQPGAPPPPPPVLAGGTSNGRHASPRPPARQL
HTQSENDAVSASKHASAAAQPSHGTTLTEDRPAMR*
>TCRU_1533 hypothetical protein, conserved
MQRRRGVLHARDGVGGPQLVLVQLQGRMAWRVMPSLRGARRGCAILAGESRRRRHELRGE
PDADENYAEHVEDAPLLRGCDIQRRGCCVYFLSQQYAAASSHQHQAHWVHIP*
>TCRU_1534 hypothetical protein, conserved
MRVPIEAAVPRVQRAASHQRQRPNRVQTKPTVNRCMRLDVADQQRGCSQHNVLQQHDAPR
ANPDVRQMDLRGLHRVNLRDGDVAVQREGK*
>TCRU_1535 hypothetical protein, conserved
MSGSVRNVTLVNCTFAGGASLYVVGWRSDPPAGQRADVLISGLESRSGGGVVVANRYQPG
SRVTVVDSVLIAERRVAYRGAYDLGDASACLVLHNVNLTGSVLTIARSHVAAVFRDAVGV
LVVGGVALSSRGALYVDGLLVQTALGLCVSVEGGVSASGGSWWRLLTATSCFASTRCLCV
GL*

>TCRU_1536 hypothetical protein, conserved
MEGTHPAAYRRVVVSGSKDPVEYFVRTKGDGRTVVPTQTETRTGWLMWPAALRSQLRHWM
RAEQVSLRCLLASRPTRWPLLKGIQEHLFPEGVPAVWSAHCSVRFIGLFLWWEDGLLHFL
DHCGGGGSWGNMPTASVLAHRALVAALCRRHNPPLQDESDVFLSLASNERSYCYVFRAFL
LDNEFANGYEGCVAAGFECRFFFFDGRCLGITGACRCHRRCEGRCFSHPKRGCWEDVFHS
CSGGRHRRGECACSPPYFLYCSAATTGSDRQPH*
>TCRU_1537 BNR repeat-like domain containing protein, putative
MKGNKMFLLAGSTALSDLNGSWKEGSLEIKLVVGEVTNSTDSGPSKRIEWGEIKSPLNGS
TLAAHKGNLTECLASGGSGVVMEDGIIVFSLMAMSEENDGVYSMIIYSKDNGSTWALSED
ISPAKCLNPRITEWEGSLLMIVDCENDQRVYESRDMGKTWTEAIGTLPGVCVNSGSGDYP
DLSLRVEALITATIEGRKVMLYTQRGHAMGENANLLYLWMTDNNRSFFVGPVGMDNAVNW
DVASTLLYLDGKLHLLQRRGIGEHSVISLSRLTEELSTIKSVLKTWAQNDAFFPTCLYPR
RVWWRYCQTHRPAVTSGTTSTFA*
>TCRU_1538 hypothetical protein, conserved
MLWTDEKTLLQLGQGDVDPLLVVLRGGAADTPGGGSGGGRGGPASSVRGRDGTTDIMELP
VICRARACLPRSGQESHRTRAQSRDSMPDVCLHTRNGPCHTDERLACGVLLPFLLDFLPV
QPLDGGVEFHVPGWDASLLQGLCNRDFVVSGLIAWDTAVRWGKYKVCRVNSLHQGKQHNP
NLFSNAVTHGQWGSSECLSCRRGVRCHQDSCGRSGCSQTRRYEMFSALFSGKALCSL*
>TCRU_1539 hypothetical protein, conserved
MRQLIHVTSRSAVLLVLLVVMMFVMCCAGGCFAASLTYSYSSDKAMRADRAKSIPAVVRD
VSFGYEGASQTCTVIGRNGWAPTRINVSTRDLDGTRKYCSSERYCAMNSLLAAASVKVTF
FYAEKREVFVSLYFAATVR*
>TCRU_1540 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGGGFADKVVEAAAGVVASNRTDEENLILNWYVLTQEEC
ANESTTGGKLNVTAERICMHKVMKEVCDAFYNKTSGVTHDRDVKFICTYYATIPEEPVEP
PTPQGPPSHSAVSNATSDEGTPKNAPESDVAGRGEGKDDDKEHGNTKQKAVETAAVESIT
RSTDSEVSTAVSHTISPLLLLLVACAAAAAVVAA*
>TCRU_1541 Mucin-like glycoprotein, putative
MKHVNPSLTPKELADENENGTQDIQDPSTDVVSNSNGTSDEPGKTGALDQSAKNPKLEVP
VETTKTTTTTNAPSTTTTTSTTKALTTTTTTTTMAPTTTTAPTTTTTRAPSRLREVDGSL
SSSAWVCAPLLLAASALAYTTLG*
>TCRU_1542 hypothetical protein, conserved
MPGKQSRMAGSGAHGVKGQSIFQSPGGTRAQTVQAAVGIAARATRTVRRTSGLPAAEAEH
RHRPKSTTAQPIPESGDVVPPCLGVSQAWAREGTKLLCTDLQQHGEATAEGMIAVLPFAG
NFSSGRLPPGEAVCASHAAAAVDSACSIPSVQIPVELSRLPHGMLRLAARTVPRCISNHV
ITVARSVSHAEVESFQSAARSARAACFRRGSMPACRGMPSSVPAVWDGRW*
>TCRU_1543 hypothetical protein
MRASVKVWLQEQRRRRNTLPPEEEAHIQRIKDRLRIGSPLCEPYGSHTESSWRKPTPVSS
ATADSLLQHNAVLLSRLEDVEEALRYSEKERQRLRTQLLQASDENRRCAMQLIQLALDTR
RGELLLEEQLFRERLLRHESEKRQKFLWELDRRLSSNRCAHASHNERLRSSPRVSLSKQF
YA*
>TCRU_1544 Leishmanolysin, putative
MHADRLLVEPLTGRVIVPRYSSGTCAQFTIPSSHHTVGVFGADMYLYVSAGPTKGSTLAW
ANFCSQLADGRPVVGVVNYGPSSVTDSVYSVRVVVHEIAHAIGFTLETMKECNMLKKVEG
VRGKAKVLQVSSPKTLEKTREHFNCMSATGMELEDEGGERTASSHWKRRNAKDELMAGIP
ELGTTLR*
>TCRU_1545 hypothetical protein, conserved
MDEGLLAVVAGVVGACSVCVTAAGSPGDASGDADAVVVPMDVSCAQSDGSLSYRVCVAWT
KCSPAAAEAQHENYTFSGFDVRMHGRNGELGAVCHVAHAVHTCSSCAASCATEEEGATVA
FTANVTTHKYACPYEVWWRQFPPMEPSIRLHGAAMLTGRASVGCRHPVKGRMTQNLVGQL
RRK*
>TCRU_1546 hypothetical protein
MPFWCSGDVLTIHSSRNFPRNVLAAAVNGLSLTGIPRAHCLPQRGGERSLRHECIKPSIS
MFQLMAMLGFLLGGVGTTFMFRTKANSGLVSDVLVAVLDAGLRSTVLGTPAAADRRQSSF

*
>TCRU_1547 hypothetical protein, conserved
MRKNPYLAHYFGAALDSSFEEEGINAAANFAYFPNSKHMTQRVFCPSRESEPSNGSSTAV
CTPPSNVTPGIRVAATRARDGFPSSPPEYTNRLPPLPLSASRRSTPVEVYTDRQNSFYTD
LSITRSNSPMGIRTHQTPEHPSIEIFNRGAPGWGSMIRQSHAALAEVRELLGAEKATPAA
SMPVANRVISSVESDGGHDEVGTETKVSPATSLYEGENTRTGTTSSYVPMSCAENHPVDV
SLVPQSTIALPSAEATSQRPAPNASSREEEKNIVTNSISSHDAPNKIGGPDPPALQQSTA
TVPLQVKCFVLTLNPDAVACALKRLSRQPPYVYAMQNNESTVQGESNMPEKVPPVVSTGR
PKSRLHDERKKLKSKGQDRKDGVISVASLYGILERLADVVRPQSESRCVDSNEKRGDLDG
SFQPPHSLNVSGEKGERIDTYCKERSMREPVVAPKVLMGNAPRIEGRDFPLNDHREAFSS
IVPTSQLQSVGVNVQRPLYRQRRTSSARRPSASRAPRTPSYALPTESWLCKGAELNDAPV
DASFIMEGSKTKGALR*
>TCRU_1548 retrotransposon hot spot protein, RHS3, putative
MTLVGMRMATTGEHHTTASTVRQFTECLAAYFNGWEESSRDMSWEIIYVQQTGSTLMNDW
QRCDVVNSNNVSDDESRGIAAFWKEEVRQYQVSISYRDFRRDEALRSVQ*
>TCRU_1549 retrotransposon hot spot protein, RHS3, putative
MYPLGPIPRHVFDEEAFSERCGAVKFALQSINEVTAKEHFSRGGESPWYSEDPSHKPVKV
VREIYAGGVILFNAPISACLEERTLERLPSVAE*
>TCRU_1550 retrotransposon hot spot protein, RHS3, putative
MKFTISTNIEDVLFKGRVRVNEMKLNDFLTRELDGRDIVDTNRDVLLEEFFRDPTKYIRD
KGALNEMQASDAYARMERTVREEMIWKKLYASFAIGVSTIYLGGHWLLRR*
>TCRU_1551 retrotransposon hot spot protein, RHS3, putative
MVWRCWGWLHVVLLRRRWALAVLPTGVAVRLHGAPTTEPCECHAQRHWDSGTKQPRLCFG
ASGTCWPQLGGASGMLHSTGVVMAPRRGSCDGSGAAARHVAGSKVWPQWTMSSTNMRLSD
FLWNYVGGRAAVDERLQCDDGDVCSGAG*
>TCRU_1552 hypothetical protein, conserved
MAGDEALLHIFVGTLSADKTTREQAEATLTHISADPRLITRLIHFSCQELPFHDVPAEMQ
QALQAASIRVRNVLGRSDWNRNPYFTEETKSAVRECIVPLQCGSHVPELVRRQLLAATQN
LICYDYPHRWPSLMPQLRRILDECGAHLCVLSDASSSREVATLRLKGALGILRACCKVYN
NPIKIDADDIEAFIDAFCPLLLSLTEMLVSVWAQELLAQQTPPPPPPQLNGIPDPSFQFS
TKRKEKCMFVLSLWHNELSHCLRIALKCIHSLTEARWPRFLCDQPGMDRLCKGCLGQLLD
ASHKTLLPLYRLRILNSDCGDSNPFSLFHESAVWKLLKWTQGMCLKMMQDLMFPKRCERR
ARAAAKYFCDHYLPGFVQHALDLVRWHATPRHLTSKAYIMSLEILTMAVDGREAYRSVIA
PNAEEIFTSLIFPRLTFSAEDAELWTSNPAEYVRLQTSPAGDLYSAKVVSSGLMLTLAAS
SKPFHDADFVHHVVQYVLERLTTHAKAAAQGDMEAARVVDACLFAIYQFNKVLRSIGFGD
DRVEWLLTNYVAPAAKYPVGFLRARSILVLSVFASKIHWSSPQAFQFVLSEILPLLQDPE
MPVRMQACASIASLICHPYARDVIAPCISDVIQHYFYAMRLMDSEGVVRTLRRTIKHYRD
VLSQWALHLTEMLVQHFLHVLERVLAEEVKDSEFTPFTDNTGGDARLDPLVSDEDAVADI
IMTADEVLETLTTLVRAVSQQEVNSSSKASGEGGLILQMQERIAPLLYVVLSREKGSCLG
FMDASLMLLTTILSLSSAVASPMWRLLPCIHQLIVQGAVDYFYQMLPPLDNFVSVSPEQF
LFFPMSDLCAVPEFAANMASMTPAQIVCMMCDTVMQSSHLLHLRDLSAVPKVYDSILQNL
WLFKQREGGDNTTATAMADSLVEYILQAALRVLNDSSSQEKQRRSLTLLFANNVLSAILA
SAALTVRMLSSAGVLLPFFVHYIRLVQEETMQVMLRSYDRRLFVMAIATLARLQTEQAEL
AASLEEVLCGVLEGEVLEKYSHREGAMVITEVGMRESLSDGDAYDEEEWSGETESDSGDD
DEMEDEEDEEEEALGMENDKCLQSLLHSAADVLKRDAAAADDGDDDEGEEDNLLDETDFV
APIDARNAWAFLLESFRHASAAASTRFCQLVGDANSQRQLQSIMQLSDAVEQLLAARGRP
NAADPHSPLPHPPVREKLKPHFL*
>TCRU_1553 hypothetical protein
MSEVLLLLSMAPGSNSGRFENPSMHSLSATRSVHLGDTTFGEGIPPSVDDFQVKCVGLHQ
PPLYEEERHQRMLIMLECKLEFMTLVMWCFAIRMRIEKELLRGRMQSVQLQEATLQHRMT
RFAHVEDRFGRPVRNPTFRVLLQDEFFEREHIALQETVEFLNVWARMIPARISMMQGPAF
FAEVMASLRSQGHAAFFFEPNVLATAYPDKRLSALRKTVRGLKNDLATIHSEAEVLSFTL
DEEFKVDEAEITLNAMKAGEEGEVLTGRDADYCANVMRLATKQMDKLRGSLFRLKERLHE
TEQSLTSTKRSLLDEKEHSAHLQQILNATEEMAAAVASQCQLGSSRDNSSAQHEDVARPS

GDAPSTYTKGVLQELRRSMLMLKKEVDWQKERAQRGFCDRDAVLEIVYTQVERLAALMPP
SHSLNELKREDINMTNIASIMEEIIAGLMALKNDRSSNCVKDVQTPQTGPEERELAAMKA
TIEQLRSTIELLLSEKGKAGDGRPAVASAAPPVPVLNSQTDVLTMALRRLEEVRGEKIKL
AHELEEMRRHPRLAGWRSRHGTAAAESEEEAEHDDNMWVQSVHRLSEANTLLQEELRLER
EAGQSLRTKLKESERFITELQKQCRRLRLSGRIDLCEVIEQSGSDRDDDDEEEDSDDSDG
DSTARIPFEEKKQREVVKNTEGMGLGEQMSTEYYAQSHSPHSTVLTDTSCSLGPLVGTLG
SSHFMDQENHMACVRDQKRLLKALCGIHGIKLATLLIGKGSQQSLCNMHEILSMFIARSI
SLHTFFKCTGASAQVLRHVAVIYPLPPNEMPFLHWRRMLHPLKYQRGSSSKENNGPSVEV
FDLCEEFQALGRYLRGCMDVCFSHDGRFMYALTSADSAVIARLCSSECLNIPEEHQFRFS
AFLPKGMTPHRSGSTASGNGNGTVSNNVMSTGDSDQSPLPIDMLGWCGRGGICAWALDCM
QFDSAAEKARFERHLKSEYRLVLRLSAKEVQHFVGGSVELMGLTVVGRTVSRLVMSLTAY
EALSPPHRAQILQWYGGPQGILLLNVMNIESLTGAPLRRLLAMVQWHGRWPLSKTPPREA
LERFGFQPHQKQQRRP*
>TCRU_1554 hypothetical protein
MEEAIMSDIILVEPCAFYILGDPVADDTETTCGARKSSAGLLPASHAHAALYEWIRKFLE
SGWGKCRGATAGLCELVEAETALRELIALDESQVYMYRITSCHLTCLQREKQRWERELAM
REAVTKYQLQRLLHLEHHFHPAKGEKSVDTQSTLHQAGFLMKEMQECLAELHAPVLIRAQ
EAQKFAEDRLQALMRVLEHQTGRLRSTQKALNDVCLALNDLAACANVEARCKEGSEIAHA
AIREEDGVFCTPKEVIDAVQERITELEMRRMHTAHEANSTGATNDTFDALTVAVCRLEET
RADFYALGRRLGPVDSRVAPEVLRRLSEVDFMKPPLTPPKCLSPSLSFSPSANVGPKGFV
MESHAYEIHQAVLHEQRELVMMLNDIWGMRPLLLRLCTEGDAEQYAQRPLSLYAGHSLSL
HQWIDVDGTRPTKRATVFYPTPPERRGEVPKEHLESVLVEKAREARDALDIIDLRAEGEK
AGVYFTGNAVFFSADGKFMYCCCGTADTCTDARRTLMLHVVGMLRRRLGVPSANCFCYYS
SSFPLDASLGWVGAGVCAWALDEMRFASHEEKESFMLHLRETYRTVIRLTREEVRNFAGE
CVEIISYSPNYGPTRRRLVVSSHALRSLSEHNRSTLMAWYGEGGCIVPDLSTIERMGGYS
ARSMLLSVVTHGSDTPPPSGHGFFSFIGIRARERESACMEVTTTYKRKPN*
>TCRU_1555 hypothetical protein, conserved
MQQNEFNSVEAELREIEEDFASGQMNAFGTAATKENFVRELRRIADIETQVFYKTCGLLS
ASTSEDHLMRAMMLASADAPCAGGGGGGASSSNNSDEGNTTVATTRSFGRENNSSNSYAT
KSMKKDVANPPKMSGGFSPGSPSESRGPGTGDSASPGFSYAGPPPWSNDAGFTDRPFQDV
ARHFKLLEGEFTAIGEHLRQISKHVLQLNEIAERVRSKGSNLGP*
>TCRU_1556 hypothetical protein, conserved
MHRPDRLVISGSVTPAGHPRRKGTAPGRLSSGGPSQQRRQQQNDLVDSPQALSSATTTTV
SSRTVSSLCPFQFGAMPTVLDPSHGNAVSAGTQSSSPLLPQGRQATAPSGSHVLSVLEGP
LPAEIREIIHSQCSGEPAEVAERHARRLLSTHRRVRVYREELQSAVEEVGDVAQMLQRHQ
TVQDALRVELKDLDAQIERLVRERQLCELQLSQEDEARQRDEVKLRDAKERVNVLRSTID
TITQESLAGYVVLRQLVPNLNVENYVA*
>TCRU_1557 Acetyltransferase (GNAT) family/Acetyltransferase (GNAT)
domain/FR47-like protein, putative
MPLIVRFAQGKDNDVFRDAAIIRDSIFMQERGVPASLEHDSHDAYAIHLVLYDEDASDNQ
KQRGGEKKSLPIAAARLRVVRHCGVHAYDTPVVKVERVCVRRPHRGKGYGVFLMKEVEKY
AREKMGISTLVLHAKLPVKKFYKRLGFHETSDEFMESNISHITMSKM*
>TCRU_1558 Protein of unknown function, DUF607, putative
MSPVRTAVVAGGGALRLLRSIHLPCAAFHRCGFSSRGCRRGVLSVPVEDLTPKSIALFHS
YGPPTSGTVPVVTDTTAFTRILNEVLVRDDSGANDVIRDLRRFLRQKREELAPLLAEKHR
IDAVVDNRYVPLLGCLVLAFLVTQFVVLFRWVFIVFDWNLVEPMTYFLGYTVVWAGIVFH
CYYARELTWETMLDTVAHRRRVHLYEKAGIDVKKVERLQREVCGIERILSKYGLE*
>TCRU_1559 hypothetical protein, conserved
MSGAPFIPELSLGTVETGGGWGVGEQFARLPPASVQAESRTPVYTVAPDSGGFNVHDSDD
DSATQEESAEAETIEAEVVPTTHYRRPSMEDDNTFIDHGSTVPPASPSKDLFEKLEMRGD
GGDYSKRGPNSIPSLHVKFLRPVSRMMVGPQVRAMVVAPDGASLWAAFGDDPVTLLDFKG
SELNISRALDVTQVHSMTVVRVPVAKAVTFKPSRGAHRPSYFAASKPQVDEGEEVETYAL
WCGVTRGSIVIVDLTNFSMAGVIKAAHAQTITGMWYLGTGKVWTAGYDKALKVWDPQTRR
RLKSRNIATIISDLCYVRSCKQVWTISDDAYIRVFDAAGNNVQLAHPSPEKPENTLRMRS

EMRFITYYESANLIYVALTRSLAAIDPSTCGMPVVINATISSMTFLENTALVTGYGEWLQ
CTKEAIGLIDLSDPHVPSLLFRGGPLGGSVTPVRMRFLTAVPFAVVAQEAGRSERYLSVF
SYEDSKAFCRSGGVTSIPQQRKITLEAPSTRRPVAASQHAPSPSFAAATSTPTSALSPYP
IVFATGKRGSVMREESNLSSGHPQRAAVTSSRADGNNQRQRHQHSPSAPFSQNFTPIQNS
NSNNAAAAANTAVSSRSQSTTPAMRTSTAIYSEDSRNPSKSGINGSAERSVAVQLTTPPE
LLTSLTKIENKTEDLKALFAQISAPRPLLDDFSKLHALVSRMAMNNQLGLNLDEEEMENI
ERDYHSLEGRVIATAVERLRKTAAASLLSSVPNSTRLRDNSGRRDNVGSVAATSPSVVEK
RANAVTEIMNSSKAEETAGSVGGSEIAPESLLRWVAQITRSGQGERESHRRQLESLQRHN
TRIVERNAALINGIVRVEQAIRTHAQRLLEDADAAAAVISSDASCDSSAHVHAQRHIQLL
NQSLQQIEQVSVSSSPKEITEAMGSFVTLISRLFSTQQVLHGDDIARRVPYDLSSGNAHN
DQVLDTSRASAQNGSTLLTTRSHFSRPTVTSVLSMRPQRMRGIVEDQIASVEEFVKDVGK
FWSRLEETQKVIYVPYESGAKPDLFQDFMQFAVLWHLREAQVMVDVCRKESVMVMAEALL
GDIESREGMVGSNMAGPRRTSVPTALLSSTEKAMHSGGGKNPNSADIKKSNKGGNASILV
VPAAAETIRSDSARLVSIGLELESVASRIRESLKAAEQNLQMGVAKETIGGFFSIPTEKF
FIDATKLRGMLYWERVSMHLLYECLECLEELVFHCDEQPRAFRKDNFKALEQQVVDWRLF
LEDVHGECTQLRSVILSSQQESCTGRMSAAATASSVVYDRSSSLGSREMSRNSDGDTTST
ERTTQWVLLFGLYVQYAERTDATPLLFASHDSGDTVSAADFGLMALLDEVAEIMETVRAK
SAALLRYCQKIQGRIARVVEDVVVNEETGQVFVPACRGGPIAERYCKGFCHDMS*
>TCRU_1560 40S ribosomal protein S12
MAEETPVLEVSPAVVDAVMDATPENLEDALRIVLQKSREVNGLIRGLSEVARALDRRTAH
LCVLAEDCEDEEYKKLITALAKQGEVDLINVEEREKLARWAGLTKMDSTGELKKTFKCSC
VAVRDFGERTRALEFLLSHLR*
>TCRU_1561 60S ribosomal protein L18, putative
MGVDLTGVQKKKRVVRHHTYSTNPYIKLLIKLYKFLAQRTNSGFNKLVHQRLLKSRSNRA
PISLSRIAVCMKRKSVWLEKGKKAPIAVIVGDVLDDVRMTRIPALRVCALRFSKSARERI
TGAGGECLTFDQLAMVAPTGKNTFLLRGRKSGRESVKHFGAAGVPGSHAKPFTSNRGKER
QRSSARRRAFRHK*
>TCRU_1562 Uncharacterized ACR, COG1678, putative
MDKIVRTVYRQLYKKAASVDKDIAMRSVLTCSPQRLYDHRRGVWIAFDLAKQSGWPESRI
FLDSLIRKLNHGRDFFIPQAGRDADDDGCRGGSSEGNRSGGNDSGSSNSSSSAHENEDGN
KSNKNNTHGGGEPSPTLLQVLRKSFEETPFTIGQMNNAFAALKELAYVTEMASKHYGSGV
SPPKEFDTLPKPKLTVVDTVGEMHHLSLTKGLSDVLERLSGEEKGMVSRKSEEDVRVKEE
TKDGTGKGDEDNDDDSDDDNFGLSGKTPGKNPFETPKAVHMLLAHPQLYEFFRYSVMIVV
RSTPNEAAAFILNKPLENDEGMLMQVNSTIRLNHVHPILGKHLGNHTVMIGGPVSRGSFD
SSILLLHRIPDVEDAIPVSQSLWVDGNYDVLQKKLDDGTADAKDIVVICGFSGWGAGQLA
GEISSGTWVVARGSADDPAMDDFIFALARHAGESYCGAPQQPLESASSSSSSSRRKAKK
MPQGGECRIRSAAAWAWAYSALGPPYADLARNQKPFMQDPREN*
>TCRU_1563 hypothetical protein, conserved
MQQPASLSVSAPPAPVIKRAVPVKLTYEEVRRAAMFSVLDDFASQKQYKCRVQRLKDVGG
NVQVIPNPAVDTVEAAPKGSSTRLLREHSSASWSVYFYQWSLFGLTSISSVATAMGFYLT
IYHNRMFLPLGPMAAAVTWRLWDLLEAAWEQQRYIDNAARLRDSRKGNPMNLVAKRTASQ
EEVEPLEEMM*
>TCRU_1564 hypothetical protein, conserved
MNFEDPFADDLQSLDAVMAQLAAEQGRRSRPPPPESGTSSLSTAIAGKSAAVLEGRTGRR
DAVSIKSLGKQVQPIAAFATATRTPASTAVGKDEPVPWEMYDNPSTTARTHASATTSWGT
SLVAHVGGRDRHDAAVVGRGDGDDDSDKEDPLAFLERAPSLAAPVVEQSQATKPVGADAA
SSPQRHMEDEGARGQAERRDLLSSLDAVGMELDQIYSTLDRLQIQADTELTGLETTIIEK
QTELAIGEDRIASERRQYESYHQRRLKDITDRTTELLQRQVEEVTSMEKEQYEAQLRALT
AEMADVKNRIDQLLQQRELLLQQHRYDEKGIFLALADEEEANEKKTAADGGVGTDAAAGP
TSSTSSVETKMNAALRLLWRHHNERMESLASGVVRFLHQETMDVAREVRERHELAYLQDA
VTRKEELGEFMQEFLRRYREFFQHRSEVRSRKIAALRRGLQEATEKLRLRARQRLEKRTQ
EVAAQMDEAARRFEKLALESAACVRRKAAAVRESDDSVAKSQRADLESRCQMERAVTEKL
QQSEMETLQQQLERMRRLGNGSTSEDDSGVLQKQVAEDICAARAESITGQVRELESSVQQ
LLRQQLLRNQAHGDKGEGQLFLTDEEIFSRMAVQEKEAVVLSLFEEVQKRQNELSATRQR

CGELREGIAFKMQEEVQTVRQQRLAQESRLASVELLRMAWEREQRELLQWGCDMIVTHGD
SASTASSTARTQLPAATTTMDLMSLIVGRNHAIMEERSKLRTRRRQLLHTIEKERENAVA
KQRETEVRWAQFCEQLVGLVAEEHAVSAQRFAAATEIAKMAALRELISHDKELFCRRREE
MQEEVERLKGKLQATLTQQAEYDALQQKIALEQTALAQQQRQLAIQQSRLGRPPASAAAE
EEGETRCPPAKRPPRSDRPLSPGEASLRRPVETLQEVTARDNIPVLREKPQWQQQGREAR
RNTLPPSMARQNTGRSFSHTSVFTEGIGEKASAV*
>TCRU_1565 hypothetical protein, conserved
MPPRLASKVGRAGRRGMTSAGITRRRSGPTPGEIVAATFANVELSFTKASMAEYSKRCER
MSRENELLRHQLEEHESDSIKVVQHLKEKLQCAEKEVTEQRSEIERLLAESADAEEDLRC
QYERILEERDEQIVQYATIVQRLQSDLKGAAQHVHKREIHQLELKRLHDEIEEMRTRHDC
ELAALRFQTVDRKMRLVALEETMRERFQAQVEKESERLLEAKSRALLEDHESLQCERVRL
TQDLEELVQLATVKNMECADVRRKGELHQRACEEALRRIVLGNRRARDSEAKTQRLERRV
KELLREKNEMREELSRRYETQIHELEKTLAETQNSLQCHRNELQRLRRIASTIVGQRSDL
ERFFYVALDDVRRMRSKAPRRKQVASPVQLPSLAADNNGNVAYTGANPRHSQQQQQQQAS
PLILEALPSSLATKGGPTFLTESPASAKGNFNTPAASTVNTVPSSIPALSPTGPSSSVTL
PSPPPGAAPGRRCGGSARPTRDAGNSNNNVLLINLGENGEGAYLNDLSWEDKEKIIKALL
FFINQTCYQKLPGSQPVNSEATLMET*
>TCRU_1566 Protein of unknown function (DUF1014), putative
MPSGPKSNKYVNRHAAEARERDQERQANAKAAREKDREDAMWTEDDPKQLRKQEKQRETE
EKMRRQAELKAERKEQLEQEERELGQKVPQKVTRRQLQKDLSKMLSDYDKLKEKERQQQP
GALFKDVGAALPESNPNRMARKDDRNNSSNEIKATGGVSDALSALQSGMGTGGASVPEDR
HIGRRARVVYKKFCEEHLSRLREEKPGLRRPQYNDLLWEMWQKSEMNPFVQRSEQRSRER
LEQERRWMEGEDDDESDGGNEAEKE*
>TCRU_1567 hypothetical protein, conserved
MSAAPIITGRCFWGRRTTPNGPLVYTAVGSHKGSDDRRRTPISFIGNTYYERRFGGLRST
QSTPLGTSLALPSLRNGDILVKMGSATPASLRGRRIVDVTGIQTSFFDASERNARARCCI
DDVVHSMHMHDGHEVPELNRGTVDIGRLTVLCAFPVAGTASLLVLENASQALLKRRSLGY
RSEEEGVQLVRVIAESCRAAALRRICLHPVMRNDCIVGVRL*
>TCRU_1568 ATP-dependent RNA helicase, putative
MPQRNVCQQCKAYDEGAEDPQDGRFYCNSCWAAYNGFSGDTKNGATKGGRRGDKEKKVRA
PRRKELEAMNNLGHDAQGVLRRLEGMYASCSHKRRPETLATSLLEDVSMVMADTDKQQRA
SSFVGQFMQRQRAITVVSHLGEPLSPRGDRVGCVGRSAYQESRKVPLDILLSSVDDIVSQ
IYVNFDESMTQVILNALNRVTTCDTQNQRDAMRVRVIDELLETLGDEHYDLLQCVMHRPR
DIFLRLLEEFCTLEDDDDNTGAGNTSAASPQHALTVRFVKTAKQRSAMREVVFAHNGEAT
DQRWLAHMTQRYRQLMRESDLDQLFKRDLSVIGSSMPSGATVVQKKDHIRIHVPPPTQKV
MPMTERVCVATSLPEWTHAAFQTVTHLNAIQTTLFRTAFYTSQNMLVCAPTGAGKTVCAL
LVMLRCIQEHFVEGTLNREFKIIFVAPMKALAQEMVENFSRRLAPFAMVVRELTGDMQLT
KREVAQTQVIVTTPEKWDVITRKQSNEDLVQQVRLIIIDEIHLLNEDRGPVLEAIVARTL
RQDELHADQQRPTRLVGLSATLPNYKDVANFLHVDLEEGLKVFGPEYRPVPLEQTFLGLH
TGAKDKEHQLDWLAYTEVARNVREGHQVMVFVHSRKQTVGLAKYFVEEATKHDQGNLFKP
SGKLPTEAVKRGGSLQGRELTNLFSSGFGVHHAGLIRHDRTTTEGLFRDGFIKVLVCTST
LAWGVNLPAHTVIIRGTHLYDPRRGGLVPISVLDVMQIFGRAGRPQYDTSGHGIIVSDEK
DVGHYLRLLANALPIESQLQKTLADHLNAEIHAGTISSIVEGSRWLEYTYMWQRLRVNPL
LYGLKIADVRRDPKLKTVRYELVSKVAEELANAGMIRYNPQTGAVDTTELGRIASHYYIS
HESIATFNQKMRRPDETWIDSLDIGSAMNVIASASEFSQLRVRQEELDELQKIHAMLPKK
VQRYAIVGESADETSVEWKVTTLMKAYISRIHVDMHSLASDVNYVMQNAPRISRALFEIG
VQRGRPLTTTVFLTLCKCMEQRCWEFEHPLKQFSLDFTDAVQSHLDKKRPSMMLLQEMTA
REIGSLVHNQRMGGVIAGLVATFPSVSLNIDVQPITHTILRVKVTITSTFTWNSRYHGSS
ELFWLFVEDQDNNFIFHHEAVSLKRKEVEMGVPVVVDLSVPIVPEYDMYSVRFYSDRWLG
SQEDFTFSVAHLHLPDDTQLTTRLLPLAPLRREVIPEAYHAIYKGFPQLNAVQTQVFHAM
FHTDSSIFLGAPTGSGKTVAAEMAMLRVFEQCPPGSKIVYIAPLKALVKERVKDWTARFD
RHLGRRVLELSGDVNPDIAALVRADILCTTPEKWDGLSRSWQVRRYVTAVRLVIFDEIHM
LGSDRGPILEVIVSRMRYIGWHRQAPIRLVGLSTAVANPADLSSWLGVQEKWAIFNFDPS
VRPVPMRVYISGHHGRNYCPRMAAMNKPMYNAICEKSPNKPVIVFVSSRRQTRLTAMALI

GFLLMEQNTAKFVRMDVDEVTALTEKVSDPYVKHCMQFGVGIHHAGLLGEDRTVVENAFL
AGKLQILVATSTLAWGVNFPAHMVVVKGTEYYDGRTKNYVDYPITDVLQMVGRAGRPQFD
TEGVAQVLCHEPKKGFYRKFLYDPFPVESTLHKQLHVHINAEIVAGTITTRQDAVDYLTW
TYLFRRLVKNPSYYGVEDRSPKAVTIFISTLVANVLDELEACGCIASPGDDEEDDLSRKV
TGMSAVGSIDDEKDPDALTCTVLGRLCSYYYLSHKTVRYFDLHIEADSSHVDVLKALCEA
EEFNELPVRHNEDKLNLVLSQSLPFPINPNNAESPHVKAFLLFQAHFERASLPISDYHTD
LKSALDNAVRIVQAMVDITSNNGHLYAALRCMSLLQCMVQGIWWHSSTLLQIPHVTAGML
PMIASRCGNLEHAAQVANSSITALQTLKAVLREDCGLSETQLREAMAAIQGFPLIDVRLC
LSRTPDRTSSSGDAEHSFDGSETAADVAYTLTVHLTRLSVHNKHVVAPHFTKPKDEQYWL
VVGNEKTGELIALKRVNRLVNCVEMTLNFEWDDEWAEFAEGGTVALSLYVVCDSYVGLDQ
QYNFSVPVPVGM*
>TCRU_1569 Histidine phosphatase superfamily (branch 1), putative
MTRVQHAQASKRRSTQQQQEFVGLVDELLLLRHGERQDHVDRAWRATSLLPEADPPLSAA
GRRQALETGLMFLQKRKHRKVRQRALGMLSLLLISPFHRCIETALIVNIVGFDGKLAMFI
DPLLSEWHSTKLFSRPPRLGGSYMFTREMITFRPQWEALGSSLWTFFRSAGNGTEYGIDD
VMTTRWLSVLETQHAQNPSFLVWTSVLMQESLRRNLHSEGGVVQRVLGGASRSDLSGINY
PENKKHMLRRVGEAVELRFDANAGETAGVPACVKAAEEQEAKYLPRRFTHRPRMASAGEA
TSEERAVLLPPARIMMVTHAEVVAMALKHCCPKHHSLDSRFSVPYCSLTSLSRVNDYYCV
LDDGAPDARGPRRASEKSWCVGTVGSTAHLQTTILLR*
>TCRU_1570 hypothetical protein, conserved
MWGSWLDQIQKRLDDVSGLAEQAITLGGGDEEEEEEEDEGRETEKVGNVQGTSGGRSTSP
QPSPEPKLQQGTHGTTFPIHADDTVDRYSLPHEGVALAAAAASMPFQTKNASCFVPATAT
EELTGSAVMTAVGGTEKEPFPVVGLPVRLVESLEAHVAPTMPETVVEVAAAAPKLTTEAT
TPAAVASTGIDAIAQDEAAPHPHSCQQSLLAGDGNEEQLLRFQQVLAEELEVSRLLREEK
CCLQDRIGTLEKELRDLRLFKKNALLADPKKLEALEREGMELSTKLGNERERYKLLYEKK
TQLESRVETLEKKLAQCALKEEEFQQSIAASHTDCEAAKQHAEELRVFVEVQESKLQQLQ
RQLTSAKKSHAELVVEHEKELAQQKAELIFQRESMSGALVSLQREKEAIASSLQRTQMEY
ERRIQELENKLLQANRRADQAELRLTDHERSVLAPLRELRAALDDVERQKRLLMEEVEYW
KGECSAAERSRESEKKHFTQRLADAQSEVQVAHDERLAAEQELQECRGKHSQVHKALERA
LERASDAEAKKEQLSIALEEVVRRMEDAGSSNNNSSTPNSISHAGVGEMTRHSPISIEGG
ANSTRVPLFQVETTESVGDVCRGSRSRAERELVRQAVEIERLRRVEEEGAEAKRKLLALA
AQHDLLMQMYGELQEELQKSQLERPSK*
>TCRU_1571 hypothetical protein, conserved
MSQKLLLHVDVLRGRNYPQTEDDPCACSTLVRLFLYNNNLQETIADVFKTGIQENSNAPF
YSAGVDFDVPAGLESVVLVVEVEETTRRTEPYVLFYGCQPVSMTGKGKCEEVITLTCTNP
VEKPEEAAQEVLLAGEDPTSCPVLTIRYQVIRQKNAEEVRDVHADVELPATPALTGATSI
VPKGSRYVWVNLTSDPRWTEAFRHTLVESWRDRAPLVGNAVAKEGLQASTKGASTSRSSS
QPTRLMDIRSIGDVIIKRWCCCRAHEVLTRLRLCAEAFDRGERTIHFSQERELSYRLQRK
ERVCLLQELAKASLVKMGISELRDTLDHLWIFFSIGIKHDPAGTRALTYEARKKVREASF
DSKDKAILQSSLLNFLVPSLTMDQCNEIAVADMESAERAGNILEETPPTGAKFGSNAMSA
PASEVDFSMALIEYIGALLDTLTETELVAALKAFEPAVVNAQQRIKAKAKEEITSMRSNF
REPMRRELTPYNPGDGIKIDHLDRLGRRKKSYHPR*
>TCRU_1572 ferric reductase transmembrane protein, putative
MMSHLWSDGGDTSVASNSSLEHSIVSCSRNTAGELPSLRLFLTGESACGTLPQRKIDVST
GRIDAAVEISFVIGDADPRTVLVFACGPAGLVRSARDAALSLGVDFHEETFLL*
>TCRU_1573 hypothetical protein, conserved
MVRCRGKCPRECLVQLQVVTPQKLGGNEAGEAVLSSSLDVSALCEAIGHKMSVFCGLAVE
ASAAGLQVEAVRHDTDGVYHVVLRLPQATPLAVTALRASCASTALGPVVGGARRTVRQKK
PRQEETAVTTPVAVRVVHLTAVKAA*
>TCRU_1574 Mucin-like glycoprotein, putative
MMMTCRLLCALLVLALCCCRPSVCAAEPEPEAAASSKATTTPTSINPGANRSVTSQSTPA
TGTPPVPGQSDPSSTGPVASPGDDGGEGSGSTSTEDLGPNGVPNTLQADDNKDTTGPPSD
NGLSEERANSESETSTEETTTTTTKAPTTTTTTTTQAPSTTTTEAPATTTTTRAPSRLRE
MDGSLSSSAWVCAPLLLAASALAYTALG*

>TCRU_1575 nucleoside diphosphate kinase, putative
MFIGATKPHTTLVAEHTFLLCKPDAEQHHRYILQTVSDAGFQVMAKSFIITPALAEEIAS
TFQSVRKRMYAERGVDKLFNGGKTALQNEQNAPQGKRRDIMDTGRASLLPTSFASAFIGN
AGGEEVSNPNNISSRRRSGSVPKRHCSRDETHQGILAEILRLTSRCADGGEGVNAGLPNV
APNNRAVDGRGVSEGDGRQDENRMQQEQKPERRLATGTVLKNTMIEAMSYQDLLNEHVRH
LAFGGTCLAVELSRHNAVEKLLEIVGPENPIDARRAAPHSLRARLGTDLIRNAVSAASNL
AEASHCISAVFGFATRYSAADIRAHTAMPEAGGVENNEQVSGVPAIVRPYCELVSAPYRA
SPRGPVALEAAFRIGKTNPQAHLSYYTGRPLYGRANEKEEDDGTGRRGPSVDSHLWKQKA
EQLEQQLAQERMDLTLHAKLLRARELDLLLREHALENATNNLFAPAQPFKATLEAQSLPH
ISPLSSEEQLMRTHLAPALMQGKQLSPRSKGDVATSRQGLPEPHSPSARYFSTEAYTPEV
RGVLPVIEAEDVSLLLTKPVRLRALYVALKHHCENCQLTQDEVLALYDRSPSIQLLWMDD
HREYFRNYVNLHTEEPVSFDSFVSVLMFLLRQ*
>TCRU_1576 hypothetical protein, conserved
MQTVIQQIHQANLKAVLLSRINLFFIIFNCVAMLIFIVTWSVSIAKEGGGVLARYAACII
SFILLAVATFLSAMVHRKQPQLLLYYAHEAISILALILTAISMGTNDVVVDLCNTKRALS
NTQCGSHTAELLAQIMACISMGFNYASTQQRIVNFIDKGILDGIRGRSGGMTQLP*
>TCRU_1577 hypothetical protein
MRLNNPFLTQRDEMEMGGENGNRRSLQENLERCLHSEGGDELPVDEEDEDDGGDASNDDC
PTPPYVPCRYQFGLSAAAFVIRLD*
>TCRU_1578 hypothetical protein, conserved
MPSSDRDSTQEQVLKSPAAPTAATPKAKNENPGSADAVLVQQVQKVQSGLESGTELRKEE
SVLTTNKQQDGTFDSHAESTPTSRSSEKSVAASNGPDKATEDEISNKKTTGVDAVPEAAK
DDGNKDDNKKTPIKTTAIANGTAPTSDSDGSTAVAHTTSPLLLLLIVACAAAAAVVAA*
>TCRU_1579 hypothetical protein
MGEGGEIFFSFFILLLIFVAFGAVLLLLIYGVRCCRRKIQRRELERRQNAHDERERQRAV
QLLEMLSILREPMTFPASVQGRTASLASSTRSPASVSRTMRRGTRMGNSASMHSEGGWLN
ERKDSNDLVQNVPSEVETAAAETASTQVLRSSTVSFHR*
>TCRU_1580 hypothetical protein, conserved
MAFSGMSATFVSLCVIFFTVILIFVSSSYLRRRHLRLLEGNITARRQQRAEADLRDNDRA
RSRRALMRQAILRLVERGEAYQGIPLVSTANGTEMLADRQLRSYRARNGEHRRPELLLMQ
DGRHATVSSIVSMVQANHTPPPEAPPGPNLLQMLVEISARRQGSEPLQRGETVDTLLEQL
QHLQEEEEEEEEEEAAREREAQPDADEVYGKGLPYLLNPANEGVVYFIDDDAEYDALLCQ
QHLARSKSALEWILTPLLKRKNGPSFENPRRAME*
>TCRU_1581 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MKDAAKGRSGDSTPSSISTSDSVDAQRKAEEEGDNEMEALNPNEASILPLVNKNGQGNVI
PSFSGEQKEQKGQLLGKSGAGGASALSTVTSSPAGKESVKHLASGTSPDGHQNVDGGSTA
DGYQTVDTGYGDKTQEDGPLKTHTGNLAKAEDANGPTTMGVGKDGTTVNTEVSTSSAEDW
ETVVEKNVHEEIKPQNRDVNGTALNSSLGNLSRGNNSDAGTMRESGLLPSLLLLLGLWGI
AAL*
>TCRU_1582 hypothetical protein
MARLICVQNVCVIVLLPMRACWLFGNLTGTERRDEYLCVNATVHGALTGAERGVTFEFAG
AGTEWLVGKLAHNQLCKFVNSISTVLATANIHGVSKEGSSTVLLGLS*
>TCRU_1583 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MVKNVFLYNRPLNSTAMTAIKERKPVPKRAPEPQAGGVPQTIASAVSGPEKNSAAPAVPM
TLNSHAVEEASEGGAAKRNASWNEGAQFVVPEVSLNSAGSGLLPSLLLLLGLWGFAAL*
>TCRU_1584 casein kinase II, alpha chain
MTDQDSSGRIIIVTRPVPASPRPPENNGDVSHVTTDCKSQKNTGENTVEVKRTLTENEIR
HHETGVISHPFWFVNNNMPPSYWDYERMTIEYSSGEPYELIQKIGRGKYSEVFRCRNRIN
GELCVLKILKPVRLKKIHREISILQNLCGGPNVLRLLDVVSISPEGTPVLVTENLEPAES
FRSLMNSGSLSNFDMRYYMYEVLRCLHFAHSHGIFHRDIKPHNIIIDHQRRKLRIADWGL
GEYYIHGQAYNVCVGTRNFKAPELLLGLRLYDYSLDIWSVGCILAEMLFRIFPFFRGQNN
EDQLYRILEVIGTEDLTRYARKYDISLPRFLFGSGGLFKRMKKPWYIFVNDQCESWCDVH

AVDLLDKMLRLDHQERILAWDAMQHPFFDPIRSALREDPQEQYPQ*
>TCRU_1585 hypothetical protein, conserved
MSSSPPATLTAEEVEAVTMSGEALLQLASRLNGAAFVPSSNSQAGGRMWGDHGSGDGGGD
APFVTVEDGAGFMELLRDVIEHCPANLQARGESHYEQREYGAHNEGRSPHAATMLQKRLL
ALHHVVFGLQPELLATVLSLLHAPHMMTDGDAVCHLFQSALLLLQTVVFSCCIPSEHLGQ
GWRGSYVSVEAMELSATCTDLLDRLGAVGIVSDFLYDDFPLTVRLAAAQLLFIMLLRDGS
TVAQAKSSYVRDALSSPERLSILMTVLTSTDAYINSVAAHATVRNLTTDELAMPENGASH
STTLTETGGLSATSATLPDLCLSLRLHIAACVRELANSHYSRLTGPEVLDVLLRLSDTDP
SGDLRALCIESMHVILRHCASSEWATVSFKKELAALCATQLGREGHHDALHATLCLLETL
ILRDALDNSAGDISKADDGEVTHRDLCLCESLLMLFADRALAALIGDAVSPLGERTKKHS
SGRGVNESQPRHRDPTYHSTQDRPQFLQGRKMATRDIFCNVTTVSCLSARCLRLLVQHAP
YYRNGAFYLVQHRPSLSRLLETSVRLAAFHEIRCRENALGSGYDRGISNSIDFEGGGDGV
NVDEASLVLAVELAILVGLCLAQDPRARQLVAAEFCNFHVEAQQMRSALISNLNLVSLSY
FGDAASGDIFEIMDVTGVRLNTLDAVMWDTPDRPSRAAVHHLFTTQESRWNKGELRILSL
SSRINGNKDLADFSDGDDGKQGRENDVNATMNNNGNNGDNREGKTRGGDMYALLQTSDHQ
RLQRLTFIVLSYAIHYTFKAATGDAAAATRFAAAFRGTADDSLRELIATLPSPSFKTTSA
VEEQRRTSRVASTAVATVPAAAIHDSRAQKNLRYYDAYMLDAGKQVPEAKGQKSSAKNSF
LVSARRGQLQRPRDRLTSSAPMKGASSSSSTSTTTDGEEESAKNAPDGPVPVTAETAHLI
LQFHRGLRLFRDLAQFYNKHPTSMLSRTTVYQATEEKGMVRRQGKCEAQRTIAKILQEAE
DASLLSQQPTTTTPTTTTAQPPQSQRGRVTSLGLIGVNTRSWSINELQEGDLFYFCIPHA
QLTTEALQYTRRRALKHSRHLKKVFAITPQSAKSRRWLLHDAIANIMPGVVHALSQFIQW
FDVYGEENVKLPILIYFEDDVGRDDDDNKNKSGSQRYSQDGNGREDSHPAGKKRRSGDGG
GRSAVLPSAPSSMFRPTPSHPQGQGDASMASSLPRAEEVALHAGNLISLLQQVAFYLQRR
DQLPHPEDGLRSREFSTFVASPMPQKGEDTGHPSYASPSITALQHDTGGAGTPIRAVTNS
ASPLSTARNSVFLRDIEREIERLQKLDVYGDENGTEAAGGFLLPEMAVSPYGDTLTPHAF
GKIDGFGRYENDDDIIEEDEEEFDELKGGVER*
>TCRU_1586 proteasome regulatory non-ATPase subunit 6
MATAAVALAPTADAAGSVLEPLLDKAEDLLADGRRAEARHVLEGIVATDVAADDAEGLRV
KERSVYRLADILSLERQVDALVHLLSVIRSFFSLLPKAKTTRMVRKLFDLIRTSGASLDR
QMEVCSDMIAWARQEKRTFLRQRLQHRLAEVQFARNERQESLITLQALLREVRRLDDRAL
LLDIHLLESRIYYSIQNISKARAALVAARTNANSIYCPPLAQAEIDLQSGVLHAEEHDAK
TAFSYLYEAFEGFHQLGDQARQARKALHYMILAKIATDSPDELAALLSSKNVLEYRGQDM
DALRGVAEAYNNQDTHFFNRIMQENKDSPFLADEVLQRRLTEMYTSLLERHLLKLLEPYS
RVQISYLAYLLKLDVETVESQVSQLILDKKLAGIVDQQHQCVVVFDEQDAKVASKNQKQQ
RQQGMVSGGGGERGSSSAAGPTYKNAKSTTEDGGEKPTTTLYQDALEALDKYDRLVSALF
DKASGKFDALVEENLKRRQEMKTDKKKDSKKGEEKEDAEKKKKNAN*
>TCRU_1587 ribosomal RNA methyltransferase, putative
MGRASKDKRDIYYRKAKEEGYRARSAYKLLQLHEEFNILNRDEIQTGVVDLCAAPGSWSQ
LLARHLREEVGGRNEKQSSGAPRIVAVDLQEMMPIEGVQLLQGDITSEATAREIIRLLNI
KEDTASVNDAYVDSEEDKSAIQTDKGGRSTARRPSLAPGGRNSYSDHTNSCEKKADLVVC
DGAPDVTGMHELDEYLQHHLLLAALNITTFVLRCGGTFVTKIFRGPNTPFLVAKSEVFFR
HVIIAKPRSSRNASMEAFMVCQDYQPPAGYRPSFDRPLTTTTRCFTPAAPLPPAFMHLQS
EGRQITQEEKKGVEDQACMMESVIVPFLACGDLSGYDADMCYDRDSDVPVLPPVHPPRQA
PYMTTACKNDEDSVVATNGAEDIMKRRRVE*
>TCRU_1588 ubiquitin-conjugating enzyme E2, putative
MSGLSLAQARLREERKAWRKDRPFGFWARPREKPASSAPLAFSSQVPQDATTLTSTAAPT
ATANASSSTTAGSTGSASRSHTAPTASTGGSNNDAKGLLASSTAAGSGGLDLLEWEAGIP
GKPGTPFEGGEFRLLLHFTEDYPTRPPKCVFTPVLFHPNVYPSGTVCLSILNEEKDWRPS
ITIKQILLAIQELLDNPNIKDPAQEEPYKVYMRDRKEYEDRVRQEVAKHHKKRMV*
>TCRU_1589 Kinetoplastid RNA editing protein 1
MKRLTHRGRCRPAGILTCDAWRNWRRVSRASMAMAHSSHAFMILHNRPRSLRWVSTSSQT
AGETAASCIPSSSAAGDDNSAVHADACGACEAFAPGEARELHFHEDFLFEEVDVHFLLLE
EAHKKHGVLLNVPPQMSPSGTPPEVPEVMFPAVQLERLRGMQLAYEPTHLPPPLHTTGTR
KLIIDDASPMATLVTKTSIASTPTTTKSATSTKGGGGTAILVRHLPPDPTMRFHCTACGK

AFRLEFSAEQHVKLKHPSDSKAAVGTGPGEGEIIEEALATAVTPTSPARTAKETTSKATG
AEKGGPSASENGAAGGAGATESAKTQQPSKDGGLSGAEVSTAKMPYDKATLALPSEELVD
ELIKEIWDDIAARRDDIPKQNDPNAYVPFNAVVEGTADRRKEIEANAKPTARATPEGAAP
GIKKPSMLSSGSMSAARAQKPGMSVPIKELVKKYPNPFGDSPNAVLQELEKEPINPFIPQ
EELEAQLQVARETPPLASTPNGVANGIPLGSKTKTSSATASAAFVTGTDSGRVQDKLKDR
LRASRPSLTRSASLRRFVCPLCAEKKRKKAEAQDSNAIPSFRLLDALFDHVESAHEGEEL
SEEQLHSLYKTQRSSALHAPQPSGNSGTGETSDGAVDPNTHAFKDDDTIGMREETIQDAV
RAASLPEMLQKAAPPAAVEQKALNVHVRAGSNTVLLGRIADVQHGFIGTMAVTQYVLEID
GENATSNKGDEGAKLSPESEKELIVIRCMGDNFPAALLKEQVRLGSTVLVQGTLRMNRHI
DSASKRLHAYPFVQVVPPLGCVKVIG*
>TCRU_1590 hypothetical protein
MILPKGKSDMYGRDAHVPSLRSEYHPSEWIFLLVVMFTATVCGGGGIGFILPVTAMHDAS
MDMTSALAPTPAAAVDVAASYSHAYSADACASYTSCAECVFDASDGILSPSMDCAWCVIT
HRCMRFNVSFLTSNLTPSSSSSSSSFYAAATAKTCPDWRHAKFNANCPDMSCSAAHTTNN
IYICRPITIFWILLACILVLLDLGFYMWLHAIRQLPWKYEPRLSQLLTGMPTPTLQLITP
VRVNQEQAGSEGREVPTEVDMKEQTSNYHHSNNINNHVDDEKGDPHEHNSQHQQTQKQKR
VLSNCPICKMAQPAPLPPGHVCFWCDIARFGFIPLFIGTSTAGLSFMLLFCVSLKPWFAD
GFYAYLLLSAYISYALFGAHVYFRRASRVHVEAARETLYISLAIFLHGRSVLSVMPSLSE
GDIVPSASASTSAQASPLQRPVQPPEGGVGGKALLQSNGLTTEWIRQKKGETAQLLNMED
LEHGIRKVLRQTLSRDECVLWCEKPEVSSVILYDLWLYLDLLAGLALGIWLFVASSVKDS
SYVLVRLVGSTSMCVIGFVLILVFACLLMTTLSSSTRLYVLTDNRLLTIFNGFISPTVTE
TELRSLRRASIYGCKMWTAKPELTFSWEVPVTERKLPPIKSQNFPCVVHVEEFLKYFKMV
APKFMPINDQIRKGIRHERKAWRLHLFFCIVLLHFLPIITFYPLFVPGFLSLLLLIIFGV
VVLATVHRGVRAQHVTHTPLNLVDHWAPCDLRRSRSGSGGRASPLARLVADGNSTAENLG
SRPKTVKFSSGLELPRSRESRTSSPPPPARDRLK*
>TCRU_1591 hypothetical protein, conserved
MWGVLLTLFLVALAPSLQFPFIAAFAVQDAAATNSSATGDHLPGVDLHTLVEENATLILA
GDALRYVYVAPKRYVHMVHLALQDDLSRCFCHFYLQQQFLTGGDLDAETVVPERRDVDAC
KMSYFSLLPGFNDVPEELAVHFTATWSMPSRDYKKNPSGHVTQLTLPQGCFTGLQRVLAK
LAGRSGNHPLRRCTVFLGIHPSSMMKDPSNVLSFNTRLCGVMCGLAIVVLVISGLMVLVT
VLFMSCRRWNAEYGMDEELGQAGAVDGVISSDHTRRGSLSRCRSNEGPERKMPEESQLRK
AGAASGRRASRAPAVGFR*
>TCRU_1592 hypothetical protein, conserved
MVCVDLTCVAIRLTPVWVCLIAYCPNGKRPTPLQALVRVMDYGFSVEAFKRKPIVLLTHM
FVHANESHLAGNLTSLMATLLEFGGPSVQRNVEEHNVWVSVRRMVGSFAVFIGGGIMGGI
GGQLMFNDAQLACRHKRWMSLLSVKGETNGTPLDAVIRRAKSWLERMKYKIDKKRTDSIF
MCGASAGICSLAGFNVSYYKRWGTALTMVAPEVIALVCSLLSSQTRLANTAWLPAGEVVG
HAAHVGGFTAGVCIGLAWRWFSRVYRNARQRKQRTKKV*
>TCRU_1593 hypothetical protein, conserved
MWRAPKQHAATSRRILQLRCIAHKEAGPSPHDLRTFVIGYGASKFRYGSELIWAVATDSA
KNEMQKTYATLARIVSGVPSTVDPESALLEANTPPLRVLCLRARLSIFENTRACQMDWMR
RPPPEPPPRAGFRISPLSRDELYAFVDAYTKDYGITESSPREERFFRSSIPPWFAASAHR
ATIGVGLPIDHSITDEEELIREKRRVSEEALALHSHRSWILATDGGVDVPKSAEVGILLS
SLNSSEIIEKASINRGARPCSYRTESRALLLALERLIAPRIQHRRKTLLVVTDGQSLLAA
LNKGPLSQTDWTEDRIWQRLLTLACAGWSVRL*
>TCRU_1594 Protein prenyltransferase alpha subunit repeat, putative
MHDQRKVSQEFDEKTREQRLAEVQAFTSAYGSLLRQRDNRVYSEAVLQQLSELLQKNPEA
YSMYNYRRIALLHLWGKMREQREEKVEPADAIENTTQVVGDTAAGGLPSSQSDETKQHAP
QGEIEWLKEELKLSSMILVSDYKVYAAFMHRRWIFAQLERLAKDALFANTATNTAGVAVQ
SDSDRVECPEELRFWSSALMKEKKQCDMLLAADERNFHAWNYRRWILREIARMEKLLAQY
FIDLNASTSKNTAGGEVPAMKQEEEEEQQQQKQKPQPRGGSGGDNREPCGSFFIPEELKE
MKFTTTMLRRNFSNYSAWHQRGVIINTALQRLQEKCEDDITRDVALREAWGQLEEDLEFF
ITAVYCDPADQSAWYYVQFLIRAADTLERISPAHHAVRIEFTTRPIQACIELLGEEKRLG
DEAEAYWPRYYLFTVLLSSFGAGNSNTDGKDRTRAVVTAFASEIRRVLCPNDSSGDSREI

EEDCVWCLRELASELVRADPLRAGMYKSLLATVTS*
>TCRU_1595 hypothetical protein, conserved
MGCKNSKAREPPADTVTAAQANIATNKNSSTAPTLSPAQLHVKQTGETKRNNAASPTSRG
NNGEASENESRIEQPKKALGPGGNDVKQAASNSPSKQELDDEGNPLLLPNGDWVRTEGTP
FYYSVEENLYFHPPSCQFYDPTNGMWYDPEKDEWYYDDENGAQE*
>TCRU_1596 U-box domain containing protein, putative
MSIHGAITFFLDQDPGAIGVSALSCLASSLNEPGVAHSLVEQHRPACKEVLSRIVAVAND
AGKNPNARILALESLYGISNVPDVRFRTGDLLDAVQKLNESFEEFLETQSTGNGDAQLEM
LTVLLFRCSDYMRLKAGDLLRQLYNNDDARLVSTLQMIMKKRSLEWNIVHACVRCMYELT
TPVTYFTAPDENLPIETTKVTAFQEKITTILIHFSEGKALQELFTELGARWAIAVGEERL
ERILEGQSPVKDSVCDGVAMRFLGLFRYLAVMLLNLADFCERMDLVRGYQRSFIAQHQSF
LGDTVIPFLSLTLLCWEASCDTTLESQNNPFMNVAISVLRLLRFALYRPSQALQESLALS
LRALTRHVHRLESLLCKEYVGMLVIVLTVEVLCNVNAVNVEPLTADFTALVNLISTDTNP
LRPGAHFTVAQAFTYCLSNETSMYCAPDNESVSLLRQRLRFEDAEMANEAARVVQALEEQ
LGMLQTLMMELAVGQLIGDLSLFASYATGSISSGQAPPVKTGACDTKQMPEKAKKKTKHP
AKYVCMLTRKLMREPVVLRNGHHFELDALQEVVDRVGHVDPLTGEAFDEEIEVDMGLQQE
IARYRIKMAARGDDEAAGQ*
>TCRU_1597 hypothetical protein
MVVTDPLDRHSVDKEDVVTVGEVASLGAQSNVIPPLADRKAEVGDGGALQLIPLAIKREK
NLQSIPLVPNPRCRGQRGGLAVGVVTSPHIFPLEVFLCIVLPIPLRFVIEEDVHRRVVTE
AVVVVRVKNDAEAGEFHRSAHQRAVVARPVSRDPQRKAIGAGALAMQVKPHDNLKGGHVQ
RLRVPQVPHLPGTVCRQADVIVRDDGGAADGPVPQLVFSVVVAQERRGKGVVLNHTLRRA
VVLLRRHPRSIGR*
>TCRU_1598 Leishmanolysin, putative
MNFDPKYMTDTAWSVRVAAHEIAHALGFSQESMREKSLVKKRERSVRGKHRRMVAGKHVQ
EKAEAHFGCDSLEGMVLEDEDGSWEKEIPHWKGRHAWDELMAPPSWCRLLHGSDDGDVCA
YGILPRELEDGGADELGPSQWLRLPGQ*
>TCRU_1599 Leishmanolysin, putative
MFCDAKDTETLRCTSDRRHVGTCTASIVEDKESLVDKDVCPVVSLEFHEVSSGTTYRKCS
DENVDYLRVSLTGGGSWCLDAELLETKDGDSHKSVKGVCTQVSCGEGTVRVKHLGSSVFQ
P*
>TCRU_1600 hypothetical protein, conserved
MELLRLLVSLLVIAQQRLQPATPRLAQLLPVAVLRVPHNDAVHSDRKHHSGQQQHVRRVR
PRSAVARRKMVGRTHHAQHRKQHKARSLHHRQEGRAHHVREGNHARTRKQHSRHAEVQDV
AASHGRVHSSNQAHHTQHRQLEHAPVHVAAPHARQHAAVHPLLRRGVPIPDGVQQALVQR
LPRKLPVPREARARVASNEVAHASRERHSVQHANDTDHAVLHAGVGHRQCKHGAEEYAEV
HRVRHDVRQAREAHRRPRTRRVHAAPPLEGRRHTVVHAAEHSGEQRVAHHHPQRIKGSEH
RQEVRQRNGARTLLRRGARHPRKHAERLHLQDGAQPAGHHHGNSRRTRNNAGDRREGAGS
GGQRVGRDRERPKQHTLAAAKHRHSVAANDYRLVGTNEVTAVHGHSQLQDGGRIRRVAHP
RRVAQHRSPRTAEPARLRRRHRHEAQVRAELRFACPAERRRQRHHQPCRDGAPTAANVVL
RQAPTSRRRRHGECRARHVAPPQSAAHRRRRGPRG*
>TCRU_1601 hypothetical protein, conserved
MIGTAAKIEGGATFEGPGVWAEWPVGKWWRNQRFHIVKKEFTLVVTATIGAAPAGSGSAL
MVAVGGAGSLRMVGLSVTADNKREVAFDGEAGEVQHGKWGLERTYRVEVGLQNGMGSVCV
DGKTLGSSATTVTRGAQLLDVSCFYVGGDGCSGSGCSQVTLTHVCLCNRPLTRQELQMHV
LRGKQTEVDCKERKATPRPGNFAAKLPRDPGVDAAAREEVPVPAKGNLAWETAPLMSMAL
LFYCFKKGLVTAPSMGLCLGHFLALLQGVRGDVACL*
>TCRU_1602 hypothetical protein, conserved
MPSLSRRPLAIGSEAEEGSSTLINEQEQRQQACPPGQTPPLVGRSNSHYGGRMSRNDYHS
ELRNYFYSAGIPAIFDALSTALLEEKPEEPVDFILSWFRRERERVLTNAEEKNMYNSNDG
SRSCDDSSKDESGTSPTLSLSETQLPL*
>TCRU_1603 hypothetical protein, conserved
MTAMEPYSFATVLGDVFGRSVMHAEKRPYVPKGSRVQVSFTTATTTTQLQASQQLGIPRR
VKKEREDDDKGDKKGETRREAEAVDDNLPVPVALTGLISTDPSDGKCLIRRTATDGDDGG

TLWESKVIPSGKRIGCIQIAPDSRAGMLQVLPHAAVFPSPLLYVADTVGNVYAATLPASS
VTAAGVESPAKRPRQEKVNRSPFWGIIVPATTSDSEIAHGACGWCGIVPFFSQQLVCCRE
FFFDIRLVDVPAETVVRQYGTIQPATGTTACPGIPHGVVVAEGPVATLYDMRCPGAALTL
TTDPKPDISLVTSRLTSPTSYVADVCSTCNEYEVAAAVGRSLCVYDVRKWSCVSVSTNIL
KYEIGSISPFASGKAVVVAGIDAEVRIVPLQKASPVAAASAPAHAGGNGIARNEKVQKEE
EGGSAAPNSFRNRIDSAVCCRSTWNGGWVESLDGSNAIGVSADHEVFLSF*
>TCRU_1604 hypothetical protein, conserved
MTRVASQCFLTASHVLESRFTIHKDLPLISTFLDEEVDLFWRFVIICLWAFCIYMRGYDT
ILRGCSPIALETVILLLRVLLLGDDILIKREELMALPNGTGHIHRVHSAPGASVRNGALQ
QRQKERIGPRTAFALELFIWFLLIIFTIDLTNINRASVALFLVNTLYWARLGPTSVVFFV
GIYVLMTYFCCPAYSLRDSFLTLSGQRSWVYRVYSSFGLAFSLTLFLTETQCLQRVRRAG
LWKVLMIPRAFEKNVANTPLRGFSAVMRHLTNYLFFLGFNFYMALSVWFSSMMFEWTSDT
SFTGIVCTPYALSAILGEGWTGDFQRMLREAIACLSMYLVIAIFIVLFVPTDSLSFAANG
VSSAFFVLYMAAHSPRRVHSSFPLVMVWLGMVAVNAYWHVNRVGVNAMHMTWYKKLLCVN
TITSGTLFMLSTALHVYRWEWPIDPSAAALTATVNGVTRLSQSTRTDHKVKEKTNNSTSL
ISNTAEKSAAMMSTPATVSMPGKKASYSIEKVTSFALSLSSSSTSRPVENVASEVYPEAS
INAAELEKCDAMSGGSIRPSSSNQFDKPTTIAFDESVVTENFLCECAHEPRTNSAASEEE
YEEEAQRQQEEEEKAAQYDDDDDYLPTLAASEEVLPTPPVMKKEKKEEKGEVQRDTSFEE
TSSAPLPSQSRRGNENENVLSSIAASDSLSKMEPLSQSLVLSSPMQTSSSVSSEERRGSS
AGNGKKTSERLAATEGGNWKRNKSHDRFAETVVDKIRSSENVSHSLQLVEKVVQPLPLRG
AQQTSTQIPPESTTVSNKTSATTSFSRRAALEPVVNARREHAPNKTSPSGKEPIAVSNQQ
LPSQVSAHRVTNTEFTGNKRQNGKKSSSRGDTTATEFKSQKTLPSQSKRSEDRRRGAETS
AAAKVAASTASASRLGSKPNNDQPSQGNKNVGGGGCVTAPQLRSAQNHLTSNLSSSLTVA
ALKSLTEEKKAWDGQQSSARDETDELSLHLRGKSTSGTKNKFNSRVSSQGDDDNSLDLAQ
LHLASLPESEPERSSSRRRGPTPTFEASRCIPQSTLHSLENFAKAYMPRLDTSGLGETER
QGEAADGKDTQGGSSTAHLSPTTVKHVSLLEAAASAAASRSASGFAESRGAVPQQMMPQM
FAMSSIRDAHGAAIYQQVTPALRPHVAATTQFDSHAMAMPQTASQQQIPVVLVAMGDGRL
TYCPVVASSYSPAPHIMMQPQHMESAAMPQQHQQQGMVYQHVPISHPQQAYPGAWSHLSQ
QLNAPN*
>TCRU_1605 hypothetical protein, conserved
MLDDYVAKKNGKLHDAETTERHLSSVVDQVLNYLRNGVRVTKISSKGSARGRPYFLSEDC
KRIHSCELDHQGFPLNRKRPPVTMWICDIEKVLIGLYTTAFVNHSGEAQLAKTRQEAVFD
NGTHRHDATQNITSSSLGTNNHRAFALLLRGGKSLEMVCEAGSDCEAWLVALKRPLHLRT
PAERLLEERRGT*
>TCRU_1606 hypothetical protein, conserved
MQQPEQELSLWQSAIWTKEQQLEMVQLDGARGREAIMRERHSIEAVRRTVREERCRQRRQ
WIHQIKEINAKFPEQVRPLAEERKKKREQATAKEDAAERALAADTKTIEEYLPRLISLED
IPVSPEETGII*
>TCRU_1607 hypothetical protein, conserved
MKRVNAIESNREEARERQLSVVRERFKHEAGKMIKELERRGRATLDEIERTLEAKKRESG
ALQADRENRIWEYEHTLEKI*
>TCRU_1608 hypothetical protein, conserved
MRVDGNTVRLNCPQPLRDAGFPVAEVLFDVDLALDVPGASTLFRKLCATAAPNFTQERKN
TVAISYGVRSSPKRQLMYGSAAGEGYAACVITEFIRLGAKKGIFALSCHVIGSTEHRADL
LDADNELGVIVGSVREGPRVRMAARIRVSLDGDARAAMDTIVKNYEKCFSPCCLKSSQCL
SWRQCLRICPTPSFFSFAAMMVRRSL*
>TCRU_1609 hypothetical protein, conserved
MTTWQRKNGKLHDAEATERHLSSVVDQVLNYLRNGVRVTKISSKGSARGRPYFLSEDCKR
IHSCELDHQGFPLNRKRPPVTMWICDIEKVLIGLYTTAFVNHSGEAQLAKTRQEAVFDNG
THRHDATQNITSSSLGTNNHRAFALLLRGGKSLEMVCEAGSDCEAWLVALKRPLHLRTPA
ERLLEERRGT*
>TCRU_1610 hypothetical protein, conserved
MQQPEQELSLWQSAIWTKEQQLEMVQLDGARGREAIMRERHSIEAVRRTVREERCRQRRQ
WIHQVKEMNTKFPEQVRPFSEERKKHEQATAKEDAAERALAADVKMIEEYLQRLISLEDI

PVSPEETGII*
>TCRU_1611 hypothetical protein, conserved
MKRVNAIESNREEARERQLSVVRERFKHEAGKMIKELERRGRATLDEIERTLEAKKRESG
ALQADRENRIWEYEHTLEKI*
>TCRU_1612 hypothetical protein, conserved
MRVDGNTVRLNCPQPLRDAGFPVAEVLFDVDLALDVPGASTLFRKLCATAAPNFTQERKN
TVAISYGVRSSPKRQLMYGSAAGEGYAACVITEFIRLGAKKGIFALSCHVIGSTEHRADL
LDADNELGVIVGSVREGPRVRMAARIRVSLDGDARAAMDTIVKNYEKCFSPCCLKSSQCL
SWRQCLRICPTPSFFSFAAMMVRRSL*
>TCRU_1613 membrane-bound acid phosphatase 2
MTAGGVYLRARYVAVWLVFLLLVHVGSGKAAVTLRLVQLVHRHGSRSALVHHNQTQICGD
VPCGQLNIHGKDMLIKVGTFLRERYNSDLNNPFFPSESYDVEVSYTRSTDVPRTLQSAVG
LLYGLFPNRSAAFPVIHTVTRGTDWLLDGGLSPFATVFYLLDDAWKHDVGNKEVDKIIDF
STLQAIAKEAFSEGYCSDPANRWDCAYVLFDIGAALQADGRIGSFKLLKANLERLRSFSR
FYYSSQYAYNSSDEQHVRMGSQGQNLAQQLLANAELHMQGKAKYKLYHYSAHDTTLMPLA
ATLGDIGPESMMPPFAQLYAFELLYDDSTNTHSIRAMRGSPEQTPDTKHRFSWDGFQLRC
MDSNGNVYNASQNTCLYQDFKRFVDSTRPTDPAGLCYLNDRYKALLKCPTREGKPLNKHC
MAYRKLCPAWSCDSDFTLDPVTLQCVCTAAYCMEKGGEKGGKALGASGIAGVAIASFFVG
AILAACIAVIALGWYFRWGASDILVQPA*
>TCRU_1614 glyceraldehyde 3-phosphate dehydrogenase, cytosolic
MTEGKKVTIKIGINGFGRIGRMVFRAAQHRNDIEIVGINDLLDADYMAYMLKYDSTHGRY
GGMVEVREGALVVNGKKIRVTSEHDPANLKWNEVGAVVVVESTGLFLTDETARKHIQAGA
KKVVMTGPPKDDTPMFVMGVNNTMYKGQEIVSNASCTTNCLAPLAKIIHEKFGIVEGLMT
TVHATTATQKTVDGPSQKDWRGGRGAAQNIIPSATGAAKAVGKVIPALNGRLTGMAFRVP
TPNVSVVDLTARLERPATYEQICAAIKAASEGELKGILGYTEDEVVSTDMNGVTLTSVFD
VKAGISLNNHFVKLISWYDNETGYSHKVLDLVAYISAH*
>TCRU_1615 UDP-N-acetylglucosamine pyrophosphorylase, putative
MGDLSECIRRLLGTGQDHVMEILEHGSEKDRSSLARQLTIDLYGVDFHHLNHVLRACLER
EKDHSSNTAIEPPPNNFFFDVMEDQRARGKHVEELETLGYEAIHAGRVAFLILAGGSGTR
LGADVPKGLLTCSGLCEKKSLFQFHCEKIRRREELATFRCGGVPSAKIQLLVLTSIQNDE
QTRQFFQENNCFGLAKEQVQFFTQSSFPCYDEETGRFLMESACSVCVAPSGNGGVYSALA
EVPRGEKETVLQRLQRLGITYVQIGNVDNLLSKVADPLFAGYALKEGAHVVVKSSPKKSP
DESVGVFARLNDEWGVVEYTEIGERAKEVDATTGNLKFNCANISSYICSIRFLQAAAKRM
ETFTRYHIARKRILTANGPTMGIKLEAFIFDLFWLAKECVDPSTGSGDGFRIMQVNRSEE
FAPIKNAEGALSDTQSEASRLLLSLHTRWLSAALISIACGGGVTAQDAKEALAALQSKGL
GVEISPLVSIGGEGLQPYLSRAINEILHGSSNRVVILHPDELPQEPGNM*
>TCRU_1616 Mitochondrial SSU ribosomal protein, putative
MRRRTVISFGCVRVATSAVGVIGMGANHRHHYQQQRPITTRGQFNPIHDFTYAMERGVRA
RDEKKFEKLITNPGPLRIAYSPDYLDWLYRCYKAKGKYMDARAAAEKKFNGNIISGGAVT
TSSGEMIHPLPGAPPPGMFLRPPNSFRRLSGEMKRKHAQETLDEVSKAQGMLDLFERQPQ
FPAIHIDRCTRFHLVELFKEMVLERSLEAVAIWDKALLYRAILSERKASYPASFRYIFKA
VEDTVFAHSSVNCPSLEAYYYFLYLVKKYYIDNAVEAHVVLRCHREPNATDLLFSNPPPK
DEVDVRNVIEALQSEEATFHAASSATSGTAKHDDPAATDEKHTRGENEQKDSANANAKHP
CRFAPPSSYPPIEALWRCEENVPLLEILLFGEFNLIVSENPFVKFPTAHAFLTRPYSTES
SKGPIDGASLANVIAEKRGHLLPSFPMNVASAIDGRAQELRRLQQKHHRDDTVSFQTLLR
STHVDDNPSTFSSYSDWSYFNPRAVRAEERDRLTRKGIDALKEYDSATEDIYRRSFEDAQ
ASNFQRVTEAWNTFPPYLPTLPHFVSIIKKDSHISFLLHVGLPERCSSAEAAAKHKEFER
RIYQLARTLYHTALEFHKETVRRVNRQKVNVAASLLDSFFEQEWVAMLRESESLENSLEQ
GAWPDKKTDMARRLGRYIPFARRSLDENGFPTDARADDYARWMEAPARMKGAA*
>TCRU_1617 hypothetical protein, conserved
MSLADVFTFAPATGHFFSTSERVALATSIPLLMEKSKRRTVLVWGKVYGFKNDYTIVQAF
DDDLVAQPVIYYSIDEGLSFVFLGTTESLMQRTMDEVLNEKKKRMLMYRMRGPFMGDPSY
EYRVVDELAGSTSSYKESLRLVLFIDAHDYHCRVAPRGAYYRELRNTTLPPEIKRNSAFT
GLRRAYNEALSLRNYYHLRAENPYIELIAKEEGTQLHAKSGLERLEEDQHIDSIFFPISD

DLPGGVWRLRYDPVQNAVLGRSAKFVGSVFYHVPGTNKYGTVYMGDGNINHDIAFEL*
>TCRU_1618 hypothetical protein
MGQHNSAENAATGVRAATSVNDDGVILVKAENTKERPVPPYELRAQELYESSVRRIQIVP
PLLRTSAGLSPLSSAAEPTGLNKLYQRMSSIFFSQAVLMEQEALQQQRQQKAIDTSQEDQ
SAAKDESNCPLAQGLREFAFCWRAFETNAAQQANAGSRAIDAALVGVNLTLEGVKGAAVE
QSHIAELYNFVEQESHALLEEVTLAVNLLQNDFAVLLRDTWSLLTDAERTGVQTEFHAKW
KHTTLD*
>TCRU_1619 recombinase rad51, putative
MMSVEHCSCLNPSLKARLQNAGLLWIDEICRLLKKHSDREVEGVTSQQKEGTDASLSSTD
AASRRLLERCPQLTQAEAVEVMGAVLSLYRGNDPADSDYHIPPETRTLEEMLKVEADKES
ERVTTFCRGIDTLLGGGLPVGAVSEVCGAPGVGKTQMLMQLAVNCLLPRELGGLHGSCLF
IDTEGSFVPERFREIAHAAVMQVKEIILRQGPEGVIGDTVVATDEDDLTVSSLIDSGSGS
GSISALVRSRKRGRAEGTGISLAALAGFFTVDYVLQQTQYLRVMDVVSLMALLNVLPTYL
ASHSDVRMVVIDSIAFPFRSFSQLGVYQMGNEAPEGGASATAVTSKHLLWQRSRLLFRCG
QLLQQHAREQNICVVVSNQVTSRTLSSESGECSRVLIPALGDSWAYGLSTRLLLKHRHNG
IMEKETNTEREKCHENVVFIAPAVDGGFDVGSAVNAVQHRVVCLVKSPNQTRGHCCFSIS
QKGVRDIYRVWL*
>TCRU_1620 hypothetical protein, conserved
MAADARTDDGDLRRAYTRSMPAVLRPLWLLEESMRDVQVQWEEIIEGVMVEDVSFSSVRA
AVLHVERLASQLKAIKQELMPRLSHFSQQEEDSEQPFLRYCSCAARPTVNRDNSNCELAQ
GEQTQAARLAARVWVWGVCVGTIMNDLELLSTSLSFAASTCLLDKFAEEVRLTEASTFFL
GKDEGVASPLSDSDLLLTCQLLYHLFTGDDAAAEMTCHRLLSLIEDCEERDDGKECRGCI
LSRLVRIAECVAAEDYGALRVLMKVDFFTGVDTLCSLPPLIIFFTQMMLDTVVHRQLVRG
CFQNVWRPVINVDRPARDESPSVPSEAMKNSPCSSSRLSFTTKRRLMKCCTVFRESLPPR
VPWPIPEDLMDRCFRMGL*
>TCRU_1621 hypothetical protein, conserved
MVVTSERQASAVLGVPPYVAARAFKDVTCIKEFGATNFVSCCILETAHDPSTVGVVRRVT
LDLPGIPQSILRERLASVEEGPYRTCIRMDYVPCDAKEAHRSAFGVEGTKRLLNASTFAT
FTAVSKNPNRCFLEISTKFTVDIDVSPDGVQRAAENPTYHDIDQFWNLYVTRAATALEDY
LLSTAFATTERQIGGGFEKEFVNAENEYCQWAAKNCDKISREEAMQVLEKALNAWQRERC
ELKHQQLVNAQLMADAAGSAAVAASAHRLSLAAMSEMSFSDHLAPKPLRRTTATSIARNT
SAEVITAPKNWVPEVPVVDNAVDLNMLKPVHVPFFSPGGGRVLSVDPAESEALQKVQTES
RDAASPHRPAAKAFQKELLLSFLTEIGTINERVAQTIFNSLDTNHEGFVTERGVSMVLSQ
MDPLGLYEDRNGKMLQMEECRQVVGTGIFRNISISQSFCDTHPAAAGSAAAAAMDAAPHN
IASKGETKDHEAEGRDGFAKELSPLQALIRRQNEQKKVLQDELIKKRTAELMNNYAYRTR
GRLHYDEFCLMMLHLLKDY*
>TCRU_1622 hypothetical protein, conserved
MVSNEGPAAECVIKVLRGVSWAVVGGYGVALCYRFGVFRKVFPKSTVNAIESVVEKVKKR
TEPLGDARRYTIARLHLIHVYFLSSLGIMVAAAGGATFFAFPKVPIILPIALTLVPSTLL
LLLPKGMMLYAGRVACLLTSCFAFGYSFGPVGWIAWDSLGVFLTVMVSTMAGLCVPLFLT
RGMISYVLSSQLLSCTLSLAAVTTLPLVLRSEGVRPAVSFPFASKNVTTPSSNVELLLRA
DVNVLLTLQLLSNWGINLLHTLPTIVRFVQWKGDEGELLDCVDPLKESICICAGAAYVMW
RSFRWACRRLLLAVAKDDTKGTSKEVQDQWGHFAKLSFRTQHVSGVSASVLLVLWYVRAV
SELQRGETVATLEALRRVCAHMSPVGLLVRRM*
>TCRU_1623 fibrillarin
MRGGFGRGGFRGGGRGGGSSARGRGGASRGAGRGGPGRGGRGGRGGGAGAKVVVEPHMLH
PGVFISKGKADSLCTLNMVPGVSVYGEKRIELGATQGGDEKKEYRLWNPYRSKLAAAIYA
GVGSIHMKPGSKVLYLGGASGTTVSHVSDLVGPEGMVYAIEFSNRSGRDLVDMSKRRPNI
VPIIEDARYPMKYRMLVPMVDCVFMDVAQPDQARILALNAQAFLKNGGHYVISIKANCID
STLEAPVVIASELNKLRKDRLKPLEQASLEPFERDHAVVVGVYRSVKKKTE*
>TCRU_1624 hypothetical protein, conserved
MVATHPRATYAARPEGIARSADGLQKRQRGCLPLMGAEDGSPIHSTTSHQSPQASHHTAD
APPDLSNCPTQSSRRAVELIRQRRSTVVRRITDVSALGRLREEGERGGPRNVDAVNVGAE
NSLAGQFTTFLPHARTADQRGEPCGLFDGTVRRGAIDLTAARQEAAVHVANEWNPAGHGD

FEV*
>TCRU_1625 hypothetical protein, conserved
MNQFIRSRTDWRERVVFRLAWITASRWFEIAVFTPNNFKLEPDGTLSWDWSVAPKTARAD
PHCFLRFVRARGRDAFDIITLCGTLQAKEKLTNLTNAHVERALALWGATARSIERGALRH
AAPIVETYNLDPHVISQLAKHFDSFYLSKNTVRYSGK*
>TCRU_1626 hypothetical protein, conserved
MYGSAAGEGYAACVITEFIRLGAKKGIFALSCRVIGSTEHRADLLDADNERGVIVGSVKE
GPRVRMVARIRVSFTGDARAAMDTIVKNYEKYFFPVLCEKQLMPELEAMPSYLPDTVVLQ
LYRDDGEAEFADYMDANSLTFVALGDAGRPALCGSDAAAQLHYEGAQRALVSAAGIVSSI
RRRRLCIPFGMSELSQLLRRAYNTEKGNRSNSLTGSTETALLAHAFSDAAWAEESFHCLS
TTCRVGNVVSTGIRYVTRDLAVDKWRLDQDIMELRDELMIARTAYDHRHCGHESNRPFQT
WRRKG*
>TCRU_1627 hypothetical protein, conserved
MQQLEQELSLRQSAIETREQQLEMVQLDRAREREAVMWERHSIEAVRKTVREERRRQRRQ
WIHQIKEMNAKSLEQVRPLAEERKKYEQATAKEDAAERALAADVKMIEEYLPRLISVEDI
PVNPG*
>TCRU_1628 hypothetical protein, conserved
MLDDYVAKKNGKLHDTEATERRLSSVVDQVLNYLRNGVRVTKTSSKGNACRRLYFLSEDC
KRIHSRELDHQGFPLNRKRHPVTMWIRDIRKLLIGLSTTSFVNYSGEAQLAKTRQEAVFG
NGMHRHDPTQNITPSSLGTNNHRAFALLLRGGKSLEVVCETDSDCEAWLVALKRPLHLRT
PAERLPEGRRGT*
>TCRU_1629 Protein of unknown function (DUF3676)/Trans-sialidase of
Trypanosoma hydrophobic C-terminal, putative
MLYNEELLGNELRKLNAGKVTIPSLGVEKQPTGQVTSTDVSVASESKSEESATSYEELTE
SDTDEQEEGIVNGPVPAASSSTLFAGASISESAIAAQSAENSFSEDNAQPSGDETSWQTT
LNEAKESMQRDSDVQPQDLQSEKLTVFSDVEKSSESNDTEEPEEDGGTNDRSGGTTSPVA
ASLSMETAAASVNGEHQVQQSVEPSAENDDVRSTGTVTTGAEESLSLEAGERNSERTMGS
DSSLTPSRSDAEPTSAEDTDNISWTDGAEVSSEDGNGVPQTVDTAPGNTSTAPGDTKIPS
ESNATIPSDHDILLEKEHLGELAAMALIGDSTVHGCVSRVLLLLPLGLWGAAALC*
>TCRU_1630 hypothetical protein, conserved
MAYNHISMDDDGVASFTGGPWHQNGADTEMAPESGMATASIAGVPVIDPTMTPGEFIRRC
QQQYYFEFSWEVPFPRVPAAPLLYLPDAFKELLSDPSPLGVMQAELDAMSEGVLERIPLA
YYLLRPEVVEEARNIAMECEQRVEELQRQAAVDGLPERLTWRPEEVNPYLEQADAELLDT
DIDLNLVLERDKPSLTLLQRPLYTDMGLVPQEQRHLERLARIVPETLRSQSLFYSSQGPH
AMGESLDSSGGIGIPLYYGEEWTQAGFGNGQAAMEAQQKWLDGVRKSFRFARTLDTHHDK
LLELVAQTKLGLDCKNPAAMCLTRRLWQLLFEGTNKGQQRSVWHQLCRFSSNYDDRGEAE
EQLRRAVVDLQLPHSELWLALLREYVDLLKEYTLSLSGGTEKRKEQLQISGKELDPFEQG
AFEPDLQTGATLRRVGKELGADRQPVAIFPVEILPLYPAGFDKAAEEMRAGSPGHIEHLG
ELAKALHHVVLPGALVNEESRIRGPHALVNNTNLLVADKNSARQLSHGLTVSYHTSRENT
FEPLVSENNSTSSYLFQLCTVEGGSPSSLSNASRRHVVYNRLSVRNLFVKSPNAEIPPYE
RYVLMFGLEGERKRQREAHGDVKESPVSTRRVE*
>TCRU_1631 Ankyrin repeats (many copies)/Ankyrin repeats (3 copies),
putative
MADFPKLARIKLDDENMEKIHCAARKGQTEEVKRLVEQGIDPAIPNRFGCTALHLACKHG
QIETAKYLSSICDVHGAWHGQRPLHLAVLSNKEVLVEALVEGARERGRNVEIMLNECDDV
SVDDIGEHQKHTDGQTALHWCVALGDNYLPMLRLLIRLGASPTAKNKENVTSMMYAMEFK
NEAAMEEMVKGVKPQQLRLDYQDKEGRTHLHYAILHNRQDYAMRFIEMGHDPQMEDDNHE
TPLFLALRAAMPDLLTYLLQNVDSFSVQQAPFHNGSVMVAERIQWLEFATDEQARTECIR
LFQKRLDEVSFRPEETEKKRAKPTVKKMKLAPSAPLRSRSIGNASALRSRSIGGRISGK*
>TCRU_1632 60S ribosomal protein L4
MTARPSVSVYSASEDKVVGTCPLPAVFTAPIRHDIVQFVHTNMAKNSRQAYAVNRLSGMN
HSAESWGTGRAVARIPRIGGGGTSTSGAGAFGNMCRGGRMFAPTKIFRRWHRKINLHQKR
FAVVSALAASSVPALVMSRGHKIENVAEVPLVVEDAVQGYEKTKEAMAFLKAIGAVDDVN
RVNESREIRAGRGKMRNRRYVARRGPMLVMPDNKGTRAFRNIFGLDLANVNALNLLHLAP

GGHVGRFVIWTKGAFEKLDSIFGTFTKASMVKKGFMLPAPMLTNTDVTRIMQSEEVRRVL
KPKKLQPKKASRLTQPTNGFRNRRLRLRLNPFQKKESSILKGLRNRKNREVRHKSKAVRI
AKAKKSIAGGAKKK*
>TCRU_1633 hypothetical protein, conserved
MCSTEKRVVLGTRRATRATVPEWNRQPSPSWTPWLAELDRAIAAAPHAEGGQRRELRRRE
ALREASESRWHTLRSELEGTDGNRQQVVRPCLSPSFLEHASHEFRWPNAQQTPEGQPPHE
AVGDESNTAPKAPPSATDPDECDGPHPINMADPGRTIRLLLLGPAPGPDGINGEALRHLG
RVARCAVPWLFDIRLRAGAVPRNWQRGAVLLLPNPERTASNRDSPPTCNAEQLPQQAHGT
HPRRTHPGRHRLPVGSAVIWLFAGQFHPRPIAAPQGCHASQCFTTPHGGLLCGPRQCLWH
GGP*
>TCRU_1634 hypothetical protein
MWRASQRSQVWCWTSSEPSAAAPPREARKRTRAAVRGGGHCEGRAASFCPKRRAQRHDEA
VRFSGGVLRVADDGGTKTQSIATRLASGRGCSFASNTASSTLLPLVVHATILLACYFAGS
GVQRDVGQASNTMR*
>TCRU_1635 hypothetical protein, conserved
MQHNRALQRRHVRHVDEGVRHQTRRALAEAANPQLRAARKHAVAQRHVQRVSEHIHRAQV
HRHSDRSAEHHRVEARRRTPAANRHRFRQRHATHAALRSIATGPRRRHVERQARVAHTAG
TAAAHAVGERRSQRIKARQRSRTAVARHHAHGDQAGHAVVAAALQHPAAGTVALHRHDAA
RDRQPGDKRNAGGSATRNRHGTAAQRHPRQRCHRRRLAHRPHVVQLQPPTGTDRPTVAAH
QRRRNRPLDAHEAQHRIKHREALAKHNAAAAAHNRHVRHGEHRVAPQTENRRGRHMHRGS
GRTARRLQQHAVKHHRARQQFHTAANVHRRPARLQRPQHSVAHTQLRLQQRRRMQHKRRR
HRVRQPTQLRVAHRPRRHNRRVTDRHVRVCWQVVHKHKRAVVAGQPAHARLQAPVTRRLA
AVAPHVDLRTTVAHAVPQFDAQHAGEHCRHVEHHSHAVRDGHAVHQHRVHGVANRDGSVH
RTAPQSQHHRMHRGHPRSSCCQRQHNKQRHTHSWNGHA*
>TCRU_1636 hypothetical protein, conserved
MFYCTVCGALFGNPQQLMLHQQSHSVDMQLGGGMQPQYALGAMPNLPIGMYPMAPNLLQS
DSQLLYAGGLGGGLQRGSIDSTALTRRLAPPMIAGNNAGYIIPAKDMYMNEQLLQILMNL
RHPSTEVERLQAELSRFRQQEQEQEKQNQEKQQQQEQKQRQIPQTRLILDSVLNEEKDVD
FDSSTTSCSLLGPATYALRLDYIDGLDIQIPLEDISIGLDEYRLLSGLENHLLEAVRKRY
YASATIEKANSDRILLSLKDPLEFTLRHSHELHVLIITFTCRETTLFWASLRAHKEGMWI
TALRRSPVDVSTCLETTSSCLPETMLCGAIQADHSQDVFVRTAKQMSSTEQPRLILVEDG
KRLILTSKQKPNGELPADKATDESRHEDMPRAVLEDDGDVPKDMKLVKSLLWNLQFDSNG
TLILPRNFKTFSLSRSRLANLSQELKTEASVLLQIRPDGVLPHLEGFAGHGKYNNEVNLN
ISFVTGIPLNAVRSRVLVYLIENIDLETVEVVNKADNPAVLLRPPDEIQYSTVGEGVLFP
TFNVSMLGIFVAEKTHALVIIEYVTSTKSGPIVFGHASFPIHLGSRKGNFLSRIRLGDPR
RPEARDIHSVISLEAERNAMEQYSQDQKEDALNSQALYNSLFEPPGRYFNCCPCGYIMWS
LDSDPDSLYFDFPDEPKPVASEKDLYVIWQGMDPKNIPFSDDWETILKAFMGMASPMGNR
INYILPHNAKRGFYFDIESLHNMGTSHALYAVASDLGEGGPDEIVLTLHRDWSSDVSAPL
FKEPLRMLTGMKYDSYFTAILYLFKLSNLRSIKEHGEKEVKISSVGWSMIRLDLGEGILR
HGRYALPWFSGVPPPEMLEQLSSEPIEKVFPSFLCENKIEFMESKSTVVVSISDAADVGQ
IVGDHPGRPLPQKLFLSKGEKESFPSGVYEGAVGYTQQQMVTAMELNVKDVERAVNACLK
AYIRENLEE*
>TCRU_1637 hypothetical protein, conserved
MGSAVTCVSFGNRRRDTPPKASQDDNEEEDMWQQRFLMEVGKDSTSLTRDFPRIPVYVRT
ATRNNYYEPQREVQRVEKEQQQKTHVEMTGCSEDAAHHCLALRSDRVRTSIELLLELCGE
DTMAMLSAWQTEEERLGVADASSLLLAVLLMSGMLQLKKETEGSEQCENDAPGTSPTAPK
REMSTAETNTTVPNGSTEYGKADAVLLSASPQYIVQSKALRLMQYMVQSAVFFSIQWITG
VFRFPWCRHMHDIVWTAHVYSEKDRNREGMEEGDIELIIVQHKLTLRHYVEPKELRKKPR
FEVDWTCTICIDPRHLLHDTSNPPTMGENAEVRQITAEVLAARVEMPPKTACCVSRVWRK
RRDALKVRLWNRFQVELDLVPALHGRTAN*
>TCRU_1638 cytochrome b5-like Heme/Steroid binding domain containing protein, putative
MDAHNTHVSFADVPCVSGPSSPLQQQPQSPTPQESGADVSPFVNDGTFRIPVTSDIVGSI
PRVKVPRQKGCSMRDWSVCLEKQKQALKQRTLKHQREEESDERCLLAKNCGRRMLPRLSM

REVMTHATHDDLWIVIRGVVYDCNKFQYFHPGGEKILRRCAGRDCTALYEYFHPWVSCEG
MMAPFAVGVIEDEVHV*
>TCRU_1639 FYVE zinc finger, putative
MGEQLPTVGPSRQQPLPSQLSSQIPPLMFYDAESVLCAPVTPQQVISFNPREKGPPSRVM
PDGSEYYGDLLLDQPHGIGIMLFKSSSSFYANGDRYGGGWKNGLFHGDGIFVTSSFTYQG
SWFEGQMHGKGLMTYSRRITDLMLRGISVFSPFDKTHAPLEYRGDFHYRYHRHGHGIMRY
ANGDTYDGEWGSNCRHGRGRLITDDGEIYEGQWSKDERHGNGKITYVNGGEFKGSMMRDK
RHGEGVMMFPNGDEYYGTFYNDKIEGHGTMRYKNGDVYEGMWKDGLRNGEGKYSLRKKGA
TVEGRFVNGLIQGRGVVRHPGVSTFVGEFDRGERRHGTLFWHDSAPGEGACYQGEWLGET
MHNRGLLWYRNGDFYFGRFLKNKRHGPGNIRYADGGEYSGYFVNDMREGQGILQNSNGSI
QAGMWHNDVFIEGYDGEWDGVTFNGIGHLLLRKPPACVPAGGSNSATATSIGTSGGGSGG
DVSPTVATTSAAAFTGMQPTFEHFGLFLHGVRHGAGVLRIAGHVIMGIWKHDVLSCETGS
WEFPSGDLYLGGFKNGLREGPRGQMWFTDGSFFMGNWQLDAPLGNGSFYATDKREPIYAP
EETVADATSPAAAEEENTHSSNYSGVMNLFINLFRRKALPENKEKRRPIGFREHFVLQGE
WDIARLPYAIYQTLMSRLISSSSLIATGDGAGGGSEGGGNSGSNSGGAVAAGTLPSGNNN
GSGVNALFKPPAMIPVGVQEKSGFVFFKSGICLRTEWLHNHPRLMLPHRPDAPLYNKIRG
VIVTDDRNGGGTGGSKICSFCEKPFTFFRKETQCTFCEQHSCTSCLHPIEVRGRPKIEAL
LRLRMGQNSMNSDANNNNNAATGDTFVLPAQMPACVDCARVALLGLEFNVIWIPMHYLSV
SETTTSSNASTDEKETETVTATIASSEASDKAENSLLKFSYSMYSSSLCSNAPYVVYEGY
TCNCIPHIYGSLWWGKEGYYLGAFHEGRRHGRGVQMMANGEKYVGDFSNDEWHGMGIYCA
DDGSAYEGVWEHGKLTSLLYHGELDEQYRRHGRGQSYEADGSRYNGEWQHGQRHGTGILQ
MKDNVVYSGDFAFGRIEGEGKLLMETSVFYGSFHAGKKQGKGSEHFGDCVIEGEWYDDVL
TGFVRIYDVLTETVYETTYQNGNERDDCFVPPVMVDDAYCQNCAQCHATFSLFLRRHHCR
LCGEVVCDSCSQRRASMPLHFKATGTSRVCDRCYRRMEERRMLGIRRYANGEVYAGCWTC
GRWVSRGLFSRADGSVVVMDLAGCPLVNGQDKTSFANTESKLELPLDASPPVEELRKLPP
SSCTEVDAFTLWWSMMLSVAELSLPLELTPCRSFTLLRAPQMKPLRLFLEKDDARDDGND
DGGGTRGNDVRDAAVVRVARYIPSIAPPAPEPPVRLSDDSVLTSSPPPRPMITDSHIMRL
VTDGRMEMFPAVPPPSADGNGVVMLSCYQRGPLLPPTPPRPSPGRNDRIMWDSWQTRPVP
QYRGNPETKTQRGVADWQHVPFACPFLRPVVTDVDRAVRGGNATRWLPTPFVGPQVFTVK
DKSAGGVLVEQKGAPSSSTS*
>TCRU_1640 chaperone protein DNAj, putative
MQHTGDGISSRSPGLRLVNLLFSDYLASPAFGTDVLQTILSTSAGYFTRRRSDPLIHSMN
MIPHLILLRLVECLVLETLLKSGLSIFHDAGVFHVVFQYVQQYRFFHCWITRFLCTLGNI
FLPAGIRQLLDRRIAETVLIPATTSSDPLKAMPVEYRESLRYYRYMYDRSVPYAVFVSGF
VCEMTHCITEQLVWLAEFYRSRHKHTSRWRLLKPYISSLAGNTTQMLLVYSARVVGAWAG
RCVSREPTGRSVFWGESVALLALSPAIHRVTTFITMQLRNKLEMLCPATPEDEREDFHEE
EMREEEEEEPTAFRMQFNNPSPSGTAQVDFYEVLGVKDTASAEEIKRAYRKAALANHPDR
VGHDEAAQKTARERMTSINQAYETLSSESRRRRYDMARQMGTDLGVVKHFENLSTPVVLG
IGLIGILGFSLTASLLLCGQYFAAFHQLTGTGRNPLRYLGIA*
>TCRU_1641 WD domain, G-beta repeat, putative
MGSGGSTSLGGRITTVKEKRKSEPRKLKVTDYTNRPLTARFGRAVFASRMLAELPPPPTA
EDDGQYAWFVEDLDRPGEWESYTPDVSERLDAAWRSGQRECLILSKKKRICTVDLNAMVQ
MAAGSATRSRRVKRVEVEKCGDSTVREKRHFSPDPFLEEALDDAGRGEDMMANENGENGC
HAEEGVVGEADNTDASRLPCLLRSVAAHSTTPYTLAFSSDGRTLLTGTRGELLHWDLETA
IVLTAFDVKSSTVLSAAYSSDGSRVVCGGSSKIAWLFDTNSPDAQMTFAGHTSKIYGVDF
LAGGERLATISMDKTLRCWDVRTSICMQSDECHTAPIFTLATSKRCDWLALSGGDDHVVC
SHDFRVGSNSVTARFCGHRKTIWTCAFRGDENQFASSGMDKALNIWDLRQPSEPILKVFY
HMHPVHFVEYMPHNRGILTCARDWTVRLTDAVSGEPVWRVKAHVGHVFRARYHFGTRMLA
TGGGDGLVNIWRYDNADKW*
>TCRU_1642 Nucleoporin
MDAWRCSVCRKTKELSGKHLEGKTSVRSDCWPCAKKRVFVRESPAVSRSAAQVVTAPFLF
NPNLSTSLEKSTTAASRMPTTGVASNPFIASAAFTNKTPFASAPNTWKGTTASSKPVNAA
AEAFAAAGKQLETEAPARKNAFLPSEKAFPIVMHSAPATDRPRQSPPFAFTSSPTAVMPL
VNDNAKLGNVTSKNGHESSNKPVWRCSVCRKTKELSGKHLEGKKSVRSDCWPCAKKCVFV

LSHPESCVSSEPNLSTFFSTTMKLTTSPNNRTRDVISISHGASPMPSAKRLWQDPVVPSN
DQEANAFIMCHFSQQPSAKEQLDQTRRSVSLESSSPSVLLPSLAMTFEGEVLRGYRQQLV
DGIRTRTVWHDCTLYVLAPENSEGKGPNTAGASQLGAAAVVFLAAEHKLALSPFRRMRRI
FCPDEFTFAAACVYANTFLAGHPTSSQQSSFVVYGPQVDHTVPMTRWGSIIESCTHARQR
VVSEEQRVEGAQSIFRRSGWLTLPLHATAEAIRLLEVQRQQEHAEKNATECLGVDVVFVA
ETMRLEDLPQAAALALPVKPF*
>TCRU_1643 hypothetical protein, conserved
MRRGGGHRVAMSVSATAFPVTASSSFFFYRRCCISTDRCAATAPQDPGPKAFLLQLRRCF
ARGALGVREEAATNFMEESDAVRSHETISLRQILKCCEEVCDAERPLACSPEEWSEAVQL
LLYALARGKRESGDESVTTQDPSAENSTPWCVSLRLFLHTAPSGGESHAEKTPVHPPASC
VSLLRCCVRHGAPVNIVRAVYQTLRLSVPAASGSPVTGWHVPYARFLFMKAATEEMTVSF
SLHKEALRVLLLDAAEDGEMLQPAGLLLSLEVLRRLVTRRKNEEGGKLQENVGMNKVEDA
LWSRLQRGTDVVSVARDVCCCVFYNRHVSHAMKREAFCLFIAVGMRLPLEELRSFLCTVH
RDDVSAASGSEMTPQLFLETLQAVTEILSKGVGGGLASYGAVTRALAEPSNVMHSHSTAV
QRFVLVWLVDHIVKGLASFQRQVITVGSVKESSHCAMESWAECTHAALRCLQRLFLHLPD
RLHGAIKRRKHELYVARQQAFCLLFQAALDGAFYTFVADRASSASERSPFLDVMSVLIQA
YGEHDWRQPSVDVFIECLHAWHRHEVLRRVFCHVCRRDERRWRIGQKCDSTGDSAKDVTN
SSRRWRLSLRLSTCLVVVESSCLHDDPTTAALAVKQTLRSLLAVKFSEQPAQNVDNGEDV
KAHGVNVDSPAENRVLEGRSVAEWTQFIREDIIPRVNEVFCRTGTDTTQQWLGDLDAESY
HSPVVEATPGTTFIHE*
>TCRU_1644 prefoldin, putative
MERYAFAEDYKNARGIPRVEYISDMATFVKNNGGADALISRLILDSSKYEHTEKRLVSSM
ANLDHKIPTIKKTLHALNFLKKRLQEDQTPVRSYYCLTDAVFGEAEVVPQETVHLWMGAK
VMVEYTFDEALQLLEKNLANAETNLKATKEDLAWVQEQMTNLQINISRVYNYDLKNKRTN
GGAAEPSA*
>TCRU_1645 GTP-binding protein, putative
MPAFSGKQKKKQLQERRQRKKQYGEEHEDIQRGDVIHHNGNPHGHDDDRSSNRNEEKDYE
KVEYKYGADRKGIRSAFLKETAEEVAARKKRAYEPLKQRRFMDKNGIPFGSWFNMPGYTD
AALMPFAVEMPTRGWALDEATLENNNQCDDNICSKKNDEVLLENVSLESRELERFEVYLK
AVDNYPLPPALQTLQLSSYERNLDVWRQLWRTVEQSDVVLIVCDVRYPILHLPLSLLHYI
VRQCKKSPLVLLNKADLVPRHVLDKWLEFLPLYFKATGVVSADEAEEASTGIVCDIPLLP
FTSLPAEETAFGADGNGNPARRRKKKKRHAKLYEQLRTGKLQLPETPTRDEYGDDDEDAC
GTSSQDEEENNKSGRVKCDGEYTYADTDNFKGMYKAERELQCDKRGYNELRIVSDMISLL
LQKCRAMCANKTHVTCSTDGEEAFLRIGVVGHPNVGKSSLLNCIRGTKVVSVSATPGHTK
HLQMIPIPSEHVVLIDSPGLAFPVFGLPRSIQAVVGTHQIAQTRDPQSGVAFLAYHLQLE
RLYGLRKVDGADDTVEWSPYELCESYAKKKGYFVKHGKGALDVHRGAIEILQEAYDGRLV
LFFAPPDITWLESGQFRKEICPHLLMELHLPKTVGE*
>TCRU_1646 mitochondrial DNA ligase homolog, LIG k-beta
MVVARIGARTEMWRRCSCLGRAIVQSVDPSLLFGAGRPRTKQQAEKYKELKNTTIQAAFP
HLAACWVGPCWGTVMITPHHISPLCLKMAVWRCSECLQEFEMSIAKFVDQHGVCPLCKKP
QRSLETPNKEPETTNGSSTEGKNGDSNLGSATAMTMTTTTKNELVYAKAPRMIHTNYRSV
LHDNPEWEEINIQPMLAQKWETVAAELLNPGPGEEKELLLASPKIDGIRCLIGYNRRRKE
PKFFSRGGILLECCHGLVPHVMPLFEADPTLVLDGELFAPQCNFEELNGLVRRLEKFTTP
EMRERQAQLLEYFSFDIMHSSQLSSPTAPFSERYRLLKKMVPTCGAKRISAYQHDEEKRK
IIRQKQRPDNAAAEGTIKLYHVPAAQVGAEEMDEVLEEACSQGFEGVMIRRPGFPYEHGK
RSFGLLKYKTMHDAEYRIVDFLPGQGKFRGGLGAFICETKTGIRFNATPKTTYENRLALW
GKRQELLGKYLTVQYQELSSQDVPRFPVAKAVRGASEEEFL*
>TCRU_1647 hypothetical protein, conserved
MAAVAAGGVWQKALAQLQARSWNVGRAPTARCWLDFFRFCATPFSTSTGQNRPSILTSSL
PTPVRLLIAESIIDVVRLARLQQLFSTSPGGMFCDLQDDGRHGSREETAASFWAGGVPED
VNGVFLTTDASPSMPSSEMVEVLSHWCAAHEAPHDVAQLLGWLREAVGFLRFFTPQSISH
LEGGAPQQQQQRRLYLTYSELLRVLHHGLFTFSLRPQANGVEDVSADVSVHEEVALLAIW
LLQKLRNGDAEDGLVDSSNPPSSVHVDRNSNNNNNKKKALNKMENMLQETQMLLASRGAT
QAWLLHLPGVLRDCSENTNGPSSGAVNDTARRIIKMQRRSPVCGIASELLLFTSSSTSSP

NVCVPFVDRFALESEAAVYAMHAQLSSIAFAGKA*
>TCRU_1648 hypothetical protein, conserved
MRGCGVLCAGHKRAAVIATTTCSLGPPTLSPSLTLRPVACAATPVTIPIFPPPMRGSFID
RNPVWASFNEKHTAKSFRHRIVSSADVSLRPPQFYLSNEKSSAGEAAVVQKRAEATDSYG
EQLDEISARWAAKFYGRVTFGPRNYPYPSSRWLARRFKMKKHRIIKRFRFRRYKLAAVAN
LPFAKMIRVGLLPELKSSKTKKGDDVEADLSGRLVSAVRSSGGKKKGNRGRPKSKYQI*
>TCRU_1649 hypothetical protein, conserved
MARYMFWRRRGAMQGVVEGHFWSLTRYRIGRRFLGLDYADNVILFPAYRKKTWGGWAAVT
LGATNASYLTSDTSSANVLEDGYPLHWRASTKLQAFIAEERNDWNKRKEEVIARRAAAIV
EEGEAASSSPSGTSRNNGAANNAGEKGAHEYDEQHFRDAITIKCTSPGFSQRHLRLRPLT
TILYKAMYFYIWGIAISVIVQAYLLFRGWLNPPAREGLKNIENHVLHIPKLIFSLCVSGF
AWLLQKTQPLVDPLLHVLEEKFPRVNWSVASPKVIATKAHQLAGNEEAAQQLAAMEAERV
AAGRAARQQADAGRRTWWKRAFFALFCLFSVLCII*
>TCRU_1650 hypothetical protein, conserved
MTERSLMIRHAVTGRYFAVGMDFPSARVFDVATGSLAAVVEVPPRSRTSLAVLSLTALAL
GEINEPHAAEEQRKAMDVVGMSGACHAAVGLSNGTVLLHNVPKDELLQHLAVSDTQQAIT
AAAFCGRHLFCVAGNRSLCVVDCLRGERVGSQLRVQQDAGAIAVMRCREDDAANGAPDVG
CKFLIFVSGPTNAVYTLCLGSEGAQNTVATMERLVSFASQASRSDFAWMSGTTQHPIVVT
ASAQEGVVRVWDAYPSVSGQTTSSRCRRSLLCGQRIMGISVYDPTTMNSSANGYRNGVGG
SETFVAATNFTGAVLVWNLGSALLTPVADPVPTPPTLRIVSKEISARLLFGAFIQGAAGE
YPSLLVLRGRFAVPHFESVDLREAAQRASMVSSMTPATSSLAEEGAVYELPTGPNSERAG
KIDAVHADMEVLDHAWATHCLQQQRQQRLAARAIYTPSEGFVPPVSFHAASVKDIPQNKL
TLEQRLKKLSLSSAAPSQQQQQQEHSHALGLATVPLYQALHASDASAVMELLTVASRSAE
DIRATVMGLQLPYCLELMQIIAQRVRGATSRSPLFVWIDAIVHYRGVEMYQAQQLFKEQQ
HQEEKKKKSASSSIYSNGVDDPLLPTSTTAASSKANPSPPKEFVAPLLHQYRNMTALYDP
LAAMYGRLSIFKSVRPSEKGVFVNSDAGIIFPTMFTEIRCAGGEYRTMRVRSKRDPHARK
NKKRSAVALLRKARRLAAAEEAGAAAEAKGTSEDNVEEDYDDEIDMDALDQMRLGDDTDG
EEEEEEGESDADKGPGKRARGEQTEMIAEAERGSSYGIESSTRSSEVEFDTASDDDVHSA
AAENDDDEEDDDEESSSSISSGVATADMFDDEEYEDDDDDDGDDNDGMGDDMAELLEVQG
EDKEREGRRHKRVRTEH*
>TCRU_1651 Cupin-like domain containing protein, putative
MTDVVEAPRPATVAEAFANTAKALEQFNIERIRVEGLSCKSSITHCRKHDKNNMEKEEDV
RTLTEQAFMREFVFQSRPCVIVGALEDWPAMQRWRDDRYLFDLDGHLSRVRRETDDAAAP
SSEGTAATGDVAVVPKNNDHDSSDDSTHPREREEEKDGLKRVTVALTPNGRADAVTYVTY
QGAREEGRENDVDGEKDNVEEHFIKTEKLFMAAAEIRATLPELYHLLRENPLYPPVRPVF
VDLRRPAPVVAYAQMQNNCLEVEYQHLHGDIPPELDRFGERVFGEPHEAANVWFGTPASV
SSMHQDWVENLYAVVRGVKEFILLPPWEGVFVPKPELPSAAFSVQRQDGVNGYVFSGTPV
HDGLTIPWMDVEFTPAALEDVSLMPTNMQERLHPLVVYVQPGEVLYLPAMWLHRVAQHAD
DTDRLAREKQLTSSLQSAQDPPLPLIAAVNYWYDMSFTNPAVVMLREFGLLL*
>TCRU_1652 hypothetical protein, conserved
MMEFDLLDDAEEILQPLCLCLNQDSSRVGVGHHKGYVIYRIHRRPAPAGTEEASSSSAAA
SSTGPPFYTTIEAVFPPRRGTQCSTPSTWDVHEGAPSPHAAASSTVGTSRVRRMSGDHRD
EVDHDTLLDALAHSPLLQRMGKPLESREKEENQVTLEGTSVNSNPVGTSATTLASTLLGK
NFLRWTEEKRDAPLPTETGVGAMALLYKTQFVAVVGGGPYPVGPKNVVKIFLTGDMWADR
EICVPDPVEELRLDHRLVIILTTREMRLHSFETELCIFSVPLWADTVPTSRPSTSTSPLF
SASVSLNSTRLQQLNLGASVTTASTSTSAASATRFVAPLAIDYSKKCIAFRNAMVGFSLV
RYDAEASLCNRVNAELLSTVSVAHEHALSSLAMDLNGDIRSSGSNTAYGSMRWHIATCSE
RGTIIRVWRYYERRGESPITVDTTASSAPHSSDVAVKSTIAEEDSSRTLPGYFVRVREVR
NASLPTPIFQMRFLGEAFLFCIAWNTLKIFFVGEQEQPKPYDISTKDPSKTVITQNSYSS
LHHLSVVSAYFNSEWAACECPFPLTDDVFLPKWVNTTSGELRQHLLRGMGSSSRMTVSGN
GVEGETSRVSADPEIPEPVSLLNDIQVSQSRSQSSLVGTVTARSKSQDFGGILRRYVLQM
APMVESAGRVARNYWGFGGESTEAARSGVNEVTNDYSQKRDYTTMTEVAQSVVVWWEQPT
YWQVEYMTKSLSRLSTNTTTTTTNITTTGEVFPNRTKCPRPTVLYCVTCDGSAISFEFDP
VKGKIECSKATAVSSLED*

>TCRU_1653 hypothetical protein, conserved
MTPRTTSDDRSLKRPAPLWDRMALAAGRTACLSLSMRLDPPRCLSPPRSVGLPVGLTAQL
LAGLRGPAERSVFSRSTAAEIYPFPRLAASNRPHEFLSSDTLSAIEALRLGPPAVRGDTT
EEIGAMPPSLADRGRTAGSVFSHDAAESHAT*
>TCRU_1654 hypothetical protein, conserved
MAMLTGRVLLVCALCVLWCGAGGVYTEDDAGVTSPGASASDGKSFQEPPPIVHGGSHNSV
LTASDVNEQTHETDKEVLLTKEVAGSDEVTQTSGEEIPPPSPSPKKSKGGGGPPQEDDLN
LEKVDENVMQPEKQRRVEEGLETLGDGEAGVTKQNEGIGVQPQDHETPVQEEDTINGEGH
QQTHGKDQQTNVEDIPPRKSAGDYSSGEHKGNDGSNEKEEKEGEEGVEGRERHRAQEREE
AAHVSGAPKVNSTDIQQEVQRTHAGETPTGIKQKAGEEKDDETEEEREEQKKQNQENPPG
KEQETITGANATNQLNTMPGDNDGSTAASHTTSPLFLLLLVVACAAAAVVAA*
>TCRU_1655 hypothetical protein, conserved
MHPVPLVAAMGVRCDVDGGASACVLRRAFLLHVFALLCVGKVVGEDMCGSERGWLPASPR
ALGASIHVALLDGVSRHPGCGEEEDGEDLLWAEGGWTGQSPSVSFPVLLAVHTESVNLGE
CGMKGLCRFVRATQSSSLQAVVTVRCGAVPFDEGRTRCHGCCAPRPFIVSAPGFFFLRSH
NILFCFTMNLLWEL*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MEAACFAARTSSISGCECVCAAGGYGDTCLPAAVPDCLGPLPPPDAKDTEVRCVHGGSID
SVDYPDPGVRGLCLVNVTFTAAIVLDLSYFDAPQQTLNITLLKCVLMGLSIKGSGARVHV
NIVSSMLDSGELEFRGVFGVSSQILVAGSTLVTTSGHAILFVKFALSANMTLLLLDNYIE
GNRYAVYLSGGVVVDGGGIIVKGNTLSTTKGDDGVESSVCVTSVDVKNGGYFDVENNTMS
SVNGVILFGDTTVRSAGLLRVADCTFVGGTEIFDSALVYLTGSVTLEGGAQWRVEGNNVS
AASVLSIPYSWQKLQLSGSGTTVVLANNRQVEGSALFARLFKSNTIVALPARFVVGCNLK
GNEELLYDGLFPEEVVLFRCGTCNDDSACYMPGTESVDRGSCSCSCKDGWHGASCLPFEV
PDAVVPPAAERAVDGDTSCVVNETLTNLTLKMWKTHHCYAGVTFSGVGAVLTFFLNSMPL
HLPVNITLTGCTFLEGAALQFFGGAEAAESSGVLIRVSRTVLRSSVVAFLLALPQRCDIA
VTEVDAVQTFAIELPGTVNNMWSVLLLDDFVLSASTLLVSNVKAHATKRDALGLYSIGAL
KLVGGSSLYVRYCSFEGYTHVFYLHSLSVSDHSVFALLNNTMLFGASLLYQHQGFSVSDH
SVLRVVGNSGSVRYAIYNDDLWTVQRSSWLDWRDNKVEVGAMFYDTESAFVSIDGSSAVT
LTGCRMGSTGLSVSLLKRVGAGYRFVAGCLTVAGRVVTTAAELELNGITNVTTVAACGQC
TKEGDCFAPLTTAVIGCMCQCAAGGHGDVCVPAPVPAGSPPITPPPVPPTPLPPPVGECI
SDMVYPEVAQAVGGGLSWLCYRNVTFSGGGMSLTVLIGGMKGDVANVTFDGCTWRDGAVL
LLLGNTYAAVGSLNILVAGNTFSDALLSPEGVFPPHTSITISGNRFTVTRLVPRSGLKLD
CSSCVAMNGLVISNNSAVVLSGNVFQSVTASSSAIYAFGSSLRVSWHSVFAVVGNTFHMA
GGDSTLINLEGSSQSLSLSVLNNSAVVIRGNVVSRPVSYFLLLILALRVESRSAVVFQGN
DMQGSSVVFYPSYSSRIYYNSWLQLSGNLCHASPSEAFAFLSPTVNLRDSTVSLSGNRFM
SSRVTPTVLRISTGSRDNTNGAIVAACNTGSGGEGATYVIPSVYNATVLTCSDPCTLAAS
CFPAYTTTASSDVCACTCAEGGHGDACLPVAVPEPPSTDGADLCVCDVRVDEVVNAGLGT
SVVCYVGVTFAADVVVDMASMSGSVRKVTLANCTFVGGASLYVVGWLSDPPAGERADVLI
SGLESRSGGGVLVANRYPPGSRVTVVDSVLIAEKRVAYRDAYGLGDASACLVVHSVNLTG
SVLTIARTHVAAVFRGAVGVLFVGGVALSSRGALYVDGLSVQTALGLCVSVEGGVSASGG
SVVAFVDSDFLLCKHAVSVRGAVSVSGSAVAFVRSEFVSTEDYAVAFYSTVSLAGGSMLL
AKSNVHDGVSREMLYTAGTVTAAGSTLSFVRNRALLPRMLSLSLSLTAGAHLRVACNDAG
GRVLSTAEEYAAAGFGDAGSIDVVGCDACDRNTHCYAPGTASASMTNGLCVCECGSGGYG
EACVPVGAPALPPAVGTAPSVFVREGVTVRSVFVVPAGASEVTLRRVVLDGVSPVLYVPW
MARDGVRIVVQNVSLLNGAVLYVMGGGALRGARAAGSDESGPVELSMCDVEALNSALVLT
GTFPAGSVLTVTDSLLVAARSTPLVYLPGSRSSPYAPVLVLSGLRLLRSVLVVSGVALVT
VMTGGRTVVVDGAVLEVVGGGVALDAAVLGGDVALYASARVVASGGAVLRVSGSQVYAAH
GLVFDSGVVANASAVVVNENAGVLTDGALLELRGPASFGSGSWLSVRGNNISGKILSLPS
YPRSADLVQSTLTLYGNAGSGPVVMDGTVALVGAGRRFFVGCLTLNGQALRPMDYRSAGI
IGEFRPAACGVCDADVNCFAAATRAMSASCGCRCAEGGYGRDCLPVYLPHVDGCNRTPAM
PPLSHTATLMATRSLTPTWTPSLSATRYSPTQYSQTETLQVTETVALLPTRTPTASVSST
LWWSDVACPTLAVKTTADGGSLTQNDVRGGGSAVAIRLMVALPPPFRWARDPQLGTHLSF

VSVSTAQPRGFGGPWGAMLRNATWVRNATNPSTVLELAVPVHRGYFIGADETIVIRCDAA
AVSGGCKGVLLGSFTISSDTLPAAASALSAITGVVAGAAAVAVVVTGGLGSILEMQALGV
FARMPCASAQERASTVALPYFLSVFAALDPLWMVVGNALLAAVFGCVHCGVTAAFQRWRG
VDAASAWAAMRFPSLTYVVAHAMHLGIFFGSVLALAMPGARVQHRVIGVVGVLYGAAFPA
GVCYLIARHTGASFERYWQFSRKPLHERLLYPVGYWHPAAQQRMYGGMLTNMRDSHVYWC
VFQLSVLCVVCLIAAVQSPVGGCHVQYFCMAAVLLAGAGVVAFTNMMRSAFMTVTRTASF
VLLAALCLVSAANHLAPSDGGAGAYVAIVLLLTAVPLAVTVYSFVVWYAEDRHWQELREP
RRGGLETLLRDEESDEETPKPQEMTSSLYATGTTVASSYRPPAPPSQPMAGDTHSNAQSP
LDRASSASRMVDYAAM*
>TCRU_1657 hypothetical protein, conserved
MESTRPVAYRRVVVSGSNDPVEYFVRAKDDGRTVVPTQTETRTGWLMCPVRLRSQLRHWM
RAEQAALRCLLALRPSRWLIVKGIQEHSFSEGVPVVWSAHCSVRSIGLFLW*
>TCRU_1658 hypothetical protein, conserved
MVSVRLTAQLQRVKKVLATWKKADERVSQLCTSESVGRDTLPGTACSADIKITDGLVGFF
SGNFSDKTWRDEYLGVDATVKKEVAAALR*
>TCRU_1659 hypothetical protein, conserved
MGTTTASPLEKVPRSVGCGVARRFACSPTDRTAQSSFHCGHSVGITRRGGVRRSRSLDED
GLVVFWQLIPSCPSPLRIALAARLAQHRPGMVLMQECPSDEAHWLQ*
>TCRU_1660 hypothetical protein, conserved
MYVVNLCSLTLAISHVAHFASTILRLCPAAVICDLNSHHELRDGRSPSTTAGEDLAATSS
GMDSELSDDPAQATRISGRGVSFPDVTAQRVLRVSHWKSTRLHGPGPPSGIADCGDGGRH
PATGRHAATTETCCLFPA*
>TCRU_1661 hypothetical protein, conserved
MPSVAAAACSVYTASPGGSLLRAEVLCKREDRNHALRRGFSKLLEVRAKQLGALSSPGLR
CLEAWRHHVPVHWDRLCCGTVGTATSLRLGSRHTARPSHCPSRTCYDPHCFLHTLCLRAS
GDWDMDWPFTPCALDSPSATLCMAWHLVPTKY*
>TCRU_1662 chaperone protein DNAj, putative
MGSDVFELRGNRALYDVLGVPRTASDVEIRRAYYKLAVVYHPDKNPDGVEVFKEISFANS
ILSDPARRRLYDSERLRTHIEGQARAYDPMMDPNVELTAEELRQFVERKRLEEEGKKKER
SEFEKQREEEMRRRAEYDAKNPAFKQEYERMRALVKEGVAQRVSTVSVPRHSTTAELMQR
LENKLREEGERRQENSCGAQESKGGVRCTASTSVKRSMMQDFRLRHNGETPAPGTISMNA
NRQATSSRLKFVSDLANNSYSCDLEERLCKFANFDYRSYVENGIVDGGSVLEDAILADAL
GNYDRRR*
>TCRU_1663 50S ribosome-binding GTPase, putative
MRLFYRPLLDKTFRHLSCRPVARVLAQRLLNSPVNAPVMSQREALVARLSDEVFSKGNVH
LKNVNTLSALPEGLHSFPEVCFIGKPNVGKSSIISCLLHNRRLGRSGSTRGTTRILQFFN
VGDAMLLVDTPGYGGWMGRQLSQNLAERASAFAILFRYLALRKQGPLKRVYWVMEARKPI
QPRDEEIFAFLREQQINFSVILNKIDRFKGDKVALQKQVNDVWDFLGSNQVPVLGIRANP
KYPERCLNIRALQHDITYYCTQELVRAEDLTYKGIRELSYAPPSLEELTAVEQRYPVESF
ILPQEDNLSLERFVLMHEEAKAKWLATSPKAALLSAKEKVANHLVESSDKRYKDGGSSNE
KNKNHNTVALPTSCLAVEEGSGPQNVFNSTTAKESTSSSFFEQAETPRRFCVRASLRSTR
QHQPEEDVFWTKRDASTPEAYAKSVSSRVAHESPPSVFPNKKPPLPFSAPLLPQLPTSLD
KETHTVRAINGVPIEKSMITTSVAQLPLHQEGSFEHFAQHSTSGDYDRLLSAELAGQHTF
LEEGEHASLSEGETLSLQRSLRKSARRKQLDRILEKYVSRVRKQRSLYMQAEGYMCPWLA
GAGQPSRVAVVGFAHGYSFMGGGGTLMKGLKRTGFGGKSFSAHTMKNRGRATKKTGYWAT
*
>TCRU_1664 hypothetical protein
MQVTVLQNHLKDASEETQSLPLSTFVKLYNYYDIAVREKILNTLCQYRSSFNVELQQRAM
EYVGLIELGNDELLKVLEPLPSFKEDDFSLVLPGRAQREEANVAVSLNISRDKREKLVAP
RADKGPDKLNSSDLLVINRDVPLNSGGESDVDLEALFTVNSTMQLDRMAKENELLRRRFI
FLLEEPSGVLYSDEFVELHCEQQYRGADARVTVTVRKKMAVGLEKVHVETTGVDVGLLLQ
SRNERGDIASSGVLRVEFVARSWPPFREAPTVRLSYKRPGECTTETKILALPIVTTRSLS
PYDEKDEMAYDTLCKQMNSASVRTRRLSAGCVTHNGAIEEALKGIGFCVIHPVDSAEWKA
MAAHAMQSHGILSYEPAVVKVFSHSPGAFTAQVITKSHVLSVAISDVLGQTLLSKGQTEC

QERFSVFGGNLTPLLS*
>TCRU_1665 Adaptin N terminal region containing protein, putative
MSMRLLRGFPVPTDSLLKEKILLVLRRIVQATDRVLRDAQTQQKQKGTMNRVSAMNAVFS
EVVLLVLQWDLDTRLHNECLDVLSWFVMEKKDSNLRYLGFSLLSQLCSARSSYNDYRTYC
RQYQPQVVVALHDPDVSIRTKALDVTVCICDAETSREGIGALLSYLPIADGLFKENLVIA
ISHLAEV*
>TCRU_1666 Adaptin N terminal region containing protein, putative
MDMRGLAHFIQDVRKATSSPADEKKRVDVELVKIRSKFRSTAEMTTYDRRKYVCKLMFIA
MLGYPVEFGHMEGVKLLALKSPAEKLIGYLSATVFLHENHSLLTLATHMIYKDLLSEQEF
NINLALTAIANAGGKEFAEVMSSRVKSILLSDRWNVHVRKKAVLTYLRIYRKYPDVVDLG
DVIPVVTDLLLSPLLGMSGCVAVFLTGCLNKSNFHLFHFRTQSSH*
>TCRU_1667 hypothetical protein, conserved
MQEELPECFRVVSQQRTCGDEAVGTALEDIHRFVFEKSQRNMETLSPELLSSCDLAVKKV
GGQLGKRNPLGIAHLPMGVAIVEMIARLTRILFWGITACSEMSLPRKLKMIEEDGEELEE
VLLPRFFLKLSVSPIILRDVLMKAPWDVFSRLYGTESALPGEVRECVPVEVRFVLSSLKV
NFGCEFLFHICFPVDLAGSHREAVTTAAEAIDSHMATAFNLGGGLSVAVEADCDNKNIGD
NTNHHLFCDKRCTRSSLLGRSTSRSESWDFKTGRKPLFSSGERSQFTQFIHSRHCLPAYK
LTRRRSGILPGPGAGIECADDLINGAGHYSPATVESHVSSEEHDGETEVLAPETPVKKRV
RAEKGVVPPSPLRPTRE*
>TCRU_1668 hypothetical protein, conserved
MGIGVAPSTRLQYARMLRSMFEMNRTPLDMMILGLQKVAARSETKQARPLTEEEMNQVIR
SRTDWRERVVLRLAWITASRWSEIVALTPNNFTLEPDGTLILDWSVAPKMARADPHRPSR
FVRIREAGRFRHYKAMQDTSRKRKAHEYY*
>TCRU_1669 hypothetical protein, conserved
MPSAGFSADRTYAKVACIPRESKNSYIRCSSHVMACDFELPLFAAPCSEVLCAPTSMVDG
KMAEKADKAKRTARLGLHDKKRLPLPFPSGNFNVAGVWNDNGSPSMERRIRDDGGRCLFR
GIDDSPTIVLDGVSQSLAQANR*
>TCRU_1670 hypothetical protein, conserved
MVMRRVFSVVLVLALLCCCSCVFAAKEEEQEQEVTQVNAECAGDGNVARWQLPGKSLWYN
CTDLSTVVAQMICGMGVGNCAPEASQSRTKGVAKDGVFKINVTSPTPNILESWWKRKVEP
KAATIESGPTTRPEAEPLGPQEHKAPGYTSTTNSDSPPAVAAGASGDPPPPLPQTATPGG
AVANPAAGATATTDPSAAALGASDPAPSGDPQGPANSASAASPAPESPPDPKPTEGGDHS
SHEPPVELREETAAAPPTQLSQTGEDEGAAKGAEEDTAANTTDTASSEGNATAAGMPAPL
SSAPTTNALENSVGTDACFHGTHLHALPPLVLAALTYGTLD*
>TCRU_1671 cyclophilin-like protein, putative
MQGGLRLVRVAHITVLARVRMGAISINHQQSLFSGSSVFYCASASGGHVSDNTLTTRDEK
GNSLIRVKRLPLTLIEEVPLPQRVLTDLELVMMAWCEEHARQYAMIMMAIRVAIFFLLLI
ILYVFYRTQLSSERMIRGVAHMPADLRIGSVVYFDIAENGADIGRVVIGLLNEKCPLYCE
YFHRRCTGSGDTGDSFRGMQLAAIVPRHCLIFGDGREMTHDVTGFNPHYLPTEHLGTGSW
RGALSSIAYGVNKESPNFAIHVSAGDYAPQIFALVIGGFDVVERINAGGSKHGNAPKKGF
TIVECGELCTLAKSHIVPMPWKLYESISKGYDEEKFGERIPRDFLERSDEHSTARVLNST
TGQEKIGKTVPWWRFLW*
>TCRU_1672 RNA re-capping enzyme, cytoplasmic
MLEFEGSSLFRHHIVCSLLTNKPVRVSGIHDEDEPQGIIATEANFLKFIDRVTGGSKFEC
TDNNTTLTFYPGMILGGNFSHEVPSCRCVSYIAEVAVLLLPFAKLDTKLTLVGSTQGEMD
LSVDTLRTVTTRWLQLFGVECSVRIIRRGAHPGGGGAIELQCKALRKLTSVDATTRGRVR
RIRGISFGSRVAADLAHRAATAAKGVLLNLLPDVYVVTDLDNSKTHHGEPSSGYGVLLVA
ETTSKYCVISQETTAAPREPPEAVGKRAAELLLDQVFEGGCVDAHHQMLVLILMALSPDE
VSTVRFGQLTGSAVSAVMLLEAYFGVSCATKGELSMTGENAPSSTLITCVGSNTVNVWKK
SG*
>TCRU_1673 leucine-rich repeat protein (LRRP), putative
MDLSLSHKGLQSFDASTLLLEAPEISLQGKSVPLGERYIAVRTLDLSHNSITRFAGGQAL
SGLAVLDLSNNFLDTLDASSLPGGLIRLRLAHNKLQSLQGLSAFVPKLQELNVGFNRITS
RRISDLPKGLAKLLCRSNLIDSVRPFLGLAHLSSLDLSLNQIFDTNELSRFGELRALRYL

ELRGNPVMSAPEAVPSLLAAVPKLISLDRTPLSQAGENRMFKVNRSRSAKRDQSNSRQRT
SSRLLSNGSGSRRHYGKGETDMELRLLETRVKELARLLKDAEKTELQLRYQKKILKEQVS
ACAGVIDSQAMELERVGRRIKDLKCEEASLREPVAELDQTFEQTHASLVAHRLNQSAGCF
*
>TCRU_1674 tryparedoxin peroxidase
MSCGDAKLNHPAPDFNETALMPNGTFKKVALSSYKGKWLVLFFYPMDFTFVCPTEICQFS
DRVKEFSDIGCEVLACSMDSEYSHLAWTSIERKRGGLGQMNIPILADKTKCIMKSYGVLK
EEDGVAYRGLFIIDPKQNLRQITVNDLPVGRDVDEALRLVKAFQFVEEHGEVCPANWKPG
DKTMKPDPEKSKEFFGAVA*
>TCRU_1675 hypothetical protein, conserved
MALVPYTPSEWCDIGARLWDMVCQCGEIQVQMTFINGNQMSDETLTVAASSTGLCLFHGP
ISKAWQDSTLIGHIADLRAPQIPNFETQALLPAMGAARELGHQQGLITAERERLNIDYAN
AVADVQNRNARLNSQFQEAHHNLSVRESTIAGADNLVLELQQQLEAAHAQLREREFNLGV
LTAQLQEREACHNAQQPVRDAETAVRDESPATRHVANDGVTTLPHQTDILMAGGVPSSAA
RRSSAAYRRPHGNVGRPHFHPSTPLPSRTSPLDAQLPMEEDRSFCAFDVTT*
>TCRU_1676 Protein of unknown function (DUF3720), putative
MGLINAVEAADEGGLGGDAGSSQDKSKESLQDKKLSGNTEGDAALGSGGVVVADPPPPAA
AAPLQKPGGRNTGEEGKQEELDKKGNEAEGKSRGEPGPPKPKPEQSSSSASGGPGTQSDV
ELALEVTSEGNKFSDDALKQENAGKTEVTKLSDGEPEKGKSNMALTETRGSQAEQKEIRL
PTLPTTQVDEHYSSGDTVAKQQLQKTQSGMDPKNNSQTKSAVTITASQHNEPSADHAGST
TPSPAASGDAANNETDKTTEDGIPKNDSAADGEEKREEKRNENMNANPRETPVEASAMKP
TKATTDDSDGSTAASHTTSPLLLLLVACAAAVVAARE*
>TCRU_1677 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MVPNASKKRPSFANGPRILVASNASGIVSVTCGGREHVAADNTDEVNERSATGHKTLVLE
NTVAGSGFVAEGDAYGLAQCNASGHDNRPLLQKLIAQYSGSGGSPHDCFALRNFAKLTLR
ELTVDGTVRVRVYWVLLLLLGLCGVVAVL*
>TCRU_1678 retrotransposon hot spot protein, RHS3, putative
MAGALENSICRSICGVFSISFTKFIQDEVLLDTIKASPPYQELKKEREEYYVLLGASHKL
KKEHIVTLRHWSNFKRKDTVTPLARAQINKAYSQILREERREAEEKARRERQELLFTIHT
RTDDAVLEGRVRVNKMRLNDFLTMELDGRGALDANRDVLLEEVFKDPKKYIRDAGVLNEM
QASDRYKRMERAVRDEMDMAEDADKLYNKGMYDLLRSLAQPATSTWCQGLVLFTREEAKR
LLFMLQTR*
>TCRU_1679 hypothetical protein
MSDTDGPREPSESVAFVVELEQDMGRTEIEIVEKEERKNIMCRYKDAVSLLTSAQKCIHA
LTCCGCPNNSFWNTNSGGRAALRERWGRRSNMRPYAMDATDMQQRKEGSMAFSLSVPPLV
WPWNPLRAIALQKSATQSENGFSHIARTPAAEARKCQGGLCSAASERLTCGSLSVSLRGD
KQLHEDGKKRRWNSSSNLCSKAGASRSVSLAPNDLVRLQKKTVSHPLVRSQHSVGSQCFP
SRREYHSLNTQTDFSIRLPKALIDDRFRRLNILQDLLRMELEREAIEDWQVLRDEFIRLG
CKPMEVKQLGRNLRCEAGDLEGRAGATVEISNWEREKRRQERRFWALELHNQQVDTVGSS
STVR*
>TCRU_1680 Protein C21orf2 homolog, putative
MKPQSVTLREQTVLERTKAESLSAVRNLNLWGEGFTDVTIVERIPGIEVLALAANQLTTL
RPFASCTSLRELYLRKNDIKSLAEVKYIKDLPNLRTLWLMDNPCAKSSHYRSFVLRCCPN
LKQLDNIEVTETEREEAKKKLSEEDVKHILEHGTVAEADLSNKRQQPNSSAVSKAVEKGS
LASVGGQPSQYGRTKEKEKEPRQGGNWANDAPRESSCTPTSNGVPYTTVKTQQAIITAIV
SLIPELTLGSLGVLQKEIKDEVVRKEKAVRNRSNCPQ*
>TCRU_1681 mitogen-activated protein kinase 2, putative
MSSEIEPHILRKYEIQAQLGQGAYGIVWRASDRRTHQVVALKKIYDAFQNATDAQRTFRE
IMFLQALSHPNIIKLLHVHRATNDKDIYLVFEYMETDLHVVIRANILEDIHKQFIIYQLL
KTLKYLHSAELLHRDMKPSNLLVNSDCSMKVADFGLARSILSLEKEQVARPALTDYIMTR
WYRPPEILLGSTRYTKGVDMWAVGCILAELLLGRPIFPGRTTIKQLELIINVLGEPTPED
IASTNSQFAEAMMKDIRRTHTATFAELLPKASPDALDLVQKLMRFNPNERLTAEQALEHP
YVAAFHKVQDEPSAPAPVTISLPDDTRFTMQEYRERLYQEIANARRRVRREAAAALSSKN

ESGGVVTRAHPPPSAAAPVAEERREKVRDAAVTHTSSSTAARPNSSTATRTALANGASRT
TLASRTSDATRPAHHTRPVVSRHGLNGSRTMQK*
>TCRU_1682 zinc finger protein family member, putative
MMRTSPRSIQQPMYRGGQGGFQQQHQNYHQYQHIPGRRNSNLSPVSGGRGGNMGAPLHFD
RHHTIRLVCPRSNTVVCTRLNRVLPTLAKAQSGAAVCEDFMYAQSCPYGESCTKVHVPKE
HTWTYITPDINRSTGLFEPGFIVHCYGPRMTQYYPIQSEFVLNTRGSREYVKMYNEHGDN
FKAKFKLCESMLTRGECSLGEACDDIHAIRNDVWNMESNTTHIAEPELLANYPRLPANIT
VRAFEQNSKDSFVDYPGDQVLLTLGSRQYLTAFEAEGTIPKKKMQHCAHFRTNHLCRRGE
SCRFLHVVTDTAGSPVNSIVGEVSPNSTSRGDSPSSDITVNPRVRHNGPWMSGSQVALMV
AQRFTGATDAASPKVNQGTVGEPMLSNSGTESNNPVFMAREEHQASGEATPSILPSRMIF
PNQATMDMSGKMRMISPTRRNNPYAMYHGEE*
>TCRU_1683 XPC-binding domain containing protein, putative
MSQPGTPLAVELKTVSGRKCTVDPPFTAQRLVDAAVDQLHLERSTIKLFVGRRLVYMWKP
EDSEPNQRLRAQVTVPKGGSVLVVGKPALRQKTHPSRAKGVDTSKGSPAADGAAEKKKPL
LTPVASAADDGMYIRCGSSDRGLYRFLKPLVFMLGRRGLHHLFLVAKGQYGHLPESFQDH
PVMVCIVEYVDRDPGRLKEILNTIQEEEPGLMRWIETHAEFFLNVINTPPQWRDDTSPIW
LIRHAKKVYSAENTKKTDKSELVRAVTPSYKQMELIPEDLADNGILLNEIGLPQDADSSE
VNSNPDSSRTASLESIQSTAVMESSTKDLCSEEDSLLDITIQELQTVYRAWELAKERYGR
TVGNLTDKKRLESELKSRVRDVHSTLMRAMESYILNPPSPASLKKLLLIGHRAWSESEQW
FIEKEHVFNALDTALGRLLFNAGKELLMVRNSTHHQKESNSSNRKSSPISEFQQFPALDL
TIRWITANGPSILAHQLREYSLQQSVSIVMYSQTSCNQVYAYVVRDGDVKIAPIVVDEHA
DRELKELERLYEVMSQTYAPKDAMKMRRVIRSRWAGLLGKLYQRLLSPIEGFLPRPALKP
HVPPSEVGQICIIDTWAPDHIPIPFPALWNPADGASCLLQWAVFKANRPWDLISSAEVPW
SNPVANSPVITRVAAPIVVRPTMSVVEETTCSRTNMVTYVNTSDIGCVSVGDKTRSRPLK
GANKVEYGELWQNVPWEHWIQKALGTFHAGIPTYAFLKGKDSMQNGATALFIHEVVFAEN
ESITSTRSSSPPNGKGKKVLTAREMPYNQSADLFVSHVVGRDSGVGIHRAALLPTFKVAG
RDPAETYASFLKTLVATNDMTAAKAYRLAVLISWHTDCREEPWRSASLMLFNYGGTMNTL
SFLHSEYCKKRYLKSLHVFRGGDANFNKDAEKQQNEAQLLRNQPSICNTADGCYVRKHGI
DAIYEVVLHGLSIARPQGEVAILDNMIQCIENNRSTLEECVKRRREGKDVVQALDTPPAE
LVFAPSLNSDGGASFVSPVRDIVTAFRNGGEENSSSGLPTRDMRRRKGNQPPNSRRPPSD
S*
>TCRU_1684 TPR-repeat-containing chaperone protein DNAJ, putative
MSVRHLGGALRWVVIESLEERLGAMQERLQGWGVTAVMLGTDAASSDLQQCREVGLKRDI
NLAAEYAAAQKEEKQPFVPTEDRSGSQEPLLRRQLRVLEQLSALILEQIAKCRGAGEETR
LGGLEEELREAVELRSSATNCLQACLTEEGRTSSELNTLSSDCTSESSNLASVYRAVSST
SNDHNEVKGNVPSNECRAASAFFAPSRNGELFHRRSASALETDPQFTSVSMEGWMDRKSS
SPRAGTTNKKRPASSSTPRRPQKNTERFYVYGVAMVPERPKTKRPATAKASRRDCMCGGD
HGSITSHCGDLEPKEMKEFNLTDKEVEVVDAAGVGVSVVVRRMLRPSRQQTQSKCRVSPD
SMNKIRMTYRPALTVRRDVRKSRLQEIVPGLRESTEAAAVAVDAARAAVAASSSSAPHTP
CASAVQGSGKQQSSSIGHLHQGSEEWKKQGRKRSGYTTRRSRSFNPDSEFIQVCRERGNR
CMRNKQYEAAVKAYSEAIERDPENDIILCNRAAAYFLLNQYVLTLMDCESVLSRSPSNLK
AHWRAAKALLYTNNVQAARRHYRVAREMCVNLVEERAIAEEMKALRAYEMYYVYMKECRW
IDSVECADQLLRAFGSTGVVGLPWQCRKLEALLNLDSWRTLEDIKRLRKAYPKYAELLFL
HAKCLFYCVHDPNSTGEILELVQAACRQKEIEGCSKDSRYTHLERTVVSFEHHRDRGNTA
YESGDWMEAYTAYTRCLTLDPLNKSLIAVTYCNRAAASMQCGRWNDALSDVHRSIQINGN
NAKVYARRARIYLHFMRDKARVGIDYLQFAINDLRRAVELAPTDENRQQLAEAMKLKERE
ERSKDSRSSDGNEDTDRGRNPNETPRFCSNDANSASGGPRQKTYGHSGDAPNIFASENSK
AHCTKVLGLENTAGLDARSLTRAYREAALRWHPDRWIGSGPGEHEAAEQKFKEIHTAYQT
LKETMVR*
>TCRU_1685 hypothetical protein
MGLAAAKEGNKSGKDVETKRTHSRVCRRDSSGSCEDGVTPFSVVSAKRSNKLRDNFVRPE
KLSTNNAVRSLFFTANPEEWDEVIVISHSPQVAYITTSSNRQASVVGFSNGTAHSERREE
ENIYKGNNNDNNSRNNWSRGRLASRNNSLDETVVQVEQRAVTSPSGFVVFKRPPPHSESA
KVAPSPSIDHCSRKESSKVSSSPIHRKTVIDRSMDEDVNRPLRGSVVSEGYRHSVTGSEK

ASTCPKGLSRRSLLPLRLESIDVTGIRKKSDAIQQWLNEVEREKNRRVFPLNARRPRSPA
RNPVEE*
>TCRU_1686 hypothetical protein, conserved
MPGFSQGFSAFIDNYILLLAARFHAPLDAVSFFEGDPDEPWEKVARCVRDALLHPQTEDE
RREVAHVDFSLFDAQLCRERALYFTWRLREEAANDATKSAAAAGASARIQITQKMSGKPK
NRAAAPSQFDITRDSLRDEVEQIYTAVRKNLPSTFGPRPPKNGAANNSRGNEDVGEQLGD
SSTDEDDDDDDEALDAVEFSLRSEEEMKRDVAIAEARDALLGKIQEMQAEFFAQHRRWID
VPFDIDVVPTHGKAVDGVVPELPPGAKAADHQPLSKSAMREALAPAYTPAVSEKKKTTST
VKEDEAESPLNAGTASPAHLLEALRRSIHVNRPPRPSQMREEDYEADYGDVANAPFSSEE
IRTETEFGIYQKINQVNDSRVPQENSLSRDSLKRNVTFQTTRASRWSILEYDGEADEDSD
DAS*
>TCRU_1687 hypothetical protein
MESLSSNAALEGGRDKREATHEADAHLLLPSRRTWLESSPLPAKHQFFFPSNRSSASTAP
PNGSASPVKAAPVTKQVEGGAGTDAMRKELIRLYDSNAELREQVEKLQACLHHRKMVLAN
EFEWNCCTHLAELREALMAERLRCEEKERIIAALREELSAANQAIEFLSRTQKVPLKESA
GTRFQGRLLDGWDRSSSLVTQDDPQIVLEEEMAALQARLHREKEEQQQGEKSGTGCLLEK
QIGAENFSWSRSHSGLFPTPNSSFGAGNGAGKRTVVTGANNCQRHTTSPTLATLDSSEQT
STLSKRTARTPPASSSRAFVPQTLADINTLTVATPFKTEAEPWYDEEEVKEVVSFSRASR
LRVAMSPRRFLRPSNVKTLSQ*
>TCRU_1688 transcription factor Tfb2, putative
MNPSYFDQVLGYPEREGLMTQCPALALFCYQEFVAAIQGGKRVVDPLSAKDEVAVLLSAA
TVSEVTARVFATVEEGATLHPFWRTLRAALESAWDPVQGGDVHWRLYEVAGNARFYGKAM
PRMPLAQLSFQNTLDASRSILHMTTACALAGSIDPFGEKRGQPLASMLQYYRLVPTSSET
REITSEGLSFCMQPLQQQWWTLVSVALDRILVLTKNSGVTRAELWQLLAVLFALDTSQFV
YPFPEKEKDLAAFQILARLSEVGLVYPLISGGRRCFALSPHFHHAVCWSSTAPLCTAALL
DSGGNSMGRVRREDEDTIITEANFRLYAYTRNPDLLNILNQFAERDAEVDQMIACYRVTR
RTFAAALKRGIGSSHILQFLAVKAHPSMLRHHREGDSKKASGLSVLGAGTRFKNASDIRI
DEIIPQSFCDQLMTWEKECRRLIFSRNLVLLRNVTAVQKELLLNALSSGGERHAVVHQEK
GYLVVQREAYERVLAPLIPTE*
>TCRU_1689 hypothetical protein, conserved
MMRRAPEWFTRGRARERFHQIWPWALSCTCAAMYFINREPFDELAATVVSKVRRPLLKTM
EWIELHDVDPETMALELPPDMIFGPLEFPKQMRFLLAALRADNELADGYLARVLVDHMDL
SLDVPILSESELLAAGGRDLLNFAIDDFLGQGTRKMRKHVFFQPDELLRLINFISVYPTL
TEYFVKKRNGVELVFRALTHSRDEYARVMALRSICLFCFTQREDGDVERRVLQANGVKPI
VEAYKQSTGDPTDTRYITLVLSSIMRHYPKEGGKEFLDADGVQAAVNNLNISRYKGLPQH
IRVLHDAQRLPPEASGKQTVNARIEDADFIPVAIGVLDVFPEFYETAGDILSLLEDIVPS
QTTPLNLLEYRAMPVLSKFFVRWKDDNLFQTDGTRTQVVRLFKMLLDDKTCQKCYDPSVA
SYELQECLRTAKEAIREEEEGVGHGLQHAVS*
>TCRU_1690 ADP-ribosylation factor, putative
MASSEEEKRVAYCKQHNVHHLFELLATKLLLDRPENPFEYLREMLSKVEESEKSKQSYDP
TVLSPPVNGAVEPLKKITLGTFGLDNAGKTTLISALGGQIEVNTTPTVGFTPTKFQTEKY
DICIFDLGGAANFRGIWVHYFHDCHGLMFVIDSAADDAVVRESLNVLRDLSQHRYIKGKP
ILVLANKKDLENARGTKVIPNGFLDKLFGRNTAYRVVASCGIEEDPALEEGVEWLLSVVD
KLHDTLEARVNCDTEEVKMEAKRKAAERLAALKTAS*
>TCRU_1691 cAMP binding protein, putative
MPMTSFSSISHQLNGVQEHRHSPLLSSRPVSSGVRSGYEAIYPSPSKPRRESVFFLAQTP
KPIDFHSAEAQEAMEVLRRLLCPVIMRRVLRIRKRKRWPGENAMRVYTTNSIHHALRSSD
SIIADWPDEVFTLIAEEALYFYLEPNEIIVYTNESYISSGVVVLLYGEVKEQKDHLDSST
SLTRPQICRHVAPAVFCDQAVLCRDVSTSLIAANGYADVAVLPARWVWNVINSYVLQHSG
GCVLDCLKFSIAPICEEIVNKKYFPTSLVLRRSWMWSLFSSRDRIRLARLMTVKVFCIGD
TLFCEGDYYPYMHIIRRGIVKVVVKNQPLLELDLGSSFGEVSILFDEPRCCRAVASTMCE
VYCLHRKHLMKYLRKKPQLYNAVIQTALERRELWLEEGKNRNIMGLAGLLAGVPCLSQST
EKVRISLAMAAKPHLLPPNQTLFAKDTLCDQLFIIGRGSVMLVDGNGDRVVRSTVEFVGE
FCLHPHRWPTNVITCTSVDGWSLSVTEIMSTLSTINAGAQAVEICRQGIELYRAQHGSNS

VIEEITGSGSHLPTVPDAVDAISLAKRETLSYTGDSRAPAQLPSSLLEQSEGKNIDFDWN
AYAMKDKSTLPLEDEEGTDVSKRSERREFEQNVENELGWRVGGMISVPNKKSSSAVDCDF
SADVDEMQQVLVEQIFLMPTERQPILLRQINQSKITLIFDDELEPLEELSSENTTANNLA
LPQYVVPSPVVYTLDGITAYSDGNPLPATEAPPIISPRTGLDFAATTTRRRSHTPEVQLS
PPGQFGTQRLFDELGSLTLRSRPQSGVPSHSRSLRPTSGFSLRRTPPRTASAGCNQRLSR
SVSFCSRTSAMGTLTVSQVSENISTSAQGNASSWTKANSIDLSQKAKITASMFQSALDRY
VKLDDQSYFQEMVRVCLPSQPEEQWFEEDTRKLAKRKEGLILLLMHVRSCKGIEIDKAVK
SPIVKVSTNARVLMRTPVMENLEEPVWPIETASFIHFIHADSEVYFKICDAEDEGKIAYS
ATLPTSDIRENGGVGLRSLPMQAEELGLSESTDDIGARIEVCMMAVTASKYSSLNKRLDD
HDDEDSSEDGTTVYLQILGVHGLKHRIEAIIRVSVEGDGQSREILRTPKVFPKTRSPSWP
GQGSFCAVKSDGVVSFDLYHRDAFLASYETPADILAFGGTGIYTFPLLRAQGGPDEVYGS
LSVSILGLKATSVERQASCRPSRVLLLHLDSLHLTSDLEEFTPDPFVIVRGVNGEVILRT
AFSFSTHNVKWTEDEASCFIMCPTLEGCSVIYRLEVYDNNESNKIGTAEMTVTPNGTRRH
RMELPVGTRGALTVVSHSFPVQEVPRPPPSRRGSLLNESNEEGFLLSIDVRGCDNLQGTG
FDDLQIDPLVTARIGRRRVLVAPLVSGSTVPRWSYPKATFVLPVLPELLSHFTLEVWDTN
IELSDVLGVARISIKDLCRTGTHHFPLQPHKDQEFGRRQNLGTITLKTRFGRMNGEIISD
GSSDLLLTGSSRGGSMLDTRLFQTPGDATEFPVTRVCVHISSCSALQTDASIKFIKVTMS
CLQHVFLEVKKEYDASSSVAWSIGEAHTVIDLRSIHRRPLCLSVACSSFSSVNDYTDVGS
ALVSFSTLLSASEVISVHSFFLTDSPSGEEGVGTIENVDRTRGTSVSLDTPTVTITLLAL
EMARPLSTGSG*
>TCRU_1692 hypothetical protein, conserved
MGPKNNSQSKSVATITANQHNEPSADHAGSRPPSPTANGDAANHEADKTTEDGIPNNDPA
ADGAETAEGKRNENMNANPKETPVEAAAMKTTTAKAGDSDGSTAASHTTSPFLLLLLLVA
CAAAVVAA*
>TCRU_1693 hypothetical protein, conserved
MSVNFCFATGFFILLLCVLLTAFEPWLRCDDVFGLDGDDHISVLRNGDAVFIDAVVNKGF
FSQTNEGGNTSSDDAKPSFSADVDTNQVLAVIVMSAPSLPEGVISSITKARLLHGVRTAL
LAGAPWIIVPGSVEERRSAEKFLWELRSPSEALFPDATLSELPAKVQKLAVQMRDSMSFD
TSLKNWIRHGRLLKRLSHASHVDEEMKVEDMSSPRLLRYGAAEWILPGFLWGEAGQSEEA
ETMTYAEQAVRLMKQRLLAVHADFQNEDGKERPIEKNARAHRGCFNVIVVSSMHNERYAR
AMVYSTIRRDWGASSSLGASQKSVLQIKQQEQQKQIFSECIHVLVTSAGDVEPTWEVPSP
LFVRGPIQSMANFSLQSSFVARFLGVYAHAIHANYRRWFACMQVSLLSYGPLSLIYEICT
IIVAHLTETLSVRDLAYSTFDQPN*
>TCRU_1694 hypothetical protein, conserved
MLYPPQKSVFSAVGQDGTQLHGDSMALLEASSTRYIQQLEVEVAELTQQYDAACQLLYHA
VLVQDASAIVMDECEARGLIVKDESAAHSELLWLFFRVTTMRRQVESAMMPRGSERATAP
PQTESAMNWGKIPECVVNALQGSLREENERLTRLLEAIPQRVCSALTVRDAAGVLPVTSP
SASHDLAQADAARNGSTDVKQHLESIVTRIDEIFKSLRQTGKPDAEPTRTEDLVGIHVAS
LQNVVKSLENLSIRIEEILDRYNNDVNSNSSPRSNQTPKAEELRASQAETSFLTSKVPQD
MPLLRRLAYSSVATLESLFSEYMLAIERMQMMAEKEMHVFSSVQDRWKMLRWNACMEEKA
CEIQRLQREVERLESQSVIRDAKDAAAANTNAATTTNATQATKFPPALAQLYAKFAAPFI
PTNVRIPRATKMKSIVTLRTEAMRAGARPASALSAADGEAALVAPQSTALVVRGADAAFK
GQNSSGTSKPEVEKKDNGVPPPEQPARHASVESAASSASWNATQQEEVHQKKAEENVAPQ
KLDRYASVSPRSAATISSGALPEDVAVMTDDGAARKAASPSVVVGEKRESGTMGIVIRRL
QRDGSMSSCTTSGTDGTISSVQVEGGEAHDDTHGASKPAVVENSFDESSDVPPKTRQSEL
VTSFSGANSKKDRRSDGVDSPAFAVLLEGRGKELASGSQHPINQTVESSSLSSTSITLTL
DTSEKSGNKRQRTAAKRNERTRNKRLSSDWDDSSPRDVVGEKKKGAKSHSPSTRARTVVS
GLKALSFTSHR*
>TCRU_1695 hypothetical protein
MSEKDAVLYAYEARLERAERGSLSALESQCRAEIRASELSKERDVYLRALKELFSRNEEL
GKCVEKKVSSSQSMSEGSVHTPELSPELCEKDAGTELRHSEKYESLVSLFQIRLANSEVW
MNMKSLLVNWMAFVLKKKITAPQMGKIRHFSSQAITSLTSEALEGDDKDISLMDKEEEEE
TGIRREVEIVEEPNAELKATETASEEQKQETEEEENAQKNEGREVSKVVKALEQHLALEP
PEKIYDTTKQSSRSNLHVCTSDLDSLSLAKKNSNPVISQGTADPCLAQEEPISSGVSIID

KKERKAEVEDAEEALSSAVESLHSLQDGSEASAIIATLLSLHRQGVGVWRRRAFLVEQQM
EEWGAKVSTLSGLLQQQMLPYTFVLYEIYTTAMTDKINIFLENFCLMNCASDKMCGAYER
SVMESSFFIMLRYWGKWRLHLEASRLVMLREKATRTVSSMAEQHEQLKAIAQRAMMRIRD
FEGPSGRNEGDVAEI*
>TCRU_1696 tRNA (Guanine-1)-methyltransferase, putative
MRNKDEKGDAADPPSLRKKRQIWTAEEQSAYWQAKKVERKRRSKEAAAQRRALQQKEWEE
LDDKERERRRTEAIAIHERRRALEAKEHAMCVQHLADTSLPVLVFDLSFAWCMSAADCRS
TVSQIKFSYSALRRHAFPMRPVITSINGKETIETSAHSELLRSLCAFEGFRRYPFPIHEE
HWSTIYKKEQVIFMTADTENVLERLDPGTVYVVGAFVDHNARKFLTRDAARRHGVRMARL
PLEESMEVGNRCKVLTVNHVVEVLCRYADRGEWRSAFDVLPTRRVNAGRQKRSRALNGVN
IVSSDNDGAVLHETDERCHDDVMPQA*
>TCRU_1697 kinesin, putative
MADQGVVAAPTDNAVKEAADLTPAQRVENFKDQKKALNKSTNDVPQPVNRCLVYCRLRPG
NKTDFKEGSFKLVSVEGNSIVLKGERRYDFDKSFDDECTQEQIFDHVAVPCVDHAFNGFC
SALMCYGQTGTGKSFTMCNTTPGLEGIIPRSARLIFERIQADPTRQYEVIGQFVQIYRDH
LGDLMVGSGKERVEVRFDENEGVELTGCTSHVLRSPQEFMRFYHVGNERRVVTATAMNPE
SSRGHTALMIRIFSEKLDDPAAGKMRGKITFIDLAGYERFSKTGISSDNPIMKDEAKCIN
ASLLSLGHVVTALSSSGPHIPWRNSKLTRILQDSIGGRSRTSIILTVGPSSDHFYETTNS
LQFGLRAMAVKVSAKQSVVVNYEKLAHNLQMLLDEKQERIALLEIQIAGRDAERAELMER
YNKHRAEIDLRYERDMARLMASNAPPEKIEGLREVYRVEVENLHEQRDEEIQYQEEAHSK
EITKLVREQTEQEAKRRAEMKLAQERIIEDFQKKLDNAREGKHDDIVNALRQLAEKDSLL
ASRANDTARLHEHIEVLTQQIREMGGTPVEEAVFPETFLDVGQVEEIQQRLEAEVERHRE
KEVQLYAEVERLSRICSERVEEINKLHDENEQLRSDLSNKGFDVGETDELTKYLRDRRAK
MIDSSEMETLRVTMRAEMEELKAHNVELKREVERLEEERAQQSLPLTARIFGTARNSLST
ARSVLPAGGAPPLTGRGASQLRQYFLSDDTKSLSLSFNGETSKKAVKELSDQLTFSIQEK
NALLNRIQKLEAELKSHGVESPQPYVPPIMLGSSVLPNIPSLVAPSPDAAPNADVDVLLR
VKDAEVDEFMETIERQQHLLATARSNDEHYQQVISDLRQAIAKAGLPLPESQAIPAPVDC
IAMDDYMNILRAVRDSERKMVVRLAEREGKDPLEIDSVLEEMNRELIFKDELVIENASKM
QFVAKVCIRLKSQLERLGITPCCQLPDSYKELIEREKCEMEEQTEAQRDLEEKLSMLAEE
KQRLNKMLSSMRQEREMDIVVMRSVQERCKEAEEKEIYAAEALSRLTREKSQKERALEET
LRLATMDLMQYQAQLAQIKELENTGGFARILKLLLRR*
>TCRU_1698 hypothetical protein, conserved
METGQYTEQGIAPLWHTDLPTCFTTQLTNKWRSTIRQDTHRYLLCGTRPSDLSGKDLITQ
EVLHRQELVYLARARCGESELWGRLYWAVRDCTNQCRFCNISPEQSAYMRPNNDPTAPGT
DTVPPSAREEDVSPVRRRTVTRRRKEKCPHCDSTLTGFSGLVSHCRLFRQEHPPPLPELK
CDFCNMVFPTRRSTAPHRIRRAHNPDATRHRNSSAMRRSLLPQDQPASTSTPIGPQEALH
HLLLECPGTLAVRQRLGIEQDLRLGKFSQWQLPHSRKLLSLLDHLFGTQMALYS*
>TCRU_1699 thioredoxin, putative
MRLTVPLVVVFLLVYLSYFHVHFFAGVAYASNVANDGERPSRVVELTDETFDSIVMDPEK
DVFVLYYVPWSRHSVAAMRLWDDLSMSQSQKRNYLTFVAARIDGEKYPDVIERMRVSGFP
TMRYYTRIDKQEPFEYSGQRYLSLVDSFVFQNT*
>TCRU_1700 Lys-63-specific deubiquitinase BRCC36, putative
MEKRAPLEKVCVADTVIQACLAHAFTTEQEEVMGLLLGEVTVHHGCGTTAAISSETVRVA
ATVSPAISTGAKSFGGNVNAPTPTPTSPSTVRKRANVWGAWILQRSVRRADRVEIAPEML
AGASDEAERYTKQVGHHTRVIGWYHSHPRITPYPSQVDLRSQGSYQQMESGWVGLIFSVF
YSDATNRNGVSIHCFQTGPGETHEKVEIEIVPVGSMPLRSLPPCEVTHRLLHVFRSEVNA
AVELVRRRCKDAPDAMAAAFALQEVQLYTLEKLIAQPTLRHLRACISYMEREVKRLEKEL
AAQNS*
>TCRU_1701 protein kinase, putative
MWSLDDFDIGRKLGEGRFGKIYLAREKRTKCAVAIKCLSKDMIRYHGLAHQLRREVELQE
YAGRCHRHILRLFAYFWDDVRVFLVLEYADGGNLQTLLDTRTQHRVSEEEARRILRPLLS
ALAFLHERDVIHRDVKPDNILFKAQAVKLADFSWAVRLDRRVPQHSRRYTLCGTMDYLAP
EQISHRSRSQGGVAQRRPMCGLSAY*
>TCRU_1702 hypothetical protein

MESLLCVDEASRLSCEEALKHPFIVGNSCSLHEASAETELPSAVSFQCSPTPEHWDNRFV
RVSLPTYGKAPAVVFAQRRQPQPQQRQQTNNRSGGGGSSRNSINSSNSATCKWVATAACS
RSLSDGSFVTVSSSHSTERITSAPDLTTPNISSAPQREWICSGRAIANGETLKSGSEEVA
TSSQGASLSRPRNTHSTSDRSGLATTQIGNFIGFSPLILCPNDANDNAEENEVDEREADC
VVQLRFDDSLLSLSQLTAASASTVDAAENL*
>TCRU_1703 hypothetical protein, conserved
MPLDLVGKLHRTVYIEGCPSTVREDLLRLLVTKCGTIEGWDLMGERLIVVFSSMNSISTA
ITFNGTAFGDLTSKLFLWVATESPPAGVTQQMAIADRGDGAVGAPHSAEELKSAREARER
RLAAIRSELAPEIEMAESTENKEARMLDLCVRQLKALGTLTSHALVEAEKKLEEISTHLS
ASQNLLESLRREKLGKATALPAEQAEGPDCTADANTAVVAAELPGVLGERDDEVARRVEA
MVAAAEDIGQWRMRFRES*
>TCRU_1704 hypothetical protein, conserved
MWTAVRGTSALRRVNSPILRCRWRRSATFTSSEKAASSRAATLRTGTYSVKGYDFVEGFH
VLGPGAALSRLKATLSMYGLLGVTVISSIAYYLTTRTYELTTDPDPLPKSRFQKFPSDYA
VLQNRWTGKRHVIALRDGDANDNDTREGKQHELEESAILKKRIRVNWLIHSVRLYLHVTD
SIVVVDLDAEFDPYHFALKRNRGSLTTSEVANHVGEPATARLLCRSRLRPIVIRNEYQKG
TLPQYERTVDTVTRELFGERYRQAILSRSGSILHPVFADELLKSGELNGKEMSWTDVVGD
NEAFSAEIQRRVQKKLGEKVILLQFSMRVL*
>TCRU_1705 CDP-diacylglycerol--inositol 3-phosphatidyltransferase,
putative
MRPKANFSSVRPTQIYLFYPNIIGYVRLLLSLGSFVVLGNYPGLFLTFYTLSFVLDAADG
MVARLMDQCSHFGAIFDMLTDRASTAGLLLVLNHVLQPMPDWCTTLFAFLVFLDVASHFC
RMYVTLFFRKESHKDTSESIFYLLRLYYSNRKVMFLLCVGQEFSYILLYAYWMYSEVDWV
RRVTFPLLTVLGSLNVLKQVVNVQQLMDGMYHLAVLDAREREERGKKN*
>TCRU_1706 Isy1-like splicing family, putative
MRNPQLLSIETHGEVVIRAKNDEINHLIAKKNSWERRLVALTGEEYKVASSRKLYFGCAK
ELPEAQVEMSTAEEVLTGDALDVSEPESLGSQSSEGIASYFKSSYLEQLAASESDDLLCR
IEKAAEHSLRLEHGKNNGNLFLKRFNEENSLYVVDVDLLPEEEYRRRILDAKRELLKKRL
GTLKK*
>TCRU_1707 histone-lysine n-methyltransferase
MTGLTLRRKRSRGLTPQKQSFDAAVVFRRDDLPARPKKPLQDEEGNGTPHYPFRLPLRNE
PNENGCYHCLTKRCFCVLFDRMLNHVYSNLYCKRITEVAGSRHLCAKSLLPTFVSRMVRL
MEVKSEDTFYDLGCGNGSVLFQVAFLTGARCVGIEISEHNANVAKTAWESLKPQLESISG
RKMPDLKIIAADMTRVLAEKTMFNEEGGKTAILLSNLLFPKSLTHYLSERLRRVPSGTRI
LCFDDLYPHSRSVAAIRDPEAFEIFSMMDYRWQERSVEWCSMDGPFYIHRRN*
>TCRU_1708 Glucosidase II beta subunit-like, putative
MQARQPQWDGSGVALWSLVGAVVVLLVAMLLPWKTLLDDWSNWNEGSAKQTLLQAPPPRR
YTDVMTHSEDTRRQEGESKGRPEPSCYTLEAYSMKFIAPAQRQEATPQHFYRCGTRLMDL
NTEVNRSKREICTAATEKNPTLFSTLRVYLESAFEEKAHLQQRDNVAAQTISLERVNDDY
CDCLDGTDELQTSACSMSGAVLPLAHMRWKQYLLANAHVQLYEEEEAPSMRRTERLLRRL
GGPVLPFRCRSDPDVWLAPSRVGDGVVDCCDGSDETTSLKHHPTHEVHGEDSWRSRVTAM
EPYLGMHSGAASPLYPMASGNRTVAAMLLENGFTSLMSCRRVKEERLNNARTLHEVVKRG
NAIHKDREANGWEKYGKKLVEHITRKKTELDAVSKEFETRRSQIAKKMEKMGKSDPISAG
ISPEEVQAINHMYAELQKRGASLRLVVMILSFRWLGDDFEYYPLADAHFTVPVNRVLETA
RSSSPEVQRVQASRRYNDSYVIESIPVHVDNTSYREFSFYPSFYLVGARNLTREQSAIII
KRAYGLEENESLNVSGTENFDESLPVVFGFWRPDLSEVTIDNFQSVDPSGNGVLRRRLFM
SDPAPVMGGVEQILQHERLSYGGRHRRVMRLGPTDLREQLQQALQGANNDTEIEMPQQKN
TPDLASVRIFSGGISCALDDAMDNSGRLGEEEEEEKENTPRSHGRVVYVCDEEDLVLEWH
RNGKCAHEVVFGTPSACPPWVKEASATRVRQAEEALQNDE*
>TCRU_1709 hypothetical protein, conserved
MNGAGHNGGGGCGTPAGARQGQQQQQQQQPTDMFVACFEAALDEELRGQEISSGFRVCFE
KISSPYGFIRNEGLREALQRLCDLSLEAAEEAARLANKTPGTTTTTAAAGGNTTATQPHL
PYDAIRSAVMPRSAVDPHSTATPMNHAASGYSASWERTQRALNGAHYTMSVFHRVLVPRV
DERSQCNPGGPVTIELSEEAALAWNTLNHAQRTTPPPSPSPVGKKKELDITLTEVTYQEQ

ELALRLLQGLSLVVYDQRRVIAEGLLITFLVEVWQCCLQHIQALFSLRRRITALEKTGDT
VSPTPHSFEEGPVQLVPELETVIVATIDAMEAACHYNPIALTRIVQQGGVRALLDLGLCP
YAPYDIRCAVFDTVSVLMQEVAPFRRAVAAGAAGAAAAGVKKGNEDELIQTMIQQAMAGY
LGRQAAPPPFLMDRASASKFDSAVRDWFSQQGLSHVVSAVLELRDVRGTPIAVGAMPKAE
VARNVQRVNQLREKHLQALLQAVDGKRAAL*
>TCRU_1710 PH domain containing protein, putative
MNLGVDARFPLDVSFDILRRVLDEESLVLAQLAYIVGHLHDPILQSCGHGNVATGPWRSH
GNNKSNAVGTKQQPAILRFAQYWELFANIATLHGAQSTIVGKLEEVVNNRTHLLDQQQEQ
KKEVKSGHGAAKNLHMRSSSSSSSSSDGGTDEGMRGPQSILELFCSAAMRHYIAEHMMYS
LNYSRNIAPRVMELWRLWRCRCGKNTSAHLSARERQELESYMGFLYFLWHAFGGEDGVPD
DPRVIFTRLPETLLVKSQKPKKDRTGHNTAVVPVKMPDAPSIPPNWRGFETLLVLLATPL
ASLRRYMHVARCIIESQSLPIPVRQRLQVDFVDLLVLRLAEEHSIVFDELAKQDISHIMA
LIDEVSPPAPSEAHKKKFPRIRLDEDGSRTLVHYGRLIKRFRRGRHERLVFLFSDWLCYV
EEQTNGRMRLRASISLESLRVVELDDTAEVVNGFDIVTKDMRLTFFAPTLEQKRQWVDAL
RNTTEAYKVKVQQLASPRRQDISQQQQQQQNKSLGHLACQTRVTALPLSHNSRLRRQQR
ADHALQRRLERRSTAELATTNSLVADETPAHVMGIDAGRKQPALSFRPLHGNFDVTYWAQ
QSTETVHKRVRSSDLLRSSWALQSPHDPNACEPKAVAPGMDPLNHGNISTTTDAADCSVH
SEDAPASAGHSPTSPWVPPRAVLSRLLSERFQEPSLHPLYSGGNANSPLPENVSENEGRE
EPDSLYTTLLSCVATTEVHKYSFAAEEDEVVLENDEWVPTCDETPDAIRPEGPAVHISLK
HLVGETDSDHGSNSQSHSNHFEEEEEEEEEEAMWSPR*
>TCRU_1711 Coiled-coil domain-containing protein (DUF2037), putative
MDVVPSLHGVIETPSDADTVLQKLADGGYHRARVKTLPVFDRIAGGLTWGILSSRHRLHV
EFVENATIREKIRISEKICNALKHMQCPIDLRPHQIHGLDYSSLLPVATWLLKRVEATRA
ENAFFLEKQTAWDFSRRFGTSLQSLLSEKEMTAQSGGDDVSLLPPTQESLCFSRRRPAPL
RQRISEVADRHSVGKPQGGQNFSRLVHVSSALLEYGIRYEMRDSVLMLRHVSRGVVAEDE
EVAREVRELEEEEMREERMLEMIIKKMRENRERMDGKMSLSKVKTLMQTTKISESLQKLS
AEYHARQQERQMQQDSVQAMQRKLQQKQEATVRYRQESETLRLQCEEAEQQLAEAQSRLQ
DAKAKVARRTAKWTEYMHNLQDVYQHVMADPVRGKLLQKLQGLLDQKEEQRLLLEETRRD
GKQRLKAAKANCVALAERSANAEPGVDDIWEKERAKYVAELRRKEAELSAINQKASDLLR
RTDAFPTRLELMQIHMRICELNEEVSSKYEELRAAFARHNTRMEILKCLESEDVIMTQLS
GKMEWCLRQPSWVSKSVSVELIREQERVVTQLRDSLDAVLRRNEDVTSKMTAARREYESL
LVRKQQHRDMLGLLKQTIEEQNARMEPQP*
>TCRU_1712 hypothetical protein, conserved
MEAVGSTVETAEASDEAFNSPESHVWNSGDLKGSGCHATSVSCAYFTRHPLCNGQHPIAS
KNMLSPFSSFWGLHVAVPFLVVLPQENAELSSKEVHQGVNTATVDDAAIDAGAISSPFSV
PPERFLTWHEMCKILVLCGVKRHHCHEAVRQLWEYLLFLCYKGLFESDSKERGNHGGRDT
TQVTDSHTCKPSGAAEDFATLVRYDTLNDVLRSRIHCGGATDKSTVVCFAELVVAASVAL
GNRDLGQLEEVMQAPSLSNRYTLVTAKHTFDRCIARLLINELRGQRITVIPLPRWNVTQA
IVQNRRSLIVFCGGTSGCGKSTLSSLITTNICFNTLLSTDTIRQSLRRTLRREEFPELFL
STYEAHRAKGSGGKTKPRAGKEGNECDPQVVIAAYEKQCEVVLRALDGILEKFICRNQVV
LVEGVHLLTSYMQRKTVELKARGVLCVSFLVCITKEERHLERFRTRAKCMALSPQRNKYV
SQFHHIRLIQKYLLEQAYDHLHLKIINNTNLDKSLMDVHTHLLDAIDCSTSPSWNETEAA
AFGRADATRHAVASDADMHGRLAPKEEAGKSKEGNCGFLHQPFADPNISGKRMLAFLLKW
RSEKKKRRANNTSFYGKFHHTCHVATSLFAPAKRARSAESLTSFRLQSLCVASCSGNTSD
ELLMRAWRNNETQCFYVCDSDKAMAVVDSDGYERPRWKCSPSISSGTAFPIPRHKLVQKH
PQEATHAVSRRGCFLEALTAAEDPPAATVTATAAASRWGKSFRSSSADAAIDAVEGNRAA
VRGNKQKRFLPRHAAHGARENGEEIKEEIPLWVEKEEEMENGSRCEFPSLMGS*
>TCRU_1713 Methyltransferase TYW3, putative
MNEWKAAKPERNTALSLSLSLNLSSICSLQRGFIGVGWAEKDLVIGHMWEEADSSALLCA
VQRGELDEKSPAAQKKKQNGKRPSNRGKELSPQYQQRKSSHVAKQKQCEKEFLAHKQQVM
INLSSNASDHSPKGGVDHKCLPLMHLLNTHDDYVTTSSCSGRIALFHSVIIPEDRGAAGP
PASLKRGGKDALGWLVVKHDVLTEREIDVLVSCLCDDVKDGVVTETATTPLEGATSNKKD
EEKEQQKEGELDGVWVREGVLQASSPPVFGMVALKMEPFVMHVECRTMESAKRLLSAAAT
DAGFRNSGVTPPGKKIMCGIRHASGLGLDVPLIIDGVNYVKGQHAYLRRLLHMANAKMHG

NDVRLHRLEDGVAARLAAEEGAKKGLRVK*
>TCRU_1714 prefoldin subunit 2, putative
MTSTNNSGSNNTPSEEAIVQRYQQLRQECLSLVSRISELENELHEHKLVAEALRPLNGDR
RCHRLVGGALIERTVAEILPELDDNVKGIQEALEQLNKILAEKQAVMEDYARKHGVTVAQ
QHGQNPGCDTNAESAKKPGAAEQSGVLV*
>TCRU_1715 hypothetical protein, conserved
MQSFYGREACNVELPISDVAILLGAMVLANVTATGDINGVTAAKRSCSFVRQSAGRPIHL
PAPGMAWNLLEGWSRLGLRRARSNALQRSSYTQPSPNTATRCDFIASC*
>TCRU_1716 60S ribosomal protein L11, putative
METHAVSEKKATNPMREIVVKKLCLNICVGESGDRLTRASKVLEQLCEQTPVLSRARLTV
RTFGIRRNEKIAVHCTVRGKKAEELLEKGLKVKEFELKSYNFSDTGSFGFGISEHIDLGI
KYDPSTGIYGMDFYVVLGRRGERVAHRRRKTSRVGCPHRVRKEEAMHWFERTYDGIIFQA
KKKKVMTRRRRR*
>TCRU_1717 ADP-ribosylation factor, putative
MGAVMSWFDGLFAKKDATILMVGLDAAGKTTILWKLKLNEVQQTVPTLGFNVQTVEYKNI
KFHLWDVGGQKLLRSLWKHYYEGANAIIFVIDSNDRDRVWEARQELEKLLQEPLLVGATV
LVLCNKQDLPHRLTPAELVEQLGFRDHSTTGLGAAMRGRQWFVQGCCAHTGDGLFEGLDW
LSSHLPDVS*
>TCRU_1718 hypothetical protein, conserved
MPFCNVKPSEVSHLQNVAKKQGANDVATADYTVLLVENMMKRYVEGRSSVCGSTGTDKST
NSLSPSWFDAVKADEARMMRTFPYPSLFLHPLPLEMSEHPDTPSPLLLATQTATPVGDDS
NTEDAPRREYREMVVLDGGASEMVTVLQGECGLAVVSPRCRSTGPRSVYLLSPDATSCTI
VACRVGLHSHLRERLVATTGEMTESGDGALAWRCCKTFTAAMGHLDCAQGVAEVLYEMLW
EAALPAWFHAALRDGDGAVGECGEVGAALDLLERLRRIAQTTTTATTTTESSDSDTPMLV
AEWFLVGGVRSREKTLPVLTAVLSTLFVAEEQDDGGANLPGGKRCILKPSFHLSEVLGGK
ESDGADADLVRIEHRLREDGVCFWSLNTVLRQWAMGRAGELYSCPASLGLLVDVGGGCCW
PATVQPGTRKYPLAALRNALMQPGYRWTCPLEREGTLRVRRGVATALAASYFGLQPVPPT
ESVCDVSLAAYVAAFLRRCEEGGETEEERASVSLPILVRRGVWEKMENIRMLDDLPDNFF
LMASTTPHCEPSDFAALGRQRLGFMSEFCVDDVFEKGTVGILV*
>TCRU_1719 protein phosphatase 2C, putative
MGIPLPKPVMTQLRERHGNEIFRCGSSCVNGFRESMEDAHIIYLQPGWGFFGVFDGHVND
QCSQYLEGAWKEILEKEKMPMTDDRMKELALEIDKQWMDLGREGGSTGTFFAAMKKDDNI
HLQVGNVGDSRVLVCVNGQARAMTEDHKPNNNDERRRIEDCGGRVEGNRVDGSLAVSRAF
GDRDYKTNTTGSQLQQKVIALPDVTHVDLTWGSKDFAVLCCDGVFEGQFSNEEVVEFIKL
QLETSDDLAVVAGRVCEEAVNRGSRDNVSCVIVQFKSGKDYADTDHLEVVPGPFSLPKNG
VFRKVYGIMAQKAGCTIHEVLEKRYDQLVSMDKELLQEEWQWFKGGPPASLKGKDRTQWF
ADLLEQHAAESPSDSRSEQLERIQLLQQQIGVPLPVLLSLMAGQTQE*
>TCRU_1720 eukaryotic translation initiation factor 5A, putative
MSDDEGNFTQQGGEQTGSLTYPMQAGALKKGGYICINGRPCKVIDLSVSKTGKHGHAKVS
IVATDIFTGNKMEDQAPTTHNVDVPFVKTSTYSVLDIQEDRTDPSKPAHLSLMDDEGETR
DNLDMPPNAELAAQIKEQFEAGKDVLVVVVSAMGTDQILSFKNAVEK*
>TCRU_1721 Protein of unknown function (DUF2009), putative
MGYENVLLRLTDTEREDLQLLIAALKVSEYTDDVDDIRHPNSREERMYRCMRELFDTTLG
LCIASGSVSREVREEVARGNTDVRLTISILIGLFEIFRRHKRLNPFSNRSEFGKLTMLLQ
DVQKRSIQERLHISHSLLIPVQTVGMELRRVGAEELLTDRDVDKYLVTHGTEKAAVLQKL
LDRYGGSECKPVVERCLRSIDDVSQFIEGNVRPLRWLRQIILEEFLPLDGNPKYDLSIRA
GVNGAKFSHDHKRHCQYVVESLTLWENVQRNIFDFWQVSEDDMLIDGDGHYTFVNTGQGF
HRMCRAPKSYSRMARCVNEADQEMGGWVGIKVIHLGDRDVPNPLVFIDKYTVIPRIVQPI
MHTIMEIEKIFSPSSPEEHPGLRNFFRAKFNSYKALRMMILSDFFRHAFDGSGDDGGSCI
DGRLTSAWNWCHQLEKKSYYDAFVLTGFSGFD*
>TCRU_1722 hypothetical protein, conserved
MNFGRILLQAFRVRLMTASDPGIPLSDIRALLRTAVHEADAFARATQSLAERRGTQISLR
CQLCHVCGHDTSTRNVRSVARRKPLAAQTAVKKRQRSCPLLMKADDGSPIHSITSRHSAQ
ASHRAADAPSDLSNRPTQSSRRATELICQRRSTVARRMTDIPALDQAI*

>TCRU_1723 Alcohol dehydrogenase GroES-like domain/Zinc-binding dehydrogenase, putative
MATNAKGYAAPSAKAPLAPFSFQRRAVGADDVSIKILFCGVCHSDIHQARDEWGGSLFPM
VPGHEIVGHVTSVGANVKKFKVGDTVGVGCMVDSCERCVECKRGLEQFCVEGTTSTYNSR
ARVSGEPTYGGYSDHIVVKESFVLLIPSNLDLAATAPLLCAGITTYSPLRHWGTKAGTRV
GVVGLGGLGHMAVKIAKAMGAEVTVFTTSEGKREAARMLGADHVVISKDPGQMKAVKNTL
NLIIDTVGNTHDLSPYILALTTDGVHILVGLPENPHPPVSPFLLLKGRKSIGASLIGGIP
ETQEMLDFCGRHGIVSDIELISIDYINTAYERVMKSDVRYRFVIDMATLGQ*
>TCRU_1724 ABC transporter, putative
MHAFRESRLLREAVCLLVLVLLPSCVWCEETGVSPDVFLSWYKKLLLSEPSRDPSGLGFR
SFMSMAAFEESDDDKCMNGGIMRNGDCKCPEDSNFTGLRCEMCQRNEVCAAQLDASSVCQ
HALAIRGSGTQFECSLNSPFLSILGGGRAIEAVVALNCSTEDGTAFAAGEGGVCSLTLFR
IEPHREFVDPFFHCNTSECSMQLVVQNKGNESNDPLKPSRAFKAVVLTGQVVILTICALI
ALLRFVSSTLGYRRKAKIVVGLGVSLTISTVLFISVMLILMRSEASDVYAVYKCKHTECH
CSKDPPEGYDPVCSKSLVGNKILPLIRNSIRYACNLRTRHCQLTMEDITLMFDLECNASE
CVDTKKFPNEPKMVQPETVQAQRDLLFILTLVLTVVVLLITAHALWLRSASRKRAAEFVR
MFGLSEPQPQLEKRCSLDVASDSSGTPAKTSLLEKREPQQQNRLSLRGDSAEEDVSSNGT
ESIGLSFHRQPGGSHTSDARRLLIAMPHEADRIEYFRRLTKSPFELQLMDLAYSLPGSRF
ASKEETRTRPLLNRVNFTVRSGEVLAILGPSGAGKTTLLDLLSARSKQGRTTGTISLNGT
PVNTASAKSIKQYRNIIGYVSQEDTLLPALTVHQTIEYAARLKLPQAFSNTTIKSIVRHM
IEALRLQQCEHTVIGDGSGLRGVSGGEKRRVSIAVELLANPRILFLDEPTSGLDAVSAKR
VMESVVELAKESPMQAYAPHYFAFKPIVIFSIHQPSQEIFELFDKLLLLSRGVSIYCGPA
CIAAETLEKRIERIVGGAKSVPRSADHPNHAEYLMKLEDILDDTTRMEIQAEDVSSRFGM
MQHEGTEFFREPRENNGTNGVSECEALVEGDDILRNASTLHVYYANVYQQLALLSSRAAC
CLISSFHLLLCHAAVTACVGGLMMVLYHDQRLDLPGALNRAGSITFMLLVVSFVSLSCLE
QLVVERKLFVVERENGFYRTLPYLLSKIFIDILPLRIVPAMVLASLIYFPMGLRVDDGVH
FFWFVVIVVLFSICITLIVLCIGIITGSFGAAALLSSVFILWNFVFGGFLVQSETVPAAL
RPFQVMSPFFAAFEALLVNELDGQACTFSPTDETGKPSSTSIPIMCLQYLSNIGLKPKRF
NTDVAQLAGSILLLLFTAWLLLAKFTSIAR*
>TCRU_1725 hypothetical protein, conserved
MQKTLFPAPKSNDYQWRNLYLKQYGICTYAPPMPQNLEVMTANALRLKSREKIDDNNISA
STQTVSLDSEEMEMIEASGSRHSAPSPSRRKGGSVSTQGFRRSFLDVQRRSTVGDFLESL
SDQQLFSANVFSFLSQHEGEANSSQLLRNPLGLDAPSSLRFPSILRNSQVNASNRTAFPR
GSSVDEGGKLVPDPADDLLRLQRETWQLLMDNRIMLWFEREAKKRGRIAAGVQRRLLEVV
TWKLEGQKKTPNKKPGEDKTSNDTAIGTTEEGKGKDGAVKIIPMDSEVEEDKPELGEEEK
LMQTLEQFAPFFAVISAPEVIQRMTTSLLVAKKRGRRHEVPRMVGLPLFSQYNTWRETYE
NRVAWSLSPFSFFLIHDHSYNHAHISALYVLLDLIGSSFHLHTAECLKNENKRQTAIDIR
QRRIRSAKYSLSNVSLCPLNVAQRLTEDILLAYENSTARTTLSMALCVQEFLTELVLDPD
TASSFLSNAALRRQCGTDIVVPGNDAGVFSATSKKNENSFESMEDGTKNEQQEPTKDEAG
VMPAEESQFIDWSSLRKLTDTTFDELFSLVNWFVDTPTANSLISSEARTRNDSLVLANTS
PARGKKGLTSQSLAFNTSLLQESKKSSQQQALSDESTVQSKESGYIVGYVREYDATMTIV
EAITRHELQRQRMAETRSGEQRQRNSVTLAHRKNRRKRLAASRTQTYNDSAAVPDLHAGA
TLLSTPLTFITTYIRLHGATWLMELLERLFSILRRESVLLYVNGLEMEAPRQTSFQGSIS
QLSLSGDRSNDGVSGFGPEVGCWRNSGQKRATHNQRLELLEDLICQDIQYVMGEFCSALF
GKRSVTRLPQGISTLLTNFCTTVHLHLLQQHVSFDITHDKPAIAVRKCLTEMRQKRVTGG
GTVNMWSQNKPDSIERLIRNIEGNRLAKFILFDCWILPTLNNAVEFGYISEEASNHLRWN
LDAFARYLKIVLNSSFSNAENADVYIHTILPRRTSLQSQRGRTTPSVEKKGRAQSEAPLA
PRCDIVKLPPLINGVYDIVSGSLMQLLRDPCDDFVDDSHERFTFGDGSSSVDFPSQKDAN
TSCSLKDTRKCWEDLSPALSYLNESLGITSGDADVEVYEDEVDVTPVRILNIFAARACSN
TSTKVVVTEYEVAPSIAAACISKTFSLVSGEHPIVRNAYLSGALVGQFRSSPYLTCLIGV
LLHPHTASRFLENILHNNRAFYNALLQPLQDENLLNLISPLVTTRNQLPLVDSNELLSLI
AAIPMHSTDTGSCVETKAGDSERKMRDSLTTRETKMKNLQLAAWEATTSNLLQKRARATT
GDILPPAVNFHPQIRRIGPTDSYQSLRATAEILTREMGRAPLCFDTWWRAMVVALTVKAM
NVIEECSETKSMQWENWCNSQLHEMQRESRGLCTYFTKNKGKNIDISKEKALSYTKVKSR

LGSSVLSSVTKVPSARTVEEQKKVTKGKKRVHSSLKKK*
>TCRU_1726 hypothetical protein
MSFRRGSAEEEGEKVMGAEGVPAYASELADAFACKLREMEALHYAAELDTLAGMRCVQMY
AEVLTGLTALGRMRWTTNGGATRDVE*
>TCRU_1727 Aldose 1-epimerase, putative
MTIISSENAKEYSSHVEPFGDGHKITLKSPNLRVSLLTQGATVFSVQYRVPQLAGGDVAD
KDGWVELVLGLDVPEEFAKDKLYIGSTCGRYSGRIENGEFELNGKSFKLLQNDGENTLHG
GPEGFSSRPWKYILLEGEEEIGISFHLISPHLDQGFPGELFVTATYVILKNEPATLKWNL
QAVLAASTPAQSTVINLCNHIYWNLNGVPSRPRRLPEPITNHHMQLHSGYVAEMQELIPT
GSMKSVEGTPHDYKKLRAIREGMEATQAEGRDPPGYDDPVALDKWDSKLHEAGRLFSPKT
GITLQLDTTSPAVVVYTANYLPENASGEAGERFQRHSGICLETQYFPNSPHIPSFPSTVV
SKGEKYDETTVCHFKYTPKS*
>TCRU_1728 hypothetical protein, conserved
MNIVTSYFVVKRLPGSIFLGEASLRHRDARQEEYMECIRRNAAHAEVVSLHILIEGTEAY
RQFRQRVMEDDYFFQSKEMRRKIVPVLWPEAQPTYADLFQHANKLLRGKLTMICNADVYL
PQVGASVRELQKLFDSDPTRRLSVALTRYESEDRRDAPLIEAYRGSHDAFIFRPPTEASF
VESVRHPQNCYKAENIVLYELQRHGYVVVNPCRSFMLVHHHTADLRQWLPAVDEERYARA
PPCTIAEALTMLRQTNRS*
>TCRU_1729 FtsX-like permease family, putative
MRNALYAPFNDTQNSSDTSRPDTRLIRQHPNNSRRLHDSPSEPFFSGSFREKSGLSGRGF
FSLCAILRLSCLYTISDLIHRPRNCCIGVLAVVLLVLFSGAVLLGIWKVPYVLLRLGELS
AGEMDMVIMGGSVDLPFINYTDMGPRIERSPYVKGATPRWIFRGEASKHKNVFTNDNDSV
SPLTEVARVNVLLIDSERERKIGIGRAWGHRNTGFSEAHVFYSLLDYLNVRPNLGDRINI
QFSPKPLLQDDMRSENETLFRIEKPILGNDVNSILLYNFFQTNGITEKSISVWDVLNFDI
SVSVVDGIYSARGKYPSALGNIVIVDYKQLIPAFAEQSCSFGPQSFTPKRGIFLPSTMDM
FGIPTMLSQFNILEKVPTLAVTMTDRSNIYYLPTEDRTKEMVERSNVIMRQGVGLDFNGT
VYFPLSEAMDSFDMLKIILVSSLTCFVIGIVALCALLFYALLNTNAEERRFEFAMIRAQG
LNKTHLVILLLTQSLAFIIPGLATGGAFLVGLNALIESLLSRFTAATPRILFVPLIPLFL
SLGLGLVLPLLTGWGLLSRVLGGSLRDALDVYRQVSNETKVVMVKLEEMGISTWQLILGA
FLVVAGFIVYYLIPFSFIFENMMLLFLLLNLVLVVMVVGICFIVTVAEPYIQLVFLWLMV
WGNEKRLLTIVKKNLYDHQSRNAKAFMMVLISVGTIISSGVMFVMLSNASEDMTRLTNGA
DINIASSAFDVPLDERELNAFLEKRRGLYVEQWAYHSFPLDNYPQMVHSSRIGTIIGTRN
PMCIVAVSEHFFNTVFPEYIMEEAKDSRYSYKLTVDGKYDLVRSMYERKPLPSGTVGQII
GTGLPFGVELPNILNKKTYIIPALVSSAVRDSMGTEVGGSMILEYNYRVSDTIVTTRFGI
EPRGLMRRVSGFPDISPFPNKLIDSEVLLPRSYFKTLVKPWAMDFGDNENFTLAPGTVTE
VRQKKLFVRLRKNISTKQRITFLNEIQAHLDLTFHSASDTHEMLKDLRVIREFIMYFFYF
TSVICISLCTLMLWITFVANVRLNSRTFMVLRAVGCRKGQIARIILYEALSIVLSAFLLG
VVVGAIVGVTLALQLVEVMVLPFRFTLPYELVCVLFGLSMIAAVVGSMLPFRTIANKCIS
SGLRSL*
>TCRU_1730 amidase, putative
MITEKITRQNRQCVPLHGICGFAPGRIPAYSNGSDSIFTNERHYVQHYFMGYKWQCVEFV
RRWLFYRKGLALPQYDFAAQLIHLREVQDVCTGTAVPCQFIPQGSEEPPVADSLIVYPGS
RKNIVGHVGLITHVTSTNVYVADQNRFFHDWGEDTFSAEFPLECVDGRYYIRDPDVECRG
WIVFPGRPNRLDGDPPLVSPHISGPPSLPRCRRIKYVAQQLWSWFTGRETLTFRPL*
>TCRU_1731 hypothetical protein, conserved
MRGTWREQPNILHPRHTGCSFFLPGDATRGQQRSDAPPAASPHDARDRLDPAACSLPDPN
VRSLLSRYRLENERLRDQLKAHAVQEALLEQRLQELSARNTALHLHDFRKKENDAVVEML
KKQLEDRECEVRDLQLQVKEQAGRIAAFEEAITRPLHGTDESPSPSPSPAAAAAAAAAAA
VSVSSSPPLSASSLRTHELLCQVLSSVGFLTRVFNAVKHCQTLPHEGLGCPRSRKECTAR
CLRAAMRGNQETVGDMMGRGHGVSCEALALAVREEVMFCELSAVQIAAQLLAAEHAPAAV
LAVEEAQKETPPLPLEDDHPTATITKIAAAAKEGKKEGEEGEEKRELCAARSISTKEQNV
STVFTAPRATRKPTARPTVNDCEVQ*
>TCRU_1732 hypothetical protein, conserved
MSFEFAFHDVSNDAIKHMTPSEALQKHLENAQLAHRVCVAKALKAEEAPVEKCALTWGEV

LIRYQAWAEYRPPFQDSVAQSKYKKYWTKKRQAEDDKNPFK*
>TCRU_1733 retrotransposon hot spot protein, RHS3, putative
MVLASDEGWPYSWNRKENKSTHDCYVNCEVDRVWQIVKGDLIAWLSPHGGTDCKPRRRVL
IGTPGIGKSMAAGSYLLYQLLHCDAEKLQVVVHCFGGRGACVSDKTIGAVTRCSDEEMCV
SELRSLRGHGRNVYIIYGVAKEGTPPPRHFAPTSGWGMIAVSFPKVANYDEWAKQPQAAR
IIVNCPDEVDVKAMRAWMTRDETKEKQAERWKEVKNKCIFWDRFHVTSLMRRRLMNAVER
*
>TCRU_1734 Cyclic nucleotide-binding domain/PAS fold/PAS domain/
Protein kinase domain/Protein tyrosine kinase/Kinase-like, putative
MWRSSVHPLVETFGATEISLLEFDVIGSTPQRSVENLRGHIRSLVDSVEKEATLVTVIQL
LESERQGLSEPSTTTVDTRGGDNNNLSPASSLMAKLSFNYESHPSGGEAPPTPHNSNWNS
VNTAGRELPSQQERTREFVETEDAAHVAERAEAKRVNEDEMERAAELDGCPQPPPPLIAS
RGEPLVSYGRRAAVSAESLPLNVIRSYSPPVVAKSPEEERIVRAGVMACHLFSNMDSKDQ
SIIVQALKRVTFPAGTDILKQDGASVEKLFLLTQGSCDVIKNGKRVHTLLECSTFGEMEM
MYNLPTCVATIRSVTNCVLYTLDQYTYQNIVLAASLHKREKYEALLSNVQFLREFSDYDR
MQIAEALVTKTYRQGDYIIRFGETGKWMHIIVEGEVAVVGRNIGKKCEILRLKEGEVVGE
LEFLFNDLTVADVIATSRRVTTAQIKRKHFELITGPIQDKLKEYIVNSGRYTHYLGGAKD
RIKSELSLLGKRSKRMATNAERENAFLHQVDVNGEIILPVPKEKVFAVEKGIVLDKENNE
RVNVKDAVSGPDVESSSAHVLFRFPLMPIHKNSLAVIALCEDGSILLWNERMVRLTGYTA
EEAIGQHICSFLLETKDQKTMHQAICDARHYTGDTEGFFDAKGGVYRRAYTFARMDGLTK
VQLKLSVLPSIVSHGKDAAEIVLAVGEETNTESQQVLDKSQLLMDQISSVLSDGECSYED
RLHRIAMVLNGFELTCRAMLASTEHVRVVNIRQMIGQVMMDYGAQCVSSGVAVRQRFEGL
YAENAYLNAKLLPECLRYAMSNCAQHLDDVQVTITAKITENNGMDFLEIEFHDNGPGFPV
DLLDEIHEGRFSEKYAQVPRVRAAMERQGGSMIIESVPGNTNVRFIVPFVPVKERLNDML
EHHAKEFDNSMSLSCVGSVTQASGNTSASSFTLQSCRRLPVWKQNFTTVVVEDTPAHRNM
LCRFLWEQKHAVLPAYKLDDIEQLIDVVDILFIDPHQSIFGETNDTIDPVALLREKARRM
AVVVTGVDMDGESAKAYQTAGFITLKKPCNPIQALQCIREAEEMISQYKMEDERILQTRE
TLSKNSRGAWKRGKLLGKGMFGEVYEATEVLTGGKMAVKEMKLNRRDVQIEQFVNEISAM
CNLRHPNIIHYFYCEENKEENVIRVFMEYGSGGTLQELLKNKGNLEFKEYQSLLRDVVEG
VAYIHSMNYVHGDLKTANVLLSAEGKGKIGDFGTARRVRDGELLYQMQGSPLYMSPECLA
ASERDEDGVLIGYSFPSDVWSLGCIALEMATNNPPFSHLKNVTGPAGVMMYVTNLHDIPD
LSPLFDGPPSIVEFVSACLNPDPSKRATAAQLLHMSIFSEAPDEDMKSALKALKRAQLLH
VLNNFVAFQEPVELERRKSHPPYRYKVRRETEFCDSSTEDKNPAGEEGEELGENYGETGG
MEKEEHAATPTARLYRPSIFEKSKNNHPNMSSTGKGIPPDGCSHKKSGSLVRNSARAEEE
AFFESSLSSFYSPDNEEGGKEASAAPAEEGKGRESKTVITTSKRSSVCPQSPTQVTWREE
FVSSFTEKFGFFPLEHCSVDFMGNSMDNTRVGAAVDVDSQDGPQKTPKTQHELGPREREY
RARTLQDDAGLLKRAFVQPFKRSSQRSSLFKFSATRQPKRGVKNMFLVEDLQVVPERKSQ
DVSSPHASNFGTTPPSFIHYGSVPRQRRFAVAPHLASPSPVMPTRATEENTGLFPSFNAS
TEVYACSPSPCSSGTRKGVFSLSRELTSLQNALSELLERLKDIKPMEVERRWCSQSRQAA
GGMFSQKTSECREDETCKVDSVAALRDLVGRIEGEFMSLKSQISAL*
>TCRU_1735 Cyclic nucleotide-binding domain containing protein,
putative
MFDHRQTLNEELLEEAMECADRSPSREYGDSRPESTSAAAATSTTSEVAAVKPGRRIARV
IEEVMRSIEGRARAVTRKKFWHEEESFETCSSRMNHNAEDGIQMYRNMIPDPVIIKGLPT
HDEKEMIAFLQNTEHFCLLRHDEMREVVHASLRREYLPGEVVLPEGGHAPHMYIVVGGEV
EVFAPNDGGTDSPQRSTRAHPSPPKTQKKWSCRAGGTYCFLDAAQKEDDLQQSRVFHKEE
LCPEVLPLVEECEAMTHCGKVKPGMVFGLDLCVLKDASPLRYVAGITSERTVLALLPLRA
VQQLLGKSPCFSQSVGRHLGEGDIFIPVREFCRYVFMPSAAMNEYLPLWTILDRYTKIEN
VIHTKLKSNTIDTAAWSYALNRLPENVTTTFCFNLVLALPPFVATRMREEAKKADVRHFL
KFGKNKSTTNRTAITYIRTKERRRCTWHLGMEGKTLVLLRDGYTDLLDFLSMLCVHIIES
NKLRGRVQGLVHPPAIDILDEYLNNREADESAGVVRDKALELERIQEVLKNLPLTKEEQK
GLLDLWQTDCLVKIYEVMMHREEFNVRVDPGVSRKFQTNPFVEWALNLRACIMQKMGLNS
HWVPPDDLCIDIVSSNTHCIKNLLSSFHRKHRQAIEEYARRDKRLGPLESWHVEEDAFYA
STTGLLSTERTDLMDDYAKALEESGIMVLVDTAMTGLQVDIIPVHALNFETIDTVLQESL

KRISGCQGRLDSKSWLQMCQPRPLTKKSTDEMSSPFLSSPNHHSRLDRHFIINMDFAFGA
QAEGICRAIFSVFGRRIRSVNVMGKAGGLVGKRGDIQLPKEVLMSKSSLIVEDSQDELRR
CRNQGLTAERLRELAGPNVSVHEGRIVTIAGTMLQNVRMLEFYKCIWGCVGAEMEASFFA
RVIEDFFRQGIANRELETRFAYYTSDLPLASHASKRTTGVSLSVPMTVKEGVPSLYAIAR
GILENILLPR*
>TCRU_1736 retrotransposon hot spot protein, RHS3, putative
MWRCCGWLQVVLLRGRWALTASPTGVAVRLRGAPTTEPCECHAQRHWDSGTKQPRVSFGA
SGTCWPQLGGASGMPHRTGVVMAPRHGSCDGSDAAARHVAGSRVWPQWTMSSTNMRLSDF
LWNCVGGRRPLMKDHNVTMEVFVQEPDDYVQDQRLLEEILNVTAHQALEAITKPLHEGVL
SLGQRRDYERKGYDHSSCKGNTKQSTHAGTDRSEAGGRGKAKTNARNEIYHFH*
>TCRU_1737 retrotransposon hot spot protein, RHS3, putative
MYEEFISALVKELKELPPPSPSKPRSSVLKLNHQGHPTRTVGLGELENGVTRIPMEYRVM
YKPEAQNFPLVDGFFFVDSPRKTLVGLQMTTAGEHHTIPSTVNLFKNNMAAYFKGWKKLS
RDMSWEMIYVQHENSTMITNWQRCGPVNTKNLSDAEKEIVAFWNGNVHEYQFALTTDFVN
KIRAK*
>TCRU_1738 hypothetical protein, conserved
MVPNASKKRSSFANGPRILVASNASGIMSVTYGGREHVAADNTDKVSERSATGHKSLLSE
NGVAGSGFVAEGDAGGLTQRNASGHENPNCENSPRSIPGAV*
>TCRU_1739 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MGEGQDGPAVNLEASARSGGNGETAEETNGQEEKQIHPHDGEANATALSSSLGNVAQGNN
SDAGAMRESGLLPLLLLLGLWGFAAL*
>TCRU_1740 Mak10 subunit, NatC N(alpha)-terminal acetyltransferase,
putative
MACDLDETWVECMGEFKEFIGKTGNPWRCYTCEGVEKETMLSAPEVMDAKTDPGCGYGSI
CSLNCLLKDGTIPSAATLTGEALLDVMDLIHLKELNYLQGFSLTSGCLEFSYFFCMDLLK
EQNLTLYTYCRALARCIDLTTRAVMTMRVRSDEEFIPWFKALDPGEDVTEEQIMNELEEA
ACKAESVAIAARLRWRKLFLSILSGFILGSKKSDTEKACATCQEACDLLGSVEFRREAEP
VQDGRFFRDAEVGYWASSFTPTKPLPCAPFAEALQTYKTLLSQLASLKDLYILPSLQCIT
EFVEALGARKPLLLMRSVAVILLFRHDPSESFLHGPSMPHRILQELADEHGAPLYLKIFA
GDEEMLEGVLRYRIQKTMDSSKIPPDQLIFLRQQTVDAVRSWAAEMSRVYLVHLEAMLCN
RGLAHRRLMNALPHLGSLQELSYTTDKSVFLSHIPSASPALEAEAAKRMPLLAIYVNQHV
LHVIQLLVLLTLELNLFTQAELIPALWYWNFTQRAQIENLGLLTPPPATVIPETRINRRT
KVPLYNLALTTRTSGHPDTVRLTILEAERMIADAVFVAACIMEAKGLIDLTSPAKHSFMT
VENTFNHRMKCLQHIRSPPFTPYARCIAAKPDISTKQNADTSTVFLYAQKASEIAVNAAE
ILKQLIASKELDKARKRVIQTHVENMERTARAVGASLASFATVCDNDEALQGYKVSVEYP
FDPAMLCFTFRKKEAR*
>TCRU_1741 hypothetical protein, conserved
MSDDRSLRRTLLPWGRMTQAAGRTAFRLSLSSHLDPLRCHLAPRTAALPVGPHRAAAGSL
ACSCRAECPATEHGHRHFPVPRLAAASQSPTRVPVATGSLSAMEALRLGSLAVHDGVTEE
ISMMPLSLADRGHTVGSVFSPWHCGIPRNVTADADAVVARFLPQGCVNVWHVDCLTAGKR
RNWKGVREKKEGAHTA*
>TCRU_1742 hypothetical protein, conserved
MISMTFANGLRLCGLQCSMEPRLTEASRQRPDILIVGLDTYAITDVTVTYAGRVTAYVSE
ESMEEADALRAARDRLTQKRQKYRYWALANGLDFEPFVMLTNGAINPASRRWLRRILGAR
VLAYAGAQWVAERQ*
>TCRU_1743 hypothetical protein
MATQREEYRALVTGSHYTNTTACLERAHSVEWPTTPATDPRQDPWLQERVPTRRYLHRRE
WPNWLDASRTVMLGYNASAPDERSRKQVAIMDLVRHHLRLPENPRSR*
>TCRU_1744 SLACS retrotransposable element (part), putative
MQREYGTDHTGNGSERAAGTGIGFRATYQKRFEATTHVFNNGGGRHPMRIMRVGLPMEEA
YPSHAETRQEEPAVITLQPEKRAPIHLTQKLLMQQYLSTWISEEHVRTGEQRARHYPKWA
MTATKSHKYGDAVALDFGHWDKQAMGVEEVPFVILLPHHNGTAEYGLVGLVATNTPNHVV
AYIPSARRKDTEWVMIDGMVQKCSGSP*

>TCRU_1745 hypothetical protein, conserved
MSDDWPLKRPASLCDHVPGSAALQLDSPDSRAPCGPHRAAAGSLACTCRAECLATEHGLR
HFPVPRLEAASQSPIRVPAATDFLSAMEALRLGPLAVHDDVSKKICTAPLSLVD*
>TCRU_1746 hypothetical protein, conserved
MASYNGDSRCALGTHPHTLPCLSFGVIAAGHCCERDGTTTAPPLEKVPRSVGCGAARRFA
CSPTDLTAQSFHCGHSVGITRCGGVRKSRSPDVDGVVVAWQLRTSGPSLFRIALLLDWRS
NSPAWFFCRSAGTGVPQRQSSLAAVTSTRPAVGVPVAWPSWCARPCRASACSLWHQLRGD
HRLPRVPTGQPQHVSGEPLQTSTAIAHAALFASNIRRLGPAAVICDVNSHHELRDGRSPS
TAAGDDLAAIPSNIDAELSDDPAQPTRFSGRSVSFSDVTVQRVLRVSHWTSTPLHGVGLP
SAIPHCGDGGRPPATGRHAAATETCRRCSA*
>TCRU_1747 Concanavalin A-like lectin/glucanases superfamily, putative
MKLSYTADVKWVTEIKNKITKSSTWEPNKEYQVALTLHGKKVFFCIDGKLLGEEEVLPTD
ETSLGPAHFCFGACGQKGRNEEREKEDVNSQKMLDQNSPVTVTNVFLYNHPLNFTEMTAI
KDRVFISTRGPESVAGWKNGEKANTTEHAVVVSLSSAGTVGVCGCVRNVRPRF*
>TCRU_1748 Endonuclease/Exonuclease/phosphatase family/Endonuclease-reverse transcriptase, putative
MEPFTWLPAERYFYPLLNSIGAHQRYTYRLRAVCDAQRQKLLLSGDIEQHPGPIAVIQMN
VSCLTPSKLATLMAQGADIIAIQETWKSSEQIASMHTGDYVLYAQSRIGKGGGVAVLVRK
TLRSKRIPLTIPQHDTSLEVVVVQVALDQNRDLIVASAYMRPPPQVTQSFRRLVDCLPAS
SPVPLCGDFNMHHPQWEPFLETSPSEVAAEFLELCTDAGLTLVNTPGEITYARGTRERSC
IDLTWSKHLTVSNWSASVSPLSDHYMLTFTLHQAFKDTIPSAPKFFYSWGKCKWDLFIKD
FDSQLPAYDYKKQSTGIKAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEQSGLPRTARP
AIYSYRRPTVRQKCNGQGVNSFSYSESACATRIYAASAI*
>TCRU_1749 Reverse transcriptase (RNA-dependent DNA polymerase), putative
MLLGDGQHTYKTARRAANALNRIFLPFHPSHKAVRPSKGINRQSASLNINASFLFGQQNN
NESSATFTSGSSLSSSSEPQDKNEAATTSGVVAHLHSPLDAPFNRTELLAALRNTPYGKA
PGPDEVYSEALRHISSKGLRFLLRCFNHSWTTGTIPAEWRRATIVPLLKPGKSPELPGSY
RPISLTSIVSKVAEKMVLKRLLWVWTPHPHQYAYRSMRTTTMQLAHLIHEVEHNRNHYFQ
VSLPKKSGIGNQLRYRPHRTLLVLVDFSKAFDSIDHRVLSRLLANIPGVNCRRWLRNFLC
GRYAKTRVGHRHSDRRPMLRGVPQGSVLGPYLFSLYVHPLLNLLNCFAGVTADMYADDLS
IIVKGQFREDAIPTANMVLQKLHAWSQENGLAINPSKCEAAWFTLPTHTESDYVREGRWP
LVVAGCQIPVMTMGASRTTKLLGMDLDQRLTPNVAATKQ*
>TCRU_1750 RNase H, putative
MIPRIRHRRKTLLVVTDGQSLLAAVTKGPLSQTDWTEDQIWQRLLTLTRAGWSVHLQFCY
GHCGAHANELADQYATQTMESGQYTEHGIAPLWHTDLLTCFTTQLTNKWRSTIRQDTHRY
LLCGTRPSDLSGKDLITQEVLHRQELVNLAGQGAGNLSSGADYTGP*
>TCRU_1751 hypothetical protein, conserved
MEALRLDPLAVHDESTEAICTVLLSQADRGHTVGSTFSPRHCGIPRNVTADAGAVMARSL
PQDCVNAWHVGFLTAVKRRNLKDAQEEKEGAHTA*
>TCRU_1752 hypothetical protein, conserved
MRRGIPRNQGSFDLGSGKIRELFVVSKASCPRILTNRGARWGSALAVFGATDQSKIKAPS
GFSVKLLGIKAAISDQRLAVIHASRKTTRSLQSVRLRIS*
>TCRU_1753 hypothetical protein, conserved
MVCQCGETQVQMTFINGNQLSDETLTVAASPTGLCLFHGPISKAWQDSTLIGHIANLRAP
QIPNFETQALLPAMGAARELGHQQGLITAERERLNFDYANAVADVQNRNAQLNLEFQEAH
INPSVRESTIAGAGNQVLELRQQLEAARAQLREREFNLGVLTGQFQEREARHNAQQPARD
AETAGRDEASATRHAANDGVSTIPHQTNILMAGGVPSNAA*
>TCRU_1754 Protein of unknown function (DUF3682), putative
MASGVLGENGSHMPDGCNKTAITVRLRSVLPITAVEAANEEVSDTSQHANNSGSDTNTGS
GGGEGGGSAAGAGGPSASPAPPPTGGTEGSVGAGDSSVSGGSSGNSTGGHVTGGISSDSS
ESPSDPPAAPGVDSSARSSGGTAGSSGNNSSNTTGDSQTEDQTPAAAEAHNSSPPEGPAG
TTSGTGHTQKEEEEEENEKQQQSGEAQVQQHQQHEHPAESGEESAKDKNALRTNATANTG

DSDGSTAVSHTTSPLLLLLLVVACAAAAAVVAA*
>TCRU_1755 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MPSPRVQAALQQPREEIKAQASTAEEPHEEEPRAAASTAEASIAGKTSEAPVAQATLQQP
QQESNAGQNATVVESANTEHFTVDSNSHAVGETTGDAGTVRGSVLPPSLLLLFGLWGFAA
L*
>TCRU_1756 hypothetical protein, conserved
MAMMRTGRVLLVCALCVLWCGAAAVMCDGGAEMQGVEGSGGSQHVSGDPDGRGGQGETEV
PFPPESDTVIKSLGVGDGRDPKQLNGVVVTPPANPDRKEEEREKEKSKEEKVVAEQTENT
VIPKEDEKISQLKSMSEDEGETAPLAAEETPPASTGVTSTAQNGNSPEDLTAIPGKERVL
PEDHSDQPQGGKNPADGLAAKMSREKGEAPEAPPSPLAKNEKHEVDLKATTNNEKDSLEN
GVSVKKTEVLLEDKEVTSNLRKEGLASTTGNQESDPSNSHAESTPPSNSGASNASNDDAD
TDTNEEILNNDSAAGGAATEGAHQGENKEDNTKETTPLRSAAMINETAPTGDSDGSTAVS
HATSPLLLLLLVVACAAAAAVVAA*
>TCRU_1757 cytochrome b5-like Heme/Steroid binding domain containing protein, putative
MQKARRVGAGKIYGVIIASAVVGFFVRVLILSYNKRSDASDWTWGCRFFGNRAKSTIRPV
EKLECRGFTKEELREYDGIQKGDIYVSVKGVVYEVAPQFYGPGQPYHAYAGHEISRCLAK
SDTTAKEANKNWMHDCNEEEIEALEWWAKKFDSKYPVVGWFVADEDFYLDAQNNTLQTM*
>TCRU_1758 ZFP family member, putative
MPPKKRSISKKKKKEVLPDPNTIPNGECDYYIGSWSHYQNIDAISDIAHTVLNQHTSADG
EVGELPRTNILIPACGLGVAGSHYGVEVTNNIVVESVPRTSMKNAGQLKEAGVAGEEALE
PEETVEEKQDVDKSSEVNEPDVGASLSACDVIVHGTVHIDGIVTRIVIKPDLPEPPVVPQ
TKRTSSTKRKKSAKSIEEEQRRLAEAAKIYEEKVNAAVAAAREEEEYRMQYAHPNRWSNV
VFTNITFTGQVIVSHAHVTFRNCLFSARVVDVAQLLVTQYCQVECIRCTFECPEKCSMYG
LPMGKLTFQKCLFTGNPKTLPSEKGATDEARTLRGKAVGLHTDSCCVTVEDCQFKDLETA
ILLRGSHPDATAEKPAMVVRTCKVENIFGSGIVLENVRGVELMKNEFAQCDYYSLDCVKG
KDIRVFQNTFLSEVRVQRHAHVKLMHNRSGTVPLALKEVDNPNWQPVY*
>TCRU_1759 Retinal Maintenance, putative
MSDVDQLIEELFPNGGTEPHSGLNVRSMTHEPPASKADWDASDEERGDATDAKIVSVKPQ
ASVDAKKNFISDPSKSYFDESDGEDFGPAGTVFTFAVVPFPFFPSDLGGACVEKCFVTNM
GSKSLPHPTIARLLLFAKEGYSDRLTQIQLLERKGAFYALDAKFGNGASDRYAENMGCSG
GCPVMVCRKCNYGVIRLQGAAWNDGEGRIDLYLTVRNYYPDWSRLANSFPVGKAKGAEND
RVLGPSVGCAAYCCQCSWLTVKSAQEIIETRLSHTVGYVGKEDSCCFATQLPLMQGERRR
PPLWVCRGHMPHA*
>TCRU_1760 protein kinase, putative
MLADVSDSNRRRLSSPHVENGIPLNGTLLEEARTGDTDVRNISNEKTNPGMWGKANGALK
RRKPAAKLAQTRVTVGMHLKRWIITGRLGAGSFGETFTAVEETKDCGDGDEEDETADNLA
VSHKIRTSSSPVEVCIKVEKENKNVLRIEAAALKKMQSCPQVARYLGSGNTGGINFLVME
RLGPNLAELRRSTPIGTFSHYTTLRLGISCLRAIRGVHQLGLVHRDIKPSNFVIGLGVTS
DPQTCYLIDFGLARRYCRLNGEVRPPRENAGFRGTSRYASLASHRQQELGRVDDIWSLLF
MLIEFATGTLPWRKYKEKEEIGRCKEEVIGPGIVQNLPREFRPFLAHLQTLHYEDEPNYD
FLLSLLERAIERRGYPPDKPLDWEHENGTVYRVDFREEENVLKSPIRQTSTVAANIAVAR
ENPLPRPVPVEYAFRKPLDVSIVPAPEAVNININRPTLAARLMPPSPQSEEEAVEQGLVG
VSDVSLSPGISRRDHLDNGNHTPVCAGTLPWNYSRVTPNPGGATFVSANKQGVGMENKRE
DHGRDEQMLAENMELIDSGGRFSPREGASPMINDNQADKGAHLGSLPLEEMAAAQYPTPE
LMSPQNQRQQKQQQNLHRGTRKKVSFAKDVDLAGNGGVSPYREEKKAEKAKRGINCECSA
M*
>TCRU_1761 rhodanese-like domain containing protein, putative
MSVREAIGEKNFLLRRTPANPKYENVKAVVESGMTAEVARLMKRTGANTERHLGECFLRV
RPKTLAEYILLLKRQEEAKSMGNSDGGFAHPMDEYRSPNARPPKEYLILDVRSEEDYRTC
HIEGSLHYPKRRLVHATNPFLPEMFEFKNKDNKCIVLYDLEEELTVGQSVGKILFEKGVD
NLAVLTGGLREFVQDYASLIVGKCPVPIVPRDNRLLKRAEALAAARSETQRSMFTHKPKS
LSNSLAKPRR*

>TCRU_1762 hypothetical protein, conserved
MADGGAAAAVPVGTRPAARHAPELRAGVDGAADRLWWSVGSDAEQRDVGAQRDESVYRPG
AGCARAPRLLHWCRRDDSHSLRRCGGVWRLQGCATWVFHHRVQHAARRCQRPLGDHRRCC
GCDGCCRGGDRRAGLHPGDAGTRRVCENVMRLGAGACEHRCAAVLPVGVRCP*
>TCRU_of Trypanosoma cruzi region 5/Dispersed gene family protein.1
Dispersed gene family protein.1
MRFPSLTYVVAHAMHLGIFFGSVFALAMPGARVQHYVIGVVGVLYGVAFPAGVCYLIARH
TGASFTKYWQFSRKPLHERLLYPVGYWHPAAQQRMYGGMLTNMKGSYVYWCVFQLSVLCV
VGLIAAVHPPVGVCHVLYFCMAAVLLAGAGVVAFTNMMRSAFLTVMQTASFVLLAALCLT
SAANHLAPSDGGARAYAALLMLLTTVLLAATVYCAVVWYVEDRHWQELREPQRGGLDALL
HDDEESDEELRKHHDRTSSSYASGSAGASSYRPPAPPQWERIIGSNEGNPDTIDRQPQPL
AVDTHSNALSFLDHASTTSGSVNHAIP*
>TCRU_1764 Tryptophanyl-tRNA synthetase 2
MQRTGGARAGNQHRTRGGGTNGIAPFFRRGIVFSHRDFGAALDCVRASFATGTHRAYLYT
GRGPSAQSMHIGHVMPFLLTRYLQDALGLPLVIQITDDEKHFFRDIPVSGERASGLVVEN
IKDIIAFGFDPRKTFIFRNTVHMGDMYPTVVQVQRMLTLSAVKNTFGLKDSDNVGKAAFP
AVHAAPCFSSAFPRVLRRLAGDPPLKCIIPCAIDQDPFFLLARNVAPRMKCCAPALLHTK
FLPALKGAQFKMSSSAEGNGVITLHDTEQEVRKKVRKAFSGGGGTLEDMRAEGVNLHADV
AYQLIRFFCPDDNLLAEVTSKYSRGEMNSAEVKDLAADVVVRHFLSGWQARRAGVTDADV
EHFSGIRSILL*
>TCRU_1765 protein kinase, putative
MGCSQSKTRTKEWGGPQQRRRSPLKNPSERHGEPVVADAEIPPFSPDKELVTWYNAQLEE
GRRIFCAPPAALDKSPLPGTPVGSSHTKKKRSFPENVGNDEALTLYQVSPLNHVIGQGYF
SRVMLADMTVQSTTADALAKNGIEAHLHPRKDLSHMASPGSTTANLLDATHSASRKYLIA
CKEYALAGDSAFFIYNQLRKEVKRLTHLTFNPCLLKVLHMEAVYEDSSTTENDTGGHLKL
FKGMASHFAGEGLAGGSKKHGFRKQGDRSSAGNSHKIPEKVRIYMEYAKYGTLRNMLLSE
IPKKFGKTYMHELTVRAYLREVLIALAFLHENDVVHADLCAKNIYISDHITNVYTTCFPA
YIADIPAGKFATVPAEWVRRVLALMDPACMQPQYYSGEVDKVHNDSVMTHLGWLPSVEAS
GMQNHGDTEVAPAVPTTRVEEEQGHHFHTITSGHAVASAAAVAENSYRQNNADENEAEDD
RCRWVDEGVRMYLQEHSYNDDDNIPLPSPLSSLEGGNVFMSPKLDGVKILRNGSFSRSPL
LPSIPPLLLNQTVSGEYSHNTMKRIMSSMQNSSTSACPQGDESLKQMNPDALAVNSGHHE
KHEGFLVRSPLARRSRKPLIKLGNYGRVRPILVGDSDKDVHKLGRVTHLAPENVQGASFT
SASDIYAFAMTFIELTTPNDGLFADQRPTDMEPPRTRQGKSEYDAAWLANIKRYLFKNDN
IVPLPPQLSEECKAMLRLCLQYDPARRPTAVELLQSKYFLLGHWVNVATKNRKIEAPWLD
TNYEAAAEAAGLPRLPSETGIYDVGTLLRVRAGGKKKPAKHI*
>TCRU_1766 hypothetical protein, conserved
MVMYDPAAPNNYRDVKVMWWKRAREDERKNDISRSLAAAAEAGSSPFDMPDMMRMAPRDE
LAYDILGGSGDTMSLHLSAEELHQRRVRQSAALGITTAMNLEREELEAAHKARVAAGMDR
KGRIGQKLGKLMSVAVTRENATKTNTTSDHVGDGINTSAGEMTPATTMATSTTTSLPGIT
APLVFQRSELAAGGYVVREDVGALEKRKTHYGKPSSTILIRFVRDGPPVEVFDDTSNKNV
GSGTLRNAFLENIQDLCGQCGVVRSLRYMVLDDEKRAALRARLENEREEVSAASADVETR
LAREMIRVLVRFDTVANAFKALEMLQQRHGSNWDVCFFSTQLFDVGALGPAEGESLCCA*
>TCRU_1767 Serine hydroxymethyltransferase, putative
MSKSLVEHDPDLADVIEKEKERQYRSLELIASENLTSRAVLECLGSCLTNKYAEGECGNR
YYGGTEYCDVIESLAKKRALQAFKLDETEWGVNVQPYSGSPANFAVYTGLLQPHSRIMGL
DLPSGGHLTHGFYTAKKKISATSLYFESFPYKVDANGVIDYESLEKISEVFRPAMIVMGA
SAYCRDFEYVRLRALCDSLGCFLFMDMAHTAGLIAGGVLKSPFPYADVVSTTTHKSLRGP
RAGMIFYRKKGRNGEATDFERRINEAVFPGLQGGPHMHQIAAIATQMKEVCDPAWATYAQ
QVVKNAKKLAAALIARGHRLVSEEVDNHIVLWNVRELGLTGNKVEKLLDFVSISVNKNSI
PGDKSALAPGGVRLGTCALTTRGMVESDMERVADLLDLAAKLCVSLQKQVGPKIKDFVDA
MRASELACQLRLEVEQIASSLYIPGLDLGTMKYKGGIPPAA*
>TCRU_1768 TPR-repeat-containing chaperone protein DNAJ, putative
MFGFIKNFKGSLVVTALLVALLAVGNVLCTGVHDDEVTKQLLLAGDAALRQGRSQYQEAL
AKYTEALAHNPSSVRGLYSRAELLSMMRQREECMQDLDRLLQLDTKHHRGLALRSSLNAQ

AGHLQEAIRDVEVLLPLYKEMKKSSKVAEYEEKLRDLQHYTSAWLPLRKKLEAPKHSAGD
ITESEYKTCVALLHDMIRKFAKDNVGMRLQRAECALACGDNQAASEELKYVVQKEPQNLE
AVALAARAYRALGAMEQARAELRMCLSLDPEYAACAQLHKLVRGQMRITKAITEALDAKD
YQRALQQIDEAEGLEENPPYKDQLLLWRCTVTVGLRDTEKGLSVCEEAIEFLGAENPASF
DVHLQKVDIYLMQDDLKSAEEQLQNARRLQPNHERVNEYRQRIENLKRVAGRKDYYKILG
VKKTANDAEIRRAYRHLAKTLHPDKLRSQELSAKERQKADERFRDINEAKEILLDEKKRE
IYDSGEDPTKPSGQGGGQPFYGHPFTFHGNPFGHGGGQQFFFRFG*
>TCRU_1769 PX domain containing protein, putative
MSKWASVPGENDEFGERNEGSGTLFSCSYVVHIPPPVSGPSLPANAIDIVSITLPHVRLA
PDVTQKVVTWYEVLVRSATHQWSVLKRFSEFVELYKAMEKANLLQLARQQLERTIAAPPS
RFFPSQRRQQRLEEFVQSLLQTMKDLLVSLLCSGSPETEVVGDFSRQTASLVTGSAFSIF
IRFLTTTSYNALLVSALAGRDSTAHMTSGATTDCLMMDERTHVPPAKIVHLPKQRFTIML
QLPGVSISTVFVECSEDSREIVVKGAWNNHINGPDSVLSGTIDTLGSLSVTSSGGLAETV
LFTDLCATADTTEVLVDTFPVGDFQMEFEVPPPFAVREWESQYAGGVLFLTWRNDAFNVS
NPTKNT*
>TCRU_1770 tyrosyl-tRNA synthetase, putative
MTAQKPTEMTTEERYALVRSVGEECIQEEELLNLITKKPNIRCYDGFEPSGRMHIAQGVF
KAVNVNKCTQSGCEFVFWVADWFALMNDKMCGELEKIRIVGQYLIEVWKAAGMNMEKVIF
LWSSDEITRNANSYWKTVLDIGRRNTIARIKKCCTIMGKQEGTLTAAQILYPLMQCADIF
FLKADICQLGLDQRKVNMLAREYCDLIGRKLKPVILSHHMLSGLKEGQPKMSKSDPDSAI
FMEDTREDVERKIRHAYCPRLRQKKAEVPEDGAPVSSEEKNPVLDYFQHVIYSRPAASTT
INDTLYKTYEELEEAFVDGTITEELLKDALALELNALLEPVRHHFACDPHAAGLLEKVKS
FRKGGQTPPLTDIGPFEQSETPLAVVWLPTVIKLSVNVAVAISDAVKAFLEQHSDGEVVL
LLPEWTAFSCGEVTGEEKNISAALELNLALLQATYLRKEWVRVVRQSQLILDNPNDYWVA
AINAGRRNMLQYLGDVCGEFKAAGDLVAALMYVADVAMLKATHIISAPHERGYHEVVKKF
FGGRVTAIPAREGTVPPLHRPEALVAGADDVLFLDDTDMDTRRKIKKAYCAPNEAANPVL
SIAAWLLRERGTLTVERAAENGGNVAYTSEAQLRDDAQSGTLHPADLKAAVTKPLLEVCA
VSKAVLSSAEGKKLSQTLRQAEKTLSKRSK*
>TCRU_1771 emp24/gp25L/p24 family/GOLD, putative
MSCFPRSSCMFLQLVAVVIVLTVLDTAQAVRVRSTAQDLTLEVNQEELCMYSVGIDTNEG
AMLHYHVLHGGDDFDVSIRDPKNKTIYVSYAGEHELEDRVYFTKHLHGEYSYCIDNRPYS
GSRKSVTMSIGVTSLKRWKDRIDPLTRMMLRTDSFMLGLHQDQIIFRLRQRNLHETIEES
KTLLLLQGAAETLFILLLSFLHVLLIKHLFARKGMRAVA*
>TCRU_1772 hypothetical protein, conserved
MLRRVFPVSRAAVRGPTLALTAALRHGHHAQTQHDFSGCFLRKLTREEEESLRVLQDNRP
VSAVVPGKLFMRHWIAAEQSTVSVVNRVMSGIISVCLMLWSCGYATLGYNGHNCAHVAGW
IFIAFWLVLHTHCMAMIPLFSLIALMQLVLN*
>TCRU_1773 protein kinase, putative
MEKFTKVRQIGKGNMGACALARNNEDGKCYVIKQIDLRRMSKKERQQSLNEAHLLSSLRH
PNIINYVDSFLLKKSDHLCIVMEFADSGDLSARIKKSYGVNFRESQVLDWIIQLVLSLSY
VHQRRILHRDIKSQNVFLTSQNILKLGDFGIARTLSGTYDQARTFVGTPYYLSPELILER
PYDHRSDVWALGVVIYELLALKHPFNATSMKGLMQRILKVQYDPVPKLYTTELRNIVPRL
LNREPAHRIKLEELLELPILQRRLQEWMLTDVMPKSYIETLLQQNLLPPAIAALRKFNAK
GADVATAEVSALVSTGDAPQGAPSAPPMSAVEAPLLPGRSERISFSVVHRKLQPVEQQNP
QQQHQHQHQQQQQQQQRRPLPPPPPPPPQLQPYSGPMQKPPPDPSYLGAVRMPKRTQPVY
LMYKNINGSYNSAAVPGAGRHGSRVSLFVPRQITSNNAIGRSEPTQAPQLGVDGAKHPSL
SPEPPHGHVDAGGAAYIPASNPFSNRTSSNANAVGGPSYKNQTDTDAKEGGGQQFVEQRA
RKRNQQGSSAVASCLNPFFRQPSIGSSPLSCVPGAPNMDIKAMLQRAALERAQRRAFS*
>TCRU_1774 hypothetical protein, conserved
MEEDWSGGGGISNLISLEEPTASHLPCSVRFRVFSDPVDNVAAREAAWRSALPNSLCVHK
RRRLDEVSTCEREAVVRPLLRVLRDPIAMARRRFETLRWFDEPRAADDICARLELDRRLG
VTPSLAALHQALRRLRSLRRTRLIADLAEDLVMDAPSISVYTLLLIVEGLEGEPQRAASF
LFSLTPLVTNGTVPTSVWSSLCCELDTVARQMPSPLERCIVDLFGQLFYRVREDGPVNGS
IVVYYGQALLKSRAPIRSVVAFVQTELLSGRNTPPSYAVSELRLSAFLSDLIQVLSVRPN

GGADEREEGPPFSARERLLCCSDLVKHAYAGRLSLSQAAFDMLLRFCDEEQDYNLLCILF
LAMCALSTPTLISTARVAEVLCDVEELSHHFAGVLGQPIPMWMLYIIVRHGKSSLFTPAH
RKKNNRKELELHFCDSLARLCARDGDASLCMDVFDAIVEYGNPAGAHVFVCSLTRAMGVT
QRLFGGPATTIDVAALEPFNLETLYYALGTDAVKLEEFRFFIYERPSAFLFPSRKGSCVT
LERALSVLLDSPQVYSTVLDVSAVCALAESLALAEAFVKMMNGYAAKSGALAFVPFDVCA
AIQLTDGGRQLLLSWLANHHWLIMLPLSFTLQRLTGVTSSAMSIPPSLRQQPCTFLFYAL
RRVGHAKAAFVTAASPAAELAKAEGVHPVITVEELKTRLGLR*
>TCRU_1775 WD domain, G-beta repeat, putative
MAVPTEAAKEKPPLHAYPEAKVGTQFFSHHGIYSERYNGVCALTGSIVLMASGRYVMFVD
VVSGKIMSTPGPENGGVGAVAVHPSRRFYVVCEKLPEDPLIRVYTWPSRREVGQFVGGAT
RGFSACCFSADGTMMATVGMYPDYSLAVWNWKTRGMILRNKCYGSDVYTVLFSSFDSGVL
VTGGAGHIKFWSMAKTFTGQKLQGVLGKFGRLEISNVPGFAVLSDGKVLSGSENGLILLW
EGDLVRCCFVREIKKTAVDGAAALAVQTYDYWPCHEGTINVVELLGDGRIVLTAGEDGYM
RYWLASELETAEGEGAPPLYEPKCLFEVLVDPHAHIRALTLCRDMDEWVVLDSTGVLWRV
PFIPPNVILGSSPGRTKEPAQAALRFNGGGITSAAISPIDHTVVTGGEDGTIRLVDYVTP
CEVYKLMMPASTTVVALHFFRTDKTGMKFIVCCENGTVGLLQRGNKAFALLGQWRPHTEG
LTAMAVDREERRLCTISTNGTAFFFDIKRDISLLEPIGFCRLPLKDVRCVAWDDATSCSL
VGCECGKVLAIRAPKMEEMDHTVSFEFNCIYALVGIRQKKKVEKQQVKAATAGRVEGLQE
EEEEEEEEELGPWPVRLICPLPSGSFAVGSGAAELLYQYNLNVRYDNLTELPPLPPTGIE
PPNYVEEPMINLCYRELIPQMASVSTSGLFLVVVCEGAQVILRPMEDNGKIPHKCILTAA
AHDRVDGRITTACTSFDDTMVVSVGLDGLVVAQIREGCRAPSPPKIDAVYPSLFAEEVLA
PQPIPLSISEQKEADDRRLAEEAKQRELDAFLAKLHVVHVKYAELLAENEAAPAHQRLSD
EEMALHPQILKEMEEEKQRRVKESLYENALQLTREEIRTKKMRKRFIDNLIYDRFQVISF
SREFAVSSFRTPNPEETIQRLKGEINELLAHDANEEAIFKADENDKKEGNNDLSKTTGMN
TEGESAEGKDGLLSTASGISQWLLAEEKKWQEKVRMTRRESELLTTTMRQYLNKMDERRE
ERRRRKRGYEILLTYKPDPAVEAAQLEEEMRNEVARRGECILRTDPSYHLTPSAVSKLRQ
LIGLEEMMLNLRSGFTKKLLLLRDEKATLCKSLNVLLHRIREINDVMKEENTQSADVHLL
PIEMPEQRFAIDRDGLDAFVRQRQLEKMREDLAKKAQRGFGADLAGTQTSAKNELVTTVT
STEKGEIQKNTPSQFSIFETPSSGHCRGKNQTVTSIHKASRGYSTAVLAAAAVRERMDYE
LRVKLENVKLTEAEEEEQQMERQRLVAERKRLQCRVDSMMHAFDQRLWKLYEERAELDAD
LCLADARSLLMLHEYQILLVFRQKDRELRLQYEETKRSHEERNKEMVELQKGIGEQAALI
EKLQEKNKAFRHEGEYFIESNFPAEHVPYVTKVFLRQIKRRKHLGDVASDDDDITSDDDD
EDVNEDDLWEEACPSNCSADRWQEVLAMREKRLDYVDAISEGRRKQEQMQRRIEEHKQLS
EELNNALSLSLQAIEDFKGEKRKQLNMLHTLVALRCSQVQCLEEDEKCPDTFCRDDLVVV
SDHALAKLRHRIEELAEEKRDRRTNLKEMKLKLQQLQRERLAKQTLHAQWEEKVYEAMLL
KFGRIVNLELLESISGCREVEELKERLRMEELAWEREIRKREKKILSLRETLQSRLVHNT
HLLHDLGDQEDDRQEVERSLSQATQKVVSRMYDGSNVATAEDRRNLKFLIAAQQEEIDAL
QAEVSLLRSKGGYLYTPSPSFPT*
>TCRU_1776 hypothetical protein, conserved
MSIFGEPLPHEDDTATSLIRREGYPPLGSYDQMPQVYVCPCCSAINPSHERDHLLRTAKE
EKELERRRIMQLDIFDERAKPISTAAPRPRSINIHHDPEDDELNQPVVPPPPMTLDELRK
LRQEANKTRLIVTVHHGKNLQADPHDPTSILVRCGAFEGQTAKVPRGTGTICTWEELFEF
PYPNEEEPLEVLVIDDELPADQDHILGGIVVPPYALRNRARGDEDVLPVCREGEMHRGYG
RMKETPLGSIVVSWYVKYDGQETEPTDGKQNLESPVDCVFVVHRIFQYTDNGTTPFTGGV
LCVLRDTDDNCSASTQYQPSGVANMSTSPYYTKEGFNYLPEPPSQIMQLITEKRLGHVLV
CVPKSDEEGEENEELLVVGAVPLDFGELYRKGSAVLLVESKVKEDVLWGEIALEWCFTPH
ADVQRKLEELQLAEESKLEHEALKDKEMPPTSGSLFVTVVRGLNLTNCEGRPLIRAQVSV
FSGDMEGSTFVAPREVGEDGLTNVMNWNQEVRFIDLEGDPSEITVYVIDEDQRVSSGTFA
VEQDRGYAVVKMHDPYDEEKQMGELLVTYNRHCTTEDAAAKVSGIQNGEANKVNGNGTRR
ISTRERSERSPGSRSHQYSNDDIYERDNENEDNINDLEGYEYDDMHKGDKKHSDEEQSRS
RSRNRGYPEEKEDSRRERSGREGRERGYPEEKEDSRRERSGREGRERGYPEEKEDSRRER
SGREGRERGYPEEKEDSRRERSGREGRERGYPEEKEDSRRERSGREGRERGYPEEKEDSR
RERSGREGRERGYPEEKEDSRRERSGREGRERGYPEEKEDSRRERSGREGRERGYPEEKE
DSRRERSGREGRERGYPEEKEDSRRERDHPEEGLRNAGAGDNIPGDVVARESGKREPVQN

ERSREGDEPNYYGGYPQEYLSERVLKSGHDDNEKQEEMEGQDVAASSKPPRAVRTTLLED
KHRSSRGASPPNGPASASVPSQPHSTPHSDWSQGDTGFEPRGGKTKVGKPPSRPEQFSVP
KVPTVRQPWFPAGSTGNEDHIPLEKRESFINRTDSIRDLERRSRASEKSSGRHVSRQSTT
HD*
>TCRU_1777 hypothetical protein, conserved
MLLGDDSFTREFLVHVSIQDKAPQRLQLKVRNPLSAEDMLRQIGRQLVDPTTSCSEKVSL
RRVLPDSHLFAFSAEENCFVPVDGKPAAVLGNFVHLLVHPLSVLPPLGPAAVAPSRNSRN
SGTRCVSTPLNVDASQTKKGPLQHAQFRVRESLSAGKKQYGAHGQNGCSALQPAEDLLTQ
PRDERDGLDEAQKRRKLSVTLEVMLKVMGHILSEYSSRASDDVIEPTEKHLWNLIEDASC
RSGGVPTPSLDSVAVDAFVETVISSIHRGRLHRTFGSSTHSRPSAKNM*
>TCRU_1778 Vacuolar protein 14 C-terminal Fig4p binding, putative
MSDTLISPQTLKLLVDSKVESRQKGARDVASKTAVIFVKYPLVEAYDIVTRELREAEASL
LSVNSPMHRRGGLGAVRAIVGSLPSRTHPSEVVSLLSSIIFESFTDVDATVRLAALEAAH
ALVRQLRIQLLDVCFMQVFWGLASCINDHDGRVALLAGEVSLSLRELITGNESFKFQTEQ
FVNFITELLEPYSNTTNNEKTFDLLVVNWCVEWIGHVLDLPGDELILLLWRFLKPLLMIS
GRCGGGEVARLLQKCLRDTKDAFYRHMSVQLDSLLLIAAECVEGAEVAVTRKNALEWMLE
LLNIATDELVHLIGRVIMAFLLQLGSKDLETRLAAQNVNHRLMQLVALKQDGVKNVPHDA
VLKSVASQLTGRGNEESRVAALEWIALILHTDAAVVERGFSETFETVLILLCDQSAHVVH
KCIETLCLISGETNFDYFVSRLVDLFHAKADVLLPKAPTIIKQLQLRYQGEDLSQCEKLC
LKISSVLSVHEDKRFLEKVVITLSTLVLTSREFLPLREILNRGVDDERARTTFVGMYQCW
RYNTVAALSLCLLSRAYEHAFQLIQFMGSLEMSAATLLQLERLVRLIESPIFAYIRMSLM
EPSRCLPLVQTLFSMQLILPQGSPQHSLLYRRLKLIPSLVTLERESQARGVSKKESPIDW
SQLLELSREAQRCISDFERRLLLQRLGDTGLP*
>TCRU_1779 mitochondrial pyruvate carrier protein 2, putative
MSAANATQQVIPKAFPKILHRYVGRPRVFECLKPYEKYYVVAYLNSVYNAAPLFKWSLSI
VPLYGIFSGSVPVEKVDFNSSAALSITGLVWFVYALLIQPQNSGSRSLALVNMCLASVNG
YNCYRSWAYKRVKALDS*
>TCRU_1780 hypothetical protein, conserved
MKRCSLCCSSFQRLPFGRRSAAGGINLNKGLLSDRERGDQFTDPTVYRNKKSIVAMDKVS
RKTERLLKEEKQKEGMNALGVDSQMERELSDGSMHPLHREEIAAARVIDEDGLLSSDPGS
KYTTALRRLMEREVDRRDHMMDKFGQPPTAKEFHRLFTRLRHADDESEAIERHQTRLVEE
YGVYPSMRLDAYMLDDDTYFPGWVNALPYSIRDRVKYGSLGLTEEDETLRVTLGRMPLDR
RRQEWERQKKAREYKAAKEEMLTLAELRDARQGKRRFHWLQRKRQKRASMLRRLALRKPD
AFELWPSTVVDYSQRIAFIAQHVENGLDTKGHWPLDPEELARARVRRSQEEAERTFLLSA
EEKKVLKKGNNNGSIMHMLRALDTPEKPFKRLSRKVYANRVNAIVHGDQDEYGRKYRKME
NRAKRRMRPYESLGEIAISKEVRKEPRLYSNGLNHTDDEHWPKHVKSWADGMPSTRYAS*
>TCRU_1781 hypothetical protein
MPPSKVLLADGTEGFLSKGESYCSVTCFRGTVWALRSCGTYFDALDSRDGELLDSVSLPE
GCETIRLAANKLWLLTRTGNIILYELSGVLIGVLNADVGRIDSLHTFENDPSFFATSQKG
AFQTWDLERMAVQRVFPCEGADVLAVFPTRFGTSLLTVQEDRIALWGEEISHPMCVHFLE
SANSAVLVCSQHNAAYADTCWVGGNQWITVFHVEEKFTQMLSLKKERLIPCAKVQQLVSI
SLTRVASFDAEFLVTIWDSCNCVPVRLFKVDSAMGIGRGTSSPVLFLTGVARVATIWVLG
GNILLSWADQEFDDDRMQAAASEMAACTVIRSENAQICKKYACLLEMMDTYRKTVVDIVS
SPNRDRASMAATISALDKCFGEQMTALRSEDDRPRDMVGGNTLRKQVEYWREKYMVEKER
NRLLLSDLRLAVDRLKEVGPDSRVDSQLLDLLALNATSQARESQLRSRVLHLEAQLHKLD
TTDSHNNDFPTHDSQSNSDPYRTRVIELEKELHCALEASEEAVTAQRGIANITDALGEME
RTLHVERGKFATLTKEKSLLERETEKMFEALSYLQEELKKAIWEKDECTELLKRHQLEAE
ENERRASLLLAETKEELHLLRQGMEKLEENRHLASTLSIRDTEIIGLKRQLEFVKSMISI
RHEEGIAASSAYDAMMDIIQTMKHESPITFLLNVLEDIDIRLGHLSSSTRKWMERDDQVA
ARDDEIRVLKNRVQSLESSILRVSSLFQHIPYTIEDVESLLLEVNEYRQRYGRNEEIEEL
VALRLLELAAGCDGEQVAENAA*
>TCRU_1782 glutathione-S-transferase/glutaredoxin, putative
MVLGKGSIGRKLLGATGLIGSLAIGGGYFTYQRRLKENRSCTAEEFNAAQNQEELSWALS
HLRNPKEHPQILLYRYSTCPFCGTAKALLDYAKIPHECVEVEPMFKKEISSFAYKKVPQL

QFNVHGYNGPLVVDSEIIVSTLAKHVGMEKQLKDPEVVKWREWARGPMVRLLTLEFNSSL
YRAWCGYSYINNIDTIPYANKLFLKIVGAPVMYLVSQYITRPRLLKSGHLHEGEDVKGRL
HGEINTFIEKALLGGKKKFHGGSKPDLADLDTYGVLQSVRGHRVYEEIVQSTPIKPWLDS
MDKEVGHVGHHG*
>TCRU_1783 synaptojanin (N-terminal domain), putative
MQAVKTPRKRCAVCVKNGHQILFLSIPKPVDPPAPIELEPLMFFEDTSPSETPCMKKIVA
NGTNKWEGGWVVVPLVVNGNGEMERCRGFGKGEFSSFREAYDFCGPFESLAEYPAMFGCI
LLDTIYLLVATRVELIALLPFGGVIHRVLGTEWIPLFIPGSVPLRLSTTDRSRLKEFQQY
SYERGYFYSDDCDLIYPFPFLPNSAGEAPAFHCDWSEQLRQPFCLHGLSAGCSVLIRGFA
EEKVVQLKNGSVLHMLLLGRQNNLNPGPRYLGRGLNGNNAAGNDHFYEYIMWRPNREDDS
ISFARHTILRGTIPVHWSTQIHRTMVEPSMIFSQNEEEVVRGCDVYFEFLFRQLVSLIKY
DTGTASSDAPAALAPEVRCMSLLRQNPQSGEGVLARYFLDAVRKSDALLRRLFNDAKLDL
VHIDWLNLVKDYGVDVATKIFWESAFEFLAPQKDDAVATVGLLRRDGRITRRNCQRRFLR
VNCADSLDRTNLGCFFTCFQASISMLNSIGIEFSQFVDQRPLPPLEGQEDLSQSGLSSLS
MGGNKKTISPPFVKSWFEARNPSLSPVAVGRALSELYVYNGDIVAQLYTSSAAMHSNLLR
NICGLRSTASNMVIATQRRFENVFEDRSKFRNLELLLGRNKDIHFPSMNQAFLTRPVPLQ
YWSCALVALGVPLSVSTADLAGAVQRALEEIFSLTLPSDQLSRHSSFALGFCISLAEDEV
ASHKEFVTAVSQVTFEQPPPMTEEEGNVIQDNERIAVIEFDHDRFDATSVQRFLREREIL
RVQNCAVTLFPYAYPFQGAGGDSSGLVQKAANSLRSGLKNFVRGLNK*
>TCRU_1784 hypothetical protein, conserved
MLTFTLHQAFKDTIPSAPKFFYSWGKCKWDLFVKDLDAQLPAYDYKKQSTGIKAFTRALI
TSYRRHCPRGMHKDGPRLWDDTLMEAERIATDSKARYLQLPTPDREAEMQRTRSQFFLLL
RERLRNTYLRRVSKLNPGEPLAWKYISGRKKASLPSPTSILLGDGQHTYKTARRAANALN
RIFLPFHPSHKAVRFSKDINRRSASLNINASFLFGQQNNNESAATFTSGSSLSSSSEPQD
KNEAATTSGLVAYLHSLLDAPFYRTELLAALRNTPYGKAPGPDEVCSEALRHISSKGLRF
LLRCINHSWTTGTIPVEWRRATIVPLLKPGKSPELLESYRPISLTSIVRLLGKWY*
>TCRU_1785 hypothetical protein, conserved
MLAFSIISDELRDESSIPTPADLGTSTPPSVASIHERWLCSAKASSLTLRFSLISSSSSV
IEWSIGSSTPMVARRAEAANQGGMELRKNRSSRGELSVMP*
>TCRU_1786 hypothetical protein
MQRRWWTRPVDGGGVRSGWFWRRWEHRLCWVRRLRQGHALLRARDGDGEHEERCVRVRVR
QRRVRRGVRACGSSRTAARCGHRVECVRPRELDGAVGVRCACRRERGDAAPRCAGRRESC
ALRAVDGARRRADRCAERVAA*
>TCRU_1787 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MAPDGTAVTPEVGGRSGEDGETVGGKDGQKREGEVKAAALSSSLGNLSQGNNSDAGTVRE
SGLLLLLLLGLWVFAAL*
>TCRU_1788 retrotransposon hot spot protein, RHS3, putative
MEAFVQEPDAYVQDQELLRRIINLPAYQALEERKILLEAIYKLHHEGVYFLRQWRDYQRN
DTLTPLASGKLNGVLTDIEEKENREAEERLRREEAETQRRAQEIIFTMSTNIEVVLFRGR
ARVKEMKLNDFLTLRFGGKGVMDTNRNVLLEEFFKEPARYIGDEGVLNEIKTSYPYLRME
WVLTEETILERDILKLQQSAGTLAAWSLAAEEVKAGVHDITKQTLDAALEEVRNPAATTA
SIKLEGCYESVYNARWHHVVEVPGGEGTGMKVHEGEPPQPWTYKAVGRTLEKDDGVEQSG
EARLRLMVLTSDKGWPYTWRRESKAIRDCYVNCEVERVWQFVKGDLTEWFINFHLILNPS
PLPRVLIGTPGIGKSMAAGSYLLYQLLHYDVERLQMVAYYVGDESFLFDKTTKTVTKYKE
GTRFTNIVKSLFWRGFKGYIIYDIAKDGCKPSANLPCDGWGMIVLTSPNEGNFSDWEKEI
KPTRIVINCPEKDDVKAICVWMRQYQSKQEQEKYWREVKDRMEDLGPLLRYIFIENEYKD
RNMLCEKAVREMTLPDTNHYLTLGTHKMWDARHVSHKLVKIVRVRGDDGELTLNSLISPH
LGSLMTCKLAQLMMPNDFILLILAIKDDLLSKTLERYSVFTFLSEGFINAIIPKLKELKI
KKDAPPHLCALRVRPHERPFKPLLLPLLKDFEEKINIGCRVLYIPEAKNFPLVDAFFFLE
SNPKIMVGLQITTAGEHHTLTSTVNLFKENMATYFNGWEKFAQGLSWDIIYIQHVDNKPL
TSWQRCDYVNPRNKTDAEKEIVAFWKEKVHQYQVSVSSRDFRRKEALPIVEEEQEQETE*
>TCRU_1789 hypothetical protein, conserved
MPLQSRSKCNRFYGREACNVKPPNIDAAILLGARVRVDVTAACDINGVTAAKRPCSFVRQ

SAGGPLHLPAPGMAWNPLEGWSRLGLRRARSNALLRSSYMQPEPQHRDKVRTPSLGPGEA
AVPPAVIRDPR*
>TCRU_1790 Reverse transcriptase (RNA-dependent DNA polymerase), putative
MDWPFMPCELGVAIRDSSLGSVPGPNSMLNEFLHRLRYVARGTLRTMIHNSFANGSLPGS
WKIEDNIRISNPGKDPCRPGSYRPITLLSVLPKLTEGMTHRRLSALLPHHPRQFGFAPSR
STLDVVTPVADKISRGPCLGCRETRSSVIFCESHVSI*
>TCRU_1791 Reverse transcriptase (RNA-dependent DNA polymerase), putative
MDWPFMPCELGVAIRDSSLGSVPGPNSMLNEFLHRLRYVARGTLRTMIHNSFANGSLPGS
WKIEDNIRISNPGKDPCRPGSYRPITLLSVLPKLIEVMTHRRLSALLPHHPRQFGFAPSR
STLDVVTPVADKISRGFNEFGTVEYERPGGGAHTKNPHHRSLVASIDFSTAVDTIDHGEL
FGMLDRLPRLGPRTKRWLNNSLRGRYVRVCSREQHSRKQITPAGALQGSVLLPQLFLYCV
DDLLHRMGNIYSASALMHADDLALVASGADIHAFAAAMQPSLSLTTTWATEHSPKINVDK
SEAAAFYISSHTRSGEEMVDLLLGNGNLRIQSCPVRLLGTTIDRLPNFDYARFHRCKEDH
ATPLSTAAGRTGWCVPSHHAILFNWISPRCVTVLWRDTCPMPCPHLPP*
>TCRU_1792 Inositol hexakisphosphate, putative
MPPAVDGKGVSGEGKTPQQSEGVARREGVLPPIRPVASAPVGRRRDSSADELLCLKKLLQ
KQESRLNERYQRITLCSESAGGADISRTASDLGDVATKPQGVLGNASLSVRGAHYNPNPI
LSSAPPTAWEQKEGETGAQEARDSREEDEDESELRRLEEDLNRHQTRINHIQNEMARLWR
KPHSHRKTALSPPTPLVMQVDNDREVLELATLVYKFSTFEQQKGGNRATGGKNSSQYDVS
GVVDPWRSFSSSIAFDPERSTTSMQLGRMSMRSSSVLRITDGTIALMESLTNQRDIVLPS
PSEVGVVRSGDVLSANHILVVDLQDALRSHKWPTGIISGAPYFRIVPRLNVAGVAQPNIS
AVRTVVNEVSRAYDGAFVWVNLREEPLIYINDQAHIVRERKEPLNPMIIPNVTGRGIAQI
EEKLKQEVLKEAHENGGNVSVHMEGVNGLMEDQWESADPHCVLTLQNVFDALRPNVIFYR
RPITRNVGPQPQDFDFVFNTCVEYPRAVIVFNCQTGRGKTSSMMLIASIVRFYQMCGHDV
SLDIRLLRSESRGFRFRTIRKLISLIPDGKLHEHRLMILLELIDKVYSITEHIHAAFYTG
TASAEEAMMHLQQYSYFLVFSFYCEQRLWNFNIKIPFSEWLAENNELRLIIASIQSMEDE
LREECIVAPIAEGEAAWAASIVRHRRGNVLSAGRILYTVPMLSGDSQHVNTLRQLAPDVP
IFTCGRLSESGRNLLMAEVRQYFPNEGNILWINLRAEPMVYINDISFILSDYDTISGNSA
ELASTMHVSLKAMEQIEERLRRDVILESQEHKGVILLHHIEGNGKRSTIRVKVRSVRTPK
STMADFATEYGVSYHRIPIPFAGHMLASDVDPFLEYLSKKGGKHDVFIIHDSEGSMRTTV
ALNMLTLYRASRAISLRRLATPDEFREVLRVGQGGVVLPSAQVVSSVAVNPDELPKMPVE
LQLAATICQMLTAGSLLRVVEAAISLGGRGTRWNILHMLNHLKVTMTDAMNKVKIMRNTV
CLVRTYLLVLLSAIYIDSMGDYCLEKPFSDWVEERTEVANIIANLDQRAEQSIKYVEPRT
FMKGSVPHHNGDVLTANCMLKADHFPGCQKKGLRPELCGAPNFRKVDTVNVYGVAIPTLM
GIHNILSLLGASQEPLQAYPGENNDKEVHMGFAAPRLFEPRFSPEELSKPLRGSVVWVNL
REEPILYVGDRPFVLRNLDAPYVNVELTGIAAHKVEQVETQLMVDVLKEATRHNGMFLVS
DEGEPGEIVGIWEPATRETVKTVREVYDELRAQGIRVTLLRLPVTDEQSPSAEDFDALVS
VLLPSIATHMDRRETLSFVFNCQMGRGRTTTGMVICCLLIGLVIPEYYDELNNRYDPLFK
PDDSPLSRGEYSCIVQLKRVLTGGRQAKLQVDLVLEVCAKMQNLRTAIESFALQVKSPDV
TESQRGRAHHHGVHYLRRYFNLITFAAYLQEEYNSMKKMMRSTYSSWLAQRPELTTLCDS
ASLK*
>TCRU_1793 hypothetical protein, conserved
MEFILDAFDSSASTLKAYYEQLQQLGEEGEDCDVKIDALRALHDCFVSHTEKMSFELDVL
QTDEEREADGIEEEVAELEAELLMLTQIAEGCDAGGHRLPFPACDSFQVYGAFATKLCDF
VAKLSVLRDAMQGFLSHPHPLETESLFHITCCGVTSEKAWAEKENELHAAWDVLEAKAGA
VAVTSSDSSIEAVRGLLDEVVALGGRVVDRVADLRQLWERREKVVKQLDGQQRRLVVWCR
QQQVNLDALSDPDHIQEFCASLLEHYKVMSSNYRVLLESAEPFLDCEAVQEKLLEASESW
LHLQVKALERLRHTLFEVHADTILEERVEEHVSFGLQVGPFLEELKNSLVATRNTNSVLH
DRSEQLTEECQLLQEIMPKHDELCKCLLQFANRMRIMREAYACYRAAALSRVTYLASSSD
ILTEAARRKEDFESCVEEIQAWVDHKAKDDSWRDVREKVRGIKALLEREQQFLDQDRKET
ESEEGAKKREQINVL*
>TCRU_1794 hypothetical protein

MSAEAPALPPNTTNGDGSQRAHMEDDVVPAQRVRLEGEEEFSIRLWAARVQYMEMARMNG
NLEGHHTPHGPVLPPGWYININDPVLLTYDPYFRSHAAKADAASAPLFSAKEGRYYAESA
LPLCRVEAHSLKSCPPAGDCLTDLNREALGNVSPCRTGNVVARRRIKAGEVIAMDVSELC
VVEDTLVWRFFPRSSASCRKKKGGRSGKEEKGPIKRNGVRCTPETFSPEIVAAARQIVLH
AHAIRNGVSTLVETGFAQLLASLLLWCGDIDLLPREEEVKTAFKSLETCGNFYIGPVTSS
AALRQSQRVEAFIERWCAVPVESDPHFTALRGAAMLLLQCIPPALLSCAQKDPTEAGGCL
SLQNGNTFVVPHYGFIRRMRLHSPDRLAQLLLGFSREAVPIHVPDLPARSGFFPFLRRVP
HECRPNSFVMFLDSPASHCYGKAGFFDYNTTGRHLDGETRAEAPVSWGFPCSDRVFLPSV
AVLVACRDINCGEHISRGLFQSVFMTQPQRSKIVRQLFGVPCSCRWCVEEPDVARAFRCP
QCPRNCGVICPVGDGSRLKEWVCLQCGYRPDVSEVHRCLDEEQELARVKADKMSGLVRLL
QADTVHYSHAIVFHKIDGWCQKAWQGQDASMCLEYLDVMQKSVHRVLDPCDPQVAQVHEF
TAQVNHAVGSAHTARYEYFLALQIRLRAGMRYAHWTRKTWFMAAEKSLAEFLDSV*
>TCRU_1795 trypanin
MPPKAVRAGMRKAEKVPPPCDPIAELSSLESIHEALKKAQELRNYFQVERDKVNEFWSVS
KKELENCRHAILNADAELEEMERAHQVEMKVYKQKVRHLLYEHKMKVKHCKEESDRLLRE
AEERHQKRMNEIQSQLTQHDRQFEAAMESHEMRIEDQRDSQNYMLTVTKKQKHEKDLARQ
TALYEAKLKTLRDELELRRRAEIHEIEERKNEHINALIKQHEAKFQEMKEYYNHITTNNL
EIIQSLKEEIAQMKKNDEHNETLMYDIDCENQNLVAPLEEAQREVAELQQKRKQYEQDKR
SLGTTRAKLRSLREEIWRLRKEHKDLEERYAEVHREREELKAKFESALRQAMEVVEERNE
VLQQKLIESHALVEERDAQLDGVLQAMNLEPTAIELIASEVDSTLKQKNQMIRDLHFELK
KGEKLVNTTLVELERRCQAVNIPPLSREQFLTARVV*
>TCRU_1796 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MLYTQRGYFSGGNKATALYLWVTDNNRTFSVGPVAVEDNMNWMLASTLLYSDGRLHLLQQ
RDNDKGGVISLSRLTEEVSTIRSVLSTWAQKDIFFSNLSIPTAGLVAVLSDAAGDGRWYD
EYLCLNATVTNATKVKDGFQLTEPDSGVIWPVNTQDDNVRHVFLSHYFTLVASVTIEEAP
TADAPLLTAVLRDAGPPYLMRLSYTADNKWETIVEGKMTKPTTESRLWVPKEEYQVALML
QGNKASVYIDGESLGEEEALSTDERPIDVAGFCFGACEMHNFPVTVKNVFLYNRPLNSTE
MTAIKDRIPVPKRAPESQADDVPQTVASAGSAAPGPREVPAAPGRTTMERATTTEHAAAV
SFTSAGSGLLPLLLLLGLWVFAAL*
>TCRU_1797 BNR repeat-like domain/BNR/Asp-box repeat, putative
MKDNKVFLLAGSTDAHKEGLEWKVDNQDLKLVVGDVTPSTRGEPGGRIEWGDPRPLFDSK
YSLNHKNRLNTFFPSGGAGVLMENGTLVFSLMAKSEENDGVYSMIIYSTNNGSTWSLSEG
VSSAGCRYPRITEWEGSLLMIVDCESSQRVYESRDMGKTWTEAIGTHDQESLRM*
>TCRU_1798 retrotransposon hot spot protein, RHS3, putative
MRDNFFPASLEKYALNAFLNVGFVTAIVTKLEELQPPPSSKPRSSVPTLNPQGYPTEAAA
ITELELFDCPQDLNYRLPYLPTFPNSPLLDGFFFSESNPKTLVGLRMTAVGGHHTRASTV
RHFTERLAAYFNGWEELSRDMSWEITYVQHADE*
>TCRU_1799 hypothetical protein, conserved
MRQIQQHRGGEGHVDEAQTTHTGIRIVHGADAATVHAADLRVLRIWERERPKAVRNRSRQ
TRVTVAASSAHTLTAADAARPRCKAHGVHSARTTVQHCHGSPNIELFLVIRYGKAYCLVA
HAVDDRARVRWWWPLARHTCDGRRVRAARELVVKYRPHTPIAERHAVVVGHVHNVGGAEL
VVAVHQPAAASHGQRGCHQHGKAKTESAGHNLQHAAAIHCNVPEHTRAFVHVNARRNPRA
VLYGEHGAAADKQVRRKSVHHVRLRPDSVIVHVEDAGQFHAETALHDNRSARTPATHQRR
PRHDKPRRQKPDTVQNKRGAVPGSRMARGSRHVL*
>TCRU_1800 tryparedoxin 1b, putative
MSGLAKYLPSTINLVSKSGTVSPISLAGKTVFFYFSASWCPPCRGFTPTLVEFYEKFRES
KNFEVVLVTWDDEEEAYNGYFAKMPWLAIPFSSRTELEALRSTFGVETIPTVIAVNADTG
AVVSTKGRERLLTDPEGKNFPWSD*
>TCRU_1801 paraflagellar rod component, putative
MKNSAAAATATAAASCGSNAVGAAADSSQKRLFNLLEAKSKERILRLVMAFRNSTPLEQE
AFAQEIGVSLPREEPQRQGPGPLTRQSLSGPALGVRSRDRSYVALADRLPQLNSTAGIAA
LISPFLTETSVSASFEKHAEDTAASHDESQNQSRASAPNAFSEDQNKVSLTSKGVMTNAD

KETYEEWKEVDSQAHTFFFRSRGYQALRLARGDENAPVTEDYTKSSVFNFTGIPIDEADL
WEWFDTLDVARSGTIGVMSFLETIKQLDRGFGVSQKAEEQWVRDVEALAPDGQLTFEKFA
FLVLRLAAQ*
>TCRU_1802 Etoposide-induced protein 2.4 (EI24), putative
MSTEDAFLPLRRIILGALAIFCAFAFGTLQSLDAVKLFSYLRANVYLRRIMGSCLVVNGV
FFLSIWVASLLFSYMWTFGETFMWSSDAAVIDNESGGGKAAATMNGIGLAGKVWFSVFDV
MWVLPVYALTQALGVRWYSALYTEAYAEKKRRASSLGVQWAAKESGRDDDMCFSGASQGA
EDSFSLRSVAVSLSEIMFKALVTAVYALVAAVVDIIFPFPVGHYLAFIMNSWLYAFYVFD
YRLSSQYLFDRRSRRHIRVTLSATLKFFEIQWAYFLGFGATHSIITAAIRSSWLASSWFS
IASVTSVLFGAHIVISVEATPAPRAPFHVPMFTPFFALCGMVLRMAVGAVR*
>TCRU_1803 Calcineurin-like phosphoesterase/Calcineurin-like
phosphoesterase superfamily domain containing protein, putative
MKVFLCILLLSLGFIWVCGVGEVLPLEAYENRTLYPVIPTYDRLPLLSIGVLSDIQYADE
EEKSRRHFRLSPGKVEHAVKEMNANRSHMDLVMHLGDTVNRDIARNLQVIDSILKQLQFP
FFQLLGNHDFLGLGEEHHDHVYRLLRMPARYYSLQVGEGGVFLLIVLDGTDLSVFATRAG
TARRAETNGMKHRYRHRKNMLDVNGGIGEEQMQWLRMQLEYASKQKMVVLVFCHFPMYPY
DDELNLWNDVEVVRLLSNYSCVAAVISGHTHRWEHEQLVVAHKNGEFTIHFVKFGGIVQS
PFTSWGFIEAYEKELHLHGLNFGRVFDYRLPIRGVPGGAVLRKTTRVLSSGPFIRRRRNV
RVISRCGGDTKWLRNIIHQPVPNKTVGRTENVSSLMWVECVIFLSLVVVIALLRLMCRKN
RGRQSKFVSVRSRGAVH*
>TCRU_1804 hypothetical protein, conserved
MYVVLFFVLLLSVLGVDAEEEDVRRNDEVVARLREELAEEGVEPLPEPPRELGVHAACVR
HGVGCPDEYVEFLESLQRTPHTFPETKPRNDAMSAERSGNMRRQTPLHGAGERRAYSIKG
EDAVIEVQLENMRRLRDVMRERLAKQQSPEQQWKCKEFLWISRGLKMVEAMHSVLLQKYW
NFVMNQLLPCVLLVFVTVWVFTGNRIPREHLRSLLADDPVPVFNEVIIRRKSPQSVAQLV
MERESHNFSSMVDIDDGSSSPSAVPNGFAKEKEDSMRAIINYRRDRWFATRFALLEAYHE
AHIAGVVLRLRLALSAAVLLMLCWTLFSLVLRASEVRRNSDGGIIQHLLVMLFPSWVTTS
FVLYIGWSWIGGMVAYAAWELVSTGEALVRTGERAAALHEKILERWCG*
>TCRU_1805 hypothetical protein, conserved
MTTVDQVVVYADVRDPQLLNQLTAAVSALCKDHTIHSPSTWNSADPLWFLNFWEKERDDV
WTYVNNKVPFLRRFECFVTDSKDQKDGVVAYALYYRQMPVLSLVTAVTGIKEKTEVNEDW
ITTALYCTVARMGCSSPSDAIAVFFTFPKSAGKVLALEGECRALVTEQCRLLRDYILRER
NIPVELVGAGGCDLRSSDLVGKGAATAEEEEEEEESALYASLIDDLLSNPEFLPLREVDP
QLHGALCALNRHHNLRLLRYRLQRGIHVILSRPMSFVLEELLRFCGPQAVPPSTMLEGVV
KSIQNFEHHWLELPRPEVILIRVTGDAATNGEAFAAPRWTACLWDEGQTPALDTLSSWHV
VTVGGAEGGHRQTLGRLHDGVRDAATSVLALAVMGNTYIEGGNS*
>TCRU_1806 Family of unknown function (DUF572), putative
MAKINATYSSGYYLAPDTDYRKLEEEQRRERKRKRQQEGDDNTGSSSASGAIRQTFAMPF
NIICLHCNRRIARGTHGYVNRRPTKEKFMGIRIWELEFRCIFCKGHIYLTTDYETAKLTG
GYHCSRNCRRGEGDFYGTNQINEAIRAKQAAEEAEKGSLDALERENEVMRQIQERERLIE
ELVESRAGTEAEHTRDELLQTIQARKRSKATCQREDDAKENVPFDEGEEEAYRLFEAQMH
DWQEEAERLPKGPSKSHAGDDDKVTAAIISRYTDHGSTRPNVFMGESDSDADTEAEKGVH
GDTTTPMEKSRGMPVAAGARTAAGRRKGSALASLLEDF*
>TCRU_1807 triacylglycerol lipase, putative
MEAVGENKTHVLAESLLAHEISPDAWQQAVRPEANSPAGQEEVSGGDGNQILFSAALASK
KPPGRLVAELQIETLSTTCGRIFLYSWYFMLLFALFLQSMVSLQWEMTNICGATQESLYK
LDKWSSPCVQSRAQRSDAINWSEFAVGGNLHDVPVDILQGSTIGEEEITGSVRNVTIIPN
DFGFRRQRTLRWVGDGQGMLLDLKLNRFVRVILSMASPRDQLPEGVNWEKYPLMIALEES
LLPSDDNESSSSDMQPKKSVFFYNTSTICYRSIPRCSSVVLPQTVAVATNESRITLTIFG
VDEALANVSAASAVGIFFQRAEYTMGTIVCRYVFLFFSILHLIRFIYRKRYSRTLYEQHW
VMFLHLALYLYLDPVFVAGIYETQGASVYHFFEFHVPTYFAALLSCFIYALITASMSWTI
SSEERARYRSLSESEALRETVGPCAVFASSPTLGTAGLAVGMPPVLTSSLQEEEERCPSP
REISRRASFSGLNEIRPIEVVDGAIPLWAKFSMANYLLAVFLLDLAQSYVGGWDWGTDMT
CVSFSCLYIRYTLYSLMLIFIIVCCVLLVQLHHSLGRRPYLETRPQQLACRVFIFVFTTA

LIYFVVQVILIAFLYPQIIGIVAYQPFTQLSPVIVSTFFVNHITFVYTTTVASRRVPIRP
ENPHWRRVVWSSEWYRWLNLHGGILYIFHNERQERYFNWVQNKGKNSTEPCCEANGTAVK
KKRSTREEVGEEANAGAAVLGSEGRTCEQRAAVAENKDGDFSSESSDTGASDNDRDYVDS
QTERPHPLRTPRTRGGVVEFLEKAERHLIDRPAILIDHLEGVLVDPLQSLFLRRRGRMPF
FNLETAIDCLNLSWEAYVATERQGETEGVADVVEFVDEPGAGPSQRSRHCGDSCCPLLGG
GDAGTRNNSDCDNDDGELHLDNGDHCDNHDIRDSVKGDSKRAESFAVFTGETPSPNSRMS
TEQYGYKQLAVVEVREVQVVITVMDTTLPCHHHKHPRLVIAFRGTDNLSNAREDLRFRRR
VWREVDPLRQWGIRQSAKVHTGFLRMWISLKETVLRTVKSYLSANPTEVYSIFCTGHSLG
GALASLCAYSLRRMLRLMNYPLLEVTVYTFGQPALGNRAFQKAYDKAVPRTFRVVNESDA
VSLFTVLGGCHVGIEVDIDRHGNYICKPMFIERWFRPTQGRGFAVANHTLFSYAQSLNAV
AMRNSGGSCKVRCLEPYVCAKGAVPDDTEPHLATPSPPSSSPA*
>TCRU_1808 lipase domain protein, putative
MSEHQHPSHHDHVESCAASSARDSAPVSFEGEPERDLWTTARGHEDHPSETFQQAWGENQ
ERVKSRVIPQAPRRNLYLSSGKTPPVEASKNGTYRSFNFSRHFSSEPVELQIEGLSPLVG
QTMLYMWYAVIIAAAIVQGMEFVSWGLVSICGEEVSDLRQYDKWNSPCVRTKLENATGDL
YTIRWEGGPYGAAFESATVRFPNIVMSLASPDDWGHETDSTRTYNIQAVIPHAANTDEIF
TFPLHVTCTRSSRRCAFVQLPPEAVLNETSSETRSLTLRGVPATLARVANESSVGIVFQR
YAYSLGIFIWRYIFLLISFLHLVRFIVYKKFTSTLYEQSWVVVLQLALFWYLNPLYALNY
SKNRPSLVLNSLEFQFPTWFVAVFVGFMLSAITASMPWTPPPHGQRHVKYNLLTLSGIKG
YLCHSASVYDPPLWTKCLVVVYILIIVALDIVGESLHVKEPLEAWGGGLPSTSYLLAALI
LLGCLVCCVLLIHLHRNMGKKSYLDSRPQQLASRVLILVFVTSMIYYTFHIIMFFLRYKK
IPGMSVTQPMIQLPAIMVSTILVNIMTLIYTTRNRSRLVPIHPRDKRWKMMVWPNTWYRW
LSRHGGSMYIFHTEAEELSFNWNQIGYRIRQHKAKVMRRKGRKGGTSHSRRAVAHGPGQN
SHHPHAEDEAPSEIPTFRSPQATPTVSVTTPYIETLESRDILNMDVTSTWFLPPQTCSPT
APPAIQQSFHSRLPSEERNGSESVDQNRVLRAERCHNIPNSPCPIDWRWEPQMSSSLPPI
APFRETGEPALFDAWNQPLGRQERASGLAESGNTVTSAEGRNVGEAEEEEEEEEEGAPNV
AARTISRAREKLDRIIRGAERTLISGPLQAFEQFETFLLDAAMRPFQDLEYLPFFNLETA
IDCFNLSWEAYGTSHRPEGRMEGRIVRCTPFSISRLCWLCCCCCLSPSSLDGLLRVPVED
SAEAPVGSETHPTENEDGPQIQRSPSGYNEPPPIDVERYGYRLCAVMEALDVQVVISALD
SPEAINNGKAPRIVIAFRGTMSMSNAWQDLRVRRVVWEEMMEGETRPFQHMCFGWKPTVH
VGFLSIWNAHREHVYRRLWEELSANPSTVYRVFCTGHSLGGALATLCAYSVCKMLRQKNY
PLLEVTVYTYGQPPLGNKAFQKAYNKAVPRTFRVVNESDAVGLIRMYGCHVGIEVDIDRH
GNYICKPTYMERLFRPMKGKGFAVENHLMGSYAASLNAIARDTGCPSVACLGETNGDADA
NPVAVPEQQGEPGPTG*
>TCRU_1809 hypothetical protein, conserved
MSNQRRTSPSPSSVATTRDTTNPTGQEILQTARLSLELTRADEVWSAWYKETEDQFVDFQ
SFGDNNEGGLNVTATAGSNIMSGSAQFSSSHRTLSARRVSGQFEEEVMKSWDEDWEDEDV
EDTFDAIMGQIGRYEASRAASVLK*
>TCRU_1810 hypothetical protein, conserved
MWARTILRLCSSKQPGTTAPAAVGSSWMTAAAWASLGSEFAGVSEDKFLRPRPDKFLTPR
ATTDVAVSEELLQSMVEENEERYKGIDVRDPSSMAVYEGDRPRWMTLGSQVRAVSEFISG
HLCHHISLPEWKALFDLQYAEMDLTYWLYVLHVHMVSRRATSIPIEKFNRRREVLEEILL
TMFESWAATSEDIMGRPPLNKIRFYIKDMYYVTAVNFEEALLHDGAGADLMLLGFLMKFC
PLPRPEDVPLYTYYSLVHYVRFHTALLDRIPDDLIAKGNFNFLSPTDPRIFERYDDVALD
RVIRSWTVDGANVGESSDEAGVK*
>TCRU_1811 carnitine O-palmitoyltransferase II, putative
MKRVLAKDLSANVLKLPRLPIPSIQQTAERYRTSILPLKPADTVKAHLVKLDTFLAGSAV
TLQNALVEANKAAEAEGGYPYSYIEPIWDNMYLSNRAPLPVNTNPAILIKKVKNAGETQP
SVAASIVYGIAKWVQNVLKEGVEVRDANMDLSPMLRQFGASLFPGEKADEFLITPFEKLR
HIIVLHDGHLYAVRVFDDQLVPLEQAVIQKCFEYILSITPDTDNTTPVSVLTAGNREVWA
GAYAELVRTPENAETLKKVHEGIVVVCLDSKKWEEDDGLKNGAMLHGNKEESENRWYDKH
QVIVSADGQVAFNFEHSGSDAVQWARWVGDVLQSIESKAVATTTAAAVDTTQVTSLVEPL
RVTFGKTFAGHIRSARTEALDLISNTALGQLQLPFGKTQLKQLGVSPDAFVQMCFHVAFH
KCRNKLAPTYEAATTSCFFHGRTETIRSATQEMLTLAEAVNKETKESTTPKESERAALLA

LIKAASDRHATLAKAASKGEGVDRHLTALNRLAVERNDNAALNFFNDYTYNSCCKWVLST
SNVSYPWVERFIFGPVTPNGYGLGYVVGENEVRIMLSAFTSSPSTNVEDMNAAIGVSATR
LYTVLAGSKL*
>TCRU_1812 hypothetical protein
MKEDLNSFSISSTTSPRHTLLDGDGNGSDVWTEQSSDDTSAAAMMDTLSRWLRSTSAIFM
GTQRLSCGRAAMAAAMSTVGDDHILHGVFTSGTPFLHYSLLQNASVEVDAQEKRHHTSCM
RHYYQQEMHLRGRNGDKLFCCFSGENNEAESIHVPYRMYSKGLRERKGFIPPWYAVHAKA
QLLLSLIDPLWRIITGLFFIPHAGKESGRESQYSQSSTQQTETHVRRLCRRRGGIEKRPL
RMSACASQTFSCMFTESQPTRRKIPDPSEEVCFIPEQAARALWARSHTTREEALDEAPPA
RGHVPTLTSAQLFLKHRSITTAPTEKKLEGVPQSDVAEESPCYPARSSTKSKRAVSGTCQ
REAKTEEHDTTHAATAGSASGARITSVHWLRGSAPPDASDSATSVIVLLLCPSVTQGNEN
GFMARRMGALCEALTNISKLRRQSSYNSFNRRRQRSHQTQLGIDPPDGLKTTTMTDATDP
HFASWHAAIPVVEMISWPSGQSSEHAPLPASSLCRERMNVTVEDIGHILSHLERLRAPSA
YSSRDTNDATMEVHRDVLDSVASMPSMSRSGSYLQSDGRAGPRNLYIVGVGWSNASSPLL
QYVMLYGAQSHIDGIICINQTASSNYALVPETVSNSQRKLRALGRDRQWSARSHKTPFHS
AFLLAPAGATRLLLLAARLHLTADRLLELQKKRQRRCQKIMKGDVLCAENDAAIWDYLRR
TVGNCASGDHESRTANDATFHPALSSTCHLSSRSLLSSAESPLDFLLKVEAQVDEEMNSW
WIDDVQAGNDDDDESTRGRSLSSRGDRAAPFSSSGGWHSLMGLLDWDKLLKNQQNVSAAT
RTGIGLSGRHTLPSSPHVTSNDTLNAEVVETSHPKNDERAEPAKTTAGNDDESVFGEEII
PPSHAPARRATPPFEMARGRPDLLLSAHLLSPLSQNFGDTPRNFVAPKRMRYELKARPVP
SQNSALEVLFYRSASSAHLVSLIHVPTLFVHANDDEMAPLSTLPMRELASNPYVFTVLTR
RGGYGVFLEGISTLYRLPRLTLQEREKAMHHNKSLDGDGDCRTSKTRHWLPQWIPLKRRN
VKLTSKMTVNDSCFVPPITSTNKKKRGMKNDMETVFIIENTTWLEQLIVEFVATTVLV*
>TCRU_1813 hypothetical protein, conserved
MFQLIHVTPRSAVLLVLLVVMCCAGGCFAASLTYSCSSDKAMRAHRAKSIAAVVRDVPFG
AEGASQTCTVIGRSGWAPIRINVSTRDPDGTRKYCSSERYCAMNSLVAIASVKVTFFYAE
KREVFVSLYFASTVR*
>TCRU_1814 hypothetical protein, conserved
MAEAASCLDLKASFIVSLPRETRHLFRCRVEDGTLVELTRLPMGYKAGPEILQIITSAIA
VVTTVVHRLWAAPPLVRIDVWIGNIRIAGSKSDVTLWEA*
>TCRU_1815 hypothetical protein, conserved
MATEWGDIGARLSELVRQRGEAQVQITFINGTEMSDETLTVAPSSTGLCLILGNISKQWE
DSGLTGHIANLRAFQVPNFENQLILPIMGAGQELGRMARAHHC*
>TCRU_1816 metacaspase MCA2
MGFDFGCLLNLCSTVLKRGGAPGSNNYMEIGLNLIKIAAPYVVQYLGPVQRPPRVDVEEA
FQQAEVTEGFKPWEAPTHVSGTFRALFIGINYYGTSAELSGCCNDVKQIIATLQRKRIPI
DEMSILVDERGFPGANGLPTRDNIVRYMAWLVKGAKPGDVLFMHYSGHGTQTRATSDTEE
KFDQCLAPVDFSTKGCILDNDIFRILLSGLPQGVRLTVVFDCCHSGSMLDLPYTFVGSRS
LRSSVAGHMQRIRKGNDCAGDVLMISGCADEQTSADVSNAATCETCTSGAGGAATQCLTY
TILKVSNLSYQDMLIATRDMLRRKGFTQVPQLSASKPINLQQKFSLMTTFEVDPAVAT*
>TCRU_1817 ribosomal RNA processing protein 6
MTGEFGTPGDFPRTKDIVNGAFGLVKEYGKLVSELPWDDYDYHMAFPGFRQQIKRHRESL
VEFMDKCCQLLPEKRRTAFKTGAGTLTEQQRSAVLEAVDSLLENVDGLLDNLKGKRLNAT
DQLSLTFGSELQQSSFAVDGGGCVLRPQLTFEHPVDNSPTPFCPVYYDEKGERHVGQPGI
HPFAELIKNMSMPEEQMIRRVETPYLPLAQCPLRFVDATVDLEDVVALLLKEKEIAVDLE
HHSFYSYQGFTCLMQISTRSEDILIDCLKLRSSMHLLAPVFLNPNILKVLHGAREDIRWL
QKDFGLYLVNFFDTGIALQTLHMPHGLAFAVDHFCQVKLDKKYQTADWRIRPIPAEMVTY
ARQDTHFLLYVYDRLKTLLLNSEGRASIGNLLVHVLNESRRLSLEIYEKPQLDPDASYKI
ALGRSLGGLSSVQMQVAREIFNWRDAIAREVDDSPPAVLHLSAVLAIATKLPTSANDFLK
CCTPVSMVVRTNVTRLVQIVKDSVGDDAIAGNSESDVKVEPSSRETGPMPRIVGVHCPMT
GTLPSIERRPAPVFLKEEAAALRSTEPSAWFNAMRNVAAVLRNKRLPTVALPGQEVVETL
MRAKTVEKQLRDALETREKYDTTRTLSDVKKYGVSRHGEDEEEIAVREEEDTAAENEDGG
EKDGKAEASDEDGSKRAGMKLEEKAVALRQVYGTGGANRKRARMEKNKRYSGS*
>TCRU_1818 hypothetical protein, conserved

MAQELLKEGTDGGGASTTALSTVTTSPAGKESVDLLASGTSPGGTQAVDGVSSSDGNQTV
DTADGGKTQEDEPHKTPADNANAADAKAPNSEGGLQDGFAVGPERTSGEDGETARGTDG*
>TCRU_1819 hypothetical protein, conserved
MMAMTMTGRVLLVCALCVLWCGAGGVCAEGQEAGTLSPPPGPVHGDQGGVLSGIGRMKPS
DTDGQVTVDGGVRDRAESKHLSSHVPLVDAKDVTPAGIGGAGNGAVEEVAPEENESLQNS
CDEDGEMSEGCVKVQGSNGFPGSGGGHVDRGRQQDDRNPPLPLSDQTSSEEINSPLPAEG
KPKNQRPVSRQLPVEEEQTDPVSIRPQKEAATLESEAVRNAANSHSQESAAELTNGTLPA
HARVTEAEDRSKNVFDTHKDAAEKQKKPAHTTGKSESPAASGDAHKATASTAAVDNEAAI
KKAKSPGGASSPISISDNSNNDTEQNNARDTSEEASHSTENATTHSAGIPRAPHTTAKTD
DTTTQEESNSDGGTVKMGEAAPQTAGTAQANDTATHDESDSSTAVSHTTSPLFLLLVACA
AAAAAVAA*
>TCRU_1820 Concanavalin A-like lectin/glucanases superfamily, putative
MDGGSRGTVTLVDQRAKPSGAKFCVGRSPHSEIWHKECHAVHSEGVSPGEDKANALHLWV
TDNSRARLVGPISMDDDRERTVANRLLHSNNMLYLLHERRDQSTDGIFLSPLKEELDTIM
SVVNTWALMDIFFSGLSIPTDGLVASLSDLATSDTWIDMYHCVNATVTNAEMTPHGFRFT
GPGSKAVWPVNREELNRQYTFVDYNFSLVAMAVIERVPAGSVPLLGVKLEHSNRREFIGL
SCTAEGKWEVSLDGNTTTSSSTWEPGREYQVAIMLRDNRGSVYLDGVVVASSETMPTLET
RFIQLSEFYFGGDEGDRGSSVEVKNVLLYKRILTAAELRTIQWSASSSSGSGPDTSMRGS
IPWLLLCWGCGALRPFTECNRVGPLPRAGTHASLRAPSLDYLAYHVDAVDFILCFFFFCA
RQYIFFY*
>TCRU_1821 hypothetical protein, conserved
MHGRNGELGAVCHVAHAVHTCSNCAASCAAEEEGATVAFTMNVTAHKYAGPYELWRHQFS
PDGTIHPPARSGDADQTGICQLPPREGKDDTKSGGTTAPQVNAEPSRQHEDRRRSAAADG
PNTVDPSPASNTTTNTSETRPEFASNPNEVMVPNASKKRPSFANGPRILVASNASGIVSV
TYGGREHVAADNTDEVSERSATGHKSLVSENAVAGSGFVAGGDAGGLTQRIASGQESKPN
YENSPRSIPGAVRVYTTALPRSTTRN*
>TCRU_1822 hypothetical protein, conserved
MLPIPAIQAEDGLEARESEEGTTLGSVATTGPGSVSGGGHGTVVPGGAGDSGGGPNLKSP
SSVDTPVTHGGGAGSAGGLSSTSQGNSQGVLPEGPKPQHSSSLDEKAAVVAPAVVEPTKN
SAPAGGESVENDAQTRADRQPRLDESTKGKGNLEPTEARALPGNTIQTLQGGEKAVPDVS
KAKEPEPKTQQQTEPSEDKNDRHNTHAPTKSPDVPKGNNAKEGNNEDPAHTPVTPQSTSA
GSQQLAAVSPSTGTPTSNE*
>TCRU_1823 ubiquitin-conjugating enzyme E2, putative
MSADRSSRRKEMDFMKLMNGPRKVHPSNSVSEFWVEFNGPEGTAYEDGTWFIHVQLPADY
PFKSPCIGFSNSIYHPNVDEASGSVCLDVINQTWTPMYELQNVFDVFLPQLLRYPNASDP
LNSSAASKLLHDPIAYVSIVREHVSRHATREVALGSIPLEFRPLQEDAVRANEKTRTVLE
DSSPATSKGLTEAPNSCVDSEEEYEPESIDI*
>TCRU_1824 U3 small nucleolar ribonucleoprotein protein IMP3, putative
MVRDTAQRASVVKAGLSKSAVKEQEVALRRSKRSKFTPASTHSKGNPIHRALKYHEKKLL
RKHDFMQYPQDNWHEPFCITKYHLEDREDYRRYLRLVGLTRQLLAHLRYLPSDSKIRIQI
TQQLIDKLFTMGLIKEKLGLAEVDKVGVEAFCRRRLSTVIRDLSMAANCKLAAELIHHGH
VRVGTTQVRDPAFLVSKGLEDLVTWMPGSKIKHHVDTFNVQRDDYE*
>TCRU_1825 hypothetical protein, conserved
MSVLGVSSYFLWTQKGKTVLPLVRGSGFLVLFQQLGGFYKYHVLSAAHVTCPVRYRQIFG
DTIGLRAIGERHISTKLLKPGNNGKVEASLDLEFAQSFLPNVDVSSLRCKDEKQINELCL
LPFELDVDPIKEGTELLLFGMEAVEERANPNDDGLHLKDACIKGECRAALVSLDYGTVFL
ASLESPLSLSMCGGPVVRKDNGRCVGVIVAQVLKNAPPSDPQVTPLYRDPWLDLSQNETI
NACGKLDVAFVPVREVYDALRRCEM*
>TCRU_1826 centrin, putative
MESIKAKCTAKNLVNEKPAQKTPLSISISEKHKAQLREAFDLFDSEGTGRIKALDVKVAL
CALGYDVSKEELTQLLKQVGGSIVGGVDFNEFYCVLLAKMMQRESRSEAIRAFRLIDVAE
KGYISVDDLRPIADSLEMDLTDDELAEMVLFAHPPVGFGKNENDIKEPLTVSEEEFLKLM

GRAHVY*
>TCRU_1827 AKAP7 2'5' RNA ligase-like domain containing protein, putative
MLRRTFIFVQKGERGLYFPINHRIVDRRIASGVTVEEADVQSRYRRELRTSFATGETRQT
IPPAWSACERPTHFLSLRLPVRNVLRTRVNEMYNQILFSHQQHAPLLVPLEKLHITLGVM
AISEREETERLASIYDCVSEVFSVIHPLQLRFRGLGTFGFGRVLFIRVVPEADFGILETA
VSKIRRRVGGELKVDMKGNPHDSYVPHVTIAKIRSKQQTQFGSKIPISMWVEYQHHDFGD
VTFSQVDICRMRGSKDGYYHTEGSVHLL*
>TCRU_1828 uncharacterized protein, PH0010 family/AmmeMemoRadiSam system protein A, putative
MVEATPDMAKYCFAVISSKLKNEAIPEAPQSISDDPCPVFVSLKTVDGALRGCIGTFAAE
PLRGQLKNYAIAASCEDSRFRPVELSELPSLSCTVYVLHSFEKAANWKDWVIGIHGIRIR
YKNYSATYLPSVMSEEGWNHTQTLNHLLRKAGYGGDVTESFLDKVEVTRYQESKASVDFL
SIYSGV*
>TCRU_1829 hypothetical protein, conserved
MHGSKSTVEMGFCSVHRRKRTRVDLIPLDGQTGQMRCKFHKECRQRAEIEMVICSLHNRR
RNMNQMKEVRKGIFECLPQFACRGQFNEAILPTTHANVSHPPHFLPPKGSRPQQVFGEAH
PALSASVTWTPTFNRPRNAGVVISSDWAQADRKTWCAKHGKLTSQCEFIKDCYHVCYDAS
TCLSTPIELPSDLLVKGCKELLCSKHNALRLVDFLEKTPDEKGYQCVVGHRCRGTLATRR
ETVPEQAMHPAREAVSSFFV*
>TCRU_1830 DnaJ domain containing protein, putative
MMRFRQVLTLSVRGSIRCVFQSKAFVSVSKELPLTPEGRNPYDVLEITVTNATSFDDVSK
QFRELVVINHPDRPGGSHERMSEVNAAYKIIKEHHNKLIQRLKEYEANTKGNENFQRHKH
ARARSDDDLGRSGGVYRRNAKAAEQSSGLRGTRSLREIESNWRRFQEETEHSVSSMCNRY
ELAVEKGRFFRKTSMLNEITVRERWLRKSFVKNVWEEVHELRGELLHRGARSAQQSQLAE
EMVAFASSTQRKLNEDFQRLTQLSFQSQSQFFLQRVLFALLLLVTFIKVWGWIVTGMFRN
SLTVRFRQGILSH*
>TCRU_1831 hypothetical protein, conserved
MACEGEEATLLAVALAGEETYWLCQPIHGKRLPPEWKNCTCQWLYIVDDVDIRGYIPWYK
GDLGVVLELGVNETSRIERFAVISDSVRARKIVVGEGGDTKTYFFVGNEERDALDAKFDD
LLRRETTVSMRKSSVVGIDGKPPEERRRIISTGASELRNGGRGGNNVVFSWDSFFIVEYG
NRVFYVCSAPHGNKYGFKVERIMRKGITIFLLFQDENAGPCRVSEVQEGERATVSSVLEG
ETGKVMALMTEGREVAVGKSRGDSADSSVFEPPSKAARRENSRMNCPNRRPLRAAGVNLW
VDSDGKEEGAMNLAELFPFSSEGGDSVRTTVFSDGTCVTYNFATASKFAMKKKIAATSTD
CDMVGLLENIQLAKEQFNAM*
>TCRU_1832 ATP-dependent DEAD/H RNA helicase, putative
MSFFGELTTGIKFDVKKHGAAMKRFTPENTKLDHPFAPGNSTPICDIMEVPLPNRTLDIF
GRSRSAGTSEGVGLIEGKAQEDIRNNATTTHTPVKSMSIKKKRNLWKKNELEVEGVDVPQ
PIEHFSELVRPPLSVDGRLVSNLFERNHRIPTPIQMQAIPCLINKRDVLACAPTGSGKTL
SFLIPMFHILKSPNTEAGVRGLIITPTMELAEQIEREAFFLMKGQRWKLVQHGQSTRNKD
IFITTPRRVFTMIEKKLIDLGNTQYLVFDEVDRLWDSATDNLQVVDSILTACTFEEKVVA
LFTATLSSKIEGIARTVMSPDPIRIIVSGRVSANKKISQELVFCGNELGKIVEIRNLLRE
GISPPVLIFVQSIERTKELYDEIRCQGLNIAVMNSKMNHEERDETIMNFRLGKLWVIITT
DLLSRGIDFKNIGTVINFDFPITVESYIHRIGRCGRAGKTGKAITFFTEDDKKRIPPIAR
VMKESGSAVEDWMLEIKSDRRTRRRLERSTPHRMIVSTKKRMLVADQRMERQLRRLEKEV
INAEDEELDGQHK*
>TCRU_1833 Domain of unknown function (DUF1903), putative
MDSNICDEEVTTWRKCIERNLGDHKLEKKCSAELALFDRCIASWRLNGAKEVKIKGESEG
EPPPQCAALSCLIGTCLRNTDYDFSRCKVPMQYFKHCVKSFYGSEYVV*
>TCRU_1834 hypothetical protein, conserved
MLLRNITRCLLPRALCTSYTSARVGTSPTGLASPGLLIEKRMPTLLIDMPKVENLTCGTG
QPAQRGRRKPLVWKRRHPWFDRQWSLDLKRAKKGPLTPQFPEGVPFTAIRSFQSFAGKSW
KINAGRRRKIRLSLKRGRRKLL*
>TCRU_1835 hypothetical protein, conserved

MDRPFPPYVLDVAIRDSLLGSAPGPDDMLNEFLHRHGPVARGTLRTMIHNSFANGSLPGS
WKMGDAISIPKPGKDPCRPESYRPITLLSVLLKLTEGMTHRRLSALLPHHPRQFRICISA
FYVGRGGTCCRQITRGLNEFGIVEHERPGDDAPTRRPRRHRSLVVLIDFPSAFGTVDHGK
LFGMLDRLPRLGLEPNAGCTTTCGAAMLGYALVNSTPGNNSPQLEHRKTASRDPNSPSAV
WMICCAAWAASILPPHSCTLTHSHLLPCVRTSMPVLRQCDRSCLLWPHGLPSTA*
>TCRU_1836 hypothetical protein, conserved
MAESASCLDVKASFSKVSLPRDTRHLFRCRVEDGMLVEPTRLPMGYKAGPEILQIIITSA
IARLTTVVRRLWAAPPLVRVNVWIDNIRIAGSKSNAILWEAQVLRNADSCHTTVGRTANR
APRSKPFLGCSLITHRAVSLSERFVRSVCAVPALNSLTIAEMEVKASRFLYAAAILGTRL
CDHHFFIKTLRRRLSALDRGSCRRHPRRI*
>TCRU_1837 hypothetical protein
MRKEINVRSFGTWVVLLICGVASVTAEDVAESGRSLLPVLYDAERVHALTCCELVERHWP
LLRSWDRCCASSVDATGDNKVHASFEELLHHFWDVPLPGCNSGGISSCNRKEHSLSDEFL
TVFLKERLCADLPATHTELARSVYSVFVVEDPLHEDDLITLMEEACKSVQHKGIILWRRS
LRARNVYEAQEAVCQRHCSAKRSFFDGDVYDL*
>TCRU_1838 hypothetical protein
MEAPGLERWVQNAETFTKEIDSVNNLFRSAERDIDTCEKERKEELCGHFKRVRAKLNVLE
EELTSQIESRSEEQRQSLRNSLAEVQATVEKVNRLIGEAAKPLLNYRAGNIDHRNAVALL
NLTQSVFDNWRAVNIPMYSVVIGWDRDIFNELEGALQPTLATESEGQVELPEAIDVNYLK
N*
>TCRU_1839 hypothetical protein, conserved
MRVASAWALRSAAEVRSACRLSLSSSLKWRVLVPVGFLAVPTHRKAEFPQRLGARHALGV
SHVRHDTNEAAAVLAAHRAVCRPSDRGGVGPAGGGGVSVLSPLRVCCAASAPHQQHVPGM
ASCSGRSSHPYCVGNSAAEAGQCSLFPTSEGGVRARQFPVASYGGAASLWLELSGTNNTF
GQCDDAGGPCVCELREIRRLLGFRITSFAPGHLAVAKDKLHPCARSSVLRARKKGTSTM*
>TCRU_1840 mitochondrial processing peptidase, beta subunit,
putative
MDNLYRCAFDSTSQGLGTPFYGTETGVARVTAEQLKSYRSSALHANRVVVVGSGAVDHTA
LERAAASNFGDLVAASTKSAGFPEARYVGGEYKLWNLRYKTVHIAWGFETCGAACEDSLP
LALACEIPGPFHRSQHELGQHAMHRVLKTFSSLDHSTPTNTHFNEKCIEIANPFLQQYKD
TGLCGMYIVGRPAQSGPGDAGAMIEVFQYTMAEWCRICQKMLHQHELEQAKVNLKSQLLF
NMDGSTNSAEDIGKQVLHYGRRIPLEEMYARIDDVTPTNVQEVLQHYFYSRKPVYSYLGY
CAYIPGYDWTQHWSYKYWY*
>TCRU_1841 hypothetical protein, conserved
MSVEAVKRQILNAISVLNIPLTRLPSEQRVVEACSAAKLLRNRVLREHARVEENIETIRQ
KSLYDNSDSDDENEEFSEFEKTGFTSDLKKLARQDFIFISEMMVMENVVIPLLLAHGMNF
SSTLLPQLLKLLTAMLLPVPFYSMERPRQMDFVCRLMERCGTDEFFTLLIQSVAPVAEKR
SQGVIQKEDVVLLEVVLKMVTLFFTGRKEAMSNVIGAFARNHGIELFLVIINQNYARIES
KRNSSNMEALREEVHANSEQKKCDDSVIVFLDDQNEEEPGIVVLDENVTLERHDKTAEFG
KELDDDDVVAQQVVVEEEVEEGETEGESLDSSDSSTEESESVSNQYNARIIQLLECDEQL
WKWNMHIVTAMAVILRSTSPVELAQLVFVSKFQQRSSHQIMGMFESGKGLRECKKELDRW
RQVARSCNGAISSSGLLVRGKSSCVQGEIGVIGCTSALLGLRSKDPLEKVQDIDLRKRGR
FIKGMYDDSNTAWILPLPTKIQLAQQCLSFICLGFEPLNMMVWNRLAHTITSFESIVRER
NELISGHKSSGEDIEIPTHIDKAVLESAQNALDYLSICASLLRYTREVIRLNQEENEAPS
DDFRRQWQSISSIISLDHICHGFELLRVFSSSPDFRRRFDVVIVVNYLAELFMTLKHLID
GDIVKDTAVVVAAHALASSVLYNEKNITLIFESISRFSAKVLPPSKAGMIVLLVYSVLTL
MERCSFGGRVLFPKCKKKKNEETVMYEAEDRGTAELLESNKRIRIDVLDTLEESNNGSGN
EGDAITKVKGNEIAIHSTPVPISLEDVHLYQGEIVPPDGEGRGNSSENASFTSSSHANVS
NLTSEREVSIGDYFKRLGTVKNMRLILTSLRHWRTNDVDLNNGLVYLIRAFILEGMGNIF
FNAPFLFVMRDILSHGEDFHNALHNVCDQVVYDFFNPSFAKLLDEKRKNRSDMSLPFFGG
AQSFLGFEVALRCVRSLFSLNSTDYSILEEKGLPHLTDFTVIPLKDETQSDKDVVHEEFS
SAQVSPVRKSRRKNKVSLPENRNGIEENEKVFSVDVPI*
>TCRU_1842 transport protein particle (TRAPP) component, putative
MSHNGLVSESVVAALSMELISYVVVRHTFREDSLIDNSGNEIELNIHKGLEGLGLLVGLR

LSERLLYRQPSFGEWTPPGVSQFVARQFWKTAFGKRIDRLMHMNDIYFCLIDKNFRWLQG
FPKMRGERIVSTTVLSPYGYSEETVAEDEGASPRTERLGSVPIHKDVLIYTVGILKGLIR
VMYPTGSIEIHANLNNENETQFVLDFRSPTA*
>TCRU_1843 hypothetical protein, conserved
MSKTQNGVGNDPQLQAVNAFTEAQSLLDIMLKNFYSVERQAADPFLLRVVIAGKKKESAG
RSVGSLLPELLNVAVNTSENPLCEDNEKSAKNFAVLVEYDDYFIELIEGFERHIINFLKL
LEKHCSQKEDIICYDVRLLYLVDDVPSPIASFFVHIDKVPAMSTEGEPQDSTDEEIADTI
AEDVNNLMKLLNMVADEPSTKRKLFLDNLRVTHPLLFPRKSMIKKYLESDIFFTLSEYID
VYGKISGFTRDIELNHPVVDSLKC*
>TCRU_1844 Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MGVRLSREGEKKTFEPSYDKEKKWQVLCDVESPEDQSRTLATDTTHHVVILLRNGTQGSA
YVDGKRVGGDEQCKLETTGSNEISHFHIGGDGDEKGDSEIQDVSVTVTNVLLYNRPLNDS
EITALNAKLSIPKAEGTKTVEGTPPEEIKQATPEAETPSSHVGQQQTEQDPLRKSENAGS
GVLSTSAASTARNSPAAKESEDQSASGTYPEGHSNVDVDSSSEGGQTVDAEAGDTVQGDG
TQQPSVGTSATADTNAPTAETMAHDGTAVTAELGARSGASGETVGGTDGQKGEDIHAQDG
EVKAAALSSSLGNLSQGNNSDAGTVCGSGLLPLLLLLLGLWVIAAL*
>TCRU_1845 BNR repeat-like domain containing protein, putative
MMMTACDDGRRRVYESGDKGDSWTEALGTLSRVWVNKQGEGAKGVRSGFITAKIDGVDDK
RGVMLVTLPVYSEVTEKGDNGKGKSELHLWLTDNTHIVDIGPVSGDDAAASSLLYKSVES
GDNEELIALYEKKKGDEGKPSHSLWSVLLTAQLQRVKDVLATWKEVDDRVSKLCPSKSAA
ASASTDTACSPTVKITDGLVGFLSGNFSNDTWRDEYLGVNATVKKENGAEPAENGVTFKG
RGAWVEWPVGEQGENQL*
>TCRU_1846 proteasome complex subunit Rpn13 ubiquitin receptor, putative
MEARGVTIPPARVGHTARNSLAVKIPAGRMVLQDGIVKPLLGRGLLCLMRDSLMDELVLT
WVPVDGGEEHRFTLPQGKVQVSWVEKCKSGRVLLFDVDEGKQLLFFWMQSRSTDLAEKMM
RRLQYILERHRHYPVNAPNSQAIQMSTFRRILEEVREGAVALDVDLEALLASSKLIEALQ
EDPEFYRSRVVDYLPSSSATVTDTPVDVVSLVQDSQVQWAAVILSTMLRHQATSTYLSSL
FLDAAAPWGLGVVSFIMQIIQAFLE*
>TCRU_1847 hypothetical protein, conserved
MLRSTRLWRFRMKGGDMFVEYKIMSRDHRRSIRVEDAIVDPSVARTVVPLSWLEQLRSPS
LRLHTGYHMEEAVYVPPAYAAVDDKEGRRLSEKSTMTPNAILAGPVVLSITGQSVPVVLN
PYFVPDDTWGIRRNRDEWDLRLGMDAIEQCTLFSELRPGGLLYNKLPSSQNVTRHEPVLA
TLQRYGMKCGLAESPLVPRPWTRMRYMFIDELQRGPKLTEFVGHNPRNGTQWRFSQHSKY
FRIGVWRETIRRNDMNEGLHGHSSWQKSPQQAVPEVRLMAPYP*
>TCRU_1848 hypothetical protein, conserved
METSVEMQRQESGSPKELAGTRAQKAPEAAAEFDYRELGEAAVQEFEEYSSASGAAPGRR
GSIRFVLASIEEKENELRELEAREKAVESQLQVYSEVIGLRKELRLVKEETERVRRQLDS
INVFAEKYGNAVERDLDSAEEEAQRSHVQQVWTSVCRERPNESLGDPSSWTKVDLDNLSR
RVEAARGKLQAASNAAAKVYASQEDMINKNTEERDKAKAKLLESVGVEMAKLVETRSRLK
QLDDDQRYHFRRGTHVKQRHVSSLKEQDIMKGRVYKDESRQFGDVVLLEDECKDLTEWVN
GAKRELEDNKRSYAKEQSELEEQLQVMEDNGKEARELRAFFERENDQLKGLKQDLQHVLI
YVRMRNREAFT*
>TCRU_1849 hypothetical protein
MLSSVKNVICGAHIAPAHDGRSSVDVDAETGDVVLCDGLTGVSRFHFDSVTYHPFHAMAY
ESVLARRVAENFGGGCPYACDTPPCATHGAVIHGSLRIHSVDLFHALVLSAVGHALDVLA
ETSVGDVQLHYSMVCLYSWGVTDALNQQVVAHRHVGVYTHDTDECCRPQLQHNVVKSRED
AALDALLRRACAVPGAHSSIIFSLVAKSANASVSGVLTIALLPQLSQGNRFFQGGMQQLR
ELIAGHPVPHDGPCWLLQHLFPSKEIRSLAMITCITDDSRFYQENYNNCMYGCCPLVNGS
GSEGCFPVCEGSFNILNFRSSLPQFQPSKYRHPVKSIILPGTGLVESCEKKRGRIRRSTC
AIPVTVDDVGATQLPSSSSAETDAAKRLEAELEERTNDLQDHVASVVKGEVAARQVASEL
VSQAETVRSEIVSGERYLVELEGRVRDAKSREDELQQHVKSLEVEVEDLCEAKLIVESMM
RALMQEFESAVVSAESAEDTMLRHVDRAEEVLRLSEADAASREAAAMERIHGMIDSYHLM

APDDVFPLSYESVVSAVADLFDQFVRMKLELLLESLKLWVCRMRAEFRMDAL*
>TCRU_1850 mu-adaptin 4, putative
MFISQIFILSPRGDKLIFKDYRQDAPRNTDEIFFRKYKFWDGAQGHAPEGDCPPFFMEKH
VNFCYVKRRELLFVCTSVVNVSPSLTLEILLRIIKVIKDYLGVLSEEGIRRNFTLVYELL
DEMIDVGVSQELNTENLRPYIFNEVVRVSGSETPTGSSFLGRLRRGEFLDKTRRGDATAN
SILQASSDRKNEIFIDILERLNIVFNSAGQVVMSDVEGSIVLKSFLAGSPSLHVRFNEDL
VVGRGDANKERYASVVLDSVNFHEDADYSGFEGERSLSIRPPEGESTLMNYRLGGRGTPP
FRLVHSMELLTTHRAELMLQIRADIPVSTNGIGFSVIVPMPSICTAASVEFGLGATEQTY
EYKEEEKCVIWYIGKFLGGTEQLCKIRFSTSSPIKAATKRSVGPISMRFEIPQYSFSGLC
IRVLRLEERSSSYNPTRWIRNVTLANSYVFRTC*
>TCRU_1851 hypothetical protein, conserved
MRRVLLGTRVTGLPLWCGCRCSSGKTEGQTTRDDGHPSAAEASAPSAGEARGEYTIPTAD
ILRAVKQRDFNAFQSHAADIVQHTWKEEHSIPAVCLLFFLITWYWASSSRRRVVRSCKAT
EAKVKEEADQTLTLVNTLVRKWRQDVQRADQQLQLILDKNSELTKDIDRMTAALRQCYVN
VPATKGGPAKRVASE*
>TCRU_1852 hypothetical protein, conserved
MHVDSDEEAAAACTAAKWRAPQSATTTNLPNAALGNIVTKLRNLREELVSFDESVPDIVT
FRVDGRLFSVHREVLRKDPQSVLFLMAATHFRRYGDGNPMREVIEIPGKNSALVGMLMNL
LRGYRNPIPEAYREVCLAEARFYGLEHSWESRYPVAATGPFRPFICSDRLLSDALCAAAS
PFYSNGLHFITFGISRCETVGVGVGAEGACLSWMDGMGQCEDLALYWNDGRVTHNFGGLF
TEKTGCSFTSNALIKVELDCEENIVRWSLSGEQSVAVVRLPPKTSFAFAAVLVGPSEVRI
LRGE*
>TCRU_1853 peptidase, putative
MALQRDTVQIITPSALRARHFGFILQGGVKCIVIQDDNAKIPAAAMSIHAGQLNDPEFLP
GLAHFCEHMLFMGTAKYPREDEYNSYISKNGGHCNAWTEDGSTTYYFTVAHDALEGALER
FVEFFVAPSFNSSALSREVEAVHSEDEKNHNVDFWRIDELERSLFDPRHPRYRYGNGNIT
TLRDAPQARNVDIRAELLKFFDAHYVSEAACLAVYSALPPETVLHIVEAPLSKMRVGKPS
ALRFLPKEDPLYAADTRGLWLNVRTIKKIRKVRIVWPVKSSAALWPSMPSDYVSYVLGHE
CDCSVFGVLRREYMATAMVVGPSRVDDDNDLLCVEITLTMDGLRRIVEVIDILYQGIGLA
ARVDSAVYAQMKAEKKINFESSDIGENADHCAALASSANQASLQHCWAAGELLLEDDIPA
SEAYTAQLTPENGVVMLAWGDMPCDDAATPAPVANDEEGEDNEECEEEQGEEEEEEEEEE
KEEKDEAASGPLDALPEFAQLACNSATRFHMTKFSKCRIPDEIIAGWAASRCGPRHPALA
LPPANPFLSTEFTVYAGDGRHATVETFHTPYGVALVRKDAGHHKSFNTSIIWRCLSPCAY
ASPRNLYYMHVLRAILNDAVAEISYFGLLAALQNDIQLSAGGLVLSVTGPQHRIMEFFFA
IFEKLFTPAVLCGSVEMYRNYAEREMRALQSKRTKQPYTLAGDRFMKAARVVAYTFDEVI
EAAVSTSYEEYQAFVKEYLASGVYFDCFVAGNIPSSKDVQSRLIVGAQEILSRLHVSPAC
KEKFPKFCDTYAFPCVSSLPHAPLVDVLIYPPFDETNSNVAVLFDIYVGEETPLLRALCD
STHQLFSSSFFDTLRTRETLGYVVYSQSLRVEGTAHLQFVVQSAVEGVDGAYLLSRIIAF
LAAVEEKLETVCAEAEVKTVVNGLIERRRKLPDSVEKDSLDLLHRHLHPVDFAHKELEIE
ELKQLDSAKVKEFFRTHVANSSNSRRALAVVVHNAASVKNDVLDGADGVRRTVTLPPRRP
GKGSVEEVDNESTESVLQLPDFVVAPMSITVQKHPSPEDFHRHFPIVPGKSF*
>TCRU_1854 E1-like ubiquitin-activating enzyme, putative
MDSLTCTRGEFDEMLEDLSKRGLGWRACRRSDSFGRTLKWLEGPSIIQRDAPCGQAEQLL
VSYFITYSECYSQPQLYFAPEHPMSPQEMCTWMGKVCYGAVERQEYDAPVVSMNFCEEIQ
MPVWGLHPCDATQLMMNTSANGVRSVNLLELFLRSVGHFVGVDERLLPLHVAGQQK*
>TCRU_1855 hypothetical protein
METAAEHCLAALIDSVGSGGPIFRREAIGAIAKLSENGTSAVLRFCVTWLNEHGANSTPV
IQRCGVVCAMATIVGGVGDEELSTREAIALLQCGIREMTVNSDLTSELSQEALRLVVGLC
VMFPAEGCRELLSSLGDNTLPHFYVLLAISHLAEKVPERILPYVKEFLTRLLPPLGNARQ
DNHRMLLSRACGSLAEALLKMRFDARSPLEEYNDLMYSTLNFFLGDYSRSNERRVRTLVV
YALGCVFGVCGDEKRMELAGKVAPLVIYGVRREKGHDVLFPLRGLAGFFSYVTDGVRSSL
RPFVEGTLQAIMQTLEHLGAEDVETKEEIFAVIMAISDSFVSEVLAYLSAFLEAKKELHL
RCAAVYILRMLVLQSRNQKLFLQPFVNDIVATVKLALGSHEDSMVRRAVVECILTICSSE
ADFASAVGYSDMLSYLIRCASLHDEVDEGLIAVRDISRNGLMLVASSKGALDSQLWPFIF

EHMREYPAKPFLLCAFSSICNVITQLASRISHNSSCFYVDFSRQVNVPSPGMLVSVFLSQ
SMLIGFYRVEELLTILEAALSVAPLIDDPYAQSVEEGGGAAMPITELWSTFIPSLQQLLT
REPARELWEMEVERLVDKTMKVKQSEEWAMHLTTECLSLLQAYQQDARMFRSALIIVGIG
CSRTASRDLIASAVETAVNASNHDDPEHVIGLAKCLGYVAKKHVDTTLETLCRLAKGAEK
RGFFHSRDKTKRVFVEGSRSVAAVGFGYACKCMEIAALPSRLDTVVFPSLLTLLREGHTS
QCQISLFEGCRLVGTGIARLDSYFFKCRDEFILSFVRFMQMTSKKKTKEETHPTAFAALE
SIVSCTLLPPLGDNGTAALIEFVKISVTECHMVNAEKDVNVTNLFVQILRHRDCRYAMRM
LEELAPLTVLENDGARCLAVKLVVTVLAACRASRESGADGAAEQPHTLASMGYILGRLVP
RMMDRCPSVRMEAANGIVSGIQTARLFMENPQPMEEEVTEEILKLGKRAHAFVDDGTLSS
EKEAVSVVKSMCTILAQQLQQREDTTALIKALLFNSIFDTQKYAATGACITMHGLIRGCG
GVLDASDVREVFDGLIAALQRDNLPEQVRSGVQTSIRNLTRHHVAPCFVALLRSQLPHSE
AVINSFGAIANDTTLGELLVQHILDFVLNSPTTIAAAPTAKKPSDLQVVSPIVLSAVCAV
GWVAQTDRGASVCRNHRASLYMAIVLHLSVCHRMNDHDAVVMSGTALKHVTCGTVDDVTV
VRFDRYGWKNFFEKQKYLLAIAEAVRYWCREGLGDSNEMDRGKAADADGRFPMEPAEPTQ
LTNELAKFMLPYCSHVSPTHRKAAACVCSELIAYALGDEELVRSLVTALLSMTGCDEEAE
TRETIIGGMANILVHPYASVHGFVPPILSATLACMEQQHTSLAAKSMDIVALFAEVLEDK
SFINGSFVTIATKLRSFFEHDDAQLRAKSFDCLRRFYSLAHRGILERASVNQNVFPYVIP
MLIHLGEHVMTVSTAAKAALHECLTFISVFQHEAGEQIVRMLSKPHMHTDRETDIDDIYD
DVASTWVSHFHGMTREYVLQAVTFTRSPNEALRQSAARILGAFIRCIPRMDLSRCGVEQV
SASLVELVGTGEKSEIVRVAAARAIGCFASI*
>TCRU_1856 hypothetical protein, conserved
MENFHWDEMGIATRDDPDPLWNGYFSRRCGSCGSATSFGDPRGSQCSMRLGSRFSCRSSV
RGEGHTIDETRRKQRVIRYMQEERERAARSKLEREKHEDWMSIRALERGERMQYMTDEER
TAFFQREAMEAERERAAAEEAARAALGRRYSARNPMPRAAKERRGVMEAAIAVSNSHEAS
IAVNRVPVSYEVEHLQKKMAEIQRQEAELQFKLRRAQDDAAAARADAENARQMQRSAEEN
VLREVKRANDESALRKLAESRAESLEKRVEEMRKGVTEMEEEVQRMKREADKNMSMFREN
EKQLASLREQLGDVREKNERLQDEHKQLRVEKNAVATRAKNPPPQSVEKPKPKAKKQQQQ
STRTNASGGKFGPAGSNFSRRPLEAETNSSVDAWGEIQPLREQLERQSSALKRFSDENDE
LKTKLRDETEMRRKLEELSAQSLHPKDDGSLRRQLEQAEKEAERFRAEARAARQELDDAR
VNYGREITSLNAWCARLDAQCKRQMSELQDRAPRDELNTEPTRRKKDMQGGVGTAKAIAD
ASYASDSASSKKIQAELSRMHTRMEESEDQKQNAIAKAESLGQKRGSPPLNEQHDKLCTQ
SHKDALFKINKEVGEGKDAVRGAIAAEGNKVELVQGAKGLLPEKMTPTGAKPLRAQVVED
ASVGNGISSAVTNGLPNDAEMEEACKRTALLQQEMEGEGRAHVGDGSEDAARNARADKGT
TAAVSEKVEKKKKAKCGC*
>TCRU_1857 Archaic Translocase of outer membrane 14 kDa subunit
MSPISERFSEFAEKYRLVQAYRSSLGAAMTAWGWVQERMWPVYSTGLILSALFMLASANE
KQILADHLYGSDVVLQKEREKTVEEARKLFREESVQGVKQVVWMLPSGEFRGEYKERYGN
V*
>TCRU_1858 Archaic Translocase of outer membrane 14 kDa subunit
MSPISERFSEFAEKYRLVQAYRSSLGAAMTAWGWVQERMWPVYSTGLILSALFMLASANE
KQILADHLYGSDVVLQKEREKTVEEARKLFREESVQGVKQVVWMLPSGEFRGEYKERYGN
V*
>TCRU_1859 hypothetical protein, conserved
MLKVLHTKAAAEPILLATTCHNMNLFAIVTRSLVVVYRSTTLTVVTTLPLKMKKNETMVS
ACWSPSGRLLAIGLQCGELYLLDVESGDLIRRFVPRSDIAFAIKDADAKTLSGIIDTSAG
NEINNNEDKDCIDGDKEDDPLRQPPILPISVDGAIVACTWASVAPSTSALHSHNELCLPL
STTVSSPIFEELEREDDIPVMLLLDQRGGITFLPGGMQEVYVVVVNLQWALDPCRMRVDA
FFVAAAPPLSNVKKGESNRCSSNAVMCGENTGSHSAYLVVRERDGETSSRASSQVVRVHL
SDTIARVADREAVAICSIVEYCRMGKVSYQFVRKRWESLIRAVRKDLFLPQNALLLRDAL
MEDIARPSSAELSVYFRGLDLDALVKDTEELSRQFTHLVLQVSNVAYRCYDLALHLSQAH
SGDRQRQCLLMDVIGGLRQRCSSFLRQMRLEVDREKDLVHWVVQRAAPPGSKFFTSHPPL
RAVRHPSLLRTLHRIARGESTAFSLVDENITRGEEDLLYIVKGCLLGGREAVARVVPLLD
DINVESILQRQCEVLVPHVAAESGAECVQLHTVTVTKSRPCQPLMVSYTFEPRGDAEVFF
LAKRGSVSVEIEPLQLAEAGAAFLWSGVVDDGGRCVLLWERAAPSFVGAENMLVVAVVDE

NGAVEVAADAEDEANGEPNDTGIEAGVSRHAVLEIKGISTRHLRASVSRARGFGVFYANE
RFVVVDFYGG*
>TCRU_1860 hypothetical protein, conserved
MKQWEKEEENPQRCRRRIRNESPVGVSDVRRPLPIPLTTALLSSKLRRELQRIWDVTRAP
GKLEHEDHADDSHTEEEVVVDVPPFKVGTMEMYRRFPKQYDIFMRRHDCQAVHEYLDSIL
LSLQQTSATPSDGGNCLAVEGKMCFVRVADFGCGTGRIASMVSRHPAVGAVYCYDIATPM
LRECLINVVCSVAESRQEIRGVCICPSGAACVDGNNDNNNNNALGTTAAAAAEVCVGNDG
VTENSDGVMLLCARPVSFGDVQQGFLDTHTPCHLVVCAWSLSYVMRAQWGDDRWHAAIDA
TVAALIGLLDTSGPAALVIIETLGTDTTKPRRNNTLLQRLESEHGFERRWVRTDYNFCDV
AEAVRLTRFFFGDSMARRMAEEERTALPECTGIWTLWRR*
>TCRU_1861 Flagellar Member 3
MAEALNIPFPDGTLEVYEGLDGRFYLTNSNSTLTPLFVDDTIMKRQEMLRVCECVTDSHE
DTVAVLDKDEVLDAIVESCMDSGTSTITDCLKIVCEHLHGFGVNMCLLKQVIQKIATSDG
YSAAAVAKVEEILFVEMLARSVKQEFYLEVQGKRIAYDDEVLSATLSKHMAEAFTTVDVF
QSRFLEVVAKKYGVVDEDNDIIRGLTTVRLSRKAEIVARICALLGVTIEKTGEKKSNMIW
HVNVNARVLPQLIDPKKVRILAEKYRTIMTQDSHRHAFCIPMRCKVACWYGNYDEALDLV
HATAVAQRNRYGESAIVSIYSRRNVCEVCFATMQKNCIAEGRSLFPGVMRGFEELTCCVT
QGRRHIEYGFWILRIALVYQHDDLVTYRSCVEEAVHHFYQAIGKLPAYLTSEHGSWLHLQ
PYKGLLQCKRLLPSCSVNAKELVERSIELSTIGWASDFFMLYLWDLSLQLEAEGRYEDAI
RVLLTAITVSKKKPTVTLDLPSLLMDGAHIYRSWDPEKYSEHCLTLLREAAEKASELFGP
HSKQYAVLLNNKGAVEIELNRLIHAGETLEKAGIVFAEADVPNDDPDYIAYLENLVYLEQ
RLAARPVVQRGFLRRYPFLATRSEDFPFSDVRPLEDEVFVDLAHKRARMAGGTSDAKNLE
KRMKERIWELLRFIQDGDVLKRYPFLPAVINGVHTASLRLDDDVLFEEFARLLHASKDAN
TRRELESRLREYVVKKAEDTALQRAYMDRMDEEFNEAHEGYVNLMHPIPWLYVLEDERFN
ALTDQMQKCVNTQGNTARIQAIQEKMAQRVAEMEGEMFLWRGELAEWLSPSKLYSVHTKD
LTEDMQLRDLLRVRQFPDSCEGVSVDTINALIRDKLEALWKRATIIRSCLAVDDEELHRE
FPFLVEMPHHQRLSTLMLYEDPTVANLVMRLRTEGNDSHLQTEMMGAIKAIAARRRDSKE
LKKWYYDIDSVMSGSLSLENVPKVRDDYYVHLWQQRNIVQAQQGEKSPLMVKLMHQMQHR
IVQMNSWMRKVSANGFRRRLRLEAKYPFVERRHEGYTLEVLDIEEDEEFMSIVEQRRRLL
TSPDASSSELERLGRHANKRVRWIASQRVKLSEELSEKYPFIPNRLEGVETLTICLEENE
TFAEKAAYYNRLRDAGSNDNEMRCRRLLREMESLALAVAREIGVRNWRESIESEDLHERY
PFLPEEPVRGILLGDVRPVQQPAFRELSNKLDEQRRDPTRNAAAIRTTEEQMTALVVRLA
EERAEATERAHEQYPFLPRRVLGVRLGDIPLQEDELFAAATTERVEDKEPLLKSRAQELV
VCQNLNEAQLADNDDAVLSQHPYFVYTSRKCFPLRHLPLDDDVLFAERLREYENLMQEPS
VDEDVAAIARFRLVLRADSLALHEIEKIERIKQTFVALHPLSLEDLRHLQDHRAFQTYTG
DGAQNPSPVLLEDAKRIIMGSRKDRAARVQELDAVRKSYPTFGRSIDPEMLKDPVIAKLV
SDLEEKLDNAEGNESSVIELEEEINRQIIRHKGQIKGEIIDLEGRHVPFKEQAVDYYVFD
MEDDIVDDKYYQGLMEEYSAFENGQLPEDTSTLRRLAKQIEIRKNQIKNDNKKMAKYHKK
IEQRSATRFSFLNSHVHAIPITELHLEEDTVMLQLEQQKASQRLIDAESPTSIEKKMIER
AEAIACGSDGEGGAGGGGGTCGGISISGAECQGSPSA*
>TCRU_1862 Glutathione S-transferase, N-terminal domain/Glutathione
S-transferase, C-terminal domain containing protein, putative
MSLTLWSGVNAGNTRTHKLLAAATLANVAVTPKTCEYGRENSTAECCRNCSPCGRYPVLQ
TEEGCVFESNAILHHTACIERSGGFLYGLTPLEGSQVDMWLDFSATELDAAPAPFVQHAF
RGGQRLANAMDRVHEVLRALEAWLETRTFLVDECVAVAFAPQWHYRLSGAEGEALTRKYR
NAYRLYNTVVQQPKTVEVLPPSRLCWTR*
>TCRU_1863 retrotransposon hot spot protein, RHS3, putative
MWALDSRVEGDTLLEDYEYVYNARWSHFVEFPGGEGTGMEVKKGEPPQPWTYRAVGDSLE
KDDGVEQSGAARPRLMVLTSDRGWPYSWYRRRNKFTRVCHVNCEVDRVWRIVKGDLTERF
SPHGRTDFKPNWRLLIGTPGIGKTMGAGSYLLYQLLHCDAKKLHLVVYSFGGNTTYLFDK
TIKTVTRYLGRGASKEFLNGLWDLKMKGYIIYDVARQGTPPEEFFASYWCGMIVVSSPKV
SNYDNWMKQKGAARIIMNCPADVDVKAMCAWMKRDETAEKQAEYWKMVKERMDNVGPILR
YIFDANEFIAHSAAIEDALDGINSRDGEKQFTHGGVRLWDSENPSQKLVRVVRGRGEVGA
EVFLNAPISVCLGRRIPHCFWKRDE*

>TCRU_1864 nucleoside 2-deoxyribosyltransferase
MSGVYIAGPAVFDADTGAACQDRVRTALWVHGVVPLIPAGNVAPGAGEMRVKKVEMVRRR
DAVIADLCLFCLDGPGCGTAFEVGHAAALGMTVPTFTLDWRSMREKYGGACDASVMSVED
FGLSFSLVLCDGAEAFDSFDAALHHFLRHSSEWRGCDCGGCVRSWS*
>TCRU_1865 hypothetical protein, conserved
MPRGGRHAGGAHTAPYGIQGRPRNSPDYYCFGNCGVTTVVYRLRAAPPLVRVDVWIGNIR
IAGSKSDATLWEDRESGATHYTFLGVQLDGESGATHYTFLGVQFDHTRQAVSLSAKFVRS
VRAMPALNSLTIAGVEVMASRFYYAAATLCTRLCDYYFFIKAVRRRLSALNRGIVLETSP
ANLPPSEAGLGERLRQMIENHRRRIIKPTEKSSAALITDASLHGW*
>TCRU_1866 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSVCVADTGLAESSGTVTSRAIGTPELTLQGSNPSELPAKEN
RPSVELGIGDGAGQNATGTLRADGNGDTSGPQSSTRHIGDQSNNKAVVTADATKKSTTIE
SPENTRKLEANTNVTTLLSPAPGVTPGNSRPEAADDSATDPVPRDIVPEAPHLTDPGAKV
NTEYNTVQKTGTNGTTGQESGTRTSTEQSNKETEYAAPTTTTKTKTKATTTTTTTTTAPE
TPSTTTTEAPTTTTTSAPSRLREIDGSLSSSAWVCAPLVLAASALAYTALG*
>TCRU_1867 Leishmanolysin, putative
MQMSCFYSSSTIPLILLLLLLCVRLCSGLVEHRCTFDKRTRDGAPLPMVRELPRKGQGAF
QAYTASEPEWSPLRIGFFTEDLKNKSRYCTAEGDMRPDYEGNTVKCEKKHILTEEKRALL
INKLLPDSIKLHSDRLLVQPTELFVLPPSLVGACTLFLIPDGHFAEGITGADFILYVAAG
PTHDVNVAWGVPCALRSGGRPAVGALNFGPQHISSRQDLSRAVAHEIAHALGFSVQLFAE
SKMVTKLSKIRGKSNVLVVSSEKTREVTRKHFNCDRAPGMELEDEGGAGTAQSHWERRNA
KDEIMAGVAGIGYYSAMTMAAFEDLGYYRANWGMEEVMGWGRNTGCDFLEEKCVNNGTTK
YPDMFCVDGSFLFQCTSDHLALGVCGLFHFGRDLHPVYRYFKYPFMGGSPNELTDYCPVI
MPSGEGACTNTLNNFTGCRVGPNSRCVESDLLRFNSVTIGAICVEVSCEHKGVASIRYVG
DDTWYPCPEGHRLKPGPPFTRGHIICPRYTDICTTLASAVLKPTLDNNTFQNLLTPVEGP
VQRSLSKPLEMKKTDARKKHFGVDAGSVAVTPSLHWLLLCSLLGALLGI*
>TCRU_1868 cell cycle sequence binding phosphoprotein (RBP33),
putative
MSTGDVNGAGDILDGFFSHPSLPFNPSVGEGGDSLTKNEPRQPLPQQNSEIFQPHTPNNT
SSEATTVTSTSSSSQSAVKSIATCSAGENTGSYSHAGSNVVGTHTASPISSTPPNQGYMN
VPSMYTAALAQTTHQQNNMQQHPTHLFSGAVDSPTTATATQPEAGHTSDGSPSAFMQGKE
VMLERLMACLGESKGMAALQLQLAQVTAPSSPAVAALKQVIQHLEEDIEKLLHLRDMPTT
SAFMNGAAVYQKMSTDVPKESLTTSEVQVPNHQYQQQQTDVSVAPLFVTNAQVAATATFS
DRGIWSLSESRNATIKNGNMDLVDMSGSTAGAASMMQQQPYQHLEVITPQSGQMTSYLGD
TGASVTQAYPMLNSALLASCDDAPAMYATSGETGYNFIDANIGSLGFGDAIRGPPRRNMD
EQHPVEGEIVPKFLAFVEFKRHRVRKYECNIDISPGLYVMVDGDRGKDCGLLVQTIKTLP
DGSTSFYCMDGTHINADKIKLEKGRVLGVATAEEIDYLHHTMQQAERVALETCRKVCDDM
GIKINLQDCEYQFDMEKVSFYFNSEHSVDFRPLVRELYRLFRVRIWMENTNPHVKNTMPA
ADLGGIGNSNINEEITAMSEGVASVNYSLSQHQHKHGGGAGLTAIGGNNMTGGRRRGHRR
SLQKNTQGKDGKK*
>TCRU_1869 hypothetical protein, conserved
MAMMAGRVLLVCALCVLWCGAGGVYAKNGDTNALGGCMASEVLGRKTMDTPKGCDKTASK
LPFRSPLPITALQADVSEEEENGLNSIVSSGTGGSSGGGVDGGKVEFLIRGLPVQAVAVK
LEMILQRLLLLVLHLRFLLKLPRPMKVYGPPEVRHPLRAGNLKQQLSSQEKSKRLQAPHC
PA*
>TCRU_1870 G10 protein, putative
MNFIDAGLVRRWKLPGYEQLCCTACCVPGTASAAARTVNKHTNRHSHGRREGNGGEERAE
GTCICRVPAEQRRVKRLEGCTVCGCTGCGSGEKRKRDPVKEQAKDAPAAVVMRVEEEPKS
*
>TCRU_1871 dynein light chain, putative
MEDGEALDLQDALKPEVKERPVRLIKIERHDGTKAFLNSVIEMAQVVLDNMPPDACYKDI
AIKLKTKLDEVEKGTWHVIVGSHFGANVTNDSETLVNFKIDEMHILLFRSGPPERPMTLN
DEGS*
>TCRU_1872 protein tyrosine phosphatase, putative

MNDSNCFPFTKLSVQAQYERVQREFSLLLRQEDPRSISFATSLKNRHKNRYLDILANEAT
LYPQVTDAPWASTPYYINGNLIDLDLPHKFVACQAPVLQGIPDFLAMLYEKKISLVIMVT
KLEEGGFVKADRYWPEERGSGSIAVSGNCGLTISEDPGKAYEVEDELKITRRYLILQRAD
EPPHKFTQVQYTGWPDHGIPQSATSLEALLTNVKNSPTTVPVVVHCSAGIGRTGTLIGAY
AALTHLERGTLTDTTVYDVVSAMRRQRFGMVQRMEQYFVIYLTLMCRLGVDIKALVGLLN
SRTTAAASTAAAGGGGEGKKRSSQR*
>TCRU_1873 hypothetical protein, conserved
MADNSPGRLSSASLVDPAIEASSLLQPSNARQSRHSGRSSSVETKTFVVVVSRRDKTASW
GFLTYNKVFPLLVGEVTSDVAALLRKGDEIVEINKVAPKNYDHAIYLFQRARLHLELRIR
RTVSQEKQRHLARNYSMGTSDVVPHADAAGEAMKNSTSPPPTVNKSATDATPPPSHETPH
VGLEVGASRYPAKMSLEKILRGGRKRRFGWGNADVVDGTLSRSPEHPSVAFNEDIEKVWR
RVFSRKRARGCNIPAKGHCSEVSEVLPRPARQAIYDRRSCPFSAEEGFTSEFHDAVQHVL
TANALTHGREGHSHGLAKGTVTISPGSQHRDVETMVESIRSKEQLRDEEVAKYNAAKGVA
QCHKELEAVHNAMLRVAECHCLMREERRCNEVEKYRQTESAARTFLANYMEAVSSSKPAA
GTKRRSRRGYSRDGIHDAQKYELRSPPSSAAETACDGSATSPPSYQLVSSNVFSTTERVR
HAGGFSSRLLRLPTPPPTPPPPPPPPPPPPPPPLSSSGG*
>TCRU_1874 hypothetical protein, conserved
MSRVETSMEAVVYEDAPDASARLKRLKVAMLAFAGVPATIPAVTAILVPVELLAAPSSSS
GLRPATLARETAESRLRQVCADRVQIRRWLQHELGITMDVWVVVTVLPRDINELSLLANW
QMDRHRSPLRQADAVSLSLQEVVLLWGDGRCQAPMLEKFLLPHQSLLLDVTCCIGESSRQ
LVNPAVFSPIRAKQIAKGRTCVVAFYSAWLPLSFSTRGLAQLQQQFRDIARHVLLHMKLP
LSCPYGGEVGALQQNLVNVTLTRRNRIAEEGSEQRLAAALLATRSLKDIYSLVGVLFGNP
LANYYGEAMAFCTSVQRRRRAAGFFCYPASVVLAKPAGATGAMRHVDDVSPAEPHRKRGR
KETATEAVDEGLTWCEDTGV*
>TCRU_1875 Plasma-membrane choline transporter, putative
MDQDLKSSKYKAYNLEVLPEAELYSQHTENLHGVAVNGIPLYPNETPGNPRLSRFVVQGC
QDVWAAVIFIAMLIMSVAWGSVNLATYEPIPLNSTGHRTIAIDASNVKVSTFVLLFVIFA
VSIFGACGSLMLIGTFPRQIIFIANVMTAVLTLAGAVVAFISGVIFAGFLLVVACFFQVL
WLYLVRDRIMFSAELLKASSEVLSKYKAVFLSAFFMTATSFVYMIFWSAMCLPAADRTNA
GYDNAGDGFLITFFMLLLFWVSEVVANVIHVTTAGVTATWYFAGEGRMPKNPTLASFKRA
VTTSFGSICFGSLIVAIIRLLRWIMESTRDNQNEFIHCVTSCLLSCLESILEYFNTYAFV
HVAVYGCGYIEAAKRTWQLCKQCFFAAYFNDALIGPTLTILSLGVSALIGIVVGLVYAST
TIGAFSFLGALIVHILFFSVVESAVTTLFVCFAEVPEGLQYSSPELYAALHHADQNGTNN
NAASP*
>TCRU_C Terminus (BRCT) domain containing protein, putative BRC.1
MLRGHVFVAAPDVPQDVRSLVAACGGRVVSSVEASVTLGLVVCGGEARLDCAAQLRSLRI
PILRSSWVRASVAAGRMLPMKHPHTEYDPALFESLRFTTTMLPVHLKRSLVAAIQFFGGT
YLPDLTSATDILLHGEEGRMAGTAGSLKWRCAWEWAIPCVHFTWLQECIASGQLGVLPPP
SSPPAAATTRNGEENESSCSSSHEAAGGNYASCTLFIERQKRPRIDVINVASDAGGNQPP
QWFL*
>TCRU_1877 vacuolar protein sorting-associated protein 45, putative
MSNAAAPNFFTIVSEYVDHMLPADNTMKVLLVDEATLNFMSMACSQTLLLKKGVFLVSRV
DEHRQRKVMKGMRCIVFIRPQMSSVEAVAEELRAAKYESYAIHFSNAASPELLDCLARAD
VESLVTRVSEVFCDFEAHNADAFVSVVSPRALLPAFLSAAAVQRVAEGIAATFLALRRRP
HVRFHQNNAFARRVALELGDILSKNAELYNYKNKDSLLLILDRSSDVLTPLLTPWTYQAM
LHEYIGMQHNRLQFSDATVNEEYVFSQQDDPFFAANMFANWGDLCNNVKTYVDKCKATLN
IDRSTATMDEIKEFMQRLPQTKSLTGSVTKHATVVSHLSSIIKQRGLLDVSLLEQDMVAS
SNAGDHWNRLQSFAAKRHSGGVEATDLFRLCLIYHLRYEKPGQNSRVFTLLEEIDPHKAS
CLRKLDQYSGERSTDELFGATGVMASIVKTFVDVGNIYTQHEPVLKRTLLQLFSGRLPID
QYPYLTPPPTSAANSSQTQQQLSFRPKEVAAFICGGFTYEEAALVNAINAGTAFTGSVAN
NLHQGGVRASIGGTAVLNSEMFLNMLSTHP*
>TCRU_1878 Spc97 / Spc98 family, putative
MLAVSFLAVPAATSVNRPAVGDGNDALSLVELLVELSGSLTSGNFGKYRRGEYGRISAET
DGILRTASVPPSRDPTVIRRKRRRDVINSFFDSSTASTSTPVFSTSPAVFRSRLRQLFQN

AKQNIREVTETHAALLELLCSAVAPDIDLKEAAEGAATLSEASEAELMLYIILRTSIAAA
PTWQKPPTIPRCWLSPSITEMVERSPTLQRTMRWSCDPDPVIEAALGVDHTRYNRSAFEP
YMACQLPALLTYHTDYAGVATTAGGGVERKPYPNESLKMDAAHGVFSYWCAGEKEEVRCL
FSRKRPINVDTEGELDSPPHMTHHDSSVVHAPSSPGATVKKLFFSIFKEEYPTDSRFCSL
LFVALHRGIIGQQDPYLLLRLEGGGMGCPPQQSLMITPSKLSFSQFSETVEISSFTCPVS
IGVSPEFLVAATGNHGDEEMRRRSGNQTALNEGGELEAKDTLCARGVVAMLQWSCQSGTL
FLRLHQLCDVSERPEWRAALGQYGKSAIEALRWLLLSLQRLVADMSDRAGGPHGVSFREL
LVAQQRLRYVAEDIAVLSDVFLVHAGANWEASLVLGQISSATLLTSLYRHYAKRTANNQW
RGQHPMVAGASDGKVGRPDVIVELFLAVLDPLQCMLGAWLRAGELKDPYDEFFILPSHGT
TACGFLVDTSAQRLPEFISPETAEKILHAGVSLRVLRAAARHVTLCSTKEKRRLRFQAED
IDAAGLYQEKVEDAEDINLLLREFMESLLGYRSSSTFLEMPEVSVLTRNGSLAYWRAFYA
ACNDVLLSVGDEMEVEQKNNVTFGSIQLARVVPVNLFDGDDTTRSICTEERCGVGGGGKA
KSLVTSLSRLSRTTTAWHEAVSEELAQVAHSTSKEEAAVKTKERAALCSEYERRVLRRRA
QRQLQQWKAVRLSLNMERAAALSGCVDSLLELYARMLSQTPAEEGEEKEDKMEDGRRTPI
GKFVKPLAQIPPSAQAAEKSNATSEGKATLQLDGQLLLGNEEAPFETSIVSVFRVTPPPL
RRGSGSVWMGNMSLSLQSEQKSFTRCEREPQESAHAPEMYVVADINDEEYLMERAGPSVS
QASSREFMVAQYDAAESIVRDCFILSEAYQQACKEAAIKLLQVEGDRSCRVDGDGACMSD
YWWTNPTVDEGTRFAHKGIFSALTRNSHALHKLTEEQAKSLLHCSSYYLTLSSYTASYLT
HKALQVMLLGPYGTLYRLTQQFLDVCLMQSGRVADRMTGIWQRLTKTAIEESKFVFSNFM
AALNGAFVEEWESCVLHGRDTLQVQLALMVPEDTSAGTDVFPAENDEEDGNGAGGSMLFQ
DTAFRKRTLYSAYEHVAEEETQREGDGDGTKGRTGDDAIPLPENPFDFISRLIIVYSTPC
EGFWLLPKNAVAIYGDLFATLLFWSSVTQLVTRVWQVGINSDVAEAFFFCNFSRAVLSAV
AQHMWFLIAGFAREYRHTLRFESGVLYSYHQLESFTTDHAAFLERCRFAAMLTPAFARAR
RQVYGMVRQLEEVEQCLLCAARENAADTSVFRSVSPGGNEKKSGAAAAHITSGAKGRNGK
KRTRASEGGNERDGGGELHGSNRRKEFSPSKTSKSSPSDVSPKVKQKPGRNSGARQLPPT
EEARRRSVRNNVSRRIRSFAGLTEIFVEHLTAVRDNLAEDAESSVVPQDNEPEKHNSARG
TCRTNTCTAALSSLIRTLEMTQAAAHDKF*

>TCRU_1879 developmentally regulated GTP-binding protein, putative
MSNLQKINDIEAEIARTQKNKATMAHLCQLKARLAQLKRDLIASESKKSGGKGEGFDVQR
TGDARIGFIGFPSVGKSTLLTKLTSTHSEVAAYEFTTLTCVPGVVNYRGAKLQMLDLPGI
IEGAKDGKGRGRQVIAVARTCSLILIVLDIAKPLQHKLIIERELDGFGIRLNKQPPNIDI
RKKDRGGISISSTCPLTQLDNETIKAILTEYRMSNADVMFRGDYAADDLIDVIEGNRIYI
PCLYVLNKIDQISIEELDIVARIPHNCPISAHHGWNLDGLLESVWDHLNFIRLYTKPKGQ
MPDYDEPVILKRTPQPTVERFCLRLHRQMMKSFKHAWVWGSSVKHQPQRVGKDHLLEDED
VVQVVKKV*

>TCRU_1880 Protein-tyrosine phosphatase, putative
MSREQRKIATAFLEQLRQLSKRHPGNNRDGFDEEMDELRAVDHRVRSNVDEFYTASLATS
VAKNRFTEVRANEGTRVRLRSLVEENQESYINANYVDGRALFNVPFTYIATQAPLKNTIF
DFWRMVFENDVVFVVMLCGEVEDGKAKSEMYWPKENGVLDIGILQISSIGERRLSDLVFR
SFILHNANGEEHQVYHMQYIGWPDQGIPDTSAPLMEIIQTMGKSELSVQTPIVVHCSGGI
GRTGVFIALHVALAQFQLERKDIDIKRIVHILKLSRTGMVQRKDQYVFLYYSVQREMDRM
IMSAEKGVSLLELLRRREPTASRQTAPRPVTNTTPQSPVFSSQAAWTTTKVPQQFATPIP
TQAYPHHQSQSRELGPMPRRNFPYASPHSFSAITEGEQRLLEDYLKRQTPSSQQLVALPR
DPVLKLGKETTTKKVPNMSVLATQKESHTGIPNSTTNTEALEEQLQHWQWRNREMRFSTD
RVERREREAATRQAPEAGTKNESAPSKRPSEEKPSKMEALVEPGPTPEEVQNPFSSTRGA
STFSERSAPPVSIIITPQEAGTARNSDPTFHAGSGNSPTNGSYSVGNDSEQHGHSVATPE
KATALTAATAPPATTETKSATAPGDPAEESEASRFDRLGEALADFETLGPFPRRPRTHII
AKEEFDRL*

>TCRU_1881 hypothetical protein, conserved
MAMMAGRVLLVCALCVLWCGAGGADASNLENNAVGGCMASWVLNANKSYTPSGCDKTALT
LPLRSVLSITAVAASTDPLVTGTAENKSDLAPSSGADLGGAGSPPGRGGEGGGGRDDGAG
GPGGVGGASGSQARGSKASGGGGGGSNGGSKARVDGSLKSPASDVKSPSPVLGDGGSSPG
APAGSVGSDGSKGSILDSFSSGGRSQPDVGSPGGDASLSAPVAGGKSPPSITDESDALEK
TGAAASTKGGEPQEAGEQSGANRARNELPELSAPAESTPEAQEDSPSKQEKPESEAAGRA

ATGEEKRRSDAEAQGPSTVMSTASASNGRRRTTNSGGSSGRRKPNGTNRLANFDRRKDKN
ATVIKQKGA*
>TCRU_1882 Concanavalin A-like lectin/glucanases superfamily/Protein of unknown function (DUF3676)/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MMLGRPRENDDAAASSLLIKDKNKELISLYENKKSDGSYNLVAVRLTEKLERVKEVVKTW
KDLDSALKSCRSVSSGTVDVRKKGMCNGPVPTDGLVGFLSGNFSENTWKDEYLGMNATLT
NGEPRVRNGLTFKGSGAGAVWPVGDMGQTVPYYFVNNEFTLVATVSIHEVPQSGSIHFIG
VRMNDTDSTVLFVLSYTHDRKWLAIPEDPANVEDFDDWEPNETYQVVLQMDDEKWTVFVN
RYEIRQKRYDESLFNSHRISHFYIGGDSKNQSATGGHVTVTNVMLYNEKLLSDNLYDLQD
SKVTIPSLGAEKQPTELVANTATLVVPESKSEEITASHEEMNEDDPEKQEEESVDDPVPA
APPSTVDAGSFVSEPAIAAESAENSLSDDNAQFHQGKTAQQATPNEENKSMQRGSDVQTQ
YSQSKKLTEFNDVEKSSESYDTQLPEEEGKADYRSGESTSSVAASLSTETVAAPVDGEHQ
VQQSVELATENDDVRSTGTGTTGAKESLSLEAGDGSSERTMNAGSSLNPSKSDAEPTSAE
DTDNISRTEGTEVSSEDGKEVPQTVDTAPGNTNTAPGETEISSESNATTPSDTGILLENG
HLGELAAMYQTGDSTVHGCVSRVLLLLLLGLWGTAALC*
>TCRU_1883 retrotransposon hot spot protein, RHS3, putative
MEVREGKPKQSWTYGAVGDTLEKNDAVQQSGAAPPVLMVLTSDEGWPYSWHTIQDLPKDV
FVNCEVDRVWQIVKGDVTAWSSTHGGTEFKFERRVLIGTPGIGKSVAAGSYLLYRLLHCD
AEKLQVVVHCFGGGDAYVSDKTTRAVTRCSDEDMCISESRSLREHGRNVYIICDVAKEGT
PPLRHFAPTSGWGMVLV*
>TCRU_1884 retrotransposon hot spot protein, RHS3, putative
MLASKDNILPIFFGWFALKSSTESAFAKAIATKLTELQPPPSSKPRSSVPTLNPQGYPTE
AAAITELELFDCPQDLNYRLPYLTTFPNSPLLDGFFFVESNPMALVGLRMTAVGGHHTTA
STVRQFTERLAAYFNGWEGLSRDMSWEITYVQHADE*
>TCRU_1885 hypothetical protein, conserved
MGGGSSKPELKVGEKGAIASVAAPPPPEKTLSSGKKKSDEFAKYREFRDQLLSFSLGESA
FDYAERLFEKNPSSPEVMALLAETTVLYDKSKNKVFRNHWCDRLDLLQRGVDVSRKCINE
NPDYGPCYRTYVLCATREAEALYFIKSFLGLGLLENYNAIMKRGEKGMELLPSDSDIPNA
LGSLCGRCAYRWYSPTRPYGIWCGVPGWKEMWAKSIEFHKKAVENEPKNLEYACRLAQAY
YQSGDLQNARRWYAKVRDEMPPEDLKDERWQSLAHTELSTAFAKTSWNVPFA*
>TCRU_1886 mitochondrial intermediate peptidase, putative
MLRRVIVGGVCRRAPPLIAGRMVAARYAATIPTSTVASTTISSSPTNRDDASTRAVVSEV
PNLSFLASKTVLAETVEQTIEVCEALLNEIPKVKGAKEKHDLIDSTSNVLCLLLDPCEFV
RQIHPDEEYKKHAAYAFQKGYEYMSKVNSRRELYDVIVELDSPEGRKQLDDEEIKNVVQL
KRDMESNGIHLSDALREKVTEMNIEKEDLAMRFLTEQGAKNPFATLRYLLRCRYELAQLL
GFESYAEQQLRGTMLGNQQSVWHFLCGIAHKYRSAAEKELNLIRQNVGEVRNRQNITDDT
RARVAHSLRRDAEPAKAEEYFSVANCIRGIQCLCSEVFGLRLEEVPFEREEVFNPDAKKF
YVYDENRAFLGIIVLDMYASDMKYCQAGHLTLQLGCKPHQEALARVGLKLPERQYPVVVL
TCNVGALTPAQRLPNGRFDDESTLMHPSEVTTVFHEFGHAMHTIFGQTKVQNLAGTRSSI
DFVETFSQLFEHFLTSHEFLRLWAHRINTREPISFDIVMKRNAAADMFKHLDMLDQVVLS
AVDQTLHGPQPYTVYFPHGQNGHLGKRTLGDSSDYGRGTYNLAKILIDVCTPLSIVTPTE
SGVLGTLSFEHLSGYPAGYYGYLYSLSVARRIWSKKFEKDPLNRAAGKELVQEVMRHGAA
CNPVEVIEKYLGDNLDEIDIWA*
>TCRU_1887 hypothetical protein, conserved
MRRSFCLLAAAAATTAAASAASPTNTKMSTLYKVLTGELHFKNKVPVKECNIVHQFGEDW
ESELSAYAKALSAQQKTVLERQMVRLKITRYTVAELSDYCGDGPAHLDASAREANIEQGV
AFLKEKGIEAFEKYVAEEAVNANWKPADVKKFIDAVKSKAK*
>TCRU_1888 chaperone protein DNAj, putative
MPPKLPLYEVLGVSQDAAEEEISRVYRRMALQYHPDRNPNGEAKFKDIANAYSVLGDSEK
RRVYDATGVIPGGAAETDNEATMAERSAEMKERVQVFYATYAGSPEETEDVISCYKKCKG
NFRRMAREELLFDNKKQGEIQRLMELVRSLVESGRLNPTEAWKVTNTAAVLKQIERSLTR
ERKEAKDALDAMGLSAKEGEGGLHALQALMKRDQEAEWSKMMSNLESKYVKPTSATKGVE
QNGKRNKRKAEATKTVSAPPQKKSRR*

>TCRU_1889 amino acid transporter, putative
MKTNGNDSVCEGLLRESRGLRQGEFTGRQSLTSRISMNVARRLSVIGVAEESRTATVSGA
AINTLCNVIGAGVLSLPLAICEASVVGALVLMFYTAILSGFAVFAVVAACDATQRFSFTE
AVAFVIFPSLTFEEFCTMYSFVPFEGNVEPEKGTMELDNLRRCHKEDEILRRKRRRILMV
LVESVIFLNNYGGLVIYSRVIADSIPPVVKNFLHGSGFFVTRIFWLLTSGVIFFCLSCVR
NMDELKWTSILGFLTIFYIVLTVVARYFTSCHTPPYPNVDPADRGEINWYHVGTGIFRAI
STYGVAFGYHYNVPYFYRELKDRKPSTMMKTVYVAFPIIVFCYATTGVFGYLTFGNLVTA
KTSGGDIVRNYPDDDPVVNVGRLGLFFHFACVYPILSVCARRGFHRILMNALTWCSQTEL
IEPGRDPEQVGRREREYTAVDVTGNMSIIGPDRDVGSPEDTTRLAIVLEAFFLVTTTVAI
AAAVSGISVVIDFFGALFGVFLMLTCPGLIAWFLFSRAQLLRTSPYRFARLLMALSVLLI
FTGIVFSVVGVAFIIKNYTT*
>TCRU_1890 hypothetical protein, conserved
MAMMMAGRVLLVCALCVLWCGVGCGFADKVVEAAAGVVASNRTDEENLILNWYVLTQGEC
ANESTTGGKLNVTAERICMHKVMKEVCDAFYNKTSGVTHDRDAKFICTYYATIPEEPVEP
PTPQGPPPDSAVSNTTIDEGTPKNAPESDVAGRGEGKDDDKEHGNTKQKAVETAAVESIT
RSTDSDVSTEVSHTTSHLLLLLVVVACAAAAAVVAA*
>TCRU_1891 hypothetical protein, conserved
MNCGGVNFPDGTIHSPARSGDADRTGIRQLPPPREGKDDTKSGGTTAPQVNAEPSRQHED
WRQSAAADAPNTVDPSPASNTATNTSETRPEFATNPIDVMFPNASTKRPSFANGPIILVA
SNASGIMSVNYGGREHVAADNTDEVSERNATGHKSPFLRKRRCGQWICCWG*
>TCRU_1892 hypothetical protein, conserved
MDAAAYRRLQHRMESRGRAASSHSTCDVCGYHCSCPPHVRREGHGDDDRLRGAIGDGRRP
TRGAASSVAPNAQAWLLQRVQGVEVDITNGGIDHRRHVSCCCSCCIGYHHLFHARHGCSG
SVCGRVEEREKGERGDSLKESYARRSCSPKSSAGVSHSPMAAAHTHTKSVETDLGDAALA
GNARDAQRGLTFRPSRSSLTVSSFIRLAESVPSHFSSVGENKSNEGGGCQPPQDSTPPHE
YGDVSKGRTEVRQPLRRGTPSLLPVALSAGQTAARQSLQSIPHPASVASPQKIPSPKRQG
TEDISADTSKVTIDASAVTHHAHTTGIAPIVHMSGFTLGSLPNVSVSFSMPQPSSSHVVN
SPPSDCVPVVAHQVSFLESSASPQTSTPVPAATPVVQPTPNTLSEAAGAAMTSAGTAQTS
TPVPAATPVVQPTPNTLSEAAGAAMTSAGTAQTSTPVPAATPVVQPTPNTLSEAAGAAMT
SAGTAQTSTSVPAATPVVQPALVAGTPEPTPADVMNALREKLLLEKADAYVRNLEQQRLE
EKLAYEQEEQRASKTYGQILELLVRLRQDDQEMLEAMYENILEPVEAPFSSPASAVQRLP
TPLQRRTEHTILSQPNLSPFPAEVMTAYKMDAGKKAQSAPQPKPKAPVQAELPPPLPPPP
LVYTAPPSPRVSTATAPSIPELRHELPEAPPFASKGVPWGSAEGTMKAWVDKHFGSSLDP
QHRALLQHVLLSREAEIRRVAAAESQCKKLEAQILGAKNFVPPLAVEETARANLSQWQQE
RDRELNQALSLIYAKEEELMAVRKAQEEQKAKLNELTLLMQTHSVQSEVLGAQEEKEELR
RWKMRCDAIEQQHRFSVQRLEELQAYIEQLRNSAQQAVMNVVSSSAAARPLPSDMRGAQL
SSVNASRPTCCLETASQHSTVPLAKPSSAPRYFSPPRMTDGAFVAAAPQRESPAADASNA
PQPCLDAAPPPTAGLDRAAALKQLREEMDLECARFANETQLWHEYLKHQEERRLQLHGR*
>TCRU_1893 hypothetical protein, conserved
MTHTNTAVTPTGKKADGMSVEEDISRIVEGAAQRQELEQGITAFLRSNARHKVADVLLAL
SAYTFGGLMHVRGQGTALTSLSMWTSGTTFLLNMQVRKVFEIEDSAKRRQVAAGMSLEEK
NVFQLETVASWLWMLSSMQQFKLHKRMKYCGYSSWMGLGCCMYFTLRHTYCMIMLE*
>TCRU_1894 CRAL/TRIO domain containing protein, putative
MVEGAKNPAADGTEGWRLYDESAEKIGSSREQQVLLELKKILGWTPSLTLDASVDAFLLR
YLSAVHLSVSEAVALLKQRRSYEMSLLSLHITAPVLEVLRSGTVSVIGRDVLGRPVLYVR
AHRFIQFGLDAQDMQRFLSVVMEYMLSYCTRAPSSPSHGSRNGETLPSLHQQQIILLVNE
EVSSWHASQAALSNAHAFRSIMKKYYPRFIGLLLIFEASWDVRQGIKAAFGDNPGEEKRV
VQMVTRGNIQKYIDRYVLTQELGGSNTSVESPDNFADAVLSHWFNVRSYLSLEDPKTRPL
WQLPPSFVNINDWNQHLQRREMAATLNPDGNGLPQAQQFLSRCTSSQFDSITCTSLRRST
VLRRGLDEDEGFCSALSEVEDMFPSFNSPRLTPREVSLDMDGNNSSAAVLLRELHKEREL
RIAAEQQLRKVRLGITLDLSMATEVERILTHIHRELNVLVANVVTRARDAAANGSPPTLL
QLLDLTLLAIEMAVHKAQRVPAMKFAVPVTQSPENDSPCCCVM*
>TCRU_1895 Zinc finger, C3HC4 type (RING finger) containing protein, putative

MFSAIVNYLILLAFVYLALALIGNIVTLLELWRIRRSIHQKRPPIIIPFLVFTTRPVYEV
ALTHMANRAVVLHGLPKVNGLTLPLQLHPVPSAKVLVKLRSTTTARQNDFLLPEVRPEND
TDANEASFNTIPSSSFVHSGGGGSAHVARHSRGCAMETAALPSASRSHQMMGSFGNGGYH
QYRELSLSDLGGGYHKQEGNSGVGRLMARSQLSLQFRVETAARIEAPNLSRIQLGNASIE
AFGRDSSSAFCGALSRSDTMIFEDPKISLVAADDGSEGADLPVKLRCACIFGADDVDIIR
AVTVGTTRTFGRGSFMYHCYYTAEDEENCARERARLLDWHNRQRLGARFQFGDHTPCMPL
SGAFYEDSVTQTNPPSRRRRHLMLVNSMTSVGECLPSRQGSLGSFSTLAGRTRSMCCSTK
SNAFTETFVDVSETACFASGSRTREERGKNEKEGFEMSKYVPASIMNDAAQDLTESNDDC
MFVTAVSPSTSTLPSSTSPPTWTDSSTSDACNEGDSVETGKMMPHTEPQAMNTDEEEEAG
DVADVDRAPLPAENAVTFSDPVNVPVTNVDDAPGTNRNANKAATSKKGHCRRPREFVDIF
LTEPQQGPIIPRAYEGSILITPDALQSDANAIITTTTTSTSAPASLQVDAVDLSLAAFQN
CFKNGPTPASGNEVNAGEGGGGGGEGKDAGGEKAGKKCEKKGEKKGRDSRHHEKKQNDAE
LIPRHPLTFALMLYRRTPQEGRNSGREKRQITSHTRQQTSDCFVCVYSTANAMASLLPKS
ASAMPGGGTPRNSPPGSSLRLNDPNECREIGETYPLPGTEEVQTSLRRLQPGSAKPEKIT
ALLEAMRSKIGAVMSVALQYVRIGNDLYAVTEVSDRTFVQYREERVLMGRCGINDFSSGG
HTNEREDITASERSVWPSKYRMRAASYSLASSPQTGVRHQLVRMCWLCMRTEANVITLPC
AHFALCLGCVETLTHCCICQRSIHATIVLNEDTDQSEFSDTRDQ*

>TCRU_1896 Mu-adaptin 1, putative
MASVFYILDSKGAPLICRSYRGDIQQNPPEVFQRRVLDEEEFRVTPVFEEQGHTYCFIRV
NDVFFLMVSKINICPLQQIAFMHACTKVFEGYFTRVSEETVVDNFVIVYELLDEICDFGL
PQYTEAKVLKEYITQEGLISYLMPEEKLTVKALPAAVTGVGGGTPWRMPGKYKYRRNEVF
LDVVESVSLLASPEGETLSSEVVGQLKMRVRLSGMPTLKLGLNDKAVLGMTRRQGRLIEM
ADVKFHQCVRLDQFESDRIITFIPPDGEFDLMTYRTSKKITPLVHVDCACVSMSSTQVEM
HITARTTFRRNTTADFIDILIPIPGDADKPEAKCSLGKLRYAPESSVLIWSLRNTGGGKQ
FSCLCKFHLPSVRSSDPKALQKAPIQVKFEIPFLTASGFQVRYLKVMERSNYEALPWVRY
VTQSGDYQIRTY*

>TCRU_1897 Protein kinase domain containing protein, putative
MSGTSDEEEDAERSPPIRPITMTPLHSDLWPTVPRSARRTLFGDTESSSSSSSGGGGGGV
TRPIMAVVDTDNSTVDLSEPSPPHVEAEGAEEEAEVETHRRVPWGASDDGKRVPSTAATM
SQWEQRYKTLLPLNWGRQLEVIVMLARDTVDGCLVTTRRYRYCCETDASPAEFLESGDKS
CIPFTAAWKRRIYGLLSLRHANVSPVTDVLIDEERQELLLVHPYVDGMQPLVSALQRHPH
MIHRELTPSMLMRILQEVVDGLLFLHQHGVVHGALSPWTVLLDAEGHASVTGFAVSEVRP
CPRGVVPAGGATHPFYIAPEAKHPSFRWRHVTVAGDAFAVGALTFAMTWERQDAVYVALR
HSMVGVMHGDPKQRMSLHELALLVSELASQNTLNETASRELGGRRLSASTAGDPALLPRG
NEHRSPSLPSAASVVGILQRDPSPVLYRVTGLEKWKRTTNTTAATERRITQRKRSHHSPA
RQVLHRWRVVSTAVLFCVIVVRMSRERRQALAARLFAPARKLQLKKLRFTHSNASPFASV
LSTPRPRKPTTVEKRRSARGGSKDK*

>TCRU_1898 hypothetical protein, conserved
MARVGTTAAAVARCTRRIRAPLDHLIMSPSDPDQVVTAIRTTDAAIVTWYMPLAELQRVL
HRRYEAEQFGELTSPSTTSVSSSTGQQSPNDGTADASDGAGGGTVPLGFLTLVAGRNYPL
KQTWLERCFDPAPHPTLSLRVAVMDRIHWQRTAWMANSICRSICWGRLPQKIFSVNLDWK
NDVCIDATFDAAADRYTAPYELRVPGLGFHLTLQDTGTTLLDPTSRIVDGFLDNESALHR
LSLAREVNMQGLGGSVYRQMLWSTPSLPNNAEVVRFDPGTLFKRCFGVDPPVAKPVAAWL
VQEVEKTLLYRMEGEVEDENDPNSATTYGDRSLTERVQKKAMNRYNGFRDEVRGKVYSDL
DGRELPR*

>TCRU_1899 protein kinase, putative
MTTYRKQIVGKYELGKVLASGYFDCRTRLCTHIVTGAQYVVRIYNKSVLAEAQWMWDRTR
DAINVMRTLPKHENLIETVECFETQTSLYILMQLFAPLQVTKLYTSETASGHRVMIPIQQ
TKHYYAQVVRGLLHMHEHNVVHLGLAPDHVMVNDRDQVKIGYLVSCAYFPKGEMCHDIRG
TTHTVAPEVLRNEGYDPYLADAWSMGVLLYFMLHHGRYPHDGANTTKNIMYNRIRPPDPT
LSPDARDLLARLLHPTPSRRMRVENIMSHPFFAANQSDTDNAEGRGAGRFVVSSPETYCT
LDLATGEDTVNIQIPYGLSRQEEAAYIIQHTYRAYRSRKWQQLSQRKSSVAKDPAAPRHN
KIGRRPSFMSGVANPLLSEPPEVEDVKGFVSHRTDRRQSRGGAIAAPPDMPRFDDASVGS
GSASEIIRDVNDSVAFVLENTVAVPSSAATPALENAVKSKYSPSYSRTHNSTLSSITSPR

RGDAGRTKTASFAPRLEHDARTDEKNVENVVSLMSNIKIDATRPCPLCHRLPMQRLAGRE
PYANTPFVYQKGECIPRVLD*
>TCRU_1900 ChaC-like protein, putative
MDVTNIAKEDTPAELPPTFLFGYGSIMWKQDFAYTRSYPSCISGYRRVFYQGSTDHRGTP
GKPGRVVTLLPSDAPDSWVAGIAYELPSDPTALAAILAQLDHRERGGYRRVEVVLNDLHT
REPLALPQGALCLCYMATEENSEYLGAATEENIAAQILESSGDSGPNSEYLFNLAAELRK
IQAVDEHVFSIEAAARRILEVSGEQEN*
>TCRU_1901 WD domain, G-beta repeat, putative
MMTPRVASEDCGEELRIAILRVRLLLALHGRVSGDDNPGQESAMHAGSVTPSPPRQRTVW
AHSDSLHSVDLEEGSSDRCQLDARRTREQTHEDHSQEVKEEEKGTSITAQTLPLPPLRWQ
LPTLPQRLEAVEKRRERRQKRTDPGQKRGWFASNPVAAAAVAVCGDIDDANDDHQDEEND
RHARTSSSSAFTLTGDRSDRSSSKDTYAASHASTDDVYIHELARGHESPLNASSNFHRRW
GSASLTQGGTNANSLATHLRHHSALLAVAGVHSESTAVTAQLEFDRIGAGEEAPYASYLF
SPEARIVDLSMLPLAAERKHEGGEKKATADESRSGNGSWPLPAPRHTELVASAPEKDGCT
RVCFSPEGDCYIVGTECGKLWFVQVSIKAGHIISTTATSPLPLHGHSGAVTDIAFDDVGT
CFASSGADACVILWNQRTPSKVRRINTDGGVPVAVRFMPKNNNYLLVSLPRHHLLRLYNS
STGFPVTRKGQLIRVEATALVMEPCTYPFLFLGDAHGAITVWRYRVSSVDDIACPSVVKD
VNEARKRSQPTTLPQSLLPQEPHPSTPSSLHSAATAAGQFAVESHLEHEKRGEFMPSTIT
EGQSQFEKVAGCVVEKGAPVASLVASSMNHQQFHCLLRAQRMGQEAHERSTVKKWAAAAL
GGGWKRNEGNMVSNKKDGKISTRSAYAVMLLASFPRDRLVVLSVQPSKSTPHEYKLVPML
VIVGACRIRQMSVGTSFCVDNTRCPTISCTCEEGFVQIIACTPARLPAQKDENVKKSCLT
GQKPVQWSVMATLPVPCGGIPRSLAWSPDMGLIVAVTEEGILYEWRRVRLHLGVPHPGYY
RSGGGGEEHCRDDDDSTGGPRALHEADEWRICLQREKERQMRRYRAQRGTADSDDGSLSG
LDDLWARSGDSVSRSPEQSSR*
>TCRU_1902 hypothetical protein, conserved
MFGTTRVWRNTFLTKSVATPPISVIRTGPRWWADPERMVRQKLMYFTLGVDQLPLRRTAV
IQKDLHRFHMCKPPPRIGDTTGYKRSRAAQLTTWYRRIQYQEYHLQHLFTRHVWGLVRAY
PGNTTKIQGKADDGYVGYDSVPYHRYNRTPLPFPAREIYGRRE*
>TCRU_1903 translation initiation factor IF-2, putative
MWRLSSGVRQLAVSWIGASCGCGAASAMAQTTVRRWQSQSSRGQPGLHWDEGVVDPRYSS
EGNMRRFNPDTVAHYVKATIQNDRREMGLGEVYDWHEFAKDAVYIPTRSGPLWVGSDDPR
CAKFMRRREKMKKSPQQKARPKPGPDPAKQLEDHTLREFFTTATNLRDPLSTANNLHRAG
LIREYDIKHVAAKIQYLPRPPIVSIMGHVDHGKTTLLDYLRKTNVASEEAGGITQNVGAF
QVKISDGHFVTFIDTPGHAAFTAMREVGVAANDLIVLVVSAVDGVQPQTKEVIGLARDAG
IALVVACTKIDRQSKVDPIKQQLRDCGIELEEDGGDTQFVSVCGRDGTGIPELLEAISLQ
AELCEISTPEPSRCEVTVIESRSSDVKNEVAGIVRCGKLKPGQVLVAGMTYGVVRKVMDN
NGNILQEAGPSMPVIMQGFRVHPKPGVVLMQVSSESHAQKYYLFMKDVYKVEGRREDYLQ
LLNQEQHGMIYARKPDNNLVRTYSTKAFVLSCKAATFGMLQALMKTLYELPRLEGVSTEI
KVTEVGGLKDYDIALIGSSGQPGCILLYGESKDTNTLDVPNHVKVIRFNVLYHGIDALKE
TLVESLPKISKTRVTAEAECIQVFRASQAGRNGNAGGMRVTRGSIIGSHLTFRVLRKSSR
SKLTGGDNSPKKATGDGDDAEDARTVVYEGQIKELRRFKEIVPSVEMGLECGVILHDEFQ
FRLGDILQQFEVYEEPRDVAEEYEAAERREKIMRETAALQAQMEEEKAGGNADGAGTV*
>TCRU_1904 WD domain, G-beta repeat, putative
MTTMLLSVPQAHSEVITSLQFSPHHVSVFCSTSGDDTAALWDWRQATAGHEIARLTHHQG
PVNHALFLQEDERILLTASDDRTIAYWDARELSAPVGNMRGFGDGINKMLRIPAPGTNGG
CNWLLASACDDGMVYIYSLGPENVPQRNDQQGRGANASNTAAIGTMVDRFWAATSTVNDL
ALSPNPGLLLTASEDCAVRLWNIVADMRVTTEDRLVASFEEFDNPVNHIAVVHSEAQPEG
HPRPESGFWLYAACSEVVFAVDIDPLTGAFGDAARTLMGHQDYVRGLEFVGRDALLTVSD
DTTAIEWSLTTAEPIRQVKLHEGLVMASATSAAKDVLLTGTDGGELRAWQLPFNTEKCNG
DTTNGY*
>TCRU_1905 CotH protein, putative
MAIPNPRRWRREFGGTRKRRIRILLRFLFFSLCLLVIGVFLLLLLAANEKRTFEKELTER
EIPHYSTNEFFTRVSFVMSSAMATAWRTSSDRLEFPAEMWVERVAVRHSAATTVPLPAVL
QKATVSATLYGKSSLKLQRTKRRSLYIRSDSPIFFVTPNPALSPNPFKRNTTVALKQFIL

LSLWEDIHRIAYRTSVDLLQHLDLIFSYAQLVELRCYPPSQKSHLDHPCVPSVAGVSVRD
GVHVGRTLGVYLAIEPPAPAIWRRMKEAFSAFEELANESLREVIESVSHGSPAALQRREY
ESVMEHTARITYWRQMWRAAKKSSPGKLEHAVEIGSRNFLSFSEPRHDMSHVPSFLKNSS
LLPSYRLLEKDPWHYGLHSETAMGKTVNPKKQFLDLPQYMAWIAINTILQNGDYDDEVFF
YGVLKPIQYGNPKFQLPIYLGVMGWDYDTVFSPCHRKVWFKASVMYCAETTLDKSIYDSE
AFIYRYTDILWDMTQHIDRERFSRSVQVAENELQTILYGAPGTTMATFNQVKRENDAGVR
WIIGAFLEQRQILLRALASYFPVNEVSHCDQTSDRDAKALEIHNREAHLELMKRLSIVVK
VKGSRVSTRWGFLVGGIQSALGVDLPEDEEYQLPDAGIYCARVSAVASFFTSVGLLPPPK
GRGKWEAPGFWFVDMPLVEPSTSRGSAEFGLWSFDKKLPMLYPMTTPDAGATLSIVMPPV
WPQDSKEKRGVFVSRVLFPEQGSENSLFRWSRKNTLIFTIDAPTQKTMIVRGFSAVRFFV
SEKSEEDSFSAQRHEGENTVRGPGLFASNSSTTRLRIGDVDIEQSVPLASVAAPPQALYL
ADGLVDAKGVRFGGSLEKQTVLRCIPENASVAESVVGEGLTLRSAECPIFISGSFEISRG
ATLDVAAGCVVVMRPAAMLRVTGFLRFNGTVASPIVVTSESAENASSWQTIHVDGPTATL
YASFTFFTGSGVKGIRVANTGKHHSHSAAISATNKASVYLRHSFLLELQGAGIAAGNEAE
VQVEDSLVQWAQMGIECVQCTFTSRRSVWTHFPSWDAAYADDDNDAMYLSGGKHRVIDSV
IAHTKDDGIDSGAMGNGGSLVVHNTIVEGCMHEGVALSSDPNGHREVVISHTIVQYCQQG
IESGYASKQHTASITSSLIQKCSVGVRYGDNYHWSHCDGKLTLQNTTLAQNEVNVMNYER
RYQIPQDPEYFHSEGVLSQRHWKLLRDAARDSALPLAVAPPEAVVMLLMDVRRRELPKTG
WEGCKDMFLLPGNSTLIVDEVVDAEAFTEELRVTEDVTVTF*
>TCRU_1906 hypothetical protein, conserved
MTCVSQSIARYSLLRCIVSAAQFAGGDLCFYENYAELVAQDAVGETTTPLRIDYDVLLHF
RVVRQQQLMRIELPRLIVWRWAEANRFASELDGGEILTREDMNRPCTLIEQLHEDDMAHF
LQSVAPMVAASRRARSASRVSTTEPLPLSYFPPNPEADSVASTETPSDVDGDNANLSGGS
QEDNDREGGMDDSSENVSAVWRSQSTVPTTQRNPLLGVGADSVESAGDKSNASRKKKHVD
VAPVTETAASVVSAAVVSEEREEKGEEDRLSQCLEALGAAADTSAVQLTRGISSQSSPLL
ANFTARRRDREAPARGGSNEAVMPNTPPPPSLSSTNLRMPRQLRGKGNTQRSAATRRRPP
HVGIDGEEEAGTMPKRARKEKSPTLFSLPAGATVGDADAATRTTTRVPLVEPPDSGASPD
QPIETPNAVTPSRAGGLPHSTRSDVVSVHRGAATAVKRDATDPNVTAEAAYNFADLMTAP
ENAAHLPLFPEVKKILGELEELIPPKRRGRGAGKTKTPRPPPKKGTAGKQQRKVTAKRRG
GGIEVISKEQTKAAKAESTTAPQKLHPVAGEDDGASTPLPDAAAAALAVAAAANVVVSPP
ANVPPNVKPSYPSQHESFIQAPALPSTQKSQQKSAHDSPEVGHTSDGAAAEAATFCFPSA
CVTPMSDYHLAETASNQHREEHEEINMDTGSGPDSSAYAAPAATAASTPPNRKAISLEQK
MDKQLTSTPLGFHKPLPFAHDSPPLCHCQQRCMRHYGTLSAVVEGDSRKSRWRRVVRQLN
SLSLHLTKARACGEELRGLFLLLLEDAEI*
>TCRU_1907 MORN repeat, putative
MFYTSCSYQGERTPDGKRFHEQGIYTFANGDTYVGAFNDGRMHGHGTLFFTAERGGGQYR
GVWENGRNVSGAFVFADGLVYGSGEDTTTTDNNTAAAAEAENTATVTRLADTTSILNSGV
KGGMDGHPISSNSNRGKGSVRESLAEEWLYCREGDRRLWAEHLREVMPVLPMQAVLGGVR
VPQSSLWAVEPVVAPSVAAEAKIPATFVQGQPRSLADVPAHFWKDPQQRENVMSSMRLPT
PPFKGAQGGAGREETMVDNGDRPAINLSLRIIAPLESEAMRRAIAAAVAASARAATSLEA
RKSPQPESTLSPDSAGCLVTPGDTDVFDKKGANPELALQGTPVHLPGELEGGSALRDDEC
STVERHASQNTPLQDPKLAPCQTNEPSLAPHPLQGLSVPETPRSLTESPEEVTCRGASEA
RVDESAPSPVLQTVMYAYLSQEQPEPDAKQHDEFRQEEEEQDTQEQEHYKQDAAQEHEGE
QQEDLKNEIGSTEEDKMYLSDGNA*
>TCRU_1908 ATG12/APG12, putative
MPRKYRYQRTHTFAERQKEVATIRGRFPQHVPVVCEPASIDTVLSAGPISDRCRLLRDLD
CSKFLVPGDASMQQLMVLLRSRLVLDAEQAIFLFIDDAVLPNSACVGDLYAQRKDADGFL
YMTYSIESAFGGAAVRRN*
>TCRU_1909 hypothetical protein
MERLLKRVGLLGEQGPNTHDKSEICSVGECGSGDSSCSTNADLEFASAVTPKTVTVTSAD
GDFGAAGGSDTVAVGSSFSSGMDKHLLAVARASEFSALKRLELCQQELLQLQRMWDLDRE
TQRWTVASLREEVRHLQKQLEQQRLCGWLQRTREKAIVTRNLSTSPESGVGASFRHAADR
EAGRANGVFEASATSGTGDVSARAEETCLGRSSDGQRTHGVCASSGAEEVEDSLEFYGRL
LHDANGECGELQAELSRVVRRLHDERRFFAQQISSLLREKEEMVREHATTLAHLDETKDL

LMAARAAERAALRRLTERCPGESARVYGGRTADGGEMGTVYCSRCGCSSTACSELLRSSV
DFSVERHHCNSLAVRQSALEEEVCILECEVERDTRNAEGLRRVLERLIDEVDVHARGCRA
ANKDIVGCLREISLLWLAEGDEKDDEDDEHKSDDGMPPSLLLLGGDGPDGDSSSECAPSS
AVRSHLLSAS*
>TCRU_1910 hypothetical protein
MLEKSEEMVQLLEEARQAECNARSELFNREEALLELQRRRDDDLRELEAVTHAHRNLLHA
IRQPREGMTEENAEESFSEAERVQGIERHAVQLESENIALREEMAQRAVAHREAMEGLNN
KISKLMEELEAKGMEYTETLGKLEEFVGLLEAARAAEKSALMALEKREQELFELQAAHDE
EMRELESAMKGLDGGVLPPQGGAADFPAAEMQANTAVADVDKNAVRTMRQQLERLKREKE
ALVMELEVKGRQHEDALNVLNRNIGELMGELDSRIRGCQVSATSAKELLHEIALLRSAEE
ENEEEYNEGD*
>TCRU_1911 hypothetical protein, conserved
MLARGTSAPGETTSLSAEEMHQGIASFLGGIDEPVLCDSIVAYEFLDNNLAAHWSLARVL
SLSDHHALLQRWRAENGSNADILETLKQEKELKEEEVRNCRRSLLQQREELATVRRDTEA
EVARAKDKIEDARRLLEEVEEVRLHEAFSRRLPSAGLCLALEASIAILNQESMEDVVMGW
EDLRAVVRHPDFITRLLEYYPTVENSMDEHQDIINRYQPRLLKLQEQVRLSPRKIVSANS
VSLESVFCDWALAQLGFIIVYPEIKKSQARAKEISEAINNNIRTMKLLETQISQIIEQQH
LYKEGNNVVNCNKADSDTCLSFAEASDIAPITVPRSSITAAIPGKGSGIVIVGKDEAKRL
TSRTAMHRPLIYAALGSALEERARLEAKNTDKTKLIQDLQQEKDNVYSQNSDLAKQLKNL
EEELHKLRKELEQQKTFAKKQEEYHKQQIEKKIKNQQEMSRQLQQSKEEVKQLQQQDKKR
DKENHGYKTQLEKMEEQMEEINNKNKTLKKSIEQKNQEIIELYEHAKDLQLQLEEMHAEI
EQLRVENEELRAEDEHKTRGLQEVSEQAEDLQRQLEELRAENEELRAEHEDKTRGLQEVS
EQAEDLQRQLEELRAENEELRAEHEDKTRGLQEVSEQAEDLQRQLEELRAENEELRAEHE
DKTRGLQEVSEQAEDLQRQLEELRAENEELRAEHEDKTRGLQEVSEQAEDLQRQLEELRA
ENEELRAEDENKTRGLQEVSEQAEDLQRQLEELRAENEELRAEHEDKTRGLQEVSEQAED
LQRQLEELRAENEELRAEHEDKTRGLQEVSEQAEDLQRQLEELRAENEELRAEHEDKTRG
LQEVSEQAEDLQRQLEELRAENEELRAEHEDKTRGLQEVSEQAEDLQRQLEELRAENEEL
RAEHEDKTRGLQEVSEQAEDLQRQLEELRAENEELRAEHEDKTRGLQEVSEQAEDLQRQL
EELRAENEELRAEDEHKTRGLQEVSEQAEDLQRQLEELRAENEELRGEHEDKTRGLQEVS
EQAEDLQRQLEELRAENEELRAEHEDKTRGLQEVSEQAEDLQRQLEELRAENEELRAEHE
DKTRGLQEVSEQAEDLQRQLEELRAENEELRAEHEDKTRGLQEVRRTRSCVLSTKIRPVD
CRR*
>TCRU_1912 Putative S-adenosyl-L-methionine-dependent
methyltransferase, putative
MRLLPPLGRLLCGCGGLTRGAALPLSCRHVATATGSVSTKIGGGGGGCDNNSNGTDGGDS
DGGGLVPSCNSHGHEALVDTGTSFSVAATTNDATAASHHDGVAAVHYASLSTAQGGMPSI
VSSGSHVMSDSRLDELATQEEERRVARHKKLFEDLIVFEGGALADHDSLGTSLIMRDFIH
FALYHKKWGYYPKLHRKYRQLMTSGYFDPVPFASLRNQHDYERYVGKIHESTPACITPTQ
LFQPHYGWVLAEYLVTMMRAKFDPREPLVVYDIGAGTGALAVSVLDYLAEHFSAVYAQCE
YHVVEQNPQLVQVLRNRLITHYHHVKIHNISILNWRQLERRRCVLLGVELLSGMPHDCVL
LSGDGVCNEHWFGFQQHDNLSTVHERYYALKDPVILRYLRYLRWLQEESFHSLKVLCLTG
GRENIDPPPFTSIEPNMNDPLRVIITKLIWTHSPFRTLWLPTVAMLFLETCAAFFPRHHL
FLVDWSGVRQALPGVNGPVCQCKVRVAKDMYLRRPADSLHGNAGMVDICFPTDFEHLAVV
YRNICGAHKDISSLTHPQFWKTFGGDKTALFTTRSGFNPLLEDFEPFHVFATHHPPEM*
>TCRU_1913 palmitoyl acyltransferase 11, putative
MSLLCCDPPEGQWLDVYGDPVRPRRSGFECPLDLLQIVAWSIIILLAILHYTLHVPFLEN
TLMIVVSIISGVLFTVTIALKVSLSLSHIEDPVIFRTDLPRLEQTGLTQEAAPPGTEPCV
FCRRFVQAGSKHCGVCDKCVPGFDHHCRWLNSCVGAENYKSFCAFMGSAWCGMAFILAIG
LYVIVDAILAREKYEDLLELRYKSSNYAVFLLFLFITVALCTMGMCVLGHLIVFHLYLCC
THRTTYQHMVEKREKKRERRRLRGLQEQMQEANGGEGYGLCACLSIRKRRDFRKYKRRRM
ENSNTPQINDNCSAPPFPTDPTWPSAHGPQEPYSSDAHEMAPISPKYD*
>TCRU_1914 farnesyl pyrophosphate synthase
MASMERFLSVYDEVQAFLLDQLQSKYEIDPNRARYLRIMMDTTCLGGKYFRGMTVVNVAE
GFLAVTQHDEATKERILHDACVGGWMIEFLQAHYLVEDDIMDGSVMRRGKPCWYRFPGVT

TQCAINDGIILKSWTQIMAWHYFADRPFFKDLLCLFQKVDYATAIGQMYDVTSMCDSNKL
DPEVAQPMTTDFAEFTPAIYKRIVKYKTTFYTYLLPLVMGLLVSEAAASVEMNLVERVAH
LIGEYFQVQDDVMDCFTPPEQLGKVGTDIEDAKCSWLAVTFLGKANAAQVAEFKANYGEK
DPAKVAVVKRLYSEANLQADFAAYEAEVVREVESLIEQLKVKSPTFAESVAVVWEKTHKR
KK*
>TCRU_1915 hypothetical protein, conserved
MQGGFGGTTGFGQTSGLRPGSSLRPGSQMRPGSQLRGTQAAGVGGSLQQPVAIAAKAPVT
LEGMRAATRSGNAGPGRQVGDRSYYIGLLRPKITELTTEIQQLNEQESLIEKNSSVLTQL
HQRGKNLTEEITKLKGALADINLAVEKSTSQDANSVKDQATKLTHLNVDRRKQVDQMFLN
VKEVETQTKKNLQILEEEMQQLDRRIMAENQDYNLYNTTRNEAYAVSDAVLNLQHRVRTL
TAKQELHMAQLATDTDKRRAAEVLREILRKRQLREELTKQCALSVDEERQLLIKQVKTAR
NDIEVLERQVNETRDALGESKSRCNALDEELKSYSGENLKAFQELQEKDRELQSFMDSLP
ERQREESEKIATVQSNISLLLERISRALELQKQMPAEGASHALHALESEVDARRNQIESD
QVTHQRLERELLDRKMELEKVENLDIKINAELQAHARKMEEQSQEMIRYSDLDGLRRNVE
KRHEDLVRERAFLVKLRDSSKHQLNALSASNEALRKRLNEEAAFRSVSTLEGRLRHLRQS
NFSLEEFVRLKGKESYYLGAKTDCLRLVDEINLLLKDTDRTRGIGGGPVLLLGER*
>TCRU_1916 Ribosomal L28e protein family/Mak16 protein C-terminal region, putative
MNHDDAMWNIMGQTFCSFKVKTHDEKTRFCRNPYNVTGLCQRGVCPLSNAQYATIIEHED
ELFLYIKTAERAHLPRRQWEKVRLDASFPRALAQVDEELQWWDQKIVNKVKARLLRLKQY
IMRRRKMLLEPKVEYVSVNKRQEDKLLRREEKAEAAARLELEVEKELLERLRKGTYDSVM
NCSREAFERVLDQEEDRAEFDALEDEEDEEFPEFVMDEEDEDEEEEPSKTTAGLRPSGRM
PVRRQRLVIEEEVEHEQQQKRSRLDDLDW*
>TCRU_1917 hypothetical protein, conserved
MAASAFSSGFVSSVEDFRALFAPNSDDRLLLCYEAYHDEVTTADLTALEDAVRSAAVRHA
TKVQLHFWDCGSDAFLAAKEQLGKVRGTPLLAVVYRQAIADTLKGPVEVMIEDVDNVCRR
LSSYQRGGKVAVFPISLPRTTADAACISVDVSRLVGVGKRLMTEGKADYAEKFFHRALDT
LDAVRPHCDGDENFDGSTALCLAWVALAQMVQGKNADVQMRRLEKDYVAFCGEIGSDVAR
VRAANRLVTAAPFTWRSETCSQRKLREALARDPQSHEHRCALVVTLFLAGDMERCLTEAI
KLRTLHVPFGTTAISAIGDFIGRDHALMRSIGIDCERPSTGV*
>TCRU_1918 centrin-4
MAALTDEQIREAFNLFDADGSGAIDAEEMALAMKGLGFGDLPRDEVERMIRTMSTDSNGL
IGYGEFERVVKSRMAQKDSPEEILKAFQLFDLDKKGKISFANLKEVAKLLGENPGDDVLQ
EMIAEADEDGDGEVSFDEFKNVMMQMRGK*
>TCRU_1919 centrin-4
MAALTDEQIREAFNLFDADGSGAIDAEEMALAMKGLGFGDLPRDEVERMIRTMSTDSNGL
IGYGEFERVVKSRMAQKDSPEEILKAFQLFDLDKKGKISFANLKEVAKLLGENPGDDVLQ
EMIAEADEDGDGEVSFDEFKNVMMQMRGK*
>TCRU_1920 Major intrinsic protein, putative
MPSTDTATTQPENENNGASNVAIPSSGVTRFAFIQRWYFNEFMSAVIVEFIGTFLLVLTV
PLSGINNPEMAPFSVGFMLMSLVFSFGYMSGGHLNPMVSFAVFLSSANFGKTRMLFYFIA
QMLGGVAAAFYCVLIHGNEFPVPNMGLDFLQMLRAFLAESVFTFVLTSVVLHVAISKQRN
NNFYGFAIGSAVLVGGLTCGSISGGAFNPSVATALIVVRCFVSFSESGCTPMASLWVYWA
SEAVGSIVGTILYLAVQNVEDRF*
>TCRU_1921 peptidyl-prolyl cis-trans isomerase, putative
MPANDCVLMDKIIEGDGKTIPRQGSIVTLDYVGFLPDGRRFDSTIERGKPFVFRVGCGEV
IKGWDEGIVQMSKGERSRLTIPPSLAFGSIGFPGMIPPDTVIVFEVTLLDVA*
>TCRU_1922 cyclophilin-type peptidyl-prolyl cis-trans isomerase, putative
MVYLTRLVRRVHRGPIRNIFSYPLNEVNPVVFFEITVEGDALGQVTIELFHDTVPKTSEN
FRSLCTGERGFIQCPLYYKGIPFHRIIPGFIVQGGDILTKDGRGNVSVFGFPFLDESFKG
KAGKHLPGTVAMAHSGPNQNGSQFFFNMRRNEHLDGKYVVCGQVLEGWDLVERVAALCGS
RCGVPVSRAWITDCGQSSGAKLEEAQRALCGERALHSMPGKEVLDLISPRY*
>TCRU_1923 I/6 autoantigen

MPISPAEAFEERHLQRDDGDKVIPPSLALVAALESGYRFKLSSIEEATDSARYPGFLTKD
EFVSLCEKNPNNCLDARMMAKHVSVLAPNGLFTRVSLQEIAAKTGSSQDALSADEIDALF
DVLDRENTGSIPAERLMEAMYGDEGRVALGKQRKEYAAAKAEEERQRALRDAAAAAAAAA
PKESVPAAAAPKKEEPTPPPPPPPPQQKKKAMCGC*
>TCRU_1924 histone H2A, putative
MATPKQAAKKASKKHSGGRSAKAGLIFPVGRVGSLLRRGQYARRIGASGAVYMAAVLEYL
TAELLELSVKAASQQAKKPKRLTPRTVTLAVRHDDDLGMLLKDVTLSRGGVMPSLNKALA
KKHKSSKKARATPSA*
>TCRU_1925 histone H2A, putative
MATPKQAAKKASKKHSGGRSAKAGLIFPVGRVGSLLRRGQYARRIGASGAVYMAAVLEYL
TAELLELSVKAASQQAKKPKRLTPRTVTLAVRHDDDLGMLLKDVTLSRGGVMPSLNKALA
KKHKSSKKARATPSA*
>TCRU_1926 histone H2A, putative
MATPKQAAKKASKKHSGGRSAKAGLIFPVGRVGSLLRRGQYARRIGASGAVYMAAVLEYL
TAELLELSVKAASQQAKKPKRLTPRTVTLAVRHDDDLGMLLKDVTLSRGGVMPSLNKALA
KKHKSSKKARATPSA*
>TCRU_1927 histone H2A, putative
MATPKQAAKKASKKHSGGRSAKAGLIFPVGRVGSLLRRGQYARRIGASGAVYMAAVLEYL
TAELLELSVKAASQQAKKPKRLTPRTVTLAVRHDDDLGMLLKDVTLSRGGVMPSLNKALA
KKHKSSKKARATPSA*
>TCRU_1928 hypothetical protein, conserved
MAANELLADMRALLEAMEDQEARPIERGEGDASTEENLRTPSPSLEDKIGQLLGALRSNG
VDDWAGKPAQEDLGVRFFSQPREGAGNGRVRENTQTTDGDTINSLMCEYLGAVKQVWRTE
DPLEE*
>TCRU_1929 hypothetical protein, conserved
MKTATVNKSSPLEEVAKEQGVLDTPVVNIKSHSELAAEEGKKKKSTKPVSSPPTKPSPPS
AAVEEVRTVTSYAPTVSAVELKNAPPLTFENAVTLDRFDGSYMELRRPDLKTPWNMKVSF
GGDKLVLTSLPPISAALKTHPFLKSLRPDTNGQINWLVDNVNGTDLTTANKSLRAKALDL
MKKTNKISLLLRPLSK*
>TCRU_1930 Dynamin family, putative
MRCWVAAASLQKGFDHFCFTPRAFWTRGVLSSLAETSCFYPRRRRIRHVPFSPSARVLQN
SCRGFTSTSAATMRFEGIGRNRQKPAVREWDEHGTAKVQQSTETTDTALREIESAISALR
NDILRQYSDVFSFLPSADHRHSMVMLLGNHSAGKSTIINYLLGRAVQRTGVAPTDDGFTI
IQRGDRDSEEDGPTSLSDPRYQLQDLQKFGMHFVHRFKVKTRQLPPSSNVPYGLMIVDTP
GMIDTPVHVKDRTSLEGQLRGYDFLAATRWFASRCDVILLVFDPANPGTTGETLDVLTKS
LAGFEHKFLLVMNKVDMFDKATDFGRSYGALCWNLSKVIEMKDIPRIYTTFIPVKTAATE
ELEATTPLVSSLNLAPLDSATKTIEESAAVSVEDRVAVVAMQEFVRERNEVMEELLKAPL
RRLDNLITETEEGARRILLAGRVCNAILWKYRQKQMITVLASSALLGLGALILTVGGISG
TTMSLAGITALAAAGSLYGCLAYLKRLESELLNDSDAIFDRLFIGREKSLDLQLRWRNIV
KPELLDLASSSATAGRGVITTLPTLSLWGQKSITSILKNDIPRLRLRVADYKNTHHIRGG
KHPASTYSGNR*
>TCRU_1931 glycogen synthase kinase-3 alpha, putative
MRKLSGDLKATTATPLTPPVTTPQPQPDGTDRSKSAGGQATYEPLHVLGQGSFGVVMMAR
VRETGKMVAVKKVLFDRRLHHRELLLLRDHLGPATHAGQAGTRNHDDPGREAGKTDPSST
NNSAGEVGFTPLGDLTSAPTTVSYHPCIVRLLDHFTVAGPNGEQYLYIVMDYLPLDIHRL
HHIYLRQKQQRMPFILVKVIMFQLARALMFLHLRGICHRDVKPSNLLIDPETGVLKLCDF
GSAKVMQPQGVNGPREKNVSYICSRYYRAPELLLGSLYYHFHVDMWAAGCVLAELLCGEV
LFKGASTVDQMAEIFKVLGAPSRQELLALNPQGAEALFHATGAGLEVTPTSAANTATSSD
YLQRYHALRIKALQWQNVLPPNTPPAAVSLVGELLRYTPAERLSAAEVLEHSFFDDIFAE
DASLPNGAPLPVSMFEVTAEEMEALPPWLLERMASAEASARRRHVSAGGSGKVVPPQKRQ
EQEGRK*
>TCRU_1932 pyrroline-5-carboxylate reductase, putative
MKIGIIGCGNMCECILNGLVLSKEYPPEEICIFNRTAANLKRLCEQYGVQAGKDAVDVVR
RSNVVMLGVKPYAVCSVVEKIRDAVTEDKIILSVAAAIKISSIEKALGHARKVVRVMPNV

PTRVGVGLTSVTPNALMTREDTALILKMFSTLGKAVEVAESQIHAVIAVAGSAPAYVFMF
MEAMGDAAVHGGLPRDQAYEFAAQAVMGAAKMLQDSDMSPAQLKDMVCSPGGTTIEAVRS
LEKGGLRSTVIEAMIACADRSKVLEANLN*
>TCRU_1933 TFIIS helical bundle-like domain containing protein, putative
MSSNSDDQLLLGLPTDNLADAPNTADLHGGGEMEGEEDAYLDLGPTSERESNDDEVGDGG
DDEGAEGENQSGGAGGGENDSSVAQLSDKALRRIKSKTEARALGRDLYKRWKKLRRRSNK
EERQRHRHHSKTKRKSRREEKKSKDKKRDRKRRRRVNDDDDDDKDSEHHGGERNDDSTED
RYDRVHKKGRRAAATKKKRKRSRGENPIALGDEDLGAAPFADLDEVLQVEEAAAKNSGGQ
GVKGVHTEPKVKKLTADAQRDVLRKIAAGVVNTMREARLKDEVEMNERRPPLHRVAIRES
VISQCRREALRSFLIEEGILQELSTWLYDFTRNELAAFELRSDALDILLSFPIDGELEVG
VTRNGDEILDAFTGMTREHLIHTDLGSAVNALRQSKQEVHQNRAKAVRLLERLSRAMAGG
VRSGRRGGSDGVRGSQAGEGGLSSTVTWKCKEDPTVAPPFHTVQTGTEAFQSALARPDPL
DPFSYLRLPPRRAPKVHVTNLGGNVGVGG*
>TCRU_1934 hypothetical protein, conserved
MSKQRRESALAVVQRLNASPVRLLPPILHNATDGGLRQSDVLVVGGVPGTGKTTWAYRVA
AQHLSCGGVVTFVFVPGSGNFQMRRFMEYLEMFVVTPDPCALLPLCISSVSVAGDSVMEA
RRKALLGALDRLEVVHCVDINDFFVYCNHGAVGTSSGVGSREVAVPLFIVEGCGGKGSYL
YHLERAIGHAVPLSHWLIGCLQRRRRCALIIIEDWGSEDVAMATRRRSTREESFSPFVLA
VEEESEFLRYLHTETPQKKAAFRHHFAKRQRAGSTMTVTASNAGSGCTAPTQVPLSSDLM
VRDLHSHFAGSLRFFYLYTQMVSVATSGLSPVASLLQWRLTEQNAGGGNNEHTELPTESN
RQERWPPPPPTERTACLRGEVLCVAQL*
>TCRU_1935 Domain of unknown function (DUF4586), putative
MTQLSVYGGLFSDPPLISTDGDPKRTDPYDKMDTIPSRYLGKGMSIGRSGTGQNAEVYFD
KKYLTLASPEQNGNKDLGAFEDADTRMRREAMESKKKNISEKVFLLPSYPKWSDGPGSYS
GCFQDRPYPFIVPGENDKKSRRRKKAAVTEVTDKNKSSLPNIKTNRTKKGTYGVPGTLLD
NPKYNDNWRQEMEKLDALRAKREKNVPQPKPMGSPFKIPGVTHDFLDELHATGVSAVYHY
EPVEEKSPKRKGRVKSPAAVAVFTQERPMSFKRTKSGQEGCIADFPNTWIDPDALERERN
KGKKKNRKPKPEYVPSPPKGASGIWKPNSFPEASVVQSCLRRFY*
>TCRU_1936 RNA polymerase-associated protein CTR9, putative
MAVYSQQARVALEEVHDAFSQGEIDRAKLILDGIDTPNEPSREELHDLFAIRCVRASIAA
MGGERSVASIMRDTVSYALHRPVLLYLEGLAAMASGTSLQTARVKFEEAIRADRYFVLAR
LGLAAVSYHMKRYKRCFSHYRVVLETLGSSCPPIVRVGMGLCAYHLNHLDYAQRCLERAL
EVNEDDELALLVLLVVFLDRRQIPKVIEVAQRLRGILPENATVLLKVAELVYFRAVTQDR
VKASANPIRRLLAEVRRVATVEESAMADYQEGRLCLALGDLSNARLLLESAMQVLPNLLA
ARIHYARFLLLSGRETEAEQLLLRINKDHPNHKEVLQLLAVYASRHGLHEKALEYSRRLT
EIVAPGDIRSWSIASWCARLDKGETKKLMSHLARIRKEVGEPVSMKLMANIAALGGDTEA
LQRIIDCELGADFLGEPNLPVVYVPLVFNLALLLEETDRTRARQLYIFLVKQHGYFRPPY
IRLHVLAKDDGFLKQAVAWLVLLQQVLPEDPTSLASIGEIFFENGRVGAAMTALRSARGR
PLPVALAFGAAFLWCSQQHGKDNRRFLASAKDRFAFVLRRDNGNVLAAHGLACCLGLEAD
YDRCQCLLDRVGEVRPNCSYVRRHHEAHMANVKTLSDSFKQAIDYLERDPQRTPLQTSSL
AFCLACESRYEEAIAALTTVVAENPNLPLLQYNLALLHCAAFVYAVSHKEAITPEKARDL
RHSLATGLSMAFEFIRQEPRSQAMAVAKTFLKTVCAYCLDVNDGSISRLILVGQRDTMEY
DRQSKLWQRVYDEFQTEKRNEEEQRQAEARQRQEQEVQLAREILEDFRRSQLDQPTILDE
EIRTRLEAYRAEFGSAAPPATDDAVQPIDPLGTTSTAILGGMNLEEDGVGWAEAERDEEE
HDVKVEGTDVSA*
>TCRU_1937 NOL1/NOP2/sun family, putative
MSRNQFRKGGRKRGRKEDNWAADTRDLSTLTNDAFISYYKGHVVEEAEWEVFMEALRRAL
PVALRVHPSVSSAEAVLEYLKSRLSSVLPITTIPFIPDGAALQCPISRGDLKRSVELREL
KKVISAMSEGGYLTRQETVSMLPPVLLQVRPGHRVLDMCAAPGSKTSQILEALIPSMEDG
VVVANDINTSRLDVLLHQTNRSAAAHSHLIVTSYDATQFPLLPSESKFDRVLCDVMCSGD
GTLRKSMDMWPRWNVFQGAELHNTQIRVLLRGMMLCKKGGIVVYSTCSLNPVEDEAVVSE
CLLQAKGAFRLMDPTSLVPGLVAAPGLDDWSLLTKDLKARLHTLQEAQVFAETSASNGIS
YRATMFPNKARLQEQNIHYTRRVLPHFQDTGGFFVAVMECLEEYSAPTATTSSKKSETFK

SVSPALQKEVRGALGLPEFFPTDQLLVRNETAREQKIYFANKAVCEILPRLGPRVVHVGS
KVFESYMKYRNDKLRFCSDGVGVLIPRLPSSFVVEIGPEMLLQLSQSKLGESLLPPLPPH
HSFVFKCNMAIVGAVYIAAERACPCQISAKVAEWQVALTKLTLGQPLVECNEEAAADTDR
VGGDKNTD*
>TCRU_1938 hypothetical protein
MSFIDDNDFAVDEEDEEEEVVAESLSRSFEPGEEEEEISAEEEEEEEEEKEGTEEEEEEA
EEDKEEEETAASELDVSCSDGNNENTLASSVRPNPQKVPEATTVLTSSFGSPQVSKATEA
PVQSSHVISSSSPSLTPFLGAEGAGKSELVVPSPAQAPARRVRLSHRFLDFPGKTASLRD
KRQRCLSLSEETKAAKAVLATFELSLPTTRFDEQLGNILSNLL*
>TCRU_1939 ATP-dependent phosphofructokinase
MENRLRDTSRVVRSHAAPLNEVTQEDLKVERLHGRKYMNPSKKHVMREEFSDKIEHIMHD
PRPQEGVHSELPVSISPLLCELAAPRQRIHFNPPETVVGIVTCGGICPGLNDVIRSLTLT
AVNAYRVKRVIGFRFGYWGLSKKGSHTAMELYRTSVTSIHRYGGTILGSSRGPQDTSEMV
DTLERLGVNILFTVGGDGTQRGALKIAEEAKRRGANLAVFGIPKTIDNDLSFSHRTFGFE
TAVDKAVEAVRAAYAEAISLNYGVGVVKLMGRDSGFIAAEAAVASAQANICLVPENPISE
DIVMALIQRRFETSRSCVIIVAEGFGQDWEGGTGGHDASGNKKLTDIGVVLTKRIQAWLR
KNKERYPNGTVKYIDPSYMIRACPPSANDALFCATLSTLAMHEAMAGATNCIIALRYNSY
ILVPIKVATSVRRVLDLRGQLWRQVREITVGLQDDVRAFKEAEVRRELEAISLVRERLIG
QLSKL*
>TCRU_1940 vacuolar protein sorting-associated protein 4, putative
MSVDFTSKAVDLLKRATTLDEAKEYEEAYRWYMDSIEVFMTAIKYENKNPTKKEMLKNKV
RQVMERAKMIKEYLDGSKEGDSNVGNAGSTAQKTASASKKAKEEEEDKQRMRNALGGAIV
RVKPNVNWSQIAGLEGAKEALKEAVILPVRFPQLFTGNRKPWKGILMYGPPGTGKSFLAK
AVATEADGTFLSVSSADLMSRWLGDSEKLVRNLFEMAREAWKTDGKPAIIFIDEIDSMCS
SRTDGENDALRRIKTEFLVQMQGVGHEDDGVLVLGATNIPWSLDSAVRRRFERRIYIPLP
DVQARYQMFKIHIGDTPHTLTEKDWYELARMTDKYSGSDINIVVRNAMMECIRSVQVATH
FKRVTGPDLKDPTRMTNNRLVPCSPGDPEGFAMTAQEITEPGLLMPLPVTMQDFVKALRT
ARPSVADDDITQHLKFTEEFGQEG*
>TCRU_1941 protein kinase, putative
MVQSQRCERCGEGGATLTNCVDCGRYLCRRCVSCAGQCADCTAKVEQSALGCAICRNMEN
AYYWCAACHSIVCRRCVLQSYKGRPTTVLCKSCQMSSPLPAPVTLCGRCKGVLRDESTWY
YCEVCAEPLCRNCLSSSFECGVLKCLTCCPAPVRLLSGNRQIRMFLDDELKTLVASISRT
KSQTAATSATTGVSFSKYRHLRNREKLGEGGQGAVFKCTTLDNEVVVSKEMTFDDGDRAA
FEARLIQAEKMRMLSHKHLIRYLDVIGLENPLKICVIMPYYAEGDLFKYIKRQRGPIEEH
KLCSIILQIASALHYLHSQRPPLAHCDIKPDNILLLNREEQVLLMDLDLCRSCDVQSSAT
SRVLYECHGNSPTFEYRAPEMVKSAGSTESDIFSLGVVSFVLATLPEFAMLRNGKGVMTV
LNDSDWTPDSLARAVRAAIEAHTRVYSEELIDLIIGMLRHRPASRPQAIEVMMRLTEAME
NRLLRCGI*
>TCRU_1942 hypothetical protein, conserved
MLKDRFAHLRIVDSDSDSDDAQAVRQHNLASLNKPTYKSSTETTEAFPTAAAAAPTSPFS
FPIAANVKKDIASLAAPAGEPGGSSSHTPKATFLNEPPSMVRGSSWKLSSDKEIQSLRLG
GGSVNSFAAASTSGSERRKVQQCERSELPDASSAVPSGLRPLSVSERFEEGTHVEEKQVT
PQGDAEMAATTSEKAEEWGEGLEETHKMETVEEPPTQMTEPMAVVGSKEELRIVATDLSE
PLPAPADDAGRAAVKRFLEERYWEKTHGYDPFKRRMPLFVAIEHCSPKNVPVRSNLPERN
ALEANPEAVRAEEPCQHEIEQNYPDSEGVGKFLDEELAVALRDDRLLKEGGEGMAGPAPN
MASVVSVDDDNAGDLLSSTQPAESGGIRGAFREHQGEAYEEGGQMGDPIITDENVLQEEA
ASEMRTSATNVKKEMEGDENEERTSFTEGSQPHLPGQVDDASKVLLSSKAALNLPGNIQE
NEYAESLKLDENNQRSIRSNVSNFIVESDQKGQSERGSNEEIFLANEELLMNDGINVDSL
REKREVQSANESAVQQNSRTSNKSEEPLQNSELTVESLRKFNARSFEGTHWERYNEGEEY
TDSSLYKTCFSPGTTEAGSFRMGKGLPRRFAGYNDCGGASLRRQELAIPPFHRRLILDME
EKFRREKRSMEHSLKEYTFHPRTTCTPRGHLPQRRRNPTNGGSTESPCQSLAMTPARSSA
RHKVLEEPLPTFKPEISKFARETQRPKIPYHERLYSPRPSPARAGPGGALNGTSPHLSPR
MVELIDGATPPLFRPEISPMAKAIENGAPFYERLYQVKADVEPSREGKSLLQSPPISPRR
PTRPIQLSPRLLERPAPPTETLPYSFHPQISPRAMSMESHGPVYERLYPIKDERSVILQR

QEKKFEDFLASFQPSIAERSNGTNADSRVMGRDVVRRLTEHREQSQRYVDPSLTFHPFIT
QKARDLKNENSAVLP*
>TCRU_1943 60S ribosomal protein L13, putative
MPKGKNAIPHVHQRKHWNPCSSQKGNVKVFLNQPAQKLRRRRLRLLKAKKTFPRPLKALR
PQVNCPTVRHNMKKRLGRGFTVEELKAAGINPRFAPTIGIRVDRRRKNKSEEGMSINIQR
LKTYMSKLVLFPMSYKNVQKGEATEEEVKSATQDRTRFGTAAVGGFVTPAPEAPRKVTEE
ERTKNVYKFLKKNHSAVRFFGIRRARQERREAKENEKK*
>TCRU_1944 60S ribosomal protein L13, putative
MPKGKNAIPHVHQRKHWNPCSSQKGNVKVFLNQPAQKLRRRRLRLLKAKKTFPRPLKALR
PQVNCPTVRHNMKKRLGRGFTVEELKAAGINPRFAPTIGIRVDRRRKNKSEEGMSINIQR
LKTYMSKLVLFPMSYKNVQKGEATEEEVKSATQDRTRFGTAAVGGFVTPAPEAPRKVTEE
ERTKNVYKFLKKNHSAVRFFGIRRARQERREAKENEKK*
>TCRU_1945 heat shock protein 20, putative
MWDPFRDVERLLNRMQSVTGTSFLSTSARGSWVPAMDIVEREDSYKILADLPGMSRNDVS
VEIEGSQLCIGGNRKSMLSEEEHKNVVMAERGSGRFERCVRLPSPLEEGSVKASLRDSVL
LVEVKKVTDAVRKRSGISVKIN*
>TCRU_1946 3', 5'-cyclic nucleotide phosphodiesterase, putative
MGCGATRDVNPLPPPDVDFRSGGQLLKLGGSLKASGGKEPLMRMPGKDKYIKESGAVVMD
DRQKSEGGGGNRASVGMLILFCAPGTDELVISYRENSSGAIYAKRMTDKELLASKDAAGI
RVSWGLFFKSLASDVLNNRAVVRYSTSTSKDVHFNILSRKDRGVKYDYTCELVMVSGLGA
SAEQNAVVEYFVEPMTRMLQVRRRVSACSNRGDALEKLECDHVVKMAALRRYKARLKELL
NTVKPLREEASIISEKTMNLLLEAKSLESKLQMMRGGIGDEQPLDILYEKGGAQYFQHVP
HAEFYYPKEEKVDQGILACIRAAFPLFPGATLDGIMTVLDRPELQPLLNDFSRPLVRDMF
DVFSGLDRWDYNVIELEIITNGNALFYTTYVLLYKLDLVAQFHLDDTVLQQFLLGVQAGY
HPNPYHNSMHAADVTHINYYIMMIAGLKEKCHLSKEKVLAGVIAGAIHDFDHPGLNNNFH
TKTNAYLSTLYNDRSILENHHIACIFELILHPAYNVFAPLSNEQMHAVRETMIEMVLATD
MGNHGNLLRKFKLRMAETTDWRTEKEDVLLALSMSIKMADISNCARPKYIYAEWARNISR
EFYNQGDAEAACGLPISPFMDRKRKMADFPKGQISFMTYIVVPMVEAISEFLPSLCFALQ
HCNENKDAWQSFIEEHT*
>TCRU_1947 hypothetical protein
MANELITLQVVLSAFVCIMVVLVGVFLCCRGRRQDHPATTMSCYTPLLFYQSSSRVAKKC
GDQGPSFMPLSPSDKCRISEWLLEVQRAIDNSGKSLAVPGLSDPRNPTIVDSLAMMATVQ
FCSDTSDKIIMESSASEYATYSPRVSAVEGATEPLTFHLDPLSR*
>TCRU_1948 hypothetical protein, conserved
MDLLLDDQRETPSFSMGLFADRVNSILEAPLPKCLLLKGEKAGERFIGSTVGLSPRGAVS
PRRTTISSSAVTTAVRGNGCASQQGKPIYEALLERGRLMSEKKEAMRLQALEEELSELRP
APSITYAAARNTPRRQQRIEDRLLQRAKEAEMRRELQAKQRKEELLKEMSVIAPFQPNIS
RKGRKATPRARNMAEKTQMDWNRQREQRREAARTAKLMHELSEVRGTPVINPRSECLAAR
RRKKEGLLGMSAVDALIERDRIAQLKRWERHELEKRAEQIPQITLYAATLQRDGDAAERL
YAESYKREERRLRQEEQLISNGAAPFTPRISPHAATTPRFRNVEDELMEKHMQSIALKEE
AQQRECEQESRCHRPIINPVSEAIASKLPESTCERLYRQTRGTPKHRDPASRDLSFSESF
ISGSRVASLPESMAESLQFYEESRQERLRKLREEQERIQHKECTFAPLTNKRDSNFGGPE
DVAARNQQWLARKERKLRELRRMKEAEKVKDCTFKPERESPTVNSTRYGESVYGGDGTPW
GVQEYLERQEEARRIKREREMRLQRRPSSAPRPSTTTPQEFLLGRRDGVSVRSLRRPPQV
SLMSPGKEDDPPIPQEPQHKHESGLSVYERIYNRIYNTVASGGGLGKIGDSDGAETSLCI
ASSFYR*
>TCRU_1949 acyltransferase, putative
MSLSCYLRLPIGLIVVLFLCTQTFGPPVAEQQISESIRSITAQYKKLVERAINETMRSLM
DHLDSNRDGQIQLEEFQSLAAAALQRVRNVRPITQEIGLAFSHITWTELMWRYFLLQLLF
LFSLFVLENLRCLIFTAPRRLLLDDSYLTTTPPEVGPEIALTYDTPWTTYERLKMAFFAA
TGLLFLRIFFLLFFAVLATFFMSLCGWRGRTRRGNPLWFAVWSNAATVLAHIGSVFAGVY
HIKVFGRFADASECKVMIGNHSCIMEVIILFILGNFPSFVTRKENCEKVPFFADVAECLS
AIIVDRKDVNSRQQTADAIRARAKDRNPKSPQLLVFPEGTTSNQRALFMFKQGAMVPGEP
LQMVCVSFPYKHFNPCWTGRPCGGNSFSDLLMRLCSQFVNHLEVRALPVYTPTEEERKDP

ALYAKHCQQMMATVLRCSVSSCKYSDYESISTGKSRS*
>TCRU_1950 SET domain containing protein, putative
MGEVVPTASRDWSLNKEKESGRLFWWNCKYSISIWDSNLNLGQPRHELTDLLVWQAFLHF
QIASVYKLCFVCHQPEGNEDMKVCCFCGLTVHCDCSREATAEQVAWKPANFGFEAYLRAC
FNCEDVHVPVKIRANREASNAHRVASRALSIKEEYPEHILRDILCLAEKAEQPHSSSEDA
SLVASLRRVLTSFYQSEESCLFLKREKRPEKGGGIGVVAAKDIPAFTVVGVYPGYLDVLS
GEHLKLGRPVTKYALKDLNCADYDNVVFEEFQGTFTPFINEPCEFEESNCGWIQEDKHRE
GRLSIMTARKIEEGEELLIGYGPSYPRSYPYRYDVLTFHKTETEFDTPCFALWRWTSTDE
SDARLVSYVGYEKSKDFYFFWGEQEE*
>TCRU_1951 DNA repair protein Rad9, putative
MFLSFSVTGASVRPFMHLLQTVAKQGEGLFFEPHRDSLQLRVVNSTRSTHMLVGIAARYL
EGYRSIHGNSVTNSCEKSGGATSETNLPRHEDDRDEFFLMLPTKALLATVLRQSQGLCSV
HVRYNATSASDMVSCDTLQWECVMSGGIIKKFLLPLAEGRPERAFFSPDRFSFDACAAAW
VWGALLGWFPASRPRVVVQPLESRLELWVVDSDEPNVMQGAHPPLESGKGGGAETKVVAS
QEHFLFMRQHEPRGEGTAVSNETSEVGDARAAPRSRGLSLPGKIVEVKPFKQVCLLADQL
GMMIRVRTGVEGLPVFVEAITVQDAQQAAAAVAAATVKDAVAAESSNAAVQQNVFGRHSL
PSENSFRVTFSMYIAAFDVPQRALDSGEGFTASSRRSTNSATTVTGEERGVVTASSLQEV
NAPLVSASAAPPSSDGVPLSGIAQRTPFKIAENMATGQVIRPTGVTNEKNPVVNSVCSPQ
RVLVPASPTQVPSCALDGPSLVGSTPLRSGGRISSPSNGEEMVVRATPEVGGIVTPHRGD
KRPRGGESVDGRFPQESVVGCTAGTTDTTAMSFAPTASFVAPTNLSPNDRRQAGEQQGRE
GPIPSVSARPSLETRFPLDFNAFMQEIAEEAKEDPEESEEDEDLQRFLESCVSLLVLPVT
PATQPK*
>TCRU_1952 E1-like ubiquitin-activating enzyme, putative
MRQEEESKQKTLDATVRDDNPYSRLMALQRMGVVDNYEAIRQKSVAIIGAGGVGSVVAEM
LTRCGISKILIFDYDKVELANMNRLFYRPEQKGMTKVLAAKQTLEDINPDTEIVPYAFSI
TSTEHWQDFVDALTKNGGVQPNSPVDLLLCCVDNFQARLTVNYACLLHNIPWMESGVAEN
AVSGHIQLLLPGVTPCYECCPPLVVATGMPEAKREGVCAASLPTTMGIVAGFMAQNTLKY
LLHFGTVSEYVGYDAMRDHFPSITIKANPECRNETCVQRQQEYAARRAAMGDAAHPLHQA
NKQREEREAKERAAARAKAKATASAAEWGIVIEARGKEDLAVHAPQPEGVEAVSVEYAYS
SGAGNAAEHAQEEFVMTDGGESLEALMAKMKALQH*
>TCRU_1953 2Fe-2S iron-sulfur cluster binding domain containing
protein, putative
MASEEPLNEIPGECPTPGDLGHAGWDVLHTAGAVYPYKPSPLQQEAFRSFLYSWSHVYAC
SHCSYHMRRYLKRNPPVVTDKLALNRYLCEFHNTVNKNIAKPVYNCDPMVVLRRWHPTFP
DMEDQPTIEEQIAEQRRLEQAEAQKQKEKELQQKQVQTSSLGDMKASRERLVGRWRSEKS
ESHEYANNNPNSVGAFATGWSASSRQHENAGDAAAKSAPAPLAESREKRWWIFGKNGSGD
KNAGFSSTTGTPSKVNSSGGGSNSGGMNGSLDDDEASVMAILKRLKACMVYCPDKDEKSN
SV*
>TCRU_1954 protein kinase, putative
MRAGSSAVATVTPAENALLSPGVPFALTKKIATPQQDLVDSGGNSGISSQKRVSAVGSVP
PVRCAVAAECREAEVAPNVCSSLGSFVDLPNSKGNQECHRIHPLRDFLETYKIRRLLGHG
SYSVVFEVVNRKTKERKAAKFLIAKETQLARRKQGAECGNGKDKGSMAIEGGRHISNNSN
TSTSLPESLVKEITVSFMARHPNLVHTSDVFVEDVEDLQRRVQRYNSQLFIVSSTSSSVT
AKRRVKQEPLLVVAKKNAVSHVSSTTCDSFSGRDNGDGDAPEQRQGSFPAKPASSAVVKS
AAETNQSAIEKVRQQLQEGKMQCILVMELLTGRDLFTLVSRKPLNEARTAAYMMDLLLAL
QCLHSQQIVHRDVKVENIVIDPQDRARLIDYGFCEGLHWSSNTNAGCSGETHKVCDGTLT
QFCGSYHYVAPEVIRAAMRSRLSARPTDAKEANNNVSVKLPPISMTGSTGICGNLMTPRT
PAEDKNSRGMHSAASIGILRTLLTPGPMGYGTSVDLWSAGVVMFVLLHSTFPFHDERRSS
LLKLISSGRQTVRPSPLLSSDAKDLLRRLLTHDARHRLTTAQAVEHPWFKRLLQRSGME*
>TCRU_1955 prefoldin subunit, putative
MSILKGKEVEVTQDDQHRICLFARLHRRRRELVAELSRRKEEIVRLGDAADELMITDNAM
YLFGETFMETDNDEAEEWLEKEKGRLQTEQEAAEAELKLVEVALGELKANLYASLGSQVY
LEDE*
>TCRU_1956 hypothetical protein, conserved

MDRPPGPMHDLIRRAYEEMRLYSNYYAAIRIITAGLQLGERDSEENVLERQTSRQPFFGQ
SGTLQGSCSHNNDVFLSDRSGGSFTESTAVGKSRVISVSEGTKIVRVAPQLRGGFNRTQK
FRMLLLRADAYSALKRHDKALQDAQAAVLMSHERSAEAHFVMGREFLRLFQLEASVVAFD
KAESLLCSSPIFSENPCVEEISAEDFWAQRGYHMEDVQRLKLNRCSMEQEEQKAHGVLLG
QRVDDGANGVLASEHALVTSTSSEGLNVANPQLLYWRQLAKEARALHKMSTSHILPIGFL
QTALLFLDHQMSTVRFGVVACLENTTSRNFRLTGCSSPDAAFRNGMQFPDTIPPGCCGIA
LLQPRGRWGGFVCSVCYEVADNAVCCFFCFETSFMGSNRCGVRFASERRSLEFACGLRDP
NSNTSGSSSSDTTTREFVNFKIPNPSLWLPTHVAPLPSGRKLKVSGATRSNSRVIMFSVT
EILSVRLRSVELLTALEFAGPVVLKKMSAVNRRYRELVNNLPPTMFFGSSRCLYPDYCLL
SDRTSSPWIVHDKEPVRWSFVFDGRLMNRELFMVSDSTDPQNNILYFSGESCGSIETVVF
YGDRRTLIAQIKGSWVPFSSTLYFCTSSGRTFASCFLNRNSELTLVWEGASKKNKSEDVE
YVMHRVESVRRTGFGGTTSTVSNLSTVNGFGGTEESNSMLFSSSSGVVLASPLAPSRGNR
GSLVEKYAVWRSQGTNAGSAACGITRQTNNGMELVAEVTINPPSAQTVTKGSVIAEITFC
TGADALLVTLMAYCRFQWDG*
>TCRU_1957 phosphatidylinositol phosphate kinase alpha
MPYNREIIASISFESEPSSRNNSPIRGGLNDNVKARESLDATGEPVSQQNEATRDIIRCM
KWALAQSITSISHPAKQRPLNPKKDFTIETTIEVEVKKNNTLGLGCCGGAAAVKRRSSQV
MSVRESGNSKVNFTYSDTDGADDEEGPQVSFKFTDYSPMCYRHIREFFNIEPRAYCDVLM
RSRWHSTPTPGKSAAQLFFCGKDWVIKTMTTEESEFLRSILHRYYFFVLDNPHTLLPHFV
GHHRLEIAGDKINFIIMQNVFATGNAIHEKYDLKGSTVGRFATEAEKRKQTCTQKDLDLN
RPIHVGPARRQQLIEQISKDCDFLKRSHVMDYSFLVGIHVLPMHDSRRLGTSVMGGKEGI
NMLSSTLAFDGTLASGVLDGQFNQTNNVFHISPNEPVIDGRCFTADEGGMRSTDQPGTRR
EIYYIGIIDILQKYNARKYLETSWFGLVNDSKKISSVPPREYAERFLAFVSSIIV*
>TCRU_1958 hypothetical protein, conserved
MNPPSKLGEFFGIVDDFFKKTFRDDSRVFVAVKSRQYSESFPGKQLFFTAPPPSPLESGK
TDVQTPATAQETAAIESKKENYMTFSPRLTINKDGTGFGKIKLGCGLCIQRVCRFEQGLT
LTSRGVVATNVKLIDLLEGLELKGRVSVNTIAPASEDVSVATIDYQRRDFYTTLGYQRNG
LGSSDLLVDCGTKFFNLLVGAGFERQKLSYLEHHDASAQMDVLYAGLGFTGVNWSIGAKM
VRAHDAWNAARVAFYQRMAPNTMVACGYNFDLLESRAHLSLGFSQGFRLRLPTILQQRSE
EHLDEWTAILPFVGAVKAESDGVCAATIRGIFNGVIHWALIARRNVMLEKSPVQYGVTIS
MESG*
>TCRU_1959 AAA domain containing protein, putative
MADNNMMGKVMAWRTGRLGFKTTVVTLLCILLNILALYLLRRLFPALRGGGDHRHTHGSR
RRSSSRDGNSKKKHKKHHRNGEVKNSLPNLLLLLGIPGSGKTTWINQYIDRCDKSYIVLN
EDSVAGKVVAAIDDSSWEEGVREAFIGEIVRHLNEKQNVVLDDSLRVMDEEFRRSIMEAA
PPCNLLVKEFPIKALFAHARLLKVAEEVTDRRCPTEIEMEELETNFEKARACMKTEGWKQ
LLDSSHLRSKHR*
>TCRU_1960 hypothetical protein, conserved
MPSLNSLTIAEMEVTASRFLYAAAILCTRLCEYYFFIKAVRRRLSALNWGIVLETSPANL
PPSAVGLGERLRHIIENNRKRIIKPTEKASAAIITDASLHGWGAVFIPDSGDVKIAGEKW
EKKPFLIMQAEARAVRLASSAFSAILPSTMDVWVDNTSLQGAANKGSPKSHAMTWDLRKI
CLFLDSRGIQATFAYVRSAENPTDGISRGRVFIL*
>TCRU_1961 ATP binding protein-like protein
MEKLSENALLRIAENIERAVDDEMEHIDNLDDDELMELRRKRLKALREMGERRDAWLRKG
HGQLQEMADPKEFFNAVEQSERVVLHFMRRSTLRCSILERHLRAIASKHFETRFCYVDVE
RLPALAERFNVMMLPTLMLIENKKTFHSIIGFDEFGGTDDFSTDTVVKVLSHYGMVNERG
MFSDDQSAE*
>TCRU_1962 hypothetical protein, conserved
MNVNIQALHPSLQRYLPGHLPKRQRRLYTGKTNSKKFQVAHLADVETEVAQRLPLPGRLA
QSLLFSPTVTRAVVVDETTDQVGIGDSFGTHPRNDNTSIPWASVSDKKDSKAVQNRETAT
SLLAVKATGTEQRFNKETFYFGCPTLGGAGQLEYNDPSDPHGRNHIVSAWNTRHHFLPAI
WFSRATQHPAVADAMIQGSNPLTTNMKSEGPHKNTNGYETPIKELNEKKQLTSVEAQPHV
PTECTPLPNSHTWPDTYNPPNLYDVPPPKLRYQLTDYHSTFHHTKGEPNSFMYISEKERF
RSTKEMPLSTPTNTAIYTYGRRRYPTKDNEKQNK*

>TCRU_1963 histone H2A, putative
MATPKQAAKKASKKHSGGRSAKAGLIFPVGRVGSLLRRGQYARRIGASGAVYMAAVLEYL
TAELLELSVKAASQQAKKPKRLTPRTVTLAVRHDDDLGMLLKDVTLSRGGVMPSLNKALA
KKHKSSKKARATPSA*
>TCRU_1964 histone H2A, putative
MATPKQAAKKASKKHSGGRSAKAGLIFPVGRVGSLLRRGQYARRIGASGAVYMAAVLEYL
TAELLELSVKAASQQAKKPKRLTPRTVTLAVRHDDDLGMLLKDVTLSRGGVMPSLNKALA
KKHKSSKKARATPSA*
>TCRU_1965 histone H2A, putative
MATPKQAAKKASKKHSGGRSAKAGLIFPVGRVGSLLRRGQYARRIGASGAVYMAAVLEYL
TAELLELSVKAASQQAKKPKRLTPRTVTLAVRHDDDLGMLLKDVTLSRGGVMPSLNKALA
KKHKSSKKARATPSA*
>TCRU_1966 hypothetical protein, conserved
MAMMMAGRVLLVCALCVLWCGAGGVYARDTLNNSPGVCMVPGGFGKKTSYLASGCNKNSP
TLSLRPALPIAVIQAEDTEEDAGSDITPGGGGGGSGLNSARQDGSGSSQTDSVPGAGLLP
PAGVSGVGGDPSGSVTPGGDSSPDRSVGTGTSASFSSTLQGESGKKVLQRDEAKDQNHQL
PNGKAPDTPVVETQSRGSDTTRGQDVGGASTLSGKEQRSSEEPEKKDGDSDIPQTVNTPE
DPNKELQEKGKALLELSNGSLPEPKTDHPKTNPEKEKNGGQNTSASTDSPAKQEGNSEDP
VSTSDTAESLSTVSQEQTAATSSNDSFSPFQREISTEKTTVENSQPSDTARTEKRQSVNK
EKIGDSDGSTAVSHTTSSLLLLLLVACAAAVVAV*
>TCRU_1967 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MHGRNGELGAVCHVAHAVHTCSNCAASCAAEEEGATVAFTMNVTTHKYAGPYELWWRQFS
PDGTIHPPARSGDADRTGICQLPPPRGGKDDTKSGGTTAPQVNAEPSRQHEDWRQSAAAD
GPNTVDPSPASNTANNTSETRPEFAANPIEMMVPNASKKRPSFANGPRIVVPSNASGIMS
VTCGGREHVAADNTDEASERSATGHKSLVLENGVAGSGFVAEGDAGGLTQRNASGHDNKP
QLREFTAQYSGSGVSLHDCFALRNDAKLTLRELTADGTVRVCVYWALLFLLGLCGVVADL
WAKECGIATPRRERVPRSLRVLFCYLHFTVGFVVFLE*
>TCRU_1968 Dpy-30 motif containing protein, putative
MKMEQSTVETLGKGIFQSHTSVLVAYADTYFGRRLFSQLYQDSNADKAGKSYKLFACTWE
KDGAQVLVEERVAATLLTGAELDAAETDAADTDFAQALDSSSGAQEASLAPPPVATTVFA
NDPGTDSLRVFWRGDTMAMLHAILQADCIVMEMRQAQDVFDMMHALSTKEHLKRKRVIVV
SSLLTWYATPPIQMDPMDENGGKSNMEGDFEEKEEEEDELEEEEVEEEPRPPDQREVDAI
LGQFDFIEGEDNGNDNINDENGNETEYNVELFTEDQYNRRIPHAKYYNWREAERVVAAWN
SEERNIQTCVVFSGLQYGEGEDALQPFFAQAWNRGKRGLPIYGDGTQLVPTVHIRDLVTF
TKRLIETEEPPALPYVFATDSGTVSWQRMVNAMNHAFGGEKTFHVPSQEYALYSNVELFT
LNMRVDNQTMQNLMPAAEDWVAQSGFVANISKTAFEYVTAHHLQPIRLVVLGPPLSGKTY
LAEALAQRHYHLPTFTMERVLEEFKAYIAALKERLEKFRRHLYETEKKRREEAKKRAFLR
FRKKAGDGEGEDEKEDETEAMEAGMQSENGTRNSSAADEVPGDKKKQRVTVGEKDSSDME
ENLVDFTLTEEELHAVEELVEEWFQQNDRATQLRETIASMERVLAMRIRLQPAANAEASG
ATNPKKRKELAKSKRGNRSGNKKHTTEEEDALNELQENAPFQDKALALMMRWRLSRADCR
NQGYVMDGFPETVTQARLVFGDAPLEIPETMEEAAAGGAFASNSNLSVLRTHEVNAAPPS
KEPCEEARLPSFVFILDAAENYLLDRLKALSEKLNEPPGNEEKRLARFEDAITVYRKQFL
DTDYSLSNFFECARTVAKTLTPGGRGVTVSFLKVDAEPLLSPPPPESQYSVAPPSEVERV
ICERVGKPRNFGPTPQQQYQEKVREIKLLEEERQKELRAVMEQSEREKNEYIRESEQRSQ
VENTRQEIEVMDRNSLELRKLPLREYLQHNIVPLLSKGLVEVCKTRPKDPVDFLAEWLMR
HNPLDDSCFEL*
>TCRU_1969 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSARATAGEVKTGEEVNVQVIVSEVLNKLGGEHNSDTDVDAL
RTGKAASGAGQNDNGTPSSNSELLVPIIDTLKSESPKDVQEQALDGVTETAKEGKEKPLN
PEVTDTSDAQQSTSLTAVRKVSENETTAANTTTTTTTNAPTTTTTTAPQATTTTNTEAP
TTTTTRAPSHIREIDGSLSSSAWVCSPLVLAVSALEYTAVG*
>TCRU_1970 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGVFGIAADDAGGGDGSAGENLIALWLTRLRMECAEEVIRR

KGSSANASAVEECMRRGMDGVRAVLDGRRRWRRQQFAVAAADVAGDVSDPESSSQGQSGS
DDGLKDKVPLEPALEPPPEKLDKAPGNGDALQTPAEIPGLPETRSEKMLNEKNEKEVKDD
RDPVKRIGEGVSIDIDEEVDGAAEISDENPKHEDEEATNTRERNGGEGSLNNEDEISGNH
HVSDDISAGLHVALPSVSHVNGKGTQSVEGTNGTVGEKGLAGQTIVQQAEGSPAPEEPTV
EFIQKEDTSKEAKEKGHQVGRGKEQTTIEEKSTEGAAAGNTAEDSHVTEAQTPEQSETSN
TNGNVEKAEEKKRDESTKNEEKSTKEKEREKNAVKSKNEEKEETKEERVADEKETTTVEK
KMAAVQSLTKINTTTPGDSDSSTAASHTTSPLLLLLLVVVACAAAAAVVAA*
>TCRU_1971 Glycosyl transferase family 11, putative
MSARVARSMYRRMLKIVASIKRVGAEQLALERYAEFLPCTVEVRKGESLHALLRKAFISA
SLSAESLASGFSFIKDATESLPDLELLSLWNAYCLDGEYEMLYGVALLSAALQQAENEEP
THAGELGDIVSRIRGEVRLLVNEMKEAVTATPTPSSVGRHGLDGRPSSLETAVESLWKRG
FDVSERAAEDLTALSLLRKRRASVFLLNVLLTVALHELGVPCTLVGTESHRPWIRVQKSG
SRPLFMSFAHAGVHSAKEVLRLDGHPPTSTQWWRAARWDGSGRKHILSRMLKVQLMLLSS
SLESPLRTRQLKTCRTQILFLLS*
>TCRU_1972 DNA-directed RNA polymerase II subunit 2, putative
MDDELLLQLNETEEFVEDGADYTVDGEHAGSTDIDSEDIWEIISSFFREKGLVHQQIDSY
NDFLLRIPRMARSLLEVVPRQDEQFEPGTQTETEPDQYRLSLEDVVIGNPSHEVSGFSRH
EMHPLFPNECRLRDLTYDANAQVTLGIRVYRSREEQPYRTFLQNMELGRIPIMLKSMRCN
LQNKDEDELPRLNECPHDQGGYFVISGTEKVLIAQERQAANHVYAFSRQKGLLCEIKSIV
EGSLNKPRTLQILMPYKKKGPGHGYENLLCRVAQMDELIPLFVLFRALDMGSDKEILQTV
VPDLKDAAMLEMLRGSMEDASTLQIFTRDEALWFIGKRLGKQDSRENLQRDAQGLLMRDL
LPHMGVDCAADRSKCLFIGYMVHRLLLLALGRREDTDRDFLGHKRIDVAGALLTFQLNHF
LVQVRKEMVKTVHDYSTNRGGVVSFGRILHSRLITDGLRRCLATGNFGDMKSGNIKTGVA
QTLNRLTYSSSLSNLRRIQNPISASSKATKPRNLHCTQWGYICPVETPEGGSIGLLKNLA
LMCLISRGSDHTGVVQAVQARITGFHSIDLPGLADVRVARVFVNGTLIGVHRDPERLLRD
LRARRRGGELSNEVSIVRDIRDREIRVFSDGGRCLRPLFVVERSRIKLQKTGIGELLEPS
KTPGGKREISWNRIIKKGYVELIDCEEEDSLLIAMTMTEVSKNYYYSHCEMDPSMILGIC
ASIIPYPNHNQSPRNTYQSAMGKQAMGIYASNFNMRMDTTAHVLFYPQKPLVRTKAMSYM
RSNDLPAGHNAVVAIACYSGYNQEDSIIMSRSAVERGFFRSAFWRSYKATEERKKDVRET
FENPDRKICRVKRADYTKLDADGLIKPGMPVMGGDILVGKTIPISEAKLENAALNDTRLL
KRDCSIASRTSEKGVVERVMLTENSGNRFTKVKIRTIKIPNIGDKFCSRHGQKGTNGIQF
RQEDMPFNRDGIVPDLIINPHAIPSRMTVAHLIETLAGKVACYKGSEVYATPFCSVVVED
FGKALHQLKFQRYGNECLYNGHTGSPLDHLIFFGPTYYQRLKHLSGDKIHARPRGPLQPL
VRQPTEGRAHEGGLRFGEMERDCMLSYGASQWLRERLFRVSDYYSVHVCNICGTICAADT
EQNVYKCQGCDNDTRISQTLMPYACKLLFQELMSMAILPRLGTGPL*
>TCRU_1973 BNR repeat-like domain containing protein, putative
MPQPRVTEWEGSLLMSVDFENGQREHESRDMGTAWTEAIGKFSCVWVNARSGVSQKENLR
VDALITATIEEREVMLYTQGGHASRKKRSTALCLWVTDNNRTLSVGPVGMENAAD*
>TCRU_1974 hypothetical protein, conserved
MGLSCSHKKKGETVFKGKTTTRSSTWVSKKECQVALMLQGNKASAHIDDHSLGEEEVPLT
GERPPEVLRFCFGACGGHESHVTVTDVFPYSRPLNFTAMRALKDRVPVPTREATPTPPEK
VRVVDSVREHIAGNITEEK*
>TCRU_1975 5-histidylcysteine sulfoxide synthase, putative
MDPEVDIMTDAGFRESVDGIPNGCVKIAEYCKAQFKAHARVEPKRALDFACGAGRVSFEL
SALFSQVVGSDFTARYLIPAYAMLERGKCTYSTLESSSLQRVAKMAEASNYSWDTNRKRV
TFFQSDPTNLHSHMKDFSLIVCWNTLERSSAPAAIPLHMLSRLEEGGLLVIECQYEWVEG
GPSARENRGETSLPHKGFAEEEIYNLLGAESAVERVGEPFEVVVAFPESDSVVKLKKIHL
NTYLKKKSN*
>TCRU_1976 kinesin, putative
MSMGRDMLIARRLESDTVSTSFRSLSRQGEKRFPSSGPATGQSTTGAEAVQVAVRVRPPN
CSEASQELAVTMDPSRSMVFLNDRLDGQRMFSVDMPIWSCVGRALDDSAPVTQSALYKRV
GRPLLAHAIAGFNSTLIAYGQTGSGKTYTMMGEVGSNVMDDNEDVLNKSEEGIIPRLCRD
MFQEIQRRSVKSASGESFSWEVQVSFVEVYCEKISDLLNRNTPVSLREEVVGNETFFALT
GVRRVPVSNTEDILRALKIGNGCRKKASTSMNERSSRSHAIFIVELTEIISIADSEGEVA

SAPRRSLAIRLVDLAGSERIGESGVSGQRFKEGVDINLSLFTLGLVIESLSDPRRRNIKP
PYRESTLTKILKEAFGGNSKTTMICTVAPSQTHRSETLQTLQYASKARCVMNKPHVDENP
SATILCKANEELLKLRCQLLEAGQGGAQHRYLILQLAQAKQRLRQEQESSRRRKAFFEKQ
KEELAAHFRKEEEEREEYSSKLQQLSAEVKRAKLEQKEKERELHHALCKAEECRQENESQ
RELLEKRLNRQSKDMLQRQRDAEGRVQQLESTLGRRVDELLDTVENMKNELKNKGCNITE
RGEELPEQPASRERELNDRLLEARSMIEQLQAKIDATEFDMARRILEAKREAQEKERELR
DEIEKADHDLKLRGTDVQKQWEEEMNTLRKKEMRVLLREAELAELEQELKARTAKQGNQI
ERKEKFAEKTKEMEQPASREHHATLRLQFELQRASNCLYSSETKRRVEEEEEESDDDNNK
FYKLNRRCAQLGKALAEREAVVRIKEEDLNAREREFDRRQQQWEKEAKGLNSLTSAHTIA
DFNSETEAINEAAKTPENELKARFLSIDTGTENLATRLQLSEEALLRRKLWGLECAEGRE
RNALETQEDSELCIIKTQMQLEEKEMRSFKDELRVESLQQRNCQINANWFNCVQELCFAM
EKRFREFLDSSRISEHDLIKLIEDATLPPCQRSGQHEASNHARGMDAFEIRQAELRLHAE
GVVEEESPLTLRTASFEQPQRPWDQEPHWEEDEKKEYLFEREAMDREKMAEHCRTREDFV
ATREQLHRRELALRGYAERVHCMFLEQTAAKRANSIKDWERTEREYIAKMYQLHNELRLC
RDASEGNQEGVQKLLKLKEAEFHEAGNRMRCAVEQLEADEVQWQKRLADEEQQMRMYRLS
LEGDGGQYIRGVEAKQEELERREAALEERSCLIQQEAVEGEQKVRRMEEQFKLQGAEEEQ
SRQERAADIARRRHDVASSLEENERTFLGQEADLRELIAKNEEVKQHIQQCDVELQRYQR
NYIDLRRLLEDREKLLLREHAHRMNGKNSATQLTEDLLYVNELLKKQLEVWIQKYNVLKA
DEKLECERCSWRNTRDATVCRCCGNPNLF*
>TCRU_1977 hypothetical protein
MDCKRSSTSSMPFFAGDGIETASVSFYEESPSMPHDSETAFLQGFPGESSGESMRLADTQ
CSYCRRGSNGWRCAKNEANLLPWHSLEQQCDLAAMQLLEQGRQHHGPNGRRRSQFEPLTG
MTDFIAERSLEEWGDSDNGDDPVLKASPAIPLALSTRPPSVDVQGAAQQQEDTLNELDES
YPEMPENKTKMTIMSPRADSCKEGLGASRRCRLDDLAERMEEGVEQLVCEEGDSFGDASP
PLYIFVAPPSAPADDDASARHREVSPGEHTQINVKGEVQNHDGKCERNPSGSSGTRHFGL
LKPQPLSSPPPWKVELQGTPSSKWRANSLPPQTLSDRFLTHLNEKSFSVDAAWKSATARK
YQQRHLLCTPSTKNIFLDFGSPCRPRSAVIGSWRSLSSHCKRAGLKTPEVPLLLKGSGYG
LFDS*
>TCRU_1978 hypothetical protein, conserved
MKAAGSTAVKFDPNPLKDGVSSIYTPGDGAADVLASSHISRQINFVDDGKLFEGHFTLHT
RGLKSLIQLLVDQQSEQQVIINDLQDQMNTIRQQTSKVRRAVNAAPMFVAPEGGTDTGSV
LKEVEDLRRRVKRLEGFRALWGVHHEEVEALISTYGDPVVTPEEYTAYLLNLQPFRQLRS
DAQNSAVSLVERRLSISAQQRSRESGNRKRISRDDDLRIPTERDARDNSRAARDRRIRED
EPRSPVERDARDNSRAARDRRNREDEPRGPAERDARDNSRAARDRRNREDEPRSPVERDA
RDNSRAARDRRNREDEPRSPVERDARDNSRAARDRRNREDEPRSPVERDARDNSRAARDR
RSREDEPRSPVERDARDNSRAARDRRNREDEPRSPVERDARDNSRAARDRRSREDEPRSP
VERDVRDNSRAARDRRSREDGSRADAERDARNESRAARDRRSHEDAPSGFDDEGESLRQL
ESRVAALEQRLRRGVVAVHSSSRAASANSGHSSVSPIEVVDEQAREDLEELERFVVRRFK
ELEKALSKSRDATPAAATSSVRGAGHPVGRSERLSHGRSVTPTESGGSNAKRSNEAALAN
KDNTNASESKQRKERNAPTDAAVVDQVAREDAFAALDQVANLEKFVNRKLKELSVAIGKE
LGPGPVRPSGESRQAVSLEPQPQGAMVDQIARDDAARSIEAVQELEEDWGKRWQSLEERL
RIIGRASVSKGSLQASAAASSIDRKAREDASMSLMRIQQLEREISGFRRLLQRQETPITS
EEVAPPDARGDSGVVFPVPPKVQRPATFPLTGKGPDGAVGSTDVEYQKRMQDLEQEVEQR
MKEVNRALATLRSTQSGFPVGNSPGATDAFGGKEPQISNQVVFNSRDTDSLELLEPSVSF
SRFPASQTAVLVMKSREAAGVGSPIRIVEPMREDAIVLRSPQLEGFGTPLVKREMPGAET
PSQGMVRNEEEQLRQMRATNGGGTESWQGVYSSGPHLAPHGDGNLPVTDAAGGAAVSTAA
NANLNSVPMTLANADLRSHPSNSRLPVGAVGRASPMDRTGELDQLRSHSTVLHKVSVSPR
GKMGERFLVEQNALGHITPCVVYNCAWCAAQKQGISAQTARSAQ*
>TCRU_1979 hypothetical protein
MPAVDVDLTAIPDMIEAQLTLSYSRLAKLVRLIVDQGNGHDVDIDKLNSRIDALARENAE
LKALVESFMEEKSRESWVQKSLDELRHEISCVSDDCAESSKQMASAMEEVHLRFDDVDQR
LKSESTARANEVNQINTFVNELQEVIRDMRLTLSQCHGFVEVWEGKAEKTEALTRRDAEG
GFQQSTEDRVDYLRSLPVFANVFEEMDVLRQMLRQQAADALSAKSAAGAIRRISTAEVAA
SGVPSTSTVDRTVIDGLQESLGNALKRLKELEERQTPAFVRTQLQQQHQSAAWRGEKEDI

IQLDNRLQNVEDRLRNLSFQASEGASLEKALLTDVDGRLRSLENRIDGLPLARPLQQEQQ
SGGEDRFPVISGQQTSKAQPQSQPSAPAVSTRRLPAPMGKDVPTGETGESMALPYLTTVP
FNGRVEASNAKAVQGTGNGSNSGVRSFVNQSNSEAQRNPKAISYQSLPQSQATVQDDGVM
RRLAQLEENSAVLEIKKADRQELARLEDALRNILQNPAVLPTSALSRGIMPHRPMSQQDA
RGINATESAYCSPPRSSMKSPPPGRPMFVGGSAHQLRDSAGAATPATLSTFHTV*
>TCRU_1980 hypothetical protein
MTALPVYIARCRQCGNSRRTYNDPRLGRSVIECKAACYESHYEWDFVEECKAEEAENTAS
SVPLPSEATPASKGTGASKKHRRMTSRCTVV*
>TCRU_1981 hypothetical protein, conserved
MFALTRHFFRGVAPDELRMQLRLLRGIRRAARRELRQRRCRHRSAQQDCSGFSTASSSSS
ACCSVHVELPPKNDALESAIALALSENRDARTELEFTRHFLTGSFLSLASPVGAWDPYDT
KPQVFALDNYVALPVFTSLPYLRLFCRRFQFTVRDPSGVLWADGVAESAEEEKAGAKGDT
LPLPDVSNSGWWERQVQRHLFATALEPMKSPVNEQEINSVETTGEKEDISWLHADDLFAS
MDATPVEDTSSEQKEDRVLKRKGRTSRVGRRHKTTLKSGGNTGSRRAREAGGKTPHEGGA
APNQDALKEAFWAKVRSTAPFCIKQATPLPVFGPLLRPFFVGYFADVDTLLHNASIVPEN
VDIVLNPVSPIEFVLAREATDRVLHKDQLLHLAYRRVERELRGEFHRFFRYLSPEVAWAR
SACVPFSLPGRPDEVSYELVILLQSDDIHRTFSSLRAAKLHCLLMGHTDLDVLPWDAAAP
YVREASSLFYERGASKDKNCEFQGDLGVFEQRGPIQTINVAQPAESFYHDPTAAYTESHA
VFTEELKLKRRVR*
>TCRU_1982 hypothetical protein, conserved
MASEAGPYPNSPRLGQTEMNDLVRRLYHQQMDRAARREEERRRELSKSCAPPRYIKREEE
GELVRRIYDQQLERFRQSKEERERRIYEETHRCDKKLPESEIQEQVDRIYGQELAKSKAR
REELCKRYLPEMEPKKVSKAKLKESVERLSHVDYAKRDEELFKKHVYPYDPPTVKISRDD
VEAMANRLSTRGGS*
>TCRU_1983 KU70 protein
MSEYSEWLEAAVGMGALDEATDQDTLQQATVYQQRRDAVLCLIDCQLSMFQGGIRSSDPG
EISRIGADNTPGEDSTPAMLNSVATSGCSKGRNTTMRKQSTDVFFWPDVGGEGAERRIPA
GMATGDEKVTDPEVTGNRINNTPFRDAVRCVLKLCQDKVLMSDKDLVALALYNTNKRHNI
YELPGLYIVHPFSLLSVQSVRELEGLAASGDVSSMMYEEFKKNIGHAQRNEVHLSDVLWA
AQHMFLSLHSNLIKYRRVFIFTNDDEPHKGETSEKERCLARVRELYEAGVTIEVFAIGKS
PNTGAGEMGMGRGEANFDALNRATRVADTQLQGGVKQREDTVRFTDCVDAERHFKHEGFW
DQLDRGERFAQGMIEHERLGAVHVTGGVEVFDHLLNAVRRRTHPQRPFQNYALTIGISVG
GSPVPTMAVSVYHPLLPATLPRAEWLDHRTNAIVPRRAQLVVKRPLSSFDSHRLNEQETT
NDAKKAEDSRVIGTPRPNKEGGEETLETVVNPDHLLYSTIVGGRRLFFSAQERQHIFLTA
TAGAPVGFSILCFKHKEDILQHKHVICKSSFLRPNPYDGGEASLRLFVQLTRTLVRGNKV
AVAQYVAQRGAAPRLVALAPSSPAVPVPTCSLPAKGLGLYVVPLPYSEDIRDVPSLPCFN
PATIPSQEDVDLAAGIVSCLSVSYDINAVPNPSLQLRYQALKEMALRQATESGVMMPEKS
GNKPGTMADMSLPDSEGMAQYAPIFHDFNAKLLGPSYDAARLCPQPKRSEFAGEKSLRTG
SGGHREGDDVVDNAAIHLVETAFEQNALPTLTVMQLKAYLSALGESTAGARRKDEVIEVV
THVLLRQRGERA*
>TCRU_1984 hypothetical protein, conserved
MMPSASLPPRPRHTFSLRTVEKLYQRQLESTGAHVRPEQIPTIVENVQRSLLRVEEVLNY
RLQCPASTFHEEKERPLLSKFERVRVGQILANAVLDLAIISMVGGNEMADAVTSTRKAPS
LSSSHVAAPSLHPYGTEELSDECKHQKLESNLHVGAVEETMELPEVNLLLPVPTGGGSDA
GSEASLSVPGRTIVSSKNCRSISKNVSPLAERLPHMPQRVQRNNTITSVDSHGNCSNCKP
ARASLLSQDMVPYQNPLSHVESPLSPVSVHFKPVLSMHSGADSSSTYPLPRQRPRRYYDI
DLQKVSDFTRCLRTVQRLNFTDSDFEKIGLRYAIPGIRELHPKEVQFLLERVDESCKPHG
NPFLCSGEEEFFVKRTISMASTGGGTDADVCSVCLTRRETNPKLVHTPSAVTADPQLPGH
GTLKKTRVSYCQSFTQQQGPGERDTPTNDTGDSSPQSASIKEQCLPLFRGGKETIVQKKD
LQIFLAMVEARLKSVDQEINGRLRFSGTDLASSSGEDDTAYIA*
>TCRU_1985 Protein of unknown function (DUF3676)/Trans-sialidase of
Trypanosoma hydrophobic C-terminal, putative
MGQTVPYYFANNKFTLVATVSIHEVPKEDSRPLMGVRMNDTDSTVLFGLSYTHEKKWLAI
AGNRATSKLVDEWEPNKTYQVVLRMDFYSWTVIVDKKEIHHQRYNTSLFDSYRISHFYIG

GDSKHQSATGGHVTVTNVMLYNEELWGNDLDELPDSKVTIPSLGVEEKPTGPVTNTGASV
ASESRSEESTASHELADGDTDKQGENSLHNPVLAASSSTVVGGASVSEPATATESAENSR
QEDNAQFHPEESVQQGTLNEDYKSMQRDSDLQPQELLSAESTGVTDVEGSAESYDKEQPE
EEGGTNDRSDESTSSVGASSDMDTATETVDSGHQVQQSTELSTENDDVRSTGTGTTGAEQ
SLGLEAGDRNSERAMGSDSSLTPSKSDAEPTSAENTDNISRTDGAEFSSEDGKEVPQTVD
TAPGNTNTTPGETMISLESNATAPSDAGILPEHGHYSELAGMALFAESTVRGCVFRVLLL
LLLGLWGAAALC*
>TCRU_1986 MORN repeat, putative
MSMTVPEVILVGQKTRYRHFARGPRDLYAPEEMLPDPPPQHVWSYCVSREHNNTVYFHND
ATGRSLWVLPSLASDGTEAGGGAEEVMRTVGSVESASAAQKHVKFGTTDEKSHEAATVRR
AVMRQSIEKAMSQAETQKPTETVQKKTPTGSVAEILNNENSDSNGKGHASPVRERLAVWR
AKRAQQQQQKEHDGNDPVTSSYGEAEGSRVNHGRPAFSDPNTATTKMTSSLDNKIPSQIS
ECVAASKGSGFKKGGQPAKEVGNLEESGQCQQEQQHNSLEKDVYDERQRLFLEAHEELQR
EKAAALQKERLALEQVARLQEAQRREEEERTRLAAERKRLEQQRLELQKRVLERQRELLA
KVEEEAMQRELAAQLDNFFENKSRLEQQAQEERQRVLSFEDAIAESLLEKAVKNHTTTPK
KERIIDLRLLEESDEDNNNRHGVSGREETCKSRNSKERQDFLQQKRQKEQKQQRRERITY
SPSLVYVGDVTGGECKTPVFLQRQGRGTFFYDIAQKHFFDGEWSGDKRNGSGALSLPHVA
VEGTWRDDVLEGSATFQTRRLKGKGEFKQGVLDGNAVVEIDCNGVFAGSVKKNGAVVASG
AVTLASGDHVEWIRDENSSENNNNNNNRQQTSAHSKNFNNGSGRCRIRFENGDVYVGEVE
NYQPNGAGTYRFAAEGQEYVGNFQNGRLQGRGTYRFANGNVYIGQFYKGLFHGEGRYVEQ
DAYTYEGFWEYGTAHGRGKLIFANGDVWEGEFDHDRRVNGHYTASRLFQL*
>TCRU_1987 conserved protein, unknown function
MGYTRERTHRHFFVARANAFFSRLPIARIQRSLALEAIKQGRMKPWKHTKEQILGAPITC
NFDYNPRPVRLIGTVMDAHTEETSIKGGLKVYARNEETNMMLWIPVGNPKLKYEVTATKG
SFQHYLDERDKWDEAWLTGRARMK*
>TCRU_1988 ADP-ribosylation factor family/50S ribosome-binding GTPase/Signal recognition particle receptor beta subunit/Ferrous iron transport protein B/Gtr1/RagA G protein conserved region/Ras family/Miro-like protein/Elongation factor Tu GTP binding domain containing protein, putative
MGNLVARLRELFSSERKLEMCLVGLENSGKTTLLNVLSVGHPIETFPTVGLNVKMVRKQG
VQLKVWDLGGQERFRSEWGRYTQGCDCIIYCVDSSDFQRTELAKRELHKLLEDKALHGLP
MLVCLNKIDLEPHMSKEECVEFLNLQVLRDNPWLVIPISALRQININEVVDWLVKNSHS*
>TCRU_1989 gamma-tubulin complex subunit, putative
MATHLWANFVTSLESRDVSFQQVQHATDRRAVIVEAGFNDPITIAVLETEWMKRCKTSGP
SSTAKEAVGVPATVAAPPAPLCAQFADYTKLEDVPEEIQDRVVATDVLAAVIGYGGSLLQ
ASRDGFIVSRYVPVSMRSLCKTIVPVADSFVALRKVERAEYMGKSLVAMALGEVVSEICT
SFAHEIANLQRWAQGRAMPLMGVVSEVLRAGHHIVRLRQVLPTDTIMDEEGTLSMVGWRL
LNHIHEQSERYSGSREDDELLLLLLRRASVPYLRLLHRWMHEGLLEDPYGEFFISEARPP
AGKASVSATLNENTTTGMRNVVSRIFPNTAAADDYGEATLEEANAFERRFSMNKNMIPNF
LLKTSKIAKMVFYAGKYCCLLREYNGTLPAFGDLAEHMLVWTDADKLHRKIEESYEIASG
EVLQLFLGPQVDLLGHLISLKCYFLHQRGDWLVDFLDSSEELLVKSPVHVKAHSVRVLLQ
AAIARCCETDPYHSTIGCSFSDGTIEQYVNGSFEPATDEAAPRGSCGRKSAMRIETHRCI
ELLQLEADLKWPLTMVLDSVVLRRLNGIFRLFTWLKICERNLTTAWTDVDVPHQPPQAYG
IKHQLIQFIRQYQFYAAHFVVEPLWGRMMGRIGQADSVFAVNNALQEFFEGVELGLVLAS
SQRFRSLSRILEIATSFSEMGRREVSMRLRAEELGKALQSTEERFLKALSELASPVGPDY
PQLIPLLTWIDFSGFYNRNGVYRVLYSAGISTETVTSAGADRRRH*
>TCRU_1990 alternative oxidase
MLGARRNIMARKTVSAAVRTTVLHVKGPMVALFFSNRCCSVNPAIPTTGGSDAAEVAAKR
EARPALQNDHDQSHGSSLYMPFMGSSSRFTFASPITTISDINALEGERLTHSPPQRFSDH
CCIYLVKLLRWCADKLFRERYLHRATMLKVIAPAPPLAGAMISHLRMILKKENPAYIPGK
GDFATETRGLLAQAESHASHIRILMLMTEITYVERIAAVFLQATHFAIFAFLFLLSPRVA
FRLMGYLGEESVVIWTHMINDIDLGKVTERALPQDAIEYWGLHKLKYTRASAADVKRFDV
REHCDEEATTGKHQQTSDVAEEEEITLRDLILLLRSDEMLWREACHRMADEMNLIRKSSF

MSSFLS*
>TCRU_1991 retrotransposon hot spot protein, RHS3, putative
MSAGSYLLYQLLHCDVEKLQFDVYSFGGSTTYVCDKAIKTVTRHVGKGASKDVLWDCVMK
GHIFYDVTEKGTPPAEYFVSSTGWGMSVVSPPNVDNCDEWEKQVKAGRIIMNCPAEVDVK
AMCVCMKRGLKPDEQVEYWKMVEEHMEKVGPIPRYIFDAKKFVAHSAAIEDALDGIKSRD
GERHFAHRE*
>TCRU_1992 Uncharacterised protein family (UPF0172), putative
MSSSSTPSVVSSVEAHAKALLHCQKYPTQAVSGFLIGKRLTESGASDSVFVADAVPLFHT
IMMTHPHPMLSVAYAQVSSYARTKGLVLLGYYVANERAGDSGISPLTTNVLRMLHEKVST
GHNPLLWTIVGANRAEGVDVRPSYYMGGKNYLPAPELTFGRWNSDTLSCEAITSNTEAIE
VFENAVDAFKQFQLVDFEDHLERVQLSYLEQTVQV*
>TCRU_1993 amino acid transporter, putative
MDTESGNIAPGNDPVVVPELGSENGSGVKWRRTSSGMGALRCFTNIIPYGGLLSTTFNLA
SATLGGGVISLAAGFQMSGVAFSIILLVLVTVCTVYSVGLMMQAVEMTGYNSYAELSKKL
FGRGWDHFTVVLTWLFTFGTCVGYVIAIGRLLEPVLSDPSLPEFWRSEAGNRAVTSAIWF
VGMFSLSLPKEINSLRYASAVGVICIYYFIACIVVHSVQHGFRGGKLRDDVAMFKSGNGA
IEGLSIFMFSYLCHMNCFSIFGEMRKPSARRMTLHTACSMALCCIAYIVAGFFGYADFGD
EVTDTVLVFYDVRRDVLMAIAYAGIVFKLCVGFALCMQPARDCCYYIIGWDVATIPAWKN
CLFCGVMALCALLLGLFIPVLNTVFGLLGSFCGGTLGFCLPALYRMYCGNWSLGTVGIVN
YVCTYLLLMAGVVAVVFGTGASLYGVVR*
>TCRU_1994 Cullin family/Cullin protein neddylation domain
containing protein, putative
MVEKSCKYEEKEDERDRPCEEVVAASRLREAYAALDRESFGTLGVQALSPRIPCASSLLE
TFPSLRELFTVTLNLEVLLRRREGDALRTIREKHLKWYKRIFHTLHGVHDIHALLRYWVK
GVVLYEFCEINRHMEKEDDDEEINNDTGRQNCERGGVMRAADYAMELREALRRFPRLVAF
LFLSKSQEYWAQTLSEVIKEDVGSNLSDGLKLNVLQRLLMKVLQCQRQRRYGVLKCEHFG
TVHPHCHNNGNPLHVVEEVRQKLTVGNPSVDISELIQLFSHPARDAEERLVITVLQSVVH
GCRGFFQREALLSLLEPGINEESRHVFLLKIWPQYWNNELEVMRELPAVEEACVKGILVK
LVFVWETGNGVSVQETSNAPCGLRPYYIFHLMRATLQPLLDALFALDAAAEEGETRSTLE
LLLDIANSMACIEAPPRRTLRLWDQVGAGAALPSSIPREVGYVVMADVCRAFLEVRLPSA
VDHFLSGGEIPEEQRWPRLIAYLIRTEHLFHRLCEMRLLKAKLLDNCSAVPCFYGILKNA
IANHLQRKRNADLFVETLLGIMQTYLLYGSHEGAEVRRVGGGGREKMVLVSLHNEDEVMS
AVRLAFSVSSIDRFLRLYKELLAYRLLFYAVGRARDGSVDAMEARREKLQTEKLVCEYLH
ELLPFERNAIQQMIQMCMDMVTGNNAPEAYDPQALQPEQCGHGADTFSVRPTLRLLSRLA
WPSYPLLTDVPKPLHNVMDQFARFYHAQYSNRRVVWLRTSMETITFTVAYPQAGKVIVGS
LELFNIFHFLSEAGTSGTTWTLLAQRIGKDKTLLQRGLKKLIHDGFFKIQMGSGEEIVAL
NAAFKSHKPRYHFLQPPPRVGALLEENGIINEEVHRSRIASIQAVIIKHMKTVRTCLYDE
LFCWTRQQNPQFQLQNSDFKLALEMLIEKEFVQRDPSQKQRFVYKA*
>TCRU_1995 hypothetical protein, conserved
MQVKEQRAVKQKQAPVNLSVRASAATLFLTSVRRLTEAHGLSFFALQRGETAVRCRALTD
LLTASSMEDVLKQGALEMQRSLATLRQPAEEWSRRWRCPHAEQEQGTQCLTQPALPSALL
RLLVDMGITKASEPFSVVGGLPPAMEFWEGCPRKSACLAAYSPSLHPLTTICINAIEAIT
EITEDLPLESRVAAAKHFLSRQSEKNRIYSEQGDGEDNTAKNNASGTADRSHPAQGPTVR
LFCLSPYASYAALYEAVNKANDSESLFFGGEACEVLLVYICTMTAAGSVGPTTLNDNPEI
WGRLRYQQAGDAESATPGNRRGNHDELFFIAATLGDYLRLGSAFSWVYGWQLCYAPQGPP
PRSLPWLKLFSPTALSAAISTSL*
>TCRU_1996 BNR repeat-like domain containing protein, putative
MSRRVFNSGVLLLLVVMICCGSGAAAAVENSDSVADPTFEWRSITDDEGVTVDSLRVPGL
LKVGTVVFAVAEAQCNKGGEGSFTGIASELLTDPTDKNRWKY*
>TCRU_1997 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MLAGKYSRTAAAKDAQERGAGEWGLLLAKGELSDGDSGSNKKVQWNVNQRLVDTLFKREQ
DSLMQLVAGGGSGVKMEDGTLVFPVEVTKKGESENDGEEGKSVSLLVYTSDTSDDSSWKL

SKGMSDGGCGVPSVVEWEKEKLMMMTACDGGRRRVYESGDKGESWTEALGTLSRVWGNKH
EEQTKRVASGFTTATLGDDNKKVMLVTLPVYSKEKGSENKEKSELHLWLMDNTRIADIGP
VSEKDEDEVAASSLLYESAEGEDNNKEEDKLIALYEKKKKGGEKPSHSLLSVRLTEQLKR
VKEVLATWKKVDEAVSKLCPTASAAKSALTDNDCSAGEITAGLVGFLSDNFSGNTWRDEY
LGVNATVNHNGGAEKAKDGVNFRGAWAEWPVGRQGENQLYHFANCNFTLVATVSIEKAPE
GDNPIPLMGVRAGSKGETKLMELSYNSEKKWKLFCGGDTTNELSSHWEAGTAHQVAIVLQ
NGTQGSAYVDGKRVGAAPCELKNAESQEISHFYIGGDGDSAEVREVVSVTVKNVFLYNRP
LTFSGGDADLEEAPHLPPANPQPTEAVPQSVEGDQKAMPPAGKPSEAPGEQATLQQPPEE
RETQENTTVGESATTQQVPANRSQGSVGSAAALNSHAVGGATGDGGTVRGSGLLPSLLPL
LLGLWGFAAL*
>TCRU_1998 BNR repeat-like domain containing protein, putative
MEVVGKAVDPFQGTTPAPYKWQEMTGSEAAAGSLRVPSLAEGAGGVFAVAEAQCSERDGA
CGHAAIASTHMGTGGGGSKAISAMDAGVSLLELVDAARGTTRAREKVQPTTIVSGDSVYM
ALGDYEKKTSGDEAADADGWRLLLTRGTLTEDGGQRKIMWGDIRAVDPVAIGLTQFLKRV
IGGGGSGVVTKNGYPVLPMQAVEKDGRSVVLSMRFKMRIEAWELSSGTTGSNCKEPSIAN
LEGNLILITPCAAGYYEVFRSIDSGIRWDMSGRPITRVWGNSYGRKGYGVRCGLTTVTIE
GREVLLVTTPVYLE*
>TCRU_1999 retrotransposon hot spot protein, RHS3, putative
MSGRPESIQGSNVESQSSTVSQGGQRRARSEFEGDTDHSSATRRRLEEIYRPQWTMSSSL
EEILLGGSILRTDMMLNDFLRSNLGGRGVVDTNENVAMEIFVLRPTIFINDNEILGLITA
SPSYRELEKRKTLLEAINKLNDKGVVSLGQWRGFKSKNTITPFARGKLNEAITQVQTAES
SEVNERMSRKEEERRRRALEMKFTISTTIEEVLFKGEFRYKDMNLNDFLLMRFGGRGIIA
TSENVLLEEFFKDPAKYIRVKGVLNEIKTTDAYLSIEGVVREEMDKGEDVRKLKQAGVYN
LQKWSEATAQVKESVHDITKSFLDAALEEAKKPTMTSAPIKMEGCYESVYNSRWSHVVEV
VGGKGTEMKVKEGKPEKSWTYRAVGRTLERNDGLQQSGEVPPRLMVLASDKGWPYSWNVL
HGTGNDLCVNCEVERVWQIVLDDITKWFSNFDLTLNPSPLPRVLIGTPGIGKSVNAGSYL
LYQLLHYDVEKLQVVVHCFGETMYVFDKTTKTVTKYKGNIASSSVLGGLRQRGMKGYIIY
DVAKEGTPPNPDFAPSRGWGMIVVSSPKVSNYAKWATQVRASRIIMNCPEKDDVKAMCAC
MKRGLEPDKQAGYWEMVEKHMDNVGPIPRHIFDEGSYIDRMDAVNDALSAIKDTDVEEYF
TLGGEEKKWYSEYPCHKLVKIVRARKVEGAEGFFNAPICTDIEFRIADRLAEKKGAKDFL
LLILASRGTLVSQLLENLGLRAFIYGEFVIALLKELKELPPPSPSEPQDSVLKINHQGYP
TRTVGLKGLEGGVTRIPMEYGVLYIPAVQNFPLVDGLFFVDSPRKTLVGLQITTAGEHHT
IPSTVRLFNERMAKYFNGWEELSRDLSWEMIYVQHENSTMITNWQRCGPVNTVNLSDDEK
EIVAFWNGKVHQYQFALTTDFVNRIRAK*
>TCRU_2000 hypothetical protein, conserved
MLASLSRNEFGKVEFDFITCTICPAMKTIFMPTSGSTLEMRILLSNILGLTVESVEFYRK
ETKGFFPVLDESMGVGHYYVLLRIRGGKGGFRKQLEKKGRAFARARRLRGSNQTAAHPTP
TKGAEVDLSKETEGKERELTEKMSSGEEILQSNTVLICKIRDAVRIGVKRTIESLVCTGT
*
>TCRU_2001 hypothetical protein, conserved
MRRVAHSRFGAGGYRCISGVAPMLYFPTNPTSKLTKDEQVKRNTSIAIEMIKRYKGPIPP
QYTRKSTSTIEQLEKEIDALLGGAEKMRKSTTDDQPMDKLTLMERCLRHALWSYHKEEGR
CDFDQIAKWVVYTPEDEVKLAQLKREAESKKKLAAFRKRRAEQGLPSALLPKNNWAQEYA
TVIDREIVTAKRSRYDALAVQTTECDDKQIEAVLQEYRKPAQDRRLDELVDLLERFKPVL
AREAIMQRLTIKHLEGQLGVWRYMDWCPEVRDRAELEVDITGWQWWSPLEERRLLPVRLR
SVNEVREIMAKAQAKKAAEQAEKSPKAIQSGSSDSARDRLLKEVLALQARINQREEIDSS
KNDQKKRAHH*
>TCRU_2002 stress-induced protein sti1, putative
MDATELKNRGNQEFSSGRYKEAAEFFSQAINLDPSNHVLYSNRSACHAALHQYLNALQDA
EKCVSIKPDWVKGYVRKGAALHGLRRYEEAAAAYNKGLSLDPSSAACTEGIAAVEKDKVA
SRMQNPFANVFGPDAIGKIQAHPKLSLFLLQPDYVRMIDEVMKDPSSVQKYLKDQRFMAT
FMVLSGLELPEDEDEEEEKVRRQQQKQKEKEMREEQEKKRAAATELSSEAKEALRKKEEG
NALYKQRKFDEALQKYQEALAKDSTNTVYLLNITAVIFEKGEYAACVEKCEEALEHGREN
RCDYTVLAKLMTREALCLQRLKRFDEAIALFKKALVEHRNADTLAKLTACEKEKEKFEIE

AYLDPEIALQKKEEGNTFFKSDKFPEAVEAYTEAIKRNPDEHTTYSNRAAAYLKLGAYSQ
ALADAEKCISLKPEFVKAHARRGHAFFWTKQYNKALQAYDEGLKHDKENAECKEGRMRTL
MKIQEMATGNSADGDEVAKRAMADPEVAAIMQDSYMQLVLGEMQRDPSRVQEYMRDPTIA
AKINTLISAGIIRFGK*
>TCRU_2003 Repeat of unknown function (DUF1126), putative
MTSPTPGALGHDVPTEYIRTLDPKLLPPRVGHNWLDPAFRKVQDKPQQLELEFRGKRAFT
AKGIYDHTPPKGLGLTAQQLLHALSTRRKGGIEADRRAQYTTLSDKVLRFYAFFTEKAPD
GCVEEYWHRRVVIDFFPEDNTVLIQEPCIPNSGLSGGTFLKRQSVRADPRQREEFPDEEF
LSLNHFNVGRSVRINAVEFFLYDCDVFTREFLTALGVEVGSPVSCPDSSFMSDWKRYQER
MLSGKFGILSQEYHGDEAVRAARFVHDSGKVLRFYSLLDERNKVPVGIVRKLEVLYFVED
DSIAVVERPTSNEAVPSLFLSRGWLPKVGSIAKANELTFAHRVNGMRQPYIGPEGHYTAI
DLGVGITINVLGRSVFLYDCDDYTRSYYLETYGVKLSDAVDCSIDYGISPESRVTAFRLT
STPASVPLTAVASTGGEHAFFSDKRTGPKTKDVLRFLLRLAPPCSVVERQRRFTLTYYTD
TDDAMVFESPVRNSGFVGGCFCSRRRLPKQGGDAEAYYTISDFSVGGFIVVNGHKFEVMN
MDEHTRNYLAGKNDPVMNDERLHLLISAFRLFLGTRFHSFKDAFLGFDRDKDGVISVTEF
VGHLQDLQITERRLDGEALFNHIASCSETGYLTMEDFVRWMSETATDKGQKNYESIDVDE
RAVMRKALLQLCERLEARCLNSLQMFRLASTMPRAYTERRADIYSLANPHRDALVTPVQL
RRCIEEVLGGNPSPREMDALLSFFFPQLPLEEYRSRRDGDLEHALDLKAFQKKYHEMNKL
LMLSEPSKQQQQTQQRQQE*
>TCRU_2004 phosphoribosylpyrophosphate synthetase, putative
MAEEETDIYLSPADSHVAVHEHLMRIESAFYYSPGDAMAAVHPLQGTVSPRRGKDLPPMC
IVSGNGNRPLAEAVAMLLGTPTHQTLVRQHANGEVNVRIDESVLGADVYIIQSTTGNEVI
DVNTAVMELLLLIRKMRLSNARRVTAVIPYFAYSRQDSKKGVRNTLSASAVAEMLTQAGV
DRVTTLDLHSGQIQGFFGNTPLDNLQTNQEFAKYLRNQSWFDPNNMAIVSIGSGGVERAR
KLADRLNIGCIVTILKRCNASGGKTLQPVGDVKGRVCVILLGMCDTGQKIEKACELLQAL
GAAKITACCTHGILTPPCPQRLNDCDALSEIVVSDSIPQEEHLRLIPKLKVLTIAPLLAT
AINMHTRDECISALFDTPPHPVENQLPPPPPQVLSSQSVH*
>TCRU_2005 suppressive immunomodulating factor
MSSAVTLRELDTLERADQPLLERFERCRHEVVRVSASSILHDCIAVTTKGGFVELINIDT
GAFRLFLSHLGDTPLESLLRCFSLVPSLYTARGRHHLLYSLAYSNELLLADMEHGTVEVL
ARFHSRPSVVFCDGDYMVCGEGCGQVTLWRAPCEAAGAKLFWRRPVFSDTVLCISVQRDY
VFCSSADYHFYVLTLESGEVVAALPHEPSPAVAIQSAANSQVSHTLTVLCLPGVLSVYSP
PPAQEDVSAATTIANSTWICTALLRLDVQISCASCCAGLMALGTASGVVLLASMITTNGE
AVERVRFDVGFSVIGIQILKNGELVVVTSAGDVWKWTIEDLLPREADMMEGQEEEEEEVE
NLFVPQPHMRPPDTRWVKTTTTAEAEAGAAGTATSGERVRMSDEEEIVVEVGDEASSTSS
ALWSESCHPVQLEKSTAGLGNPTGDGITEGNAVPLLRSISHSERTIHVNPIHISSSTKST
DTATAAVVVAHGDTATEDHVITVRGVDKSASVAVISVNTDEEKDEVNHSVDDDHDDEYSE
HSFQPSSISIVAGTIGAADAARSVILAPLQIEPNMNSHSVPHVAAATPTTITPTTTNTSP
FNADPSAHRDGTQLHQEDGVVATAQKAKDAPFPPVSTSSACSRALKCLLRGTELGPPAVI
NGLRAGRRMDPRKARHIVENSCTDAAALPEPESQSSRILVDHRQALEEAKFDYAEYTKAH
LLKAESLRYRYPVKLPVHGLHTHLFAAAVPRLQDRPNGNMESAEDGDKRKKRRKQQLQQK
QQQPIIDDLMNATFQNFTRRKDAALEEERLRSGPDIQQHFCDSLLFGPVDPSGTVLFEET
RVQLAVPNMLFLPMPLPPTPSVF*
>TCRU_2006 Exocyst complex component Sec3, putative
MATTGDELRSLVELVFRQRHEEVLTCESVVVIGRGASNKGSKARLLALCRPFAPSTPSSP
SSVSQTTLNVVRVESGRVVKVKLVFVVARLVDVSHDGSFDATFNFGGSGMISVAFESHIQ
REMFVAAVRKVQRDLQPNVTTVSRDVRALLTDALGAEVEADAAARVKSLRHEKRRALTAE
DEQRLQHFLGRHGFDDIRSTEKSLSMRQKEAELSSVEVLLASVGAWEVVRSRIVELVGDV
EELESRIAQYSRQILSKKEQLQRIEHQSNTLQRKQRNLRKLHEHLEGLCGQLSLPPQTTA
LLLRLASVKDEDLVDFFAEGNNAQVLSVAMKHMRSLLQNKKLGTDYPITAVTERRAFFIE
QRRMIAHRSKAYILATIGKYETTYLADRTRYSSKGQLVWRIHSELMAQLANIRDVITALL
YIDLEGYIAVLRRYRVSMQRIYALEMHKFFKHMRTHVKKVGSRGPFLLGTRDYSMDEALN
SRMETATITTAAGGETPRRLWGVGSSVASTPAASWTLTPHTGEGDGGKDGTLCLELPTAR
EEGLRLYDVANVRADAATSAATPGTTPNAIPAAATSYSFTSLASGWTGTFAGKLRPDLAL

AMVLETTFSVVLQEKETLQQCFGIIEKAPTEDDTSGLSRPFDDDPLLACEENPAKLLNES
LLELFGGDKLVQFSPSKAGASSSSYSWPQDGDVGLIGVNKNNNNKHSCSSTIGNNAVQAE
KGCYLLRQLVGIAEYCGEKCDRLYAVPVMAMLGAYRRDGTPTAESSFCQMLLQALEHVVS
STISRSIAEQTTSIATCRKRHVVDPRGMLSCFTKLPVFIHHMETVHNALPPAVCNRSKYA
SITLSFVDQTFEALNYITNFGGTEPRREKKLSFIESIEKRASSWLEGLDNNPVKRGIIQQ
YRHHAFFCTFYTSLPSTAYAVELLRERYESSRRLRDHYEEVYLTRILLVKDFPEFGNFAL
VAEDLAQSHSREELRHHNALSVEAMGRILQCLPREVRSGISSSSRRMKKHFLRDVADRKE
EKLFHCALLQHVWQHFSTLLLQKIEFLETLLRWPLYAGMEMTITRAEVLSLLQAA*
>TCRU_2007 hypothetical protein
MDAAGGGRALRVELDGANRLAEFRLQKVIELKAEVLRLRRLLLSLRGGSEALERVGLKKK
KRNSGESLATCMAESTKSGVTRLTQEKRRVLSSPSPCIYTATAAAVSTEHVMSPGPRVFS
VASCMSRGASRTPIAAQRRQESSAARCGSHRLSSPLLLTSSSSFTKAKPKATTRPFIKLH
TGVELRGPKTFRRVPPPLSLSSCLEGAAHTTSMPTATTTALDVFSAGATTPPASPSSRFC
SSLAIRQEHEGVLEALAMLRGIVLRADRSMLSTLTTLSNRRHIDHALPTALAEFKQCLLR
VHSSLGDKLHDGEAWCIDEAERDALEVMEVPGMAAALRDVVITYDYTACIHQNILHKEDG
MVGVRLGKAFHEFHANIYVLLALAQCVPAALR*
>TCRU_2008 Thiopurine S-methyltransferase (TPMT), putative
MQRCVLRRISFSLPSGDELEGQILLNRFRKRYGDVKRRSWVPHAITASRLQGWIVVGGIL
LGAAVFIGPWLVDEYREMLGYKFVPVPPSAMPHTSPVWWENEWRKGNPLWRAGESTSTFY
RGPFDFVRAVTGRDMYDGNTFKRGRDRKRRPRALVPLCGDSPIVKELAVRGFEVDAVDAS
ETAIRACVERTERALEVDVYKRIHLHWRDIFAPELWQGPLRDVKFDVIYERQAMTSLNRE
QREDYAYLMRQALAEDGVMYVEGIFRTGRVHGNTVRGPPFALSQLELKRLFPETEGFMVR
CEETNDAITKLSRENRILQRIPKELYVTPFHCAVFRAKSVDAAAAAAAAESAATLP*
>TCRU_2009 guide RNA binding protein, putative
MRCILRTCLHHNHHLRQRVVATTNTTNNAAAAALLFGVRCQSNSLIGTIHGGELSLPSDP
QGGSQLSARNIAMEALQMKKLHQERGGNPMLAQQARRVLFATSIAGQSLDARSVALLLNT
AVYFGMESDAKLVRECIDYCLKNDKLITVDVLPIVVTACATLKSRDAREVIEMQAQKAAR
NAKYLDSKGVANIISAFSKTGINHEKLFGFLSKRVQTLARVGEFEAAHLVIIANAFSRLR
YRDKFLFGAIARRAMSLRERVTVNELVPLIVAFSKIGLKDPKLSKRFATKAMEYVDQMNA
EQVASMFMAFAYFGIRYDQLFGVLTNRAVELIDEFNAQFISTTLNAFQRIGINNPELFDN
LAERALAVVQDHDARDISKTVTALAHFGLKDEELFKRLASHAASIADQFDALGLVNTAHA
FARTNFLQQDMAVALSERSVYVCRQIDAGEARRLLWSLAKFQVRDPKILTPVFNRCLALH
QDFFSDPTGSEEIEEIFDIYGPNFCPPLYQLYVSRGTAPQM*
>TCRU_2010 hypothetical protein, conserved
MLNTKKNATNNTPTAAAAAAEEEAGMTVRQRLRLKRELEEKRKFGLAPLAVDEVSGNEIS
PNVPQLISQAPWYYGTTGPTLDHQRLKCVDTMDRLQDQHDTVVVLGKAKTYTAGACGNCG
SSTHKTSECYKPRKKVGAMYSGKVTSVDMHVERTEKSYAQKRDRYAMGASGVDLLQQASQ
EGEEETQANGNLHANGEMIVKKHPRLQDVFATQTAVTGEGAEIKELPKHLHNLDDDSAMF
DPKTGSMRGNPNAADPTRTFQGDLQRYRTGDYYTYLDMQLRFLNGESKSIVDFRLDEQLQ
KQRRQERQQQKDEGNSNNNNNNNSNNNRSVDTEEEMTRDRLLRSLYGESSCASAENSLRM
REAIAGFAAASAASLSSSPQVASSSSLALSSMSTPINLPQVRIGSATRNGHACVYGSYFD
REGFRWGYKCCKRLGKDAAACQSTPAEPSVAAKAEGEVLGQAS*
>TCRU_2011 Putative intraflagellar transport protein D4
MNVYFSKRVAVPTSTVITSIAWNEEQGWLACGGRGGLLKVLKIDNSIGAKGALLVNQTLE
GHSADVSAVAWNHQYRKLTSSDESGQIIVWTLHKGMWMEEMINNRNKSTVCDLSWSADGT
KVCIIYEDGAVIVGGVDGNRLWGKDVKRELAKVTWSPDDRYILFGTKNGEVLVNESDGGH
AVCQLRISCLEGVESLSGLSWHPAWVDSPDPPATLAVCYANGRMQLMRDINDNRPYLIDS
GILVSCIAWNPQGTTIVVCGVISTAAMMGDRPASQPSSPSSSLVVAQFFNTEGVHLRTLR
VSGQHCGGVTWEGDGLRVCIAIDAALYFANVRPAYKYTYFSKTVVFAFYRSDRAEQGVMF
WNTRSNERFIRYIRGLFYIDSCKDVCMIVNTSADGSHRVVQLLNAIGSPLEVRMMDLEPL
VCGMNSSHIVVSDEENIYVWQFRDPDVVLDLLDPISVQASRRETRDRIVHVDDIVRPDSP
PSLVTHTAVTNDLICSLCLSEEFLFVARESGLLQLYRFSPLHLVGKMVLPSRVQSMAANS
NSTRLSVVDVSGIMTVFHIDPMKLSLVPQKIAPEPNFEHKDVWNVRWSKDDPELFAVLEK
SRMYIFRGTEAEEPVQSRACICKFKSLKVRALQLDDIMHDPERPRKEHVIEFETRELREA

RQALQNLSMKEAYMYVENHPHPKLWALLTEHALAQLDFDHAEMAVVRSKDYPAIQFVKRI
KTLDDPQKQRAEIHTYYGRFDEAEKIYKEIDRKDLVLDLRYRLGDWFRVVQLVQEGGGDE
SHMQRAWENIGDFYADRQKWTKASQYYTQCRQLHKLAHILFLQEDYDLLAQLIPSAEHDK
GLLLKIGEMLFAVGLGDEASRAFLAAGEARLAVAGCVQLHQWDSAVAIAEAHKLKDILPQ
LARHTKSLIESERLPEAIELYRKAGQHEEAARLLARLGQRAAATDPLRAKKFYVLSALEI
EKYRKKKVALSDDGTAAVDMLLSEERAATSERVLDAAWRGAEAFHFFLLCQQHILHRNLP
HALNVAMRLMEYDDLISPVDSYSLIALTAYLAKNFSICSKAFTRLEAAEQKDAQQQNQQE
GGTPAVAGQLQFIDMTMDLDVSKQTGVAHRNNACSHGAAGGGSTGLSGTTTSLQLTNRSK
GTALATQFKYPTVSLREPRRRFADLAAKIFTKHKPEDNSADRVKCPKCDAFVKEWASSCA
RCQKQLGVCIFTGRCITTEDFWQCAVCHHCIIDVEGDRFRNCPLCHTPMKHGARG*
>TCRU_2012 MIX protein
MLRRTSRRFVSAKQFFGTEAQPLEPYTVKSLFLFSFIASIAFLSVLSVKETKKAGPIELP
DELEAEKRRRNDPRRPPWPLLHQRIVLLREGKAPHDDLALLWEQTRHYYPADWLVPLEVT
QVLKYTSGAYLQNYVADPDKLRKDVLMQLLNIKYGRVKDPNGGRINRDVEEIISMAIEDL
ENMDLSPSADAALVPTHT*
>TCRU_2013 hypothetical protein
MPDAEMPETRGGLVLFPRCLSRAFRCLRDVPIMHFVAVTKVNRRGKRQRRFLVITSMHLY
SCVENGSIQRSVPTRSVAEVHAWNGELPQVGLRIPSEYDMLFFMDSAADVTGVVAALQSA
TRDGASGRGDGGALRLVEATEALSVAAYCLERPKGFERGMRGTFGWLIGSAGDVPAAGMD
HDALRPFVSANAKGLFVKSSTAAAAAASSSPPSSLTAAGGTVPAAAEETGLPGASNGTRC
LSKDYSDDEGADAVSFSVPPPHSPTIGSAEAGAEQRTKKKGTGEEKTAASVISRHDNNMG
GAAAALAGGPALRDDRRQLLEEREQWCLLLAAERRDTYRLRQAISDLRGQVLALTSDNIK
LRTELLNQRVTWHPKQSS*
>TCRU_2014 poly(ADP-ribose) polymerase, putative
MSPKKLSGAGKAPAAKKASAAKKASAVRKAPAGNKASAAKKASAAKKAPAAKKASAARKA
LFPAVNNTVKIIPAKGAAPAAATAPPAATNVGGNSLTPATDITGAKVQQMLRKGRGVVDS
FSGKVDTCHVYEKGSDVYQCTLNQTHVAANNNKYFIIQLLEDDAESIYHVFTRWGRVGYG
GQNKTVTFSSLGQALYLFEKTFCQKTANHWRSRAQFSAVKGRYELMDIDYGAAEDEAEKS
GESSAARGPAEKPVISALPGEVQGLLKLIGCKETMKRLMAEYAINTEKLPLGKISQGQIT
RANSVLKSLEAEMKKANPRLEELSDQFYTLIPHAFGRSRPPLISSESILRQKMEMLEALG
KLEVAVSILNAEAPEEIHPLDKLYRRLNCEITPLSRDEPDFRRIVEYANNTRGPTHKFHV
EVKQVFTVRRKDEDDLYGSFKRLGNRQMLWHGSRITNFIGILSQGLRIAPPEAPCTGYMF
GKGIYLADVCTKSANYCYPSRDTKTGLMLLCEAALGKQMELTDSKYMENPMPGTNATKGV
GSYFPDPAGAEVVDGVLWPKGRVRESRISSSLLYPEHIIYNVGQCRMRWLVHVGFKYH*
>TCRU_2015 hypothetical protein, conserved
MTSAICPVKGTAVELPWKLLVAAAQPYQTLSGPALSVNFHRQPTVMPFQRLPFHHCGVSG
RYYHSLLHSLAEFATTPRPVRDSHVRMLHAPMEDFWHAVGFFNCTYLTTYAPFTHEHPAM
GAVELAPSSHRSHKDLRFSLYSGEHQPISTMILTGLPSGAVDGKEKDVIAPLPHIEKDEE
SLRVANIGDVKRLADGSILQRAIFTRDSQQSRDVVPPWWVDVCVAEFCQTLALANLLAPH
VAGEGRNCTWNIAAQQALTQGELLTDAPFDIVSAVPRVFAAYRTPPWRHRIGLPLFSADR
QPLCVALRVELRQHGCTLTAGTYFLVEVEGHT*
>TCRU_2016 Zinc finger, C3HC4 type (RING finger), putative
MPKHRKGSRGVEAKDIGNFQYERQSDSPGVARRPTAAAATRRDVNPAVLKRAYMLHNFQF
VLRPDVYEMKAMPGLPQGKRRLNEMLLSSDAAPPWDAVTAVVVRGTMEQFQCPICLEPPT
AARVADCGHVFCLPCMSQYLSRLKQENKQRTCPVCHNFVTLGMLRPCIFRPIEPPCLGQR
VGFTLLERRGGCCVLLRKDDPRWHDAAPMEDELPLPLFHEPSATFSRYILATEESECARR
RLDCTAIMDALQQLNAQPRPLTQFDDGVLRFAEEALEMVLQETNAQSPQSSVRNSPPIAP
KRPNVDGASTYYLYGESEGQPYYMHPISFKMLRDDADTRGVPLPNTVYAPVEEIVTFTQD
EASRKHYKALAHVPLHGTIKFCLLDLSDVVLPSTLKTFAPSLARMREARTWRERGEESSG
EDTSWQEYLRRYRAISPHCTEDSGVSPEPVPSEYSGVSDLLISSVVTAWSEPGGLSGDSS
LETRQRATKRHDTPIPSCWTAENSRRLFATPPMRPAMPTWGGHVFNPHKPSSAGLHPTQR
PGC*
>TCRU_2017 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative

MDGDGYPILLGLSYNKEKKWQLLCGGETNSKDLSVFLGPETKEDHVVILLRNGNHGSAYV
DGQRVGDAQCELENTDSKGISHFYIGGDGDKTRNQGDVSVTVTNVLLYNRPLTFSGTRAE
VEEVTDSSSKDILSLSGDPQPTGTVSQLVEGDKRMMPPATIPPEAPVEQTTSPKPQQERE
TRKNTMVGESANTQHVPANTSQGSVEKAAASNSHVVGGATGDAGTMRGSGLLPLLLLLGL
WGFVAL*
>TCRU_2018 hypothetical protein, conserved
MMTMTGRVLLVCALCVLWCGAGGGGCSETPPGSPGTPPHEEPQNDNGAVGVTGGGVQTGK
QAVPQAPALPASGLPEVPARPSQGTQPGGGEASGTPSTTKDSMVQNTEVKKKEEDEEEHG
GNEEEEEKQEEEEEEKKQEEEEDGTEEEETKKEEAGTGTTEVTSAGGQEQPNLSSGAAGA
SNKTNPNSTQTTGDDDPAADGAGTPEGKQNENKDANPKETPVEATAMKTTTATTGDSESS
TAVSHTTSPLLLLLVACAAAAAVVAA*
>TCRU_2019 mercaptopyruvate sulfurtransferase, putative
MDIVKKVKIDLPVSLAPMTRSNACGHQWKVFLTVDDIARSFMEYQVFDVRYNLADGNYGK
NAYAKGHIPSAIFVDVDEELSGPLTNTTARHPLPDAAKFVEWCKSRGIGSGKSVLCYDDI
SGAMGACRMWWMLHALGVEAYVLNGGFQAYCAAGLPLETGLPESRTQPLETWPYGVEFRR
ALTIEEVPPNAIMVDTRSKNRFLSTVRPYGADTLPGHIDNAISFPWDSILLLTDQLKCLK
SEEECRSNVLEALQSVWDAGHSNASNCVFYCGSGVTATLNIALLCHLGLGDPFLYCGSWS
EYAGQFSFSIARRIVGEHGMLFKMMSPCLGDNPKAPASDAATVIVDGKIVPQPDAEISSA
IAHMHLGERAQVFFKSRRVVVIEVLPK*
>TCRU_2020 hypothetical protein, conserved
MSNTLCLLEFVCNLRWVLSYAVQRLDPVLEAHYAHVIERARQAESDVFRSYSSVKSLVEV
SRDALTLAQEGIVYLLVAEGVLGHCPSTMHSFLLRATASSDSRALSDCTCQSDVSSLSQL
QSARNVYQAHFLFIRWLVAEGLLTDEELLDSLGDEADASACGQKSRFELHVSMAKSLSSG
SPFALQAHVILTRSLILHHCCIILSVDDILAHVRFLDPMCSGTLESIEDALVFWMHHVLK
VMHEKKMINDQLYGFAAKELGDSLYHSVQSGVVLGLIVHFYKQNILPLSHICTASGEGEE
TTRCRERRLQNWGSLLRVSEELGLWPCLYADEVELYGAVVLQLHVLRFVGELFAVLATQA
EDLEEHGEDAYCMPLQQKKKNGTTAQSQGIMDVGRERKRNEATLKNCRVEKGDDIISMGK
GDEANVGSSQNSSSGYPSVHSRRQYDVMMASLQMRGVDIGVSGPPKSYSSSMKKRESAGA
AKAKSGVRVLASTASMRATAAASSSSSSTSSGTAGYLSRADSRRFIPEKVTLSKNLSNME
LVQSHLNSAEGVMRSDVVQASKPIAINPPRLPFVTNANAVTTSPISSNSPVTTALSAIAP
DLSQESFHATLYMESVLRAFNLCDQVSFLGAKDSGKLFSPNSTVNGIHSNMKERASCTTT
ESSFPINSAGNLGSPPQSRKMETARKLTSLSRSHSNLRGQGDMESEGVSPMTPELATDQS
DAHSQTALTSFNQQHLSSLRSQCQRRRSEAHRKLEERLKDLLRDLSAVDHSSVQSTAAFQ
TLLRTLEKQQAIIKRLSSRLAAMNGGNPLWHDDVWSGNEGAPGVSEGPGSTHLLCCEFNC
GSDDSGQHAETEISSIPDAFLDDEKALLDH*
>TCRU_2021 PIG-P, putative
MSLKSVAPVETASSGVSKGHNVAINGFIAWLLIITVFVTYFFWAFLPRHVLDRTLMSYYP
DKYWAVALPAILVISTVYYLSTSFLLVLHRTNPLTDGFCVADADAKEDYHGLESLSDAKE
GVPPITEIPVSVASRLLFQPWT*
>TCRU_2022 Endonuclease/Exonuclease/phosphatase family, putative
MKSHLVAVLGLWLHVETPQQSVAASTTETKTTPPLERVPRHARCGELKRSACRLSDKTAR
SFRCGHSVDITRCAELQKNPETEEDGFISVWQLNVAGLSPVKKIASAARLEQHQPDIVLL
QKTNTQSATAAKLYGYNSFLQSRTGRGGGVATLVRHSLPCECLTLPGTDLLETIAVRATP
QDRPSICVVNLHSPRTATVQSSSFITAIRCSGPQLLSRVN*
>TCRU_2023 60s Acidic ribosomal protein, putative
MDAFKTLLGASVATEYEFDEFDGKNLRKAALEGNLGGGVADAAAAADTGAAAAPAAAAEP
EEEDDDDDFGMGALF*
>TCRU_2024 60S acidic ribosomal protein P0, putative
MPSVSEAKREYEERFNGCLTKYGRVLFCLMDNVRSQQVHDVRRDLRGLGELVMGKKTLQK
KIVERRAEDKKASAYDKLLYNTCIEKKLLCGNTALIFTNEEIPVITAVLDKHRVQAPARV
GAIAPCDVIVPAGNTGMEPKATSFFQALNIATKIAKGTVEIVSDKKVLSAGDRVDNSTAT
LLQKLDISPFYYQVEVQSVWDRGMLFLREDLSITDDVVEKYLLEGISNVAALSLGAGIPT
AATLPHMIMDAFKTLLGASVATEYEFDEFDGKNLRKAALEGNLGGGVADAAAAADTGAAA
APAAAAEPEEEDDDDDFGMGALF*

>TCRU_2025 hypothetical protein, conserved
MPRVLIVLLTYDDPECGGAADALAEHLQRDCAVMMDRCQLTVKPIAILHNASHRDALYRT
LQDLFQVKPQDIYVITFLKENNFEEYRKVRELCNGVKPCCIKHQLLTHVANYSDVGLIIR
NLVRLVLEEMRREA*
>TCRU_2026 hypothetical protein
MSDHYENASEANSLSPLLQTPLLSTRQYFVSPRRQNQQQVPTDGIWSLFPWFLGPSGDSN
VSARAQRNRSLPASDGGENSHRVLPSLELANGMDNGNEVKHRQQQIHPSSLSFSLAGFGS
QFDDMQPLVTLLRSSTTSTLGNSEEYRSTPIRRLRRCVSPVHFFHFPTKNFLPQTRRQAA
IRIVRWWRSREALSEKRRVHALKLIQRVGRGYLCLKQISRRVEVTRDSSSFARSIRLCSS
ISMWLNKLGEKSNTRFPADKLGVVLCESRGQFNPGQSYCSRCCRNTSGSMSRNYVSFRGL
GKGVRGARLVNFDPEKKTASAQAEESKNAVSSDANNLSGSFINENADFIYSPALSRNEGA
DIFYLPRISQRTHAKKEDEETQPQNEAFFCTFNNRVSLEPFSVKVARSLRSRDYNELGPW
SLQSARRSTVERVCPNASML*
>TCRU_2027 centrin, putative
MSTTRAAGGRLTAPVRTAVPAALPRKRRFELTDEQRQEIREAFELFDSDKNGLIDVHEMK
VSMRALGFDVKKDEVLRMMQDCAARDQHNQPLMDLAGFTDLMTERFAQRDPRQEMIKAFQ
LFDENNTGKISLRSLRRVARELGENMTDEELQAMIDEFDTDQDGEINLDEFLAIMLEDED
Y*
>TCRU_2028 hypothetical protein, conserved
MMRQCRRLFMMEGERKFTFPGTPASHSTGGVPFYGNIYAGRVDTQNYIPPMQEGSGLIKP
KSSLWDDPQIRAKMDRCPYFALCDQVLWHNMDPAYLDPGLLTAEEHQLLLLFSRAYYEKW
KAIHMRPPNTLPRVRIKYGDTHLLDEMLELLDVPAKVRQSLVKEFQLDDASLIAMNPDCW
ETAYLDPFNRDHFSGRVLEFAGMDEPLREKFFLLLQQMRRFVVVRKDTLEEQRIVLPFSS
AITLFDLYKHLGLTPYNGQLKMYDYVDLQQTQHVLTLGDEETYFDLLVTTFFKANIRNAT
LSDVADDTDYTARYTITVEPYSVPEKRIGRWF*
>TCRU_2029 Aminotransferase class IV, putative
MQSELSGILSRIPATVIGTILADESCETVWFFNPKSREVISMDALRSLPNPPSNSGADAT
ERHLVYGMMRVRNQGVMFERDHIQRLYENCVLAATSKPLTDEATLPFPVEGVTQSIRDYI
LSEHKESSDINLKFVTWLPPFSNSLTTAEAWQRFMSDFSYVVYFIKSFFPPKEWYTEGIR
ISLLYNARRHTPNAKIIQAPLRSRAKSLQDSSGAFEVFFVWDKEAHFLVPEGSRSNYLLV
TEDGRLCCSLQKDILRGITLHTVKRVASTTGLADIEHRPIYVGDLCLAKAIAMLGTSPGV
LPVREIQFYYDEESKANFISSLDDYEQCMKEKGECPSLPRETILSNGGRLELDSPHNTML
AQLREAYEAEAFR*
>TCRU_2030 dolichyl-P-Man:GDP-Man1GlcNAc2-PP-dolichyl alpha-1,3-
mannosyltransferase, putative
MNEFLSYLSLNLGCSFLFVGILLVLRLRIHEAALRRFRPEAAETRNPTDVASQKEAQRPL
KVVILHPDLGIGGAERLIIDAALALQKHQRVTPVSVCIVTNHHDPKRAFPETVDGTVKVV
VSGAWLPDHFLGRAKVFCATCRMLWAALMICYCYPDTDCIFVDQVAAVLPLLHFVATPIP
RLFYCHFPDQCCDANRDAQGRFLKPIWRVHKLYRRLFDYLESWALSFADSIVSNSKFSRG
VTVRVFPHLDSVIDAESDIFYPPVSWATKDLLTDTTPDLENDELAPLHNSLENRTVVLSI
NRYERKKNLPLAIDAFALVVAAVSNATSRSPLLVMAGGYDVRLKENVEHLKELKELVAHH
NLTDDQVLFLQNISDVTKGYLLSQCRCLVYTPAMEHFGIVPTEGMVCAKPIVAVNQGGPC
ESVGEGGTLCDPTPEAFAEALTAYVKDEALAKRVGAAGRERALKLFGMDVFGEKLATRLV
TLWAKKNGELNSAQDEEGVKKQKSD*
>TCRU_2031 hypothetical protein, conserved
MGSLVTPGETYRILAPSSSLREHLTDSYWCSAMEEVCDGKLDGVAVRYTGQNLVLMQFRP
KRLSPAGYRYPLSMSIPVEYLVPVASRPVDESTSVGGSFYSSHEPGNSSLSANGFARLCI
VCGRYNVPDMVRRRHGFKCRTCVGKKSSAKLRLEGARGKDELEI*
>TCRU_2032 Sec7 domain containing protein, putative
MKANGHVSSLSSSDGAECWRRDCLVLSNQTQNLLVAIRSNGRFGANARFANAGRITEHPL
LRQLKALQREIMTPTLVRYISEEAILRPFCDLYSSEEMGDTIVGVALASLSNLIDLRCSF
ITRNGLEMILKIVHGKKGEASDISTYEVVLARTLQLYVSCAGHPCARGLPEDLFIRILRR
ACKVALHPMVSPLLRRTAEQAMKSIVTSLYTFVVKNRPHSSPLEVKNETAVNNEAGEEEE
SFLTGANMLRYICTLIMGSDNERGSNSDIQRSVNKSSPKAAAVQLEGLWLVQAMLLVVND

SLCEPGWEELLHSVQQDLCRALLVTGVSTENIIVLSLILRTVHIVVKIASIHVVPQTFSF
IRVLHLDPIMRMTEDLRSGPSSPRRNISSPSMATSPSMPTGSQAHRSITQMLDLYERREL
LLESLVEFCGDADFSTFCYAQYDLSRRFPPLFDRLCAVLVENCFYLVDEDSSSALRREER
TGASFDFGAEGFLTQMDALALEAMFGLLRQTSLAVSHPLPPPAEFTSLILSRLEQKKLLM
EFASLFRRNAIKEGIPFLLGKATRVPAGSSYRNIFGSGVADTPAFVLVEPAGGREVGACL
YYLSDVLDKRALGEYLGELGRELPAPASGEGEEGAAALAAWESEREKSHLQAGTVRFYEE
QLKGFLQEFDYRNKSLLSCIRETAYRMCMPGEAQKIDRVMEAFAKIWAKSNFDAGKEINP
FCSEQGPFILAFSLIMLNTDQHSGKMMKPMRKEDFRRVHRDSDGGNKLPDEFLDRLYDDV
KAHPIIMAEMIDAGFSNDVTWALEMRELALAKDVISKDALMRCSMQVTGSNPKDQAVAQA
LHAFVFSSLWNNCLTAFSNTIYMCGISLEQYLMAEGDVELESTKLDSSLTPAEEAYNVAL
DGLCFLAKTATMFGVVSAVNHVVLVLLSQLPLDMQDANGSLVRLGNQRFSLHCLEKLFFV
LHDCMPMVIDAWGELGNFFSKSFLLGVFAKEPNVTSSTSSSTDCTEVWEELRHNPRIVVA
GAKRATSEGGWFAALWGSSISSERAKAQEGEERRAMERVKMLFPTMEEFLRMIDKLEDKA
HLQFFRALCETGRMKSKGAADSYAASYMMLLITEVVIRRSTDNVVLECYMKLCQQVTSSI
FATINQPKSLRSQQSNNNSCNDGSGSGCNSNSNSNKNNTTSAAIEYESSLTEPSQPIRPE
AHEYWLSLAIRVVKALLRAFKHFICHYLQQEVGPQVLDLLTNAPSKVFTSVVAPLLSSTL
LELLSEPQYLPHVPTHSILVRLLNTLCMMATACSHPLVQWRTRKALTIMVKEEHYDILRD
GEDVINALVTYALESYSEDEEAVGCVANASEVDQGENLESIADDVTTICRRLVAAHDLGS
TDNENTEWHRVWIASLRGLCALVVLSRQYRDRSEALLCLQHCLLDSDIKRLPVASISLLY
EDVVFPLTEQICAPSSAADPAPSRSTKTPADTAVNPTSTQTFVTSLLSSFSPRPTAKVAT
KNSADPSSAARERNQIVAIDLKCRVVGLLPKVLLHYAKSLRETPEVLQELWQRILGTLYA
LYTAPTESSCNTVTADAQDARELRRCNALTEEENVLREAIQETIKNMIYVLSATLSEPEC
EEVMQQTPYFWTSTKNLLRTFDFAGPLLAHIDALDG*
>TCRU_2033 IgA Peptidase M64, putative
MRFIALLRGLLLACLILGVVKTCRAADGGPKYREVQRVSVDWRTRSITFLSAGYTAEEED
QFQSDVNKCVDALYGRVRGVVSEPWSRYASSLNIYAVFQPSVGSDNTVGKNETLRNERLD
LECSISHFYPFYIYCNLSAVFALSTHAPTKDLIVVLVNDPKSVVGEGGKSLAIFTNAPMF
MPFFVIRELTKAIASVSSEYVLGVEEEHDVYVPNCAPSIEAARARWDYWIDQGLADKTPS
QGCFFNNYYRPSESDCMMRNSSIEGLCAVCKEQVNLALLFADPNFSRPTTRCTRTAQKVQ
LDKSKDIQLNIGEITGMTNMNVSWMLGDGAIFDAAHSSQLVVPKELWKNWSLPTELCAVI
TDNSPYIRPVGDTKLFRRILSYELFSDKSAPFEMKMCGMSDSCTPCEGSICDDSSGFNLR
DVEWKKKGVAKAGKRNYVISIVVCSSVALLVLLIVTVLYLWCYLKRPHELFSTLFMDILI
RKFIFILSLIIVGFSIFSFASVLLFLEADIILYKQLLIPYVVITVWAYLITLLNIALVIF
RLYAAVIVCGALLLVNGLVHTILGALWVIVAIFEGDFLFGYLASRWMKTAIKNPSEIELI
QSRLQCSGFFVSCLEVTSSSCPKESESNMYAKPCEEFFMLDLYAVHGTITAPVFVTGILL
VVVGLLDIVFLIRSFYLSKIGIQRRKYHSDPKAAVLPLTFAEARKLRRMFYRVSGKTNRT
LAGRSVTRFLEKVFRTKLEPEEKKKIEDAGPVTFDKLMSLFFPHFITSRMDPRQLTPEET
QEVQGVFELQNCQYEKFCRFATASGALSPETLFKLFLFYTSDHFTVDEGEFISLIKAEAE
TNCPDASMCRGLTAFELEGLRHVWTALNPRILGDLNDEQIALFYQWTHSEPLSGDSHFQE
WKNSLDVRQRGSIGWGEFCYPFAQRALLWKARRFLSNMEKEVPPEMITKNLVEQRFGCEV
ANAIFLPYEDEIPIERVLEYVLLSSKSK*
>TCRU_2034 GTP-binding protein, putative
MDQHDEPKAVTDSVESALEKRAAATFDLHRRLAAVVLADSEGCGCLTEEDDDGDVEYKWR
LTDVTPARFKHLVTQMQFRVGEGNGQCLYELGIANDGSPRGLPRCEYQETVETLQKMAEA
LGLDFNILQEFLLRSEPIPLWCGEILITQRQAELQDGKVAFCGTAGSGKSTLIGVLLTGY
LDDGMGSARQLLFNHKHEVSTGKTTSIVARAIPIDSSEGKNKNSTLCRLKGIDSSSRSLA
MIDLGGDVTKHMLFGLMSRRPDFTGICVSVEQPVVEVTLYARVFRAMRIPFFVVVTKLDV
AFDFEVDAFLFELAVEFSLIGCDSVLLADVDGVDSFQRSWNKSNQVPVLRVSSADGSGIE
LFRHFMSSLPIGCMPVTPDGEFEVFLDGSFFVRGVGPVVHGHVVKGSVELGCQCRIGPDS
EGNFYPVIVQGIHVGGSHVTRVRPTDEATFALSELPRSVDMTQKGKILVPTSVSVCWEFE
AHLKVLSQGMTPRLQPILYTGNMRQAVKIISPLPNDADVFYKGCLVRFQFLYHPEVLREG
ASVILQWNPEGIAVGEVRTVFSHAPVPVVG*
>TCRU_2035 hypothetical protein
MPGQTPEKSHVIETLAMQLKAAHQQRKVLFDTLHKLEMEREKTRAFCEAELVPLREANMA

LVSSTKTLKSKLDGGNQRCFSRRTPKEDKMVGTSDHASDHQALLSNVSQPERTVQAPSRF
MSLCTGEKREENGTLPGMSCDFSGTVSEPLRDTLMDGPAKQLSLANHPPLGHYVTSHPLH
DGPSELLQETEESTTSASVVNALLVQLSLMELLLRNYREAFVSRDSLQIHSTNILSDFYL
MARDVLGGEMASAVVQEALQGMLLSNEHEVIRKLFFTLFHRYRAAVSHFPSRSI*
>TCRU_2036 Coatomer subunit gamma
MPSDRDRYRYEEEDEEETLPFEGLEKTSALQQCRVFNDVRLDISSCLRSMTQCLYLLCTG
TTLTETEATDLFFMSTKLLQSTHPKLRRLHYVLMKELSPLVEQRFIASNSLMIDIKSNND
ASKCNGIRTLFKVMNSSLYASMDRTIVEALTSQSSNVVCAALVTGLHIAQVNPEMARKWG
TQLTEVIRSCGKAQYAAIALLHKMRKNDRLSVTRLIDQAKSGVIRSPMALCLVIKMCTEL
MREDFEGSLDIYKFVTSMMHNNNDLVVFESVKSICSLRNITAKEVSPAVMVVQLYLNTQS
AVLRFSAIRVLNEVATLHPAAVSPINSEIENLVTDPNRIIATLAITTLLKTGTEYTIERL
ITQLSTAGYLRELGDEFKMVIIDAMRVLSAKFPAKYNVFLGFLSKLLAEEGSSQLKENVV
DVTMEIAKSNPDSKESVLKHLAEFIDDCNYSQIVRRVLMYLGEEVPLTENPKTFVRYVYN
HATLEGPEIRAVAVSTLAKLAAYVPSLRRSIVVLLKRTCNDADDEVRDRAVLYTRIFLNN
DENIIRSMVCDVANTVAMSRQARIAARSAVLNTVAEDIGRQKAIAKEAESSTEETSAVSH
AVLQGREKMRKIKQLLELGEPIVSSEPVPLTDPDSEYVVTVMKHTYISNIVLQFKVKNTM
EKVTFKNIAIELDTDEVGVEPQYFIPIESVAPASTSYGYAVLRYEEEQYPSGTLECRFKF
AMQEEGGDVEEEEEYPLESFDINVSDFIAPVNLGGTFETQWEKMQLEETTGTYSLSSMRN
LTVAARELVEFFGMYVEGGKPGKITTASHTLQMSGTMVNRARSLVLITARVFIAKDKSVA
LQLMLRGANAELREYLSAALLA*
>TCRU_2037 hypothetical protein
MSNCAEREFGRNVTNAPVGKTAFVGLPLTANAPQRSGAVERIRQPQKRNDREEGHEDAAH
VVTAVGAKRRCTEEGILCQPPCGAVGQVEALAVKQRSVMNPACSMSGSVSSIEAYFDEGV
EASRESSPACAELLRAVEEAETAVMVDLRCVCGGAPGSLHSPLLLESSSSPPVIPLLY*
>TCRU_2038 molybdenum cofactor biosynthesis protein, putative
MFRLATLLLAKKKPLKPPSRRGRAAAVATTARRTMKSPARRRLPSRTRTPAKRAGGKGET
ASVIPNIDAPNRQPHHHHDQKSSGDEKVGTNSNMGSGVANTSSSGSDNVAVQTTAMAKTT
EATVDTSEKKPPYCLATAVSTIVVPPAANFLLENMKQTLAPSLQRPNDGGVSSSSSEETR
SPVSQMEEFYTSKKGPLFATAVIAGTNAVKQASQLIPFCHPVRIQKCSFTFRRRVVAGLS
RTSALPHRVVLRKRVSPPPPPSRARGECSVLYCFCTVASDDSKAGVEMEALTGASVAGLT
LYDMLRTLPGSQEDGLSIGESFVLAKRGGKSDFTKILMSELENVPEPPNAPAPTPPATRD
TGGEETAGMLTEGGATPPSAAAAAQSESEGNDGKSKSDAPAPSSSGSGHEQPQRDSGGTP
GDADDNAATPDELEEKGAWWKSTAREKKLQQLHPRRRYESQEKTPMEDESPPTKKTKSTP
ATTAAATTAAIAVRRNKNTEYALAKKKMENKTRLKMKAKVAKIRPKRLAIPLAKRRVESS
IPEDDASAAADDADDHEDVVVAMKKKKKKKENREVAVASNNKRAPLKKTAVHDSADADDD
SADVENDEEGEEEFAVDTFENEGDLAPPARREKKRPRRNVRETAKMNDNVADEDKDDEAD
EDEDDDEESFHEEEAVDETREYDDDEEEEELPARRQKAAKKRNKTPPSPPPRRARGSEVT
RPVRHDSWDNETEVESEFDQDDSEAHEFFEEEGEEEKPPPTHRKKKTGKTSRTQRQTARR
*
>TCRU_2039 SelR domain containing protein, putative
MTHCASHAETDGSKDIDDAAWRRKLTPEQFHILREKGTDPRFGPYNDHFEPGEYLCAACG
TLLYKSEMKFRCGCGWPAFWDCVPGAVREEPDSDGVRTEIVCNACNSHLGHLFRGEGLCN
PPPNERHCVNSTSIRFQPSP*
>TCRU_2040 protein phosphatase 2A, putative
MAELNEMIETLYAGKLISEQQVAQLCDRCKDLFLEEGNIEVVYAPVTLCGDIHGQLFDML
ELFRHGGRAPDTSYVFMGDFVDRGYHSVETLLLLLLLKVRYPDRMTLLRGNHESRQITQV
YGFYDECYRKYGSANVWRFCTDLFDYMPLLALVEEDVLCVHGGLSPDINTLDEIRVLDRK
QEVPHEGPMTDLLWSDPDDINGWALSPRGAGFIFGADVTKAFNHRNGITLIARAHQLVFE
GYKSMFDDNCCTVWSAPNYCYRCGNVASIMKIGEKSRTDRSFITFGAAPAEERGHLTKKP
PPEYFL*
>TCRU_2041 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGVSVVAADVAGGGDGGADEYFVLRWHAQLRRECAEAFGRR
TEGRKDAFAVDDCVRRGMDGVRAFGDGRRVWRRQRSAVVAGVDTTDDDSTRGSSSEVQTE
TDSGSLDGRPPKPSVKPIPGEVPDGQESGKLSEASEPTINGTGGTLDGEGEEGDVSQDEG

QDDKDVKDEVVDAAVGNGERETPHKEHGEEKEGVKEEKAGSTTKEREGDENNAAGRGPAQ
GAAASRPPSPVDVSNPQNPVLDQDGAGGERGGAGPVVLPQAAGLREAEGAPAKLAPGGDA
AGKETERQNGTAEQVATKEVQTAVEDSSAEAAAAGKESKGEKEGENVSEAEKEGSHGNVD
EEAAGKNGGNATKKLQKEATDEAKTKKRNEKKEAENANNTKEEPDEEEVKKATQEEEAAD
KENTTSARILTKINTATPDNSDGSTAVSHTTSPLLLLLLVACAAAAAVVAA*
>TCRU_2042 BNR repeat-like domain containing protein, putative
MLLRGTLTLRGIVPLLLVRPIKYTWRAHTVLGAAEGKEGLGVVHHSTTVTKGHGVFLLAG
GSDVSYEGGCWREGGLELQLVVGDVTNPTGGKQSGRIEWGGPKPLSKLISSASHEGERTE
FIASGGSGVVMENGTLLFPLMARNEAEYVCSMTIYSTDNGSNWALSEGMSPAECLDPASA
SGRDHFP*
>TCRU_2043 hypothetical protein, conserved
MASVTIEEAPSGNTPPLTAVLANTASNRTMGLSCGHNKKRETAFEGTTTTRRSTWEPKKE
YQAVLMLQGNKASVHIDGQLLAE*
>TCRU_2044 BNR repeat-like domain containing protein, putative
MEGGTLVFPVMAVNEAEDVCSMIIYSKDSGSAWALSEDISSAECLNPRVTGWEGSLLMIV
DCENGQRVYESRDMGTAWTEALGAISAVWVNARSGVSQKESLRVDALIAATIEERKIMPY
SQRARLGGEKGHCAPPLGHGQQPHVFRWTGCRGQCCGLDARQDPAALGWQFASFTTEGQR
*
>TCRU_2045 CRAL/TRIO domain containing protein, putative
MEDVLTAELGPVSVAHRAALGELRRRLGICHTDFDCWLYAFLENKKFDVDETIAKLQRRA
AMEVQELGAYEITALGSSGGVDGKACCTSDGMARGVIQIIGCDRRGRVCLYVNTVRDTCE
KSLRAEKTRTFDAILSYATRLRRDHKSCRVVMLVNQKDASLLKNIDLPFQVSIALRISKY
YPGLVERIYVVNMSRLLAVVAKSVFKGLPRDVSERISVVSETEMKQGALLQWFDAAVIPV
ALGGTMDRDTPEHWRAFADTVMRHFRHLQDAVVLRGMSVKEWELEELQRDGAVGGGVEES
SVAHVPRLFDAAEQHRNVSGALLAPRASLSSGEAAWRAWSPGDLQLRECLALEQAYAIFR
NEIVESEFLQRSSVVQPAWEVLRRQQWLQCHVRSRHHRLAVSLAEERRWMVHVTGAAGAL
VAVVSVGVLYFCCLLHTWVWCLFGAWWVPAG*
>TCRU_2046 hypothetical protein
MPGTDTSTRSAGPLASPEGDPSIAVYPDTLVGLASAPNGPLDCPFSTATDPTVRCGPPTP
ADENDVDGRTGATIHPAADCLSKQQQQGDAKQNSSSSSLTNALDVWREGRSVGSGSPSFS
GSSPCLDECPSQSPYLSEDADDLDRLLNLLSYFLPSMQSSDGGPIAVRADPSATTGRFGQ
PKTNSLAKACSYPSVSTEEARWTDGAEDTNTSFSVLLRYQFPTEDPHEDVKEDRAHAPGI
CGTRPVHPQPFLVSDSRSRKGGGGCNGNVFSGTCSVSFGAKNSVIERQ*
>TCRU_2047 hypothetical protein
MGHNNGKHKDPEPTSPPVTTIPPATTSPPEPMPTFSPKGTRTGTPAHTASPTLMETEART
ATLSMTVPSPDPIPDGDSRAIPRKIIFIVCSVFIVLFIVIIVVVFMHCLRRKKRQAGNRT
WEDSVGSSHGGSNPLSVEEEVGESKEIQQPHFYPYMPAPPVRLSEGRRLHLSEGNREAFR
SIRMHQINHMNEDEATRFHLLRHAETAFVEFGPFVDSDSD*
>TCRU_2048 hypothetical protein, conserved
MLLAKDNVHDGGSREMLYAAGAVTAAGSTLSFVRNRALLPRMVSVSLSLAAGAHLRVACN
DAGGRVLSTAEEYAAAGFGDAGSIDVVGCDACDRDTHCYAPGTASASMRNGVCVCACGSG
GYGEVCVPVGAPALPPAVGTASSVFFREGVTVQSVFVVPAGASEMTLRHVVLDGVSPVLY
VPWMARDGVRIVVQNVSLLNGAVLYVMGGGALRGAGAAGSDESGPVELSVCDVEALNGAL
VLTGTYPAGSVLTVTDTLLVAARPTPLVYLPGSQSSPYAPVLVLSGLRLVRSVLVVSGVA
LVTVMTGGRMVVVDGAVLELVGGGVALDAAVLGGEYAFYASARVVASGGAVLRVSGSQVY
AAHGLVFGSGVEANASAVVVNDNAGALTDGALLELRGSASFLSGSWLSVRGNSISGRLLS
VPSYPHPCGPRAEHADAPRECRQRARCDGRHRCAWGCRPEVRRGVPDAQRAGAAADGLQV
RRHHRGIPSRGVWRVRRRRKLLYCCDEGDVGVVRLPLC*
>TCRU_2049 predicted C2 domain protein
MNGKSQFKAHDTESSSFSLLHGSARRSRHSERSFHSSPRRNGDFSSSPSPHRRQRPKNGH
SGHDPFHYNDTLPPNAVGRSVPPEMLSEDDEYHTPYAAPLDADDSNANSKQKLELRVRIE
GVKDLVPDSRAMQTPPSTFVTVQTAYGRGKTPVIYNNSNPPFNDEFMFQVNNPETEEITV
TVVAVTSTGGKKIGQCALSVGNLMQRMERRQWVALVRHPGTERAYECGEILISLYSENSG
TDVYSSPLKEREFREKLRALFRKDAPQELHRLEWYVGKCVEDYDGAYAAIFGRYHKPHCE

SAAFQLTINSVADLTMKNGSPTTRETCYVKVTSSRFKKVTKMVPYHRRAVFNEKFDMVID
NPKADSISLAVYSANHKYGECLVSLNGLQPRVPKERTHNIVYAAGTGDACYCGTIKIVLC
TVNYGTESPVSDAEDEKRRIRLRNYLWKYLRDDLHRLDPIVASISHMNSFMGKLVRAYGP
EPRPYMMMLRIQNFHRNEKEEKPKTYAVVVRMGPEIYRTAGVRFSQDFIFSNETTFPVYT
AEKGELFFMVVDEADANDAEVGRVVISLRGIVRESLFQLQLPVYQEALTADAKVVGTLSI
EGIVHGYGLVKEVISPNKKKYFCQRVEALLSHYDPSQLHRVEYLLGEYVGQEERLIKELT
DTLGPETGSAPMRVCIVNINDFAPMCSCFVKVYLDDVLVLRTKDHHAAKSLAFDIEMKNE
TTVSIANPLHSTLRFKVCEHRLFRASRLLGVAEMSLRNMVRDELNLCSLSLFDEGTREEI
GVLAVEVQSPGFVKGTVTMYGKPRNGGKGSAVEEVTRDVTSLMRKYLPQEVPHAQPLISK
ATSLRNAHRELLKRFAPDPIDFTFYVHIDNVNMFRVEDKDAVEKGNISISASFLNEEMRS
YLKVKWEDRIDTCKYFPEMRMDISFLRGSVSTRRVPPLEIVFYEKSAPAAQASSVVSKRN
TIYKSLLLPERELGRILLSLRALLTRRVYRLGEAFTVPILRSASRSVTPGGLGGTVPEVI
MGEITLHITTPAFEHIPHRLRFAPKKMEHYNRGYVRHFEKRIAAFYRLYDPSSLRELHFT
LYERHVASARWPRSLYDWLLMLIKQHGPEPINEFGPPPKLSFDDDSEEEDEEDEEEEEEE
EEEKRSQENGRHATGTITRREEMVNSLPSSRLQSRRHRLIRPNTN*
>TCRU_2050 hypothetical protein, conserved
MRVRLRVTEGGNARCAPCTTEATITWVAPPYDEGKAIFRDHAQVCTISATSGSLLPVVPW
GGDVRVWSRTVSPASTEQALLRASVPDPESIGTGRGTPPKYVDTAAPQKHPSPEEREVAS
GATTATECSCPATPRVRRRRRRR*
>TCRU_2051 Leishmanolysin, putative
MPIRINVSTRDLDDTGKHWISERYYAMNSLNGNCECEGDVVSSAHGIILENEVVPAAVNP
HADRLLVQPLEGPLIVLHLPRAAFAVGLRCVLGIVSSVLPMLTWCCAWQSAVGGGALDDC
RDGCEEPRDRDDIDGMELQDGDGDGRTLDSHWSQRHAKDEWMAPIGSAVYRTELTLVAPA
DLGCMRAEWEMAEPMRW*
>TCRU_2052 RNA-binding protein 38, putative
MPVHPEFIPLAKQKEMFAISSWRDSPQTAAAAQPMVPSPAILPEAQCDKDGASQVKGGHR
SRRGRRGKNRLVQRQQDVDDFFLNCVLPKGVSFATLNSELQCNATMPLRAYDIGTPYALF
TRRNCGALSGGMEPGNTENASGSGATATAATGTKAPMPPGGDHSSSTNNNTNNHNPNTTN
TVTIAAADARIGTSSSEAEAAVVAIASGDGLATTTKKSNHPVVTFSPFRTPMVGASGAAV
LTPADDSDDSPGDAPPPDLVLPPSVPSEILSKGHLISLLYAESGEAEKTSEWLQKKWPQA
TVMVVARNRSILNSSLVLKGLPSLAKTERIIEEVEKFIPQKPSYIRLHRGERGVFKNVVF
VKYPNREVAEESKLRLERFFIGSRQLKVEFKKREKGTAERESEASLQQLVRDLRVSTEHE
GFIYQRSDLTKDELKLLKQLCHSYGLSFDLSEQKVTVKRILPGNDRQSPALRPSQTTPLN
WTQATPGALRPMDFKGIRHWGEMRSKYSSLGIARPKGPHDVPPFASGRGRPL*
>TCRU_2053 protein kinase, putative
MYDYSTLVTILSCTAVFKQGCHPRYNSGPVALKVTAAPPLPLASRRRGEEEGLRVDHEGD
RERATALLCDGTVHPTIHEARVYALVCPHPSIPVFVECIEDAFDTSRFLAKEHHRGVRRL
PVLVTQFVKAASLDRFFYSFPVLRWSIAVQAAHQVANVLQHLHSKGVVYGDLKLPNVLLG
SEGHVWLVDFASAVILHSGVAVSEKRSAVEVEELARGITFHLRAPELFSTTQTPGTEAVL
KHPFMVDFWAFGAFLLELLTGRPCLGTFAECSGKYTREELHARAMEGCSLARQRYGGAKG
PHNADRVWDALGDLLAGLIQHSPEQRLGFRGGWGDVLQHRFFDLVGPDLLEPFPEEYAEE
NDELMLGL*
>TCRU_2054 hypothetical protein, conserved
MRRSSLFWKSKTLAQMFRKLKLAGAHPDVVWAVDAQKAQHNGEEMIRLETMMHRRSSAHS
NSHGPQRIAESFTFWLTKQQEAHHGRRATALRSVTCTINPAAPNNTVKQQLSQLFRDAGI
YEDFDIDGTGVEMSLESVLRHADERQNEHLHQSGVLYIRGDKAVEMLRRFGVLLIVEENG
ITYLVTLPEMHPQPQHQEPLDRSSSTYTPAKSLVDPNGEIDPDVQEYMRERGLRAFDLRM
AGSHSSVERFVSAFERLERMYDVHRGRSMRPCVCIVFSLNSPDNYVAEDGCIVLSVQRMP
AWEEFLLTLPQEVWQNCVQMHRDWRIGNAPKLRARQRQLMKVADMFHFFRLQLDSGIGSR
VDWQEAFILRLMKEEMMIRNTVRKYNLKSELLKKRGEIHVAFTLRSAVDPTKEIGYRIGG
DGRLFFNFSTMTTGQMLRVLKDNLHRLETFQKQHDNAVATLEHLSRSIPVDFSVDTEWKL
REEGNLVNCLQRFVHTIKANQAQLTAFLTMLLKNSTMVGVPKKRMVWIISARFDTMPSGV
VFVPWDVDFESIKKNLLPRG*
>TCRU_2055 hypothetical protein, conserved

MSDGNRRIVPGTQLCYRALYATIVGDQSNDCLPGTTVKMSSDGPILVDHVMRVARRYVGG
NATSKMHKVVAFAGMDSASKAMKAELLSVVEELRRQNQQYQRELETRTQQLELRKQEVQT
LQNKLRVVHSEAKKRGYNFRDLADRGNQRGVEHKKSFDTDRHHGGRDSTPPRSSRIGSGM
GGTGEHTRPPLPPLRVDDALSSTAAPPPSPSLQTFQLKHSHSPPSYSQESRLVAPNGTAN
AAPSLTSPASLDGGSVAENGGGSDMSVGASVSKNALPQLGLEEDVRGNCRDVESGSLDTK
EDTPGNHPPLTRKNGAGAPILPKQLLHENPGAMAFCHRCRLFLAPHPVSVTNHLQSEGHQ
KSAGASPASGTTYTQFGKLVQKMPPFIEPITVVSDEQKRKVTATGNNFFEGGLDIVNSTC
SICQEIITTQSYKVHESLPAHRRRAAEMKADPAV*
>TCRU_2056 WASH complex subunit 7, N-terminal/WASH complex subunit 7/WASH complex subunit 7, C-terminal, putative
MLTSIDFGVDIGKDEWEAFQDKLHFFVSGHEKMLMEIEQTFDCRWDPVLWDPHTDTVSLQ
LGAQAARQGQLTTSIADTLGRSQLHNRLFYRITLCFAGLVLEMDALTEEAFDVLIPPLAM
FGDDSCLEVDITDEEAQRGAGRMLGLLQDLWKWVQRVRRVVQQTVRQLAALYSPLRERDK
YRPFTHVRFLRVWRSLTDIFSALLSVEEVLQTHDTLRHGLSTYRKLLAHVSRNRDKFDCD
DMTMELFCRLLNKIDQELLDDGVLQRLVMQSYEVPEEQVSVTTNNRLCAEFTEVLDHLIC
AVEEKVGTPREGNARRQYIGILGMYYFHLHLFQQAANEVTRRDLCKRVFHLHLQIPVIYI
HGFHLFRPLMWLSRRVPDELNRHLWDPSKEGMSAIKKACEKSGMEFLPQLNQLTTSVSAW
IAEMETTLPVDPSHYKAFLHDTALLVQRGILLAEHIQRLVINYIVLHNCADVAIPLQHVD
CVSHGVELLMMIRAAFHAKTGVIATTYNLLISSITYVMERHLYEMYLLFGDVIQTSSEDV
TDQYSAVRQAIALLHKPQTVENLVCLDLVLSTAFNRCQVKDGSVAMAQKKYEDILIAFSQ
LHRLVFYQRSLRVATDCDFLYWHRETFYPLFFERMYQRPLRSNYLPYLLMAMHDCRTSIL
SSRHVEDAHTLLDAYISYIQKCIQNHLIKTLCIDIENDLRLYTHSVVLGQPFRKVDAAGR
KCDVGCFTRLPPLRFFHEWLHIATEVEHYLDAQFYNLNALMANDWKTYEEMRNLALVRYG
LRICDGYLPGSIVDQGLDVLVITENIQVFVANYTYNMNEQLFVQRPSTTESKHLHTLHIR
HIANSIRTHGTGIMNTTVNYVYKCLLKKLAILSQFLYDDHVKSRLIKDAKFFIAHKEELN
GEYPLSRAENFIREMHKLGVADDGQTFLDKFRHLVSEIGNALGYMRMMRSGGLRAIADAA
VFIPFIDNVVRLERVIDPDAIGSDEEEEEVEMMKEEGMDEEAYKAPPSTVEAVRVVDSVI
HNMRMKLSDGSEYFRMLLEAVTKRLKDADKYEHLRNFHMIIPPICVLHVELMIREKEQLV
KKNKDGIFTDDGFALGCSFLLKLFGLSDLFESLHWFESVGKHYVERLLTMQEGIAERTKE
AQKRKKPQRRDASHEEEEINNMHLTATMVDYAIREYTALEEAFVSSKVFFHSAIPDGEDG
ETEEEEEN*
>TCRU_2057 glycerol uptake protein, putative
MNGSRKRPRNQDHNAKAPAFLQKNSVEYLFSALTLCLAVLYFIVIDIGGISYWNSELLEN
GLAPAWPPFCWLGSKGMDVRDDQWYQFTMVLPIIVPAFGLFLHVSRRLRRIGGGNELWSL
YMLHIIAGLLIGFGVSGPGFVFTVILLFGNFYGLNMLHNRAPFKVFMAIMWGTHVAVLFL
NSYFGGYKFAWIGLQFLDKLKTPILPWTVHYNMSVLRMIAFNTDLHQAIVESSERRAKVI
KKHDATCIECAQVREAHAQKGGGSIPFGLEVGGLRCYKFRTEYPLDVREYNLLSYLGYIF
YPPLYIAGPISSFNAYVSYLKEPSRAINEKGLQRYGLRTLFSFLVVATTAHYIYLTSIIM
TPSLFSTISFPRKAILFYLQLGFLWLKFNCVWKFFRFLALLDGFDVPEDMRRCFSNTVSI
QEFWRDWHASFNLWIVRYMYIPMGGNRMKHFNIFPIFFFIAIWHDIELRLIHWAGIICIF
FLVELLFTHVLFCQGAPLTLMLARRPLLWRHLRTLGACAMMLQLAIVNLVGFSIGLGGAK
QNLREMWMESPLSFRLLMLFYFYLAASIAIQARDQEKFEEQQRRIKYGLVSARDGTSVLV
SAVAVDGSG*
>TCRU_2058 hypothetical protein, conserved
MSSAQVEELERRASAAEVAIEELKKSMQARPQSGAENNAALELRLRELLKLMEEDRLECE
VIRVQRDELKEENERLRAQVMKHEYRIKHLLQTINEIESGKQQN*
>TCRU_2059 60S acidic ribosomal protein, putative
MPKSKRAKIVPLTKTRAKTREDKDKLINRIRKALDDYTDVYSFTLSNVRTNILQQIREER
KGDSCLFLGNNKLIMIALGRDEESSQRPNLHKLCKFLVGSCGLLFTNLPKKEVKSYFASV
GAQVYARTGQTATSSLVLRAGPLPQFTHSMFDHLSKLGLPLKLDKGVIVLLQDTTVCEAN
DTLSAEAAQLLKLFGIQSAEFRIDLTAHWANGAASRIVGRNEENVTGKA*
>TCRU_2060 hypothetical protein, conserved
MVACIIPFVALIFACVAAAGGVFYCAVFLLLLSLCVDGELVCAEVYTQVTGVMAMMMTGR
VLLVCALCVLWCSAYCRCTEEESVSLSRSGIGDSRTGSGVSGENGVKTDKTKTMKTASEG

DSHPSERDVSDGGSFDQAPPDKSMCKEKNDGSTVKPLTTDGEVLLDSQETIATHLKGTDT
ELADPNINQNHKNPKAIDGIDTQLPGAPAAPKAQPSPSTVPTANKTVSSKEELTAEETPE
HSRATRNPNEDSETKNTTDQALKPDAGGIDTLASEDASSPSIDDAATSEAAANTARVGSP
TASLNNTDGKNEGLGDGESPTPSPSAAEPETITTA*
>TCRU_2061 zinc finger protein family member, putative
MQLLAPLIEAKEGYTYDADGTLCMVVVDPATRKLLIPCNFIYATRAQHRATIPSLCQLFL
HGRCRQGTQCHQVHASLDAVVALRSRVGKLPCCCVFHGDEDIADVLNERSWLSKVVLYVP
EVSFEGGYVPLSRVGYTVPISKILNEVSYEIAHSLESYTEAIREGRVPHEESPVVVLEAG
DIPICRLHIRERCRFAEECSFLHLCKDVAGGDPELPLGRRSRLKATPSEPDCVVSESHDS
NMPHKAFLSPAAGISAGTNACPISVRGFPLVQRGGASVYRSSTNKLCVNGENSLWVRHMH
GSGSIDQELDSSTVEVSTVPTPVPKLRSLGCSDIRPLKRRSVVRKKLSSRVIVSCESLLH
CEGDPEAAEEGTPELRNGGFTEGCRKAFSVRGTMSNSMAASSRDEGTSTSSMSLSTSHRC
CAGGKWRHDPYNLSRSQMGC*
>TCRU_2062 C2H2 type zinc-finger (2 copies), putative
MPDITALRASCKAILLRHQRGLSLELPCIVCRQRVRGQESIMQHYVDAHGIHTTNCDNIV
DLNGFLVHLRELLLFRDDERMHCPVCREDCGDEASLLEHIEKEGHSRWDIDTIPSLASFC
MADVNKSEEAGEEEEDSANGTNVVESDDDGDDEDWGVEPAVCLLCDTASEDCLGHMIDAH
GFDFRAAVRSHEGVQDVYDVIRIVNVIRKCVARGLCPFTYGDELAEAEACRCDVAASSLE
EHLRNHPLHNLPRVVPSSDRELIPVLCADAFISSVVVGGDLLARGEEDPEYPMVPTNAEM
AKKQTARRQSEGNA*
>TCRU_2063 hypothetical protein, conserved
MDDTLIVKLLRLVRNGRSPLKGCETFTFGDLHMLDRGPCIADEETLQAHQAKKGLASQVA
LVVYVKGAIAEIWRFQDFRVPGVVSPNSKMPSAIAASQGLAITEQQGNSLKILIRVIFAY
LRIHELFVDITYVDAGDIVLRLVVDMDELPRLETDSCVKKVWAVDGLVSVSVTYNRLWRA
SLKQEGDLILVSNTATNVKGECPAEQRVGSVLAHCSDSVGSGRSFPTPHFAPAPLPSSVG
SSFLLQKWPKSPTLGMSEFSLPLASTSMTDNNYSYYKTPSQGAVAVAVAACGTRTPAVRG
FTFASVPTFAAHVNDSASEGESDGTSNQEQLHELLEICEVSLQEATTGVQEVLDILEKPL
LP*
>TCRU_2064 cyclosome subunit 1, putative
MQSAFTIRVGEKQAGGVRDVSVLHNGEVHFSVSHRSVKWAFLTRFPAPSRRKRSLDPAFV
LPESTCANSELELNLDSTGGERTGAAAHCGSEAVQEEYLCVFHRDEPKNRHSHYTAHQSS
TICSAYNTVHPAAVTHFVLKNIAPTTVVPGLRGVFVHGSQQSSRGSSSRALQVEGFLFHQ
AADLWWMASQLTFRPVYVSAGGSELITRLPSNPIVTMMSVSSQVDSGSATPGYALVDAII
LTQFQTYKGRLMTVAVRGSEICLATTVLVEHLDSLLWVWWPQRLHVPQLHVKATDVSVTI
SESPDAPVQALFLFDAPHTLLHVLRTPNLLTGKGALELLFTISTNCPPVVLPSLRPCMMQ
PIMVCHYPSMNEVTLYHVPTILEHPSSSNSVATISLATTLPKDFIVNGVLYQTGSAVAFH
ATPRSSGNESERGEKHAHELKQKTCVVSFPSLLEEQHPLVHFILEALELVLEANCVASLQ
CELLRRAWESKHLGNVWDFGIGCIELIIEVVRTSMIGRSRRSNILENNNNNTGAGGCNEN
DGRYFLKNALGHEEREEVRLCDVLLDPIALNADLLQRHSLCSPCAPEKNGREAFQYGPNV
IQLWTQHQCGLSVFVLHLLCESLKLQERHWVLLEPLAHMNLELSKLMRWTQYVWYYSTCL
CVPETSGFANRSSVVSQPSPAHEFQRTLPEHILLERFVFYAGSSSDAVLSGAPPILYTIF
QRALAGKARMSGGWPAIKGVLSTSPLSMANRLFFMLVDCFDTPQAQHNHASRWWFLLCRG
LLKYGIDPKFVSLELCVGVAQPIERALAIAKDQVDDTWDNDFNAIIGRLDRLQQHAPTLL
RYADSSGDVVRAAQERSIGRQYCATLNDDDGVIMRPDFPKHWGDPRMDIVQTMLNTAAPI
ALPSQLDGADAIYASLKTLSRRATALPVGRGIFTLCTQNFRLRDSVPIPRLNLEGRTSDG
ITITNSSDEFSSENLIWPLFHNGCAAGLRFLPLPQGHGHVKEEQSITRHWVLYQTRNITC
LASRSGLLLAAGLLGHLKLLQRTDIYSLLVSPQSEFSGRETVTIAVMLGLSCSLRGTCNS
IVFNCLSMHVQSLTPATEDIEVSLDAQTAALVSIGILHQRCPDAFLAEMLLVQISRLPSD
EHFRDREGYALGAGFSLGLIFLGIGSSHGVPNVENRLLKFMEGARRETVPSTCEGLEVFN
ERNPDSGHFLTRALLLRNTKDSFRSHCTRVYEGDCFNTAVSSPAAVVALGFIYMQTDDAS
MAKKVSPPNRLVGLQGIYPELCLLRCMMSSLILWSSIEPTCEWVRQSIPSCLMRLVKSPR
QSGLAPAQVSYLMMNLGHCLAGVILALGMRYAGSMDADAKALVLGELKGFMRGRIGTTGA
AIITIQRSTGAFQPCLSACTVALALIMAGTGDAQCLSVMQKLYKRTNVKYGDHLALSMSI
GLLFLGGGQLTLSNSLSSVAALVMAFYPVWPDTTSDNKMHLQALRQLYCLAVVPRVIETV

DVLTNRSVSVPIRVIVHRGRLGQTEPTSVVKELWTPLPKGKEDQAVRMVTPCLLPDKSTV
TQIEIRSAQHYNLTIYNTGSNVIDDRGLVVRVLEKNVVHTDSETFLRSPSEELVVHWIKR
LFHGEPQQRPRPIEATVILDNVNLLFAAQESFLSEIGSTENDFSPDFVMNARRTLAKRYG
GLLQHCGAMSSCHPLAQIIMMRKSLYSAAVSLLQSLRDGAECSCDLAPVLESLRFYNTAT
EAETEGGNGGAGLVTSVVMKWLSQALHFYGLVSSMGSLSQVLADHASFLQRREQRFLALH
SINQQLLLHPRVLEDLVECCVEYVE*
>TCRU_2065 intraflagellar transport protein 20
MEDDKLVMFDAHGAIRMYDPEKFDQLMKTIEVEKRFTGRMDDFRNVVNQTMSIVERLGEA
IEQEKLRAIGSRNIVESEAEERFRTVQEAKVRLREKQTELDRYIAEYDSLCKVEQEQKLI
IQRLSQSARD*
>TCRU_2066 GPI alpha-mannosyltransferase I
MPCHSDRSWIDGVNIRRLLQLGGIVRLILIIYAHFHDRWFRVKYTDIDYMIILDGAREMW
MGGSPFDRTTFRYTPLLAVLMLPSVLVANPFGKLLFALCDLGAAYYSYIVLLKFATERSA
KWMVSLFILFNPIMVVVSTRGNSDILVTFMSLVVLAKFAQSKYFQAASVLGFAIHFKLYP
VIYSLPLVLGVWEETKAETFFQKLKRAVPTVTLCGLLVVIFFTIPTMMCYKWFGQQYLDE
AFLYHLYREDNRHNFSPYWLLMYLNMARSHLGLESEYAPGLFAFVPQAFVLSFVSYKLRR
NVAHACCIQTMLFVAFNKVCTVQYFVWFIPFMAFLFFHPRGAEGDGKRPGLLKAVAAIVL
WAATIPLWMTTAVPLEFYGRSDFARLWVVSCIFFLATVSLSSWFARIAYRLQEAVALQHK
AKGEKTTKVA*
>TCRU_2067 calpain-like cysteine peptidase, putative
MTTYFAGLSLREIYEKKCVELHCRKNSAICQLLSDVPDEYQSLVFIDLSKNFLGPKGILP
LLEIVRCCRNIRVFDLRAQQLDNVAIDALCLALRQHPSILRINLSDNPLTMNAGVSLLQL
VRENPVIEFMTLERTGIGNSIVQAIKCQLERNRRVKEMVAERELGLLASPGSRDVNSSTN
EEKSGRERITPAKIFRAAAAAAAANGGLNELPPDLAFLAPMYEDSFERKRLKAHDIEAAL
LSFSHSVHEFLYDDNPVSVIDQLCEQQYAWFYDHQFAADDVAVQHRATAMYRIAGWRRIG
DIYPSARLFPDKDEESRLVLPSQSPPSFSWIFVCVDAVFNDLESLRSTVLGSNSLGHGVY
GLRVHIDGAWRYIIVDDLLPVNNKDELIFTHPVNDKYFWPCILEKALAKLNGGYPALSLS
APDYPRSRLSSRTERINRFSITTRGHSVYSFDGTSFFTSSNYQGNNERQTNCAKTLSDLS
GGVGIVRFLHHEQFQLDEWWLTMSDVHSAGAMMVAVSRSANGTLPGIEPSHAYRILQLQQ
LSGARLIELSSFWTKMQWKGDWSDESVQWQRYREVDAALRNQRSVAKNSSFWMSYTDFIA
AFAQVHLCHLFQGFHQRTIEDEWGRNSAGGSCHEQNWHLNPHYRLKISQESPFFINLAVP
DTRFTPTDIDSLALHIIRHEQYPVRYASDREEIVVATDYVFTDSISFEGIMEAGEDYWVI
PSSHTGGVMGKFLFRIFSQSGFIIWKEDPSYHWNTLTYSDTVECSGEYRTGDDNAQVALC
FGSHATVGNMENKTGSLIVKAQAPDSDETALGMFLVKTTLVEGRPSRSVGVLRDESVVAS
SPFITDEIVYLEAKVHPGERYTLVVCVHPVGSQAKLKFTIWSSLPLPQLTPLPVWKKKSV
IVSWPQGSGSYYDVTRNPQVEIYPARILDTFVIRMQVKDCSYTDPSIVFFVLANDGRQGE
GIKGQIPADRVMVRSQYVRHHVVQCELLMTESMDSLLVVPCLQPAGSFGECTISVATESA
EFMIRALSTG*
>TCRU_2068 ferric reductase transmembrane protein, putative
MEQPHLLPAVPALEQDHFLNEAQGGSGATFCMEWLCRSVWTRRFVSISSIFLFVFVVARA
RTTFWTDVFVYHPILMAIAFVAIIPELLGSIFIIQGYARDPRMRCGLMQAHRRYALILKI
ISAFGIIAVEWSKFRRSKAHFVTWHARIGGVCELSQVLETLLGLTIYYRLLDHRITTSQR
AKMRLAHRYLGAIVVVTGLISMSLGMLSHFALRVFEVTFLWLFFAILPVVLAVWAYYGVS
*
>TCRU_2069 hypothetical protein, conserved
MGKLGAGLDVNERRRPVGSLFMEAMDRDSIRPRVRRTLHHSLAERSLPNTPFSPRPDEPG
RTRAFSAGGRRHFPDRSCGNPIVPGPPEVHSARRAVPKQMASHLDSAAQAIYEEKPILYA
RQRCKQPPFDEKSPAVVPRPHALNTSPLKRSHLSLGSLAPKDEPPKERAVPPPMIKKPIR
FGRRHTPAPRSKSAEHRRVGIKMVHPLPHWESVTEKHAAFTSYGIDAYAKKDIHHRNQSN
WEIGFIPPAPFRRSVSTENRKNNAATPLNMNPWRGRRYSCSPRQRDYDIISWTPRRALRM
DEETGIEEGERNMER*
>TCRU_2070 Domain of unknown function (DUF814), putative
MVFYFTLASDPSVFCYMGRDKYENEELIKYGWPEDIWFHVDNHSSAHVYVRMPKGKGMDD
LTPEMIEECCQLTKANSIEGCKLNHVRVVYTPWSNLLKTKGMDAGQVGFHVESQRRYHTV

EKKNNALLNKLEKTKITKENVDFKALREERDAEERRAERKALLEKQQREKEEMEARKRAA
DLKSYVSLMDETKMHTNQEGVPDEDDFM*
>TCRU_2071 hypothetical protein, conserved
MTSPRLVLRLACVRRSLLAPTFPHCQSRASTAFSSDAALCRQTAKVLYSLERFHRQNSSQ
NERRKVERQAWRELQKLPDAVADSASIHDVTDIVAAWCYFSRFWALGMHGPEETADEKQK
GGLLERNYIDVPLVERRAPKARSPTVDEAPPPRANPLDEVIEF*
>TCRU_2072 kinetoplastid kinetochore protein 16
MEREIDRLLRMIDELAAGVEIWKQKALSSMDFIDKEQKALGSMVQQLSIRTAARKEEMMK
RQRQRLEELRSACMERFKEVELRF*
>TCRU_2073 ribokinase, putative
MNRLHVLESHEGSNGPTVVVVGSCFLDYIAYVDRIPRIGETLTSKSFSKGFGGKGANQAV
AAGRLGARVAMVGIVGSDGDGDEYIANFKRNGVDTTNVYRERNGATGLAMIFVDTKTSNN
EIVICPNATHALTTEFLRRQSDNYNRFLSQSCRFLICQNEIPLETTLDVLREAHKRGIYT
VFNSAPAPSSAEVGVIKPFLPYVSLFCPNEVEAAMITGMEVSDGASAAKAAKALQALGVR
NVVITLGAQGYVICEMGSEPIHAPGLRVKAVDTTGAGDSFVGSMVYYMSKGMSLSEACRR
ANVCAAFSVQRKGTQSSYPTPDELPADARA*
>TCRU_2074 kinetoplastid kinetochore protein 7
MTEVCGEETLVPSYPVSPRPRRQPMASLSTNQRSYSRMSSKGIFGDESPLLLSPLPKYPN
RRRSVTFADETEATVREERPYYTACETGNTPGKHPSESPFRRPIIKTTSRTNNATDAVVA
VNMNRRNDTTSHAPVAPATSPTIKRGRSSSRQRRAARRHQAELYHGFYDDSFVEDYVLKA
KKEIEGEEEEKIVEENLKQQEKELAEAEMRAAQATVKISALQQAKEYLLATANARCFSPA
CSSSERRDSGFASSRSCHHSLKKEPSLIQQADGEVEGVGDIEQRRRHLPQKPVKHSMPLV
TQMDDMDEKGSGKRIRQASLKKGGHSLPIRHDGQIHTEDDDDENEDNNMSKRKKAKLERI
IARVIEQQAKRRHGKRSVVVIDWDCDGCGELLASDADVEEEETDNDDEEAAMTRAAARSC
KEPMSKKPSNAASASATAASAASTASRQKKQSNTRHVSVRAPSRKRGANSASVAPDLGAD
SLLLEEDQPVLLRRPATRRRAPTRSISYMSPEAEDDSVPDHAVDVSRKPPRRTPAPKATG
RGRKAPAPTTGTALSPHRFPSLVPSSLAVAHVSQSFTSARHNSHANVEPLDDPPLPPVNS
RRRCRTTSAASRPPTTVTSSDDPMAVFFSASFPSPSKFEEMMLAAGGLQETRKVGRGHPR
QPALLLPDSILRRR*
>TCRU_2075 hypothetical protein, conserved
MSALQPLALLVPKQIQSLVVDGGAEIVVERRPDEKRCLFLRFFDEAEREEAVRGKSTCAH
IHEQVLEDLKWARSTLWNDRRLQQYFYSRDWMTWPSLPELSSMVELVRSAKETDEVPDFS
GSNALKKALGIIYMEVTYPGLHALKEENLAGTLLAFGTTRRDNRIVGDTMHALLGRGDEQ
RIGSSLWVLDLKTPSFTPDEAILLSLTARVREKCLRVMQPELGVADCGGSWSAVLAAHRR
GIEELGPRLFCGISEGLLQFAMAPVYLAKAMCEAAERGLRVRLRVGIYLTVLQRTEVFVM
TRGSCQSAATDDKLEVKAAFVERTGRSYDACAAAGLFLYLLEGETLEVAIRLRFLGPLAG
KFDIMETMPLTATTQITPVLVRHNPFAIVHGPRVVGTFPENCEVRKALSELLLSRDSSVL
PATPEPSQQSMAMKTNYTSATLTGEQLRRGVDDAIFRTLSQGPMTRAALSAHDNMARFRG
LANFEAILKDSLKRNAVHQGKKYYLRE*
>TCRU_2076 ribosome production factor 1, putative
MGKGARSKRGPRGPAKKQHAPRHRAAEVDPALVELYRSTRQPVKKSQLFEQLREQKKDAK
RVRREARERERKQLKENAPAKAIPKTKERLRRPDVTIVEEKDDAEIVRDEADDEFAAYYN
EARKPSILITTGEHPCFRTKQFVKEALWLFPNSTYRPRKDYTLKEITQFCINREFTDLVV
ITDRLKEPYNLIISHLPEGPTATFRLSNFMAHAQLKDPAPRTEHYPELIFKNFDTRLGRR
IHRMLECLFPATRDYAGRAVATFHNQRDYIFMRTHRYIFDSLEAVRIQEMGPRFTMRLLS
LQLGTFDTQFGEYEWFRKKEHDSDKLEWYI*
>TCRU_2077 Vasohibin, putative
MKSLATIRAIVEELAPKNPYTGLKDLPEIPRPEESSIPRELPSLQQIPYVQNVLNMLSYN
FLPQTFFCLEKHRSLDSIMLTSKEILAEALPIRCLEATFVGLYLTHGMKGVDRIPLSFKS
RARGKSFHHIVLVIRCDSLYGALGLSRRSTLMDKPMIYKNLFELIMEYKEQYEAIGHQLV
DFKLGLCASHESHSRKAPCWRYIAVSFAKWNSPLHLTSPHPSDELPTSENSKVSSEDGCA
EEPSVLANVSNLLDRYSELLTIISAQYEKCTTPFLHGSTRESHPICLRDLHEMEETTARQ
ENMRRLEAICNGRLPCLVFDVGTKKRAASRSTSKKRIETSRKTATVTRTSATKCTAAATK
KYSKKDIPADGQKETQHKQSQMEQEQELQQLPLVMEHTSSLFSSLALSGRLNNSTSVTQR

SERSGLSPSKRHSLPFLENKGNEFGSLVSQNGDSWRIPFLPFDVNGVNFNDLL*
>TCRU_2078 glycosomal transporter (GAT3), putative
MGVPVLNSLRDGGLVVSGTLAFLICLVAQRAKLHRYDAAILDIRTPDDTRVTRSFFGDFL
YVAKLALPTVWCKEFAGMTVFIILFLVKSILHVAQSNANGQILKAIASDTPENRVQNFFR
VLLLRAAVSMMAAVCSGSIEHLRPFLIACYRERLSRYLQRRFYSHLLYYQATVLDGRLET
ADTVIATYCGEFAEHLAELPYYFLLPMFGYMTSMVVLTRNVGAKAAGLACAAVAISVLIL
QKISPAFGRIHASLLAREDDYRRMLTNSLNNVEYIAMHNGGSYTRQKLERQLGKLKRALD
HFALAKGHFDFLEISFSALLQAISSLVIFRGAHQMKTKSMNDIYVEIQCMQDLIENVKSF
VVNFREVSHLSTFTVKLAEFDSTLTSIAEGCFIRSSGASPKSDCNSDFPVSYTHVNYIVR
PKWKKDFTLFAFSNLKLMTPAGQLLFNDLDLEIKSDQDWVILGENGCGKTSLLRMISGLW
RPTEGSYSMERGIKLLFAPQHSYMVPQCTLVEQVLFPIVSSKLGAKELDSFKEAIRLSGS
HSVIDVLGGFDSPYVGADPRTADDTYDWDSLSGGQKQRITMARVFYNILTMDRSEQTPVV
LLDESTSMMDETEQAVLLNLRKLQVRMISVTHREEVITHHTHALRILPGGNWTATPVTTR
VNID*
>TCRU_2079 hypothetical protein, conserved
MDVHSRCWLHVEHSASFSFDAENPIKVESIHVRLTLKTGNEEGIMPRGGGEAKTSEMKCV
LWAKCVPTITVADKLFCDQPPFIVASFLLGPEGVATATSLSWEIGENVSVSICLTGLTET
PEFLSTPSEEPLLCPTNMNNTMEPIKEANKSSHLELESIYNVTLTFAGVKANWGFQQSIW
QPLLCFRWFELQGHIREATVPSLPLEKRGKRLNDTRAKKRRMITGDIKEASAVSSCGNYV
LWRDGTLGLRQELVPYHRVYTPANAEKRVRVRRFPHRFADIVGEIPFGSSVEAIGRQVDG
YTNETYVLVILLGAPDAATVAETYNLQCIEPNKWIWGWSKISSRNGLLLLVEVTDTARSS
LPDYGHVERLGEPTYYTSVREERSVRIRSGPSLSTDVVKHLEPNEVKVAVAIHHFTSIND
DSSVRLLQQFVEWEEGGFSLLRNNDRVYLVPVHLQQQPRHFPVCPRPAPNSPEIIPLQRK
RCRTVSPANNRKRPDTGTTPPPDLWSPADIPETLAAGLKKGSVRLEELPKINLNGSPTHS
SASSNS*
>TCRU_2080 protein associated with differentiation 3, putative
MALPVSCLERRETQREEDDCGGTERPSAGDEVANEPAAAGGPPKKVETDVDYIAPQYQTT
FLQNLKTLKLWAFLCSFFCIAGSGFVIIYNASFLYAALADEEVDNAIKTLLTVLNGVGSA
AGRLLMSYFEVWSQKRKAEDRVSIIVSVYFADVFVILSLVLFLVVPRAALPLPYVLCAIG
NGFSAASLVLVSRTVFAKDPAKHYNFIFLALVCSTIFLNRLLYGEWYTREARRRGVDVCL
DCACVQLPLLVMLGFNVTAFISNAYVHWEYVKFNRQVLDERRRLFEEQQEGGGLWA*
>TCRU_2081 Bardet-Biedl syndrome 4 protein, putative
MEGGVTSSASHARGDLVSGDDDAGSHVQNAEALNRDVTRKASSSPAPTNSTATAAAAAGT
FSVAKSLLDIRERRNWLIHQFYVRQEYADCLNVIETQLQESGGVCEYALYVKGLLKRRTG
ELTESFNLFQAAMLINPQNPANRRQVAQALFFLGRHRAAIDMFHDVERLCEANGMGNDWV
IQYGIGICYMYLKDYQKAEAAFVNSITIQNHDCTVMQLGKVLVLQQDYTRAISLYEKYLL
KFPDNADLLTALGLLCLKVENPPQAFHYFGKCLTLNSSNPTAIMAAASIMQDNGDFSVAL
NKYRVAVSKLPHSARLWSNIGMCFFAQQNMHAAVACLRRAAALGPFEWRIAYNMGLVFLH
LKQYASAFHHISASTYLHGNYAPAFMHLGVCLALMNDVDNACAAYTRALSIEPDPLILLN
YCITLLNCGQEEKAREQLAKFMQVWHEKSETQQQAFGPTFLRMVRLLTERLCGRSEDANS
SSRLPTE*
>TCRU_2082 hypothetical protein, conserved
MRVHPGLEMDAVSLIREEIVRLREETERSSCLSDESLFRDARSSLLGLLNKEYGGSYFKF
VVGFMLVPFFVLLTVILLYLSAKMLTEWIALRRISGRMSCHPLIREEMHARELSQASRRS
ARRRTAFVVTLKCVIASSVLFLFVGSRVMMEVLTRGWIKGLLVPLSTDGSFAATEDDFDP
WLELYSGLAMLLSVDWFRDIQGLLTFSLLGSSLMVVGLRLLRSASEDVVSMRTDCISSLK
LLQKIDDKQKERGQEIMRRQMATLISMLAEQAASIPEVPRNGNVVPPLSVVENGENSSGE
EEANGSSAENNREE*
>TCRU_2083 Mitochondrial ribosomal protein S18, putative
MNRMGGSVYANAMAQFAICRQPWNEYINLLTKQDSTPYHVEPQEKPAYRGRKRGREGWLF
GQQVQLHYHRFPDEQLLTNLTRWRTGETVGDIALQQFRNAQPFDIEDKDPQGMQRPSPEV
YMKLNYKNPATISRFLTRTGHMYPADILPLNPEAVAKLRVAKAQAVRIGLYPRFGNPFWF
RSQKFRPKAYQENYDPTTYSTKHTMEHFAYNWVQTDRIRRYFKELEELQKNASNGARGGS
ATTAEQKQQNQFYAPENQPISMHRNNISYMAEVERSMKNPTVPGLMSTKGMKKKFHNLYS

STSTKRMGFSNPTLGIKKV*
>TCRU_2084 Glucokinase, putative
MNIKEFSLHELCEELKTPAWNVPLTFVGDVGGTSARMGFVREGKNDSVHACVTRYSMKRK
DITELIEFFNEIIELMPASVIKRVKAGVINVPGPVTGGAVGGPFNNLKGIARLSDYPKAL
FPPGRSAILNDLEAGGFGVLAVSDAHVFSEYFGVMWEGTQWRTCEQEPAGSVIGRGRCLV
LAPGTGLGSSLIYYNPMNQQHIVVPLELGSQTIPMRKDIDYIQTLHAELKLLPNYENMVS
GAGLEFHYRQVVRGSRPPCSAGEIAKLASEGDANACKAMKKYHEYLMRVGSEASMALLPL
TIVLVGDNIVNNAFFYRNPQNLKEMHREALNHEMERFGFQSRVTYLRQKKLLNLNLMGCY
RCGLDLSVGKKQKAQL*
>TCRU_2085 hypothetical protein, conserved
MRAHAGRAQPGVIIVCEGLPCGCHNGATVFLTGASRAGRHRSCQACRQTRHAGSTNAGTR
DGPGSSATASSRTPRAADPRRTTGDSASSTAGMPSSLGTGTATVCGTAPARTTVRLRQNT
RHFLRTALALLTDHKEPSVSVVPSLPDCGDRPASAPAGTSSRREHRNSLSTSERRIDVLL
PNLRQSALVRPQYEGTCRTCSAWRYNSLRGPPMRMPQWLDRLPNRRLARRSPPKLPSMPA
GKTRRRHKRGHSRWTRLFRHRLITDATGC*
>TCRU_2086 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSVCAAGSEDKAEKAGQGATLQDSWGSSGSDNPGAKVTEDDE
HSSDNKPIPSEGPSNTASAPPTPTSAGTEEGPSGLPTSQDGGGASGQPGGSEENNLSPGS
TGDSDKSAVKNPEHNKEVALAGKDVKEQAPTTTTTRAPSRLREIDGSLSSSAWVCAPLLL
AVSALSYTTVG*
>TCRU_2087 hypothetical protein, conserved
MHEKLKDEEEEEDKDEGEEEVDDGKEEDGGEEKKKQEEKDDTGTTKRISSGGQEEPISPS
RVEEASNKTKPKSTQKTGDKDPAADGSGTQEEKQKENKDANPKETPAEATAMKTTTATTG
DSDSTTAVSHTTSPLLLLLFVACAAAAVVAA*
>TCRU_family, putative Se.1
MEHGVTLLEDPMTPRQPIMSSPAPYFFAVEDASVSRVVEDWMAKVLHRDVHIFALGCTPH
RRLQQLPRARIAPMAMRSKDIMLDFAAPEVLVFHLSMQNGFFQLLSPLSPPN*
>TCRU_2089 syntaxin binding protein 1, putative
MEEPLAALKKLHEYHPGLVQGVEPKAKLAELGSSVRAPPEFRERQARLSLHIDICARLVA
QYREKRLAEVCEVEKDIVVGHQPFRKNLNGVRHLTRDAAMPRPVRLCLFLLLVAASSTDE
LTEAKKQQLIRDGGLTPDAHLFANLEHLTRRAGSVQRYSTASAQSGRSTSASAGNAATDE
DTFLKHACMMMETADRNRTLRIGLSLASMERHHAMGANGASGGQNSGAAGKTAGIFQGCG
GNVENHPDLGGGGGTIALTTPQRIVLLVLCGVACSERRSVHEISKRYGREVVIGEPRCRV
LRCVCAGNWHPTAL*
>TCRU_2090 kinetoplastid-specific dual specificity phosphatase,
putative
MGNVACTDAVPFTLEDIQLSRQAAPARLMELLPEAVIEKFTRYQHNLKAFMFRQGAATGD
AVKRMDSSQVYLQPLDLAQAKIKLTESAVYVLLHVQCKPPAAIDSNYHATVGTRGGDRPH
RESDGTQCSNEETLLWARVLTDMFTPRGRATAFATNIDKPSFSALPSTGLENAGVGAGGN
SYGFTASSGMGGLDFRFSVHILTGNKADQLVASVALLHALRIEQSLMESDEVVRRLFFNY
KPSQGMSDAKLASLSCMPIGEIVGDRSFSHRSPRIMEECPKNAIFRILHNIRCKTSFSTI
LPTPFSARGNLSRDSTPRGMLNTTTTNNSSSIYQQATMQSRAGVASPSSAQGPPVLEIPR
LRFAAEAARQRAVDMPLNAPRQSTAQTPRLTQLEGASSVSNATSTRTTTATVGSTLLPVI
ANLHLNETLNRRCATELSLENDEIRMTEERVKKLRAAAPEATEVLPWLFVGGEEAAGDRI
QLLAKGITNVVNTVAFSMGNVHSDIFRYLGLYLSDSPDEPIFSLFPVVIRFVEEARLKGG
KTFIHCHQGVSRSCSFVIAYVMWHQGICYDRAFEFVRSKRQVCSPNTGFYVNLLLWENQL
STPVFNKIYAYVPYMEYLFPFSFRLALTFRGSQRSQDDDSQIVNPFVHVVHGTDESYTVD
PRLSYGILLGDRGSRSEDRVMPIKSYFFAGSDCDAIVWQEARVDWDAFIKYSFYQGQKKR
STNSKGEVITFTPMPPVEQPTQCLWELRDLGRVINEGVFSQTCRASGGTRYPNVVQGQVQ
CWNKLLARDDLVFRLSTYLAEEQRVNLTSQSRKRMREEERRRLSKLVSSASTPRLSSYKG
GSGRNNAGTSSVVVNAANSTNTTNNAPLTAHTSFSIAAPSSRVAAANTAAMDLLPLVQPL
PTPPLVTPATTTTKSAAASAKTSLPRKTKSSIPSTARSNSLGGEVEIYAYPFTGPPLTDI
LDVADMEPDGCYAVVVPATAAAATTSWRHRVFLWLGRTCSVGEAEAWQTYRRSLKIDKDV
RLWNKTLLQSPLEEVAHDGEEPDDLILALE*

>TCRU_2091 hypothetical protein, conserved
MNADDGGAIESATSHQSAQAAHRAADAPPDLSNCPTQSSGRAKELICQRRSNVVRRITDI
PALGQLYEESERGRSRDVGAVNVGAWNAPSGAIHNLLPHARTADERGELCGLFDGNIRCG
AIDPTAVRQDAAVHVGNGSNPAGHDDSGVTKTCGVIRGEAGAPLDKGRDESSNPRPDRLE
GTCCRTTRVDNSESLVRNCGLDTQQS*
>TCRU_2092 hypothetical protein, conserved
MLVHGPVSKAWQGSTLIGHIADLRAPQIPNFEKQALLPAMGAARELGHQQGLITAERERL
NIDYANGVADVQNRNARLNSQFQEAHYNLLVRESTIAGAGNQVLELQQQLEAGRAQLRER
EFNLGVLNAQLPEREARLNAQQPVRDAETAGRDEPPATQHVANDGVTTLPHQTDILMAGG
VPSSAARRSSAAYRRPHGNAGRPHFHPSTPLPSRTSPLDAQLPMEEGRSFCAFDVTR*
>TCRU_2093 Concanavalin A-like lectin/glucanases superfamily, putative
MLKGAGAGAQWPVDMNGPTVPHHFANREFTLAAAVSIHEVPESGNVPLVGVGMSDPNSTV
LIGLSYTHERNWSFMTPSDANPDEPALFDWKQNTTYQVTFEMNTDGCYVFVDGRGLYMKK
ADEESFATLLEKHRISYLFIGWGSARGTESSRMTVTNVILYNHTVYGEGLEQLNASTVPI
PQSGVAKQQRKHEGDPSCGDSTVHLSVSPVLLLPALVLQLWGMTALC*
>TCRU_2094 BNR repeat-like domain containing protein, putative
MSSCGDGQHQLCVSDGHGTSWYPNRVSINRVWGNSHDRKGYGVQSGSTTAVIVGEKVMLA
ALPAYSKDNEKGRLHLWVTSSVRVHGVGPISREGDDAAASSLLVKGNNDELLSLYENKEK
SEDGSDGHFAVRVAAWLERVKDVAKKWTDLESALQ*
>TCRU_2095 hypothetical protein, conserved
MDGQMNPQQSSGTRHSPSLQQSAAKAAGNFSEGLDMFDIQLQNDCANVPGSFMGGLGGNA
ATVGLSPSPPVTLSAAMFSSIATATHGLASTMSNPQTARRMVQEVAQVILRFISTPDEPQ
PENLTDEYGRQLILQFADELQRSAAALTTGMTSGGGDGRLTIDKEVVLSLKNGREGLPPP
GADVARPHHPYTGYFSTMNSASPRLTTQPLWRGTPPNFSNGLHSSNSASGNTNAATTATI
INNNCNARGSHGATESFSPAGVGTTVHPQANLTAPSLSKRVGGGDVFRPRPQHPKSGSRT
LMAHRRVVTSTKKVLRSASSAFSECSAGETGEVSSSMSRTTVGTSALAK*
>TCRU_2096 RNA-binding protein, putative
MAMRRAVLLCSPLSPPFSSSPSSSSSSSAAAFFNGRSATVEEQKQTSDGGRDVDLALRLQ
DQLAKISEKVAHDNDVIRQQATAFAMLQRQQVVLERRVVAVEEETVQMQQKIAETTRVAS
DVVLQHRNVEALVRQMEKLVLSHASSPKNTKSSSGIASQAEEAKSNALGVSTNPKLMTTP
SYTSPSFPSSASSMGNSAVAGMGAQISALSTRLEALQARIEQLTLEKLVLNNVQLHAQKL
QKDQQQQQSLVEEAVSRVAAAAEEECGGGSGTGSGTVPTGHSTKSLATLLRNTGAFPFKD
STGATRVSSQKVLVRGVPVNFGASEVRDLFSCVGSVVSCVVRRMPVAPVATKARPHVSRY
RSQQKQQEEKEACEGETTDGPTSGGSAANFTTSTAEENERVFEVTYQKVEEAVRAILQLD
EYQLHGKHILSVEPVVSADIVAAMQHLERELNRR*
>TCRU_2097 kinesin, putative
MGKKTSKAAENIKVLVRCRPLNEKEELQGYKSCVDVDLTEHTVTVKSLVGEPDRWTFDAV
INNTFSQRDIFTQFIRPLVDSVLEGYNATVFAYGQSGSGKTHTMTGKIGDAELQGITPRC
FAHVFERIAEIKEASPNKQFSMYVSFVELYNGKVQDLLARQQVPLALKENKDKTFYVQGS
HIPQVKSPDDIFRHMEEGAERRRVASTDLNADSSRSHSVFSLIIECTEISEDGDSLSVTS
KLNLVDLAGSERQSKTGAFGDTLKEGCNINLSLSALGTVIDTIVKGRGHVPFRSSPLTML
LKDSLGGSSKTVMFANIGPSEHNFSETVSTLRFADRAKQIKNKPVVNMDTKDQKIAELTE
LLHELREKLKRYETEGTGSLEREVEELREKVGEMEVSLDSAVRAREADAVDFENVKAKLN
MERQATTSRVIELEELIGKLQNDMQIMESSVTDERLQREEVLRLCSQYLCGEEDGGKPIA
TANELEAVLQENSHGKHSVELARLQNKIQKLEVEARQMRKEHKTVTRELEEKLQEALASL
KSAESKLRKANRESNEAGDVRKGTSQPPGGNGASSEEVAGLRVALENAQQELQEKGIAAK
LETKLQEMQDSHEKITTAYLTQLKQAKEALGAPGADDSLIVQQLRAILAEDDKTYDFALN
HMSNMHNVMHGLKSAMREAQTVPLAAISGNADASRETIKKMGNLDAHEAVMYAGMLSNLH
DAVDKAQTHRNRLLDAIAALPDTPVNFKEELSKLVSENDELRKMYKDAIKVTETAQARVV
EEQRRTVSEESVQAQIDSVRKEYEARERELLAAMKLDENSGDGKAVLALLNKNASGGGAV
SEAAQKEIESLRSDLEEERVKCEKLVQSKEAQQVELKALRQEVAESESRYVDLEGKMNEM
VSDYERQLANAHGSTEKIADLTARLKERTDQLDQMRGLLEKQKALIVKSNEKCEYLQQKL
REVNARAERTEEIYRQKLQERDENFQSVLNQRLEEYARDHHDDVTKQEEKSKKLRKKIKK

IENEVDRLKEEYDCKVCECEDLRNTIEEQKVELMRLLRRMGQTEEEAEVYEKKEKIQTAL
ERAKEEQRRKKDLFALGEVANVRRGEY*
>TCRU_2098 guanosine monophosphate reductase, putative
MSVSGVGSIPVALTYDDVLLVPQKSPVRSRKDVSTTTRLSRNIKLHIPIVASNMDTVCEH
QTAIAMAREGGIGILHRFCSIREQCEMLSKVKRAQSFLIENPRMIMAHQTQEEALQGLQW
KGRKGGVSCLMVVENFSTRKLLGIVSKNDLHFADANEPVSKLMTPLERLVVSTNTAITLE
EAREMMREHRTSNIPILGKDNALIYLVTLSDVLKLTGKKHASLDARGRLLVGAAVGVKKE
DITRAAKLVEAGADVLVVDIAHGHSSICIDMIKKLKTDPRTNKVDIVAGNIATGEAAAEL
ILAGADGLKIGVGPGSICTTRLVAGSGVPQLSAVMECTRVARKHGVPCIADGGIKMAGDI
CKAIAAGADSVMVGNILAGTEEAPGRVLVKDGKKVKVIRGMAGFGANLSKAEREQSLDED
VFAEMVPEGVEGSVPCKGPLAPIVRQLVGGLRSGMSYCGATCINEMQQNARFVRMTGSGL
RESGSHSISKL*
>TCRU_2099 cell division control protein, putative
MSRIRFKGGAWTNSEDEVLRASLTVYGLQNWERVASMLVRKTAAQCRERWENYLDPRLHI
REAWTAEEEEQLVQLQSLFTNQWNLIARELRHRTGMNRPAWLCEEHYHTLLDALEYERQQ
KEGGNNKRNESLTLEDFLAERRRHRAYHQGHETRASKADAVNSDVFEKEMVEFAVSRLAN
QDGKKGLRKERKKQLQHTSFLAKLQSNREAIESGTLSAKAKKRMERAMLEDRAGPSDTRL
QDEILEDDDVGSSGGSDVGNDESKRGQKGVFRPIDLGADKQEAGIQAKHRELVKNLSADM
TRLQQEATVSEGINVELLRLASGTSGSANRQVEDKKTPPITSKSSAAPGASPATADLDHL
FASLPEAILPEQESVVGARASVDELFGTLPEPLLGGRVSRDKFNVAVATPEDYEAEEEEE
AEVSYTVSPSEPSQAPLTALNFSTEEGRSWLREAKRRVLVESESVFLNRKRVRHHMSSPT
EKTQLMMTTKNGEEEKGQLEGERKEKEEKNDDNDESTWCIVRALVEQQLPATARDLLEAK
AVPDGFLAKKAKREEDSSARYNNTQEYVKEKGGNEEEKDTTIELAACVAAVQDEDGADFW
KDVGATEATVQLEELVHHQREQVAANTANDTEAYQHLERMVRICFAGSRKELRGEDIINR
VCVYWGWRLEEAQRRLAFYSAIREVERQEMQRRINDVTSRLTEIEQKERTLQERYRSMRL
AE*
>TCRU_2100 Putative methyltransferase, putative
MLRWVVKEVESPYGNVATVHWAVDDGDDDNVEAATDAFDASLQQQLENAEDQLGAVLWNS
NAVALRYLHEHVLRDEASAYRVVELGAGVGCLGIALAMAGARVVITDLKELLPLMQKNIE
MNAARIRLRSNGQGSCTALALRWGPPPRLKKRMKKQQEDEISLGSKPKETWPYAGPSPSF
LALQQELDRVDMVVLCDALYGNARDWPQLLYTLSEILAANPSCEVINFCEQRVKNVEGDF
LRLLQQENSKSVASDAEDGKENEEESLESALTRMRGAYEWWSATEVVREGTSDLGMTVCA
TRIRWVPRRKRQELVSSVSASSSSLTAVVGASECDEGLRGKRRRTKL*
>TCRU_2101 hypothetical protein, conserved
MTEMCFSPCSIFPGEVEDYYCTSCHTTCSGLSLLVGPHTGHNRVPLIDAATYLPAALQRD
ANALVMRIQEEYIRPKTTHCNTLHATLAHMQQERQKKRRELEELQRELGTLDEKIDNLTE
ECAMALCHWSHQRDGFLSQVRRLLRGADALARTLGIRENQPIGSERRVDVDIAAPTKFPP
PFALRAVRKELYEVRRLLTQPLEWLEQEDEEDKEERSEGGKELRLSRSVRNGADAVVSHR
SKKEDYGQLSGTSRTPRHVNDHTLVSSDAEAVLQQLLAAHMKRQGEPHTQKSPSARAYVA
EVEGTSSCNSQKDVQVTAERRRWKNDYKRRERLLHEGLNVYMREGFFPGRTTTKIAGGVE
TDVNDMSSSDSVKEAVAHLLRNSQNDIFINTTPHQQRRPPSCALASEED*
>TCRU_2102 hypothetical protein, conserved
MLRDTPVCRFGTLSTALANIALFTANSIGVCDPFSVLVVGGTVFRMLLLPATIYGDCCLA
RVACALPELQSAHQDYKTIIDHPRAILWEKKVAAQKLKNDRERIFRNHHTDNVRLVLLHL
VAMAGSWYSLCIPAQQLSEFVGTSAVTSPMIVYAFGVTMDPTIGVAATLTLLNTRDHLQR
RMGFNDGLDGWIRQIKRHMTLTWSAFVAVSLLGQCFAGPVFLSYLFPFQLAPVWLGISMM
SSCKIILVNHTAPMRALFGIQDYPLTHGMHGALTTAEAHEYRLEFTGVDAEERRDMWQTQ
KKALDYECNVRLHRMLKQIGLFDSVEEAEHEAENLRRKLDVVRDRQKKRKQEQERNDAEL
SSSMAFCEADIVGPSAESVAERHFDEIQAQNNARRQRGRGL*
>TCRU_2103 hypothetical protein
MGNAFFRWEACEADAAVDTLTFLAEDPNAPRFRLKHAAVGTALDSHSTGFCFYSRYVFLE
VFTALQVLLAFFTLYLFNYMGTIRHYYAPRTVLKEEEGFFFPPKEKEVLVPHKREALAAV
YLAVVVIGLCFILLVAAYILLTNSGWWASLETKRWEHDKQAAVSSQPSHGELQHRVRSSG
YHLRRLGIRWISWTRPYYAFPRRYLPDFDYRHELHAKFGAPSTRGDPKKMYFVFLSPFVF

MLTFMDIMTVDEMRVTEMRVSLLQGLLLACGPLFLFYVASILFMSMMMSQRSCFGDTMGV
LYA*
>TCRU_2104 Protein kinase domain containing protein, putative
MSEIAQVGNLSGLNATTRSLSRLTESKEGEWSELDQAELERFFIETQQSSATPESLCFMS
ILGGVQITTPHNETPIFGATETNKTSCSSTQPNSTVACSLPPVWYGLPRSTPNTSFRLEP
LPEVAMDSLQEKKGEKRRWVDPLSSSTLRDSLRGMQPVSLQNETKGSQTEAWKSNPVQPL
ESRLQSRQRCNLWTCGRNKLPVSPLEALARCGCHLSAHEKEEVLGFQHVYYCGAHAKCAA
LASMPPSGLKPAKNEPSPLSFDDHDHNYRIIPGDHVGYRFECMEVLGRGTYGIVVRALDY
AARPIPKQCALKIAKNLPRYAETLRREADILDFLWHNKPEVRRWIPQVLTRLTFRSHEIL
AIPLFGLDIKDLLRVNLFRPMPMALTRAMTAQMVVMLELLSDANVTHADLKPENIALFDR
SLSDVAFPPDIQRQISLEEQERDGTKLDDDGDDREHDSPLFLDSINSLSSLHTRGVPGMA
ASEEIENDGEDDVVTSHIAILDFGAAHVGKSCIYPVQSTFYRAPEVALQLPYGPAIDMWS
LGCVVYELATGVPLFVAESDKELLQRHITVLGMPPPEVLQRLHEMRTSSGDVEEKKGEEE
EGKMRDLFASLQVERTPNAERPSAQFLNLLQLLHIQEREEAIISNKQTQQMRQQKKHTDT
HLAKEAYPLVMATSPSSYDGDDDDDAGETVSTLLLLDFLLGCLMWDPEERLTPDEAKCHP
YLVPCLKEDFMQCDEKAPLVRTRSTGMYYLHTHALTRGEVRILEAAEREYAQRRAKGKVV
TNGMHPLMRLNVRHAIQPLRRFTSQRFGDDTSETPLRVSCRSIRPVRIAVGDSLQPYTTK
FFDPIEQVEVSIMYFDEI*
>TCRU_2105 hypothetical protein, conserved
MERDFIFPASFAGISDQQGVISVLQRHDAVRVRAAHRIPSFSVAVEVVYQFLRSLPPPLR
WSIREVRVVAAPSASNFTVELTSECQRHAELDVAKLISCHGEEAERMSDLTAVSQEVRLT
CAVESSMQRTRGIQDTAHSTEGMGILFEGHWKGKEINKGEDHWNGIPAVLTTKLQAYLRL
LAKKQKEHQPSSLFFHLRCEVRNLFYCMPVRQRCAAGWSYTSYRLRAERQALLLTAYRMA
VECVFAPLYLSLNEGAGSSASFYLHLSNSGDGRNKAANDNADVFYVHNYPVQRSKEMVEQ
LKKRRRMEPESKNDDGDRSCTLRTAHRILFSFFPHLRLCGESLECSNGIASSRLREVVVD
PGKFVVLFLIPAWDTHDATRRVGRRPSALGTVVVCRHTESTACYVVDESHRIYLQVLNSF
TTLCPIIVFLEGNLLESNDATLRRMFQSAERKYLCGLGTDTPRAIQTPTREDSLSVVGKL
METKDASGEQKIVGTALRVSFLAQRLSSVNGTKRARCFGGAPISSFPRRTPFFPINLGRN
LCGTSTLSQVRSAMHLTIDPSLFAPRAYSGPSVWPGSGEMENKERTPCPFRAKHLIAQWD
RKFLLLQMNDVGEPSDTSPFDEIGSPSSTSINGMPTMGVPPVLCKQAQSHHLPPPALYIV
DPHAIHERLRLEFFLTTAESYVRRDIGPISVPVHIPEEIRRDVTTYEDFLARWGWRFAHE
NLQCTGLRSAMASKSRYTQLSWCCVAVTQWPHLEIEGHVLQLETIDALRKTVEELVTVLP
SWQMPAATEKESSKECDWIVESPGARVVPSAVLEFLVTRSCRGAVMFGDSLSTATMAQLI
GALQAVEQYTLCSHGRPSFAVIHRRKM*
>TCRU_2106 hypothetical protein, conserved
MAMMAGRVLLVCALCVLWCGAVFVSAAGDGDGDGRGVVGEPLPESPESRVESKVVSNALK
EHVEEAPTPAKESSEEEEAGEDEATLQGEERQQQQEGENALQVNGRKAPEILVKQNETPQ
APKVEGIPTAGALEESAKTPGLKAPTLKVPQPPAASADGEADGGPVGVEGPVSGPPSGGA
S*
>TCRU_2107 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily, putative
MAATHGGHDGKVHDSGEMGKKWMEFCGAHLNVLSGALRSATSGGRLDIVTVFIEGRSVML
FALPRQNNIRRATSVLLLYMTRFYPIGPLRADGVSKNADTLHYKGGELFALFEWYAGQGR
VVLAHLTEQLEEIKTALRNWDAVDKNVTTPCTSTSKEGTAFDDACSTPMPTDGVVGYLSN
EGERDCWVKEYVAASATVIGTAAKVEGGATFEGPGVWTERPVGKWWRNQRFHIVKKEFTL
VVTATIGAAPAGSGSALMVAVGGTGSVRMVELSVTVENKREVAFDGEAGEVQHGKWGLER
TYRVAVGLQNGMGTVCVDGKTLGSSATTVTRGPQLLDVSCFYVGGDGCSGSGCSQVTLTH
VCLCNRPLTRQELQMPLLRGKQTEADCKERKVTPRPGNFAAKLPQDLGVDAAARDEVPVP
AKGNLAWEMAPLMSMALLFYCFKNGLVTAPSMGVCLGHCLALLQGVCGDVAFL*
>TCRU_2108 hypothetical protein, conserved
MAMMTGRVLLVCALCVLLCGAGGRCEENGADVVSGGGPGTGNDDKNSEALCSPDLSSLER
QEEGAGGAAGGFADAQGGKDISTSSTGTNILKVEKVDLVVDPPNPIENQNKSKDSTKAGT
GTINQTASPSKPQSPPPAGPPPPPLPEAEGVKLTKTPEKQDSSVGHQSTQHTVPQVKELK
KQQQNTQNQIINEKHESERLQVQEEKEKQRSEEQLEQRERPHEEEREREDLQEEIRDQQK

KQEQQEEEHVDSIKQEKEQDQQHQHQQHETFAKNSDGPIKNETAVGTNATASTGDSDGST
AVSHTTSPLLLFLPVVACAAAAAVVAA*
>TCRU_2109 hypothetical protein
MDVEKWRRTLQGFVSSSALQVRPAPLQKVLQSARLEVNHPPLPMEDWMKLYQNMESRFST
VQAGLSLQAQRLRSEWSGLQEPAPGTAVDDHADNAATVLAASIERLRGVLLNACSSLPGN
AMESNADGSA*
>TCRU_2110 eukaryotic translation initiation factor 1A, putative
MPKNMGKGGKSFKAGNAKGIMQNQKRDIVYADPQEGEEYAQVKKALGNLRLELQLADGSK
AIGSIRGAMVRKVWIGQGDVVLVSKRSFNKNDIVDVIHRYNPAEVRALVKDEVIPRDFRS
SDERDAKNAHSDYVFVAENDDDGGADDDDQNVLDRNKVVLDDPLATFDEL*
>TCRU_like histone chaperone, putative AS.1
MATRVELRGISVVGSNPAPFSDSIVLKVLLEVFEKPPAHAIDVKFTWKLIWDFPVDQELD
EFEVGPLTTLGVHELTLQSDPPDFSKIPDPTGPTALIISFTYEGREFLHIGYNAVVTCEG
EMPDVFESAEQLRRHLTQCFPKQLSIVWDERPADAVGNPSDDDSGSFDVDKAEECAGEGD
MDGEHASDSGDGAPPLKRVKT*
>TCRU_2112 Sedlin, N-terminal conserved region, putative
MLMVIGPDDASLFECAKSVDGESTHLSRQLMLYASLDLLDDVLWKTGDFLLPAIDRPLEG
KYYVSAYVGFAPIKLLLMQEQEPNKNTRQFMNEVYGLCVRYLLNPFSFPNTPVRSTLGEK
VRRLYERYS*
>TCRU_2113 6-phosphogluconolactonase
MSFKPKIIVCGSPAELSGVACKKIVEIIYASERTNWPLSIALSGGSTPKMLYSLLHEEHL
HLLKEERALRFFFGDERLVPADAAESNYNMARQALLHDIPEDLVVPVDVGCVGKVSKVAC
NDAVKSADAYEKKIALLLGTQKVEGMEAEIPVFDIVLLGLGSDGHTASIFHGSQAESEMH
RAVSVGFPSPTMSPKVWRVTLTPITIIHARHVILLATGKEKKGVLNGIIADTPTEVPVSR
FLRNCKGEVTFILDKEIAGNLTC*
>TCRU_2114 BNR repeat-like domain containing protein, putative
MGRPQTTPETDLFASHEGDWTEFIASGGSGVVMEDDTLVFPLMAKNEAEDVCSMIICSTD
NGSAWAFSEGISPAECLNPASPSGRDHFTWLLTARMARGCTGRVT*
>TCRU_2115 Nuclear transport factor 2 (NTF2) domain containing
protein, putative
MLGRDTVAGVACSFLVTYYREFVKEKEVVGLVELYGESSLITYAGYNEETTVVAQGRHEI
AQHLGKMDDALGRRKVEVRFADFTPLPGGCIHIVCQGILYLRGQRRAFFQVFVLAPTQYR
TNTYHIAIDYFRVMVVEVEQIPEDSIIMTPAQVAQHLLEEHERRKRMEESREQLRRQQAA
AEALRLQQLEEAARRKEFHQTRGEQEPRHGRHERQNNGTRNDGYGNNTSNRRDRVEWNDD
RRGDRTDMRTLIRNEGSVSRNNRPERAERNNGRYDERNERNGERRWERHDGMRGERNDNV
RAREERGVLEEGPAPQSTRPLRSREQPSTAASKSENGGSKPSIARPVPRSKAALEKRLEG
RAEIEENNIINRNEAVASRRVPEETAMKEETRKKTAAPRVAAAATAAAAATGSTRDPARG
RPQFNRTGSTDYARLVRVPKYVTLTDIKAAVTSVLGAEPIDAYWYGRSSADCVLQLRSSN
AVEQLVRDSVTVLESRLSAAKFYP*
>TCRU_2116 cytochrome c
MPPKARPPLPPGDAAKGEKIFKGRAAQCHTGTKGGANGVGPNLYGIYGRRSGTVEGFAYS
KANQDSGVVWTEEVLDVYLENPKKFMPGTKMAFAGLKKPQERADLIAYLATLRD*
>TCRU_2117 hypothetical protein, conserved
MSYQLYLHRSFDIQLSPVAAAIIDWAPTRRDGQVSSDLSSGLSSSGESTNTMGNRKGSKP
ARDGENEDKMGKLMSRSHAVESPYATGSSETVSLEATQKAHGPTGASMPDGGPREVRSSH
KRMYPWLGQRRLFLLNSYAVVPLVTRGSLSLNAGLFAGFGVTGGASSPASSIGTSCVSPS
TGRASIYASDVLQLECIWGRMQWAGVFNVVCFSWPSASLPLCEFIGMTPRTDWSMQVDRL
LFNWSGFCRVFVRRGRHCRRDSLISLNSPADSALSSHGDVNAAQSCAAKNNPPPTPPVTL
TSRGDTAISGQDEHHAHPRAVKSPHRTERPRAAADNNNNNQTNNKNKHHHLTDDDETPPD
SDGGQISKRRKSRDTTAWSHLARKSSQTTSHGGEGYRWWRLEELRCGAGLAVKNDLASGV
NLYCGCSAHFGRALTVSTHVDVLRRACCSITSTTSSLDLAARLRMNLITWHRTELDFGVG
WRPFKQVSGLTCRLSHSMGRTSVGITIKDVGTQYKLLRCSRCAKREEHEERQEQEGRSWP
WRRRDSHDDSMSQENVGGTTSVPTLSTTWSLSDWYDPYVGWVWRLGGSIFSSASLSSSPS
AASPAEGVAAHAPGLRKRLSQAMRAGLDYADALSRQTEFDLTLGLAEERNYSRKPRCFVV

LSAH*
>TCRU_2118 diacylglycerol kinase, putative
MQTKSLDILHACEQGDKKHPLGKCPPENFSLSCYSALEGGNCTENGSAEVPRGNGSGCMQ
FRETSNGPNGFETLPVMVNSPSRGYDSVEIANLKTDYRPMTSPRDGDPEYEYVLCIVNPG
SGERGVAEHVLDSVRAVIGADRVVTLDAALFADPTPLLEAIRRHAVRSISQERKKSALTR
VTAGGNSDADARGDGVYSRGLERRGTVIVCGGDGTVSFVMEQLDAVRDMMQRTERGSFEA
GARARGGALKPRFVLPAVAVLAIGTGNDYSNCVGFGNGYSRHKLSCLCCCMENAIEPLIR
NVVTAPAIPFDRWRVQLVPLTAIWEQQERQRQKKQTPHLTLGTKHEELVLSVNPPRGDME
EKKIQEGKKEEVTVTEDTVDLYALDWDALEADETCRKYNFINYFSIGFDAYVLQKFDFFR
RKHPKFCSTRMNNKLVYGVYGLKAGTRCSSLRPCIPQICVPQLAQHSPIHTEASQRSSGQ
TTETKSMMTLSLPKGSKTLLVTNVGSYAAGTRPWKEGKGKLYRDDHLAQPMIITPVCVND
HKMEVQAVGGIFQMGLLQLGIGKGASKLAQTREMFAFVLCNPTDISRRENPRYGEEMLAG
KEGVEEHTPLCMQLDGEAIGRINRPTVVHITELHRPRVYVRCRNPRVVRYPIKDEEDAF*
>TCRU_2119 hypothetical protein, conserved
MGCRQSVAKRPVAPQEAAAAAQYGESGKFGEHCNASSATAMELTMRVSAKKKVHDAGNNT
PHAGEQQVTRGKVRWVSTKKDFAASHRELLGRFWETHDMERLSTLLVRNVPVSLQETTTS
TSFAWTSTQREDGSSMTIFSPNAITVSSLAPLDGRRTRSARRKRALPHHSRWVSLLHTFS
EPHLGGGETGEHVSTSCAPAHAREGAGACKLSGMRGHMHPLSGSGSPNDADVGSCSAHVD
HGAATGCGYPGAKKLFAFRLSEMPSTGKGTSFLRKRKMNPCMGVHAQRWDRVEFFSPNIH
SIAIAVAQTQPNSANSFFTNVTSPGSPLSRLKESHATFNASFDTTKVLAPVLLTESLSST
VSQISLGSPRNAEHSTRFPESSLYCHCLALPASHIQELQAGGELIPTSFLSPFASTSFGG
NALEKTTVDMDGSPLHDATICSGNANMTLDNNKKSASTANIEANVPRASVYGTQGKMELQ
KLNLGVRELISAIDEKKKASPLREDTGGHTTNMCSSSELQQSHAPKTILSGIIVSSFDLS
IDPFRWREEQYKCNTIKYNGARSCVREQFREGIVTRVMYGGVFVVECTSHLALQKLEKAL
KLKKWSDRKKKISALSKITTFPRDHNSNHVRDGAGRVTSSSCYNSGMECSNGGSFLEYKS
CNDANQLELYRVAYCVGGMQIKWESYPKTEEQSPRSDMIGTHTGCPTLTPWINLKTVMKL
AHSWARHLLSTPELAEPLAVYVQSFVGIIPALRLVSDWNCQLMQLFTESEDQEDDDDELS
TDCGAGIERGGLPGMENNFGEASPFEDSSDLSTKTGGGLSVPTVLFTCRPMTQYFKSDGH
VSKSTLRSSANISLITSKRTSETARRPSSIESLQKHPRPERSRRATARAIHESVPKVDQC
KSSARQREGGFLTPRAKGDNPHVPRTAKPNEKKEGTNERNVPVTDPMMNEQTKLEFLTPY
LPPPLSFEGEDGEAFWERSMLEAMALEKELKDVMDARRKADDEFYRLGGIIHSLQCAFLP
NSQLGEIEPLCAYLQTAIDDPMELPHRCCYFAGPDWFSCLAAVLTNPRNSIAAVDISYRL
TFSSLPQLGMLAGLLFHECAMPFLQRLSLQCRRIFFLKCGEKNELSRNEKVGKLWSRIIS
RHVSKKDHERRPEFSRPTSIGFDEPRRGPPFFLTPKQAKRVLVILTESLLDNARQPHFTL
QLREFPYKSFERDSKVFHKVFHVFSRNFMRHATSNDNNNNNSHPHHHDTDGAGRKTKKKK
NRTEEENALLRDRESTTSSWTDPPEVVFSNDPHPIQCAWDEAERQPHCMLMRHREFLPTR
WSAHHKNHPYAGRHEEKDQNHSSCYEKMWVYGLGSEYLEFAVFCELGAQLLEKAPEIFDA
VQAALSHRGAGKGTKKGSNGGKLLAQTEFLLTC*
>TCRU_2120 U6 snRNA-associated sm-like protein Lsm2
MEGALVQTIPSVLAAGGHVQHSLMRVELTNGIVLTGRILQLDAVTMNMKLDAITDIAVRR
RCGGGGGKKIEWETDPAALRCTSSVVIRGCHIRYIDFIDEEASGGRGLQELITAARTVRP
TLV*
>TCRU_2121 hypothetical protein, conserved
MLRRLVSSHGCSNGGGTSGGRCVRPVKEEPPVFSSLVLQRRFSFKYATKLQHDEMRQPFY
IHEKRHGIFSNEKNIKKSRRGLPFITPLYTRHMNLWETDTDASNNRFFRGYVFGQRELHQ
LLGRPHGFEANNTDGSNDISAYEMTTDQRYKGIPRPAITNLHYEPEWNYTLYRAGTHGSQ
LSNPRSPLTAEVLGDELMKIRDIKSFDHCKAWFDRLQYLIKLHYDAVGDIGEFKSRHTQH
VHEFFVAFHDALSSFDFGDSYLFEQFHAARPSELTDLFGIFLEMESNYVHEDYCPRCSLP
YSTTRYCGEGDANTPFRKHRGRWAPHQRWGREWYAVVARRAEALWYRATEDPYFGTPQHT
QRQTEALLRVYVQTKQRGKAIDFMNALRGSKEFLLGSICITPEMQESYDRLLDTTPHPHL
LTNGFTLESNAAKYTGEVQKVPFSPLQFRIDMEMNKYRRQQKEEGAVRVPPAMWRIDTSA
IVPYKVDPKTKRVINWREVKEGIEKSFLSTGLPKEAYTGSEWREMLHLKSIIAGRAAKAA
ELERRLHTDKVKLLEVASKSKIASETNTSTSSSIIFPDKDGYHVFDTSVASLRPFGVSQS
GAVFQSVTHTYPSPHAVPYNDPVHGKQFILDTTNESCHLFGGFEHGDRLLIRARKSDKND

NNPNSVLAVKGNEFEVIVLGVSKEGSDSEWQLCAMHVDPALQREHGIVFLGTDCVEIHER
WASVRYAAAAPHVKGRVTLLEERRTAREESLGQIVGVRDGVLFVQWRLLRGGGSEMDRSV
AEPIGTVEHVRNTYQITEQGVEELMHPPSWRTPFRNDFAEERLEELRQAPFKRENWVSLI
QGRYTPKRKRFGYTQHTTMDDFETKEYKDRLLSKQFFHNPQAFEVIPDRRDRAVTFGGKW
EYQRTHGLPTVDRNELENGWSEVEAVTDAEMHVIEQALRDISGRRPGNFIKSPTKKSTLQ
LNESWWEPLEFGWEQHNKEQKALVDPTEQRLIDSTSLPFGGKIPPFGTTIGIGERIREIA
EDYAKGFGLGPHGHSPSHDTSQYNTLNAEEDRVRELGYKDALVRLFDEKMAGKDVHQWAV
EQCADGEADVRQLLLSLHEWRERGRPPSLMLLQVLSKYLEQEIAAFNEGVPASVPKLSLQ
TVDGTLSPSGNSGERSGTIWADVEPTAYALQYASQANHSSLDEPFILQLLKSAQLGGRNA
QFTDPFYNAYLENSVVSEFQLGLAALAGKGVSPSLLAQKTSQLHRGSVRLSGNVIPFVKS
RELAHLLERMGLSSENIAVVTRGLANCPEQESVGDDFAVPVSVILTWGGPGSGSSTSVAD
RKGNATQSRNEQQRKGSAALSSAIRQLGQKRSSSKNWQNEDKMMVHVIEELALRDDGLVM
DIQYIVRENRRNPVLRHEFFAALLPVFAGKHEKVAQLYDEYCEGKYVPNITLAIEAFIAF
LCNVTKHADVYPGSSYFDVDTTNGPHAGQYTSLKLLDPLDGPFIFDNIKAEHIETVERFK
QHGIQVGPVRAPATGFIAANSKSLSYFTRRPEEVVYVSTDADQGLRRSLERSAHYKTIAA
SPAMQFLLHTQNGAGLVATFNRFFYRTMPMLSFYQRILKHYSDNVQPLRQKAQNSVRGLA
RVLENERSAAMEEFRRNSERYWRNVLEGRSVEQAMDGSGGSGGGGTTPPVSSSPSQSSQE
AMATDVARAIGSGRTGDQKGGAAKQQQRQQQQRLQKQQRTAGDDGGVRTTFASRQGGSRS
MTDLLSKLNKPKGSNTSGTAKGPTKRGNPKSHTDGGRGAKP*
>TCRU_2122 cullin, putative
MPTSLGDLISIRGSSSGSSSSNGSRSGSKHDSGGCRSDAKRVDCSCIRERDVFSRLQDRP
SVDDLWPGVESYLVHAAHTIRTGSAEMMDRLRDVRHRMNWYAVIYSVCSGHPQKSSEVYH
RLSLFLLNDLEVNVLRQFLRRNAPCGSPPSSSLCLQFVQQYKLFMAFRRVVLSCFSYLDQ
YFTAKFRLDPVTALCVKLFYVVVYEPMKEALIAEVLELADAARTAYLNDKAVSSACSDVQ
QALLSIVEILSTVKAFSAPYDANTQSALTHQKKDNSNPCNYKRGVGEGRNMLAAFAAKVG
RMQSPSTAPNRDPPRTMGESPRSPLNKSHNSGHSRVEQQNGSEGHSISSSPLAKDWDAMA
YRSLDGIRMLRERLERRSFGDLLAAHVMRSSSRNKSSHHQHNNGAGIGITSGGCEGSANC
SVDSAGVVIVEITQPLHFLIFAEFGLRYVQAAETYYRNRREMQFSTPEGWMDYIPWVQGC
LAIERSLMRDVNAPLLLSALRERIHHVLLVEVHRSIILAKEVGFRAQLDAWDSNTEQGAG
DMWKDGSSSSSSIPPMGAAMSGTCSDVDAATSPAAFFSAQSTNPWEQLSREELGDRIKEF
VATFVSTQDEACWTLLASEFASKVVVDTAALFFTYMSQLEALAPQQLQQGEKERPGAQQS
ASSPPVQPRKTVIPMRRRRSLRADGLPSDRNFLTQQDLAMALIKGLVDTSIHYNKLICEK
FNEHPPMQVAMGDAMREILNPERWGQLVVGGAMHGGVAAVNRGELPSVLLNHDAAKKTVA
VLNRLATMRGSREIAVPQFLAMYCDQLCRREMDDGVTDPTDHILYLITLVDDKDVFLEHY
KLLLARRLLFLPSAQRNMDREHVMMHKMHHALGRTLTYGLEAMLRDHEVTASMNEEFSRS
DVALALPTRLRVQVLTSVHWPTYRVVPLTPCDSLALVMKNFTDYYIGVHPSRMLHWIHTL
GTATLHAVFPKGDKEVIANNLQAHILILISDAYNMDRGGAASSGANDSHTAMASRRSLSG
REIATAMGMEFCDIYMYLAPLVKHKLYNLLVRVDPSAVAGTGQTTQSSPPLSPPNARNAA
AAAVDDDDDAAATPSGTAPGQLLPEDHFTLNVEYTHKLRKFGLPVARPSRGEGFKGSVVS
STHVERTTAALSDEIEASRRIQMDAAIVRIMKSRRSLRYYELFDLTVQQLSKQFVPRPRS
VKMQVEDLVCRGFLRRSEKDTSVFEYMA*
>TCRU_2123 PPIase, putative
MDLKATSRLGCTLTRGSPASGTRYASHSRPIERTSCWMELACFGGFPKVPSLSGSMVQQR
QDLLASTKGAGEPEIILRIEFELFDDESPKACANFRHLCAGQSTSRKGQTYCYQGLTPCY
RGTYFHKIIPAFCVQGGDLTMRVNKGANHFSSFGRGWFSDENKRRRLNEVGLLLMANNGP
NSNGSQFFITTSDSEEKALNGRHVCFGRVVRGLDEFLREVAPYGEINGNPSRFVVVVDCG
VGPLPETLGITTSNSWAEEQKRHKAEGDNSHEEVGFEDGAATVAGAANAAASVEEEEEKE
KELEETTNATEANKQPPAMNGTS*
>TCRU_2124 Domain of unknown function DUF221, putative
MDLSLKPRSTWDDQGLWFTLALNSILLVVLSGLSIFCLTAPLLWLRRLYRTNHTITVSVG
PSGFPAATTPLTPSSSSPSASPTPPRQRVGRVLPYRCSLFSLPSLRDWLSIEEEVANLES
VVQPLSTIASPKDDEDDTKRHISGEMEMSKVNKRENTAVEDTFLVSATKAKVPFDPQVAL
YLAFLKLFATVFVLGGVFNFWICVLSGTDNYLEKYMVRRDIHGCQSLGDNETACNDRAPF
CKYVETDCVPVRLRGLYDLSAQNISPHSWRLWLVGILDLFFSVIYVVAVLFFLYRFDAYI

KSVMHLQMENALGHRVAIVRGLSADMMSEKRFHQGYLVEEAYFRPRGGKGGRVGNGDSGN
DNNGNAEEDELDVYYQYHCTGLSCLFSICGLGYYKTTRRDAIFTRDCSVRQLLFPREPPE
GMYESMERTETAMKELQEAIADQKAYSKKQRERMPVARERGEDVEETLMMCAPFPSCCSK
VPKVEYRKRVFIAEAKRLNQFIDATPARDAKGSAFIIFSDALEAYEFVNLFESRRGGVSG
AQATIAGPPDGIIHFNLTTDRYTGWLRTAVFFFVYILLLFFWAVPVGFVSSIDNLVYIPY
IGKFVLWIYMKVPETLRGAVTSFLPVVMLELFNLILPFMIRCFVIAMGVVNRDSLRGGEL
FLQYLFMVLTGVIFQAALQGGLSQLADVLKDPSGEAIIGFFLAIVSPNGGYWYAKVITAA
CISTWLNLVDPLPLIRAFLRRKEVSVQRVYDKLFKPCSFDWPQFYSFDLTILAMGLLFRM
TVPLLAILVGIYFFVRYMTQRCRLYDRYCPRVHPLHDCTVVSASAQVMRAASWLYCLGGI
GGVLVMSLRKHVGGVVLCSISLAVGILLLARVHSVSRRWVNSLANARRFLKHRAVPQTRY
GAMAKRKATQNRTQRTDKPSAPPQSTNVLSEGCSMEQLATELVSQTFETDGDVDNRAVTD
RSDSSTDDNNGVVGGDINAREGATSFGDQVPIPATELLPHNPNIISRYQPKHQRLLHIDA
EQEIQRMEKTVFHVESYWNSSFELIDDVGMPL*
>TCRU_2125 coatomer delta subunit, putative
MPVIAAGVVNRQGNIILSRNFNEVSRIRIEGLLSAFPRLLESSVNKQVTYIDAGTVRYVY
QPLEELFLVLITTKNSNIVEDLETLHLMGRLIPEFVDTVTEATLEAKAFRVFFAFDEVIV
GGKRENTTVEQIRTYLEMDSHEELMVREEKRLQMERAKKDASRKAHEMREKRRKGMNPYS
GISSEDPGYGGFGNTSAPVIVSGGGVDSAVLTHQFEGVSSAFTTSAAAPAPKRAGGLTLG
RAKKADITSRVLKEAGLPSPAPANAAGAASSQQPSSLTTGAGGGVESKKGVHEGTVEGLH
ILVEEKISAHLNRDGEGGAVDVRGELSVLVSDPQLATVRLILSPMSSKFSFRAHTKVNKE
MFAEDHVLSMRENKPLPVQQMVTILRWCLINSDNARPPITLSCWPSAGSITVEYELDRAN
DAIDALRDVRIAFPLHGTRAQEVTPSVGTWDIVNGCVVWSIPLLDAQNHPNGNVEIELAD
GGDGAASGSEVFFPVDVSFTSCRTVAKVQVVEVVRTETGTPVRFSQESRLVTESYTVPA*
>TCRU_2126 hypothetical protein, conserved
MDKLASRSDAAQPSSSLDEQLLRLLQQQVAIEECLSGQRALMQRITEGFSVLREWASRHA
HHDLSLHDLLVLEAYGGGSLCHNEEALQEVEKEGDEGDIHRGGYRHCGPNDMAIPAPHGD
RNENGNAHHPEYSKCERWQQQLQEAKRAYRSFIRARVLDEGCAAPDNPAQFHALTADSFY
LLLPQLTEMLKELVGITPGAARVQQPSSSLFSLSTSPSFASLADWCASLARVLRFLELGL
KHFPEVLDNSPLRPCLVQSLLQLQEDGNDRSHTREEAVLQLRQRAEKLCAHLHRLPVDGV
HNYE*
>TCRU_2127 hypothetical protein, conserved
MQTVDKSADAVHNADDVDMRESVNALKGKEPAAALAVASEPHIDKADVSLFPSPAHGKNE
NGGSRGGHPAYTDEGRPSHASSDVRKTNTNEGFKTNRCDAAGGPYQNEGISNPSEYLRWR
QRRKNLTSADYWRAAEKERVIGLGTVGLFQDQQPDSPPPGEASACVNGTIIVGPPGYVRK
VKDYNDWREKHSELFSTLRNQDERERQCMRLRRLHEKARQREEEEYEYASAVRRLRRRGW
SVLGNAPRQVDHTRFNQIKAEREAFRAECEGNVVRKIQEASKQRENILQQVAMYKEEKAR
QENIVRDAARQEREEQNAKREEYLTLLKERAANTRAIAEEEREFIRECAATESKYRQNRI
DILRERVFAKTYTNGLLTNLSSTLRGAGRQYPPGDWRNTFKSPLRRLPNASDDAFRKQWV
TELQEERRAVARAEVELMKRLQTSAQREAAYRDNCERAEALRKEKDALRERKKQQCEEVQ
LFHKVLRQQEVEGQKRREEVLRALRESKREAASIIRQAIEEEEMMFQTLEDEELRQLQER
VAQMKKNKTFPPRMALSPPAERVL*
>TCRU_2128 hypothetical protein, conserved
MSMNTSPERTGLKIGTALRDSRLRRSPERQSVPVSQELSFIYDLKREFDRIADSGAFIIR
AVDSLSKTDAHALDIDVDVVLNDIEREEEYIFSPIPHYLQSEWKRMVSENESAINDVVTK
LDTVGRLNEDGKLRADYSESARIVIDPSVPLLMPFSKERYHASPQRKTAPSCYHSLFFGE
GEPVVFVPPENNKRKDIEKLNKEREYWKKKFQRAPRSDVVEQKKTIKVPNDFVPSCAQVD
HSLVQQELQKRNEIEKNKAKKETPVKRKTVSPAH*
>TCRU_2129 dynein light chain LC8, putative
MSADRKAVIKNADMPEDMQADAIEVALQAMEKFNIEKDVAAYIKKEFDKKYQPTWHCIVG
RNFGSYVTHETHSFLYFYFGQVAILLFKSG*
>TCRU_2130 SCAMP family, putative
MYKFGGETKDLRNIYNFGDISQRETEPPKDLSLAENRAYLVDVEVHSDNNEEEMGHRESQ
QPNSRVSPTAQGVPQSSAFFPEFSHSSGLDVPQKPSMENTSDQKNSKEKQKENSKVKIAK
EVLGINKKNTSGMSPEEKERVLIEERWKRAMAEENRLNALEEQVTHREQATNSSGLLPNF

PPKFLCIKPLVHHDISSVPEVRRQFVRFNFINWIATCVLLLVNMIIVIAVVFASHKEDAK
KFNTSQNTVLAILYLMGAPLSFIVWYWQIYSACSTGRHTKHLLALSGLVIALAFDIFMIV
GRTNYAACGVSLAIDISKTKSKFAVLPVIIVLFFWVVEAVILCYCIAKQWMYYRLDVNAQ
EEVRRQMRNVIGI*
>TCRU_2131 hypothetical protein, conserved
MAMQRARGVRLNGGDNRSEGTELSISRVIRAVQGSKSHKLSSINALLQTVVQSAKNVVKG
TDSQRRFNAQFSEFCRASLVGISDLEDAVYTLEKADGVFGNDSSDEQGVKSIGAVEFVKE
VAKFISSQTSALGVQYLEHVGISAVAAATKTQQLTTTETKRGSKRGRFDDTRQRHVDYRS
SPRKRMGASPSLAPAWETDALLLSSPANKSTLARGGATDSYHGAVKLSGIPELSMWLQPW
NLSLPNAHGVALDRVMTERAKSLATAEDSLKPPDEVSVFDICTAVATAEVLRLWEARECL
LSTGLDRATASNPVPTGKVFPPIAEEGKPMFFPKSDLRARAWVPTQVMVDLVHYGISSLA
MPFKDVE*
>TCRU_2132 hypothetical protein, conserved
MEIAAYKLFCLVESYATHPGHAVGKFVNLSGEKESFGIAFDAVQLFGHLICTSEDGMELL
CTVLRKFVEIHEVTVGTACRVNFITYVVLHAYHTLAKEAVMSQRIGGGLSNLGWGTCSPF
PSHETNSEDCDARCCWRIMNNFLQELRAKGHSLDPTDVLEEVASSIVSAGEGMCDTDGKK
AKFLSPRVLHEYLQRTFAYDPLSWGYRAGKLAVDCFLHIRSRLIEFVVEMETDKTQSGLS
SLHTFVEKSLYRVSNEGIDWLPIGGNEGCVVPGIAFIRTVRMKRSSDALLGTCVCAPTNA
FGTLVENEGFRTHLLLMFSQFPDAATEESDFGFRQLALMVKNVEKGLLVIAVQSHVGEET
LRRMESWGNHTRTVLFLVALGKKIMTQLALAFRVLPRPLGLDQQSFLQGSLFVKPLFGSH
SLRHCSGVELRSFLLALNPLNMEGVQHPIVSVVFGGRCAADQVLVERLFSRQLHHLVNML
CLPAPLNVVMPAGGVVEAYAIQHFDKKLREKSMESDISLRCFEIRLIEALRSAIIAYMES
VLQKSGGLTVEATLEHLALSQERFAAMDRDAENRESNCNGFGAFAMRSALPNPLYSRFVP
TPPLTEVSGATSAEKYRAKSTLLLADLREWEAQVELVSTYLTIGMCLDHLCFTSIMGRRS
AVRDSKEDTQMDELFFFPDIV*
>TCRU_2133 hypothetical protein, conserved
MRQLIHVTSRSAVLLVLLVVMMFVMCCAGGCFAASLTYSYSSDKAMRADRAKSIPAVVRD
VSFGYEGASQTCTVIGRNGWAPTRINVSTRDLDGTRKYCSSERYCAMNSLVAIASVKVTF
FYDEKREVFVSLYFAATVR*
>TCRU_2134 hypothetical protein, conserved
MPSPLRIALLLDWRNTIRRLGPAAVICYLNSHHELRDGRSPSTAAGDELAVIPTGMEIEL
SDDLAQATWNSGRSVSVPDVTAQRALCASHWTSTRLHGLGPPSAIPHCRDGGRHPATGRH
AATTET*
>TCRU_2135 hypothetical protein, conserved
METTVSASSSERLRLPFSRCEARDERVDPDALRLFLEHARQEAAERHQRRVSQVESQYLR
HLQRCSTLPGASMSRLQGEKGDAAPVDDGEVIEIELEESDENNDDAEDKKNDEESKSWAS
CGFTSNFSTATTTDFTRALGKTSATQHSSPTPSTPQSQSNSQGISPEVYTPLISTPEEVS
STNSASAAKVSSLMRHDGANDTDAEVWRANAAPNSAAMFPNYGRGPEDYFGGMSVQKLCA
ENAAAQQTRSLHTVDECGDQHDATRCLMHAFGRHLDVEFQQVEQDAPCSSPAGVPLETEL
EEFLAWQAAKPLRRRERLQGALNCGSHLAKVYAAVYPELLSLALFDAPGKKLAEPLTPES
PASRYIQWIASDVDCYEDLLLHLTSASKEVEQTLLEGVCEAALNAYITECVVDSILHNCK
*
>TCRU_2136 kinesin, putative
MTYRDPQRGEISPAHGTPLRNVRPSRQVSNIADPLRISPSTVARHENDDEYMSPTSLSNN
HSPIYRNNVPANHSGFGGDEGSESNFNVVIRVRPPVQRELNGYRPYVDVVRIPNDSRSIT
LCETLDTEDGRGGVYSRQTFTFDYVYDKQTLQSEVYERSAQPAVFSVMQGYNATLMAYGQ
TGTGKTYTMEGFTSEDQRGIIPRAIEEVFTSIEVSRHENMRFLVRASYMQIYNEVISDLL
KPTTARSLVVRHTPQRGVYVEGLSEWVVRSPHDVYGLIERGTSLRATSATKMSELSSRSH
AMFTIIVEVMEGDETSPTSYRVGKLNIVDLAGSEKLRQVGATGQRLEETKKINKSLHELG
NVISALANKSGGRNRHVPFRNSVLTSALRDSLGGNCKTTLIACISPALESYTESLSTLVF
ANRAKNIKNTAFINEDLDQSTLLRKYERELKTLRQQLQERDATSQQAGGGVDPCILLELR
QGMRRAEEDREAALEALHESSRAHQEELVVRKRFEERIQELEMMLQNGGFKGVPRTSDEY
ALRLDELDRERQVMEEEKAQVDRYKQLLLKQRDIMLNLTTRLNERDEMILQLQEEIDAYD
THIQTLEEALEALQRQQQQQQQKPEPNGSSKSHFSTPFSRARAEEYLQRTRVQNGDEGGE

LRYRSDANPAVLLTAEEKMLELLLAFPHVPSMAPQQPTIQVNEDMKRQLIELVRERAEKM
VQRQIDDYFWQQCREMELLKSQLLESEQKSNVLEQLLKGVKAQHPPFQDVFARTRRHIDE
QQEMVRKTYEGRIQALQQQLAQEREQRLRLMNEVDVLSMESRKALERCTNAAQRVEMNNV
CMALQQLEERIRTETKNGIEAAVLARVPAARDSSHGNNFNSHGGMIHVHGTNNNNGRDVH
GHNTAGVSSATSSTSEVSPAPATVTNELEGQLKALQSSHAKKEEEWRRALQEKDATVSQL
EERLHAVHVDMSEEIATLTKSLNTHKKDRRALQTIMEQRVKVKIDTICELVAAGPQLPPQ
EQIRLCNEVRVLQNLVNASIKAMES*
>TCRU_2137 acylphosphatase, putative
MSAPKSAIVVCHVFVRGRVQGVFYRKYTQRAALERGVRGWVRNLEDGRVEMMAEGPKENV
DSLVEWCRVGSPKSRVDGVEATIVSSGDAYTFKTFEVRR*
>TCRU_2138 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MVPNASKKRPSFANGPRIVVASNASGIVSVTYGGREHVAADNTDEVSERSATGHKSLVSE
SGVAGSGFVAEGDAGGLTQRNASGHESKPQLREFTAQYSGSGVSLHDCFAPLNDAKLTLR
ELTVGSTVRVCVYWVLLLLLGLCGVVAVL*
>TCRU_2139 hypothetical protein
MRDSDRRCWVRQPPQTVANPRFDVTAQHSLAAQLSHQILCHPSLHGVAATDGCPSGQHRC
SVQADGWFHRGKSTPPQFIRAGVFMCRHIHREGNGGPFLFHCTAGSTVATCVHRIGHMAH
STQLTISAMHAHIKATESVILMLSLSNGSRTILPRPYTHAIAQAAQLGAHDTSTGTTTAS
ASPDASPGLPAAVTHTEQAAAAQERKDQHGAAPSSPVVESLKSVS*
>TCRU_2140 BNR repeat-like domain containing protein, putative
MLLRGASTLRGIGPLLLVRSIKDTWRAHTVVGAAEGKESLGVVLRRTTITKGHRVFLLAG
GSDVSYEGGCWGDGGLELKLFVGDVTNPTGGKQSGRIEWGDPKPLSKLISSASHEGEWTE
FIASVGAGVAMEDGTLVFPLMAKNEAEDVYSMIVYLTDNGSIWTLSEDISPAKCLNPCVT
EWEGSLMIVDCENGRRVYESRDMGTAWTEAIGAL*
>TCRU_2141 hypothetical protein, conserved
MLQGNKASVDVDGELLGEEEVPLTGQRPPEVLRFCFGECGGHESHVTVKNVFLYSRLLNF
TAMRALKDRVPVPTREAAPTPPEKI*
>TCRU_2142 BNR repeat-like domain containing protein, putative
MVAGNYSFEVTGTAGNTAAAAKWGFFGAVGNVTNDGSSGKKIYWKDAFVVSLSDFETKHE
SLTRLIGGGGSGVKMKDGTIVFPVEGTKKDGNAVSLIIYIATEDGKLSKEVPDDGCSDPS
VVEWKGKLMMMTACDDGRRRVYEIGDKGGSWTEALGTLSRVWGNKQKGM*
>TCRU_2143 BNR repeat-like domain/Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MLITLPVYSNRRGNGKGELHLWLTDNTHIADIGPVSGNDDVTASSLLYKSAGSGNNNNER
LVALYEKRGDGKPSLGMVSVRLTAQLKRVKEVLATWKEVDDRVSKLCPSTAARNPSTGND
CSAGKTTDGLVGFLSKNFSGNTWSDEYLGVNATVKGTNGGATGYADGVTFRGAWAEWPVG
SQGENQLYYFANHNFTLVATLSVHGEPKGDTPIPLMGATMNDKNTVLLGLSYNKEKKWQV
LCGGKTTKELRSNSEPGTTHQVAIVLRNGEQGSAYVDGQRVGDASCELKNADSKGISHFY
IGGDGGSAGRKEDVPVTATNVLLYNRPLDDNEIRVLNANKISIPKLTDLKTVAAGATGVG
TARHFGANGDGSAVCGGGLLPLLLLLGLWGIAAS*
>TCRU_2144 translation initiation factor IF-2, putative
MRYSRIHLLKFLDTFYPLPSVMDACSFVKLVRKRTSRLAEFLEKEVLASNANQRSRSFDA
KVHVDIAKSLDALLSLKEKDVERVIWEEHKLTDERLLTCLVPYQMAANIIMRGLPQNVRK
MCVEEIRDEEDYYLKGITKKGHNKFIQWIERDVFVSTGLNYLRRLSPLRHARIPVIAVMG
HSQHGKTTLLDVLQKTSFSEEESRGTSQSIRAFTISASESGFSSVTFVDTPGQRVFTETR
FHAQIIADALLLVVSLVDGVQIQTLEVIKVALNIDKPILVVLNKLDLYSDPGKADEAMFN
VLMDLREAGLNVVMVHKPKDIERLRACESSTKLDAQSSKEVQNTLQLFAPMKKVDAQYKG
SKTHPVVNLKRSCAGVCISAKKRENLDLLWSLIELMSSTLSPFCHSRMGNYTSHSCSHQA
VILESSKHLFDEESFRLRKNVQRLQKRQDATNERQKLRLEKNSVSARIHSALNNDRKKLQ
SSNPTSTNCLVLTVIVREGCITKGLLFVADQTRGRVDYMIDAAGNFVDKAYPGTAVIIID
VHSNTGCPGVGTHLLSMPFVDERDRVFEYRRWLQWFIECFPNRLNLLRPRGMDVSFAHLG
DYGQIGNTHCLEYQLLYGPPQNAFSTGINSQSTEELSINGSKPLEKSIAEYLSEKNLEDR

ERHNGSPLEDGSHQKILMEDDLEVTLQTTWTQLQPRKRPETQEMHDEMIKSCIQIGVLFK
VDSWHSARMLHREINRLGTRKVAFHVVGMRFGELTADDIMFFGRAMKIAVCYRTPLGLST
DLDQYLEINDTWVLQTDDITEVILFLKWCAVALHKEHAPDDYGVTERSHRSYLVLMKDKS
GKSPGKKMDQQKNSRHRRLLVTPNF*
>TCRU_2145 IQ calmodulin-binding motif containing protein, putative
MDTAEDGDYLQFATKLYAASKPFLAIKAYERAVSEVEAAAAATSDPKPLPGNKLGSGNAL
FKDFILHCNAFGVKAATSDTKMAGDFLRLGFKELQRRNYLQGDLDANDPSQFFIPIQEDR
GIAFLVSLILSNWACLLLRSGNTREAAAFLQLALTNSMAEELTRVVLLNICAVDVHNCLF
SQVRENAMEALFEDGETEEEGQEKMDKDNAAREDVNGLLCAFAYHNVAIAEEYLQPQEAE
SHYNKGKEMLASSPYQRWSSVIECARRRFLDIVQRRRYEATRRREAAEAEMEAAKQVEAT
VRRKVRATWSATARQPSAKPGNRGKKYKKRISGLTNDTKDESIELPPISEYLRQKMQTQG
LSNVVVPILRVVDVRKFVFGGIPAHEDSFFPFRESVNLNNVAMVLLCEETPLQVVDEAEL
KDTGPPRKTIWTPFVPRRDDTLIIVPPKPKPGAVLSRDAANIAKSFMPPPLSEKSIENAQ
RSVTAFKKILNHRLLMLLRAENAFEEKWKATGIVKRALVAFNLAQDMLKLKETIKWKRET
RAILENASARRIVRFFRLIIERKSNSAPIMREARVKYFEEKAAIALQKYARRWLAVKELR
SLQRQRRAEILRVMKIQSTYRMHATRSRYIAYKEEQNEALRFEKETVAREFAAIQIQCAY
RRHAYRLRRWYEGGEKRQFILHHFRSSREYYATLIQKTFRGFLVRRVYGPAVYAKRCYGR
NCYRAALVNTCATIIQSVFRGYRVRRATRIPLQQHLRQCVVQRAREKVESLRRIQNEAAR
VIQCAYRSYSARRVANELRTLRERERLLRRNRVYPSFRLEEQVY*
>TCRU_2146 High-temperature-induced dauer-formation protein,
putative
MGTSSSTLEVGKAIRLLLVDTPVDDGIFNLLLNTALSKSELERALPFSTLRVMRHYYTRN
FALLLFKCIEVVSQIRNASLESASDVQSASQGLQNALCLMRRIIPIAMEGGDTPCAAEEP
EKRGAPASNPPVEGANLPAEEAKDEKKRTLFTATFVRSFFEENLACNDAQPEQMLPFLPG
QNTTLSKFVGRLLVDCCFIRGLTLAASSLPAKESESHPCVDESLLWYPGVGGKQVEGTST
QPMNGTMHALRQELLYTLTALLSYPLFSPPGTRDTLFSEPLLNVDENPLLPTLVASTLNA
ILAYKPFGSIPYTSHWVGPEEMVVLMSARFLSALICYPGALLDGSTQTRHTKSPEESDKN
EPKENVEAKDREDGTTTEQLNSPPLRIVHSARDLISAITPEEAKYVIERLKNTIGLKVYS
NRTVLPDSQRCFITQDEFMMLLWRLIELSPECQLAFAQQPAALNYIVPFVDYALNAKRDP
KYFPHLQLVLFLLLRLSETRAFCLQCNALFHERIPFEFESFVGTYNDLLIIMLCSFILLR
HELIRPLHVTCSAIISNIAPFMIKISPVTSEKLGLVFTSVSTRYLAYKALFASNEVILDD
AEIKADQVVLLNIVEAVAGVLQYHEGAAATLLAAFIKHKSLVGEVSDIFLAEGSNAFRVR
LTSPFLIGTVRDAITAVEGAVAAAEEAGIMDIVSVICKTSLVGALPTPHRIIVRRLYSNS
SMEQWAMATTWSSLYMHTPPGTFGGSKSIKMLRFF*
>TCRU_2147 Zinc finger, C3HC4 type (RING finger)/EF-hand domain
pair, putative
MPPLILATECNEELRCALCLDSWKDPVELVPCGHIFCAVCVRGMNTCPICRQSVANSKRP
NRTLVNLALAVPVKCASCSWTGTREQGNSHTCRTDTKMASVPSALAPGPKYAFVEPTSQE
PWHQFGLSREEYDQIMALFVFFDNDESGGLDRAEVGRLARWLNFARTDHDIDRMFFLMDT
DGSGTLSLNEFLTWLSHNRPDPNALYGLSQSEYNTIMMQFRLYDTDQNGLLSIDEFARLA
VRLGDVNNIDSGRRLFRCIDTDGNGVVDLHEFLTYRVRTRRK*
>TCRU_2148 mismatch repair protein MLH1
MRRIKRLSDNVVNRIAAGEVVQRPSAALKELLENALDAGSTFIQVLVRDGGLGLLQVTDD
GHGIHRDDLPLLCERYATSKLRSFEDLSRITSFGFRGEALSSISYVSRVTVTTMRRVDKD
EASSGTLAWRCQYLDGAMQGEPTPCAGNPGTSIRVEKMFYNSAVRRRALNRPSEEYSRIV
ALISRYALAFPHVGFSCRREEGSGGKAEVFFPKDSSSLANIRLFHGPAIASHLHELKCVE
AGAGGGSPETVLAKGGEAGEDCFLITGYTSGMALLNRNPYLCIFVNNRLVESAVIKRAID
TVYSGILTGGNRPFTVLFITIPPDRVDVNIHPTKHEVCLLDEEIIVAQLSESVRLAVMES
AARRQLDTRHILSKAAALAGDRGAHVSQPSPLPSSIVVAGIAPAPCTVVRVEPQRGALDA
YCRRMPISKKEEAGEVSSENAVEKQRPETCSHPDPLTAVKSEETIIQEEQHAAGTSIVCT
ASNEDVTASLITSIMKFGSTDAADRDEGEAKKRLKEEEREEGEEEEEELGYVMQQFKRQR
KEIQRAAGIVTTAEAAEEEKEGAEAVYASAASSACEDAVEPVPDERGDLLLTSVSTIVSQ
IRQTTSPTVQSLFEKLVYVGVINGHMFLAQSGTTLYAVDTLRLVRLVVYQRIFMRWSIAS
LPAPPQMLLQEPVRVTDLLWFALQHDVPPQTDVSLAESTQRTVRRMDRCLRQWRCMLLEY

FSIEITHDGYLLALPFGLNSSWPPSPRVVPLFIWRLAAEVPYREDEAACFTAIARHIADT
LYGLRLHDAWVEPRVSPSPGVEPPEGGSVPSLSDAIRFALLPCVTSLKLFVPPADALIDG
TIQTVVSVEELYKVFERC*
>TCRU_2149 kinesin, putative
MYADDTGGETPLEDFSDFPVERSGVFSPLNKMHLPISRRRMVLPVVHIRTRPILPYLGEG
KNQRHVWCLDHQKIVVRSNKLVPSRCRTASPLKSNGTPRSAPTSPFVSSPPRQHSLSGWL
SESLPPKMLFARKTPRKHHSESSRSRGTTASATKIGNKTFASATPEVTPLNNSGVIRREE
HFNFDFVHGEDATQEELFEESVLDFVDMALLAQSVAIVCYGPTGSGKTYSMMGSTPGQSL
KKIGKVVPAVDGLLLLENRPIFDSKNRGKVVPLAERLSNSQRSNLTSTGTALSDTAALVS
TTASTAIPVRETLTPAVKIEEEQQQPHRQQQQQRNFISPRRGADANDMEGSSLSSGLSQF
DLGFSTYMDAFGGTRNEMSLTGISSGLTESMTVPDEGNETMGLLPRIVLILLERRGERVV
LGQNEPSVKATPGNRSGNGKEKSQETQKQRHNVSLTLKELTLYGVELYMDEFYDLLDPAK
RAIPNISDIGGLDAFCQRLNIPNSLAVSSSCGGKRASGGGTGSTSFRGGGVRVSSVEDFR
RCYKLATRNRVMKGHQRNDRSSRSHAVFILQLQFDLADSQNAGSNAVTQSIYSYVAMVDL
AGSERVKETKVEGVALREAKYINKSLSAFSAVLLALYQRSSHIPYRDSKLTRLLRPCLEL
GRVLVLVHVAPCSAEETISSLKFAEQARYTNVQSHSLLNAATEVVALFDDMTDPHAEELM
ETYHRTEVEYAQLCAEVRLAHLSRETPDGSLTFAESPGENSFTLQELAQNKKRDYVIGTL
VKRHMHRYKALEEKRLQESVAEIEREWAFYVENVKRSRKQDMENLKLSIEKLRSANARLA
EENSKPVLRDDHVMAIQQRLKELSTEINNYAREKLLLMEGMRAIRQRLALQTDLERCLDQ
QLREFQQVAAGGGDNGARLPVDSIVDEELGEIYHQQLLLSREMSLLRRESTCFVRGDRIW
EGIWARVMRQELLLAVSIDMEMMEGILLRPQSLRWVLEANGMTPDAARDVVFPTSSVARN
VKILLDTLETLKKQSASNPYGSGESDARDPPLPHVPLLMSNGDEVRPVPTLIGRYGDEAK
LQEAAVRKLVEEGIFCEATFFSMGVEELVRRRLPATGLMQQTNYKVHWGCLRLVHPPKDT
SSYSLELFQRTYSGSDKVRDRRVISIPLSEPQLRIKLHVIEAEGIVHTSPWDDGSVATEA
ALPLIALELQGVHPVTNTGAQQYQEREKDVKSRGHTHYIAPCATDTGGAHNGNGLLANGA
ESSSARDFLLSKRLDCGGELLLPSGCMAACEEGSGFFLFHFPERIVARKTRTEAVECIVA
ALSGLTLPFFPSASRCPSSSSMNADTSIGDISVVTYQHVPYLLLSSNGGSLRGGDAKGLP
VLRRVGVQSLGYFSATQICFYFQKEDSRRMTADGDALSRFPRSPLGRVAMPLSTACAMLG
RLGALTPFSGSGVGSSSNGHAHIGSNNAGAAQSVDETESMMWRMQQLYAFRRKTRARVRQ
QIFDAEDIKAELLYSYSDSEFMRGSYIKDVLKEARELIDLQQPQTSAALALRGMIRATPG
ICRELCGAVVPWTLWHWAHRWKALQLTHSHQQALADAYDMEDDEDSMDGSEGAGRLSMMA
SSGTPRDDGGQAFIVFEELPCFLACME*
>TCRU_2150 PH domain containing protein, putative
MDSDEDLQLPPPKTPINLDDSDDDLPPPAALAVKGPPPVKPAGPALTSPKNKPVALNKNG
VSSPLMGSPLNNTAAQRGAQYLDPQQQQLPFTSETRARVNPAKVYKEGFLFKQQPSWPYS
NQKRYCVIKNCRLYYFDSQESMKEGKPQGVIDLTSAKLVDPGNEAKLPSSFGIHVASDRQ
AEGGGSVKKERTFTFSVMHAHELGEWKAAIQSVVGDPAEDEKVHWFEKMVQGVY*
>TCRU_2151 Protein of unknown function (DUF3682), putative
MAMMMTGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAI
TVPLRSALPITAVEASTGTDNAGGKKNDPNSSGTSNAGVNGSDPAAVTGRGSGGVPGGDS
DASSGAGAPAAAGGGGSGGSGTSAGGHATDSVPSDAAPPPANAAGHSGGPPATAPGVNSS
AGSSDGTAGSSVTNPSNTTGESQTGDQSSAAAANNSSLPEGTEGTTSGTGQKEEEEEENE
KQQQSDETQVQQQQQHEHPAESGEESAKDKNALRTNATANTGDSDGSTAVSHATSPLLLL
LLVVACAAAAAVAA*
>TCRU_2152 hypothetical protein, conserved
MLVPHGRVSGLLFTVNPRQESKALRELQLYLHPLIADLEEAHKRVEEHVDDRGRCDNATT
EKQSSSKMSTDAEGKITPSTSSLLAAELAEYITTRGGQRRHEMRRIPMKEEKSDVSDDED
EKKSTDNNNNNNNSDILLNRSSDDGSHDTDAGRQSSARKRQRHETEGSKRSVINSLRWLA
PLETGCKGHLMVSIPFASQEQGENEERETGATTAETQIVKSEAVEASTPRTASVSGAASR
GQGEPPHSILYNPLVHIVVERIFKDIEENPRPLLRNCFRLMPCELTCCPTLPEMREALGQ
LVGAHFPPTKGPQRLHRVSLAFSVKNNTGVENKKSYFHAALETVFPVNRFVLIPAARIKG
PDGETEAVFCAFVAHATCAMGVQRLFSHRGGYNLHALSAKQLELSSSV*
>TCRU_2153 Mucin-like glycoprotein, putative
MMMTACRLLCALLVLALCCCPSVCAAQDVPAQASFQTMTTTAEKPGRKKKRSEVLFKENV

ITTTTRVVDSKPEDDTRGTATTLPSPSAEGERGKGKTGTSGVVPAAEQEDTARDGQTLTG
PDSYSIVATSTLQREGTDGTSGTQSRTSTAAEQATEEAKDPAATATTKTTTKAPSTTTTT
TAPEAPSNTAMNTEAPTTTTTRAPSRHREIDGSLSSSVWVCAPLVLAASALAYTTLG*
>TCRU_2154 protein kinase, putative
MEESHPSELQLPAREGDEFKGGGDDRGGEGDAVGCTQEAGRAELLDYKVDWDEVVGEGSF
GVVYRGRHVSNGTEVGVLTLKGSLELREELCKEAEKGVMLLLNQWPGVIQLLGTFDIAEK
DTVTVMSILQLRGVEDMQAFFMRDVVQKEEKKVKGELEDDPASIAPEQSSSFAGCCGVEE
GACSRLFNENEAKWKREEEETDKGEAKTHRAEEKKYAAAGVAGEKTQSLPPPASLAQRQG
GALSVGKYMVQLGSVLGRGKFGTVYRGWHREEGYEVAVKILKGPVSKRAKMLIEPRELGR
LQKLDHPNILRMFGAFRHEEKDRNEMTLALVLELCQGGDLKEFLARNDPLSERQAKHIMR
QLVDFLCFLKSNRMMHRDLKPANILLTTTNIDRAVIKVADWGMAKQIPTFGSSICVPDAN
VMFESAVGTVAYMSPERLSRELYDFQAEVWALGVIMYELLFARHPYLHSASSVRTPEELL
NAITRAEELEMSCNVFLSENKRKEGNVFNQHHSEVSPFSRECYELMRHILDPDSKTRYTI
EQVRAHPWISQPEKMRATEEVKAVTNTVEPAVAHGENLNTVKVIKAEDVVAATTKILKAE
ESVTTEMAATGPSAGVTGIPLRVPSSEDEVAGPLHFQGLGSNWSPLQRQQIIYQAFREYF
YILRYDVLEAESDPGRGLVLLSYAWELLRAVARAALLEEHRLSGGTVCLDASSSICYSAR
SFSRFALPDDIKLMENYIHETAQRLKRNLPCLTTHISMGAETLTFSTGSMCGMEASGESL
TPLPANPQKLTYPSAHTLLFERTVSLIRAAATEELMLSDSHEQDNVMEEEEVRPEGERYR
QKRMYEKAIAILRLILQQVVVRCQSSLHYPFPPVVTDTEESNGMQLLTIPLVPLEDEADQ
RTVQALLHTVEKHYRRLVNVK*
>TCRU_2155 retrotransposon hot spot protein, RHS3, putative
MWRCCGRLHVALLRRRWALTASPTGVAVRLHDAPTAPPCECHAQRHWDCGTRQPRLSFGA
SGTCWPQFGGASGMPHRTDVVMAPRRGSCDGSVAAARHVVESKVWPQWTMSGTNMRLSDF
LWNYVGGRGAVDEGLQCDDGGVCSGAG*
>TCRU_2156 hypothetical protein, conserved
MGALPSRETQRRGVYSHRHGRNRRNEVVLIPLTAEFFPDEHSPLFERLYQARHHRTAKYY
YRAVRPANTDWDSDYYCQTIAHAYGLDLSDPDGPDKDGLFEKSFTDSIEGLYHRLIRETE
YCMCESDEELRQRYMVQLQQQQQHQRKQQQQQQERRRSTRQFPSSTHEEYFGTGLNAYVS
GYMDAVMYMQGKEQHTHRNKDGTHVTSPAAFYLRPVPCAIISRYDAQRPHAEEGVEFLGT
TVKVLGMFGLFPTTIPMTVNGETVEQHMLKATMFVDKDVGDQILGNVVMLAVHMYVRQCL
EARIRAPYIPMVPFILRVPISNIPILQFVREMRVRLQSLLDAGTPRSGARPVRGGSSGSG
GGKGGSSAVGGSGAASTTDCADIGDTYVGKFDADAFLFEEDIPSATSPRQLFAEPSEMKW
LRNHTSQNTNPEGTLPILMMSGVNVQTTPLKHLSMTNMSHVRLPAWVTEASNEGSLPKTT
TSQQQKQSKLAFLLACRRSRFRIWVEDGRLCVWASAAYARRGCLLLAQQLSVTVDSKAFP
LPRFWNYRGLLRGGMTVPEPMLHNDVFVVAHDMPSVGLYQGDILRCSTPREIAERQKQQQ
QQQQLLLSQIKHSGGMSSTAATSPSSEAASTRRGFSNYGVLSAKEPPSPSEQSSQKANYT
SNHTSNIFLQDPKEAPVGAFWVHVSFDRENSGPSNSEKRRRGSAPEAQQCDFISYRQTNV
EEVLLSWIKKICIQARDFLEPDEHWVRDPITRALVHVDRYVIRRVEHDGMRYFIGITPRF
VGQQRRLEKVLVELKAMQGEDPSYACGDGNNDAEENSEADEGSAPEQASMVHGGDASVAL
LVEEVEEEEETTIHASEAVPSTTQEGVAPCEECNDMNVRLK*
>TCRU_2157 J-binding protein
MLESAPPQLLPKKGRLEISELAPQQRTIRTAEEIETAYNEAVRKHPFYDNADHTIDFHDA
TVFRDARGVVGGVFLPGALPAFAATMAADVLRPAAVRTSLRSNMFGGFAPLSGIAGYFDY
RGSPVELKCRKTSFTYENVHSWPNVFPMIDYVSAIYKAVFPEQWAAQDAAVPDIVRIHGS
PFSTLTVNQQFRTASHTDAGDFDMGYGLLAVLEGKFEGLSLALDDFGVCFRMQPRDILIF
NTHFFHSNTEPELNHPRDDWSRLTCVCYYRAALGEPACVAEYERRLARAKEIGASPPPAV
DAILQKDNGNNFNKPAPTFPYLLTPFGGAASVCSLHCCTAKLLRLHELLLENPTLEVILF
GESLRTDDGLPRREKEQLISVHLPVVVKMSPSGGFSELGGALKAAEEKQYFFEEKYLADE
LGPDLMSMWTQSRAHWLRLVKEDWERLCRRDPERTKFTWNNSSAMNAAFFDLCEVAKQMM
IGLLNKETPSSAENHSFWILFAAHLNYACTTENGMPRDAVGMHKLNVKLKDFHFGGTRYL
KDMPPEEQERRLERKKRIEEARRRGSSAHETHTDNWLLNDTFDYQQEDRKVEFEENGWMT
PEAYVKHLGLKPCGDVTAAASPTEPIHVLVVLPRPAAATTAKDVKRDVPLATSEESIRLL
MNPAAQRVLRGKARNVALPSPLSFGGVKITVLFDGDDIDCIHPDFVILQHLLATIEEDEA
AKARVKYWARVARYCVFVVETDVRDRRHFLLREEVRVAYEDVAEDCFRSLHAAAYSTKYN

RLRTTPSLIALCNRKNIGLRFKFRGSPLNTIALVVVGERLD*
>TCRU_2158 hypothetical protein, conserved
MLQTKDSSEHEEGETISSDTQRSASKEIPEATTPLSASKSGSGIAGSTVGKGGVNNPQPP
AASVTQHDSEGDTGPAALPASTSELQAEEIPNAGIIATTNDDDSDSSPAASTAERPTAGT
RSTQASGDASDLEQSNNDDVNDDVAHKDKTVEFETASGNRDTQADNDERYTTVPENATNK
TSNTEITADSDSSTAVSHTTSPLLLLLLFVACAAAVVAA*
>TCRU_2159 Endonuclease/Exonuclease/phosphatase family/Endonuclease-reverse transcriptase, putative
MEPFTWLPAERYFYPLLNSIGAYQRYTYRLRAVCDVQRQKLLLSGDIEQHPGTIAVLQMN
VSCLTPSKLATLMAQGADIIAIQETWKSSEQIASMHSGDYVLYAQSRIGKGGGVAVLVRK
TLRSKRIPLTIPQHDTSLEVVVVQVALDQNRDLIVASAYMRPPPQVTQSFRRLVNCLPAS
SPLLLCGDFNMHHPQWEPFLETSPSEVAAEFLELCTDAGLTLVNTPGEITYARGTRERSC
IDLTWSKHLTVSDWSASVSPLSDHYMLTFTLHQAFKDTIPSAPKFFYSWGKCKWDLFIKD
FDAQLPAYDYKKQSTGIKAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERIATDSKA
RHLQSPTPDREAEMQRTRSQLFLLLRERLRNTYLRRISKLNPGEPLAWKYISGRKKASLP
SPTSILLGGGQHTYKTARRAANALNRIFLPFHPSHKAVRISKGINRQSASLNINASFLFG
QQNNNESAATFTSGSSLSSSSEPQDKNEAATTSGLVAHLHSPLDAPFNRTELLAAPRNTP
YGKAPDRMKSTVRHCDMFRQRASDSFFVALTTVGRPVRSRLSGDALPSFHS*
>TCRU_2160 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGLSVVANGGTDDLVSGRDEKNAEHLSSSDLSLPVRQGEPT
AAGGGRGSTNSQEGKEASMSNTGIRLPQEQEVKLDAAPHKPTGNEYENKGPTEAGADTRN
QPAPPPPPISLSEEEDDELTKATQDQDSPVEQESTQNNEILQEEPGNELNTQNPLPQEQH
TSEQPQVKQEHGKEKQRSGQLEQREHREEPKDQQQKQEKQDEESIKHEEKQQQQKDEIQD
QQHQQHEHPTENEEESAKDENVVRTNVTAAKGDSDDSTAVSHTTSPLLPLLVACAAVAAV
VAA*
>TCRU_2161 Endonuclease/Exonuclease/phosphatase family/Endonuclease-reverse transcriptase/Reverse transcriptase (RNA-dependent DNA polymerase)/RNase H, putative
MKQYENIRREDYPGSAGHLNVVPGSSTLAREEAKRLLPICCTRRGAGRRTNGSEGHQMEP
FTWLAAERYFHPLLNSIGAYQRYTYRLRAVCDAQRQKLLLSGDIEQNPGPIAVLQMNVSC
LTPSKLATLMAQGADIIAIQETWKSSEQIASMHTGDYVLHAQSRIGKGGGVAVLVRKTLR
SKRIPLTIPQHDTSLEVVVVQVALDQNRDLIVASAYMRPPPQVTQSFGRLVNCLPASSPL
LLCGDFNMHHSQWEPFLETSPSEVAAEFLELCTDAGLTLVNTPGEITYARGTRERSRIDL
TWSKHLTVSDWSAPVSPLSDHYMLTFTLHQAFKDTIPSAPPSAPKFFYSWGKCKWDLFIK
DFDAQLPAYDYKKQSTGIKAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERMATDSK
ARYLQSPTPDREAEMQRTRSQFFLLLRERLRNTYLRRISKLNPGEPLAWKYISGRKKASL
PSPTSMLLGDGQHTYKTARRAANALNRIFLPFHPSHKAVRFSKGINRQSASLNINASFLF
GQQNNNESAATSSLVSSTSLISCISEPQNNNESAATFTSGSSLSSSSEPQDKNEAATTSG
LVAHLHSPLDAPFNRTELLAALRHTPYGKAPGPDEVYSEALRHISSKGLRFLLRCINHSW
TTGTIPVEWRRATIVPLLKPGKSPEVLESYRPISLTSIVSKVAEKMVLKRLLWVWTPHPH
QYAYRSMRTTTMQLAHLIHEVEHNRNHYFQVSLPKKSGIGNQLHYRPHRTLLVLVDFSKA
FDSIDHRVLSRLLANIPGVNCRRWLRNFLCGRYAKTRVGHRHSDRRPMLRGVPQGSVLGP
YLFSLYVHPLLNLLNSFAGVTADMYADDLSIIVKGQSREDAIPTANMVLQKLHAWSQENG
LAINPSKCEAAWFTLSTHTESDYDREGKWPLVVAACQIPVMTMGASRTTKLLGMDLDPRL
TLNVAATKQCAATSQRISQLRCIAHKEAGPSPHDLRTFVIGYGASKLRYGSELIWAVATD
SAKNEMQKTYATLARIVSGVPSTVDTESALLEANMPPLHVLCLRERLSIFENTRACQMDW
MRRPPPEPPPRAGFRISPLSRDELYAFVDAYTKDYGITESSPREERFFRSSIPPWFAASA
HRVTIGVELPIDHSITDEEELIREKRRVSEEALALHSHRSWMLATDGGVDVPKSAGVGIL
LSSLNSSEIIEKASINCGARPCSYRTESRALLLALEKLMIPRIRHRRKTLLVVTDSQSLL
AALNKGPLSQTDWTEDQIWQRLLTLTCAGWSVHLQFCYGHCGVHANELADQYATQTMESG
QYTEQGIAPLWHTDLLTCFTTQLTNKWRSTIRQDTHRYLLCGTRPSDLSGKDLITQEVLH
RQELVHLARARCGESELWGRLYWAVRDCTNQCRFCNISPEQSAYMRSNNDPTAPGTDTVP
PSAREEDVSPVSRRTLTRRRKEKCPHCDSTLTGFSGLVSHCRSFHPEHPPPLLEFTDFCD
MVFPTRRSTAQHRSHCAHNPDATRHRNSSARRRSLLPQDQPASTSTPIGRQETLHHLLLE

CPDTLAVRQRLGIEQDLRTESSLNGSCFIAGNFCRCSTTSSALRWHCIARRAGKSRKKNI
GPISREGDDAAASSLLVKRKDELILLYEKRNGDGTYSLVAMRLTEQLGRINSAVKTWKEM
DSALRVPTEGLVGFLSSTLDGTAWKDEYLGVNAAVGGGVTSTESGVTLKGSGAKWPVGSM
GQTVAYYFTNNGFTLSATVTIHEVPKAGSIPIPLIGARLNDTASTVLFQLSYTSERNWNF
TLHKKDFLVKPSGDVGNWETNTAIRVTV*
>TCRU_2162 hypothetical protein, conserved
MQHDRALQRRHIRHVDEGVGHQTRRALAEATNPQLRAVRKHAVAQRHVQRVSERVHQAQV
HRHDDRPAEYHRVKARRRTPAASRHRLRQRHATHAALRIATTATGPRRRHVERQARLAHA
AGTAAAHAVGERSRQRIEARQRSRTAVARHHAHGGQAGHAVVAAAPQHPAAGTVALHRHD
AARDRQPGDKRRASGSAARNRHGAAAQRHTRQRRHRRYLAHRPHVAQLQPPAGTDRPTVA
SHQRRRDRPLDAHKAQHRIKHREALAKHNAAAAAHNRHVRHGEYRVAPQTEARRGRHTHR
GRGRTARRLQRHAVKHHSAQQQVHTATNVHRRPARLQRPQQSVAHTQLRLQQRGRVQHKR
RRHRIRQPAQLGVAHRSRRHNRRVTDRHVRVCRQVVHKHKRAVAPGQPAHAHLQAPVTRR
LAAVAPHVDLRTAVAHTIPQFDAQRAGKHRRHVKHHSHAVRDVHAVHQHRVHGAANRDGS
VHRAAPQSQHHRMHRGHPRCHSHKRQHNEQRHTHSRNGPAPHTVPAARTRTRRTPHPPTQ
TGTNRALVVCCTRPVDRSSCPAKPVLQMANQETQFR*
>TCRU_2163 protein kinase, putative
MPPKRPVLENLRIDPPEKTVSITDTLTLVVKGDGGLEMRVKESFMASGPAFPAQAAKQKD
DKNDVSMEKIRFEDLRTCQELGKGSQGRVRLARHLPTGKRYAVKYIRLEEDTDGMRQALE
SELRQVKALMHKNLVTSHEAFFRDGRVYIVLEYMDAGSIADVLRRHPNNFNEVMLAYVAR
ELLQGLEHLHASKVIHRDIKPVNALANSKGEVKIADFGVAKRFSGGDVETLSAQGSLIYM
SPERIQGQPYSFNSDIWSVGLTIAECALGAYPFASMKHSLYDLMQAIATRTARVDWTADG
REHSSELIDFVDQCLRPVSSRPTATELLHHPFIQKAANVDPAEAGRWFVTQS*
>TCRU_2164 hypothetical protein, conserved
MPPKENKKNSKSDKDLQDDEQQLNEDIVKMGIRLSALKAEYAGQLEEIFGLRREKKELEF
VCAKFEDDLRLATLNRVDVLTDFVRQYKTEEDEKIRTCTDLDETLNRLEEEKIRLTEKAK
KAETEHEDAINSMKTEYDSFSEVD*
>TCRU_2165 hypothetical protein
MHTNLEENASTVSLPVHFDTHGVASYEAEGHGAGDLDCVGEMQMDWKMGNSLHFCGKDAE
LSPVNFPFLSHHHKSSRVTDWEKLFQIESELQYLGEEVGFFLQKLGRSLVGNDPLDSVDD
TVELGEALQMVESRLNSIFAGCDDSGMSQRFLSKDALHKATDCSRALMAYRGVAEAAESM
KKLLTGVFNYRVLLPFGADAMKRAREVSLLLDDMEKVLDSLEARVETLRELSETRLDVLK
RGLDDLSK*
>TCRU_2166 cullin, putative
MLEEDKEAIRRMKADFEAIAELTESEFKLNTGFARRMNHYSAVYTAATRTTNMRSFSDAF
GYYVDELLYTDFQEMLTRYLLKYRDLQDSSQMRLFGKILKLWNHYKVLMKWNMRAFAYLS
RFYIVNCSKPSLQQVALNIFLEQILKKNVHVISRVTQDLLCLERNGESVNRDQIRGAIEL
MSSVSVEKKDEIYTEQFLRPYMALTKSHYEGLVTEWSKSFAPSELLRQIEQAHNEEKARC
MCYFLPDDRKIIMTHVEEVLLESPATVEKLLKSDDGFVAALRGRDEALLEKYYNLLSCRT
NCLAYLSNLMRDEIIAEGKERLLQHDSQKKEMDFRSCVGDMLQLQDDFMQLLARCFNSNA
IMMKSMREGLEKVFGGSVHASRGPQRSVPFSELLAYYVDAVLQGNEGSTVEENLEKAVAA
LAYVTDRDTFLAHSRELLAQRILFPRKKMDEATERSLIQRISQRCGVSSTSYLEGMLHDV
DIAEGFGVTEKLEAVGKAPNFAFSVLVLKKGIWPPRIQGECFVPPRVIQEKLSAFQKIYL
EGTTGRVLTWSYSNSSGDVCAVFKKGVKILSMTGIQCWVVLAFNELNELTPNDMMSLFGM
SLEDAKPALLPLLKCSILRGESDATTIQPQAKFFINEDFSSKWKKVRVPMPTCRRDGLLH
GEVIAKKIEEDRRPAIDACLVRIMKSRRVLSHSSLVEECHQKLSQLFSADQKLIKQRIEE
LIRKEYIERDHKNPSVYQYTA*
>TCRU_2167 TFIIH basal transcription factor complex helicase subunit, putative
MRLFIEDVLVLFPYEYIYPEQLEYMTELKKGLDQGGHIVLEMPSGTGKTTTLLSLLIAYI
HYHADEKRKVIYCTRTVEEMTKTMGELRKLLELWNTDELGSNRPLRGLCLTAKKNLCIES
TVASQRYPEDVDAGCRSLTAPWQTSNRCAYFDNLERIPFELPPGAYSVEDLKQFGEAHQL
CPYYLVRKALRVVDIVVHSFLYIVDPIVAEVTKGYFNENAIVVMDEGHNVDDVCIEAMSL
IITKEDAAQAKENVKQLNAAADHLKATNRQQLQDEYDRLVNGLAMVEMARSVDSMMMPVQ

APSIPSEIAEEAIPGSLRQANHFLSFIQRLVDFTHRVVCRISRTYVADPLTFLSKVRDEC
AVDIRHFRYLTERLKVLMNTLQITNSHKFRNVSLIAQMYMTLSTHYTDDRYEKPGFVVVC
EAHDPTRPAVPDPVIRLVCVDASLALREAFSKYRSVVLTSGTLSPLDIYPKILGFTPVIA
KSFQMTLSRKCIAPVVVTRSTESVNITMEEITSSFVVRTNPLAQDIVSSAYEDLLRGLGK
TVPDGIVCFFTGYQYMGEVLLGWHRSGFLKELAQYKLIFIETQSVEETSIALANYRRACD
IGRGAIFMAIARGKIAEGIDFDRHYGRAVVMFGVPFLPPNDEPLRQRICWMETCLGIPGN
EYRNFDAMRQASQCIGRVLRNKTDYGMMLLVDRRFALNDKRKKLPIWIQQCLKENTNLSV
DAAIAVARGFFKEMAQPWEHKKDLGTTLFSKETLALKGFLKPSKRSFPCRVTEKCSNSAE
ELVHGEGDAIRAVKEPEHRKRLRG*
>TCRU_2168 NLE (NUC135) domain/WD domain, G-beta repeat, putative
MPVRKRQRRNTVFTEAGAVDEIEEKDKNVMVRLVDEKGVLTGAQLLLPVTATPKQLDELL
CSMLDESARGTPYAFFIDGDQVHDSVRDSLFRRQQEAFVDKMMKEGRRFRQQDVSKLEFE
LPEETVVDIQFKPQAKFMVRPVTRCTGALEGHSEAVLVVTFSPDGEALASGGGDKEIRIW
DVYTLTPTEELKAHTSWVQVLSWAPDGKHLVSGSKDGTIIIWSHDGMYGNFKGKRHKAHS
SYLSHISWEPLHRNIDCNRFVSASKDTTLKVWHNVTGVQFSLSGHQACVTCVKWGGEGFI
YSSSQDRTVIVWDASNGTPRHILRGHAHWVNFVALSTDLVIRTGAFDHEEKKFDSREEMQ
KYAERRYQEVVTRFGYHERLISCSDDNTMFLWAPQEQTTPLGRLTGHQGAVFHIQFSPDG
TLIASCSADKSVKLWNAADGKFITTFRGHVAPVYHVSWSLDSRLLVSGGRDSTLKLWSVS
KRELVEDLAGHCDEIFSTDWSPDGQRVATGSKDKKVLIWVH*
>TCRU_2169 hypothetical protein, conserved
MTNMETTASAFSTASPIHLDCPAACPFGHGANNGDNSRTDSHDDSMHRGSSFPPVISHNL
CDELGKCFMQPPIALLSRRRYQDPAVMRLHAALAFREMRSSANESPEPQVSSSWTTNSAA
SPKNSLSIGYDDDAMSSFLSTPANGSPIKFFRRAKSFVFPSVRSSASLASGDEVNHVSSV
VETTTKLKNCPFMNCYWNSQQQRQQQGIEDGQEGLIETEKQEETIEGVQSPCFVFDAMAD
PSQGAERGMSDSDVKFRGVPTDSSADIVAAWEMDDRERKSHDVDDDAALSHHEDDEVVGV
TAEGNFIYRRDIDAEGSRFGRGNVQNHQDDCPFLDECRDADTFPAFIPTAPFCTPERNIF
ATVLSDRAAVPNSHEERVGVWKNAAAASTTASLTNGAAFPRGGSIGRSRQKKTPEWTPND
AEWCSLLLRYRVCENADETEYKELISAVNKWHEVRLRYPMEALERRLREGESYDRPPFVL
RW*
>TCRU_2170 BNR repeat-like domain containing protein, putative
MGRPQTTPETDLFASHEGDWTEFIASGGSAVVLEDGTLVFPLMAKDEAEDVCSMIICSTY
NGSAWALSEETSSAECLNPASPSGRGHFS*
>TCRU_2171 Concanavalin A-like lectin/glucanases superfamily,
putative
MRWWRNAVKDSDGLQVTRLESRAIWPVNTRGDEVRHVSLSHDFTLVASVTIEEAPNGNAL
PLTAMLANTESNHTVGLSCSHKKKWERMCEGKTTTRTSTWVPKEEYQVALMLQGNKTSVH
IDCRSLGAEEVLLAGGRPPEVLRFCFGACGGHESHVKLTDVFLYNRPLNSTAMRALKDRV
PAPTREAATTLPEKIRVVDSVREHVAEDITEEK*
>TCRU_2172 hypothetical protein
MSHANSTVVVIILILGLLLLAGTSDGQRMSLPRETYPRPAKDGVNPAAMFLRWAQLVNSF
VEALLNAAGPATVADKLKRNAPTDMEGSELRAISISPNYLKALQNGDVKRAVDHDDGLKY
LLPPKRTLPPHSCWSGYLAVPNTTNFTCGIDGSKTADEYSNMTDYQRAGCRHDEKVEAVC
LCPIGTVWVKRRFDREWVCYPRLLLVSARLEDKHICQDSLGGSLGLRSSYNPSDFCIHTQ
RKATLLFNINVSYRWTENDELADILAAKNNHLVFGKLQYDETYITLLRGISGLPDVLSRS
PKLFRFGVTPNASHLDAFGVVEGHPLQRDGAFEHVVYPFREMTLLYHGQVVQKLSDSEVM
NTFFSGDRNFTLQQVTRDLSRLSDSHITSGMMYMEIGFYGTGIPFGARHSHLWITFKGTL
PVKGNYNYDQSPSPAIIAAMTFGGAVLVITMVTILCYLCRRQKDIDDPLLANALEKQSQM
MRKKKD*
>TCRU_2173 hypothetical protein, conserved
MTNRVDRSRTPSRTSAGPYRNPSRPGILGTYCDPPTVARSVEFTSSTLEFGGIAPRSTIV
PSTDVTFVMLTRTCGIRRAVLSLRPPIRSCAPPASTQWRSATFSASANASIERSSTATVI
GPLNTTESKHAVARPPPIVTDSVSVTPLTQPSAVSPPPPPDLATGTSNGRHASPTPPARQ
LHTQSVNDAVSASKHASAAAQPSHGTTLTDDRPAKR*
>TCRU_2174 CRAL/TRIO domain containing protein, putative

MHSTGSDLCKADSLVTCYSGMAEEYYDDVSGTDLGSELLREADEWKKVMRFFPRSMSLFF
MEELQRWRIAVDSEEIAARYKILDEHIAVRREMDASLPEINVKATNWYKRVPVQLRFLYR
FGFVALGVLNGVYFFAALVFLAVLSANVIATLFFGFFVRWNYIFPLGATLAMAVIQGFAL
CSRAVEMLVAMARGKVIRPFETIGTKLGSVAQMCLFAVLVAMQFIVFCVYATFYSPLRGL
QVSFAVGWLSAVFIVAICHLVFFFDWLNARQRLRRGRHIIPLSLFVLLNLHEAAERDLDV
YAITTSSYFICGIPVLLSLFLGIGFLISRIVGFAAAVCAAAVLASFTATYYLDSLSNALS
GKLLRTAVWIASLVWVFDCYVFGFLNDGRKWYVPVVIASIISIWFLFISFICLKKDEFHV
LLRLTFVSLVILFCATWISSFPIVGWRIGVFCVCLMIHNALGMLVSRAELTNIGGVFVVS
AAALLIIMSCTLLGWYGTSPHCTLARSLPREAAATPLTPLAEYHRYPVCSLRTASGLVIT
DLALLTQLVNSYGTDAFFFDFENWFNSTDFSYGGVVQEFFSGEGKWLLHRFDSTVYNQTV
LVLHNGDALSSMLAMTAWLGSISLSPLHIFLPASWSNNIVYIISFVTQMIDFPWRRYEQQ
LVNYMQGIRAVSTKGLILTGSGVAGGIASIAGAHAQIQTVVFGSPGLLHLLRLTGLSLAE
YHKYVLTVGASNGVLDNVGGQDITMSQKLYCNGNAVTCLSMEYISRELIQSCDTSGRRHI
*
>TCRU_2175 hypothetical protein, conserved
MAMMMAGRVLLVCALCVLWCGAGGGGCDDTPQALLSGSGGGTVVGTGAGPSGGADNGLFA
SEPNGESEGDRLERTDLGQINSSPRGGTVGLDNKLAVMPVGSPVTRNQVLSNEALSLQSP
PSPKPSAPELQDLPEGPPLSGGRQGGEADNAAGGVGPSGSSSGSGVKSMVSASFSAGTLS
PPIPLTGMFCRAARVRQPP*
>TCRU_2176 hypothetical protein, conserved
MPVGTARERRRRRCSAGRRPCDAHTPRRCARSALVPFCHGQASPRRRPCVVALIEADGGG
VPAALTGGGGPVPRSPLAAQRAAGGPTTPRAACVLPVSADASSVPRFPGTSQAAVSKGGA
THRSEREAGCGYKIAQQRIQYTAGARGQDKRRVAKGQFKRTQREGPNHIPATRGHASTKC
ADGSGDRGKWDSDDATDERVSLLPDFVGAYQRYTCRLRAVSDAQRQKLLRGGDVERSPSP
IAALQMTVPSLTPAKLATLMAQGADMIAIRETWKSSEQIASMHTGECVLHAQSRIRKECV
AAVLVRKNLRSKRMPLITPQRDSSLDVVVVQFALGQNRDLIVASTYMRPPPQPTQPLGGC
*
>TCRU_2177 hypothetical protein, conserved
MTMGASRTTKLLGMDLDPQLTLNVAAASQRISQPRRIAHKEAGPSPHDPRTFIIGYGASK
LRYGSELIWAVATDSAKNEMQETYAGLARIVSGVPSTVDQ*
>TCRU_2178 hypothetical protein, conserved
MPVVTARERRRRRCSAGRRPCDAHTPRRCARSALVPFCHGQASPRRRPCVVALIEADGGG
VPAALTGGGGPVPRSPLAAQRAAGGPTTPRAACVLPVSADASSVPRFPGTSQAAVSKGGA
THRSEREAGCGYKIAQQRIQYTAGARGQDKRRVAKGQFKRTQREGPNHIPATRGHASTKC
ADGSGDRGKWDSDDATDERVSLLPDFVGAYQRYTCRLRAVSDAQRQKLLRGGDVERSPSP
IAALQMTVPSLTPAKLATLMAQGADMIAIRETWKSSEQIASMHTGECVLHAQSRIRKECV
AAVLVRKNLRSKRMPLITPQRDSSLDVVVVQFALGQNRDLIVASTYMRPPPQPTQPLGGC
*
>TCRU_2179 hypothetical protein, conserved
MTMGASRTAKLLGMDLDPRLTLNVAAASQRISQPRRIAHKEAGPSPHDPRTFIIGYGASK
LRYGSELIWAVATDSAKNEMQETYAGLARIVSGVPSTLDQ*
>TCRU_2180 hypothetical protein, conserved
MRVVSPVSQELRRLPSAREVPLIVLSEQRAAGTRWRSNAFNTPPGPGPRQAKSRERTIQA
HTARRAKPHPGHQGARKHEVCRRQWGSQQWDSDDATDERVSLLPDFVGAYQRYTCRLRAV
SDAQRQKLLRGGDVERSPSPIAALQMTVPSLTPAKLATLMAQGADMIAIRETWKSAEQIA
SMHTGEYVPHAQSRIRKECVAAVLVRKNLRSKRMPLITPQRDSSLDVVVQFALGQNRDLI
VASTYMRPPPQPTQPLGGC*
>TCRU_2181 hypothetical protein, conserved
MCSQYGPLRNSSQRGGPIAVSVANSCLRVAATQKFSKPPSAVHPRNIGRQATEDSIASEL
KGLAGVYQHQRSPMGSAVELASNTALLGKVRLEVIGSVMLHFVYRVCQLHRRGTHTTARM
LVRTRRPQPKQSPQCHFLSDLTHDGRRADGSI*
>TCRU_2182 hypothetical protein, conserved
MAKGFLRVNWRACGGWLILQWRRPLPGTTERLAVSGLANGTTPLVAGLGSKACQRVRVPY
GCDSMFRVLSGCHGLRRMLSRRLISMHSTMSVTKLPVHGPAGTHQCQETLPDPVLVEGR*

>TCRU_2183 hypothetical protein
MGGCVPLRQRKHGKCGEGSERFEVCGGWRRGALAGEPAGAESTVSFCKPRVHAGGVGDDS
RGSERRESFAGCEPGLFWWQKTPGALVRQEAPVAANIRINAGDADGIVGDG*
>TCRU_2184 hypothetical protein
MPTISHVTVNNVLLYNRQLNAEEIRTLFLSQDLIGTEAHMDSSSDSSAHGTPSTPADRSA
HSAPSTPVDSSAHGTPSTPVDSSAHSTPSTTVDSSAHSTPSTPVDSSAHSTPSTTVDSSA
HSTPSTTVDSSAHSTPSTPVDSSAHSTPSTTADSSAHSTPSTPADSSAHSTPSTPVDSSA
HSTPSTPADSSAHSTPSTPVDSSAHSTPSTTVDSSAHSTPSTLAGNGATRMFLILPDGAA
ISAFSGGGLLLCACALLLHVFFTAVFF*
>TCRU_2185 hypothetical protein, conserved
MAKGFLRVNWRVCGGWLILRWQRPLPGTTERVAVSVLANGTTPLVAGLGSKACQRVRVPY
GCDSMFRVLSGCHGLRRMLSRRLVNMHSTMSVTKLPVHGPAGTHQCQETLPDPVLVEGR*
>TCRU_2186 hypothetical protein, conserved
MCSQYGPLRNSSQRGRPIAVSVANSCLRVAATQKFSKSPSAVHPRNIGRQATEDSIASEL
KGLAGVYQHQRSPMGSAVELASNTALLGKVRLEVIGSVMLHFMYEVCQLHRRGTRTTARM
LVRTRRPQPKQSPQCHFLSDLTHDGRKADGSI*
>TCRU_2187 hypothetical protein, conserved
MVCVRCRCWAAAICDCAVAVRGVAAVSLLLLPLCVDGELVCAEGCRQVTGVMAMMMTGRV
LLVCALCVLWCGAGGADASDLGNNAVGGCMASWVLNANKSYTPSGCDKTALTLPLRSVLS
ITAVAASTDPLVTGTAENKSDLAPSSGADFGGAGSPPGRGGEGGGGRDDGAGGPGGVGGA
SGSQARGSKASVGGGGGSNGGSKARVDGSLKSPASDVKSPSPVLGDGGSSPGAPTGSVGS
DGSKSFILGSFSSGGRSQPDVGSPGGDASLSAPVAGGNSPPSITDESDALEKTGAAASKK
GWKPQEAGGQSGANRARNELPELSAPAESTPEAQKDSTSKQEKPEGEAAGRAATGEEKRR
SDAEAQGPSTVMSTASTSNGRRTTNSSGSSGRRKPNGTNRLANFDRRKDKNATVTKQKGA
*
>TCRU_2188 BNR repeat-like domain containing protein, putative
MSRHVFNSAVLLLLVVMMCCGSGGAAAVENSALVAAPTFEWRSITDDEGVTVDSLRVPGL
LKVGTVVFAVAEAQCNKGGEGSFTGIASELLTDPTDKNWWKY*
>TCRU_2189 Tir chaperone protein (CesT) family/PDZ domain containing
protein, putative
MNANDVLTVISPDDGKRFRINIKGDIGRLTIGRLKQCLATASSYSVPVADQVIKFNGTPL
TQEDEVCAAYGIMNGSTLTVEHRANVDPTTDHTASFVSPHRQALEYQTIRQQEEILGDEV
LGYDNTLQVKIDQLQDQVEAAEKKKMKIAREKEKAERELARLRLQEEVAEKQKRRLTQLR
EREAQRAARRAADLAARREQLKAEEEATRAVALQKLDNERRRASLEQERAVYEAEKERLA
KEREEYEQRAKEREVNIRKKEIEIEQQILAAERDRRELELSRLVSHQNRLLYHERVGRPP
PPELTHEGMRRGEWSGNDPFSLPVATPEDKNVAWGKTQEINNNNPPNQQWQLNQKQSYRQ
SDARHPSGPIKSEENATANAQFEDSYQNRPRPPRAAENVVKMMLPGRDNFALAHGGNDVY
NARENAIDNLVCMGRDLGLENTLEFDNNNTCVISVDGQYNLIVTFDATTERLYIYSTLMT
NIPHDPVLRLRVYEFLMEGALLGREMCGGGVGASIKNDFILLSSSIYLPTSLPTTLSTLA
PQFLFSLNKWREKLGELLSTVDMQKMTSPSKNGHSTIEDTNELDSRHTPEEKASRRIASS
TRSSRTHSTESGAGRPVIGIEATDSVMINGVPSRHNGGVLVVNVGGPAALAGIKPHDIIK
KINYKRVTSLRQFQREVSRLIVGKMVPVVVERSDVLHTIFIRVGSA*
>TCRU_2190 hypothetical protein, conserved
MRTGSFLRKKASRVGCFLFGGVTVAASSHIHRASWHTSTRCIVSGGVKNEKAGKPAVSSV
KRMPPPPPPAQKQQQKLRASSSHIYPEPPLASQRPLLDVEDIIRALVEVFVAYQKHLQNC
NATKTATISNMNKGGGTDVNVPFYPPVPLEYVEEQFESLLLRLLPAGLTRGDGDASKVVR
FSDNSADADKNRRQIASRIQSSGVFHLTSTRRRNSQREGASRDDGETFFLRIRPGVRELA
VEIAAFLFSLEPHNGTVRKAVPLTVIRRMSLSPANVAFVRHELANDVRRLLLVYTHSVFF
LTKNGTMVQLLEPSVGGGESVLHAVSLNTTAATREQAQELVASTTQVNNIPEGTNSTETT
VTTGPGQLSVHFASGENDTVVHMGKRFIAPTAIERYRLSQRLIPFLEFVPLTRTVINTNN
GGNDVSSAVADTEDGFVDFVAVRNRAVEKYPSLAPLLAFDYNDLPQLCDGPLFSALRALG
VEFCLGRPLPPQCQRKRRQQQRSTTAMSSLPVEMGLLFLRRIRTSNEAAASTPISPTGEK
MPLRLLLLDLQAELDATVMPQWRRKWWPWPSHIHPVEYGITEGEATNGAERHEEELWGHA
FLRVHAAVYEELAATPAQWMPYDSTPVISLKETSYPVGVSANSAFVQHLLRQLTPRQHEK

LHDILLRGVQGRVPPLIQHEIEESVACLFFPYGQSSRSHGNIIEQNSNNSSGDSNREAQQ
ELIVFNKYVEGFYDKNLSLQLPFVRPRTLSEEPPLVYRRLLPAKLVLEILCCLHREQLRH
AEEIGLEVIDDDEQVADGDDKNCFLSFVPLRQTLQPASRTYVRDYIGDLAMIPLLVSCFP
RYFCVPAIDTVSSWSSIGLTREGRHLAQLLEASSKASDGRPLPYRSQRTGCFFTDDTRQQ
MEAFLLWR*
>TCRU_2191 WAHD domain of WASH complex, putative
MPAAMYNDSATTVCGYVVPVPLTNGDCVTMLSVIHALEELDQISSCVFGNIEAAVRNSRE
TLEGLQERIETCTARVKQLQGRREAMVVKSRSRFPNGCYRPMHLAQAPRERRGRFLRHRQ
DVMPVLLPVDESDSDSEYVLENEGNAALNNGESNGVSGQGKRGNLECKNFYQRPIRRLEG
TVEEQEPVRPQHPLQRVELGDVMPLAASWRYHTVAERGLGRLPRQLMSVGSLLLFNTREN
LYKEYHELDVLKQQREERVVAAKRRLGGAADVHRDYMTRLSSDEYAFIPLMEEVANLMDD
LPEDLPLEGIAEVAWHAYALEAADNIAPSWQRRLGDESEVATENAGPLRGGKKAHGQTLA
ITLGPAETPTTSLINPSSALEAPPPPPPPPAGKAPPPPPPPGFKSMKAPPPPPPPPP
PPAMMMKTAVQPARTMTAIPPPPPPLSAEAAPLPISPIAPGPPAARSLPKLGNPPPAPPL
PPPPPPRKNAVTRAPSKADPRPAPKVAPRSNLDTLSSLLANRRKGILGMHSDEDEDDDVP
QSAPSKGMRGVKESASQASTAPLVSVPKSTPPLPPSATGKLIPRRVDDDDDDDW*
>TCRU_2192 60S ribosomal protein L10, putative
MARRPSRCYRFCKNKPFPKSRFCRGVPDPKIRNFDIGKRRATVDEFPVCIHVVSRELEQI
SSEALEAARIQANKYMVKRANKEVFHMRIRAHPFHVLRINKMLSCAGADRLQTGMRHSYG
KPNGTCARVRIGQILLSMRTREAYIPQALESLRRAKMKFPGRQIIVMSKYWGFTDILRSK
YEELRDAGKLQQRGTHVKLIVPKGKITQYNLLA*
>TCRU_2193 nascent polypeptide associated complex subunit, putative
MSTPQVQNPPVEDDEVPTLEAAEVPQVAKQTKRYAKAMAKMGLKPEPNVVKVHIRKHGSL
SFLVNQPELYRFPGTNTFLVFGEAQLGDTAMEAQEAAARAVSGVVPETESRVEEVPTTAE
TPETPVPAEKTDDADAEDGGELDEREIKVVMSQGNTDRAGAIRALKNNKGDIVNAILELT
M*
>TCRU_2194 chaperone protein DNAj, putative
MLQRTCSGSLYAVLEVARDATPQEIKKAYHRLALRLHPDKTGGTTTEQFTLIQEAQSILS
DPRQRRVYDTFGRMGIESLRQFGDGMVVMTTAGIRCAFFIIAFWMLLWLLTLVLAIVRLD
YNKGWPWAAVFAPVWVALVPLLLIGGLLVFHGVTRREIASTLLGLMCFLVTFAVAMFVVG
LSGALTWTIALAPSAAIYVFQSCFILRYLLPFQFRNGFAEFIPPGSSVCLSRMYWGFLLE
TVFEKLCCFSFISLALLRAAQTGGEDTSKLISFWIVFTPLILYFGCMTLVSAARRFFAGT
VEGQSCLLSRLCRALVAAMGYASLLFMACMLAAKCEAEQNHKAVSLHPSAAVALLPLEVT
LALAVLLPSCIFYNAELLFGDVSTMDVAEDDGSLAPGGDDAFDRGGFMHNFMWNNYAKNG
GRGETAAGSSEAYRGEWAPDPPNLKTTYQGI*
>TCRU_2195 hypothetical protein, conserved
MGSDLSVVVQACAPVPHVIHETWKRRGSSFGAEKNHALPMSYTELRLVCRESLNPEMLTE
FPKEEVTPSPVRPIVTDTTPHFLSFLDLEDAALFSFLHDALRCKRCRGRIGFVVDPSVCI
GQRLYEAEQRHIFTQSFSIFLSKLVAVMKFVAPSCHDDWTQGTEGESSLDGDLVDTRPNT
PNKPHSWIPHEFFLLEIQQGLLDDVSGPWLLRDIVDHMGHVLHYHSAVSFLCGSSNQSVI
SSGDMQKKLMSGETSTSSCVLTRVRAYDDINETSLSDSDTAEFVFCRSLQHVLLSQNNMS
RVGLRKCLLELLNSIEQDQLSSARPLQMIDVRENDESDATQRFIAELSSYTGVQIIIGTS
GKRWRHRAHYFISKSLSHRGIGGVGMTHAFPEDAPYSRLNMEESILSGLRGDQSLLPEKS
EPHSLGNTGDSVQMMPHFECEGKSLFASYSEEPRNEEVNKLNAAFTFTAAAAAAAPGKKG
GKMEPKPSDSTPRESLLLDEDDVNGGEVDEKRMHSLRLDGAGELEAEAGHHKEIQELKTS
IMSDSPATPPVSFSRIQKDETGIVSQDVISSMHEVEGTPADCIASALPVESLDNLESSVS
VPHIVGRDQTSVADRVASVPPSQLEKKTRPKPRNAPPAAKGGKSVRASKRLQPNRHDTAL
KESKFP*
>TCRU_2196 hypothetical protein, conserved
MGVSARSQKPYVPIDTCSPGGTWIEEKRYNKVRHESHKRQACKVLCGNWQEEKSLEDDLL
AQQPLLPGSVPADDFVQTAVLQASLDVIREGKNGRYAGGYQSTPYLTIDARNPHLRLLQT
TQRHDYCEANGDVRRLRRPDMGARSRALLEVALKAAKEEKEACDREQQTRLSRLAEDGGG
IYLSTYHKSHCREEELPIINELRNDYLSDEPVTLYTGNPVTGCTMTVHGKTPVEPVEGRS
RFGRHTYFTERKYML*

>TCRU_C Terminus (BRCT) domain containing protein, putative
Pescadillo N-terminus/BRC.1
MHRKQVWAKRVKKERLKKKFLTRMQATRLLQVDSVHFRRLCILKGIYPRALARSKQKQSG
NDKQYYLAREIKWLVRDHVAERMMAYRAWEKKVRRAEAMGLADELKVLRSKKAKPQYSLV
ATIKERYPFFIDAVRDIDDAMSMIALYAFLSPEVMSETTIETHHALTSGLHERARGIIAR
WNRYVARAQVLSKGFISIKGYYFEAIVRGERVRWLCPHEYAHKFPPGIQQYITLSFLEFY
VELMQFVLYKLEHELQRDVAEQQEAEDEENNTHAEDFRLPDKEMTQSISDVKKDTLKKGE
LMQEELRKARRVFDGLTFYISREVPHKHATLIIEACGGRVATAYAADNITHFVVDRPALP
PGFERVDRIEYVQPQYLFDCLNARMLLPPNGYRIGEELPPHVSPFTVAITNSPEDIAAVE
EAKKNHPKIVSYVPKRVHEIRALVNPQYTPLDPEGKASDLLLHDESDEDHALVPELGADD
DVSLSGDELLEASHRPKWEEEEVTENVQRSKLSALKVAKQRKMNLMNAPTDEVVARRRLA
QLKSRESRQQQEPSGQRLKRKLAEMKRQEAATRKMQLQVARKKAARYYKMVNSVVQGSQR
REKMLEAKAKQVADGRIAKKEDGRELVNVRVEAKRARAAASGKPLREKKAANPYKKLPKW
VR*
>TCRU_2198 Peptide deformylase 2
MGLFPRRNDACRSALRAALRCSARLNSSRTAYDNNNAAGEAAYMAGNTVHVEHPIVQLPA
RSLWCKQYPLDPAQVRSGGFAEMIERVRAARQYYQYPSLCAPQIGWNVQMFTLFDGSVFI
NPVNLDLLEVEAAGSRSGMPIAEAEAQWVASCRREGKTCFAWEPCASCCFLMHYIERPAT
VRIRAIGADGHPFEVTLEKMRARMALHELDHLSGVLFTRRIPDTNHVVPLEGFSTMSEWS
DDYPSLEARSTYLYTTYTPPYTFTTDNVEDAQLLDRKFEDGIYPGCEHDRRMRIESAALE
ELQRAQWRMEKNCSEEGDSTQCMRDTDDEQQHEDEETEEDVTAQKGTL*
>TCRU_2199 hypothetical protein, conserved
MERASQRSSARSSKVNAVKGGRSSPSAASRSRADSLKGNRWGNGNPQASSPANNTSNGCA
KNSPRGDIDGGSQRNLNGLAQGRGKNGARRSSQRPKEMSREELLSLLFRKPQLKEMRPEM
HRLDLSQRDDLRFLYEMQHRVDPELVPVRNRMYRANWNKMHQSHIFDTEPASKPQASTTP
VKKNDDGLGSLARFVLCSEERNASPVRGRRHGNYSAGRTTLRLFDGNSKESELRAASQTP
RTGVRRVGLKPADKLGANLQSRDLLCEVGASRHGVRTMEAVKKFESTQPKLTLPPQKLSR
RFAHPARSFSASDNDIFGVRKRRERMMQRASSCTSARTTEPYGSEDLEGSTRHRQSSLGS
TSVIDEKRSNHSTIQSKNVPFGEEEPRNGGTPTRHQKSRRGGSLASRSSSVAPSPSVRSW
SHPRSTRGSNSEMLRRHNDVIGKQRNNTSATTVSSKISVISEGGEYSASLFPTPRVRTGR
ARVPGHSITKSNIVFGDLNLLNSPRHVQRRIR*
>TCRU_2200 atypical dual specificity phosphatase, putative
MNEVLQLLINVERHPIYVHCLDGRHIVGLVIMGLRKLQFWEVNCSHLEYQRFTRSVQDEV
AFITDYSGPIAVPMRIPSWLWKGTWFDALGKPRRIHVGIRLKFPSVSRNMESTEGSGSVP
SWGREGVNCTSTNPSTRNLTPERLTSPTRTAEGPTSPLHMAIVTPNTGNGAESGVAYVDL
PSITPAKLIGPAIGARHSAFAIQTEKPLAADLRLLSLRTSAETVSGSSAVTAPPPLSSML
TLSSRGWDIGEAFSVAGMVPQGSSSAVAGLPSTATAIGSELSAVSRSTTQRGTPLAGGMK
LWEFDDDTNGSHFSMQHGVHGMVNTSLQRWNEWNHSSASSTRYSSRSRRHLQYFVAEAAG
YGPSSESVASTKKTRRRNSL*
>TCRU_2201 hypothetical protein, conserved
MYVVNLCSLTLAISHVAHFASTILRLCPAAVICDLNSHHELRDGRSPSTTAGEDLAATPS
GMDSELSDDPAQATWISGRSVSFPEVTAQLVLRVFHWTSTRLHGPGPPSGIADCGDGGRH
PATGRNAATMETCCLFPA*
>TCRU_2202 leucyl-tRNA synthetase, putative
MTPRAARNMAYQDYVINGKTGVDPSPLFEVEGAKLVGLPLSAPLCPYATIYTLPMQTITV
PQEYTLVKLKVQNATEHPAFLAFKHIIGDRPVILPGATLRVETVCGQTNCWISPNFSYKA
YTILNKTGEEEIFIMTPRAARNMAYQDYVINGKTGVDPSPLFEVEGAKLVGLPLSAPLCP
YATIYTLPMQTITEAKGTGVVMSVPSDSPDDYINFTQLVRKPDYRSKLGIKNEWVDFDMV
PIIEVPGEMGRESAKFMCEKLKINGPQATDLLEEAKKLVYQAGFYQGVMIAGPFTGEKTS
VAKVKTLQLLTKEDSAIRYYEPSRLVMSRSGDECVVALCDQWYIEYGKKEWKEAVLKHLE
NMNMFFPGVRNGFEETLNWLADWPCSRTLGLGTKLPCDESGTMLIDSLSDSTIYMAYYTI
AHFIHTSTEGKLRLDGRHDNVLGVTPEMFTDETFDYVFLGKGTPESVHAVNGLPMDAAEK
MRREFTFWYPVDLRCSAKDLIQNHLTMFLYTHAAIWPDDTSNWPRAIFANGHIQVDNEKM
SKSKGNFMSLAETIDLYGSDATRLACADAGDSLDDANFVRETAAGFILKLTTAIDGAQEL

LGKKHTLRSGEYNIFDKIFSNSMNFIILQTERFYVGMQFRGVLNLGFFELSNEFSQYKLN
CDELQIHADLAERYVEVMTLLLAPLAPHFAEYIWTSVLGNKKSVVCAAFPEPTGPVEYAI
LVANRVMTDVVKEIRSQVAKMQKKRGPVDEVFIYTAASYSEWQIKALRLLRELYEANGRS
FPVDFSKKVMSHKQEWMTKEILPDVMAFLSFTKMNVERCGEEALAEAPAINDAELLKGVL
ANICKLSGVPTVHILGHEDERYPEHQAARRKCRPGEPAIVLPVKKK*
>TCRU_2203 hypothetical protein, conserved
MKRSSPWSVGESAARGVCDEAVAEEPGPSRVPAFVLPACLACWHAWQLRWRPAHEVPAKK
TVAPLRHPHVRPVKPSERQAEHVGHVPSRCGQTGALRRRLGRRMSIRRSLVGKELRSFSR
EEVPAEAEAGGSPQ*
>TCRU_2204 Leishmanolysin, putative
MSARKHHDCDDIDGMELHDGDGDGRTLESHLSQRHAMDEWMAPIGFAGCRTELTLAAPAD
LGCMRVKWEMAEPMRW*
>TCRU_2205 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MSRRVFTSTVLLLFVMVCCGTGGAAASDGKPSEPNYKWKDVKSEDGVTVNSLGVPGLLKV
GSDVFAVAEAQCKKDGKYFTGIASQLLSMETDNKPEEVLKNAKDKTQVLEEGVSPSKKVD
VSRPTTVVNGSDIYMLVGKYSHEDAANCQAGTENIKSGILLVKGELSGEGDKKIDWKTTD
GVPCTLGDQHKSWTGLIGGGGSGLKMKDDTLVFPMEGTGGRNTVSLFIYSPDNKSWKLSK
EISADDCSDPSVVEWEKDKLMMMTACDGGRRVYESGEKGDSWTDALGTLSRVWGSKQKGN
EKGVGSGFTTAKIGDNRDVMLVTLPVYSKKTEGVSANGKGELHLWLTDNTHIVDIGPVSG
KDEDVAASALLYKSGDNNKEELIALYEKKKDDAEKPSLGMVSVRLTEQLKRVKEVLATWE
EVDKRVSKLCPSEGALEDTATDTACTTDKITDGLVGFLSGNFSNDTWRDEYLGVNATVTG
GTTKVAEPSDGVTFKGRGAWAEWPVGRQGENQLYHFANYNFTLVATVSIHGEPEGATPIP
LMGAKMDDGKNTVLLGLSYDKEKGWMLLCDDGKNKEHSSYLETKTSKHQVAIVLRNGNQG
SAYVDGKSVGDESCVLKIADSKEISHFFIGGDGGRAEGQDDVSVTVRNVLLYNRPLSSAE
IGSLKPNKVPISPLVKEPSSPSPVASDSIIPPITPVNKNAQIAGTSSTPAVTHRTQQRQP
MGSSGADSGGASTSAVSAVSTPSAEKDSVKEVASGKSSDGAQTVDGGSTADGEPTMEKRE
GTDVQKEEVQPLNREVNATELNSSLENLSQGNNTDAGTMCGSGLLPSLLLLLLGLWGFAA
L*
>TCRU_2206 hypothetical protein
MSEGSSHERSEGGSSVSEGSSHERSEGGSSMSGGSSHERSEGGSSMSEGSSHERSEGGSS
MSEGSSHERSEGGSSMSEGSSHERSEGGSSMSGGSSHERSEGGSSMSEGSSHERSEGGSS
MSEGSSHERSEGGSSMSEGSSHERSEDGSSMSGGSSHERSEGGSSMSEGSSHERSEGGSS
MSEGSSHERSEGGSSMSEGSSHERSEGGSSMSEGSSHERSEGGSSMSGGSSHERSEGGSS
MSGGSSHERSEGGSSMSEGSSHERSEGGSSMSEGSSHERSEGGSSMSEGSSHERSEGGSS
MSEGSSHERSEGGSSMSEGSSHERSEGGSSMSEGSSHERSEGGSCRHKGVSIVILLLGIC
TFAVVY*
>TCRU_2207 hypothetical protein
MLRHCEATRGTSTGSGNESGVGSSMSEGSSHERSEGGSSMSEGSSHERSEGGSSMSEGSS
HERSEGGSSMSGGSSHERSEGGSSMSGGSSHERSEGGSSMSEGSSHERSEGGSSMSGGSS
HERSEGGSSMSEGSSHERSEGGSSMSGGSSHERSEGGSSMSGGSSHERSGGGSSMSEGSS
HERSEGGSSMSGGSSHERSEGGSSMSEGSSHERSEGGSSMSGGSSHERSEGGSSMSGGSS
HERSGGGSSMSEGSSHERSEGGSSMSGGSSHERSEGGSSMSEGSSHERSEGGSSMSEGSS
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HERSEGGSSMSEGSSHERSEGGSSMSEGSSHERSEGGSSMSEGSSHERSEGGSSMSEGSS
HERSEGGSSMSEGSSHERSEGGSSMSEGSSHERSEGGSSMSEGSSHERSEGGSCRHKGVS
MSFYFWEFVLLR*
>TCRU_2208 ubiquitin carboxyl-terminal hydrolase, putative
MPDLTSIMNGREEEGNEMHVVSLRTTPASASLFETPFILCPLVNLGNTCYFNAGVQLFAN
CIPFVYGLRNSPFRHPFIGSRALKYCRTGGKASQALFQAFAELLYDMEFARLGQGEALSP
LKALDCLAAVHPAFEGRGQQDCPEMVNVLIANLSEEGRQNVELEALLRSFEEDALTRAAS
DAVLVDVVGRDNIPNSHSTVGMDFRSMPHEHATGVLIKEETLKLCSHSAMDKEEKIEIPP
SFLFAEKPNMLSFNFPGSWWTYNTFQLMQTVNHDNERLDRKERARKDRPQQNTFCPPKLH

YNSVTDCFTGYMLSEVQCHTCNSTSRIVEEFSSLTIDVSSYSQRMQYARRHPEARCSAEQ
RPFMQQKSRGPLQWWNPFVWIGALTRFFFSFFKGFSDYIDYPITLKECLDIHFEPVVLKG
SNSYHCASCDNVSEATKREFLLSLPEYLLLQMKRFEYGTCFNTKKTDPVIFPVSWDIGEA
GDADALRLSDYVHESVMRYMAPSVPCRSIISTDICTNAIENMTNPMHTQQVDSPISESME
GAYTEMQSPIYTYTLENVVNHHGSIMGGHYTVYARKKTEEENVWLSVNDEEITRVGVNEV
ADSEEYLLLYKKQPLQPRSEAVLTLRRKAQCLLSLPPSDGKVLQKEEFTDRHDKRDAKGK
RVVYISRPWLQRMAFMEEPGPILNRLCYCIGEDQGHKANSRQEVQGSHNRRGRMSHGLPV
EWFYVPLRCDEYDAFYKMYGGNTALTQREYEELYEAQHQVS*
>TCRU_2209 ATP-dependent protease ATPase subunit HslU2
MLRFSWCRLCGGSSSTVAATSPLAPDVLAVAKAQSAQLDGLSPRKIVSILDTYIIGQSEG
KRAVAISLRNRWRRRQVKDKELRRDILPKNILLVGPTGVGKTEISRRMAKITDAPFVKVE
ATKYTEVGFKGKDVDSIIEDLYMNAKTKAKRRLEAERAEEALAMTLDVVYGSWATRRRAS
GGDARSKYDEDGEDGGRAPFTDVTLEEFKAKYKTEFKDDLVTVDIVPTPPKHNRQGWSKA
EMDIAGLFGSASEVRLKTRVTKRVEEAVPLVLQDILERLLDETQISTLARTLAEDDGVVF
IDEIDKVVTDAANNDADVSSTGVQQDLLPLIEGSDVTLKDGTQISTDNILFICSGAFHLA
KTSDMIAELQGRLPVRVELQALKEEDMRRILREPKFNLLLQQKELMKTEKVDIEFTEDAV
DELARVVTTVNANGQNIGARRLHTVIERVMDKYSFNCQDYEDKKVVIDANVVKEATSTLH
TNIDLAKYLL*
>TCRU_2210 catalytic subunit of the vacuolar transporter chaperone 4
MPFSKAWRSAVYPDFREQGAYINYKATKDILHRMKEDIANPSTPDELYNSLLLQKCRVYK
WCEKKIKELLTVAEALMAASDYLTEEDTKTNLSLVLNTLGSGNMKCLPPNEARLLADSIT
HELLRFVECCNLNTDTIEHIIGRMYRYAVLGPTGKHWNNIMTEYDYHKLSIHEIFYLLSK
VYDRVTETENMRIVKRSGIPAGTVGSQVFDRRSVKYWVHLQDLPFVIARIIPHLPHSTFK
ETYQTCKERNIPFTLGSPVSSVYWDNNEFLLYHRRLERLEGATLIRMRWYGDPLESDWNK
LGPNDSVFMEIKVHHEAWSGERSNKRRFALKEKEVNSYVHGELDLNPALEKLRAKKASKK
ELHNFMDLSTEIVTKIDAYDLKPVIRTQCSRAAFQRGIDQSIRVSIDTDLRVCAEDFGLG
HHWRYSGVDAPVSYFPYAVVEIKLQCAENERIAPWIEELMSCRYMESVPKFSKYAHGIAS
LYGHTPFIKMVPYWMHQLDIDIRASTKPEQNQWDPTVGLASGCWERTTDRAIFGVGHAQT
QTVGASEAQFLPRTDYTRVYQKALHGIRGEEVATPATADNFQDAEAEGGRASGTAGSRKQ
QLQPRLPAHTLQYDVDRRHKAYTTFHLYPFAEYGVESLCFTPASGKNAAAEVLLGLIPWQ
TGKRIRVPQKYDPKTLLTSERYMLKWTEHATRLGLVGLGVIQFGNSMTLPGDVTQLSSFW
RANFHIVLGIALVLVALMTLMYALMTFKARSRRVYARKKIRFDDSWGPTVLTFFLAFGIC
VIAMMHILGRYGPMLTGDDNF*
>TCRU_2211 Domain of unknown function (DUF4586), putative
MFSPSVYLSIGDEYDKPSATPSLGVKSGGRSFVVPMKRSPHITDAVFQKPFISLAVGDEY
VAVPPHGTFRQPLDEKKAGMTVLVPFKPPSRPHKSNGSGTYYGTFNEGNPPRHEAELPLI
DTKKAGTPAAATTPEWPKRRIYTNPGKKGTYGYVGLTIGKAGEVQYIADPIAPYTTSTRS
SSPRSQKPFKAAVKSGGCFDESPNGFTTVYSISRPLPPKKPPMPRPPLDVKPWKPAGALL
REIIKPPEYQEDPYDLKEKRIREERQKEQSYKPWCPAGNDPYRHIFHYPVRFDPPPLNE*
>TCRU_2212 NRDE protein, putative
MCILAFVTQCSPRFPLVLINNRDELIGRVTHPVGVDKSTGLLWAADGVAGGSWLGLNVHN
GRFAVLTNCSRCPTAPLAIDGISMPSDWRGAMPLAEVVRRMKVHATPAEDGGTDVFLTFI
PDLSRGCIVGDFLKEGRVPGDCLPSSSLLTEEAMNVPPSLLSSPYFDGYNLLTAESLFDP
HQVQLLYSTNRYAAQHRSPAEHGVVHCLQNSYLDNWMEPKCTLLRKRFEEALKTFFPTGA
TPYDAEYVADSLASYCLCLEPNFDLQQEIQGGNLSPEVVQGYQQVLDAPLPYKGYNGEAE
LIQLYGAGLQPPVHFPTDSYKEHINFQLRNIFVSNGMYCTRSQTTVVVETMPDGEGTVVH
FSQRNCNAGKAHGPWKHFTVQSRSII*
>TCRU_2213 FHA domain containing protein, putative
MRGRKGGRKGVKGKCAEKVSDPLQQGAAERISSWEVEQPHEETQKDSIEESWERLAPSAN
GPLVARLVPLSADGAELSAIDLYRDVGRMMLGRSQQLFAECRIGVASVSAQHCELAVNPG
SLKVTIRDFSTNGTFLNGNRLKRGMEVELRSGDRVSLSNPAKESKPDAPSVEFVFQRVSS
EIKVDVLVEELTCPVCRGLFIRPCSTIPCLHVCCAACISQWIDAGHKSCVQCRANIWEVR
PAHKIQSCVEELLKSNPQLARSDAELHEFAKNDTIPQGGKNLRKRPHDEASEVNSNTSSF
PQDSDGSDSFHYSEMRSNDSHVVDGNPRQSCRHCRGASSVDGFRCPTDAPHRHCRACGTS

FPYRPLCSRPQNCQMCGATYCNLYYEGEGGCRAFLNGHLVRPKDGTPIRTMPRTVFGGNT
VERNILSDYLSTKGISLGMVWSECMEKFRAREWVPNIVCANGQLTEDSPLCVKCMNAVVD
SLLFFYRLKVPRHELPESVTNRPNCWYGDKCRTQFHKVRHANRYNHACYQEKGKE*
>TCRU_2214 kinesin, putative
MENIRVVVRVRPFLPNEGSSRCLTVRGNQVVIGDERQFAFDEVFDMDTMSHTVNDAVAMP
LVSAFVNGYTVSTIAYGQTGAGKTFTMSSLSSDVVRRMSAALKANVTAEGGEKPEFRVSA
VELYNENICDLIASTISSSSSIAMASVASLSLREDPRCGVYIQGLSEVAVESEEELLAWV
ESSSANRRTASTMLNATSSRSHALLTITLTHNGVVSRFGLVDLAGSERFKKTYGRQRRRG
SLEEFGNESNCMSTNDKAKGSEVASRIREGISINTGLLALGNVIVALCERKAYVPYRTSK
LTRLLQPMLSGNSKTTIIACVSPDVSSFEETLNTLKYADRAKAIRTTPFQVASGFSSLEE
AEKTILSLRRQLGMAQQQLREEQLPIMYSFPVVDETQLGELQNLLTRERNLTRRLQEDLF
NAEYTAMMEVEKRKQIEKRLLTLEAQQRCRLSQSIETDNTQLLDANLGEDGAGHTSYLAQ
NPAEHDEPQVPKAEEAVDAERLSMPHEIISVSRNNIDESKLENLSREIQSKERLIHQLTN
QNEDAVRELEYAKRRQQEMQDVKRHLEEELARAEAKLEATQMQRQGKEEERQKLQTHYQL
RLRKAEEEAAEYRRKVQEATTIISGREANAEMMKQLQSQVVEMSDELNRQRHALREGQQR
LHKVSASHSQEVNQLQKKLRDSEAQVARLQVQLQRKEREIARVKKGGAGVANRRQQTPTK
TTTQQAHASNTPSVCLSEDLQKEIDVELISLINLEKELDELTADRDELRDSVREAQERAG
GMTKWKDAMNGFMMRLQQLERNLHSEVLNEEIRLEYNREKASIEEKLRQLELLEPVLAQA
SKQLEEMDNNIDSLQEARKYHLRRVRQMQNGTLTPVNPTVRASELLRRGVANHTEMV*
>TCRU_2215 hypothetical protein, conserved
MTVGVSNGDDDVVSFLQHAGERYKEHKELLRRKHLEDERKKCPFKPTVSGYAEQVSRQSN
IRRSEAITKRLHELHAKRLQTVEAQRVKSRKRQEEEMTAEMRAPQVTERARSLVSRDPVD
VSRKWLEKREEKFARLREEALRRDLATLREVPRISQYAQEKSIVERHLGQRIEDYFMAKE
EARRERMYWLAEKSVGMNSSFGSSSFFSHVGDLPMQKELPQPPFTPRITEYAKQLRRSGN
VVDRLLADGRKGRRTPQDTSCTFAPRVAPASLEMSRGYYSDPNTLVYERLYRNDASKLRE
MRRKRMEIDLQNDRTGIPRISETSRLIVERKRSEAMEQARQKSPTQRLHSSSRDVHADAR
EKQRLMEARERKEKENCTFKPRLNAASKKMWRHQLQLLQGDSDARTAAAARELLWKRSQK
RMDEEIRRRRAMVEAREMAECTFHPKVGRAPERRVDRELSVSDRNEMWQLQRAQRLRQAR
MELERTQLSECSFHPTVDPVFPLPAHDASAVSGYEAHILRQEESRRRKQEAQDWWRPKVV
PPGGHGASRHTLSVASEPRSSHQRKQRNLRSEGQSRALFSPRSRDDSSADMDGIQFVVYQ
APSCASSVSPRSVASASPPSYKHHHHHRNYHGDFLHSSDNGIAAAVQSAKPSPVDFMINH
HRAILDSSRRR*
>TCRU_2216 hypothetical protein
MRRTDGIDMDADGLMVNAVRSAAYRQKYDETNNTRWGGLLVDGDHDCEEEDNGDLPPRRR
SISLNQLLYSEPLQRDFMARTTTEKLSPSVNNHHDDDNNNGGLTAIQRLIDAQYDSCAIR
VNNHRSGNSERKKNNKKNNRNDDDDIYSEVLEGKCDWDSALPPRPVCYSKETILKETHMR
LGDREDAEASRLPDKRETCSVGVQCEMRAAKKAATLRHLEQLRQQSLSGDPESIARLLAR
HIRELEMERFGHSSAFTSALLQQL*
>TCRU_2217 hypothetical protein, conserved
MLCPRRCATVAAGDVYCRGMRGSGRPQASKSSTHALHSLYRRLRKEGEDRLTLERALSTR
PLEKNIQLGLRLLHYHTRLVNIDREAREVAFWRIVRQLQLAAARRYFAWRIFSLRLRLRS
TAAISDALVYFLFLTVCFMLYQMYRVCRIGVTRAEERYMTLAIPIKQTFEALEDAQERRK
SLRREMEKDVLQQR*
>TCRU_2218 flagellar protein essential for flagellar pocket
biogenesis
MLVINVAADIFNSKVNFELNFPHRPTLLEVSRATEASFSNEIALRRPDNVPPHNFHVAKI
KIYDEERNKWVDLTSEGQLMDYCQLYAFQPENQWHKESQKEIPAAVKPPTSAQRHPGTHS
ASAVGRGNSNGGVPQAGTIAAYTGNRTPVSQRSESQSFRRASLHTSTSGALVPKINAEAS
QEEKHRVLFAELDSKGSRTLGLGDFKQGFQTFNLDLSAETVEDLFEKADTNRDGTVSFSE
FERFCRLYPIMTDCLFFRSKAFWDEEQLKREIQAERQAVRQAEQVVEQARKSLEDAEQDV
VAAMDAVTVAETDLKDRTDRLRDLTRDMDNAKREKERAIREKKECEKELMSTKEREKEIR
KESQDIAREAEKLDRRAAALSSEAVGADDKVRQLEKALEEARRAAERAHLSAEQAARDAD
SMKQRVRDSTKDVDDVLRQIARAEDAVRGAERNVVDADNSARELEGMGRDLSREAEEASQ
RRYQYEKAVEDAKNSVRVKEHQLDEAKRHVDDRDALARQKETELMEQRKQRDLISQHERA

LIEQELRLREQRDSLEERETKLMSEASSFLGNLRSQLQGGRS*
>TCRU_2219 Unconventional myosin
MNEPAIERVAVQQQVYYYLPQKGWLRGVVATVLDGEKKAHVVNATTGNKETVPLSQIHGY
MDQAFDPSDPDLFHLSDLHVATTLYCIKERFVQLKQQYSLMGEMLISVNPFRLMPFNSDD
HREKYLNSAQNHLLPPHIWQVAHRAYSQIVIRGFDNQSVVISGESGSGKTENTKMLIYYL
GELSHMHSSNAMQKSIADKVANCLKWSNPLLESFGNARTVRNDNSSRFGKYIKLYFDPSS
GVMVGGQTVTYLLEKSRLLLQSVGERNYHIFYEMLAGLSPEEKKELGGLKSAQEYKCLSG
GNTFVRRGVDGKTLDDSLEFQNVLHALTALDVDADVQRSIFKVLASILHLLELRFKSDQN
DMACFEDEAPFLTACSLLQLDPALLRECFLVKSHTSLVTIYANKTEAEGFCGAFCKAIYV
GLFDRLVDFVNQSIDAHGEVSRCKYIGLLDIFGFEKFTRNSFEQLCINYANEALQNHYNK
YTFLNDEAECEAEGIEVPKIVFPDNSECVQMLDQKKIGVFSMLDEECHFKAGTVERFTHN
LWDQWANKSKYFVLPKSTVPNQFGVNHYAAFVNYNTDEWLEKNTDSVKEEAYQCILNSGD
PFIRTLTPKDSLLDKRKQTVALRFQEQLTALREELESTETQFIRCIKPNMEASPDTLDNC
LVGNQLESAGVLQTIALKRQGYPMRRTIEQFCRYFFLIMPRSAIKLYKQNKLKAAAKDFL
AHYQKLYGWQKPHYAVGHTKVFVRAEVWSSIERLLLRRKAWLLRRCVPFLLRWVYTNREQ
KRLAEERRKEELRKAKEERERLIAEIKARGFSLEQMEWVEELATLFSNVDVSTLIDIVAI
LPKRDESLATLTEMQQQRVDGSLPSTFMRVMSESEVRPSVVQALVEGGVATMAGLSQCDQ
AQMKQFGMTDAEVAAVTRTMLKEQSARVKLERLQSSIGTAQLEKVVGEVKRRVMTQSDFA
TKVEKLVRMGFPRSHAELTLTHYNGDVQKAAERLLHGGVEKHLHEEPPHGSKGRWTSLDP
EVQRLVKLGVPKGAAKRVLRQTSGNVDEAVRLVFPPVS*
>TCRU_2220 retrotransposon hot spot protein, RHS3, putative
MKFTFSTIIEDVLFKGGVRVKEKKLNDFLTMELGGRGVVGTNRSVLLKEFFKDPTKYIRD
AGVLKEIQITDAYARMERTVRDEMDVEEVVRRLHENGVDNLLGWSLATAKVKEIVHGITK
QFLNAASEEVRNPTTTSASTYLEGWYESVYNARWSHAVEIPDGGGTVMKVKEGKPEQSWT
YKAADGAIEENDGAQQSGAPRLRLMVLTSDKGWPYSWRENKSTRDCYVNCEVDRVWQTVK
DDVNKLFSSHGKNKLSPEPRVLIGTSGIGKSMNAGSYLLYQLLHYNAE*
>TCRU_2221 RNA polymerase subunit, putative
MSIFYSYVVRDVLEVEPVYFQGRVTVSSTSSFAAAAAKVAEEDVEELLDKQHYQVTFEDI
LMHRLTERYVGKIVPGCGLCVAIHDILQYTQGIVRGPSASAWLTAQFRLCIFAPTPGARL
RATISAQTREGIYLTLEFFQFVFFVPGDLLVAPSSYHEEKKCWVLHVEEEDDDDVDGGEE
KGVLESALNPYENGDEVIVKVEHVIVRELVDFHSNVGTKSQNNNININININSGVSVDGKEG
SPTSQSPMEVRGSFVGTGLGPVLWFEK*
>TCRU_2222 eukaryotic translation initiation factor 2 gamma, putative
MDENDIADFTMDENTFVTNEQNERGLATQDINALNLDKINAETFEVMSRQATVNIGTIGH
VAHGKSTVVKALSGVKTQKYHREAVMNITIHLGYANAKVFKCDKCELPAAFHAFPSSQPD
KTDCPTCGSPLTLKRHFSFVDCPGHDVLMATMLNGAAIMDAALLLIAANEPFPQPQTLEH
LKAVEIMRLANLVILQNKIDLVGEVHAQDQYHKIRNYIDSTIGSNIPIIPISAQLKRNID
YLLEYLCHIPLPTRQLNCPAHMTVVRSFDINKPGEVDIENLRGGVAGGTVTRGIIRVNQV
LEIRPGQVHAQTGGTFSCTPLRTRALTLKAEDNSLQYAVPGGLIAVGTTLDPTLTRQDKM
VGHMIADEGSLPEVYAEIEVQYFLFEEMVGRSKQRDRNAKRVQKLNLQETLQINVGTLTA
GATVVNITKNPDIAKLTLVTPVCCTLDEHIAISRLVEKNFRLIGWGIIRRGVPVKLN*
>TCRU_2223 ethanolamine phosphotransferase (EPT)
MGNSTNVVYHIRVLLLTVAFLTGAFIFADSMLSKKVMLSNMSTEVCRGMQTVDQVVILLI
DALRPDFALPALSEYYSTGNDCNASTTRGVGAFQRRNTTLTYVEGKLKDTTHPSHGFFFL
ADTPTVTSQRMKAMMTGTVPAFFELKANLNTEAVESDSLLHQLRRRSILLGDDTWLNMFP
DDDDDTTPWKRTHAGPPYNISDFETNDNNVTKNIFPTLLSETLEKAPSDYAKLIIGHYLG
VDHVGHRHHADHPEMDRVLARIDAMVHNLTHFIRHQRKTRMRTLLLLFGDHGMTGAGDHG
GDSFQEVETFLYAELFDGNNASSSSLNVSAEAVAKSLRRRSELTEDRWTDEFGEGTIKEK
SCRNMAGVPPQKLGVAQQTDLAPTISILLGVPIPFSSIGRVIPEIITLADPDADLNTVEA
CNWRQLMSFFNQAGVPVMDAWKNKSLTWRKRISLMSHFGRKSRNEMRRSGMFIGSSLFMA
SALSWFRNKDVLGIIRRERLIDTWALIIFLFRACAVFANSFILREDVEVLSLLQLLLLTA
LLTTTHMRVAMFLFALQVTLRVMVPLLYRSRLQISHTVAMPSLLEQWVEANAAGKEWEFT
GLFLGAFVFLCASSCTLDRLWVVGQSLLMFVCHNHFPLHHIAPLISFMLTLFSRNGSGLR

YMVFVLWASSLCGEKYSIGAATAFYGAVLPSVVRATQHLPGFSQAVLLHLFSWVAFFTQG
NQCLFSTIDFNATFVGNSSEHIFFGGVLVTVRTLNAFALAPMAVMHVYRAQRTHGWHVCY
LLVYLAVVQSAFSSFNGYIQKAHLMLFSIFCPKLIFDLLIFLMTFIGYAVASCI*
>TCRU_2224 aspartate aminotransferase, mitochondrial
MRSFFSAKIVSAKAPLEIRRAASSFFASVPLGAPDSILGLSAEFQQDSHTPKVNLAVGVY
RDDANRPFVLESVKRSDTGSDMEYAPINGMRSFLKAAQKLCFGEDSRAIRDGRVASCHTL
GGTGALRIGGEMLRNFVNDCSNIYSSDVGYANHAGIFKAAGITLPPYTYYSPATKGIDLP
GMLKSLEAMPERSVVLLHACAHNPTGVDPTQNEWLQVVDVIKRRNLLPFVDMAYQGFATG
DLDRDAFLPRYLVENVPNVIVAQSFSKNFGLYGLRCGALHMVVENPEEVGRVLSQYALLI
RTMYSNPPITGARIVNSILNSQELTALWKEELRAMSGRMQDVRRRLVKELGECGSVLDWS
HIERQIGMMSYTGLTKEQVEMLKKKHHIYMTLNGRAAISGLNSTNVSYVAKAFHDVSK*
>TCRU_2225 hypothetical protein, conserved
MGSPQRNNGSHTAVYGLSEKDLVDPVCSSAFPGMRYKGLDSGRPFQVEARPDLSSSEQLE
LSSLTSEEPCALPATVLIGGASRCVGTVSPGEYETMEGEDEEPESSSSLDNSGEYAPLGF
TVVTGGPLRALYKPKTVSYSADESEDSNTELSFSDAPLVMTVQENRGQASVQRQKERNIE
VLECKPEAEAKEDVEEQGQLNAIVIRNLVRRLRDPNVQVAASEFENLEWDDPNFEEELQT
LKQIASYTEVKETMMKTAKDGILESSSLMDQKIKDAVMMLPEITVVGVKDKFVEQVGTYG
TLNKIGQEFVSPNSPKKSLLGAPREKIIIVGNNGKVAVLSKEAYTGSRFAGKKKMTESMI
FTAGGAEAAISFKESRVGSCNVEKKKRKDHLLTSQKFTIIPKEAAFGEEEKPTRRMRRED
LGRKSVVIYEIPELINGEIVETEYMDTEDARNGDKDEEKQTMRHSRNKETTRKGRGWSVI
NEIVSDAAQNGYAANGDENLLSKKGRVPATRRRRRNNQNRSITFAELLEVEGEEVPLEAL
GTQTISLPSSTNPHDRETTETIVENEQATHTPLGYAQVFSQDSCKQRNSADVLQPLIEKN
VTGVVERAKDGKSQQKKKKRYRPVSDRQKSRELEYSLVVDEEGTEIAESEDALGLNDGRA
STVSRLREKHSLDHQGAAKDANCQLLPPLAPATSWRHRIRSKKSLNASLSVTELPEPTVS
EIPDTTMDPSKVAKMSNQGESALGMTHNARKFRRARSNNLNRSATSFVFVPDEEIIELKE
KVEESLDQTTSRGNTLNEGILLPVLSRPRRRKHSSAAASMTSLDIAESSTMEFDLDDTIQ
STWNRKRSK*
>TCRU_2226 conserved protein
MGRNKKNKSAAAYGTEEMPSEEKSPRDVPSDESSTHSDNSSVVVQPVAKKKVYHGNKLSR
AAGGKGKKEEQAHQLPVPAAKVSNMEDEKTTREVEVNRKDDCNAGESADGLAGQLEEDLA
IACFEPVEVLYCPICTFPAELCEYSGMYEQCRPWLLEHAKELAEAEERGRKRRALTERER
LERLVQGRGTKKAIERIVLVEVTQRKGRKMTTSVKGLDLFGFNLKDLSREWKKLFSCGAG
VTSSEELKQSSIDIQGNVAAQLIEMLPERYNIPKGAIYQMEDKKKVKCYSEK*
>TCRU_2227 hypothetical protein, conserved
MPLKYFRRLLLSALVSEGSKAPLFQRVAKKTARMERDAPEKVAVWTRAAYVEARKDAETL
WVKLREVLYGDTNIKRVEGDKDSQNDRRE*
>TCRU_2228 hypothetical protein, conserved
MISIKEYIHLIGDSVNDADTARLAEEAVNAPSLFFYGSLFELHSVQKLRNNPSFAWIPQL
MEILCYGMVDELHLLPDSAKKHLTPCIYQKMNKLSVLSLCIRDGTGGMLFIRDVQGAIGA
STPLEAEELLIEMMSDGLLHGRIDQRGGVVILQDFAAREVRIEEVGRLREKLETWCRNCD
AQIEMLEEMMKE*
>TCRU_2229 hypothetical protein
MTFDGKAVMESDLPLTVEELVANYQSIRHLNEELCAFIDNIRVECDSIAESSPCAAQALR
DLFLNFSQGKPAVASFLNANDPHSSGAANGSTSSACTGGGVVLEGVVVKNQKCNEISHSA
AGGAKKSRFLRFVEEATRDYKEECGVLRLKMMAMESEQKLLLQARKNLREQEKKYATCMS
ALNDCRNDLALSRSHCTFLLGVLKNGESTVTASTMKNIIEQVGECMLVENGGCGGSTVTV
GSTEAEVDSVHSLAVRLVEAEIGLQESQAAVKSLDTKVERLSYGNDQLKARLETLAEERD
ALKSHNTQLEGQLNRLLLLFHDDAEARRGMQGTEEASSVVTCRAEEGPERDELKERLQRL
SCDNRALQNTLLQLQRQINDSELRAEELYSEGGGEVLVLKEEVARLREALREKQFELQRN
HHDWEKAATRWELLDKVHRTVIYHMSMRLMHDVARRFLPRSQEDTSPKAPAAVSEDTKEN
SSDLALSDDTAVAVAVSSSRNSGNDNRVKELLSLIESKDSEHRLALRQWQHVNQELRSAL
ASLQKDLKQKEGHIKVLEREKRSSDIHTTTCLEGVASGGHGDCGGDDLLNTQPKDLEQMS
GLRWKEIQKENETLLQRVAAMQKENSSLNVLLGDFRARCTSLEQELAKRVGAVSRQLVGG
AALTDTIPIRNLQRILHDVLQENLILVARVKELESR*

>TCRU_2230 Fcf2 pre-rRNA processing, putative
MASSSVKAIMAKAVTTSPTFFSDSNSVKGRKEQKDAIRKERKERAATLSQWYGMKKVNLG
AEERRELELLQFRNFINPELKHQAPKKSNTEQSEFVEFGFFAGTGRNKRRRLKSFADEWI
AENPELEQVVARRLKRNVRLNRKTKQLMAKKAAREAARVKAKKSSKRFKKKDMIL*
>TCRU_2231 retrotransposon hot spot protein, RHS3, putative
MRLNDFLQNYFGGRGAEEFNENVIMEDFLSSPNDFIQDEVLLSKIKALPSYQELKKEREE
FYVLSGASNKLGDERLLTLRHWREFKRKDTVTPLAMAQISTAYSHVLRVERRKAEEKARR
ERRELGIYVSTMIKYAVFKGRVRVDKMRLNDFLAMELDGRGALDANRDVLLRSFLRIPRS
IFAMRKYWAECRHPIVI*
>TCRU_2232 DNA repair helicase and transcription factor protein,
putative
MIVGANGSLFVNNTHPAYPHLVDFLTSCCEPVSRTLRMSEYVISPSSLSAASAEGTYSTA
MMRNFIRYFRLDEQHRLPVDLAKLSALERQLENGEDVAMGTTHESEESKGKKQQKQEEDE
DRLAPKRAKKENGERVSLVKQEATEETAAPSRRFFSLVKAVTIQPEPLISHALCFPDALR
PLPPDLEQMLLEEERSSRVRIVLQPQLRSFQRQQPHHHSQGQIHHEDEGRLVYFLVSQDR
QQMEFLVSRLQEFLVPVSLHGVMRWVLSDVDRGVEEKSVVESGRAKTLRRLFDTPSVSFA
SAMDDVGSCAAAAANSTGRKYSRVVYKSQVKDGRLRNVRERLFKELGVRADLFYDYVQDG
ALDVRDLVLAEHVRLRPYQVASLERFRCGNKAHQGVIVLPCGAGKTLTGIGAATILKKRT
IVMCINVISVLQWQREFFRWTDLSEDQVTVCISDKKQMPGDVFITTYSMLVAKRPTAPEQ
EQGEDARLTSRILASVEEQAWGLLLLDEVHAALAHHFQEVLNKVKYKCVVGLSATLLRED
DKIGDLRHLVGPKLYEANWLELTRAGFLARVECAEVQCPLPLPFFREYLDSQAEEDPFAR
RGTSSLARAVVCFNPYKLWCTQALLEFHRNRSPPDKVIIFCDDLEGVQYYARHLNVPFMD
GKTTEVERENLLQYFQHSNDINAIILSRVGDVALDIPCASVIIQVSGLGASRRQEAQRLG
RILRPKPPSLDNTCSYFYTLVSQDTHEVQQSYGRQSWLRDQGFAYRVLQCDSLLKELRRT
GGKPCCVGHPQWWYETLERKLPSAVAAKGSIWLPFSQEASRRMHRFFVNGREVCELDSTV
LNDTPRAAELAVSGLGEKWIVRFSASNAPETFGTVQMAEDNPTLVRRICYGPLDAAHDCL
KGEEECIQYILGQMRYRIKRRSNPR*
>TCRU_2233 hypothetical protein, conserved
MGTRARDQNCEISTSVSRVEGTIGISSEFVETDSRNGGLPGKEMDLQRRTRKLRDEEAVS
AFTTPKEVKLATAGEWKQRNKQSNSKRPQGRQRPGPGSRSMGDEGAGAGGSTDNFSGDAT
AGDRKVNRPARKGSEAGTQRSSIFHSLVFPGARVDCKQKDVIAADGGGGVEGGENGGNQP
NSVSPGTTQPDCLFDDAIEGESSVQEENGLMGEEFLQIIQSPQMRGLGGELQAEAARRAR
REKVQAAENRQQRSLRRLQLVEEMFAKALERRMKAMQRIAADPPADRLIGNHAMQHIPVS
MLPGELRRTALAFMDGVTRDVNSTAGTVPFAADKNEVSRKKFFLTDVDEAAAEEQKKEPI
DAIDAGVGLQETEEEEKTNFPNLNGMEEEELLRKWRELGYTAVYLPATGRLVYPGESSVR
NRSSKKPYVPDRWMSRQPLPPVHLVQRKLPPEFILLHGGMKSVGRRRPLPVVCRSGKK*
>TCRU_2234 Ankyrin repeats (3 copies), putative
MRAMIPPDLRALARVLNDVDSMQVSELFTPVGPNLPVHELEMLLEEINGAPLSAKEFRQF
QMAIMEERHHLRGVDLTTVAESQVGSALSLTSRLDATCTEAKVPLAHVFPQMKEAHNFFL
RITSFKCSVKQAPVFYRLSGALCSLLLCALEELQRYMDEMASSTSKSGGLKLRAEGQNYL
EGGGEEDTMPWLNEGAHLPAELECILADIDGGVGFHLAHLRWYLEVSQQNTYFDSGAYLG
DVSVRKIWNAYVGKEKPACFADTFSPALQFFPEWSRVAIMKVVNYRECGVVSLYTLKRLL
SVWGPFLLLDRNMRDVMQVGLFELEHSLEYHKKAFARRADAQEGDCLATLTDIPGEVVAL
VLRCQSEKQARTDGENGLATRTIRFTQETGAWVAKGLSGAEYETVYDAFCAFPELFRRPC
GKCYQLGESSEGDVQWGEFSGAVTNTASGLNRACFRNNSRYVKTLLERGSALVVNSASSD
PAISTQFAWTPLLCAVNNPNSDPGDVVRMLLEAGADAELCDDAQCTALYYAICNGYVDAA
RVLLEHLPQLSTSRSSVPLLVALGAHHFHACESDIRRLCDYIPSVDMLRVLLPYQTSLPL
LRLCVEIIRGKLRGEERLRQPTDDTSIWCPDGELELRTPEEEKFLLDIIAHNSRLCQQFR
EDVSSAARLLYNHCYFLSCREAFNQNPVDDQASSQCVESAPAQESS*
>TCRU_2235 exonuclease, putative
MGCSGAGTGVDRVEGGSSRVSNGSGSSGSNGTKSCNRVTHRRNAEGQWEDIKLYFSTVHR
LVQNREELTFVLDTVLGTGWCVDVETSPKDSESSCSAGVTLPLSQAAISGIESPRAPSFS
DRTTEHKPKQQGEADEEHQQMVVIDKLKVHSTLNHKAVPFESRLHSVLASPPLSAAPYYF
SGRSASTPAADPHTNSPVSFSTPPLHQCGGVAMEMASSAMPSASTTVSNGTTPPAGPSLL

SSNTAFKLESREDMIRRRTAAAAAAAANYAHTTSGNYYGNRSRGTWSGSVSPLLSFMNPA
LSHSSCPYDYLLVLDFEATCEESTPPSYLHEIIEFPVVMVDVRLQRAVAEFHHFVKPKVN
PKLSEFCRQLTGIRQEDIDNALPLEDVIRRFERWHAQTVPPGSRTMLATDGPTDLKEFMY
IHSVSRQGIRFPSMFYQWIDVKRFFAHFFQCQQGKIKAMLDALNCPFEGRLHSGIDDARN
VATIVIRMLKLGCSFCEIPLSRLPYGATATTASLVAPEITTTATETVKLDKNDTDASSS*
>TCRU_2236 exonuclease, putative
MQSARTRDLAAEVALIRKELRPLPESALDGTDDGAEDDGGGALLHGTGTRFEILMRGAKR
RTAAQSAGTSDAVDRHNGSSSQSKKRLVPQIFSHLLVCDFEATCDSASVAYPHEIIEFPV
VCVDTAELRVVAEFHSYVRPTKNPRLTSFCTALTGITQAQVDAAPRLPEVLRHFDLWLRE
VVYPLCRRWRKEHLEGLNKCLKASQKRRFVYDETHNPGWIDCERMICMVTDGPWDMRKFM
YECSVVRDGHLFPPLFYRWVNVRHSFAEHFRMRPRKLNDMLRKLGLSFHGHPHSGIDDSR
NIARIVIELLKRGYRVHHVSTINYENAAAATAVAQLLGESDEDGTKPPHQRAEGRKKGRK
NPTTTTAARRRGEKGHQAQ*
>TCRU_2237 hypothetical protein, conserved
MSHQAKELFRVNVSRGSAADNPSTASVTAHSSFKGGSTSPWSSPLAAGSETQGNLAEKTL
PRTPSGATLLHESQRQEKDQQNHHHHQQPNVRTAPNSSVLSLRFESPSFVMFRPHTPPRI
RPTSELPPTRDATSVLRGMPTVLKASDDTLHDVPARPPQAPAQPRGLDALHTIDTSTHET
RAASQAAMPVSSTVAVMGEEKTVRGTICRVCSLCGISVILVGTFVEHQQQWNEHVDSWAH
QRNVQLRALARRDDFISMESTDVASSPPLSQGMIRTLGDISASPVLLQKEEASAMAISPL
RAIFFPHRADGIQADEDIFSPHEKRRGNVSPTAAPSHVFKELFDEENLAATPDAKSNEED
HVDICRKEERPDALWKVGSRRRRKAMLRDKRGGESSRLAERTSEVVSVNERGLSRVKKIP
HTDYAASSEHSGSASPRRERQLECTLAKFLIQKEGRQLLACFRRWFNFVLVRMMSDSSLL
IRASSKRGPAAAADLVEEAFSAVSAKPKCGEESLLHSSAVTLEKREDAALPAAPSHIEND
QQREDQMLNKTATGDGEREGPFMASRVKDFAHFIGSSSSSSVEMEMARTDVSWYVHRTVR
PLHRGSGGGSGEGLRTPPWESDTSIEEMLSTLTPALQERVRAVLSGEPERSRAFPKTSEA
LNIIRYPSLGPNLSPGGPRVLDTDGNHSISSSFPMAHVTRSGSGDVMQGIIDPQKGSSSS
FSTHVGPIGRRPTGGDAKPGNQEVPILMDVEALNFPSPPAELSGMPPLRQEEPLGRLSGE
TAPVEVRDSPSHLRRQKSLEGYQKASSEEKPSPSPPSKVCDFIGQDGDEKTDSAPHASYF
SQPSVPRQRRGEQEGSPSWRQAWREELDVGKDGANEEFKGIPGEYYCYYNDAYHRVLDPT
CEEYYDARGRRLPIFFVRRSTRTRAFSTRRLIATTRPKSPLGPGRLNPYCSVCVARYFLI
VVDEYMRPITVTPRRQRGASGGNGEAHTCACPGRSAKSSPSRGMRDAFTRKKALQSPRRT
SSWERQDSSFPSPLPHSFPLAMKSDSTGATTSGHASASPKLVSAAQLGDSKAPETSQDPV
PEENKRLRRLERDLRRRVKSLLWRELPQCRGSQQWVDYLTSLKEVLQMLEALRSAASVQ*
>TCRU_2238 hypothetical protein, conserved
MQGEGSRAALASSACRAKTPLLLHLGRVITPQSLRRARQYVDLLANPPSPPHPFGVFLEE
AARLRSRAAAAATHNTARCAENGEGVSSGSAVVGAEDADVSSLLELLRREHGYSTGSAMH
RIWVQQPREYLAGMAQRIADLVLTRVMPLVASERKGGEYSHSQSEANNTSRKTQFVKQER
GNYDIHVRFLPSSASSLQVHAPIAKVFCAEITVRDAEALRRLEEDADLLRTQYTSVAAEG
QTVQSALAFWRAIKMDAAAEEIEGPSADDALSAVVLGRARNPADEKCARRLSAGGADALW
MQPPNKRPRQAAASATASAGINFSSRRKLAAPQTTGLEPPRVPLQSTAGLVAVFYLAFSG
TLYTGVLCGAAEEGDPYPAPVPHSTYAASDGSVTGKRVETTATPLDAEPVFFLPCTASNS
FVRGLLGL*
>TCRU_2239 cofilin/actin depolymerizing factor, putative
MAMSGVVVSDECIKALTDLRQKRCRYVMLHIIDQKNIAVKAVGERDATFQQFVDSIDKSS
PCYAAYDFEYETNDGKRDKLILVSWNPDSGLPRTKMLYSSSRDALNAMTEGFQPIQANDV
TELEFEDIVRKVKSHRQC*
>TCRU_2240 hypothetical protein, conserved
MTNATARERNKAAVQRLFARGRSSPAPWTCPPVRCADGTLLPDMRLSKQWQLAQEVGCGH
GDAAAAAAVSAPHICAAGPGSSSCSCYIMNRKIARHEWETNTKEKRRLQEGSPRSHEREK
EQRAAMDREQAILRYELSIPRRRVVDHFLHLTASQLDLCHTMPTAHTMDRLVEQRRGRWV
LQNPYRQLLLRGEPVMTRIMRGEFYAPQRNETKATNFPQANKRHVRIASNINHAMHFNRG
KRGSVDRVQQSAEKSALT*
>TCRU_2241 hypothetical protein, conserved
MPTVVSLVATWAAEHSLKINADRSGAALFCIVSHRQSDEETADHRLGDENPRVKSHPVRL

LGNAIDRHLNFGVHVTVAARQTVPRRHQLRLGAEAGASRHTTRSFLVGCVHSALHHGGEA
IAPCPAPVHLHSLEVRHRDSCTASLGPRASKKDTSVHLAANLAPLRRIIGFRAPTQHERL
TLFRCIEDVRGAI*
>TCRU_2242 hypothetical protein, conserved
MNKSVGIASRADVFLQEYFDACNDEEKSEEEFDDESDQDSPNYWRSSRLSPLRGKARLSL
HQRNSVQQALMSQESLSRRGRDAAAAASLLSRPFIATAEMREGMTGSATVSLNNTMEGTA
AEGFLFDAFCAFRQSPNGSFELSPTPREGGPPVWSLRKGIVVAETWAAISFSLRSLMEAL
LAGANEVARAQWLLQLLGGSLSQEGVSVMEDAFTDYSQTCTGEEGLLLAARLVLCRFASV
GRGLVQRIMSWTTQVQEKWNSINPNEFMKPDLHKCIERLLLPLRRCIHLLERSCSLAGER
PSTIDSNLTGTNVNTVTRATTLMDHLIVRMSALQDSNTMDIYRFYMVLLIYCGWPYVLLM
TSAIFGFVTDIDADAWRSNIPRIFRLSFSHIRVGDHGRNDRKVVMLPTDILSFVLLCVGY
EPVEADGRCSEAGGKPKRDVNRARRRAAFSSMLSSRSFILRSFAAFTRKKVLLGWSRRRS
ADWRPTNAECSTGDEWLGFIQKGEKTTSHSVSTAAALSLTLCGDGEDEFLSLWPNFSTWT
LCVEEKKTHHDFILDDGTAGGNGKPLQLWLHTSLPAARWVTASLLVPIAQVVKRLNERRL
AELLSNEIARHRVGYHSENNLENTDDVCYDDDDNTPAIRFDMNSDAWNVGSSTVSMRRGG
SLSLIGGGRGAVATKLLPNDVTFQDAVRLIIDIALCRDSERIVYTFLYRLFNEPHWWYRR
DAVGYKYTGTASTFISTTFADAIRGKALAQFVRLSVAPTSESTLSQGTGDDSALEVLRTF
ASFELVFSFPWDIELILLPLNLSVSWGGADAIQEKYASYFWKNRRCGEEAKVRRGNTEKA
AGKTGAQEERQQQPLDKQAVKARESWSYCFGYLCSLYYAQISLREQRKRLQQRDIFSHNI
MSALGSSEEGKKHTVRLTRGLGSAYFELSFAVDSLLSFTQNIVGIVARELEGELTKLGKV
SSCMALCQRIDALLLRLCTVCFPVAPGLEDTCPMTDSLPIRESITAVLAIALNPTSLPLR
HITSRTQNAIEALVAVVRALPATSVLKEKLSSLLVLLTFNRFYGK*
>TCRU_2243 hypothetical protein, conserved
MEGCPGGKGGRTHRVAGACRCGEDSIPGVDPDIGPRVAALRTGAMRLLPALRQACTRPAD
HKEPSVSVVPSLPHCGDRPASALAGTSSRRERRNSLSTSERRIDVLLPNLRQSALVRPQY
EGTCRTCSAWRYNGWRGPPMRMPQWRHRLPNGCLARGSPPKLPSMPAGNTRRKHKRGYSR
WTRLFRHRLITGATGC*
>TCRU_2244 hypothetical protein
MLENDSHNSSEHVFCMEKETERVAREESPMERYASLLLCEADRHQRLRQALQKRLRHVQF
VPNSVSAGLLGLLVSPSKNGFSVNTADDADASSAILKQKATHNDADIVPQLTSELISHVT
TDWSLVEASQEEVIKHICELPTSTDDEFQLIQLIQRDKIRRMEDMYLLLEMCFKRMIMSS
CSRAGEESAEGPVAFPVGAHNDVVKGELLSNEKRVIGNTNFFLPAVPELLDLCDTMDLCL
SQCQETRQKIQHQKNVVCGAFGVLAMKRRRVHLTTVIRMLHFIEQRHKQTHDINIFLKAG
RFAEVVLSLHQLRIQYEMRKPVSGSEEETLEMMCEATTLGQTVLKKHLYLCTQGVKALGL
ALQNRLFQVLDSLQDTCLVWSKDLVCSALRLAYGAHALCCWKGKPTRALNQHSSNNTGNL
TAGRLMEAYVMDKLHEVVNENIKNSEIGGGGIAVLAESVTLSEVRRCTSQLLTKVSSFLR
AVLLLQRCFEALFASESRDNCMKDDCLTFEQAIESFLGDDFAFCKALSSGDEAAVRNYIY
DVISLKKVYEDCCGIGRHAVKEALRLVLSYQTHLPLENLTLLELLLSYRLFFHFVDICRP
VFPTDDDFAGNITAEMEARLAMLVKRNYLTAQADTLGQLLRNDTGIFVGATEDDLPPLYP
LLPCELELEGNAAHKYLLVPPVRFCYCSKEKVLISHITCSEEEEMVMLNPFLNTQAFLSP
EAIPAADTFRIRLFSSRDALEVFTFSSLMGVKMMVENTMYAQMFRRVALALVYVNLGITS
LYVWYILSYFVSSGDQWFFRSTAVDGELKQFARLLRDEYLPRSFDWNKVDSSPSLVWRSV
VNSRQHLFAAVERATGLCSVLSIGAAFKAILSALKPLLPVDELGQLDSVKELMGRLCTCI
SQNGLRLLSNQLLSSNAFAILMEEFHWDGSAESFPIAVSKVKGSCSFSYPVRQVMEAFLR
CQHELRELYRDAPSVSLRRLLDHMILNVFTGFVEGVSRIRKFNSFGEQQLLHDAEYICHE
MFCAQPTLNRRPIIFYVQRYALAMTLSSGLAELVTTMHHLYTTRQLIALTARLDLSKRRD
VEQLIQRTHVRDEIPYCLIEEIA*
>TCRU_2245 hypothetical protein, conserved
MMRLTRRCLFITKISKISRPPASGYEIAELPNEKVFMEFLKYYNTKCVLAVLHSGSLRST
AGEGGAGTKIVEDPLTRSFISSINAMNMGNPNETKLALVPGPHAPRMVEEYGVLTYPTVL
LFMNGKCVERVVGARTREVSIKALFTLRNAGRNIFSRE*
>TCRU_2246 Protein-tyrosine phosphatase/Tyrosine phosphatase family/
C2 domain of PTEN tumour-suppressor protein, putative
MGPCTGTCLKVPNEGTCGKEGNTSAPNGSTCVLPELCLNDLNKLLGEEFNETDVHHDEGN

EVIQEYTKMKNTASETCLSTTMMCIRGAREMEEELGAAKKQLEDLMLDQVEFFSHSLENV
GNGINTAAGQIDLNIIDEILSEDSFDSDDAVFFRMAEEDPVPKPTEIGSSLAVLVSQNSA
LAMMRSKVSQLKRRYKMDGFDLDLTYITPRLIAMGFPAWGTEKYYRNPIDQVELFLESKH
GGHYRIYNLCSERPEYDSPKRFQGKFKRFPFDDHNAPCPISLVIDFIRDATSFLEEDAKN
VVVVHCKAGKGRTGVMVSCLLRSLDPIGIPDAKEALRVFGNARTYNGLGVTIPSQCRYVY
YYDRIVRDFGGQLPPSRPIKLYQIIVDSSIKSCGQVDVYFTVEENGVMKIDSRHLFHGGL
KRDPKGFFFLFEEEPTLQGDLRFTFHQRHRLFNEELFYFWINTSLCSNYERFSLKDRELD
GRLSKGKDGDTFCKDLAVNVIFVD*
>TCRU_2247 hypothetical protein, conserved
MSKVVPLPGITFAGASYARNERVFDSLPKNDKRRIRRGEVIRFRGAPRSFERPRWNISVL
DEAHPFPQLPIMHSLHSFEGVEVLHREFPEIVRGAKHLETKCRPGLWTTRVKKGSPRDVD
SARERWNSYLSRVIASECSERKKELRSGWDSSKKSWTFTGRIGDPKESQRSYVELNKTKK
ILNMDAYNSPLSRVKKMNESIRAAKRNEKMRKEQTSLTHVCASGAPAVFKMSNIDEWWHL
DPTLTAAETTAASAVNVNKGSEQ*
>TCRU_2248 EF-hand domain pair, putative
MAVLYASKAKCTRFKAIVERTRRLLFTGASGANGIRALSRSLGIAVDAGGKLVDKTTFVE
CLKSNDVPLDEEDVEAIMSVLDRTGDGMLDPVDFIAALRRELTPVKRTWIIRLWYTFRQN
TNGTIFIEDLVNAFNPAGHPSVLSGERSEKEVREEFQGTFNTTTNPDGVLTRQEFEQYYS
CVAGSCLDDASFVALLRGVWPALAGKSGQHVTVNDERENICGATFKASQTAVQKGAVNKV
RQIAADFDGIIRTSHRPAVMASPLAARQVSLLLRVKDAEGAFFLTREDFLATLWQQRLYI
AKPEEALEVLDTRGDSSVDYLLYLTMLLPQLSPARMMMLERLWELFPKDTCGTIDVLELH
NSFNAKDGEEKNAFLSAWDVRLAIQRRVTLEEIVDWYIPMSATVQLDKDFEAVLKRQWNL
A*
>TCRU_2249 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MLQDGKGFMYVNGKIVGSPETIPTLETQGHEITQFYFGGGEGDINSNVTVKNVFLYNRPL
SVGELKMVKKSDAKKGNGDGSMRGGVSRVLLLQLLGFCAFVAFY*
>TCRU_2250 hypothetical protein, conserved
MEATTKSGDKITLDTTHDTGFGFHPGEIVHFTKSLRNGKLALIRGVADGLLWFSVFRTVE
EAEAAEALRAPVDTASCRAKEEFIRQFGWVLDLKTNPAARGGGV*
>TCRU_2251 PrimPol-like protein 1
MFWCKSTFVTHFAADDCQLFPTQQKLFDFIDAQNEEEGQQAHSAPKWLPFSIELPSEEEV
VRELASRSLRASAAAIPTHSGSGGARGRLFRKRPLSMHGEDTRKTDDEAKYLCEGKRQRR
VVLREDYAVFYGVTPLSSQTRMFLAATVNGLARVVREIEPLQQHLYEVIREGAPCHMYLD
VEREKDYSAWLPVVSVVDDDSEENRVIYECRRAEEYSAALSTALWKPPRCCAWNCRLRAD
NSETTTVLLTELRRFLCSTYPALVKSRDSENHGAFEDEDDTVLPTDDNSTAAPLGPGVEV
MVMRSLDATEKEGGRGGKFSQHYVVKFGGQWFNSNADVGRIVGQFVEYLYERAVADPCVH
VALFYHDSPKDFAVLPPSQPSRHLPFLPLRCVIDTAVYSRNRMLRCLGSCKLHKRSILTV
ERNVSANFPTGTIPTTADRVALFFDSLVTLQVGHREVILVPAPTISTFGAASSNEGCKYG
SGETQLTKDVDRARYDALAEHVAREWSIVGGVPCRVSSVRQRGGRYLFFLLDGSRYCSNV
GRQHLSNNVYITVDLQQRVWVQKCFDPDCALYRCAPRAIPDDVWSTNRHDWTSETPTAAL
ASHASLRTIFQPPR*
>TCRU_2252 hypothetical protein, conserved
MVYRRSRLSLLSRAVPPSKLQALFLRCGLRDIVEAHGDNFAREVAMRSKYQLFSPLFAPY
FTMESHHLTMLGDTIIDDFLSQAMLRYAIHAGLVLTTNATRQLNAVLHNHFTLRLFAKEL
HFDELAVPLNLDSLLADDGGKTTGDRLAFLEPQYVGLREHDVAGTSFQVTPLRAGQSPLG
WMFSHFIGALQQTLGSDVVRRVLSHTYGDVEMNLPSGAAALLLRTLQHFPAGNVTEAVLA
AQGLPLRFVTKTRVLSDEATREGEEDGDEVAGKKSVEEAVLCSGFGVQDATRDAMTIDGI
AANPGVLASLAAGPGGIDAINTWRQRAQRELQEGRGLLRDAIRDEHDDDDGWLHPEERER
YRRGAAFYNAVDFTAVANYFADLYGIPQPVNAQRVTLLKFRNSVRDPLFYDTRSDMRNGV
PFSTDGEPLAQYLDRFNRPHRRLFEVSLVVGSGEGRTAGRAIATRYTVARESACRAYLGA
VLHDLHTMKERNSTAV*
>TCRU_2253 hypothetical protein, conserved
MEENPAEEDVNEINTTLLELQDAFATALRNAGVLGKLRAQLRAAAISVIRGDPYLRTAAV

GKTILPAALSPEGRVALILIEEFARVHGLQQTLGVFEEEGNLSLVGELERNTARRLRGSL
ESSALEQLIAAAMAREAPQLQGKEPLMTSGSVLPASTPFVSDEREKEREQHAGARQQQQP
KKEVRAELETPCHPEIAAGLKEYEDSINYSIVSVTDLPGVDESNYDKIENF*
>TCRU_2254 WD domain, G-beta repeat, putative
MDRPFETHIRAEEVEEEEEAEDPREAFLDLDDPNNEILDESKMAEIEDDDNDDDGGGRGE
EETQSCGARDVDEVGDAEDLNGIPDREPDRDDALCVFRGRDGHPLHAVTAHPHDTQIFAA
SGESDEVYILQLASDRRTVETRAVLQGHSDTVSLLAFSPDGTWLASSGMDSAVALWSTST
WELRHCLRDLSGEILTLLWHPSSLVVLAGGEDAQAAMWNVSKGTLAMYFAGHGGPVTCMA
WSPDHKKLLTGSGDGGVIVFNPKFGEQEAYITKGLSPDRASVTALCFLGDDDRCVVGCED
GTMHVISLRAGRAVASMQEKHSQAIESLCISHSSAAERISSLPLLISASCDCSIAVWNTA
DLTLRVVFNVGESVIPAVWAHGHFVVAGCSDGEVKVWDGRSLDQQPLLRFMGHRRMILSL
TVREVSGVVATASDDGTVRFFSLGLQ*
>TCRU_2255 hypothetical protein, conserved
MAQRVPYDVVYCTSQDDAFPIDGLGHGLLPNAAAAANVTNASMLRNCKGWQSARNAKMPQ
ALVLRFPGNVELTQMRILSHECKIASKVEVLFFALKGEEMEMHPPSFRAIHFTKLGAVDF
NSNEQSNYRSKERKTIHMHAVAYFVKLLFHTPHRNAQNVFNQVGVYSIECHGQMLSRVWC
SPDKTPVIGNNKNKNGRSMSGGDLTESVRSSEQLHGLVLDPTRRRQEQQKREQVEEEKTP
LRPFLRQELRSPYSAQQQTRQQLPQSPPLTPVREIIPHGNDIPVFRSVRIVEFEEFFIRR
SEELLALKDQAVAVEDFDTAKLCRDRLNLMNRRSKRIYQIEQDKVQAIIEEDFDAAKEAK
RVMDAMIERVYKDAQLPRPQPDFDQYECIGETFHENLNYNPPRSDMADVSEERTRDKSPR
DTGGRDDGADHSISSNGMDADDHRYKNERDSNNNNNNENKDNIRMDIDEYRDSDAHEGDT
MPMVSKFAQRMVDMVRDTTYEIDKVDPPPQEKSDDNPPTPKIEESTLQPWERRVAQAIMA
ASSETNGPAVLNPYVKNTREALDLLGVLGTFTTCCLFSKRFKLREAVLDVLMERMGELYQ
ASPSAMEEALLRFLDMNGHGLQDTIPNVVAAGCAFVRMVLADEHKCLSSVLAPVVNLLPR
LLCCAADSNQRVRDEALATLTLCIKTHSLTNTTILTAVLAHPLDKERRRLPSCGPRVQVA
RLTVFEQLVTAGHMGLRNHTESVWGKLLRPCINHQSREVRDAAVSTITSLVQERKILLTP
KHVNMIDNAAIRDQIKAVVEKSNAARTSGEAGDAVGAAAGAGTKCRPNTQGGKAGNGRGK
PRTKRVNSDVAV*
>TCRU_2256 ZIP Zinc transporter, putative
MVSCSEEGIGVRVVRGDLLQLLLENCAWATARMNDVALFKIGVALSLTSVTVLGMCTPFL
CVQNAKGNTPPRPRTQLMTSSRPLSLANCFSAGTLLAISLVHFMPCALATAGNGVSPTAL
CAALMIGVLFPALIERNITESVAQSGYGHSHGLFLAHESYQRLTLMPLIMLPMCFHAAVE
GVLLGLEASVAALMGSAVPLFVHRFFDGVVVGVCIAKEVRAEMEAVDEVTPLNAAEKNTT
AGDFAATFRRRACRFPIILWLCIMPTALLFCVVLTGDFHVHGVSEALHRGGLTRPSDGAE
SHLRGSWHKESKWLALTQAVGSGFFLYAGLTTLTLEELKGTRASLALFAGVLFTSLLGAM
ETH*
>TCRU_2257 hypothetical protein, conserved
MSSDPFSITLKTAVNTRAPLSDRVSWRRQVKEVVSAKSALHRGIHTTYDAAYNFVPARTD
PSDGNRFLSLLRSRVGAAGSGKSARLEIVTAPVAEEHLQCERKQPAVPRHSLPSQPEEEL
QVSSNLRFFEPVLTRHMPSEWETEQQASSRNVLPVASHGFYSTARKIEHEDDDRRSGLVG
NTQRTVDIMRKRASNPLLCPAANKYHSFRPVRPPCVTDESGRPASYCLDIVDCTQLAPTT
EEQLGFDMGPISRLPNTATLSQALDVQQRVITHMGTSHPLFVGTAKVMETAVPNYTGHAP
CHPRNIAAIRGNDTDPLRLWSKSFMTLAEHGGGVDAGNNCKNPLVRKRGGIRAPQSKELP
PKSEKGIRSTVEGSMLQATLKDTLPAEHAINQREDKALISLA*
>TCRU_2258 hypothetical protein, conserved
MRSALVWQRGSSKCVGDVLDAIIDKAGICSRGDKDERTAKRDGEGVTRWKHRNRPPEGII
AAVMRGSNPFFVSLRPLTNATSKKKETAEGPRVNEAVTRGREAVPKREKRRGPKRTAAGC
GNKQRINVPVTATAVQSCVLSAAGASVASTTPPSPCRARRLTARKLRWLSNGVTKATALF
KLFKTLSLYGQSRLVKNRRRHCCRSAEKGNGVDGGEARLHAAFWSALASVLQQRRLHKKQ
WHALWEAQSDGQCDVQLLRAFPLFGLLVVVERMRWRQDNEDPCTVIAEVVGSALGVVMHE
SRAFIGVALLREEKKLRVLSNHPLIGEGMRRKSTDNALMGDEELPTGRILRVSKMFPGGT
GTAAELRCPRETTRCVVARVAPEELYDNFTAFSPLVGRYL*
>TCRU_2259 histone H4, putative
MAKGKKSGEAKGTQKRQKKILRENVRGITRGSIRRLARRGGVKRISGIIYDEVRGVIKSF

VEGVVRDATAYTEYSRKKTVTAVDVVNALRKRGKILYGYA*
>TCRU_2260 Zinc finger, C3HC4 type (RING finger), putative
MPKKTGGKKKGQSSPDGSEPRKRKNNKKATMEPRDVDEMQKLQELLGDEEQPLGVSNKSL
EGLLSLRQPQELAVRLAQSLSSLRARLAELELERLNRGSEAPGLSNIVARRAQEKAEKLE
LEIQKTERVTRRLKIISSLVGHIIRLREKTLTETHTAMEAEVQSLQEKIRVNEELIRERF
VSRVNMLHRYWLWRTLQELGDQTVGWTFEEELARGPRYRTLGVQNNIVSETLEQQLSWLL
VFAEKEKIFREHVRRLELLVEELTDINDALEEALTCRVCGLLFEDPVLFWPCGHVFCLVC
FDTLSIAPSLFRCPTCGSMGSEGYVHNLLIAESVAKWMFKDAGYGDIHGALSLIRLHLSK
FRKEVISSRVAQLHQQLTEARQKETKVEELSQMDITYRDF*
>TCRU_2261 hypothetical protein, conserved
MTSKTPSRRLTDILRSNSKETLLRNAAELARVSTSLPAEKLQTRFLRNMHLISPKSLRLL
CDDAVLSRWFAFAVYKPPFCPMRRAEANKNYHHVSVESFVEAALRSRTVQPVLQRELQPE
EVKVRVLNDVDMYASGPVVVTLADRHTFSTSLQSVTMRYDVLVAGHMPLKEPCSVEADHL
FAPLRRDSNTEDICSYPDTTARATRLPAEAAPSSCVCTYQVRRNAYYSVHPVSLLEFTIT
APPTPLPPRLEAFVCDHLGTFVLGDSDTPATTRRTKRTAKTPSTASESTDRAQAAAKASR
SVVAMHGDCDFPRVFTHLREVSIQTDVADVAGGFAAKKPIEFHCRKCFEPILQRERIYSL
KGRRIGLLDGSWTPEAEFL*
>TCRU_2262 prolyl oligopeptidase, putative
MGVGGRPYDADEYDATIVWVPSDYAFHGDKFTSPLRPIPTKNPVAVVRIPVYLCRKKALR
SCGGNPMLLSVYGSYGECCDVVFENERLSLLDRGFVWGFAAVCGGSELGAAWRKASCGLQ
RATSVNDFVSVSFYVQETGWCAAGQIVTHGSSAGVFVATAAMCVAPSLPLAVVALVPCVD
CLTTLMDDSLPLTVSNWEEFGNPRDDADAYRLLRAMLPMDNIPSVGVALPHMLLLTAWHD
TRVGFWESLAFTARLRAREMEEGAATR*
>TCRU_2263 hypothetical protein
MFTVCSNSYSEVHVIPCDAGVEKCVSEVPVFPTTANDKGEGLQNNTCAVHCFADRNFCMD
YDIDHHSSLFGEGVDAWVVTATKSSKGLEKFRVAYVLDEDEKACRKDAVGGGNRTLSDPS
CWQSLFAYDTCIEVEDVECMRDYLLLSVGRAASSTVLLLPVRVLWDRWRDCHGRNMPSLS
LQDDTVDLRQVASRPFHSSGEVRFSFAQLLQEQRLKKDNNSNEEKENEGCAHRFY*
>TCRU_2264 Prolyl oligopeptidase, N-terminal beta-propeller domain
containing protein, putative
MRANGASQGKKGRGGKRTSKNTGDHGRRSAAGILSLPKYPRKEHRIVHFGDVRTDPFYWM
RDRRNPEARRLLQHENAYVESVFAKLGGDQLFRTLFSEMRAHWKEDNASLPF*
>TCRU_2265 GTP-binding protein, putative
MQSLGKSFQRSKKASQRSQREKYRGLLEGERNAAILQEEERQQQQRQKGAPLKSIWETNN
LEEFLLIADAREKGYEAERDIRVVVDGTPHVVTNDKVLPMSKESVDWLKLSELLTIPRRP
KWEYGMSAEAVQAMETSAFFDWRRLLAKMEEEHKVVMTPYEKNLEVWRQLWRVVERADVV
LMILDARNPLVFRCADFEAYVRSMCNAAGKSKEIIFLLNKSDLLTESQRSEWATYFAERG
EPFIFFSAAPAAKTSPETTGEKDGSRTATQEGKQNEEADDGDEEEDEFLDADGHQVDESC
VPELLRHRREKRRHNKKSLRAPVEVANPYELVEQRRAEKARRSQEKQQASRVAPPPTENE
KARDARVSQLQALHPWAVLDPVQLLDRLALWRTVYGIRDANTPLMVGLVGYPNVGKSSTI
NAILGCKKVVVSATPGKTKHFQTLVIPNERRVALCDCPGLVFPSFASTREQMVCDGILPI
DTATDALSAVNVLCRRIPREVLQKQFGVSLRAEDDVDESHSLVEHFLNALARRRGYLGAH
DRPNKSRAARDVLKLYVDGALLYVEPPPNYAPSKDAGVVGLPAAHVDGKDSDGWEDVECD
SHDDGSDGDEWDDLDSAAEARAISEEGDVSMDAHADKNDEEDEDVDKTASLMFYARPSGI
RGVLTAQEAFNAEANANRIRTLTSAALRRKKRTNHQLDPVMDTFVNNDGEVELIIDDDDG
IIELVTDNSRQNAEGKQQQQTQQKRRSKRQIRRELKRLGAGPVNPTSRKMQVQGY*
>TCRU_2266 zinc finger protein family member, putative
MADSEENPFVVDHTDGNTEPFLTAAELPSPAAAGGMEGGRVKDEPQRQQQQKDVEEAKGD
VSSLIPLCVQHASGPQINSAVFGYDIAQMQKRPWDDPAVNLKDYFNYGFNETSWRLYCAM
QAGGEASLLTGTNAFLSQPAGPAMKNNAMEEVVEGDGASYYVPPQGSSHAYYAAPRDNFL
KTKLCQRFALGRCVKGDQCSYAHGHGELRSAPPVQHQHHHQQQQQQQQQPPSCILPPFH
VEQGYMPSMGMPPTGVLEPTVAGNYHVMPKRQRSPDGAEGQVYDASY*
>TCRU_2267 dihydrolipoamide branched chain transacylase, putative
MRRIALWPHRICGARFFHFSRPRWGTIIPYKLADIGEGIQKVDVVTVFVKPGEKIEEFDK

ICEVQSDKALVDITSRYAGVIRAVHITVGESTLVGHPLVDIEVDDDVKDDASGAEPQPQE
AAAVAEPTTTSSSSSPGKQKIKAASTTPTTTAVKLLATPATRGFARECGVDLEKLSGTGE
NGRILKKDVLAHAQSHGNDEGDVVVSLLTGIRHVMVSTMTEAGKIPSFTACDEIELTSLL
KFREELRRNLTPRSPGDATPKLSLLPLFIKAASLALLQHPQINSHVSQKCETFIIRKAHN
IGFAVHSPKGLIVPVIRNVEQKGTMDIVQEVNELVELGRKNRIPPEHMRDGTFTISNVGT
IGATYATPMILPPQVAISAFGRLQVLPRFDVDGNVVRANIVHLSSTADHRVIEGAAMVQF
NNALKGLLENPQQLIA*
>TCRU_2268 hypothetical protein, conserved
MVSLRYVREQQEAAVRRARFEEARRIGSAIGVQRARAYAAQKSAQAVKVREDMRKQWECE
VQQQAALIDRVLYDGQSRLGEGMRGAAELTAAQQRNASDEINAWVAEHALERERHRIARA
TERVTRALQDEPHRSIVGRKKAVREVEDKRSKTRIAQPSPRLPSFASHGSPLAGALSHTA
IMQARTPTPVASVVMVTADNDDGHRRAARGEAAAVQFAEERKRELAGEREKLQQCQREAA
ERAAAYLSERDKEAKEAREAARRRAANMAALEQRIVAEPQDDNSVSGKVLETRRVAMLKA
QEEVEFGQLFLSGPLPLNDELSLKEDNDDADEMRPFPLSSVSCLLPGESEVVVQLHPRPF
HVYPIPEEAPADADDAEEKATSEAGSNAPNAASVAPQPTPMSPQLVVSTKLNSSPSRTLR
SSEQSLPLEVPPSSSLSLPPPLSLFPSAATAKKPDVAQLNLSTHDEPPNLALHHEQFLRN
LKALQDKLAKVSSDSADVNETVDVSTCHGNVTLSSMSSPLSMARRPGKETREDEYEAGAT
SIDTSANSGSSSNGGSSSTSSSGPSTSSVYSRSYPTMTAEQLKAALLKLKLRMRSA*
>TCRU_2269 hypothetical protein
MDSAREALLAETKRLLAALNDENRELKAENTRLLARCKTAAERLTSVSVEKEGLEKDLKH
INFNLMHQLRVKVGAVKEHERRAAQLQATVTGLEKQLQESRLAQESAVKESKMQREQIAV
LESRLQQLTERLFRTEAEAGKYADDLNAAISGHREAVAKIQHDGAERLKQVEEALRVSRG
NEAGLERVVEELRYELGRAKEVLRQSHCSSSEGQRRTLSARSEALYAHEQVLTACNASCQ
QLRELQQKLRGLESLATNASHHVEQTLERGEARLREQMEHFIGTDEALVAFLCQRIMDQE
EALRTAREELARAHHRLRESEGELHKVRAEKQSYEAELKSLTALQQEMQTIRAERQAHGR
IEEELRAEVGRWRHEAERSASQVTEFRRLLQEQREQSEAADRIHKREEDDVDEQLRGFSA
AVSQALRKFDSTTRHRRRLSSSAGGVTLSHAPSTQLTEYAPDGNMSSPSVVRVEPSSGAP
SHT*
>TCRU_2270 Nudix hydrolase 2, putative
MYRKNVCVAIFNEDLRFLGCRRIQDNLFQFVQGGIEKDADLLHAAYREVYEETSLCKEDL
HFVGEVPPPSGDPREFRYELRRTSNLRNFGFQGQEQRVLLFFTDSGNIEKVNVIPPKETC
AQQEFSEVHWMELREIIDRCPREKIHIFLAVAKVGVPMARAFLQSRSALKKDSI*
>TCRU_2271 Putative methyltransferase, putative
MLSSRRHNILLAPKLMFITRSSTAEQQKEELHDAVRRHDSLVADNLKRRNGSAHATYDEE
VAVHFPAFQLAILPPTNGVHREGLRGSLATHVTEEFRRFLVQPWTSAAKRHVLIVGSRSV
GYLQRQLAMDTGHSVFVVDHALSALLDAATALVPRYGPRVHFVRSDAPFLLQRLMPPTTA
DVCVVPMPVPFWSESGSYRRLVTREFLCLVHRVLRVREGPADPRGIVTFTDTTPLAEFMM
EQLEESRLIVPWTRKDPAEIYGRWLPIQSPPDREFQQQRLGDVVAWAASKSGPTSTQAEE
AVQSFDYKRRYYRALSRQEA*
>TCRU_2272 hypothetical protein, conserved
MVFCPSSMALGRALLLSPFCHQPVAIPAAPSLRRLLLEVKPRSESSREEVVAALLEKLPA
HCDRVKKDMLHARYASRYYRSRYGRGMETRGKQLRGLLEMPDDEVRRWAQSRCVPVRDPL
APR*
>TCRU_2273 kinetoplastid-specific phospho-protein phosphatase, putative
MDPPSVPSSPQAPPEITPPGMSHSFRTEAFITLEMAQAVTINREKLSEWHHKIRSRLFSL
VSGFFVRCRVEDSTDGRALYKVGRIKTLKPDWSVELDLITTEEILSGRSHTNYDCISNAK
ITPTEFNSFISKVPPELLPNIFNTVFKMEERLRMLESVILVEPAFHGKRRDDKRTQEGSQ
VGGGVANLPEKYVFSQNVLLCEDDFVNLPQTVTIVDLLQNAVGQKGVAEPDTPRAGVAPG
SGTKPRAFDEAVASHSTMLQLQDMRNYMNSPTQPPVDAARLIETIRRAANPTHNGFSYEN
LPEFCKLVISVCSQCREVVAKEPLFVRLKSPITVFGDIHGNFADMAYFLEKVVGFDDIML
KYTTTHLLFLGDYVDRGAFSLECVMYLLALKVINPSKVTLLRGNHESPEVNGDMDVYGYS
SFKYQCLDKFGRERGIDVWVAVNEVFQFLPVIADIDKKIFCVHGGLPQYTGGEDKRLEIL
SDPSFPRVPVVQCTDPTNVAQRMMVNDLLWSDPAPPNHQLDKYGFGPNPRGPDIKTFGSR

AVDMFCERYNYQYIFRAHQEKADGLRLSDNARVVTIFSTSDYAGHQNGAGCILVANGKMR
MAIKKPQRQESKEVKGPVSPRTLGKSVPGFVPRLKRL*
>TCRU_2274 Transmembrane amino acid transporter protein, putative
MRKPSARRMTLHTACSMALCCIAYIVAGFFGYADFGDEVTDTVLVFYDVRRDVLMAIAYA
GIVFKLCVGFALCMQPARDCCYYIIGWDVATIPAWKNCLFCGVMALCALLLGLFIPVLNT
VFGLLGSFCGGTLGFCLPALYRMYCGNWSLGTVGIVNYVCTYLLLMAGVVAVVFGTGASL
YGVVR*
>TCRU_2275 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MAHDGTAVTPEVGGHYGENGAMVGGTDGQKGEDIHAQDGEVKAAALSSSLGNVSQGNNSD
AGTVCGSGLLPLLLLLGLWGLAAL*
>TCRU_2276 hypothetical protein
MADNATLVMALLFAFFVLLFFLLTANVYKRHLEDKKQRRRQERLRNCQRAEPFAPPVSLP
VVVDAVVVFPSHEEAQHRIEEDGAPITRVPSELPGDGLTTSHEYFASAEPVEEGNALPRA
RSGDVLQGVPVDRSLRLPDVNAASRRLNTLSGATYRLRPASAVYGSASYLPRSSSSGSGM
TAGDVPGVLQQSDAASCPETASPVHVCEAPPRAAAAVNAEGRTVPTTTARRPPVEEGQRT
*
>TCRU_2277 Cell cycle checkpoint protein RAD1-like, putative
MSVYCRVAQPHILLKALAALTIAKDSWVTVAFTEGVVVLHVEGKDQSITSTARLPKALFS
EYSAKDVRFAVHLVTLRDALLLGGPALLAPVVLARVVLAYPMGDARLLVELTDGDCTLQS
TLATRPVQERLLDLRFGETSVANQMVLLGDVARDAIEDLVAAQCPHAVVVLDPRSGVTLR
GEGGPYGAVTVQLQRSSEAILSALDEGTHAHTRVLRSHLALACGVRPGGKLWRASGAVAD
VAPGMQGTSGGAAQPTFGGFERLLFQVNEARQLSVVHMPRDHDVPVTVTVTVSPAHGLYD
E*
>TCRU_2278 hypothetical protein, conserved
MLQGNKASVHIGGHLLGEEEVQLAGERPPDVLRFCFGACGGHESHVTVTDVFLYNRPMNF
TAMRAPKDRVLVPTREAAPTPPEKNRVVDSVREHIAEDITEEK*
>TCRU_2279 hypothetical protein, conserved
MVMGGSSHPHFVSNAEGDGVSRGDARELQLTWTPTHSQLPAAKHSAAELISGGNCESAQC
GIEEHSNAAPDVIVFLPEIEEVTSLVRPTVRDACEQKAEVAAQHRLKYASFGSPSTSSSF
MHNGECFSFYEECLPIDTAVNDRICACEEQSILTTSIKAEDPGIISSQGAIARVGRNCGE
GLAKRCSPISHPLTRQETSGMMSGGTSSTNGTAIHQGTLVFAPRPDTEGSLFVAPSASCG
IAGPREDMFLFQAPDSRRESTLSPENLIAVATPRAIDPFCLDSSNVQNNLSLPLVVADDS
SDVKLNFTRSFSRTDNDPAVGRQVNTPNLGCELYRQSGALRSFGGADEASEDM*
>TCRU_2280 Putative methyltransferase/Methyltransferase small domain containing protein, putative
MHYEDFGVITAENGASSLSFELACATAMDHYIRCTAPHDKQETDKYMSPCSTGLRVYEGA
RVLAAFVARFGRVLLPYTFEYDTFRYPSSWVVELGCGCGLVGFTAATLFPELSVAFTDAS
VDCLNLIGASAERNGLTLIQINGKGFSGVFENNEHRVLVAYPLEWCEDDTVRLISTIRRF
SNSPNHVKTGDIRMVLGSDLLYYRVDIKALLTTCKCLLQSSEETASKDQCNTSLAPRLAI
LAHFMRIPDGDAKLQMVAYELGFGIVRVPLEAFVDADVIKNRGWNGISVVLLFLRSLPHT
DLHCLNIGSLCEQHEEEDLAEVKRIFSVCHISFPSEALVCYSKKALGNNADAFVDCEKGS
DLDNLPFFF*
>TCRU_2281 hypothetical protein, conserved
MQDTLAQRKAHEYYDRPSRTSSGSLECAVALHKTGCAEARCSKRGHIQFGLTRDLAVGEA
RRSVRPFPEYYSIFVEVHRTADPGVVAGRIDVKGELRKGRNPG*
>TCRU_2282 hypothetical protein, conserved
MRPTPLRGHSGLYTQRAQRNRKNILAAQTAVKKRQRGRPLLMKTDGGSPIHSTASQHFAQ
TSHRAADTLPDILNCPTQSSRRATELIRQRRSTVVRRITEIHASGRLYEESERGGLRNVS
AANVGRRMPLAGQFSTFCRTHEQPINEESRAAFLEAILDVAPSTRPRHTRMLRSMSEMNR
TLPDMMILGLQKIAARSETKQARPSTEEEMNQLIRIRADWRERAVF*
>TCRU_2283 hypothetical protein, conserved
MACVDGLVSEREYALAGSEQLLEANRAQLQERKCQLGLVNAKPQEREARVSAREAQQAAW
ETEMAGREEAPATWRGPADEPVTRQNTAEDGVTKKPHYTRRLMVGGAPSRTAQRNLTRER

RQVIPQTSRGNFW*
>TCRU_2284 hypothetical protein, conserved
MGVASAWAVRSAAEERSACRPSPSSSLKWRAVVPVGFPAAPAHQEELTFHSAWERVMPRT
LAMCVTTLARQPQCLPHTGQSAGRRIVAGWGPAGGGGVSVRGSLRACGAASEMHQQHVPG
MAGCRGRSSHPWLSRTPVRRRAGAASTSRVRAVSMRVGPSRLP*
>TCRU_2285 Protein kinase domain/Protein tyrosine kinase, putative
MGKEKRGEKHVRKQLEESSVAANHGGTVIPGENVDGRDALSWTQETQRIVVDTLVSLQSS
SNVDNTSSVMPATVRVPRRSEDKVASAAKTRHIDPLSASDHLFREKERHTNLFAFPSVLS
EGHTEKELLCHYPYHREGSLHQSYGGPKKRDSSVFMPPISNDPQTSIGSLSGITAPRIRD
RETGELHDTEEHCVVKRRNSKRENQKLTCMTHGPKPFCMKQSDLTLAFSDCAKKTADVAE
TNKKTAAQALNLRTTECCNDEASFECLGISLLPSQHENSSRASVPPRSPHLESINTLGYE
MSPIPREQEETGRSKLRKKHFYCCFKELPLSSVLIPYFLVLMCLSLFCLLTPYYVTTVII
RESVEEFHEHARLEINSQLEGALNVPTLLSSIFVALYVVDERKPRPNDDVIPMGFEMSQR
FCAALQNMDRYKLLTFIYMASLPRDEIAHCARGFHGHYFATAVRRKSDGALNALVAVDPE
NVTLVEPPLVLKKFSKPFILKDLIYNFTPTKKLIDSWKEDVIAGNEPRMQMWNVENFLSP
RYVYTYPFFEKDGTVSFFKVALDLRRVLGKIFAEESDPISLVRVALLENDGNDSNMTVIA
TNFNVKWQGESGEGEYEFVFSKGGNGRVRTIGKAGEYMVPSPKVGNIKDPLMREAFLHVN
MNEVMSIVRSGRNFFTTFPYDGSVGTFSVCLTQSELNATMVLAVVVPPFYGERFEILHVV
SLIGAFVSTIGATLLVYFVFSTLVSRPLHSIAAELRVTAKVDVTLARTSINTPRIRGIRF
ALLEIDKLQSVAASLKNQMRHLRSFLPEGVLPLRYATDEERKAKYMDGGIQSEARNADMR
DGVEGAQASSPNFMCGKGMDIARSLLQDPRENINVFEEIMCSVVSVHILDIKTILEHTGE
TANIVVEAARKYGGGVDVFLPELFNLNFPRRGDSHLDKLDATFCAIEIHRNLPDAVRRCC
AILVDSGVFHFGICGGPEKKEPVLWGRATSTELIHVQRRYGVSLAILQNTVPFIRSRVHV
LPFASVLVDSADMSSKVTFHIVIEDIVNEGSWQCVEETYLNGFRYLTAQACTEARMCFES
LVASPYVTPQLMRLLRCQIAQVQQCDVKKRSRFPSEWRVGGSDRVDTLTSKFSPASVDNS
ESIVSGLHPPSLTFCGSRRRLTPSALSTSASSTHVSSAGQAIAHEFWDKKNVRWKRASEN
FPESGRFPVFLGISDTGTLAALKFIPVSSLPDCGYNDMESLDLALTRAQTLYHENLVQLL
GYGQTKEHTCLIMEYVPGGTLRDTVRRYGRALPLMAIKRFLVGILRGLEYLHDRGLVHGN
LRPEDVMAAVEGLYKLRGVSMACTAEAAAAMTEERLRAESCLNRWAYSSPEVFTTGKKGA
AADIYAVGVILLELITNQTPWRWMEGTVTRPLQNISPAEDENIRQQNTKKTLVELTSILS
DYDRMKVAQMERKISLVEIPREGDALIQEVLKSCLVTDPEGRKTASELLQLLSSMQ*
>TCRU_2286 Tim10/DDP family zinc finger, putative
MQGQMMVMHAMEHYSMLDLANDVLEKCWNICFDVNLTRKELVEGDLPDSKLRKMEACQRK
CIARHFEVMKLMNGARELREKEALQGLPPGSLSAE*
>TCRU_2287 iron superoxide dismutase, putative
MLRRAVNISIARGRMALMSYATLPDLLKPSGAPAELPKLGFNWKDGCAPVFSPRQMELHY
TKHHKAYVDKLNALAGTTYDGKSIEEIILAVANDAEKKGLFNQAAQHFNHTFYFRCITPN
GKAMPKSFESAVTAQFGSVEQFKDAFVQAGVNNFGSGWTWLCVDPSNKNQLVIDNTSNAG
CPLTKGLRPVLAVDVWEHAYYKDFENRRPDYLKEIWSVIDWEFVAKMHVQAIK*
>TCRU_2288 50S ribosomal protein L2, putative
MWRHWAASIFAGGAVYRGCLRFLHDIRGGTVGSPSLVCAKITRKGTTADVHFFAPALSVA
RRGVKLSNPSSKQGSQHYGVEPKLEAGKDVQLKHTEMYDGYTDDFGVFKEGPPTTLRLEY
VRSPEHGYSQQLLQKDIWSPFQVNANMMIYTPFYYDWKGFASRDYWGHRSGTNPGSKVLL
GHYRRAEERSWGYRVMVNHKPQKRIPKWLACIVHLPRKKTFVGFFLYANGAYVAELLTYK
QLPRICYNKPFQGCMPTIGQTVALSEVTYGKELHSVEMYPGHGGVICRASGTAAVVLRGS
EPNLVPLLLPSKEVRLFDNQCHAVFGRRAGVMYRYQRNFGKRNVEENMPHRPKVHSKTKR
VSSHPAGGGNGGSANLLVPLDWRIHPRNCVKTKYWLSGYILRGRQYNKSQTVADIKSKTY
SWANRDPVYR*
>TCRU_2289 ADG2, putative
MPKKDRDVWDPPEDRKMVEEAPSAFMQHFQDRAVRVGKDGSNAQLVRVKKTKPIQWSDGN
NRNKEGRGSIPGPLGDETSMHKWKPMMLKLPLRNRSHVRGIVAPDEPKAIMPPRRLQAIN
HTICVESGNGLGRHTRPFFDAHVVNRMDAHDAPNPAMAISPDCRIENMRQTVAAATVMSP
RLELSDVTSISVDKSQSPEVLSVECVDVSQPVKPIPFSRPLSDTMGLVDAGEGLRKSLAR
LPPRKISGSSGADEATMMPRPKNTAVSPPLPLERNEKKKKKEDRNDVLSREDEVDDFSVQ

FEDDNSEFRACDSTDIPIYQPVGFLMRPRPGAVKGENKTSIIAAKKRNPSTGTRRPESEN
GACGTRQDYHLCTHRKKGSSTGIQEFATSAPVKTSGINSHPSRLQPLCLPLPPRTSTVSV
TSSGALTETKESEQEEEKKKNPAYKSYNLKDYKLMMEQVTHLKLGGLGPADTDEQRQAKE
KMHRQCQYGKLVEKKAVERIREKQQRRIIQKLKLGEGGDADVVLTGTPNKMPQQPPPPER
IQAKERRSRALDYARNLPRPELPASRKPRDENSISTLESCTPQWRSQQDEAAWRREQRLK
ELEARHRIDRERVAAVKRQLGY*
>TCRU_2290 hypothetical protein
MSAFSNSPVYKQILRPLRSNSMLGLCVMTGCMSVFVYWWYARSIRATLRQTQESCQITAD
NAFAQSRQLLKSLGDDWAQDMKSRDDSVRRLELQNVEQTRSIARLDAAMKMCIAPGPEIS
Q*
>TCRU_2291 calcium-translocating P-type ATPase
MALLSLPATPSTMDASAVTKSLRVDAKRGLSADEVEERRRQFGSNELPTKPSTPFWKLVL
AQFEDTLVRILLFAAMTSFVMALFEKNAGDFVEPFIILLILVLNATVGVWQENRAESAIE
ALKSFVPKTAVVLREGKLVTVGAEDLVPGDIVEVSVGNRVPADMRVLELHSTTLRADQAI
LNGESVEAIKEADAAIGQQERFPSSMVYSGTSIVYGKAQCVVVRTGAFTEIGSIERDVRE
QEEVKTPLQIKLDEFGMLLSKVIGYICLAVFVINMVRWYSVHTPTPDEPWYERFIAPAIH
CLKVAIALAVAAIPEGLPAVVTTCLALGTRRMARHNALVRDLPSVETLGRCTVICSDKTG
TLTTNMMSVMEIFMLGVDGNPREYELKDSRFNVMPNVVTCGGKPVTSALETDGALSMLTN
IAVLCNDASLHYNTKNGQVEKIGEATEAALLVMSEKLAHATDPAAVCAFRKLAEQKWKKN
TTLEFTRQRKSMSVHATSTAGAKLNSLFVKGAPEEVLRRSTHVMQVDGVVIPLNDALRSR
IIAKIDAMSGSEHALRCIGFAFKSTQPVRELKLSDPSTFEQIESDLTFVGACGMLDPPRA
EVREAIDNCRTAGIRVVVITGDRKETAEAICRKLGLLLKTETSGLSYTGAEFDAMNPAEK
RKAVMSAVLFSRTDPSHKMQLVKLLQEQKLICAMTGDGVNDAPALKKADIGIAMGSGTQV
AKAASKMVLADDNFATVVKAVGEGRAIFNNTKQFIRYLISSNIGEVACILLTGLCGLPEA
LSPVQLLWVNLVTDGLPATALGFNAPDEDIMQQPPRHVDEPIVNGWMFLRYMVIGVYVGL
ATIGGFLWWFLSHGFNWKDLTTYAACTDMQDAKCAILADPETARAIALSILVLVEMLNAL
NALSENASLITARPSSNIWLLLAIFSSLALHLMIMYVPFLAALFNIAPLGVDPLIVKEAQ
PFSVLVPSNFDDWKAVVVFSVPVIFIDELLKYITRHMQASRNKKNN*
>TCRU_2292 Ribosomal protein L9, N-terminal domain containing
protein, putative
MRRTGIRRVAPWVPPPRHDVKVTMPPPPGGEVGGSFGVSIGYSDRIACTPYWKRMALSNY
ALRMKENATRYPMSEHRPGEYDIRYLPKPYPCTIRNRPLLEVGEPRQIPSIQIPVIFLVN
LYNEEKNSWFGRKYETVYVSRQFMREELMPQRYAIYATPEAYALLGLPVVDHGIHKEIPK
TPREYEKLLERQKYDEERWKYSIEYLFRKYEAGPPELLDRAEDTWDGTEVLAVSSTAGAA
RHGETVQRKGAIKHRKARKIKLF*
>TCRU_family, putative AB.1
MRAELACIWTAAVTHDTPTLKQVAKRFGCEDYALFASCFLQHPYEAFSAETNLTTKATME
MMREQVRNRMHEVNNIVSGLPKEYALVLRNIMAVKAINRELQRPVNRPLRMLRYSAVVAR
RTSSRWQLGFMLLRAWWSEIISSLLMLYAEWRYPQLMQMLDDSLQVQISG*
>TCRU_2294 AmmeMemoRadiSam system protein B, putative
MVYSRRASHANSWYEGSAKVLKATVDDLFERAKDFQLGGDETLIGIISPHAGISYSGPTA
AHVYKALRNYIYGPKGSNVTHIFLLGPDHHKGFDGVEMSGAQQYETPFGALSIDTSVVSS
VFQSLKAAGVQTTRTSQSTDEEEHSIEMQLPFISHILYHPPAGLTGAKNRIQLVPMLVGW
TDRKTEERIGAVLSSYSQDSHNIFVLSSDFCHWGSRFQYKYHYQKSEYPAIADAIIAMDH
EGMEWLEKRDMNGWYDYLNKTHNTICGRRPISIGMEAVKNDRSTTVRFLHYSQSNRCASL
SDSSVSYASALITHR*
>TCRU_2295 hypothetical protein, conserved
MKSRQRRAPLSEGVAFSYELFGSVDIKNEEFLNFTGEKGPGHNSEITEFLRNKSFAHGRE
PVARQPSYLQFQQAVDVGNGTAEELGGWNNSFVSLEDAAQHVWFISQRSSGAMPFARNFT
TADRFLKYADEHSLFPTEPQEAEMEAPNEPLTAAKWLDIQTTNKALITELLTQFPVSEET
INNCHYLDGMDALSAHSALGYFFFNLMCTPIVPEEETGRSRQTKSVIQRSLEAAMEDKPR
SSVPAAVPVAVIVFPRWIITVHEKPFHELGDLLRFLHINCSDHGSSATPRRRRQVMTAPF
IFSSFFQIVVGHQLDTVSLTTALDRMGDYVFKVEEKAKEREEVIKRITNVRRSFAECAAE
LTRREHIVSILLQPHMMNSFLTQERVVCQQLESARAHLLRLSKDVGDSRDTVVVTNWYHN

ATRTWKIICRGNKATRQMLLLLEIMNIIYPVVAFQMLYTMNVPVPFDSGGDPPVTNLYAF
FVVMGIILLYLLLCTRAGYALFKRKRWSTRLLAE*
>TCRU_2296 heat shock 70 kDa protein, putative
MLLQALLVLSAVVVAVAAPDGTGKVEAPCVGIDLGTTYSVVGVWQKGDVHIIPNDMGNRI
TPSVVAFTETERLIGDGAKNQLPQNPHNTIYAIKRLIGRKYSDTTVQTDKKLLSYEVVAD
KDGKPKVQVEVGGKKKQFTPEEVSAMVLQKMKEIAETYLGEKVKNAVVTVPAYFNDAQRQ
STKDAGTIAGLNVVRIINEPTAAAIAYGLNKAGEKNILVFDLGGGTFDVSLLTIDEGFFE
VVATNGDTHLGGEDFDNNMMRYFVDMLKKKKNVDVSKDQKALARLRKACEAAKRQLSSHP
EARVEVDSLTEGFDFSEKITRAKFEELNMELFKGTLVPVQRVLEDAKLKKSDIHEIVLVG
GSTRVPKVQQLIRDFFGGKEPNRGINPDEAVAYGAAVQAAVLTGESEVGGRVVLVDVIPL
SLGIETVGGVMTKLIERNTQIPTKKSQVFSTYQDNQPGVLIQVYEGERQMTKDNRLLGKF
ELSGIPPAPRGVPQIEVTFDVDENSILQVSAVDKSSGKKEEITITNDKGRLSEEEIERMV
REAAEFEDEDRKVRERVDARNSLESVAYSLRNQVNDKEKLGGKLSADDKSAVEAAVKEAM
QFLDDNPNADKEEYDEARDKLQSVTNPIIQKVYQSGGGADGDERPEPMDDL*
>TCRU_2297 hypothetical protein, conserved
MESGQYTEQGIAPLWHTDLLTCFTTQLTNKWRSTLRQDTHRYLLCGTRPSDLSGKDLITQ
EVLHRQELVHLARSRCGESELWGRLYWAVRDCTNQCRFCNISPEQSAYMRSNNDPTAPGT
DTVPPSAREEDVSPVRRRTLTRRRKEKCPHCDSTLTGFSNLVSHCRSFHPEHPPPLPELK
CDFCDMVFPTRRSTAQHRSRCAHNPDATRHRNSSARRRSLLPQDQPASTSTPIGPQETLH
HLLLECPGTLAVRQRLGIEQDLRLGKFSQWQLLHSRKLLSLLDHLFGTQVALNSYTHL*
>TCRU_2298 hypothetical protein, conserved
MTMGASRTTKLLGMDLDPRLTLNVAASKQCAATSQRISQPRCIAHKEAGPSPHDLRTFVI
GYGASKLRYGSELIWAVATDSAKNEMQKTYATLARIVSGVPSTVEPESALLEANMPPLHV
LCLRARLSIFENTRACQMDWMRRPPPEPPPRAGFRISSLSRDELYAFVDAYTKDYGITES
SPREERFFRSSIPPWFAASAHRVTIGVELPIDLSITDEEELIREKRRVSEEALALHSHRS
WILATDGGVDVPKSAGVGILLSSLNSSEIIEKVSANGGTRPCSRTTESRALLLALETLMI
PRIRHRRKNPACGYGQSVSSSGSKQGPAQSDRLDGGSDLAASLNTDVCWLVRAPAVLLRT
LRGTC*
>TCRU_2299 hypothetical protein
MESLHAVVDGRSRWRCQLSAVSPAAAEDVKGNANTGKVVGEENLNTVEVDKKRNNEVSLP
RQSNELLVNSGQPATESQKKLPHSETDLVPPPKETSDQGQHSGEKRKEEEEAEENDGESE
HEEEDAEDTEEEEEEREEVDGGGEKEEKEEEGGEKDETDGVEEEGKEDTGEEDEDGDAEE
GEKANEREEDKKEEESEKNTKKEEDEEKDDDNTSEGMPAGGQEKRNST*
>TCRU_2300 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCSCVCTASVVAEHVVTSEPLKPPQGTSLGIKSPDLIILADQQD
VGADALSPPVKAVKEGKPRVSSNAENGEGATEQAGSEDVDTKSRGSTENSSKSVVKSSEQ
NPEVLRPNEEANLPTANTKTMTTTTTKAPATNTTTTTAPEAPSDALNSAEASTTTNTRAP
SRLREIDGSLSSSAWVCAPLLLAVSALACTAVG*
>TCRU_2301 poly(A) polymerase, putative
MSTVDKAFLAKKVISSDGPSPKEEEHNVSLVDWCVAGIEPEEEANRRRSVLEHINNIVRA
WIRSTMITEFRMPAEAATQVEGRIFATGSYRYNVHASGSDIDIVLIAPNRITREHFFNTL
APRLQHEPRITELHCIRDARVPLIAMVADGIDIDLSFGSIRQDRVPEVITDDLLQGLDDQ
SVLSCNAVRVAHNIMDLVPHKASFRQALRFIKAWGKARGIYSNTFGFPSGIGWAILVAFV
CQCHPNQNAAGIVVRFFRIYHSWFSPNPQESGRENRAIYLTETMRVKTNLGRGWDPRESK
SDAMALFPVLTPAVPYGNACFNVTLTNLRQLCTEFARGHEICSSSLVTSAEEAKSRFGPH
GIWSRLLEPVKFFGEHKYYLHVLVSCTDAEAYQGYVDAVESKIRFLWAGTAESRGYALEN
VRHVRIRLNPRRYEAPEEVETRARLLKKTSRSSGGGNGSMEVSSHQTSGAVDDSSAPKIF
SCHYFIGMSVDPKAPSGKIDLAPSIRAFHGIVRQLRQYKEGITRLPVITVEDISKIPAFV
KTAVGFKETVVVPDADHADDAASPAKAHDENGARSTVAGEKRTREEGEVKHDADAAIEST
VTEASSPSVANISGVIHGRTKSGAANNKAVDEDEPDLEEALGLGF*
>TCRU_2302 Myosin-like protein
MSADDNDSLWLQKSIHISDPIPETGEKAHLQNDGKQEEPKSASKKTADPEIELTRTPFSI
NSLRPMHCPSQRLSCRLSMANSAFASFQELDELRARVSQMTRERLKWSNVQRDLEIARFE
LTQAREELKTVRDYVKTMREELDGANSRADRETRERQTLETQLNDVMEKRRAETQFLKQK

LDDVEAEHTRRLAEMAERTELECNSRSETLRGDVAKLSEEIEELEARSIQLDRERMQFYK
ENEELRGQLKGIQEKYDDSRRAVEEYSRRCIELEKMHAEFVKETEKSHAEVLNSHMTLSD
ERVRQITESKDEMVKDLRDELQAQKEKSRALIDDLSSLRHRCQIAEEELKQQGLDHQKEI
KRLLDEHRLALCQQQLQTESLLREAKGGRLSMEEERSSLKRQLTRTSEELSTVTTILAQR
EKHISHLEKELATAKDTALRMEQENISLSKEAEAAQEALGHAEERVQRLMEQQDTSDADY
AKDLRELKDQLATTQEELVRVRGELSSTAQEKMRHETECRGVISGLRTKLEEARYDADAM
QQLTREKKHLDEIAEEYRGKYLSMCKKVENLDIELTAATNRCTLLEKRLDEELRRSLRNV
STSPTPQRQNGVEKRLRSASSVNVPLSLTTHPRKKSRSVEPRVFTISGFDASELLTEIKQ
LPHATVAECRSNTPVPSNLTHLITNGQLTIKLLTALVRGCWILPDVYVRDSVRDQRWLDE
SAYGFRHERPPLFQKRIGFTEGFISSRHYSTAKLITDEGGATVETELRVADIVLCTHAEH
GTLEECTHAMTWDKVVELIYPVKIGDTQ*

>TCRU_2303 HECT-domain (ubiquitin-transferase), putative
MCSKEILSACAPTFEDIALENRKLLELLGILPNNRAVLHSLMQMMSCMGELSNLAYNNET
SLSPFEQGEVRAVVGKMAVCLATFGEAFDINVGQAAMDTLADQFHRASNSTLGRSRAERK
KSFLSTLVAEDTAKEEGKSHAHARPNILLSPTSNRDFFGFLDELVTYSRSDFEKAELKWV
APLPDGTIQELVENGSAINVQYNDLPKYLECVQRYRNARTNEANRNKPEAETAPFVTSQR
VKSASVPILPDNSQHDKERPISSPGVMDGGLMSPGTLMFPSASDTSVAKADIGDFSSAEL
CSSDADFCAKVEGLKRGQVTGLQIAQLNLTFSVPRNGRLVELIPNGIHVKVTSANVAEFL
RLLGDKSVNQCGRIRRMESIKKIEVTGAGSQDLSREKDKFSPTHFSKDIFAPYEDRTSFL
VDFDASDEILPIFIKEREQQQRRAESQYVRVVCQGDLKAWRAIIDEVQNNPAALKKYGVT
FCVPAAVVVDATEEEQITKVHELMRGGISTPVEDSQLWLFSRLIEQFSHSFL*

>TCRU_2304 hypothetical protein, conserved
MRSCSTYASEDVFGATARGGCSGVPAGLCPPSRVPTPPRSMDLLDELFSSPPVSVPSGSH
LVSGVPVRDDAAAATCLPADDFAAAPVSRHSIGDSVGAGPNVCDVLSSAHSERLEEVVLV
LERIMNDDVPRWYEASVILQSLLCRSDSGSMPNRVASDGMGGDPQGSSVWNDGFVNTHRN
LVSIFPFLEFVQTFKHVSVFPFLQVPRLAFKLRQCVRDWVESHGGVRAVLSDSSLVLDLQ
TLLKNVNEVFVAVVATSPQSASEALLLSSLTDVCRYCIQLVCTCLPHGNHLFFATTMQSV
MHHNSSVMPHLEGELKAQEDILQLLVVARSTAYHRCSEDIQASVSPLVAELFSLLDTFSS
SSMVPLDKKKVPERRCKLSGLRLNSSDTSEVIDAFVKRYWNVAIGSPIPP*

>TCRU_2305 retrotransposon hot spot protein, RHS3, putative
MDAGSYFHYQLLHYDAGQLPMVAHFMVIGAYLLDMTARAVPEYMGESSTVKVVKGPSWRG
VRGHIVYDVAEPDNRLSTCLSLLEWGMIVVAPPERKICGHWASERRAARIVMSCPDESDA
EAMCVWT*

>TCRU_2306 hypothetical protein, conserved
MLRVTSLFRARAIIKRRTPQLWGAPGAPIIRMRGHHVVWKFQSYDLFVEHTHKRRNSDAR
LLHYLGKHCPHPQKSLWSPDTPVAQDRHLFMLTTVDVDAFKYWFGVKRCRLSMRPWALLA
KAGLLPPSLRQNSKIMPKPIFDKEQLMRYYLANRKEEATIEREDYLNYKNSLVKSEEERA
AERPVAPYL*

>TCRU_2307 Archaic translocase outer mitochondrial membrane 46 kDa subunit
MESPINPAVWKFLFHGTVAALSAASLFSLYHERHNILCSLDTPFTALRKAKTDEERAAAA
EVILNKLKEDAAQKKDSSRMSAMRHGGTLLRLATLSKDGSNVVGVSMAIKAIVRVFGADA
EGCRKLYMLGGYRTLLTTMSEAHRQGQQALMEEIAQALQTLTQVNDAEVVLETDVPPGSE
GAYALACIPATVKMLRLLDPQSPILFLDALTGIFANVCALRVGALAVGRGVEGRSGMSYF
LRLLEHSNQGVVEHCVLNIRYLARAGIGHEELAEEDNLQRLAEHLSVNGDPRVTNSILTI
VLLMCDSHHGAKFFTCLADKTDIISGLFEIWCRASEKMLRDRAEMLVQLLARVPQCTAAV
QRLLERYRVQIAERRAKDEEARRKQLQQMRQSQMMQQMMMENMGMGMGGGEGWW*

>TCRU_2308 oxidoreductase-like protein
MSRIVDSAEEELPSNGQEEGKPTSLAEREARWGFTLEELLVATKVVRTLFHNPSLFVGDN
YLHESRLYTMITRDRKTKRENREVYKMIMNAEKSRRKRFKRMQDIEAIRRTEMKRERREA
LNALMQRPTTPMLAIEGPSETKPTCERPELGEGDMLAETQREEDALDSFSAYDRQIIRLI
GAFENIIRLEETYDVNPTAPDWLKISQLVAQVYRYLPHAFGSQMPSALFRGAAPAMTPPA
QREKYTAVLKLRIAHLCLEWMKLAEVTKNNEEDDENNTSDGRNNTRIRNILSTQEDVFVA
DSTLLRKVSSLRKCGDVNSLSSDVLCAVQHIVPGTDILRSLEAVLAEGVADDRFVSHDGN

GASTFSAEASLNLFIARRLYASSRVREWGESPFKVNTCPPTSEDEEPDSYSVFDDARMYA
AGQTVPSDEVLQLNRWIACHTCRVRYNKLHPYYYSLCHLCGEYNFNKRLLTRDLRGKVVL
LTGCRIKIGFAMALSLLRCGARLVGTTRFVHEALARFQREADYATWGDRLHLFALDLRDL
WLVTQFCAFVRQHFPKIFAIINNAAQTIARTREYTAHVRHVEAFPPEELHRRLYEDTKAG
EWHRFFLSHTSVTIGEPLRIEHHPHEQPFLDDVKAVANGKDMVHEENVTGEKQQSIVATA
RTADTHSLIFDRYDTQTEESDRRETNSWMMRLAEVPGSEAAEIMAINALSPLIINGKLKP
CLLNREGDAAPSEERFIINVSAMEGQFYRYKQVTHPHTNMAKAALNMMTRTSGEDYAQDG
IFMNSVDTGWITDESPRLKKERRAEQLLLCPLDEIDAAARCLDLIYTNSREYGKFFKDFK
EIPW*
>TCRU_2309 glutamyl-tRNA synthetase, putative
MSASNANVESDKLILTNAEEGKVVTRFPPEASGFLHIGHAKAALINSMLATKFKGKLVLR
FDDTNPSKERGHFEQAILDDIATLGISWDIGPTFSSDYMDLMYEKAEELIGKGLAYCDKT
PREEMQKCRFDGVPTRYRDIEVEETKRLWNEMKKGSAEGQETCLRAKISVDNENKAMRDP
VIYRVNETPHARQGTKYKAYPTYDFACPIIDSIEGVTHALRTNEYHDRNDQYYWFCDALN
IRKPIVEDFSRLNMEYTVMSKRKLTQFVENGVVDGWDDPRFPTVRALVRRGLKMDALRKF
VQAQGMSKTVNFMEWTKLWFLNTQILDPSVPRYTVVSNSLKVRCTVEGQIHLQECEKLLH
KKVPDMGTKKYFKSDVIFLDTEDVALLKEGEEITLMDWGNAYIKNIRSSGELSLITDADI
VLHLEGDVKKTKYKLTWVPENPNAEVMELVEYDHLLTKKKPDLEEKIDDIIAPVTKFTQE
VYAEEAVQTLKKGDTIQIERRGYYIVDSVTPKKVLIYIPDGREKVNHLGAKAQYLKSLSK
DGISSAANDLAAKRAAKAAKKALQKQNSQK*
>TCRU_2310 pre-mRNA splicing factor ATP-dependent RNA helicase,
putative
MPSKKPIRFEDLGLSTPLPRVLSTTREQKKKEKHEIKKEKNARLKVAEEQLSLVKATVEK
HKAFVKKEIALQKEKKAERRKAIFALQECIRQKREAEEAIQKQNSFIAHENYVSNLKIGR
AVDEKIQEEVQEAIDRETKELAKYAPKNVHILVCRNPEIEKTRKDLPVLREEQAIVEAIN
NCSRTCVLICGETGSGKTTQIPQFLWECGYGDPKGSVFGREGAILITEPRRVAAVSMAKR
VAEELNTSFGGMVCYHVRYDNNLSDNFKVKFATEGIVLKEIQSDFLLKKYSVVVVDEAHE
RSLAGDILIGLLSRILPLRNDLHLEELRKHNGIVSKTNIKPLKLVIMSATMRVEDFRENN
RLFSIPPPLLNVDARRFPVTNHFAKRTELRNYTDEAFRKICQIHRKLPPGGILVFLCTQQ
EIESLCKRLREHYAKTRIEYYEQSYSKHSLVVQRRNDNDERDFDSEKDKSASFDEKDEFG
LAVEDYALEETVEKKDLNFSRKRCRDTADEDEASFEEDEINGELNSLHILPLYALLNFSK
QQEVFREPPRGKRLCVIATNVAETSITIPNIRYVVDTGRVKTKTIDESTGASCFRIGWTS
QASAEQRAGRAGRVGPGHCYRLYSTAAYSNLMPKHGLPEILRTSLESVVLLMKYLGIDNV
GSFPFPSPPNEDELKRALTHLTLIGALDSQIERRITTLGKRLIAYPIPPRFSRIILEALD
RKLPDCILNMVVAIAAVYSTTTNVFTSDGNGLKWKARDLKKPDDERRPFISSLLNPGSDL
ITSLNAFGVYLNDSSSGNCYRYCLVQKSLSEARQLKQQLHVLVRQDAVVEQVGDTIDAND
VGAMDSGPHITNIFLPTLSKEQELLLRKLFIYGLKDQVARRATIQECRDHGVEYKDKKAT
KAPYILLGRSMISYIHPSSSIARTFPPPEYVTFAFLQRSVRSETKDPVTMMLGLTVVTKE
WLSECGVILE*
>TCRU_2311 hypothetical protein
MSTTNGNNAGWVNSSESLSLAPLKKDSPLAATLDKENLKTVSDTCGCVNTTTSPLAVVNS
GDNTVEELQRRLKCAELNNSILRGNIETLKAVVNQLAAQLDLANNRLALHEEKENVHALC
HCGREGKDTESIDDEASLTTADYERRIAVLYDTMLEKDATITALQYEMESREAEASALLR
MSLEKKDKEIIRLMGELDQLRRLHNMERYARVRK*
>TCRU_2312 hypothetical protein, conserved
MAPNQFVELVDTVEKYATRGSNECGCRIDTREESIPSNTLVGYPFANAEGVGVHLSYRKG
DITLSADVSSNPKATWRDVLPTFSWTRSLRGQQHEVLLRLAMTPLFAYSFSHPQFTCSSE
VNFMDGFRSKFTTSTQLSMRNQLGACVEYDPSRSGVIDYTVAFLRAGCSAVLGGDFVVQY
NATRGLGVHTRIPVKPFMGAVALVERGRVIIGTEARSPCGAQMMMNLDLVNSRVMLAVVR
NISTVWKFTFNYSAPLPGTSSAARRFGLVFTSQDAP*
>TCRU_2313 VHS domain containing protein, putative
MVVLSFLENVKDAASRLIPTPYMDIVVEATKPELPTPQYESVAFLCDSANSSGDAAEDVV
RAVRRRITDSDAKVQLLTVLVLGTLIKNCDNALHVEVASQKGLLRDLQNVATRTPCVTEK
ERMAKEECASCVCGCAIWFTGHPDGRLYILTTISDDVRHAIGPSAFEGIQHDTTQLNSSV

MRQQQHNPRFNRQSRQTGRQQHQQQQRQQGLVVDAVGINFPTEEDLAAMLDCCMTLAEYL
NNAKVQPDGSIKPDDVISGFRDKILADHKRVTVLLSSDLKLNNRDTLRDVFDSQSALIQR
LQSDVKLHPDQTPAPSQVTDVAPTERYLPQVTTPNPPAAAAASSGGQGVGMTPAMNPPMS
QVEPVAVPTALEAGTREAAGEAEGSQPCPAQEASKVMENLFVSAPVTESLAPAAETSSRE
YNDNVDLLLTKADMPPSEPIPSVPEKKEEVLMAGKEENQSKQEETQKQPDPHEKSPEEKS
KQPAGEDDEFDAFLEGRLSK*
>TCRU_2314 kinesin-like protein, putative
MEEQNRKPTKAKVFVRVRPFTEAEAQVCPEDSPVPREVVVWDKHRILTVLDAANGFSPRK
NGQFDIDNVLWSFRDEERPKMVLHTQKDVYSAVVAPMLPQIVDGYNAAFCIAGASGSGRI
YSLYGDDVDGVNRGVLPRFAENIFHVFKREKREDSSLTCEMEAIDVLPNETYMDLLAQRR
KSPANAAEEPKLTNDATEGMKLQGATRISVGKAADALSVLRQLARVVPKRSSCHTVQFRF
VETFDFADPEQQDQVISKSRRINVLFVLLRNMPAAFQRCIDVAVEHDSGENPLAKVPTRE
TAFTKLFPELLQQGYNLSFLCCVSPFYEHTRETVQTLTLATKFMKLKCKPRLIQDEALME
LRNLSDEVKNLRTEVVKQTESAQIVQHELNARELELMRQEAAHHEAEVKLRRTERELALA
KHALAINQFRTRGHRKQFAKERVSKEKLLGATKAEKDETDKSLEAAKKQNEQLESGKNEW
EKKLRAQEEKNAAFQARLLADEEKEKRIGKMRKFLAASPEERSRILEEEAREQARNDVNA
QKAEKELKFLQGAQEKADGRCRVLEKDYAAVYAAEKGTREKAELQNNIAQLKKEIAEAEA
AIARMKAELDKRPPGCNCVLM*
>TCRU_2315 Pre-mRNA-splicing factor CWC22, putative
MTRYVPPHRKREVSDVDDGKSTGNDGGKTTSEALQRESWQALSRSITGIINRVSGENVQL
SATELFRENIIRGRGLLCRSLMRAQLADPDLSDVFASLVSRVNKEFSIIGLLLVKRLVVQ
WWRLHRRGDWTALRCVSRFLAWLYIFNVVSVDVIYQIILAHLTAEKRCDDDVDQAAALFR
DTFRAMSQRDVAEFHAHVLTPIRDLLAMDDDALRLSPRAQTLLETCLGEVQKWERVKHTV
SIIPPQLLLVEACEQKCHEVDLDDAAKMNAEEQLDRFVFDADYDAHEDAYETARCAVLGD
DWETELLEQVAAAEEEEEEEEEGEGTIAREEEARGQERSAQEKQSSMDAAKQVVDERERQ
IRKDVYMAMRSSVRADEVVHKILKSMPSQTERTVCFMVIEGCCEESIYKRIYGMVAERLC
KSNTKFQLFFAEAFRTRYEHAEDLVEKQIEYTCKIYSHLLRTDSLSWHRCLSVLDIIESD
MSQRLMIQWLLQGMVEALGMRAVQERLEKDKELRSSTVKLFPVDANEEGLERAVNLFEAM
GLGELGTGVRAQLEKVRRSRRMTLNTNSAPNYNDRFSGGVANDQKGHKRSRKNMMEYI*
>TCRU_2316 vacuolar sorting-associated protein-like, putative
MEVAFTVSPDERQHVEYLADLFAVIVAIEKVEKAMLRDLITQEQYDTTIRRLLEKYKSSV
SYLEQGRNPYYTTIDSFWENYGSKCPAARARIQLGLANDHQQKDGHTNTTLVLECGQYFI
TLMDSLKLQQTAVDQLYTLLTDLVQGLRRLGASDQEFHQRLVAWKEKLDTMKASDELNER
DTREFAFVLECGYQAFYAYLSDTSRTSSGSMKY*
>TCRU_2317 SWI/SNF-related helicase, putative
MGHRRKRQREEEESVVVTATHAPNEPAAVVPAPAQQQQQESLLTLSKSCRRRTAPVTSSF
LFAPTMFLPQWQRVALSTLRQLHESQAEEHRAATRGRTLQKDLTRYHEDLHRREERLRAQ
QREARARLGNKLFTAIEKQWSRRGDVFQQLLCVEFDDVKQRHTERRQEDLLREAENLTRS
LLDGIFSGTKNHGSHSDGDDSRGIDADEAVADALRNAEMTGGASGPVLESSLSLLDTQNG
RRPLRDYQRSALRWMTNLYTKKLNGILADEMGLGKTIQTIALLAYFAEYKNDWGPHLIVV
PTTVVLNWKAEFQRWCPGMKVLVYIGTPKERHRLRKGWMGEDALHVCITSYNLLVKDRCV
FRRRPWGFLVLDEAHQVKNFMSKKWQSLFDLQAEYRLLLTGTPLQNSIMELWSLFHFLLP
FASAFSSNEEFREWFSNPMEDMVTGRTFFNEEIVRRLQSLLRPFMLRRLKKDVEAQLPSK
TEKVVMCRLSRRQRLLYDDYMQLTETRERIRGGAGGVLGVLLALRKVCNHPDMFEERRTL
SPVALDCLSEITLLVPRDILLQDNDFRGCYRFQKWRLCIEDVSMSVKYDKEMVFDDTWLD
CLGLRLLWNDQAFECPLSRYSPENFRWPENVPAEQVFGADIKDSMSDTMWSMLCQQVEER
QAWVRQRHQTTATLQAQRCRGIETSMHVWYPRSLEIVSHGRPGFLPSWLHPNVSQRVCAI
LPIAEKTAVYVPRVAAVHPPRLHCRLPVVHYRAFCSHTRESLAPLLALGVSSSNGHARRG
VFDASSFLSELWPLHVRRCFSFPDKRLLIHDCGKLQFLQHALKQLRREGHRMLIFTQFVH
MLNILERFLAIIGIPYLRIDGSTQAERRQAFVDRFNEDDRITCMILSTRSGGIGLNLTGA
DTVIFYDSDWNPTMDLQAQDRCHRIGQTKPVTIYRLISEHTVEENILQRARERKKLNNVV
IRGGQFHAMASVDETYEDSAAALAALSDPVRLRSFFHDLDEDATIVADEQQRGEAHASKT
DMGEPVDIREEMMRLEDQEDREAQQNVEEELRELEEQRRNDEAELGDEEEEDEEYEDDDV
EEEGGGRSRRRKRKRELTGAELEEGLMDVSADDNALDAKNADMSRGVLPMVIQRRRDILR

RQRTPLDRLLSVRFGTCHAADARKRYDALCENYATRVGEGELPAFKTKFRL*
>TCRU_2318 hypothetical protein, conserved
MTAHTVLRALVRRAAAYERPFNSQDSLLIVRALQALRYRSDDVRGVCEKCAFAIASSRIT
VPVERAIEALSGLLSLQAGALPVVHEKLAERLTEVTPQTASPRYVQKAAVVIMKLGRRYC
KPAIADHVFDVLTQLLPSHPNDVALRLAVISVFMYTSSALKYEVMCCKGTARNEDLKEEK
DKRVLTLLEAATHIVDAHLLGALRGNSTLQAFHIFPVLSWRSLIHDTSKRNGQACIDGMN
SPADHDYDRMLTKWERVENAFSEELQFSTVVPGGYAQFMFDFFPTLGRNNTSGVAFNLAL
LDVVCHENFRKALNSYDVAKIAMSVSHALLNRRSSAGPRTGRTLTGVERAKDEEGGGNEN
DPEKLEERTLLRVVGSLVQQLCFFDAVAGWSRPDGGRVDQVAVGAVWRVTQKFVCNFQPG
AGEVQQTVAQLVRLTKGIASKLRDVWSWVLYSMSLCARTTVYNDGLRDGMEILVQESSLA
RRPEELPLRSCVQALYAVSILMVPSTEEKELMLRATQASMRVQERVQVRRAQWTPEHPLV
VSMLQRLLNFRFREYSGDDIPMLLQSLSNLLEVTTAQRAQPLPAIQQMMERVFYYMQGNR
NLDWYRMHGVSTTYTLLSMAEFFPVDCKQLRDAVKQFFFYLESEEMIELSVLRRWLELLT
LQKRRGVNTTWLCEEILKLLAVQVHCACTGRKEPFHFLMNVLESAHEIGASIAFVNSSEE
VSNTRRVTIHLDLEPFLHDGMLKAVDAAQVLRIMSYEVQSAGLVRVHGDHIVQLRRIAIG
DEPAAVMRVETLLHLLRANATLQASKALFDTRTLEQIMVSLCHQLTENRKALIQRGDAGK
IVYALLSSQILLRLGCSLRSYKGLAEAVGEVLDTLEATGEERPETLFQLRLLCGQ*
>TCRU_2319 hypothetical protein, conserved
MPSLRPNSCFLHAPVNAVTVGTRWICLAVGNRVLVGSVDGESNSDFKLVAELPRGAVITA
LEQHVVDDANCKAGVILVIGSGDSVFVLNHLLLGWRAGDHHLTQLVLEDMARVLRIRSLG
PGAGVLVITAISSAYILCEESLSWVRASEEAPLLVRYAATGLGVALAADAVLERDGDGMT
VFTGTYAGSIAVWRLPVAAAQKQNNEEETEATRGALIPFSWINAHRQGCAVFAVKAITLR
DRMEADQMRFCVATCSDDRTATLYISDDINCLANMMEELKWTCCWRGAGASFSRRRVFDV
SMYFTAENNGTLFFATGSEDGSVHAFVFNFQELLNAASTKNLKEITKKNAFLATTVGRRL
LHRGHQHDGRGVYKVALLRNPTFNTIAVVSCGFDGAVYYTPLSVHASRRGEIVSQKEKPK
RHVRGVVCDDVGSLLACTEDELIIFPLDPKGKERRLSIPITDAKKDIPSCIKVAAGSIWR
GRQQYFLALIGTTGGNLYGMWYNLTGTQPKSQEEVEEKELVNIFVLLHASSSRASKVLLV
QGMHWQERVLIAGIHADGNLILLEAHTLDERASEVRVTRRCAGVHTTALSICIFASPMED
DEKEHRTPSPKKQKRRRQQQQQQEHQRTQPRYLGIFVGDDEGGLSIDLVRINDYAYTAT
TLLFREPLFRESIASVIRETRHINSPCERITVLSTQGEWRVVLVNVEGQCVDIVPVSSPL
RLPWRISSVLACSETVAVTMFGTDISVYRRRLSRCSWHLVEEYHGVRAPRLLSATIPADI
SGAGGLSVFVCHCSDGMQAEWFACDSLSETRILSGGAIIGREYNTALFLPSPAFAVICGS
ENSMLTVLLTPHSPRMGMDAPLTITGPHDSNILAMAMCVTNGDGSMMRFVTVGGLATLVL
WEWSTYHNWRVVAHVSQQHESTSAFPAANDRKKEGRGVPRFLSVCTTFEEIVVGGSDGIL
RVFSSNDSLRLLCEARFPTSTPKPMMAVDTLNARNRLVVVGDTSGTVGVCNVANGSFTTH
FTWAKSAVNAIAVGRRIGFQSQKQEEQQQRYGQKREEGEKGKGVEDTFAVWRVLAAMDSG
DVVLLHVGVLAIGVICVVRVGLTSACGVSWITGSPNDDTDDDAAVAVNGECLTYLQTCGV
QSAAGGTEMLRVAWHTRVNVRGVSGLAVVSPTRRSACAVVVGEGVEAIPLYADRDNT*
>TCRU_2320 UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase,
putative
MVGLVLEKEVKYKPMLYVKVLGCHFHDARNGTGHSQVVPTSMCVHHVREDDYAALMARFG
NDTSPVARVERYSEEVIYPSCD*
>TCRU_2321 RNA editing endoribonuclease
MRACVITRPAAVARARGRIKCNYADIFSWGSSPPEQDGGVSKGEMNRMKSRFYNSGQRRC
TLCDEYLEASFSTHCCHVGHIARVGILERATAILQKETAEVMTSSAREPASNVAQMVRVL
LETWWKRLNEVEQETLLDYKRIASLSSPSARRRLWRVRFLLEFLRDREVIRDCLTLAKGT
PSNEGSFVRTKRFERSEMIGDNIVKVVVPDRLVRLFPPTEGGVTYKLACIQQLLDSNEGL
LQIYDYIDLNSIIGTRLPNNKTKSDVVESLFGELQTFLWASEVACGLNQYPAIPNAEHRY
VRALVEHLLNELTHMVIMWRIESTLENAKEYLEEQIQLKLQSSQQCALKGGAGGCTVVKE
VECDRGRYAVLPLLLSFPYPSASAESRQHRQRPSTPPPVRRVGENGTPQMLFTTSIPKPE
LMVSHYRPRLRVVRSSQEYRLEAVKALTMQRNLFTNILPASTSTLLGSRVSAKGEKQQLG
HLSFPGLAEGKYPTWAREVRIAEVRRSVEEQMARRGVYVETIDWGSMLAALARTLTGFHA
IRAPRLQSEPTKAPTKPLSPPTVAAAAEVFPPVEGKLKIVEEMCIPPLKPTVE*
>TCRU_2322 40S ribosomal protein S18, putative

MSLTLQSEQFQHIVRLLNTNVEGKRKVPFALRMVKGVGIRFAYMVCKKAGIDVERRAGTL
TAEELERISEVIADPAKFKIPDWFLNRQRDPKTGKTEHLTSAMVDTRLREDLERLRKNRV
HRGVRHAYGLRVRGQHTCTSGRHGKTVGVSRTK*
>TCRU_2323 hypothetical protein
MMRPTLQPIAGASGMTAAPPPAAGAVGLGTRTRQTNFNQMVLAALSASRLPQRPTTPPAS
TEIDGTGKALTECQDTSCLPTSLLVKQPEELTTTSFTSNDKGTTTIADSDSSTAVSHTTS
HLLLLIVTYAAAAAVVSRPV*
>TCRU_2324 hypothetical protein, conserved
MRQLIHVTSRSAVLLLAMVFVMCCAGGCFAASLTYSCSSDKAMRADRAKSIPAVVRDVPF
GSEGASQTCSVIGRSGWAPTRIDVSTRDLDGTRKYCSSERYYAMNSLVAIASVKVTFFYA
EKREVFVSLYFAATVR*
>TCRU_2325 hypothetical protein, conserved
MGTTKASSLEKVPRSVGCVAARRFACSPTDRTAQSFHCGHSVGITRCGGVRKSRSPDEDG
LVVFWWLRTSGPSSFRIALLLDWRSTIRRLGPAAVICDLNPHHELRDGRSPSKTAGEDLA
VIPSNMDAELSDDPAQATWTSGRSVSFPDVTAQRVLRVSHWTSTCLHGLGPPSAIPHRGD
GGRHPATGRHAATTEACLRCPA*
>TCRU_2326 hypothetical protein
MRIVRLEQDDYLILFRGLMLASAHFSDLREATEPVKAETDSGWNDDDFDEDEMQFSNPCG
ANLAASMSVGRVQMEEADDDEWGDW*
>TCRU_2327 heat shock protein Hsp20, putative
MSAESLPSDESEAHQQPQPQKKSTDIKKNPANSYYYWHGHEKERAKVGDVAPMPTPQLVK
RSEACEAPAIAATTSLVTKYSWCDAENAVTVYVDTKVEGQESLADGTLQVEFKKRTLSLS
YVANVVSSKATPLQRKKQLLLHLSKSINVDKSEYKVKEPSGQVVLRLVKEKPSTWWELVK
KNAGSGDDSEEDSEAAEEGGVSQNDAPA*
>TCRU_2328 hypothetical protein, conserved
MAAPSLTGSECDNTNDGKKSDEYYGDDLHRGADYLRVFVHESQEGLNAVPTIPGLAELLA
FALSPAVISAPCVEADPFTVEFTQQLSSGCAAGPALALSHVSQRCLACDLMPVFSKPLSP
VFFWCPIRNTLRCGGYLFAWPSTHVTMLNGCVFCLAGTRETSVCADSTAKVFVDGWRRK*
>TCRU_2329 hypothetical protein, conserved
MRTGGRANASSVEECVRQVMESLHAVVDGRSRWRRQLSAVAVAAAAEGGGKENPNTVEDE
KTSETLATSGKASTGKTTAVASEQTSVNPAPAIVPPARETLVQGKHNETNAKEEKEEEGG
EKDDSEEEEENHKEDDEQEDAEEGEKAEEREEDKKGEESEKNTKEEEAKYGVEEDEEDKE
KDDDNTSEGMPAVSKEKRNSTLGPEEAPNKTNTEGTQTPGDIDGSTAVSHTTSPLFLLLV
ACAAAAAVVAA*
>TCRU_2330 Ring finger domain containing protein, putative
MYFCYVCQQFRNQHALEDVATNCEVCQSPIIEIVRDQRHYNELQAIVGRQQEQQQENQPG
NFLAEILHPLWPRLAENLGEHIVIQFTIDEGPETSPRPCVSVDDLIGSFVTLPNGLQESD
RLEYPEAFVSSSCPICLDSIVGSGVPVVILPCRHCFHKNCIREWLREHPECPLCRAFVVP
SQDTVASQ*
>TCRU_domain containing protein, putative RF.1
MYRYRRFVCGLAGLVHRTAGRRLVTGGGGKPNDKASGSEGSNDGDAYGSSSDIPPGIDAQ
KLRAMQEMIRSQPLEKQVEMMKKALEFQKALGRIPGVGKLAQKNIEVMEHLVKTVENQHR
HMQQNNPQDAPKPPEFSDTKSGLFTGKNNTFSGLFQAVNAAAANAVAAGGSGGGRESRQG
SSGPTIDELKKVNLGPEIEELFAELASMRAKKNSYREKLHAKEEECEKLQKELLQMRETD
ASLRTKLRKVEQDVVLLNSENMELKEHEKEWRQVRKKNELLTDTVQKLQKSDAAQDRHRS
DMLQTQLKEREENLRSLQRKLERLRRRDPLLKFSRLCSDVVRMCDTERDSAKELSDGAFA
SLQSCYEREQDAAWKTAAMQEGAGANVYVAVVRRLFLSRLPHVNYDALVNVEGDVAVLKS
FVEESGYELQHVTAERYVIAAPAAATSSPTFIGPYGVGVALFLSGKMDESTYRLPFKLTA
VCPNVSTTLFSNAHRATVHYDTARSSGPGGQAANVTETQIIAKLLIDGELAYVAEAQDSR
SALSNREAAMERLSKVRRQQYNEQLAKQHRAERVERQLVQMIAEHLKMNSDTSAEVMTTD
GIVDMVRTAVEKGYVSRADLYLVYGLQYLSRAATSASVST*
>TCRU_2332 hypothetical protein, conserved
MRRCFVKRHGRLKFPLGNGFLTVGHELHPLVPSNELYYDPPKLRHRLDKDGYLYFKNIVP
RIVLNEAMDDLGNQLLQCGWTTVEDRAEQVSRDGVALGVPFPSTGQLPPPQIKYTESLRS

AVSGTGVMALVRQVFGGAVNVTDVQSLHLAAPKETFGLRMSSVYLNKGTKLALVALVPLH
DTPFQMGTPVVVKGSNSTESYAALRRTYGQHEVESGDIRGDGCYTHDPQELLPLGKQGGI
DETTGRSITIDVNPFVSTAFELGDVLLLTVYTMYAFLTNTTNCWRIMVEAVWTMEGDDVG
PDPRYVGADAPGLSTWYADRDDPSKYPRTMNEAKQAWGLLPGVPSEA*
>TCRU_2333 dual specificity protein phosphatase, putative
MRVAGRGAVPASELTAGTRMVIRDIEVENFKSYAGKHCIGPFHKTFTAVIGPNGSGKSNV
IDAMLFVFGRNAKKIRLERLSELIHSSAAHPNQAYASVTVHFVRLAETPENEGDPEYRQE
VPESLLSIKREVYKSGSSQYFIDGVKTTQREVVEKLIAEGVDLEHNRFLILQGEVEQIAL
MKPKSEREGEEGLLEYLDDLIGTNNFAERISQASKAAEAAQQTRLEALDRERKLRAEREA
LDDAKDSAIAFVTKDNHLQKTLIVMCQLRMQTLEEKLAEPRRLLTEIDERIASMKKTVET
HSKEKAKLDEDLLKRKKELAEATKERDTVRRKKETADAEVERIKSGADEQTKARKKAQEQ
LKKAKEELQKAELQQQDADREVIIHQQNFEESTQRVEKLQKEYDSTTEELAHVFVPLRQE
LEKTKAAFAPYEKAVVEATEQLDTARSRLASLDNGRLMTQEQLRKIDAATERNRNRVAEI
EELLQDANKNRYKEELQRLQEMLAGAAERKHSVNNAIQEIKNAYREGEADDRAMEFLLAQ
RSLKGYYGTLRQLGRIADEYDIAAGVASNAWGFHVVEDRETAVAALELLRKNNIGRATMM
VLKEIEREVGDRMNAPFTSPSPKATRLFDHIVPTNARFRVAFYQAVRDTLLVRDLGEARE
VAFGSTQRARVVTVRGELAEPGGSITGGGNTPRGAKLKAARSPQDKEAARVALQRLQGEL
VEAVEEERAAQEQLHKMRQTQRHLSSEQISKLRVELGTLRATLESDAKKRTALLQEMEEN
SSGSQSRREAILEEVDEAEKSLQAANKSRLKHQSDLERIEQEMDAVGGAGYKALCAELKL
QQERREAEENAIRECRRLSHRLHATQQRKQSDIAELEEELKRINEEAAQGASGALAAAIA
TSEEWTRRYNGANAKFAKAQSDVEDVKTAVPVAHKALIEAQKLLDDEERFRQVETAKMAD
ALQELAKFEQKIEGCEEKMRENAELYGIETLQLDVNSGTDGDESIDEEEEKEVENEEYEE
EERTKRSKKNKNRNNNRRAEEDEEELRRRPGKQQSNCIDLRNMSFRLSPEELARCDYEHS
VRLAKSLSEETKRLHSEIDFRAVALWHERDAEHRKGKSHYLSCKEASDAAERGLLELKEE
RRGRFMECFVRVQERLREVYQLLTHGGDADLELVDANDPFEGIHFVVRPPKKSWKQISNL
SGGEKTLSSLALIFALHDIKPTPIYVMDEIDAALDFRNVSIVANYLLRQASGAQFIIISL
RNNMFEMAHQLVGVCKVKDVTRTLVLMPRGFQRMVEAELLRLQRKRQATDMVTFSNGDGE
ICRDEGGDEGNDEAEGGNDARNHTAEAMNNGKRVKKKRRAS*
>TCRU_domain containing protein, putative P.1
MSAKEGAAAKWDECVSPATEACRHFSRPPPYPTPSSAWINRLEEGNVHETAAGRHAVEGM
REAPVLGYRAKRRDPVYPENSQNCTANALVELECILMYVETVTKSLAQRSRVPIPSESVR
VISTSVVTSRRLVNAEQHDGAPQYSLAMGLHDSANSLLGCLAKLEYMSLFQKNELDDIER
KVNTTAGDVNIALDAMVLRYTTHELSDVKEFFLGNQPTIEECRRMVHGVSQTAHQILLLR
RAVVGRDLALAKKLFSEHQTEYQKKGGVTRLHSPFFTWMGKRWFPAMEAWRRIVAQAHEQ
AETSDVLSAIAKGHQETFSQVDLISDILLPGETLSDLLRKELDEPFSHLAESLKKTRHHV
EALRVAVAKPQVGKLTECVCAVEELVAAGRVRSVADRELLKEGKRLIIRLQQVENVEAAL
RLAAQVGETVSLFRTINHANEIILQLGIAGDAAATKEIVARCSALLEEMKSSKGIPPAEL
IARRVDAASITVAHVPSQIWSAKTTMAYQAACQSLAANTAQDLARINLERVLKGGEDCQL
NTTGSTFDDASNISLNSHSMRVAAAKGPFPKFKGARVADLRTALKRANELGLNGQLIQDG
EAVLRSVEALKLKVHFDAQLRVVLIADPENATFDEIYKKVSELCSRQEGGGASNSAGRKL
RLRYQDSDGDCISLLTQEDWDVFVGEEAPNGVCGAKLELYCDYMQLPHAHVTDTLIETQP
AVEEALSSPEKVAVESHVQTCIKKTNPRSARATPQRRNVANNGTRFFRSRSAAVGLRHSE
FLFRYRTPQRTNFHESRVQKPHKLLDAVAEREDAVNVASVGESSQTTGQERGGAPAKDAL
PGTKPGLSGRGRVNSLRLNSSLSSSTNKPKLLIPIYQERKSRTLTKAAVTASSAAGNCGG
GGDATASTYATTSTNQITPVSTPTPTATSSVVTMPTNTNDHKNNEATAAVNTTPSASPPI
ELETVKKWNDDDAPLELRTVVSAASTSKRAVISVKGGENSVKQLAKKRLGGGFTVTPCSR
GIGNSSKAVGTDGVPNSNTPNTASITVLEEKREWSAEMFMRSDICTVVSEQTNQPPSVTN
CVGRQRPTNVTSLINTTRVDPAIVPPSNASSVKKKAEVLQQLRHLREENQKALKAALNRR
RTGK*
>TCRU_2335 hypothetical protein, conserved
MAVTHWVHGGVVPPPLPMAKRVLWLVLMMSLYVDAASASETLKGVAPFRCMRPFESLPRF
SPANMDSGENCRLGPFRVINAKAMTQCVRDDDDTARAASPTCSVTLRVSFQTEGDKRRHR
VGGAALAGSDEAFGSEAYRFSLRLRAFNDSIVEYKGFDQNGYSMCCHFIEGSECSWEVKE
EEGNSTQQEAATPQKDDDGRASHAPRRREAMVVSCPIRNPVVAGIVFHGAITKPLHRLVI

TDWEARLELWRGRPHEKVFLGRVLVPFRLTEDDIASAQSNAAATTTTTAMTATDSSASGK
MAGGVLLVTEDVVKERNGYEDL*
>TCRU_2336 hypothetical protein, conserved
MGTRRAVPFPSALLRQGARKLTEDSSRRRVIAEGSGNNRGRFFCKNRRIDNTLLVVEEKT
TGLRRRWIAWPRDRNRHDAYEADAPLLHISHYLPPVMAEAASCLDLKASFLQVPLPRETR
HLFRCRVEDGTLVELTRLPMGYKAGPETLQIIITSAIAGMTTVVHRLWAAPPLVRVDVWI
GNIRIAGSIGDVTRWEAQVLRNAVGRRATIGEDRESGAAQYTFLGVQFDHTHRAVSLSEK
FVRSLRAMPALNSLTIAEMEVTASRFSYVAAILGTCLCVYCFLIKAVQRRLSALDRGIVQ
ETSPTKIPPAAVGLGERLRHIIEDTTVSESSSPRKRRRPPSSGTHRSMDGEPSSFQIQAM
LKLPEESGRGSLFASCRPRRTVRLALLAFSAILPRTIDVWMSNTSPQGAANKGSSKPHAT
TRELKRIYGFLDPRGIKAFFAYVRSAENPADGISRGRVFTLEELAKGWNLRRGAAGSCDW
RSSNSATP*
>TCRU_2337 hypothetical protein, conserved
MPFAVFPSHQCEQRRHLGQHCGVPPQISNSILGKVERVNVHRQQREHVWVKIACLHDWSC
VPQRTLFCGVRRGIPRSQRSLHVSSRKICKLSLRRSVLRNVIVSNASCPRILTNRKARRE
SALAVLDATDQSKIMLQREIVGS*
>TCRU_2338 hypothetical protein, conserved
MTLVPYTPSEWCDIGARLWDMVSQCGETQVQMTFINGNQMSDETLTVAASPTGLCLLHGP
ISKAWQDSTLIGHIANPRAPQIPNFETQALLPATGAARELGHQQGLITAERERLNIDYAN
AVADVQNRNAQLNSEFEEAHYNLSVRESTIAGAGNQVLELQQQLEADRAQLREREFNLGV
LTGQFQEREARHNAQQPARDAETAGRDESPANRHVANDGVTTLPHPTDILMAGGVPSSAA
RRSSAAYRPPHGNAARPHFHPRRCPPALLPWTPDYPWKRTAVSAHSTSPRGPRVYGMRAP
PESLSTSGAHTNAGNRRTSRLNLPLTIWSSGSARWKACRIPPIES*
>TCRU_2339 Scd6-like Sm domain containing protein, putative
MSAERAIGSTITLITNSLIRYEGTLGQIDGPNNTVSLTNVRVFGTEGRGQEAGLAQIPPA
DQLFDQIVFRGSDIKELTVFEEPHNAMMDPAVVTALPARNNSGKTVSVNQRNGPSSGNTS
AQYHQTHHQHQHQHQHQHQQQQRYGGGGYRRGGGSGYRGSRRVDGHTGQDFRPATGAAKE
EFKDDFDFSKSREEFEKKKSEFEKAKEDAKVHSKAYDKSSFFDKISCDQQDRALRMDREG
VKRADAETFGSEMVGNMRGPRRGRGGRGRYNGRYN*
>TCRU_2340 hypothetical protein, conserved
MPLLNAGKNARTELSGASNLANDGAPPDYSGPLSQNFSDNPTAVVGKDTRPSNSSKSTSP
LFTATPTTVSPILEAPTKEEGGKKDCRSLRTRARHAERRKKDGLITATSLAGAGRRAAVW
VEQWDRGSRATRLLILEAFISLHSSSNTNRMETDLGDSSMLFFTRITAWLRLTCKLGHPL
RLLLAAISLFVRGVRYLTCLVEVGGAQTLIDTLATCRLVPDDRREIALLLLYMANAGRVY
REMLCDDDDIDLLLHAMRCESDLEILDLHAALFLVLGEGNSPRVTSRVQSGVIGMILHDE
TTKGAMLQAARVLRIFQSSRDRMYADAIARDLLEDTGTVSVVGIESNFSTESARQLLEAL
FFLLSHEDLSLRVEGLELLTMVAKNIQLTGHILTRCFDVLDEDRLAIEPKDNLSAVMVFR
RNQISFGSAAVNIMLLDTKCEARQRLTFDIIARRSAHFSLLKYLRLLESGYTTSILDCCR
ALQLICRGALMQERHGVTGGAEVGVPLGKAANYIREVVGDTLYSVLLYEDLTEDEAFSIA
RSVTSSEL*
>TCRU_2341 DnaJ domain containing protein, putative
MNVSGFRAIARCGIQRGFNDCVNRGLPPCARRSLSASLSLSITSVPHASLFAQSRTQFAQ
VPGKRDQEAFLSQYNPLEVLDLDESCTVEEIDEAFKRMSAKYGPNGPRPDAQLLDRVFRA
HAILKDPGSPFYLRAHSSETDRHRLQFQLLPKSKRRIIGFQVGILVLLLAGLAILVFVLI
LRPMKRSIRAATR*
>TCRU_2342 hypothetical protein, conserved
MMRAGTGGKFAAVVRRSLCWCPPGRGRGPALNVQRRTVITGQIPTSPTGGDAPASSTPGW
ELRRGHHLHSSVGLHTSFPTACGRTFNPQLYYEVLQACCDQQWLQAIQRELRNDKEWMDT
LRREGGVAKAMNALTESTHHDDEFMMKLRDTLKTDKKMSLTLCAIQESYERIRNKRDMHE
TQVAADGGDDPYAAMRRKQQGEFGHKYPSF*
>TCRU_2343 hypothetical protein, conserved
MISPLLLWARAHQDQKQQNEPRGEDCIITPFVQCFYALGGCSRINADNTLQSTKEGQDDD
SKWIIYARHRRRLYLHHARELSQFSDAHDYYRLMMWCHDQRLFIHPAVCMRRHPSLYRDH
IFAVSQDVDRLTPLLAIPEALAIGFKDISSAGDFDNDLRNEKREKEFNELNSGEGTDADV

CRFFFDSLNMIVSDLVAAKSSPLTDPRWVFAELLGKVRTLKNAPYFEDDVVLDSETTGLA
DVLLQMIRNYINGGPLVGKLDRAELRWAVSVCLSHSTPLVIASTRSIGMIPIVHLFPHGG
KETNSFLVARTSRPNSTERIAAFFSKHHGYDFMRDREGKWIFLVPSRPLQSGEEIRLQAM
TPVCGKDSEAEKMWRLSCAAAPQEYMTSSAVAHMQRCLTRELIERGGDILAERCGGAPS*
>TCRU_2344 hypothetical protein, conserved
MAGLYSVDIGAASSSACGKFASVEMNLSEKLISWAQSLGKPLRCTSCLLKIQTTEKTVMY
RLRTKYHVGDVSERRFALIFPVSGCSGAVTSIMARINGRLVVGQLVSVEDSASGNLRRFK
MATDMPDENFTDIRQKHPVSIYSITPNASDVLGGKAAEVGAEVIVEIRWISKEMVWCEPH
ALQVLYPFVCAPRLPDEIACRAVFSSPVKMVSSPNCRNGGGTLDWKLNRRCCKVWLTPRN
AEKVLRREDDVFILTFYFQGALDAKYQPGTLAPVLLVIFLGIIVWMMLTKDLSV*
>TCRU_2345 hypothetical protein, conserved
MDESPVGTPFYAAFGEFKDGYNREEAEAGIHEAFRLRQRARQKNYVKELMLGSGLGKAAK
RTVQSGLYQPQTALYLPTNVVSAAAAVADAGDVSEECEESGDADEDPIGNFLMPPGLALL
SNSPSSVMNKFTRTEVEVQTLVEVERQLEENIKVAEESVARECASFSFENLLESLSLALA
VVEEGDAQIQVKLPVQEEDAVPLHGAEAVMAYFREHMAPITLTLLATLYATEWMLQYTMT
FINSMFIENEKEAQLREELLARCVRWLGKINRFVAFAFALEMASESYEAFAEMQSLAEQH
TEELLNGIEGDINSALLLSFPKRRQGLLGRDGRIKKRLQQLLQLLHDVETSWLPTVKLQR
DWKDEFLTRIYSRIHTVIAPGYLSAQLGFIDESLYEFVADGTVLRKQNAMNATRGSNGQR
TSFRQSLPRILVATQVERRIVDEKLTFQQIGMLVRGSASRVIGLQLCMGTRFILRQCDTE
YDAQWGFSMSHSQDSPNAVRDAVESVSCFMESLKMQLKEQMDYQMGILRHFLI*
>TCRU_2346 hypothetical protein, conserved
MSFTTDDAPAAVRNPTRSSGGNGDCQCEEQVQADPMPPVVAHYPLGSWERHLLEERLRAI
KDCERERLLREELEKECTFQPRLATSRSGEDEPQKDFVSTDQKQRHVPVFERLAHRAKER
EARLASLAEEKRRNEEETLRHAFRPRVNTFSEQRVSFASNEARIPVEERLLHYGRSVEQS
RRLLQEQRQQREIEEMRQKAVIRRAQSNASRDKRQSDIAGRSKRLLIEREAQRAMAQNAL
LNAHSFRPKVCTTSDAIDRTLKAKKSVRDRGLALYEEGMRRQQQRQAETVQRQAKESSGL
HKPATNPLTDDWIHHGQHRALFRQDFIKRQEIYQRVKDEHQRNLLSALEQSERAEVPRVN
QEMLEQQVERLYLGAQEIRKESRKRMEEHINSRECPFRPQLAPGTAYVIARTQREEDVVK
RLASVPRSRRVSQYSIFDTAYADQKENEKNSPRKSKVIHPDEAAEFFYRQRKALEDREVQ
LREQKQRLAMEELCACTFRPRTCTDEYFHRRQREATDQAQKPIEARVSGVSAYLQRQAEA
KRRLKEQESRYSNLGRGLPCNGAGSTVITPFQLSSGRGRHPHGLNPRWNELKLFNGEECD
IRCHVDPYSNNEISMALRGKLVEGSARSRGQ*
>TCRU_2347 hypothetical protein, conserved
MNQSRDRKAVPADRDVRARRKHTHRAEQRVTESVADDDNVQRPNSGVRVAQQQQHGAVPP
RAAIKPDIRHVARHRTNQHRQAHAAPAERHVAVAQPRQPAAHCMRHLGVHHVADALTNWR
RWRRGQHWRRRRRWRASRHRHRDAHIAVPSSSALAPAVNYRRRQRSKAAAILRALPAHRN
RRHVVDAVQFQLCRRRHHTSRDRQTPSNEQVAGGSTR*
>TCRU_2348 hypothetical protein, conserved
MCTQNRCVYPPKLQYRTYSELPPTSVSVPVEYKPNKPCLGAFALTLLTNSEDALNTTFFS
ITTLHMLFADSGNRTSENCTASTSVTAMSQCCGRANANKATEDRITVWLTRIRTPADSDA
SLPPTNCSTAP*
>TCRU_2349 procyclic form surface phosphoprotein
MCLFGIVDAVEDFFKSVVACACCLIIGGPALIIAGSILLNQKDLRKAFRDAVNEFDPTPM
NDWTGTINKVPITVRRESLNVKGVDGATSVFAEAVVPVSENFLSEFPVSVNVSAVTPFNR
MAPFNIMRNSTYFCFSSDCIDGKDCKCKRDVRSFGEKCTARGGRYNQTPTWCKAGNICGE
CLETLYLRKLYLVVREVSNGKYAEDTNLRSAMYAFGDLDNDYQPGVPSTVTVRLYSSKDP
YIALQRLTRGTNDLGLNSRTVGIVLIVLGCLFLLLEIGVCTALICYWMRPKKTSSGAPPY
LAPASQGISTSGASGNAAPNFYAQPAQQTGQGYKYGQAAPPGYTYGQPPQGQPIPPGYTY
GQPPQGYAYGQPVSPQGQHGYAYGQVPPPL*
>TCRU_2350 Leishmanolysin, putative
MAAREHHDCDDIDGMELQDGDGDGRTLDSHWSQRHANDEWMAPISCVVCRTELTLAASAD
LGCMRVKWEMVEPMRWWRNSCCALLQRKCSAPNMSEYSQMFSEAGVHAGRCTLDRYSSGW
CVDEVSMKGQQNVRWTVAPSLVPHWM*
>TCRU_2351 hypothetical protein

MASLVVYTRGPRSAGQRPPVATEHGCSSQSSTLPPPRSSESTVPNRYDWEWNGGSDIERV
VNGHGRRGSSEYVHGNVRAVSPVSYGGSNTSERNVSGHLEGLDASPERIYMEKDRVIRQM
ADSVGRSRRNSYDDDSFNEDDYNSDEEEEEEEDDDVPRIAIIGGRHNEQFVREILYGTPR
AGESPKDPHPHQQQQERYHTEPFDREFSTTGTGYGESGLRSDSKEERRVVFLQRSSQMRQ
EGHQQQQQLHYYTQSKRFPSTEQLPDKPERIVKLSPIRQRPQAEVTRTRPALLSAVKSRS
FGVVRSPKRRESFSEPVHGRHMSYDKGGTRGHDASLSPRRHSRHEDSSLRRRSVDSNVKS
PSVSKDKNRRNERERQQRLRKLKQIRYSEEVDDGSRVRRLPSPSTGNDFGVKETKMKHRR
TRTMSGSTSSGSGRENSRKSRKKRRAAGVEDDGNETQKAAVQFKPVFTAVESVPPKAKKE
KVFCDCCRGKKEKSQKEKQEADDSAKREVVRRPNEKTGNVEDEKPSALEKAVHATRKTKS
QPQVPPRRRKRRPSMPPSDAAGSAVKTRERAAASAS*
>TCRU_2352 MORN repeat-containing protein
MSLPARATQSQPADVTFESHQSGIQRVMMCPIEFGTCTGIQTEQLGKNAGIGLKQQNVCL
RHLYTGEVVRADSNHNCGNSSNVFIPHGVGKLVCFFYAKGGTVGFAGKPGSPVGLPHTVV
ISEYGEVEELRDAILLTFSMYTGSFSYGRRQGKGRLTVYPHYFIDCLWDNDAPLLDRTPC
VLCFFSKDSMSPTDEKSQMKPTRVGGNSGKDMAANVKTQYIGMISLISSGLTPHRGTFAG
LAWAEQARFVPDGIGEILYPQGIRYCGFWQCGQRHGFGVEYDPNKSTVYMGGFVYDQREG
SGTLHYCTTGVIFSGSWKKGSPTETSNAILPTSPFILQGGLWKSYENWSFEHGALMRSSV
PLSGIWEPLFLAFDEKLASAPWDHQGTSPTTKTTTATTMEGLDNDEKDHADEKNILLLSN
MMQSSEFKALLVPFQRCYYFLYKPCVGRGRRNCNGSSSLGEDAGHSLTQWAFPSFSSPAA
ARSAPVSRSSLLTAYDDENRPLSNSHDILRSRWASLRCFQQEKSYMKSLERLSPLVLQLR
ELGSDYRQGFGEAPGGGCWSCPSWCEEMGVVGGNGDNSKSNSSNISNGIGSGAIRCFHTE
SVVESLAKRMSPVKMFERAMRDLASFVSSVRLRLLSYVAAHPLACDVSVSKRVLAVCWDS
VYALVAPVIHELAAAAEAEAVIAASLALQRCTSLGPHDFIPMAVAKNFDYFEEDRKVTKW
LARLFSSPTHHSRRVVEQTINGQLLCFSPHVGSGQETPAVYFSPACMFAAFDSVYKISLR
LFPQHPLFQERWMSYSVLEAFNYAEGIVPRDALSPPAVLRILHFLAAEVNPRYPFPGGST
ELRDDAITSKGWEKALHVTNGNGTNRKDGRDPSAIMESDTVDLEPWLNSFTALYSAPKEA
TEVVSLLDFFRDGVDRLKSVYPSVRVNSLRPSAMDATVLEGGVLGIVYPLDELAVRTRFV
LLAASEWLRNRQQQGGKECEWNINDGKEVEMTTDGENGDTSRKANGLIRRVLSLPISVMQ
PALSQQADELSYEAIHMHEDGLMHSVEQRRQQEMSSIANLSSEVLLWIVECIGRVLESPN
FPSAVTSSMAPRRTSMQPRETQQLRQPDPLPFNLGNKERCDSPADFTVATPKESSWGGAV
SDQDEGNVVGSQYLRYQWKHFISNNMTFPNRSASLPLGDTNESHANTSVSAAATTSELLT
EAENLQILLLQSFLAEVGLWITLDMHSCYDNEEDVSSTSLAPYAISPREEKTVRRCVGKE
AILSLQVGLSFLGSRAWEVLADAWLAACLRLRANASAFPHARRKCNPIDALKCVH*
>TCRU_2353 Replication Factor C Subunit 1-related protein
MSLPPRLSSCSLVHTVSLSAFFADGFRLASSSSPCLSQHHTGDAGQCCTTAEERNVPSPC
GGPAEYRAGEKRIRLSLSCTSTQDITPSSEGKMESADLLSGDGAEAGKLLPFHKDDASLL
LEPAAASLIRLEPSGSWLGSLPRSVPEKCGGVSGEEQRWTPSLPKEGNETANSAELASLL
HTALLECYRVEDELLKRGREVAVSKKETPHCAPKLVTEEKMERAEMRHRPSPSTSSSSGT
FERMVGYIHAQKRRRLEQSERLEIQVRDIARVKELPVLVEDAVRYAQQLFEWSCKCGGND
KGAFLAEAGAVHSDESKLDDTCSPSGTTPVFAGSTASDNREANHMLYAKFPPPLFHTSSF
AAAVGRLLRWVRTWQRAMPGGVGVTESIPTKAGDKTQRNGSTKGAASRKMSTKGVLNLSS
ASCQQRKRHVRQLETRGNSGFLNDDGGEREEEDDGRVAMASNRKKEEGHKHKRTALQSYR
DDWICMADQMLGNSNRHITPSPFRSGSPFESLEEKEYGLATDRVIYDEYGNRLRSVRLAK
KMAEERALYEEAQKAREQRRGYFARAEEETRSTRRALFDEVSDSGSDEMSDDSNEDVTNI
AVLHGPCGVGKTAIVYLVAEILGYRVVEMNTSVRRCPKDIDRLFSEVTRSRRLSGLAAGK
AMVSIEEELKKLKSEHAAALAAVSATASEISKTTSSKKTKKRNVISAKAVAAFFRPRVRA
KSSEVILVDGSPTVSATVPPHDKQVLNHAEDCKYGKRDGEANVTVEPMCGGHEGTTRTLL
LFEDADVILGDETMKSFYTAVRDLAQRSKVPIIVTISSSASSSSSPATTTMQEPEAVQI
VPLDAAQVSHFFGKRTPFTAIEPMSRAALFAQLLVVAAVERGLVMVQGGAAPHREENDEV
ESSSKHNKRRTAEPMLPSTPLELVMIKDVTKFRQIADAIRSEVYNDDLETPSRPLNDPSD
VRLWLNRLQYLLLVEQWPASATSMGSRHDECIFGGTCILPSKTDACSNAMQFAGVKSHWD
TQLGRVLRAPEYERPAVSSIWEWQEFQYAEEIAADINANYKCSDGVIGETRGSNNSNGSV
VLTTPQVEVPIAVELAEVLQGVFPNDVFCQQKRKGGVEFVDGVRRRCTTTTRERIEAFGA
WWRRTKKTDAVKFHVAARSATAYEDLIGFSCLLQQASPVGKGISG*

>TCRU_2354 WD40 repeat-containing protein
MLEESVRHISGLSPTPRSGSRSDTSVVGPRKKTDQKAQLLGKMTLGDGLICVDFLSGPNI
LAIGSTKAVHLVEVTPMNLPSQAAGADVSSTPHLASVSFAMRSCGMFGNVAKVEALAWYP
NRNEAVLAIVQLSRSVTVLFDALSKKGDAYMAQQWIHSSRCRTLVSSTVAGSEPLSAAVV
SAASMPSTPFGTAMQEVQPSPFVERDPDRPCSMVEVVINTGFLRVERITWDPHNPYTLAL
TSNATHFELWTIPLRDKKVYPPRLILRPPAHDERSVTRGVVFSPFDPNLIVVVVERANAG
KVIVYDRRHVEVLWSMETTGPCLSAAFHPIFSDLLAVSFRKAKTKTNSRVQFFRVQSDVI
AAPSTTETNHSGGEKLASAPAPLESTDVLPPIDSIDSLNRLRWRPCGNAFQVTGGEACVE
TSDGSIDATSSKLWFATTALNGQEISVWDAANGFSPIFSIRTVCHGREFVRQGAHHMNPT
LQELPLQEPTDCVWVNALTLVSIFKDGGVVLTSLLDEKTTSRDTLFRCITDPNTQLSAGS
DVLSLSAILPTAAVVADYFGRSFAVRSSSSLLREYYTKIINAEKRELLEELASGKKNAVG
GGGVLSSPSPSSTAVSLGTVKHHKDSSRATPTGGMMFDTRYSPLPSHWSTQTPLQQASFE
RRFPSSLASAHAIAGSPNSGRRLEFLFPLLFSLVPSPSPVLTVATTTTRAMGVDRVVAND
DAETKSADRFLRRSPYLVAFDSRHRSSRGGLETQSESGLEGKACSFPTRHGLDGAAATAK
RGLFGARSASANEQSLSEHRGIVSPMISLMNALAMTSSFSPTQSEEGNARRTNLFTPVGR
TSGGAVSLLQETQAGCANLTSEYGAEGGSVEKIPAQPPPLGRRSLVKPVIDCFILSNETC
GWAYVEQTSEEDTFVRYALNWEMGFDTSRKMRAHRHAATEEIAKTETENVDQCFARMMGH
NSKVCRSRERELQAATKAISEGRGNVPGVDGATANSGKGTGNSEYPLGSVDPRGRLWAAA
AYAWRSHNVTLITSLVCSYLEYTSLVGDVQFCAVLYLLFCLWWKQRGMSVRSYACPLFPT
DEKPAGNAQEHEKTREATNGSPWQWKMRALQWVEQYVTRLYERKLYVPLNELLIIVPEVM
GNFSAGLPRAEDVAQKLFTCVYCGTCPKSELVPRAPKKGERLFLHTATPATSVDVSEGTN
ERLGSDDDSSDSFESSLSSSHFCMCVQDEPADSGACNDSVLVAKEKVNGGGSAHPLANSG
VPPRNAVCSRCRNAPLMTCVICEEVVEGMYLWLLSCGHGGHVHHIKEWLEVSNECPRCGI
PVLRPEEKLR*
>TCRU_2355 retrotransposon hot spot protein, RHS3, putative
MKLNDFLTMELEGRGILRANRNVLLRDFFSDPTRYIRDAGVLNEIQTTDAYLRMEGTVRE
EMGLEEAVRRLHEKGVDSILGWSEATARAKKSVSNSTKQSLDAALHVARNPTMTNAPIYL
EGYYESVYNARWHHVVEVPGGEGTGMKVKRGKPKQSWTYEEAGRTIEKNDAVRQSGAAPP
RLMVLTSDKGWPYSWEQGVESLPDCYVNCEVDRVWQIVKGDLNKWFSSHGKKKRSPERRV
LIGTPGIGKSMNAGSYLLYQLLHYDVDKLQMVAYSFGDEASLFDKTSKTVSIYEGGTSIL
KIVKGFSRRGVKGYIIYDVALKGHQPSNTLPCKGWGMIVVTSPNTKNYESWAKLVEAEQI
IINCPDESDVKAMCVWKEHNGQVEEESKEEAKEETEEETEEEEETEEEEEEEEEEEEE
EEEEEEEEADYWKKVKRRMDKVGPLLRYIFDDRKYIGRIDSCKSKVKSMVLPDTHYYSIL
GSNEVCDDNHISHKLVKVVRVRGGKKSELPLNSLISSYLGNLVTCKLAKLMAPNDFILLV
LGIKDDLLSKALEKHSVFTFLSEDFVSAIIPKLKELKKRKNARPQLCALRVCPHGRSLKP
CILPCLGKNKKKFNIKYRVLYKPEAQNFPLVDAFFFLNSNPKTLVGLQITTAGDHHTIPS
TVNQFKEKMAKYFNDWEELSRDMSWEIVYVQHNDNKPLDGWQRCGPVENNKLRPAEKEIV
AFWDGKVHQYQVSVSSRDFKEKEEALPIVEEQQKQKKKQIRR*
>TCRU_2356 hypothetical protein, conserved
MAAPSLTGSECDNTNGGKESDEDGDGLHRGADYLRVFLHESREGLAAVPTIPGLAELLAF
ALSPAVISAPCVEADPFTVEFTQQLSSVCAADPALALSHVSQRCRACDLLCVVQAAASSF
LFVPNKKHFALRWVFICVAVDARDDAQRVCLLFGGHEGDFGVR*
>TCRU_2357 hypothetical protein, conserved
MEAGLPAEHRAVARISLIGGVTAEPSNLLDSDILLRLMGHVIAVAEQPSDSLDDIMARRV
GVSLPLYPTEPALARCCCVDDDAVTEGIAVVYSR*
>TCRU_2358 hypothetical protein, conserved
MQPRCKPHKIVEAFRFPVAEAPAHLLWQPGELACEPRAERHTAQTVRDDGLLRRTLHCVC
VGTPLPHPHNSPRLIAAVQHRTLTVKTTRHAVSQDCVFVCPQLYCRLRRHNVKTEGLQCR
HAARGIGTEAFMRGRTTAGNGVEPQCLTGPVVDEVSTFPQNTIKACGAPRSAQIVMQSSG
PSLRQRTQRVSPDAHHTFGNRSASRARVA*
>TCRU_2359 hypothetical protein, conserved
MLPRRKHVALVLRDADCDASTSACVTPLATVTTWLEMRKCTIPRGSRDIPTCIWTDGMEH
AESTAAAAWDAHTASPGGSLPRAELLRKWEDRNHALRRGFSMLPEARAKQPGALSSPSL*
>TCRU_2360 Adenylate and Guanylate cyclase catalytic domain

containing protein, putative
MKARRVQFVSGVVTDAMLEVESVTFIDPLLLGSRLNRFRRNVIRLMPTLEQQFFVLANYL
GDTSRGSAHAVIRSGEASAMADLLRRSLLTFRWSLEPAKLLAGGDALVDHLPVKGDVFLV
GLAAGDAGAIARHVASHVGVRVFVVFSEFALLYAEFVAAFHGCEGADRVVFATSLPHWND
ENSTSVTTKKFVVAVPEKKRTPLSLMGFAAMGLMEVVISRMDSVSAELLADFFYKNVAVT
VDDMLYGPFADGRACASTESGAGCGVNYGAKRISVWPLARALDPAVPLLFHAVNPSMKYV
ESAAGGLTARQLIGVIVGGVAAALLFVAVVLYFCRDSRNNANAPKNRIHPVTLVFTDIES
STALWAECPEVMPDAVATHHRLIRSLVAKYRCYEVKTIGDSFMIACRSVFAAVQLVGELQ
QVFLQHDWGTSVIDDTYRMFEEGRAEEEGEYVPPTARLDAAVYRQYWNGLRVRVGVHTGL
CDIRRDEVTKGYDYYGETSNTAARTESIVNGGRILLTRASYFALSTAERKHVEVTALGGV
ALRGVPKPVEMYQLDAVPGRVVAGLRLDRDDGAVDDYSDVGSGDGSGSTIRGGPSGYVAS
VLGVLFGTFAAPQRLKALLPLCQRWSVPVPSGAGAGRDKEACRAAMERLAAKVCGVIEKR
AYGTSFEEGLRTLSLSDNAFFWNECGLRLRNSAFERNGLPVDFRRRSLLHQASLSAAGEA
WPAEEDPVATIHVRRPV*
>TCRU_2361 BNR repeat-like domain containing protein, putative
MEDGTLVFSLMAVNEAEYVCSMIICSTDNGSTWALCEDISPAKCLDSRVTEWEGSLIMIV
DCENGQRVYESRDMGTTWTEAIGTLSAVWVNARSGVSRDLSLHVDVLITATIEGRKVMLC
TQRGHASGKKRATAHCLWVTDNNRLFSVGPVAMENAASWMLTSNLLCPDGSLHLLQGRDN
GECRVMSLSRPTEELEEIESVLSNWTQKDIFFSSLSIPTAWLVAVLSDAASDVTWNDEYL
FLNATVTNAVKDNDGLRVTGLESRALRPVNTQGDNNLRHISLSHNSTLVASVTIEEAPSE
NTPLLTAVLADTEPNHTVGLSCSHNKKWETTFEGKTTTRSSTWEPKERIPSGTHAARQQG
LCAH*
>TCRU_2362 Glutathione S-transferase, N-terminal domain containing
protein, putative
MSLTLWSGVNAGNTRTHKLLAAATLANVAVTPKTCEYGRENETAECCRNCSPCGRYPVLQ
TEEGCVFETNAILRHIARLDRSGGFLYGRTPLEGSQVDMWLDFSATELDAAPHRLCSTPS
VAGSGSPTRWTACTRCCVRWRRGWRRAHSSWTSAWWLRLRRNGTIV*
>TCRU_2363 hypothetical protein, conserved
MVCVRCRCWAAAICDCAVAVRGVAAVSLLLLPLCVDGELVCAEGCRQVTGVMAMMMAGRV
LLVCALCVLWCGAGGADASNLENNAVGACMVSWVLNTNKSYAPSGCDKTALTLPLRSVLS
ITAVAASTDPLVTGAAENKSDLAPSSGADFGGAGSPPGRGGGGGGGRDDGAGGPAGVGGA
SGSQARGGKASVGGGGGSNGGSKARVGGSLKSPASDVKSPSPVLGDGGSSPGAPTGSVGS
DGSKGFILGSFSSGGRSQPDVGSPGGDASLSTPVAGGKSPPSITDESDALEKTGAAASTK
GGKPQEAGEQSEANRARNELPELSAPAESTPEAQEDSPSRQEKPESEAAGRAATGDEKRR
SNAEAQGPSAVMSTASASNGRRRTTNSGGSSGRRKPNGTNRLANLDRRKDKNVTVTKQKG
A*
>TCRU_2364 hypothetical protein, conserved
MAQQRIQYTAGARGQDKRRVAKGQFKRIQREGPNHIPATRGHASTKCADGSGDRSKWDSD
DATDERVSLLPDFVGDYQRYTCRLRAVSDAQRQKLLRGGDVERSPSPIAALRMTVPSLTP
AKLATLMAQGADMIAIRETWKSSEQIASMHTGECVLHAQSRIRKECVAAVLVRKNLRSKR
MHLITPQRDSSLEVMVQFALGQNRDLIVASTYMRPPPQPTQPLGGC*
>TCRU_2365 hypothetical protein, conserved
MCSQYGPLRNSSQRGRPIAVSVANSCLRVATTQKFSKPPSAVHPRNIGRQATEDSMNSEL
KGLAGVYQHQRSPMGSAVELASSTALLGKVRLEVIGSIMLHFVYQVCQLHRRGTRTTARM
LVRTRRPQPKRSPQCHFLSSLTHDGRKADGSI*
>TCRU_2366 hypothetical protein, conserved
MAKGFLRVNWRACGGWLILRWQRPLPGTTERVAVSVLANGTTPLVAGLGSKACQRVRVPY
GCDSMFRVLSGCHGLRRMLSRRLISMHSTMSVTKLPVHGPAGTHQCQETLPDPVLVEGR*
>TCRU_2367 hypothetical protein, conserved
MAKGFLRVNWRACGGWLILQWRRPLPGTTERVAVSGLANGTTPLVAGLGSKACQRARVPY
GRDSMLRVLSGCHGLRRMLSRRLGSMYSTTSVTKLPVHGPAGTHQCQETLPDPVLVEGR*
>TCRU_2368 hypothetical protein, conserved
MSGTSLADGSLRSSWETGDTTRIRRTREERMPHGELSTLPLLSVLLGVSEGLVHRRLSAL
LARHRRQPRLTPRRTVSDVVTPVRDKTARGPNERIAVECGRRRGGVPRCTLTVAALSQSR

PASRLRSAPLTMGECWLRPAASRACTVEPNTGCAATWEAAALG*
>TCRU_2369 hypothetical protein, conserved
MDSAVNWELASTLLHSDGDLHLLQRRSNGEGRAVSLSRLTEEASAIKSVLSTWSQKGSFF
SSVSIPTAGLVAVLSGAASDGTWIDEYPCLHATVTNAVKDCDGFRFTGLESRAIWLVNTR
GDNVRHVFLSHHFTLVASVTIEEAPSGNTPPLTAVLANTASNHTMGLSCGHNKKRETAFE
GTTTTRRSTWEPKKEYQAVLMLQGNKASVHIGGQLLAE*
>TCRU_2370 eukaryotic translation initiation factor eIF2A, putative
MQPPALASLPVILRKDDSLVVASFSEQQRTLTEVEGTLMTGDYRECEVRFNPVKQTAFAH
ATTTHVRYSELVPTQDEYLWGLKQIFEVEERNVVALSFSTLGTVLVTYAMMDSRRPEGNM
VLYDVNTGNVLRRCVQARWPGMVWTSDELYCVRPVQGFLHVMDGNLRKGEVPVLFKMDLQ
LPQDKEIELSMCPGSISLLALFKPFHKQVQGTLFIYRLPNLLEGLIYQVPFGRAESATVL
WSGSGNHIALLVKSESDKSGRSYYGTVAFFLVNVMGRSIKEIKFPSGESVHDCQWSPTTD
QVMVIHGTMPRNKTTLYDKTGMALMTFGEAPRNTILWAPNGRYCALGGTGNLAGDFVFFN
LHPSDSSNNMKNVHKDKNTRVPMAPKPVAASSSEAAVMIGEFNEKSSVQMWAPDSHNFFC
ATIFTRLRIDNKLVFFKKNGEHLLTQKYPMLYGAHWVQTQDTRLYPVRSASPRKETDKSS
KPQPYRPPHASAAAAALLRRPDSSAPMQVKPTVPPGATVVVQKKKRR*
>TCRU_2371 hypothetical protein, conserved
MVCVRCRCWAAAICDCAVAVRGVAAVSLLLLPLCVDGVLVCAEGCTQVTGVMAMMMTGRV
LLVCALCVLWCGAWLCDAAETSSSAPHRDNAEETMTPEEVTEAIEKLAEGVLDMIRVSCL
MSFITSVNATLPAHNDTEVEKCVNKTAVGISGVTPRGRPAAATTDATFASPLPSSSSATS
A*
>TCRU_2372 hypothetical protein, conserved
MYAAHKKDINRHKSFHPLTYRNLSKVEQRQQEEEAKKKSAKERKEELRHDQEQRRYDDLI
LAASADSVSGQLAKFRQVENIFAAEGKKANASSSAPPVKDELASIATPLVRSGALAFKKE
NTEHDGDEKTEGRKRGREDAAGLPVGGDGSAVDGPREGKKAVTGFISTSNAAQLRKELDK
LQKERHDPLRRIEQFQNRTVAAEAKRRELGTGAASVSNCVDTEKDAIRSRIHELIQMKRQ
K*
>TCRU_2373 phenylalanyl-tRNA synthetase (beta subunit), putative
MPTLAVARDYLFHLMGKNYTEEQFEDVCFKFGVELDDVTSEREMFSREQGMVGGANLEEL
SDEVIYKIDTPANRYDLQCAEGMAVALNVFLGLMRAPAFKVLNRCSPLYRMTVDKSVRNV
RDYVVCAVLKNICLNERSYRSFIDFQEKLHSGLARRRTLASVGTHDLDKIGDNNFIYTLK
SRESIRFVPLNQRGRMLDCAGDGLAEFYKDDRQISKYVPLISGLSHYPVIMDREKQSILS
LPPIINSDFSCISQETKNIFIECTAPDHYKANVLVNQIVCAFSTYCEEPFTVEAVRVEYE
EATPDGTKVEVTPNLDPAVIPVYIPKVERLIGIKLDSPQHCGQLLERMLHRVAKMEGDNI
FVEVPATRPDVLGPTDLMEDVAIAYGYDNIKYVECTTRGKVTQQPLSKLSHLLRIEMANA
GYTELLTFSLCSRDEAFAHLNREDDDVAVHIANPRTMEFQICRPSLMPGILKTLNANKSH
PLPLRFFECSDVVLIDNEKNFPPLIRPHSEYPNCGACNQRHVAALHCCSENSGFEDIHGL
VEFIMKKLSISRKGEQNAEAEEDTYTLERGTDGAFFPGRCMDIFLHRKDQKVCLGGFGVV
HPNTLRAYDIPFPCSYMEINIQFAQ*
>TCRU_2374 hypothetical protein, conserved
MIITEAVFACLREWHDATLARAFFADDEGVFVLFSAMNVLPGNVETNEAGESATALELHT
RCCQGSRLFLESERLQVARLLRFRPLFQEKKSVSVSDGNDVDECSTASLTSPDGRNIIAR
LLLELHASSCWWRQGEFVQNMLRTPRFSLADTAIIRHRCAAVVVTDETSSASQLKSLDAM
PDGDSHAKKLLLPRGSPPSFLQGVLSSYLVKWLRAKRTQSLSHLTSNTPMSLLRVIFFLK
RPRSSEESDEHSNDESDELIPCVSLLMALFGYTLTQTPPRNTCDASEAHKAWRQLCVDMQ
CHFCGGRPRLTLEKTVAEEPLDQPQLQEQKNEEDVMEGEHNKRMESGETLMIAEPTSRQE
PGEPVGLENRAQLELETSQTSINPDENKNVLAHVAAVCNSDKKEASPHSRFCYTIEVSEQ
DEISGHHNTCPWKALFLSAVLADTTSSFPSKEVLFNLCNADEEGGSLQMCFKLPEVAKLI
KCWRRSLYAESVWKEMYIRHPLPAALSSVIPSPTDSGTEAFLEGLASRSAEGETFQLKPL
TPLFDDRSPWDSYFRVASFLKASAIVDYGGVEVRGKDTTEIRKPPKVEEERHWKAVYDMG
RRCMLAAVEEGGSESAVELSEKFKEQYRHCAQQDATGGHTSLPLEGVMHKLLHLLNSTLS
VDLLHGRKVSLGGLFEGPKIAAQEQKNVHSFLDALDDVVENATHEPPATEPTDPAKRPLL
IQGNNNDTTLKKGGGGGKGGTSGARQKQPKQPQKQKQHQYHHHQHQQHQQQHQRQQHQQQ
LRQQGMPMLMAQHVLLPSSSPTEGVFPFPARGSGSGVLPTPVPVFQQQQQPPPHLPFQPA

LHGIPFTNCNQKTVLGGDSIGVLDDAYMQRPSVMGQCQTTVAKPPQARMGGRGGNHRGAR
GGGRGGGNTFKG*
>TCRU_2375 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGGADASNLENNAVGGCMVSWVLNANKLYTPSGCDKTAL
TLPLRSVLSITAVAASTDPLVTGAAENKSDLAPSSGADFGGAGSPPGRGGEGGGGRDDGA
GGPGGVGGASGSQARGSKASVGGGGGSNGGSKARVGGSLKSPASDVKSPSPVLGDGGSSP
GAPAGSVGSDGSKGFILGSFSSGGRSQPDVGSPGGDASLSAPVAGGNSPPSITDESDALE
KTGAAASTKGGEPQEAGEQSEANRARNELPELSAPAESTPEAQEDSPSKQEKPESEAAGR
AATGDEKRRSDAEAQGPSTVMSTASASNGRRRTTNSGGSSGRRKPNGTNRLANFDRRKDK
NATVTKQKGA*
>TCRU_2376 TFIIF-stimulated CTD phosphatase, putative
MPSHISERFASVSTSLVPGNRISIQKQGHASEGSVRRVPLRLANLTTGGNISGRQGFTLN
PSMPAENSLKSYIFPRGSLSKRLRCIPASNNLSSSLSLSHAPSNARLVRARAAAGAADGF
FIPPVRAVDEGKLVVVLDLDETLVYSRSGRIILRPGINRLFDVLRGRCETVVWTAGEKSY
AMEVLQLIDSSHCVQHCIYRHEKWWTERPGYVKDIAALGRPLHQTIIIDNTPDCLRAHTR
NALLVRDFRGPCGGSSRFDNTLFVLADVIDDVLNGSENSIDAFHDHPQLQLRSVECESGS
TIDVLTLKQDNFLDPPKGNNVIPYNTQRASRRRTMVGM*
>TCRU_2377 kinesin motor domain containing protein, putative
MAELAGTAGRIQVGVRMCPPRQGEKVIVHADSDDQRAVLIDAEGGRASTMFKFDRVFTGG
QDEVYETIGRPMLKEAFEGFNVCLFAYGQTGSGKTHSLFGDLNSKEGYGVAPRFAQDMIE
EAQLRVESDSAATIKFFVTMIEVYMEKVRDLLAPRARGQEPESLEIHEDSQHRVYVKGAG
VHSVLSLERMLELLKKGNANRQTGETKMNETSSRSHAIVQITISQKYGSLDMRDVESVVL
LVDLAGSERQSKTESTGVAFEEAKKINQSLLMLGRAMNSFSDRKGGDAFISLRASKLTRL
LSESFGGNSKTWMLATVSTAANNLTETISTLEYAQNAMAITNKAKVNDTKKNIELKRLRE
LVASLEGRLDVLALEKQRKQEEIGRLTQERDKLRQEVAFADSVHDARDKLELALNNIRLS
NIALRRRVEAASEGFIHSLDNKSCFLFFKGRCSITLESVLRGQRRSFYIGLLTESGVLTE
ATLHIQLFPCEHHANERNDPMQFIGKSLRFCLHVVGASGIPKAFVAHTFCKFTLLHDREE
RYFTTSTAENTQNPRWGYVKVFEIPELTAEVIRCFCEHTVFAFEVFAFNA*
>TCRU_2378 kinesin motor domain containing protein, putative
MGEASKAASRIQVGVRMCPPRQGEKVIVHADSDDQRAVLIDAEGGRASTMFKFDRVFTGG
QDEVYETIGRPMLKEAFEGFNVCLFAYGQTGSGKTHSLFGDLNSKEGYGVAPRFAQDMIE
EAQLRVESDSAATIKFFVTMIEVYMEKVRDLLAPRARGQEPESLEIHEDSQHRVYVKGAG
VHSVLSLERMLELLKKGNANRQTGETKMNETSSRSHAIVQITISQKYGSLDMRDVESVVL
LVDLAGSERQSKTESTGVAFEEAKKINQSLLMLGRAMNSFSDRKGGDAFISLRASKLTRL
LSESFGGNSKTWMLATVSTTANNLTETISTLEYAQNAMAITNKAKVNKTAKDLEYDEIQK
LAWVLQIRLDDEAKGISALDAQIQGLRGEIDCMKSKLTVASDSKVETELKEALEDREELL
LSLRKGLIEQRKISGFSAALVCFSGTCKTSLANIPFGSYEVTTLVVPCYMLAGPPPFLIC
HIHVYLTEESSVAVLLRLRELQHLPDYATGGVQVTVWFEGHYSSAVQTPIVRPNGGNPQF
SLRQMYLFGPHTEDLERFFQLDVLNFRVEGIMSDLTS*
>TCRU_2379 ubiquinone biosynthesis protein COQ7 homolog, putative
MIRRTFPRILGLPSRTFANSARKIKIDEVLRVDQAGETAAVRICGYQLLWMSPLDSAVPV
VKEILKDELVHEKTMNDLAKKHSVRLTALDPVFHVGGFAMATLTALLGKEAMMCCHAAVE
ITIVNHYNDQLRELEELENGGVNLNDDDAKALKEIKDIVAKFRDEEEHHQRLGETNGAAQ
AFCYPLLYNGIRLACRMGVNFAKKV*
>TCRU_2380 nucleosome assembly protein (NAP), putative
MSTYPQHVVDAVANCNEKVKSLQTETESQANQTRIEYRKKLELLFEQRQEALDKIEGFWS
GVLSATETPLRPLFNGTIDPKIVRAITNFKVTTSVKDGFLCRNVSIVLRSNMFAEQGTIY
REVNTQLKTISLGPIKWKSGTERARQDSVFRFFTVECNDEGFIDETLDAFDTVFQNPFLA
LESTEY*
>TCRU_2381 hypothetical protein
MQSFRANKRDVENILHDFSTFLRQFQGSNGLRCFLDQGKLSLLSAIGEFKQSSDEIYDRR
MKVLSQTRVSLMKLSDHFDAVGNAIETLFAQLDGLLSELHNFKEICENHLEMATETFSEQ
AEFISINSLKVKLRALSQELTSSIRTNCCGIQSSSIEQLDKAYLDVKCEVSRTQTAFDVW
RRDAEVCESKLLKSRSGSSHDQVRELEFKLRRLLERLHESGDKYHEALQGSMNKTSFLLE

QVSMATWAACNVFFLHLSVFFKDTMNVFELVASALSSVKNNRSVSRRINLEKQAAAAAAT
VATASSLCTTTALPRLVEEKTAPSTSPTHELEYLFSAQLGEGSVSHINLTEDEINRGTRE
FTDIDDIFK*
>TCRU_2382 hypothetical protein, conserved
MLKVWLREPHQSDDEAIKLMVDEEADVSDVLLKAPELLRVQQLKPSEIRAEFEDTVLSNR
LLVSSVFEGKKEGTFVIRPRPGVVVPPNGVPKVSSVPAGRGGDGKNAPPLAQNNVHPPPS
SRRNQFDKSPRVNSEEFKRTGSLGGDRRKPPVARSTSRGPTPPRIVGEGTPRDGKANFDV
HQKERNITSRKSTPNRGTSVSSFDRRPAVRSRYRDPKNVASRFRQEAEKVRVPSKRNQVD
AVCDSFKPQWGKPLCATCNHLKQAHWEAQKIKSSGVEPNIPVENDGSLSKNAQLRCPTPN
ENVSAELKIDGGNNNMNMANSASLPLREEY*
>TCRU_2383 mitogen-activated protein kinase kinase, putative
MKKLGLVLDAAAVEKSQRDLQSYQIKNNNSLQLRAFLLNESGMFTKDGRKLPGSVTKEVI
DDTSKRIIGRGASGAVYFAKLKDGGPVALKHIPITSKPHRDEVDRELSFFSSQSNSPFVM
KNLGAFWDSEEAAIVIPMEWMAYTLKDLSCFWEGIEETMLRDIFFQVVSGLVYLHDTKRV
IHRDLKPSNLLIRDDGYVKIGDFGVSKLVHTLDVSSTYVGTMYFMAPERLEQGAYGFNSD
VWSLGLTVLSTITGKNPWAPPEEMNIFQLLGRIAGDTTPTLPEKPAYSEEARDFVKKCLV
RDPQERPSTAELLKHPFFKGCTEASAVANVKQGVDYMTRLINSDAKKNGLLKRSPEDVTK
EVNAKLDRLGDL*
>TCRU_2384 enoyl-CoA hydratase, mitochondrial precursor, putative
MLRKSLFLLNSMDPIVKYAQKGAVVTLTLNRPKQLNALNAELTNALAEKLLKCDADPSVS
VLIITGEGRSFVAGADIKAMANQTFVEFYKHNMLRGLDTIAAVRKPIIAAVNGFALGGGC
ELAMSCDIVVASEKAIFGQPEIKIGTIPGAGGTQRLTRLIGKSKAMEWILTGEQYTAEEA
ERAGLVSRVVRHEELLPTVSAMAEKIALNSPLAVSLAKDCINKALETTLAQGMAYEQRTF
QATFATDDQKEGMAAFVEKRKPNFKNA*
>TCRU_2385 hypothetical protein
MALAMNDAKTYVLYFTEGGQQMLLPVCPGTSAGMPPSAASQGTPFVWLPFQDATELQHQR
PAFVATKSGAGAPLMAVPTNYILPWAQAKQPIGASYLTPGPNGSAVPVVPISPNTNLQNA
HENYQHSSAEKGVKSLFPDAKNPRGARTGDEEKSANRFEEILSVRNFTSPVGSVLVRGRK
MSMNVPPLAKRRPPLCRNPPGASSSAVNSNTPINP*
>TCRU_2386 hypothetical protein
MPSTSRMSVFDSSVTTSKMASLFRFSLISFSLMRQFRSEAPANMEKVWKSSSSRLPKVRG
SLRPLSVTMSSLLINWATATIDPSYVTGMQRIVLVRYPVALSTSRLKRSSEYASEILTVC
PVWAT*
>TCRU_2387 hypothetical protein, conserved
MVCVRCRCWTAAICDCAVAVCSVAAVSVAFSLCVDGELVCAEGYTQVTGVMAMMMAGRVL
LVCALCVLWCGFSGIAADGAGGVPDGSAGECLFSRWRAQLRRECEEEVSRRTGGRANASA
VEECMRQRMDGVLAVVDGRRRWRRQRPAVAAAAAAENADELGKENTSSERNVLSGGNGSG
SEDAHVRGGNLHSESRDGVVRPEGATSEELNVNSNSHTEALPTKEIRQVIPESISPVSSP
DSKEVEEDTASKDDKTQEILVSGEQQALQSSSSLGGNSPASDQGAELTAAENPQNDKKGE
AEKEKNLSDKNVPTGIDPSSTNSNDNAPTKLQAETLYRHLPMRIFLPHITPTRVLRRRFW
TPLLFLLPQ*
>TCRU_2388 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MNCGGVNFPDGTIHSPARSSDADRTGICQLPPPREGKDDTKSGGTTAPQVNAEPSRQDED
WRQSAAADAPNTVDPSPASNTATNTSETRPEFASNPNEVMVPNASTKRPSFANGPRISVA
LNASGIMSVTCGGREHVAADNTDEASEHDATGHKSLVLENGVAVSGFVAEGDADGLSQRN
ASGNEYKPQLREFTAQYSGSGVSPDDCFALRNDAKLTLRELTVDGTVRVCVYCALLLLLG
LCGVVTVL*
>TCRU_2389 hypothetical protein, conserved
MLLCKQPGDTGVFATATQHKIKIYRLSSSSQLLRETKAGAATTTTTTTTSVAVGEGMQTE
SNTAGNEWGSAFTRTAPSSPIASVPPSMTRKRCGTPIDASCVIPLSQFREGEVLSVAGGA
ARGFGRLYISHLQPNPPEGKTSGDESLANVPLTLSLSCARDDTLRFLYSGKTLGAWIGAE
NTVSALCTTSVNGAPYDAGYHNHRAEIVASGWDPLDASALAIGRRSGVVQLLNIENSNGM
LSSTSLPLNLVAAESFSVSNGCQASFGTSPTYPSAVTRNTERMPLSVLSVNVVQERLLKG

TLTSLDWAPRSHTTVVAAERSDGIGHCVEVMDLRSPDNGIRYLGMPFETTSPASTMSLAG
TGSSISEVCFAEFVACDCSGIYVATVGSQSRRDVAQLWDLRMTSRPVCRQSHSRVGYTSL
NWSTHEIPTVIATTRNGGLRVHVFSDFRSETEEDEGALTETEGNRTSGRSVYAPFYSSLS
KRTAKPFDERFHPQPRVPAASVAWLDGCRSHVRCSEGAMAEENGVGKQGEQRAQHGPSQR
VAGGSRTDIPCLLLLDAETGELYPQVFFPVGCKATMIVDVPLCSAGPNVFILDSRCLFEG
QPERKSVEPDGTSFNNNSMGSAGTHINYDPYNEMEKGGVAFCNSAESTPTNCAGMATLAA
VNATAKGVYTGNTHVDRHLHRLDRLRAGFVPQSDKVLSTLLKEQSDREAYVLFRYGWYAQ
RYLYPGRATLPVPDVIPGLLELLERERRPINSGIPEAFCGVRKLILLAAGWVTDPREERL
MLTPAGGGGDDDDDGHVERTVQLPSRLFSPSEPTLAGFPPQHQPLREKSTTVSSNLCSRG
SADEGMEATDLFLPTSQGELSTPSASSLKPADHVEMASFQEAVERRVAILVFMLRLNEAA
ALLCHYSHLHPLYSTFAMLLLAATANRNGVPPTLTLDVSECSFWIELCFFFMNAFWTSAT
PSTVPEERKKDYRAKKGVANNNDGGDVDEDHIGEFYRSPPSARRECFASFVRCFPQIPLS
DRIALATLLLLDPSPTADGESQCNILSEVLREMVQQQFYTNTTGGCSLFLAAAVEGVRGS
CVPLQRYVDETGDVQTPVAYVALYGSGKGASWRQWNEAYRSQLNAEGHAILRSLHDLSCK
KLARLREQQSGFSAKRHAVPPPEAPLGRLVGLSSPAVGLMGVPFSGLAGGAAAETKTKPK
RKNKRNVELRCKCGKVVATSPMESADTVTIMGRRQQSLCGSINCLTPMCVVCGEPMFALA
SGYDVDSSFTWCTVCLHGGHWSHLRDWFAKHRKCPAEDCLCTCYCPSLSP*
>TCRU_2390 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MNCGGVNFPDGTIHPPARSSDADRTGICQLPPPREGRDDTKSGGTTAPQVNAEPSRQHED
WRRSAAADGPNTVDPSPASNTASNTSETRYDFATNPNEMMVPNASKKRPSFANGPRTLVA
SNASGIMSVIYGGREHVAADNTDKASEHEATGHNSLVLENGVAVSGFVAEGDADGLSQRN
ASGHENKPQLREFTAQYSVNDVSPDDCFALHNDAKLTLRELTVGSTVRVCVYCALLLLLG
LCGVVAAL*
>TCRU_2391 retrotransposon hot spot protein, RHS3, putative
MKQPRVSFGASWPQLGGASGMLHCTGVVMAPHSGISGDGSDAAARNVAGSKQRLQWTMSS
SVEEILLEGDTLSTDMKLNDFLRSNLGGRGVVKKK*
>TCRU_2392 hypothetical protein, conserved
MRAVEAADGDDAMNDTSSAENSEESASGAEGKGAAGAAAPSLDAGVSEADEYKKESNAFK
PNGNAINTGDPTKGAANEF*
>TCRU_2393 superoxide dismutase, putative
MRRTLRHGYHAYVPKGALLKTDMLASSPQLVTAVFRETEAAAERADRANDDAGFFSRPRL
NYPVASGIPAFISRRQFDVQYNIFHHDAVATLNRHTLGTSLEGHSLETVIRRASFDATQA
AAHTAAAEHFNYCFFYKSLRPWGTAVPKQLREAFQLQYGRDGSVDVVEEVKRLFTVVVLS
HQERCGWVYLVWTGKQFDVVEFPHGACPIGSDLIPLLAINVHEGAYSLDYGPSGLEQYAQ
NYFRACNWFLAERYYLQATGRGVELRCMNVSG*
>TCRU_2394 hypothetical protein, conserved
MLQGTGRRLFSTFALNPETTVAPHGPPRGLINRYVSMGLPPWAAWCNKINRYSLYRMSGV
APRTLLPKAPHEMDVIWLNERVRERVRTSRGVQNVYRQLKYPYVKTGIHYSDVLCHWVQV
PMVEAAMFEVERDGGFDNFVLKRSGPELRSTYGERVRRHILVRQKEIRKNFVLDQQAKHL
ADAICGEVLSLRDESAAEAVLAKYGIEKKRFLEELARIVVARKEKANAVAVTAEEPLP*
>TCRU_2395 hypothetical protein, conserved
MMKSLRRDAAGRGRQRKDRSAFWVAPPQRYVINRHSPKAVPHSLSVVVVVDPHMVEPTAF
LQPIAPLANDKRNCGAAGNGDAIFAEPDSASDQVVPSFFRLDVYVWDDTTLREILEEVLA
SSAAARQVLLPSDAPATATAEVVGEASRPPASTGAEKAEKRGGRDGGGDDGGNGNLKDDD
DDGASVELDDGDDSVGGDAADEEPASKRERTEGEKKQRDETRMGAPSAAKRAQPRDRRPP
PTPAANVRLFHVFVDSDKKPQVRDIALLRVDRPVFHAGDYTTMQEMRTFKTGGRGWKNGD
LLVLSPTTRHYRATPM*
>TCRU_2396 ABC transporter, putative
MRTQSDGDAGASREEALSLGKVVNFSWENLTYRVPVEDDDGNVTYKTLLYNLSGTALGGR
VLAIMGPSGAGKTTLMGTITGKLYNAKAKLDGCCFLNNTIYSQRYKKLVSYVSQDDIVMG
KETPREAIKFACRVRLGLNMEESEKLVDEVISRLHITECQHTVLGIPGILKGVSGGERKR
ANVGTELVTNPCVMLLDEPTTGLDSVNALRVGKMLQELARRDMRTVIATVHSPSSDLFDV
FDDLLLLAKGRVIYHGPTEDSVAYFASLGYQVPPRTNPSEYFMNILQLPDEELSQLWVAW

EDYVMSPAANNNHCLMVVQGPITRQDEFLESQLKVKKSSCAVQFFELWKRSLRMFCRDPA
AFFGRSFQTLFFAVFLGLFFFNLKLNQQGVQDRAGALYITLINNFFGACMHGISAYPPER
AVFLQEQANDSYNAVVYFFAKYLAEIPFQMLFPTVLDLITYFMMHLYRSPGAFFVNWFIL
VLLATFGYTFGLMFATFFESSTTAFAIIPVIFLPLLVVAGLFANTQRLVPYWVWLNYLSF
PRHAYLGVFVNEFQRLRVICDPVTPHCTYPNGEAVIEQFGFENWQPWRSMVALIVYQFGL
AMIGCTSLYVQGMRRRGKLAFKKNLGSRVASPRAIASARSNDELSDSDATPMDEIPTPSV
AYTDTVPLDKDDPSRPGGGGARGMLTTPIVTPKADTRGQS*
>TCRU_2397 arginine kinase
MASAEVVSKLEAAFAKLQNASDCHSLLKKYLTKEVFDQLKGKQTKMGATLMDVIQSGVEN
LDSGIGVYAPDAESYTVFAALFDPIIEDYHKGFKPSDKQPPKDFGDLNTFIDVDPDKKYV
ISTRVRCGRSLEGYPFNPCLKKQQYEEMESRVKGQLESMSGELRGKYYPLTGMTKETQKQ
LIDDHFLFKEGDRFLQAAHACEFWPTGRGIYHNDAKTFLVWVNEEDHLRIISMQKGGNLK
EVFGRLVTAVGVIEEKVKFSRDDRLGFLTFCPTNLGTTIRASVHIKLPKLGADRKKLEEV
AAKYNLQVRGTAGEHSDSPDGVYDISNKRRLGLSEYEAVKEMQDGILELIKAEESAR*
>TCRU_2398 hypothetical protein, conserved
MISRTAVRTAQEKQGRVHRLDSATVQRLFPPSQIAQWPQGYLPACGVARFLDPKGLPLSD
VIDCYSEMKADQRHELQRDFAADYALWCRGVLADFVRRLGDREGRRFRRYTARTRAMHDA
EVRELFGLSSYAPPHAKAGRRYEFTPYAATQTYAMLPVSRCDGPSAKAHFTTFPQVRNVM
HTEFDSMGPSRALSLLTGDDLVPTAEMLQALALYLRRRLEEITAGEETFRRSAHKSAGSN
GSCRSSSTPEEGDNSELRSFSRETPVACFFGNGRLAWLLNNSELLPFRVLPLQPPSYAAR
RERQQRHLLARSGILADLTEKGVISRSFSTIFPCESISVQDALRKYRPCIALVEPHTDRD
WLCDLRGFYSVREVLLLGPVDSPAMGSFAFPLLTFGVTPGPMSYWTYSNTLQRVTAASRI
QMPMDPPHVLQGYTRHAVDDISAYLLSPNDCPAFGCQYRSLSFVRTVYPVVIGQPARFPT
ESSALQEE*
>TCRU_2399 Protein tyrosine kinase/Protein kinase domain containing protein, putative
MKTRVPRLLLEESLFDDRSHLISIHNAAPEENSLRAMQPTHMNAAMMGEKSERTEKLAEF
FALSRSQQAAELANALLRQFAFRTYKTSTPDIVPAFNNAFPRTAHSLTRKSLVLALLDEM
GLTEERVASAEDAETEHFSSTCNPSRRMTSVENSTVSEWEREDTVLERLLRHVLRQFHAQ
HPCWCQSVNPDSSTTTSSSTGRNRNSRTVYLREWRKDRKNCDFVSNGLDSMAHVASPVEE
KELDASALRRFFRDHPTEDEQVFVVANELLQQHIRTPHRKPMETPLSGDVVSEREFSSSS
ECVTQPNMSRVDSLNGSICENRKEDGVKLPRERLVLIELLKSVHEASISSRVLPAIFEKT
VAWSSSNAMRERTLDTTVSNPTSTYSSGTSLEALSRQIGSNTTSGGEIQDAQEFCGREKR
RRLPSLLSLYLQSHLQEKSPSMENVNKRMLRMRRDSPKLTSASVSFRESPSACVFSPVMS
SDAHCNIGSVTHYKFSSPSNIVSVRSMEGMTRIGRGSSGELFAMRRVDTGELVAVKRIYI
TDLSREFVENELSVLRRSIGLSDDAGGGVNGNKSDGAESVKPPTSRETCDTDKDDDGNSE
ANDCRAVIRCYDAFFDGGSAFIVMELMDSGSLMDALNARFGRPFSEEECRAIAFQVLHGL
RYLHETIRQLHRDLKPHNVLLDKQKGAVKLTDFGLCSEQLQSMGFNQCGTYVGTLAYMSP
NRVDPASVYGKESDFWSLGITLIQLALGKLPFFPNVFVIAGFATHPPRLTTAFMSGEGKD
GTRGEKDEDSISSLTPFSEAFEDFIAVLLPTSRERNHVIPLVPAEEENNDSTQSCAYAFS
EHCGDASSYSPADVEYGADEGDETTENFGGGVGHCSIAPFTRWILSRSSTPDSHTDAMQE
LPPPALPEPRGMPQVKGSGNDNANAIRQDDAATEEGHLTGELTSTALLQHPWLRGMTWEK
SRAIIAAVSLEP*
>TCRU_2400 hypothetical protein, conserved
MSADLLHFSETSPRHHFESATALRNAVLSKGDEYSEYERSILEEINELRRDPVAYSFVVE
SEATVGYPFVRDDPEPAECTEMTLEQLRVYIEDFRRERREVRDFLQHLQKEWADAESAMK
ERWSAEDVERSKKSKRGSATVRKQRVLVHKEEDYAGERQRAAQELTDHYTQQAREANSKL
TQIERSCRWAVDGANLIIKCAHELREANAVPELEYSRSLTLAARDVGKECHGAPAIGMQS
PQASLFSPLLPLSSTTGDEDRIRFTQPPSTASTRQGSSVLRSSIVPSSPAEENRHAALPP
KNSIRHDAGSVVDALFTRREENSERAPTPLLKVGTNSLQKEPPHGFHSHDFSSECDYLAK
LAMKACGKYGYYSAAIRGVRICGAFSPRKMLIQMLLGTRVPQFTVPAPTAPSDSCEPFTS
SQTKQTKATPLLWANGRLLGIGWVRAINGTVSVTVLVATSFEELSLIHERRDFTLPQLHR
ILNTSCSAYTRTEQIRPAVMHIQSLLGVQVVEPVAHPILVDKEQRVARLLVRADPNCVEV
TATVSCVSEAIPSIPLLDRELLLVQRSRDDIEKVEILLDTQAAWHRWSGHPLLVHMFERD

KTARGVKSFKNIGFVRVIPLQRGDGRFMDSRQFTSPSSKREKDTAVVGVPPLLVHKRYVG
PMEGQAESCGWPLVTVNFQELCATLIEPLRGKWIACGEMQHVAIQIPKVAYLDKSIKNVR
VLLEKEQAFFEWEATSGSQERMNEVITSKMATLKVAENELQEKEGPMQQELAQLQKNMVK
KRGKEMAKLKRQEEELRQRMDDMKKNVEELRQSLSNAQEDLVQLGREYALRVKRQRNLRK
EYERLRDRADRTKPLIVEVVLVTDETTRSTVAENTRLQPTNNACTLYEGDVRLTLGFKGC
ALLLVNEQEVVRWEVRPG*
>TCRU_2401 hypothetical protein, conserved
MFYGSIPLRIAFPVHRDTTKVPRMLKEVGTWLYRQETVDAFRVWCKANGVRGHNNVKVVS
SMHYARCLRAARHIRPGQAIITCPHTACFNFLVVAKEMYNLNGAAATHNFPLEVNWMNYD
ERCKFLRGASMAELVTAGWMCRIASLEESSFTPYIRWLLEDTRGRDGVANGMSKERGEDS
GLVDHYFSEMATDACEDPEVFLENLFRSFAALHLRAVPIESAAICLFIPGTNFFKAKSDE
MFVPTLIPLVDAVPQLEDDAHNTVVQYFPHDRSDKESLARRCRELFLPEEEMRAMEARLS
QGDGDSGFFALRALCPIEEGDHLYLRGVPKLGDAAKESMTVKVMEANRLMSND*
>TCRU_2402 WD domain, G-beta repeat, putative
MEQKEGTGRSLVKRHAFGIRPDVYGCLNWVEEGTLLYPVGKTVVVHNLNSNTQRFFDAGV
HSSGLTALAVSANKKFIAIAEGGIAPQIQIIDSVPRKRRKTLSVQDLGSESFVAMAFSVD
GRHLATQGGAPQWNLFYWNWERSKPLALTSVIADLKVEGMNESTSRFSLLHDTRTKEPHG
ASSGPPPVSCVTICPRDPLLIAVSGLGMMRFYRYVDGVLQTQPPINYDLEGVSNFLTHTW
VTGDRVVASTQTGELMIIEGGVYKRLLPVPPPTRAQLTNPTVLSLVPSKGGFIAGSDQGT
VAIYENASGSSGEYSIVYTVPVPTEEELHTKKCALEGDDTRPSATTAAGNRAALDSNASG
SSLADAPDPSSLKPWATKGSKRIFHVNTGVAQKVTAAPAEKTRPQSGIQGMARMDVLREN
SVVHLSLDQLEETMALVTHSGQILAFNFSQQWAKRTADDPPALLPICQSFHVGGIIGVDC
SVRRPFLVTSGVDKSVRIWNTSTHRLEMCQYFPSQPGPVSIHPNGLYVVICFTEKVLVMS
VLWNCLHEHRVLNLRNVTDVKFSVGGKYFALAHGNLIHLYNALTCDVHGQLRGHPQKISC
FQWAATSPYPTDNGMVSCSLDGIIINWNISELRKDGEYADKRYQYRVVVADDKNMWAVGD
PASSAAETQCKSMLREMDRFSSVEASSPTTTTDYEFRDSTITTLLVSPKQRLLFGGTDDG
SIKFMNFPLQLGLQEVPIVAHMGKVARMVLSYDESIIYSVSADGTLFVIEVREDGRPAQR
DAGYCGDEVLVLASDVEDRQIAIESLTHTAGKLKAEIEGEEKRRSHEQNTRMRERAEEFK
SEVSALEAEYAALWSAKAEQERSFVAVRLEKEAEAAPLLEELERAGQAEVQQLEDECTEL
QHQLDWSKSKYMQEVSDLEAQIERERREEEERFNDVVAKRKEGMQKIRRQVQRAKETNAE
SRRRLELDTDAELESIRERNRQDLEAIRERYLHMKGESAIMRKNALRMEKEAEVHRNELS
ILESAKSALMAQLGELNQRMSQLHQDIEERDAVIGEKEKRIYDLKKQNQELEKHKFVLDY
RIRQLKSQMEPRQREIAREHQLINEKNVELENLHQNNITLRQSIEGLKADLAQQQLQIKQ
TMNHMKDFETYKSRVKTDVGELAPAMQDPALLREVVERLYQRYVLARDGRLAAQVDQEIK
GEFRSQLEYLSTSVDALRRKCKADQEQHRCKVSEMMVENLSLIREIHDLRAELVDLRNLS
VAAADEKKRRARMEEFKKQASMSSRQNVSCSPTATSPTRPEVPQELKENREEIQRLRAFV
DAAQQALGATASTRRATGGTCMFPPITQ*
>TCRU_2403 TFIIF-stimulated CTD phosphatase, putative
MLYRECCRPLPRYASTGAYGAWMASCRMYTSSLSSGKNRGVSDGKLFSRTQSSIHMYANK
ENAWKDYTDDRFYGAKRLKDYWRRMLSDRGVRYYLFGTIIILAVAGSKLWRLQEQQKSTF
GLIGPKKKAYRSRLTIVLDLDETILSYGDKAFRMKAGMVVRPYLAELLDYLSSIDAEVVL
WSACSERYMRQVLNVIDPSGVRVSQYIVRHRDWFTQDNYYEKNILWLKRPLEDTLIVENR
PLSVRSCNANAILVDDFIRGEYMDNGQDYPPKDHAMRTLKEIIQDLEESGRSVQEYLADA
KHRNKDIKEIPCHLAFRQLPDELARGVFYFIGGKYRPGADMRGRG*
>TCRU_2404 Phosducin, putative
MLGSGKSSGMVNEATNLKANQNLTSAIAEMGTKEYMSNRDMDDVVPTHRRRMEEKPRDNG
VPVYDPVAEKEREKQERGAVPRDIVERDDDDDDAELLELRRRRVAQMQRQQTKEVEWRQK
QHGEYREISQDEFFGIVVREKGGSDDVCVHFYHKDFETCRVVDYRLSELARTVLSVKFVK
IDAEKSPFLVERLRIKTLPCCVLFHNDVAVDRIYGFDGCMTEDGTLDPVLLRDRIVRATN
PGPEE*
>TCRU_2405 kinetoplastid-specific dual specificity phosphatase,
putative
MSLSHSGLPSAEIERVFAVLRFVSQQQEASLSSLSLPAAGGSEGDTLNAGTVAALAKGKA
GKRVSDPLIIPEDVQNKLEAFRMAVTNIPVQMEKVQSARAALRTALRDAYPNKLEDVDQL

CDCNVFVLKATAKGTPHFMLRDVYALQAMHEVVPGLYVGSYHPASERELLHRHKVTHVLC
CIDVMPRFPSEFTYMKISAQDMPGYNIAKFFPQTFEFIEDALIKQHSAVLVHCGAGISRA
PTIAAAYLIKKLRMTAVAAIELIQSRRHVASPNLGFRQQLRAYQEELGIFPEGAEGARPR
AGMSLQINNKG*
>TCRU_2406 hypothetical protein, conserved
MHGAGVESCLASAYERRADAVLRLAEELECGSPSAGQCSSPHFFRALVTAYLVQNDAVNA
TWALQRWATGPAGAGEQEEEGGVRAMLERVARHCGRCAYGEAFREALGAVGGGTGRDVEH
LERWLLDYLAARHVHQRRTFYGESGGMEKLAVGLGVTVADLEARLQRVREDELRHIGREV
SGGPCEKTRDTLCCMLQVGKAV*
>TCRU_2407 hypothetical protein, conserved
MLKAPYMRAAAVGRKIPLLPLEYYSGGRHGAAFMLAELRRLDDRKDSSISNTAPSLALWL
YRSSLLRRLWLEGIVCDAVVADGFTAREFTALLHRILQTPRFLRGENKATQDEAVKLVWG
VQKEFAWRVLGAIVEENQWFWTLREAWDCATTLVKDSVFPDDVMSLSLLLPLARRMATRE
GSGCTLHEGLRDLHAQKLHGGVLWFLARRATSSPRPEKQLLEAATKAACAVPTFLIIKSS
DGKLNGDDEKQMASLLQMTHGSGETSQESVFSPFWHVLLYEMVYYAHCILCDATAKERHQ
VGTLLSLRRVLCSFCRHSLVRPVLEFHCAITAPWRKGLEKDPSALNARYGPLVYREALLL
DAYALMTLGHVGETAIDVDDAAVKEVMMIQSRCLAHLEALAQNEPDAGIDRDAMGLHRGA
RAGVERRLCEGIRLSFKLLLRRGAYEVIHQILTRCPSLGGSWEGGKALVMLGKHMEAVSI
FTNFLESTRKQFASGIPHHIRCMMLEAVEGAARSYLKETSDVTGRLLSLYEVTRNWGFPV
PAAVTFAAILRACCTGRNGTEGFRNWGRKKRLDLMNALLRHHVTVAAYIGDGLLLETIEI
FVKLLAECREGALSSNLDLLPLLQRAHPGLPVYRVAILHFLRVEYKDAVNALLKHIAPSS
ADTTVLLTPLQELPLAALEALSRHVAQAESEEQRVVSAVLSALEYRRFAEEQRLPWQCHL
CRHWNKKNASACKLCGSLELAVVRCHACGGFSPTSASGCLVCGAEKRRNTSDQGVSHVRE
DCTIFPLRRWRCGRCNHTNEPQHLFYCSKCGSVQPEMVEALTHTSFDCRVCSHHNPLGLL
RPWCPACGTLSTVAAAGPPKTLWRCVECRTLTPWILTHCHGCGGSKPAPTLRFDTPWFTR
VCMSCEAINPAWSVVCHGCGVKLATDGGKKEHEVEEREQLVVHSARGEVSAGEPTSTSCP
HCGNLYPDHRDMFCRTCFVLRPNSTCLLWVCLHNNCLGVNVRYGERGERGLLVCSHCGVS
HNIAAAGGYHSNPLRYRELTSVEKRRGCGKDPPTGDESLGMQSSQLPSALLLPVPSAPRV
CAFCGAYLQLQNIARICHVCFYCGYSLPHSSDASAAEHDIALRLILSAMLQTVHRVKQGL
LSSTTVLSPLRSMLMALLRAQEVQLPWRGCDLLNGMRCGLQSRVPVLENDTVHSSVCDVA
EIIRTVCEIASSTTVDEKATAKEGTKSSWTKKRPWVHLALDLVDLMNRTTEYDELGFDVL
AQLCMEVRPQQRSHIYRETHWTYLRYMKLPREFIVNDVVCPTCLLPKARGTGEAGNTCRC
TVSLTDSGATDASVMIKRA*
>TCRU_2408 hypothetical protein
MHSQASAPTPSFSTASETVVSSSTLPTSETRMEVLQRTLHLLRQEVLVPYFEFVERLRVT
NNRAVRVQDVVETLYTASFREKGSSA*
>TCRU_2409 UV radiation resistance protein and autophagy-related
subunit 14, putative
MSSSVFPDEFRCFRHITHIYARNLPLHPMGATVQAADDGGIAGSALDTPTLCDGARLGCR
TSQGQRCVSSYFVLSLPPGKVGKMAAEGGNRRIYTSEVRRETQQPVWDHIPKETIEQFKG
ITRFVFSLYYCTTHPEEAIASPETDCLFYEMLIQTSHVQYVAASMTKADSLPNLPYHVEN
RPNSFVVLLRCMDGVFFPKHQGVQMDEGGEGMDFIKTPYLHEDSDPTRLCVDAEVMRARG
KSINAPVEKITLGDLKTFATATLAWTYLSELAVGRRGERQAYIDDMMDSRRGEVAIMAQR
AMLEARLAKAREDLGCRSSELLELRNRYKEEQESMMLQMAQLEKLRSSTALEEVQQQEAN
KMLNEQELPLSTLRAQLGTVRRLRFEELRTMFPIHVDSAGLADTICGHYLPVKGKEVGVT
SDVMHDWGLALGAAAHLVATAATIYGCSLPHPLLLCGGRCCVMAKPGLPVAAVVSPFTGP
SDVKLPLYCARTADRPLMSAAMQLLSEDVAALARAMGHHDIAANARDNDGRLAVILKQLL
LLL*
>TCRU_methyltransferase, putative EMG1/NE.1
MSRHDLARPARRSVKRPRNTSNGSGARSDVYHPLRYTDSTKQAMVPPPTERAVVVILENA
GLLLGREGVVDAYDRAASTEIANASLKDVRPDIVHQCLLALFDSELGWQRRLRVYISLFA
RSGRTIEVSPALRPPRTFRRFKGLVAALLRDGAVRSVDGTVLMRILPGSVAPVVPCGAPV
IGLTNAVAAPVRTATQLARKALADPVDDNLQGGVKNVAGFFCISCTDEAGLDSIDYVTQQ
ACLSAYPTTAHVMCARICEGFARAAKTIDPAASKSE*

>TCRU_2411 hypothetical protein, conserved
MLAQGVAPRVAQAPAVRVPTLEPSTSSSSLFTGTRMFRSNPNERQMQASTLSDHYRPAQV
GTDQQYCPHTAQLRELESPINTVKIEELLRSVRATSTAAVAAVGELTDDSPPPRQITSSQ
QRTPCEGCQRRSASPDRVHTARSSPMKRTPRGESPARPAWNQNRPTPRVKPTVSAPRTEP
RRVTRDASVENRSRPWMEGMKLKNSSRCKLTAERDKNHQKFTPVIQSQPSHQVPTCARKA
SSVGVGMSSRTVSGGTGGLKTGNDEVAFQPRVEFLEESLRDVQQRAVRAEARCEELEAAL
QALALEHRESISRLEGRNVQLNARVQHVLQWIEHVDATRVAREVFAQEVEMERTNESGDV
EVPSQSLSINNDVGDSPGIEKAVKATPVRVPPTPPMTLQIQHR*
>TCRU_2412 Meiotic cell cortex C-terminal pleckstrin homology, putative
MDSIHEAHLERILENRRRRGGNANYNNRRGSSTATQTQQWDAIKNVETPTLIKYELSPTP
RGVPGHSTADEAGQCENVARATRDEADSGLGVCIEKRENKHYKRERLIANSSGSEHDTGS
FKYSSSPRFGDRDNSNRGRCRFRGNENLQLRWRPLGNFSSFFVEKNVEFGRRNGFASARS
PSRTVPLLTYGSSDSPTLRWRGVSSRRGRTVSPHALSTWHVGAQLFQRQDGLRAGGLGND
RRSNCRGGNGENRSYGRHDSSPKIYMDSPRGVKQRSNQRRHSTEAAKIPFGPPDERNWQA
AGSVIYTGNAAKEEGSPFVSSRQRRRPPGSPLPQGAPISMADRNSMTDPNNDVVGLSSTR
TTIDIRTSVSILAAGDWFYKWNGNGTSVSPRWVWVDSQSHLLLWAHKETHESTFAGAIKL
EKILQVVFRELERRNAEGVQLTYYVLLVETSRRILQLATERRMKADTWYEALNNVMSYLR
SRKFGASFTSPIS*
>TCRU_2413 transcription initiation protein, putative
MAEELNVSELADLLGDDELLDVTSPLVAALPQSATSAELDGKDVGSKKKHKRKGKRLRHE
KKHRKLSEIEENNESEDDNNETPRKRSKYVIDAAESGDSESEGDDFIVGSDEEDEDGDYV
GGIPTYEPRKTHIFREGEENMTSEELARAIEERHRASKKEGGKTETLLLAGLGKGNMSSL
RYTSHLLPQDTDPRVFAVKCRPRMARLLVARIVNKCYAYRIGRNYEKRKVDLGIISVFCL
DHVKEYIYIEAHRKVFVENALNGLDGLFRYKITLVNPSELMQMMERRPSPEKLRVGSFVR
LRQRQYRLDLAQVVEVHPISNQVTVKVVPREDFVGKPFNKIEIRLPPRFFVPTLAAYVQE
RGDFYRWGDLTFDKEGYLLKTVSSRMVISGTKMKNPTVEEIALFFNNDRERVREAVARFA
SVGHRGADLRIGNTVRVVSGQLRETVGTIENIFLDTNTVSLSCPVPGRKEPIKVRVELAA
CVKHFALGTHVIVSSGERAGESGTVVNSSGDVVYIFSDRATASRELTVCASDCHQSNLIG
SFGHTSGSWRLFDLVMLADTSSVGCIVRINRNDICVLTDRSETRYLSPMQIKAAVASPRQ
TTDRLNNIVTRGAEVIIQTSPNTPYHLVGQTGRVEQLFGSTLFVRVRSVKENAGLVVLDA
RSVLLIGGRTSTKHIQQPKQLPAVQLNPHNATKGDVSVPHPRLTSEDWATNSEWYEIDAS
*
>TCRU_2414 MORN repeat, putative
MQKENDRMRKKKDETREEEEISIFHCDDGSVYEGRVTRREIPVELPLGMPTPAPASTLRG
QLPPEVMPQIVPIQHGKGIFKDAGGTIYDGNWIEGAMCGEGVLQFPSGATYTGGMRANEF
CGTGTYNWPDGSRYEGQWENNRMHGFGVYVDAQGGRWAGKFYRGCGVGLLGEIHL*
>TCRU_2415 GTP binding protein, putative
MPPKKKDEKSQPPRTILLGRPGSNLKVGIVGLPNVGKSTFFNVLSKKGVPAENRPFCTID
PNTADINIPDDRFEKLVKINKPASIVPAQIHIRDIAGLVRGASNGEGLGNAFLSHINECD
GIIHMIRVFEEVEVTHVEGDLDPIRDLEIIFSELIMKDLQVVNGLIDKITPIVNRGIDKS
KKFDLEVLMKLKEHLENGEQIRCCQWNGKEIDFLNTLQLLTAKPAIFLANMSEKDFIRQR
GKWLVKLKEWIDQHTGEPLIPVSAEMEANFLNMSPEEAEEYCTANKTKSQVHKIVTTAYH
AINLIHYFTAGSDEVKCWTIQRGTKAPQAAGKIHSDMEKGFICAEVIHWEDYDKLENEAA
CREAGKQHQEGRNYEVQDGDIIFFKFNAAKGGKK*
>TCRU_2416 mitogen-activated protein kinase
MEGYETLGILGEGTYGVVVKARHRATGRIVAIKKYKQAEDDNHVRKTSLREVRVLKQLRH
PNVISLLDVFRRDGKLFLVFEYVENTILQLIEEKRHGLPPDEVRRYTYQLLNGVDYCHAH
NIIHRDVKPENILVSKDGVLKLCDFGFARQLSSKGKYTDYVATRWYRAPELLVGDVFYGK
AVDIWAIGCIFSELSDGQPLFPGDSDLDQLALIMRSCGPVPDRMVDIFERNALYRRVAFP
RTPMEETLQKRFKSCKASWLELLTSCLRTDPAERPSCAALMNMPYFTEDNFRVEYEAELR
ALFTQCQTPAVDASNSSGLVAVQPKAPLFPGEPEETGEVFLPLLAMPPRVLESEDGWSSG
NKRTSRGGASLGNGCSGASPFQQLGTLWSHYLGTAINGGVNNSGELPSISTRQMQTHHTM
ATPIFNGNKNASKPENKANKEMLISSIQTLKMAGGSTQVPLNPPSTTSQQGSKVSGVLQG

TSTHSRKNWKNQGMASKKADPMGGWKLGSLKKSIKLGYPMFPALPSGCSSPVSTAFTTTS
SVALNALSVLRDANSNTVPKSMPKTHTNTVPTTTTTNTNTNTNTTTPTTTVNSSNGDGVV
NNNHPPKSKRKQSKRTPLPGGTPASPPRVSGNTTSRHNVNGQKCSLHDVPSKR*
>TCRU_2417 hypothetical protein, conserved
MTQAKNEDTDEFAMAIAPGRRMRVYSPAGSLVALARALQECAERIHLGPHGLLAASVSVD
GELRLLRPRANDVMRNTAGLEAWQVLWRVFLADNSTPRTRAGSHVNRGAYQRLSDGQGRL
LLTCASLLRQLLSPNTHYPVAGSPSSLRNRLRLVRVLREITTPGEMRYVSPVGDDEDDDG
AEQQRGDDVIGRMVRASLRDLQPYVYGVAGSKVTRRVVEGCIHFIMCTHVEDDVLTKLRQ
LLVRFLWSSSFPNGEGDLHSIVARARDVLIDPTSYIVPCQGESVLHSRVLPFGTFLLPTV
SPEISPHQGTVTPFFTLERHGDGQAERVMFLRIDDQGGLLQFEHSNRKEKIDTDSDMDAG
DCSNDGSRVVERQWTTTEQEKAQWEAARMLYEWAWMHGVTAVLTPSHVPPVMKTYGLRYN
VTGNRDKERECRRPIFMVDEVDEVGFDALLRRLQYWRHEKLTERCGAQEDPVWCPTAAVL
RRDVLELPGRAEDVLFPFSRLAHGPLLEVCSSANVKEFMVNECSNVRVVLLELDQGTLLE
ESARGLRRLQGLGSMLLVAPTAYQLRMYTDLLLKCLASVRAAMDASPSSGDASPECGLGF
VRAGGALPIALSRQLRLSAEALKCQMRRLEGTSHVDDAHATANLPVVAAVLQMLSEVLLE
LPRRLAELITAHHQPLRHAWLQLESDAISRAKSHSANSLTSLREPPLHVCIREDVSFYRR
ARMPPPCEVGHGDGERSYFCCSDTESSDSESDEDEDACRQERLRGPPSLGFVEPIATTAG
ALRAAITLLRLTLMDDSGALETAGL*
>TCRU_2418 dynein light intermediate chain D1bLIC, putative
MKGRSDAVERKGRSGFLDADMEPSGANGVLQGDAAHLDGAALPTEDGPGMPQVTVDPTKD
LWQNIILNTRENQVTQTEVNVLIVGTSGGGKTSLLRRIFSGVNTSSSSVPKSFLRVKPTT
ALDYSFVRRNDRHIAQVAHFWELAQGMELSQLCEVVITPENVHTMVLAIVVDCSEPSTMW
DTVVYWMKRVDRRVIEIFQKMRAKGSATPDKLLSRAKRLVGMEHPDLNRLRLSGVPTMII
CNKLDAFAGEMTMLKTLVRSMRFVAHIYGAYLVFTSDAEAIKLRAVMNHLVFVSTFDLKH
IELDPERGAVLVIPSADTFADIGEPAVSDMGGLQSTGDAELDRWKAPLDAMFPAKQSEGR
MQNDSFLKRLYDTGENGFGEPTVDAVRKQKEDELEQYRKSAFKREKSTKDDRGKSKEKKE
KE*
>TCRU_2419 hypothetical protein, conserved
MMPCRADCCSHENEVVEAQFAGWDSCTATQEVPAAEEECLDIDYAAEIEESSRYVFSQRP
YCRNTALAVCGGDGEQGEFCGVREEEQEQQVRELQSHVFVTRGERVQLQDDTLSPSDRRA
SLVFLMGEARRRHLALLSRHGASEGSVMEAIRQWRAFARRFLDELDRWGHEHARRMLSNM
FLFELPGKSCNLLDSGARVRELIRNKERVLQELRERNQLFLTAEANLPQMDTSPCVSMAS
EGEELEMFPTAADSLSLMAMAQLNDPSFAKFQEGREVELCEFFSFSLDTSLKSGEGASSS
DCSSDTDEYADACRSPPSTTGDLWLSAPCQ*
>TCRU_2420 Rab-like 5, small G protein
MSEERVKILVLGPSRSGKSTIANFLAGLRETPTKGYYETQPLRILEVEIGLDNLKVGGRH
VVGPKKAIVQLWDLGGSSKHQAGWQAVAANADGIIYVFNPEVRGAEKELVLWHKNFALDQ
DKLDERNNFKVRVPDKHSLVFSHHSSMPELAVGDNAIPSLPKQLRGVRAIETSLDYQSGN
FKEAFDAMVEQIVVSRIVAEEDEILQKEREAGDAPRMVR*
>TCRU_2421 hypothetical protein, conserved
MDGKMTALLQQLQHVLATWDAVNGEGEPGTIKLSRNRGGANHKNLFLASVDAAAADNNGN
NTKKDHHADDESCGVVGKSSETYPPWLTEAECNQSGKEVVERRDGDAALAAALNGTGFPD
MSVDPSLSRQRITKVELARAALALFTSNSGIYRPILQKTLGFIFGLIDELLEEKMDLPCR
EETPQNFLPLWMATENEEVATAHERMRKMEVRMAKLVDEAATQRDHLKAEIAATRAREAK
LEGLLKHQILLSHAKGMADEVFLGPGDKETDALYVRRLIARAENEKAIDELQGELRLLQN
ERNELSNRIQQLMELNGKYARQCVELAARLSVLTDHNIAIAVDCKRHQNEVLVEKQRSER
YQVEIQVIRNVLMTLFMNRNHSVQSWWESLREKRMKDATQVLLNLIEASKRFPSTPQTSE
GSKTSRHTTDERRQGSELEEEDDSDAKNKETSSPYQAADENSLCHMWIPSAGNNPETPEH
LRSLSSVEYIRINPPVAERAVYVILSEWACDAELRPLDIFTRDYVLRAMKSSDASPIFTL
QKSDQASAAEEANSHLPITYALDALSRSCYCGSLTYAFGLVTRRRVNANLFRMLELDAAI
LISICRYLDIKRSLPGKPRGLIPVVQFASLLVAMYPSYPLVRLQQLLDAARNDAGNQMDS
MELLNYNVLLPERLFLRSAFITVENAGALWDTHFKHLLYKFVCDDVEGSWQAVEDALCLY
ASRVNVASESQLLYQAMSELPKEGRKYWLPSIRVALSCWDDLRADTASVLLDGMPRVPVK
AAASYLRGQLLIRRGTCPNSLRENEELLSGLQERWNKFAGSYEKLNFQYYAQLVEILDGK

RHAVWGPASMATDDVMRHIGPSDDLSVGALLARLQRTKETNK*
>TCRU_2422 Golgi transport complex subunit 5, putative
MFADSALMSPDFDEEAYLRYALHDPNCQAEQARLASCVKAVREEVHKILSENAEDMLQQV
TAACRAQRDVAAVRQATFSLMGSTNRLRQTIQEPYRVISANITKLGNMNTAINILRSILK
FIGLTTRLKSQPSQDLARASRTLREVEELLQTSNIKGIEVVDNRMDTVERAAVTIRTKAQ
EMLRHGDAQDASGVAISLQCLFTLGLLPRVLGSLMTEQKREVIRSLMRDLDPQTIVDEVN
HGGSSATNDMNLRMREVLFSRIKSALANVSQHSQVVVSVWRVLVKKVDPVTHTSYLSVVE
SPTSVLGDYWHLVTEKLCERLQAVQKRPNFLAVLAKDVIQYQNLLTGFLGSMNELLKILD
RLMEMDAAALKRTSGSSPSSKALHTSTNTTTNATASEELKRLWLSQVTQEVDERFAAHIM
DRHRERLHHILSKLSTILPTASGRSTVSMKVDLQRPEVPAAARVLDTRGYTMLATQDVVT
YRQNPHTLGIVLDCILQCLASFMQPVTETTGKWPLPPLPSVSGDATASQMLHICVSNACT
LLCNDLTALLASLPEGELFAADFLNDWWASNGSRREEQGEKSGSATNDQKLVVEKYHQLR
GFTKRFNSISESVVQPFFRSVSVLFLDSILMCVDGTLEQEVAGIGQLHSQMRHFMSCFYY
LFEPQTPTLDEHSRRLTDNLLARLIVAVTLTYPFTTKMQKHLMNCLQQIPRVVLSFGPAF
GHGTVGRSTMSLKGQIHQLTVWYSLPEEVSEKPIGEWHTILLTLPPILARLLLLQRVLHP
GIKTKKPYTLMEVTSGGFMEMVEAIVLEQLYTSDTPPRSIRDGTDGVPRVTRLGEVLVAV
EKCFQESVAVSDEDASRGPTVRWMESLWAQLNS*
>TCRU_2423 NADH dehydrogenase subunit NI8M, putative
MSWRARFTPSVASLTVWLNPKDPNCFGVRNWWRNNLPELQLLNPSCTFTIQELSFGEPHM
YINYTPTDQRMIRLAGATEEECEDIMEACITYGMNHAVIERPRTDDGGDLVNQPAIISFG
YTESFMSKLEVSPPAEIGQRTPEGVDDPGQKPRMYPRNVGCKLMP*
>TCRU_2424 Amino acid kinase family/Aldehyde dehydrogenase family,
putative
MATVPVPVERKRLDHITSRKDLKFAKRIVLKAGTSTIVTESGFPSVRRISNIAEEIFALR
SEGKEVVFVSSGACGIGRNVLRRQDVMVCSAFDRLHRNCRPFSSIGNNTFAAAGQANLMN
LYQTVFQQLDITLAELLLTHHDFLTDDRRENLQDALDNLLSLGIVPVVNENDTVTANRNN
TSNDPFTDNDGLSSLVARTINADLLIILTDVDGLYDLPPSDPKARLITTFAPDNAVVFGA
KSPTGRGGMNAKIAASLAAVRGGVPAVCICSGHRMGTIGELLQGKPNVGTLFVRDPTDLI
ASEAAAAEGRRTMEKSAREAREGSRKLNTLSYLERKKILLEVANALDTNREKILDANAVD
LRVAVESNLAPSLLKRLELTHGKIDTVVSGIKAIAEDKDPLARVLSARMLDQNLVLCKET
ASIGVLLVIFESRPDSMPQIAALALSSGNGLLLKGGREAEHSNAAIHSVIVEAVTKASEG
KVPSGVISLVTSRADVYELLKLEGFIDLVIPRGSNEMVRNIQRSTSIPVLGHADGICHVY
VHPDADMNMAAKVIIDAKLNYPAACNAAETVLFHRATVENGDAKILVEKMKEAGIKIYGG
PKAIAASLARAGAVSMHTEYGDEQITVEVVEDMDAAVDHINKYGSHHTECILTSNVDTAS
DFVRRVDSACVFHNCSTRFADGYRFGLGAEVGISTGRIHARGPVGVEGLLTQKWVLRPID
PELYATVAEFQSGERTFTHEDITNAMILQEEN*
>TCRU_2425 Serine hydrolase (FSH1)/RWD domain/50S ribosome-binding
GTPase/GTPase of unknown function C-terminal, putative
MVRVLCLHGKRQTGEIFEHQLNKLCRFLSGVAELEFVDAPCVLTGEMVTGDAVVTRSWCE
PKDGGTRDSYAAGDDFVRRCMNSGGSPYDLLLGFSQGALLAARYVMLQKMNGEREYGPPV
KAVIIAASPDPRRVFPEFVASYLYHMPQHDINRTGFLGAVPSLHIVGEKDAIVDPAESCS
FAEACRPQSELLFHAHAHSIPQLRSVLVSIKSFIERIAVYTGERGETEKTEATLERENDD
DDDDDSGSLDAACEEEIGLVTSMYGEECVQRNKTPVVFLPLLLDGVSDEASDMSLSALRI
CMTLPRRYPAELPKLDVVGGPATHHVFFERWKLQLITKTLAYLRDDLGVGNAMLLPAMMF
AGEQAASDVAFLRSVMSAKASASAAPDGSAAQHLQQQQQEINAWWDADGDDDDDRSACIV
DAEQNAQQTLEGNPPEQAFNELSAAVFDNHHPNSRGGVLELTIGLIGKPSAGKSTFFNAV
TDPDSESKAAKVAAFPFTTIEPNVGAGFGAVFCPCGILSTSSSPCDAMYGHVPVGGALCR
RHPVIIKDVAGLVQGAYKGKGKGNQFLNDLCDASVLVHVVDGAGATNADGSACPPGTGST
CDDITWVRAEVHSWIYDNLRAKWGGIRRKPEKLRTMFTGYRSPPSFVDGVLRYMGITSEA
ELMSQLPVWRQPELHRLVALYVRLRFPIVVALNKSDIQSVAGELHADLQRRYPHEKFVPM
SAKVECHLLRLRQSGLVEYVSGDSSFKEKGSSGDGRGSLMSPMVSMALAEVRQFFGSGRT
PTTTGVQEVLAAALFLCPIVLVFPTVSMKLPLPSLRECLVFKSGSSAGDVFESLLRANLL
DGKLVRFEAVCAERLREGHEPTSLKKDAALPGRHVLVRVLTNKRQLVL*
>TCRU_2426 hypothetical protein

MRRAATKDPAEPASLPPDDSLQFTPIGGVESTFIEADEELIRTAGVATLEADRSQREVER
WRLEASAQMHCLTKVRREKALLLREVLQLEKSLEEAREAAAVPTSKETCSLIHGGRSILG
DVCDPHGDGIIVVPGTFTLETKGGVTAEEVELRYLISRAISSLDSLQAEIAALRQQHADL
WHRKREITEDSKRLNATYQRQKKQREELLEKKLFVEAAEADPAFREALQKRMELKDLVRH
AADRRAALKQLRMERASMIGHLLEGAMSRERDACNLHVRIAKKKGFIGHPMHDMLMALQK
ENKEIRAKYLQMVRGSKEEDAVLSDYLDVLEERLLLDWMADASHDKAV*
>TCRU_2427 hypothetical protein, conserved
MEPTAGSAAFSPSFRPGFTSGTHRRALTVDLMGLLDSKETDGMGWEVATKGRAPVYVAFD
PERLWQIPDGGGAEEVGNNRAFHGVMVVFSDGPLCGDEGLPEVGGDACFGGCVLKFLMLR
TDFMRHLSSFSAPLCSSTCEHREEEEEKEEKRERDGFRAVLLFTDVKMEGTDDDRALSVV
YVQLAKGWRHAVDRVAVQRRAAQVIDAALSLFPSSLWVIFWVDFTGILDAKDSLLPHEIR
DAWSDLAAASASTPSAPRVTVLVEPAAALKLRQDGAKVTGEAAPILAADANLSTVKETLC
MSSGRRPFDDSQRGSSASERNCMDPHEPLVSGDVDGNGEKKGGNSSDDGEDELIWKKYKR
TKTNAQDANDGSTSHLGHPAHEESDDEEDELLWRKFMCVLKEEAEVSMNNATQGLSCLFL
ECPGDDLFSSPGDDASIRELFASWSSLGSGHLPRTIVLIAGDDNLLERTLLSWVRVPWSQ
NALILPVFGVSELVTGQHSQEGVELPPSRSSLPSAAAAASLSMNRDAASASHRFFRILNF
AVRYFGIDVHHSACLSVTQPLMQAAWLLDFRVVGDYARVFSWVMQLRAGNSAVQGLLDVE
RERERLFAELCATNELARKLRESPRRPEILLRVMGSMRVGVVRPVVYDAVALASKSLTWT
RVRRSLDTALSLSPEQRSRVYRYMASFFTKNVFCVSVDIVRSCDSDYFLGYHFSAVGYLR
YELSSWVRRHVFVELQVDFQPLLEGDPLGAETEPHWSRVFRRLSCTCTPRRHEVLLCTET
GEKKCRHLAQLLYWSLRPRPSWNTSFFKKTFADQNHAS*
>TCRU_2428 hypothetical protein, conserved
MFELWDKFGKRNIAEKEEKNGDDCYLFSALRRLHAKLLAAQPEFTEEDVIIIAYPSPGGS
PTHSPSTSPRDRDADCEQDDSSWNTGGEKSSKSSTPTRDTGNGNVALTPPGQGSTSSKIT
AMGTGKELTSRDFLALVRNFDEKALLRNRKAASDALKLLSDAYALTWRDKRYFTSATLMT
SVGSSRLMAASARELGGRGNSSVLSTVRRPLFTPSSSFRAPTHKPPQNLVLLMGKCVESL
LVYANESLSLRTMISSNVTLLRLLCFVCGESRKLESSSCGSGWRDIDEELNELVSHWQLF
SLSLPLLVALQECYLLEFLLDAALPPTVCSSKYDGIALVLHEKKRRLMTEMMSSRTGFGS
ITRGLPLISLAAIVSMSIFAEPKLRARVLDRMTGEGLLQTIRDELESTVNNFKRLMTGES
DGQSPRTASCSPSKRSGGFFSFFQSKARRVRREEKMLTGMQDSPLRRLGSCLEILQNLTA
PNLAQEAAPATTMKGVVRATAWASQIEDVREICTSLLNLSSIMAGSDTPFSFLRPLQEQV
MECVRQIASYSAVLYGVVVETVDSALSEYARERTNGQRDITAPLLPLLVELLCLKQHAEA
NGECVGRWFTCLTECLVPQAFDVPVLTCNRAGNRYSWSKGVRRKSSNSRCDAPVLARNLR
REEIISLSPYFRFASRLILETKWRDGAEPFLARIALLAYNVLLTQARRPNLIFGQASACY
DAVAPLLETPNGVLPGGSSSGTRELCGTPTRRSGKTPDSSSSPGRKRCRSVSGGATNTGD
EVFVPSPSQSPLFLEAYSSFSETEKGRDSDGVSRGEGSPSCALTAPSWRQRLSLSAFLGL
FGEAFPE*
>TCRU_2429 Miro-like protein/Ras family, putative
MSFEGDAALHSFTEGGAELAFHDSQVDALITKNENCAVFPTLTPNESESLCISQSVPLVD
GGDLPLSEKIAVGRTAEQEGHNSEERRGPLISDEEEKAANPSCMPNKILFGLASVGKILD
PSSVNATIRREGPTAGGMRHCSTCPESSLCAQSAEDTAIMESDENTTAALKPQDVQEMLQ
WLGVKRRGDLLSRYLVMGSVAATQHGHGVNDACSLGSKEKHVDPQMRNLLLQEVQRTGSR
GRFPNKQIFQRKLVLLGHQEVGKTSLLKCFESEPYFLKKLPDVKTTTGVEVCSQTICVGE
DCVQLILSDFAGHEVYHSHTRFLTDRSIFLLVWKISSVGQDFQSSGISVKEEERLYKWIA
EVYAKFPRAKMALVATHLDELRVQGQRSVEKILLRVEKKVTSFMQRIAATDPTTGKIVTN
EIVGNFAVSCKTREFIATGGLRRFSVRKLSALLHFFAEVARRDCMEDTDFPAAAIPGRHL
KLLEMLMNEKKRFPEKFFMPLRDFIYSAVQFGVASDEELLQIARLMYSWNIIYLFNPYCF
SDNSPIMLRPLWLSRLAAALFSYAQVIRTPLHLRSLIGRLEYTVSVAEAADMHLMSKGFL
RWPLVRVLFRAPLFDILGHEPDDLDYTVAVRFLISLSLLYPVLIPCDELALLEEETPIDI
EAGQPIVREPKITRYFVPSLSPYFVPDSLRRLAPVLFKRGPKLRFLFNLLPDEAWWRFQF
RLHSYQQVVVLQEPCGALLADNKGDDDDGGDAFDEYRLLEADEEHNRWNDAMWLSGDCCR
VFLYREGLQVIRVFSAETKPHAAESVLEDIERTILSLLGEYRGLQRTVQIECPEPNCNGW
LMSSELLTGTRLKCQICKQMISTEDVVAFAAVECVEPRRSHCFSDTLLKEAGELLCFSLN
PMGCMQFCEYLGLDHTILCGAISKDSCNTDGDEEVTQTEQNPDYMYALDKVVRAAMLRQL

RERVEEEARRRRMLEPAPTALQVSF*
>TCRU_2430 hypothetical protein
MQHDVPSEAAKGDLYTKRTFGPGSNDFWAGTGGTSSSMSGCERAAWVPLSAALVVMLWAT
SPTRRAVDTVGGNELARRATVLGAQLAPGKNGTRPYFFNATLFLSLRIALGLRKILAAYG
RGPVPSTASKKGLSQDGRVVAFGAAGGKPSGQRRIVSAAWQKVKKAREERKTIVVPPDRI
*
>TCRU_2431 protein phosphatase 4, putative
MDSIDQFLETVSKGAYPRESEVMKLCQTAHNILDAEANTHVIRAPCTIVGDIHAQFFDLI
EMFRVGGEVPDVNYVFMGDYVDRGHHGVETFLLLVALKVKYPTRVVLLRGNHESRQITQV
YGFYDECLRKYGSVNVWRYCTEVFDLLPLVCVVEEKILCVHAGLSPMISTMSQMDAIERR
CEVPHEGAMCDLLWSDPEDIEAWGLSPRGAGYLYGEEVVRTFLETNRLELLCRSHQLVME
GYKVMFNDTLVTVWSAPNYCYRCMNVASILELDEHLNKNFKLFEAAPDDAREPSKPSLPE
YFL*
>TCRU_2432 BNR repeat-like domain containing protein, putative
MRDGALVFPMQAKGKDGTSVLLSMRLSKSENKWELSYTATGKGCRDPTLVKWKYEDEDDE
RLFMMAHCAGGYYDVYMSTPNGVSWYTSGESINRVWGNSHNRTGYGVQSGSTTATIEGKE
VMLVTAPVYAKEENGKGRLHLWVTDKARVYDVGQVSRENDDAAASSLLMKSGRDNKELIS
LYENKRSDGSYNLVAVRLTEKLERIKEVVKTWKDLDSALKTCRSGSSGTVDAANEGYVQW
SCSH*
>TCRU_2433 Concanavalin A-like lectin/glucanases superfamily/Protein
of unknown function (DUF3676)/Trans-sialidase of Trypanosoma
hydrophobic C-terminal, putative
MGQTVPYYFANNEFTLVATVSIHEVPQSGSIPLMGVRMNDTKGTVLFGLSYTHEKEWLAI
TEDAVDLEDVDDAEDVGDIVKWEPNRTYQVALRMDCDEWSVFVDRKEIKYTEYNQRLFDT
HRISHFYIGGDSKNQSATGGHVTVTNVMLYNERLLSDKLYELNASKVTIPSLGVEEQPTG
QVASTEVSVASESRSEESTTTEKLTGDDTDKQEEGIVHGMVPAASSSTVVGGSSVPEPAI
ATEIAGNSRPEDNTQLSEDETSQQATPHEGSESMQRDSNVQPQYPQSEESTGVADVETSP
ESNDAPEEDGGTNDRSGESTSQVASSLSMDTATRPADGEHQVQQIAELPAENDVRSTGTG
TTGAEQSLSLEAGDRSSERAMNSYSSLTPSKRDAETTSAENADDVFRTDGAEVSSEEGKE
APQKVDTAPGNTNTTPGETGIPSESNATIPSDHDILPENVHLGELAAMYLVGDSTVHRCV
SRVLLLLLLGLWGTAALR*
>TCRU_2434 hypothetical protein, conserved
MERSPDSHRRRMPWTAAKECVPGVVHGSKGKMVLDGARRVDVECVDRASQVYPLEALRTA
AATCEYDIFRGKNIFNWSLRRNQMCSGNEFTARSGRRGRTTKTPLAPSFISVVARPQRSP
RQYDLRIFRGGMRCSVCRHCSPSPSVGADVPVDASSCGFRTHPLIDAADTPAHCWCFWHD
RCTAPAAGAVGMGTRTQQTRFNQMVLEALSSSRRLQRRAQKSTGQERNQMTAREAILFYI
TPSQTAGRIHNNISH*
>TCRU_2435 Mucin-like glycoprotein, putative
MMTCRLLYALLVLALCYCPSVCVTTEEDNPSTGSDPQEGEGRTNGRQKGTSGNPDLTTKE
SEVESEGGTQDIQGRTTDVISNSEGASGASGEPGKTSDVDQSATNPKLGVPLEKTTTTTT
TTTTTKAPNNMNTEAPTTTTTTAPSRLREIDGSLSSSAWVCAPLLLAASALAYTAVG*
>TCRU_2436 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MIAFVEGRNKNKRFSEVIDLSSSDIVAGYIKAPETWQSLVAEVTKDDWKAHTVLESVDNW
NHVGVANLPTGITRGNKVFLLVGSYEERRENDGDIWKTEAWNIKVIEGEATQSTEVEPSQ
PINWSEPKPLFQTDSPNNKGELKEFLGGGGSGIVMGNGTLVFPLTAKDENDKVVSLITYS
TDDGQKWEIPEGVSSAACHSPRITEWEEGTLLMVTYCEDGRKVFESLDMGKTWTKAIGTL
LGVWLKSGPELLEVSLRVDALITATIEGRKVMLYTQKVRHSLEVDEPNALHLWITDNSRT
FHLGPFSVDSAENMTFANTLLYSDDELFLSQQRGFRAGTAVSLARLTEELNTIKSVLSTW
AQLDASFSESSIPTAGLVGFLSNTSSGGDTWIDGYRCMNASVTKATKVKNGFKFTGPGSR
ATWPVNSRWDIKQYGFVDYNFTLVATVNIHQVPKGSTPLLGASLRGSKRTKLIGLSYGAD
GKWETLYDGTKTVQGGTWEPGKEYQVALMLQDGKKGLVYVDGVIVGSSAMLPTPDERWTE
VSYFYFGGDEGDSGSNATVKDVFLYSRPLSVGELKMIKKVEDKKGNGDGDGEDKKGSGDG

DGEDKKGSGDGKKGSGDGSMREGMSRVLLLLGLCGFVELYGA*
>TCRU_2437 chaperone protein DNAj, putative
MRRISPVIFGVRVVSFATTSVAFLQARAGGGLTDEEQRELEEEEFRVMDAAREEAELLPI
AHRLAAKADALDAELRRLSYVLFEKPQLVMDTRSATLTGRPTSILTVMRRYNAGSRHTSC
PAGWVKPLGSSSWIVQAYKGVHSAGMRLCGRAKQEESKRPDQLVTLTGDLDYIRRMKHLH
ALNFYSRMNLTPKRHIGFSLYALLWNVVVAVQNAVGCVIFGAMRGVRDNEACVGIIKGTA
IGILRALQFLAYGLLVSPCIHIPCGLCNSLYGVWNAVSGTLFFEVSAGRWQYSTALDAVW
LRHDIQLEQRAIRGVGRLEFRRKNMRAEERWQQRLASMGFSFDKINQKMRRTGDTRRPSS
AAWKEGEHAERGGAEEDPYEVLQVKRSATQTQIKAQYKNLAKVFHPDVVQSRHGGPLSEE
ERRDAQRRFESISQAYQILSNPEKRKSFDLGGAQALRLHESKMGRFMSRTPEEMIQSVFG
GEPFREKILGSLLRSHWHLRNEAQVSVSLHEFEELQCLRCRELTAELAQILDVHANSPLA
TGYQPRGGGHGRSEVLHSLLSELGGSAPKPKSRKSSQRSAKNNATTESMFDLTPGSNEYN
CFSRDFEERCERFTRRLSEACFGRELMYEAGQSYVISSQRFLGIRPFYAPKLHVYKKIFS
GVDRVYAAFREKIDDRAKNNKEWLAQKVMIEYFSMEFDAVVADVSVILRYAAQNVLQDVT
LNEEQRRRRCYALWYLGEQMVRKGAPWVAMSRDDAELMAYLQQAANSASTTSKPGPF*
>TCRU_2438 macrophage infectivity potentiator, precursor, putative
MAFCLLGVLFLSCITSVQTASGDAASHEERMNNYRKRVGRLFMEQKAAQPDAVKLPSGLV
FQRIARGSGKRAPAIDDKCEVHYTGRLRDGTVFDSSRERGKPTTFRPNEVIKGWTEALQL
MREGDRWRLFIPYDLAYGVTGGGGMIPPYSPLEFDVELISIKDGGKGRTAEEVDEILRKA
EEDREDM*
>TCRU_2439 dynein light chain, putative
MAGTVAVVKESAMSRELQQDCIDCAAYALHELGLHEQTAIAQFIKRELDSKYGSRFHCIV
GRSFGSYVGHDGQYFVYFLIGDCAFLIWRTVDTFEERVFYVPVDDLAIGRLQ*
>TCRU_2440 transcription factor IIa, putative
MTKKAICKGHTLAPCGTSDVYEVAMRNFRRFLLERVAQQEDEVFAARARFQLQRAGDREH
FDRTQSRRIKSEGTRKTGLDNFVRNGMAATGSMERQYAAEQEFLADQQKLYVEHEEELQR
AYPLAFLDDESAGVIAFNLMPILRGKFESLAREQTRRRKELENPTDKTKMLSDLTVPSLP
QSHGCVLVNNVENPQIIRVKKENEPDVDAGLEAGGEACVNILQTTTDQSTSSRETEDNRD
APLPREESVKDVNDGCVSVDAGRGVVNPPWVSHIASGGEVEFVRVALMCRKKSLLARQEE
KRRCLKSLLTPLTPCNLQQLAKEKLFLLKLEEEDGARKEAEIWRLWRATRDKINSNGSLS
NADTDGEGVAAATGNGENAEDRRGEGTLPCSVEETGDDKTTNGKDWNEYYSPSRAIEENR
RIRINCLFSLGSQAASSGMRNSLFDFNTLRWETITLDDGATTIDGGNNSSNRLESMAESY
LWPQHIEAEIKNVLFGEAVRSRRRWLSFLEPQGTATQEESEEAEDDGSAGDGVPTRVNGT
KGKRKMPIVLAFPRCGRKVWLKLDGLEEFVARDVRFYQGYLHP*
>TCRU_2441 CAP-Gly domain containing protein, putative
MAQARGCELMDFVSVLPVPPQTERRRGVLRFVGSTDFAPGLWMGIELFGTIGRNDGSVMG
KSYFSCPAGQGVFVRPELVVPYMSEGEGPSGTVRKGDEFLAVVEPLRAELTRMQEELQQR
EAALREAREELRNVMALHDAKSVELEREREEKSRMIMLTMTACRNNVTATTQTDEDEAVE
VKDLEIHRLQQQCADLKDLCELQEDEIHRQREHADDLAQIVENLRREHEEERVRMVEKIR
SLEEEITQRQKATAEDSAKADVEDMHLHAFQQQQEKEALRILKERYEQLYAERESERQEQ
EAKWKRATAEYEEALTQQREYKNRLLNEIRQLQHEIKDMRHSRERERVLQVPLSTLERDE
YESQIYGLQWELMGVHEEMFSKRYDHFLAPVSSWNLPADVMRALSEEIMSLERVLPFTTP
EKCQQSRMVLFQMHPRDAEGGTIAAAPL*
>TCRU_2442 ADP-ribosylation factor family/Signal recognition
particle receptor beta subunit/50S ribosome-binding GTPase/Gtr1/RagA
G protein conserved region/Miro-like protein/Ras family, putative
MGFLAWILEWIRGLFWQQEMEVTLVGLQGAGKTTFLAAITDGTESVRLHDTIPTIGLNTR
KVTRGNVCIKVWDIGGQPRFRGMWERYCRGVQSIVFVVDASDISSLEEARRSLHDLLGRP
SLYGIPLLVLANKNDLEGACSAETLISELYLLKLAADRETACYSVSAKNYTNIDVTLKWL
MRHSKASSSS*
>TCRU_2443 hypothetical protein, conserved
MLTALHITLPHRRDHRDSQQHLPNRCLVVNEDTCEASLISTEASLKYASGAAHELYESRS
RFRFGHVAISPHHGNIFVTQVAPLIYDLCRVFLRPLCSNEPRMESRPLTPTTETTTAAGS
DSNGPGISQKGWDTVTARRCRRICKKTWSMSRTVIIYGSHSATERRALFLHLAKATSLAL

IQETSAMGTETLEKNMCQVSFSLVDLYHAWGVGDALDPNAVMHDSIQLQRLKREEPRRSL
NEPKGMDFVEPTRQTLEDRDSVSTCLLRALQRIDPPRALRTNAEKEDHAVKSTLVLTFII
SRNSRCRVGVPRPRNVHSAKSEKLKGWQRDGFPKEARFHLILLPDSTAAAHGKQGAKELG
ALAGALQACTMWQNEIVSAEEEEEGEEEEDDARTQCANCVTATDGHMDASFSTTTSTPPQ
FSWVPLRESPLLLYLFESTIYYSHQLLQSLRNLRLSKERRRLFSDRSPSGSSNISTHSQN
AARVVSFSTNTSMEKGSCWMSTDTNSTNVIQCIAAGIGQCLLIVCVNSGWDQYYQARSAF
LFAQRATNQFAQPYMSLNSKTADVSSIFSTEHGKGNPHKEATPTLTEIQPPQQLRQKQRL
HESFLSLEKTGTEVERQLWSSPRRREKTEPRRPQAEDSPVFELAPSEVAVTESEDIVGRD
GNDVPSHNLSPPTLSQGIGMNPIQQQVKSKTGLVTKITGPTLSLPERNTSPYPVQQLFRC
NQDDPKGAINKVFDESGEENASNSWEQPETARKNQIYPKYSGLCESPSSTKGVNLGPVPE
ASSTAINDVLQKQGLLLQENERLRALLVTLSSRQADAGREQRESTTLKDVCDITLLESRK
AARSSDLDELRTALSITTKKARTLQKTLSRSIDENRKMRRLIHSQMKKCCVEFSRIAQGT
PAEQGSNGSTVAEERIYRWEMLLENTVKQILRSVRGDSFVGSDDDNEEREEEKEATRTGN
GDRFGSQRLQVKNKENSSLANCGCAHMQDGMQPCSSCNGSHQFINGGADLSLSEKAQGRN
CRAFKRDAEVEDAVNSPQYRKIDVQLSQLLHIAYSLFLGESSSANDDDDDHSVSGGNMHK
TAEGAEVEGCNRTHCSLSRSVLDILSPHQQGTRAKDGRAKEEEEEEWRLVCKRSPETEVC
WRCHSSRRTRCNAAYTKFLEILRFLRSHMTINGSFASDSYRQGMKEAEEKEEINGRDSAS
PSRHARVSSLHSRFREKLADGSPAGASSRDGGTLLLKARQLSDSLQKRTNDRVNEQAAVQ
YMQSELDKEREWRRQLQDELLRLRLCLSKCESKFDFIDETVKPKLSKDIAQLEQKISERK
RQEETVRKRRAMFMSEIQKRLQKVVYENDLTLLPSSSSSFSLSPRRL*
>TCRU_2444 Vps53-like, N-terminal, putative
MADGSKVRFSDAVEKALAEVCPPRDPFDEPDFDPVDYLNSRFPDESSLAALPAFLEEMTS
RLTKTENDLLKAVEAQATNAATADRDLHNAKAAVVALYDRVSDIKAKTAKSEDTVRELCH
HIRELDTAKTNLTVSINTLRSMQLWMLQLQVLSTSFERRKFIQCRDALMEAQKYSVMFDS
MKHLSKVREINDKQAQLCRRMEHYIRHTVFGDISLDSLDETLMAEACAVVDLLGKESIRK
IRDQFIEKMLEVYSLRFKRGSEDAKLERTERRYVYIRNLLEQNEGLFLNVFPRHWCVPQE
LCVTFCLRTKAELDYLLREAAGNIDVVVLTYVLQKTIDIERDLTRMMAWKEEFPGRSEVP
DYRYNGMILSSFKAHMDLFVRNEDKLMGDALSHSLVGSSSDVESIATGSTNAMAGGAVPG
WSIEGDIHVGATLPVAEDLFIFIKESLKRTIRISQQDVLLEMAAVWRKHLIRFAETITTL
LPSPAASREDMRRACVIVNTADLCQSTSQDLGDEVCARGEVPAKELGFDQVTEAFSTLYS
GAIQCILQGTELKLAPFLVEYSNAAFVNRRPEEQDIHDESIPIRSMSAVLHDMVLVCSAV
LPSPILRFLLDKVANSVIPMFTDTLYRMRRLPPDFALGLMRVDSAALEKSFLQLPNYNDP
DRFAPSHLMGYMKLVRREFDRLNRTLKVLQVDASVDTFVDVYYEAMLPDDRSIQNFVRLV
ELKGRKREDVRSWIANLSKKGVVEATKRDMQRESSLGIATGTTSQSAAGSNGISSGIKIS
NIFSPTTANTYEHPSTGGLSNAFSNLVGRAGSNSNASTTTMPTAGATSAATAEESFGSRF
AKAARSTVTTMNFLSNFKKEGGNTGSGAYGPLR*
>TCRU_2445 ABC transporter, putative
MGKPKYLKKKQEATAVTGQQQKSSSGSQANPELNVPQSSGAMVSFANPVFRDGVSDILVE
KIDVSYQGVSILENATLNLVTGHRYGLVGPNGCGKSTLLKVLGYHEIPFPKHVDRYFVSH
EVEASDITALEAVVSVDKEKENLEKELEELALADQEDMAVNMRMDEIYKRLDELDADTAE
ARAGKILFGLGFTPEMQQRLTKSFSGGWRMRISLAQALFINPTVLLLDEPTNHLDIEAVV
WLENYLSKFKKILFMVSHSQDFMNNVCTKVAHMARGKLTYYDGNYDQYCITRAEKESNQM
RRFQWEQNQIKSMKEYIARFGHGSAKLARQAQSKEKTLARMVRGGLTESIAKDRQVNFGF
PCAGPLPPPMLQFREVSFAYPGRDPLFRDLELGIDMESRICLVGPNGAGKTTLTKLMCRE
LEPTSGYVAKNAHCVIARFHQHFVDQIDMSLTPLEWMGQEYSSVSDPTILRSALGRFGVS
GKLQMTPMSTLSDGQKSRVVFAWMAFKTPHLMILDEPTNHLDIESIDALADAVNCFEGAV
VVVSHDLRLIAQIADEIWIVDKGSCRKFDGDIADYKEHVQREVNRMTEDYAKRK*
>TCRU_2446 signal recognition particle protein, putative
MSDVAKWEKQLERLLVDGSDSSKILTTIEKILSVNPKHVFALRCKVVCFLHQDKHAAALT
VLDQIAVVDPALPQVSQDYAFQKTYCLYRALEHRQAQHVLMNDAPHTAEHVPSRHLLAQL
HYHLEEYEAAAGIYEALLTEGKFRDEHEKTELQTNYAAACSAIDAQRTQSIVRSADEKNA
DLLYNAATAQLEVQEYAAALQTLQQAEFLCAKAYPTSRLRSFQDACSRSDTELRSLLDVK
GSPERLFFNDVAIIWVQTAYVHYAMHNEEDATALLNLVLRYRPSSAVTLAVASINWTAIQ
RHRDFFDTHRKLKSAQNPAVNNRLTSRQRLLVRYNTAMLLLHTGNFNAFKRQVELIANEY

PDSDLTHSLKLALAVRESKKKRQPDEKTLTEYLKNYQQSVRAQKEHARNPSVGKLLPLIA
AQIFLENGDLEHAIESLSSAPEEIRKKPCTLMTLATWKVQLGDVKGAKQLLTEFAGAAAK
GGTVVKPILFWAVQFLTARGLYADAADVIRDMQSALPVLQNDKEARALLALCLSHYDMQA
ARTCMETIPEAGFTGTQTEKKLLASSIAEATLQQPSRKHIEALGYHRISADGHDGNNNGA
KVKRSRRRPMRRPPKNADARLDPERWIPMSHRSYIKDLPERRKRELKRLRAIEQEQKRHE
AEKRKAAAH*
>TCRU_2447 transporter, putative
MDRFISSAVTVGKVILVSVVGIWISQHFHNKEKSLKALSYISVKIFLPCLLFSQLAKDLS
WDMIHKYYWACILPLIPMILGFCTALAFRSFIPAELHGLLQLSCTFQSIVSYGLGIVLNL
DISWWSKEDRSEAQSYVFLFNLLHSLFLWSFGTMIVEKGAMALEEMKATAAVATAVSAED
DGDDAITSMRNTSGALVEMEECFGAESHQSAGQLEAYQPAPEINSTRDVVERENKSTADL
TWPEYIRVQIPYLLSEQIIASFLGLLVALVPPFYLLAKNPVGEVLMGGISFLAPGAVPLQ
LLVLGVNVTADDEDDSKKLPIRFLAVVILLRLFFIPAICFCIIHFLVVNALMPYDKPFIL
VMLILTSAPTAINTSSICSIYSYKVKEYTKVLLFMYMACIFTTTVWLTVYVWYLDS*
>TCRU_2448 hypothetical protein, conserved
MAMTMTGRVLLVCALCVLWCCAGSVYAGDRDNNAVGGCMASEVFGTDLSHAPSGCNKPGI
TVLFRSTLPITAVVASDEEVTSVTMQNDLGSRENSNAAGPAGPAGPTGPADLADPADPAG
PADPAGPAGTAAAGVPGAPGGGGGGGTSLGGGGTDEISSVSSGGENEPPPPLLKAENEAI
RVPTVGEDEAKKAPQSHDNSVEQHSGENQEHLHEEIRDQQKKQEQRQEQHENNINHEEGE
EKQQQQEQHQQHDHSAKNSDGPTKNETTVGTNATASTGDSDSSTAVFHTTSPLLLLLVVA
CAAAAAVVAA*
>TCRU_2449 hypothetical protein, conserved
MGSVLQPEGQRDAVRDGEADPRVFAAHGAREPICVERCAHNWGRVAARHCGAVCVVRGRS
MAAIVRDVEDTELLDWEEVAYVAARRECITDCLCWRGACWSERGVPVRA*
>TCRU_2450 Leishmanolysin, putative
MASRSMVRNGAVRGWALSVVVDSTTAAMAAREHHDSDDIDGMELQDDDGDGRTMESHWSR
LRARDEWMAPIEGAGDCRGSAPHRT*
>TCRU_family, putative Se.1
MRGGLVRSRPTEVGQPREPSNGVCGCVRDYIFHQMLDAVHGLSNVFFCDAHAASALSCSL
RLHELMEHGVTLLEDPMTPRQPIMSSPAPYFFAVEDASVSRVAEDWIAKVPYRDAHIFAL
GCTPHRSPQQLPRVRIAPRAMRSKDSMLDFAAPEVLVFHLSMQNEFPQLLSPPN*
>TCRU_2452 hypothetical protein, conserved
MVCVRCRCWAAAICDCAVAVRGVAAVSLLLLPLCVDVLLVCAEGCTQVTGVMAMMMTGRV
LLVCALCVLWCGAGGGYAWDFGSESLNEHYYGANGAFCKILPKMYSCELRINASKLQEAA
SQKNNTQSGTGTGQPNAGGSSGRQDQTLEESGSGQPEGTAGEGTQASQPPGEGGTETPTP
LSSPPTATATATAAQTSATRTPDESDGSTAASHSTSPLLLLLVACAAAAAVVAA*
>TCRU_2453 hypothetical protein
MQPASAPCSRRHPNRCHPLIPRVAPRPVRLQRPPVPIAILLLHAINVVAVVVLPRCHRGS
RRLHHHQQRPATHAGSIPHHAAACHVRAGKPDSMGHQVRGDAGGEASVKQSGRAMFMAPA
TGRPSSSVAHGSAHTPPGAAATHSTVSELAAPAEQCSAGTVNRLQTLPVASDGTTNEPSS
GCTSRRSACSLTAAGTTSSATAFPCADDTTPFLQPNAPSNAFAVQHQEKPQRLLLPHGSA
VGALMRTGTHRSLQTTLHTCNASCAPRGTSPTTPGDAHTPPARTASSRKQGYVRMTAGHP
PAIHIAGIITSSSSCRPRGDVDQPTHGACGRKNVMA*
>TCRU_2454 Kinesin motor domain containing protein, putative
MYEAAEQQLALVSRKTHRLGEVLRQQIDALKELRTARMAAFAERDELRQRLRVVEERANA
VDCKHNEAECCLRRTAEEFAATQLLQKQYENTLAELKGRQRVVVRVAGAAPRSGGPAWEE
ASRDEYPKKPPQRTQEKQQQQREGEEEERNYRARIAVTDECTVVDLDRRRTFVVDLAYAM
TSLRRRMPSESALAAAAGISSGAAASEAIPAEDKTTQNFMIDEDLFATLRLEHVIADVLS
GVNMVFLSFGPAGAGKTETLFGTKAAIIQHEMLQKRGRKQQQQQQQSSRHSRRSGSNGR
GMSVEVLSKSPQVCGATAGLLSLFVHGLFNSLVSHAVTHVSISCSFVELAMNQTVDLLLR
QPGRPVSGSGGNNTTLVKMFSAAAGSASTASISCGGPGEEVTAVRAETAEEVMRLFFEGL
DRLGRWRRSFSSFLLMGDDNGSNTNGPQPKDEHVVMAHRGGVSHAIFALRVENFNDKGHY
RRSMVSFVDLCGPPPSGAGSVMRPLTPEEQWVDESLQAVCDAIAATSSVKPNEGKNDAER
AGAAFDQLPSSHTNCMARFLRPIFGGNAKATLVCCVDVEMHSKEQVLNAISYAYFFKRIQ

HQAVPYDIPPELQRLNLQMSAFLSGEGGDDDGEDEDNDNDVITSSVGLGTARNSLAPVDA
NWHCEGYSRA*
>TCRU_2455 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MLYTQRGYFSGENKANPLYLWVTDNNRSFSVGPVGMDNAGKKEVASSLLYSDGNLHLLQR
RGSSEHSVISLSRLTEELKEIESVLSTWSQNDAFFSNLSIPTAGLVAVLSNASASDDTWN
DEYLCLNATVTNATKVKDGFQLTEPDSGVMWPVNTPDGNVRHVSLSHNFTIVASVTIEEA
PNNNTPLLTALLGDAGPEYFMRLSYTADNKWETIVKGETKPTTESRPWVPKKEHQLALIL
QGNKASVYIDGESLWKEEALLTDGTPLEPFGFCFGACDFADDDEEDSPKKIGKKPRVTVT
NVFLYNRPLNSTEMRAIKDRIPVSTRAPEPQVKIAPKPAVPAVPAVPGPREVPTAPGRTT
VGRTANTQHAPAGRLTSAGNEGPAREKGDGGANGDAGSAYGRELLPLLLLLGLWGLATA*
>TCRU_2456 retrotransposon hot spot protein, RHS3, putative
MRRAVKGEVIFDEDIRRLCDKGVNNLPGWSLAAAEVKAAVHNSTKHFLDAAAEEARNPTT
TSAPEKLEGCYESVHNARWSHVVELPDGVERKKTGTGMGMHEGKPEQSWTYRKADDAIEK
NDAVQQCGAAPPMLMVLFSEKGWPYSWNMIQDLPEDVFVNCEVD*
>TCRU_2457 TPR repeat, putative
MSSNQKEESRAPSRQAVEEWLERIDDIAAAVEEILREDPMEATIRRQEREARRRQMQIDE
RKEKVKMRYDPRHYVRFESDEVIDKLLKEAEVRGETTRREVKDESLYTRAERVSLEEAIR
LKDDAARAVKASEWERACELYTTAIKLDVVDADLQRTLRNNRALVQLKLKRYLDAVDDAS
YVLREEPMNLKALLRRATALRHIHRPVDALKDVEEALKKDPANQEAGDLAQWLRRVKREQ
SVGAVFQHRQPEEAKCLENSIRMLTSAVKELHNCGAIPTGESLAKKESEENAEKKPLIQA
VESVRRCLGVVQMFHQGAAVFFLLLDGLNPLIELVCKAIIGGWSELVVSIAAGSPEQMST
CGMTFVVSARLLALVLLGSETGVEGIELSTVTSLVRKLADVLSIALQQKSLGHRDGATLT
LTVAILQVLEGLATRCPILVHAHCVSVLVEAWKVMKKRQPPPQLLFFYCGILEALIKEPS
VCASVAKEMEEILPHAIEVAIEAGPEQLKEVGLSLAVRATCVSSACAKSLGSSELTRTFS
KVLPLSQGESRDSPVSPRLEEGLYAVVYNVLLQAESRSQYVAQWKAVTDPGSSGDFSFSL
HTWRTLREQVVAEGKSTRRITVHAKMMAVLAKFSPHDEALRGAMLEGEETLWAMLWHALS
GLEPPDVGPSAAADNQNFANRTEDEEKEGEVEAVIAAAAWELVEHATTCIASHYSQNHLL
REKGLSTADRIAVLMHIIRRAGPQHVVALGNAGLIASFVPSASCSHFAAMNGVDVLLEGL
RSVRDLIFKLEHDGKRGSTQWIHGGAAQKNLAIALSRCCVVESQRERLRELKGFETLHAV
LEPHSA*
>TCRU_2458 hypothetical protein, conserved
MPHVSYQHNPRSIADDPLYVAAGSAPYTRSDTPVSFRVFPNGTSSFGSDLLTSNESIARR
VAETREWLGRMREEVREAKRKCKAEEKSASLLCSVLRASSALMTERAKGRRSSRGRARQF
RFALYSFLDGTPFLTPQALCRYNTALAEMLSDDHLELIRRHVFNYDEEAFANLLYADEVA
ESLERRAPYGGGELVPEFVQRFNETSRRALERLFAAPGGLADATINAAHRVPIVADDVEN
VAVHGE*
>TCRU_2459 Type IIB DNA topoisomerase, putative
MLGDDEIIGAAEAVVHAYLVVLLHRTDAAVTEASSQTHHRHSAPCGMGGQKMPQFCETKC
TFTEKKMNALRRTARVLYVLSCVVDMVHQGLTCTERDVYYQNTSLFRNGQRDVHTSIENL
CRWMDSTHPLRNADDPESIGRRRYTREGLRIAASGKSILIGYISFDIPKRSPVLSSLSQT
TQMTLGNVSQTQFCFEKTSNYLTGTVEMNGMRHSSGILVNMAVGMRGCHFRGAEGVGSLP
SAVILVEKESTLRTLVVAEGVLGLGAPLNRCSFLCSKGYPCRASRTLLHKLHCELPQLPI
LVLVDGDPHGMRIALTFLGLFGGVASTRRRKQKKRPFASAEFISTLLPARWIGVRPSALP
HQATGRAPLTPLDRRVLSQMMARVVEALSLLEDEVVDATCSGEEINIIRGTLNNILREAE
WMKEKSLKCALQAWPDGPLHLLMDSLEPGRPV*
>TCRU_2460 Flagellar-associated PapD-like, putative
MEFLAYEDGTLRSEFYRTSDVVEEPIFNPRRVYHQESKVSRLVLNGVQEFTGQEGALGFI
HSPKSVLFDNFTVGESYTMVMVLTNCANRSKTFRVLPIPIKYRDVLRVEYAPPPRIPTGL
SWKVRVIFTPEENMDFETAVGFRTEERVFFVPVKAYRKRSCVSVDPECLDFGVVIFGEKS
TRVLTLRNDGALAAKVFISGSFRKWMEVFDKDPQNDQESLVLSIKPVANQLLVNPFSTCR
LEVTFSPHREINIDDEIELRYDSDGKDHIQRVPVKGFGGSLPVYVSSASIIDFGWCFYEN
RYCEKILITNTTNVSVNVVPEIPPTLASSMIFSPETACIQANSTFDLYFLFTPFRGMESN

ICSAIKMIVSGQTSPIAVTLKAQITERGFSLEPKKLEYGTSSMNEEIILPLKIRNNSDLP
QTVGFLKLPVNVHVTPFQTIILLPKEVFEVKVGVRPPTLGQYTQMIKMTNEYGDSQSVQI
TGYGNKNVVQFLKPCFSFPACPFGGETACTNVLENRGSVPCGFRLISPTDVLRVYPSSGV
LYPGKTIPIVLIFRPPEPQPIIVTVEENVSRPGGKGALKKRKERENLNATTGVLDQEVVS
LDTLYKDWESNVIDEEWSRHCTFLVKCLSTMGTEKFLNLLQVNCTVVKPTLIARYLSRSL
QKIVVQKVSSKRNSKKSPPLVNLTEETSVVEMSGGGTHLDIDFGEVPLKQLSEKTCLLQY
NGERSISLQVRPVNTLSPFRIVKLPPAKLSQKEECTMGIRFHPTEYGNFRDTINIASVGA
NDIALSLSGICRPADLLITLSSDITGDRFNSIDHFSFDTVLVGQELRQSLYIHNLGSLTV
EVTAKLLSTEGKELKWPESHSFIIESDRFTITGNCKVSIMSIFCPRVAGTLSAFLQLSAG
AFHNTILLKGRASENLVFYTFPEQSTQMTETSFVCTGLQPEVFPPEGSSPAYPFQVLCVA
GETKTITVGCVKLGASFECIVCGWSESYHENGWKLEPMKVNVPSGGNVLFTLNYNPKREI
GDVSFCTFFFTTKSSQPLAETKCHVRCTGTMKV*
>TCRU_2461 RNA-binding protein, putative
MVPYQTFNSAAGQPVNVYQQIPPTSASRDPRTNIHIGSKLFVGQVPAMTTEEQLRPVFEP
YGELLEVKIMRDPLGRSKGSAWVRYETNEMAMNAINALHEKHTVPPQTNPLRVQFATPNS
VRHQQLQARYAVELKVPMNQYNFGGQMGGGTQQSGMVMLRSGASPNVVPPISANVGGRYM
SAPFGGGPMESSSIMSGPYTSSANCFDGVNSSGNRRDLYSPLEQPQGTAPQLYQQQQQQQ
RGGFSSPVVTPPSVYNQAPSTRQPTARNNNTKSGGGISMGSFESGHGMVNPNSNGAPTMA
NEMSTLDAGIALWEARNNNGLQGQEPREAAARVRSGERKEE*
>TCRU_2462 ADP-ribosylation factor family/Elongation factor Tu GTP binding domain/Miro-like protein/Signal recognition particle receptor beta subunit/Gtr1/RagA G protein conserved region/Ras family, putative
MSSKACASSIKIVLCGPSNAGKTSITKRFITDTFDEYQDTTVGSAFFSKQLYSKAHNTNV
RVEVWDTAGQEKYRAMAPMYFRHAAGALLVFDETVLKSFEELEAVWLPELLPHMNDSTEF
IVVCGNKCDAVLTEEQRESLQKAQEACRARGITFLHTSAKKGHNVHESFGGLVDRILTRR
EKEAAAALAAGANGGDGRAKSTLATRIGSEDNGGIKRSNCC*
>TCRU_2463 Zn-finger in Ran binding protein and others/FYVE zinc finger, putative
MSFNLDDLFDTGSRQQQQQQHGGPTYMPPPPPSDPPPPPVFMQQDQFGVNATALPPPPPP
PPPAAAAAAQTVQPFEAVGHAPIMTAPYQTYYAPSPTPQAYGGNGYALSSPPIPSSESPS
ALLPQAAYYTAPTPKPVAYGSSYQTSPGAPIVSPSTVPPTLQSTAMPFVPSPSHPEPAIN
APTASNSTSVFAQEEEDRKQLEKIIQLRKELEKERERERKKREELETWGCPSCTYRNSLD
VNRCEMCDSNRPGYHPPPDVVSPSTIKSDAHSSSSSPLKKVAISSEVAGPTAWVCSICLA
PNEAHNSRCKVCRSYQKNGKPITGGNGNPTGATSDVYMPPTAWLCGICGKKNAATAARCG
DCNSYQSNGVPVVDPEPKAQIVAETVPTTWKCSVCTLENSVSAAVCEACQSGQRPRHLAP
PKTNEKKKSGNEPRKNDVPKTWSCSTCTYQNAIAKEKCEMCSNERPSQYKPPLPSGAKKE
AEDSGEDIQWQEDEVARECNRCHLPFNFTRRRHHCRACGFVFCGACSSFQLALKKNGPLE
RVCVSCYEGQK*
>TCRU_2464 40S ribosomal protein S27, putative
MGFFDSDLSYPTVRSERMKHKRRRLVQGPNSYFMDVKCPGCNAITIVYSHATSEVQCNGC
ATKLCRPTGGKAMLTTGCGFRKKADH*
>TCRU_2465 Dpy-30 motif containing protein, putative
MSVKDGGEESDEMLERLAAHLREPPTFPSVPIYALPDQQYLEATVLPLLLRGLEEVAKAR
PADPLAFLAAYLLGNNPQRTSHSLMGDEGRRVPLQGIAQMAADIISRK*
>TCRU_2466 ATP-dependent zinc metallopeptidase, putative
MSDNHQLEYKRGLEDARRHRSRTEDNWVRASVGPLLWFGVPFAVAWLYLRRQAPASAKIN
PFEGMMEQMMPIKKRQFRVDVKGTKFEDVIGIPEAKQEVQQYVEFLTSPNKFTRLGARLP
KGCLLTGEPGTGKTLLAKAVAGEADVPFFSCSGSDFIELMGGSGPKRVRELFEEARSSAP
AIVFIDEIDAIGSRAGKIGGSVSSEENRTINQLLAELDGLNTGTDAIIVIAATNFQDNID
KALLREGRFDRKVNIEMPDKAARVDIFKHYLNRVGTGDPRGRKVDEEGEPLPTNENVDNL
ELARELADLTPGVSPATIATIVNEAALQSGIREKRLVDKESILEAVDNTLVGRKHRNRQS
VTSLRRTAIHEAGHALTAWMLPSVKQVLKVSVVPRGHALGYTQRAGAEYHEYQTNATLLA
DMVVMLGGRAAEETILGNPSAGAMDDLQRATDLALKQMMAFGMDANAGLLSYHPESTQAG

RIFVNYSNTAQRIAEEEAKKLVSLAYELAVGIVKANKAKLDAMVTELVDRKELLTGDLER
LWGERPVSPTVEQLVGKLMTLQGN*
>TCRU_2467 60S ribosomal protein L10a, putative
MSKIPPAQLSEAIQAVLTNRKERKFKESIDLQVNLKNYDPQKDKRFSGSVRLPHVCRPRM
TVCLLCDLVHEDIAKKNNVPTMNQEELKKLNKNKKLVKKMCNQYDAFLCSESIIKTVPRL
VGPHMHRVGKFPTVCAMSESLPEKVLEIQSTVKFQLKKVLCLGTCVGHVEMTEDQVRQNT
VMAINFLVSLLKKNWQNLKSAYIKSTMGKPQRIY*
>TCRU_2468 serine/threonine kinase, putative
MVSSAKLGEYFLGKKIGSGNFSTVRQCTDAKGRKWAVKIIDKGRLRQENMEDQMLREVAV
MRSLRHENIVALRDVMESNNHYYLILEYVPGGELFDKIVQLKRLDESTARQYFHQLIAGI
YYCHSKGFAHRDLKPENLLLDANGTLKISDFGLSNLQQDFLLQTVCGTPNYVAPEVLMER
GYNGLSADIWSCGVVLYVMVAGRLPFEDRNMNALLAKIERGEYQMVRHVSEAVKDLIARM
LTVDPKKRITLEGIIAHPWFALGWDPQRLHEAAETNWA*
>TCRU_2469 hypothetical protein, conserved
MKTSLGLQPSEEDDIKCFLADIQYRLSLHCCRVLAQLTAHTGKSFLTLARRGRSPTRLEM
GGERAEDIGKRDEFSMHEEAYRSVLSAITASCTLGHRSCHALWGPRGCGEHRILRLVAKE
CRQRDGTLVLYLDGDTLNGDEDGLSSIANQILTFLKSPQSSRLRAADWSLRTGAFDFGLL
FGFPKLLQRDVAASGERKSDNDDANKTTRRRTTANRQNKSGKENNKKATRKRFRSPSPID
SGSEDESIDGDESLLLVTSTMACATGGVSSALPALQRSLLLMKSYGTNLVVCIRRVERFG
IWCDQLLYVLSGLMHESDGRGGGMSLVMTSSTPDIRQLEKRLSSRLTCETRCIPLLPWTA
DRVTRACLVEVKESLQSLLESRAAVKKRESKKKKTLSSETSLRSRVETLLFPHTGWRFDV
VSAAQEGWKQQGSETLGPFTASSNAEAQLLVETMLEMLTAAMAELDSAFKLQDESVNDSC
FAGRITQASGQLRSLGATAGRVMASVTSAFGDVCSGSLAFLHEKSRRNIILWLTGRLKKS
GGSKSLRGNFTTAPEAVRALWLSTSSKKPFRNGTGATAVTAASASSLSFRGPQPLFDDLL
SDCRLVDLGYCSRETFLVLVYVYLRHEAGVARTVVDLLEDVSSSMGTQAAAALDRAAFRV
AIADLHRWRIISIAGGDDVGIVSLRGSSARLREFLQSVLRRADYCASVLGLEAREMTRLR
SLV*
>TCRU_2470 dynein light chain Tctex-type, putative
MSVETPSDTTSAQDVAVDPPIPTQSKEKAETRPEISAEEEQPAEPKKVSVTLTPVTHPGV
GLHDDPDSADPEEAEKASDHDNAMEISGIPPNDVKNIILQVLSPYFDDEGGEDDAQRYDH
IKAQGWIQLICDGIMEKLLGMRRPYKYVVHCMIMRKCGAGIHVCSSCYYNQADGWVNHAH
DLSAHIYAVVTVYWSVI*
>TCRU_2471 Elongation factor Tu, mitochondrial
MFRAAIRGALLAPKKEVFHRNKPHLIIGTIGHVDHGKTTLTSAITTVLSKHGNTKALDYF
AIDKSPEEKNRKITINATHVEYESEKRHYGHIDCPGHMDFVKNMITGAAQMDGGILVVAA
NDGCMPQTREHLLICSQIGLPALVCFINKCDMMQGQEEMIELVEMEVRELLEKYKFPAEE
TPFVRGSAVKALEGDAENEGKILELVKKCDEWIPDPPRAVEKPFLMAIEHVFEVGKDKKA
VVVSGRVDQGQLKVGADAELSGFSAKKLTVKVASIEMYHKILEDCMPGDSVGAKIVGSGE
TVNLSKENVERGMVLSAPGATTLFNKVRAQVYVLTKEEGGRHTAFSPHYRPQLFFHCADV
TADINFPESEKLAGELNKKYGRDAAEQKKKETELKEFEKTLVCMPGDNREVLLTLAYPMP
MEKGLKFTIREGKITVGWGSVTECLALDPKVSIEGIKHTKAVTGKGKKK*
>TCRU_2472 Iron-containing alcohol dehydrogenase, putative
MFRFSRPSAAASTFFMPKVSYLGVGALDSATSKMTKLGFKKPLLVCDTGIEKAGILETVM
DVLKKKCQMDPVVFKDVHPNPTAHNVETGLELLNKNACDSIIAIGGGSPQDCAKGIALVK
ANGGTIYDYEGLDKAEKDQYPLVCINTTSGTASEITRFAVITDEKRHVKMVITTDTVTPL
VAIDDAQLMMGQPPSLTAATGMDALTHAVEAYVSVGASETTDACALYAMRLIKQHLSNAV
KDGKNLVAREGMCYAQHLAGMAFNSAGLGYVHAMAHQLGGFYDLPHGVCNAILLPHVESY
NSFVCARRLGDVAVQLGVSTTGMDDKNAAAAAIDAIRALSKEVQIPSGFEQLGMKEKDIP
ALAESALKDVCAATNPRQGSKEDLMKIYRESM*
>TCRU_2473 hypothetical protein, conserved
MNTPTKLGDLVIATPSSLAAGKSCAAEVGTTATSRSRALVVQHKKETAKATVKEVDVLHR
GLKRLETRMHELESRVQYVNPWVVQYMWELLCELRDRIGMNYSHQREKAWITGLRRRREN
SRGDQPLTESGMKTPLKQGSTEARTGTAGSRGETLLTTPTHRFEYSNEGVEGEQQEDDDS
ILDTSVSDESDDGRLPFRENGVVTTEACAQGGADFVQSSPSIDDSKRLKVGRTPKTDGRR

LARHMATLGARWEVYRITQEESTSRLGIALEESTQRSLLISSLSCSLATVLHQREVVLAS
SASSNSGNVHGMHRNATQRQGGIATQRRRERFDDLDVPSPPRTEIPVGLSPIQLAQSPSD
FFSPERDNGGRGGNQERSRRAVRSATDVVDDDSDFFSPNNRRQKSRREHEMTALACSVLE
APEFMGRVVNEVSRQLAAQIQQTDMSGERHLSSSQSLPSALVLTAREAVNAIAGAHDEAL
YHQLRECLAHEQRQRTTKEESLWQRVTEYEEMWERRTAAERQTKEEVLQEHQRLLALGRE
DAESCSEIRRELLKLCGEVVRAVEGMPDTFAASRPSTELDDRQTNGTDAIRDEKVFLRLE
TLSAAVSSLYSDLESLRNKSKGELAPQSEWCKQTESRISTLQESMMDVQEAVSIMARKSR
AAEERLDASKAEKEELTKWTERIQGLEQQVEALPSIFTTAMSPPLPPPIETTATTGIEMN
LMSVEDAMICVQRNILSRRAKLETSTDSYFRALSALCATLQQLSHLYNVGTGTFGVSLRL
IFAMPPLSVPSSLATACQAYLREHSAAELKEAMEALNVTQQVAKVLYDSYYWMQSHILVV
DDKAIEASLQNMEDNIVLAEGGNFTERAEPLSKSNVVSSCRKWQLRSATTDGKCRTEALS
RSKEASFLQEPKIATTNLTVTQKEPSEKAMPLPSLQNNTCPESKSGEEDENHQQERPTGE
LTSLTALESLAMASPLRTMDAHCGVMHHYHHHFNCSREEGHNFAPQFLREKEKERTFSPK
PHASQCSETQWDARETRWGNAAQHIGVLYHDGSDFAEQTTPLPVSSLNRSHIDVEKGIGR
MGERMAQNGCTSLDLPPTPSVVNECLTLPTAVSSFVDPQQATHTSGRGSLPLKDLQPFYT
AVTRPRPNSHSNFDENNSDGSAHERATRFVSRLVGDEKDKGTRHSLHRHQNLHLNLQKKF
*
>TCRU_2474 Zinc-finger double-stranded RNA-binding, putative
MFHTPVCGRSAGAFYCPSCNVYCSDSRTAALHRSSLKHKKKSGELEMERQLYKEDASVTV
EDVMALVERKRVELGVVPWSQLRFTEEETHAD*
>TCRU_2475 paraflagellar rod component, putative
MGEGRCESFPHLETDLPSRNEACQNAVGVLEQILSISDLHMTARATLHETQCSSVPTLSS
MTETIAHNSQLVCERTVALLKKLVPEPREVSEGEVAGGRQLSSPKIADLPSFVQKSRLLH
ERVQRVAVTLGGLKHSRLLGEESAGRRIITERASLAIKQLLEVLLAVEATVDETPLSSRA
GQGTARSRYFVLDSQRSSEPLEAPSTESSHAASEMLFSGEINKGNPPKSISFENGSQGKK
INRNSPRYLTTTRLRPTAEKREEREGSKTCTSCCEGKHLPFLQDERKESSSNSFYSCFSA
SVSSGNADTMGQSSSLRPYDKKGASPTSPKFREINCGNADSLETIASTHCIPLEELCSIN
TQLLAFKNKLLPPNTTVRVPIRNEDLSTAVPTRVNVHRRIFQGKLWRELLCNEDPTFTSR
WKELFIEEVVLLFGIPHRWVSDVQLANDTQTTLTGGDQAVKFRVRLPLSLEANEVNTRIQ
NHEFISMLLLYEELQKKKEEEGIKEISQSDTNSFLSVASRDNPESMSPPEFANTAVPNSD
AGSSDSRSGSGFDDCHNCLSNKIKNDKLLLDASSAIIQKETLSRDGLIVQEKYTRKLVMK
KSTQNQHMPGHEQQGGKKPVDVSLPTYRNHTGQQEPQIEASDALEEVSPFRFPNTHPACV
LPPLPPQSFAFPRHEHVSASTVDEEKTELSASSPSPSPVRTDCEVNDADYKEKSIFGNGS
LLMNPHLPESSEREFVLGPRKAWEPTVQWFYTSHEKVISGERWDLVLEKERDELRRTFIA
EVAALFELPEENVTAVEFVLGSLHATFNLMHDRYLKAAEIDALLTVFDFPQVRILYHRCV
EGVNAFPPVPSNKMSGSGYERQNVNANDLRMQLPPDNSIAGKNTSSFRNECADEKLVRLA
SEESLFFCGRQLFPVRLSMNSLQENAATPDNEPITFAHLALLHDISTDALVRANPHLDAF
GVNDPLPSSAHIVIPRLTLDDDACGFKEGYEEHNSNGTTPILVNQTTPGLGTANADEKSC
SKSSMNLKDAAREMDSNGQALRQRSTHFHSDGNLDPISRNCTVNVSVGSLEASDSPVVLP
AACASYQSSGTLIGMREESPTAVVVSGSDGEKRTVGFGLESTPFKQLTQESADGNGHALA
AGSEPKGVHKRWHDFASLHQVVKQHLLAPPQRSRPFMRHVSDLRVKPSFSTIRDAAVRRD
QAVLLMLRSTEQFILLRFFARWQYVARIRKGHCEYLALQRVPLEGSPTKSPIQETESLNS
RFREKTLGGTLTPQHVVPSKTRSLRGQNAELIAKTIEAIARTEKRGVSSRNAHQNIPVQK
KSFFPAQQNMQEVSSGTHAISVSAPMRTFGGDHSLQSGYEFAHTGSRESSRSPSSCSSSP
HLAFSGMSSDHSSYSASAFVHRPNVVPDLGISERPPLGLCVSSLLTVTEVHGEAEAAGIQ
RGDQIWEVGRHRVRTLKDFRKILASTDGTHICVGIRKKSSGALTRIRLRRGWRGPLESEG
SPSTNSSPLEPRIISMLGKAGSAFLASAMNRAHSAFVPKSVQQSYLPLNNTEHGS*
>TCRU_2476 DNA-directed RNA polymerase II/III subunit, putative
MGDESNAIGQEALLYDKMFRVMRTVGEMMCDRKYQVADKIIPSSVEEFKDWYTDPREGVI
YRDRMTVPCERIGVSQRSRAMVFFSEGLSMETMKRYHTQASEANCDRVIIVVQGRINAIV
KRHVEDINRSSLGLKIQLFDEDDLVVNITHHELVPKHTQLEDEEVKEMLQAHALELSALP
RILSTDPVAAYLGLERGRVVRIERKSMSAGFYVTYRQVV*
>TCRU_2477 DNA-directed RNA polymerase I subunit RPB5z, putative
MGSIEELKIVRLYRAYNTAIQMCMDRGYTVRHPSAVAQAVRDPCVYSYEHGLDYDWFLQR

FVTQRAAASGAERAEEDEDDKVSVPTNQNKLLEENKKRILMRGAMRLVCSAELDGATDDE
EVSLSKRGEKKGSLMLVFFSASPSLSMSELQEFREKALLKEARCMVVVSAGKIPPMVRRG
ARELGGFLRAGTGEEIMSIQLLEEDELAYNIARHDTVPQHEVLSPEEARLFLQQRQISLS
QLPRILKEDPMVAYLGLARGSIVKIHRDTKESGPYEMYRQVI*
>TCRU_2478 30S ribosomal protein S8, putative
MLRRTIVPLAKVYGAAPPNGTGQKQPVRHRLLHGKRERQGSLFAIANDVKYDEKRLRQQL
NAMLEEERLPPRTRLEHNKANGGEALPQRRLVDLPGVERRRDLPADPITRLFFQHKGDHA
LYYGTYDNPSLQDEDRIQIEKREPRYWTYNVFTPVYDFCHRIREATEQRKRFVIVPSTVE
TRGCARVMLGHGLVAGFRDFYNDRAFAVELKYFQGDSTINVIEPCAYDGKTEFEWSPKMM
RRLMNTHGIHNRLVVYICRTADNRVIDHIQAVKENVGGRGLIMVH*
>TCRU_2479 ethanolamine phosphotransferase (EPT)
MDLFLSVSPTDDRPLVPPQLSYLTEHVLTPFYDLVVLYYPASWTPNKVTLFGIFMTLLSS
LLLLTGMPPTTLFEPPYATIRPASFLGEDSKWQNSFGPTPLHPTTLRPLWSSIFPSGNWL
LFTCGILNSIYCIADNTDGRLARRLKKSSCIGEYLDHGLDCVTSLLSTCVALSVFGISFS
NISLAVVTVAMATVFSHTLNYEKHIFIWGNRFVSVDEAMIFFCVVHWIPLLFPGLASAKV
SPALLYAVLPEKWAHALLPLRYVEAIMVIYWASQVYVILDIALKNWKMIFRITTLALLLN
TVLMLGVIPYQTAQLVKVDPAGYVWGPFSYVAIWFITVSCTSSTVVHILIYSHCARLPRV
DPTALAGLLFVWLAFINCPAAGMMISVVWHIAQILCYVDGLQNRHLEGSQKVKVV*
>TCRU_2480 hypothetical protein, conserved
MDLSSIVLALQGNLAFLPRAVSVLFNHANPLSEREAAKLSEFTREQQETGAPVTSVPDNI
KQLMERPLHRLSAVTVIQCILGAARVPSLPVKYQRRLQRHLLPLLCKSELLSLEEWSHVL
RQTATLPMGHSAIPLRCAEEVLKAAVPALFLSKNKSAEEESVNEVQKLFLKTFSVVVSHY
AKRYTRCFQRSATQKMPTSKSNNKRNFLYSTPFRRLQRILDVNWGHTREAWLEIVETLSP
AEVLILSLATPWNYPIKNGTLMQVLKGSPTLLFHLFSDRPSPGSLWVECPNDAIQTCIYN
MGLTNCSRDNALDYLVVLLALSGKDKFEFFKSRGMDGFVQLLTPFVNNVKTLNVAVAQEW
QELYALLFLHMKAEEELFPLFVQAASDVVVNRCRAVTEKASIITLTASVMHAMSDAARSK
AAAGKLTRMIERELASPAVDTAAAAWRLLREARLEDEVADEIRSALKSVKNNEQLRRVMI
IHISPQRAPADVITSLIEPLFEECEEAEAYRPDAFLALRIAAQRRFNAVAKLCGILCQAD
VVAQLGTVADELNGLMETAVALAQISLFAPMALLLTHRSGLLRQQLSSYVATISTDASAI
IALWDSLTRTVFGLEAKEKPKILSSNAVGALLTVAPALLQHTAKTPVSTTLCEVLLCCGH
DHIQGTDPYYFHTKSFLLGRRRTSSGVVQSQVFERLFAGEHAHLFKLHSEALVSKICENF
NGPTHLGTAASRGLVLLLSFITSPLSLQQAFENLLDATKKSVDYLISLDARDRAIAASSV
TALQEYETKALRERQLLKTYSDKPPKGMSEDDYEDMKRRDAIALEKGREVLRIEIEKRRH
EIEEMIRKNKVPLATIRTLGATGRFPIEGVAVLYPYLQGILNRNDVPEVLERLIVDAISG
LLSKTIFADMGENMACTVAQLHDKPSLTVGDVSRLSTMSLHLRQAITHMIPAPLFVVLLP
FSRVAFKAGRGGNAVQTTIPVATQHQIMGLLLQNLGQPKLPQPTETLQLLTNILQNFPSL
FKSVQQGINLLMALIPASNLTALELGLFNPADAVKEVVASAYHRFSHFLTCRRALVLAAV
SLHDSSLEVVKSMQRVTQDPVYSFSLDPMDWNDLLYFLRNYGQHQASHAVRIGETMRELF
LLPSTTVAQQKLWLEDLKKIAGQGAIVSIQVLSSSLMNDAFQGVLLFLCEMAESPSTEPL
MRLILSCGRVVLNDCAIDVLKSLAPTLQTRLGKPPKDLTDAHKELYFATSTVWLTIISCR
LKETVLLESIVEQQSSTLNKSSSAMVHRAVCTSMVEITKNEEVRASPKLDEFVEKCLKQV
IHASSYIKKKAHAYGLVGVLQGLGLTSLRRYQIMEIMKKAVSENRTERTGVMLLLEVLSE
EMGAKFEPYALAMCGGLLEGVADKDQRVSECADDASRVMVRSLTAVGLQQLIPRLVDSLS
AEQAKRRVPPLNFIGYVAFCSPKQLAATLPEITKHINACLFDVNHNVSTAAMNALRRVAG
VVSNAEIREHVEVILLALRSPSTETENALDTLLYTRFVNAVDPASLALIIPILSRGLSSQ
MPHLRPKAAQIVASMVNLVNDPKSLKPYSEELVRLLEEAAMDPMSEARTTSAKAVAALSA
ALGGKMVDDIVAWCFTILHKSHVSSIEKAGAAQVFVEVVESCGDSILYDSLPTIAAGMLD
ERPLVREGFLHIMVYSPSTLSPSTFQRFLPLSFPWVLEGLSHFSDRVRDVALVAGSGIIN
SYGTRNLSLVLEPLLSGVVSEVTTLRQSSMLLASKLLIHLVQQIRKRMRISLAKENLAGD
QDKTEELERILEQEAEAAEDAENCGVLQMEAARDVEKRGISILGSLEEILGTEGFTQLLS
AMYCGRHERNLNVRTDTNNAWQTCVASLRGAVKKIFNGLVNVLVLFASSENLDCVEMAVK
TIEFTSRLNEMIEQLIEALCDRYHEKSRRSKLGALTCLANIVVYIDSRRLIGVGGQIVGC
VLPGMQDTDPRVQECARDVFAKVSKSVGPRLIEDAIEAQIETSVRGVVEVVKVKPVAALD
IIFKYLAQRSVYTQDNLELLDAILDVDEAYEQMRRYSDDMSRTLLAFLVQGLEGASETYQ

KFIEGLSREFEHLPVEHWEKGLRSPATQRGALLAAEAYGLGVSFDSIETLTAVFRAAIEA
LGSDDDELRSIAVSMIPRLIASLEQRVVESLEEEEQQDLTTSKRAAGRYLLQYLDAFQNT
LGVTARAFITETEPEFNVLGEGEPARIFDVFMNFYNRGLDYGTSVQKVQAVECIQDLLSF
APRHVSAGAANTVAGRCSKVLFTRNEGTVVLALVRLCLQLMDYPASGKEKMVEGTMALAM
FNASLCDKGEARVLALRVVIRLLQKSEKYAELILGTVVTKKNSVDTALLRGVMCRFVSVV
IRYSHFTKALSHITKLMDFVLPTWEWAETPATAAFAGVAVAALCKSASTTDGQLAELQKK
ALVMISSKGSAALGGFAFAYSLVTCCMERADPTFIRAAADGVRTAASVGASDKLTITWLL
RAAAALASTGLIQASDLKPEAFVPMLRRVDVNDELMMSTAQYYYEVIVERFPEVAGALAG
IPREQSTQWGIVGHFDADLDDEEAADTVY*
>TCRU_2481 periodic tryptophan protein 2, putative
MQTNFQLASVHGMLYTGGNVAFSPDGRQLYSPVNNYISSIQVQQEGHRSLPCSNSTIQCF
DLSPDGDLLIAIGRRGVGFFYAISAGVVLDTIAFPPDCEVRCVKFSPCGKYVAIALENTL
QVYTSPAQRVVAYHACHRVENLHAALTLPIMNVEWSPNSEHLLLCGQDARMKIYPRQGRL
QQKGMAIQQNALVGHRAGVHGAWFMDDACSCVVSVSADNVIITWKRTNVTRREVLQAVAT
AQMKARIMQQEDESGDDDDGAGRAPKSFLEKRRLEQLKLEGVRVSVADDTYLPDILRCAY
EIDKKYLLTHKGNVSVTCFHRIRGLVAIGYNSGIFAIHSLTTADEAELTLVHLLSISAQS
LTAAAFSPTGDFVAFGSAQLKQLLLWDWKSEAYVLKDQAHYYDISRVAITADSGSIISCG
DDGKIKVWKASSGQCYVTFTEHTAPVTGVVTCAATNAFFTCSRDGTARGFDLVRYRHFRV
YKTPEQTQLSCIAVDPSGEVLAVGSGQTDRIFLFAVQTGKLIDQLQGHEAPIACLAFHPS
GTALVSGSLDHNLVFWDLFNRGDGGDRMKGDAEVVDIGSEVLSVTFSNSGRRLAVLTMRQ
EISVYETVVPTEPIIIKTFQTSFDAAGGWNKTVGPRSANYNARFNVIAFSPEGEKIVAGG
DSKWIVMYHATQGYMLKKWPVTTNQDVQGAEEQYQWRQMTEAGHVDDIDVDDADIHLRRG
KIMEMPGSRHRHFATGKRQTALTARTMDLAFSCTGTEFVAATTDGLLMFSTRVARPKFQP
LQLSANITTQQVRDQLDRGEPVMALMGAMKLGDKMLGVECLRRMPRDAIPVAVSSVPSVL
FPLLVQWVSTEVEESRGIEQALLWAQSLMLHSNECTGGFAQERSAVIPALKVLQRGLQQH
RALTDLAKENYFSLRYIIDMTKMQKDILQPAATVE*
>TCRU_2482 hypothetical protein, conserved
MRGQSTEVPLRPKNLQSSLGISSGINTLPGITSIMRNEFLPLMQCLEQGNDVLCKTYIVE
LALTLSRFDALLKEEERRVFVCAFDALVRRLLKDLHHLIELESFLHQDLLMLMELAERCR
RVHHLYDCHTRSSSAGDAGGRSRGVRSTSSRSSVAGNALDVKGQRGTLDPPEACVANCTS
AELQQLFQSDVGRQLHPMNSMTASGTWSAGGNENTTNQPSSSTIPAQTSVQPFRLLGMVL
PRNFISKRASCWTEDFWDFLEGRIPKGEIAALARLLLSEGDNKNENFTPFSNAHRDFPIH
ASTKPTRTGSNNRDASASFVAHVDATLPKRMMQNAEDNDSLSREMDGSKCDEAGTAFLGG
RAMNQTAFFLNVLVEGLLFGGSSSVSSLNSSFGSMEDAEQNSAVTDAVNESRCSGAVPQG
DMIGRFITLPSPAALSLMPMLFPSLRNYAEDFTRLAEGFVEAVEGNSGGGNSSVAASSDI
TRRAQSGFQRIKGVHATATSGGPFGDNSMDPLHPATTLQMMTDASGFVRPNDVVLYVLLR
SLQRVDGQPATTAASTHLKTGGTEESTPKDFSFEYAAAASKTQMQDNAATPTLFSRIGVE
LESMIKQVQEYITSSQTMQEQIREEVTLLIFRVISTTFDFLLPAVQFVDLRVSILYRKWL
CDMYRLLWEEDLLDRFSAIVAASLASSSNDNVCGVSSSSSQPQSTTPRRGGGESKRHLGK
GDSTGGNTTPAVGGITSKNTSNHPSYGKGSSIVASSETLVKKREEKLRWIAPGNAYSRAA
RGLTGSGSEFMSLSSTLAVHPSKFRSINKTPTDVGLYGFGVFDDPTVLMAELLLEDKVEE
IPKSNGFVMTRLMATLLRDGISDKLCHLHLAPERSLRDGGVAAAALHDSQSSTVRKTTTP
SARSVKQPTRKKNTISPHHSPMGVRSAHSTPENKSSVPQQRPSPRYPAVTNVNDVKALYY
SVLCDTEVALSPLDPIRAAVVQNTVDFLVSGMRLPKEAYELLDAYLDDVGIEPIQPPVTR
RVALDGTSEATRGGAAGGDNPLSVSDSPFSVTTIRRARQMPSDTHSGTGGKTHTSHASHT
PQVKRGGPVDKETSAAALRLPLIPKVIPSWNTQEETEQFLVILALLRREYIVLRAELGLL
QPAPPKQSKEVFSR*
>TCRU_2483 hypothetical protein, conserved
MPARRSSGSACTKKNAGECAPQSQTAPANLPPVNSVLQELLMDLGLTETAKMLEEESCRR
LQFLTSATVEHNNFCGNGVQTLDVANTGEKSARGNSKEAKTTLEPKGKDGNGSPLNVPCK
TEGGTETQQPSSQPDTARTAFLWNFMHRKTGGDDETKNAGALQELCRIGIALPGWDAARA
TTTDGGDNNNNTTELVALTPHLRKLFNVFLDADSCETEHGEKKSGAQSADILPPEWVSLL
EVFFSYVEVLWAQICLVEAVSWADFTSQGWFRHRKNILERLSLLHEKLQRLLLDAHQLEI
NRHLFESFTPSWGENQKADGLFNSEEIKKDPSQLYSSANEVMITTKDIHSGIIALFCRGA

STFRKNIEEVSTWIILHCGQYNKRMESIDVSERKLKEPISYTESGETSSSEVKTEMEGSS
ACKPWHMLMGVVRRAVLMGSGEVSDASFDAGEPSFISSPALRWAQVFLRIQILAWVVGSV
AEFADVWLQNSQGFMEMTNCKAEGCHETRRRLSIVSASLGFWYQNCAAQISEIIDGTKGL
RKDSPSYTDNGQGKGLSQRLPRSRRAKMADEKENIGFTLVNTLKRAVHEFLAGTTTLVAP
LRLSLLGHEWQSETGANLPNHKEFCGTPYLHDNMNNEVDIHMALLHVLATGQPYQLGRAP
KPRRTPLYFLLKKVLSAPKILLDLQNERVPADIQLRSMENPAANMFLMSSQRNGVASKFF
PNGNQGRATQTEKAMNEPVTVRTYEGEISVSGEATSGFLDSQQVLSGGTGIGAVLPGISE
ESVEPFMFPTLSLPIHFQALVSRMAHQANEFTQSEGSVSVGSDEEAVSSTEYNLDRPSDV
ILNEVQIVSVTPCGSLLALLTTKSRLVVFALRAANGLNQTNFNDQLQDSFCEQLVLDVVL
MKGLKDPYWYEQLESFLSFSPSGQFLLCSVQNAPPFVPEGDEASRSHHATTGKVFLYSLH
RAECGQIDASDVSRHGAVGEEDRLYAAFRIHKTLITVARWLDPRFWRGNSSSSVLPLEEG
SPLWKHEAQRRLAALQCLSSGRDNLILRWSPADGSIIQSIATFPVFDILFSPLMQAFYTI
NQYGQLSMYDAWNERDIESAKDNVVVVSQRGLPATLAAMQSSTDLRERSFTQKSAAPVKD
GEMQDAFFVGTRIIGFDRRSLARGGTERESAVSRMSRLVQEKGLPAGTETKEGNRLGRRI
VQQLLRQDGDHLVPHTLAVIEPSSGSDKDFDGDDDDDYNHDGQATRGHRNHQGNTNGGVG
GGFNSMPFLRARHFRGEGKKLPTLSNETKGNNDVSISGEAVLYRTGSRLVFEEISQLLCQ
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GSRVKVIGLRKQAGLTNALNSGQTRLPIKRARCSYVSLADLGVFSNCQSQRDDGNDDDDS
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PFFEKLQEDCIPRLSEGHRSNGCSRQQAHGHCGAPDSASSILSFPSPLPHLKLMMSCPSF
LGQLKMALGGVSPANGFQSAASRSDAEGKANTATLFYDVPFAHVAQRELCQALLSNETPM
SVGENGLPSTGGVAPAVAVNTSMNSASKPQKRFLCGVVNSVALFYDHVKGGVFVFSSDEY
GGLFMAGGLIPSRV*
>TCRU_2484 hypothetical protein, conserved
MHGRNGELGAVCHVANAVHTCSNCAASCATKEEGATVAFTMNVTAHKYAGHYELWWRQFS
PDGTIHPPARSGDADQTGICQLPPPREGKDDTKSGGTTAPQVNAEPSRQHEDRRRSAAAD
GPNTVDPSPASNTATNTSETKPEFAYV*
>TCRU_2485 BNR repeat-like domain containing protein, putative
MEDGTLVFPLMAKNEAEDVYSMIVHSTDKGSIWTLCEDISPAECLNPRVTEWEGSLLMIV
DCENDQREHESRDMGTACTEAIGKLSAVWVNARSGVSQKENLRVDALITATIEEREVMLY
TQRGHASRKERSTALCLWVTDNNRTLSVGPVGMENAAD*
>TCRU_2486 hypothetical protein, conserved
MGLSCSHKKKGETVFKGKTTTRSSTWVSKKECQVALMLQGNKASAHIDDHSLGEEEVPLT
GERPPEVLRFCFGACGVHESHVTVTDVFLHNRPLNFTAMRALKDRVPVPTREATPTPSEK
VRVVDSVREHIAGDITEEK*
>TCRU_2487 hypothetical protein, conserved
MRPHIVDGRAHSAAGWAGGHQSAARWSAGSCGAHFGKRFWRRQRRAGLLSEGGTASPTQR
VICDTEGTRRHVEEWAGVAPCLCAEPPLGARCPGCARNRVLATPTGACHTVYAPFLFSWA
SLQYGHLTAVKKPTCQIGLSSCGRDRAIMASSSAASLRGIPQCDGENMMFTERPRCIKES
SIIQISSVTQSRTASGTTRSASILDRDSVATRIRVGDWDVSKQKGMRCLMPSSVARHSAL
YERASLPAAARWTSTGRSFVVVEPYNSAADPDASSARDEETSVHNSKSKSPREE*
>TCRU_2488 hypothetical protein, conserved
MATIRRKAPRLFTGAVFTEEISRGLMTFSDRHNLTSDVWVPKKLVGKMKAGATLLPNAIL
CDVSLIPGCGAVDLKTIGFERVLVNAAHTTDVEFFEGYRNDILNGLAGALPLTVTGAPHR
DVRLASLAVDGSQRGFQSPYWLRRWGRKRQWVNAEETPFPGRLNPTDCTSYEPHTFTNQL
FSRAVVRLMRRRASRYGYVSRTWITLKEGEAHGTQLDAERIKDGPPIFVSQFSGSGQVQA
VEFFCADQFEDCTVFPTQREIDLAASGVFIGAEKVRGYPLLASLAVESSSSDRHRRMAEE
TAKLSDPVVFGATRALEPQFLGSEFKESLRKFSLLRGFSKPHFFFHTAETAKYLRLKPQE
QGILYNPPATSIGPRPEQSRHCVFNVQQFEEPAVVEEIIFRTPTFFFTQVPIAGPMVVEC
ARAQCRNREYSQMWLPARALDYLAGAWAISPGAVVVPRDETLLAFSPKMYNASEVSIPSE

ALEWWPNYKPHNMHNNLYWGQVRMLLSLRAWERQYKSPLWITQKLMSRLGITTKRQTRWK
LFLTGKPFEKPPTVLIDDDEYTNMEEIKNPDVLMASMSNADSDINVLAKKG*
>TCRU_2489 hypothetical protein, conserved
MNQFELFVASSESARSDAWRYLRRLRELDSRIDENMQRLREIAETVVKPTVTQITEERKR
KNGLPHGNEKRGRSPPGTVTSGAFFRGHGEDEDDVSSETSVVLLEPSEAKLRVEYRACRH
RVLRYALEREAVAEELKACGSEMKKCLAVRMAKLRQTLRGVEYSSPGTSS*
>TCRU_2490 Papain family cysteine protease/Protein of unknown function (DUF3586), putative
MTYTGGVLTNCVSKKLDHAVLLVGYNDSATVPYWIIKNSWTTQWGEDGYIRIAKGSNQCL
VKEEASSAVVGGPGATPEPTTTTTTSAPGPSPSCFVQMSCTDAACIVGCENVTLPTGQCL
LTTSGASAIVTCGAETLTEEVFLTSTHCSGPSVRSSVPLNKCNRLLRGSVEFFRGSSSSG
RLADVDRQRRYQPYHSRHRRL*
>TCRU_2491 hypothetical protein, conserved
MNTAKRATTRKAQVPSEKTVSETETRCHSALLVIGTYHSVMAGLVYRRNKFGMLFSVKHH
EGCINSVAVGERYMATSGTDERVFLFTNKNQKSLTPSERLRLRAAGESLSVRLADLGHIS
PPSEVRCLLFIANSQQLLCGCTDGQLLMYRTRDWSVGLSLPLHEKGVVGVATHPGSDGAL
AVTIGADRHVAVIDLARGRLLSKWRYNASLEGTEVKKRQEEEEEEKDDDKKDGTPRVKRV
KLERRDGPHTVKFSPSGRYFTVMSSHAFAVYETATVGVVAIYRTPSPQPREELHVFAFVD
DDAMIFGNESGELLACRGPWKLEETQPGECTLHPVAIHVPSESEQHADEKKKSLRHPTRH
TTRLKALYCVERTVFSLDATGTVIAWLVEEVADATMTLKFNCSANCQGRVTTMDVLLL*
>TCRU_2492 metal-ion transporter, putative
MQSEVELLLRSGGAAKADYDTTGLRPQGLCPTPVERAAIEKVLSATEERRKRESKFLYGA
LIFCFVFMIVEFACGVFAHSLALLTDASHLLIDVGAYALSIMSLKAASRALCGKYNYGWH
RAEVIGTLVSVFSIWALVVWIVIEGMTRTWNVVSCSRMPAAVAAITQQRGGSGGEVVADA
VLASSRRCEEINSPIMMLIGVLGMLVNIVCAAILYCGGSHGHSHFGGHGHSHSHGEVTNC
ESDLEISINGHTKDHSGHHHTNDDDDCGHGNSDEKEEHDYDHNHVEKKKSKKGFALHAAL
LHALGDCVQSAGVIFAGVFIYFANKHAFGVPSYQYSIYNIADPLCSLFFAVVTLNMTRPL
LGDLFGILMESTPPGIDYLALNQALLSIEGVVSVHDLHIWSLSSDYVALSVHLVADDAAK
ALRKAQYVCEVLFGIRHTTIQVDAVANGADLCQGSCASPNCGKEYQTIT*
>TCRU_2493 hypothetical protein, conserved
MSSTAAEMRSDTGIVKQEINECVETGREAVLGAKASLEKPVRSAVEKVKQGVRECTEVGR
ETLNGAVTKTNQSLNATKEKAQKLADEGKQRIGDMIESAASYVSGAGEANGEDGGSNSYA
AKIISVADQYVESGRKILNDAKTSAEAYHSAAVEAVQSKITHGRQQVETYATTAKDSVEP
LVDSARGLVNKSAKRLSKTSEVIREQKTACMDKLDTVRTKVRIAVDESKPHLQTICDNGK
SAVFKRDARLALTAVAQLFAGVILLMNAFFEEALKLTFVKNTTSYVQNCRVTQRTRELLT
AANIPQKVDHLPIVGHRVVVAVTIFLSEVKRSMLEMKKKNRCVSPKPAGAHDAKELREDA
IPHGRKTQRKEKLEA*
>TCRU_2494 hypothetical protein, conserved
MPPSSRRKTASAAKREKSGRIKKANAKYQNQKYVPEQMMQRGRGGAHGRSGGQQAERGNG
EQRRQRSARTDNIDIHLAAKVSAELRVDLSKFKCQLNATEIFGKELSQIFKFVPPPFVRQ
HLPEDVKSLRSYISKFERGAPSIVHAFIVWYEWASYELNKGKGHSYSSKKNGVEGQDASV
AKEDENDEREEQDGEEARKEKDHGKVSQARAALSKTVREREHIRALLQMCLRHNSSRRKE
GQHAFLNHLKAKLSEDVDCHSLKSLRETSHHAVPYALSRLLLGMVTEDMAMILLHAHTLF
LLLRDTTVTPSVILSLIGEELALDVRLKASKARLEARAAKKDTLTQEQQQQADEELDDID
PDKINDPTRGERNQQMIATVFATAVIVANPRKLRLEDAQRLVHYLCFAYIEQKALRVLTA
NLFFNIIEKFPSLWEDKTVLEWLSYAFFLYPKLEYYRPEGVQLLLRLMMMEEKPPGMKRG
VPTVVMKYAAMDPLEPSTVEQIANALFRKEQVTMVYPMVHPVWTDWLDIVAQRCAAGESM
KEHLSTMVHNAIAPYRRGNADTPRRALFQQLVSRLGQLAVQNDDAEQRAEILQMASKTVG
YGRRTIAKATDIADLRNMPLELLDAKVRDLLRHYRVTRDSDMSASANRTWVLRELRSCLY
VPLREGVKCTYIDDAAEALLEFGFYPPPPHRDTRSMNRAIFLFAEVFSFTYTAALSRPKC
TLSPLDIIRAYLEAEKREATRYTTGVSQSVFRKARNRIVEALENSSKRSVLFYAERDMHI
LLVLLFLVLSTDDYTNDEAKALATSTVPDICQFFLTGTLETIDLFVDVLMALTMRSTAPI
HVIPLMTCIRRIATGYLLKFARHVRERLTLDLILAPLREAFHTDDRERSRQAKARGETEK
EDSDDDEDDDDDNDNDSNKDNDEGSEELREDENEEEDGGDTTGTSDTSESEESVATESTA

ATAPDDEAEEETTSDADELSDKEDFMEGDQEEGEEEEEEAPTQQYIDALKGMIGNVDLQF
IYPVDTSNKDKSNVVRAIQIAARVGASMRCPLMLHIFQVLLAVCRENVKSPDDVIFNSAV
SSTQILMMTKNRYFGRFLVPEELFQLLSDIQSYCRKLDHVLVRKESQSAKHAVTIRRRMA
LLRDLALRVFHFVAFLAYKNHAGEDVRVTLLEFYKSIFCDRGWNDKKRLPGIKRDMHHYR
HGFGWVVLPSAFEKFGEVEGIAGPQRVRVFKGCCQMIEAMLPRLSGMGASLKTATGTAIT
SFLQSTTVRAVYEMKYTLLYDYFHCLKMVAKYNSRVHLDTAWLTSVVEEAVNDDSLQMSA
ASIRLLAGMERLLGLTPRAKETKAPVPVKVLYQQFEKQGRKEKAVFYKRAKRVRAKVVKA
LVAYRNGDLTDAERALKRRRREAMKIDDRLRRQVLREEKSRVLTKEEKEEKRKRIMIAKQ
ERIAKNRERKRRLHEHREKAFQRWREQKLASAAAME*
>TCRU_2495 hypothetical protein
MADFAPDGASASRYFQSDSNFGECGVCLCQWVCPLEIFPCRHIFCEACVESVDRCPECSA
TIEQRRQPNVAILELQKHSKGRCSVCGWVGTFENFNHDHVTCNAKPSFSSSSLNVSSTSP
PLGSRVGRGYMLDRPETNDAGQSSPDFSSQQEQQQKQQEVRSRVSPPKLNANALRPVSSI
SLSAEGIRRWKETVSCVASDYGLSEDEFKFMRDIWPEFATLNSTRTNLELQWCDACRMLR
YMNLPSHPNDVIDLFNMAMQPIEGGCVSFESVCLWSSVYRRDPSRMYNMNREQYSCLLKY
AQIIDIEKTGLFNEDQCRGIGEQMFLRELTDLEWRSIRPLVVARAEEFRGNIPCAYPTAV
SQGQQMKLSLHEIILLYNRFFDPTKKSTGMAGGNNNGLSEALQQRIQFMLKH*
>TCRU_2496 hypothetical protein
MSLYSAEVVPCEVQEVPLSDVVCPDVPETNKERADVPSAGDDVARSTESAVPLAVDASDV
VEGGVSAMDEEERTEENEEQLPQNGEEEQNCGFVAADHEADVESDGAASKRRRLESPARD
STDLKSGGAAMDAAAAVPIEEDGLTKVISANASQTLDGLAESPTQHA*
>TCRU_2497 hypothetical protein
MPTKGTGAEGMTHRLLESAVFLSVVAAAKIEELVGDTTVTLKLVLETLPQLSNQKDAMVA
VSDETMSTETLGLGKEEVLPLQLSHADAYQLLAELEDVLEALSQKQF*
>TCRU_2498 translocon-associated protein (TRAP), alpha subunit,
putative
MRSLLSATIFPLLFVLLALCLIAAPAVRAEDMGEGGAFTTGGDADDDDEEGLGDAARKYP
WASARVIFPDKPMNLLHTLPAGSEKNALIAYRNNQLSHQHTVVLIAGYLTPLNLYGQVIQ
NFSVVRHARIVQPTDTTSFQYTFTPDAMLEPNDYTLILGLYYQDNVTNHTYFVTAFNNTV
TVDESLETDPKMILLYFNLLLLFGGVAYFVALKLGLVALLREKRGGDSSRRRVEVGTNGE
GYDPDYVSKEHHRYKEALLQRHSSSSPTKKRN*
>TCRU_2499 Tim10/DDP family zinc finger, putative
MQLEVKQESFRIEMLMSRLQSECFNLCCKDLTTNELSMQEVRCVDRCSQRYLRTHDIIAN
AVDRGQSSGGKIKL*
>TCRU_2500 hypothetical protein, conserved
MRAFCPAMRVTGRGALRCTIRWSLTVKEDEAFVEQMRVLLRRYRALPLSRITALFSDEML
DIMSNISGGLRRYFQERPSRFRLEILPSGVTVVMLAGDLRSVGPGLPIVGQALAHLAVSP
QQQMTVSQLFCALPALEQRKCGNEKYLESFLLKYPSLLTVQNGMVRMAPTSFMQLRGGVP
APLPTSRARVVKLQSPVPEPPTSSNTAVEDAKMNKLMALLYGVVPFSYYVPLSFVTGHSR
SYMAFSPGMPVDDVLEELQRVTATTLDCRVIGSGENDVFLRMMDAERRPYINDETRLSSR
YEVLPLGAPLLEAFLTYAAKGPDHIQRLRSGIAMSDLKDILPSELLKRLHLYDSTQEDAA
CIFVFDRLRHLFDVNMTAYMVRPWEVLAAHAQPSSLTWQTTPIPVVLRHGLMALEKKPLS
PEAFLNALPSTSRKQLKCAYASVADFAAHHSLYLFLKDGLIWTPYLAAVSQGARVPASSR
NASSGRHLTDAAKAKMMMELLPLHHPVDWSRFCTQPSVRDLPFEAGNMRQEFFERHKECF
RVYEPLGTTALIVGRRDGIPPPAKLLRPPCNSLGDLVRQVALLSIDGAQEGNILNQLSKE
ARLLVKRYGTLEDIARQLPMWFDVRNEMRDPGNALISYIATDQSRPPCEKQKPADE*
>TCRU_2501 FKBP-type peptidyl-prolyl cis-trans isomerase, putative
MYDSCSSVDGEGGFSVPVDKKNIPARKSMRSLFAQDALQSKQGVTSLRYEDQSKKNKTVS
LSVMEGNSAPGYPPNAPSPLQTAVQAVTIAYSGDTSMGACVVAVCVPHANAPIATPLIAI
VDREKRPRCRVPMDGGLQFLQNESSPQYASLYDPSLGSHWTLMFKGRRECTEFFSAVHTT
VHYTEIDIGAAPRFVEWNNETNAEEGALQVKLASGDVASISYMAWLLRRMPGTRFFSIGK
MVEEVPPEAPCEVLVGDGSLMAGIEEALVGMQRGASRLVFVPPKKTSIRMGMGNPEVSPS
DTVVVHLTCQDVAVRSDMRGGHKATVASPLEKRFSNSGTQAKTTSPAPVTQTEPSSKPVP
DAPAVVGGDLSTLLQAILLQMLQQQQNSSGSSISSSNNTNNNNNSTGCDFGNGVSGQWSA

LERSIDRVHIQLSSLYEKIDRLAIAETLEKNNAAIERIVKRVVGKAPAGEVDVEEMAKDR
DGLLATIERLKKRLEEETNNYHRALEAMGRHKDEVHGLKNDLRIEQETHESRMRQLEEHN
RLKFVEMEVRHRQAIERVAEEKLREGREIGLKEGLQLGKQEALEAAGGHSDREWKDRFFA
SEQRALQLEAEMQERESHHISERRGLQEQIDALHEMTEKLDQRAQHARITRQTGVEETSR
QCKLLRRAMNAAYTHMEIQLSGMDETVNVTDVLQMLMVALRSETDTFIDEIKKQAEFFCG
LDSQSEVPMEGDKSRVQTDENASDHLEATEAEAMDKKRTTALFPGKEQKTSMTTELAEDE
CVKIDELPPVPPQDLSSFMCDNPPNVFLESVEPVAKDDDISHDFVRKDENKNGDLCNVAA
VTSRLPKSESNDDESDW*
>TCRU_2502 retrotransposon hot spot protein, RHS3, putative
MDHWVLYEPKVQNFPLVDGLFFVDSNPKTLVGLRMATAGGHHTRASTARQFTEYLAAYFN
GWEELSRDMSWEIIYVQHADSTPMNDWQRCDVVNSNNVSDDESREIAAFWKEEVRQYQVS
VSYRGFRGDEALRTEEEPSK*
>TCRU_2503 retrotransposon hot spot protein, RHS3, putative
MPGGIVRVCVQCEVASCGGSFWRRGDGNGSEGGEAPQSWDYKKVDDTLEKDDGVWQSGAP
RPRLLVLTSEKGWPYSWRWKENKSTRDCHVNCEVDRVWQIVKGDLTEWFSSHGGNDFEPK
QRLLIGMPGIGKSMAAGSYLLYQLLHYDAEQLPMVAYVVGSQSFLFDKTTKTVSTYRGDP
RIDDVVNIFSLRGVKGYCIYDATLACRQPPAGLPCRGWGMIVVTPPDKNDYERWAKKWTL
LQS*
>TCRU_2504 retrotransposon hot spot protein, RHS3, putative
MGLNDFLQNYFDGRVVEEFSENVYLKDLLSSPNDFIQDEVLLSPIKALPSYQELKKEREE
FYVLSEASHKLNREYIVTLRHWREFKRKDTVTPLARAQISTACSYVLRVERRRAEEGERR
ERQELGIDVSTGIKYAVFKGRVRVDKMRLNDFLAMELDGRGAVDANWDVLLRSFLRTPRS
TFAVREYWAECRHPIVTIRWRGL*
>TCRU_2505 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MLYIQRWYASGKNRATALYLWVTDSNRSFYVGRVAVEEAVNWEFASALLYSDGNLHLLQR
RGNDKGRAISLSRLTGELKEIESVLSTWAQKDIFFSSLSIPTAGLVAVLSNASANNETWD
DEYLCLNATVTNAKKLKDGFQLTEPDSGVMWPVNIPDDKVRHVFLSHNFTLVASVTIEEA
PTADAPLLGATLGDTNSPLTMGVLYTADKKWVTIFKYEKKPKSGTWEPKKEYQVALMLQG
NKASVYVDGKSLGEEELPLQSERPLEYLRFCFGACEMHSSSVTVKNVFLYNRPLNSTEMT
AIKDRKPKEEKGSGDGEDKKGSGDGSMREGMPRVLLLLLGMWGIAAI*
>TCRU_2506 hypothetical protein
MATSRNYTDVEEQLRAWQRKQEKKIVVSCMDWQNIESNLPLLIPIIGITLVTCFVFMLIP
FIGRMKSGKQNPGLACRYSANLGSSRALLFASRFNAPLFSAFLTIWLLLCLANVVFYLMQ
VAAKDPTWAERVLTTPDGFLEPMVLLYIVQYWGISSLLIHVIFTSHHYMVGCMASFLPFL
VSFYQATRLQGDEVDDWPVIAIKAALLFSFFATVAFTVPWMRNEYRIAMREIDAHTSRAL
GLRRKTGKMPERKK*
>TCRU_2507 Protein transport protein yif1, putative
MSAFSPYNSASPQPQPNSPAPWGGNPQEIMLQMGLQYGQSMLQGGEQKFMRHMPVISNIY
RYFRVDNQYVKRKLGILLFPFTRSFRKDEQGPGCEQEVTGGSAGFGGDSAPFSPISATGR
TYPTTSTALPTNNVYALDLYLPLMGAVTYIILSGFVHGLHHHRVTNEDLLGFASALVFWF
LGEVFVLKMVSYILRIVPDINVLELMALTGYKYLTVSIIVFLRELLQFESDAYYIGTMAT
YILFANGVFVVKNVMRMYEREGRTPPNARLLAYSAAFLQAPLVIWLAVKPFR*
>TCRU_2508 chaperone protein DNAj, putative
MLAFSVPEIPRLEDGAEEISFRVDPKLFFGLATRVRVLPRGLALQQQARTSAQVWVEEQL
QHSRRHGDPHAMSGSDLDESDDGSTGGNGEGRRQQTFRRKKFVKLTDEDLGVDWYEVLQL
SQNDGSTEEQIRTAYRRRCLETHPDKQKDHSDEAFKKVQRAFDILGDSETRLAYDSSRPF
DDSIPNETLPANADFYATFGPVFERNKKWSSERDLPSIGDDNTSLKAVYRFYDRWAHFQS
WRDFSHLVELDEIDDSMCREEKRYYARGNERQLNHLRKEEQQRLRTLVERARKNDPRLRR
KREEDEARRQREKEERELKRRQLREEEERRRAEEAERERLQREEAQRKQLEIKNEIRQAQ
RDLLAFLEQHGLLDETTTNKLLPHTVRRPNVVWIFSKVSTPAQAAAILSDVMSCSTERRP
VDTTRGSEGVGNRIGDDDEEEGLTVEAVLRFNALVEENERRIGVTRYGEPIKKHPPSSTD
VVEVAKKITPKPTANWDEEDLVRLQKATAKYPPGAVDRWRKIAEMLRGKFTEEEAMRKLN
EITAALNHSNNSGQNTRTPVQKQPPLSNTSKFPPSAGGAAAAVPPVLSTEDWTVKQQKML

EQGLRELKEYKERDKFQKIAAMVDGKNAKECFERYKYLCTMNKRK*
>TCRU_2509 hypothetical protein, conserved
MLCSCRRAAVPGCGDEWGPNTERLSRRRGATHCGRTRPEGPHGVLERPSLCTQPQLKAKE
HGLPCSDGDVQTKNEKSINRVTEQAHRVELHAWLPTAQAMVGRVLVRLSV*
>TCRU_2510 hypothetical protein, conserved
MGTTTASPLEKVPRSVGCGAARWFACSPTDRTAQLFHCGHSVGITRCGGVRKSRSPDEDG
LVIVWQLRTSGPSPFRIALAARPAQRRPDTAFLQECRHQGAPATRRVGCGDFHQTCSGRA
GGVAFLVRHTFPCQRLLLVAPTAWRPPPSACAHRPAPAFTW*
>TCRU_2511 hypothetical protein
MKLTALFQRLLFLVVISGSALLHGVSARASSESELLCSPLEIEPYQKSFCVINVRDSQQE
PTMAFELEEFLVTPQSSVPQADLKLSPLQRGVDVTTLTFDVSASEGTSITVNVMYISGNQ
SFPIRNSGVVVSVLNWPAVRMGPISCNVPSSGLVLRGTTTCGAALYDASNRPAAVHQSDV
TFLEEKDLGFFKFISGMGKLVFNFTAASFPSMTAAYFTLLLTLKGSKDVYSTNFPLLYPD
LFPAASFSTLSCYNETTPIVCTLRALDEAGPVRINMDYFRIAFDMPDNNVERGKWVDNTK
AFDVYSRAWAQEDTVFLSWKLKVNNFINTERLHVYVVSSTPGNGGKRVEEVRGSPFLFVS
GVMPHAAYVSLRGCRVSSITSGNRTQCFIDLHNGVTGDVRYFNLSSTLGAVFENITYLPN
GPIYKTPVVSFVYVAPVLNTRSEDFITLIVGGQSAIRSPFHMNVFPRRSSEKNEDSETVR
GSNALVIGVGLAFFGVIIGTGSFIALRSTLRLNRARQLRAMQKVQMVEMEEEAGCSATGK
VGIEPVPQPHHPQESESD*
>TCRU_2512 hypothetical protein, conserved
MASDDLADENNVLRTRVSVLEQELKQRTADCTKLRDELRAFEELKKKNESQRELILALRG
ELDFLRAAHLSAVEALEKKKKEDRDREHRESIQSINARLGADASPKNGSPKASAPKLGAA
GGLVPTSSGPQVLLKSSNISSLGFAPVRRPVDFLGGQQNSLQQCGTAGSGNGDEDEAARL
MEMVHDEALLDVKYAEVADQEEKELLERFEALRRR*
>TCRU_2513 zinc finger protein family member, putative
MSSALCFVCSRCELPICSRKDLLMAPVAGGTTETAFEYFLEDVLALDISVPCYSGDEVAE
VSVTVSEEILASVLPPGAQQLALEAVVASQRSEQQRQQQVEQNDVGTSLSSPRGGSSPGS
STAALPHSSSSSSGDNAEVPVEIAPEEANSHNATGTSSRGALTSENSSYQQAIQALARYK
RVQETRVDLVCVREDVLGCGLSRCTRDRVAQSSSASSPPASVEEAQSSSSPTQWFSHPGN
FIVEESFIKVRRRTKTARYPWFDAYDCRGRLECPDCHLGLGYLFVRRSNEHPGSEAVAVA
APSAGHAETGDDGTAEEVPEPQQKRERKEEGNDNEKKQKQQNDGDENVLQYPSTFLGLEL
KKIRERQWGLRDFQKRYQRSKELKTFREMFPEAEELENLYSRLTALRMQSELYNNLLRKH
KERNDVQSALLQSQKERIHTYEEKLRTMQQIIEAQREQLEMQGRQIKHQEELVKNHKSQV
HTQQQQIHVEQLLLTEQSRTIESQREQLNLIQAHLRARLMKEKLDERCEQLTRLLYDIGG
ERRSQILTTDTATTTLQRLSRHPLPPPHLMGVVGYDTREVRETETEERGMEYRSTDGLCQ
RPTSDAVAPSRDDLVTSGQEGVGAAVSETRGCPSRASPAFFTPKGLDGRSAFGRSPDVSQ
RTAAIMRRITEERARRGVGKDSLPSGDISLGSAMANDERQNSDGACALNSRNVSLLLSKK
KE*
>TCRU_2514 CW-type Zinc Finger, putative
MRGAQGAGAAALHSAGDGGEKNVASTARYIPMPESLWALRHRFPNVTRSVLLQCVRCHRW
VAQPVTKHPPDELATYPTLLGKAASKTKGDRHQKPRKEKEEWRSPRLRQHYQKVVEAVKP
QKPRIQEEPKERISLYIPNPANFTCQWSYCALEDVWADLRDNWLGDLYATLDGAMGNEEG
GNSSSKSTRLRRSPQSQNERINEELTRELHGKRSERLAKKPYNGMDVKQENSESNGSAVE
PPSRGRIAQQVDKLIHHDEAVVASFCWVSCDSCGKLRHVDQPFPGGAPFVCALALNIGSC
SVPEQEGLGPIFSSETDHFSAGDKSVAITGDAALRVAIEAQAFAATSTAAVASTGNEATK
LTARSEHRGFRRSAGGLPSACKSRASVELSLPLLRELTSALRKRALGTFVKNIMMIPEEV
RAKREDVARASLVVSEDTRHMDSVSPKRECGESDVKDVQNSNSQREERDNPNQEQEEEEK
RSGATGEEKDTNGASDGTVTCVAETHRGEEAPRPYRRLGCPPRRALCKTREGTCPEGALT
RVDLLPLPLRETTRSAEVAELPTTVKLEAVRMPCEVSNSIRTIHESPNGNSAKREASVFP
LEAPTVSSAEVPIRESLTKNISGRKRTRRQSNLKDVEENNSDDNKIHTTQAAKPQGVKRR
GRKPRRVENDETNNTVNEEEVEIIHWVCCDLCDKWRIVPEKISEDTEHWYCNMRADGTTC
SDTDDEIRMKRLEKSGRRRGRKKKKI*
>TCRU_2515 guanylate kinase, putative
MNPPLDAIAVCGPSGVGKGALLGRLLRDFPDRFGYSVSHTTRAPREGEENGREYHFSDRA

TVEKMRDEDGFIELCEVHGNLYGTSVRAVAEVRSTGKVCILEVDIKGAQKIREKTGLLNA
LYIFVTPPSMEDLRERIRKRGAENEEVLQHRLRTAEEELRFVEENPTFFSHIILNKDLDA
AYEELLRVFNEAFLRCNMSKLERNSE*
>TCRU_2516 YEATS family, putative
MRQGDRGAAAVEQEHVLYTGAMLIPFCVGSVALPLSLCRASSSSPLLAAPLSVPRRKSKT
RRRGEKKNQQGTSHEGDGDNPHDYNAGISRCTHIRYSYLRDGSSAAQDLAYRRALYTSGD
VRMTSVSTSEEKAVTTASQLYAVVDRVVFKLPNSFPEPRREIRHPPFFVVDDTWAEHLVE
MEVHFHPWLGIAPFTVSHMVLLQKRADFTPQLLSSTFGQNKPPPTVILESSDTGVLPSSS
LAVATTRCHSKQREGPPSEAHPLVVGEHDTDNDEFYAEERGICVKFEDLEEFSIVSERRD
AIRIFHPTLNVARFLATVRTMAQPELEPPPSFCFFPKQKSAPSHVQLNNENVPTVDCCRT
AEKRNRSNDTDGENHSGALDGGLLPPWCFPFEAIMHAHEPKRRDGAVDAMRAVLAALRKE
QSELREGIEQKISLAMNNAEELRGVIQKMRETCAILKKPVR*
>TCRU_2517 chloride channel protein, putative
MSLRALSKDCEEVEGRCENLPQSCFTPFIYKIGLVSPGRDLWNMLLKKRRRFFLPSERQK
MERYESVDTYEPATIVYKDHLESRNQEPRWFIWVFVFGLGIASSVIAIVVVSLLHVLNGI
RYELLGFGLRGFSFNDSNRYAMTNRTDLDIAALFEGVGVGLYGIEPRSLKKGYLMWISFS
LVLSVISSLICLLVPESIGSGLPEVMAYLNGVHYPMLGSFRVLLAKVSFIIFSVASGACT
GHFGTIILTGAMLGAQALQRRRYFRCDSVHIIECFRNPRDRRVITVIAAAAGVASAFGVS
IGGLMVVVELISTILPVRFAIYVFAASLVSSLTLQIYFSFFSYFSLRDRHSYPHGELISE
MVQFFVSCVSFEDLVRMHIFYFIPTTLIGLFCGVLASVFVRLSSFALGLRRWLEQRLETK
AVRYVLPVLFTGIYVTIHFWVAAAVGSGGWSPPAPSPSEPPRIGSDSIRLPMLQQTMSNE
SNPAGLHGAMGGPCVAVPSTLLTTLNVTSISYYGANGFFCSAPTAVEDQVHEERWGMKPT
LSVLHAYASLAFANADSAVQTLLSWHTEEMLGAPVLVIFLSIYFLASALFLGVSLGGDTL
LPGLVIGAAVGRLFGIGVNYAAVSVVGAEAASSWADPGCFALIGAGSFLGGTTGLTFSIC
TILMESTSDFQHLLPLMMGITIAKKTAELFTENINTILLQMRCVPMLDFENEVHKYPMFD
ARHVMTSHVVTLETVCTIEQILYVLRSTRHNAFPIESVRDRTYKGIIVRQQLEILLWHVY
FTPYPSICTYELGKKVEARLFYDKLLGTLPPLETRLDVRIDLSPYIDHSGFCVLDKTTLP
RTYTMFRTLGLRHLTVVNPENRIVGIITRKDLVTDRIIEGIFAAEESRRAIIEGKSLALP
DGALITAGGSDSNSISSNKRMDKTDGNASYSSNVLESSARRQQIAGKEYEFYRTGDWLVL
GRYDGVWGDVAEGIEGLMHPSASTVAAIRAQAATRRASFVQEPDAGGPNEVNPRHVAKRE
SISLLDCLPDVIQTRKTP*
>TCRU_2518 hypothetical protein, conserved
MFPRRTPYENSPARRPNIITVATPGVTSSRSQISRYTGVDGVDVLENACSWQPSNNCITN
EVTAVEELAAFRRGRGNYVLTAEEDPPFLYHASCRVAPRLLHNVMASPEMDEIAYNKFSL
NPLNWFMMLKEVIVSALFSISSKRCMYSQARMTNLGGERDQAACQREIRRAVRIIKERQS
VTQGDNDVTAHSSPGRPLHLKLVLFGCSRGATTTFYTAMKLPLELAQYVSLVVVEAPFDT
LHDVIASSCWFPRFALWFFCNFCDYGGNEPYSFVPGRVQLRCPIAFVMSVKDTRVPNKLT
RRLIETVKNECPQIPAVEVLELKHSRHPLMAVGNREDQDAYVAFMERLYDTYCS*
>TCRU_2519 hypothetical protein, conserved
MLPATAKSHMGAYVSESPAYLSIHGNNRNSDTGASQEEGEVLENSSGNEEAQCPTAPRLI
DDYPEPLTGKQRELLHRHTATMVHRFEMLRKGARIIERGYNSLQSLLSRLEEEKTRLRAS
LDELAKPAETQILGTSHTEPTANPTEVKATPGSRRPGGLLRSAAFANMHSILNAAKREEQ
QQRSNVTLEREKIGKTTRLKIIEDDLAEQKQYLAPLAEKYQKSCALLEATKGKVLELLRL
HDEMQRMEVSYASRFFLRASGFHESEGVKGTASYDVFFAPAKYTDEVQDMIREQVEEILN
EYLAYRSRVDPVLESLAEEQRNREAKRKDQLLQLIGIDTDNIEVAASKDLGFTTNMVTKT
TNDAAPPALRRKDGAAAVAGQISDVEDDNDDNDIGGESQEKKQRDQIQSALAALDDFEEL
Y*
>TCRU_2520 hypothetical protein
MQLHSPDPYFYDNEIDRMLEEMRAQRQQQKRMNKQRKECADNGRKKRGFMPADIFSSLLE
RQKSMKKTQQRARSLPKTSFLAANEGEKSPPLNDFIAHTTPQSQEERDATTDAFNDDSSV
ELLRRELRIARKENALLRRDMYTTLTTIGRYLAQFAGKNSVRRKLDVDTGEAENTAGLSD
NDSPTLRLPSATSVWELCERGALRLGPEEAALVRSLNEVIASSLERYVGLEKQFAQQGPI
GLQPEREDNCVMRQQHTSGEEGVADI*
>TCRU_2521 transketolase, putative

MNNSKKDELVANCIRCLAADVVQEANSGHPGTPMGMAPIAHVLWSEVMKYDSKDPSWMDR
DRFVLSNGHACALQYAMLHLAGYNVSMEDLKKFRRLGSRTPGHPERGFTTGIEVTTGPLG
QGIGEGVGLAIAEAQLAATYNRPGHNIIDHWTYVFCGDGCLMEGIGQESLSLAGHLGLEK
FVLVYDSNHISIDGSTDLAFTEQPKQKYESMGFHVIMVDNGDTGFDAIREAFEECKKVKG
KPKLIVLNTTIGFGSGLAGTEKVHGAPLGDSDIQQLKRRFGRDPSKKFYVEEEVYDVFKQ
HVAVCEQKHEAWKAAMKKYAAEFPKEAAALEAQLKGELPSGWKSQLPLNDASKIATRKAS
ENTLGTLFSIISGLIGGSSDLTPSNLTRPNSAALTDFQKATPQGRYIRFGVREHAMCAIM
NGIHAHGGFIPFGGTFLNFFGYALGAVRLSSLSHHQVIFVATHDSIGLGEDGPTHQPVEL
LAFLRAMPNLLVFRPSDQTETSAAWALALENAKGPSIICLSRQNTVPQSASSMDGVAKGA
YVIHSADKPQLVLVSSGSEVSLAVDAAKALAAELRVAVVSMPCQELFDQQSVDYQKTVFP
DGVPVLSIEPYVNYGWEKYSHYHVGMPGFGASAPGGELYKQFNITTEHVAAMGRKLAAKY
PNGNAPEKRVHL*
>TCRU_gamma, conserved domain containing protein, putative
Elongation factor.1
MASSGDDSRCAPGTHPHTIPCVSLRELDELKIDYSHTDTRTVAAPYFFQHCDAAGCTTLW
YNKYNKYNKMQCMTANLIRVWLQRMEHVGQYALGAALMFVEQRRHDIVALCVLGGRACRR
F*
>TCRU_2523 hypothetical protein, conserved
MMGDCENTSAFQKDTVNESAVRECKREAKKALCDFFYGDHSGEHDASHLHSICSPDVGSG
GAVDQQAQEQILTLRETGKPAPPTTPQGLSEESPDTPPTPASAGASSQAPPIQASTEPTV
LAKQAEPNTAGSVPPKQSQGGAEAMRPPQEPPKVSSIHDTATQGDPPTEDRAEQTLPPAK
ANDNSSDHSEEGTAEESTVDTPASGAVQTEGNESETPGSGLKKTKTPHTTVEGSNTVKPG
DSESSSTAPPAGESDAATTTTPNNHDARRLNNNGNNTFTEEVDQKEAAIKPKSAPDGTDT
AAANSEASTTAINISTNTTNKTTTGDSDSSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>TCRU_2524 hypothetical protein, conserved
MMVPNASKKRTSFANGPRILVASNASGIISVTCGGREHVAADNTDEVNERNATGHKPFVL
ENGVAGSGFVAESDADGLTQRSASGRENPNYENSPRSIPETV*
>TCRU_2525 retrotransposon hot spot protein, RHS3, putative
MRLNDFLTRELDGRGVVDNKRDVLPEEFFKDPTKYIRNKGALNEIQASGRYLSMKRAVKG
EVIFDEDIRKLCDKGVNSLPGWSLAAAEVKAAVHNSNKHFLDAAAEEVRNPTTTSAPEKL
EGLYESVHNARRSHAVELPDGVERKKTGTGMGMHEGKPEQSWSYREADAAIEENDAVQQF
GVAPPVLMVLASEKGWPYSWHTIQDRPKDVFVNREVEQLWQIVKGDLTAWSSPHGGTDFK
FERHLLIGTPGIGKSMAAGSYLLYRLLHCDAEKIQAVAHSFGGSTTYVSDKTTRAVKRCS
DEDMCVSELRSLRGHGRNVYIIYGVAKEGTPPPRHFAPTSG*
>TCRU_2526 PAB1-binding protein , putative
METTYSSNADRLEYLYLNLVGQVVQVRLVDGSSLEGIFVSRTDVDADTEAGILLCCTRCL
PSSKHKPLDPSCLELLEDTIIPYRDVVMMEVQNAKIRTEAPGRTDTVRSDYSMNKIDWAD
EGANELLDSEQHQTGAWDQFEANEKNFGVKTTYKEELYTTRLDHSKITEEQRAHADRVAR
EIEVSATRGIAHRMEREEFLKDDGGMDEGTLYSDVQRPQEKKKTYVPPPVAAARKAAGEM
QTAAPAAAPVTTPAAATAAAAAMAVDDNAMRHRRMEEEKIPMPHDNHPRSPGFNPAAVPY
TPMKTGAASAPVLDFMTLLADTIMSNEQCYESLPNWPGTCMYYDQDDSSYSQQNYENAVV
PPSMGAAPQMYVTPQQGLPSHHRAYQGGGGRMNPSQQVPMHHMHAQSFHQQHQHQQHQHQ
QQQPQQQPFHVYGNYMPQHQHNAPMQEYPPNKGAPPGPMRNNMRQPKSSSASRVEPQQPV
TANTSVAPPPVPTVDSAPTPTPEVKHAPKLQRGRGGTAPQRGGDGDGTGDAAGGNPGAAN
PPAGPKKRSGK*
>TCRU_2527 hypothetical protein, conserved
MQRAGCGIVRPGRGCHTTPLYCSLATISTGVFDHLPFQHRRQHAFNTLPLHDANHFGGRT
AYLREIGPVNIKKSGRRFKKDLRTVQFNVDIWCAQQTLRKRWKQRDWEVIEVPFRLAPAE
QQRVIPEMYTDVPPMTDPERHDFSNIRNKVYDREELQGVLFGASGPLPYPPLQRIDRQAM
TLDKFL*
>TCRU_2528 hypothetical protein, conserved
MPHTTPTAARREEEAAGEKRDVSSRSGSESGSKNNTNDNDIAVEARRPSRRALHRHAVKK
FNERRKNEERRRLADERDGKLLDRNNATETVAGGSEGTPVSHTDGGGELQATQLLRVNPM
EKSILINKWEFEFFFRTIPSELLQTPAESKGPDTAVVPPSSSSLYNEQEQSLVVLNDDRH

RNSGGSISLKTLMQSSITKSIHVRRVEGVPPLPMKTPMQPGTDLDQPTRNYLLPDTTYNV
HQHAPGFERDQNAAKRSLLACAVQEWRGGEENVLLLSTGEALRSVFESTYCDEKPLALEV
RRMGPTLLIDSHNERDFRTRVRDMREKALLGKALYRIHNDVFSWKETDDDNYEGAGGGVL
SLPTHRVGSLALSKEIRTLSRYSHIFSWEIGLMDVLVGIDTPIVIDRRDNTEFVLKLENT
SVVMTPQEIQRDALRCWFDATLANVPHVGIYVHNDGIIQRYEVRKVQELLGIVEGSMATA
AMNFTMNVLQWLVKQCKKDGTTYAVIRNYESGYLEIYEYSRDERLEKFLPDDGACGKGNF
VGVNDVINNSKFNRGREKSGVEEITETQRAEEEKSAEENERLNWGLATMCFRMGMHLKDS
EQKAPDAVSLLLRSFAVYFMQRAKMDEACSHVCEIAKCLPALIGRLIKNRKAAIEEAGGI
IQLPEIYREAFLACGRFEMRLQEAAYDETLSVAIRRAFLRCILPCSAALCVCVARTMEEF
AAERRVYMQLRAENNRGSHVHIHSLIAKDLLQVVVEGLLRLEQMNRILKSGAALTKGMPL
GTNVESMALMDTKTEILDVTPLETTVWELYTDVVLLVMSDRTPFTADVLVELSRRIKARE
QRRRCGGGSKDCDHEDNHNSSGSGSTETIVAGESTLAWLSALTPDVVSLSFTALRFLTKA
GLQSKRLLSKTAQVYYHVGHHYFLTDRYTKALESLHRAQSLFKAMQQAPADTVFGACCTS
SATVTLRNVQQSLGELYIRMTRLKTRTVPTEMKLSLQQPLLMGEVQELSQEEENFFRHAV
DSFTSCEAKEQLASALRKYASRQIGQVAFSGQQADVAKGRHIFSMLRKVGELTSNDVEID
WEVLRLFTCSAHHAALQHRAELILSQWTAGGGTPEAGAVRMPLKLMSTVHPVECALQMAL
VSLSLLENKKKVKMHQVMGLLRASVAHLMVAIKDAHAASKTPGALLVRAMSTWKARCTHE
WVCRISIMMSLRAMRVMVRLLTGDKASEAKQLLRRLIEMEEKHSEILNKSEICTGKCQFW
RLSETLMESLQDVAKW*
>TCRU_2529 Zinc finger, C3HC4 type (RING finger), putative
MGNRQTVQPLIGGPRTFYLVSGGPRIRYVGHPSSAGPLIFHIETDLMDDNEAVDRAETIQ
LPVAVPSRQKFRLVQLDSKNRESGFLLSFSIVMSEPGQTLRVLAGVDIEYRAGEGVQLMQ
SEKSQNPFCLLEFVSPEEFREEIEVSEVLHPEKLNKAIFRYSENGARRLTYAPIAIELVY
EAPTDRAPSKSPDCISPSSAKSVFASRQECENSMSHNSHASFAAKLLPQTERMVQYTFLD
IPEGALGRTKVSLLPKSEPQEGAARIVYEAKILRQLLQHGTQVYELDDVFDLGGDGSENN
LDGNDEEEEEIDLCVICLLNPKDTTLLPCRHMCLCYECASILRFQQNNRCPVCRSNIDRV
MTL*
>TCRU_2530 hypothetical protein, conserved
MISTRYKVIEKPGGLGEVVQVAVKDIGVNTGENTPALFVSPLQTLTTTMGVNSWSQKETT
TCAACARRQERMFQLEMQLQQLETQLRVNNILNALMNSMEAQGTAAGESAGWDYTSRPHG
TRRRLQRQSSPLNQEKEDEEPNETLLEMMREELKRQDLLHALMDLMERPTYAERQEIKKF
VPKNVKALLFTPSKNVFSIPTPEKSM*
>TCRU_2531 Ras-related protein RabX1
MSSSSAPGGDCDYIFKIIVIGDSGVGKSSLTVRLSEDVFYKDYASTIAIDFRMHQMNYMD
KRVRLQIWDTAGQERFQSVATAFYRGANGVMLCFDLTHRPSFLHLDQWIERVRQQALPGI
PCLLIGCKSDEARSARQVSKEEATAWAQQHGISYIETSAKEKENVQYAFQEITKEIFLDM
KDRNGKPMASGGKSAGRSESVRLDSQGGRRKTSERGRCC*
>TCRU_2532 small GTP-binding protein Rab7, putative
MSEDLAYKIIVIGNVGVGKSNVSSRYCDGTFYEDIVPTIGMDFKYCHSTTLEKKPRTVRL
QIWDTSGQDRFVTLTTAFYRNCNGVMLCFDITNRVSFEDVDEWYDRLRTNCPNMPPVILV
GCKLDLVQREDVNDIGISLGSQRQVEKSEADAWARSHNCLCYLETSAKENRNISEAFQQL
ATYVAQSTTPPLEGGRSGINGRHGRPINREIEGKKGCCTAF*
>TCRU_2533 hypothetical protein, conserved
MILGVGDGTFAILFVTVIGIIVTLIGSYVQPRLALPIGLVCFLLPFLLYACILSAPHGRL
LPPLPDTPYNRERRLPPDAVVVDQLLPVRIGVMILLFLAFFAAVGYHVLLVIWEPPYKAP
RVRCLREQLKELHPTWYR*
>TCRU_2534 flagellar protofilament ribbon protein, putative
MNSAAQNAPAISPTATMSTGPLDTTSKKRLFMMQRAERLRDPKVRHMGIDKEALDDQVRE
KEALRRLEKERNEFFDRQALLMDRHAQALQKEVNEIRAGREKELQDYRETFQKKHMRREW
DLNDPTWKVKDLPARVGDDDPRNGVSSLQKFEGEDLDFKNRRREQQLQQRDWAQQQVEEK
LAKKWMEQEANHAFDERNEEVNRRIYEVERNIAEQRRLSHKNQAEFNKALAEQKRREAIR
DKEEDTRKGLEEIRYHLEGDFLNETETMVGELGKKVKSDRYKGMTAEQKEQLYKDQALQR
DAMRRRRLLEVEEEKHWGQQENLQLRMANALERQRERERRAEREAVAAEQKKQKEAAEIR
RKKLDELYTNAVDEDYYKYWDLCM*

>TCRU_2535 Zn-finger in Ran binding protein and others, putative
MQRCVASLAGTAFFGHLRGPSQTLALGCSSRAYMISATPCCLGRRIKGKRSRHREPAEGD
WLCQCGELNYKSKRECFKCGAPAPPLPPGVRRPSLPGEDPHDWACPCGQMNFRGSVVCHK
CLQPKPAPPPLPGKEVTLWTCPKCKGVNRSIRNYCFKCSAPSPLLTFKPVV*
>TCRU_2536 hypothetical protein, conserved
MMSSRLNNLESVEGFSSLLYGGDKAALQLLTEIGWSGMAAAMGLSLMQKVLQESTSAYAI
FFVSQTLRQLVESKFGTADLVPLESFLSWLIVQRHNSLNASSVDVLIRLLCAVVKQGFCD
APELQSFPHRVTAALKLEESNCSDGHIALSCAILVAFIEEAERAEGTVRSLINHKRMIKC
LRNACLLPIFRAASQCLKRLQQTDGKAICGLVALVKRILLFDFTCSCDEAADDVMTCEFP
LEWAADLVDQGLLVKLFDLYATPVTDPSFLCDVLEAITPLVSVNASLYSSRQQQAEWMNK
ILSATLSIMESRSHLEEATVLREFCRLLNRIKPNFTIDEMRRAPCYQRWVRAVAEFTKLC
FQNWHHARQSFLSLTSIWAKLVGSQSYCKDGCTLFELLAPDVCLSYMMSHQEQAVRFATS
GEASLFGEYILDEDAETSSLEFEFVSQILRFCGEEAEKYIVKEISSLLEALKIPEVRSSP
ELFCVCERLAFIITLASSWLGSYRFSRNGRALDSTVLLACLNVVSQSSQMNFSRSLPSAT
SRHFHRSLLAFLRFAWHITLLNRMDGSKKLQESLQLSLAAKDFGTLATFILGLVVDEVLD
CVSSCSEQTVFEAIHLLSEMAQSPSTAVVLRKLPQFDGTRLVLDASNVKTSRNAAVFYRV
EYHLSRIRAQVHFLGCNSESSRADFLRPLFEELEMCLRRGMAVADGQLDFFTRVICLWRG
VFRSCVGQNEYNMLLRRFFPCLFLLTQQLQNHLGTVCGVQLLRLINEITENRYRRINFGA
NGVEGYHLFREVSRSLEMAVHLVRRALGSGELCLGEWGLKCLRILIHTGRNILSGGYCNL
GVLRLYEDKALKTCLTVLWQAMMLVDRHRFCQYEKLAKAYLMLAGELLRDLHLWFLCEVP
VGELLHVIHMLEISLGYCISGSASLASQSADALGIFTGVLCCAECDSVEHRDRVCGSLLH
TDPSLFSRLLRLTLDVVLSRKCPSSKAEVLLRSLIALDGESFRRLAGEFAEIALSAGKDA
EVRAAFELLGSSACESVRKNNRSLFTKEFQHFSTLVTGCLG*
>TCRU_2537 hypothetical protein, conserved
MPPPKKSVALRHRAHMIASSVEDQEAALMEWRARAQQGKETLQRIRSKMDAHKKSAETTK
RGGRWLAEWASLQREAVSRDLELSKAYASCAHLLPQSLRNKLTEQEEQKNELLGYLSERV
TRIRKELERLHKQKNQPSQEALRTLSESISALRKELLEKKVTDVKAEKMICGEANGETDK
QSPMETLQRLIQSTMKTFDGICESIDGKINAALVETYRNALQTEGENTTSQAAACIDRRV
GTVLQSQNDLRTVSLILKTYDSEVESGTTAAAISDELYDRVQRALPHLSKMSARRVVDEA
LRQKRGRVYMRSVILQYKKRSTELLESFKKAVMAEEEIMKMRNAISEETRMREERQQKTQ
EELERLRIAREAKDASRRAEEEAKKMEEDEKHQKLLCSREAEFQERLRRLREYQEEQREL
QEKERVVQQALAEENALKKAIQKDHNAKRVEERKKEYEEKCRLRKKHQKEMEELRKAHQR
TLETFFKGIERRLGVTYDAERVLQPTTSSQQSVPFVSFSEASQFNLHGYTVDDIMKDPRF
RLQLALMEAGLHQTPYGREVISRGYHVPAAQRPSEENPLSMEY*
>TCRU_family, putative Se.1
MLDAVHGLLKVFFCDAHAASALSRSLRVHELMEHGVTLLEDPMTPRQPIRSSPVRYFFAV
EDASVSRVVEDWMAKAPHRDAHIFALGCTPHRSPQQLVRARIAPRAMRSKDIMLDFAAPE
MLVFHPSMQNGFPQLLSPLSPPN*
>TCRU_2539 hypothetical protein, conserved
MGRCPITYPAMDVRDIETVIWKGEYLSAMSGDKPSSWCLDTLPNNTTDARDPKEAHLGAV
MHAALRCLGMRVRLKVTEEGNIRCAPCTDGATIAWATRPYDEGNVVCRDHAQVCTISANS
GRLLPVVPWDGEERACGAGRLHRHLLNKDCQGHPSPLRRALRPAAAHHRRMLSRLFPRSI
R*
>TCRU_2540 Leishmanolysin, putative
MRADSTYWIRVAVRDEPFLSSWCAATIHRHWEGWMPIRINVSTRDLDDTGKYWISERYYA
MNSLSGNCECECDVVSSAHGIILEGEVVPAAFKLHADRLLVQPLEGPLIVPPFATGSVCS
WFTVRAGHCSAGVANAKTVLCVAAASGGVWAPRSATLEDGRPFAGAMHFACQFYFTDASP
PASPRTFRPMLLGSNARTWQAAAW*
>TCRU_2541 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MVSVLLTAQLERVKEVLTTWNEVDKRVSQLCANSLAQKDLSTDTACSADKITAGLVGFLS
GNFSDNTWRDEYLGVDATVKNGAAEAILHGGGVKFHGAWAEWPVGKQGENQLYHFANYNF
TLVATVSIDKMPEEGDTPIPLMGVKMNDGKTVLLGLSYEKERKWMLLCGDATSNSGELSS
TGEPGTKRHVVILLRNGNQGSAYVDGQRVGNEQCAFGNAESQEISHFYIGGDGDKTRKQE

DVSVTVTNVLLYNRPLSDNEIAAFNPNKVTIQQLKDKSSEPSPVSSDSVDTNASPATAAA
QQTGTLSTPDGTHPTEQRQSMGSSNAGSGGASTTAVSTITTPAAGEEPVVQVAPVSSSDG
HKNVGGGSFSDGDPTVETREGGTNGHEEGIHPQVREVNATALNSSLGNVSQGNNSDAGIM
RGSGLLPSLLLLLLGLWRFAAL*
>TCRU_2542 BNR repeat-like domain containing protein, putative
MMMTACDDGRRRVYESADKGESWTEALGTLSRVWGNKHEGNAKGVRSGFITAKIDNRDVM
LVTLPVYAKTESEEKEKEKGVRHLWLTDNTHIVDIGPASVEGGDEVAASALLYKV*
>TCRU_2543 tRNA-methyl transferase, putative
MSCTAVRVAIALSGGVDSAVAALFLRRCVPRWGDVEALWRLERPLALCEVVEALEQQRPL
SEVVALAPATGNSHDPAAAVKYFPLFMKNWDDAFESDGVGRSWCEAAQQDYNDATDVARA
LGLLHSREILPLHNYSACYVEKCFQPMLDAYARGETLNVDVLCNEEVKFLALLDALLTAG
RAAYLATGHYARTVHFPLLSCENAAPTSLRVIARPFSARNDLNDQTVFLSRLSKGQTLRA
IFPLGHVFERKSDVRAVAEHFGMKRISKKKTSTGLCFVGEHYRRAGRGGSCAGGFRSFLE
EYMAPNCTALQKLTAAGQQTTFINAENGNVVEASGLALHGDGDGVLLPAYSLTIGQLIRG
KSEDGKTVRYYVQGKKLFSFRENYSKGDNEDDDGGYVRHLHTVWLVDRWDHPLLYGKVAK
IYDMKLSVHPQWLGNRERSVRLHCRCCARHQESLRPALICFDWSDVSEKNGCIRVATATV
LFEEPVRALTPGQALVAYISLSKEGAEDAAGWFVVASGWIA*
>TCRU_2544 hypothetical protein, conserved
MKGNTLRGAEEYVTLESAVLFELAVLKNGGYFDVENNTMIAVSGIYFYGDTTVSSAGLLR
VADCTFFGITLFFEPALVHLSGSLTVEGGAQWRVEGNSVGAASVLSMPNSLCKMKLSGSG
TTVVLAHNRQVDSSKAFAKLLPRGTIVTSPAWFVFGCNLQGDEEVSYDGVFPEDVVVFRC
VTCNDDAACYMPGTESVDRSSCSCSCKDGWHGASCLPFEVPDTVVPPLPERAVDGDTSCV
HLV*
>TCRU_2545 retrotransposon hot spot protein, RHS3, putative
MWRCWGWLHVVLLRGRWALTASPTGVAVRLHGAPTTEPCECHAQRHWDSGTKQPRLSFGA
SGTCWPQLGGASGMLHRTGVVMAPRRGSCDGSDAAARHVAGSKVWPQWTMSSTNMRLSDF
LWNYVGGRAAVDERLQCDDGGVFSGAGWLRKRPAA*
>TCRU_2546 hypothetical protein, conserved
MMVPNASKKRPSFANGPRILVASNASGIMSVTYGGREHVAADNTDEASERSATGHKNLVL
ENGVAGSGFVAEGDAYGLSQHNASGHDNRPQLQKLTAQYSGSGVSPHDCFALRNFAKLTL
RELIVDGTVRVRVLGVAASSGIVWSCGGLVSRRVWNCDSSRRTCAALHACFLLLFIFYVV
FFLE*
>TCRU_2547 BNR repeat-like domain containing protein, putative
MKKPYNTSARWLWNNFVRNCWAGSWGVWGNSYGRKGYGVRCGLTTVNIEGREVLLVTTPV
YLEEKKGRGRPHLWVTEGARVHDAGPISDAADDAAASSLLYSSGGDPISLYENRSEGSYG
LVAVHVTTQLERIKTVVKRWQELDEALRTCRPTATIDPVKRGMCIRSILTDGLVGYLSGL
SAGSEWMDEYLCVNATVHGTVRGFSNGVTFEGPGAGAGWPVARSGQNQPYHFLHKRFTLV
VMAVIHDEPKKRTPIPLIRVVMDDGDRTVLFGVFSPMMGGG*
>TCRU_2548 Gryzun, putative trafficking through Golgi, putative
MEFLSQLYNDDAYRDYLDANPSFSLAVLGRKNLRIAEGLSYFFDSRVRFRINYFSDVKAF
LNKGVNVSLGAEISGILKSNWCSKHLRLRCSCVLVCLDWDQLGETAIDEVWLSGVCSQLK
EYTRSFRSKVIIALVTENTMRTSANSTAQIEKLQYDLKMFFGSDFKNFLPLYESGMGKES
AEKLFQMAVGLATKYHKDEMSRLKNSKLEPSYPLVRRGFKLGWHCLVLNDTKNAQKHFEN
AYRTLRKIAPFWPAMELRICGTILLFRVLHIVALESAISSDDMYCRLCEDHIMWIGRAIP
CGSPEFKPMAGFLRLILVGECYEWLLRNCRYVADETRRDYLFAAMGAFEEAIKLNQPSGS
SKRHTVAPVFVGTECHLESHNCIFYSNNSMRTLSVRVKDLLSEIESHNSLSLDAFYISVG
VHASFHAWEQVFVCLERFGRLRIGTYKEAEAVHKIWMCAMQSTGGNLKENIQEDVLFSYV
SLCFGPAVGMEQKNYMKQFTELMKQNKLNHFSLSYPRRGHFAPFTILCRFQDEHHVCATK
TEIQFSLFTASIEMIIVDSLYVVVSWLSSDGVEDLSMYLVSDKGLKLSSNTPSSASLTLA
LDKPGTYHCKSVRGRVNCAGIQINVEWRLEKSLGGNPFLRGTEMLGSISGLLYHKPWISI
VRPVCGVDIEIPRNIAGIEGEEVNFDIVVNSKQDLTGNGTLVIHDVPSLYEFVWDACQEK
KMKMGEGLRKGYRTVILDNIAFISCDHPLYVTLNYRCLRAGKYMVPILFYYKSGNYSDVE
ILKRIQLNVFYPFSTTYTFLKVLPWMVTPIKGDVIVGSETTLRVPEFSRVSIQHERFTLV
HPRYSTRDDVPTIQSNRDSLVYIAHTEREDHSDNFASSKGEEIILLASMECRAPQGLMVK

NLDVVCTQDASLSSVVVSLLPCHVEHLEVLTLSIKFRLLNAGKFSLGFIRMILAPGNGAQ
HIISDFPLPEVKVEDTPFVLSLRGPSIAIIGSPILISFDITNKTENFQNCELLMEKNNGC
FLMNGRTQWSFCLAPNTFKSTEIILQPLCIGTIKLPSVYLRHSTGLASGTCAVCVSDSQR
ICVLPS*
>TCRU_2549 Dos2-interacting transcription regulator of RNA-Pol-II, putative
MSGEKVDNIIERAISMGLNCDEETFEKLRQVPLLQLCRMMSRYLTDEKHIIEALFVLSLA
TTRRKTLLDEEAVVVLKFFLEKLSSLQTIETSVECITRVIEYLSSQRPCSKIVFTELANG
FLPNVRLQALPTRVRRSGFKILKYMVSEATVSWLTTPVLCLLLEAMDEEGEPELVLHMFE
LYYFLSFFVDKNNIVPLKEQYFDSISSYFPVVFSRPPGCSVTREELKRSLTRCMTCPLYL
DPCVSFTLSRLSSPSSFVKQESIAVLLELFSPESAHDMNDLSPHILPVVSHVRNEVIKGV
SLGFSEGDSYIRDCMNLLSFIGKRSHGVLSPVIASWIEPAISGALTSLNSGSATCSAYAT
MFYHLARSDASCGTSLLSHFLPLLLMNLNEIDGGKENAFIILSAVFTGILDLCTTDEVHH
GLSSTLDDVKRSLELSSPELFRLVETLLLALKMAESSSKIIMCELLSSLLSLDVYLHPWM
PVESVQLSYENLLLISLQGNEEIHIKVARCISRIGHLEGNGLNNAIVHLLEKETKFNATG
IITLFNALLMSSVPVALLAMELLLNPLRSLVESRLSESDVFSLCRRALSENADFSEEDIL
HLLQIVVSKNLPASLEFLCELLVRISLCSIEKTVLQMVDGKRWSILVIALLSSCDSDVLH
VSETLEHWVTEMLNAVQEEEFRRVTIQGMSAICAHAPNALEGFLTRSRGLDPELQLAVHA
AAARGLIKAGLAMDGEVKGIILRLLDAICSGVDIDEVLTATFFSPSLGSNKCVTLLVPFI
QAVRTSNIPMPDKVLNVILQLLGKEAIGLEFDWSSILEVCENLARQKPSEGHVIGILQLL
DCVLLRIDSKVFFMKRILTNDGALFQMLLSAVRSSDLQARCTALRLLSEVAMFAVQLTAT
NNEDELNYKRIIAREKEGVLHLTQILLADHKRVVRRAAAQCRHQWYKLR*
>TCRU_2550 thymidylate kinase, putative
MKIVVFLDVRSEALCTAVASEAATVGDSVELVNCHNSVVQVLRRKNKQQETVNTFICLIT
EKGSLKDAGVVYALFRRRIAVLSLEEGSIASTSIPLLETISSLHVDLSGGLLQAQLLAVK
AFFSFNASVSQVIVFEGGDGVGKATQARLLVDRLVDEGHRVSSIEFPSERNRYGELLREV
LSGKKGGIQDLDPKLFSLLFSMNRFAFLPELQYWMCRGTKIVLDRYYTANCGHQASKFPE
EERAGFIGHLQLMEVSWLRLPPANLVLYLDLPPHAAFSAMKVDPNRGSLDIHETAQRAYK
ENVRKTYLWCCENMSNWFHTDCCDCAGSRLSREETHNKVYEVIERQLIPIA*
>TCRU_2551 hypothetical protein
MGASSSSEELSGTAAFFGAGLIAGDALAFCAGFRRGASSSSEELSGTAAFFGAGLIAGDA
LAFCAGFRTGASSSSEELSGTAALSSVLHCFLEGFSPSDDG*
>TCRU_2552 DNA replication licensing factor MCM2, putative
MSPHRKRPREEKRTRHTHESDDDRDGEDEEELGEDLFGENYERDYLNPEDESELAEDDVA
DDDDWIDDTSDVSVISESGRLAVDALLDRRKEMEQRLREEQRELEKGVFSDVDDEESVIS
AESDYYNAADPDDDGGEEDEAGRNRVGLNNGEDGDTDYTGGNKDDGVYVRGDMEAMDFDW
RRPQCDLIEWLAQELPRRVVKNRIYNFYLNYVENGVSVYEQKVNLMTRENEQSFELSYSH
LGRAYDSVLALWLVDVPDLMIELLEDAANYFVFRLFPHYQKVHRRILVRICDLPLCDPIR
DFRQIHMNVLVRVEGVVIRRSPVYPQMQAVRYDCVRCSYIIGPIYQRGDKEQRVSMCPSC
HSKGPFRVNMTLTEYRNHQTVLLQESPGKVPPGRLPRSLEVILTNDLIDRANPGEEVDVT
GIYRNNFDPLLNSRQGFPVFTTVLHANNVVRRSAEVGSFRLPDDERARIMELAKHPNLKR
KMLRSIAPSIHGRDDIKLGLLLAMLGGVPKDVGGDQSHRIRGDINVLLVGDPGCAKSQFL
KFVEKTANRAVFTTGRGSTAVGLTASVHKDSVTGDFVLEGGALVIADRGICLIDEFDKMS
DQDRTSIHEAMEQQTISVARGGIVTTLSARCSIAAAANPIGGRYDPSLSFDANVNLTTPI
LSRFDLLFVVRDEVNVELDEKLATFICHSHIRNHPRSQEENKRTERELHQQLSRLRYALE
NASTEEERHVIEGQLQELRHHLQEKPREEDEDPSSNKPLPQPLLRKYILYAKAHCHPRVS
NIDANTIARLYTELRQESKHGGVAITVRHMESVIRLAEAHARLYLRDFVRDEDVNAAISL
FLRCFIQTQKYSLRSAMENRFRKYLDSEMEPIPLIQHHIRVAVHSIRAFERQISGGVEPT
KVRIDVAQLEHCTANISSEALNTFFESEEFKKDYKLICDPATGARLQIEHSLV*
>TCRU_2553 hypothetical protein, conserved
MPDANSVQSFWRENLIPRWHELLKNECEAEYSKETNLSLKDLAVNCCLHHAMHELCKDLY
PKLFKKTEFSNVEGVCKEYAAEPDEVKCPKRQTQPPPATDNSVKVSVPEALGKEGDLGET
PEEAPLADLPAKPTKGPPSSPMGGQPTNADDVPAPKSEERPVSTRPTNDSREGDTDTITD
TDQEETSTSEAESAAPTPPVASDNDDSNETDKGTGEEVPNNAPESDDAGTEEKQDENKEA

NPKETPVESTATKTDTTPGDSDSSTAVSHTTSPLLLLLLVACAAAAAVVAA*
>TCRU_2554 retrotransposon hot spot protein, RHS3, putative
MKGMYDSVYNARWHHVVEVPGGERTVMKVENGEPPQSWTYKKVGETLERNDGVRQSGAAR
LRLLVLTSDKGWPYSWAGTEPVCDCCVNCEVDRVWQIVKRDLTEWFSPHGRTVFSPKKRL
FIGTPGIGKSMAAGSYLLYQLLRYDAKKLPLVAYIIKKSVYLFDKNKKTVSDLGSEDVFV
ELLKDHTERGVKGYVIYDVAEQGREPHVGLPFTVWNMIVVTSPNINNFKGWTKQNGPTLI
VMNCPDESDVRALCVWMKRNEPRGKDEYWKQVKERMDEVGPILRVILDAQKFKNRKKDID
KVINDVDGSNAKHYVGVMSDKLWEAVNPSHKLVQIVRVSEDSEDETYLNSPASRVIASKM
YIHLSTKMHSREIIKLLMHPDVFLLSNVLEILGTATFMCRGAVNIIKKKLKELKPPGRRA
LQLAALERNLEGHPTEAVGLPTKKGVSGKKLARYKVMYKPAVGNFPLVDALFFMESPRKT
LVGLQMTTAHDHHTKTSTVKEFTEYLSWFFKNWGNFHRDLSWEIIYVQHPDSKPMNGWQR
CDLVNSRSRDEKEIKAFWDKEVRQYQFILTPADIKKLRAI*
>TCRU_2555 hypothetical protein, conserved
MGMGGSMYGMGGPMGMGGSMYGMGVPMGMGGSMYGMGGPMGMGGSMYGMGIPMGMGGSMY
GMGGPMGMGGSMYGMGGPMGMGGSMYGMGGPMGMGGSKYGSVVDAASRRDGFLARNELIR
ANIAPVKHSNNNEEKNNEKAPSPVPKKYEKAISPVPKKDEKAPTPALKKDEKVISPALKK
DEKAPTHAPKKDEKVISPALKKDEKAPTHAPKKDEKVMSPALKKDEKAPTHAPKKDEKAP
TPAPNKDEKVTVADSGSSNTTNLASKNDKPETAVANNAASEEKAAPKSLVSTSLHSTENS
ADKKEGSAEKPATKEDKKKEESKKETLKPPTGTNIRGVVVIVKTAASASSAAVTMKNATT
VTTSGKDEFSFDEVITHTDPSKTMESVMLEDLRCHWLAGHNSSLLIGTTKGEMKDAFNLG
TKFITNTLSVLEKEGCKFDVSVTMVAVKGGSEVKDLFKSSGAAYENIQLASSPVFGPALR
GMTSKKLTKSSECVKLLEDGLGKHDKEKELLVAFLVLKQMKKSSTGDDTVYLSTLCLVVA
GEEVSHLTGIKEKKASEPWTLLRYAVGGASNTVCLLAVSAEGKKSSNVNAVLEVGKTMRE
VRNGIPRSGNLMHFVEFTKRELTKQRAAAVKDESVKRVVVRLEKMLKDAEEFLANPDSEP
KTY*
>TCRU_2556 Protein of unknown function (DUF3720), putative
MGLIKAVAAVDGGDGAGNDSLENKDKSPQGGVLAGTKDNEAPGAGGVQGAAGDENGQLPA
AGREGNENKDVDPGIKAATDSQDKTNDQLSSSSGSTPSRSGEKPSSTGTSEMTQLPKDTV
TKLDADLQDKRESSEGIKAEETEEEERQKIKAHTGSSESKNNGGETTPPPLTSSDEESPI
SDQENSQNSKKVKNEATLSESKTASEAPAPPSKDATQGQHSHDTDTEDPTKNAATGSPVE
PTTSSTSASGSGDHVHNKADEDDAQSSEEQHDGIETGNTNVVPTLSETASQTPETATDAR
TNDTTTVGDSDGSTAASRTTSPLLLLPVVACAAAAAVVAA*
>TCRU_2557 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MVPNASKKRPSFANGPRIVVASNASGITSVTCGGREHVAADNTDEVSERSATGHKSLVSG
NGVAGSGFVAEGDAGGLTQRNASGHEYKPQLREFTAQYSGSGGSLHDDCFALHNDAKLTL
RELTVGSTVRVCVYWVLLLLLGLCGVVTAV*
>TCRU_2558 Concanavalin A-like lectin/glucanases superfamily,
putative
MGQTVPYYFANNDFTLSATVTIHEVPEAGSSPIPLIGARLNDTASTVLFQLSYTSERNWN
FTLPKKDFLVKPSGDVGNWETNTAIRVTVQKDNDDEWFVYANGRRIYETDEGEMAQDSNA
DQFGPHRISHFFFGAGDKKDEGSSPVTVADVLLYNHILHRDDLRNLNARTVPIRHPAAEE
LDTAVEVTATEEEKQKVRQLTTSLADVEEAPIAQPTDSQSVRVLAGSESSAENVTDGLSP
RTAATNDTSVPETNHSASEGSMSPEDRLALITDAKLILHDLRGDSTARVRVSCVLLLLLG
LCALVAFF*
>TCRU_2559 hypothetical protein, conserved
MQHDRALQRRHIRHVDKGVGHQARRALAEATNPQLRAVRKHAVAQRHVQRVSERVHRAQV
HRHSDRPAEHHRVEECRRTPAANRHRLRQRHATHAALRTTAAGPRMRHVKRQARLAHAAG
TAAAHAVRERRRQRIEARQRCRTAVARHHAHGGQAGQAVVAAAPQHPAAGTVALHRHGAA
RDRQSGDKRNAGGSAARNRHGTAAQRHTRQRRDRQRLAHRPHVAQLQPPAATDRPTVAAH
QRRRDRPLDVHEAQHRVGHREALAKHNAAAAAHNRHVRHREHRVAPQTED*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MPGTESVDRGSCSCSCRDGWHGASCLPLEVPDTVVPPLPERAVDGDTSCVVNQTLTSLTL

NMWKTHHCYVGVTFSGVGAALKFFFNSMPLHLPINITLTGCTFRGGATLQFFGGAEAVES
SGVLVRVSQTVMRSSVVVFALALPQHCDIAVTEVDAVQSSAVQLFDIRINILSVLLLRNV
VLVASSLLVSNVNAHSLRYGGFGLHSVGTLTLVEGSSLYARYCSFAGYKHLFYVNILIVR
NHSVFALLNNTMSSGAGLLLQQHGFSVSDHSVLRVVGNRGSVSYAIYANNLWTVERSSWL
DWRDNDVGLGAIFYDSGSPFVDMDSSSGVTLTGCTMGSTGLSVSLLKRVDAGYRFVAGCL
TVAGRLLTTAAELELSGITNVTTVAGCGECTKEGDCFAPLTTEVIDCKCQCAAGGHGDAC
VPAPVPAGPPPPPTPPVPPTPPPPPVGECISDVVYPEVVQAVGDGLSWLCYRNVTFSGGG
MSLTVLIGAMTGDVANVTFDGCTWRDGAVLVLLGNADASVGALNIVVTGSKFRDALLSPV
GVFPPRTNITVSGNRFAVTRLIPRPGLGLGRPSCVAMNGLAISNDSAVVLSGNVFQTVAA
SSSAIYVVESSLRVWWHSVFAVMGNTFHMDGGDSNLICFEGSRHSSSLSVLNNSAVVIRG
NLVSRPVRYFVYFFFALRVESFSAVVFQGNEMQGSLAVFYSSDSSNIYYNSWLQLSGNLC
RVLPSNEFAFFSSKVNLRGSTVSVSGNQFLSSTVLPTVLRIPTVSSDLTNGAILAACNTV
NGEEETNYVIPSVYNATILTCSDPCILATSCFPAYTTKASSDGCACACAEGGHGDACLPV
AVPEPPSTDGADLCVRDVSVDVEVNVSFGTSVVCYVGVTFAADVVVDVESMSGGVRNVTL
VNCTFLGRASLYVVGWRSDPPAGERADVLVSGLESRSGGGVVVANRFPPGSRVTVVDSVL
IAEARVAYRDAYGLGDASACLVVHNVSLTGSVLTIARTQVAAVFRDAVGVLFVGGVALSS
RGALYVDGLLVQTALGLCVSVEGGVAASGGSVVAFVDSDFLLCKHAVSVRGAVSVSGSAV
AVVRSEFLSTGDYAVAFYSTVSLAGGSMLLAKGNVHDGASREMLHAAGTVTAVGSTLSFV
RNRALLPRMLSVSLSLVTGAHVRVACNDAGGRVLSTAEEYAAAGFGDAGSIDVAGCDACD
RDTHCYAPGTASAGMRNGVCVCACGSGGYGEACVPVGAPALPPAVGTASSAFFREGVTVR
SVFVVPAGASEVTLRHVVLDGVSPVLYVPWMARDGVRIVVQNVSLLNGAVLFVMGGGALR
GAVAAGSDEGGPVELSVCDVEALNGALVLTGTFPAGSVLTVTDSLLVATRSTPLLYLPGS
QSSPYAPVLVLSGLRLVRSVLVVSGVALVTVVTGGRTVVVDGAVLELVGGGVALDAAVFG
GDVALYASARVVASGGAVLRVSGSQVYAAHGLVFDSGAEANASAVVVNDNAGVLTDGALL
VLRGSASFASGSWLSVRGNSISGRLLSVPSYPRCADLVQSTLTLHGNAGSGTVVMDGIVA
LVGAGRRFVVGCLTLNGRALQPMHYRSAGIIGEFRPVACGVCDADVHCFAAATRAMSGSC
VCRCAEGGYGRDCLPVYLPHVDGCNRTPAMPLLSHTATLTETRSPTPTWTPSVSTAHCSP
TQHGPTETLQVTETLALSPTRTPTASVSSTLWWSEVACPTLAVTTTAAGGSLTQNDIRGG
GSAVPTRLMVALPPPFRWARDPRLGTHLSFVPVSMAQPSGFGGPWGAMLRNATWVRNATN
PSTVLELAVPVHRGYFIVADETIVIRCDAVAVSGGCKGVLLGSFTIRSDTLPAAASALSA
TTGVVAGAAAVAVVVTGGLGSILEMQALGMFARMSCASAQERASTVALPYFLSVFAALDP
LWMVVGNALLAAVFGCVHCGVTAAFQRWRGVDAASAWAAMRFPSLTYVVAHAMHLGIFFG
SVLALAMPGARVQHRVVGVVGVLYGVAFPAGVCYLIARHVGASFTKYWQFLRKPLHERLL
YPVGYWHPAAQQRMYGGMLTSMRDSHVYWCVFQLSVLCVVCLIAAVHPPVGGCHVQYFCM
AAVLLAGAGVVAFTNMMRSAFLTVMHTASLVLLAALCVVSAANHLVPSDGGARAYAAIVL
LLTTVVLAATVYSMVVWYAEDRHWQELREPRRGGLEALLRDDEESDEDTQKPHDLNSSSY
ASGTTVASYRPPAVPLHPMAGDTRSDTLSLLDRASSASRSINYAPLER*
>TCRU_2561 retrotransposon hot spot protein, RHS3, putative
MVLISDKEWPCSGVVGRCIRDCHVNCEVERVWQIVKGDATEWFSSHDGTDFEPKRRVLIA
TLGIGKSMNAGSYFHYQLLHYDAEQLPMLAHFMVSGTYLLEETSRTVSEYMGESSIVKVV
KGLSRRGVKGCIVYDAAETDNRLSTCLPPLEWGMLVVTPPEAKIHGHWASERRAARIVMD
CPDESDAKAMCAWMKRDQPVQQQAE*
>TCRU_2562 hypothetical protein
MADMAEGIATLPVLLAAREETRVHEAVRRRFKNPGDTEMCMEAVERHGCVAEALEHAGEH
CRRGVEALHALHTSPARDCLEAAMGLILTRQV*
>TCRU_2563 tryparedoxin peroxidase
MSCGDAKLNHPAPDFNETALMPNGTFKKVALSSYKGKWLVLFFYPMDFTFVCPTEICQFS
DRVKEFSDIGCEVLACSMDSEYSHLAWTSIERKRGGLGQMNIPILADKTKCIMKSYGVLK
EEDGVAYRGLFIIDPKQNLRQITVNDLPVGRDVDEALRLVKAFQFVEKHGEVCPANWKPG
DKTMKPDPEKSKEYFGAVA*
>TCRU_2564 SKIP/SNW domain containing protein, putative
MSSFSEDGGAFAECFFAQYPLGMGRKPLPPVVMEKIAGRRDVRATDAIAGPTHGISSHPL
FAAVPNTEALIVGSSDLSAGGVSTLSAKGSVVQDSDAEALAETTEKTKEALEEVLRGRQA
QKEDFSGRNIRRVPKTKPGLEIVLPGDVGVTGVHDPAPIVRSPTRAKKDAGNSGEGSSSS

SSANVAAVPFSIGNWKNKRKLIIPLEQRLAQQADTQAGSGGGISEQVMNLAVAMQQARKE
VEAEQAAREKARQEEEERRQAEREAEATQRARELLEKAASSMMQTSTERRKESREERLDR
IRLERELREREKQQEVRQRRLAKAAARLGITVEALEADKDLLKTVDEAAAGGHGVSVTDY
ATPSSSSYLGAKQEGSSLEQKPPSLYADDEEDGTRPARGIRKGVFGSAVISNEGIRREME
ALARMEEQEGGIKDGIRLRNDDESTDDDDDGGGDGLGLDQLMKKRRRL*
>TCRU_2565 Acyl CoA binding protein, putative
MPLFDSSLSQDAAKARELCTWTTRFPRNISGKHFFLDHELGDLEATARFEDRQKLLFYAL
RRQAEHGPCTGAAPSIWWTRERTNYNAWKQLGDMSRFEAMVNF*
>TCRU_2566 Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MVSVLLTEQLKRVKDVLTTWKEVDGRVSNLCTSLIAEKDPPTGDVCGADKITAGLVGFLS
GNLSGNTWRDEYLGVNATVNNKQGAASTLASTDNGVKFTGRGAGAEWPVGKQGQNQLYHF
ANYNFTLVATVSIHNVPEEGDTPIPLVGVRAGSNGENKLMELSYDSGKKWHVLCGDKTTT
KLSSTWEAGTPQHVVILLKNGTQGSVYVDGQRVGSEECALGNGESKEISHFYIGGDGENA
DNKEEVSVTVTNVLLYNRPLDEAEITAAFNPNKANIAVQLDGSVEGDAIETSPGGGRPEE
QRQSMESSGVNGVSAPTVPSAKTSSGGEGSATQLVSEESSDGTQNVGGGSSPGSDAPVET
GDRSTVQGDGSSQTPVGTPATADAYDPNAEAMGHDGTAVNPGASASSGADGETAEGTDGQ
KEEGIHAQNGDVNAAALSSSLGNVSQGNNTDAGTVRESGLLPSLLLLLGLWGFAA*
>TCRU_2567 BNR repeat-like domain containing protein, putative
MSRHLFYSAVLLLVVMVCCGSGAAGVAGKSSGPQFKWRGINESDDVTVDSLGAPSLLKVG
NDVFAVAEAQCKKEAGGVSFTGVASQLLTKKTAETPEEVLGKPKDETQVLEEGASKGQEK
KVDVSRPTTAVKGNDIYMLVGQYGSKDCLSSDEGGCELLLVKGSVSGGGDTNNKKIDWKD
TESSLQRIFGTQLDSWTKLIGSGGSGVEMKDETLVFPVEGTKKAEEGTEEDVKTVSLIIY
SSTDNTNLKLSKGMSDGGCSDPSVVEWREGKLIMMTACAGGPRRVYESGDKGESWTEALG
TLSRVWGNNKKENVKLVRSGFITATVGNDGDKRNVMLVTLPVHG*
>TCRU_2568 hypothetical protein, conserved
MEVLGRRGRGIMSLAASFSAPTAFASLEDTGAVTLWDTRLKRKDYMCVDDGAIKGNGEAT
ELLLASDRHMAVVLAENIVMAYDLRQQTLLHSFKHVSEVVAFLSGTHPHGASTTLIADEN
GAIIPFDLSRFAPTTCVSERYFGVEKTLSKPSFGSLSNYCCGLGLLQVKQRQGVCALGMD
GRGAFYMDPIDPPVEFCLMDDLATARGQFVNPPLPTTCHFLGEYIATGRANGIYSIATVD
ADDNSVVEVFAAPGHASNGLSVVLWTHDGHLMTCSICGEVSMWDVMPLLLQDPPVDETEE
GELPSLEKACNVRETTSHHSVVNCGTILGSGVFLAGDTMGFVTSCPILQA*
>TCRU_2569 hypothetical protein, conserved
MNSNPVAVLGLWLHIRTPQQGVAASTTETKTTSPLERVPRHARCGELKRSACRLSGKSVR
PFRSGHSVDITRCGDVHKNPGTEEDGCITVWRLSIAGLSSVKRLLLLCDGSDIKLTPFFC
RK*
>TCRU_2570 Domain of unknown function (DUF4201), putative
MYEYDDQQIKEEALQSKAAAVIQQRWKEYCARREAEAAMLTTSDRGKLVAIAAAAAAAAT
AGDTAAAGGEEAGEDPAVYLDEYVRLVEKRRDVIGRSLACQRQLARYFAAQRQRKGEERP
QPVSPEAEQQYWVAVKQLQEERRVVQDRKEASGTLLSEVKARHQSTIEEALAQEEQFRQY
IRQLAEESVFVRTHQRLTAEEIDAFLKKETEQRREVRNARIRHILLCHELKKLQKTAEQR
DQQQDGMNLIDFEQLKIENTNLNEKIEERNEDLLKLRRKVTTTIHVLTHVKEKLEFMKIE
NAQLRRQVSMTEDELNELRDKLAQTKRRRDHFITSNIKMRESMPMVGSEKLLLDYENRKA
ACNTMRQNVLDNAAKHKELLAATGRNQVVLNRLQKSLASGIPANVGEKPFNMLAS*
>TCRU_2571 KH domain containing protein, putative
MPAAPTTLLSSPQLDLIADPHARSLLEEERGLRERCDKNRAALRKILREKSSCISEHAPK
VNSFVAEITSTIDALVLKKDNLVVELDKLKSLQFELSNLRRDLRVLEHDISTLAQAARDA
EVLLESEMCELKRMREEREARVGRMRFATVEQAEKELHRLERELAKAGDENCNTAVNLSR
RTQAARARQERQEIAALDARVLAQDLRVEKCRAEIEARTAERQEKEEAKKTLKEHLQALN
EDPAKREVQFNAVRSELAKVQQELAEALRRRKEKRPASNEMDSLQKEHDALVAEMQADDK
RLADLRKQLPCRTFAYPPELKMALVGKGGATLEQLQVDFGVAVCIDGVENGCGFVFGGEA
DVNAAIVAIGEIIAAEEACSHKVVLRYDAALRTHLIGKRGTNLRRIELESGAKLDVERDA
VTLRGTQKAVEAARELVETFLKGQHRAEMPLLADEIPHVIGKNGTVINQMEKETGVRSLR
VDREAQKIIAIGEQTRVEEAMRRYKELLADVRQSQPVAECDKTTQGDVAGSDGRTVQDVE

AATGVFGHVKDSMISPSGTSQSAEAAHVLPHKAQRTEARVPMERSLMQLLTTALVEVNRG
PGGDSEEKRELEVLANEENREEESVRVKGAGEAVEKKEMRHDKGAGSRALTPLQVIHQRS
QCKHVKPVHSEGIIFLCGEPKHIQHARMMLEEFALQYRPRAIHVSVPEILFTCITQPSGK
KPSLVSEWSKGYSPLLSIELKPKEEEVIVGSFIAEEARAVAETVREFTKAKEESLVRRVR
PFPQNRIGTLLGKGGKKLRELEKKTGTHIVLRRDAGEVQVFHADGDDAALAEAVDLIMTV
AKS*
>TCRU_2572 Cilia BBSome complex subunit 10, putative
MASGDAPVEILPTSGFVFNEVEEPAELLCPPKLLPIKSFTLERLEKLEKRVTDEAKAKRA
QRQQQQSAPMWSTNVAPTKEAVGDATSE*
>TCRU_2573 Thioredoxin-like, putative
MTDAIDVTTYADDRALGQVAPSLEKLVPIRGAKVAIEGGKVYVLYFFNTFYRGADPVNEE
LTVLSEKYGDRVVFVAISNDADREKTEKYLNKTIVDENTKKPLRLAPPHILFDEKKATGK
TYAEASNLTVMSCPMAFIVGGDGKIAWRQQFLQTFTISQSNFEAQLNHVLAGEALESNGP
RPVVQVEEEAVEVEEEMSLF*
>TCRU_2574 hypothetical protein, conserved
MRHGYVSGISGRRVNPDDGAVEYSVQWSGEDGVCDTWEPRCNLPASCAGPVSEVDAREET
EALHRIASWAKRDGTFEDASDATPPAPDLTPPLHGIVVHSSSNNNNNSAGDEGKSLVSLV
ALGERVLADATSHGLNPTKKRRLQGQNEHDPSCGPALLLEKCWREQHAVSFMHTCAISTC
RTPAAQEFELGKGSDKCRDASSIEIYGIAPAALVRSGQVYDNAKNCDPLAGHAEAETLSG
QCNFKSMPAHTTQSSVRGKQEQLVVRYFIMENNGENDQTLLTMPLCVFRRYYPQLLLDFL
LRHALVMESS*
>TCRU_2575 60S ribosomal protein-like
MRRIAFLFPTLGRVSAARGCAKMTSNSNPKLDELASAYSQLTLKELSELQRLIFKKLGHS
DEFYEKALLRGLGGGGGGGVTMPAHAVAAAAAAAAAPGAAAQEEAPKAEKKKVEKATYDV
KLAKFTPDIKVKLIKELRSVTSLSIADAKSAIEKCPGLVQTNMRKEDAEKLKGLFEKLGA
TVELI*
>TCRU_2576 histone acetyltransferase, putative
MSVFEARQKVYATLHGTFHAAIVQEVAVDAETGQYLYYVHYVEQDSRMDCWLPASELKER
RQGRQASKQQTNKSGGGGITTRGQSRLVAGKEDEVSRGPNTPTSSAKRSNLQNCVKVSTT
RARKDSSFFSRPKNIHSICMGPYEVATWYFSPYHLARPQIQQGLKQNAELFSGKMELQLR
QENKKSAFQTAVVPTSFVLHICPFCLHPFTAHEDVVRHLQIVCPRHPPGNEIYRDPVRQL
VVLEMDAVVEPVFCEHLALLSKLFLEHKALDHDMTPFLFYVLCAVQPHGLEVLGYFSKEK
QSPEMYNLSCILVLPQFQSRGIGRFLIELSYELSRREGRIGSPEKPLSDLGEKLYLGYWG
DVIVSALARAIEENHCATLEYLVQATYLSQADVLRTLQYLRLLNGTQIVVSEESIERCYS
RRLHRERSGKNYVFYPHLLSWSPHMYYELKEQDVAPPIYVTQSEELEQNAASKGQRVF*
>TCRU_2577 nucleoside hydrolase, putative
MVRRKVIIDTDCGGDDAIGIMSAMTHPEVEILAILAVWGNVDVEQGMENLGKLLDLYGRD
IPFYRGAAGPLVVNRETVQWGGFGRDGFGDAGFPPSPRVAAQSKKHASLALVEILRDAKP
DEDVVYQLVCLGPLTNIALAIRLDPSVFEVLGSETESAVTVMGGTSEGKGNSNLMGEFNF
HCDPEAAFVVFHSTGIKHPIQMVNWEVTVNCAMPWRFYDEWVGRRETSEGLRPVNQNKTQ
WFIEKMFQRLETFTRPDEDGTRADTGDAEATQDVTCVIPDAVAMLVALDPTSLEDSFLTY
VTVELQGRETRGATCIDWYGTEQSMAKKGRWRNCNVITKVNCDTFLEVMQRIVDFPL*
>TCRU_2578 Cornifin (SPRR) family, putative
MSIPPPPVAAVPVPPTAAVPAPPTAAVPAPPTAAVPAPPTAAVPVPPTAAVPVPPTAAVP
APPTAAVPAPPTAAVPAPPTAAVPAPPTAAVPVPPTAAVPVPPTAAVPVPPTAAVPAPPT
AAVPAPPTAAVPAPPTAAVPAPPTAAVPAPPTAAVPVPPTAAVPAPPTAAVPVPPTAAVP
VPPTAAVPAPPTAAVPAPPTAAVPAPPTVAVPAPPTAAVPAPPTAAVPAPPTAVVPAPPT
ATPLSASSVPPVVSVPSGAVPQLSVAAPFTGTSIALSLPAGIGVPSQQAIHEESRRSLEE
AAIQQFKSAAGDHYLDLDDVVRDTICKLFFLSNYDVGTMMNSVAKSLHCLGRYDVGLLRN
DDSTAFTLIQSPPFNEAVVTDETQSVEQCRRAIQEAKIRIERADTRSKARFFDAARAGTK
PKEQPGRVPSTCVRKEAKVKPATFRKTSYEQIQEMLRAYQASRVGRGRGASASPGVPQNA
SPERDGYLLWRYGGNYPKENYYTHYRLHGLKK*
>TCRU_2579 Calponin homology (CH) domain containing protein,
putative

MPLPKCWQTISLPELAPSRRAAGGTAAAPGAAVFVPPSVSSLNFDEEAVVDTDRKIERHR
YAKLLLHHVARYQQFTSTDLFAETFLRDIALQDGVTPQARAAAATWVMKLMCSSSSKKWL
MEPLVDALFPAIYRDYDEQKLDHAPPSIQALVNDRTLLRDNPYFSHSMYVQDIVTINATI
ETLSRKIQRTFPAIMQWKRLVVILAEYVRNTIKRRAFSAWRELARRRRTDDLLRRNVIIR
HEKNIRSSRLQAAFFRWKTAVETSRTEYLTERLHQAAFQLESAKNQFQMQCFRSDKLQLS
HEQGQVEIQNLIEERDELLRSVEELKETLVLREKEHQDRMKNCVREVVTLVQQQRCILRR
AIDARLCVEEITAGWLDEAISEFKSKAADEEALPPGYKFLLKWCNQIYFRQRTKKPLRVS
NFAADFANGEAYLLLLQYVFSGDQLATIKPPPPPMWLSKVNKTERLNRVCQFAASTPLAI
ALEPVDLSEKREDKIAAAVAEIFLYHIREKRVMYTKRALQIVSDVALRSEPGANNFAAAI
NTPTRSESASGKDSASDSVGVFDDGFGGAASFHDEETLRRQVMEWGCELEQWEAELQRNV
VQENKLQHCGVTIAHDAAHMMRERSKGQPLYVVTSSTGLIFTSINAKNMEDLRTKFKMPN
PQGWKTLVRVALKNVLWKHLRLIASHFYHFAGVDARKMSEVQFWRFVEETQVAAEPLAPL
VAMQIFDAVVSPQIASIWRVAGKDEKREKMLEAVQEQIEIRFLKPNQFTEILVRLAVARY
KGGIIEATEHFLSELRLPVMEHILPITLLFYEPESQRVMSYFQHDLARVFFFYMNHQLNE
SLKGRSHKMQGCGRFMARLSYTTYIKMFADCDFILPEQDGESGSVGYQRKTRFMSIDEVL
KMLEDVQRRIPSISPGELCFSLFLETFGVACTYWWPDPAVPLSRKLAAFLSRLVEKLRAV
FASDVLILGNPPCVSLEGGAHVELF*
>TCRU_2580 DnaJ domain containing protein, putative
MEAVAESYFTSGDMKAAATFYCNLMVLHPRYVKMARICRVLADPSAVPQPHRYADIVEAL
LEPTVTHEALFGVDAGPADINKAYQRWTLLVHPDKNPYPRAGDAFKRLFTLKTMALETAN
AMKERKDCENLLHGGRRRGRKNSNKKSDAPAARSRHDANASLSVQSSVIDMTLSELKKKQ
VILKSLKRKDIDDNELPELRAALRRVRERRFCSRPTTPSVLTAPCMTTPSLSPEQSVLST
ASCPPHGFHPATEKQKSLTPPPLPKIGTLLKTVALDEQIQSSSTVNSSQCVLSDTVLEEQ
LDELFTEEVRPGQEQTTTDVEPELPENEDVKKLNEKNGIENTCSIIRKPEIANSSPSPPA
SVTDDGVPLKDAVKGSIIELIRGIQEIKVNRTKLRLSCDLTFATYEREKQQQKREADMKG
KFAE*
>TCRU_2581 hypothetical protein, conserved
MFCRLRAGSRLGGEALRSEVLVSQRRLLNINRSVQTRWEAENQAASQKRTDYDFDKEQWS
KQMRFASMDCIMNPDITPIRYTTITGLNKAFRRFMTMRKLVERRPDFNPEDLKKLFVQLK
TISHSLNPEDLKLLQRITTHGEASRIGKEIKLGMNEEFSKKSWKSLKMQAVQNTYQIELD
YFQLVNCYMGQMAQEDWLQITYKCEYRERPDEASEWQSMCEYPVFEVRLGDGVQSSNTHA
FIVVGVMRKDGTRYGKDSQDAAALRKQFDRSRKWF*
>TCRU_2582 Leucine Rich repeat, putative
MHGKEHRPRGCSFDGPLYDISGYLLSHPLAFLAASPITRQVAERIVCETLLRSTVMHQTG
KNQLEGELWLPHSGAWCGQLSNLKYTLWWIRRQADANDGKLAALFFAYRSSIEDLTDVKD
LRGLRFLFIPEAILLNKTLSPLASCPTLKHLWLRSCRTLTRVEALSHLHSLKSLDLSRTG
VTDDGLLALTACHLLEEVDLSGCDFICALPFMKSMGCLRVLKLRNSGITDRAISAIGAAT
ALVHLDIAGCFLVTSLNPLGGLKRLEWMNASWCGIRDGGVEGLSCCGNLEYLSMARCWDI
HNVNVLGVLSKLQVLDLCGTNVDDEGIAGLSRCASLCSLSLSDCFCIYSVRALAAMPSLK
EMDVSYTAVTEESLSLLPSWVRVVRKPVCVVSSNDSITFFRSPRTPLLSITPFVG*
>TCRU_2583 Miro-like protein, putative
MPSPLTVYVLGSPASGKTSLLRQLSCMCENGTLRTRPTHDAPTKGQEVYSLVIQAPQPKA
LSCTVEIRELGGEMAPVWEKFIQSFMNSIKGKGGPNCALMFFVDALSPHLLPLASVMLSR
LKGSDGVCRNWPTVVLLSKALAMNAMTEEELWFFLPADTCKNIQVFSVDSWNGLGLGDVL
AWLSGVASSC*
>TCRU_2584 SNF2 DNA repair protein, putative
MPVPSHVSVATLQSVLQTVCSTGEPAIIAPSSFLGELDTVVDEVKRHGMKLASIPHGGIT
ILPPVPISGTELFDFCAEYCKAQTHEERLAVRHKINNHNFLMQDPLLRMPCRQLYNPADY
VLRIVHLCSELVSASEEEYHGAYGVAPLLHINPVQDVCGKLRSMFQSGSLYVKPWILEEE
EERREMDESNRGVLFNSDSFGNGRGGSSISSSERSVDENDVADEDLTGEEVVDNATDTVV
EYLSEKDFDVVTESGIFYDDSGERVHAIYLRGGIKKELCQRAAIAIEEAATTKNLRKAVN
GGKTNPETGIVGYYDYLNNPTQRKCRETEFTRRNWSSVVDSCEPFLVALNKLYSECAPTH
YKLQRIAIPHHYQLFNTVFSTMTVNRNFRTAVHTDRGDFRSGLAALCVIDGVFEGCHLAI
KKLGKAFRLETGDVLFFDTSLEHGNTEVHNFDYCWKRVSVVCYLRNGLMSQICEMERRRW

LQKQMLKQRLLDRSRQSVINLNATDPNLPPIYLPGRLLEVLSPVQQAALGFVVDRLSKGN
GCVIALTMGLGKTLLSLALCYSHMYDQNPRDVLILAPKIVLTHWTGEKQKWEKYGLVFSH
FVVSDGTDSVSFEIALKRYKQQLNGELPRTSHVFVINPEYIRTVLKKLTGFRPSLIIVDE
GHRVSSKGSKLKDWLEGLRCTARVILSGTPVQNNAEELYRLIGWINNDVHSVLPPRVFTD
LAGTINRYINGDDSALAAAVSAQRYIQEWMCSYVFSVMKTDLPPLNDYIIICGFSSIQRK
MLEDHFGMEGIDGLTSIKASEHRPYHLSTHPLCFLGFISGVYKSLNGNHKLTPEAEEELE
SQEYASQLYSLTEDDIGLIDECLSLVNSGFLTEFVGLSGKMTVLISILHSIREKKEKAII
FSQYVGSQDFISRTLTSFDIVSSTIRGRDCHERRRRTIEKFREDEKITCLLLSTQIGAYG
LDFTAANHVILWDSWWNPQVESQAIARAYRRNQTRAVIVYRLASEFEDTIVLKTQIRKLA
LFRCIMNEEASRAVPPEELLDCVDTEEDEGRRFLWRSLKKSYLEGGAPAVSKVFRHGDTV
RSESWS*
>TCRU_2585 hypothetical protein
MAWWNQLTKQMLLRLSKHPTVHRYARQGMNYVRDHPSGRKVSSAMSNSWVEIRCRVESST
SAFRTLGFDGNNKNGGYAKQVFTLWNEYKGRVFSFIVVNFMGILFFFQFGSALWQMFKQM
VSTLFTEPEKKLKKNEGSSRAINVYVAGAEGIEEKKKKVILQQQQQQREQEEEKHPVEME
NVDQFSFVFSDGTDAHAKQSMLRLERDIFGDVKKPDFSTSFKFRMGEDEEFRPSAKK*
>TCRU_2586 phosphatidylinositol 3-kinase, putative
MSSPSELFEGLKVDFREELEAEDIYGSKNSEGFERLFERSEKCKRNVTQLSTILQSLIFQ
ENEIETEGELEAIIEYIVGTGLYGQSSSLEAKEFRKKIRASFEYEWQEFQKENSFISSSR
AMRTLPYRFSLPSLEKAQLEMLTELSSRGMSNGSLGTVLLRIWYIDLVGCTCSTLRGFPF
DMKASDAILITMERLFLITNFDKSKSQGIMYVFKIQGRKEYVYGDEILINFCYIRDSVTQ
QREVNVVVEPHEKTLLTDPIFVPSYSYFSKTSDENHHVFYKSESPDDISTGISVWDIEGK
LVVKIGENLCNLVFTSERAKEEGVREGDLLYLALLVEVYHGAKLVCRPQMTKWTVCNDLV
ASNELTTSSSVNWGKETKLTFDMLVSNAPREIKLCISLLATCGERFCSVNSLSAEEIVQK
AEERIGVKKMEECHLSPVFFLGYASVQVFDYMACMQTGKLDMRLWSTKKKANPMCPIPKN
SNKNDMGFSLIFPSFNKPVVIPNVAPPDSKRRDWEQQLLDSDLCLVGNLRESKIEQLRQL
KRILASDPLTELTTIDKVLLWKHRGELILRPRALAKFLLAVNWLRPYAVYEAHTILPQWA
PLQPMDALELLDIRYADIVVREHAVKYLNGMTDYELKGCVLQLVQVLKHEPYHDSALFRF
LLRRSLQSPHMIGHYVFWYLVSEMENTSVSERYGLLLEELIRRMPERKVYLRQLYLADQL
FECAMRVKDAPKKDRIDCLREHLQGLRLPRRFTLPINPAMECSGLDIGKCKVMDSKKFPL
WLVFRNYQEEGDPFYVIFKAGDDLRQDLFTLQLLELMDSLWKSCGLYLHIIPYGCITTGE
GVGMIEVVLNSDTVANITRKYGGAQAAFREEPLMNWLRQFNRERDEVERCLWNFICSVAG
YTVATYVLGIGDRHNDNIMLRQDGTLFHIDFGHFLGNFKTKFGIKRETAPFIFTPMYVYM
LGGQSSPIYLYFVDLACHAFNVVRRFGGTLMTHFMLMLSTGIPELQKIEDIGWLRTVLLI
DRSSEEAREHYRLQIALATSNFRTLFNDYIHIMTH*
>TCRU_2587 ribosomal RNA processing protein 4
MNLTTCIVGDSICGSLGDSKLLEPEGVVFLRGYSTYEGNRPNEVAAAQEGGGEIIAAING
LIEVTDRVVSVKGISTRYHPEIGDIVIGRVKEVSGNRWRIDISAYQDAVMLLSNATEPGG
ILRRRGRNDELTMRHIFDQDEIVVAEVQRISSDGVVSLHTRCGEKYGKLTGFGMLVLVSP
ALVRRAKHHFLKLVILPVGIILGTNGMVWVNPNVAQRGGTDNSLYFNEQTDVDVRRSVAR
VANCIKVMNFARLPIFAKTIEASVKLSIDVGIGPFDVLHNSNYDLITNAVMEAITKRKRQ
RS*
>TCRU_2588 hypothetical protein, conserved
MPLAVFPSHQCEQRRHLGRHSGVPPQISNYALGKVERVNVHRQLQYHVWVQIACLHDWGC
VPQRTLLCGVRRGIPRNQRSLHVSSRKIRKLSLRRSVLHNAIVSNASCPRILTNRKARRE
SALAVIDATDQSKIMLQREIVGG*
>TCRU_2589 hypothetical protein, conserved
MGTSGGLLSLCPPPAGARKLTEDSSRRRAIAEGSGNNRGRFFCKNRRIDNTLLVVEGKTT
GLRRRWIAWPRDKNRDDAYEANVPLLHISHYLPPVMAEAASCLDLKASFLQVPLPRETRH
LFRCRVEDGTLVELTRLPMAHKAGPQILQIIITSAIAVVTTVVRPLWAAPPLVRVEVWID
NIRIAGSIGDVTRWEAQVLRNADGRRATMGEDRESGAAQYTFLGCSLITLTVRYP*
>TCRU_2590 hypothetical protein, conserved
MEERVPPNAWIALQAFVEDGSVEAGAFLRDLLRRAAFTANITRRSLPPLFFREAVMKFYE
GTLSASSLLLVTILNRLFCMQFIPDAMARPVNDERPSDLADLLQFYVDSLGAANLPAPVM

EQTYLCVSSLLLLQSNVSVVEALLAVFGGAVPEVARETRSLMKLLSGIMSVLSDHRVSIG
PVRRSTQRMRIQNNMHLLLISIIEEDVSAQASIITQGVSFLMEVSVHEPQEIAPLFWAQL
PSSTFWRLALERLHQGTANEDILRAVCAVLRAITVLDASAVSLLLSALEVVLDSRTHAPL
LHVCRIITSSLESSVEEVVVRFGTDHVLYQALASGAQTLKRVLEQPEAVVASSSEVGLAL
CEGLSVLSQVLMVLPVPEMDSTDDPDDYAMFVEEIQRRNTQKKEAFGRLEGFLKGCLTSL
LVWLGRLTAHDVRSIAAYITQNDSDEMAVWHDELSVALFTTYERLCTLLSPSQDKEIRAL
AAVGCLTVAAWDAELSYIALVPYGDAAIQHQQLQHAPLMPVVVSRHQRKWGPEQRECVVS
SLMALLRVAVMISGDVAAAAAIGESLRELNAPFLPCIAECLWQGLYLPCGEDKTPRCVLA
SYLSNILEQGDISLPTEAFENSQMDDYSLAELRSCVLRSLQDVLRVMDLLQRMEPEIVQS
HRVAERITKWVQKTVATGLLEIELYTRALQQWYIVNPFHFCITWRLIRPLEPTSAAGLLA
DALERFVSCKNESGDMNWPIESDCFSPYVLDTIAQSPYAPRLYRVLYSLISSNTYMGDGS
AHFRLRAVVRGGNTLLQSQYCSPTLTFELFYAASKEYVKLRHELSAASSCLGTDNDDDDD
DGDLLRGISMLGKVVRMDGVRIPSNAPAWLHEVRNAVDEFEIQGVFKAI*
>TCRU_2591 transmembrane protein, putative
MWRQSFLRLCKGATATATGSNGGGRCVTEELEGRTNNIFSIRRAPNSLYEDKMHSNSLTD
HPLTHRTSRDELAYRKRKLTERGNYEQAAKAEEEAERRDTEGRAGAETREYYSAICFVVL
GYLTAHGVVFKRFYPDDLRPYYSPDRGYSDDVAARRQDLEAVDELIGMNVMESLYSKRKE
VFKSQMA*
>TCRU_2592 hypothetical protein, conserved
MLEPREDYTSMLALTPQHVAEEMKVISLLRQELRNTHVNYDENPVAEPPFEPAHRTVDAK
SLRTLKCTSYPFIVCEEAPTSYQAPIPYQLESVIERLREEFRSLEENLKNAEALRREFTG
RQRSTSPSHGSHSRDGSRRHPKEQGNQTRKEDALQLFLEVVGRDARFANLSKEVSMVRWY
TRWVSSHSFICLEEALEQVEYVLSEGGLTTEADLVEAMQQFSFVEAVSTLENDRRDVVEA
ERHRMHSHSRTFREHVSPLAITAATSSFLTPEEKYWYQECYNQTEHVMTMLHHVLHVQFT
SKGRDPSLVSLGKFCPINLEVGSNLISMKETTSVGEESQILSDAAMRALRQERDVITNLL
QKIQDRQENGVMLGPTRDQYRNSLLAAMVVYKCLVDDMVMLRSQKRLAAEFLAEYDDWIL
HLCGTNDQAVIRRLGITPTGGSPPMPLMGRNTPRGNSKSHSREREISAPLFCYSPIGQLP
RHVEEVCESLMSLLKLSRRSSGTDNSTGVRETVYRRWMCLSLRYTCMQIVRGRWPGDLLL
DCMDDIANNLIRLVSEYNSNPGAVQSHLTELNAVLRCFLGLVADGAARRQSQREFPGINN
GTASSLALASATAPTGATSVARHSFDVSVAFSLDRDISSMERAANISDEDEDVWGAIFDA
LWFQADPTGCAHGGFLSCKDFGMDVEKPFVFLRLGSITLPDRLPKTAEGRRRFPKVYMSL
HYVTHTADMSPARSLAEVAEGDATLMASTSVVTRYGYMRRILYIFSILEQRQLLQDYACR
VEEVELVPIENAVFFSRKRDKKTITTRLFYSALPPPRNGDDASTGEKYATVVGLIPPAAV
HLMRYNAIPTGTEYPVSRSKRSTLTTLNLLLGNMLKKIALCRSPLLDKMYNMGDTLWELG
VGAAEEKDNDDGSQGKPLVLPILRAFDEYISSPGFEKSVKEADDEMRQQSAQHVNFYHCP
Y*
>TCRU_2593 protein kinase A regulatory subunit
MAEEENTLSLFLEACRKEGVKQPNTILMDFFRSNPSPSQIEEIDLSHNYVGNRGILAVLD
LIEKLPSFRFLNCSNQKLYNTDLSEDSVRGNATVDRIVEVFKVHPTANALDISNNPISNY
AGRKLLVLAQVNRRICRVELSETRVDFDLRKRITQQCEKNTIALWEAQASEGADEERGFG
EGPVWVPKQAPADLTTIGGGRNRRRTVRSEGIDPEKAKLYQAPYFEKSEDEMNLITKLLT
HNVLFSFLNTKDIKVVAGAMQRATFKHDDCIMEAGQTTCNKLYIIQSGHADIIKEGQKVY
LKTEGTAVGELELMYDTPVVATVKVCTDELIAWVLDRDTYRNLVMGTAIRRRETYIQFLA
NVPFLGGLDSYEKLQLADALSSEEFSPGEYIIHYGEEGEWLYIIMEGTVEVIGRDADGEP
TKVCEFTQGDHIGELEFLNNHRTVADVVATTHVITAKLNRRHFEMCLGPVIDVLKRCTND
PKYEYYQNVLKTGAAQPSYVDDV*
>TCRU_2594 hypothetical protein, conserved
MMTTTDRVLLVCALCVLWCCVAAVAVSAAGGAGGDGGAGEYLIAGRHAQLRRECAEEAGR
RTGGRANPSAVEECVRQGMDGVRTVVDGRRRWRRQQFAVAAADGGSGNDGRNSVSSQKAV
SGTGTVLPDDPKLKSPVAPGPVLADTTTGGGNLLIPAGSLETAKDKNGEPSRETDKGEKA
TVENRSNEGTNGDEQVDNAAIGKPNEDPENKKGETLQVEERIVKTEEHEVKNGLEENNTE
TDEENRNKAAEDPEGDDEVTILSSGGQYNEEGERQTEKDSGSIKKEKEVNGGGATDGISA
VAPVALQPASPVDVTDRRNLEKKNDGDTGGNRDAGRTQTQESAGPSQTEKLAAELITEEE
AAETETGAPGKKTQPEDAGKEQTTVGAKSNQETPVAAKEANNKKEVPREEEDAETAATNE

NFDKKRTSGKDNAHNGAETTRQENENEVEKAEGTHAEAEGNEEQTGKKNFADKDRKLNDT
ATPGDSDSSVAAFHNTSPLLLLLLACAAAAALVAA*
>TCRU_2595 chaperone protein DNAj, putative
MVKETEYYEILGLEAEATEHDIKRAYRRLALKYHPDKNPGDQEAAEMFKRIGHAYEILSD
EEKRRIYDQHGKAGLEGGSMDEGGLDAAEIFSMFFGGGRRPRGERKPRDLVHEMRVSLED
MYNGKTKKISVTRDRICGACEGGGIKPGAERRTCVACRGQGVQTFVQELFIGMHQRMQQT
CQSCGGEGTTVREVDICGRCRGSGIVKDQKILEVHIEKGMKHQDVVRFDGEGNEVVGVRL
KGDVLIILAQKPHDVFRRVGNHLIMNYTINLQEALCGFELPVQHLDKRLRLITIPCGQVI
DPGAAWVVRGEGMPLPNTGGLDRGNLVIHFEVEYPTRLSAQQLKSIAKALGVTESFPRVT
GQKLTLSDVSQRQSRRRSGSQRANAAARRRQMQMAGGMDEEGFTAFHGGHSGAQTVQCAH
Q*
>TCRU_2596 Leucine-rich repeat, putative
MSDGVVLDGTTLCAVACGLTSLDMIPLLCGRTADGQTEDAPPPPPRSITEAHLSFNAIDS
RSLCRLSHLAATLQTLVLDNNELQEVSSLPPLPGLQRLWLNNNRLVGLDDVLTVVSMQCP
ALTYLSLLRNPCCPSELDGHLPIEYTRYRLYVKYVLPKLAHLDTDSFTQAEAKEAKKKGK
FARPARVKTNNGAAEKRPITVRVNNNRDTEQSGNNSVEREDLFASFDARRHEGAGAVTYL
SEHRTVYVGRRSEGNRFICDDML*
>TCRU_2597 Ribosomal protein L14p/L23e, putative
MGKEKANVKGCRFRVSLALPVGAVVNCADNTGAKNLYIISVKGYHGRLNRLPAAALGDIV
MASVKKGKPELRRKVLNAVIIRQRKSWRRKDGTVIYFEDNAGVIVNPKGEMKGSGIAGPV
AKEAADLWPKISSHAPAIV*
>TCRU_2598 hypothetical protein, conserved
MSQLWVKRAKAEVSRHSRLLETLNRVFPMPFEERRSRVGMVTYGTYRWFRYFPIVLVPVV
VMGAILETRDIPQEHVFTSLHLWLADHGMFRHDTVKALNPAFEDERRAIEWKANDRKWRF
TGIDMPSEKELREFAAINIQRQGLSSSR*
>TCRU_2599 hypothetical protein, conserved
MKSVEYKLARLEEQNASLRQKLRHQENEISRLSVRESQLKEARRMPLLQKRLNTALTERE
ELECQLAETRGREARLSDEVKLLRMFIKISENPEIAETARQYVSHERIQVELKVLGEQLR
SIATERDEYKKRVLLSCEEAECYREKWNASLEEKRRLEEYIKKLVAEQPLVPTVIPSPSC
RMVERCASCGADTATRKTNEDFDLDEMQYLRRSLEEEKARSEALQETIDALYEQQRGQRR
SCSLERRITSPPASGSKPDIAGKDGTSAGIYTLRQKIDFVESECRLVKNRWHALREQNKI
LLSRISELELTEAAGRGQIQQLSGECEQLRRELEFVLKARKLIACHHDEPVDNEAPKEKN
GLTP*
>TCRU_2600 hypothetical protein, conserved
MCARLARCDPRLLDFVTWAVLKGCRLFQRVHITPLGLVATSTIPAYDFVAVVPTSATLSV
LTLAGDESFPIKVSPQNHGDELEFWSDLTLGSFALIGYFTKALRTGSPRGVRSYLDVLPF
DPGMPIGNVADAAQKSPGYAEMIKPLKNFCKAQDVEFDLTFRHAYCLFRRHAIPFWTNTE
AGSGGHPDFQHSPFATLGHGDILGMVPVLDLALHSPEPNASIGYPDADMLQWLAQEKKAG
IQVEKGYFAMQAQRDIHKGEVITVNKNAYFNFDDATFRAWFGYPNVSQLHQSAETVKIPT
ATCDDIMETDNLELTDM*
>TCRU_2601 hypothetical protein, conserved
MKHRFHENCSVATGVIPSLLPTCYTTSSLTPKWVTAIGVVSFDLELGQILTHLFPPLPLS
IRQETDLAFLCFPDTNHTEYGHSLHHFIFPLNKKDCDNTRRTVFRMPRSTALSSASREMP
QCSVLHCKLCDEEYFCSSIYLQQRDINNERGTQQKALVFISLYGFPKIFETILEMVYGLV
LDSCNVAEKLETLYNDICSWPAPLPTKLYTGLHLLGKPIQSFRTPYYTRDQIGFRWCEDG
LGREEKCFLARIRLLEALEKPCPDPPTIQRCLASCVLGPSAIEGMGEYIEKQLRLPLDVR
AWRPSDVLAVIFAVRMRKYEEVDVTPFPEGILDEDSENIMNDDVRHLARQFPRFCQVTPQ
VAAVQNQELGYCRRLAKRLLFEHKDFIVNVDESGAPAMFSEFDVQGILLPHLNRLWKLWE
ILVTGEPLCIVGSNLSRVSAAGFCLYSLLAPLSLSVVLRPYLTINNSEVDGLLPRAGPFS
PVILGATNPFFLRHWSSSPHVLCLGATESYELQTHKTLPHSSLKKSNCQFDVKTNMFTSK
HFLVRSEKHLWDECTANCSSVGVLNLPIAARSVAGATLNMDHNESVRKTFLKTTEQFLLP
LERAVEVEFEKSIPLFFYGDYVPSRVQIFSVLERSSDSDLPLHIFKGRRGMLKVYWRFMN
TSTYSCWLRQKVFSLKRALLLRSNSFENVLLLEPDTCRRYEVFMSLQYMLDAELRRPLLD
VLLLKKLLYLTKSFAILRTCLTSDNSNDEGASCGF*

>TCRU_2602 proteasome beta 2 subunit, putative
MPGFSFANVQRNLNLQRQGLQPPKTLKTGTTIVGVVYKEGVVLGADTRATEGSIVADKRC
KKIHYMAPNIMCCGAGTAADTEAVTNMVSANLALHRLDTGKQSRVHEALTMLKRHLYRYQ
GHVSAALVLGGVDVEGPFLATVAPHGSTDRLPFVSMGSGSIAAMSVLETGYKENMTLEEA
KELVASAIRKGIFNDPYSGTQVDLCVITKTKTELLIGYDKPNERKYPKQEIRFPPGTTPV
LREEIRQLVTITDVE*
>TCRU_2603 T-complex protein 1, eta subunit, putative
MIQPQLILLREGTDTSQGKPQLISNINACMNVVDTIKTTLGPCGMDKLIHNGRDVSISND
GATIMNLLEIVHPAAKSLVDIAMSQDHEVGDGTTSVVVLAGELLKEAKACVEDGMAPQII
IKAFRAALSVAMKTLQELCVPFDPNSEQGRKNLVRCAETALNSKLINTECLFFAKMATDA
VLTLDSDLNLDMIGVKKVSGGSMRDSILVDGVAFKKTFSYAGFEQQRKKFESPKVLLLNV
ELELKAEKDNAEVRVKDPKQYQSIVDAEWKIIYDKMEKCVETGAKIVLSRLPIGDLATQY
FADHDIFCAGRVSTDDMARVALATGGVVQSTLSNIPKEALGSCALFEERQVGTERYNFFT
GCKNAKTATIILRGGAQQFIDEADRSLHDAICIVKRAYKTGSVVGGGGAVEMELSKVLRE
YSRTIRGKEQMVIGGFARALEVIPRQLSENAGHDSTDTLNKLRQKHYMAGGAGKWYGVDI
INGGICDTFERFVWEPTLVKRNAIQSATEAACLILSIDETVTNPESDAGKKQAAAGRGGA
AMPISKAGMGGMFKGAPGVTKMKGRAGR*
>TCRU_2604 nucleoside diphosphate kinase, putative
MTTTSRYAFKVDYYDPQANLTRQYLLLYYTEDATIEMHDLKTKRVFLKRCAYPSLGVQEL
FIGATVNIFSRSLKLVDYGDEATRQHFSAAMGEFILIITENGFRSVGTIVDKIISQGLRI
KNIRLVDLPDNMCLQFGISSRCIVILVKGSEAAEKVVLLNEAFQNVTVVVSNPTDVGLLS
DVAFGPGKTTAMMKNCSICVIKPHAITSGYQGAIIQRLIDEGFYITALGMYTLSLTDAED
FLEVYNGVVPEYKRLVEQMSSGPCWAIEVYAENAVTALRAVCGPHDPEVCHVLFPHTIRS
KYGIDRTRNSVHCTDLEEDAPLESEFFFSLLQNL*
>TCRU_2605 predicted WD40 repeat protein
MVKVKTISRSHLEWTKDRNGEVPRVNRNFDTKYNPMAKQTEFTRAIRAAKLDRMFAKPFV
GALSGHHDTIQSVAVDYTSLSTVVSGAFDGGMIVWDVFTKRPKAIVDAHRHSVDGLVLST
DGVACFSASRDKVVKMWDLDFPSDDSKVEPLAEYLGEFPFSSIDHHFHKSIFVTSSDAVH
LWDVNRTQPLQRFSWGDDTVSCCQFNKVETELVACCMSDRGVFIYDTRTKASHSKIIMEM
CCTSVAWNPMDPNTFVTGSDDRNCYLFDMRVPGRPKSVFQGHINGITSVDFCPTGKKFVA
GSLDSTLRMWDIHQTTKSNSTEMYHTKRMAKVFSVKWSPDSSYIYSGSEDAILRVWKADA
SKPVRPLRGPERSSFNYMRSLKDRYSGFVEVRRIANQRNTPKAISRAQLRGKKAEKREFV
KEASRRKHDDIKPLAQRKVYQSLN*
>TCRU_2606 calmodulin-like protein, putative
MSRAALMKESFELLQRDGKIPKASVPTALRAAGLNPSEERIKEIMNTVTDLDMAGYEALV
AKHDDKTDTPEAVKEAFRVFDKDLDGTVSVAEFRHIMTTMGEKYTEEEFRDLIQGFEENG
VIHYEKFVNKMLAPFTDHGNLEDVI*
>TCRU_2607 hypothetical protein, conserved
MASRATVFQTDVLEWLLSNKASLSRLRKERYALEKGVMDYLYEFRDMFRDVKEGESKEGE
KKLEGVQESVGSRSLSQFYESEELAKRMKWKRVTWDEDADYNSFSRRLLDNDNLLKNVPA
FSFLSIHVTNDPSSIQFVRFPVCKKSIELGTLTNWVLQERDPISVEKYLPSRKNKLRSAF
TVDWVAGEVKVIDTASVQEVLTFLHTVAPRLQAVQVRMEEQQTALVENVQDAKIRVGAEV
KFNEHDTTFWDDPKRKDNLDYVTPDDVEKFLQGLLKSAFLYRWFLKGQGLRVLPPGKPYF
IDMEKKEIQIPANFAEFNWRAAHKRFEKIERIFSTMRAFWWLWFSLAMVIIGDVELF*
>TCRU_2608 hypothetical protein, conserved
MGLEKQIASLETFFRHVNYPLQPLHYETKVVLDTFFEKGGFLNLCDLTFASYGTKGRAGG
ARSLSWMDIGNLKPNGKDASALFRLLAPGGHLCNLLEAVSLPSKDFATCLKRSWKENLAG
ESEIKFPFYTFDIPISALYSLSYELLAESADTNWYTLSRSRCPPLFLIPFWNPPLATRFE
AEHGQVLTSFPCSPLSYFILRMFFYLVRKVEESGVEMVCLPRLDTMGKRVVSWFNILIDY
FRDVPCVELPLYHRLLTAYIQYFVSFSFIGRLSSKRVLEDVQWSTSDVMAALLLSAPNLL
CMKGFRRPELEIYRNSCRDVFSAALLFKMIPFLTECILALRKTDSEESFANMSKYSILPQ
KEMRLDSAVSSAWDILFFDLSFYRNTLIALRQSLISFEKFRDCRREHFNNSLELWYLLIK
PSENKDVRETYVVHHYEIYSFFLIDVFSMVLRSSFLDSIDVAGASMLLRCFEVFSMASIR
NVFHELSSNDTFSRSSILDNIIQYLTLNWADEDGTVHIVKVFGKEILELAADFCLAVESR

IEKGDLDPAVTFQLKGLLDLLLNVFEGLQPVVEKCRQMHASCRKPNADVRTNSTPTEIKK
KLDTEGEKELFFKGIRRSCGFSGPLNLRFATENGLLPGTSYPAAGTSLGNEFPCLLAVTR
LLDAFFEKILEAYYSVWIPKCSRGHGMWLLSSSKFACINHPEESAVWECVFCEEVYGACC
RSNPYGGDGKKMVRAENSQSDFKFCSECYAFIPTNTVFYTLSMSGTVLCPECASRPFKRR
SFRFFAAYRTWTIICISCLLVTFFYII*
>TCRU_2609 Sperm-tail PG-rich repeat, putative
MIKEELPLFRAKLPGLYTGGGTGPGVGPGSYNVTSNLSKPIHGEAPFGITSERFYSHHGT
AVPGVGTYDIITNDYRRGDITVVPFFSSLDRFFCPRADEVPGPGAYPHDGNKWGRCGRSH
AMGAACSKGTENSFSIGPGSYDPNYGSGRRANSRAAHFGGYSGRDAPRFNDIPGPGHYDI
AAPDNSLYNNKPSSMFSTKTLRSTFGGKSVNPGPGSYNLPSYFQSLDEYRVANPESFSAF
GSSAPLHAPGPTDSPGPGAYTGDIAPRRPKAPPKTKKACTFGSGTGRNRMPPGTNIGPGA
YEPTKPNKLQKYQLASVPFRSQSPRFPSSKSTEVEGIFEPRRPVVRVPLRIHPPRPRDSA
INVAAKMSSRKAPLDPVYNVNYDWPKPTCTSGSYFGTAPRFEKKDSKTSIPGPGQYDISE
KPSLGGGGSLNGTWGTDGRFTSGNEVDNPGPGHYRYESTFYKKSFNSTIGSSEKM*
>TCRU_2610 Chromosome passenger complex (CPC) protein INCENP N terminal, putative
MFRRGLVHRRYPFNKRGPRERKSWKHHVLTDPPKPIQWRDPKVWTKDLTTMKSFDAPQWD
LWQSRARSEDIDEALQPFMDMPQSLKDRRYDIPWWANPFGAWYLQNILSVELLKLPSRTN
AEKVAIYRNQKHSLSSKKKGEAAQDDEILANIIKERWRTLEFGDRDAGYPCTFSDYIQFL
NEWFKSLDEEGMQRLREHFDRRIRPLLAVMSPVDILWLEALTQNSPHNKEQLQRKIAFQT
SLGTPEFFDMSKRLRYEINEDYKVRDELGPELFALWSKAPERWPPERLSKMYGLDFTLVR
KILVWHHFKACYDACVEPDWTLPKRLFALEWIRDVRARKHGLFYGKMRFAEQKITFYSDR
FLFRDLVNRREASYANVWEMDDPYRFLQTEQDYEDYWGDNYDVYRRMFPEMIGKSGEPVQ
QYGQMPVWTGPHRQHANKSQHNWMFAEIGVNVGHEALKKLELDPTNEKRRRFVIRQPDGT
LRSAKMSEMRAWYWKEEWADFRFWAPNMEWGIENTPSQEQYQEHVPDTPDADFRKQRRIQ
SRPVKWFYESHYTRTGNFAGFQPLRFMQRRTEREVRWPDVINAAVQIQKRKPDAYIFKAI
PEI*
>TCRU_2611 hypothetical protein
MSTESFEVSRNEAVEKSGNVYSPPPFSYYVTRKEEDSAEEPISSTSKPGNAGQNMETLAG
AGELPLGAAAQPFSARNVGRFLEQQRYLREINRPHTISLWDQACVGHLFPGMFEGTIDAI
ELFHILKMLVMIAINSVTVAVNVFYGTTSVSSLEWAKPMSRVVFLIEFLVVYFFFFFLIV
VILHAIAYGNVGANLAGDIAALSERITSFSSLRVVAIVSPDFAINNIFPIVQNAVSVSEY
LRATLFFVLWLCACVLAMAAVVLKVTQIEFASTLSISSWTFGEFIQLVGLTMNLARVNDS
YETETQVLLDAVHRHFCSPGMPKDSFNRVECLYTRLCDYLSLPRPKKYEFFDAIFDYHFK
LAQEQKNIPLPMKLRKMLNYLAFILRTDNAVLRRLLQMSQSPLPFFQMGRDAFFQCFNEH
DELGMLVAVWRSDPASLPVKLFGMENKGVFNITYKCEDGRHAWDADNLSHILSHSESEKK
FHKDVVDACL*
>TCRU_2612 PRP8 protein homologue
MGISQDGLNMRCYTTTREGISWALENYAKALEQEPTEVAPKHFAPCRATLSEDLQGFLLV
PTGGDWNYAFKGATWRESTEFDVSADIPVFFFAAQHRPDHFLNFARLSEEEETIDMADMD
DTMA*
>TCRU_2613 Leishmanolysin, putative
MPIRINVSTRDLDDTMKYCISERYHAMNSLNGNCESEGDVVSSAHGIILENEFVPAAFKL
HADRLLVQPLEGSLIVPPFATGSVCIRFTVRAGIVPLVLPMLAWCCAWQSAVGGGALDDC
RDGCEEPRDIDDIGGMELQDGDGDGRTLESHWSQRHAKDEWMAPMGSSVYCTELTLAAPA
DLGCMRVKWEMAEPMRW*
>TCRU_2614 Mucin-like glycoprotein, putative
MTTCRLLCALLVLALCCCPSVCVADTQSGPEKPPNTTTTTTSQAPDPTKSGLGDDVNTTS
LSLSLPGSPSKEPVVERGKTVGGEEGLTGQEAPTVTEDTKEVKNGTTGPISGNNPPAKQT
NEESEASAQTTTTTTTTTKAPTTTTTTVPEAPSTTTTEAPAVSTTRAPSRLREIDGSLSS
SAWVCASLVLAASALAYTALG*
>TCRU_2615 hypothetical protein, conserved
MSLAGQFTTFSRTHEQPMNEESCAAFLMAILDVAPSTRLQYARILRSMLEMNRTPLDMVI
LGLQKVAARSETKQTRQARPLTEEETNQVIRSRTDWKERVVVRLAWVTASRLFEIAVLTP

NNFKLKPNGVMVLDWSVAPKTAKADPHRAPLSDRRRGQDAFDIIKLCRTLRRSVRLTNIT
NAQVERTLAPWDATAHSIKRGALRHAAQIVETYNLDPHVISQLAKHVNPFDLPQNTVRYL
GKYTTMLTQVSSRVVLM*
>TCRU_2616 retrotransposon hot spot protein, RHS3, putative
MDEVGPILRFIFNEKKCKDRFNECEGAVNSITGSMLQYYTGIGTGKSCESNHVSHKLVKV
VRVRKDNIESHLNILISPHFERETLAKMKREMRRMDFTYLVLSIWDYVIPQILEDEALDA
FLNEDFLRAIRSKIEELKLTGRPGSHSCALKVHSNKSFTRKEVLPENPSKRIAIEYWVLY
RPTAKNFPLVDGFFFVDSNPKIMVGLQITTAGEHHTIPSTVELFTERMAAYFKGWKTLSR
DMLWEIVYVQHKDNKPLDGWQRCGPADPNKLSRAENKIAEFWKKKVYQYRVGVSADDIKQ
RVSSVENDQQGKSAN*
>TCRU_2617 Leishmanolysin, putative
MISEVPNVRGRPKVSVVSTPNAKAMARQYHSCPTLEGIELEDEGGPESVLSHWKKRNMRD
ELMTSDVGVGLYSALTLAAFEDMGFYLANYSAAEMLWWGNNSGCGLLEKQCLTDGISEYP
DLFCNWFWSAGYDFCTYDRLSLGRCGIKWYDEALPEEYQYFADPRLGGDDLFMSRCPIVE
AYSDTGCTNGVPLMPGSIVGPNSRCVKGQDLQFDDEYVGDVCVDTRCGDGTLSVRFLRDD
AWHECRAGETVTPPSGPWRGSIVCPQYADVCTAFPNISGYPIPVVEPPLADDPTSAEVAE
*
>TCRU_2618 clathrin assembly sigma-adaptin protein 3, putative
MIKAVIIINTAGKIRLLNVYEKDIPLGVQQELVRRIHRLISRRSADLCNFVDNFRDWPTP
DTRVVYRHYATLCFVFIVDSSESQLAILDLIQVLVEALDRTFENVCELDLIFHSDRVQLL
LMEMVMGGMVLETSREEILRANTEMQRIGSSKAGTGAAAVTGYH*
>TCRU_2619 hypothetical protein, conserved
MKLVKFVNCDAPNVPADMLQLSVEEQRICVVSNQRSDGEHETKSWHLISAAPSMDGVYWL
LNDDNTPIGPINEILLATRDNANSARTKVPEGVKECHIDGVDLRSKMGKQLQRTREEYGQ
TFKTAARNAALLMDADRLRVGREEKVRKERKRVVEAIENGEEPIRKTRGKKEDGNKSNGG
SKKH*
>TCRU_2620 Arrestin (or S-antigen), N-terminal domain containing
protein, putative
MGVFNRDRVEVELTLHGGGAAYIPGSTLSGVVKVFVKKKILCRGIRLNIRGEEYAKVHCG
GVVRQDTHIHYDRMYALARDVSNNNGALDSPSLLFPDSDDEVEADMRKADVLLPGTYTHM
FELILPVFLPPSFDVRDSRGVSEVRTTYTAKVSVDITSGFDVKCIRKFYVLSAIPEMQRR
QWMEERMKAALVSYAELPQYHVMERFLCPRQGRFVLTEVSISPTVVLMEDCVGLANSYGD
NGEIRADVRVFNDTQTVLKTVRVQIKNVVEMKLQDVKCVRRVNVGEPFIFSEIIHPGEER
SFVASIRPPLFFPYSSLEPHENDSVDFNRYTFLPLIPPRKQKQYILYHQPLMNMVTSFVD
SRCVVSVDFPGVNAKGTIKANNVLILATTVDGNNRARPIPCECDKLSPISGVILNNTYSS
QLHQYDHDRDSDEMRSESPWNYRHVKDRTGIFPAYTAGNWNPGKEALT*
>TCRU_2621 DNA repair helicase, putative
MYDAGSFRVPFPFQPYPLQLHAMGAIRDGLAGGDVVVLESPTGTGKTQVLLNSVLSHVFE
PVLNTEGEDTASLQKRSLPSLENAAPPPPSAEVVGRGHKRQRRQTTSVNQQMKDVTNEVD
EDAFLLEQNTYEEACERQRQHKIMGGASSCFSSSSSSIGSVKEEEENVAEWKPFLLRLQK
PKVYFSSRTHTQLQQLTEELRRTVFAKYLVRPRLRQHVAIGSEQMEEPLEPALDEAPHML
RYVHVAGRQQLCINSLLKNAAGNNNERLNELCLEAMKYEYSKEGREARKEHEIRNKCSSL
PDIEENVPLGEVPKGCGYCRRERLKILRDYVDISPRGISEMREIGQRVGACPFLATRELL
RGADVVLIPYSYLVSPEMRYALLSGTATNECETVANMEEVTTDQGLDGNAAASHVHNDMT
LRRGSILPPNFTGDVIAVDEAHNLVDFCRSATSSTVSEPDLSLVRRLLDAYYTRYEKRLL
TRNKQRIREMVLFVDKLLRYLHMKSVTQTNSVAAEVWNFSSFVFDAHVDNVNVYRFLAFL
NESRLLTKLHGFVAFLSMQKKEHAEQKQHVPIPLGPIKQNGGISHSAVSETFRDGSNNLS
LLAFEYNSKSVTSALYRFDAFLRWYSRSDEHTRVVLRRVPVEKESESNEAVLLQLLQLEP
GTHTFFPLLRQVQAALLAGGTMKPMALTCDLLLRPPNPHVAPSATTEEKKSMMNLENKPG
QSLTEKKVFFIEEGHIVPSSSIAVFTLGSGPSGHRVELQHATRHQWNRQFEEIAAALLNF
CRVIPDGMIVFFASYDVEELFHGFLQRSGFYDKINEVKRIFRESGRLASSKVATNSGVEG
KSLSHAVDVMLAEYTRWIGTEGSGGALLFAVMGGKLSEGINFNDELGRAVIVVGLPYANP
SDVELQLYLSHIANTRLLRDAGFAASKTLAVDTVTIDRSVPFNSSAEWSLFTDLCIRTVN
QSMGRCIRHADDYAVAILFDARYGERPDIRRRIASWMQPSIHVNRNFGECFRGVRDFFLA

RRLVPVAENVLCDSHRH*
>TCRU_2622 arginine N-methyltransferase, putative
MPSRKNLPPYELGQGQQRKKKVFNTKNVTNGACSPLTRTVANESLLATEGEKNATSKSLY
GDPAARISSNLYSISDRIRLRAYQSVLKGIKGKSLLHIGCGMGLISLMAARNLASAVVAI
DHSAIVDAAQVVAKQNGLQNISFFRGSLREMMGNFPVKKFDVILCEWMGTFLVNDPLLED
ALFARENLLAENGVMCPDGSSIHIVGVSDYAFYLDTVEYWSNVYGFKMEPMKGLVRQEVE
TCAIPASNIVTSTSLIHTVNITEFRDADNKDADESGFTVPFSVRATRNTTVNYLTFFVDA
TFTNPHDPGANFVIGIRPGGNNAWTETSVGLPQPLPLKCGETLSGELRVRVLNRERGVTL
VEVTAQTDGKVLAEKTTGSYTYQRF*
>TCRU_2623 RNA editing exonuclease 2
MLQRCRILWTADFRTSPKISEEFNNVLNRSGWGFDHVAIDMGALAGAAGRLTRDLIGQDR
DAETVKVLHRQVTNVILRRIQPKKSLAIFIDGSEPLWKVRHMRLYPGKKFEGKFYRSAAS
PMVYLLEDKFRQVAVDLRTPPKEFVISGAGVPGPVEGKMSAWMLDLASRALPDGAVTLSP
PLLSSTPAEVTFNDTICLIGGTDLFLSALGATPFHNITTLTLQQGEMKSLSMSESLEWLA
MDHLLKGEAATQGDQGTGRQELQKRLAAVRTDIVLLYLMANGISATDLSGLGVNFKELME
AYMAEESAGASHEHIFEETPNGTSLLLSSAVLERVLSRATRKTGGSPKPCQQSADYLEVL
LQTHAMICGGGIRNFCWTPDDNDCVPEKPPKIPIERFLAHLKHLTTLTREGGKGGGGEVQ
GDGAEKKTTAIEKEQCRVTAGVEASVDWTFALTGLETLLLTAPRAELIEQIVPVFTRGHS
LPAGIADDIVSTKNVMEAAQKTRNILQVIKGNNSEEGGGAVKDHPALDHHPSHYFVRTPG
CRGPPPGWSYQSINLGVRAAGFGVRYRTGVGASAATSRVLDGVGVASKNTLFVYAADKNG
VWSEEPCGEIHSPVLPTPTEELSTLRVLTWNVQFNRHSGERTPLGRDGIDWCTPTRYIAL
AKTMETLDADVISMQEVEPAWCKYLCEQQWVRERYALSCNEDSHAIRPWGVMLLVKRHLR
VEGMHHANVAAFAGHTSVMPEVTITVSKNVPVTIGSLHLLAPYNKNNVSNRTTQLENLTK
RMRARPSAGGVSTGAIVMGDFNDYANNYFTFPPELGFKDAWSLLNPENNKNEGYTIDGDR
NPYAGQIIEREFFGRADRVLFASRHLQPIHAELVGTTSVRALGITKQVNCDKAVPEYLYP
SDHFGLLVEFQVM*
>TCRU_2624 hypothetical protein, conserved
MAAGDGGNSPQQSSHAHSISHASIGERNDDEFRTENEEFIEEEGYSSVGAVFSKFLERVR
RTHPSRIAWVLFLIFLVTSGNAMQVVGLNFWLRSFPKDGAPGNFTTLAVSSLLFGLIFFF
MLVVYIIVARPSLAYLRCACGWRILFLIGLADAVNSYMAIYAASHTPEVLQALFTSLVPV
YAAGFTKWILEDTRKYWNVWILTSFFLIVSGVVVASAYHFAHGFGGDSKGKAWWSLIFFF
SVPPTVLMNIWQNLYMIQFTYDPSPEESHFFPPQPRRPRRGSMMFSDSVKKNGEEEFNAD
GNDGDAAFSPCETTHAPESSNGERHRFGEIEIPSTQSMQGTDTVVKLVMLACGTTIQFVL
IMLTLPMDAIPWWGGSKSVHDAWTNFYEGIRFVFHSSKNSLYCMVYTLGFLFTYVGSAYL
NQYSVTLCSMIGQLSSPFTALILIIVPKWNLEKGYTPWYLSLLAIVFLCVGSFIYTLWEE
KTDEEKRCGERRLKEKLMLEMQHSALSTRLRSNSTFIFTTEE*
>TCRU_2625 hypothetical protein, conserved
MVIGAKVREKSAAAARYWRHLRFKTLRRQLVTPHVGEICLPSASFEVDGSPLPPVRMKVG
TSHEELLRWFQLEYFGFFQSKSSNGGPENDRTNADVCFHVGPPKSLGYPYTLVSEVNNFT
EAVRRSEEYAAWEETDTAVGPHSTRWITQQLLDGFVSRRVVAHVGLACTNMSQTLSTACR
LQLELAPSDVSPYYFANDLLTSWGIFGVPDPKSTEFRTDDVTRLLQFAHASTVLPMYRAL
WINGAALCNEKGDAVLILGPRRSGKTTLALHCLAAPSPRLRVVGLENFHLADSSTLANIK
PSLDGFTALLMGIPASVKVGVGALLGTLRPNPTLAEAAHTFQLSPSTIQQLIRNNELTIW
NMGARHHIHIAEAFGRQRWCPTIIARLKGILLLNWDVRELSMPHARVNPQVMKWESKEKS
LGLLKTLAETKRGSLFKGHYLLRSLYDETTAMEMLENLFNENEALPPPLYELQGSVSFDT
AAQLVCNHILKQNDS*
>TCRU_2626 leucine-rich repeat protein (LRRP), putative
MGREQSADFEKAFADLLLAGLRRQGEVHGDERVRSIMRRVLVERGGDGREETGTVASAVF
SLAGAGLGDKGAIAVAEALLKLGSPQMVKSHGVRRWTVLLNDNGLTDRFSAHVSLLVSRC
APPVVLLDARGNAMTPAAIQRIEEARELSPAPCALRLPPTAGTAGVAAAASLRESASSAS
TAGGWRRGLDAEALRKRRSALFASGAASSTAVGSELGGRGRPRSRQSEGEAPRDVAAVEV
AARAPSSASGPAPEERSRRMEASGRRHSAGAGKSEKREEEAPPRGGDCGEPLDETANLSP
LLAVVLDLSNAVPTGRLQALYGTDDIWGVVASSGGAVSHAFPPKQTPFLRAGIKSTVSFH
SLTVLLRANKNASKKRKKKGRKR*

>TCRU_2627 ATP-dependent DEAD/H RNA helicase, putative
MSSRYRELIAIFGEFLEENDFHVRISMDRVGEVKTLFSAKTIPVESETEAAIEVVTIEAA
RRRDALRRTCNAVLRTRHSDQHVDVGTIVADEEERLAWKFLIGALAAKNSEILPVVEAEL
LLAAVEYHYATARPELCDMFVHLSASEMFFIDGDSLFMAALSPQSVDWDLIQPLHVIYNA
QKLLYDMHCRGARFHVVFFDSLLWIWESAPAKLFMRENLRKTLMSLSENNAKVGLSISNF
SSYYSEAFETYVKQWEPEFILMSDGEQLGRLNPLQAFFVRPSAANNTHDSRRKANYTDAD
EANPYRLRRQYRSIVEDEAVGDKAALYYRCIHLWAATRRLKVAYSSRIIYKENAMVVFTV
RVDGASFERAVTIESDVQALAQSMEHEVQLPAISSASLGLLDEEDLSCRERVVYAALHAY
LRASARSEQEHQLCQALAITTYITGYLNKEARAQQVRPNPILAGFLNEISPFLLAVWRHA
DCTNGNGQEFDLIDGHLFSAVSQQLRTASVSELFDEYGVEDIESTWGVLDDQGSADIVNA
PLSYLPVIDSVDVEKLQPYPLITHELVERLAKGFGISTHRADAPYPTDFGAANELAGWDI
TTPFDRLNDVIDAEGDAIAKSMMTEKEAKNVQEYYKKFVRNALKQAQSMGISGFAAHELA
MVCSDNDSDDDAGGNSANNKTAGAKKVNKEHAGQRNKKERSKEDEIRERSNVIAATATVA
EWHKQMNHLLHAVDMSHGRTTNRDRDESINTIMAAIKRLSQEKFGKNFDPGYTLGGSTNT
AVPLKLEMWRLLVAASQLREVEFAFAMEDPALKDSKGASKKKDSKSEYKMLYGFHVINQF
VEREAVKGNQWGQLDPLRKAKPDMTIVEARSYLRWVYLSFVEMHIQLKLKCRVVKLQLEN
WRAERERARLAQESPKIALGIPLFLYCHHHVLAVIRDEGPRISSEDIDTVRSALKHFDLP
DSYYNKLDQCIARWQNMTLGTLLPSLLPQDKQLFETPEMLQLIHMGHLLERPFVREHDYR
VAFNPDNWQRELLDIVDGRGSAVVCAPTSAGKTFISYYCMYKALRRTNKKVVVYLAPARA
LINQAVADVCARYGSKKYKNPGRYIYGALGGADYHQFHDSCQVLLTVPETFETMLLSPKY
TDWVELIDYVILDEIHSMESNGNGDVWERILALLPCPFVALSATLGETQQLCSWLNRVQG
RLKEQTEEMSGKMRDFEVHLLPSEGKSIQRWNDIKKYIYLPPPGAALTHKKIKAQYDNCY
IRDLHPLSILTADQLQRGFPPDISLVPSEVVSLFEKMHSKFNEVVWPNYSSLQLAKTLRA
QLMLIEPSKYFEAETYITQERARQYEAEVKNAFAYWAYLGHEGCELPENLVEEDLDDFSA
SMNMAVESILRTFAQKLNEDEALLERHAADGMEKKKRMLLRQQHLQLLQQQEQENEPNQE
ESMEQKSEEQGGAQEEEQEKETVGSVSFPGSRQFIREHILNVLRELIARDMGPTIVFSFE
SEDCGDLVKYVVEQLEEAESRYRKTNEFALYKARIERAAAAQEARRKQRESTLKQKRLTT
GDDGDVEVADRDMSDGEGEDELFVVPDVLPEFTFIGEKCTVEPEVVDSLMEDCEKEGEDL
LLRALQRGIGMHHAGVKGKLRAHVERLFRGRHCGVIFSTETLALGIHSPCRSVVLAGDHI
LLNPTQFRQMMGRAGRRGLDYLGHLVFLGITMRRIKRLMTSSMTVIKGNVQMDPISNLRL
LQLYDFNTLRHLKNEAGWKTHVLKLAERLFVNPLFFQGRNSVAGGNMEGFTVEWLQMLLG
YFQREGLHFSDHASSLGSILQDAMYVFREAHVGNEGFTFIRMLTSGVFDKAHYSPLYDKK
LNSGVLDEPLAELLAYLFSTHQTCGVPLEMHRSALLDPAVSTLWEGKTGPTQHRAVLSPI
DVCSPTIHAFDNTDFFALLSAFYNYLASHLAPQTGAALRLPCMKSTNKKCRIFGGGSTEF
LLKQKLQESSVPYKARSPFVAISGCGDLFTSVDDVTFTLRDGLYCDRTLLPILDLADGWR
HDGAQILINACLLDFLRAKAQIDTTRKNYRFTLLEELNGLSQSLSYAVLNRAEKILSNLA
GLVRPTKLPRAKVLTAIMPDESEEGIFMAGAPRLLEVAERLNSLQPQIQKRLAEELLTAK
WAKRISEMNAQRKD*
>TCRU_2628 GPI inositol deacylase 2
MVFALSEFGEHKGHKHTHGGAVAVPFMGLEESHDGAAHYVRLEEGHDGAVVLTKRVVRAF
VWLAAVAAVIFAGSMLLFQIASRELIKKNRALSISSVVGNYWLNYERVYPVRDEETERNG
EEAAWPYALYRLFCTCERNLASSGKKAPAITSSKLLVFFIHGNLGAYDEASQLGCVVSRL
ISVTSEVYTFDFLQQANIHRGKLLQQQAAFVAHTLGLRRWGSESKNITSAMDFQGEEMAK
STDHLEKQDDGTGVWIVGHSMGGVVARLAVEMMRNSGTSIFLEGVITLNTPHRYPPIFMD
AAMFRIYTNLWQPSDRDLALKNSWHRAPHFYSLTSGSLDLQVEQWLTNLAGLDENRFPHT
MFRTEDPTVCGKSLSHTDIVRDYCVLEFVANIIAKKITGLRHTPIHARNPLASFSGGVTA
PLWWANKSVTSHTLPVAALSFYTALVLSAIYPTVFPPMAKQRFISNHRISCFCWGHQVAL
PRGIPTMGGAVIGSLFIGICSRIFFVQIRCFFLPCSSICGLPWVADDIACISEARCSHLP
SSFVAWLGPALLGSWVGLLVYYLICGLLRLSLLIWTVLGSCHLYKTHLLRHIRPGVNMWY
CFFMLVYPVTAATSTVFLELYQRTIVWLAFILLMMPLRVFVENAAANTPQPTASADASAP
VAVYALLHALNVQPTFAWKNKKLSGTADSNNILDECIRVSEVFLHVLLLTHFLWPIFRSF
VLQKSGHLPLLKLSSSRGSFLCMATSVVFILIYMSLFAMNGLPVEVFRVVWTLLWGFPAF
LFVSTVGLDGVLVERFAPTSLRVI*
>TCRU_2629 hypothetical protein, conserved

MLTSDLQRLQRLFAYFKKNTSSVLGGCCALIELIDEDDLTNWYVLLKYEDENKKEFFVSL
RIYFFEELQRMPLVFVIAPRIIATFIHHGAICSLELMSQQWSVDAEGIALLIRSLHATLN
PFSHDSRVAVDELNSGRDGGNQQNRLLAAEGIGATAAPAVSLSAYTREEHELGIRHIRQS
HPHLFRACTRKDSQPQQQHGSPAAKSVMNSTPSPNSISLSTSYAYHGGAEKAATMKAIIH
SQEELQELFLAGGLVDAELDVGYHCSLDGSLRIGVDAPSVKCKLPTAGNPILNYTMKISP
YGWEKNDEKLTTTTIPKSGIDIASDTTQAVGECSLTAHHSDVPHKWKGEDRKKFVSRQSF
LTPAISADDAEQENKPHYHSKHRGKEKGSTCMGIERSKERRKVVLFLEGEAVMDTGDSNT
LSNAQEGRRPEAPCTIPAGCTLRLEHLTVYGAIVVLGTLEMHDCKFIGHFSSEGEGRVEI
SQCRVCVDSAETRREGILVLDASTLEIRDGTTVRRREYTFTEGGESVPVCAAAPFLLQAF
ILISNSGTLRIHGGCHIMPYGTEKTIFAEQDASVDIADCSIMAGYSSAVSILGCHAFFSN
TRFYGADCVELQVSDLNRPTGLNVELGGLVTARHCVAEYLYFGFSVIAHSVSHFFGCHAE
HVVNGYTIDASSVTIENSSARSNHVGVFVLNKAKCNIMNEDDHVLSFDERCRLLLKSREN
VERQRKFSFVETHLGEEDAETSSSFSSVSSCPIVLQRSPAAAVGDEEKMDHPNVGISALA
DMNRKLFMSHMFSGETATAITASASIFPLSFRGGLFSLEVRDASMVAKGLLLVDAQETSI
YVYDQGVLTLTDVIVWKTLASPQQPCGVKIVNSRANVQRCLVADYSFGFAAIQGTVVRFE
ECMAVGGTNGFTVDDAHCTLHHCGANTEHVGVFALNRSTLRMDNLNAPKCKEGWLSCVLK
GHLHGLESRSSDTICIGVTVQRSLDSGFTCYNGGCLRLEKCTVDISTSGSTETNIGDISC
RHFSPSGRDCSNPAFSSGAAAAALDGSEGGLNRAKIGNTTKANSPHDEMPGTSLAYSSQK
NCGVKAWSGSRCLAIGCEVRHVTFGYAAIGPDTELEASHCTAKHIVNGFTVDSAKCRLSR
CSTNSNHVGVFVLSHGTCTVRRGSYTARMYSIENRNGIVHIEGHVKLSGFSRIGLYVYDG
ARLDTLTDSMLDIKVRKDHAGQQLPPELNLTGPSASPSGLFPSCFAIDKGNAVIHNAFFG
GGAQCAVSCGDGANVYLHQCTAEFCNIAFNALSGSQMYLSNCCARDVRHYALIVHRGGVS
RVNRQSPIPSAGGILQGRIRIEGKCFLEHVILHPTTDVDSEQFETIQPSLPLLSSSSSSS
APLLPYGSEFFVEKTPLNPSLPKSNFLIYVTLNGTLVMDCCLVLLEEHHRVLEEDGGGGE
SIANSVIVAEGCRATVQLRNVLFQRLTAAGTGSLGSFEGSMSSHGSVLLPSNTHGSVISR
KKTTWYGVVLLQGAKGDIHGFSEAALISGSASTIRGAAADNPLEASQARTHFSPRSSVEG
GDDAISLLENHNVPTEYEFLYRSLKKGRSVLSVGEIVPLRVYLTRASSLTTENVNVRKLV
ASGGSTIDAVCCFFAGADAVILSGGSTFRAVESRFVSAVFGPAMRVESATVHLRKCRGYS
THKEVIVARSATLTFVESLLFPLNLVNNETSGTSFSAGERWLGISSRNDEECEIGKGDEV
LILPHRRRRDGGGGNEGAIVPKSAKQGDTSMPKTAVPTCLALENTPIERRVAVPLGVPLL
SHARAEETRSDTLPQDVKCLQPHDDGIVDHAPLVLEGVQNELFRGNCPTEEGPRRRHIST
REAGVPLLQCKKGSCVTEEALELAESETGSYLGRRQHFDVRLEHSYLYCCGATRIEGGVT
ADAFSRIEASRSTWFSGLISAARKVLARVYGT*

>TCRU_2630 Aminoacyl-tRNA editing domain containing protein, putative

MEKVKRYLCSCGADYIIPKICEFPESCATAELAAERLSCSPSMIAKSLSFTLMGKKGGVD
CMPIVILVSGDAKVNNNKYRNKFARRPVMIRREEVEELVGFAPGGVCPFGVNENVRVYLD
ISLRRFETVHVAAGTANSTAPMSIKELERFSGFVEWVDVCDGWTE*

>TCRU_2631 hypothetical protein, conserved

MRAVASARINGFFFSNSLAGVSISVRCLSLSELAKAFTELSESNGAPVATGPAPAPHEAR
VRAAFDMKSAPLTLGGNDLGPLDKASGLRLGSSRDDSNNGAVTFSTAYSERLSNMSGAQL
AFALEKQCRQQHVGQMLQCLVEVWRRLRETSLMSVIITDEEARGEVGGNNVAFTSFRSDR
LLEGVLRALAKTNLDEVQQSSRLVRELGHDGISVEWVTEFGYLLMQWLAARAASLSPFCS
ATFLHLIAQQKVFHSDAVLETLRDNIEVHIARDAVRQAGIAFSSKISSSRVTSAESVREF
DVCAFAVLLDAIARWQAKFVRLLGGDGLGPQIRLHDGRKVTETITRRQHPILNASFYNVV
VDGLVRGVRDGSLHLTRQGSPSTFFFLTLALAKIRWLRADCVEVLLPQLHEALRVFSGQY
LGVVFLLGRREVKTCNVETTDLLLQTLLDAMQKRGKRYISADERRRHSSDAVALPTSLST
TQSADASSWISTSVGHEVDLSTAMAIADMDTDDEDLQLLSASPHLESVGDKGVRHFSETE
AINSGVSSHSSPVVFATSFMDIRSMPVLLDSLNHILTTTLEHCSAQGQETQRNAVELKAR
TLYEALLNDTHGGVKSLYALQESPVLVEKLLSSVLRIPYETHHPLIIELAYVFTRHVGAR
HVVPQDIRKSTVAAPHWQWRTMSLVELLVQHGVILPETYVMTDSVIQFAPRVLSAVEAEK
KRLLERHHERQQQCGKQKGREKKKKKTVRTSEVFARFSRVVLQLKQQM*

>TCRU_2632 hypothetical protein, conserved

MRRVVAKSVLSIRRTPRWTAAHFATSRPLLNDITVPHDVTGENQTRNEGRAKPWRHQRGG

GPKSSTHGHNGPVKDRFPPILTDLSDPRRRLAILLDASSVEPRVFYNTVLPAAKKVGVPV
LVRIFAVQLSSEWESHVAGSDGAKMSGRDLSSSSGAEAGEKTKICNEEQEEKTTGNTSLC
PPVEFFRVERFIPVSMQMEADANHIFDFRRQNKIEAVCFVCTEVDRGVFEGFLPNIAGNG
FNQYVLDELGMAKEVLEDGRSADGSP*
>TCRU_2633 Protein kinase domain containing protein, putative
MGEECPSLPSDVSDRWMRRCGVREIVDHLIMDLVTAHPEDVMGFIHEWSAPRRTGGPMHT
GTSYPDGAQREEAVSSERRQSHFSEELASFEEDKGCVEDENKDAGARLVRATEPTVQELS
SIYPDARGSPFTPLLSEEELEAYFRHSCPVSLGKSSLGICLGRGNYGFVIPAIVKSEAKE
GADQKDENEYQSDTNALTGVGNGRLVAIKVSRIQAIWSLDEAESLRRVTVCRQSLEDEVQ
MLQKELDALRDAEANDALQSQQEEQQAAHPGCNVSMSLLESRLHAQSFLLQGARLVTSLV
GDIMYDVRRDAFWFPLEFYPSSLRECIQARSKLCTGSPPSGSSFPDISLNDLGETVMALL
FSVQEIQHVARSLCRALQFLNVSCSLCHLDVKVDNILLSTPWVPGEPELGKANSPPAGEL
SGAQSNTAVPTLPQVVLGDLGLAQPLDAPIMQLGDFSTMAPEVYWASDCGNANYAAYRTS
VFCASSDMWSVGCVLLQMINGLEYSSWGPSDMFAALEENYVSPALRHPEVWPMELNDFIA
RCFERDPRRRMRAGEALRHPFLLFH*
>TCRU_2634 ATP-grasp domain containing protein, putative
MLRLALQRSGVAIAACYAVPSASMCGTAWSAMMVTAARAARFESRRYKASSAPATTPQKS
AGSSRGHGSGTSHAGSGQVTGSPSTAGHLSGNSSHNGATASMTVSHASGTNNNNSNNSNV
CNSGGSDGGGSSGGGNGNMNNSGGVSWLRRKKQTKKVLKRKAGLKKKQVKKSVSVANTAS
AHIGGGASRNAASGGANTTSSTTPTVTASRAVNSRRIKRKLEPKKKKMATPKLRVCVLNS
SYEGSDSVTADIDNYHCSPAHWVKDKKRYTFTEVSLRKSESYLRVRELVTSNNFDVFFNL
CDGGKDEKRAGVEVVEALEEHNAAFTGTDSHSFEPSKIDMKLLVGAAGVNTPNFVLLEST
EGLAKKCRHLRFPVIVKHLSGYASVGIHKDNRCDTLDELKVKVRAFLAEFNHALVEEFIR
GREGTVLACADRGSLFGVKVFKPLMFKFLQNDDDFAYFEKKWTMECNENAYSFLPHNDPA
YPQIIDTARNAFRHIMNGVGYGRVDFRIDPKGDVYFLEINPNCGMWYNQKDGGDFADVMV
QGDKSWDHDRFIRNAIIRAVREQAARRPWYFISHDSKGNFSTRASKTVRAGKSLFSDAIH
PIPVVAQALYKLGEEDPTVGCVILRGDRPHQAVAIRHSCEPNMQFMQGRTLTLVSKRRIN
VGEELTVDYATLCDENMPPFACSCGTSNCRSVIFPSAPTPRTLEGKNIRQMLREKKKAWY
KEKEDREAERILKKRASKGKGNSGSSASSPSSSPSVSSTSAAGVSSNAATGVNGSSNSGS
VAHGINSKK*
>TCRU_2635 CHAP domain containing protein, putative
MIHTARKKQFGLSALALFVLLLFLLVCVTLGLHWWRDTSGPALHPPRSRFDPLAHCATPH
GTLLGYALDIPAFSNCHRRWNSKSQAFVTLEHPHDVRQEPFLLGTLRSRSTGVRWVAAEF
IARTYYLHRGMSFIYGAPDAPEYWSALEFHGPMVREREYETLELLNSAEATTAKERKRLA
PRVFDVVVWSPMEERDLPEGHIAVVVQVEDDVEAAGGEDRLRELRKLRLQPRLLYIAEQN
FDNTHWGGKNYSRVLRFQWRNGREAVLQDPLGLPIIGRVRPGRPKQNTDVEDDL*
>TCRU_2636 CHAP domain containing protein, putative
MAAGFVENKSLGRVACLAFVLICGVLLLWGWRGNKRNPLSAEGNPLFDPLKHCRTRYGTI
LGYALSVPAFSNCHSSYSAERLVITRFGYPELVADHNDGSKGNYCSGSPWSSMEYTARIL
FHYKGIKYFEMPTPQEVWSTPYFFNPLEAAERDKERRYEPVRVANYEEATTAKERKRLAP
RVFDIVVWPAQMEHELPEGHIAVVVQVEDDVEAAGGEDRLRELRKLRLQPRLLYIAEQNF
DNTHWGGKNYSRVLRFQWRNGREAVLQDPLGLKVLGLVRIGKRTVIFEDEDGGDL*
>TCRU_2637 CHAP domain containing protein, putative
MIHTARKKQFGLSALALFVLLLFLLVCVTLGLHWWRDTSGPALHPPRSRFDPLAHCATPH
GTLLGYALDIPAFSNCHRRWNSKSQAFVTLEHPHDVRQEPFLLGTLRSRSTGVRWVAAEF
IARTYYLHRGMSFIYGAPDAPEYWLALEFHGPMVREREYETLELLNSAEATTAKERKRLA
PRVFDVVVWSPMEERDLPEGHIAVVVQVEDDVEAAGGEDRLRELRKLRLQPRLLYIAEQN
FDNTHWGGKNYSRVLRFQWRNGREAVLQDPLGLPIIGRVRPGRPKQNTDVEDDL*
>TCRU_2638 CHAP domain containing protein, putative
MAAGFVENKSLGRVACLAFVLICGVLLLWGWRGNKRNPLSAEGNPLFDPLKHCRTRYGTI
LGYALSVPAFSNCHSSYSAERLVITRFGYPELVADHNDGSKGNYCSGSPWSSMEYTARIL
FHYKGIKYFEMPTPQEVWSTPYFFNPLEAAERDKERRYEPVRVANYEEATTAKERKRLAP
RVFDIVVWPAQMEHELPEGHIAVVVQVEDDVEAAGGEDRLRELRKLRLQPRLLYIAEQNF
DNTHWGGKNYSRVLRFQWRNGREAVLQDPLGLKVLGLVRIGKRTVIFEDEDGGDL*

>TCRU_2639 CHAP domain containing protein, putative
MSFIYGAPDAPEYWSALEFHGPMVREREYETLELLNSAEATTAKERKRLAPRVFDVVVWS
PMEERDLPEGHIAVVVQVEDDVEAAGGEDRLRELRKLRLQPRLLYIAEQNFDNTHWGGKN
YSRVLRFQWRNGREAVLQDPLGLPIIGRVRPGRPKQNTDVEDDL*
>TCRU_2640 CHAP domain containing protein, putative
MAAGFVENKSLGRVACLAFVLICGVLLLWGWRGNKRNPLSAEGNPLFDPLKHCRTRYGTI
LGYALSVPAFSNCHSSYSAERLVITRFGYPELVADHNDGSKGNYCSGSPWSSMEYTARIL
FHYKGIKYFEMPTPQEVWSTPYFFNPLEAAERDKERRYEPVRVANYEEATTAKERKRLAP
RVFDIVVWPAQMEHELPEGHIAVVVQVEDDVEAAGGEDRLRELRKLRLQPRLLYIAEQNF
DNTHWGGKNYSRVLRFQWRNGREAVLQDPLGLKVLGLVRIGKRTVIFEDEDGGDL*
>TCRU_2641 hypothetical protein, conserved
MLCVDAVHRDVLVAKRLAACSETPALGRPTLPLASGSLPITVSDPLPHSNGTIVVTICLE
RAFAGNRQANPHPASVIVRMEWEVFFSVAYPKEPCVWRLVDGLPAQSSTDVDYRVVRLQS
FLMEEVLSRLPKAKKTYLAAYVGEAGGGGGATYHRSSRGDTATLRSQTELSTGTTLAEMY
PGLGSGGRNNKNNKKRQNSSSCSKQDNSHNNGNNSNSNKGAVGVVVSPFLSDFAFLCSWW
AALELDVGCIISERQNFILRNISSGSMVLLEEDAGSRSYIRQGRGVHFLDEVGGNRVQNP
GRGFAAVFMPRGDVVAWGLRQLPQIAKKKKEEAKSNTVTGTANPSIFGTASHEMVPQRCG
GSWSGYCTGYMETSGRPGYHNQDDQYHLQSRRAQQALRITSVRSDMAGAVLPSLLVSSNI
LRTGVYELNDICLYANDPSVALCQNALILREGKALKDVSNAFLMLRHLIKGVSPHAPSRY
ALQLLAPALHELVKSMQEQRKPFWAGVALCCVLLPAILNDRPMPFEITAHLIDPVECYRC
VSIVAMIFSTVRATNKFREAELTRSAILSAYRCKKPPMSLIRKSVDCEESKSNSGKIPPV
YQIPITECAVCGMPLLRDTRRGNGTATGNPFNTGLGSGDDAVPASARKDGCIIVQCVRCG
HGGHVAHIIAWWNDKNVRCCPKGCDCLCIY*
>TCRU_2642 cytochrome c oxidase assembly protein, putative
MSSDPFRDAPATGGDGKGVVEGIRQRREKLELYQSHSHKMKSLMMNSAGIRSGLSTKNER
ALNPIWTNFPTKCVKPIRSVEEMREKLQYFTKSDDVMVVRYHQNRCTACNAVDKSFEFLC
HQSADRLPNLKFYEINKDEVPELTKNLVRYPQVKGFSGGHWTDLEFKPPADFREELYMAV
EREVKRRKDEARPVTALEAEEMYFSAAGPSMLEVLEESIVKFYAKSQVRLHNYWKQVSVR
RSWFFKKFIEPKVEERLREEWQMKSLFGEKIMYGPEPKIEEF*
>TCRU_2643 50S ribosome-binding GTPase, putative
MSKALPPIKPLSPRGRDAYNGSGRPRTALQTPLTPPEGNARVPTATTTTGTAQSSTIRFL
SREVGFSLGPVQDRFLPPYNDLEDPHLAQYWARREVLIRELAERRHELQRQRRLERRRRE
MLRRRFERRRRRELEDLSAKKGYASQRREIEEEEQERQRSARSRQPHPPQTNRSFSGRNR
SWGRGYDVSAPNNRPATASCGAIMDYSKKTPPSQRQTSARKANQESSLHKAVHHRPSREM
PTETKKTAKADTSAHKKRVNSAKAVAAAKIRAAAAKAAADTLEREPSESQSSLNTPIKCK
YPQEADTRTEAPAQPKSFKKADVFSNFTASTSSSSLSSSSSSRRFRRNGRRQRNNKYNSN
KKSAASARSAKKRAASPLSSKEFQTVVNARRTTPRYDEYDDDYESETPASAKKRPAVLSS
KEFQAVVDARHATPRNDEYDDDYESETPASAKKRPAVLSSQEVQAVVNARHATPRNDEYD
DDYESKTPASAKKRPAVLSSKEFQAVVDARHATPRNDEYDDDYESETPASAKKRPAVLSS
QEVQAVVDARRTTPRNDEYDDDYESETPASAKKRPAVLSSQEVQAVVDARRTTPRNDEYD
DDYESETPASADEQPAVLSSQEFQAVVNARRTTPRNDEYDDDYESETSASANEQPAVLSS
QEVQAVVDARRTTPRNDEYDDDYESETSASANEQPAVLSSQEVQAVVDARRTTPRNDEYD
DDYESETSASANEQPAVLSSQEFQAVVNARRTTPRNDEYDDDYESETPASAKKRPAVLSS
KEIRTQVKYKASSSSSISRSSTSSRSGDSDSDESGRGDPYHELGDASGKLKGNQKKKVTA
SANGLSPGVSLNKSAKFSTSSPKSNKKGLSENHMVKDSSHVHDEY*
>TCRU_2644 hypothetical protein, conserved
MAEAASCVELEAVFLQVSLPRETRHLLRCRVEDGTLVELTRLPMGHKAGPEVLQIIITSA
IAGVTTVVGPLWAAPPLVRIDVWINNIRIAGSKSDATLWEAQVLFNADGRHATIGEDRES
APRSTPSCGAV*
>TCRU_2645 Reverse transcriptase (RNA-dependent DNA polymerase), putative
MHCNAPKHRTATDFVGHANAFDTVYHEKIILEIRQLSIPNHIVRWSAEFLSGTGAVVRID
KLASFPNTSVRGAPQGTVLGPTICSIAMNSLCSCLSNAPSIRHGLIVDDPTLIAQHSNRD
TINSAPQKGLSAVVEWTERYFMKANAGKTGCTLLGNSNTAPLRLA*

>TCRU_2646 hypothetical protein, conserved
MDSTERHVTSQTQKAARATVPERNRQPSPRRRHSAAQTPTQRSATRSIQKPLAHAPPQAQ
GHGRQQPADSTPCVRSSSPERASHEIRFSNAQQTPGGQPPHEAAGGKSNRTPKAIPAATD
PDECKGSRPPITMAELDRTLRLLPLGLAPGPDEINGEALRHLGRVAKRAVPRLFNRRLRA
GTVPRNRRRMVVIPLLCNPGKTASDRDPPPTCNDGQLP*
>TCRU_2647 Endonuclease-reverse transcriptase, putative
MTAEGLDGQLCAGGPQINGADVKAHTEAWNRSIPSDPRGDTIARRCIENVLQVVNSGECT
RYAKRQGTSAPNIALSKDCAVTHWAAQPSTDSDHCMILLDGLIGDDDTPAVVPRRARKSL
AWKKAN*
>TCRU_2648 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MVPNASTERPSFANGPRILVASNASGIMSVTYGGREHVAADNTDEVSEHNATGHKSLVLE
NGVAGSGFVAEGDADGLDQRNASGHENKPQLREFTAQYSGSGVSPDDSFALLNDAKLALR
ELTVDGTVRVCVYWVLLLLLGLCGVVAVL*
>TCRU_2649 Vacuolar iron transporter 1, putative
MSEAKRIEVKAITDYKSTARARTAFLKGDLEMSRREHAKPLPHEEFHSSTASDYIKSVVF
GGLDGIMTTFAIVAAAVGSNNSYVTILIFGFSNVIADGFSMGFGEYVSGEAERENALAER
RREEWEVENAFDLEVDEMVQIYEAKGLSHEDATTIVNIISKDPKLFVDFMMTEELGLLLD
LSDVHGPKKQGAVMFISFVMFGFLPLLAYVPGKGRGVDVVFVFSCLLATVSLLVLGSLKG
YLTGIGMIRSATLMVFNGVISGLVSYSVGMAMESLLRARIGDGP*
>TCRU_2650 hypothetical protein, conserved
MTDADDTLADYWAWCAQNGVVSKKLFLRRGLHGFMPQFSLHVAESVRAGAVVATVPYLVT
LNTQTIRGDMKPAAVPPIHAMCTFLTRRRRMDLVTARSLWLASCLACYRRLLAQGHALSI
APLLSRLIMPELPSPFTSTHIRCYPAIVASLPEGVDVAALEESVFSSLWKRVEGQLRVTH
AALHFYHQRRVTNIPRHLVPSFDELSMAYRMVLHRSLLLPIDCVPSSPGDLADLFTEQPD
LDLLPTLVPVVDVIRSSAVARTLLEAKGGGVRGSQDDSTAANCALYTCTQSDFVSSGTRR
RVVFETEPLSSRRVVVCATRDLKEGEELLLDYGSE*
>TCRU_2651 hypothetical protein, conserved
MSGALGRGSYRSVVAGTRNVPHRLTYYPCAYELMQLHKAHKEVIRHFYVRDKIFDNKFPT
TALANGLFKFVPNRRESYHMREVMESIRRRSILMHRIQQQRAINAKVVEELEKGYGKESA
AAMLCFTTPDSDAYFNPQRYQSVANAWPNYWQHPSTSHVVPKPRWRRVPELGGITRVQDP
LTEQANDY*
>TCRU_(FEN-1), putative flap endonuclease.1
MGILGLSKLLYDRSPAAIRERELKNYFGRRIAIDASMTIYQFIIAMKGFQDGQGMELTNE
AGEVTSHLNGLFARTLRMVDEGLRPIYVFDGKPPTLKASELQERRQRAEEAQQLFDTAKE
EGNDELMEKMSKRTVRVSREQLEEAKKLLQLMGIPVVQAPSEAEAQCAELVKKNKAWAVA
TEDMDALTFGAPVMLRHLTYSEAKKRPIAEFHLDEILGITGLTMTQFIDLCILLGCDYVP
KISGIGPQKAWEGIKKHGDIETLLQSLDAGRHSVPEGFHYEEARQFFLKPEVTPAEEIEI
QFREPDEEGLVKFLVEEKLFNKDRVLKGIQRLRNALTRKTQGRLDQFFTITRPVTKLNTC
DAKAGLKRGHSAIALSGTLQQKGSSGHKKVVKK*
>TCRU_2653 hypothetical protein, conserved
MDVSVVLAADVLSSSDTRHALILVGQRSVAGGSGNQEQVVCIVSDAFPCTDMDVIMEQVE
CLEQVLPCGIAFLGVFLPGDGVKDLAALRHSLSSHLQVSFFFVAKYDNEGRVQCRLLQSG
RMLSVTTPDTKPVLVTLACYFFSPLGQFPFIVRSKDENITSNVVLDVTSTVLMEHNQIWD
SVDALYAVQLGSTEGQEKDMLCVHVTFFPFLSCGQGVYRAICTLLPKVERRPQCVMVRVG
SRRYPSLVYQWIFTPTERGSAALSVKQWDELKELIEDGVGEEVQPSQIVTDTFLGAPSAT
ASTTIKGSNNMRNKTQASEVSNTFQREKAKGDFLRYMPPLLVLFCSLFLYFCCTK*
>TCRU_2654 hypothetical protein, conserved
MPRRDSVAGEGTLPGIPPSAPGGETTNGGPDREGRRAESRDNDDGNGDVAAGNSTARVGE
EIVEPSIEDLVEEAEINLDAPCANLPLLRAQELKIIGRCVTFLGETTVEGERVLLHYEGV
VAMITKDTVMLLQVRRYTKEDFLKYQEMIEAEKRDEHKKDDHQELHGEMDRNGNGRAHAG
TEEMMNFHAASEATSNDDVHHDMHIVDCNILAAQETRENAEMPEPDPPLTRQNRLLGTRT
MGPVPFMTFSRRRIHNVVFGHDPQNSLYSIFQNPSRRYFDMQCLRMFVRRYLVHTSQGNN
PRKINLRPFIEWRCNCKGIADDLLVNVAKQELAYLIKTEREMAKAAERLANNRRNFFHTY

QPTHRLFRATGILFLTRIPAQTFSLAILEMLVSLLLLGFSAYSFATAPPILIYGYVKDYT
FSVTFAGIVSLLASGMTAFHSLRMRIPLTFSIHTALRLVAATVAIALDTMALVMIGGAVS
YSHILGYLFRLAQESAELCYYYALHNCTGFGEICGPDNMSPICMQHKCPSNRTTTCTQPL
TATLIRIFIPFIAISMVLVALFMIDHLLHYRLLQASRLLMARM*
>TCRU_2655 ras-like small GTPase, putative
MDHVDVAGTRDMGSAPSLTALQVIIPYGSNSNNNNNNNNNNFYSGGVCFTRCPSITANVT
RSLNVSCGGDGSSFSNVWSLAKPTLDPSQIRFCPEGCWVPDAQVMTCMAHECNVSFSLFN
RKHHCRLCGRLFCAACCSHVITIRSTRGGLSACCALSGAEGQETPTSLPAILGATDDNSA
GGTSGNPNPSSLYPSQAQLVQQQQHSTSHLEPTATTTTHRICSACYYEIQLVVPRRDQNG
EVRRRCRGELKMFQWSLLVKVLSYLSMHDLLEASLVSSDLYFISRDNVIWYQYNMAQRRQ
KEVQLRIPPRRQNSSLSLRRRFLQRQKEPPRAFGIEFGDVSSSDASKRVISLHARYNFTQ
FLDFARRQEMARCRGLSSFSVAARTLFSSPLKIAIIGSMGVGKTLLVRHFVVSHENGGSS
EGRISPKLGFVRYAKMVHLTGSLAADVMLHIYDISGELRFEELRRFLCSNCHAVGLCYDP
RRKFTLVEAADVMMGVEPALGPQPVVVCGILCPAEPARQDLHEAAGTQELEVTEVDASGI
TVRGRGSLQCAWDNSECLFQQLVQSLLDRLAMATATSSVVSAASTARLAGDEKEATVNCN
IAQELLRITLDPSPLDVLMDSN*
>TCRU_2656 hypothetical protein, conserved
MATGQYTEQGIAPLWHTDLLTFFTTQLTNKWRSTIRQDTHRYLLCGTRPSDLSGKDLITQ
EVLHRQELVHLARAMCGESEVWGRLYWAVRDCTNQCRFCNISPEQSAYMRSNNDPTAPGT
DTVPPSAREEDVSPVSRRTLTRRRKEKCPHCDSTLTGFSGLVSHCRSFHPEHPPPLPELK
CDFCDMVFPTRRSTAQHRSRCAHNPDATRHRNSSARRRSLLPQDQPASTSTPIGPQETLH
HLLLECPGTLAVRQRLGIEQDLRLGKFSQWQLLHSRKLLSLLDHLFGTQMALYS*
>TCRU_2657 hypothetical protein, conserved
MQHDRALHRRHIRHVDEDVRHQARRALAEAANPQLRAARKHAVAQRHVQRVGKRIHRAQF
HRQSDRPAEHHRVEARRRTHAANRHQLRQRHATHAALRAIATTAAGPRKRHVERQARLAH
AAVAAAAHAVGERRRQSIKARQRCRTAVARHHAHGRQAGQTVVAAAPQHTATGTVALHRH
DAARDRRPGDKRSAGGSAARNRHGAAAQRHPRQRRHRRCHRRRLAHRPHVVQLQPPAGTD
RPTVAAHQRRRDRPLDAHEAQHRVGHREALSKHNAAAAAHNRHVRHGEHRVAPQTETRRG
RHMHRGSGRTAQRLQRHAFKHHRTRQQVHTAANVHRHPARLQRPQHRAAHTQLRLQQRGR
VQHKRRRHRVRQPAQLGVAHRPRRHNRRVTDRHVRVCRQVVHKHKRAVAPGQPAHAHLQA
PVTRRLAAVAPHVDLRTAVAHAVPQFDAQRAGKHRRHVEHHSHAVRDGHAVHQHRVHGAA
NRDGSVHRSAPQSQHHRMHRGHPRRRRNQRQHNKQRHTHSRNGPALHTVPAARTRTHRRP
HPPSQTRTNRAVVVHRSLPVNQKSRLANPFLQMTNPEKQFR*
>TCRU_of Trypanosoma cruzi region 4, putative Dispersed gene family protein.1
MYALASELRVDGGSVFSIQNSSWSAPSTEYYKGACGFKDVVVDGGSVLQIVSSTFRLGFA
MLITNTLTVTGGSWLVHRDNEFRTAYVLYVVNENGVAFHDRSVWSILHNYFTYGSYSSTI
LLMTSKWSSPSDARPIIYGVCNEARGSPVTDYREELNIGVPVTILDCGACTMDAVCFAAR
TSSISGCECVCAAGGYGDTCLPAAVPDGLGPLPLPDADDTEVRCVHGGSISSVDYPDPGV
RGLCFVNVTFTAVIVLDLWSFDAPQQILNITLLQCVLVGLSIRGSGARVYVSVVSSMMDS
GALEFKGYFGASSQILVVGSAIVSTLSYAFAFPEFSLGANSTLLLLDNYIEGNRYAVYIS
ETIVVDGGGIIVKGNTLSTTKDEGVESSVFVYAVDMRNGGYFSIENNTMSAANGVHVFGC
TTVRSAGLLRVVDSTFFGSTRVSNSALVHLSGSVTLEGGAQWRVEGNNVGVVSVLAIPHF
WHKIRLLGIGTIVSLAHNRQVGSRMPLFNIFLASIVVASPARFVVGCNLQGGREVLYDDV
FPVEVEVFGCGTCNEDAACYMPGTESVDRSSCSCSCKDGWHGASCLPFGVPDFSLPPAAE
RAVDGDTSCVVNQTLTSLMLNMWKTHHCYVGVTFNGVGAALTFFLNSMPLHLPINITLTG
CKFREGAALQFVGGAEVAESAGVLIRVSQTVMRSSVVVFALALPQHCDIAVTEVDAVQTF
EFDLPGTVGKTLSVLLLHDVVLSASSLLVSNVKAHALRYAEFGLYSFGTLTLVGGSSLYA
RYCSLDGYEHLFYVYRLSVSDHSVFALLNNTMSSGTSLLYQHHRFSVSEHSVLRVVGNSG
IVACAIYAEDLWTVQRSSWLDWRDNSVGVGAMFHESEFASFAIDGSSVVTLTGCGMGSTG
LSRPLLSQAEAGYGFIAGCLTVAGRVLTTTGELELNGITKVTTVTACGDCTKDGDCFAPL
TTAVIDCKCQCAAGGHGEVCVPAPVPAGPPPPPPPPSPLLPPPPPIGECISDMVYPEVAQ
AVGGGLSWLCYRNVTFSGGGMRLTVLIGGMTGNVANVTFDGCTWRDGAVLLLLGNAYAAV
GSLNIVVTGNTFIDALLSPEGGFPPRTNITISGNRFTVTRMIPRLGLDLRRPSCVAMNGL

AISNYSAVVLSGNAFQTMTTSSSAIQVVRYALRVTWHSVFAVLGNAFHMAGGEGTPIHLE
GYAESLSLFVLNGSAVVVRGNLVSSLVQYVIIFVCFFCVESRSAVVFRDNDMQGSSAVFF
SSHHSHIYYNSWLQLSGNLCRVSPVGAFAVLNPTVNLRDSTVSVSGNQFMSSKGTHTALW
IYSRPSDLTNVAIVAACNTVNGEEEANYVIPSVYNATILTCSDPCALATSCFPAYTTTAS
SDGCTCACAEGGHGDACLPVAVPEPPSTDGADLCVRDVRVGVKVNAGLGTSVVCYVGVTF
AADVVVDVESMSGSVRNVTLVNCTFVRGASLYVVGWRSDPPAGERADVLISGLELRSGGG
VLVANRFPPGSRVTVVDSVLIAEKRVAYHDAYDLGDASACLVLHNVNLTGSVLTIARTHV
AAVFRDAVGVLVVGGVALSSRGALYVDGLSVQAALGLCVSVEGGVAASGGSVVAFVDSDF
LLCKHAVSVRGAVSVSGSVVAFVRSDFASTEEYAVAFYSTVSLADGSMLLAKGNVHDGAS
REMLYAAGAVAAAGSTLSLVRNRALLSRMLSLSLSLSAGAHVRVACNHAGGRVLSTAEEY
AAAGFGDAGRIDVVGCDDCDRDTYCYAPGTASASMRNGVCACVCGSGGHGEACVPVGAPA
LPPSVGTASSLFVREGVTVQSVFVVPAGVSEVTLRHVVLDGVSPVLYVPWMARDGVRIVV
QNVSLLNGAVLYVMGGGALRDADGAGSDESGPVELSVCDVEALNGALVLTGTFPAGSVLT
VTDSLLVAARPTPLVCLPGSQSSPYAPVLVLSGLRLVRSVLVVSGVALVTVMTGGRTVVV
DGVVLELVGGGVALDSAVLGGEYALYASARVVASGSAVLRASGSQVYAAHGLVFGSGVEA
NASAIVVNDNTGALTDGALLELRGSASFASGSWLSVRGNSISGRLLSVPSYPHSAELVQS
TLTLYGNAGRGPVVMDGTVALGGAGRNFVVGCLTLNGQALQPMDYRSTGIIGEFRSVACG
VCDAEVRCFAATTRAMSRSCRCRCAEGGYGRDCLPVYLPHVDGCNRTHGIPLLSHTATLT
ETRSPTTTWTPGMSTAQ*
>TCRU_2659 hypothetical protein, conserved
MALVSYTAPEWSDIDGRLSELVRQHGAIQVRLTFVDENGPSYATLTVAASMRGLRLVSGK
VASRWEDSSLTGHVANLRAPQVPNVEAQVLLPIMWGGPGVGAPTRARQR*
>TCRU_2660 hypothetical protein, conserved
MLRSMSQMDRTPLDMAILGLQKIAARKETKQARSSTKEGMNQVIRSRTGWKERVVFRLAW
ITASCWSEIVALIPNNLTMEPDGALVLDWPVAPRTARADPYLALRFVRIRGQDAFHTIKL
CRTLQENEKLTNLTNAQVTRALAPWNATAHSIKQGALRHAAPIVETYNLDPHVISQLAPH
VDQFDLPQNTV*
>TCRU_2661 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MLQGKKASVYIDGKLQRQEEVPLTGERQLELVRFCFGACGEDAGQKTKVTVKNVFLYNRP
LNSTEINALKDKAHTLNGPGGALAGWAALEGAAAREHAAVVGLTSAGSGLLPLLLLLLGL
WGFAAA*
>TCRU_2662 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Protein of unknown function (DUF3676)/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MRDGTIVFPMQAKGKDGTSFLLSMSFDPSDKKWELSYETPGKGCRDPTLVRWEKYEYGAE
LFMMAHCAGGYYDVYMSTPHGVNWNGHFQPITRVWGNSHNRKGHGVQSGSTTATIEGKEV
MLITAPVYPKEENIVGKGRLHLWVTDKARVYDVGPVSREGDDAAASSLLIKDKNKELISL
YENKKSDGAYNLVAVRLTEKLERIKEVVKKWKDLDRALKTCRSGSSAAVDPRKKGMCNGR
VPTDGLVGFLSGNSTQTEWRDEYLGVNATVTNGEKRVPNGLTFQGPGAGAEWPVGDMGQT
VPYYFANNKFTLVATVSIHKVPETGSIPLMGVKMNDTDSTVLFGLSYTNDKKWLAIPEDP
AGNVEDFVKWEPNRTYQVVLRMDHHYWTVFVDREEIQKTKYNESLFDSHRISHFYIGGDS
KHQSATGGHVTVTNVMLYNEELWRDDLYKLKTSKVNIPSLGVEENPSGQVTSTDVSVASE
SWSEESVSYEELTEDDTDEQEEEIVDDLLLAASPSTVDAESSVHESATAAQSAENSHQED
SAQLSGGETAQQTTLNEAKESMQRDSYVQPQDLQSEKSTVFNDVETYPESIDTEEPEEEG
EADGRSGGTTSPVAASLSMETVAASVNGEHQVQQKLELSAENNDVRSTGTGNTGAEESLI
LEARDGNSERTMGSGSSPTPSKSDAEPSSAENTDDVFRTEGTEFPVENGKEVPQTVDTAP
GNTNTTPGGEGIPSTKGAARHSDNDTFTGEIADLLAMGEFAESTVHGCVSRVLLLLLLGL
WGAAALC*
>TCRU_2663 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAATVVSSAPDATRAQSVWPEDLIQKWHELLKNECKVENP
YENNEDLKELAVNCCVRDAMNELCSAFYGRTVMENKDANVEGICKVYAGKPDDVVNCPKP
KTNLSPAAVTPVKVSDPEAPREKEEELRKTPEEVPKAPPEEVPTPLAGTPLTNSPANPTK
VSPSPPLKGQPTNAEEVPVPNSEEGSVNTGPTNDSEEGDTDTVTDTEQDEPSNSQAEPAT

PTHTVASDNGDKETDKGTGEDTPNNTPEPDVAGTEENQEENKNNKPKERTLQVAGIKTTT
ATSGDSDGVKATPPLLLLVVACAAAAVVVAA*
>TCRU_2664 DNA replication licensing factor MCM5, putative
MEADAGLVHVTNFRGGLLAGDDEGERQPDEAVDLKLIFKDFIERFRISNDHLYMAMLRSN
LAGGLFFMEVEMMHIQQFSSTVFNALHSTPTRTLPLCEHALWELAHERKLFPPFARQSTI
QLQLYWGVPPTPLRQLAQASVARLVCVSGIVVKASPCHARCVRAAIQCTSCLSKTYINGG
RSIDLPPHCLENLGRANGALGFGAAAGGVSGTQRKCRPNPYTLLPMECEYEDQQIIKLQE
LPEDVPTGELPRHVTVVVDRYLVDRVSPGSRVQVAGIVSVQEKRGSLEGGRKKGKGMRGV
AGLRAQYLRCVGLMYITAKEGGISVQSVNLNFSSRVRSQSVMSWQAEDEASFKRFADQGH
VYEKLAQSIDPAIFGLEDLKKSIVCLLFGGTRKKQGSNYLRGDMNVLFIGDPSTAKSQLL
KFTEKVAPIGIYTSGKGSSAAGLTASVISNGNGDFVLEAGSMVLADGGVVCIDEFDKMRE
QDQVAIHEAMEQQTISIAKANLTTMLNSRTSVLAAANPTLGSYDPLLSNEDQMDFQSSIL
SRFDLIFKVLDPRNPEIDSRLAQHVVNLHKGGSGRYANTKSSPVVERSFFTKYVSYARAT
RHPRISEEAMSVLLDFYVNIRREAHQQILEALSSSTSSGSKPQTPIIQITARQLESLVRI
TESMARMRLDVLANRADAEEAIRLFKVATVDAIKSGVTDQTMTAAQSELVLRIEEALRRR
VALGATVEQNRLLAEMSRMGFDAKLVDRALYAMVKREELEWRKQRTLIHRLR*
>TCRU_2665 hypothetical protein, conserved
MSVFGLPPQNPPGAAPSKAVMMPGPFASVFPALADTSQQKLPHPQPQQGKHAPLYGLQPV
FFSPQPNSPVLSSHEQNTFNAPPSVFSRTAGMQQSFGSQNTLTVTPSIQKTVLPSNSSAS
GFSAPVFGVSSAFGTCPIPDNVSARSTAPASTSVFQQFSQKGDVLQKPQRSTTFGMPKSG
MNTLNPAVALPQPSQPFTMASPVFSKEESGNVTFNPMASGAKRGRGGSTPFGGRGAGRVD
VAPPQFGEHSPRRARKEPPPTPPQQKQKFSSAFVAPVPAPATKGSWQPRQPVQEQRQMTT
GGIATEQLLSTRVFSAFMRKILEESDVIREEAADFLEDAFFGVVGSHGSGEFPTALQQML
AVWHEVKETQPQSSIKGEHWVVLFALGCHVNFLTNTILAEVNEQHGTADADNNNNDNTNN
EGSNDDNGGAGDQKDIVLGNKWAALTNSCTYANIMCDIFLQLFSNQAENHVPYSVLPFVL
RRVRNTFELANDEGVLAVQSNMKTTLLKLYRYVRVPTLQQEQHSVVEQQRTAAYACVLGE
LMLHSYAPSGRDEFVQSFHQHCSNMTEIRCALYHHYAHNLLQESLTDTVIQEAMELLARA
FVILPESAKENKRLLFLKLTACGLALGRVPSPEEQEAYNVAELEDLIVAVRSSNWMLFEI
AMRNNSEFYVQCGIHNVLQVVGKRISLLMVVKYYVNSFSSRLHVQDMIDYYEMPFTLYEG
CHVWLLPLLVEKRINGVMESGVLVLSSANPFDAYSKEALTALATRDQGE*
>TCRU_2666 par1
MTVYHEQFALVPPQYPRRAVQEAENHRALAALYELVENAIATAENYVAYTEGRLVPLSSR
GSELLAASKELRERYRHEAPCGWTEQKVMQHCEQEVTVEEMAELLLRPPLDVSGIRSILR
TLQETRTQLPRGRFLLMRDNLSALKPHQPPDLVRDLSDVCGALYEIQYVDLMAELRAELS
ELDGERDKVQEKLKDAIHLYERALAKGDVVEVERAHRQLIAARYEFVNACAKLMHQILGE
DMASQESGFAAEMEALRRDATDSISRFVEALHERRQAFRNDLHNCDKKRLEEDGNHQKCL
EAYNAEERETAAQIGQIVEQKKKLVEELRQKARELRDITLKQKEMVEAQVRAKRAEEERV
TAYNEFVNMEEQQKHRLLRCLAYFDGMEELTADLRSYVDEMVTRIPQQNLRQVIDQLNDI
EAEAFMNAYSGFVSCCGELTVKKMHRLDTLERQARLLEHNRDSAMESLDPNMSNYRLELD
DIIEQMKGVSGVINALNATQDAGEQLFQSVEKGVLAKYERSGTPFVHPLQEYGIKSVEER
NRFVDRSMHYVENEERKVFEKRNVLNRMRQAVEEDEAATESAIRNLPAAPEY*
>TCRU_2667 hypothetical protein
MEARSRDIAEALRTAEATNAAEQARLRALFPMCADLPVSMEADNESLNLLRRRSSLLSDA
FGNSRAIDYIDRSLRRRVSLLALAPEETTIEFCQESEVVAFDVRMNRNVGKHRRLRHTTA
ANQRDGDVRGAVRNEGKAVLEEQGAKSRLEGDELGSELALKAGENLAAVLVDGEEEVARR
TIQQEEVLRRVEHCLSAVDACEAASREGLMMDEKSALYAQFLSSLMEQEELARNVVDNDH
NSAMMKLLHEKAAEEASVCRNEELAAALCGMMGEEADDRARLQQSEENKRNALLDEWLQL
EESALRKLVELNEVQLLDELMLEESDSRRKAALGGTDRASYRARENLCDEESLDRNRLHD
VESGEMNDLHKMALTERHSTISKAKIEELCDAEAQGRIAITANEEEGDVELGIMKLVVDE
MLLRQEIEEEGEHLLASTTNAFDELCKLMDTLNEMLLAVGSTEGEERAKLMDEENKAREQ
ITFEVEEGKATARDRTINTLNELLLTVKKAEREERAKLMDEENITRGEALLEAEKEEIEL
RRRRKMEEELRFSMDEEKKCRDVIVANEQEDINLLRRELEVAIAVEESVAKMIGSEEEAR
RSIGDTEEYEWGQLREEVGKASLEAIRAQEERETVEKEAQQMKRRQDAQALIKSVVFAYR
IRRRLANRFQNRKAQENKNAIAEILRMEFNTRSAICDEERLECQKIDEAKRSLLSLIGTR

AARTIAELEKEEDDARHELMDDFAFHLSQLQRASRKALAKRQDLIPSLKQLQEFEENEDR
MHATTVFTATGRRVGLSLSDDTGDEGDEEEEFDTPLTTGKYKGYTLDSIGTFLLQYERDL
QRFKASLEKHRVIVAADHDMLKKARDNATQDMVHGGTGALWIPTRPLPLSDLVRGPSAQY
RRGRIVDARGQRPVSRTTDAGGRAATPSDVHFFDGLVK*
>TCRU_2668 hypothetical protein, conserved
MKSRDFHSGRSGDVYREIPRWCLRKIPLLSGEEVESIVHMYDDNTGESEAMSEATHSTEA
TAARPTAVSNTTRQDSSLQLRLAGLPMFLQTEALVLRRHEQQYRQYMKELIDLSECITMV
CDGTLRHPSPNSASHVAEDSPAARRKKDDALQRMFRRAEEVEVCARNAAVERVRSAQRML
LAAAVAKHKKRARREKAHEEEEDALRVRRRRL*
>TCRU_2669 leucine-rich repeat protein (LRRP), putative
MYSRVLGLTSDGNEKEDGADGVVLLRNEVSEFTPAEIQALSRLELSDDPTPNAGHMPVDG
CSAPDVGCNGSRRKRRVNTRAASSFLRGEHQNCCRSFKSLLLPEERVGGKDSMADAVLST
SQLHAEDRALRDTSVVECFLNLTHLYVQHNHITSLEGLSLLVQLTVLVVHHNEVESLRPL
ADLGALRFVDARFNSISKLDPLEDLPRESLRYLSLSSNPCCRGESAVAAERDAYRQSILQ
CCPLLEMLDDLPCQISSSSDGDDSVVEGKEEEEVPDEGRTSSLPTSHDDAPEHCSHFRTR
ISHLMRIHRTPSMNASLPSPAVRNSSGSNDATTTARLCQQFEHRSGNIRKQAFDHAFKLP
CPDHSRWAGESVKRNGRDDDRDDDDESDVLPLSLMQERETKSRLYADIHFALGTSNAQVQ
QLMGNVWEDVGKVLRTRQALVRHRRERMELQRKQPSGAYTESLALLQKENRTTNLDKYRR
*
>TCRU_2670 hypothetical protein, conserved
MVAIYKPVSDCVWHQMPMDVRERIRAFRERAVSLERYHTRNAWSADFINAPPPGMVGRKP
GLVAFQERPKRPELLSLGNGLNDGGVAIVQRSSSMSSSKFGKSRHSLHFRGELWESVVKT
NEFGLKASFITDVVNATGLDGSRIEDVAFVITNVLIVTFTVSLPENPERMTEVHAALQRC
NFPRTTATYMRHRLALF*
>TCRU_2671 nucleolar protein
MAAAKTELAMELNDVVCFERLCADREWRNTLGKVIGFPTSTHVRVELFERAEQTNHSVSI
VDEKLQEMATDTGKLAVWEEKLELDHQLQQAVEEEDKASEKLFKLRDTTQQRQSKASARV
RETMEALDEARKAMTRVPPRQWRDVRAPGRPTESLVSICRAVMLALQEDRVKSWDGMQAV
MRQQNFTERLMHLDCTVTPLPLARRKKIVAELGVFRRELHGGNSGGEIGRREPSKLNRQP
SAAHATQIEMAMRDWLLAQVACSETREAEEHVVGDFFLEYQEQTNLVREVNSMRENISAL
KEKILEKKLAICGDTPLAALLIKDAEASKDTMFIKCMSNGRHVTEMLLRSSVLVVFGAKK
EEQLEDDENALFLSLTPEEVMQLRDAARAANEVHDLEEIEALYALSVREEEEMQELKTRM
EELRHKENFTEDDEEEMRQLDAALTDVVRRHETTQWRIRHLRALGRDKRFLKVRDVQDDM
VYSELNLTFSGDKWGVLLANTEYLMMVETALCNDLSHALGLPPGNMSNFRFAIKSLLVKL
TVKHSRDVTAEQLQALANEAEFLGLRGLYERITFRKSYPLNTPSQRLEYEEILRMQRIKE
NFAGAGLPEKLEDFADDSEGETDDENYRRPVVEIATVRYEYGLEARYGYPTLAHVGVPAG
FEALFEKGRTQLRAAMYPEEEEEAAEAVENAAVEDAEEKLDSVEKEPTAEEPLGNTEAEA
TAVEAEDVHAVHTDHVDAADHFEHAELSEHAEHSEHAEHSEHAEHSEHADAVGSAEGFLE
PKETLEAPKDGEQRDPDSQDKETHEL*
>TCRU_2672 microtubule-associated protein
MRRFEGDDWDLVVDNNRRKLEDAFSRETAAALGVSPRQVVLLDCRVGSLLMVFKVLGCAM
SDAEITERTEAHPYDEVYALYRPRIRSFECVDAAVPRGFRADADEVWTRSRVEFEGEDWD
YVLAMREADLLRAFSNATAEAFGVDEDHVRDVSARYVAGNLHFDFELRRPAALTKADVNA
RLKECAYAAVWALYEPRPLQEEKKAVTTHELGFEGEDWDYVLERRRAEVKDVLAVETARA
LGLEREDVLEVEVDAVPRSLIAFVTVRHPSLLSDRQVEETLARCEYRKLWALYETRPLES
SVLMRRFEGDDWDLVVDNNRRKLEDAFSRETAAALGVSPRQVVLLDCRVGSLLMVFKVLG
CAMSDAEITERTEAHPYDEVYALYRPRIRSFECVDAAVPRGFRADADEVWTRSRVEFEGE
DWDYVLAMREADLLRAFSNATAEAFGVDEDHVRDVSARYVAGNLHFDFELRRPAALTKAD
VNARLKECAYAAVWALYEPRPLQEEKKAVTTHELGFEGEDWDYVLERRRAEVKDVLAVET
ARALGLEREDVLEVEVDAVPRSLIAFVTVRHPSLLSDRQVEETLARCEYRKLWALYETRP
LESSGAVRPRLIVAEEVEAELDSITFLRNALRRARRERDEYLALLDPLLGLRGERQRILD
SLDAA*
>TCRU_2673 microtubule-associated protein
MSLEHVAEVKGGPGALRVGEMVVVMTRRVEEQTAHWTLGSVESAPYLYDVEIRLWEKQMD

VDWQEQFNVGESQEEGELIMHIKKTKEELEGSIQHVTELTKKLRQRRRSILREIDDVENH
ASQSRAAVKAAYIDVKGISYHHWHELKSYRAPSRMVLTILRAVMLLLSEDDAKTWPQMQR
VLRDPHFKSRILDYDPDKELSRERGDYILYECVRKKSFRYDRAVQGSQAMGPIYYWVLAQ
LDRSEATGKQYQLEKRKQESQKELRSVINEIHKQQQRMAEYQALMDSADDQLHAYRALQR
ESASLRGGQLTETRLREVAQQRYETSFAGAAGKEYLRAAFYTWKPTEYRIMVLRKSVLVN
FGTVPQDAWDKNNYTLDEPQIRMLDDALQQRQSVEETFYEKESEQQQQQHKKKEEEEIEE
GLFHPVDENYVPKSKMSVDWLERTFEGEDWKYILDRKRLAIMDTFCDETAEALQLPRSDI
SITQMTCGESNNLLMVSSEVWHDGSRSRGDLMDAMNAYLYPKLSALYSNELDGFAKLEKR
FDGKDWQYILTDHKNDIEYAFKNDTATALGKTMEDTEIQNITATAEALIIKYLLYIKENQ
AKKAKKAISNYKYPEICQLYSRLKPNTSTEDKIYSTKRIELEGEDWDYVLERRRAEVKDV
LAVETARALGLEREDVLEVEVDAVPRSLIAFVTVRHPSLLSDRQVEETLARCEYRKLWAL
YETRPLESSVLMRRFEGDDWDLVVDNNRRKLEDAFSRETAAALGVSPRQVVLLDCRVGSL
LMVFKVLGCAMSDAEITERTEAHPYDEVYALYRPRIRSFECVDAAVPRGFRADADEVWTR
SRVEFEGEDWDYVLAMREADLLRAFSNATAEAFGVDEDHVRDVSARYVAGNLHFDFELRR
PAALTKADVNARLKECAYAAVWALYEPRPLQEEKKAVTTHELGFEGEDWDYVLERRRAEV
KDVLAVETARALGLEREDVLEVEVDAVPRSLIAFVTVRHPSLLSDRQVEETLARCEYRKL
WALYETRPLESSVLMRRFEGDDWDLVVDNNRRKLEDAFSRETAAALGVSPRQVVLLDCRV
GSLLMVFKVLGCAMSDAEITERTEAHPYDEVYALYRPRIRSFECVDAAVPRGFRADADEV
WTRSRVEFEGEDWDYVLAMREADLLRAFSNATAEAFGVDEDHVRDVSARYVAGNLHFDFE
LRRPAALTKADVNARLKECAYAAVWALYEPRPLQEEKKAVTTHELGFEGEDWDYVLERRR
AEVKDVLAVETARALGLEREDVLEVEVDAVPRSLIAFVTVRHPSLLSDRQVEETLARCEY
RKLWALYETRPLESSVLMRRFEGDDWDLVVDNNRRKLEDAFSRETAAALGVSPRQVVLLD
CRVGSLLMVFKVLGCAMSDAEITERTEAHPYDEVYALYRPRIRSFECVDAAVPRGFRADA
DEVWTRSRVEFEGEDWDYVLAMREADLLRAFSNATAEAFGVDEDHVRDVSARYVAGNLHF
DFELRRPAALTETDVNARLKECAYAAVWALYEPRPLQEEKKAVTTHELGFEGEDWDYVLE
RRRAEVKDVLAVETARALGLEREDVLEVEVDAVPRSLIAFVTVRTCTSTSS*
>TCRU_2674 Domain of unknown function (DUF4457), putative
MSRLPIWGDSQQVWPGSTGRRVLHMHTDSATGRLSSGDSFTHCHALPLPMEIVNLGNVEG
ISDWSKSPGQYAMKCIQRYTGSPTFHTSDTIPFSSDSPRRGNSSAAPAITTILAPPEEPR
GQFDVCGGTRGDSGGLASYLAEEMPRGRFIVMNLLSTWGAPEEVGINGMEFFNENGDRII
PPAECLKKPSSSLQSPPGSTGGKIPQEKSKIVDGYHTILYTTPQSSLSLMVAYPIEGSSS
DSANASAGTDEVPRSDLANLVNGIHNTHDDTKLFTMPFNPDKHHLICFAFPKSVVISMVR
VHNYGGRGRVHTSKGVRLLEMTVDDELVFRGEIAPNNGDVVPFHRVGLENCENILFTEEP
RVLRRLLACPATETSVQGRAWGKERRTTIGVLPREIIGHSTTISTVLFGTVNEDKSKRMG
GERSVLIPAAVPVHAKGKHIIVQNSLGNFENATATPVTGIGYQTSGSLSMFSRYPQNVTS
LCFLLLGTWGDTEKIGLSGLRFRNAQGEMVSQRIAHWYVRFPSQRHESDVGEKWEDQLVH
LFDENAETAFTLPCEQGIEVIFIFDTPLPTLGFVEVANYSLGEHTFSGVKEARLFLSSAT
PNWSPDALVAAYSALWEINTATSCTTLNLHGIFEATPEEGVSLRKAPAFLSIPRFQVYDL
SLAAELRAFEGGSGALRNSLTHSLSASMTIRAEMALRRARMALKPRPEWFLEYQSYLTPL
LPVAYVLKVSLGICARSAMDLRKYAKKWMVNPLRACTFADENGETIQVFSRDGAKDTEGH
GGDVAGGVSRSENTHAFVTECLFTPRPNALQEDEEAAAVAAQAGIRVSLFQASLSLVYVF
DSPFCLSLLTLNRPLLQEEECAAWVRQIRVFMDDALVFDSGDVGVPRRAPPATVGPSSPL
RPAGEGFLPFAVGGGGAGNAVHRMRLKPLVFFTLDTVQLEEARREMMVAG*
>TCRU_2675 TLC domain containing protein, putative
MGRYGAYDLYVAPFVRDFTVLLPMVAVWFVLQWAMPSLYTRIFGAYFTRLSPKKREDVVV
RSVSVLNSFLMTGAAACFLSNLYAHNFTLPGEYYGDIPGYCFFRISIVSYFVWDIVVCFM
YGWGELWKIHAIASLLGAYLLSFPFSDHYASYFTGMFELSNAPLHLSVIMRTLDVKALNP
FVMAMEGAFALLFVVIRVLGGTIVAAAWLKLSCIRLVANYYTGGRLLHGEVPVVIAMTLI
VVIQLLQYIWCVEVVRRVIEVLAPSATTRWKAKQVRTDAIQLDK*
>TCRU_2676 deoxyhypusine hydroxylase, putative
MTQDFAAYEEEYKRLLDPNEPLDSRIRELYRLKQSIFRTPAGVHVLAKAIDTTDSVLLQH
ELVYNIGQCGLEEACPILERVIHATDVYDTVTRHEAVESLGAIASSSSKPILERYMDPAH
EPHKAIRDSCELALERIRIRELRGDAALKLPCNCPYVSVDPAPAFCDANTDGPVPFTVEE
LERLLCDTTGATSLWRRYQAMFSLRNMGTEAAVMALTRALRGDTVSALLRHEVAFVLGQM

EHPSSQAALIEALKDETEAPIVRHEAAEALGAIADPKALETLANYAEHKEQIVRDSCVVA
IEMHKYWSRFRQHGEAAA*
>TCRU_2677 hypothetical protein, conserved
MENHGVAEVDLLAEQLYADPDPTVRRRAQATLGVLAKEETDSHLYYAILRQSNSQYTLLL
IAQSIVSWFRSTRKWMSSEEQRELIVVHCGGCLTRMFDTGAPKHVVSSLLTAYARLTKLA
FENEPFLEAAVDFPLEMLIREQKGSSAAVLSLMLLNVMVQEFSRHDTSKSQTYLSFVAHR
HCSGNFREGPLLKIFLAALKQLEGITTDSVHISEVVKLLESCFLFDFRAIMMDETEGLPF
SLFPTSWKSTLLNKQNLGTVWGQHARLPYPHCATLLSGIVNICSVHRTLFDSSEERGEYL
EYTLTMLTEVTMIQDGRLKIPHYVELFAEACTRVLTSFGYRELRLLKAFEPWVNALSILS
VEVVSIPFGQEGSFSTASSILSFWATLTTSKRRSYHDASQRDIEDVVMQLLQNFVKARIC
NLEVNAVDPNFLINDDSHDLNNSVIAQSASYATICLLDPLTCISDLVTHLNQHFVAPILS
SPLSTGWLFYLVGSVVGPVVAAVEEGGVAKCSHLLSFVVWCSTNRLRAGDRDPAMFGPFV
ECGSLQFLTHLQTVFSGARQAPLATIVTNVFGSHSQMFQFILDSAGHNLLRGAEDARAVD
IIRTSAAVITAACRDATPELLQDLTFDLPPFSELPLAQSERTYKLRTDLMKALWFIRRSE
PTTYEQMTSYLSGIEANMQQTLNNELTSTSFVAGWLRDLRGACQAMNDEGNLFSDFLEWV
CGHSHVFVDVLNKSGESPVIVNALMRFLCELVATGRYGRFYLRPSGNSAVGLVLFVNLCA
FIEKAEEAVFSDYRIASIAESSSDCEKTLKPWMLSMNIMTKCIRGSFVPFGAMMYYNDRK
YENNAFHLVRKLTMLEPNVFRERAKFRAAALDLLRSMTEEQLYFPLTHLESNELLKLVEI
VVSICEDVDTPPDVLLHGLSFLGFIAGLVRDVKEILFTPTMQPSRGDAAAPPPLSLSHSF
VPILSSPSPASRAGQASPMSRFTREANGKLARLLAPHQELWQHLISVAMGIIAYRDHAVS
ASSGVVYPIFEAHPPFWYNFVEQFVASYPKRKQLGIREALSILTNASESQEKFFSEVFTF
RQALRRLNT*
>TCRU_2678 Sedlin, N-terminal conserved region containing protein,
putative
MPETEYPTWAIAAVAVFGRHTTPLFIRTFISPREVLEHPDAATCANLYAGEEDVVRLHFL
LFSSLDRCDDILRERRKQQQLEKGSSIASRQGPGSLRTVVGVSAGADVRFLGRLLRNHKF
TSYGFQSASGIRTILAIVGDIPLDAVLPLCRSTYEAASAALCNPFRTPRMHAHLLQSWSK
SGSQEPTILPAEYAENLRAAPTPERVAEEPSLAYSHGFREQIRTIIEPFTVTARSALI*
>TCRU_2679 Domain of unknown function (DUF4460), putative
MYKKALHSFFLKVHPDFFHHNRSQQLVNENSVARLNELLSWAKAFKSGTLRPPPATSITL
AFYTKPDDGGVGEDAPGGNQQRAAPSSSFSQGGFKAEKSSSPFLIESTFELADNFTPDDA
HRGSVERSVNKFLRDLLRRAACIDGITESISSAEDATAERAEARPLRRRPGPHRRKVEKP
KSLLDEATESMTLQWSITPAPTLDELMEADQILFARELSPLQSASALHTLRQHLGELRYP
AWESMPLIISNEFNIGEVAGTLTIPWDFTPLQFLAFLARNDKAILHCREAAMRFANTLEQ
LISEISHELDLDDILISCSHKDAILVLQLLQRNKELLRGYGLTDLTLEIGTRHAMRANGM
VIISCELTADELRPWLKKLQPKLALHKRLYRISKQLLEATMWHLKEFRTMAEPGGIDAFN
NDYTYAQRLEWAKELFRIGSSLAPWDWKEITFVLAPDVDVDWAKGLIALPYNFNGDAFVR
YVEEVQHEAKRRKREELLEDDAMRRQGAEDKRQQEHDEELMVQDDENKESGEKLSQDYLR
DMYRRTSPHMEEYLASSSHRVDTLSVERPLSHAVTFNSDAEAEDQLKWEGFYADPYVDQV
PTGDLDDVAHTFMLTNRWHREEAAKKMLEQLRDSYGKKSRRFDYQKMGDVLEINNAKVQP
KGFPTIPRGLRPTQ*
>TCRU_2680 hypothetical protein, conserved
MPHRMGIGLVERHRGGVSRELPGPAAAAAAAASGVGGGVIDEGDNYDEGPRPSSFVPTPE
PRVPATASTAASASFLHAGISTSPRSTRAERNTLGGSLSMSPAMDGASLRRQVRRRSSVA
HVRRLDLSTTVMDGVEWSWLCRDVLPTMSSLIYLGLAHMGLTDKRLVELIRECHLDSVSR
STALPLSSSSSLLSRRSGGRVASKSIMFGDASFSPTSREFSAGRKKPARALPTATGARGR
RELRGLSVLDLRGNHLTHRSAAPLGKLLLCVADTLDELHLSGNPLQDYGLQILGIYLAKL
KLTSLRNEQHFFSPSLVQQYAAILKRKKREAEHEVRLRHGVLQGPTHTKTDEWLRGENGG
RNAKEEEDDACGEAKIHLGISFLDLRDCQGSARGISEVLAGASRAHRLETILLAGNGALA
AALIPPKSTCTDGEMSPLATGNRGEGPSETNPSPTANRFSSFQELQYPCALSAVNLCRVP
LSIMCTPIGCRELFLNIFFCCPKLILLDVSRSLDFSKLPNSLLQQVLMDGREPSSDPRTY
WRLQRELEGVAEFTLDAVMIGRQSCVGSILCELVAHAAFNAQRRQTVAPSAFCHLKELYL
NGTGVTDVAVRGLAIAVSSSGSTGVLSSLTVLDMADNLLTVNGCLQVMHAFILDWPVTPS
VLSTLALQGNAGIYHDDNDTILLLQQVAEAAVQKRCEERQRRDPVDGKGFPSPLSIYLGA

VHAAIFSISSGGVTASTGVPRTHTTRSSWRTEGDNIAAAAAEEKETVKMARKREQGEVLA
VHESDFDREFPTFQLGEVGPAPSPQKAVRPLMEGPVGASFISPLGAQMAAPCDVSSIPPG
ETPRQFLFSMPSTPLMPQRTADRLRPPDQQNRTPLRQEIKEGGQRRRSFPILSPLVVDDS
SFIAGGSTTEFIAGETHRGSVFNIQPPTGVSSPSRGAGVVPRLTLAKGDDRRAMDVATAT
HGRYCNGGRGITPPSSTTNDHPVLQDRQTAVQRETSFTLASSPNSKAFKFGCLFASMDVS
KGRDSNVEKGNALTRSRVSGEEINKYNDGGGGGETDAGEKGARVMPETAKVLTLHGDKIL
GLKEAEDGESPVTVSYGGGAVGRERQTASKVEVTSSAVDGKWRMNTAARLGRLQKQFLSE
PLDESDRPVMMMTSTAHFRSDKTDTDDSTAVATAGKDATVMKPEPIQDLLLQKNGIGEEN
MRSDPVIPALGNLDDMETASLRPIKGRREKSFVMSYYHPMGHILCRGWRLLYRNDSVGED
ARGCVERDVWTLLQPLDTEQGSAVVSSVSFVVPSAEDMDNDAEYGITRLKIVSNERRSVL
AERLQHNANMENGIIAFPRLIAAIRRAEEDTVDVVAAMLDAAHGRLPPEYVGCTAEELVH
GRHGNEDELMAELGAAIAAGGSDEESQASFNEEECAADQLPSFSSTVDAFPLAEEPVEGI
AEDSQLLQSQKQTTELSEKSEEAEEEAIMPSAALSHESPLFNVADRPQATSVSAEEPPAD
TPETASPAGITVQLETGPATSAHAASATTEGVGEAMNQPARSVVGRMKTFLFSFPHREGH
CLCRGWRLLHRPDSVGEEARRLLEADVLSFLRPATEEEEKNADNDTRKISGDVYDDASAM
KAVESVSFTWEGSSSSTMQLQVVTSERRAVISQRIQQNVVGDEGMLPRFSELLRSNANYD
TIHAVETYLQRQASVDLRERIANRYRSIGTLVHYYHGDEAAMLVEIGAASMVDVEATVAP
AAADSAAVTSIPSREILEGESERGAKEVMATGDGEEAHRLLECGDGVQGLNESSLHLQET
LTGIHSNENVVEKEDHHTAENTPLSRRSPLSFLTLSTPIQREGDGRSVELTPHGGKSGSS
QHIHNSAANKSEKTVTKNEDVSSPSAHMQEAFAERVRRLQYLAYSAMAKGAILLDKRQRH
KLRICKGKWGRQPVTIAVEWDVFLVVYFLRGTRFGMKSHKTLVLVHPVASGVRCCVDVDN
NVGGRVHAIRIRLERAHSPDELGVPLQEIEERLHSVSMLNSRSRSMASLHASLIPMQSVT
NMSIGSKSSSVDTVDSVLSAPSTERLLQRSVSFQVTLSDTKKAREAVAAICGVVQHAVKM
IQQTISEQDRHAVARPLPATRTN*
>TCRU_2681 Reverse transcriptase (RNA-dependent DNA polymerase), putative
MDRPFPPYVLDVTIRDSLLGSAPGPEDTLNEFLHRLGPVARGTLRTMIHNSFANGSLPGS
WKMGDAIPIPKPGKDPCRPESHRPITLLSVLPKLTEGMIHRRLSALLPQHPRQLWICNSA
FYVGRGGTCYRQITRGLNEFSIVEYERPGDDVPTRRPRRHRLLVVSIDFPTAFDTIDHGK
LFGMLDRLPRLRPRTKRWLNNSLRGRHVRVCTREQHSRKQLASTGAPHGSVPGP*
>TCRU_2682 retrotransposon hot spot protein, RHS3, putative
MSGRPEEGLYGNLESQSSNVSQGGRRRTRSEFEGDTDYSSTTRRRLEGIYRPQWTMSSTV
EDILLEGSTNRTEMKLNDFLRSNLGEEWVVERNGNVTMGMFVLRPTMFINDSEILGLITA
SPSYQELERELKREQEERKILLEAIYKLRREGVYFLWQWREYEGRDTLTPLASGKLNGLL
AEIQKEERREADERAKREEEKLIREAEARVRQEAEERVRRREAEMKFTMSTNIEDVLFQG
GVRVKDIKLNDFLLLEMEGKGIVDTNRSVLLEEFFNEPTEYIHDARVLNGMKTTVRYLKM
GRAVMKEVDMEKVARMLHEKGVVSLEQWRNYEGKDTVSPLAKGTLDAALSRVQTSTSVVK
STVLEGLYESVYNASWSHVVEVSGSEGTVMKVEEGKPKQSWTYKEVGETREKDDSVQQSG
EAPPVLMVLTSDKGWPYSWEEDEFIRDCHVNCEVERAWRIVEHYLNEWFIPHGGTNLTPG
RLLLIGTPGIGKSMNAGSYLLYQLLHYDVEKLPVVLYVIGNDAFLFEKTTKTVTKYMGDF
SIDDVLRSLSIPGVNAYIIYDVAKGGRKPYQIATTRGWGMIVLSSPNEDNFDAWEKYKSP
KRIIMNCPEKDDVKAMCVWMKRNDSSVQAEYWKNINGRIDEVGPLLRYIFDDSKYNGRVQ
SCKDTLNSLSRIEAEYYLHFGTKEMLGGDKVSHKLVRIVRVRGVHNIESTFNGLMSPYLG
NLTLCKLAELMPPNDFILLILAIKDDLISKVLEKHSVFAFLSEAFVNAIIPKLNELKMKK
NKDAPPHLCALESRPHERPLKPLPLPLLENFEKKIEIESRVLYKPVAQNFPLLDAFFFME
SNPKTMVGLQITTASEHHTIPSTVNLFKENMAKYFNGWGEFSQGLSWEIIYIQHADSTPM
TGWQRCGPAKTDNLSDDEKEIVAFWEKEVHQYQVSVSSRDFRRKEALPIVEEEQEQETE*
>TCRU_2683 Amastin surface glycoprotein, putative
MSKLGAILYGVVGFLAFLFVLVGTPIDQFRAKEKGATGNTPCMTLWGIKEDCHSTKYEFT
VGEDFRECPSVLRLFRMAEAFSIISILLLLAATALGVAAHFCLKSLKIFATLLLVVSIVT
VGLVWIPMAYFYNHDVDNCLGTPLKTGSKYGGGFVIIVIGWCLIFVAVVLLRML*
>TCRU_2684 tuzin, putative
MHGVTPLFVLKIRDGSSPLRIYNEVVALACDRRLCHVIIEVPIESLTIAMTALPRLDFHL
VPNFSVSEAFRYTHHLIDPLELTHFVEVVGTNSNDLDELLAAVRHAHMSATTYTNQKLVK

AMRQLQAAWAKDPSLREAVIKLARFPFEEGQSEGYDYSSLRNEALRDIVMYNAVADVWMF
QQKVFHTAACCWQ*
>TCRU_2685 BNR repeat-like domain containing protein, putative
MSRRVFTSAVLLLLVVMMCSSGGASNTATSNSGNVQLPHTVDLFLPNQTLVVSKDGRSQG
TKRDAFVSPSLVSAGGVIAAFAEGRMETEYQGGPSIKPSSDVVAEYIDAAWNWSTLVEKV
NKGTWKAHTVVCAAEEEESLGVVLRPTTITKGNKVFHPAGGSDVSYEGVCWREGGLELKL
FVGDVTNSTPGDPGERIKWGDPRPLFDSKYSLNHKSKLNTLFPSGGSGVLMEDGTLVFSL
MARKENPNEAFYTIVYSKNGGKK*
>TCRU_2686 BNR repeat-like domain containing protein, putative
MSPPNCYNPRVTEWEGSLLMIVDCENDQRVYDSRDMGTTWTGTIGTLPGVWVNSQSEDYP
DGGLHVDALITSTIGGRKVMLYTQRGNYWKGQTERTNALCLWVTDNIRSFYVGPVGMGNA
GEKELASNLLYSDGYLHLLQRRGNGEDSAISLSRLTEELSAIKSVLSNSAQKDVFFSNLT
IPTAGLVAVLSNAASDDTWNDEYLSLNATVTTNAKKLRDGFQLTEPDSRVSLPVNTRANN
VRHVSLSHNFTVVASVTIEEAPSGNTPLLTAALGDAGPEYFMRLSYTADNK*
>TCRU_2687 hypothetical protein, conserved
MLQGNKASVYIDGELLGEEEAPSTDERPIDVADFCFGACDFDDDESSTKKKPSKKPRVTV
TNVFLYNRPLNSTAMTAIKERKPVPKRAPEPQAGGVPQTIASAVSAVSGPGEVPAAPAMP
MTLDLHAVKEVSEGGAAKRNTSWTEGAKFVVPEVSLNSAGSGLLPLLLLGLWVFSAQ*
>TCRU_2688 quiescin sulfhydryl oxidase
MWLLYHSITVNVDAGGDTNPLEAIQEYVRYFFSCEECRQHFLEFNFTRDEDPVLQLWRAH
NSVNARLAPVKEGADPFVPKRQFPDAEICGNCRNSLGAFDESEVAVFLRKWYEWDPSTIS
TSTNESGNSSYFFRPGRPMPLYKDPKQRHRDGVRYDSVPLHVFLTVFVTVAVLNAGIFRT
RRRSVRSLLHQHCRQKI*
>TCRU_2689 hypothetical protein, conserved
MLQGKKASVYIDGKLQRQEEVPLTGERQLELVRFCFGACGEDAGQKTKVTVKNVFLYNHP
LNSTEINALKDKAHTLNGPGGALAGWAALEGAAAREHAAVVGLTSAGSGLLPLLLLLVLW
VFAAA*
>TCRU_2690 hypothetical protein, conserved
MLQGKKASVYIDGKLQRQEEVPLTGERQLELVRLTKPRCGEDAGQKANVKVKNVFLYNRP
LNSTEMTALKDKAHTLNGPGGALAGWAALEGAAAREHAAVVGLTSAGSGLLPLLLLLVLW
VFAAA*
>TCRU_2691 hypothetical protein, conserved
MCVVNLCGLPTVIAHAAHFASDIRRLGPAAPVAVDLNSHHELRDSRLPSITAGEDLAATP
SGMEIELSDVPAQATRISGRSVSFPNLNAQRVLRVFHWTSTRLHGLGPPSAIPHCRDGRR
HPATGRHAATTETCRLCPA*
>TCRU_2692 RNase H, putative
MIPRIRHRRKTLLVVTDSQSLLAALNKGPLSQTDWTEDQIWQRLLTLTRAGWSVHLQFCY
GHCGVHANEPADQYATQTMESGQYTEQGIAPLWHTDLLTCFTTQLTNKWRSTIRQDTHRY
LLCGTRPSDLSGKDPIAQEVLHRQELVHLARARCGESELWGRLYWAVRDCTNQCRFCNIS
PEQSAYMRSNNDPTAPGTDTVPPSAREEDVSPVRRRTLTRRRKEKCPHCDSTLTGFSGLV
SHCRSFHPEHPPPLPELKCDFCDMVFPTRRSTAQHRSRCAHNPDATRHRNSSARRRSLLP
RDQPASTSTPIGPQETLHHLLLECPGTLAVRQRLGIEQDLRLGKFSQWQLLHSRKLLLLL
DHLFGTQMALYS*
>TCRU_2693 peroxisome biogenesis factor 1, putative
MQQSSFEIFIDSSRTDAFVTVSAKFLNDCLSPFYGSKTPPVVPLRLSDGKRNLYVGCLTR
KSHNLEPCKLLMSVILGRDLELENGAIVYCVPVYHPIKASRVLVSPASVDESEVAEQNAL
RIETQLLRQVQVIFPGMTISVVVFSDVHARVVVQRIEDSQGRELSSGCAVMSEGTEFVIA
TRSRQVAEKGTKPMWAILRCHPYGTYEATITSLTEEKASLFLNPATAERNHWCDGLVVGF
WDLACMSQILESKEVTPSFLRTNAWRAPIKYIKEMPEGVCCCTVFGQTSNVVVFPNPEEN
LPTVTDKDVAEDHCIFSSCKEAGFDRVAAVHGELSQELLRHLSGWFSRETELNTSLGEVN
GGNGNVLLCGGKGSGKTALVAAVLSRLRDVHVCVVQCGSGGGSRQLVSLQQALAECILCA
PSVLILDDFDAIAPVQREGAVAAVTGKTKSTLEEMLHCFSDAFTFAGRGSVVVLANCGNR
EDVYERLRSANCFAKITKVEALDRKARLALLQQIFPKESADTLEQLAALTENYTPFDIKK
VSVRIKSCSTDGDFPSLEKAKEVIVRFTPLSHTGIHFLRGEKQSLDSIGGLSNAKKILYD

TLVLPMKHPELFARLPLKTRSGLLLYGPSGCGKTFLVETLVNAAELNCIVVNGPEVFGKY
IGQSEQKIRDVFERAEAAAPCVVFFDEFDSVAPQRGVDNSGVTDRVVNQLLCYLDGVDER
KDVYVVAASSRPDLIDAALLRPGRLDKAVECPIPSYEERLEILLFCLDKISANLSRQEVE
DIARGTVNWTPADLSGLVSSAHIFVTRRVIERLSLDVAEMDFERSFAVANVGRDTTLEKI
EDTLKPLFGTVKKGQDLNLFTQMEMEDMKQALAVTRPSLTSKDILEYERMRYMFTGGDTG
NKRSKVGRKLAMR*
>TCRU_2694 SET domain containing protein, putative
MEFLFSEGPPRRFFCANRKTYREVWPYLLSRRVPAARSFLRWAARNGVAVHCALKLQFHS
GRGCQLVATRRIPAGRTLVSLPLTLSLSAAPPSEGKSFVHRWDPLETLTGVVVRELHNPR
GFHRRYLEFLHDLYNVDTIDMSTGRTLLHRELETMYMGNSMQAQGVSNGPCLPKEVFVSA
SQRVEWVRLHSLLRRMEQSLPHFASKSVPWGLSMVLSRAFSDDYGGLTLYPIIDFCLHSF
EPNSAVCFTSANSAQGKGVGLRWHDTDQFCAHLLTRRAISAGESVTLMYSPRRVVSTEDA
EYWKLRWGYVPN*
>TCRU_2695 ruvB-like DNA helicase, putative
MPGIKIEEVISTTKRQRVAAHSHVKGLGLDADGSAKPSADGFVGQVKAREAAGIVVELTR
SKKMAGRALLFAGPPGTGKTALALGIAKELGTKVPFCPMVGSEVYSAEVKKTEVLMENFR
RAIGLRIKEQKEVYEGEVTELRAEETDNPLGGYGKSIAHVIVTLKSVKGSKQLKLDAAIY
ESLEKEKVSVGDVIYIEASTGAVKRVGRSDAYIGDHDLEADEYVPLPKGDVHKKKEIIQD
VTLHDLDSANAKPNQGQDALSIVNSLMKQKKTEITEKLRHEINKVVNKYIDQGVAELVPG
VLFIDEVHMLDIECFTFLNKALESTLAPVVIFATNRGSCRIRGTDIRSPHGIPTDLLDRL
LIVRTTNYSIEEIVSIVDIRSQVEGVKVSDASLELLGQIGERTSLRYVVQLLTPALIIAE
TNGRTVIEAEDVMLVDGLFKDAKASAQLLHEHADEYVYQ*
>TCRU_2696 Tetratricopeptide repeat, putative
MKRILTFHSYMLHAATLDRLVGGMMNRFSVTSAAFAVRVCSTQPPFSTRCTVEELQKSAA
EFFERGEFMNAIKQWESVIESMDKADNNNNNNNRQYVLMSCLNNLACAYGEIGDYARKLQ
LLERSRDMVERVYGMDHPQYGMVLYNIASAYEEMGRYQEMEDLLLKSLEIHERKFHSKHA
KVGRVLLLLAEAHGHLGKHGAQLQVAERALEIVRRHCGPEHIQTTIALLTFSRAHGANGN
HAKRLQIAQQAYDIQERKLGALNPQIALTLLELADAHGANRDYFHQKDLLEKAIELQRRA
FGSQHTQLVSTYTALGDAYGNLDDRKNQFASYREALDIARQRYRGNHIVIGAASNKCAWG
YLRIGKVEEAKTLAEEARRIIEGMVSEKHPAAVELRATLQELKRVTGGTGKNV*
>TCRU_2697 hypothetical protein, conserved
MPVTPNDDIVEISRRCDFLCMALASAEDGVKTNPTQRYMYLCKASGERPNHTFLHFSKGT
CGTRLDLHRAYLSQRAILPILLTLPFCPWLEHINLREERLTTTLVELLCESLRNLPCIRT
IDVSMNPFGSFGVQALLRLVLRKRSIVDCYVGDTQSVGSLLRRLQMACERNRRDAVDMEE
EEEEEEEDEEEEKAFSTLPAECPGS*
>TCRU_2698 amidinotransferase, putative
MATLMMLQSRFFGSKKRVHDNKFITVTEVSENQAQQDNCLVIDLQRKIEERLLNDAKARV
IYLNLNEEPRTMRSAYENKVGALFVNDSISVHHFTDARGRITRRLIFLYPMSKLRRGELP
KVQLLKKLDKTVKSEEPSGLELVDLRDFESHDLCLEGMGAMNFSYNGEFVYMALSDRSSE
KLLDVVCSPENLNIPKEKRFVFTAVLPRFSGENKRCVGEDVVHHTNLIGWCGKGICAWGL
NFLRFSSEEKKEAFFEHLEATYKKIINLSAEEIRAFAGNACEIALSSEEEERHVLCISNE
ALNSLHHRNYQILEEWYGRENIFVFYAETLERRSGTSISSLISCPVTHGEVLPAPGEVTA
LEVAHVDEKVIANLLNR*
>TCRU_2699 ZFP family member, putative
MFGGGEEYFREPPSIDRDTLRRFALFCARLRAAEKPGKKTVAESAELARGVGDNEMAFEL
VVGALFRHIKSWTGNKQLACWYILDKLCKEDRDKYGYTASKYILEIGRDYIPFEDPVLGP
KYESLVEHWEGVFQSHVVDALWLAKKDRLWAIEHPNEVLQQKEEEERQWKLEEMAMEDED
GLNDYGQPCMDYLQGRCFWGDACRLYHPPGEEGTMPLECRLGDWKCSSCGAINRHFQRRC
SSCVREKPQYKKGRKPTAEEALLSSPDPNVYAVLRRQFGYDPNVVEEAVAHWKTRLETTS
IEEYKEERRAAYRMRILGRAPTSKLEESIRLQKNYPDIDIGLPEDVVDPCAAPGRMENES
LLPAGTSPVSAVGLLAQTIVERGARDPKLPQLLFELAHQVKQVARDSGIKLSLTQCETLM
TACKIVFSAWGADRGATPFVPLFFKELRHTEDGLGLSTEQQEHLTSITKEFCTH*
>TCRU_2700 hypothetical protein, conserved
MRLSRRVQLNPEVIDSSLQRLNCVSQNIIEVDISPTVLALLTSVAPDVVRQRVAELPSSA

AGDIGKEEAIDFGGAGMNTALALSLHTVLLSRNRLTTTLGLVQFKNVVRLSLLGNRVRRI
EDCEALSLLPSLQYLTLEFNPVTSLPHYRAHILRICSWPDTLNSKNCRLRKLDTRSVLPA
EVERAAQCLQREKVTLGELVHRMRFLALLSEAEKRIALHNEIRRRGFMLQDSFLTLTVES
IVTRCSAQLLALVDVSTASHLARRLMGGKCRICAVTPESSFDDDNSNEKELSQLATSFGH
SLSSSKTLSLQHPYQAELTAFCKDWSRDVFRRATTSLDHRICGLLLNIAHALGEELTVMD
VDYLNKLWFTQIAKVDSCKFYQFQNPKEKPVANGSAPTVAARSEKPCEGINGSMKESTWE
EFVRVPLSPSETHPHAPRVEAMIGNEDVLSLRSISPITQQTVKCSDVVANCERQKSSCDA
PEHSFQKLPEIERVPNDGNNGDELKKSPKVEKCNSDWASIEEFPLMAPVPFPAPKDELAL
EQELFHKLKCHVRRRILRVWRSKVRRKQQETLCANFIQRRFEGFLALSAPTPHAISSTLQ
MLPRKEQKRVLFQLWREQTRMSYAPRLLRLAQLFSRWRWQTYQQEIINYFAAKRRTRTLT
EVWHCWAEALHVHIADRRNRSGEKIQNIAVLPVATSGFQSPVRKGCSRMMMSSDRRLKET
HDVFLEDCSSFKVTTDATPGLTCSTKPSVNGAFNVPQMPHLEGTSATASRISLPMAIPKM
VHSPSVQPLFSCEKATQTLPPSNDGVAEECKDELCLEAKKAVEVMQADRLRLVDRLIALE
QRVCEESLRVQHREEEIEDLKQKLKAMTVREECVGSTIGDYQREIEHLKVIVRALREERR
ELLRPIFQ*
>TCRU_2701 DNA topoisomerase IB, large subunit
MSKKEKNLVKEDAVVKEEDDDSDRSENREELNWWELENVQFSTKGQKRWDTLCHNGVMFP
PEYKPHGIPIYYEGREFKLTPEEEEVATMFAVMREHDYYRNEIFRRNFFSSWREILDRRQ
HPIRRLELCDFEPIYQWHLREREKKLSRTKEEKKQLRLEAEKEAEPYKWCVWDGKKEQVA
NFRVEPPGLFRGRGQHPMMGKLKKRVEPEDITINIDEFSPIPKPPEGHRWKEVLHEHNVT
WLAMWRDSILGSFKYVMLAPSSAIKGQSDMLKFEKARELKNHVDEIRRCYIEDFESRELM
KAQRAVAMYFIDKLALRVGNEKGSDEADTVGCCSLRVEHIELKPDHVVKFDFLGKDSIRY
ENEAVVLPRVYELLRRFTKGKKTGDDIFDMITPTVLNDHLKSFMAGLSAKVFRTYNASIT
LDRWFKEKPVPPSASVADKLAYFNKANTEVAILCNHQKSISKNHHNLMHQLTQKSSYTRT
IIDALKRAQETTKKKSLEQAVKEYFAEMDEMQYKWLEAYGTEEQKKEYDEIVKNRGMPRQ
SSSTSKSNGSRSNGKKKKRNSGDGERGKKKRAKSAKKSKKQKKGVKKSKKTTSHKSRSRA
KNAEVSESEDDMSVADIVKKKSKIDTSNKDGRRGRVKRDRGGNPKLKAEASDDEDVPLSA
LFGA*
>TCRU_2702 mago nashi-like protein, putative
MTTEVPCEEGAMTMPEETMESHLYHLRYFAGHTGRYGNEFLEFDIRDDGTLKYGNNSRYR
NENIIKKQARVSPAVLEEIKRVIITSGVLESDDERWPQPDRNGRQELEIHLGNTHISLVT
NKITSISEVEQTDNSKGLETFYYFVRDIKSLVLALVSLHFKIKAC*
>TCRU_2703 serine/arginine-rich protein specific kinase SRPK, putative
MPKFNKKTRGWCAKKNGKSAPTKKKTKYIDPCGTNEVDASINTAIEEVESHEEPLGQPHF
SKIKRKKNDKLQLQEIGRLTLKPGMTVAQAHEKANKVYQQKPLQNIPDPSFEEEEEGYEE
GEEDHGGSDEDYSDTANERSVEYRKGGYHPVVVGEVYHDRYRVVRKLGWGYFSTVWLVWD
YVTKRYQALKVQKSAKHYTEAAYDEIKLLGEIMSSDPDKTCCCARMNDYFEHTGPNGVHV
CMVFDVYGEDLLSLIDRYEYRGVPLPIVKCISRQVLVGLEHLHSLDIIHTDLKPENVLLS
SPKHAIISLMKRYHPPPLHQRLRLVERDPKTMTKSQRRRYYKKLKAIEQNGKKNENISEK
GNQCATAKTHKNSIEQNREQDQAEAISESETDSDWEIERLHHVVLADFGNSCWTYRQFTD
EVQTRQYRCPEVILGEPYSTPIDLWSAACLIFELITGEFLFDPRKGENYSRDEDHLALMT
ELLGDLPESMRLGEGKYRSQFYNSRGALRNIKDLNFWSLDDVLYRKHKFTRKKAEEIADF
LLPMLEFDPQKRATATEMLANFEHFFEIKEDDYSPFCFVSSDADREMVEASTSNEEDSET
SGDSNDADDESENNSLGREKTRCGNKEMDSAQFWDEHPLLAREFLEKRGLSLLDIHDLLA
GKELEDPAAHKSALEVIHLLSEEAADARGEGHADRDGDATSRVEELNNSIGDAGSD*
>TCRU_2704 homoserine kinase, putative
MSDPPKKVVLRVPATTANLGPAYDVLGMALSIFMEVTVEHADEFSVHLEGDGSEHISADR
ENLMVKACELAFTEFAKKAMPPLKFTMKSNIPFGCGCGSSSAAAVAGFVAGMKLCGLTMK
TEEEEALLQVIARFEGHPDNAAPAIYGGIQLGYKDNNGRFLTYRVPTPASLLVVLFVPKN
KMKLNTHATRNLIPSSVSLEDTVFNISRSSILVLALCTGDLRLLKSCDDKLHQKQRADAL
FPHFRPCVDAAMAAGAHYAFLSGAGPSVCALVGGRHGDPLTQPRGERIAESVAEAMIQAA
NAVGVAGRAILTQPSDQGVHCVGVTTIRPDMEYISI*
>TCRU_2705 hypothetical protein, conserved

MAMMMTGRVPLVCALCVLLCGAGGRCDEEERAVSGSGDEPPPGSAEHGTPRKETQELKVG
APGVIETASPPSLKPTGEDKDDDDEDDAGGDEDDDETDEAKEKRREGQSNKGGTVLPDTG
SGERNLTGSGQETGQSNVPAGGISPSGSQLSNANPLRTEVEEKNDTDKNTPAAENALKTA
NGENTLPGGIAEGNPPSPPEEGFDSREQDGEDTTSEDEKNAPPPETAATPQSHRDEGSEG
TGEDTKATTVTANTTDTTNTQNSDSSTAASHTTSPLLLLLVVACAAAAVVAA*
>TCRU_2706 retrotransposon hot spot protein, RHS3, putative
MERGGAWPRPRLMVLASDKAWPYSWGACEFNRDCYVNCEVRRAWQIVKGVNKWFSGHGGT
DFKPDPFVLIGTPGIGKSMAAGSYLLYQLLHYDAERLPAVACFICN*
>TCRU_2707 retrotransposon hot spot protein, RHS3, putative
MNCPDESDVRGMRVWEQRSKPPQQQAEYWREVRGRMDKVGPILRHIFDEQSYDDRIEKCR
ETVEETISPETQYYTGLGNSTMWGGSSVFHWLAKVVRIREEACKGGFSLNLPISDHLCNR
TLCMLAKLMQQDDFNSLIETQA*
>TCRU_2708 hypothetical protein, conserved
MVPNASTKRPSFANGPRILVALNVSGIVSVTYGGREHVAADNTDEVSEHDATGHKSLVLE
NGVAGSGFVAEGDADGLSQRNACGRDNKPQ*
>TCRU_2709 Reverse transcriptase (RNA-dependent DNA polymerase),
putative
MDRPLTPYELDVAIRDSSLGSAPGHDNMLNEFLHRLGPVACGTPRTMIHNSFADGSLPGS
WNTVDTIPIPKPEKDPCRPVSYRPITLLSVLLKLTEGMIHRRLSALLPHRPRQFGFTPPR
STSDVVTLVIGKIARGLNESSTVEYERPGGGAPQATLVTIARS*
>TCRU_2710 retrotransposon hot spot protein, RHS3, putative
MAAGSYLLYQLLHCDVTKIQVVVHCFGGGDAYVSDKTTRAVKRCGDEDMCVSELRRLRGH
GRNVYITYDVAKEGTPPPRHFAPTSGCGVIAVSFPKVTNYDDWAKQLQAARIIVNCPDEM
DVKAMCAWITRDETKEKQAECWKEVKKHMYLLGPIPRHVFDEEAFKERCGAVRFALQSIN
EVTVKEHFSRGGESPWYSEDPSHKPVKFVREIYAGGVTPFNAPISACLEERTLERLPSVA
K*
>TCRU_2711 retrotransposon hot spot protein, RHS3, putative
MKEKDTITPLARGTPNGVLTQVLTEARREAEERLRRTQEMKFTISSNIEEVLFKGRVRVN
EMKLNDFITRELDGRGVVDTNRDVLLEEFFKDPTKYIRDEGALNEMQASGHYLGMKRAVK
GEVIFDEDTRRLCDKGVSNLPGWSLLLRR*
>TCRU_2712 BNR repeat-like domain containing protein, putative
MSRRVFTSAVLLLLVVMMCYDTGAAATNGAASCPVSSPGKHFAWRDVKEGEKVDSLHAPA
LVEVNGGVFAVAKAQCTKDEGCVFTGIASELLEFNGETLKEELHESKLKTQVLDECSASE
ERQCPSQAVKPDSSQRVMNLRVGRPTTLVKGSDIYMLVGNYSRTAANNPEESV*
>TCRU_2713 hypothetical protein, conserved
MTLVPYTPSEWCDIGARLWDMVSQCGETQVQMTFINGNQMSDETLTVAPSSTGLCLFHGP
VSKAWQDSTLIGHIANLRAPQIPNFETQALLPAMGAARELGHQQGLITAERERLNIDYAN
AVADVQNRNAQLNSQFQKAHHNLSVRESTIAGAGNQVLELRQQLEADRAQLRREFNLGV
LTGQLQEREARLNALQTARDAETAGRDESPAT*
>TCRU_2714 hypothetical protein, conserved
MSEDEEDIIVLQVCANQRCLGIEDLEFDEESGEMYCVNCRELYARAEDEGFRLLLTDEDM
PLINMIFNCFDGGKRYWTYEDFDRFRGYTGQSSETAINSHEALRDFFKEEYDIEISKGAT
GEYVVYKQNLEEMYGGYIYNNINALIADCDSLEDAGMIRTATLE*
>TCRU_2715 hypothetical protein
MLEVSTVSSPTSTATLRRKEVQLFHRAQERWKRRIAAVSVHELRLEAEKDHLRQLRRHGS
SRAHQTKSPGLFQEKGKCEPAVTVTEENETSREGHAEARDEPQPHLASAPPRLPPPPPPP
RGK*
>TCRU_2716 PX domain containing protein, putative
MVSKYPTIRLNVVDASPSGEDIVLKLCTMDPERPTRILSVIEQRYSQFLLLHATMCAFLA
EIELPPLAVSGFFGGFDANYLEDSRVSLEVFLNSVASHRLLCNDPDFLSLIGLEQDMCRE
QREEENPKREEYKKWAVICFMTVPGRAIFLG*
>TCRU_2717 hypothetical protein, conserved
MKERMPSVAEVESLIALTRRSLAIPPRNVYEAENAYLANVERLKEARMKLGQFTGEYVER
LLREMDKLEQDLNDMVIRKSNPVDALLDVDFDAEGMDNDLDEVAAAEKEMEKKRDGRKKQ

GGRHTSNKKTQAKADTTNKKEGIGGTSDLTPEGAVAQEEEKDTATVAETADVEVEVLAKY
NECSSSEIPQEVLGPGRCLMVPNTPLVRLDFTSPVDYDGILCQCRVTLHRAVVTALTYGV
SSTTASNCVAAENSLEIVKADGDDEPPCNVSGAIRHEERQDAEDEAELEEMDEASVIAKL
SKQLVAEYDAAQGGKEDEESGTNLLPLDVPPKLCDSLRSFTFLPWVILMCHGGYFAGGVF
LDKKPVVHKSFQRYVVRKKQGGKQSSNEKEGGSYGSVGSQIRREQEVKWKTDVRDILLSW
RNYIDAAAIVLYVAPGPHNRAVLTDFSGLPAITTGNGERAVSPVSLKDPRVRKAPLTTHR
PTFQEVQRIYMTVSTCTVEYVRCIV*
>TCRU_2718 hypothetical protein, conserved
MADESFFYGLLSAFFRSAAYSCLTGCLHSAPFEALRSFIQGDVTIIMAAPSLTGFECDNT
NDCKESDEDYGDDLHRGADYLRVLVHESREGLNAVPTIPGLAEPLAFALSTAIISAPCVE
ADPFTVEFTQQLSSVCAADPALALSHVSQRCLACDLMSVLSRPPPPVFFLCPIRNTLRCG
GYLFA*
>TCRU_2719 hypothetical protein
MHRHAWRGQIFWDFDVRQRHGGSPGGAAAGRGESCIGAWSLLHGLAAHGGAAARRRTGLA
AGTSVGAAARAECAAASGAQRPTAGAARGGAARRVVFCCEGGGGLCARIAGEGADGAAAA
RGSC*
>TCRU_2720 hypothetical protein
MQNGFSQREVPSSVIDSGRDSPFPSQLPFSATRVPLLDNTVNRDDWDNDDNDDNDAGGGS
SNSSFVDLDQIAVQMNVRVEDLLRALQNGLGGGGGYTAPENRLRSQFSFAGSTSLNRGDD
NNNGTRNNCSGIDFFSYVDHDNESNHADNRSGENESGMFGVLRQHLSKEALSKTQLLSFA
VEDSNLSSQEREQQIREGTGTETVTAPIVFLSTSSTRGSGLHLSPIPSTEPLMRANAPSP
LPSPSPQPPRRIRFGSRVVTSVCVYSVNNEVYFGLQFRQHWSSWAALLCGFLLETVFEVH
LDWFAKVGSATTHDTIPIAHWVYTYRSLFSVVYGLLWLLCGAWRDGVRSLVAVTAEPLGV
CMKSLAVTLVSSFFFSLAAASMVLTNEMSGSSLLFTTTVMHCLWILFYRVSRAQMVFLVE
VCGSIMLIVGNVLCNVDGMRLMGLRDTIYGNLLMSGGSLLFATAFLVMAYGLQRGLCSTT
GLTVAVGIELFFTTFIMGVCYGYSMSSGVGDSLIAGFQHANAMHSCLLAAEDLFFNVMYL
YALYHLDVLSVSACFSLKVAVVPIVEHFLVWRVAEKVPPVVRARWGPLLFVGVGVVAVAA
AFVMFFASVRRRFVARRLFHMRGLRRVPDPYQKKKRGRHERRQRLVAPSSSW*
>TCRU_2721 hypothetical protein
MSITLRGELSQSRNADIRAMETRNCTALVTTVGIIMKGMRMMARSEMAGKTISGVSSCPR
MWYRRSTTAIMTGGVASLMNDVSTRQTCTPLRYCSSMSRFASMFAMKRGSHVINFAMRIP
EKNSFVAFTRASVVVARRLRSRIMRRITSALSGSVVLRAATATSALHPTSRYKRKMENTA
TIGELQRYMQNCRNSSARSTSVLTILIILPVLISGIANDLGATTRHFSNITAVSALRKRR
PPLMLM*
>TCRU_2722 60S ribosomal protein L19, putative
MVSLKLQARLAADILRCGRHRVWLDPNEASEISNANSRKSVRKLIKDGLIIRKPVKVHSR
SRWRHMKEAKSMGRHEGAGRREGTREARMPSKELWMRRLRILRRLLRKYREEKKIDRHIY
RELYVKAKGNVFRNKRNLMEHIHKVKNEKKKERQLAEQLAAKRLKDEQHRHKARKQELRK
REKDRERARREDAAAAAAAKQKAAAKKAAAPSGKKSAKAATAPAKAAAAPAKAAAAPAKA
AAAPAKAAAAPAKAAAAPAKAATAPAKAAAAPAKAATAPAKAAAAPAKAAAAPAKAATAP
AKAAAAPAKAATAPAKAAAAPAKAATAPAKAAAAPAKAATAPAKAAAAPAKAAAAPAKAA
TAPVGKKAGGKK*
>TCRU_2723 hypothetical protein, conserved
MSHVTADLEYFKCDMCGVYLHKDIFCDHRRECKGLDSKELKKSQCHQIGMALDKEARHRI
ASRMVDGATLVPVELAERHQQARVRRNVANSYQAEIDKRLQEQLAPERMRALSAFLSE*
>TCRU_2724 hypothetical protein, conserved
MRRSLPWSVGDQQHVASVVRRWRKSRVHLECPRLCFLRALPTGMLGSSVATSARGACQED
DETIAASACEASLTIITPGRARRTMCRHAADKRAHSAADWAGGHQSAARWSTRCCGAHVG
KRFRRRQRRAGLLGKERDGTTDTGSSL*
>TCRU_2725 hypothetical protein, conserved
MTASASAVTLRGIPQCHGEHLKPTVRTRSTSESGTTQISSATSSCAASEPRRSDSIAERE
SVAAGIRVGDWDAAARRGTENCLWPSSVAGHSARQEHARLPAAAR*
>TCRU_2726 Protein of unknown function (DUF3522), putative
MRPRYNRNEASWVTFITCCLSHLALLPAIRYLQKRGMHYEVCVSVFSTLVSFLYHSSESL

RTPLFLSTIRWHRLDNIGAISSITIVCLHVCSFESEKLVNYLKYFFLFVTIVLQEADPWN
ILYTAIPILCALAMVLVAMLLSPIRRRRIAGKNLYVGMASSLLGVICFLRGLDEDRDTYR
AWHGLFHVLVGMGIYNIFLALGDWGKGSYSRKMSMTSPSFDV*
>TCRU_2727 Protein of unknown function (DUF3522), putative
MRDEPAWALFATTVVSHVPMIPTAVLFYKRRYVYEACVAAFGLASSLLYHTCQSFDVEMF
LDELGWHRLDNIAVLAGVGMWFVFLCTFKDPVVERSVKYFTLLASIIIEEKDPWNVAYTV
VPITLFACIPVAVFLYTRQVPAIEYRQFIIAAIFMCLAVPFFIAGLNDTEDPCRIYHGMW
HLFGGISSYFMWLMVKTPGATGPYPKFGSITVRGDTLL*
>TCRU_2728 retrotransposon hot spot protein, RHS3, putative
MVLTSDDEWPYTMNAPHRCGNDLCVNCEVDRVWQTVKGDLTKWFSSHGRTEFKPKKRVLI
GTSGIGKSMGAGSHLLYQLLQYDAKRLQMVAYSVAEQTFLFDKTTRTMSEDVVEPDTLNI
VDGLLDRGFKGCLIYDVAMKGCQPSTSLSCKGWGMILVTSPHAS*
>TCRU_2729 retrotransposon hot spot protein, RHS3, putative
MNCPDESDVRAMCVWKKHNRPAQRQADYGHEVKGRMDNVGPLLRYIFDEQAYDDCIEKCH
EAVDGMAFLETGYGFVLGDSMTWDDNNVFH*
>TCRU_2730 BNR repeat-like domain containing protein, putative
MDVARKAGYDSFRAPSLVEVDGVVVAVAEAHYKNPKESELYAGIAAKWLKGNEKKWMNGK
VVGMNHFDTKVDRLLGATSIVYYGEMNALFGGCGM*
>TCRU_2731 BNR repeat-like domain containing protein, putative
MIGSFRIIRLPRTASSLWSLNGGQRSPHDDVVCGRQPQGLGGGRKGESVDGGIRPSFTRV
GQLTDASGARRAGWLCQRDDRWTERRPFQPAGVFLEGGEEAGRVDLRLTDMQRIYDVGPV
SAENERFAASTLLYATDEVRSLLVEKEWIKLYYSHGVAAADDECNIAFVDLTEKLEDVKR
VLVAWKEKDA*
>TCRU_2732 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MEEEAPSSGVLAPALSSTPSVVSRQEVLESKIPVSGGRPEGGREHLPSNAAALMMGQAGK
ASEGSSHNGYTDGWPQRSISRDFFFESVHKEPSTANTLAGDKQHDDPEGETHACTAVGTN
SGPDSFSSTDMTPADVATAAPEPGADPATAHHNGNVLDGAGAAPAHSSTTPGKTKVPSEF
NAAPALGSDPFDLESVTALVSVGLRCGNTVHGCVSRVLLLLLVGLWGAAALC*
>TCRU_2733 hypothetical protein, conserved
MTTKWSPPSDTHPIIYGVCNDARGSPVTNYGEDLNIGMPVTVLDCGACTVDAVCFAARTS
SISGCECVCAAGGHGDTCLPAAVPDGLGPLPLPDADNTEVRCVHGGIIGFVDVPDPGVRG
LCFVNVTFTAAVFLDLSYFDAPQQTLNITLLQCVFMSLLIKGSDARVHVNVTSSMLDSGA
LVFEGHFGASSQILVAGSKLLTMSSYAILFLNFFLG*
>TCRU_2734 hypothetical protein, conserved
MQRRCGVLHARDGVGGPQLVLVQLQGRMAWRVVSSPRGARRGCAALAGESRRRQHELRGE
PDADKPHAEHVEVAPLLLGCDVQRRGCCADVFL*
>TCRU_2735 hypothetical protein, conserved
MFQLIHVTPGSAVLLVLLVVMFCAGGCLAASLTYSCPSDKAMRAHRAKSIPAVVRDVPFG
SEGASQTCTVIGRNGWAPIRMNVSTRDLDDARKYCSSERYCAMNSLVAIASVKATFFYAE
KREVFVSLYFAATVR*
>TCRU_2736 hypothetical protein
MLSCRGRGHSHSVCGGAPRGLSGAQRLVGIAAEEWLKGYGCHWSLQRCVVRFLLVDTLDI
FGSDLRVRHLLGDRGAVAESTCEAFCNDWSARVSASGVCLHIVDGQEDAAAAWAGRR*
>TCRU_2737 retrotransposon hot spot protein, RHS3, putative
MERTVRDEMDMEGDVRKLYKNGVDTLLKWSLAAAEVKAAVHNSTKHFLDAAAEEARKTKK
SSAPIYLEGHYESVYNARWHHVMEVPGGEGTGMEVREGNHHSHGRTRQLAELSKRMTVCG
DPVQHFLGRWCLPRRRDGRTRGIRYRIFLMTFL*
>TCRU_2738 retrotransposon hot spot protein, RHS3, putative
MAPRRGSCDGSDAATRRGVEGTRQPQWTMSSSVKDVLLKGKESITNMRLNDFLRNYFDGR
GVEEFSENVIMKDFLISPNEFIQDELFLRTIEASPPYQEQKKGREEFYMLLEASNKLSHE
RIFTLRQWRDFERKDKVTPLARAQINTAYS*
>TCRU_2739 vacuolar assembly protein vps41, putative
MPHVGSRIANVARSKANDVWLMTAVVHVATSDLGKHYETLYRRRGAAIRVDPRMAVCSFC

HQPTLADVVIFGCSHTYHANCVIGYLAGEGVLLVQPADVDVGRFFNHPEEYLRPGSRKVS
PRCLVCCEVRGAVK*
>TCRU_2740 U3 small nuclear ribonucleoprotein (snRNP), putative
MRRSVIRLRKEFLERKQNERVHEAIHARKEQFREAVSNATPLPGHLRKDALALKKFTELD
DDQTRTLQTSVDDEYANAGVEDPRVLVTTSREPSQKLLEFAKEIRLVIPSAVRMNRGNLS
VRQLMDAARRGQYSDVVVLQESQGVPDSLTVSHLPLGPTVVFTIHNLVTRHDIQDVGTMS
EQHPHLIFENFTTRLGRRVRDVLKFLFPVPKPDATRVLTFDNQNDFVSFRHHTFRAVKGR
EVQLTEVGPRMELAPYRITLGTLEMDDAETEWVLQPYMNTAKKRRLL*
>TCRU_2741 L-threonine 3-dehydrogenase, putative
MLRFSLPLFAAAVPRVLITGGLGQIGTDLTLTLREKFGADSVLTSDLVTPPEKHPLAGGK
GYQQLNCMDRDAYEKLVKDFKPTWLFHLPAIMSVRGEAEPQLAMNLNINSTRHALDLARD
YKMRCFIPSTIAAFGDKCGKVNTKDDTILNPSTVYGVTKVFTELIGTYYREKMGTDFRSV
RFPGIISAATLPGGGATDYAIHMYHCALLGKKYVCPVRRDEPLPMLYMPDALGGVVKLME
ASDSCLKRAVYNISGFSFTPEQLRASIEARMKRPLEVEYVEGPAQSIAHSWPDSLDDSNA
RQDWGYETKYDVDKMTDDMLRQIPVLHGLPSL*
>TCRU_2742 zinc finger protein family member, putative
MPSKGSAANTTTGSQLEVFDSNFKCLYTVPSHLVVHTPPARFNISRFVICRNYRCGEADS
CPKGEGCRFVHADVDYSTLEGQPIHVNYIWRDEKLCIYERLPPGDVLEVLSHSGSEKPDL
IPSERILVTRRALSYREDNSRRLSHCVHYYCNRMCNRGENCNFIHAVYVDPNVEGDFKRP
PAQSMSQFNSSTRSSQTDASDSPLEWKSQMNSSLRSYGRLPSNKHFGSQVFPKTQSADSL
PLNVVPQELGPFCMAASQSANEAVTSVPLNGSNMSFNRNNNSSVEYNKIFEDAHILRIER
GTRGSGMGSFTPMSQTPMMSSLGLSCDSSGALPIPGEGAKNIPRVAYKTFEGSIGQGFLG
SPCGFTVSPATPMQGAGNFSLSFTTPSPCQMPLNSPQETVLAACGGVITRNKAADRHSGH
MDKLLRVYRHNPYKPIN*
>TCRU_2743 Long-chain-fatty-acid--CoA ligase 5 (EC 6.2.1.3) (Long-
chain acyl-CoA synthetase 5) (LACS 5), putative
MNTVTASNLLENSVFSLMDQENIRRMVPHDKIQWIWQYGAQNEPLPGTETENMSAVYRRV
GTNDAEHAKLCHEWYYGDNMPQRFKKICEEGGSRNAFGYRPVLRVSKEVLKDQNGLERAY
DITYLTETRYIDFDTLWGYITAFGRGLAELGIRPNANVAIYEETRWEWLATIYGIWSQSM
VACTVYATLGEAALAYAFRETECSAIVCNAASVRNLLRMMREDLIPSAVIIYLGELPPDV
EAGSHRIFSWHHIVDNGRISEEPLRITTDNDQLAFIMYTSGTTGNPKGAMHTHGSLVSGV
LACADRVNDLIGPFEVGEAYCAYLPLAHIFEFGVVNIFLARGSLVGFGSPRTLLDTFTRP
HGDYFEYKPVFTIGVPRIFDTIKKTVEARLAPRGSLERRIFEHAFQSRLRALKDGMETPY
WNEVVFGPFRYLLGGKMRTMLSAGGPISAPTQTFLNVVFGLMVQGWGLTETVCVGTKQLC
GDIETVVAGQQERICEMCLLDVDEYKHTDTPEPRGEILLRGPFLFKGYYMQEKLTREALD
EDGWFHTGDVGSITTHGRLRIIGRVKALAKNVLGEYIALEALESMYAHNALCMPNGVCVL
VHPARSYICALVLTDETKAMMFAKEHGIEGSYPDILRDPAFQRKATESMQATARKADRQK
FECVRHVRVVGDEWTPENEILTAAGKLKRREIDKRYADVIQLLFVEEC*
>TCRU_2744 Endonuclease/Exonuclease/phosphatase family/Endonuclease-
reverse transcriptase, putative
MAIQETWKSSEQIASMHTGDYVLYAQSRIGKGGVVVVLVRTTLRSKRIPLTIPQHDTSLE
VVVVQVALDQNRDLIVASAYMRPPPHVTQSFRRLVNCLPASSPLLLCGDFNMHHPQWEPF
LETSPSEVAAEFLELCTDAGLTLVNKHPW*
>TCRU_2745 BNR repeat-like domain containing protein, putative
MSRHLFYSSVALLIVVMMCCNAGGAQQTIKAAPDPRSLPKTYFVWRDKKGEETVISLRVP
SLVEVKGDVFAVAEAPCKDGGEKVFTGIASELLTLSDEESKELGTNAVKTQVLEECPFDE
KSACHIAGQDDSKTQTRVLLSRPTTVVKGSDIYMLAGNYSWKRAAGVQGADGGYWGLVLV
KGNVSNEKSQKRIFWNDTYAIPWNYNKKNESLTRLIGGGGSGVRMEDGTLVFPVEGTRKK
TTNQVGTEKDEKTVSLIMYSLKDTNSWKLSKGMSDGGCSDPSVVEWKDKKLIMMTACDDG
RRRVYESGDKGESWTEALGTLSRVWGSKQDKEVKVPLEAGSPQRRLAVMKITEM*
>TCRU_2746 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MHDDTLVFPVEATKKGDAQKDVKTVSLIIHNSKDTNEGWKLSKEVPYDGCGDPSVVEWKD

KKLIMMTACDGGRRRVYESADKGESWTEALGTLSRVWGNKHGEEAKAVRSGFITATIGDV
DDNRNVMLVTLPVYSKEDSKKVTGNGKGKLHLWLTDNTHIVDIGPVSDDDAAASSLLYKS
AASGTNKKEEELIALYEKKKEDEKPSPGMVSVLLTEQLERVKEVLATWKKVDDLVSKLCP
SGSTEKSASPDNACSPTVKITDGLVGFLSGNFSDNTWKDEYLGVNATVKKKEDAGETGAT
NTSDGVTFRGAWAEWPVGKQGDNQLYHFANYNFTLVATVSIDKVPQGDTPVPLLGVRLND
EKKTKLMELSYDSGKKWQVLSGDKTFKELKSALEPEKTHQVVLVVRNGTQGSAYVDGKQV
GGDEACALENMDSRAVSHFYIGGGGDSAVSTGIEEEMSVTVTNVLLYNRPLSSEEIGALN
PNKASIPPVVHEKAQGTQSQSSSAGQPPSGPKLLNGNEGVGGGSTSTSAPSTVTNSGKEQ
SEIQPPSAISSGGSKHVDVASSSDGDPRVGAEAGGAVQGDTPPQTPVGTPATADTNAPTA
TNVAQVDTATTTDVGVSSGADEETAGGTDGQKREDIHARDGEVKAAALSSSLGNVSQGNN
SDACTVRGSGLPSLLLLLGLWVFAAL*
>TCRU_2747 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGLSGVAADGEEDAEKKKDESSGGPGPDADDGSAGLQAMQFS
VKGGPEREDHSLGAQTGNSTNEQSVVVISPPESSIGPEEQAEEEEEEGGETVQKEKLEST
TEEEETPKLTLPQEGEGPPAPLTTRKNEKPAETSDATPGKGQSSSGDVSTRPELHKTPSE
EQPSSTAPQAPASAAAAQIKNESTTSADVVSGQQIKEESQHDMQSEGASGKEENVPTTVT
KKDGPTESNAESTPTPPSASKDAITNDDEKSNEEVIPKHDQTPDGETMNEASQVENNEGN
TNKTQTVEAAAITNNTATPGDSDSSTAVSHTTSPLLLLLLVVACAAAAAVVAA*
>TCRU_2748 hypothetical protein, conserved
MLTSEDPAAKHAGQAGQAIRPPPSPESDGTRPSGSSRGDSSVSPLSTAGISSSSVLDAPL
VQSTQPSEKGLQSETMSLGTALPNEQPKEITESKAQQGFSTSEEVAKSPDDSGDAVEKKK
EKGDVGPKATTSLSSTTSNPPVTQTTPRPPSAEPSPTETELQAGEETSTENVTITMRNAT
ANTGDSDGSTAVSHATSPLLLLLLVVACAAAAAVVAA*
>TCRU_2749 hypothetical protein, conserved
MRRRLDSIHFVSAFMHADDRTLVFLDAYILACGAAMKAAVSLVATWTAEHSLRINADRSG
AALFCIAPHRQSDEDTADHRLGGGKPRVKFHPVRLLGNAIDRLLIFGLHVTVAAGQTVPR
CRQLRLDAEAGAFQHTMRSLPVGCVHSALHHGGKAIAPCPAPTHLHSLEVRHRDSCTASL
GPRASSKDTSVHLAVNPVPLRRIVGFRAPTQHERLTRLRYIEDVRGAICSETTPSSIHWK
AATTISLPGDAVLKELRSVFRHMGISRTTSAPLMLSSELLPGRCEPQRGGRLPATARQGR
PGRCQTIGR*
>TCRU_2750 hypothetical protein, conserved
MGVVSPFPETSQAAVREGGVAHRSECATGSGCKMAQKLIHCAAGARGHATQTVAGGQFKH
TRREGSIHITATRGHASTKCGDNNGDRSTCNADSVTEERFACCHGRAQTQSQEYCSTADP
RRQGRGAAMSRGITGLGSTGHQAVSHRPLAAWRNHRRGHDCGPPVCGEIQLEVNCLLLRL
CARRMLPLQWTRHAPFRQSTSLWELSRLQHGMLRLAASKVPRCISNLVITAARDVAHAKV
KASRSASRRTTATCFRRGSMPVCRGRPSSVPAVWDGRWWSDSM*
>TCRU_2751 hypothetical protein, conserved
MAWVDVVTSVLPATSIWELAPKPPSNSNAPESSIEDVTFTCTRAPLPLTDRPMRTHCSSV
MLSVCSGASKLHRSSTIAAVKVTLTKHRPRTPGAGTSTELMLPPCTQRTSVSSASGSGSG
PRPSGTAAGRHVSPWPPAAHTHPQPLTLLVLAAKHTASTVQAPQSNTVTGEPILSSSP*
>TCRU_2752 hypothetical protein, conserved
MTKRVDRSRTPSRTSAGPYRNLSWPRVVGKYCDPPTVARSVEFASSTLECSGIAPRSTIV
PSSDVTFVMLTRAWGIRRAVLSLRPPIRSCAPPASTQWRSVTFSASANTFIERRSTATVI
GPLSTTESRHAVARQSPTVTDSVSVTPLTQPGAPPPALAGGTSNGRHASPTPPARQLHAQ
SENDAVSASKHASAAAQPSHGTTLTEGRPAMR*
>TCRU_2753 hypothetical protein, conserved
MHRGRGRTARRLQQHAVKHHRARQQVHTAANVHRRPARLRRPQHSAAHTQLRLQQRHRVQ
HKRRRHRVRQPAQLRVAHRPRRHNRRVTDRHVRACRQVVHKHERAVAPRQPAHAHLQAPV
TRRLAAVAPHVDLRTAVAHAVPQFDAQRAGKHRRNVEHHSHAVRDAHAVHQHRVHGAAHR
DGSLHRAAPQSQRHRMHRGHPHSSSSNQRQHNEQRRTHSRNGPVPHAVPAARTRTHRRPH
PPTQPGINRAVVVCRTRLVDRASCSANPFLQMPNTVTRFRQVVIPLLLLLIILLLLLRVI
TKTLKR*
>TCRU_2754 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-

terminal, putative
MSRRVFTSTVLLLFVMVCCGTGGAAASDGKPSEPNYKWKDVKSEDGVTVNSLGVPGLLKV
GSDVFAVAEAQCKKDGKYFTGIASQLLSMDKGKEKEEVLKDARVTQVLEEVTSSEGEKEV
DVSRPTTVVNGSDIYMLVGKNSRTLQAGDQAIGWGLMLVKGHVSGENQRDKRIYWNDTYA
IPWTYKGNQHSILKRLIGSGGSGLKMNDGTLVFPVEGKKEVDTQEDGKTVSLVLYLQGTE
SWTLSKEVPADGCSVPSVVEWEKDKLMMMTACDDGRRRVYESGDKGTTWTEALGTLSRVW
GNKHEGNEKGVRSGFSTATLDGVENDNKKNVMLVTLPVYSENVEKGVLHLWLTDNTHIAY
IGLVSEEDEEEITASSLLYKSGKGNNEQNDELIALYEKKKGDGDTPSPGMVSVLLTGQLK
RVKEVLTTWNNVDQSVSQLCPPSAEKDRPTENDCSAVKITDGLVGFLSGNFSGNTWMDEY
LGVNATVKNNDDGAATGYADGVTFQGAWAEWPVGRQGENQLYHFANYNFTLVATVTIDGV
PKGGSIPMIGAKLNDSENTVLLGLSYDKEGKWILLCGGKTNKEHSSDWEPQTQYQVAIVL
QNGNQSSAYVDGQPVGGDEQCKLETADSKEISYFYIGGDGSSAEGQEGVPVTVTNVLLYN
RPLTSEEIGALNPNKAPISPPEDLTEAVVVDTPSTAVGGPVAQKTVSVSTPGGSTVKHES
SASSAEDEGTVGGTDAQKEEVHPQAGEVNAAALSSSPGNFSQLNNSDAITIHGSGLLPSL
LLLLGLWGFAAL*
>TCRU_2755 hypothetical protein, conserved
MGLIHLENLEQCQDEWRRKTEARVNQETLMDPPRLDSPRSLRACALCGIDPATSLESLSL
RQHFEQVVSGAPWVDRSVSTSVRAQDALNACEESGILTGSTQQKMQAYSNFLRYEENRRD
ALMLAQELRRQLIAEEIFERRRRVHVDRGSGLVSSLCELGSESRLEHDVLQVSLRPNGGT
LAAEAWPVPPSGGTAMVPMEPKKQAKGKEWQPLERRWLGSPPDENTTVSAAAKGTLTETA
LEDDHKSMRTAAATVAGTAVEAKEVQILEENAPPAPPISSREQDEVFYYYCANAMVTGRI
SKCRETSFF*
>TCRU_2756 hypothetical protein, conserved
MKDSFGSPSFALAGEVMVAFAEGHKDYNGPQHTSDLYTSEIVAGYINATEPWSSIVADIS
SDDWRAYTVFTKESSKDRFGVALLPTAVSTGSDVFLLVGSYYLIRDATGRRWIDDGWDIH
LLVDKATQSTDAKQGELIEWGAPTSLLASIT*
>TCRU_2757 BNR repeat-like domain containing protein, putative
MRFVGGGGSGIVTEEGWLVFPMMATRKNDRGIESMLFYSKDKGVNWDVSRGIPAADCVDP
RITEWENRELLMLAYCVDGQKVFRSRDMGDAWTKASDLLPRVWITTQAIPRGEGWRVGAL
ITVELYGRKVLLYTQKVGYPPGERNDKALYLWVADSNHTVYFGPLSVETGAKRAFANTLL
CSGDALYLLQGMGNGKMDGVFLFRIIEELRKIKSIVRNWMEVDAFFSGLSTPTNGLVGVL
SDSSDADKWNDMYRCVDATVLGAIRIEDGFKFTGHGAGGIWPVNSRGDNKQYTFVDFTFT
LVATVVIEKMPPGGSSVPLLGAMLEDGMGTKFLGLACAENRMWEKCLMGKRGRATFGCRK
KNTRWHSC*
>TCRU_2758 hypothetical protein, conserved
MELIRKRRSTVVRRITDIPALGQLYEESEQGGSRDVRAVNVGTENVPSRAIHNLLPHART
ADERGELRGLFDGNIRCGAIDPTAVRQDAAVHFTNGSNPARHDDFGVTKDCGAIGDEASA
PLDRGRDESIYPQQDRLEGTCCLTPLTEEGMNQVIRSRTD*
>TCRU_2759 hypothetical protein, conserved
MQAEARAVRLALSAFSAILPSTMDVWVDNTSLQGAANKGSPKSHALMWGMRRIYEFLDSR
GIQASSAYVRSAENPADGISRGRVFTLQDLAKGWNLRRAAAESCGWRPPKSANS*
>TCRU_2760 TFIIH basal transcription factor subunit
MSELGEILNTAQISKHYKVIQFLLSHANVEYTLTQLDFLIPRGASLQRFPEAWREYMEAG
RCGNQCIEVFHRIVDVPDVGVTDDRAVRNVRSKKELVLVCRRPELHRLEELERLLLSPAK
VPDREGCVALHTNQVILQEKLLKESQQRGLLYYLPDHYMKAYECRLVKGFRSPFKRGESL
NVFLCDDEADAVLGADGTAGQLELPVGVVAQSMLYTRRGVPVRGKNSIPTCLHVGERVLV
IFDRVLSPSHDSSMSFEAPALRVSLGKPRKNLDGALPVDVRVKASRRTGGTQRSFMDVRA
QAKGNVAVSVFVDEMETIVPVEVIDEVTSMPGVMIGREALPALPVPDGICIHDPALWGGR
IAGQGGEGEEFRGEGRKLAGTVLAWWLNPSPAVLKVRDLTIPDSETMSAASRAVWIPHQK
DEAALRVVRKTLQEQHAAEVARRIRRKRNRNRELRNCHMVHFGFDASVPFGGEMQDR*
>TCRU_2761 hypothetical protein
MQCRGGNSTGSGGLKGSFLPLGAYRRVPREATILWKTTMDTAKEQVAVVWETVSSWEGSE
VTSSDSCASGINDPSLEDVGLWEEHLQIRMELIRRLNPFRQGPPVGGAAHMTASAERNGM
TGTKLGSIRTQRACGSVTHGECVGEDILFPNHENLCTAPKTPQTYQKVRRNPCECTCRVR

RLAPAEWSELLRLGSEDVVEL*
>TCRU_2762 ribosomal RNA-processing protein 8, putative
MFGGSKGRKGGKHVRSAKKENSAASTERHPKKVHRISTDPTKKSHNGSTLKGPVVSHSGG
NASRDFANDRQHIPFKNKLEERAYKKANRIPLYTPAPGGKKGDSDATAKRSSGASSAAQR
RAIMKAKGDDAVLEHFRTKLSSSTFRLLNEQIYNSPVAFASQLLRDPSTYADYHNGYRQQ
LEQWPLKPSQVVVDALLGDRRGRFLANKAKSMPGYIPTSWVIADMGCGDAQIAQAMRPKG
YTVHSFDFCAVNDYVTVANATNVPLDNNTVDICIFSLSLMSTDYVECLYEAFRVLKPKRL
LKIIEVRSRVPHPKRFSELVESIGFYLDYYDTVEKYFVAYDFIKREDQAKANRGVKHDPR
EVLVASLYKKR*
>TCRU_2763 glycerol-3-phosphate dehydrogenase (FAD-dependent),
putative
MGRRSRRFAARVAAVGVAFVSSWALYHRWQLRRSAVVLLPVDTTMNMPQSHAMRLQLLGS
STKKEPFDVLVIGGGATGLYTAVDAAQRGLRVALVDADDFGAGHTGTSPPLIPGAFSYIQ
RALRQRDLVWLRRGVEAWRALTVWSNVAPGLLENGVSTLVLSCHLLELMELTTAAVIATL
LSAFSGDWRPFRFVRGNVLRKELQEAGKGMRGGILVEDAFLDGNAASIALARTAEALGAV
VLNYASVTSITNVETTAELKGQANFAVIVNDVSTPSGVGELAPRAVTVYTRSIANCAGSW
VDEVKQLVPGNAMDAVPSAVKRHQVRSYLVLPRTAVQTATPNNADLLFGADAFSVAPTSH
SFSSVMMLPWFDGCVLIGPSLSSLFRLPSKSYAVAPTTVLTLAGTKNNNGCNIHDVYISQ
RKHLFRALQVSGVKVDEERVLSCLSSIVPIIASPPHVPLAKDIFMEGCHISSGKEQPNVV
HVYGGTLGFARDIAEKALDRLLHDSGAFSTAETAALRPCQTSRLALVGAQSRDATSDVVS
PVKRIQRIVREEYAARLLDIVARRKHTAYSSPAEALAALPAIAEIMRCELGWTAERTKVE
LEVTKAFIRSISFA*
>TCRU_2764 Transmembrane protein 231, putative
MLREFCFRNAALFHEHYKVRYIPRGLGSWIFYILCLLAILVAPVFIGLAMRNFWLRSNSF
MQMPHVYFTNRCVLRYTTVKGQEKLWTCSNEFNEKHINVQEQLAVLPFFSIYEDDRDGDG
RVDFVTMILSLPINDVGDIEKDVTPSDMGDAVFQVDFLPEFFYEFDHHIVTLKMRTAALF
SFKRDHWIPGTEGGPLSAITEGDLLFHSTEPLIASPNVRYTRTYIDSPFDNVTDVDELLN
VPLFASQYTLRNQSLQFKPKLETVGGLALLRDENYNRVLGEDLDALGAFTWRIKLHIQRA
EVNYVPSIQEALKWAWVQYFCIAYVLQRLLWWLRGILVKTGVLGSTAFFHRGWKSS*
>TCRU_2765 zeta tubulin
MAVVVVQVGQCGNQLGDELWRQLKLTTNSGALPSPFFTRDRRARCVLVDSEPKVVTAVYE
RQKDVLRAENVIHGQSGRGNHWALGYYGVNDPLSHRAAENAVVARPFQVVKDQRRCDSHV
VRNALRAIHAETRRTDDAMEFEAIIVLHSLVGGTGSGMATRLLEKIRYYFIEPVDSSLTV
DECEEAEMMRHDGLDGMMMEKRRASYLVSITVAPQAVGELSTQGLNAALTLHALQENANA
VLLLRNDDCIRVQEDSCAGGRPRGRGNTSFSTPSFSSIPSCATFKEINEVFLTMLLPILL
YGRSTNAVGELVLKCSPNPREINNILTILPTPQRHYLRFKESVTVSRLYVLRGAKQSMPG
VYPSVPIELIHTARSLRNPNLVTSREEVQVPKELLKGLKETAATRRSVSVALLQQMEGVL
VLNEARELNAAVLFRLLRSAAMKVKAGAFLSTFEDMGMTAECIQAAIREVATRLSAAEEI
*
>TCRU_2766 kinetoplast ribosomal PPR-repeat containing protein 3
MRRVNLFARGGFFIGTQCRRAVISPVDRISGANRHSAPRTSYQFAVRDEERGLYDHGVTP
DARILMAEAEAQYRASAHWLHAPPGGVAPPELRLDSDGGAVSCIAAPFAEEYVPSHKERY
AHRGHVGELSMQRAAAPKFLLNEHASLNLRKERQFCELMSSPMPSLQKAMELERLLHDFY
LQRLALSSRNVEAIIALWAQCSVEERLAGRAQVPRLTSSSSAGETHVNSVAAVDAVPFLP
AMKRLYFHARQTHVAPTPLVLECLMTTLAAVTSPDSSVFHFSNRLLLDADKYVVLPTRTT
YAAFFTICSLHNAMSFAMARFKDAVVELHISVDATMATALLKGLCQNGLVEEALALLARI
EHVPLDVQFLNASMEVLLLSAQPQACFSAFDAMQSCPVQPNSETYALLLLACERSGLWCR
TTAILADMQKRRVRGDTKTLNLLLKGLLMERLHSYAKQLYGTMVKKNVEVWPALESQMRL
TGKNRRKEKKPKQPSPMASSTQTSEPC*
>TCRU_2767 hypothetical protein
MAILPHGFIEAIHASPLRCVLYVMGAGSSVIAQLTSVAGCSRTLLDARVPYAMAAALQML
DDRPPKMVSATVARQMAQHAYHRAVEYSNGDDDGTLVGIGSTSAVQTDRIRHGKDCAFVA
AWSERQVVEFAMELPGHLARAEQEEQVTLLLFKALAECAKVPFEISFVVEPKRLSYIVPD
SPLRSLLQGEIKFLVFNTYGELRADFVPYVAETSFAVKTENSWKALLFPGSFRPLHWGHT

ELARAAVRAMATMKGKLNSTSTDISSPSWNVPDASNVRVTYEIAVDNADKGIIDSDVELK
KRVQQFLQRGARVAVTRARLFTEKALLFPGHGFIVGIDTMKRILDPKYYDNSREAMLRAM
QFIREQGGYFVVAGRASGGKDAVWEDLTSIEVPAEVESMLISIRKEDFCVDVSSTMLRER
SKSTC*
>TCRU_2768 SSU ribosomal protein, mitochondrial
MFGRTAFLFRKYRQKSKAPDLKTSFSKTRNFKKAEKIAIETVDGEVVKGRGKLRRRSHSA
LKKAIGEMEHPSIWLWYPWRMNPEPPTPGMPQRRALKNLHGAVFTDLTPVQKKRQEQMLY
GINIPETRQMKFEQEHPLLASALRQLDGQPKGFPFWYKKYPTRRHAYGNRFSIPDEMLEG
YGEEMKKALSKEMMSIQEKQFAQEAMYMERYAEHDFDTTSPAVLAVKRALKCRVLRNHLL
TNPHNNIIKAVLANTEKKLSHALRKLRKVDFKKYWEIIRDHDVQDVLQPSNLVTYRQGAY
WKYDWNAGLAISTNLADVLDPRGLNGCVETGRSRSEVARDLGLSYTRPLQENEKKQLSHQ
ALYYERLAKFKMEQPEAARALERERFVRKFSGMFAKMDIKSGAPDFPSTYRKLLGTKVVR
WASKRHGPA*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MDGTVALGGAGRRFVVGCLTLNGQALQPMDYRSAGIIGEFRPVACGVCDADVHCFAAATR
TMSGSCGCRCAEGGYGRDCLPVYLPHVDGCNHTPGMPLLSRTATLTETRSPTPTWKPTPS
ATHYSPTQCGPTETLQVTETVALPPTRTPTASVSSTLWWSDVACPTLAVTTTAAGGSLTQ
NDIRGGGSAVPTRLMVALPPPFRWARDPQLGTHLSFVPVSTTQPSGFGGPWGAMLSNATW
VRNATNPSTVVELAVPVHRGYYIAVDETIVIRCDAAAVFGGCKGVLLGSFTIRSDMLPAA
ASALSAITGVVAGAAAVAVVVTGGLGSVLEMQALGVFARMSCASAQERASTAALPYFLSV
FAALDPLWMVVGNALLAAVFGCVHCGVTAVFQRWRGVDAASAWAAMRFPSLTYVVAHAMH
LGIFFGSVLALAMPGARVQHRVIGVVGVLYGVAFPAGVCYFIARHTGASFTRYWQFLRKP
LHERLLYPVGYWHPAAQQRMYGGMLTSMRGSRVYWCVFQLSVLCVVGLIAAVHPPVGGCH
VLYFCMAAVLLAGAGVVGFTNMMRSAFLTVIHTASFALLAALCVVSAANHLAPSDGGARA
YAAIVLLLTAVLLAVAVYSVVVWYAEDRHWQELREPRCGGLEALLRDGEESDEETQKPHD
VTSSSYASGTTAASSYRPPAAPLQPMAGDTRPDALSPLDRVSSASCSINYALLDRRRCFA
*
>TCRU_2770 hypothetical protein, conserved
MRELCNDVYARSLKETDDSQVEGICKEYSGKPNDEVKCPKPQTELLPGTGATVEVSVPEG
LGNEEELGKQSEEAPGAPPEDSDTQPTGITASPPVEGSPDKAKDVRVPNSEEGSVSMEPT
KDSAEGDIVPIADTDHNEASNGKAESTTTTPPDASDNANNKAENGTRENIPNNTTESDVT
GTEGKTD*
>TCRU_2771 hypothetical protein, conserved
MKKVLAAWKERDACIAREYGCGNEKNDKKRSGCGGDFGKGLVVFLSSTSTVNTWSGECPC
VNAIVHLAVTCTPDGGLTFQGSGAWTEWPVGEQGQKQLYHFADYKFTLVATVSVPEVMEG
IDSSFPLMGVRMNDNKSTLPFICCGRRKISGR*
>TCRU_2772 BNR repeat-like domain containing protein, putative
MDATRVVCWDLLRVTFLFGVSGVVVAVAEAHFKNNKDGKLRAGIAAKSMEVNGGTWANGT
GMMFDYYDIKVDRLLSPTTIMADGETCALVGGYGESGAPWTKVAVDGYWSSRYARSTVLS
EDDDKYKREFEWNQ*
>TCRU_2773 phosphoglycerate kinase, putative
MSVAVLGSKRAVYDIWPLKNKKFFVLVDPQNILGETTDSNATLNTIEYLLKKQGAVVVGA
SFGPLCGIPLNLPRQQREDAIVAFRREGGRGFSNFFSSISSRMKMEVLKGVPGLVLPSTC
SVDGKTGKTLVFSQLENATKFDALHRVFPKAEFPPVSTFPFVEELAKLLPGVTVKFASDC
LRPPLHQLKPGEILVLENLQFYRNETSSDQAERMAMAEVLAADIDVFVNESFATASKSHA
SNTAIPKILYHGAAGLSMDRELAFFSKFLTQPARPIAVVVAGRNIPEKLLMIRSLIGRVD
KILIAGLVKIPFLSAKGLSSGKSLNLPEVVKRKLLNSRGGDFEEETITCTQLAEEIMSLC
EAKGVELVLPVDHVVSKRLTKTNDASAAVVESMAIPSDVYAMDCASNTIALFAKYIRECE
CVYWAGTFGWTSLGYHEGTRAFATILAQERKLSIIGGRSTARAVQQFGLASHFSHISGGG
VSCLELLQGNLLPGVEALSDVAPELDSKSTFSVDELLRNLPLFSRCTSHQLKSVARKFAR
RIHACGDYLTYRGDRHVSMWVVADGGLVARFGDNTITIPPRYIGRGQTVAMYDFITQSFA
TETVQAALSGTITYQLTSSSLNDLLHEHPDLAAQFLQNVSEPLCLMANEEYQEQTSLCPA
LRRAAACSRVPSSYGVPKEWCLVEDIVQDVVSAVVLQKLTMQYIDYPALPPNHQVKHIWD

KIKCHGALFPAVGASVLRAFVYHKVLPLGLMHASIVTAVAAAPLRLVAMGVTWRGLTYKA
ILDEAMVSVAVSWAPAVAYAGFLVTQRRLELLKRSRCSRIVQLLIMAIIRVVLGFVVFSL
LFRRCDEIGSTSLLGIFRKDAFKAYELKQVISVFLRYVVHLLLGVVRKTSAYTKSIQHGR
QLLDRK*
>TCRU_2774 hypothetical protein, conserved
MSCCSKIPQTADKELDENGVYLENITKTFKLFEKSIAETLNTYQMLMNSFEKVAQCFVEI
AGGSSKNMVGLADGFKEGMRKLRDGPTLSGLQMDITRYVKEGLPPLMAERNKVYKLYKRA
KELKKAEDTYRYKIGEMEKDFARKNRPLGESKSYVKLGKNRERATIKYQGKKQEFVTAME
MFKDLVERFLGTSLPGYAACTSSFSRHLGQVMEAYVSGEHSISSANGSPLNQSKHRPSQR
NSDSTVDQLAHGNQGKNPLSLEEQYYQVE*
>TCRU_2775 hypothetical protein, conserved
MMVPNASKKRLSFANGPKIVVASNASGIVSVTYGGREHVAADNTDEVNEHNATGHKSLVL
ENGVAGSGFVAEGDAGGLSQRNASGHENPNCENSPRSIPETV*
>TCRU_2776 Concanavalin A-like lectin/glucanases superfamily,
putative
MELSYDSGKKWQVLCGDKTFKEHSNTWETEKTHHVVILLRNGTQGSAYVDGKQVGGDVPC
KLETTDSKEVFHFYIGGGGGSAVSTGIEEEMSVTVTNVFLYNRPLSTAEIGALNPNKDSI
PPVVSDNAQGTQSHSSSAGQSPLRPELLNGNEGVGGGSTSTSAPSTVTTSLGKEQPAIQL
PLGISSGGNKDVDVASPSDGDPRVGAEAGGAVQGDTPPQTPVDTSDTADANAPTATNVAQ
VGPADTTEVGASSGANGETAGGTDGQEESTCTGQGSKCHGTQQQSRKCVAGE*
>TCRU_2777 hypothetical protein, conserved
MLDKIKTFVSRQAGQKARNALVSSSGAPPSLKEAFDRAMQMTNTLFEEREWQCPCGHKFR
ASGEWVATLPIYCEVPSCPNPKYYVDGPGRALLEANPSGVKLQEVKDAPSLPASSSSRGV
GARFHNRPK*
>TCRU_2778 hypothetical protein, conserved
MRSCLVGCVHSALHHGGEAVAPCPALTHLHSLGGRHGDSCTASLGPRASAKDASAHLAAS
PAPLRRIIGFRAPTQHEHLTRLRYIEDVRGAICLEAMPSSIHWKAATTISLPGDAVLNGL
RRVRRHMEISPHRNHAPHAEHRIVVWGNGSCSGLDVFQPRHARDALDGVRRSAVEAACAS
IGLCVLDPPRCHSTPRTAAFPVGPHRAAAGSSIVPIAHTSSCCHRYPLGDGGAMPWPAGG
ARRIHRGYLYRAAFTGGSRSRSFLHIFPMTLRDPTQRDSGR*
>TCRU_2779 Endonuclease/Exonuclease/phosphatase family/Endonuclease-
reverse transcriptase, putative
MDCDCLGLPQTARRPVCDGIIATFVRTALALLTRYCDIIRQQQDNNSICDECWPLAQPAT
STRCQGLVLFAREEAKRLLPIRCPRRGRRRRTNGSEGHQMEPFTWLPAERYFYPLLNSIG
AHQRYTYRLRAVCDARRQKLLLSGDIEQNPGPIAVLQMNVSCLTPSKLATLMAQGADIIA
IQETWKSSEQIASMHTGDYVLYAQSRIGKGGGVAVLVEKTLRSKRIPLTIPQHDTSLEVV
VVQVALDQNRDLIVASAYMRPPPQVTQSFRRLVNCLPASSPLLLCGDFNMHHPQWEPFLE
TSPSEVAAEFLELCTDAGLTLANTPGEITYARGTRERSCIDLTWSKHLTVSDWSASVSPL
SDHYMLTFTLHQAFKDTIPSAPPRHLSFSAVGGSASGIYSSRTSTHNFRHTTIKSSPPAL
RLSRERL*
>TCRU_2780 Reverse transcriptase (RNA-dependent DNA polymerase),
putative
MHKDGPRLWDDTLMEAERIATDRKARYLQLPAPDREAEMQRTRSQFFLLLRERLRNTYLR
RISKLNPGEPLAWKYISGRKKASLPSPTSMLLGDGQHTYKTARRAANALNRIFLPFHPSH
KAVRFSKGINRQSASLNVGSSCISEPQNNNESAATFTSGSSLSSSSEPQDKNEAANTSGL
VAHLHSPLDAPFNRTELLAALRNTPYGKAPGPDEVYSEALRHISSKGLRFLLRCINHSWT
TGTIPAEWRRATIVPLLKPGKSPELLESYRPISLTSIVSKVAEKMVLKRLLWVWTPHTHQ
YAYRIMRTTTMQLAHLIHEVEHNRNHYFQVSLPKKSGIGNQLHYRPHRTLLVLVDFSKAF
DSVDHRVLSRLLANIPGVDCRRWLRNFLCGRYAKTRVGHRHSDRRPMLRGVPQGSVLGPY
LFSLYVHPLLNLLNSFAGVTADMYADDLSIIVKGQSREDAIPTANMVLQKLHAWSQENGL
ANNPSECEAAWLTLSTHTESDYDREGRWPLVVAGCQIPVMTMGASRTTKLLGMDLDPRLT
LNVAATKQCAATSQRISQLRCIAHKEAGPSPHDLRTFVIGYCASKLRYGSELIWAVATDS
AKNEMQKTYATLARIVSGVPSTVDPESALLEANTPPLHVLCLRARLSIFENTRACQMDWM
RRPPPEPPPRAGFRISPLSRDEPYAFVDAHTKDYGITESSPREERFFRSSIPPWFAASAH

RVTIGAELPIDHSITDEEELIR*
>TCRU_2781 RNase H, putative
MIPRIRHRRKTLLVVTDSRSLLAALNKGPLSQTDWTEDQIWQRLLTLTCAGWSVHLQFCY
GHCGVHANELADQYATQTMESGQYTEQGIAPLWHTDLLTCFTTQLTNKWRRTIRQDTHRH
LLCGTRPSDLSGKDLITQEVLHRQELVHLERARCGESELWGRLYWAVRDCTNQCRFCNIS
PEQSAYMRSNNDPTAPGTDTVPPSAREEDVSPVGRRTLTRRRKEKCPHCDSTLTGFSGLV
SHCRSFHPEHPPPLPELKCDFCDMVFPTRRSTAPHRSRCAHNPDATRHRNSSARRRSLLP
QDQPASTSTPIGPQETLHHLLPECPGTLAVRRRLGIEQDLRHGKFSQWQLFHSRKLLSLL
DHLFGTQMALYSQRCR*
>TCRU_2782 hypothetical protein, conserved
MPCGGRHAGGADTAPNGIQGRPRNSPDYYYFGDCGVTTVAQRLWGAPPLVRADVRIDNIR
IAGSKSGVTLWEDHESGATHYTFLGVQFDHTRQAVSLSDKFVLSVRAMPALNSPAIAGVE
VVASRF*
>TCRU_2783 hypothetical protein, conserved
MLSHSSQLCSLWIESARVIRLDHCRCPGRLVSTGLGVSSEIRKTNLNGKSYTLDPVEMEP
VFGVNRASDFSEKGGLCSTNETNEKNVLLSGGDIVSRNQKEVDKVERVALVAEKEHEEEE
PLARNLHNTIGPTPYRVSWYDYGSVSPSKRFTYWAYRRLKELPTDWQEYYRRMLYQEISA
ARYVNQTWDCFMMVVDGYRKAKWILKKYGISIDESLIPKPYNNFWEETTHEERVWAHRRS
HQMKELQALYRDEDELVFGAHTMDRREVSHGSIKNVQTGMQGGTPVHALDLPAPCESEIK
TSPQIEDMSSALMSSIEDDKLWNPVLRSRIHTRRSREEVELYSFEDDEEDENSPS*
>TCRU_2784 calmodulin, putative
MADLLTMQQITELKEAFAVFDKDSDGSITVEDLGEVFEAIGQKVSRNKLQLMMAEADLDA
NGVIDFPEFLTLVATKLNDPEEKELELRRAFSIYDLGKTGFINVTDLKFVMGRLGCPLST
EQAFEMVNEADIDGDGRLSFNEFRRVMNEGWP*
>TCRU_2785 conserved protein
MMIQSLLHYSEQNNVDDDGDFPPLLRSVIRPASHCPLFDLKIEEEHTWPCANLLNGNARY
RVQYQNGAHLVMSDNRLLVVCNSEHFYCPPWNTPIRDACVQRQGANGNSILAVGLADGLY
LALLQRNPQLQVTDDVFLTMKQSVEKIVFLRDGEMALCYGNAQVEIYRINTENLQKVSLV
SINRNHTLNLFQAVASLWDTRRYRDSAYDSGNGRMFVLSDIDLTVWAYKSTDAFAAVCSV
RIQENVVAVLPSSQLHRYAMLVFNDGGRQPVIVEETFAKRSDETRTVIRLGAVRPLPEDV
LLDTVELACQDAEGNTMLYDSRKCTLVMLTVASPIYEDIFDVVEVVSPLRLSTRAVGVAC
VSELQDLSASFIVYGKGGILCRIGVRSLGYMFYGLLQKQGLTDVIRASLHRLGPKRGIEA
LVGAAFAGASNEVLSPLLQEFMQPSFCENEMRVAPGVNGIISLVNREITLAECLWNAPFS
WHLIPDLERIALQLWAWHEKLEALLRPYGWLDCPKQLNLSWNGFVATSHDHFTIRTALNT
QAMLLETLLKGLRDAGVLCWLYSLLLRGKPGIDTMRQNRLKPIVWGDNPSSTIASLCMET
LSAADGFVMSQLEARKNVLPIRARHAISIHLCISGNQPDAALAYACDNVRSLRHEQVFEY
VAEKLEGTFPERMPHLRLLLCWLRYNRGAIVELLEMLERYRISESSEQLKLRLGVVLQAV
TEYPALQHAVVRWMVNYPLEDDRVMGFAELLEEHSVVIDEPQTLTALFFVSWANRNRRPA
LAARGFCDIARGRRRLALPSRILCIKLALEFAPTVSEQLVYFVLLLQEELAEAIEAAWRA
DAAQSDSWREGKVEADVDELRHSYLDERRLFQLAGEYKEQGGAKVQLDLLKVHPETPEKV
TVEVLHDLLEFLIRKGMSATEAARNVVREYYDGYAAGLPLLPFVALLAQHGVSTEEIATL
LQSSGVPTYAVVEFFFHFLDERSEGLTFKKGSLVTTLVAMLAQLSGESRDICAAYLLERI
QNLLEGEQKAMAATITTNKILQESDIMQLQRAESLLKRPRTVSPP*
>TCRU_2786 hypothetical protein, conserved
MRRTTAFLTSQLLSLATTKIASTASEGTIVGAPNIGGGGGLFFADRAVKMTRLTTPGFSL
ICKPSILSCESPDAAAAVRLITEEPGKGPSARIQLVGMCTVSFFRSHRIVFHCTGELGRV
QRHEIGLKNGDVLAVLRGCDLMRDWKSVERTLRSVAGEDPEYMAEEILLNLASDARATKN
GNALNNAGSSGIDDDDNINTNASVDDKEVSTSDSSMPNGICIMTVVRNRPSEELPQPPSY
LNWSMACGGEKQNGSQKKAGWGR*
>TCRU_2787 hypothetical protein, conserved
MASVYHRKITISAGEECTISGSGAIELQLLSGVVDVAGVLLKAKETHVFFLEADKRCVIL
YTLEGGSVQATAGFPFETLKTATGMASVVQLCRRSLSAERRTKVLVIGKSHSGKTLTAHT
ICNLLRDDSAGELTTAPAAAVFLMDLNSESNCLHAPGCVSAVQVEHVLWPGTTSAPTLLP
FSFFIGEATPPSAENILSFLHFVEQLQECTESLLNGMNHERVHLVIDAPAPASDIKESVY

FRKLIELLRPTHVVTVSPQDGSETWSTFLQEDVQRVLPDCEFSHVSPVVRRCTTSLREQH
LREYFAGTPQFPLGCAKVVLPLTQLQFVQYEAHGVDEEVAVSCRKVAMTPTFVGCICALS
HAEMIEEVPLAPVAGLLLVVAVDEEHEELVAIVPACDDLPRRIVIVPNETRAAETPTLSV
TTAMASIEESVAV*
>TCRU_2788 Protein of unknown function (DUF498/DUF598), putative
MRRSLLHQSGSTVNWKIRVRRGVQRFVRRYVPDPRDDPLTEVPMNAETYKKTYLQQEGGV
RVGIRPGQSIEDYMAERDKKWLEEQKLTTQRLVEEQQLPTTSDGQLFTGAGTRASYMNVD
AANKLVKTPTPSDYEADEELILMRRQLQVENEAEYRRFVAEKKRSEMTMEETQKRRHPHP
SDPNYDPFKITPGYRPQDSVALAQWLKRQRESGKTASGLSLQTKEGQERYYNEEKMATQF
HANPFAARVEEPRGLSKMRVTAYSPDSIFVNDKEVIGSCIVTDKAYYHWNVSSFEEVDER
TLALLLHLYPVPDVIFLGTGRNLHFIDEELRIAFQKRGSVIHCLTTPQACGHFGVQLSVS
RRAALAIINPIPTNGYGVECFGDFVENDMFSLSDTQLGVPPIKQFSSTMFKPNKVAEKYR
HMQGTGFGPKYHQLSDGRLVRPGTSGTKLRPLLEPGEEVQWERLPSYYHWYPKEHLHDYI
ENTTMREIQGKPTGDPTERRLYQSMRGGKPDKENAPTPDLAPWDSASIPITKFPHERNDD
EIVVEDPKTGRIIGMDRGTYERWRIMMQERREGKPESDPVEYDQERFVTNKDGVVFDLSK
MKYRPIFEGRWNPRRPQSTGRTNPIMT*
>TCRU_2789 tRNA intron endonuclease, catalytic C-terminal domain
containing protein, putative
MEKLEDGDPRQRRHIGGDAAPATRKTDKCEEERGGEANDDEKIILRIIRTHGPLFVCENP
SLFLQTLPQARKKHYRSDHLSIEELEYLGHSFDIVFKNEQDSHRRACLRERHATFCRVYR
YLTDEMGLRLRHGSQFGAAFIGYRDVSGHGEYLVYLGPLSRLEEVAAVRVARSVAKEAWV
AEEQQDGSGFSFTRLSPSVSGRVSRETPRQLVMGTNGPKTVS*
>TCRU_2790 hypothetical protein, conserved
MLGGRKLRSAGACETPSSCAVRPHRQLGCPGTQVAAPRIQTHAQQAVRPAAWAIRPQKGA
GRLYGLSSGVVVRAVVGTPWLEGARPVAAHSVPDGNAVLSVRGANVVRGDHAVADASRSI
EDGASRQRENRRCLPMRRRRRGFRGGYAPHVLNISEACEPFVLSGCAEPNDPPQRCWIGF
QVDRSIPR*
>TCRU_2791 Glyceraldehyde 3-phosphate dehydrogenase, C-terminal
domain containing protein, putative
MATARATMASLKEWRGGRDATWKIVPSATGAAKAVEKGIPAPNGRLAGMAFRVPTPNVSV
VDLTARLEKPAAYEQLRAATDAASEGKPKGLLGRTEAEVFSTDMNGVALMPVFAVKAGIS
LNDRFAKLASWYDDGTGYSHKVLDLVAHTSAH*
>TCRU_2792 retrotransposon hot spot protein, RHS3, putative
MLAAGRPLMKDYNVTMEVFAQEPDDYVHDQLLLEEILNLTAHQALEAITRPLHEGVLSLG
QRRDYERKHTITPPARGKPNGVLTQVLTEARREAEERLRRTQEMKFTISTNIEEVLFKGR
ARVNVMRLNDFLTMEPDGRGIVDTNRDVMLEEFFKDPTKYIRDKGALNEIQASGHCLSMK
RAVKGEVVFDEDIRRLCDKGVDNPPGRSLAAAEVKATVHNSTKHFLDAAAEEARNPTTTS
APEKLEGCYESVHNARRSHAVELPDGVERKKTGTGMGVHEGRPEQSWSYREADDAIEEND
AVQQCGAAPPMLMVLFSEKGWPYSWHTIQDLPKDVFVNCEVDRAWRTVKGDVTAWFSPHG
GTDFKPKQRLLIGTPRIGKSVAAGSYLLYQLLHYDAEQIQVVVHCFGGGDAYVSDKTTRA
VTRCSDEEMCISELRRLRGHGRNVYIIYGVAKEGTPPPRHFAPTSGWGMIAVSFPKVTNY
DEWAKQLQAARIIVNCPDEVDVKAMCAWMTRDETKEKQAECWKEVKKHMYLL*
>TCRU_2793 Concanavalin A-like lectin/glucanases superfamily,
putative
MCTGPVPTKGLVAFLSGSPTETEWRDEYLGVGATIKNTAAAVNGVTLKGAGAGAQWPADM
NGPTVPHNFANREFTLAAAVSIHEVPESGNVPLVGVGMSDPNSTVLIGLSYTHERNWSFM
TPSDAHPDEPALFDWKPNTTYQLMFEMNTDGCYVFVDGRGLYMKKADEESFATLLEKHRI
SYLFIGCGSARGTESSRMTVTNVILYNHTVYGEGLEQLNASTVPISQSGVAKQQRKHEGD
PSCGDSTVHLSVSPVLPLPALVLQLWGMTALC*
>TCRU_2794 BNR repeat-like domain containing protein, putative
MSSCGDGQHQLCVSDGHGTSWYPNRVSINRVWGNSHDRKGYGVQSGSTTAVIAGEKVMLA
ALPAYSKDNEKGRLHLWVTSIVRVHDVGPISREGDDAAASSLLVKGNNDELLSLYENKER
SEDGSDGHVAVRVAAGLQRVKDVAKKWTDLESAPQ*
>TCRU_2795 hypothetical protein

MSDAAVPPKKASPKKAAPKKAVAKKTPAKKTAKKPAVKKPAAKKRAAPKKKPAAAKKAVT
KSAKKHAAKKAPKKAVKKAPKK*
>TCRU_2796 hypothetical protein, conserved
MTRHDAARMDELAAEVANEPSEYSPVLRRGLRVLRSTVDDGRLSTSALLPDRVRYASVKE
REKAFSKHYGHFCAYYKSSCFTSVILTRLAIGTVEYFDENFYPDCVEDVDYSLRLRLLGF
QERNVLYGKLLHRGSSNIRFANEMETPDALWYRRVRSLSANKPYAMMKWGPQRACSGGYK
KPYDGMVPAEVWVKDETRIQRIRVHGHDEEQGIPKVECDRTLLHPVRTKGR*
>TCRU_2797 RNase H, putative
MQPHDGIQCTAPGHGKAECPSYPAQAKTLHVVTDSHSLLAAVTKGPRSHTDWTEDRIWQR
LLSLTRAGWSVQLQFCYEHCGVHVNEPADQHATQTTATGQYTEHGIAPIWRTDLLTCINT
QLTNKWRSTMHQDTHHYLLGGARPSDPGGKHLITQEALDQQGTDKHCMSRVRGIRALGSP
VLDCERLHEPTPFLQHLTGTVCIYAL*
>TCRU_2798 retrotransposon hot spot protein, RHS3, putative
MAAGSYLLYQLLHCDVEELPMVAYVIADRKFLFDKTTKTVTRCSAASSIMDILDGLSDRG
VKGYIIYDVAMKGRQPSAGLPCEGWGMIVVTSPNTNNYESWAEQTEAEEIIMNCPDESDV
RAMCIWKEHNGQVEEEADYWKKVKDRMDKVGPILRFIFGN*
>TCRU_2799 hypothetical protein, conserved
MTRRAKRTRPATPQDEHAIPLQQQVNVPVLNLEWIQSRLHPATLESLMQVWGLVGRLTFP
PSSSGKACEGSRRIPTADAHLLRKAGIIEDASSTITGGWIIPFSVVEEKTNGLRRRWIAW
PRDKNRDDPYKANAPLLHISHYLPPAMAEAASCLDLKASFFRVSLPRETRHLFRCRVEDG
TLVELTRHPVGYKAGPEILQIIITSAIAGVTTVVHRLWAAPPSVRIDVWIGNIRIAGSKS
DATLWEAQVLRNADSCHATIGRTANRAPRSTPSWGCSLVTHTGRYP*
>TCRU_2800 hypothetical protein, conserved
MMTVSATISGLRWISGNTAKHWKDSTLTGHIADLRAPQAPNFAFQLLLPIMRAARELGAR
QGLTIAEGRRSKPHYAAADVQNRSAQLQHRMEEANDHFSARASNTAVADGLLAGRERHFE
TTPGTKGTHRCLGSAACSLGCGDSPGQRGVPSSRRGPPDAPAHGYENSATTPPHHERLMA
RDAAAPTIPQPSFTGERRRDNTLASLGTVGERVSLTP*
>TCRU_2801 Histone methylation protein DOT1, putative
MTVQRYYLLGGALFFFFVYCLVRPGSLRRLAFASGIGFALGYGLPALNNVRKHSFKAINE
PIHLLTPPADFRSMYHRIFEHISERYDELGQMEIGEEHITVMQNVFAQIGTLDFDGIRKM
WTSVIIPQLRSSISGGALVNDSQNLPTKIEESVVFCDIGSGVGNVCLQILAETHCKKVVG
VEVIPSRFRNAKTALANAKLYYPEYFDGKEAIFFNDDFVNCVSCLKEQQVNVIFAHSWMF
DDELMEKLTELVTSVPTVLCVVTSRRLTEKVLQISPIKLVSQVYLTADWNEQAPFYVYTK
N*
>TCRU_2802 serine/threonine-protein kinase a, putative
MTDTKRMANANSGLPQPPAEGDAAKSDPLEGILGTHPDCKYIKKKLLGQGSFGSAWRVEE
RETGTIYAAKVMDTNNMSSKDRGFVTNEVKCLSRCNNANIIRHHVSYERGGMLLIIMEYA
DGGDLYKQIKARQQSTRYFKEHEVLFIFLQLCLALDHIHMNKMMHRDLKTANVLLTTTGL
VKLGDFGFSRQYEDSLSNPVGSTFCGTPYYLSPELWRRAPYSKKSEMWALGVVLYEVIVL
KRPFGGRNMDELIDNILHARRQPLPNIYSEDLRNVCDQLLSLDPKYRPSLRQLFQQPFIR
KGLETLRRSVLNHNRIPQNVQKDIACNVDEVLNSDIQDYESSRVVPRRGIVTRHTADRGW
QDCELLLDEEAVVMRDVATGSEERVELNALTSVCPIDAAIAHEKFVFAMKNQTGKAFWFK
EVNETSYEEWLVALQNALPF*
>TCRU_2803 squalene synthase, putative
MEYMEELYAMVRMKWRLRRIEKGIACNDEDLRFCYDILQAVSRSFAVVIMELDEEMRDAV
CIFYLVLRALDTVEDDMSIPVDFKLRELPKFHEHLHDTTWCMSGVGVGRERELLERYTHV
TRAYSRLGKAYQDIISGICERMANGMCDFLTRKVETKADYDLYCHYVAGLVGHGLTLLYV
SSGLEDVRLADDLTNANHMGLFLQKTNIIRDFYEDIREVPPRVFWPREIWEKYTDDLHAF
KDELHEAKAVECLNAMVADALVHVPHVVEYLASLRDPSVFTFSAIPQVMAMATLSLVFNN
KDVFHTKVKTTRGATARIFHYSTELQATLQMLKTYTLRLAARMNAQDACYDRIEHLVNDA
IRAMESHQKPNGESVARSMLMRYPALGGHLLYTLVDNVVGYLGK*
>TCRU_2804 hypothetical protein, conserved
MNSLGDRFRCVVALLSGDAGNDDNTAAYHVAIVMPAMGAAALEEEVAANTVAFGAANKMK
IVDWGSDTAALLAAAHGPALAHVSLLRADAVAFADARQQLLAHHDPTLLLLELACEKAMP

FAAEYTAGDEWSWIRPPSSYFAELTESERDAAVCIPAVMRCSCPLVRATASLLSPSLWMN
SAVTLNGMLREVGYKVGCLSKYGS*
>TCRU_2805 inositol polyphosphate 1-phosphatase, putative
MVSVDLLHVLTVCVRGALAAQRYIALELLKVQELETQLPALPIMDQDPQTKKVLLALLHQ
AVTVKVKEQLSNKEDAAAMDLVTTADVVTQAVVEHVLRDAFSDMPFTIVGEEEVASVSVK
SLAERCVEKYYRELTLVPYQTELEAHACRRGSQVTAATWKELRERVGVFIDPIDGTNCFV
EGLWEVPLTLVGLTLDGVPVAGVVNRVFGFSVAQMISENSSRSSTSLSYVWNFGLKEPFI
VHEGRRVVPAATYKIVSANSVLRVIGSSTTKSQCFADVLEKLFPIEMHGARGAGNKLMFL
ISSMLAGSPSVQSCDVFISPEDTIKKWDTCAPHAFIVALGGELHTLRGDVVRYSLHGKDL
ARLSSGVLGVSRRSKLEVARRIKWSSSSL*
>TCRU_2806 hypothetical protein, conserved
MSTNPKYGREALRARFADAAKSVTELYRTAVVSYDAGYRDALLFVHRYILLDTPAAMTTD
VVLPHSGQPPAKTASPLASARSPDAERLLRFIQNTLKRHEAVSAASRGMSRRRKRSPGWI
ERPACGVCADGESSIMPDGGRGAPCRRTSFSARVFEESGAEVHDMLSNVRIAHPAESDSG
ISDDEFAAER*
>TCRU_2807 nucleoporin (NUP54/57), putative
MFGVSSSGFGTAANTAGGFGTAANPTGGFGTAANTAGGFGTAANTAGGFGTAANTAGGFG
TAANTAGGFGTAANPTGGFGTAANTAGGFGTAANLTGGFGTAANPTGGFGTAANLTGGFG
TAANPTGGFGTAANTAGGFGTAANIAGGFGVTGGLGFTAAGGFGAYAGAKNNNMVGMEQN
IQEFGSQSTAGRYLLELDNAYNALHPNCRFRAFLYNMCAPGQSTMAVERERFIAAQAGGG
CKEEELLRAQERNPDPLRMYPSPIHFMQELKARAEKQQEVITAMTKHVDVLISKSERFRE
MDEANVAQYRELMLEQVMLQRRWYSLLKKVETLRQLGLPLGEESRIARIVKTLNLQLSAP
GVYRTALSELQPFLDAESATVASLLRSRPGDEAREPVVAKEDGMLQRRTDPQLLKNWTRF
AERIQEGVEALIELLEKDSADMRAIRHRVGLT*
>TCRU_2808 Region in Clathrin and VPS, putative
MATVWRSFKFFELEVLKGPLSRMEMTSCCYGHKAIFVGDGEGFVYALNRGGTTTTLEFSA
YKGAVTHMKHLRSRNVLVTIGDDDALNTGIMRVWNLDAVSESAPPYREHRLFNAKHPPPS
ETIVLRTNYNTELMNSLKFRGRDGDAVNAIPATAFRTVVVDFDVSEDLQNAAVALVSDEI
VVLRGDLEHDPTVKICRIRSGVARGAVAFVGFPGAKFTPRAAQGKQHLFGLGIGNPNANA
NSSSINSNTAVAHALYTVFADCVTVWQVTGAAEYKEHRCDPPFGAAPECCCLTDDGQLVV
TSATNDQIAVFGSEAVLSPSARTSASLPVFDPTLFGAVHFAEVEGHKRRIIAHRSYVVVL
TQSSTRSEKFTLQCYDILNGLRCLSRTQESSCTNVAWVIADAADILVVCQETKHEEFVAQ
RVMRLVETELQARLEQLFQKECYDVAKRIVRRLHAADASQQMSIQKKYGDYLVSKGKYAE
AIDQYIEAIGFLEPSYVIRIFVNGQHTAELTRYLEELHHTRHGNLANRSHTTLLLNCYIK
LRDEARLSEFIHRDDIRFDAHNAIEVCRQAGYYDAAIYLAEKYAQPHDYVIIQLENLHNP
KKALAFIRNLCVDDAEAILLEVGKDLAGMEPRACTELLAELCIQWKGPARRLADPARTHR
SSPQDYSFRLQQQQQSRPSHRSEAKDFMHVFVDSPVCLLYFLRAVVESGVLDGGGESQRV
VYNTLLELYMTRELKQCIRHQVTPEGAEVYTVEPYERRLEQALTFIEAYAGSYDDYHALA
LAEQQEFEEGVLLLLQRLHLSSDIMQYYAKRLEEGATPAIRRAAREKLIETCRSRLNRDG
TDNDNNSNNNNNNTIGGPGADHSRANSGSSRGRTDESTKELWLSLLSLLVRSPDTEWQDL
VQVLQYIEEQDLLSPLSVVEILSTNPRLQLCTVREYALRVMRKDEQRTEAFHGLIDTRLK
KLRELHGEIDALQTKATVFQAHKCFHCHAALDLPVVHFMCQHSFHQRCLNDITECNVCAP
AHRRLAAEQREAEERYGDPKIFFERLGAAHDADGFSVVAEQFGKCIFAAPQLRKEATLFF
GDPMVPGAVSAAGACGGRSGPAISSEDEDDYDDMRRAAMEDGEEVYDEDGELLRPEAIEL
W*
>TCRU_2809 hypothetical protein, conserved
MGKGREAVTLETTPDLNFVKSGHLNMLIYTNKEGEQVKVPVNSLEFLEDRRVVRSRSMDQ
VNFNNDCVFKVTLEFMEPMACLEETAVRELTDWVLCSCRGHASFYSPVEKRLVLQQCFVC
LQSNIPELLDPFILVLYLEKDQWLVERVLR*
>TCRU_2810 ribosomal protein L7/L12, putative
MRRVQTHTKAEILFRWFTIGGVTGTAMPRGMQAFPLRDSAKTIETIAEAYVNMDLATMRK
FHESVLKNTTRTCGTSRLSYEQALLQGIGAGNSWSSTGTVGVGDSALSSASSPTREEALA
SDNAALAKKVAEKTAFDFTVRKYPSANKVKLIKELRAVSGLPLHEAKTAVEKCPGVLVKA
MARADAEKLKALFEGHGAEVELL*

>TCRU_2811 hypothetical protein, conserved
MAGLLGLFIATVELLLFFIFDLILARVLNTLKLDHPELEECAPEDLPDLDPAAIVDTLRH
NLEELYDHQHRRFTGDTKEYTSFNETNVEFAPVPPPPPCNREKILHGIILVCGPAAPLFT
CLQFLFPTAFGWCRFLLPVWMQYAALIPGLAAVFVFAARTTHVAQYSDVSKQQWILLMWF
RLDFMCIMSVVALCGAGAWLVAGCMFAVALYLAHRVMRIEKRLAHLTHETQLVRGEVDIE
HVYLPGSEQAERALASSDVQGYNALK*
>TCRU_regulator, putative Ma.1
MDFVPLASFEFLNSLLQGVEAQGCLMTVRLEAFTCRSTRKKKQLAASMAHYANANTPPLA
PASHAGLSPPPLQLDRRLPVVFAPVDPEDIDDRLVYLVAALNSIYGEDGYDFSVLTEEDF
VVCNEAQVRAEVDVTLHSMSDSCRPAVEQFWTLVSEQVMDASQGCEYFRFMCPTCDPMVS
RSLFSQHYFLYNRRSRLLVSLLIFAEGNAYRGDDGVIVGNGFYVERDDADTDEGNNSSRG
AWQSSPEPLSSDDGVGGKNLHYYYGH*
>TCRU_2813 KH domain/Domain of unknown function (DUF1771)/Smr domain containing protein, putative
MERVVQITRVQVGHVVGRGGATIKELQCTTGASVEIIDGPSVRITGDSEEKVLAALERVQ
AIVACQKNPEYEGPVGAKLRREADALGARRSKLFDEATARRNEGDAQAAHKLVEEAKEVG
RQMEEKNKEAAAAIAHYNNEGKGKGDDYFDMHGLRKEEAMTMLQFRVQRLRAKPSGTVTE
FELITGAGHHSAPGKKQLLKAATVAYLQGEGIPFTEVSAGSLMATIIGTGEAAVAAPTAT
AMAADAAAKKDEKKAAASASASKLQQKTEKRKEKGKCGGLCTVM*
>TCRU_2814 hypothetical protein
MTNVVLLDDALVEMEGDACHLLYREEDAGVWKVAFVTPPTLVSLSVQAPPTAMAAGDAKA
DDADEDALEFFSD*
>TCRU_2815 hypothetical protein
MWRARIACSGFVLYFARRSVVVPSNTDAEKLFQRIVHPNYDEDTNRRLSGSMLVSCVAAI
EFRRQRMEVKGKLGPMDAFLGNDMLEFLVALSKMCDQRGSLAVVEGICSNVHDDLQESNR
VAFAVKTLLNALDILCNFSNGAHQRSFAVDAVKLLQLELSLLEVLVRVEGGAHGNVQEAC
YHMQRMQHVLENRGIYTLSAVEQRRWMKRMRWLTTVTYSHLKDCSHEDEEAFKRTLRSLY
GEEGTFGYINKLRYAVGVLLPFLLKNAATMMKGRKWQRKRNAACKVGDKLPPQK*
>TCRU_2816 hypothetical protein
MPSRRRRQPAYAAAEQRKKTTEMQQQPEAASCEAGAPDEAKKTEAVAPEVSPMAPIPPPT
AARQGGQAAEVPPTATPTSVAPTDAKRAVLTKMVTKRKPKMAFLFDNEETKGAEHKEEPS
GTKEAVPKRKPKLPFLFNEEGTHDGAAAQKQPQPEVPQANPVVETAPKTNTRIDEVKKET
IEKISAEADWSGAAPTRTVAATPPRQKMAISKNVKLYRRMRREPHEATNNTAAVEKAEER
SNNSAPTNSTYVQVEMKKTQQLHTDDGKASPPFTEPTEKTLHESSGKERHEHTAEKFSEA
PKEDVKRKHTATMSKLMRHGRHFQNCKTAVDSPSNTSENAQTQTKEEVEVPEVIEPGATS
EIAQRTPVCNDQPNLPQSLDGIRAVENSKTAEMPRHTTKKHEKKKTKKSLVKRKFMKEMA
EKQAASKQAEEEAARKQAEEEAARKQAEEEAARKQAEEEAARKQAEEEAARKQAEEEAAR
KQAEEEAARKQAEEEAARKRAEAAARKKAREEAERKRAEDEAARKRARREARERAKEIVK
QRRAKEEAARKQAEEEAARKRAEEEAARKQAEEEAARKQAEEEAARKQAEEEAARKQAEE
EAARKQAEEEAARKQAEEEAARKRADVKKLSEKGPKTRPH*
>TCRU_2817 kinetoplast-associated protein, putative
MRQSNPVTDKTVVAAAVAQEVMDVPLVSVHACGASSASDASAAVPSESKLLAEALEFPNS
SVTIDRFDDNELVARRRSTDDAWEIGLRFDWTIKTLAIGSMPSFSLTDPRRLHPFMQRYQ
SRPVWFLEEVNGAKANNIREVMDILKKSLTARFVFRK*
>TCRU_2818 kinetoplastid kinetochore protein 8
MRSTTPPLYYKRPEGVPLPYCTAAGPAIEVPPSLRVPPATTANNWGYPTAPNAARVGSVE
YTKYGTIPSFTNTVPSMPAVANPFNPTNPSPRTSLAADNPADLIQQSAARWSTTANQSAQ
ALSALEAEEASILLEEQAMKAKLAELQLTRQRQSEGQLDLSHGWAALLDREERYFTEPLV
DLSEEIMAREHQCALLRDQLQQAEAHLEALRREYQEYDTVVEEKNKLEAEMLRVREGFLE
IEGRRKACRMRAELLFDVESKRAVKASHHVRELDVQLKEMTSVGPLSELQSAPPSRSASR
GVTFAPKVMHLHVGSHAKGEQEEEEADDEDAGLTQGFGGTSVCLQNDGDDDDVGGIGGRS
VAYSLSVVPKRQRVEVPTT*
>TCRU_2819 Endoplasmic Reticulum-Golgi Intermediate Compartment (ERGIC)/Endoplasmic reticulum vesicle transporter, putative

MRWLGQLDVFPKFDTKFEQDARQRTAVGGIFSLISLLIIAVLVIGEVRYFFSTIEQHEMY
VDPDLGGTMEITVNITFPRVPCDLITADAIDAFGTFAEGVERDTVKSRVAASTLEKISEA
RPLVDEKKKITKALDPSGAEKENCPSCYGAEPEPGACCHTCEDVRRAYSLRRWVFNEDDI
SVEQCAEERLRKAATLSSQEGCNLFVNYKVARVTGNIHFVPGRMFNLMGQHLHDFRGKTV
RQLNLSHIVHTLGFGERFPGQVNPMDGLVNSRGAVDATEEVNGRFSYFVKVVPTQYQSAS
ILGVGSVVESNQYSVTHHFTPSPSAELSAAAAGSSPVMVPGVFITYDLSPIKVFVIEKHP
YSSVLHLVLQLCAVGGGVFTVAGLVDSVIFHGVRRVQRKMQQGKQS*
>TCRU_2820 emp24/gp25L/p24 family/GOLD, putative
MRRLVTQCPHAPRCTAHASVVIVWLLALFLYGPYGAVGFGTKIDAEDRECFVESLAAGGS
LAFTFRVTDGGSFDIDAVMYATTVAPLNSVEETTRLHYSEALIKMRENTTTVIVNEWRRA
NEGSQSYTAPSAAETKHGLPAEITVCFDNSFSRLSPKWLLFQFLKRDVPEVDPESTTRAE
AEIETKLHKHGTVLFELATAAERMRQMGESNRVRYESLASIVMVGLVGNIVILALMAVYQ
YMTLTRFLIRRRAK*
>TCRU_2821 retrotransposon hot spot protein, RHS3, putative
MAAGSYLLYQLLHYDVEQLQLVVHCFGGRDAYVSDKTSRTVTRCGDEDMCISELRRLRGH
GGNVYIIYDVAKEGTPPPRHFAPTSGWGMIVVPSPNVANYDEWAKQLQAARIIVNCPDEV
DVKAVCAWMTRGGTKEKQAECWKEVKNTCIFWDGFHVTSSMRRRLMDAVER*
>TCRU_2822 retrotransposon hot spot protein, RHS3, putative
MKRAVKGEVIFDEDIRRLCDKGVNNLPEWSLAAADVKAAVHNSTKHFLDAAAEEARKLTT
TSAPEKLEECYESVHNARCSHAVELPDGDERKKTGTGMGVHEGKPEQ*
>TCRU_2823 retrotransposon hot spot protein, RHS3, putative
MITYKTSGFLKKFLTSLRTKRWGPLLGLFTKVCTLSGNVGTMKEKHTITPLARGTPNGVL
TQVPTEARREAEERLRRTQEMKFTISSNIDDVLFKGRARVNVMRLNDFLTREPDGRGIVD
TNRDVML*
>TCRU_2824 retrotransposon hot spot protein, RHS3, putative
MSERHGEGNDDNETSPASTVLRGRRARARAESDGDSGQPAVPRRRVEETRRPQWGLFSWV
EDVLLGGKARGNYMKLNDFLRGHIGPSAVVDERYNVTMEVFLVEPRNYVQDQKLLEEIFN
LSEYQVLQEMRGLRRDTYNVSQMGVRSLRQWRDFERKDMVSPLARRELDAALRGVLKEEK
IQMSEGFYDSLYNARWHHVVEFTDGEGMGMEVREGKPPQSWTYKAVGRTLERDDSVEQSG
APRLRLMVLTSDKAWPYSWPLGPSIRDCYVNCEVDRVWQTVKGDLTEWFSTRGENNFTPG
RRVLIGMPGIGKSMGAGSYLLYQLLHYDAEKLPVVAYSVAEQTFLFDKITKTALHYVGES
TFLKAVEEFSGRGMRGYFIHNVAEPIHEPSVRLLPRGWCMIVVAPPEESARRGCKKQLRG
RRIIMSCPQESDVKAMCVWKKRDQSAEAQVEYWQEVRGYMDGMGSILRDLFSERDTNARL
SAAREPWNGLPHQMLMNALA*
>TCRU_2825 T-complex protein 1, beta subunit, putative
MLFANQAQQVLREGASEEKGERARLMNIMGAISVADIVKTTLGPKGMDKILQGMDRTQSV
RVTNDGATILKSLFMDNPAGKILIDMSKTQDDEVGDGTTSVTVLAGELLRNAEKLLDQSI
HPQTIIEGYRLATQVAREALVASAEDHGHDEKMFYDDLLRIAKTTLSSKIITVEKDHFAK
LCVDAVLRLRGSGNLEMINIMKKLGGTLGDSYLEPGFLLDKKIGIGQPRYLENAKILVAN
TPMDTDKIKIFGAKVRVDSVAQLAEVEASEKEKMKNKCMKIIKHDINCFINRQLIYNYPE
EIFAQHGIMAIEHADFEGIERLAKALGADVLSQFDETEKVKYGFAQKIDEIMIGESTVIR
FSGLPQGEACTIVVRGTSQHILDEAERSIHDALCVISQTINETRTVLGAGCSEFVMARAV
EERAKKTPGKRQLAMLAFANALCTLPAIIADNAGLDSNDLVTRLQASHYQGNNTFGIDVV
KGDVADVKALGITESFKVKNSVLGYAAEAAEMILRVDDVLRAVPRRRTQ*
>TCRU_2826 WD domain, G-beta repeat, putative
MSNKYSAPEKASGAQKKEIAVTNNVNTDITKVKICSGHTRPICHINYSEIIDGTFWFVTS
CHDAKPMLRNGETGDWVGTFEGHKGAVYCSVFNQDATRLVTGSGDYSSMIWNAITGEKLH
TWSHPKYIKSCDWIENKIATGCFDGLVRIFDANDYNAEPLSFDSPEKVNQVKSTYFIDPT
TMVTACENVIMKWDLRDTSRPYLRKEIPGLNFLEYTHHHCIVAAHEKSVSFIDTTTLEIK
SSFTTNEDVECASLSPNGQNVAAGSKLKAKEFTLDGAELESHRGHHGPIFHIRWAPDGKS
FASGAEDGMARIWPSHDIIQVYDGDN*
>TCRU_2827 hypothetical protein, conserved
MMMMTGRVLLVCALCVLWCGAGGGCEEVPGVFPSGVSGGIERERGDSEDSLRSEPPGAKK
LAPETPPPKVQQQEVISPPPKVPPVGSEDGAGGDKEGKAGEEGAKDVGKENRGDATSKEV

KKPENHPKSVKSPQSRENEGLQSPSLNGTHGVGTITSTSDSLTVNTNQQDLSSPLQPPLP
NSSPHAIPSSTSAAGPDNEKSRENGNGTKNSQMPVVGEIQERNGTCVKAVASTSGEENSR
LSAKRVEEMSDATKKDNSESSTTATAALRSDAGTEGTPTTNHPNQPSTEGATPPETTSDG
EAASANKYDTVSQSAGSTTAPTTNAKTGDKTKPVDSDGSTAASHTTSPLLLLVVVVACAA
AAAVVAA*
>TCRU_2828 hypothetical protein, conserved
MQHNCALHRRHIRHVDESVGHQARRALAEAANPQLRTARKHAVAQRHVQCVIERVHRAQV
HRHDDRSAEHHRVEARRHPPAANRHGLRQRHATHAALRTATTATGPRRRHVKRQACLAQA
AGTAAAHAVRERRRQRIKARQRSRTAVARHHAHGGQAGHAVVAAALQHPAAGTVALHGHG
AARDRQPENKRRASSSAARNRHGTAAQRHTRQRCHRRRLAHRPHVVQVQPPAGTDRPTAA
AHQRGRDRPLDAHKAQHRVRHRETLSKHKAAAAAHNRDVRHGEHRVAPQTETRRGRYIHR
GRGRTARRLQRHAVKHHRARQQVHVAANVHRRPARLQRPQHSVAHTQLRLQQRRRVQHKR
*
>TCRU_2829 chaperone protein DNAj, putative
MHYRTLGVKRRATQEEIRKAFRSAAVRVHPDKPDGSVELFQSLQTAYEVLSNEKKRALYD
AELAKKMSKLRGFKRPPPLDNIRLPVHYKLADDEYYAFETAPDCLKCSFKHGDIISWNNK
LGCFIGLAGDNFLYWRQDDQTHASKLCQMGSFGMGGIKVVVRANFMLARGRFTSSSLPSR
SADTANSGSHRQVAGKQHDDAGKSAPVTHGEAMKKGRPGRLSDAERLRRDIMRRERERYY
WESMAALAEKEEKQRVRLIEKIEADMEDELQSFRNWLEAGGVAVGGEEPAWVRHARRHAF
GK*
>TCRU_2830 protein kinase, putative
MSSPAWSVYEGDWGSFCDDADNVPPTLALKGCGLRQKCLLQRGAQGAVYLGEDADGNVFV
VKRLFTQRSEFGVRGVSEGSLREATLLTYITERSRTLGPEPLFGVIRLERIVEAPFQELC
LILERCAFNLSRMVFYSRKRPYGAAVLFPETPTRCPILAKMNVIQYLMRGILKILQFLHE
ECHIIHRDVKLGNLLVGEDGRVRLADFGSARFMHEAVEKMSDARSGEYTPISLRTTVIYQ
APECLLGERSYTAAVDMWAAGVVFAELLLQQHLFHSCSELAMLSDIWKLLGTPSDDPSFS
SGEGAVTYAMRTESTIARKFPEGIVSAEGLDLLKRMLETNPKKRITDSEALRHPFLCGPA
VESGMEEARRLWNKKVEACMQETVAQPAAMGMRSFYVDNVEFDEESGENDDGDGGIATLP
TCLDCFPHILSDVNGGYDI*
>TCRU_2831 Intraflagellar transport complex B protein 46 C terminal,
putative
MPPRRAIDDDEEITEEEEEEELETTSGSEEESSVEDSAKGLGAGTTGPKEALLVNKPNDE
KYVVEGARHVQTPPDNVTGSKVLYKSRPESPRGMREGNKPETSLGSQSLRQAQSPQESLQ
IPSDMDIRKLRNNPNDEMVRVEDALNIPTPRGKGQEEAGGLLLRNAPHDEAIPLSTRGSS
VGTPRKQTGEKMGAMSPTDEGSSADEEAEEVETQSRGYINQRPEAIDTEAHLKTNVIPNL
EYKPQDYAKINSTASREMQELFKCILDYQPVIPDLPAKLRPFIPDYVPSIGDLDPFCKIS
RPDGRPDGLGLFVLDEPSVSQSNPAVVLLELRATNIHSSGGLAEVVDSFEDAANRPEVID
RWIADVKKVHYKKPLPTTNYQMPMPEIESLLQVWPPVFEDFLNSDIQFPPPTIDMDLDQY
VRTLCCILDIPTYNSLVDSLHVMFTLYQEFRANQHFQHE*
>TCRU_2832 cytoskeleton-associated protein, putative
MGHEEQVDMPMVPGAAAQSVEDFSNLPLNALLAHKSWKARKEGFEQIRNSPKSLKAHLLE
KPRKLMCESNAAAQEALFEALSALVDVCDDEELNILVGEPLRVVIEKGITGRPRAVHASF
KFVSDLVGAAKQAEVFDALLPAFAHKAPKNRMAATQLCAQIVGEYGVAGLPTKAILRAMQ
PLFNDANAQVRKEASSLCCQCYRFIGAGIKGFLTDLRDVQLQELETLFEDVILGEAPRRS
IRGLLPAASTKPTALTVSLVSHNGNTNDISDDAYESHDEVPVLSRLPRNFYRVALDKTAK
WQDRVAMVQDNLLPLIAAAKIRVKDDYHELAGMVRELLLDPQAPLMLLGFKCIQELARAL
RAAFAPHARSYLNPLFDKMKDKKTSVVEHITTTLEILMRYKCITLEQCQDEIELTLQSRV
PNQRLALIQWLLRLTVKLDHSCFNRLSRAQVILGRLMNDEKVEIREASCMLISKLITFLG
ETNFQSLLASLDEKQRIKLAKAINSESNLQCTPTISPAKKTLRVERREGSSVAVSRSLSI
GETHSPSHVSASLRGHRHSSLMARHSSPELRRQHPIDDSVSLESTLPSKEGASNRMLGLM
NGDTTVTQLLRSKDWGNRYNGVMKIREMVERWSKKECTEYLDTVLVYLRVDPGWRESIFQ
VFQGMLSVIQELLLRATEVSAGASYAIINGCVCRLTEPKNKAYVRNLMTQIAKFQGISFV
TRHLMGEVTSVKTPRLMQECNEYMTQLLQTFPASHVDAKGIIDYVRIHCFGQQFPAVRSS
GVALLVALRLHTGPLVDNYMNNTIPALRTAYEEGVSHSNGNKISHRGTGCDVHRAFSPVS

PSRMQKTENRLSEKGTGQHGAVVNTAPSRVENRTGFLSRGYDQTQHITENEESPMRADVS
HQLAPLIKQITIAKDWRMRLDAVKRVEELMYASNKNIAPNLVTELLRSLRSRFEEANKNF
VIDVLRTISLVVESAGSEACRPGMKSILQGVLGMLGDQKMSLRDEATNVAYLALDCLGLD
LVLQCMQKPLTSESHTAHQTALEIIERGFQKEPEAVVSKQLVISLVPAVVRLCMSRILEV
RVAAEGVIGKFLSLVGDEAVLKAMQSLRPAEQQSVMAPIERQVQIFLRTANEEEARRTST
LASMISAQVPASHTPRSPRSPRAASKNLSISHKSVDFSQMSQGAPASCTASQRTSMSKEA
LQPFAPSLVQPSASVAQSTHPQVRREELLSMQEIMVGLRSASASTAASTCVEFLERVKND
EDCGTPEIIQVMVERLYENIRFFDLGLALGLIRCLKAIFERPRYTQWCHSSLLFRILGMI
FDCLLSETFSLQEEVIKALNNMTLKLLEGCPGNDVFSALMSRMTRYSAIYTENGKKVDLK
YIQVTVKCLMRLDFDAVSPDNVVLCCHEYLLQHPPSAFRNLDDLSIRTVKTILQDFSRRC
GTPLLDVSNRLVGTQDLVTHFIRACLENQERAARAISENEQKKAVDANMQLQSHPQQQQQ
KQRDASPSHPARTRRGQNVYVDPNVPVTPSEAPLGPRGVALVAMEEKSMASIFSRIRNHL
TSKQGIEELYAFLKQHPKSPEFEQQFRRCSEAFRSYIKRKLDRQLQDDPTKPPGFSLPDV
LRPMP*
>TCRU_2833 hypothetical protein
MDPTVPPFCDGVSFTLCDDDVYAFGGAVPEIIWRLNLATHTWHEIPCTGSVPAARKNHAA
ASFAGNLLLCGGEPLHASFLQPPKLMPYYELSLDTMAWGLIDTIGAIPLNRSHHACSVVG
ESMILLGGKPLLSKDEGVLTNERLNEFIQAGFYDVYIFDILPRFWRAVVALGPAPLLWGH
SAAVYDERYILVFGGMDVSANETVVISRYGSPHHRHDPPVAEVSDKLYILDTEQMKLRVV
SPAVQYPTPPRAFHAAHIDGVRMYVLGGVTVTKHGNLVPFDEMRVYDIIEGKWNLMEFPL
RFPAAVRRLSFAYESQLVVVPNMTSMWCLDVHKQAASKGWKEVPTSHVKVAAIPATSEAD
EYNELLNPRRRTAYDDIPCGQTDGVELSQSMPPSTSPRAPSMQFDMIMDEIHQLRELLTQ
RGPRQPSPHSPQQKQRNKEERPPTATVTEGLQTAGNEVESTKMRERRRRGREKIKKFTHQ
KELILQLTRRLEHLLERKKEEKQEETTGLFAVGQQLSQRTSDEALEADPLICSLAKHCES
DASVPSPQSPLHDTLISFQREGVGKKGQISFNDQDGTLEKWTRLIEILKKSPMKPSSKAF
RASVVMI*
>TCRU_2834 hypothetical protein
MSLSVTQSVRDEMVAALLLALDYTQGVLETGIDTKNVNVFFRNVLSRVACRWLPCILSIF
ILLLVTLQKRVLNARRRQLPDVIISSERSKNPPSNTVGAESSTGRNIGAEESTGMRRSHE
AQRVIDAYFGPANNTVVDDFDADGHVQKLLKHFNPSNTTTTSES*
>TCRU_2835 hypothetical protein, conserved
MEEFYNNPFRHDPAVDDVCYASVQFPSMTASNTETESCRERDFFSISSALRFQTQLSEAL
RANSTLRSTYEAHIETQRNEIDRLSVENNELQMKLTRLEAQLRSLLLEKDCSTMAYKREV
EKNALLEEKVGCLEEELNSLERRTRELRAAYNRTPQQKDGCETTFSRTRPNLLQQQRESH
YTEQGTPSSLVSASDLHSPKSLLESERNNRSGEKQKWRAAEEAAASWRTETATSMKTGLG
GRTPKPCSKATPYPTQVMDEENDVVVKELEKRLLRECQTRDEIEKRLQKMESTRIRSGSE
RAKKIALEREFIAAQRAVGETRMRLRELSALVR*
>TCRU_2836 hypothetical protein, conserved
MKGLEEWLASSSSLDDSNNADAVSAPPVRGGRGGEGASSTDARTRNEEMRERMRNLLGDR
VVKAVLEETSGVGKAAAPQSVSTADNYCVEEDGGRRGDRHHEKNSRGGSDRCIRPSSREY
RRVEVMVVDRGTQTTSTVGCQTDPVENYAPYMGYPLTHCCTCSCGKRRPGGGLLPREEYS
GEPPLRFKEQLDMIKNSIDIMIARYNLPPPPLPRVE*
>TCRU_2837 small GTP-binding protein Rab28, putative
MDSGSSAPEDTEPEYKIIVVGNGTVGKTSLIRRYCEDGFGQGYKQTIGVDFYSKKVEIPG
SQAVSLQIWDIGGQQIGGTMIANYVHGADAVCFVYDVTNPVSFKDVEDWRQSLLALQGNG
EGRKPLMVLVGNKTDLPNRQVTADMHAKAASAYDMESILISARSGDRVNALFVMIAAKLA
GVDISQQELDMTNRVVLSIDSRLQERTQGLRATEGKEKRKSSNDNCWLM*
>TCRU_2838 hypothetical protein
MAHKSDSYPSCPVTDISVLLDGSRARGQYAAAMVAMNRYYTMLYNSLLSLSFGLGLKFDP
FLDDELAEDDEGPLLRCLGMGSICSHDGNAVLRVRYEEECRQLEAQRSFLGAALEKKRLE
CEKLRAQGRAFRMEVEHMLPLTLAVNRKVRLSVPSDGETLLLSMRPAENPTAPLPAKSTA
AVSKNTPLLTMAAAIAAVEDQIRLQEQEVLRNGKRFSIKGTRHVVLQALREDLQDAQEAL
QRDVMSLEAAKIDALEAEEEKSRLILELEMVTWAKNCGEILFKEISERSAVLTQRVAKVQ
RMHQALQRVLSAGVQVTGSTSPRTDVKHNVTKKEEEEEEGEEEESSLENLQDSVRQLCTV

QESLFALNNCVVDLLDDVEEIETVLNELKTHSNALSSSTGTHLKVQKWRSRFLQEAYNDA
VLELLSWQARERLTVTAAAKLLKQFRRLCIVNNIFSTHFEALARAVMDSGTLWREVHQML
PAAQMALSIVRNRNC*
>TCRU_2839 AAA domain (Cdc48 subfamily)/AAA domain (dynein-related subfamily), putative
MGGGLSRQEELFVLGQWPELLESAMGTDNEASKENADGSKHASSTFRMSFYEWQALISLL
DSVVPSEVPSRLCTSISGQQLLNPIVVVMVHACCWVDGSVSEQKFAERLTRLQEDLQSQQ
DIPRWGRRSKEEDTERELVNKALRVFTDILAQRGKVPTPRRGDRVGIAAVESLISWDHSK
RPVVVLAHAFIVGALACIHPEPCYAESAIHSFRNLQQAMDEAVSSIWRGKRGVKGAACKI
GEWQAVRRLETILVRRQREADVADFLAVEDRWWLPSNTMVPHASSKASLEERWEAVSSHY
IGQQHVWAALKTHFLSSDVFNAEKPTVIVLFGPSGFGKSELARRLACVIHGVEVGELETS
GKLVYIHLPSFCTRDTIYSLVDPPAAHVGEGVLLSALRRNDDAVVVLDEFEKGTADAIQN
LWLSAFQKKGTLRSLKEASRSISTEKVTFVLTCNIAADTILHRTNEYLRGTAEEQAAMRK
EWTEVCRDVCRKTMHDPFVNRVDYFFPFVPYTEEEKRRFIHLQLRRVLLDQRAKDRRIYV
TPRMVKALARKLQTFHASTIECVVRPLLVEAVQKGWDTAVLTVVELVSGTEFVALPAVDK
SDGVTTWNSLPGAKRALEVCELPYGATGALPPVEKRRTDMVPGGNSGGGGGGEGSKSNIG
SLRATADRATQPIFRESNVVPDTRVGVDRKYALRLETAVEKELQVELNRVKELLVMKEKE
IAYLKEKVFQLEKLLAFFLATTLMCLLFLSFLVGMKIVFVMGLVIFMGLWLLVEMPLQLL
MGAIRVLYGVLGPVGSVIAVLVASLWGSQALRHAVVC*
>TCRU_2840 hypothetical protein, conserved
MGPKKGLKKTEEKALAVEDPVVVGCTRSLAKWTERVTANGRKIQQVQYVLSVLSSQMEVC
NKELADVYDCANLLTALRIVEYRQKLNPVPPAQPAKKLRGKRDGSGRLALKPLPDENSTE
ALVAAMDEKKRQKVRSILVSLFRRNNIDSPVPNTPTNTVASLGAGAPTASAETAVRQEVN
TSLCLPADAASISTSADLRRPKDVPPELWDEISKLRVKRVDLEGRSAMLMSGIDKQLARF
DLLVQNHGIATYAAEDLERRIQELRVGKSTARAL*
>TCRU_2841 CRAL/TRIO, N-terminal domain/CRAL/TRIO domain/Divergent CRAL/TRIO domain containing protein, putative
MTDTMSTATQRELECVAYLKQKISPTFLDPEDAGFLTDNTYLRFARARNAHKEKALAMLS
ACLDWRKEFKPYKITHGDVANAMKQFTITPAGRCRKGRPILVMTVGVPNACEVDERVKQL
VYLLEEVGQRCHEGITWIIDFSELGKHPRDARSSETRKTTMKILQDYYPELLGALLLYRT
PWYVRLLYNAVRPFIDKRTRKKVFSLGHDENLLLQCVSRDQIPESLGGTFRTDASKPLWE
*
>TCRU_2842 PH domain containing protein, putative
MMSGGMQQQRQRHACRASWLFKQAEWRFAWDRRFFVQDGLRLAYRVGENEAEKKAGYVIS
LQRTVEPPGSHTFRVWLKEGECWTLRAETEEEHQRWTSSIAAALMQDAAEELHDVREGFV
LKKGAWTGQWRQRYLELDEYRLAYRMNKEGEVRNRFVIVSADASGEEGREEELLVSTSCG
EQFWLKFASKEQFDDWTGVIMRGLRRTTSWHWKTLVSPQSSEYASVRVQYHASGAGNGPC
VYCYGGTYTLSSRRYFEASKLFLPDIHRVSVGKQLSFVQLTGEHKCISLDILPYEEGPHA
KLRPPPLFGAALCVLRSPSESLSSPVLPNFYASTPPLECLLLVGGRSETSVFRDVTVDVW
WCVLQGRSSRWQRCTYDANVLPGRTFHTLTAVSSRSALLIGGLDSMNRVCADCFLIFWPE
DETEAFITPPVVKFFCYLPEPRAFHVCLALRDVLLLLLGGRGVREAAPCSSLFVFLSSES
EWRELTVEPPLPVMNHVCAEVVFSSSGEQWVFVLGETCTSYPTLRLFQLSVQSKLAVSRE
VAITVGDIPRRCCGATMHHAGGYLYLIGGCYDGNQRNDQGQAVLFRDPIRMLIGDSEGGG
PVTTLRQ*
>TCRU_2843 Putative papain-like cysteine peptidase (DUF1796), putative
MRRWVSLGGWCGPGLMLSKLGIRPVEEQLPFDMARCSFDGLLEFTRNGFDNGFFPGPLQR
RPFTPDPASVWLLFRGQHACITHFDINADEVVQEFKRRFDEWEKMITCPTRPVTFLRTCI
AENARNEVELVPQWHALLREKSAGKLDFCTVMVMHDQGPTTERVASFAEEDAAGSPCVVW
NLAFDKQLPVEASLFDKCHDGYAQIIREMNRNEAWYVSTSPLRLVSPKPYKALCLVEGVP
ALRGSCTGFGTTHSALLGRCLYCGSTNGHEVVRDAFDSKKPWDNAEDTTLLAKWITSNGD
KVAAVEATALELKRGANEVLLRLQQLIQS*
>TCRU_2844 pseudouridine synthase A-like protein, putative
MPVAPNGLSVGDFVGGPSKKMTRKKNREERPFLFANYPSRKVAIRLAYHGHLYDGLAKQE

ETSNTVEAYVVAALKHVRLIPQDGPIDLARCGRTDKGVSALGNVFSLTVRASSWPTDSPQ
KPALDYCAMLNSALPVTIRIVGWAYVDDTFDARFSCVGRTYRYYFCHRGLNVEAMGNAAA
RLKGVHNFRNFCKTDVVNVSNYERDVRSVGIFASEAFPELVSYLEIHANSFLYHQIRCTM
EVLFLVGRGLEDPEVVTQLLERGDRKPVYPLADGTPLVLWDCHFKNLQWNISKRAFMAVE
HELQDIATALFLRASLANSMRSQLLTWYNGHTDSEGKTIMAQLPEVQAADRWSVTGCDWT
DKRTHANMRVRRYDLFALSRQREHGASGHLSSRPYTKLLERETERTFDEEVEALSQKKRA
RFESNMEKK*
>TCRU_2845 hypothetical protein
MAGSLATAFAPSETMQEIDEETAVYCRSHDVMWLGFVRDLLSTLRKAAHEVQAKSEGQLE
SRHLCVGDFGQFSRLSTALELLQDCCLKWEECRAEAEKGFLEYYFAMHSLNSGTEPKTGA
VPVGKFMSNLFAGVPGTVGGDRLAEELRVERKRLCLADALGLPLELPRGGDEQQLPQGML
ALERALKSFRVVTDETLPGYLYCTIQPLLCEMTSCWLLNGIFADTPLRLIGTAEGMRLAK
ERLELHASSLRFLLELAENEFCRCHTATALESKKELEEMLLRVTVMQTAATRDGVVGQLA
KEWRMAAEEARAVLASTEKTLLGVLPGQLMGEFDKLFQLSPHRVMDHIVHSFQLPLTSTA
PNHDVDRVVRCDDVPTAVAAVGALFDGMSLEEVEYLLQPSDPDNMSTTQREEGTFLAKIQ
AHFYRLFKLLLRACCLQGGEVLVMLWPFFELQASPFLCSVPHARLAAMLQRHNYALFDAL
LGTPWRVKAAVLLGGGWVRAARGHFAQWLSERRGEGRELLPIVVFKQLWREDDKSDVENG
TQNPFCISLLRRIITGCGGRLMNAKVAVLVPAGGATVLSRRYSVFPMMRHASCEVGGTDA
DETRGGKNNVSCFMMTEAKSRPLLVALLQATMMPVFSYSVCGATPLLFVSDGLDSKKQMH
VLDAGLLAGNGVG*
>TCRU_2846 epsilon-adaptin, putative
MSKLYRAQTQQGHSRGFFEYIRSVGESKSKQEEDAIVTRDLAELKKTLASNNIEKRLLKE
YVVRIFYAEMLGVSAEFAHIHCVNLSSSPDLLSKRTGYLGTWLTVGPEHDLMYLIVSNLQ
RDMKSSSFLDIAAALTAASKLVRLELMNAINTEVVGLLRHPNALVRKKAVSTMHAFYRKS
EGLIGDTKIFRQMLCDADPSVMGAALPLFADVICTDPTSQRELISIFLSILKQIGEHRLS
REYEYHGIPAPWLQIKLLQMLPILIGDEPSLARKCEEALREVITRADNGLVIGYAVMCEA
IRVITLIPTIPTLVELAAEAISKFLSARKANLRYAGIQALSQIVRLDPKYAHEHQHVVMA
CLEEADDTIRRKTMMLLLAMCNEDNVEVIVTRLVKSLSQTTDKYFREEFTRRICDVVERF
SPGAVWYIETMNKLLLCAAEHVPQMTIQGILKLIVEGEGKDGEKDAAFRTFCVEAYFDLL
EGSQKNLPEAFCRVAAWVIGEYGFLAKRISRTMLLDRLCDMLERAECADTRGWIIMAMIK
IVAHAGAMPDNVEDLITRFKDSRSVWIQQRCYEFTELVKMPVLMKKVLPLDGCCEEVDLD
ESMGFLDGIVQEALLAGARPYEKRKILLGVKEEETLRTDAYELVRTDVVNENELDPENFK
TEEPHKLVIRPAVKRWGLKNLEEDITPTEGNPTGGPEASEATGSMDCFSEGAVLHHVDPH
APSSLSTPSAAVNLPMPREVSKSSKNKKFLNDIFSVGNKKKLTVRGHNGATESLVHAGKG
SEENDTGSLLSIHMEYVRELATTGVVVRIVGKVGVENVVISMRAPPNCTLRVVSCSATSA
TVDGTAVTLNKLQANQPVEVEMQVLPVGFPKEGRVLVEITYRSAVPGDPQCASVSRALSA
RDILRPPAQMTTAEFGQTWVGLREECKLQMSSATPLTPQSLQNLLMERASLRVVEAIRNE
LITAAKLIGTGKPVLCHVDVVGPNAANLTVRADDKGFAAYVAHALSAP*
>TCRU_2847 ATPase family associated with various cellular activities
(AAA), putative
MDAYTSLLNLNFMSAWRTGNSLIDMLIAMTIPFVSNWVARFFSVIWPAYVKKFIAWILPR
DAEVIIQHGLTDRYQRAVDLTEGSVLQEAVERYISHELKPFYSSGEVVYNMVSHSDGPDR
KTMAQVLEEDFRLFCRPLKESVRLGNGIAFFIRESEDETPSKSKGAVANGGGEKGGRLRT
KARMREVFLREKSGGRDEGDKVLAFVQAALKWHVKSLEKTSTRKRYLYQPTRNKDALGGN
DGALTRVLRYPLYDMKSFSSLFFPEKEKLIALIDQFESKTGRFAVPGFPHKLVLLLHGPP
GTGKTSLVKAIAQHTGRHIFSIPLSQVRTNQELISCMHDQLFEVCKNRQFWKVSLRPEKL
IYLLEDADATSDFMLKNKTKSTAKKSQGKQATCPPNKDAITTKGLLEAFGGILDAPKRII
VMTTNHIERLDSAIVRPGFVTMRLYMGKFTKEYAAQMVRHYYGPEAATEERLKCLKEVLQ
RASDTEVYFSPSELEQLCAEYEDIEELIEVLKKGSREEVF*
>TCRU_2848 hypothetical protein, conserved
MLHEAYAPEDTRSVAWSRQKKVAFLSLISGMRDGTRPPSVLLLYGPTGSGKLTSVRAMLR
EQRDAVGRPLLVEVLHSCESTPQQYYSFLMDTFTEHQLAGNDPCESHLSASSVSADDSSD
VKGRAQRPCEAQSRQQPRVVARVMKLYGESLISPLHARTLRFLDHYDAWRRAEFLGKCTG
DGPNALGGSILRRHFVLFVLTTHDTHSDKVALGKLLPSRVLTHPCIYSFHCTPITTRNLT

IRVKDVLRMEQRRQTCGVRCHISDEHVDFLCEHSNGDIRQALLQVQWRCLLGERGLNEAA
FSSTSAGTPKKKGPRPKLKKPKNVMDLVDDHENVSAETCTLQSSLAPEKGFEEEVEKAVL
FRDEYLDVAHATARVLTQKYTVSSVAKELNIQPEKLFSYMTNNMPIYFRPDQMQEYAVCA
AAASTADAIRSAEVFGRRRQTGAELHTARLASDDDSDGMGVIGLDLMALVLFGKTYEVCH
KDVCIPAALVAQRPPPYQPMAYPRLRDVEPTRKRFRNDGGGYIEDEFGRKRGRDEEHKVD
FTEQEWRQEFLRRIEPRAMGGGSWQGADADILRETLPAIVNRCASLETVLLEYAPYARCI
VLDWSPPTASRGVRDGNATALSSNVESFKKRPVETSFKPPGPKKTLFSFAERRAPSLQKR
PCSLLRYKILCCGLVERPPVRAEHFFIVKRHDDNGDDGDDLLDDAASDPNAPLPLLPDGE
DIEEYDD*
>TCRU_2849 RNA pseudouridylate synthase, putative
MAWCDASFSVIYGNEELVVVNKPHDVPMDGEACPVTVEKWAWAYLAKGGCADNSAGGGVE
KEEDTTRTAGRGRGEKKMVKFVHQLDYATSGVLCVAFSREMAARLAHCFEMRTTRKAYLA
VLLGMMPTTSAMQKKLDTDTGVDFLRGSPYASHVRRISMDDVPGVCFIRKCVIEASGHEE
GENADCCATLLEVNLPVGYDTTDHEGFRMTVNGRDARGSVTYLSVLQRGHMTHPTSGCPV
PVTKVALFPRTGRRHQLRVHCHAIGFPILGDVTYARIPTPRVASKVTGAEEVATVGAAES
INAPNEIDAIEAWQRMMLHAWRLSFPVSVEPLRSGSERYMQKKKRRRETLGLAVAGGDDT
TVWTHFETEDPFQLVRPE*
>TCRU_2850 dendritic cell-derived IFNG-induced protein
MDGVAFVDGKPVPCVMTLSQVQALFPQGLVGLCECFGGRSHVFPDAEGTFHLKGGASYTL
KLSGAAKWPSQGEGKGEKQGPCAWAPSLSTSTSTAAKPIVDSTALYNANAEDEQCLFRSA
NASPCYAEKSVRDIFHSASPPDALSDARAGKVSYNVGTASSLAEDDAPRTAVDCSGELSF
CLPLLGTNDTPGKHIQDRVHEYVFLPTIAIRIVDTLEFQRLRSLKQLGTTVFLYPGATHT
RFEHSIGVAHLASQMVRQIALCQPELNITRADTICVTVAGLCHDIGHGPFSHLFEHLVNR
IREKKRIKDTWHHEQMSIRLLRRILSRINLWEYGLTDEDARFIELCILGLAPKSPWPTNV
GRPPYKRFLVDIVANKRNGVDVDRLDYFLRDSLGCYGRAALDVHIPRLFSACKVLCYEGE
YQICFEEKMALSLSDILNVRAKLHKHAYQHRIVKVTDYMVSDALYEADPFFKVRGTNGKL
ISMSECVEDEEGFCQLGDWVCNAIAASSDPRLAKAQSIIQRINERSLYRVVGTAMFARFQ
VRVTEESIREEILSYCMEIEADLVLRDAIDKTLIVSFVVITFGSFDDNGLPDDPINKVTF
YNPKNIELGAFKLPRTRVSPLFLPSEYGERMLFVMVREEALADVVTAAFEAWRERYERHL
GVAVPTSNRRKDESPGKGSARPRRFSENRDVLSGNDFVSFEEMQRQVQTAACEQEAHQPQ
PQSQQQQQQHFQRGVKSARSPSCKLGNLQGERTDGNDENNERVKRICTSVGRGNVEEKHT
DTCTHEGGAVE*
>TCRU_2851 kinesin, putative
MEQRINVAIRIRPPLQKERFDPLCAHKADDGRTVIIKDEESMGAPSTFQFDDVFDGGDDQ
CQLYTQSVQELVDDALQGANVTVLTYGQTGSGKTYTILGSLSSGDLTEESGIFSRVFHDI
FAYREAVKRERHLLVFISAVEIYVDDVMDLLSKRKRVKLRETPEGALTPGVNIIELRTVE
DVIQTFNMANSYRSVTSTKINDCSSRSHALFFIDIFQMPLSASSEPPAREQLIDASGIPI
SGDIKGLVRSRIALVDLAGSERVKRTGVEGQAMVEAQAINKSLAALGTTINAMYMESNHI
PFRESKLTRLLKPLFVDRNSRLLLIGQISPPSVSAQESRGTLRFCDRVKGLKAGSPAFFL
SQEDEESYIRSLRQQEELTAELRIAGAECYYRPMRPLFMAYVKNISVDEARRASIDLLQR
DASSIVARKEEECMRAMEAEIRAKQMERVHAFADKMNQMIDEYEALSHAVKKEKKDAKRR
KEEQAEEQEKKLIGAKKAKKTRLKMEAKVEKLNIALKEMERHAEEMEAAFTSPLVEDTNE
STEELTTGETPKDDSVQLLVENFHSHATELNRLQDLYAQWLGATQRQRSQVRRAKLFSSS
IIMDGTLVYDIIDFIIDRSVDIADGVSHAEKKFSWNDIDGFSSLLRSGERLYPPLVTTPS
SKAEVCEPSAYHNVTFLSSDESDEENSHHREENRMLRGDSRSFSSSEGPNTPIKGQYDAL
GDKKAQGTFKQPEWNGLQQTANLEGEFILQGRDGSMADANGDDTDDNCYDEEKKGEGEER
AGKQPRQNKEENTNDEEAQSLESTRKRDVRDNEYLMRVYDSPTLVHDLIRFLRGGTVMLK
HGRSGRPHFRYFWVTISQNSRKLVWTEPESKITAERSSIDLDDVSFIQLGCFSKVFRRHP
VASTDPSFYRSFTLGLKGGGRTVDIVAGSLPDFEAWIVGLSNLVRVDPVWGGKLDITKEA
HFEQLNCFEASLCEMNYIYPSQYILLKKRVKRIAMRTLGVLEQCGNDATKAYKILGGIHP
PAVNEKGAVYLTKGELRFIGLNDMDILRITKVWILFQQMNLVYDENFVPATTFGVTERH*
>TCRU_2852 hypothetical protein, conserved
MTFRQPRLSISNSLLPTAVDWAVMRAMREWHNGVEAADASAISSEGHVTEELSPFWIPKQ
VVGFLAEALLRERQSSQMPFHTPVMDGTRMTTRSGTKQVESVYFAKGTRSVSVFGFSFVN

AASTPICSAVDSCTCVSYELPISESGDLIRFLMGKMSFAAPSRLSSLKASCGDNHSLGKG
CFPLKFGSPYWIEGEGLERRWRGVTISPNATPLYVGRSSRWLINAEQTNDASRFDSLSCT
PFRRHQCLTENGVHDVSLDFSARLAEAFLEMKRDPEKTHSTPTKFCEPNTTRRTCHGHHC
FYERQQQMTDSPSNLWVDAGVIERSGWSLQDAAVGVELPPHQLIGVERNAVSGVNSATVK
AKPIVVVNAEFVCERDSLLDVIMYRPECIGLQRNQFLGSRATTQLALLAHTMNYTSPTWI
QATVAERAGLCVKKGRAATGVEVKIKESYQNETSTVVFINADELDLTQERIAELRNGSV*
>TCRU_2853 WD domain, G-beta repeat, putative
MQRRTTSPSRGLGGRLQGTASGVTRPGVSRPSAVVRELHKNDGTNPRGARGRQIASEMES
LMEDVYGGAVTQRPPPSSGAGGEYARFKTTFNASGVPRSWQSGPVDATGRCFNASDRNLL
CMDVYMRNKLCVVGSADHGLKVFDIKTGKEKKNLYTKNYGHTEWVTCCKFLQNTGQIISG
GMDSKLCLWEATGPVRCSDLLGHTGSISQLEVNDSSKIVISSSYDRTMRLWDCGGDGRCL
STLAGHKAPVMMFSWCGAQVLSGDRQGTAKVWDLETGDCLATMATKRGQIGSLWHLLHTS
VGLLSVIGDQGGVVTVLDFPRLGSKPIFQDVLHPGGVVSGIRSIDETPYLVTAGADKIIL
TLDPRANFSTVHRFTDHRDFIYSLETFGPLVLSGGGNGWLLVHDTVTGKCCYGLGANAAA
VREIFASPEHLVAAGDDGNAIVYDYL*
>TCRU_2854 ESAG8-associated protein, putative
MEVTHQQPKSCFSPFSPFLQEITNTNVLDHENKENIPPALFGKSHNEGGSGCKSGWKNGG
ITQLLNNSLNSCCCTPVTNRQRAHHTGLTPGNKCAAGPRGVSALVSTNTNIADISLITES
DAGDLKESNFFITPVKRWDGAGAGATTNAAHAAATPCFRQGKLCELFNESVSLPLPVSTP
NVSVESTLLPRSVLLESDDDDSVKEVQSIKKPCVSEVPRSVVPRQLDLRSSQEDPSQQRP
VEGQKAFPASASMHGNAHPAPQHHAVQHSGPPPAYPRHEKRQNVTRVVGKTASLIAVGGR
RVPIDKLHLLLRPATSEGKSGAKVNDSTTGGKGSVSSSAFDPITPAPLAPSLRPTPTAAK
AVKVVSPPAAAPAPLIRRSLPVHQHCDYVILEFARGVVMRLQVDSPHPLPVIGRRYLAAI
KSSRSPYDNVAYEDVGVCVYLQRHHGDANTTSGPVQRSALYDGTIIREVGEHIAADAARL
QELKKACNNAIVECRKQFRFLNLPFELVDVCYTFDRSICIVYYNIQPQEGTSSQPNVSRL
LRMLQFNLRTKVFLKGITSGE*
>TCRU_family, putative Rio2, N-terminal/RI.1
MVKLDVSLLRFLEEEDFRVLTALEMTMRNHDVAPTALIERIAQLPHGGCRKRLRCLLKHK
MIYHENTMYDGYAMKYGAYDYLALRTLSKRGTVAAVGHRIGCGKESDIILVKDEAGHECV
LKLQRLGRCSFRSVTRNRDYKGGGRTRHGESWFYLSRLAAEKEFSFMKTLYDEGFPVPKP
IDQNRHALLMELVDGTLLNNITALGDPEKVYRRSLDLMIKLGEHGLVHGDFNEFNLMITE
DMRVIVIDFPQMVSTNHPNAAELFSRDVENLANFFHRRFKVTTLFYPTLEKNVERKAELD
RVVFASGCFSSRQQQDLERLLQTQLTAQDEVDSEEEDGQEEDEEEATTLSGNASVDVVSA
GGANACGVHAADGSEGEGQAQRHPPGEVGDDDNGETSSVARSLDEVVDEAAIERRGQRQQ
NVNFNPDGTVNEEYVRSQVRRNIRRQDNHQFNLGLHRNVQKGRQKQKIRRQIKQGMSNGF
FD*
>TCRU_2856 Kinesin motor domain containing protein, putative
MSVKVAVRCRPLILDERKDNSVVIVRMNNNEVTVLDCLEGVGGKFCFDEALWSAQVVVEG
NANPHASQEMVYKSVASELMNHVVTGYNGCIFAYGQTGSGKTYSMMGTPTDFGVIPRAAK
SLFTEVRGLASSGVESCVEVSFFEIYNEKVRCLLCPSVDGFENSTLRVREHPNFGPFIEG
LTKFVVSSEEELLRLLNDGNKVRTSGTTAMNAFSSRSHAVFVTTLTQKCTNGRLVKTKTS
KLNLVDLAGSERASKSMAAGKRLTEGVNINKSLMCLGNVISSLAEEQDSGRPRHIPYRDS
VLTWILKENLGGNSKTVMLATISPSSLQYDETMSTLRYAERAKRIVNRAVVNESNNNEVI
AALQKEIEQLKSQLRGASGSDRDSLSEQLAASEKFQKELQMTMDEKLMESRRLMEERKKD
MQRLEEQLEAQRGEIANLRQDNAEKERKIHELLQKIEVVKKRLGGGDDTEVEELLEQVAV
LELEQNAVSTKHVNTAADASRVADDTVLRLENLGNVRPQLIEGGKITVRALARAFEAVGR
ELPAAGSAAALCEIKGNDYFAQNVNAVEKELRGENPLSSLTTADFDAGIDEDLLLEELLE
FDEETVQEHGDQMQEEGTLDSAGVNVNGDFDSDLVVDEDEEIELDESELEFDLDLELDEN
IDGNASVAEKEGGEEVGEAFSGGICQSENDLNDNDINAVAARQELSRAENVVNDDDYEKA
SHVHEETTPNVTQVPRETSINSNIMIEVAAVDENGGNNATNQSVVKDTSHTTTKNAATAT
DTLMDADKFANASTQSTGNGLLSPFSTVTTLVIPSHALPNNRYLNEVFKVIKRNDAAILG
NRKDRIWLVDFFKRRFANLDMAGYMSFQYPASNLFRVEKDPLNSKRLTLHFFDAAHPYEL
EFTSTGRRQRFYEISMTLRRNSVMWCPSLCLPNEKNVILHVQGTTIRRPNAKTVNVSGES
KFTVSRMPYEVLDMWYGCFSMKDRPLPRSAAVLGSFIPRGSHEMYVIGIMDVPASFIGND

VFSKYFLEYLGSSLYYVLANTAVFSKRRQNNNALIVIVRNSFILRTSHIEAMETTPVFTD
DIPKDAFTSVGCTLRVNEATIGIILVNAKPIDCSLQRRAAALRSMMSSYPFGDTLVDIGA
RFDYFIVSGAFNFGADFRHDDMLLAQIKARNLMSGLVEAAPSSAILNATEPIRIFFAFRP
GVCNLDVKQYTTSRALAAPNAFISADVFCQRAYLCVFGEQVPRVQLVLDKLVLASPNLRI
PSVEAPELRISADWIENSPLLTALFKGGDAYKLSGPAVPVVAPTTSNTVFLRLQTITFSM
LGIPGSAKRREKTVIASGSLPLKNMLYLGEVVEFSTPLYYRTCYVGNLTGTLFLSAYERD
TADLAGLESERDVIVVSCYENQILEGKNWVSTIFSQHHAYGFSTEDATVECSREGHTLPD
STKWVWLNLWRHEVFPHDAEGWTYSEGFDQPFFSIKPSKTTIVRRRRWTRAMQANDPVTY
HNFLMLKREGSSFS*
>TCRU_2857 hypothetical protein, conserved
MGKRRRTISDVTCFIESILSCRRIEEPDASFSLSRVSDGTNSGSSRSSSCSRSRSRSESM
NGTSTNDRSAVSRVLTIPSGSMNPSDSQKSTGGAFATEINFFCRAEEDLADMSLYLARVV
SSARTPDAFVALVEHFSKYGAETVMLSLKRSGTQPKLLGHLCSVPDGGLTKGYQQLFLRF
LAFLVRLCDTEVLYEEELMKFLLRCCQSHAEASVNSAASSKRPSHWSQGARQAAVVPARS
LKLSEIKRSVDALCGEEEDNSHASLALRVLLEIVFRQNRNTSHPSDPNFFIVFAELGGFK
IVSALLETEECADALHLLEAVTLCEGLRGVYASELRITTAFLVRLITENEKQICKVAPRC
DEKNAALRVLTNVTGLVPSVLSGSPQLSRALAIVAAKTLTDAEAVSDTLAFTLCFTTNIV
KWEASQKCDEFTSVLVESPSFLTRVACLAFSAYHAEDMEKNVLAGYYALLLAVLSLCESP
KAQLRVPVMTAVAHATRGTAALKKVEDKPMTLIVAILQEFLLFQGSAGSLTRDSLVSMTG
IIDSVAECNGIEVSSDE*
>TCRU_2858 FHA domain containing protein, putative
MEQYFLVDTASGKRELLRPGKNVIGRSATVSAVDGVSFVSLESPSFTISRVQAVVEVASN
GDAWISDCNSTNGTFLAISEGNGIRLDPHCFYQLKPGNRVILGDVEMRLETSACSTNEMG
DQKGVMPSSALSSLNTSHPTNLSGAHSEILCASNDTRVATTANATNTIEKPSDAVESEAN
GAVLQKSHECLSGKCSNDRVESTPYHEGSVFLGRKRIRSSSDITPPSGASKTVSSLLRVH
WVCFSGMDGAEKADAQKLAKKLGWQTTDRIVDADILVVGSPVTRTPKFLIAVGRGIPVVT
GNFLKDGDTAQLEKYVPALSHGSHTYSAASLRKVIFRECKTPILQGVSFQLGALPRKLRA
VAREIILGCGGDIVRAQSTDALSLTEESLDSVYDSVLRGESL*
>TCRU_2859 hypothetical protein, conserved
MRQTGWVKDQFLNRGVNHFVVFSSLGRVMESSGDFEDEEKQQLAYTILQQTSTLLRSGES
VKRLSMTFDDFVYIATTIAGEGENLGVVLKRNAADVLATT*
>TCRU_2860 hypothetical protein, conserved
MNKQLLQTLPLAKGKDIHSRVAKLALYKECIALAKNVGDPLVRQHTLVEVREKWVQNRGC
GGHSLQLQIASALDRISYGRMCVSKQRLRLIPNASEKYDWGVSNPLEYHERRLTKRSEKE
SPDAFPHGAGKRDFVPMTNWGYGNMDPDAVMRHKELTDRQHFIGPHWRGKPKPMVLEDLS
FEEQLHVHFQSKPKMKKTPKKHY*
>TCRU_2861 hypothetical protein, conserved
MSSALLLESAKATSILLASEVRLPREDVGAAFESIGAAEKGYEVMYTVTVVDNRDWRRIF
LCRNATEATKVRDSFDEAQFDVYALRKYNDARKFEPRRSVPLLVPSSAVMQREYRVVTRE
EAASRVEGKSGAQESMKTANTSLNCSGEPMTRDAAPQEKPTIVNNVSMGNKLPPPPPPPP
PPPPNESCRSPIRSPQTLLKTPLSGKKHTRTADTAKKQSEANLKKPCVRNKKKGKFEETR
SLMKLAKASAKNKIGSDSSRISGPKTANTTTTFACSSILQNLLDKDEENGDHCSNSSNSG
ISFERRDEELMDEELPTLDVAVSSKENDDIILCDDAPPMVFCTPEPVAGTSKKEQQQIQH
NQRRHESLGSVTQPKLTGFFQRDVIEYQKQYIREVMTDTVIENGEYFCKDKVCFRHKETK
EVISEEEFYRRSADIMRSVRSDSQNVNSNDRDTTGQGSPSTPAGSVKRVSAEAARGSKPP
KIEKQLRSQPKTLFSYFKPTSS*
>TCRU_2862 Calcineurin-like phosphoesterase, putative
MDLIALEEKVRRLETLEVNEMRLLLNTVMDLFLYESNVPNVPLPVTICGDIHGQFPDLLH
LLALAGEISTTSMHYIFLGDLVDRGFNSVEVVTFLFLMKVKYPEKITLIRGNHETRQVST
AYGFYDECNRKFKTAEVWRHCTDVFDCLPIGALVEGRALCIHGGLSPDVNTIDNIHLLQR
KQEIPTEGALADLVWSDPGNIEGWGISQRGAGHLFGANVTREFLYRNGLNLLARAHQLVQ
MGFKYHFDEEFVCTVWSAPNYCYRCNNFASVLRVYEDESREFVVFEKVDRQYVEDFPEKL
QLSYFL*
>TCRU_2863 Protein of unknown function (DUF1193), putative

MTLIGLLSWMILLLFGEYNIIHPHAPWPQNALQNGSSTSEPLASPHSLPPSSIPRKHDVN
KARASPFLFTPPEFEEALQTYENNLGIVEGLMGNLDQPTTDFTDIIESTGPGVPLPYDSS
RVANAKEWEACDQRNAEFTPERDVLCQSYLAELNNMRYIKAMSSRLLYGRTIKFRVRYAH
SEIEAIVKVSQRKFYFEATSEYLAFSIDRALNLSRVPTSAFVPLPLNYMKVATAYSPFFS
QWINRFIFTYNYTTRNFFPCGFSGVSPDNEILCAYVTIQLWMHDVHSALSSFLSLPYEYD
SAFAAKYYKIGDKLWPPKSSRLRAIGDLLDRFIFDFLIGNTDRGMNDHNNFVYGGCSFKT
TCQRPPKAKRILGLAKYAFLDHGSSFYSHREPKGNAFFGEEYLIPICRFRRSTYESLRVY
RKRNSSGPHHPLTTQIRQSLSPYIFRVTSISVFEKVQGRLEKILRIVERCLEQYPPSEVF
SLPEYWELRIPEEEEEDEQEMSDSVNSE*
>TCRU_2864 Zinc knuckle, putative
MYGNKGPPKKYSNPRGVTDQSGASRVCQKCASTEHWTFECQKAADATRKTTARLSRSQML
RWGIKRRRQEFVPEPTEREAYTAHAKEVERMLLTEARRDVLQRQRLEKSRDVKDDSDDDG
SSRGDDTWNDVKSKESKQSAILKDEAYIKEEKKDHMEM*
>TCRU_2865 dynein heavy chain, putative
MGRLNSAVAENCVAVTEKVLKRRLGITANRAHQSERTVEFVFTASNDRLGEISSALFREF
VQAACGSEQGRTKLGSVDVSVDAQKGLQSVLFTDVVCVHNFRFDELPDDSPAITAVAEAT
YFRYLAKHSDAQAYAVTEFPKCLTAKGGPRLDVIIAGYVLFSLLSDDGDEVKLRMYIKNI
DEVLGTMCTSSFASTVLPHSWSNLDRLEPHQLVDLLEETQLAISDFWTDSAQDTRARSQV
IFLMTTIGSELREYFSKKTLAAGGIFGDSKSATEMALSCCDDWVNMCRNLTTIDWGAVWG
GRFEDLQLRVVCDRLRVVASLRDLVGEMVELLNASGELHFLRKETLWEAMESIDIFQTTA
AVEKQWDAALSAFYRRLEPVEHRCAAALRDFFGERGNLAPQTILNEVVKFRQLIRRPVVA
KELVSERDALLAKLNERLQGIRLEFEHRSESTEDDLFLEDEDRRCQTGRFMPGVVNNMIW
LRQLRGRVEEMIKMCKSLLLDLQNAREFVLAADTLLEEIGDYELELYKHWAMDVEDNSHA
LILDANAPLMDIDANGRVEVNYPERLVQLIREVRIFRGLGLRITGEIQRMVDQGVCFYRN
GVSLKQIASTYNSMTKDIIPCTRAMLLEPALFFENIITASGDRKLTWRNVEDAERFIGKL
RTASQSLTDSNRRLHRLHKEIEAIVVELFSVDLLRSRERWMGKVHTIREKMEISGFKNME
NWKLFWDVQLYKAMEYQYQLGLESLHEVVAEMKADIVYDQETGLAALRPSLEVIRGQYYQ
RIKDFMTFPLGFRGCGENEFFKEMPARNERGIFAVMQHAAQLFKKVQQELKRFHPLLIIG
QCGRNGNPSLEEIVGKTLTEVQHWEQGIRLLKQKGKEINGEELFIKCGCITLCTASIKGT
VEDHLYKLSEVLRVTLRRSAENHLRRIDAYLVEVSGSLDSTLTKLDEIGAANVHHAYLVE
QRPAMEVEFYHFYNKNMLLQSMANRAGLDFAKTRDEWDRVMRRLDSYESEMEEQMDKLKG
VIEESVKSWQKKLERFTNQWHELKPKSADSPNAVQFVKDQQEKFKALEAEGEECVQQCKY
FQLEEPDIEPLHDLGRDIEEYALMWSMVGKFNEELGVLRAEPWLALRAKLYRFDDLIKVW
QEKLKEIPNNPITVQIRTLLDSWSRCAPLFKFVRGDGFTPGHWVELFRLLGTPNATQDTL
QFGDIIDRYENILRHEMELKKLHSRAQGEAQIREALDDVRSWGTNAKFTLCAHPERPGVM
LITEWKDTLSALSDNQALLLSMKESPYFSIFASDANKWEERLACLDEYLRSMNQIQRKWV
YLEPIFRRGALPHEQERFARIDKEYLQVMHNIAKDSRIAPLATHKEYKEVLRNVLEQLDR
CQRALNQYLEAKRDSFPRFYFISDDDLLEVLAQSRNPLVIQSHLKKLFMGIHGVRFDTQK
EHILQIHSLEGETVQLEEPVRITDEVEEWLSKLDVAMKDTLRVHLVRCLEKLDIGAYATQ
ILCTAGMIDFTKKTEEAIRESKAGGLLKLKANLQSQLRDLTIYTGGSSDVVVVLKLKSLI
MDLIHNIEVVDTLIRNGVEKETDWLWRKQLRYYLDHNNNCVLRMVDAEFNYSYEYQGNAP
KLVHTPLTDRCYLTLTQGMQLGYGGNPYGPAGTGKTESVKALGNAMGRQVLVFNCDEGID
FKSMGRIFTGLVKCGAWGCFDEFNRLKVDQLSAVSQMIQVIQEALKNGESHCHLLGRDID
VNPNAGIFVTMNPAGKRYGGRSKLPDNLKQLFRSVAMSAPDNELIMETILFSEGFENATE
LAKRTVEVFKLAAGLLSYQQHYDWGLRAMKSVMRLGGSLIHQYLMDRVGGKVKLTPQDVL
QKECEILIKSLRVNTLSKLTFEDAILFNNLIADVFPGVPIKEIDYTELHPAIVESIKELK
LQFVESQVQKILQLYEALKQRMGVVLVGPGGSGKSTLLRVLRRALQRLGVSVPLYVMNPK
AMPRTQLLGHMDNDTREWFDGVLTEAAKKVVKEENDVHSWIVCDGDIDPEWIESLNSVLD
DNKLLTMPNGVRIQFGDNVSFLFETHSLEFASPATVSRMGIIYLSEEDVNPKMMVATWLL
EQPEDSRNQMRSWIDEFFYKAIDNLLATGNLIVETTRTGLVASGLSQLQNCSNKAQFTLA
LVYGLGSYLPEENRREYAKDIHYMTGERVLDMKDPLGTRYDLQHGGYRSFEFQPAFELSV
EDLYRYPMIATIECQRNMEVMRAWTKPLRPGVYRPFILVGPEGCGKTMLLTNLFAGISGT
RVATVNCSAQTEAIHVIQKLKQTCQMFNTNQGRVLRPKEAERLVLLLKDMNLPKPDKYGT
VQLHSLLQQLILYSGFYDTDLEWITVERVQIVGSMNPPGSMGRYPVAPRFLAIVSVLCMS

YPSRESMQIIYSEFFNIMIQSHKLKFELPGKGAADIARIMTIVYETIAIRCTVDVSSHYI
FTPRDVTKWALNLLNYNSVDIPDAIGYEGRRIFIDRLISPDERTKFAKLIYDNLIFLVGH
RAGITEKETTYYVSWMDVASSRVKKLNATSMDELKKSAEHLLLNYSREFAELDVQLIPEV
CAWIARVDRVLSQERGNLLLVGRSGVCDRAIIRLVAYNLHMEVMTLAITREYGMKQFNAE
LKSVLCKAGIEGQHVVLLLEDHHFGNNPLFLEYVNSLLSSGEIPGLFTQEEQEALLAPLR
EEAMGEGMSPYAYFVDRIARMLHVCVVMDPTNPNYEVHCRSNPALFTRCNVYWMGTWYSD
SLKLIPRLMMSNVFKALDMRSDKKEFSLTTEIVHIHRGFAEKFSPQHFKTLCLTYQRIFN
EKSTAIAEILDRLQSGVSKLDEAQENVDQIATDVADKKTLMEAKQREADEALQQIQANME
EAGNQKKNIQRIHKDLEKEQRAIEERKRVIEERLSGIQPMLDAALSSVRSIRAEHLSELK
SMKQPPAVVQDVMEGVIILIASNFVTDINWTAIRKILAGDIKSDILNFDLDNVNETARWK
LERFIQSHENSFRREVIGRASKAAAPMAEWLKAVVEYGKVLQTVAPMREELKGYEANLKS
GNEKKKKYEVKLSKLEEHVEELKKNFGEKTMEAERLKDRLEQAEQLYQSAHDLLVKLASE
HDRWASQIRAIRADQHLLPKRCLLAAAFVMYLGNEAEDVRRRTLDGWKERIKQLDDFNFF
TFLRPQSTQLQYKAEGLPDDELSMDNAVMMQEQVTTPLIVDSSDQAVNWLRNNLKGRGVT
VDVCSVSDERLVSALELALRFGKSFVVTDVDRIESFMYPLFRKELRMEGSKRVIQIGDRR
TVDYSDGFQLYLLTPSTDLRIPPDVLSYLTPINFSVTLSGLEGQFLGTTIQHEQPELEEE
KLRVLQKEEKLKLQLSTLEEALLNDLASSKGSLLENKTLIDSLNEIKTQAAEISEALEKS
KQVQEEIDMKRNVYRPFATTASETFFIVKSLKGLSHMYQFSLNFFMGIFRDTLKRHTEDH
TDAETKIKALKTTFVRLVVSSVSISLLKEHRPVFGIYLARSLHPKECTSAEWDFFLDRAI
ASEAEKKEVHMPTWVLPDSRDLFRSFVVLFRELLPKMNLQEADVWLQWMRTTTPEAEYPR
FLMQLTNFQRLLIVKTLRGDRLIAAVNRVACDLLSVNSWGDNRTLASFVKRTESNTPLLL
ITTAGADPSQELQSLAYHQVGRDRFHQIAMGGGQTDEAIRLLRLCAETGDWLFLKNLHLV
IPWVPVLQKEFNLLTPDSKFRLFLTSESHEEFPSILLSQSLKITFEPPPGVQQNLLHTYK
EWEGTAFDSKGTRQKEVLFIAAAFHAIVQERRSYVPQGWSMMYEVTSADLNSAADIVLQQ
TKAETDWKAIRGILENAIYGARIESEFDMRILQKYTQHFFDPSVLSDAKRQANLFATLRV
PGTGKLADYIKVISELPESDVPSLFSLPPNADRVVQLLKVRQLTDNLQHLNGSKAESSLS
REEWTSRLTPVLQAWAELTQPHSNLLTLSATESQEVTPIIGFLTAEMISSLRLVSLVDES
IGDLRRVTEGTALLKEDRRAEAAAMISGEVPSHWDGYFHGSPRILPWLQSLLRRATTIVE
WRKMAVNRELLKSDLSISSFFRPQTFLHALRQETAHSLHEPLVSLKLAISVSSPPEGAPL
PVCLEGLLLQGAFIDQSDMMQPIETSDEPALFPMPKVYVAWMSKPPAAKTSVAVPLYTNT
TKEKFIMDFLLPCTSEVAVKAFILAGVSIFLEP*
>TCRU_2866 Replication factor-A C terminal domain containing protein, putative
MDALSRGFCASAIKGVLPHGPGESWALLWPSPRVQVVDIQRYPKIVTEPFVVSRFYVAVS
DSASLIWLVVPPGSEMEELIDTFQIEVGSCITLNEYSVVAAKNALNVVVPLSITYSGNEL
SLLGNPTIEETLFCLSTEALTKRRGAVKPNFSRAIESYIKISLIDLVDTKGHELEDYAMD
LRIIWKGKPRHLTASGSMGRFVFDCIGVDRNGDAVSISCMGQSGLYDIFSLGDCVCVTNA
CLTSRSEAEDTMRLQLNERSFVVLRGEEAVSNIPTHPCRMFGARSVTNLINYSNVGDIVH
VEGVVTSVSSAALVNTRRGRVERSGISLQDPASSSLIDVTLWEEFSRSVRPNVGERWCFC
GFVVGEFMRRLTLSSRYGSGAFQMKMTPEKSLLPVNRTEKIPFMSLENKDSLQVVLDLEE
ASETLPVLAKIKRVRVPLTYVACRGCGKQIRSKALSCAACGGSTLEERFFVRLELSDGIC
AVSAVGFAQIGETLFGMDLPTLMKQREKSPGFEGNIARDVVGLPLLFWLLRSPDDSLLHV
VKCQHIDMARCAATLLGALAQMMGPNFDASRTE*
>TCRU_2867 hypothetical protein
MPYNFLRPNRLYTSEEKVAEEENKECDDDNNDVKIQRELNAWRLHMREERRRRLLAAASR
AERTRTAEEPSASHVSPRESSHEAGRGGESHHQELTALQQYRRELGEVTSGVQKGRNSLW
NLRVPIRRQRRVKTNRVTYHEARSVLRDYIHRPPPPPANVQKTPIGTLRAYKDALALSAR
ACSEAPTSPPLWHQRPLRNISVHRRRNDFSKFTSVSTTRSTTLRRKHTESSFANRHVDRK
LKWCQCDVQRKRNGDPSKRSFRPVLEATQAYQSAIKQEEEKYNQHRQCHEKRFPFEKEPS
PQSSVSSQCLSSRRSATQPMVTHAIDSPQARQPSHISYIRHGVEPEEPFHNPVVNPPAAE
EAVSPQTSALSETGTASHYEERSRRESSPLLRKLLSKLTLSSPSLYRPDLYQGNTIPFTS
PVVRTVEPHPWPPVGAKGQG*
>TCRU_2868 PQQ-like domain/Protein of unknown function (DUF1620), putative

MKCSTPLFLLVLFLFAVVHPSLAIHEDEQGLRDWILRFVGHVDHASYQPGLQPNHVYLAS
KPGAVAALSLSDGGLQWRKLLSEPQVCVAASKHEVLVSSRSGTVHLLNAANGEIERTFKL
SLPIGSTVESCAIVEGKVRVAAMDTITAYIYEFGLVTEDDMMKPRNNFPIGTDVHALRIS
GKHIWALRTSSANRYSLTGDVEMTDVEGGSYGSSVTASGDAVVFSGTRIAVVRDDGKTEN
IACENCDVGVLYSTTGKFEGTVKTTADKLGFTVFFPGSNVHVAYDSAAIIAPTVLLAVRD
RLHGAQVILRTYNGHILAVSEKYGKMWERLEGLAHLSATVIADNPAHEDHFSFNKVALAI
STYGVFYAIPISEMGHNIRVLSDISDVILQKTAAFSMESVKIERMFLSGTNVVTVVVASP
EKRVSLAVDYSTGSVMEVKVHENSLFVSPTFEVTRSLELHGAVSYNNMHFFTANVSSGLI
EGYAVSESSEVVPLWTVRMPYPLVAYATGEDILRTKTVNHLRVFPNKTSQADEVRRKYPT
RNVFVVAHYEPSEDELTTLVVTAIDSVTGSVLATARHRNVEGPVHMLVVEHAVLYYYMDM
EKVRHCIGVWEMFEEEPGRVLRKDAGATIPQVIASFFSRFKRTFSSRATRPPVVTVAVLG
VYGGNLATMGVTTSFNGISRKSVVLAFDSGRIATVELNRLLAGGQLPLDDKGNQATHVII
PSTSLASHKLRVAKPSLIATTPTNLESSCHVLVSGLDIFYVRASSGKAFDLLNSDFNKNL
LITLTCGFGVLTCAARYFVSRKALNLLWK*
>TCRU_2869 Alpha/beta hydrolase family, putative
MNLVRRVFSSGSTVRALPISESPVLLNYTLSTFRWHLDSRPSSKAILVHDLFGSAASWQQ
LLNDDLSRLPLSQFTPTTPLELYAVELRGHNHSRGLPCPKDGDNYTLASAADVVLHQKQV
LRTEAKLVGLGFGALVACQAALHSPKSGFDSLTLIVNEPSQLLCCDPSNYSLPSIIRGMP
RGMRSLGEVEEYLKKTVNNAVERALIFAVVELQEDVPGFRFSDDLLHFHGPFKGAADIAE
DITFERRVTVVVCGNEAVSQEARERFTKHFPRATFVQFQGGSNPGIAGLYKQGTNFICTF
LEALEMLGTVDGGEKEEK*
>TCRU_2870 PX domain containing protein, putative
MEFLVADAERMYTVNGRLQHLSYWSYKILARSFLESYQNPPLLNSIRAAQNFSKGSGYVD
FCTWHRYSEFEWLAAQVELEFPGMLFPPIPSKETDGTVDKFTELLTSVKENNSTTRENPL
VKKRMRQLQLTFNAIAQLHELHESPLLKAFVTLDELSWCAFREEREKKMKTSILTIFKAK
GLSIIAKLRSFRESSNHDYTLESPLDSVATRQSDLGELLNTCFAQVEYINKYCISEWRHW
SDVNKLRGSIQGSPMPWTACYGGHLVQHSKHPGLEGVVREINNDAAVVEWNGQGGRLSKV
PLDELNYPSSGISDPAIFALQELASQVESYFMYLSRSSGVAVLRDVEDLLWFLSTYANRC
VRVIRRFREMRSEVRYLTRVVEKKASVEQFEQLERLKQILSKGTSRFMEQYNNFYRCFMR
NSLMEVAQKFGQVMTVIMSDDQWNERLSVAKTMLTLSLPLLPEEREEIFAEDASKRDSSP
MKQVNGLEG*
>TCRU_2871 hypothetical protein, conserved
MVHIVGAVKQQLRVSLDERSVAALERAFNTLQGLRTGFVFGVLPSSTAFNELHILCCEAA
IGLEQWGMAESCLKIFAGKRAPTRALDARALYCEGLIGLHNIPISFRGRAKVTSHLRCAT
KIVTGVKIALEEWPKEAHTLAVGVEHLWLAIRDLFIPGSFDSVLDIVAFVLALHEKLGLG
GPFSQLQWSTRYAMCLRGVGRHQEAVSQLSTASELVSRVGSERLQLQFLRVQIAFWASLP
ATRTKQDYTKPVLQALYVAQAFFCGMIDEFSATADLIAAHEKLLLDPEKKEIKLKSRKTM
EAEITFSDPALVMDVLSEVVLGLALCGADEVCKISLPSLLQGDSVRPRLFGEFAQAILRA
RACGALGLAKALDASYLTRTMADALFNCIKAVEGTMDNARMIEDPSERAYTLQIGCVILW
NLSLPLLQSETRGKLRHTLKRIVVLLTNYGSCLTGLLVHVAYESSLIEFEEDNPISAIEQ
IDRALSLNHCVVNAEGKMVFPMDFALLSLRRRCVVRKTIDSSVFSAREDQVIHLIEQART
SNSASNRLVLLQSAVKKLPPLGQVLDPGTLAKERGPFLRERSKIGRAKKHSVVVEPPEGQ
PPRVITNPAAAHIYYLLLKEAKEEKNPSMHAIVEKVASSLTCIDVLNEADSKELIVMKAE
AHLSMAEVLLKNEKSSGGTSSDSTADALSHISAAAKISIKLCAAGNREEWIAVNACLSLI
GWYSELFRKGLFLPATVALGELYVALNQTHVDPNREYKLFHDICFAYIMSVLQSYISSKG
EVDGELSCGNLAETLRKTFLYPICEANNPMLRRAEEVCREVMGKWRLPSQRKMFCTLFVC
IQRLLDRSPEDSHHPQEQLLFLLGKLNGPVSMEEKRILVNKESLDLLRMDPSVELCGRLA
THSMQLPENERVTLELCRIADQLYQDGKLGWGTKTLIGNHTGKEKGHSPNSASSAAVLAR
GAFPKPTEDDWYWYSDILLHQATVLGRLGTGTERSKRHELEKRVIVAITNSAIAASHGPT
CTRVSQITDAYYAFCCTADYFSGALRQLLLPSLRILLSPSMLSILPLSSRGGGSSTEGHA
EREALLPLITNMAGIFLTTLSENGAHEEGIKTLNNLLAVLPTKCHKVFRTYEAQFRSNLG
LSTAQLVNKVRGGDPEIEAAVWVAIAKNAAANADSTKSWLKALEVLERKPLQRADTLLQM
AEWMATRNAVSRHELITLLLSALDSVERFSDPQMSRLPEEGMRQEGSSRCLRQTMAFSLS
GRTICLPDAGSMRSGNNLTGGVGEPASLREIMTAIRIMYLLFVVAPEKPLEGHTFTVCKR

SCASTILHYVFCMWNIVSTLIRSKDAGKENALKENLLEIPEEFHAWQGFCADPQHIDFIR
VSCQDDAPQNTDKLWGMLFDVCEFLMEEHWEQFTFMIFSWIEFAANWRYGSLDPRTMAVV
RAVRFKCLLAGARSGWGNLSSMYQVEAPTSEYWSAIQEILLSAENSSHFSPWPDGALRFT
DFRGSTCYCVLSEAEDLFLLGRVQEALRWSGKVLNCALHIGNIDAVVRCRLLEARARILR
GEGAAVAKQLSEIEEEFVGLTFRLWTELNLVKVDALISCGHVEKAISLARNLPQALGLRL
TKIAPDGLAGDISNDLLKDCTRRILCECGRQLLAFLRLSLRRSSFPGESEDAARKYLAEV
GDQLQKMDDWQSLSTALCIKQNLNPPMDEVLLTTDVEKGKELLELLYTEYCEALRVTELI
RSEMNVVAPFSLYTKSLATHPSILRAYDEVLVIRARNCLERELLRDFIILQYDQLSMEQL
GIPTGGPKILDTSVLQYMRDPAAYEQMKKNMTAGSGKESPEGGFYEEYNPTRDLECALNH
FFIPQAQVEGASSAEAEAMLSRTVKLDGECTPLQLEAVICVAFAEFQRRLKALLRAEDAT
LAVTLTGVAQIREDKGIGFRENDMLTRKWVRLIPNIGQLDTRRTSRKRALSVSRKSRKSL
LTEPPKKEEGPVNLWVNEDSSLPSMIQLGAKHARRLLEYKELAKCYICLAHNLVLSDDYC
AAGTAIEFAQAAEMCGFLLDIQSALLQSSPESNLIRFLERMKLKASFLLNTSAFDSMRNL
LMNTSSMLKLFDLGCEWPAEPNKPQPLYSDSCALSVVREESTKYFLVALRCPEGGVHSRR
VQLDINSLIQCGDEFETFKQTKKVEIINKNASVKASLEETSAALLKSLLDRVQYLLAPLW
EDFNGILSWLAPNCHLFLCLDPILQSLPLERLPPCTQFLSVQRELSVFNIRNKISTRGGK
SSSGGSLFIVDPFGEHETSLQTLFGPESRPKGATSEVISSVRDKYGCFCNPSQQYIRQAL
TANSRGILLVDLCGSFTDIVSPETLMELNLEHFLAVLVAEGTNDSSLRREQKQRTSKTTL
SLYYERQFIFSLLLLARGVQCVVTNALLPLSPEECGLICRRWLPAILAGGKGLFEAVRGG
TGEGADSFASVFLFYGVPPTVKQK*

>TCRU_2872 hypothetical protein, conserved
MYYLRSLFFTPEEVFSREHVRNEIAREKLSRAKLQRKSEEETHMAEMERLDNELREKREL
FAAAAKPLLEEFDDVSLAQHYYQEISNIVTSHLHIVSQLADREFSEFGYVSKKLISVSLN
LAALKCCMMGGVPFERELNTLLKDADSSDLSIVATPLCHVRSIPPAANVRATAFDLARAI
EEVGKDGPTREPVRGWLDLFKFRTSFSPTMLETRQVEARRAAKQFLSHIERGEHDKALVL
AEDAYVKVGHEVSAANAVLLESAFGAFRDTVLPVIASDVFLRYARASLDASRFACVEKML
KE*

>TCRU_2873 GRIP domain containing protein, putative
MEEISGGCAEDAGGEVGRLQEELRKAEERMRLWKEKTQVAVNELRDRIVKLTSERNELQE
AFTELKNHQEQQRQQDVDGGSKYTADGALSSSSYSSLVYVPAVTIVRSIVQWTITTVDVF
FPILLKKSEFALGLAACTSQELDKCKRRTAQTLRLQAKNIEALQSEISGLQQQLNEALAE
VRERNHAIDSRDQALSVLQNRLEDLEAANLRLESSRVLLSNKPNAEQINMFEERLEEELE
NVRREFVSRENVIFDQHRDEIERLLAKHEEEVAELRAELEEKILAAETAVDATAAAKVDA
NRAERNGEGAYIDLMRDFEALQDELKVTQGENEKIMAELREVRGKLAHFNGNGNSNDNSS
VASQKEPFTLPEAAVRIAELESGMMRLSEELCETKKRLIAAKHQANARDVSRSHVLEGQQ
LSYLKCIVVKLLGAAECGDVGRNLLPVLSTLLNFNSEDLQELYAAHPDWVKRRF*

>TCRU_2874 chaperone protein DNAj, putative
MRRTARFLVYEKFEGAVSGDRGYMTYQQACSIFGFQMNDRLEAGEIKKRFNKLVLRYHPD
RGGSSEQFQLLREAHKILLTHRHDKGDGASAKGSFINFRRVNYDNVTNTIHRQTAENPEY
RSFSLQDMAFFFFVTVVMGFYLYRAWRTQMQIIRSRWSYTEDRLTTEATHHDEKLWHPW
RSDQGTRDMMDNIGILQGSVKRELVEEKRQLAPSVYMPWQPGGPFASGQRVESERDTQLS
GEKH*

>TCRU_2875 cysteine peptidase, Clan CA, family C19, putative
MMLYESNDELADGMEEKLPYVGLVNQGSTCYLNSVIQALFHLPSFRQTLYFMAHPERDPI
ILALRNIFSQLHCATPLVSTKELTDAFGWGANDAWVQHDVHEMMQKLFDRLETICKGTPQ
ENFIRDLFYGELTYITRAVDGVDYISYRNEGFYDVELLVKNMDTIYESFELWAKPERIEG
VSLEITKGGPCTSHTVERSQRFVRLPPVLLIHPNRAEFSMETFTVRTLPGKWTFPTSLNL
EPYVLPMELEKNGGTGLSPFYELRSIVVHQGIAENGHYFAYVRFGDQWVCFNDMYVFRVS
EEAVMTSASCSSDTENLNKGSNERASLLVYVNTSVSKDILTEDFVPTHIKAVAEEILAER
ERIQRERCETVTFRYITERESLVEALDDPYDPPVNVKSTSVPTFFSIEEVHAAIAEDIGQ
SPDRIRVWMYDGGIAADVFEAHLHNDINRREILFVEILPDKKEKFSQMSVEKAFFALVRI
IHEDSLGPCKIIHTRKDLERLMGESEEENKCLICLQGPSLWEVSVDRVLVGGNVILCPVS
MKKEHALELLRQRKLKEVEVLLLDRRGTGMWTPTGTIRLDAKSSYADAQEKVYEHLVAAH
HSPPISPEYIGFHCAGSHARNPSIAVFPPSFLGSMKEGMFSLLWHGEDTMELFVTLLPAP

LSSIDTLRVVLLNVGGGIRPAVHVEGRSYKLGELFRLAMQQTSSCLPTDLFNYIMYRLQK
RIPVLRLILIPNEKNQRVFENEDDEVLECIGLYVMDVLAEIRKGFFRVDVVFYDRRSGEG
RFGFPTNIALTESYEETGMEIAQRVAEKIKAAVSVEEIGRWIVAVKGKSGVIRTVGPKEV
LKSIMKDLNEELECFMIDRPRSLLLDGVDDVRQGIEHSIIIKDPSLQDSRSKSAQHGEM*
>TCRU_2876 conserved protein, unknown function
MEGVEKVAAENPLLDRLREKHAELFRQRTSELQKTLETEHSFASRKMHNLPPSLDLISDE
IIIALNEIGTRCEEYAVPQVGQLLRDVRTMMNRQLREAYASLEAGYKSAFHKLEEEAEGS
RRRPEASSTAQKSVGRAMWKLQAESSPPNEESSQSTSSFKERLGKRNTVPKTLRLRDTFL
ATLGFFAETTAVLLRCEVVRIFLYDEYENLKCCARFPFNSTLGDPTSGNDMELMLARELH
STVCKKCIAVNGKEARLVAMRERDRDALEEELQQLGWHSMTSCLIFPIFSSAGCGRPFGM
IHAVNKQGVSFDRTGTFDENDEVFMSVTARLLGCLLTRYPTKLFVLSVGEKLRNCIPSSL
KGNEESHLPPILQDEVKGAAEVGNKANQMFTRVLLYRAPINVIYQTRSLRKEVRKLESLN
VIDRALSTVEFDIAALEELWRVGREENIIMYQQCQRLNEQLNALQLLLRNVLDAIGASRV
LCSMSDLVRYIQALEVYARQENISMITELISGVLMSPRTGVSVPPESGETSSDRLSPSEM
IRIERRVAQTPLKLKFGAQAPSNVRTYSYDPEKKREKVRFLNQLAEERETDFVAKFAVKP
VARHEAETKATIAKKVNQPVPFLVQFGPTDYASKRPFQIGNS*
>TCRU_2877 hypothetical protein, conserved
MRRAALAGSLVRLNLVVKKQQQYRFSAAGSKGSPGLVDHCKLLQKIHMDQQPYHVKRKRI
QGVLRKMETNYIHWLRECGTKESLLVLETLAGVSSYLKKGRSATVNVQQRDKEEGEEWTG
ASPYFLPGVNDWLCVLLERGARHASRPDECMTLLWAAAELELADTPTLQHLCRQLLKEEY
TGSAAPGELVRVIQLVSLLVKRCRMPIPQIDYLLCRLSAASLDSRESINVLSSLLRMRER
NSVEVVRAVSRRAVEHVATYTARDVIYALEAIALLNCCHESYAGAVLNRCIALHAELKPA
ELGSVCKYVAMLNVSRRNNETAFFCSKELRRLLPALLRRAEQLLGRFSLRDARCVLGCLQ
QHKVHHSVVFSRLTPLVSEN*
>TCRU_2878 hypothetical protein, conserved
MLRSVKGIECLFTGNVTALCATPRRKHSRATTTHLDEEPSSHMEDVGKKGGGEKTKGGSE
TSEESFGKRLFTSWQQGVVASIGAVMGIGAIGFFLYAPVKEDTVHHTAVVASEALGDLRL
REQAIQLSKGVVENVLTDPKSLDLVVRLVVQVLRQDDTRIAVSSFLRSLFEDHYTQEVTK
KFVLMTILDPWIQEQLRGIAKDLAKDLLNDPEVKRALVNLLTDSATTSLRDEELRYGAAR
AMRSVAKRTINPWS*
>TCRU_2879 NADH(P)-binding, putative
MPAAVNFEVDRGALVFERPRYLGRGVEVFNADDVPITPYGSFIRPNEYPKKFNINEASSI
ACQESESVQMPLDLFASHEDAGSAMQSQPLDQSFVPSTTGSLVCDERRLKHQLHRILLIG
SPGLVSTHVAAGLLKHGYRVRLLERDYRGKIFLYGLESLIETRPSRLSLFYEDDLSLAVA
DCDGVVYVNGPDTSEISNENDIERLFVSSIQDVFLSIKRNGKSVRRVVLISPASSIFPVE
TTLVAKTRGLKRGQAAALKEAERLSYKAGVPLTILLPAMMVGPSLLGEGDGNVQALVLLA
EQQRRFTSPIYYNIVDVRDVAEACALVLMAPRAEYQKYILSGGEMSLAQIACALQQCIPR
VSPPKRHLPVWLTRVLLHLGILNFLGFEFCERVACERVGWSYVLSSLKAQRDLAIQLRSA
QTAVVTAVAHAMNVPVAVQQPNVGDTHTSGKVRNQLRQSRLWRGLQLVGVSVLFATIGFF
SGKRLFSRSKVI*
>TCRU_2880 Peptidase family C78, putative
MSDEVQFFLSLKDELPLLILRKSGQTIAVTRDEPSVGSILPFSPRVCDLVRVSDEDVLRK
TYEDGYFTAVARNWRIKAKVNVSLDPIEERTHWLLFLGRNKGTAEKSKTTVAKSFKGTEK
DLREVVNWLKSLSVEGYCEVYLASEPSISDLRVTGEVGRLCLCRGDERVNEQVFFGDSMD
EIAICLEELLSVFFFDCVREAKAVFWPPSLAHPLNIHYGAREMRVAEHNAALLPMRPLLH
LGQRYKEWPMTINLPTVLAASVPRTGQSWEKNLICNIHAHLSTNSVINGGEKFVVSGAYD
YYHYRVDGFKDDGWGCAYRSLQTILSWFQHEGYMNEPIPDICAIQNILYAKDPDKMNRKE
FIGSKEWIGSFEVMIVIQHFLPGMDCMIRRMESGSDLETDPSVQQTLVNHFRQKRACPVM
IGGSSYAHTILGVDANLATMEARYLVADPHYSSGETSLKTVVKKGYVGWKEAGKFFESNS
WYNLCIPQLATYDPR*
>TCRU_2881 Rgp1, putative
MLLSASLHRRWYAPGDVVRCEVCLHGFSNSSESVSNGVAMRFGRMDNYFADIDIDAPTVV
RVKSLVAQILGACVVDSRRIQYDLGGDRAMDERCRIVIEDTLSKDHNVYGLFCSDEFSLV
SNLPLRERESRALVVKFTLPQYLPSSFRGQCIRFYYALFLHGVYCDPRNSNAPVKLRIPI

QVFSAQAIVTPLLLPVSFPLERFDFQEKVSFLQSAPSSALTGPLQSHLVPSEVEDFHAHV
LSKKALNTQANQLSKQRTPLQFPLSLDGELALTVVVASTTVMIGESLSGIFVVQGNPKFQ
PVKILGSLEFLECCSSKHVKKGIFRHQLPGWRKELVVAQTRVMEELDWVVLDRATVPFSV
PFTNPNTYASMHTDVVTLCWQLRLRFLWCRLSELRQCRATCREELKIEKEEPELVVPLIV
VPPSQSEQHPCRGATLQVLC*
>TCRU_2882 50S ribosomal protein L7Ae, putative
MTDKNEEQQNTEEYDYDRQLYRCPISWPITSDKPKMTKKLYSLIKKTVTRNKKGILKGIK
DVTKAIRKGQKGVLILGADASPYDVVSHFPVMAEEAKIPYVWVPSRQDLGTATQCKRATS
VVLLKPEPEFQSSYDKIVLAIEDLNSDE*
>TCRU_2883 gamma-adaptin 1, putative
MSTARLRDLIVAVRRCRTSAEERALIKRECAIIRESFRESRASLRTRNMLKLLYITMLGY
PTEFGQVEVVSLLAQAEYAGKRVGYLTLQMILDENDEVLTLSENHIKQDLAHDKPLIQSM
ALNAVANIASEVMARDMLDEISRLALSSNTYLAKKACLAAIRIVRKVPAYAEVFLELFTS
LFIDHSPAEMLSAVTLVNECLRLPQGEPFLSKYRVMANAAVRVLKQLVLSSRVTDQDVLG
VTDPFLQVKILEFMRIIGKGSAVTSEALNDVLAQVLTNTDATRNVGCSIQYECVKTIYAI
EGDEGLRTLGINTISRFLSSNDNNQRFVALQSLLDYASRDADAVREHQDIILDCLKDVDI
SIRRRALDLTVALVTENNLRLLVPDLVSYLTISTEEMREDVTFHLCRIIENKSPSTEWRV
EYSLRVLRLAKRFAPVEFATRLITLLSNESTEIQTSAVVSMWDEASYPFDALHQSRKAFL
VAAVWGIGEYVDLLLDAKGIQPEDVAKCVAEITTNTVFNIIKCYGLTSLMKIASRYPSAK
PVVLPVLSNYTTSLDCELQQRACEYMTLLESFVEEAAFCFSRMPPICHVEEDVEVQPVPQ
VNLPPEFLQKKAAVALEDLFEVNSKPIVMTHPVENKNRDKENNVVAIDDLFGLKTDVSSN
TAPLQTPSGAATSAEMEPAKPPPEVHVFDCDDFTVSVSGVVQGAINANIIVFSRLPTAME
NLSIQAAVPKTSMLNIGFLTSTVIPPYGRIVQQLIVDNSNSNKNPRLLTLRVKLLYTVDG
APRSQMFQVTQEL*
>TCRU_2884 ubiquitin-protein ligase, putative
MFFAFDSGPGKTPYENLLDLCTVLFISEEGSELPVQRVFHAINDSLQRAEEDGDVLVLAA
RALALILDRFSRSLLISGNSDASRAVKKCAETVFSIVKKRHVNFRYTKMSEKELSEELLT
CFSLARNSQEVAAVAPSTAEQLKFCFNALDESKWTSCRVLKHCIGLMRRGELKTAGDHEK
ILQLLQHHLASLCYVDIDHEWDDLLRTVVEGILTYRVWCATQLPLRKRRRASGGGSNAMK
TTGIIFDGVPLNNTTEALLAIGERILFSGTAECRMELTLACLASLVETSSLSMEATEKAI
VWVSRLLKQNSTRVAGFSNPFLRSRQDAAKREHLRTSPFQALPNLQWIVPPLTWSSLVLL
SKLCGANFGFCGEYMWAWRGEGGEYYPYLRGTRQKLTAMFFAADKNKKVLQKRHVIDLCT
MTDTSALTLVVSRVYFQPIPSVVVFDGALSIPPVYTHISEELSALLQDALRPLSFGHSKT
AYLARAIRLHVICGGAPTNSEDVITAFRSLSAEQKRPVVEAISSALMQHDKRWAPVLLEA
GVADALTAFPASAISKKAAVTTSSEQKGPPVADLIRSAGSSPRMVAMKIPPVTELPSFLS
HASPAELLAFIEALEDSTLSISSLKRVCGEIDLDPQLVCRMRDAAHNYVLRILHQTSVAH
QEVKSLARRVSGFSHFIGICRPTQGGMNHVLCPEGHPLCVHFSVNWRCNVCANSNSFGSL
ACRECDYDLCSDCSNTKLSRMDVNVSALVGDIIRYWREFRGDELSDEGSSQRGLKHSVLF
TSKGVLSAGLSSSTLQGEDVHYAEMGNCCECNISVPLLVANSMGHDVLDSPLQIFLRTFG
PLHQWGEIESAIVEVLESCGGEIFESGVSGIPVSVVRVLQAISPYISLSFKRDTAHFLSV
GCYRFGLYHLQDVNASVRGTVMGEIQSNGLATKFTVKRETGAMTQALFNAFVQYPSIRNK
VEFNFEGEEGTGEGPTQELYTELSQRYREMATLWHERNDGALEAFPTLRQVHKKEFFVLG
ASCGRAFVDGYTMNVSLIPLAWPFIRSPSVSMKNKWTLLIELEPELANTYKRMVRSTDAE
LKEMDLEDENGAVLTTATVKAYVERRVEESLSHAILNLYWFSLGISSVIDLRAFWFLSDD
EMSVILCGASRESTEEQLFGEEALRSAIVEAHGYSGGSREVAMMISVVGGEFTREEQQFF
LEFLTGSPRLPLNGLAGLGRKITVVRKELEGSGEQTLPSCNTCFLYFKLPPYTSRAVMKA
RLLTAITEGRKNFSLS*
>TCRU_2885 FAT domain/Rapamycin binding domain/Phosphatidylinositol
3- and 4-kinase, putative
MTDAAEPSIDRFFKESASALGRQFSIIFRNLQSAPESRLRRVNECLSDLLDLLVAHTKEI
IELGLLDHIFQLVNETFDGSVKRGIQALRVVFDAHLGDQHEERSRCVALLMRQAARGKCE
EDCAFMLNELGEVLQENVRSTSDMLGRHLNRAIVMMRQGATVHERAVGCQILATMVETSS
SVIKRNPALLDSLNATCSPLFLLRETVESFSMWHRHALVGLLKNIVEKHCIEISPFMATQ
MSAVMTEFMENADENVIIVGLLTAIETVAASPTLQSAPWHLKKIHSFLMERDWNTYPKEV

CIMVPRATGKALLLFRDDEGLYYGIMRCFLSYLSDWEEDVAVVALSTLYDILGEVNIAPH
VELAVDVIAHFIVKFPFYQLPFDALERLRAQCGEQSVARIYTLFDIIGIDMEYTNLQKLS
ALLRFMGDRKQSIWERFRLLQIDISPHVPVDVLVRALPFLATLGRTEQIGELIDLMFHEN
LKVRQAAVDAVVILCEKLILQSRSNDNIHQLTQRLDNTVTSAVGKLLDVAVADRDAELRY
NVLCRFSPLFDAYLSLQDHLDALLMARNDVSRRARDRTLVLLCRLHPCNPAIVHSQLLRQ
QEYMLREIEAKDGSMSAAIYQASLLQMTAEHDRLLLQPRTVELAVLARLQREPFASKSFS
VALLNLLRLILDRTGPHNHCDANQLLQPVIHIVNGSTSSRRRKAALETLCSILTTIRVTK
QSSYVAVYLALARIIRSEAEEDEGVNYAAMKALSVIGAVNPVKLRFILKTLEDDEIEEAE
EVVTSALACYKPRMRVHPHMTERYPSIVLYLLVKTLQQSADPEQQAGTIATINSMVREIP
GNQKAILLTHFLPQLQSWLADPERDHLYEGILLLMTELATLLRQFKDVIPSNTGSELLHS
VRQFCLLPQASQKPLNAGVVELLDEVARGLSAQEMRDHRWAVEFIHQRLSQDKNDLDLVL
RAVKSLESFLAVLHEKDLQVVLPHVLQCIEPEDATPSALRPKAKDINAACFDFLNQIMVK
QPLLVKDCCAEIVHTVMWYIEKSKSQDEMEMGFNTLAFLVEVVNRQAKRFILPIRRLAEQ
KGFSEAMFTDLLNSAARGFLKVRVPVTKQDKLDPDLPLSVVSHLPGLSRKDFEEEMMNTL
NLGGDDFEVMDVSHPSGQTIINLRFFGGDDSAANFRSFTRKAQETQSVLRRNLGILKLDQ
TQLNECKVDEALLQKIATIPVANKKKREQSWIAWLHKTSVEMLANSQIQPLRCTAELAKY
NSDLSRDLFSFAAAAFIAQLDKNQRALVMDTFTRALEMSPNDIKQILFGFAEFFESERGK
NELVLVKRIETMNCVVEREDTEKKFGINYDQNARGIAVTKLEPNGPGAKAGVPVGALLVA
INGKKVSAVSEIVSNIRGEKKISLTLKYEVEEQRKPESEPLMDLEVLARVAFDSQMHAKA
IFLNEVLFDQLFNGLGEQVSGRQDAAVRSALQVAERLIEFYDHLGLNMVAKGLVKKMSAK
FSGKIIAPEQFGFDEVGALEQLNWWGEALARYESRMMNTDGSINTSSLLGVLRCLDALGE
AIEMEVLINRNWHQLDWESRFEVAPLKAKVALSLGRWQQFDELTEQSGVMERLGMVERCA
TLFRQGQYEELLEFTRERRESLFDLFSESFMESYNRAYDMLVELQHLRHFEELVSFVNSG
EERQKMLKELWQTRLAHMSSRPAQVKTLITINSLVLTPAMDLTSQVMCIRALSKSQWTSF
ADHMLNLLLGPTGDYQALCHQDPDVIHVYMKHCYTTKNRRETLRLLSEILARLQVSPGDD
RAEAWGSCWLLLGEWTMHLFPDKGDEAIEQLKKATELCPRNHLAFHSLGILHYDMSRDPN
TPVEVQTAHHVGSITALFKSVELSSNQGNGVMEDVLRILSIWFSHSALLEINEAIKEGID
RVPDYVWLKVIPQLVARIGITAKVARSILTELLVRVGSKYPHALIYPLTVTEKSPEAIRQ
LMAERVLKGIRVSNGPMVGEASLISNEMVRIAILWAEKWHSHIQQAAGKQNDVNAILRIF
GPLFWELENPKTPNECAFEKTYGPTLRHAKAALQNNTLDQAWSLLKQVYVQLNKSTGERR
LLMGDLSPTLGGIKESIVAVPGSFVLGQPLITIQKFHQAVIVMPSKQKPRRFGLDASNGQ
KYRFLLKGHEDLRQDERVMQFIEFVNTIFFADSSSSAIGLSIPQYAVIPLTDNVGIIGWV
ENTETIYRMLETRRKENSISIYEEVRMIVRNGALRNIEEYHHQSKEQRKNLLNQVFNNTP
DNELRRIIWDKNDTCEQWLEYRGTYGHTLAIMSMVGYVLGLGDRHLNNLMLQEKGSVVHI
DFGDCFEVAMHRSLYAEAVPFRLTRLLVSALGISGVDGVYRLTCELVMKNLRRHCENLLS
ILEAFIYDPLINWRLANVGDGERSSSRAEALVKTGDNTLLNPGETNTKDPQMQLSYSVAR
VREFVACATLDQLNEEETRNMQGDLALARVRAKLTGEDFDSMNGSSFLQNSRREFCDESG
DASSCGSQSYGDSQKDSFAIGNPALTTYLSLRAVNGSANCLDVPHQVDRLIQEATSLDNL
AEAYITGWAPFW*

>TCRU_2886 TFIIF-stimulated CTD phosphatase, putative
MSTGRARNTRSAGPPGSGYRNFRRGRGFLNLERRRKRKKQRLTNSSRVCSSASAAELCLI
ATDDFHDRGEQDSSVLSDFDAINDVIQEFLLESDDEEEEGGFNHVSIFHAVKPFFGYSRT
TKESHRRQARKVVSMLPSRLATSGASVTPGLMLAEAMLPGIGGKGFRRRQNKALLPSDKG
LPLSPLCIVVDLDETLVWARRGSVYLRPYLKEFLDACHMEGCEVVVWSAGSPLHVNNAVR
AVSDVLQRKDWFHHIISRHHKWYRDEEDDAKDLSILGRPLNRVLMLENSPRSIRQQPRHA
VLVEDFNEPTKRDNSLRIILELVRRLVAVLRVASDSSDVDVPRLLAEDVALVDLSFSLLD
NSKNERNIFCKGLLYSPQDTFACRSYGGENPSVPRGNGA*

>TCRU_2887 cytochrome c oxidase assembly protein PET191, putative
MEKERKSICWRPKNALIECIVGTKCFEEKGKIEDCISANECFLERRNWTLCKVNATNPRY
RIRGNPYDVATEDQKKIEARDERIRRRELEEEGIFTK*

>TCRU_2888 Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase, putative
MTLPRRPYEALRGHFERCLATPLRPMNLLTLAGNDKGYIHTAVEQLGARTARSYRAIYSE
VQKRSLDREINARLSPLESICRREFECCVELSEVAEVYLRKMERGEICDADTSLPNEIID

DAQVDSIMKGKGYGGSGNSGGDSSVKRLIDVLESLRPHENLFDIVVNEEWICSPNFNNWL
SRFCTRRVSWRVIHEHLLHLVGPGRYSPIIRTDPNVGSILRHTGTVVVEQYVRSIQSIHG
GSMFIHMEEQPDLFTRVPRGRLATSSKVDCPIFPTTSMPPAPSSRVIYSVEGHLEYVFRE
LMKNACLAMRSRTNSIELQVCFASNDTHVVVDVTDAAGGIAPDAVEKLWLFGWTTNSSFD
NKMGGFGIGLPASKCYMDLWGGRIDLYTTEGVGTTVRVIFPKAPTEVFVPKGTSSSSD*
>TCRU_2889 hypothetical protein, conserved
MRRNVEAAGVHLADCTLLDYRRELELEEKAAATKRSQQYSTAQWKENAKCPGKTAKQLVS
PYIRVDGELISTNIALSSLLRAEEERKERLALEEQQKKETEALFQLHDGMRTTIIDQWSL
GMEKLVLLEKRDCIRAQCQERCRRASDWWDALAEQHLADEILLWADEEQVMARERDEGRA
AYRQRSVHTRK*
>TCRU_2890 hypothetical protein, conserved
MGHNRESHAIPNYREVLLMQQRTASFLMVFSVIAIAFFVLIVSIQTQEAICQTRANTAAF
NVYAKAEIKNGSFADALIDALKRNGVHAEPLEIKSQVRTRIDVFDTLEKTLFNSGFRLLR
KPDEFGVTWRLRYLEHSVCQTERRISMEALPNVDYEKVSYDVMAINTHGDRAFLYEAEVK
TKDRDRITTFPQLQSLFPGFNARTASPQMVLTDSVVTLTAFAAELYYGSTSLDIELQMEQ
RSREKGGKLYWRVTLLTKNILAESNLKGVHRIVSEVVQNRSVLCDPASCGSAFGDPFLQ*
>TCRU_2891 dynein heavy chain, putative
MSAESRNGQPRDEEDPRLAWLAARVKSCLYGVDDDVIADLYGDTDSRKVILEIFDNPKER
FLVISSQEATTTEGNAVGGRLSMATPRKPPPKLIATTRAIKNSNITGSTNFPPDRTRCIF
FLRVQNVQLTRELVHNWRTETECPIHRAFEISCMVVPSLSSFHTILKYAYGPIVEDVVSS
AGRRRCVATKKVANRQLYTEILNWVHRVDMQMTGFRNQVCAERRLPMPQTLVSMGYSDSG
LKSALANEDVIKQIDITVSQWQAEISYAMSLDPQKEGPLGEIEYWREKYSTISALYEQIN
SPQAKFILKVAKEAECNSFHLISTTIQHFFRLYAEAKDNVKFLGTLDRHFRTMHGVTPGS
GSLQPIIDTLSSMMTGIRMVWIISRYYCTEERMVGLLEKVGKLIAQKVSQHIDFRSILGL
PFSEAKEKVVEGQQCLLKWKATYVNVQEEINSSEREQPWNFNQKRLFETTDYMSDRCTDL
LEVIETVEYYNTVLGAQLKTVLTDTSGIERILKDVERVKRPFETLTFDPFERKATHNWQV
VYSNFVNTVANLDHEVSEFINKIFDDDLRSAESAFELLVSFKGIVSRPQRAGEAFDTASL
LSEKADRILAQYFSEVERVRSIFVENRDNPPLTKNQPPVAGAIHWSTSLFQRLKKPIVRF
QQEGMLVTTMGRQVRAKYVEVARQMKEYATSRFIQWSEGVRQTTTASLKMNILRKGNGDT
YVTNFDVALFNVIREAKYLDRLGFEVPQEAINVTLQDESYHANVDALKAMLLNFNCELQG
ALDGPERVILAKNIRELRLALEPGIHDINWTSLGVTDFVANCERAITKFRNLSREVRKRA
DHIQTQVVNKIGSTKLIPEFEQLLQAGGELPELQVFVDTIERRRTTLVDACLRAYHTAKP
LLTKMESQLVGTHTGKCLILESYYLHWEQRIWKALTRMVLNSLLAFAKMLGYRGSSTVKR
PPLFKVLIFLTTEPTFSPPHQEITSAFHKVQSSIIESTQRFQRWMRGTCIEFTQGELVPR
PAEGEQETLFTYYKDINSLPQVYKLQGIINRTIQTHLSALATNIKMLQRYRFIYLADKKL
SVEQQAKSQFHWIDYDAKFQLYFNMIADFDAEEHIHDFGFMRCDESAFYAELVEHVHQWI
AMEGAQMNDTVRVRMQKRLESIVRINKDLQRPCENIEDLKFVLEVMHDTRASSLDVEQDI
SEIKYIYESIMHFGVKVDPQELKEALSFQGLWDCTLARLHELEKDLEPKKLRFREYTRAE
VANFLQKGKSVLKEFREKGPSRADIDLQEGNNLKKEWREHLTQLQAKRDQLTKAEKLFDL
PLTSHVHLQQLNEELTKVEAVYDLYEQWVAILKRWNRSSWKDLLLEDLQTTTDEKVKRAR
LLGRTHGDVHPFKAVQQVILNFHSSLPLLAKLKSPALKQRHWVELMRVTGKEFSIEQINL
DDFIAMELYCFADDIDNIIVTAAREQAIEKDILAVKEFWSKAEFSLVPYEPRKGDFRCSV
HSDTSEIQEAVDDNILKMQSIANVKWAQPFIDDVKLWEKKLAMINDVIAVWVTVQMKWQY
LESIFKGSDDIANQLPKETAKFNDLDKKFVRIMNETAAGPNVDICCNATGRLEEFRYLEE
KLEECQKELSNYLETKRYMFPRFYFISDDELLSILAASGAKSVQDHMLKMFDNSAHLIFK
DGEDETICGVESQEGEVVIFDRPVATMGAPVEQWLQEVLEESRSTLRDVLKAGVYYYPRM
GRLDWLKKYHGMVTLTGAKIWWTFEVEDAFNSLKKGKKSSMKDLSGKLTRQLIDLVGEMD
KDIEKQYAKKVNTLIIVDVHGRDIVDRFVRDSVTDAREFDWESQLRFYWERDGDTCVIRQ
CTGRFNFGYEYMGLNGRLVITPLTDRCFMTLTQALSFYLGGAPGGPAGTGKTESVKDLAK
ALAIQCVVFNCGEGLDYKAMGTIFSGLSQTGSWGCFDEFNRIELPVLSVVSEQLRSIQSA
LKAGEEEFLFGDKVIRLVPTVGVFITMNPGYAGRVELPDNLKALFRPVVMVVPDMELIAE
NMLFSEGFTTARELAKKMVTLYQLAKGQLSKQHHYDWGLRALKAVLVMAGQLKRGAPELT
EESVLMRALRDMNTPKFVAEDEPLFKGLIGDLFPGLDPTRAPQENLSKAATKVFKEKGFF
VDARQVDKVVQLYETMQTRHTSMVVGPTGGGKSTVIDCLCKAQTDLGLPTKLYIINPKAQ

PTTALYGVMDPLSRSWTDGIFSNIFRAINRPNESGARERRYVVFDGDVDAKWVEDMNSVM
DDNKLLTLPNGERIRLRPTSSLLFEVGDLQYASPATVSRVGMVFLDPVNLGWKPFMYAWK
LKRPRDELDTLNELIEKYVEPLVNFMFDGIDGEVVTDPPKLVIPTNELNMVRQLTTMLHT
VSPQQVALEPKALQCVFLFCCVWSFGSLIATAEGRVRFDAFLKKVSGWNLQDVGENFLTR
FVGSGSLPERKTLYDYFFDLEENRWKPWHILVQPFERPPGAKFGSLLVSTVDTERNMWLL
NKIVLNRTPVMLVGESGTAKTVTIQAYLKQLKQRSLEADTAADEDVHLEEMLLELNFSSR
TTSLDAQRAMEDNIEKRTNTVLGPPAKKRLLVFVDDINMPRVDLYGTQQPIAFLKLLVEH
HSWYDRKDLLFKNVRDTQFVAAMAPPGGGRNALDPRFVSLFTIFNILFPSDESINTIYGQ
ILRDAYKTMATELGDLPSQLTSMTLSLYQQLFAALPATPTKFHYIFNLRDLSRVYEGLCR
ATPEMFPDTKSIVRLWLNEISHVFMDRMADSSDKEFVALLARKEITRHFPDAAEFALAEP
LLFGDFGDFEPDSDVERLNIYEDFGAEFTRARSLVEMMLEEINTPTKKMDLVMFDMALDH
LLRITRVLSLPRGNCLLIGVGGSGKQSLTKLAAAMYRMGVFEIVLSRNYNEDAFREDLKR
LYARVGVQKEKVVFLFTDSHVKEEGFLEVINNMLTSGMVPALFTEEEKEPLYSSVAAEVE
ADGLAPSKDNKWTAFVARCRDNLHVVLSMSPSGNILRTRCRNFPSLINNTTIDWFQKWPS
QALEAVGNRMLQEEEVSEDLKRAIASHAVYVHLTADELSMRFLGEMKRHNYVTPKNFLGF
LANYSRLLITRREEIDDLVNKFAIGLEKLDRAQEDVKVLQEELAEKEVILEEKQEVNERM
TKEIKEQKERNEKRKAEALLMEESLNVQSAEIEKESAEAQEVLDLAMPALEEAMEAVKHI
NPKSITELKSFAKPPASVVAVVRMVCVVKGVPATWDSGKIMMGQNDFIRSLIDIDSLAPT
LNQGKINEINRILKEFPVNSNDLKKVSLAASGLMIWVEAMKAYWNTAKEVLPKQARVREL
QEAKANAERQLSACQDEIGQLTVSLQRLQERLDAGMHEAQLLQQEKAVMERRLNAARRLL
DGFGSERVRWAEQKRTLADVRNCLVGDCLAGASFLSYLGAFTFQYRQEALESLWLKDIHE
RGIPLTNDFQIQHLLTDEVSVSQWASDGLPLDSLSVQNGILTTMSTESIGKGRKSGRVRF
PLCIDPQMQAVNWIKRQHKSNPRFECASFSDSDFLKRLEFAIQYGNPFLFEGVDEFIDPI
IDSVLDPQFREDSGQRVIRIGDKDVVWDPNFKLYLCTKLPNPEYPAEVFGKTIVINYGVT
EDGLESQLLNYVVASERSDLQRQSEELVQTMAESRAQLKELEDTLIRELTLATGNILDND
DLIATLENTKSSASEVQQKLEQAKETARVTEISRQEYRPAARRGAVLYFVISELSMINSM
YEYSLSAFLHDVFGYSITKSDASFEIKDRLNNIIRALTYNLYCYVCMGIFEKDKLMLSFQ
MAIRLLTQENRMDRSELEFFLRGCVLASKDYPSNPVEWLTERQWNDICKLSTTCQVFANL
RNDVSENLEEWHQWYALDRPEDPSSVIPCGYTERISEFQLLCLLRCFRGDRVYTAATNFI
SNCDLLGERYVIPPILRYKDVLDKSSSTAPIVFIVSPGANPTEEIIKLAKKEVGIQKFRS
ISLGQGQGEEAMKLVEVGVVRGHWVLLQNCHLLTKWMKDLEKVIEKMDQTPPQEEFRLWL
TTEPSKDFPMGILQRSLKVVNEPPNGLKMNMKNTLLKVTEEQLDACLHTAFRPLVFTLAF
FHAVVQERRKYGKIGWNVVYDFNETDFSVSMRLLDTYLTKAYKNGDSIPWDTLRYLVGEA
MYGGRVTDSMDRRIVKTYLEEYFGDFLFDTFQPFYFYVNDEVSYCLPADSTDSNKRVTLQ
QMMALVESFPKDNTPEVFGLHPNAETGYLRNAAEGMWASLIELMPRSGKAATLGGESRED
VLLKLTDEILSQLPEPLDRKRIMRKEKERANEMGHSNLQPTQVVLLQEIERWNRLVGVMI
ISLKELQKALSGAIGMSNDLDDLASSLHNGQLPWSWRKMAPATRKNLGRWLAHFHLRCKQ
YNEWAMNGEPRCMWMSGLMVPESYISALVQVVCRRYKWPLDRSSVVTKVTTYMTPQEIQE
RPKDGAYVSGLFIEGARWDPNKRCLAPQRKKELISEMPVMHIIPTESSKVKSVATFRTPV
YVTSDRRNAAGVGLIFEADLSTDAHSSLWTLESVALILDSDD*
>TCRU_2892 TPR-repeat-containing chaperone protein DNAJ, putative
MGRTILKRHGEATLEYTYLPKPRKSANTEFFSGGLATMPTDWTLCLRQASDEEGACRRLL
IANEAIERQRLVRGLECCLPEVNASFTRNEERGIRLLEAKDYGGAYVSFTRALQQKPHSK
IACYKRAVCSWHLLFYDECTKDSRRGIEMDLDLVSLHCRSLLLRERYQEARQGYEYALGV
LAPLMNDPRNIKWRAECEAIPTLKKFRNSFKEGKWEEVLRLRDAAKPLIDDTPLVLLEAR
ALLHVSPNMARLRLLSYVPTIPRPVSANTEMSLEEKLAWRLVEEHYLQAAVLLAQSNAYC
GSSFLEIAAALVQTCLVISPSFGPALVLGHYLVSLEEILSRVRSLFAKERYAEAIPLIHD
GLLLDKSNQRICSTLYCMRAEAYASLGKNSNVINDCTAAIGMDSGCVKAFVLRAEAYRRM
NQRAEAAADRLKAVNLDPSFRHILHGDEEQFLRHTEHPRSSHGNPGSQKRRSNWYDAFAT
KSEIPPKSGATTKDASSDAERASKLGAKTTLYDVLELPHGSSISEVHAQFKKLTLLYHPD
RLVKEGEKKQQAGLERFKLINHAHSVLTDTNEKCMYDFSLGLNVSPRV*
>TCRU_2893 small nuclear ribonucleoprotein SmD3, putative
MSTFSIPLKVLFDAIGTTISLEVSNGELYTGTLSEVQDNMNVLLISAKKTKKSGKTVDLN
SVFVRGSSIVFFQLPDALRTSPALVKAGQVLTNALDNRGDGKGFGARRVVKRGRE*

>TCRU_2894 Major intrinsic protein, putative
MTFSPAMSEIVAEFVGTFLFVLTIPLASLGVGSLAPLPIGFMLAAMTFSFGYISGAHFNP
AITFATFINGKIPFRKMFFYMISQILAAFLASLYGSAIVGLRIPVPSTDVALVSVWQAIL
CEMVYTFALASVVLHVNYSRQRSNEFYGFAIGMTVLSASFAVGGFTGGAFNPAVATGTQL
VGCIGGNCKPLIFFWIYWVAPLGGSFLASIAYQILDTHDRVAPIELSGQVF*
>TCRU_2895 hypothetical protein, conserved
MEIAALLAEYLRAPVSSRGELVASNPCLFAPDVVEALDDAHDMMAQVQKQARDACRTIDD
VMGNLDLPSLPRLTPTERSELVVTEEVMIAQFVDELSLLLSQRETTPCSLKGTLSASDEA
CNFARPWHQQRSVVLEILSFLPVECTFNVAENVCRLWRTWLCVPADSRAFWAGCVQREFP
ESMQTLIQLQEVDLYESDWRTIAMMCSTDEEKDDLMAEEEVTAS*
>TCRU_2896 hypothetical protein, conserved
MTALPEQPSHGGCDGSTLPMPALTARPFDWGALVADVRAEARESRRAVEKRTRRLATLNM
RLRKKVEENAGTVLAIQELDEKIENAVKQEKCLLRLITAAKKRKAQLQADVEEAEKRLEK
MTPCHQQSTPTAAAASVVVKNSLSRARKSEMEDCVVVHENCEMGNLQHRLHVTRLLYRRM
QEENNQILAILADLNFEENLTTAKLNERSSSNLTAHHFEFSNALQDLIQSFKDVTHAAYK
PH*
>TCRU_2897 TPR repeat, putative
MSVVEELRSDDEVDPCPVSEVPAGCERVVDVVACERLKKEGNALFVSGKVAEALEVYRDA
LKAAPIKPIQKEPKSKKGGDSRADGRPSAPETQASSAPAEGGGNSGSTACNENDTKNDVL
DEESNDGGVDYTLTSQIYCNAGLCLTKLEFYEDAVTDLTEAIRHNGLYAKAFIRRAECYY
LLGKWSNAYGDYEEYEKLGGVLDADGRAHKAAAKAKVDEEMKKMLGDLKDMGNRFLNYFG
LSTDNFKFDKDPVTGGYSMRFEK*
>TCRU_2898 50S ribosomal protein L14, putative
MFRRWGLRLAATTTDAAAKLPAGNPVNKSWFRYNLIIRRKASYRSRWGTGAEGYGTGVPF
SDQVKLHCVDNTNCKHVRLISKATAERFAHCRVFPAVAHRVSVQRFKSGRGEVSRHRVKP
GNIYWVCLLSRRQTNTRMSGLQTNFDRNTCILLNDQRVPLGTRVMYCAGRHVNHKYHLKA
VVLANFFI*
>TCRU_2899 hypothetical protein, conserved
MRGQRSAKFAEYTATYAILKRLGLHDTVLIEKRDASVGYGVFVRDACDAGTPLLVVPSRR
ACSVTTLERLGADVRMVETGALLKLHNLNDGVVSRVLGCSANQWATLAWRLAIEQQRSLS
PWWGWLNVLPSFTSFRTMEENCERLCRLHQAPLLPYWMDARRRIEEEVVAAHEIFAEENV
VPSFCYFRGAVDIILSRAQHLPLCWTTAEGHPVELGILPFIDLINGHDGTDRKRNARVEV
AFAVEELPVWYRSWFVQESERGGIDGEKELRRLMEEHFFAVVVLERGLIASEEVILEYEL
QPWDTGSLGSEEELLLGRLLRYFF*
>TCRU_2900 WD domain, G-beta repeat, putative
MNCMHSVLGAKIIPGKDASLNAGAAPIDDGRNWPYQSAEYGCQDLLAYSSYCHGSGDVFL
VDMNSMQLVQTLHGHNAPVTCVQWKPPPASYLQHGLFLITGDRGGAVAIWDVAEGVVLNS
IQVPNSQPIHAFSYLAKQHLLVVTRDGSNFVYDSHLVGKEPFGEFEFPVRTEPTDSFVPL
RVCTSKLSSTQASCFVLGDRLRVIGSLETAPGKSGVALQMKDLVYDSEDGHETVLDATFS
EAHEDVLYFATRNSVGAYDWKTGLLLNEQVLWHTKSDVEFRRLFSSSPSSWTESPQELPF
LYSFGTDQRLCAWYNSQKEKVTTVSADVRGARIVSKTVSNVVQSRTTANLFAVIFADGSV
ARWRYLVERRRWSLEGFFSFALLKPTRLCVVGDNIVCCALENGHMVLLDVMHNVTLRRIN
IVHSGGTRIILLSPHRWGESVWMVTNKSTQLRNFHQVTLFDCRSGSPLRVLRKPTIPDST
RMKEITLSATGTFLLLTFLDGTFEVWGVEEGDLIYTFEGMGVAGVSWAPQSFLSCLTGVQ
GSPQLLAIIFTDGGMSLWTVYKDRVVKNRDVTSLFSGGSIPRVNCVPTEEALILTHGMKL
PLVVSLGSFGFSLEAFKSVSPNNPAIHVAVSKGEGMCANNTRTEKNNSVVLVAIAFTDGA
FGVWNASSKERLSYSRATLINLTAKQLTWIADKLFVLTTNGDIAVLDKSLTSANSNVSCK
FHRRPLQTSAFFLPAHRTYIQTLLETQTMCESPGAGNLQSASSPSYLVQSIDSQRRPCRG
PFGQVITEGITTLAQELDLYKETMVPRHIREPMQRAVAQKRTEEVAFWVARFFGQEEKQR
FWLQFCVNKYFCHFGSKAKDEIQPSDGVEEERKWASPFFYSHCNRFSEAVANPDVIRSNR
MCINEHRIAALEATKSQNTEVSACRLIVARELLKLQEAQRAIDVLMDANLESDHFSHLAN
LAVMIAASITARESSSFSLFSNTTKRAAALHLARRDLDAAVEKFILSGDYYEAGLALQSC
GKWGEAAALAKVTSMTPNQKKEILYRWCSYYAKRGEIMEVARMLFSMSSPSEALVLLSES
VQLIDVAGLLAIVLLEDSFFSSWESLQKVIPSPLRDEDPSGALSLGDVVLNVLADYCSVL

NSVGNVVTERMVLEIIASLKRGNRQGSTLSA*
>TCRU_2901 Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain I/Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain II/Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain III, putative
MSVEKLVQEWISWDRDPETRGVIEKLWKDGDTRELQILLGNRMEFGTAGLRSKMGAGNSQ
MNCLTIIQTAQGLSAYLRATFTQEKLSSGGVVIGYDGRYGSKRFAELSANVFTNAGINTR
LFGQVVPTPFVPFAIRLFGCVAGVVVTASHNPKEYNGYKVYWSNGAQIISPHDKNISKFI
LENLTPLGSSWEAAAGVSDPFQEVWDQYFATLKAEYKPLAANYPVKVTYTALHGVGCPFT
MKSLETVGVPRHCISVVRAQAEPDPEFPTVKFPNPEEGAGTLTLSMETAAEAGSNYILAN
DPDADRLAVAERRQDGNWRIFSGNELGALLGWWTVFRIRRLGEPLENCYFIFSIVSSMIL
RSIAKKEGMHYAETLTGFKWMGSLAESLQRESSARVVLAFEEAIGYMFGTRVFDKDGVTA
AAVVADMIAFLEKEEKKRLSEKLLEIFKQYGFHFTCNSYVIARDPARVSEMFGAITKMQN
GSYPKEVAGARVLHIRDLASGLDTQMPDGRATLPISASSPIITFYFDNGVTMTIRGSGTE
PKLKWYAELITEDPLREKELAVFVDKAVEELVRPSYYNFEYRSNL*
>TCRU_2902 hypothetical protein, conserved
MTSRGFNAAAARNRKQYLQLLRETAEVAVSEGTTSFGVNGVLKTSSRIRLHEAALKLPEN
WVRNSTTRLQTSLEGVVPREKLLTNDLFLCALIHPSYVSSRSVRASVAMPIELTLTGSST
LRLLKEVAAVHGMAGLLATEEIAGIPSGLHVEDLLLYEKSMFEPCGQIPPEEVRMAAATA
LCGAVVLSEGICSATALLDRLREGKKE*
>TCRU_2903 actin, putative
MAVVEVGWTIRAGYIGDARCTRQSSSICFRDGPMETSFPSILMAAEATGVDIIQSVWTVC
SLERGMNQNVEQLEYIMGNKLQCSKDDPLMLVLPEALHERTDLVRELFRVVLEAGFTSAL
YCFRPSVAWTLASGRTSAVVLDVGHNQATTTAVLDGYALRNTVASSSLAGRSVTGRLIEM
LDREQLDSLESIKRYRVPSIRNWALDDMVNDIKRMACFVRVGHSNFSLKEEPLVLRAPDG
NSVTVSASARTEPYEMLFSPPTGFGVSLAELLVSCKKRLDPEWLQQAVPHVFCGGTSQAP
GFCDRIIKEAQKRDSCYFRYEKEGSFHVFGAVDGAWTGASLAAASSSFASLWVTRADLEE
EGDSVLYRKLLY*
>TCRU_2904 hypothetical protein, conserved
MAFPLEIAVGERLLSLSTVSRSTDIGHNGKQPLSSFYFVGERLPDGGIQWFLSPLDGYKQ
KRLRVEEAVVEKDAGNRDVFLRLGDSTFRQYTVKGSPSRIQAIVTNRIRQDELNDSSANS
RQSSYFLSSSSATPSMVSQPGTQEACLILPGKDANLYDGLEKKSLRVTLRLPSDEGDGCK
EALTKQEVEGEKNDTLHLPPVRVPQKPATRINSNVRPTGSIHLRRLLGGQ*
>TCRU_2905 serine-palmitoyl-CoA transferase, putative
MSMSDFISLVLTQIVEHPFHILIEIVFTAALTVALWRKQARRRKNHSKAAAFEMPSLEEQ
ELRIAQFQSQMFRADCKTTSNAVVPNALGTAEVDSREGCYVTIRNVSDGSLLRCIDFATE
DFHSFSTHPTVLEVARKTVMAYGVGSCGPRGFYGTIKPHMDAERDLAKFLGVEDAIICSL
SFATVSTIISCFAGRGEYIILDDGVNLAVAEGCTLSRATVHKYRHNDMTHLESLLKKVAE
TEVAAKKLSRRFVVTEGLFMNSGDICNLPRILELCHTFKFRLILEDSYGFGCLGPTGRGT
HEHFGIPATSIDLYVGSLSTSLGAVGGFCAGTRKLVDHQRLAASAYVFSASLPPYITAAV
SMALTILHEDHTYPEKLQSNAKLFREALRQARFNSDKIRLLECEGDVSPILVLRPTEAYL
KEHSQSVEIELEQVVQLARKMKVMLLRHLYSADEQCENYPALRILVKGKANREEIQNAAK
VVVDAVKTVFP*
>TCRU_2906 hypothetical protein
MRSRRWGPTSTKDCSFLEPLNPNAQSGDMTTKVLLGRETLATSKHDAFLSSQVSAEASLR
EESTTPIALLFFERMQELLSLLRRYMKRWRRFAREHNILASLEGIQRGAVIKQFLRMFYK
WFLFASRSAAVRNMEHSLIKEASLRLASRYLKLWRMAVELRQKRSRQILVLRGIRYGAER
SLARRQYLRWRAAARRKVELHRRLAVLSESRTIHLAHFFFVTWMRWRQRNFYTTQLGLIK
YAAFRSLARCTLQRWGLLISRRIVARDMERCSLERFVGGFLLRWRRYAHTCKSLRCIGHK
AYWRVARRAFGKWKMWLVRIVVTLQLEKRNTVLLVQVYFFRWLMFYRVHRLDYNAFLSSL
LL*
>TCRU_2907 Protein of unknown function (DUF501), putative
MQPLEASNKRGAFGTAASQESYRVADLELASCKLHGGAAVLCSTAGKVGRKARSAAAGAT
LFWLTCPYLNIIVARLERHGAIGALQQLVDENERVAAQHVASHARYEERARSLLSDQRWA

FFDSHFVSIPESSGGRKYGNGAVGHAKDLKCLHALVAQSLCGAPNPIGDAVLQYIYLFSK
KVEALRRPTKSSYLEEGGDEAEEENGPASASFFDDISVFVDFVEGWAKKNEEERAKFPVA
VDANDYCSAACSVLTFLEGRPPRLRKKHRIN*
>TCRU_2908 hypothetical protein, conserved
MDADDGGVPAAAKLTGEQEARLVARLHDVSMSHKQETLRLLEARIYPTMPSKRIPKEAIE
GSVMRQVDQEMMKRQAAREEREKRIQEEMKPLKVPSETVERSTCRLYTESMQRKKANLEE
IKKRHLYAGPPMVQKKFSEIREYVTRLAVPKKREFTIDEINKIYGLAAEPVNAMGVSGGA
DAAGGEAHNES*
>TCRU_2909 inositol-pentakisphosphate 2-kinase, putative
MRLLGMGCSSAVFSLLDNEERGGEGKTKEGETIALIIEQIFESGRNPLHGLIDRVALRLS
RAMTFACSTCDQALADFIGFRHEISLTDELRKCCAATVSLSLQEHCRGAGHAHIIPNFAT
NPAVLIGNGRGSRWLVVEIKPKGVWRPPRVVGILVDGVEYYIHPVKLYQCRFSLMQLLKY
ERRGTGVAPPSDSSTAYCPNMLLIGDQPSIKKGIRHLIRYPANNFRLFFTENSSGEISDA
DLDDLSTALHESGILKVLENLQLFGCGSHSDWEVLDIELLYRWSSAREISDVQWIVRESD
ASSSLKVECACQRGTIERWTDEGRIKDISTRFIAPPIGLKECINRFYASTTAKDVSVLVS
LLNGNTMEAAAASPAVGGPTGSRPRLEITQWKSLYGGVFVDFGFPNASICRVGAVDVDAK
VHKSLSHYFILDKNVLAAWERWKSTRILSLR*
>TCRU_2910 hypothetical protein, conserved
MRQTLWLWQWKDLLSHWKMYFHSGQKLTRRAALQLLQKTVDAARSSANGPGNSPLAKKRN
SEMIWKTIARHNVHWADCLALMNVQWAVLSPEQRHFIQEGFTCSGSGRHLPCLMADVWHP
ATDLSSVYARLLVSETIVQFAIVVYAAVRERPHLGDVLPVTPQVLLRCYFLGRSQPEVAL
QCCRVIALSSTKDISRIEREALAFEYIMLHAKKGQWSVALYLLNSSREIRPSAKRLFRLY
TFQASQWLRAIASVVPMEPHIVAEAITHAPHWSYALRTFERWESAEAICALLARPDCVAA
MGWEASLRLCAEARVNSYSLIRFIFTTVPSYCPQLMQLHATAIRPAGEVMYSGTLTRRAY
KFVQSGCWAEAIGLLCGCCYYDVALPLALYAPPGFALPHSLLKYEEAVHRIKLSTIVSAD
ASFEEQLAVALHGDGTRLKNLHTNNRLRSLILAQRLLSPNAAGKAMDGAEEEKCEVQCFT
FQSEKISRLVCRSAGIKAQRYFMQVIPRALRRHHFGVEEIPASELYTSERYMTFRSSNEI
VSEREACNMLCAMVVEHLRASGKLTGQVFLREIAHCLASGKVRLAAADCHALPLAVLRAA
TYFHRLDAVVTTRIALSTPSQHLMTHPEALERGMNALVLTGRWQRAISLLQRTKRPYPES
FAVVAYAAPRSLAIKALNMLWKDHAKSQWVLLLQDLIQGDIRLAQEELIHCSSRINSHVD
EGKILWRRRVLGACCALLQSSDSMQYVVRAANISSFCSLDVDEHGLQRLLPLLSWNQALT
AITDLKERGEVVEEHWALLVCTKPSISLDVARKIISWFPYSFLLNSVFLHQYAVLHGDLV
TSIKAMARYHALVITEYRRCLTYLRPFLVFLKNALHQFDDEAWKKASVWSLVRRLFNQVV
EDPKFVHWGRQGRKSIPFSLREEGPLAALFIVGFLYHRLSRALQMPVPAAIMSRLLRSAA
LSTNDSQCALYFFKSLKQPNDVERSLLVFALRDCDDAMTVLLNTGRFIGPRPDQVLLWSD
PGLGSEKWLEAIKLLSQSPPSQERLERLCASWTKEESLRALKLLQRTHGNSAEVRSYVEL
VESLQQKKVKSE*
>TCRU_2911 50S ribosomal protein L13, putative
MHRASRIAAAPFKSVLRRHKHHPEGLPLYNEMSKQWLCREGERWWILDAKGEQLPRVAAV
AAQYITGQHRPDFTPGMISGDHVIIVNIKDVVMVGDEWIRVPITWQTAYPGGKYRIRLTD
MYERDPCMLMWWFLKDEVNRHFVRKLKTRVAPLEKAWLYEDSVHPHGEKNPRPLCWSDPV
VRGWKYTDPQFIRRWKPNEFIT*
>TCRU_2912 V-type ATPase, A subunit, putative
MARDHNPYEAEHRMGSVKAVSGPVVIAENMSGSAMYELVQVGSFRLVGEIIRLEGDTATI
QVYEETGGLTVGDPVYCTGKPLSLELGPGIMSEIFDGIQRPLETIYRMVENVFIPKGVQV
KALNDQKMWDFKPRVRVGDLVTGGDILGTVVENSLMYDHSIMVPPNFQGRVTFVQPSGNY
TLVDEIVEVEHNGTKRSLKLMHRWPVRTPRPVAVKESGNHPLLTGQRVLDALFPSVQGGT
CAIPGAFGCGKTVISQALSKYSNSDAVIYVGCGERGNEMAEVLMDFPTLTTVVDGREESI
MKRTCLVANTSNMPVAAREASIYTGITLAEYYRDMGKHIAMMADSTSRWAEALREISGRL
AEMPADGGYPAYLSARLASFYERAGRVTCIGGPRREGSVTIVGAVSPPGGDFSDPVTSAT
LGIVQVFWGLEKRLAQRKHFPSVNWLISYSKYLKVLEPFFNTFDPDYMRLRSVVAEILQR
EEELQEIVQLVGKDSLSESDKIILETAKVIREEFLQQNAFTPYDKFCPLYKTCWMLRNIV
TFYEEGQRVVAESAGEHKITWNYIREKLPHIYNGLTEMKFRDPAEGKEANIDYFKKQNEE
IINAFASLLQ*

>TCRU_2913 Nucleoporin
MLFRDRQIIDRGNEILAYISHLDAAISSAEASKERLSELKSKQGAIAAMMQRVEDAVQPI
YAKVRPNFTRLDEQREATYTAVINLFDEVEAFRLRLSQSVAQHNRSLRQLRECDDLERMA
GLVDCQLSALERCSKRAEELESEMDLLLGKNSAM*
>TCRU_2914 NADH-cytochrome b5 reductase, putative
MKFLAFSAAAFLGAAFQSYTATPDRVAQCRQENVFGTKFKPFVLGEVINLAEDVAVFRFL
LPKPEMEFDLMPCSTLQGCFKEGINIVDQPMRFYTPVTRNGTKGYFDLLVKKQVNGRFTE
HLFSMNVGETLLFRTVQYKLKYRKNAWEEVGMIGGGTGICPLLQFLNASLDTPGDTTKLS
LLFANRSENKILLKGMLDKLSQEHSHRLKVYYTVDSIENEDGSYNGYVGYITEKMLQETM
PKPAPKNLLLVCGPDPMMEKLVGAPPSVLKAMSSGQAYQPAGAVLNNLADVEGTLGRMGY
TKDIVYRF*
>TCRU_2915 Endonuclease/Exonuclease/phosphatase family/Endonuclease-
reverse transcriptase, putative
MEPFTWLPAERFFYPLLNSIGAYQRYTYRLRAVCDAQRQKLLLSGDIEQNPGPIAVLQMN
VSCLTPSKLATLMAQGADIIAIQETWESSERIASMHTGDYVLYAQSRIGKGGGVAVLVRK
TLRSKRIPLTIPQHDTSPEVVVVQVALDQNRDLIVADAYVRPPLQVTQSFRRLVNCLPAS
SPLLLCGDFNMHHPQWEPFLETSPSEVAAEFLELCTDAGLTLVNTPGEITYARGTRERSC
VDLTWSKHLTVSDWSASVSPLSDHYMLTFTLHQAFKDTIPSAPKFFCSWGKCKWDSFVKD
LDAQLPAYDYKKQSTGIKAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERIATDSKA
RYLQLPTPDREAEMQRTRSQFFLLLRERWRNTYLRRISKLNPGEPLAWKYISGRKKASLP
SPTSILLGDGQHTYKTARRAVNALNRIFLPFHPSHKAVGFSKGINRQSASLNINASSILG
SRTTTSLLLHLLQVLHSHLVLSQRIKTKLPPHLV*
>TCRU_2916 hypothetical protein, conserved
MQNAYATLARIVSGVPSTVDPESALLDANMPPLHVLCLRARLSIFENTRACQMDWMRRPP
PEPPPRAVFRTSPLSRDELYAFVDAYTKDYGITESSPREERFFRSSIPPWFAAFAHRVTI
GVELPMDLPITDEEELVREKRRVSEEALALHSHRSWILATDGGVDVPKSAGVGILLSSLD
SSEIIAMSVTKPRCTPMQLQDGIPCASSSPREADDPSYPTQA*
>TCRU_2917 C-14 sterol reductase, putative
MPRSSRGASRSRSRTPRRATSLTRVRAPEPKQATPLNPRTVEYEWGGPVGALALTVLLPA
FVLIINVQCGEEQCAVTGIYNLPTEILETIRASLSQLPFAIGLELAWLLLHALLYMVPIG
GRVKGTKLRNGKTLVYNMNAVYVFVFTHAVLGGLHYNGIFRLAGLAEMFAPLMIASIIIS
TGMSIVLYLASFRAPTVLLSLGGNTGNPVYDFWMGRELNPRTGSLDWKFMCELRPGLIGW
SVLNWAFVLKAVEAGTCTPSIIIIALLESFYVFDGLLLESGTLTMMDIVHDGFGFMLCFG
DLTWVPFTYTLKTKFLAYHPVKVSNAYVAFSCMLAVFGYVIFRGSNRQKNKFRQNPHDKA
VMNLKVMETSRGKSLIISGYWGICRHPNYVGDWLMTFAWSALTGIEAILPYYQPVYFAVL
LIHRQLRDERQMAEKYGDADWKKLCSIVRYRLIPYVY*
>TCRU_2918 hypothetical protein, conserved
MPWIRLEAENGLRVMAPSFSASPRMEGIDKLFEYPVRARSFHCFRGCAMPLEKDDNVDSR
LCLMEEILVLVQRQQMGGKLGEVTIAVGGPAASRDELTVVLDSAFDVVRRTNYSGARLIF
DALCTSSTFAPAANDEVVEYDGLPTLQESHWKERRVSDWRDSDKMSSNKGGRSEVRSSLF
VRRRALLFFVTQDVVPVNLLYCRVSGVKSHGCVSSVAKAAQHYRKGLQSLESSAARACKN
LVDVIDRTLVAAYNVNKSAKKHQSLWGGNFDKITFVAVFSINGLLFASPLFFQLTDHRNR
LFIAAVAVDQLSRWPTERSLSKQTPLIHVCDLLLKCGKDGLVLNLVFLGVGNAVSCVFAF
RTAGEEAFWDAAVLLRFIKEHLRTPRAALRLGAGTDDGDDDEEEEEAAMKKEAREFAPHF
LLCTASIYPTTWFHRLLYEMNKLEEEAPKTFLQGTNDVSNGKLPPRLHGTCDCLPFFGQH
GKKTVKSTPFVWSTDTVDLPLDIAWCVASSHIVKEEANACSEGREMGHYALFSILSGIAG
NEGELGRYGVGWFNHCWRHTSIVGTRGDKENGVFDYYTTEADPTKFLGGLASIGGGPCAP
GFYEVREGGGCFFRQASRFEARAGDDGPFFTSKLVTFPYSLLFEGNGAEDDARTDEENGG
HLMTALYTMNTHKVKDAECNALLQEMLLMEGDLTEWEEELIETLRRRQHRSPSVNAAFAL
CHEAARCVLEDVWRCSIL*
>TCRU_2919 actin A
MEATLWDEEPAVVLDNGSGNIKCGFAGEEIPRCVFPSVTGVSMNARSSGSSSSQRVYVGD
EALQEKGLRYFYPMEHGIVFDWDQMERVWRHAYEQLRVPPERQAVLLTEAPLNPISNREK
MAETLFESFGVPALHVQIQAVLTLYSSGRTDGLVLDSGDGVTHLVPVFEGQTMPQSVRRL

ELAGRDLTEWMMELLSDELDRPFTTSADREIARRVKESLCYIPLFFEEELQAAEEDGINE
DVKGKEPFTLPDGEVIHVGRARFCCPEILFNPALAEKPYDGIQHAVINCVNSCPIDLRRQ
LLGSIVLSGGNTMFKGMQQRLQSELAALANKRAAEDVRVVAASERKFSVWIGAAILASLT
SFASEWITRTEYAEQGAAVLHKRCDSLSFVSK*
>TCRU_2920 hypothetical protein, conserved
MHSPSSALSCDSAESIYNLLSAVQAQANADEEEIKTRRLHIANCEREMERTNEEIRFLSE
QHEEALDEVRAKRLRGEEQKLRHAGAVEMLQCTREEVAGVVDALFACELPLHPVAAAAGA
SFETPQESLPPAMIRSATTSLKEKIRAATEQRQSQVTEPQRLFTAVAQEASLGNDAGNVF
AVRFRQDAASEASSDPTNNTAIVSECAVVEVVSSPSERPRRKVITFNDAQLEGHIEKNHS
SPSSSSSSTAALSEAPPRKGLEQQEEMRPAAVVSVYGVLNMKRLPRRTFWQKEPRLQK*
>TCRU_2921 hypothetical protein, conserved
MALRLTLLALGSRAKGYENRVMVYAHRRHRSWYQPPKLPHARSPLANKPPEEYGNTWDPR
SGVDWYYRMRRRGAYRHWPWARWSDDPVRHHRETPFNRTFSHNSHGSNDGVPLWNYYAEV
GQEYNTPSHFPLHYMAPFIHQYTGKMWSRNDIERHLKLIEERTGLISIQDVHDNLPRLQE
WGEVEMGTVPHGLLQHVEMLANDIVLQNRKKGFRRKLHENGVLRTSTMERYYALPHLRSG
PPMPTTLQQPSGAFPWGKYTHMLGGTKIHPLHRPDGFLKENMYPP*
>TCRU_2922 ribonucleoside-diphosphate reductase large chain
MLATDLTVRKRDGSLQSFDANKLFARIERVSHGLDPNYVDVKILTEIVVGGVHDEISTVE
LDKLIAETAAYSVTKHPDYGLMGGRLCVTALHKTTSASVLETFSILHKHKIHDTGRAAPL
LSDEVWEVVQRHHEQLQRMVNYDRDMRFEFFGYKTLERSYLLRVDRGRGEREIAERPQQM
FLRVALGIHGEDMERVKETYDHMSLGYFTHATPTLFNAGTPFPQMSSCFLVAMREDSIEG
IYDTLKQCAVISKSAGGIGVHVHNIRCSGSYIAGTNGQSNGLVPMLRVWNNTARYVDQGG
GKRKGAFAIYLEPWHGDIFNFLLLKKNTGKEDHRARDLFYALWIPDLFMERVKSGGKWTL
MDPHTAPGLSDCYGDDFKKLYEGYERENRGVRTVQAQSLWFAILESQMETGVPFMLYKDA
CNRKSNQKNVGVIKCSNLCTEIIEYTSRDEVAVCNLASIALPRFVDKERRIYDHQRLYEV
TKIVTKNLNRVIDRNHYPVPESRRSNELNRPIGIGVQGMADTFILMRLPFTCQEARTLNE
DIFETIYYGAVEASVELAEVEGPYARFAGSPASQGQLQFDLWEQKPRSGRWDWDALKKRM
MKSGMRNSLLLAPMPTASTSQILGNNECFEPFTSNIYVRRVLSGEFPVVNKYLVMDLIKR
GLWNEEMRNQIIAYNGSVQNIRGIPNDLKELYRVVWEIRQKDLIEMAVDRGKFIDQSQSL
NLFLENPTSSQLTSMHFFAWERGLKTGMYYLRSKPAADAIKFTVDPNTLKGLVKEDDRKQ
VSSATPSNEDCLNCGS*
>TCRU_2923 hypothetical protein, conserved
MQRSIDRPLGRGGNEARDKRPRKHISFARDGVKVCFVKPPPRSMNHCYWFTETELVAKKG
LFFEVEPDIDVSVDVMCRMQLTSVASQPWKYPRLFSKGGGAGEKRPKGRSSERVFLEIKA
TPSLGSIGVSRRASRWLTVASVEEGQLEKVRVILPAGSYALRCVGPRPVQVFAQVWDVET
RLD*
>TCRU_2924 hypothetical protein
MTFCIYGTSHHERLAVALFRGSSLTVYRQTSVHGKSDELFTMEPVMVLRHCHEGGGVEQV
VFVQNGEGLATSGRADGRHICLWALPPLPN*
>TCRU_2925 hypothetical protein
MNAIKLLTGYLLVSFEELGVVGSLFLAAAGAVVVCAWTAWWLRPRHSVASSEEVKFDKDV
GEAALTGKSETAEAPARRKEAKARSDKDATGRMTAPGEPKGEDSIQPTSVLRGYPEVDSI
MVSPCQRYLFIHCRNKRRARLYPQNRNRAFMERGKELQEKHFVSVDEAVISATGGDAKVE
LYAAAFSYDGERIMISERNSDTFFLFSIGTKCQLTLQSSCKLPHRRLVSTLPPWGVAGAA
YDLIVMTYDNGCEVEVFSLQSKEFLGKAKFKVGNALAWAQRDLTIAAAGSFLSRRNFSGR
RSSRWEMPWPGRSETSPLPRLGHFSRNRGWRRCRFALMETGSNY*
>TCRU_2926 calpain, putative
MNACRYNPSEEEFLYLPQSVFLNNFSSMQRCHINCGDRLTAIGEWDKTSCGGNPKFTTFR
NNPIYLVENKSSRPVRILAELRHQAPVFYDADSVGHYHQTGLALLQHDGSVSVLSGIITN
STHNFIQKGIMLDTREVCSRMEIPPTSTCILIPYTMKRGCLGKFSVSIYPGDSSVNFMPL
TPLSVTHGFCDVDVILTPGSREGKRIEFVVNGACDAHLLLRQNKITDPASIKKGDVLAED
DVMMMLYDEYMTRLASTGDATSAREHSLALQLPSAGRYSVLLACPNKPVTGNCPCSLYIY
TPKQVATRILPRPTNGTPQILPFLSLPQSSKGAARGNVKGKVIGAGDVATGTGNRPVETQ
GMKLPNPPRNGRPTYHR*

>TCRU_2927 hypothetical protein, conserved
MGEEAFSYHAAEVRAVHLALSAFSAILPSTMDVWVDNTSLQGAENKGSSKSHAMTWELQR
IYEFLDSRGIQATFAYVRSADNPADGISRGRVFTLQELAKRSGGVLWLEDPKVCHFVINN
I*
>TCRU_2928 hypothetical protein, conserved
MELIRQRRSTVVRRITDIPALGQLHEESERGRSRDVGAVNVGAENVPSGAIHDFLPHARK
ADKRGELCGLFDGNRSRAIDPTAVRQDAAVHVGNGSNPAGHDDSGVTKNCGAIGDEADAP
LDRGRDESSNPQPDRLEGTCCLTTRVDNGELLVRDCGLDSQQFHNGAGRDLNFVLVRGAE
DGEDGSPLRLAVCQDTRAGRVRHYKAMQNTSRKRKAHESYDRPGRTSSGSLECHGAFHKT
RCVEARCSNRGDTQFESTRDLAVGEARRPVRPSPEYCSIFGEVHHSADPGIGAGRIDVKG
ETAEGQEPWLRAEERFFHDFYHNHAATITRRVARTRLATPQDEHVIPPQQVNVPVLNLER
IKSRLNPATLERVMRVWGLVGWSPFPPSSSGKAREGSRSIPTADAR*
>TCRU_2929 hypothetical protein, conserved
MAEAVSCLDVKSSFIVSLPRETRHLFRCRVEDGTLVELTRLPMGYKAGPEILQIITSAIA
VVTTVVHRLWAAPPSVRVDVWIDDIRIAGLKSDVTLWEAQVLRNADSCHASMGEGRESGA
TQYTFLWVQFDHTHRAVSLSEKFVRSVCAMTSLNSSTIAEMEVVASRFLYAAAIFGTRLC
DYYFFIKAGRRRLSALHRGIVLETSPANLPPAAVGLDERLRHIIGNNRKRIIKPAEKASA
AITDASLHGWGAVFISDFGEVKIAGGKWKKSFLIMQAEARAVRLAFSAFSAILPSTMDVW
VDNTSRRITAA*
>TCRU_2930 hypothetical protein, conserved
MASSDDDSRCVLGTHPHSPPCLSVGVSAAAAWSMAEAVGAAERDEAPRNKRSNLLDETTM
ADESCFVAFASYIARSVPCRRLTGCLHSAPFEALCSFIQCDVTIIMAAPSLTGSECDNTN
DGKESDEDYGDDLHRGADYLRVLAHEYQEGLNAVSTIPGLAQPLAFALSPAVISAPCVEA
DPFAVEFTQQLSSVCAANPALALSHVSQRCLADDLMSVLSRPPPPVLYWCPIRNTLRCGG
YLFAWPSMHVTMLNGCVFCLAGTRETSVCADASAKVFVDGSRRK*
>TCRU_2931 mitochondrial carrier protein
MYPGSTYAMLYKVLQRVIKFAGQSYMRDFLESRFGHIFLGDAQEQSKQQKQQKQHTHRRN
NHGAMALEATAGCLVGVFEVILLPIDRMKVLNQTNKGAIKNRSFFRILRQEGVMRMYAGI
GTTAVRNAPGSFLLFGGVAWTKEYVFHLEDYSDATVVQNLVSSTVGGFLGVWFTNPIDVV
KTRIQNKRFEDGRVTGWSVMTETFRREGVTAFYKGMLPKLLTSAPRLVFSYTMTQFFIRC
FRGEKPKPLRESK*
>TCRU_2932 Transmembrane adaptor Erv26, putative
MHYEYEYYNFRGSGKPPYMRYGPFDVLTFLMSCITGIAILFSVTCAIGYVADVAEEFPTR
AKKILHTMTIGVLFVHGLILVLDQLSLWCSLVSIITNVLYLRILSGFPRVSLTHPLTILT
IVSLVVELLSWYLFFLFSPIMPEHLGSYRFFSFTAFLWLIPLGLLVSLQIEPVGLPGIGF
SASPQRHTDIAAEGRKKTVFNLLRGWLTPVMD*
>TCRU_2933 small GTP-binding protein Rab11
MEDTNLTFKVVIIGDSGVGKSNLMTRYTANEFSQDTPATIGVEFMTKSIKIEGRDAKVQI
WDTAGQERFRAISRSIYHGAKGAMLVYDITNQTSFDSIPTWLQELRVFVPATCSIFLIGN
KCDLEHLRVVKKEVADRFARENGLSFLETSALEKTNVEKAFEWLAKSVYDLVVAPVDAAG
GRRPPLNAAANAKRPVNLGASNDGQAAGKKENTSRCC*
>TCRU_2934 ABC transporter, putative
MDFVKNFPPLLRDIEGLGEEYGVQSYTLSATTLEEVFLKIAHGDGVGAIPAVETQPTVLK
GDYSEMDEKGNKPVELEGDFSTTQKDTPRLVAHPSIRSRSNSGIETMSQLQTIWEAEVIK
DEFRLMFSQLKASLMKRLLYALRDRRTQFIQIVFPVVMLTFVLLLQLVEFFSYPSLLLSS
NMYGERVLIDLAACNGTINVSIPFAKSTSFGIHDIADTGDLYKYLIEQQKTPSLNRYTSI
SCNDVVYRERKILLYNGSALHSSALSLVGYYGSVLYAQLRGASTAYQEDIFLTRNFPMVQ
TTREHATSEAIKTVLMGILAIIPFSFIPSTFVSFVVRERECKACHLQKVSGLRFSIYWLS
NYIFDFFCYLITAILAILIMLAFDRKEYISSEKIGATFVLLLMYGLSCIAMSYAVSFLFK
QHASAQNVMLLVNFIAGFFMVLLVFILEMFESTKTAAKGLQWTFRIFPSYCIGEGILNLS
LLKGKEDVRGKRISPWELDVVGIPAIYMACEVLVFLLITIFLDHPTRRMRTKRALHRGNG
EAEEIADEDEDVAMERRRIQETENNPSEDIVRLENMRKVYSNGKVAVRNLSLGVKSGEVF
GFLGTNGAGKTTTIAILCQEMAPTSGRAFVCGKDTVRDSRESLRCIGYCPQFDALLELLT
VEEHLNLYAGVRGVKSGERETVVRDLMGLCELTAYCSTLARQLSGGNKRKLSVAISLIGG

PRVVFLDEPSAGMDPIARRGLWTAIQGISCSCSVVLTTHHLEEVEALAHRVAIMVNGSLR
CLGNKTHLKRKYGSGFEMVIRMADDEMRERTEEFIAMYFPAAKLNEVRGNRCTYALPATT
ILSEAFGLLEAHRNEVGIADYTLSQTSIEQVFLRISEQAQQEPDSVNVTAA*
>TCRU_2935 hypothetical protein, conserved
MRLSNYCLAPTLSKATRLQLGNIKTEYGYVSTAAGSQEKWGFIFKVRRYPLLSCGYTLCL
MSIAIGVVGTYQQYRDMVIMTEHISYEDVKDRCLTPIPGWARIRNVQIASPLGPMTYRDP
TPLDWLPFELKLGHVKQASY*
>TCRU_2936 proteasome complex subunit Rpn13 ubiquitin receptor, putative
MQRKGRGGECVIQFRAGKMNFKDGKVEADRRRGTLSFFKMPNNDVKMTWISGTDEEQHDL
PRGEVKFSQVEKCTTGRVFLLDFGNRRPPIFYWLQEKTTENDSTYFSTIQELIGGDLRPS
DRKRAEFEVVLQGILRNMRNGLEQDVDLADIIGSKKLLDALHEDPAFFMYKLHQFLPEGT
DPTADIVEQVRNPQVSAAAASLGLALRDPLGFLETCSAFGINGSNPCVFGFLSGVMKLFK
KGDDNSQ*
>TCRU_2937 DNA polymerase epsilon subunit b, putative
MQDYRAEIQFMARAYQYRLHPSALKSFSDHLSTIGDSEKRRDALRDLFALLHKLCAGDRF
VDDKKMRLAITQQSVRDRGISEREGVSTVFPVPLEEIPYVYMDEKTGEIKVQRAERDIDR
FTVLRQRYLFTRRRCLRSGLFRRDLNKQSLNQDLPPLLSTIALEGIDPSENVAVLGMIRR
GFNEICLEDLHGRVRLTFLGGVPPLIGFVGDGFFVLVRGQWSSGVLVVVSIELPPAERRE
DTLRDIGSDYDLFGYRPTDMAAAHLREKNSLQAVIIVMSHVHLDQTSTVNKLVCFFKEMQ
NRTESELMNTTLVMVGDFSSSTIHYDDISHLPDPFEGSNRYKLLMDTLAMVITTHAPSVA
QHTQVVLVPGSNDVTGLLGVLPQPPIVSVFTRTLQARLKKVFFAPNPCRLRFFTHEIVVT
RRDFFRSLQGSGRAFNRSVVETPNSISSFESVAKTILDEAHLAPEVKEGILWKADGALSL
LALPHLLVLCDSTEQWECTYKGARVVNPGSFSLASTFLWYTPADGECSLSSIDY*
>TCRU_2938 DTW domain containing protein, putative
MKRVREVYTEGAEERRRKIIDFIRSLQFSVPLYRLRQQEGRRPCANCGKRRQYYCYDCLT
VVHPESHPPPLFLPLNVYVILHPGEIRGKSTSLAASTISPDLHIVEYPKVPSSLELESTL
VLYPSSQSTELSDIKDLDSVKNVVFIDSTWQQSKAIARDERVCRFKKVRIKSQTSLFWRF
QSNDPTYLATVEAIYFFLREFISNKRKHCAEESKKPLYRGDVDDLLFYYINQYVAVQQRY
SHDTTMQYTTRHFDGYILPSSSWDELVAPPPKDLKEGNVI*
>TCRU_2939 trypanin-related protein, putative
MPPKERAVATRSKAKGAANDARKNKSIAAVPSAPPPPIPDGRELWLATDTLQKEKAMRNY
FQLERDRIISFWEVTKKQLEDLKTELRQRENDKAEAQERQEVEKKVFKQKIRHMMYEHQL
QLAEMISEAERTLAIREEEYRQKERNSGGEIRDAKLMLRAQENEHRDMTSALTLSHDQEI
AEQQLAFERKNKEMHLIYEKKMKDLRDEMDQRRREEIGLIEKRKGDHIAELRETHERTFR
EMKEYYSEITSNNLETIRTLKDEVYARKRTEAHNERAMMDVAQRNKKLTEPLAKLQRQKR
ELEQELINYSSDRDKLREMKMNVREREQELRTLSWENEVLSQRFVKLEEDRDIILNKYNN
MLQDIQRKATFRRVLVQNKLELVQSQLEGRDARLTELLKRVNIDPEGISEIEHRVRDLSL
EKDAIIGDLQHLITQLAAKQQVIVSTYEAYLRGNGISGVSG*
>TCRU_2940 rRNA processing protein, putative
MPVYDVAARKKRPAVVKLNGTPKEVNEKNEARRKGKMAPNDKKKNNAEGEKTAAVEFSEP
AQWVERMALTSTKSLPADLNADDDPRREEVFIQQALLSVSRGISLLEEAAVPWRRPADYY
AEMFKDDVQMGRIAAAIEDSKARVEAQAHRRAMKDQKKYGKEVQAELLRQRAKYKREMGE
RITEWRRKRKGNEELKEILDDGDAKGIQSAHTAHRVRTPKQKNLRPGGVGGSKRRPGKNA
RRRR*
>TCRU_2941 hypothetical protein, conserved
MSSQWLPDFVLQRGQEAESYSSTRGRLSNPFDLVTEDACIISLERKSRHLTEVFAVRDRI
HKKFRGFVDNVASEFVLKSSLTQLGINAEDIKINLDRGALRAEIRMNLVALSPLGVLMLD
YIGEGAYIGKLFALEEVRRVRNVSYINRLLKTLDQAGHFLLNYGDSSEPDWELKIVDGRV
VAFLPILEGTFAYSGEVHGLLPTIGAALKHRTRYKELLRLHQEFRLNYTRVASPEGVLLV
RGLAMHLRTLFGRVVDELLPKGLKSMSSRVIEPDTGLKQKLQKRTFVFYGESSVELTHVP
IEFFTLESYREHVPFSLRKTLSQRCGCKADVLSVFRTAPRGNECCCTYICKGGQFSELTS
ADWVVADPKPLPYVGYEDPGRQQEIAQQAVYQECEYSILSAIAAGDITSDGVLMTRYFPS
PSLKSLILSCSVGKKVRAIFFTKASRHHGQFFSQEDSGLLCDLNTFGILVFYVDEAHGEI

YQFIRRQDRDCGVFVPVERRQEYLLATFFGVYGSNLMQGDFEAELRFLFNGILRLRQYCN
HPLLNPGKTLALVTGGGPGAMEVGNRVAKSLGILSCGLFVDFGSLSHKPGATINEQRNNP
YIEAFMTYRSNKLVERQSDFNLDFPIFLTGGIGTDFEYALEEVRRKVSSVPPNPVILFGT
LEHFKNKITGRYQENLRSGTIKGSEWICSIPWLVTTGAEALEIYKRFFNGQLPVGPGHPL
NDLGFVVASEYLANHPM*
>TCRU_2942 hypothetical protein, conserved
MMAGVLGPEVIKELKAIHCVAKALGAVKTSPHASFSPDDGTITVSQQSGEDTAAVLGDIG
KKLAAAAERLADAIEAQMGEFFNHMREKEASSVVGLLRTRSVVPDFFKVMGKNEVRAGDT
NAASRSCEIPEINGSMQKNINSLTSHQSDLRGATTLLQTCLFLMMESVLTRVNAVRAAVY
IGDVSENPRVLCRVAHIHADDKLPLEVSYANSSTLITAVQGGMAVNFNNTKMHPNKDDRE
ANGHSRPFEAHLRCHLRVQSGIVVPIGNYGCVLVAEKPAGMPQGFTSFDEHHVWALAILC
EGLIPRYPRDVFVKMSWSPAVRTLRHCSRLPSILKPLARASTLPRTGLTVTSAPSLDTLA
SVPRKLTILRASGNSPSIIGDPKGIPRKHMTTEGIFREAAEYVRNIEDLWQKAVHEANQL
QQVVEEHVRNLEEKTHQITLLEEELRRLKRHAFGL*
>TCRU_2943 60S ribosomal protein L5, putative
MPFVKVVKNKAYFKRFQVKYRRRREGKTDYQARRQMVLQDKTKFGTPKYRLVVRITNRDI
IAQVVQAKVVGDEVVMAAYSHELPQFGIQHGLTNYAAAYATGLLVARRMLTKLGLANKFE
GTKEADGSYSAVRTKADDQGDDEKRFPFKAILDVGLARTTTGARVFGVMKGAVDGGLAVP
HRPNRFPGYDKEKDSLNAKAHRDRILGLHVAEYLKQVREEASSNPEESTCQFSKYIKDKV
VPNELEGMYKKAHAAIRADPMKRRARKERKEGAAVKKYNTPKRTGAQKKAAAKEKIAFLV
ASIRERASK*
>TCRU_2944 protein associated with differentiation 3, putative
MTGEHLIEVLATGPQKAIYEPRRFALLLLGSYGCICSSLSYAFNLIAPEMQSLYNLTGRD
ISTISTVGLVVGYFLVPYGFIFDHFGPKPIFILSMVLFPLGALMFGLSFRGTIEGSVVRL
SVFNGMLILGCTLFDLAYMMTIMSHFPISRGPVVAILKSYIGLGSAIVGSIQLAFFDGRP
DHYFYFLMVLFLVTGVAGFFFVLLPSYHLTGYEEKHLGVEEKQRRLARKSVYLRQKPPTI
RLAIGIAFVVLLVIYLPLQSALVAYLEWGRTQRIIFASILIAVIVALPLMALPVSCLERR
KTQREEDDCSGMDRPNASDEAANEPAAAGGLPKSVETDVDYIAPQYQTTFLQNLKTLELW
AFFWSIFSIMGTVFVIIYNASFIYAALADKEVDNAVKTLLTVLNGVGSAAGRLMMSYFEV
WSQKRRAEDRVSIVVSVYFADVFVILSLVLFLVMPRAALPLPYVLAAMGNGFGAASIVLV
TRTIFAKDPAKHYNFIFFSVVFSTILLNRLLYGEWYTREAEKQGGNVCLGRSCVMMPLLF
FIGLNFTALLSTVYFDWGYRRLSRVVLEERRRLKARAAEGLLAVNTSPVVGTGPQEGEED
AGNRTTTAPNDMQAVRP*
>TCRU_2945 hypothetical protein, conserved
MLQMDRTPLEIVILRLQKIAAQSETKQARPSTKGAVDKCIRSRTDWKERVVVRLAWITAS
RLFEIAALTPNNFTLEADGALILDWSLAPKTARADPHRASRFVGIRGQDAFDIIKLCRTL
RHNEKLTNLTTALVERALANWNATAHSIERGALRHAAPIVEKYNLDPHVISQFASTSTRS
TFPRILFDICGDTPKC*
>TCRU_2946 rhodanese-like domain containing protein, putative
MGQDNSFENIEQKKALSLFEMEALVKSKMDGENSDVYIIDVRDGFEVEEFGSIPFSVHIP
STEVRRAFRLREAEFMGNYKSRMPRKFDKIVFYDQRSGRAATAVEVVEAMGYQRATYFSD
GFSEWKSKSGRSADEDL*
>TCRU_2947 rhodanese-like domain containing protein, putative
MFGLTRWLRVKVTVEQVAAVVQAKLSGAQSVQNTLLIDVRSTGEVAATGVIPTAVNIPLK
LLEFALGEEVEAEEFEKTFGVQKPQPGMTQVIFYCTHGVRSAIATEIAGNLGFTDAKNFA
GSFTEWQRHHGEPCDNGDVPLK*
>TCRU_2948 Rhodanese-like domain containing protein, putative
MQNSLDYAAIKDIVANKLRGELKTTHLIDVRGRDEVQSTGLIPTATNIPLDELESALKAD
HESFQKTYAVPKPLQDDTLIMYCKKGLRGLEGEKRARQCGYTNTAVYPGSWDDWSKNTKE
QKEE*
>TCRU_2949 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MSRRLFTFALLLLLVVMMCCGSGGAAAVGSVSEDEHLSKWVDIFVPNKTQVLAGEDDSKS

GVGVSFASPSLVSAGGVMAVLAEGIISYNPSSATESFVYHSDIVAGYVNAAESWPSLVAE
INDGTWRAHTVLSTVNEERHVGIARFPTTIAKGNKLFLLVGSYIMMQDTKDDFWKLGGTD
IQLVQGEATKSTEGKQSKSIKWDEPKSLLGQIAPQAQGDSKVLWAGGGGSGVLMEDGTFV
FPLQKRKENGEFLSMIIYSTDDGSSWTLSRGMLPAGCRGSCITEWERGQILMITDCDDGQ
RVFESRNMGTTWTEAVRTLLGVWVKSESEFFWDKSLRAGALITATIEGRKVMLYTQKRYP
TQEQKDKALYLWVTDNNRTFYVGPFSVDSAENKTFANALLYSDAELYLSQQRGIKTGTAV
SLSRLAEEMNTIRSVLSGWAQLDASFSESFTPTAGLVGFLSNAASGNTWIDEYRCVNATV
RNAVKVHNGFKFTGPGSRAIWPVNSREDNNQYGFVDHNFAIVATVTIHKAPKKSTPLLGA
SLGEGHPTKMIGLSYGAGSKWETVFDGKTTAQDSTWEPGKEYQVALMLQGGNNGSVYVDG
KLVGSSETIPTLETTVLEISHFYIGGDEGDSDSDLTVKNFFLYNRPLSADELKMVTKRED
SVRGDVSRVLLLLLLLGLWGIAALY*
>TCRU_2950 hypothetical protein, conserved
MGTVTGELQGDAFLRANLEYLASLEPPAICPVLPRLPGGSGLLPDDFQLPPTATAGEAAS
IILQVNAVEDVSLPMAQRLRAMAPPATAAVQDNETELPTAVGDEAQQISVDEVLRSMESD
EPASQRRGRRQRLLRLTLTDGFTRVIAVEDCRKGCDALREGVAWGTKLRLYAPLQIRHGV
LILKSQQTVMVGGFVLELQEFWERHAKAMLEEMSGRPKRRIQQLAEVPSRVAPVQIHNGT
RTNVEHNSASLPPPPQQRLQEAGAEENAAAPAAPSHSNTMASLHSANAVNQPPPLSFSLS
ASQPQSLSAWQSHHPPTAPFRTVAVIREVTSELTIREVSARSPEASKRFSLLVLLSTPPV
DVNSDVPTGEAELVVDLGHNWLQQALGVDPDAFRALFLSRQPDDVAKLNTLVESVGWELE
NFGVAVFVLRQRETDGVVEVVKVERL*
>TCRU_2951 profilin
MSWQAYIDDSLIGSGHMHSAAIVGLSDGSYWGYGGTYIPQPDEVAHILKCLGNFSLVQSS
GVTIYGVKFFGLQSGEEGEMKYIFFKKGAAGGCIYTSKQTAIIAVYGNPGTSSSLQQDLE
KKEGAEIAVNPADCNSTVKRIAEYLISLDY*
>TCRU_2952 hypothetical protein, conserved
MRASYSPFKSKSQWTVENLAERIFISSPRLFSFSHRVLVSLRHPYTSVVVDLVDSDAYRK
KNRLEELLGALLQSRDEERKWVRVATMFDTKLTAEEIDSFRRKISLHREIRLCIEALWAD
LGGISNGAILEDSYKAFHFRLYSYILRIDNVSVVTSTSAAIAEDFTYDKRGSVGVEFGSF
AVSILELADNWTKTREVEDYIHFLRSIHDNCIVKNRSYSLKEDTIPSYKAPVFFSSGLVC
RVQEGDNVVYSKKKI*
>TCRU_2953 Ras-related protein Rab4
MAEKYQQLIKLILVGDSGTGKSSLLHRFVEDTFSEQQAQTIGVEFGSKIVQLAGRKVKLQ
IWDTAGQERYKSVTRSYYRGAVGCLIVYDITQRSTYESVPQWLNDVRQLAGKDVVVMLIG
NKSDLSDGRTVQHNEASLYSLENGLLHFETSAASGEFVSEAFLKVAKTGLSMTAEEVNIG
GDRAMEVAAKQESRTGYSCAC*
>TCRU_2954 Protein of unknown function (DUF2870), putative
MVLIECKRLPKDEYSKDYDVFLVSIPGVTNIGEATDVLQQMRNTRVRIKWMMAAAKQLAK
DFCSEEQQHHLLGPVADAERYMSLERAERRLTCTQKELDDLVDAFKGGAMILFPAECSGT
DAVKRLAQLLDDDNTTDTERSKAHRLLSIIDDGATTEDILQGVATMWWSGKQLDRAADFT
KYVGKNEKTKITVKLTAKDAPAPPREPALDAKAQSELMAYYFRKQEEMKKMIEDEDLSYG
NSAWANPQGLKSQLHGFDSVKFKPG*
>TCRU_2955 hypothetical protein, conserved
MVTRDAWLQGLSAVGFFLTGGVEELQALADVIAGVRAGVSATRSVAVGKTCFTLAVPRPW
FPRLHARHHPTLCTVLPRRLDLIASHIEPSPCGRNVVSKRSRGRRARHLHSFVEVPWERN
ADLSASGVSLLLLPYSVSPWVLSGAPAFYWMIGAAEMWRVFAAPSFSTFFARRVRDGFRL
PHCMGCCKAIHYATRLCCGCRAVKIFDVVEVPLEGGVAILRRG*
>TCRU_2956 hypothetical protein, conserved
MTKLAAHRSLRNLPLHERQGCPRKGVGLINGGVKTGAQCGERDAGIGCNCELHPECIQQG
PAQIHDSIGGILQAFQRADPLDQIVKGKFNLLVVLLPALVCTPEVDNDSGGALIPYTRGP
RGDVECAETAVLFHG*
>TCRU_2957 hypothetical protein, conserved
MTLVPYTPSEWCDIGARLWDMVSQCGETQVQMTFINGNQMSDGTLTVAASPTGLCLLHGP
VSKAWQDSTLIGHIANLRAPQIPNFETQVLLPAMGAARELGHQQGLITAERERLNIDYAN
AAADVQNRNAQLNSQVEEAHINPSVRESTIAGAGNQVLELRQQLEADRAQLREREFNLGV

LTGQFQEREARLNALQTARDAETARQDESPAT*
>TCRU_2958 hypothetical protein, conserved
MDGEEADVTKETKEGGPNTSHTFSVDAAPFEPSVNVSSNLANGWQDASSALTEQLSALGA
NESWPYPAQYIDMFALNASMRAMVEAAAMMNVGAKRYSGAPIVKTTSPPKKGSNASEASR
KREKGSLSIHAKPWSPSPETGLNQKEGDTYTHLKKGWVKVPYRGEMVIAPVAFKEIANDF
VHSLTVRPIEKPRIHLELYNYHCARCATHSFFGRLSCRDADVILKGIAGDIPPLCVAHLI
EQVTGAVVCALFTKGDCLDYEIWLETPDKAAHFAKTISDAMWTCPMFHGYAVHTKTEEEK
AFLHEYISSLKDDFPEETPYPMRCVEAIASSTGKVKG*
>TCRU_2959 hypothetical protein, conserved
MFITKTSEPNVSGFPVVDSLQEFSKVLTDYGTAFSDFSCFTRELIDPIVLPKGKTVLDVF
RVCFDDNASLLEEYHRDRKDSNQKWEPWRPAQTGSPQFSGQRVFTCTTTIKALVSKSCPF
TEYQRYAFMNVGGHEPTLVVQLSGQAEGLMYADVFRAEALLVFTQSDSGVAMRVFGYIQF
LRDVWVKGKILRTSLDNEMPICYRKLGSMLIERLQQEGGISSAEGPEKSSPLLPSSPSAN
AAEVLKGSSHVSGLVWRTVVYIEFVLEILSALLCLNSLFKTYFFTASKDIAGAQIPVLAT
GEISVNLTDAEQTLNTEILSLLVVDLLRPVLLASLLCLLFVIQLFLRKTVFRMKR*
>TCRU_2960 EF-hand domain pair, putative
MVSNRSLSAPPGGGSLANDSNHFGYRWGELSVGGFSPSPPPSNPWPNRPQTFSRYESSAD
WRKSPSYGGNRHGAYFRRNRGGAYGRVSHEFNRGYSSRSASALEEQDLPFPPQGRNGRFN
AHRSSSTPVWSQGPSYPTYQTPSPRYNGRRSGSSSSVSNSAKGKAEIPLLLASAFSEKQT
TRVRASLESSSTFSQAGIRLKLLEYLGYWMSDVLTGAAVEKLIMETYREADLKDTHTSVG
ERKKYSFSEFSNVMNTGKIAGDRHVQEGEKVNGSNRATSHLLSPSSSFSSLSLSSVSFHR
SESKNTSEGAAVRREQETQGKWERGTGTHFRRDSGTDASSNTPEGRVFSLVRSCGVESMA
TKQVFLTDEPKILPQQTAVLQTSSLIQATYSHVPRFYFPKGAQKTTEETLVGPMKKKHEN
PHLRVLEGMVIPTAVHTNSEERAAVMSDDVFKRHEVKKVPIAPLKAVEDKCVHMIIQKEF
GRLPVPPKIIHGTRPQSSAAKGFIGLNNGMQTRQGLNYRIQLTQAMKRICTQCFGLPKYF
AFLIVRILQANVDFGNSGVVKSGRSSSTMALSSPATGLPSASQTEVMVRQLLDFFETYLR
GRCIVRRVFEVLLLSSRVATSGSETSTRIGNDWRLVYDGEKQQQRSYLLPDDFRAYIEVL
LEHHPGLLFLKQTPDFQSKYLETVTHRIFYDLDRFNRGRITYAEMERSSFLDSIRQVDAT
NDINSVLLYFSYEHFYVLYCRFWELDKDRDMLLSRREFMNYAPEGVMNPIIADRVFTGAG
RRKACTQKDRINYEDFVWFCLSEEDKSTPTAIRYWFRILDLDGDGLLSAYELRSFYDEMK
KTVTSYAPDGAVPFEDILCQIFDMFGLETSCSLRLEEFLAKPEAAAVTFNMVTNVVRFLQ
FEQKDPFVTHQNRLEGGLEQSAWDRFARAEYGRLSNAMRKE*
>TCRU_2961 Alpha/beta hydrolase family, putative
MRTVRLTLSTATASAPPLVKEAGKVAAATTTDKPRREFTSLRIQPWQRNCLGASREQMLP
PSLFYHGTHLGPRPLIILDHTTKNTAEAALAAKKYEAVLSQLSWEYGAVYIPLHVDFPYT
TSGLIEQTCQQVCAVMDALDVHWTHFLTYSYGCLVAAYMAASEGFPHRIGTFISLDTPLV
TRELLQNMEQREEIAKAERDVNVPEANLSFAKHNLISSLEEPLPCPAGADKSLYYDYLFN
PAEIFQSDGLVRCEERYVPVKHLADVRHPMQLVVPSANALADVTVHKEFFGLRRPVVLKG
CQRHEEIFRDESAKEIAKVLETWLQRFEPDAYIAKRYEQAAAEMSQLMMSSAPATTQADG
AEGGDQRKKKKEKKKKA*
>TCRU_2962 hypothetical protein
MEVPIFSPHGYTGYAKKVFGEDCYVYGPTTEHCEILLSNVDEDVSLHIDGGTPTTVYAND
VALLDSWMMTPVLISSSGFVTIRRVQATGGKGAASSRGSGVLPPVSTRGGSGNYGELSFH
TTASSPVVAPSLPLGVLAPMTPVITCRVSTKCWPRVFPHGDNSTDTQLVQYFKEAVVVSV
RTMRLLGVEEGSMVQVDFHSEASVLAASKVVFSVTSDFVGEEFSFDSCLRHFIAPFFLQR
CRAISVGEEFEFKNHDYGQLHVTVVAIEDGLLKCGLVVDSTCIRLVAQPEAPPKLQGHGS
GRVSESSTPRMRVPSARKSSGSVRGSSLPRNSHSRMSEASPRPKLPPGARSSTSGKPPPI
VGGPPRVHEPSPRRASRDVEPHGGIASFSAYSPQTFDASPTLIINQMHSPTSFTALKVAR
ADRAPDDDATAAITIGTTVTAASAPADVSKVAVVNPAARTSPSSRVQDSDGVKIPPVPSP
QHRDTLPTTEHAPDAINPSNFATESPTEHSVSFLEKPQETESALLLQSGVDFLEVDPQED
LEARRFETHSSRKSETNSVDNMASAASSPTGGSWSQREVHSAISTTDRRIVACSGNLSVA
TQHDAGSVEFRSVEVQTDRESPVKEIVCDISLGNTQGALQEPTEAAPRQDEDEEEGGAKN
VLGLSSIHLPHTVSNLTVSSTRPALEKYGMGTRCEKRNEGIHSLEAEEEGVSGKDSAAEP
IADDFNEALNGKSQESAWSVPNQEEEGKGPKNDFSSNDAFKILTHHSGSTKATEMRLEQP

LTVTKDVAFRAGRIVEKWLDVKAKWQGLSISHLLKRESSAVIQEFQHFLALYKELKQRHA
DYLAYLDSPYGHTVRGDLVLRISLLAASNMEGDGGGEIKPPWRPAELRGESAETPSEKAN
DDFKNNNTCDANSKSCAAALATELLKLSVREVSAKLGCGVLHIFRVGGTCPALYCTLMKP
YADGPGEITLMGESFPVEVLQTTILEDLCEAREESRRDWVQLSTLWKEAISGVLQHGVFT
KHMQKVRQLFFELAFLLHCPGEIRLSVRYQRHMDPFPPNSAECVAQTEKTEGDFNLTGTS
NRSPSTTSSTERKAALSNSCKEFLPHLQELQDTYYLYFELLEPFLLHSMQHLDTVSTLTD
AMKCEELVDFLKVSHEAQMLEQRAEETGTPLPLAVVEEERAAFLKLVKARKAGEIMPLPQ
EWWEADNLSSKNKFP*
>TCRU_2963 hypothetical protein, conserved
MSDTADLVEEMPAGRDGELQQPPMEERQPVRRIVPEIFFETQNYYQPQPQPQPQTISRRT
NGGRMRLDGKPPEAPQIQTPVQPAAAPRLLQLSRRGRGPVLERMKIRAASEASRENGSGG
KAAVQQKRFSRGGTATRRSPHGDGRYGAYGKLLRDAARELAMRSPSGVRSADGGSPASSA
RKKERGRSKTASCGRVSPEATPTIHSFSVSARGSTSRERRQQNVSATKDSPGDIGEAVAT
ASRNGGRQSSSSVSALRRVVHQPGPIRPENGCVLPLPCQMARRKVGHGRLIVFDDLLWKR
EKEHRWPLPNGETKVIAPSRVPQLTTEAPALPAVLEVALADHYLAVLMTCPQSEVERVVA
KLSPNGFSEVVQYLRQTYSAYFCPNTRNYTSVQPQPTQSAQRAEWLIKHRRHVQGRTRSI
ASGNAKKSNANGTYNPISKEVRQFLKLFTREVCMTFMDEGFAACTMRRERARAEQPQEVQ
ARGVPLPADVLDSLYSQVVTQLLFQILGWTEKEASRVLQTVVRQIKRCFPPSPNLSPQM*
>TCRU_2964 phospholipid-translocating ATPase, putative
MNEAVEMVRVYNNGNRDGSDDESSLCLPIPPMKPFSYVRLVRGWLNMDVAEANEPRTIAI
GCDPAVWSGRSYPKNAVNNRRYSLLSFLPLALFYHFRSVFNVFYLLLSLSQLIPALKVGF
IVTYFSPLVFVLLLSLIKDAVDDIQRYRRDQIANKEKVEKLFPDGSTGVVLASSIQVGDL
LVLRSGQRIPADCVLLRTSEKSGTCFVRTDQLDGETDWKLRYALKLTQTLNNETLCRFRA
NIRCEPLHKDIYKFVGMLDVAGLDAEAICLENTLWKSCVVASGTLIAAVLYTGVDTRSAM
NSSKPSTKTGLIESELNFIGALCFLFLVVVSLFLVFLQQFEGDWIVMFLRFLILLSAIIP
ISMRVNVDVGRMWYSYEMFRDSKIDGTVVRNTNIPEELGRLQYLFTDKTGTLTKNKMEFR
VIQVGVDTILNYNEVDRFRRIMEAFFVERHETGGLNAMDVGKGGGLLSQRTFPRDVTSVG
EALLALVLCHNVSPVMEDGRLEYQAASPDEVAFVKFCSSIGMTLTHRDVNCVRFTTPAGR
TVHYDIIKAFPFTSERKCMGIIVRERRGVGEGGYKYLMKGADTKMASVLRLTDWLYESCQ
ELSQVGLRTLVFAQRTLTEELFETFLAKYNEANADLGDTRNSSLDAAMRIIERDMKLVCV
TGVEDELQDDVTTSLETLGMGGIKVWILTGDKVETATTIGHSTRLIPRNGVVEVMASSTE
EDAMRFLEKLAARYALLSRGACVSRPWTLILDGTSLSFCLSESVSRIFVEVSQTAYSVIV
ARCSPTQKAAVIHTMRKYCDKRVRMAAIGDGGNDVSMILAADVGIGVEGLEGKQASMAAD
FSITKFAHCVRLIMWHGRRSYCRTCRMSQFIMHRGMVYSVVQAFFSLLFAGTTMSIFNGY
LLMGYTTIFTMAPVFALVLDEEIREKDVSEFPQHYKELLKARSMNTRSFLQWVWISIFQG
GTMMFLSLELFSEELFQLVAVAYTSLLLTELIIVASTAHLRILWEQRRRHLYLFIAAECF
SIASYFLAVVVLPETIDRNFFFSSGCWWRVTVITLAIIIPIYTIWLVSKYLLFNQKLAYS
LL*
>TCRU_2965 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MMMTACDDGRRRVYESGDKGGSWTEALGTLSRVWGNKHKGNEKGVGSGFSTATIDNRDVM
LITLPVYSNRRGNGKGELHLWLTDNTHIADIGPVSGNDDVTASSLLYKSAGSGDNNNEKL
VALYEKKGDGKPSLGMVSVRLTAQLKRVKEVLATWKKVDDRASKLCPSTAAKNPSTGNAC
SAVKTTDGLVGFLSKNFSGNTWRDEYLGVNATVKKGTNGVATGYPDGVTFQGAWAEWPVG
RQGQNQLYHFANHNFTLVATVSIHGEPKGDTPIPLMGATMNDNKKTVLLGLSHDKEGKWQ
LLCGGKKTKELRSNWEPETTHQVAIVLRNGEQGSAYVDGQRVGDASCELKNADSKGISHF
YIGGDGGSAGRKEGVPVTATNVLLYNRPLDDNEIRVLNANKISIPKLTDLRTVAAGATGV
GTARHFGANGDGSAVCGGGLLPLFLLLGLWGIAAS*
>TCRU_2966 Asparaginase, putative
MYLWDHNSLTLEDSADPSLEVGPDTEGEEVLLINARPYTLTGVSAEKGGLSQGFIDIKKN
KDLQKAGVPPFRVMELDVLRHSADQNHDDWVSLAALIRENYHKYRGFVINNGKDNMVATA
TALSFMLENLGRPVIFTGSCIPPERLYTDLYRNLIVALLFASCSQINEVCILFDERLFRA
NRTIQISRSAISPFDSPHFPPLATMHGKMSIHRTFLRPYPRGQFRVMDNMRDVVLCLKLG

PSMRRRVLLRSVELTEARAIVIIAYGGGNAPTRGGYMKEIVRKAVERDIAVCVCTQNLYG
SVDLGTYAAGDQLLEVGAVSSRDMTIEATIMKLKYLIGVGLSTKEIKRFFGDVSLRGELT
PPASQL*
>TCRU_2967 hypothetical protein
MSVNEASQPNLKNKETKAVSDILLACSVCGTSNVLPASSANVLKGTNMTMFCKTCGGATI
QRVVVSYFLGDHSKDSVDALAAPGKSSADSYSQASETDMDESIWRRLQDALVNSGVSMAE
FFRCDTSTRARLISAVGFNSAEIPRLLEFADANATRSMLSNVMERMQNPFETTAAATLRI
GAVAGEQAINPGPMKEVKNRTSAEFFRNSAQDERVFVNTPHHSAQIDGSMLSLKIKEDGT
LIARCSVYPHLPAEFWCSLCGVLVSSRCHVSGIHKDHPFITLRQAAEAHVRDLSTWSERC
RNQLNVANTIISNLQHGRDVLNDSAKHEEEALDRHFEEIVQGLTQWCQGLKSSMRLQIDA
QLENINVAIKRTNKLIEYYAERLKRCDPLLQSIPPMHQEDKKSEDWSLRVMDLVSQLKTA
SQEPIPMPRITVPEVKSFATVTTYMELLKAVSVPAGIRIPDVLDTGYLNFPTPSVLGRET
FTLDVPKDAKTRGILIYSGRTLTRSQDITPTHSLVCASQIFYTGITAWEVHVDRLGAGPG
RILAGVLMAGTDGEGVVWDGQRIVGPNEGECRALSERYRIKTGTTLRFVLELEAPSYFLV
CYYEDEVVARVPLPPALNGWIPAFSVFGPQDQLTVVPISAAVAENLLTDAKPEEKKKREE
EMKVRLGEQEQRLNALHQQLLAVNSRIDQDQYEKLNHASHARQEIRGDGSNDKGDADPSI
LSSPFFWRVSPQVPGDGYQSANNKHRLDSMHGAGAVAATGELTSPSPLLAPNVDSGQRNE
KNKRNASYSPELQNLLNFVDSIK*
>TCRU_2968 UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase,
putative
MAKPKLRRKLKRVALLLILFIAATTVLFFRLATTDDDDAPEPNNPRHSRAAAADDAALAY
IPRSAVEKWGRQEYLVVLGIPSPDDEARRTRRNLQRTTCWRFPGVATRANGFTGAMLVLY
VLGRHPSHGYDYSAALLEEAAQWHDVVALPMKEGRVTTKKKIGGSGSWGDEAEIGVTRKT
YMWFDLALRLFPTAGYIAKGDDDIFLRVPLFVAHLRLLPRRGIYMGGHVGLAIFVKRGLP
GSTFMVGWCYTLSRDVAEALVSYKPLRRLAYLPYSKEREEEFALLRFHCEDIMVGWVLDR
VIKYQPMIYVKVLPCHFHDARNGTGHSQVVPTSMCIHHVREDDYAALMARFGNDTSPAAR
VSWVSEDVIYPVCD*
>TCRU_2969 hypothetical protein, conserved
MNADDGSSIRSATSHHYAQASHRAADAPPYISNCPTQSSGRATELARQRRSTVVRRITDI
TALGQLHEESEGVSSRDVGAANVGARNVPSGACQLAWTTASLWSEVAALTPNNFTMGPDG
TVISDWSVARKTARAHLHRASRFVSIRGQEAFVIIKLCRTLQHNEELTNLATAQVERALA
PWNATARSIKRGASRHAAPIVETYKFYPHVISLLVRRVDFFDLPQNAFRYFGSYTTMPTQ
VSSLAALM*
>TCRU_2970 Alpha/beta hydrolase family, putative
MNIRVSGNCRGRTVVFLSGWPDTSEVFRDNIMSALAPRYRLVGITLPGFDRMSPQVQRVK
RSRKKEEAAEKGSLSSKMDFLRIPRMGYSFEDLVDFFEIALLAVMEHRPLERPLLVVHDW
GCIIAHEFLLSRPYFFSRVVMLDVGGDISDPLLTKGGECDDGVGGGIWAHWWRCVHIFIR
HAIVIAAFLIIPTSVGKGILRFILQIARWPSYKYTRHLSALGNDTDGEEEVLMVPICAQK
STVDVSRKPTRFLDVFNALLRFTVFGGDSEQKQDVSTLAASFYPSQFYYAKSRRLYTLPP
HPTASGIHYTHYRYRSARTQKTNGSASKNTSNSITTQNGVHPPTAPSHDDEASLNFVEVD
PLNGWIYLRYWIFWISRLLPSSRRFFIPISVPVLFLYGTEKPIMLHSHEWIKYIEAKGET
DGSEVVSVAGGHWFFAEDRNKGQVTKRIAEFLDADKFEAQISQSWKGHLYGGERDSYTSY
VSE*
>TCRU_2971 hypothetical protein, conserved
MEVPRLLRFSNLPPLSSAAAGPRDRRVGSDAVSAPLSPPPLPHAASVIGTEANRSTVATQ
TEESAHAETIHRAYSPQQRSIGTWTAPVKSTRATSPIPTVLVDAANNTEMSGAQWEGQSH
ELLQKTTLLQEQLCRNNFLETRQISMELAFTSAQERIKQGEERHKAAISYLTAARDEHRL
ELERLELTCRQSLFDHEAELRSMLHTLLGSWRTATLSTEQTRNGHERFLRAARGYSQFED
NTFHQLILDEVRHREEVKDSEWQSLLSLRQLRELAENCQRESSRTTAAINLAEEEKRAAI
MAKKAVEEKLRDVLEREKELRLQYLHVLRLPTTTIVSCSHQSNAATSVEEDIPVHARFVR
AHKEAVDAVRAQRRHTIGQIHIF*
>TCRU_2972 Haemolysin-III related, putative
MHELLTVQQVDPWLQFNPHIVSGYRPRMSVRAALRSFFEWHNESFNVWSHALAACFVLYL
ALFPPTMEISTTSTVSGCGVGTSGIAATDVSLTPHDRRWLGSSSEHLLGASSTTTFRCTC

LVFFFIFICSVVYHLFMPCTTSESLYRRLLSCDVFGVVICITGTSWSLVYRGNACSQNWS
CHVGMGALLLSALFVLYGAVFNASCGSFGRFKAIGFHSVLRFLILLWVELPKVQSQGYHQ
AVHCHAMSFVFLALGAVINALRFPEKHLRRATRLLPTSSSSPEATVTSRCWRWLGRFVVS
GEEIDYTWNSHGFWHYCIILSTTMMLLGCYYDLEEFELAKC*
>TCRU_2973 hypothetical protein, conserved
MTMAVEELPPLRSTPAIDRLRDAKRRFALSESQFASSRLGDRWSASPRMTAQESSLKQPC
TSSSSSAANAATNGSGGQREGTRHATLPFSGLSSIHRHVVGDSDTNSLLTWTLFDSNCRN
TPRGAAPIMTGVDLTPTVASSFGVPGSEEAGSTAPQVVASSGDGADSGRVFGSDGPAAMP
TASCKKQKHYLSDVPTHDIYRQRYNSQRVEMSRREDDYRRRRDANRAEVARLISHTTRLG
CMMNLQRQIYNEIMKRPLRTLATTEPVMNTAAPLPSKRSSVSPLFLSVRREASGPTKVES
GVQVALKLLKSRFASGCYLSTNMYRKPLFSEPAAAPTLETPLEAAGELPSAAGATSTEKV
AGSGGENEKSHNDDNTKRECRGVNEEVVHASSSPHEHEEAVTFHSSLLINPATAPTMIYE
SCIHHASGRKEEENPTSANQRRGSSETLLTEEEQRGLRLLSTVRGLRRQTEELTTAVLHA
AGEWGCWDSPGASVFRGLFLSPRTATCIVEEEKAAELRLMHMAALEEAARGEVHPVTAAL
RQQCPFRRSLPPPPSVLVQMEMFNLPGMRQQIRRCQEQRQHRQLQRQEEANAKDGNSREA
IWRPFVQHVLLPEAAEHFSKTEEEAEERGKQRLQQSPVCVEQDADPVDAPVDVGPPSQLA
TNLTVIKMGEQHDHQGSFASLKPRHVHPFISSSSSSSSSYEFSFSSSYLSSQSSTEDGRQ
TASAYSYASSALLSTNMKFSVAALSEGEESASEAQRGIIKEKKENEEEREMSKKENIPYN
SQREVLPLDRRGLAMTKSSDNPTSTSLGPRVAGELSGTAVVPIFRAEAACEQSHRGNKKR
KSLAKRLLSFFGACSCGGSRGATVSGRKRRSAAS*
>TCRU_2974 RNA-binding protein, putative
MDLFFGNIVGDGCGNNYIHNTNTENFSSISLGKTNEFFDALGVIGDERECAEEGFIGGEI
KAEATHSPPLNSCATSFLHSITSNVADPRLPSGVRGGSAYDEGAWMTDVVSSTLPMTTLD
ARTSVESSFAAKNSEAEASVTANLPTVITPKSTPTNVAINSQQTSATGDTMRLTVRNNVY
VSELPAHWNTDKLRSVCSAFGTIISAKVVHDGATNKSREYGFVMFETEEQAALCVESLNN
CSMAGRVLACRLAHEKAMPAFAHAESISWSPCTTTNATPSTGFITPQEGPIESGRHFNPE
FFEASYTPPQNGQPNSTIDQNAYSGLRKSRNVFIQGLPLHWNTDKLRGLCGTCGRVLRAK
VVRDATTSLPCGHGFVLFETEEQAAACVATLNGFVAEGRTLTCRLTREKRSSLQFSMSNA
DGLTTTPGMPPLSPSGRTSVNTESLVTPSTNVLAPIGIVEAVATPQNAAFMSVPNYGKWP
PVGMVPNCAGGALPQTLQHAGLTSSPSFLGHATLATPQSYATVATAGSIPGFAAQPTEYG
IVPGMEGQFASLSNVSNAYIITLPYSPAGMGQVTGSNSSLATVALAATALPLPMGTAGNS
TGGASVVPSELVGGYIGRP*
>TCRU_2975 hypothetical protein, conserved
MSGTAGDAEITPSCAEVEEEGWLLLLAAFIGCFVDNREGREEDSLGACGAVGGDTEPSGD
MTGTAGRYVLDGVRRALRYLVHDSDALRAKRELEHVVDAVSEGFWRQLRSTRRPCRRGDD
AKNDLGGDDTTRDEEKMLQLLYRLAGVLPHSTTTLNVVLPAELLYVVYYLAYTQCGPQAW
QVETTDSRWVQLFFGPSLCACSTMMKSSMTNDFAASTALFSLHAHGMEPGGRMPQEENMR
LHMTRFFSRCTAHGDTKNVQLFVDAYHAWLMRDYHGVLEHTEKLFQLLPFGEENQSRLLW
VMLQSSHFIYVFSSIAITNTSHPAAREELKGRLQRVRVESNSDSYERYVSSVWGECTSLH
TCPSLLCAAYNLVYCEISHSGGNHHGEEEGDGCLHDEQQPQPSTSLVCWQEMFLLTLRVW
LRAKRLTEEGCMTESRDLLLHTLERLYSHSCRTRNNNSRSVITVFSPPLTAGANAIDPGG
AASGGGGNDATKEDASISAGKGETHVVILLMSSMWLRNLLLVNCAALSDTRTPLHLMDHL
RQPLTAAELLYLAACPTIAAGGVHSPIFALFPIDGAGEMKPATGVNESLERMPLPVRVPL
LSHRLWKLRQQLLQELPRSPDENCECEDHRVSLQREMIHLCESLAMSARGLFGSLDLSFT
DCAPHRIVFDAIMMACDVQEDILRSAALSLANASTFSPPTSPCSSSSGSGSDKERTGGIM
SETSNIVDRETNTDTMLTSYIMCTSAGDSPSFISSVTRVHDKSRSSIDDNNENNNINDDN
GDDDSDSWIMKNRAALLISPSELSQASSFVACTAVAAQELYWFSYRKSHEWMEILQHFFP
QLPLVVQVCQLRVAAAAFDRGIARLARNLLAAFHENALVASHVALALFASLHVVPAERCI
HEALQKHPHSAEMRRLYRVICGHNNISRQELQGNGDEQEAKGWVRKHLIRPDFTHRYRGV
LPVKYVACEQRGYKAVYVPLVMSLVCIGVLVLCFVLHLRDVDLTTERTILKDDAVFRWSF
ALPSAFLTYLGFGVLLYGFAAAALVPFLTSRRVGSNNRVQHVAMFLHALMEWNCLEHDTP
NQLVFCLRGLPLVNLLTGVQLVVSNALWLKTHTGKPCISNEARIIPDECNRVFTGWGAVQ
LLVIVVLLAIAVLFYGRAWRVLRYRDVLVGPPATFITIFFIDVAALLVFFPVIFLCCVLL
EPLLFFITVVFSVAFGSPLLTEHLPTVPTDMVLASTVLPRIPTATTRAVGRWGGLTALFL

EQVTLQIRERLRASMPPLHWFPSRHQDCSILCFHEVLQPLSNDGKDASNSTGGFILQFLR
LAASRGIAVCAFLQDIINWRIHRIPQDSEAAVQLALLRESFTAVVVPAPANVTSTLNDLW
GVNTKVELDTCATRFATPPRWKVSSTTPYG*
>TCRU_2976 hypothetical protein, conserved
MPLDVVWTRLLARGAFFLFLTLLLATSGGAAHSLAVYPIVEDPLVNYSVVASQRCEDAGM
RLAAPDSLEKAKHMESLLSRCSSSTGSVLFGAQVVECDATISLFLFKDVFSEPSSPVAGD
AELCDSLAGAAGRKNVPGMFGGTLGLPFYHVDFKDCKHPNCIRPVLLDYDPAQRYGFEKP
QSNEMNLLVWKLKKTEDGKTLFSWEGVCSKGTAGCPFKGVQKPFIPNQVICESDGPMTDL
AAICFESYVDTTEAKKPVDGNLWIIVAAVGSGVLILALLVIIFSTNSWRQRRDMKRREES
EDISAPYKSKRENGSSLKLQHQGSLAGEGMQRQGSFAGGEMPRQGSFAGGGMQRQGSFAG
GGMQRQGSFAGGGMPRQGSFAGGGMQRQGSFAGGGMQRQGSFAGGEMPRQGSFAGGGMQR
QGSFAGGGMPRPGGFPGGGMQHSKSFSGVGMPRPGGFPVVGMPRPGGFPVVGMPRPGGFA
GGGMPRQGSFAGGGISRQGSFAGGGMPRQGSFAGGGISRQGSFAGGGMPRPGGFPGGGMQ
HQGSLAGGGMQHQGSLAGGGMQRQGSLAGGGMQHQGSLAGGGLSRQGSFSDAEEIRGETK
DDVKLKRRVSFTGTYVLL*
>TCRU_2977 hypothetical protein, conserved
MMESPLSRGGYVSPNRVGTGCNSSLAPGGRSVSPGTNSLTLPAVNQKVAVEGWCRGGRLR
HHKVNPSLFQEGETSLLFVDDGKGGKRESVTRPLEEPLVDAKWQCGMKNPVERKKRESTT
SCRGMLALGNNGGLSRQQLLTLTEASKGGTTVPLTDSSSQCTETSRDGGQQRTRRVAKNG
LEYDPKTYGELLPATLRMHKAGCMQAGIVSSAVVNELLAERDAQQANRGALAMNGEGFYT
VSLQELQGFLGEMNQFQERGKHMRRRWRRHLLCVEAPSSAAIRVVNEDDDTSSESLQEPD
SDDKLKLTLSKRQQQTSEATRAAISTWREEINALQLRGGNPRGAVLLRNEIRKSQRAVEK
ASQGVTLSKILMIQNETNVKTPKEEEQREPLRGQSCLSAEEISWRTENTMSQRTVSPTPP
GLGAAGVVERTNDGGSYHGDKRKGSDSDAVHRRLDTQLVSLLNRGKGTTVYGLDITRRNR
SCGAQQHVPPANSLPSLQPASGKSSPMDFSVTWTGDAKKNPELKGRHSHYSIQRPSRPLP
VEYGVGEQSSLRLKALITQWRLEDCQMEVRNQEDIRRTRELLQELIPKRAALLDESLKCS
RENARVILQKHRQHIFKRVAEKDSEERKQACFGYVDLLEENYSGVVAEGSLAAIRKALQK
TRDLIKVSPTRCNARSFQSILKENFLIAHLVEVPVRELLWRLAELFGMTRSQYKSAMSNA
YQLLNTPRDYQARFREIERTIVCISTPAERRIRLTLHRCRFFLANNTVGTSHVVSAIGGE
RSRELSEIYVQIKSENQVFISTAVRARISNDDDTFSWDVSQRDGKYHSLCGANFMDQAFR
FNFGENAELVVALLHNGLVIASGKFCLSDCTFNPRGIALLWLRLSGEGGAEAEIKLTLAM
LAEKNQQKKTLRN*
>TCRU_2978 hypothetical protein, conserved
MRGGRRTAAIAASTFFLAPRRRRFPQLTTLVQQPRYCSSESSAKKIFHYRPHQLSGQSER
NVELNLGASTKKLSSVHITLDSLAPPSTLTADTAVEYLAALRGLHRSLGIMASASRVRWQ
AREFLIRGVPKPNDNETQALWTMTEELACAITVSCAHFEISILECPYGNESVEFLQHLWQ
ERQSSSSPLSSICSCEEAVLLGRLTMAVLDLLVNRVLYLDADGYELLSQLLCRTLLPAVM
CVLQDDVLFTPPKGEEGEDKDLTNTQAAALTVLLSSLTKAAVAQWARRSSDSEDGENVAL
FGTPTSLPPSVESGVRIPRAIKVPIVPLSLAKLARIVQHYATGLTPLRVRETALPLLRFF
TLTQCVPLFVEPHDECGPHGTGEGSSGGCEQGTNMASLVASVTRVLQASMDNRTFFVSHQ
VSNITSTYARILSFSPIQSKKEVGNDGHAVVASTSWCLFEILMMGLKSNILYHVEPLSPT
VVMPQLCECVTAFSKKYLFSDLAALLNALAKIFHVLCEQHNNLWIQQQQQQLQQKQDQPV
KVNGTRSRFERRRTTASVVRSSMLPKDEGGQSSLTSPALPLTGVFFVSNDDISEIEGELE
VLLDACVAVMERHMLSFWNTRQALVPRSGIHSSTSGASASDKSLKVLKEERGIAFSGVGV
SLAKALGGRSRRLKKSVSSRELVMIAEGVHALSWRPFVAFQERLLALLSSSVGQSETTPS
QYACLVRFVLRAPPVLPSVIFHSVGDRLKRVIHAEAVTTAVSKRNGNEDGKEESTNMASS
AEEVPALVIAAAHARSLQDTPLSLYDACAVVFAFAQKMKKSALPLLHDFFVRTGKRVFSD
CETSPEPCQDAATCAALMMFVASATWVLCQSAPILPGDHGLTFIAASRDYAAEILAASTP
EEKLNAAKSFFSLSDLAYACMMLEPSCDSQGSAQLTQVRCFLQETYKAHTSQCDSMEVTQ
FITDYLAIPPLDISYGDAVKMKQKEEENEKKSKEFLQLSPWMISSLRLRDRLEGNTRLST
VMFFPLLGGGRDDISRVLNVTRMYCRTFATLVTTLRLLAAADVELLKDDAVLEVVFRKVS
QLTRRTARPLDLFQFFELYGDYPQMASACLSELLPEARCFEAKNAFVPIVQVNAAVRAVR
RMRKRELRQRWFATMTPLIVSAVTFSREPLDVVLELTEHIGNDDPELLQSVLKSSASMQM
IHETFRFTVSGDVLLRLLQQLQNASTSHPTVRGLHAASRELLQKTNAHIPLKQLAQAMLL

PSVEGTTLGRRLKKLFVFRVTVLLGITRPRASRPTGQSAVKSEEDPPTTTLRCSHWDESL
DCLELEHWMLLLRFSHVAEPSSYRLLMTIKHDMDVAARRMGKLALSSTPAKGEKAAAPEA
AAGSSHEGAVLLLEGKEEDPGYEKGVEEWSDKRHRSLAFFYAFSDHTILCLRRSLGAFQF
ITLVCELLHQASIFSPDLAAFSRESNSHERGCMYDGSASPLSDERVWPFLRLAIGLVEEM
SADLGGFLRREREQGRRLNHGEPRTAQNERNEELEEISVDIGAILKFLNVLDTYDPRRRE
RRLLLLSSASPSRLSLSHDTPNVFDDVMQIPHRYLYRLLLQLPQHWGKVTPAASFVDTPR
VRLQNISSVFDYCSAPTEFHSPFGTPDASVKAHFCLLSIFGADRPLISDVWMPIAALQSQ
QRLIDRSVKAQLFGALMRCLVRDGESLAATRPRLAELGPRDLARVAQTFLGGGGGGAVVA
AGNDDHYREEYDKWRSGRRAEAVIALELLTDMLPSASAEDLHDIVMMLLPPPSAEPKWEG
DKRQTPHALLYEEVAEVRRFLVHVPVVMGNDTERFPLPVLYGILLRLHEPHRLIAPAAAQ
MMLTNLHAVDETTKGQELPEHEGEEEDVGEQVLEDAVSGPRKKQHYKATVALLRRVVSSS
SSFSL*
>TCRU_2979 hypothetical protein
MSTAPGGAVDDEIQSRLSKLSVYKRAEYHCVEGIAALRESLRDVVRLEGEESGTNDHGAS
KAVQNSSGSTSGGGGRAELAKARQAARRAHQQLDKLAKEAQRAARREDGGCDADMKELMR
HVESAKRWYRECFRVVPPIEGGYERQGDTGGAPGLDDDLHARQCTQHGATSMTTPLLAAN
FNDVNSNIHNGRDGVTSSRNASVTAPQPTVSDEEFLLFLDQVRRNDELADVALDRISHGL
SRLHENALNVTSELRTQEGLLVAVEEKVETTHANLSVLNKRLRKFLAEKNKCDCFMYAFC
CALLLGVVAAIAVLLKK*
>TCRU_2980 lipin, putative
MISSISGFLSLNHLDMTSGANDVIVVRHSNGRLFSTPFNVRFGKVKVLRPSDKVVQVEVN
GKPTSAVMKMGSDGEAFWLKPTPWSEYVSGRPESPLATATAYMNGGFSSHGNSGSRSPNR
NVENLQPTEPVSESMNSPTINAKAENSVAKEPLLEEDHEGHLKVNAVARQSGVDITEVQL
AEETVVAAEMAMQRIAQMTIEYDDYMRETVLLEKDEGILSTDMDKLECRPGALENALLSV
DDDTNAPPAILANTFRRSDRVYMETAGKDGDESGSVSVEIHPEKKECGHETPTARVAKES
ENTDKEVLTTPKKRRAMGSQKSLAASDEGLDTLDDYLFEDPINPEEYGGEFGGYNTGGTP
ASVPVVQEAGSEFPNLPLKTSTPDEKQCEEPSLSREKLEEVVYFTRTLIPTEADLRKLNL
VEGHNQVRYITHSSLRGEVAVDANVYLWDSTDRLVVSDVDGTITKSDLWGHLMPLIGRDW
THPGICSLYSKIDRNGYKFVYLTARSVSQVSMTRNFLWNIEQDGFRLPKGPVLTAPQRFF
TALTQEVSKKSHVFKIACLKSVLDTFPAQSKPFYAGFGNRFNDVVSYTATQIPQHKIFII
DPNSVLHVYNVRQTYKNLAHLVDVTFPPIVKRIHHHHHHLHHTPRETSDNLQSPDTLADA
EDGSENFTAALVGTRRIGSPGPAFLDVRDSQLLYDDDGSRLTSSPFDMRPLPEDNVGRVH
ATASTTPLENHADLNIDQEFHSFLYWRVQPADLVAEKKETKENENVSKGPKQHGNRKGSR
WLTFSLGTSSNHNNSDGLEGKSEDELNTRHVVGASESTGAQHSAPKAVAAAEDGVPKTGG
TTQDSSRLPEGNSTQERSENDNV*
>TCRU_2981 exosome-associated protein 3
MDFDDDVLPLMREMDAKLIRMQSELLPLLASLNEDVLVTKYSVDEQARVSLATAFILVLL
TYAHDRMQHVGGKKDMDARVQLKLERVSGYIKKLREITQLDNQLQGQKAVTAAATGGGKG
ARKHRREEADGGDVERRELTDANAADDPYGDAILFTEIGRGAGRPLSSLVQSLLRHVTDS
SAS*
>TCRU_2982 BNR repeat-like domain/Protein of unknown function
(DUF3676)/Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MMAHCAGGYYDVYRSTEDGVSWYTPGEPITRVWGNSHNRKGHGVQSGSTTAIIEGKEVML
ITAPVYSKENDKENKQKGRLHLWVTDKARVYDVGPVSREEDDAAASSLLIKDKNKELISL
YENKRSDGAYNLVAVRLTEKLERIKEVVKTWNDLDGALQSCSSVSSATVDPRKKGMCNSP
VPTERLVGFLSGNSTRTEWRDEYLGVNAKVKNGEKRREVPNGLTFKGSGAGAVWPVGDTG
QTVPYYFANNEFTLVATVSIHEVPQDGSPVPLIGVRMNDTSSTVLFGLSYTHEKKWLAIP
ENSGDPEDVYVWEPNETYQVVLRMDDDDEWTVFVNRYEIRQTRYDESLFNSHRISHFYIG
GDSKNQSATGGHVTVTNVMLYNEKLLSDNLYDLHASKVTIPSLSVEEQPTELVANTGTLV
ASESKSVESATSHEKLNENDPDEQGENSADDPLPAASSSTVVAGSSVSEPAIAAEIAENS
LPENNAQLSEGEESQQSTLHEVKESMQQDSDVQTKDLQSEESTEVTDVEKPSESNEEEMP
EEEGEADDGSGGLTSPVTASLNMETVTGPAYGEHQVQKSIELPAENDEVRSTGTGTTDAK
QSLSLEAGGSNSERAMNSDSSSTPSKSNAEPTSAENTDDVSRTEGAEFSSEDGGEMPRTV

DTAPANTSTTPGDEAIPSTKGAARHSDNDIFNTSEFADLLSTALNHDSTVHGCVSRVLLL
LLLGLWGSAALC*
>TCRU_2983 minichromosome maintenance (MCM) complex subunit,
putative
MSISGIPQENVKWLWQMYCASLAPLSFEEEVVVEMWRLFAAFLAPLSLQPSATASNQASS
AIATFTFTVDLRSDGLTAEMRTALVNQPQIVVPLLEFFRAVLDYQQNSEEHRRGALGSKR
LVCSVIGDDACATSFDALGASLLGQLVVIRGTVVRMSPSRVVCVKMAFRCGLCGAIVEVS
TEDGVLIYPGSCRGRCRGYKWSPLVEQGKCEEVQVLKIQEQSGVYDGSTGGGNIHKMMTV
ELRGIWIDAATVGESVILCGVLFARRSEGRADATQQIAVRAYSIEGSRHDSERSVLLSMN
SLEESAQFYEMARHPQWFARLCASLAPSIFGLQHVKEAIVLAVVGGTAHTMRTRSNIHLL
MVGDPGLGKSQLLRSACTIAARSAFVCAHTSSSCGLTLTLTRDPTSGETAFEAGAVVHGD
GGITCIDEIDKGVTEHRALLEVMEQETVSMAKAGMVFSVPVHTAILAAGNPAGGQFDESK
AVTANLNLSPALLSRFDIVVCLRDPHTECTRSLSEHVMRLHRRHDEVGARLAGCKSGGIT
LPVELVQRFVAFCRHHCHPSLREDASEVLKSHYLKSRAETKDDELAVTPRFLQALIRVAE
ARAKVELRHEVTAEDAEYAVELLRQCSGSLRGNPHTLSVRPAAAKKMSQREMIINALKAE
VCRTGVNALPYPVVLSACEEAGCRNANAMLHQLNEVGVILQIGDKYQLRGV*
>TCRU_2984 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MGTPATADANAPTAKGVGHDGPAVDQEMNASIREDEEAAGGINGQEDYHAQHGEVKAAAL
SSSLGNVSQGNNTDAGTVRGSGLLPLLLLLLGLWVFAAL*
>TCRU_2985 hypothetical protein, conserved
MTQAAGRTARRLSLSMRLGLLRCHLSPRTAVLPVGPHRAAAGSLACACRAECRATEHGHR
QFSAPRLAAASRSPTRVPVATDSLSAMEALRLGSLAVRDDVTEEICTVLLSLVDRGHAVG
TTFPHDTAESHAT*
>TCRU_2986 expression site-associated gene 3 (ESAG3)-like protein
MNQTFKGAFFLLQFFLVLALLIAASNWEKDSSLILSETLAKDDVQFVKAESESERPRVVF
LVIQTRKSPGWCRMMLSSLLSEVSVVSIGFGKRYNHAKRPLWILDYIDNEGLRDEDVVVA
FDGGDTFITGSFQVKQAVDRFLEATAPTAAVFNVTAVHRGEATAPLLFSSEGLCFAPLMK
ILISSGPRKHARKCVWYYSKVWEAMNASADQGMVPFTSAKGLFLNAGGMVGRVWAIREAL
KAYKKVLGLTDQWWCDQSIWSLLYVWSLTRTTNVSLDFRIPYGILNLDYHHNFFQCPYKG
LVAHPAVIHLPGGQRDWAPSMPELMNHTTWFSKLKSSLQMTRDGLTQLSNLFVKIFTCDG
ETRFRRFGALCSPRKVIDPDWLLSPLRK*
>TCRU_2987 retrotransposon hot spot protein, RHS3, putative
MVLASEKGWPYSWHTIQDLPKDVFVNCEVERAWQIVEGDLTAWFSPHGGTDFKPEQRALI
GTPGMGKSVAAGSYLLYQPLHCDVKKLQMVVYFIADRTFLFDKTSRAVTRYSDEDMCVSE
LRSLRGHGRNVYIIYDVAKEGTPPPRHFAPSTGWGMIAVSSPNVGNYGEWAKQLKAARII
VNCPDEMDVRAMCAWITRDGTAEKKAEYWRMVKERMDNVGPIPRHIFDANEFIAHSAAIE
DALDGIKSRDGERHFSHGGVRLWYSENASQKLVRVVRARGEVGAEGFLNAPISVCLGRRI
PHYFGRRDE*
>TCRU_2988 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCCPSVCVGRSTEETIVVREVDDVKEPTSSSTLSSESQVEDNSH
EERGSGTGSSEEGKTKVPVTPGSSGAVTQSNEAKMPVQTGEKKGTTEDENGTTAPKSQSK
GSTVEQGEADVGGVKSLTAPKRQSGDAIDTVHEEDGSTTGPQSRTTKSADQTDRETKDAA
ATTTTTTTTTEAPTTTTTAPTAMTTRAPSRLREIDGSLSSSAWVCAPLVLAASALAYTAV
G*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Right handed beta helix region/Dispersed gene family protein.1
MWSVVGACPRSRHRVRHSAIAAMRVALLFLLALAAAAAWMPAVHAVVLRLRGGTVDRAIT
VGRAVDTVLMDGVYITNGVAVVFDVAAMLPGALRIELRNCVCDGGAQIYVRGYSGEPASD
RSLEVSVSGLSGSYCSLAFVHNLPAHTNVTVRDSTIVTAGPMRYSQLSGLTDAVASPLVL
HATSLLQTQLRVSNTVLRSLQAGGSAVHVGGGVDLLSSAVVLDGVLLEASGGPTAFAMRV
ASSSRLSLRSHSVFSVTNVSVVSSGGGIVLGERLTVFDSVLRFLRVEGSVASSLVRCGGG
TVGSGGWLDLHDVWAVGEASSVASLSGVTLSGGAVSIARCVATGATLVSGLTITSGVVSV
QCNRAGGRVLQSSGDYRMAGLPSVSVVPCDGCAAALACFDALTASFSDCVCGCRAGGVGE

ACLPFDVPPARFGDGGDGAQGCVSGVTLTESVTVGGVRATACFDSVVFSGPITVAVDLRS
MDAFADALNVTLRHCVLAGGAQLRIGGLSESTAYLMPHALVNMTNVTSLEGTIVLHGAMP
LHSSVLLANSTLRATVGGSQYVPMTPGHAGSRYGPALVLDGVRLLSTRVVMTRSSLVCGG
GLCAAILVERSFVVNLSSVFYMDNCVVMSRAHVMYALASDLRVSGGSVFSIQNSSWIASS
IEIYEGACVFRDVVLDGGSVLQVVSSNFRLGFAMLIAETLTVTGDSWLVHRDNEFRTAYV
VYVIKENGVAFRDRSVWSILYNKLTYGLYSSTHAHMTSNWSPPSDTLPIIYGVCNEAMGS
PVTDYGDDLNIWVPVTVLDCGACTVDAVCFAARTSSISGCECECAADGYGDTCVPAAVPD
GLGPLPLPDANDTEVRCVHGGSISSVDYPDPGLRGLCFVNVTFTAAIVLDLWSFDAPQQT
LNITLLQCVLMGLSIGGSGARVHVNVISSMMDSGALEFEGDFGTSSQILVAGSTLVTKSD
HAISFFGFNFGATSTLLLIDNRIEGNGYAVYFNDALAVDGSGIIVKGNTLRVTGGVDSSE
TAIYFDVVDVKNGGYIDVENNTMNAVNGVYLFGATTVGSSGLLRVADCTFVGKTEFSDFT
LLYLDGSVTLEGGAQWRVEGNNLSTDSLLTILYSWHKIQLSDKGTTVVLAHNRQAESSNV
FAKILPWSTIVTSPARFVVGCNLQDDEEVSYDGVFPGEVEVFGCGTCNDDAACYMPGTES
VDRGSCSCSCKDGWHCASCLPFEVPDTVVPPVAERAVDGDTSCVVNQTLTNLTLNMWETH
HCYVGVTFSGVGAALTFSFNSMPLHLPINITLTGCTFLDGAVLQFVGDVEVAESVGVLIR
VSRTVLRSSVVAFALALPQHCDIAVTEVDAVQSSAVQLPDTVNNKLSVVMLYEVLLTASL
LLVSNVNARASKRDAFGLYSIGTLTLVSGSSLHVRYCSFGGYTHLFYLDILSVSDRSVFA
LLNNTVFFGTSLLYQYRGFSVSDHSVLRVVGNSGSVSCAIYASNSWTVQESSWLDWRDND
VGVGAMLHDSESAFVSIDGSSVVTLTGCKMGSTGLSRPLLSQSDAGYQFVAGCLTVAGRE
VTTAAELELHCITNVTTVAVCAECTKDGDCFAPLTTAVIDCRCQCAAGGHGDVCVPAPVP
AGPPPLPPSPSPPPPPPTPVGECISDMVYPEVAHAVGGGLSWLCYRNVTFSGDGMSLTVL
VGAMTGDVASVTFDGCTWRDGAVLLLLGNAHAAVGSLNIVVTGNTFRDALLSPEGVFPPR
TNITISGNRFTVTRLIPRSGLGLRKPSCVAMNGLAISNDSAVVLSGNVFHSVTASSSAIY
VVESSLRVSWRSLFAVMGNTFHMAGGDGTLIHLEGSSESSSLSVLNNSAVVIRGNLVSRP
VKYFILFFWASRVESQSAVVFQGNDMQGSLVVFYSAFSSHIYYNSWLQLSGNLCRESPSE
AFAVFNPTVNLRDSTLTVSGNQFMSNNGMAKALWIFSGSTDPTNGAIVAACNSVNGEGEA
KYGIPSLYNATILTCIDPCTLAASCFPAYTTTVSSDGCACTCAEGGHGDACLPVAVPEPP
STDGADLCVRDVRVGLEVNVSFGTSVACYVGVTFAVDVVVDVESMSGSVRNVTLANCTLV
GGASLYVLGWRSDPPAGERAEVLISGLESRSGGGVVVANRFPPGSRVTVVDSVLIAENRV
AYRGAYDLGDLSACLVVHNVNLTGSVLTIARTQVKAVFRDAVGVLVVGGVALSSRGALYV
DGLLVQTALGLCVSVEGGVAASGGSVVAFVDSVFLLCKHAVSVRGAVSVSGSIVAFLRSD
FSSTEDYAVAFYSTVSLDGGSMLLAKGNVHDGVSREMLHAAGAVTAAGSTLSFVRNRALL
PRMLSVSLSLAAGAHLRVACNDAGGRVLSTAEEYAAAGFGDAGSIDVAGCDACDRDTHCY
APGTASASMRDGVCVCACGSGGYGEACVPVGAPALPPAVGTASRVFVREGVTVQSVFVVP
AGASEVTLRHVVLDGVSPVLYVPWMARDGVRIVVQNVSLRNGAVLYVMGGGALRGAGTAG
SDESGPVELSVCDVEALNGALVLTGRFAAGSVLTVADSLLVAARPTPLVYLPGSQSSPYA
PVLVLSGLRLVRSVLVVSGVALVTVMTGGRTVVVDGAVLELVGGGVALDAAVLGGEYALY
ASARVVASGGAVLRVSGSQVYAAHGLVFDSGVVASASAVVVNDNAGALTDGALLELRGSA
SFLSGSWLSVRGNSISGRLLSVPSYPRSADLVQSTLTLYGNAGSGPVVMDGTVALVGAGR
RFVVGCLTLNGQALQPMEYRSAGIIGEFRPVACSVCDADVRCFAAATMSMSASCGCRCAE
GGYGRDCLPVYLPHVDGCDRTPAMPLLSRTATLTETRSPTPTWTSKWTPSRTLWWSHVAC
PTLAVTTTAAGGSLTQNDIRGGGSAVPTRLMVALPPPFRWARDPQLGTHLSFVPVSTAQP
RGFGGPWGAMLRNATWVRNATNPSTVLELAVPLHRGYFIAADETIVIRCDAVAVFGGCKG
VLLGSFTIRSDMLPAAASALSAITGVVAGAAAVAVVVTGGLGSILEMQVLGVFARMSCTS
AQERASTAALPYFLSVFAALDPLWMVVGNALLAAVFGCVHCGVTVVFQRWRGVDAASAWA
AMRFPSLTYVVAHTLHLGIFFGSVLALAMPGARVQHRVIGVVGVLYGAAFPAGVCYFIAR
HTGASFTRYWQFSRKPLHERLLYPVGYWHPAAQQRMYGGMLTNMNGSHLYWCVFQLSVLC
VVGLIAAVHPPVGGCHVQYFCMAAVLLAGAGVVAFTNMMRSSFLTVMHTASFALLALLCL
VSASNHLAPSDGGARAYMAMVLLLTTVLLAVAVYSVVVWYAEDRHWQELREPRRGGLEAL
LRDDEESGDETQKPHEMTSSSYASGTTVASSYRPPAPPRPVAGDIRSDALSLFDRASSAS
CSVNYAPLDR*
>TCRU_2990 Leishmanolysin/Trans-sialidase of Trypanosoma hydrophobic
C-terminal, putative
MDSCPIIDPAMDVRDLEAVFEKEEYLSARPGDKPSSWCLDTLPTNTTDARYPEETYLSAA

THAELKCLGMQVHVKVPEKRNVRWLPCTEEETIMWDTPPYNKENVICPEYAEVCTISATG
GSVIPVVSWDDEERVWGRTVRPEFLRQSSPEAPVPVAESIGSGRGTESENVDSAALQSKP
LPQGDAEAAVAQHDHQAGNNNSTPTGSEREAAPAASGENNNSPTAAVAGAGDFETTHSED
FFTTEVESPMGEEEQSAPEEGANPTTLQSRETTGDGDAQPVQESVAPLAGSEGLLPKQSE
APVPENNHSESGSGASQEDRLALLNDAKLMLHDWNVDSTARVCVSRVSMLLLLGLCGAVA
VL*
>TCRU_2991 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGGGYAEDVGVVSGDPGIRGERGGGDKSSLADGSHGGSG
GSNGDSSHESESEPSDSASNEKSLNPQVDEDEDPNSSEQPLRQGKGGSKGKQDHSQSVPQ
NGSPHKVNGAETLDSAAQVQLSATPNAELNTNVADGEIANGGRGNTGHNTGLSPNSSDSS
APPVPPAMTVPTGDTNRTASKDLQNINETTSMTPPSHSKTAAEALQTPSGNGAPKQHRKE
TDTPDLKDAPASHTAESTAKSIYTMGSDGAQKNEEKFDSGDQRSNGKEPQDGLEDRNTDD
APTASETETETATTQKNATPKFGDSDGSTAVSHTTSPLLLLLVVVCAAAAVVAA*
>TCRU_2992 Mucin-like glycoprotein, putative
MMMTCRLLCALLVLALCCCPSVCVTAQDPDSPSSSPEGTGVAGAEGGVGTGTGAEPEVVR
KNEDGPRNKETTTPNTEAISVEVQTLNTEAGVAGQSGSVNTKGQDLEEIPGPLQKPDAAS
AREAVKKANTEIKPSNTTTTTTTTTQAPSTTITEAPNTTTTTTTTAPEATSSTAMNAEAP
TTTTTRAPSLLREIDGSFRSSAWVCAPLLLAVSALAYTALG*
>TCRU_2993 HPP family, putative
MLRNDSEEMQEGQQGGDGNVVLMPFSRDDDDTGMVMEAIGEEFVNAPVSTSSPTLGPREE
SASSRFFLVYLRRLRGAGEKGPPFFAPSVDLIPTFLFTTVIMLTLGVADVYGFEPHGLQA
YLPAFAASCALTACFTTAPGAQPQALLGSHLLAALIGLSFAHATHSLEQPLGHLLASVFA
VAFLAPVCHIFGWFQPSSAATAVSAAFYENGQKDGGYIFVIFPVLIGVSIIFVLSWLLNN
LIPWRPAYPVWL*
>TCRU_2994 glucose-6-phosphate 1-dehydrogenase
MSGSENRCRFQKEVDKFFDTLRERTLRDHPQELCEYLMENAKKVAAELRGEVCERIPDAV
SPELRSRALTIVVLGASGDLAKKKTFPALFQLYCNGMLPRDVNILGYARSTMEDVEKWKK
DTLAGFFTRLDERGCHVGNFLRRISYMTGSYDRDEDFARLNERILRMEEAFQGPEKGGNR
LFYLALPPSVFVGVCRGLSKGAMQKPELGWVRLIVEKPFGRDTETSEQLSNQLKPLFNER
QVFRIDHYLGKEMVQNIIVTRFANRVFSALWNSNSIACVQITFKEKIGTAGRGGYFDSIG
IIRDVIQNHLTQILSLLTMEKPRSLSAEDIRDEKVQVLRQVVPANPAECVLGQYTASADG
STPGYLDDPSVPKGSHCPTFAVLRLHVNNDRWHGVPFIIRAGKALEERLLDIRIQFKDEI
RPFGESTQRNELVIRAQPSEAMYLKLTAKTPGLLNDTHQTELDLTHERRYDVTLPDAYES
LIHEALLGNSTNFVRVDELDAAWRIYTPLLHAIDRGEVKVLPYAAGSCGPEEAQEFFRSS
GYKTTNGNAYKCSNA*
>TCRU_2995 Protein kinase domain/Protein tyrosine kinase, putative
MGNTLPACSNGMRRFLSYLGSFCCSSKHPTRVVVGGVEYNVERLLGEGGSAYVYKGRDTR
SGNFIALKRFTLKDHQYKTQCMEEVALHRSLCPHSSIITFYDSDIVKRPGPILPELWIVM
ELSEAPTLANYINIRMAVKQSFTIREVYEISHVVVGVIAHMHSQSPPVSHWDIKAENFLF
EDSQNLKLCDFGSASRLYYEPQNALHVSIAEAELGERMTLLYRPPESLDLWSRQRVDTKC
DIWSLGVLIYLLIFFEMPFEANVMEIMDGIPRRFREGNWEEVPREEFKPVVEIVRTMMLV
KDPVKRADIFDVSQRLSALSHIPPIPRPRPGYQRPQDSRF*
>TCRU_2996 hypothetical protein, conserved
MGYKAGPEILQIVITSAIAGVTTVVRPLWAAPPLVRVDVWIDNIRIAGSKSDATLWEAQV
LRNADSRRACMGEDRESGAAQYTFLGVRFDHTHRAVSLSDKFVRSVRAMPAPNSSTVAGM
EVVASRFSYASAILGTRLCV*
>TCRU_2997 hypothetical protein, conserved
MIENNRRRIIKPTEKASAAVITDASLHGWGAVFIPDSGDVEIAGEKWERKPLLIMQSEAR
AVRLALSAFSAILQSTMDVWVDSTSLQGAVNKGSSKSHAMMWELQRICFLILAEHRKPLP
TCGLRKTPQMAYHAVVFLAL*
>TCRU_2998 hypothetical protein, conserved
MGLFTGGRGGGGGDAVGRGAVSSLPNVADAQTVVLKQTRGEGREEGALSPSLIDRSKSQQ
LVIRKGDARVGFFDTDAVDCILRRYEKEMTVADQLMKKKQRKQQEQGLFHLYDYEEDRRY
SQWLKDQEHVRATLKIHWLDMIIDKPLLCLTYFARVGTTAGLFHGAGRSVYLYRTMDKVY

IKLHGVSFAGIALHEVSLSVIKGALVAAAGTVGVVVGEAATSIARSAATGDVSVPERTWA
NVWVCGTSSGFFAGGAFAALHASILTPWGMAVAVTGFTALSSLAGLALARIAYHPFASAR
QGRTYDPYWHPWYTRRVNDGGGTYMRGKYI*
>TCRU_2999 Gim5A protein
MSACAHTYLSDTWNRDKVMAIVQFLPMALEGPVRNAGCDSLAESLGNLSKMADSYRAVTR
LSLLLNALSSKTLKDLAKPKGDALVWRLEQVSHAFHIGFCLNEHTAVLAGRGVLNSGLTR
FGGVAVVCWLYTLLLGIARQAYLLAKHSPRGSCKALLPEDAEKKVVPYTHEECKRAVVNL
VKMSCFAVFAMTCLPEGRPKLLQDVCGPLVPLHELIRAIAPNKLHLSDTVRGLLAATASL
CDFY*
>TCRU_3000 hypothetical protein, conserved
MPRGGRHAGGAGTAPSGIQGQPRNSPDYYYLGNCGGDDGGSPPLDCTSIGACRRLDRQYT
HCRAEKRCDIVGSQVLRNAAGCHATMGEDRESGAAQYTFLGVQFDHVHQTVSRSEKFFRS
VCAMPALNSLTVAEMEVMASRFLYAAAILGRRLCAYYFLITAVRRR*
>TCRU_3001 DNA polymerase theta, putative
MQPVTGNGGETTAEQKEDDGANVSGCQQEQQQRTVPTETIWVHDSPATSSRSRADAAVAA
TSNVSKHRGDYCRFKDVLMVCEPLLQGLLGPVGIDVEMNGTTAMLRDPNGFATALDSLEK
ASCDSLRHFHDSIQLFFIIRGDSFYTLDSSVCSPLVFLAKLLSVPAVTKIVHQAQPIYRL
LFMFLGTDRVEVRNLVDISVWSAVVERVCGPRPYTKGFADSQSLWQSLPETSRESIEVQL
EKAKQERWCEGTLKAEEGEATMVLSSSSPSSSGEMPLPQLLGRFKSLATLYAYYEAYLQS
VESSGATGNVFMSLFTVCSLETRVSFLCEVMSYHGMFVEKNMLDSMVADLEQQIKALIEK
GNVALRAMATASNESIEMETVDAWNLIKTLQSQFGGPWTFAKGNVEEQMQQIGAYLDEKQ
SCADSNVARIWLALHERREFKRSLMEGFTKGASMHARLIAVPEEMASTEGGGHSNPHHVG
AQYRLFFSVHPKWSVHHATTSRLFCSRPCLQTVAKNPPISRTAPSSSPPVTIFTNPEWTL
RHLYGPPPGCTLVSLDFNQIELRVMAHLSGDPLLVQQLRGGSDVLAEMALRVMQLPRLAD
VTPYLRQGTKVVVYGLLYGMGPESLDLRLRQLHKETTPSAEQPPLSARQFLRSFNQCYPA
VQGFLKSTRLRAFHEKRCATLNGLRDLSGEPDGNRRKQMAVALAIQGGAAVILHHAMVEV
HEKRHELVPFLPAAAVALVLSVHDELVYAVPDGAVSFVAPKIKQILEQQAAALSLSVPLP
VSMKAGKSFGSLQSLPV*
>TCRU_3002 BNR repeat-like domain containing protein, putative
MRVGDSYGRHSLERSPREYPVADTAAAGHIFRNPHLVNFDGLLLAIVGAQFNGSVRSGSA
SMQLMARISVDGGRTWRSYAGPEDLDAFAALPHRMSFPSSFGPLGSLLAFVEGYDLRNGA
IIRFTDGWGGSGLESVIHFLETGPGRSGDLSMSSVSMSIRPPYPYKSDDLIGFLNDASTP
ITKMTDNTLVFPVQFLTRGGDTASTIMYWNSDQQHWTLAKSATHAGCTNPSILEWEAGKI
IMITSCKYGRRRVYESTDKGEHVEGGSGDALARVEQLIGRFWAPHSEWIYHCNYWQKEGD
PPHPAGIFQTREQGRDSPVANRHEPHLPRWPATHWVWCNLQLPVVRE*
>TCRU_3003 Paraflagellar rod protein 2-5
MSAEEATGLEAARKQKIHNLKLKTACLENEELIQELHVSDWSETQRQKLRGAHLKAEELV
ASVDVGTKWNLTEAYDLAKLMRVCGLEMSQRELYRPEDKAQFMDIIGVKKVLQDLKQNRN
KTRVVSFTQMIDNAIAKMEKVEEELRRSQLDATQLAQVPTRTLKQIEDIMNATQIQNALA
STDDQIKTQLAQLEKTNEIQNVAMHDGEMQVAEEQMWTKVQLQERLIDLIQDKFRLITKC
EEENQPFKKIYEVQKQANQETSQMKDAKRRLKQRCETDLKHIHDAIQKADLEDAEAMKRH
AANREKSDSFVRENEERQEEAWNKIQDLERQLQKLGTERFEEVKRRIEEVDREEKRRVEY
SQFLEVASQHKKLLELTVYNCDLAIRCTGLVEELVSEGCAAVKARHDKTSQDLAALRLEV
HKEHLEYFRMLYLTLGSLIYKKEKRMEEIDRNIRTTHIQLEFCVETFDPNAKRHADMKKE
LYKLRQGVEEELAMLKEKQAKALEDFKESEEALDAAGIEFNHPVDENNEEVLTRRSKMVE
YRSHLSKQEEVKIAAEREEIKRARLLRTGGGGSGEQPRIGNNTAPARLE*
>TCRU_3004 mismatch repair protein MSH5, putative
MSGICDTEEEIATYEVVSLLVFYHEVGLASYDSATCQVSCSESAAALNRGEEMFIGTLMD
VPGDIVWVAQFLLSKKPKVVLIPSGGSQILIDVANLCGVNVVLTAPREFDEGRIWDLLGV
LWANVTRLEWHSRICPHHHVMLMALSALLPYLQRSELPIADVAEVPPLGLLYIEQETLSG
LQLLRTEPHPMDYQGIGRAKEGLSLLSVVDRTCSVLGRALLRQWFLLPVRDESELRRRYD
VVSFFTMQENYDLMMQLRRALRHLRITNSIFTKIRAAKHTTNDYESLLRTVRGFLRIASL
LTPRAHFSPMFLRIVASCQTNQLEEISRLIDEGVSFSRDPGAALSKTYVHIRPGFDAKLD
ELCAHFIHLDEVLANVAQQEARCLPPLWGLCSVVCVFAPCWGYVITLPRFSLPVGREDIP

GWELLFQTEEGPFFKTPLTRRMDEEIGDLRSAILVREGEIQRELDKRLIVLSPALIPLHL
CAELDCLMGFALAALEGQWSRPEIVKEPGVLVIERGFHPIFARTAAHQVVPYSINIRTSN
QRVCLLTGANGSGKSILITAVAHAVFLAHIGCYVPCTHATIGLFDTLMSLHAVSYSSRDR
TLASTTKELHSSFGNELVSMSRMLQRCSTRNKEGGAGSGRSLLVLDEFGKGTLSLDGAAL
LAVSIRSFISFGDRRPIVLLATHYVEVLQPQLIPREEIMVLEMQTTLVPTARTGGEGGED
VCEGFIGGSQLVHSYRVAPVQALSSMDTIQQKGMTSHALRFALQFSVPPLLLQRAWDLIV
TESL*
>TCRU_3005 MORN repeat, putative
MPGARHNFGRGFPNGDQYDGETIEGNINDGKCGFFETTGGAKYVGAQLLGKPHGKGKYIV
PGAMGYIYEGDFVNGERSGNGVCTFSNGRKYEGDWLGDKMHGNGTLYGAEGVDDFVEYVG
PFVEGERSGADGRCRYVNDNIYKGLWLHDKRNGRGELVLGRASSTPGYTPRMGEPHIVAY
KGKFENDAPSGMGEFLYSDGSSYVGECVGFSRHGEGLHRKLNGDTYKGGFQLDRRWGKGV
LQNKYGEYNGEWRDDLLEGHLIFRGDAAGAVATDLIFYEGPCVSGEMVGNEVVAKYRDGS
SYKGAMVAGKPNGIGILEKKRIKIPGVGEFMLRYEGDFMGGVPKGSGTGTLTLLTADPRT
APSPPISAEVRCFIPQLDVSGQYKGMWLNGLPNGDGDWQWVNEQSYRGAVKSGIPQGSGV
FITPKVHYEGSFICGLPEGYGKITWRGTEEKKEDTYEGSWKEGYLDGEGKLILHDGSTYT
GGWKSGIKEGNGVDSVVKKYHYSGELKEGKRHGKGTISMLKEGFKYEGEFVMDELTGNGT
MTLEDGTVIIGGFANGKPHGNVKITLPTQDGFQGEFKHGVVSGSGTLFYNGGKYEGEVAD
SGNPLPMRHGRGVYTFIEGDVLECTWKRNVLHGDGIYTTSTGDRSTRSYVDGVLKAVSPQ
STDAPPSQKGFPIELSEEEQQQQQLHKKQVVSIRRSLPNRSPSNSFQRSLARQMSSSGT
TRSTVAMPKVKSSSISIMTTPKPVSPRSAAVASPSFSFKSVLRISESPVKPLSAMTIVRR
RTVTGVAGNGIEAGGSSHLTPFSRFHDGIKGLPSCTESSEEWKGAQLNTSYPVAGGDKGL
VQSTVVRREAREGEIHSLTEALRRINEQIWQESFMAGLPVTAGNEGLKLTKASRLDQLES
LQLERRNIVDKLSVILR*
>TCRU_3006 thioredoxin, putative
MKVAVGFLQHCLVRRRTGTSVTTVFSTAPAASLSSWTCATRRHIATFRGHSREFLDEVNR
EKVALVYFYAPWREPRNRVYVKLEELLNKGRPAVRGGSEATSSTSLASSSLSSPSAAAAS
PSKDPAAEGTLQPGALADPKSRVDPEVLLKSVREFCVRARANGRTVRIIPVNTDENPKLG
ALHDIRSVPTFVTYRDGRIVGRVEGFSEDQIEQLVKELLQEDSGDTPVTDQAKRNWKSKE
CEETKKGEKK*
>TCRU_3007 serine peptidase, clan SB, family S8-like protein
MLSGTPPFFLMTLFSLTLMHFLLSGVGTCAASAGDAAAAAAAAASKRPLAMRRSPLQKWL
HADWLKIHETPLHWFVQKHHHQYPHTGENSTSHVASACDSCRTRRPFLTARTAGLSGEDA
SLLDSDDGRYVVVKLDKLRWKERRNVRSSLMRHRLEDTHIIDELHMLVYVDSERAAQIRA
ALEAEDRGVSPLTSLTVLDVYSTPTGARLKLSRAIRFSMHRCGARHDKSAVDNKPMEEMD
LRWRLPLDVRTALGRENVVERSLQSVSSKTRNVSAKCQWNIISSIAGKGLVRWVLTLSSG
GKKEEEKEMDVVCHCSAFINTVVSHPAVRWMEVAIEHVAPLNFYATALVQNGNQDEREPF
RPFWDAGIDGSGELVGLADSGVDFDSCFFSDPKESVAIYPEVNHRHRKVISFVPCDLFPG
ERLIGDKKRGHGTHVAGTLAGYVLDDDENSKYNGVAKGAKIFFTSLGVPSQPLLTLPIDI
TEVFRPAYKEGAHIFSNSWGFFAPDEYTAVEKSMDALANQMDDALIVFAAGNSPNSGLLT
PCRTKNMICIGAHKNTFDPNTQNTIAKFSSPGPTYDHRVKPELVAPGDTITSAFSDGNIS
TNQCAVVSMRGTSMATAALAGSVALMRQHLRTLENISSPSSALLKALLIHCTVNLNNSRL
SGFGRLDMSLFFTPTGIIGWFRDRDSIGHHASKVHHFTLGPNLLDVNEIRVSLVWTDIGS
AMEGSAISLVNNLDVLLVDSKGAVYFAGENKTLDTTNVMEQICLPISWELAAGFRVFVYG
GSVHEGNNQPYALVVSGPGLSYVDNASIMSGVVCPNNCSGNGNCFGGICECHTGYRFIDC
SFCDEEAMCNGHGTCAAKDLQCKCDNEHFADEHCSSCKPGWYGPSCSSNCTCSERGKCNM
ETGECICQKDKTWGGSGCFSGPNCEYCCEDFAGEKCNVRSYWCREDGWPFEVNDTAGGYI
EVNGYGTYSPMLVCRWVVKAPRGRIIRLQYLRFEVESPTDIVVLYDDASDEAEPIRVDTG
TSAQGLLFLSSSNALAIVFSSRWSHVRKGFLMHYSFEGPNNSNCTVPCVKNALCDVWGGG
FCVCNEGRAGWDCGVEVGSDNKVIELQEEDKRGATYFTPLVNEELQLNLKHQSPNWVRTD
VYLALESSIFTKQQGEMALRAAAIRSTPSGAISIKKEKKIGWTSNCRYARISLSYRLSAP
KGELNISFTLLNNASLLSAANGNASYRAAAYLAKSEPQDIYETLDTDDRLLLISCSSDLS
SEVPLSVFGDFLNRTNDASEGRTGVSAFVAPLLLFVFFASGFFWVPLFFTWRPRQGLALA
TIPTEEVMVLTSSSVCIGAEDDARIESGDGLFSSISVFSETHEVGETSTGAA*

>TCRU_3008 ABC transporter/AAA domain containing protein, putative
MGDCGEWRSNPFNEMDGDGGNQEERNQPNILVPEVSDAASEEDGNEVVLRLRGIEKSYPI
EGTEERVVALRNLNLCEDCGRDGFGPIRRGEFVMIRGPSGGGKTTLLSIIGTIDLPTSGT
IELMGTVINGSTPDSLLADFRLRKIGFVFQTFNLISTMTALENVELPMTLLGALSAKKRR
IRAFRLLALVGLRNRLYHLPSELSGGEQQRVTIARSLANNPQLLLLDEPTGDLDTLNTIQ
VMDLLVHLNRITKTTCIMVTHNPDVECYADRILYVADSRFVKEVRNSCPQRLVYEAYVKN
LEKREAESTAVVCSFQDP*
>TCRU_3009 Zn-finger domain protein, putative
MSCSTSQGEEASKEAGDNTRMLPSTGEERNTEHSGVSQDEEEREEQQQPQRHEPAASIFH
EDAHETPDADHDGEMECWICRSGGGTTQNPLITSVCKCRGSVGWVHRECIDAWVFSRRRA
SCPSCGATYNILAISDVSLPQTFFEQLCFFFWDLILPLSAKALALLLGIALNGFVVPCII
GVTFYHKCFFNNGDAATRTSEYSSNSSETALLQGPEEGASTFLDVWLWINVMAYGWICVT
LWRCTKTGWCQWRAFFEDTDAVFATATEEVQEEEEDDDEGEDEDEEDDDDEEEGPRLQPN
TVVGMLHWILDWSLERTGSSQKMLRPRILELGTLVPLSFLVNFTLGKLLLCLILALGLVL
RRLLYPRKRINDPTRRFAEAQERKTSATEIDIALWFITYLSELVLFSILMTTFGGIVVHF
ALSPYFLTFPASLSAFAGELTLTRLLAYWLVGSFCSMILLHVETAIIVPLFAPGVELYFV
RSVDLNLEDDTAYWKFVLAQVFDTDPLGVSLDFIRFCCIEMTLLYVFLATPIYVMFAAHD
VMIKDGANSTLTSPLAPGFPVIMVTPAVDGISAWLESYLVPEKSRLLESYYQFFFSLIEL
LGSCFARFSLGVILWFTRNPYWLKCVANTLIVFGTGTAIVCVRLFPIKHMQLKVLRHVVM
FIGRHVVHLEDYLFDKERLSLLDSWLRGDGQSDIPLPEARLPSVFRRREWALPPGTAHPK
YLKLRVAIFSFLFFVTSSALFWIIPMAVMTPLLTVLPYSVPLLCLSANIIFFVFNPKMYF
TAAAEFMLLCIIFVIGVLLQPLFFCASLRNISRLQLIQETMEYYHKLRRTVGVYNGEAME
AA*
>TCRU_3010 hypothetical protein, conserved
MRSSFNAAFGRLLRPALFHALWPGGCRAFCITKPTRPLLCLSGGTPEVLEVELLLPDDVD
EGRNNKSRTNVDGDDVDDFPELEEYEASKEAAAETITTIDTFARAKVANFAKRMPHSACE
TSSSASHLLAEVREVQTAGDEEKLFHARVRVPLPPEYGERWGEGLASTEKEAELVAAMHA
ERVIDAMGFPMFQLTSKQKRHAEAARNAGRWAPMPGDDPRPPSTPSPPRLQLLREGATKE
VERRLQIDKMEFSNVTAGAFTSMKLTLASPFLLDYGSVNRIKQFFAAYNCNIQRYSRVTP
LHKCVSKEKFGGSGSGEAFSHTGADNNNNNNNNKMFVAQIRLPIDGRFGERIACGKSPTK
KEAIALACMHAELIIDALGLALYPSDKEKQETHADECRKVNRWCSGPCGYEYHFTKPSPP
PLQLVKESSVKTAAEVDSAASLESVLLSHAKAIEKFENVTELQRIDPAAHHIFVSYMAQY
REDAKEVGSLFFVESLGVKGHEVYRATVTVPVPFVAGTTASTGSASVHDGDDVAVSSFVA
IGIGTSEMEAETTASMHALSVLKSLDRPLLGSSTVGREKFQQRNLTRDTVIPPPYRYVVA
HLGRIVVPGLSPARNIGGLPLAARQRGFSSEYHEARIQGARAGLPKSDWSLDADAEGYII
QNPSVNVQETRNYVHTLPSVRQADRFALVRLRDYLERHGKRLEAAVTSSMLETDEGLKRW
VKKVVLPVPEAFGHVVAHGEAYTEEEALVMCAVHAELLLDELGIALYDLQALQERHCDAA
GMLGRWAPYETHSTRRAVPTPPPVRKEHADSCLWARLSKETRKEGTAPCGEGIKQTVSST
HPPDGNYKAADGENHTDATATRKAEVVSPSPGVTDDALFDLAGLVFVHPSEFFRHAPRLL
ESYCGRQGVDISRCMRQYNVCNPLYGFVHRAIMEIPVPPQFGRRYALGCALTKKDAFFLC
CMHAVYVLGELGIPIYIGPKQAEYAAIARSKGRHAPNPGDPLRPPNTNSPPGLKSLPDMH
MEKPPLPRPPNRRECHKSRVWQGYVTACRGYIKKMKEQVVWDALFTKGKAPRSGVDLEDN
GLDVVEALPLFTNVKSRLPQKCAAARLPAPPPLSFRFEVYGRPPHRRYLVEQPVLGTPFV
ARGMGEEGQEAVTRAAMHYEYILGIISGTVQGNSETGNFLRNRHGDLFDPTLRDFTPRGK
LAIMALHSTLRAPFLPLRLTLKERNNSAAGVQLVYVSLVEIEDESGLRMAGKGEDRIHAE
ESRNRAIAELYKQLQRKATFQAVAQLLQTYPALRAEGAAHMLSETKTMRDLRSVLAGRKD
PIPLPLEEFPEGAGVATLLRGGEEHLDSPELRLLFNIVERELVSMPTPAPLNLPVAAQHL
LRTMGLVKTQGGDEKNKKTIEANAIRVAVALFSLCLPPLLPMREGASPLVIGALPLQLAK
LLFAGSLLDCLESCIRVVALVLSSFIGENDVCRSGDVVELAALELSQEAKRLATVIAARL
RELSKQLKKLTSPSHILTTLVDSSCVVSEGTWGPLQEGWGKKDEGRLRLAVSFATFPRAF
IQKKVAADGVLRLITVESRDRQRTAQIAVPPNLAKSCNASSDPASSSLSPCHSSFPWFCA
FDGASAGEGEELPMLGTFVPPCGLLLASAPCDESRMLVIPDDVPNMAIVDGFIPVVMKST
ESLATITELRLTLKDHWAVLKPLPVDTQDIVDKLLVSEHSLANVLQAELLD*
>TCRU_3011 Integral membrane protein S linking to the trans Golgi

network, putative
MPIPLGAPLSDPKFVFLQILYTLSMFFIMLGVVRVVLGVLSLTFIDSSALSVPLFTSLGY
CFHVPLRSLFAVRVEDVSDGSAMRFFLMHLLTACFFSGPLALTIQRRKFALDFIFTLYAM
YYVFCCLASWRLTGGGFAWWVSVLTGFCVLYGLTFLLCGRRELQDIFFPLPTAPAVAVGG
SGGICNVSNLAGGGDGDVMMATLGAAAEANGVDVDGCSFSNGCSSPSAVTEAVLMGPGSA
RKRRQ*
>TCRU_3012 hypothetical protein
MQLPHGIVRVSTPSHHGSQRRRARSAYPFTRSFLADTITSNDATISPPLAATAYPWRNAV
PGKCILKTPRARDSSSIVVVAAAAAKGHRRRVHFDEGSILTKGINGGVLDRDDAIGVSLP
ISGINAPKKSLNASVAAEVPYTVAWGEDSEWFKELFGLKAPPSRGSKRNVGPIIERDLTL
HSNTKEDPARCTRFVGHRAIISLSHAMPNTPLGGASWGNTSNFTDSARSAVHVSSSRSRP
RINAVRRVPEDHAHARVAVGRGGESNRFVTPPRLRLAPKVSSTKNCFWDRPKSLSVEWKS
EWQVIPPQRRLCNFTAPQLCFVNFGRDGGKNGRRRRGEWLVPTNIHA*
>TCRU_3013 hypothetical protein, conserved
MDLPPSENPALSESGPLAFRARTALLEQLRDLHRQEQQQQKRRGQLRLSNNGPQTGTESN
NDDDSDDESDNSAPMAVRFVRGCPPLTDPSWAMEELLRIDPNVALWTGTGLSTAVWAPPG
SGHCPFGTTQADFIRHR*
>TCRU_3014 XPC-binding domain/UBA/TS-N domain containing protein,
putative
MKLKVNCSMGGEGKITKELVIHNPAATLSNLRAAIAINFRLPVHGFRMIHDTADFACEKV
LLRDSGICDGDLIVVDAKREREDETGGVNKEQKTGTEVGPNQQQRYEPKQAAAAPTALVA
NTVTPASAELTVPERNANAAEEPDGLGDGGTAAGDDDEEEEEEEEDGPAELLSHLLETVP
NLVEMRQQFLANPAEIMQQIQERDPRLLELITSNYQEFLDLVNNEDLVETLQREQEEAHA
AIFGEEEELDEEVEEAVSSLLAQFTVRGGLPEEADDESTEAQNYLERPLTEEEEAKVEQL
MQLGFTRDQCKVAFFKAKRSLERAANLLFEDPPQL*
>TCRU_3015 hypothetical protein, conserved
MSSVVQTIAASVGGRFLLLGCADGLRAYDVHSLGIVKKIIPSAGETPATRGCRAVGGPVR
VVAVLGETPLIAFVLEGGVTSELVSEGDLEGAAVSGRSTSSVASTSRVLCLYDASKGQRM
AELHFETEVVGIQMNTRRLVVALVECIHVFDLLTLEHLAELRTASPPNPNGLLVLSELTT
NVHGEAVSYLAFPQSDQGYGDVWVAQITEKPMDREGEWTDVVNASGGKRCGFVERVSIVK
AHHRAVVCMAMTRDGTRIATASERGTTVKVFEPSSARLLCHFRRGVKAARMLSLSFDTSC
ASSGLRLAALSNRGTLHVFRCSSTGGSELVVHESLLPYTGSEMRSFAQVTVGKASTASCA
SPSLGLNCKMGNELQCCFFSQNGQFLYVVLPAPCVMEEGTARIQDAAGSGTSLLSERRAD
VGARWMLQKYAIHMHGCELVNSHVLN*
>TCRU_3016 Rab-GTPase-TBC domain containing protein, putative
MKNRVRTGALASFWPEETTPSDCSSGGCGDGGERAALDEIPGRGVGAHAPDPVDTSIKWT
EMTPEVFSPVDWASEERLGFPPSSNLEVRAAEMDAEPLLRLAAQRCEKHWQSYSRGLPLL
ATANAKVEEFMRRAMWHHGIPQHLRGVLWLTISGVASKMDENQGFCRALLKRHGYIRGEY
AEAIEKDLHRTFPEHRYFADGGLGIRKARNVLHALCWRNPLLNYCQSFNYLVAFILLVVD
DEESTFWLMCHLLENLLPNDLYSESLIGTKVDQLVLQALLQERLPRLAQHFSEVHFEVET
LVSAWVMALFINVVPVQTLLRVWDCLLAGWSHSSEHSCVPLEVVLAVLKLHQNELLRCND
AGDVLMCLDHATKRLFDAEKLVRLIREMRLSPSNVRQMRRSARPTVAEEQYRREKRRQEL
LEKNHLGYEKKNGGIIQMWRSEEKEKDDVVVTVEDPQPISEAGISGQHREFVPAPPVESR
QKEYRERFAGTVFVEVNAWHQIQKGKSRLGNAGGAVDEDSERPALSECAVGTRRWRRREE
SVGLEMESICTANRDQEEAEHQ*
>TCRU_3017 hypothetical protein, conserved
MARGRRESSAVAASSSSSKSPPGKKGGRKLPVVKSTSIAAALRQASCDSNESAVILRGKA
GVGVKGQGACTADVQSHPQGSRLRLQQSAPQISFWKGICRPTLLVQALAKIGTLVEAETA
LLFANSRVRYPFSALTVERVLTAIQAIVDAAELLRTVGTDGNRAVFSNDAMCQRWRVIGK
LIELAEAAVPMKVSLLAGSTTACESVTAGLPPVSLWALNGRLKCLQRLLQLRECHSRILS
TLRLCKTRNEVSAALFGPSMIEAATIEPMPGVAYWHQGEQFVIKGLMAEVNDITPCSESW
GPSSITPLRVAGGSYVLHKHSRFETLACLLRVAEFIGLPPFLRSIRVAGGRSRVFQPQPS
KMKSVDDGSLHIYKESLPLLFPSSDDLDPRHFEAPASNHAQLVQEELVKLAGQHCCFGAL
VGEADQVVALLHESAACLQRRKMASCDERTVAIKVEREEDDGGGRPLRRGVMDASGDDPL

RAYAESLLQAAKEENSKKNRVRWLCGNRWSPTMSYYALVIATALPHKTNDVMEAEEDREA
GRRVDFVASYYVAAVLELTRF*
>TCRU_3018 hypothetical protein, conserved
MLRITSACRGGYMMYHRKSMGTMKYSKWKGAHGGVSHFYGRTPMVEEVKRNEPITLIDRR
IMHYVHRSRLRHFQLFRSYQQKSNATECKLREGEMLRRRWHRKLQKSFIAFMQFKTMKVL
EDQAKLVNTYGQAAVNAALGDSWDAVSDKEKDRKYVTIRRQVKALPVVSVVPKHVATMKQ
IHNDRFNYRWRVN*
>TCRU_3019 hypothetical protein, conserved
MNQVIRSRTDWKERVVSRLAWITASRLFEIAALTANNFTLERDGALILDWSVAPKTARAD
SHRASRFVRIREQDAFDTIKLCRTLQENERLTNLTTAKVERALAPWDATAHSIKRGALRH
AAQIVETYNLNPHVISQLARHVDPFDLPQNTV*
>TCRU_3020 retrotransposon hot spot protein, RHS3, putative
MKLNDFLEMELEGRGALDANQDVLLEEFFKDPKKYICDAGVLGEMQASDRYKRMERAVRD
EMDMEEDVRKLYKNGMYYLLNWLAASAEVKASVHAVTKRFLDAAAEEARKTKKSSAPRYL
EGLYESVHNAKWSHVVEVSGGEGTGMEVREGEPPQPWTYRAVGGTLEKDDGVEQSGEARL
RLMVLTSDRGWPYSWNRKENKSTHDCHVNCEVERVWQIVRGDLTAWFSSHGRTDFKFERR
LLIGTPGIGKSMGAGSYLLYQLLQYDVEKLQVVAYIFGGSTTYVFNKTIKTVTRYLGSKT
SRNVLYGLWHLKMKGYVIYDVTEKGMPASCFAPCGEWGMIVLSSPNVGNYEKWETQVRAE
RIIVNCPDEMDMKAMCAWMKRGLDPDKQAEYWKEVKERMEKLGPILRYIFDANKFIAHSA
AIEDALDGIKSRDGEKHFTNGGVKLWYSEDPSQKLVRVVRGRGEVCAEIFLNAPISVCLG
RRIPHYFGGRDE*
>TCRU_3021 kinetoplastid membrane protein KMP-11
MATTLEEFSAKLDRLDAEFAKKMEEQNKKFFADKPDESTLSPEMKEHYEKFEKMIQEHTD
KFNKKMHEHSEHFKAKFAELLEQQKNAQFPG*
>TCRU_3022 kinetoplastid membrane protein KMP-11
MATTLEEFSAKLDRLDAEFAKKMEEQNKKFFADKPDESTLSPEMKEHYEKFEKMIQEHTD
KFNKKMHEHSEHFKAKFAELLEQQKNAQFPG*
>TCRU_3023 hypothetical protein, conserved
MPYRLLVTKIPLHVGEEEFYDYVRAHVSGEAVVNALLIMLPGGGGASTLISSSGAALVDY
SAKNAADAARRVDFYVDGVAVMMKAVGSVPTPGRHTELLAEEGRVAYQRLRRGLSHADRC
TARTDAAAGQKRQRKDENVVVVDDVDTNMKGMRETDNQKAEEVELRLVGIPHDVYGSLFD
EGVAGSGSHTTRQSTVDLFTDVALTIRRATLGELLSLRRITDDEAVIRVFADTADTLLGR
AETGLQLLIQSTATTEDAKEFLKEPSDQRILFVRRPRPQVRITGDNFALATKHDVVGAMA
RIMELTNAKVAGFIDPFGNLLLPSLN*
>TCRU_3024 CRAL/TRIO domain containing protein, putative
MYSPDSTLELRLPRDLFLFPKQNAGFQIPFFLSTEEEAAKVRPPAVVKTLEERLQEFSEG
QREILSSFKKAVRDAPWYSEAEDDDWLLLRYLIARNFDVKKSFCMLEKSVHWRRKKDADN
WVCEACLKDPNRHMMQFVGWDLQNRPVCFMAMRWGPDRKEPLKHCVATFNHLVKLMPLGV
EQWVCVTDFETYSHIRDSSPKMGLSVIHAIQDHFPERLGLMILVDAPKAFSVLWKLLSAV
IEEKTRKKVLFTYKKSKPTIESEFSKIFPPALAEYLCESYERSRTAALPATPVWYPAQSN
E*
>TCRU_3025 membrane transporter protein, putative
MEETYVRLPNGQLSTDCGHYSVPTQRQLLGDLMRIGLPLSASQVSQFSFIIVMFFFAGHL
GVQELGSVSIAIGILNATGFAFGSGLCGALETLLSHSYGLDRRSTMYGVYAQRMFIILML
FSVPLAILLSCLTPILIAIGEPTYVAEEVGSFCLICVLGLPAIMLLELLRRYYASQHRSN
PVFLTLAMAAILNPLVQYICVFFGGYKGIALGWVILLLLMDITLVIYLRVSGLYRHTWGG
WNMAAFQNWIPMLKLAIPSLGMAFSEWSAMEVNSVCAGLMSSVQLGAYAISSQLSNLCWS
VVSGFFMASTVLVGNSVGEGKPQLGRRYAMLSFIVVFALSFVNISLLYLYQEQIAYIFTE
DPEVVSIFMSITPFFLVYHLLDSIQSNFLGILRGCGLQVIGVFIVFVGLTLVGTPLGLFL
LFRCGYDVKALWIGPIVGCTLLAIPAYLFVFFRRVEWEKLKPHIEEQFEGSINFAISRET
SSMAF*
>TCRU_3026 MATE efflux family protein, putative
MSVNIHSVANDSFATAGCAGGMEEEKPLSVDITTLEIVKKFLVTGLPLSVATLIQFFIIT
VILAIVGRTLGVNELGGAALALGLINATAFAFAAGSCGALETVLSHTYGMHKSSGNSGTM

YMYGTYAQRMTIILLVVSIPLGVVLIYADMFLEYIGQTKEVVYYTGRFCHIAAFGIPSTQ
LFQLLTRYYACQHETKPLSFVMVAASFFNPISQIVLIHFFGFEGSPVAWLFLYTFIDLSL
VGYAYCTGLYKKTWGGWNINAFKNLKGLLKLAIPSMAMMLSEWVLLEVISICAGFAEPHE
LAAFYITMQVFGLCWSIPSGTMIIVCVLIGNAIGEGKPLLGKRIANVALVMVVITALLDI
TICWLLEDRIPYLFTSEESVVVVYRRLLLFVLPYHLFDTFQSTVMGILRGCGLQKLGALI
IGCALCLVGVPVAFYLFFHVKYGVESLWIGPFLGVTAVGFPSYIYILYWHIDWSKLKPHH
DEGIVVLEEEEEGKGGSEEAREVTVEAREGVASCS*
>TCRU_3027 Fusaric acid resistance protein-like, putative
MPGHHAEKGNGDGRRNNDKNTTISEGLISLDGEMSSFDDAIDKQNYHKGNGSFGLPRYVP
RYPFDQSRRESVLNVPWHLRKPGGLEQCTFFDSFRSVKFWRQSEFALRITLFAVLLPASL
IAAELPNSPFVSKTHCLSAAVLASKVTVGEGLAYVVTWTRAGCIWLPLATIGAAANLGNY
IIGWCFFYTLLLFLMAIFTENMVRRICLLLFNSCMFGILMDPQRGTVYPSRVMSDWCIGT
GLCLVATFLPYPVFSKNKAHRALAEIARNTGTALTGMSSCFWSESNVTRNMAMTKVRMMT
AAIDLLMQRFRTAHEDSFYEFIFEGFEPWEVREAKVKLFERLRANLRGLSRVLDILESKP
WVVDDSERSRAFGALIQQHVLRFSNSLDKLTEELASTSSFGQIRQLHGHFVELNDVTVKL
QHEFDQARRRLFYENKPGTLEEFVPLMTFFIFSIVNFRDTMLQFDSEVQRRKHLLRNSIK
RVVDKTMLEPIQYTFRFCRRLVTQWRRREIQSLIEAAKVSAAMILTVGFSFLIGIDKKSL
SGPNIIAFVSGANPVEALQASIVRLTACILGTVMGFFAGSYSSTAVQKVASLCVLMFLGT
FFRTDKDYGIMAVYAMFVLIPLDTVGHTTTEDTLARMNQITFGILIYVSISVIVLPLSPG
LILRKKRINILLRVSEALTSLCDMFSEPLPIDSMHCSTLPIYRESIVLDEHYESSNLPDA
DFLKNASTRLMVRVDRPMLKISELLDEIEGRLEATYPFMGFARAERGIVDADYPAKSCEK
TTYHLYRIVSLLRTAWCSWEVLRTQKHYAPDTRHVLHCLQPIAWDVCRSFQRFVGMLCYS
LRNPQVSLEMELIQVVLELIQATEELHLRKNQMMLFIICNSVEKHVRYKKEPDFFTADVT
TVQSAPHKEKGLMALGGLGRKRVDDGGSILPLLRKGTKANLEEDDSPEPPESVALSDNFV
MPITGADAEGLHSFTLSMQMFADETKKLLMCLEEMLDHLRKKM*
>TCRU_3028 DNA repair protein RAD2, putative
MGVHGLWRLLDTFGEVTQPSDWRGKRVAIDASIWMSQFRAKCTSGENMEQCILEGFFLRI
LKLLFYGIEPVFVFDGTATDLKSTERRRRAERRAALERSALTRRAQQIFKAQLASGLLNV
QALDQKGPVKTAGRPPSPKKETDAGMLQRSSLTNISDTATGCCSTNPRSLLRKRRREIVL
EPDAISRTLTNSFLTEAEEWIEERKRGELCVEANLLFYSSTSLFMGPRGVLEDKINGPIK
AAVLPEKDTNPPAYMSLSSLSSEEASLVISDDDKTSINDYETVSTGITSSRGSVVIVGGH
TETFPDRLREMEEITIHSLHDDSCDTWLEKDMATCDDILSFCNEGDSSGGSGHSNSDHDD
SVQLWNPGTQLICQSSAETTRKHREVSDDGIERPKAASIGSVEETTSEGSSSPVTKNLMG
AVDVTRSLETPSPSHPPQTLLPKPITKGAKAHQVIPFELLEILELLDCCGIPFVLSPHEA
DAQCAFLSQQRLVDAVFSEDSDVIVHGANVVLRGFFSKNRYVVVYRQSDLAMCGVDKDVL
VALALLLGCDYAEGVDGVSLLEALRIITAFWHQESVQGPSHVLDMLKRWRDAVAQRRFVW
EEEGVLLQSYLNWRRWSTLRVAADFPQVPVVDAFFNATVDADMRPFAVASPEWNRLRTFA
GMHGLLGDVTCQQRLELAQKAFLARELQRNNERKQQQLRLTDFAMPSHAKEKVAYKKQPP
KFAAALSALRAARRSGVRVDCCHY*
>TCRU_3029 methyltransferase domain containing protein, putative
MPAEELHCSEETRKRPRDPPFVVDYRPYTARQLAHALQKRTTAQKEHWDVYYRHNTVNGY
RDRHYIISEFHELRETLERLKEESSLPATDIIWMEVGCGVGNAILPILEEYGEVNGWRLV
GFDISFVAIALLQEKRHSLPENCQEKLSFCVLDPVEEDISVAGSTSASPLAIAESSVNFV
SMIFVLCSIPVEKHLVVLRRVAFCMAEGGTIFFRDYCVNDHAEKRFGTHRRVEENTFTRS
NGTLSHFFSLAEVRQLFKDSGFEEVELLVVEREMVNRKKGTSMHRKFLQGRFRKTGGAKT
TKITKLDKEFLAHTRVKECV*
>TCRU_3030 cyclophilin type peptidyl-prolyl cis-trans isomerase,
putative
MSVVISTTRGSLLIHLRYTDCPKACFNFLALCASSYYDGCLFHRCVTNAFVLTGDPTGTG
KGGESVFAPEQRYFDDEGLGTVHHDSRGVVSMAHRGNKPNTNASQFFIIFQPCPSLDTKH
TAFGCVDLAWNDGESERTLKKLEELRVDDKYNVLDKDAKIVGTTVLYNPFAEGHIKLDV*
>TCRU_3031 Iron-sulfur cluster assembly protein
MRRFTSTPLAANAAVASLRTLYSALVEDHYNNPRNMGKLDKTDPNVGTGLRGAPECGDMT
QMQVKVNPDTGVIEDVKFKAFGCGSAIAASSYASQAIRGKTWSEALKLTNKKIAEELSLP

PVKLHCSMLAQETIQAAVENYLSKNPSLKSKVQKKQSTEASTP*
>TCRU_3032 hypothetical protein, conserved
MSTSAYRVASLLRQENNKLCSDKEKNTLARLTRDVEAFLDHAADVPPVVMETPYDDGETD
LMEVHLSVVAGVLEPCEPASDVTAVDGVFMPTAKNHVAMDRKRVREAQAMLNLLGALSTD
CKMPTASVAAATRCRLSLGSGEKADFESDDESIAVFDADELENDTSSSDGESNVHGRPPP
RILELN*
>TCRU_3033 hypothetical protein, conserved
MPPNARLRIRLIGPSGHKSEYHCATLLGNWQEERMSFGLKDPAKEPLEGQTTYLASYRGT
NNDEELLAAKPPGCFCAEAPVQLLFYHGDIVAPPQSQFTVHELSYTRPTRDVGANPPKTI
LDKEGISQRREKTEALRRAMGFSGHRTAVGAPSSLGRNTEAAPLAYSTRCATERDNEYTR
TPRRGHYQPAKLPPIGRLQAKERFLTTKNVTFDATGEYLKDNIDEYPAASSECWGQFMAY
KDDPMNRTRLREEYER*
>TCRU_3034 hypothetical protein, conserved
MEGTPPLAYRRLVVSVSKDPVECFVRAKGDGRTVVPAQTETRTGWLMCTVTLRSQLRHWM
RAEQVALRCLLASRPTRWSLLKGIQEHSSSEGVSAGWSAHCSARSIGPFLRWEDGLLHFL
GSCGGGGSWGNMPTASVLAHRVLVAALRRRHNLPLQDESNVFLFLCQQWTFFLLCCLGVS
AEQQVCKWLRGMCDCRV*
>TCRU_3035 hypothetical protein, conserved
MEGIGSSFPLMGVRTNDHKSTPPFDLLWAKKNKWEIIFNGSRLALPADAKWELNTTHRVG
LEMDYFKELLVYVDGLTVYDGGGEDYSFFEETKTVLGFHSVSHF*
>TCRU_3036 hypothetical protein, conserved
MKTKAVAASEARVPAPKGAPESSHASESSDEPANGSVAMDEARQYATSSSPQRQDSPAQP
LGNKKGPTVSRQTFSSDVIGLATPAAKGEMKEEAASSGGMAPALSPTPSAGSRQEVLEAR
KPFGGERPEGGREPLPPNLAASTMGQAGKADEGSLRNGTEDDWTQHRISLYVLRSVHNEP
ANADTLTSEEQDADHEEDTHVRTAVGTNSGPDLLNGTYATPADATTATPAFNRDQTIVRH
KDNV*
>TCRU_3037 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGLCGVAADDVYVPPGDSGTSGKNGVGVGVQPPVLSESPGA
NEDPTDKDTEESEGGSLESDDLDGQSLLTETVKDGVVADVSKDGLPRQEEGTIVTPGQPE
PVPRVELPSEAKATRPLAPNPQEQLPNTPTEDEPLSTGLGGNRPSGNSRKRPLYLLQRTA
VLPAIKLPEAPRTKVCTMIPCMGPRLRCKTTVRETRN*
>TCRU_3038 retrotransposon hot spot protein, RHS3, putative
MTLFGLRMTTAGGHHITASTVRQFTECLAAYFNGWEELSREMSWEIIYVQHADSTPMNGW
QRCDVVNSDSVSDDESREIAGFREEEKHQYQVSISSGALEETQLSEVRNSHGNGKRNWGG
KGAVLISGKN*
>TCRU_3039 retrotransposon hot spot protein, RHS3, putative
MDVKAMCAWMERDGTTDGQAESWKMVEERMEKVGPIPLHIFDASKFIAHSAAIEDALDGI
NSRDGERHFKHRGVRLWYSGDPPQKVVSVVRARGEVGAEGFLNAAISVCLGRRIAHYFGR
RDE*
>TCRU_3040 MSP-B, putative
MCHTMLLLVLLLCCVSGSVAVAEHHCISEEIEKKVGPRTTAVVLELPTRGGGMMRALTAS
APEWAPIRFQVFTEDLNDPSKHCTAEKQIRPDFIGRNLECNKRDILTKEKRSIILNSLLP
RAFRMHTDRLLVRPLTGRVIVPRYSSGICAQFTIPSSHQTEGVSGADMYLYVSAGPTRYS
TIAWATACSQLIDGRPVVGVVNYGPSFVTNSENSVRVSVHEVAHALGFSVWLLQERNMLK
EVLNVRGKAKVLQVSSPKTVEKTREHFNCVNATGMELEDEGGEGTALSHWERRNAKDELM
AGISGIGYYTSLTMAALEDTGFYKANWGMEEPMSWGNNSGCALLTEKCLMNGVTQYPEMF
CTAETTLISCTSDRLALGYCTIYLYTAELLQQYQYFSNLKLGGSNSSLMDLCPYVQPYSN
TRCSNGEASIMHGSRVGPRSKCLKGDGLVDFMGRIGDVCAEVSCEKGEVSVRYLGDDAWR
QCPEGSSITPTGLFTGGKILCPKYDDVCIIFDPLRGGGDVSSLLSVFPSISVILLVFIFI
SMC*
>TCRU_3041 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MLVTLPVYSKEEGNGKGVLHLWLTDNTHIVDIGSVSGKDEDVTASSLLYKSAGSGNNTNE

RLFSLYEKKKGDGESSLGMVSVLLTAQLQRVKDVLATWKEVDGRVSKLCPSTTAKNPSTG
NGCSAVKTTAGLVGFLSGNFSGNTWRDEYLGVNATVKKGTNGVATGYADGVTFRGAWAEW
PVGSQGENQLYYFANHNFTLVATVSIHNLPKGDTPIPLMGATMNDNKKTVLLGLSHDKEG
KWQVLCGGKTTKELRSNWEPETTHQVAIVLRNGTQGSAYVDGQRVGDASCELNNTDSKGI
SHFYIGGNGGSAGSKEDVPVTATNVLLYNCPLDDNEIRVLNANKISIPKLTDLKTVAAGA
TGVGTARHFGANGDGSAVCGGGLLPLLLLLGLWGVAAS*
>TCRU_3042 phosphatidylinositol-4-phosphate 5-kinase related
MFTRRAVRFCTRRLPSGLLLDGTFNPKHPDFLLEGCATTPDGRVFRGHFDAERGFPLGGS
ELEDDGDLYRGSFNAQWQRHGDGEAWLADGTYYKGRFCEDELVEGVVRIPNGTTETVFEG
LLRDEAFVRGTLTQHDFTYEGEFLDNKPHGRGRLRFATGAEQEGTFFAGKLHGIGCKMKL
DGGFVYVGDFVDGCIQRGQLFTPTYTYDGEFNEHGRAHGEGSQTYLANEPRLIFAGIWEN
GALVRGTCTDEYGAPVDWKDNYELQAKVFSEDGGDVAVAINSYGAAKLKEADTLHREMNQ
SYVKDAERVRQETGRYPSKMSLGYEGSIQQERESLERASRKNVEDMRNIRDSMEASHADV
NCMCEKALNDATIPINENTARMQYARQEGAQQLAAERVDEQFERFMKTFSRETDGNASRR
IIDGNSPWKAYTPKG*
>TCRU_3043 Metal-binding domain-containing protein
MDDKTLQCTLEVHSGDGECTRRTFTVEHLPRTLREVVELLKAQDLRLQRGDFEFSVICGE
SGSPQQLLADRDVNNLFSSFASERLLFKVTLQERVGGLVSSMLADDSLVHLRIYHRGNDL
VTEKRFIPPRRGVREALVIAVRDAIQQPPPASVGMQLYAIVGEMCDQTALKDEDAINTFL
RSCMVTRSVCRLTYQFDNEGVINEADASIQTKNLGVNNAQMPPSDPIQANSATPQMPKCN
DGDDVLCETPSRAEDESDAPCETPSRAEDESNAQASSVAPVNDVNSALVSKSSSHNGSPA
SEPLTQMDAVSVPPETAVSAARNASPLRELAKNGRQLLDGAGHLKQNDGDPPAVTLTAKY
EEAPRPIMLVAEEKVPAVAVSGRCHAVDAKIKKEKLRIEIECAFGDSTVVFPFSWRRDSA
SVLQSLREACLIALEVPRDENVNLYDRKGAVLHTEEDTCKRLESILLSGCTRIGLVLWSG
HPCTSGLPLQCCVSWGTQQIVMVCTVEREMALMDLRRAILDEYGMDYRTIDGLHLFLSNR
EMEAESELTSSRAYEQLKAASLHEELVNIRVSIRDGPSLCLSMERNLPLKTAAFVEEALL
VLGDRPHSNDVLKIFEECSGKTGALEKDAKDFIALVIVMLSEPRILTRERLTSFLLKTAA
PCNEEGVLEVLNRCVAIAQLRVVRRPFDVLKRFFRRLYRVIQIPEGAKGIPLTMVTRQLA
QAGLSDAKGLLRRDRTILAELQENDYTELFLRLYFTDANMITRAVVAARLSGIGKIRSRR
VMTSRGQEMLREDFMHEIRHAFDGIRSTDVLKFLRSQEPHPEPKFRCLLSVMGSLLATHP
VQHPDHWFVERFRGKVADALDVKLRTFEDSVVSTPQLYRLCWDVLKPDMHHLLLLPESPV
ASAFACWAFFAVQLICVNRHLEFPPVPLVDLQKFSLVGLPISPVEIARDDALNVVSPAAA
ASGGNDGGAAAALPFRTNKPRIKYKYSYLCHDLCRDVRVERPLK*
>TCRU_3044 wd40 repeat domain-containing protein
MLASPQCTLGGELLAANVTPISAVYCDPNGGLWAIHASGMCVFYFSASAVADIISSTSSS
PSASFSGVAAIGAKSKAPSAPIFECGEEDQILAVVFPTTRNASRLFACIATTEGRLVLVD
TEEPVNVLRQCDIGTLFTAVTPVPMDAACEAAEDGAGVLVSSFDGTFSEVVFVHWEGDDK
AVVSATGLFRIRGNLHNVILDEASKRILTITQHGEVDVWNWRKGFDETLSFGMLAYSADE
YGEPSCSILLSGGRLWIGTMMGYIVVFHLRPGVSDGSPRHVWQAHSNAVAIRSLLLMSLG
RHIWSYAADRQALVWDAEAWTLQGSFQFPGDGFSKLHGGLRCMDTIAWGIDETAGTVTWF
TVKEPFLRADCGLPFGRDECVMPRGEVERLHLLETLVSHLCSQLLHAASSDEGTAVRERS
SSLNDEHTPKNGVKEEEEEQNMATPPHIDLALQQLDEDHPSARLLPPAVASLVVGWRMVR
RTLADAGMRSRSFLEDVQVLLQDNRRHKELQAQVRRCLAELRQELQHGDACDTLDDVVDI
FRALVRRVEEDSPAASPAHSAIDRNRQTSSRTHSGSTDDAIKTVPSLVEASDDVRARRLE
EDLMYERQRRERSEMQLTEAYDEKRELQRQLTQSMRLQEDYEERLLSLERSLKTAKKAAA
VTATEAARFSEMEANLNEAHHTIHVLQDKLEGLMRERQESLQTAQENKSLHAEVQNFQAK
EQVARRALASFIETQDFMLDKLSDVLQHTNTDVELYSEVSSLYETFCSRVEMQHGFLVEL
KRGYARQRDKDT*
>TCRU_3045 leucine-rich repeat-containing protein
MPVERTLGKEVNVDLHTSAGQPYDVQQLQSEFHAISPAEAYGELCQRFQCHAIAAVAAMF
PSGVGQWNGTTELNLSRLYVGPKGVRPVVEMCKRLPALRSFNCANNYLTNDSVYFITRMA
MFHPALERIELSYNEFISWTGGTFLTELVVRNTNIKEVGIRSTAIPTRVAEAVFEQTRRN
CVLAYQAVGRMPKPTNHPAAIHMRTMKRFFMDIQENGTVPVSALVDGFRERLRILGQERD
LSKYTESFFETLCRQVPQDRITWEAFIVTLRTDGSLYDAEFVKKVQRVFLEFNIEPSAGT

EGFVEVRDLAAMFTRLYGEPPTSKELASMRSLLGLNDTMTLHWDEFLPLMYIRGPKDKCM
AMGWNLSPLYIPTMLHF*
>TCRU_3046 hypothetical protein, conserved
MDYRDRVIALYQCYAPEKMAGVDAQLSKYEGREEEFIQAIINKYGPEPDSAEGIAENEYN
AQEGEEDEWYAYYRQRLVNFYTIYASEKIDSVDNQLKKYAGREEPLFEALVAKYGPEPEY
ENADENEKEAADKTNLSYENVGENENKTGSKEKLSYRDRVVALYNLYVPSKLGDVDAQLE
KYRGREEEFIAALEQKYGPEPSVAESASADYRSRVVSIYERYAPGKLGNVDAQLEKYRGH
EEEFIAALEQKYGPEPSIAESASADYRSRVVSIYERYAPGKLGDVDAQLEKYRGHEEEFI
AALEQKYGPEPSVAESASADYRSRVVSIYERYAPGKLGDVDAQLEKYRGHEEEFIAALEQ
KYGPEPSIAESASADYRSRVVSIYERYAPGKLGDVDAQLEKYRGHEEEFIAALEQKYGPE
PSVAESASADYRSRVVSIYERYAPGKLGDVDAQLEKYRGREEEFIAALEQKYVYGSGSAL
PSLYVSGTLSPVVSEKAGSSHQMVLMGMALTTIMEEESARRLELLEAFTAGLMSLSMDAE
SERRLKVEHQEQLAAAVFEEFFIRLQIIAEEAMGRPVLEHPHFPFVSDKSADAVARFFAA
LGTTHVNGKAFIMASACRLLFFEAVGEELLEEPQGELVSLEEFRQLLTRACHCEKDVVAR
LQSFVSMAKRQERPTVLAAPQELCAGFWAYRCVKPCVAEDWQRVWVVLENDTRLVIRRPN
IKKPELTIPVGQVIKCQLSSMLGTQAPRSCAKNGLYLQLSSGVNPVLLLLCPQRVANAQA
LVKMFFRGFPQKTSGMTRDVVAEAKDTLMNKGEVKISAPAAGEICRTEDACVATIVWCCR
GGCSKFVRSVWTLVGDSIVHQAVGEKENFTWSLATVRDVYLVNELGMRPPVPTAKHGFVV
LLEKGSLFCCTETAAARDAIVGYMKRVVFKHFLQSNQKRASALTSLMTEESKEGKGGAPL
ASAKHRVPGVAHSSSRR*
>TCRU_3047 hypothetical protein
MNVLVNGSLYRSRTGTLEIKRRFGFGAVLVSYEGNRPCIAPVDALGRFLVRDGCSYDVYS
LQTGESSRMTRLALQRDARLSQRETLLSEVPSQLPERKRARSITAKTPRRKGNYVRFVQI
FLKSFQSVSFADAAKEWRLFSEELKRTAPVEELLERVRAKGAYQPSLA*
>TCRU_3048 hypothetical protein, conserved
MMMGYDYQALKERLLSDVHLLSVDSIIHMLSQAYGTSSDGSDEANYLIQHLLSRPLKPVV
CRELLELLATVGNSEVAQSLRMKAVECIRGEYGQGSFGKHDPIRDLATVSIAFALERQQT
LAVSAGTRMLLEELIARCHGMSDGVWDRYSGRVTGVLAVALDVLASFVQTGKKSPSLTGI
YHQLEQFPESWERGSSPSAVITECAACVCSACHLLRVFSLLKTPFSTAASPSSVETTTLG
DWNGTHGSLTEALLRRCTDVFSREGTLLPRAVVFDMWRASTGVEGTSSAVLQPLMELLLN
YTEKHPADFPLREVAKFFGTDCHRFPAEAFELFVRCLRNESDNVVSSHLDMLVSSMEGVA
ARGDKALLQRLQLMLFLRPIGHEKALIHAVLFKTPQLVRLFNCCNSASDLTASMQATLLE
LMVSSCGRCTTMEELNTAASLLPHIERGSLKDALAWALAANAQRMHPTVTPDVQKALLIV
YLQKGGVAVEEDLLQALRRRA*
>TCRU_3049 conserved protein, unknown function
MWETRLISPPRRSLSAPCATIRHVCSFSADEDVERELRAEVVEAASSLFNPRLRITRAAF
LFPSFTASASSSGETTKGTDAWQALLNSRVCGRKEVVGEPILFDRLRTANSQINLLNSMS
GYTLQRCAELEEENISLSRTLKQLLDENRQLSERLQSCLRELYDERKLVAVLQSELEASQ
HEKSAREVSK*
>TCRU_3050 hypothetical protein, conserved
MHTTEVESVPRRNPFKNQWRTNLPSFHDCLASLGSRENFRSFGEVLAAVSPPPREIVGSP
CALNSPKMNAKLDFSFFTLELSDTTLPGTPPHPVERYQQSCASSTERTPRISDEDGQGEG
ISLTPRQLPPLCPNASPIAHSPSAVGGSCSAPRTEPQEVWLTHSVERAHPALLKEKGNLE
TLLVMENSPASIDHCARCGGMTPLISGGDFFSGNDNGVGQWGCINQRVNSIIPPLCEWSD
GKWLRDPINCYGDFAYHHPLIYRVSAGAARDDVIREMRFL*
>TCRU_3051 ras-like small GTPase, putative
MPDIPIVVLGGGGVGKSCLTIQYIQGHFVDKYDATIEDVYRKPIDIDNQPAVLTIVDTAG
QDAFGAMRDQYLRKGEGFVLVYSITDAESFQQLKRIYAQLCRVKGDQSVFCVVVGNKIDE
VNYRVVSTEEGNQFAAQVRCPFLEVTAKNRGMAEKVFETLVRTIRNGGTACEQRVANGVG
KPPCTDARGSGATTHPNMKAAPQVVDPPALPSPAYPKRKKRRCVLL*
>TCRU_3052 DNA repair protein, putative
MARQTRDVTSARAFTCLPPDAPWTLSQHFSPIVTLAIHRIGKVEVSIGKKKGNDFDSHRN
GDCMNKVRDYVVVEDVEMVGEEEDVVCVEPATSQRLLLPRSDEVDPCMEFANRVIQGWCR
DTQRGRTAGNASNPVFLLIVFGERALRRYVCRLTHTLEDFQTFELNGFVAAYQARHGADI

RRRAEAPATEKTTHVNLRTWFLANNDEVMEEDEEVAGNHNNDDEDVGSEVGNAVKKGVGI
CIEKTPTRTLSQGPSFLFSQSSRLSHNPAISNDGSGGAESVSLHQLILSQAPLTPPSEEE
EKQQNEEKQRERRHPGTLLCLDSVGAGIALLSVASSDCNLPSPSLRVAVVNGSLLCASEL
ISMVKGVHDAFALPTRILVVEQELRFLRMLEMTQDALEPQSLRQLRVQVLVEQLHESPVT
DRVLEEEREAFEALAHAKATLTGSLLADRDTLRTVQENLDSGLILQKNLGRRQQGLPGLC
GNELREVQTSAVSGSAPTTTTALEAPLVVFDERELRSLLPYALYRRGIELVPLTLATADY
VLSPLYALERKSAPDFIQSLFSGRIFTQLAALSRRYEFPMCLVEFDRSAPFRLSFSSPSP
AATSDVSGPVAHFEGGGLFARIARLYASFPRVQVLWSRDPTQSAGIIHEMKRTCAREAVD
PSTPSLTRGNIDPHDSAMEKEASHLAARVLSCFPGITPGNAARVMAVCGSLAGLATIDES
ALVEAMGEENAKQLYTFLHDDLVAKVF*

>TCRU_3053 retrotransposon hot spot protein, RHS3, putative
MPERHGEGNGENGTSPASTVPQGLTRARARWVSRSGQPAATCRRLEETRRPKPRLDSEVK
DVLLEGELEVELIRLNDFLREHCGPRAVVDEVHNVWLGVFLMDPDAYVQDQQLLGQILDL
EVYQLLQRSQKLVMDTMKLHERGVHRLEQWWGFERKDMCTPLARLKLDLALKVAPKEGGE
EMLEGFYESVFNASWHHLVEFPEGEWMGMMVRRGKPKQSWTYRAVGGILEKDDSVEQFSP
PRPRLMVLVSDKAWPYSWMLENSTRDCYVNCEVERVWQIVKGDLTEWFSTHHGESDFTPE
ERLLIGTPGIGKSMNAGSYLLYQLLHYDAEKLQVVVYRIAERSYLFDKITETVTHYAEES
TFLKVMGELSGRGMRGYIIHNVAEPILEPSVRLLPRGWCMIVVTPPEESDHRGRRKQLGG
RRIIMKCPEENDVKAMCMWMRCGSPGRQAVYWQEVRDYMDKVGPILRDLFSERDTNARPS
ATSEPWDGLPYQMHMTTLA*

>TCRU_3054 hypothetical protein, conserved
MVHTAVARALTPRGATTVSRHDAACPDACPCRLHYANNNPTREASLSHGFSRQYGVLNPG
AKTSQSSMKSQEESMMEPAKKYRLAPNGMRRPTLRSHTECTLYSIELMLRPSLKNASVSD
EPSNTIEENKLAVMMRHRQLQ*

>TCRU_3055 DNA topoisomerase type IB small subunit
MTEVTPLKAPLVTGAPTPPASYPPTKVPVKMPYVLPKPPFAPVVPMRPPAPRLKRDGDDG
HLAVPGLADTSKRSRVKDPERRGRAMSESSNSESSSNSDSDDDSDSDSHSSSSGSSGDDE
SFSSSTEGSGSDETRSGDELTLFEIAKARGLVNERVDNKKEEEEEEVAPVGPPPRPPIVR
SFPNNVDLALQRYEERLNREENMIRIKDDNKAVSLGTSKVNYIDPRIVCSWAKEYNVPIG
KIFSATLQKKFPWAMGAENFSF*

>TCRU_3056 Protein of unknown function (DUF3720), putative
MGLIKAVEAVESGEGSSGDPDQPQDKSKVSSPDKKLDNNTKGIGASDSKGGSVAVQPEAA
PLGSGGSDTGGQERGSNVLGPNEEKEAGRMDQKDGKGTGPHNEGAEQSSSLPGSPGPQSG
EDHNLENTSESDGASDIQLKKEDAVEAEVPKISEKEEPGGGKENENGKALTGIPDSQTKM
KETKTVQPPPLLTKTAEEARITIGIPAEDSTPAETNGHSKPENTVPVQQLQLPQSDMKSN
SNSQTEGIASITANSQNETSDGHAETKPPPTENGNFANNEADKSTEEGIPNNDPAADGAG
TREEQNENKDANPKETPVTATATKTTTARAGDSDGSTAVSHTTSPLLLLLVVACAAAAAV
VAA*

>TCRU_3057 hypothetical protein, conserved
MARSGRSFFVSAAVGAFAPDLSARWPQRVAVTLCSRRYAATLLLVCCFGDNVPAAVRLPS
GGKCVSAVVESRVGCLAAEGIAHPTQHRSCRASSITPQHLSRRQQHAARQRMPLPPRVRL
EENASAVVFRGSHCVAQWRAQNLFAESAHDTGHWPRSVCVVEHTAVESLFPPRGRTPDFP
SFSHPGGWLRDDATTRHLFSQWRGNICGAMHWEYERRMQ*

>TCRU_3058 hypothetical protein, conserved
MVRGRSNTPCKRPESGRGAGTRIALDKALFSVVSAAGCDAIHPPDDAAALLCRLVPSTPQ
KEGGNGAAKNFALDVEVLILDAVEIVLAAYNEFTASSAKEGEETFKSLLMRASLTNLRSL
ATLLSHRPPFSPPVLAALFQLTILVVKHAPLQALDEEGCRMLLCLLELLGCLPRGVETAG
TPSIQRVARITARNVMRRVGPRLCPSAFSASVEASEKVAKSAVLREQLERDIIPWVERHL
LPLHAVTGAAAQADLKEDRRLALSLLEFMLLSDGDACGPMSSQRISIYYLADTVASLLEE
EDEGGIDGPDREVALAFLHRVGRTLSNPAAASLVSTSREDGAHEGCVQSPPLRVRDVREF
LRAKDAAYVAEFTQLHERIEEEQENQAILQWQLGELTKEHERVQREIQEGILHSFNADEG
NTSVCTLMKGDSTHNTTSAAASLSLGERARNILSFLRPVEDTTIALNEQKRRRSLF*

>TCRU_3059 RNA-binding protein, UBP2
MSQQMQYYAPQQQLQQAPAQMNPEPDLLRNLMVNYIPTTVDEVQLRQLFERYGPIESVKI

VADRETRQSRGYGFVKFQSGSSAQQAIAGLNGFNILNKRLKVALAASGHQRNRNGVSTGF
GAYGGYGGYGGYGAYPSAANPYAQQQMMTMQHPYMMTQSVPSVPRQ*
>TCRU_gamma, putative elongation factor.1
MQQPKTVEVLRSQGATFGPVKAERKGKDAAAPARAEKKPKAAAAAADGAEEEDEAPREKK
KPNPLDELPPSPFVLDAFKREYSNTDTRTVAAPYFFQHYDAAGYTTFWCRYKYNEDNKMQ
FMTANLIRGWFQRMEHVRKYAFGVALIIGEERRHDIVALWVFRGRGMPAIVEDVEDTELF
DWEEVADVAAQRERITDYLCWEGPTIPRPVLEGRVFK*
>TCRU_3061 hypothetical protein, conserved
MRRQMYTREELIALREALALDTFADPVPLDCPMRTDSDLTLHQTTVRKRNKEDWKVMSFS
KRISAFNGTIGENNVTTRPDIHRANFGEASITLCRSNRTEEYTDCDDCGCKVIMPPRLQI
PFVTIDPMRRHYNTSSRDYKKKAEVNIDMERNMVARLRLRQQRQPTKKNPTEYREKQSRY
KEVPDSCMVFATSSPPKTEDASRGAFVHITQMIGLGSSTVPQQEVGSAVSISNVSLFNSM
LGSRYLGFTRSMGLWHYLSKTFDGKYLHVLEETADTGPSNGATNNNPIGRHHNGNESSIG
PDDSGTTPAGEEKSGSEQVEETHGNYEVLKQRRPHRRRTNRTHAEKRVNRQLKEFFSEMK
TSGEDCG*
>TCRU_3062 N-terminal region of Chorein, a TM vesicle-mediated
sorter, putative
MFIANYISSWLSTYIRWFTKHWNRNSISVSILKGCIELKDIELSTDITAFFRASIPLERA
SVGRLRLTVPWTALYSCQCELFLEDVLAVFKQHFQEEVADDEGNPLEGKKRIVELLDAIR
YKSQGNTETKRQGFLERLKWVIFRNMKLVVKNFTVRYELIGTSPLSATIRLQYLSCIAAN
AMNEPFFVTDDECDLYRIILFQGLSFTVASLDCIETSNRSWRTDSLHSFTSFLIKGMEKE
VEKFGYVLKPSSGRAFGSLQFQHPKLQLGAFILVHSCGIDLDFKKIQGLLMMTSYVVSFW
PCDKDEKKLRPIEKPSTVIPGSCAAWWRYSIDRIISNTRGCVKRTAFHWATYQDWKCHSE
EYYKHYLLTLGAPWLFGLDVNKTILEEALSSFSIGYLIQIRQEARFTLEEFRLTGRVFPR
HYGDTISDRGFGYKVAVVEVLKDSVVNSPMQLEVSISLGVPKLPLFLRGHNMHFNIDLTD
MSLRVSRSADLLQILFSAYSIQAFSEVSGFNRVNTVFIIDGTKTTKGVVVTYLRNGKNKD
LSFVLTSFKIRYNQCIAGKLIAEFYMLESENALGWDNFVLYSLHDVAYPLKTQVNIGNTA
LKLGKLEVCFEDLSFEVQWRCSRLFVSEISNSPFIDLKNVFLPYTTDSSIFIEESYICGD
LYSFYVLKNMIQDMMVIYEPIMYWLRKRDTIYSTETMNIFELKSPFFMVTLPGEGTFLKI
RQFAIHLSLGPTWILRASCIGMACDGVLSDTNMHLMVLGGTNKKEIFLDGPLKNSDSDLI
VYATFEEGHLIVDNRLVGLVEFLNDLLFAMLFPAEINPPVFLDESVMIPSLEVLISCSNL
SFDVLGESSGTWNLPFRLSCNGQESLLVEFKRFPDTHMNTTVTFGRCFLCSVDEFTLILP
SYSNKGVLQLVMDWRPPMELVTEEKYSTLTASLFVVERYFTFHLPALHEFLHQFNRNGSA
LYRLRSLGSRLHFGLREPNKEVYSAPLWPHRTIIKLDAKNIIMFYHPWYKKELSDLSSNT
EFFVRTSFSSCKANWSFDGFKGHILMELFLITGLPRVMKSSCSCASNVLSKNNVLLVELR
QDVTYDLEKQKEAFSIVMRGKDMMKIPQMFKTPIGAKPSSCAADMMPFMVSFEEAYEFIE
IVNAAFDFSSPQQVTVEISPRHERVLKINVAPFLVYSPSLFDVAFVSWEGIDFMIQKDGN
FEGTMVGISLLYDASLRAIENQEMTVLWDHLHTVKKATAILEVLGNQDTEEDFITLKKKS
DMDSVMLHIGGVFLHITEKKLPLLLHQFMEVHNFFCSNTLPLPLLPRENVIATSELNYAL
MNIQFDEVHLGFRWNSRMNGIYGELHCALFAFTWRSNGALTLKDGVVQLKWFDAAPLGES
MGSVDLLLQEASETVPLIEHISLSTEESRLGKILVKISPIHMNLSFDTYLSLVELVVYHL
RLELRRPARRTSGDFVSVETLGKGTLDMKKSLSSASYLFSCGNGDTLTSFSGAGFLLQSG
DVTPTWQFSLELAKVRLTVDTERRVKNGDRKNFKPLLWLNLTNIIFDLFPNGTSFALDEV
RLSFLRETSVVSLSGLQFSTSRASDSMPSVPEMVYMVQSMITRFFTPDLLTCFDRLIKTP
AEELAELYWETTHPSGSDILCRFHTEDSTRDNGGNGDNRSGSKKGNYRKMEVLTVGTPVW
ELTNDLVLSRNGGTVLQFSNVNTNNIHVEMNGHSILIETPRKAGAEIVMVVDGGISLTFC
NGRFFLPCLLSEETRMRRLERLGEEALLLPFIALGECSYIRCFKVRYATTERHNLQHFYH
EEQKQQKEDGVIESVRPQRWKMHAGIHSVVLHVSSERQKGIVKATVAVEAKISLHGKKIE
RGEISLENFSVVTRTMDSTTNNTTNTTTTAVSRSSSPKSNSNMSASAMDNVLIAPVSIHL
CISESRQFAFSLGRVVVDAMVGDLLLLSIMARELFLFARHVISFQLAPTEQEYRLQIEHV
LGWNSVGMRGDQHEEGGDARQRGEAPNEEPTNKMPVLSLALFLPMMEVKLSNLKYPLVQL
SLADIVWKVNMFCTSRTTLLQSQQLNIRVYGKGRWDTLIPPKAVISLEAVHSWSRRTRTE
QVELQCDGFVLYASHLLLSKMMHIHREWSEFYSTIFELSHHAQEASPPIGLSNILNPVST
ATHRFINVFDDVFYLFVGKDLENGEIVPLPSSTAVDLTLPFNRAEDVRVYLYPRHCIELN

ENGRHVRNNEGLRRDMQHCHVVASQLQYGRAFGLVLDNLLVVISCVETEGIQKGMPPLSS
VNARCQQYGDRGAKPLNLTNQANLLPPFRKLPMASFGGIDEAGLVIVRIHSRRSLYNGIG
MMIEVRQYILADSEETPMSEDFWIVPPNSEYPLVALCNRLELRFSLDGDVYGTSFSTPSL
ETGVVLAFQRIGNAVSNRENSGFLPVSVFIALRRFPESGSTVIHLLPRMTVLNHIGVPIK
LSLWQEEGTEEEKEEEEEEERLLNHRDDSVSSTSNHGERGSSITANSGQPSSRWPHWRRR
SSRRRLISLGEHGALPHQGALSICRCSYSSGLLLSLSFTQTGGETVQTERTTKVCSSLKR
RVGREPCLIQLRDSSERSFYVQVTVLHRTIILSVGYWVINLTEYPILLKDSYTSRHLTAG
QSMNTGIPPSRGLPFLIGSRPAEFTVALLKIGLDEEWSEGIPTQVGSHGVAESPRRMVGG
VTRSCNYVIQFPRVQEGRPAVLLLTPRWVFINNANRRLKVHFTFPVAKKMPSLKKLSSRE
QRSPRASEADTDSLPFLTLRPGEHQFSCIGTATGNMASFQDTLEDAVPSVTSLFSDTVRH
KNLAEFYEAHRTASISVDGPGHAVFNLWASLKRQPAVPSVFYGARIANHRSSSLLPQSSS
DCPEFDEDVAFVTGRISVTVQHIDNVLAVVIKSIHSTNMVIQNRARSVTLAVRQKGSQRR
TVIPPCQNRFFLWEDYRTDPVISLHVIGFKGAWFEVDFSRGSYQVQRRHTSELTENVLSP
FSFRACISTRNAQRVTILFTDENFPPHTSFDDAWHRSVGRTISFPSLELLWLMEGQSTGD
KPHLSLVLRDLQVQTLVAGNTHAISIILKRLQVVDVRRQAIVVLHRANPATSNATEVSTG
GRILSWLWRGEEVPQQDFQAVYAAMMSPSGVTRVTELSFVFTPFVLNLSDQLVVSLWQEY
RGLFSFFKNNGSKTTLVSEALSSTPVSHHEFSQRLMARMQEPENCTAEISVGNTSLTSSS
AIPIVNYFNQSETHEGPALLFIDQAHFSRLTVFLTFSRQKPDLLWELLGMYTLMIPKRLE
QKEFSWNALVVENGTTTWGLLLAQAQRWLMDGALRQWPKVTRLGDIVDTFKRGSNRRVTL
AGTPAPRLADVNNFSDGDDDKKEKDKRENEALSSSRRML*
>TCRU_3063 PUB domain containing protein, putative
MDVAEADWILERSPPDALNRAISTVFRRLLANIVLEPENPKYHVVREENKFIRDTLNPLP
NSVVEALFAGIGFKRAQNANSETIYVFTGNTENIKEADYFLSHLEDRIEKGQRKEAEMHF
VPPETKVNREREERRQQVLQEIQRDAEKRQGETTGSEPPTLINAFYPGDYTLVENLIEKS
RRTLLSTGRVRNFLFEGRHFTLRRMAHGRVYVCKEGCGTDFLEAHWHLFTGKNLMYSYVA
HLSPDASAMMHLGVEHGYQYNSLPGTKNFRRTVHFSAKRINETNGLLEYIEHPDRPSETC
IYCGKPFSELFL*
>TCRU_3064 Glutathione S-transferase, N-terminal domain containing
protein, putative
MSLTLWSGVNPENARTHKLLAAAALANVAVTLKACEYGRENETAEYCRNCSPCGRYPVLQ
TEEGCVFESNAILRHIARLDRSGGFLYGRTPLEGSQVDMWLDFSATELDAASAPFVHHAF
RGERGSLLCHFFFYFSRIDCMARVAVTRAYGLYGVAAAPQQKVFFSGGVLCVRPCANNRS
VGKALLYFWLTIELCPCFAKK*
>TCRU_3065 Mucin-like glycoprotein, putative
MVTCRLLCALLVLVLCCCPSVCAAGSEDENEQSAVPKIDEKEVTGKGTDPRPTTLQPQTR
EEVEGSEKQETNTPTHTSQETAKATGTAESESSSNNTQDQGHEDGQSTEEGTENTNTNTS
NEQHKESNAPTTTTTTTKTATAPEATSTTTTEAPTTTTTRAPSRLREIDGSLSSSVWVCA
PLLLVASTLAYTTLG*
>TCRU_3066 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MTAHNTESVNIPKLDHAKPEPRGTPSTPAGQQPSELGHLVGSSKDASGGVEGADSQNRGV
NATALSSNLVNVSQENNNDASSMRGSGLLPSLLLLLGLWGLAAQ*
>TCRU_3067 hypothetical protein, conserved
MRAVEAADDDDAMNDTSSAENSEESASGAEGKGAAGAAAPSLDAGVSEADEYKKESNAFK
ANGNAINTGILRKVRQMSFNFAPPVNFLLNPAALPLHRLGESPFRG*
>TCRU_3068 hypothetical protein, conserved
MPMSQPRFTTNPERIARLEENYNAGVEREKIPVAEREKLDLECLNVSSAKLRFLYQNSME
SYGPDVKKNKVKEYNLKHGSDLSRKWFGIF*
>TCRU_3069 3-oxo-5-alpha-steroid 4-dehydrogenase-like, putative
MLKRHGGNLSSTWAWLLVAVVFLLITTVCMVLLQQYVLPLGSTTVIESASYFHLVMAAMT
YFTLRFVEVAPFGRHATSTTAHVTMPAPLSWALQECPTLINVVYYLLMEYPCHALKCGSS
QWIRLLFDDPFGQAAHAISEGITSLHVGLLLFVIHYLHRTFLYPLIIGEGAPVPIKITLS
AAVYCLLNGRLQLLANIRDGPSAPRFPLLFTSHMALFWIGIVLFFAGMGVNVLSDNRLVR
LKKQPPRHSRKIPHGGLFEYVSCANFFGEIVEWCGYSLVVWSTTATTKPESGLAAFSFSV

YVMANLLPRGYAHHEWYKKQFGGAYDTLRRKAVIPYVY*
>TCRU_3070 hypothetical protein, conserved
MYVEQLRRGIEEQERRVSALRQEKQYRDSLLSEVRGLINHVEPHLFHELNSDTQELLHTL
ENNVSVRGPPTNTLRGSGPHDLDSSTIPLFSKEMEERIMQIEEQPPHRERRPRHQRHGER
KKKKGKRGATRRMETSPLALTELEIKKREALMAALDSLQLESFETLPAEKGVLLWLSDAG
TLHQQRNVEEVAQGEWVGEEMQTYYSDDFEELTDVER*
>TCRU_3071 hypothetical protein
MSAGQSVVGCGDVSTADTHGPGTSSKFLPSPLYGTRAEVSATDGGASPLIKPPLYATNTS
GGGPMTAKTGMDESTGFAHDAEEGETPARNPARASSIAASPQSLCADEEDFSDRNAAAME
ESYFRRSAAMSRVQSGAVNAPVQFEGSFLGQTVMLGQSTQGRANTMSPSVIVSRSLPQLA
GNANCGDGGAQEICEECADGPSITVSLANSTNDGVGPWKRVQLVSFSAPGIAGASPMLTI
PVELASDAESPNKQRANPPRHRSIKDPAAPIGMHNSQQTAASSISFSDRTPQREGSPSRP
PSSACSTMDMSRQLNISGMSGSMSFRPPVGGVSLADLPKGSPLVFDSSMNSVTPTRGTPV
LSTTVQQPKPCPVNRTTSAAVPQFVTTFCGRSSGLATGNGLPLSRGVMGGSGGNPLLSSA
MSHIFTDPHELPAAPKSQKPPTAPMSDSDVFRPWLPLGLEQDVAAAEVTGWTPLGNGSEM
PEQSCNGPILAGNIVNDRNNDGDDDNGYGEKSMSPARPEAVGSGFSVNEDDGNPFFGATS
TTLMEATLLEMNLQDGSISVSVRPPPSNQAAKGAEDDRQGKNSQEARENRVVKPTTCKDK
VGQSTRGRRQPSLRNQSESQMNKETHGVVKPDTTVAGTTPAVLSTEEPTPTRHE*
>TCRU_3072 protein kinase, putative
MVGGKDAAKRAGNAKRSDDKKNGKGESGNKIGPAAHATVATHSDNKREHKTAKAVHAKPH
PQKKGPEKPGKSKNKSKDAGKSAENLNESLPLLPPSPRSNGVVEEAAVAPANVTNTPIVE
DLERNDDNAGVSFSGMQISLGVQSVPPVRREKRSGSGSTLCKDGMAGLFRADQRAGESLM
DNSDGGARWPKEAPTSNWTAGSTEDRDSWVNAVGGVTAKNKSRKETAGSEDDDDDEDAEE
EDDEDDEEDDEEEDEDGEEEDEDGDNDDDDEEEEEEDEEDEEDGCNDTVNKGEGWKQEQI
TVKISREGDRNVKVLYVTRRTKFRAFAKDIMRRFAYNRLCDFDMYCIDAAGDHVDIDVSQ
DFKNLITQFLQTLRLEKQKNAAVDARPSSKSSQSQHLPPKASRRFSARGVLRRSASLSRP
GSQTVETSPVADDGERSSTSVLRLYVRDSYRVRKEEQRRMHPSIATGQSQLVQLGLSSQQ
QTHRSLQITGSVGEDSSNEFFTPGHADFLPIGSSNISVNFSSTARFFSQTINFREDEDVQ
WSKMGLLGKGSFGSVYEGITSEGKIMAVKVLEISLDEDAENVASIQREINLMRSLKHKNI
VAYYGCQTKELSSGARQLEIFLEHCHGGSLSHLRRKFERAKERFSISLVRTYAKQILEGL
AYLHSMNVVHRDLKGDNVLISALGEAKLADFGCSKRIGTATMQQDGCGEKGAGYQTMVGT
PLFMAPEVVKCEGGYSKPADVWSVGCLVLEMLGRQPWIFRSNANAFQIMYQISKSTSMPT
GVPNNCPADLYSFFTRCFEHDPNKRATAEELLKHEWITCPDSKLQEVLEEAGGE*
>TCRU_3073 hypothetical protein, conserved
MMSHVRERQHRRSFRQALLRAAVTFWVLFSLCGRTLAATRTLEISYDMLTPPPPPPPTLS
ELNERLRLPHSSSSSSPFLRDGDGTSLCSVDHGCPLSSMAWASGTFTMSDVLTPASFLIA
SNLTLKLSLCCGYKYNGTLLRDEALYDVFLQVLLQASPFQVLTREEKRRMFPREHVIIMD
TVRQRRYDANYVLTTEDFRQQNDGDGDVILLVSGAVGEGILRIPLYRAAEDLATAAPANI
NLKIANVAIKCKCPHTLLVMPLLQVRPDTLLPVSVLGLGSHCGVHPLLPPTTPHHGENIV
QLREKAWAASVAVAPSQLPATRVQWVVTDTRTGSIVLDELLHVPTRTDSSGALLRHHANC
SYFEVLPNHKYEVNLTVSRGTAVQRATGFFILRLPIDRPQDVERGPPQLHFGFERRLRLS
ERTRTYLELQGALSPQHQPAEYFGYWENTPLNDQPLPQILKRIRHNPYAEETALYPMFVG
RNEIFFYVRDVDEVCDPVLLEVQEVWALQGILLQPSISPLTACHDDVPMEALPLKHVVAT
IRSSLQLPVRFQGTSWEPLQEQNFLEGRFDCTERGAGPCDIRTRVANGGTSGVLQMRKRG
VADLAWVVRVEVNETALVPPHSLDPSVARIVANTVDEGGVVVVEVRSRPAVVVRRMSTMP
NNVNVTLAMRLRRMKVHPPRSLEIAVDEVPIGHWLVAAPLLLLSVDDAFVAELDTSGVPN
VPQRLREGTLRFVAEDPGEAIDLGVPYTSRCPPRVVEHTVTVVALAAPPIVPALVPFYTE
DDCVHLRAPRPRWKDEDARWHVPHCEEAPQSPPYIAGLEKGKRAEHNVSSLEEEEVQEVQ
VCGIQVYRWCDVVWTARNPVAAVTQTFSLRRCQSPPQLLFHKDGLQEPRDISLSVYALPL
IEWLDGYDDVPDDMDVGGSAKNTTAQVPRYTARRVIPVAGYSATVGYSFNYSGLQQDFEV
TFKYAHDAAHQLGVTQQHFERVGDDGLSDEMAAAAAAAPLLLRRSLLSLDGDKMRDDRND
RNTNDNDNNDSMADDKSILRVGDTEGAVNLEQQVAERARERDYALDLASDTRFFFTHLSG
LRKVWFNGLDNSSHYPLLYKVWPSPTATGPSRDAAEFARRGMCLLQRGNISVFSVNPRGV
VPVVENGVLPFCYPSFLFSRHPWLSTKYKFDFSWSCEDDGVIVVERRTPTASILRHNGPA

NDTRCSLTVRNDLTETVQKDTFLLRRVYPTPLPPTFAILSGNAAMGECFANGTTRSKQTT
RLETNGSPDTTHRRTRTRWIFGKKLILHVDAHVGGRTSRWTALSVVPAVPSPVGTGRLLD
SIHFLPLPRHPLALERGFGDATVLVSGIRVPGLYTFGYYHPDPMYPGVCPNSSIVETLHV
VHAQVIEKELTVCGDSAVLKAVPIPREIGCEFFGQWEVVSLQTSENETWTSGANFTGIRF
DHGRRPRTVVRGLPFGILTVRWAVYAVSPTDPDTQRNDEERQEKQRGLLVDYETVRLLVL
TENLPSNRLVTLSQSVYLLATTSTLHWVLTETEASSSPLTLRRPRLRVETVSNESSTGSR
FGAGHQVVIVTNLPIGLTRLQYELHLSPRAFGPMLTKRCPYVPRQEFEIERVSAFLSANT
TLSHECDAYSGRGQISICLHAEGAQSRGILFTSSSSLPSFGARLVEPASFEAIVKSGAAR
LEARGCSLPWWVASQTRWSNVHADATGRCVSVTVTAARHLHPQEVSHHMFLAQEQLGSSR
LCPHGGDFMTSEIIDGATTWGDGGSTRNSLFRGGEIAQFLPFLHFATLTREERSMRPMLS
LLGVPDIVTTELDISNEGKAVVVLLRLDTAQPKQMGGYVHAAESSEDGRQRHSLLANCAR
GTVRASDVLNFWTEVNRPDGAEGRTAREWLEYVAAVREKHVGCEPLFVSLAHLLPRPDDT
EATLRRRQLYRVPPKEQRLVTLDVIEQQLEGLQREYRWTREGIDVTGLPPELQAALARRR
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PPHEPFTVPHNLFLRAAVHKDVLCGTNVSAGADPASLVLFGRVEVIDVPPAVGASPAAIK
QCEVEGGVPVIQVSVSGTTFAAMDVFPTDRVLLEEVHNPNSTGLTETSPEVGLLPCLQQM
HFGMRVAASSMTKKHLYLQLSPCPFFQMLSHADYDEQQDSELLQKKLFLPRLLRITLRGV
LSEDSHTKGKTSVSFVVKVLPTLARLHLRTLPAPEEGTARSSWSGSIARRPLLMCEGDVR
RRGAEFGIELIGDRWHDRVGGRGIHDDDITSLPENAWYENGAGRIGISGTISSSRSAVDG
ARYRSPHNVALINSFSIVEHHRLDSAHHLLLRHGGLYRSDFVNYLFSIMARPEITQRHQF
VYRYNDTFVSVRIPAAQSDLNDLFHGDEYDGTFDDDHLPPIRSFSTIEEILFAVPGIATE
CRGCLLADTTYFMAGDLTGLWFFPPATSPPLDNRVLVEPLRVPFYAASRVPREWRFSTLC
PTEAWDNLQLFLRHWQPPRLQRGSAPYLQFELVVYNLRDILGGEVPLSRRPNAILTGLPV
SLTKLLKEGRGRGNSLAEVVFQVNTTAAERAHATMAADFSRYGRRHLHTVHDYLRDHRGS
GGALAVNASVFLKVCVPSTAAVPEAQCSIVSVTHTLLIMEEPRLMSYYGRPRQGSWRSIF
DPASLLHHAGTSLTGYIIFPRLPALRRTLSLGNTHDVAPARIGLTVALFVAVVFLYAMAT
RLWAVICTLLWATLLFLVPEIIVGIYFVMHFLFWAFVM*
>TCRU_3074 chaperone protein DNAj, putative
MRRAAILRPAIGVFCGNNPALWGATLPLSASRRLLTGAAPYGSVPADIEESRHAQKPHEE
EVVRGVTRQTVTGAGGGRAASDACGDGGEEPAAAAAAGYNPWEVLGVKPGVPSQTLRLRY
HELMREVHPELDPKGVGNIPRLNQINKAYEIITKSPTLDRRYRNLVSDTQYFYYKFLPEW
MARNVDEMPRYWSWVKWRTPGAFQVFLWCCGCYMIGRFYAAFPLLTTVFLVSVAFDILFH
TMTAPATCSMLFLYAIMTSQSHDMAWLTSPKSFLRRELGY*
>TCRU_3075 Colon cancer-associated protein Mic1-like, putative
MTDVSTVPPFMVFRKPVFRFCTTAAAAGGGAGGNDASRVTRIYIDEVANDVVVFSRASRQ
VCFYQLRLREGPGNYEATTAEIASNSSLLQPDKNVDAVADCRKDPCEKVRENASSAANDV
EWMRHHPALPADAIALTVSSREGDGELLPVRYAKRCPIPLHCGYHDTMTCSSDSYHSGDE
RAYLVALSIDTRSVLFVLCHAYMGALPLYALATFQCAPKSLRFRDDFYPIQAYYWAEELH
GTQSPSCNFPTRRASSMVDLPGGKERQQHERRNVPDDDASSLTPAKFLSAATSRRRILLC
VTTISLDLVGVDEELLPCATEEKVGSRELCVLLRRFPTHSDYWHYCPAARTLLSVNRLKS
RILKSFEVSDEGLRPLPALRLQDEDSDGGGDEDWAISGDENSEMSLLFSSPACMDRPSVR
YPVGLLVLYRQLFLCSLSRHDGGAMLYRYISAENGSEESFVRYALLRPDFSLNLRRDPVA
LQVIDNLVVLHVLRQGISCAFDIACGEREHDVKSSLSGGTSESVATSMPASAPAAARIGG
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ARGGGYETFLPVLQPSLSAALMMYPPLSANTSTCIHMDDLYSHVFVYGTMPLLLDRCHGT
VHLVGANPFAIAATMPQTSQRVQFYLHRQHCAGGAVQSLLHTMLSKQESLDLVAHAFEIV
TTHHATQQLLQISRQNGDKKKTGTPSWAHDPLFLSVTAAIIPQTNGHACFMGSTAALRRC
LPVEDEEGPLPCGPPWRRWGGVTLQDFLSTCMTSFDGFPVPGGGGDGDGRVVLSTDVSIG
QLVMQREVFAPLADVVLVSPPFAGGCSGSGVRVAARSEVETATTKTQAASAREDCEEETI
DARSPSESRNSKGQLYFARYLFYALFEYASCVMRTGLELVDELQRLLIRLLHAAELHCGP
LRQLLLPGMITDQVPTAMVLLPMGGEYRRLGIDMLLRLRAHLLVVQVLLAERRPLDAMNY
VYANIQNSQDTGDELLNPRVMNDILQCALDAVVDREGNCEGCGINRRRSLEFIIVFEMIT
GALMQQPSIGRMLPPDYHTMRAKYMQLLAEGLGG*
>TCRU_3076 Fructosamine kinase/Phosphotransferase enzyme family,

putative
MPEPLEETFSRVLSAKVARAKRVFGGDINETYRLEMEKDDVVYFLKLQRGTTADFYAAES
LGLSLLSDVARTPRVVQTGEVNGDAYLIMTWIQSFPSAMRGGVRRNMAELGRMVAIVHRQ
TSPNGQFGSSVAVPLAGCKTSAGWSKDWATYYIESLLAPQVALARRKGYWSDRREAMFVA
FSKRFCAFYASKKNVQPSLLHGDLWGGNVMYGESGEPYLIDPSSYYGHREVDIAMTRLFG
GFGSEFYTAYEGEMPLEAGHASRVPWYQLLPLLCHLNLFGEAYGSSVDSAMAHVL*
>TCRU_3077 hypothetical protein, conserved
MSDGSANTLPPPPALRHRRLVAESTSEMNSGNWVSESASNHPMSTAQSPNSPTVVVATTV
NSTTTTTVAAAAAAASAEARALLEFGEGYHRILEELGNPGYHSIKALFYGEEGPPGNTVP
SITVSFELFEAVQNRFATTKATLERTKEDLHTRHQQYALLEGQHEQLQGSYNLLEQRAND
LERKNTQLLQDIAKQGVMSELLRQQVTRMKSEAEMIEEKMAKRDEDLQVLHNRIAEGLVS
LSQKETVIANLRRQLGYGGRLKRDGVSGNLVGESDEYSPEALKRIADDVEGRSTEARLRL
CVVELEAKVRSVIDERKYVMLRHTMYRNHVQIVTESYEALCMSREDAMGSHVCEAPPSFA
VMAESTEDRMMLNNNNNNKFMRSSASRLSPHTPSLSERHARNLSPPFQESDFERRRSQGI
ASKRNSVTSRGDSYERTDMSPMTAESDTQPQRSPSPQNRFPVASMRTSSLENNAGDKGRA
SSPSYTKSVSPASKAKEGTRPRESRTKRKLHPATTGSMDHSGASLPLVIQHGESQGQKSP
NDYSNRGDNTATPPNKIKKRTKNAGARDQGTQTEWHAGKRPVNNPQLPPHPSSAGRHNTT
GSHSLNPRSPSLSLLAAAQSADLSSTGNSASDKAWERAGFAPRESASTGPFGSMLPVFEQ
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LADLHEFLFPLKGNEQQGGTKPIPFYLDANNADAATQAEYLLTVVAADTRVLLHILNRSQ
RDLSVSGGLHPSPKKMPRGGLQRVLSGQPSETSSSPNEKPLVIARTGRSPLNGAFDVRPV
DVDGAGKTPSRRREITETTSGTNSVSASGKIHAADKLDTSLVADSPGGLSPAKRLSESRR
TVTTGNVSSLLSGELAGAGENEARRSGKGGRISASERTTSGNLSRVSQSLNSGGVSRVGN
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ENAGAEQRGHFRQSSSLVKDSEALVGKQKDLQTTSQTAKTTPFLSLPELPIRGGDDEGSK
GQAINQEGVTAAADPGVGAGAGTIGSKSAPVLPSLSTRQRNMTYRGADRGQQGSKRLVWN
AAVVRFDFSKLFDPKMEGQAPSHYPPGRQQPSRSFIPARSPKETFFRRALNNKGVTGRRQ
FSAHHGATPGIAFDTDKGTGFANAFSPAPSNYLLPGFCFSPYMHPTTSIPSKNTAEGQFN
DLVLGGTAMFTPSSTERVRSLSHSPSPPRSRWPQDPVMETRKSNPNDFAVTDHWLGDLPS
YSNNAAHQPPAAGFASRVGICTQEPPYWNKFYSNEQVLVHILHRDPEFWRLVRDSQGRAR
QPPKTFSYWMRRRLFRGRQLRFLLGLQHPRVHPRCMPLRLFNYQSLVRPSDLYIGSSRNS
TLAPLVLGRQWYAKRRPRFTSLVKRVHPFPMKNIEPQKEFVPLLIRGLTLRPLPAKKREH
*
>TCRU_3078 hypothetical protein
MAVTQHDGAAASTRPATSLRVLELSDEFVKLLGVERDAAESLQIVFAARCRQLLPVRRGM
HDDRNKGTNEKFSTRVASRVVLLTGSGTLFVLKNRLANGCRMVERLEFGAHLHPHDRQAR
RRGQMTRRQRKTHSDEDEDDEAFHFFGYGSTHRGWPLVRIEVNVDEKPIKGMQSICITGW
AHRSRKWVPQTAGPFFPGAGQTVRNPKTGSSATAAAFVGGGATSLSNPSSSARRHEREGK
GNNSCNTMKVRFVLALQFYARLGLLGSVLALKIKQIATHFGRLGIMTFTLNHFSQSLHHA
RQNMALFAAESLSSLPSPPPRGDGSLAFLVSLRHLFRLRDVVQWVKKRKRHRRISLKDVV
CNGIPMPPTMTVYESEDGEEKDASLRSSSSSVNSSLSSSELAAMYTTDEEAEREAGLAEL
EDRCFSTDNTLLDDDIFNARIIGLLDDITRVEGILMAQRPQGQ*
>TCRU_3079 hypothetical protein, conserved
MDDIYRDGESTADLSQLQCRPSLRLASFPSTPPPPTPLKYRDTNTLGNSKQWRSLHCRRG
LVATARTAPTSPTRSRPRAAVVRRPLTPTFSAIPPLHRPVMTEADEDHVNSNSSSRFSLV
CDVPVAGGTNERRVSAGDGEGGDGGNEEQEESLAQSSRWVSFSFASALTSRRQSESRPSS
PSPQPRAAIIPSNFPNLHLSEDEYNMAEGVDATTRCSPTTTTPLLSLGRPPVVFNDTPEE
ARENREEDGDGGEGRPIKKGRESLLLTSAPFSHTAEVTHFLPTATAGAMTFPIGVEGLPT
LQSRGKRERSALSSPLTTSFVLCGTDSSFQGAAESATISLGRGEGDVVGKAMWPNTDSHL
PRPRRLVETTNLEESVERSVLSVASTATMRQPIPTAEGGGSLVLVDGPTPTPWRGRLAPV
VTATAESKPCGSMVLDVRCSDAAVAPVALFTDVLAGCSDDGSAQKGERSENDDNERAVSH
DSRCCNATGMTTCEEKDVTRMEKTVGDGCGVVDDERLAMPNSIVRPSEELKALIESAREE
VRRASKRILAALHAHRCASCDKSDCVQSNGKGSTSGVADDDCTWVGDSPQLAFGRSLTGP
SGDGAGSPWISKDTVVMRRNLAARAGCILRRLRGYDPTDVGILSLAVVIRVVRLVLFNDA

TADALPVCRSEGSADLFWGLTSSSSVCSGTPERKRTRQEVCAAEESAMELCMSLWRCFRE
HFGERYAAKRFGICGDVDAENSGEDNSCSGSQSPSHAFATCFPRVRLQLGLPGQSLPPSP
PLLDTRIDYNVFAASLAELN*
>TCRU_3080 hypothetical protein, conserved
MINYVLKSWAQLDSSFSESFTPTAGLVGFISNASSGGDTWSDDYLCVNAIVTKNAMKGKD
GFEFTGLGSGAVWLVSSREHNGPHTFVSCDFTIVATVMIQNFSKLSTPLPGAGLDAPVST
NFIGLSHNADSRWETVFYGIKRASGSTWEPGKKYQVALMLQDGHRGFVYVNADLVGSPET
IPTLETQGAEVSYF*
>TCRU_3081 hypothetical protein, conserved
MDSCLIIDPALDVRDADAVIWRGECLFAMPGDRPSSWCLDTLPTNTTDARDPEETYLSAA
MHAALGCLVMQVRLRVVEKGGVRWVPCTDGATIAWATRPHGEGSVACRDHAQVCTISAAA
GTLLPVVPWDGEARAWSRTVPLAITGQGLRGGIRPRCGEH*
>TCRU_3082 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MSADGCGVPSVVEWEKDKLMMMTACDDGRRRVYESGDKGDSWTEALGTLSRVWGNKKGVK
VELVGSGFTTATIDKKKVMLVTLPVYSKGEKEEKGELHLWLTDNTHIVDIGPVSGKDDDE
VTASSLLYKSGGNGGKKDELIALYEKKKGVEETSSGMASVLLTAQLEKVKEVLATWKKAD
ERVSQLCTSESVGRDTLPGTACSADIKITDGLVGFLSGNFSDKTWRDEYLGVNATLDNEG
VEQVETGVTFTGRSAGAEWPVGKQGDNQLYHFANYNFTLVATVSIDGEPKEGNIPLLGVR
LDGEGEKKLMELSYDREKKWILLCGGETHKKHSSTWDPETKKKDHVVILLRNGNQSSAYV
DGKRVGEDVPCALGNTDSKVISHFYIGGDGKSAVSTGNGEDVSVTVTNVLLYNRPLTSEE
ITALNTNQLSIPKLEDLKTEARDAPPPAGTEPHTLGAVSSTIRGGHQDTEEKLLKISNDA
GGGGASNSAKTTMTTHSVGSQSAEQLASGGSHDVNKNVNVDSSSNGNPAVGTVGGDTKQG
NGSPQIPVGISDTADANTPTTEGEGQYGPTVNPEAGVSSGENGETVKGTNGQEEEIHPQD
GELNAAALSSSLGNVSQGNNSDAGTVRERRLLPSLLLLGLWGFAAL*
>TCRU_3083 hypothetical protein, conserved
MTFPTYEDDFPDDALRDPQLFYLTTRRNAGLVLSDEGLPSRLVPKRRAHEEACCSRLVDA
CPVRSLFTTVERLIRLIAEPSTHCTVLVLLSNADRTDRMMVFHCWKAL*
>TCRU_3084 hypothetical protein, conserved
MESTYPVAYRRVVVSGSNDPVEYFVRAKDDGRTVVPTQTETRTGWLMCPVRLRARLRHWM
RAGQVALRCLLASRPSRLLIVKGIQEHSFPEGVSAVWSARCSARSIEPFL*
>TCRU_3085 Leishmanolysin, putative
MLTWCCAWQSAVGGGALDDCRGGCEEHHDIDDIDGMELQDGDGDRRTLESHWSQRHAKDE
WMAPIGCADFCTELTLAASADLGCMRVKREMVEPMRW*
>TCRU_3086 SKP1-like protein
MPEEFDSQEVDFTKYCVLQSNDQPPVEFKVLREAAMMSGLLKDMLDDQGDMEPIIPIPNV
SGRTLRLVVEYMEHHYQNRAEPIEKPLKSKIDTIISPWDRDFLYTHLVKDHDEKQHEVLI
DVIMAANFLNVKDLLDLTCACVASMIRGKTAEQIRALFNIESDFTPEEEEKIREENRWCE
EV*
>TCRU_3087 Organic solute transporter Ostalpha, putative
MASEQTPHTDGENSSAGKIRGLDMTWALNPNLTYAAGVCVAIACIISFADLRDHLARFDY
PQLQVLVLRIIAMIPIYGLFSLLSLVLLDMRFFLETIRDTYESFVLYMFFILLLKYCGGE
GQLLRSLKAKRYKGVHLFPFCWLPTYPLDTAFYLRCKRWVLQCALIKPLCSFLAMLLNPL
GVYVVGKFTLNNAYTYLSIIMNFSLTVSLYYLVLFEVELEKELHYAKPFLKFLCIKTIIF
FSFWQSVMVNMLLKVQLLYTGETEHERENVSAAIEDLLMCFETLPVALLHRAAFGRSKLD
EEMAAVPMYMKDENNNNIRSNIDTALSINDVIEDTIATIFYRRGKLVDQENTEDDYANEN
ERGNGSKKRGGGAAAVPEADDGFVEAVVAYGRDPTLEELVHHAIASDYGVRADGLLHYDD
DSDREERNRDMNFADTDVIMRRTRYEEASEAVKVDTDLLQSHQLQLQTNTPQIYCVVCGR
FDREMVRRKNGYKCKECIGVKSKVLLRTYQQEVLEQTASASHGVVPDA*
>TCRU_3088 40S ribosomal protein S15A, putative
MLPTASQGTKPAKEKMTMMSVLANALRCIASAERRGKRQVLIRPSSKVVVKFLQVMQKHG
YIGEFEIIDDHRAGKIVVNLNGRLNKCGAICPRFDCTTPDFEKWVKNILPSRQFGFVVLT
TSLGIMDHEEARARNTGGKVLGFFY*

>TCRU_3089 hypothetical protein
MAGRRRRRDDFDGGTPLRERAAHLRSRTGHDAEFAVGRLLHPFRAEFNDHFETSLEALRD
IAVVVDQLRLLLRPSAPENFVVYDPYYCAGTVVRYWNTLGVQRVIHANRDFYKDIAEGDD
PDDYDMLVTNPPFSGDHIERLFNYLVARKKPFAFLVPDYTATKDWYRTAVRRHFTPVPSS
GKGDINASRHTRPKLPAALLQPPPFLKMEQTASAEIALDDTKNKKQKEDNKCDNEETIPI
GTEPFYLVPRGRYDFSHPKGVGKDHSHFRTMWFVWTGRHTTEVLRGTKVEFARRHREDST
QRQVSPDVVHGLDALAEGHYVQSGLRLNPQRRAKQRNGRR*
>TCRU_3090 60Kd inner membrane protein, putative
MSFHAVVRRAALHHVAPLCGTTGAKTSAAAASPLTFFGGFGGRRFGTETILVSVRCISWN
PANWVGNSPVGRESHRQIEDELPDVFAQQPQEVDDFIRPEKSVFERLEDFWDWIVSFMQP
VEKQLEVMRSLRHSGFLGFDFGTWGNVFFFYGIVMRLCTLVPSLYSHRNALRMSYIGPQI
SEITNNQNRVKNDRTLSTAEKRVIKDGYNRMKYALMKKHGCAQWKSFFTMLTAPITMSAF
FSIRRLAVYESDLEMAPFLWVKDLTMPDPTYGLPLICAGMFLVNFELNQQMQRGGRSSSG
IYIRWAVRAASLVGVYVFASQPSAMFAYWIGLSTAGLLQPLLLRWQPFREFFQFPDPPQA
AKSQIIAEVKGLSMVERLFLSKEEKLRREKDRQALWEERSKKKFERVEDYDDVVFDVDED
LSKSTRKH*
>TCRU_3091 eukaryotic release factor 3, putative
MSGWAQPGGFNPNANAYNPQGQQGYYPPQQQQPQGGGYGGQQGRGGYGGYSGAYYPPQQF
QQPQFGGYSGAYYPPQQQHQQPPVGGYSGGYYPTQQQHQQPKGEYGGHSGGHASQPPVDN
IGNTAQQKQQDQQKVSAVESGKLSLGGAASEPVVVPKKGKAGTLSLGKKKTEDDKKKNED
TKAAEESKKGTSAAVTMSDEKRDGTPSNSKMSTEDFREYVKREIAKQREQNKKEFVRDPR
PHFNIVFCGHVDAGKSTISGHLLMEKGLVDQREMEKLRREAEVHHREGWEYAYVMDVSED
ERTKGITRETGAAYIETEKRRVTILDAPGHKAFVPSMIGGATQADICVLVISSRKGEFET
GFEKGGQTREHAMLVRTCGVKQMICVINKMDECGWDKGRYDEIVGKLKPFLRQNGYDEEK
AKNLCFIPIAGLTGDNLIHHSSDDVCPWYKGPTMMGFIDNLVLPETKSENDVLCIPIVGS
YKDDGRVFIYGKVESGSIALGERLQILPTKLEAFVEGISIESTEFEKCYPGDNVHLRMRG
VDESDIHAGYVATSIPTTLSAVEYFQARVVILDVKNIICAGSRVMLHAHAAQEEVSFHKL
LAKVDKKTGDVLEKEPTHAKAGDVVIARMELERSLVLEAHKVFDKMGRFMLREDGKTIAI
GLVMKLYESTKESLAKSGKA*
>TCRU_3092 protein transport protein SEC31, putative
MRLKSTPLSCAFAWAPSHLGTPTFLAAASLAGAMDEEFSNEAFLEIRLVDVTQTDETEMP
VVARTFIPERVFRVDWCSFGSACGMIAVACCNGAVYVYDASVMMKNYQLNPHSNTEEPLL
CAITEHRGAVRGCQFNPSQPNFLAIGAEDGKWDVWTLEDPRDPQQVPVMSDAAHTAAIVH
LQWHPKYPHIIATASSNCVVNVWNLKSQTLAVSLNVSKGGKSGASANAIAWHPVVATQIA
VAMDEKDSAIQIWDLKKSMVPLREMRGHESAVTGLAWNPGDASMMASCSADGKTIWWDPS
TGEKSGALQQENSYVIDVQWSPVLPAVLATSSFEPLLCVSTAEDVSTAASAGGPVPKWLK
RPCGASISLGGFVASLVPNSTKKVGLTCVLGKSAMSPATSQDLAFCDTLRKIPRDSEERV
KWLREQNYSLLAAAAACKDDRTPILAYLNEETSTHDEGEDPFETMEASQKSFEDVAAAHI
AAGRIREAVEVCLDSCRFDDAFVIAYLQGGTLLQRVQQEYAHYTLTQSRQKRHVVYAAAI
ASGDFGSLTESENVPWKEALSVIISFVGDGFSDACDRLGEALKKKGNREGAMTCFVCSGN
VDAVMQLWREDNTSLGRIMRDALLLEEVTGRRVTSAFFSDCLYEYGMKLVGEGVLTEGVP
ILQRSASIGNHSAAVMVDRLKFHVPVGQVVFPFAMMPLSDSPSPSCATFITQQQQQLRAQ
PQPQPQQQQQPQSQQRFPMPGQYQQPPKPLQQPPMPGHHHQQQQQQLPPSLPQQQQQPM
QSPNFYLQQQQQQQSQGITATRSVGATMPQGPTEAAPQPRLMPHPISSYSSMKQGAPVSS
GSPLAMASAGYSNGMPSAPPRQQPQFAPQGGYAAPQQNYVDPSRPLPPPPLPSGLRGASV
PGGQALARPTQLAGIQQMQQPMSSQGTGVAPPPPPPPHPGAPVVPPQQAGGFVGSSHPLP
RVSANASTYSSGVNDDTSVGNINSQGAISSLYGNPSASTVPLAPSTNAAASVTAPPPIRP
MMPVPGNPPFGVTTREDSMGGSLTNSYGIGNATYQASLTPLENKVLHQNNMSWPPKAAVT
PSTYGLQPNANKSSMPSPYGSSAVPSAMASRVPGSVPFTASSTVDDADLSHFDITSLNPS
YHALAQKLCADVQQVSNAQRRLVISKAALELFKLLQRGALSPDVVFLVSNYVNLMGTPLA
KNAWRQLSDAHFDVVQPFLNLKFLSNNDGVPN*
>TCRU_3093 MORN repeat, putative
MNLVKPALHARGTGLRDSSLNFPAFSGSSLSTNSTVFLTSDVNAVIEEPISLLVSADDSG
ALGEQHSLKKRAAVLYAGEVRPYTADEVRATAGTEFASGKAVHVFLGHYRQSASASGLQE

RSIKEGPGSMYFADGGFFLGNWVNNYRCGMGAFYSSCGYTYEGEFEDDLPQGHGVEHFPS
GEVYVGEFLEGRPHGRGVTYYPRNGSIYVGEYSRGEKHGRGVIFYENGDVFEGSWVGGRR
SGEGISTFLETRDRFNQSKRCNFRRCVRAQWHGDKCKWETVSSDPTHEAPSLSRYIDEGL
VKPLEKLEIPFGCSVGNLYMAHELVREIPPVLLRRAERCFDHLDAMCTGEVPFSTLVAAL
ESSSSREAIVQSILKAIPLSYAASRDASPTVHLDFATFLRGFFPHISEADIQRHVIFELP
LEKLFRLRGVLAGMVSSKKDGFLYLTHGFQEDALFHIASRECDGMRQFAVGGPEQTRRES
VTSAGAAQLTMEELNAAKGFLGGVRVPHGLFLWKKIVSGIDRLSFRELLEGLYPCVTLQT
LRRCELTFFSTHVFQGYLQAFSKLDEFHLGSLSIQAMDAAQREFLAARAKGHERIPRPAN
ALEKFVLSGRRRSLVQWEIADIALSVPFAKYMDRSKSGSVTLADILRHAYPNVPCAATRA
RLSLAALPPRRDPHVTEGQMNGTAAAGRQNSSGSSISLLQCCRCCICTMCAAHGHPLGAC
*
>TCRU_3094 60S ribosomal protein L28, putative
MTHSTDLQWLLVRQNSKFLQKRNGIRLSSDPFNNNANWTKRHAGFLNTKAAVVKTKGDRI
LVTTKDGKAGNKPKSMYKKAVMDAGVEASVVSKAVAAVRPDLASIASRRARKMASTLEHM
KKVRAARKERSSKITFQRKAVRPKRH*
>TCRU_3095 sterol 14-alpha-demethylase
MFIEAIVLGLTALILYSVYSVKSFNTTRPTDPPVYPVTVPFLGHIVQFGKNPLEFMQRCK
RDLKSGVFTISIGGQRVTIVGDPHEHSRFFSPRNEILSPREVYTIMTPVFGEGVAYAAPY
PRMREQLNFLAEELTIAKFQNFVPAIQHEVRKFMAENWKEDEGVINLLEDCGAMIINTAC
QCLFGEDLRKRLNARHFAQLLSKMESSLIPAAVFMPWLLRLPLPQSARCREARAELQKIL
GEIIVAREKEEASKDNNTSDLLGGLLKAVYRDGTRMSLHEVCGMIVAAMFAGQHTSTITT
SWSMLHLMHPKNKKWLDKLHKEIDEFPAQLNYDNVMDEMPFAERCVRESIRRDPPLLMVM
RMVKAEVKVGSYVVPKGDIIACSPLLSHHDEEAFPNPRLWDPERDEKVDGAFIGFGAGVH
KCIGQKFALLQVKTILATAFREYDFQLLRDEVPDPDYHTMVVGPTLNQCLVKYTRKKKLP
S*
>TCRU_3096 palmitoyl acyltransferase 7, putative
MPQTNSTEWRVFTSLGASLRQLSVEEIANHSSHSFSASLAHSRSILRVTGNNVARSTLSG
GGGGSGRQSSLWPSDNRVELKIAEVGEKKEQQREYSRCHQNDNFHVKADDHGVVSGADGE
LGISMQHKHQKGAHSRKGGYSMEVSRELVPSAAASVVSGVRPESITDAVEAFSSGEQKQI
NEDGIERQFLQDKAEAKKKRRKRRERIHSVMSIKASDVDKGESEVAGMSSIARHSVECVS
RSEDPPESVFFDGDGTGQIPNCVHFSDVYTEDTAVSPFRVVAHRRVELCGHGSKGGDEPE
GLEVAMNGAGESLAAKGSMSREHDIFFPQIEPKGCLAEEFCVLMPAEKQQNCPREISSPG
CDRDLIPSMETGEYIGSPQQFISSSPEIIMRAARGSSCGSFSPTEETVNSFQVSQTESDL
SSFMVRYSKPPFASCCVDRSNPDGWQCNRPRRHAFQWPLHFLQIIALTLTALSTILFGAS
ILPTYVLLYRSGGFSNCLPEMVVLVTLTGSAILSTCILWAVISFRENGDISNEGEPCTYC
RRLTHSDARHCKACNKCISGFDHHCKWLNMCIGEKNYRIFIAFLVSSALSMLLAFISGVV
LLARWWSYLSPYSLFFRIGPIVLCVLMLLAVPPLLHLLGFHIMLHRLGLTTFEYLIQRRR
VMRDPHAAASATDAGKELHAHEVREP*
>TCRU_subunit alpha, putative protein transport protein SEC.1
MKNYMMMAQPILALLPEVSRPQRIPPIKERIMWTAAALFIFLICCQVPVFGARPGQTSDP
FYWMRVVLASNKGTLMELGISPIVTASLIMELLSGVKIISYDVNDKKERAVFEGIQKIAA
LFITAVEAMAYVSSGMYGDVREIGTIMSGFIVLQLMLATLICILLDELLQKGWGLGAGTS
LFIATNICDTIIWKSFSPSTINTGRGAEFEGAIIAFFHLLVSRSDKMRALKEAFYRPQLP
NLTNIFATLVVFAVVVFFQGFRVPLMTKSRHAAADRQPYMIKLFYTSNMPIILQASVVSN
INFFSQILSRRFGQHNFLINLLGRWEERAYSQSGQMFPVGGLSYYLTPPATLYELLNDPI
HGIFYVVFILFSCAIFSKLWVTISHTGPRDVAKRLVAEGRWLAQARESEEDMARLLEKYI
PVAASFGGLCVGALTIFADFLGAIGSGTGILLAVTMINQYFEILQQEGKDLGYGFLKQKL
A*
>TCRU_3098 hypothetical protein, conserved
MSKQLFIISAGASAALLQAATAIVDKATAGKLSTTMTSMAEKNAVVVGPETPVGVHTSVT
AAPASPDPAYAGVKTVLVRAVLPRASPEKVQLRDALDVFFAAGINMDAEVKAATESFKKS
AEVAVANAKAIGVNRVTLVLKQATKYNNVNELFRKVSTETIEAAGMTTEIQSTSVATNHL
IMFPESLGVVLLNDVTSTEKIELAYAGVLGGASRTYHTVSGNKISAGHSFKSVALAVAQE
LRALGMGSEATKVEAAAAKNPRAVLSSL*

>TCRU_3099 hypothetical protein, conserved
MHASGRDGSRNHPSQSFAGVPDGCAEGNDYRAHVMHGDRSPLEVMGQLPREPLRVDATNY
SALSRTGWRPFGLPITSSIEYDAAASRGTSHGLSVRRVSESHAALVNNLTKRNSSSLLTS
NMQNLTDRGMLWSDLFAFGDDAQVEHQKHVTNVNIEEICLWTAPVSAGRCVLPGAEVGIV
PTRPKKFTRAATLSDFQREPATVSTTQGADNNAATTNFDDSNRGSVSCMRDVLNDGASVM
SSFSSENSLLTQRVATPFSANISQRLDIARRRKRGVFALFGTIERGYFESFSRMFRRNQL
VLEVFLENVLKSNQDLYPKEIDFLDFLRQGQRTPDEQFFMDPLISWPLHLLYEVSCFYVS
AKLHGYHDTFETIRQQGGLFASGKGIFAALAVAMSPTEEELVHHASRMYRATFFVGLVYS
KMEKRLQTHLENSPQRSFALLLVNISTISLQLLLDEVNKVSFGSGNCDGCCGRNKCCVIP
MSKLEMTRIISSHSAIVCGHPLDLERLSTVLVCYAESTGVRVHMEYLLTTVPENSTFYNQ
WQHLELLQMWKDNGVELEDSELQLTLYSPVDGQPWKNSSKCTLADCIASTTTCSSQDLTY
SLQHMRGGDVLLDFSGATPCMSQLIAWTRRNITVLSEPADCVSTNVFPSPRRSPEDGIIR
ETLARCARINTVLQNMKWEGKPYRACVLDLTTSFVDLGLLISSEEFLKTYSGVSYLKGST
TVRKLSGVSTTRYHQHELSADVRSNSGKDMAMNSHNDDLFCAAGGHSASAATGTIRHVIQ
PNEKLPFVVDIYQDSPVVRYYEMQSKGFLTRGAVEFTQRLSLCTGIAFPPHTLLMCPTVL
ALMELWDTYGFLRHKISDDE*
>TCRU_3100 inositol-1,4,5-trisphosphate (IP3) 5-phosphatase,
putative
MRSLLDGITSALRIPQQQQQQQNEQSSQGPVGGTGVTVAPSYHQGGSTGASAAGSLPGSS
LYGGSNISCSFAAEKLPDLPFTMLLLTQNIGCICSRCDGGNGEEVAGGGPETATTKGISD
AVRTRVADFLLELRLLIHEASSREFVLHLRKEKLNAEGGASSAADAGGPSSEVPPLLDVI
VVHFQEVGGKGLNTAFNAFFAEALKTLLPEAAWSSGLLMETNSDMQRFTALGSIVFLSSR
MCPISSILSFRHRTFVAVADDPATYGSSPTFLFHGGKFSGAGSGRKGFLLTSLRFGTVVV
NYLNVHLYHDSRNTDAAMASPSLYSVQRQEALLEAMAECMVFISPEDPLFIFGDFNARLD
THNLLKHLKETQQIDVKILVKEVQAPDRFWELFTEPQNAGMIKKFDLELQRLMDVVAQQS
GVELAEFAIRFPPTFPRIPEREFAKSNQKQQIEMSGVNVEASEYGVKDDDPKLGNERRKK
AAGKEKGTGEAKPSLVLPRITAIPTRGYTRQRIPAWCDRVVWNPAGLELMTGQRSLSPSV
SSALGKSDGATDSSPRYAYRSFVLAHTDHDCVALLF*
>TCRU_3101 pyruvate phosphate dikinase
MESKKFVYYFGGQKADGNRDMKELLGGKGANLAEMVNLGIPVPPGFTITTEVCGIYQRTK
GLPQEVVEQVKANVRRVEADMGTNFGDVENPLLFSVRSGAAASMPGMMDTVLNLGMNKAT
AEAWIRRAPHLERFVYDSYRRFITMYADIVMQVGREDFEEAIGHMKEKRGTKFDTDLTAK
DLKELTEEYLVLFQRKTGFPFPEDPMTQLFAAINAVFRSWGNPRAVVYRRLNNITGLLGT
AVNVQAMVFGNINDRSATGVAFSRSPSTGENFFFGEYLVNAQGEDVVAGIRTPQQIGQSL
SLRWAKSHGVSEEERRHRYPSMEETMPENYRLLCEIRAKLENHYRDMQDIEFTVQDGRLW
MLQCRNGKRTIHAAVRVAIDMVREGLITKEEAVLRIDPLQVDHLMHPNIEPGAAKSNKPI
GKGLAASPGAAVGQIVFDADSAKEWSARGKKVIMVRLETSPEDLAGMDAARGILTARGGM
TSHAAVVARGMGKCCVSGCGDLVIKGKQFTLSGRVFREGDYITLDGSKGLIYAGQLKLQS
PNLKGDFETILQWCREVKRLGVRANADTPNDATKARSFGAEGVGLCRTEHMFFEGSRIDA
IREMILADTLEGRKAAIRKLLPVQRGDFLGIFRAMKGLPVTIRLLDPPLHEFVPHEDAAQ
AELAKKMNVSAEKIRNRVKSLHEMNPMLGHRGCRLGITYPEVYNMQVQAIMEAAVAVSKE
GCRVVPEIMIPLVGKKEELTFTKQQAVKTAEETLAAAGQRVDYIVGTMIEVPRAAITADQ
IAEEADFFSFGTNDLTQMGCGFSRDDAGSFLRHYCSLGIYSKDPFESIDQEGVGELVRIA
VQKGRRVKPMLKMGICGEHGGDPTTIGFCHKVGLNYVSCSPFRVPVATVAAAHAALKEKR
QMEQKYKAIAAKL*
>TCRU_3102 Adaptin N terminal region/non-SMC mitotic condensation
complex subunit 1, putative
MLSVNQLSGSALFSRAFDSTIVREDLLSQNTPRQLSALQQVVAFMTIGRDMSGHFSDIAP
LCSSTNLAIKRLVYLYLMHNSHAQPQKAVLQAGVFVKDTVNDSPLIRGAALRTMTSLLVP
VMVDFITAPLQRCLEDSDPYVRRIAAFGTLKLFYIAPNVCEELGLLEKLKNQLHDENACV
VASAVAAILELRQRHAPISLEEAIVENVSRVLEAASDAPGWYQHYLIEGVAVAFKNNSLM
LDMERAEKIIDGVMPFLSSFNVATVMSAVKAMTSFLLQASALFTLSAHGNDGSNKVEKAS
QLRDRYGPKLVGACVSLLYECSLEVRYAAFRNIRLLLKTGLVFFFKRHLGPFFVKYDDPI
YIKLEKSELLLELADIEVGEIILSEFAAYATDADEELVRKAVRLIGFLAAKLEPLAEQCV

ERLLGLIDTGMSHVMQEAAVVVQTILRRYPNRFLRVVRKLCEILDELRSPESKAAVVWVL
GDHAEHVENAGDILEMCAESFSTQPEIVQFALLTAAMKIYLSSECKDMGRSTNFLQRVLS
MATQSPRPDVRDRAFMYWRLVTSDTEAAKKLVFTFSKGLSFTMADTLEKRRLQSFLTDVG
SLTAVLHRPLHLIYSNETGLNENDEEEEDAGDHFGEKFIRRVVCDDEMAGTMANNLVSKG
PNIRDKESMHVALPADEGNGLEVRMCWSQLGNKLLLNCHFSLVSGEGYTRHAVVRALQIN
RNIHALGLAQECPVVELEVGEKEPETLQLMTGTNNEKSPMRDLLVAVNVDPIGTRYFLAP
TVPPAMLLLPAASIDYGFFAHQFQQLHAPSWTMPTTLTPTRTDQTRYTANALRLHGLNLV
YTSKLHGSGILRLFISAETIAAQKLFMEAAIQDDLVVYLGVRCKDPQVPPVFGAYTLSVL
SVAEN*
>TCRU_3103 HIT zinc finger, putative
MGFGNAQDIFAQSLQEERLAKLCDDNAFVNVTEVFKRQRRDGALVNAVDIEVNFLEPSAD
FSSAPPRVHLSRCLMEQHRAYTRALEEDRRDHKKEDGASAAEPSSSSSSSEDGDTDMTTN
RVKRPRDFESRSRGRKKQAREELHDGGVHVNKISVNVVQTVSDVGRERRNLGGWLQSRRS
IPLELTVPGPSYMAMAAPPPLHLGGYHLCSVCLLPASYKCVRCRGALFCSIKCHVTHDAT
RCMKFIV*
>TCRU_3104 40S ribosomal protein S5, putative
MSAKAPKLFNKWSYENLQTTEIALSDHISKTATYVPHSAGRWQKKRFRKARIPIVERLTN
GLMFKGRGNGKKPQAVRLVKHTLEIIHLLTDQNPLQVVIDAVSKGAPREDSTRVGSGGVV
RRQAVDVSPMRRVNEAIYLMCKGAREAAFRNLKTLPECLADEIVNASKGSSNSYAIKKKD
EVERVAKANR*
>TCRU_3105 40S ribosomal protein S5, putative
MSAKAPKLFNKWSYENLQTTEIALSDHISKTATYVPHSAGRWQKKRFRKARIPIVERLTN
GLMFKGRGNGKKLQAVRLVKHTLEIIHLLTDQNPLQVVIDAVSKGAPREDSTRVGSGGVV
RRQAVDVSPMRRVNEAIYLMCKGAREAAFRNLKTLPECLADEIVNASKGSSNSYAIKKKD
EVERVAKANR*
>TCRU_3106 hypothetical protein, conserved
MRGGFRRGRFDRLPQPGAVNSYSEAIYPPRVYHYYTQQSGVAASSSAGVIVPSIDDGVGE
TRGREAIPQGVGPVMDKKSPPLLRDFVGCFIDGNQHVANSRAFAILDSGKEPLNVLHYPT
LLGVNRKDEDAGAPIADKNAAHVSTAGDHEIRRWEDSLGLPAELRIYGLAKSTGDMSTAA
VDRLRIRPSKRKRIVKPIRRGTKVVVLPPACTEDAQEIKKVRRIVGEEGETEGGNRAQPR
RENDDRNEEGSGGFDREDDEASLSYNIDDDDDGGDLDGPEGSGGEEDFF*
>TCRU_3107 MRB1-associated protein
MMQGNDSAKSFLEKLKYGGSNTAFIDNSAPPDADGIIVRRLERQYASEPLSVLGIKISDD
GEVLSTESGSPAAKANILPHYMIIYVNNQFVGCRADFEDIAAQHLTLIIKLQTTSAMSEL
MAKILDDEEKVETENGKPSTDINELLRTTPRYGFLSAEHPMFLRWNHRIQTQREARQLLR
QATREAEEQLAKEAFEKIRRELEAEEAKQRESQQVAQPAVNPVPVPAPKPTEEFLLKHVQ
DESSFGRVEEFTEKMDEVQEEASAEELLKLIGAQPNEEKAPVNIVPENDGEVRFFIIPTE
EYKLSNGMIATISVKKRSGPFPKPPPGKPPKGLRGLAVNKPNGAVTSMKSFESDVVCSFC
YLRGHNVDECAEKKEQERRLAFVPKERQICRDYLRGRCLRSDCMMRHVSKHSQGRISPPR
KRDRERRHRSRSRHHRGGSRRRHHDGRRRGHRSRGVSTERHRRRR*
>TCRU_3108 PUB domain containing protein, putative
MASLSEEIQRLSELFASGALSKEEFKAAKEVTIKSYTPLAATAPLLGEVGRSREEAEVHT
PFPNVNISEFGEDAAGQPQREKAYTVLEKILRNLLQFPGEEKYRRLRLSNPVLHSQLFSV
PGAMGFLQSIGFARCASDDGDGDEWLRLPGMPCRPFLEEGLRAIHFLRTRSREVVARNQD
FLRLRRTLSLEVRRERCEKAKAVGELRSYIVSEFCSDDAGDGLYSSQINLDKLETILTNV
LRCPSEAKYRRLRLGNPAVYAAVLQQRGGMEVLAECAGGEMVEEAGEAFLLLREGTVTEG
KLRCALQAVHAARLAVREVQEKTEQRVREEARAAVRSQARLEREMELRRHCPQHNSEGAE
LCEGIQRVGGRRVPVAEALRFLMGKGRAEEEEEEED*
>TCRU_3109 AAA domain (Cdc48 subfamily)/ATPase family associated
with various cellular activities (AAA), putative
MVITRSQSRKEARSLICTSNGNKDDAPGVVGDDNQNSTQERLGRGCRIPREPPASYDSMY
VRKALLPSAMRRAENEELQINSRYPQRDAAKRAVLRMSSTLHSLGERTRRNFWPLEDNNG
DGDDESSSNDGTEDGTASFQSLGRKCNGNRFTNLPRKRVREPSINSFITDDSLREGSNGR
GKDADEELLVEDPSSLSSAEGCISEGEGRRVFRKAKESTVKHIPINHYLDEVMKASERKT

KKGDKQKCKTHRRRMEDMFLGLNEAHGGPVGAGKGGEGRSITETPAPLGDITPLHIDTSV
SFEKVGGLPGHIVMLREMVLFPLLYPHLLQTMNLTPPRGVLFVGPPGTGKTLMARALANE
AASCAQRKIAFFMRKGADILSKWVGESERQLSLLFEEARRRQPSIIFFDEIDGLVPVRHA
KAEQSQAALVSTLLALIDGLDDRGQVIVIGATNRPDTIDPALRRPGRLDRELYFPLPDAA
ARRHILSIVTQPLLPLDHPDRNAIMEELTTRCEGWSGAEIQALCTEAGLNRLRTSLPQLY
VTSRRLQIPNNALTIQKEDFFVAAQRFKTSVRRGTESIVKGLEEHLEHLLYSTRMKLVSH
VASMWPSAAKALANERRDCSNAGDAVQELIGFPIPHTVKPMLLFLTSSVERNVYGVDSYE
FALEKAALAFIKALPSIRIFTLNLPNLVVDRGSAPMMVTATGSAVPEGGAGNFEELGFPL
NNSFTSGHIYSCIMAIQRSSGPSLVLLQGLDLWLAENGYPITNEEGNEGDGTDEERAQHK
KQMESFCYYLALLRDSDVLIVAPTLHCEVLSRFFGGTRLNTQIHKTVGNVPCAPSVDDLQ
RFLQYVFHVVELALLHCTHTVWEELHEDISPPPPPSMEEVRAARHGTLELWRRVEYRRRQ
LRYVLSKWLGQYLVSRKFSILCSADLDFTPSHDLYDEWRQHTQGSRIGLCDVMEKLENEE
YTSLSQYHDDIDMLVRNVRTFFRTRSSTDQRYRSRALELKETTVLNLYKINRNVVQFCEQ
YKDLAEPDVSLSSISPNDDVKPRIEEPTESRAVQSTVKGKRKPYRYYRDRRRRRRKVRKT
PKVRENDNLHKIGDENEEETTREEGRSANRDELKTEPAAAEALPRGEEEVDDHAVIVERN
GINSSDFSSSIAQCDKAAEIRVSMEMLRGLSFLELHGVFQAAMSLLEEEVSRRRNQQQTV
SVSPFTGTSEVGSTSFFLWMLGEAVRAAVKERRTSD*
>TCRU_3110 leucine-rich repeat protein (LRRP), putative
MFVSTSYESKLIGDEGLYAAIEAARLARSLRGATIRPHVRGNPLINPNSILLANTPKRWE
ARLLSEKAEQEILEAISGGDKAVSQYLQQVQIAIPEEKDLEKLRAVVPRIHHIQPHPVMR
FDEAKRLIQLMSLHGANITCLNFGNGALMPNDHTEASPAEVMAKMEELKQRFPLPTPKPK
KNTDSEEEEEEEEEDIDLNNNEELQKWCQNQQLEYTDYNQAIRLRAAYELDAFRNICEML
MHDKKVRVLLLGKNRLGAPNEEERVSLIPLRLLAKVIDANETIKVLDLSSNELGAHGFGI
IGKALTKNIAIVSLDLSDNQLGMPMPDLDEDPEYQEEDPVFGETYNGLEAISEVLKKNKF
LRHLRLRYNQIHSGAEGEEPPVADPTEMDPENDATTPDVDGWQDLPLWRLVGPLREYHRL
RALDLKGNALGPEGARMVATALAENHSVEMLDLTDNGIGFRGLHYIAKLVLTSPHSVLHT
LILRRNNLAGKKGSKAQRKMALAAMEAMSVALNGNTKLRRLSIAGNYLGPTLCAAMLSTI
STASALEEIDLESNDACGDVTAPHDTTVMHLIALALYGTALRGNRPSLAVLRLGSNNIQA
AGLRVLFPSSATMPTSLREVDLSRNSIRDGLEAVNHLLISSPVLHRLALAYNSITTAPAL
HRGIDANESLCELDISHNKLGSLKEQYCSDPQAQVRGVEELLQVLIKHPSLEYVNLSYNE
FEGVHGPLLAELCSGNKSNNSLRRIDLSGNPEINQQDIDQMVQALATKPGIEAFYISSSY
PAQLEKVATLRPVGQDAVLDPAAQRHQQLSLLKLLQETVYQSPSLIDINCDLQKGVLSEE
DTGTDEGEVIGEMRRRLLLNAILMPYGK*
>TCRU_3111 hypothetical protein, conserved
MRGGNSAAAKGSSNSGEKKKRTQTHLCETGVASAGKKRSKISCFPLPPHDSTTDNTEPPS
VRVAAARQHVMSIDKDSSVTSPVMGTTISSATGSRSGVLVTDPWVILQPQQPPFLRGWAA
QRSNTRDSNNAKTAERCVLPRTTTKSTATIPTRMSLCQVAHEILKSNTVENDACFVDGRV
RKLQRLELHFATPSERKQDFTRVVDPYTETMRRLEEEHHRRFRRALYVLQQMHPDPWWRL
QSSVYYDVGVPDLLACDENLLFSRVAGEVRDAGVTWLSLKNSTL*
>TCRU_3112 START domain containing protein, putative
MSSKKNNEGEITSNGSDSSSVVYQSPFPITGPEVQHGGRTYRLVTKKDFFTFREFADSLD
GFEMQYNRQNEFISWNKKVAGEPMRIIKVFGVLPNVIPATLYDMLQDATFRALWDTHRID
AFRVVKLDENNDIGYYAAKSPVPGVSNRDFVNQRAWINSGNNEYAIFNTSVPHRDVPIDY
LKVNKVSSDSVVRGISKITGYLIRPWVDNKGALGSCITYVTQCDPGGWIPAPLINYISTK
VAPSTLKTVAQAAAQFLEWLPKQENYVKDWPETADPFDTPVKNETIAFAKKKWSANGHLE
KKNASDERLVQ*
>TCRU_3113 MIF4G domain containing protein, putative
MTSSTADHLYERAKLRRLNLDPAPQRSVFAARSSGLKFDVKKATALAKRFKNYSAEASEK
TILMQLDTVSFGKFLSEAAHAVVQSLCHGTKMKPADAHSFTVVCSEVHQRYEDFWALVRK
ELKENIESVVDTGSLKLAVERIEEYASTTTTTTATTFISGEGNVSTGTTVVSSGLSAPPS
AAAKGGLTPSLSKSPVDEFNRLRLVARVFCEWWLVGLFDDAKPLLNLLKLLQKLAERNAA
TPNSPLAVATVFSITALMIREVGIEILGKGNAVLSSLFTEKKGDENGPERLRDLLGHCGV
FTIDENSEAGRKTPFLLGPAGARLAFNATTKKVGPVENAVAHQAEEVSWARLCEIRNASA
ENYCNDEEKRHFFGLALASTKACLRAYKQRKEEIEKWWHSVNDQAEFRGKTARFNNDEAR

FRFFQEHVERLYVVCENLLGMLGFSPPLPVDLSIVEQREEVEAVRISVTRKFHPIVGAET
LNRFGDDEQRIFYEYVPEIETLLDEVFLSSLTAEKAKWELFSRHSVIGGAIASGTGATTS
SGLSAIGSGGVGAPGGGDGGDSEEDDMDVEAAANTMEEGKGQHNTETVKLMERRRLRLAK
LGVPAALFNDYAEVLKLLEELGECTTAVAIDEWCERFVGEAIVPLRNSSENVVGARLFFT
NCRMLLTLELRHFLRFRYPEKLPFMARCAAIFDQYFHDVGIYLGARLEAQWRREYSTSTS
KRETSTSCSTRSDEFLQRRVGATGRYLCELMKFGTIPPSRVLNLLNIAVEDLKQPCSVAT
ICAIIEHGGLFLVRNHATRRATEKLIQKLKTNMMNEEMKAECSHMVTEAFSFLQPATPSL
VAFPSPAQKEESPLERYVRSLLHERLCPDGTKFVLDGLLRMPWDDVEKREMLIRALRSVH
QMSLDVVPLVVDILKELAHADHVHVVQRILYEVAEDMRRDLEVGAVTPELVSGSSRKSMM
ISEPYTTHRPLQWRLADCFFLANFYRVRLVSFRFVCHMLLMLLLYFPFITTHCNDYTRLR
CFVTLFRECIPSLPWIVNSRTGDFNRPRSRTSRSAERIATLHQLLRKLVAQLYLYRFSLA
EPLPLQLQVCLEELLHLLRDNIGRDERYRETWNKLQEKLKAREKGSQKEAEDTSKNKNSQ
LGIKSSQKLVFPETLEEAHAYAKSVAEETVLPANAWYEKVYEAIKGSQNDEPLFRIFAVE
NQKELSLCTSEVVHAEGADAENSRHASLDLLPEDMEQGDEVSTDRSSDAYEDENSMVRGM
TRGSCSSVGSISGSESLSDSDNVDTSVALSATVSDTTSTGEEEEGEEDEDEEDEEESEEE
DEDEEDEEESEEEEEEEEEEEEEEEEDGRFAAAEALRIRLEEADLDAQLRALMSENPRETT
GHAASAAVARGTSVERLMEQDLVMGIRMHRQHQRQCAKNTFLLPTAETAKEDTVEEVRFT
LLRRPPPNTSAAGKTGTAGVAASTSSANTAVASANVVKKSDFAVLSIPRGAKFAQNAMMS
QERHRQQQEELREITRRINHMHEVERSVHAAKPKESK*
>TCRU_3114 hypothetical protein, conserved
MPSTSTRRERSNLGKGSTGSESASKRPRREVTSDNSNAILSGTVLHNKADALLLPWLFEC
HRVLRAATPPFAVSAGFIKELLSPRYLKSSLNGVQQLTGCLLSDIVRLSSGHASGEERAN
MLPFDTNYADDVLCCLTSPFGQVARGEAPLKTCEQLIERASASHIFGYLIPHCRQPVQER
LTCVFVGVQQAAAGAFTGNEAPATSDNTITIVTAAEMGRILIDILNATRSITSDELAPLL
KEITAASPTLLRRAEANRKTGNTVDSNPLANVARKKTRAPGAVIAARVFLEKLDVIHPAI
ASYVVEMVEQGVGEVAAAEVTGDDVEKKRHGLRGVGRAMECLVALMELHVDLVGQLIPGI
LPYLEHEITDIRLLILRGFFMAFGAHEAAISTYRSAFVTLLSRFNDPKHTLRIEMVQLAA
SAISASTHVSASLAEERVCELLPFVEMRLVDPHALVRRAAVIAYSDVVSAAPSLVTSDRM
EKSLGLRVADKNPKVRQAAVERLSSIYQTLLYPWMPNVVMQCLNAEGGVSLLESSFESML
PPPSRVMPSDASFTTFSSSTSTGRRSAQASMALFDFEKESATRERTYVDGFAKMCSHLNF
KSFNKLLTFAAKKAQLRLTILRLFQMRAEVRNTDLKSLEGQEMINNIHRLLNFLQTMTHS
ERGEWDALFRSKDDKVSKAFLSCCADRHFHYAKERELLVKTMKGRVEGHVFRFVQESLSR
QMMLPIEVEHVNELLARLREALNGICNDARTKVSAEMRCEVEGLLRALLVFGHTAPSFLS
HCAVPLVDFLELVCQSSNTTIPTSWVILLLDCLTEWAGYAKTTGVDNKEHDGGGASVNMV
SSRKKGLFTTLGRLCVCGHEPLLRDATPEMVGAVCKHAARCFTALVGVNGAQESKALSQL
VNSIFARIRSTTTPATSSVVGWLKALTAFAKNRTVAPLLQDESLTRSITELLLAAVRDKT
DAEDLAKVKAKRADVLPMSLAGAVVDAATKCLTAIARCQSADGIVTAVAPTINILLAAYK
AASERESNTVGACRRRISINQQLAKLVIRPSSEIAKELAVAVVLSAEEEMVVRRSVQKKM
TFHIMHNQCDMRYVALLILTVVSEETKSGYQHLRLLLQQVGDHLRSKQRSSGATLSSPEA
LTCFLEYTIPFLVFFMAHHTFYSSEKENHFVAYQRVWHLLFEELYRHGTQCASFVVELLA
RIKQADEAVDRESHAARLLCDLGSRVMQACLGQRQISAEALKRYPGRVLLPTFFIPSKSA
TEALNTIFLDAKVHIFPHAPFRAPTAAATGGGGGMAGDKTPSLARVAEADVGDDNLVLTA
AKAKFDLPPNVRQRIDRALDAFIGSMTQEEIVKVLWSEVKQRLREAMVGGDDNGDSNDDE
DDVDEANVMEYAKEQLRQIYERAPPQ*
>TCRU_3115 hypothetical protein
MEPELITLSPLFIRLLRVGTTTAYALRPCFATRLDVYSASTGSEGGWTPCALLVSQHGEM
YLFSAEDGRVINAALLSPGPIANTEKARIDIVTQHTLDAETDTQSVYIRCRQQLQLMNNG
GEGKGKGLMPTQAVAVSDKAPGALFPPFSYLMRFHCRNAQVMLQFFRIITNFADPKKREF
NLRKANISLRGELDHSLFIDPLITVPRHQEREHQKQDTNKWSNALSKVSPLKLLSRLPGG
RNSVYMRDVAKFEKKRLLDAGERIELPLQDDPSLLLKPNSVCEVNSANAIGREASAEVSP
GKNEHAGAMANALLVKEGDPYSTVLPAVAKFYGWIMDKIPQFTLSSSEDILCMYGLPGFE
SQFAVFFVNPRIQNIVENSVGQLLASFPGLPDLPQYRIIAREAVREEMRWNFGVTYRELC
DAARKLIDDISIDQLVIDEERAAIQKSHDVAVEALLAESQARWQKMLEEEGHVFFDANHE
PKSVTTGQLLAPLCTEETEWRNEVAEAAEALEVLELGIQRIRNTIVADSDEDNDDSSGKQ

DSLGNNVGGVAFMPSRGGKGGNSSHFLSLQEEAAFLLQEIQRERETLLSMQLQCSSGDRG
PKDIVEDDVEIKSMRSEYNARLLQQQQQIDTLKQELQKSAAMFGINARWMEEQNRRPGLA
QELLNSTYVV*
>TCRU_3116 hypothetical protein
MRRGLLSTHPVPSPATDRKNHETTGDQGDRGTPEHTLARRAAMRSTAGMLQDNWPREGKP
RVTLRDLNEKVALSLSIDSGLLASPTNVTKMATEFAEAIERVQLRNSLLSVEQECNLRDE
LSSCLQRKFEEVYHLALEKERQHQRNTRDSYNSELLIAYRREQQAKHQEQLEDLQQNLEA
EFREEQKEQRRRAYQRRVKVLLTQQGEKKTEYQNALEQYYTYREGGQPASGTFSPRDGFF
QVRFTCEEEIALRTSAESMSRDQVMCLRIALRRLKKRVKMTKEHTQRCLSQRQKSVFAAR
NRAQERYLSIIADQQNELRMLQHWHNEMQKLEREAKEIMRSYTEQRLRRQEHMQREKEGQ
VSSVTGSNGEEGTGKGGSALNAKCSNGFQRGLFDLLL*
>TCRU_3117 hypothetical protein, conserved
MSQTEGAKQSGKSFRGTDALPLTLLRRSCPEFISAIASVKEHQVKKASNKNRGSNLEFGQ
ELDAAVPPQCIRSGTTRTNTDEPFNVRDDSASAAPQASEGLAERMQEKNASTMAPKKRRR
DGMISLSTTAAPSSSPTAASASHRIDDNNIGAAAFVASGSRNRRALPESPRSFLREALVN
CSRREEDAIPDELVANFDGMAFFQLLQQCSGGVCVSLERAEEAVDGQNGSDYSTSPPSPM
TKSSSSLNGSGNLPIGRLSKRELQAQLSAALAWASSAVHGVEDENDDGGDDNDDDDGDDA
GVMVRLPRAILETASQIEHPSLVFELLHCKDSKGRSKGAGACCGKNTYTDDTEEDDDDER
EEEDEEDRSFLGDLDDLKETTEKVNSLSLHTINELAAWWGIPVEGGNGEVYRLTITEHFR
LLAFTICAVVSNTLEPQPLFSSYAGGNWRQDGNNATIHSSGHKKAAADAANGASDAGVKE
MTPRREDDQDGPMRGLLSLRHDICTLSAEHLRYFANIFGFPDRCCSPEDIFAAISAVAVV
TFFSPLPTPLLEKVCHELSISTVEENTESVDAHQLPELLAEKISHYFYSPRYSVPSVSKL
SFMPQMQIHEHAPGRYTCTVDNAKLMKVIMLQRLISNRFSCNKIRWHALLTVINDKLSFY
VWHRNTGPITAHMIVRTQDPKKKRKNNGISGGDNNNKSKNSDFSPNPESSLRESSALFLE
REVEAAPGELMGFENFVSLTVALHSSTMSQSGYRLYNRVEDRLVFQYAMDLICPNGAPPV
EEKRKKSSSNHQNGKSTCANRGLENSMEQGRVNQQATTDSAATATANAENEKRRKEWEKV
VIKLEKSESQQREAVDQAWNSGYRQLLSEHGKSYQKALQKKKDRERKMLLAKVGPSPELL
RELETLTQTVSATRAQVTKLAKEKSKEEAATKKLQEQIEEGKLEVEQLRQQLKSSNELLS
SLEAEAAACITRFKERGEAKRRKQRDLAAALRIPEMSSTRHETLAINDLQSFWAPSSTNG
ANSQLLLLSTLSATSSSPARSPQSSAIAAPGVNPNLAFSFVGGGGSGLCGLSIPLPRASE
ENSCGVFSPPLQSTAEEVMGVGISTWASMTDPLSFGEGGKGGDTANTFGTPSAAVLFSPQ
PPPLQQPEAATHLAGVDTAGGSAAGHSSSFTVTAPFTSGGAAPRFTLDANACPFTPTTMV
TGRTSCNSAPHTSFGVKTGAAPVSLHSPLSTSPTTVISGNSPVFAGGMFPERPRYTSVSA
PVSGGVASNEAFSTDPLQSSAPLFAPPGLSSASGKFLQPTSKALSLNFTTAPWN*
>TCRU_3118 hypothetical protein, conserved
MPPRTVTANSHNHNGGSAKNNSKPNAKGSHDHPRSKRDEHAAEETAPPSGPIIKTQITNT
NKASSGKSFLDALRVGASKRSNNNTSAAVEKPTVATAVAKTETVAAVVEPKTVTPEPEVT
TVESLAVEVNAASVEETAQQLASEQPVVEQNSATPTPPVQQKEQQQQPVTLPESDAHFSW
ANDDDYSFVNQFTQPHREEQVQAGAPAYLVQYPQDVIDAQEKGTRVIFKAPGENQTMASA
VAALQKESRELQDSRRVFEDYCKQREAELNEKRAQLSKFERQLQEQSENLQQERAKILEQ
QQKLQQQQQQQQQQHHQQQQHHHHIQQSPVRSAPAAPPAPTQHGPQPAPGYTYSPAMQE
NMQWCPPPRPDNWALGHGPVVPPYEHNRYYQNMNYQPPRGKSFVPRSGDIPPHMGRGNPM
RSNPHMQSNFNNRPMGAGEMRGPMPDGGVNPMFNQRSQAGYMQTNNFHNQW*
>TCRU_3119 hypothetical protein, conserved
MSALESVLQRVRVRVAQRRLRLDDFFADFDSLRSGRITAAQFRRALAINSIQLSDAEFET
LTSAFAALPANKTTGSRTPRGGASNDVNYVAFLHALRVEDPPAELLTTLRRKGKMLSDEE
ERTLETTFRSLHYAVRVRGIHLRKLFEDFDPFHSGKVSASQFRRCLPFEGLRDDILKLII
KKYGDEDGGVLYAAWCRDIEASTSLKEERLSASISPHISPHGVSAPLSLDELLSVLRSQF
SMYRLRCDDFLKAYDHFKTGFVTAPQFESALGQLRFVNFHLTAEHIDTLTRAYADARLGG
TVSGTNEEVFPRVNYVQFLADTNPRREDATPGLTNYYEMTRTPGQFLSEVDADEKERAEF
VLNKVRRLVQSNRIHLIPTLHDFDRVRKGIYEHRTCTQSRFVRSLATNKIFLSPEEISLL
VKWYLIRNADGSPSDEVNYYQFVMDVDNSHSLQLTSARLMRSTGMGELQNQKGGSYSRPA
DTLSEVLAKVAMQAEERHLRVNEFFIDFDPLRSGMVQTEKFSVALGIAGLQLHPQEIELL
QREYKSTKARDHVDFDRFITDIGEFAPTAVPSVTTKFKFTASQSTKGALSAISKDALYNP

TEKLTDAEREFLPRLLARLSHDVATHHAMLTPFFSDFDRLHRGKITKSNFLRSLARHRFV
LSPADTSLLSRYYASPEDAELIEYTRFVRDVGQGEMEQGIREKKTGVSSSGMNDTMMLRT
NTASVCLGDGSPHGATVDEEFVERVLTKICCFLQERKARLSEFFPDGDELRHRHVTNTRF
RHCVSILGLHLTEVELQALEAAFAHSELKGHVDYPAFFSVVSEKLQAGVGIMAVTQRRRG
LYTSTDTASVPAAVPANEKSVALKEGTASGFEKSTKILEDLQAELYQSAMDKVRRTLASR
RSVSLSAFRQYDRARKGFVKEGQFFATLMSLGVQLTPAQSDAIRKVHSIGGGEMGYTKFS
LATDDERFA*
>TCRU_3120 hypothetical protein, conserved
MSLEDRGVVAIWEGEWLWLRRQLSTVRQTVWMFGALLGPVFDLAAYLATAKVCVARADRF
VTEQTLLASEQLRRRHWILPAIGITSASLFVLFKSSPWGTYRAFRNGAVTAALLTCFLLP
REIIDAVDAELPFSTRDTRGVEGNARDIGEK*
>TCRU_3121 FHA domain containing protein, putative
MEIVLLATHNLQLLSDSGGICAVPKKSSDNSEKWNELQPTYVRHGSVNNYKRCRLRACFF
LKNDGNILSLESEAKSANGGNTPMILLLPLGRDPVGNSAVITFKMAAQGPLLSRSHCVLQ
LSSSRLLRISHDPHEWCAMSVRDCFSLNGTFVNGRRLASGACSPPVTFNPCNFRSWKEPL
MTLELGAGAKLSAGESLLEKQLFLRFDVFVRFVGERKDVGLIRRCLEGSCLANLGTKDIA
TCFLRDGNSACRLFSEPAAVNISKDVLANEECVNTLQAEEVLTLLCENCSAAARRIQLLN
SAKAPGSTTAVQQHIPLACSTINNSCQCLYSTILTCRRECGTNNDDAETLTWRPASPNCT
SDLPLHASEHPTEVGAAKGETRGNESMAIFLTNRRFGDGLQGSLRDVLLTPHKAGSKSVF
GRGKEEPGNCASSGIASNSTKAVAHSVPGPCRDGCKQNYFLREPPLDLSPVLVKKKLLAK
SPLLEPPAKEDCMTNHCRLVSSFEEMQRNEGTNVMFPTRKPPEVIEATNAGLTKDKDKLA
EASKAVQQQLSTIHTEMEQVLSWRSGIDSLPSSQDDRAIVLPRHGRVKEEGEGELVPYGG
FITVKKSPPLCDLAAGTGQAEWQAQTAKKRGVKRKRVVDMKETMKKFVAELIAGTDGASP
HE*
>TCRU_3122 hypothetical protein, conserved
MAWNAWRPLGTPSRQSQISMDLFDKWRSEQDMSIADRGSDADPAKEEEHNSFMMRQNLNA
YICYKQLDEYTSCLAKHHIIEHTDRGHEINTKNNINERKCRGTHKAYVACMGSQKNQETL
LHSAVLHNNCREFHAELMCCYDKNRELETKTSEPLCIPFYRRLLRCGLNHLWNDYWRALT
RFGEAEEFHLYELSRDDNKKQEFLRVITSTVEQQQEYLRNRREQEKGYFLPRPDKDVESS
DEKMKAAAAVLAQERQ*
>TCRU_3123 40S ribosomal protein S21, putative
MTTIGTYNEEGVNVDLYIPRKCHATNNLITSYDHSAVQIAIANVDANGVLNGTTTTFCIA
GYLRRQAESDHAINHLAISKGIIRIKTGKKPRAKKLKNVKGLGVRGLPRGALQQRGARVL
PTQRGVAQRGGAQKGNVRKLQPQQQKQRSQLNQRSQQQKQRPQLNQRSQQQHGARPTRKE
EGGRMQRGGRDAPQARKQQGRNEPQARKQQDREAPQARKQQGRDAPQARSTKSGPNRK*
>TCRU_3124 hypothetical protein, conserved
MSYPNYSLTDSIRAALAAHGVRNARVVIDLLPGNGQVGVSGNENGMNGDWHVVQTDDMEI
IINEREGVLLMEGTPAQQPLEPPKTLPPPRAHSPFGTVSAPPDLLVGGGGARQPKKHHSR
EKVEGGNGYDFMENVVEPTTKSDDALPHGSFVGDAPSSGSFERKVPIVPLEDLHKVSLSS
DLPRGEGAGEGLPHDPTTPLPSSSLLKSPSALFPTPQAPDDRRELRSNSSLLPATQPGSN
RKTSVVLVEKLKAPAPPVKTTPSGLMPVFSILNTEHSEQLERLPSNASSRKVSSVHLVES
PVVEEPKHQPHVVEGSEAARKPGILVTGASSKTGQTDSKPGVVGGNGELKFPHFGEQSSK
MSVSSEIDVSVNGKMLKTPTPHVDFWKLSGKQRLQEMLQEQREMEQQDRLSRAKHEEIIQ
EAQKVLQRLEQNKMASKDEGELPSLPQISLRTGPASSRPVAALCASPHCSSLSPSNANGV
NGIKVLRFTLPASGKAKEEVVSQLSTSPGGSQHLSSKDKYSMLLQEQERILRQNEEGEDE
YKKLVERAVAFHEQRKEQRRLHEEQGSEESEEDDPVKL*
>TCRU_3125 histone H2A variant
MSLSGDDPLQQNAMMGPGSATADQTSIVSGGKHGGKGAAARGKGKGKGKGKRGGKTGGKA
GKRDKMSRAARADLNFPVGRIHSRLKDGLNRKQRCGASAAIYCAALLEYLTSEVIELAGA
AAKAQKTERIKPRHLLLAIRGDEELNQIVNATIARGGVVPFVHKSLEKKIIKKSKRAG*
>TCRU_3126 Zinc finger, C3HC4 type (RING finger), putative
MAVRALLQVAEKCLVCRVCYTLLRSPVVFSCGHVFCKACAERFIEERPRCPLCNHAVMSR
RAITSLPTVASLMGLVQDVAKSLRLQQTAHVAAVRAGNIAPPRLTEKIVGIQTADEKCFP
TAAVRDSLASTPTVDDDADEKTVRVPTIHRNVSMPETQFLRTSPPPVPVLTDDFVAWEDA

ETQRISLRSPIASSFSRSLQNHCYQCVAVRRCIGELSVGAYERVGCCFLCGLDIKNRTQV
RQYLQQILNSDPTCDHMRLRRLNEVTLSDFLGSMWDLHLPTQIVKRAASGMCRKHGRSGT
FLSSSTLLVHQACLEWCVLHERVRDAVALKVAVMGTQMQQLDGSLRASTCFFCSNRGKCL
ILCERCQRKSYHYPCALLTGAGVCNILSETMSLICATCLQEQEEQGEGEAEEEEELLVLF
*
>TCRU_3127 ssm4 protein, putative
MPVESTASRGSLPAIVIQQAITQQVATSTSTDVSYQTSSLSPSRPPSALRVEAETRQGYV
YQGKLLSLDDDYNISLAEATSWRDRLCDVERALLAVRGFPAPAASPATRRRYVGSVFIRS
SNLLMVRFLEYDEPGANGRRDNSHGAAGLRSAFKSMVSKVKRQINMERKRNRMERQKRLH
LAQTPVPTKAANDGSGMRSRKDPKAGSNRRRAGRFSS*
>TCRU_3128 hypothetical protein, conserved
MTALTVPFVCSPTEDTVPSYVLYSPQGSRPLAGLHVEGGTVSRYYDKETRSQLIRTSPSA
HISFLRNTKSRVGRISSSSSSSLSTNGGGSLASSQRVVILQIFCEESACTAFSLTVELTL
QDKLGRHRILFSNTFQKLQRCAQHVKVPLRCVAPGVWSNIVLDVHQIHATLYANSGGRLS
TAELINSRRLLSVTLGCSSVCRIRRILGMPQLPPSYRELATAEWPLSLRLPPEVHAYFWV
IRTCEEEFLQQRIADGPYHHLEAFIHVNSTLDPSISAPVQKKTLQKPVPAVPFQSLSVSS
VVESGVLRAVPGASDRGGGVDPHVALMSVAAGENGLSASCTKGCQADGSEPKWQSGTIEL
SALAGSPPRSVPRCDASVQTSLPAAVVTAKKGGATEQLQVVGTRFFDTFASVTESPVKMV
NLIDMTHVVFDDEEEQREEEAGDGEWWPRSKNNGSEVNKKETVSVPVAFVAPTPSRCLDS
PGRPDKKEVTNMRGAQPRETVLNNIDKNVPEVMHAPSLNNYANTLNLMRQRVKCIQALIS
ESREHDVSLNEGEISPDDDRCATSGGNNNNEHNQKHGGCEDNDHQGERPWPQLSAEGKHV
ILCDGSTQKQQQGLFSSRCFIVPQEHRPEKIRGVPFQNTLTPCSTMRTTDEGVAHVCTYI
PNGGEKNMVGTDEEDEEDEGFTVNVCTSGDHERPAVVVPGESNALSKQAPVSSLCPKPHE
VDRLCFDSSFLENGFIEPSSQRPVHRTTQLVEDDSMVLSGPLSPDYSGSITSPAPAAAPS
VTQAQRTRATHHRGRLGEQARGEIVKLEAFQALASTETNTPPPSPRHGNGGEEVESSIST
AEYRRPSMSRDGIAAGGFSAAAANAGRFISVGSNCEVDGEKDKEEDDARQPFCLPSLPPK
SPSKKQQQYQHPRPLASREDSSNLLSSPLVPLTRRCQHAHIGDTKKECTVKSANNYMSNI
RSMPLSSTQLTKPPKGADDAREKIENAGDSLVFDPLLQCCLDLRSNTYVVTIRSPEGTQH
K*
>TCRU_3129 hypothetical protein, conserved
MSAAVPLAARIAKNRQLKLLAAQSRHLAARFSDIFGDASVRTTRLNDRHFESTVFYSFSG
LCTLRLASEIAESLSEAVERVRGAALALFYSKADLRHMLQAVDSDVFAELNATLDSMDAK
AVIHLARSKKEMLDATASQFMVTVTAQLPLKDEEITEVGESGGKEYNIMTDIAICRSTGQ
CPRDAIKRGFALSLAELDEYAVEEQRSRGEEAWCYLQSVQRDELQRDWESVALSVFLSRS
LGDGNLDTIEWLPPREETDTVRVACFPRKESRSLTLTIRDASGNETLLTLPLHSPPLAFQ
RVLVGDDDGSARIVHTSALAWPEKWIASSALMQLCTILNAGVRAPETISCGTAGVALTSQ
EISFLSVRSFAEAHGTLPVTAVPYSIERCLFMVNNRVALCFAKKCGREYFGGSSMPLICL
GVVSNEAKKLGQGIHLQLEVKPSEGGAECQKYRNFVTTLLRRAKKEALRGRHETKLQKVT
AITAGLLGHLWKLFFVIAGLAEKEGMNPLRDISVWSPTEIPFSGNQQKKQQELSSLLCQL
FAVDAQVVKKPSWGGSFPNILHLSSSSLGVQALPVCHTLETPEMTLKRLLDDASPSMAEV
VEIASKTDPRRTVEVAAQQREIEQSSYYCPDILLMIQEMRLELHMPQRSFPTLEFFQKAV
HDVPQRVQEIAMGTYGDVPVYTRVVAHWGPNLRVEVESDMMGLTDNYGVYRFDSPHHNHC
GPLGLLLSVVYTMYERVFPHRRTVPLIGLNSPNRRRSIDFLLYSWFMASPQIRCFEISTR
AARLAAATTAMAKKSSDVAEMTLSHSVGNYIIRAMLFYDFCGQRVLFAETHAPTLWEAVR
RVNELAVSLNIPKQDFFPTRATTRRDSRSFYTPPDGCDSEVAFVLRALMSATRSQLRVFF
VRTNDSTALWIEGMIELQVPIRQIRCAVSVTRTRGVVPALVLACREALRCASDEEEAVRL
LRSAHDAGPLIPRDNFPRFSSRFYTPVNLLGEVLQGVAGKYHCTYTIDSKTREVVCLLHV
PAMAGYGNAARDSVPFPLGIGRGRSKKVAWAAAASQALQANFPDVLPQVERHKKLCELLH
RPDYLSLLDCPEGFKIEVVPDREKESGGGYKCTVISRQPSNVSDVNTTAEVSDVEHPKIL
FEYSADRSVDAYLAAADALLDRLQQQRQERTAAQMGDSVFHLWDFTSNYGKSVWHACCGA
LGVAFGGKVSLRFEGGREDASVWESEVPMRVQLVVRTWSPADERVIETPLHMLNERRIVG
YGSLTGLYEKGKPSAEQLIFASTHLLAEAIISYTDEQTRKCLQRLLNLFQQLKEGEQSCS
RLNAKRRVESYMELTLGCQCRVVVRQVACGMVTAELGAWLPGHFRESRVPVVLSACTENT
TGKALSGLEESVRQVVESLWAIVRRSCAC*

>TCRU_3130 hypothetical protein, conserved
MAQAVYATLLLICLLAAHSAAGIFIVDSRPSGDYCGGYMSLVNGRITVHPTTSEFDISLD
VFGEKYLCKEEKYSYNETTGQMFLDGVNDPDDCLGTILRDNGLKLSVTYLQGEDAILLDF
DVVTVKLSRCS*
>TCRU_3131 WD domain, G-beta repeat, putative
MSLEINRQFLMGDGSKVTEPVIPYISIDTTKILEAHKKPYLTKAEHVKFTGEISCLCTVG
STIWVGEVSGKVSVVEVDTGKFLNIVLDHRGAAVIVMRTARGYVWAGFADGYLRVFNSLT
IELLFEKKFHKDCITDIALSQNCDTAYSSSLDSYVCYWNTSFFAIESPRVLGDCRGAVRS
LVLFHDLLFSGGDDSKIIEWNTVSKERKHVLAAHSAPILVLTICNNFLWSGSEDGVVCIW
SLSDLDGGSPECIHMITNPHEGPITILKTVGLKVWSVSMGQVYIWNSSSFELEVHCRLSK
EHHAFLNVMETVSQAFCSKTWIAYKNTGDITIVQSDDLLPLPLQNLCFWGDVKDTKDKDQ
FIDQLLESQKSLTSELLVLRAKLATLTPQQCQKEATDRFELAKSDGTEKATLLNAVPKSF
FFDSNEIMDNMTNLTSLRSNKDDHGLSNIPFSIEGTNYSNFASHMPRYAMVDTHALLERL
IYFREQVGEIIGSSEVLYENNCLYLTDEKGRPPIPIGFITLSELTENERITLMNICGGSR
PPFLIPALTPTNQAEICQFIRGITSRLRGYRSIPSLASSEKRILINDSSNSVHALGKPTK
CLSFFESEPDGVGFPPLSFYLNKIICEVMVGARRISQNYNSRLSNKRVDSMGKAFQGLKQ
RRDAGQKQSSLSYGIKETESNEGLAFFSPDVDVLSLKEHFLPLNDGPQSKGSDDDRRNAT
LMQRITFLKRQLVGCVTSHSSKQVKTCARNLPPLTYTDEFSDMESEMEELSAISFGLIRR
LCRLVEKLETEMQEQKVLKSIFGAVDDSCRKNHTDDTRQQFPGLVSLFNRMQESNLVAHE
FVIQHLLEVGGKIALQYGCLMETMLQRQNPSAYSSISWGYESGRSNVQSSSLLDSLNEYS
ILVEKVHAVEAVFFADRT*
>TCRU_3132 hypothetical protein
MGSWRSDACGAKRPAALKCEWRAFRSAEVPSLGRIGASSQLHSEASIISERRSPLVAGRK
GSLKRAFSRATQTDEDDFVLSEVFSVVMATELGSSTADCLDWAIRMNRMTLSRIQRAERL
SDFPLSSGCGGHDANCALQSSANFPLETILRIAHFQNKKHQLLSVCFLGQKANSLF*
>TCRU_3133 vesicle transport v-SNARE protein, putative
MSDVAMYDEELKGLEEQISSLLRALDSATNLDQRLEKYNKAQDIMKRLHKTHHQFKVEVR
LLEGNEQEVYEKRGQIHLLRINQLKMDLQSKKVEETPFSAARENSVLSSNSPSNDGKDEA
RAVARRVNTIQTSTLGSLAMTERLLNDTETVGIDAAAKLRSQTEQIQRVNENLNELDSDV
NRAKKELTAFIRRMMTDRIIILFSVLILIGIITIVVLKVTKK*
>TCRU_3134 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAVFGHAEGLAAVGGSSGGGNSAGSEGGSRGGPDVNSPLE
PLSVVEGSKGNMISSLETSPSVGGIPPNSLSEEGDGSQSPGETLTSEDELSSDVSGPSAQ
TKTPGQSDSPIVKAPEKSGPETKTHISDKQGEAGSTEANEDATENEKGQSEVVKRDTFSA
PQSPPTPPVPAFPTEETPLAPADLRNSVEEDRNTPPSQTKTDLEAPEPSVEDAEAEKHGE
GATTSDSMNDAAKGRSGDSTPSSISTIDSVDAQRKAEEEDDSEMETLNPNEASILPLVNK
NGQGNVIPSFSGEQQKQKGQPLGKNGAGGASAVSTVTSSPAGKESVKNLASGTSPDGHQN
VDGGSYCWWLPNGDHRIWR*
>TCRU_3135 hypothetical protein, conserved
MNQVIRSRTDWKERVVLRLAWITASRLFEIAVLTPNNFTLEPDGALILDWSLAPKTAKPD
PHRALRFVRTRGQDVFDIIKLCRTLQENEKLTNITTAQVERALVPWDATAHSTKKGVLRH
AAQIVETYNLNSHVISQLAKHVDPFDLSQNTV*
>TCRU_3136 retrotransposon hot spot protein, RHS3, putative
MSSTVEDILLEGSTSSTEMKLNEFIRNYFGGRGAVDTNENVSISVFVLNPEMFINDNEIL
GLITASPSYQELKIELDEREILLEAINRLHHEGVFSLEQWRDYEEKDTVTLIARRKPNGV
LTQVLTEARREAAERLRRTQEMKFTISTNVEDVLFKGRVRVNEMRLNYFLTRELDGRALW
TPIGMPCWRSFSRTPISISVIKEH*
>TCRU_3137 retrotransposon hot spot protein, RHS3, putative
MEVREGKPEQSWSYRKADDAIEKNDAVEQSGAGRPRLMVLTSDRGWPYLWEWEEDGSTHD
CYVNCEVERVWRIVLEDLSEWFSPHGEADFKPVRRLLIGTPWIGNSMAAGSYLLYQLLHY
DVEKLQVVVYCFGGGDACVCDKTIKTVRRYVGKACKRFLRDLWDCGMKVFIIYCVTEKGT
PPAK*
>TCRU_3138 hypothetical protein
MSRNSRTKTGTNRTMTSSTTSRTRARNSTRNGSTGISSIMNSSTKTGKSSSTITGNSNTR

SRSISSTNRSRNSTRAITGNINTGNSSTMTGTNRTMTMTGRTRSSRNMAGNSRNMSGNIS
TRNRNSGTGTGGTSSTMTGNSGTGTGGTKIGKSRNKTRGST*
>TCRU_3139 hypothetical protein
MSSGVQSICNRDRSILAYRRRVDVATSIANKKTAELSSLIGRSCVQQKFVNCPLGTFSAP
TLAAPTSLEPPRSLPSYSWSKAGMSVLRRATVERRLRISPSALLVDCVGQFQISDEASVF
RCYVCAGRWEVMEWMGLPSSTFISSGQPPCRFLTAVCTASDSFWVRLGGYI*
>TCRU_3140 DNA repair protein, putative
MRVCSHRFLRITCISRVVKQATLPTTDPAPVQGFYSSLQYDDFGALDVPDLATTLLPFQK
EGVYWMVQRERDHIGGIMADHLGMGKTVQMIGLCLSSHHFNKAIDETHIQTIQSKTANYR
LLTVIRQLQRINVIANCSRINRPAMDLRALMNKVEENAAPSDESMDSVRQEVDKWLKFAS
KFHPSYEKRATAFLYDERKRSFELIESRDLRTLVVVPAALMLQWKSEIEAKVKPSRGLKV
FLYHGTNKSITNTELELYDFVITTYDTLTSSAQFALTPIFDDKNMSFNRREAGPLFHVRW
KRIILDEAHMIRHANTQRWRAVKELQGFHRWVVTATPLHNTIEDLQNLLHFVGLPRLPLL
PGFNPEEVLNDPVLQRGIARSIQPAFLRRGPVMIRNGKEEILVKLPPKTENVVMKRFSIH
ESKQYNSILARSRTALATSERKEGAFHIFAMMTRLRQACCHPWISEGRALSVSVCGICRS
EAVSTVTTKCGHYFCYECLLLRFREAVDGEEMAVRLPCPTCGTTITNSSVFKSYTLTSSE
RIAKFKKRDLEMSTKLRMILDSIDTMKKEYPDDKMIIFSHFTSFMDVISVALDKLEISHL
RLDGTMTLTNRNTVIRRFQASDDVRVILASKTATGVGLNLTAANHVLVVDPWWNPAIEEQ
AVHRCYRIGQKKHVHVTRIIIEDTIEQYCHEICQRKKEFGDAILRAATKGDSGASVAASR
LRELLSRLNYIPEKDKETVEGTVPGVER*
>TCRU_3141 hypothetical protein, conserved
MVDGGEQTLLGGTETGNSFDNQKSLSNSGSLKEFLSSRIRDGFASSAYWGATGEVPPREP
NDVAGRKPHAFEMEINKKLVPFPEDKTSLPRTLDYTLVGLHRLKGDGSEIKPQLNAAQMR
FLETSSNSLKDDTNGGKKPNLMETTTTQNRTIGKGKFDPDVLDALSKGLEDLEDSSKQRD
HLKNMPLEGPAPNHYRPTSWDYCDMSGIDPSSYWVTKRDPNAPGGDGFLPVYKSRYNLVE
KEGPVRREKTTTMLEQGRNVDKGPLKDTMKDMNTKSLPEGYQPWSANEWMSTTHDYHAPY
NVAEAAATNRRSATIPLPRTYHTLSPAHEQSVLSLSQRHMMRHSGNWATEYSDSYLNRFD
QAEVNKEHSKRSIFDIRYGTYTMHHSAHHPRDDTATGEMYTPSEVVPGQYTTMSQQPLHA
RNALSQRANNS*
>TCRU_3142 hypothetical protein, conserved
MLRLTLFLQRKTIQSYPVPPKTRHFNRRWSSSRTNSYNRQYWRIVMNENYSRPSFWVSDF
RHRYLMRTGSDFQGQVPASPQPGLYQGFSDVHKLLANHPKPQRESRHLPVMPMTPRVAFE
HANEKKIDFAKKMRSDRRRVEELKTLEFWGWYMKLQRVRGRWCREQGVSSRGVYGPAVDA
AELWG*
>TCRU_3143 Sas10/Utp3/C1D family/Sas10 C-terminal domain containing
protein, putative
MPKKNSLKKRTRREVEEEEIVEDLDLDVDEYNVEEEDVIHNRRGKAKRDEQAELAAVLPS
DAHKFEGYDDDDDERGAHLEEETLALEANKSMRRRVIESDFDVGGITSGMKRKTNGESDA
ELNVAPVVEAVERDYAALSSSERMSIVQKESPELIKMLEEMKQYLAEVKELAKPLQELFF
QRRFSDADRNLIQFLETKVQLMLSYCMHVTFYLLLKTEGKKVSGHPVIDNLVEIRVYLEK
LFPLEEKLQYSLNRLLSGKTTAAARLDALRPLQHNERGVLATNTEAKKRRKQLEAMKEAE
EIEKEELTTMNRIQTKKSATLKETSSFDRKTMVSALGYREDEDQYFAKLVAGGEEEDEGT
QGLSLIERLRRRQHSFADGVAGNPNYSSDEEAPVVGDDDDDEANSGEDDLLGEGEDGVEG
DYEMLLEEEQVRLMRAKTEESRPKPKLVEPEVDRRKTSKKIETHRGLTKSRPKDRKTPRT
AQRRKYEKGMRIHKAQTRTCQPEPEGGFIGLPAIKSKVTQSIRF*
>TCRU_3144 SNARE associated Golgi protein, putative
MERADAILAREREEINLLREPLRVLWLALVMCVKYVTRYVTTHLTPSVLRVVVPVLLLMT
ATSLFWIDSPAGHAFNALDTDRDGLVSPEDLETYYTRVLGHQPGIGQQARSAFPQNSSHL
NKAQFVGWWEEGQGDMLRRDAFFTQGTWREVEYLLADALWWLVLGILSSVGLGTGMHSGL
LFLFPHIYLACSSADSCGNTNFWTYPVNRFYGPRDRTFTCITPHVTTTVPPTLARLLKVV
PACIIWGAGTAIGEIPPYALSYAAARQGKRHAELEELSKYDVLNRMKMWTLDKIQRYGFW
AILFLAAWPNMAFDLCGMACGQFLMPFWSFFGATFIGKALIKVNMQAVFFVLLFSGDNIE
RVIRLAGDALAKVLILPAWMSSHGTKGIVEMSIAPIVKARENIAARARGTEEIDLEERGG
SFLMMFMHWIVVAAVAWFAKSIIEAFAQNEQEERDKWTLERVQKMISHRRTRADIKSEEL

RQLIELARAGEVGTSRSPIESIFMALFTIMAFLGFVMGFYPVFVLGLSLLGHTLMFGLCT
NESINRWTFCGVRAALTAAALFSLSTQFTVQG*
>TCRU_3145 Domain of unknown function (DUF4539), putative
MDSQLLLQREASTRGLTLTSLCQVGTLPTSQKVACCGGLLETIVAESAQDCTVLLRDATG
TVHCAIHGAVSSRYPDVLTAGALLLLRDVTVLVTSSLMRPVLIVCLEHLAALMLPEGPPE
SSQSHAVGFTSTASPFTEVPPQGEEYVSNMCQDTLQEVFHETPHEICLGPVTSVAATTLP
KDSLIPSGFDNDEDCLQLADDF*
>TCRU_3146 btb/poz domain containing protein, putative
MEGEAPLKRLRKGRDDGRLAREREPGGTHGAGSGEQSSSAPSSRGDMRVCINVGGSCITT
LASTLCSEPSLLSEWVSNDFAGLPRDANGNPFVDRDPENFRHIVNYLRGYELPLATEKIV
FLAEDAEFYRIEKLRALIDPPARWRFVSGPGVSKDSTLFSTENILGICGNEPLPTRGKSI
LVLRVDKCELVSIGLIGTEKPFENEPLQGQPHSVAYCNTGELVQCFETEKTYVSGTGFKS
HDIITVHVSFSPGLTAKITFLCGTVKTYETEWPAPTPPLRFAVSLHGTSAVTLERCVTGD
MSDEEGREEIGGVSEIV*
>TCRU_3147 protein phosphatase 1, putative
MSLDVDAIIDKLLGVRVSKPGKQVNLAENDVKNLALRSREILLAQPALLELEAPIKICGD
IHGQYYDLLRLFDNGGFPPSANYLFLGDYVDRGKQGLETICLVLAFKVKFPENFFLLRGN
HECASINRIYGFFDECKRRYNIRLWKAFTDTFNCLPVACIIDDKIFCCHGGLSPELQTMD
QIKRIARPCDVTDAGLICDLLWSDPEEGLSGWGENDRGVSYTFGQDIVEKFLRKHEFDLI
VRAHQVVEDGYQFFAKRQLITIFSAPNYCNEFDNSGAVMSVDADLLCSFQILKPSVKKPK
FYQ*
>TCRU_3148 Ankyrin repeats (3 copies), putative
MSGATAVEEDNYHREATTIAEAFFDCARYNDGDDAKLLLAYLSATPSLIGAKDEQGRTAV
HLAAANGHIGILEILMEFGPSPDVPNHEGNTALHFAALNNQLEAARRLLEWGWHASARNV
FGKKPIQLIYGKKYEAMETLLLGYDDEIENYTRGTVSLVENGDDPPPAPAPTATATLAGS
SCLHNTPVHQLCEDLSPEENSHHAEAKSTLQAKHEDPTRLLGSADVDGIE*
>TCRU_3149 hypothetical protein, conserved
MEPRVWRPKFFNPFSERRTLRRHLPIYRGFFRVMPLHRWSLKDLQAILGYAALHPSLFGF
PEQSTCIVNTAYFLPSHRSRSRGIWVFGSERGCKSIIVPASCNTEPFDALDAKLMEPLFR
WNPGVEYLYLSRFCQPMALYLVPYLQRCTHLRTLTLEGWDDATAIHRVVMACKNVDVLDA
FSLDDPPRKWKNELSVQSLNTLIEMHPKLICVKATRVYLADWHEATQFSRCKHNIALVTF
SCDYVLLHYGLFLLLLCIPCYFVFKGMWRLLEGMLIPAYQFFWSVIAAVVVFAALLVLDV
GVWHTYGRGWVQMQKYVILARRRWDAAMRLQQKSLTVS*
>TCRU_3150 protein transport protein SEC13, putative
MQLDAVFDTGHSAPVTDTAVDAAGKRLASCGEDGVIRIFAINNESPDEWDLLAVLEGHTG
TVVSVSWAPPAHYASTLLSCGEDFQVILWSDFGNAKGWAKVYFTTLASVPWCVAWAPHEY
GKMFAVGCASGSVMIFVGKDQQWSHTEFTAHPNGCSSLSWAPSLPPGMLLMAPLESELTA
SGAHPPAGMPLAPPRIVTCGGDRSVTVWTLCGEEWRPQELPLEVEASWREVAWAPGVGMP
FTYIAAGSDEGFVVVWSQDGSARGEWNRMVLPQQEDGVTKLSWSLVGTFLLVSCANGTAS
MWQECASSQGWERACELLPSGN*
>TCRU_3151 ER lumen retaining receptor protein, putative
MNYLRTFGDMLHLLAIIILLGKMLRQRSAAGLSLKTQFLFALVFTTRYLDLFTSFLSLYN
TLMKIFFLTTSWHICYLMRNKSPWKATYDHENDTFRIRYLIVPCIVLALLFHGKPRGGWL
MDFLWAFSQYLEAVAILPQIFLLEYTERYEALTSHYLAAMGAYRFFYLLHWIHRYLVLDR
VNVVSVSAGLLQTVLYVDFFYHYLTQVVRRAKQRYDLAR*
>TCRU_3152 protein kinase, putative
MNNYQIYDEVGKGRFSIVYKGRRKKTIEYYAISSIDKSRRQRVLTNVRFLRSAEHRCIIK
FHNWYETNNHLWVITELCSGGDMRQVLNLDSRISRQAVQMFGTDIAEGLMYIHSRGVVYG
DLKPSNILMDSTMTMRFYDFGLSCDFNTIRGDGTVGTPLYMAPELFTKDGIPSIASDLWS
LGCLLYEFGTGKPPFNGSDLASLIRNIMSEPFCPHEALSDELNSLLESLLVKDPIRRATW
GDIVTHDFWQGRLQLPTAPFPPQPAFERRQRMAVAWASGDWPMSGEELRRHVEWAVESAK
RNYTVSQSASEGGPSRCPAVTEEIDLQDHSAVTDATTEGGIAASRVDGQKDGRRLRAGPT
GAALDATNSQFLRKKESFRGETANDSHTAANCDQNATINAVSNAEVSIVMNGLENLHLDE
LMAHTSDAHIRPLVMNSRIERFVEQKYDSEKMGFEPPAKAEIKTFTEQQQSDFIKMIYRT

LSSSSLSHEEKLNVLCYFEDVCTDAAIANFIVNSSIMTLCLKMVSQRNAPSNYRATAASI
MSILVRHATFIHTDLAKANIFSSIIEVYGEEDSPRVKRKLTACLGELLIYIAVQRERDRN
VWGINANATLQLYLTVLKDADDVLRHYAVKAIENLASVSDHGVALDVFAKKEVVTALLTV
YALPPASIRSEHMRSSAACAALKLAVLKEDLMPVVMESPHLKVKYYSEVIAEVTAPKTAQ
SLLTFLNMALVKSLVAIRNPIMERWGKDTINIFSSSSLAQEKGKKIIESISGVAEAVVSG
LCGVCERASVAIKGKMLLLIVLLGCMDGKLLLRLSSNKLIGCIDGVLRDKDSYVQRCAAC
LASYLGVFLEAQLVAVAKGAPSGTTSTILDAVCNVLSARNLGMMVELSDSVFVSLGTCLE
KVMSSPVYVTYEEEFNRVVGLLTQNSERVLKHRRAVVNELFPLYIHMLGGSNIERRFSAL
RTLSAFIAPLVDGSGLVREEKIAEAEKLDHLMQTVAASLPELLKESEPIPILALRLLATC
GERRSKAFANIATVELVGDLVQYMLRSKQSDLSVPLQLLLLLALQTERAAEIMDYLAAQE
FFTAVLLKTLTMAVAKELDHLLEPCCELSVFFLKHAVNNTSSRMAQQCLLLLPQHGMETL
WLPLCDSPVRSAAGNAAACVYHFVQLSPAAQQDLMTTESLTLVREIISNTRDNPTAVLYV
LRALRYIWERVRKRHVQKLSEWLLAALKAIVREEDPDRELYSEAVAFMEFIGG*
>TCRU_3153 dynein heavy chain, putative
MLEHHLRPDRKFSLTNAQGEATLSAFSLTRSEETLSRKGVMSPVRDKQQATERRDPTSPR
SLIGISATYNKSAILFPDAHKAAFEPKVQVPFTYQRGRIPRKIEIERRRRQYEFHDVQEL
VELAGLTLKQLAKKDSQELPLEVFDDTSYDCRNPSEWMEIAGQNENENGRYLPAEGIYEF
INEDFRMRPCRVIAWDAAKNELKVLWGPTPVPGETPDVVPRFFVRLLAEDPIVYVKRLVS
AQQQREKAMAWIRYRLCCDAMPLEGLSGLDSGLGARLRHLGTGMPHLSKAVFPDVEERAE
RLIAEFTLAWKRSHNRILLQDRMERDEVLLRTVANATQMSLEELVRGPNMAIQRTDKGKG
DSVIPIGNFDFEERERSFTFSTYYTQPEVVTALTGVRSECIKVLEGSLFNLPKARQMQLA
KFQQLQEDHMSSMAKYLKGEWTENICDVIRKSFTSAGKGWLNVHESKQEIYEMSKLKKFF
TTVKFMMEDTLFALVYTSLQDFTVFFEEVSEFTVNVIDMNHVENKWPGSDADDCVEKQPL
FMIDLAERDGSFTYSISFEDFEQTIIQLFNDAIYCTDAIPQVEKFVMSQYFWRREGEGPF
LDSVKQEEERVVLLRNRVRDALRNSMEPLRDYLQVYDELLPLIRLDKKEFIMFYEQQGHT
TDEMKEEIRQHLKAKKVVAQKLPAYITVGNYVVDCHSFGQIMANKEQELAKLVMELICKM
AKARTTYIREEFTKIVRTVEKQPQNPEKLYELKNFILSLPERISELSVEIEDMRQYYNIL
DGFQYELSDDESRQKWEAIAWPRQLSLRVQEVNKQLEKVEEELHARLQKYSEDFSKKVDA
LQRVVATFSKYTDASEAEKVAAEVKVNSIEIRKCIEEARSINSDQRLFGDKLTDYRNVFD
LEKEFKPYSDLWLTTYQWQDCYRRWHADPFDSLDPDEIESVVANAFKTMTQLSKTFKDKN
ATLKIVEEIRSRVEEFKPWVPVVTSLRQHGMKERHWKGLSEKLNMNLVPGETIILLDDIE
PLLNHKDVIVAHCEVAAKEAQIEKCLKEMRAKWETRMFLIESYKNTGTFIVKDASEIVEL
LDEHLNLTQQLQFSPFKAFYEESITDWERSLNLISDIVEQWLECQRSWRYLEPIFSSEDI
ALQLPRLSRLFERVDKTWRRIMGTVNHQPNVLEFCIGTSKLLESLRESNRILEEVQHGLN
DYLAEKRQTFPRFYFLSDEELLEILSQSKEVKRIDAHISKLFEFISRLAWNEKTQISGFF
SAEGEHLPSVRPVVPEGNVEMWLQSVEKMMKSAVHDQLRQAFYDHTKTPRSRWVLRWPAQ
CVIAVSQIFWTNGCEEGLNVQGSVKKFFRLLESQLDELVDIIQSPLKPRERINMGALITV
EVHAKDTVELMKRNEVSSIHSFDWIKQLRFYFDPDDELCHVKQVDAHFVYGGEYLGNTGR
LVVTPLTDRIYLTLTGALALCLGGAPAGPAGTGKTETTKDLAKALAKQCVVFNCQEGMTC
NSMAKFFKGLAWAGAWACFDEFNRIDVEVLSVVAQQVTDLQQACLTKQYRIIFEESEVVV
DPTHAVFITMNPGYAGRTELPDNLKVLFRPVACMVPDYALIGEIRLFSYGYKKARSLAQK
MVMTFKLSSEQLSSQDHYDFGMRAVNTVISAAGLNKRENPNEEEDLLLLRALRDSNVPKF
LIDDIVLFEGIISDLFPGTKVPSTDYGMVVDVLRQVVTADKLQPVPTFISKCLQLYDITT
LRHGLMLVGPAGSGKTMAYTSLQKALSECAVMQSKRNDLCSREYMKVYTHICNPKAVTMD
QLYGVYDENGEWRDGVLCVLFRRAAKYGDEGNQLGKHWVMFDGPVDALWIESMNTVLDEN
KKLCLVSGEIIQMSRDMTMMFEVEDLLVASPATVSRCGMIYMDPTACVPTSAIAATWKAS
LPAFMVSKNEYLAELANTYLDKLVEFIRANLKEYVPSTNIGLVHSFFRVMDGYIQSFAVP
KPQPGQPVMSPERAEILEKCITPLFFMSVIWSLGATCDEGSREKFSDMLRTVAQGNNHAD
SLPAEGLVYDYCFVYSAVPEDEEQPRWVHWDDLCDTCEIGRMTKFEDVMVPTIDNTRQKY
VLQHLLTQKVNVVAVGPTGTGKTVSVSDLVLGGLPDRFLGLTFTFSPQTKAGVLQNSLMS
KFDKRRSHVFGAPIGKHFVVFIDDANLPQKERYGAQPPLELLRQLLGHGGFYNFTGGIRW
NAIIDTSFVMAMGPPGGSRTQVSNRLMRYLNYVSFPEMSEVSKRTILNTILKGGLSQRGV
KSEVIDLSSKLVEGTLSIFRRCCKTFLPTPSHVHYSFNMRDVMRVFPMIFENDGNSLPNE
EVLVKQWMHEMQRVFYDRLICAEDRQQFISFLNDELTQLGYEGGYTSLVPEGRLIFGDFM

SERERSYRQISDMNALSIFFDEQLSAYNDANENVMDLVLFLDAIEHVCRISRVLCLPNGH
CLLLGIGGSGRKSLTRLACFLIPDMDVFTIEFTKNFGVKEWHEALAKLLLDCGKDDKKRT
FLFSDTQLVHPTLMEDVAGLLTSGDVPNLFEDQDIELINEKFKGVCMSENLPTTKVSVYA
RFIKEVRSNLHVVLAFSPIGEAFRTRIRMFPSLITCCTIDWFAEWPGEALISVASAQLAE
TDMKMEDMEMEHLSECFKSMHLSASETTERFFLETNRRSYVTPTSYLSLLNNYIFLVENK
RRFVLEQCSRLENGLEKLYDTENRVVELETQLKAQQPILERKKTEIQEIMERLRVDRKDA
AEKETSARHEEVIATAKAEECSKMRRECADRLAEAEPALQEAVKVLSKIKAAEISELNKY
QSPPKGVQYVMEAVAVLLTFGNCPREFYTGPPGGKKTPDWWLCAKSYMKNANQLLDTLVQ
PPEKGGFDREAMDMPLIEKVKGYYDNEEFLPEKVRTVSVPCMAMCQWVRAMYNWFFVNRE
IQPLRQRLSEAESELRRVNAALAETRKKLDAVIEAVVALEREFTEAVDTQTQLENDVEET
SQRLHRAARLIDGLGGEKVRWMELVEQYKAQEKCIIGDMLIAAASIAYFGPLTGPYRRSL
LDTWSGILRGFDIKTSEQMDLVATTGDPVQIQEWQLCGLPKDPLSTENAIILTNARTWPL
LIDPQGQANAWIRNLHKNDNLQVCKASDEKFMKVVEGAIRIGLPCLLENVGDSLDPALEP
VLLRNVFLIGSTPHIRVGDSAIPYDKRFKFYMTTKLPNPSYTPENIVTVSLLNFFITRSG
LEDQLLGKTVEKERNDLEQEKQKLTRDCAEKSLELKKMQENILRMLEEAEGDILDQEELI
NTLERSKLKSTEIKDDLQRARETEKTIDETRNKYRPHAYRGALLFFCVSELSMVDPMYQF
SLQWFINLVLFAVDKTEQAEDIDTRVKNLTEYFTYSFYTNVCRSLFERHKLTFSFFLCTS
ILQQEGSLNGDEYRYLLTGPTGRGGNAANPAPEWLTENSWNEIQFISANLPGFSGFDKHV
TENCEHYKKLFDSFSAHTFPLAEEWKNRETNMQRLVITRCFRKDKLAPAIQEFVKHYMGE
RFIIVPQFDLMDAYKDSTCLTPLIFIISPGSDPMNDLLRFAEQMRMSKKMDKVSLGQGQG
RKAEELLTNGRERGQWVLLQNCHLATSWMPTLEAVVESFTPETVRKEFRLWLTSMPSESF
PVSVLQISVKMTNEPPMGLRANMTRSYYGLNDEDLDHASKPKEFKKMVFALCLFHAVIQE
RRKFGSLGFNIAYEFNDSDRNVCLLQLRKFISLYDEVPFDVITFLTCEINYGGRVTDDWD
RRCMLGLVKTFINPSVLEDGYAFSPSGLYRTVEPFDRLYYLNLLGSWPLNPEPEVFGLHD
NADIACAQSESANILSTILSLFSREESGSSHTSREEMLMRTAQGIQEKLPRLFNVQEFHE
KYPTRYEESMNTVLVQEAVRYNRLLRFVQKSLAEFSKAVRGEVVMSAELEAIGSSFFINA
VPASWAALAYPSLKPLSSWVDDLVQRVQFIQSWYENGVPKALWMGGFFFPQAFLTGTLQN
FARRTQVAIDSVSFRFGLLDEKDPARVESPEEGTIVYGLYLDGARWDAKERTLAESRPKE
LYVEMPLIHLDPKVDYVNDPKDYVCPVYKTLARAGTLSTTGHSTNFILAICIPTNVEPGH
WVKRGVACVVSLNF*

>TCRU_3154 hypothetical protein, conserved

MAQKRLKGKSHEKSGGALRKSVGDSKKKTVYGKRRKTIEAKARANYASAVESRVASRVPS
DQRGRLTVVKPTAGQTSQREKKKHMKKPLTRGRRRKDAKKA*

>TCRU_3155 hypothetical protein

MASALFSENKQLRRRVRELEGEVSFLQDQNYHIQRVNDTYRGKVLQYIESLRSKGRRGSS
PAFATAKDLEELVRRLRAHDITHSSSRPQVEEMTATVFPKGSITREGDDGLMNSTSTLSR
ATQEGEGGVHVAGRSNAPRKEAFSPKGKKSQGNESATVKNAQRATVLNLTAENRKLVSLV
DTLQSRLAAAGRLNSSLEKKYRALSSLMGCSGSSGSGRQQDVTRDKMPGLPELEKQLREL
GEENEKLRSENDHNKELCQELSHYRILLSRKNVEFEVLRQRESILLEEINDLKGKLAKTT
ETLQTMGTALRLGKVREKRAISAMETLQKKNEEQELQRRQQVQETRMTASEIQPAFLSAF
IARVAAALERHHFVLSEYTLACHMLHVILHGRLTGQRAQESMWAIDFGWKSIVTETLFLA
AEHLANLIKIFEETTMIHIASVTSSSLAKSGMDAPVAKASEDGDRRGCLDNPATMNNNKR
LQPPIQLFTDDGNEVALKSEDEDALLSSNPVRRESRSIEGSVERSHAQMVDAATITVSPV
QISLAVGCSLPVSPQFPSKGTETISPLLISRAVGEDFGIEGCALVFPVACAASFQHDGRR
EQ*

>TCRU_3156 hypothetical protein

MDSTSRKEAVETLLRTCSRGGDREDVARLLLLQQITGERVKDVAGELDGASIVDEVLFHG
EGHGTTLPRITPPPLFTIGAKELWEAFPSWCRDTELQRRRCGGDAVHGHSFVCCAWNLGR
VVGELSFPSIRGWAAAYRSPWCHRYQLPLLTRDGSGGDNNNNKNGESGMRCTTSLEEEAN
AIEAAQREGRLMEALDYGEPGAVIMELQQRLNQRLEKYGAQYFYTPCGAAGKEMGVRFAS
PWATSAFVRNLSSAEEVISGFVTLEVIALECVDIAEEERPVQAASSLFDGDEMWVKGGRE
EDEWPSFSEMTNTFSSVGRRRWSAGHSFQLRVNPTELLIRHDTAHLIANPKYHGDGSVGN
AANDSSRMWLFHKDQGRPETLPFPRRTCRNHDLVTTLERGEEEWPTFLENLDLDALVSLL
CARVEKSDNAVVPLGVSPIVRVTLPLVAPSPKRMWERALQKRSTVVAAAAAGVAAMVRNR

SGRG*
>TCRU_3157 Modifier of rudimentary (Mod(r)) protein, putative
MLRMQPYVDELKSRFGKVTVIHNSSAETLLQVEHVIPDRGYAAVLCVTLGVHFPRTPPIV
TYFDGRKISLASPDGSAPDAWDPSKSNLVDAVGNAFANLANLWGSVVPPSMELLTSQLSS
LSDSMLQDIVSNPNCLESYAYQLPFFKAIRDASCQTIDDIERVANENLKLQPVVENLRAE
VEGLQRSLEQNVQSMQKMLRATPLLNSIGTPESLAKTLATDVRTLDAQCEEIAKKILQLD
CATDKFRFDNLLEEYREKAKERHFIDLKRRAYCASLT*
>TCRU_3158 methionyl-tRNA synthetase, putative
MSLKLFSEKANTQALKALLCCHHVKRPVELTLSGAYTSPVLHHPALKQPIFSANEMVRLI
LHDKWRDDSAGGSGGKKTGCYDGHWASVSLEEEAWLEWEATTFTCAVHPLYTQRRVTPEA
AGAFEYLDNKIHENDCRGPCLAPVGEKGTSTKSPSFLVDCIIWCAVLPALCEGGLLGEKE
REKVPHLLKWFESFQSAREAHIAGAVESLAVQEFADFLRAPRVYKLSPKLSKVFFITTPI
YYVNAAPHIGHVYSTLIVDVIGRYHTMKGERVFAMSGTDEHGQKVAEAARQKGMNPYDFT
CQVSREFIDCFEQMGYHMDYFIRTTNESHKKVVHELWSKLEAKGDIYLGRYEGWYSVSDE
SFLTAQNVTDGVDKDGKPCKVSLESGHVVTWLAEDNYMFRLSAFRERLLEWYNNNPGCIV
PEFRRREVIRTVEKGLNDLSVSRTREAVQDWAIPVPGNPNHCIYVWLDALSNYYTASRLR
LGKSGEELELVEDHRVLERFPADIHVIGKDILKFHAIYWPAFLISAGLPLPKTIVAHGWW
TKDRKKISKSLGNVFDPVEKAREFGFDALKYFLLRETGFSDDGDYSDRNMIARLNGELAD
TLGNLVMRCTSAKINVHREWPTPDAYNAKDEALIQLIKELPGVVDHFFLIPDVQKALAAV
FDVLRAINSYVTENAPWRLVKTDPDRLRTVLYITMEGTRLATLMLSPVLSQKAPVIFDML
GVPEANRVGVENFGFGVVPSGTPIGDAVEGKVLFPKISLDKAQSA*
>TCRU_3159 hypothetical protein, conserved
MDLSLKHGRILLLLDILRIYGRLRSLILRHKCSCPLWGAARELGHQQGLITAERERLNFD
YANAVADVQNRNAQLNSQFQEAHQNLSVRESNIAGAGNLVLELQKQLEAAHAKLRREFH
LGVLTAQLQEREARHNAQQPARYAETAGRGKAPAT*
>TCRU_3160 hypothetical protein, conserved
MPGSDAIVSRIRNVFSRDLPKIHEAIGGILPALQYADPLDQNVKGKFNLLVVLLPALVCA
PEAENGSGGALIPCMRGLPGDVKCAETAVLFHS*
>TCRU_3161 hypothetical protein, conserved
MASGVLGENGSHMPDGCNKTAITVPLRSVLPITAVEASTGESVSDSTDIYPDSLSVPPSP
PPVTGLPEALKAPKAPQDPPESDVGQTGVGDRLSLVPNDDSSGAGGGFEENGNSNKIGVS
ASEFSTVVGASRSSIPPEVGGSENKSGAPPNLKLESPETNELRERILVETNKDTQKVSKL
EENPESSRKKEKANIRGTSEEAGKNEAGRSGVEAHGPSSVLSADGQLQRQGTTVTMTQPP
PPSPEQQTSAVSPSPGVDTPAARSREAGDLEEGKGIPPARTASHNSTDEKRKAPPLRSEK
ESAAPKPPSADGVLEQNSEDTTTKEAIKMDAHTDGPAATSEQSTSASESGVVKRNESEDG
DNAQRPEPKGQHNDPDAVNTKAAPTASEAASYTAKTVPARKNDTVTYGDSDSSTAVSHTT
SPLLFLLLLVVACAAAAAVVAA*
>TCRU_3162 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGGIVADDAVPAELEKENKSESLKDDPSVDKTDTHEPQE
GMIATQQNGLALKSTTNPLELEEDMDEDEEKEDGKGKGKAEKDTRSTEQTETQKSLTKDG
ETSKLTSAPGTPSTPIPPEREGQETPSETPPGPPTNGKPAEETGPPALTGSQNAAETTST
TSPSHSKTAPEAAETPSGNGAPNQHREDAETPDSMKDGPTSLPAETAVSSVSKSGIGGTQ
KKEDKVDDSDQRPNTKESQDGIEDGNTNVAPTFSETAQKTPETITVAKTNDTTTTGDSDS
STAVSHTTSPLLLLLVACAAAVVAA*
>TCRU_3163 retrotransposon hot spot protein, RHS3, putative
MDLECGVLYLLAVGNFPLVDALFFMESPRKALVGLRTTTANAHHTQTSNVRLFKERVASY
FNGWEEFARDLSWEIIYVQHADSTPISDWQRCHDSANLTEAENREIAAFWEEKVHQYQVT
VTAEMLLQNRPPEVSNN*
>TCRU_3164 retrotransposon hot spot protein, RHS3, putative
MQVFVQEPDAYVQDQRLLRIIFNLTEYQVYKLHHEGVFSPEQWRDYEGKDTVTLIARGKL
NAALFQAQTSTKVVKSTVLKGVYQSVYNARWSHVVEIPDCEEEQTEMGMKVEKGKPKQSW
TYKEVGDTL*
>TCRU_3165 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-

terminal, putative
MEDGTIVFPLMAKSGKGVVYSMIIHSTDNGSTWSLSEGISHPKCFAPRITEWEGSLLMIV
DCEDGQRVYESRDMGKTWTEAIGTLPGVWVNSQLFFRDLSLRVDALITATIEGRKVMLYT
QRGHASGDNANTLYLWVTDNNRLFSVGPVGMGNAGEKEFAGTLLYSDGKLHLLQRMASGE
GSAISLSHLAEELNKIKFVLKTWAQKDVFFSGLSIPTAGLVAVFSNASASDDTWNDEYLC
LNATVRNATKVKDGFQLTEPDSGVIWPVNIPDDKVRNVSLSHNFTLVATVTIEEAPSGNT
PLLTAVLANTEPTHTMGILYTANKTWETIFKGETKPTTESGTWELKKEYQVALMLQGNKS
SVYVDGKSLGEEEALLTDETPLELLYFCFGACDMKNSPMTVKDVFLYNRPLNPTEMSAIK
ERIPVPTRTPEPQVKIAPDPIAPAVSAVSGAPAVPAVPAVPAVPAVPAAPAGNEGTAREK
GDGGANGDAGSVYGSGLLPLLLLLGLWGFATA*
>TCRU_3166 hypothetical protein
MKVQIRDSKFKGAYEPVNDHPRRRIATPTLQEHLNDVKYFHRMAPTTQSRGIKYRLAAIE
NRLEHGVRQRYQRKVQQIPSTSQQFQSSSKRQEHQTVPTDSPNMASNGSETPDAERFAFL
PRDTSTDECKCRVLRPLDRFETKLRPQGDGSMWLAIRSSRRGKTVQKVGW*
>TCRU_3167 hypothetical protein, conserved
MQLVLGHCGVSRNEACDTKSEKASDLSQLTDTWSTGVVALAERIIRARQLKPEAHRSAVR
GDWELTRTDPTLTRGVEAALARLRTGVSHKYGWLLRPLQPAIPRTCCWCGSDAAQQTRKE
LRTETPPPPAGPTPPRSDGRQTARCAASTAAASLVS*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MEYRSAGIIGKFRPVACGVCDADVSCFAAATRTMSRSCGCRCAEDGYGLDCLPVYLPHVD
GCNRTPAMPLLSHTVTLTETRSLTPTWTSTWTPSLSATHDSPTWYGPTETLQGTETVALS
PTRTPTASVSSTLWWSDVACPTLAVTTTAAGGSLTQNDIRGGGSVVPTRLMVALPPPFRW
ASGPQLGTHLSFVPVSTAQPSGFGGPWGAMLRNATWVRNATNPSTVLELAVPVHRGYFIA
ADETIVIRCDAAAVSGGCKGVLLGSFTIRSDTLPAAASALSAITGVAAGAAAASVLVTGG
LGSILEMQALGVFARMPCASAQESESTAALPYFLSVFAALDPLWMVVGNALLAAVFGCVH
CGVTAAFQRWRGVDAASAWAAMRFPSLTYVVAHAMHLGIFFGSVLALAMPGARVQHRVIG
VTGVLYGVAFPAGVCYLIARHTGASFTKYWQFSRKPLHERLLYPVGYWHPAAQRRMYGGM
LTNMKGSHVYWCVFRLSVLCVVGLIAAVHPPVGVCHVLYFCIAAVLLAGAGVVAFTNMMR
SAFLTVMHTASFVLLAALCLVSAANHLAPSDGGARAYAAIVLLLTTVLLAVTVYSVVVWY
AEDRHWQELREPRRGGLEALLRDDEESDEDAQKPHEMTSSSYATGTTGASSYRPPAPPLQ
PMAGDTHSDALSPLDRASSASCMIDYAAM*
>TCRU_3169 hypothetical protein, conserved
MLLAKDNVHDGVSREMLYAAGAVTAVGSTLSFVRNRALLPRMLSASLSLSAGAHLRVACN
DAGGRVLSTAEEYAAAGFGDAGSIDVVGCDVCDRDTHCYAPGTASASMRNGVCVCACGSG
GYGEACVPVGAPALPPAVGTASSVFVREGVAVQSVFVVPAGASEVTLRHVVLDGVSPVLY
VPWMARDGVRIVVQNVSLLSGAVLYVMGGGALRGAVAAGSDEGGPVELSVCDVEALNGAL
VLTGTYPAGSVLTVTDSLLVAARLTPLVYLPGSQSSPYAPVLVLSGLRLVRSVLVVSGVA
LVTVMTGGRTVAVDGAVLELVGGGVALDAAVLGGDFALYASARVVASGGAVLRVSGSQVY
AAHGLVFGSGVEANASAVVVNDNAGALADGALLVLRGSVSFVSGSWLSVRGNSISGMLLS
AAAVSAQCGPCAEHADAPRERR*
>TCRU_3170 hypothetical protein, conserved
MWSAVGACPRSRHRVQRSAIATVRAALLVLLSLAAVAAWVPAAHAVVLRLRGCTVDRAIT
VGRAVDTVLMDGVSITNGVAVVFDVPAMLPGALRIELRNCVCDGGAQIYVRGYGGEPASD
RSLEVSVSGLSGSYCSLVFVHNLPAHTNVTVRDSTIVTAGPMHYSQLNGLTDAVASPLVL
HATSLLQTQLRVSNTVLRSLQTGGSAVYVGGGVDLLSSAVALDGVLLEASGGPTASAMHV
ASSSRLSLQSHSVFSMTNVSVVSSGGGIVLGERLAVIDSVLRFVGVEGSVASSLVRCDGG
TIGGGGWLDLHDVWAVGEASSVASLSGVTLSGGAVSIARCAATGATLVSGLTITSGVVSV
QCNRAGGRVLRSSGDYRMAGLPSVSVVPCDGCVAALACFDALTASFSDCACSCRAGGVGD
ACLPFDVPPARAGGGGGDTAQDCMSGVTLTESVTVGGVRATACFDSVVFSGPITVAVDLR
LMDAFADALNVTLRHCVLAGGARLRIGGLSESTARLVPHALVSMTNVTSLEGTIVLHGAM
PQHSTVLLANSTLRATVGGSQYVPTTRGHAGLRCGPALVLDGVRLLSTRFVMTRSTMACG
GGSCAAILVERGLGANLSSVFYMDSCVVRSQTHVMYAIASDLRVGGGSVFSIQNSSWSAP
STEYGEGACVFKDVVVDGGSVLQIVSGIFRLGFAMLIANTLTVADGSWLVHRDNEFRTAY

VVYVANENGVAFRDRSVWSILGNNFTYGSYSSTIARMTSKWSPPSDSHPIIYGVCNEARG
SPVTDYGEELNIGTPVTVLDCGACTVDAVCFAARTSSISGCECVCAAGGYGDTCLPAAVP
DGLGPLPLPEADDTEVRCVHGGSIGSVDYPDPGVRGLCFVNVTFTAAILLDLWSFDAPQQ
TLNITLLHCVLVGLLIKGSGARVHVSVVSSMMDSGVLVFQGDFGVSSQILVVGSTIVTMS
GHAILFVKFTLSANMTLLLLDNYIEGSCYAVYFSVALVVDGGGIILKGNTLSATKDDDGV
ESSVYVYAVDVRNGGFIDVENNTMSAVNGVILFGDNTVSSAGLLRVADCTFVGGTETFDP
ALLHLSGSVTLEGGAQWRVEGNSVGAASVLTILYPQYKIQLSGSGTTVALANNRQVGGNT
VFAMLLPWSTILTSPARFVVGCNLQDDEEVSYDGVFPEDVVIFRCGTCNDDAACYMPGTE
LVDRSLCSCSCKDGWHGASCLPFEVPETVVPPVAERAVDGDTSCVVNQTLTDLTINMWKT
HHCYVGVTFSGMGAVLTFFLNSMPLHLPINITLTGCTFLDGAALQFVGGAGATESSGVLI
RVSQTVLRSSAVAFLRALPLHCDIAVTEVDAVQSFEFELSGTVNNMWSVFLLGNVVLRAS
TLLVSNVKAYATKRDALGFSSIGTLKLVGGSSLYLQYCSFEGYKYLFYVHSLSVSENSVF
ALLNNTMLFGVSLLYQHQGFSVSDHSVLRVVRNSGSARYAICNDELWNVQRSSWLDWRDN
DVEVGAMFYDTESAFVSIDDSSAVTLTGCKMGSTGLSVSLLKRADAGYRFVAGCLTVAGR
EVTTAAELALHGITNVTTVAVCGECTRDGDCFAPLTTAVSDCKCQCAAGGHGDVCVPAPV
PAGPPPPPSPPLRPTPPPPPVGECISDMVYPEVAQSVGDGLSWLCYRNVTFSGGGMSLTV
LVGAMTGDVVKITFDGCTWRDGAVLLLLGNAHAAVGPLNIVVTGSTFSDALLSPEGGFPP
RTNITISGNHFAVTRLVRRPGLDIWSPSCVMMNGLVIANDSAVVLSGNVFQTVTTSSIAI
YVVRSALRVSWHSVFAVVGNTFHMDGGGSTLINIDGFSQSLSLSVLNNSAVVVRGNLVTR
PVRYFLLLILASRVESRSAVVFQGNEMQRSSVVFFSSHSSYIYYNSWLQVSGNLCRESPS
EAFASLYPKVNLRDSTVSVSGNRFMSSTDRPTVLRITTGSRDITNGAIVAACNSVNGEEG
VEYSVPSVYNATILTCSDPCILAASCFPAYTTTASSDGCACNCAEGGHGDACLPVAVPEP
PSTDGADLCVRDVRVDVEVSAGLGTSVACYVGVTFAADVVVDVESMSGSVRNVTLANCTF
VGGASLYVVGWRSDPPAGQCVDSAGLSRVPAAACWWRTDTRRARASLWWTRC*
>TCRU_3171 damage-specific DNA binding protein, putative
MCILSHLHTPRLVVGLLNGYIADISLEAVLMGSAARETLIRLQPVQLFNLESHNAVLCLG
EVPLIIILCDTGFQLTGIDFNDVAACAIIEGSHISSKYIFLSQSENSLAFGNIVDLKKLN
SCFLGLKATVTRVKYIAWWNVFVMSVRRNEKDQILLLMGHELANSWVPQNELFSIELFSI
ELLENERCVFFETVVLGGSNESPNGNEADKDKAILLGTTFAFPDEQLPRSSRFIWYSVEQ
GKLISERPQLRQIGSKDVEGALQCCCIVPNYVGRIALGINGCIALYSWNAADSVFVAEET
ICIGTIVTRVLPIFQGDASYMVAFDARHSCFFIQVDTFQGSLEIVARDSEPRGVMDGAVF
QLGNIYNICFGDDYYNFFCLSRGASTLPSASNATSATVSSGKLETSAQYHLGDMVTAMQL
GSFAPCSVTNIAVPIPTTLIPGICGPQVVFGTSHGAFGTITPVSNETYLLLKALEVAVSS
VVPALGGFEHVTYREVLRAGQERGYSRNASFENANVVSSGVFEKRRKRYLSRCVCSGDLI
ESFLTFSQTIQQRILREAESRIKSCYFSMNSTLGEFFEHNDLDNSFAERSDACLDECKTI
GDVNALFSESGLPTLPLTREAVNEFLQNMQRIH*
>TCRU_3172 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MSADGCSDPSVVEWKDKKLMMMTACGDGRRRVYEIGDKGDSWTEALGTLSRVWGKKRKEN
VKLVRSGFITATIENGDYNKKVMLVTLPVYPKDTDKGQNNEKGRLHLWLTDNTHIVDIGP
VSGEGDDEIAASSLLYKSAESEDKKEELIALYEKKKGGEKSLGMVSVRLTEQLKRVKEVL
ATWKDVDSRVSQLCINSLAQKDPSADSVCTDKITDGLVGFLSGSFSYNTWRDEYLGVNAT
VKDGAAGAILHGGGVKFRGAWAEWPVGEQGENQLYHFANYNFTLVATVSIDKVPEEGDNT
IPLMGVNMKGAGNSVFLGLSYNNNGKKWILLCGDGTNSGEHSSNWESGTKRHVVILLRNG
NQSSAYVDGQRVGVGASCALGSTESQETSHFYIGGDGGSAGSKGSRGVVLVTVTNVLLYN
RPLTSEEIGVLNPNKALISPLKEEPSTHSPVPSASVVPPTPLVAATAQQTGISSTPDGTH
RTEQGQPIGNSGAESGGASASAASTVSIPSAEKDSVMQMASGKSSDGAQTVDGGSTADGE
PTVEKREGTDAQKEEGIHPQVREVNATALNSNLGSFPQGNNSDAGSMRGSGLLPSLLLLL
LGLWRLAAL*
>TCRU_3173 hypothetical protein, conserved
MELICQRRSTVVRRITDIPALEHPYEESERGDSRNVCAVNVGAEDVPSGAIHDFLPHART
HDERGELRGLFDGNRCSAIDPTAVRQDAAVHVANESNPAGHGDSGVTKTSGAIGDETDAP
LDK*

>TCRU_3174 hypothetical protein, conserved
MVRYAKRPWYTPVGFMSYAPHSYGALLVFVGTTAVFPLRYKISEYFERQRDGPHVELRRK
AVLYYNEIERMHRRQALQNLSSMQEDESSHRLSATLQGEALRMGHVDQEYNYWYAHQRDA
LRAEKLLAEVRELQERVSQAQ*
>TCRU_gamma, conserved domain containing protein, putative
Elongation factor.1
MHFLTTNLIRGWLRRMEYVRQYALGVALIIGEERRHEIVALCVLRGQGMPAVARDVEGTE
LFDWEEVADVAAQQEGPTIPRPVLGGTCVEVGVACL*
>TCRU_3176 hypothetical protein, conserved
MALVPYTPSEWCDIGARLWEMVCQCGEIQVQLTFINGNQMSDETLTVAASSTGLCLFHGP
ISKAWQDSTLIGHIANLRAPQIPDFETHVLLPAMGVARELGHQKGLITAERERLNIDYAN
AVADVQNRNAQLNSQVEEAHKTYR*
>TCRU_3177 cytochrome oxidase subunit VII
MPRPFGVWAPATTLAEYRARVPNLSAFSLKWIYSAKREVYYHPEALAHFKDHQQYKDAVD
TVRAMSVSDKFFGEGQKLPRRPVIKLMGALLVEGLLVYAVIRYYYGVYVPANNPTWRKVV
NKEWEEAINTSPWDHMSHVWQYSDQYAAVMGDTASPGPRKFYIPA*
>TCRU_3178 ATP-binding cassette protein, putative
MPIQGVCESEGLRQPSPVQSEEPLLGRGMSSVQFLGKQKESTSKLALTFKDITYTLPKCS
GRSEILCGISGYVRSGEMLAILGPSGAGKSTLLDILAKRTVSGEVGGEVLLNGRAIKDAA
FRRITAYVQQVDVMQCFLTVRETISYAAQLRTPPSFKRREVRARVEEVMRQLGIDGIQNK
KIGSDLVRGISGGEKKRCAIAIELVASPSLIFLDEPTTGLDAFTALHLMKIFKELTSLGT
AVVFSIHQPRSSCFALFDRLLLLNGYGEEVYFGPAGEAMSFFAQIGVVPSAPENPADFLL
DSISVPPEEELLACGDEARLCHVACGQSAPNIAAAFRDRLLEGIEREIDAIDDTFMQIGS
ETSMAKDVSPYFRSVWTQIRVVSMRGVINKIRDPMAVIVTFAASIFFAVLTGSVYFRLGL
DQPSIRNRMGVLFFIVMNTSLHSVSVLNLLMEDRPLLLREHRNGMYRPVAFFIGKIVQDL
PIKMVSNFVFDTIAYFMVGLQPRVDKFLLFCLICFIIMLNGYTFCLLVSTVSKNIQVANI
LAPLVVVVYLLPSGGVLMSVEAIPLFWKWIKYISFVRYGLTTLVINEFDGLKFNCSPEDV
ICVRDGKLYAEMQGFYTKDFWRFIGAAAGSVGVYLLLAYIGLVLVRTRGSG*
>TCRU_3179 hypothetical protein, conserved
MTSTANDEAATLWVQHAVECLHKNDNGCDDGGEVRYADLLDFMQSAPPPPNSLHAMWEQC
VWRLQDEPEALYLLRCLANSSRGGVYSDASFLLDARASLPFPCVSQEDAGGAEAGNGLQR
LVARIVALRLVPSTTDIIQLGWSVSLAGPETTPAASSSLRPMYCTRTHVVIQLASGRHLS
AWAYGGVGLRLRVGTVFCALLYPSRTENQEMAYVIHNVSEITAADDSVGSLAWSRSIRRD
NFASYPSMPGQFSFEQLVESFSPEMAGQKLCKSLLLLVVVHTMYRAVRCRARRPLHALLL
GAPRSGKSALLRAFLHLLGPHATLVGAHVVHGQQRSAAISQAITATYPHVRQQLLLGGAV
STFDALVVDEVSGRGCANFVEGFITGVCPIFSGGGGVSATMIRSHVIPTHVQVTAAANDD
LLAAAALIPKFSVVARTTAQLSLHNAASIGEGVIAASVASSQSLSRTPSRSASLCESSPG
RLDSGVFCAGPLCEELLRAAVEEAPPASVLERMIPAEAFTSFYLSRLREHWHGTKALGTT
TVTNSTPPLALVLSVLWELNLARLVLEHGCCHGERATGWSELLAEEVWQCYTHHLWALDT
AAVATARERIKKQAIPCGADFSAVGSGKKRKISKKAACVALLRMMAHEQRESGADSVSEA
STRAFFQQLGGEAMTGQSFSDVIQQLLDAAMIIQRLSAYAVVAEA*
>TCRU_3180 hypothetical protein, conserved
MEEFGASPPDADLDIASRDYARRVQGLRNDAYRQAVAEIAGELYGAVYMRAYRDALEMHR
GDWGGTASSSPSGCA*
>TCRU_3181 hypothetical protein, conserved
MRRWQYCLVPIACNSSARAITTTRGLLGLEQLQDVPASTSRRPRGMHRGPGKRQTTEKEA
ERYRFIKRWDLQMREGWDELEAFKGLPKPKQQFGNEAAEIVWPYAVLLERVVKVHPFTKS
IYVYYGQRQSTPLGKLAAETAKRFAREFLIPITFHNSQVYVETEMLLEYNETPWVVVHAL
DGGQRILPVHPAAEDTPIDAGVTQLLREVVKTCEALAAAVANPKEVTRMLNERPLQNQYV
RVNYQWFGDTPDERCSHLVRWDFDPAEVEPIMRQRTRHVLNWLNHDGNLPNHNSVRVNVF
REKTRLRSPQTTSGPKTFFNSVGSRANARSSRFGGQSAVGK*
>TCRU_3182 PHF5-like protein, putative
MLRHSKQEQQMCRKMPGASFGYVCDQHDGRCVICDLQFDEVLPSMREVHVCDDCGFGKEG
EERCIMCNSGKTTEVAYYCHYCVALEKDRDGCPRVLNQSRHQRMATLRTR*

>TCRU_3183 hypothetical protein
MNINEKISSVLGYVRDSVNPYTRLVHSAMNTDKRSVPFYQMEEVREASFQSDHACEMIMK
ALAPSLDESSSIVLSKALSIFRVLFVEGANGIRIRMARVRGSLSRIANLQDVGRGTLEAS
NRDLARAFLEAMDGNSDALVSFPTVQMSGAREEEYTSPQSYKSEFQTMHEKERRMYRRQC
EEEKRRSAVIVRGRIYGTFDGSLSPEKLAEQVVACPKKRFAQTELDSFVSAAIATERVTE
VCAALDQHLQGARQTLQNRYKVLLVVEALVSSGVKEAQDYYRENNVGICRHLTMNSVENP
VKAEAAQSTARRITQALQAPLLSSAPAPTVPPRHVIAPQQPTVSQLDDLFSGVSVQKKPA
ATSFSHVPLLQDISADAVIEDIFGPAPRLQSAPLPPTATPTGNGTFTPTPSLPQLFEQNH
KQGEKQQQEQSTLSFISQNFPPSGGNFISAAQQSTPDFIGSFQGTSTAAGELASQANSFG
TSSEQRVGDARSDADKLRLMQQIQAQMEMTRRMLEQQQSALLALQAEFQKK*
>TCRU_3184 NUC194 domain containing protein, putative
MTVEEISFALRADVAALRFLLVGLQGSASDACHVFDNMERRLRSSKIALFSAHETVPLLE
CVLSNEESGLLRVLNDYCEKMRFSGTDARDARVLKRAMSFLNLFFESFQESVTIPQVEEI
HSTVWHTFMLLHRLSKHVEVQAECLGVVSALLRSCGQRLSPARLDVAKVVEVCVLILERK
ITSGLRLRSNAMRLLGCMCGVYTTLMSPHAMRILHAMVSVGQHLLASDEVEQVIGEGLLL
AFSDYSGGFSLVFNGPDRDTLMLMYHLIKKAILLAGTCQNYRFCKAALALLGKRADFLKE
CLMNDMQDCFTALRHLWSHRNAEVRRATHAATAGFFRALALSWSGDSQRHDLAPRLRYML
HALEATMRDKQGRHRDLSFAIMAFGYMARPLVSCFGVDYLAITFREMVKRCEVLFTLTSG
PVEDVVRLLPYFLSALASMLLELPPMGSELPQLLNFTLHTTLFLYPRGMCSENIRSTFGS
ALLKLLTAIRYCHGVEFGVVLVARWLLALACVPFSRWDPKKGLPTAVEDVTMQKSYILLW
ESLQSHSHSVLDWGSPWNLSISDAMLDSLRMALRRELVSAELEMLRQFDVSLLSTEEEEE
ARDGGDTDFHWPVVDELGEMQLCSMEDCNVFLRFTSFFIGSLDATFSEAIGLEEVAAVLV
ESLVSFATRHTHIAGGYTCLHELLQAGWRAGLSLSHAWIFLRSFSRTCLHCLTIYTDGLQ
IQSALCMISMNHFGLLETAQLLYPIEVVIRHADDTAAVADALEVLDCCLEKDRALVMPPF
CALLSQLTVFNPVFGQLHSLLVRHGAQLGDGVQRGVNDEVLECCHGTTPALPCLRRHMDG
AQLPLPMGSTTLFLPLGSLLPRATMLSFQERDSQLRLAACELLRAAVGWCIEHNVDDLYG
ELFDTVIVLAGASAAGLGIQVMFGALLRQCARCFALRGGRGAKVMENAIFRGTAVPHNAS
IRRVSIEALAEYVQWSLKYELRLQLLQEDGAQESQLKSVLLWVCLTLRGPSAWQRLGAAG
VLDRLLHLLRCERAVLPFVVPFTRALLAALASMRMNEWDGGDEREGDGGGRAAVSLAGNL
CRCVRRLEVYVVTNYELLVDMWQDRNVAEENEAVLRDILLHAYREGRHSTSGAALLRLFA
AICRCMPGYTEGDVGPRRWLLTHLSVLRDFDLLETIPGRRLECGLQMHYMLMSNALFPST
LKRARTEDASLDEESTYFRRVLEELDRYVAESAAGCSDSVCISARVLFIARHLVRVLSGE
VGTVASKLLLLNRSLPQFAVRLLLAPTSLGITPGPYYEVQRLCGRELVAALSVSLRSDEG
RFRELVDSLREHVPATLWLTPQPTLLEFFLSDPHTAVHTLRCLAVLVDLGLWAEVLLLPS
LSHVIQRRLLEGLLEAVRDECVVNSQWGTIFCHMLLLLLLSPLPPPSLDDAKARKDGENV
TNVPRGFGLREVLSAVQQDEERFVDRKTSPVFLAAILRGDWRDAGKNGATLRCLLTELFQ
VCGELLQRSGESSLQSAPFVALRGLLHDFHQGPKPAAETWALAMKRGVDALMHIGHGGSP
AVLAFFLEVHRCCLRVGGSHFLACYEYDILADISAAVDGERWTMRPHTLLTSRVAVHLFV
QGVDVLCDAVAAASAGNERPTQSYATLVEQLMRRAINDELPLDWREVDDGSINGIHYAFV
VRALIRLVRCTAALDSALLLSLVPLLHQTDMPQYTALVTAVSSVLQKLPSEALVELCHKS
RELQQQCGLPWAVWWGLTHRLLLPSLRRLLPAVRDKFFLQHVVGLVEEASAPPSGAATLQ
RKTRALIMLEAVFDMTAASVLRGPINAAFTGKKDGSSGKELIIALIKACCAARVFVPPAT
FSPEAFHDALNYRQSAHRCLVAVLVATQEQEKVFTRLLLNSPGGGVWNQIVDTSFKHFFY
VETNFPHMTECTAKECSDWEVRKCVATFQRLAESNTGILRQGTEGEMQCVYAVENAVDHT
FLTANLPWLSHALVMHDEGDDKPHNRKREEKENGAPRVKLDGVWISTCFGALLRVTDFLL
SRFAVNPADGWVKEIIGLFSSTAIHVNVRLVLARLIQMRASSFTPAANALRDSLVSLVCE
EEMGEGGVHYVARDLLELLFHWGETGAMNFTTEAARKLMVFLFRGASHPSEDVMQHNLDL
VRRLVSLLKPLSPVCDRDLLHVLRGQLLEFSFGIRMCGLLIDNGVLLSSVAPASLVDLYH
SLVSCFKRNKNIAKVEVEELLVVADVVGKELRGLRDFAETDALLLRDTVRSALLCLWSRS
PGVALRVLCAIVQHDSGVVEDIPLSTLLANFMSRDATEQLAALHVIKCTLSRTAEAYATL
HDIFSGHLFTLSAPVRVALYHLLVELFPLLAAAEKERFMNAFLSPDAMQIMCGNEDTNLA
FFKLAVRVYEVAPSSFLLARVAEGLKEPLPSVRFMLLEFLDAHVLPRDSYLSRLAALKEA
ITPQTVGHDVWLKNAAVLTLSLCHTAGATCPVTGNLIASPPSFAFLGSCFLNDPLKRHGV
PHDLCPRASRGGLPWAHSESEDLFLQKHREEGAEKPEASITRALPACSEAEFVEFQIPSE

SFVAPLQLLCMHDTETARCFLGHIEASVAV*
>TCRU_3185 Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MNDNNKTVLLGLSYDKEGKRAVLCSGQTTKEHSSPWESQTKHQVAIVLQNEKQGSAYVDG
KLVGGDEACALKSKDPRVVSHFYIGGDGDKVEGQEGLSVTVSNVLLYNRPLSSEEIAWLA
KNTITNPKPEDPKTSVVDAQSSATSGSPVQGAVSLRLRRRQLPLEEKPLKENIGAGAGGV
YSATSVATTPSSDASQTVVTGGGDMMLGNGSPQTPEVSVSSAEDGVTAEGTNAQGEEKGI
HPQVRELNATALNSSLGNLSQGNNSDAGTVRGSGLLPSLLLLLGLWGYAAQ*
>TCRU_3186 hypothetical protein, conserved
MATEWGDIGARLSELVRQRGEAQVQITFINGTEMSDETLTVAPSSTGLCLILGNISKQWE
DSGLTGHIANLRAFQVPNFENQLILPIMGAARELGRVARAHHC*
>TCRU_3187 hypothetical protein, conserved
MGEDRESGATQYTFLWVQFDHSLQAVFLSDEFVLSVCAMPALNSSTIAEMEVVASRFLYA
ATTLCTRLCDYYFLITAVLRRLSAHNRSIVQETSPANLPSAAIGSGERLRHINEDNRGRT
INSTEKASAAIITDALFCG*
>TCRU_3188 hypothetical protein, conserved
MELRCFLVHCGNPSFGTSYVDIPPPPSCGSERHHGAVKYLGRHSPELYWRLGNNPRYSRR
MMSLWVENTSPEEIPLTARVHPHVAQRLVLKCIGKNTITVSRRTAGENRILLRCNESVTL
RVGDKVGVAHLVWMQVVLALVSVNGAVKAPVLVQQEEGNDAQYFSACRTLCPRLQDPPLP
PVVRVNVAWMKLPSAIRAALAISVWERQLAADSGAVATAALTSLRPTTFAASPEAGDGME
EAAAISNSSQVIQEGGTITTSSETRSKRRLHASPSGSQGVESQLISLDVPPPQKKRRTSV
AETAVMDNNLRVTLPENNTYYETFDERLDDAVRFLESRTEITNSLIAAGPPVPELLGESP
PCEGRSVEVKKWARRSKSATVSRTELRHGKKQKEKELQLSSGHVEGEAAGGKNPFAGESQ
VVYYRR*
>TCRU_3189 phosphoglycerate kinase
MALKEKKGIDQVDVKGKRVLIRVDFNVPVKDGKITNDYRIRSALPTIKKVLECGGSCVLM
SHLGRPKGVTMAAAAACGDDSVPGYEAGATLKPVAERLGELLNVPVVFAPDCLKAASTVE
KLSPGGVVLLENVRFYVEEGSKKEEERDAMARVLASYGDVYISDAFGTAHRESATMTGIP
KVLGHGAAGYLMEKEISYFAKVLGSPARPLVAIVGGAKVSDKIQLLDNMLQRIDHLIIGG
AMAYTFLKAQGHKIGSSMCEEDKLDLARSLLKKAEDRKVTVLLPVDHVCHTEFKAVEAPL
VTEGVDIPDGHMALDIGPRTIEKYVEVVAKCKSAIWNGPMGVFEMAPYSKGTFAIAKVMG
DSTQNHGLMSIIGGGDSASAAELSGEAPRMSHVSTGGGASLELLEGKTLPGVAVLDDKE*
>TCRU_3190 Phosphoglycerate kinase, putative
MTGIPKVLGHGAAGYLMEKEISYFAKVLGSPARPLVAIVGGAKVSDKIQLLDNMLQRIDH
LIIGGAMAYTFLKAQGHKIGSSMCEEDKLDLARSLLKKAEDRKVTVLLPVDHVCHTEFKA
VEAPLVTEGVDIPDGHMALDIGPRTIEKYVEVVARCKSAIWNGPMGVFEMAPYSKGTFAI
AKVMGDSTQNHGLMSIIGGGDSASAAELSGEAPRMSHVSTGGGASLELLEGKTLPGVAVL
DDKE*
>TCRU_3191 Protein of unknown function (DUF563), putative
MILGTLLVISPGLKELKEDVWPEVSDGAFPDNLIQRGPGGGYLLQSRRGREGPPLQLEHL
RSFCSKYAPGLENAWWKRENIVNFPIRSNKSKDIRLPPYPIFPGPVCFLGGSSYFDGDDL
DRRRNLGGARVKIFPSWRRLTDNVLMDMQNNSYIRSLTFVPAIAIVFLNFFSLGQMYHVL
NDMVKEVMVIMTEVGNETTPWKYSELGKSPTQFFALPRAELLWTRENLATALPQTTHFLG
AFSHPTAPTRYFFNDIPVLSRDAVYCTCQAMFTCEVPPDETFEQKTVAFRLIGDLMVRYM
NETPHESAQEVSDDLKKKQVVPLSILRRFSHIPQIAKRFWETELKVMAKYKNREPGDKTQ
EPFVYRPRLLLINRNFREIHDYQAVAALAERVGFNVQVVYFEKMPLEDQVHVSRHADVMM
GMHGMGLTHVLWMDGRRRPRCRALLELMPFGCPRTLIHFYKLFADTVGIHYEYIEAADMY
LKHMGGLHTSKAQQRDLEAVKAVMRACKFDYMYRGFTNQVAMYNMSVLEQRLVAALQRLK
QCGVA*
>TCRU_3192 lysophospholipase, putative
MIGTPIENLTVSQIKEELRTFYGIRDFSDVVELKDLQAKLTTTRNSQLITHGLQYGPLLQ
VGNRKNPNGVVTLLHGLGDSAHGWEPVAHELAGSLPHLLFLLPTAPVRPVTINGGMSMNA
WYDIKEISAATDVSRQDGETVLISADYVKSLAYTTTQRYCIPKNRVVYAGFSQGAAVSLA
AGITSRIAPAGVAVLSGYLAGGNVVLSRLCNKEIPILMCHGTEDGIVPFEAAQQTKKALE

AAGVASITLKSYRMEHSSHPDEIRDVVSFLKKVLPAIDSKA*
>TCRU_3193 beta-ketoacyl-ACP reductase 2
MLSCASFSCVFRRCAGGTGAAAAIAGSLLTSGQCWVSVRHYHQHTTCLLLPRKLSQAKQQ
PLFPGMCRHVKRFEGEHTYNYGHHTFTIVREGSTFFILPLGFLIAYAATLFVPMSFQLEA
MYSVLLIAFSRYFARGRKNRDWKDLKERHVIVTGGTSGIGRETASQLAAMGADVTVLSRN
GPNVDVAMAYIKKFAKSDEQQIRFTALDLADFIAVRDYCKRAQQQRMAVDILVNNAGLMQ
QKQVMSRFGDDEQLAVNLLGPFLLTEGLLPLVAENGGRIVYVSCSAHVAVKRNIVSTYLS
GRGLWSPRIRDKFDGLEQYGFTKLGCIYHAQDLAVRSYTNASKPFASMTPATVASILTPS
NGRAHKSNSNDGNSNTPRYTTCVAVPGGVVTNLYRYVPLATTFRWCRYFYLLFMRTATEG
SQVVVNCCVREELVNGGYYQNCRYSPTGLSATACSVEERKSVLAWVRLKMQPYMRWES*
>TCRU_3194 hypothetical protein, conserved
MVKISHEDTQRIKTAFLSYAQGQDKVTEAMIDQLICGAFPGLSWEQLQEKKKGRAAANGY
DRSAFFSLVASDEQYVRFIAQHFPCAPEEEKPPEIDALELKTQKGF*
>TCRU_3195 RNA-binding protein, putative
MDDNLAAEIARIEAELEADRQFRELQQRQQQQQQQQPFGAMDATSAFERASAAENNPHPA
QRQRMFAHGGDPMAAQQQQPGVMAPTSGQPHQFSKDSDGRSIFVGNLPRGENGGPTTTPE
ELAQFFADCGQILNCTVLRDRGTGELKGTAYVEFASYTAMGKAIDTKNNASFKGSTIIVC
*
>TCRU_3196 Leishmanolysin, putative
MLWWGNNSGCGLLEKKCLTDGITEYPDLFCNRFDVYDFCTYDRLSLGRCKMKRHEEALPE
EYRYFSDPRVGGDDLFMSRCPYVRAYSNTGCTNGNPSVMPGCVVGPNSRCVKGQELQFDD
EYIGDVCVDTRCGDGTLSVRFLDDDAWQECQAGETVTPPSGPWRGSIVCPQYADVCTAFP
NTSSHPIPVVDPPLADDPTSAEDAEGDEGEVPRKRPRRL*
>TCRU_3197 hypothetical protein, conserved
MADESCFVAFASYIAKNAPCRRLTGCLHSAPFEALFCFIQGDATIIMAAPSLNGSECDNT
NDGKESDEDYGDDLHRGADYLRVLAHESREGLDAVPTIPGLAEPLAFALSHDVISAHALR
LIHLPWSSRSSSRVFVPLIPRWPFRMYLSVAWRMI*
>TCRU_3198 hypothetical protein, conserved
MEHAECVAAAACPELNCSANGRTAIMPSVVASPCCQRSVRNSLVSSRAQACDAPRHGGAT
SLPSGIGCAAVLLGPRLCSASAVTSSRREHRHSLPTSKRVMDVLLSTPRQTGTHPADYKQ
PFMSVVPSLPHTEEAGLPRPPPEPPPGVSTAPPRRTTSSGSTSPCPSCSSVFSSVHNMKA
HARRTNPRTPIVAEGLTCGFCDSSTVFPTGASRAGHHQKCQAYQRAKNGQRTSASSNDSR
SPSATPLLQPPPAAEPRQSTGGPAAHAVGMPPSSTTEHPTIWEHTLSHDSTIQKGKLATS
LRTARRPLTNSGCKV*
>TCRU_3199 hypothetical protein, conserved
MGTTTASSLENVPRSVGCGAARRFACSLTDRTAQSLQCGHFVGITRCGGVRKSRSPDEDG
VVVVWQLRTSGPSPLRIALAARLAQHHPGMVLLQECRHQGAPATRLTGCGDFHQACGGRA
GGVAFLVRHTLPCERFYSWHQLPGDHRLPRVPTCLPQHVRGEPLQPSYSNCSRCSLCEHH
SSSCSYCG*
>TCRU_3200 hypothetical protein, conserved
MMRRVFCVVLALTLLCCCLCVFAAEEEVEEEVLPVDAVCAGDGENVGRWQLRGRPLWYNC
TAEASGLGKMICGMGAGNCAPEDVKKRVEGNAKDGVFEIKFHTPTPGRVKSWWESNVEPK
PATAASGPAKPAEERPPVDREEEAPRDTTTISSGSSPAGVGGSAGALSLPPTTPRDAGAN
AAAGAAGKTDPSPPATLQAQNPAPSGELQGAAHSASAASKSPPDPEPTESGEHSSHDPPA
GRQEETVDAPPTRLSQTGEDGGAAEGAEEDTANTTDAATSEGNATAAGMPAPLSSAPTTK
ALENSAGNDACFHYPRLHTRLLLVLAALTYGTLG*
>TCRU_3201 hypothetical protein, conserved
MAGNFGAASWMDEGALARVAVVVGACSVCVTAVGSAGDVSGDADAVVVPVDVSCAPSDGS
LSYRVCVAWKKCSAASAEAQHENYTFSGFGVRMRSRDGELGAVCHVVSAVHTCSNCAASC
ARKEEGATVAFTMNVTTHKYAGPYELWWRQFPPDGAIHPPARSSDADRTGISQLPPPREG
KMTQNLVGQLRRKLMLSRHVRTRIGDGLRRLTDPTPSIGVPHPTRRPTRPR*
>TCRU_3202 multidrug resistance protein A
MQTEIGEKGINLSGGQKARVSLARAVYADRELYLLDDPLSALDAHVGERIVADVLLGQLA
CKTRILATHQLHVLSRADYVVVVGDGAVRFAGRHEEFMGSPVYKEVVAQDARQQQHQEKE

VREGEGDDVLDGAPVLGNGAPPGAGSPGRAKGAMMTSEEKAVGSVLWSTYVTYFRACGGV
SVVVIVLIIFLLTEMISLSSNVWLSMWSTQRFGLSTQTYLNVYIALVLFGTVTVPLRFSV
AYSAMRQGSRNLHRLILRSVSIGTMQYFDTTPLGRIVNRFSRDVDCIDNQLQMTFLFLLR
VLYSIFSSLAVAIDSQPYVILALLPTVFFYYKLMVLYNVTNREIRRVGSIVKAPMISLLG
QALVGSSTIKAYGCVASIMKESLRRIDRVCASSFLENATNRWLGVRVDFLGNVIVITIAL
LGVIGTMMSFSTHDIGLVSLSLTMALASTSQLNWLVRMIGTMGADMNSVERILHYTHNID
HEEVPEMDRLVDELREKNTEGGDVTATVLVEGVSGGSEGRHPETTAGWLEFREVEMRYRA
GLPLVLDRVSFLIEPRQKVGVVGRTGSGKSTLLLTLMRMVDICGGDIIVSGRPICAYGLR
ELRQQFSMIPQDPVLFDGTVRSNLDPFLDSTPAEVWRALELVGMRERVELESGGIDGRVQ
EGGSNYSVGQRQLLCLARALLRRGSGFILMDEATANIDHALDQQIQRTVMTAFNSYTVIT
IAHRLHTVAAYDKIIVMDHGVVAESGSPRVLVSDPSSRFSELVAALGKQEAAKFMASVGV
AAAS*
>TCRU_3203 hypothetical protein, conserved
MNVFLLSFQCWVQATQEEAQSPRSAMPSTPQIDEVLPRGQQRQAEEAADRDKQQQQCHHR
ESEACPACRPSRCFGPCRREKLLAVCQGILAGSTSPLSTDSYEEQPCLHPSVVCRGRSQC
SPQRGRMPLAILVQ*
>TCRU_3204 glycosyl hydrolase-like protein
MGPSSPATATLREVGREPQRVRRPTNVMTDVPLNILTDAPQEGLLWPHQRHDLDALYSTQ
TCKLVADGPNEANEGDVLMRVRLFRPNCRRRVHGGGEGKVRKGPCDDSAHPIVGLMPHQS
AASFFPEEVLMDETDVQVGPSTLRSIVEEEKEEGEEKGMRWCASPTASPSLRCRLRARGD
AEGKSRLVWDSGEFFVGISLRMTATQDELSSGLDANFSFNPEYKMRFFGLPLSHASGLRL
PDDGEYRLFNQFHLNQTLLSGTRMHGSVPLLYGIGRAPIRYGKKSLYGQRRRAIGILWLN
GSPLHVRTATGGVGGETTLSFRSTAGATRVYLLPGPTAEDVLLQYYTLTGFPMMPPLFAL
GYHHAHRGYGKMDELLNVSAAFLQAQIPVDTLGIGLHYMRGKRIFTWNLTRFSNPVKLQD
DLWRHGGRFMVLSTVPYVQVDPRFSLYIEGKRHEYFVRTNADSDEIFIGFSESGANVWID
FLDSRARHWYGGLMKYKRFLGSTNHTFFSLEENEPFLQGGVRGTLPMDAGHRGAVPHEVI
HNLYGMLHAMAAYGGQLRRTQFYRRPFLITQSYFAGTQRHAAVRLGYNAASWEHLRSSVE
LCLAHSIAGISFVGADVGGFYFQNVEEELLVRWYQLAVFYPLFCTDANENAPLREVWRLV
PHVRARIRDAVQFRYALLPYLYTIFWRAHLDGELIIRPLFFVYPQDPLAYVEPTMLGQRF
FLGPHLFVAPVLTSVGTRDVLHTVQIPQEDLYNFWSGEFVAAGTTLRVSKNISYSHLPEE
EITPLFQRVGTVLPTFTNTSGMRSTHDAANYTLTVTLPRLEPFFSGGGEYGGSGISDQIL
AQGDLFVDDGSRHINYHGRNANYHAFCALALECVLFPGKGDLVLRWRAIANSSCCDVLHV
LRSSTTDVTDGESFLLTRLRFMFATPEEKKHVTLVESLVDDQRMTLSLGGSKPSLLEVSG
VALPLLAGDCHGNGADSRGSSRPVGEVHLKLNFSHDSWP*
>TCRU_3205 Leucine Rich repeat, putative
MCDVQQKRVEKAPSARRLHEMITAKLLHRIRSNDPTLCTLRMCPELITSPGMLDALLRNS
TIRSVVFVNVTAKTVSEVLFAKFLACLYHLPLYTLLAGGNLRLPAHYMRHLLELVEYSCG
VGKGCKWSSEENKATVVKGAASAADEVVNQATNSSTDDLKPMAKLEFVDLSGSHITDSHV
MWLGRMIFHPRSSLRHVDLSECRLGTVGVRSLLLEELTLNSRLTAEVADNTQLEVLDIRW
NGITEDFALRVFLDSLEMNSSCTTCIRAHGNYISSELYQRIVDREASMLSIIEGKRQRRR
QTRRTEAEELRRQLQQQKEGQQQQQKQQVVSSSSGALGFLLSVVSDSPSSLPCLSLLASL
LHTQE*
>TCRU_3206 hypothetical protein, conserved
MRRTIAALTATPERFSILGTTHPKPKRTGFGRNNKMRSKPSDNVAWYDKGPVEWLPRPVR
LTYDHLDQLRDWMMRETLDGKTEEFNRIRDMHREWSQHPLMPVLGDVEPKFPLNLFKQNH
RAKRRFLVRWHKANTPANWLWMPRGPTVVTPLHHTNPSQYPESWRQMVRKKK*
>TCRU_3207 Cornichon protein, putative
MDETHRFREAVAMQIDWVHVLITERHRPHTTWKIRQAAFFAFMHFCFLMVFLGHFVHNIV
TWVLAFLLQVAALLLSIFHISSVTDYADKMNNAMELEQQLNPLIIAELSIRCFALLHCLL
MGGWLMGIAGLLELAYDYWIFRRGDFLVDATTAWKKLGALEMDSRVRLAYQGVMVIASIF
SFIHFLVSM*
>TCRU_3208 hypothetical protein, conserved
MSSEGTPQLAALKQPSDTTIIDRTMHLFGTTQQSSHECEIESLPLEFLSTNRVVSVLEKA
IERLELLGLLDTTAPDEGATRPFFPAIGSTTNVGDAGRNKSSSFTPRKAAVMVARKEEMS

TRTVSELNSALLAVASTQRTGRPTVADLVEEQQRLELRYGELLRRAKKARPSPNEPELDP
SCFAAVQDTERAAVMEELRQTSRRLREHNKALFIQLKDNPNDVDNWKKIGNERSELIQLL
QALIRELTSGYNAAKAAVAQGGLPRPNSRRKRSGVSESIGTESREATMSLVKNRFGSTIQ
MKRSVRGPTGPRIPLTSFFERFAKLISDEQNAQRWADELLLKEKEMNQNVKQLQYDLKAE
KVLKEKDIAERRQRIAELKVKVRLEKKHVKEQSEVVRAEVEALNEARQRAARDEERVVLE
QIRGLEQEEQMESRAHADFKEHLIERTEAMDELASQWEKKNQTEIKRVEARKIDVEQMRQ
QCAERLQKALKDKEFELQLKSQRDEERNQEEAERTAAEAQANLEYDAVSQIQSAIRAMFT
RQALIILKKKNRKKRKAEKK*
>TCRU_3209 hypothetical protein, conserved
MGRRTLSMQRRKRCKPEGKKEKEEVVEFMAATSPTTTRHPQKGRKTRMTEEETAALFLAD
LAVATTTNGDAIAARETEGGLSEAVKKGENASTTKIKSKKSSPMAPKTTRSRKRVPADTR
KTSTVKPCVLGSMDLSAMPLEEGEEDPSVSAEVLRQTAAFLARLTPARSQQFWAMRQMAR
GELSGRSAARMRRTELTSDDNVREWDEEDVEFTSSEGVYDREVSSVAGKEEMSSYSEGEG
EEDFAWPKIKENKTHAAAKCKNRVTNKKRPRGGALFSSNPDIWDD*
>TCRU_3210 UDP-N-acetylglucosamine-dolichyl-phosphate N-
acetylglucosaminephosphotransferase, putative
MGASNSVFVALCNIVKSFCTHSFELSAIIFAGVVAYVICMRFMDPVCMKLLERRICGIDI
NKTTLEKRRKIAEKPLKALEEEERRLVVPESLGILAGAVYLCVLVLELAIVFGPSMHKLD
GAITAITVMLLLGFVDDVLDVRWRHKLLLSAIGTFPVMLTYDGSVSIAVPRPLLPYFSTS
FVYLGVFYLLYLGLLCIFCTNSINILAGVNGVEVAQSIVIAFTCVVYNIFQLRLETEFQD
GLGGSGDMYVHKMETDGGGSMHELMAIALLAPFIGVSIALWHYNQYPARIFVGDSYTYFA
GTVLAVAGVTGQYGKTLMLFFLPQLINFALSLPQLFHFVPCPRHRVPRWNAKQDVLQNSG
NYTLLNAILWVYGDMHERALTNAVVKMQVCCCIFGLLVRYIFASYMYDHIQ*
>TCRU_3211 GINS complex protein, putative
MSTASSATATNGVGIHFDNDTAAVAAVGGGVPGGRGGGSSSFTAYHFASFAAMEVTVIIV
PRFTMPRVSTAFGGRYGPFAPNYPVELPLWLALHIRQTDTCTINPPPFMTIPYLRNVVEK
EKENEATFEALPFYFFEVVKKLCENSAAAEDVPHVAEVIRLVGEIKAIRRQKLQRSMAVF
EAEGSPVYIPGIKLTNIVNNELEYLRRSFSKVLQQAAEMKRRREQLIGGAVEGMTPLRPS
RGAPSTPAFSSAAVDARMSTHSGIDGSFITSTAEDTTAPTATLHGAEQQSVSSQGPTTTA
SSAMEPTETLTTATESIASPPVKKRRTLRQT*
>TCRU_specific WD40 associated putative domain containing protein,
putative PQQ-like domain/WD domain, G-beta repeat/Utp.1
MEGFSPFRVVGAVCGEVPVSSTVLYGAPVLMVATGRTFQLFRGKELSMLRGGPHFHSRVR
AVAQTGKYRFVAEGPHVHGFTHHKPIWTCTHHDITQSKVNHLLAADDILFCIGQDKRVAV
RAVKSGKLLGEFLIERSEEVRAAILPTGYTNKLLAATAEGSLHLYNFKTGVCLWYAQRES
DAQILSLAAGRYKDIIAYGTSCGRVVVLNLLTNEEIMMFEHKYQGAVSALAFRVDKSILV
SGTTAGEVVLWDLENRCLEGVLTRSKQVRSEVEVFETPHTDAIHSIVFLPTDGTTMVTAG
ADNALMQFRFDTVDGLGMLVRERRGHMGSCTNALFYNTDLLLTAGTDRALRVTHVFSDRA
SWELSQGKLGRRGREKQMGREALKATPVIAMASCTARNYQWSSVVSLHEASAKMCCWRMD
TRSLECKLSGITTSMHTARTVSLSDCGNFAVVGYSSGNVAIISIQNRSVKQLFDVALQPN
DLAHTSSVECVEIACGNSVVVTAGLDSRIKLWDLLTGCLRCALQVDCPMSKSCLHQPSSL
FIVAQHFKIRVYHCNPDVGFDEDFLATPVREFDGHNGPITALALAPDSYRYVVSASGDAV
LLVWDLAAAACVGQYRLASPATSLSFHPDALFMVSTHAGERGAFLWSNNLRYGFVPEVVT
DPKGRRIEQLPLLHFPTAHGGDELQEDEQEQHHQDEEEEEVSGGMNFNGLQPPGKLTTTM
SGRKEEEEEAELFDASKDSALIRRQRKQEQWAQLDGIVSGGLRLAGVPRSLWFNLTLLDQ
IKEKNMPLLPPKKRDVPFFLPTTQELRPTFLVVASSGKAGEAAASQTHFVGASLLERTPV
QRMLMQGEHEKLMLHLLALKTPQAIDLEIKRAVEYTDGVSYSKEEIDCIKSCVCGLFSFL
AVWLRRRENVDLVQGILADVIRSHGTLLTKCGGEMVAVLEEVAQLQNAVRHSMDHLVGYP
SCLVGTFSGSLF*
>TCRU_3213 hypothetical protein, conserved
MQDTSAQRRAHESCDRPSRTSFGSLECHGTFHKTGCVAARCSNRGDIQFLPTRDLAVGEA
RRFLRPSPERIPIFWELHHNADPGVVAGRIDVKGETAEGQELWLRAEEPFSHDFYHPATI
TRRATRTRLATPQVELTIPLQQVNVPVLNTKVDPEPVEPGHLGETNASLGTRGAVPFPSI
LLR*

>TCRU_3214 hypothetical protein, conserved
MGRRCNQDRLRPRFRNHRQVLGELEPYSTYCESPGTSSDNFRDSIAPSHRVETARELGVR
HWLITAERERLSNDCANAVADVQNRNAQLYSHVEEAHNDLSAREFHIAVASGLLAGRRDA
VSRRSAHLSERAAR*
>TCRU_3215 Leishmanolysin, putative
MNFDPKYMTDTAWSVRVAAHEIAHALGFSQESMREKSLVKKRERSLRGTHRRMVAGKHVQ
GKTKAHFGCDSLEGMVLEDGDGSWEKEIPHWKGRHARDELMPPAVGAGYYTALTMAVFAD
MGYYRVNWRMAEPMSWGHCSGCDFLVNKCNTTDNLAAKYPHMFCDAIDTETLRCTSGRCH
VGTCTASIVEDKESLVDKDVCPVVSLEFHGISSGKTYRTCSDENVDYLRGSLTGGGSWCL
DAELLETTDGDGHKSVKGMCAQV*
>TCRU_3216 Sphingosine N-acyltransferase, putative
MGTLRFADGTIGLPANMYAMPLDRAREYGFVSHYNHTGDPAMDRHANNLTFTGEQLWWLV
TNPVSLQMHLNGWGGVGLDAAALPQLLPCLLWAVVLIAVRLFFQRRFAWLGVQLQVVVPG
TSQKKVCAGTGANAIRLNVGQRKKLRKFQTQLWLAVSYTASTVFGYMVQRGEPWFGLPLS
EANRISILSPHPYNPGRWILLYYQYGLGFYLSECFSHLANHDIKRSDFLEYVIHHIVTIA
LIVFSHCSYEHRFGVYVLFIHDASDVMLAVSKTLSYVVKAAEAREQRAARNGGNGAAPAG
PPACRLYRLVFSSTTVLLSFVVFVALFVFFRLICLPFLALASVGLAVKIRTFTVCYWVLV
VLLQVVLQGLHLYWFALIVKLAIRALFGGPLDDIRSEDDEENDGH*
>TCRU_3217 hypothetical protein
MLDTAPASRRCGRRSACLHSTPCCGHVEPAGVPDCAGHPLCGRRDEANTTQPAADDVLAA
PRSGDEGERLHRRDARAVRPWAALVARLWIFRRAAGGGGGVFFSEGASEGETAGGVGCRS
QRLMHATRVPCHLSHIPQRRAGLGRAKVS*
>TCRU_3218 hypothetical protein
MDQLNVSASILWSNARHDLFPADVVLGDVAVVASAPATIQFLGNSEMSFEGGMALVESCC
TGRNSQMFLLVFTESDMSLARIFVAVQSCDIVAHVEPLGGLRSLALCVDMDGQLRYLVVG
PLPTSAMMEACFATGSSAKSESEIADPSTRYPLGHESSVRVDLPRVVDGSSSCVTAEGGR
NCRGGSSADDVVKISVGLLRDKVLSVLSAQRPHLFEFPWNVSKGMMTWLKRREVLEALSP
PSLGRAVYLIAGHCTFFASSEAACNATACHASDRRPIGALRGLVAVIRNALVLLPLETNC
GTSPGTLVVRWNQLLGYQASDVLKCTRVFHVAMSDGWKKHDRGAFLPCGIWLSIIFPSWS
DCNAMEYALRTAYISATGIECRVLERGKNVTVGDAEVWGGVWPPSLKGTKSAKCNVSSTM
MMMEPGSAVTTRRNLARKAELMPPSPKITTDLVVDCDGRGEACISRAGFVWVLIHQTSSV
LLLVDHVACRSMTATAASGGSRNPSEIADIFIDAFTELRSTPTPGGIVGNGVDISLVHAA
ICAECSLRRIPPASMDPCLCCGSVTKPVRLSPLSSLAVESHETIENFFPMIMSPMCAVII
VRFIMEHTSEAWDAVRERVLPAREMAVNFSEHIIPNLLIALDEMREFPFILSFVFKNFFM
RLPPLPHIHDSCEEGSAKSQAAALHLVVQLYFTGLCLHARETYGLGLQTGNLWEAFHSLL
KWCGNVIEAVLLGEENDIRSVKLPEETMRRALTVRDPPADHPLRRLESLWIEHAPSMITA
SLALTAGGGAIGDEAAIHPLADAADAAERGQAKNLQKGPTKPSARQPTEYLSLGPFCMPP
ASGKEIFFADRKRSLRRGERKQELMNEVSVQVCHLSSHADLPPAAAQEGVQHQNQHRCYY
PRYGIETVEASVQTVRTSSQEEALLRSHLQLQTKVRYLERVCADQRPTSSATSSMPLAAD
VSVQFPYLKAYRSHLEHVTALEKRIDELKRLSDERQEELFAVQKENYALKKALCEATSPS
GNQPAPFHVAYLMLCREASQFMLEREEHERDTIIFSECKERTALLFSLLRSFS*
>TCRU_3219 GTPase activating protein, putative
MSKVDFVADQPRPLEDFIAVTGLKLGHAKECFERFGGYAPALASFAQSYPSLPTDYFEEV
GRVEKNAEVINAELKLIYRRAREIKSQSGKEDEGVWAVYYTRPSTPESKPQNFNASSADK
APKPFGSFFSFTSTTSAAPPPGPMNFGFGAQPAPSSSEAAPVSTTFGGFAQKKTTEEKKK
TTNNERTVKYCEATHFTGPLFDMPLFWREEVEGRCPLLNLDKGFLEENRDVLRKRLEKWV
KKAEFFVKPVQYLEVDDEDEETIRVIIKDADRTFFHPEHRNKFVNFLTAMHNEFNAYGQA
MSYLAGLCLLVLSEEETAAVLRYVANVHIPGHWAAEAVGFSTTAWVVEGFMKRKFPDVAK
HLEELKLWPDTYLQKVLTGLCIHVLDFKDLFVFLDLFMDGGVKFLIKYCLAIVEHFRSDL
LRIKSATAANEVYEIMRIDAKVADSHDVKAILRRAPLIDLGAEGDLIDILRMEAYNTHVA
PRLQRAPKTEAFEPCAVCNERKPIWWNDDLGAVCTECRDAAPELSYTKY*
>TCRU_3220 rib72 protein- like protein
MNEKTVYNALPKLPGFSFPELHHPPNHSRRQYCSIHDGTRAVLDARPIRRRDGDNGEGGE
CGGLSRAKIFARFPAWNSMDDKVLRFFAYYMERVDESMVERMRVRKVKIYFYLCDGTLVV

VETPAVANSGLPGGTIVSRCKIDGVDFFSFYIGSTIQVRGVEYTLVDCDAATRDFCAAME
VPQPEPLGYPEDAFEASVKVVKAPMDELHATMRRNMEVAAANATGAHATLLSPEERSKAR
NFFEHDREVLRFFAVWEQRLFRLQYYIADQTVSVMLEHARNDGRDPISVFIRRTLIPKDP
KAPLRDTETLNHPLGAPVVYISEEDLRTGTRINLFSREFYIFDCDNYTRAYYEAKGIAQP
SFPKPPTEADILAPKPKSPPPTATQLPIIKSVQGASTMVFEDHSSHKDRLKLTRYTNDVF
RFAARRVNPSPEDEGRMFVFCYYLADDTVSLFELVVANSGHVGGKCFARAVVPEINEPGK
LCVGARVKLAGVTYELIEMDERTKRYIAMGMPLMDEDYFRTQELVHRVRNVILQRFSSVT
DVFRRFKSTVDGLDKEDVKGLFLECGTRLDAAELDRVMARLDQDNDGIVNLSELTENLLL
LQFVSDFVPKNETFRSIEKGPLRSFRNLEASKTAAREADEALRKLISKSEARRILLIRAF
RITSNSTYDGHLSVEDFRRTLKDRMNFSLTDSEVESLVYKFYYLPGLEDWTARRLPVKEI
QRLIMC*
>TCRU_3221 ABC transporter, putative
MSCCRAEVNEPVTPSSASSLESDDQIAPKQKGNEPQIEDYSIIAPGFSIKGSVAQFDAVE
QNKSSVSGRFSIPVSWNNLSYSANGTKILCGLTGTALPSRCLAVMGSSGAGKTTFLNAIS
DRLTTSRTLKLTGKRQLGDLEYKRHYRRMVGFVAQDDILSPRATPEDSLRFSLRVRRGTS
ISETNKFVEETLEELRLVHCRETIVGIPGLVSGLSGGERKRTSIGVELICDPKILLLDEP
TSGLDSVTSVKIVHLLNNIARTGRTVIYTIHQPTAETLTYFDDLMLLTGGRCAYHGTMAK
SVEYFESIGFPCPERYTPSDFFMKLLQDPEISKVLVKKWKSYLKHGVRTPHTTAVELNPN
PSESPTAKNIESYLGRFGSTSCIQFQELFRRFSMDLSRNHVYIFSHFIQAAFFAVIVGLI
FLNVKDDLAGMQDREGVFFMVTMNRAMGQTFIMVNSFMQDKALYVREQMVGSYSPFIFFL
SKTLVEFPMRVFFAFLECCILYWMVGLYRQAGAFFYYFAVIALLTEVASGLGFAIGATFK
SLVVASGTAPVILLPLAMVGGLLANTDRLHPYWYWLEKPSFIRQAYILLARNEFKHIDHI
RCDGRGKPPGFCKDKPQNGEDILRQLGFQQKQYENWVLWLTLALLYIAFRGWAVISLYSA
ARTKF*
>TCRU_3222 40S ribosomal protein S8, putative
MPQNEYIELAQKRYGRRLDHAERIRKRDARKAHTQAKHLRTVRGIKAKIASKRRYAEKAE
IRKKIREHEEKETKERVKEKGPKNALPSFLMDRSEADRAKVLSNSLKQKRKEKAGKWAVP
IEKVKPVSEDEMMKAVTSGKRGKKSWKRMVNKVTFVGETFTRRMPKHERFIRPMALRFKK
AHVTHPELKATFHLPIIGVKKNPQGKMYTGLGVITKGTVIEVNVSDLGLVTPSGKVVWGK
YAQVTNNPENDGCINAVLLV*
>TCRU_3223 hypothetical protein, conserved
MSSRSERHNQSSGNGTLHSGYDMSQREIPVTKSASEGMSRVEQRLRIVKSSRVRWTTDTQ
GETLDPSPQPSVSSIPTAVEPPCATYPAFDLARLSKHEQHIVDALLAEVVDAVAFPSVQD
ELAQ*
>TCRU_3224 Domain of unknown function (DUF4496), putative
MLSAQGAITNELVMIECTSSQEQTAKEIFLLSELERVWTALSTVLRGHLIEGHNVRIANF
GSFWFETRPVVSDGVERYYARRVHFGMDSNFALRYNLDSNKVPQEPPRLVYVKISMADVV
SIAEVPARTASMALREFFSYVGEGLFRHKVFKITFLDVASLLIKREKSVLEIDPSFRRDI
FAIDSRKWPPRVREAAESVVMDIGRPATASSVLSRPSTAQLSRQIAASRPIEPRPAFVTS
APRDRLFSEIEKEPPRKLPPRSSFPVEDSSRSTDNDAAACVKESIFDALSSDEYPPEEPE
IEVIEELPRELPPLRAYEEEAARPVVNTGRRSFHDHSSVRELLYGKAIAQVEPLMRGRRR
YINRDSDAVAALMKSS*
>TCRU_3225 protein transport protein SEC23
MDLNVESMQQQQQQQGVEHLPRWSWNLYPANRIDAARMVVPLGCVYAPIGSSCKEVYYEP
LRCVCGGILNPYCVIDFRSRTWGCPFCETKNNFPQQYVHISDQNLPLELAGWNDTVEYVS
IVKRDPPVFVLVLDTCIDTESELEGLKEFALDALSKLPAEVRICLITYGTTVQIHELSGV
TDYPRSLVLRGSQEVTVETLKKVMPEPKLFVGVLSNVKSVVTVILEELQQDVWPVPKSHR
PLRCTGAALSAAASILEIVSPNTGSCILGFISGICTEGPGIVVETTRERFIRGHADIRDS
TAAASFWESSCTFYDSLMHRIVKQGHSLSCFTASLDQTGIAEMKLCIQASGGVVLNDESW
RKEPFRQSLHRFFERRDDGTLKMGLNVTMDVITSTTWKVMGVIGQCVGTGKKSSSVAEYE
VGMGGTCQWTACMMDCTTNFAIYFDTTAAHPSEAAKRSVRYAQFITKYEIGNEVRTRVCT
VTHQAQCTTSMPELSASFDQETAAVLLAREALHKADTTPLFDVLRWLDRTVVRLVSRFGD
YVKDHPSTLKLPPQFVFFPAFMYHLRRSAYLQVFNCSPDETATLRLMLLKSSVQDSIIQI
QPTLYSYRMDAPPQPVLLDSAAIQPDNILLLDTFFEVLVHLGSTIAAWRRAGYAELEEYA

YFKEFLQVPVADAEILVAGRYPTPRFIYVCQDDPDARILYNRINPSRSYGGENDQKYGTN
EGELVYTDDASLGVFMEHLKKLAVSQ*
>TCRU_3226 hypothetical protein, conserved
MMNREKVGRRLDLVNSSAGSIISLAAWCALQASSADVIFAAIDERMRNASTSKETRCALL
NVIHELLLTCAANGVPEAGKRSVLMAVSKTLPGMVQAVRGLAGADAEAFEQNLSKVVSWW
SMLNIFPRAWIAQLGVKKEAEQPRDTTGGASMPVQLSYIANLMSRYNEMKEECLRVSHAS
PERAASLREEAIQQLTKIREVVHCKLDGGVSLVAWLDAERNALEGNLPSMTSSVVGQKEE
DDVLGSFF*
>TCRU_3227 hypothetical protein, conserved
MGQGLTCGATLGVGLSLSVLPARLSVTDHLGICAAVAGCGLCVDFVSDCCAKEGRVIIHR
DVLLQAQDVLRHVSTFYTMCDSNPIARFFRQKHEWLVLESHGRRYYTVQKNPATGDVLMD
VRNSLRAANDVGLSVAGRPIHTGEIRLHRVDLEFDLPNDLQVAYMIAWLRKEDPRWSFST
ENSRHFTTRARYALNDF*
>TCRU_3228 WW domain containing protein, putative
MREAIFYVPPRRSYATSLGTERQLKTRSPPRGSSSPAPRPNSQPLPRHIAAGTSADVGAP
PLPRSASYSLGGEIARQSGAETASEMRELLHLLEQEEKKTTVLLESQEMRIRALRLMEET
DAPLSLRQQAMTISGVHFSCNGQQKPRTESQEMGGKEAVQTVCDGSYASHERPPLVLREI
QPSPHRDQHQELSLYTQKPSSGSVMPTDADVKCEAVTPALTSLGTHNGSNEELNGARRMG
SQHKTEQQRQQQLPVDGLSDSEALAREEWRLELSYGKEEAATTEPQPLVKRNPSPAVAAA
ATKAAEACSATPAEGGGVLCSNWEEPRQREAGRTYDSQTATQEARGKPPSEALEEKKGGA
APQREQQEVQEGNAAKTKGALRVCGTWKEYRDANSGRLYYVNTETKQRTWKIKETPFANE
*
>TCRU_3229 hypothetical protein
MVSRWVDENSLSKLLEALDNLLLDDLKYPQTGVPSKLHVTQAVLTPRYSDIFLGIFPKIS
RRIASSIYDMATCANPSLLEWFYLLNANGLLDGMKVMIPSGINTHENILMLDCVELGRCQ
IMDGTTETNAVGMCVYLNILRASRLFEDSSAAPSLNEG*
>TCRU_3230 Got1/Sft2-like family, putative
MTIPVEVVDQEVVNDNDEQCFQGLSWSSRIQGYVLFTALGFFSSFMGWVSLGIGYYWKYS
VLSTLGSLMSLASTFILMGPRAQLNYMFDEYRRTSSLLYISSLIITWIVAIAYKSALLCS
LCGLLQYGCLIWYSLSYVPYGQEAVSGFIARLIFSR*
>TCRU_3231 hypothetical protein, conserved
MPSQTGLRAGRGQSQTVTVHILNDRAFPQWMRRSLPWYVGGPAARGVCDEAVAEAPVHLE
YPRLCFLRVLPTGMLGDFGGDPRARRLLRRWRHCGIRMGGPSNYRNARLSTSGMCRHTVD
GQAHSAAGWTGGRQSAARWQARSCGAHVWKGFRRMQRRASLLSVRERHHRHRGFIVIRRA
REGLSKSGQESHRACAQCRHSGTDVRVNTRNRVLATPTGACHAVCAPSFSSWTSFQCCRL
TAVRQSTCQALTQSCGRNRAMTTSVSAVTLRGIPRCHGKNVEPTA*
>TCRU_3232 pumilio/PUF RNA binding protein 7, putative
MLQYGAAGGVREELVNALLDVFSEIHEMLSFAQGSRVMQKLVAYASDEAVLTVVNALLRE
AEEERKKSGTIDEEEKEEEQHEGAETDDDNDGNGDGEKKADQPALKAKPSRREQREINRK
KHYKVTSRAIVSYALHNHACYVIQAILRECRSRQLEHQRKQLMDELKPFVFELAVSPWAG
RIVLETMFQSGSAKLAEVMKNVVFLKAEAWLSDVPEKNTRGGSGLDPTMRQALRRHREEP
DEGRKEKFPDDSSKKPPRKKLYRTIKK*
>TCRU_3233 zinc finger protein 2
MSYPNRYGRGMAAPYGTVQLPVGWQMAYSAEGDPYYIDHNTRTTHWQIPAEVLQRMNQGQ
VYRGRVRRGIDRTKLKTKMCMNIQRGGVCNWGDNCAFAHNSEELTAVPHGGNQRGGDGNP
YRMRGPANNNSNNNLTNNHSMNNGNSAPNAAELKQPKKQEQQPQQQGIPAPQQAMPAQTQ
*
>TCRU_3234 mitochondrial carrier protein, putative
MQTRKVQQNENFSANAGVDTEKENLLSSERPCEQHLVIKRDSYTTLATFFAGGVAGACSR
TLTAPLDRIKIIVQEGHLVTGPYQRISIFKSARLKDVFNLIREDGGWRAFWRGNGVNCLK
AGPEFAIVFSLRRYLLSLYEDGVEEEERRELEFISTGCSPLDSELYRSAVSVLPSPFDRY
GTLTGVPRLFVNFSIGACAGFGAQFSLYPLEVVKTRIAVSKMTEFRGGIREVVMATYRNG
GIAEFYRGLTPNMVGVFLYRGLEVGMYSTAQQQIMMYRMRNYGMSRHNAALSSMETAVVG
MFASMIAQTVSYPLNVVRTRLQTQGINGREIKYTGMMDCFIKMIRGKGLASLFSGITANY

LKALPASSCMFVVFELVQKLLVGDD*
>TCRU_3235 hypothetical protein, conserved
MARETAQNDGQADLPVAEAERKRGQVQCGAQPIPEDEGAAPPRHEDIATSGWVRLQVFSR
GLSEAQRSNGVRLDFVPPFFGYIRLEAGCLRVRRCVCFVCCFGGGLGLFHFVCPYLFGAV
TAAARDMALSCS*
>TCRU_gamma, conserved domain containing protein, putative
Elongation factor.1
MQCVTANLVGVWLQCVEHVRKYALGVALMFVEERRHDIVALCVLCGRGMPAIVRDVEGTE
LFDWEEVANVAAQRERITECLCWRGAC*
>TCRU_3237 hypothetical protein, conserved
MHKDGPRLWDDTLMEAERMATDSKARYLQLPTPDREAEMQRTRSQFFLLLRERLRNTYLR
RISKLNPGEPLAWKYVSGRKKASIPSPTSILLGDGQHTYKTARRAANALNRIFLPFHPSH
KAIRFSKGINRQSASLNINASFLFGQQNNSESAATSGLVARLHSPLDAPFNRTELLAALR
NTPYGKAPGPDEVDSEAL*
>TCRU_3238 hypothetical protein, conserved
MKVIPPSLLALQQHIASLPFDVLIRRIHSSSQGNPARSLEAHFIGARSHLARGKGQGFAE
LPQVSGEQLASTSSQNAETVVVSSLQLRELLSERLLQDVQQPRTRLQLNVDDLSLILANA
VRHKFSFRLTNTTLRRFTEALNGVWGKDAASQQIEALSRVMEACCDGLEGNDLMTWDDLA
NLVAMVEQRWSLFTKSNSLCCLLLQFFSSVIAVEVSTEAPMPGILRADPVLLKERCLQLV
HDATDILADTLEAGIPLTWSPAELQGMCRVVKQLRHYEHVRSSLKTSSLGRVRFWKRTAA
TAPAEPADAVPVYKQLSRLVTTQVLSNSRLVTDVEAMTLAQVAGVFSSVSFACGTEAILR
FTVPVQNVLKRVVVADATSMRHVICIGEASLHVEGASLLFVEAVRSISRFAFVLTSAATW
DLLCRVCALLEGAPLSLRAVVVMCLCSLQGSLEKSRRLPSSASPEFASFRLAVAMVCTLL
AQHKVQTGQRMEEIIHSVVEAAPMMRDGGKIGASTLVRCFFFLTSTRSHANSERQARAIH
LAMAEASRLLNEKNEDHPIQLTNAEQSMLRNSLKRYREMLAHSEAKRNTFLQGAETQHDA
PASSPRDADAPSAAAASRQERFSPSASKTAKTTGRI*
>TCRU_3239 hypothetical protein, conserved
MAGVADSAALLIPQLLAENARLKMKIGIPDNERVLQSVLQGQVQRFFDDARRTLENVMSN
AVVLGGKAEEEGKEESEGETQRVSALVETLRVLGAQNEEMVQKLSEMQTQCVAGLNGKLE
VLTCERDTLRQRVLQLEEELAAASAEATETGEQPPSLLAELRYLRASDALLRQQLEELRQ
RSKASTEEANKNVREGLHDTLKLPRLLEHLGEMRTRVYQVETERELFRLQMEESQKRGGV
WHALREAQLEEKVALGQSTIQNLLTRVAALEAREAEAQTTAETHKETIGRLENTIQSLQT
KHTSSDEALASKRRRVEKEILDNPDSVRRELITFWQEGSDELRQLREEVEELREKERILR
TTQEKLTRMERTRSTVTNKLVTLAEEIGRVREENQSLRAQCVGLEVERDYLRSSLASAIS
HHMQEEELQQCSAAIRDAAVKAAAASLSVVADPQAIQQAMRQLQELKNEVAQLTKQREKI
HRYITLHEERITALITREALLENEVTRTCNSVADNGSVLQRVKRAEMQAFDLLTGLAEET
SVHTEGGMRRKETFLGMEQRITEYEQQLETYQEKLSKVIKERDDAKKQFEELQAEMRSTL
TARETAMTETLNSNAALMKSTDSLRLENQQLRASYNVSVLFSEKLSTALAGLLELLRAEM
SFAASLNNMLTELRAEIVQLTRRSANAWNTREGEVQEVVEAVKRMCGYILQAVEQQQRGH
TLDETVHIRHLMETLKKQEQRLKETQEMFTHACQELGEGLAQRITAALQSADVMWKKHTA
TLLEERQHLQAQLGTEKDLLARIEQSMAAPANTNTTNSATTTTVDTGVKAAEESHASHHQ
VLDAINQFLAMSSQEVAEKVGEEEQVEEEGGEYGNPSRGFSGAVVSVTDDTGDIRAAEEE
EGEEGEEDVTQSSPGQR*
>TCRU_3240 hypothetical protein, conserved
MCSLLAAGAATIRLVSRRQRTIHGDAVPIFTSTRRYVNALYRAPPVQTVPTHNSSGEEVD
TELFIRQFKELFYALKQTQLVEQIHEMRTCPYYECLFTADLIFQHYDIVLPMPKYGREHR
SSEISETLRYLRACGASGDFNHILQDVKGGAASGGDFVSTSHGILMAYGTARTNKLSMMA
LTGSGAADEAAALQQRALNVVPIEVSPDAPPLADLLAFAGKRTLIVQDTVHGRHAAEAAA
SSIPKIPWQILRVEPGCSFLSHLCGVNAVYDVLVDQDYPHSMERIGEAGLNPFPVEWTEP
RKLGITMRSVCLIARFARGTMSAGGYADSDGHRAASFTYHSRGIAKNTRLFQNGHRRHGD
NGAPLEAQLRSGELPEPVYQRPPRYAPPMHRPGGLMTSDAEGRE*
>TCRU_3241 oxidoreductase, putative
MGAVHSQAQEKQGMEEKYNNNGTAPEGHTIRCEGWTIEKPIRSWSASAMVYVDNVMVPPP
GPGQVRVKIYAASVNPVDVKRPRFGRNNGFFSWCNENFGKVGKNSNSNIGAGVSEIVSTF

TRHEPPEFPFPYVMGTEGAGVVESVGWDNDDMEQRERYGLQVGDRVAFLADITMANGGTF
CQYALAMADAVGKIPSPTTDDVIGFLEAAVMPCAVGTAYVALFDKLRVSSGRSIFISGAS
GGIGSAAVQLAKYAGMYVLASCSTVNVAYVKSLGADYVFDYTASDVVGECLAHTRGFGVD
YVLEVADAALAVHHADALRFGGSICVLPEHMPISSEVFFRRQLSIGYVCLTGLHADPLTR
GNLRHVVETCMKLYQLGAFKLQLETVPVERADTALDIISAGHTRGKIVLTIFHPDDMPHG
DDMMGTRRRKHAKVQSGQAAPAVSIQTAAPPPAQ*
>TCRU_subunit A, putative Chromatin assembly factor.1
MDRLASLLSGMAPGQIEQAVQLLQRYTAAAEANRQTVKGEEAPFLSSPNSDAKTDDAGGV
GREVGHPSPVKAERDGLNAPAGGLDAVSSVIALALEQTIRGGSAVAAASGDGSNDDDDDD
ISLVALAQKRQREAGKKSPTAAPKKKNKAQNVTAEDKESGNITALEDHERKSQKTDDSGT
PSRKGTSSAKAAGSPSSQQQQQTTAIAARGLASFGFVSTIKRTTVTVGDKKKLFTPFVQD
RRLVPSALRFWCHDKDAPASQKEPSVPSCVPREEMPMGGQQVIAVDEESSLMHLPVTSCG
DNEKAQDAQRQRQFEGAARRYVSFTAMIDDTTNFIDKGTQQEPPLQCPCAYHVSIAAPRA
GFRDEVIFCGFYAIGYDPCQSRPPYFGTYNSQDSLNMEELLQLARFDTGKEMPQMSNIDY
EYDSGDDWDVVENDEDLGASSSDTEDEEDSDYSSTSDTDNDFINDNDDEDDDSDAELQRK
MVEERQRRLNRLRHKDKLVPVFSGPFVGIPRLEHPLRECDRMERLACTLDGASFTAMMEQ
EMRGLGSAAALISLSDANRSGYGGGGTVPTENATAESLDERVLQQRLVAAALRNRRDMLP
DEIDAMHAIIAANGKIFPKAIVEALQRQQLCAGVARAEILRTIRRHYELKHKMMVRRPEP
WSPTDERLFKKRLRQMAGGSNVNRKGSTNNLTQSASNKDDNNNNNSNNFDQERGRDEEEE
ADDYEDDEDVPLLEIAIKRPRAACEAIEGKNE*
>TCRU_3243 hypothetical protein, conserved
MPPKGKKTVSRGKKKKLEKILDPDERYRNALDKMHYLSKESRAEITNSCLRRILTSIKAF
TLAQPPLEIESLMSREEQVNKEIATGVPMKVLPDIVRSLGLIPTDKQLRQIGWMVLNHEE
LQKQQRPQPKWEGVFAKFPQDNAKEVEDEYDNDVQGKLTLEDMMENPFSETVEWAAVEGK
ELIADREKLEAVLLDIMHTGLLVFDPANVQGGESASKFERVVTVLEYVNPEVVDNIFDVL
WSTSYRQKTGDGVRFIYSSDLTRVLETVEESEKSGEPPFESDELEDLLLFVGDTGRGTIS
EDAFALIAL*
>TCRU_family, putative AB.1
MTSAAHVRAKATRRSFWQLAGVSTLLVGSTGGGLFLYYRYARLPEQWRVARLSRMQPPVR
RTRPFVAGTSNRGNEDINPCDGYGFSNELLLTGEPLWGISAVYFYGLVLLRSVMLLTRMV
PVIWYAFLTYGLHLCGEQVLFEKLRDALTAMGPSYIKFGQWMATRPDFFPPTLCAALEKL
YDQTSAHSWSHTEKVLRRTLHEATPSDGIIEDNGMTSLPDVVEATKTSRKQVAMKQRHNA
LYYLQEIETVPVNSGSIAQIHRGVLREEVDGIPAGTEMAIKVTHPRIREHIAADVTGMRW
FVNILTFLWPSTVYFDLKRSVQEFSFFVQSQLDLRQECDNLQQFIFNFRDFPGVIFPRPL
PSLCSQDVLIETFEEGEPLQGIQSGENYYDLAERGCHMFLKMLFEDNFVHSDLHPGNLLL
RTNPGAPVSSVSASLLLPSSDAYYPDGKMKLLHELVVLDTGLVSTLSKKERNNFIALFAA
VACGDGKLASDLMIDRMPKQRRPQSGVKREKFRDDMQAIFDIVPPGKSEGFKLSKVRIGP
VLAKIMNTVRENKTPIDGNFASLVLTVIVGEGLGRRLAPDFNIFSEAAPYLVALLEDSEL
YFLASKLRETYGTPALLRDSVHFVRPERTATYAEMGVKKLVKTMGHMWRQLTGEATDSDV
ATVEK*
>TCRU_3245 retrotransposon hot spot protein, RHS3, putative
MWRRFCRLHVALLRRRWALTASPTGVAVRLHGAPTTEPCECHAQRHWDCGTKQPRLSFGA
SGTCWPQLGGASGMLHRTGVVMAPRSGISGDGSDAAARHVVGSKVWPQWTMSSTNMRLSD
FLWNYVGGRAAVDERLQCDDGGVCSGAG*
>TCRU_3246 retrotransposon hot spot protein, RHS3, putative
MIAVSFPKVANYDEWAKQLQAARIIMNCPYEMDVKAMCDWMKRDETAEKQVECWKEVKKH
MYLLGPIPRHVFDEESYIDRLGAVNGALLAMNPSDVGEYFTLGGEKKWCSEDLRHELVKI
VRARTDEGAEVFLNASICARIGSRTADRLAKPLPRRIFCCCYCDRMVLLLPKLWKN*
>TCRU_3247 hypothetical protein
METTRRQVIAVALLGSSEYDGDEEEGEEAWNMRGSSVYRNGSDSTLANQMSLYRISLATS
PPASARRGTRSRRGALIQPASTAQEENRFACSEDESAESSEGVERLPQNRLFNKVRSRSW
AFVTLSGSVHGMFCVQEGSLNGSVKPLNDLADQTDSGASLFLLFEQHGWARESGVNGVPC
RCSSGSPLSKGRNLSLLT*
>TCRU_3248 cyclophilin-type peptidyl-prolyl cis-trans isomerase,

putative
MNLFIGGSVHAAGAYTSPYPQNARNSVVYLDTAVQEGYTWFGSASMKPIGRVEVELFDDT
VPITARNFRELCRGYQNKTPEGKPLHYKGSVFHRIIPGFMIQGGDITKGNGTGGCSIYGV
RFKDESFDSKAGAHKGPGILSMANAGRNTNGSQFFICTVSCPWLDGKHVVFGQVLRGFDH
VKAIEEVGTPHGKPSKTVLVSDCGVLKEAS*
>TCRU_3249 ribosome biogenesis protein, putative
MSSIGGFRRRAPKTLKTRHALKKYEPKVVENPKKILFLRGSRTSSVVNDAMTDLAAITKP
YNKKLKKRNGFHPFEGREHLEFLGFKNDCSLFCFTSDNKKRPHNLVLGRQFDFHILDMVE
LGIVAADRLDLERVKGMDVASLGGKPFFVFEGSEFAADPAFIRLKSLIIDFFRGGTETEV
NLDGCDRVLAFSLRSENGRDACVAPSTECYGSGPQQERGNTVLCMRHYALQKPSTAAGMP
KTLSSNIQLVDIGPNFDFSIRRAAFATPAEFKVATRVPKEVLATLRSTAENVSSDAMGNL
RGQLHVGKQDVDQLNLRRFKAHRKRGRHGDGEDGDGGEKDEEAPQKRRRRRHGGGDDADD
DARPETDISETDI*
>TCRU_3250 hypothetical protein, conserved
METSGVQRVPAVLLLREELRLMDEVIRGGGRRRVYRHHLFFRALLALRMALEKMLPHFAQ
RRATPPQWAITRLLALAVRCGEAAAVELSVSRIDTLSLAALSLAISSRIGCLLGALSSRE
QDVFSGLAPADEGSSSSNNNKKKKDKKREGVNFLVTIKRGRQKRSRSPEGVMSLQRPTIG
CVIEAVLH*
>TCRU_3251 zinc finger protein family member, putative
MQKQQLTLDAAYKLTLWYSLFCEAQSRQERTTECRSHDTRVRHIAFSLLKASLPRKSLKS
CCLSGACGRDSLTHKRVHFGRPEICPASGGRDDVCQCLAHATAFVGCPVRLMVRDYSSSA
SLTGDRYGGLRCMLRHMTLQSVTFSGTSDPHDAQRVVEELSQTLMSHTGTLGRLSLGGIP
AHVVISPLLRAMTMVDSLTELRLEDCGIQEVDDIVSYLNMAKHLRRISLRGNSGISEGMA
KLGGAVATCRSLLSVDMGLCRLRDDHLYHFLNNLHGFLGRASFTFDVSNNFLSNLSFEHL
RDAPAAFRATVSELDLSGHNLEKCGVVASAMLLRLTALRGILLDQCELGSRDLQRLCRVL
SQKERRWNLLSFRGNALTTHDIKRLALVSLAAGSSLCVAGNSIGTGVHKLNLTLVLPFLC
ELDLSICDIRDEGLLQLANALEKVGPFSLRVLRLDGNDIGVEGKKGCSGLQFLGRALRAS
YAPRLEVLSLAHNRLLLRPLLTLVEQVSSTLRELHISYSAIANDYGEVMSLVKEIIQRQK
GGLGFEQLDLWAMRAADADAFCSGELETWLEGQRAVRVITGTK*
>TCRU_3252 hypothetical protein
MNITLESLAQALTVLQQATAADLSGETETAVEMYVAAKNELDAVAPYLPRGHADVVRGHA
EEVKRRIDGINCNRWAKEGKSEFPTFPLEYVPKPVPVEEFRVPLNPTFRVLWLMRLLERS
IRQGAFVAPDLYVGKEVWYQNGGGAALTHTGPKIRYLTALCGAMEKLRAVANLNNTETVT
KSLRKYLRTAEELTTALEMEIGIRTDGGASPRSRIERGMRGLFHKGQQVLRTWMNQEPNM
ELCLIWAVNTLGQAQLFERWIIYYSQVHMSPAVTEIMGFLHRAVGLLYSGPCSFLLRDMA
ILIERHQEKCRKSITRLLPVDVKLEGGTFS*
>TCRU_3253 40S ribosomal protein S33, putative
MTEVAATKKEKKAPQEEVVVQQTDQAQVGLIIKVLGRTGSRGNVTQVRVRLMAEEGSPDA
NRTIVRNVKGPCKEGDMLSLMETEREARRLR*
>TCRU_3254 40S ribosomal protein S33, putative
MTEVAATKKEKKAPQEEVVVQQTDQAQVGLIIKVLGRTGSRGNVTQVRVRLMAEEGSPDA
NRTIVRNVKGPCKEGDMLSLMETEREARRLR*
>TCRU_3255 CDP-DAG synthase
MNKGLSKRVLSPLKRTASGSLSSIESLPPKTEAPEKLRTYKDFINRTIFTIAMAYVFLVL
ISLGVEVVIPLVIAIECTMFYEITRINQRARKDRQLVSMFVLKLWFLGSTIFLVTSHSIR
EPLVATFPWLLRYYANFGMFAFGLPMIGIVGFVLSLRKGMYRYQFIQFTWIVMTLLFTVI
QGGIQIKNMMRGMIWFLLPVSCVVNNDIWAYAFGKMFGRTRLLALSPKKTLEGFLGAFLF
TMAWSFWFAGFLGYFPELYCPKVDFHSSMHCEKDPLFVQRAIVLPSFIQKLTGNYLTTIQ
CSKAQQHALVLAAFASLLAPFGGFFASGLKRAFKLKDFGDLIPGHGGITDRMDCQGMMGV
FTYVYLMSYVYSDAKCPSLHDLSSCALRLSDEGKIRLMRLLNESLSKGF*
>TCRU_3256 thimet oligopeptidase, putative
MALRIFADVETASKCAVLFPKNVSACQVVAEEAKLRAMEKLNAIYSFEGNRTFDNTAVAA
DIAAAEFDVSLSLLSVIMSVSTVKEIREEANKQIVELKSFEIDNFQSNKRLFEALKEVSQ
SSQYKEKYLEGNKDKEYSYWLDEELRNFRRKGMELPDNKFQEVVALEKELSALCTTFSRN

ISEDQSEILASAEELKGVPVSIIDGLKKADDGRFILKMDYPTFFGVMKNCEVAATRQSMA
RAASNKAYPVNERVLKEIIAKRQALAELLGFSSYSHLNLSDKMAKSPDVAKAFVDELIPR
LQQKWKHELELIKKNLHESCILTEDGRLREFDVAFMMNQIKKIHLNVSETEIQEYFPLDV
TVKGLFDIYQAFFDITFTRIDNGFELWHESAFTLQVKDNATGKTLGHVIMDLFPREGKYS
HACCHSVVPPVLLHGSEDEFSPALGVVIANFPAPLKDCPSLFLHDDVTTFFHEFGHAIHG
LMGRSRMATFAGTNVKWDFVELPSQMLEEWVWEPEILQKITSHYKTHECLPSNLVEAKVK
SRNAFIGRDSLRQLEFATYSLEVFSAPFAGGKDPNKLDTAELMRSIRSRISPDIKCEDDT
HFECGFGHLTGYGAGYYGYMWSKVFALDVYEYIKSRNGLLDPVLGNHYVSNIIGIGGGQD
PTAMLKKFLGREPNSDAFLKTIGV*
>TCRU_3257 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGGAVLVSAAGDVVGGDGRGVGESLPEGAQHAVLLPSSPDSS
VALKEGTNPLQKRLEKVPALAKQSSEEDDEAGDQDVEDVTVPIEGQQQQQEEQEMYGVET
SGVLIIKKEAPQAREGERNLTAAPMEGSPTTPGPQAPTPKLQPPPAPAILRPEAGEERPS
PPQASGVGEGDGGPVGIEGTGRNVSGGGSLVGASDASRVTGEATKGPKGSEGPVSGPPSG
GASSSPISNDGDASRKNGGAPSTQDTTSLKNNEQSRPTTSSGNAPLNRETPERSTPDAKQ
HSSETQENETSRLPDGDANYSATGQSAVGTKGSSGVSTTASNAPTTPLPQLPAPPVPTVS
TVTGAPAEKPTAEQSPPPADSTTVEGLAATTTAQTNDTATPGDRDGSTAVSHTTSPLLLL
LLVVACAAAAAVVAA*
>TCRU_3258 hypothetical protein, conserved
MDTTHLHATCAAQPEGLLAAQSVIKKRRGAAGCLRGRKKTAPSNPPPPTNPHTRRRTVPP
TLHPIFRVARINRREGQWSLSAKKFTVARRISDIPALDKLHEGSERGDSRDVCAVNVEAE
NVPSGAIHNFMPHARTADERGELCGLFDVNIRCGAIDPTAAHQDAVVHVGNGSNPADHGD
SGVTKDCGAIGDEAGAPLDKGRDESTYPQPDRLEGTCCLTTCVDNGESLVRDCGLDSQKF
QTEDGRDLNFGLVRRAEDGEGGSPPRPAVLQDTRAGRLRHNEKLTNLTTAQIERALAPWN
ATAHPTKRGALRHAAQIVETDDLDPHVISQLAKHVNPFDLPQNTVCYLGKHTTMLTLVSS
LVALM*
>TCRU_3259 hypothetical protein, conserved
MVALPFHISQYLSALWDEAAALLDLVAPFYRRLFWRICTGEFPLSSEICGSRRVDSPPHG
PRVLSGSSPHRCEGLGGRPRDGKTAVCGAARGKETSVWISSIRTSGRRKSVVRRDQCAAK
KWRQQENRRSLPRGVNLLAYRSAARRRVSP*
>TCRU_3260 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MIIYSTDNGSIWALSEDMSPAECLNPRITEWEGSLLMIVDCENGQRVYESRDMGTAWTEA
IGKLPGVWTNSQPEVSQDESLHVDALITATIEGRKVMLYIQRGYASEENEANALYLWVTD
NNRSFYFGPVGMDTSVEEELAGVLLYSDGNLHLLQQRDNDKGSALSLSRLTEELSTVKFF
LSTWTQKDIFFSSFSIPTAGLVAVLSDAASDDTWYDEYLCLNATVRNAKKVKDGFQLTEP
SSRVSWSVNIPDDNVRHISLSHDFTLVASVIIEVTPSGNTPLLTATMADTNSNHTMGVSY
TADNKWGKMFEDKITTESRPWEPKKEYQVVLMLQGNKASVYVDGKLLGEEETMLTGETPL
ELVRFCFGACEMHNFPVTVKKVFLYNRPLNPTEMRAIKERRHIPRIEGVRAKAPAGSGLL
PLLLLGLWGFAAA*
>TCRU_3261 transporter, putative
MFGVTVLAVTKVVVAICIGAFASQRIPNASVTVRDFTFVIANILLPCLTFYNVASSVNAE
LLIRCSVLFLFSLFVIGSGLLCGTAASKLMFRVSCSGIPHGLRDSLRYTLIYQDAEGRHV
KRAARGRRHSPSLKPVVCVLVSGALETQQVEPEEVLPLLEPPGVEYEEQPFYQYASLIAC
SLQNTVTLPLSLLQALAESLAWIDLAAGTSFIFIYSLSTTASLWGFGPALVDRAQKETNK
RRKIRELLELHKKLQGCCDVATQTEVNEEFSLIASPIGLNAPPFLSGKQPNAKFLSTIRE
AASKKILHEEEGEKNASKMMAAATAHSTGEQTDIPPGAWRWCLAAAPATVETFHYNWKER
GLIRVMYARDFEDETEAERQKRNNFFPFLRALKNIGVRLFKTVAFTSLIAGLVVGLIPPL
RWLLFEGPLSMLTDSIALVAQGSIPSSLLLLGANLVGSTSLTAPAPEVRLREAEQNTEFP
LDDTSADPKDTEDYNERHEVIEFDEHASFTLMSLQQQLQQAPVVVSTATSSENSTADSPD
TFFSGNGWMSAVRRVFALHGVWKSFVFGIIFIRLLVIPAAGFSLVLLLRRTAPSLFGEKR
EQNVLILVLLGELAAPTAINGTILFNSRQYMPGVWSRMLFFQYLICTLTIVLWCSLSLWI
VT*

>TCRU_3262 N-terminal region of Chorein, a TM vesicle-mediated sorter/Integral peroxisomal membrane peroxin, putative

MLEKYLSAILVPYFSKYAENIDSKQLNVDLWSGKASLNDLILRPSILDALLQGESGSDVP
TSSGVASTPSCSSSTAVHTTAASTAVSSCLPLTLQRGVCKKVSIVVPFTQLRSKPVVVEV
DELFICVCGSTGSRDAVLSKAAKLDAQAAHKARELEQFEAERRRMRDVAAAAAAAKEGGN
NTAAASPSGPAGTRSGHGSGFMADPGDGVAPAPSLLTPLTTGRDGYFSHLGELVVNNIVV
KVRSVHVRYEDESTKSVMGVILGGVEFTTIDSITGEATFIDPSGLSRMHKRLEFKGMQFY
CDDPLRYEREPGDYFISKMTDVSEWHAAMRNRVEAGDIEMSTVLGPVKGHVDVNLVFKKF
IKNLLHDPYLTARMKLGPVTAKFNRAQYVSLMRTVSLLSNWTGGVELFPRRPTAPILQDP
AVWWRYAIRAVRTITGAPRRERLLQRISEVCIVDYHVLYRDVVRKAEMSADKQRAYRFIT
RFMTVPDMIAGRKYVYTQIANAIQLKRKDNEAKKAEAQSNFAKKNTGWFAWLRRGPKTPQ
DIEEEEAAFEELERSYGINPNDPEGAETTMVDVSALPKSYCWLDAQFDLPMFSLRLDMGK
RETVTLMLHSVRTHLRKFNAANSVQLRFITENLTLSNPVQDNALLERLPSLVEGIPLSSS
AASAWKIDPTSRRSSSMSSSLLPLSPKQQGGVPLLECSAAFNPIDAQKEPQLKNTQLDFA
LDLRLLPLRIVAEPSIIDHVICFFQFPKGLDLASIVRSTKSLAATVGQAASSELRRAMAH
SKSFSISVDAAAPYIIVPKTLRGSVEEPALAVSLGHVQFETEPLTETEKQSRLASTTTLS
EMNEDLMYYSSSATFSNFYVEIAPIGLSLERPGKGFMLVPEVAFSAKVLQIIDDSIENRE
RFIVRMEVPSLCMACSVSQAYILSNMVESWLLYLQATDSPYADEQLPPSLEATLRGGERA
SQSAVGGLEGPHGFTHTNNALMRNRKGEESESDDIPASPSPLGRSREDLPYVRLHLKVKE
LGILIYEDEPETLQPMKTPRFTMAFSTAEVTLHVRTLQKCVSMILEQPYCRDAKEPDQLI
LSATVIRCGVKTAPDTPIRVDVELEPSLRFCFGTPCIQLLETLMDIVNLVGGAPRVLKEG
DGEEKAFSSQLLRHFTGSTAPRGTTTIRPTSQHSQVNLVEELCSTYDTNVVKLSLHVAGT
TVVDIMDRRRKKRVPRKDDSNAESGEEKKTAEERVENEKNDKEEGEKEEEDYPFAHASFT
EVTLSLTKNGATLEVSGGVGQVTFALAEAHDVAPAHRTIVQYKASPSRTPLRPALQQDGP
FLDTHLVRHESHEHINFSYRTSLPVVPIFETDCKGKRHLSNAAELRFSSFVEIEVSSSTV
LLDVYSILTVTQYFSSGLFARVTQLTSRPRYDGRVTVSSPPVQPPTLLTSLRVYARDLFF
ILPIDTRTTGDGYFQVTVDHVVVQSSLLSAEGKQTMNISLREIRLLHTSLKEFAAVATGS
EGENEEPHTLMPTTTLDMSVKTPLDPLSDEPLHVDLRGEDVTLQITETDIVELCRLASGN
LRRMPPPPSVHAVVSAPKSPQLVESSLAPSISPSSSTMHMPERPADISFVASESGLNLLP
IPRAVPPYMDKENTGREVRVLWRASKVCLNLLDESTNKMRFRVEGNGFIFQVFVPSNDVT
VGWESLELNDVYEVTQRASMMLCGESRVELRNILTSTEILQKNFGMRSSVTQTSDRSVWD
LWSGRVSGTEGYSVDIDTELLEVPTVVVDFTLRRFAVSDQWLAVHDFVCNEAVMAALQPM
MGAAEASPSSSLPLSPDGNDAEAKRRFHCLIKTRTVNVPFLTTSREEFIEADITSLFVDF
LALPGVSNVTVRMQDLEVRHRASAERILYRQSDTAPNAGGSQEELLRPVTDAAPIPGVAF
SGSVEGEASAAEKASGGDILAFSGSFDAGAERQKVTVSLGQLTALFSMPLIMQLVEYCTR
PDQPIAKISNLGVMRERREWLARAAENLVQSGAFSLSLLWRQPRIILAGDAQDLGNNLRS
IEAQLGIMRSTVSLDKRNGNYTVAMKVTDMAIPDMLEKSSLRLSYALKDRRENVDVVLDK
TAALLHPEELEKLLWVLHRNLMAPTTTISAQRDRAGMKTEASLEAPVSPKKKDEKEEENE
KVQEGVTHVEEATLRTIHFRAEGVVLAIHDVVGINAHTASLSGIDVEVAPSGDVRMTVGS
LTILEHFTNRQLAQSLGDQPITVCMSSAEKTVNVTLADMRFMLIPKALGSIFNTLLSVQF
PPPLEEILVIETGTELSPMDTHGKSPVITATEAPTTESQTMTEPSSPVLSRCILVSLNHC
SAVAVLGSRDVCVAELKDFIVDWRAYTDASMRLTASIEQVIVRDAFSTSTLYPEILQPLL
EGATDTKGQTPSGVIEFSFISLPHRNLNSNKKISSSGHIGEGDADRSVPSYTYQLHCQIP
SFAIVLVPEVTSAIVRLLSEVKEHISDVNREKAYDYVADKTVQTVQERQELTQVELTLHR
SSIILVDSANSSKTMEMCPGNFFVRNEICCHRSDESTPPAESYAEVFRLHINRMSLNVLG
APAFSHNSVIEINVLRGIGENSASSLMELTSSAELSSSDTTSVSLVIPTLSAHLTRGQLE
CLLDVMGAWRNSGLSGIPVEGVPVVASSTLQAAGGGSGGSGHPEGAASGATPLATSLLGT
MAMKKKSNSGNSALLHSGNTANVTPLSPDTLTPSNRGRSGSGRGGATGGSITLKANMQRF
EANIDGVFQLDVDQLDFKYSTNPGVNTTATTIALDTIALRHHVCGVSDLRADIHLFVMRK
AQLTSTVTVQVSLAARMSETNTNITMDSLQMSISPLVLLDAREMLYGPFCTKVLRLPLSP
IPVCRLTTDVHVLGSDLVLDSHHIIITTGKTRCSYKLDLNQHKLYLSGTPTAQIVLDDNC
QLILTNGCIVVPGMYALSSFVSFGLNATLFTTDTCIIEKQVHHGRNLAPFVKPSKRRSKA
VPDSYLLSGNKNAVPSSLPSVKPLPQSGVLSPPIATITPVHAGSPSNSTSNFMGDDVRTI
ASFQCKEFTMRTLSEEVEEISVTVTASTSFLYLQQTENGVLTQRSANISLKDMHTSEEDE

NTLFPTTLELSLAGADTICIVANLSGLELCLRMALLRSLLEFGNDFMTAFIGEAMLQRHA
PQVALENEDLQPLVDLPVAGDCLSCGSPGASLGESKDATGVLCYHCCTGRRTLPATEINF
DVPLVDLVLLGGQGGMLQLYTSSGIAVTVAPDKEIQLQMKLQVYNLNPHANIWEPLVERF
EAGISGNVTSSTYKIKVDRFDYVFSPDNMKLLSQLAAEFSPTSKLHRQLRKKLRDNVHKV
LTGEKPLKDGMGGDTLRSMMNIQQVSLVQSPHYNEDDKICAFVVVTNYLNESLEVDGKTV
EPRGGRLEFAATSSSGVVRRCGVVGDGMTIHWAKSPLYVRGHDMLAEVRLEFSRDEEAFR
LHCAVRLHCYPVHRSNMIICFENKISTFVEVVRGLPAVSPHERFYFHSNFSLDEKLYLRP
VRLADGEEYTAAVTKQTNVTPTLRMLLNASFITLVCRGSKNTHNDFIFRMKEQQDGVRAG
IPTFLISIEPQLYIQNCLPYDVFFSIGGAGSKKQQRYCAVVESAQKADVVLGDVGIDELA
LHLELQQNHSSTGGMTTTYRTQRGISLSRGFTRVTLTAASKETQEMRIHVQCMGNIILLG
TPYSIVNFTPLDLQVWESNSLGELVSKKRTNFGILPKKMQRTYAASPSGKDTTEFFVNIS
VGDMWASAVPFHVQGRGLITMIERNVAVSRVGTRSVFHFVYLTQVDMYGTRFVTIVPRWI
LVNCTSRSLYVAQALKQSASAPGATTTASSSSSSATAAVAVGESSGGMSSRSSGDYKNWS
ARLRKSGTLLSPIPTLSGEGSLYACSKEIMQLAPANSATPFFSTLNSTPDVGYGAFLLQD
THAPIRGDPVSLEEISSTLVVVHAAGDTPEMDGSDRIVEVSVATQGPYTFVTMQDPVVPP
YILINRTEKTLDLYDTQDRFLAQVKPGCVKPFAMDVRNGNSRTRVSFARDFAATCFVGHK
SILAAVNSPVATAEAKTTMEIDKKGEEETLSFVEFNFQRRMTPQEASNPLGIEYNLSLGP
FGQQIVEIVYSTGSTERTLHKYQPSPPSPLDVVLNINVLSISMVMTDRDVLFGAIVDTRV
HFNREGTKEVFDFSIKNFQVDNQTEIKPFFEVAVVAIRNSPDVTCLSGHVERIVVPAKAI
LYLNEVRLDVVPVALRISDNVLVALAAFGAQLSTELPSRQTSPTEEELFDKAQSTVSAMD
TRVIMERMVVNPLVVRLWFEREVDGHDFIREHIQIRTAALVSMLVRSCEDVRIATPGIAV
RKRSSSAGLMLKWLIQVYLDGIRNEIHGILFQYASSLPLLGVPIKLVSGIGSGAMKFFQE
PIAGLSRSPKAFAMGFASGSSALVTEVMGGGLGAVSNLAKTGADIMGAASGGRERKRTSL
LHGITSGVTGVLTKPMEGAAESGATGLVRGVGMGLIGVVTRPMAGLLSDVSKVTGAAAQL
CDESYIPDVRRLRKLREFHAMGAVAEYESVLSVYEYERGEHDGLRWKGNTFIPTDGPQWY
PYTKEQAERARGVSSSKWSLEMANTNFEGWRFSTKYYGVYTREQVPTARVRRRRWVAVLR
SPLTSRVVRLVQRGATTVSGSHAAGGDESRRGGDTTTNTAPTRSSTGAANVLPAIQGPRS
ASGAAVSHEATTPTAAPVTEGQQQQQQQETLPEVSVLPRETSLPNEQVVELYEYESKLPL
IGWGSRFLPAGCSHWQYRDGRAAPRKSDFQLRQGWVWASAWALASAGRSGGASSSAPPDG
WEYVQRENTSSLPTLRRRCWRRTARRVQ*
>TCRU_3263 hypothetical protein, conserved
MGAPNDAVALRKYGRVPFFPGANCAPSTVARRANSFPPTVTAARRVGEVAHGITTSAALR
GTHAARPHPYIDDDVPPVPAQKSLLPEPKVLFVCVYRPPFAASLGTPYCVVQSNHVCGIV
LHWAGARHAISLLSEPPGGWAVPFLGISTAP*
>TCRU_3264 Leucine Rich repeat, putative
MPPRPVKPTGKKAGKSVRIRHVAPRELYIRACAELGLAPNSGLIDLLSMYQESASVEFID
VSRNYLGDKGVIPLLAVVDRCNNLREIILSENGLRNNAIAALCNSAVRHPSLRRIDVSDN
YISEGAAAHLQRLLEDNPRVCELGIDNTKIDVEWRLKLRDLLRANATAAAAAAAAADVSQ
QDVKIGPN*
>TCRU_3265 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCAAGGRCDEEIAKDPVGPSGAPGNLGKDGMEKADRSAVGHGE
LGLVPEPPKDVSQGGPSERTLGGTGEDAVDKNKDVLSSGRGYGFKSPSPEKQPPGTDDPA
KSIEEEVELQQQRNDGKELENQPQLQVPVAQQEHGVLPLSLPHPQSQQSHQNTQQQQPQP
QILRKEGGMPHEKGSEKGTQELDKLKEESQDTELQNKVKEEKMKQELKNEEKGGEHQPQL
RVPVEQQEQSALPQPPQSMQQPSPPQEQPRQQKQQPPHGKPADNEQESKTDKNAVGTNKT
ANGTATPADSDGSTAVSHTTSPLLLLLVVACAAAAA*
>TCRU_3266 Mucin-like glycoprotein, putative
MMMTCRLLCALLVLALCCCPSVCATEPPEKPKVDLNTSVPSPSGTGVKEAPQANSKSLPQ
GINSGLDQDNVGGEIRVLTDRDSQTDDAHNSVNREGTDGDTGIKSPRDFSEEKTHEETEG
RAKTTTIKQSPEDDRKAKPEANTNATSPMPSAPVIKPYDASAHTTMTTATREPTTTTTTT
TTRAPSNTTTTTTTTTTRTPSRLREIDGSLSSSAWVCATLLLAVSALAYTTLG*
>TCRU_3267 hypothetical protein, conserved
MELEVASDGDVYARSLQEARWDILQGLNVAKDWGRLEERHPFFRDVILDAKRQAKLLASV
LTATEFFLQRLLWCCENDTAPSFVDANRVKQWRASLAVFISLYESSPVPTRARWLAESRE

RADGTCAVSVDGDEKYNSYDHNKVRGMDDDDVDDDDGSFVENRLKDMVLQCLAIGRMWCR
QLDEEDEMAVKVRHALSVMDAFAAPKTLDW*
>TCRU_domain/DAK2 domain containing protein, putative Da.1
MVTTKFIDTPETAVDTAVRALCMTRPHLQFIENTHVVVNRKIDPTKVLIVCGGGAGHEPG
HVGFVDCGWLSAAVSGDVFASPPTIHVTAAIDYLHAKQGPNGPGVLVVVKNYMGDILNFQ
FAVHEAQTRGINVEMVMVADDACFGLDDINCRRGIAGTILLYKILGAAALKGENMAALKQ
LAGRISSGMRSIGASLSSCSPPGSKPLSTVPDGLVELGLGIHGEKGLYRIPFEGAKTLVS
HLLGILLCGGKKRGEHKEGETEKEWKGAKVALLVNNLGSTTDIEMGILTHHALRQLQQAG
MDVVGVSVGRYMTALEMHGFSFTLLRFSIQDDIAFLFDQQQTPLLPFTVPQFSISPAVGP
RSALQLAQEEKCGLQCNGLLGRVLENVFETLKNSKDYLNELDAAVGDGDIGSGTTRASIK
ALEILPHLPLETNVSKALVLLAKAVADVFGGSSGPLYGAFLLGAASAVAETMCRDGASSV
DAIRAALRAGSANIQRVARSKKGDRTMVDVLEALNENPQVNDANSIQELARVCVPEAKKA
AAATALLPAKHGRSRYLQGKELGQPDPGAELVVLWIEAAANTFLSGGKL*
>TCRU_3269 poly A polymerase regulatory subunit, putative
MYAGLFKKRPREADAASHGNAPEDSGDASSRAAGISSPTLSPRTVYHYPSMLPFPTVIDS
EFPAESYRSRSKDVKAAIHWGQRKLLLSEIQLLSIYARPNVSYHIVYAGSAPGTHLAFLD
ELFQSRHTWELVDPGRFDRPVLESRPNFSLRNEFFTNVTAYGINARRLLEVLPGLGTVYR
CVALDGAWSTKKEIHQKLQSIVGTIDVARGTEDIPSMYEPRLDLPFGFELLCYVGMERSK
PLLFVSDIRSGSVNLPNFEDHVAENMRAQECWCQILQGEYSMLKFRLPYTHKKIGFGDSS
RKVNSSLIGPDGTVNYLRGDILLPIWTRPTSTEGRLVVPRGAHRVPYKVAQVENCFFFFN
ARVREQVHFNHILLPDENLDHHYDAAAEVNCLLKYLQFLHPELREASAAVLRREVKHIST
SITAHLRVNFQDVVRRREYLLLKQARSGQSEEEGDESDNEAVDADIAPNCGAQLGSSWET
FAKEIIQAASKERARVVWRRNVEETGSDVRSGFWVTTIMRQ*
>TCRU_3270 hypothetical protein, conserved
MLATRVGVGRLWCGDRCLPPRHLAAVVRCMELLGDDDAVDALIREEESRVRQFKLFHCTD
EERRRQYGAVSRPMLPEPSPSPPKVKLTGIPLEMLPVEAEEMLVHEYEQHRSAKHDVDID
LRRRGLPPPYYDGPLLTLRTRGPYTRFEVLACRPPMRPRVEGKKASQKDCSQHYPRPLRE
KPKEDTVAMPGDSLRRWKYSMGLLDE*
>TCRU_3271 transport protein particle (TRAPP) subunit, putative
MLMPYRDSVRSSKSDKASSRNTNEEAKVSLSAFSFLFSEMCTRAHNTPSKASNVEEIEQR
LTSLGVLVGARLIMLSSLKDPLELQRRPITIEGALKLFQDKLWSRWFGKPANDLQRETGS
DRFFIFDTEPIVLRYVYPSPEYLDGEGRWSINYASFMGGIVEGALKAIGFAAEVLTYHQP
EPSKPHQSIFAISFAKHVWDRERRLRG*
>TCRU_3272 leucine-rich repeat protein (LRRP), putative
MAGVLTENLVLQKTKVDSIQRVRKLNVCAAQLSDIGVLRRACNLEVLSLSLNDVSELGVL
ENCRRLCELYLRKNRVEDLNQVLHLSDSPYLTVLTLAENPICQDPNYRRFVIAAVGSLRR
LDDIDILPQEREEACRVFPNLRAIAPPPSMYCDPARGKVRPGSGPTSGTVSLAKLTAQRS
HHNSVSAYADDHAAHGNGDRRGSLSRSPTRTHATKRRSTHLEFSHHSQFEPMNHSIHTKR
ASSGNGGMGAIHLQPPQIGPTETGVVQAVKVLLSELSAESLEEVRRFIDALK*
>TCRU_3273 Ribosomal protein L31e, putative
MTRAGFKGKVLGKERKQALLDARKKAVASRKARDDRRWKRVLAKMDSEKRKKYHGVGNTA
EHSRVRGITRAALRKRTGRKPDNITMEATIHLSKLLKRKTFHKRAPIAIKRIKAFVARLM
KTKDNRIDASLNTYVWHKGVKGVPGRVRVHVERKSETLEGGKRKHFYTVISNVPVASFKN
LTTKVTEQ*
>TCRU_3274 hypothetical protein, conserved
MAGESATAPANVEEWAEDDGGFFSAFAEEAAGGFSRRKRNRQAHEREVEQQQAVQRAEAA
EDEAIVMARAEEARRQIAAKVFSRASPREVRQALKKAKKESIPKKPHGEGDKARQCNFSS
LQKRQKKRRK*
>TCRU_3275 Peroxin 19
MKNPHDDDELDALLDDCINTMDEQERRHEEEVRARDAAREAELEKGTADSNQSGELMGLL
QALMNGENGDGNADPETLMNTLNEEITRVSSLIDSLPDASEEERASMTEVREIFDRLTKM
SSTNEDDAAGGNAMNSDETLAEAFKKYMADIEKTSGSSAGNAAASETPRNTSSTEAPTAT
ANAAEFEDVIAGLSGMVLDCLLDPGMLRIMKVMQRTYPRWLAANESSTSVNDLARYKKQY
DVVNSICDLVGDGPIDRQDETKTSQLVSLTHEFASLGPLPPDLEKLDAEEEQCE*

>TCRU_3276 replication factor C, subunit 3, putative
MTNEGRNSTGHAAKSSTLPWVEKYRPVTLDEVVAHEDILSTTRRLMDSGNLPHLLFYGPP
GTGKTTTIKACAYYLFGKDRIRANVLEMNASDDRGIDVVRQQVREFASTSSFYFASAPAA
PTIAAFKLVILDEADQMSGDAQAALRRIIEKYTKNVRFCILCNHINKIIPALQSRCTRFR
FAPVKKSAMLSRLKFVAQEEGVRFTDEGLVAAFRLSNGDLRRCLNTLQASAMSAGEITEE
SVYRVTGNPTPADVRGIVEDMIAHDFAASWEKVHQTVSEKGVSSTDLVREVHHIVMAMDL
PQESKCFLLMKLADVEYYAAGGAKETTCISGILGAFQLVKEALTQKRHVFALANF*
>TCRU_3277 hypothetical protein, conserved
MSSSDDEWRNPPDLLARRTAGRRGGEDAMLAARRQAVQRQHGSAALAPPPTQPPAQEPLM
VPEQLARKTMPPPKRETGVTEEMLESLRQELEAKKKVLTAAKEKENSLREKWRALRAQKL
AEIAQLDVKLHHHKDAMEDVKASAEREVREAEDAQQQQLEEERIKVASAVREQYEPQIVA
LRSQLEGLQQQEAKLQAELGVKDTVKDLLHKCVGSALATILQRVNDLFAAESSTMESWED
EIQRLVRHEVRSSFAVTTGSEAQRERED CQKLFQELLEFWRKAEEEEREHVLKMDEQLIL
DMQSMVHDDLDRLQREELSMEEMYVESREAWASQHQEILKRELDAAMSRRTAEHEEQRAL
RHQLHLERLKAVEENHHDMLEKQRWFHEKHMALLREQHVKEERLAEQRSRVNAAMQADAS
RATEEVNRTVHAVEALLKRMKEYRAAIEDGRAAIDSDRRRALEAREETLTMLQELVTKQN
VSVGEEYNSLMATLSRLEGLRRTMEQHLEEERLWLGKQEANFANGKTEWEREYRRWKQMV
EDEKSNIQERFGRVLAELREATVQLAEEERDAKAEQASMVSWFRTASESAHAEVSQLRQR
EEDLRGRHEVMVKLLNDFQRTTEQVDEQWRQLRQERQGLMKESEALRNDEMQLRQSRQYL
HLLQEQLDAKRIETAEGHGRINALRRELQLSKEAVENLPRQIPEARHQMLPAAPPNFCHA
MPAARQNANRLPLRVLHELRGMLGKNSRQIPVRAVVSESPEPAVDLTFASTAAETSPVHR
RMAPQHEQPRSYQTGKPEHTYVDPVDSSRDTSTHLYDTSNNNFTSLINFSDTESTRHSLH
TSS*
>TCRU_3278 cystathione gamma lyase, putative
MSSQKHLVSDFTEGSGSWQDQTYGFDTVLVHGGVKPDPVTGAVLTPVYQSTTFVQESIGK
YQSKGYSYTRSANPTVSVLERKLCAIENGDYATVYSTGMSATTTAISSFMSAGDHAIITD
CSYGGTNRACRVFFPRFGMEFTFVDMRDLKNVEAAIKPNTKLVFSETPANPTLTLTDLTE
LSKLCKAKGLIHVCDNTFATAFIMRPLDLGADVTLISTTKFVDGHNMTVGGALVTKRKDL
DEKVRLTQNILGNAMSPFVAYLQLQTVKTMSLRVAKQSENAQKVAEFLETHPAVEKVMYP
GLKSFPQKALADRQHLNNNHGGMLWFEVKGGTAAGRKLMDTVQRPWSLCENLGAAESIIT
CPSVMTHANMTKEDRLKVGITDGFVRVSCGIEEAKDLITALKTALDAL*
>TCRU_3279 EF-hand domain pair, putative
MISLNYHQRNTQAVKVILSELYATWSTSDEGAFDIQKALEEILNAAHLTNKSGHVDGGQA
QHRYASRLDDRDDNCQTELRALEVSSSHHTDPNVVSQPLSPKRSTSPPPSSPGQMRRRLS
DEYQRTPSPVQTPRFFGVDELDYPHRAGSPGCIAPSSPSASSHAKPVVDPMAPVPHVSNN
SGATVSPPAAHSLGDLNLDTIINAAMVSGDVFASIETVTNGSVSQSQRFVHSSGSFALTP
PENVRRATYNDIPTFYGKAEMRGALHAISETEEEALRSFFAIKGSALNRKLLSGSTLPID
STKTVRKGQFGKLCQDVFKIPTWMKDALFRRIAAAAGVSESAALTYEQISSYYYNVFGPL
TVNRRLFELIRGDSNNEYLTLQEFKDMVRYLVDSHPGLEFLKQPEFQEYYCRTVAIRIMY
SLERQQNGQVRWFAFDRSDLPEVMKELDEKDVNLVLQYFSYEHFYVLYCKFWELDTDRDQ
LVGFDDLCKYGQNSICPSVIKRVVEGSGRPLSSGKLEKLDFEDFVYFCLSEEDKNNSPAV
YYWFKVLDVDGDGILSGYELYEFYRENHQRFLEFSESPEGDLSYADMMCQMIDMMGFSLS
KEHQFGLTLSDLRACPTPSNFFNMVFNAQKFILFEHRDPFAEHQQKMRPEKTDWDRFARA
EYDRMASEAQ*
>TCRU_3280 RNA-binding protein, putative
MGKTLGLSSLELKALSVPSSLRFLLGVEYDVLLCVTEVGKRRSCTIRFPVLGINFQKLLE
LCAERFGLCCTQNEDHSLLSGTAIIPPLRYIDYLPGALHAEELLGCLGVKPVTNPKRYGA
SVHDFLASFIDYSGYNTDASLADVHGTGFYLTLDHGLSTATHSHLVKISFHKGCSLEEAL
REFEEFSGWTTFDIRYEDVDDKLAGGVVVMPSVQDACDLFEKYEDEDSDDEGGLLPFMLR
PVSPLTSVPSVEDSALKRLRDHQWGEIEKFWERFPKWKNCVVVSNLYESASLEEALALFK
DLTVTASSLVEDNSPARRRRVFVTFATSDEAKTALFVDGKSTKGKTLRVQVSPPYLNESR
RGRVLESRPPSLSEPPGQQPATEKRPVSLGSPAHAREKRDAAASNNPEASTPSGRNRSSK
KAGDDKNWNAPVPKSRTPIQDAASAPVPGAAAAREGGDQKKTATPPKQSQRSPIIVASTM
NANAREFVPSSTYQASTTSPEYYHSSIPMAYLDENYGQPPPCYPAVALGPVGMARPMGVV

PRSLRSGAAPPPYSSPPPYSMVSGQSMHMVQPPPPPPPPSS*
>TCRU_3281 Histidine phosphatase superfamily (branch 1), putative
MSEKKVHITASGNVIRSDRPSHLEPPEQIIVVMRHGERRDGAVGSPPEVDPPLTENGIVQ
IAEVAKKLQALLGVKRARKLLLIVSPFLRTLQTAQELQRCAIGELHHQIIDNTLCEVYGP
VRIKSSTAPLLSDVIVKNGLGELPLWGETIELASKRYVNCFFRNCHRYSDKNLLLVTHGD
AISAIMAALYPLRTVYETEYLSFIVFQRDSKSVSRGDLESCQLITSSGVQWLVDGPETSL
AETNTLEADGFSGSGLLVRNSKPPPNAGMCGYGCVDSNVGAIDGEWMAINDTHGTNRHEL
ASVSLIFRCMVIVSQWATIYLWSNKGNAAIYMIMVIAFELVSVLLHFNNLNRLRLGASLS
RVELFHRLTRNQFACVFCGLSPPFQRCTFSLCISLLKGLGIFVLCMAAAFIASLFQNSGF
ISMRHSYAEIFKSVAKVSVFALFFLIDTCRRLSDLEH*
>TCRU_3282 hypothetical protein, conserved
MNADGGTDETTARLVSRLAQRSTLSSDAEPFIPSFLRAPATTTETQHKNGEENAVELKRG
KVLETGLKQLYCNAETYTQLPSVESLATTAAVASTALCTFGSMTEEQLQELEEYLWNPSQ
NNNESFQDDERVFANDDDGMDPEEEEWLFNQMLEAAGVTQIEETTTDEIGGS*
>TCRU_3283 protein kinase, putative
MDRSRSDGEKPRVFSRTSTQGSSVFESSNSQFSMGLGIVEVPPDSKKHYDVSGFQLKKNN
CSIRPPTGNEETQILSFSPTSSSAVSTRPCGPISSSKTTDGQASVHRALFLRQAFFSPIR
SPDGDRGIHSDTRSNELWDKSKQEIADGDVMMSSSPLANFSGSSHLPKARPVDGAAIAVT
SEFVPSNPGRDELEIKRLLPNVKSSSETPFFNSAFPRFSTGENYMGSSYMRDEVDAAAPN
ITLRRYILSRPKPAVRGRGLYRRLYFMLISLVLLPFIFIALLFGLHYWASTNVAEELHHY
AGASLSDDSFCDRNFLELQHRQIGPISKEGFICVMGILLALIIIVIGGAFILWLFSWRCV
ILTYLKTLEFIRRAAPMLTQIEPLGPEQLAGAPKPVPSFFFWHCNRGENNKKEVLSQGIV
EKVVLLGNTLNELKKYIPSTVQSDVISAVLAGHSLDSSTAVSTMERKGRRISGPSPPQED
VLAAAGDLNPLQIKVQAHLPLYVKKKAATFTGGLRHSHGSGNNFGFTQTAGQRGSSNKLS
PPHRRFICPAGSLSSLILSTSSSVTLTAENDRALQSVGNRGECAVSEAAETRITMLNDYG
FSLQQTTFLVCRLFLPKLELNSDASAIRDSVNQVREMSQRFLRIVLRVAKEENGFSFNIC
LDSVIVVFYTPSGTNCVNLFQPRNCALRLVSELSKLESEWAAASSTPLNWGIAMHMSLLM
IGVSDIGSHRFAYLYGEELQLAYRVAELCMILHCPLIMLQSCYDLFRVCMMAVPVDVICR
ETIRGKDRIYLYELKIPEEGEDLDTKREYYKPLTVAFGLMCGRQFADAAQKLAGIVEMDH
NVSRLYRLCEYFLQMQEKGTINTILSPTENYVRKEPRWEPLESKAVKFLDKYCVREKQQC
IHRRREVSGNNEGNEENGTRDYHAARFFEDGHEVNGLRGEKFSETHVRTPSVRCDDITEA
DDFLYSTNTPSELNPSFAVPMSPVIATHDTEVKRTSTIPLQSICNPGEPQQVRVRYISRS
TAASVTFPEVDSGNNDVPHHWTDVRNLQESSKNDGGNEGSKYVFDVYEPLGRGTFSTVYR
GLHPNGNIVAVKKYPFRDRGENNSWAQSVRFEIEVLSSLRHKNVVRYISSFFQDEYLYII
AEFVSGGSLSAIVRTFRRLPYNTIRRYTGDILRGLQYLHKRQVVHRDISPNNVLVNIDGV
CKLSNFGGAVVFAMQRNEFCSNSSNATTAGIFAPRSVVHASDDSGSATGTVILKNCFGTP
ACMSPEACSGVVDPKNDIWALGITLCFCFSGRFPWPEEELNDVNAFVDKVRRGVLSPQVP
FDVMDSQAADFISLCLRRNTSSRPSATELLFHLFVVG*
>TCRU_3284 riboflavin kinase, putative
MQNHSNKAAFKPFLLSGKVIHGYGRGGTQLGFPTANLELDDNVRAQLNPYKNLVLFGWGS
VIAIPGKENCGEGPYPFSMSIGYNPHFHGLDLTAEVYFIHEFAEDFYGAVVNILVLGDLR
EMGAFVSLEALVDAIKDDVRKTEEALQKPELKRLKQHSFLAPSLAPSEELPQFELAVV*
>TCRU_3285 hypothetical protein, conserved
MYRSSGELRKYAQCVFALYCLDDGLSISRFRLAWYVLWGKWPEESVVQMLFDKKDKSTGG
NEDPTREEGGIVGSGGLAEKDKHHDGGTPLAKSFPFSALRRRINEKEFVRFAVTYHDTMG
ADAVGFGVTEEDGEYATVDMQSAFSGVVRARHWLQFHALAGSKGYVTLDDLIATEKVDWL
YPPMSGGSASGLMVEQAGDDSSTMPQDDGDRRLAVLSHVFAIIDDDHDGKLNFEDVTRHL
AKTA*
>TCRU_3286 class I transcription factor A, subunit 2
MPEFGTQVYWHNIPACPPPWKDEEERARTWRISQHIVGAISDQRHLLEPPRAEILAKRLL
GRFAPKRVHRYWGIVCEPYLSPLHGLNMVMSELQVRPIAIEEAKEAVNVVCEDYNAMTQQ
QQKSTQSGIPSQGGVKTEISTQQSNTAAMDLREAPLLQVVKILCASRGLEVSSFSRAELR
SKGRLGVADLLPRRRVIMAFDRSKPKFVFATAVSVKKKKDAEKSTVCYIQLVAPTSNPVP
WRQLLKREIPYLPPNECVVVAVQRHHDDEEYDDDDGDEKKSGDDGPYLGDANVRSEVLLG

GNESDKDDLGEEGDAQPRQQHEGENPQKRHKCGYEDKIDFSDTSKVSESSGSTTASCRSD
EAKRKKFVGREPIFTAEEKLQNDPLFETPVAVLRKLPRKTRGVHDWIQRLINPVARKRLY
AINY*
>TCRU_3287 inositol polyphosphate kinase, putative
MAACESASHAPGDEPIVVGGHKGVIQRGPKAPNDSATITKKSTGWEVLMYLSMALRIDET
MCELAEMAPTLVAILSPEEENSGVWITVEKEENRPLLEAFHEELRKASVHTHGYSEVMDT
ARWSVCLIDVTDGMLLPCVADIKIGYIRHSPHTPPEKMARIKKKRLIQPLAIRLCGALHY
FYRTISNEQCIERETCEKDIGYLLHTEEDHRRCLRAFFSSAVSMKQEGSGNKCGESEVLS
ARLKACCRHVEKLLSFFTSSVGCALLERTAFVSTSLLLLYDAVSRVSDNVGNNDAADVRV
YLIDYARVSDRRLNFAEENIGFLRGLENFLFLIS*
>TCRU_3288 hypothetical protein
MQRKLPRSESPRNDAPSTMSIATTTHGGLTRSTGLSSLSLEEEDSRQRGPLQARSQHVMT
FVGELPWVPHDDTDNEQPPREEDVVTGNIPRQIFIEDENVFLSRFVRPARLVAPAPAEGQ
TSGTNSSGGDGRSRRRWLPLRMDYMG*
>TCRU_3289 dynein light chain type 1, putative
MAASSTSNVTGRRRSGLRSSTGRLSSHSSMAMIPEMEVDPRVANLSRVAVYIDVPDDTLK
KIIDIAVEAYKRFVLAPTRNTWRKEEGARKELERELERTALRDIAEMIKKNVESTFGGTW
HVIYGRSFATYVTHQTRSFCHFQLDGANVVVWRHGG*
>TCRU_3290 WD domain, G-beta repeat, putative
MWAFDSPVERGIVLRAKDSDKCKISPLLAENIHDLEALKEEFAPYPSGMTMDTLFNVLLR
HIGKKRGDSDGFGLSQSNWLASRGETPASPQMSPRGIVKGTVPKRPQKTSMLPAGRPSNS
FSSMPQKDALGALRDGLYMSPWKVGASHQHISGSWTDINAFENLFNRLDSDSDGLVSWDD
IMQLAVEEATQSITIITEEMRSYSLSRISSQEKLVRLVHTLPDHKSVFAIASRADPLLLV
SKEDFSVVKQFRLKDFDNNHPQLIEYLPVPDVLLAYSVNDKTLRGWWNAVSVHRMGTLSP
LYLGDTIRRIRTQPWKFPYSFFTCSSNGKIVHWQLPKQRSLLEISRVHAYEVLHKPDTGG
ITDFTVTDEWIFSTGFDCRLFSTNIETGRSILVGLPHDTIKFLEYNRNCDCLPTVSYSNR
VLLWDVRSSSATPGATFRDEGGRPHTADVIGLCNAPGLPQIITCDSVGMMKVWDLRALRC
SQTLYADGTAMEDMNVDYMYSDQAINRSDRSFLFQALRKGDPKCIRSIGFFPNTQEVVCC
SPEAIYCLRYNHRRDGHTADVEVVHAAFYDPYHSTIFLQGSARTSVWDAVDGFRRRLFDR
SSHIKVPYWQQEVIAVCLDYPRNRLFFAIAGGTVEVRSSKNFVLLETFAMHEVNAQEMLF
SMKHKMLVSISNNGFLTLLHEEDSGHSISNIGLSSLPLRALSLSDEAGLIACCDENTLFF
VDYKQTKLTFFSVKLNVPVRTAAMLGTYPVLATSSDNGELTLWSTPPAEESYTPLVSFFV
GQSSPSFWRRKTVKNFSFSRSSPDRREQAEVSSFSAPLRSATEPDEEYPHGESSDFSEKL
GEKEKQKMGFTNLLEAIAADEKASGASTAISFDDVLHRLFVADQKGSLFIYSCCSFLQGF
GFRRCSFENRSRYALWGMNDDFRTLHFPILLQTLSPHNGYITFMKWFPGLSAVVTCGSDH
LVKILDYDGKETGQLRLDRLPPRSLLDETDGTEIKAYAEKTPQCFTIPFSLPPPFPALKR
CKECARIEVELKDSRNSSLKELAKESLPLPAANMYQCGSLAPLGETELTLPQPSAFVGVA
SEEVNCNRGKETPSPPSVSLRLVALEEKKQWRPRREVPCLFRERKHASATTRTSFSGETV
SGRGSARQMCRTTPLRGMSSTIEWWRPRSVPTPPSFKTKQHRGAPTCSNDNNDNNNNGNS
GSSGIEGARDDFKNFSGELCFSGNSVSPPSPVSLKLPEDLSAEGPKPVLDSSQNILRESG
GRFLKRNQKKKWTFIRTNRSEDETRAEMTEQSGSFLDSVLRTYEKELRRCVRGRNVMKRL
CGNSPTARMTISSPTGHGASR*
>TCRU_3291 Major Facilitator Superfamily, putative
MFRTYNGIRFFRVFLTLWITYAAYTMVRRPLTVARADIQRETGFTSAETSLVDTMFVFSY
ALGQFFYGRLKGRCGNKEMLLRGILLSSAALAILGLSSRLPAFCVAWAINGIAQAAGWAT
CISIINVWVFPKERGRVMGWWSTNMAAGGVIGNAFAAFLIGRGLSWRTAVEAEVGLLLAV
GGVVLLALVEHPNAVGFPSVQQVEGGVEFAKLSFDCNSAPLSKDGEMYMNSPRSTNSSLE
ENMNFRHKDYDDHEEPFSPTFLNIIQLPGLCGICASYFLYQLVRYGFMFWLPYFAVHELN
YTTEFAGYVTCAFDVGGVVGIVASGYFSDWMFHGVGRTRVILLLTVGMVLGSCCLAVFSR
HFVENALFFMVAVTFVGFFAFAIDSLVSGSFLLDHLEHIKMVKQAGAISGVVGGVGSAGS
TFQGVFTAVLISRSWPTLFYGFGVAGALAGVSLIRPLRSELLRARKRSVVF*
>TCRU_3292 ATP-dependent DEAD/H RNA helicase, putative
MSFPQTEKNGITSESPAREFNTNEHGDLLNSAGEPWRGGRFQERGRGRGRGRGRGRYEGD
GEWRRSDNDRERGNERFSWRRGSGDAGGGGDYEGEEGYGGGWPRGGRSGYNNNYNRRGGG

GRGSRQYGPGARKEQWSNWRQGDPKRDAGDDYSEPHRGGGDNYDVEGGRGGRGRGRGGRF
ADDDRELEERAQRRSQGATDDTDQQEPAQQSEGQQQQQPPAQYGRFDVDSYERPRGRGRD
RPYRGRGGYFREVEEERQQQPQPQPQPQPQEQQQRPRVSEDPISTNPSRTQRAPHLRKNCHD
EREIEQLFEHHHQQKGISLDNYANIPVDIIPNNVEPVESFEDLYVEPALALNVAKCGYKQ
PTPVQRYGIPVCLNGDDLMACAQTGSGKTAAFLVPVVHYILKHGVSPARERVSYPIAVIM
APTRELALQIYDEVRKLTFRTDIFYDVVYGGTPYPTRFENDILVACPGRLKDIFDRGIVS
FSRVKFLVLDEADRMLEMGFEEQIEYLVASRYTDMPQTTERQTLMFSATFPQRILNLAKR
YLRQHYYLLTVGRVGSTTKNITQKIVRVQESEKMDKLFEVIYQQKQTDLVLIFVETKRAA
EELHYALKSEGIPSATIHGDRRQFDRERALRDFKDGITPILVATDVASRGLDVPNVAHVI
QYDLPKEMDDYTHRIGRTGRAGNKGTATSFYNKNNRNLTVDLYNYLKEHEQDIPLWFEEE
KENVEGERFLGMSRGRGGGGIGGRRGGGGDNYRAAPTLSNSTWGESAPSRGRARGVGRPQ
NNSNVDDGGF*

>TCRU_3293 aspartyl-tRNA synthetase, putative
MRRQRWVLQRHCSGSFTATAIGRATIRQGTSLSSLTSLGATAAKPATRIRGRVETTRVRG
KIAFIHLRQPPCHSIQVVASAADIVRRVKELTPESIIDATGTLVPAERPVTSASCKNYEL
HAERVDVVSRAATPLPFPIKDCNTRLDTRLNHRVVDMRTPLTASVLRLVSAVCQCFRKQL
LARDFVEIHTPKMLGAASEGGSAVFTIDYFGQRGYLAQSPQLYKQMVLMGDAMRVFEIGP
VFRAEKSLTHRHLTEFVGLDAEFVIEHSYTEVLDVLESTVCAMIDHLQEDHAALVRQARE
SLADMDAAEGSPSALGRNQEKEEASIVCELSEETLGAFGCLTTDATEAHLTTDCYHGRVG
VGSIDTQRRNPRQPKVLRLTFDDAVRLLLDHHVVDQPPTDFSLPQERRIGELVRERYGVD
VYIIDQFPLTARPFYTLPHPHKTESTCSFDMYLRGEEICSGAQRIHDITLLLQNMERLQV
DAASLKDYVDAFRYGAWPHGGFGLGLERIVLFLLGAKDIRQISLFPRDPKRLAP*

>TCRU_3294 Aminoacyl-tRNA editing domain containing protein, putative
MPTSLETRLASLAARFQEIERSIMKLRHMSHGTPNAPSAAAATVTPTVAAQYRDPSELQE
LQPCARDTPEVAALRKWCLKHGLFSARFRWVPSDYYQQSLQWRRDILEAPSIYHLCKSIV
LENTHCTHTDCSHRENSRYYIAVFPYTERFDDRLIMRFVMDMNKGMGKKKFNFRLADPQK
ALQLTGFGHGAVAPLGTTEEIPVIISDRIAQLSPPLFWMGGGHVGCKMCVDVAEFLQVIH
PFVGSFTSPLPVEELERLVD*

>TCRU_3295 hypothetical protein, conserved
MTLSRRQLLCPVLLDIGSSRSVTLPQFHQEVRSSLLREVDRILARQGGHSRLPQQSSAAL
ATSPELWIRPCGFSAEQPLLQHDSWKMPWQAHIHAMRQRGQMPSAAASAPQIGRETETVP
LFGTLSLPLSVRVSNAAAKGEECVTMMMEFFRVDAFIPVHVQMYHVMRRILERRDLWGVA
AVGVVVPTHHTEYFMDAARRMHERVSRSTLSGCDDVPTVLVYNPKGLQFQSP*

>TCRU_3296 katanin, putative
MENDIALQQAIYSSLRSQKKYNQQCQSRSAPVNRQTETIQPRNGLRNALLREGIMPAVPR
SAQTGILAPVAVSHYRFSPPRTECVGSTDENSNSAGSPIHLQRVSDRVPGWTQMCSGGRI
QRQNTLGSQLVFIGTEAHLEQTPKICCSDLLLLRAVAPLPNDQSMSCFTAQVQSLVSPGH
YAMFGMGVTPNAGEELHGFPLILIHFDASGAAFISVERWHMTENDTFERLVVLEPMKALR
LIRDRVTLSLVITSQCMSLSINGELLYPMIVAEGVRLGEALPILLSTGGKIIIRDVTVTE
GDKPPVNRLYGRPSSLTVSPKKSDATKKGQASLEDRHSPGTRASRSENRVPTTKRPTATR
NTTTKEGKSRPGGDSLPSGINADFAERIESEIIERSPNVQWEDIAGIPDAKRLLKEAVIL
PLLVPELFTGVVQPWKGVLLFGPPGTGKTMLARAVATSAKTTFFNISASTLISRYFGESE
KMVRTLFQLARHYAPSTIFFDEVDALMSSRGGNEHEASRRVKSEMLQQIDGLSTESDRRV
MVLATTNRPWDLDEAMRRRLEKRIYIPLPDAEGRMELLKKQTSSMSLDPSVDLSIIATSK
TVGFSGADLNLLVRDAAMMPMRKLIADRTPAEIAAMKEGGKMVLPAVTMRDFEEAAKKIQ
PSVSQQSLKQFERWSEELGSV*

>TCRU_3297 Programmed cell death protein 2, C-terminal putative domain containing protein, putative
MTGVLLGVFDGYMSLGRNALTSETKIGGTPTYFPALSDAEKATIRGWTTCGVCGHPMFLL
LQAFSPLPSAPDLHHRMIYIFCCNSAACVTQPSCSWCAFTLQVDAVDENAAEDEEPEDMS
RCDPLRSSELPPHTFPPCFVEIVAEPKKEIVVPTELEAEMIRASEEKARNAGITEADIKE
LERTIDLKDKPSDHEFEKFRRRMAREPRQVLRYYVRDPLGKKKNGAPAPTASPLFMHPRN
VGNRARIPPCDSCGAALMHELQLMPTCVYYLRVGEYIATGKSAADEGVDWGSVTVFVCSK

DCSKDCSGVVLRRAFVLVEKAPELEDEARETDGRQNLRSFINSS*
>TCRU_3298 hypothetical protein, conserved
MSRDAKPFFRRPTLADLVAGRQGSNVSQESNSAGTCQGVSVSSVGSTVPPVSVNTGGRPI
YAVEEAGAHDDSFARMEQSGQWKLEKINREKLHDMFVKENGIRRDNVIRLLKKIGINSSL
NDAALQVLFKENTHTESSILPEQWVALVEKLLRVREDATEGTAQSNEVLASKPRNDEQPK
SVKAMQRKDTVSSQRNREVLPERKDENKNNVSINNYVLNGTREHPGEVFEKKWITGSEAT
DIALLKLFIHCGALDRKDRGIELLPEDFRRVTYLRRNILPPKPIVWDATSKIADWCLQNS
HSTSYETDDLCMKMSNFLDLLNDEFLDLTGGKVWNDKAANSSPPTVCMVLASLAPVPLQR
LFGKEVVDHLCSPSTVQNVLKALGGSRGLFSTSNEPMSQNGKEFGIPPPLPPPASNNPQR
PQARLLPFSSSSACIIGMGGGGGEGCFTGMDGAGIKKKSPLVSYSVGSRSSSTLRGANGK
NGQPRYMEPRPLDEISASIVARSKARRLIDELRKNAIPINRYECFARIDYVQRAIFDDAS
LGEEEEEEEEEVGGNVSRDAGARAHRRHRYTRYRARPPDVTGPLLPGMYKMGGLGQPLQR
RARQETFERLYRLRFGQVRGVGNGSGYRSTSLKSAALLASRSASERGTLAPGQINPVKVE
DSKKVGCAEERPMQQADDAPTPLYQRRQIRGKMTRRGSRPPLMLANLFAKQIVFSPPSSQ
PPTPNCGTVSTRKGQKRNG*
>TCRU_3299 hypothetical protein, conserved
MSLLTRVAPSRLVPGAKGVFITRPLKKFTPVEVAPPPDAIAPPYLVNLLRMPPHKISLRH
FLALRHQFSSGMYFNVATLGGWYLIVPGSHAPLADPAGLRAWRERHHHRYEQKAAVRRRK
TDEVVTATHGSTAKKSRTTLMDSCDGGKRNSSTAVQGDNDTNMEGENEENEEEEVHAGPS
ATASSSVSFGETVSRASLLSESRIVIPEGHLFEINDGVLWETPPLNDLGNPAYWKHHTAR
MQLYEDTSISAEQVEFIASPLNTEGIQNVSGYTEQERHVQQQRLFQVLTHKANVRLNVDD
NTRLLTLMPIIDLKEGDELLLHYGREWWSQRLLSTLFMSVPDNEMRDIRWIEALFKKPTD
VSKPFPQLCSAVARRKMPKRGKRGEDGKASDVNDGSNVDAATQRDNLVLYNAVTRRKATD
AEALIFAVRRSCVNRNFFTALVGTGGAGVFDVSNCDDEVPLRRLRLTLLQSLHLEHVSAD
MTGVPAERSEVQFAEDEEDGSLIL*
>TCRU_3300 intraflagellar transport protein 172
MQVKHYKTLLASQPGFARVQAICWSPNNKRLAVADNNRFVNLYDEFGERRDKFPTKAADN
SAGKSFVIRGMVFSPDSSRIAVAQSDGMVAIYRIGLEWGEKKAICSKFPQSNGVTCVCWP
NTTQGVELVVFGTLEGKVKVGILKSNKSQSLYAHDHAVVSVANYADGQKVICGHLDGSVY
QYTFDSEEANEVAGSKKIFHHSCAPYVLLWGEHICAAGQNGHVTFYDRNGQKVQNIDYKV
EEEGEFTVGCFNPSGQTIALACREKFRLFDYNLRSRKWEEGIVINLPNSYSFSAMAWKYD
GSRIVTGTLTGAVDMFDACLKRYRLRGAFEFTYVSHNQVIVKRLATGTRIVLRSNLGYEV
QRVNVYHDRYLVAYTSTTLLVGDLISCKLSEVPWRLSGREKFVFENPQVCMVFAAGELCL
IEYGKKELLGTCRTEERNAHRISVRVHEPNDNGGGGEQQARKFIAYLIDRQTIQIDDLGS
GITVARVTHQSRIDWLELNYRANKLLFRDKQHQLFLYDVEEQTRTTLLNYCTYVQWVPGS
DVVVAQNRVELCVWYSIDAPDRVAVVPIKGEVEGIERGNGKTEVIVDEGINTVAYGLDEA
LIEFGTTMKDHDYNRACDLLDQIALTPETEAMWANLAIVALREMKLQIAQRCYAALGDVA
KVNALNHINELAAAAAKASDGLTDGYDHYTVRAELFMLNKEYKRAEQVFLENGKIEEVMA
MWEEMNRFDESINVAEARGWPELANKRAQYYNWLMETGQFEKAGEQKERDGKLIDAINLY
LRGGTPSRAANVVSANDLRPEPQLLEAIAAALFKAQVFEKAGDFFEKLKMDDRAIEAYKK
GHVYSRAVEFAKRAHPDQVAALEEAWGDYLVGQKHVDQAINHYIEANKYGKAVKAAIDSR
QWSKAAHILEGQAVGADNDKTVKGFYKNIAHHYEELHQYGDAEKFYIKAGSVNEAVEMYS
RAGMSDHMYRVAQRHLSQQQLVALFVDQAKQLETKGDYAGAERIYLKVNEPDQAIVMYKK
SRDYTNMIRLVQAYRPDYLLKTHLSLAAQFEKEKNFKMAETHYVAGKDWGRAVNMYRDRE
LWEDAVRVAKVHGGANAAKQVVLSNAMVVEAEDGVRLLMKFSLVDAGIDAALEAQKFDLA
LQWSQLAQPAKLPYVYLKYAMYYEDQGDFRMAEDAFLKSGKPREAIDMYLHQQEFENAMR
VAEGYDQTAISSILQANGRELFQKGNHREAEALFLRANTPEPLLKMYMDSRLYTEAQRLA
KEHCPEMLGEIAKRIALQSNDPKEAGAVLEEHGEYQLAVDTYIGATPERVPNPNVLASLW
VRAVKVAQKHDRNMLKGVLRIATEKLKDAKRYVEAGKCLEDCEDYKGAINMYVQGKKFDL
AEYLAKRISPELEDYVKRAIVQDSIENGGMKDAKVVEEIDPEFALKAYIANNDWENAIRI
AKQLTPEKMKYVAGLQMKYHLNKDELANALDVVEELPLDTGDFRFYDTWLDMAEKLVSMM
PLKAESNLKLDGFHRSLINVSESMATSGQKPEDVERANALAHIIHAYYMAPRMLDLSLGD
YAMKLLLGLPRWIPYIAPEKAFFDAGMAAKNAGSDAIAFLYLNHFLDITEKIAEGATDSS
SIDDSKFDCTDFPKKYLLPKSSSVDVAAEEEVNKWVLTISIESSFDPHLPTTMDPQNHVE

MFEGALRSPAGEKFPECAVTGYPIIGGGLTRCRNCQRPANPEDWNRYVVLGKQCPWCGVA
DSPNFSM*
>TCRU_3301 trypanothione synthetase, putative
MDNTDKQRGVHASETEHVSFGGLIGVTDCGVPVFSNGEKKFFGERISLTLDCRRIEAATP
TTVIGTYDTLGYKWLCLEFARRYLLMTKGVWLASVPTAEDIWEIEEIATSVPTGTPVPVE
REKHGDTTNMPSVGDLLVWSRTEDSPYGHLAVVTHVSDNGVCVAEQNYEFKRWQQGKNYS
RRFDCEKREDGVTVFVGETHLLGWVIIKAPPYDFSLGDLPDKYRHIIGPGHIVRRHLEKD
VLLPWLNPSQRCDFFLKRSLTVGGYMGEDAVAEVHSVPDGFYMMDYDMWCRFRFATKNLH
AVAVEATRLILNSRDSETLLVQYFGLPKELHLQLRRSFETIPSMCGRFDFGYDGKEIIML
AYNCDSSAAMLECGDTQEKFARHYGVELGTSTGSFLYSRIANYFNCLIQNEFLCPHHKIV
HFMIDDDDEERYTALYVMNAAESAGFRAKLCVKLSGFRFGSTTGEVDRDASPTERRSVVD
LENEEVLLVWKTWAWDTVLQQYVEQRTQEGHGVSTKPTLSDILLNEHIRVLEPLWKAVTG
SKAILPFMYAAAPHHPNMVPASFYRTKEIISAPYLTKPVSGRSGKSMTMYDTEEDPEGVA
VAPHTAAAPVLGRPISAVLFDDAPAGTHRVPFDNIQENLTGRLFDSVVVYQSRVFLSRYE
KKYSPIFCGWNVGGEFGGVIVREETFNNTKPSSLVIPSRVVRQHIPLHAMQESTTSGEV*
>TCRU_3302 hypothetical protein, conserved
MEEKKRQRAEEKKQYDPGEDDEDTEDSADDPDHKEGEGQKEGDAGSSKKGKEVNGGGGAD
GTPPDAPVVLQPPSPVEVTDLQSIEEKNDDGTGGERDAGRTQTQEAAGPSKAENLTAELS
TEENAAETETKTPGKKTQREDAGKEQTTIGAKSNPETPAAETEAHNREGVTKEEEDSGKA
TTNENFDGRQTAVKDDDHNEAEKTRQENENEVEKAEETQEEAKEKEETTEKKTVAAKGLN
LNSTAAADDSDSSTAVPHTTSPLLLLLLVVAAATAAAVVAA*
>TCRU_3303 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGGGAADGDGVVSGASSGGVVEAGGGPSVAVESIAVDAG
GKDATSNEHGTRSSEPVVQVDNSSSSNIGQDASHVLDPPVKI*
>TCRU_3304 ribosomal protein L15, putative
MGAFMYLNELWKKKSSDVMRFIQRVRAWEFRHQHTVVRLRRPTRPEKARMLGYKTKQGFS
VFRVRVRRGGRKRPVHKGITYGKPKTSGVLGVKLNKNSRAIAEQRLGKKYGNLRVLNSYW
VNADSTFVWYEVVAVDPMCRTIRRDPRINWIVNAVHKHREQRGLTSAGRKHRGLRHKGHK
ASKLRPSVRAAWRRNNRMVFLRKR*
>TCRU_3305 leucine-rich repeat protein (LRRP), putative
MSKGYTVVSVMKQTQETVINESLIRDCIYLPPACTTEEERLRFVGVREENQRHQRVKTTM
ETMELHKVTTLLASYRRIGKIENLVGLCNLTKLALDNNNISVVCNLGHLKKLQWLDLSFN
QITEICGLEDLVELETLSLFSNNISVIQGLETLKKLTSLSLGNNRIEALEDAARYLHRLG
SLRILTLKGNRVEKQPHYKLRLLAFVPTLQFLDGCVIDPNEVVSAREEQRENLMPVDEED
ERAAEVAKVEQELEKARKDYERFNCPDETNFYDELFHLELDGRGVVELLRVDIIASLSKE
LLEKYQMEFTEKARELTEAMKAIRTRRDEDESAFNTASARYRQKNADACKAIIKQFEKEV
KAHIPRTMWCREVDTGAIPSEVLSQLQIRLREVRHQLLEKEADQYDALESLNAGTIGKWK
GDGIDVILQTAFENFLKMEADFQVALRQLFDSVFEMRQKQEHATDSYHLIKQDESIMAII
DNKEEYQKVLGDWFELRRKRLEEMEQMYISNEEKLLRERSNRILDEEQNRHRARLNEIHE
FVEQMKGLLECAW*
>TCRU_3306 hypothetical protein, conserved
MENTRRKEPPLWLNPAVHVWITKNDIPVVNLRDISEKLRLPRSAFRADEAPRTPDEESCP
AESASSNGEKTPEPTKTESLNALLGIAQRRSEKQTTPPTQLLAVPSNPPASGGSGASKEP
EAKATSFPKTQPAAAMDVEFVQGVNLPGEKNTVTPVQPQPDGVQSVALFHDPVWGEVGSS
YDIDCLAPREEEKIDVLSSLKFGILSENVNKNELSTTGTATTTTATPPAFTASNPMSEMM
YQPPPHPPAMTSSPQQIAYPQGISLGASGWTTAPPPGHGVAVHPLQFVGLPFPFMSQAAV
MAVPQPYRVPYQFYQMHPQAPPLAPVPPQAGAYQTSPNPDLYQIAAQKLANQQSSSPRPG
TNVGAAPFIPGGKSV*
>TCRU_3307 Protein of unknown function (DUF773), putative
MEQQVIAVHYQRMEEWLSDRKAVLGKKHKKEFFRLMELAPKLEQLVRYEIPAQHKQNKRL
SSLLDDAYGSIEDATKARKNLEERKKRFFQEYGLVESQGAEEEDLEAVIEAKIASSTTSL
NEALREFGRSPHLESFREAYVRAAKMYSMGMYDDNVFSLHLPWLDRVYQERFYKSKVDIH
HHEQHQKQRAGERDQVAVKASTGPCNIDWGDEDTVDLVDVGETVEIKWDEEALEVAVEGA
VRNCSENNKRMDDGCEEKPTDTVKGIFTIDVSNAAHRKNILTELQAFACFASERSSMDDE

SLAEPAAAVEVLVKKLTASTEAVFVRMKTTPTLRFSFMEEVRRLQRGIAAASMRKSNSQA
RVHQIQEEIERLGPQLDALLIAAGNCRDECLAELLKMFPGRTVTIVGDINKYL*
>TCRU_3308 ATP synthase, epsilon chain, putative
MFRAFARRLVSRTLPLLQVPNHDLPEGFEFLENKVVDKDIHATHENLETLRFTLTRQDEF
LMRENPVKCVTVTGVNGEYGIYPGHAYKIVQLVPAPLTVEFTDGTTKKYFVSGGFAHINN
EGSCDVNAVECVAMEDLDLSAAEKALAAQQASLGSAKDEKAKAVIEIRISVLESVISALK
HHH*
>TCRU_3309 glutamine synthetase, putative
MSGLAEKRIACRLTYIWLSGRDSHHDIRSKDRTAYLTTEEVAKHPKELLADGIFPVWNFD
GSSTKQALGADTEILLNPVNAYHCCLPRLSTTVPWILVLAECYLPNGEPTNDNSRAVARR
IFERAPEEHPWFGMEQEFFLIKDGHPYGWPPRGFPAPQGPYYCSTGCLCVHGRRYVDLHY
EVCLQMGINISGTNAEVAPGQWEFQVGPCEGIEMGDQLTVARWVLLRILEDDGLDADYRA
KPIRGEWNGSGLHTNFSTASTRNENGLRVIYEYVERLKKTISKDIVLYGAENNERLTGKH
ETSKPNEVTAGVGTRGTSIRIPNAVAAERKGYMEDRRPAGDADPYLVSARLFASCVCIES
PELDLISSFHERNWMKFGDLS*
>TCRU_3310 hypothetical protein
MELCARNPTLILCNGGRDPANRLAELMDCSSALLWVSMPEALQLSEAKRRQSRSRSPGFH
ERLWAGLCIGARRIVVIPACHGLASAQGDRCLFSGGIDGPSHPSHVPHLSLSAPPPWQGL
AGLHVERGSLG*
>TCRU_3311 BNR repeat-like domain/Protein of unknown function
(DUF3676), putative
MRHKINTESASLRVPGLVKVGDDVFAVAEAQCGERNGAGSCAGILSKHLNISDDSMDILT
SDISLFCMQHGDTAASSFWKTEVLRPTTLVLEDSVYMLVGNQSRTTPPVEGPNERGLLLV
KGTVTVDGGNNKKLVWNETHVVEPQGKGKSHSLTELIGGGGSGAILRDGTLVFPMQAKNK
DGTSVLLSILLPNLGRKWELSLETPGNGCRDPTLVKWKENEDEERLFMMAHCAGGYYDVY
RFSESGVSWYTPGEPITRVWGNSHNRKGHGVQSGSTTAIIEGKEVMLITAPVYPKEENKG
GKGRLHFWVTDKARVYYVGLISRENDDAAASSLLIKDNNNELISLYENKKDGAYNLVAVR
LTEKLERIKEVVKTWKDLDGALKTCSSGSSATVDARKKRMCNGRVPTDGLVGFLSGNFSE
NTWSDEYLGVNATLTNGEPRVRNGLTFKGSGAGAVWPVGDMGQTVPYYFANNEFTLVATV
SIHEVPESGSIPLIGVRMNDTSSTVIFGLSYTHEKKWLAISEDPANVEGFDEWEPNKTYQ
VVLQMDYDWTVIVDGEEIDRNRYNKNLFDSHRISHFYSGGDSKDQSATGGHVTVTNVMLY
NDDLWRDDLHKLHASKVNIPSLGVEEHPSGQVTSTDVSVASESKSAESATSHKELNENDR
VKQEENSVDDLVLAVPFSTFVAGSYVSGLATAAESAENSRPENNVQLSEGETSWQATLHE
DNKSMQRDSEVEPREIPSTKSTEVADVEGSAEGYDTPQPEEEGGTNDSSGGLTSSVGASS
DMDTVAAPADGEHQVQQNIEHSAENDDVRSTGTVTTGAEESLSLEAGGQKFRENNGLRQQ
PHSFRD*
>TCRU_3312 hypothetical protein, conserved
MTEAAGRTAFRLSLSMPLDPLHCHLTPRTAELPVGPHRTAAGSLACTCRAECPATEHGLG
HFPVPRLAAASQSPTRVPVATDSLSAMESLRLGPLETHDDVSEEICTVPHSLAD*
>TCRU_gamma, conserved domain containing protein, putative
Elongation factor.1
MRCVTARLIRGWLQRMEHVRQYLLGVALMIGEERRHDVALWVLCGRGVPAIMRDVEDTEL
FDWEEVADVAAQRKGPTDCLCWRGAC*
>TCRU_3314 Vps23 core domain containing protein, putative
MGEDELRRCMSMDSLREHYSQAAATEINKYISDFMVYLGNFGNISCSFSMKANQRLFVLQ
CPLFVTPPRNDNTGAQEDNKEFPPLFVEVYFPPRFPSVPPCCSVNSTNYKYKNVEKWSIR
QPSRIVTSNGSVNLPELSLLSGATPPYSLLEILLALTEQFEIEFPLIPANQVTQSKANTQ
TQGHRRPSTNTSSERRSALERRAAELLMLHLLSKAEGYLDTREQSLNQFERLYRCGGAMR
EARGLLEEKKTELLAYSPAVDKVEDLVGRLTQLPDNLEVHSTCIEPMDDLQTHALELLSD
IHALDDALELLERSLKAGQLSCEEYVRRVSDMGRKQFEARFLFARVAEAVNRSSAKTAQR
LPSIPPRVYSRPVLGDEPIKVPTKLNSLDLLLKEFPEVGSEMVKAVLNVVDGNLSDARVQ
LRAMLS*
>TCRU_3315 WD domain, G-beta repeat, putative
MKEDSSPDSSTDAIAEARRLPLPLPPFEENPNALVLHHEASKLSNEIHFSAPVAPLGMDE

TENTSMSFSGKLSINMAEANSEKAMHDGAKLWGDDKPLKLPEISTATGKSEVDSDAELPS
RQRPKSWKEDEVTTQTALASQLHRATFIPLVNTHHPLDTHSRVFQSGRNVRSRPSVLDMS
LLTIDDPHEEPLGSETEFYSGATWLALTILGMSPLHPNTSIVHPFVRIWLVNGVTGSNLV
QIGGGVAPFVLTHPIDLRLRGTRAPWWGAKFNLRVQSNIVHDVSSNAVLLLEVLEMGTEN
ICGFSLRRDGLYPICWGFLRLHDAHGRLNTRNRLHVQMFPFPQRASYLTKLMQLLPSFFF
PSSFSFSADAIRTVAADGSPASPNSYHGVPDKTENFSFKTSTPPDIFFVYRDPRNRKVPY
SAGMLISLEVNKDAHHPGETAIFPYEEYLLNQMSVPNEFLPKSIVHSLSPFSHPMRRVRD
VSLSLVNTAALLKSYLREKEERVLPPTDVLQRVQLRGRVSCVAFSGGTVWLAVGVTASME
HVVQLRHVLMPEIPVIREFRGHVGHIHHLFFRNDDKLLLSCSSDKTVRVWRCDFLSSPMD
ASRDLQSSCICTLPHTFPVYDGIFYQSHIITCGYDPHLFLWRYDKEHPSSLEEMRLNSTL
LRSTCDSRGNFLGSSIFKTDLAFSPGGESFLGELLCKTPCEEEAIIYSVCASQLHRVWSV
DAFGNLLVWRVLYEEAKDGKRIWKMSLRRRFKCHGATRVESHGGRVLVKCDKLPVAYLFD
DSSQQLLHKISFHQKPYVPAVTLLPDGEAVVAGTNNGRLLCWECGSGILCTPGDGYGKAQ
VNFSIRSIAWSGAQQLCVVLGTEVGIGHVIHGTETTMTLGAVIGTPRTMESVILCKDSSA
SELFRARFAGELPAQQRNRAFSRSTSVAVNLATDRNTRFYGVSRASDKNVSGDKETRIRQ
IISMWRGFVGQHSRKKQEAVGEAQSDPTAVYIIEDR*
>TCRU_3316 T-complex protein 1, epsilon subunit, putative
MSLAFDEYGRPFLLVKEQAQKERLTGVEAQKSNILAAISVSNVLKTSLGPRGMDKILVTQ
DNDVVVTNDGATIVDLMDIDNEIGQLMVELSKSQDSEIGDGTTGVVCFAGALLEQANGLL
DKGIHSSRISEGFEKGCEVACKRIEEISETVPVSREEYNYLLQTARSTLNSKVVNRERDR
LAKICVDAVLSVADMERRDVNLDLIKVEGKVGGCLEDTCLVNGIVLDKDFSHPQMPKQLK
NPKIAILTCPFEPPKPKTKHTVQIANAEQMSEIHAQEQEYFRKQVQLCKDAGAELVICQW
GFDDEANYLLFRNDLPAVRWVGGVELEMVAIATGGRIIPRFEDISGSKLGTCGTVREVGF
GTTKDRMIFIEDCPNSRAVTILIRGGNKMMVEEAKRSLHDALCMVRNLIRDNRVVYGGGS
AEIAASLAVLNYADSISTVDQYAIRRFADALESIPINLALNSGLDPIKALSLARIVQVEG
KNPYAGVDCMDCGTIDMKQQQVFETLQGKCSQLRLATQVVKMILKVDDVILTHVEEEQ*
>TCRU_3317 protein kinase, putative
MLDEKLYALKRIDVKEVTEATNAVERQGRKRGLVKELNMIRLQRSREPPRHLMQVFNAVA
TLDNERQHLYVLMELMSFSVEDAQKMLSRFPVHEMMKMTQSTFRKHLAGSALVQKQTEKL
LKQQSASCMHLTGRSSYNVPEDWELSIDRQTPAPEIILSILASDVLKGLRELHEEYSIVH
CDLKPANVLLDFNKRCFKIADFGCGCQMDPNTQLVRRTGVDLGSKLYKAPERLQNELAFA
EIEDEMLLVEFTPAADVWSLGIMLLELSNGVNPCSSFKSDYWNYVNNLKLSRMVKPLAWS
SAFYDFIVRCLVRDPSQRWTVNMLLQHPFILRYSGVPREKLNSFMERLKNESETFQRRQQ
RELLEKQILLSTGKKAHDRYQKQSWTRWKSFTGFLSVAPQFHDTEKFPLLS*
>TCRU_3318 septum formation protein MAF homologue, putative
MSASHSNGPVMVIGTSSRRRADILVEHFTGVYKEFITISPEIDEKEWRSTDPFDLTKLIA
RAKMQAVLEKLKDMHPAPKHGVVVTFDQVVVKDGEIREKPTSVEEAKKFIASYSNSSVRT
VAAYVVYIIDSGKIKVGEKETVTYFSAYNDNVINRVLARGVCMNTAGAFVVEDEDISCHV
VRNLGTLEAVQGVDPAALELLIKQD*
>TCRU_3319 hypothetical protein
MESLLRRLQTVADVNDDDIDSLGVLEEEEELHNMPTDRGELQRRLRHALSRIRRASERWE
ALQSESCKIEFELAALRQRFITSRKTWLLVHQFDRKTIEALLEERFNAESKGQSVTLDGN
GNRRNVKHGTDGLSHDITYLSSLQEQTATLKELLCKYAEERDKYKLEAQKLRALQGTQGT
LSEGGPIATLGKYSENSPFKEDCTLQDYVEQLEVELRRQSELMSEMELQRRVHWVAWEDT
RGEREAQLQPKRKMERGLVASRQGEDAGNGGALSNFLDSTEFLKINTMESSCESTAPAAM
KKRDGDEKVNLSLDPTSNAVEELLKRLEESRAESNAREEALNALYEDVHFLRERNNQLEQ
QLADVEAQLEQLRLDMMMTQDECRLEKGRNRELMEELECVQQQLQRQGRELVSANEEKRR
LRLQASFPSSCGEVHRAFLNMNSLPNVTAYGSAESVSGCGSGSVRNGKQIVDGVVPSMHQ
DVGRTPWGGVKSGGWLDQNRTFRGVMFLIGRRRRLIIGFFLSLFIAMALIMQARLGAPVP
DVVLSQLQSDLRACQTQLRLRDMTN*
>TCRU_3320 vacuolar sorting protein, putative
MVLVLVVGDLHIPQRAAAIPEEFTQMFSPGRINIVLITGNVGCREMYDYFRTVAPEVYCA
KGEFDQWSHTQLKEIHVITVEDLKIGLVHGHQVVPCGDRDSLAILQRKLDVDVLVSGATH
HCKTFEFDGHLFINPGSITGAFTPAHLDVTPTFVLLDIKEKTVTSFSYVYTRREGAAGGE

NFTIKRKVWTKE*
>TCRU_3321 dynein intermediate chain IC70, putative
MTDVSYSYSRPRREFGRMPEFHANEGEILSDIPPNRTVKNYYTKLDPCETEIQNVPSLSE
SSTNTERIKLRHRAQSHVEGGWPHVVDPTEFEEKMKYCKKVEREESYLSSCRRLVQQCTD
KYIKQNNAIDIYGSYFAEGAPPEDESLGPASAKIVSVFKDPNTEKRTAAAISWQNDGRKF
AVAYCRLRFQSSTPTMNTNSYVWDVMNPNTPVETLVTPSPLCSIEHYLKDPHIIAGGSWN
GVVQYWDTRQPTRPAARSLIEESHKDPVWSVKWLQSKSGELLSVSTDGEVYVWDCRLPDK
PVELHKLPEDSLTLLPKSNEGGSKGILGGLCLDYDPQVGGPSKYMIGTEQGTILSCNRKG
KTQAEKIGPNTFNAHHGPVYSVQRHPYFSKYFLSVGDWTARMWFEDFKFTPLFSTFYHTS
YITSGAWHPVRPGVFFTTRMDGYLDIWDLMLRQSTPALSVQVSDYALHTAKPTVEGRHIA
AGGIDGNVTLMELSPSLQTIMADEKAAIGQMLENQSIRDKNLDRAVKEKRAVAKQRQRRS
THVQAVTKEMEDLDEQLEKIEQEYSASINEERDRDLRLQEELEVQRRKLLEEVGDGIDVD
DEK*
>TCRU_3322 Mucin-like glycoprotein, putative
MMMTCRLLCALLVLALCCCPSVCVADTDTESAGVPEDEDGGRRADQLATAVVSPHEETVP
SGLPVKEPGELQGTTTREGKRSTDKLPKSDEADDTVQTKGKNGTTGTETDKNTSTDQTNA
PTKTTSTTTTLASNITTTTTTTTTAPEAPSTTTTTTTSTTTTTQAPTTTTRAPSRLREID
GSLSNSAWVCAPLLLAASALAYTTLG*
>TCRU_3323 Mitochondrial small ribosomal subunit Rsm22, putative
MCIRFCRLVQVFRLRGSPIVISAAQLNQRNLLSSLSSSSTVSEGGHHMREGAMHQPGESG
QQAGSSSTIAGKETWSQFSAKMRHGRRRIRVIDVAAKMSYEYQMLRKMCKRRPSMRQWAV
RDDFCDMHPGVVVMSPSMQAAFMKVFRLKDKGLIRQCMRDIIPVIEYRNREEPMRLQVNA
AEMIPENEPDTLNQKKRELFERREKGENFAELRLHDKRSQAKLRFKIRQRLLKFQRQLAV
ANAVASRTVLYSADDAIGYFLFRGAAMYAGMHRVFFELSKQLPHFVPKTMLDFGAGTGTA
TLVAKEVYDPGALAYPLYRSLRQTMQGNESSRIHQLAELRYDLKRLQRNNAEKKKVRFMA
VAALLERGEVDPAELPEDLRREIAEVAAAAAAAKKERLSREAHARHRDVVDGTEWESGDP
LNVEHAILEDPNDVMDGEEHDELHDGGSIHKKTWWEQFVDLESETAQQRAAKRLRPLQEV
TAVEPSPGMMEIGTMVLHDDVPNVIWKRYLLPEDEVIQHDLVVAAYSLSEIATVENRRRV
VQQLWKMTKGVLVLVEFANLNNFNLLMEARDCLLEEKDVGLWDWQPTIVGPCPHEQRCPL
RHCKAGVKRKRMRVCSTEAHYRATFVEVWARHMPLKVGVEPISYLIFARNELVPERALRR
QEQMKKAEEAKRQERDAKQRELHEASLSVKDVVFERLSDEALHRPETGVPTPLQHALSTD
NVEPLTPLAEALRDGAVSTGEVGHMPTDVPRLVKTSNTRYNRLIFPLQMPPATHKFNRAF
VDAGYQRQRAITPAEMLVVRAEVDRMRERVMRMAPKYMRVVRDPRCCGKVQADFCTPDGD
LVTGRVYRRFYGDRNRVSAHSTMRWQHIGGWKLLKRLKRGSLFPHDVPLYAVTKHPQVEF
PNTLLDARHSIVEQTAMQHNDPLSLVETPDDQLDREELRLKRRAQRDAELLQKVEGKLEE
LFGAKVKHDTDLGNGRIDSRREITEQEWADAVRRAKIRTVQHTKNAVPFAAKQRAAQRAL
QMRRRNIKREMASNRRR*
>TCRU_3324 hypothetical protein, conserved
MSDGSEPQWLVARLGNLLTAWTKNGGSSELAVQLLDVYWRFMRAVHHDVVLKETQGAALA
TAACIPVWEMLHFYGGSFGPLCGSRKAFAVTLLTALYPKTRDRRCLYQHLGCITGLGFPR
VPLLSRLPMWTEIMKCPMDGGHESDAYSEVVAYVKNTVSAEACILGGSSLHSLKVKIKVL
MEDVLPQCQFVRGEAEAAFVTANCPSAIVISMSDEPSLSIRSHEVLQQTIWKYLILLHVH
LPEERRTLSNYLTTSAWSQQSLKLSDDSVVTYAAIMAPIVHEAAVCASLMPSVASDASDN
APLIHPRVLEVLLPEEMASKDPRPFREDLTKAFVADRIKKRKISVAQSTVVGVRELLAES
IPQEIAFFGESSSCRDCDKLTHFCRNVLLSPVTGNTVAGGGLSLRVMRCMLFSRKRRRDD
GFYEGPVFLPVVSSLFEMLDEKAENASLSTLERIATAPGFQ*
>TCRU_3325 hypothetical protein
MAGAASLLIFVLCVPLSVRAAGSVRATVPALELFRVVFSGSDWQYVYETVAQHHDTSVGR
AAASTLINPVSAAVAELLTTSLSTPPGVTGLSVRGCEIDATGGLSVVYAVTRFGGGGELT
NTQINNLVRTADAFYLRSFYWRNGGRVTESIFVRDATLSAQRETCDLGCQYAVGVAVPIL
CCAVICIPVFISLVSARRASLRLDPPPPPPPPCAQVCCSRHAATLTSSYRPFGAAASSES
GGVANVSLIAPEYVPVTEGLEGCPTGYRPPVERTETDDVYYTRVAQQAFEAEKRRREDEN
CWRRANGLPLLPEPSNSTRKPRVLVVEDRQGTVQDTVMGLDPEERAAVGCTTPEEQRRQQ
PRRFEPHVPLRDGVAGVSGVLQAAESFHASVSTMDPYRPNRRPVVPSSTVVPMHALGVRH

EQPRPSSVASVLESTGCGAEHNTPANSLHTPLPMTSGPEDPQTGILPLTAAERRKMPLRD
TGLIGGEIVARAPSASEVRGPSNGVRSIVRPFLTEGKPQW*
>TCRU_3326 transportin2- like protein
MNSEEIYRPTPNDVVNVLRLLHDNGVSVQNSKKAYAELQQYQANPSFCILLSYVFGAEAC
PIQELQLGGSWIQYRRLAGITLKNNLEKSQYSLGLVAVKEAARCTLSVLGNPSDVRIARV
AAQIIVKITALTSFGWWQECGMGNLSHLLLNELFEAGDLRTLSALYTLQYLMEDLPKEVG
AASKDIIERVVTLVLDQNTKTNLQKAAFRMCFNIYEQAEQLDWNVEGLSPLQTGLTAASG
TFAGVCTALLEQGCGGDIPLLIQVLRSCAIMLEYLDYFTPMPDAEMTKLIDWWIRRTIDL
VSSRVDVGEYNLQLKTAAMDLLTAALKLYDRMGGNGPISFLMEPIPLMLPDLVQALVTCV
PMSIEEMNGILANDDYRLRDATAVNYHLNEASKDISEDTFMDDDCGAATLRASALRCIDA
LCVFSSKETFPHLIEQIKILWGADRQLKEASIVLFGTIANGCYTEIELTVPDIIRQLIDT
VMSLSEDIFVVSVAIWSLSRILEWAFICDEKILSDIVAAFVSRMQSTSKRVQQAAVSALN
TAFVTGHNMGATARLVETFPYLSESIIACLPIYCDGNLSLLCDLALHLIAVAEDLNMTSR
IGAAFKSNRIERIKYFETSYVALYINGVPNTHVDKDIFSIDRFVAGFLTRFPDSETSLKI
LGVWHAALKDAAERDIREDEDLLCNMMLTCCNFLGVTSTAALTEWSRQTQGSLASLGFQF
LVTLPKQTVKSAAVTLLHRLLKFIEKSAYPNGIGEKLLVALTSSIRAIDDSYDKLDLVRL
ITLMVEMYFSEFPQIASVAFAAAVDALRSDAYNDSRWLFSQMAYDICHTLDAVPGLLVQS
RPDEISRIMAQAENTCDKSSATISLMNALLSAEDIASAIFPDVMRLIYSWQQAACNFPGT
REKISSMLLFYSSKHGEQLREHLSALHPNLREMILSTYSIS*
>TCRU_3327 metallo-peptidase, Clan MA(E) Family M41
MRRYYGKFESVLRQQTLALRFKLSPGERLTTVIIPHSISIQRRSYHDYSRQTAYPPPPSP
SSMQQPPVPPYVYQGGPPVPPIFNNQRVNPTGFLGAAVPELGTKERPIFVLSAPQQASWA
TRLWLLLLLGIGFSCILNLLDELSTRIQENNSSVRASAISRGAITGMFGSADVKPVDLND
LDVTFDSIRGCDEAKKELEDIVEFLKDPERFYYLGGRLPKGALLVGPPGCGKTMLAKAIA
KEAGVNFFYATGSEFDEMYVGVGSRRVRELFAAAKANSPALIFIDEIDALGGKRSRTDHA
YSRMTLNQLLAEMDGFSSKESIIVLAATNTPDALDKALTRPGRFDTTISVDPPDMKGREE
VLEVYLNKVKADASVKAQEIARGTTGFTGAELSNLVNIAAIRAAVLHKTAITVEDVEYAK
DRVMMGAESKKIIPEEERRVTAYHEGGHALAAILLEKEGADPVHKATIVPRGNGIMGLVQ
QLPEKDKYSQRKKQCLARLKVCLAGRVGEEILLGVDDVTTGASSDFHQATQMARNMVRRF
GFSEDLGFVDYESSDTPEGAYMSEETKRKIEKEVASLLKDSYKEVKEILLVHRKELDSVA
QHLLQHETLSGEEMKRILKGEVLPARPTKENLQASSTQKPPKGSDGMKGRRRPVPIS*
>TCRU_3328 hypothetical protein, conserved
MRRVHSQLSISSLAGGPLSSASCRCPPIAACCGTQARHCMGPSREKQRSRPNADPGTGNQ
MSLIEPPDLTQHIQFGMNNLEHVMVPEVPEERRNRTDVEKEHEMRSRFGEYGPGERLTKS
SQQMRRDMLQEQQDVDGLPWEVRWRKGLIPTAEEMIQEVRDRFDLYIQDPIEREQEWYLH
WKDRSFKIQKDRMIWPQGYTDYLDHYDEHGRRRVLPSDQRWSDTSWKHLADTKYKDRMWL
IEGEERKAVHESLREDRTLMEEEEQRQLEMGNVYNGIVSGVVDLDPEQTYQALSGTADPL
EVARTKMKIQAYGAKQALQDGRKPGALEVDPISGFPKADMEPLPTGITVEQGASIAAEAN
IRNEMLEQTADMARQAGHDAVPVLMKTHHNTSKQHGDRPVLRSLVEKKIEETKRLQKTHG
ACKLETMENVLHNIESKIVPTLDAQDKGALPEEDLLAASKANSTSQYGVLESETKKEAPS
GFIHVTKRPQDAEPNIPVELYNTPKEYETETIPEWYRETLVETEPLIQAYDLTHDPLETR
EAVKVEYYQPPKLTEETRITNDEAIGGISAFDEMKMHKLQSLPELVEGYKPLPLFRELRK
GDQKEGETGLTKGATEKKKSEKLRKERQERLKKAKVQYDPDILLPSLPWETDSITDPYRG
VAAEDAVDFNKPDMEKTWRAYRDTFRQSMTEFGSLTQVTTEEKCEQMLMDTMDRFRRGDV
GEHPTIPEEHEAIFRMIFEAHTKHFLADFYKFKGNRVTEAKTTKAEADEILRRASAKCKL
LGPSFMNFIQEMTSLELDSVRKNPAQRYVIMIRDRKYESLGKPFMNWITNELGEFILTEF
KSVEQLETNLEFLRKHVNDAKFKCPMRVEGVTNSARDAAVEAFFQWCRGALCFYAGKQLH
QMYIEFADTRFRTRAEDLFEDSIECFSNYAKAANGVVQIPIPDSDPPYEYDEKEFLDGEH
AVYAEISGQLDKAEGLWHSGTSKRWYPVTDETEYMWYNERRGRLTLAMDISDRCLENVNK
KTHPSIHPFPERARPFLEGAPLTQETAEHLWMRHMGDLYNEHSEFMFRQGRFQTGRSYRE
KCLNFYHLAIRTARERLPSSWKAPLLTEAKYLMRVYEPGCDVERHLREVEVVVDKLFAAK
EPRHWLEPFSDLPYRIALVHANLAAFGECITNRVNARLKNRPSNELLLRGMEKRAHGGAY
LPELEEYFSVANEVAEEVFRKKVLRWRSQEHEGSDPYLFWTHLYFAFRVQPKNADEVRKM
WDMYEPAYLYIYTQGALASRNRGQKLINDALRRMCQILLSGDESEKKILLRELTNVREKL

AHLIDRRELDRTIYALQAHLADPTHSTFTYGSSLLYRDAVRHERIANNPNLRSDIAAKEY
AELQKRRESLRAHETTLSPQQAAKLQERQSSASSMNEEALGSQPDLSTREIFEAEGR*
>TCRU_3329 hypothetical protein, conserved
MTGVGGGVPFGDFLREVGHGIDTHTSRMREDILLLLSPYIGEQLRLMRESLRAEAERREQ
VLMDEKREIEASLIVAEENIQKQKKLVQALALTLGDAHKRLWWRRRFRDWLDWILKKRQQ
RQLCRTMIQTGNVMRKYHFYVQWRLFAASRRQRKHALAEESRWSRREAELLAEAEALKGI
VEEERRRSDGLEEKMKAAFVRGVCALNKEAVQVLRGAQTVEEEVEESKGVPPRLYDARTV
RLPSARTSHTPSTTARFEGPPIQKTTTATTAPAATATITPIGPVCSQEGYSYQYTGVPQQ
ASSQATCPVHHFCPPGPPCHVCYAPDTCAYNVRSSPHQPFVVSVDPSAVRSYGDTPASQR
PPHVARRSGRTERPRVSR*
>TCRU_3330 hypothetical protein, conserved
MDRRLNHTVMTHVLDALNVQRKSALLSLPFEAFATTSFTGNKTSSSRLLSGQLDTEKEMM
PFVRDAVLRAVERSPQDCGGKKTAEWPEVGTLMEGRRLVGIDLACTRLSGSFNRSDLSGA
NFTGAFADHSTFNLTRMQGCKLAGAQFHSCTFLASDAAGVDARRGRFSQCVFCRANMTDW
DVRGATFYCCVFKLSDLSRWVYDSQTTVVEPVDWGCCRRLGWMTPSEDCGDCLVVGKGGG
FPSLGPREETSPRN*
>TCRU_3331 hypothetical protein, conserved
MLKIENFIRILSAMYMTQDNETRRVATMEVLKAEDQMNSDEMLQIGMGLLRVSDHGAAVQ
AYGAVLLRHAVASGCLAAEKVPCGDIMMWYLNEPSLGRLLCGDLVDLITECMIYEWPERY
THLMEELCPTQAQLSKQPRKLRLLRALVVRFMDPHFGNVPVSRMKKLKSTLSSCSRVILA
EVIQALFDLYTAAGGEGSHQLAESALELIVDCLTITVHVASSLAISQWWELGLGNALSVL
VRWLPVAPEALAATAALLRCDGVSTATATTMNQQLLALVTAVLDCVEAYVMEVNYGILEE
IMELLLDLPDSIVQAVVAPVSQSCLVVLRVPSIYLATSACHLLKRLGDAAFAHVSPLELM
MRFASLIPKNKFHPEFGTDDEGKRLSEQQYGSIEPFERGFAEFRSLAGHLLTSLARIYPV
VSNQFILQILTTLCDGRGTLADPRTQSGFVTQQSLTFREWEATQFLLTHLSESFKYSSDY
VSQTIAALIAKQTEDMVLYPVYLNMLSSFWSCKDDAALGVWDGTLNIIFSCLCKRQKDQY
DVDELSARKRAVTLLVTASSQHAARFVDLCEPFIKRIEQLLMMPSTTPHERNFLYEAMAA
LTSVLPADEGLHRLQSFFTPVVKMLIQRVQSLDQMKFNSIIVAQGSDLQNERNMLRDSVA
IVAGVMRRCKTSPYLVESFTEWTPYIVRLMEFVHGLRADQLPPEYACILDMDGGVREQYL
PGRSRKSVPRQSNKEKARTALMDLRMSLYQVVGALSTFLPSEALRGMLQMLTSSAELLPT
HTMRSLIVHCVFPIGTSHTDLIASILPICGVFFARVARRISARPEDEIIDTKQLFYFSKD
IFTFMRQNILEKNLLSGNVPLTNLVIEVALTILESGSNVYDVPRFINATIDVSRSGCSGN
SAMEAQVEEFAVLAFGRMLEFSVRADDAVLSFNDRERLVFFLSDTYVDRYPTYTAALYSR
FSRDQIDALHTELVMTNRFDTKRRRFKEFVLQEAAKNTRIS*
>TCRU_3332 dihydrolipoamide acetyltransferase E2 subunit, putative
MFRRRVVQQLSSAVASLRLLTITPIPMPALSPTMEKGKISEWVTKVGDAVASGDTWCKVE
TDKAVVSYDNVSEEGFVARILVQNGEEASVGDTVCLIVDEADGINSDEVKNWHAEGAAPS
RAEEPSAAAASPSTGPAAPVTTSPSTSGARVKASPLARKTAQELNVSLEGIIGTGGGVGR
IVKKDVEAAAASGSARPSAAAEAAETKVQSIPKQMPAPDVATVAAASKPTPAVNDNYTDI
PVSNMRATIARRLTQSKNVDIPHYYLFEECCADNMLALIKQLNAKGDGKYKITVNDYTIK
AVARANMLVPEANSSWQGDVIRQYNTVDVSVAVATPTGLITPIVKNAQARGLADISTEMK
ELAKKARDGKLQPHEFIGGTVSISNLGASGIPGFTAIINPPQSLILAVGSAKPRPKISFN
EETGKYQVGTEVEMAIKFTASFDHRVVDGAVGAEWCKHFKDAIENPLSLLL*
>TCRU_3333 hypothetical protein
MVSKGKQLSVLIAGANGSIGRELVSLLVSHPDVGRVVALSQTPIPINRWRSSFPRIHPGD
ALRCLSVVSVDWDKIAADAAHVPASYVRAGVWSNESEANPGLLDAWRRIRGSAAATGLRF
SRPRNNGVKGNGGPRKAARGSNTGGPCGGRGGEKNGTNRGVNGDEALGRGGRNASRFPTT
SGSRSKAGYVKMSMGDPTASAEARNKFLNELLETNFYKSVFSGHHVVINCLSSRNRFMRS
EVNAVDHQYAIAFAKIVRIFNCMVHAEPSEEEEMLMDKHATKQNSVLWGEIYAACYGHAD
CRWFYTGEELEEKRDGEEEDVLPTCPEQRLSRGGVGTLRQFTQVSVMGGSLWNSLPYFRA
HGEFDKELLALFNRNEDDIQDNFMQRRGTRGDEDDVDDDRDYALGEEASVMARRRAEMLL
RRDVVKLWDNSHLTIWRPGLLQRDNLQLVEKILGVFTSRVDVKHLAEAILEDIIASLEDE
RGFNEVGTAKVIGGNNVVVRAKMKEAEMEWSWHGKRIVTTSADS*
>TCRU_3334 methyltransferase domain containing protein, putative

MANAGDAQEVSPVRLVEGDVLEREHVLKVYDAIASHFSSTRYKAWPKVQAFIESLPKYSL
VADVGCGNGKYFTCAQCYRKATVTHIDDVGVTVEADDLEDACRYVVGIDLSEGLLRLAQE
QQKKLASASQVISRTDLLRADGRRTALRGGVFDAVISIAVIHHLATQAGRVEAIRELLRL
VRPDGLVLISVWAKEQPRKRSRNDEADVLIPWEMHEKYDKEKRVYQRYYHLFVQGELESL
AVEAGASVRESYYDKENWCVILTPT*
>TCRU_3335 hypothetical protein, conserved
MRKNNRRTEAQAALIVSPEWLDRTADAIASRNGVLLTDCVTIAEEGEATELPSAAVLKNI
EAAVEDLRCTLMERVESSHSRHRGTPGCCADDVKERQLYVDVLVRVAVTGALARYQRMEP
QSGHSNGAGEDNSGGEKPPQRYFDTLARGMLHVFEAFQEVHSMQRSHYTPRRRGGSTVGT
VGWDTLLLLHFVHRIPRVARDASEHVIDEATGQIVRSWRKLLLSLQTADPQESPEHSRRR
GALAVCNGLLSILFHRYNTHQCRILVNSVAQSEKIAESTGDWGKSILRPAQHMIAEVVNF
CYYKGRIMLYDHRFEDAYDALRKAYYLLPPPGEGTEVQQRNKQRVRFYLTVAGVVHGKVV
PEEILRTDDLIAFVFMPIFLAVQRGDPHAFANAVDAFGTLLRKRGVFFLLQRAKLYCFLV
LLARTRTALGMCSGVDNSRVPLPVLTAAYAHVVDEGRKAATAQTGAAGSNQKRPKRHREE
NDENKTSVMTDDEMTWWTAKLIASGLVRGYISYEHKTIVLSRQTPFPTLGIAPP*
>TCRU_3336 hypothetical protein, conserved
MLQGNKASVYVDGESLGEEEVPLTGERPPDVLRFCFGACGGHESHVTVKNVFLYNRPLNF
TAMRALKDRVPVPTREAAPTPLEEIRVVDSVREHIAEDITEEK*
>TCRU_3337 BNR repeat-like domain containing protein, putative
MRGIGPLSLVRSIKIHGGHTLCLVQRRGKGVVLRPTTITKGNRVFPLTGGSDVSYEGVCW
REGGLEPKLVVGDATNPTGASEWDGSMGRPQTTPELIPSASHEGEWTEFIASGGAGVVME
DGTPVFPLMTKNETEDVCSMIVYSTDYGSVWTLCEDISPAKCHNPASPDGRDHFS*
>TCRU_3338 Mucin-like glycoprotein, putative
MMMKCCLLCALLVLALCCCPSVCDAKDTPVQASSQTTTSIKTEPTDTNKHTEPEDLSTKS
VITAKELVVNSETEDEANGPATTLRSPPEGEQGKGKTGSSGSVPAAEQDDTARDGQSLAG
PDSHSSVATSTLEREGTDGTSESQSHTSTAAEKATEEAKDSAQMTTTTTTTTTEALTTTT
THAPSRLREVDGSLSSSAWVCAPLVLTASALAYTAVG*
>TCRU_3339 BNR repeat-like domain containing protein, putative
MLVGIYNLDGASTGEDITDEWGLLVARVNVSNDGDRGNRIYWNVTYGLPGTVFKKEHGSL
TGLFGSGVSGVHMEDGTLVLPVEATKKGKRENNAEEEGKTVSLIIRSSDGAGWTLSEGLS
ADGCSDPSVVEWKENSS*
>TCRU_3340 syntaxin binding protein 1, putative
MPRPVRLRLLLLVAASSTDELTEAKKQQLIRDGGLTPDGHLFAKLEHVTRKAGSVQRYST
ASAQSRRSTSASASNAATDEDPFLKHACMMMETADRKRSLRVELSLTSMERDHAMRPNGA
SGGHNSGPAGKNAGPFQGCGGKWENLPDLGGGGCGGMIALTTPQRIVLLVLCGVACSERR
SVHEISKRYGREVVIGEPRCRVLRCVCAGTWHPTAL*
>TCRU_3341 BNR repeat-like domain containing protein, putative
MCCSGGAATAQVGSNADASTPGSALTGAIAGEGSASGGVEGLQRVDLFVPQKTQVLPKTG
TTDSGRRDSFVSPSLVSAGGVIAAFAEGHINAKKTHTESTKPSSDVVAEYIDSAWEWPTL
VGEVKKEEWSAHTVLGKAEGEGSLNVVRHPTTTMKGNKVFLLVGSTALSDVNGSWKEGSL
ELKLVVGEVTNPTDSEQSKRIEWGEIQSPLNGSTLAAHKGNLTDYIASGGSGVLMEDGTI
VFSLMAMNEKNEVDV*
>TCRU_3342 Kinesin-13 3, putative
MSSSRICVAVRKRPTADVDKDIVVAQSPHLVVNEPKVKYDLTPYTERHQFTYDQVLDENS
NNALVYQRCCSKLIGTLFNHGNATCFAYGQTGSGKTHTMLGNDHEPGLYAIAAKDIFSRA
APLNAEVYISFYEIYGRKIFDLLNNKERLVAREDAEKVINICGLSEHKVTDIQGLFDIIS
RGSTYRAAGQTSANSESSRSHAVLQMEVRETHNRRAKTIGRISFIDLAGNERGADTFDCD
RKTRMEGAEINKSLLALKECIRALGMGKSHVPFRGSILTEVLRDSFVGNSRTTMIATISP
TSAHCVNTLNTLRYTQRVKDLGGESKPVPAERAERRPAKKSKPFEAPPPIKSRPEWVDNF
LSPEGDHAVEDDGNSGNEMAKPPPKQRASRSIGGKGRRSKSEVIVRDPKIATIVQNHIEA
LEDGSDEEEEEEEDNAVQLGALAKNEEKQVRKVHAHVLEEIAKAEEKLVAFHRRHIDTKM
TGIKDEIRAIQAFEDSDSVDEYVNRVRTLLLRQKQDVETILGLLNGITGMLREEEELSST
LNTSLKGGK*
>TCRU_3343 Fibronectin type III domain containing protein, putative

MPQEENIVCHAVVLRMGELFGEFGLEFDSSHLANDVAAVTKWNLHIDLEDFDGSPELCFD
EEMSIEKPRKVVKLRAGRFYLARVRVFLADTLTWSAWSDTVRTATLHAVLGQVKEIGEDY
VRVQWNRPPRDTSHIIEERDIQATQAIADILDLELRIMREDEMVQEFCDRFAVGVRTYTV
RGLRPGAAYIVMIRYKTLINTMKNWTEVGRLYTKSRNIISLVSRGEDAIKVSWHPGPSPV
DAVGYIVPETTVHLYEVYLEGEDTTTNTVQLPEQQREYRVEGLSPGTLYAFYVRSLTIEG
IWGCRSEPCKVRTAEIPELSVVASGETFLSFTWMRGHEEAEESRVEFCLQSFTSRHKQQE
IIQVGPRAEDKVIHVRGLTAGTEYSMSIRTFLQGEWGRWTEPQRFRTQFKVSLSFLERGE
DFFTITLEDQNNTMSDSHFNVMVMRVGKGDERFVVLDQEFKREPNEPGFRVGSLQSNTVY
EVKCRRWQHNCVTGYEGWGDFTAPIQIQTLQHLALHVLDIGEDFAQIVWRRGVSDTAPLN
CLTTQTFPDLKYEVVMGCVDTGEDYIVHKQVLQTNYTITNLQPATTYIVSVRACNELDQW
GLWSKVRLRTLASVVTSVHEIGEDFVRLMWQREDIDDENVKKDDNCNDNNCRPIESLVNA
DAFVSRYAVFVCSSEDGESIPSTLSGYHMGGNSEVARYEIVTSEHTSLRMNDLLPDRDYV
AVVRASTATGKWGLWSHPLRFRTNPQFRIPVNNLTIGENYVNLVWSRDAHPVVDKDVFLG
DLSVTGQQLRIHGVDTPYSKDHTLPADLRELKIYGLSPATAYTIQIRVCGKGGDWGRWSP
PVHILTRDTIVTRAVEVAEDYIIIAWERRKVANPKNYPTGRGIVTSYHLRVYNNSGIHSE
VFLGDGDSPYLISNMTPDTYYCVEMKANYNDEEWGLWSTPMWCLTMKTLEIQTKLISEEF
SCIVVKRPYQQKRLPEDDGNRASDDRIIAFGQFRPNLMLCVTSPILNPTPHISAGTTRPR
HQNSSLPPDAADHRLIYQTEILCASDDTDHTIPNLRSNTVYSVSVRSKLVNGEWGIWSQP
SLLFATVPATQVEFTDIGEKFLKVDWKRSAQRIPPQIKNPSAVKCGLGTISASRVKVREI
GGSLQRTYELNNSLKTLRIDALSPASTYAVSVQTYNDNYEWGVWSEEEKVRTIPVIDIAV
QHISEDAVWVAWKRKSDVSNFVNYDTALNVDVIPCTYEISIVGGGYFNYTKEMDTNTLFF
RGLQPDTLYNFQVRAQSFENQEWGIWSTQSFRTKPRLRVTFGNVGEHFAIVEWRRHLPSS
IGERDVNTVVESEDVVQQFRLKVERAGSKETYVYDLSPYISSFRLKSLQPSSEYRVWLCA
KGYEGVWGFWNDEAIFRTLPKLELEVTAIGEDYVTVSWKRGKWVGETVADTDAVVREADG
AVSGYKVRVLDINGMEVVSQFIGFRETSCTLSPLDLSSVYSVEVSAKDTYDEWGLWSDAK
HFMTLEAVDLRIISVGEVFVEVEWGRCRELLRRRRARHGRRRRRNSILSSDENRSGGAVG
MNETEGIYNGGNNSADGSSKEENSSGMELPDTDARVSASNRTNDQEGPYQNEAHNIAERN
DGDEDGEEYEFDYEEEEEGEEEEEGEEEEYYYYYEKTLLHGDDGVLNWHLRVQGQRVFGG
QPGAEDFAELCIAADELQCVIDSLLPYATYSVSVRGQDKGGAWGHWSEPRKLVTCPLLAL
TADSVTETFIHVTWNRPPATLTLPEGFICFPPANDIHNYQVHIEPLATETPFDEQDEPLV
DGARVYETSQPSLRLWNLSPGVRYRVVVREQMINAQGEFVPNAWGCFSAMQVVETVNPMK
VVPIEIGEDYCLVGWHRVQRPADIASDISLVTGVAKVTAYELRAVRLDEMAKKEYQGPLA
LDAVVPLEANETSYHLVNIVSNTIYALSIRAQMERYWGPWSAVTKFVSQSRLEVKVRAVY
EDTFVVSWSRPLPEWALSRADSRNLNGETGPRREKKPDADFVVEEVTDENEATGDESINN
NNDNNSKGGNLSVESSNDFFATVLIGDYSVDRYELYVDGITCDMEQCLTLPKEQMSARIG
GLKHNQIYSVCIRSQSAKKHWSMLSRRESLLTLTPMCVDLSHYTETMTLIRWFRAPQDIM
VYDALLEGRRAEEERRCDERERQDLFELKRRAQGMEESVERKYLSDHLAVRREHNAARRM
DALHHLRIENVVLGDAEVTGYHFKFMGKVGGCMPSIPGVQRMLLQQRGTHSSRRRRQESA
KKSAGRMRRQQNLEETPTHTLGDAAAGNGAAPVVADDEFPSEDASLIDVQLGSHVTSVVV
KDLEPCASFSVQLRARNAAGEWCPWSQRESITTLKSIELHQNRFGEHYINLYWHRLPAAF
MQQMEDDEAQLHSLNEEFGHMSAKDLEDKKRELPELEYNVILERLKGWCELKRQVAHVRS
QLSRGLGDVIVHEKTPVKGFQLRIIHESGKFMDYYIDNKNNIHHDNDTNDQANNDKTTMD
TTDTVVTSTTTPMNFTFTVTGLVSNTMYIALLCADYGVAWGPWTTPLKFMTQNLIQLSIT
YISEVFVEIEWYRAPNKRIPPGEENDVLTSDTVSSEGRVCQVRITYEDEENDGKIVEEYR
TMRSCNMFRIDKLRTDTKYTFAVREWDAEGDWGLWCAPKKCVTLPGMETTVKELGEDWAE
ITWRRKERRVDYDDDIDVLQYDLEKLSYYLRVQELPENDDEDEAHAVPLEEMRENTTELI
ISDEMEGIFTSNHMTHGVLPLQEHPAEFEGEKDGLQCLIRRFGKDVVSFRLENLRPDRFY
NVQVMCETAENRLGAWSSDQYFITMSKIKISTQNIDEQYVDLVWQRLPPRQHPNLNMSRV
FTGHYMTIAYVLEVKGADDFYLHEQLQGHNNTSYHLKGLSLNTIYSARVYSINDVDMKSL
WSETLRFVTLDRVKVQPFEISEQSIILVWGREEQRPSCAETGGKYDPTISVGSRESGNYL
LRVYQGCEFSRCLLLEKNFPGDVHKFSLASLTPNTPYVVSVRATNLLGEWGLWSEERCVY
TMKLICAEIAAVGEDYIRFLWKREEPDELQIGDSLNSPKQPNKSGHDVFTEELAEAEAIA
INVDTTDNDVIPERRTSEGVDGATGSVCVQPSTEANVEMSGQKRHSMRGVNRKKYPLMDR
PERKGVVYNSANTIIDVYVVSVRRADEAEDYTIEVPGDATSFTVPSLRPDTRYSLAICAR

YGSGQWGVSSAYVTSGTLNLLKVELSGLGEDYLTAAWQRLPITYDTSTVSHGRKEDAIFY
ELAVHDFTDVSFGEEDVEDLAPRLRRTVFVPAKVWSCTVKELFSHHRYRVCVRRWYKPLE
AFINDAPCESPSTDDEQILDAIRRNHGLPGTWGECLYDVTLRDMMCFLTDSAEDFFVVRW
ERDPRAPALPVLNPFVQMPVQGYHLRIDEMQWDGVTVVTSADSTHIDQSLDANETNYKAQ
NLRPDTLYRIDVRCCVDNVWGRWSRNLFVRTLPKFFIDIANIGEDYAAFSWQRPRRSSCL
SDGTEVFCGNGDNIERYHLEVVGIEHRFHVSKKFKAARNNYRIKQLEANTVYSVSVRSFD
TRFDGWSLWSERVLFATLKPMHLTVGTVAEQYVMVEWDREEQTSEEYSEIVGEGGGIVQL
GNPEVIAYQLCVFFTQHTPSLAVVDKQFPKDVTRYCLGSLSADTPYVAVLRACNTESRWG
LWSKEGCFQTQRILELCVITVGENCVRVKWERSEVDFHEDGRGAGTRAEPIIYQLLLKAE
TETIERLIQPIDCGVTEDDFKLPTYLLEGLTPNTNYLMALQPGYEENRWGLWTPTINFKT
LQPISITPTTIGSNRLVISLCRGVETPSTEADIVATGNEEPERTAPSGSIVYYQLVLLKT
DEQQIAQEKERESEPNFLSTHATLFSTVATQRTLSISAAAVGAASVAAADATAAAAVEPN
SIVAEDAGEVDAEEAMYASPTIPAASVAVDAESLAATTDEKPVLPKGRVASVVIEEEPPV
PEGYDRGSLSRSAFFCPPAKKDNVVLTRDFEVNKEDPTNTICELEELESSTLYKIQVRAL
DENGMWGTWKELNVETAPFPPHSVAMHRINAQFCMLQWEPPDNRYLYRYVVEQAFAPSDT
RGKTKGGTEWRVADTVEDTFCRVRFTVPPNKMRCRVKAARVGEGHEFSEFSEPVKLSSGT
PPEPVTQLAITAIAYNFMTVEWAQSRSEISGTSRQARTLTYRIYLGIRDHTPIFVTTVSR
TTSYTLEDLEPSTEYTIQIVVENADGMSYNNPTIRAVTKSEQDSTVTRHEPGEPPLGSIV
ESISSLRRTLLPEIPSARPTLVPQPPSRSKRKRISGRSTPGAATATSSTAVTGTAAVSTN
ESRGNYRSMSRTGSAPRIMEMNSKRGTRDRLPSLKRKR*
>TCRU_3344 Primase zinc finger/Mcm10 replication factor, putative
MTRNEAEDNADDDEDLFAVFNTPEPAVDLLAAPAALRQSDSFFGGGRSVSVTEALSKSAS
SPSPSIMHFVCASTQDGCEMGSVTRQPPAERVHAAAVREPNSGINIRHSTKSCEQLPLVL
VEHPYSTFIEMRRSLATAGTPPLLTVIGVVIRRTDPKQKNGKGAYGIISLWNMRGPFPTP
QDELSILIVGSAFDAHYTKLAIGLVLALSGVQRMEGRKVTLSGNTKAENTTLTNSNRPGA
NSSNVCSTNLELLKVVKGDQIRVLGYAVDLHTCEGTQQRSGERCNRIVNGALSKFCSNHV
ANLRRVARGKASSPSTTNPQKPLRSNVSSTTFRAGVTRVDPALTNPKGVIASKKALQSMV
RQQPGFLTVKGSCGLPTTTPAGSDVVSAAGAYAGVVPGGALSVTGMCRDVGRVFRSPQAL
GVTARGRAVLAAAVDQEDAKERQRLLQLALKPSELGAKHPRNEGTSTPKSPRTTVAEDVE
AVREQYAPLTGGSSSSSFAAMRCNGFEEVCRHRQDYQHHVITKRANGTTSSIVSAVEQYL
RGDGVLAKTRASIVQEETSQQKNTASVSKSLLGTVAGSIESVNDGLRATDERRRFEQRME
RRLMQEKALEALVAVTEQKVNGIYCRQCERWYLRRNERCKMLQHVLETRATIRRFIECEH
CGYKTSLLGDVRPSKMIPRCPRCCADAMWKASNAAPEMAAPRKDPPPL*
>TCRU_3345 peroxisomal membrane protein 4, putative
MPVSTSDAPGLRRVALTSEAARLIDDMIRSGKYKELLDAIKGFRNGFVYGARIRAPHALV
LNLVWTNAPYRVMARKIYQVTKRHSIALGCTSLTFSLLRAFLRKLHGGPQNWHSALAGFF
VGVIFWGEQNPVTVQMSMYMLSRILSALLFILAGKFGWKFSPGAFRIYSGVLWMIVMPLF
LYYGDAMQPSMRSSMRYIYQDNEKYSSWYDLLCVNSDTSF*
>TCRU_3346 hypothetical protein, conserved
MRYSFEQVAKKETGGLCRAVAAANATRSELMKAYMQLAEAEIRALPKQRRLLERLLVQSE
EERRAAANERRQLALRRRDELKRKLRQFKEEGDGDGASKNSSHDEYARQWAAVYGGLALR
REQLAHVLSCPSTAVHVTTFADAVDSLAPFISAVHRAITFLEDKKDTETYTVPTQLLYTQ
LEQVTKMQLQVTSLLNRERHTQSLLRENTAEFFKGQERILAWCVEQREALHDLKGLKDLR
EFCASFMSNVAVMDTNFLVLLERSEQLASNRAVREALVAVNRTWMELAIAVYHTIRQVIR
REHANSGVEAACKWWVDTFEQRLRRILVEARDIADHMEMQSEPLMQTIHRRSIEVLRDLA
LPHTISQHISEFTEREDSVAPHEEALRDALVMRLSLLTQTFVGDVKYDGQREYADRLREV
SDYLDAQATGAVYTQLLERVKKLRSMVEEQLRLLPAGKIVTAADA*
>TCRU_3347 btb/poz domain containing protein, putative
MESIETVEVVSENGARFRYHCPVKLLRNMSLDASHYSPQFTVGGYTWRLHLQRRATAASG
EEFLSIHLQSCTNAAVVAQFKLLLQCYEDPPSSKGHIFRCTFKKSGSAWGMNEFIPMWRL
IQQENGFVYEDEGSGALYFDIDVLLKIVDANGQSYGNGGFETNVLPGRSGSPPAHLNFHQ
DPNRALSRMRSPMEYRGVGPTRSTSARGHLIVAPENGFIVGGGQAVVRAPLLYPFEHLEA
LTDMTFDIQGVRMKAHRCVIAARMRPLLPENVLPLQPGCVVTIAVTTDVFSAFLRYVYTE
ECPQQGVLPPEALLDLYLLSSACEFYELSGVCLNFVRPLLTNENILHITLTRYNAGDEVL

NALYLRVLLENYDFLIQDPKFEEIPGHLFRRLSLILRDKEPVPQVTIPTSKNTLGRQLAW
LAESGEYSDMELVVGPKHLIVKAHRYILASRCVLFSQAINPRSSVAIPPFTAAEFDFSQR
SWQKLLIGIYRHHLESYRDFSAEDVAIVFKMHSVFGMDGHLKREADDAFNHQNALRLLIY
AVKHQVPELHERGISYVASNFNALIQNDPQAWELVSELPQHAVVALFRMVVESQR*
>TCRU_3348 hypothetical protein
MPAAVEFPSLVAVSVVLVLSPCATAAADGGVPLGVPSAAEFSPGPLAAAWPPGDGDVGSA
SPPAGVLRVAPDAAAVPGSGEPSPVTPWFPAAGNCDCSCCADCGSVVTPEVAGSPGSADL
GKFIGPVGAGGSGDGGAPPCWFNSSALPSSSFERPEPLPSEPWASLPAEPSSLGSPLPSP
PRPAID*
>TCRU_3349 UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase,
putative
MVGWCYTLSRDVAEALVSCEPLRRLAYLPYSKEREEEFFSIGTQREDVMVGWVLDRVIKC
QPMIYVKVLPCHFNDARNGTGHSQVVPTSMCIHHVREDDYAALMARFGNDTSPAARVSWV
SEDVIYPVCD*
>TCRU_3350 UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase,
putative
MLVLYVLGRHPSHGYEYSAAPLEEAAQWHDVVALPMKEGRVSPGKKVGVRGAIGTEAEIG
MSQKVYMWFDLALRLFPTAGYISKGDDDMFLRVPLFVAHLRLLPRRRIYMGAHCGGNILM
NNRSLSAHFMVGWCYTLSRDVAEALVSYKPLRRLAYLPYSKEREEEFFSIGTQREDVMVG
WVLDRVIKYQPMIYVKVLSCHFHDARNGTGHSQVVPTSMCIHHVREDDYAALMARFGNDT
SPAARVSRVSEDVIYPVCD*
>TCRU_3351 hypothetical protein, conserved
MGKMWSQLRDLNPPAEAARCKSLRRSRRAPPAGQGIAPPSPRGSLWRQERLWAIGTLLPG
AELGSVCDHAHWQDTPLGRSMRGCRQLRGEAPQGARLSGESSGSAADPDTHAPSEAYAAS
TANRLTPSKASLACRGWKTPKPAAAHSAPDNNAVLSMRGVDAVRGDLHVAADASQSVEDG
ISRQRNSRRRLPMY*
>TCRU_3352 Acyl CoA binding protein, putative
MPLFDSSLSQDAAKARELCTWTTRFPRNISGKHFFLDHELGDLEATARFEDRQKLLFYAL
RRQAEHGPCTGAAPSIWWTRERTNYNAWKQLGDMSRFEAMVNF*
>TCRU_3353 hypothetical protein, conserved
MRSYCRHCMFHVCVFLVCTAVGAHAGGRLASSESVGCCSFSTVTGDTAVSLSVPSLFRRV
WLHLRHGALLRFAAEGVSTPYAFFSFSVSTPRMLERCFPWIGVLHDAASRYFGPGVYLDS
RWRSPEVADRVWRAMTPKGFAAMWCCRCVTGVLQTNCFRTRNGPAEYLFLVSGKEQASCE
VHYSGEVNAADTEGEREHEPSCMMSWLRPLTLFVMRTGKTSMVVFAVTSCASRTNLSWLP
FPCAGGPQYVALCYTEMTLMLLSLSFFIFSPPLSLGSLTAATP*
>TCRU_3354 hypothetical protein, conserved
MLFTLPRQNNIRGATSVLLLYMTDMTRFHPIGPLCADGVSKNADTLQYKGGELFALFEWN
AGQGRVVLAHLTEQLEEIRTVLRTWDAVDKNVTTPCTSTRKEGTAFDGACSSPMPTDGLV
GYFSNEGEKDCWVK*
>TCRU_3355 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MNAIKDRKPVPTRGSESQAGGVPQTIASAVSGPEKNSAAPAVPMTLDPHAVEEVSEGGAA
KRNTSRTEDVQFVVPEVSLNSAGSGLLPLLLLLLGLWGFAAL*
>TCRU_3356 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily, putative
MSRRVFASAVLLLLFVVVMFCGSGGAAATEKANAGKNDLINIQNLQRVDLFVPRTTLVLP
KKGTGPVKTRDSFFGPSLVSAGGVIAAFAEGHMNAEYQGGQSNKPSSSDVVAEYIDSAWN
WSTLVGKVSESTWKAHTVLGTTDGTDNRVGVVLRPTTTMKDNKVFLLAGITDAHKEGPEW
KVDSLDLKLVVGDVTNSTSSKQSGRIEWGDPRPLFDSKYSLNRKSKLNTFFPSGGSGVLM
EDGTLVFSLMAESKENDGVYSMIIYSTNNGSTWSLSEGVSSAGCHNPRITEWEGSLLMVV
DCVNGQRVYESRDMGTTWTEATGTLPGVWVNARSVFWDVSPHLDALITATIEGRKVMLYT
QREYTSGKNKVSALYLWVTDNNRTFCVGPVAVEDNMNWMLASSLLYSDGYLHLLQRRVSG
EGSAISLSRLTEELKEIESVLSTWSQKDVFFFGLSIPMAGLVAVLSDAASGDTWNDEYLC
LNATVTNATKVKDGFQLTEPNSRVMWPVNTRDDNLRHVFLSHDFTLVATVIIEETPTADA

PLLGATLGDTNSPHTMGVLYTADKEWVTIFNGKKTTKSGTWESGKEYQVALMLQGNKASV
YVDDKSLGEERLQTLLYWVRFWWTIIPGIPWESCIPRIKSGRRYSNTRRQTKVALGSLRK
NTKWHSCCKAIRPLCLLMASRWGRKKRCQQMRGHLMSQAFALARAV*
>TCRU_3357 hypothetical protein, conserved
MEMMMTGRVLLVCAFCVLWYGLSGVAADVGSVEEHGTGKDDKELKGISSSGLSLSKGKEK
PAAAALGGRGTPDLQGGKDNSMSEEGENILQEQELNLYDNPPKPNEGENENKGLTDAGHD
TRNQAAPPTPLPGTSGESPEPPILPAVKGPPASAGVSSQEPPTQASTKLTLPVQPAELNT
AGSVTPVQSQGGPETM*
>TCRU_3358 Reverse transcriptase (RNA-dependent DNA polymerase), putative
MIHRRLSALLPHHPRQFGFTHSRSTSDVVTLVNGKIARGLNESSTVEYERSGDGAPTQHP
RHHRSLVVLIDFSTAFDTVDNGKLFGMLDRLPRLGHRTKRWLHNYLRGHYVRVCTREQHS
RKQLASAGAPQGGVLLPQLSLRHVCDVLHRLGNSYSASALMHTDALTLVASGAGIHACAA
AMPPALSRIPTWAAEHSLKINVDKSEAALFHISSHTHGLTRTWSISILLAETYVFSHAQC
ACWTPRSIDFLILVRTLPPLQSRPCHAATNYGRSHRLVRSTTIRNPFRLDTVMVCHCILA
MQLSLALPPPASIIWKYCTATVVKHPLALVHQRKIHLSN*
>TCRU_3359 protein kinase, putative
MMERSEYGSALWWWEKARAVEQGALAEESPLCRSSQAARLEKECVMRMSRGDYAPFARRP
RLANGENDGVPHSDVVSTVTGKETVSQKTASATSSFRFGPLVTAPESDAVSLEVAAGCLP
HRFRDRLGNVWKRALNPIEDPSTDITPVYMAISATGTLAVLKVCQLTDAAARLTRAEVDA
ALEELMGLRVNDSLVQYLSYCYVPPHRVVLVMQYVPGGTLREMKSRYGRKLPLTAVRRNV
ASMLRGLAHLHGRGVIHGRLCPENVMVGVEGRWRLKGMLLGAAPLILHQETYYVSPEVAA
GGAKTAANDVYALGLLLLAMLTDSHPWQWSANAALDRSRNELDSLLADSTAFREALRNGL
LTPVPTPADTDETLRTVLEACLRTAPGDRPTAADILFLCNP*
>TCRU_3360 protein kinase, putative
MRFAGSDASSRSSAPLHGDDDGHASRPGRQVNQSREEGSGVSEGASHKRQPSRALETMHV
ASARRHNYGIRDSRGSDVVFLRTCESQARQGPSVKADTKKESANASVSELQKTEDVATRE
AVSASSRGVASSSAVVYKNEDCLGADKVFRLSDNAGKDGRSSRISRLSGKASLTVCDRWG
AMDSAVAEGEVPALPKMTNLNAKSQEMSEVRMTAASFPREVLSRTDSAHLLIRHSPPLRS
TLTLSLRCWVLCPLVVILLVVAAVTMALSFATSKSSSESVFLSLHDVVLDSIEESVGDLT
LTKMARMAVSTGSMYFSKNTFPNLRADILMPLEGGMMSRLCAVLRDMDPAKMVSSLGAVS
LTRQQAAVCFNSRSRPGNFVGTVSRNGVIKGFYYVDSVTLEYKTPLEPLEKVDPPMSIDD
FTKSQRFEKVVEKWKTAVEKGEPMLSEQYWVTPRHPPNYVVFVYPFFEVYEDGSTGVGYI
YSTMFTDDIASIQWYSPTESGIRVMLVDPDVRAEQLLVVANSWGQPLANVTNAWLATVRG
DPVKFMHVEDVEDPIMREALKHVDLCAAISSGSDQNASFLYGGFDGRITAKRIDVQGGVK
FLLVVVTSRSYYLGPVILYRNVAIVAGIVVLLLVTVACVAFVECCLVIPLRATRAELKLA
LGGAPVSARSRRRAVLREVRELEDVCTTLRCRLDKVRLYMPDRFNARVAAAGYGSPFRSE
CGIDKASLDGSNSEELKRVTCSVAYVYYTPRTVRNPTDAVVELIMRAVVKIATDCGGRFE
VQRPDYCVISFGAQLRGKEFAAEALEAVEFARRLREELTACAELDGLYRVIVESGVFLSG
VISGGGRSHFVLLCRNLHYRLGGFLPHTGVVAAVTEETALLVRGRCRLLPFETVYLEDAA
TTWWEKARAVEQGALAEESPLCRSSQAARLEKECVMRMSRGDYAPFARRPRLANGENDGV
PHSDVVSTVTSEETVSQKTASATSSFRFGPLVTAPESDAVSLEVAAGCLPHRFRDRLGNV
WKRALNPIEDPSTDITPVYMAISATGTLAVLKVCQLTDAAARLTRAEVDAALEELMGLRV
NDSLVQYLSYCYVPPHRVVLVMQYVPGGTLREMKSRYGRKLPLTAVRRNVASMLRGLAHL
HGRGVIHGRLCPENVMVGVEGRWRLKGMLLGAAPLILHQETYYVSPEVAAGGAKTAANDV
YALGLLLLAMLTDSHPWQWSANAALDRSRNELDSLLADSTAFREALRNGLLTPVPTPADT
DETLRTVLEACLRTAPGDRPTALRLQEVRCDRSL*
>TCRU_3361 hypothetical protein, conserved
MTDLQEGSIYARVAILQWAADILHGEYASFGNIPAKDIAVLLHAIFNTPCEGGSMDTGGT
ALVSLHNIQFCEHPTPTTLFLNAKRVLSLVQTLSSSVVDGNGDMNVAEGCGGCSRPLSLP
AVGNMTVSAWMEGKAFVEELKMWRWIRAEAFRRGLEKEELERRAQKFLHGAANPSKVPSS
HESTTTGPALELESGPSSGSVGKHVTSPRKRSREKDTGAPNAPEAALDSGNGASNQVKGP
AATDIKPESGRDGGVRNCMRTDIVVPRGRRGDESTYISSQYDKVPREDKGEAVSLPHMTC
DGVAVAPKLLNVLEEVKKELKERKVAAEASAAACGSITGSITTASRGSEPHVIEEACGSG

HPVVGCSSCPAIFSEALQQNYSAIERLETARRLAVAACLKKDAAGLLEALAFI*
>TCRU_3362 hypothetical protein, conserved
MLRRPCVSAVDMFAGASSAIVAVSPRRGISTEQKDITRSGQPHPPAVPHNEPILPMDFNP
HIEWFEYPKEIFDPKYPYTREESIRMTEESWESTMDEMASRYGMRLNMTTKPTYWMAWSI
MVFYSWYTLWGCYRAMGTEPGWPHYRQIVLNQPNVPTLEEDDIYLDQWIRPEMREKHAKF
DLFWNWKPLVNRDGAKTTWQIPMQYHDESEWRHMTSPN*
>TCRU_3363 Protein of unknown function, putative
MREYGRGLNADDAPPPRSGGTLLAPLRLTQQQQQEQRQPSEVVPLLQHLTSSGEGLQQVR
MKMGAKPLQPIGTMATGAGSQRAGQAMTEHVPLNSAPTHLSESKAINSFNSSSHSPLQSF
EPKADGNDTMNSTGQLKQAPFFPIRLEEPRGAALEPSIPRVRQTVVFVEGSSCSQPPPET
ANSREPTPQLSHEKEQKINANSSTSGWNANYSPPFSEANNTSLPLNDVCSVSNPTVGGSR
TLPVTRPEPQINENPPKIAASIKKLGDINLSAFTQWCSENVLDPNGLTERRLGRRRSRRW
ISSTWDLVSATTVRSRKTKGSSVSMGGATKRTTSNGSNGGIFTPEDSTLKIPPRETREGL
NRRLKKDAQSLYSLELPTFDEETGTLGDACVFPRSLAVDVAVEHVISQERGELRTKATGV
GILRFLKEFDESCEIIYLYFWYAIAHIRRIKSEKMLIGRYINLERIVRGAFPRYKAEMPT
IKQIGCILAKYAPTDESISENNSVAAAREEVEVEEAVPPFFPAISNVHLLGGPGSIVSEE
SGRTAFVSQYPKKKRPRTGSGGADIIQAFDEAVDKSLLQDPAIISLCNEAINAFTVVQME
VYELAEFAQRCFHRLAVLFGQAFERLAEEKDEVLTAFTFIVPHVVYYVFVYCFPNDVVAG
IFNAALRMNLYRIFYFWCSGLVATYVRVNGWPKPLTDGKKSLLKFIAQQAGSPTLSQSTA
SVISPISPKRGGSAFIAQGESNSQGVVAAIGNSKSLSSPTAMGEERLEALADDTFEEVDV
EVANGHYRIALEFKKYAKHVNYLLQELQKRTEDMHREAAHSSLIPTPTDIENTSMGGMAQ
PDRFFNKLPSVQMSASPQLRTVSWNGGSAKKKMPETRQLPRKSTLLIPSNNHDAAGNYDE
AVLPAISQANGAVKKTKALPVNNDCILSGFPLEHTAIHVKQYMMRPTGVAPAKVPLPPLN
VPSTEGTNSNEAASPHADKHHTLPSLRTVKVPLPVASPFFQHYSSKRLASNAAGINEKSF
PRKSTRHDKPHPFFSECVVPTSMGSPSSSISHATATRNSVGSLSSSTLAPSISQKRGVGA
KNPTNSLMLPHVRRKAIKLMLIPPSDAQLRPLKFKSLTREVTRRQLEIERQMDRLSGREQ
ILRRKYDAETQQGSRRVHQLLSECHSDKQKIEAYAGFLSDKRKKNEDTMRRKQKFPLERI
KR*
>TCRU_3364 hypothetical protein, conserved
METPRDVPSTQQHPFNFTGQQPEETAHRSFHFTCTLEDREKRKRAAAVRWTSPFQDTAVK
TSGRKHCTEVPSVNEPPPPKTTSLHVVAASNDTTKAIASGDGPLSLEILLHESQQQLSAL
LWQKRRCRTLQAALDASLERQKVLENALVESSGESQETREQYRAYVATTAEELRQTRKSL
RASETALRVIEDEVGGLRRENERLRQLHQQAEEDHTVRRRQQERMEDQLSCLLAEKERIQ
GELSTSRARCRELETLQNAKETTIDESAEGNDETKNMDKKKIIHGNDDNGGSDAARRDEI
NTIITLLEDELDRRRAEMDAMKESTEAFREEVRRVFGMACKRLTVVSQRGAQLTSVLACD
SKQLQRGMEEDVENGGDMDSLFATLEIIVRRLEQQWCCLEEKVMSRESESQKQEELQNQL
DAMKKAHLAELQTIKSTRQEATERLHQMEIRYTQLLRAMERQSQMVLAATNTDMRISRGN
RTSRTKEKPRNKQEDGDKNSDDSSSNNNSHEEYMEGRGEERGKRMACEKETFQTYEWHFG
RKEFMTCETILDPSYDRMVYTLLRRTRQATRNAIRQLREARSKHDTLLKLQEEKQRQSMA
ISEERVRYQATVKRLQTSLKAAHDTESSLKTKIAAVMRTAELERNSLVRRAEAAERDVQA
KSKQERLLQRQVREMLEEYEAAKQELAARDDKIAELSAELAEGQSTTREKQFDLNTLHHR
CEDLVRMTDVLETRVRREIQNQDVFYELLRKLCGAVAVLTLRLSTVAEERDALWRAYEAR
ETDCRAALQVLQEFMKKEEEEGQELELGLQKIGRVLPSHHGRSFYVIVAVVIACHRMQHL
LSSRYSRRHVMFAVYNEDDNSTNLRSSGRDLSGFALSPWHMLKSRNVLSLVASVPRVSAA
LRRQSGGTRMPFVHLPPLKTLLSVIASRDRNGTAEHEVNDTLEQILALAELNNNVEANRF
WLEAHISRGVAYAASAAGGGGGGGAWTRRGLPCVNSQPIHCRGMLAEKLHYVLHTVRDAA
TEFRQKMRQKDASIQIAEEESHQLRSMVQEREGIAAGFAQQLREYEEHVATAFVGRDVYQ
ELQDRLRAAHDALQEEREARRKIEEVNAALRQREIELTRIVQLLRDEVRSLSIELAEQTS
HDDSHCQRIDAYLSTLRLSPSRRKTMNTSRESNNTQLYVPRSVKLTSLPFTAISSMNTHP
NTNNEDGANLDEAVRQVLSGLASRLEQAEGNPLQP*
>TCRU_3365 WD domain, G-beta repeat, putative
MAELSPVALLPGGCQQDCALPVISHANVIVYCSAAAIYMHTPNTITLPASAGAAVGTERV
KNENETFHNYPLTRIFASGVVGVIYSFDFNDEYMACVTSTTNTVVWRIADGENLNDKRVP
SCVGEFFRREGGPSVVRIAGKYHILYGTKTGWVVSVNMNDGTTMHQLRLCVTYKSVNSIS

LSTPASVATKAAGGHWEGTETQVGYVTVVDVSISRPDTIVVGTSEGYLFVLSIHPANGLR
QTASLRPFSAPAVFEDKPAADSTNNGSDALNEMGWLPVTAMAFDPNNPNFVAVGSRDGGL
VLVDIVSTTIVQTYAVNGEPVISIAWLAGQAGEFVTTDGESSKLHVWSVSTRTAVAVWHP
VAGCAIFGIAAFAPEHLFIALRSGSVAVFNTRTGQIEMQTEAGHTDVMHTCRYAHHDKDQ
LATTSTDGTIRLWNTKQLVLQNTLDVGRVIVRSMDWSLSGKYLAAGLSNGEVVCYYVHTQ
REHWRVSVTTVSTVYFVSWSCTESGGHIAASHRDGLAVISARDGKILRHYKTKSPVLGIE
FDRKHPKHLAAACQDGQVLVFHISSSREEPALILTGHMAAASSVAYNPTVPNFLLSCSHD
TTLRLWDLYSGASHTASVSCRVLRGHTNSVNAIAWCSIAPYIALSASSDCTVRLWDVRGG
SNLATVRAHNAEVIALSTHPERPPVFASVSHDNSIIFWHLGLLRQVYLEAALGRIEHCIV
SDGASLLASAAASSFVDPAHLVTGDVVQELNKELKEANLAPHKRMERLVRMFEFPCGAVD
LARAAGFSVDPQDVSNAKCTVVPTSRLVEVHGKWGKTNVEKSHGKTVTNAGEEYKKSRII
EAAEFMLQIGKVAEYCQLMAEVGEWDRAIAAAPVVSRDFWRSLCLKAAETMEAAGNTRAL
RYFIMAEESARAALLVSRQSNKNWDLAAVIAQTCPQRVVNETSTEPPHNTTVDTNGVSAV
VKGLLNARATALENAMNPRIVAATKLAEGANDDAVMDLIHSGDVVIAHLLVHTVPLQRQT
TIDAGYRLSMLLSCRQRQWDTALICATRHSNPHDGLATVLAFYQEAEEKTRSVDTNGVPA
PVNERMKTFHEQLLLECQRLQLPLDAESIQRKHATDGLGSINQLAAMALSPKTPVGTVTS
EELLHTMSNFIDSVLQAALQDIDSPNAVFYLNQAFSATCYVSLPIQSASKGANSTTPTGF
STTITGNGTHSAAVRRFLAQVFLLAALMCVKVYRFPNFLNPTFTKARELAEGDNHLMVLL
SKAQQSLGSYSPHSVEVGCPTLGASIPSYDIEDGIQLKSILTKEPLAGAVHVLEDGVSLM
GKSEAFQWMLCCAFSPLASGARFLPL*
>TCRU_3366 hypothetical protein, conserved
MHGRNGELGAVCHVANAVHTCSNCAASCATEEGVTVAFTMNVTTHKYAGPYELWWRLFSP
DGAIHPPARSSDADRTGICLLPPPREGKDDTNSGETTAPQVNAEPSRQNEDWRRSAAADG
PNTVDPSPSSNTATNTSETRPEFANNPIEMMVPNASTKRPSFANGPRILVAPNASGVMSV
TYGGREHVAADNTDKVSEHDATGHKTLVL*
>TCRU_3367 hypothetical protein
MEEKLRNASREELLNHVLTQRLLIRHLHRRIVELERLVPLTSNNLDSRGGNEANLSPPVP
QRDPPPPAKLSEGLREIDRILRAHATGAVRLPQEVVAEFLYIQKELSAVESGQNTAESTE
TSALPVTFSSDAFLVSRTPVVSTSAVSDASIHSTPYGQRSGVSRRFSPPSSLIQRTQKHL
SMRERNELP*
>TCRU_3368 hypothetical protein, conserved
MQFVVVDGSWPVVPCAIPRSQLLARSVKDTDRGEDGGGQSVLPGHALFTLCQEVLDTSAS
KTKAPPELATLDMTFLRDPQSGPLGALRLYTFKSVSHQFFAVEDLVSSGCLIVFTSHWAS
LTSAALLTGVRTTHKEKDDSANSSRRRIENNTGSGTREVSASRASSLMGRGRSVLQKFSR
AETYFTSVASATQRDFEMVNELLLSGTIRMNAHLESFLCSVCGNLPRRTMTTSCCGAVVC
LVCAPTLSSSSVLREEVVCAVCGEMPLTNPEAHVSRDAEVMRLVRELRVLYHPQVSAVAC
RAMPGETQPPPTPFNVHHAGLPVPMCDMNEPTGSVLGSVFMGPS*
>TCRU_3369 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MVAFAESLFGYNIDEHHLLGIRPYEIVAGYIKAAESWPSIVAEVNAGKWRAHTVFGSRNG
SDRVCFLCRPTAVAKDNKVFLLVGSDTVGYYSDDDVWVQDGWDIKLVEGVATQSTDGRQS
TLVSWAQPKSLLKHIPNHTRDQLRDVVTAGGSGVLMQNGTLVFPLVVNGEKYPFSSITYS
TDNGNNWVFPESISPVGCLDPRITEWEKGHILMIVDCVDGQTVYESRDMGKTWTEAIGTL
SGVWVRSQPGFRWDEGLRVGALITATIEGVKVMLYTQRGYASGKNRANALYVWVTDNNRT
FHVGPLFVENNVNETLANALLYSDGALHLSRESIVGTRWGISLARLTEELNAIRSVLSNW
ARLDAFFSKSSTPTAGLVAVLSDEANDGTWVDDYRCVNASVTKAAKVKNGFKFTGPGSRA
TWPVNSREDNNQYGFVNHDFTIVATVVIHQVPKESTPLLGAGLGDGSGKKIIGLSYSMIK
TWETVFDGTTKAQKNTWELGREYEVALILQDGHKGSVYVDGVIVGSSEAITTLETQGHEI
THFYFGGDEGDSDSNVTVTNVFLYNRPLNSTEIRALKGRAPVSTRGPETQVEGMATTEHV
AAVPGPVELPAAPGRTTMERATTTEHAAAVSFTSAGSGMQPLLFLLGLWGFAAA*
>TCRU_3370 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative

MQNGTLVFPLVVNGKNHPFSSITYSTENGSTWVFPESISPVGCLDPRITEWEHGQILMIA
ECFNGQTVFESRDMGTTWTEAIGTLSGVWVKSRSGFRWDVSLRVGALITATIEGRKVMLY
TQRGYTSRKNKANALYLWVTDNNRTFHVGPLFLEDNVNETLANALLYSDGALHLSRESIV
GTRWGISLARLTKELNTIRSVLSTWAQLDASFSKSSTPTAGLVAVLSNTASDGTWVDDYR
CVNASVTKAAKVHNGFKFTGPGSMATWPVNSRGDNSHYGFVNHDFTIVATVVIHQVPKES
TPLLGASLGDGPGKKIIGLSYGMDKTWETVFDGTTTAQINTWEPGREYEVALVLQGGNKG
SVYVDGVIVGSSEAIPTLETRGAEVTHFYFGGDEGDSDSNVTVTNVFLYNHPLNPTEMRA
IKGRAPVSTRGPETQVEDGTERRHIPRIEGVRANAPAGSGLLQLLLLLGLWGFAAA*
>TCRU_3371 hypothetical protein, conserved
MTGMDTAWIPFAVLYILYQIPPTMMEVYSYYSRGGLVSIEDIKYDDTFTFHFQWLHDKDI
YLKRYCDRPISEAGKAFFSWLDWSAEAYDRSVYVMRRNHARRDGEVSMWKRYIYGPFVFN
WPKKQWLRGDDSCGMRMPAWGVGGEARARQEYFAAKAKGFDKNWHYQIMRKIRREQARKA
SADAAKA*
>TCRU_3372 HECT-domain (ubiquitin-transferase), putative
MENFFTRIVVDAESSVVQRKMMKEIAAARDNINSDDEGRQTVGLLDLCNLLNMATAATIA
SIRPSVFVPPVLACLKKEHNVDLMLLAARALTYMVDAISSAVYVLGSEGGMEAVLRHLLE
VKDIELSEQCLTCVEKITQSSHGALMGLQKGGVKSLLAFVDFFSSSSQRKAWSSVAAMCR
RVDVTTFDRVEDSLNDIRSRTNHDDGKIGDKAIACLYRIINGVRTNPELVALAYGDVSPS
LLCVLTRSDVSENTFTMTLSLIGSAISYSTEVTRKVIESGLMECMLALIAHSSKHQLPLL
QQQPQQQLQQTWRSFWESPILGTQNPPGSSFSQDVSLLPNSTTTQTTAAFRERRLTMEQT
KTLCIALAGLLPRITEGYLAYGNILTELLAERAQGMAHRRGFFSLEASYEEDEEEEEEEE
EEGETSNSDEIRLRIFDEGIPLEKNTKFSRCGLTHMCDSCGKLCRPGDWFRCNKCADFDF
CGECLLMNWEEHTGNSAQHTFCDMLEVFPGFKRSPTPAKARKTLDDALNTERKELYKSHP
QLLDTILGGLTKMVALFNESETHIVRNHSLAFIDRAVCLASPQQLAGSGLVEASVCELIL
SAIADPSLVLNVQVMLLCRTLLEKLPNVYKNAFVREGVTSALIKAQQQNQTSTRRSTEHS
EEKRPLIERLVTISDWRELVVEEAKSMLSMFSSLSEETHVMRLAEFVSLMEEGQFQEAFD
ILRTALLNDITTFELASSNVLRSLRETLTRVNDIKVVVTLVKTLAKEAPNPPCALTRFVR
HLQTILSQLDQFRPPSFGEVSSIHVHIPVHLVPHASEQQKTKPSFLAKGGGVLRRPPAAA
PSKESGAPPRSTRIPATRRSSGTNIASTLAPSTSNSTKGPLEGRDIMVSVEPLTSMDALM
SFVASNVLSGEMEHSDSRRRIEDEDQVEEVLPELGREGRDETSVSGKKLTQEKAQQTVYL
RYESHVLPSSMTILQVIQQFHSNSLSGTSLSGRKKKKSGQGSGTANATTTTNTNASNTTT
AGGSNGSSGGGRSRQINSMVEELRRGTGEAITLHYSTVPFGPEYTMELSRSTVSCIAPTD
PIRVRLPSKDIRPAAVVEVMCALHQDYPFSSRFLTAAQKDVLTLLGTIYKTLRCWSELLL
YLGYCGEDEMDGGVWSPSTSLGEFIHHRLNNKAMRHSSNLLLAGQHLTTWAVNLAMDCNF
LFTAMTRKFLFEISFCGTARSLVQMQENMEKYGMRDLLNIDHQFIRSYRLHRVKKRVWRH
HALMCAMEIMGKKQVNDSVLLEFEYYNENGSGSGPTMEFFSLVSDELREMKLQLWRRTDE
TPDEKYYHPQKGVYPRPLPPDSPEIDRVEPYFSLLGRFLARALLDKRIVSIPLSPVMLKM
LRGDECGIYDLIDVSDSLGSFIVALSIATHHGATTIQLPGSSTSCSVEELSLDFTLPGDD
AIELVKDGANKSVTFKNLFDYCDAVTGFMLRTGVERVIKAFRSGFHEYIPLCALRLLSVS
ELHEALHGHADLVTVEDLEANCQADHGYTMTCSHVRQLFEIIASFNEEEQRQFFLFLTGS
VHLPVGGLASLRPKFTIVRKTSSEPKVREQDQLPSAMTCQNYLKLPAYDSKEQMERKLRQ
AIDEGCGAFLLT*
>TCRU_3373 exportin 1
MESILDTSRPVDVQEFDRVVQYLSTGTPQEIMKAQGVLTMFKDRPDVFAQAGTLLSKSQN
LTTRFFALQIFDETILHQWNKFTDVEKGDFRVFVINLIVGECKSFNQIRSRKALLTKINS
TLVSIAKREWPLRWPSFIYDICSSAGPNEPLIENNLNLLRLLGEEIFEFAEKTLTSRWIK
RKKEALKNDFCLILQLCLSVLGTSDLALLKTDLECMEKYLAWMEPTLVFNEEVLMYIASL
VVGDATVAPVAVRCLSVVCSLDTDEGAAGDSQAQIAVRVFRTAFNNILNALPTSHLSVEG
RIVQMYEMGMDDDCGFISGVNILLISFLKRYYKLILYDDILLLSTHQMLVGMSHIDNKEL
FKSCVEYWWWLGEKLLRFPSPTPLHKKLSGVLSNVRFVLIKKMAKPEEVIIVEEDGELRR
EHMSDVEGLQLYNLMREALVFLTNIDPYDTQHIMTELMQKQLDRSEWSWHNCSTLSWAVG
AVSLALSEEQESSLFVVIIRGLLDLCKEMLGKENRAVIASNIMFVVGQYPRFLRNHPSFL
STVVRKILEFMKELFPGVQEMAVDTLLKIASQVPDQFVSLDNRKKSIAVDIAERWTELTS
LLQPQQTQTCFAAAGLMVQSESLERRALLLNLFLQDVNINFKAITERAAAQGASFCRDSS

SMMELIHVLRTFSSIASTCGTAFIDEMGIIIWDLHGFYRTFFAAQNALIAEGGPAAMVQQ
QDARYLRLAKKEILCIFERFVDNTEERDFVAANCMPSILTVVLEDYRDSVPEAKEPGALA
LVTACVNKLTTRLSGDCAAILDHTFDTTVAMICRNTEDFPEFRVNLFKLLQALNRHCFDA
FLSYTSRKEDVIAGMLWVIKHTDFATMEVGLLALDSFLENVAKSELAKEFFTSFMQRIFV
EVLVAAMDSLHAAGFSLHCSILIKLFSVSDMFPPQTPVVGRVALHEFLVENLSVIPTLTP
SLITDFVSFAYESYCDEAEFRRRFADFLIEMQVWGAEEENRLQAEEERRLRGEINPGFAS
PSTGPPEEFRPSSF*
>TCRU_3374 mitochondrial carrier protein
MSSTYWNELLASSKNKNVDAVVAHSNAEKEKTDLHASPLSHTVSSQFASATSTLIYYPFD
MLRVRFMSQDGTTYRQHNGQTYHSIRRALVTIYREEGPRALFRGCHVAVLGSVAAWGIYM
YTYRSLCCMADVSSFLGRTGVSYLASLTSTLVSSPIWFIKTRMQLEDATQSRNYATFRKG
LRHVLQTTGFCSLWRGVSLQLTLIIPNALNYPTYDFLKEIILRTRLEHSTKRGELTVTET
LVCSTVTKVLLLLLSHPIMFLKVRLQDQRWNMGDVKYTDIRHSLLLILKREGTRGMLRGL
NSSLLHSLPRAVTHYMLYEKTLGVINGYI*
>TCRU_3375 kinetoplast polyadenylation/uridylation factor 2
MRRWITEPTRRFALTIELRRCSTATKDNESLRPSRSSGKKGTGFFGIDQSKLDLALKLHE
IDFDTVVKATREALAKERARKDTVFGDGMNIKDLIPEGEKESPSAATSLSPASSAGVAGP
SAPATDENVRDDSSKRMERQMFRGIVGARDTHTTNSFAVVREQRKAEGARYGLMDALRDC
LLAGNWVKAMHLFESAVETSCKAVQNSFSANIVIETEETERLETLRRINATTPPRSDSTG
SSMHPGVLRWSGGHFYLLLKLLLSKHRVAEAERVWDVMKRIGFVEIHMDARTLNQCMKLA
RNTTLPDIVSPLKESNRHTEDRIKTFRTTFLLELEELAKKKELSLDGRNKELTRAARLAE
LVKNGRERVEDKGEVDPLNEGGLKVGDFSGLLRRCNSEESTARVLQMMDKLQMPRGGEVF
GALIAALRQPHYILTPHDMTGTVVGTKEEYDAHRKQRFERACQWFEQCPEDERSADVYNE
MLQIARGDEKADEKFQNVLLEFRGAPLALANAPTEGENKDTNNTDGEQGKKKKQVKLLPP
HWRVSPNGRTYEILIFRCKYLQEWRLLWALYDEAMERRVKGTQRLYQTLLEVAKYHPPQG
CDSNAVIMELYEEMKGRGIEVTGIKGTVSVLNAWCATRRRRRW*
>TCRU_3376 hypothetical protein, conserved
MAALESLNFNAETAIHYIHCVLSNVPMTLALSEVAPMVVPNPESPIVKELEAIGCRIVPH
QLNMFKEPLERKFGFVNFFIREALRAESQGKVHELVLLWISRELADQLASVNVSVTLGQP
HDCYSAVPFLRALHKECSFLDASKVSDSKKLETFLLSKIHFDDAGSNLHKNNGVDGVDAE
EEKKGDGARRAVGSFRISSLGWKELLWLSRGHSDLPPILITNGNISTATCDQEALRIFFE
GALFPLIRVLP*
>TCRU_3377 Ankyrin repeats (3 copies), putative
MSFKEFVHAKGIVWKQRAALRSIDHDGAMKRVVNVIKDGNESLLFDWMNTCDDINVRDSW
GNAALHWAAALGKLNAVTHLLLAQADVNVVNMNGATPLHCAAICGHSNIIRQLLRSGADV
MATNHEGQTMIDLLRYMGWDNASIQQEHSRNVSPLSPSGLENFGEELSFSDGASLGSLKA
YAPPDSPYVYGFNVEVKNHHHDLRTKEIGELSCVENDASNDVAGEELVCMQWHAEMEQLF
SRESAERNELISKYAKWMLQVTDTMKSDHSAPTERERKEVGVVLDAKYSPKGSDQFLLHL
AGDAESEELRVKADDVKDSPVAKAYVEPLETSTITPNISSEIIGGDVLLAREHSEDAEQP
ELPSLLRRIPCGNSQISKSAPVSNAPKASIEHLPPLRISPSTNSSPALFVNEKKPADSLS
LPSCNLVTGILSQNVAHRDTPHNSILTISTHSDKNKIKSCSNSSPANHIHCGEKALPPLK
LNKVNYNAAASVKEASKFRQGGVFCGEKRNANREYLSEEEKRIYEEFLRRSALRYLGRIV
ELRKA*
>TCRU_3378 hypothetical protein
MRTTHHLKSLINDLEVYERELKEKVQQKEEELKQLLQRIGPVTVIAGLPPSSFSGPWQLH
ITREADGKTDSEGVLSPSPCITEERRHLQYTVGGGDSVGKHRSEKSNAKQRKDTLLSIDI
DAVSSISFASTSSAESVETLEMAQQLLTACDRAKDRQARRVRFVSRSPQVLSNAVEALAA
VTAVEGETGGKARGTPLPLSQAYQALTGEGGDTDNKDVDALMLIRNITATSNMGLEATNH
ADLASRVHEDNEEPCYIRGRRKPQEQQQQQQQRQKEEVQLHPLHTVTSDASPTNAEDILA
VVELPKVNSTPGSCVTRSLRRHRSESGQTQQLCSGPPAKRSQISVSPTVSAAWPHHVSDT
QMEGRGAGIILACGPTLFFE*
>TCRU_3379 proteasome regulatory non-ATP-ase subunit
MAEEYEIGLTVRKVAEEFLKLKMDYERKNDDGCKRLLESIKKKLILLPTFLNPTAHSRTR
SEELTLTREVLEHGVLVSARLGDLDSFELYFNQLNVYYTDIDSSELPESPLYLLILGLNL

VRLLVRNRIAQFHSELEKIPNQIHGTNTYIRFAVLLERYLMEGSYKKLLNSRHQAPSNEY
IPIVGMLESTVRQEVAECIPRSYNTLSIDKAQKILMVDSAEEVRQIGRCHNWQLSADGRS
FVFTREEDLARKEVPFQEMLKNHLHFAVELQRIV*
>TCRU_3380 retrotransposon hot spot protein, RHS3, putative
MDATAIVTNCPEENDVKAMCIWMKRNRPLQEQAEYWKEVRGRMNKVGPILRFIFGKQACD
DRIKACQQAVDGMNASKFEGYLDIGNCPTAATCFKSL*
>TCRU_3381 hypothetical protein, conserved
MARMCASRVTWGQRGRRLPEHSRAFGSGHDQDSVGTKACVWKPSSPRPLREGHALHSERV
RLGGNATALYLWATDNSRTFHVGALFVGNAMGETLANALLYSDSALHLLQKGVNEKGSAI
PLARLTEELKTINSVLSTWAQIDASFAESSTPTAGLIGFLSNAASEHKLIDD*
>TCRU_3382 hypothetical protein, conserved
MKAHERTKTELQQAPKIAALLQRPSCDKQAGNTGGLATQVRQKHPDSKKGTTPKMEIKYP
CAVKLEAQQEEEQIHTKTLLPQRRRMLLRHSALCAQNDTYASVHKYNTVADSMMARRSGR
REGATHPATTPRWDHHRSNFAVQHAAFGAAAVTDRPTTAQHATEVDLTL*
>TCRU_3383 hypothetical protein, conserved
MLANTESNHTVGLSCSHKKKWETMCEGKTTTRTSTWVPKEEYQVALMLQGNKTSVHIDCR
SLGAEEVLLAGGRPPEVLRVRFGACGGHESHVKLTDVFLYNRPLNSTAMRALKDRVSAPT
REAATTLPEKIRVVDSVREHIAGDITEEK*
>TCRU_3384 hypothetical protein, conserved
MGGPLQPQGQRDVVRDDEADPRVFAAHGKRAPLRVVRCAHDWGRVAARHFGAVCVVRGRG
MATIVRDVVDTELLD*
>TCRU_3385 mitochondrial carrier protein
MSTSSEKKHTPWVNAVAGGLGGAAAKSLLSPFQRVVVMQQLGEHKEYSTLQLARHIREQD
GWKGFWKGNLTSMIIRVPYSGIQFVLYSQLKFFFQDICERYVRPRKGSAGDAHHRGETLE
LFLMKCGAGGISATIAGVAVYPGEVVRLRLMSGERQFNGIFNTIRCIYAETHSLRNFYRG
LGASLMQRVPDILVSFAVYETMKYRLIEKDFLSSHPSYKNIVSTVAGGGAAALASILVAF
PLDVAKRRIGMSGKGKSGVVYAGVRDCLRQVYAQEGIRGLYAGARVEAIRCVPQVVLMWF
FIEGFQSFLTDHCVH*
>TCRU_3386 phosphatidylinositol kinase related protein, putative
MSLPVNNQTFSTSSPSLIGFFDTPAASALAAPVMVADTAMLKARLTAIVNDVQMPNPKEA
QKSLSDLRLFLDAVAEQSGTHIQNIFGQHVTNNILFVVMDSVVRPALTQYCSAAGRRRSM
ATRAAGRGANATSRRQHELTALAAASSASLVAEEELDALRNNKAKKLCTDVVRPWRALVE
TLHHNLPSSLLLAQASSSLGTSSNADNEEARMAAVGAAAIGTRGGQGGHAKEESAASNAF
DGQWMTSRAAANRTEMSSVADLLSTRHLWARTANHTSLPLLWKNAVPLFSITRHALEVLQ
SEVLVAVCGQEYAKLLLHLFLFNGYLSNLQPGIIMELIMRLLELIERTVYEANSTDTTVA
TSTNRTSSPLLAEMSPHLDVGNQTRHGVEGHVEDDVYHPHVEQGTTFAALLVQLFRAPQL
MSAFTPFEDEATLLLSTSTANNGTMPFIMQRLVRLTTQRHMRPTSALRLETHLLIALKLL
VTVARDDCPLTSAVPLELVRPLCHFFYTTTRRDGWRMEALTFMTTQLCVCFSAVLGRNVR
ADIERHRPHGVRCSQEAAPNETNNEKGLGGNMSEGTTSACDSVLVSPYSLTLLHETVLPF
MLQLFKVVRSEFGHVSRRELFHFPCPPLAPLFEFGAVVFYLACSTHEAYMKLPSLSSFVT
PAASPAPAASASVTRIPTVSDDALSKRVFAQEKQREQKGIKRSREEEDVMGEKTGEHSRR
KKRETPPQPGETLLQLFRSLFFLDSVSDDATAGTTGKTRGTGGKDDVGNLTEKDTETERD
TDCLLRVSAAAGGSLSAAAVQDLVKDGSLFMLHLLAHPGTTLGCSESQCTLLVEHGVLPL
FPYYGVRLETLLLAVLLAVTPRASLMCQQDVFRWLVRRYMPTVTTQRDDESQPKEHVYRL
LSVLLGRGVVGRWPLWINGEERARLQAAAHFSAISTRIRAVLYGVSKSLPKTVANVPQHT
AALPPAMMASLIATATAGHRSKTGLSTPLFMAMLQFLSLYQHYGAISAEIIAAQRMARKK
HLPEDDLDANHVTTALKDHSLPHLPSAAVCLSTGVAFVISGLSHAVCFLPHDESVVWRHD
TDTAAAASTCSSSFMQALCWAEEYLLAACFTVTENELGWQHLPIAVGGAMSDPAKNKETS
RGHGGGGGKTAASLQRMKQLLARSRYVMDAMFIAPEKHVPITVCDAVEGHWLLLHEFFAS
STEEPLAGIDAVRTEKKGVGNVTNEDEETDVSELFLGRLRRGDVPLGFVEILSGEVMRAV
GELAERAKVIGAACVGLAGGSSLQQPPSPPSQQPQHQQKQREVDEDAVAMAHRTLCIHAV
QLMHLLLRLFRLGIWQLPQGHRSCPKGCEGSNSDNTNNNNNDTDDSNKIGKNSSEDDLCI
LSDIPHMQLFDHPLSILRRLSPEGRLYYAVMWICRHLATRLLRGSVVRDRVLMRSLLILF
HDVGTVLLSQSFALWEPRQVVLSFVGVVSRRALDEGLVKLASWQPTNVTSADAVAAVHAT

MRLSCSLLSAILTLVRRTHVLAASADPLVIPARVTAVILHILEKDGLIPATMEAPKGHRS
EHLMNHGSETEMSSTQNVSNLNPFLPFSLAVVDAVLGLLQVLHEAYGDTQARLAARQLLE
TLFARYRYSLAESIFLTFSHYAPPHHAVVSSTVADGINYDEESEEEETMSTNTCNREDVE
EVAHRVGQNLQTPGGTMRRGKEKKRGRNAHDDFLFEEGQLLEVFVDQLTDVSRNDMPVLT
PQLQCAVLSSIYGVLFRCESSVAEKLGKYLFSFLSIKTAYVVRRHTALQVRWLFNRFTHR
TYAVLQELLYRAREGIASISPMHSATSLRALGEAAHAAPMLEADIICTLLECWATQGFAH
KGLLLECLEFIGKNTRLRERGFATATAMTGTAESETWMSAQELCHYHCERLLFDWLWRLG
HPMEAFPVVCFGYAGLQQMWQALMPTLLPLALLCSARQNGAEGTSVFLHPSDLLWRLAAC
HKRSGDATSNNSRTRELLVGCVRAYFPDVMARLLVFAALSKRHGRSGGVGDVQEIAEAAR
IALEWMGSTFSTEYVPFVRHYADAILCRLVEIVGTMTPFVRVRPLQEAVTMLCDIIANAP
GLPSTTGPGVGNTALDDFHHDDELSSLATMTTVDRFFASDGGDHAYVLLQQLYAGLTHDV
HRGTRHTMLALLFEQIVRHWWGRELLQRVPHILHTVLRLCGNILLTCVDVRARACNVLLY
VWTQAVSNTAHLLSSSLPTRIVSADEAFISTVMLTLAEDSRVVASTWNAICRADATLEQQ
DWKLQHARYTAESFVQNEDVDEHEVIVITPGANEEAEEHHRHVEKKGEESACLHLEKNDG
QTLSVMEAIRQVTRILPLLKSTVHVSGAPASSFYTDAAAAVDRARPAFVKLIRVHIREGE
AQSRLQGRVGLVKKDEDVARRIQTVYEMCCRAVQHLLTLVCMGDAFDLSSQTMMATPLTR
MRTTTTPTTTTSTAFKLLQETTREVQLSVFRLLRALCWCFIEAGAEGHVDALLYPVGAMQ
RMLQGWPFDKVLHCVYRQHVEQLYRLAFDVDADVARVASTTLRGWLCGITTDNNGGEAIG
EGMDGASENVIMSTRTCAVASITHRRRGVGDEGDLIRRTLEEFSGDETKQEGDVQRASSL
PPEEKEEKEGDVKGSHASSVILLKDILPFRRQLFDAQPQKHATVLVETSLKVASLLDEVV
WDALRVHEDESQFLRLFLVALIRHYNLHHRFSTVATVLHHVLLRPFSSRSGGLILFIESY
LPIVLLHTMLVRESETQRSQRAVWSRALETHLFRRACGFLHMTRLFLRALNVCHSVLMTV
VRSHGVWSENLESNPLSRMSPSELEAAAASLTFPLFVRSEYGELPELSDVRDSYWLSDID
PLVLASAAVTCHEPHLAALFTELSGESLLGRRKGIPSAAMTIVGQPKCSVLFPSKRRPSS
REDASREGHRRMLRGDETEAEMTQRLATYRAAVYAVLVDVETTLRFRDGSDNGGMVISDS
RSSSIDGTSVGGGGRNGSAAVGNNSSVMQTAGDGGDLNFYMSPWEEAFFLQHPARLMERE
KSRGNWHAVLLLIDRIEGAMRPMRVSSGIHRSYFACGFSSSRLLVEKANALMQLGAADTA
VQMLAAALKRHAPPLLFAAAGDKRRGKHEVKEETGAEEEEEDYFLQLRSALAATLWRLGR
WDLDFLEETEGTHRHHKQRRDLLLPSLVSVEEGIFYAMRAAHHGEHHNVRRWTTQALQRL
ACQFDETNWFQSMLQAEALHDIEECGRLFLRPHSSLSSSTSSTVEAKRAGGMRRPPPWVR
ASLVHVHAPYRELELLDSVHHRLCVLYRQPQWWLSHLENSSERALRSNRPVLVHQWLSAY
SEFTGGDVESQCGVKKEENEPFQQDGTIFEKLITSHELPAIAFLALVQARAEFVGGRPHR
AIAILQNTERSSSEEPTSVMNGLLFPMPANAPQMPAIVQQLVVWAREARLVPLSQLVRDP
FLLLSVKNDRTGVCCLQLARLCHTLVRDITARLHSEEYRKLQESIGASHRIRVELEQQQQ
MSDGLSDAEKRILQRRIRTLAVETTREEDEWQREVEMYALYRRSALNAYARFLERSGPAE
SDSLLAVFAFVSLWLQQDERLDERRLKAAGSAASVTSGIIQKAIKNVPLHKFLPLFSQLV
AQLGTSLDDTNLESLVLHIAMENPLHAVWPLLALANGENFGPAVATMAHGGGSSGLHVVD
EKKVTLARQILRTLKSPTNRHDDEDEDGAEDDRSTMKEEENKNKGRRCGWREKIVTEAER
LSAAYIQLAFYRVYNKHRPDHRIPADFMIIEKGVRDLLIPPPTFTLPLFSLASRSALPAL
LQQLPKIVRYENTFTTPGGINLPKALRCMLSDGRIVRQLLKSEDDMRQDSLIEQVFCLSN
QLLAQDKRTCRLHVFTYNVVPLAPTVGIIEWVDGTIPLGQYLNGDPNGGGTNANRLRFQT
GAHERYFPGEPTTLECRARLQEANKSQKHGVLLDLYAEFSPALHYFFLEHFFTPQEWLER
REAYTRSVAASSIIGYIVGLGDRHGNNLLLHTQLAELVHIDLGFAFDQGKQLPVPELVPF
RLTRNIVDGFGVQGTEGSFRRHCEGTLGVLRGQRELLMTILEACAHDPLARWAVTVLPPQ
RQQGRPQEIALQVGEEEEGEAVRRTTPRQRDLGVSRGKPTYADAERVLSHVAEKIEGYES
GELLSVPTHVHKLLQTAQNTELLAQMFVGWSPWL*
>TCRU_3387 Zinc-finger of C2H2 type, putative
MSSVKALNPSLQARRDPYYKRNHMGRVTCTLCDVCCTDDNNFLKHIAGKTHCTQLERMER
HARREERLAVEEELNREACRRASQEKAARELLLQQQDQQAGSRGGATGTDIASFAPFGRP
QFNYCTENDPELFQTKVWIEFFFPQAAAGVRPLHRWRSAREQDMERPPDDSVVYLLVACE
GYVTIAVKFPSKLPRTSASSSVAMTAKTMASYGSEVAVTASDEEEGRYHCSWDPLKKVYS
LFFILG*
>TCRU_3388 Cyclin, N-terminal domain containing protein, putative
MQEEHGKAVGQNGIMRKEDVMKNTHETILSLCRKILGDPTVTRRAQLPCLSFLWGLPWTE

PLIFIYEGDSWPSVIYPCHLFEVSGGFLPVAANNGATAIQHASLTNFETGASGLSIEDED
YAIKVSRFELVGTVFSFESYRIFSRNTSQLNPSMKPEYNRPVSSAVIRVITNESGTPSDE
KAATHRIMQLKRRELWQIFFYSFIPLIGVTREHLEKRWSSCLTNGLSQSDMESGGISSSA
HSSQALNEERSLVSPNHHPGISIFHASTRQSSTLKANSLKFNDGIKNSAASFLTTEGAER
NSDFSLRWDIFRHLFDQEERYRTDVERCWGYWTNGWDKVNRFDVVDSIDCIITSLGSSRE
AAHVAATYLDAFVCMSQTVVRDATYFSGVLLACAMLSCKQVDRFFPSIKAFLRYLRPQHS
ITATDFHRYEMHVLKTLNFCLQPVTSLEIVEVLLYLCGGPAAQQDAERRYRLRELKRWND
GACGGGGGGNNNVYDNNANNNEKNTSDGYRKWTDDSFTNTYHLRWNDLCKLAHFIADLMI
RNTRAQEFRHTIMGLAIVAIAAEKTSWVLPAPLVELLPESCRVSIHAGEKAELDCESYEL
LVRYAATMRCRCEQDGTETDAVSPLWRALALVHECCEEFGTGEQIANSVLQRRYNINHAA
VMSGGF*
>TCRU_3389 hypothetical protein, conserved
MWGGVKARAHHGDIFRGWSASQGLENLRRKLYREPRPWYLAWSLHHHKHLLSDHHCARLL
AWCTTVMDLEKRKTAKRQAYMYSQHVFQTMVHSHKVGSETYQEFFRLCAAGRDLTTAFRW
QQYLVETGHPFSLSHYTWLLHIAALSPNDESAEDMAEAVWEMYLARYFHLVKHEVTDGNA
TLQFQTSDEETRELEGLFRAFKQLRSKIYHCAKPELLEFIDALPDGSSNSVSNDTWPPVI
RHHTFRHLEAGASWTPPTLSRPHLRDSILHESFTNDLEQAAFAGNVQRVVELVDEYLRRI
SAEKSKESAKKHQAGERDIWHCFSDPSAVAFRKPLVEAGGVTAELYHYLIVAISATKPSL
ALRSLRCMEESNLQVLDLTRAVMIVRCEGSSADQQALLREQIKEIELRRKIDEDYDLTRE
VELFWKFCYTDFFHYRNALSRMELYLILMEGLGPVRVQELLIEAKLHESCSMEDVVVVDE
NFRAAAAVYFRSCCGEVDVNKALDDITEKMPKLDISLVGSIPHFSDYALPEGEFVATDVS
ALRNKLVGFKRIFLLDSSFVETSEHFITVGQASDVENEGSSLLLIPYCCLQQMSLTIEQE
NDIVTMDEALQEANKAEPFIASQRLRSLFALLRDVNKNRRTRVLHFSECLMAHSVMESQI
KAAVLDPAHSDNDHLFLLLAMIRTIAPEEADVVLCTDDAALVKIFHDDKSASFFVGKISV
MSSQPPPQVLQNGEDLIDDNPELCMSMDFEPKLQTSTYLGEKNRVLEGTAMLPSKTQLPE
VDEDVLGTAWLDMLDGEEQREKPMDLASRTSYSQFEDSKTGAAREMKHVGEKENEKEEDE
GEDDLAARENERLMNTYDSEHAVVPVGALMAKASSLGSVFEQFDVVGPDAEVERAMASPA
PYETPGQSSLRPRRRTLLEMEARRNRGASNRQRFRLARRLSNISGGRVPFNFRYRVLEVN
IADPKNKSFVDAYKKGMAKKRESFKRKFKKSYLVGGISP*
>TCRU_3390 Pestivirus Npro endopeptidase C53, putative
MEVSCSIADKPQTFDYFTERYYHQYVVRNCKGVEDNNCRLLVHSNGLCVLCLDGSHAAIQ
SHRKGFCTDEELDASHPRIESVTFGSGRGNAKLAPQNVCLVGKRKKNATKCQEDTNICVI
TMTDGTLYKIPACVAGFVLELNPAVQERPELLVTAPHVEGFIAVISPNYNKLDLGKYQKV
WEATGGDIVDDNDADDCTKKYEPQ*
>TCRU_3391 hypothetical protein, conserved
MKSNNNSQTEGVAPITTNSQNEPSDGHAETEPPLPTENGNFANNEADKSTEEGIPNNDPA
SDGTGTREEKQNENKEANPKETVPTTNAATGDTATAGDSDGSTAVSHTTSSLFLLLVACA
AAAVVVAAWE*
>TCRU_3392 hypothetical protein
MDWLPVPLHRTDNNKLGLCTFIRGKYLVSTVLPRDVVAENSAAVTRGGGNGGADGAGRRS
GRCVHVAAEVCGATLLKREIELVEIRWSSNATSLAGTFLFAIGRCTSVVVLQPTGDTHSG
KLMLQVVHYIEAKGVVASPPFLPFPPIAVGAARSGHTMLVVSHGTSVAFYQAPEFSTKLF
VAVDEVVTCVGSYERRLTMGLASGAVVDVRSGMPIAKLQSPPLLIDRIEGTSNDEETWLV
ADTSGECTRIYRRRQGDAEPRTECVLSIARVRRAADQPAALIMGCSRMSESLRITSDSAP
QFVQHPLQHLMIARGPLLAFFTDGVWLLAPQ*
>TCRU_3393 glycyl-tRNA synthetase, putative
MRTALPSRLENLVRAEFEDTCRRRFFFGLAFDPYGGSAGLYDLGPPLCAMKANLLSYWRQ
HFVLEENMCEVDTTSLTPEEVFKASGHVVRFNDAMVRDTVTGECIRADKLLEEYSETRLK
DATLPIETKQEMQTLRNRAAGMTPAEMKAVIEHYQVKSPKGNALSEPFPFNLMFSTSIGP
EGDRVGYMRPELAQGIILNFKRLLDSGNAQRMPFAGACIGTAFRNEIAPRANLIRVREFT
LAEIEHFVNPNDKSHEKFESVRGTEFWAWSRELQDANADPVLMTVGDAVAKKIIDNETLG
YFIARTVLFLEAVGLRFLRFRQHQRDEMAHYAQDCWDAELLTSYGWVECVGIADRSAYDL
TQHSAASKKDLFAREEFAEPRIERQLQRKLQKGAIGKAFGKNAGEVMEYLNTAPEATCVA
LGEKLASGSVEITTANGFTATIKPEMVQFEFKEVKVTGRNYIPSVIEPSFGVGRILYALL

EQSYWVRRDESAKNEKRAVFSMRPVIAPQKVAVLPLLVKPELLRVVEEIRGDMVLRGIST
RTDDSGASIGKKYARVDELGIPFCVTCDFETDGCVTLRERDSARQVRIPREAVADVVAEL
SRPLRPREWSSVETEFPAQSTAA*
>TCRU_3394 Snf7, putative
MLSRLFGRGDKQAKAREKQQSGGPGSVSQTLEKLESAYELLEKREGVLEKKMEMELERAK
QYHAKKNTQAALQCMKRKKAFEEQLTNISAQKQNLETLKFTLQNQNMNNELLEVQQRVKN
ELRERNKKMDADRVEENMEELQEEMEKANAVAEALRQPLDSQLLDEDELMGELMAELQTA
DVKVAESAPALPAMPSVPTGKLPKLSAKEEEDEDEEALRALEAELQS*
>TCRU_3395 Leucine Rich Repeat, putative
MLPIVKEYMTECAQRRVEPYYGFIEHAGAGEIVTDLDFAPLHSVRVFALTLLRCGPRSIA
VRGPKLQVLALRYDSNKGMHHPPRQSKRKVSYTTLLSQRLPEDVIVAAQNRPVLRSLIDG
VRVACMTYTGHLVRVELCGLPLREIREVVTRLFDVLQHCGLLRVLNLNKSKLTDQLFTRL
TTTVNTFPSLKEGHFSECGLTDGSARGIHSLILLNRGREQNAMWRASLRDGGGGHVATFA
RGLEVLDLSGNCLSDATIRRLGLAIAHDASLRVIDMSRNTVTTAGLKEFLQRGTLQESAV
ESLDLSKNLIDTKDKFFVGDNFACQHTYGEQLLLTRLDSRERHRSASTAPQLEVSGAAVP
QLRSSAADGAPLEIHHPRAVSPEDVGAGGLRSRESSPAAVLDTREENAEVCSQLLRCPGM
ERPQANRSTWTASPEMFDRQSNASRRNGDRKASERSRFSYQETGKQQENQPRLNQCPPPH
QTAVPFFPPLLFAPTGSGDGSQQQQQQQWCGVPLYVPVPVSSLGAMAMPPPARSTRDVA
VGTSPQPDTMQQSTSRSLSTTPLADGDVTDDGTAFEKMMMEPLQTNDWELADWRRNEQRF
LESLIVRLESHENATTEMLERNYQATCDRLGAIQEEFSRQIHELLQEQRVGAERFRGELR
EELLSERHQQQQQDPEAAMAEQLAQLIDTGMKRIHDQMERRSASASGTAAKAAGVDLQQ
PTQEYLRVVKERLSSLGW*
>TCRU_3396 eukaryotic translation initiation factor 3 subunit 2,
putative
MNIQGLALHGHMKPVTMIKFNREGDLLFSTAKEPNISVWYTKTGERLGVFNGHSAIAACD
VNNYSTLLVTGGMDFKAKLWCVESGDELANIMLKSPARAVGFAHDDSKVMVSTSRKMGEK
SAIQLYNLPFAVPKEDYIVHPVKTAFNPCAEFVSEGDDITFAVWGPTNDTIYYSMSDGSV
AILDVETMRTIRTQQPHEETVNRIGFDCNYYTLITASKDKTARLLDSRDMSVIQTYRSDV
PVNDASISPCGDHVILGGGMEAQDVTTQGGQTSFEVKFYHKVHEKQLGQVRCHFGTINAV
SFFPDGRGFASGAFDGLVKLHRFDENYEAAPGAKPVWSPDSS*
>TCRU_3397 hypothetical protein, conserved
MCIALGIVAEDDEAWRIASEAVAAEKEPVFSGNNGPFVDVWFGEQKLFGLVQRVAPNDFI
QVAQECGEKSDDAAATLRMRVTHNVSFVLHLSSVPHAMLQARGAPEDKFVNFMQLVVDYA
SLLRRGMKDEFLGVDPESDAEYIRFTPQ*
>TCRU_3398 S-adenosylhomocysteine hydrolase, putative
MTDYKVRDISLAEWGRKAIEIAENEMPGLMELRREYSQSKPLKGAKIAGCLHMTVQTAVL
IETLIQLGAEVRWSSCNIFSTQDNAAAAIAKRGIPVFAWKGETEEEYQWCIEQTLKGFSG
DGFPNMILDDGGDLTNHVLDHCPHLVDKIYGISEETTTGVKNLYKRLQRGKLPIPAINVN
DSVTKSKFDNLYGCRESLVDGIKRATDVMIAGKTACVCGYGDVGKGCAAALRAFGARVVV
TEVDPINALQAAMEGYQVLLVEDIVEQAHIFVTTTGNDDIITAEHFPRMQDDAIVCNIGH
FDTEIQVSWLKANAKERVEVKPQVDRYTMHNGRHIILLAEGRLVNLGCASGHPSFVMSNS
FSNQVLAQIELWTQRDSGKYPRGEKAQVYFLPKKLDEKVAALHLGKLGAKLTKLTAKQAD
YINCPVDGPFKPDHYRY*
>TCRU_3399 hypothetical protein, conserved
MLAALLPSVVLFVLALVAFSGAVTIVHGGFIRLAIGALIVALLISIIFSSCAVLLLEASS
SFPTDVVPVIFLRGALGAIAQPTIAGIVLLAMLVVLAMSTSRVCGLVEEIQILLDAHKAV
AEAEVISSTKR*
>TCRU_3400 hypothetical protein, conserved
MDALYLMSRAQFHQAATHISLYREDASPGYRTLGEECLRLVGLNPSRYVYWNVPNMSAYF
GKTVPVDVHGGYVLVDEGAAGRLATSYGVLRYAYLSAAVRAREGGRWRYDFMTMNITLAV
GVAGGFAALSVGRSRWAWMRRHPVGGIAVSLLVFLTGTVASRQAIRVLGVGIVTAHNSHK
KALTKLNCADCFDDVNLYTAQQVEDLRKQEIPRQPGMPPPPEEFVKRFERGTQLQIKMLQ
ADMDEVRAEKRRIGSHFCDVHRGLREDEGYAASVVLPISPVDTQRASERLRAERTEKKAE
*

>TCRU_3401 oxidoreductase, putative
MSAKKRAFDVLVLGAGAAGCAAARAIALRYPNATVGLVEQGTRRPLPLVMRVPLLTPLVA
SVRSTRGFLRKYHGVPEECIGGRQLKYVRGCALGGSSCCNDMRYMRGTTRDYAAWGDPMW
SFEQLLPFFCALERNSRGGSLFHGNSGPLDVTDVPRANVGFELNILWFESCEALGIPETM
DFNAGAADGFSALQSLIAKGVRVDVFDALLERDRHLFPNLTVMPETRVQRILFDGKRVSG
VENRVGRDVEVLFSGRVVLCLGPLESPALLQRSGVGAGGRVAEIPDVGRNLIQPTSATIV
FGVTHNANLRSKSVSWRNAPYLLRQWREYNEERSGAFASLAEGAAFVRSTPTAAWPDLSL
TFFATPNVRWCGWRPFDGFAVRVAHHYPESRGEVDAVDEHNIRITSRMFSSRKDVQCMDE
GMRWVGSLFNDARSAFHIDEKGRPTSPFASLGVHVRHPRNALHTQQGAAAFLAEHAQGTG
DLFGTCALGKVVDSTLRVRGVDGLHVADASVVPTPTCGASCVIGAAIGSRVASILQV*
>TCRU_3402 replication factor C, subunit 4, putative
MSQQLVPWVEKYRPKSMEDIVGNADAVSRLRVISKEGNLPNLLLCGPPGTGKTTSVLCLA
RTLLSDQDGGDTTALKEAVLELNASDDRGLDVVREKIKLFAQTKKTLPQKVNESSQQKIN
LHKIVILDEADSMTPAAQQALRRTMELHSSTTRFAFACNNSHKIIEPIQSRCAVVRFKKL
THADILKRLTYIIQQENVTYTDDGLEALLYLAEGDLRSALNALQATHSGYGMVNAENVFK
VCDQPHPLLVESIMDGCLQKKDLPSAHKELQRLLGRGYAASDVISTFFRTAQNPKLFRNE
QQQLAVLRIIGETTMRIAEGVGTPLQLASMLARITMVNTD*
>TCRU_3403 hypothetical protein, conserved
MTSYAELLAACTEFQENFASLNGKYNAAVQEVQNAKEANERLSKQLEAMRSSEDKLQHTI
RELKKELHEAHAYKDRYLAANVSVEHLKGRLENARRAVADKMLEHEQQVEQLQGQIRDLL
QRVSVCADAQTTQKLKKQVLELEERCAEQSGHLLEEKERGSQQLLASHTALREQQARNLE
LEQRCRTLEAEITQMRSVVRRSADLQNEAAVAREKSASDARRAVMQAESVAAELRETRAR
LNAVVAQHAEEMEAAKSAADDEKSQLLERVSQLSAAVDDAVASRNAEQERYAVLQRSLHE
RVEAVRTETRLEVTVLQKSLSDARAEGQQLAWRVEQTKMELEESRRAVQQREAKLESCAA
ELRQLQTRLDAVTQREAWLSAERDHQLAQLAAAREQAQHLAASQRAHEESNLAGERLRIQ
LQFLEEELQGARRLAEASDSHVRDIEEAAERRLRALRSELKSVKKNARAERAKADAVRRR
LVQALLEREANVLPQICLQTQRPHETVATAPEQQRPAVGLDVLTLLRGQTEQAAALHHRL
VELSR*
>TCRU_3404 14-3-3 protein 1
MAEGIKWHNAAIQDELVPKKSPLEFKLPDSAKELVFMAKLTEEAERYDEMVLCMRKLVKL
NSELDTEERNLLSMAYKNVIGSRRNAWRIITSIESRESAREKSENLQLIASLRKEFEAEL
AAICDDLLALLDTYLIPASQGGEVKVFYLKMKGDYHRYYAEIAPEAGQRQAALDAYAKAT
EVANSSLASTHPIRLGLALNFSVFYYEIMKEHEKGFQLARQAYDEAVTELETLDDEAYRE
SNLIVRLLRDNLNLWTDEQPSS*
>TCRU_3405 DNA topoisomerase III, putative
MPTWLNVAEKPSVAKELSLVLSSGTCRMGNSLSRFNPVFEFDFEGKQMLCTSVAGHLMND
EFPPETRSWQNYPLVNLFTASITKHVKPEMEPVKKNLEALGRRSSNLVLWMDCDREGENI
CFEVMQVVQGVNRSISIFRAHFSALTRRDLLSAVRSLKAPNKALSDAVEARQEIDLRIGA
VFSRFQTIKFRDAFSGMPRVLSFGPCQIPTLGFVVRRHREREGFVQEDFFTLVMRHGQTV
FHGCRGSVFDQLAATLVLETMLESAGPNAEALVVDVVRRPTRRHPPVPLATVALQKLAAT
HLHISSEQCMTWAESLYQEGFISYPRTETDSFSFTDDELREIAGVQRENPEVADYVGAML
DDSSHKFRRPLKGGHDDKAHPPIYPTKLMRAKHDNRSALYNLIVRHFLACLSPDAVAATT
AVTAVFGEEKFTTSGTAILEKGWLEVYPYERWHSTCLPAYQQGERFVPKDISLEKHRTTP
PPHLTETALIALMDEHGIGTDATIAQHIKTVLDRGYVKREGSFLVPTALGIALASAYEVI
GLLSLLQPQLRAQMELAMSDIVSGKASKAQVVDAAVKLYTEVFQKLSLGSKEMYEELCCH
LSPAAPQTSGTHAYGTGRIEKRRLVHCGVCKNPMDLIEQTEGERDTWCVRCHTCLKDYRV
PNGRLNQLSSCGQSCILCGFGVLEIRNTEKQTSYTVCPYCFTSPPPGTDMESFTGFRCFQ
CLADCPLAKGIESVAIARCSACKQNDIRLCTGSRGAFLSCRGFPGCTFSVTLPWAKGVRP
TPTMRCASCQAVMLQFNFGGMPSVPGLEEGDCVCVFCDGRLQDYISVKGGFTRDNDHTAD
REHANQQQQQPQQEHPAPYSLPSLRGREANNRSKPAKGSATGTLCECGVPAKQLVSRKEV
SKGKRFLTCAARKCSFFQWLD*
>TCRU_3406 hypothetical protein, conserved
MSDILGKNQQTTPVGVPVTYYETCRRIEYLASLGMPQVTPYTEPTKPLVATLPEPRELLL
GEGTPLSSPSPVLLPVEPRRTVTPSTTSTLRGTCRKKTELEKFDMDAAYAAFIQRLEQRL

DEEEAKNSKELGSASPLQ*
>TCRU_3407 CobW/HypB/UreG, nucleotide-binding domain containing protein, putative
MSAVEDGEDCPELISAKVPVTILTGFLGSGKTTLLHYVLSAEHHLRIAVIVNEFEFGKTI
EKGLTLKSSQKPDDEWLELNNGCMCCTAQSQTVKALESLMTRKGTFDLVLVETSGLADPG
PVAAMFWQDEAVCGSLFLSGILTLVDAKNICRYLHDPVVSGEAARQILMADRVILNKCDI
ATEEEQGRALAEVRCINPVVQVIHSSFSRLENLQEILFLNTTRRLVELGHLHQDAPSGIT
AVSLEFFEQPNFLALRDTGDVDLICRDLLYKDHDPPFEVVRSKAALWVKKAGQYSLLQLQ
TIGELFDVRPMEGQSVPMGCSRVLILGKQLDKDVLRNIFLRYMRVDADP*
>TCRU_3408 tubulin binding cofactor c, putative
MEERFLKTRAEREEARQQKTAVPSSVTWDKLEFEQQARDFERDVMQFIADGGVRAAQEGV
NRFKLLVQEATSNNVLTSHEMARSNATLSRLQALIDAKRDTTNRAKAFKFSSQPKAKGAV
IMEMQAAASATQRSNEEQSHASNVYGYARDRTLFVGPSKAVFLRACENCEILILPVPGTV
FISDCKNCRVYVACHQLRLKNATNIDVYVWCASTPIIECCSEMRFGPYSCWTGLLHSTVE
GHNYATHEEWVGRVGEQRIDEHTANSYKTVDDFQWLRKTPSPHWGVLPQEEWAMSTERFI
QGEPPAK*
>TCRU_3409 ADP-ribosylation factor GTPase activating protein, putative
MNPLARRVERNRDEVRKLSQKCGNRFCIDCGIRGPLYVVTNFRVFVCSTCAALHRSLQHK
VKGISMTEFTDEEVACLNVGGNDRAARVWLASYENNKPPHGSDIAVRDFIVNAFENMAYV
NREELERFQNDLKAVGTGASCCHLPHTMNLPLPEHGPQRPLTSLPPEQPTKEKPLPPEPS
SSSTGLQDLSSAPRPQVELFEQSTPQTSSSAPVNFSAPTTDDDLFAEFVAAAAPPASSVA
ADVPTAQRPLDGWLNSVTSGHPHVNIPVSIPPGVTMGPGPYSTSQPLSAGKMEYPPNMLS
QPGFQGPFYVQQEGYGGMTRGNFFQLQPQPQPQPQQFQYAFSMGPPAGPNGVPYQAPTAQ
GQTPSGGSATLMNMCGVDFFQEPPANPWGNFNSSESTKTEPVKTKSEPQNDIFASLDPFI
GKW*
>TCRU_3410 hypothetical protein, conserved
MANSAMPWAYQAVVSYSRMNAAANRGGVLRAAKCGGLSLEQQSPAPNLLLSQSANDVRRA
VWLLHRPRGVLGLVVSPRPGTHYGSMPHEAAPLGSPGVKRVMRHLRSLSFRVAGDGPTCP
PMVVHKNHLIGWCLGGKAAPLYAHTIDELARLKPGRIKTLSPENAFVCVNYYEWDDWREV
SMEPGWSWHHADEHVANGLVSGQLSPDELHNLAAEVA*
>TCRU_3411 hypothetical protein, conserved
MKDVKDEAEGVEGRKPPTFSEDEDEEGSEENDEDEDTEAQEKRNEREGDQEVAVTSDPNS
GETNLSRSGQEKDTAIVSTQGISPSNSQESIVNPTQPEVEGKKDTDKSRPAVEKALRPGK
GENTLPGGVAEGNLPSPPEEGVDSRKQDGEYTASEGEKSVPSPETAATSQSHRDNGSEGT
GEDTKATTVTANTTDTQSTQNSDGSTAVSHTTSPLLLLLVFACAAAAVVAA*
>TCRU_3412 E3 ubiquitin-protein ligase KCMF1, putative
MDGESNVASTPIPWSLMLEYERADAVLQLFRQFSFFHADKLLLIEREEVICSPGMDSERM
EYLVIHGSVGNARKEAFLKLLRLARLTLVQDMASQVVVCPQIGDLLPNTMLHPLWETSQV
RSFKKWNRIYWAMRCGLLKKIKRRREMIQAHVEQVLGLKAENLVQNSSVEAAGISHVNEE
AFYNSFWNLLELEQEEQNAPLELYYTACSEERVNLSTVIATVPTLILLWASWDITSMEWL
RENLFNVTKILKANTLQTFSSTYSSSMKDDPWVETVMRFVQLPRRIVMYRRTRLKRYLKR
AQIVLISVDREKAAAVDALNGLFSEVSGWKSPEVPLIPLWCGPDGLQSDLATELNIAQLP
FFVATQLPDKQTRKLGDGRFPRICYITSHTEGEIAPDACMKNNEGEEVSERGFRLMNWHA
IEKKEREIVMSAISRFLAASDAPLRFIARVDRTYQMNPASLAQVKKRLKPEVTSFVTMSG
TISTLDLMKLKEKISVLSRVRNFFFDVKIMKPSIPLLIQLNPKTPTRYVLGSARNITCSE
CIRDVLIDKEHHFRCIQCDQSEGVVCWMCFAAGKHPQHHVLLRVPTFSETTLNLLWGPSN
VSPLALFCGKLVSNINETHVGVYCNGCSQLICGVRWKCAMCYQYDLCDCCDEKRNRREAL
KCEGDASTPSGGISGPIHTFTPPSTHPKEHLFLCIRHGCGADGDACLNPVIEKNSLPLFI
SQ*
>TCRU_3413 developmentally regulated phosphoprotein
MRRFSGFLRVAAACLCRNKVDFSDLQRELQEVKKRVGVIEERQTLQSLLAFYSSRPMQKL
SNLNEVIYYCLKTGYNAEIFCHMELPVLLARLIMAIDTLPCGLNAMPSVLLVRNTYLDSF
KKLIKCDFPDNDERILHFRRVVADIEEAHSKRDVLGTMAMGLLELKKLLSRHGQYVFSQN

KKPSGSAFELTLDEALMDVTKPMDNFSLRMVNYNFISRMLLTLEENDDDMVGMVDLKIDL
ERVVRNAVDDAKEVCTQHYGDCPDVKFIISKDANTMRFPHMSSTITYIVVELMKNAFRAT
VESHMERNSAGMVDCSNLPPVEVLVNIKKNAKHACICVSDEGLGMTRAQCELAMTYAYTT
VKRPIIQHGADEDSEEERNGVSPLAGYGFGLPMSRVYAQAFGGDLVMSTMEGYGTRVYYY
IKP*
>TCRU_3414 Enkuring domain-containig protein
MSGENIYNVLQEGAPVTTGPYTGNYEKHFKERPKPAYSTFFEKGKEYDGSHVRYFKQRHA
VFGPVIGDTVDPKNFLRSGRGVKHSVPPVQQRKIFTKPLLDHGISKSRNQGRERVAAKPN
ILSAGEEADELRDANGLEGGYGRNGEKSGVLTTKESGAQSGEEILEDQGNIDWKHYNGPT
GYVKESGNGQHGNEEKDFAAHGANIDQSLHSANAGYLGGKDLVDGKKDFATSNIIQVSNM
VPKRRKDQPENPTSRKTFGQAPGYLHRVKREIDEEKMRLKSIEEMQIQQKIQNMKKFVHR
LDKKEQLQLLEKLRIKLNEKSAELIKMPFLKDTYTQILRRAELEKGIKQIEVAIAKLDKD
AVFVYNDDPRCIHWTKNAALEEATLFASEREN*
>TCRU_3415 hypothetical protein, conserved
MGARPRAQDYGPRHAQLLSLEREQHRVVTDRLYQKVQKLSLKWAQEREAHASTTLLLFKT
QMEVCILQEESARHAIAAAEAEDRIGFTQLEGSREPVGSHRKGADSCVLSQFFSAAPRKK
PHILYAYDSDLLRALQRSEAYIAHLERYCHEHLPCFSPSAFFASHYLHGSPCSETWSSAL
AGTALDGDTASYVPLSPYIRTIM*
>TCRU_3416 rhomboid-like protein
MASRLLQRRGVSLVGPAKSTFFALYNAQKQGMCVSACRCPGRAFSSTRTIQEQKNTGDYL
AGFREVKTYEGKGEEGEGGKEEEDPFSAGPGQGYLPFPPPFHTFNVVMLLFLANVITYFL
MNFSGSDSLRDFIVDHFTLSHENAGKIYPLLTNAFYQENLLQLLIDCWLLWQFGNTMLGF
LGNTRMTFFAVLCTLGGSFIHLARQKFELYYGMDPLEVRGRCYGPNPFILGLIGVEGLIF
RHLNFIQQPPVPFLVLTAFVMVIDVWRIFTTRPEEHGASTGGALVAYFFWALPTRMLGLD
KLTAAL*
>TCRU_3417 Protein of unknown function (DUF3808), putative
MSTEVSSGSNDGPSFHHHIQDAVHMIWNNQCSEAEEILFPYKEIHPRYALEYANKYLVQT
LMNSTNESREILLELFKVADSLASAAKYSEPMFDFDVENDGDGTGMSMCLPSKAERKISK
KSFNGRRKAAEKAGQSFVDNWKLECDVIYADALLMRSVCQLMMNSYFKGGVNLRRTWGLY
HKLIQVVEADRTNQIPNELKMCVKYGTGAFYAFLALVPANLMRLLNVIGFISDKELGEQY
LTEVFESNGVRSPFAALVLCTLYLFLPTGLGRVEETLAKAKRILDAMNQKYEHNTYFYGY
SNFYHRKRGETAEALMAIQLAETNAERAGLVPILIRYLHADTLFMDLRFEEARDRYAALL
DHLAKTKESFAYTGQVVLSLAACFVMLGDDAQAIQWLKKVGSMYNSRSKNDANSPKFASR
VLANPRLLPLCGVYMLYINRDLAHMKVEQAERLLEELTRVTKGKDLSGPEPENMFTLFVG
VIHKGCDRIDEAFGYMSKIFANEKRVPSDSMVLPYAYYEAGELEYRRGNYENAKALFTKG
QSLKGDGNETLMNRYNIALKQLKRTMEERKGA*
>TCRU_3418 hypothetical protein
MMTAPAGREQIIAYDSDSDDSVVEDVAPHRTVAKRAEMILAQQQRFRSVGEREAGKRELN
SLGGAYGDFCRGAPLSMWVAETACTPRKLSKSDKNEACATAALQTPEKNRNARDDEILVP
SPKTGGRVCGYRSPLPKKTTSPSIVSDISLASACKGGAWGGQESIGRNSPTASEVVPLTP
DGSATSSLLSQAERSAVELLACDIDSVTRECWRASQEQLLPSAIYAEEDRLAAAAAHTTS
PGGTAKRKRPRGVATPEKVNDGTARCLQFETDSSMRSLRPSVSEMALKRLNKQTQQRLAS
RCLMLPY*
>TCRU_3419 Protein of unknown function (DUF1637), putative
MLNFKTVLQRKGGQFCSASITKALAQLTLLDLKSYVSEEAAQRCMADCNAAISEHAFSLH
DALHSSGPNCWKGKLDGRVGCSTLYETDDIALCWFVVPPGGVLPLHDHCTMVVWQRILFG
RIHITSFDWAQGFEPVDTQLCNRRGGEAIVVFSGTSEARSNASSPASLVTSFGPHEGGVL
HEIENESTEPALFVNVMTPPYNKPPNNIECMYYSLSRLDGGRATPLESQSDAACRERLTV
GQRVLLTPRPTVGKMPMNVFIPIQSPW*
>TCRU_3420 procyclic form surface phosphoprotein
MCLFGIVDAVGDFLKSVVACACCLLIGSPALIITGSILFSQRDLRKAFSDAVKEFNPKPM
NDWTGTINDVPITLRRESLNVKSVDGATSVFAEAVVSVSEAPPTELPVFVNVSAVFPFLR
KAPFISVKKLFYRCFSTECKYGKDEKCKRECRNFEAKCIGMGGVFVFTPTPCNVGEVCGE
CRLIFYLRQLYLVVREIGNEKYVEDTKLRSARYAFGDLDNEYQPGIPSTVTVRLYSSKDP

YIALQRLTKGTNDLGMNPRTVGIVLIVFGCLFLLLEIGVCTALICYWMRPNKKSLGTPLY
LAPASQGTLTSGGPGDTAPNPYAHLVEQTGQGYTYGQPLPQGYDYDQEAPPAEQQDREYG
VSLYTQDTHGSFSPPNADNK*
>TCRU_3421 Cathepsin propeptide inhibitor domain (I29)/Papain family cysteine protease/Peptidase C1-like family, putative
MWNLICCFFFVATATTAVATAVSAITVTSNEDYLAQYTFEKYIADFGKRYADPEEHRKRA
AIFKENLAKVRAFNGVLGRSYRLGINKFSDMTKEEFNAKFNGRVAVPQSTRSPQRASYKH
TKATFPEALNWQEAKDPVLTPVKDQGSCGSCWAHAATESVESMYAISSGKLLTLSTQQIT
SCVNNTRKCGGSGGCGGGTAQLAWEYIMNTGGITLDAEYPYVSGGTSVTGSCVLNRSMPR
VVNVYGYASLPHNDYEAVIEALVQKGPLAVSVAASDWMFYTGGVFDGCGKDGENITISHA
VQLVGYGTDNKTNQDYWVVRNSWGEDWGEKGFIRLLRKKQDELCVFNNAWNTVGGGCADD
PNITIVACGMCGILYDVAYPVVTKPPGRGRFLWAAGTAFGGLCVVMIVLVILSRYRGTTP
KVCEAFREESEALN*
>TCRU_3422 Monooxygenase, putative
MFHPSLRALSPVIPRNLFNVVVCGGGIVGAASLASLQQLRSRFLSEISREDSTAGHSVYA
SRLSQLLLVDSVPRPQYDAQNVMHTLRTVSLTPVSSKLLDNLGCWRRLQTKHPYYRIALR
HEQTNSPFFPKQNRPVSYFMSYLLGGNEATAEPLLEFTDLNRPLGFVSYNAEINTELINV
IEDQQKLNDANVAKDRIFFGSTVTSVSLPPQDVVDGALGGAVLRSTSGDDSLNFSLLLGC
DGRGSSLRELLATGAVQHDYAQTAYVCTVRLEHMDDGNSCCFQNFFLNGDVIAMLPLSED
SANIIFSTTAARARELMAASQSDLVSELNGRLHAFAPKDIPRILGVHEGTVNGKQVRGQG
TFPLRLNFVLRPYSPRCLLLGDAAHGIHPFAGQGLNLGLYDVCALIEVLEKAIRSGQDIG
GVCAVGQPFASEMMLHTSSMITAMEGIYTALNAAPSLSCAGMKVLQGLPLVSSFGKQCIT
NFSSGGLFARRHSDCFLLL*
>TCRU_3423 Transcription factor e(y)2, putative
MKHTECKVEGGPVSSGARIYEEMSNVQKQLLRDYLSCRLGTASNWRKAVSQRVEEVVRRR
AQSGESLDAHDVVGEVLPFSRSIIPSEVREGLFRQISDALRLRDERD*
>TCRU_3424 hypothetical protein, conserved
MSGTKGEIANKIREGAQRRGEEIQRIRQLRRERREELKERASNASSAGNSSFIPYILISL
VFLSFPLSEPKVDWLLVCLFLALNGTWTIFFRSTSWINWAIMCVSNIVLVRWSPFIPDLP
RIISQLSPTHVAVYVSGNIFLCIILYFGYVERRAPWNASSRKSGKKSTRSDKGDGEQVES
LEEFARRRDWMNRLDLAASGMILGNVALLIVLGVVPLDLFMQSLRQFFSFVR*
>TCRU_3425 hypothetical protein, conserved
MAPKKRLPRRHHAADGHPNLENAAAERIDAVTAEPLHPLKFVEIMSPDGTLRLFYNTATL
IRIATDRGMFMQPPHFREPMLPSLQRHVEEIEGRTFRFERSNVLIHDLGDGNDGGIHVLH
RHVYFDQIMDEFYLLNPAELYVCPSCYLHWIGTRLIPHLTVTRRRIEYVDGDPNPVIDPL
DVFAHMQGVQNAAADETDNSDTADVVEEVDRVPLTIPSMEAVPEWDSPLVHIVFRRAISW
RRHVRRHHNDSGTAAVDYRLKEFLSQYISQYNRLLEMKNRKQRRRGEGNLAGVPEMTVSR
YWHINARYNRLRYNRIVETVERAEPHLEECVNQTAFPNENVMSTFHSNDNDSSAGDFICD
SESSSGTSGSGDESLQSSCEEADAEGTKQNRKRRRAISQSTSSSLSSVEEDEEEEEVSEG
QRRLFKSGILAPLPEPYRNYTYEERRVLDTLSRRVAKPTMLYIPPPQDEIDDDRGDEDVD
WGQIGETIESASMYLREKQQRQNSATATSPADHRSGREGSTRGQEEPTTHECAATVKQMT
GALPVAFPVHRLMLDEDSISPTTTVQDVFVLEGQKRLLLDDSD*
>TCRU_3426 hypothetical protein, conserved
MSEWNAVVPLIVSGASDAHEVTHAELCAMVRGMEETVENTKRRLKQVDKIIERQRVVVND
VRISTSRFEDMFTKTNSDLQYIQQQLEYVVVSLEKERGIVADHTEQLRLFAMESNRRDGR
SADVLDDGTSLLFWLATWLYRPLVHFAKGCYTLFSPLINTLQSLSLFNTDVLMRRSEIGV
RLRHVETNEDLLKRLQKGSLDPTSLPKKK*
>TCRU_3427 cis-prenyltransferase-like protein
MHASVCFEDDARVLGTLFADTSDPVFVLNCCRFCSVDALTEGFEVIVLFFVAILFSVCLP
CACCSLWRKPALRAVSRYLRMCEMLLEAEGQDMCLKPQACPCDEGANSGKDATQHLSILP
VGCSLNGILNHGVRHLAVIMDGNRRFGELTSLSTVSVDAVTKLCDSILEEKNPPGSSVER
CSALVSLLRHTTLDGHRCGGEKLIEFIDNCLEFNIQMLTVYAFSTENWERSALEVNVLMA
LFYFFFERVRSSAREKGIFIRFISPAFERIPISLRKLMLLVEEESRGHRPRRIVVNVCVS
YSGREEVLEACNRLLRRVDKSIPISNAEFMSHMLRSITQEGHEAEDATVLADGGGAEPQV

LLRTSGEQRLSNFMLYECAYTEFFFTKKTWPEIGREDFIRLLCDFSQRGRRHGR*
>TCRU_3428 WD domain, G-beta repeat, putative
MDEPPTARFVSEEESKQRSEVGEAISIPSSTLVEFNPRSDTIRGELLHVVVGWLIEQGLT
SSAQILRDEAAALLRQEHNERKALRAISRAIHEGNWDTAHAQLKKLESITKPDGSANSEV
PLRIVSLLQLMPFLLAQQQFLEYVDEDDGQRAHVFFMRRIKPLEGTISKDHFQQLIYLLT
CRNVSEAGGMFPIWRGWTPTIGRSQLQSLITKFIGYCDSSPYCRQYEGNFDAGPHIAFKG
LEQILANSLSYELLKSQHPSLLRGLATHSVHSILQPLGEQLVPSNLIASIDVNEVRCGNA
AARGKNVRLTACEPFLQVHAVVVGTHMGSILWVPLEKKRVESLSGASCDACLKLYQYNTP
VRGMTSHERQILLSWSACQAVVLNLGSIMGSASDLLGTSECWMDCVANTFTHTAEVYSSC
FFPSGFILATGLSDGTVAVWDMLTGAKMFQRSFSTSAIESLTSNRSGSCYFAASKEGLVR
VVDVTTGVLLFTFASPVASEISSIALSPSASLLLVSYRSGMLRLWDVLTGDILPQRFEGV
ESHTRKGASVTFGCVDSHIISGHNDGYLYIWDIGTARSRESSILLSSTAPNGTAEPFQRE
MAGLHSSSIPGRYYWPMGEAVPPPVRTKLHRSSITDVKFQHHYVVTCSDDGMVCICSGLL
NHSR*
>TCRU_3429 adenosine transporter 2
MAVIGFQSWPEFFVYLTFLFFGVSIMLVSNAIKAAPSFITGYYKYAQGDKNAKPADPVFW
NNVLTYFNVAVFGTQTVCEAFMLTPLGRSIPLRPRLIVGLLIPFGEMLALIFIPLARTSE
IGAKITVMIIAVVSGLSKTLCDSTTGALAGPFPTKFYGSVIWGLGVSGIISSAMSIIIKA
SMSKDFESVQTQSRIYFGLAMGIQLISCTLLVVMPRNPFARKYTAEFRYMRAHSNERAPT
SGELVPMGSVDTKEDSAPQVEYDIPSSDAQCKKNVMDAEGDADNMEDIDQVANITSTQQM
LNAQIATVFKCIWPMLLSCFVVFGATLLIFPGVFFAAGTSKDWYPTIIVAMFNLGDFLSR
FLLFFKRLRPSPRFVLAGSFLRTLIVPFLVLCLRGIIPGDVPPYIMCLLWGLTNGYFGGM
AMIHCTRTPSLTMAGQRSIAGIMASLSLLLGLFLGSSLAMAVMKGLPR*
>TCRU_family, putative Mn.1
MVEKVKATTRVALESANRWTDNVYLLEHHISQRMGLTPRELRMRLQLPADVDYIEFDELV
PDREANPKTTAATLERMSSSPQRAAENAAGGVVEAPSRSPAAEEADTPAAINTSSTHKEE
EEAAPRNGRKDTRNTQQRIKRGRDDGTVAAKQSQSVVADSPRNDASEDAPRRTVARRGRK
KKEL*
>TCRU_3431 BNR repeat-like domain containing protein, putative
MEKGELHLWLTDTAHIVGIGPVPGDNAAAASFLLYKSGKDGGNKGEELIAVYEKKNGDGK
PSSLGMVSVLLTEKLERVKKVLATWKEVDERVSKLCPSKSDADCASTGTACGALKITDGL
VGFLSDNFSDGTWRENYLGMNATVSNKEAAEQVKSGVKFKRHGAVAEWPVGTHGENQL*
>TCRU_3432 hypothetical protein, conserved
MGLARLLFRLFFIVLFVYASAVGAVLVPFPPSFFVTTGTTIPFPLATPVAQSGAIYVSNK
TKQLRIDNFFLGSQYSFIADGERRRGYVLESHAPGSFGASYEEKGSFCRTFKMTGDVTSF
GVPDEFLKHAEGNLVRGVEVTRYTGYDRDSTGPLQQVDYYVRNMTFKLPGEKKGTVEEFV
FTIPWRVQTQRQQKALKELTGAPVTVPNWRYFGGPFFDEVITPDEPFVTHLQRLMEDTIV
TVDFYNFVPIAPDPSVFKVPSDCEEVDAGTASSNVDISLAQRLLVDLSFYTTAGRQTLRE
KSKDT*
>TCRU_3433 hypothetical protein, conserved
MYQLDAVPGRTFAALRLDREMPDLDDGSDLASGDDSVSTERSGPSGYIASVLAVAFGTFS
APQRLEALLPLCQRWSVPVPSGDGEGREQDVCRVAMERLAAKMCGVLKKKSF*
>TCRU_3434 hypothetical protein, conserved
MSTYRDRLVAFYEKYAPRKVGQVDAQLEKYAGREEDFFSALVQKYGPEPGNAAGTPAASR
GASPALSESATPTTMDRMSTYRDRLVAFYEKYAPRKVGQVDAQLEKYAGREEDFFSALVQ
KYGPEPGNAAGTPTVSRGASPALSESATPAVAGAAEKNSLADHHQPTSSEAIKNTVAQKV
DANARNISDEDRRERLRALAAQLGVAVESDDPLQVLSALVDARRGRNFGTTSPVRDADAR
VCRVLNESMYAPSTSRLTASVKAMMMMDSRSPTDLSVMLDAVNEEEAESRTTLELLAADD
FDIILAAQRRALRSVGRDGALSSLRASAEAALLQRVWRGWHDTAADYVKQAMHGRHHHRT
RYQKMLFSKSVAMYYDRIARSKRQQERRRRQMDAANAQANAMRRRRLRETIAEHGNLVNR
NIRAVLLRQSPGAHNNRDTPETPEQSPDAVFTHGKAEPQRTHSQRLAQSPYWHGDSANRH
GSGDRRNNRSLSFYSYGNRSARLLAIEKDFDRLPSDARARVVRRLQKWDILPKSPTQHFS
RGFPHLQSMRERGEQLARRLDTLDAFAAVADEEDTPPQWWKSETELRQYLARVLIDAFDA
EEREMLGLPYEVL*

>TCRU_3435 Phage tail fibre repeat, putative
MAAGIRAVETDVLQRVRLAADRILRVRLAYEAVGNALGDGSVRMATDTSDGEDDSVVAKI
RELHVCLTDSLESLVAFLGDDTGGATRRLHDGVSFEAMVKELMKECRSASAAFVDITSLV
RDGVEEKEEVPGGEATTITTTNKKNNPKPLVCCYEDLVVCVRRSLTRARGEREKNKRLCE
ELRRVLATTTGTVSVAAQSSLLGACLSHADVATDNISSFSDSLASQKAKQLFSKEELVGS
GDSDSCQSPLGSRHSFEIVHQVRSHIASKVAEVQELRTAVTTSVEKLGGTVTSPSVASHV
IANALLDVVRETSASIADVQALIDPDAATVRSGPPRLRDLVSCLQVKVDEWETSMREARE
LVNSVMNVNDPNYSLAASPGRSLTRKSKPNPVVAGRGDESLSLNRTFPVSSESGSIGQLP
DGRSVADASPRKNRAFTPFSSEAEGGGMRGKFVQDAVLEIRAKLIGIRQLTNACATAVCL
MGGEEGVERQALDILPVQLLQRAQEVNEVIQLTQDAVSLLDGTEGEVGGTAGGVAASSCP
SIRTRVRRLVEGMKALKDENESLRLQEIASLKQKAFLLQDFEAMRDKFASQEKRLGEEYQ
KLLGECNELRGTIDRRMQEIQERDDTLAKQERRNTELEEERERLHAECDQLRRQITTLRV
TRDDLQVLEAGPKEAAIILRRASAFLYGRLQKAINQISAVSSSSSSTSTLWTAAEEKVTE
NHLQEDKPEGIVKALDVNDASVSAAQLMAESGRELRRCGQAIQQIELHLRTETQLRHWVR
WVCVRTKEEVVSEEAAVRTLLREACRNGAVLLSEKMRVLKERDEMRCLLQQRLEELLSKH
DEERAAWKRRLQDLNETQQLPFCSSSAASNVATVREGACEVQREGPRAHSRLEQWIIENT
TVPLPNASLQRAAAAAAAAAAVVVEKTTEMCGAPLECVPAALEFMPAVGGDGAAGEWRPE
EPLSDGVKCVQKLAEDLSRCRVLLQEQLLMMGEDNDDDVSRSEERRDDGADQRASLSRLM
ERHKSSLKRLVSERAALHVAWQTAQSEVLRLHRELHEGEARYTRDTEEAGRRIGDLRAIV
QQKLVADAKTEREMEEIQSVMDQHLAVLYSYAKEEEAVTRHLHELCRLMRSKTNVQKQHA
RLHF*
>TCRU_3436 hypothetical protein
MKRKVRRPVRRPRHVGLSLPKLANPAQETETDDEDGNAPLGTSFSPSLQAQQSVRLASTS
FKFSRAVSLSRSNTSATENIEGELWYVTSNMGPGKRATLAMQWVTCDDHKLTVSSGWSER
GRIIDMMQFDGIRVIFSFSHVHEHFASSRQAPITRIVRRDDNGNSIYVNVCKKDKEYSRN
DYQPPRRAMREFRLCEGKLRPRYYYFGIEFSEHRDNTGAPRRRQRRLIIFATDIKSDQQA
WLDYFASLGDLKCRSISRTSNTHGCFSVQDESHCQSLQEPQSVGRLNLEERDWGSSRSYE
PLEFAATGRPGSESSPFLVDFDELSESHASAFPRSRHNEQLRNYLIAQLTDEETRLRKTL
FVEEENDRRRLCAVRQAFFLAFRENNSFSAWTSTRLAKTGTTDDATLAACGLFFPQCEEV
SPETSQCEEFITDTIKMLQRTITEKNNHINDIKKELEELRRQLTVDKNKIQTLEEKHRPN
VCNKDVNGKKGNKEATTPPNKPGGQEADDRVRHLIGTVQELKERLRATELARTVLEKQNE
RRRRELEEQLAQLGTERDALAERVRELDTRLGSATVSLHDAEHECELVAGLLGVPTVEAG
RESDASVAGRLRCVSGALCVSWGSRTSADAVSWRSNWRSWAPRGMRWRSVCVS*
>TCRU_3437 60S ribosomal protein L8, putative
MGKTVLTCRKGNGSVYQLHGHKRLGPAKLRILDYAERHGFMRGVVKTIEHEPGRGAPLAR
VEFRHPYKYRRVKELMVAPEGMFTGQSVLCGVKAPLAIGNVLPLGQITEGCIVCNVEAKV
GDRGTIARASGDYCIIISHNHETGRTRLKLPSGQKKTVPSNCRAMIGIIAGGGRIEKPVL
KAGNSFYRFRGKRNCWPKVRGVARNPVEHPHGGGNHQHIGHPSTVSRHAPPGQKVGLIAA
RRTGRIRGSRAVKGAWHPEE*
>TCRU_receptor peroxisome targeting signal.1
MDCSTGAAIGQQFAKDAFHMHGGVGVGPTGNSEHDVLINEMMMVQTPTGPAGEWTHQFAA
YQGQQQQQQQQHPQELAMRHQQNDAFMLRQQQEMEEAFCTFCTTHPHSHAHSHAHSHQPQ
GLVGPAMMGPQIMPPMMFGPGTGGFMMGAPPMMPYASMKFAGDAAMAAANNTTMTQGATA
TSTTSVQQELQQQSSDNGWVEKLRDAEWAQDYSDAQVFTLEGQSEQTMEEHAKNSEFYQF
MDKIRSKELLIDEETGQLVQGPGPDPDAPEDAEYLKEWAAAEGLNMPPGFFEHMVQRPQG
NNEQAEGRLFDGSNDALMDDGALDNAADVEEWAKEYAEAQEQLQRVQNETNYPFEPNNPY
MYHDKPMEEGIAMLQLANMAEAALAFEAVCQKEPENVEAWRRLGTTQAENEKDCLAIIAL
NHARMLDPKDVAVHAALAVSHTNEHNVGAALQSLRSWLLSQPQYEHLGLVDLQEVAADEG
LDEVPEENYFFAAPSEYRDCCTLLYAAVEMNPNDPQLHASLGVLHNLSHRFDEAAKNFRR
AVELRPDDAHMWNKLGATLANGNRPQEALEAYNRALDINPGYVRVMYNMAVSYSNMAQYP
LAAKHITRAIALQAGGTNPQGEGSRIATRGLWDLLRMTLNLMDRSDLVEASWQQDLTPFL
KEFGLEEMAV*
>TCRU_3439 threonyl-tRNA synthetase, putative
MSKAATTSAGEKNKKGAAPSASDAATVDLKSLQEPEFWKARDALFDELLAAQEAKYNSMQ

APITITLPDGKQLPATSWLTTPIDIAKRLSNSQAERVIVARVNDELWDLTRVFEGDATLE
LLDWDDPEARHVFWHSSSHVLGYALERVFHTRLSVGPALEEGGFFYEGDTGRPLSETDYK
SIEIAMQELVKMKMPYQRLTVSKADALRLFGYTEFKSKILASKVPENGFCTVYRCGHLID
PCRGPHLPDTGRVKAFAVTKNSSSYFEGKAENAVLQRVYGISFPKQTMLTEWKALQAEAA
RRDHRNIGRQQQLFGFHEVSPGSAFWLPHGARIYNALVEFQRKQYRRRGFEEVVSPNMFS
SKLWMVSGHWDKYADNMFRIVVEKEDHGMKPMNCPGHCIMYAMQQHSYKELPIRYADFGV
LHRNELSGALTGLTRVRRFQQDDAHIFCRMDQVQEEIRGALVFLDDVYRTLGFKFFLKHA
TRPENKLGTEEMWDQAEAYLRAALNSFCGIPEHLPDPFKEGATFTFDGRRDTVKKLRALL
KKQAANRENKDTEKKEEKDDEWKGPTHAEAWEENTGDGAFYGPKIDIVVEDALRRRHQCA
TVQLDFNLPQRFGLKYTLPTSTVEGGAGAEAKEHHTDPNAPNVGTDATTTEGKPEAGDEC
LSSYEKAARELCIDRRLDANQARPVMIHRAIFGSLERCIAILCEHYGGEWPLWLSPRQVI
VIPVSAENTAYATKVRDAFYADGFHADVDSGNATLDKKIRNAEVARYNFIFVVGQVEEEA
QTVNVRTRDNRRHGTKSLAEVQRWLRELVDTYDLKY*
>TCRU_3440 RNA-binding protein, putative
MPSGDKKIDTRNGDGHDDNRSDYCDDDYVPPAQRGVLFFSTIPRDMRPQEVRMHFNEFGK
ILRQKFTPFPKKERRPGGPLLPLQFMNGYLEFAHAEDARRAAAAMNGTPVACKRRRKCHG
QLWTVKFLDDFTWDTLLEQKEETRRTRRQREAEARSAERAINEAYRAAVLGAMRRKHTRG
EGGASPKEPNECRSPKKTERREQNVTGRMLRDVSVSSDSVGAAAVTPLEVVKKKRRKE*
>TCRU_3441 C-1-tetrahydrofolate synthase, cytoplasmic, putative
MVVGVPTAALLQKEDNFLVTLCSRSNDLEAVKEVSRQADVLVTALGIPRVVTADFVKPGA
IVLDVAINEDCASGGEMPSGSRRVCGDVDLASVREKAAAVTPVPGGIGPLTVAYLMQNTL
KAHLLAKNHINLFSPLASTQGNAEWNNEGHTEADFKRMGVDTHDCAGVGKVG*
>TCRU_3442 SLACS retrotransposable element (part), putative
MEVNLPLAPVSALELPIKNDSKLRRMFSATVVAGAHCEACGWALPMEEAYPSHAETRQEE
PAIITLQPGKKAPIHLTQTLLMQQYRSTWIFEEHVRTGEQLARHHPSWAMTATQSRKFYD
AVALEFGHWDKQAMGVEEVPFVILLPHHNGTAEYGLVGLVATNTQNHVVAYITSALHRDT
EWVMIDGMVQKVQRRPINTHKVILCLYRRLMPETGLEEDGEDDEQELHTHKRERNGRTLV
SAPKGSRHFQSQKSEEAQDDSSMEDGFGKNGYGQPPGSATHFSPLASSLPSTQTITQDSF
LTPSAPRKRGRCGTEKEVESEGGGNKGRGFVCEEDAGGILQPSVPPTSSQPNQQTPQGQF
LNEKEEEITMRRAQPQETPYNNKNEPPPHQQSSLSQKEEKREEEGVGDEEGELLTPQHTT
GQEDSRHPFSHKTTELPDPVWCLAGGCHHNFSGPRRGEHPRSHIHAVHRKQVRMDITNEA
LISQGLVWCDACGEVCLASQRARAAHRPRCGHHTCRKENLATQREEYRASVTVSHYNKTA
ACLERAHSVEWPTTPATDPRHDPWL*
>TCRU_3443 hypothetical protein, conserved
MLSENVTVKEKLPDQTAEDGSASRPSENFTVSPLTSAEGAANETSHNSNEGDSQSDASGE
GNSTVAGTNPLRPTRDESANESTEDIAALLQNFVGPDGSDVTTVWVRTPLLLLFIALVCA
VVR*
>TCRU_3444 hypothetical protein, conserved
MTEEALAQQVMQDFMATRHAGSSVELLRSVFFARLQQTIAERYPLAYNRLLLAWHWRGKW
RCFADEIVGLRCFRYMLMDCAETRDLEVHIAPSELRRCLHGGNHCAVQLTDGSVGALLRE
HLLQKGALHCWCDETVRAAQADGGAGCADRALWRETRLRGT*
>TCRU_3445 p22 protein precursor, putative
MYRLFSRCKTNKLKRVFSHALDASIKNEGVAQQRKRQVLPRRHRKLHKLTIREENEEGLR
DFLPPKPVVPTGWKLEHAKGSNRFDLRKSVEIRDCGKEHLHAVAMMEVKEYEGTYRMDNG
EREEEEYLFFTLFVQKNRFPGALEFGLTSIDMELVMDSLAIHNNREELEDAYGALSVSTS
RDGISNRIIEKSNLSCRSCRDNRYRGPMLSELDDDFSDEILDYLDERGVNNGFAEYMMAQ
AHFFEQEEYINWIRLLRQFAQ*
>TCRU_3446 Ring finger domain containing protein, putative
MDSAVEDLIRAMDINKAKHDSASLWRKIRNMREESQTVDEFLFKRVLLCSARCVLAKLEE
SGGAEEQWIGYLDFFMEAVRSFGTRYADPLLGTCEEVFHLVLGYPEKPRDLFHEYLFCLS
AQRHQCMGMNPNLAGTAPKCPMLENKSTEVALVPEVPLNEVRQYVNDLPQRLTFPLQNGV
VRMRLGNPLPIPDVGYVRGGYRCDTCCISNIQVAYQAMLYDDMDKAGVRSAVHFRNLANR
VGFDMCVACAVYFYRDAVLRLSQFLGDHSRTFRVCPDADVQLHSFSTEGNVVKFTVSILP
WGARPIVWIADKEEYNPPAAWRSAVKIESCNQYDPSRRNGGSDDDQCAICLQLLANGTPV

LETPCKHCFHVDCVQEMRSMMDDECPFCRRENVFTSCVNLTGQLNMYKVQVDLPNEAKEI
VLAVGSLLTSDGEYNNPTNIAACRSILVRHSCIMDFEAEWERNSPVS*
>TCRU_3447 SPRY domain containing protein, putative
MENPHVGFDSTPATSTFTPNKDETAFRHAVSMNFGKVALSEMEEEEGGCEYEHLVGREER
EVLCVPRGAASTLQGFGWKANYEPKKEESLFIHLNDAKNKTYETSTVADTTFRQFDHSPD
GGRTERQERVREAVGAVKASDPGTGMAHEEEEEERGIQKLGKDPGTAWGATKRKDDPEEC
AGRGVFAFQHSMFLNKPQTVAFFQNYFVPTTQSPSSPTPMCENKTPIDYTQRGKSHSLFS
GENEPVPTETEVVLSLMNGEESVSIPPTSRSVGRYLFSTQRECNDKDDLMPTAEGTHPVF
LRRELMELEHNAAAFLVEEEHVARCSLEEEEVNGRDLLLNAVQLDLDTLCFGEVDMEGDQ
RYTTPPVNPKPYSPVLDNMDDHNELFLRNTRIGSNIDDDVVTPLEKLLRESSPNARNLST
FNSPANGVYANIYEPPSGKVEVATSKLSSGASRIGLLAKNAPKPLSFEAAQSHLSPWCLL
ETQRHQLEMERRLTQRDRDNLERALDARHQCIQIPSDAHAQLRFEPSDSFTRERQLILGS
FGITGQKNSQADTSTPQKEGKERGFHHHLHHHQQREQQAVLQPQTHEEGMPGVGVSPISP
HTFVSSPSPPKLLAQKQSPTEATIFAEACEAKYKESLTAMKELIELYQAFIKKKPQSKIL
SGESQIQVYNSNVNEPAAFSIVTYEKRLARIKKLCSSFNTKTSVTHYYRRILHTPPLPLS
LLPENVADGISQNYMSALVKGTIIPHRSFVEGVENTRRTDKSGAAKYPSHRFAGFCESGV
GYVVQKVKPTPFVADENNERRGTLYCQNADSYLPPHRRIKTPPASLGWEKQISTKEVSVL
WPVLRWDAQRSENILISRNGTTCMVDASRLLQLIALEKEQTGKAVPCAKIPMFALGTVGI
AEGEFVFEVRIDAHPSSTHTPPSVFAVGITTKYYRGVHQKSPAYLFRSDGTIVACSDDET
GVPYGCPYHCGSHITVYLSLIRKELHFSLNGQPLGVAFRFRGVEDPEPLFPLVVLGGEGH
SASFVPPSAPQLPQHVIPPAHWSMHVVQSH*
>TCRU_3448 B9 domain-containing protein 2
MAELHVIGDLMSGENFGRRSYFCIFEIVTGEHWSVVEGRTSGCTHIMQSGGEGSVLWCFP
LDVHFTTNSIEGWPKISLQVWSIDQYGRKDLEGYGVAFVPPPSIEEQEVVVGTWKPCYWS
PSFFTRIYEALRLVVLGGNPVLRDKALIHTNDERFKLQTKSGGTVCLQLNVISRGMQRLG
IRYS*
>TCRU_3449 repressor activator protein 1
MSSSMDGTRSTWRGVQFFVDVDVLLTFRTVTLSDLEGQPGQPQRRIAVVDGKAVSVVSYP
AASFFLKTLRATGNSVVLVTPWKTEKTASLLRLFGWDAFDEIRTILREPGHENFRLSCLN
CTLEEYPFSVVVTTSRAAWHTAVWSQVVEVRHETNYPCQSLALLRALSCCLRIAECRVRF
PHTAVSSCISFSRARLFSQYRFYLSPEVTDPSSVVMMINEHGGYLVSKYEDATHYVIEEG
ENSFSCTLQKPRLSREDGERSSSLSSSDSEGSDSSSAALIDVERESSVSLNSDSGEEDNG
GASGEFKNFGVNEEQEKKTIHVAMLPPVTTNESMTATEFSTDSVNSSLILPVVNGCHETE
EHDWTTWTTPSTSAKTTTAITVTVLWLQDCIDGLLVYPPQVAHSSNDNSQWNISALLLAA
LIPPSDVEPISLSCLNNIAEDYGFRPLQLSQMGGEVNLATVLQKQWGSVLHVEMRGGELF
LRQPSIPPNEAGQEMERHLAFIAEQFCDAWTNAIRNNRLRNMTDSGTQTAAVLMATSGAN
TDVVLLNSEGATVDPSPQGRLLLMHALGPAEWAKEVDASHMTYNAIRVTEESVSLEPSSS
LALVNEPPTGYESPPEVKEVQAISDEKAPARFAQRGVEAEKGQPVVDLAKPPPGGEREFV
KCFIPSDGLGDERETLDKDVLLRQPPFRNYPMKLTVDQQGIHCLFVTTFDAKRFYQEGYA
EVRNRFLPILPEYAEEISSTVGTRKRRRSRSPVTKRSASNTSRGNRKDAFSSNRDSQSFR
GAPGMEKNVDTGGSTELSKSDLELLGEIGATFDFACQHVDVVERYALNELSDPVFRKQQH
QLLRVVVKLKRIIKRGN*
>TCRU_3450 ATP-binding protein, putative
MKTIALISGGKDSILSVLLAMRYGHFPVVVANICPTGDEGPEEVHELDSYFFQTVGHEAV
ESIVHCMGLPLRRAYIRAGQSKVQDLHYSKERDDEDEVETLYRLLHSVKEEFPEVEGVTT
GAILSHYQRYRVEDVCGRLGLHSLAFLWQRPAEEVLDIAAVLHVHAILVKTASIGLDPRI
HVGLSLEDVRPTLEKAQKLYGTHGAGEGGEFETILLDCPLFRDQCLGVSLLERVIVDDND
YSPSGYARLKVKLRDKTMEERALSKELLLRLPTLTFPSDRMCHLPRVDQLINVYNEELEW
EKSFRPSNIDAKFWGDNCCDVYESDVLHTEDEVEYCVTGVLQRIVEDMSGRNREVFFMLV
FSPSIRYFVFFFEAFAHFFPNPQPPGCAFAEVSDKKAFCLEVLSAPREFIQRATLQVRSR
SCCGPVSMGPHSFSNLVNTNAERCVIVSGCIGLVPVTQRLAVTEDMPEILNLSLSRLSRA
LGLEEDAVRTFFVQFAFMYANSVIGLTHFGAGVPFATHATFFLRDMRFAPLVPFLWRWCA
GDFARLLPWDNPRACIEKDGVLFRILHVTRLPSNSEVEIVLERRGLRLEED*
>TCRU_3451 RNA-binding protein, putative

MNYDYMFVYVNGEKMGLLEDGRLALYQRFPVGSVLYDPSELPPREVPISADAAEYGVTAC
KLIPYGHYEAYIPEPATGDLHPMTGENVCVYVTNLPPNTTAEMLGRYFEAFDMVAEADVF
TAPSGECTGRGWVVFQDPSKLLMVPPVLEFFPRLFIYTSLSDKIPTRTTLQLSSVPETLV
TGTDIASFSEPTLNHNRGGNHRRMNGKASGNFLKISTAANAGVINTSAYYFVALIRRDEV
EKSVEEGVFWTNPANRRAFYATLERGPVIIIFLLQEYPVIFGYARLLPDGSADKNGFSSC
TVEWMKHHVFLKEQEMRNIPSVPISKMGDGVPLKPEIGESICHLAEQHPTHSTIPERLGQ
SLPNNGRHVGRGGGVVISGNGNVGGFNSVGGGGLFHSIGDRGTLRSGIGITSLPQPLGTR
PATRGGHIMNNRIPQRRRPYNDNSNTYVGYGGSAVPPRKL*
>TCRU_3452 hypothetical protein, conserved
MAAREGSVCLCGGRRSHDAETVFAGGSECPNSPPIDDFTHVLRSAHVNFGHVSPGASSIT
ASGTVREQPSPIVERITQGLLASSLGCARCAQIDGIRESLKCVEASYLGEIAQLRRMVGQ
IDGERMDAVNRMEQTLLTFERGRQQSLSKDCEIQSLIGQLQQMEDRSQRLEYELDSLRQL
YRREIAFYHQREMFLFLENERCARAALSSTEDGWRSALETRHLSVVEVDGKIHRSYPHQN
FLFLDFSKENEGGSSMRGGLSPGLVRSLPPSITRDTRKNRNGGGGSKTSDIKGGLLTELW
QSKRTLNELNEKLQRELRAREDQISTLRQQLSVREESLVQSSEERAEEDNLKREMQEEID
DMLRTEFFLTQTCERHRLETEAMEGRAHLLQWLLQRHVLFSQERNLMFLERTPEKQGLTE
KVWTPGTLPFFISSNDDVKPDVYVNRSKYSLSCQQQQQQQQQQPDELYAVVSQAVSETLQ
SVLTHQPFLIKRTAEAICATEDELHKNSNNFVQKMHYDEDDNVINAAGINASHEKLLGDV
RRVLQEFCAANPPQEIVDLSPVIDALKKVARLTSHNAKVMDDKLNDMLILQSAVARELAL
LTTPSAGRRVDESPSSNVSATASLSIVDAGVTGANNKASPISRRAHPKPLNLDKSPAGRG
EGNAPVILQAKPSHEWDVAESDDESIPPIPVFSSLRKTPYDADEL*
>TCRU_3453 Nucleoporin
MIAGRKRGRDEVDDALLEEVTAAIQSVAAETEDIVGSVGKVNGAVLASLLERFRQMEVAL
NASGGSTVQLWKLIVQSQRNRVADALNHIAVADDARRKGHLIAALQEQLLSSASLAAEGV
SSGLCRAHETAVALFSSQLAGERETNNKLILHVQELLRHSLEAIQVSSRRAMKAELLSFK
RDILVARLQSSLSFYQNASLRQHEEVMALIKIVRILASKGKDADLAETKLRQAKTHVKLL
ENHLELAGIVEAILPPKFVPPRQGTEPPNEDLKRTAPEYFALRLLEHKDMTLSELVDSWQ
KQEARIMAAEEKYRELELSLESLRRESLTVHQGFLEEKRRREVVEQRLVDLVRERIRPSS
NDALVQQLTLLRADHTKALDDLAQMATLVNVTRERLFAEQQRNALLEKKLQQMQDDSAND
EVANTLASLRHYYEEELDRFRNGLVDADTRSAVAAASSEIQQKASKNASNALMVTEQTLM
DMSAALNRVEKQLLIDQEACGFSSSERIAESAVKVLAESEVHLNRTIPTFKRMIEESEIR
QEKDMAFFERQVKQLLESLQSLLPTVSHSEVTTGAEIMMVQQQQEVQSMMREALVHALQF
VSDNLVTNEISKTRLLDTSISDARQISLLFEKVQKLTVDRDAALERLARCERIIDQHSLT
AVERVLMHEVPVEESLDAMEAAEQITTLRKEVSSLGAARTAALAELKELRKELKENNHER
EFAVARFELLEHHNSRLIKSIEECLAREVVLIEQVHQLQRNLQEGKKMELPVLPTGDSNE
TTEMERFMPLMQQLEQLTGGINEMKEQLSQVQRVIFSSPAAEGDVTEKQLLCNGVRQVAD
ALREALQHAELFRHALPLEVTKDAALSIVGSSAETMSNNDGHEKAETISELGRSVADTPE
MDERDEELVRLRSKVETHEQIEQALRKHERDLQEQNEGLQAKIFRLLQINRQLLEELKTT
RASSTTSANKAPQG*
>TCRU_3454 hypothetical protein, conserved
MLVGVREYRREEIQRICGTSAEALVSYYTLLRNKNEAIMADVTDARARKNMNFDYYMTTA
NSLFEEAVRPIIRTVLPPISSPQVVVVVDGTETTRFHTLLDPEEGILALFWRLLMDAAEF
RSILEAVYIAVVELDDNNRLRDITCAVTAEKEPIIFEDAEDLFTSVEDASYMEIRTEADI
ARLMQHALRVALPERHQIFSFILVPQKASGLPNCTIQFVALSVSEMARGMRSTRHCITTA
ASLIESRSPSMTFSGTKLSFLLKPALLGQQPGLWISCFAPTSVAALKQRETFKESFCIAH
TLCRVYSSRVGASVSEACQRIGFKEGDYSNENCDEQVELQPRKDVPKPSLLGPWEKTRRR
LSKTTSLHPSLSVSLLSSSFSLHSTPNAGQQKKGEERGNSPTYGINDEHLSSLAAPQQKP
TGLLVTPSERRTKSLDSNKTGFKKRRDVTSNGRRSLSRPSHDRCSSLEKHPYNCSARYEL
ETYKRVMEPAMNRLREDIQHYMTLLEDARRQIRRIKRVNNEEVEVEKLRDSLLTAKRDCA
SLEAEFTRREEMLQSRVSELQTRCEELSQQLRGQTSCAAPEGEKLPHKSISTQTHNPVPY
FPPLSSSPPPPSAPLPAEDGLVAFRNFPKDSPRKDVQHASQWLEVVNYHQRELEDYAERE
RSYRNRILLLEQKLSERESEMAQVRAELIRRDCEISLETVSNQRREHEKKMDQCQFEDVE
YLRAKLFEANNVSSRVEQHLESCINELKEERRQREASEAELRRLQGLCAQHMETGAVKEM
IQMVKESYERHVNHLQREVEELRGVAHQAVSNEMISRANSSTTSTPRQRPQGHQHGGMVS

PAIETLQAKSMFPSKPSMPDETNATNDVPSTHSKTIPARSGVRRFEDFMKEEPSYTIRLP
KALDRANLS*
>TCRU_3455 Pre-mRNA-splicing factor of RES complex, putative
MKRPRYDSDDDDDYAEGSLLPYALENKGDFLMAMGVGGRESSDESLRSVEEVSVAPEKCK
EKERQDAEQKEELMESFFSPSMVVDRLQRQALRVDHDVPEHWKGLLSEGLLQVYFTTLSY
AEKKRMVDDKLLSQYLPHDAKRFPPLGRPTDRKWDNAFGIKPGWRWDGVVRGVGSL*
>TCRU_3456 phosphatase and tensin homologue, putative
MSSSIYSREDEKRLSELLERVNWGGELSEEERLELARLKRLYQEFIEEGERRLRLRGGHE
KAAATNSDGPGDVLLTLQESVACAGKAAYFWGSLVATLVPGYFGRKVGLTSGFLHWNFIT
DRLILGALPVVTRVGSSGNHLVQIREQLESRKQKLGLVIACLEDAEVQGFGLQMISFADE
SSWHEYVSPAVRYIRLPMPDTTANISFGSVLYAVKQMHHCIKEQNCVVYVHCKAGKGRSW
MVTMCYLTSYGGMTFDDAEQLIRFTRSQINPSPSQRAFAAQFASRIPAQISGS*
>TCRU_3457 hypothetical protein, conserved
MDLSLGETSDAIASLAEGCSLEHIAELATQCESHLASVEAIMDATENALRTSQGPRRLVL
WFFIDRLAKQHANFLDALRPRLRGLAATAAPAVGTAEWDDFKTLLKSSIAVVFGAPLVSL
ILLEIDPDTQKETASTTSTTERSQGILAMHSNAMRTSGAFLTKTIGTQRPAAAKHTLQVK
TIDSQMAMNMASSYAPARPQEIAVPEIHPDADAPHGHVKALPSDYLKNYENTRRKRLREV
MERNRKEMDRRQEEELLHRVRGTAIQNGKMPDYSDVVMPLEFPRDEHGVKRGFFPLGVRF
IREAIRSCGGAVELDVLVNRLSTLASKETVAEFGDVREFILIHRPTFRITNERNRWIVRL
AGDESSDPTWESLQCPLCSKVMRGRNLARHMGCRQCVTTQIALGLHGEVHGPISELSFVA
KSIIDRGNEYDDWDLEWFADCLERSANCRRFKLSSQSKFAPILKAMRVVRNRWLARKGVA
NVSEAAVDPSDAAVANLFRTIGRNVNRLPIPWLEMGDMVDICCRFSDLVLPPFNPPPRPA
DPRISLHNEYPGFLLCESEVDDEDDPSDDEDAFSDDEAPTFVFAPPVELAETVFTAGFER
DTKRLQHRMRTAPPLVLQRVLKGDRSQTQREMYAVAKDASGLNTPS*
>TCRU_3458 mitochondrial carrier protein
MNTDDVKEVCAGSIGGALATVVEYPLDTIKVRLQDDPSRYRGSLSCITEIARLEGFINGF
FKGLPAPVIGAAVENATLFCTYRVAINGIQDVFYEKRFESDTEPYSVVFSAAAVGGLVVS
HALTPAELIKCKMQVQNTLPGHKRALKNSLHCAMSIYRSSGVRGLYKGHVSMLARETIGC
GVYFLTFQWVIRNMLHEGQSFAEASPFVHFLGGGCAGVVFWTSIYPIDALKTKIQTGKGG
YGELSFVRGMMQLYMREGMRGCMRGYTVTALRAFPGNAVLIAVYEKVNLLWEMSHRSRCT
SVCSASCVGST*
>TCRU_3459 wd repeat-containing protein 19
MGVQKKFELSTKELGGGVILFSWNSSGTQLAVYSANGKLQILSPDGKKLNTSSFPGVVRI
AWDYSSDTLALIQKNNSNVTLQSTGKQSSDSIDSGLHELCFLAWSRRGSHLAVGSTKGTF
VVINSETLKKLPVVGTHTKAIVDGKWSVDNTLVMVGEDNVLSISEEDGVLRRQVSLKLMP
LSVTLVDLSQRGEKKSPISTAALINFGKTLEHFNLETFKAQPVPFESKLGTVTVCDFISG
GLVCVGFSSGAVALVNASVKGVKMCGVVRSFHDTVNALACCQNFSMCAAVGENALKFFRI
ADGSIVENAMERVELGGTYGTLRGVEWSKDGSNVTLSTEQGQLISYKLNVSAVSTTKGTF
IYFLSSSRVVTAKSLQDDRIIYNANVDIEPAIIAAARGILAVCAGHNVLFYTTEGNEFSL
LRRADFPSAISALKVSSRIAAVVCDGKIELNEIRSGENSATFPENGTANIISLDMTEVLL
FYATTEKICVVNLIDFQCVVEHTPSIGIKRAVPNTSCTRVALIGKNDALYIFNPVTLTLI
QTEGFEAEHKNILWDQGDYGILVSYDSKTMVTFVYSPHSRYGPTSESVVIKDTNTENLVT
PIPVGYTPVALFKGKVTFQTSSGSLDFAHLKSHNQAMTRVPNPEAFYTNFSLNHLRWASQ
NISTSQEAEDLAVKALHVLDVELAIRLYRQLSQPSLVLCLENIKHINEKNLLIGHISMIM
GFFKDAQSFFLRSSQPLCALQMRHDLMQWESALALARQMAPERVFILSKEYAQQLEYRGE
YAKALEMYRAGERAMPKGHASTQLTAAQEEVKSHNAVCSKGAARCLLRTGSIREGVKLAL
DSNDEALIMDCAEILESTRQFEDAAHLYEKASEFEHAATLYILEAKNLKAASRVIPKISS
RNIIGMFAKAKESEGAFKEAELAYTQAEDWDNVVRIKVEKLNDLYGAYVVVRQTRSAAAA
AIVAKMCKKRGEFGSAVEFFVLAKSFQEAFELAKEKNCMSTLEGALLNQAQLLDGIAPAS
NQAEFAMIAQYYEQNGKPGQAGLFYHIAGNFPLALRNYLDAGESEDIEKAIQVVGKSRSD
ALTNRLIDYLMGETDGEPKEPSYIFKLYMALGSYEKAAKTSVLISTKEQEMGNYLTAHKT
LVDAYRILRDKKMHVPNDLRRSLMLLHSYVIAKPLMKIMKDDETASRMLLRVVRNIHKFP
KHISVIYTSTALQCLKSGFRKSAFDNACIIIQNGKYGTELDEKTRKKIEGIVRRRGKEEM
DDPPEKTSPCPFCDAQVPETELDCGACKNTLPFCIVTGKHMVKENYSECPICQFPALYSS

FVTLLRSSQTCPMCESIIDVNKVQKQSDPDLKAYLA*
>TCRU_3460 ubiquitin carboxyl-terminal hydrolase, putative
MAKKWLPIESNPDVLNTYLRNLGVPNPKVEFCDVYGLDPDLLVFLPRPVRAMILLYPITP
EIDAADAKTVEMQAAEIKAFMAEKDVFFSKQTVENACGTMALLHAVMNNLDSVGDVRKDS
PIDFLRREGLHGNPEERALLIESDPNLDAAHMGASAEGVTKNQPVNANIDLHFTCFVHAK
DQCVELDGRKQSPLLHGACMDNEQFVSVTAEAIQAKISRNKESFRFNIIALVDKSS*
>TCRU_3461 cleavage and polyadenylation specificity factor, putative
MLRASASSIKLTNLYGAPTGDTYHPSTPFANLIEIDGVRILLDCGWNDEFDVNFLDALMP
YLGDVHAVLFSTPELVSCGALPFVVEHIPTGTCVAAAGSTAKMGLHGVLHPFLYLFPNVK
TWRLENGLDFEMTVDKVYSAFRSVTEPYGGKVTIRHRDAEVECYPIFSGRMLGGHGWLIK
YKIDELFYCPDFSLKPSYALKRFLPPTTSTLLFIDGSPFHLSGNTGRKYEEQLNALIREI
LGTLRNGKDVLIPVSVVGRGLEILTIVTHLLTEKGGDNYTVVFASIQAAELVAKASTMTE
ALLDEIILSERQLFANVVTCKTAEEVLSVAGPKICIADGETLDYGVSAELLGHFLQADAD
ERENLVVLTGAPKPHTNAFTMAAAKKGDAIDLRYTIRSPLGKEELEEYYLQIELEMEEQR
KALEGGAYEVASLEDENSDNDNDAGKEDEKQLRVTQQCTPGLVLPSYMTFVSKHLQFPIL
ETAASLANAMFKKVDYAYGLPISEEMQFLMRRKAPARIYSDEGPEGIQMHNDAQAEANIP
SKTFVNTAVVRKNSRVFMTDLSGFADAAIMRSLLKSRFSFAKKIVLIRGTVDDHRALYQF
CRSEKVMKCGENVFFPRTQRTHLELATHVYSYMVQLDPTLANALPSALRRVKESRSSGFW
DVGWVDGALESSFFSLTPEDDERQSVKRLRAEGNGGEIKDGVFTLVPLFGERAQQCARER
ELRGMQRGLFYVGDVDLHRLRDVARNEMGLRGEFHKNAPMLVFDAGLCVRKSANGNFSLS
SMISPSVFALRKTVYGQFSQTL*
>TCRU_3462 hypothetical protein, conserved
MSDTDVLLLNLEVEAAAARNADLSRRLEMITEELGCSSVHMTGKPELVSQGTQTGFDILR
EVALNLDDLLFEIAEIMFRLYPSTPIDLSIRRGDGSRNLEELSHRCLGEMRSLRVAWETK
LEGYNTFIEELQRAIGSYYRSMEEMESQMQEKELEFVTLQKHNVELSRQCADMEAQLRAA
REKNESFRENIASQMRRTRDLEEERDQLLKRETVLANTVASLRAECVLGPWKNTVTKRDT
LAENSVHSFNVLPVRGSAKPVVGACAGIGVADPAINAMWACQGSAVNRAFPEWCVSAEKV
VDFSCKMRNSR*
>TCRU_3463 hypothetical protein, conserved
MEIHEGRLDGWIDLVNAGDATSLIAVFREVLSSTPLDPSALGTISTFLEAHLFPSALEVD
LPQLFSPMPTEYMEAALSEARAHALDPREILSELLAIGEALAGYALVVYLRLIRASFRQV
FFDTLGRKKGLCASVEEQFSKTHEIMLAWYPGMDRLFSRIISTICQRDAAPKMVRTVNNF
GHGDVDSDDVDEKEVDDLGNMPLLVEPEALQVLVLLSLDLLLMVGEPHKIMPLLLMVRTS
IVAAQPYNESGEFLHRTGKDLREWANFFCSVGDKRTELKEEPYSTQNSPIVATIKESERM
REKIARAVLEISPPCELFSHLQKCWSNEFTKDLMDSVTYEDNEHGKDASDARAFATLHAL
KKEKDSLHILSDDDYEREECNDEAFSASLSLQKIGAMLILCDFMTLEGFSDQQLLLSKSP
ESFFFLTGTMVLECLKSSSLNVVMTGLAFLSTLVPQVPPYSVCANGELNTKSGEIHEFGQ
KQSAGCTWGFHTKRFELIFEVVKSLMNISATSPCECHREVSRGIFVLLLRRFASKLRMLV
YSLFLALTPFASICSLMLHSLREEWNGSQFSPNNSEFDFLQNTLPTLLLKAQKNWLSKMR
FGELTFVEPMIQSINFVRCVIIEDRKRRPEDALFRFDPNCAKVQLREEDSGGGKGDRWNI
YLCQLLKDVIPPLRIMVLESPETSATAMGLSGGVTLSPLDRFALSMSMDGLGEQVSLAA*
>TCRU_3464 DNA-directed RNA polymerase I subunit, putative
MIRSHLIVVDEFASAAESLRVTPVQERRSSAYLTKYEMVRVLGERARQTVNGSSVFLSSR
SRVNERSALELAERCSDPYSSSVDPIFIAKMDLLQGRISMIVQRTWPNGKIENIPVSELL
IDKTMLNMQA*
>TCRU_3465 elongation factor, putative
MRRFLRGVTRAQCRVTHLCSLRHINFREDLRNIAVIAHVDHGKTTLVDSMLRQSGTLVEA
RNRVMDSKDQEKERGITILAKNTAIFLPKRTASQSERRINIVDTPGHLDFSGEVERALQM
VEGIVLLVDAKEGVRPGTRYVLRKALSLNLKPIVCLNKIDRDDTSIKKTEDAMQDLFLET
AENEEQLEIHFMFGSGRDGYMNDTPKKGGTLDPLFEKIFSTVPAPHCKGDDALQMLVAQV
ELDESTGHKIAIGRIFSGKVSVGDIVTVALEEKEVDALVKNIQLFVGVERSNVQSASYGD
ICILTLQEPIGQKVPVKIGCTVCQQGVVDRFPYRKPDEPTYSLVMQASEAPWRKKEADER
LGTILALQKRLEREAMVNTALQLSGLGTPHITLMGRGPLHLSVIVEDMRREGYEFEIQAP
RILTRVIDGVSCEPYERIHLEFFENLVSDMVSFLSNTMGEIGEIRQLSNGRVLMDCVMPV

RFMSQVPLRFHTLTKGDGVLNHSFETYRPMTSVQVTRETGALISVENGEATEWSLSGQAQ
QGRFFVLPGDAVHYGQIVGENSKTLYQNLGINICKRNEQLGGLRSNANDKAIRRRASFTA
FRATFEDCVAWVTEEELVTVTPKSIRMRQPKFNGKTTMRNAAQKR*
>TCRU_3466 electron transfer flavoprotein, putative
MFVRTIPSHFTTTSPLWMRVMVGVKRVVDYTVKVRVKDNKVQCDGLKMSVNPFDEIAIEE
AIQMREKKLADEVIAVTIGNKKAEEVLRTAMALGCDKAIHIVTPDGEAEGLEPLVVAKIF
QKLHEEIKPDMWILGKQAVDDDLGNTPQLLAGLLEIPQGTFASKVEVSDGKVKVTREIDA
GHQVVELQLPCVIAADLRLNTPRFPKLPNIMKARKKPIDSRDVSSLGVDTKPRLVREAVM
EPPLRKAGIKVKSVEDLYDKLHNEAKVI*
>TCRU_3467 hypothetical protein, conserved
MRWSLALRKVTRVPTRSVVLSDALRYHPRYSVPRKMVLSNSFNTVDEKNRFLSLRLILEK
LSGNVGRRQYRMMCDITRHFERLKEEGIDWHELKWLNRTELMDLFDNILSLSRTERAVLL
PAIEAKICGVLRRSDTRHSTSICVNQGVAEHGWRCGLYGHTNDVYFEGKAKANPTVLQIY
HRSSVRSVERSGVRVEVRTAPDFSVVGRFSHPLSPRVWSTPENPVFQVSTIGYEFRVHPE
DPRVVPQIEAAAREWELHAGVTQQVVWEMLEMYAVERNPQPLELKSGEMGAPDCPSLYSS
AFTVRHDSIAGSSDEQGAVTEQRMISTDGHEVPWFKEPLTQKFEGGIPVILPFAPSIVVK
SSFRQVTRTFPVDVERQLLQPVVDVTCFVHPQACFWWSEEDEERCLNHIVEYAKRIPYAL
PFNLYLRVDTTKNFRDAPSRVEEMEKRLAEKSHYFNLRRFRESTAANSEK*
>TCRU_3468 hypothetical protein, conserved
MFRKIYTPLTREVTTTMCAASLSLFSCTRWETSGRHTPPNAGDEDEEDFSMIFNDDFHFL
DECFGESGLDVFDYIPEHEAALLGHDKR*
>TCRU_3469 Mannosyl oligosaccharide glucosidase, putative
MEAHVDLFSWVALLSSIISDVELHLGAAETVPKRLWTVWLDTVHWDAANQRYADRAGCPG
DSFSPYIGYVNLYPFLLGIIDNKGRALTIVELAKTELMTRYGLMSVSYDSVRAARDAGLR
HENRWMGHVWLSANVLMLHALRTKYIDILGDPAGELFKRLRLCMLEISGGSPMMQEAYNP
VTGAAESTVSLVGYRAMLLGLLEDSR*
>TCRU_3470 hypothetical protein
MGEVDKSPKRIGVLSADNGSSSDRPNKFYHWHSGSQTLPFIKNETDIVQWLLEVDAARGK
DTPRDMEQEELVAFFKGRSQQGGTLMASVSTTANASIPPRGEEDEPHLTRSVARLSPHIA
FSAAYHGKPMREALSSAPQTGRSSLPCGTSASRFSGGGVMMKTATAAGITEGLGGYSPGF
VPKQQKQHHQQQSPLVLAASLGRGFVHHLVTGNSSSCSVPDLSLPPSLGTGAPVTFCGTP
VKRTVNGETTSTTAVLLETTCGGSDQTTPLRQRILPVADRIRQPPSAPHHDRRRRDMGLT
LCCNGVTNTKSRSLQQLRLNNPPKLCPPYAPRLLALVTECPTTNTTTGDATGPAQHLNSL
LPGRRGVGVLSKETTATQGR*
>TCRU_3471 glycosomal membrane protein
MSDFDKFVKLLGQTDGRDKIYKFVGGVLKALAALDAVECRRSAYKSVSSSITDGRSLMRM
AKWMGDIPKMRSVFAKCAEGGRMEMTALIMFLRVLGNFLYILGDNVAFLMRYKLVPGQPK
RVQYHSKVSQFWGFFFAAVLDLLALRTALQKRASDAATSCKEAKSALINLTKDASDVLVT
MAAVGYMKGVWHPGPVTAGALTAVSGGVATYLNWKKIK*
>TCRU_3472 hypothetical protein
MSVPFKYRQHIRDIHESFHDGKPISEEELMSVMDIIASAEHQALIDQYRAKCPLNSNSFL
SLMYELQKASKISYDDLVWNYIRGALKRGVFNGEDRTDLKTLRSTLDPLMRAVRLDVPNL
YKAHAPPDGEGKITVDQLCDVFRAMYPANQIVYLEMYKWSRTKKVTKGRGSITELAKNFE
VMTPPPFAVSAPPAVPTSLSVSKPPQPREDTPSEMLKGTTNAAVVDDSTETASTQQRSLR
TQEKEFTKEPQEELEKLSQLPEEGPNLPDRSVPTEKWKITSEADGEAKKPAVEIQLPDVG
ETKLRDSTNPKVEESAEASSIKETEANIQLTPSLFSEKKLENGTVSPESLPAATFPSPPL
DPHDQQEPLEGEKDAVKNFIASERPSVSVTSLGSFPYCDLPPNVQVERRPGLNFNPSYIR
DMEPPVRKQKSFSDGDNKPSLPPRLRGHEEQPAWEHEEVLLDAMLSRVVPGKPVDSQVME
YLKELARQEEELESALRAEMENLTSNMLACEIVEQRMIILRAQRQAQCFDRMESRRCKLL
EEMEKYLSGSRKAHGQNKVLLAGIKESGMVSCRKDGHSSNHDGNTTNAREKPTDFVSMFT
PPPPLLSAERQRRTLKRDLRLGEKLQRMQSRSPRPASMRRVSLPQDPHFQAQQLPSCMEP
EFLQGSPTSHSFGNTSQRGRWAKKTTPRQPVPVVHSRPIQQQKQQHLSPRHFGGEDFTIL
VNSGSRSSQSPLPRQTPNRGVHPHLTTRMAAEVLTSSQLQRKIEERLEARFSKAFQAY*
>TCRU_3473 histone acetyltransferase, putative

MEKKSDRKAEEYPRQSSILGTPCSVRGPDATVRRGQLLEVRYLWTPASLHVDTHAPLFTP
PLYGFVRLKDLNHRLSGWFSLEDIGLKEAKGGGGGGNAAAGTVSPPPCGSTRIHGPILTS
VYREVTLGMIRTRREEKLLDFFEERLLRDCRTPTTIRYFVYLCKFVFAPWYYAPYGIFHR
EYDPLAPISMADQERQGLRLSEETGGINPFIRDAYLCPFSLRIYSTLEQMQHETRCYRAG
RLRPPGREIYRDESRGFSMFEVNGSQKVTYCRHLFLLGKSFLENKLAGHDVHNYFFYVVC
LHHRHFPQYTDDPSAMYFVGYFTWEKQVADNNLACIVTLPCFAGGAAQQKDSGGSNGRPQ
LGHFGQFMIAASYELAYRRKHVGSPERPLSDLGASAYDRYWRRVLVAWMHTLVTESTTVV
AVSDGDSTDDQSVIVEATTPAKGRRSKRSRAGSSDRNSETDDDVDVRAAQTETLKVTSVR
GIAQQVRLEEPDVLRTLLNMGFLHLNAEDRSLRLVIPVPFVRREYERAREQAKDQTRAEF
EASLLTSSGAAAVMASSRQQQKQPGVAR*
>TCRU_3474 Protein of unknown function (DUF2826), putative
MLRLGDPHIVVVLTNSRGTAHTDALSGRSEASFEALQGAECVDAATTCMECHDGTAGCGW
WNTCFSEATERELLLLLASLLPFVASHADYCLSAVHGWCVSTSDVVCRHSTAPAKHTSRR
MLWLWIWCCECSRHYFARLLFTAFRQMDASPPESFTAAPCAVLPAQDSPVVWRLADSQTP
LRWDMQGCGLPLTVLGTAVWMRQPHERMYCGTIKCVKYAESQRLQ*
>TCRU_3475 Mucin-like glycoprotein, putative
MMTTCRLLCALLVLALCCCPSVGASEDEPEGSSKTTTKNTTQPPVLKDKAGPKPNVGDVP
PPPPSDPSHPTAGQPGMQSNGSAEQPRNNAGYGGSSNVTVPQLNGEPIELQKDDKDSMTE
DA*
>TCRU_3476 hypothetical protein, conserved
MARDAAAPTISQPIFTGERRRVNTHTSLANLERPHFPHSENSPSRSPDSEEVSGSNEVDL
DFLEFDVTTWVPRIWNGGILGILFEIRSACDYWHRGDAHTQIAFDISGFVDARRGYIGNP
TSSLWTWAGLYRGPSGCRL*
>TCRU_3477 hypothetical protein, conserved
MTEAASCLDVKAYFFSCLFTAGDSASLLMPRGGRHAGGAHTAPSGVQGQPRNLQIIIASA
IAGVTTVVHRLWAAPPSVRIDVWIDNIRIAGSIGDVTLWEAQVLRNADSCHASLGEDRES
GATHYTFLEVQFDHTHRAVSLREMFVRSVCAVPALNSSTIAEMEVVASRFLCAAAILARV
YVTTNFLSRQCDDDYPHITGELCWRNPGEPSAGSDCLGRAIATHHPEYNRKRIIKPTEKA
SAAIITDALFCG*
>TCRU_3478 hypothetical protein, conserved
MNQVIRSRTDWKERVVLRLAWITASRWSEIAALTPNNLKLKTDGTLILYWPVAPKTARTD
PHRASRFVRIRGQDAFDIIKLCRTLQHIEKLTNLTTARVERALAWNATAHSIRRGALRHA
AQIVEAYNLDPHVVSQLAKHVDPFDLPQNTFRYLGSYTTMLTQVLSLVALM*
>TCRU_3479 D-isomer specific 2-hydroxyacid dehydrogenase, NAD
binding domain/Acetohydroxy acid isomeroreductase, catalytic domain/
NADP oxidoreductase coenzyme F420-dependent/NAD binding domain of 6-
phosphogluconate dehydrogenase/TrkA-N domain containing protein,
putative
MYSMLYFYRQTWRSLASRAEHKWDPFLMVELRGRKVGIIGYGDIGQASAKLLSAFGMEVT
GVKRSASTKEVDEYGVRLVHGDAERERVLRESDFVINILPGTEETKRFFNKELFSMMKPS
AVYISIGRGITQNEDDLACALRDGVIRGASVDVFEREPLPAKSPLWDISDDKLLLTAHSA
DRTANLVPDSVRRFIGLVNEYAKTKRLDTYLVDPVRGY*
>TCRU_3480 hypothetical protein
MPSECRGGGRAATKVSCYEATAIERTFRGEGPVQCPAVDAQPRCLDILEADGAKFPAGRL
ACLWKLANPAAAEIASWHCCFDAVWRLGCVRSDFCAVRCFSVWGKPRHRNHI*
>TCRU_3481 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily, putative
MGGEPREWIKWGDPRPLPKLISSASHEGEWTGFFASGGSGVLMEDGAIVFSLMAVNEKND
GAYPMIIYSKDNGSTWLLSEDISPANCADPHITKWEGKLLMIVDCEDEQRVYDSRDMGKT
WTGTIGTLPGVWVNSQSEDYSEGGLHVDALITSTIEGRKVMLYIQRGYASVENKATALYV
WVTDSNRSFSVGPVGMENTVKGELASALLHSDGKLHLLQRRASGENSVMSLFRLSEELKE
IESVLSTSSQKDVFFSKLSIPTAGLVAVLSNASANNETWDDEYLCLNATVKNATKVEDGF
QLTESDSRVMWLVNIPGDNVRHVFLSHNFTLVASVIIEETPTADAPLLGAILGDAGPEYL
MRLSYTADSKWETMVKGDTKTTTESSTWVAGKEYQVALMLQGNKASVHIDGKSLGKEEAL

LTGETPLEYLSFCFGACGMKNSPVTVKNVFLYNRPLNVGELKMVRKSDGKKGNGDGSMRG
GVSRLLLLLGLGFCAFLALY*
>TCRU_3482 hypothetical protein, conserved
MSLLETVHAEGNYHDKYEYLSDVVGHLFRSVQGLVMYAEGSLNSLESLRHGLCGVWGRHD
NEGDAGGQKTVNPPLPNSTLATGPFPSSLPSSTVSAAANSPMRQPQEQQRLAIFEEERAR
LEMLAAQLKYAQRHCCEVVEGLGKGKEELQRQCTAHQQQLEHLQQVSLRNNTQELSRALK
ANEKALVQLREDLQQSFATERAQARERERELEQRCVHQSSEVRQVTEMLALAREQLQMEV
ERRNQAEQRVQEAEEAAAEAQRHCGVAVSELHRDVEAEKDAMEAKLQHLQRELIARRAEA
VCVRQESIALDANVTKMEFLLEHGYERAAAEQHYTLLLTREAARHAQIQIATEQRALRER
EATAQQCYEDLCSLLECMREDEFKAEAQQREAEADTEARRLIVSVETHTGIIPKKKKNDE
CGAVEEVDDGNDDGAGGKTQVLLHRYGTPTTLTGVVTCLQNAYEVVRRHQRYMQSTVDVA
KERVRQLQQEVATLRPRLEQLMAEYEKQQVNFKRIWNEQTMWERQETLKGLLAKQEALLA
TVNVEREALQVRWSTLSEEYRALERRNSQLHERCAVKEAENARLLGFLRAKQIASPSSFS
PSSSTPQQPTSTSSRSPGVVRESPAVATTNANETAVGNSPDTRRTETSTLPRHPVSRGSS
SVAGLSGQARTSCSSFLDEEAAVSNSAVGVVLPLGQHPHDRGVWRTACRFGRSVRTTAAA
TATMAEEEPCKPN*
>TCRU_3483 hypothetical protein, conserved
MSSKTGTSAIAGQPKAAALVATVFQTSLDNLLLAATRHRSMITLRDAVQSARIKGFSAED
IFHTFVLACDTLHGKRPYRPLLMQTLSDLGKMASLRMLPMSCNVIHVICHLVQKLLGRCP
SGNVNLLQSSIRSTTVRGRSGFDSIASSLLLDGASTLDAEFREGSTSQYPGSDSAIDTHP
PDEELHMRILQTLMAYLSACEFGNAALADIMSILFLVYTQATPESMVEATCAATIEERTQ
ALLRCLRSSSDAKQLEDDSASFTAQIQAVAYAKDLCALCSGATPKWLKLSLPRLGSVSGG
PSDYIFAGIWTPPRRLRLLLLRTLITHFTESERIHSIHETNVFFTQYLNEDVVSLVVGSG
RKPLHVQRHPEEKNVEQNMGTMNLVDLVLPDEQPNNEEFYLTQQLGVIAISKALPVMRHA
MPILLRHHVMLVKLCSEGEDGELGGNARRMAVVLTLWQKVIADHEILQQLLLLTGSNSVL
LPNRPPTVSSANIPSPKKQGLRRPTRASEDDAAALLLDSPPDQGGAMADSTNEKHPFADL
VTVTAELLSDIIVASGGMLNLDNVRANDNRSHPGASASAAAVGGGGGGGIAAAGVMGGGS
HWSAISMAFSRPLHLSSTPKATPNQEDGESSSPERALTSIMAQRHPATGQAADILSFLTI
TSQSFARVVEASKLGSSPTKTCSGPTTVSAREELTALFISLHSPLLRCFALAAQHLQGDD
VIHMVLKGVTHLVQTSCNLALPAQRESYLQIFVSRLYMKRDKQLLEGELVGTRSKNRVAE
DSALPAKVTGAALGVGHGRNLPDKVTPQMKHATVLRRSLQSLQEKLYVLNCVISVANCMG
ASLEEGWRPVASCLILTEPLLKDYHRLMEQQQKQPQYGAVDEITLQDALRNADRVRDALQ
LLFINNALLPDSLALEDLLKSIVMETCNCAPSIYLLSIRLVSECCSLALMTVAAGRTDVS
FAQLRRLWGTVKPLYLHVFDPVNMVKLVRVCLHSERMMEMVAGIFEQLVEDIAVVTAQFC
QRLNKSFSDMRAKEQKQRGEEKDATLTFHFAAGPYATAALVARLAYLCSSPTRIQQGTTS
TKCLVHDNGDVAKDDVETERRQLLASPTELLAVIYGYLQQPRQRHEKMQQEDVEEDVAKN
DREAVETVTRGASLMVLKEVLKLVQGFGEELRGAAWEHLLHLLRHTAAPSGAKRHPHPTT
APLTSVKQSIGIAFRALETIQHSCITSLDDEGLRQLIRCGGAFMTQQFPGLEHRLNINLS
AVQLLWSIADYVVSREKGDNKNDDILWCTLLMQLYDGCLDVRPEVRQSALKTLFSLLQTY
GGRLSAECWKCVFIAVLTPLMEATVQAANTCVVNSGTLSMPDKLRFRRCSSVKQQLRRGS
SDSGLTSFSDSAQILYGGYANEEEQHIAMLLAHLGEQPALFESMRVTIMDAVCRVFVSHY
QAICTVLFVNCSDAQQRTDREMLLRETISLFIGLCETSQLVARTTSGESSALSAVRALHV
LMTAPGMTLLTENELESAWRAIEQLLRRDGDGANTMRKQCTTAVVSTIVTSLGDVVAMRI
AEREQQKQQKQQQQRHQTDALVPATNVKAPTSSTFFEQLCHAFSSTPSGLRGGNGGSTGG
RARHDYFPDYIHIVQESLCSFAVADSYFFPSRVQTAVIGVWKTLWPMLNEDERGAIIKIA
LQQFPTRHSIMSFITQGTNSRGRKNREGVEEKITLTVTMAEPSPCQKEEKEERQISLSDS
LPPGAHPSFLLALMDFFRFVATESEGEAVAENQQQKYVMFNAAPALIRAAGVLLLLEYAS
PALLEVPGSGLLFRIPADFFDRAERCLTFFLVDTLWGGKSTPLCKAPSSTPPTVMYGFSA
SLATSRREGLLAFAFLFSSLVSIASNQLGAFTKNGLHDVSTRDETPEHLRCASQRLESLA
VLIGELIPNVIRRSGDLASTTELLSVLVPSSSLESPLLAAVAKRSLDVLRRWSVSSSPSS
PLLSPSSEESAGARGKVTAVGAEGSSSSRQKDDDTEGPQMTAAADAVALSVEGSDLSLDG
EELSNRLKSVARASMGARNLAVLQRFLSNTANEETRQMMKTTLQTIVLLYPPNLENQKPP
SGWHSSGVMPAAIEGNGASDEVKNNRKKENDTGEAREVLQGILVELARLVEHTGDDAELR
SMLSRAMLGICASLGFVPSA*

>TCRU_3484 kinetoplastid-specific phospho-protein phosphatase, putative
MSSNVKQFNALRKEELVQRVLELEEENLSLRQEMEQLRRRSTVIRHYDTNSLPSLQRYSD
EPQPTVSPTGIGRPSSKGKKGNTYTVSFSVMLIENGTAISVPLSSVIDKSYMRPDLRDAD
TPVVASSLMRDDYDTESFARHSMDSLCVDRSLSASADEPLGRSSELHGVSLACATTSVAG
GWVCNGSGGRPSVLLEFIPTDDANEPVPQDPASIQSALVSSQPREQQERCQQGQDGRHWS
VRHDIRQLSLGRVLNKRSISLDPDALVSHHTLRTFHKQLLDGCGVLSPLSSYGNAIYHYI
VKTFAVRNGCRHSSSDIEGFGRTLCSLCGEVKAVLQREPRHGSVVSPCYVFGDLHGNFLD
LFYFLDNLISFQDLRYTPHRFLFLGDYVDRGEFSVEVLAYLFAMKVLAPEKVLLLRGNHE
DTLVSGDISGYGNNSFRAQCQNLFGHALGEELWHRASETFAYLPLTANIDGRIFCTHGGI
PRYRGGVDDRLHILSRSDFPAFESFFQVPEEDTAYMRMCRQMAMDTCWADPAEDESTLDK
WGFGANPRGSGVIVFGSVAVDHFLLNNNFEYIFRAHQEKSDGLKLSKSARVFTIFSTSAY
VGHENGAGVVLVADGKIRLIIKSADDTARTPVVAEEEEDKDEEEEEKEAEIEAEEREEKK
NEKMRKSSRLVR*
>TCRU_3485 hypothetical protein, conserved
MRVSEDKRLRGQSLVPGQRNVHLEPGLTVSSLFDTHSGHKEKVVRVFDEKGCLTTREVGV
KRFQFARLSIFYMIRSLTWPVLCTYLLLLYIAILFAFAMVYFIWGNVCGAWEDAKWVTAL
YFTIVSLAANGGYFGEPTDTMLQPDHTCFTGRTVLVMLLSYTNIIFVGIVAALVVGKAEY
GGRLSQRIVFSDFCSLTSVPGRRDRCWRLTFRMANSDKQKPIAHGRLRLFIVTAESLKDR
RISRGEMRRQSLAELPEEQRSSKGGGKSWRQRLPHEMSIVSMEQEEGGIQLLRASASSLM
EDLSPADTSLAVTQGQLSPKSPRGRQRRGKRRRHEEQKPPGTKCELATGRGKEGDEDHAA
QTKKTCIGSAPTCGSTIAVAISEQGRGISDPSPFAEAGIEAAQHQRHQERLPLKHPASSH
PTSSFAAAAAAGVFAAGGNHEDGFERVSIHVEELRWTSSNEQYLEARQGQLSLWFPVSIT
HFIDRRSPLFRYVDQEKMDPAMLLSQSLSSASPTLKTTGEKGNTIGSLRSFQIVATFDAT
EMESGATIVAKRTYTLNDIITHYRFSNKMVQMRPGSNEVLIDYHYFNEMIPVSGMEPTYT
STSESDTTL*
>TCRU_3486 hypothetical protein, conserved
MEKYRKYGDAATGINPFVLMRTPTTFSVVVAAVLFPLRLAGALLFLTALVVLDVVAYFFF
LIPGMSCVSWCLLAPCQRELLRCLLFALGNVGITRASPRATAVANAAGGDATPVAGDVVV
VNMQSVWDMCVLEVAGRLPLCVVAFYIGGAAGANSGGDANKKKTDHDSRHDTLLVMEPSP
FQRWRVWWHIYHTGSLEFLRAAAGGDCGDYKSNTEPVLHLAALQQRCERIGVPIVLFAEG
SCTNGKGMLRTSPLWVRTAPRRVFVCAVDYDTTAVHTVLRPHRLLSFIFLMSASLHGSRD
PAWYSPPFPTATVRMVALLESSLSSDSILATKTTAGDGATVMWEEAKVRQALCAASNSRR
VLAVGLHEKCGYAEACVGVKAGSVSN*
>TCRU_3487 hypothetical protein, conserved
MSQPHNGYEQLPWWKRIALDDAYRRRIRKLATQRYREELHLLQEFPREIAPAAWDDGRPI
PQSSQHICVEDGTRAWATKYPESIVKVSGFQKLQTAAVATVISGPRAEEHEAYILEEVRR
LYNEEKASERLYGLSYFWNRQLPPNGFIRVWPSPLSAMWPSLLISEPFTPMYKTLSAPGS
SAELPPGMNPTCMTDPLFVHVFRRNGEYLGAWRQSLFLIRYKVICWALHEEERRRTCGAV
GRPVLASDKAFPDVATTQMLKNVPEFQLPLLRLQRETVTFSAKTCRLNLQSLSEPLTWEG
IVPAPTTYRAEQAYLNWHSLHRSSAVVRQAVRDVFNLLPQNEDGLITKTTYVEFFLDLLN
LFFPMHISSANISIAEEEWVYRGTTELMRFETFYEKFFSFPFIFFRDLSKVTRDQYVEVW
CLIRVCLLENEVSVLSCLQDTAVLGPPNSVTSGGLSFNTLSPAANPSAPRPVVDYSRTRR
PKRILEATLCSLQKLKDLGRKKAPPLIGKILGVSYDDILRLGGTRFHNTDNYPLHSAKQL
AAVMVKENLQKLMPSHAIAVVHAKGKQLLAETSRARRQQELQEQLQKKDNPGRSMDSEFS
SVLTIASLSKNENEGEETEGSSDLVIMNRSNSFRGRSLAEKRRKKMMGWSHVTTGRHATL
EKIEEARMKKKLIETSVFYRHRRLRRNAEHAKILSHISRSHTAWEVCRHDIYEIPPEKPD
EEDKLLAFVQDLPDDFFDDENSLRVRYGIHAALLKERAERSKNCYPIEPVLSTSSMTMAS
SRDTPKGNEQDSPATCMYTALTADDTTNGSSRGGAVSSVHVFRTRRRTPNGEGASRMSNS
PGLTSLVGDGSSPSSSCRMNSSSTPPSSASSGTMRGDPPEERNGSRENARDMASLEEWSK
RKEELEPKRAFYIRLNFKQNMDVNYKKLLQKKPHRLFPLSMPTARKGAPSTVVKSRLQEG
LRPSGAQQTF*
>TCRU_3488 hypothetical protein, conserved
MTAGGGVLTPSSAGAQIIHLASRLVVGVRLHGTIAAFHPRTRGQLKCRPFLRYFAETLHR

LRCDVTLFVPVNSRTGPQQVAELSTHEFPCEYRVVHDPTSGAVDDCSRGQRRGGGGASRG
NFQDLLNRVATEQQTSPSRILFIESEINYRFSPVQTLVVEAFQAHRIRQRRRSMGEAAEA
EERRQAGEHHAALLESEYSWTQGGRVSRLRHAQPSAPFSAELHGDPQEEAKKDDVRSAAL
AINREDYTLVALAGMLVELAAADVAVADYLRVEPLVEKLTVPFHGEVNYLPMENCDDMEL
WDWAAVEVREARRKEEAETAVPEVEEREEHRDLFK*
>TCRU_3489 leucine-rich repeat protein (LRRP), putative
MNLHAGGLSCGASSIKSENTVATTTATKLKGSAELTSLVKVSSWGKGSSNLCDCSSCQKK
TSENFMTEPKFDLSLHKSPLLPQMMTHPSAIGPHTVSPPQSAKTQDSVELPSSGKDAATY
SRTAANTSLLPPCTVERQQFHQYYSHPHQQHHEQPPASRNLLASGGVPLQRYRAKLEECA
DLHCRLQDTCVELSVTREHLCSVKVDRNNLINEIERLRDVLFVTTTELQSMQQRVEELER
ENKHMSVELRGLQSLSMCPSRRMEIITTLRATPYDIDAGKSENIYGTNTDSFAPGVMGAR
RRLTNSAAALCLESNPSLLRRSLTCADTVKPTDILASYVCECFRTEVVPHMELLRSLYDG
SRLMAVDPPVTHAQLSALKRVLVEAAAGTTRIGGAGAASIRRLEKRPLPRVGGRRLNPLT
SAKRWNCQVELLSFRCENWHASTSVLLYMIRSLESVRHVEIFSLTDVAFLRQLAEALLMA
PHVEVLSLPELSLADEGLAVLFSFMVRQEQLVTKAPASIVETKSSIRTKYEPLGPNEPQK
GIGVLSHNRDHKEDEDDDGAGGIGGKDEEGEEVSCKLGDYSAQFSSEGRYVKPQFSIPCL
DLSRCRIDHPTGLFRTFRGPLVKVLVLTGCSALRDAHVRDVLEACPQLHTIDLSGNEGLT
TACVRYISQHERLKVLRLENCPAIKRLELANVEVLFSSLAYVTRLYAPELCRLPVPLTQS
HVLFDLYAPKLREIILKGIVVDRGTLAAFMHNGSNGFAGEREPSSSLRAHSSSARLVEKN
FLEEQQQQEQQPPREGEGEDEEMEEKQEFQEEQQEQQQEEEEENQHEPGDVPQLLSVGFI
GCLIASASELNSFMKQQTQLLRLSLHGCHGLVDSSLAWLPHTLMDLDLGGVAQLTGSSVD
VIATRLPQLIKLSLKNAGTSIQNADLHRLRGLGNLEVLNLLGLPQLFPEVVAAVVEALPQ
LRVLYHETVVVARTHPTTVLQVNRIDEEDTTHHDIQHCLKELLQLRNETALALWMEAQLP
KPAQLLPCRNGARSGTEMGAKQPPLTINTTFYEATQLELSQQGRFTMALENEEEEEPSTA
ENGENTVEQEKPDVLTISSDHEEAMPHDFFDGEGDNDEDDENEKSKQSLYDTHRRTESGM
DEKSRLAIEQTPLGPWGAADIVAEHRQNSGG*
>TCRU_3490 hypothetical protein
MDAEVEETGKPNSAVVSPVDNEERQHVVDSEANGDPAAMKAKSSATDPKKVPPCDEYPTE
APKYFANNHHNNRSGSRRKRKGDGGGGGKKEAAEEYPIEESGASSQRLKGADVHPTTSPR
KEWKGDCRPVRKRESSQKNPRISPQKVYSAPIASVSRHSEKLTQHYGKASPTARQKRGQQ
QQEQQQQQQRPEYLLSMGKNGEYVSQTPPAEEGGRRGRVRNQAFLEHYTSVYMKTPRAPR
RQQKLRPINLGGEGGKTFLNEAAQAYDRKADDLHRDDEYPVEDTQDGQVPLLGHTHKSDN
NMESDSVESKAKWIPFSRGVNHLSSMSMVNASSVKKEFMEDNVPSRDETQRRISSQRLLQ
TRCQNDEFQRCLHELIGLFNSRSEKDMVTSLGFSYACILAGKRRQKPSEIPEVWFMSRRA
LLLPQHRGAAERAQETTQLPLIYSNSNNNNRRNESSASFAENVPGTKKSGCSNERRGNGL
QSVRPAQQESQDAFAELELEECEQGRNTDGFKNVESTEKLDDVHCEGEKHKELLAR*
>TCRU_3491 retrotransposon hot spot protein, RHS3, putative
MLTRDPHGDFDFGRLGTEIIGMEGHGFLLNTQRLMRGVNKFYCEGLNSLRQWRDLGRKDT
VSPLGRANLNEALSQVLNEERQSRRHKKANKLEGSCESVQNARWSRGVEVPGGEGMGMEV
KEGEPPQPWTYKKVVLSLEKDDDVLQSGAERPRLMVLTSDKGWPYSWKWKENKSTHDCYV
NCEVERVWQIVKDDLTEWFSSHGRTDFTPKRRVLIGMPGIGNSMAAGSYLLYQLLQYDAE
KLQVVVHCFGETTYLFDKTIKTVTRYVGSKTSRNVLYDLRHLKMKGYVIYDVTEKGMPAS
WFSPFNEWGMIVLSSPNVGNYEKWETQVRAERIIVNCPDEMDMKAMCAWMKRGLDPDKQA
EYWKEVKERMEKLGPILRYIFDANKFIAHSAAIEDALDGINSRDGEKNFTHGGVKLWYSE
NPSQKLVRVVRGREVGAEVFLNAPISVCLGRRIPHYFGKRDE*
>TCRU_3492 retrotransposon hot spot protein, RHS3, putative
MKQSDFILLVLRFWDYVPPCLIEKYAVSAFLNKNLLRAIRLRIKELRLPGRGESHRCALK
VHSGKSFARKEVLPPPERLSNPVAMDHWVLYEPKVHKFPLVDGFFFVDTNPKTLVGLRMS
TASKHRTTTSAVRRFTECLAAYFEGWEELSRDMSWEIIYVRHEIYRPMEGRQKFEVVNSD
NLGDDENREIAAFCREKVRQYLAALSSADARRGEALRR*
>TCRU_3493 BNR repeat-like domain containing protein, putative
MVAGNYSFEVTGTAGNTAEAAKWGLLGAAGRVTNDGSSGKKKIYWKDAFVISLTDFETKH
ESLTRLIGGGGSGVKMKDGTIVFPVEGTKKDGNAVSLIIYIATEYGNLSKGMTDGGCSDP
SVVEWREGKLMMMTACDDGRRRVYESGDKGGSWTEALGTLSRVWGNKHKGNEKALEAVSA

QRRLITGT*
>TCRU_3494 Adenylate and Guanylate cyclase catalytic domain containing protein, putative
MAMRWVAAPYLFFALILLLALFSPQGAASQAAVTDLHVRLWLMRKMNQVRLKGTPLAFYS
GMNASLWARNCTVAEGVRVEVVEKEEVQEGNIAVLEEEIRKDTNVLALVGKQSGEFLQLV
LPLLKKYDLVSFAPFTGSSLMRGWNPNLYFLRADPAAELLALLRHAWTHLRVHRLGFMYL
QGVSFGDREYEQAQRVMLGMGYNLSGVFTVKSSMSRGAKKEVFDAAWKAFAKTQPQAVIV
FGPPIHDTVKFINRMLTDNRTAGAYLLAPLMLQDFFLRAWHGAVAGGVEFEPGQVITTGT
SPLAKDIQYAAVQRFQKVMQDYLAHSGQKDYVDKDHFLKDDGDGAMMVAGWIAGEVLSQA
LGNREWVKNRTSFLTSLYNQRRYMVDDIVIGDYGGECKSEAASQGATCLCNQGGRTVHID
KVMGAHRLKPFKGVMRFPLSNCNVSYVKIPPVFIGLYLLMDDNVFAFTACLQFDIVFAAA
SSLHERWWEQGMLLLDFLQSNTYDSAGDLRSELQSRRAHAVLGVVTDAMLDVEGMTFIDP
LLLEPRLNRFRRNVIRLSPTLEQQFFVIAKYLGKTSGGSAHAVIRSGEAAAMADVLRLSL
ETFGVSLASVTLLAGGDVLADHLPAERDVFVVGISADDAGAIARHVASNDGVRVFVVFSE
FALLHAEFVAAFRDCAGVDRVVFATSLPHWNDESSTSETAKKFVIAVPEKKPDASGNDGL
CCHEADASGFLADGPYQR*
>TCRU_3495 small glutamine-rich tetratricopeptide repeat protein, putative
MMSDTAEAHSTTSQPLTEEHRKLVFSFMRMLRGVNSPDPERVNTIVKLLGDEYGVNPAGV
GGCHDTGVDVFEAFCQALQSQESKENIQQNEKFKAFLDLIQKKGYFAGAEPGTEEYASRL
EKAKQKFEMRNNPYQGMSAEEIKNKGNELMGMAKYKEAIAYYTKSIEMEPENHVFFANRA
AAHTHLKDYDSAVIDCERAIAINPNYSKAYSRLGTSLFYQEKYARAVDAFAKASELDPTN
DRYKEDLKQAEEKLKLMGNASSGSSAAGGFPFGGGMPDFSQIAQMMNNPQFIETTTRMLE
NPQFSQLVANMASRFGGGSANPEELLQSLGSMGLSGTNDDGTMRTPFGNINRERLEQLQE
DEVKNNPKFRAIMEDVRQNGFQAFQKYMGDPDVMDLMVRFQNTIMGGNNANSSP*
>TCRU_3496 Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MNGDENPLMLGLSYDKEKKKWRFLCGGKTTTEHSSDWDPETTKKDHVVILRRNGSQGSAY
VDGQRVGGNAPCGLENTDSKEISHFYIGGDGDKTRKQEDVPVTVTNVLLYNCPLSSEEIT
ALTPNKAPTPSLEEKPSDPSTVSSGSVVPPTPLVTPNAQQTETPSTPAGTQLTEQGQSMG
NSKGAGSGGASTTAVSTVSTPSAEEESVVQVTSGTSLDGTQTVDSGSTADGEPTMQTRGG
TNGQGEEGIQPRIRDVNAAALNSSLGNVSQGNNSDAGTVRERRLLPSLLLLGLWGFAAL*
>TCRU_3497 hypothetical protein, conserved
MPSDRHIPGNASYLSGELLLVEVPKMRYGSGLPFLQHRAKTAWEWLRHGLCSLRRRCDRR
AVSRSRPRSSAGRWFRWDFWRLRLTAKAKFPQRLGARSAMGVSHVRHDTSAAAAVLAAHR
AVCRASDRGGVGSSRRRWLFRAKFFACLMYVIRAAPTACAWDGGLQWSQQPSVFVRNTGA
GAGRCSLLPASDSGSRARGLPVACCSGAVSSWPELSDTNNTSSQCDDAGAPCVCELCEVG
RLLGLCITSLFPGHAAVAKDKPHPCARSSVLLARKKGTPTM*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MDAFGDALNVTLRHCVLAGGAQLRIGGLSESTARLMPHAFVNMTNVTSVEGTIVLHGAMP
LHSSVLLANSTLRATVGGSQYVPTTRGHERFRYGPALVLDGVRLLSTRLVMTRSTLVCGG
GSCAAILVERGLGVNLSSVFYMDNCVISSRTHVIYALASDLRVVSGSVFSIQNSSWILPS
TEYGKAACVFKDVVVAGGSVLQIVSSTFRLGFAMLIANTLTVTDGSWLVHRNNEFRTAYV
VCVAAHYSMVFRDRSVWSILDNNLTYGSYSTIANMTNNWLPPSDTRPTIYGMCNEARGSP
VTNYQDDLNIGAPVTVLDCGACTVDAVCFAARTSSISGCECVCAAGGYGDTCLPAAVPNG
LGPLPPPDARDTEVRCVHGGSISSVDYPDPGVRGLCFVNVTLTTPIVLDLSYFDAPQQTL
NITLLQCVLMGLLIRGSGVRVHVSVTSSMLDFGALDFRGDFGASSQILVVGSTLVTTSGH
AISFVKFILSANMTLLLLDNYIEANRYAVYFFNGVVVGGGIIVKGNTLSTKKDDDSVESS
VCVNSVDVKNGGYFDVENNTMSSVNGVIFWGDTTVSSAGLLRVADCTFAGGTEFLDPALV
YLSGSVTLEGGAQWRVEGNSVGAASVLIIPHPQYKIKLSGSGTTVALANNRQVDNSYPFA
DLSPPDTIVELPARFVVGCNLQGDEEVLYDGVFPEDVVVFRCGTCNDDAACYMPGTESVD
RGSCSCSCKDGWHGASCLPFEVPDTVVPPAAERAVDGDTSCVVNQTLTDLALNMWKTHHC
YVGVIFSGVGAVLTFFLNSMPLHLPINITLTGCTFREGAALQFVGGAAAVESSGVLIRVS

RTVMRSSTVAFIRALPQHCDIAVTEVDAVQSSEFELPDTRMNTLSVLLLGDVVLSASSLL
VSNVRAHATKRDALGFYSTGTLTLVGGGSLYARYCSFDGYTHMFYLYGLSVSDHSVFALL
NNTVFSGASLLYQRNRFSVSDHSVVRVVGNSGSVRYAIFNDDMWTVQRSSWLDWRDNDVE
VGAMFYDSSSAFVSIDGSSVVTLTGCKMGSTGLSVSLLSRADAGYRFFAGCLTVAGREVT
TAAELALNGITSVTAVAVCGECTKDGDCFAPLTTAVSGCKCRCAAGGHGDVCVPAPVPAG
PPPPSPPLPSPSPSPPPPPSPVGECISDMVYPEVPQAVGGGLSWLCYRNVTFSGGGMSLT
VLIGGMTGDVANVTFDGCTWRDGAVLLLLGNVHAAVGSLNIVVTGNRFIDALLSPEGVFP
PHTNITISGNRFTVTRAIPRPGLELDCPSCVVMNGLAISNDSAVVLSGNVFQSVTTSSSA
VYVVGSALRVLWKSLFAVLGNTFHMGGGDSTLINIEGSGQFSSLRVLNNSAVVIRGNVVT
RPVKYFLLVILALRVESRSAVVFQGNDMQRSSAVFFSSYSSYIYYNSWLQLSGNLCRESP
SDAFLFLNPTVNLRDSAVSVSGNRFMSSTGMPTVLRIPKRSRGLTNGAIVAACNTVNGGE
GVKYSISSVCNATILTCSDPCALATSCFPAYTTTASSDGCACTCAEGGHGEACLPVAVPE
PPSTDGADLCVRDVRVDVEVNVSFGTSVACYVGVTFAADVVVDVASMSGSVRNVTLANCT
FVSGANLYVFGWRSDPPAGERVDVLISGLESRSGGGVLVANRFPPGSRVTVVDSVLIAEK
RVAYRGAYDLGDASACLVVHNVNLTGSVLTIARTHVAAVFRDAVGVLLVGGVALSSRGAL
YVDGLSVQTALGLCVSVEGGVAAIGGSVVAFVDSDFLLCKHAVSVRGAVSVSGSAVVLVR
NEFLSAEDYAVAFYSTVSLADGSMLLAKSNVHDGVSREMLHAAGAVTAAGSTLSFVRNRA
LLPRMVSLSLSLAAGAHLRVACNDAGDRVLSTVEEYAAAGFGDAGSIDVAGCDDCDRDTH
CYAPGTASASMRNGVCACGSGGYGEACVPVGAPALPPAAGTASSVFFREGVTLRSVFVVP
AGASEVTLRHVVLDGVSPVLYVPWMARDGVRIVVQNVSLRNGAVLYVMGGGALRGAVAAG
SDEGGPVELSVCDVEALNGALVLTGTFPAGSVLTVTDSLLVAARPTPLVYLPGSQSSPYA
PVLVLSGLRLVRSVLVVSGVALVTVVTGGRTVVVDGAVLELVGGGVALDAAVFGGEYALC
ASARVVASGGAVLRVSGSQVYAAHGLVFESGVEANASAVVVNDNTGALTDGALLELRGPA
SFVSGSWLSVRGNSISGRLLSVPSYPRSAELVQSTLTLHGNAGSGPVVMDGTVALGGAGR
KFVVGCLTLNGQALRPMDYRSAGIIGEFRPVACGVCDADVHCFAAATRTMSGSCGCRCAE
GGYGRDCLPVYLPRVDGCNRTSGMPLLGHTATLTETRSLTSTWTPSHTTEHYSPTQYSST
ETLQVTETVALPPTRTPTASVSSTLWWSDVACPTLAVTTTVAGGSLTQNDIRGGGSAVPT
RLMVALPPPFRWARDPQLGTHLSFVPVSTAQPRGFGGPWGAMLSNATWVRNATNPSTVLE
LAVPVHRGYFIAADETIVIRCDATAVFGGCKGVLLGSFTIRSDTLPAAASALSAITGVVA
GAAAVAVVVTGGLGSVLEMQALGVFARMSCASAQERASTAALPYFLSVFAALDPLWMVVG
NALLAAVFGCVHCGVTAAFQRWRGVDAASAWAAMRFPSLTYVVAHAMHLGIFFGSLRALA
MPGARVQHRVIGVVGVLYGVAFPAGVCYFIARHVGASFTRYWQFSRKPLHERLLYPVGYW
HPAAQQRMYGSMLTNMRGSRVYWCVFQLSVLCVVCLIAAVQSPVGGCHVQYFCMAAVLLA
GAGVVAFTNMMRSAFLTVMHTASFVLLAALCVISAANHLAPSDGGARAYAAIVLLLTTVV
LAVTVYSVVVWYAEDRHWQELREPRRGGLEALLRDGEESDEETRKPHDRTSSSYASGTTV
ASSYRPPAPPQPMAGDTRSDALSLLDCASSARGKIDHALL*
>TCRU_3499 hypothetical protein, conserved
MHRGRGRTARLLQQHAVKHHRARQQVHAAAKVHRRPARLQRPQHSVAHTQLRLQQRRRVQ
HKRRRHRVRQPAQLGVAHRPRRHNRRVTDRHVRVCRQVMHKHKRAVAPGQPAHAQLQAPV
TRRLAAVAPHVDLRTAVAHAVPQFDAQRAGEHRRHVEHHSHAVRDVHAVHQHRVHGTANR
DGSVHRAAPQSQHHRMHRGHPRSCCCQHQRHKHRRTHSQNGPAPHTLPAARTRTHSRPHP
PTQTRISRVLVACRSRPVDHSSCLSNPFLQMANPVTRFRQIDIPVPPILILRVIPNTLKR
*
>TCRU_3500 Transmembrane amino acid transporter protein/Tryptophan/
tyrosine permease family, putative
MKNHSQTAPYGDDEGAGNIFFPVLVTDRNSFSKAHRNETSLMSCCSRERIMEMARSTKNI
DGVLHDFEEGPPTAEMLRQRKRKSLPQRILERVFPPGSMLSSAFTLGSSTLGGGILGLPS
AFNMTGYILSIILLVVVVILTVFSLWLLARSADVSGKRTYEDVMKVLMGRFPACMVAVLM
CGFCIGGGVGYIISIGNLLTPVFANPGVPYFLTTKPGNRLITSMIWLVFILPLCLPKQID
SLRHTSLLGCICILFFVICIIIDACQYASKHGFRSELEMFGTGNHAIEGLGMVMFACLVQ
INAFEVYHEMSHPSPRRMVRDSIIAMSGCGLLYILVGFFGYMRFGKAVTDSILLMYQPGE
SVLFAIAYVGIVFKICVAFALHQLPMRDGIYHLIGWDVYLIPWWQNAVFCTFLSLVLLLA
GLFVPNINIVFGLVGAFCGGFIGYIFPSLMFMYSGDFTLKKKGFLLYFLTYFLLLAGCVA
AVFGTGASIYGVAV*

>TCRU_3501 hypothetical protein, conserved
MSVKDPQSRDNEGLRPPSLTGTRGVGTTTSTSDSLTVNTNKQDLPSPLQPPLPNSSPHAI
PSSTSAAGPDNEKRHESGNGTKNSQQPVVGGIQAKKDTGVKAVASTGGGENSRLTVTTVE
EMSDATKKGDSDSSSAALRSDAGTEGTPTTPDSSQPSTGGAEQPSATPDREEASDSTENG
ISQSAGSATAPTTNAKTGDTAKPVDSDSSTAVSHTTSSLLLLVVVACAAAAAVVAA*
>TCRU_3502 retrotransposon hot spot protein, RHS3, putative
MKLEKGEPPQSWTYKKVGETLERKDGVQQSGTARLRLMVLTSDKEWPYTWAGTESTRDCY
VNCEVERVWQTVKGDLTKWFSPHAGDYFKPKKRVLIGTPGIGKSMAAGSYLIYQLLHYDA
RKLPLVAYIIKKSVYLFDKTKKTVSELGSEEIFVNLVKDFTLRGVKGYVIYDVAEQGREP
HVGLPFTLWNMIVVTSPNINNFKGWKKQNGAMGIVMNCPDESDVRALCVWMKRNEPRGQN
GYWKQVKERMDEVGPILRVIFDGDSFTERKNDIEEVINAVDSSNATHYIGVMSDKLWEAV
NPSHKLVQIVRVRKDSRTERYLNSPASRVIASKMYVHLSTKMQSRKIIKLLMHPDIFFLS
NVLEMSGTAIFMCRGAVNIIKKKLKELKPPGRRALQLAALQRNPQGHPTEAVGLPTKQGV
SGKKIAGYKVMYKPAYPTFPLVDSFFFMESPRKTLVGLQMTTAHDHHTKTSTVKEFTEYL
SWFFNGWEELSRDMSWEIIYIQHPDSKPMNGWQRCDVVNPSSREEKEIKAFWDKEVRQYQ
FIFSSEDIKKLHAIQESTTEKKQEAAVGNH*
>TCRU_3503 Concanavalin A-like lectin/glucanases superfamily,
putative
MKAKDGFKFTGPGSGAVWPVSSREHNGPHTFVSCDFTIVATVMIQILSKLGTPLPGAGLD
APVSTNFIGLSHDADGRWETVFYGIKTASGSTWEPGKKYQVVLMLPDGHRGCVYVNGVIV
GSPETIRTPETRGLKSHSSTLGATRETSTAAM*
>TCRU_3504 retrotransposon hot spot protein, RHS3, putative
MDVQGSWRHSRKDDGVEQSGEAPPVLMVLTSDKGWPYSWKWKENKSTRDCYVNCEVERVW
QIVKGDLTNWFSPDAGTYFTPEQRLLIGTPGIGNSMNASSYLLYQLLHYDAEQLPMVAYV
IGSQSFLFDKIIRTVSVYMDDHRIDDVVNVFSLRGVKGYIIYGATLACRQPPAGLPCKGW
GMIVVTPPDKNEYERWTKKWTLLQS*
>TCRU_3505 hypothetical protein, conserved
MIDITTVPTRSLTCPFPLVALDAAAFHETPTSRLLLLLVGRDRACVASLQDHKICLRRVV
LQYHRTLTAGACRSMNSKDGHIFALADTSSTLTVHRVPNLSSGVVPVDQESGTVFLGNAW
DKASRIDQVVSIQGSSQVDVICTRQGETNVAWAISFEREEARMIRVDGDLERLFPQQEIT
PGCFVGGTPHGVSLISPATGETLIQLKLPSGNRPAEAVQSGYAGNSYYYAVVTACGTALM
YDQRRSEKPFWSKPLWDSRSVNENGDAGTLMAYCCEGVWAVRAAERLHCLRCTEGSVVCR
SFPLPGGLHSSQFTTAGLHFTNDVLHFVGTNNF*
>TCRU_3506 monothiol glutaredoxin, putative
MFASRLLLLRLTRASHGPEKVAPALAASIKDIILKDRVVIFLTGTPEEPRCRFTAQMVDM
MQQMGVQYSFFNVLDDDDVCEGLKTYSDWPTYPQLYIDGELVGGYDVCKNMLLNGQLTRL
FQEKKLL*
>TCRU_3507 formin, putative
MERETLVMKEVIIDPNRERNVGIVLQFLRLPIQTIEASVRTFDELTLGEEHISGLVKIIP
HAEDLRPIEAWMRRNPKASVARLHQLSIPVRFFMMTMKIGHYAERLQCWNLKNEFKGRID
DLEVKICRTLEGVSAVMESTQLPRLLQVVLAVSNFLNTGSRFQEAKGFRVTQLPQIIEFP
TTNNNRVLLDYLVEIIDQQDPALHNWTEELLSAAENASNFDVPGVAGELKSVRARLQKCA
SLVRAIPDDKPWTTKLGKFIYTAFPALDHVEQLMSELNAKIELMPAYFCENSSSFSMNDT
MRCLANFAKKYNRKRDQLAAKQMRLSRLAAKDAENSENVTEDPNSRVNVNESHKVQHSLQ
EPKIKVEKERSKPSSPAPYALMAKGDRKGTVGNGRGVGRRTESLNNGSCSNSSNGETFSE
PRLLLFQ*
>TCRU_3508 hypothetical protein, conserved
MFSTRRLLTGAGGAEMTVPYTRGSYHIVPKKYTVGKRIAVRSYLDRNRTELSDRTYMPQK
AWFEPYTPRRFERDHEELSYNFYNLETKLIWTAFDTPEKIGMLIHDETIKGAKHLYNKEF
LDAALHWTREGRYWRCIGITKPFYNKKTLRVHCWHDRGVQIGTLVLSQAMRHALMDLERA
VRRKELGLPPNYIWDRWGPIGFIDGSKTDYLPRFSHNPYIDPDGVEVTELDVAPFNTHEQ
IKERYSEFIEPDLTPFSGVFRSPSHGALTLDDVPEQAAVELFRQLKSKAGTPVFSAGGAE
IAPADMRVLFYLSADPQRMEKARGVDSWQEVCEMLAPVQEVCDEKIEALRLLQNTRHDVN
RVRTFYEEKCGFADFMYTPDKVITAAVLCYLQELHRICTETEWGKPLALALTDMERVQVM

GREAFLVYRHIEDAILDKRRRIWATRFAGEANEESTLDYLLENFGRRTEQTRNVGTTGAE
FDREQEPIGRQVQRRVLDSDKANKLAEARQKRGKMWSQKKSVFDSLHQKQLQNVTYGVR*
>TCRU_3509 hypothetical protein, conserved
MDADGVPVRAHLSMPSAAEPSLAASTIDRGKFASPPATPFQFAQPIPTESAVTFYFVVFL
CNRSPIFHSNRIPLRDDTPPYTPGDIVYFGPSEEVAQQKLQELAFPLGFGCKSSLTRNGP
LWNSRLESVQKRGKVRYHRLMIASTFVVSVAVENGELRTMQTKYAAVALVVTCPADRPYR
QFLEENFDAVVRNMLHVVLSFAMKATQLFFFRLSPTTVVGDLVTELERDPQAIQTYGTLG
AILVNAFAHSHAIPRLHSRISCTDVFNLSRSSSSQPHNTTETVGDLLSGALRVLCSFSET
FTSRFIAGLLSLSNWERWGSGQSNVDPQQQGHRIGDDGDRVDIYGDYWNRMEMVERSSSG
SGDNINSIGLVSPVLERCKNIGNNNNNNNNNNTSSYGYTESNAATAGAQVLHRLDFNSVS
RTTSAVSTTAHSTAPNTDVVCSLSSERVGRVVIFCTDPELARCLLILAAFFFRDHRATVG
MSSRLCDKAPFAGKVLSCIYPSFPVQWVMEEYDETRMDRLLSFPYSVDNLLLVIAPRVGV
CNRIKLEKKFSLTPILVEKFKKGFHPVCPFQQRTLSVVKMLPDKMISSALREARRLQEKS
HGTVNCAVFFEFFMLWLVRQSQLCHSQQRFAEVEATSVSVASTPLKVEGSTHVSSRIGSH
VTKLFSFFSRKNGDVVDRRCFPHRVFSGTASPSIDVSATARPGRVFSDNGSDGMFGCVHE
NSQLMSLLTKCWTSSRDGP*
>TCRU_3510 hypothetical protein, conserved
MATHISVSNEHVSQPAALAFQCCRCNQRVICCPGCGEANFILVDGVSSPTCFTTNAARGR
GSTGVIINGRGGVTWTRRPPAKSNGASTPALPHAVPTAFELFCRDAEVQREVGMDDNRIV
EVVGGELEDESLYDRRRLHAECWLAADAETRKRYELAASALAAAITSKVHRVAGGDAPRN
VKKGKRRSAALESPVVATLLPCCGDVTDTSSSVTTANVSNDDGKMLGAYRSPMTAFRFFC
KREQQNYKNKGALMKAWRSMSLADKKPYDDEAAAIRVATRGKRSTRVCKN*
>TCRU_3511 Sec8 exocyst complex component specific domain/Invariant surface glycoprotein, putative
MAWRYSGVAGNGTFGPSPTSPFSTASMRNNGQDNGNTGFAVGSGALFSGASANILGAGAF
LRSNALSSFGTQKQEIDEELRSKGEDSTVESEGRWPRREGNGSLAIADAPPVFGRSQAPT
RSIAGALMSNLARKGDILSVADASEAGVVLADKGRTVQGSSKTELLAKKLFYHPPNVRED
EYDDDEYEEDGDARHVDREFVRGANFLFSQVDPELLLENFVPFERGVEIIANEGGTEATE
TEIDERLAPYYDLQEDIDVMLGRYIEAHHDEFNEAVAGFSKMVLAISGSDEMLARLKQQL
TMAAASFDNLAEQLQVLRMRAAKALLMAESLKRLEASLSCESEVKQLTANHHYLAAVKLL
RQHKARLEMPEVSNIRATQMLRDYVNGTLENMHVTVVENLMSCVFRQGKLYEADAQLVGH
MLVDGASEKTVGAIDALVALHEKSHYSDIKADKTTLGFSDVINSIDDDPYDNDGDDVTRN
YLRFIPLCVKTLQELGKLNCCYETFFSKATRSIEQTIAHFFRLYGAWRQRAVKSTSIAGS
LDAATVRVMKLQAEGLASPTVSYDEAIALIQQPELIAMLNALFVQIEKIVRNADYLIKVI
LVSYFPFLSSCLMKPGGFYPDTTYHDWDVSQTPLQNPDEMREILTAALSTTLSNYGAQQK
DDGNNAEMVALKRLLVKLDVDSTFERLKALLGRSVCLRDVLDLIDAATEAVIRENPGDSE
EEVMVCRNSLSTLTTDMVLEAFRRDVREMHSQWDLQVLSSQLSYYIELIFRVLCDAKELE
EDFGDEVALKPFLKHRNLVGRVHRTAELMSSGAAAAADNLFSLEKLLSTQDTSGLLAMME
QTGYVSFSIVAAVKYAQRELRCADEGNRKQLRDRSMAASGNFVYSWRSGSALLLQQAMTL
KNWFVFTPMNILTCHESVRQFYRRCAVRAPRFVEASREEIKNSLFHFLQKTYIPSLYVFH
LQQLRQLFADMSEAESFTDEASAGEGNVRKSPVRSPSSFLLPIEPLVHHQKVQQEGIKWP
IVTLRHGGENGYPILTCVHYVGQVLQKLAHICRTLPDKLAEAIQQNVTETLLSELTIVLK
KKFYLISHQTLYHCLLHTEFEEAFAGRPSARWQALSEETRLWDAHNAVDADLFRYYAFNN
ERRTSGHQYNHVSHDFLGCDVMENSKEANESGVDASIGAIPPAEIALKGSGVVVALAMLC
YSMEWLCDVVLQTVWQNGWHYGISTDCLVPGTVFFKRHDRWSTSLAATKPSDSTRWTRLG
GIMRQMYTISQVCLFYLSLEARFAAFQYIPQLRDESYNIVATTRSPDTFVQAYNRRIINF
FALLKLHLSEKKLKYVGITVAKPLSELIMVEIAHLREKAISHAGLARLRANLLSIETALQ
LILPTDDDVRGAVKHYFLRPATFLRHLPNKDVANDLITSGDYKHFSMHEMEELIRLVFRR
EASDEFVTAQIQLLHVKLKSVAPAVATPEMTPSASLTDENLLPAEHNPQQFERGEGSEEE
ETEEEGEEEESDTVLQPGGRGPSRHVDPTTKMATSPSADSQNPVFPTGPKLAVTRH*
>TCRU_3512 40S ribosomal protein S11, putative
MTAPEQYARVHSVDLTLQHEKAYQRQTAVNENSHNPNKKHVNMSGHIRYSKKIGLGFKTP
KSAINGKYIDRKCPFTSDVSIRGRILRGVVHSTKMKRSIVIRRDYLHFIRKYQRYQKRHR
SLTVHCSPCFDPKPGDEVIVGQCRPLSKTIRYNVLEVVSKSAPGKLGRKFSKN*

>TCRU_3513 ATP-dependent DEAD/H RNA helicase, putative
MSSGLADFDGDDVKVPIVSAQPHMGVGMGTHSAVALGGFQDFCLKSELANAIRENGFEHP
SEVQHQALPQAMLGADILAQAKSGMGKTAVFVFALLEQIEKVPEGQKPHCQGIVVVHARE
LAYQIEQEFKRFNKYLPYCTTGVFFGGIPEDENVKQLKKEVPAIVVGTPGRLSALIQRKA
LDVSRVKWFVVDEFDRCLEDVKMRRDVQTVFLKTPKEKQVMMFSATMTDELRNVAKKFMN
NPTEIYVDQRAKLTLHGLAQYYMNVTEAQKLRKLCDILDAVEFNQAIIFTSSVERCEALS
RQLQALKFPAMAIHSRMEQPERLRVYESCKSNHTRIIVATDLFGRGVDIDRINLVVQFDM
ASDADSCLHRVGRAGRFGTKGLTIAFLTDEEKEIKRENRKYTDHGVMKELQERFEMQVRE
LTDISTQLNQSQYMNQ*
>TCRU_3514 LETM1-like protein, putative
MQGSWATLKKNCRNFFPGLALFAKQTQEAVDIWLRIYNRQLNYGPKDFVEQSETFSPDYH
KRFHSQDKNMWVDMELSKEVSQEEIAKLMRYKLDMWRMVHCTGSVLVIGGYALPLALFWL
ANDTWVPSAFNCTAEELKAWRHAQDLYRYRSIPSYLTDTKWHFDFHAYPWNETQERAWDD
LFEKNDVWRDPKLVRHAADMYDGFIKFELIRRKSLRHLCRSMNIPTYPMLTRMCNGTRVR
DYWNLAWCEDYMVITQKLHEKMTDEDLYDYAWRRFLAPYDKNLTREQLMERVEGYFTFLG
PEFLEKGKAPNLVILTNYVMGYYNDPAFLEEDISELDKNDYDHLASWGKDAFLRRLEFEN
GPLRDQVEAHTQKLLAEREAVAKKAASSADPVKTG*
>TCRU_3515 hypothetical protein, conserved
MATDEMAELPTVTLFRYPACFAIPTADPHALAVECMLRFVGAHFVKRDAPLPVALEVPTR
DGSAVGCHENGGVVRKTGVASCLQQIEDSVHVDKDVLPVEKRHLSLCVKILVVNSLLPAF
VYLTHCDLDLFDHSIRKGVVPKVATLWQRLLGNYRRGVLERSGCCGRYSSVAEALEEAEK
GLRALQTLYVGNSNPPGTFFLGTERPCSADALVYAAASSFLHADFANHHASLAVVKMQKR
LQGECTTLVKYIERVRQMYFEEYSAFYTLRAAPSCAAGAHSGNVAPEPDDLFKKGRRMVV
AWTIGFSLLYFTLSNANLILEALSELQVDEEEEEEEGKEEEGKGGEKK*
>TCRU_3516 hypothetical protein, conserved
MLEGDAAPSASGTVAGIQADGSGPEFNDATPSNLRKQFTIPKLDEKKLDMKAQEPHGTTT
PFVVLDGGMSSGTTTTTVTAVTETSSMPLNSNAPAFVFGTGSRYTGGNVIAVDSPSASAA
YLLSMQCQNPQYQLAHAAPTDQEIFLTQSVLQMCPREVLLWVLYSLAEESPVLAPFIRMR
CEKALHLILQQQQQQQQQQQQQQQQAAAAGHFATHAAGAGATAGSAPWVAHLPASSYES
PRANSFTGNASPHVGSNRKGRGGKVREEGICSLHNNVRSMNHLQLNKQTGLYECVHGFHC
LEDGGSAVATPCNFNNVSTTSNANQNVNDSHASNPNSGRPHLVKMSSGQFRQTKDVKNAT
SEKTGGVKKIFPNTTRSSSNSSHGNNNNNNGKSQGAESGQDGSNGTLWHELSELRKKDEN
SGFTYEMDTLQNILQTVRELAAKEGE*
>TCRU_3517 choline dehydrogenase, putative
MYRTLTLRRANYNVAVVGGGLAGCLVAGRLAMENLSTIVLEEGDDIRKKPRWYRSIPCSL
LIHRFARRNYESCENFTTPQKTHRAEDPLAPVMIPTPRVLGGGGIMGGRSWNLGDQNDWD
GAGWSFREELLPRVQRLENLEDPPPHRGKRGKFFISRSQALSPFFKVFCEAMSKDTALTS
AFNGKEYHVRPGCGRAESFVDQRSGIAHTTLQSYLIDAIALKRPLEVVCNARVIGINAVD
NTKVTASGVTYVRPNGETEHVGADAVILCAGGIGTPRLLACSQGTLSIDPAVGTNFWDKP
QVKMQFRTRIPLSHNCFMEPIVQMCIGINLRYGNPLHALCSAYDDMICYWSSSGEQTPDV
KFIFQPFTMNNDGSTPKGVEHGVQIIAQLVRPKSRGCIRADGTIDPKYLTHPDDEKALCK
AVARIKELTKMLPFSNIFTDMIAERFESASIYGGASFPVLDQATFRVKNTDNVYVCDESV
FCSPLIGDSLPYMLALGEKFSDGFLRKPDMRSKSEAAMRGMNKARIIY*
>TCRU_3518 NIMA-related protein kinase
MENYIQIRVLGKGSFGSAWLVQRRSDKAQFVAKEVRLGGMKPAERESAKHEIEVLRTLNH
PNITRYVDHYEKNGSLYIVMEYANGGDLYTKIRSRKGVRFTEKEILHYFSQICLALLHLH
ERHILHRDLKTQNVFLTNDGVVKLGDFGISTVLRNTFELKRTVCGTPYYFSPELCLNKPY
NNKSDVWALGCILYELTTLTHAFDGNNMKALVQKILKGVYPPIHSSYPPNLSKLISAMIQ
IDPKLRPNVSQIILLPYVRDSLSSLQRVVEVAHYNQKPCDPSEERKEPARPSQLEAMRQA
EDRRKEEQLKAMKFAKERQLLRQQIEQRNRENDERLRQIRAQQRQAEIEQNQRRKELEAR
VREQRREAVKRAKAQALVNKQREEEWERNLREHAEEYKRRQREEERCVRERAEQEALHER
LFKNNNNNNGNGYVEKPAPSVAETAAELYREMRRQAALNKQRMLEDVRAMPGRADSNVVC
VAEVQMPKSPPPARQHRVNSLGKMQPEEAVEVRRQVYWQMRREAEENKRRALGLDEAPDV
ALPKRPAASPQAQQVTPQHEPKQGQEKPQEPQKQRQPEEAAKQNQSVVYAKRVVRNDAPQ

NLPPSPAAVEGIGHRAPDGEPETANDDDVGRKRDEDYSALQTAIDAALTQDEKRADAKDF
NDEAFFDTDPSKFMLDGQTLILPNVQATDPLMHRIESLRLFLENKLGESALIASYRQMNN
IAVDDDEAMQRVADMLPEEHQRFIPLIAQLIVCEDAFNRHLLQ*
>TCRU_3519 Microtubule-binding protein MIP-T3, putative
MSEAYVEKTQTELGAIISSPKLTEKLLLKPPFRFLHDIVTSFLSATGFPKGLYPDALLDS
SNVTEKTIKIEFLTQLIAAVEAGTGKKVSAQPTKIVAGQEAEKTNELLQLLASCAKLTAE
QKHAAVQKAKGGGGEQPAADKKAAEQESKEKEKEKEVEREQKAEERRKRKEEEKRREEEK
RREEERRREEEKKREEEKKREEEKKREEEKRREEEAAAAAEEGKKKRRKEDESLTVDESP
KVEQQRQEAANASGKRQKSGELHGSHNEEKEGKKKHGETLEERTQKTGDEERRKRHEERR
RREKEAAEREEIPTADESLTTVTRAPRVEQRIASTAPTPNAAASAAGKAPPRTKPTHEVV
DGSQLDAVPVSGVIREKKRTPGGKAQEAEDEGEWMRVAEQQNAKAVTSGSGDGGGVNEAE
AKGYLGQQALKAKREQEEETARRAQEANARALQGGSTGGGIIIHSSKGGKSGAAVAESEL
SKLREQLQLLTKASNPLGKLLEAIFDDIDTMARELEMWRSEARSQALAAADARRETMESL
QEVNAQLQNLEDAINDQILKTHNIRRSVINNGNAIAGMVRMIVSPEIGKR*
>TCRU_3520 hypothetical protein, conserved
MPGREAVPRTGNANERRRPAGAPYDTALTSSRQKAIVQKPNQSKQQQEPLAVAPACEMCL
ALLQSSQKVRNALEAVLTNARMVFLDDTLHHQMDDERWVRVLRAIGQDKSMYYARNVTMK
DPPH*
>TCRU_3521 peroxidase, putative
MWRSLRKSYALFSCCTSFCASASTSSAHAGETKGNRFRSPASVGSSTGGSQQREANPYKS
WEHLNHKWLLMMCVGCLAGGLAAGQVVDVDDNTLRPPFLKESVLADIAKTFEFRPDLAAT
SIRVAFILAARRAGFATDNIDESCAVVSGLEDIAGVLRHLSTVHGLSTEDAASLLAVAAV
KFLKGPCDVIESNWRWGRNDTDTTLPRKKQLAEADSGLIALPTILEGLGGLTDEESVALM
ACHGVGEFHEHVSGIDGVSHIGSQYKLSNDYYKFLLANERRFFELEVPRTEENKVIQRLP
KDFVCVYAHVGKKQKKRQCVFNRREVEALLRNKKWRSLTERYATDEAAWAAAFQSAFTKM
IECHFKRLRPYNKSSEQMHTE*
>TCRU_3522 WD domain, G-beta repeat, putative
MDESIIRVPFYASTSAWRTKAQLQGLLRNHPSVIADSGLLAAPGTIFSTARLSLHNSESA
LALGMNPLGGGGSVGLMSVEGPEPTLQGATHIRWLDLPQDVCVSSIDWCDDHLLLGSTRG
RILLVKAGPYSVTESGEALDPSRCLASGDTQPMVGDIIVAPSSHAVSTLVRSVRCNAEVN
PSSVVGVVESRAMVWDLEGDFHPVRAWTPGVSTEVKNNGQHEVLLFANWAPHCDSIVLTG
GYEGSLILTDTRADNTRGHGLTLPMRRGYMARCADFNTLLPFVVAAASSDGTISVFDCRF
PEHAVRTISSLQGDVASLRWLRLHSDLLATGGIDGTVAMWNLRFPPTYCVGRAQYKYPVV
DLAATLSSVEQRLFGVTSGGELTLTGIALPALSALASWPSSRAKPQQVGEEKPHLRERES
RGVGLLYARRLREAYEIITDCAMERFTRKDTAVAMALVALTDVMLVPKFDYKEMIEEKVG
RLFALEETSHTQALEVFDELLTRSSERLCMTLPLRKVRDLMKPNPEDVKKLEALRLNLLL
QRVLYTGNPEAVIAGVQFFAANAGNLELVDTDTACGIARMLLRENYVEGEKFIRAFLSLL
IQQDGTVLARTLTRRLLIVVQEPLMTEGLPPRQAKRREERFLRNLVAAQEAVHVQLTILG
MGIEKHEQVIATVNRYEKACLEKGESGIFGWLGMKPILLFLHSLTADSNYATFFWACVQL
IEVFAKCPGSRQVESLLFITVDRIHSAAKHIQSQLNQAAETPRFSLPALREVGNTIRSAL
DFLLVLLRVQLECENVAIESGMLEIPPVMGRIFDILSTSSSDLLEAWATLLEKLEDCKMR
DLVRKCCLGVVRNFSSQIEELMKVSSKKEDDEPLNEILDTCYHFIDTFLKGDDE*
>TCRU_3523 hypothetical protein
MSSFDRIHEKTAPSLELLRAQLQHMRSFDPHTAISVPCHFGQRGIPVSESGEVSVFLSPL
SSVRDAFLMSQEKWDANDCMLQQLDSRLRLYQENGAKKRGDLVIAMDKAHTEMEQLQNYA
AQFWSDMEENLRLLRQLLADSKNMAEDTPGRPEARITKIIRGLGDEPDCCADNRDEDECL
MSRLEEMRRTQDVIRQQLEESSASGTPSSIAAAVERIQAELQKERDGADAQLSALKESFV
IVVQKTLDELEVLRRDRLETEALCLRILS*
>TCRU_3524 hypothetical protein, conserved
MSLSSSLASSLGSIFSRGGFSGDTELEKRVALPRVAPYVNCLPIEILHRLFMEVIENDNY
NFAWIGVLSSVCWRWNCACQHAVIWEFVSKRIFVAYPLVQRLHSAPLDQSDVRLLNKMRR
LGAPEQFITQHDTMEPLIAPTNRTLRKAMEEVRHYLQSRSYYEYVQRRRVFVLQMFLSWA
LLSFSLFLGTTVCSAEGVALGALCSPSMAFSLLWMTYLSIVTIVIANVVMETHFEPKPLF
YRLRKNKPLIIRSATGIIVGIACIAFPTLLVQINFAREERFPWLLCGITPMVSLCMWQLY

VLLSYVAPEVKQHIHEQRTGFRPMAIMTFLLSNVPYVYPAFFAGTIFCIFQYVEHGGRMY
VLLAIIPVLTSLVVLTLLFMLDFFLTRRAKDFITCGCLFLVLLFPLSLMWKEFRGLSLLP
VATASFLFYVTHLKLMAMRALQELIDGALGYRNMRRIR*
>TCRU_3525 hypothetical protein, conserved
MEVVIEANAGDSAFLSASEKREMIDTLAEMIASTIEGASVTDVHEALASHNITPGGWREL
VQRKVEARRQRKGSDVVSATDSAPVTQDTPLPPTQTPTTRTWECPNCGTQQEVVDARRSL
RHSGTSLAVRIFSDTSPVGCSVCEGVISHVR*
>TCRU_3526 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MGEEEQSAPEEGANSTTLQSRETTGDGDAQPVQESMASLAGSEGLLPKQSEAPVPENNHS
ESGSGASQEDRLALLNDAKLMLHDWNVDSTARVCVSRVSMLLLLGLCGAVAAL*
>TCRU_3527 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCYCPSVCAAGSSQDPAKDIPSPLPTQSQGTGVSGATNPSTTSSSA
VAGAASPGKIEGSGTQGFSGAGQALSEHPSVVAAPAGSRGPTIPVSITKEVPGGSGSSGS
PGPVADTVQENGDSDTTDSKSGNNPSTDQTNTNADDSAQKITTTTTTQAPSAPTTEAPTT
TTTRAPSRLRGRRQPQQLCVGVCPAAACRIRAGVHRSGLKRCVRAVRASTQSRGFVCVYC
GPM*
>TCRU_3528 ras-like small GTPase, putative
MGGHSKKHGKGGGGGGGVGRNRPPEKRKKLTKDLGVPDLKKVGQNLTRTARNRNRSVFSI
PFLRGEAKLPSIVARTVAGSGEPPQTEEERMASERRSMRMLALQCAGKTYQYEAPKQWLD
EAEGQDCMYDEMDRRCADKSLRRFYKEFQKVVESSDVILQVVDARDPLGCRLTQLERNIR
SQFGDKGKKMVVVLNKVDLLPSKEVVDRWIHFFESHEGVECIPFTTTAKGTVGHSYVANM
FRRLRALALNEGTGAHKSIVVGVIGYPNVGKSSIINALKQKHVVGVGNMPGFTTGNTEVE
LRSDIRVMDCPGVVSPGEDSGDVVLRNAVKVSNLADPFTPVQRLIQRCTQVDTDDPHSQQ
LFAAGVHPLALFYNIGTFDTNDTIGFIRLVGQRRGRLRQGGEIDEEGTARMILQDWNDGR
IAYYTLPPTSDLFDRETLTTMAEEETAEGVMLTAAERLCGPQVVDSLASGMQWDGLPTFH
ISWERRDGTSRRCTRYDKMNTQNGVES*
>TCRU_3529 hypothetical protein, conserved
MHPDPLHCHFTPRTAGLPVGPHRTAAGSLACTCRAECPATEHGLGQFPVPRLAAASQSPT
RVPVATDSLSAMESLRLGPLAAHDDVTEEICAVPLSLVDRGHPAESTFSHDTAESHAT*
>TCRU_3530 hypothetical protein, conserved
MRRSAFCLQSGALAILINAVSTRRVELGPEDVYKICALLKTKEDALLLQKNRAFLSGLHA
EYQKMDPDAVTPFQRTFIDGVFAALPSALLTFSDPSYSSPSCIDDERGARKSDVTAVSGK
QNQPWSTMTTTKETCANGFATDINNTSNDENNSTSSGDNTAISRGNAVVRSDEEPTVEER
IAAIWEVVQEYQSTNFLGTDGSQKIQKHCKALELQLRQMKPFEVASLVRALATVNYQDYT
FTNLIARRGCEVASKLSLSELCRTYFNLSKLQSHDSMVAFVNQIEAQMDKLRHEQIQFVA
MALERQPQIASAPARMVPKLLARAVSHFSEVDSVLYHRALLIVAARYNLSRHPAVLKTIQ
DSSKHLENIAERDLLAILHSLVDLGIPAGTPGLAELLGKAEAIVTIIDIRHVDVLMDILS
VLPIDTSGIMTKLMDRLIVDGGKLSIPQITFIMDLLSSYPPAKDNACVAALAFSASLRAE
SFDREALEQVVLSLARLNQFSDDFYTLVSVLQKNKGGFRSFDNFASLMKWCSREVALDVR
GQEMITKGILGLAPSMNDEQLAEARKLLTQLGVNDKNVHQMIFRRAKQLQRESGSRWTRR
GYSSATDDFT*
>TCRU_3531 BNR repeat-like domain/Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MSRREFTSAVLLLFVVMMCCGISGATPANEEEVKNDLINIQNLERVDLFVPLKTPVLPKE
GNGSVTTRDLFVSPSLVSAGGVIAAFAEGHMNAEYQGGQLTKPSSDVVAGYIDSVWDWPA
LVEKVNEGTWSARTVLAKAEVNDRVGVVFHPTTIMKDNKIFLLVGSSDVFYENEEWGTVD
LELTLVVGDVTPYTRGEPGGRIKWGDPTPLFDSKYSLKHKSKLNTFFPSGGSGVLMEDGT
LVFSLVAMKENPNESFYTIVYSKNGGENWLLSEGMSPPKCYNPRVTEWEGTLLMIVDCED
GQRVYESRDMGTAWTEGIGKLLGVWAKPRSVFWDVSLHVDALITANIEGRKVMLYTQRGH
ASGKKRATAFYLWVTDNNRSFSVGPVAMGNAVRWELASTLLYSDGKLHLLQRRESDKGRV
ISLSRLTEELKEIGSVLSTWAQKDVFFSSLSIPTAGLVAVLSDAAGDGRWIDEYLCLNAT
VRNAKKVKDGFQLTEPDSRVMWPVNTRDDNVRHISLSHNFTLVASVTIEETPSGNTPLLT

AVLLDAGPPYIMRLSYTADNKWVTIFKYEKITKSDTWESGKEYQVALMLQGNKASVYIDG
KLLGEEEALSTDERPIDVADFCFGACDFGDDDEEEASTKKIGKKPRVTVKNVFLYNRPLN
STEMTAIKDRIPVLARGSEWQADDVPQTIASAGSAAPGPLELPAAPGRTTVGRTANTQHA
PAGRFTSAGNERTARETGDGGANGDAGSAYGRELLPLLLLLGLWGFETA*
>TCRU_3532 hypothetical protein, conserved
MGLSCSHNKKWETAFEGKTTTRSSNREPRKEYQVGLMLQCNKTSVHIDGRSLGEEEVLLA
GERPPEVLMVLLWRVRWARISFDGDGRLSVQPPTELHCDACTQGQRPRSDKGSGSDTARE
DSSG*
>TCRU_3533 BNR repeat-like domain containing protein, putative
MIVDCESGQRVHGSRDMGTAWTEAIGALSAVWVNARSGVSQKEACVWMPSSPRPLRKGRR
VMLCTQRGHASGKERATALHLWVTDSNRTFSFGPVAVDNAADWMLASTLLHSDGNLHLLR
RRGNGECRVISLSRPTEELSAINSVLSTLTQKDIFFSRLSTPTACLVAVFFDAASDDTWN
DEYRCLHATVKECSEGQRWVTIDGTCVQGNMACEHSG*
>TCRU_3534 hypothetical protein, conserved
MAMVMTGRVLLVCALCVLWCGAATVVSSAPDATRAQSVWPEYLFLNWHELFRNECKVEKP
YENNEDLKELAVNCCVRDAMNELCSAFYGNTVMENKDANVEGICKEYAGKPDDVADCPKP
KNNLSPAAVTSVKVSVPEAPREKEEELRKTPEEAPTPLAGAPLTSSPANPTNVSPSPPLK
GQPANEEEVPVPNSEEGSVNTGPTNDSEEGDTDTVTDTEQDEPSNSQAEPTTPTHTVASD
NGDNETDKGTGEDTTNNAPEPDVAGTEENQEENKNNKPKERTLQVAGIKTTTATSGDSDG
VKATSPLLLLLVVACAAAAAVVAA*
>TCRU_3535 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGAGGVDASNLESNAQGGCMVSGGLGAKTSYSVRGCNKTVLT
RPLRSAFFINAIQAEAKDVKDISEEGDNLKLGSIPQPPAPPPAPETPPPPDASDSDGIGR
SELGADGQTGGGGGGSSGISNGDEDSTLKVPVPDDKSSSPIPNAGDGLKNTGDSSVTQKN
NPSGTDEPSKKPLNVPAQPTVQTPEALDPDQNENTPNTQGEISVEARGKGASGGGAGESD
VNSKGSSSVSTAKSNPTGKTTPSVPSAGETPTITATPNDSENPTGKNDSTAASGTELDSE
ATKKSSKDDAAEQHSQERDKADLVKSANTGHPAYTAASSISTYGKGDAQGKANENGDDPE
RHDSKGTHDALEADNTNVAPTASEAAPEAVNSTEKNDTAPTGDSDGSTAVSHTTSPLLLL
LLVACAAAAAVVAA*
>TCRU_3536 cAMP-specific phosphodiesterase, putative
MSQEKTGLQRPVLAQLSPIAIRGHSDEGVKKLRRRNDDGCFGEALFKGNAPARSLLFGDD
ACHRRVENLYLLDNNPTNWSGIKTNLKREIPLLQDPTETFARMNKVMHQTLKYVKEVESI
NFSSRGVIDFNGEVMEDHQRIFLSVCTSVFANFSFSCQMDVEKLLSFLMALFENYSKENA
YHNALHAADSVQMLFLILREKPATLIFTENEVILAFLATLSLGFVHPGVSNAFLARIDHP
LVLVYGDMTTQQSAGLTALLYLLNREENRFIDLFANSGTQPFSQFLREILVETVLGTAPR
LRSSLLRDLEKVAVADAVELNDIPILLAAVVILADNALALRPHAQFVNLAGLMVTEWLRE
AYEEEQRGMDPLVPNLRKQIYENGLGMAVDYCKVWLRPLITNIRALVPQDLYDNMEGNTE
APSMSEIQDFLVHLDSSNERWNDGSVPVIDIIRRITMHATSLDRKASKRAILNAASNRAV
SGFLSRSSSMCLSPNGARMSAEASEKKINQQPSRCEHYFSFLRLYDTYEKEGRPAAEFAA
QLVFLALQLNPEYIGRYTHKGIDVCSKEECEEIAELIMKKEEAPTTAEVIASPLRDGEQT
DGFILRLMEMYAERDRERERNDTLNSAANPTSNLRRTLKCYNPVYGGMYSGKKS*
>TCRU_3537 serine threonine-protein phosphatase PP1, putative
MSLAHNLLEKMLTLTKSATQQQILIREEDIRSVLDSVRDVFMSQPMLLEIRPPVRICGDT
HGQYYDLMRIFEKCGFPPYSNYLFLGDYVDRGKHSVETITLLYCYKIVYPENFFLLRGNH
ECASINKMYGFFDDVKRRYNIKLFKAFTDVFNTMPVCCVVSEKIICMHGGLSPDMTSLAT
VNEIERPCDVPDKGILCDLLWADPEDEVRGFLESDRGVSYLFGEDIVSDFLDMVDMDLVV
RAHQVMEHGYGFFANRQLVTIFSAPNYCGEFDNDAAVMNVDEKLQCSFLIIPAR*
>TCRU_3538 hypothetical protein
MSVLQRENLETSIAVEHDSTLLSSTDSEDSCGEGCGDAGIIPLNVMYAMTGAIEKQERDM
SREQRAQKITQEREMLSRRQLLRERVELLRHRLASTREPFEEGQEEERRANAVGISMELS
ISGSEIHAAHAIRQTAYLPWSTRLWHSLYNKVRYFFVAASFITGGNVYASEALNEYYQQE
TYD*
>TCRU_3539 3-beta hydroxysteroid dehydrogenase/isomerase family,
putative

MARYDLGEWVQSRVLRSVASPFHGVMREESTRHECNLERGRAAASPDMDAAGCATMQESA
RHYIFFPRQNTMDVSRELDTPAAFSTVTLIGGTGFFARFVADQCLRRGISVTVLARDLEK
AKNTLLPRLRCNVTKGTEIVEEHNMDLMEGDCFLRYTSSMKRGNFAVPLQLEILKGDVTS
PQAVQHAVRQASIVVYMASAKCSSWWRPWAKSNVPGCVKVDVEGLRHTIDACSLVDAHLV
AFVPLFNRSSWASALQWYRTLFLYRVGYLKATRRQEHLLIDDDGSPSALCLQHGGPMRFT
LFRVTDIVHPSFNERVAIAKNNNIADPVHLIPLRRGDVDANLLANILLRAVALCRSSIGS
RIDVTGCMRNGVGLAHVDSLLHGLRNE*
>TCRU_3540 hypothetical protein, conserved
MWRWRLCDGLEVVGLPVTFGLSRRCCHSNCPQPPSWVLQLRSDAKESKTASSYDVKIYDE
LAWRKMRFIFDKELWDPARMSSILRRRLCLGNEEAEYTIIGEAFAFPDREDAPVVNEPQH
ACRLLWDHNSPSEKLLVQLSEHFPPLLWHAVRPSLDSLKRIFSEFLEVDAQHMKKHLPYY
ESVQNSIETATKETLSGTLSPVSIKDRFVEDMRRRDPKTLELDYPHEHNIFLGTSPHFRL
LEDKMMKSNPFVFGWPLLLSDGNEHLEGTPLRMAAFRTIYSKSLLMFHTRLDLQVDHRLA
RLEEGDEEEILLEVPVFCTVNYPQNTRLCGGRPLVQRFNDVMGTSYPFDTPVDVLAALAK
ETTTKGVRELLEELKFLTVASTRAPEVERVIRISEDQLSSNRILGQLAYTIIYLALLSYE
RFVEDVFEVYKGHKSDLVRVACAKGAGIVERPDLIEQLVAAEPEGSRCRKMLQASMHGPP
TTARA*
>TCRU_family, putative CBF/Mak.1
MNAKITAALKRCGQCATYQELCGRFDATVRPLLESCLSAALVRPVRDHVSPDECSPRVAE
LREALRAANAGDDVWFFLFRATATFVERSAKKRGRNGDTAISAIVVNVFVLFYGRVIPDL
SKLRLQWGFLKKERSKFEANDSYVRSNAAERRKALMTSVLSVFSERAHRHYFTALWLPCL
HHAAAAALHLHILHRIGDVILPHLTNPLVVADHLSGCFSSGGLVAVLALHGIFLLMLDHG
LEYPQYYQQLYTLVTPDAFASRHRYDLFRLLDLSTSSLRVPSYIAAAFVKKVARVALLSP
SPVLYFALPFIRKVLQRHPNCLALIHRSTKEAVEAADGAAETGEVEQPNKSGKIAKEEAQ
RLTASLFDGNDPFLEEASLEACHALHSTLWELTALERHFIPTVPLMVSAFGSTAEDQAPL
RYEKTYARLFTAEVTRPISKSQLPTVAYREPQEEDGTSAVLLV*
>TCRU_3542 protein phosphatase 2C, putative
MFACSRRLFSAASVQPLLWFGRRGAFAVPHPSKAKNGGEDAFLVHTSGIGVADGVGGYAR
IGVDPAVFTRNIMRFTRQALEKDQNRGTISALEALNYGFAETQKRGKPGGCPVSLVTLVD
GRFASVLNLGDCGTICLRSSKLFFATEAQQHRFNCPYQLPEDPPSAGDRTTLEVSEGDVF
LCASDGLLDNVEMSDILRRLENVEREGCQRVAETLVEEACKNGADEKFDSPFAKNARAMG
YRYTGGKQDDVTVVVAQLTRLDIEPNVCPGDIAEFLKLPTE*
>TCRU_3543 Iron/manganese superoxide dismutases, C-terminal domain
containing protein, putative
MLGITSALLCVTAGRAALVASELQKLVPVLLPLLDPPIAKGVNVSAAQLIVASGHTSRRN
DVHLPDCPVMAHALPLTALAEHSAFLRHPCRACLKRRVHFLSSEHFCMHLEEKCSQSGGG
MPVEWESIAAGQFGLFTHFTDEFVMYATSRREPGWTWLVYDKERPEGHRLVVVNFPANRV
PLVLGLWPLAVINMTEGRLLSAIGARTKTSAAESSPAPWSRAARNPLVAEASTATVAAMA
AAVTDTVDDLHGSLSSIRAQVAQEAVLKMNWGFVLQQWKQAESYYKSAERERKVQAQRTK
MEREAALAEMSKLRGSGATILTSDTVEITVAGSDAAPEKASRDLKASTQTTKEPRKEEEE
TANVGTATQDPHCTQLEDGTWQYAYKNGDLTLLRPDGTRVFKKSDLTTTVFADGSTLYEY
PNKTSILDRVDGVRVTTFADGTTKEGRYK*
>TCRU_3544 hypothetical protein, conserved
MRRTFSYWASRAWRVHSELIQGWIAAASSEPRKLQQARSYLYDLKLEDAIEEVEDATDLV
YFMHRVSYPAGSHLETKVGQFLSRLSEQLTRENLLEIVKRLNEQPNSGPLWSRVLFEQPW
FSGRVEELLEGLTLEEHVTFCAVVWRSLLPMLQSHSSQHATRGAAVAVSQQLALLTAQRI
ERSNDCQAVCLCAQLGVPLQGESLAVLRELILSLTRGGKLSPEQMITVAEAILAHHSTDA
EWLDALQVAICGKPPGSVSASQVIAMLRAVTSARSGHLSKMFEDLLLRVLPEMSPEDMLD
CCRSLTAMPNAASCLRKELQRLLCSKTSLGKGTSDRYDNALLLQLRGMSLIAPSEATKLL
LRFVDQLKGTEKISSPSMTQILLRCMRDLQLFPPELVSHCKNSFLQNTPSNFTQEDIAYL
LYAAAHAGEAVDGIFFNELLNRFAATRKFDRRKHKAYHGKLLSIPTVTMVLESFNVAKGG
RLSVESKVYAVLRDAIEQQQPPEGIKMEDAMYILKLLVHLGVDDRGLTTLLLTRLSKAIG
SMTPIHVRTLCEVLVALKSRDVLMFRALLSHLSHISPDHESITSTALTARKLKFVPYFEQ
SVLVEHVTSIEGWSLSDIVLVACTCSEKQRKAFLALPGAEVLSQARPEELSTLDLFLLLS

ISNEDREKTAAMAATLRSRPPIAAGDLEVEDVWRAFVNVADDKEALAAVCRSGAATLQTA
DENTLMRFLEAASNVPELPNVFFRVVGRTVLRLANNMTVENALRWLELYVGHQIRDDSVG
KALLSKVRTRSHNAASLVDKTLRKASTMYGKTYNTQGKLRKNKEKVEWRYFHQD*
>TCRU_3545 Predicted membrane protein, putative
MNVGTPTAGGPSLSFQLLLYGSAGWSGIWFVVTLGLLIYKGSMLHFPPAALPMEIVSALL
LLVIDFAALSLGTRGNLAEEVGTSCLAIGLLLVAAVGAIYYMWLQTYVMMLDLAFSAILL
GLNVLAVLAGVYAVQGVIRAKHSPRQRFAPQPHGLPSFMRDKVKRHKED*
>TCRU_3546 Uncharacterized conserved protein (DUF2039), putative
MPSKRLVRHGARGSQQVHMNKVKFDPYRFKVNDQRLPPVVLAFMTSLCCRRCCDILQWKV
DYGKYIPLERQRKCNCCQERTVTIAYHHICQRCATERARCAKCQKPPTLGNSTTGTENRG
DDTNAEGNANADIREEEEEEEDEAAEAMSAGMPKGELSGKYVFVDQEDSDEEFWPLRGLD
IRQLKQRKKELARLQEKDRVCRLRERERRTVLRGALRGPGAEEGADDSDEEI*
>TCRU_3547 hypothetical protein, conserved
MFVGRWVYNKGQTVGCLSHLALRQKHDDNEADAVANTLYGCVLFLKDDVVNCFAGGGGEI
VSVATEGDLMNTVLQWARGGRGLCGEVPEVTAPGASLPFYSTSSGPWFVIERCVGDPCSF
GVIAGFVCRYVHNGDDVDGVGGCNLDQESCGNGFLWEWGELINCTTISQLSLYLDSLPLK
SVK*
>TCRU_3548 flagellar attachment zone protein
MVLLNTLKRDTPQLQNGQTVAYEYLIDDEHWQWTLGTVVSLKDYTAVVQQWSINQGDDAA
LRNIVSNEIEKEMKRMRVFQERLSTSRDKLAAIRSENEDSVSAARSVFEVAKEQVKAVDE
VHMREVTSQARPSPVAVEVLKAVLAVAKNDPAINDCFSWYDIQMEYRKPGAVMDFIYVDV
PGRYYPTPDTILSSLHEPRFSLAAAARDSEAIRSLHQWVVSALAYQEAHSRLTSDMRIQA
QNDAIGAAISGMKACRMKVMKLKEELSRRNSSAARGQVTSFIKTSVHSTIPLSAVISVVP
IDPSVTDCALTDDEVDVLYEDASWLRFQLKDQLSRTMNEYIGAMAELHCLSMYTTELEEK
RLYLQEHYTRNVIRSHDRTILNFHDRDTSGKNKELQDIIDDLKKHDERWLFADGLKVTTK
HAKKYSGKDWGKLLKNKPEEVLARFKFEQALACHVPDDCIQNVEFHLEPDALVTSFNVRH
STELTTGEIDRRLEQFPPREMNRLYHDPNGAKVSLDRAIVEVCRAIDIPETKFQGLYFDE
FVEELGGKGHLVDKDAYESEIGDLLMLLDKIHNENRSLQCTLEKSAEEFRRQTASTLREQ
EALRQRNNELHAEIGRMRDLVEKLKDLADKQASELELFKLQKNQAIQMRTQRNLSTFKGD
NTAEPLYCVTLDELHEQMKQCELLENEAAQLQKQLEDLNQTHDNLLVHLNTVTQEKKGME
TENEQLKEELQIAQKAASDAAQERSELLHELARKRAECEELAKNLSQISDLLDALKTSEK
EALEGIEARDEEIHDLQKQLEDALNNQNVGARALELKERQNKELMEINQRKQKELNAHRQ
KRRTAHEARSLEPTLQLYTVKDAGFEDALDPEELLREPLLSITMDEYTNQIQRSNQLQQE
NDTLRQQLQQLSDDMETINSQLREAAADNQNLSDQLRAKYEEFVKANNTIQSLYRQNETQ
ENELQQKNIENAKQAEELEKLTIENEKLADELEKLATDNEKLADELEQKAAENERLADEL
EQKAAENERLAEELEQKAAENEKLADELEQKAAENERLAEELEQKAAENERLAEELEQKA
AENERLAEELEQKAAENERLAEELEQKAAENERLAEELEQKAAENERLAEELEQKAAENE
RLLDDKKSLEEELERNVLERGRIESECRSRELVVGGLESKSRELEEALVALSAEKYNAVE
TIEKELTDILVQLKVVEGVNGALRRLLSDKEKELVFLRAHCELWTDPTEVKEKVVTRHVK
VFDGDEWGKLLSERPEALMAAFVIDAGNACHVPGDQVSAVSFFTERQ*
>TCRU_3549 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily, putative
MVAFAEGLFEYNVHGHEFFGIKPYEIVAGYIKAADSWPSIVAEVNAGSWRAYTVFGSGNG
NDHVCFLYRPTAVARDNKVFLLVGSYTVGYDSDDYGGRWVKDGWDIKLVEGVATQSTDGV
QSKLVSWGEPKSLLKHIPNHTQGQLIYVVTAGGSGIVMQNDTLVFPLMVNGKNYPFSSIT
YSTDNGNNWVFPESISPVGCLDPRITEWETGSLLMIVDCENGQSVYESRDMGKTWTEAIG
TLSGVWVISQPGVRLYEIFRVGALTTATIEGRKVMLYIQRGYTSGNKRATALCLWVTDNN
RTFHVGPVAMDNAGKGELASTLLHSDGRLHLLQQRDNEKGSAISLARMTEELKEIESVLS
TWAQLDASFSSLSIPTVGLVGLLSNAASGDTWIDDYRSVNATVMNAVKVHDGFKFTGPGS
RATWPVNSREDNNQYGFVNYDFTVVATVTIHQVPKKSTFLLGAGLENSNSKKFIGLSYSM
NKTWETVFDGKTKAQISTWEPGKEHQVALMLQDGHKGSVYVDGVIVGSLETIPTLGALGH
KITYFYIGGDEGDSGSSATVTSFFLYNRPLSVGEPKLVKKSEGSMLGGVLLLLLLLGCAA
LWPSTGRNAAGPLPPAGAKCTSPRTFLNN*
>TCRU_3550 Paraquat-inducible protein A, putative

MYNLTCGTDGFYCSLPCTNGIELLNLRLYGLNEWDRLVVNYIGPFVTQRINELFSSMIIP
FCNTTDNRFQIPIKESPDIISVPPTEVIVPSVLVGFALVFGSTFLSIRKHRKSPVYLLDG
SIIPLWRVLLEDTLLILMIVVNALAFIWSNCTTAARIVAGDEVTLLSFSLMETSTNLYKA
GLRPFAVLVFVFSGLYPYLKLFTIMTCTLVLQKPESMILKVIDYFGKLSFLDSYAMVVMS
SGLQMEGIANVKIIAGFYVFLAATVLCVFTGNYATTFWRCNTSLRMRSNSIPRPMKEVPD
EALLLAPLTVNERHIVEMPNTPRSNFRSLFWRVLNALFVAACILPPWITPCLSYRVRGAA
TIIQPNDRNMTLYELSSASTSLLLTCVFTICIAPLLYAAFYPRLALLASWGAADAFLLAC
VAGIFQLERFVEFVIGTNMRSLYTAEARLLWPMIPLLIASVWQWVLAAEHVFGLSEFIRN
YRAKPLEALAS*
>TCRU_3551 Protein of unknown function (DUF933), putative
MAHGWTTKVGATAKEASGEIHSDMEKYFRRARVMPYSEFLSKPNLEAAEMQMEFVDAKYI
MKDGDVMIVEHNTPI*
>TCRU_3552 hypothetical protein, conserved
MRSAEGACPRSRHRVRRRAIATVRVALLVALALVAATAWVPAAHAVVLRLRGGTVDRAIT
VGRAVDTVLMDGVSITNGVAVVFDVPAMLPGALRIELRNCVCDGGAQIYVRGYSGEPASD
RSLEVSVSGLSGSYCSLVFVHNLPAHTNVTVRDSTIVTAGPMRYSQLSGLTDAVASPLVL
HATSLLQTQLRVSNTVLRSSHAGGSAVYVGGGVDLLSSAVVLDGVSLEASGGPTASAMRV
APSSILSLRSHSVFSVTNVSIARCAAAGATLGERIAVLDSVQRNRAGGRVLRSSGDYRSA
GLSSVSVVPCDGCAAALACFDALTACAAAVPAAWARRACRSTCRLRGPVAVVVRGAA*
>TCRU_3553 amino acid transporter, putative
MSTNLRTYASDDPLNDGVELVEDLQGQAGLPTGDRMDVAKIRIEKLNQERQERVARRRDP
QSCLKRGLHRIIPYGGIISSGCNLASSSLGAGILALPYAFNTSGLAMALVYLVVVGLLTI
YSFTLLGIAGKRTGLRNYEQVTRALLGKGADYFLAFNMWLFSFGAEVSYMIYMGDLIGAF
IDSSQSAPDYVKSSSGRRLITSMVWLVAMLPLCLPKEINSLRHISVLALAFVFFFVICVI
IHSVRNTITHGMRDDLVYFRTGNSAIQGLSVFTFAFICQLNAYEVYEEMYKPSVARFTKS
AALGVFASFTMLFCSGFFGYLDFGPALTGSVLKRYNPIEDKMMGVAYAGMVLKLCVGYGL
HMIPVREAVYHVLHIDVKTIGWWKNALVCGLMATLSLIGGLFIPSITVVFGLVGGFSGGF
IGFIFPALLYMYSGNWTLQSVGYFHYIGTHFLLFVGVIGVVFGTAFAAYGEAMH*
>TCRU_3554 hypothetical protein, conserved
MRRSLPWSVGDQQHVASVVRRWRKSRVHLECPRLCFLRALPTGMLGSSVATSARGACQED
DETIAASACEASLTIITPGRARRTMCRHAADKRAHSAADWAGGHQSAARWSTRCCGAHVG
KRFRRRQRRAGLLGKERDGTTDTGSSL*
>TCRU_3555 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSVCVTTSEGKAGESVSRVDEKGELDGATDQQSATSSPQTRE
EEEEKEEQKSSTPTHTSQETAKATGTPESESNSNNTKDQDHGQSTKEETENTNTNTSNEQ
HKESNAPTTTTTTTTKAPTTTTAPDTPSNTTTEAPSTTTTRTPSRLREIDGSLSSSAWVC
APLLLAVSALACTTLG*
>TCRU_3556 Protein of unknown function DUF84, putative
MIIWAVGTTNKAKLDSVDIAVRMCFPSYQHDVRPVAVLSIVRAQPISAEESQQGAQHRAH
EALRLVPEAHYGVGLEGGLEKISGRWFECGWMYVIERSTGRCGIGSSARFEMSQKLMSKI
LDEGKELAEVMDEMTGETDVRSGQGAMGVLTAGYLNRAESYSHGLIFALAPFLSDHKYWD
*
>TCRU_3557 diphthine synthase, putative
MFTLVGLGLGDASDITLKGLKAVHEADVVYLEAYTSFLINSSAEELANVYERPVLVADRE
MVESGEVLQEASDKKVVLLVVGDVFGATTHFDLVVRCHEQGIPCRSIHNASIINAVGCCG
LQLYRFGQVISLCFWTETWHPDSWYDRLMSNREMGLHTLVLLDIRVKEISDENLARGRNV
YEPPRYMRINEAIEQILEVEQKKKGGAVAEDGSTMSIALARVGSNTQQVVAGAMRELRGL
DFGDPLHSLIIAGDIHTCETEHVNLFRLK*
>TCRU_3558 hypothetical protein, conserved
MRGATRPLRYLCPTGVLMNFFPLGMYSGPINAHVFLPNNNLDGRATNHMKKIDGLTKDPQ
LVFSRNDLKLQCEYCRFQWVHDTLCVRCPAQPNHNKREMWLQPTWMWGKQQPYQYYKYMP
AVRNPRTGMPLAREDASGMNNERRGQGLTTKTLNIEKERRGISRAVSNIGKYNTRWQTRF
PFPA*
>TCRU_3559 hypothetical protein, conserved

MSADPDAPADPNRRSGGHIVRNMIYRHDSARNLEIVTGWQDQGTREYNQKIVPPAKMELH
SKHPCHDLNTQLLRCSLDCPAEMKLAGRIATCNTERKALMVCLTKQKHWKPEPSSAWYRF
W*
>TCRU_3560 cytochrome oxidase subunit VIII
MLRRTGPAVSFTTSHRALMLRTSRPLLGGDMNSKERFKAAWDEMPLHLLGASRKQVFEWH
WKCMYQLGIRDTTRMTKLRVLTNWVGLFSFMYLTYISVFYSSFYHIYYEDWPEEFKRENA
RAYAQSKGSDVWAADGKFIRPYFHISPPMLTMTAEDI*
>TCRU_3561 hypothetical protein, conserved
MFAVNCEAALLWHPVVHHSLLLLRTLRQRHTLVLEPSCTTASRPDEFWRLSQAGNYVSIN
ATINSDSVFLEGGEEEGRGLALLHISEGGLHRVQNPQHILYFISSSTLLEQKQQLQTYLD
TAFVTDHVLRAVDDVLLALSTDEMEVTRQTHSNLMDLVARLETFLESENDDVMQETEKWS
TWPLFTTLKFLVEEAGLLLGPFPRVAKAYRQLQDSKPVVAHTRLVNRTVNLALSGEGLFV
QPPAWPYRGFLREVQRKLADYTADPAERMMEGVLGEKGPLKARVSGARFGLQPVSARMPW
NMQREKMGRS*
>TCRU_/ S25 / CI-B8 domain containing protein, putative
Mitochondrial ribosomal protein L.1
MSRNGELCLKKVIISYCPNRGSPNTRQFLATHLPRFHAKYPSVTIDIRPRLWAETSITGL
YRDGSERSYKTKYMSSMGIWLRFHRLVNTANDYDLPFSASHLHFQRRSVQGTWNPWLWHY
ETDRRRTETPQWRRKLSEEEWDYYLGQYSAQMKQEEEAIQQRVAEHTEIPLQNTREVQER
WKQYVLPRLQTDMEFNLSHYKRQHARGQRHEPVTMGEYRLFSVPDHREIGQDAVDMMRRR
EAKHQEEWWQHRKSQLKPPK*
>TCRU_3563 protein kinase, putative
MQKSLSSAVSLVDIDVVLTPQTVLSEVKTGVVPLIPITDAIRCLGQNHGSVRDCGSAASI
ATSPVCSLNNTLQSLSAGTLRGTLGTSLNVPDRMIIPLERLRLFGGHVLGKGAFGEVVRG
ELNMLCPTVGYGSAMSMTSCVTLSPQSFTNSTPGQPISFGEICSEEDHLPTGRSSAGESV
VGLLRSNGQYNHYCSRSMEENNLTLPLYCGSFSTDKSARKLLLLTPRVHSRTISRELCGG
PSTMHDDVLTDTSNSFQQHTLRHAANRGDTVVSFGPRNEMASYASEEGVIVKSVAVKRVD
KFRLWRRQKFVKSFQSELNITATLRHPSIVKVYGVAETDAELFLIMDVVEGGTLEDYVKR
KGLEDMNIMAPRFLTDVVLGLEYLKTVGVAHRDIKPCNILLTEDHHVVLADFGSACYLHD
NAANTFAGSAAYMSPEMVGTGKASATSDLWAMGCILFELFVGRPPFDSENCMLVMRKIKE
YQDGHLEYPPYFPEAAKDLVQRLLRRDPMDRLGSDATGGFDVLKTHPFFGGIDWKQVLRM
SNLIFRCADFSADLQQSILMEDENVVHCSMVLKESRVFFKRTLRRRLLVLTDLPRLFYVD
MSTRTVKGTIPIAPDLYVEYDTVEAFRAVTKKRTYVFCDPNKHAYIWAMRVNDVVKRLST
AGNCVDPATRQKKDRGKIFHRRYESR*
>TCRU_3564 hypothetical protein, conserved
MGAAPSAEILREAPFRPARNDSARVISLIPMTREFFPSPDSLIFGQLYDSRCDPYVRYYM
RRDEDTDIRLDVIPRIEFTRDEYYEKCMELSKSCQPCETNKDLRQKYIAEPSQQHLLRPI
PCAVAFLYNDRRDAPEGSVPLGGAYVTVIGGIGCELKESDASSEAMRLDLMIFLRRSAGD
HNMVRAMLLASWLFYTQCIDICKLPCVPMLPVTFRALKTNIPFLCFLREMRSRVGILHEN
TVEHCMWIDGAFICGFITAEHAVELCEAFAEQYRTQVEFKSSSKLGIKPLPVTSRTTNSP
TSSEVASSVGTEETSSACRGLTLSRLHKQFFNLAGFIEKDEFIIPASTHSSNEVYVVCVD
ALVRVEQCEDAATSDAGGKDGSDASLLKVRRGDIIRFVPEAIESQHTPGLAAGGTAKGAT
EEAGVTTEVVEDADIFHSKRGRWQVDPVIHLENVLLSFVHEECKSAREAQPDDPHWLRDK
ETGEPVSDGGFRIWCFDRKGVRYFYGTVPRFANAFRNRSEPARRGASHAEAGAGDQAAGE
GMAPQRKGTSRKKLSGKGGLQAHLARDKGMRLGYYKDAGKAQFEVARRMPLMIMNDMNQG
AVCPFYPSMAPFAPVQAQYPESPPLMMMSPALTYGSLPAASSGEPSESCDGGIQSNVGVF
NAMDASSPVPCVPMVQSMGVSSAPPVQYVPYAQPMPSAMQPMQNAYYCVYPTMGHTGMQS
VQQFSYVPAQVPQRPDGNPLFIVRQ*
>TCRU_3565 hypothetical protein, conserved
MPPFLFLFLLEAPIFYGDDCFCSPLRWHEGDWAPACWVHSEGSGWCAPCLTVGVGRHPPQ
PAVRRHANLSWQREVKDFALELDALRPFSLRLCACGAHGSFLQCDVDGVAAACAFVHVLC
GGLLFLSHGTALVCGRLGGAERCEELSVGGCRLRPAHWGLPHTRGFSRQPIAAPWPWIER
CEGLLHAEGGQRDAVRDGEAGPHVAAAHGARATVRVERCAHGWGEVAARHCGAVCVVCGR
GMAAIVRDVEDTELLDWEEVAYVAAQRERMTAACAGGPDDSEACAGGTRVEVSVACL*

>TCRU_3566 retrotransposon hot spot protein, RHS3, putative
MTTSAPRYLEGCYESVHNARWHHLVEVPSGEGTGMRVEVGKPEQSWTYKAVGNTLEKDDA
VQQSGAAPPRLMVLTSDKGWPYTMNGTHRCGNDLCVNCEVDRVWQIVKGDRDKWLSNSDL
TLNPSPLLRLLIGTPGIGNSMAASSYLLYQLLQYDVEKLPVAAYSVGGSTTYVSDETIKT
VSE*
>TCRU_3567 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MSVREGTSLQEEVPPPLGTEDIPKADVERPIYEEEATSPEWATERQTQETNAPLVENGDG
EDVGTAPGNASILPGETKISSESNATPLSDHGILPEHGQLGELAAMYLIGDSTVHGCVSR
VLLLMLLGLWGTAALC*
>TCRU_3568 Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MVSVILTTQLERVKEVLKTWNEVDKRVSKLCPSENAKEDPSPATACGAAIPTDGLVGFLS
GKFSDGTWRDEYLGVNATVKKNDGVEKKENGVTFKGRGAWAEWPVGAQGQNQLYHFANYN
FTLVATVSIHGLPKDGDNSIPLMGAKVNDGDKNTVLLGLSYNREKRWELLHSGEKTSEHS
RSWEQGATYQVATVLQNGIQGSVYVDGQRVCESLQSNLENTKSKMISHFYIGEDGGNAGN
TGGDEGASVTVTNVLLYNRPLSFEEIAGLAKNKINIPTPVAARNSSPAVSRPKRSSESLA
GGASGVGTARHFGANGDGSTVCGSGLLLLLLFLLGLWGFTAL*
>TCRU_3569 Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MDDNEKSVLVGLSYNNKEKKWILLCDGGENKELSSHLGTENSEHVVILLRNGNQSSAYVD
GKLVGSAEFECENTNDEEISHFYIGGDGDNAEDQEGVSVTVTNVLLYNRPWTEEEIGALN
PNKAPITSPVTENAPETVLQPPAKPQPSEHEPLTTNIGAGGVPSAASTATTPSSDVDPTV
VTGGGDTMRGNESPQTPEVSASSGEDRETAGITDAQGEEEEIHPQAGELNATALNSSIGN
LSRGNNSDAGTMRGRGLLPLLLPLGLWGFAAL*
>TCRU_3570 hypothetical protein, conserved
MTYSVRKLRLLVDDPGGTLRDNLAIAQSFFAAEDDRELEEFRSLMDLEVHYANFWGVARG
PHAALAVFDNERSALRLTWPSRVMALTANTFERRGYVHFLSGGVASIPGIGNWLTRFTQS
RVRESLVVKDGKVKFRDLSFEWGLAVH*
>TCRU_3571 hypothetical protein, conserved
MRHTRKHFKKRGRDDLPMVDMEREVRDVASSNDVRTLVQLFPEEIEFLLMRLPPVTKVED
LDTLSERLSGLGGKEELGFSPLFCPLLIDAACQRGIFPLALSAGGDRYIFAPKLHYHRCL
TQLEPPVEGFPMANDAKEGKFKVGLLQVSKKYLSGRNEMTRARSFDVFINRKEDIAPALS
LIVSQHGENWMCRALRACFVHMFLNQERYRTKIVVVTVRRHCYGADSREKAKTADERVRD
FAEGDHVEEGDLVAAEIGFIAGDIYTSATGAYSLSGSGTLQLAVTGEAMRSVGCKVWDLG
MAMAYKSQVLGCVTFPREKWLRLVREHVADTSLAEKIEGRLREKFSEGVAVRTLLSLADK
*
>TCRU_3572 ribosomal protein L36, putative
MPARKKEVPKAEAPAPRTGIIAGFNKGHKTTRRARAPSSNDRYALPHKKLRAVKAIITDL
VGLSPMERRVQELLRVGKDKRALKFCKKRLGNFKAAKKRRAKMEEALRHQTKKK*
>TCRU_3573 Domain of unknown function (DUF543), putative
MTQRVSTVASEKVLLPRESLTEAEKWRYAIDNTLKLCGLGFLSGAAFSLIVFRNVGPRIA
VTALGGGFGLGKSYVDMRYVFGHEVVAEAVWTAEVVKRTNHGTAAFNEGETAGPQ*
>TCRU_3574 ATPase subunit 9, putative
MMRRLALQPVARRAVATSPSALVVRRASTVAISVQGLHYVGTGLAAIALAGVGLGIGTIF
GNLLVACARQPNLTKMLFNYAILGFALTEAIGLFALMLAFLMLFS*
>TCRU_3575 BNR repeat-like domain/Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MSRHVSTFAVLLLVVMMCCGSGGAATAQVGSNADASTPGSALTGAIAGEGSASGGVEGLQ
RVDLFVPQTTQVLAKGGTSQETERDSFVSPSLVSAGGVIAAFAEGRVYTVNAGRQNEKTS
SDIVVGYIDSSWGWSTLVGKVNESTWKANTVLGTTDGVDNRVDFFYHPTTTTKGNKVFLL
AGSFYEHKQTVGNQTYSGFKTQLELVVGDVRESTSSKQSERIEWGSLSSPLNGSTIAAHK
GNLTRFLAAGGSGVLMEDGTLVFPVMAKSGNGGYCSMIIYSTDNGSTWVLSKGISPANCT

DPRVTEWDGSLLMIVNCKYDQRVYESRDMGTTWTRAIGTLSGVWVNSRLYFWDLSLRVEA
LITATIEGRKVMLYTQRGSFSGEKRERALYLWVTDNNRSFYFGPLGMSSAVEEEFASSLM
YSDGKLHLLQRRDNGEDSALSLSRLTKEVSTINSVLKTWAQKDVFFSSLSIPTAGLVAAL
SDAASGDKWYDEYLCLNATVTPNAKKVKDGFQLTGHSSGVLWSVNIPDDNVRHISLSHNF
TLVASVTIEEAPSGNTPLLTATLANNNSNHTMGVSYTADNKWGKMFEGKITTESRPLEPK
KEYQVALMLQGNKVSVYVDGNSLGEEEVPLKGESTLGLVHFCFGACDQKEDAGHKTDVTV
KNVFLYNRPLNSTEMTAIKDRIPVPTRGPETQVEDGTERRHIPRIEGVRANAPAGSGLLP
LLLLLGLWGFAAA*
>TCRU_3576 hypothetical protein, conserved
MSEMPEEFTDSADEWEAPVQNRPEVDDKPQRTQPLLDKLDGEERELAGEVVHVEFHLPDG
RIVRRDHLMGQTVACLKAHLEDIDGVPYEGTTLFLGDRPLLDPLSLNDLPFKGGECNEVT
VRIAE*
>TCRU_3577 U5 snRNP-associated 102 kDa protein, putative
MDAAPTLLPQKDKYEQLLAKYDWSSPFPPRGYQFGVGRGAKAFSTSAELSSAVGAAAAPF
LLSTPETSGLLDALDRLEEKRQKRRRDDAKGARQAATAHESKKPKTLLSMEDLATVGSGV
AGHSLVKRKARTEDMDVVDNHVFADETSVVTAGDLLRSQTFTTKQTLENILGMGSPTEQT
TWITHSRAFREMGLSKKAHQTLIEGCRLTGSKGPLIWKERLEHTQDPAAKRQLLEEAVKA
CSGCEELWLLLLEHEPPHGQLHWLQQAVMVCPSSEKLWLRVLLHISAPRDQKKIIRKALE
VTPKLSSLWAMLARLESYETGKAIFNAAAAEHLSLQIIVEAAKFEEFHFSSRIKEGKRTE
EGSLQVLGNERIQQFVHQAVGSFLIVEEEKSRREWLEAARAAAFERYVLTSAYMYLYFVS
DRKTKSLFVPATWIEDIVALVPDIWRTHETVCAMWAAMLILHQIHGKPLCGDTHIKEKEV
EVMTVALRLASSVAIDAALSALLKQMTFTDASNLGNQSVEEEEEELGRPGTTELALSPPN
GTTTSATAASNSLPLPLTCVFLCTLLHMPWLTTAEMTIRIAKVLYDRGFYEGASHVLRLS
ISQHPTNCFLFPAAAKTLLAIGREEEAVEMLLRGTELVSAESDIVWVKLAVHQRSKHKDI
LPLIDKALCLFPKSEKLWLLRLEAEGARIKRLLDDAAMRGVSTLPFIIELRQIYSKALSE
ANCRFSPTVWCYVGERLESVLLSSASAARALLLEGVVVCGRKQPNKKAEIQAAFGLARCQ
VERIHSGRETALEVVKETLQLLPKNNGSFTVPVGELVSLSIDLEAPAARGRAAAQAVQHW
HVRDPLVFGSIAKVYHAAGKYDKALEQAMKAVKMSEGSCGDAVALWLKLASLTAYRRLVK
ALMCIADEGELSNTEEPIPMSLMLSWLWNQIALDSDDSGNATDAGSNKQHTPKINGGPLW
VLVAKIKDPSNVTLLGYRDSVESMLQKVMDLIEL*
>TCRU_3578 hypothetical protein, conserved
MSSVFNTNAFLRLTTDTVRHDMRTMLHWDPVGNRVHCAMRDAFFLVIDTPRFFTYTHSSY
GAMRRYIRQARINKGKVNPEDFRDVDTNVLRESLIRYAQWKGPLQKIDFRWFYWMYALMI
GYVLWQGLALQKILDEKVERSGVSLEERRRMFDDEYEEDVRPR*
>TCRU_3579 hypothetical protein, conserved
MTLAVPQCLLRLLEDYTLQALDAAHDVSDEFEEELTDLTSRAIRIQAVLQLIRECEKSRH
ATSSLASSKAIMRNTPEAFTQFALQALGQMSSELTGIPATGARKPQFNAPSFGLLPIGRP
VSLSEAALELFAHNTKVVFRRVEKRGRDGDAVEGEHRQESLKKSVFSRLAAEQRKRRLVL
YTARTALFPRAAPLSSLSVEDIEENLPPFVPPAVREFAALNMEAECEMLTAFYRVDAKVQ
LLRELPGLGSLVRQLRESLRAAGVLLQCASDSMNEAGEQPWFEFPSVSEGVIRIVVRQSL
VLDVTWESARGGQWRLLALHWLLRVQTLPEILQVKTFSMHTCENEVAKGLFLYGGSLRVQ
PAHHEATLRYLSSCLETGLESGCMGALRVVNAVAMEVIEAQCKVLREKFFVGPLESNFML
DVRPGTHVAMTVQLPSTMGSVHGGALHVKCNLCMGTIVVERRRGTDTQTMQQTDFYTDSL
ARLKHSPVVVVDMESLLWQFAFA*
>TCRU_3580 cyclic nucleotide-binding domain containing protein,
putative
MRADTTQAFLPSGEKLYSFPERVVKEVRGIALAVIRCLFCPILRRHLAGMHRRRVLQLMR
GSGELEAKMLHALEQLSAPAQVAHAVEMGAELARVSWVMKQVAASADYRVFTQREFVQYL
GEPGNAVVVLLVGSVTRRVRMARVRGKSVLEKTIFRSFTAPGSAVQGDETSQVSRASSAL
SLRRSSVSNVYSEKPSQCTVVCAPAVFGEYNTVGGYPWTEYIVAESPLVVTASLSKNAYC
EILGAFPRHIQKQVLLMALQSREKLIPLFAPMTVGRMRLCPLLTDLSEENVLHLMDYLVP
HVKAAGMQIGELNAPQHIFFIRRGTVYIRNEELFLADLSSATQPKCRSLLVEGHTFGERQ
CIFREALGDSFYAVTNVDLYALPFSVLIQFMKQQPDARKIIYASAKAASLVLENDYERMR
FVPSSVEEMGTVFLGSALMSKLFHRRVSISTIGSRRITPLAALAGNTGKMDGKVDQSACG

VSPHFIEQIRRIPLLDLCSPDDAFYAECASHWNMFLYDAGEYIVRRGGECNRLLLFPQGG
AAVVLNEKNASQCLVDSSTPFFRQNFSLVPRECIIGYTCVRRHPWALSVIALENQLEVWE
IKRVKFLELLRKHQLERKMQEIVLQLLQPLMCLPSRSTVLDMQPLLAPAPNSLWSEHRIP
NLHPVSLCEHLRFPVWKEGDLPLGSYNLQNRRNTI*
>TCRU_3581 adenosine monophosphate deaminase, putative
MVKELQASTETENGRSAPGNTDEAGTDIITQQLARARLCSHNKTNNNSNSNNSNTPTKQN
PSAGTSAANNNNNNNGEGGTGKFAFGNFYNVSIDGDDGDRDFLKCAEMIANIILSRQSYK
SFDKGEMEVFFGSDATDFIVQIDVQQAGEESVLSFDGGIFRFKGMRTKIVPWETYVRDVK
AVFSAIESGPCLSTARTRLTTIAEKSRLYSLLNGGVNLSCSKKTFGGGIYSICARVDNAL
HLPTSVTAQNLLDFIITTALEQPRTPLFYDEKGKAVHLMEYLESHGVTDPRELTVHGLGM
QPPHHRNKFQYYNVLDTNLNPSGKFGAHLLQAVFSTNGPKEGDLFGALIRPELEKREFKD
RQVVATEILLSFYGQNAEELQRLAAWVRRQGFNSFEMNMWTLCIPRSAPLRGPNEQPVTC
VTFGDQLRHIFYPMFMATLYPTDPAWADVAALLRKTGAISISPERICHAENLLTDALDPD
EIKYEDVVNDHCFFYYIWANLVSLNALRTRLGLNTFNFSPSVLEVAPAYDQLVSSFLLAD
VVYHVTSLEKSWIMQYLFMYCRIGVVMSPLRDNTLSMSYFDHPFVRYFAQGLLVSISTSD
PLYFHHSTSPLLEEYATLMKLHSLLPMDVRELARNSVINSNFPLEMKRKWLGDDFQLIMN
RGNDIWRSGVCDARLDFCTGCLIHEETVLNLVLSQVCKKGEQPLSLSFLSTRNPTRIPTG
ATQQLRDARRANYTDWRIMYPRIDIFRNDTQVPATEAVELLCDVISLRKKYINFHVREVD
VNVEDVFTDSKFDESKWEYNSYYGVFLLFRIGKSPPWPSFIPPVREFIRDVATVREAVMS
HRGLQHLAEQRLHLLERKFLLHLSLNVSKEAGAKEEKEWNNRDFFTAHKVDTNVQTAAGM
NARTLLEFFVEKALHHGHDVVFEEDNQPVTLRQMLERYQINATRITVDELNHLINSNSHI
RTIFLEVDNLMKGRYFAELTKRTLELYQEDAFSFSENRLVIRGESKDEWWKLAQWFDRYG
MASSQNRWMINLPRQYRRLRQEGAVRNFGEYIDNIFQPLWEISLHPAEDTKLHYFLTHVS
GMDCVGDESKIDLPLTATYPHDWDSDLNPPYNLYLYYYWANITTLNEFRASRGLGTFSFR
PQCGELGGVEHLIGGFLLADGINHGVTLSQNPVLEYMYYITQLGVAMSPLSNTAAASAYL
SNPFPLFFHRGLNVSLATNEPLYFHFTREPLIEEYSIAAKLWQFEFNDLSEIARNSVTQS
GFPPAWKENALGKLYYLNSALGNDVRKSRVSDIRVAYRYEAYQSELNFLSGQLSGGRQMP
RAMRLLEEEIAIYEEVMRTKVVMPAAGDEDDGREEIRSPAARAVRIKAELDALERDMQRM
KVLAMQMGSENRGIVEAFHRIRARLKTEGLTVMGNLNDCFAPLDTNGAASETINRVSENF
VKEAA*
>TCRU_3582 GPI transamidase subunit Tta1
MSGEEDWRLRVDMPWAVACVGALLVALGVHYKALCEDRTDLSLPELRASMEAKCRLLGDV
FERPVMEPFLHPVPSQFGVAVWVEREQWASPVHEALDRIEEAIGRGSYKADAAGSGARRL
RLIQRIVRVATSRPHSGTQDDSLSLVSVATAQQLGLGLAQHVCTVDLRGEVIMHGISFFR
RASSSAGDSRVQCFSFDERQAYCTIPEDVSSTWLSREVPAAVATLMSRWLQLDSFRDAST
VRRWALEREAQSCKYALRALQQLELSVNAHPEMPAPLDVAETIDRLQSLIDAGELIQFAR
AADDLQFHPLLLPQLYIPWDQALVIHFSILLPVMMTGILGVRITVAARRRQRAVAKLQEA
TEAKKND*
>TCRU_3583 hypothetical protein, conserved
MTKSSEPPRGRMRVEPSIPLDFSSLPAVQEMIEENNRQTRPKRRLKQFEFINEVFTRLGD
RAINDAAAVPVLSSFLQECVEKHGTLPRSSALAKVLYLWSENGLVGEGQSLLGEVLQADP
ALRKNAFDEKVATVSLRLLSRSASVDVDLMNKILAMLPEGAHKRRLFFPLLQHAARTKDT
ALAFNTLRMGQNKKIEFWDADYHQLLCTIQHAATEGGNTTKLLDELLEAMVDHHPVVGKR
NAEALKHMMGGEMAEINDKTGECSRCGTKLFSFDFTSIDRATLLSDIETKLIAPRVGGEN
HYEPERIVTPAEKDRRWREFEAFKETLTNCDYDVVIDGANVGYYGLSSWYREAKELCLRA
RGVDPTTVPEYQLCEVPLPVDVPPKFSLIDEMLAQTRCVGRKPLVMLHKRHVESPSKESS
EWLLKWKADSALIACPGFMNDDYCWLYAAICKPDCLFVSNDLMRDHHFMLLSRRSFLRWR
QRHRVTYKALFQRATGTATLLLAMPRPFSVWVQRGLLSRTHWHVPVLLSADIIDQATNRA
SGKQVEVDKDGDDSCDAWLCTAAKNLLNRSE*
>TCRU_3584 hypothetical protein, conserved
MLLFKRPHLRACESHADIAVDLAPLSQLRNYAEFEELLREELQKIYGNAPAEFHGVITYS
TRDAPQSFRGCFTERQLETLHQYDAAVEKINHLSSEYRVALEEHERLVEGNKDRKPTQKR
IREEEKSRKRLRAMKREVVAAEYNKECLSLKLKNLFSIDVIRVPLH*
>TCRU_3585 hypothetical protein

MAANSLKCPFSSKMSVSDGVVALDSDEILVSPGAVLVLPGAVSTVCGTPLPSSEETSAPS
VQEMLSVSSADVGSASLLEGVRLLSESIALSEFPSPASRLRLCSAPVVPVPVDHTPSFSA
EGSVLFCTWCSLSTVSVAASISDDAPTEDVDSPLLSLVPPSSTGISSSLLSEDLSNSVTP
VNSSDGSSCGCGSESCCIELLSSFSVA*
>TCRU_3586 hypothetical protein, conserved
MRKYTIPRGSRDRPEESRRTECSRPSLLRRQHATSVLSYREAACPELKCSANGRNAIMPS
AVFSPCCQTPVRNSLVLSRAQACDAPRHGGTTSLPSGIGCAAVLLGPRLCSASAAGNQLV
RHTVRVALAAILTVVRTPCACVPSGDWNMNWPFTPCVPDSAIRDCLPGMAPGPVGVLNVF
HRLLAPAARTERLSIPPSLTAACEVPGKRGTPLPSANAGRTNAAQGELPAHPAALCPARG
ERRTGPPSPSPFSRRPDRHLDCIRHR*
>TCRU_3587 hypothetical protein, conserved
MDRTPLDMAALRLQKIAVRSETKQTHPMTEEEMNQVICSRTDWKQRVVLRLAWMTASRLF
EIAVLTPNNFTVEADGTLILDRTVAPKTARADPHRALRFVRIRGQDAFDTIKLCRTLQEN
EKLTNITTAHVERALAPWNATAHSIKRGALRHAAQIVEAYNLDPHVISRLAKDVDPFGLP
KNTVRYLGRYTTVLTQVSSLVALM*
>TCRU_3588 hypothetical protein, conserved
MKASLEFYSKSGAHAITGTVGTLTPGSPLAFLVLWMRALQLHREPNKQFMDLGGIVLRAF
RMRIVIKSDPSIPIQKLRARLRTAFHEADTFARVAQSFMDRRGTKRTVRRSLLCQLCLIY
GHDASTCNVRSKRVFPELQTKV*
>TCRU_3589 hypothetical protein
MKEEVEDGSTGTKTAVRLDVKVSYLSFMIRDDEESSVLFTVESSEFWMIQHSMKLTAQYT
MSNASIQSTYKSKNCHVLKPFCFDMTVRDVELLINAISACSAQVNATRLELELSDILLYQ
FYQLAAHRQDNSWKTMKKKGSKGGDASPAIAVPFISPFSRNRRIEINSVVICEICVIPTY
DRRVRPPEDVLFRGSPIGTFIPSLRRATIRLPTVRFRDVSRKTLMEVCNMVQEVLFFEFL
KQIPSFISSVFLLPTLSPLGNILTRVGSFIFGSGGASSELPGAALI*
>TCRU_3590 hypothetical protein
MIRLEVGGVKYAQQSAPFPEELSGVFSDCDMDSDTSVVACEKYTHAVVKNWNVHLKGVSE
ADAVKELLGLWMELRHMMNSIQRRNVVNCTLLRGGHYNLDRTGPWFFDSPGEMVLVEDCT
FLSCTSGMHMVVCSGTHVCFRRCHFSSFFQHAITVEDECASFVCDNCIGEDFGGESNATG
AQAEVEKKTVQKFLFFFHRGAVCLTLRDECKLTLNLSTVDLRFFTCLKKTVSHLRLQRGR
LEFMEKGALHGLVSRMDLDLDWTLRHRDDYATLSSSLRVGSVSIPVLLFGTMRCLRGVWN
AEVPFSEASVREYPSPVKTRGFSVARWKALVRVSIIPVELCPPSGGAPLISFILDSTSVV
SRRETTGEAFLEARSGIQQLSLPGNFLRNRMFHFYGICSLCWWLLARRIFLVRHVTCLSP
HVSFLSPAGKSSAFCPS*
>TCRU_3591 N-terminal region of Chorein, a TM vesicle-mediated
sorter, putative
MVKTEPTLEAGAELMKVIVITFSGVAVCANAAKEQPQKIVEIDHLSMRMTSVYSSAGILC
RKNVAIVFDGVSSLFFDEDALRSLTRCAVSHGIMKEVPEYCRPFYKLRSLSSRWSHAKSC
VFAFIRDRRGRYNFNSSHLHFYAEARTSYLALLDYCHRTRDIAEKREQLADIEGDIRYRD
VVLFLRRKVQERYSTTVLAGSTGAGVTPPPTQPSDARQFVVVSSLHVDAKITCVRLPAET
TVWLRDVAFVKRHGESNFSVGNVTLVAGGKSQLLRAPDSGEPFFSLQQTESNGMTFVRTT
LEALRFITTSNWMLQLVQPIMVAMPHVLRAIPETNCNAPETKLSNRCEKTTSFVFPLIDF
HVDDLRLHLKQLSLTHIERTSGDSRVGLLMKELSVRFGEETDVLSPMKVEMTEEEDILVS
AVTLNVSSALWEYLCHVRTESGTMPYYGLVTCQALYQECSQQRVAH*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MSSTVALNVLRISTVSSDLKNGVIVAACNTVNGEEEVQYSIPSVYNATILTCSDPCALAA
SCFPAYTTTASSDGCACNCAEGGHGDACLPVAVTEPPSTDGVDLCVRDVSVDVEVNVGFG
TSVVCYVGVTFAADVVVDVESMSGRVRNVTLANCAFVDGASLYVIGWRSDPPAGQRVDVL
ISGLESCSGGGVLLANRYPPGSRVTVVDSVLIAEKRVAYRGAYFLGDASACLVVHSVNLT
GSVLTIARTHVAAVCRDAAGVLFVGGVALSSRCALYVDGLSVQTALGLCVSVEGGVAASG
GSVVAFVDSDFLLCKHAVSVRGAVSVSGSAVVLVRSDFSSTGDYAVAFYSTVSLDGGSML
LAKGNVHDGVSRGMLHAAGTVTAAGSTLSFVRNRAVLPRMLSVSLSLAAGAHVRVACNDA
GGRVLSTAEEYAAAGFGDAGSIDVAGCDACDRDTHCYAPGTASASMTDGVCVCVCGSGGY

GEACVPVGAPALPPAVGTASSMFVREGVTVQSVFVVPAGASEATLRHVVLDGVSPVLYVP
WMARDGVRIVVQNVSLRNGAVLYVMGGGALRGAGTAGSDEGGPVELSVCDVEALNGALVL
TGTYPAGSVLTVTDSLLVATRPTPLVYLLGSQSSPYAPLLVLSGLRLVRSVLVVSGVALV
TVVTGGRTVVVDGAVLELVGGGVALDAAVFGGEYALYASARVVASGGAVLRVSGSQVYAA
HGLVFDSGVEANASAVVVNDNAGALTDGALLVLRGSVSFVSGSWLSVRGNSISGRLLSLP
SYPRSADLVQSTLTLHGNAGSGPVVMDGTVALGGAGGKFVVGCLTLNGQALRPMDYRSAG
IIGEFRPVACGVCDADVRCFGAATRTMSRSCGCRCAEGGYGRDCLPVYLPHVDGCNRTLF
RPPLLSHTATLTETRSPTPTPTPSQSTTHYSPTHYGPTETLQVTETVALPPTRTPTASVS
STLWWSDVACPTPAVTTTAAGGGLTQNDIRGDGSAVPTLLMVALPPPFRWARDPQLGTHL
SFVPVSTVQPRGFGGPWGAMLRNATWVRNATNPSTVLELAVPVHRDYFIVADETIVIRCD
PVAVSGGCKGVLLGSFTIRSDTLPAAASALSAITGVVAGAAAVAVLVTGGLGSILEMQAL
GVFARMPCASAQERASTVALPYFLSVFAALDPLWMVVGNALLAAVFGCVHCGVTAAFQRW
RGVDAASAWAAMRFPSLTYVVAHAMHLGIFFGSVLALAMPGARVQHRVIGVVGVLYGVAF
PAGVCYFIARHVGSSFTRYWQFSRKPLHERLLYPVGYWYPAAQQRMYGGMLTNMRGSRVY
WCVFRLSVLCVVCLIAAVHPPAGGCHVQYFCMAAVLLAGAGVVAFTNMMRSAFLTVMHTA
SFVLLAVLCVVSAANHLAPSDGGAKAYAAIVLLLATAVLAVTVYSVVVWYAEDRYLKEPR
EPRRGGLEALLRDDEESDEETQKLHDMTSSSYASGTTTASSYRPPAPPLQSVTGDIRSDA
LSLFDGASIAS*
>TCRU_3593 hypothetical protein, conserved
MWKTHHCYVGVIFSGVGAALTFFLDSMPLHLPINITLIGCTFREGAALQFVGGAESAGSS
GVLIRVSQAVMRSSVVAFVLALPQHCDIAITDVDAVQTSEVQFADTISNKFGVLLLLNVV
LNASSLLVSNIKAHASRYWGFGLYSIGTLSLVGGSSLYTRYCSFDGYTHILYLITLGVCD
HSVFALLNNTMASGTSLLYQHSRFSVSDHSVLRVVGNSGSVSYAIYSLNSWTVEQSSWLD
WRDNDVGVGAIFYATESTFLIIDGRSVVTLTGCDMGSTGWSVSLLSRAAAGYRFVAGCLT
VAGRELTTAAELELHGITNVTTVAGCGECTKEGDCFAPLTTAVVDCKCRCAAGGHGDVCL
PAPVPAGPPPPPLPPVPPTPLPPPVGECISDMVYPEVAQAVGCRGCATAT*
>TCRU_3594 RNase H, putative
MIPRIQHRRKTLLVVTDSQSLLAALNKGPLSQTDWTEDQIWQRLLTLTCAGWSVHLQFCY
GHCGVHANELADQYATQTMESGQYTEQGIAPLWHTDLLTCFTTQLTNKWRSTIRQDTHRY
SLCGTRPSDLSGKDLITQEVLHRQELVHLARARCGESELWGRLYWAVRDCTNQCRFCNIS
PEQSAYMRSNNDPTAPGTDTVPPSAREEDVSPVRRRTLTRRRKEKCPHCDSTLTGFSGLV
SHCRSFHPEHPPPLPELKCDFCDMVFPTRRSTAPHRSRCAHNPDATRHRNSSARRRSLLP
QDQPASTSTPIGPQETLHHLLLECPGTLAVRQRLGIEQDLRLGKFSQWQLLHSRKLLSLL
DHLFGTQMALYS*
>TCRU_3595 hypothetical protein, conserved
MLAFSIISDELRDESSIPTPADLGTSTPPSVASIHERWLCSARASSLTLRFSSISSSSSV
IEWSIGSSTPMVTRWAEAANQGGMELRKNRSSRGELSVMP*
>TCRU_3596 Endonuclease/Exonuclease/phosphatase family/Endonuclease-reverse transcriptase, putative
MEPFTWLPAERYFYPLLNSVGAYQRYTYRLRAVCDAQRQKLLLSGDIEQNPGPIAALQMN
VSCLTPSKLATLMAQGADIIAIQETWKSSEQIASMHTGDYVLYAQSRIGKGGGVAVLVRK
TLRSKRIPLAIPQHDTSLEVVVVQAALDQNRDLIVASAYMRPPPQVTQSFRRLVNCLPAS
SPLLLCGDFNMHHPQWEPFLETSPSEVAAEFLELCTDAGLTLVNTPGEITYARGTRERSC
IDLTWSKHLTVSDWSASVSPLSDHYMLTFTLHQAFKDTTPSAPPSAPKFFYSWGKCKWDL
FVRTSTHNFRHTTIKSSPPALRLSRERL*
>TCRU_3597 hypothetical protein, conserved
MHGRRHGLQSDCATHVLNTPETREAFVRCGCAEPNDPPQRCWIGGQVDRGILICCAWAER
CCAAVAVPRFQAVEVSGGRTRCGRLAAVVQRTVDASNQKGSRGLPGRPSRSAEPQLTAAW
HGLPCSGGDVQTKIEVSINRIAEQTHRVELDALVPTAQTMVGSVLVGLSV*
>TCRU_3598 Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MHHYDGVSVYVDGEEIYYTKDYEDGEDYNFTQRLRTLLGSHGISHFYIGGDNKSNSEDIN
VTVSNVLLYNRALNEAKLNALMKKDAFAAAAAKVPAQEVAAQTTNVSEPSRHPANVPVIT
PEAQQDATSSPRIQHSPAQTSESESGPADFKQTFPDIIVPSTSAGVGMAEEDSPQNGNTD

DWAPYGTSLDVLEGVHDEPSNANTLASEEQYADRDEDTHVSESVGTNSDPNSFSSTNVSG
GADAAPAPPSTAPGETKIPSELNATIPSDHDILLEFRELAAMALIGDSTVHVCVSRVLLL
LLGLWGTAALC*
>TCRU_3599 BNR repeat-like domain containing protein, putative
MLEDNSYVLPIQALTRDGKNVSLVILAKGTHYGWEFSKDTSDEGCIQPAVLEWNDEIIMM
TSCDDGSRRVYWSSALGKWWMEEYDTLSRVWGNSLNRTGHGVQGGFVSAMIDGQKYILVS
RPVYTEKNGKETGRLHLWLTDMQRIYDVGPISAENENVAASTLLYATVEAQPLKVEGPKE
EKKLYCSYEVAAGGDNYNITFVDLTEKLEEMKKVVAAWKERDAYIAREYGCRNEWENYWR
SDCHEALTKGLFGFLSNTSTDSTWADEYLGVNATVNKGKPAADGGLTFEGSGAGAEWPVG
KMGQNVPYYFANYKFTLVATVSIHKEPKGSSSIPLMGVRMNDAQGTLLFGLSYTHKKSGR
*
>TCRU_3600 hypothetical protein, conserved
MDAPETGGNSQSAGSPAPAQNNLDGQDTSITNAEAQSSIKPHTAGDQNFNDDETGGENER
KAAVTGEPPSKQQPTPLQPVQPEQPTTDSHTRPKEERDFEEEQSPPPAPSPTNSREGIPA
TRELEISTEEKRQTSPSETQKGLVGQEKTSMDDAEEHNTEGTTPSDSVKDAVASGS*
>TCRU_3601 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MLGNGSPRTTEESASSGANGETAGVTDVQGEEDEIHPQAGELNATALNSSLGHLSQGNNS
DGGIMRESRRLPSLLLLLGLWGFAAL*
>TCRU_3602 hypothetical protein, conserved
MDSDHHLPSHTAGTEDGIPRQAGMLPRRKHVAISLREADCDASTTACATPLATVITWLEM
HRGTVQAAAVTFPQESVRTEWSRPSVLQRQPAPS*
>TCRU_3603 Nodulin-like, putative
MVQLVDDLFRMRMLMAGVYLGLGISSTYGFSIFTDHLRHKYGYSQSDITTISTVGNCVGY
CSFLAGMLFDYAGPMVVLPLGGLLGCLGFVLFGLTFDGYVVSNPSVIHFSIFNAILYLGC
PSMDVSSVMPLMLQFPLERGYVVLIMKTFNGLGTAVLMAYFNGWFKAANSDQPEDNNYSG
YAYFVGGQILLCSLIGTYFTRLPMYFPCSWRKKRLSSEEAAEREKTLDLYMSQQAPMRRL
RIGVMLVVAMLIFSTTQSIATAYVDTSHVGYLAISIVAVLLMASFSVIAMPFQFLGRYTP
VCPTHMEGIGKATTGLEHERTGETICEGAVADGNDLRANVVAVPAPQYSGSFWSHLLTVD
LWAVWLACFGMWGTGTVMQMNAAQIYRSKNNGKFDTRTLTLYVAIMSVGSAAGRMAMGYL
DMKLSALQRAGKTRTLTTIALPIGPLLLVAAYLFFAVLPGSVLLLPFLLGAMGNGVGWGV
GVIALRMMYSEDIGKHYNFCFTSGAVATIALNRFMFGEMYDAEARRRGEFPSCNRPRCVR
NQMFILLVVNVVATLAAALVHWRFSRFTRARLDERETPDSLQDGKDMIGMGSGDQATEED
HLQS*
>TCRU_3604 AAA ATPase, putative
MMTSAAPLFAITGRGNDVKHARELIASIGGVLTTKEQVADYLVVVKGAGRRRVEEYCQHH
HHHHHQKQLQHNGGRGSGNLTGHTTSSNGIRDLHSRGGRLLLLDMLEQWSTRGKVPERDV
SVEELEGMNLLSSAGAERDQRFYDIPEGFLKRSRVTLDPHGNAVDEADNSVLVSSRRAAP
PLTATPPPLGKTATSPALLRPPMVPAAVPLAGAVVFKTPLQHDVQRRGVPRDDESVPQKA
AGNVASYGPKNNGVVNPMRAAFQRRPKPEWDTYFADAPGSCGAGDAQWVGDATTNKKKTN
DSHSSSKVHVAPQNRAATAAAAPSPSECTPSNQAYPSSTARGEAAVAPKITRQKKNSVEL
TFDLSKRGTRCPEMALRGAKSNSEMNAHESTTKKRSDEKATVEEGARKQQQETKEKKQEV
RTKKIRRDGPKSRFYHSALNSKPGKSRSVELPTSRQSKVNHDDAPCRRTAGSGVLASDGS
FGPPPPLPPRPHESAGMRSTTGAATTTTQAGCKSTPAASRLARPLSTSMPSHPPAVATAA
VTTKAANNNSTRVTHGNSLLQRVRQSSYCKGIPEETCLAVLQQVVDRACPVSFSGISGLE
VCKRILYEAIILPAKCPQLFTGLRRPCSGLLLFGPPGNGKTLLARAVSRECDTTFFSISA
AAITSKWVGESEKMVRALFAVARALAPSTIFVDEIDALLQARGGAHEGEGSRRIKTEFLV
QMDGAGNDNSEARVLVMGATNRPFDLDEAIIRRFPKRVFVPLPDAPARTQILQSLLDTEE
TPNSFTPAIWQRIVAMTDGYSGHDLRQLCEEAAMIPVRDLLAEKMRNGEELTAQAYHHDL
LRPLTLQDVETCIKARHPSCCPKQLKALSEWSETYGSN*
>TCRU_3605 chaperone protein DNAj, putative
MSWHGGSHTWLFFFLLRGVLLLLLLLPLEAGEVVVVAAAKSAPKVEEEDFYEVLGLGKER
DDASERDIKSAWRKLSKKHHPDLAGESQREVYQRIQRAYEVLGDRKKRKVYDILGIDGVK
KIEQPQEQQQQQHMHSFFSFFGGGHQQQQVDRGKNEDLVLLVPLEDVYSGAAHTVKLSKT

KICRTCRGTGARSKDHLVRCPHCNGEGRVLRRVQLAPGFIQQMEQPCAHCNGQGVFISEK
CLTCKGKKTVRSTSSISIDIEQGIPDGHVLTYELEADQQPNQVPGDVLFTVVTASHPRFT
RSDNDLTVTVVLTLKEALLGFSKSLTHLDGHLVELEQSGVTQHGERRKIAGEGMPKHHVP
SERGDLHIIFEVEVPSLLTKAQKEALERAFG*
>TCRU_3606 hypothetical protein, conserved
MGRSPDPHCRRMPWTAEKECVPGVVHSSKEKMVLDGARRVDVDCVDRASQVYPLEALRAT
VASYEYNTFRGKNIFNWLLRRNQMYSGNGFTARSGRRGRTTRTPPALPFISVAAAVTQPA
PIRLADFPG*
>TCRU_3607 AAA domain (dynein-related subfamily), putative
MAATDENPLPVTEAEYELPEMEEDHSDNADSDCEAPEDTSRRRRKPAVDTTLNEESDDEN
EEDSKKDADKRRGKRRVKVVAKIHNDDDDDEREKEEEEDVNGFEQQQDTLAEGEKMSRGR
KLWQEQVAAVQGLSHHLCEQLRLILAPTLADKLQGDYKTGKRLNMKRIIPYIASQFKKDR
IWLRRTKPNKRNYQILVALDDSFSMQCNNAGVMSCRAVALLAEALRQLEVGELGIACFGK
ETHIVHELHEPFTGESGPRAFSEVTFAQKSTSLKILLETSLDYLDAARERMHGQTRSTTQ
QLQQMMFIISDGQITEDRLELRRLLLRAEENRQIVVFVLLDVKAAAAPTAAVGGGGVASV
GESCVAQKETGSLSTAPLAAKDLSQLSPAERLRRLKAEREARLHRVQSSSVLDMQLVEFK
GGKVVRRSYMEEFPFPYYLIVRELETLPGAIADAMRQWFELLNVQQ*
>TCRU_3608 hypothetical protein, conserved
MESTCPVTYRRVMVSGPNDPVKYFVRARDDVRTAVPAQTETGTGFLMCPVRVRSQLRHWM
RAEQVALRCLLASRPTRWPLLKGIQEHSFSEGVSVVWPEHCSARSIGLFLR*
>TCRU_3609 hypothetical protein, conserved
MADSIKALEDELNRQLEILAEERKGLRALQRKMNRAAGGPNEGDEDSRGRQLLTANKKLR
QDLERLKREGAVPESSPQLIGVRNKIAAAWKEVDEVEQEVDTLLLLLRDRKKVLERERKC
NRSVDVLRGRQREEQQSLRAKMKELEAKLKRLEKRDVMLRNRFTQLQNQVLLNVTEKDAT
ALRKKHKQQMRTIGKLQKRREEQASSWIKVLENDGQRLTIREKMAKSQMEKEIAELQALV
LERNEEIAQLRHRLAKSFF*
>TCRU_3610 endonuclease/exonuclease/phosphatase, putative
MAKSSPTSVCHISLTNGEDITEASRHCITKPSGLSLFHHRDESTTCASPRAENGCKIATT
RQLTLIERREKKHYSTSFPSLSAETLLDESRDAVAGDAAIVSSTLRGWSVRHVGKNMSSL
VLDGKVKIVSYNILAQRLVSTELYPHCPMFALAEDYRCSLLKRELADAAPDIIALQEISV
DVFEKPGLLGDWLSSNYCFAGDHVVVTDVKGRPRYERDELPKKKCDVHVFKETDVSSQRR
GGEHASWVTSPPPETDGPLQKRSEMEGVCVLYLKDRFDSCEVVPIRFNEIAAADKHLTQR
ERRSLQVGSHNVALISVLRDRVMPNMIYVIGTVHLIWQRTECQLWQMHHVLREMEQLKKK
YEKISTGGKDEPALVSLVLAGDFNSDAGSPPIRYALSGTPPPGSDVMNYWKLPEEENSSG
CEEAGSPPLSPSDTTSEAAGVRHIGSKRRRYRITDTVGHSISFTDSYATYREQHPWHVST
VNPSSNGEGGVLDHILVEEKHVVCTSVMRLSGRTELPTKDYPSDHYPVGVIILPRSSLK*
>TCRU_3611 hypothetical protein, conserved
MSGSTPGIEFRHTVDRLSRGVCAFLFLLRFPPIPSPDCSEEAHVPGIDGVLREGSSHDGV
GVRRHVAWIPQCHGENMEPSARTRSASESGTVQIFSVTPSRTASEPRRSASIAERESVAA
GTRVGDRDAAARRGTGNCLWPRSVAGLSARQEHARLPAAAR*
>TCRU_3612 RNA polymerase Rpc34 subunit, putative
MSSHVANAKQRILSSLSLAGQEAVLFTTLQRDLALDQRTAADALRGLMEGGKVVLRRGNG
DGSVYVALSNSMPEGPSLVLDAIRSSGNSGIDQATLCSKVRLPKSEVIKSLQLLVAQKRI
KERRCFSNRAKRIYLLFEFEPSDEITGGTFYGGEDSREMDVWFVDGMRRLIVALVAQRHS
VSLEQITQHLHESHGSGAAGEATLGVGDAVVVVTALPSGSVVTSANDNKGGNKRISQRDA
QLLVQTLVLDGVLDCVTPSVGAPPQYQLATGKNVLRHFTATPAAVGGWPSNGVTTPLEDG
REGHGDVFAGGLWNPAPVAQPSAWAMPAVGLPCLGCPQLSVCFASSNSVVNPCNCAYLNE
WLS*
>TCRU_3613 serine/threonine-protein kinase, putative
MWQHHNLSSPTLGPREAKPTVQTSRRGCTRSDAWCSSLAGGGHDDPSESVPNSRVSPRAS
SFAPPQRTAPSPTESTSQGLFELQHFNHHKQQQQQRRQKQQLVIRQEDIRDDDFQRLEVL
GDGSYSVVVSARHLPTQQLVALKEVSRRRLRELKLEKQLQWEINVHRTLRHPNVVRMLSY
YITPQTVVLVLEMCPGGTLLQKLKTMPGGRFDERRASRYVRQAARALTYLHGHGIAHRDL
KLENIFLDAHGVARLGDFGWSKALVEPTVEQDLSSHHDNFGTAPCSAVKDVSPLCSGGRG

RLTVCGTLDYLSPEMIIGMPHTFKTDVWSLGVMLAEMLTGAPPFYCVSQQDTLNAIREAA
PHLGDDVQMSSLARELVLAMLQKNPDARPTMAEVLQHPWTRQNGEKKKKK*
>TCRU_3614 hypothetical protein, conserved
MPPKRSKGVTFKLVHPSYDDAEYEGAKNVAIMVEEQELRKHLPTTATRRRRQRAEESDEE
ESATVSGWAREWATTTSFASSTAQADAGRLPEEDAYMNRHNFLRAQDSEDDEEDDDKLFA
DQEEVEFTDDFLREVVFGDGDEEDEEEVRSAGGGAKSVTEHDGFVYVQHDVTKRGVDRQF
TQMMREFNVDARLNDAYTDDPRAHGALGVDQYMRALEEFVVERAGVDYGTAEPRRNKGLI
HQLQNMALSAGTDMSPKGELYTTTVLPDKQARFLEEFQREAEEIRQAARERMQRQQLDGP
AGNFEDAVQATEQDDDDHEVYVLREVEDKENRLDCETAVSAYSTYFNQPNVIRAPSPGRR
RRSHGDFSAAAATEKTTENGKPEDEDVVSKRGKQLLALARHKGETREEKKMRQQLAKQVQ
RERRDKKRELKQAYKTLETDEAKRVKESQTAKKTVHFF*
>TCRU_3615 RNA-binding protein
MHTSEQEKPGDIVEHPSDEMYSHANLFIRHLPRVVDENELRIFFSPYGQILSAAVMRNIH
TGENLGTAFVRYATNEQARTALHECNGRFLHGRAISVHWAKKRHDNTPIGDARKKIFKLF
VRNIPLDVSADELARLFACFGPVGSVSLHKDTAVPRNKWMERRIGFVAFLAEGAAEKAAE
AVHNTRPFPGSGSIPLMVKLAEDVPARNRRPGAAVTDSIRRGGAPNDMVRTNATDRTMTR
APVDEGRVNCCRSDFSTWSFLRWSRCNSPQPTQSANTSSTNYPCNLMPQPFYGCSAVPTP
SPMRDYMFFHEANRQRVCAPGMPPQDHADAFLQQAPCLPQPNFFTHAEKDAATFHSLGAP
QKTLGSSCSSLCPAESEASTPIAIQYFNEWSARPATHDGSAASRQGAPITASTSFCSAYG
TNIAEESSVSNSTPTATEGRKRCTRYTHNPYRLHQQRLSECPTPPVPV*
>TCRU_3616 Cell growth-regulating nucleolar protein, putative
MVSFTCNYCHDVVKKPKVNGHAAQCGVASFTCVDCMEVFDLQTIKQHTSCITETEKYQGR
WRQNRAPAAAARRCVDGSDDGDGDGNDNNKRQPLRPPRPPMNLSSDSDSDDDTWVTGGKK
KAVMEKNKGRNGSPNGCLQKRAKTTSPSNKNMEAKSGLKRQKHEELLELPRAVTAADCIV
PSFVLGTDEEVAEVTRWIIEEAGETPLTVRALAKKLVERYNTRIAKHVRHAIETAIQNGK
LLVEGGTVNLP*
>TCRU_3617 Major Facilitator Superfamily, putative
MGDLPSNERIGSRVVFSAQRSPASVLEDPLAQQRESADFALERTRENSEGSGHNASNILL
IDPKKISDFMRFRVMFIGMLLFISSSTQGLHALFALYMEKVYMYDVRTMVDIFAAGTAFG
LFVFPFGAMYDFFGPKIVIGIATAITSLSHLLFGLTFAGHIDASKTRFCIYFAMMNWGCY
AFDVAALPAILTYAPRDRAQPTGVMKTFSGMGASLISCMFRGFFKNRYDHLMYFLMAIVL
GFGLIGTFCLSNAPYEVTRWEDSRISLKERLRRHLIRNRYMSQLLPKRRFYILSCLLLVM
NVYLSIQAVCAAYFQKEMTEGQYRGIAIGAIAIVLGILLLLVPLHALDGDTPQDHTVLER
AREKERKLAELRRLRLAREREEKDAEKEEERAQKAVAHQNAGDVAIEVKELPRILVDQSS
PHADGHSVLYDNSLQHKDGEKDDEDGEETQHRRYLPLDPEVSLFEADDLIPIEARDDDAS
RNSRQRLGNTSIATRVSVSNVSLAARRKDNEGAEMDFITRELSTYDRPHVETITVCGEVF
VTPVYETSFLLSLTYVDLWLLFYTVFAVWGVGITLTANWNIRIMVGSVFKGLDYQTYVLF
ATLAGISTAFGRVAIGGYEVLLLYIGKRRGVMLPATIALPVPSVMLSLALIFYLSFPGNY
SLLVVYIIAAVAYGFSTSMTIYVIGIIFKRDIGMHYGFCFLGAALGIVLLYRVLLFHVYD
HHKSGLTPSLQVNKEGICMGKECLQKTLIVYLILVFLSIGTSIWLHYRYWKLVHGKLKHK
RVITHFVKKRLRRINRRREKCHATEEGAQQQQQEEEEKR*
>TCRU_3618 hypothetical protein
MKPAVAHANPDRADCRDFALRIPVLVPQMISEDAETVHGRNAKREINAGYQHPHAEQIIY
QLYHDFLSPRSTTSKEGIQLEEPDEETAHATGRKNCLPSCWKGQP*
>TCRU_3619 hypothetical protein, conserved
MPGISVSSSAATTAVRSEASTEGSRTISDLSPSSSEDDARPKNTPDGDDASHITEDVVLP
SAGTPMPHQTAAQTDATATPADSDGSITVSHTTSPLLLLLVACAAAGTAAAVVAA*
>TCRU_3620 Tubulin cofactor C domain-containing protein 1
MSGRYAGNTYYGEGDDRYVDAYPASPLFSTNQVVFCVNPVLFMNCGILLDAPSGLTTSAI
MKIRQESSNSAAISLAMWRDIAVNVIGIRESVAYSVFEVVYALTGSFVQTPVAPQVNGNL
VSAKSIAEYRQEGNRALLKKMGGSVDEARWPAASVSRQVSLPALTIFLLAQLILEHPPRA
MLGEISQELIMSSVRQHLHDYITAVAITRPGRLTVGDAQELKILLREFVNGVEQPFGTSI
GFLWPRSEKTIDITILSQFIRPRIMLPSELAATTTSVSFRNNVVVRGLRGTVYIPPCPVM
PNNNTKLMISSSYTIEKCSQSSLYITSDLPHTRLSQLVNCTVAIGPVGGVLCIDRCENCN

ISALCAAIVVSQCKNVTIFVCTNTPPVLSSYDGVNTLENVRFAPYNSHYSTLEEHLASSG
VNPKLNLWNVGLPTSQYVLPPDDFTPICFPVAPHTSAVITTRTNPCPLPRLYAEALERRL
QRFHDTSAQLQEAYQRLQAEGRKDLAEKLRGKVHTMFMEWLRRTGQEKGLISLLHQGTES
HSQN*
>TCRU_3621 chaperone protein ClpB1, putative
MPVYVTEPSVYECISILRGLKERYETHHGVQITDNAVVVAVQLADRYITGRFMPDKAIDL
IDEACANVRVQLSSRPEEIDQLERKKRQLEIEAKALERDKKEKSSQERLRIVKGDIQRVE
ELLQPLLARYNEERQRVDELHEMQTRLDEKKTKLERAERMRDMELAADLKYNAIPVIQDR
IRSLKEKIEQQKASMVQEKVTEVEVAAVVARWTGIPVKKLSQTDRERLLQLSSHLHRRVK
GQDEAVERVSEAILRSRAGLSRPHAPTGSFLFLGPTGVGKTELAKAVAAELFDDEKHMVR
IDMSEYMEQHAVARLIGAPPGYVGHEEGGQLTEPVRRRPHTVVLLDEVEKAHPSVFNVLL
QVLDDGRLTDSHGRTVDFSNAIVVMTSNLGSEHLVHVGNSPKGLEATREKVWQVVRSYFR
PEFLNRLDDIVLFRRLGFGELHEIIDLIVAEVNGRLRSQDILLEVTDEAKNFVLENAFDA
EMGARPLRRWVEKYITTEVSRMILAQQLPPNSTVRVLVNGSQGKLAFSVKRSSL*
>TCRU_3622 Major Facilitator Superfamily, putative
MSEDARGSSHAQSTFRGDWEALHNPNVRRVLIFCFANGACFSLWLPQVFQVLISRTFGDT
TVGWLSATSCTAQVVGAVIAGLSDELPRQTIIRLGAFSGITAAALSIYALSVLQVHIFFF
ASVLWGMFSGMVSTGVEVLFADSVETGRRDFVYNLKWANQTLCDCIGSATSLLMLVKLGN
EWKLSSMKVLVYTGISLHPIAQLFLFTLKDKYVLDESTGGHVPQCAVVVEDTDAPDLTTK
PKLLPGASESFMDSKESLESPRQPLVSENGMKNEDLSSVSVISRSVASAGAVVLQHEAVI
AQLTMRSAQKYHEYMEAQERRNPAARLVAAVWHHANKLCEWSTVPYLLCLCDFFLVFGSG
MTMRYIPLFFVNDYHITPVLLLSASIVSSITTATLSFLVRYMGERFVSRVAAVFSARFIG
ATLLLLMGVTHLHLSILVPIFVLRNALMSCTIGVTRSVIMDCVPKSSRAKWSAFESFASF
TWAGSAVIGGYIAGAKGYQFTFFITSMLHYVGICVLVPAAIVSQNMERAKRARWRNEKAE
EKERKKSLRRLRSTGTASLLAAAEGCEEKDQLLGRDRTSLQ*
>TCRU_3623 GRAM domain containing protein, putative
MDKWTGRVQAVSNSVAAVDVSVGDVVKVLLAVAEQYAADMSPVEAMGRAISQGIANASAT
LVSCLTDLATMSEAMKDAMNANPKEAHSLMMNLFNVFVKQLTVYYKENYEAFKKAEVTLR
QQRALFWSQKSEMETNNDNTSDFTLLPAEEPSPFNISLVAFNAPKEAKKKYADGKKKKTR
DSSKDTSVVLPSEQHSEKQQGKPAKGEGGGTNVCVDAPSTNVAEKNETAQQGNGGDIPSK
VKSFSTEPVVTVKEPIYLHVASTVEDALGRLVLSSRPNVFTAPEVIENRAPIATYYIKLP
APGSMGPLLLSNYIALGDDMQADLMCDILQSDCVEVVPFESPAGEIIVENPSDLHELPAC
GWRVGSSEDHRQAFYTLYILVTRGEKMTPSLLIQESLLIDSEPQEVMHEITAVPDAPQIA
KVTVRGFGPAPARSASPTKRYTSDRLLAIVNITKSTYERNGFVEIKKEELRALVRQMHPH
ELQLLREEELLTRPNSNLTTAAAAFQGTVELASLEQPGEQQGWGLTDVAKGAVRGAAAVV
LAPVSVGKVVGNAVLDASGVTGAIKQQKEVLFRKSFPNLSSEEIIETFSCALVDDGNPIP
KQGFVFITPRWLCFQAGLLSANFSLEWDEIRDIQKQRTVKVLENAIAIQTHLGGTYFLTS
FVQRDQAYADMMKQWLRR*
>TCRU_3624 hypothetical protein, conserved
MSDHTVYPKPLVVTEERLKEAREKQLRQQALKEALEEQIAQTRRRRIDHHAPNKKNNVMK
EDGVRRQYTFTYEDGHGRFIQRDNSPEPREQPTRTITGTSTVDMTSDNATALSIISGHRK
PLEPVPSKNSQSNSLPPNFSMSTSEANPLVPKRTEHSGQPLPVDSGSSSRKQNGGMNNIS
PRVRDLFPQGASPKSGLRSAELVDEGGCQKNCIPRNFNLEDVKRLLQGPQASPRPAQPPA
GGGRSPFPLRNIPQKHHTGHLPPLDPLEGANGRQRSEEPSTGVDLAFSPPHDFLGAHPPN
VKSPRLLKLKQLSTPRRLSNEGRGRPTVNALAPRNGQARVTENTVERLQKELESRDVQMA
KMREKEKNWEEQVKQLKIELKSAKKKERDLNRLVKEGPRRAETAPDQPFLSPPTLSAPGL
PAKKGFGAPSPPGQGKKQKFARSRVFNQQTFRPISAPSDAASSSYVPQEENVASLMQESF
KCASVLTRKTAFGLPEENANRPVPIEYEHLLQFVKEQIITQQQADALWRLFSNEEPPLTL
LRRQSTVAQPSDTTVITNTDNYLVLENGIENSIYNASDAKRKEKIFNEEIDRKELVCSNG
HGHEELELEGDTFETFAELHLEESFSQEEAGDE*
>TCRU_3625 hypothetical protein, conserved
MIVNNDERSIDFSQNPSGELDDEVLTSLRDALQGNDNYCKLVFDNNRLNDDAIGILAAIL
KGSTPIEHLSLSSCQFRDVDFTHIANALCVKKVLRHLDLSKNPEITSAAAADLSRVIRTL
PSLRTLLLIGTGLQPKNCSNILAALKQSPSLKVVELPYTVGFKVLDSFRKLLEERNGDEL

EDSQKKKKKKAAKSEAAPTDSGDGAFCCSKCDTWKATSMPKLVLPPIHASQTAGQKPLSN
SCGPSNSLRMMEFRCWADPAVKNAAVHLHVLDKRCHLWEVYQKEKKEKILARRGVDEKNR
AVKVRSRYGGYDACPNL*
>TCRU_3626 SH3 domain protein, conserved
MRYFRVLHNFDAQDGVELTVKKGETVFTAESEVREGWIKVEVLHDPRRRGFVPFNYLRET
TESLSREQEEGSRGIGRELGGMSTAPMTRQPSAVPRETSVTFTSGALDYGDRLQNMYGVG
ASAPSPVSQRSRSAEQGMRRVNENSMTTATKGAVMESLLPSQKVPSSPPSGADPVPERSL
LNNPSAIVEAFMKNELHFKQLIRQRQDALAQMRTTVEEAMSELAACKEKNFTLARKLREL
DQSVEKERGRWKERIMEEKAYISRSMSSE*
>TCRU_3627 hypothetical protein
MTELLEGKCACMEEFAASAIPTVLLLWRGRRDDAAVAHGSHLDVVHQSILLYLLRTLDGM
CGSDVKCVEQTESALKLRLLLWISFKALYLEPPGGGHEFPGEWRSEVLRDSKAAERILAS
DIFLGNGGAVHCQKVEVLSWLVVEVLLQYRCYWEHVDMWGSVEGCRTHPFILWAVGNLSE
VGTEGAHPWTLSCVQQRAVEMIVLLGADAVLLERNRELFTDAYLRTLVAAGREIFTPELF
GGLTSSIRDGLIRGDRLYHDDLCVLLETLRRHVSVDTDEGRVRDLRTVIDVLLNTACPFS
CEKEIMRGVEAVCAWFELLGLQEDYRHVLTEGAIDGEVLRSGLSLHEVQQMGIRNEMDAA
SLLRVLAARPNRRVMPGDSRM*
>TCRU_3628 hypothetical protein
MENVSDNHMNGGKGDDSLEDLYACDSLFDESGSEDDLFLAANVEEQLLMPFSCFTEKDLL
SVFNVSAPYGDPVRLHPEEEPPKETRLEGPGVLRGVRIPSPKKKRETCTHRKNKSSTEKN
TRPAGKRKEKPSNTSSNQTRRLRTKGFIKALTPDDLKDDEDYKR*
>TCRU_3629 hypothetical protein, conserved
MMSQSLNALRSGTACFPTTIAQQRRWITRLYTSYYPGVLYPNQLVQHKQRLPPGVSLSTA
LKARTQTRQEQSVAGREVPEEKETRGVSWTDASSTDVMHTGNARRQEKVSVATGRSYVPL
GEVAKLELQGDYCMEGGLFQEALERYGVVAKAYSIAYPENHSQRIGILLKLASAFRHVGR
LDSSKVNIENALKMLDASSRPSLELICEALLELGLTREAKSMKKEGAEAYEEAVEVLNLF
HNWGESHRMLRLLPRLGRRFNLNFEEKFVYFSPFDYDRTFAIADQCMERAEKVYRETGDS
NGIIRVLQCRKEMIDKKFFNLRDFAGRIHTMRGHWMRRAQHLTNAPTPDELLRYTPTIHQ
VYRDFKYELTAPIGREKEVMPGVNRVVLDMGNPYRRRGRLSNKMLRDADHNFANYVRREE
YNA*
>TCRU_3630 hypothetical protein, conserved
MSNTVPPHYVRLRRQNLTIFLHCDVNHDTVQAIKERYEKLTGRLFYTVRLYLGRQSLDDF
STLYNCGIEHEGAELIVVHSKALKTDGTGEYIWEDLEEATQLPQPSREEAKETKEGETSL
GSREGGETAGEGGSASLLTRPEEKSHMSFEPNVGFVGV*
>TCRU_3631 hypothetical protein, conserved
MHRHILCEALLHAQYGRRDAPCIADFPTDVSRKEVEEVYLPFLTSEEAQLRQNLILGDVE
IIGYDSGSLLAVAGDAIAAGLVLSDMLSEVPASTVFPTSVGPHSSAR*
>TCRU_3632 replication factor C, subunit 2, putative
MACISVAKKPRIESKPNATPWVEKYRPMTLSEVKSQEEAVCALRASLQSSASMPHFLFHG
PPGTGKTTAILAVARELFGPDYVHSRVREMNASDDRGIQVIREKVKVFAQTAVGNVGHKV
QSDGQVYPVPQFKLIILDEADALLPDAQAALRRMMEDFSDVTRFCILCNYVSRIIDPIAS
RCAKYRFKPLVRETLYDRIREIAKMEEITVSDASLEALDRVSGGDLRSAIMYLQYAQKAH
GSDLTKENFLEVSGSVPMELLEKYLKALVTKDFDGMYSLTKEIVGQGFPASQLLSQLHQY
IVGSSCPLNSLVRSRIALKLCDVERRLSDGGDEFLQLLDLGTTICSL*
>TCRU_3633 RNA-binding protein, putative
MSSKPSDENGVQFNTEMDPEAELQEMQRQVSDLQEDLRLKTLQETAAQDEGHRKSTGFVA
TKNTSIFVGGLDPRTTEGELRVFFSSCGTIKRLTMLRDKFTGQLKGNAYIEFEAPEQAAA
GILKDGQSLHGKPLNVAMKRDNIPAFQRGRGSSGFSRGGYRGGGPGAMQQQMAMAATMMA
ASMMGGAGGGFNPFGGMARGRGRGRGRGGVH*
>TCRU_3634 leucyl/phenylalanyl-tRNA protein transferase, putative
MGLHWRAGENYLDVLSLSPFTIHGCQPADAEGSFLSEQKFPLHARFQESSGEYMATLWAL
DTGRAYLVGVGPSTEESSTRDTNLESCLGVGRNGVDAPVKFFIVKTCINRGPLAFLAANT
ILDVRLLYRDDFLDCLLSQRSSWMLIEHFGWENTTLLQHLFYHSLFAIPDAIREAPVYTL
PNGSKGRFCLDLKQENIAWRKSKKVRRIMLCDLFAVAVNRDIRDSLCLAREYHLEKKGNT

WLKESYIDLLVDLAACPEYGVKIMSVELLEKSSGNVLAGCLGFSLGCVHHDFTMFTMQRS
PEGFGTFATKLLGEALQQCGYNLWYWGFRLKYMEQFEGKYGGKIICKADFFARWAQNRDV
QPNCTLEEFFRSGRGMLPYFVSAE*
>TCRU_3635 Hsp70 protein, putative
MIRDSESHAESDRLKRELVEVRNNAETQANTAERQLTEWKYVSDAEKENVRTLLAELRKS
MENPNVTKDELSAATDKLQKAVMECGRTEYQQAAAANSSSSSGNTDSSQGEQQQQGDQKK
Q*
>TCRU_3636 Hsp70 protein, putative
MAADNQMMGQFDLVGIPPAPRGVPQIEVTFDIDANGICHVTAKDKATGKTQNITITASGG
LSKEQIERMIRDSESHAESDRLKRELVEVRNNAETQANTAERQLTEWKYVSDAEKENVRT
LLAELRKSMENPNVTKDELSAATDKLQKAVMECGRTEYQQAAAANSSSSSGNTDSSQGEQ
QQQGDQQKQ*
>TCRU_3637 valosin-containing protein homolog, putative
MGPKKARYKPPIRPNADGTGFVRESAGKMEETPTRERGREGHPGLGAVRLSLDLSTPPCM
GPSDVSGAALSLQIRSNNSLPSNEARLSPSSFRALGIVSGAVLHIVAGNSKAYAEAFISS
SCHAQTIELANEVAAALADKQANVSVMKQPLPSAPLDLVVLEIAFDPPEETAAMQLEGSV
KLPFLQVRSAFRRQYRNRLVYRGMRAIVRVATQPFCVEVVQCVQFGADVKDQRKKKQIQA
MLGFLLDCTVIRDGGCEIHIENESSENSQDLLKGTCNLQHVLVLGESGTGKSRFLQQEGR
DAATLKCRHVETILVQELPQGEMSDVSTATVLREAFARSKVAAPSTVLIDDLHLICGTKG
SSTAGSLWAATVVAATLKEELDDIWGRRLDVCVIASATSTESLDRSLLTPERFGKRVTLL
TPGSAEERYVCLKTCLKERDALDSVSEETLLTVSQEAHGFTQCDLARLVEVAMVENFKMT
GNVAVSDEALLAAAKLVRPSALKQFEVSVPNVTWNDIGGSEDAKKTLQDCVAWCLGKQQW
IFRKFKLSPPQGVLLYGPPGCSKTMLAKALANESKMNFISVKGPEVFSKWVGDSEKAVRD
IFTRARAVAPCVIFIDELDGMCAHRGSGGVSDRVISQFLTELDGLPAALNEKSDALVFVA
ATNRPDNIDTAVLRPGRIDRKVYVGLPDVSERRAIVSIHFARIPVATDLDADYVANRTEG
YSGAEVVAVVKEAAFLRVTMDAKAAHITREDVDAALQKVRPRISPSDVAWYKRWSMGRSL
ALR*
>TCRU_3638 E3 ubiquitin-protein ligase, putative
MSYVEEEYYESEEYAVDYEGNGGEWALVSPAEALRRPVGARAEAWLFTTLSISEVLGDLQ
RDVEKVNEILGLTPEAALLVLRHYGWKMNDATLEKYFNEMDKVNSELRITEAAFHSGGAG
AELIRGDQPIECPICGDDVPAGESVALGNCRHFLCVNCLRTNLLCAVKHGHDLLDKRCPI
RGCHSLVGLNLFKELLPAREYGQVQRRFLNDYFISNRHMCCCPNEATCEGVICVKAIRES
SLEVQCHVCKLKFCFNCLCAPHAPATCDMMQRWERMVQENEPSLALIQHMTKGCPNCAVR
VEKNMGCNHMTCVRCHHEYCWVCLGPWSEHNAGYYNCNKRSRSDKKIGKDFFLDCFERWD
NHKRSIALEAKSLEECSKKVRKLTQHHKDTSTLDRTLSVLFNTQRVLHDCRVVLMNAYIA
LFFSEKTGTSLHYRIHQLELRTEETSRVIGVSPELIHADEIECQSHQALHWCNVLRGDGF
D*
>TCRU_3639 kinetoplastid kinetochore protein 15
MAENDGTICRFEVQGRISSMAYGDATNACLVSTIMNGTHIFNMDSSCGAPTRYVAQLESF
PHQIIGGDPIISSCFLSSDSSLAVGSSVGGIAVVSRSSRSVVRCYNFQDEAPVLSLKEVP
HEPSLLLSASPVGVQAIDVERSVVRLSLAVPKPRVVGAVAITRNSFAVANYDGKVMLYDV
RCGIDPVTVLSVPDQITSIAVSPDTRALVAGTVGGRVFVMRCLVSKLREEAFGTGKTRSP
VRCVAMHHGRIAAGDISAKITLLDSGDCPAPTMYWTAHSLLPHVVATSSWGVSSVLLRKD
SLWGAFTSPESAASHVVMLPP*
>TCRU_3640 heat shock 70 kDa protein, putative
MFARRLCGAGSLAAASLARWQSSKVTGDVIGIDLGTTYSCVAVMEGDKPRVLENTEGFRT
TPSVVAFKGQEKLVGLAAKRQAITNPQSTFFAVKRLIGRRFEDSNIQHDIKNVPYKIVRS
SNGDAWVQDANGKQYSPSQVGAFVLEKMKETAENFLGRKVSNAVVTCPAYFNDAQRQATK
DAGTIAGLNVIRVVNEPTAAALAYGLDKTKDSMIAVYDLGGGTFDISVLEIAGGVFEVKA
TNGDTHLGGEDFDLCLSDYILTEFKKSTGIDLSNERMALQRIREAAEKAKCELSTTMETE
VNLPFITANQDGAQHVQMTVSRSKFESLAEKLVQRSLGPCKQCIKDAAVDLKEISEVVLV
GGMTRMPKVIEAVKQFFGRDPFRGVNPDEAVALGAATLGGVLRGDVKGLVLLDVTPLSLG
IETLGGVFTRMIPKNTTIPTKKSQTFSTAADNQTQVGIKVFQGEREMAADNQMMGQFDLV
GIPPAPRGVPQIEVTFDIDANGICHVTAKDKATGKTQNITITASGGLSKEQIERMIRDSE

SHAESDRLKRELVEVRNNAETQANTAERQLTEWKYVSDAEKENVRTLLAELRKSMENPNV
TKDELSAATDKLQKAVMECGRTEYQQAAAANSSSSSGNTDSSQGEQQQQGDQQKQ*
>TCRU_3641 chaperone protein DNAj, putative
MRRSLRILALDPFAVLGLSRSSTKAEIKTRFRELARLHHPDAPAGNSEKMEQVNKAYNML
IKEGAYERMRMKSSGVKARADVRRPSPFSQESERQPQQREEKETPYEALSEEEVAKLSAL
DPTTERVTPTGTYMYQSRDDGSWTELDRPLVRAHQPRYASYAAQADMSEELRRRSIEKEK
EENSKSILQRVADRMSDSADLPSRNPAALRFYFILAFVVLYFTYQRTFAWGKHRSIRADF
YSSVEQKREELLEVYKENRDALETSVAAAAIVFLVASQRKQETDPVVPPTPEKHFREIRP
PREHFYVISGG*
>TCRU_3642 hypothetical protein, conserved
MQKPPPADPSWSDEEELDRNGSGRDSSSDESEWGTVTRDFRINGILEDEEGGGLLGGDDE
KQLYLPEPVVSLTTTPKPELPRLSTENLPTGCHVWVVDEDDVHLLLREHWDDSYRAVCNG
RLCGTVVRHSVNVTLVSFYDEHLEMNYGLSLPRICLSNVPVESYNRSPGGSNRLIQSCFG
LGNLDPRAVRFREDAAAPKVNRQFYESLSVMEVQVPQSLPQLAAVQKSLSEGAYEEALKL
LDKLPLNAVNRVDILVLRSRANIFLGRYEEALKDALEAIEEEPRWVKGNLAAARAFSGLC
KFEKAAQQIHRAMLLLPHSHELHKIGELNSFMLSLQMGLPRNDLDLFLDSQYDKRLVSSR
RFKKDEIVYKGDQVIFAMESIFSTPSGRCCVCLKTEGKMMRVPVDLDGNSSEELACYCSV
ECQQRSSLFFVMELGRHRVAVERARDLISCTLPQRVNQVSLDLTYMATRLFLMICVTHDR
LLSIRRSQRRLNDVTNSNASGEESDQSAASDKTEFLPLQAALKHLGVYPLPTDQLSPSAR
DKMYVLYNTLTAFFSDKDKQTYSSALFYALCEYVRTFAVAVKVREAESMLYYLPKVMGAI
RHVEASEANCTVVINENGTDLALVASRDILPNEMLSVPDWNAHNTS*
>TCRU_3643 hypothetical protein, conserved
MAEAVSCLDVKSFFIVSLPRKVRHLFRCRVEDGTLVELTRLPMGYKASPETLQIIISAIA
GLTTVVRPLWAAPPLVRVDVWIDNIRIAGLKSNAILWEAQVLRDAAGRHATMGEGRESDA
AKYTFLGVRFDHTHRAVSLSERCARSVCAMPALNSSTIAEMQVVASCFLYAAAISCTRLC
QYYFFIKAVRRRLSALNRGIVLETSPANLPPSAVGLGERLRHMIENIIVSETSSPRKRHW
LPSSRTHRSMDGEPFLFSRLRRR*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MLLAKGNVHDGVSREMLYAAGAVTAAGSTLSFVRNRALLPRMLSLSLSLAAGAHLRVACN
DAGGRVLSTAEEYAAAGFGDAGSIDVVGCDDCDRDTHCYAPGTASASMRNGVCVCACGSG
GYGEACVPVGAPALPPAVGTASSVFVREGVTVRSVFVVPAGASEVTLRHVVLDGVSPVLY
VPWMARDGVRIVVQNVSLLNGAVLYVMGGGALRGAVAAGSDEGGPVELSVCDVEALNGAL
VLTGTFPAGSVLTVTDSLLVAARPTPLVYLPGSQSSPYAPVLVLSGLRLVRSVLVVSGVA
LVTVMTGGRTVVVDGAVLELVGGGVALDAAVFGGEYALYASARVVASGGAVLRVSGSQVY
AAHGLVFDSGVEANASAVVVNDNAGALTDGALLVLRGSASFVSGSWLSVRGNSISGRLLS
VPSYPRSAELVQSTLTLHGNAGSGPVVMDGTVALGGAGRKFVVGCLTLNGQALRPMDYRS
AGIIGEFRPVACGVCDADVRCFAAATRAMSGSCGCRCAEGGYGRDCLPVYLPHVDGCNRT
PAMPPLSHTATLTETRSPTPTSTPSLSATHYSPTQYGPTEILQVTETVALPPTRTPTASV
SSTLWWSDVACPTLAVTTTAAGGSLTQNDIRGGGSAVPTRLMVALPPPFRWARDPQLGTH
LSFVPVSTAQPRGFGGPWGAMLSNATWVRNATNPSTVLELAVPVHRGYFIAADETIVIRC
DAAAVSGGCKGVLLGSFTIRSDTLPAAASALSAITGVVAGAAAVAVVVTGGLGSILEMQA
LGVFARMSCASAQERASTVALPYFLSVFAALDPLWMVVGNALLAAVFGCVHYGVTAAFQR
WRGVDAASAWAAMRFPSLTYVVAHAMHLGIFFGSVLALAMPGARVQHRVIGVVGVLYGVA
FPAGVCYLIARHAGASFTRYWQFSRKPLHERLLYPVGYWHPAAQQRMYGGMLTNMRGSHV
YWCVFQLSVLCVVCLIAAVHPPVGGCHVQYFCMAAVLLAGAGVVAFTNMMRSAFLTVMHT
ASFVLLAALCVVSAANHLAPSDGGARAYAAIVLLLTTVVLAVTVYGVVVWYAEDRHWQKL
REPRRGGLEALLRDDEGSDEDTQKPHDMTSLSCASGTTVASSYRPPAMPLQPMAGDTYAL
LEGPRLCCAPQPAVVNGTYSVVGRCFYRCVSILSGLFQEFFPFRDDYVEGDCTVALVAPV
VVLYRTVISWSCVRGTQRSFYAMEEGSSESPSGSNELQLCLTVDLHAGGVTALRSKAAPE
*
>TCRU_3645 hypothetical protein, conserved
MNGLAISKDSAVVLSGNVFQSVAASSSAIYVVISSLRVSWHSLFAVMGNTFHMAGGDSTL
IHLEGSRRSSSLKVLNNSAVVIRGNIVSRPVKYFLLLILALRVESHSAFVFQGNDMQGSS

VAFFPGFSSYIYYNSWLQVSGNLCRESPSEAFAFFYSTVNLRDSTVSVSGNQFISRTGTP
TVLPW*
>TCRU_3646 hypothetical protein, conserved
MARGRRHVLRPANRRTQRRVRQQHTRVQRHRAMQHDRALQRRHIHHVDESVGHQARRALA
EATNPQLRAANKHAVAQRHVQRVSEHVHRAQVHRHSDRPAEHQRVEARRRTPAANRHGLR
QRHATHAVLRTAATTAGPRRRHVERQARLAHTVVAAAAHAVGERRRQRIEARQRSRTAVA
RHHAHGGQAGHAVVAAALQHPAAGTVALHRHGAARDRQPGDKRRAGGSAARNRHGAAAQR
HTRQRRHRRRLAHRPHVVQVQPPAGTDRPTVAAHQRRRNRPLDAHEAQHRIKHREALSKH
NAAAAAHNRHVRHGEHRVAPQTETRRGRHMHRGRGRTARRLQQHAVKHHRARQQVHAAAN
VHRRPARLQRPQHSVAHTQLRPQQRRRVQHKRRRHRVRQPAQLRVAHRPRRHNRRVTDRH
VRVCRQVVHKHKRAVAPGQPAHAHLQAPVTRRLAAVAPHVDLRSTVAHAVPQFDAQRAGK
HRRHVEHHSHAVRHVHAVHQHRVHGAANRDGSVHRAAPQSHHHRMHCGHPYRQRNQCQHN
EQRHTHSQNDHAPHTVPAARTRAHNRPHPQTQTDINRAVVACRSRPVDHNFRLINAFLQM
ANQETLFR*
>TCRU_3647 RNase H, putative
MPPSMHGKAATSILPPRDAVVNGLERVCNIIGIPHSHNRAPLIQHRIFPWDTVSCNKVEF
NQPRFAQDASDDVKRTALDFIYSSLGDFDFELWTDVSSSLAELASGSAALLYGSTTTNDL
PVEVHRAAAGRLACSYRAECLATENGIRNLIPFCLETSQSPTRILVATDSPSRTEALRVV
PLAMRDYVTEESWIMLLSLIQRGHYVDVMFSLSHCGIPRNEAADEQAMIARSLPQEDSPI
WHVDFFTAVG*
>TCRU_3648 mRNA export factor MEX67
MSAPYKKKNTQNVPCIYFKRGACTNQRCPYLHVRGKELGENADAAPIGNGSTDAATNLLS
TMLKLVFEKQQHRVYDASSGMLDLSELRKFPDLKDVSNSINFNTQSFCRALCSSIKSLIV
PPPSAMQLKGNDITSFFHFASQMENAGLHLSLRALSLEANDIKTMEALQGIKKFSNLQEL
VLVGNAVARRDDYRAEVKKAMPFLLGLDGEAIMAPPLLLPWPRFTNSDYTDAQQHVLQFV
QCSLLNPLQAGDAAGVPQGVDAVSDFYAQKAILSISLSSPEAAVSTPARTVKSSPVGGTQ
RNVVREIVSFRLKQTESNHNLLHGVKSSVVACGRTKVCSQLEHWLYPKNFLVEHFVHSSA
SASFLDNTYLSGPSPAIMKVPVTVVTLHGVMAWTHLSPQNQSSNDRVVIYRNFSRVISVQ
QNDAGRWLITNDMVSLYPFPGDAASPSTKGDANASTQISLSECRILFSPREDRSRAEVLG
RKKNVPLEVVLALSQHVSNDAELITVLNDIGGVPLSMYEHCATLAGENILESIQVCRIGN
RFGLAPEEGLELLRRVGGNWCAVEEAMAAAVGVTPQAS*
>TCRU_3649 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MGAKLNDSDNTVLLGLSYNDNENKWILLCGGGENKEHSSHLETKKSEHVVILLRNGNHSS
AYVDGQPVGGDEKCKLNNTDSKGISHFFIGGDEGNAEGQEGVSVTVTNVLLYNRPWKSEE
IAGLAKNKVTISKSEGPKTSMDTQSSATSGSPVQGTVSLSNSARQLPSEQEPLKENIGGA
GGVSGAASVTTPSADANTPASNGEGKVEPAVKKEMSVNSAEDEETRGGTDGQKEEVQPQV
REVNATALNSSLGKLSQGNNSDAITIRGSGLLPSLLLLGLWGFAAL*
>TCRU_3650 hypothetical protein, conserved
MAMLMAGRVLLVCALCVLWCGAAVEAEGDGSGGSAEPLPESQEPEKSPEGTQDFGHEAGG
LKEELTPTSADEDDEDDDDGEGAEDEEEKQIEGPSGEKGNAAPDPVSGEKKLIGTEQQTR
QSIVSAEDIPLSGNRESNAILTQTKTEGTKDSDKNPPAVENPLTTVNREQTLHAEGNLPP
PPEVDDSREHDGKDTTSEDKKNVQPPETAATPKSHRDKGSEGTGDDTKATTVTANTTDTT
NTQKSDSSTAVSHTTSPLLLLLVVACAAAAVVAA*
>TCRU_3651 retrotransposon hot spot protein, RHS3, putative
MKQSNFVFFVLSFWNYVPPYIIEKCDVSAFLNEDFLRAIRINIKELRPPGRREPRSCALK
EHSDKSFTRKEVLPPPERLSNPVAMDHWVLYEPKGKSVPLVDGFFFVESNPSIMVGLRIA
TAGGHHTTASTVRPFTECLAAYFNGWEELFRDMSWEIIYVQHADE*
>TCRU_3652 hypothetical protein, conserved
MSRHLFYSAVLVLFVLVCCGSGAAHAVGSVSWCVRLLQCAEIFVLQETPVKPKDGSESKV
KDSFASPSLVSAGGVMAVLAEGTLARCPTKQVYPADFVAGYANPAWGLSSIVAEAIKDTQ
RAHTVLSTVNETGRVGVARQPTATAKDKRAFPLVGIHE*
>TCRU_3653 hypothetical protein, conserved
MSISQSDDSGNLNGGNSKLNRLKNCLLANDSNGAIHRSEVRSALCSGKDMRTNSPFITTA

KSLRDDKGGKDFSLDATSEKCDLESALKNYQEDSEKLGKQLLTLKKELEAEVSSKRVMEE
KLSMLESIVATQRKEILLLQRKVQSGVSELSEKRLESALREIAFLKSKLGGVGETENSSQ
GDVFLQLQSNLNKLVAEKDELLNCVRKQSMLLDVLERQKLHLEAAILIDISEKELERYFD
VARP*
>TCRU_3654 hypothetical protein, conserved
MACITGDDTGLVKVWNISRSTGATLAFSYGEQSRKRGIAGMCWLDSSMTKVVFSMNDGIV
SVLDLEERSLLLSKKLGFVAGLPNSLIFLKENFVMASKDGKVLIADASFEEKKIFECNGP
VEAFHIHRKFGMFSMGGKDNALCVYDVSAQEVSVPVFRAKNMRDHVLDVPYPVYVTGTCI
INPFVFCTTTAYHQVCFYDRRSSERPVQEYEINREIDRRPTTLMQWNCNKFLIGEASGDI
HLYDTRRGFASRAKLRGGVGSVRSMAKHPAGHQLLGVAGLDRKARIYHVPTGRLLLTMYA
KQKVSSILFDRQLPLADNTGAFSGIANNKQPSKSAVLGDEIWDSMDPVVDDITEVFPLGQ
NDNGNN*
>TCRU_3655 hypothetical protein, conserved
MASCRTGRLPMPDDPLFNPIHMGGLRSSARIAGVGLLAVIWIMYQKLYHSHHYITYKGPD
NPFARIRHRRYPGGGFLFGWGNNGLNRDCGLKEWECWAGYTGKEYTY*
>TCRU_(PEX11), putative Peroxisomal biogenesis factor .1
MQNDTLRVLGSNPFENITAKTRLRQLLQTHQGRDKLFKVVQYFLRIKLWMDSVSYNQNYL
PGAEFTAVERNLMTIVNTRRLFRVGRFVGEFVRMRLTLIKCSELVYIPVHGGQWIALFIQ
CQMICDMFARALMCVKSLCEDVAFLTQKGFFNSQVADQLISVSIRCALPVFLIDLFLNTL
RLLQGIRDASQKPAKKELLLSMETFSLLSRYDHVDKLRRRMSKSNPLGKGKVDDDEEEDE
EEEVQMLEVGEENEIIVNSYQELLWKDFELHWIFVTELKLLLDLFVALSNLNQWKGVGGL
VSIGGLFSGLLSVYRVWTYGR*
>TCRU_3657 hypothetical protein, conserved
MAMSAGKAQRLPKVAPLSSMAYGKRNEGDWKSTLKLFVEEVSRLKEETDALKSTRNDIEA
SWQKAVEKMKILTDENCLSQHALESLLDEERKKSLAVVKEKEDLLVKLKCADEKCAAKEK
EVRRLADMVETEKIRHSVSVALHEKTMEKKESQYRAELHLQEKRLEEMQHELHQQLKRQE
SELLAKDILLEKERKRWRNWHEGYENENSSDMPQIKGASCACRLSPEATMNFADISSSTP
FMAHVPFSVPPDDDDARNVSKKSRLEAARQQLRRINGKSKEDVTLISLSKLNHLQEHFRH
*
>TCRU_3658 N-acetyl-D-glucosaminylphosphatidylinositol de-N-
acetylase
MSVFFAVTFLALILAVLLQWQRRSAALRPRILGDVLLVFAHPDDEAMFFSPMLEHLKRYD
VKVHFLCLSNGNYEGLGALREKELGLSAQFMGVHRNNVKIVNHPALQDGMNKMWDAGLIR
QEVLLYLQKARNVRTVVTFDQWGVSHHPNHIATHNGVSLVKENMPPGIVFLSLRTRSLLG
KYSGVLAAVQYITNFSLLGHQHRFVFLVPPISFLTSFLAMRLHRSQLVWFRYLFLAFSSY
TYVNELEELKAS*
>TCRU_3659 endonuclease III, putative
MKKHAFKPPPNWERLYVRVKELREGLDAPVDTLGCSKLFDKAALHETRRYHILLALMLSA
QTKDHVTAAAMHALIRIGCTPEVIAKMPEKTLDGFISKVGFHNKKAKHIKEATDAILKRH
QGRVPHSYEDLIALPGIGPKMAHLFLQEADGVVLGIGVDTHVHRISQRFLWVPSTVKTPE
DTRKALESWLPRKYWGEINGLLVGLGQTICTPRLPRCSECPASDLCPNAFKEAKRSGKRG
RVPDIEDVDTR*
>TCRU_3660 RNA helicase, putative
MGPNRQRKPRTTKTHRGRGGNRTPTSSTAAPSMLSRAGREMIIDVLHHAATGGAVPVPEK
HFDANAGIRITLQRNSPLTPYETLQRLYEGLGFPPDLTTQYVTDLQGASKIPAFTSITEL
LAEDGPYQSFLVNSCFELFSHMLFYSRGEVDVIMASEEEDAILENELETIQSLFDESFIG
VRQIDDKEFEGCEMYFSFSSGSGKRVVVCVRVPDQYPADPPLILVQPCGNQVGTLPILGV
FHADTKELPAALRRSILDAAVETINGLAGEGCLVALMSSLHGVIASLEVMPISTCNSGIK
EEERPGKEEKINLDAQRKAFVNALTATPGVNPTSTEDHHASYPMPVKIGLKTVGCVQDEG
DIVRREYLKTDKSLDAKLMAEWESLRTSGTMKKAREQLPAFQVREELREIISKHQVVVIG
GETGSGKTTQIPQYLYEFMCESGMGGSANIVCTQPRRLAATSVALRVAEERDEAVGGVVG
YTIRLESCVSRRTQITYCTTGIVLRRLQVEKFLGSVSHIVVDEIHERGVDTDFLLILLRD
LIQRRSDLKVVLMSATMDSELFARYFGGAPVISIQGRTYPVQHFHLEEIIPMVGYILEDG
SPYANREAKREERRRNNRKQAINIDPEEVDDAREMELSGQSLTGKLNAAPKTLETISRMN

LDVINYELIESVVFYIDTVMKVDGAVLIFLPGMAEIMRCMEQLKSNPRLSNSCLMYNLHS
SLGSSEQHGVFQRPPKGKRKVVIGTNIMETSITIDDAVFVIDSGKAKENRYDARKSLSQL
VTVNVSKANCRQRQGRAGRVREGFCFRLFTSAQFEALDDHQLCEMHRVPLEGLILQIYSL
NLGDEVEYLQKALSPPEERAVRGSVRALTTLGALTLDKRLTSLGQHLANLPLDVRIGKMI
IHGAILHCVDPVLTIAACLAVRSPFLSMMDYQAEVEGVRKAFAGEYMSDHLVSWFAYASW
VFMQYNEGSSAAKKLCARYYLSLPALKQIQSTKRQYERYLYEAGFIEEAPIHSSHERFLY
DPVITLEDRLYESGGRQFNANAGSVKCILSCVVAGLYPNIARVQTEAGKKGGAFLKLTTF
DGSEVMIHPSSVVGREKRFLSPLLVYVDKIKTSATFLRDVSVVTPLHVILFSGGGLEYLP
KYGELVVDDMVAFKCRGEDATLLKHLKDQLDSALSQKINNPSESWESTSSVVVRAILRLL
KDDLESVRHLTVVDHRQPRTSLTAPLAPPEEAVARERQDAKRRTQQRCFVCGEADHMARS
CPRQAASLKGGPSVRCFVCGAWHHPTECTLASRVS*
>TCRU_3661 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGGALLRMSRLLSVLLRMLVDVSRNHHNLRRHRQTSKAQ
KYHQQMFVCQCSRLPIHPWKEPMEMMSKKSNRQERVMKEFEHKNNTVNTIDKMTNMSGKE
RNADDPKSGKEGEAPGKDPATERGLQSTPEDGSPSHLPNDARRGNAQEPRNASPPGNDDR
RQDLLNVSQDAPVKFAPDTILSSSSTGGHGADNSHGNQREAKKAQQTSAGVKQHDAEFGE
KSAAPTKGEGESQLPVTADETKSNTTMPGISVSSSAATTAVRSEASTEGSRTISDLSPSS
SEDDARPKNTPNGDDASHITEDVVSLSAGTPMPQQTAAQTDATATPGDSDGSITVSHTTF
LLLLLLVACAAAGTAAVVAA*
>TCRU_3662 BNR repeat-like domain containing protein, putative
MVALCGSGRKVFESRDMGKTWTKAIGTLLGVWAKSKSGAPLEEGLRVGALITATIEGREV
MLYTQKVRHSMEASEPNALYLWVTDNNRTFHVGPLFLEDNVNETIANAMLYSDGALHLLQ
ERANEKGSAISLARLTEEPNTIQSVLSTWAQLDAFFSESSTPTAGLVGFLSNAASDHK*
>TCRU_3663 BNR repeat-like domain containing protein, putative
MSRRVFTSPVLLLLVAMMCCGSGAATAVGSKSGEVQLPQWVDIFLPNKTQVAEKNGCASG
VKSAFILPSLVRAGGVMIAVAEGRTKYNDTHKSGRLDSSDIVAGYINAAGTWPSIVAEIA
KTEWRAHTALGGLNGKDHMSLFYLPTALARNNKVFLIVGSYERTYNYDYETWVQDEWDIQ
LVVGEATQATDIQHSKPISWGEPAPLLSHIPQRIKDDLDQFAGSGGSGIVMGNGTPVFSL
MAANRTNHPFSMITYSTDNGKNWVFPEGMSPADFFYPRITE*
>TCRU_3664 retrotransposon hot spot protein, RHS3, putative
MLAAGRLLMKDCNVTMEVFAQKPDDYVQDQRPLEEILNLTAHQALEAITKPLHGGVLSLS
GNVGTMKEKDTITPLARGKPNGVLTQVLTEARREAEERLRGTQEMKFTISTNIEEVLFKG
RVCVNEKKLNDFLTREPDGGGIVDTNRDVMLEEFFKDPTRYIHDAEVLNEIRASGAYARM
EGTVREEMGLEEDVRRLHQEDVYFLEQWRDYEGKDTVTPLARRNLNSVLTQLLREESREA
EERAMREEQVESTLTTTIRGVLFKGRVRVMDIKLNDFLTMRFGGKGIAATNRDVLLEEFF
KDPTKYIRDKGALNEMQASGHYLGMKRAVKGEVIFDEDIRRLCDKGVNNLPGWSLAAAKV
KAAVHNSTKHFLDAAAEEARNPTTTSAPEKLEGCYESVHNARWSHAVELPDCVERTKTGT
GMGCMRGGQNSHGRTGKLTTLSKRMMLCSNSVRHLPC*
>TCRU_3665 hypothetical protein, conserved
MTMGASRTAKLLGMDLDPQLTLNLAAASQRISQPRRIAHKEAGPSPHDPRTFIIGYGASK
LRYGSELIWAVATDSAKNETQETYAGLARIVSGVPSTVDQ*
>TCRU_3666 hypothetical protein, conserved
MCSQYGPLRNSSQRGRPIAVSVANSCLRVATTQKFSKPPSAVHPRNIGRQATEDSMSNEL
KGLAGVYQHQRSPMGSAVELASSTALLGKVRLEVIGSVMLHFVYQMCQLHRRGTHTTARM
LVRTRRPQPKQSPQCHFLSNLTHDGGKADGSI*
>TCRU_3667 fatty acid desaturase, putative
MAKSSNAFFEQLFEPQGRGDYYWSKNPQPHEMRRKLMLKKYGRQIKELYGPDPWIWRLMT
PFIFLQLYLGIRASEMSWPIYLFLAYFVGGTISHSTFLAIHEATHNLAFKTREYNDYYAI
FLNLIVPIPYAMMFKSYHAEHHRYLGWELVDADVPTLLEAKLLSSYMGKFLFLTFQVFFY
ALRPCMIRKIELEKRHFINYIVQIVFDIIVYKFFGPGPLMYYLFSTFLGTSWHPTAGHFI
SEHYVFRGEGRQETFSYYGPLNWLTWMAGYHVEHHDFPNIPWTRISRLHKIAPEFYDDLF
VTESWPGALYDFLVDTNVNQCSRVLREKGAFQRANLLPNVTEDASVG*
>TCRU_3668 cytochrome oxidase subunit V
MKRFASISLVAVSTCRHFFGKGWDNASLDTIYSCMLRKPEVNDRVRSQYASTMDPRDADV

LRRLGEVAKENKTFIRVFLPPHLGDPHRLLKCYSLMAYPILDDKGGQLKVEMDGHHLDAF
ADPDDDYAKVVIPHIELVEYLAKSLLETMKWEATPRGAASLLESLYRGADIPDHVFQTPA
VIERIDEFKDGNKVTQ*
>TCRU_3669 protein kinase, putative
MLPHPILATEDDRDYIERSILSMQEHVENFFALLELVYLESKSEQTPRAHALFHSIQSTL
KVLGTVPSSSYRKNDSKLTVDEELPKGLERMRRLFFDVVTVGPESLVWKKPVTRLAQEAA
QHAKNIQIKFPSSSTLVRKGVSRNSFCFLLLILIFVSALILALVTMVVIPFIGPSPSVAA
AVGILSAVFLVGSGSCIIFCFVMAVRALQELFDRLLGERMHANLIYQPSSGLSDEASPCN
TTTNQLRVKRGRDTRRGYYAIPYGDCVGYIEGKHVDAHVVMIGFDSNYLITRWNMAAEVM
TGFLESGCIGKPLSDLLITPSGDVPHDLSTLQASKGDVLKVKLRAFATAPVTLCTIAAPI
LNLSGKTIGSILICANAKDNLGVFRSYIRDYLTSEVSVSLSELIEKNAVDTRGKAAISSL
QSFLSCALDKQVQEMAREMLTEWEWTTAEQLLAQALRSFAVRHEKQIDSMFPATLCLHPN
VPKAISTLLDTIGVSCMVKLEVLSQTVNVFALAVTITPHCEESELCLNEEELQDAIMPLI
RSICGNMCKDGKDINLRFPCQVTAFLEDGEDAFKAIEKRGEQSIIDQTRAIVNCTVNVLA
LITDLVDQHNLSMILLKTMFVSLTTVRQRDDLERRLKAAPNDVDVIICDRGWLNSARDLI
ISSDHSAIVVPMADQGVFFAPEEFQYVIRSPISGNEVRKVLMDIGTAVSLRKNAATAREE
RERILTLRQDSPWTKGKLLGRGSFGAVYEAMSDLTGGKMAVKMFYFSADCDESINKLLNE
IRIMCSLNHPNIVHYFHCERKENNINLFMELCDASLGEIIIGRKPVPPTLTVVQILRQVL
TALTYLHTRGVAHRDVKPQNILLKGDTIKITDFGTAREGKASKDVQGTLRYMAPEVYRGE
AHSSPCDIWSVGCLACELFACPPKFMDNSLILAEMTSAVPYLENVTSSVTLNDFLRKCFQ
DDPEKRPTAADLLLHSIFSPEFSYEVESLLTVFKKKLMRNYSFSITSQK*
>TCRU_3670 hypothetical protein, conserved
MPSPHSLNSVQVFLGNLPVESVREDLEVEDVPQNDEGLRLMAADANWSGVLLLAERLGAE
ADADTIQGLACKLRYTLVQVTAYFSMQRYAAAKKLVDAVGDLNSDRFTDPVTKESIVPFS
LRFISALLPSYCGSAVETQCRLYVLLEECQKHAGVAVSPLRKARVKRIQRALVVSYYQTE
KYADAIRLSEEMIAAERYDDGDYEGADFRVLKQMLQLQQLATLCLHCGNIFLAEDVFRAI
DGLSTADESDDVQNFHRFLTTINRALWLTFNDRAGEASQIFREVARGTSEFCRIPNAAEK
SSSVVPTVSSQRQTSTAPLSAAKTQSTLCHKAFHQLWVSAATSHLSCIPYEATLNKNPTT
LMASLIDTMEGYLRQNPVELLHSDAFLGNSVRLYTLEGGAHRKKLDLLADMLEVFRCERG
CIPSLENMV*
>TCRU_subunit 2, putative Biogenesis of lysosome-related organelles complex.1
MRQPSDTEEPLEPKGSFNSDCISEPGSAPSVSVVNKGAEALDQLRRAHAAMQQYMTAEME
AYAEDWKLLGKCNELMESRCQEVRASAKDAVKELETTAGLMEHSLSQLASIDRIEAQLAT
LTEAVNRIDEYSKALADRFKCT*
>TCRU_3672 hypothetical protein, conserved
MVFSSAGDAEQPLFVRPFNCTSSHWAAPVVDPCGRGHVKSSALCIEESVRKRFEPWELGL
IKHNALQEYNLLKNASERRDLEREESIAREEIVNDATSLLAAVIEWRVEAGEEVMSDRAL
SRLLERLRKRATTQQRQYEINEDALREEGRMGWRREVEEKARSKQREEAMARWRRECEDS
LRAAAAFLMGMERRERRDEVAEEEAAWAALCTEEVNARAEAERIAYENFMNSPEQVALRK
EQERIEAAAQAAAARQLKKFLREQEHLVKSCRHARGAGSVFETLPSRNLCVSCGVKFDET
VGYYVRMRGSTLVPPETWSPPKDTSLAQRNSRSSIAKLPPITQQTKQQGRKSLTGAALDG
STRVSRVSAVKKA*
>TCRU_3673 hypothetical protein, conserved
MEGTSQLCGLFGDDREITTRSGSCASGDAADYGDGGGDGGNGSDVGAAAVVVDSTASSTR
KQASLNSFEQRHMDDDDTMTKRHCYYDCDPEKTTDRPALSYNIWPEVKTVTVMVPTMFTT
AGGRQICVREKRHIARGSPYWRLLFECPLHEGAALSSHTDEEEGLNKKKKDEKVEGGEES
GAAGPHRGLLPAWRRRPREANTYSTPSLATSLRGPRCRSSPLPPSDEHGINEDCGDTSFT
FSYSSFTRADGSMIYLSRAPT*
>TCRU_3674 hypothetical protein, conserved
MDYNLEYSEEQREYLERVGMREYLETFVAEVVRQKPNDIYAFLHDWASAHCQKQTKMTPT
EASIKIQCAQRQNLAIKEMRSRQRKVNELLEQEETERVGKVEMEG*
>TCRU_3675 Cytokine-induced anti-apoptosis inhibitor 1, Fe-S biogenesis, putative

MSSKPTQAFSLKTRQAVDEDALLTEEDRVVKEATKGEDCTTRRRACKNCTCGRAELERKM
LAEGKKVEMPQMPAGGCGNCAKGDAFRCATCPFLGQPAFDNTSDGKVKLNLTDDI*
>TCRU_3676 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MKDGTLVFPVEDTKKDDAEEDGKTFSLVIYSSDTPSCTLSKGMSDDGCGDPSVVEWEDKL
MMMTACDGGRRVYESGDKGDSWTEALGTLSRVWGKKHKGKERGVRSGFTTAKIDGVEDNR
DVMLVTLPVYSKEEGNGEKGVLHLWLTDNTHIVDIGPVSEEDDAAASSLLYKSAGSKDKS
DELIALYEKKKGESSLGMVSVLLSEQLKRVKDVLTTWKEVDERVSKLCPSSAAKNTSTAN
ACSTTDKITEGLVGFLSGNFSENTWRDEYLGVNATVTGGTTKVAEPSDGVTFKGRGAWAE
WPVGKQGENQLYHFANYNFTLVATVSIHGEPRGDTPIPLLGVKMNYSENTVLLGLSYDSG
KKRAVLRSGGKTTEHSSTWEPETTHQVAIVLQNEKQGSVYLDGKLVGTEECALGEAESKV
ISHFYIGGDGSSAEGQEGVPVTVTNVLLYNRPLTEEEVGALNPNKAPTSPVVPGIAQGTL
SQSSPDGHPPSGPKLMNENEGVGSGSASTSAPSTVTTSTGKEQSAIQLPSGIFSGRKKDV
DGGSSSDDDPTVVTVGRDTMRGDGSPQTPEVSLSSAEDAETVEGKNVQEEEGIQPQAGEV
NATALNSSLGNLSQGNNSDACTVRGSGLLPSLLLLLLGLWGFAAQ*
>TCRU_3677 retrotransposon hot spot protein, RHS3, putative
MVLTSEKGWPYSWNRKENNSTRDCHVNCEVDRVWQIVSGDLTEWFSSHGRTDFKPKRRLL
IGTPGIGNSMAAGSYLLCQLLQYDVEKLPVAAYSVGGSTTYVSDETIKTVSE*
>TCRU_3678 retrotransposon hot spot protein, RHS3, putative
MIVVSYLEVRNYGEWVRQVRAERIIMNCPAEMDVKAMCAWTKRDETAEKQAECWKEVEKH
MYLLGPIPRHVFDEEAFNGRCGAVSLHWN*
>TCRU_3679 vacuolar type h+ ATPase subunit, putative
MRFSAPVTLGAAIGVCMLSAMGVFAATRREACLARMYPQSAGFYGALGAAVALVFANLGS
AYGAAKAGVGVAHLGLSAPEKIMRGIVPVVMAGILGIYGLIVAVIINNNIKTEPHSYSIF
SGNLHLGAGLAAGLAALAAGLSIGVVGDTAVRAYGKQDQVFVAMVLMLIFSEALGLYGLI
IALLMNNQANRYGALCEVE*
>TCRU_3680 kinesin K39, putative
MMGADPNAIGGADAGVTPRLCLELFQMRERIEAEGHSKWSVEVGYIEVYNERVSDLLAKR
KKGSKEEVFVDVREHPTRGVFIEGQELREVSSLDEVLGLIEAGNRVRHTAATKMNDRSSR
SHAIFMLLLREERSMQAATGQTITTAGKNSRMNLVDLAGSERVAQSEVVGQQFSEARHIN
LSLTTLGRVIDMLADMTKNKDSQWSMPPYRESKLTFLLKDSLGGNSKTFMIATVSPSAMN
YEETLSTLRYASRARDIVNVTKVNEDPRARRIRELEEQMEQMRKDIQGKDPAYVAELEEK
LRLLEAEAQKRAADLQALEREREKNEIHEKMLRATEAERQELLSRAGALERQVEESRRQA
EYHERANQRLKEEHAQRERELLEQMRRREDEMERIRRRKEAEVMSGQEQLRKTMEDLERE
RRDREEALRVLGVWKEELNAALSDSRQSQEQRAELERQNAQLADRMRQLESEREAQQRLL
HELELLRDEHESLQRAVVLLRTEVEEMDQRHDRTTYHLLAVMELHAECYEAVVARLGVEH
ERQLNQNAQWDADERAALERRNEEGLAERDSALSALQEALAECQRRLDESETAEEKLRVA
YEALEKEKGGIHENMRLLQQAKTEVEQSLEAMTSERDELRENLLSLKKDYDFVVTSCARL
RVDMSLADLEHQDELARLRIDNDAFAAELRRVLWKLNASEVRLKYLRSLCKSAGLGGSAE
SGEDYQVTRSVLAMRRT*
>TCRU_3681 retrotransposon hot spot protein, RHS3, putative
MTTTGEHHTTTSTVRQFTERLAAYFNGWEELSQELSWEMIYVQQADSTPMNDWQGCDVVN
SNNVSRDESREIAAFWEEEVRQYQVPISSRDFRSGEALRSEEEPPK*
>TCRU_3682 Glycine cleavage system P-protein, putative
MSQGTPPVILRNVIENPAWYTPYTPFQAEISQGRLESLLNIQSMIIDLTAMNLANASLLY
QATACAEAMYLAFHHGRKERMTFFNYRGTSSHLA*
>TCRU_3683 Protein kinase domain containing protein, putative
MTHEVVSRWYRAPELLLGQRHYGPEIDVWASGCVFAELLRGHGGAFFAGDGDIWQLSRIF
DVLGTPTPTSWPSAVLLPDWGKAHFEPKRPLPLREFFPDASECALDLLRRLLCLDPQKRL
TAAGALRHAYFSEYPT*
>TCRU_3684 zinc finger protein, putative
MDDGQHTGSLAFLAAPQDSLRYSEGSDVIHVLIYVSAARCQVILVAVIDGETVLMLAKRL
VDVRFRLGRGSLKSIRTAAREILLQKLRFSSESIVVENEANASDVASHCKHLVLSTLSAS

ELQHAHDGDPMEGFFCSELRNENKDGMIC*
>TCRU_3685 hypothetical protein, conserved
MEQAEFAAEAAHEAHTLPHPETAYFEPNVPEKREERNQALRRCSAVLLEARAKGLGASPS
PRWRYIHGVVAPYPHPLESVVLRTDLGRVCALPRQQANLLVRHFVRASRAITPYTAAACC
TPLVPGGWEMDRPFPPYVLDVAIRGSLLGSAPGPDDMLNEFLHRLGPVARGTLRTMIHNP
FANGSLPEDSMSGSDDGDSSSPSQVDISWLPLSSMVKKSDGEDSLGQ*
>TCRU_3686 Concanavalin A-like lectin/glucanases superfamily, putative
MARVCSSRVTWGQRGRRPSGHSRACGSTHDQELPGTKACVWETSSPRPLRERNSCCTLGK
GTPSGGTEAKALYLWVTDNSRTFHLEALSTDHAVGETLANALLYSDGALHLSRESIVGTR
RGISLARLTEELKTIKSVLRTWAQLDASFSESSIPTVGLVGFLSNTSSGGDTWIDEYRCV
NASVTKAAKVKNGFNFTGPGSGATWPVNGREDNDQYSFVNHRFTLVATVTIHQVAKGSTP
LLGAGLGDGAGKKIIGLLYSMNRKWEKVFNGTKTAPESTWEPGREYQVALMLQDGNKGCM
YVDSVIVGSSATIPTPEMQGHEITQFYFQGDEGEINSSDVTVTKVFLYNRPLSVGEIKMV
KKSGVKKGNSDGSMRGGISRMLLCGIVALY*
>TCRU_3687 hypothetical protein
MGPAPGADGMRGEALRHLGRVAKRAVPGCPKDDCTREPSRGIGDVESSCPSSIRGKRIQG
VIEPQSTLQTSGCWPVNFTSDQLLRLRAACAAMLHNTAWRLSLWNAPRPSTRWTMKASCW
ECGDCRSVMERNAGQQRSSIAKALWFASTNSHLPPRSPHEARRKEQRCAPSCPSSS*
>TCRU_3688 hypothetical protein
MERARAARPHEEPEQRLLHLKLILSVAWRTKRDTLRAFHLALVQAKAMYGIAVWHWGASP
ASRSTPNSAQYQRSKMISGIPKGSRMEDAVLETEPRPLPDVVLGRRFRCALLCETRGSAL
RPSAPIVRRPAPGL*
>TCRU_3689 hypothetical protein, conserved
MSRALWSHDAEQRLHGNGCGLGCAVCGGGAVGVSSLVPVLAKVAGGGSGGIPGRSGTPGD
LALRVASAATVLLAARRAFCRGFASLRGGVQRDKKRFSCEVFCVSVVGRPGRTNGACVVW
RVAVVVAAIRICAEAGQRSLFLTSEGGVRVRGLPVACYSGAAGFWLVPSGENDAFGQCDH
AGGPSVCELREFGCPPDCRITSFFPGHAAAAKDKPHPYALSSEPRSEQEAHDSTKYRVRC
REGARSQGVEEEGLACED*
>TCRU_3690 ubiquitin-conjugating enzyme variant Kua homologue, putative
MSSVKEGKTGVFEDEFSIRKANAKKLAAGYTKQKRFMECCYLSFATYLWFTQFIIVARYF
VHSGEVNLVHLAWSPLMVFFAMTLADFIGGMAHWGLDTWGTPETVVFGKFIRSFREHHVD
QVAMTKHDFIETNADTTLPLIPVLLLQRYYLFSANTHGKYEYNIDSENVGRHVFLLTLTI
FIAITNEVHKWSHMAKPPALARFLMRCHLILTPRVHRKHHRGNFDVSYCITTGWLNGFLD
AVNFWRLAESVVTALTGALPRANDQNLLGK*
>TCRU_3691 Myosin head (motor domain), putative
MAEQSVSFLPGMHCMCNHPQHAWVPGIIDSFDGKHVSVSTMTPAKEQVSKLLPDDVFVCE
KNVVDEDVHDLLNLSVLHEGTLLNCLKSRYFRDVVYTNIGAIILALNPFNFNIPWYMENK
MSDYLAEGETIQHNIPHSWVVAHSTYYEMRRDGGNQSVLVSGESGAGKTEAAKIVMKYLA
AVSALSCTEEEKKTGEFVGLRMFQSNPILEAFGNAKTVRNDNSSRFGKLMRIKFNRKGLL
TGADVTKYLLEKSRIVTSAPNERVYHAFYLLLQGRDRERYGLAELSRYRNVIAGKAPTIE
NVDDAEEYDSVNKAMEICGISQANVDSVWRCVGAVMSLLNAEFIATSTDTCAIDSKTNHY
IANGCRLLSISEEELKKELTTTTLIIREGPVPTTLTKAKADDARDSLCKALYDNLFDFLV
NAINKTIDTEDYTSWVALLDIFGFEDFKVNSFEQLCINLTNETLQRHYNYFIFSRDMDEC
RQEGIDVTAVVFPDNSECVELIGGKGGILSILDEDCLLAKATDNSFLDKVTNVFAGKCRF
FERPRLAKAPCFRIVHYAGTVTYEVDGFIEKNRDTLKDSFKILLNTSGDALVQTLFPMPN
PESRVRYTVGGFFRNQMKELMVVINATNPHWIRCIKPHPAKKPLHFDGVQTLAQLRSCGV
LGTVQIRKAGYPIRIPHVEFARKNKVLVLSEALDFSDAVGVAHAVLKSVGFDSRKAQIGR
SRVFLKSDAYQQLEVVKKQRLQVFLRVAVGGALVSLARMRTAALLRRRSTEIVEVFLLWR
NSQQIYRKKEYSFRREEIISNIFQLLKLQKNEMEARNAFVEERENFYNDITAKRSRLLEE
LYEQWLAEKPHHDAMALEAFIAAEECSRKEMISDALNELRQTLVLLEEDYDASRRREEKR
LATEFALEAAAQREAQRREAENARLEAERRKEEERCLAIAYWDERKKSMEQQVARREAEL
KRLREGVFDAMTSLNISLALKKQEPVLQARQRAEYPTAQFRSCGVDLLRDPSLGLCGLQD

GVTASPFSSAYNNVKKAPLRSCSRRENITNEDKFKQMDSFSEKVRLGKERVCPGRTGSLD
IVRRLRHLQAMGEKSFVTKPGDLEDSLDPYSPNWKPPIDGVVRFPDGFSCNLREAALNGI
SNQKSERCDGTSGRGRYISQSTMDFGF*
>TCRU_3692 hypothetical protein, conserved
MLKEHSLALRELFDKSCPYIEDRDNFVALFALRAHPFYRAFVIVGANADAAVRVTRSRMK
AALRAMEECNPAIADLEGALLMHEAELLSASNTIKDLRSSIKEAQEKVEKSEKSVWNAFF
LKGEEGKEREMRSTLSAKPNLQFLEHLEAALEILEGTVGRWRLRLALCKEELALYKQEMF
IFGRAGVLSCSDPGKERERDDERPLLGENGNRSDDVTKKYMFPPREEGKRNSPVGVVYVV
DRVIKKAARKVTEAPLHQGVHLWSLMSGGRGVTGFRGPSSADAATPQFVYSAEEEKRLTE
ANLVLQDQQKTASAEDAKAVEASVRELSQLTSLMNEQVVQQKEQFSILLKNTETAHNNMH
KGVIEVQKTLSKFWNSTRQLILCLWVSTLVLLVANWIIR*
>TCRU_3693 PHD-zinc-finger like domain containing protein, putative
MVQNRKRKKSKAGDVPMRIALNYEAVLPLVLVDNMDEVRAKYKPYKIIEEGLSEDSADDE
HTVSKGRLATSQPSRKRSRMPSTVDAVAKGFALPSARVGWGAQALRESTPYGLLRRRDLF
DRCCYIMDLEDYVWCHEKKVPIPFFVDAITKLERKYVMHLEAAARGSEAPTNVVVFNGAN
NNNNLYLSGENRVELCGVCSLPELSEESECFLHCRRCGCQAHVKCWILEALPPNAKNWLC
PCCVVARREKGVGRCHFCGRKGGVMLPFVSGVGWKSESSVGKSLFCHIVCSLALEELAID
AKKRVVHPVKRSRKSNHLARCVFCNSESAGACERCHHPRCFDSMHPSCAQQAGTLECYRA
PHAISATGPWDGCRFYCRAHFGVVVESPSGFAGIGEFAEAEALRHVNFADFVDEKRPVRR
GRPPNARVTPAALDAVKKYWVEKRLQRLHDGVKIVENVQGGRCDIVSVSLRPEIMKITPT
EVRLARFVCLIPELQHYINASVEGVLPIPDEEYDDVEEYRKAHSRTRYAGNTRKLYEKMQ
SVASHINVFCELAELLHQRAVVWRELLETDLQVLEARCHWGAEAN*
>TCRU_3694 hypothetical protein, conserved
MASRAWVDDADRDVEEQLPDFVKQSHVLPAWATVSSSSKLMMAAQKRFRDEDLDELLART
EPLLTSKHDRKYAALPPVLSVLPLPRDSARTVQWHRNGQLAVVGGNHHLYLFNAAGRFVE
QLSKTDVEKRIECTALEASGEDVLIVGHQSYTPDLLVLSTEKLIPLKFLFTRDSAVYRNG
RRDNGKHDFYITNVALPATNSSARLVGISSGATVTVGSLSSGSVTHRIEMSDPVVDILFS
GGPHELTVATRNKLSVFDLRKSAQFLRETCDDGTVDITTFATSDSALAVGSKSGIVSIYN
KGSSGPVKILKNLTTSISHLAFGERSNGDATLAYSTKGQKSGFRLAALPECRVVPSFPPI
SQRHQFIQSLTIAPTIPVLSVGEKQKVTNYAL*
>TCRU_C-terminal conserved region, putative PS.1
MQQSLKNQEHIWAVLQKMRMEMNECFAEHERMLRQAHGQLKERLDKIESAFVARNGGVGQ
LVGNSSSSLGHLDHATPVYTRFVSDKKGSPAGMRVTMLSTPPNERMQLMPPDSRGARSDV
LPQPVDPTDWVALAAPSRQEATPAVSPHNRWTNDDSIQAEKTPSVDATCFEALNNLMNDD
DFQHSTLESVIPSYTQDDDSKQLQSQPNLGTYTKKNDIIHMGAPGSSQTQHFTKSLKVTY
MDGRPQAVPIPDGPPDEPDKLGIDVNAQCKVLVEFKRKRVLQFESKEYVPPGSYVMVGGD
RGEDLGLVTYTWCETTKSLKGELGEFGNGSNKTVVLCVGLTGSTLTRSIGLGAGTVLRLA
DDSDVKQLHTVQVELERRAIDVCSQRVLERGLPMTIVDAEYQFDKKKLTFFYEAQQRMDF
RELVRDLYKSFRARIWMELVEN*
>TCRU_protein, putative AB.1
MLKRSGTICSLQSVVRGAAKIAAAIVDASVGNVNVVDNSHNGEGGTPARAAGRSHTSSPP
EVLPRSVVTQLHESKDDLRKNAVYMSVPSTRITRAAGFASLFVQLGWDHLVDRNGEGILS
SQSHKRVVNTLRRMRGVVLKLGQMLSIQDPATVPQYVLQLFEQVRDSAYAMSREQLDQTL
AKEYENINWRKDFFLEFDDEPIGAASIGQVHRATIKGEGDTQIEHVAVKVQYPGVATSID
SDIANLKMLISLHLLPPGMFVDRILQDLRQEFLLECRYKIEAAKQVRYAALIKQEPELQE
VFVVPKVYESLSTENVLVTQFVTGIPVDRLANISGVQDLKNYVAERMLLLTLTELFRWRF
MQTDPNYANFLFDAEKNKISLIDFGAAREYSKEFVKDYMDVVAAAARQDRDRIIEKSIKL
GFLTGNEMKPMLDAHAASVELLGRPFRHHDKPFDFSAENLPSKIQEHVPTIIKLRLRPPP
TPVYSLHRRISGIILLATKLKATVNSGEMFWNIYNSCRTNYE*
>TCRU_3697 hypothetical protein, conserved
MDAILVIPNASSTMVIDAEAAAVVELNTLLSRSGLHFSTASTQLHIMPETVYFLSREDVA
VLSRFARVLVKNASVQCDFSALWGVLWGHAKEVENVLNQHAQQPLDKEGRPQETALRQLV
PHLMLLAHVFHTLRHIEEPFARQEVKDAVNIVQKEVEMVVRLALKVTRVFDSALRNPQRT
NENSLRAVELCLAALEMFIASIASRKTIDVSPVLAFFNSDLVWRFSGVGVIATESYCEAI

RRLIVAIFLRQDDFVGVEEVAVRLLRHRLTNRPPFDWEIFRRLYVLRDAELSSVASLTPQ
YGILRYMSIVQLCVESLLLSDESWTKSLRRQTVKSLHQMNKKEMLSFFQVSLLGAVEGMP
EMNFSDDAELQRRSVVTHLTVQNTSKDCILQPSFLRILLAHGYIVPQINHGVLKRTSIIS
LLRAIAEQLFQLPLIQSGEKNSLTDLTLIPPVLTKRVLRLIVDAAASDVEMACDVMLEVH
QITWVIYEANISQCASLLSAQRMPVPLRRLSVSAMELLAIFFEPNAILCSAGHSMTLESL
ARVFAVLAFYSSAKKDAGNMEKKATLRLINNLGMKLSSLARMMTAEEIKSFFHTVILPCT
SKEKLIQKNRQQYALQEAYLRAFSSSAVALAMDEATILRHWVDTALRCIRNTLSGALSLA
GLDFFTAIFLSRRAIAPLFVPTYVALMIPIKNKTRYGEPSLFLVRHFAKGVRATCQALED
CDEQILAGMMQNPNSSLKTFLLEIYGEGDAAPSLDNVRPISCVLLIVSALFDKVCLILGH
TAKAQTTIATASRQERIARFQAYFSALINLLRCRSRPVLHRVCASVEAVILEHLHGVPRA
QLQWMKYTTATVDLIEGTGKKELVEWLLMLEEKARGSIPHSQL*
>TCRU_3698 retrotransposon hot spot protein, RHS3, putative
MTVVGLRMTTAGGHHTTASTVRQFTECLAAYFNGWEELSRDMSWGMIYVQQAASTPMNDW
RRCDVVNSDNVSDESLEIRCSGRKRCASTQCQYHPETLEETKPSEVCKDNNNRKID*
>TCRU_3699 hypothetical protein, conserved
MDKARPFEYVYRLPATTIEELRYAECVYDRQVLLNETWHSYALRKGRINEVDNEHVKWIT
RTWDEEEKARVDQRSFLDKSNAQGEKQIFAREENLMLKRKKSAAIVAHIMAHQEHLLSDR
IVCRHNLHVDFDLLQENKFIGEQNIIFIEEEFLRLFQEKGLDGFCDALFLISECHRIFCL
MKLNIRLRREEEERRRIREEQERAIEEERRREELRQKELEEAERARQEALEQAKMLERKK
REEERRAKARSERERLKSHHGVHEIGLSEDKSQTLAFVDEVLPVTENLSSVLEKLDLNN*
>TCRU_3700 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MLVTLPVYSKRVSANEKGELHLWLTDNTHIVDIGSVSDEDAAASALLYKSAEGEDNKELI
ALYEKKKGGEDEKSRSLWSVRLTAQLKRVKEVLATWKKVDERVSKMCPNLSAEKDNPTDT
ACDAGKITDGLVGFLSGNFSESTWRDEYLGVNATVKGTDGGAEKKAEVATVDSEKGVRFQ
GAWAEWPVGKQGENQLYHFANYNFTLVATVSIHKAPEGVNPIPLMGVKMNGEPKKSFGLS
YEKGKWKLLCGDGPKSGEHSRDWEPGTTYQVAIVLQNGTHGSAYVDGQHVEDAPCAVETA
DSKGISHFYIGGDGGDAGDEESKDVTVTNVLLYNRPLTVTEVAALNTKKPSLSRLDGENE
LAGVAHSPEKGVPAPRGTVSRPILGDLQPTAPEPLRTSKDAVGAGASTTAVSTVKTFPAG
EGSAKQLASVTSSEGTQTVDGASLSDGGQTVDTGDGGGTREDEPHKTPEPGAGSGENGEP
TEGTNVQEEGAQPQDGDVNATALSSNLGTLSQGNNSDAVTVRGSGLLPPLLLLLGLWGFA
AL*
>TCRU_3701 hypothetical protein, conserved
MSLAGQFTTFCRTHEQPINEESWAVFLVAILDVAPPTRPQHARMLRSMLEMNRTPLGMAI
LGLQKLAARSETRQARPLTKEGMDQFIRSRIDWNQRVVFRLACMTAIRWSGIAALTPNNF
TLEADGTIILDWSVAPKTARADPHRAPRFVGIRGRDALDTITLCRTLQENEKLTNITNAK
VERALAPWDATAHSIKRGALRHAAQIVETCNLDPHVISQLAKHVDPFVLPQNTVRYFWKY
TTVLTQVLPLVVLM*
>TCRU_3702 ubiquitin carboxyl-terminal hydrolase, putative
MATVKVKWGKELLELTVSLQSTVGAFKEKLQQLTQVPAERQKIMGLKANASKDDATLSQV
GVTDGKTLMLLGAAAEPPQTKEPPPSPAAASNTTAVQAPAAATRMPTGLRNIANTCYMNA
AVQMLHLVPELIELLQSRKNDTLLHSMGELYKTMEANKDPVTPLLFWNALIMQNSTFGEV
DEHGHPMQHDAQEVLNTILQQLNNGIQETHKNLFSGTMKRTSVCKEIPDDVSEASDLPFL
MLSCNINAEVQMLETGLYASFNETIPVRSEKLAREVLYSRTSRISILPEYLFVHLVRFSW
RADTQKKAKILKPVSFPLVLDTFTLCTDALKESMQEERGRVLARRDKELERRRQVRQKTQ
FDVTTNAEEVSTGAMAGDAHNIGNKSGYYELCGVISHKGRSAESGHYVFWGKPEDQWFVY
DDEHVASVTEEDVKRLSGVGEAHIAYVLMYRSRDPRTKATTIPL*
>TCRU_3703 Protein of unknown function (DUF3676)/Trans-sialidase of
Trypanosoma hydrophobic C-terminal, putative
MDGRSKEPEQVRCGLLATWGRLCRTTLRTSATGGHVTVTNVMLYNDDLYNNELYKLNASK
VTIPSLGVEKQPTGQVAGTDVSFASESRSEESATSNEELNEDDIEKQEEGSVDDLVPAAP
SSTDAEGSSVPEPAIATEIAGNSRPDDNAQLSEGETSQQATPHEGSESMQRDSDVQTQDL
QSEESTEFNDVEGSSESYDTPQPEEDGEANDRSGKSTSSVASSLIMETVTGPADGEHQVQ

QSTELSAENNEVRSSGTRTTGTEQSLGLEAGDGSSERTMGSGSSLTPSKSDAETKSAENT
DDVSRIEREEVSSENGEEVPQTFDTAPGNTNTTPGETAIPSESNATIPSDTEILLENGHY
SELAGMALFAESTVHGCVSRVLLLLLLGLWGTAAPC*
>TCRU_3704 hypothetical protein, conserved
MPVGLRVVCLRPVMRSSIAVAASPLCCTPLCTARRLQASDQFHRYLHNPHIVQPDGVDTL
PRTKGDQQQWLNTEQWVGYSDTYLKRHMQYPPTNEQPNAQLNSSHALLYKCLRTCYECYG
PLAEELQALHEDPLHPRFHEKIAHVKKEKEKIAAELDRVYAALHPTVKTVYDAYLVRRFF
HLNDWVKHVEQKRYNLLCRLSPDHIEQVKRARGVSAHFIDRLQRLEAAFTHNPTLGLLEG
EEGKQYTHDELVMLRQKAAYFRNMRQLGASQQEADVHTH*
>TCRU_3705 mitochondrial exoribonuclease DSS-1
MSAPRRVVKLVQFSGSYLNGTWTRKFILGSLLQRYSPTPEAGGTTPSPSLPKVTRESVAL
DKELLRLQRMLGEVWSLPVRPLDALSEARIFRLLARYAAGEGVLSLEALSELNRVLACIH
GAPQSVEDPQQMECLLQVLKYVEPGDNLRRVAFSGELHYPPSALSHMQPYLTEELQQDGG
DPFDSIRQYVDGPAYAIDSATTSEVDDAIGVHTDPSTGEEYFVVYVSDATVYCPFDSPLE
QLTARLLTTTTYLPEGVFFMLPKPIVEAATLREDRPCRTFNIRFQIDEVTGELKNYSISV
GWLRKLRRITYDEVQVLYDAKEEGTEEVARPSWMEAEDVRALHRIHLAARKRLEERRARS
LEHFIDANLPEPHIKVEAARVLSVEDQVVATKDARLAVAEMMIAANEVCSRVAQANHLPI
PYRGTRELSMDHEAARSYSEPQGVTEVASLDPQYVYFAEAIQHAIRQLSAVTRAVYFHTP
IYHAGLNTYNYTHSTSPLRRYADMLVHHQLKMWLWRTSAQNRGRAVPTSSPKRTVVAMIE
QPIAEHTMATLCSMISNKQEQSRILQDNSQRYWVLRHIEQNILKKNRQYRFICLVGDTRG
VESAPEYTRFVDSSHWDQIREDKEFGDYATSSNLQSVKRTVPFIGRWQQRRCEYRYVSDI
YIPELQFAHVVLHSLPNVVIGAVVECEVLTVHPTQGQLTLKVVNVWSGGDERQFESMWKK
ALLPSLDS*
>TCRU_3706 hypothetical protein
MKVESCREANVAPLLPLSVSFPFARQELHEKGSCIFGNWGRCLKAQPNDSPVPRMEIQMG
NRWQGESSESCVHRALSWSHREESEKPCGIKAHRCRSRSASPMAVDAIGGSIPVLGTTDN
GGDIPSASGENSVENGKKEVPLGRCEALLHAREDRAPVLESAYCSNAPNDRCLEEKCEEN
FSFASSRRSTAHHEANPHSTASMPTSEHVHGLAQLMDGLQHAILQLSGEMRELRLAFQQM
RGSFMSGRQKTLSRPPLVGPMAVTTPDQPQEEPAPSSSSSSLTFPRRTEDLSFYSASPPL
HPEGSTAFLDAGIVNAVSDGLKELEALPTFLPFEHRVVI*
>TCRU_3707 hypothetical protein
MQFDEFNFGSPGYQISVSESSSGSLQRSLPAPVLPLAPTVGGRVVLTSKNCNHDAFIWED
KEMDLLYLQCAMQHMLVGSVLRETERHLIVRFDIPYRCLPPVISSRLVKRCFGEVRGEEG
ASDKRRNKVVDDDSDKVEKEEGGDRLVGKEGQDGEGDKSASVADVALPRFVPETDGVGGG
GVGCPTSRPTRFVVGIVPVLALTHETVLGSNSRSNAGGTLSANEASEKSQLIATTAVSGA
YFINENQNDVLHVSLSVTRSGCVSLLQNLLEQHDKLECVSLAVANRDFKSAANHIMAVID
ARQNLLKQQKEMCKGIAESRQSSPTWLQPNPQAPGTDARRQTEEFIPEDRRSRFVMIFDQ
ENESLSCRGFQPHSLTTPNEEECRCLSKENVSAFNDKGSSSIVQSKTDVVDLDSASINKM
HKLHILWNSGKAIKELAPLYAFLSFLHFQDGHYEQCLEDAMTALAHDTICIEAYTRVISG
LMALGLEKEAILTAAVAVKRCLVLSPQFARLYQLVHVRFFYHRSLGNHSIVDVSLRLRHS
SIADLGSAKDGSNISKTNRQPRRPTTVRVPGLSNILTSPLPFYCVPPPSLRKILSGSSPP
MDYFLRNLRVRAARGFERDETVFSEEVSLQVLLWSLPDCEYENSSKPFSDDNADLANPWM
LCRSRFCAYCGHPLVSKSVLLAGIREKTSRAMADRVRWNFSEKKPLPCLAGCGDHYCDEI
CRNRAALEYHWIECALLPVDESESEDETPPRDGTMTGEVTRTHDFFSPAAPCGGDDTHAS
LLEILPYAKVPLRRTDVRSLVNICRRLNNRQSCLGIADLSIGSLRESLWQEFSTSSVNEA
MMERERLYLSSIQACCSVIPEIRAVFGSYYASVGTAILEKAPNAITAPLLVMGRLLASVL
HLIMPTAATKNDIFSRAKNHFIGLEHRCRERSDAVKKIVARYASRGFTSGGASPSDRHDI
HGLCLAEEVLQQIRVPFFADTNLLQPSTVWELLSEPPAVKSTANNDDASSGAAATTQSIR
RGFDRAVELLRAINDIVQSRLRDEVVAFSLSKASDPLQWLSPESVSAGGDSRLSKSQSDD
ATLASRGSDQSFAGSLPFLTDVGSLAVWLVEEHSKVGFHMAKRPSVWTFGRLLGFLGKRR
FMEQFWDFCVCSYCVVPKCVLTVGVGDSVPEHLQEGWKKICREYTVLVAVMGPLTSLVTD
LSAFGGDVCSRFFKDAAPSGQRNPLHLRKGDSPAASMLSINSLTHESEEPHSRATPQSMG
GGENKASPQADAIFSAAMPLGNLELCSKTSFDRSGERRVTMKAQRPITPGEELCYEGS*
>TCRU_3708 hypothetical protein, conserved

MADNVVPRQRKKFIKGTNIIVQKSATDGVEDAHLRMMYAIAADDKNEVLWWRNTLRPERN
LTHPSEAFLQGIKALRPSARFNTFDIEKARLRRLVKQKKDKHRFLERRKREVAPTAAMKA
SINPHKVPRTGGQAPEEEVRFLSRGRKSSKQSAPNETEKKGYFHKWKKRKMQKIGKGL*
>TCRU_3709 Right handed beta helix region containing protein, putative
MVHPEVAQTVGGGLSWLCYRNVTFSGGGMSLTVLIGAMTGDVANVTFDGCTWRDGVLLLL
LGNAYAAVGSLNIVVTGNTFSDALLSPEGVFPPHTNITINGNRFTVTRLIFRSGLAIDRP
SCVAMNELAISNDSAVVLSGNVFQSVTASSSAIYVVRSALRVSWHSVFAVMGNTFHMAGG
DGTLI*
>TCRU_3710 hypothetical protein, conserved
MRVASSSILSLRSHSVFSVTNVSVVSSGGGLVLGERLAVSESVLRFVGVEGSVASSLVRC
DGGTIGAGGWLDLHDVWAVGEASSVASLSGVTLGGGTVSIARCAATGATLVSGLAITSGV
VSVQCNRAGGRVLESSGDYRMAGLPSVSVVPCDGCAAALTCFDALTASFSDCVCGCRAGG
VGEACLPFDVPPARSGGGSQGCVSGVTLTESVTVCGWVRPAGR*
>TCRU_3711 hypothetical protein, conserved
MHGRNGELGAVCHVANAVHTCSNCAASCGTEEEETTVAFTMNVTTHKCAGPYELWWRLFP
PDGTIHPPARSGDADRTGICQLPPSREGKDDTKSGGTTAPQFDAEPSRQHEDWRQSAAAD
APNTVDRSPASNTATNTSETRPEFAFVRNTKVAPTPSGRRPTPVTEPQGILLMMR*
>TCRU_3712 BNR repeat-like domain containing protein, putative
MLVTLPVYSSKGGNGKGELHLWLTDNTHIVDIGPVSGDEEDVAASSLLYKSAGSGDGDNE
GEKLIALYEKNGGNEDTSLGMASVLLTAQLQRVKEVLATWMEVDERVSKLCPTESVGRDT
STGTACSADIKITDGLVGFLSGNFSDDTWSDEYLGVNATVHNKEGATKTSDGVTFQGAWA
EWPVGSQGQNQLYHFANYNFTLVATVSIDGVPKGG*
>TCRU_3713 BNR repeat-like domain/Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MEDGTIVFPLMAKSGKGVVYSMIIHSTDNGSNWSLSEGISHPKCFAPRITEWEGSLLMIV
DCEDGQRVYESRDMGTAWTEAIGTLPGVWVKSQSFFRDLSLRVDALITVTIGGRKVMLYT
QRGNFSGKNKATALYLWVTENNRTFFVGPVGMGNAGEKEFASTLLYSDGKLHLLQRMASG
EGSAISLSHLAEELNKIKFVLKTWAQKDVFFPGLSIPTAGLVAVLSDAASDDTWIDEYLC
LNATVRNATKVKDGLKLTEPDSGVIWPVNIPDDKVRNVSLSHNFTLVATVTIEEAPSGNT
PLLTAVLANTEPTHTMGILYTANKTWETISKGETKPTTESGTWELKKEYQVALMLQGNKS
SVYVDGNSLGEEEAPLTDETPLELLYFCFGACDMKNSPMTVKDVFLYNRPLNPTEMSAIK
ERIPVPTRAPEPQVKIAPDPIAPAVSAVPAVSAVPAVPAAPVAPAVPAVPAGNEGTAREK
GDGGANGDAGSAYGSGLLPLLLLLGLWGFATA*
>TCRU_3714 hypothetical protein, conserved
MRGADVAREDPHVAAEAPKFLEDSISRQQNTRRCLPMRRRRRGFHVGYAPHVLNISEACE
PFVLSGCAEPNDPPQRCWIGCQVDRSILL*
>TCRU_3715 hypothetical protein, conserved
MWKRRRRHTPGSRSGWTPAEDDEIGRLSRSHSTEGADRIDVYGFLREVKQQERDFRLASL
EDSGHLSSEAGAQPSARSSLQWSPEYLDDVSVRDRPKRATRFLYDGKANRSAGTHTGSSG
RVRPRGRNVPPFVRRPKSKPAGQLLVVDDDGSEYDSGELSSLFANDDEDLTLFLATFPEE
LQHVRLRTEARGVLGELKETSSLLVNYATNVRHRLPEGYVATAPHESLSSATAMAEAAEE
LKTKVRIDELRQRFELEGYEEHPELWRTLQDLRQKVLEQEAFLKESLMDVVNLSRPLPGE
DRDAFAIRLTREVNEYAKSHRLDQRDLGKNTDIKDDYTAAVKGFLESFALTRGRRPGHDV
GCQCNPFLKESLMDVVNLSRPLPGEDRDAFAIRLTREVNEYAKSHRLDQRDLGKNTDIKD
DYTAAVKGFLESFALTRGRRPGHDVGCQCNPDDLGYVDEEIRRTEEEMEDLYFHARGLFS
AIKLTIVAVGNVMGFHASLELESTCKRCFYIFESPRTLWPCGHTFCQQCLPFMFTEQGEL
ICEECGSLCEVGYTPNLALELVASYQVMQHTDYDDDDDDDGDGEIGCVVQRRSIEEVLTA
MLKDLMSTQTTIADAPRKTAGKAAPHPLELVM*
>TCRU_3716 retrotransposon hot spot protein, RHS3, putative
MIVVSSPKATNYDEWEKQTKASRIIMNCPDEVDVKAMCTWITRGLEPDKQAEYWRMVEKH
MEIVGPIPRHILDADEYGRRTKDVMRALRWINIGDQGKDFTLGGEKKWYSEDPSHKLVRV
VRARAEVCAEVFLNAPISFCLERRIPHYFGKRDE*

>TCRU_3717 retrotransposon hot spot protein, RHS3, putative
MTTTGEHHTTTSTVRQFTERLAAYFSGWEELSQELSWEMIYVQQADSTPMNDWQGCDVDN
SNNVSRDESREIAAFWEEEVR*
>TCRU_3718 universal minicircle sequence binding protein 1
MADNAMTRGSRACYNCGQPGHLSRECPTRPPGVMGDRACYNCGRMGHLSRECPTRPPGVM
GDRACYNCGRMGHLSRECPNRPAGGFRGVARGACYHCQQEGHLARDCPNAPPGGERACYN
CGQTGHTSRACPVK*
>TCRU_3719 proteasome beta 5 subunit, putative
MIADFESVLRTDFSLDDCPRIGPFTWHNVPGLDGSDEGDEWDAPTLSSYGSIETRPRRND
DFRVIPSTGEMLTEDPLSTSNRLQTDMRMWKLMKTCPVPRSVPKLDMKKGTTTLGFHFDG
GIILAVDSRASSGQYISSQTVMKVLEINEYLLGTMAGGAADCQYWERVLGMECRLWELRN
NCRISVAAASKILANITYSYRNYGLSMGTMVAGWDQFGPSLYYVDDKGTRVKHELFSVGS
GSIYAYGVLDQGYRKNLTVEEACELARRSIFHATYRDGASGGIVTVYHVHQGGWTQISRD
DQTKLYDRYVL*
>TCRU_3720 tRNA pseudouridine synthase A, putative
MRRLLFPQRVLLVTLLWQQQQRRWESGGEKRSGVRGASPPPTSPKRQKKMSPAASELSRS
EDVAKREERLDVERHFPVAMSHLKATPVSSHVAEEGRKRRWREVTRVVNADGYAPPNEDA
QAPPSFFNEGSLDIRGGTKKRGARERMSSRRESISPDVLQLSAGNTRQHGLALAEESNLS
PADPTIEPEGEEGRSTYGDTPVQLTDMLKERLMELKAEKVREDRNDTYLPRRLRLLSDQE
VQKRLEEKKAQSEIAAKPVSTAPRGRITTLADVFKEHAGNDEAGPGQLMTSAAATNNSVV
MDAIFRRTADFIPGETPYDPLADFAKKSLGGGIGKSGTPDGSVFLLRCLPRAGFCSRREA
LSIIASGQVRVDNVVERNPFRLVRAENSIHVESHSGRLRFAPPRLWMYHKPAYVIVSRND
VAGRTLITKHARILGMDHLVPVGSLPMRAHGLLLLTNDGELSRLLENPKTMIQQTYLLRV
RPAIDPLLAHKLNTEGILVNGKRYNNVEFFVNPAMKSRHSLKVKVRGETMPVAHLMQHLG
RTVERGGRISFGPFSMSGLPVGSIREVTVPPYYMQHSGAVWKEFIERDWPFFRRQRVSRL
RRLSRYRELTPRELEELDNFTYEELKDALSFESQELKATSEEELRRMSVRPTLNEEPLPN
EFASADVDGNGVFPAEEEIVEDITAVI*
>TCRU_3721 hypothetical protein, conserved
MVRVGGLERPASSKRRQSASRLSSSSLQGGAVAGRVLRKADGAQRRNRSEGQSRKLSLKR
RSLKAGGSTNAQRKRNGRSNRAYSVRSHSAERGAAAGAQGKTLGTSGRSRPFSRAVMDAY
VSRIQRWFRRLVLGGVVRCRGLLVMRIREILELQKRLLELRVRMAKRVMSEAFNTYALSI
HSDSEMRGIRKYKPVVTLVNAFMRAKKDCVLRSEKLHIIYQRAVRVIERAWAKCVLFRSI
QQASVENKMQWLLIQQEEIERRDYIRQRLLFLVECHQQCYNHPLLMKAVIAVRNTECWAG
IITESPLHLTDRICSFVNLSNEVTLNTSSARDFRHSIMMQTLRSQASSRFASPNFGRTSD
SQRWSCLNEEKHKGLIFQTTNEQPSVKHRFNVRADTAFVHGLLQEMGKLDFPSSMGSRPR
VLASPRDLTDAAVSTTCTARVQSTEHASELTNSRFVWVGNVILRECLRSSPLFTEFCIWN
NSKERGWIKGGKATSSSYVFEDAVNACFLHPAPRRKSRERTLSPMDFSVSVASMGKAWAD
FYVFMDLTGDALKSFSCNNTTSDSSPLASLMVSRRSKGRALLHFLLGTGAASVTRTSGKL
HTPTPSPADQTQANWAPTKIFGSEFDIKYEIERLLVREYHRRLKLQDLYDAEVAALGWII
QRGTATTRNAGEARTNVKESRQQFKKARVPLHLPPTLC*
>TCRU_3722 Peptidase M76 family, putative
MVALWGRGKENRNDVEEGEEGVKASLLHQQCEAAVSEVLATVNTVQYLIKSIEEITGKPF
HRERIKCVTLNRGIHSGGAVGNNGSGPLDGNVMAGYMWRRAREDCEKGDILLVEELMVGK
AGNSGTNIPDKRTIETVERNLRHELIHAFDDTRGVIEASDCIHQACSEIRAARLSGDCFV
GEELKRGRLDPLRSGIRCVKRRATLAVEKNPVCRGFSERAVERVFQRCYSDYEPFAAPIY
AMGSYGEEKFK*
>TCRU_3723 hypothetical protein
MATHSYYGGYSLIRSSAYTANSNGCGNSCSSKNASSTRDGTRTAGLARMNFASCNSDWMP
SLATSSAAEVRSTVMPVDAVGDVASSASAPTRTPLIQALLAMQNFYRGVPLCVTNTTARN
ASTTTTVTPPAAPSAKTEKFVAATTAEVSKRAEAKKMLPTIPMPIGGDTWTALSDTVLAA
KTGVVASRHALKRPVAPMAVGVTDADLDREMRSTRKGPEPLFRDLLAFSSPSETPTQSAF
ACNTNNSKRRDPVPADELFSFQQHEQEQKQHCPVPPAPISVSPLLSPNRENSLAPEEKLQ
MFQKQSEAPGGFYDEGHYALRSSPKELQMGLASFSSTPEERQQEKSTIPVLSGGINGASR
QGIQRNQLLREGDEDKPLFDEEDEDALEHIRQVINIVLSVNASENASADTDASCKPKKGL

EFGMEWLNTRYHQSEQQNSFFQGF*
>TCRU_3724 phosphatidylinositolN-acetylglucosaminyltransferase, putative
MSSERRRTHTATSSDEFFAGVSVHWASSTGSAARGWRKVLYERQPFEDNYVDPEQFMRDL
RQNVNLKTYEYGKVVMDTFVVVQQLSFVALFLFAFAKMYSEEGNAYALAWINATLFALSF
VFYVEMQRQQAMEQGETTTPLLQHVVKLGRQVLPLVAVIILLSPALQTLTATYSNDTIVA
LSTFAMCIHLLLTDYSYLNCYTERYQQYTAVSAATFGTILVASRIKNFFCSGPLITFGIL
CFALSPIPRHHLKRTSATAHVGLTFALCGLAAGCLMQAAIFAVLYCLLVVAVSLFIPWCF
VTLHGSMKKQINGPWDEAKPTNSAAAAEWANAGLLR*
>TCRU_3725 neurobeachin/beige protein, putative
MFKFFSVIRKLSGGSANVNAGLRGQEEEEEEELLAEFTKFLTLPSCEGIRVELEKLECQC
EVSNHVHHPHSPDSGLERSVLHLLRTESFQPALPSRLVALLLRRLESCFTGSDETEITGF
LQDSLPTLHALLMTDASRFGTTMLALGIDNHLLLVLQFVRAKLINRTLSGTKAPMNITAT
QTKEQEENSFETETNFSLNTTSQPSLARRCVLVRILCETLRLLLAIHVSPTATAVSVTGI
SHILLEKGVTRYRTDSNFLTSSAAPRLISPSTTGVTFGGWGSGDSLATIDGMLTECGHLF
LYFSKGALDLHVPADEEEEEEEEEGELVAEAICSLVLLISNLYQEPSELIIHITLSGIGV
QLARFLVAEEPGKSLLLLRELSFGLLLVSKFMRESPLVTVQAMSSVYFFDNLVGTLQILG
QQYECARMDESYASAREDALKELLSVANLEAFRVRKLSEKVIHLSRPRFDRLAEDNTVDE
FLHCYIGLLETQRFVKSKMEVRRDPAILRVFAEIELTLIKAFLDSPTSLSPASCMYETLM
KYTIASLPLHEMGKPEKRHVTLIRPLINAGLYRILFYEPTFKSFRHDPRLYYAAVYLLHY
MLIYPLLSLEDHVEDEVGIILDAFLSNEAEEHSHELPEKSAVMCAILLSAVCGPNATHVL
NSLMQRNGIAMFAAIITRSSISDSRKQEKEGGGSSGGVIVGEWVTYLLTQLLRQPEVQRS
VLVDQADVAFSLLSVRGIRKNVEQMVVSLLSHRCVEAEYSQRMTPLVNCTWEFVSQCMKI
QQGEPLIATLIEADDEDSLLLSILYCIRASIRALAADLPCWGSVRQLQSVLCGSVTDAPD
PFLCLLHRVVLPWHGVRASHGLSSILHTITMLVQGNPALRVRLFQTMDAEQLVTCFQSAW
FSSRGGSWLQFVHSILALVYEEEGELREGDRPPKSKKKSGAATLLADVREDTVIQNPELL
LPLLRIFLKLTEFSTKHRDALEYLLARLLRTLKASLVSLWMLANAGLFEVLTALIPVVTG
TALLEMVLALIMNITSHHIGVRETKQFLMGIAHTQSEEERRRLVPIVIEVLSVSSYMFLN
QQTERQNYIAFREFSGQTGVKAILSEFPQDGYTVCMWLRMERREDGRMPQCIFSLQNMEK
RTILELVATAHGLSVIFLNEQRRTLDLDLSCSIPSQTWTQLTVVHRQAAFPFSGNEFLCF
LNGMEVAAVSGVQYPPISLGFFYIGTRGEDVEQRSSRRSFIGQMTAVYFLMRALTPKEVM
EFFVGDTGVTSMKQYATHIAVYIDPRFCERGQVHNLATLMRGKASELPLITYEGTIACNT
NSIIDSICVLGALHTVVVPLLVLLVNPQLPFQCRIPPAKRKSVPETTRKAVDDLLKLVES
LLLSNTVRADVLEVGLFPMIAHVLQQFMEYHCSNLAQRMCNLCSALLPNGAIFDAAYTVL
FLSGDLLHACSEETQLALIKTQTAMCGANKELCRRAHALDLSNFVVSEIIHVYNTSSPHH
ASMRREMFVLLEVMMVEPITMNDADALLRLINFAVKQIESMVLLEILERCRVLIATRKPL
LAAYMGKKDFAAVLLLLLEDSRGMVQNEALLLFCLLVGRSRRTQELLNPTLLSAREAAHV
ACDISLSWLREKLHAVQVDVGLYITLRAALTGRFDAPINDCTELKRDDKILFAPAFTPLL
QMMKRCQEKSLKIRAMSDIAALVQQDPSAWKSVVSVPGWYASVVDLYLSEDDLRDMQASD
ISSFLASTTMIFVKVLFHALLHEAYGASELELLVAYLVQQRAHVLLNAVLTGVVKEYSAL
FSVRHNLLGGAHFGLGSQQAATNFTTLLFLVEDVLFYSVTTYQAYGAARPLESLRKRGYT
EEEELVLGPMKRHARDARRKEQGEGGEEVEEEEEREESADALGGQFFIGDKAMRFRTDPD
GVWLHATLAVCTMHILTTHAAVLNAGGTNSGGSLDFYMRGRRVRKGGFLRLFVRLFRVTC
NFILRDAEQVEGVVLMVGRWIRIVEKEQSSFLLLRRQSTEQREHSPLSGSMIMILGLHDL
LARRLRFSVEGSSTRFEDLNYEILDCIKCLCILYRRTLAQMQIFHAQSPAYESAPRTRKD
TLDWLCSRKRERSIVEFVEVASRQDYDGFIRHCTLVMERDRLTEKGIVRLIEEEHTKVMA
HLHQIITGLSVARRLMLDALEQYLQATSKELAETETLKERFAPQTARKLATVVFNTVWRR
FLERCKGTIWDFDPAGQHSTKYVRLLEVEQQQLVRRKLVFDSNGTDHANITTMGSASLVL
QQAEQQQPCPRGGEHMLLSTENSGNDEEDEEEEGKDEEEQMEEEEGMELSGVAALPVATE
ANQTVHFSMACEVPYMMHCWSATMVIRESDLCIFFDEENKAYNQRIAEEAESLLIKPGSI
IYPSGHVKILAPGRRFRMRRSAVELWFLDGMSVLINFATFPDMRAAVNNIRTAAGRHKLL
HSPLYIFQVNPKKDPMLWRRMEQWRDREISNFEYLLWLNFFGGRTLNDITQYPVFPWVIA
DYTSETLDLESPSTFRDFTLPVGICGGPQSRARVEMRYEATKQLGDIPAHYFTHYSSSAV
VLYYLIRMEPFTTLQIILQGGHFDHADRMFHSMASCWHGVTTNSQDVRELIPELFYMPEI

CMNTNRVRFGCKQGGEAMDSLELPPWSHGDPYEFIYRMREALESDYVSSMLHHWIDLIFG
YKQRGKEAIAALNVFNWHSYEELDKNRDTDVDRQLLIDSLDNIGQTPIQLFTQNHVERRP
YDLLDPISCSMSVKTIDVQRTCSCVARVALFASDRVLLVGGNGTALLFRLIVAPLTKRAR
RACSAGSVGSAAATGAGENSVAASAGSGGLPSLSNMTPSASGRCGGISRGRPSVDMLEEV
ERRTAPLPTGVVPNTSKKAGGPCETENVAVLSFDNEVFVAFGGLFDNTFVIRPLDSSSVF
AEERLSAHRGRVVRITASSNSRYIVSGAEDTTFVVWSCQLQQGRTRLRVELLFTVYGHED
NPTAVDLSPVLDLVATASRDGVLMLHSLTSSRLERSLRHPENFSIDRVLIQASCYLPNIL
YASALDHVIHQIGVNGVALRSVTAPGRITSWCVTPNQYILVTTKSFTNLNASDESGGTVF
FLHSFYLSFLNSVPCPLRSFGATLTCCAAHPSNPQVIVCGSSEGSLSLLRVEL*
>TCRU_3726 Sec34-like family, putative
MLSDAEFSHRLDVALAQMPKIFQHAIPFSDRMLEFGGSLLDTTVRFGSSINRASSLSPAV
ELRDPQKEQEAQAMEEMLRDIAKAESESRVEGLQRWLERAAEGRRMGEQCLSVFNDLSSC
LGSMCDVTAAVQEQSNLLSSNASALMVRKTKLEMVQEELERMIKHFTRIEVLTREAENPV
LSANSTRYPSMLQEMEEEMQFLSRNPNFLSSKVYATRLALSQQRAFQCLKDAIVESVRSA
QNLTVGSDVYRDAFYRRQRGTSNDAANTEDRALKTTTILPLPGVDGSSDAQRAVADALRR
INAIFCEKLSEKASLRRMLEAIGGDGESKDEVNDNEIFDAYRESRVLVVGPLLQNWLEAW
CSVDVTAKPMPKLVNHLNSLMKIALAGEKEVFDEIWLREDFSARVFQQLVAGLSNEVYHV
FRSQLLQVDELEELARTIEEIQWENTRQDNVAELSELLTKLIQDTQERLIFRTSVFLRQS
IMRGGPTKAMLREFQSDGVKSDDSYIPALSNCVALLRILYPSLEFSVFSVFAEEAIHCAL
TQMQELARLMSQQRGENTAIKGLMCQLCHLIHLREELSRIDENITVVEKRIDLSKIAQRR
VEIVQSSRESKKDVETEIKVCCERLVQMLFSGVSAPLSGVARKKPDEIRDAVSALEQNWT
TQKELLRLFIPNATTREVLLRPVRARIDELLHETDSIQQQQQQQQQQEQPEQRTEGGTK
TVVSAPASVPTAGNSFAPGQVEDGGTAELLQQETERQTTMPEKNNSFPARRFGSGLV*
>TCRU_3727 hypothetical protein, conserved
MLRSSYIWFHGQAARSNSVLAALLRIRQQHQRPSHPINRRDASLQVISPSRDLAVSSSLE
RQQLVDEAMKILRKEVRGGDALSDVDAASAAFCVEVGKLLSVAAVFGAATTTPRVAEALQ
WVRTNKKQLVSTRQVMSICVPLLNLKDGKTAGRRFVIEELSGPLLQALESPASPTVSSES
DLKQHRSAIVSVFSLVGRLLESDGGDADGGKKAMGEESVFPVPPVEDRPMFYQRTLLFFT
KAVDALLTLAEQSLPPLEISESVYILQACQRLERDSEGKSIEEVRAGLNRVRPMIDAALG
PSTAGTTKRPGDVCQLLSVVSKLQDTHHMTDLSRAALGLLPLALASASAKDICAALQVLV
RLSGSSPEVTEPLLLRRVLEAVRPKLFLIAETHPASMRHVECSLLMSTLSRLEEELADDL
VNLLCGCFTASMDLAQPAQLIPFLQGLFRCSEAASRSSADTHNVPFWEVARLPSVRPCIE
KAADRVIAWAAADAITDSESAQLLLLFSQLRYTRVLAVYVALEKKLVLTVDHLSRGLSND
DSNGNVAESISSSGRIGNGDDDVAGLVVGGDDGSSELKHKSLAAANGIALTSVLMNALYA
FQNEAVTIVREEEECLQRAGKLYETLRQGAVESLTRTRNPKAFVMLLHVLMPEGKRGRGG
GGGRSATLESDVTAASVVNSASRPLDAVAPQVCLLAPVSNAYEVGAIAKAVGEFMAHGLI
GEEGAQRAMEAILERSEAVELSSYDAQSLLEGMRRVRVVSIPPSLLHRLATQLQNTPQKT
TMMLRRLLPVLKTITMKPILQEALIKLTEVAMANACTIMFTNASSPPPLRDTALLAHVLA
QLYDLSLEPLVLNLVVKEEMGMTEEAEEETKEDENGEGEADFLDDGTTDEPDEFIHHQHH
HHLLTVTKKAFLALGDVACSSLQQNVDSADGLTCTLIPPQEIVMLVQSFEKVGVRHHALL
YEVVPLVRDMSGSMEPLELSLLLNAFARLGAWNGRVLNTLASSVAAQIKTCSLKQCQSIL
QALQSSGFLRPGAFLSTTEYKTTLLRDWRPACTPTTQASIDPLVVLATSVVERMTTLVER
PESVSAMLESQSLEDVAAVVRVLGFFVQPPQPAFDTYFEMAMKKLVLDSKDIMDDSSPLR
QRKWLMVALFLKGHLGKLRRYHRQCISAQAMADSITAHETTLLSLTPGLRLMAEEKVADL
YYTCCVFAMVYNVKFSPEAASTILKVISEKLQEEDVARNPRRVSSALRHLTKLSSKHIGA
PGIVHKIALDSAWHLVAQLQGNAAEERNCSSPECSSSAAAVMLEVLCMSHLLALPYLVEE
KQKLQQVLFFFSNHLRKNDISRLSAAECSILVLSTAVGTAMQICCQVNVAWLDEVQHGIL
LKEKHLSVHDAVNILLAEALCCDESIVQAETVRCASRVLVGQMGKTDWTGLRLLPELYRL
ATAGDACFMAWCKRLQQVAGDDTTAPVAGGVLEVFERVLPALLRALRSAEKGTTPTLCWQ
CRVDVAEQYQRCAETCGDERGLADALAELVKKETCASS*
>TCRU_3728 aldehyde dehydrogenase, putative
MRRTSCTFCKAVFDLKNAAKLTTGVVLDRTVAFINGAFVTPASAATITVEDPCTQKAIGE
VPNMGKEETLQAIDAAKSAFEGWKNMMPRERAVIMHRWAQLVLCHSQSLGIILSRESGKV
LAEGVDECLYAERYLEWYAGEAERVYGDIIGGPREGVVTTVVRRPVGVVGVITPWNFPSS

MVTRAVGGALAAGCTVVLKPSELTPFSALVLAQLAAEAGVPDGVFNVLTGNAEPIGDALL
DSFDVRKISFTGSTRTGKHLYARSASTMKKLGLELGGNAPFIVFDDADLNRAVIGLIASK
FRNAGQACISSNRIFIHEAIHDAFVARLVEKTRETLRVGNSLDETSKMGSLINGAAVDRM
EALVKDALAKGAKLELGGKRIPGPGYFFEPTILTRVRHEAMDCSKREIFGPIIPIIKFSS
ESEVVQLANATPAGLAAYIYTQDYRRQSRVSEQLQFGMVGVNDVGLSSPCAPFGGVKESG
LGRDGSKYGIDAFVDIKYVLESRI*
>TCRU_3729 hypothetical protein
MTGKWQEMEVDDVLTEMEAFIDASGIRDVALIAASDDAFTRDHLRELEDELDRQQPRPTK
ELILNPVVKRHLYFPLTHSSGGHITQLPLPQDQIFRLGARVVNCRAVGSVPFGAVGTIVR
LLATSHDAEVVYDEPFTGGSHFDGRLRQPRGGLSKLSSLLVLNRPGDDDGGGAATESERT
TVSILRALMQKSQQQQQQQQQQQQQQKRGSVPMAESVSVIPKPRSATEDASVSKTVTGMA
PASAAVTISGGAGGIRLSDLVGKLKASPEHSDAASITPPTVPEEQKDARPSPVSLKPQVA
ITTNTSSVAAGSNDKKGNNGNLGVNNTPPQVETRTLIPVQSGNENNAVVENRLQMHLRGG
GSPEEKNSGKRLKMTFTVPREIASGEFTIRRGEAVPFFRRLLKLRLSEELGKTTTHR*
>TCRU_gamma, conserved domain containing protein, putative
Elongation factor.1
MVCSKQKDDKKMQCMTANLIRVWLQRMEHVGQYALDPALMIGEERRHDIVALCVLRGRGM
PAIVRDVEDTELLD*
>TCRU_3731 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGGRCAEEKADEVLVAEPGPSLSGGGDSPTKQSKNSSPV
PGPLVLPPKQQKDDKSEHLHAKESLESEEEVPLKTQEGENKTQVPQDGVQNGNQSIPQEQ
SPHQALPPHQPPSVGSDAVSPGGSSVGSSSSGVISSPHGGGDKGTTDIILSNAPSSSPKG
VLPAEEAETEHHSLPNENAAERGNVGRAAAQGNEDPFPLEERRTQDGKSEAHQTEESSKD
LNKQPQGNGKIQNGSPNADTPQLQTPHGRKTPETKGNNSHNTDISTNLPDAQEPKYVKES
NNENPASTPVKTQGTSTGIQEEAPASHPNGIPSLQQENFTGMKTTENVQPPEVAATNKLQ
TGDKSKDVNSDGSTGVSRTTSPLLLLLVASAATAAAVVAA*
>TCRU_gamma, conserved domain containing protein, putative
Elongation factor.1
MCEGGRCSHTFASSTHVAPLGSLSQHPDRGSRGVRVCYKHKKDNKMLCVTANLIRGWLQR
MEHVRKYALGVALMIVEEMRHEIVALCVLRGRGMPMIVRDVLDTELLD*
>TCRU_3733 BNR repeat-like domain containing protein, putative
MMAHCAGGYYDVYRSILDGVNWNPDGEPINRVWGNSRDPAGDGVQSGSTTAIIEGKKVML
ITAPVYAKEENGKGRLHLWVTDKARVYDVGPVSREDDDAAASSLLIKDKNKELISLYENK
KDGVYSLVAVRLTEKLERIKEVVKTWKDLDSALKTCRSGSSGTVDALRKGMCNGPVPTER
LVGFLSGNSTGTEWRDEYLGVNATVTNGERRVPNGWTFKGPGAGAVWPVGDMGQTVPYYF
ANTKACACGDGVYPRGAEGGQQPHSFDWREDE*
>TCRU_3734 hypothetical protein, conserved
MKSHLVAVLGLGLHIRTPQQGVAASTTETKTTPPLEKVPRHARCGEVKRSARRLSVNTAR
PFRSGHSVDVTCGGDVQKNPGTEEDGCINIWRLDIAGLSSVKRLNLRRDWSCIKLTSFFS
RK*
>TCRU_3735 BNR repeat-like domain/Protein of unknown function
(DUF3676)/Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MLVGKYSHTEKQVEGKNERGLLLVKGTVTVDGGNNKKLVWNETHVVEPQGKGASLSLTEL
IGGGGSGAVMRDGTLVFPMQAKKKDGTSVLLSMSFIPSKNKWELSLETPGNGCRDPTLVK
WKENEDEERLFMMAHCAGGYYDVYRSILHVVNWYPYGEPITRVWGNSHNRKGYGVQSGST
TAIIEEKEVMLITAPVYPKEDNGKGRLHLWVTNNARVHDVGPVSRENDDAAASSLLMKDN
NKELISLYENKKSDGSYNLVAVRLTEKLERIKEVVKTWKDLDSALQCCSSSSSGTVDVRK
KGMCNGPVPTNRLVGFLSGNSTQTEWRDEYLGVNAKVTNVEKRVPNGVTFKGSGAGAEWP
VGDMGQTVPYYFTNNEFALVATVSIHEVPKEDSSPVPLIGVRMNDTSSTVLFGLSYTHEK
KWLAIPGKSAASQFVDGWEPNRTYQVLLQMDYDYWTIVVDKEEIDHKSYDKNLFNSHRIS
HFYIGGDSKHQSATDGHVTVTNVMLYNERLLDHKLDELHASKVNIPSLSVEGQPKGQVAS
KDVSVASESKSEESATSHEKLNESDTNEQGENSAEDPVPAASSSTVVGGSSISEPATATE
IAGASLPEDNAQLSEGKTVQQATPHEPKDSMQQDSDVQPQDPQPAELTGVTELETSSEGN

DTEEPEEDGGTNDRSGGSTSSVGASLSMATATASVYGEHQVQQSIELSAENNDVRSTGTG
TTGAEQSLSLEVGDRNSERTMNSDSSLTSSKSDAEPTSAENTDDVFRTEGAEVSSEDGKE
VPQTVDTASGNTSTAPEEEGIPSTKGAARHSDNDIFNTSEVADLLSTALNRDSTVHLCVF
RVLLLLLLGLGGIAALC*
>TCRU_3736 trans-sialidase
MPRLLLYVLVLFFLFNFCPNVPAHALAPGSSRIELFKRKNSTVPFEENGKVTERVVNSFR
LPALVNVDGVMVAIADARYDTSNDNSLIDTVVKYSVDDGETWETQIAIKNSRASSVSRVV
DPTVIVKGNKLYVLVGSYNISRSYWTWQPDGSDWDILLAVGEVTKSTVDGKTTANITWGS
PVSLKEFFPAEMEGIHTKQFLGGAGVATLASNGNLVYPVQVANMKKQIFSKIFYSEDDGK
TWNFSEGRSDFGCSEPVVLEWKNKFIVNTRVDRARRLVYNSGDMERPWVEAVGTLSRVWG
PSPKSDQPGSQSSFTAVTIEGMRVMLFTHPLNFKGRWLRDRLNLWLTDNQRIYNVGQVSI
GDENAAYSSVLYKDDKLYCLHEINSNEVYSLVFARLVGELRIIKSVLQSWKNWDSHLSRI
CTPADPATSSSERVCGPAVTTVGLAGFLSDNATQNVWEDAYRCVNASTANAEKVPNGFKF
AGVGGGALWPVSQQGQNQRYHFANYEFTLVASVTIHEVPRDATPLLGASLDSSGGEKLLG
LSYDEKHQWQPIYGSTPATPTGSWEVNKKYHVVLTMANKMGSVYIDGEPLAGSGQTVVPD
EGTPDISHFYIGSYNSSNMPTESHVTTKNVFLYNRQLNAEEIRTLFLSQDLDGVEEDKDS
SDDGDENDGDDSDGDDNDDASSLSAGGRNLVYVCALVLHLLVLVYF*
>TCRU_3737 hypothetical protein
MKAKCLLFVLEIIVMACVAQAETCRVNTSDTGESISLEYLSNYGNVSVMLGDVKIDLGVS
FCWPKKFSAFGEECDFGYMIIYEKGCEGTFTHSDNVSLENDTLFFTIRSPNTLMADVYVE
CDESINGLRALSANETEITKYVFRFASTTVCPGYQPPGRDNFPSKGFLITIVTGIVGVVV
VAAALFQWKSRSPSVEDYSQLI*
>TCRU_3738 PPR repeat family, putative
MLLATAKCLPKALSPYAKALRHVALRGAVAFGPSAKEMELDMYRKGTLPPDYRPPVQGKW
DDTIERWAYAWQFPAEEEQEDIVGAVERNSSGMQALLEFGNRLLQSPPSAQPHSGKYSKV
YPPITGGPNNGLTGLISHSSNYEHLEQAVSELIISSDTESFLHDTMTAAELSARADVPVA
YIDDNSELSNASKELACILEEFGLEYTEDGLITVISALSQQQYSSMSRAIFDFACTVGLG
PSAELYKALMRHASRRGDVNESMALIEEMKAKGITPRIGNWHELMRAFHQANDYPAVSQI
VDNMKMYANIEPNEVTFALQLKALAKDSSQINSLAESIQLFDQMENVYGFIASRPHYDAM
MYHLSQSPKPEMRLRCEELAHKMELMGIVWNANTYLNLIRSAQVVGDISAVEKYLSKMRD
DGIVVGITHLSWAIQAHAQSIIRLDYAAMREKSEDPLPIWLEHLETCFGIYELVVRRGWT
MQLPFVNALLRLCCQTTMLAMEHSPDQTTTIGRFEEQSNKIWNQTFEEWHLKKDVYSYEC
YIALLAHQQRIDEAEKLFQEMVLKEDLTPSKRTYDCLIFMHLSSGEEGGTARALRYLEAM
ERAGIQIRPSLLKKIVRVNNAAGYKRDMKRRARRIMQAREEYFARKEQNIGFNEDAPSSS
VSSKADVDSEGNSVLTPLPISASSTLAWWEQWKRETASKHELFAEENTDGTPKGETFDEK
NEALRQLGINSAFPTKDHLPRLDRQKILPQIRSEEGEMAGSLWAMDGGEFSYPKDGGGPQ
GWGIRLWRERQVVKQEYQKVIDGSQPVPQLSAIGNAVRTTSTQLEIEKSGARTPGELSDH
HQFPHHCFDSGALKPPLETAVPVPLSGELVWQGESRDNLAPYKSDEEIALENDNTFFSDL
SEEAERKMDASVMAIQKREENALEIKGKGVTRRSKYDYLEKWREMYRHGTLEVPEGPTLR
FGRSPDDHKDTMAALVREWYLRNRKTPATLEDLQRWESDSQREKEASISRKALKKRKRIR
SHHKGE*
>TCRU_3739 F-actin capping protein, beta subunit/WW domain
containing protein, putative
MRESTNKAEDVAAAGASLLAQYPPRKGRMILDNIVTLCKYRDAEAVLNIIYRQVSPVDTP
WPVLQCPSAATQWLSATPHYFIAFEYNRMGDSYRCPLCNKYVSGDKFVSFPLGSSGLLRQ
MESAANRVFVEYAELYYGKESTASVYTWECDPANTESKMGLAVMIKHRAKSPNGNRPGHF
SLREKRGVWQSAHVGIVDISSGAYYFQSSFYMDAFVPLGSLPNKPDAVGRFNGSVASRLF
SFESREAIATPDLDGLIASIGEQVQLTENSFYGRLFEIYFSKAQFVAEGMRVIPQSTLFL
PPQSRWKEQPAASRVTEESSQQADVHVIGQTSDTNAMTHSGAVRLDYQFAEGSEEIASPL
PRGKESTVVDDWKEAYDDDGNRYYYNEVTGETAWEKPDVGKLVLDILRNLHLMHSPDKYY
RRLKKYFRQYETELNIDTFYSLTNEDQMLELDDGSTMTALEYIVPAYGDRRKIEVYIAQN
ARKDA*
>TCRU_3740 amidohydrolase, putative
MNNINVLISAVQPEVVQWRRHIHENPYLAYEEQPTADYVASVLTAMPAPLEIRRLTPNSV

IADLRGGAGEGPIYALRADMDALPLQEESGEPFSSKRPGVMHACGHDAHTAMLLGAVKVL
CQVKDKIRGTVRFIFQHAEEVIPSGAKQLVQLGVLEGVKMIFGLHVSAATPAGKISTRSG
TLYGACNDFDIVIKGAGGHASQPELCTDPIVIAAEVVMGLQTIVSRRIGALTAPVLSVTT
FHGGTGSYNVIPDTAHLRGTLRCLDRDVQALVPGLMEEIVAGIAKAHGAQHEISWLEPNI
VTYNDHAAFLIAKDVISEFVGADAFLEKEQPLFGVEDFSEYVAKTPGCFCLLGIRDEASC
SVYTEHSSKFKVYEKALEHGVQMHVGFIVKLLMRST*
>TCRU_3741 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MMFCNAGGAEQAEEQASERNYKWKDIKEGEGVTVESLGVPGLLNVGSDVFAVAEAQCKKS
LVSFTGIASRLLTTQKVNTPVEVLNGAEDKTQVLEEDGSEDPKKKVDVSRPTTVVEGNEI
YMIAGKYSPTAATDQDGGAEDGGLLLVKGSVSEESGSGKRIKWSDANAVPRASVGELDSW
TGLIGGGGSGVKTDDGRLVFPVEGKKKEVEAPNDKKAVSLLIIYSLDTNSGVLSKGMSDG
GCSDPSVVEWKDKKLMMMTACDDGRRRVYESGDKGESWTEVLGTLSRVWVNKKSEGGVRS
GFITATIGDDDKKNVMLVTLPVYPEDASKKETDNRKGKLHLWLTDNTHIVDIGPVSDDDD
AVASSLLYKSGTGDNKQKEELIALYEKKKGEGKPSHSLWSVLLTEQLQRVKDVLATWKEV
DETVSKLCPSESDAKDVSHDNACSPTVKITDGLVGFLSGNFSENTWRDEYLGVNATVKGN
VGDTKAKKTSDGVTFTGAWAEWPVGEQGQNQLYHFANYNFTLVATVSIHGVPQEGSPIPL
MGVKMNDDGKTVLFGLSYENGGKWQVLCGNGTNSQEHSSAWEKEKTHQVAIVLQNGTQGS
AYVDGKSVGGDVPCALENKDSKKISHFYIGGDGSSAGVSEVQDVSVTVTNVLLYNRPLDD
DEITALNPNKVPIPPLVVGSAQGTLLQSLSAGQAPSGPESLNENQGAGGGRASPSEPSIV
TTSGEEPVRQSASRASPGGSKNVDVASPSDGDPRVGSEAGGAMQGDTAPQTPVDTPDKAD
TNAPTATNVAQVDPTDTTKVGTSSGANGETVGGTDVQEELHARGGEVNAAALSSSLGNLS
QGNNSDAGTVRGSGLQPLLLLLGLWVFAAL*
>TCRU_3742 dynein light chain, putative
MASATSVKEAIARFEEAEYRRRTSEMSEEEKANAPRVVAAEEPRVLLIGMLPPIVKMDKD
IATLVNCEHLGLSTNGIEKIGPGLRELKKLKILSLGRNVIRKIEQLDIPQLEQLWLRVCD
GASCQSLWPLPREAGGRCGSSCGTRPSGPAGGTGATGRCSTASLGVLAA*
>TCRU_3743 hypothetical protein, conserved
MAEAASCLDLKASFIVSLPRETRHLFRCRVEDGTLVELTRFPMGYKASPEILQIITSAIA
VVATVVRPLWAAPPSVRVDVWIDNIRIAGSKSGATFWESQVLRNADCRHASLGEDHESGA
THYTFLGVQFDQTHRAVSLSDKFVRSVRAMPALNSLTIAEMEVMASRFLYAAAILCTRLC
D*
>TCRU_3744 hypothetical protein, conserved
MAALRLQKIAVRSETKQARPLTKEEMNQFIRSRTDWRERVVLRIAWITASRWSEIAVFTP
NNFKLEADGSLVFGLVRGAEDGESGSPPRLAVREDARTGRLRHYKAMQDTSRKRNAHESY
*
>TCRU_3745 hypothetical protein, conserved
MVHTAVARALTPRGATTVSRHDAACPDACPCRLHYANNNPTREASLSHGFSRQYGVLNPG
AKTSQSSMKSQEESMMEPAKKYRLAPNGMRRPTLRSHTECTLYSIELMLRPSLKNASVSD
EP*
>TCRU_3746 hypothetical protein, conserved
MQAEVRVAHLALLAFIAILPSTMDVWVDNTSLQGAANKGSSKSHSMTWEPQRIYEFLDSR
GVQASFGYVRSAENPADGISRGRVFTLQDLAKGWNLRRGRRGLVVGGPQSLPLRK*
>TCRU_3747 hypothetical protein, conserved
MSPATGCKNGAGGRYDDAAVVPEAYDNDVMSWSFCVSSSPSSSSRSSASSPPRRGSRSSC
QWRSSTYHTTTLYTVAKSGTVVSSSTIAAYALAPPSLGARWLAAPTTHSAARSTKLAVCI
TVRKAERIMFVKATTPAPASSTAAMQKYWTWQPPTGGCTAAIRPTTHSTDSWNTHQYTWL
PLMFVSMPPYIRCCAAGCQYPTGYSSRSCSGFPENCQYLVKLAPTWRAIK*
>TCRU_3748 hypothetical protein, conserved
MPRCIACATTYVRLGKRIAAHAVAASTPRHRWKAAVTPQCTHPNTAASSALPTTIHSGSR
AANTDRKYGSATVLARSCAKAHGILANTPSACISRTEPSPPVTTTATAAAPATTPVIAER
ALAAAGSVADLIVKDPSSTPLQPPDTAAASQRMTIVSSAAMK*
>TCRU_3749 hypothetical protein, conserved

MRGVHLAPRHAQHSAPRRNNARTRVQRIFATEHSRVQRDTATDKLQHSAVHHHRPPTSHH
GHEGHAGHNQHGPHKPQARQHQHRCVRRGLQAGKIHKRRRPRGNQQGVRHRQHRPRGERA
GQHKRTVQRLHIAHRQLHRPALVAPRRPRTAQRSSAHHVQHGTVQQRHVLHNNPHAVPRH
PRHVEHRTHAVQHNVAQRHLARAGRHNEHRLHRHALADKHSRRSAHSGRQRGSAHRHARL
VVPTAAARAHAHTVRHARRRRPGRVALRVPVAVVAPSNVDAPGVAKTSSSVLLRRRQDTA
TSVVARHPHMRPSQKRQAQRQHPRQQRSVAQKAQRAPSSGHGASGVEHLPRDAVVHVALR
QQHRPAIQTHRRIERHRVVLRRRKFAPHKRHSGARHAHSPTHRHRVLAQQEVAVNKRHHG
AAAGRDTALHRHAQPQRRLHRQPVQVQRTT*
>TCRU_3750 hypothetical protein, conserved
MPKPEAEEQSSTEQDTEDSPDTEEVTTGKKNVQNTVEMGIPSSSSSAASKPPVQQTTPIL
AQSPAAPSPERSALAPSEKESTAPSFSAGEGSRRAANVAQNSKEEKNEKLPSENETQSKA
VEQPSGNDVAEQDSPARTTASPIPASGGADAQRNEDADNSNAQALKSEGTHKNSETGYTN
PASTAGDAATQTEKALADAKTNDTATHGDSDGNTAASHTTSPLLLLLVVACAAAAAVVAA
*
>TCRU_3751 hypothetical protein, conserved
MGGFGLRAFIFFGEFVGALLEELKELRPPASCGGQYAVLKAIPQGHRTELYGLGSLKNSS
ERENLKYRLPCTPETKNFPLADPFFLCGLTTEDPGWAADGYGGWAPHDRQNCEAVQ*
>TCRU_3752 retrotransposon hot spot protein, RHS3, putative
MAAGSYLLYQLLQYDVERLQVVFHCFGGGDAYVSDKTTRAVKRCSDEDMCVSELRSLRGH
GRNVYIIYGVAKEGTPPPRHFAPTSGWGMIAVPFLKVANYDEWAKQLQAARVIVNFLDEM
DVRAMCA*
>TCRU_3753 mitochondrial glycoprotein-like protein
MQRSMRGLWLLRPSVPTSSVSRLPPLLLLLQKQQHARRFMSDGGLNGVDASSGEMAVARR
ALPPSDFPERSFLKCIEKEMQDEALRLDKEEGPPPPPSGWEMYHAPGTSLFYGRRWWVPP
TPVTPTGQRVAPRVLERHTIRVQLTTRDPSLDPECDVRGEHFPFSLFVQRVADGAGTSAA
TVHGSSSSPPVNHAERAHEVLGEEEERGLYEQSIEVRADFVEGELVVDHVVFHGTFKPSA
AFKSRTNTHSNATETQETEGNKNESSRVSTESEVHYNNMFGGYPGPNLDEAEEEVLDGIQ
AWLAERCIDDQFGEFVGQYSVWVEQMEYERWLRQLRDFVTA*
>TCRU_3754 hypothetical protein
MSDARLRGGPFCSAVLDHIAATETATSELEEYLKGLRARHGVIEQELKELAEELLKLGFR
PSIAALQERSQQLQAAFHKVDELKETMDQINELILIVFAAVKAIDSAPDVMGKASSFLAS
FGLALKSERANAGLWSRVPSYAMLKSRTPKEFLKGVRTVFAPLCPNDGSRGDCNRL*
>TCRU_3755 hypothetical protein, conserved
MHESQNKEGAPQPPPPPPTIPSGGPAPSSTAGEGGPLPDQENLQKLNKAKKENTPSRSKT
DSEAPEPPPGDATQGQHSHDTDTKDSTKNAATGIPAETSSTSSTSASGSGDHVQNKADED
DAQSSEGQHESLETGNTNVVPPLSETASKTAKTTTDAQTNGTMTKAGDCDDSTAVSHTTS
PLLLFLLVVVCAAAAAVVAA*
>TCRU_3756 hypothetical protein
MSTLTTGEYTPCPSPPQFSTPVLPSTSVFSSLNTWVLVDPSHIESPRTFFDESFSAIVPP
AVSTANQTIRSSSAGSNLTCGVHHQEDFSSGWSILSTKQSQLQSGNDLCDLVASEHSFSN
NSLINRKNMDGFQSGESNDEIDQFGLYNSMPFASREYPCGKNLRRRTTLPFRKCSGFYCP
TSISCLAFHFTYLSEMGNGGATYTLFRNVVHPMGAWHWREKIPSESSDGPSPEMSVGTMP
VHNHAKGWGGNSKNEPSFSHHSDDATGENSSNRSNDSSGEETSVVSFFLCMPFLRFVLKT
IAMMASSNENVTRRSGHRRRRRRRRGGSGRTGEGSDSRPCLGERIFGEIEALVTCALHGI
LVFML*
>TCRU_3757 hypothetical protein, conserved
MAGSQVEGGMSKGEQLIGNLLVDALDDRFRQERLNVEFAFVFDTTVDTVLDDLVEALAGM
GLRLAIPRGQCALLYDNSCNNASNGSATHAGESLHKGQEVDGVGGAELHVEGEEEDDSRR
MLSGADVIFNAPEVEAFYNLNYRCGLHRVATFRIVKRVRAPLPLRGVSRGTSGKENSDGS
GDQAATEGLSVYLLHRKLQFDDLSNELLAPTNIEGNNEAHGDYKKDLLRVREMVVAAERS
ILTARQQHYQQQPPREPHWSVQLSKPPSRHEWLCAVEAEATAYVRLTAKLARDTTSVVTR
QETARRTLENEVAEFHQRIDEVKMNVVRREALQERVDRLKIEIEAQREKEQELLRSLERA
KISEVKRTPPVRPVASSFFGSYAEQHPQRTPGVPPASEAGALRTHRDVPLSSRLLSPPRP
TPPLTPPPPSSLPHEFVSNYSAIQGSNTGIGAATGSQFFSPSLREDVRQALAPYMRSSIN

AQPYQSDLQRLRQLAVELSHHLRSPNPDPVERRRLMGEIRSLRQEVERQREEESRVTPNP
*
>TCRU_3758 UTP--glucose-1-phosphate uridylyltransferase, putative
MKMVPDGGEPTCEELDALRERLSSPELDQRHLFNGWPASAEEYTEEQRRLMLELFRFRDH
YSGGVEQYVRNAQRLFKGLKNTRHEYAALELPPYVYEAPSLFDRSEELMNLEREGLGYVK
KSVFVLVAGGLGERLGYSGIKIGLPVETATNRCYLEHYLRWIKHIAGPNAPFVIMTSDNT
HERTEKLLRGLGLNMTNVHLLKQETVFCFNDITAHLAIENGKLLRKPHGHGDVHSLLYRS
VDRSSGKRLVELWQSQGYSYIVFLQDTNATATLTIPVSLAISAKHRLAMNFTCIPRQPKE
AIGLLCKVRMFGSNIERTINVEYDIFESLAASLTELGGDRAAPGSIYSYFPGSINTLILN
MDDYIPLLTEFCGVVPEFINPKYTDDSKTTFKPCRIESLMQDIALLFGPEEHRVGALRFS
RFTYQPVKNGLQDGIKKFAQGLAAYCAATGEEGFYEAIRLRLQAAGLNLPTRPKDAYDVD
FGAGLKVRLFPIIVADAMAMGVSVEDITQRLLPHPEHVKVSARSVLLVEGCVRIESLDLD
GALRLVGPTDENAAPLVINAMTVKNAGWVVRPLSADESADEIYRIRGYVIEEKEMQAVHH
AKL*
>TCRU_3759 XRN 5'-3' exonuclease N-terminus, putative
MGVPKFASWLTKKYPEMVLDVIPADVHGLYIDLNGLIHPCCHSERDPSVAARPEEEKLQC
ICFEVEVLLATVRPHDILYIATDGVAPRAKMNQQRARRYMSRAKIVSSGTEVVEEVVREF
TPNEMAEVDDDLDDIRQLLMQDALYGGVNFQDDTSETLNGVANIADSLTPVTPCHDKSNN
HEAHAEAWAAFDGLTDGTLEVTEFDSNCISPGTAFMVKVTNAILTMVQDKLANGDPLWAG
LRVVFSGANTPGEGEHKIVDFLRTQSSYPGFNGKGAHVIAGLDADLIFLSLSLHIPHILL
LRDRDRNPYAVRMHDRHREKIQVQPHKLHTESEKNTPDLARELEERTEGNEIHVDADNEN
SKNSSSEGSGEGKPPGVLEANTNYEYYDIDTLGSCIVSELHGLCQLKNFTPNNKKAFSPE
LLVSSNGYHFYRHAGCADGSLRSVSKGDDKSHHDKESWRKFLPCASQANSKVIDDFIVMG
MLMGNDFLPRLPGAFCGESVMDNLLELYVSNVLPYGFLTSGYHEIYLPQLQRLLRSYAKI
ETVKFRRFALSNKKMTPKEAAEPLYSPLDEQWRQTYLTSTGLTGNLEEACKKYVEGLRFV
WRYYSGNASTCSWSWHYPFHHAPFALDIADYLQRCDLTNLPPPPLETTPPDMFLQLLCIL
PPTSHALLPAVLGDVMLNPPEELRETFPSMWRVDYTAAYGKDYLAEVLLPFANVSGLREV
VESSRPYFTKEEQERGRQINYHLVLGSRTSGFEINGNICELNANDAAIWDLQREGLRYMQ
LWDSPPERGRPKTYSCTTLVPWVTCDARGRVHKRERLSRSERRKHRDDVLSDASVTLINK
GPSFAAYLFGFTASFLLMAMTLFPWLSLSILQVLAVNLTAVAFSFFIGIAVHDPIVGSGV
QRNNIRFTFVDWLCAGCLSLNFSCNDKCFCCRLPFDSKRCLAVFSGTQSVTPPLYDPNHA
AYMETACLEIPGRKPTDAS*
>TCRU_3760 WW domain containing protein, putative
MAVIPKAGQVFHGEDGTFSIVLPDTCDPNNEPTQEELLDYANWLGIDAEKEPHLLWIARQ
GLRTPLPAEWKACRTGEGDVYYFNFLTGENSWEHPMDDVFKRKVEEERAKLVDGEGGSSK
TRKKSKSSSTAGGKGDRGVEKRRLEKGAAGYVASPERSGKGGKLSAVMSPTSSTSTSPMT
KGLPATALRFGRLGALGTPEATQRLTPDVSGLLKPSNSGDRSFTRFGFGGANASTSSLGL
AAGGISGGIGSGKLSLTKPPDGVKEMEAQIRRRIDEEMDTRLRAMRTRHEKRIMEERTAM
EKELQKVKEDGECAVAAAQQRHAEGVKQRAQAELESLRRALEKEHKETKGRVESLRQTLQ
RERVSMESTLQERLEEVRKKLQLSHSEGLIRQREASAARLNKEKARLLEDLARRLDAEAN
ELEKKTQTTVENFKKTLEAERAKLKEELNEKGMEHGDRSASSAVAEAEAQRAYEAAVQKA
TSDAASAMEALRREYRLKEEKLRAAKEEENCQEKESSTAMTSFGDANKNDGLKRREAEAE
AERLERALKQKIAQYEAETQRLVATRQAAMMKNIGPLRDNAESGDQGCSNKTSSKNAKVG
HFATAAVQEQRRFEVASRRLETKHAQSMDRIRREHEMILREKNLFNPRQSSGYVEKIQEE
HKSWLKAHPPIALTMPQLEPVPAVPGLMDVSPVPMPGQEEQQKSVDIAVTGAKKKRAVED
SKKLAEMEAALSREMKEAVAAYHEKRLREIEAQLTQYRVAQAEEYQRRSYQMAADIAEAV
SPQSSQLRGKAEDPVPRLNEVSLEEAKVREEEIRRHLQGRIDALEELKWHARDELRQRQE
EAQRKTLTLTPATTALQRPPPVPTDTFFPGCQEQKISPRPCQQQQQPHGLLTPVLNRTLS
TIAPANSLWSSTRPSPTKPYHWLSADNAASSLFWQENHAPSAGAGNVEKVLPSSLSQRDV
VLEDRLHRASLLLKKKKEELRAQQARMERARDAWRRDMEECRRKRDRKHALMLRELKEVL
EEKAVQLNHEVMELKRATQWLRKRTVRYKQTLNIQTSNLASAEETSTADHTAANGSGRII
SLLKDILANTELLGSYVASTKKTDAKTLRHGRCRSPASPPNSRTYPHPSRHGDALSSWKN
AGPSGVTRWLMEQ*
>TCRU_3761 membrane transporter protein, putative

MPSLNNSFVGGAAQQVDIPQSISTREIFKRIIVITIPLSFAQLAQFSINVSVIAVVGSLG
VNELGGASIAYGLINATAFGFASGFCGALETVLSHTYGRDPMSKLYGIYTQRMFLLLMIV
GLFLSPIILFADRVLLLLGQNPDVIVFTGQYCRISVWGIFPTMVLELLRRYFACQHLSTP
LSVNLVVGAVLFPFLLIACVHTMGFAGAPTGWCLLMTLMSGSLLLYLIVTRKYKDTWGGW
DDAAYRNWGPLLSLAIPSMGMMFSEWVSLEINNIFSGFGTREELAAFGITFQLSGICWAS
ASGTFIAASVLVGNAIGEGKPLLARRMAFCCLFMTVTIALLSLIVVSLAKNLIPRIFTDD
KKVISIVHSLLKYFFVYHVFDAFQSGVMGVLRGCGKQKLGAYVILLVYSIVGVPLGIILF
LKTGFGIGALWFGPAFGVMVAGFPVYMYILLYHIKWGELKAHTDSQELSGVIVEENVDEV
LVCSNDSSEKSENGEEGNSKNDDKKTILNGKTSQNNTPTLTRSPSPQPIGRQKRYQVETN
VAREGTE*
>TCRU_3762 hypothetical protein, conserved
MWSGLKLERLIYTFPETTTPTGWSQPDPHLSSLLGEADTNEGDSSAVSGEDVNVEHRHFN
NGERRRKLAVRPFTVPASAMAEEGGEEGSHVHLGFSFPGEGKFDEEPEAVLWRPQGNCQW
LNEESDCSQRSAMSCPARPTKTTIQLGDPGAPIKKNRERKYICNDADENSNSRVGPAMYH
QLEFFQESNSVSFPCESSALSHITPLDETGESVDLANHMSHLTVAVSPIQKRLLFTGVLD
DAVDAPSGRDVGDDKGVGSGLQSLRREKRFLEEMDTNRDAANSNSMACTMPREPHRKFRR
IDAGENDRKSLDNHFHSRR*
>TCRU_3763 Concanavalin A-like lectin/glucanases superfamily/Protein
of unknown function (DUF3676)/Trans-sialidase of Trypanosoma
hydrophobic C-terminal, putative
MCNGRVPTDRLVGFLSGNSTGTEWRDEYLGVNATVTNGEPRVRNGLTFKGPGAWAEWPVG
DMGQTVPYYFANTEFTLVATVSIHEVPKEGSIHLIGVRMNDTKSTVLFGLSYTHDRKWLA
ISEGAGDVEDFHEWEPNRTYQVVLRMDDKEWSVFVDGEEIHNKKYNTSLFDSHRISHFYI
GGDSKDRSATDGHMTVTNVMLYNEELFGNDKLYKLKTRKVTIPSLGVEEQPTEQVASKDV
SFASESWSEESAIYEELNEDDTDEQEEEIVDDLVHAASSSTVVAGSSVSEPAIAAESAEN
FRQEDNAQLSEGKTAQQETPNEDYKSMQRDSDVQPQDPQSEELTGVTDLERSSESNDEEM
PEEGGKADYRSGGSTSSVGASSDMDTVAAPADGEHQVQQSVELATENNDVRSTGTGTTGA
GQSLILEAGERNSERTMSSDRSLTPSKSNAETTSAEDTDNISRTGGAEFPVENGEEVPQT
VETAPGNTNTTPGETEIPSESNTTTPSDTDILLEHGKFGDLLARGEFAESTVHGCVSWVL
LLLLGLWGTAALC*
>TCRU_3764 DNA repair protein RAD51
MNTRSKRGKRKGVEEVEVHEIANTSPDPVAAPEQQQQQQEDQQNVDGANNGGFRVIQVLE
SYGIASADIKKLMESGFYTVESVAYAPKKNILAVKGISETKADKIMAECAKLVPMGFTSA
VVYHEARKEIIMVTTGSREVDKLLGGGIETGGITELFGEFRTGKTQLCHTLCVTCQLPIS
QGGAEGMALYIDTEGTFRPERLVAVAERYKLDPQDVLSNVACARAFNTDHQQQLLLQASA
MMAENRFAIIIVDSATALYRTDYSGRNELAARQMHLGKFLRSLHNLAEEYGVAVVVTNQV
VANVDGSAQMFQADAKKPIGGHIMAHASTTRLSLRKGRGEQRIMKVYDSPCLAEAEAIFG
IYEDGVGDARD*
>TCRU_3765 plectin, putative
MDERLRKLRLERGQALLESCRMRDFDRSPEETARLKQRGRVLYEERLRAEEKGSPCVEMR
YHSDAVIDLCSIPVKEGQAATEKTHGLSYLPPQSVELLSESRRDGDNISTSHDCTTAIID
YSILDSVREQHIRDVRQIEILTKESHLLQETIEKQQEALTKLAAELAQRDAQIQCNLKND
ARKLLPPDEKETGVRYDGGSHHMQEMVPAMRPRAQDNRRNPHLETSEDLHDAESLLARKQ
VEIQELQLKLQEKILYCNKLGEENKNLNKNNQQLQEDVVALLKKVCMIQEELINTTEEGN
LSQKTVIYLEHKIKQMQSEYKPHTPVPESTHMEEELERLARQCADAEATMHRMEAEMAAE
NAKLKEELCRMQQSHEEEIEAALLEASDRIAEHDDLLRHKLEEQEAELEARFLEQLNSFK
EPGGDSDALHSLLSLKEENAKLKEELCRMQQSHEEERQAAGAAMHRMEAEMRSQQQTQLA
GPPRRAAASSTNPFASMGALSKEPGSFPDQGDDGDDVFGVGTEQHPTATGDAVSVDRQAE
PEGLVTELRGRLAELEAALSAPHWPGIALWERWSVLHGSAPMRRRPCTGWRPRWRQRMPS
*
>TCRU_3766 plectin, putative
MQQSHEEERQAAGAAMHRMEAEMRSQQQTQLAGPPRRAAASSTNPFASMGALSKEPGSFP
DQGDDGDDVFGVGTEQHPTATGDAVSVDRQAEPEGLVTELRGRLAELEAALSSATLARDS
AVGEVERLARQCADAEATMHRMEAEMAAENAKLKEELCRMQQSHEEEIEAALLEASDRIA

EHDDLLRHKLEEQEAELEARFLEQLNSFKEPGGDSDALHSLLSLKEENAKLKEELCRMQQ
SHEEERQAAGAAMHRMEAEMRSQQQTQLAGPPRRAAASSTNPFASMGALSKEPGSFPDQG
DDGDDVFGVGTEQHPTATGDAVSVDRQAGPEGLVTELRGRLAELEAALSSATLARDSAVG
EVERLARQCADAEATMHRMEAEMAAENAKLKEELCRMQQSHEEERQAAGAAMHRMEAEMR
SQQQTQLAGPPRRAAASSTNPFASMGALSKEPGSFPDQGDDGDDVFGVGTEQHPTATGDA
VSVDRQAGPEGLVTELRGRLAELEAALSSATLARDSAVGEVERLARQCADAEATMHRMEA
EMAAENAKLKEELCRMQQSHEEERQAAGAAMHRMEAEMRSQQQTQLAGPPRRAAASSTNP
FASMGALSKEPGSFPDQGDDGDDVFGVGTEQHPTATGDAVSVDRQAEPEGLVTELRGRLA
ELEAALSSATLARDSAVGEVERLARQCADAEATMHRMEAEMAAENAKLKEELCRMQQSHE
EERQAAGAAMHRMEAEMRSQQQTQLAGPPRRAAASSTNPFASMGALSKEPGSFPDQGDDG
DDVFGVGTEQHPTATGDAVSVDRQAEPEGLVTELRGRLAELEAALSSATLARDSAVGEVE
RLARQCADAEATMHRMEAEMAAENAKLKEELCRMQQSHEEEIEAALLEASDRIAEHDDLL
RHKLEEQEEYYEKILADKTRLESLSVDNSVLGDALFWKEEHDKLYERFEQLQTELRSYLR
DTTVHQDVEAVVRQGAPAEEGKCVDGPLQAALNEVDLLKGQISVLQRTREQEEEKVAMQE
RDLQELRERLRAEEKSRCEFSQMYEDAAALLRDGATSVEMLLQEKRARIEELESQTEKMS
QQVLSTEEQLRFVRVELEQRQQEVDEGTERYFRLEAVHREMGAELREVKRLLEERQRTLS
QRLERVQNDMEKQMHDASEEIRRVCCEHEQQENGLRREIDRLRAELQAAQTLAATMPFTA
QTNNHQLVHLRQKLDEALSEKMQVVAELEAMQQLLRKKESLSRGRQQGAEDGTEAGDSGQ
SLDARINSLLQRSESLEVRVQQLTTEKETLLQEKDALELEVQCARRMVEVRELACQRQTD
EVKQSRTQISAMKDDLSFRIQSCNALRQELNEAQEQAAELARAYEDLQLVTFAERRNLLL
REYMEAILLAKAMTVPRVMQDVLHGIMQAHRQLLRRCSENQRNLLARCDAIEQTATEAMV
EGERQSNELLSIIEDAKVEQQQLQEIIERLEMELAAANCVARESTEEAAAVKKISTEATK
DAREEASKAKSDLQALQLEYNSAVNTISLLETEKANAARILARANSRLEELAAQQQEEVA
RLQESLIEKTCLLRDAQEVAKNKLEVVEQQAEEYKAQRDDATKRAQAAQASLDRVLPRLE
RLEAEQAAREAELMDTTQQLTALSQRSTSTEVVSRRQVEALNASIAELRSAHAALSEECT
KAHEHITELKNQLTASEAEIGRLRTRKAQQEQEAEAAKARLTELESLYANDTSDAATWRR
GAERRSAALESRNSALQEELQASQKQQCVLQEHVDALEAKLRQMSDENHSKDQQQRRFIQ
QLKERCEILEGEIGKLDEAHANLSAERDTLHRDWLNAKQDVGSLENHLEATNQHNEQLHK
ELRRQKESHDAELQMVRRTLADAQEEISRCRCTLVEAEARENELNHVVYALKKEKARCVE
ELQQMRGLAESEQELLVRERSQRQEQVAELQEEVVQLQKDLHAVRQECKGLECKCTQHAD
EAELLRRQLTDRTDRCRTLQQDAAAQHEQLTATVKSLRAEVATLQSKLEEALDTLAQKQR
EYEQCEERSLRKMEVSRLSEEILRKEVADLQRDVQQLQQKLAFTATAAHDAEKTGAQQQA
TISKLTEELERQNTQSTAYLKEREQLQSALRENTSQLERVARKATADLETALAKTNELHR
SNVEKLETALRREQQTAQEVRTARDRALESLEERQGECEFLRAEVARLQQMLRSAQAQVA
STQAEVRSTVTQVVVEAGLPQEGELSLSSVVNQLLLRLNRLSHAAVLLDVEVSQFKCFEK
ACEAHAAALRCVIDATRSSQQVPASSTAPTSPLLPMCESSSGSSTHSLRQRSFSSRSRVL
QDIISSVSTFAHRLMDHCHTIRGMLDNMEAAVVQCETKFVGDPAVTHLKLVVVATLSELQ
LRTSRQTAFLSQIFDGAVMSTALQEAIRFLRDDETYVLRPFNELLMPSSSSPLSTPRWGG
GVQESTFFTKTRVPAADTASMSQHLWRGSAKKENELQSRIVVDPRQQMESARMPGEEPRG
PSIPATSGAEASVASVTTAVDASTGPESSSANWCVNHEMQDAA*
>TCRU_3767 hypothetical protein, conserved
MKSSDIFHAYRYTPVFLKARQHDSGVNQYGLKPVNAYDFINPTNLVNFGRGTSFDNLGVR
RAGRGEIDSSPSLGGSPVFTQAKLVGLSGEEQLTMCQSETMALRVCMARGGQDTCERESR
ALDACLSRVGHLRRAMSEACGEFNDWFIQNVSDNHTKPFQHRPHDWRHFYAQEKLVRERQ
QNGHAYGRRPKQFSFGARYVKTEGYGKRPRLPYNK*
>TCRU_3768 hypothetical protein, conserved
MGNPKDASSLAHILYEQCKGDATSLNRLLRQRVSPRGNRFERDTPDTFLYIERSKNRNIV
AYAARLLDAVTQKSVSSGAGRSCIMDHSNPVHAYFIVLESAKFKENQENVVMSEIKELNF
IERRLAYGCSAKPICRTMSDSMKEGIGPWLKHFDTHALTYVALPGHPLLLLLLPPLGGAT
ENSAEAEGTGQTNSGGGNEQEATDTLAVLLGFVGGVLSVLQRVYVCSVEPKHFYQLPTVK
YIEFFGVSLESGLDTYEKRKN*
>TCRU_3769 metallo-peptidase, Clan MG, Family M24
MPPKGGGTNGKHQHQQQQQQQRQGGKKGSKKSDDDEFDALLAKAVKETQAALPKAENGH
HQKKQNSGAGKQQQKKTSATEEVRDDGTGVKVVSTADHVDNPYPQVAPGMKRQTWPEPTV

PVCMQFTSGNFPPGEICEHPGEVNAYRHSSEEKRAMERATEQEVQELRHAAEVHRQVRRY
AQSFIKPGISLISMTDRIERKVEELIMKDGLTRGQAFPTGCSLNHVAAHYTPNTGDKTVL
TYDDVMKVDFGTQINGRIVDCAWTVAFNDEYAPLLEAVKSATYEGIKQAGIDVRLCDIGE
AIQEVMESYEVEIKGKVYPVKSIRNLCGHNIGPYVIHSGKSVPIVRGGEAIKMEEGELFA
IETFGSTGRGVVQEDMECSHYMMVPGGDKTQLRSEKAQHLLKHINKTYGTLAFARKWLDR
DGYDRHLLNLNQLVEAGAVNRYPPLCDVKGCYTAQFEHTILLKPTAKEILSKGDDY*
>TCRU_3770 hypoxanthine-guanine phosphoribosyltransferase
MFIRLFAREEEGEKEGKICHMPREYEFAEKILFTEEEIRTRIKEVAKRIADDYKGKGLRP
YVNPLVLISVLKGSFMFTADLCRALCDFNVPVRMEFICVSSYGEGLTSSGQVRMLLDTRH
SIEGHHVLIVEDIVDTALTLNYLYHMYFTRRPASLKTVVLLDKREGRRVPFSADYVVANI
PNAFVIGYGLDYDDTYRELRDIVVLRPEVYAEREAARQKKQRAIGGADTDRDAKREFHSK
Y*
>TCRU_3771 hypoxanthine-guanine phosphoribosyltransferase, putative
MISSQQAMVHVVSRNADGVIVVDGKAYPMAEELVATESVIQRSIKAVAKQIADFYRPLSH
RDTHGGGGVAPISDENPLIIISVLKGSYIFTADMVRYLGDYGLPHVVDFLRVASYRGTSS
TNKMKLLAETQFKALRGKHVLILEDIVDSGKTLRYILDKVQREHQPATLKVCVLADKPGG
RRVTMQPDFVCLTVPNKYVIGYGFEVNDRFRCFRHIFTLRPGEARRYPAHL*
>TCRU_3772 serine/threonine-protein kinase, putative
MSVGGGSLIRSETFSSRSFGSLREAGNVNVSLERCASACSDSKNNHADDSGRVISQWDRF
PRSHQIGTGSFGNVFLCHDMLPGSPWYRQPVAVKAVPLDALTDSGVMLAMNEVAILRHLR
HPNILHYIDSFLDEEKQMCLVSEYAEGGDLTFLLRRSWELSGGSNNKGSCHSHQWEEHER
EDMREGSQSANLASGSKNILTTRRAVSVLDDTQHGQARPYNWIESYRITDIVRQCLEALS
YLHQCYIIHRDVKAANVYMTKNGSVKIGDFGASKLVNLTDPLANTFIGTPFYLCPELCLG
EPYSFGADVWALGVLTYEMYCLKLPFVADNVLAQIHVVTEGQYDREALYRAHTFSPSDLQ
SLETKYGAAFTQQERSLHMLVVALVERMLVVDALERPSASQLLREFFFADPHSSSLGTVS
RPISRESLPRPDSSNTRESASQGLISRCLTSTTESNKETREATIEAAALIASSVSQSYGT
LLEKLPKERRNDIIQAASRSASLAGCLRRGSSALQATIDAVELGDTVCLASHEVISETVD
KIPWLRHAEAFSLLTLHEGHEDDVVQVDWIDEEHFSLLAPRKRRCLSLSCARPDGDKEVD
LSETRGLTPTAGRKMAGRGEDAEETRAVATPAIHTFHVDEKVRSPPGSVGRCQGLSTEAL
EKILRKKIMASYVHRQWRLKAMREAYAVHEEERSRLRAELNELYAKSFFEERRGMMTCGE
DMEMSSTMNMPGNLESTQSPHSIAAAAALFVTDATLGPVIGGDFTKTAGIERTLRRLTAS
PGYSTTGYRDGNTSLLTNEVVRIARDAAAVAERCKKWAVQPPARLDFSKRQVDEVDRRSA
SSVTDSERGTNMEVYDTPVTLCILPDESYITRQHKSPPPPPVSGSAVAVGSLVLPMTVTM
KPISRRTRLDGIIWRVKTTLKAHGLDHVLFFPLDIDNANEVDAEELGIRYFDCVGDIIEI
SEASDWYYVRRDWYQRKGLPWMQLYMVIQ*
>TCRU_3773 hypothetical protein, conserved
MFRRLFQTEASDASQLSVAVSLGASRPKASSRGAAAAESKVKEITVRLLRRLRSFFRTHK
NILLGTCGAVVVGYMCQWIRRVCGERRNIRSAQDNVKRPASGWGLRWFWHSPFGHMKGFS
GDTVGDSGQSPCCPSGRSIFRQTGEDDDEINFVDATESAFRMFQRRVERTHEAPLLLVLS
ELESLGRRWQSQLSDTNTALEEEHEEAGNMNAASAGIRTEETVDETLREAILRKAVEADE
LLTQYVVQLDLAPVGTSSALKKERKASIVAASALAERIAKWMSLPSRHQQP*
>TCRU_3774 hypothetical protein
MGATCAKDTADGNIAHASSISTRSRGRRRRGRRSRMFAQSESNIQRCGTSSVVAFSGPDA
PSHAREELLPEQEDVLSIPSVPFGITLTAPALENVGTNCSSAYHTKTKPIVTGATAATTG
MGESAVNDTKRGPEECFRQWAPVFREVTAEPESTAVCMNGMSDGPSPPSSRVNDKFAAAS
SGSTPKTTTTENYTECSVEGLSAVVSMKRKYSVGFSHTSALFTCISCHEEEHTDAPSPHF
YSSALDAPGDADTKSRGKKRSLLPTLISKNVAVQPDGDNNSKTETKQQKEEDEEDDEITA
KKETLIKDEMSGRALIEKEELDVREAFLCSYARERAFPQRLDQEVTPTGAVGAASASQRT
SHLGDSRSAKTSSLFTFSSIGEEFLMHAESDLLRPPVVGENFIEENSMWSSVVSSHEKGV
DETCQGSNSHQKSLQFPRWEGSGLLSPTPPPPQNNSTMVVNIMSHDDNDVNPNTHFGEQV
RVERLCGERPYYEPEDNERKTQLMGLRADHKEASRVRVLRSPSLVCLRDGYFNAAEMDGN
DWKPSCKLSLSAREFHEGLIESPSLIHSDLPGSCGAHYQRYGASLHTKSLTSLDTPVLER
TGTAQHKVLPCRRGGLIPPPPSPPPSSLSRRAEDEERESRGSSRHMWQRSYTSPRPERSD
GSVSSFGYLYSPRAEPVLSTCTVVSGAVAGMATTAIPCGVVERKSAKHFCRWCDKPYECR

EVCAVAGESHAVLRLRRKHEKEVKKRAQGLLRCGRIREAISELKAAGII*
>TCRU_3775 Costars, putative
MVELIIDTNADIDLLLRELQRLNGSLKKIDAGRGAVLLWGEIYSDSTLQDLFQERLASVM
SAAKKQRAIHFPRERLLIGNYEEVEVELLAPHLRILPESAIRSKSKQEERKAAFKEAKLR
ALEAHKEKMLRLAMQGIDLPSGKSGSPQTTAGGAAERGDENDVNPPPAPPIVGDGGDVIA
EAEGKKSDDNLLPPPPPPPPADDDDDDESESLEKEGDDDEEDPPPPPPPPEDDDDDGEES
DEDDEDDEDPPPPPPPE*
>TCRU_3776 hypothetical protein, conserved
MSFRIVAFPYSPPAGAPYADACLPAQPGERLRLVRRVDPWAIVESGGRFGLFPIVFTRDD
YQGCPRMRTAARENLVETISLSPEDKIVLEEKDSDNVLNHAAGVAPPHENKQDKAEVFVV
PGCGINSDCKNELDNSNKISSSGVEDHHPKYVDCNAAAEEEGWRTKKDAPFLKMVPRRCS
GQRVSGRRRDGDCCQYETEGRGNPHGECLADARWEKNEEKEGEEETVNCSRHVRVSVIEG
KEQLVSPPQQARPVVQDCSSDALQELRRQYMELDAEMGWLSHVTENVRAERQRVRDAHAS
DAQQRAAQELANTEEMERLIRNIAAKDAELKAARKYAAHLRSILLANNITGDFLKSLPPT
PPPLSFSLPSFLQQIQEQCNDDKENKDDAYNNSHEEEDDDDDVSEPVEELARNPNAAAE
VNAIKECIKQEQETLQDYHEQHNQLIAHMKRLRRIQAAIEEESCALRESEEALEAVAPTG
SYEVVRDGGFISGGPLQPVGSGKASVLTQGGAGEVDVAMREGFAWPAKLPGLTAEEQDAL
SNYQRLFNKYEAKHQYWQKQHEEATETKLSSVNEKLRAAISKGDMALNELLQRTENLKEF
VTKYGPVAESIREQVAVSQRILERQREKCGDACAAYEAAAASKNRDQKR*
>TCRU_3777 hypothetical protein, conserved
MTAVHCVGGSRGYGDDDQPLHLSVVEAIRIQRELKRHGGEPIATEQGGRMFAFQYASPLQ
MLRRSTTVRNSVSSCLQAEKEKGQRRRAGKRSTFSWLSASYCRAEPCIGRRKGRGLTQVL
LAREARPPPFPSVAARLENDIALGLAASMWQSGNVVGHCNDRLAHLLVLSSTVVQWVGHE
VQNGGEPRVPLELREAFMAAIEHFVRLECVVARAMLLTSVEKELQRQQGEYAQRQDLPEG
SPSGTDVTKMSPAAFSVAVESAARVIRGLVEPATLAAAAVAPTWQYSLVRTAADVPNRYD
ILDAMAYVLQPCRHLTVRRTFCAVTRQLALEVLWGAGNEKFGTRGGAAALRILQHINTRP
FFLTVEERMAGQRFLALLERKLRSLMALLPPNALDEASQPTRELIDAVRLFCTPLV*
>TCRU_3778 ABC-2 type transporter, putative
MSTSRVAGSSYFSASSASSLSLTLGFENLTIQRDKRVVINSASGIIYGGRLTAIVNCSGT
QSDSFLLGALTGREECASGTIMMNGIPLDAPAYLHRTVLIDEGFTALEELTVRESIEYAA
SMRIATSAFTVQEILEELMLESVADAVVHRCSPYVRRRVSLGRELLLNPLVLCFDQLLEG
LRTHEAQEFMRLLRRIAAPMAVSLDLITSRSPFLLPPRPSSSPASVVSSQVLPNNAGTAV
PMTDGATLAPHSLATNSQRERMRIVLVSMSQPRWAILKFVDDVILLERETCVFCGTVTGL
FSAIRVDPTAGLAENAINSLYRLASSSEKSLVDIFAPSGNAERVHQSVVQFFHNCAVGRE
MLEGPPYSSPGAHVRLYYMFKYDLLKVRHNLLLKGVVFLAVFLLGVVLAAVYNSQEGQSG
MQNRIGIIFFLVSSTFLYSILSLDSHRREYNRFLRHRTHGYYGVFTYLTYAVLYCIMERV
FFLSVLTFAGFCVSNVVEKWNYYQFIMELVLIIGVLSFCSHFVVFFFCTVIWTRRFAMFA
LFAVYTLNLLLAGIILNLTTLPKTFQFISNVSLIRLAYESSILSQFLGRDFGCGESNETM
CYTGPQYAAFLGFKKSRMWVNVWILAGISVLLIMGSLCAMLWHRPPRDFC*
>TCRU_3779 protein phosphatase 2C, putative
MGIWQSIPVPPEVVQAAANNTSNWGVPPEDIPEDEKDVEELVLQTWAFCKARPSPAQNYR
SDVEERQRRRFVSWRKRASFIELDCGEDSFFVSNTYKVIGVADGVGGWRDEGVDPALFSN
SLMENAKLFAETHRKELNPEIILQSAFDKVLNDRKVKAGSATACVAALRKEDTGKHVIDV
ANVGDSGLLVVRNRKVLHRVHEKVHGFNAPFQLAVVPKHLRGRAFSDKVSDATREKVEVQ
KGDVVIAATDGFFDNLFNAAIASDAGWVGKVEGSVFERVPLVGFFLSAIIADEKVAYIDP
QRVAQRLVQNAYKISVDEEAHTPWASMLRTFGAADAKGGKKDDITVVLSRVTTRDELNTS
NIW*
>TCRU_3780 transcription activator, putative
MGFDNPFATFLGKRRVPRTGLKRHRIEGDVSLESTQEYRTTAEDVVADAASATASPNAAE
LSCAEKTSSVDTAFSSPVKVVLLSDERDLEEEEEEEELRLLLGGHHKVSVRPKEVAAVSS
SEGADVAAPTATTPVALRDLPWTTRSNAVLAEIAERFAVQFRWELRHNVELVRVFEPFFS
DKAVRRIEAETRGPQFLPAPVATPENTGAASGYMLRSYQLEGVQYLLNNFHRGSSCILAD
DMGLGKTAQISAFLHLLKTQHTIDGPHLIVSPLSTLTGWTRELARWAPTLRVVKYHGERK
GRASIRTTRGNRHCVFVTTPAVLNQDRGFFRKRAWVVAVIDEAHVLKGRDTIISYVARKL

TACFRLAVTGTPVHNNLGEVWSLMKFLYPSYCASYDSSGDDDDPIKAAEDCAKLLQYVML
RRTKGSIELGIPPRVDEPTCMIEPTRLQRQLLFRMTEQALNGDKANATRLQAHFTHQRIV
CCHPLALRILGVEVRASAQAGWEERLASAGIELDEASIIAPSAKMIELDRMLREFKANGH
RCLIFSNFTSILDLLQALCVLRGYGFERIDGSTSRVERELSMIRFNAPGSACFVFLLTTT
AGGVGVTLTGADTVILFDAHYNPQIDRQAADRAHRIGQTRVVRVHRLCLKNTIEERIHNV
ALRKASLGDFIVDGGSCKGDDSSAPALSAHQILLLFGNENRIINYPRCHLSHMDVVDFDH
DNSVEETMVEALLCNEVEGLPRSHATTKKIRGVRSAVVGVTHHCFVCGEIMRPLEPLYHC
AVCPKAYHADCIGERRPKAGMIGPRRWTCPRHSCVSCGKVQGFDGAVFMCTECPSSFCFD
CLDSRYFELDDTRTQFVHIRREYPGMEAEGMNSRRSIYYIACLRCCGLLSSSSSSASSSS
SETESDAVNDDAVVPEDQNDMDSMEEELVEG*
>TCRU_3781 RNA pseudouridylate synthase, putative
MHQVRGLVQRSSAATLRLLEKNVTPHDVRTCFIDTVFVDGFGAASAVQLLHPVALQQLLA
ELPKSEALVCVQEARKVVLASKNDTAPIGTWLKKLNHLLCIKDTTQRTVTELRCRQSRFL
AKTEGRLMAHDFSLVEAFTNRLLTREIPQQEEKELFLPDEVAMYRGVVEELVRLNPQAAL
ALAMNTKLPSLGSGASAALAALVNLDVPAATLSFLESFSAKDEMSAASETCATQVAVCLR
NKLWELRELSADDPKRVALRESLATACRFNVDPGVVFPTDAGAIQRWGSQFLHEEMWPME
RGRVISDIVRRKRLMPRRVSLDCLSNWCLTDLERKWVSAMLADGQGTNMIGGSDTAVYCS
ALSCVLKDPKRCLVDSRLLRQYALLLKRGELEPSHSSFPHFIEECGECHGNDERPEELSF
LMPPQSSPSQSSSLKSQTLMDALVALAPQCSYWRTLLAEKQEGVEAFVAPQGHIHVTVKL
PRVHECVEAAMQAARSSSTSSFSFASCLPVIFEDNDILVLNKPPHLASSRHALSCTQMND
KRATDVVSLILASTKNGETMRGVFRQGQVHRLDAETSGCLVMAKTDCAADSLRHQMGTSA
AYSQCNKVYLALCAVMEPDLRRIPLRGVLRDPMDPKISTKYRVIRFFRKARVALLECRIQ
QGKKHQIRRHLAAAGLPILQDVEHGGAACTTPLIDRVALHAAALTLVHPRTAEVVTFVAP
LVMDFAETIRQLQ*
>TCRU_3782 TFIIF-stimulated CTD phosphatase, putative
MSQDAASFFRGVSAKISAANQSYISRRARRRVEEEEEDEPQQPIASPSLSTLLSTTQNSS
APCVATSVVGRVSKTAMTTNVAGNTFAIGRSSSKIVSSVVKDEHGDGSGGDFSELSMQSE
QISSTLMTQVRQIPRSSRRESLSLTGNIFLHTGREPATGSNGASSGGDGSVSDKNENGAN
NNSNNINNNGNNNNTGSSSIVSGGGNSGDTEVRPKVHLSALLIRTRRIQQMPKNTSPIIA
KNHASLLPLQMRQYHGKKTLILDLDETLVHSSLTLQPKQHDLILSMKTEPEVTTIYVAYR
PFLHEFIQAVAGLFEVVIFTASVSMYCNPVMDAVDPEGILGSLRLYREHCSILNGAYVKD
LSLLGRELSQVAIVDNSPVTYLFQQRNAIPIPSWFDDPKDNELKRLIPVLEALAQAAEVY
DVLDRYNAVLQLQQEQMRPENKFARR*
>TCRU_3783 hypothetical protein, conserved
MTSVTAALLRQQDDECSTAVLHLLCDNDAFKRLAASEGEAILRRDKEDEEKLAVGIGIAK
AKGILSGNPDVGSVTRISVAGMTAQQVTEEIMKYLPSKKGNAIVMQGLSGTGKGTTVNKL
QKLLPRCVTWSNGNVFRSYTYLSLEALKGEPIRTELLTPELLAAVEKQVTFEQVENGGFD
IVLKGSIRVADIQNTLLKRPEIEHAVPTVAQQTQGEVIRFATMAVGKLKDAGYNVILEGR
AQTLNHIPTPFRFELVIDNITLLGERRAAQRVMAKAFSDIKNHLDGATNKMVEEAIFRAL
SEL*
>TCRU_3784 hypothetical protein, conserved
MSIFGKKTWRVQDIIRTDGAQEIVSILKITHPFRRQRIVVVPAPRFAQESYYNDWVYQPY
AKEHRMYVSNDIFNPTYVYLARILIRRGVFPGYAYFHPMGFPDCIDLNLTRREFIAREQP
LKTPTPLILLTPNMFRYKRHPWIPRRVINIVGEQYVTHPREEHQSMLFVLPPEYIPDAVN
TLQSLGFQVTDHTTAVAGEAKTLKKLHHWSDIAQLVVLGYLWFMVALFFLNESQRMRRMF
HEYKREMVEKAGKDPDEMGL*
>TCRU_3785 HpcH/HpaI aldolase/citrate lyase family, putative
MSAGGAEFKAELRAGKPKFGVFLNSASHLLAGQFSHSGYDWLLIDMQHSPVDALTLSQLI
AAIRTGHAKVMVRVGSTEDRPGIQNALDSGADGVLIPYVKTAAELSAAVSCCFYPTVGTR
SVYAPQQCMNAKGLLGYAGEANKNVVVAFQVETADCITNIEEIMAVKGIDIAFLGQNDLC
MSMGLYEKYVFPDMYTSTELNDATEKLITAARKNNVILGLFLFGTDRVGEFLQKGFTFIS
IGSELHHALTQAATHVKVLEQIANVNGKPWKHQPSALV*
>TCRU_3786 retrotransposon hot spot protein, RHS3, putative
MPGNQASAVPQGDVQRRARPESEDVTDQPAATHIRVEEARQPQWTMRSSVKDILLEGSTL

STNMRLNDFLRNYVGGRVAVGEDSNVTMQVFVQEPDAYVQDQQLLRRIFNLPEYQELEEK
KILLEAIYKLRHGGVDFLEQWRDYEGKDTVTPLARRKLNAVLTQLLREERREAGERARRE
KQVELTLITTIRDVLFKGRVRFMDIKLNDFLTLEMEGRGVLHANRNVLLRDFFSDPTRYI
PDAGVLGEIQATDAYARMEGDVREEMDMGEDVRKLKQAGVYNLQKWSEATAQVKESVHEI
TKSFLDAALQEANKPTMTSAPMKLEGCYESVYNSRWHHVVEVSGGEGMGMEVREGEPEQS
LTYREFDESLERDDAVQQSGAPRLRLMVLTSDKGWPYSWAGNKLIHDCYVNFEVDRVWQI
VNSDLTELLSSHPGAYFEPKRRVLIGTPGIGKSMGAGSYLLYQLLHCDAEKLPVVVYVIG
RQAFLFDKTTHTMIRYMELSAMEHFLAFVSSRGVKGYIIYDVAKGGRNPSVFFVPSEWGM
LVVTSPNVDNFEEWRKHKGAAPIIINCPEEMDVKAMCFWMKQIQPTGEQAEEQAREQAKY
WETVEERMDEVGPIPRCIFDVLEYGIHLNAIDATVKDINASNATDYMGVGGDKIWIDEYV
SQTIVKFVRVRAVPGIEVGYNAPVSHSARVKITHHLTNMTPPVDFFNLLLRGYGYFLWVV
FEFAGTAAFMNPHAVDIIQRKLTELQPEGRSRSRFSVLSNKPRGHPTRSKTLKKLSDNPA
GMDLDYGVLYLPAVGNFPLVDALFFMESPRKTLVGLQTTTANAHHTQTSTVRLFKERMAS
YFNGWEEFARDLETFRWWMPFSSWSHRGRHWLGCRRLRQMHTTPKPAL*
>TCRU_3787 protein kinase, putative
MEHIRKTNKKLGVGARGVVYEGYDEERGRFVAVKEIPFFDDGGVGTGGGDDAAEEDPTLV
EERRAIVREITLMERFEHPNLVVYYGARRSAVGVQIIMELINGGSLDAIIRRQGSLRESV
VRSYTHDILEGLAYLHDTARVCHRDVKPANVLITVDGRCKLTDFGVSKLLDDNVSMRTTV
GTPWYMAPEVVNGNADEDVEGVEDTKRYDGEGSCKKRVHKNSYTTAADIWSLGVTVFEMI
SGRKPFGGEMKNPAAVLFAIASSDGTPPRLPENCEASVSLRAFLDLCFVRDARLRPKARE
LLSHQWFMETSGQTCHGLLGNNMRKNSSSSNNNNNNNCSKVPGVVMPPPGSNQTSLPAPL
NMLDTADIMDAESLLSPKKCSPKSQRSEVKRRIPGEIGPAFASRALDPSAVRDKNRDGGF
FSSDGHYVDLPISLPLVLSPLRKREK*
>TCRU_3788 hypothetical protein, conserved
MAMMTGRVLLVCALCVLSSVAADGAAGVVSGGEDNSLKELFIPVARLKARQEQTLKESAQ
TATEAAEKAAAKATAASEAAETARVAAAEAALKTAAAAEAAAEAKTLAETAAEAAEKAAA
KATAENAAEKAKAAAEAAETARVAASEAAVQTATAAEASAKAEEAATKAKTLAETAETAT
EAAEKTAAKATAASEAAETARVAAAEAEAKTATQKAATAAAKAETEAEKAATAEKEAATK
AKAAEEATAAKDEAEAAAAEAKTAAKEAAKKAEAATEEAKTAKTAAAEAATKAAEAAAKA
KTLAEAAETAATEAATKAKAAAESAETAKAEAKAAEEEAQAKAKEAAAKAAAESLRGTTV
GEEEAKTATHDQDNSVEHHSGKKQELLKEEEPELHEKEQHEKQQSQQREHSAGNGEESAK
DKTANGTNATAIKDDSDGSTALSLTTSPLLLLLVVVACAAAVVAA*
>TCRU_3789 retrotransposon hot spot protein, RHS3, putative
MAAGSYLLYQLLHCDAKKLQVVFHCFGGGDAYVSDKTTRAVTRCSDEDMCVSELRSLRRH
GRNVYIIYGVAKEGTPPPGHFAPTSGWGMIAVSFPKVANYDEWAKQLQAARVIVNCPDEV
DVKAMCAWMTRDETKGKQAECWKGVKKHIYLL*
>TCRU_3790 Protein of unknown function (DUF3720), putative
MMTGRVLLVCALCVLWCGAVFGHAMEDYCGEGGGNGLRHTSNGGDDGVSLKADCGLLFTR
MVLIKAVEAAQAGEEGLSDTLPPGNSKDKALEGNTNGSEAVGSGDVGVAGQAAAPAAPTL
GGSGTEEQERGSNVSGTSDGNVAGAKKDHEGANAGDSKHQRAEQPSSSSSGSSDTEGVKQ
PVVNENSKSRETSDSPPQEEEEEEEEDLRTKPDSREEEAEEELKNDKMGHEAPKETPGGL
TKHTEIQTATTPLNGQSSPEALEDVKQSEEVQDERDSNHNSQTKSVASIAANQQKEPSAD
HGESGPPSPTANGDAANNDSDKSTEGGISNSDPASDGAGTAEGKQNENKDANPKETPVTA
TAMKTTTATTGDSDGSTAVSHTTSPLLLLLVSACAAAAAVVAA*
>TCRU_3791 glycerol-3-phosphate dehydrogenase (FAD-dependent),
mitochondrial
MVSAARKCLGAATAAVAGFIGFSYTNPSWTRRRFDSRKTLPPLCTENPSREECLTRFKAF
DSPETPMDVLIVGGGSVGVGSALDAVTRGLSVGLVEMNDYASGTSSRSTKLIHGGIRYLE
KAVFHLDVQQLKLVAEALRERTIMIHQAPHLCHEIPTMIPCYDPIDFIMFWCGAKLYDLI
AMWERGTLKYSGFLTPYDTMKKFPQIRYANKKGELLYGSVQYYDGQMDDSRLCLSAAMTA
ASHGAATANYAKVEKMEIVQNTAGEKVVKSVVNDRVKQHKFTVYSRSVLNAGGPFSEEVQ
KLMEDKNTLSIVPSSGTHIVIEPKYCPKEGATVFPSTDGRVVFGVSWLGGCIVGTTDKKC
EVTEDVRPSEADVRFLLDSMEDYVGKVPREAVLSAWSGIRPLATLNGGSENSTQNMVREH
MIAVDKDRLILSVTGGKWTTYRKIAQDAVDSLWDTLLKDRIPFKPCVTEEIQLIGAHNMA

SVPAAAPSDIPEDVHRHWRSQYGDRYNVLLEMVRRNPAALKKLHPDEPIVEAEVIYAAQR
EHCERVQDFIARRTRLSFLNVDHAKAIIPEVTRVMAETKRWGRSKKNEELANAFASLDSF
RAN*
>TCRU_kDa subunit, putative NADH-ubiquinone oxidoreductase complex
I, .1
MATAEEIGPGGVNIKGKPIFLAVEHTRCAPSTERELSDQELLAWKSFQLWRSTLSVERRD
NVYKSLTNSDYTNFRLAHHIMGTPFPVVDTTPGIFDVGKSVRWYEHAISVAVALAYGYWI
RSKASTRNARMMPMSRSAITLLTFFSMDLCFFYRSMYRLTGYLPNDYECRKYGVMEDKER
LERKKVLWEKYAKYKKEWCRRFDYHVYGIRPGENWSFFSACLFPAWAPMFNTCTNYPPRK
NPYFLTATPLRNIFAESPFTYEIPKDETVPLVKERPEFKYLYRGPEREGIVNGKN*
>TCRU_3793 hypothetical protein, conserved
MKSPQEDRPRSLKALCEAVITNSLGEGGKRPYHKKRKEEENEEEEVKRSLEALFSSGNPV
LGGLPAVKGLRDAVRLFVKKHAYLIKKTGGNDVAGASNEPVNLRDALLSNQEAMEKIRGE
WKEILENMYAVEGDDSTTPPGETLETDTNTPSNVLFLDAGHTGAWEELQLEEKTPCSDAR
GFLETCVREWVEEGLPIEKGKPGAFVRALREVIDTELDSIVFDDHWEAWVSSLLMCVELR
TKSSSSTSWEVLTLVELIYSRCTPQRKLLLLDFIAKEIQQPFEGVPILKDFLLQLFHRVL
LCTAENIVGFMDDEIAQLVLKGLRVIADHLASFDTMDPQARWLKHILVRPSLVRDIASLP
SREPELINKLTAAMPAPHAVGLMLIMLPLWMKEPGDEWTSTRIFDKLVDALLNKHVLDDL
VEDAMACVDRCLRGLHTEKRHEHFGKVHSFLLSQEYSEVQESVGRLLRLLLCFSIPSAYD
PGKSYRLLPTHLRSLEEHLLRRLEKWTRKNAAHKIVVGDFWWEILRWHAADLPKVVARAV
QAMCRDERHVGSPWDEGHLVAISYSVSSWRGLEEVLEDEQHAGSLNYVALLLNICAVASR
ASSRSQQERQQQQKQQQPPVSLNPTACWLLMRWCTNACARLGLFLATTEVLRSLTDDKDV
TEGGLLAIPVEEFDSITHMPHAIPAQELNQKCMLATILSVRLWIATLSPLSQTPSVAELD
VTGKLAQQLQTYWVNYDSNVSMPDKPFGEDSLLLLLCVLSMNRLTRVRKSGNHSQEYILQ
DSLKRLLAERRGHDPVWHLLQFLLTGVGSEHLAAILVHRFGTAQEVPLQIDVDTYETSVL
HDVGEKELGAMKDIIGLKRGDKERETNLLPVLQLLLQLHGGDVSRAVAAFKKYPTSRWEA
YGRCMDLAAGVVERLIKSFPYLEERMRCEGVDVYYLSLLCTRRWLRDSVKLPDLARVSIE
KFMRLGQAAWEGVVADSLGKHIEALWEQFSEADGLLRLCAESVILPVSPFLALCLATDFS
LKENV*
>TCRU_3794 SBF-like CPA transporter family (DUF4137), putative
MSSGGGRGEGQSSQIWRPSPEAQSIRDLSSSCTGEDVGFIAGSNERVVRLVVGSLSVVDW
VRGQWLLGLFILSIGMAYYHPVSAGIAASAWTRILVFISFALSGASFPDIDRSATLRFMG
PTITMFVMSFILSPILGAAIYVIFRSSSGEDNYLLVGLMCTFCLPPSVILSVAATRSSQG
NEALSQYLSAVGIVCGVIASPLLMLACMLFSYSSKFPVTADLMLFPATAIGPFFFGVIAQ
KIFAWASHRRITGEDRESLRIAKAEMACSELCNGSLFYWRQRAVQLNSLVLLLVNYFMFS
SFFVQSIAPSLLTWRGVGLISFVELTLYTVMCIVGWLLASLFACSPEERIALFFALITKS
EVLVVPIILQIFHENRQAAVILLPSLIYHLIQAFTTGMLSFPLRRWRCQYNCRPGTTLLP
LRLSRVNRSPSTKP*
>TCRU_3795 phosphoadenosine phosphosulfate reductase-like protein
MRSLKLVGTDVGDIDVAQACMNHALTRVELENCDRVTDLSALATVPTLEEVHIRDCRRVR
CFGPLGQTQTTLRKLVLSGTPVTKAQLRELTRLGQMELVVDNCGDDPKLERPAQSLVKSS
IDMIREVAGRFKPEEIGVAFNGGKDSVVMMDLLECALGPEMLSRFCVFTLGASGREEFGE
VVAFREAYLENHGLTGVKTDVSLSMKDGLAQLKESKGIALVFMGTRSSDSVHQKKSVEPT
TAGWPEMLRACPVFHWGYEDIWGYILAYSLPFCILYKMGYTSLGLRGATAPNVLLRRGDG
TFRPAWELHDDLEERNGREVNSS*
>TCRU_family, tetramerisation domain containing protein, putative
Sk.1
MIRSGAAFNPMRRTPPPPPHIDTFQLIPDDYIKMTSADGHNFLVHCNCARASPLIRKCFA
DRVDLDLPAVAISWGETEKSPPTIHFPTLTAARLEVIIQYMYYKHRYEGETEGRPSFDIP
VEAALEVMKVAETLQC*
>TCRU_3797 hypothetical protein, conserved
MSKKARAAPPSEPSVVSPIAFEKSYMICLRTADDRLFLVDRNCAMVSGVIRSAMRKESHN
GDAVTSSVNTPPEAYEMTTIGTENHETITLEEISGDLLELGLEMMYFKYRYDGDPERRPL
EPQHSPENRHKLAALSVLLDM*

>TCRU_3798 HIT zinc finger, putative
MHGSEVELLDAELDDTSGEEMRSLSSAADADLEWIPEENEADESQLIHEDYYAEGEENEE
DEGPHFMASALSKAFARDLVNQKLQQQEGENTGLGSPCTAEQEAVEGKVKKAKICCICSD
AAVYTCPGCGARTCSNVCVQMHKKEFQCKGERDIAKKVSLSEFTDGQLQRDFHFLEDVSR
IISNCRRGFSKFWRYTFRALPPPLHALREAAKKRGVVCQITSEGMTKRNENTSRFDRRTE
TITWRCQFNFHDPDFTVVTDWGSERHRLGDIVAFCWSTNPPLPCFHINRRYNRASRWIGT
AEHNEEVVGEEGRQEPMTEEGEGETRVENVATSSRVFLDNKAHCQEAWSPCQVSITPLSP
AEARNEKAVAAFLEMEPVIILSRAERLGMRQKYFRMSPSCTLNEALRTLFFINEFPVFDV
IHVSALEAYPLVTEADKEFIRESFRAAPRPARPECRPRPTKADLSPEEAARFAKVPCRMF
LAGSCKLAEGACPYWHCAYNEVPACRNFVKFSICERGSSCIFRHDTAAVTAARKRMREER
KHPCERRSKRRYE*
>TCRU_3799 hypothetical protein, conserved
MQEAEKTFRILQEALEKAVRFFSIGVTVDGVPLTQQQAVDVLDVYDTLLDAEEPESYDAR
RYVLCRSLECGFMRFLAEILTQPFQHLHEFDAQVTQPFLPLRMKAVKALQRLLLACSDMG
EDSCVSCFRVAVEEEIIPLLLRALSESPYEPLRLGAAETLFIFILRISHGRTGFVSTGGV
NAMCRSLMGDGSHTVRSMCASILRELVNTHVAEFNNPATVKVILKSLEDTSADVRTLGVE
ILEQTLRLCTSSVAYVLQDAQSVLLPLRRILDDDPSVEVVVSAARLLETCCEVADMMHLH
TFFKFVVSMGLVKVLLLRIRDGGEAGAARARGLRLLIQHTPASYELPRQIFHDTEVLAVL
LKGIVDAGRGRTTPGEEFAAFQIKSLELAICVAIILTQSPEYREVLMEELKEYPQWAAAI
KNAVISLLNAASLDYFVNIELRDVTGHHLNALHGVPWEADNTPQRVYIYRLFQEQAQRVI
MMRENALFDEEAPSSSRADARDILEEEKQGKKVRLTFILLVFATNITFPVESQAAVKEVV
DEPPSPQPRPGSRAVPRFPPSTLAGSKHREHVLSPNGLVSPTKWRNKIQSKKLPDEKEAM
AIAYDKFNSSMSFVMKFAQQFGKTKQKADDVVETEDGYFLRMSRLKNPWHAIVKHQKLKT
WQVKDLRVGDLFYFSIPFDEIGIKALDVVLYKARRHMMYLKKELLITPHNSKGRRWFLDD
MARNIMPKALEYLEDLKELIQSRGADGVRFPIFLFREKELHFGERALHPGNIVEVLDQIG
FYFSQSMDKIVGVDKSRLQQLAEQLDNIEGNADMPDTSIHFCSVGPHDTTAEGMKLDTEE
ANEEDYDGGYGHGTISSDTESDF*
>TCRU_3800 Amastin surface glycoprotein, putative
MSKLGAILYGVVGFLAFLFVLVGTPIDQFRAKEKGATGNTPCMTLWGIKEDCHSTKYEFT
VGEDFRECPSVLRLFRMAEAFSIISILLLLAATALGVAAHFCLKSLKIFATLLLVVSIVT
VGLVWIPMAYFYNHDVDNCLGTPLKTYFKYGGGFVIIVIGWCLIFVAVVLLRML*
>TCRU_3801 hypothetical protein
MTALPRLDFHLVPNFSVSEAFRYTHHLIDPLELTHFVEVVGTNSNDLDELLAAVRHAHMS
ATTYTNQKLVKAMRRLQAAWAKDPSLREAVIKLARFPFEEGQSEGYDYSSLRNEALRDIV
MYNAVADVWMFQQKVFHTAACCWQ*
>TCRU_3802 hypothetical protein, conserved
MLQGNRVSVDVDGESLGEEEVPLTGERPPDVLRFCFGACGRQESHVMAENVFLYSRPLNF
TEMRALKDRVPVPTREAAPTPPEKIRVVDSVREHVAGDITEEEWRGTTPLEKNLHYKESL
RRVWSGVSPDDRLASLNGVKLTLRDLGGNNTVRVCVSSVLLLLLGSYLGRGSLLSRRVWI
CDSSRRMCATLPALFCTTVFYFYFIVFLE*
>TCRU_3803 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MCLTSSAAESTSTGTACTSVVTDGLVGFLSGNFSDGTWRDEYLGVNATVTSGVGAAGTTD
GVTFRGAWAEWRVGKQGRNQLYHFANYNFTLVATVSIDKVPEEGPISLMGVKTNGQGNPV
LLGLSYDSGGKWKLLCGGGTSKEHSSTWEKETQYQVAIVLENGSQGSAYVDGKQLDGNEA
CALGNRGSNEISHFYIGGDGSGAGSQDDVSVTVSNALLHNRPLTFSGGNADLEKDVAAPA
EAASHTVAGGQMTTAGESATAQQLLPSPSQGSVGRTASSSHAVGGATGDGGTVRGSGLLP
SLLLLLGLWGFTAL*
>TCRU_3804 BNR repeat-like domain containing protein, putative
MSAGGCSDPCVVEWDDDKLIMMAACDDGRRRVYEINAKEDSWTEALGTLSRVWGSPKGAN
VRGVGSGFTTATVGNGDDNNRKLMLVTLPVYSKG*
>TCRU_3805 BNR repeat-like domain containing protein, putative
MSRRAFTSAVLLLLVVMMCCGSGGAAADEAASGEGSSPETYFDWRDVKKEETVGLLRVPS
LVEVNGDVFAVAEAQCTKGDSVCDFNAR*

>TCRU_3806 hypothetical protein, conserved
MESTRPVAYRRVVVSGSKNPVEYFVRAKGDGRTVVPAQTETRTGWLMWPAALRSQLRLWM
RAGQVALWCLLASRPTHWPLLKGIQERLSSECVSVVWSAHCSVRSIEPFLCWEDGLLHFL
GSCGGGGSWGKHAHCFGVGAPRTCSCVTQEA*
>TCRU_3807 hypothetical protein, conserved
MGEESFTYVLSPVTSTQNFAHRVADENLPSLEESMEFTEKMTGTLLIDYDGFIEDLLLGF
CRVPNGAHDSRVGVGRGEYAAPAGAILPTTIKAVGLDPSSSASSLFQDGAWPFVWAQFER
DVTRETLIIDGAPCNDALIALQRIQKLLADAYDELPSRITAAKTHGHGKADECGGLASRF
LNTAWGFLGNVQVAYKKMVRNKKLAEAARIAILIAQQTVMAFPVELLHAQFSRSSQGNFK
DKDAAESKIVYIGERIASKENDDEKSDPPHKEESRRMIVRVERRNHGSRLPYARVEKFMH
VFTLDESANASIKLELCIVIEVSLFTSDQVELNWEWRRPPHTFSGDAAAAPPQPPEEETQ
RLNKGEFIHAFADF*
>TCRU_3808 Amastin surface glycoprotein, putative
MGRANHAFSASRNESTENSKSVPSQPEQEAVSPPPPPPAGDLDISPEIVTLAFVLNSVFL
AVSLGTAWFLREQYAAGPNGENVKEAFKLWKTTRWVGSVRTSMRSDAIACTPVRQRLLVL
QILAVSALFISLITLVAAVVRRYFLQGNSGIRLALIYCVAICFIILTVESAIGINVYTFS
FVACGEGSSYHSHAFELSVGFALTIAAWAITAFAGIVVYNKVPFPRDERIVAYGIQAFDM
LAFIAFLFSTVACAIPLWFYKDSARRILTEVFLWKERYSILWATNASSNSTSVKKLGCDS
LSHYFLAAESFGIVSVLLNGTTFVIGFLLVKGLVGVTKYALMLGYISTMVAFLQWILLIC
IYYGDWCSGRVAYHRKKYVMAAGFALSVTAGVLMAVGTVALTLTESIRRRHFPSAGPCKK
IKEIFVEMCQ*
>TCRU_3809 flavoprotein monooxygenase, putative
MWKRCWRLLGSTNRYTDGSGRRLDPSGLPKELELPPISNRAYPVRGENWQPVLAGEPSPH
KGNVIISGAGVVGLTVAALFALRGWHTSVIEQNVSALKPSPVVAQPPVPSTGTNVEMTDT
AQYRFGPFLGLQHALATRRAVDALEAAGLNIRELRQCGVPVSGVMDHPGAYNSWLTRGLT
EHHPFAIKMLSMDLLTLRQLLELHVHALPTGTCRIFHEHVIEAVYPLKQQLVVKPLRESQ
THAWRMQQKSACKVNPSEDNAGPGTREREDDAAEVIVRRGYRMETSLTLHRLKWEKKFST
EAVDYDLLVCAEGADSQLRDLIDVEGFAADGDFGMRWFLLRSKKLSHAHIHRWLHKRRKS
PKQVDVCSPFQVPIAIAFPRQDRESNGDDAKEKESSFALLVYGPSSDIERLSDEEALRSF
CPDLAENDTTCQIISFTRTVVPYPTIYCENLFNSVGLPSAVVVGDSAHTCNPFWLQGLAM
GLEDGVNLLNQVDAYSKHFYDAIKQYSQERGCSGDALREITDRCLYYERMKHINPLVRFQ
NSFQLAMNMILPRSFNEYYSGASVNHLYSKSIEEMLNGRGYTSYEYAEKQQAKHRAFFHL
GRVYT*
>TCRU_3810 hypothetical protein, conserved
MRRCICCDAVITELLSRASLRVQRRRRGASENEAKKQVFRDVLTMSLLRIAAATRGGGAP
VQAVRDAPPRREWQANDWHSSLSDKAKSSSGTSAEGTPRFLRALLLKSRKENAVVHDAKR
VPHAPTAAKLLTDAEDGLCASETLSSTATEGADAVGAVATWYAAFQLFSEAVEQHTVVPS
IEHINVLLGITVREKRWQQMQQLEMFLEKILVSECGMCLSETPCKMDSILDVSGSQQTAF
PLQPNSETYEWLMAAAVSRGDWVEALRCFDDVRDEYLPVSDSLLKLALEAYRIGGVHSLI
DPGGNGHTNKKTTLAPLRTDYRGPFLHCAASARPASTSHGVRTKPAAARYLWEAALMLFS
SFLHRVQESDTVALFMSMMADAGKHQVLLDTYRDRSRTVNFGEEILPLVSNASREVGDWA
LNLCLLQHILASPADTERAAVGRQLLVDALLVLRRTQHYQKIIGLHVQVPSRMWTSRARV
MVAQAAMVQRDLPLLLWLFEEEETMRVETNRDDDGGRRTSHIMDTGLCYPFGIAAVSPVY
PSFPVEMYDIALRTIQLELIHRRFHSTPLRESAVSRLNIPQDLAALSIAIYEKFLRDSKH
QISTNEGVPFDASLSVYAPFVKLLQTSANEGAGVGRCTNGLPEGIWEKALSHVALIRRPD
TIVVSLVTHLLQRENQWEAAFNLLSHVIRSEEVSREADGPSRRRHSRLSSPNGVKVDEAN
HSDRYTCTAITAVAIRYAVWSAVRQPSAAVHLTQRALATGWIDGSMAMQLLEGVEGILGK
EEQLQDHWQDHDGNLSYASNDAVHALLKLVAMHDKREGGLGSFGSLFLKTLQLLQQLQTR
VEPPTSLLSDLTGNLEEVVSGLAKEGNDELRAKAELVVPVVLHAVWHQISMSHMSRWTLW
QECLRCLRWFCSPLSQHSSFVLQANESTLRVLRAFIRRCDRPEEGFVESVAVSWLLVEAS
PSALEKLLSLLDLLPDLVDRAVWLSHELLLDALVWCGRHRVKGLLRRLARILLPLFLKIL
QRGVNSTARKATEPRHCLRSETLTALTVAVQCLTSGPHEEVLHDWPLVHQLLSLLLQANE
FITAADTAQTTTPGRITALAESLAAVLDKLRRTFHFLTMKISLDAHRRRSQGSEGISFSR
DDEAKHLTSVLESGAIEYMDLCEAFAQRFFTEAGVDWMALGAEMAACLEKVMNCVWDVNY

TLYVWYTTFSPFQSGSSVLKPLQKRYRWLMCLCVLFLPASCITPLRVGRWLVVMSGDGES
AVTLTQSEIKGTETETNMIAALLHDITTLEAWQRCQFTTISHGGEGSCHQSRQLIVPLVL
EAIHSITIGVSEHVPSSFSQPTTNLAAAAVREALPPLKNGYSARTPFDDHIALVSPWQLR
TMQKAGCTLIYMLLCEGQAELPQMAKKAMSWSCCSHALLEVIVSAAQSTSAETFKALWTP
VALVDVFGLLKAQNCFWALFGRPQTAGGSQASRVLSLLTASPAVRAATRMDEDICTAALL
ALDPVDVMGDTEHVVAVRHTVCRLLAAFPKILEKRLLLLLLAGQLDDLQLTVMDILSQHI
VKVTGGRSLGCSPTLMRSIAMWLLLRPPCVAPCVMPCNAAPLQMFSDIMISGELRSADHD
RRMTGTMMRKEQAQNVSSSSREKSEEMMKAAHIRRWLGWEKAVQLLNDALQAETPHVDLN
KAFFGAMEIYGTYVSRRWEDDFFKALLEQNKRNPSSCNHTSSLRRLMGELIDHVAYAPSL
QQSLFRHEPVEPSELRQVGEKLWKCLGTACKEQTVTHADVWKSVFILLQRVLQNNLPFSC
QDTGELVFSLFPVNCLMVERLVPHLLRHGVVRNPSLPEKQESVVDIPLVASSMLLMLEMA
FPGRAVNMVLYRLYEKVLGEEAGCDSGGVTPPLSSSPAPVTSRQGAWRSLIECAVYFLTL
PGLLDGSITENIFTSGVAAGNNNKGNNAARVRDAFSTTGAVVGLVFRFICDDAVYVLSTD
DKLSHMREDNMQECLLRLLELSGRCVASLATELLLLSGTKRMEEDSAAMKRIVALFLQSA
LLMGSWRDIYWLSSRLLVSVSATLQLQRGEEAKSLFVSSWCWIVGCLPAMVAGSSRTSSS
LHSQVTALLKMIPAAFLQQNYLATAAAIVEKKGFGDGCVEARQRQLFYEFLMGLHERILL
KAESTLRDEGKRASSFTLRLSVIRPVVQVGVLLGLHNVGATEAGKLQSSLLFFLADDFQW
RRLLEAVKAECKEATTSKDLLKLDAANGGSAVSSWQVALKLLCLADKELFQTLSLKNGER
KAGAEEIQKIKDALHVFHVSCFAQAVPWEVAIDLFHRDDGPPHTALVFPASYTEQLIRHC
PSWSMALELFKYSLSRVPHPTKVQQLLAYLILYRMRTDPTWGKGGQTLLPHSYNSGGKDV
GLLSWEVACWCYNQLTQDRAAPTLPQRNMIEILRHCVFSPSAALSMYEAYWKQEYRLTEG
VNVFLSLLRAARLARNEELVLRAMWDYIRCCDEHDGVISKTSCGSVRHHMFTAGGNATLC
RSFTHVCESNIVSRQAAMELVTALKQRGRIGEMEELLMVTSYSRGVADATEERAR*
>TCRU_3811 tRNA synthetases class II (A)/Threonyl and Alanyl tRNA synthetase second additional domain containing protein, putative
MSTAPTFVRVGELACQRNPFLRGLRARVVLCEPVSMNKPAGGSGKGGHNSTNTNPSYNVV
LTDSVLFPEGGGQPCDHGTIVYGDEEVPVRNVQRRGDTCVISTPCPLEVGEEVEVRVDWP
RRFDHMQHHSAQHLLSAVVEKASQCRLPTVSWSLTHPYSFIVLPTGNKIDSDVVAHLEKV
CNDAIARAIPVRCDMYPSKEAYEQALREKVEKEDSGENFRQSRSIPSDVTGPIRIITVED
GIDQCTCCGTHVSNLTQLQMIKLLHQETKGDTLKLFFVTGDRLCRYYGDMYFREKELMKE
LGGVRPEEFVAAAVKRGKEYADMEKRLKNLTLELMKAESEKLIAEAKASLAEGAGGGIVV
YRRDDVGGDFFNALRDAIRQACPECLAVLAWGSPVATATAGGAMGRAKTGQFMVIGPTDR
VESLAPSVCIALEGKGGMSKYGYRGKGNLAGWDELVQKLRLS*
>TCRU_3812 hypothetical protein, conserved
MDANTTEKVEKKRQEFLSKDAIEEMRNFSDQTSSRVRHGLLPRDYHQTVDKAHEEKMHAY
ISPRRTWRQNVYVLRNFEYWRLRAEYYPYIERSDKYSDNFFIRGISCHPRLSDYPGCRAV
IQDYFICRDKNKVMQLFNMCAPLKEQFCACINEVFIKNHERGDKKFNANRKEYFENQRER
RFSKMLLQAEESADQRKKLQD*
>TCRU_3813 hypothetical protein, conserved
MMRAVMRAACSADSVNWGEASLLAADVLSVLLASQAAASLKTGLRFLSDAVLMVPRLLFF
LRGKADSAMLDRVAYAFLQPLWRVASGGHPLLQCPATSTDDAATQLRLSLPSLFELRVPD
DEAPGAYVTVDGVLSRCTERTRELGTHLLFYLCGEAPCTGAAPPAHTTLASTLFQR*
>TCRU_3814 hypothetical protein, conserved
MGLSCSHKKKWETAFKGKTTTRSSNRKPRKEYQVGLMLQCNKTSVHIDGRSLGEEEVLLT
GQRPPEVLMVLLWCVRWARISFDADGRLSVQPPTEFHCDACTQGQRPRSDKGSGSDTARE
DSSG*
>TCRU_3815 hypothetical protein, conserved
MPASCLSEIAALTPNNVTLGPDGAIVLDWPAAPKTARADLRRASRFVRIRGQDAPDTTKL
CGALRHSEKLMNPGTAQVERAEAPWNATAHSIERGVLRHAARIVGTHNSDPHVISQLAGH
GGSFGLPQDTVRYFGRRTTTLTQVSSLAAQVRRETPRKDRNPG*
>TCRU_3816 Concanavalin A-like lectin/glucanases superfamily/Protein of unknown function (DUF3676)/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MKDNNKELISLYENKKSDGSYNLVAVRLTEKLERIKEVVKTWKDLDSAMQSCRSVSSGNV

DAHKKGMCNGPVPTDGLVGFLSGNSTVTEWRDEYLGVNATVRNGKRSVSNGLTFKGSGAG
TVWPVGEMGQTVPYYVANNKFTLVATVSIHEVPQSGSIPLMGVRMNDTKGTVLFGLSYTH
DKEWLAITEDAVDPEDVGDAEDVGDIVKWEPNRTYQVALQMDSVEWSVFVEGKEINYTEY
NQRLFDTHRISHFYIGGDSKNQSATGGHVTVTNVMLYNEILSNYTLHKLNASKVTIPSLG
AEKHPTEQVTNTDALVASESKNEETTAASHEKLTGDDTEKQEEGIVHNLVLAASSSTVVA
GSSVPEYATAAESAESFHQEDNAQLSEGETSRQATLNEAKKSMARSSDVQKEDLQSTELT
EVADVEGSAESYDAPQPEEEGGANDGSGGLTPPVAASLSMAAATAPVYGEHQVQQSVELA
TENDDVRSTGTGTTGAEESLSLEAGERNSERTMNSDSSITPSKSDAEPTSAEDTDNISWT
ERAEFSVENGKEVPQTVVPAPGNTNTTPGETMISLESNATAPSDAGILPENGHYSELAGM
ALFAESTVHGCVFRVLLLLLLGLWGAAALC*
>TCRU_3817 signal peptidase subunit, putative
MHSVSQRVLEILTMSVSVGFVGLLIVVASSFSPLGPKNVSPIISVFNVSMSPLMRMPMPV
IYAQGQKPPPLRDYVFFKFTLRADFSPVWDWNTKAVYVACVARYRTENYVLNEVILLDTV
LKSKAAAAQWSLENAQKYTLEDAHPGALAGVQVQLSIRYQLLRYCGHSPMFEVSPVGKEY
PVLELPKTYGSVKMKDWAL*
>TCRU_3818 hypothetical protein, conserved
MLANVVLQENRALKKRLKVLQELMEKERVAYESLRIASSGLFPGDVALPVGHTTAVAVVG
NDGEEKGGGGVGGGAKVTVAAYQQLKAQYEELRCTFNTLQKERLRQGDA*
>TCRU_3819 40S ribosomal protein S17, putative
MGKIRTKTVKRASKQLVEKYFSKLNKDFYQNKRVVMDVTIARSKKLKNKIAGYTTHIMKR
LARGPVRGISLKLQEEERERRMDYVPEVSHVDQAIQDGVHVDKQTFSMLKRMETGVPRHV
ALTTVVAPVTKKGGRRAPARK*
>TCRU_3820 hypothetical protein, conserved
MVQLAGLSRAYAVLRQLELLRQQDVLDPLPPDTETETEAGSNLSDTGRGNGKNAGAPTTL
TDCCAAGKGPRLESSPIITTAAKSSGDGSRENTTHAPQCTEAYVKDLPSLQERMSHQSVD
SPMVGNGERERRLVEEYSYDTTESVTSGRRLSPHPSMDGRAQALQRVLQEIVARRRQAGE
KAVTPDHDDVHKLTQQDPYHRAGVAFRPSGRCSKKISSRLLSPSRGIDGEEDVFFDESPL
SFGICTRGTPGREAGQRIYNSHEKSCADEEETRNDVPHAKEEGEEYSPRAVPLVYSPPRR
RKDLLTYSAVSEYTKSLLRQRRQRHEKIKAETQQQQRCRTVDAQRRLDTTPLNATLSPIA
CIENPDKDVSYNLSRNLEFDSLQEETVIPPLPLFIQELLVMGSAEMQEKLRGMEGCCNGS
AMWCRDWFALTALVNSPDAIRHVILPLLLLELLEQNESNEQDASDANSRMSHILCALIGL
GGLAAGVLSLLLDMLTKSLGCPRLVALAIRAVGGDEGLHALCRLARCEQMDQGVHTAAVY
GIGTLAYPALGHTDVYCVGAPGLNGTIVFYQPPVLVGYVEVGNDGERRRETSLQCPPPYR
PTHVILSAELVRNKLLQFTVSRNFRRATGIYETLPLVLRDFARDAPEACRLQGLSDDVQE
TLRRCALELEDVSHFSARVLPFSYDPHYAGRKEEVFAVEEVLMNVLYNRKTTLGVVEQTL
VSIASLPDFATTHAAFPVLDYVIKCVTRFEREGDAAVEGEKAVLVAGLVALGRLLRNEGT
PPAVIDTACVVLLHNLDSSSCRLRHAACIGLGEVGAVVNNPGVVARALTDALSDAAMNHE
TVAWALTRLGLRGVRVLLDQISPGDGKSSSRTSGDWQEKKNGSRHHAAAALPISTRMICA
RALGKVDFLTVSLGIHEDARRLQEELVHRLAAAITSAQMEEELALECAYALAEAVSINLN
GKTPTPCRDEEAASYYRSETLNEAFQVLKGLVESIPLPLSVNKALFYSICLYGGAHGELY
ASQTAIQAPLVALRAAATFGLRACGGRVIRTVVMALNDDDAAVRVEAFDTLDAVGVKDVL
RVLRTRPHKHTQQVIAALRDSLLRDMGRGAKRQAARDLYAALLRA*
>TCRU_3821 DNA repair and recombination helicase protein PIF3
MTRSRVRVSPLELMRRGASAFAAASLQAATNTRIARRSCAVLPALFTADVSDGKKPAKQS
SQRNEPALLPHRSHVVSPEGEEAFINPFTGRLTSSSSRVAKELLRVGFLQSAVNPFRLTW
DAKKWHAAGAAAVKPFQSSMVGWRKNLAALLAREDAADAVVEEVQRLYSELTSAYLPPKL
DTMHDPQLSAMEMTPDQENAIRCALRGYNMFVGGGAGTGKTVLLKAMHRRLTEMGLRVAM
TATTGVASVQLGGCTFHLAFGVPVGAGENSKKRWDANAFRAVDVVIIDEVSLLDAELFDA
FELEARMARLQPLPFGGLQVIACGDFLQLAPSDSTFSGPCYQSDAFRHLIAVRLVTQMRQ
AKSDPLHKLLAQLRVGKFDRKSFALLDRHVPGDTDNVTYIFPRRREAQLLNEEKLAELRS
EEMTFTPQRGPLQLVGKFTPPGLIEFARKKQPVSRDEIVQVLTEEVKRVAAVDVVDHNVV
VMPTRSDKNGMLIRLRNPDDIVAARANGVGGNAKDYNSCSNTGGNTSRSGNMRDVHEISA
DRWKTILEATAKRLKATLRRIYEEDPQGFVPISVSMMLADVASQPNAEHLMPLRLKLGCR
VMINRNLSRTVSNGSVGVVEAFAVPNPDLFPRRHETPVRTMYGRLLEKNMFPKLPIVRLL

DGEVVQVPPLSLMVGGTPATFFYGHELYLLPMQLGYGFTVHKVQGLTLQGTVVLDCKHFF
ECPHLVYVACSRVRTLDQLIVKNIKGDMVIVKRSALEFSEKLRDASVITNLLPPDGCTRA
SWVDRLRPRLMGLSK*
>TCRU_3822 R3H domain containing protein, putative
MSAAGSREEMLEALQKAKQAMARRVPVVTLQETPSEGGELQLQDAETQPSFSRPRPHVPS
EAKTNRSHFFDTWCRKIEMFVADPTKTVLELPNDLAANDRRELHSLAEKYNLSHQSRGSG
ATRQLVLKKDALHYRMPDARPDNIETIKQNAGSKQSKFHLRRFLQDPDAAVGSIGAFADE
ATANMVRRLDRATDEYRRAVELGYSQEELLAIEAGESVEEILRRGGDGRLLLPSAVEQAS
GDVGSVPSVATHGGNDALHAIPPDNRKGKMYEEVCLRCGTRAHVDYDVQKWECNGYCAQC
ATQTIWKLVELDGVKEELVHPSFKRDRKRNFQEMEMEAAPAMREPEEIDKDNDEDDTITV
EDVVDMASMNDFCAADVNWIRSFATHHQPRGSGNILSAHIVFCIEFEDLFSMRIFRDFLS
LEDKKHAMKERKRTREESNAADQKDKGHCGWFLRLFEVKETGVPLSTLLEEISLCIPERY
DCLAVAFPNMSVYGAVASCVCLIQSNKVEESSLEILQRKYGKRSIQFARDLCAVLLNGGE
TASVS*
>TCRU_3823 eukaryotic translation initiation factor 4E, putative
MNPAAQEFVPRKKCAMDSNAIHMMGRNPPQQQQQKQPPQISPPPATTTKLRATAPAFVPK
GSLFPMATPPPTSFLQPPVSIPPPALAPPTVPQYADPNTAVGSGLPGPKSFSPSAPPYTP
ANPKVVAKFSSPPKTSGSPNPDPKKTTRTPSPHPEQQQEEDQPNEEKQPREEQEPKPDQS
PLAQKAQTLGVANRIDSARQEDSFGSTSAADETSSNALQQTGALGEAVENDFSGSVLPSV
FEVSVVAKPPPAEAIRFNTVWALHADDHPTPFGAPLAYDPVLVHLVGDVECFWRLWRYLP
PPSALLPAFTYHWFRRDIKPNWEHARNKNGGTITIVIFDRDKPGQNSKQTMDDAFMTMLM
ACCGETLAESTTNLNGIMLKVRQNKPTTVQIWTASSDQRKLKALAGSLRNLLEKIIGAKP
LQKLEYFSHQQTQVGGAGSLAGRMKGKPTRITPDFTL*
>TCRU_3824 hypothetical protein, conserved
MEAGDILHDIMGGNGPPLPQLQAPHEQRHESLPRRSKLVFLYSSDEEGDVDNSEKTRGVG
VAKVTEVLTLNLLPNDLREMRLEAELAAQHHPHAALQSPGDTEQQPLLFTEDTAGENVSF
AVQGRVKVVDALPLRECISSFGNKEVPLRRHLHAEETKRLAYARKRFRDDGDNEDRSSVE
DAGQCGAASGNVVVAEPRPVFDGDGLVRAIAVGGYRLTVDEHELQVSGVGEDVVTGEVDI
GHDTLEDDYFDQEDDDEEEEDEVLEEAVVVAVVEQLVRCCEVGELDESLREAGERFLVKA
RSCLQRLQTGELDLAAFGDEVQGDILRLSRAFQRFRRPKDAPVVIDGVVMDM*
>TCRU_3825 membrane-bound acid phosphatase, putative
MVQAAAALLGGIYASENATIVPTIISTAPERDALLNVEAFPSSTITRMINAKAFNATLES
VVDEQFPDASVVEAMGAEVGLDAALCSAPATRMVCCQQLQKLAVMYAAMGATDSAPTVMA
NKAKLDAVAAAYFHVSQGYNASVPQDVARGSLGLPLARELLRNMRAKMLPVGDANRNTKI
MMQYAHRVPIQTALGHDPSDATPLGETFLVDLLRDDATNAYFVRLRYAAATNGAPAAAFF
PFRCLSAADVPTDATTADGVICPFDDFTRFVESSSGTSAAGAACYLDEETRKKFGCSVEG
AAPSPECARYRAMCPAQACPGGQVYDVRDDSCKPRVVLSDVISNGAGVAVGIAAVVLGFL
LSLFLMHLCPMLCLTKGASEMHGDCPGNVEVSTVPRQ*
>TCRU_3826 BNR repeat-like domain containing protein, putative
MTATIEERRVTLYTQRGHTSGEKRATALCLWVTDNNRTFSVGPVAVDNAANWMLAGNLLY
SDGNLHLLQGRGSGECRVISLSRLMEELSAVRSVLSTWTQKDIFFSNLSTPTAWLVAVLS
GAASDGRWNDEYLGLNTTVTNAVKDKDGLQVTGLESRAIWPVNTRGDEVRHISLSHNFTL
VASMTIEETPSGNTPLLTAILANTESNHTMGLSCSHNNRWETTFEGKTTTRSSTWEPKKE
CQVALMLQSNKASVDVDGQSMEEEEVPLTGERPPDVLRFCFGACGGH*
>TCRU_3827 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCVAGGGFGEEDTQDEFCNNTYLGVLTLLANRTDKEPAEKYC
KNAGDKTECVDTLKKNIEVALENEKKMKDNAPDRERNVAHGAGSSVGNPTTTSSTTVGAD
NAGVSSPLSLKVEGGVGAQIHSQAGGASRQPHSDDGRSEAERSHRLEAEGSNQHDVAVQG
KTIHNKDEETPQTGVKSTEAREDTDGAPAPSQDPPNTTESHEEKSRRVAAPDTTPALNTS
SGSNQEQTSQSSPPSGSETTGSSDSEGPEKNSKNAQISDAQLKDEEQHHESTAGNEEGTT
VESAAVQSNTTTPADSDGSTAASHATSPLLPLLLVACAAAAAVVAA*
>TCRU_3828 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative

MSADGCSDPSVVEWKDKLIMMTACDDGRRRVYESGDKGDSWTEALGTLSRVWGNKHDENV
KLVRGGFITAKIEDRDVILVTTPVYANTESEEKEKEKGELHLWLTENTHIVDIGPVSGDD
EDAAASSLLYKSAEGEDRKEELIALYENKKGDEEKSLGMVSVRLTDQLQRVKEVLATWNK
VDKRVSQLCLNSLSQKGLSTQSVCTGKITAGLVGFLSGNFSDNTWRDEYLGVNATVAEKD
GAQKADKGVTFKGRGAGAEWPVDAQGENQLYHFANYNFTLVATVSIDKVPEGDNTIPLMG
VKMKGEQEKFFGLSYEKENKWQLLCGDATTNSGELSSIGEPETTHHVVILLRNGNQSSAY
VDGQRVGGDAPCTLGSTDLREISHFYIGGDGVSAEDKESREGVSVTVTNVLLYNRPLASE
EIAELAKNKITITKPEEPKKLTTRPRSPAVSATGVEGTVSLSNAAGQQPSEHEPLTANIG
AGVLSSAASIATTPSPDADPTVVTVGGETVQGDGSLQTPGVSVSSGADGETAGGTDAQQE
GIHAQAGEVTATALNSSLGNVSQGNNTDAGTVRGSGLLPSLLLLLGLWGFAAA*
>TCRU_3829 hypothetical protein, conserved
MAASSFTDSECDNTNDGKNNDEDDDDLHRGADYLRVLVHESREGLNALPTIPGLAEPLAF
APSPAVISAPCVEADPFTVEFTQQLSKGCAAIPALAHSHVFQRCLACDLLCVLSRPPPPA
FSWCPIRSTLRCGGYLIAWPSTHVTMLNGCVFCLAGTRETSVCADNSAKVFVGGSRQK*
>TCRU_3830 hypothetical protein, conserved
MVLLWYNIYNKECEEKNKENGSLNDSAMKSCMRTSMKEVCGVFYNDNSGETPDPESDRIC
KEYAGDPDGAFQPSASQAKPLPTAEKPAVAPTPETSKDEAEEMGLTPGPPAGAAGDLPAK
PTEGPPPPSAAIDAASNEMGNGTGGKVPAGAPEFDVVGTEKGKESEANDGSTKKTPVETV
VMRGVTAPEDSDGITAVSHTTSPLLLLLVACAAAAAVVAA*
>TCRU_3831 P-type H+-ATPase, putative
MLPPSKGLTTAEAEELLAKYGRNELPEKKTPSWLIFVRNLWGPMPFALWVAIIIEFALEN
WPDGAILLVIQLANATIGWYETIKAGDAVAALKNSLKPVATVHRDGAWQQLDAALLVPGD
LVKLASGSAVPADCSINEGVIDVDEAALTGESLPVTMGTDHMPKMGSNVVRGEVDGTVQY
TGQNTFFGKTAVLLQSVESDLGNIHVILSRVMVVLTSFSFTLCLICFIYLLAEFYETFRR
SLQFSVVVLVVSIPIALEIVVTTTLAVGSKKLSRHKIIVTKLTAIEMMSGVNMLCSDKTG
TLTLNKMEIQDQCFTFEKGHDLRSVLVLAALAAKWREPPRDALDTMVLGAADLDECDNYT
QTEFVPFDPTTKRTAATLVDKRTNEKFSVTKGAPHVIIQLVYNQDEINDQVVEIIDSLAA
RGVRCLSVAKTDSQGRWHLCGILTFLDPPRPDTKETIRRSKQYGVDVKMITGDHVLIAKE
MCRMLNLDPNILTADKLPKVDVNDLPDDLGEKYGEMMLGVGGFAQVFPEHKFMIVEALRQ
YGFTCAMTGDGVNDAPALKRADVGIAVQGATDAARAAADMVLTGPGLSVVVEAMLVSRQV
FQCMLSFLTYRISATLQLVCFFFIACFSLTPRNYGSADADFQFFHLPVLMFMLITLLNDG
CLMTIGYDRVVPSKLPQRWNLPVVF*
>TCRU_3832 haloacid dehalogenase-like hydrolase, putative
MMLGVGGFAQVFPEHKFMIVEALRQYGFTCAMTGDGVNDAPALKRADVGIAVQGATDAAR
AAADMVLTGPGLSVVVEAMLVSRQVFQRMLSFLTYRISATLQLVCFFFIACFSLTPRNYG
SVDADFQFFHLPVLMFMLITLLNDGCLMTIGYDRVVPSKLPQRWNLPVVFARSIILSAVA
CSSSLMLLWIALEGWGDETYPNSWFKALGLAQLKQGKVVTLLYLNISISGFLTIFCSRTG
GRWFFTMAPGLVLLIGATISLFVSSMVASFWHTSSPGGLLTEGLAWGDTNSERLLPLWVW
IYCIVWWLIQDAVKVGAHMLMEWMDLFGCVSKAYGGKVVEQYMENKITEPAN*
>TCRU_3833 hypothetical protein, conserved
MQDTSRKRKAHESYERPRGASPGSLGCHGAFHITRCVEARCSNRGDIQFGSTRDLAVGEA
RQSVRPSPEHCLIFVEVHHNADPGVVAGRIDVKGEAAEGQEPWLTAEERFFHDFYHNHAA
TITRRATRTRLATPHDERTIPLQQVNVPVLNLEWIKSRLNPATLERLMQVWGLVGRSPFP
PSSSGKAREGSRRIPTADAHLLRKAGIVEDGSSTITGGWIIPFSVVVEKTAGSRRRLIAW
PRDKNRDDPYEANVPLLHISHYLPPVMAEAAFCLDLKASLFQVSLPRETRHFFRCHVEDG
TLVELTRLPMGCKAGPEILQIITSAIAVVTTVVHSLWAAPPSVRVDVWIGNIRIAGSKSG
ATLWEAQVLRNADSCHATMGRTANRALRSTPFWGCSLITFTVRCP*
>TCRU_3834 hypothetical protein, conserved
MDGVHMTNGVAVVFDVAAMLPGALRIELRNCVCDGGAQIYVRGYGGEPASDRSLEVSVSG
LSGSYCSLVFVHNLPAHTNVMVRDSTIVTPGPMHYSQLNGLTDAVASPLVLHATSLLQTQ
LRVSNTVLRSLQAGGSAVYVGGGVDLLSSAVALDGVLLEASGGPTASAMHVASSSRLSLQ
SHSVFSMTNVSVVSSGGGIVLGERLAVIDSVLRFVGVEGSVAPSLVRCDGGTIGGGGWLD
LHDVWAVGEASSVASLSGVTLSGGAVSIARCAATGATLVSGLAITSGVVSVQCNRAGGRV
LQSSGDYRMAGLPSVSVLPCDGCAAALACFDALTASFSDCACSCRAGGVGDACLPFDVPS

ARAGGGGGDTAQDCMSGVTLTESVTVGGGRATACFDSVVFSGPITVAVDLRSMDVFADAL
NVTLRRCVLAGGAQLRIGGLSESTARLMPHALVSMTKVTSLEGTIVLHGAMPLHSTVLLA
NSTLRATVGGSQYVPTTRGHEKFRYGSALVLDGVRLLSTRFVMTRSTMACGGGSCAAILV
ERGLGVNLSSVFYMDSCVVRSQTHVMYAIASDLRVGGGSVFSIQNSSWSALSTEYGKGAC
VFKDVVVDGGSVLQIVSGIFRLGFAMLIANTLTVADGSWLVHRDNEFRTAYVVYVANENG
VAFRDRSVWSILGNNFTYGSYSSTIVSMTSNWSPPSDSHPIIYGVCNEARGSPVTDYGEE
LNIGTPVTVLDCGACTVDAVCFAARTSSISGCECVCAAGGYGDTCVPATVPDGLGPLPLP
DADDTEVRCVHGGSIGSVDYPDPGVRGLCFVNVTFTAAIVLNLWSFDAPEQTLNITLLQC
VLMGLLIKGKWCARASERSLLDDGFRSVGVSG*
>TCRU_3835 hypothetical protein, conserved
MVYPEVAQSVGDGLSWLCYRNVTFSGGGMSLTVLVGAMTGDVVKITFDGCTWRDGAVLLL
LGNAHATVGSLHIVVTGSTFSDALLSPEGGFPPRTNITISGNHFAVTRLIPRSGLDIWIP
SCVAMNGLVIANDSAVVLSGNVFQTVTASSIAIRVVRSALRVSWHSVFAVVGNTFHMDGG
GSTLINIDGFSQSLSLSVLNNSAVVVRGNLVTRPVRYFLLLILASRVESRSAVVFQGNEM
QRSSVVFFFKPLFIHLLQLLASGERQPLP*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MSSTDRPTVLRITTGSRDITNGAIVAACNSVNGEEGVEYSVPSVYNATILTCSDPCTLAA
SCFPAYTTTASSDGCACNCAEGGHGDACLPVAVPEPPSTDGADLCVRDVRVDVEVSAGLG
TSVACYVGVTFAADVVVDVESMSGSVRNVTLANCTFLGGAILYVVGWRSDPPAAERVDVL
ISGLESRSGGGVLVSNRFPPGSRVTVVDSVLIAEARVAYRGEYDLGDASACLVVHNVNLT
GSVLTIARTHVAAVFRDAVGVLVVGSVALSSRGALYVDGLSVQTALGLCVSVEGGVAASG
GSVVAFVDSDFLLCKHAVSVRGAVSVSGSAVALVRSDFSSTEDYAVAFYSTVSLAGGSML
LAKDNVHDGVSREMLYAAGAVTAVGSTLSFLRNRALLPRMLSASLSLSAGAHLRVACNDA
GGRVLSTAEEYAAAGFGDAGSIDVVGCDACDRDTHCYAPGTASASMMNGVCVCDCGSGGY
GEACVPVGAPALPPAVGTAPSVFVREGVAVQSVVVVPAGASEVTLRHVVLDGVSPVLYVP
WMARDGVRIVVQNVSLLSGAVLYVMGGGALRGAVAAGSDEGGPVELSVCDVEALNGALVL
TGTYPAGSVLTVTDSLLVAARPTPLVYLPGSESSPYAPVLVLSGLRLVRSVLVVFGVALV
TVMTGGRTVAVDGAVLELVGGGVALDAAVLGGDFALYASARVVASGGAVLRVSGSQVYAA
HGLVFGSGVEVNASAVVVNDNAGSLTDGALLELRGSASFVSGSWLSVRGNSISGRLLSVP
SYPRSAELVQSTLTLHGNTGSGPVVMDGTVALGGAGRNFVVGCLTLNGQALRPMEYRSAG
IIGKFRPVACGVCDADVSCFAAATRAMSRSCGCRCAEGGYGRDCLPVYLPHVDGCNRTPA
LPLLSHTVTLTETRSPTPTPTPSLSTTHYSPTQYGPTETLQGTETVALSPTRTPTASVSG
TLWWSDVACPTLAVTTTAAGGSLTQNDIRGGGIAVPTLLMLALPPPFRWARDPQIGTHLS
FVPVSTAQPSGFGGPWGAMLRNATWVRNATNPSTVLELAVPVHRGYFIAADETIVIRCDA
AAVSGGCKGVLLGSFTIRSDTLPAAAGTLSAITGVVAGAAAASVLVTGGLGSILEMQALG
VFARMPCASARESESTVALPYFLSVFAALDPLWMVVGNALLAAVFGCVHCGVTAAFQRWR
GVDAASAWAAMRFPSLTYVVAHAMHLGIFFGSVLSLAMPGARVQHRVVGVTGVLYGVAFP
AGVCYLIARHTGASFTKYWQFSRKPLHERLLYPVGYWHPAAQQRMYGGMLTNMKGSHAYW
CVFQLSVLCVVGLIAAVHPPVGGCHVLYFCIAAVLVAGAGVVAFTNMMRSAFLTVMHTAS
FVLLAVLCVVSAANHLAPSDGGTRAYAAIVLLLTTVLLAVTVYSVVVWYAEDRHWQELRE
PRRGGLEALLRDDEESDEDAQKPHEMTSSSYATGTTGASSYRPPAPPLQPMAGDTHSDAL
SPLDRASSASRMIDYAAM*
>TCRU_3837 hypothetical protein, conserved
MLQGNKASVHIDGESLGAEEVLLAGGRPPEVLRVCFDACGGHESHVTVDDVFLYNRPLNS
TAMRALKDRVPAPTREAAPTPPEKVRVFDSVREHAAEDITEEEWMGTTPLETNPHYKQSP
RSVWSGVSPDDRLALSQRSEIDTA*
>TCRU_3838 hypothetical protein, conserved
MKVPENQPEADISLLSSSGGRAAGIPGQESSEFPSKVSRSSEASGTGGDGQYKNTNGTAK
PAVAAPKPVSVTQPKPSGIAGAGAGEGERLEDPLPEKPVKETAPAAPSPKASSRTASSPS
KKKDTESTKPADDPQKKDKITTTAATQNATTEGHGEAASSSSAEDDSNAVANNADEGNVE
NSNDGSASRAAVPDEKQQREREDGSEKETESVPTPKAKNEDPGSADVVSVQQVQNAQSGL
ESGSESGKEDGVVTTNKQQDGTSDSHAESTPTSRSSAKRVAVSNGPDKATEEEISN*
>TCRU_3839 Mannose-6-phosphate receptor/Autophagy-related protein

27, putative
MERGKRKVHLVLRFFIYTFLLAGLLSCTLVARAEVASCVVGTYNLSKVPEANLLARERNS
DGTSQGPYLWNIVLCVAQSGFVKQYSKTRDRLGKAMTLQSIIVNDGYVQAVYSQWYRDWG
YQMNLDIKCGQEMELAWPSADYEVRTYYYYDTNTEMLNATVLTKAVCPVQPSGGSARGCG
GGCAFVVIFFVSLAAYVIVTVLWYYLRQGKRGKDLFPHPEFWADFPYLLKDGMVYVYTKI
RLCIGRGSSTTQYEQM*
>TCRU_3840 cyclin dependent kinases regulatory subunit, putative
MSARDFFSITDPVQKEQARHMISKLQSKILYSEKYYDDEYEYRHVVLPKDFARLVPRHRL
MDESEWRQLGVQQSVGWRHYMFHKPEPHVLLFKRPKTQ*
>TCRU_3841 hypothetical protein, conserved
MPLMNAGDGSPTTSHQSSQASHRAADAPPDLSNCPTKSSRRAMELIRKRRSTVVRRITDI
PALGQLYEESERGRSRDVGAVNVGAENVPSGAIHNLLPHARTADERGELRGLFDGNRRVA
TSTRLQYARMLRSMLEMDRTPLDMMIVGLQKIAARSETKQARPLTKEEMNQVIRSRTDWK
ERVVLRLAWITASRWSEVAALTAKNFTLEVDGTLILDRSVAPKTAKADPHRASRFVKIRG
QDAFDIIKLCRTLQEKDKLTNLTTAQVERALAPWDATAHSIKRGALRHAAQIVEKYNLNP
HVISQLAKHVDPFDLPQNTVRYLGRYTTLLTQVSSLIALM*
>TCRU_3842 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MMMTACAGGPRRVYEIGDKGESWTEALGTLSRVWGNKKGGQATAVRSGFITATVGNDGDN
KKVMLVTLPVYAEEGNEKGKLHLWLTDNTHIVDIGQVSGEYDAAASSLLYNSGENTDDEK
LIALYEKKKKDGGKPSNSLWSVRLTEQLKRVKDVLATWKEVDGRVSNLCTSLSAQKDRAS
TDDVCGADKITAGLVGFLSDNFSGDTWRDEYLGVNATVNNKAGAAAALASTKNGVKFTGR
GAGAEWPVGRQGENQLYHFANYNFTLVATVSIDKMPEGNTPVPLMGVKMNGNENNVLLGL
SYDSERKWHVLCGDGTNEELSSTWETQTQYQVAIVLQNGTQGSVYVDGQRVGNGECALRN
GESNEISHFYIGGDGGSAEIKGDVSVTVTNVLLYNRPWDDTEIGAFNPNKANVPVQVTPN
AQETGTSSALDGKHLTERGQSMGSSGAGSGGASPSAVPTVSTPSAGKDSVMQVASGKSSD
GTQTVDGGFFSDGEPTVGTREGGKNGQEEEIHAQNGDVKTAALSSSLGNVSRGNNTDAGT
MHESGLLPSLLLLLGLWGFAAL*
>TCRU_3843 MSP-B, putative
MCHTMLLLVLLLCCVSGSVAVAEHHCISEEIEKKVGPRTTAVVLELPTRGGGMMRALTAS
APEWAPIRFQVFTEDLKDPSRYCTAEGQIRPDFTGGTVECNKRDILTKGKKSIILKSLLP
RALKMHTDRLLVEPLTGYLIVPEFLSGACAQFTIPSSHHTEGVTGADMYLYVSAGSTKGS
AVAWATSCSHLADGRPVAGAVNYDPSFVTDSEYSVRVSAHEIAHALGFIVRIMKERNMLK
EVEGVRGKAKVLQVSSPKTVEKTREHFNCMSATGMELEDEGGNGTASSHWKRRNAKDELM
AGVSGIGYYTALTMAAFEDTDFYRANWGKEEPMSWGNNSGCALLTEKCVINGVTKYPEMF
CTAESRLFSCTSDRLGLGHCTIELYDAPLPPQFQYFSNPKLGGLPNTLMDFCPYIELHEI
TKCSNGNKALMRGSRVGPTSKCLKGDGLADSEGFIGDVCAEVSCDKGEVSVRYLGHGKWH
KCPEGSSITPTGLFMQGRILCPKYDDVCIVIDACRGGGGVSSLLSAFPSIPLILLVFIFM
SMC*
>TCRU_3844 hypothetical protein, conserved
MTCLRLISAKIAKQLEGSTVAGHFSNRWAFQAPNFDAQVLLPIVWGRPGSWGASKGSSLR
KGRYYARTTPMPLRTYGIGLLRFTFRRKRHPTTARHVKLTLRCLAVFLRKAETLFQREAP
TSRRGPPDGPTHARRWRKYTEKSTASFDGLGRVSIRVFPTQSCGGETAGQHSEFSEQFGK
IHFSFFFAVASPPSPVKENFGLEGQVLHFLALDVTIWAPRVWNEGISEVVVGPRSAYSYK
CLHQADAQVQPAFDGLVSCRRALEIERDPADCFMDLFRAPLQTFQLQMMTTESSVPISEL
RAGPRTQQQRSLRCRLCRICGRDASTCNVGDATRGSYSQRRWPSKNGKGAARRL*
>TCRU_3845 hypothetical protein, conserved
MELICQRRSTEVRRITDIPALGQLHEESKRGRSRDVCAVNVGAENVPSGAIQNLMPHART
ADERGELCGFFDGNIRCGAIDPTAVRQGAAVYVGNESDLAGHGDSVVKKIAARSETKQAR
PLTKEEMNQVIRSRTDWKERVVFRLARITASRWSEIAALTAKNFTLEADGALILDRSVAP
KTARADPHRASRFVRI*
>TCRU_3846 hypothetical protein, conserved
MHRGRGRTARRLQQHAVKHHRARQQVHAAASVHRRPTRVQRPQHSVAHTQLRLQQRHRVQ

HKRRRHHVRQPAQLRVAHRSRRNNRRVTDRHVRVCRQVVHKHERAVAAGQPAHAHLQAPV
TRRLAAVAPHVDLRTAVAHAVPQFDAQCAGKHRRHVEHHSHAVRDAHAVHQHRVHGVANR
DGSVHRAASQSHHHRMHRGHPRRRRNQRQHKKKRHTHSRNDLAPHTMPTARKRTHRRPHP
PTQTRISRAVVLCRTRPVDRNSCLANPFLQMANPDTRSARSLS*
>TCRU_3847 hypothetical protein, conserved
MQRRRGVLHARDGVGGSRLVLVQLQGRMAWRVVSSLRGARHGCAALAGESRGRRHELRGE
PDADEPHAEHVEDVPLLRGCDIQRRGCCAGVFL*
>TCRU_3848 hypothetical protein, conserved
MQRRRGVLHARDGVGGSRLVLVQLQGRMAWRVVSSLRGARHGCAALAGESRGRRHELRGE
PDADEPHAEHVEDVPLLRGCDIQRRGCCAGVFL*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MVYPEVAQSVGGGLSWLCYRNVTFSGGGMSLTVLIGAMTGDVANVTFDGCTWRDGAVLLL
LGNAYAAVGSLNIVVTDNNFIDALLIPEGGFPPHTNITISGNRFTVTRLIPRSGLDIRRP
SCVAMNRLAISNDSAVVLSGNVFQSVTASSSAIHVFRSALRVLWHSVFAVVGNAFRMDGG
DSTLMHLEGSRHSSSLKVLNNSAVVIRGNVVTRLVKYFMHILSALIVESFSAVVFQGNEM
QGSSVVFYSSFASNIYYHSWLQLSGNLCRASPLDAFAFLLPKVNLRDSTVSVSGNRFMSN
IVAPTVLLISSVSSDLTNGAIVAACNTVNGGEEANYAIPSVYNATILTCSDQCALAASCF
PAYTTTVSSDVCACTCAEGGHGDACLPVAVPEPPSTDGADLCVRDVSVDVEVSAGLGTSV
ACYVGVTFAADVVVDVGLMSGSVRNVTLANCAFVDGASLYVVGWRSDPPAGHRADVLISG
LESRSGGGVLVANRFPPGSRVTVVDSVLIAERRVAYRGAYGLGDASACLVLHSVNLAGSV
LTIVRSHVAAVFRDAVGLLVVGGVALSSRGALYVDGLLVQTALGLCVSVEGGVAASGGSV
VAFVDSGFLLCKHAVSVRGAVSVSGSAVVLVRSDFVLTEDYAVAFYSTVSLADGSMLLAK
DNVHDGVSREMLYAAGAVTAVGSTLSFVRNRVLLPRMLSLSLSLSAGAHVRVACNGAGGR
VLSTAEEYAAAGFGDAGSIDVVGCDDCDRDTHCYAPGTASASMKDDVCVCVCGSGGYGEA
CVPVGAPVLPPAVGTAPSVFVREGVAVQSVFVVPAGASEVTLRHVVLDGVSPVLYLPWMA
RDGVRIVVQNVSLLNGAVLYVMGGRSLRGSMAAGSDESGPVELSVCDVEALNGALVLTGT
YPAGSVLTVTDSLLVAARPTPLLYLLGSQSSPYAPVLVLSGLRLVRSVLVVSGVALVTVM
TGGRTVVVDGAVLELVGGGVALDAAVFGGEYALYASARVVALGGAVLRVSGSQVYAAHGL
VFGGGVVANASAVVVNDNAGALTDGALLELRGSAWFAFGSWLSVRGNSISGRLLSVPSYP
RRAELVQSTLTLHGNAGSGLVVMDGTVALGGAGRRFVVGCLTLNGQALQPMDYRSAGIIG
EFRPVACGVCDADVRCFAAATRAMSGSCGCRCAEGGYGRDCLPVYLPHVDGCNRTLAPPP
LSHTATLTETRSPTPTWTPSLSATHYSPTWYGPTETLQVTETTALPPTRTPTASVSSTLW
WSDVACPTLAVTTTAAGGSLTQKDIRGGGSAVPTRLMVTLPPPFRWARDPQLGTHLSFVP
VSTAQPRGFGGPWGAMLRNATWVRNATNPSTVLELAVPVHRGYFIGADETVVIRCDAVAV
SSGCKGVLLGSFTIRSDTLPAAASALSAITGVAGGAAAVAVVVTGGLGSVLEMQALGVFA
RMSCASAQERASTVALPYFLSVFAALDPLWMVVGNALLAAVFGCVHYGVTVAFQRWRGVD
AATAWAAMRFPSLTYVVAHAMHLGIFFGSVLALAMPGARVQHRVVGVVGVLYGVAFPAGV
CYLIARHVGASFTRYWQFSRKPLHERLLYPVGYWHPAAQQRMYGGMLTNMRGGRVYWCVF
QLSVLCVVGLIAAMHPPVGGCHVLYFCMAAVLVAGAGVVAFTNMMRSSFLTVMHTASFVL
LAALCVVSAANHLAPSDGGARAYVAIVLLLATVLLAVTVYSVVVWYAEDHHWQELREPRR
GGLEALLRDDEGSDEETQKLHDMTSSSYASGTTVASSYRPPALP*
>TCRU_3850 hypothetical protein, conserved
MEVIRQRRSTVVRRNTDIPALGLLYEGSKRGGSRDVGAVKVGAESVSSGAIHDLLPHART
ADERGELCGLFDGNRCGAFDQTAIRQDSAVHVGNGSNPAGHDDYGVTKSCGAIGDEASAP
LDRGRDESSNPQPDRLEGTCCFSNCVDNGESLVRDCGIDTQQFHTGAGRDLNFGLVRGAE
DGESGPHRAFNFVRIRGQDVFDTIKLCRTLQEKEKLTNSTTAQAKRALAPWDATAHSIKR
GALRHAAQIVETYNLDPHVISQLAKHVNLFDPPQNTVRYLWRYTTLLTQVPWLVALM*
>TCRU_3851 hypothetical protein, conserved
MGTVCVDGKTLGSSATTVTRGTQLLDFSCFYVGGGGRSGSYCSQVTLTHVCLCNRPLTRQ
ELQMPLLRGKQTEAGCKERKATPRPGNFAAKLSQDPGVDAAARELLPVPAKLEFGLGNGT
ADVNGSTVLLFSK*
>TCRU_3852 C-terminal, D2-small domain, of ClpB protein, putative
MREKVWQVVRSYFRREFVNCLDDIVIFRKLEFGEHHDTVDLIFAEMSRRLKSQDILLGMT

EEAKLFFFLVNDFDVEIGARPLRCCAEKYIATEVSRVILVQLLLPNIVVRVLVSSSQGKL
AFSVKRSSVA*
>TCRU_3853 hypothetical protein
MDAAKLLEPSRARCELRTVAATFFEEYRENVETDAVLGRRFMPVYVTEPGVDGSNSIFRA
LGERYETHRGAQMTDNVVGVAGRLADRHAASRFMPDKAIDPIDEACANVRVQLSSRQEEM
DQLERTKRQLGIEAKAVGRDKKKKLLQERLRIVKGDMQRVEKPLLAQCNGVRQ*
>TCRU_3854 zinc finger protein family member, putative
MDLDYASGLHAVISWSNELNNEVACMKTREDAAAENFGESILSNGAGTGVCQSNISEDEN
WRPIPMRGDALPTSLGSSLGLTEAVHTITNKLASRNYSGASASQNSLNAFTVLLENGVQH
SQPYIEFDDIWGSDATQSNAVVKDNESCQEMPQALFIPSSASSGLVGSVGEERRDGITEK
CGEEKVIVVVDPRRSKLRVPLSAISPTKALGIRAQNPSLCLLFQSGRCRQGVNCHQVHVD
PEIVQRLRRIVDSLPCCCTFHGDCNTHCWDAKANSKRGVFISNVWVPLSHVAYTSGLARF
VTNKVQRPLSFGVLCRLHGKTGGCRYGADCWYLHVCREILETKFAFMTEANTKDSKTEGT
FTLLPNAAPMFPSVMTEVQLAASSRQQQQEQTSSFLPAVTQFPMMITSPFSTKDYKSNGG
INNVFPHRDTAVASAVPCMWVHSASPPQGSALAFSTVAAGAGAGGAGMHHEGLQHKTSDE
KVLPRRVSSMSQNIPNESAISVSIGPPSSPAAFAFSLGNGNTNPSPVSSLPYQLVEQTQV
SGMNVMPMNPSPSAAYSAMWFSHQQQQKQQQQPQQQEAYMPEQTRNITVPSAFVASSAGY
NLRSRLEEFFQPQNNPGPSMTLLPVISYLL*
>TCRU_3855 hypothetical protein, conserved
MYQRSLLFLLFSKPITQGYVAQLPQPAPTRRCTSWRRAFENNDEVRKKYTPDAERYEEWY
KATYGLESLSDGCAASGATSNRRLDDTQNMESVPSLDDFCAVEEEVEFCSRQFNHNTLVR
*
>TCRU_3856 NADH-cytochrome b5 reductase, putative
MKALFAAAATGFASSFCYNRELATCSAAKSPFSTTEFRPFTLMNFYDESHNTRVFRFALP
EADMPLNLEVSSCITAKYTGKNGEAVIRPYTPINKSDQRGYFEILVKRYDNSKMTTHLFS
LKKGDTLEFKGPWVKIPIKANQYRHIGMIAGGTGITPMYQVARNVLRVPKNTTAISLIYA
NTRKEDVLLGNELNELMETCPLFSPYYVLSQAPSDWMGGVGYVNKEMIKSVMPPPSSAAD
SIILVCGPPPFMEAISGDKDFKTSPPSQGELKGMLKELGYMQKMVFKF*
>TCRU_3857 leucine-rich repeat protein (LRRP), putative
MIEDAEHAYRRAVEIIEVATIPPDPDAPSLHMWRLRPSEEAAFLIQRYLNPPPQWGIKLS
LSATFLGPERCVSLGRKLILNNTVTTLDLSMCDMQEEAAVEFFHCLKRNRCLKHLNLDGN
NVGDKGATAAAECIHNLETLHMSCNDIHDKGAIAIACFLRNSSKIKTLNLRANCITFYGA
YKLISALEPILERLSPALLERISIEEPVSSSDYDDVLNLSARPSTQGTFDVNGDIATEES
AEKASHGKQNRIPPEDVYNETLHTLWLRHNRDIPEELFKIVETILAKRFPQPPKGISKKK
IALKSKRE*
>TCRU_3858 hypothetical protein, conserved
MKKEQVLQQEESDSALARRLHEEINGPGNVQPGAGSIPNQASGVKLIECPACTFINTITE
FVPGRSYTCEQCFTPLSVPASNETIDAPDSNQKMVMCNACQYMNRIPLGNFDAIVCGACC
HKLKGKTPVSETQHPQLPPASTRPLQVRCGECSSINALQVGMEVSTVRFECGSCQTVNEV
SL*
>TCRU_3859 protein kinase, putative
MGRVGEYEIFETVGTGAFSKVKRVRHIPTDACFVAKIIPKSNQRVENDIRVEISILRRLK
HRNIVQLVEILESPNNYYIILEPVFGGDVCSLVLSQDSSLEEEVVSGLFFQLLAGVRACH
QNGVAHRDLKPENLLLTEGNVLKISDFGLSRLHKQSNFHAQIDEYAHTLTGTLAYVAPEV
FCGTYDAFKADIWSMGCILYVLLTSCFPFGYTTDARELEERIKMGRICKLPDSVSEEAKE
LTLWLMSLHPEDRPSLDQVALHSFLKRYVPMKHILALIGSKQPPPLAANPAEFSSEVVEE
EKQVNERGRPLFGKEAPREYSLKPCSGGSSKPMGQSGKD*
>TCRU_3860 hypothetical protein, conserved
MLRKRYRPLDPAEERSVDVEHKLQVGLLYDEQSYCFRWPDAPLTSMLRRSNASLTRAVHG
NMVSFTQSIIAQPPIFTIDSIATEHGKRDFFASVSVDRPIISFSSGNVSPSARYTETQRY
KRHPGAPIETSTEDSIFSFNAQQLKDLRDAGAFKAFREALSRSAPDSVNLDNEAELESIA
RREMENELTRLEWQAFHESEKTAPALQRIFLLTTAVPFMEDTKKHGKEASTQVSYGWQRI
VYDLWIKWRRETPMVIGDTLTDTNSSPWGSPLLTGAFISSLAKEYFLTGNGEPNGAIKSG
RLREKRGGKDKLMFPLTSPRRRGAYGYLRWRIDLYEPRIRSAWGGSRGENGDRGSAKMLS

AAEVNKLINEKLPAALADVGCDERMDPVDALALTDIRSEVETWRHWLTYV*
>TCRU_3861 hypothetical protein, conserved
MSKSSQQSTRKWIGQRALARAEDATNRKANAAVPPPAPASHEHNPSSPPPTLVQLPLSLI
FERQEAVDALSNLYHNAETVRKVETGDPIFDLRDASKVHEEIMECLKAGGCA*
>TCRU_3862 hypothetical protein, conserved
MDANDGAPPSEPQGTPVLRGDKEQPVQQTANELQAPRVEAIEEANENIQAVQSGAVVEEP
LQQEEREASEGGEELKPNLVGAEVSSERKPREELEVIPAPVATIPTSIEEEEIMQPQQPS
HGTQVELGEDHPSPTPSVPAPSASPAAVTSAAELSSNGYIVYAQNDVIVDATVYPTGFRI
LVKAPGSPGGKIATRFVYESVASNLGTHPEVIKVYCKGKRIRFGETIDYEIGELQAKGRL
WVDVHFNEDKMPPHLQKLRKDDNVVRCLQLRSRPDDISPADLVAARKRGLTFDEAINEFR
QRNKSKDIVSVVLLHEPTGTRMPFLGGYRLKKDPSRVFLHASTQLRAPGDTSLEDLQYGP
LPRDGVSRRTQTYGVSRSCQTLRECSTQTARPDYEADDNYDEIVIARRYFSSVQLLALQT
EKAIIMQKMYRKWKARQVYRELFAARQAFLERAAAQAAAEEAEKKLREEFERRRRATPRT
ADDFSTLRRELEAWRAAETTRILTDRTLSEVAKRAALTELTKRELHLLQELETLRRGVVQ
NRRARRFEDILSLMTAPKQCGIVSVTTRAAERARELRELYVALTETPSSVEARLDVLLHI
KWTVKEFDSPLTKQIVELVDRESDLLQRGRTACSLKGLRTRLEHLFKRFIATPEYNPAVD
EVVKGPTFGADENGEAASMVAARRRLKPSNAV*
>TCRU_3863 Prp18 domain containing protein, putative
MSFAGLQKRLKNKAVATTTTNSTPPSSDAKTDTIESSSSVYDVAAREARANHEERKRQRS
PHDKENTAYNPTINERNGPADMLSDHPSVEKASSKTLTETEFLERRHLAEEVVLQCAEAM
SRNMELAATSIDKIDIKKESEVYDMSGLPLPLCQFLEQRLQRSSDATAMLISTCEEEEHN
LVSALRSPSNLPMLFPPQVEDFVTTLRTLWLALCWHWVMALRGKEGNEGKEVSENGWSYN
VYLLSRHALPITVRNTRGRDVALALQAWQEAYRVRQNMLDFLAYILHDMGVVLRFSGDDA
SKGDENLRIVPPKIADSIFCMVQHLRRRDFTAVLQAYVELTMGTANWKLGLFSGGEVHMR
RSMERIERRRIEHLLHNERAVRLLHVLRELIEFVQKNEVMLLHTGIFAREKSMKEHSP*
>TCRU_3864 hypothetical protein
MKHLRVTLRGEGAHELNQLLKVLKARVARPRVGLEQRQHEANLSIPNPLPGVELKIVGTT
KPENDYFDGARTKEFYVLRIDLKHLLYRRVSVTGALRKGQPRLGEARNEAPRIGCPSRGG
TKQQSCLLQLHGEFATRNACEQVSHKGDNKTFLRLVTGNAGFVSAAILLAADAKAEAEAA
VAGVTVLHAVRDFHA*
>TCRU_3865 hypothetical protein, conserved
MRLYFADQQRGRTQHDVPQHHNAPHVNPIVQKLDLRGLHRINLRDGNVTVLREGECKHNN
RGSHHRLAHADQDASRLRRLSSPNKLQHGTLTEYASSERDVDGEMQRHTVE*
>TCRU_3866 hypothetical protein, conserved
MDNCVVRSRTHVMYALASDLRVGSGSVFSMQNSSWSAPSIEYYEGACVFEDVAVAGGSVL
QIVSSAFRLGFAMLMANTLTVTDGSWLVHRDNEFRTAYVVYVANENGVAFCDRSVWSILD
NNFTYGLYSALTYMTSDWSPASESRPIIYGVCNEARGSPVTNYQEELNIGVPVTSLDCGA
CTIDAVCFAARTSSISGCECVCAAGGYGDTCLPAAVPEGLGPLPLPDADDTDVRCVHGGS
ISSVDDPDPGVRGLCFVSVTFTTAIVLDLSHFDVPQQTLNITLLQCVLMGLSIKGSGARV
HVNVTSSMLDSGALEFEGDFGASSLILVVGSTLVSTSGHAIQFQRFSLGANSMLLLLDNY
IEGSNYAVRLFFVVVDGDGIIMKGNTLRGAEEDFPLESAVFFESAILKNDGYFDMENNTM
SAVSGIYFYGDIIVSSAGLLRVADCTFAGITLFFKPALVHFDGLVTLQGGAQWRVEGNSV
TAASVIGMPNSLYKMRLSGSGTTVVVAHNRQVDDSCPFAKMAPSNMIVVSPARFVVGCNL
QGGEEVSYDGLFPEDVMVFRCGTCNGDAACYMPGTESVDRGSCSCSCKDGWHGASCLPFE
VPDAAVPPVAERAVDGDTSCVVNQTLTNVTLNMWKTHHCYVGVTFSGVGAALTFSFDSMP
LHLPINITLTGCIFREGAVLQFVGGAEAAESAGVLIRVSQR*
>TCRU_3867 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MSRRVFTSAVLLLLVVMICCGIGAAGVAEQSDEAKFKWRAVTDGETVDSLGVPALVEVNG
KVFAVAEAQCKKKDNETSVFTGVASQLLSTEKGKEPEEVLKEAKKNTQILEKGASEGQKK
KVDVSRPTTAVKESDIYMLVGQYCSKDSQNSGAGGCELLLVKGSVSGEGTNNKIDWKDTE
SSPQRLFGAQLDSWTRLIGSGGSGVKMKDETLVFPVEGTKKPVGTEEDGKTVSLIIYSKD
ATNWTLSKEVPDGGCSDPSVVEWKGDKLMMMTACGDGRRRVYESGDKGDSWTEALGTLSR

VWGNEHDKNVKPVRSGFITAALGDGDGKRNVMLVTLPVYADNDKEKGVLRLWLTDNTHIV
DIGSVSDDEDVAASSLLYKSGETNEEELIALYEKKKGDGDTPSLGMVSVLLTAQLQRVKK
VLATWKNVDDRVSKLCPSESAEEDTQTDNACGAFKITEGLVGFLSGNFSNDTWKDEYLGV
NATVKNNDVGGKKGEATSTEKGVKFTGAWAEWPVGSRGENQLYHFANHNFTLVATVSIDG
EPTKEGSIPLMGAKMDDDDKTVLVGLSYDKENKRAVLCSGGKTREHSSTWESQTQYQVAI
VLQNGTQGSAYVDGEHVGNVQCELGNTDSKGISHFYIGWDGGNTVGDEGVSVTVTNILLY
NRPLTSEEIDALNPNTAPISPPEDLTAAMVDTPSTAVSGTIAQKTVSVSTPGGSTVNHES
SASSGEVAETVGGTDAQGEEGIHSQDGEVNATALNSSLGNLSQGNNSDGGTMRGSGLLSS
LLLLLGLWGFAAL*
>TCRU_3868 Leishmanolysin, putative
MNGALSSAHGNAVAEEVVPAAVKPHADRLLVQPLEGSLVVPSLATGSVCSRFTVPAEHCS
AGAANSDTVQYVAAAPGGVWALPCATLEDGRPVAGAMNIARPPYFTDASPPASPRT*
>TCRU_3869 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGGGYAWDFGEKQELNEHYYGANGVFCKAFPTMYSCELK
INASKLKEAALQKNTAQSGTGTGQPNAGGSSGRQAHGSEESGLGQSEGTAGEGTPELNKP
GEGGTETPNKHEQPPTATATAAQASATRTPDESDGSTAASHTTSPLPLLLLVACAAAAVV
AA*
>TCRU_3870 BNR repeat-like domain containing protein, putative
MDFARKAGYDSFRAPSLVEVDGVVVAVAEAHYKNPKDGELYVGIAAKWLEGNEKTWMNGK
VVGMNHFDTKVHPLLSATSIVYYGEMNALFGGCGM*
>TCRU_3871 BNR repeat-like domain containing protein, putative
MARYASGKVSAGCGNREMKAFEWDYGSKSNPTDLLRYCKPHPGRFKQFLGGGSAGVRLED
GGRYVLPIQLLNGGGRSVSLTILAKGFTHDWEFSDYTAHEDCIQPAVPEWRAKVSA*
>TCRU_3872 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MTPADVATAAPEPGTEPATAHHNGNVLDGAGAAPAHSSTTPGKTKVPSEFNAAPALGSDP
FDLESVTALVSVGLRCGNTVHGCVSRVLLLLLLGLWGAAALC*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MVDGARAKHHDSPVGTCLGWWMRSAEGACPRSRHRVRRRAIAAVSAALLVALALAAAAAW
MPAVHAVVLRLRGGTVDRAITVGRAVDTGLMDGVYVTNGVAVVFDVPAMLPGALRIELRN
CVCDGGAQIYVRGYSGEPASDRSLEVSVSGLSGSYCSLVFVHSLPAHTNVTVRDSTIVTP
GPMRYSQLSGLTDAVASPLVLHATSLLQTQLRVSNTVLRSLQAGGSAVYVGGGVDLLSSA
VVLDGVLLEASGGPTASAMHVASSSRLSLRSHSVFSVTNVSVVSSGGGIVLGERLAVIDS
VLRFVDVEGSVASSLVCCDGGMVGAGGWLELHDVWAVGEASSVASLSGVTLSGGTVSIAR
CAAVGATLVSGPTITSGTVTVQCNRAGGRVLLSSGDYRMAGLPSVSVVPCDGCAAALACF
DALTASFSDCVCGCHAGGLGEACLPFDVPPARTGGSGGGAPGCVSGVTLTESVTVGGGRA
TACFDSVVFSGPITVAVDLRLMDAFADALNVTLRHCMLAGGALLRIGGLSESTARLMPYA
LVNMTNVTSMEGTIVLHGAMPPNSSVLLANSTLRATVGGSQYVPTTPGHERSRYGPALVL
DGVRLLSTRFVMTRSLLVCGGESCAAILVDRGFYANLSSVFYMDNCAVRSRAHVMYALAS
DLRVVSGSVFSIQNSSWSAPSNEYYKGACMFKEVAVDGGSVLQVVSSTFRLGFAMLIAET
LTVADGSWLVHRDNEFHTAYVVYVANENGVVFRDRSVWSILYNNFNYGLYSSTIAHMTSN
WSPPSDARPTIYGVCNEARGSPVTDYREGLNIGAPVTVLDCGACTVDAVCFAARTSSISG
CECVCAAGGYGDTCLPAVVPDGLGPLPLSGAKDTEVRCVHGGSISSVYDPDPGVRGLCFV
NVTFTAAIVLDLSYFDAPQQTLNITLLQCVFMGLLIKGSGARVHVNVTSSMLDSGALEFE
GDFGASSQILVAGSSLVTTSSYAVAFLDFVFGSNTTLLLLDNLIEANRYAVYFSIGVVDG
GGVIIKGNTLIATEEEDGVESSVCIYAVMKNGGHFDVENNTMSAFNGVYVFEDTVVSSAG
LLRVANCDFVGSAEFSDSALVYFGGYLTVEGGAQWRVEGNKVSTASVLIIAHAQHKIELS
GSGTTVVLVHNRQVDDSCPFAEMSLSNTLVDSPAKFVVGCNLQGDEEVSYDDVLPEGVVV
FKCGTCNDDAACYMPGTESVDRGSCSCSCKVGWHGASCLPFEVPDAVVPPLPERAVDGDT
SCVVNQTLTKITLNMWKTHHCYAGVTFSGVGAVLTFFLNSMPLHLPINITLTGCTFREGA
ALQFVGGVGVTESAGVLIRVSQTVMQSSVAYFSLALPLHCDIAVTEVDAVQASEVKLADT
ISNKFGVVLLQNVVLTASSLLVSNVKAHASKRDAFVFYSTGKLSLVGGSSLYTRYCSFDG
YTHLFYVNILSVRDHSVFALLNNTMASGTSLVHQYSRFSVSDHSVLRMVGNSGSVSYAIY

SLKLWTVERSSWLDWRDNDVGVGAIFYATESTFLIIDNSSVVTLTGCKMGSTGWSVSLLS
QADADYRFVAGCLTVAGREVTTAEELELHGITNVTTVAVCGECTKDGDCFAPLTTTVSDC
ECQCAAGGHGDVCVPAPVPAGPPPPPRTPPPPPVGECISDMVYPEVAQAVGGGLLWLCYR
NVTFSGGGMSLTVLIGAMTGEVANVTFDGCTWRDGAVLLLLGNVHAAVGALNIVVTGNTF
YDALLSPEGVFPPHTNITISGNRFTVTRLIPRSGLGRRGPSCVAMNGLAISNDSAVVLSG
NVFQTVRASSIAIHVVRSALRVSWHSVFAVVGNKFHMTGGNGTLIYLEGSMHSSSLSVLN
NSAVVVRGNAVTRPVKCFVLFLSVLRVESQSAVVFQGNDMQGSLAVLFSRSCCRIYYNSW
LQLSGNLCRESPLDAFAFLLPKVNLRDSTVSVSGNQFMSSTVTLNVLLIPTGSSDLTNGG
ILFACNTVNGEEGVRYIIPSVYNATILTCDDPCALAASCFPAYTTTASSDGCACRCAEGG
HGDACLPVAVPEPPSTDGADFCVRDVRVDVEVNAVFGTSVVCYVGVTFAADVVVDVASMS
GSVRNVTLVNCTFADGASLYVVGWRSDPTAGQRADVLISGLESRSGGGVVVANRFPPGSR
VTVVDSVLIAERRVAYRGDYDLGDASACLVVHSVNLTGSVLTIARTHVAAVFGDAVGVLV
VGGVALSSRGALYVDGLSVQTALGLCVSVEGGVAASGGSVVAFVDSEYLLCKHAVSVRGA
VSVSGSAVVLVRNDFSLTEDHAVAFYSTVGLSGGSMLLAKGNVHDGVSREMLYAAGAVTA
AGSTLSFVRNRALLPRMLSASLSLTAGAHVRVACNYAGGIVLSTAEEYAAAGFGDAGSID
VAGCDDCDRDTHCYAPGTASASMKDGVCECVCGSGGYGEACVPVGAPALPPAVGNTSSVF
VREGVTLRSVFVVPAGASEVTLRHVVLDGVSPVLYVPWMARGGVRIVVQNVSLLNGAVLY
VMGGGALGGAAGSDESGPVELSVCDVEALNGALVLTGTYPAGSVLTVTDSLLVSARSTSL
VYLPGSQSSPYAPVLVLSGLRLVRSVLVVSGVALVTVVTGGRTVVVDGAGLELVGGGVAL
DAAVFGGEYALYASARVVASWGAVLRVSGSQVYAAHGLVFESGMMANTSAVVVNGDGALL
VLRGSASFVFGSWLSVRGNSINGRLLSVPSYPRSADLVQSTLTLHGNAGSGPVVMDGTVA
LVGAGRRFVVGCLTLNGQALQPMDYRSAGIIGEFRSVACGVCDADVRCFAAATRAMSGSC
VCRCAEGGYGRDCLPVYLPHVDGCNRTPGMPPLSHTATLTETRSLTPMWTPSVSMAHYSP
TQHGPTETLQVTETTALPPTRTPTASVSGTLWWSEVACPTLAVTTTAAGGSLTQSDIRGG
GSAVPTRLMVALPPPFRWARDPRLGTHLSFVPVLTAQPSGFGGPWGAMLRNATWVRNATN
PSTVLELAVPVHRGYFIAADETIVIRCDAVAVSGGCKGVLLGSFTIRSATLPAAASALSV
ITGVVAGAAAVAVVVTGGLGSVLEMQALGVLARMPCASAQERASTVALPYFLSVFAALDP
LWMVVGNALLAAVFGCVHCGVTAVFQRWRGVDTASAWAAMRFPSLTYVVAHAMHLGIFFG
SVLALAMPGARVQHRVIGVVGVLYGVAFPAGVCYLIARHVGASFTKYWQFSRKPLHERLL
YPVGYWHPAAQQRMYGGMLTNMRGSHVYWCVFQLSVLCVVCLIAAVHPPVGGCHVQYFCM
AAVLLAGAGVIAFTNMMRSAFLTVMHAASLVLLAALCVVSAANHLVPSDGGARAYAAIVL
LLTAVLLAITVYSVVVWYAEDRHWQELREPRRGGLEALLRDGEESEEVVQKPHEATTLSY
ASGATGASSYRPPAPPLQPMAGDTRSDAQSLFDRAPVRAAALIMPFWTGEDALLDEEISA
VSPFGV*
>TCRU_3874 retrotransposon hot spot protein, RHS3, putative
MIVVPSPKVGNYDKWMKQEGAARIIVNCLDEMDVKAMCAWMKRGMDPDKKAKCWRIVKER
MEKVGPIPRHVFDANEFIAHSAAIEDALDAINSLDGEKHFTHGGVRLWYSENPSQKLVRV
ARARGEVGAEVFLNAPMSVFLGCRIPHYFVKSDE*
>TCRU_3875 retrotransposon hot spot protein, RHS3, putative
MVLTSDKAWLYSWKWKENKSTHDCLVNCEVDRVWQTVKGDLTKWSSTYRGTEFAPGRRVL
IGIPGIGNSMAAGSYLLYQLLHYDAEKIQLVFHCFDGRGEYVSDKTTQTVREYAGGKASK
EFLYDLWNCGIKVYIIYDVAK*
>TCRU_3876 hypothetical protein, conserved
MSRRVFASAVLLLLVVMMCCGTGGGAQAGVGSNADASTPGSALTGAIAGEGSASGGVEGL
QRVDLFVPQTTQVLAKKGTDSSRRDSFVSPSLVSAGGVIAAFAEGRMNAKYQGGQLTKPS
FDVVAEYIDSAWDCSTLVGEVGKGRMECTHCAW*
>TCRU_3877 Myosin-like protein
MEQQDTSDADYAKDLRELKDQLATTQEELVRVRGELSSTAQEKMRHETECRGVISGLRTK
LEEARYDADAMQQLTREKKHLDEIAEEYRGKYLSMCKKVENLDIELTAATNRCTLLEKRL
DEELRRSLRNVSTSPTPQRQNGVEKRLRSASSVNVPLSLTTHPRKKSRSVEPRVFTISGF
DASELLTEIKQLPHATVAECRSNTPVPSNLTHLITNGQLTIKLLTALVRGCWILPDVYVR
DSVRDQRWLDESAYGFRHERPPLFQKRIGFTEGFISSRHYSTAKLITDEGGATVETELRV
ADIVLCTHAEHGTLEECTHAMTWDKVVELIYPVKIGDTQ*
>TCRU_3878 hypothetical protein, conserved

MAMMMTGRVLLVCALCTLWCGAGGGGCTEDTAGSESGLSNRGSDEVSEGASGQTASGEAG
NPPVQQSRLQHVGGSPSGGSRSQADLQPQSPAIQKPSPSGSEPTDSLSHSQSSGEERQDV
PDEGPPGEPGISPNQEKNKNVSIVNQQSIDPPSHSGNGDVVSSNSEERTEDTPSSTEIIV
AAPSEEGQERENATPSLEQPRETSTAAPAITTQTSSTTISDVSESNTVKMSEASPQSTGT
TQTNGTTTKIANSDSSATVSYTTSPLLTLLLVVACAAAAVVAA*
>TCRU_3879 hypothetical protein
MGSAAIRSVSPRPSDSRNAGSNCSQHVVGSHNHTTGNASNAETGHTVPQSPNTHEVTLLP
ILFFTEPKNAQSNNMSLGVSSDKKDQHVSSPVVPGDEVSVGLYADGNIVSAERQSTYNSH
WVRQASRNEISDSFEGRNSDGHISNQQSFQKDGRCEGLLHKRRSNEFHRTGPRVCLGSSL
SAPEMHHNSKIGSLSSILQRGSSTRHVRSAGASGVFLSSEDGWNEDDNNPAMIKTPSLKC
LQEAESVVVALEDAEEKERQRIIKLIEEMKEHKLQLISTISSAFLPPCE*
>TCRU_3880 hypothetical protein, conserved
MLSGRTLRSAGSRKAASSCAVRPHRERGCPGSQVAAQRIRMHAQRETTCRPAACVIRSQR
GAGRFKGRSSDTVQGVLGVPWLEDAHPAAAHIVAEEYPGLSMRGADVFREISM*
>TCRU_3881 retrotransposon hot spot protein, RHS3, putative
MGAKDLLLLILGSRGALASRALEQLGLRVFMYGELVCALVEELKELRPPERNEARDSVLK
VNHQGCPTRTVGIRELEGGVTRIPMEYGVLYLPKVENFPLVDGFFFMESPRRTLVGLQMT
TASAHHKITSTVNLFNERLAAYFKGWKKLSRDVSWEMIYVQHENSTPMKKWQGCDVVNPN
NETDAEKKIVAFWDGKVHQYQFVLTRDFLSKITEMRTQ*
>TCRU_3882 hypothetical protein, conserved
MLAHGPLSKAWKDSTLVGHIANLRAPQIPNFEKQVLLPAMGVARELGHQQGLITAERERL
NFDCANAVADVRNRNAQLNSQVEEAQINLSVRESTIAGAGNQVLELQQQLEAAHAQLRER
EFNLGVLNAQLQEREARHNAQQPARDAETAVRDEASATQHASNDGVSTIPHQTDILMAGG
EPSSAARRSSAAYRRPHGNVGRPHFHPSTPSPSRTFPLDAQLPMEEDRSFCALDVTTWDP
RAYGMRAPPESLSTSGAHTNAGNRRTSRLNLPLTIWSSGPARWKVCRIPPLES*
>TCRU_3883 hypothetical protein, conserved
MVAPLMLDLMDFRRMMCKISVPIRLLVLVQNGREAMLSLCLQELERVYGWSGRLVVSRHP
ENIGYSAATNIGSRLALSLPREKVPFVFVTNSDVKVPPDLLPNLLRDVHEVTRHDAARMD
ELAAEAANGPSESSPVLRRGLRVLRSTVNDGRLSTSALLPDRIRYASVKERGKMFSKRYW
HFCAYYKSSCFASVMLTRLAISTVGYFDENFYPDCVENVHYSLRLRLLGFQERNVLYGKF
VHRGSSNIRFSEQLELPDALWYRRVKSLMTNQPYAVMKWNGLKACCDGCKGPYDGMVPLD
VWVKDEARIQRIRVYGHDEEQGVPKVDYDRTLLYPVRTKGR*
>TCRU_3884 BNR repeat-like domain containing protein, putative
MSRRVFASAVLLLFVVLVCCGISGDTPANEEEVKNELINIQNLERVDLFVPQKTLVLPKG
GTGSVTTRDSFFAPSLFNAGGVIAAFAEGHMNAEYQGGQLTKPSSDVVAEYIDSAWEWST
LVGEVSESTWKAHTVLGTTDGTNRVGVVLRPTTTMKGNKVFLLVGSSAVFYESGGNWS*
>TCRU_3885 hypothetical protein, conserved
MQPLPSCSISDTRYSLPGSHVLLGVVFVPSNTVSHVLFMPYDKPNNLPAETVLQTRTQQR
SALLRNMVDGHRRHNSESVVCKAVLVIILPAVHRPCCPGPRSREFEPVFDLRCLLRSCIH
AALIVDPRVVTGRIGQSCHQTRRGYGRLGEEGVQSRPSTEGGIDRIQLISQAGK*
>TCRU_3886 hypothetical protein, conserved
MLDDYVAKKNGKLHDAEATEHHLNSVVDQVLNYLRNGVRITKIPSKGNACRRLYFLLEDC
KRIHSCDLDHQGFPLNRKRPPVTMWIRDIEKVLIGLSTTSFVNYGGEAQLAKTRQEAVSD
NGTHRHDATQNIIPSSLGANNHRAFALLLRGGESLEVVCETDSDCEAWLVALKRLLHLRT
PAERLLEERRGT*
>TCRU_3887 leucine-rich repeat-containing protein
MGCKESSLRSPDVKKEDDELEAKKAGGKPVGTEAPINLDGDSSNNASLSKLLPLNGRTRS
PLLERPHGSFELFTHEPLLDGREAPNDMQLVSFLANEDNGFRMDDEYFLLSDSGTSTPLL
FRTEPLRRAQTGEGTWEWWYDQVENLRITKDNSSRARLQDIPNRLTRQYDAKKDQVELDL
GWCYMERSAPYVLGRLFVSPYLREIRWVTSLRLDGNYFTDDGFGNMLAVMGVANESKTVF
PLLKNLYLNNMNLDHRSVYGILFYVFPIDLSSAARGTQVPRIAGQVAGLPAEAYMPFHGA
PHAPLFPSLEVLSLCDNPGIGNNGLAEILRCFVAPHYERRNLPVLDLSRCGVDEVGVCYI
NEYLEQLRIADKRGDYIVVPRRVVLFGNRHSSSSKSSVDGNTAGSGVTLLM*
>TCRU_3888 conserved protein, unknown function

MYSKGRDALRRLDMVLESLRQGALKETRATREEVKRSLIREDVHRQNEERRQQQQQQQLG
IEQEMSSSPSVGRVGDPSMASGGFSTSSLVGCGGNDKSSGMGGAKGLPAWYDGDYTTAPR
RVEKTKNGRVSTADCDERESSNGGDAKLHDEESAMVVDVTQRVSQAERKLYPILLADVAE
CANADEKNRGGNALDVGGSEVIEWDDRGAPVRLRSTWMPVSPQTLVPVSRTVDESKESAR
SDVMHSRRTSAAKTMTTTTTMQTISSDKKLCTQLHEYTWKEDPLAPMPMAGRPAEEGPSP
PPVGLSGTSSRGAVNRMRQALPFSPNRGNSTRRRNRPPLSTEGTAVAESSASAIARQIRQ
AVVKQPTASVEVNKKKAGSESFSSFPVIHGSSGRCSVLYEPDEAECVITHVLNPVTAFFC
TSCGVCVAREIVTGEPNSCTACGEPFEALPPLPSPRLNGCLLDTVVTETKSVVSLREEGV
PAGISASVKKCTATTSTMTTTTSTTTRDISTLPMTAKVTAGTQAGTSWSMPPLAATAVQG
LYFLRLWDQAIAL*
>TCRU_3889 Isoprenylcysteine alpha-carbonyl methylesterase, putative
MLQYLVRQVLWTISVSAQLLAAMGLGFKWISMAIRLLVFALLILWYFIPHICAYIMSPNI
IRRVSYRSSKRTRQRNLQIFLQQVKSIPPVRRKENGREVSEDPAEQRSGPDMDAVELLAT
KLNPADGRLMMGLPRRLSSPTRTTEVLDDEKVMKIGSFSDTVAFIQSYYATASAGEHAAS
NGVPAGEHKNPDWASDAAQEPNSTGDSEDEEDEEDRNNLHNRAALDIYLPIPLDSLFRMM
EQEKKISPRSRLQHKKFPVVISFNGGAWIVGFYLWNFLLAPLLAARGYVVFCPDYRNFPQ
TDMEGMILDVSDAIGWVINNAGRYGGDPEDITVIGQSAGAHLTMMSILSQAQLSARAASG
GTAPSDMAYNVPRYNPRVSIRQYIGLSGIYNIRGLVKHFDRRGLYRNVLYQIAGGRSNLP
RYSLNSYFDERRCGDTGEVLPENIFDFLPQRMYFIHGDADCSAPFSESANLAFFMRNAQR
ARLAEQYTNGGQTMGICLAPPVDIKYILVPGATHTDAIIEECLAARESHVVDFLCYYSTD
NEERDKCLNNSNGFRDVNNKRDEDDGQLDPSRHPDGVLPSPAPHNERPMLIRLSSYVCPF
*
>TCRU_3890 hypothetical protein, conserved
MMDVDDVITRHRARLDEHRKFLHTSPAGSTNPPKSPDGINSSGILKTVTRFHAVGDNTFS
PLPAWPGSEACFDVSPQPDINSLKPGRDKKGRVKSEPSKKLLREPKTLMGSADVTPEKLK
AQAASFSGRALEAAPRRASSGPVLMLSSDNKNNNNNRNRKLHDWLAEEERFFDSQLKAVG
RYYVTKPEAMYAKSQLWLESRERSLQRLQEESQRDVLGECSFQPNVAGSRSLTRRSSSTH
AISSFCEDPSVAAHLERMEEARQLRVEAERRVKGKKAGTWTNSITVPKEFEFAKKVAVIP
SLRKPLVNVVPLHDDDEVKEEGAKPRTDGNCAGVACGDLLVNTKAVATQRKRHGGEEEEE
EGRKREEAKVRDASVRSAKAVSQLKVVPLLEATIVQLKEELARKDEQLQAQKGELALLSR
ELEVAKATVRRLSLQDVVKVEEGEEERGTTPGPTSPMDCQESTESNA*
>TCRU_3891 RNA pseudouridylate synthase, putative
MRALEDGEHSPGDRYPLVMRATHVYDAPNNNSSNDDNNNNNVGFHETAPVRVLAVAPYKF
TFSAPVKGRWLGLPLLTVFAKEFAYIPPVAAGNETPRASRDPRVTIPAYVEELRKGLLCL
RGREEECRAAGDAYADELRHLRPLPRPNENADATRGSPVEGMATCSDAETMTLLLSAVSP
RLLLRQKDVILHHVLRREAPMPDGDPVHILRYDHVPCGSPPRRLLFVRKPHGLPVHPSGR
YRKNSVTSILEDVFGGTDAHRYRAIPLKKEDKRRNVPQPADSVECVAIRHKRYDFELVRV
WVGDGYVTRDAWEELRSRMTRQTPHGLKVFVVHRLDAATSGVLLFGLDSRSARMTAELMA
QKGVPDDKDAFMPVAGCTKQYIARVHGRFCADKLAETQHHCTYGDRKLFASSSLNESLGK
LSARPACWLRVDRLIGCLSYHKSLYWCPDAALTESWLNEKEKWEKDAKEQQQSASMVKGH
AAGRKRGAPFGDAAALEAKHERMRQLTRGGRAKATAASDGEVNNDSRHPEESTSKIQMQR
LKESMKQAITLIRLLAYDAACDESVVECLLLTGRTHQVRVHLASLGHPIRGDKKYIRLAA
DSPSIPLRTDLRDEEEEDEEEEEEELKGYLSSHGIFLHAWRYTLRYAAGEAPEVLEAPPP
AWALTGEEGGAITDPMASSCV*
>TCRU_3892 60S acidic ribosomal protein, putative
MSSKQQLACTYAALILADSGKTDMDSLLKVTKAAGVDVSKGMASAFASILKNVDINDVLS
KVSFGGVAPAAGGATAAPAAAAAAAPAAAAAAKKEEEEEDDDMGFGLFD*
>TCRU_3893 Asparaginase, putative
METLPPASANGEAVVSRNPILFVSYNESGGRRYTDDLFPRKDRRVLVLYVGGTIGMAWTA
NGVLEPCKGYLTQVVRGMGELQQRPEIAPFDIVEYDELLDSSDMDGRDYMRIATDVARNY
DAYDGFLILHGTDTMHYTASALSFLLMNLAKPVLLTGSMVPLVEPYNDARRNIVVSLMLA
SNPSIREVCVFFNDCLLRGNCCCKLHHTFGAFCSPNYPVLGMVESTGFHLREQLLLPQPS
GPLKVQSNMRGRVVVFALHAECDKKVMKQLLLEDEVAGGTPTTTPLAVQEESPSSSTEGK
DNSEADPDNKKKRKNTQDADSVAGDGRRINPAVANTCPGPKKLMDAVLLEIGGVGALNSE

SSLVLRELASVAKARDIVFCATVQEPFGSLSKSEICRLRGVSPDLIYLHMTTAAAETKLM
YLFGKGLSPAAVRKLLPRNLRGEVTPGAACEANL*
>TCRU_3894 hypothetical protein
MEAGSGQKDRNNSEASYFLQNELARLREAKAGGNCSRVADDAGITMNQSRMPGRENETPR
AQLPNEFDRAHRLRQVQQELPTSQPSFRQAESRIDSVRLPSEALRRAVRAAFGPGRFVLD
DGTAVMLEYAHDFIVLRGPQSVRHSFMALLLRTLLKHVESLPQQEQGNSGKERQNLSSTH
VISSSMAEVGESREDDPTGPPLYVLRRAIGMEKMEREKAQLAQHDAEHECALIKTAWDVE
RARYREEKQRLEERVRQLETDLKRNRDSLQIALHRLQEREPQKREVSGDRHADDVEALSC
QHGEDIRSFPGEGGKSKIHGIPSVSLETGDTSSVLPCSEGNDITTTNTAGNTSHADFSSL
ACGKCGKTMNLLQREMDLLRNEKDILSRQLQVSVGVVDELRNRLQNIEAAAVQLFSSVLS
SSEVVLTVLKGAAAAPRLFLHRCGGVDEPQVQALVQSLSADSTAAPPVEQRLAELTALLE
IEHRALKASLDFAVHERDAALQANREEAFLTSPEKAAVSAPLTRRTNLDGRIANTSSATT
LEKENTELRIELRRSFEDIRQLGQAIERSHAMYQELQEKLRTADRCMREKEKTARSMGHQ
QEIALMEAIKRERSLEIQLQRLRQQNKMSAVHHSNTPIVHSEKQEKTFAHLVTTPSKKSC
AASVLTLDESRNKYPFHHRHNTDTRENDSVSRNDGLQSGPRTTPTPLKGTGAPTPFSPSI
VLRRENFEEALNAIHPS*
>TCRU_3895 hypothetical protein, conserved
MDNEVTWSSLFLPLEEEVVFASFITILCPLQRQRQQQQQQEMFSRRETSSEGDEQTRFAS
GSILYHAADEDAMGSPLFALYGERADAIVCVLANRSVVFFDLTDGHEGPKEIRRFSMGKP
HGVNLEKATCASMIPLEVVYMCRVPAMAKPPTVAHHTSSNLGTTALASKASVSDRTMYLR
GVVGSSDGRVDVFSEYGFVFGFVAHDAPVVAVAVIYCPEDLDEDRTHPSSGGTNVYRLPL
SGREAERWFLNVTTGMGFVTCSSEGAVYVWKQQGLIMKSEMLEKSVFPSRTFKWHVVQPS
NGAWLLGGLGGAQVSLLVHTTPGMEHELRVRSTVTFEDVEPRVKLPGSQFTRTTAIASDE
KLALVARGRKVYTFVFATARCELLFTARHTVTGLFLSKYGLVAAACDSGGLLYVVIPKLM
LVLGHYNVRGGGPIRSVSLHVVSRLLTIVAGNGSVEVVLMPETWNDGPLSRLHYLTDLMN
STPAAKALYSLVSLQKRQDDSSSDLVNATQQSAAHESLLLARMAIPEETKRYLRPTTGLA
*
>TCRU_3896 hypothetical protein, conserved
MLRRAPCLLATNIPRSAWDPAHFNTNWSDSYSTEIAARRHWPAKKWSIGLEPRTPRDWLQ
FSYRNLAYAYNGALRACQSFPEMLVCYKEMKQRGVKVDVDTMNVLLTRAARYERVQVDDV
FLLFDELTALGARPDIAAVETLHTVLDHSAAMPYEWREARRRQLVELYNCLAMEEIERLA
PHRVDRLLKEQIKRYRDNLRALKASLSPSVYRRYLHTMHSASMLLEEVHNFLWELVESDH
PAMEIPALQLRIPFVGSVMRRPETDTNEKLLKYTDFEDTDVCSVFLAAAERAVDADLHDT
RAVSERRIFLSLLTMISYSGVLYTSDLMAQLMEMVKYSTHASSRDSDAQRLLRYAVRGSS
AAQDDLYRSLWLKVEMVADSRVLGRYIGAREPWSPIRVCFDERGLFKSYPPLVHASAKKT
SAIEADATSGSGSTTMEEEQRQQRERQGMSTEITSHTSEGGEEMVEGVRGAVVAEASEAS
GVKDVALQEASHGEQRTVEALDLRWDDIHRLIERTRALTSPPTERHPQQEKMEIFTGIAV
YLRTIATGRRYCSGEEEAGGEYPAESRERALFAVGYELDVWARLFELVQEVRHDMEKFIT
DNAVHHVEPEFECWEALLITLRCILDFCVVRTQEKGKEERAAVEELFEKTMKLRNELVEE
SRTRFGGRMRILWLQEA*
>TCRU_3897 hypothetical protein, conserved
MGMASRWMPRPEEPNAEAPPLRFGGPLLMQLVRYLPLLMRLLTHLPGFTAGFILTCLFFA
VVGRDTLRNEYAPVAGFHVVALMLLRELVAPWREGKKKAAFVRQRVASLRSFADDVQLQW
RDVLD*
>TCRU_3898 lysosomal/endosomal membrane protein p67
MRRERIVKDVIFGVTLLLLATAILATGGVRAEFWQNDDVTTVKVRYNMKTKEFSVTEGEL
FGAVAATLEVHDTFLQNGWDVVNAEADKEFLHSGPIETRDEMLRIAYQAMGYGEGYTTQK
RMEAQLNNSFLGKGGLNEILASSPEAVKWIQEHVEYMDTADAVDAYGRQLKNLLALLDGM
VAGYNARVGAGGVLLNRTWLFYLNFLAEIGDVVASVSSQNTIAGLRETNPRHFLDLHCSA
LVKVTEYDIYFSHATWSSFNSMLRQYKTYRVEHRTVTMSSYPGMIHSIDDWYMTSERLAV
METTNGIYNDSLYAYLNPKTVSEFLRVMIANFLATDSPSWVKYFSLNNSGTYNNQWMVLN
MAAVANPKTPMPANTFWVAEQLPGSTYPLGVTAADMTEHLNKYGYWASYNIPYFENVYEI
SGYLKKEKEFGDYFSYTNCSRAKMFKRNESDVVSLESMKRLMRYNNYKEDNLSLIQNCTG
AGMNDTCNPPFSAMLTIASRGDLNPAGDAKNYGPLYEYLGRRDHGATDAKIATWSGMVMD

LHHYTSHVICGPTNEQQPTFEWKDDLFTPMPPTYGLPKVYNFTFMKYVTNVSPKSPSIDN
ARNKWVGIAVSTAAAALVFVSIAIVLVRSRRRAKYLHEDMLLAH*
>TCRU_3899 hypothetical protein, conserved
MIITSAIAVVTTVVHFLWAAPPSVRVDVWIDNIRIAGSKSDVTLWEAQALRNAGSCRASM
GEERESGATQYTFLGAQFGQTHQTVSLSDEFVRSVCAMPALNSSTIAETEVVASRFCMWR
PFGARVYATTTFPSRQCDDDYRHFTKGLWRRHPRRTFRRQRLVWARDCDTPSRTQP*
>TCRU_3900 Protein of unknown function (DUF3720), putative
MAMMMTGRVLLVCALCVLWCGAVFGHAMEDYCSEGGGNGLRHTSNGGDDGVSLKSDCRLL
SARMALIKAVEAEEAGSGLSVTLPPGKPKETSLDNNQGGGAPGLGGDLGVEGQPEAAALQ
PTPGGSGTEEQVTELEVVDPHDKNVAGDKKEQKDVNAGDSQHQRADQSSSSSSSGSSGT
ESVKQPALKENSKSNEIPDKPPQEEEEEEEKDLRSKSDGREEEAEEKETEEDKKKASNQA
PTETPGGPTNKEEIQTATTETNGQPSPEALGDVKQSKEVQDEKDSNNNSQTKSVDSIAAN
QPNEPSADHGESGPLSPTANGAAANNDSERSTQTTGDYGPAADVAGTAEGKQNENKDVNP
KETPVTATAMKTTTVTTGDSDSSTAASHTTSPLLLLLFVACAAAAAVVAA*
>TCRU_3901 40S ribosomal protein S3A, putative
MTLGKNKRISKGGKRGKKKTQETMSRKEWYDVVAPKNFEVRQFGKTICNKTQGTKIAADY
LRGRVYESNLADLNKTQGDDDAYRKVKFVVQEVQGRNLLTQFHSMEMTSDRVYFLLRKWC
TTIEAAVETKTADGYTLRLFVIAFTKKQSNQLSKNCYAKTRLVKWVRHRITNLIRQRLSK
VNINEAVTLLTRNILRDRLAKRCNPIVPLRDLRIRKVKVVRTPRFDAQALLNAHGEIPAS
AEGEARVVEEAQEAPAAEATA*
>TCRU_3902 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MLVTLPVYSEKAGNKKGVLHLWLTDNTHIVDIGPVSGEDDAAASSLLYKSVENGDQGNKE
ELIALYEKKKGESSPGMVSVLLTEQLKRVKEVLATWKKVDERVSELCPSENAEHDSSPDN
ACSTTGKITDGLVGFLSGNFSNDTWKDEYLGVNATVTNGAEKTDNGVTFKGRGAWAEWPV
GKQGENQLYHFANHKFTLVATVSFHGEPKEGVTPIPLMGAKMNDNENPVLLGLSYNNKEK
KWILLCDGRENKKYSSDWETKTSEHVVVLLRNGNQSSAYVDGQPVGGDEKCNLENMDSKG
ISHFYIRGDGGSAESREGVPVTVSNVLLYNRPLSSAEIAGLAKKKITILKAEDPNTLVDA
QSSATSGSPVQGAVSLSNSARQLPSEQETLKENVGAGAGGLSSVASVTTTPSSDVDPTVA
TGSGDTMQGIGSPQTPEVSVSSGEDEGTVGETDAQKEEVHSQVREVNATALNSSLGNLSQ
GNNSDAGTVCGSRLLPSLLLLLGLWGYAAL*
>TCRU_3903 twin BRCT domain containing protein, putative
MLVTTTAIYGEELDRIKKDLHQQGVTYLAELTTSTNVLIAGRSEGGKCRVARERGIPCVT
PAWVRLGRCFISRIGEFEMGRSLLGLEVCSTSLSMDEVGFVRRACETHRAKYNAFLTRRC
AVLVVPNGKFVEDQSEKLHFARKNRIDFLPYDKFMKRYGFATELQQNLAPVSRQQPLGNG
IQGLVVYCSPESLMTETISSLFEKVGVQRVPVLTPLTTHVLVLEPTDEVFPQRPNLEFVS
VAWLEECAKQQKQVAVESYRVSVFQLPVITFTGVPREERMAILSCLEERGLPFLMQEDFV
LGRMADDSSGQRNTTHLVTGRSALLQSSKVAALSCRVHKLRRKECFLVDVEWLRRSLEVG
SWVDLTKFSLEVPPISAFGWATKRTRKTLAAATAPDINNQMAEDYDNKRGLSSPCSFARE
KGDEMLPSRSLELLIEELESKTSGRGSASTTPIIAVSQSVWPKKSSFQERTEDHSCKGAH
LERSTASLSLEANLTSVPVESQVIVYKRSELELPKKLMRQQQQHFVLPCTEKTGGDADGF
LLTEGAVYKTEESPRRPSGRFCCIMISKALMHMEENLERLQALGCTLAKTVEECTHYVTG
KPSRTEFFLCSVAAGKWVLAPSFLEETLREGRIVPEEAHEWCPEIAIAALLRNSVVDLVR
ACSLQRKRTVRSFSSWRVALCCATESRTESFSRVLRSGGCRVIRPYSSPQILNTLKSDFE
ELRDLCFVLSDDNVWEASQLDILAVHLPVLRMEYVAHCLCVEVPEPDLYLVQGDSGRLRK
RLKVV*
>TCRU_3904 diphthamide synthesis protein, putative
MESAESELGLPSNYRFEIDKCVRRIKEKNATRVALQFPEGLLIFAAPIADILEAKTGAEM
VILGDVTYGACCVDDYSAVALGCDFLIHYGHSCLISIKDCLISSMMYVFVEIEIDIQHFV
DTVRRLVSPETRLACIATIQFVSSMRAGMQMLRDHFQHPVIIPQNRPLSSGEILGCTSPV
VDPATVDMVLYVGDGRFHLESFLIAHPTLNALQYDPHNKTLTKESYNTTEMRTLRKEAVK
KGMSAKSFALIMGTLGRQGSPRIVDRIIQMAERQGKTVNLLLMSEIFPEKLSRLQDVDCY
IQVACPRLSIDWGYAFDKPLLSPYEAEVALKAVEWGNEAYPMDHYSKDGGRWAVYTDKSL

E*
>TCRU_3905 ubiquitin-conjugating enzyme E2, putative
MPSTPTPQCVRRLQKELSALCREAESFFFTRPSAKSILVWYFVIKGPADTPYEGGRYFGK
LNFPPDYPMKPPEIIILTPNGRFETNKSICLTMSNYHPENWSPLWGVRTILTGLLSFMVG
DELTTGCMTSSDELRRKYARESRRFNAEKMPVYKELFPEEYQKDLEELKREDNEKNGRTS
GSAGCGANTKGGGVMESQEKEQWRGLFPALLGLFAVLMGAYFWPW*
>TCRU_3906 hypothetical protein, conserved
MRCGGRWIVERSDGFVIEVEKPGVSVVFGRDIGLPSAQRMDGKYVSRQQFSVEWKASSLH
VRQLGKNPTFYSMEFHTLPGDGTAEKELVCCREEETREGKRMGDGRKGLNVILVPPVSNE
KFLASLRGGAKGIEPATLHFPGELNLPRFTVRYVVADEKSSEEKTSREMLTVPLGSSKSD
EVEDDERANQPWMTGSWRGILDSVLHEQQQQAER*
>TCRU_3907 dihydroxyacetone phosphate acyltransferase, putative
MARSDTTGVTRRWKFRRSVIVSGDSTCWLSAACAISLATSPIFAPNAPGDPKSIVVMNRF
DVSRGIFYGDKCQAIGSCTSSSFAAFESLCRDLTKGVEIMKHVAFAVDAPQMNETECFVA
DVQSDLYIYISAWSDADSCGHAPLSSLASLRKSGGYLVILCDGATQRSAWEAAQTHLPGW
TVLGFCVPSFAPPSFDLHLTRSFVRRCHAMKGILECVSLGVAMGTVKHLPVGFRDPLRVV
PLDVALITAMTAVLLHKDNGLGFISADAAMMKLGCAADNVLVWGMVAEYLMDYYGRIGPA
ALGDLPFPQLLDTQPTLQLSANVSDWVNYGVSLMMPFRCYYAHQVTQRRKRILGELPDST
TTEYIRGALGSIDAAVKCITAVAAARVSPSHAVDYSDAAKPPSASVSFNETDYQLLLQIV
TRDASLRELLPLILLRNVQWDLYIKVIAQAVLEGVALQIFKRPLSLPPPVPLYHNDIVFH
GTRRVPSTSLIPRRWFSDVHWTARVGVKPDGERFAASPGLTKESMSRILAHPSVLRIMGE
VAKNENSSEGAVRERAMAILRTVGDNLNHFQLRLFGFFVRRVLFRLYDEVSLNSGAFKRL
YNLVNTPRVGVVLLPSHRSYVDFIIMTYLLVVMGFSPPHVCAGDDFLRMGPIARLMRGSG
AFFMRRSFRDDQLYYTLFREYVRQLVLRRRTLEFFIEGTRSRTGKTLCPKLGILRFITDA
FLESKGELDDLYFIPISLSYDELLETRLYADEQFGVSKPSENMGNLFRARSLLKTRHGKI
HVYIGEAFSLRHFQDQPLQCPAPFEPRGEKDLDASPRKNRITPPRVLLNLAWHATHSIEE
NTVVTPTALVAMVLNVFAPTAGTVPLAEVYRHMTWLHTNIVRRKGALSDDCANSDVETMT
RKGITHLQEFVEVLSDDAEKIRVRQDVGSFMGITICSNQLVHVFRDEAVVAVAARMYGEV
QAAGNVLRVERQHLKEGCRQLRQLLSSEFQDYLPFCPYTFDSWFEHTLLRLLSCEESNTE
SEVFLSLGGTTAEAEKRKQDRGDNLSIERPNNVFIPMTRLYRFLIATLSPFMESLFFVSL
ALSAVVEPGSERVVYKCLLLKACQACILELYDAKRVAHPQSGGSGLLKSALEGIAMLHGV
EIDPVAKEAAYLIPATADRTVLLERLQQLMRHVCDMRSSSPKLLRGEEQKKAREDILKEY
VKQLKRMKRPSKM*
>TCRU_3908 hypothetical protein
MIRLTQLKNNGGIKFRRRTRRTLVILVAALGALAWIIAVSLLRHLGGSATTETAVKTSST
PVTRSRDPTASTNANTGRSSPMFVKGNIAKGENSISLPHLYPMHRHLPANRSAVVEAIQE
KQMRRQEHCWVTAPHSPLFPSPSSVGATLLRPLHVETADAMLQQEYFFARQKPTGSVSTG
TFYSGYDTPPTAANGTAFPWWVSKKSHHHLPCTAEVQKRLHEYQNEAPCSARRFLLSGIK
EGGHGLGSSLIVISFDFLGALRLGRTLLIVAPKSDKKWQFVARGCLRAGRRSLDCFYLPP
SRCKLPGGSVRVVRRGRDAASISSRVIRKYSVDIPGLDRNTIPSDEAFFGPGHQQWACFS
RYQKWVKNPANMAVYGTFEKGIDARLTFMLAQVFTYLTRAPQPWFQAMIEYHLSPLGLIA
PHMVRVDPTPRNRCIVYVQDRGEVAKMREYYNVFGCHTVGLSIYRDYVAAISTSSKSAPS
QNSCRVFVSGGTPRQSFLWLKKEFEDDSYEVLSTWNLSTLKAGSESTRWGASSPASSWVD
LYAGVASTNWICAVQSNWCRMINFLRLTHGRVDCGFIDIGVLMLTSVEAREKYCVISDFP
TKPFSNVIGR*
>TCRU_3909 hypothetical protein, conserved
MWNALSCLEAPPLVGPKKVDTPAVVVPVSACEEPPAVSEAHFADAAQTEAVVIEKKSDFC
EEPPTHADFATLGDASTEWDAFSRRRLGIAFHRGAAVLPGFPVLQRELRANTPHDSPSRQ
VMDVDLWNSYWSAFSDRFASQIDYLQEYLKAHDGESERRRVLVAASLDAEPYMESFKCSL
TAYARSFGALEHVSRERCVVMLQFTSPRSAEIFAAWAFSLTLEDIFTEADASQQAGAHCQ
LLVRLISHDAGKITSTLRWGSNIVLSTPFVESLFKGVFDAVSVTYHDGSFLILFASDYAA
KTALHSLQRSLLEVFGTTLSFSEQQPELGGKSFLMDKLGSESNLPR*
>TCRU_3910 Shwachman-Bodian-Diamond syndrome (SBDS) protein/SBDS
protein C-terminal domain containing protein, putative

MSARIQVPLSQRRHTNVAVVRYTKNGVRLEIACYKNKVISYRGGIETRMDEVLQVERVFT
NVSRGLYSSEKEIEAVFGKGTSEKEALQYILDHGELQVAQQERAAEIDQMFIDIAVIISQ
KCVNEVTQRPFPSQVIEQALRSIGAAVKLDQPVKKQALAFIHQLIDAKTIPIARTRMKLR
CIVPDEPSLEKLVEWCEINGTSILQKVVEVGGSDAALRIHSLLILLQPHLFRDIERFVKT
EMPPGGSVHVIENAAMDVGEGDVMDAELIARANAHMTGAGGVGNADKSHCTGSSSNPHAE
SNRGRRKGKGGSRKPQGVQRVLGNDDGTDQQTVTTAELSSTPAVVGENDDELKVALSKLV
LDETHGSRDEDYDGKGRRGKKKAKRRQGEPHQKQQQQPATPQKAVEVDEQKESDEEVLVN
RKQRKQAAARVKVKDDKRNEYWNDADDDDYDCGYEDEDAGEGRD*
>TCRU_3911 Spef1
MTVPLTEEDLHELYLWVDDIPLSRPKRNITRDFSDGCCVAEVVKFFFPRLVDLHNYTPSM
SMKLKRDNWETLNNRVFRKLHFEVPPEEINDITAGVPGAIERFLRALRTKIAQIKARREK
MSALEMGHGGSDDENNDGGDDRGGGGGGWTTSGRPWAAKRQPKYPEHRPGSGVGADPAAY
RSPSNVRNVSEMQPSNQSSRDNKRNDNGDDATTSFRLLLDEKDRTIFELRETVSLLSEKV
TKLEELVRVKDEKLNAYREKLGRH*
>TCRU_3912 tRNA-dihydrouridine synthase 4, putative
MERLNDDDEREDLYCVDHGRLKYKHTDLLAMLRDAQSAIIRFSEENHDIIADVVNFASTS
ERKNTLRKLEEAYLGIVKVQAPMVRCSRPAFRKLCRLWGTDVSYTHMIMADSFTCSDAAR
HADFSMYAGEERLVTQIASCSGPVAAEAATLLAPYCDAIDLNCGCPQRWIIKEGLGSALL
QKPEVVADMVRCIHNGLSGGVSLPCVVKMRVDNDVGRSVDFARHCEAAGCGWITVHGRTP
SCSAHAPVRLDAIRTIRECVSVPVVANGGVNNPQTALKTSLTTGAGAVMSATGLLANPAC
FYVPREGELLLFAPQRHGIDVALEASMGPCRGADEGASTAGSENSAWLKGLPGCPVEVIS
DFIRLSCVTDLASKATSMHLLKMGGNYLSPTERVFLAQMHSSFSVVSAFQQLGLYTQDGR
FRVVESVT*
>TCRU_3913 hypothetical protein, conserved
MTLLGAVLAFYEVSGVPLALICTSPSVRQACEKNAAAEVGLWKLSLESDGSRRVIWQPSV
PVRHCHKTDVMCSVAWWCNRLMPIGGKAPPTRLDLGAAGRLLDTHLPIVFVFRSLVELTL
RRAPIKDVNVLGKLPMLKRLDLVQAQVVDGGIIGLGESRSLVEVDLWGCTAVTNANTLGK
VPTLRRLVLAETCVSDDGIAGLVDGLSINEVDLEACAFVKSVGFFGRLPVLRRLLLVSTS
VDNNGIMELGSSMSLVEIDLWGCSAVDDVNSLGGIPTLQKLDLFGTSVTNEGIKGLRRCP
SLEEIDLTRCEAVSDVETLTKIPRLRRLVLLHTQVQDVLELVSMGVTVII*
>TCRU_3914 Uncharacterised ACR, YggU family COG1872, putative
MKVSSFISQLRPGWFHLTVHAKPGARSSSLACHPAVTDAAIEVRVGAPPVEGKANAELVE
FMQMLLEQELARVRAAQQHTPLESNGAVMNCVYGGHSKKDKRKNKPNTKMECPVNYPEKV
RVSLVSGASARHKTLEVAFPGTQEELISVLQSAYVS*
>TCRU_3915 hypothetical protein, conserved
MLRRTQRWLLLNVSGESPSFRSKPVRNLQMDVQMSPYKEQFKDYWSTPVPWADREYGEKP
KIGAPIPTRRAATAIVVGKNKHVAVDKVERGEDNDYKVLMMFREGKNRFVRDQFIFPSFP
ISLEDSSEDWGKILRRRGVKTAWNDLHHRLCAMRALFAQMNILLVPKEGGGLVEVEGPPG
PKKWHLLVHSQPTAMKNLVDVLELPMETCLSQLFPFRCITTPTTETFRFDNLVYLVPFEK
IPDVRFTISTVGEKLVWVSPMEAMARFNAGIMNMPTPNIIAISELNNECPTFADVIKRKP
HDDYRSILPELYRHSQTKVATVLLPGDLMHPNTTGEDKAERYIRRFVYEKDYPFGVRAVF
EERPATPEEMNEPLIQEAPKLLEEANEMDMVYADTPYPKREKQPGEIGRTRFPVPSYSFQ
EGAENEEGVIPVRNRNIESVGDLYSHTN*
>TCRU_3916 hypothetical protein, conserved
MEIIDRPLSELIKEQKIGESLRKKRRGHGGQQNTRNGGRGTSRNGRGNRAMGRGSRGTAG
NDQGRRYRRPLRFRSNGGRFRRLGIGFDDRRGFNSRSWRRNALDLGDDRRDRSVKSTATQ
RRRKAAFERNDRVRELRRREALSRARSRFSRD*
>TCRU_3917 hypothetical protein
MSNDPSDAAIICATSDTTYMEEIILQNEALLLEVEQLRSVVKGKGLDQLQQLRGENERLQ
QLLKLSESQLAERTHQLEVLESAYNRIDGVHSAIHELTEQQKALSEMKERCISLEVHNTA
LKTELVKTSESEEELRKALQEAERSRHVLEEEVNKLRASVTETKSRLENVENLKCSAEEA
LEGAKASIAKLQAHSEDLEEKNEAFKRRLRDAEQEACEESRIRNGRHTLIEKELEDLRAK
EAIGAKRLMEAERVQARLQEELRLAREALAAKEQDTSRTLLQQRDQVERKLKLEFGNLQR
ALEERERLLRQQVEQNIRLKEELTMLSAEKDILMRRKQGEPVDVLQLQNRLKELSDETSK

KEALQQRFQEMLKSSTATNSDIKHLFAQMLDYQERRDEEMRTMIAIERIKTEDMKNMYEL
NLEKLRAEQKSLVYEIQTLKSEGDASVTRRIAPAEAEISHEGTQYGAVAVGNSLMPQANA
NPPMFVGPTERVHPVARVGGSDVGGTSGSIAHDLWQRSLTRADRVQTTAINYEPARLRFP
HEERLSLLACPRCTFLNQPGITKCEVCGASL*
>TCRU_3918 Enriched in surface-labeled proteome protein 11
MTVWYFLQSALVALFFFKDVSALERCRPIERLKGLNQEILAMPRGGFYAGYEYFCAEDAP
RQFHCHCGVDTICKNKTDAWGRNVGVCACCPWWMIVLFAILALVAVVAISTTLYVWCCRG
KWWFDGYPPPVKAIMCRRGAATVVPATGPLPPNLFRGYRTSEFVSEPTEQPPSRVPLAAR
GGEAPRYLYHENRRHSSPPQNPPHSLQQRLSERNPLSHR*
>TCRU_3919 hypothetical protein, conserved
MSASGSTSKDASPYVCLSAHCDLLHFIGPVPHPYGGPKPQTIAQRASQYVRFSCESCEKA
PTVTVKCEHPLFPPIPITRTSDGVPSFPLTGIELARWAYRENFESVASQSQLNPHEKKVD
VPHPPLQGDSARVAHESALPEVASTAPLEEPEPTMESGRSSCIVNFHALRRIFLQTLFIL
NLPHRSPAVSFRLSLHDPRPFGVTSFFLLPRCAEKLAALAHPAKVTLTVARTTGGDTLQC
SCDCLHKKDEEEDRITSLQLLWELKEGDEREQYAKDPVELDSFLTRTMIPVLFALPEGLA
QLIESEGVQTSRAIGWSQRRSFHLLALIAHCVWCEKVAWCIMNRFSVSMGLCRLQKARLK
LRNSASLESTDKWESTLFFYPTAFNDDRHQTTRGRLEAIDVTATSCAALIQVTVRGCDEE
MEWEWNGEIPHRSSAGLCDFTELIKKRY*
>TCRU_3920 ATP-dependent DEAH-box RNA helicase, putative
MRRLLCKSGLLAPAREMRHERDFRGRNRQRRQRGFGEGRSSSNPRNNDDIGILQIKFHTI
PALQVDMRAETQIESFLRSQLREDGSSMLLSTNASSLPIVRVINVPRSTLKRAVLEFHVR
GIPVRALGQSTRAKRARALCFMHAARLIDHFSVEGTDNSAAPLPLEEGTELNAQKKYLKR
VMSIRKTQAFGPPPQPEEYDCWEDYVDESRRHIERQEQERRNEAFQLLRIPHTGNPLVDR
AAEMTEQERCTDRLALQKLNNELLGVSKGVNIVRISHRVFVATLTLDSVTNLVATGVAES
SQEAKQRAAMHALNILTLVKEQRQASAVDGKASAFAGRGSCASPDAVSLSLTPRYSKMLD
FFSLFFGVTPAPVFTREGNSYICHMDLDGVKCTGQGINRFEAERHAIENALGEMELYDER
LQGINSIIAQYPNIQPRCVPTAKLPEALRNEIHAFVQRCRTELHFPVDGNTVGNEGHGGT
PEKILTDDVLDAETRAAIKALEDVRRDEAYARRLRDRLCNLRADPKYLEKFHMRRSSLAI
ASVEQRILDAMDQHRVVVVCGTTGCGKTTQVPQYILDREIMEERGDRCCIVVTQPRRLSA
FSIADRIASERLDVVGKDVGYAVRLDARPGRHITLCTTGVLLQMLSGMPSLDTVSHLVID
EVHERDINCDVALALVKELLMEDKNKRLKVLLMSATMQSEMFASYFGDVPVISVEGAVYP
VKVCYLDHVAHLFQHSSPPGYYSPMFDALSSATTSQGRNTYRGRGGYRGARWQLTTPPKT
DYALIARLIERSVEVDLHGEVEGKSVLVFLPGWKELVAAKQALEALNGEQRYHIILLHSS
VDAKKQRECFSPAPEGFVKVVLATNIAESGITIDDAAVVIDTGLIKQTSWVSRATGTQQE
HHASSYSTQLALQYASRANCTQRKGRAGRTQGGICYRLFTREVWDVLPSFQEAEIHRVPL
TQVLLTLLSLGHTKPKETLQRFIEPPSVKNVEASMRQLRSLGAVTADEKLTPLGLYLSRL
PCDPRIGKMIMMGAVLRCMDSALTMAATADVSPFVTSREVSFEVRQKRHAFSMGSQSDHI
SVLNAYNAFCARQGDGVFASEQYIHRNNMRIISRYKQQYRDILRRSGFIRDGESFSIEAP
EDEFIIPNDDAVAPLHVDSGLLSLDAADVTLVKACLCAALFPNVAVLDPSPLLQGGKRAK
TLVMRTAAHKNISPSKDSACRRLGPPRAHGVLTPKEFFGRDAESGAEAPVIPSMFYIYQS
IFCVQESREEFLTQVSSVSLWALLLFGVGEADMRFDPLLQLCIVGGWIGIHIDASSFATL
HALRTTLHTCVWRKYQKPDDEKNNEALEVLRRLCKEVLQSPPNDKEQYLNRLVDTGRILS
PSKLEPMTTDTNDENFAWE*
>TCRU_3921 hypothetical protein, conserved
MLRRWPVCAVATEVPTIVATTTTAKLWGSVRAASSSATGNGTGENAPSVAEAADGAAYRE
SLIQAILSRDKEIFELKRQHELSMLRVEQNQRRILKDQEDRGMYYEQNCNVHTFDTISVG
LYTQRNTLYHTMSVERLRNVKLLLTLLVTLLTCFYLYYRYMINPNWVYVEKPLKIIGSRV
GALNDIRAQLGSQEEETMAMRSKLRE*
>TCRU_3922 hypothetical protein, conserved
MQGLPHDVDGHFGIRVAARSSKLRARQEANGRAHVAGSGAQVPLRTRTILAPRLQLRTYH
DNTAMRDALEELKKACGHFPLDDAEEMEKMNPTNSSAGLTPSQLNQMPGHLIVYCFTYCD
LESLCELGRVSLRFAALSNANLLWETHARLRNVTTSAPESAREDLRRAVVEQHERWQAEV
QRHEREYEALERRLRERAAAELAAPVDVNATLANNRPGRFFGGNSNGRDAGNAADQEAFS
AQLEQLETVKLDLLRGIREMKSELAQQQRQIEELQMWVAKTEEATCEAGNTTAACEAEGI

TFLALQAFERRICRIVLSAVNDLPTVLRRGVDDFATMELLCLFGAGDVGGRVRQRWAAFK
RFFPPMSEDYGTVRYLLMTGEPPSSDRARECIASLGGVIRRVQRMTDNEIVQIIM*
>TCRU_3923 Endonuclease/Exonuclease/phosphatase family, putative
MTVASSDDDKQLDRSHRSDGSCCSISSSISSSSTSTSSTHGDDGIPHANGVVRVHQGRSL
FSGIFMCYLSLFCVIRYLARLLFSGFATVRAARDSETYAMQKKEDDFLCGNQKNSERGGG
ITAKGIQALRSQFRLDSDTDTETTSGRSFSSAAVSGEARRRLRANLLIRQFFKKEKTESM
LRALRVHACTWNVDRQPPPNGNNGFYEWLLGRKLMGKVTTYWDLSKEARENSNETTPPFP
IEEFPDIVIVTLQEVEMGGVVLVREYTETGVMWTEAIVDALNKISEHRVWYKKVKSVQLV
GLVLVVVARVEHINYVTNVRVSLTRTGAMRGVWGNKGSVGIRATIYGKRFLFIAAHFVAH
KHNERTRTLNYHASLKDLMFEMPAGVDSELDVLETFSTAARDSNMEDGIIEKRSRLTPFF
RNLRRTPSALLEKEVLDKYDYVFFLGDLNSRLHGLKGTDIRRLVRNKEYDRLICHDEIRQ
GMISGDTFDGFQEALIAFPPTYKLDRKTDLYDTSRRKREPAWCDRILFRVCLPCEKSDDD
DSNDHNVDGVNRNDGNNKQEGENRALYGSFPYLNSSTKLMYSMPEFSVPVDNVNGPLNRT
DDDVVSLQSSTSSMSSEGAVSLLGKSDSVLSDMHYRSCYLETLSKMRAQNLQISSFTHRD
VSLDETESLPTFLAARRSTCTDKRFKFFPMIPNKMLVFDYHHVQALRHSDHRPVCAQFRV
SVLSFEKDLVDSVLQKVNEAFYLEENYPLHD*
>TCRU_3924 hypothetical protein, conserved
MPQEEGDFDGVNPDVQARLVDLIIFSDQARRRIAELESTVETLEQTLSELRRNDTHSAAT
LRRPLSAPLIDQPFKENGLQDICSWNEQLVETVNALRGAMLKMETEAKVQIVVLKDEVER
LRRESDSLRRENDALKERVADDVLRQRQTNRVEMAVEKAKIASRVRAAGLRRLEFMEAVL
MEAHDDLYFAQRFDAAKLPVRDVTFVIHAVPNVPTQHLSAEEFTMTIYQNFLLEVAKKYG
GYHVCGLREIEVFAFYSATAALHFSSECHVGVKNLPWPARTTDIPFFAPVIDDGELLYSG
PRMHTCMYTCNPGSEVDPINGRSVYYGQEVKDALTTALQGSPIGEIVANKACVIMLFKEA
SIMNDVHDDFFLEMSRVRAKLGAGWSIIASERTVGNLFCSILPKSLERRRGIPPYYLHPS
PRFPRGNIDVDTLLPQLIASMKGVTRPCQGGTQQKPQAQLQIQSQSQQLLLHHDGWVDGI
YRSRKRAAEKRDSNSEDVVSLYLLRRDRKNIISLYNKLEAVSAFHEQTLMEAEDWYLARF
QSIDPSETVYLCTVDVGSNSSWRKITQVSMGLEEHHQLRQQLFSSALLHGKNNFGVYVNG
NNTDVFTFAFRRTEHALRFTAQIYTVVKQKCEAFTKSETCLMRAGITVGKLRPSNDSHTA
STNTASGTATDCKATRMVLCRGKALVCSGHLCDLACRGEILAVAEVIQAFQSNKSNLLSM
EYNVLKKGGRFLGSYSTLVDVYSILPKAYAYRRQLLKGGDDGSCRDECESPRSSVKAALQ
LGKRIMSREEVEQLLLQHQQLLEKSEAAMMAAEDNAWEITTQQALSLPWPVVSRSGVRST
TAERGFLYCDAVDIVAISRALPEELYKNIMGQYNYVVKEALLAYDGFIAKTDSTAAYIVI
FTEPHCALEAALQIQRGLLAVDWPQRIKTLEATLHVKSCKANIVLFDGIRARMAVHVSKD
YQSTRTFCGDDKEFVEVFGPAIETVAELGFQACGGEIIVTSFALSSIGSTLHGSMLLLQV
AMRVARIQSSNKMLLASCVPQRLWERLHLFVPAAPVAEVAKQGTGSKLRQLKVAERKKSW
WREGNNSLLSLPFSSQAPWGERVSASHSTFAFSVQASLGGAVGQIRRELSSSIGLSTHRE
VFLNIVCEILMNMSHLFRVVEDGVSRANVLSPLPPLETGGAAAISRDASPNKFRQNFSPE
NRSSGTFNMKLMHSGDSTSSPSVSISGEPHKNAVQMLDNLLRGALHRMARALGGTGKPHL
ASFSNRMSTFKSVSRRSSPKPSGQLRPL*
>TCRU_3925 hypothetical protein, conserved
MVWEWVFRWLKPRSGVEDKKTSEEILAYETLRKAQTELKRLESDIETNTETLRQCEEALD
SLFHKELQLREGLEGILMEMHDHTSVDLENTIGNNSDGIASLQQILMHIQRKRGKLHDQG
YRLHIKLQCLKAEKKGVVKSTNMLLSRLLGNGLAVQNGMGGEDGKEGEQGDDDDGSWRAV
VHSPPVSVSFIEEYREKEGS*
>TCRU_3926 hypothetical protein
MKPLCGVLFTVLFVLCFAPCSAENVPNTGTSQMAENISRAETIPNGETVGMTQTVSNTQT
IPNTEALVMTEAVSNTETVVTTKNAPTAANPPHGAVPDRLSLALATRERLPTREDKTRAD
AVAKWFHDRIKINKQPSGIGEPTLHISSADSSSGRSTCFFTPLLLMTVLASTLMS*
>TCRU_3927 G5-interacting protein
MSLNPNAMPWNMPESGIDPVMDTNTRMGQQDPRFHGYPSYYPNHHAHQMPPVMIPHQMPR
HMMGHGFSNPNHMPPMPQNEPVQSYNHPRVRSQQYNAGIMNPMHSVSTPSYKKLRPVVVV
FGYRRVGKTTVAKRIAEARNYKYISLKPKEEGAVFSPTDYVAPLVELLSRKNSFEGIVID
DIVVRNKYEPYYVHSLLQKHNLKFDVIVVLDNDLDNTKERGVDYDDSLQRQLHPESYEFC
ASYLQGEPTLVVECREKTLDEVVTDALRQLGEVNFTKDSNISLKGVELMPGCPLERNAAL

VTAILDAQTQQLKLSEGSLFPFSEPNYLLEYAIFARYAYAFRSYMITPWIQGDKASLIGY
QGAVYVHLPSYNIVFCFIDAPSTLTQLAKGNVDNNEVGFIFEATFAGDKLYISDLLMMGE
MKASEMLVTERVELLKKKLKDMNSSTVELLPWYPVQSIEACESENPQAAGVLFVNPDGVM
FGGYDSRNFLYPLQRKKSVELRVWNGNFVGDSWTFDAFCEEMGNENIVEGIPVHVPDTEV
TQHCINDGNILECIRQDCHAGPNKGRRGAKRFVFQGRCQWKVRPTTMFKQEVFVSDPKWP
FERMAQACASVKHIPPTRPEGITTADG*
>TCRU_3928 LicD family, putative
MRRFSCAIFISHRYVSVFRPHIHLSPCVICDAAAGDSQETFGTSPSCDYHPPNFFPPPDV
RNDCVVEQTSSGWSTTLERRREGLKKWLQKEHEWVGGHRRVNSAYLESCWEAFCNPARTL
TKDEIAGTIDFLAQFCEVKLDDVPTETSASSNFMRQETEQPQCQNSVPSRVCHGKEEMSK
NVFLTHVQRSISALAEIERQLLFQRTLLDFFGVTNSLNVPLFLCCGTALGAHREGYFIPH
DNDIDVGVFYEDLQRLGGTMEEDAQSAVVSLLSHVALDGHFVLLDICGTVEKGLELRFLH
HETRVALDLNVYYPPLADDAALISQFGPFVWTASHYEDAGSRRHGMYRYRHASFREALIR
LPFCDPAVASRADGFLVPPVSYLVEYFGEDWRTPRAYTYTEGLQNGEYKNIIEE*
>TCRU_3929 cleavage and polyadenylation specificity factor-like
protein, putative
MLHAAVKPSLPASGVTHSLVGQFSAGLPAGVRELILFKKNKLELWRISCGEEWVSSLSYV
ASTQLNAPPVSVAICRPPGFAVDVIAMCLDDFHVSFVQYDPVRMRLSTLALVQLDDREVV
NDVMPLEPIMRADPTGRFVAVLARRRHMFLIPLLGLTRSENGDCVTGIHLEAENNTKLKE
AMTPVDDWGDEDDYKELAEETDPSIPPEKETTVHIEPEKHDSRVADAFDGLLHIGHLSMF
SVSLAVNGVIRYVRDMQFIESSGEPIVAFLCERHPTWAGRVKLVEWRTKAVESKMLSSQI
VWVQISAASTSNRKLLLIGEVDDVPYNVTHMTPVGPFSQIPSGVICYGINTVMHVTTKRG
YGVYLNNGGMEECANSKSSAMSYGKVGWCDPKMEASTALFKVNLSLANCTASFMSIVNEM
LHLLVVSEEDGVVLTLSITAQSSSVQGIRIAILGTGCYCSGIARIGDQIVFLGSACGDSC
IAKVDMFHSDVAKRFQIIESMEAIGFISDVDVVDCTSMDETDPNQLNGVNNSSLCDTPYA
ELLGRTILEPMPSVSIAECRAVMDLAVCAGRGGTGSLFVLRQSVRNKVFRRENVNAISAF
FLETSQVHKRSRAEHEGEEGATQHPPQPSPPHLLLTGLSFTLLFAVRGESLLHVRRSEFL
TAYRTVFATEIPWLNALLQVTEKEGRLISFDGKTLLQKFNFMSEREAGKKRFVKAASIAA
DLMLFFPLLEDGTLFRLALKAAKTAPTKEVFAEGVTAFALWPEQRRVVIFFTDGTMTIKE
MESCEVCATFPQFANLPQYSTPATDESNKEARDDEALPQVSHVEIVTMRDDNTVEATVLV
VILTTGELAVYKVISSDAFGPLRLKKSMHHFLDHKAEREVIESIEMKRKRLQRERGVVEN
DTQLMRQYSRRIVPFDAIGGNTGAYVCGQHPLFLFWDRRTRELEAYRHQTLGPVRGFVPF
RIINSGYIYCCEGFVDFASMDTYCRPTGQGWLTRRIHLGVTPHFVVYHPPARSCFVVTSK
KEPFRPQRAPFDVQLNIVYDEESGGVQSITTEAPVSNMPPIAPNAGIRVPMADRFEIRLM
STTDWACTDTLLLEENERVLGAQMMEIQCERDAEGLHTAPVCVVSTAFPLGEDITCRGRI
LLLATMCTKKKRKIVLFHSEPLNGPATAVVGIRHHIAVAVGGTIKLFRFDWSNRKLVVGA
LLYAGTYVTRMSSFRNYLIYGDLSRSCAIARFNEENHTLSVLGKDRNAVSVVHCDMMYHD
RAFGLLCSDDERNLLVMGYTPRVQETEAGSPNKVLESVLSLDGEYRLSGGCLVKSLRFRS
LAGNSSVTLYVTNYGEIGFIVPIGEQANRTASWLMRRLQIDLPHSAGLTPRMFLGLSQGS
PRTAMRAKEMLVSASLLNEFFFLDIHSRKTIASAAYTQLERVTNVASLVYEECNLF*
>TCRU_3930 PPPDE putative peptidase domain containing protein,
putative
MTGNFEKSHEPFASSSTDADDGLTASPKFYSYRRIIALPATPPDAASASRVNGTASTQLP
SFCPPQRECSSLLAADRVTFVLSQVTPSPRAVEFTVILHVYDLSRGLVNRHSEELLGFNV
PGLYHSAVVCYGMEFIFGGGIAVMGAGHTRFGKKYKKILLGTTKKTLSEFMTWIREREKD
TYHLNAYHPTKNNCHTFSKDAVAFLLGPNGSIPSFLTTVIEHLVKTRLGQGVLEVLTHYL
IYPKCITNRLLREHMLERKKSAMSIAQSAVACELMSQPPPCVVLFHVDDAAKCRQVFEGL
MPYVEQLKQRGKVDQSAKMILTSTFIISTGAELIDPTIASDYIELVVRILMYTHTTLWGP
VLNSLRIALLHKVVLCACVFHPTLLALLANGVRDFLNMTPEGKLSFLRVLCNLSSGLHGA
LALNSSRFALMWVSVVGLALADYRNDAIVYTGASLAVNLAHAFVLTTIPRVSKDHGVLFS
FHRIRQLMTILLFYLRHWPPKRIPEAAMNMMLLALFFLMSSYPENVEFAATHGCRLNYAC
MLQRAQTNESKALLCLMHALEQCGHMSCVNVIS*
>TCRU_3931 hypothetical protein, conserved
MAVDAAYANLFGVEGKAAVLGCDELGLVPRDLLHIPKKSLERAGDDKNAVLVRYTLIERA

RQNNIRKVLAIKNHLIADGDVQKKWKERCKLFPDAPGVPKIPKAVMNKLMTELDTETDDD
DNIDELGLTKPMPRYGDPPASLVADGANREASNASSSTSSRARFSPDRLRRWNGSKASNP
LSLSSKEKPLKKKGHTRKLSKFWIKHAADTNSGKISSGRLSGDKRDTFWRPKPPLDPPFL
PPLPYPRRDAVTLKMELEELNEYRQFLLRYAHDSSAMAQEYHDFTKSLQEDNNTREKFRN
RAATYTVEGSKFVNEDELTPLGPADGGNVTKSTFTKGGISNHKRQLDAYVRLARLEIRRN
ISNYKKWNGFMEEMEGVESTGTIAADVRARLNVGKLPIFEEYVQMVRERTKRRENMLLND
KRKQERLNAFCEAKDRHTEENIEKIKRTQTNLFMESQVVQSEIKRRNREYENRRRRMREH
RVQVGLAKKEMGATERHMKLLFRAKEKRFEHDAEEIFRRLLKEKIHAMDATKRWDIKSVR
AP*
>TCRU_3932 WLM domain containing protein, putative
MTSLADTLTKYSTIGAATTLGWAGDEYAREYMLRLLVRAHAILSAHNWKVRHLKEFYPRS
ARLLGLNVNRGDEVCVRFRAPSAKNTFLPFTDVICTMLHELAHCRYSRHDKYFWGLYSQL
VTECEQLEVGIACGKIVGSASQQFRFTGSHRLGGSGSSLRPNCSTSMRKTLADAALKRIQ
LSRSGEFDGCGCDDAATSSSTAMGNDGWICKRCGNVNMSVLTVCDFCSDILDPIGTEEGW
DCTRCSFHNYCSLQHCEACSYPRLNTPESSQCAVQRIKVFGAPTGDFSAYGLLGRLADVL
DPILRERGWQVICLNEFSPTTPTVMSQGEFIDSRRAVLRVRLRSPNTPSEFLSFAYVCTA
ALHQLAHMVERHHGVAFFEVWVSMLNCCLMTEKVQEDVVMFEDIKGSLLQFTRRLETILE
DQRGGGKRPLTMPSMHSLVADCGNFVKRERSSEEDGMTGNIHHDCVDSFRNWVCSGCGFL
NPIGAFLYCEVCGTTRLPCTPSLEKRRGSLEAIVITDDDDDEKEGYSSCDSEDVVVVVV*
>TCRU_3933 Enoyl-(Acyl carrier protein) reductase, putative
MSVVNLCDAMTDLPLPGFCVYTMAKHALGGLTRAAALELAPRHIRVNAVAPGLSLLPPAM
PQETQEEYRRKVPLGQSEASAAQIADAIAFLVSKDAGYITGTTLKVDGGLSLARA*
>TCRU_3934 hypothetical protein, conserved
MAMMMAGRVLLVCALCVLWCVAGGVCARDVDTNALGGCMASGVLGENGSHMPDGCNKTAI
TVPLRSALPITAVEASTGESVSDSTDIYPDSLSVPPSPPPVTGLPEALNAPKAPQDPPES
DVGQTGVGDRLSLVPNDDSSGGGGFEENGNSNKSGVSASEFSTVVGASRSPIPPEVGGSE
NKSGAPPNLKLESPETNEPRERILVETNKDTQKVSKLEENPESSRKKEKANIRGTSEEAG
KNEAGRSGVEAHGPSSVLSADGQLQHQGTTVTITQPPPPSPEQQTSAVSPSPGVDTPAAR
SREAGDPEE*
>TCRU_3935 translation initiation factor, putative
MADDLQMSRHIIVNGLPNNVTPEKRVLFLRHMTKKVSEVLGHENFTIHLVLDETTGLVTG
AFLSFATVANAEDALARLNLYRFTKTDVLTTYRWSALQAASAAKEEYKPPELTDDVDADL
AHTMCEDIMARPQFFIKQGESFDVEWYWFNYMTLKDELYRKPRALKTDSLGQWTEMDRRQ
KKLESGLVYGPLTSVRPMPAWSTFGRMIISQHTSGLKVWGGRQMNMLFEVPDLDITAFLV
SPQEKYLVVKTLNDLSVWDIRTAKKIRTLGGLDLVDAEKWPIARFCADDSLVAISHASLE
PAAPGKLFIYRAESMRVLQAASSTTPKSYTFLVPGLKTVEWNPVVGTQLAVVMELSTNQG
WKVVIQDIILEDNLVREEVIAQRNFLQAERLELLWHPQGTHLVVKIAKPHSTEYALFAIG
TKSAAVSQLQVEKGLSAGRFAWQPSGPHFAVIFEDRTKVSELGSTSEIRIYNIKKQLKLL
GRFMTSATHLFWAPRGARVVATNYSKSIMHFYGINDQGMVVQLEKHALPVTDTAWDPTGR
FYASWVSALKSQGDNHFRIFDLNGRELLNKPVRHLSHFSWRPLAAPVMTAEELKQVRENL
SEYTQRYEQELKEQKEREEAEAQRVLRDKQERYIKRMRDIARFHSDKELMEKREQLIASS
PWSRMWARRMKSLSAEETIVHEDVTEERIMHRRAIN*
>TCRU_3936 syntaxin binding protein 1, putative
MPRPVRLRLLLLLVTASSTDELTEAKKQQLIRDGGLTPDARLFANLEHVTRRAGSVQRYS
TASAQSGRSTSASASNAATDEDPFLKHACMMMETAGRNRTLRVGLSLASVQRDHGMRPNG
ASGGQNSGAAEKNVGPF*
>TCRU_3937 hypothetical protein, conserved
MSMVDGKMAEKADKAKRTACLGLHDKETLSLPLPSGNFNVAGAWNKNGSPSMERCIRDDG
SRCLFRGLDDSLAIVLDDVS*
>TCRU_3938 oligopeptidase B protein, putative
MAALYPWVPASNVAYTLCRYFLNRFAPHARNICPLPFLDGPLPDEVPESLLLCGERTQSD
PFKYMEDLFDRRTQSYVRSEQHHYAFIDSKFDFKHTKARLWAELDSKVVVTSREGGFDKG
EERIGDFVYFTRVVPGGDSNAIGFYRKRYGQVDLLAEELINPTSLQQHFGYEKCHVGICR
VSDDGRYVAYTLSVEGGDRYICHVRSIDNASLFHVIRGRNIVSIEFGSGDYFYFTESNDL

NRPYTVIMQQIRPGILPPPVELYREDDEQFFVDVHKTKDNAYIIITSDSKLKSSALVLPA
SFPKVSRELQAFFRDGRPVEIAGKENWNWLEHYDGHFIMVVADQGPNHRVVYAREEVVLK
HGMRAEWKELVPYRDDVQIVDMDLFQGRIVLYEVHFAFERINHIHIIKCDKGLDDAARQA
RKDDLVLHFPPLTSVTPGLNKNFNQDSMSFVYSSICQPSRDCVFSFDSKMTAEKSWVCSS
ESLFTQHQSEQLTPWDYMWPYSIYRDLCLSPDGTQIPITICHRRDAFVQEATDFEAQPNT
PKHCLIYVYGSYGEVPSMHFQLAPYMWMLRRRWTVVFAHVRGGGELPNWGEQGKGKNKIN
AVHDFIACCEHMIKMGYTKPELMVAAGNSAGCVPIAAAMNMRGCGLFGNALLRSPFLDII
NTMIDPDLPLSLAERDDWGDPLHNAEDYARLTQYDPYLNINDRVTYPGMMISTCLDDDRV
PPWNTLKYVAKLRQQRRRKGTDPVARPLVLRVRSSGGHYCWGDTENICEELSFLCSQLDL
EGPGKVLNDMDIMTHMHNLTATGAMDHDDQEKVFLKWDNWERERIDYHVKLHNFDWEPNF
RKLKAEKEPFFWVPNEQEMQQRKVDEMFHARERDKREEAKSEAKVGSTGRAAGGNKWKEK
VKK*
>TCRU_3939 CYC2-like cyclin, putative
MSSVWKVLVRLHNVVNIPCGVCSNDECDDARVFSVVARAVSSNGTLLTECPEVIAEFTTR
DIVQASAADPLEVKLDGRGERGAAVSAEWSTNAPTIGLMLLVKERQPTCERVIGSCEKNL
VIDVSDVVQRRKIVTHIVGTEMGRVGVSLTVAPSDTAGYRRRLTEFLSQYNPGGLHLVDS
VVRGIPEVETFTKLYRKYALVDYERRVRDFFRVYGREHAVQVPLLLKEWENREEELMHNL
VLDNGPEPDNIDVETRLAVFLRAHNVSTATPDVARALRESNNTPFQLFEALTLKYGPEPD
PRSYLFPPTHYELTQTQYQLRQLRPTSVPPIRAAENKWSPQREISSNGGTKRQEEGKPFS
QHQRQQTSPVILSVTHFDPPAATETEINGNGDHSYGNEKDTRSVNFGNNAVMSWDGFCDL
LRRQGREPSDVYYMSEASFSAVAENMGYTKPDRDILIHQWQQRLRAAVREEGLTPGDAYY
GTAMKEVLNLVGLQELNLEVVSVTMVSNREHASCFANRLLTAQQRATERLAIVGEYHRLR
DIVIHGANGTAGEHNSRRNPCIVFHRLPFQNWNRKQFTCILVCDVVIGKPFVCTPLVKTA
REATEEFRTEWDCCVFHDASGGQAVAVYDPQQVLPRYMVQCHVDVTVTPCPAHPSRAVEY
YVADENAFACSHCVVLGKYRKKEVLAIEDAAAQARSRLADYKRDVHQLLVDLEARETDLV
REVDDMSIAARRLEAEKEVERIRREAEERVAAVLRALEQAEEDQLNDIKLRRECVSKARD
AADTLSEKVTTALQHTNPLQVLAALQRVQAEDELQYLRGEFRRSCIKINDTENGTRPDVP
YAWTRTAIRDDDDALTIAAATGTRVNPLFEQIEDKMQRMEGIHMNTNSLQNHGYTSSFGT
GVSTHLMETPQPEKNTTANSLYAKYLAIASGAGKEEEEKEGLIHQPMSSNVITKKNSESN
SALCALSAPPSEIRRAKEDITKGWALYRQGDPEGARRMWNDVYGCHLDSAIGARAQAYIA
EALDRDYEAAAKWYDLSLQRDPSDVMTLYNYGVLLETLLGRLEEALMLFERAHTLGDGAA
GRRAQQLRVSLGKI*
>TCRU_3940 hypothetical protein
MSDRIFWTPIRLDERRHYYITDTPQSELHIPSPAPPCGERGGDDTRIGGRAPRMEEINPN
CVVDFTRDATAASRAKLTSANVELGDDCINRPNSVYEKKTPGAERLFPATCKREGNENRE
DAVCLHACASISFLQQAFGDTEASAIPHELYTDFCSAAGSPQDKKNDLEKQQIPRVQSPI
PERPEDEMTVSTSMRGLHQRLGRRITSPLPDDDDDGAVKCAKNMLMRRENEPGGEGKCGR
YGSDAQFFPPDVRLQVSLPVHESYTRVPRPPRKKSAKYSSSPRCITARSLPLVEEQRKNA
DEWEQRAPVASPVYSNSGAVFTRVDFVGRQSAAELCGPLRSPLIPPAKLHELPREPQGRD
KTVDEIAVSPDTSAPELVDWHVLMEESIILDLTVGSEGVDEGMPLLVRSLECPLLTTNKG
WGGGDNVDGTQSISTPHEAAAEEEETMLLHSQSPLQRNATGSPPSRGSDVVVYPTSLPPS
ISPMESNSFDDECDEDGFKGVRRETALQKLLGRLAATNDNRLQGGGVGEFRGKLPFSFSS
PMLSSISEKNGSLTHHLETRHLVLAPLWLVVELCRALRPFARRLLLMLAQESGGRADVLC
DTCAEVVNSILEAEGVCHVRASRNLCRSIASIGSTDATDGHELLSYANFVAGVLQLAGDT
K*
>TCRU_3941 ribonuclease H1
MMSSSSRKKYYAVAVGLKTGIFESWDECRHYVNGFPNALFKSFKKLEEAQAFIVKKNDAS
NRGAAKSAVCVACVAAHAPTEQERLCVEPVAVTAGRKRPRLSSPPSASPSPLTLSVVEDA
AGEVELLQHVSLDWIRAREKEAVEVYVDGACRANGKGKLSRGGYGGYYGANDTRNFSLPI
PIDEPQTNNRAELYAVIYVLRTALEAESCYNLRVFSDSMYTIQGADFYMHKWLQNGFCGT
NGSTVLNCDLWKSLNTMRLQHATRYGEWLVSQFGLLPVVASTLAKKLALQLVHVRGHAGV
YGNEMADHLAVMGALYGRPADDN*
>TCRU_3942 hypothetical protein, conserved
MQTGMEVEDPTESVPLSYALLELPPKKELRKKGYRMEEINTTSTRDHPLSKWTTHTLKRG

ATYRDALDVIEEANKKSWGLLKARIHFSCGSFESYARLKPNDPASLKHTGTYDPNGVYKV
STIEASVAGRARLFPLLKPLVDERGHHTCSKKLPRTFAPQLLYKECPPPVLTQAGYDFTP
VSHNAFLLRPSDHPQGVRNVKSDFMKESCDYLPRSYLREKVGICANSRHRHCAEVYQVGD
YTADYARATDVVNQRNRVVKKDFTTTGALKSNSTIVGRRYAKAATLPCAHQTGVNEGVTA
ANTTAADNAVDKDPNDVTAPQDKDLKQSKEKPTVCFEEEQGNKVA*
>TCRU_3943 hypothetical protein, conserved
MVARMLIIIFSLLLPARLAIRCHPGAEEAVEQRKRLPAMKQLPLRELFGAWIFLNAPPLA
RSGGAWAFWEQMAKGFLRVNWRACGGCLILQWRRPLPGTTERVAVTVLANGTTPLVAGLG
SKACQRVRVPYGCDSMLRVLSGCHGLRRMLSRRLISMYSAMSVTKLQVHGPASTRQC*
>TCRU_3944 hypothetical protein, conserved
MVMLTPKFTAQRVLLATSRIPMTVAVKQGKGITQRPSAAAQSKQPRVDAVMCPEGDAAAE
RSHQHSVELKSKKFYDKDERTEQTGLKVTEARKGMDGAPAPPQDPMNMAESQEDKSRRVA
APETSHAEYIFRQQPEPNSSVFIS*
>TCRU_3945 BNR repeat-like domain containing protein, putative
MKDETLVFPVEGTKKAAEGTVVDVKTVSLIIQSKEATDWTLSKGMSDGGCSDPSVVEWEE
GKLIMMTACAGGPRRVYEIGDKGESWTEALGTLSRVWGNKHKGNVNLALEAGSSQRLLEM
TVLMTEK*
>TCRU_3946 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily, putative
MLVTLPVYPEEADKGNEEKSELHLWLTDNTHIVDIGPVSEEDDAAASSLLYRSGNNNEEL
IALYEKKGGEDTSLGMVSVLLTEQLKRVKDVLATWKKVDDLVSKLCPPKSALESPSPDNA
CSPTVNITDGLVGILSGNIFGNTWRDEYLGVNATVKKKDKGAAKNTEDTGATKNSDGVKF
RGAWAEWPVGSQGENQLYHFANYNFTLVATVTIDGVPTKEGPISLMGVKMNGNENPVLLG
LSYNSEKKWKVLCGGGNPKGHNSTSKETTHHVVILLRNGTQGSAYVDGQPVGEDEACDLK
NTEDKKISHFHIGVDGGAKADSEVQDVSVTVTNVLLYNRPLSSDEIGALKPNKDSISPLV
KELSTHSPVASASVVTPIPPVAATVQMTGTSSTPAGTPLTGKGTVDGEQWCGQWRCIRIS
RK*
>TCRU_3947 hypothetical protein, conserved
MIDEIVNDGEEDFIFNEYAIDDTLDPLSRLLNYHSSGFSLQREFLLREIVDTVKFAGFDQ
SVKMIVPLLVGFASDCEPLVRRMLVQQLPDMARYFLEQGGDAGYEYLLSRFLPIGFELLI
DKNVEVGASAFASLKELAELVKPEHVQNHLLSVVVMLAHDERAEDYRVVAARLFNGLAAI
FGKNCCVNDVLPELELLANDSNFSVRKAVGANLGEISKVVEENTAENVVLPIFLNLCEDE
IWGVRKVCITSAEGIALAVTPETRVAKLLPAYLLLLQDSSQWVRNGAHDSLGNFLHTLRP
SDLSPALLKLYTDMAFQSENGDTVYSEPCAFALPAVVKVAGKERWNEVADAYATLLKDVK
WKVRRSLAYSLHEIALILGQEITESDLVVAFELLLRDLDEVRLGVVLHADVFLGVVGQAT
RERLIPLLCHAPLESENWRILNVVAQRIGDVGVLLDPVNSTALNVIINLVVRLLNDGVME
VRRSTYRSAAMLLQHLASVGKENSCGGYVQTLVHIANLHSFRERLMFPYIAEEVAKLGAT
SLVERYFMDGLLKLANDAVGNVRLAVDSVLTRTFLVDPYWSTNQKIAQVQKLLQEKNCDG
*
>TCRU_3948 hypothetical protein, conserved
MDAKPASPLGLVRQRQNANVSPSFAPRAPAFVKKRSSAQRGAFSPLPEADGKGLSKQGSD
GGMPASIKRRELGEKKTMSNAPRVAKSILHENKIKDDTAERKMLSGDGGVLQPSLTKLRQ
QSAGDKVAGAIACNSANLRSGMRELRIARHGPIKGVVCEQLAPASCEAVTPTAETAAFCS
KKQAEFEKAIDTLNSMMEIDAKNIDPRAWVTRFTEGKAEARLSKEHLLPVWIIVHMDFVM
AIDMNGTAQHCNYGSFSVSQVTGFPPCGCIVFPLRDALREGEVRLPENVSEVEAMMMPAT
SEIRWGVPVGVLFMNPQERISVVRNICQLFLPLFFREAYPQGVPLRGVWIPAALDATSAK
PCTINIPGNVRECVLSCMRDLGVSNGNTFTGDGSLLGGTQRSCEFQQRESAQPNVAVATS
LTTRRGSGLTPEEERLRGSSQSTNCDLASPWGIRGNQPIFTARLLTSSAIVSSTECCTPC
HAVLVFTPRGLLELVAESPSAAVTVNDVKVSLLRSGLGRSLRLQRDAVRFLYAPSLPVIE
DDAWINARYVVMRLQTR*
>TCRU_3949 citrate synthase, putative
MMRFCARAGILLNAPSAARRHLTIVDELKAAVMARHEADAPKMKILKEKYKNEKLSDATI
DAAYGGMRGITGLIYESSMLDKEQGICFRGMTIPECCEKIPKSWKGGTSPLPEGMLWLLM
TGSIPTDKQVKELHVELHRRADNEAITAATKTIASLPENTHPMTQLSTGVLALQAFSKFA

PAYASGKAIKSNFWEYALEDSLDIIARTPYLAAAIYNRLTTGRAAVLNPANPDLDWAANF
TNMLGYQDEKFWDCMRLYLSLHADHEGGNVSAHATTLVASALSDPYLSFSAGLNGLAGPL
HGLANQESLSYLFEMRDKCKAAGVNMKDRKELAAGLEKLTWERLNAKRVIPGYGHAVLRI
PDPRYMCLREYCLKHFPDDELFFLVDTIYSIMPDILKKHGKTKNPFPNVDAHSGMLLQHF
GLTEQNFYTVLFGISRQLGALTGVVWDRLQGRPIERPKSITSDALFKKFKIE*
>TCRU_3950 hypothetical protein, conserved
MSSISSLSLGEALRRAYPSFPQILLPRNSLVVRGKTDIAATHAVPHVHGGAESHERRLMA
NPVFVPLVRRPCYACPGEAKDALLEFTQRHGYKSPLFVPCCLPFALHAENDIEAVPFSAS
VDGNAQGGKIETARNSVTAVAPSQTPTANIRIFRCESRVNLTDCLRTRRLQEELRRTENE
FCLLCKHARVSASVAGFDTKPVGVAFNPEVETQQSLPSHHLQLRWRKHGWYFEDAALAAE
QSKCVPFPLESAGYWSAWVTPHVDPFANPSVLRLQDIHHFILETQLALINAEAVCHYLAN
DNKIFFSLRSMPASADYWASTGDPFSATGTPVTTPRLMDTGEDDRTCFPPRSRCWFAVAE
LPERRLQIRRGGEVVQLSVSYDGCGFFLHEAPRWFLMSREAVLQRCPLSYATLRGIFSSP
EFGSKDDVLAALEGSGLLRDEVVFVLQETSTWDMYPRRRGVLNFQQSFSNDEELPRCNDD
SCMNSSKALIFIDINEAVRLMRDWSRQQQQQRSSDATNKRQSKERERVINFFASVPSPLS
AAAFITSFIHHCACTVEFVPTSPPLDPTLKHSDSMTELAFGETATMTLNDRDELERHSPV
HEQPQATTRRREITRDPNSDNDDYHNADDDCPKVDRHVYKAGHRLDEACTNPQEVPHLAT
ALARQIIAAREENKRRDFLSLPTNESFFTESKDSDEEMAVVWDLGIVWASFAYTIPAVNA
FDTEIISR*
>TCRU_3951 MSP-B, putative
MRHTLLFQVLLLCCVSGSVAVAEHHCISDEVENKVGPRTTAVVLELPTRGGGMMRALTAS
APEWAPIRFQVFTEDLNDPSKHCTAEKQIRPDFIGGTLECNKRDILTKEKRSIIINSLLP
RAFRMHTDRLLVRPLTGRVIVPWYFSGVCAQFTIPSSHHIEGVSGADMYLYVSAGPTQYS
TLAWATTCSQLTDGRPVVGVVNYGPSSVTNSENSVRVSAHEVAHALGFSVWLLQERNMLK
EVLNVRGKAKVLQVSSPKTVEKTREHFNCVNATGMELEDEGGEGTASSHWERRNTKDELM
AGISGIGYYTSLTMAALEDTGFYKANWGMEEPMSWGKNSGCALLTEKCLMNGVNKYSEMF
CTAETGLFLCTSDRLALGYCTIYLYTAELPQQYQYFSNLKLGGSAYAFMDFCPYVQPYSN
TWCSNGEASVMHGSRVGPRSKCLKGDGLVDFMGRIGDVCAEVSCEKGEVSVRYLGDDTWR
QCPEGSSITPTGLFTGGKILCPKYDDVCIIFDPHRGGGDVSSLLSVFPSISVILLVLIFI
SMY*
>TCRU_3952 hypothetical protein, conserved
MQKLLIAINGTTTLRPSAPSKARHKSPPPLPREFGVRPMQQRGLGDPAWKGEPHDAPGEV
ELLLGLRGTQGLMRGIRGWQGFARRIAVAPFGGVLECMLDATPGHSSWMRLGSLFRRRLR
QTPACRQRWEERGTLGVRQSRGIDVHGNSPVDRATAYTQSHGSSGQQKRILER*
>TCRU_3953 Mucin-like glycoprotein, putative
MMMCRLLCALLVLVLCCCPSVCVPTSEGEVVESGSKDGEKGEPGQVTDPQSATSPLPQKG
EEVEGKEEQEANTPTHTSQVTATINGTAESQNTSNNTQDQEHEDGQSTEEGTENTNTNKS
NEQNKESNAPTTTTTTTTTMAPTKTNTTAPKAPSTTTTTTTQAPSTTTTDAPTSTTTRAP
SLLREIDGSLSGSAWVCAPLLLAASALAYTTLG*
>TCRU_3954 RasGEF N-terminal motif/RasGEF domain containing protein, putative
MVMGTSAERGQTRLYVRMEGLPPFALIVSEDLSPEALEYVARQYVRDRYGSGAGTDHLLV
RRINFAGSDKLMDFAKGEKTHSIVKPFVNKTLTGTSTDHVGNNFAFVKTLPAYHGSESPE
AIRGSYRTSDAPVLNENLPEFSEDGGAAAFIPSSTYMSFIGFCRLVRMMTDPHNPQRDLF
TRVVLLTYRQFATPEELLEQLIERYEVPALSMPGENDRSPLVHQFYMELRRDIQRAVFNV
LELWVENYYEDFSNDMLFHRLVAFSKEKIDQSGAPAALLSLMAKGDRTALNSSKPTVLPG
VARGGETPTAVLIQYSPREIAAQLTILTSYVHRQLKGPELLGQRWNTDEASSIRNFIQYR
DFFSCVNNWVSYAVVSERDLSHRSKNLELLMLVCDELIKLRNWDMLVAVHGGMRAPAVKR
LSRTWASLSRETAELFTRLRKMLGSDTDHKTFKETMRKGSRLQFPCVTIFLQEMKVLEES
KCSQEGLVNFGRCLQQYRLLQTLLQGKEVRVDHLMPKNELMGTFSTWVPVDASLLMQLSE
EAEKP*
>TCRU_3955 hypothetical protein, conserved
MAAPSLTGSECDNTNDGKESDEDCGDDLHRGADYLRVLAHESQEGLNAVPTIPGLAQPLA
FAPSPAVISVPSVEADPFAVEFMQQLSSVCAAIPALALSHVSQRCLADDLMCVLSRPPPP

VFFLCPIRNTLRCGGYLFAWPSTHVTMLNGCVFCLAGTRETSVCVDTTAKVFVDGWRRK*
>TCRU_3956 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGAGGRCENSVTASSDSAVNNPIIAPVPTKGGDLPKTNKVED
SKPLEDDDNHDPVNLPEKEICKNDSTKSSKCTESPEVVSASSLDPLAQGEHNKVENSGIP
APSEKGTTLKEQELQGKLQDVETLSRDPATVKEPKIAMPAEHSSSPSPPKATVTASSTDI
SGVGDGTVQRDNMQNTLTGNDGSKSQVAQPDSASSNTPISVDEDTSSNGGAPQVITAANA
DSAGSTKTARNTTNTKNENNGDTDGSPAASPAVGNNTATTTTTTNQDASQYNKDGVKIST
EDVEQNALKTNSDTDSGTTETAAANSEVPTAASNATNKSSNTETTADSDGSTAVSHTTSP
LLPLLVVACAAAAVVAA*
>TCRU_3957 hypothetical protein, conserved
MNLRSLVPSDKQLTEEQQSHIQNLQDEIDEIWSRRGDYKIDDKAWEHMPLFMDTITEKDM
QKNADCAALASIAYDEVPPEDIAESRKQHGNRAIQLALNPEQVNKENLARAAVHSYTEGL
NAKCKDPVLNSQLYANRSLAQYIIQNYGHGLEDAQRAIILNPDYSKAYYRAARCAERVKK
YDLAIDLLSKGRCTNPPPEGIALEEFEELERVCREGMKKFQKKEMKDSIRTRVRAAETSS
LMRALTSYGIRLSPTPEVSSEQMGVYGQHQPYFDAVGLLHVPILFMYDEYQQTDFMQGVT
CDVSTAELLDEIMPFPWDDRGRYRHMNEVVVFFKIDDGVKMAEYYEVDLSWPLMEVFRSE
SYKMPMLLPVLHVVCRSSELLQHWKPQKPR*
>TCRU_3958 POT family, putative
MTVEFAERLGFYGTTFMLMTYCTIMLRWSTSAGNALINALYALTPLSACVSSSVSDGRWG
RPYSLVVFLTTYAVGLSMVALSSFPLMYGEFPLDPSVLGVALFATGILLFALGYGGMKVC
TNPLMADCVSDAYKDNETQCQVVLSQLFRWIYAITNSGSLIGIIVPPLLRSLDGRSVVMG
SVTHTTGYYFGFSLSAVSSILGLSLFVMMYHRFRRNEPSPSTVLLRTFFRAIFIRWCFAV
GRIHDEAFLSAHRWDLIDFAGYSVTAKKSTDTVASHDALSGAPELSVKLRNCTESGSGRE
LNQGREAVATEWNANEAKQDDMPSQSASSDADGLDQTWVANAKMIASVCRALVAMPIYWL
ITNQFSTNMILQAATTGLPSYIPPEVFNNVNVISLLISLLLFDRVVFPFVFVNKTPPVRG
RVVCGFATMIISMFWCGVVQINIDHRGKYDEKDIYHLLPGMTMVSPLWLVPPYIMQGVAS
ALVDTTIMEVVYVAAPTSMKGTMMAFYLMASSLSGFLGLALSPAMRPKNAQIVIFSLTGA
LVLVTVLFYLLNSPTAEAVTEASDGQGTDVAADPYTVSKEEKECLLLKGFSRSENAAYYG
GVLHHREVSHL*
>TCRU_3959 60S ribosomal protein L6, putative
MAPAKKKSATRKVAKKVSRKSPEYTTLRKSCKPGTIAIILAGRFRGRRVVILKQLPRNGP
LVISGPMKYNGVPIRRIDSRYVIATSTKVNIKNVDVSGITPDIFKRPKQEKRVKSEGEFM
GDKAKKAAEQKAKKTAKAAPKGIVSDARAQLQKTVDAALIEAIRKDPLGKEKAGYLHSVF
TIKPGDAPHRMRW*
>TCRU_3960 WD domain, G-beta repeat, putative
MSDSDNDSYDPAENSGTRAVQNLSIPPHFLATVASKSIARDVPASLPQPLAHQVEEATRK
ESTAVSSETVDLKNSLTSLSLRLRGAAGRVSSICLNTLGSTLCSGTEGGSVCMWDFSVPM
ESSALRPTRVLTPFPNRISGFQPVVSVHFASDGSFFVACQDGDSPALIAANGKQLGYCAM
GQRGMVDVLQCKGHRAPVTCSAPSLTDPSKFFTGSQDSTARVWDAASFERQSVYAVKHGS
GQLLENVVVETVAPILSLSNENKSVFATGGEDGLVQLWDTRQKYRPGGALGVLDLYSGHT
GVSAKVKPPNDEMFFEEKHLGGMVEPDTSRPMLCVRRGSEVRVVDLRKMGRSGVIEDVCP
PLTGLPFTTDTTPLVACTSTLYSQEKPSFMTCTSRKGYRQVAGGHVLQFTYMDGGYEPTM
VWRPGASEDDVLSLAIDVKHGQIFAGMQTGDIVGRVKRMAVDSFTNEPTLQTWFATRPER
GRRVVGEKSGRENTNGDDEDDDLVF*
>TCRU_3961 hypothetical protein, conserved
MLEVQSCRGDGQKVNISRSSEAVLGPPPVYDDICRFVAEYAGRLPRNAFTGTAPYEYTGC
DYALILYAIMPSRCIDLSSLCWSTTPLPAQLESNLAVFCEGCCGLQLCDAPLSSLHPHCL
RCSPTCIVHHIKVQHWLFVLSQRFPPEGSFDAVTLRMELRHTQLGEPRLATSHALSSTDV
HIASANGEDDLSLPSLHCHVIWKAPAVAVMENAERGTAAVSEAKTPKKKRGSDDDEIQRK
PWRSAARPWRTASTIKSASQRTERTSLPSQPSSNDCANSSSTICHNLAHQWVESERRRLQ
LKENIAHARQTLQCTLFANGTIDFDDILSILQQKQQ*
>TCRU_3962 hypothetical protein, conserved
MRPRSVARHLLAGVRNPRRWLYAKVVDTMRENTNDVNNVGGASVSKVRGLRPWVWLRLHP
VEKWTTLVDLGRRAPSLLEKSFCVAKGIGKEEGTSVSVVARLFRWRELKMDVAMPQARLS

PLALRRHHLLVQKLPYCLRLRLCLSFLLWVRSLRDVQDTLARLRLPYANTRRVRRSVVAD
VFPTRMMERFVDSFTTVAVKIDSEINATAEQVPAPHAWNPEQEEGAELDEIRRRKLMRKS
VTGSGGRFGRGSGECHGERESLYRPGRNRKDILLAVQDMKARPSDDDRLARRRARNSFRS
FKQSPFVSWARRKTMSCVSPPWSMNDASRSALPFPLAIDHKEDEEYHRNLIRGEGCPIDE
NGRLESVPIHVEVPPAANLLDLERFCVMAHAAVLSSLFVEGRTVCFTTNHSLLMEYVLFL
FEELTEDGWVSVSLCEEPLRPYIPAWSTRETVVVLLPSREENSYRLRDLRNMADMILQYA
PCSVLVEAVPCDQMRFYTKVLMEEVKKQRASVVTPQTEAHWRVSWVPVSHSTTFGSINKN
TNAANDDFQLGVNEILRQFYAVTFIYMPSNCRFTPRQVQDWWWHKLPSNIHIVAVNSHAL
DLLYYFPQAPFLRKKIGNSFRYRAVQRVLLGKNVHGGREDPMRHWVHRWLCLRGPYRTGL
CSAMALKEKARVLLADQENVRVDDDDDEAVDALKWERTVDYLANPSRFHWIALMAAKLFR
V*
>TCRU_3963 hypothetical protein, conserved
MSLFDDDSVSSSSSGCDEMGRMGGNEFLCASVKRDLLHKNGAGGTVNLALGDGVSRFTLT
AEENRQADERRRREAASRSRLHGAQNAEADGGKSVPGESRFYASMAEALQVRRNAREALF
LQRIQKRRQEEAGNSELVEKDLEVGVFVTPQYLAALKRQKHLSVDASHVRAGIDTAGSVE
VTDPLEVYVRQLEEKRLNAAPHFSSTVSAVGGVTADCCRQNEAKAITPAAQENPRLNVGI
DVLPERRNCDSTTHTVLSSSIETPTTVASLPDESGINLRDDDNISRSLTSFSAPLETVSP
EDVIRMARESRKRHRADRHFMTAAADRFNVRALEGIGTG*
>TCRU_3964 hypothetical protein
MPACNSSPEKSKAVLLKKSSQVGAESWPLHTSKLDVSDECFASPLSSVGMAPKPDSESYL
PILSVHCDDLDSVDETPAEQTHAFLENSPLDCGRCNEVFHLENPRAGGVRTPFASTPTMG
HSGTPRSPSSRRLSVMENSHLHRAFSVRLWNHNDSNTANEISLQNAENYFQSRTHPSMIL
RPQSSSPRSARSHGTRSSQMWRGDTIEETLSQSFSPFRSNARMWDPRAPTDIGPFPRSCI
SSRRQSIFPHTGSQAVCASSSSRELDIRPGFPKEEHHSWALTGKKGQALSGDANPLLSGS
MCPEDLSMGQKVLIEKIEQLEMRVEQSERSLAQLVESFEARQAKLEKRLTELQQQTVLVN
LRDGPSPPNSNSPGGTREPSRVRDA*
>TCRU_3965 CYC2-like cyclin, putative
MELSVSPDVQRSKGYVSHSFHNLKVPFTAARADEKAWPEAVFAGGISHDWTSSTGNLPSG
QPLAACGGGKPSNSMKCTLSGSTLTKWKSDSNVAAKLLGNADIMREGVAKTTPVMPIEEV
RRMNRCWGCQVHLRRSECHCHHQDQHHHQQQQQKPSVMSAGNPSNNEILNGHFQSARLSF
FRKTFSSNRSQHHGGNPRHHQAHHYQQHHGSHHNPIHVTGTARRSHRHRGFGAAAVEVIR
NRTLAGNSSPHHKTRSPANKGRKRHGKPCHVNEQEGHTEFLVPLPRSRLSLDGRQESSTP
VDEEVKTKFTASGSELGSGVVGDNTPSAFRLSNIAPFYECAIQQLITICGRRTSNAPEAA
HGISCNENPENLQKPKLSSCLASIRSFDMASSVNLKPFSAPPSKFSLSQHALFTRTLCSS
VGGSMQHGSGMEETSCSSNDMDPAQNEGQQNEEKEIQCVAMASGDAPKLVSEEVKEQETS
PTMVQQLIESIGVYVAYGDAAPMVLIGALVYISRITLQSPSEDVGVTNANWYRLVAIAIL
IATKMYVDGSRKWNERISKATGISLKEVQKLELDFLFLIDFALLIKEEEVETWAEWMESV
ARKRGMSTQLRTFIFGRNSCPPSTATTPLSSFAGEDAFSRSFSHIPSGNLPSTPVSLTPA
NMTPQINAHVSPGTMKSACLSQRLSMSFVLDLAEKHPIPTSHLHPSPSSFHACETPNLFF
PSPMYASLDFHRTERLFSIVHAPEEPSTPVKLLEVSQLFNDAPNSIPFTPPEQETRSPIE
FFKRSFLAEGACNSDTSSGKARCGMDVFQKNTGKNDARRLDFDTFDAFDEEQTPPHRPLN
VLSPPDQLNIALPPRAEYNCFANFKKNNSNRDIPFNNGKTFTVTAPQSLYSFPQTREDKN
VREHATRSSASGSAEKRTPRTKADTTEVTPHVNIKSKYDKLVHAISNVRDLFCVKPLCVR
DTPFNALSVATGGSGTADIGERDMYNNNNNNNNSKDVDDRYVAECDEDEDHDAFLDEFED
DRDNFFLRCRPVLTHSPPA*
>TCRU_3966 60S ribosomal protein L28, putative
MTHSTDLQWLLVRQNSKFLQKRNGIRLSSDPFNNNANWTKRHAGFLNTKAAVVKTKGDRI
LVTTKDGKAGNKPKSMYKKAVMDAGVEASVVSKAVAAVRPDLASIASRRARKMASTLEHM
KKVRAARKERSSKITFQRKAVRPKRH*
>TCRU_3967 hypothetical protein, conserved
MPVGLRECFFSVLALSEGTSLQQNIIRSADALLAGGDENDLIGPLNDAADVTAADLLSPL
LERFEVAIEHLAALWLAAKFWGTSTHRVSMLSLVTDILEAGISREADDYGVALQYATEIV
NRLYKAEMVLLRRSRYVVPCIDGCESRF*
>TCRU_3968 hypothetical protein

MYKKAVMDAGVEASVVSKAVAAVRPDLASIASRRARKMASTLEHMKKVRAARKERSSKIT
FQRKAVRPKRH*
>TCRU_3969 hypothetical protein, conserved
MGYKASPESLQIITSAIARATTVAHRLWAAPPMVRVGVWIDDIRIAVSEGDVALWEAQVL
RNADRRHATMGGDRESGAMQHTFLGVKFDHTHRAVSLSDKFVRSVRAMPVLNSLTIAEME
VVASRFCTRRPFCVRVYATATFSSRQCDDDYPHLTGGLCWRHPRQTFRRQRLIWARDCDT
*
>TCRU_3970 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MVSVRLTAQLKRVKEVLASWKKVDGRVSKLCPSSATVSKPTDTACSDGKITAGLVGFLSG
NLSGNTWKDEYLGVNATVKKGTNGVATGYADGVTFWGAWAEWPVGKQGENQLYHFANYNF
TLLATVSIHNLPKGDTPIPLIGATMNDNKNPVLLGLSYDKEGKSQVLCCDGTTKKIKSTW
EPETTHQVAIVLRNGKQGSAYVDGQRVGDVPCELNNTGSKGISHFYIGGDGGSAGSKEDV
PVTATNVLLYNRPLDDNEIRVLNANKISIPKLTDLKTLAAGATGVGAARHFGANGDGSNV
CGGGLLPLLLLLGLWGVAAS*
>TCRU_3971 Leishmanolysin, putative
MSAREHHDCDDIGGVELQDDDGDGRTLESHLSQRHARDERMAPIGGAGRGTELTLAASAD
LGCLRVNWGMAEPMRWCRKSGCRLLLLRKRSAPNMSEYCYMLCDVGVPVKRCASDRYSRG
WYLGSIHEMPAKRPMDRCPITDPALDVGDIDAVIWEGRIFVCDAWG*
>TCRU_3972 hypothetical protein, conserved
MRHTRKHFKKRGRDDLPMVDMEREVRDVASSNDVRTLVQLFPEEIEFLLMRLPPVTKVED
LDTLSERLSGLGGKEELGFSPLFCPLLIDAACQRGIFPLALSAGGDRYIFAPKLHYHRCL
TQLEPPVEGFPMANDAKEGKFKVGLLQVSKKYLSGRNEMTRARSFDVFINRKEDIAPALS
LIVSQHGENWMCRALRACFVHMFLNQERYRTKIVVVTVRRHCYGADSREKAKTADERVRD
FAEGDHVEEGDLVAAEIGFIAGDIYTSATGAYSLSGSGTLQLAVTGEAMRSVGCKVWDLG
MAMAYKSQVLGCVTFPREKWLRLVREHVADTSLAEKIEGRLREKFSEGVAVRTLLSLADK
*
>TCRU_3973 ribosomal protein L36, putative
MYCCCHVDASAEEESMPARKKEVPKAEAPAPRTGIIAGFNKGHKTTRRARAPSSNDRYAL
PHKKLRAVKAIITDLVGLSPMERRVQELLRVGKDKRALKFCKKRLGNFKAAKKRRAKMEE
ALRHQTKKK*
>TCRU_3974 ADP-ribosylation factor, putative
MGAVMSWFDGLFAKKDATVLMVGLDAAGKTTILWKLKLNEVQQTVPTLGFNVQTVEYKNI
KFHLWDVGGQKLLRSLWKHYYEGANAIIFVIDSNDRDRVWEARQELEKLLQEPLLVGATV
LVLCNKQDLPHRLTPAELVEQLGFRDHSTTGLGAAMRGRQWFVQGCCAHTGDGLFEGLDW
LSSHLPDVS*
>TCRU_3975 hypothetical protein, conserved
MAKSSRSKWKKLHKRQRAQEVAAVVRRRVSRLNDKLRLAAEGGLGAVPMQDPETRFHFLN
PEMDMNVPQNCKGLNNNFQDIVQESLDFSRPLHLQPPRTNFHGKSDPNAPHRMTQQFELL
DASAPVAGHAITVKDVERMAVNKEQEQRPNADHHANEEEGPKGMNNGDGMMEEFVFGCND
AAEETTANTKALLFCVSDAAAVKKKQKSKMAETPQAVPQRICSMAGAAKNGGRFLQVSGN
KKAKRLSNAISTRLVKSGSRAAKKRVTASHE*
>TCRU_3976 Nucleotidyltransferase domain containing protein,
putative
MHQSPGAQNTARCGKADDCKCSANCAGGSSPAVCSMRSHLKAAASHEVIVNQDTHSESSQ
ECEWPSSMVIDDEPGVVVEAERASLPLVRNDKSSSSGKAGKEGMAQSVLSSRKGVVPSAP
LPMFASALPFGSSCEEKTGSPADGEEEVRCWLPGGISGSLPRATLTPSEHVEEVGTGARH
RDPGELVHSSTINASGYNTSDDAHSQTERNRVGLSLELQQLFATGAAAQTQPKHAGIGDD
VPATVSDNNSSRGSSGAAVKRGAKDVVKGTDLLMEAVNGMNAPRPTNRKTPANANSRRLS
SPSSPRKAYLSRDMFAVSQERACETSIAKAGSFIYRNQFIHQIKSAGNTGQTDESNRCEL
NGFSPASNCFVDGNKKDKNEGTNLSGVAADGANSSSCVHARQVTPKRHPSTGNAKSVLPL
PSIDSPRDVAQSGSNNPGRPGAGAPALTSQQLQQSSVLAKNTQKLVSPAIGSSHWPFLPT
PEFVSSLQIYVNTCLGLCESDMQARHNFITRIQRVVTKVLGPHAEVRVHGSITTDLALAS
SDIDLLVVGYEPLTPLQAIQQLSRAILHISEDELQVMESEETGETSAGAAGEGSSHVFVE

VSSGVADEGVLDEKGAPIPSVAELEDVTLGPGGELDAGDPIMRMEEEEAEYRSQIERDYL
LSTRAGITSAAMVNSLPSQGPKKAAMALQGYMGPFAATPLQPPLLRSLVENGIVADLSMP
IHHQPNAGGHRLYVPTLEGPYFQVQTIVSTRVPVIKVTEKATEMRGDITFAGGEHWRSMQ
LTNRLLKRYPASRGLILFLKHCVRQMGIGDSQPGGVTSFAIYLMVLHFFNEISRHLEGIL
QQQQEKQQEREDRDNVVTNSGNEGTTGTSSGTGDGVTSGAHISGTSTPTPGAPMPLASLK
ATAVSLPAPQQRSRFDDRFSLVEMMLLQRVHPYHEEKGGKQNTASILHYIRTFLEEEEVS
VSGDEGGKDRAADLIKERTGAKLVAPLDYDAVSGELASYGQVQQKADVVFAACEALEVPG
LTLEQGENDVNIDYHDGGDDQKAVAELNHVAESKNSDGGGSGCLQEKERDETEDAADSKA
SILRSLALRLLSTSSLGHLFHDFCFYYGFTFDYDNHGLYFDPLGNSSVVPKPRKCQQRGQ
HLYMTSPFDDQYDITARMLHTREFQELCRMFVPLTTPLATISGYGGGGCTLQEVLEWISP
ETAFGELMQVHAAIQQQQHQQQRADVVGTQFSKNEEKATVPPNLSEGGGGTSLAQPPLRC
EVERRDGKSSSPHPTFNSGVEGNLPKDTRLTRRRDTILQKTSGSTTSNELRKKDDRATLE
SNSDVPSATTSLTPSSGGLILTQPGSKTISTEHGTAEMTGGWPATTPSMQRQMKRREGGA
EESAVVSGGGGAAASGTLSSSQPVLAEAAMRPLTPAGASVAPGSLTGSGAPVGGNVSTVG
GEAVYARAQHSRSNPMQHQHQHQQVPFSFPPPIPMFFVPPNGAGAGYPDPSQLYFPMPYP
PEAMLHYYHHNHHYQNHNYMMPFPYLGYEMNQFYQQSAVFDALNAAAAAGGGGGGNSAGG
GPTTNRQGNTRGAGLPSPGARQRARGGAHRGGNSDSVNPGEKVAPGRPAPVALLEEPTAA
AEGMAVDGVNSNNNNTSKNTMMAVLPEGPSTRERQPGVTDVKERLHSEDSSFLAQEVQQH
QQFLQHQQQLQQLHQFSLSHQYHQQQNGLKLRSGGQQHQQAFWGHHPHASLMMQHQMYAL
QSSVDNSVSNALCASIHGGAVFRQQQQNQQHQQQNTSGATYPVAATPFGLSRMPTHDIPT
SNLAVPISNEGQQQQKHREQISTAAHRSEGAAATSGSSSGSSSASRNARGGGTGRPHHRG
QGEDVGEGRVAEIASTEGTHGKNNRPM*
>TCRU_3977 palmitoyl acyltransferase 1, putative
MQVFGARMASRGGRTLPLTYFMQSELTTAEEAPPVDVFTAKLGNRTFHESLRNDSGFAIV
TAFLLGGVDINVRDKNGATPLHVAVSRAAPTPGNDDDESVLLSSEGPNNLIISFLIDNGA
DINSRNATGETPLMIAAATQNISALRIILSRGADTSLRDDIGNTVLHHAACHPHVLQTLH
SWIDDLPAQAARENLLHMVCRQGRGAEFAALFLIEQLGVDVNVREGETAATTGVHDGDHH
YRPIEANTATAAAAVQRCDSAPHSGVIVKEGLTPLHCAVLVGDTLLLRSLLLKGADVEKP
DATGRTPIQLAKDCAMSSSPSLLTSLLSFIRLQCSFLGLTQRNGRTAKNIDPWKVYTILD
AHSKEASSAKREANLQREAAADTSLWRLNTISDILSFGAAAALPHFLMALCALMGMPLWI
LIVFATIELILCNGFKVKDERRLNVRPLRCVGFLVGYTLVLLACSISLEDAMEPRRMNTR
PWLFLCTIGSALCAFLVMWINPGIVDSTDGQRVGIYKTIFYSKGAPPEDVRQGIDLSCMV
KKPLRAQRCRHLGRVVLRYDHYSTWLASAIGGGNHRLYIAFLLFYTVLLGICCRSTYWLS
PNQMSSEMFFDDPHFRRFANVYILFVLPVAFIFSLYTLLQQLWYIARGVTAYDVAQPSRC
PWCFQLGSRTYSLFDAGFWRNVCGFFFLREKFLNISYRMPVMSVRLQKMAKRHQALQLSS
CHDGHCHSHENGGHGHSHNGHLGQLHQYNPEQRCNAPLNTALSNVAEGIGSPATTAVVIN
SSTPASALASDPFPSVAVDTTAAATQLGFEASVGRLFQLMVQHGDTDLTAVAAANEIRAS
VLPEKWQEMVEMAQSMYGFFKSTMNNANN*
>TCRU_3978 hypothetical protein, conserved
MRTFETFLLEAANRAPFLVGEAAPVFVRRQQKRARESDKETGEGETRQLPQEEDIVRLQR
LLVDGPLQPLGLEHAVYHFLLPAFTAAMDAAREVWRTAEALRAAEKATKAKEGDDAMKKE
SEESAGANFDPIGTTTGAETSTQPQPKVEALQRALIAAQATLNAQRQLLDAAEAKLRTIV
EAVMCAFAKPKMSPRDEEA*
>TCRU_3979 Tubulin binding cofactor C, putative
MGTCASSLNAAQDVTSKKSRGRRRPQRKREEKNRPSAVLGENDEANGNVGNARLFFSWKA
APLLFDPASASFFNGKYGEEAVKEAARLRERAPIFEAANLPPHSMFLRLPGEVRGQRITV
HENSYCAILLLDHCDSVSVHGCERCFIFIGPTSGSVFLERCRHCVIVCCCAQLRLRGCRH
LQFSLSVATMPVLEESTGIGVCSLSGWFVYPLMPVHMQRAGLSAFNNFYLTVHDFTPRPV
SKQTGPGCSASGSNGNIYYIHHEVFEGTCWMLWKRLGEHDKEEVMEKALADSVPVAHEDV
ELMLTKKDEASTGVQRDAIQRLLHQPPILSCLPVLPHSTGQPHKNIGQKNSLSQLPVDSN
GLLEMFHHTVVVPFTFGTNRPLPQAVLLGKWEPRLFVVTTANGGATIALRIVREIELSRR
RAFIDRMQRGVVVQEVVDEWSRTEVDGDVLLLNTVELRCTEKLVKVQLEPVLKKVANFSC
NNALVLQKEAATAVQRMIRNACIFILALLRPASKRDGAIRGAQSIFSLAGALPPPPECTG
KTGGSNSSRSDRSPSPRQPQSSESTEDATAWKKSVLLNVPFPMEHLSVLQNDIFLRAPTT

DSGFGYAF*
>TCRU_3980 Zinc finger, C3HC4 type (RING finger)/EF-hand domain containing protein, putative
MTQYRQFTKSQEVDEVIVCLLCKDSWDRPIELGPCGHIFCESCISEYWCRSVGSSCLPGS
ERPVALVCPNCSCAVEQSERPNRVLVNKALEVQVQCTRCNWKGTREQSQNHTCHPQPPSE
KMEVPASTNNTSESDEHRSRLSSHSGGMHLSPEARNMSRANNGFAYQHVSSNDKEWKKYG
LTQMEYDQIVSLFMVFDTENKGFLTRSQLRQLAFSLNYVNRDEHVDRMLFEMGCDETGGL
MIQDLCAWLGKHRPNPQALCGLSRFEYNEALLQFRGYDLEGRGFLDWKDFRNLCLSNGYA
KTEAEAQKIFCSFARTSKNYINLYEFLLFCKHRQFLHGEGTAEAMAPGSRPQRLPHRFPG
AAAAEIAMPFSTKYKKKQYCMLM*
>TCRU_3981 predicted tetratricopeptide repeat protein
MSSLLRNNYALMMFYVRERLWRHAELVCTETIKSTDSWVLRVWRALCYDQQGQSNEALRE
YKAAEQRRETNIPALMGIALIYRRNKDTEGLSSVERSLGDSSHANDVDGWVQAAALAWAA
GDTSGARDILMRFQDGFDEHRDEYTNLATVRAWVDLSTGRGAFLEKSGALLRKVMEMEDQ
DGQTMDLDAAMGRVVFYERKFQFSLAQQLLNKLIVSRPNFTPALVVKARHLMKAEDWDQC
WETTKRILAKEKTNLEALALNTLFLLVKDARYEDAAAQLPRLFEAVKEKEPKNAALFFEY
ARCFSRLSGNYLPLLGVTTQFAEVAHRMASQRGDYFAELGYQQTFRGEYKAAMATFKKAS
STPDSSITPLLGLIRCLILTGDLDEAAKQIEFPNEIQAPNQRNAELSLLNAILQWRRHKN
HAKTIVFLDQAAEAIRQDVGTYQTGMELYIRLNPPLMLDIAKEYMQHCRTEPPDPTVPKA
DPIAEKCRRHLELLLRHVPGCLEAQLLLSRIYFVSGDLNRAQTMITKSIRHVHVLPEAFL
LSAQICQYIGNASLASQALEQALTLDFDMKDQPQYNLLHGIVLGMMNKYQNALEALQLAL
KLTKEKSRVTTKGRPLQPLSLQDHVSLYLQLAQTYLRLRDTEEARATLVEATAMFKETTQ
AGRVAIANAMIAARTDMDKAVEILKQVPPRSEFFTAAKARMANLYLTYRQNRHMYANCFE
ELVEEVPTAQSYFQLGEAYTNIQEPEKAIAAYERAKAMDPENAELAVRIGRALVSTHDYQ
RAVRYYRDAVASDGVNFTVLADLATLYWRLGAPDHAISLLTEAPAHQSEPDVGETVERAI
ERVNCTLLMCKIYRDSQKPDAATEALLRARGFQEHVLHHMMRSETQETIYQQKIVAATIA
LELGGYYASIGDAQRAKEFYQEARMYDESNEEVLLAIARLLLDGGDATACEEQCNAVLRI
SPKSEEAVVILADVMIRQHRFDDAAQHFSQILDETPDNYKALVQYVRLLRHAGRLGDAEK
VLERAEELLPLGQRHPSGLSFARGLYHRYCYENLEALRAFNAARLPVDDSPWSIPALTNM
IEMYLFSSNEELWVDTVLRDEDKNENVRIAERLLLQMPDGESRDILQGYCWMASKKRSLV
ERAIKEFKQICATSETMQQHQGSFNDEKDAKEEEKDEDERLLSDANRPPQASGRLNVPVR
VGLAIAYFIAGLEKKAAAELKRIVYMPFDPITIDAVHRARLLAAHMSILREDLKMAQGIL
QKNIEVNKSCPQTWLMMGSVHEIGMSHDEAAECYENAWKLTKERDPSVGYKLAFHRMKSG
KIVSAIDVCRKVLEVHPSYPKIHEVMDACCSLLRP*
>TCRU_3982 lipid-like atypical dual specificity phosphatase, putative
MTAPLSLSSVLAPRQMPSAIQEPLVPSINFAMVCPGVYRSGYPTRKNFRFLRALRLRTIL
YLCPEEYAESNVKFCEENDIRILRFATEGNKEPFMDISEPLMHRILSALVDTRTHPILIH
CNKGKHRTGAVVACLRLLQGWSLVSIFQEYRCFAGDKARMGDQQYVELYHPIVLVAPAYV
AEWMCITRRVTVVQTEQELLEAESQQLGWSLVAPPPLPPSPPSPQEREKRQQKPKQQEEV
QKQQSQRPPLLPSAAKGTAQSSHREGSGKNAKNDAAKLPVKSSAATATVSSSTSMISIPA
PRRAGGQGESGIDSGKTKETNSIPRKENGDRRVKNDANLQ*
>TCRU_3983 hypothetical protein
MLPPPLPLPAKEAPPPPPLTVKQEPPTPLVAALEEPSECVVPGVSSAVDLDGNSVCECSP
LKASGLTAMGSNECTAGGMIFLSHEGGSDGEQHNIRERSGASLPHDEGDGCTSRSGAGET
PNSSFIIREKLLRLLRGIASSGGEALYGATNPDVAVSGNGNGIPSCYGEEHVILDDLFMH
LLLALEKVVHEFLCRSLTKEWKSKRSKEVSPRSSSEKETARLWTRAWRQAQHRDEEAWIE
WRSALCRSWRRTRRESASRERSEALNIALFQFDPLGGALARSAPSLSRHGIEKQQAEKGA
TSQKLYALLYRVFFTCPALLLDGHTQRLAAAAGLDLNSVRQQICVTEDVGCDYDGDGVAG
FMRNLSCRKQARVDKADLTALDEVERLFASDRRALLCRIELGQSPPLLSSPFTASFPMQP
AGSPHSPRIPSLHARTPKTRSSAASVPQYIEPTPIQLRPPSFAPLDCFSPTARIPDEVRR
QFAGQLASPSNYEQAVCMSDNQPDTLEARKAKQKDGSEGRRAFWPADGRRYVSTSLPSQP
RVLDGAQSERRLPSALRTPRSVSIW*
>TCRU_3984 DENN (AEX-3) domain containing protein, putative

MQPSALAHTISLHRVWFPASESSGNGLGDKLASSAELEPIIVIKEDGDAGKCERQGIIEQ
CALLRSVLGRFCWPLLVKLGNLAAQRHATGRHDLHWVGATSPVAEEGIFVQVPSCHFTSE
CMRAATSGTAMDVIYYNSLGSRWWRDGENKGDSCESIDLESADIFDEGYIYGFAQFVDVG
YATEGLMLSAFSTSPLFNMLRTVVLETVPHLFCAARDFYFDRRTVSRAEEKRTVSAVYAE
VMSPLREIVDTRSAACSTPANRHFYLSFSHTRVSIVRPDDLRYPFVNAPLSTLFLSFSYD
ALRVIHSLLLQERRVVFIGATPQHASACVVSVQAMLSPFIWTLPIVPYMPPEACEILEAL
GDSGFILGSTAEMVPHLMLHSGLSSPQRCSSSNEKVAENERGRIWFADGRTGVVGVSPLD
ADVVPFTMLDLVPPSEKVKEAMKRIVSKEARQLFSVALSSTAAQDLGIGSLWSSTLKQCV
ALADLEEMHGAFLEYSVTRLVGNYRKGLIPASNGIVDAGGSPAHRLRLQGGVAFIIDYTR
FLPYNLENNATLARRIAGTRMFCHWEDTVASLETVGVLRSLVGEFVRSRLRSRQRGPVNS
PPRERETPATHYYLSHPRMLGMLRIFYTRSMRRFPELYSDLQGSDLARLSEGASVFFTTG
NSSTTTKGSSLSCNNGNSSSNSGGKNSMRSFFSKATKAVKNSLASRYNRIPVQVFVQAYG
SFANKTNYEKDPNKPASLSKTFKSNATATAAAFAPTQQLSYPTIPLSPTATAATDVDDDL
CGTCSNLYGAYVEDSDALRSLSTSDDQSTPSVVCRRLPLDVIHQFGRYHTLLDSRTDSMY
TTGGRGGTASGPSVDELKRFLEFGQLFAADSGVWSVLESKRLTLLSMPEEISSPSPEQQQ
QQQPSLLFACNNETNCGGVVFQAQPLPFSMDLVTRAVELPPVPDTLSFNKQSGNATAAMG
GSSDLGSYQGSAGAAGSVMDDFFSFATTHSHSSSESANAFKQLEEFFQ*
>TCRU_3985 spermidine synthase
MPGSELISGGWFREENDQWPGQAMSLRVEKVLYDAPTKFQHLTIFESDPKGPWGTVMALD
GCIQVTDYDEFVYHEVLGHTSLCSHPKPERVLIIGGGDGGVLREVLRHGTVEHCDLVDID
GEVMEQSKQHFPQISRSLADPRATVRVGDGLAFVRQTPDNTYDVVIIDTTDPAGPASKLF
GEAFYKDVLRILKPDGICCNQGESIWLNLELIEKMSRFIRETGFASVQYALMHVPTYPCG
SIGTLVCSKKAGVDVTKPLRPVEDMPFAKDLKYYDSEMHKASFALPRFARHINNSE*
>TCRU_3986 hypothetical protein, conserved
MQKLWGHSQRKELKRNPFEVFRDYKKAASLPPASPSRGVSSDILLTLLLLFSLNAFFLAL
IRRVEYVVAGERKKKQDDEMEGASKVTSHINEREISDGATSLWMVDCDQLMKNTMVLFAS
VLSVVIPICVFSQPSNEVRSIGPAAVLMSIAIGLCVLEVHGGMRSLQAFLNGFQALVFVT
LVFLVTVEKLSPNA*
>TCRU_3987 Mitochondrial carrier protein, putative
MGAGDPRDILIGGVLQCTEAFTLGMPFEVWKTQQISGLAKGQWNSFIVEFKTLCESGWGR
FYHGTGAKMVEAALKGSILLFGTNLTLELEPMLGVNPHGAMGGMLAGFVGGVMQTVVMSP
MTYVVTYKNRNPQYHSMSLFTVLRKAGFRKAYGSAPAMAGRQGTNWALRWFFAVAFTNKY
KELVGRQKLTTPEEIFCGIMGGVLGCINQPFEVVRVLQQARQATGEQGVTTRNCVSYVYK
TYGLKGFYAGIIPRMGLSAWQTLFMVTFAGMIKERLQAISHKVELIKG*
>TCRU_3988 hypothetical protein, conserved
MTMNFGNMTLGGAAATFGGQSNPMCNYTSPLAKKFVYKEMGKVYYPLRRHVFRLKLRTAA
EIRFNEIVKRYMKDKMSFKKGCYAATITNTVELDHMGSIIPKDEYEVRRLTSYMTSKKMS
NDYKKHIQDLWTRVLFVCESSNLVGVTENAMHQNSRPGTDEEFMAVIWYSSFISTFFAFL
VTLCVWWYRYGQAPQYAEVK*
>TCRU_3989 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MKDGRLVFPLEGTTKKEVDTKEDGKAVSLIIYSSDAKNWKLSKGMSAGGCSDPSVVEWEK
DKKLMMMTACDDGRRRVYESDYKGESWTEALGTLSRVWGNKKSGGSGVKMKDGRLVFPLE
GTTKKEVDTKEDGKAVSLIIYSSDAKNWKLSKGMSAGGCSDPSVVEWEKDKKLMMMTACD
DGRRRVYESDYKGESWTEALGTLSRVWGNKKSEVGVRSGFITATIDDDDDNRNVMLVTLP
VYPEKDESKKEKGELHLWLTDNTHIVDIGPVSDDDAAASALLYKGGNNNNEKLIALYEKK
GVEETSSGMVSVLLTAQLQRVKEVLATWKEVDERVSKLCTSSAEKDASSVNACGTTVKIT
DGLVGFLSGNFSESTWSDEYLGVNATVRKKEGAAKNTRETGATKTSDGVKFHGAWAEWPV
GSQGENQLYHFANYKFTLVATVSIDGVPEGDTPIPLMGVKMNDSGKTVFLGLSYNKEKKW
KLSCGGGSIKEHSNTWKTKTSEHVVILLRNGSQGSAYVDGHRVGGDPPCALGNTDSKKIS
HFYIGGDGGAKADSEVQDVSMTVSNVLLYNRPLSSEEVGAFNPNKDSTPPLEKEAAKPSA
VSSGSVVSSFPPVAAAAQKTETSSTAGTQPTEQGQSMGSSGAGNGSASASAVSTVSTSPA
EEESVVQVTSGTSPDGNQTVGGGSTADGEPTMETREGTDVQEEEIHAQHGEVKAAALSSS

LGNVSQRNNSDAGTVCGSGLLPLLLLLGLWVFAAL*
>TCRU_3990 Leishmanolysin, putative
MELEDEGGNETALSHWKRRNAKDELMSSLSGIGYYTALTMAAFEDTGFYKANWGKEEPMS
WGNNSGCALLTEKCVINGVTKYPEMFCTARSSPLSCTSDRLALGCCAMKLYDAPLPPQFQ
YFLNPKLGGSPGFLMDFCPYIRPYAKTWCSNGNATVMRGSRVGPRSKCLKGDGLSDSEGF
IGDVCAEVSCDKGEVSVRHLGDDAWHKCPEGSSITPAGLFTGGRILCPKYDDVCIVIDTI
NGTGDVSSLLSAFPPIPLIMLVLIFISMC*
>TCRU_3991 hypothetical protein, conserved
MGAPNDALALRKDGRVPSFPGANCAHSTVARCANSFPPTVSTARRVGEVAHGITTSAALR
GTHAARPHPDIDDDVPPVPVQKSLLPGPKVLFVCVYRPPFAASLGTPCCIVQSNHVCGIV
LHWAGVRHALSLLSEMPGGMGDPISGHFDSTLNILGPRSGIVIRCPGDPFD*
>TCRU_3992 RNase H, putative
MIPRIRHRRKTLLVVTDSQSLLAALNKGPLSQTDWTEDQIWQRLLTLTRAGWSVHLQFCY
GHCGVHANEPADQYATQTMESGQYTEQGIAPLWHTDLLTCFTTQLTNKWRSTIRQDTHRY
LLCGTRPSDLSGKDLITQEVLHRQELVRLASARCGESELWGRLCWAVRDCTNQCRFCNVS
PEQSAYMRSNNDPTAPGTDTVPPSAREEDVSPVRRRTLTRRRKEKCPHCDSTLTGFSGLV
SHCRSFHPEHPPPLPELKCDFCDMVFPTRRSTAQHRSRCAHNPDATRHRNSSARRRSLLP
QDQPASTSTPIGPQETLHHLLPEFPGTLAVRQRLGIEQDLRLGNFSQWQLLHRRKLLSLL
DHLFGTQMALYS*
>TCRU_3993 Reverse transcriptase (RNA-dependent DNA polymerase),
putative
MHKDGPRLWDDTLVEAERIATDSKARYLQLPTPDREAEMQRTRSQFFLLLRERLRNTYLR
RISKLNPGEPLAWKYISGRKKASLPSPTSMLLGDGQHTYKTARRAANALNRIFFPFHPSH
KAVRFSKGINRQSASLNINASFLFGQQNNNESAATFTSVSSLSSSSEPQVKNEAATTSGL
VAHLHSPLDAPFNRTELLAALRNTPYGKAPGPDEVYSEALRHISSKGLRFLLRCINHSWT
TGTIPVEWRRATIVPLLKPGKSPELLESYRPISLTSIVSKVAEKMVLKRLLWVWTPHPHQ
YAYRSMRTTTMQLAHLIHEVEHNRNHYFQVSLPKKSGIGNQLHYRPHRTLLVLVDFSKAF
DSIDHRVLSRLLANIPGVNCRRWLRNFLCGRYAKTRVGHRHSDRRPMLRGVPQGSVLGPS
LFSLYAHPLLNLLNSFAGVTADMYADDLSIIVKGQSREDAIPTANMVLKKLHAWSQENGL
AIKPSKCEAAWFTLSTHTESDYDREGRWPLVVAGCQIPVMTMGASRTTKLLGMDLDPRLT
LNVAATKQCAATSQRISQLRCIAHKEAGPSPHDLRTFVIGYGAPNYAMAASSYGQWRRIQ
RRMRCRRRTQLWHALSAEFRALSTRNPHCWRLICRRSTSFACARGSQYLRTHAHVRWTGC
GDPRLSHHLAPVSASRHYLGTSYMPS*
>TCRU_3994 hypothetical protein, conserved
MTLVPYTPSEWCDIGARLWDMVCQCGETQVQMTFINGNQLSDETLTVAPSSTGLCLLMDL
SLKHGRVLLSLDILRIYGRLRSLILRQALLPAMGAARELGHQQGLITAERERLNFDYANA
VADVQNRNAQLNSQFQEAHHNLSVRESNIAGAGNQDLEPQQQLEADRAQLREREFNLGRL
TAQLQEREARHNAQQTVRDAETAVRGESPATRHVANDGVTTIPHQTDILMAGGMPSSAAR
HSSAAYRRPHGNVGRPHFHPSTPLPSRTSPLDARLPMEEDRGFCAFDVTTWPSRAWNEGA
SGVIIDLRCAHQCRQQDNEQVKLAFGNLLEWIGALEGGQDPTDRIMNLGRSLLNTFRMQL
TIASDPGIRLSKLRARPHTAVHQTDAYAREAQLFVDRRETQRTLRCQRCHTCGHEAYTCN
ARPRENYNTGVHQKTAEGLLYAPHECWRRQPHHLPSILTGAAPHRRCSIRYFKLPDAIVG
KGNGAYP*
>TCRU_3995 LicD family, putative
MIKGYPKSGETLGLYWTRAIVVVLLGIVVYVAVTYCFHVYYDREAAFRNALTCSMRFLEE
NKIVFWLQNGTLLGSTRLGRLVLWDADLDIGFKRSDDTDKVVAMMNELDSRCFGVVSTVR
VSLQNSVRVFRKCTKRICAEFHETIVNDGVVISVDGSSPEKELFPLQRCTVADVVSHCPH
NAPYYLKEAYGGDWLTRSLTELFQ*
>TCRU_3996 Programmed cell death protein 2, C-terminal putative
domain containing protein, putative
MAMKDAVWLGKPVDVTGEDLCSVYTSRIGGTANLFRETADYSVFRCPKCNSMNTVSLLAQ
IYAPLDVYDRLLYVLTCSTCSTEQSTFCFALRSQNFNPSYKNVSQTNDKGGCEDKRLLFE
ESADWGDGMDKGWDYDYKSVKSNTATEQRGNRSIVNEAIADDICSTEVPSSLAPPGSKPP
IRGMRFPCFTLEVFEEPPKVKPKSAPLNIQLHEAQGKYGEDVVETTVLDEADEPLHEKLL

RKYVERIGRVPSQCVRWGPSREPLQLSVISIVAPRCPYCGKKRRYELQLTSPIIYFLTKS
NEEKKHTLHFGNVLVFTCSGNCNTEAYALEYCFVEGEI*
>TCRU_3997 ankyrin, putative
MNMSLFDSIERQDLAAMQQVFSPTNVNSLNSNGYTPLYYASMKREVGCPTVKKLLSLGAE
VDLKGPDRETPLYIACFNGKIDVVLLLLEYGANVDAKNGNNDETALHVAARTGNCAIIDI
LLRSGANLNAKNVRNETPLYMAAKAGLHDAVYQLLRAGADQNVCDIDGKNPLYVASERGL
KHVVVLLKSKPEDIVIAKARADEELRLRPPPIKSTESILEEAEETVATGRPNRLDYLFPE
PVKEAKPLEIVEIIVPHPKSGSCDPLAVISNGPCRSLEEVGYDEPPAIPKSLKDRPPVKP
ERIGGTSMRIGTGVDTVGTEPPRIGCIPGDTMEFSVPIKL*
>TCRU_3998 hypothetical protein
MREAPKGKREEDKIKFHGKNGEKEDQRGRHCSIGSEKPENGLPLNSVLSQGANRNTAPGL
VRRPPVVKSEVKTSFPAPPKQPFVRPFLPDPGEESALQVGGTPKQLGVTGPVPFRPPQPV
WLNQNGPSPSGPSSDLCHSLLVAENSVAAEKAKEDSAASLGELRNPFLQRWS*
>TCRU_3999 hypothetical protein, conserved
MDIKGGECNWLLLFDIALSHGESIRQQRLRYSGLLTLLRSAGLLGPKTGVYQFLVESLWL
FHGKPLRPNENGDATKGDFPFHDLAVDFDGFLAIMNVVCVRCYQTQRCSELLEEKCPVLD
AIILSSEDQVHLRESVIYTGRRFLKPLISRCLVLKRTVISLSSMKNGWTPYINQLVIHVM
ASSAHSIVLPIFNLYAVDGRIYRGAFEKMLDDVFPNFTPVQQIGARSIFDYPGFFGIHNL
MEYSTLEIPNGKVTALELDSFAEALLMLGVVAFSDEVQYEHHRPFTAKVWSVFEDYYSKF
VGAPMVDDPILDNKYASILPAISLLFPSRVPIDKTSSFIIGGWNLTVDDRSEDSLDLGKD
YPPRIFQFHKINITPDGGNGRRISGPVPATTAGLASTLFGEELNRQFQAEHDVLIYGMRR
CAVYVNEIRVMAFQRGSNRVEVVIPSSMWDISVDTIHVHFVESKDKGKLILSPITKASVS
LRDSSGSTIFSSKDVLFVAAPLVEVIPASHVQELKSLFERHSTEAVMTFEEFSSACIELC
VDTLLAPWGDCSSFLEMYLERKSIEGPSDAGNVTCKKATIHFQEFVSAVATLFLHQLDAD
GYMPNIPYLFGVVLSRLTHNLPPLFEKKKFLGASSTSKEPPKLLQPHNARIDVPYANALR
KKALSINSLSDVKEILKGVGKGRTPMRLLPEFPAEARTVAVVSQYTDDEKGLREKVRTVS
ASLRKAFLKKEMVVLQNGLKAE*
>TCRU_4000 phosphatidylinositol 4-kinase, putative
MKASSNLSLRRRELLERLLDLSTATFDEQVLIVNKLYDTPLPTLEEVLLQVSHVCITHGE
AEVQDLLRNFMLWIAAQSFSAALRLSWTVDSVQKIFGLLGLGDRVKEIRDRIESFAINRR
GNVRDGNDDEVTEAEIMRKELRLKLYNEERQFISIVTHLSSQLCQHPDKRKRQTELKRKL
QEINNSLSTQSIIYPFGGVADPVKWIVNIAVDECVVFSSRERAPFLLRCEVILDDTTSMG
DPVASNLRLPNGSFKIATDFDEVFTPSYAQEGSGDEKDMKTDGVFQGSDRDAFVCAFGES
AEECVARMRKKSVFGKHPNWSVVSVVVKAKDDLRQEELALQLIDIFNKIWEEGGITCSVR
PHRALSVSADSGIMEYLDGACSIDGIKKLCQVSSLAQFFNEAFGPVGSERHSKAEMNFVE
TMAGYSIVSYMLQVKDRHNGNLMISSEGHLVHIDFGFMFATSPGGINFESAPFKLSQELM
EVMGGVGSAAFNYFKLLLYQGMVAVRERADDILGLVSLMTPYNTMSCFGSDPASTVQQLR
SRFRFDLETETDFALHVKELILGSVDNWRTRRYDQFQTLQNGIL*
>TCRU_4001 hypothetical protein
MKDEYDAPLLSRGEFEAIKHDPLLILERGTKAIMSLRQDEAALRAERETIQLHLQDADKD
GGFDSQRYREIMNATAELERDHRMLSVRCTDTELSNKRLAKVVDELRQEKEALREELQTL
KLTQDSLAKQHADTVNQMAVFEKAAPDDAAKMKGLQDAITKKIESLDLLTKEIVSVTNKS
ASLQRKAEQLGCERLVLEAETLALEQTTTQQERTINYLQYESAQLSEAINKRKSELVEVK
KQTAATLLELQLQLTRAEEELTRLNNAVANEKSLTGRQNIWQAKELHAKTEDLLAAHQEM
AKERGEMKNELALVQEKVYRLKNNVLVVEKQNQVLNGTLQMLEEEDQLMKTTYNERKNEA
LEEMNKQSAIVRQLNAELEEARENLYLLNSKVCKACRTAIFPSDLPDPSSRRG*
>TCRU_4002 adenosine kinase, putative
MHNGAAVKLEPKGHAARGLFFGHPLLDMLTSSSVEILASYGICEGSVALAESEQMPIFTT
LLSSENTVYHAGGSAMNTARTVKWICPEMSVCFVGAIGCDRFCEILTRELDAAGVEHLFE
YHEKIPTGVCASLVVHKERSMLASLGAATQLSFEHMKSLEVERAIKNAGFYYTEGFFLNT
ISSPNNIMLVAEHAQREEKLFCLNLNAPYISTAFGDRLRLLLPYADILFGCKEDFFAFSD
MMWGGEVMGDIKAILMRLVQLPKKSVSHPRLVVCTCGGEETLVGSEDGVLAYSVPALDKT
RVVDVTGAGDAFAGGFLAQYLSHSNIDHCVEVGHASAAVVIRQWGANFCESPPQLKAPN*
>TCRU_4003 Domain of unknown function (DUF3336)/Patatin-like

phospholipase, putative
MISQGFLHSLICILRIALDLLCEVAAGVFGIPLGSPTQLVLKKKAQAARTYDEWIIIARQ
LDELDGFQAWRLKGESRFMNFDGLVGRIGLLTTLKRKGDAEVLLAVLSTGLQRSVFGITN
PNLYRYLSGTKAVIEAYNSLLVYLIQKLARDTSVDARKRYSTFMDVARVYGSTALVFHGD
MMLGQFHFGAAKALWKANLLPRFFYGGKTGALVSAFLCCKRNLAEVFDVDEAAFSTFSKA
TLGHFDWRWQRLWNEGYFFNIHVLVNFMREHLGDLTFLEAYQLTGRVLNIEYTPEAVGVS
HKRAPLVRLLNYLTAPSVLVYSAVAASFASMPHFFERYPLLAKDLNGCVLPYDPPVMGCV
GKRSDGKVDGLERLRQLFHIKCFIVSECSFSQLPFLRLAGRTSLPARVWQAFSQEWWHLC
LFFVSFMPFQKYLWAFLSNGDIDAEDVIKVFPAASFSDFITSFQLQPFSLKEFQEHVLRG
ERGLWPFLERIREQLAAEFALNDALMQLRHMDGALSVEDENPYSG*
>TCRU_4004 hypothetical protein, conserved
MPTVNEIQPRSSGSTLYIVRNVQGRQCLAPQSQPDNMSFTFLVKLDPKSGQEFYVNVTTK
AKSWDLPDIDAERAADPSHKDGSEVSPPLQTVEAFGTTYELTQCDGDERYVPKRLPFEPL
PIHCWRPVREASAGRFLYENCETAEKVTKLPPIEYYCDAVRQIYEFYDIEGSYVDAIRRC
FGNENRLVESLSIQYGPRPLRSDEVMELAECYFQRHDKSMLGEMDSLLRQWSGNEIGFVD
ALYKEYGERPRTTRERVRAVYAQYCPSMIFYCDEQVDQYKERDDELIDALEIKFGPEMIK
GEEPLETIMQRVRCQFLKYDPERVADIENILAKHKGAEVQLLELLVCHYGPEVSPEEREK
LLKGQLQTAWNEADYACGDRWEEASNEQPVKETAAAKNGEPTPTSKETGAWNCNSDETNP
GNYNEEELNDFSASVKLFSEEWAPAISRVVTQANSVAMEVQEGVEPDMSRRSSPTVAVDA
SSMSMREANGTMKSLRLASSAARESSSIVSSSFPNADSAWRKHTEILETERRLREQEFQK
QQQCIFFEEEKQAREFEAHQRLLAIERERRSQEEAKRIMEVAQDAAMHAVRELTRLQQLR
DDESGCDERSGDVSRQKEHRQAIEALASANEALMGQLSHTGAQLRDTLASLESYSEINER
LRAENLRVAANFAEMQRQYELELQGMRIYLDDTRVRLAKKISEQEVKMLHLKKEEETTTT
NLLRELEIERNNAAKAKEAWELEKTELRTTIAGLKQQVKTIVEEREHMKSKLNSRDIVLS
ERTKEIEELYDSMKRQRVERIEVASQTEELDLSVVLTEVRASEEPSHTSNALTSLSTHLN
PSVNVSPEANDLQKAYKRSQQTVLELLAVNKKMKTESEKAREFIGILRQRVRSLEATVEK
LELRQLAVPDIPVCATEQDVVVVNLKEDLLKVGSRLLEADAESMRLKREIRDLRSLLSLY
MSNTKKL*
>TCRU_4005 EF hand, putative
MGGRTSELQSQSTPSSLEQNQRLNTKDLEEALDTVFSLGKPRSENGSFALFEFLVDAGKA
MLSPLWSNQEFQEFLQSDFGKFASAQLVRCLDADGDGRVTARDFQIMYDRDIKNLLRHHQ
GTLDRVLPFMGQCAFGFAMGLAAGRMAHRLYQSKTLILSSSVTFYSGLQYLAQFNFVNQN
LLEAAFREKVKQLADVNGDGELNKEDLNFLIENRMRYVATKLGPGGIAPGFMGYATLAIG
ILYGLRRIKI*
>TCRU_4006 hypothetical protein, conserved
MFCPDPYGAMRLMQYNMQRRAVQQMVAETQRQMMQQGCTVPNEMPPSPEGFGNMGGPNSG
WGPCRQRGGSLEPTPAGYFGGFSPAPQFLPNDLENMRIPEERYGNY*
>TCRU_4007 Mucin-like glycoprotein, putative
MMTTCRPLCALLVLALCCCPSVCAAGSTEQPEVKAAVAAISPSLVPEGPRKEIGNSGSLG
NGSGADLGITAVAGPASTAAGPESVGVSNTLQNHGTDGTPGPEISTRQSTEEASQEAEDP
AETTTTTTTHAPTTITTTTTQAPTTNTEAPTTMTTTHAPSRLREADGSLSSSAWVCAPLL
LAASALAYTTLG*
>TCRU_4008 hypothetical protein, conserved
MPQLVGCHTHVSICHQYLLRVKVHGSSKWTTIIQPNAQSRPRGWTRSRKNIGVENHVGAS
HTHHVVLVWDGEVLAHPQSGMRNNDGARHGPHGETLRVQLNGGGESLPQNNLPPLLRQHV
VRPACYCTVIVVNAQIPHRTAVPQRVEHVLRGHLDADRSPAIVPILAGGGVRLHGALSPA
RQVTHHRSRQPAVFLHHRVKPTAVLHGGIGGNANTNATHHHHEPRRQQQRGAAWLAHGSG
TMCLFRRRGQQWY*
>TCRU_4009 retrotransposon hot spot protein, RHS3, putative
MWRCCGRLHVALLRRRWALTASPTGVALRLHGAPTVPLCECHAQRYWDCGTKQPRVSFGA
SGTCWPQLGGASGMLHRTGVVMASRRGISGVGSDAAARHVVGSNQRPQWTMSSSVKDILL
EGSTLRTDMKLNYFLRSNLGGKDVVRRNENVAMEAFVQEPDAYVQDQQLLEEILNLTEYQ
VYKLHHEGVFSLEQWRDYEGKDTVTPLARGKLNAALIQILTERREAKMKFTLSTTIEDVL
FKGKTRVNKMKLNDFLTMELDGRGTLGANRDVLL*

>TCRU_of Trypanosoma cruzi region 5/Dispersed gene family protein.1
Dispersed gene family protein.1
MLSNATWVRNATNPSTVLELAVPVHRGYFIGADETIVIRCDAVAVFGGCKGVLLGSFTIR
SDTLPAAVSALSAVTGVVAGAAAVAVVVTGGLGSVLEMQALGVFARMPCASAQERASTAA
LPYFLSLFAALDPLWMVVGNALLAAVFGCVHYGVTAAFQRWRGVDAATAWAAMRFPSLTY
VVAHAMHLGIFFGSVLALAMPGARVQHRVVGVVGVLYGVAFPAGVCYLIARHVGASFTRY
WQFSRKPLHERLLYPVGYWHPAAQQRMYGGMLTNMRGGRVYWCVFQLSVLCVVCLIAAVH
PPVGGCHVQYFCMAAVLLAGASVVAFTNTMRSAFLTVMHATSFVLLAALCVVSAANHLAP
SDGGARAYAAIVLLLTTVLLAVTVYSVVVWYAEDHHWQELREPRRGGLEALLRDDEESDE
ETQKLHDMASSSYASGTTVASSYRPPALP*
>TCRU_4011 hypothetical protein, conserved
MGQSNGAKHVELKSNNIPGYEENAPESTNIEDLIKGGRYKVATRETLDMMSAIQGPKDEG
KIYPDSDVKDIKQYIIEQEGLSVGQTKRRALSQQWRFFLSSEPVQRGLDAGIIAGSFSAA
IFALKSPRNRVPAKIGLVFTLGFCVGVIAVPMMVITADGYNSRRIKALEKELFLKQREEF
YNKGKTDA*
>TCRU_4012 hypothetical protein, conserved
MAANCEGLSSENTALRVECEAQEAEIAQLRNFLQFSVTKPDVYPGQQRVTLSKGLNVFPE
KAWQQLSTDTPHVDDAVVISALEGQLNEKNRQLNACLKEIAELKSYLKEDASGRTNTQDE
NTSHLLSQISFLHNEVERLEQQVATVRADSTREAHTLAIEFNEKLGQKEKESRATTEKLR
ARKKRNVDGEDLLVRCKTLENQLAIALSEKNSLLVEKNEHCTTIRKLEAALKERKYEVLE
VQKMASNECVASGIQIKSLQEVIQVLSDERSALQKQLVQLRGELNVEKLHAEIQVGKNLL
TASTQMEPLQVAEKECQVNSVLFTAEYEAQSVQSLKHMLELKCTECDDLRVRLDALSLAH
RETLSALEITKKSLEEEIEGRKFLSDDAEKLSLQVRSLQQKCSQQALSERELQARINQME
EQKRQLRLNFTSIERDKGVLEERLQQNEKDMEQLLANKNYCNQQVGQLAHENERLLAEVQ
RLHQREVQLAYSLKAKDGELREILSAYQNAVKEAESQVEAQRSIERELEAIRATLASKEQ
CILYLQEQLNQLHHRDQQLSLDLQTFEYENGQLHRRLVQTEALVTQFEAKCNDLQQVSLA
KDKTTEELQQSLAELSKQVALKENECMLLRHRSESIQYDLSRLQSVYESESYRLRELENT
NARLVVRGVMIGDSDERLNPFREELEVTKEKLREKSMALQRLKDQLQKEKEERMKCIEEL
GAVQTSLEEALLSKERLQQVVLDQAATLSHLSQ*
>TCRU_4013 hypothetical protein, conserved
MVLVISVVPNEEGRAVDRRHERYQLSALKGNIAVFYDSRRGPPDPEVACSLSQDTSPDEA
PAQPFFVCSFDAIWDALQEDKSSTKVSDADVMEVLMADVGARVAARENVTIINRGAHAHQ
FVEKILRSLQKRIEESAENAMQVVADELAKEKQMQRLLQLENENNMQVVKEYVKSRNEFT
KPARTAIKLSPKLLRNLRQLRKRNLHFLVSEQNAAGRFTVLTAAYRGELVPPCIKGSCLT
PQSFKIKPPPRVPTSPQSSRRQKCSTPRNSYLGSRMQRRPTLSTLELLGEVNEEVVVEPL
KGNGWGKEIHFYVFDGKTSLLGLPGIPKFENVIKGFTVDFWFRIDSKEPENKRVFLHIMD
GQRADIGQLFQISYNCYDQMFEAICIYVRDSTNRVLECLMPLKLDASSEEGEEHFHHFLL
NVQSLEEGNLECLFDGQTTALQIVQQEYPVIFNAWPHRLFVGGYMDAFNRPTCVFHGTIF
EVRFGLNTTDGPQTIVRWPLLADGEKLKEVMNTTPGEHHETLLNLEKEVGCPPRTAPSLD
GNLVVTLGPLGVLGELLCNWRLEIRFRTNVSNRTMSLIGVTDKQCRMQELGIVMNAEPVF
GRERFRFHEYNITLYLVDAFGACCSALLRGSEHQNVMDGQWHTLVWKCIDSEANTYRVKV
DGVLQELLYLVREGPRRFLPFVDWICLGGHNTRSYKVQRPFYGEIGRFFISVRGIPLATL
NMDEGPGAYVLQDTSGRYNHGLLISPLTKAVRRHDVYWFPHMEDIASEGDDFLGKDRIII
HKNNVVSLAAIVFTCEFAPSGVAREVLYDVLGETCVEPRVVENHISDLRPQWKTWRALPE
SCFRTVDTLVQLEETINSTLACEKPPGHFMFVIRIGDCHVTLLNLHGPVLPSDATYNRSI
LRWQYAYAISGTKGRREILLNQMIQGVESILLRDTLTPFVTKRLGPLNVNEQSIVTEDII
RSMQNSGKPWFLSAVLHNHLLNAEYGSHIHIFHHLKDRMTVDEAASVALFNRKLLNETKK
KASLVIQRNWRAREARIEVMRLRCEREIRERKVEEINSLRMNPIMKAKETLTALLITLHQ
IDCEAIPPITDEIDELSEILSKHGYAVTYLPNASRTTLMKALSELDEDTSSFVYISGYGG
LMNVRQPPLISLHSLYISITEGAGRATLEEECGGAYRRMMQAFRDERPPPKVRKGKRKTN
RSQPSKKALQEAELAARQRDELFRMAIAEIEKEETFTREATAEEYDKEVLMIIREIKLAT
EATNEYERTYKRDSGGMHFVLPCEARLIEPYANTVYGVEELMNIALERQISPLGLQRIVA
IDLEPITPMSCGSAWVASSTGYTLKFPYQPQQRRIMSHLLCKAFDGRMPCVSAHFRYAVL
KGGIETNSDERDWRSFATYLVSKMQSVCSKAALTELREELDREVPFVAELIPVRGIVLDL

DTRERLRRERDSKEVHVVLRYGVGSSHVQPDMFAVFKNVITVGVPLREIAFKNTIYILFT
RCNKGIDGLLMEPLLKEIESCRPIGCNVPISVTTTALGVRLFFDNKDPENKLHVSQWANG
IVVRSLSWQLPVNSLLGYRILEVDHVEYLYEVKITCSLRNLNRLKKQQRQQPVPMPYSRF
LACEVLPNPS*
>TCRU_4014 hypothetical protein, conserved
MKLVRRARKSIRERRMKACLKDLSANLEKVEMRVFRQQKKERDRRRKVAGINCGIPPDVR
MGKMNPELYRIECRLYREAGLLPPPPPEGCAQESSSGVTRRIGFVDFNTIAQAVLRRSQS
LL*
>TCRU_4015 cytochrome b5, putative
MQNIISFAEAAKHTKEDDLWLIVNKKVYDITKFVDQHPGGVDTLTGAAGKDGTDDFNSVG
HSDSAKKEMEKYYIGELDPNDAEKLKAPLKTSAGNTTAIAIVVALIALCAYLIFFP*
>TCRU_4016 Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MDTAVRGELASTLLYSEGNLHLLQAKGDCEGSAISLSRLTEELKKINSVLKTWTQKDVFF
SKLSIPTACLVAVLSNASASDGRWYDEYLCLNATVTNATKVKDGFQLTEPDSRVIWPVNI
PDDNVRHISLSHNFTLVASVTIEEAPTADAPLLGATLGDTNSPLTMGVLYTADKEWVTMF
KCKKTTKSGTWEPKKEYQVALILQGKKRSVYVDGKSLGEEETILTGETPLEYVELCFGAC
GGHAGQKTGVEEDKKSSSVTVRNVFLYNRPLGADELRMVKKSDGSMHGGVSRALLLLGMW
GIAALY*
>TCRU_4017 BNR repeat-like domain/Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MLVTLPVYSNKEDNPKGVLHLWLTDNTHIVDIGLVSEKEEDVTASALLYKSGAIKTDNNK
EKLIALYEKKKGDGDTPSLGMVSVLLTEQLQRVNEVLATWKKVDDRVSKLCPSESDRPTE
NDCSAGKITDGLVGFLSGNFSNDTWRDEYLGVNATVTKKDGTAAKATLHARGVKFTGRGA
GAEWPVGSQGENQLYHFANYNFTLLATVSIHGVPRGDTSIPLMGAKMDDSENTVLLGLSY
NKEGKRAVLCSGQTTTEHSRTWEPQKQYQVAIVLQNGNQGSAYVDGQRVGDAHLDLKDIK
GSKGISHFYIGGDGDNKVGDEVVSVTVRNVLLYNRPLTSEEIDALNPNKAPISPPEDITA
AMVDTPSTAVSGPVAQKTVSVSTPGGSTVKHESSASSGEDEGTVGGTDAQKEEVHPQAGE
VNATALNSSLGNVSQENNSDGGNVRGSGLLPSLLLLLGLWVFAAL*
>TCRU_4018 hypothetical protein, conserved
MGETLANSLLYSDGALHFSRESIVGTRWSISLARLTEELNTIRSVLRTWAQLDAPFSKSS
TPTAGLVGFLSDASSGDVTWIDDYRCVNASVTKASKVTNGFQFTGRSLGQHGP*
>TCRU_4019 Protein of unknown function (DUF3676), putative
MNDTSSTVLFALSYTHDRKWLAIAEDAGGVEDLFGWEPHTTYQAVLRMTLDEWTAFVDQR
EIDRKSYNEDLFDSHRISHFYIGGDSNDRSATGGHVTVTNVMLYNDDLYNNELYELNASK
VNIPSLGVEEHPTGQVTSTEVSVVPESKSEEITASCAELNEDDPEKQEEETASMIRCLQR
PLPRLTRDHLFLSLPSQRRAQE*
>TCRU_4020 nucleoside 2-deoxyribosyltransferase
MSGVYIAGPAVFDVCTGAACQDRVRTALWVHGAVPLIPADNVAPGAGEMRVKKMEMVRRC
DAVIADLRLFCLDGPDCGAAFEVGHAAALGMTVPTFAFDWRSMREKYGGACDASVLTVED
FGLSFSLMLCDGAEAFDSFDAALHHFLRHSSEWRGCDCGDVREARVNALGPGGILCTAWR
ASPTQWPADIPCRVSQQQGRRLAPCGTAESGVCAAEFCLFSAFSAAFVWAGDVVLLPTRR
VSLFFLFWL*
>TCRU_4021 hypothetical protein, conserved
MPNTLNDNDGSESRAAQPDSASGSTQISVVEKTSSNGGAPQVSTAANADSAGSTTTALNT
TNTKKDNNDDNDSSLAASPAVGTNTATTTTTTTQDASEYNKDGVKRSTEDVKKNASKTNS
NADSGTTENAAANSEVPTAASNATNIKAIQRPQQTVTAAPRHEKSHQNNTVRRMGTKDRP
PQTRPSGSL*
>TCRU_4022 hypothetical protein
MLPGKIGLNRLLHHQRRPFFPSDVAIFTCVFQGMFLLPVDCHLKLCTLPCLPPTPIDLQK
CHCVIHAHNFGLRAGTGRDVRNLRWILRKSFRHGRIRLGFLEICLQRCNLPPPFLQFRRG
ILNKVARDGHLEIFRDHFHVQRGIIQLDKLSTVHFEKVSYFQHPAQTGVKQRANIVALLW
LQLGVVHGSKSLRRAQVLNVER*

>TCRU_4023 phospholipid-transporting ATPase 1-like protein, putative
MVYGKVRGCAWCSGCKREEDELEDDEQVEVVVHMNDRKANAPYNYPDNFIRTTQYTLLTF
LPLGLLMQFRKVSNFYFLICMILALIPGVSPISPATAIAPLVFVIGVAMIKEAVEEFKRH
RADRKANSILVDVLVNGKLEKVASRDLRAGDIVRVHNGEEVRADVFYLSSHTEEGQVFID
TCNLDGETSLKGRKSIEVTRSLCSPEGLNAAQITMYTVPPEPGLLAWTGRIEIDGKDYAV
DINQFLYRGCILRKTDWLWGFVIYAGVDTKMFRNLRKRPPKSSDLDLKLNILIIIVFVLQ
NVFLFLLCSLSVWWNGRHKNHWYIRWYLESHGKAAQWFLSYLTYFVLLSYLIPISLFVTI
ELCKVIQAYWIRRDNKMMEIVNGRWRRCKPNTSNLNEQLAMVRYIFTDKTGTLTENAMKF
KMGDIKGHLIYNENHSFSLELLQRQGVIRTAAEEYFLALAICHTIQPFPDANAPLGVVYE
GGSPDEVALVTTAAEHGFRLLERNSRCLTVEVEGERRVYDILATLEFTPERKMMSIIVQE
RNTERIILFTKGADSSVGSRTADEEDVQEYMQILSQSLLDMAEHGLRTLLIATRDLTSEM
FSEWNTRFLAAGKVLVRRNEAVDRLCGEIEQELRLLGATAIEDKLQEEVPETVSFFREAG
VMMWMLTGDKRETAVTIAATSSLLDPRRDYVVHVDLGSLDPKDPEAIEKIGADLHQVELH
LESGRREGVRCTLVIDGTSLGVVMEHYFELFVRLSKCVSSAVCCRLTPLQKAEIVRMFQK
STGFTALAIGDGANDVSMIQEARLGIGIIGLEGAQAALAADYAIPRFRDLLRLCAVHGRY
SLVRNASCIVVSFYKNFTLSFMQLIFAFYCGFSGLTFFDGWFLTFYNVMMTSIPPFFMGI
FERDLPSEVLTHRPDLFTPLSHGLYFSCVVFLRWFLEAAFHACVIFYVIYPTMVNGDYNR
QDDIYGIMVGSMSLFVLVSVVLGRFALQIRYWQLLQVLGITLSVIVVFAFFTIYSAFTRI
GDLSTYWQSYVLMSGAKFWLYQLLLFGSLIFIIDLTVLCFQKNLWPTPRDLAEREHLMLL
ESRRRKREPADQISNLGVV*
>TCRU_4024 RNA-binding protein 34, putative
MTVRLFVSRLSKSVPAKEVEEFLAKLFPEAVHIQLLQGSHSGTHKGHAYVHFSDEATAAD
VLRRLGEGPTPTFHELSIHVKRASRLDTGENNLFTPQPLPPQLAHYAYSVCATVSSSVVD
TLDGVVARCELSDGVTAVAFASEAQMTAALENYRENAAKCLPPLLPELLSSRIMRKRRRS
DEDGGENHCRDDLNESRNSGVDSVNDGPHTLENGADLVAAYERRGFVPLAPAVALTLLRD
FMEGRGRVALKDQKGHMAVMTLPAHAMALE*
>TCRU_4025 Calcineurin-like phosphoesterase, putative
MEGLPECQSVVAFALDENGEERHTDDPDKATQGNGKKELGRLMSDGSPLGTSSAGTLSPR
SLLFSAPPRKGIFLELIDSILRSGTSSPVSQAANKPMDDGRPLSADVEARRFFTTEVVDQ
LCDEVRAVLEMEKTLLNLQLKEKETLVVAGDIHGDLNALLSHILPEQSDKQLNVDGLDRK
FLFLGDYVDRGPCGVEVVLLLFALKVEYPQLIHILRGNHEEPQTSRIYGFYSEVNLKFGC
DAPWVRFNEVFCYLPLAAVVTTPRIRFFATHGGLSPPLSEAFDIVNTIERIDYGSVLDNV
LSEVVDGLLWSDPTEVIPYFERNVRGCGYMFGIRATQEFCQVNHFDFICRAHQVVSQGYN
WSHEKKVLTLFSVPNYCGFNNNLGAIMIMHVSGAGKEEEEEPRFKQFKSAVESGACSPQT
PKPCGEFVFAAFME*
>TCRU_4026 ubiquitin-conjugating enzyme, putative
MVEVPRNFRLLEELEAGEKGTGSNQNVSVGISGTDDIYLHHWNGTIVGPAGTTFENRILS
LEIFCDEDYPNRPPHIKFVSRVNLPCVNADGTVDKTKFHIFKNWERRYTMENCLAELRRE
MAQPANKKLPQPEEGSKY*
>TCRU_4027 hypothetical protein, conserved
MRVWRVSGRALRRCVGLRCVSSSPFPLPPPTTTVRSKGYGPTKDLLKGVDISKRLVVETE
LHPADAELQRRVLSLSAADVSVRTPLEGEVNFVDSGAIPQQEEIVSISSEQLASVATVIV
EQVKEKLELSSYTSEAAQDARSSGVVNAVADCLRQEMERLSATLQTQEVSFSRMLGENSD
VICARIASVIQKERSLAAANLRKTETKHLSSFTQEVTSAVANLETSLKKTLGETIAAKNK
KMEPIFEDVCLHVVGAIEQASRTQQEQLAISLQDVLERTVISAVSPDKSLNLEAIQGIVQ
HAMERVVEGTQNKVQELLKDIRKHFKKSTISVGDASDEKQLELEGLLNSYGERLEELRES
TAGLTDVKELLMEVHSLQQTNEVAVQEVRDSIKRLKKDLMGVLRGATSPPVVEAVAEDKN
GMFAEYCDKLADVADRVTSTVEQQLKKQSLDVKELLTQVRTLEKTFGETKKSALVSIPSM
QELDDDRMVTLAQSISDSILASLPPREALPKPAPAFTKEDLVEAVSAVLGPKLDELAAAV
AKMETPRPSTVTVSDVDEGTTGLGEQQLITLAQTIAESVRDVVQDVVPAKELMESLTSRE
NDAALMARLESLKETIIATVQEEMGRTHEVDLTPFQNYLDQVLAGVQEAISKQQEATQVK
VESVVETLLGQLQKQQKLLVEEERARQRSSDDDARPSIFTAEELATLNNRLLGEINEMLT
SNSTSLLSSLEAVQREVRATADRLPENFETRLSSVENSIHESYAAGKDHNASVKTALKDI
QAGVETIKGGNDAAVQVLTSINKAVSDLAQSSTASVDGIKEQLSATENRTEALYTKMTSD

LSHHFSQLQTEVQDGRRRIEELISSQVEYKGVSTSVEAMRLKLEEVSRLLENMKTSVFNS
PPSEPQHRPPPPQEQQQQQQQTVSGEFIESQLKNLSVVTQEILSEVQKYRSAQEAPAPA
DATSTKENLEAMEVRLNERLQGLYSKLNEMTQADADAAAVELPSEEVPSNQGSVSEDVSQ
HLKNVDILIKHLQTSRSAQVKQMREKLIVLRSFLATGGLNREEGSTIKTILGALDAHRLK
LREEAAGAEAALVKDVNDALQQTLERLFSSSEQTVAESTKHQLQQLQSDLDAKSERIETQ
QRHVASQLNDRLNNLEKLQEGHTVVLTKEIQNGHKEWRDVLNLAIKQEMPTALQGVIVEA
CTEPLRSVRDKLDKRDTREEQRAATLLSRVQEVSRDVSKLGGLGAEMQAAVSRSSATIIE
EILRKQEGLAERFEGHVSTMVRKEFSNVSSHIVTGTPFSTTMVTASTPLSLWWLCVLSFV
VFATIIACAYFIFAAFLVAFVPVPPPEGFLANAGIKPVGPDDTADLPKKFSSSRVVDQVM
E*
>TCRU_4028 hypothetical protein, conserved
MMMMMMMTGRVLLVCALCVLWCGLPGIAADGVGVVSDGSADEDLLLQWRAWLRRESAEEV
SRRTGGRENASVVEECAHQGMDGVRAVVDGRRRWRRQHSAVAAAVGNGDVITDKDGQARN
KEVLPPEIKDEKPVASGQESTDATRGKDQTTQNPSAAIVSRTKLISDQKQEEGERMTEKE
DGGNEDEEAEEEAKIRETPLVVPPPPAAAGGGIKPPSGASGPAAPGAILTSRSSSGVDSS
SRIGDEGSTVGISPNAVGKPSRQDKVPEAKENQHARPHDGVAADTLNNGLEQNGSAPTSG
QNENEVATLVAGGSRSSGEQITVKGGSEASRTDESSADPNTKLQESEKTPLKPSHAAATE
PKTQKEVLTSVKEETKSKSTDASANLADAPKSSEEHPASAATTMQSTSTGSQEAAATPSS
NRIPPLHEETTTGTNITENAQPPKETPVTATAMKNTTVTTGDGDGSTAVSHTTSPLLLLL
VFACAAAAAVVAA*
>TCRU_4029 hypothetical protein, conserved
MQPLPSCSISDTRYSLPGSHVLLGVVFVPSNTVSHVLFMPYDKPNNLPAETVLQTRTQQR
SALLRNMVDGHRRHNSESVVCKAVLVIILPAVHRPCCPGPRSREFEPVFDLRCLLRSCIH
AALIVDPRVVTGRIGQSCHQTRRGYGRLGEEGVQSRPSTEGGIDRIQLISQAGK*
>TCRU_4030 hypothetical protein
MAYALQPSSHDVEEQSSLNVIPKVRRSPNRPTKNPYETSSNQQHSAEYANGGETTLQTSH
VRTNTWLSRGNTVSQVTVGCSGMTVGSGVHEQQPSLRIGVVPEETDKMRDRMFNSNGNSP
YFSPDAWQGPVQPPAPVSGSKTWTNRPYLSVTVAPQIGDSFDRKLSCVAFDTATDPYADP
GLARDHSGIQTPQQQSEMTAPSAPKYLRQTPVENNHHKYAKYPSRVPNQNTNSFYGTEQT
GQTQNAGGGGWGYRAPESDIYGGNYPGQGYYSPSPHHSYQQHYPNRYQQQQQHQQQQQQQ
QQMPPSYCNPQQDHQNWRTGNDARYGYNDPNNFFLTPGSSKYPGGGGKNMPMMHSYNNSS
NPQLTNSPSPMQQWSDGPVEHSMSNMSGMESGSQRTPSSYSTSNNNSLARCVPPGPMARV
GVPPNVTSSLGANYGGMSANWRAHSRYPNNPQQQSQQHTVPPAYRPGDVGGGSPGPYQQT
NLTGRRPDHPDNLGNDQYYGHAQVNREFAAHQTTTNAPSYSQQPG*
>TCRU_4031 SLACS reverse transcriptase, putative
MVLGPVLFSIGTIATLRQLESSFSNASFTAYLDDVTVAAPPGMLGKVCEATSRAMRALGI
ETNEDKTEVLNKGGPVDMPAEYIRPFARVLGAGVANDPESELITQFVQRKAEETDRLFRA
IVELPFAKHTQWRLLSVSALPRVTFLLRTHAPAHTRAAAEWFDDRVTGVLGVIMDGPVTK
RARDIAALPVRRGGCGLRRQREIAEFAYACLGEKGKQRALTDELDAKHQSDLYETLQGPD
RKVFVSNTAAGAGRPLTDPQVHADDRGFSTYLRERLLVRVLPEGQKCVCGADASNEHVHT
CTRLQQNPRTTRHDMINMTFANGLRLCGFQCGMEPRLTEASRRRPDILIVGLDTYAITDV
TVTYAGRVTAYVSEESMEEADPLRAARDRLTQKRQKYRHWALANGLDFEPFVMLTNGAIH
PASRRWLRRILGNQDHRLTITNAYDSIVADTLAAMLRGNVHVFSAACGRAGPG*
>TCRU_4032 hypothetical protein, conserved
MMTGRVLLVCALCVLWCGAGGRCDEGLVESDDVSGSDADLPLASKQLEKPPQDTQGLHGR
VPGANENVPPASPEPGEEEDDVDDDDSEETEAQEESIEGQNGQGGTTAIGSDSMEENLIG
SEKKTGQAIVPAKDISPSDSQESNANPTQTEVEGKKETDKSRPAAKNALRPGKGENTLSG
GIAEGNLPPSPEDGVDFHEQDGEYTTSEDEQNAPPPETAATPQSHRGEGSGRTGEDTKAT
TVTTNTTDTTNTQNNDGSTAVSHTTSPLLLLLVVACAAAAVVAA*
>TCRU_4033 NADH-cytochrome b5 reductase-like protein
MGSRGAEGGGGPSSDSSWFGDGSHRASRWQKRQSQRGTPRWSYELQDIPKRVRKILNDVN
VGYAARLLLTCGVAGGVVSVLYYAFFVRLQESRPLAKRSRFAPLVPVTLIEKDKVNGSSM
VVLRFALPNSYDYCGYEPVSSVRVTSGTVRGMGSVSRWYTPISHPEQRGIVEFAIKDRDP
GVMSARLRYLERGDRVYLGRWMKEFPYKKNTYGELGLISTTSGASIALQLMKVLDSDKSD

RTKLYFLYCHHTAKDIPFRETFDAYARRNPDRISSNYNVFSLAKQTRAQDVRLGENFFLG
NIDPTIVEKALPPPAIVDPATGNIVRPKILICGPQSMLLPLCGRVSTIGNYSYWQGPFYK
YCGFLRDMGYTRSQVYKFGVSTKMLAYQ*
>TCRU_4034 ATG16/SAP18/CVT11/APG16, putative
MNAWAAVIDRQILQRNAAEIQLTECVFDAHKITQNQLLRLQQRYQEIVDDNGRLDEKCKA
LMQHVRTLELAAAGVLTSTAREGELEAKVAELQKQLQDNITQEKDYYKNLYEAKRLTDEN
KALQEEITRLKEQEAQRENVLRMLKNDYAALKQENSVVRPKLNTLISERDRCVKELLTAK
DTIARMQDTILEYEDRWNQMQKEKRNSGIGFVMGATYSDPNFGDSVRGSCAVKDPAATLR
DVSSALEVPVPTAQAYAINEAHGDRLLYATCAADGGKLLISGGGDRMIRHWDYSTGKALR
SHPCTDVPLCVDSTSHYLLAGCADGVARFWDTHALRTVELTGHREKVVAAYLSQSAHNAF
TASSDRTIKLWDVRKSTIQRTIMCSSSCNDICVGGSLIFSAHYNGSIWVWDRRTNDHGTE
IKHAHQKGVTCVRLDPSGQRCVSLGRDGAVSVRDVREMSRELLRIEDYGICCSTNLARLA
VSPDGALCALGNIQGEVLFVSLNTGRVLQERLVGGHVKAVHSVVWALCGSTPMLASIGED
KRIVAWK*
>TCRU_4035 Sec20, putative
MLDLPDSGDGALPTEFMVALERRAAVAVTDLNRTLKAHQESHSQRTHGALVLAVAAAQRV
VKLLATVKEQQPLSRHSAAAPVSLLVQLETHRIAIRRLLPAAVAAAETKRSDGAADTVNA
LRSLLHTRSLLNLELRKVQGAVDELAGSSVPLEMLQGTLQDVNATVEVAQRLVRKLLSVK
SKDDLVLRISVAIFLIVVAYILAQRLFGFFPTQIC*
>TCRU_4036 hypothetical protein, conserved
MIRPTRWQPEKKGDEAGIRSPHASFLDSPVNLTLTSQTARTQRTVPPEAEKGMGSNTLPS
IYEAKPMKATYPLRYNQTGMGEEKAKTTNLKTVTPSATTTEPYDMTHCRPKLMQRVAAHL
ARVAIDRQSNVFPLVINNPETNEPRLMPEEEKHFAPEKKILMAPALGIAAGVNVIGGHSQ
CFVMSRKEANWRMQEERESNRLIFSWWEARNACRRNEEEIAVMEGELRDPLWSFFRNSIT
EEEAQCLIELKETKTPTSGQMLLKPTGAKTKCGVDLNGGGSSSLAFVPASSDRGILMSFE
LYERLFFRVLSRVNRHFLTLLRCRATGAAEAPETLLDSRSQGHNYVQFLLQSQLEMMEAG
KSLSSGNDPKELCLPVVSIPEERCFRPMLEAETSFAVTLLWRILEQVRSMLPGTALALQL
YVRYVLPHVYENFAFYEQQLPKAGAIGEQVEQLHALPLNLVRHRAMTVATKQAKDDVHYM
EGFLKSWAWRTWRRSVVGQRQRERAMKLLEARFKRLYKAIWLQKCFDGWRLAAKEGRFVA
QLDVIDVSYKSFLSGARHAAREVQLFPELGESLTSGSSTALDKNKFFAMKLAETAQHTKA
KKKSVSLVEAESAEKQVENQRAENKESASSSNSFFAPGTKRKSVLIKMALEEPPAPPPPK
DLKEETSDEMSEADEVAPKKATFITSVPRGVREGKEASPLQNRAITTFEGMLQKLQEMEM
ISGYLREEIAIQNKLIQKLERENRSLKSKTRDLELSLFNSEEERLQYSNLLQEKELDIRE
LARRITQLKSRLRCQMHRPWQRTVMRVIGELCGASTSVSERSDDLHVARKMVASAAHKRS
NNNDSSNYVETVATGSSELRASRNTAPSRVAEEDSMVENDENSSISSTGHSATAEPGTDE
ERLFGKIAPLVIVSTRDMPDAQTILRDWANGCLEDLESLDDLKGGTLSARFNQFSDEVRN
GVLFSRLLFYLALPRYQNKTAVAQAGTEETKNKASSQLSFTLHRQQLLMQKNVQLETPFP
TYSECFGDLLNLKPSGRMSLLLQFATELMEGQEQLGDEYIKKQMALIREAAVKATEMVPL
PSVDRVEMLEIIDPYALSRGDRSATITFIALLYVRFSHPFNHKARQSAMIEREAILYLLS
GGTYSLQDQKSIAEVSKEPESKEQRSTEDEEFSIARRFLTQLEEEDHTPWQLFLSHCKPL
INTMAHPFVLRGNFWPSVAFNSPELAQMLGSLGLALNRSLEVHRWHIIVSCLVPVKTFSG
LSRGTFTGSRASPVALQAGLEREGEWVFAMEMPCVQEMFEQREAVVREAIQAGTLVKSGT
GEGHEWKDGSEFIALDKTRLLSSIGTCVNDLLQLFLQRGSFSGSCAMPALDLGSWRLLWI
DLGLVNPEDTEKSILDLEQITRIFCSVTSIVVESRKEARTSDPSADAWGPQQLPTFAGVL
YFSEFLVAVVLLAHEMFPPLGDKIKLNEGGVVWLADALSNLVFRYIGPILMKNAAEDPVR
VIRSFRANVKTEQVLIRHNKALLLIFNTYCKDICGVSGMERESLLQMLRDAMLTSTDISQ
TLIYELFMPFSVTRKADEGSKEERRREQDARPRDLTVQRRRGNVNILDPNSDVQSQTGKS
REVSVLLYDGFIEFLCVLCHFKQPNPLIPFDQRLEIFLRRGLLRPLAQRNDALSAIMSLE
RRSFKQEA*
>TCRU_4037 hypothetical protein, conserved
MTILSRPIPSKSFRSWRITAGNFEKRLCVQERTVEGLSKNKRIAHRLIYKETDFLRYRII
FSYNTSDYEMDPVKRHVAVKKTSRSSRIVLAVANSLQEIMCDWDTITLLFKDRSLATMSD
LLAADCWKRLHESLSDTSTLTEASKAETEQNLFSESSVIKDVKCISSSHSGESGQENGLS
YDMQQKQQLSFDAQDMCFIRIMSLWSWLHPLDTFVYLSLLIFALGCGAMRFFSFFLISLG

AGFTYPFRPMSREELQEFEERLCQLESYLGWRSPRHVVSTIISFALVKQVMLVLFPQLNL
MDALESVLLPSLVSLLLYRGISQLFCGVKLRVPVSAAAGTAFEEPVCPNTPCVVNDVNEE
NGFLMSNDAEGTPATLDAHEKALHDELLPEGPFSEIITRCVKFASVSNGWATREKRRSGA
VVFEKKSNYSGKTAVLVVANIPHANAGTLQHLLLDDPDFEDDKGSYAYKYDSLLEKRASV
KALGINERLVLTRYKTLQWGVAPREVLTWVSCANLFTPSQQEALGIRPDNGKGLLAFSQS
GVACLDDFVTLPPSIASDRHERAVSHIYHIMGLEEADGSLTLHLCHDVDPKGNISGTFQF
YANKQHVKKTEAMMRLISEIGPKPNIVRPYVNARDFIPLINRPVPRINKKLNGETPTCEH
TRELPPADTVPDPEAERIVKSVVEGLLPRQWKLVLDKKGISLWSTVLPWCDKKAMKTVTF
VPGATPRDLESVLTDMSIGKRLARGVESRGEIKKVSDSISIFRTTFSSPVSGIDPREMVT
REVTCYYPSLAECTALGIPCIDGAKEGSIFLHVGEDATEELPPNPKYQRGRVFMSLVMAE
EMEDKRGVRGIRVTRSASVDPGGSIPTAIVDGVLFMQWQEAARLADCIKEVAAARLKSL*
>TCRU_4038 DNA repair and recombination helicase protein PIF2
MCGSVALRYQRREMTTNDRHVADGTNPTAPMQVESPRKQPQQGAQETRKQGERKERPRLI
CLAWRARDPVSVGARDNGKSGNLRNCSDTADLVNASGGGCHLPLVTGFVESHGCVVAHNG
TRQVREHQQINEKRVDEGSCQLKKATSLNVSLAECNQREKLGRMPSSSFPHTVAKAIGRG
DHDGDALVYNIFTHRVVKRSAASVRALGMLGIGVYQDSQELDVVDPAALLKLRSKLLNKE
VSWPALWRNTLFRQLQHVLLRRTGRDEEFVVEEVRCLLRTHYQRAKTRRGVGVVSNENNV
GATDGPFSNEVSLGSSMSLQERLLTYQDLNEEQQRVVDFVLEGHNTYIGGGAGTGKSLLL
RVIKQELVRQGLSVAMTATTGIAATRIDGVTLHHCFGVNIHGECSRRAELRAFDVIILDE
VSMLSRELFESLEYQLRRANGVDLPFGGVQMILSGDFLQLGAIASLSIVHSAVFRRYFAM
LKLQQPVRQLGNDHFLRQLHELRRGIVPHDLQDTVTFLSPTESAKALMKDEESSVKLLPT
NKEVDAINQAELKKLSGELVVFPAQLQSPSLSGRWTATYMLAIEHEDPNSSDRDKLLMSL
EQYVFEFVNKVPNASSLTISLLGQRHVVLYKLFVDAFAFRVRIPHELNEKDEHELACHLR
NLESWLPAQGLGVRLREIIVSPDGLHTDADEYALTRYANNSPMMLPLCLKKGAKVMLRTN
LSPGLVNGSLGVVVGFKELKMGNLPQFLTKYGRLDAVDGYSEFLQYEHSFPVALAPEVDF
GGGRVIVIPPTTFCVGGLSNTNHYYMGIVALPLSLAYAFTVHKVQGLTLVGRVHLELSRM
WPCEHLLYVAMSRVRNPEQLTVSSFHRDLVRCATECLLFDESLPPVGAVRVLPHFFQATW
RRVPSRRKSVLRQKQVSRERAKRHHASMPTGTSRRRLSGARIVR*
>TCRU_4039 14-3-3 protein 2
MSSFTVPEKREQLIIMAKLAEQCERYDEILVCMKRVVKLNPVLSSEERNLLSVAYKNVIG
ARRACWRSITALEQKEDIKKEKNITLIKGFKRQIEKELSDVCSDILELIEEHLLPNASTE
ETKVYYLKMKGDYHRYYAEIETNTEEQKNKALEAYTQAMQYNSSLKPTSPIRLGLALNFS
VFYYEILKSPDRGCQLARQAFEEALSDPSVLDEEQHKEAALIMQLLRDNLALWTEDAHPE
GHDDGTAMEELE*
>TCRU_4040 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWWGTPGGRCDEGGTGGTPPGASASDVVGNGSQESPPIAQGGSH
TPGLEAPGIKNKNEDPDDEQLLTEDEEEEEEEEESSDEEDEDEDRDRRLQISGKEGIPTT
PPPGGGGGGKSEAAGGKLEKVNEDGPKPEKQHPVESAAQKTSEKETVDAGEAGVNQQNEG
SRLKPQENPNPVQEEDTRNGEGHQQTQEKEQQTNVEEITPHNPAGDHSSGEHNGNDGSKE
MEEGEEGGVEDHERHRAQEREEAAHVSGAPKVNSADIQQEVQRTHAGGTLTGIKQKTGEE
EDDETEEEREQQKEQNQENPPGKEQETKTGANATNQINTTPGDSDSSTAVSHTTSPLLLL
VVVACAAAAAVVAA*
>TCRU_4041 hypothetical protein, conserved
MSGDKPSSWCLDTLPNNTTDARDPEETHLSAALHAALRCLGMQLHLEVTEKDNVRWSHAR
TERRALGPLDPTTMGKAICRDHAQVCTIPATSGSLLPVVPWSGDVREHVEQDGLTGIY*
>TCRU_family, putative Se.1
MEHGVRLLEDPMTPRQPIMSSPAPYFFAVEDASVSRVVEDWTAKVSYRDAHNFALGCIPY
RRLQQLEWTRIAPRAMRFKEMVLDFAAPEVLVFHLSMQNGFPQLLSPLSPPN*
>TCRU_4043 hypothetical protein, conserved
MISSEYVLATRGARSFSKGRPQTLSHCAHYYFNYLCSRGEDCSFIHAIYVDPTISEVCKR
AAGRSHRQRVPGALRSSVESADSDSQLQCSRQRKKCGVPPEIPVTIDARNCRGDGVMAPT
VNAEGLNSWAGLNGPSEASSEGPRHSSSGEEGTLEPLVGLKCREPNGVQMIGSACGRAAM
RRARVYRHDPYGIF*
>TCRU_4044 hypothetical protein, conserved

MGLSCSHNNRWETTFEGKTTTRSSTWVSKKECQVALMLQGNKASVDVDGQSMEEEEVPLT
GERPPEVLRFCFGACGGHESHATVKNVFLYNRPLNFTATRAPKDRVPVPTREAAPTLLEE
SRVVDTVREHVAGDITEEK*
>TCRU_4045 BNR repeat-like domain containing protein, putative
MEDGTLVFPLMAKNEAEDVYSMIVHSTDSGSIWTLCEDISPANCTEPRVTEWEESLLMSV
DFEDDERVYGSRDMGTAWTEAIGKLSAVWVNARSGVSQKENLRVYALITATIEEGRSCRT
LREGTPRGRKGPLRSTFGSRTTTARFLLDRLAWTMLRISCSPALCCTRWRFASFTTEGQR
*
>TCRU_4046 hypothetical protein, conserved
MNAGDCGPIRPSQAARRAADAPPSADGPPDLSNCPTQSSRRAMELIRQRRSTVVRRNTDI
PALGLLYEESERGVPRDLGAGNVGAENVSSWAIHDLMPHARTADERGELCGLFDDNIRCG
AIDPTAVRQDAVVHFGNESNPAGHGDSGVTKIAARSETKQARPVTKEEMDQLIRSRTDWR
ERVVLRLAWITASRWSEIAALIPNSFTLEADGALILDWPVAPKTARADPHRAPRFVRIRG
QDALDTTKSSRILRLPNPNEPWPLGMPRRIPQNALRHAAQIVETDDLDPHVISQLAKHVN
PFDLPQNTVRYLGKHTTVLTQVSSLVALM*
>TCRU_4047 hypothetical protein, conserved
MAGGEPSSAARRSSAAYRRPHGNVGRPHFHPSTPLPSRTSPLDAQLPMEEDRSFCALDVT
TWPSRIWNEGASGVIIDLRCAHQCWQQDDEQVKLAFDILFEWIGVLEGWQDPTDRIMNLG
RSLLNTFRMQLTIASDPGIRLSKLRARLHTAVHQTDAYAGAAQLFADRRETQRTLRCQLC
HTYGHEVSTCNVRSRGN*
>TCRU_subunit mitochondrial RNA binding complex.1
MLSALSTAAPAAIASAVATRPAPLDHIFQRCKLNLVEFTAQDIYQVCTTAYNMDTIGMTQ
DPDFMRGIHDAFRRSDQTVLSPFQANLIADTFRKVGIISTPNEVAVPEEEAVSPESLIMV
LRTMNITKQRDERKMNTVLKLMFPILDEFSPTQLSLTVTELARLKCTNTDFLGKLAKRII
EFNDDLSPLDISLTAKSLAYCPGVSHNILRRVFQIVEERMSEFQPEDYVNVLHALNALGS
KFLMTFRRLVECGLEHVENMDAVTLTNYLVCFSTMDYRQLEHVEIYADALVEVATDLSER
DLVQAFIALQSLQLLSDTMFGTMASCAMRYAPKIDPRNIAPIMDICSTVPHPSEPLMKAL
LDRAMECTRILTPNQLGEILNLIGLYPPAREHPLVQMFGKQARLRLDLMGPDALAGATRG
LANLGYADPEFYIQAAETGFRYGFKDWSLLEPILMGLSITAQCSPTMVRVLGSHLAPMAR
SMSLLEIERANRYMKRLGCEDDFVYKAMASRVLQFVKEITPDMPEELQILLQRGAVEPST
APGVM*
>TCRU_4049 UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase,
putative
MGVHIGTSSFEDKGLPGSTFMVGWCYTLSRDVAEALVSYKPLRRLAYLPYSKERDHEFAL
LRFHYEDNMVAWVLEKEVKYKPMVYVKVLGCHFHDARNGTGHSQVVPTSMCVHHVQEDDY
AALMARFGNDTSPVARVERASEDVIYPSCD*
>TCRU_4050 UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase,
putative
MAKKKLPTLKRKLRRVAVLLILFIAVTNLLSLSFVPADDDVAPAPNNLRYPRASAVDDAA
LAYIPRRVVDTWSRREYLIVLGIPSTDDEARRTRRNLQRTTCWRFPGVATRANEFTGAML
VLYVLGRNPSHGYDYSAALLEEASQWNDVVALPMNEGRVTTNKKIGHYGCLGDEADVALT
RKVYMWFDLAPRIFPNAS*
>TCRU_4051 Endonuclease/Exonuclease/phosphatase family, putative
MEPFTWLPAERYFYPLLNSIGAYQRYTYRLRAVCDAQRQKLLLSGDIEQNPGPIAVLQMN
VSCLTPSKLATLMAQGADIIAIQESWKSSEQIASMHTGDYVLHAQSRIGKGGGVAVLVRK
TPRSKRIPLTIPQHDTSLEVVVVQVALDQNRDLIVASAYTRPPPQVTQPFRRLVNCLPAS
SPLLLCGISTCITHSGSHSWRLLQARLPQNF*
>TCRU_4052 hypothetical protein, conserved
MFGRCDHAGDPSVCELCEVGCRLGFRTTSSVPGHAAVTNDKLRPCARSSARRAEQECPES
TMYRDRCRERTRFWSAVRREREPVKVDTIHGALPVRRMLLNGFLVPRCGAMHSALRLRGI
RSAPAPGNVDRRSIQVQHRRCSQLDAEFHEAACPSFAAFSSGCGDVISCLFFVVFFVVFF
*
>TCRU_4053 hypothetical protein, conserved
MLSLFAVEVTYLIVPAMVIFVMFVAPIPGLSHYVSRAVSFVERLNFHGVSLLLLVTLVTF

VSFVVQLVDWRKKYSQGKPRFADLSLEVDWEAKKWRFERNMYIHALATVLCASIMKFSRL
YTALEKYSTAAVGAKKNR*
>TCRU_4054 MORN repeat/Kinesin motor domain containing protein, putative
MLNDIETMNLLKFTSSEEMTISMDSNKEVGGEDKVELQFPGGSKYIGSMRNGCLSGYGTY
YYASTGDKYDGHWKAGMKHGCGTYYYASGDRYVGSWYMGKKHYRGIYTFSNGDEYNGFWK
YDKIHGYGVFTIQSNGNRYEGHWKETYRHGHGVFYHGNGDVYDGNWVRGKEEGLGILIKG
TGNAYCGEWKNGEMDGKGVLRDQQFLFAVEYAKGHLVSQVPIVEGKKLQEEWSRAYDHYV
TFMGKYQRHGDKDAIEKDELRRALEKLKIESATWQRRYEELRGERSTARRRSSSVPGDEG
KRLLLPNILKVPSVKAKLRPGVAAEGATRVSSLTRASFKIADEAPATPGMTNVRRKEISP
VLPKADLDGVDCNGKEVRHVGVKKGCRATSSRSSESATPKKRNVELTEKDRELDVEHHTT
MAWEKDQLKRTIPSNLVKQEEAGQQCAEATVSEGEASGEATNFRDFGQQFETTVAERTRY
DDSCGPEKNQAQSVGNLNKRLEEVNRMNAELNLCCDALGRKLNEQRDRYQKLVNKTTATG
DGELLEVLKTDIQRLESQLKNAEEELRTQKAEIDSRGTRCIELESMLLNIARKRTTDPSI
LHSLSKKMDLARSLQESNAELARLLEESNMKLEIIMSENKNAEGQRHSAEDSASALGEEL
RRVRKELRKEQHKSKRILADRESVVAELHDADIKLVGAECALKALQGYLTITIRVHGCKE
GYSVPCIRINERDSSQIVFSEESTTQMHQFDICIDEETSLDVIFREVCRNMFTVTMGFHV
AYVTLGAIYTGKTVIFDTFVPLAINTLCNHSQRFPVDKYALTYKVGALAIGACGAIDCET
GSTVTEIRRDAYGFTVPIGVTFVETTGADILSTVERLRKRKPRDLRCHIWIQIQCVILHR
VRQTSTVGRLTLVDLCGPGPLPTQKEAVASARFANRSFGHIVAVLESLQDSQGVVQYNKS
LETALLSDVLGGNALTTIFGTLSSAVESVSESRQTLRALTMASKVVNRPILPRFVSSDEL
RWREVVAATSSAEVASPCLLEVDELRDM*
>TCRU_4055 3'-5' exonuclease, putative
MVCPAPPRQLVVVDPAWVRVDEENYNAAWKQLEEEAMECGFIGFDMEWTSRPKPVLEEGE
ETTVENSNAGTAADARDRVRVRSAHSVEPVAVVQLSTFSVTFVVRLCDIVCMARPENCIG
VSEAAAVSSTLGVVLDNLTSLLANKRVAKVGVGIIGDQEKLQRDYTAFRLCPCVELAVLA
RHLFPTAEDLMGLRSLKDFAARFAGRKLKKDILVTCSDWGSSLGALSPLQLEYAAADAEA
SFDVCLGMCRESHLIASDNIDDNDESHGISGARDVRCNVNSILQSLDGLKATTFRNARVE
KPAGNRRAAWWCKGRTKPYYDNIFVYDAEMRLVFTVDKSKAEWYVYKKGLGKVIEWRETA
AEETQKTEKEIAAIQLNFSPDLSKYNDAHIRRNLDYFRQAKENQCVVCGEKKDLVRFAVV
PLAYRKYFPSVYMSHNSYDLLLLCTVCFARARRLYDEERRRVAVDFGVPLGHLTPKELEL
HRAQLQQQMSTNISNDGSAVENIARSRSNSSSRRSNNNNTATSDRKYLLSPAQKMRIMQE
YLEIEKHREVLLKIFKYAKALRVAYEEPTVAAGCIEEDEGVNQTAAVNEKPAKPSVMPPG
RARQLATYMRLHAQRYPFAKCASERIALFTADAASKESVRCILEEGISPRVVLTRFWLRE
HPKLREMFSCTTRRSERHEDGGSPGPHENGERLEENLFVDSHGFLIVQALLEKYHTDACK
CRDHAIGEFIYRWRTAFLQGMRPRHLPSGWSAEDGILL*
>TCRU_4056 protein associated with differentiation 3, putative
MSKLEGTNTEPENDAHDAHARNKNVADLVVVEALHDNREPLSEAKRFSIVSVAVFGSIAA
SFAHFFNLFSGELEKKYHLTQRDLSTVGTVGTVFCYFTLPYGFIYDHFGPVPLFCIAAVF
FPLGSLLMALSFNGYIYGTVVRISVFNAILNIGTIMFDIAIQMTMLSIFPSSRGAIVAVA
KTFNGLGSPIVGTIQLAFFNGHPDRFFYFLMVLVVVIAVGCMFVIRLPHYHLTGYQRSHL
SEEEKKKRLATRGQYLRQKTPIPRFAIAIFFEIILIVYLPLEGALVSYLKLGQRYRLAFA
LTTIVLVCVPPIIMPLPLRILDREWWSNWRRRRCQHDKEMAKSNANNPNERAEPFETLME
NGSTSEDARVGVETDVDYIAPQYQTTFLQSLCTPRLWGVLWTLFATVGAETVLMLNASYI
FAALSGEPVSPSLRILLTVLDGVGSAVGRLLMSAFEVWSQKKKPEERIPMTAALFVPSFI
MVVVLVLILTVPKVALPLPYVLGSLANGLRAGVIVLMIRTIYAKDVAKHYNFCFLSTVFS
TILLNRFAYGEWYTREAEKVGTLVCLQRRCVLMPLLLMLGINCTSFISSVYVHISYLRFS
RRTLAERRRIKEEARQQAADICIDHSENGKK*
>TCRU_4057 hypothetical protein
MIEPRRWPLAEAWHDRVSRPPLQPPLRGPGLPFTSPLSRADVLDDGGRRAGRRIYLKNHG
KKQQQQKAVGAGSLSHGGTGRSARAYTLLQATPGRCRGVSSYRTQEARTRRTAFALLEGL
SALRGSHRTHHGSGVLAFGATFGDAPIHRVGRAGVVMERRREQRRTRRV*
>TCRU_4058 hypothetical protein, conserved
MNAHEGAEVTFALPFHISQYFSELWDETAALVELDASFYRQLAWRICTGEFRLSSGTCGS

CGIDSPPHGPRVLSGSSPHHREGLGGKPRDGKTAVCGAARGKGSCLDLQYPNQRAAEERG
SAGPMCGQEVAPTGEQEALAKWCESIGVSFSRETKSAALRHDAKTRIEGGRASPNTCS*
>TCRU_4059 BNR repeat-like domain containing protein, putative
MSRRVFTFAVLLLVVLMCCAICGAVQADEDLSAVPKYQLEEIADGNLESFGIPGLLKVGS
GVFAVAEAQCKKKDGETVFTGIASQLLTIKGDNTPEEALKKARVIQVLEKGAPTSKRVDV
SRPTAAVKGNDIYMLVGKYSRNGGQESGADDWGLLMVKGTVSDKESNKQIDWKDTNAVPK
TPLGEQPSSLTGLIGGGGSGVKMKDGTLVFPLEGTKEKDDNGKDGKTTTVSLLLYSSDTA
SCTLSKGMSADGCSDPSVVEWEDKLMMMTACGDGRRRVYVSGDKGDSWTEALGTLSRVWG
NKKGNEKGVGNGFTTATFGAGGEQKNVMLVTLPVYPKENKRANSIFG*
>TCRU_4060 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MVPNASKKRPSFANGPRILVVLNASGIMSVNCGGREHVAADNTDEVSEHDATGRKSLVLE
NGVAGSGFVAEGDAYGLSQRNASGHDNKPQLREFTAQYSVNGVSPDDCFALRNDAKSTLR
ELTVDGTVRVCVYWVLLLLLGLCGVVTVL*
>TCRU_4061 hypothetical protein, conserved
MVMCRVFFVVLVLALLCCCSCVFAVEEGEEQEPQVTQVNAVCAGKDKLGRWQLRGKSLWY
NCTDAVPGVGQMICGMGFGNCESEASQSRTRGVAKDGVFTINVDMPTPEILESWWKRNVE
PKAATVASVPAKTPEAEPPSPQEDKDSRESSSRTDSDSSPAGAVGAAGSPSPPPATPGGA
GANSAAVAAATTNPSAAASQASDSVPSGELQSPSHSASAAASPAPESPPDPKPTEGGDHS
SHDPPVELQEETAAAPPTQLSQTGEDGGAAEGAEEDTAANTTDTASGEVNSTAASMPAPL
SSAPTTNALEKSVGTDACFHGTRPLNRLLLVLAALTYGTLG*
>TCRU_4062 hypothetical protein
MGRIETESNNSGEVQQAASEGACLLESTTPTRRLELGGESADVDTNAVVRRAWEKDITAF
LASQSHTLFARDPLLELKLDDSPDGIARREQAGVSSTASPLSAASPMSAWRRRSELQDDV
RTGERRHHTGDPAESRLLLYSPLRCAAEEEEEQVIIGRDVTYPDNDVLGLHSLGQAVTGM
EHCFSTPRLIPTPETHTSRRQAASQVTTGCAVGLAAQALSPVQQANNVPFRSWKSREQQK
VGAVAVSTGGALPEAVDGGCAGRASLSQGAAKEALGPFPKDDVMGQGDLGEGGKEDAFAL
PLPLSTRKSGGCDDEDAPLFCRVTPVGRRCAVG*
>TCRU_4063 Leishmanolysin, putative
MNGVVSSAHGNAVAEEVVPAAVKLHADRLLVQPLEGSLVVPSLATGSVCSRFTVPAEHCS
AGAANSDTVQYVAAAPGGVWALPCATLEDGRPVAGAMNIARPLCFTDASPPASPRT*
>TCRU_4064 retrotransposon hot spot protein, RHS3, putative
MVLASEKGWPYSRDTIQDLPKDVFVNWEVERLWQIVRNDLTAWFSPHGGTDFKSERRVLI
GTPGIGKSMAAGSYLLYQLLRCDVEKLQVVAYCFGITMYVFDKITKTVTRYSDEDMCVSE
LRRLRGHGRNVYIIYGVAKEGTPPPKHFAPTSGWGMIAVLLPRVANYDEWAKQTKARRII
VNCPDEMDVKAMCAWITRDGRRLFFRLNWRMVKERMDNVGPIPRHIFDANKFIAHSAAIE
DALDGIKSRDGERHFTHGGVRLWDTENPPQRVVRVVRGRGEVGAEGFLNAPISVCLGRRI
PQYLGKRDECEGYFFSLAIAGEEEYSFV*
>TCRU_4065 expression site-associated gene 3 (ESAG3)-like protein
MNQNFKRTFLLLQFFLVLALLIAASNWEKDSSLILSETLVKDNVQFVKAESESERPRVVF
LVIQTRKSPGWCRMLLSSLLSEVSVVSIGFGKRYNHAKRPLWILDYIDNEGLRDEDVVVA
FDGGDAFITGSFQVKQAVDRFLEATAPTAAVFNVTAVHRGEATAPLLFSSERLCFAPLMK
ILISSGPQKRARKCVWYYSKVWEAMNASADQGMVPFTSAKGLFLNAGGMVGRVWAIREAL
KAYKKVLGLTDQWWCDQSIWALLYVWSLTRTTNVSPDFRIPYGILNLDYHHNFFQCPYGE
VVAHPAIIHLSGAQRNWAALMPELMNHATWFSNLKSSLQMTRDGLTQLSNLFVKIVTCDG
ETRFRRFGALCSPRKVIDPDWLLSPLRK*
>TCRU_4066 SET domain containing protein, putative
MWRHLLRRLGVAVHPALQREVSRAKDVYGIFCDANSVGLDEGELLCFVPFYHCIAANIAA
ASPWGPTLMGGVSSYTVAVDGVQVEYPKLSAVTTVFCALVLLLEECSLNSYLHWISIEQE
IDADTQRRLGRSAHAKIKIIKGLNKSIIGVLCEDMSKLGWNIPVEVMSLAHGICSSRCVD
VPRSNEVFGGPAFVPFVDLINHDDDEPNVAVCVDTMHSLRTLLRRSKTFPQVFEDDISVD
HCPFYVLVRAAKNIAASEELHYRYLDPHDALAGDPLFWASRFHFCPEPH*
>TCRU_4067 hypothetical protein, conserved
MHTLFDSDDEVQGAVPTNPERRERGGGWQPPPSPWGTDPLGAKKNLRGRDGVANEGEKVQ

TGASQPRQKQAHASLPTTSVFSVETHPVTAPFYNPTSVVDAVPQPPQQAETVTQQLPLQP
PCLPPTSQVVVDAGGRLPEMPEISFSLSPLRVRSPGNPPEVKYMPCPKCGSKKDHLKTSD
DTVVWDAFLELRRKTEESVSRMSSFYDQVVKLQLTHEQEAASYRDASETMINQQRKALDA
LSFEYKDLQSTNENVKGLLAKKSQQLIEFENANYSLSMRLREAEQRVAHVNDRATVAETG
RMMAEIRIKELEASLEHATEMARDLRRRISESNREQECALQEQYTVFEENRRDIIHYYDE
REKDILRGFKEAVTNIQQVMIKKMKEREEQLSKFWQGVMEFEHQQQNEVLKQMKLLKEKE
EKDNQENVLRIEQDKERWFDQCRNEMNLLEQRHNEREQHLLMDIARRERELGEREQRMRL
QHAQEEQEAKVALASKEVELKTYYQKLTEDMRVSFDREREKLTASFREQIQELSHLHMNN
ERELERMHRDKEREMAQRYRIAGYEMDDRKGEVNLRGASLQAQSALFSKFDAIEARQRER
AEKARAAFQASAPTNASHSTYEKDKE*
>TCRU_4068 heat shock protein DNAJ, putative
MFGFSDEVGSMINAFFGGMPDGLHHVGGRRRNQKASYALPVTLSDLYNGKTFELPHSRAV
ACPNCEGRGTNSRKNNVCRSCRGNGSRLIVRQMGMMMQQMSAPCDACGGSGLKVDPKDVC
TACHGQRTTEVESFLTVPVERGMRHHDEVVFRGEGSCDPYTGEPGDIVIVLEQVKDERFV
REEDDLHMNHTITLAESLCGFQFVFKHLDGRELIVRRERGEITQPGEVKVVLGEGMPRRQ
RPGQHGDLVIKFNVTFPNRLESSQVDALRKALPPPKSVDLHQCDDAEVCYVTREELDHLR
RELEEEAKEEDEGPSVGCAAQ*
>TCRU_4069 RNA capping enzyme, nuclear
MKSVSSLSQLHNEAEKLFGRRLFLAVDEEFVYSLHCFPPTETQRAGGSVFSVLYRDLVQR
TCFRKSSESTGIPRLLFSYVAEAVLCSRDGEFMGPLCSPLRKSHTAMLRSNQYFLTEKSD
GVRAILVSFCVHAFPCWVLRDAEGPTCNILRLDDVAALEEMRQQFFQGATSQSNSRSLQI
SIGSFYIEAEGSKTSNCEMETFTLKSCPESNSGAFSNGNIIMAERTQGTRHMAYCFDRSM
EQAYLLLEEYAAPTLSAFAVDGEMMLALRDLKTRETRPVYSCFDVFRYTPIKDAVGTGVC
LTRWPMSKRYDVLRDHIIASIHASENLRTQKPLLHVFAKEMFPLKNFGECVARLRRADTS
GNTGGVMYYYDGPHGWTLSDGFIFTPEKFDLVHGASKEQLKWKWPSMLSVDWSLAAIESR
TDEYVVDLFFRKRRFGHRPDSVGRSRLSSAMRLLNPFSLRIPTGRSVVAECVFDRHKKSW
SIERLRTDKSEPNSVVTVISVLESLVENITLDVLVGMLGVEDTVSNRDLKSLQEATDLEE
EGKIVSAPESPIEKKTCQLTLRATQSQMQGEHEIHLYWTVRLLSEKQHIPCIHCKVSECS
GLGFACPMDDERSKLTENLYVELANAGGSYAWSDFTVSALFDGDTGRWNIVSLHSKGDNR
KSTSVGVIEHLQWLLVHGRERVLDVMPVVNTQKPNGMIGEPMGELVEKINSHYACKTREL
LSGKNRSVLRKFNNWVKNVLISNAVSYAKSRSDKDSECGELAVADVCCGRGGDLFKWRAH
NPRYLFMVDSCLEAVAEAAGRYSVSKGLSLRIVPQDKSSVGVIAYFTVCDVFDEAGAFTV
KLDEFFNQHLKRRRLDIVSCQFSLHYGCSTEQRMSCFLRAISKALRPGGVFFGTTVSDVE
LLRQVAEHGPAFGNSLYSVRFPSETPSDPSFGVQYFISVEESVSELPEYLVPWNRLVALC
SSVGLLPVESLGFMEYSDMHYNSPIGQKLRDAVLRGGKRDSDGHALLQLSSEEREAASLF
RTFFFVKNLVENEACFVNN*
>TCRU_4070 hypothetical protein, conserved
MDCVLETPTAAVKYARTSNAFAAKRLVEAPLLNMLPRCRNTFCVSHASKHPDAATARAFL
DKYIPQQRTDMDMQRDAVRQHQQARFREFVEASERKNAMSAREKVIGVKCLMHLAAQKSL
QHAKMMNHHPIVIHSVRHTWRTLLLQLKEYLNDDGFGEIQEKEEEAQLAFRCRGALENVS
ALGVWFVGAMSIPFRRYAVRIPTEDGTLQDFVVIGLASFTYSSYVMDDRRLAQEATLAEL
ERLSKRLSVNLLFLPPLLLPEEPLRGNTDFTQTKSASMEMLIA*
>TCRU_4071 GMP synthase [glutamine-hydrolysing]
MDSPGSVREYVVILDAGSQYGKVIDRKIRELNVESRVMPLSTPTEVLRGDHAIKGIIISG
GPSSIYDDDAPKFNADLFEVGKPLLGICYGMQLLARTFGGSVGRAAVREDGQDEIWMDLS
SPLFKGLGLGEKVLLTHGDSITDSGPQLKVVARSSANIVAAVQHQQLPLFGVQFHPEVEL
TEHGMQIFKNFLTLCGCHFNFTMEDREMVALRMIRERTAQGQKVLCLASGGVDSTVCAVL
LLKALGPERVVCVHIDHGFMRLRETEEVVAALREAGVSVVVVDARAQFAEATTEMPARRK
CAPYRTRKLCEVTDPEEKRVIIGNTFMSVCDTVIRDLQLDVNNLLLAQGTLRPDLIESGS
SYASLTADAIKTHHNDTALVRQLRDAGRIIEPLCDYHKDEVRELGVRLGIPPNLVQRQPF
PGPGLAIRVLCSNGTPYKDEFYQSTHEILKALCRGDTSIELARPLGEALRDLQPASCVLP
VRTVGVQGDGRTYAYAVAISTGRFPVEAEWKALSRLALAIPKVAQHVNRVVFMFGPKKED
SPHSVTKTTLIPTTLDRLRIADEIVNSTLLKYDLVRRLSQVPVVLIPLGFEEKGQYSVVV
RTFVTNDFMTGVPALPGTPLMPLAALEEMVNSLQQLDFLSRVMYDLTAKPPGTTEWE*

>TCRU_4072 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain), putative
MSSQISIRCLPCNFDAQSLLRLCSSFGDVASFEPRSSGTGNEEGKECTADVQFEEAEDAL
AAAGNMNGMEFGGKHLRVFVKHAVD*
>TCRU_4073 kinetoplastid kinetochore protein 11
MEGSQVKELIQKWRALSNELREKNAELEKTRAALQELEGQHAKTVQDWDLEKANIQNTIS
LVWAQVSDKKEEVLRIEKETADLQLKVDERRLRNEEYWCVLDKRRQAVTTRLQELEEKDK
DAKERLREFREVRDESKQQLISAIRKLEDADQQELVDHQQKTRQMRSKISEIVASVEAEK
KSWALEAAVRGWREKNDARRWLSEEANASEKNKGVWVEAIREADSMHCDNSLKELDALRA
LISC*
>TCRU_4074 hypothetical protein
MELTPVRQRKRNKRWLFFEVPSVEELAGIPDEELARRTLPKGFYLWFFAHHMRTIYAVLS
EHVYLTRGVLDYLYDYLRWGPNKIHNKLFICSSYNREMQCSNGFLCREVHCPFNTDTAME
ASIYNVFSNANGCPTSTERKEKSLKHPPNVLLWHSLHSRWTPPWAYPTLPRGATFRVAMP
NNPKPVEEFDSGRIFVTKVVREYYERFLRNEPPTVTLQHCANYSKNGVCCFGQNCQFVHV
VSHTGERAEKDASVGDLSISSAPGNANVSIRPIPGQKGNSTTFSESCGETSGTSFPMMHF
SLSSSPSTSVNAPPRAFSTKSMASDTSMLNTQLLLFPTPLMQTGQSPQSRENCQKQIQLQ
QSLPQLQTQKQGQLQPCLSTGCLPQFNPASAPFFLLQGPEKSQPISLQQMYALTVPPQDG
NAKGVSPLYFMPY*
>TCRU_4075 hypothetical protein, conserved
MFINSAASRQMIRVQIRSLRGETMDVEVPRECTVGQLREFLIGYYGYPPATSLVYGSYVV
GDECLVEEFPFGSLVLVTSLDGAQRGYPAQQQQIVAPQQRGQHFYNQQCQQQQRSQNQGH
GKLQQPQREPFNPFFPVGDKQQKQQQQQEDRSGFDSREPKKESSASVSKHFHTRTDSNSM
ASGGTTTPRIGNDKKQPGCHGEKLRSFSCQSSPPPPQRSPHDTVPSGKTSPSKFVRNAFP
STAPVESGDGKGSLDRTPRKNSQSTPSIDASRTPRDTNIEVTRGVSEEAGDTASVASRIS
VKCMVPALKKSINLELPGDATLGDLLLEVVSQEPRLAGSKVVFRGKLLSGSDAKLNAYGI
YADALPSSLSLTNPDASGVYTLFFASGEYSEPQKVMLLEIEADTACIESIIKDGGLTIQQ
RRGYYEELMRILFRTDNLQELEGEWRSRRKDAVMRATRIQDVLNVDVSS*
>TCRU_4076 Uncharacterized conserved protein (DUF2036), putative
MTYVTLRSDFAKCSEYRLLAVEADCVRRLKEKIAVHGNEEASTRTGMDENRTLLMMKGTS
NLLLCDDEHTYRLRRVEYSNTLLLAEKRPICDRNIEALTHTPVQNSSAPVDLEKKCKYVV
IRAAERLFEAKRACVYRDLLKLLKERPVTIEELESENSARPCDLADARMAPPDGVICQHY
TFPQLVSMSRCSARELSEVLSEAGAIAYRGCVRLLQPSLLREALQAVIVFVECCEEVSWG
AVEEHFCPSVYPSIVIRVVQKMYGALEQAEGRTGAVALLHVRKVLQTLAEAAILLLTARS
EEEEDRQFHMEEKFFFPSAEFESFYKTWVESIPSSFFASGVIPPRSEKAALTSLLNDVVV
VRGACGDCYAGATVVWAPQDELSTDLSQRIEQLFELNPGRWEVGALRAYVEPLLDPGVVF
EQVVHRHAKEFRAPNQPLRYGRLV*
>TCRU_4077 zinc finger protein family member, putative
MVSVALTLNQSASANSLGSHPGCQANQTPLSATLRRGSTPQQTTVAFVEALDHLSTKLKI
PMSAVEPTNALQDDGLVPGICRLFLEGRCRQGSRCFQVHARRDVLDSLRKEALETPSCCY
LHGAPCNYEGLPFNLTVNIGSKAVGLHSLNPTNCLWSIYSEHGETLLTVSKGRVCREHRR
GLCRFGEECGFLHICREIPLDGDEYISATPVPIPRVQGRGTRAGEASASAVNCINNASRD
VSGDIHHQSLCGSQMEETNITTRTPNASSFNNTSFNGGYFSGGLNGQHGSCNNQSNSLQG
IESGYGTPCSTSRSRMSYGYRAKYIAHADGEERAIKGPLLRPLGGGAVLPRGPMGQRHNP
YGDASSFQ*
>TCRU_4078 hypothetical protein, conserved
MWEQQPKPVTSLPLRPLESTNERVSTSSSSSRSDSGSYSYSYSETESATETGTASTVTQE
PPLTGQKKFLSFPDLPLPVPQPPRPITSSQVNQPISAEAKKESPSNTNGASSESYGDSKG
YGYSYSHSSSSSEEEDTGSSSGSSYSYSYSTESTKKGKYYATQDKRLKSTHDVKPEESSL
SYTYSESLSTEKGRGEGSVTHTYSSTTSGSRSRNGSDSVGTEGSESYGYSYSSSTDGSTT
TWASMPRVKKVPGKIAESTKGTEESSTRDIKKDVATKGSQNYSYSYLCTEDEKTRSSSKH
HVSLSSTESKTSGVKAAGGSTSIGSRLSESLDIKPNKLSPLSLSAGKSEKTPSNSSTNSL
ITGSIGSGSLRDSSVITQHDTTSTYTEDTEGLSQGSVLMDVPPPTASMQTREVIVLRTPP
EEAPRFRVLPRICLVPRGSENDTLSFFLNQLMWIQSDFIRREAEKETTESVLTAIKGDGT

KSTEARSKSKTKKGTVKEEQQALGDVPQHHFIKKSLKFALKAVGVETAEERAVALREFVM
PMHRDAALSILETCAHKSVFKRVKSMFLAHDKFQSGEVPLDVTLELLGRCGIAHRNMENL
TLSICTAFPKGSTPLLCVIQRMSPSGPPIATVEGEEPKPLETKMNEEVVDVCNSALRTGG
AAVYWDERRGCIYVGNRSVMKAITSSDTAKRIVVQLEALIYVCFALEACTIEDKSLSAVL
YTPLLAALLSCTSKDVPDTKSVLVENALVSVLNPLKHLERLSAHRNLQEKYLMSGEEPIL
SDTLPERLQDFRGTMVERLRRQVTWAPNPTSDGGGFEMTPPMDPDDVYCELGIKKLRLKE
LTPEGACCYCLVSARTTSGGNWMPTVRIPVVSIKASKKNGFKWKFSRDHSQRVLFACKAT
DTICIEACYDMEESAGETVTWCVGHLLVSCRGAKSGKLPISPGSLFSGFVTPVPVAKLVQ
PSKGLFCSLRRKENATPAISMSILVTCVHSNSLPARASVPPRFLAFRRHLPLMAQLRGAI
MSVGGSQMTPLHVLRQQQVQHALVVMLNPTLMDQLQELWERTLKGKMGTKPTDIVQKQRA
LLTLATKVFSVHNNISGNQAVIKNILGRGAAIPVSVNSLAPRRPVFV*
>TCRU_4079 Leucine Rich repeat/Leucine Rich Repeat, putative
MLEPPHTAHAEVSLEKLEQLVANINTKYAALQRQALHSSNSHPTFFNGLTAEYVNSETKM
SFQSGSPSENGHASVPVDPLPPLTPFCRPHWPTYWNERELHVAASELCQCLNGGVNYRAM
CIQYQTIFELLLTMLREDIRLVRGMEFLPSGTLERSYKVLSELINESRQLLTQYGLIPGS
SIRVMEEVENKSSSEVGEMPNPDYALPVALACSDSYNNSTNNNNFIHQIRSSDKSGYGRG
HGTKHETRVTISDPLEDSLRETAYTPLHLCSSPGKPVVDDSYDVDTPMLPVEEENAATES
QGVQGAKFGGYYGGARTNLDPANQSRYQSMEELYKELYPNEGMEMLVAMTRMVFLKEYHN
VVARSREEAFLTFRKHLDEHLLPCIQSYEALVFPPAMQSSLRSEYVVNCLQQRIRPNERL
LDVLSRVGPERDLSSMALASMSLNDVDMKPFVLVLPRLCFLRFLDISHNDIHDDGVRELC
SVLERHPSLEVLDLSDNPFTDIGGTALLQLAATTTQLKAVGQQGVAFSAHIREAISRQLQ
KNRSACDSALGPAHISHLSSISNTHEPCKPAFTGRLAPLTALDGTRCVPARRRSNLGVIP
GPGTDSMVSRSLGMLRRVRLPYLTALRGGPSTDGIRESNSSPR*
>TCRU_4080 hypothetical protein, conserved
MSSNPIDFGSSLTPRGRMSLQDNDNSTSSSGGPLGTVLSVTTQTRSMKMQGSTSSSSLRT
SLQGVKLPKRRLLPAAEDDPVMNRLQFRYATKPKERMYANVPTAVNRLTASAGGELRGEV
EASTAAIHQETVGMLCRNLPLIADPSSEIEAVLGSIETERPKKTANLDDRITPQTLYKLL
HTGRALASKMASKRKAQEVLEDLKKFPNKKLDDLRTQVTRLEPPYVDQMLQAKVFNRSQN
DEDLRPREAFPITLLDSEDKKLNWRPEQECHSHVLAPPPTRKENREVRQKLSLFSPSSHA
GDSPENVAVALNVPLALSTGMGDDTGIIDQFVSYASARRRPEIGGGVHSDTVAGIPRPHP
SYNPVFSALDAVLAVSKEYEKVQQTWPGASTRQMSASRQAIIDRIASWESSRIPRSLWVT
VSDPTFPGSRLHQLDEDASSGAPKRSSIVFPAVKATGRAQVYLLADALDRMFQEIPDTLA
VLADRETAKILLPEAPENDDLIVYRDLADVERIMDLKALNESDSAHRKYIEAAEKVMEVV
DVGLVEIIRQVAGSCKERGALLDVLRLLIKDVISSCLWLIGYCKDQARREAKARRELIQA
SKEDVEEVMMLREEVRKLKQEEEIMRGANAELEQKASKYDTLIDRLKLKDKNFSRHPVHK
HLRLLMELEEDYTKMTTKGLEELYKHQNAQPSDEPKVYDAPTIHMNSVRQEEQQISQEEL
YTESYRLLAAVTEALRVVDVTCEPLYDRIALPPLGPTSKVASMRWAEIANAVGSYEVEKK
HRQHVFELFARWNEMQGKSGATSAQPSGLGGEITDSEAPQSPDEKSPHEKAAPYEFQTLS
LEAEMTDDLRKRVQFITRKDLADMGVTDCSPDEINAMYSPDFDISAFLRIEYNPPGEYEM
TPKILRDMVHDVTEVLRHITLRMNALANSGLVKEGVKPPLQAPAHPEEACMLCGRRDRVA
MEKKSRGETMQRVAGEIQRRYDEMVKKCQRAESERENYRREIQRFQIREKKQIEEWGIRE
NELRQENAALLEENRRLAQQAYSAGTSSGDVETEHGTVAFVRNRLMSDAMSLSSEEFTSE
YGDEEDEQSGPPDESENAL*
>TCRU_4081 glycosyltransferase family-like protein, putative
MLRCSPGRHYIFDACYVLNLDRRRDRWAHVQRQIARVGLEKFIQPPAKVTRVSGVDGNSL
DVEALHRDGVITDLGYTRFLLPTEEKLFGMDLTRGAIGCALGHRKIWEMIVAERRKRALV
LEDDVEFHHKFGRLLGPLWKRVPADWGIVHLGGLDLLAAEKPPRPFIDDGIRLAYQGHRE
LTAYVIHHISAKRCLELSTPMTWQVDTHISNIVESDPEAQDKYIVDPKMYVFQPSLAIQI
TSFGTDVQKRPSENPPLEDAARRMREFIGGGTSVR*
>TCRU_4082 N(2), N(2)-dimethylguanosine tRNA methyltransferase,
putative
MRSGLFNAEGLAKEPVSGFEKITEGTAAVLFPPANVKGTSASQHADCTKRQGDHRDADDI
DDDGQAVFYNPAQVVNRDLSVCALACFSHLRREEPRRKGGTRDGITILEALSATGLRAIR
YYNEVPGVRFIIANDLDPDAVACIRRNCEFNGVPCARPTLTENFPPEGIRVDEATGEIEA

GGAVIPNLDDANDLMFRLAANSTVYAGRRFCAIPSQMATNITTSNDDASVNEAHPLLQQE
LMDVVDLDPYGSASPFLDGAMRCIKEGGLLLVTSTDSAILCGGHPDTCHAKYNTIPTKNA
ACHEMAVRILLAALERVANKHRRYILPLLSLHIDFYVRCFVRVYTQPAEVKLSPCKLGYL
LQCSHCPAYWVRPMAVARMRDKKCARKKNKMPNNDLLKSSISSGNNNDNNNINDASKGND
MGNDHAECRADTLGRERFPAIPLRQENPKITPCSLRHMLPCVNTHCCNVCGASLTLSGPI
YAAPTHCVSFLLQLLQEVERRGAAKQITAEARVAGLVRLAMEELPDTPLFYQIPDIASFV
KVRCPPTPQLVGALGRMGYRCSQVHCAPSGLKTDCPPDVLVRVMLQWKREQEQASGDAEK
GSCDAAKAAVLSATAAEAINEKAGEEEKRGAGVFLLEPIDGADFSYDRRFDFRGAVTGVA
KFIPNAPNWGPKRRHQGAMHNNDEQLTQKQRKE*
>TCRU_4083 actin, putative
METTRERVPVVILDTGSHCLRAGYADEQGPRLDIPALVGHPRNRGVAMAAGMNEYEIGEE
ALVKRGMLTVGSPIENGLVVNWEHMEKLWSHVMFSEMRVTPESHCFVVPQPVNTPAAQKE
KTLELMMETFHVHSLFLGTSQVLSLYGYGLTTGLVLDSGKDRTMAVPVHEGYALGRHVTE
SEIAGETLTNYLASLLRQEGYSFGTPVEMQVLNKAKEELCYVRLNEFGVYSPVHSLGTLG
NAAAFDYNFSSSAQRPGSSPVPATEEVFFLPDGNAIPLAEHRHLTTEVLFNFGIMGEEYI
PKSRYMTELGEIFNPSFPMGISWLSFAAINNCQPAMRPSLFAHIVLAGGNVSFPGTRERI
EAEVTRLYRETHASEAVTPICVHDVECRIYSAWLGGSMLARTSMFPHLTVSRQEYEEQGY
RVVHCKCQ*
>TCRU_4084 katanin, putative
MQQRNPQRLQPLSNNPDGAPGSSLQAIKVQQKAREEEERIRLKRVKGAIVLVLQFLLDQG
YTGTLQTLQQESHVSLQHFCPADNVDLLSIITEYEQYFEFRFNRRVKLFRAVEGAQDVWR
EAQNGECVAVRRQRTASPGAPARRAAAHANNNKVNYANVANLGSAPPGGLQETQRPGGQP
PTIARGLALAQRPPTPLSPQRLRIKNQKKLAGNGAGLMAVEGMRVDVVPDPQGNNNGIEE
DEDMFFGRALKPLPSFLSVEQQELAMTIQREILDVNPNVRWSAIAELDQAKQLLKEAVVM
PVKYPELFSGILRPWKGILLFGPPGTGKTLLAKAVATECRTTFFNISASSVVSKWRGDSE
KLVRLLFDLAVHYAPSTIFIDEIDSLMSSRSGEGMHEGSRRMKTELLIQMDGLSKRRGGD
VVFVLAASNVPWDLDTAMLRRLEKRILVGLPSHEARAMMFRQILTPSASAPDLDWNLCAE
LTEGMSGADIDVVCREAVMRPIRLLIEKLERAGSPMELTGGLLQRPQVTIEDIMASVACT
QSSVQRSDLEKFDAWAKKHGSGVSS*
>TCRU_4085 hypothetical protein, conserved
MRRSSAVMPLLSGSRGYRVGWRNALLASAWSVFPAVFAQTAMESRALQAVPLLKSPRGTN
KNEGRSMGRPSIPGGDNATRLFLRRGRTTRQAPDVPREEDAEGEFQTGVSSKTGVSENKI
LRAFDRWAERSGGCSANEFLQGVHQSYYGLGVLCETLAEAAKPQLPLGKIVPFAGALAQL
KGLLTKQYAISPKGLADEVKAVAAKSGKEGLRTSKVVAEALAQIIPISLELAENMYNMWN
KQRIFDSNVLRIAATNDYILSTKMIFFHECHNMKEVHFCDDTQLSVIVVPPPANAGDGSR
RGPSVTSDRREESTTDHEIASETKLKMGEVGDSATDNAEGKKQLKGQTIITFRGRPLPTI
PASAVACAVASIDVVTPPQRYDPSFDWYYQRITGHESEYQRIAVARFFAMSNAQTILAPL
DFLVRMCTGRHLELACPPGISDMIGIPKNIAECPPAMRKLLCYYLDADGRWVLSDLLWVD
TVTTPMMPKPVSA*
>TCRU_4086 AMP deaminase, putative
MERHWHEVLIQNDEADRHFATAAPLLVKALRLIASVRALPLALNVAWWESEIARVDDSRL
VHRKAREQARKLREILTPQLESIYGSLSHLQSAKVESQHSHSLLRCHEGLIAPRDMTMDT
LLESQPVFDYKNFRAQFEGLCQVMANSLLFSACEPRIKVLQSRYRLYRAFNGVREDDFHP
TLGGGSYDRAPKLDVRRIGSCMSAKTLVEFMQQTLEEEPEMVLPARDAISPLSLGAKKIR
VEPEGLQSVNDGVGNLHEDHEERDPTLKELVDIFFGPSLPPEERYFAADGLGLLPNYAET
TGRSLDGFEKRNATQSASARSMPLLKHFLDIYAGNRGELLARLVMPMLSSIVTREQTMLE
MEFTATGRVPGEVQHIASWCVRCGLVATKKVQLALRIVQEPLSAGEVEGTAENMEDVLKN
IFIPIWMALLQPQDHSDMVQFLQQLASVVVVVSGDADVQEMPAVNDPKKYSVESGVAPPD
AFFIYHVWRNVQLLNCLAVAHLFFASDRRESEGATEGDAVNAGYFLPGQSLFLHHSPVLT
RPLRFRVCTSATSKNSFMESVMGLLVADEVMNPVDVFNWSPLAYLYYLTQRRIVVTPVRN
DITPLDSAVQKEILFMVETGLNGSVATLDPLHYNTTDNALCETLNGLQKSCRLALAEITE
LCLRSAEHANWGMKQRCEMFGGPWERASTRYSEFTKTQVNPLRLLFRESSLAHEVDLLCR
KGLTEESSFSIMSREEEEGHKALFSGFTQVRNASSNFGGFLPTSKTLAAQREILWRFFKV
PHYNPPDNVECGGKWWDFVDRQIEYPRIIISGPEITDKSQEAQALTREFNRRQYYRSFNV

HCEIPPTEEMQAAQTMHTLIALHSVNRSNNEAQPMHGAHFSSNTFSPLMKPETRKMMPEK
FSFRDGVLDVVLPADANETTRMYFRPLPTWKEFQLDVRSLRRLSHERAVQLYATKRLEML
ECKFNLHVALTNDDQENHARDAPVLFEKGDLYKCVKVDVHCHMAAGMTAKELLSCIKEKV
QKHADDVVDVERGTGRFVTLGELFAKLRTSPLQGAAVNLEDLTVASLKVKAGNGTFNRFD
EFNGRYNPFGNSALRTLFLKTDNFMGGRYFAELIRQTFRRQAEDGHVFSEYRLSIYGRQR
HEWDQLARWMVLNHASHSTNRWMVQIPRLYFIYRKNGIISSFEEMLSNIFAPLWEASMHP
EAHPFLSYFLAHISGFDIVDNESEREPDTLIETPPSQWTVLDNPPFTYWVYYMWVNITAL
NRYRAARGFSTFTFRPHAGESGDPDHMADVFFVVDGVNHGINLKRSPVLQYLYYLAQIPL
GITPLSNNALFCKYRDNPFPIFFRRGLNVALATDGALIFHHTEQPLIEEYSTAANFWNLS
MADVCEIAKNSVMMSGFPSYRKKAWLGILCELRSAAGNDVRLSKVPHSRCTFRYEVYMEE
LSHLQRKAALDIPLKPIMDAQLEGLCTMDVVGLTREQVIERRLNGQPILADTDTEADKQQ
KVHDTQMVLVRLGPRITAPSRL*
>TCRU_4087 hypothetical protein, conserved
MARRQRVPRHKEHGRRRNKNPKLSPFQREQRRNKMANQPPVSFGKNGSQRDYPISQRAVM
KFLMAKQKRLQERHQQRHEEQQKKEIGEHQQRQTKKTTGDGKLCEDNGEVSPSPATHSSM
ATAAVEAVVGKKKHHAKKAKKTSLTAPVALNEEMAASLARPIMAFKTLAEEERGEAENAL
VAIISRKKERKHRKKAEARRERVREVLRETEEQLREVLSSKGGKKRRREYPVDPKDAAFE
KKLKQMQKEKAEEAVAAEKIVAGKNIKQDRSETESQKRKRKRITFLDDGAKGGVDAPHSA
MRYPNDKGAKVPRDFCELVDVVRFGERVEAPPVFDVIPRHDASITRLANRMESSSCRNFL
KGGVASSQKERLQMLSSVGGVGEERRLERLGLGPVSTSAAAARRTGAPKKLSKEEEMRRL
REAVMEAYRRKKRIGAEARKGVDMHHQFPIFS*
>TCRU_4088 hypothetical protein, conserved
MRTALRYRLGNVRESEFTRARRLINSHDPLSTQEQVQVLHYLAASMRSSVTLLRVVAVLQ
IFLAFLFIAMLAAGHPLVYAVIDDAPPLTFGGTVAIMTSSILLVAGGLYDMRTCRRTLYI
DEAALVETNPGREQETGVHAGRRDACTAALVVTEPPRYHYFLGFLALWPTVYWLYVMRVY
HTHMAQQGPVFFGVADNWVELVLVLWQPVMHFVFARTLRSIVTGKNDLLRLAKMKYRYDK
L*
>TCRU_4089 hypothetical protein, conserved
MRHSSARRSSRGFVKHSPPIPYTASSPFFTDVGKPRGLQARKVLGLVSRLKSAVLQKLLP
IYHPPINYGDILREVPYYVQTRVVAFFSIHPSYCEDVFGVSHGQCIRFTRGPWMNETAII
VGVRGGKLWIVGCDGPIVARPLREVQKHGWEKVRPEATLLGRFREGLVGARKDVELDYSP
EQREFLQKAPDLYAEVVDDEVAGGEELDPVEVGWDGPTAGSRGESGGVAPSDGVASCIPP
NNGRTGNTNNDTRIGEFSTARKRIVLVPELLQSTNDLGWAGEGLVTVNGGGVKSFSASLS
ASVLL*
>TCRU_4090 Dpy-30 motif containing protein, putative
MTSSLSGVVSKAALFVRPKYAQERELLSVIKFKLHEAGFIIIHEEYRRINEELADTIAVQ
LDRTAFLSGSAAPSIALEDAATSRPMFTCEHATSVPTGQQDLVGHVYLYVLARRDCHVDL
LRFLCRLFADEDFTSVLKCIREKATREEATTAAVKNERENEEKSEGSHISCPVFCNATAV
AAKQVVQLLFPRMLAQDVPSTGASKEYVQAELKGALLPALVELSKAKPENPIRWLAERLL
NTNTRAPPLVPASSVNGNG*
>TCRU_4091 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MSRRVFTSAVLLLFVVMMCCGTGGAAKIAEVEPTIPEEPVPKSPFGWRDATGDETVSSLR
GPSLVEVNGKVFAVAEAQCKKGKTSVFTGIASQLLSMEKGKGPEEEVLKDAKYTQVLEED
ISMEKKKVDVSRPTTVVKGNDIYMLVGKHSHEAAANCQAETEKIKSGILLVKGEVGEGGK
KIRWDDTDGVPCILGAKHESLSQLIGGGGSGVKFTDDALLFPVEATKKDGAGKDGKTVLL
IIYSSETKNWSLSKEVPDDGCSDPSVVEWKDKLMMMTACDGRRRVYESDDKGESWTEALG
TLSRVWGSKQKGGEVEIVRSGFITANIGDGVEDDKRNVMLVTLPVYSKENQKENKKGELH
LWLTDNTHIVDIGPVSGNDDDAAASSLLYKSGDNNEELIALYKKKKDDAESSLGMVSVRL
TEQLQRVKDVLATWKKVDERVSKLCTSSAEEDTSTENACTTGKITDGLVGFLSGNFSDET
WRDEYLGVNATVTNGVATGYAEKGVRFTGRGAGAEWHVGKQGENQLYHFANYNFTLLATV
SIHGVPRGDTPIPLIGAKMNDSENPVLLGLSYDNENKWRVLCGGENTEHSSNWETETQYQ
VAIVLHNGSQGSAYVDGQRVGNAQLALQDIEGSKGISHFYIGGDGGSAEAQEGVPVTVKN

VLLYNRPLDGTEITTLAKNTITNPKPEDPKTPTTSPLSPAASAPDVEVSLHRSNSSGQLP
LEEEPLRANIGAGAGGVSSAVSVTTTPSSDASPTVATGSGDTMLGNGSPQTPEVSVSSGE
DGETTGGTDGQEGIHSQAGEVKSAALSSSLGNSSQGNNTDAGTMRERRALPLLLLLLGLW
GFAAQ*
>TCRU_4092 hypothetical protein, conserved
MCGCRILVPLLFFLTDGVKELQALAYFIAGVRAGVSATRSAAVGKACFTLAVEGGIDEAN
VRAHHPTFCTVLPRRQDMISSHIEPSPCGRNVASKRSRGRRTRHLHSFVEVSRGEEMRAF
RHLTSRCLLTPYSVSPWLLSDAPAIYWMIGTAEMWTTFAAPSFGTFFARRVRDGFRLPHC
MGCCKAILYATRLCGGCHAVEIFDVVETPLEGGGGDPPARVIVDGFTRPFEFAVPYLYFH
ELTADIAEYIQVAAVLHTFKVLSSAPSTAAADRPVSLKDSGGGSVQLIPRLESLPSFLSA
RHAHTVTLRSLPSMGGKGDDELRETVALFVASLRDRSAAVDASALPEGRRHKLCG*
>TCRU_4093 hypothetical protein, conserved
MSLAVSLSDKFVRSVRAMPSLKYLTIAEMEVVASRFLPAAAILRTRLCDYYLFIKAVRRR
LSALNQGIVQETSPANLPPAAVGSGEGLRHIIENNRRRIIKSSEKASAAIITDASLNGLG
AVFIPDPGDVKIAGGEWKRRPFLVMQAEARAVRLALSAFSVILPSTMDVWVDSTLLQGAA
NKGSSKSHALTWELQRIYEFLDSRGIQVSFAYARSADNPQTAYHAVVFLYFRNWPRCGTC
EGERRCLVVGGPQSLPLRK*
>TCRU_4094 retrotransposon hot spot protein, RHS3, putative
MTNSPRSEYYFGFGMSRMWDDNTALECLAKIVRVRGERNGESPFNAPISTHLGGKILCRL
AKLMWPNDFNLLVSRLRDYLISENFGKRAVFAFLNGSFVGAVRLKLKELRPPARRQPHRC
ALEVYSQERPARHYFLPSMEYRYEKIDVECGVLYIPEVASSPLEDAFFLHGVKSGDAGGA
ADDYGE*
>TCRU_4095 hypothetical protein, conserved
MPGIDAVLREGSSHDGISVRCHVAWDSAVPWGKCGANSAISIHQRKRRVANLLGDGIVRR
QRAKRSDSIAEREPVAAGTRVGDWDAAARRGTGNCLWPRSVAGHSARQKHARLPAAAR*
>TCRU_4096 hypothetical protein, conserved
MPAPPWARIANPIHSAPLGDRCPGQHQEESSATPTSACHAVCAFVFLLRFPPIPSPDCGE
ETHMPGIDAVLREGSSHDGISVRCHVAWDSAVPWGKCGANSAISIHQRKRRVANLLGDGI
VRRQRAKRSDSIAEREPVAAGTRVGDWDAAARRGTGNCLWPRSVAGHSARQEHARLPAAA
R*
>TCRU_4097 Beta-lactamase superfamily domain/DNA repair metallo-
beta-lactamase, putative
MKVPRFPVYIDQFYSEDNPDAVYLLSHFHTDHMKGLSHSWCAGLIICEAVTRALLIQKYG
VCMENCSVSLPLFQRTPFLRMVTTTSSKVAPDIAEEREVVLDTVKDNGSDENCGSNFGED
EMVMLYLLPAFHIPGSVMFFLETPFGNVLYTGDFKYDEYARRHLDPFFADHAVDHVYVDD
TWLHLGIPEVSPSMRGNEGTRVLSKMLSETELEEAIEAVGRRMDWRVREFSLEKNSTNPP
CGPYVVRVYLHNQFGKEHIVQRLATRLGVPVVVDDSRYERIRLLASFNETTAEVNEKFCL
VADRFVTYTNCKSFPRIEVVSSLKEIAPEELRAAAERSGGTPHYGIVMSGWALLRRRGGG
DDEALVWEIPTTLHSTPQQIIDFIALLRPMSVTPLHYKPCRGAMVLQRLGPFLRRPYVNQ
FLSVADSLKDESGEWRRCIQPSGSNKQEVVVYPPKRSGFCIGPSFKSELSPHPHNAFTPG
VEREGRKRPREAFSSSIQTVRHDDSSCSATPSLTQLAEFFDL*
>TCRU_4098 Ran-binding protein 1, putative
MAEDKHNDELMEVEEVAVSDGGVARFAPVDVQSGEEKYEVVWQETAKLLRFDEGENQWKE
RGQGTAKILRRKDEHGKYMFVFRREGIGKLAAQHYLLKSMTVKFHPQSEKALLWMAHKDY
TDDEEGFPENFVMRFTSKELAEKALKAFKDAISASTV*
>TCRU_4099 DnaJ domain containing protein, putative
MTDYYQSLELPRDATQERIRRNYRQLALRFHPDRAEPEGAERLKEVQSAYEVLLNPQKRK
IYDSFGASFVDNPVSDVLILQLGGRSILCIMACTPFLAASLVVIFTAFLVAYVAGRLVAR
DAHSVNDHS*
>TCRU_4100 hypothetical protein, conserved
MCTLRVGVFLWTLIVLSLIVLTVLVPVARDANDMTSLRGGNNFHSWRRWLAPLYVVGASS
TLLGIVTRFPTRQKHERLKDSGHDGLWACMNVFFVVGIPKGISVVVFSALIACRVDEVIA
TNYFVILALPFYVFGFLTLLDSILHRIFIQKLRGNPAGSCNIFVISIPFITAVGLVLASV
SIVSMRLNDLDRARHGAAGDVFSLHAALIPVYFLLGCFLFSTLMIFCFVCFFLLTEDGEA

SNSPHGDAATEGNDEQQGSEAHSGGEKGVEGGHDDDGQPSRKHSFFLESRRNRDVRDMPQ
GAPDTPTGSNGEMFLPQRPRQGLSDID*
>TCRU_4101 TFIIH basal transcription factor subunit
MDLWQPSLPGAGAQRAVLILQLYMRMGNYSPLTILIADALCLTFKASGATLSELAAYLGL
PPDRVEIGIEGMPKEVYCTSSDIRQDDIDEEYGEKVNSRKRNRQEVAEESTLRYYINYAT
FLPFAFAHGSHILLALCQLPIPEHLANAGIRGEGISLNVSATLRRADSRRGLCCVSCRYW
MALKDLRATVSRCPLCETDILGGMLRAIYARYEEKLASGQSLLLFGPVQQRPTPSTSTTT
ESDNSGSRSVEAVQGASSKKTSGENSDYPLARDPFLVQQGLFFHFLYSHPFVRVNDASFV
VDADEVMTKEEYDHRSRHKATVLDQFRLVHRNASTIRVKRVDQEKLDADKCREGLVKVLK
RGQLPPWLRPISVFHEGEGPLPPAAQKEEEFADHVESKTTKKAQRDSDITAIARYTAREF
FDDDYDEVPLFKPSTV*
>TCRU_4102 Mucin-like glycoprotein, putative
MTTCRLLCALLVLALCCCPCVCGTASGEAQVSTTDHPPPLPQRQTRETMSSGSKAPTPPK
ANTSDEVDLPVTVSAEGRSDVSSTTQDGIILPGQPGSDGGNKSQPGLIDNPDQSVVKSPA
QETGESKGNEDFTVKTNTTTNTTPITTTTTTTTTTTTTEAPSTTTTEVPTTTTTREPSRL
REIDGSLSSSAWVCAPLLLAVSALAYTALG*
>TCRU_4103 hypothetical protein, conserved
MRRSLPWFFGESAARGVCGEAVAEEPGPSRVSAFVLPARLAYWHAWRFRWRPAREVPAKK
TMKPLRHPQLRNSQTIGTPGRTRRACALTLRTNGRTLQPIGQENVNPPLAGRQEVAEFSS
GRGSGGGRGGPVSSVKKGTAPPTQGVPCDPQGARACRRVGRSRIAPVRSAATRGTIFGST
PGREFRHTVKRLSCGVCPSFPPGIYFSTAA*
>TCRU_4104 hypothetical protein, conserved
MMASASAVTLRGIPRFHGEHLKPTVRTRSASESGTVQISSVTSSCAASEPRRSASIAERE
SVATGTLAGDRDAAARRGTENCLWPSSVTGHSARQEQARLPAAAR*
>TCRU_4105 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MKDGTFVFPMEGTKDGKAVSLIIYSSDNASGNLSKGMSADGCSDPSVVEWKGKLMMMTAC
DDGRRRVYESGDKGESWTEALGTLSRVWGNKHKGNEKGVGSGFSTATIENRDVMLVTLPV
YSNRKGKEKRELHLWLTDNTHIVDIGPVSGDDDAAASSLLYKSAGSGNNTNERLIALYEK
KKGDGDSSLGMVSVRLTAQLKWVREVLATWKEVDGRVSKLCPSTAAKNPSTGNGCSAVKT
TDGLVGFFSGNFSGNTWRDEYLGVNATVRKGTNGVATGYADGVTFHGAWAEWPVGRQGEN
QLYHFANYNFTLVATLSVHGEPKGDTPIPLMGATMNDNKKTVLLGLSHDKEGKWQLLCGG
KTTKELRSNWEPETTHQVAIVLRNGTQGSAYVDGQRVGDAPCELNNTDSKGISHFYIGGD
GGSAGSKEDVPVTATNVLLYNRPLDDNEIRVLNANKISIPKLTDLKTVAAGATGVGAARH
FGANGDGSAVCGGGLLPLLLLLGLWGIAAS*
>TCRU_4106 hypothetical protein, conserved
MRQLIHIASRFAVLLVLLVVMMLVMCCASGCFAASLTYSCSSDKAMRADRAKSIPAVVRD
VPLGSEGASQTCTVIGRNGWAPTRIDVSTRDVDGTRKYCSSERYCAMNSLVAIASVKVTF
FYAEKREVFVLLYFAATVR*
>TCRU_4107 hypothetical protein, conserved
MKREERFSHDFYHNHAATITRRATRTRLAAPQDEHAIPLQQVNVPVLNLEWIKTRLNPAT
LERLMQVWRLVGRSPLPPSSSGKAREGSRSIPTADARLLKEAGIIEDASSTTTDGWIIPF
SVVEEKTTGLRRRWIAWPRDRNRDDPYEANVPLLHISHYLPPVMTEAAFCLDLKASLSMP
IGGRHAGGADTRWIAWPRDRNRDDPYEANVPLLHISHYLPPVMAEAASCLDLKASLSMPI
GGRHAGGADTAPYGIQGQSINSPDYHLGNCGGDDGGSPPLGCTSIGACRHLDR*
>TCRU_4108 Histone-lysine N-methyltransferase, H3 lysine-76 specific
MLGHFQRDVRGGSSSRRKLPRSVVGERSEEGSGTSKDPFVLSLRETPNRSGCYHCIEDCC
ECLWITELLAVCYGSLPTRRQVMTYRKREWCAKSILPPFVARIVRVAKISSHDTFYDLGC
GNGSVLFQVALLTGARCVGVEINEQNATVAQGAWRRLRPMIEARRGEPVEVEIICADFCS
LMRDEKFFGSSPVIWAANLLMPRPVNHYLSERFRLLPKGSRVLCLEDLYPHGRSVAKFRD
PDAFEMFAMTDFKWQTKSVEWCDTEGPFFMYTKRT*
>TCRU_4109 D-isomer specific 2-hydroxyacid dehydrogenase, NAD
binding domain containing protein, putative

MMKPSAVYISIGRGITQNEDDLACALRDGVIRGASVDVFEREPLPAESPLWDISDDKLLL
TAHSADRTANLVPDSVRRFIGLVNEYAKTKRLDTYLVDPVRGY*
>TCRU_4110 BNR repeat-like domain containing protein, putative
MSRHLFCSAVLLLIVVMMCCNAIGDQQADAPAPGPGSSPENHFVWRSKKEEEKVSSLYFP
SLLEVNGKVFAVAEATCTENDKVFTGIASELLTLDKKQTKELDASKVKTQVLVECPSDKE
ECASQPEDLAVSQSETKVRVSRPTTVVKENDIYMLVGNYSSTAVASSHETASDAAILELL
LVKGNVGGESSDSIIWGDTAGVPCVSTVEKEKVGSTRLIGGGGSGIKMHDDTVVFPVEGT
KKEGEAQKAVSLLIYTSDNAASWKLSNGTSDGGCSDPSVVEWGEKDKKLIMMTACDDGRR
RVYESGDKGESWTEALGTL*
>TCRU_4111 Leishmanolysin, putative
MLCAPTARSIPGVVGDVPLGAQDALHLCSGVWRDPWVPIGIKASTTDPCDSRRHCVFSWS
HAMNSLNDNLYFEDDVLSSAHGNSLAEETVPAAVKLHAVRLLVQPLEGPLIVYSFATGSG
CSHFTVPAWHCSTGVANADMVLCVAAAAGGVWALLCAALEDGCPVAATIYFARQFHFTDA
SPPASPRTCWLMLSGSTARTWQAAAW*
>TCRU_4112 hypothetical protein, conserved
MELIRKRRSTVVRRSTDTPALGQLYEESKRGGSRDLCPPTWKQRVSLAGQFTAFCRTHEQ
PMNEESCAAFLMAIGVAPLTRLQYARMLRSMLEMNRTPLDMAILGLQKIAARSETQQARP
LTKEEMNQVIRSRTDWKERVVLRLAWITASRWSEIAALTAKNFTPEPDGTLILDWSVAPK
TARADPHRASRFVKIRGQDAFDNIKLCRTLQENEKLTNLTTAQVERALAPWDATAHSIKR
GALRHAAQIVEKYNFNPHVISQLAKHVNPFDLPQNTVRYLWRYTTMLTQLPSLVALM*
>TCRU_4113 hypothetical protein, conserved
MSCRCTMQRLASRTPRRPRLPWLAPALAPHQQLDAGIAARHQADRKNLKKSKRPFANYFR
NEYRSSPSYSPPVTRTDGNISSYNVVRLMTDGRRTWTPFWGRATGGVRTRRKRQDVLEPP
APQFGDDGLDRTIERLLEIRFQWDLGDDILASSLVTPSLRAMTEHCLPFAPCMGSLLPSQ
ERKQEGLLGCVELDGEQIPLYVFRGRGRRKGTAVPKVNLGFNGVDTVPSVVLDATRGPLV
SSPTETSLSVRWKATNREATSVSEVLRLLQSVGRVSVIGIPQRSLLLLAKALATAEVEDP
AVSISLAIAAAEHYYDYSHTECLEMLRCLRRIAYVRGLARLPESSASALSLYRDVKQCQM
FFAEYIGDAAPFLVDKVWSRLPEHVRRLTRRKLFLDLTDFLSLAVELHGWRIPYNLPNPV
SSAMYASKYLFLRYTLMLDEPMLVEYAKCMSGATSFDALSSSSSPLKDLKGSELGAAASE
VVLSPSLLDKRKKNIEEDEEEDACTKPLVLWLCVSLLVRLTAEALGDVLRHVEASMRQHV
QLAREYEMAAGQGESRERRLKAETDLQLYLDRIALYRPRQRVYQCIGRRQPRKMRLRLIP
LEAFPEIFRHTRLPFEAETRQAHISIARQRAAAQVDSPLVAVLARSALAEKHIQRACGAL
DWAAMILTQCTCIVRRFATPVNWAQQVDASAQPPSPPPPVSPPVSHSEAVDSRFVLCEAH
VRSRVQRDMDCLFTHIPWQGLEEQLQTFSEEERQTPTAAKQMVTEEAAGMPDAYFLDDLL
NPSKGDGTDCGSATGESGVSKSQATASTSAEREVQMMLGRLQESVERFQVAVADLIDAQE
EYFLMS*
>TCRU_4114 hypothetical protein, conserved
MDAADRLKESLLDAAWVGQALELFADELRDLELLEEEEEKRFQAELQRMREVSAESTLAP
SANAEPKVMNNERKDTARSRKYGSSQPKRGAAERTAGTAGGTAKGTSGFSQLIKEKEAAM
KLAREGEFWYRSLHDMKQQMQNAREEADRRRALARRQLRFFTARSIDEYMMEEILQGVPG
MASRGKSTLADATSDEFHGKDAVSEEGSVTVVSTGTPTTDAPVLLARSGCPDTLDTECEF
TIDAVGFARDLNASLEKEYGFRPVLSTAEDKADNTTTTAATTTTTATTTANMTICQLKSK
LLTHVPGDLMSIGDSWSLTLPPVVSTHEGAAVPRSRSRSVHTTHERKVSVPLPAIIHQGD
GGVADSDALSRFSSPPPTANTTADGIAIAATPRTGTIMPKGLREAGSVPKVTTGYQSHHL
LFKTKARSGRFAYIECSAENNRVKLRTTVGAEVSTTVRFINREPNLLRVRIPPSKHAWIT
YSMVKSSVDRRVSPASPSTFSSVKPPPPSSSSSSCLASAAMTRIAPSEPLGCGGFVEVRI
TFKPQSATEPLVKEVLRLGHCRELNSRSGEGEKWHFFEVNVTCETVLPQFSLIPINHQGE
TGSVYSTAIPSTGKRSHCPKMPEQAVTTVEFPYTYVMDTCSRQFYLENTGSVAMVTLNST
SPCFKIDPSTEKAIILSGGDRVEINVSFVPIKEMRYDAEELIVTVRELEEGPVISEQRFR
LCGEGVLPRVDLVRVGTLELSAPEQDASVPQYMVPGTAPGVETKVLVVVQNSGPIGVPYF
WRTDSIGGGSPLGGVQLSVTPATGVLPPENESVFLVCLRPATAQPLAAVLNLFLEGLPMP
SAAEEAAVSDLYVRGRPIPAVLAAEEIQTMSDPYSVFQRWTREQPKDCSGVFATGFYLFA
DPVTPSLVMIPDHLEEGVECLVNCRNLRRITMKNNSPRPLHFCLDPNPDECPPEVVLSRR
DREFVDVGFEPRKGCVPPYASVTVLFQFTLREVGQHIFVFDCYIPELMELLTTTSTASVT

EGTTAPPPTQTGMIKTPPTTELYCTHQLYLSVTGVGPSVSVSTGCLDFGLIELGAEAEAS
FTVSNDNPIAIVFELQDPIMQEKGRFVFLPPSARLGAGESVEVTVYRQAVELDDSQAFFE
LMVRGGDTLAIETHATIQAPSLFLEGAVVDFGVVPEGAWVEQDVVVSNPSAFDFFYVFEL
VVVPPCINIIAPPPGVVRAGYQGIHIPIRCAFEFHPGEGKKEALMVIKNTRTRQELLVEL
RCERVQQLCAAIDLIPVPKAEKGPGSMAYTPPVLSCNLPPPPTMEIAHFLEALLWNLVEQ
SVMDEDARCSESKVTDVSELNEIERQPAVLRSYCPPVLLKSYLPDKEPVWSELLALRVSN
QSSCHGSYTVEAMRYSLKGFLEGLTGVSTKGESHAVRATAATTSTTTVCSGRLPGKRCHS
GKGRERKRRRQLGLDSSCGTERTGESDLNFSIGNVERAFWCKGIDGTEQMERERRAMLFD
AQKVLLDGRGCATMFGNTPVGPLHPNATVEVPLSIFSNLPGRYEETLRVRCGKLPYTHIP
LTLELSGKPVVLDSNTAGLTVLGGRALMRMPAVIAGVGRSRRSMVLINRIPRDLTVSVKI
FLTTATFSVVAVDEEVDAAAVTLQLQPVSGEEQQRESEGKGKVAASPENLFLPALASREV
IIEYAPDATFVPKEGASEREWRGGVIITAEVADTPFNDGFLINEFYRLHAARYPVRGGVM
KRKRLRESVPKWMRSIVRPIMMLNVQQPLISRPGVVKNNAILLATPGELTVVKKHFAMSK
SQSCGTFMSEEDKSNMGNQSQKNNSRSSCTKGSEDKGEEDEGEDTSLDEESQEDYQDETL
VSEKPLEVILAIEEERKALHAFMEQRKLEMAEHSRHYFIPIELEVRARCGVAQLTVEPSG
DVIHFPQYVEDAPCVQTVRLNNLGCAAMEFILDLPSSSFIVASARYISKNTDEELMEVDD
EEEARKRWAIAALKWVTREERQSSQRVLRAVKRPHSGDMAITEVKMANVDCIARSHTRSG
DAAFVTVTKYRLHPHDALEVQLEYCKPSKQEVHAMMRGSSIVQGALSIMYLPSDGVIKES
TAHEGGAAHALCPPPVQEVTQTIPIILSFSSPSVRCSPSILWFRPGQLLHDGRPQPSYAQ
KIRLLSSYASAVTFVIVPSCQIFAEFFSATTETFDEGVAGTHAYTRSTALEATQLLTRER
HIKEVANYWMEDEGDGGAKGGDGEKDESETEMDSTGVDFCSTECENPQPMQLEQEQQQQR
RRPQKQTVRQKEERQHVVVEDTERFTITPMQGTIPGATRGGQPGVCEISVTFKEHMNVRF
EAVYDVLINDALVEGCCFGLRGDSRVTEI*
>TCRU_4115 hypothetical protein, conserved
MGAVRGASAGMTGGERHQELSYFLIVTAVRVRGLPDTIADAPLVAELTVDSCSLLTEPLL
PLPMEKEDAMQFERPSSADSAHFLSAGRTLGLDSLHIVIPIAGDWRWGALREKASSSPFL
HGGEAASMSRGGIHVVLRTADEALPWGSASCYYPGDWFPMTPCGGEVQVGFEVYCQESGD
VSGLLVPGQMSLDGQSELAEPHSWSLAENQDVAFVPTDGGTGGCTHLSRVASKPRQVRSA
CSSPTSRLACWKRRVQTAGQASCERGRADGPSLYSDSVHLSHSAHTDAEFLHPRRSYVFL
VESASGNQLESAGGENLNPNEFRTRACQPRSLVFSHIKVSGFQPITSHGSWTLEFSWPQH
KVSPMKRIMWIPGSVDGNGAAEIQETLSIDLPLFMRGEIQTHMHAVWSGSSNNDPKTRLY
VQVEFDPIVLVVGDHEMHWEGCRSHGPMLTNGLPLTVSDLCVRFLVKLEFYEPQRDGRNG
RPTSAVPRHREKIAAAAADATGERERGRNNGVLRRGAPESVEKSATQRAAEGREGPPCVN
GVHHAETWTRGVHSLPRHGGSDVSHRTGACTEPLAPLHNRNQQQQEQQSQRRGRGTPSSQ
RSKNATQMFPDVRGLVPCYSEQRRQEVFQAYDTKNCGHMTIEQMLHFCRAHVALFDGEEN
DASILRGLRPYVASAAVRSHAETCSSSNSPPSSCRRSRSLSLERRGSPRTSANGHELSVS
HPLPLSSATSEGASAAASLAPMGFAGCESQGITYNVFEIIALRLASM*
>TCRU_4116 protein transport protein Sec24
MYYPYGGAQQQQQQLLDQQQQNYYYYPQGQQEQAGVPPTSWQQYTNPQHGGAPPAAPAG
AMHNGVQLPGQYHDPYVSATPNGVQSYSNYYPTPNYPQQQQQQPLPPPPPAPQMHPQQPQ
LPQQQVQQYPHQDATTTTTDATTTNNAAASASLISSTGAIPFANSQTDASGMQLPTQQHA
YQAQQRQQTGAFPSGNYPRQQEQCNSVVGRCARPPPRRSVDLKSAPNPRRDISQKPGNQE
IQTSSGQLPLSATGFLAVDDGNASPKFFRPTTNSVPAEERLVKDSKIFFGAVLAPLCRPL
YPREEVPLVEGRPPVRCFRCRAYISCHARFVDMGRCWVCPFCNMANEVENEYFCNLDARN
QRLDRAERPELSRGSVEYDVGPYPDYALRDEKDAPIPARPLHYLFLLDVSQKAVSSFLPD
YVDALMHSLHEMAQQYPQCRVAFITYASTLQFYNVRHPRMPQLIVADVDNPFVPLPFTSL
CWLTLGTELDLVDTFLMRLMEYAQDLRETDSVMGAAVHAATLVLAGQHGGHVILCGHKAP
QRGIGALKLREQHLLYGTDKEKDLLRPIEGFWRTTATACAKQQISFDLHMFADQYCELVT
ISQPCHLSNGRVHLFSNYDRETDATKVQAVMNQALLEEAGYAGILRVRCSSGVRVQAYHG
HFMSQDSHDMDLAHVQGSSTFFVEFAHEGKLEKTSYAYFQTALLYTTRGGERRVRVHSVR
MSVVTTLSGVFEADLEATLMGYIHEAIGNAVNKGLQYARSTAQDRVLKMLIAYRRVCTSN
ATSSLLMPSRLRLIPLFVLSFMKADALVEGTTVPIDDRVQKLFLLMTIPMHQCVTYLYPT
LYAVHHLLSEPTSGVIDPETGHCVLPGWQQLIFDSITTDGVYVLCDEQARIVYLWIGSSV
VPEVSLELFGTTNALDVGRTVFFENFGERLKNVLYTCLMRDDGMRRFVIFHEKDRGEEAF

FRQFKEENEGGSMGYDQLLVHLHREVKKSIE*
>TCRU_4117 GIY-YIG catalytic domain containing protein, putative
MDTRFHCVYLLTSLDPQCAGEYYIGYTVDPIRRLRQHNGEIVSGAWRTKRRGRPWELLCC
VSGFGEDRIALKFEWCWQHPTKSTRLKTQMTQLRGVHRLPYAVGVLHLLLRADLFARLQL
TLHIFEPEHVGRVVAELQGRVPSIPPLVATSLLRIEEITKERFMSLYLDGVSGGDGTAGD
GCVYFVTAPLSSQPEADAPSRRVRSCRYLSEEDIFRQHARVKELLEANQCPCALCSLPLR
SPYFVRCSRTPFCTLRAHLACLAMWFTYETMQKRDATMGQSTRNERSGEYSNKIKDDSND
GTMDAHASGRQLHSLSVNNADFSSPRDAGSIPDSSGHISAFEESRCASSPSLTLLPSQPC
PCPLCDEPLQWGALVHDLKRRAVLEKRWMERQRREKIEAALAERLQRLQNSSLTERKSRR
KAKPALGQKRNRGENCGDTVGDGGKEAITNWRARVMDGCDSWNDTNDFSHLVSLPPSGDE
GYACDSSRRGVGGSKHTTRMTDEGKNDSITDICDCVLQLTEFNLDEWLDA*
>TCRU_4118 protein phosphatase 2A, putative
MEGALPTGIANKTIASPTTTGTAVAVPTPPGAVGEPNSFNVDELIQYVLQGKPLSEPQVA
KLCQKGKEVLEKEGNVHTVRAPVTVCGDIHGQFHDLLELLKIGGLPPDTNYLFMGDYVDR
GYYSVETVTLLLLFKIRYPERVQILRGNHESRQITQVYGFYDECVRKYGSANVWKLLTDL
FDYLPLAAVVENEIFCLHGGLSPTLDSLAHIRSLERVQEVPHEGPMCDLLWSDPEDRDGW
GISPRGAGFTFGADISEQFCHNNGLKMIARAHQLVTDGYSWAHNDRLVTIFSAPNYCYRC
GNLAGLLELDEHMNKCFFQFDPAPRRGEAQVSKKTPDYFL*
>TCRU_4119 RNA polymerase subunit RPB10
MLIPVRCYSCGKVIGNLYEKYQQLLSEDYTEAEALNALQLDRMCCRRMILSHIDLVDELL
PYSVPVVGTMPFANPLQTSKPHRR*
>TCRU_(GCN5L1), putative GCN5-like protein.1
MSTDGDTISKAAEATGEKDVGSSQEITCPHCPIGAGNEGQETALLVCDGKQSSGNDEAHF
VRGASPLFSPSSTTTATTTNTTSVLEGLIRAHRERQAELRAVGSRAWEEVRQHAQAACDA
VTDSANAEVFAAFARERKIEMELKAIAARSSQLQRQMTAWATLFGKFNTELKEMGDLSNW
ARRIEEDLSETVHLLEELSERKRRAQGM*
>TCRU_4121 hypothetical protein, conserved
MSSTAVKKMSAERKEEEEEEENKKKTTTGLTIHSEVPYTEEEKTFLLEQLVALSQEQQER
QHDDDDKWTRTTVPLLVSMLEKVLQLAADNYEDDSNNNNISNSAGTTTTAATNQKPKGGG
ATTLAAKPLSKMECFLEENDYIIEQMQQQQRPFFTLPRLLEILADPFIYNRDAAGKLRGG
KLQAAVRRCVLVSYPLLTVQWPFTSEVNPA*
>TCRU_4122 PRP38 family, putative
MVEPHLFCGPEFVLEVPAEHPQPIQPHVLLQLQTELYSLLTPTVRRKIHTTHGSHSGSGD
LVPPPPDSLLFIDMESTPPTDAGNEDDYIHVLLLVTDSRAAAELFSIGLRNPFIALPHRM
RLRNHYAGGGGKPRAPPAEILRKKESLRSRMNFDEDLWETLQKALTPEWLQEFESRYCQI
PEGGGTVPMRDAEQHEQRVESLLRYCEREVQYVGVMDEEGNASPFLLAMGVFYRFGLIYR
DAFVHFVRHPRRPIRALALFIARYTAAPEELEPFFVPSLTDEVTIACAENANVTTSMRQL
CADLLLCDEVCEAWPPTYHAYWVEHKVRPMMQRIEAECKRREELRLTRRDEGGGGGIRAA
ANMTPTNASRGNEETKVRGSGGGVGVFGFRNMRELQAYVRERERVLVPQRILSMTAAPKE
GDGDGVYYSDLDDDDDGDDDDFLIKVRVEGSRSGRGAARSTQTAPQEVQKQKRGAERRKR
ARDSEITTNTRALVMTGAYRTVLRLLGRTEPFDRRGEHYLTF*
>TCRU_4123 NPL4 family, putative
MPTEADLEKIRRERAARYQQLSEAEKPRVEPCPHCHELPYKKEVCPETGIFHNLERHTIV
GGAVVQSNIVRSSELMEAIDRSRIRWVESRTQMVRADAVSLNLFQSFVRQLDWSLQRYGI
LYGKYDASLNLIEVHAIYEPEQHGDAYTFHYLPDKRLPNVDRIAALLGLRRVGAVCTHPP
RDIEEMVLSSREILLCAREQSRFGDECVLLTMSPSLTTGRIECQAWQTSPQAVHFYRLGV
LREKSDDYSDLESAKYVHSSIPLEVAQQETDEKGHPRVVTMAPSHDIDTRWFTSYVAVQQ
FESPVVRNLFMRVSRPGMEPPAMINLRNYMEDPKRRKVPLIEKLADFHVLIFLAESVFSV
ADDMPVIIGAITKQRPAEDAMHYGEVLKLYLEQ*
>TCRU_4124 cullin 4B, putative
MASRTLYDPPPTALQWDVGPSQEKPCITVKLLTHDAEMHRLACEKEKENAWTVAEGMLDA
LLVRLAAQSENVISSTPPFEHSTSLLSFLISSSPSASSMSSISVRIPPVNVSNRGYAADA
ACRSVRTLVELDAASAVYEKLKQSLEAYVMHILQFLTTACEPDGEGCLTFMRLVHVWGHY
RLAVAELQEVWVYLDRWYISRMHAVRSIDGLAIAIMKEALLQHPWLLSRAQVGFLTFLRQ

DFENESNVRREILLFTNLCSSIEVYFLRVEPDVLAVAKEFYTEVADRMWHDGESAEVFFQ
QVGCFLQEGRRRVQACLEANTMSKLEEIAQTSLLAAHGTDVLARDFERLVKDEKYDCIRL
AWQFLALGKYVQLGKECGAVFREYILHEGVTIIRQLTSRPADREGFVAIKAMIALIRRGE
SVIDECFAENSMVFTVQLNDALVEVLQENQTEFARQIARYIDFLMREEENDTLMSAPANT
KGDDGSGDNCLYADATATANDGGSDEVAAAATATATATAVSPCGGLLNYIGRIYALLPSR
GIFETFYWHDLARRLLQYQRPRRLDAERSFIQELKKACGVETSKFEGMFNDLKVSQELNE
RYQAWVTGERDDASAQWPPVMRVDNEEEEEGEAMSLIAELPWNTEVKLHILTSGFWPTQS
TLAVRLPSPMRLLAKSVQDFYRQCFTDRQLLWQHQLSSAVVRCSIGTVRRNLTGTLLQAA
ILLTLQEMMDTTPSLSSSQRVEAVTVGALCDRLAVDILVPAVTGSIYGLCHPKFSLLLRE
PAMGGSSAAAFPMLAGTDRLRFNTHFAVSSMRCRIPFYNTPNSGEDVSTGRNDADSMLAV
DDVLKEHKHVIEAAVVRFMKEKRCATHEDLVTAVSTLVQFPVTMATLKCVIERLIDRGFL
ERNGATAYTYTL*
>TCRU_4125 hypothetical protein, conserved
MWLENITRDLGDFTSSLMEDTKGLADMVSRIAAEVTGHSTYIAGDEDSLLAQECPLDEAA
IFALQRTDAVYLEEPREPEEKALFEEWIRRSVYSSVNAFCRDHFDGSGSGSSYNAAMTCR
QRLLDENPLVAEKYAAMVQTSDLPQRESPSESKTTPGQPSLEGGEGDVKTPKKSATASPS
DLQRITEDAFFDRYFFRLSQLRLSTAAERRKREEDEAAAAAAAATAAAAAKVASEAEAPR
KEQSKGKSLAERFMEATDELVGWKEEEPADAKDTGAGEDRNSRGVVHRTEAEWREQEGKI
AALESLVHLLQVELNDERRKLAAVLKLVQQCNLNESQMQLVHAAMETTTTTTAAANSSA
ASLSSSPPNHVENPAMGGSGAHHGDGACESGRDAAVQETSSPEAVQQQQQQQCEEEVPRN
PASPPSSSSSLENDGWTNV*
>TCRU_4126 hypothetical protein, conserved
MMRVCRPQLLRVSPLLRVWAAEEDDANAPPTTFKNVKPGRLLRLWRQIRHRSWIVYTWDE
EWTSPGSEGYLHQQRLEQVCFAPLSAYGMVPGSYCDPLLYNTKHTSPFRWHVANTSSDIV
GHWYMEADEIFRIKDWQPKNPDDPTEMFPRPPQQILKWDETVDEHGNRTFRYKYRYDFMG
PTGMWEAYPRYPFSHIYLNGQDHHGRAEGYGFKQGHLLRCSEEEEEVLRRIMEEEDKEWE
MVKRTEVVQEPWSYPGKIRPQDFKGAVERAKARFREQIKHGKETDPSEDPDYDLVQAGEF
VEPRDGPRAEWRHLWTSNRPKGEPLPYQVTFNDGITFEDNEGRPPVHPESHYEQTPKEAP
YKKYEEQDTKEEEEEQKRRKSAWDQSFKESIAKYEERYGVEAKKGDSDKKSSSDTGKSSG
GGDGSTPPPSSSSSHEGQDGKK*
>TCRU_4127 Ras-related protein Rab5B
MTSIPATSKKYKVVLLGDSGVGKSSLVQRLAKDEWNENQNSTVGASFFRYSCPVDDTAVN
FDIWDTAGQERYKSLASMYYRGAAAALVVYELPLYETFERAKYWVRELAANSPETIITLV
GNKSDLANRRNVSAEEATAYAKELDLMFIEASAKDGSRVRDIFEKIARRLVAANSQNTVR
DGGVIGARQPGKKTRQLGCC*
>TCRU_4128 hypothetical protein, conserved
MDRPFLPYEFDVTIRDSLLGSAPGPGDMLNEFLHRLGPVAHGTLRTMIHNSFANGSLPGS
WNTVDTIPIPQSWEGPMPPRELQTYHAALCFTTTNRKNDSPPSINVIAAPPTSIWLYTFA
FNIGRDDNCYW*
>TCRU_4129 Reverse transcriptase (RNA-dependent DNA polymerase),
putative
MGSYSAFLTDSRAFAHRTKLWLHNYLRGRYVRVCTREQHSRKQLASDGAPQGSVPGTKLF
LRHVDDLPHRMDNNYSAAAFMYTDEHTLVASGADIHACAAAMPPALSPITTWAVEHSLKI
NDDKSEAALFHISSHTLSDEEMVDLHLVSGTISI*
>TCRU_4130 hypothetical protein, conserved
MASKQDRISDAMKERIIQLEKELCQCKNHLSESVQQKEALECDIDALQKEAHDVVAQWVA
KSSELQTKLDESLSQIGALKNDLLINKNRNDDLQRCLKDAEAANCLQVEELHRLKKAQDD
HAARLAAIEKDFASASQQNIHYENLVSKMDLEMKQVVEEVNSLRKERDTLVETAAELREE
NCRLEATHFKARNFIGLLEDKLAGHQQLLHQFSYTMLLDEEERHARDEIVFQWGTLYVNV
ILAERKHHIQSNSLLQTKHQELEEEINLLRKEKTLLETEFHKKSNELSSLRQEYDKTTGD
LSQHVCLLEQDIAELQDAQIGQKQIVELLQKELEFSTAQNELNKSLKEDLSTEFKAVKDC
YSSLLLEYNELRVNEQRRQQELNAKITFLTEENKNIRAENDACFQEVMKENTNLRVCLAS
TEGKNLEHIERGERLTVEVFQSNEWALLFSDYSARLVNWLHESYEQIWTMHKEMNLKETS
LKEKENMNCALCEKLDALEKGFSSKQNDITQLESKVMELSSELKSSKETCEETVNDNTWL

KEQVETMRRELGELDELLNSNLNEMREDSERQQMEHERLIKEIHHYEDLLRQSQEKINLL
DERCHILSTDNEAISKTLLLTEDELSKAKKEIAVMHQRERILLEEKRKIELNFIQLQKKH
VTADSQTALLQEQLQTQEAKLQILGKSSRQEMENMKMKLNGFIEKYEEAEARVSAFSKSM
RDSENIQCNLREAYQRAKAALEEAKRRCSKDAETIQKLLEERQNLENEREIIVQKYNRVQ
EMLKSLKKDSVGKFPDEIQKLSDLCFQQEVELQQLRHQNIILKKCIKKLPVTANADKQIE
RPVFVERLNLAEGPLRRPKKRSVLNEDTR*
>TCRU_4131 hypothetical protein, conserved
MKVGNRDYDPCVKVSLELESLLQHHFQQRQHSKRILKDRLRKAELEIAHLQQSVSAYSEE
LRVERLKFDTLQRTMEDAKRNHAAELMEQEKLIRDRMCNVDTQTRLLVVKTEEFERRVQC
LQKQEEELLNREKELKFYQASFEAGIMPAQRQIEAERVRMLRAREKAEELLEEARISALA
TEERKKKLEALHILEMQFFALEKEEATERIQIMRQEILGLVGLISFRRTHVSAAEGEAAK
RIRLLEEELASKKEVFELREKEVYLRYQREEQRMRKERERIISIKEAMRQDYRLVLEGIR
LFGNEYSTEPDQLQVDALKDLEKLLFSALDDHQLEITKKL*
>TCRU_4132 hypothetical protein, conserved
MLDSVTTAAVGYGASCMSIFVLYPYRDLTKIFSINPITRLDPIQYSWVRYKGMILNPSQP
LILAFPWGLLYGGFALGSGALTGALVAGTLHGMGKVAVRTIARRVGGPRSRYDGVVYKSL
LHCLQASTKQYGILSFFSGASATALISTLWHGASLVALQGSRHDGFFEAWWDAFRVHALL
TFATNPIRNTFRSALHSRERAGGVCNFSAFLAGEVAIFREAGGVMKNMLRTMGLPFFLEG
VLRTTFKSSVPFGFTFALFLAFGGSLPGQGGRDNDGHRYHRHHMPLRRFVV*
>TCRU_4133 hypothetical protein, conserved
MLRRSIVWKQMQNKGPARPGPMLYGWGRTEQKRRLEYETVESKYHKREFNKNWDLAGVEQ
RYTDFMVVRTYFSLGTRWGTWVYNMLQFYVLAMLPVFIFMHTFHKNVEWYDERIRLASWW
*
>TCRU_4134 coatomer subunit zeta, putative
MDFLHHVQGIVVLNELGGRVFAKYYINAEMQTAGVLNTMDKQRALELGIHAAARDPKRGC
SNSMDGDVMIHGGHTVLLHVFEDITFIVIGDGSENELVLHSVLRGLVDALRQELKVSDLN
LRTLLGKYDAVLLTVDELVDEGIILETNPNSICQDVAPFVSESGGEAARKALDKVNKYLK
DTL*
>TCRU_4135 ubiquinol-cytochrome c reductase complex 14kD subunit,
putative
MRPTAPRYMAQGIWAGFRYYFGHFFYPNMYREFLSVQNAHKVERALRIQSAIKANKIDYR
ALLALPVTDHAHPYKMEYPWEKLIHTDSRDLGLYGKWYASKIMCFYEGLQYHKYGCLQDD
LINAHGWWNRAARTRAPQDKIVHGDRRVMRARVLRDKYIYEPKSRWVHPIDNVAYFGPYV
MMVCDEWEEKWGFFAGQEVEY*
>TCRU_4136 hypothetical protein, conserved
MEEGEVGMSDSVNNVRNITLRASKGHYLLAHEAEEARRRRIEEKRQRRKQELQEQQEIEW
KAFQDATRRCLKDAHLITTMEELQFRETLHSKYSEICKAHEEEMEAYTERVVSDEARRPM
TLSPLLTLTRAREKCLASARLYGEAAKMQALFSQLEECEHKAAEEHKQQMVERRVREKWQ
EIKKRSFSSYQKVFFAQQLKHLQSAERMRAIEANLRHKASEMAVSHHNQRQALHLPLLDI
RSSSKAHQLRGSRGSQLKQKVNGDHYYVPSLCDMYGSSLEHE*
>TCRU_4137 prohibitin 2, putative
MAKAPPGPDFSRVAAEVRKRLGSFGDVTGLLALVGFTGILGTGLYKSVYFVDGGCRAVKF
NAITGMKDKTYGEGANFAIPFLETPVVFDIRNKPTEVMTATGSRDLQTVNLAVRVLYQPS
VNNLSHVYRNLGMEYAEIVLPSLVNEIIRAVIAQFNASDLLVKRPEVSHRIAVMLAERAK
RFYVDITDVSITQMSFGKEYTSAVEAKQVAQQMAERAKWRVEQAEQEKKGAILLAEGEAE
AAKLIGDAVQKNPAFITLRSLEASRAIAKMMRKHGAGTFYLDSSGLTLNANATGGEGSAD
VHGRRL*
>TCRU_4138 hypothetical protein
MRAGNHPRENTRIKRVPHATRRLSVYPYKDQHFITAGSSVRRSPMKNREVYDASRRTLPR
ASIPISNGATEADFPRKELEEIAAWLASDAIFLEIESLAARTHVMCRQEETLRNDTNTAA
TAYSGNGSATRKRGLRLETNSSMPSLPLNEEAYARQIFDRDAPKQQEGNFSREPSTPPEP
YVGDTVAQPAGGQGCDVGAKIEQMISLQQLAYGRSALLQEAEDGEKEGSNSPTVVELLEE
ILQDDFNARSSSHSSPSMVQVGVSVSVPTGAESSLGDGAVSLRDASPPRSGACFVHSSCK
TDLYNVVQIPRAHYILSEVNFSHW*

>TCRU_4139 branched-chain alpha-keto acid dehydrogenase e1-beta subunit precursor, putative
MLRRIGTTHVVSPLSSFFSSVASARRLQMTAVSASQAREHADAPEAVEMNFLQAINSALD
LALSRDEKTVVFGEDVAFGGVFRCTLNLSKKYGSQRVFDSPLSEQGLVGFAIGMASAGWK
PIAEVQFADYIFPAFDQIVNEAAKMRFRSGGHFHCGGLVIRSPSSAVGHGGLYHSQSVEG
FFNHCAGIKIVMPSTPSDAKGLLLQCVEEEDPCIFFEPKRLYRSMVEPVDPGYYTIPLGK
GKILCEGRDVTIVTYGAQVGVAMKAAERAAQEGISVELIDLRSLKPWDREMVTQSVRKTG
RVIVTHEAPKTSGIGSEIVSCITQDCFLSLEAPPMRVCCLDTPHPLNEQLYLPNELKVCE
AIKYITGY*
>TCRU_4140 ADP-ribosylation factor, putative
MGQWLASAFKSLLGKQEVRILMVGLDAAGKTTILYKLKLGEIVTTIPTIGFNVETVEYKN
LKFTMWDVGGQDVLRPLWRHYYQNTNGLIFVVDSNDRERIGKARQELEKMFTEDELRNAV
LLVFANKQDLPNAMSTTEVTEKLGLHSVRQRNWYIQGCCATSAQGLYEGLDWLAANIKKT
SK*
>TCRU_family, putative Se.1
MEHGVTLLEDPMTPRQPIMSGPAPYFFAVEDASVSRVVEDWMAKVPHRDAHIFALGCTPH
RSPQQLVWVRIAPRAMRSKVIMLDFTASEVLVFHLSMQYGFPRLLSPLSPPN*
>TCRU_4142 hypothetical protein, conserved
MLTSEDPAEHAGQAGQAIRPPQSPESDGTRHSDSSRGDSSVSPLSTAGISSSSALDAPFV
QSTQPSEKGLRSETMSLGTALPNEQPKERSESKAKQGSSTSEEAAESPDDSGDAVEKEKK
KGDVGLKATKSLSSTTSNPPVTQTTPRASSAEPSPTETELQAGEETSTENVTITMRNNTT
TPGDSDSSTAASHTTSPLLLLLVACAAAAAVVAA*
>TCRU_4143 hypothetical protein, conserved
MTEVAKLPLNCERLEVLDESTMAACGRHVVYFCPLPGSALSSASSSVVEVSLAKSTVCLA
PWHPPGAALQECGVFYTEVGRIHFRRRCYCGNESVQESRDVLEPPPPASSGIEEMRVLFG
TTLVVRTAESVACYALDPTRGAEVTRLPLVGRVTLPHPGLTGDSTEVLMMDGSPAGAVAG
DVDHTLGVVMYCRTTRRVSALLLAVGPACVTMQSETRSGGLALPFESNASLRSWSFNWSR
REVLFVFADATSSSSSSDDTTKLLTRTLSLATMEWTVSSTDLTQLPFVPADVGHTHTGDT
WAVDNSFDGVVKFSKLLSGSVMREVVLQRAAGSDAIFLTAWGSSLYVLMGRRVLEVREDD
DRDGAATKTTLCDWLMKQVAREPRDVPHVPTPKRKRKEGNDIEEEVDAIVAFLRNPACSS
FAMIVRDCRYVSCTMDAAEEYSHAILDAIQKTSGKNCDNSSLVRYIAVAQSLHPLTILRV
LSVSDPSIRLTLAVLLSTKPTLVAGGVRLLEWGPPVRAFCRSVGHMQAKLFTAAMCETAL
TALAAGALGAVGLLCAVADVVMVTALGNDKRAVVSREEAAAEVTIVEAVGVLSSYAQWAL
AAAPALGTITAHVGPVRKGKKEAAVRDRVAHSILLSRSVQIEPLLLLERRHAS*
>TCRU_4144 hypothetical protein, conserved
MAPTENTAIQVNPPQGFYVNFDVDTTYVIPFTVRNDAHSMCTVRFTPPRNQHVFRINTAS
VRLAPRLSYVIEVEFITHVAQDYQDSFVVFTNTESITVPLVAKCSPDLEFPTKLNFGRVE
RDCRGLSKVLRFTNKGRRDKHVQIKIGKQSTGVKVRPLNCVAPPMGFVDVCVELLKLDFG
HHQLPLHIDVDGEAKQRTLLLEVDVMDSKGVLIDPCSGEEVHALAFAKTYLGTRSVVELD
VRNDSEQPVSFAFQAAADISAEQQNPQPFDFVPRQGRIGPHETTRVTAVFAPPMAYSPQG
WSCRRENPRVLNNMYECLYSLLFLEMEHTHTVRVTGTSTTTAAWLSQPVVDFSQCAMNDT
RDVTLTVHNGHSEMPLHFAFPRVAHFSIDPADGKVKPRCSRAVRLTFCPRRLGKFEEHLK
VVFNETEEHSLTFLGVAKSLVPPRKIVGGADKLPEDFVCARKSVTLVKEPPCAILIPAAE
TKLDAVDIGMTPAEGLQPPEPEIPAAIGKKKDRGEISLLREADHFSPVLLDAKTLIRKVF
KETPSNAVERRDCRRELQPMELLRIAAPIKVIDYKRVTVGSTSTKTFFLYNGTSATVLAE
MPTEEAQLSFSPHSQVIPAGRAAAYDVSFHSSVVQTYQQVVQIKINGRYMLRFTLQADVV
PVEVTLSRDDVVINFAEFGDDPKAYATVTLFNHGNSEAFYAWSLNNGPFTIEPMNGSIAP
LSKVTAHLTFSPPQSVLSAEARAELHVKGALDARVLRLKGIIAPTSCGWSDILGGGSAAS
RTSVTAGGEHVIKLLQVPAGLATRATVLLQNKGRNSAYFSFEFVPEWVTVTPMCSCVGVG
EVEEITLAVLHDTPGLLQAVLLCFVRGMRRPLKLNLTAEVCVAPLCILSPPRTNGEVLLE
FDSVYIGTEKALPVRFQNSGDVAAVVFVDLRYLSEYSLRCPEGGAASLAWRGRGESVPGE
TYVTIPPRSEANVLFVYRPIGLSNDERFLVAWRHIGANEMNPLAPLAISARAMVSQIAVG
RQVLEFPRTVIGSTAVPMSVAIENFSGDSVRWELILTRGDGSKKERSSDKSAACEVSPFH
VNPESGTLAPHTSELLHVAFAPTTEGNWQESYSVYIDGNHLRPCAEVRVSGFAANPRILC

DKEELVFPAVPLNVVVRETMYIKNDSFDTIDVRYSSKGQGPLTVTFPHAATFNSSSRIPV
VVEFCSPKPVTLSTSITFTSDKCETLTIPVTATAVNSFLTTAPYVIFQRGFSHIRVPEDP
VVAVGHSEEEESSDEKEERIMPLIYHDDVPAFPSSAAATATAISPMATGSGDSATNDRKH
HSVGPERRLTLKSSPFGYVDAVGQILYSKHAIENLRVWLNHSVFQKPVDDLIYTLQSTDG
RQLVEAACRLSGKKPNKLARPTGSERSLNSLQLLVSMIKSKGGCLSEVRLPYLLNYGAYR
RYCESSGADVLSEIAFATRADHAWVTVILQFIRVFYLPKVDLAAISQLYPGMKAYLSNAT
WEPAPFQAALRESNVFSPEEGLLLWWVFYNVQKCKREGLLKGRTKMLRGFDDLCDCVGVI
ACILAYVPSAATRFSLMERLVSEPKTRNDVENNVALLFAMLTYLGFPACAGPRDLLEYNS
VDWLLLVATLFVFLPRFIPSAVILLEGKLLVPMSRSLEVANASNTERTYTVEMSNAVFRA
LPREFSVNAGGAVQLSVEVTLLFNRRVEGECVVIDTSACLMDERAPVVFRLAAVPNNEPL
RVINIQTPLYTSLYYEMIVESPFPESCVATLRFAQEYKNDAGYPEGDFGKTIQNAFSIPV
GVVPFRSGEKSKVVVQFFPFARGKYEAHITFHDERQGEFSYLVVGTCTMPKVTDKVSIRA
ESGEECTQTIFLKLQNAPFERMLRAAEDHRRVSVVRAGKRSLMPDLVGVPYSVSFVNEAN
VGPNPFFRGPENVTFVAGESMLPLSFTFLPKYLGEYNCYIILASKYDVRSIQLTGKCVPT
GERGVLRFTCPARQLITQGLSVTNNTNENWLITATVTGPGFSGPKEMRVPCGKQREYSLR
YCPAWISSANGNLTLFNNTTGERCIYTLIGEAEEPVSEDVLFVDCRARERCVVTLTVPDV
SGVDATYLVETDLPFARGESSLLVRRGSTSKYSLVLHPVMGGTYAGTVKCRAPNGRYAWY
AVTVNVSPPEKEGTVEIRTDTRTPVTADVSIQNPSDKSLIFNVRRFGPGLFGENSILVEP
GAPAVYSLLFVPSQLGSFDGRLAFCSEEAGEFWYELSIVVEEAAPEEIAFESEIGVPDVM
QVRIPNNTSIERTLVVFNTNPRNFSTAPALLTIPAYSELTVDIVYTPTAIEKPQETMLRL
HNPDLGEWRYHCRGVGRPPAESAPVECVCDVGGKLSVALKIKNPFDVHIVPVVELCCDKE
GYYTLATMPQLPSIAPGAEGAISLTYTPKSVGRHEATVLVRPKTSAQEAQNFTWRFPLRG
VAEWRCRDAPRRFRCVARRQLEETITLEAPGLTEEECCLSVALELERHQQYATAVEASLQ
SKVEVSNAAKELLTVNIRFAPLRSFLAAADLVVRSGKGAAWRYSIVLDALRAEYDDVVTI
KAALRTVSAVVFDIYNVFPHTSPFNAYFTPESSRDFSVMNARGVLHPFLVGQRNPGVATP
LQVRFAPSARLPRVEGTLIVDTEEMQWSFKVIGKIEDRQTR*
>TCRU_4145 hypothetical protein
MDDWEKEYEADRRRLAEGKDVIFDVRRNDAAADVFEEKKDVSSHAVPTGGSGTSTMPGFV
PASFGPTTKTVEPSRTGDVAPPVAVPCDDDEEEIRKLYAQYGDDDSLPRNRRAMSDEEGD
ERTQDYKLHDARFSLTCLPPGWNLCGLFGKKLGRRLFFAETVTSPFKGFLASKESLVGCF
VTPNCLYLGDVQTGAMIICVDILRLHEMHIFDGLAVGLKTLDGLELFLQLPKQAERLVEI
LQKISAFWKVNVKVVRSTTDAAKVFKKEMRLVEKKSQAWRLVEDPRTGLRIVNLTGKFVN
ILSPIASKILHWVGFVNQLSKDWKGSKKAQRRCAWVTATCFFVAREEGLAGDARNIKHCV
AMQYMTELYAGPGGELGIVAAAGPPQPPISVTFESEEEKNAVLFIFQECYNYRNGGGSVK
VTHVDSVEEKIRFMKAVGEARPQLFLMRPQKELYDFLRGPSGRK*
>TCRU_4146 hypothetical protein, conserved
MRRLHQTHIRRGEGASLTFFFCVREEGVKLPDPPYALPTSPRFDAERSGAFNKAWLQHEL
PALKPLVRNSVYLPSKEELWRLPMHEGLEKIAERLPYHDVLRYIMDHNYFFLFKTLLNKP
DAPLPHVIYEDFMKCRTFSSLQNPPEEQFALPPTLLRVLLCMAAYQCILDPHYFTTCQLL
FRRLEQQQTMTSGVLSAWVYCCAASGRVDDALAHAKHMADHDVPFDETVFSLMQHPSVDP
VAAEHCAVWHSAKGILLQRRLGERLQTEYRSDSVAAHGMFVFYALTLSHVKKWEVIRAAV
SLGVSLSERTLALLVDVYAREKGLRCGPKTVRAFASLLARDGTVGHLLFVLLRARKNELL
PEFQGLPRTVFSEAEKADILQCVERRARREDGFRAAIPLLRALVQEDDPRHFFHALNRAV
CGNNNRSSIGFDSSVNNGAAPVHALSDEQSLQFLVTSVRGLLREVDTLEKTSRREAVKTS
RAAVRAEKAPGDEKEEELRTLDESGIPAGVREIARIHLIEEAERAKRAARLRTAWVNPDG
TL*
>TCRU_4147 hypothetical protein
MLSSARALLARLEIYRGDRAEEEEKELQPLPEPPRQHPPLAVDAVLTRRVALLRKRLNAL
REENGGLRREIEAAERTIATHSLPTAAILMLGFQCVLEECSRALQSEGEHVHETSLMRDA
LVHALQQLYSLKSFMKTLDSLHEAYRQVQREGVQLVLENYVGGISEDDVRTAAAELIVRY
DVLEERRMQSVSEYNLLQRSFANAVGVAVSRAMLHVGKSKQASQQTLSLLSATQQVVLGA
LDVFRHLERDVATNFARGVSVNAALLKRLHAISLSMVPQHTAPTTADLQAMTDGVADTDI
EQRRDGCYDACVQCLQAALFLLVD*
>TCRU_4148 CCR4 associated factor, putative

MMQYGNALAQYGTYQQRYPVAVSQGGIAAIPSLSKSPMIRDVWEENLEEEFNIIRSLIKD
YPYVSMDTEFPGVVAKPVGNFKATHEFYYQTLRCNVNLLKMIQLGITLLNEKGEVPENCC
TWQFNFRFCLTEDVYAQDSIQLLRHGGIDFDYFAQYGVEVTHFAELLISSGLVLNSDIRW
LAFHAGYDFGYLMKVVCGKDLPEKEDDFLQIFHSLFPCVYDIKYLLRATDLSHSLGLDHL
SESLRVRRFGMAHQAGSDSLLTGHCYFKLLRDCFGSNPPVASNGVLYGLCEDASSAATPS
STTIPGGSAHAFASFTASKNTTFPSTPLNNSVKGHN*
>TCRU_4149 hypothetical protein, conserved
MSLENENTSDIWSNPVDHFRPNLKALTLYADYQYYVDNWLHVKERWLSPWYLPWWTPMYQ
LGTWYSQRRRNLFLVENHLSYRPYRYRRNDEDRKNPY*
>TCRU_4150 hypothetical protein, conserved
MLEGPDCLQLDENVLEALVHALTADRSLCVDDCLPYILNGIAHGESDVGAQRRRGTRGRW
EHAKAAEVAESLGRALNSRAGGKEWSAAEDGWNMFLCGIGSGRRANGEVREALKALVGPA
TQALAPVLEFLVSEENVHEDRLLCARGFYARAVSSLLRVHLPGATEKECVMWLRRCDWKK
ELEELLSPFLQCEVEPLAKELAFHFQQGMKTARREEPQHFFSFLLQLYERYNADVRTHGW
ISPNMKAQDSISLLALGSVSLAFIAVSVFRGVYGWCEGSQFLASRDFTVHGVNSFIEFLD
RARGIIHGGAQLLLAESIFFHSAFCVFLETAKVAAERSLTTGARALWRQEFLAMDPPRAF
HTVCGAYHMLRCLEAVVRRLGVVFSLLPTYAVSLWERTITPCLSTFVCVCEAAKESCDSN
LDAVMVSLEVLSCAHAMHSAAEEWMEQCCEVCGGVEISTSPLERLALWRDELTRGTTHDV
KQFFARLFAEPGLLEWRDLQAWDALLRVVCSGKTPAHAVVYEDMKLSLTRLISEEQRNSL
KEYCQVTSMGALATLLGNTVT*
>TCRU_4151 hypothetical protein, conserved
MQACRQFLRHRIKRGGHTAWVCEVSLAEMSKQGEGIFSEGDTTALRPPFSSAPVARRLTT
TEEAVRRISLFYSPHTYAYGLLSALVLFDEAKRRGLLDPKVDAGKFFVHPMALVRHPEMF
SQFFGPERSQFFSAMLQQLLAVHDAEYSSVVRVCRSQGVDATRWIPFLRGLCLCVIAGDP
ILSEASFVIEDLILNGVLHDGLSVPGDYNDRGVSVADMLMEAAVELGSARLSELSLSVYR
QFLPETPYAVSKRLALCITRGERRHLDWNLRCLPRKPRGRSRLKR*
>TCRU_4152 conserved protein
MELNELQRLSAAFYEQGMRYTFTASQHPSNPGVYRFVFSRPTNATPESPVYITVDIFRSP
PDNKTDDDNTTTYCAMVEGLRWPYYFRLRGGAIDEGGFSETLLEKVDAQKCKVNERCLWM
*
>TCRU_4153 cysteine peptidase C (CPC)
MRAYFSLSIALFLFLLYATAGHSFHAEDAPILTDEFLELVNRLNGGKWTAGRTSRTKHLT
RRGASRLLGTFLRNTSILPPRQFSEEELREPLQDRFDAGEAWPKCPTITEIRDQSSCGSC
WAVAAASAISDRYCTLGGVRDLRISAGDLMSCCDVCGYGCNGGYPEVAWEYYAVHGIVSE
YCQPYPFPSCAHHVNSSDLSPCSGEYDTPTCNSTCTDKKVPLIKYRGNTSYLLSGEESFK
RELLLNGPFEVSFSVYADFLAYTGGVYKHVAGTFLGGHAVRIVGWGELNGEPYWKIANSW
NREWGMNGYFLIARGVDECGIEGSGVAGTPRIP*
>TCRU_4154 retrotransposon hot spot protein, RHS3, putative
MRRHQPVREQAEYWKVVKSQMDEVGPIPRYIFDERMYDNWVQRCHKTVDEAISSVILQCI
GLGLGGSWDRMKVLYWLARVVRVRGENFGFEFFSNLPVSAHLGNKTLFKSAKLMQQRDFN
LLISGLRDYLTSENFGRCTVFAFLNGSFVSAIERGLRELSPSPQRQSHRCALAVYSQEGS
TRHHVLPPLEHFSERIDVECGVLYVTEVENFPLVDGFFFVKSKPMTLVGLRIATAGGHHT
TASTVRQFTECLAAYFNGWEELSRQLSWEIIYVQHADSTPMNGWQGCDVVDSNNVSGADK
NETAVFWNEKVRQYQVSISSRDAPRRF*
>TCRU_4155 Concanavalin A-like lectin/glucanases superfamily, putative
MGLNSRGLGSGAIWPVSSREHNGPHTFISCDFTIVATVMIQNFSKLSTPLPGAGLDAPVS
TNFIGLSHNAESRWETVFYGIKRASGSTWESGKEYQVVLMLPDGHRGCVYVNGDLVGSPE
TIPTLETQGAGVSFFYIGGDEGDINSSVTVTNFSVQPPTECRCTKNGQEKRRLHAWGRVA
GAAAAGTLRFCGPLRA*
>TCRU_4156 hypothetical protein, conserved
MVMRRVFCVVLVLALLCCCSCVFAVEEGEEQEEVLQVNAECAGKDKLGRWQLPGNSLWYN
CTVEDNGVGKEICGMGVGNCTSEDVKSRAKGVAKDGVFTINITSPTQSVVKSWWESNVEK
DVTVASGTAKLLEAEPPAARQEEASRETSSRPDSESWFLTFILRGGV*

>TCRU_4157 BNR repeat-like domain containing protein, putative
MSRRVFASAVLLLLVVMMCCGSGVAALAEESNPVTAPNFEWKDVTDVDVTLDSLSAPGLL
KVGSDVFAVAEAQYKKDESNTFTGIASQLLRIEADKEKEEVMKDANTKTQFLEKEGSGGN
KVDVSRPTTVVKGKDIYMLVGKYNRTAVTGENRDADDWGLLLVKGNVSEENGSGKRIKWK
DNDGVSRISVGELELWTQLIGGGGSGIETKDRTLLFPVQGTKEGNKKGEATKDEKAVSLL
IYSSDNSASWTLSKGMSADGCSDPSVVEWNEGKKHDDDCVW*
>TCRU_4158 hypothetical protein, conserved
MIFSLETPPSVGIPPNSLSEEGDVLESPGDTLNSEDEVSSDVSGPSVQTKTPGQSDSPVV
KAPEKSGPETKTHISDKEGEAGGTEANEDATESEKGQSEVVKRDASSAPQSPPTPPVPAF
PPEETPLAPAELRNSVEEKLNTPPSQSKTDLEAPEPSVEDAEAEKHGEGKTTSDSMKDAA
KGRSGDSTPSSISTSDSVDAQRKAEEEDDNEMETLNPNEASILPLVNKNGQGKVIPSFPA
EQQEQKGQPLGKSGAGGAPTSTLSTVTSSPAGKESVKHLASGTFPDGHQNVDGGSTADGY
QTVDTGYGDKTQEDGQLKTPTGNLANAEDANGPTTYPVGQDGTAVNTEVSASSGEDEETV
EGTDAQEE*
>TCRU_4159 Right handed beta helix region/Periplasmic copper-binding protein (NosD), putative
MLLDDHVVEERLSVWQKKKVRTYVVNGRSKVSSRRSIAGALAIAKPYERIELVGGEYFET
ISINIPLEIVAAEGEDPRIFSRGPCLTITQDVEVYFEHVEFVSKGKSKLDSAVALMNGKS
VFFRCKMNSILIGGVARPVLEQCTITESYNGYGIQIGGAGGAEIHHCTIHTHSAACVEID
TKGVVLLKSCTIRQPSNGGHAVKVHATQSGFDDKIPVENLACKKVSISKCRIYVTSEIFR
PKEREWMVTEKLIGLPSCVLVSRGACPVFTYNEILEGFIGVTFESAGATVLEGNSIYNQK
SCGILVLVDEKSPYPDAKQNLRISGGNVIDRCLIGIDVHCLSKVKAFSGPAQEILLSQEL
PSSGKAFDWIEKVHHLEKSKSFSQGDKKMDCTLYFNGRKMKLSELKDDLCTLAKLVCAGH
PSHFGSGDASDERHGNNGGNPLKDILQETFKISLPLPNAAGCAAQLLNLRGTRGVDIVDT
RFSGCELCAIRFGPDGYGLVEDCDFINSGATAIVVSGGAHPLIVGCKFESSKGASIFVDN
FSNPLIMGNEISHNAENGIEFCNLSRGIVMGNIIFGNTLSGILVTGGSTTTIVGNFIQHG
QGDGATVTGGSKPVLMMNNFLSNSKSQLMVSEYSTPFITQNTFTYGAGCGIRFESCCGGT
VLDNTISYNDRGIVVELDGDPYVESNKISNSKRHGVMVGNNGLGTFVSNEITQSGSCNFV
VQEGGSPVVRKNVITGGHTGGIAIIAEGKGVIEHNVISDNAMGNVILLDRFTEPVIAHNT
ISNSSTGCGIICGREAGGEFFHNNIFKNKQCGAYVIGKANPLFSSNTITYESTGVIISDS
GRGIFKQNNIHSSYGSGIIIQLGGNPFIEGNSVSKCFLSGILVSAGSSGTVSENEFSEND
VGVQLGSTLGTATLEIEANLLSSTPASPTSKSNVKIGKLKPRRSFGLKKDGENINEPSQL
TPTTIRRNRIFSNTTCGVLLENAAYGILEENDIELNEKYGVMADVGYSAKRVKDKLGKVL
GYGGWKLPNLSLTGGSAIIRKNRIFNHKKCNISILNHAENSIIISANDVFEAPTGIYVGN
DASIHSIEGNTIYRTFDGVYADSGGHGCFENNKIYDCDGVGVYVCNRGNPQFKKGNVIEN
CSVSGAFVDAGGRGLFSQTTIRHCVVGVVVYTCLPVSSLVQEGEFMQSRFVTSAPVFQQC
DIEENALYGVLVLTVPTSFPLRHISRSGVGHASKTEGLMKTPGLSVFPQFHQNRIRNNCH
FGVCHEMYDSPELQDETENLSLHEENSPETKRSSTRSNLQNHIQRRLSTSMQCRFAARGS
MQEALGTSKVFSTDEHHKERMQHQVSFVENTISNCSIGVVVGGNCHPFFLRNRIINNAFF
GMFLRSQAKAMCFGCEVMDNGVAGLYVSQGSLGAFTGGTIRRNNGFCRPDGNPHDPRSFG
TLSFMQSTLAVLSVPNTSSRPPHGAFSSILRGLESYANIAAEGLLILCELVAASSVGLSL
ASGMCPIVSGESGMSYGSGLQMDKYDRGWAADGGMGVWLVQGSMMEISDSLIDTNRNVGV
FYSRNLQQHYMNLSQFPVKPAGGFPRFPGGEVISGEARSPRKGAMRWVFFTANAIHDEGY
LMQMSTSVFGEGSFTESWRVFTPPQTPRMSKQTEAPVYEGDRPYMLNRPALVSGNRIVKN
GYGVVIHLHHVMRANFSGETDTAAKETTEIPEPSHGRRANAAKKHGRRSNNKAADNDLPR
NREGKTLRVSRLKKQDEEENNSSHEPTTEKPVYPMMSMNAFSREEDFSINIEENHVYENC
GVGILCLHIVEAVCGTHVKSRLELDGAAAEYNDVCVKVTLKRMLKQPKLKFSLVPYERMT
RYAKIYSNEVYKNVAEQLEVTSRYVAISQNCVRTLLQIDTLRQPSASMASSQALLRIPLF
ASLLSAAPPGRFVIESNRFRDSTKGVHVFGFVGGNSLLLRSNAFVNMRGTAILIQGHLAS
ATIGGGNVFEANDVAIRIVLPEDSLTKEDVAWMQAMGVNTRIHSNHFCAPKQLSVTLEGG
GAPSPVFEGNKFTLHMSGSVAFFISGPNAHTQLRRNVFLENYIPVIITNEAGTSDEGTSV
ILEGNRFARNFIGLLVAGGAAPKLLRNVFEENYRTGLEIIDENTRPTVQHCFFVSNKFSE
VQPFNEEVLLFPEHGKICVDAGLEGISFDFVATIVPDNTAASDAKMRLPSGLLISGRGES
SVIHECLFQDNDIGVDVVRSAALPGAMKASSCGIQLTSCLFGLNKVAGVWIRGEEDPNGK

RALPSFNMSGSEIEHDATVFDSCFFVNNTTDAEGKGDVVALDGGFAIVRGSLFTGSVHGK
KDGMALFERNLFYAEDADAAVYLHKSARIRLVGNTIRGHKNGIVTYPAAWGHVEKNWILD
TTRSVSAAPFCHTFFVRNRIVKAKDCGILAYGGVFTENEVCFAPTGVIVQNPVEYKNYSE
IPKAEKTAFDALISENRVHSCEVEGILVAGGARIEGNCVFNCKTNMNIICPQNAGGGSGI
AVVSKNALYDGEVGLLVAKGSESVIRVNDIFDNSTLGVWVKAGALGTLQGNAISSSLGDS
AFDAEPGAEIKMLQNNIRNQFSPSYHKTLPTHREKERQKAAETMTEEIRELDRTFQKMFS
LCNSVEVVLQATLETLRRESANMDGVRPLSTTTNFVLTSKFLRGYTQTQNIVEVLSLAST
RGARYSAKERKSSLSAAKASRSVDRRISQSTSLVPNEQYRHVLIHVCDTDKETVESTQIG
KEVEAVFTSESLSSRVMFRAALTTNPSSFHASITAQMPDVIIVVVGASKKAFDTEELAVF
SVIDRLRRAPAGRRQRKKNSVLLVSTILSVEWKENIEGNASSSKSVEKLTGLEFFAAANN
PIYFKFSVAEAFTELIQRLKSHVFSPSTSTHDLDVSTSRNEGTVVKPARGEQFLSSPLSQ
FGSISFSSPKLPSTRPPLRASLNVRAEK*
>TCRU_4160 zinc-finger of a C2HC-type, putative
MQDKATLHVNHCKQSNAATSNSAGANGSSWSLVRLFDSEVTELLREQREFLAKAQANEIR
ASIFLRLRLSAQQKLVAQRNQFSERWAVQNKRRTSAMSSAMARTPNAAGPPEDLDSNPEE
EGEREEGWQCRGCLRNYNDASAFTRHRSHCAKYILPKKKHVGETVSLTASSSHVGMKSRQ
LFSTSSVGSTFKAELEFTRQRLDSAGVGLPRAEAINNCGLSSILNASGLSHSEQTRRNTA
FGSDSALPGTGSLPAETKSPNRSPSIHCFSALEERRDERVEEDGRKDAAPIFSLSRELTP
FSSELLSQPKISPSGRASIDDVPAAVADRASFEKPASLPMWVSLAGNAKFGEDGDSTAGK
TQKSLSFAQSKVVFNGNGVSGTKIQEETENMDEPLRPCPHCGRHFFAETRWPRHVAVCEQ
QQQQQRQRKSQAESSRSVQKPFSQRVSRSSNMESMNFSGSFQEALQTPSSNRGKAGNAAT
SATEKKSSKWRQQRAQLRQALQLGSARSQNNSLKSVGDIDVFEDDRVACPACGRRFAPAT
AERHIPFCQERRSGPKTMRI*
>TCRU_4161 Stress responsive A/B Barrel Domain, putative
MQPKICHVVFFRLDPAKVTTLLPTDVLQRHLSVLREKVPGLLELNFGPTGTNLYPNYVDC
SNGYTHCLVSKHADADKLKVYAEHPDHVVFANLLKSSSAAPPIRIDFELSASNE*
>TCRU_4162 NADH-cytochrome b5 reductase, putative
MRVVVSFAAGLLAAFLHRPVDDAFPAECYRSIENPLQFRNKKRDGEVFSQRYEPYQLGEV
IPITHDTALFRFLLHADEEFNLKPCSTLQACYKYGVQPMEQCHRFYTPVTANHTKGYFDI
IVKRKNGGLMTTHLFGMHVGDKLLFRSVTFKVQYKPNKWSHVGMIAGGTGFTPMLQIIRH
SLMEKWNDGSVDNTKLSFLFCNRTEKHILLKGLFDDLAERYSNRFKVYYTVDQPVEPENW
KHFVGYVSKEMVQQTMPAPDEKKKIIMLCGPDQLLNHVAGTPMGTMSAMSSGMNIQPLAP
DLNNLVSLGGILGELGYKNDDVYRF*
>TCRU_4163 UBA/TS-N domain containing protein, putative
MLFQIVSNVADKVDLFIEDEMTVGEVRVLIGQMIDADEKTIRLTFQGHVLEDDKATWELI
LRMYPLAEDTPRKLFAHVSERLRTGSASMEALRAALVSASGQEDEKAARVQARLMEPVID
LMVKDPSMLEMMLSSHPGLKQMLEKHPELKSHVCDPETLKTLMMSQIDPDQRRSLNRGMG
LQLAQLSALPGGEQLFEHLTSEYLNDMAALTETNVSSSSDNVDEAQARPDPTKEANSEAL
PNPWERQSSSLQGASGLNSMNGNTNNLFSAFGGLGAFGGSMPFAGLPGNIASLGHTNPVT
AASFLPPRMLPSSHEGNHVPTTDPTHTREASANTGEWASQLATLREMGFDNEALCLEALR
ASNGDIDGAVNYIADKDK*
>TCRU_4164 hypothetical protein, conserved
MAQQGGNIRRGGSRSNVHPAYGAMGQTEKFTRDDSTETFEGCNIQVQVRTRENGRRSPLV
ATPNHLSQKSSAVPLNSYGSEENSPPIATPIAFRGPQEFPAVFNPQALLQEPLPSTVVHR
GLYGKCRFILFPLLSVFEFVPPPPAGKSFPLFVGQVRFETTPAELIWLFRRTSGACAITV
EGRGNGCFIVHLQSESERSLVRQLHRRVLFDIGGVWFARSSEEVDSLCEYVALNGPYLSK
QAKLPRDSMVVEDIKVDLKDMAFCHPCHYSQEAVAQSFWSGSGVAWDPSNSRRETPTKTP
YCSPPTSPLAASLKMPYSNMRPQDVYQTCTPPNSLRRGIEGARTEL*
>TCRU_4165 hypothetical protein, conserved
MTKYELKLQYFDEWMMRWRKFQTDSDWTIEKNRQWWRKCNMALSAVLFGSLVVYTSGTAT
LKRQYGLPHFFDVGIDGQIKQAVLQTLTSRWRYTPQGYGRVLLTGIPTYTLFVLLEHYQE
RRRMHLYVAQNTVFGEQMRRFLNTGKIEEYLAVNIKGSLPPSQRSIYAY*
>TCRU_4166 copper-transporting ATPase-like protein, putative
MTPVSHETTGGSGGVRLYEFRVDATSPRPSQDVLEKALFAITGVTVISVSIRSEDDTIVV

KTLWTAERLERLFHGVISSLGYVVAYDVPVESRFLIEGMPYLNHALRVESHLRSLRGVER
AAVNFATMTATVVHNPKGVTATDLMNEIGIMGYSATLQGSTGCAIRPPTGTAGCIRRKLV
VSGMSCASCAAQIGSRVRRLDGVTDCVVNFSTGICLVTLDREDALQRVEEAITSMGYTVS
VSPPRNPTAAVFLNETKAALERTREIEEQKRRFLGAAVLATPLALLMFLMATTNVFDDSR
TMVFVDFVQMGLSTPIVFYYGSVFFIHAWQGLRHGMLTMDTLVAIGAGCSYLYSLGACIV
MVVAKYQIATYFDAAGMLLAFMLLGRFLEARARRSTSDALISLMNLVPPVSIVVTAQGDI
TMPSSLLEKGMRVRVLAGDRFPVDGIVVEGMSDVDEQMVTGEAITKAVKVDSAVIGGTTN
ITAMLVVEATKIGEETMLSQILRLVQEAQNTKPEIQRIADQIAAYFVPFVVMFSVGVFFT
WLLLGAFDMYPPEWRGQNETILMFAFDFFISSVVAACPCALGLATPTAIMVGTGVGAKNG
ILVKSGKSLEVVRQSRCIVFDKTGTITFGKLEVVFKKCWGDNVEEVMKVVGFVELLSNHP
VAKAVADGILLASPASTYDVVFSKVKGGLGTEAVVRCRSQNNELRVHVGNLAMMREGNIH
VPPEIEQAVRQQNNMGRTTVVGAVNGVARLLVALADEPKEEAAGVVRFLHRQGFRVLMVT
GDNEGVAAHVASAVGIQNENLYAEALPTTKASIVRQLQSEGDCVIFVGDGINDSPALAQA
DVGIALGAGTQIAIEAADAVLISNSLVDILNLRALSIATVKRVYGNFFWAFGYNLCMLPL
ASGMLYPFVHFKLSPILAAAAMVFSSISVLLSSLSIRWFAPYETRMNIGLPPKW*
>TCRU_4167 Mitochondrial SSU ribosomal protein, putative
MLRARRSLPLLPGSRAWLLRFYSSTRELRQLQSRERLILGTHGAGVVQHASVSQPLSVNF
QSSVTVAAPAADLFRTKVHEGTGTSGKDPYLRTLPNQESREPESSVSQAHITVAPTVDEC
STLDRRWESMQYWFNDQHPRLVIYLRQLQVQEVPPISPAAESLLSKFEEVAIPKLALDDT
DRQRLTKLWGNLTEEVKTLRLRYVFDRLTFESKLSQLCKEALEQMHAMSLSGTEGSLAVE
ALRRLTILERNDYIQKHLIDVTSNGAYLGFGDAVWRVFFSAVEAHKAVLFGEGTPDTIRF
AWESILQQDVVRVPDVTAPVALFLTLVCIHEGNRLASVEWRESSSSLDEGICSYDNKQQS
PLLALLNPVVKRRFVTKMVESLLRSHSSNEFSKLLRKNGLHDLSRDVALCEALNSSQGIL
EDDVAELVSRFESTGEVKTLLSSLIGGKDAAVRETVAKILGIPLATTVDWDAMMQSVDWT
NNWRRLATKLLCDQTLLVSIHKLVKNAIGAKGISRHLFSEEYADQLQSIIAIREERELNR
KLKIDRIVRELSSYQRVDQSCEMLRQLGVDMKELDQAALSIRQEGLVKRPSVDENVISRA
LEAVGNRHPNWVRAGVIAPAAIKDSIGALKAMLFIFIRLSYVPQTGLAAMAQRFRRRIGP
IGVEPFQFNIPTEVGFVEHYNNLEYKRYDWQGWYQRMVDVHNRNISLRCRVSDLKRLDAN
GVPFVDMQTERRLRILAEGRVGMGVLMLDSDKYEDQKDNMTFGSIKLSELLSDARKAQLG
EEYWPSVEMKVRKPSGQSRAHYSLIDYDRIEKKSRELYEKYRDAKKKSLFVTPMDLWLEV
RGMQVRKASEGADADGYTVDILQDALSSEDNEKN*
>TCRU_4168 hypothetical protein, conserved
MQSVKDVGVTPLRPFCSTPLTQVPDVVLIPPFYVILLASVLCCLWNTAFNYFMSRPGKLA
HTIRKWGRILRLTRRTKISNLQEPSGIPPSCGEASIETDGLLGTSIFTGDNSYDTFFIQR
MSDTELQVEAPLQPHANVLNNALRDSLRSVRKEAQHMVFVYNPKYMIVATVKSLMMLVVL
QYHFDYKGGWDRLVVCSAANLMSGLLTPVLEYGARLLLPLDLERGTRGVIVEPEEPADSV
LIVEVLGHIGRLELEDLETVLIQGSTFIVFGAALLPAVVVFCLAGVASFLWLFLPVWTLY
MVVRRLYYGHIGELEMQRPSLGPMNVFLTPAGEFAKAAFLKVMTLFLLQWTVQCSFLLGL
LLLQGGGYEEALQLEASHQFWGCYNIPEMTRFEWLCFASQILF*
>TCRU_4169 hypothetical protein, conserved
MLDGETLPSVGQSQVGNAGLSPEQRKYHVISAQLESIMGEACKEPPSGANFVSIKRRITA
LQYALEEAERRICEKQRLDDISRKRRVLDVYLRRAKKDEERRDVLEKDDGRRKQLVSEMQ
EEKRFYYNQKNKEVGGRIEKYKNSILDAQAAVIERAEAEGEKRNRILSRLQEERARTAYE
HKEKSRKRMERCREVLNRRKQQEEERRREKRAAFISHMRKLEQDEGIDAILNKRKDIHSF
LARRRNSSRAGTDDGFMEAAAPPRYKTHETLLRELKEKEEQHKARYEAEQAFRQYEIQLR
AHARQKRMERQRQNYRAQLEKRIQRNDEIIEMAREKKKRGELVKDAREAREQENLNEITR
DIEQHRNRAEKMAHRRHQDALEKNYYRWNGRAQRVILQLQDAIRADKDKNCAMDENEVFM
PTALCSFDNL*
>TCRU_4170 hypothetical protein, conserved
MLDSIDINFQDKPSASTATRWFDAISPNFFSAANLVGADPFSFVSSRRNDTIELTPSTIR
YNEDSGASPRDILSETRSPVEPVRERSRVEVSEAEQGGPTSHGERPLDNTTPSADNYQRS
RHGDLYEDAMRAQIAKRQWAAVEQMRQMMLENAKVERDCPFKPQLSSYAAKIQRPAGLAP
HNRVYNELMRREEWRTKKRQEHIRRELEGCTFRPLTLRAAMLKSSAHTHDSHVFSKLYHH
HEEQNHFVREVQPYVVEQLERHMLFKSPANKPLPEDKINSVVERLFSHGVVVQPDEVKRR

RSQSTSPPFKPRVSVNSERIVAKQRQGGQVVEDVVERLLKPPVYSNRTGNLRRQLEATQE
NEELKLMRSEYVRGLQELLQRERRRSFIEAKFNVLSSAINKERQSHEGSKRTLTEHRAEE
LVRAAVIILSPDEAEELRNIILSSGASKLNKEGFIALCEKAVEGLSNPHASPLGRVPPPR
IHAMEANLTDDDNGSYAGARKKFQRGALSPEELEEVRARRVERKRQLAEEENQKRQAMIE
EEMRQCTFRPPPPRKVPRECHVNHKVDVKTTKADELRRAHIQKTLEGEEHAGGAAAALPT
ASARELFGDGGSHPRLHRSQSANTRSPRAMSTLHTKPAFVAPAEASFEDRTFSPKRNRYE
KPRRSHTAHSDAFLRKKDFAGVPLKDRSSRRSAAVSSDRSSEDAAAADITSRGMKKCESV
AEATTVSPRLYRDVISEHAAFGRDGALTEFGRELILRQLREYRNKR*
>TCRU_4171 Domain of unknown function (DUF4470)/Domain of unknown function (DUF4471), putative
MSYKYLHDGKEHFINGVGTELAWGWSPAIDFTEILERREKHATDDTEYVAEETKEEPEEG
KTTNGDNVKKDRKFDLDIDAMIAAIQQRIPKEKKDEGSRDIVRVLLCGACDIRHIFRTLS
SLQVKSKMAAQPPPVYHFFIYEPNLRIHCRYLFFLQWLLDSMFSLDELEEQVLMFLDVFG
NALTRDITSAQSRSVSQRLLRVLRNEEGELARLVSFTEMKSKERDFVEEQIVHWAFDTSQ
AKVEDSWLRRLRHEMAERYDNRDNIIDWDFNFYLCDYTNLIKFAEYRTWRNTGIAFDATH
INPRRGFTYNYEAPNKTLCHFNAKGIGTFLGDVKNGPFFAFGAQTANTHIRAKTIDGTCK
YGNGVVSMHNVRAWLYGLLTGQSWPWGDHAFAWDDPSNYNYLPPGTPSDVAHQAVLPDVR
FHFVGLDFTRFMQHIREKKNKKFDLAFVGTSCTQLMSPEFFEVAMARNAVVVAETAKFVI
DARDGAKSAFVNKIRELARAANWEQNDVLTDLLHVDQPEPPKVDDNSSNMKTQKMALERH
QMPYQLALTRSARAPDK*
>TCRU_4172 WD domain, G-beta repeat, putative
MADGVIAHEEVLRHVYAFLQAYGYKNALLALQNESRVPFNTIDVVEPKELTEQNATVAST
SPAGLERSVLEGQWHTVLANYVDSLLLPMEVLFDLYEHIFVELLTLQGFVHAARAFFTNS
PIFVAMKKSSLARYARLQQLLDSHKNIFLDEMNKHGNGGVSIEVKEKRETLLRTLQEAIT
WNTEPYNGFLPAALWRLQNDLDGNHRSTKNPSLKRERPDDFSASSLVSSALFLHYPLQCP
KNIRRKIVFDNAERPISCVHTLLPNAVDKEKMFTALIVGKTDGTVDFLDGDSASSVGSSV
GHTDGVLSIALDAAEESSATWVAVGYRDGCVKIYNAETRKLVRRFSQVHTSGVKSLVFAG
VRNPALSGHHSWVVSGSFDGAIQLLDIREGKSLQRIADAHHSNYVLSICILAGKTGGLVT
AGNNGTLCFWSISATGLRQAGPARTLRSIDASLKEAIPTRLLPVEDKESEGEVLVLTRGQ
RALLLSVRFTDDITNPLVILMRSSICTPRPVYAGCVRVIETPALAAPLLSLFLTDREGTI
LLYNLEMSWRLGGETAGGGCRMELRPADESSIVVVDHGERVEDLNLVNVLGKSNSLLAFS
PSLSAMYLLSWN*
>TCRU_4173 Ring finger domain/PHD-finger, putative
MASGVTNGEVAAERASDDEICGICFTKIYPFDNPRGRLNSCSHVFCAHCIKEWAQSTNVC
PHCKARFTRIFTVDPEGKEKITKVRKRNYRLWEDEEEEEDQNNRDGNRVSTPIFFVCHVC
GESDNASRMILCDRRQCSNTVHLDCVNLSEQPAEYFCPDCTRLRASVSVAINSSSLSSAT
PLAATDAVSETPLNSECPKDDANYTDNSTPLVAFHPEAVPPCQINGKKVFVAPPAWLQEA
VERSNLQHSEARRPLPLEAPTISNDFAPQTSPVPHETRMSGGTPTVLPDEDEELHRSAEA
AMQQFTQRQAQKEQQIRHRRQRQPGSPSYDPALLRATAQRSKRFHSSANVPMGCAETTDV
LDPESRHREEEALGRRLALEILPILRRNRILQEHKIYLGDNGSIVAASLPSKFEGAQGER
DLYNHAMTEGRRIARERMEAKLGDARRRKERLIRVQAQRESVALAKLARIVASHRAVPKM
K*
>TCRU_4174 BNR repeat-like domain containing protein, putative
MMMTACDDGRRRVYESADKGESWTEALGTLSHVWGNKKGGSKKVVGSGFITAKIENGDYN
KKVMLVTLPVYPKDTDKGQNNEKGVLHLWLTDNTHIVDIGPVSVEGDDEIAASSLLYRNG
DNNELIALYEKKNGDEEESLGMVSVRLTEQLTRVKDVLATWKKVDSRVSQLCTSLIAQKG
FSTDSACSTDKITDGLVGFLSGNFSDNTWRDEYLGVNATVKNGAAAHNGVTFKGRGAWAE
WPVGAQGENQLYHFANYNFTLVATVSIDKVPEEGDTPIPLTGVNMKGEQGKFFGLSYEKE
RKWQLLCGDGTNEEHSSVLGIGDETPRGNFATERQPELRVRRWSACGE*
>TCRU_4175 protein kinase, putative
MNLLSSTLGDSVFPLFSADFVRGVMYQLLHGVAYLHNQGLAHNDLKLQNILLFANGELKI
SDLGSVLEEYNDQGTPMYISPEVCKYFYCAEDVEDEKNMVKVDAFKNDMWSCGVILYYLL
VGRPLWECKMDVCNRYQLFREIASQTSPIDLDYVPEPRETTETTTMMMDDSLGKGNNTSD
SSATEEISPLSLRHLLRCLLDINPATRLSAKDAIEHPSLRALQLGGSFGNDAIGMAQREV

AFRVSQSPHLQLFIKRDREKHLQFVAECCSTLNIVLPKEIFLPGTGEGGCENEWIEDTDS
PFFRSAASSLTNATVDRSIFPTTRDYHYYENKLGRAEHDLRSLLQNHAKVNMLRNYMFGT
VLVECGYRNAEEAEAKRILDLKKNQMKLVAAEQKELLQAKSARALVATSNQKYIERSQCS
GCFCGLM*
>TCRU_4176 hypothetical protein, conserved
MNCGGVNFSPDGTIHPPARSGDADRTGIRQLPPPREGRDDTKSGGTTAPQVNAEPSHQNA
DWRQSAAADGPNTVDPSPASNTESNTSETKPELAYV*
>TCRU_4177 hypothetical protein, conserved
METAPSNPPPPATPRRHRTAPPTLHPIFQIARRNRREGQWSLSAKKFTVARRITDIPALG
QLYEESERGGSREVGAINVGAENVPSGAIHNLLLHARTADERGELCGLFDGNRCGAIDPT
AVRQDAAVHVGNESNPAGHDDCLVTKNSGAIGDAAGAPLDRERDESIYPQPDRLQGTCCF
PNCVDNGESLVRDCGLNPQNTTMEADGNTILYWSVAPKTARADPHRVSRFVRIRGQDAFE
IIKLCRTLQHNEKPTNLTTAKVERALAPWNATAHSIERGALRHAAQIVETHNLDPHVISQ
LAKHVDPFDPPQNTVRYLRRYTTLLTQVSSLVALM*
>TCRU_4178 BNR repeat-like domain containing protein, putative
MNMLGVYSPDIVAGYIKAAEKWPSIVTGIITKKEWRAHTVLGSRNGNDRSCFLYRATAVA
RENKMFLLVGNDTVGYDSDDDMWVKDGWDIQLVEGVATQSTDGRQSTMISWAEPKSLSQQ
IPKHTQDQLRDVVTAGGSGIVMQNDTLVFPLVVNGKNYPFSMITYSTDKVITGCSQRAFL
L*
>TCRU_4179 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily, putative
MIVDCENGQSVYESRDMGKTWTEAVRTLSGGWGRPQPGVRLYEIFRVGALTTATIEGRKV
MLYTQRGYTSGENRANALYLWVTDNNRTFHVGPLFVEDNVNETFSNALYSDGALHLLQER
ANEKGSVISLARLTDELKTIRSTLSTWAKLDASFSASSTPTTGLVGFLSNTSSGGDTWID
DYRCVNAKVMNAVRVHDGFKFTGPGSMATWPVNSREDNRQYSFVNRRFTLVATVSIHQVA
KGSTSLLGSGLDAPVSTNFIGLSYSMNKTWETVFDGKKTASSSTWDLGREYQVALMLQDG
NKGSVYVDGVIVGSTEKIPKVGALGYEITHFYFGGDEGDINSSDVTVTNVFLYNRPLSVG
ELKMVTKREDSMRGGVLRVLLLPRSVGEGGGA*
>TCRU_4180 BNR repeat-like domain containing protein, putative
MSDGGCSDPSVVEWEKEDKKLIMMTACDGGRRRVYESGDKGESWTEALGTLSRVWGNKKG
NEKAVRSGFTTATIDGVEDKRNVMLVTLPVYPEKDESKKEKGELHLWLTDNTHIVDIGPI
SDDDAAASALLYKGGNNNNEKLIALYEKKGVEETSSGMVSVLLTAQLQRVKDVLATWKKA
DKLVSELCPSSAEKDASPENACSPTVKITDGLVGFLSGNFSGNTWMDEYLGVNATVKGND
DGGKKATLHAGGVKFTGAWAEWPVGSQGENQLYHFANYNFTLVATVSIDGEPKEGSP*
>TCRU_4181 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MSRRVFTSAVLLLVVMMCCGSGVAHAEVEPSSVPKFQWKDIKSDGETVDSLGVPGLLKVG
SDVFAVAEAQCKKGEDTAFTGIASQLLTMETGKGKEEVLKDAKETQVLEEVDSEDPKKRI
DVSRPTAVVDESDIYMLVGKYNRKDGQESGAGDWGLLLARGNVSEEEHKKKIYWKSTEGL
PRGIFGTQPESLTGLIGSGGSGVRMNDGTLVFPVEATKTMKEGTGKDGKTVSLILYSSET
KNWTLSKGMSADGCSVPSVVEWKGKLMMMTACDDGRRRVYESADKGDSWTEALGTLSRVW
GNKQKGNVKGVRSGFITATIGDGEGKRNVMLVTLPVYSEESKKEKGVLHLWLTDNTHIID
IGPVSEEDDVAASALLYKGGNNNEEKLIALYEKKKVNAEKPPPGMVSVLLTEQLKRVKEV
LASWKKVDGRVSKLCPSSATVSKPTDTACSDGKITAGLVGFLSGNFSDNTWKDEYLGVNA
TVTKEEGAAGATKAENGVTFKERGAWAEWPVGRQGKNQLYHFANYNFTLLATVSIHGEPK
EGSIPLMGVKMNDSEKTVLLGLSYNKKEKKWILLCGGGKTTEHSSDLETENSEHVVILLR
NGNQSSAYVDGKLVGSAEFECENTKDKEISHFYIGGDGSSVEDQEGVSVTVSNVLLYNRP
WTEEEVGALNPNKVLITSPVTEITPETVLQPPAEPQPSKQETLKENIGAGAGVLSSAASV
TTTPSSDADPTVATGSGDKMRGNGSPQTPEVSVSSGEDEETVEGKDGQGEDEIHPQAGEV
NATALNSSLGNLSQGNNSDAGTMCGSGLPSLLLLLGLWGLAAL*
>TCRU_4182 DNA replication licensing factor MCM4, putative
MDRDSLVELTPIRPSMQHDLSQSPTQAAAAAEAVMAGAPQMFLGDDGEVPPSEGHPPPLS
SSSALLRREDLSYIWGTNIAVETFREEFQRFLETFEMHTDSTGGWPGIVGEHVGTGGGNR

KYFLQELLRLRLQNRSVLEMDMQLLAKSCPRLYQQVVAHPMECLQMMANVAEDVCQRLAT
ASSYLPMPDDFILRVAPKNLPEIISLRGLGPQHLEQLIALQGMVVRVSKIIPEIRVAFFQ
CWYCQNVRRSVVDRGRIFEPTRCDHCGKNYSYRIQHNLSLFDDKQLVRLQEAPEHLSDGE
TPVTISVVVYGDSVDAVVPGDRVVVTGIYRAAPVRLNSTTRCIRSIFATHVDAVHIEHRR
AGRHLWKKQQQPLTPSLEAEEGLAEDPTEAARRDVFRRIASRPDIYDILLNSFARTIWGN
EDVKRGILSQLFGGTRKELKSGTFRAEINVILCGDPGVAKSQLLSQVHEIAPRGVYTSGK
GSSSVGLTAFVVQNHETGELVLEPGALVLSDRGLCCIDEFDKMNEATRSVLHEVMEQQTL
SIAKAGIIAQLNARTSVLAAANPKESQWNVNLNVVENLQIEPTLLSRFDLIFLLLDRHDP
TEDRRLASHVLSLFMEPDEGSRRATTSSSSPELGNNNDTDNEEDRGRNGNMRSQGVPMGQ
AATVLEHEGEVFLEGTNDAPYMPPRVLSQYIALARETVHPRLTEASHKQLATSYVEMRRA
RGSSRTVSATLRQLESMIRLAEARCKMRFGAEVTVEDVKEAKWLISAALKEAATDPQTGL
INLDMFSAPDPTRQTVEGSMLRLEHIIGRRYLAAGRNSATVNELRQAFNESLVGGMRPLA
IAQFMELLALMAGGEHVKSFSANSVIFADEGP*
>TCRU_4183 Dynein light intermediate chain (DLIC), putative
MQQQRGNTFLEDLGLNLLDNTEQQLIARRVVIVGDALSGKRAFASRLFAAAVQQFPSSSM
STSSSETYAANSSNSSAGGSSCCFPVLSSTGAAEAAGTMGTEGTNSSRYFPQFPHGAGVT
QAFILQRIPATRSAFLPTAEDGLSSGGLYSSGSGISGSAVLPGGVRRAMTEFFCCETPGA
LAMALPTVEALETSVVLLVVDTSVPWRLQDQMRRWYGYLNTHVMQTLRVDLPKQDEVRRM
RMIEQQQLFWQAQQQELASMRRRWCEREAIHVGRTSNDKNSNNYYYSLSVLQVPKGGVSP
LRTILLCTKTDQLEKLSREVEKLCNRSSFSAEARTVTSLENVNIGVEPWVSHALLSSLRT
SGLTLLELVGQLLRKEAIVRQSALVAVSSRVNTIATSSLSSSQHTTNMAPTTTTVSGGAV
APLAVAAAAAAPVAFGDRSNDETSPLGLPTNSHSVFVHPFYKNLWLYIFQLLYDPPTTLA
NNIVPNDILGARDHDDDGGSGVYMAAALQGPEMSSGLRSEWGSLWNSLLDEMETQVSSRF
HPHAFLPHGMDHLELLSPFVTSTDAVTLESVFPSGTDESKEADRGVLRLHDEYIQEVEKV
LATAGPNEEAMIWDKL*
>TCRU_4184 drug resistence protein, putative
MGYVSDCFRELGRFEILSIQLSNALMGISAGVEVPILTMLGRKLAYSEKTIANYVTLTAV
CRVLADIPSGILAECVHMRCLMLWAICLQVLGCAVALVMKPGSFSITVFSAFDGISAGLF
FLTRHIYATRLSKREHRGMVLSFFAGILRWSHVLGPLLLGAAATAWEKEQYYFSVPLVAA
ILAWLSIIVVGCYGGSKHEEHFHNRPKGKRGLTLDESKHLLPFAQAITAVNMDGSSHEDH
VTMLSYESTAVTCDENDYGNACGHPTPKRSPRALDCGHNESMENCEFQLSAFGSIMAEHW
SLIWRLGGYIILYVSIRANRKLLLTFAAARMDFTNSQLAFLLSFSFSFDALLFPLGGFLM
DIYGSRWSMLPAVLGIGIAFMLLPLSPTPSWLYVMAAIFGTVDALGCGLVMTLVADHAPK
KHGALFFGVMRTVQDMGHVLGSMVVSLIITRVEFVVCCYIWGVVSVVAAMWAWFIAPVVI
H*
>TCRU_4185 hypothetical protein, conserved
MSNDTATGYTIVDASESFHLIDPETGLSMTSRCVRDTAAQGSVRMAEVAEGEPRAETPVS
TVSRSAWSMLATTQVDEAGGTVPAASAAGQSPSFSESRGLESASPSHGEQLAAESINNGE
YLSSVFSRLTQINQHHNHHNDADNDEDEDEDDGKNKDNAPQRPVPLYAAEIMPASENKSN
TATPTLASSREKESAMNAVLRAQLAEADRKNVYYMRLYEQSRDELDNLHQTMSLLLHGDN
ENEFIERLGGGNANLGQGRDEWHGQRTEQQHFLNRPSWLQQFLRVIGFEAAYPAPICCRN
DWCGGRRPSSNPVAVDGENYRTSGWKRDFSYAKWHARHGRAALAMESLLLAISSDEFDAW
RSLLVEDPNWNRLRGIDRQRWYCLVAVKLCEFLDKRNSRRRNLPEKSPSEQCGASCPMEE
DMNEEVDNDGQEARQEVPTDQRVPLTADLLAPFLRRMSWCYAVGKQSDKERVAAAEAAGT
LSGGMTPPSHEAIGAALEDLLLASIATFPHSAVLFYLLASMRAIQGRQEESLHLLGEVIR
LDPSHLLREGCNPH*
>TCRU_4186 hypothetical protein, conserved
MFEILVEIAFSIFLCVIMAYYFFLSAPVEERTVGEECGTCVAGTGSGRHANGAGGYTLRS
SPPLERSRRREGAMWCNVLGRWAALLVLGGGSIDKDVWTDRIAYFIEKGAKRLDGAIKQR
RTRGSEGADAERGERTLRVSPDTVRLVCLELGGGGPLIGGWNQQHKQQQQQQQQQQQQQQ
MQQQQQQSYVPTLPVSGLFHARTGSDGNRAGVVHSESQEGGGAASPPIGAVLPRIGPAG
IVSLEAPYSVSMHEITTEGGSAAATAPAVTMAMGLQHTLRCFSVPIIYEDHHFFLLLMCN
VPLLFALPVELRIPADVLTLRCALSVRRVIFDGVLYAAFCGNLVELSFASEPQFTASFDV
YSEKSCHRQQLQLHRPYFSQASSCGSVRGTAAGERSASVPTLTPPLAGNTVSGGNRFKEK

LQEIVDLAVKRSLQSITYPCVLRGVVGKSRRPTPQDGTTGDDTSANPHEDGLLTWSLAKA
TLPLCC*
>TCRU_4187 cdc2-related kinase 12
MVTKVPKSGSLTLRPKSPRQDQRRQEDVAAVPHGQEQLSLLSSSHATNQRKSGICSRNSP
GSIPPPPSFSSSSLFGSRGCRLLSRAETGGQDEEENEELGGAGSCVCLLEPTPPPAGGDV
LEEASLAPPPIPPQQQAQTQQQQQQPCGGVIGEKRADSDGHTSSVRETRLKLRGAEKRMQ
VAPPAISGDKEKGAVTEARRIFRLSRRATAPTVTEEPEKRPENKPLKEEGEEPLHANDAL
ASSLSRQPGVATGMRESNGEVKEGEEASSKTGVPQQPPLAPPKTAPMNSTGADGPPTVRR
QRNSTDWVESMSPTPTPQGLYSCGCSPSMRRHSKTGVPLPLGPTPLDFSSVTEYVETKYE
MRTKISEGTYGEVYMGRCRATGESVALKRLKVLHGLDGFPITSLREVIALRHINNAREHA
STSDGNQDNKEDPIEEVISLRDVLLSRNHHDIYLVFPYSSCSIAGLLQRRFPFTEREIAY
VFRKLLRALMKLHAMGIIHRDVKADNVLIHHDGRVQLGDFGLCVFEGSGRRSLTPSLINL
SYRPPEMLLGITSYDVKVDIWSVGCFLAQMYLRTPPFFLAHRRHAGGGGGGGGARRQHEM
DPNRRTETELEQLSLITDVLGPLSSAGPDAFPQERCQHFAQLEQLRRALATNSATSLSSS
TPSLGSLFQPSFLYSEFNGFAAWFMATAEHRRRDASHLLPSKECIDVLAAIFQLDPRKRP
TAAQLLEMPFFQLHRTAPRRTAPHIEVEKERLSEDEVVERHIQREIVEKLVLYHDSHVAP
STEGGK*
>TCRU_4188 hypothetical protein, conserved
MVDKPLKSGQRKVYWLIGTGIFSALVLVICIAVPISVYQAKYQRMRETRIAAEIFEVDRW
VSFFRSDVIDAISTAYGLEGFALGSMKFIPTFNGTPEERVYGQEFAGFTEYASLLRVSPH
LVAQILAPGGVGLEVFPPVPSIRMLDFLNNDSMGEPTAIESVDSTKSCVLGPLYRAVPGI
NATWQLIVRDPIYDTKYNKRAERKTFWGFALVVLNVDTMMGERALEDNMNGKGLDYLLYT
VKNTSGKITPIRFSVKENPTLEEMNEFISTGTNRAVLRNRLSWYVCMRGKNRESTPTKTT
IAIIIVVALLIALVTFLASASTVLLCLKEYDGSADAPKTAPFAMAILGLCSAEQLWELSP
DRMVFVSERLATLQRQEIIRHNAYEGMQLHPYTTTIITRSVETAVRLCFSVIEELNSQPI
DDPLRELLGEDGRLLIACAVHWCTDATVRVESNSGVIRYEGPDVVYCGRMWMFAAPNEVS
ISRAARDLAMKMDEVQICSLASVFLRGVEGRQDLFTISNPQRKRLVDAANRAKRRISSSF
AVQSPTTEIVSEGNPLSAGAELFPRNGMYPPCNSEMRGVASNATAQLRGELRSGSAGSRS
GNPILDTSSMGACGRYMPEVSRGLKRFSQINGVRTLIELLPTEIACPSEAAGFDISQRPS
SSPLSRDNVGSSTDEGHTRPRTTPTDEEKDWRRISRGGQFLAVGRGSTANWSKKPLKQVD
QNVGNGIVAFSGGLRAEDLDDGDFVTEVLRHPTIPTFVDTQLRAVFEQQSLLFDFSYDSV
RTVVYYFFSAFKLLLKPLATPERNNIFNRLVTVFGIPQEHILEHLAVRCVLRYIQQLEEA
RSLLWNCEQQLRLRSLARGQMRSFTTIDSSTTNPLSEESFEELSRSIV*
>TCRU_4189 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MLVTLPVYSSKDEKETDNEKGVLHLWLTDNTHIVDIGPVSGEGDDEVASSSLLYKSGDNN
ELIALYEKKNGDEEESLGMVSVRLTEQLEKVKDVLATWKEVDETVSKLCATLLAEKDPST
DNGCSAVIKITDGLVGFLSGNFSDNTWRDEYLGVNATVKNGAAAHNGVTFKGRGAWAEWP
VGVQGENQLYHFANYNFTLVATVSIHKVPEGGTPIPLMGVKKKKNGAGSSVFLGLSYNNK
NKWQLRCGDEKTTEHSSSWKPETTHHVAIVLRNGNQSSAYVDGQRVGGDAPCTLGSTESQ
EISHFYIGGDGGSSGSKGSRGVVLVTVTNVLLYNRPLTSEEIGVLNPNKALISPLKEEPS
TPSPVPSASVVPPTPLVAATAQQTGNSSTPDGTHRTEQGQPIGNSGADSGSASASAASTV
SIPSAEKDSVMQSASGKSSDGAQTVDGGSFADGDPTVEKREGTDGHEEGIHPQVREVNAT
ALNSSLGSFPQGNNSDAGTMRGSGLLPSLLLLLLGLWRLAAL*
>TCRU_4190 hypothetical protein, conserved
MRTHIVDGRAHSAAGWAGEPQSAARWQTRSCGAHVGKRFRRRQRRAGLLSEGGTAPPTQR
VTCDTEGTRRPVEEWAGVAPCLCAVPPLGARCPGRARNRVPATPTGASHAVYAPRKPLGI
PPVRSPDCSEKVHVPDWAALLREGSCNHGFFFSGLIAWDTAVRWREHEVYIVTSLHQEEQ
HNPTLFSDVVSHGQWDDAECLSSRQGVRSHKDSFGQLGCFQTKGMRCLMPFSVARHSALY
EHARLPAAARCTSTGRSFVVVEPYNSAADPDASSARDEETSVHNSKSYAPREE*
>TCRU_4191 acetylornithine deacetylase, putative
MNAKQWLAKLVSFDTTSRNSNLELIHYCKDYLEGLGVKCTLVHNAEKTKANLWATLPGEG
GVTEGGIILSGHTDVVPVDGQKWDSDPFTLTERDGKLYGRGTCDMKGFVAVCMSMTPELL

KMKRAKPVHFAWSYDEEVGCIGGQVLTDFLREHKIRAEYCIVGEPTSNKLVVAHKGLFLY
RVCVHGKAVHSSYAQTKQGCNAVYYAAKLIVKINEIAESIKFYGMQDPCFDVPFTTMSPN
LIQGGNALNTVPAKCEFVYEMRYLPEAEAEKFEERIKAYVNDTLLPSMKKAFGDARIELE
KLSKTPPLKDANEKDPFTLLMRQITKDSTKRKVAYGTEAGQYQAIGVPAVVCGPGSILQA
HTPNEFVTLEQLDECARIIRKAIQGDGALARPHL*
>TCRU_4192 retrotransposon hot spot protein, RHS3, putative
MTLIGLRMTTTRGHHITASTVRQFTECLAAYFNGWEELSRDMSWEIIYVQHADSTPMDGW
ERRGVVNLDNVSDDESREIAGLWREEMHQYQVSISSGGFGGDAAL*
>TCRU_4193 retrotransposon hot spot protein, RHS3, putative
MKGHIFYDVTEKGTPPAEYFVSSTGWGMSVVSPPNVGNCDEWETQVKAERIIVNCPDEMD
VKAMCAWMERDGTTDGQAESWKMVEERMEKVGPIPRHIFDANEFVAHSAAIEDALDGINS
RDGERHFTHGGVRLWYSGDPPQKVVSVVRARGEFGAGGFLNAPISVCLGRRIAHYFGGRD
E*
>TCRU_4194 hypothetical protein, conserved
MFQLIHVTPRSAVLLVLLFVMCCASGCFAASLTYSCPSDKAMRAHRAKSIPAVVRDVPLG
SEGASQTCTVIGRNGWAPTRIDVSTRDLDGTRKYCSSEWYCAMNSLVAIASVKVTFFYAE
ERVVFVSLYFAATVR*
>TCRU_4195 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MVSVLLTAQLKRVKDVLTTWKEVDDRVSSLYPSENAEKDDITDTACSAGKITAGLVGFLS
GNFSNDTWRDEYLGVNATVNKKEAAEKTDNGVTFTGRGAWAEWPVGKQEENQLYHFANYN
FTLVATVSIHGEPKEGSPIPLLGVKMKGEQGKFFGLSYGSGRKWMLLCGGGTTNSGELSS
TGEPETTHHVAIVLQNGNQSSAYVDGQRVGVGASCALGSTESQEISHFYIGGDGVNAENT
AGDEDVSVTVSNVLLYNRPWTEEEVGALNPNKVFITSPVTEIKPETVLQPPAKPQPSEQE
TLKANVGGGGGVSSAASTATTPSSDVDQTVATGSGDTMLGNGSPQTPEVSVSSAEDGETV
EGTDGQGEKGIHPQDGEVNATALNSSLGNVSQGNNTDAGTMRGSGLLPLLLLLGLWGVAA
L*
>TCRU_4196 SET domain containing protein, putative
MRVRRATTMTAASSVMHRQQCRWDLSTPSVPRQQQRPFRRTKRTNYADREHVLFPDMCSS
FGGGATVEGNRSLNPTTTATTLSSLFLSTATPTEAVSTQTTSIYTKRVSLSHGDRVELQK
SALALNALATPIVGRLLYYGLTAMAYIRYSVGHVSFYTRKSVAPPLSTSSSATTETSSLS
SNCSVSSTSIQHLIEMGAYEQAAAAFATERGDISSSHCGVNAPLFRGILHGKALDCLYVG
LSSIHSRGLMTSRDIPRGTRIVTEPQRSYMDASNFLPLLADTHLRLPDTWHYTHPSGVLL
ELVTQPLPHHIMNHSCDPNVCSGLSRQFWPAAIASHNAELLNRIQSFPHFDDPNSFFTTR
DVPAGGELTLSYAHRVAPLFSGEDPLQKFFVMCRCGSPMCRHFLYRPTDDVMRYVSQLSR
SWSGGKKRRKSIHDEADDISRLLQLGFDDETVLLSLLPSRTQLMAYMRTHLASSRRTASK
GQLLACYRHVFKLLNEAAPKEQNPYEDVSCRERK*
>TCRU_4197 hypothetical protein, conserved
MSGDGDSSLDPSILVVEARFNESLGNQSVSGGGGSERWQHHEEKQQQQQPLSLPPRSRGD
VNWNASSSSPSTIEEAEGGDGDRRTADRRWSDDGSNAGNDRDGGIEKNEENEDDIAERVL
RALRCKDMLMDEQARNLQRREMEARQLRRELDELRGEKQLLMQQLRGFLDGSTPMTTASE
TGPLKDSGQLYPSMLLQRADSQLQDERAERQQDARHFMAHIEQLTAQLAEAQQEARTREA
RHAQDLDAIQQEMQELSTVVDDMHATKAALCLTQEQLAKANEEKAQCQLERDRLVRSLQE
ALRREGSEHQRTLERMRAEAGAYERAKAAAEAKCRRAEAEQLKLVEEMRALRIEMQQLVD
ENAALTLRMESSEQQLQRAQKQHVEERAAEAEARRRLQEELDAKVREMAQLRFTRDAQSK
LLAEEDGRHALFQAEVEECVQSTRQLEEALMRCERRRCEAEERETRVVAERDALRVQLQR
VTAASRQELLEQQQLTEEMRSFHQAKLQQMQQAAEHQRQRAERLEEKSEEAVREYRTLQA
LLDSTQRQMEEVAGELQELRQQRISLEAMLAETKQANNECAAREKNAAAQLDALRSRLKQ
RECAWRELRAKMQRLEESEQRRRLAEAADSLLRMRQNHHSQGKCKNNLQTCIRDKISRAK
LEENLLDNIAGVDVNTTLSTKEPSSMTAPPPPETKGKPLRGPQLDAWQAKLQALEARNAN
LERQLASRQIGHRALVEDRKALHQQMHTLQETAQGLMSALERQHRDAIKHLEEAHRRRTL
VACREASDALASHESCVRSGVARVVSELMAFIRALEANATLVPRHHERLQEAPVQMADDD
DDKENMLRAACDDITRNFLGVEGGWEALLQHSLRATSGRKSSRADGGSLSAAMRRRIRCF
LLDYLQAQLLGKPTAAALPALRRQSGNKKKALNVSFAASSDGSSESHDDWDEKQENCGEQ

PLVELLMERVRCVYGDDTPY*
>TCRU_4198 hypothetical protein
MSTAQSRAASSAAASSASSLSATTMSSTVCCTSCTPDDTPLQAIRYFPTSTSRMDADSAD
DIRGRGSRKNKQDAEGKRQVQGDSHVKLKYSESFDAYEDDVEEDGSHLHRHRQQQQQQQQ
NSSEFLLSVGTGMSAGRLQVRCDKCFQSGIGRSSTSNFVDWKQQQENKKEPRCEEPKDLV
TSALSSQVWRYEAPDSHTNSLEGKVSTSLNCGRNESASLGVCRWNDRSNHVAWRCSDDGN
NETINSWGEKTSLLLNSQKKSCVAPTSPNMQGVKMELCSLHGVYREREEEQQQQHFLFSS
HTMNDGFETSHVDSVKGRWLRWRRKSKSFAGAGVQTDSMALTESTRIREAVGIGYLLGDH
APRMGDMLRLFFVPGTIDLEEREVQRWICSVNRTRRHGVLLPELQGIDAGAQFQEFTQPK
TAYMSGEATEVNSGVVSSPTAMAAAAETRRGQMENLSVSRAAAYVYTRQKEVESISLDPA
RVPGSFLEDREKLDAYWARDESGRSNSDNSDDQMSGMKQHSRYWSNDWRKYSMEAYAMEI
CSMASCSSVQQNIDNCSVSSENKNYDKGTSLATSSLRNNSKKDEEKAFGMRCLHGGNDGA
YYFNDHDYQKEKQKGKFMTNDKRPAMDGASAWERGIMSDDGRGIGNDDRDTRVNQQCRVK
VCIAALKSHFVIMATFMPLALFIGLSVLTSAIVISGLLVVVVALLLGVLVYRHIVALYSL
CFSKNLWPTIPLGCSRGHNNERRRSLDASPDGSWLLMSPSLLELTHRFGGRWMYLLTKLL
YMGALLAAAILFMSFGFTLTGGAAAIICTLWDHSTFETLSMMESSQGCQLGPKPRFLVLF
PFLALAVCFAGPTAARSRLCWWETGIFKLVSLTVFGLLFFTMLTVQLVWTLKHSPSVFDI
PLRFIVDHAWGRRVPSLWWLQDTVSQAEFWTEWQVLAYMVLNLSLSVAQLSWFFGFGVSA
IKAGTYHFYLMPLLWRRGTVRKERPQGEEEERGQQSVKRFDQCVFAASGFGTPFYVAFIL
FMTLALVSTFLAFVGTTMSLPSLAAPSPLRLLWTAVPVNLTDTDSGSRRKMVCALGILES
SPVGVLRFTAVLSFIAGIVLFAWVPYCVLHVSSMLAHLNPVTEPEERQELAAMAFLRSKQ
AAARRRAGESHSFGLVSSTTHTTTSWSRLTRCWYRNKGRGALGVGYCGNREKNGHSGGQC
GASASSTPPAAASAAAVNGSVIFNLSSPFMLYPEQYHATTRAGDGVRVLELFKHLRLITL
EENWFRYHITEVLLLRLPFLVLVFMVSSLLVAGRFARCYEFWAFGEPDLESARPSHKSNV
VYVPPFCKEAASVPISDQLYGRLVLFAAVSGGFFMAPLVFAVPAFILLRCRWERWRCMRM
TASLAQLMQVDVRQVRDAAPRQPHGTVASPTLPLLWNGEKEAEVIRSEAREVSPVPLEVP
VGMNKGTTLTPSAALGGLAGAQFFMATQKSVEGLNAWNTNCNGTRKTAAMASTTRRIRRH
RHPMYNAPLVPSQYYQALKKREEAKHTPSTITHKFCSGLWCIVQVSVEAFPLLVTLTAWV
GAWRAVVALAYQYGIWTN*
>TCRU_4199 hypothetical protein, conserved
MRHAGAQFFNHRGNGGCGVTFLYAAAILCTRLCEYFFFIKAVRRRLSALHRGIVRETSPA
NLPSAAVGLGERLRHNIENNHKRIINSTERASAAIITDASIHGWRAVFILQTPATLKLPD
ENERWPFLIMQVEARAVLLALSAFSAILPSTMDVWVDNTSLQGAANKGSSNSHALTWELR
VICEFLDSRGVQVSFAYVRSAENPADGISRGRVFTLQDLAKGWNLRK*
>TCRU_4200 hypothetical protein, conserved
MAALRLQKIAVRSEKKQTRKARPVTEEEMNQVIRSRTDWKERVVLRPAWIMASRLFEIAA
LAVKNFKLKPDGALILDWSVAPKTAKADPHRALRFVRMREQDAFDTLNLCRTLQENENLT
NITNAKVERALAPWNATAHSIERGALRHAAPIVEAYNLNPHVISQLAKHVNPFDLPQNTV
RYLGRYTTVLTLVSSLIALM*
>TCRU_4201 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MKDAAKGRSGDSTPSSISTIDSVDAQRKAEEEDGNEMEVLNPNESSILSLVNKNGQGNAI
QPFPAEQQEQKGQPLGKSGAGGASAVSTVTSSPAGKESVKHLASGTSPDGHQNVNGGSTA
GGYQTVDTGYGNKTQEDGPLKTPTGNLATADANGPITMGVGQEGTAVTPEVSASSAEDEE
TAGGTDGQEGIHSQDGEVNGTALNSSLGNLSQGNNSDAGIVRGNGLLPSLLLLLGLWGFA
AL*
>TCRU_4202 BNR repeat-like domain/Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MLVTLPVYPEKAQDEEGNPKGVLHLWLTDNTHIVDIGPVSGNDDVAASSLLYKSGNNKEE
LIALYEKKKGGGETPSLGMVSVRLTEQLKRVKEALATWKKVDQSVSQLCPSERDRPTGNA
CSADKITDGLVGFLSGNFSNGTWRDEYLGVNARVNNKEGVEKKENGVTFKGRGAWAQWPV
GSQGENQLYHFANYNFTLVATVSIHGVPESGSHIPLIGAKMNDSEKTVLVGLSYKNKEKK
WILLCDGGENKEHSSHLETKKSEHVVILLRNGNHCSAYVDGKLVGSAEFECENTKDKEIS

HFYIGGDEDNAEGQEGVSVTVTNVLLYNRPLSSAEIAGLFKNTITVPKPEGPKTSMDALS
PTVSAPDVEGTVPHSTPGRPQPNGSVGAGAGGVSSAASVITTPSSDVDQTMVTGGGDTMQ
RNGPLQTPEVSVSSGEDGEPAKRTDVQGEEGIHSHNGEVNAAALNSSLGKLSQVNNSDGG
TVRGSGLLSFLLLLLGLWGFAAL*
>TCRU_4203 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MLVTLPVPPTEREEEEKEKGELHLWLTDNTHIVDIGPVSGDDDAAASSLLYKSAGSGNNK
KKDELIALYEKKKGSEKPSSHSLWSALLTEQLQRVKEVVATWKKVDERVSKLCPTLSAAE
SASTGTVCTSVVTDGLVGFLSGNFSENTWRDEYLGVNATVKSGIGAAGTTDGVTFTGRGA
GAEWPVGRQGRNQLYHFANYYFTLVATVSIDKVPEEGPISLMGATMNGDDKTVLLGLSYD
SEKKWQVLCDGVPNSGKLSSTLGSTHHVVIFLRNGSQGSVYVDGQQLNGNEACALGNRDS
KGISHFYIGGDGENAGGQEEVHLTVTNVLLYNRPLDEAEIGALNPNKEPIQLLKENPSAP
SKVSSDSIIPPSHPATPNAQKTEASSTPAGRHPMEQGQSMESSKDADSGGASTAAVPTIT
TSSAGKDTVKRVASGTSPDGTQTVDGSSTADGEPTMETREGGTNGQEEEVNTQIREVNAT
ALSSSLGNVSQGNNSDSGTVRECGLLPSLLLLLLGLWGFAAA*
>TCRU_4204 Cyclic nucleotide-binding domain containing protein,
putative
MSKFDKCVCEWIFSASIDRQSKHQILENVITTIDKYKKMEGKDLKTQGEYKKKLISGISG
QSRGGHTGGKRNKGSVIDYKFSRKVNEVIQRLDDPQITPLPTSLSQREANGSEDANVPLN
SAVPVNPSQNGQSLPSVDDFQEKHEINDGVESEGQLTIQSDRVETDEKYEENEMEAMRYG
FETFKFVKTGSRATSTSSSDVGDGGNAAAANRPGTDEIMDDNEDERRRHITMQGHSRLGI
SARSIGAEEMMSTEFPTAAKSSEAASFIMKVLEKHFLFSFLDDKELHKLAMVMNTEDFPE
GIKVLVKGETNSKFYIILDGSATITMFEDDPDRIETESLQKGSVFGELGLLYETQSEVSV
ESTTPLFCATLERNTYKIVVSRAEEEKRQRYFSFLENAPFIKDLPAQERLKIAEALKEDK
YTEGDKIIRYGEKVDWLHIIVEGTADVIGRNEEGEEEYVVTKNAGECFGDLEFLYHHETV
ADVVATSPFVRTAKMSRLHFEQLIGTAKELLDREVKEDASYDYYRRTMVGTSAPREDPTP
SFDAPPEYLSKLNVPLKL*
>TCRU_4205 metallo-peptidase, Clan MC, Family M14
MNGDGNTVLCHVTCGKSVGMDVKEEKGARGYELEWSYSPPPDNQREFEFPEDGLLFSSRF
DSGNLIQVERIGAYRYNMYTSPDCGNSPKQTNNRQWFHFAIRGGCRGCVITFTFVGMMHS
KMFTYGWTPVIAVCPGKPQYTRLPGKATVVSLDAMPPTPGYPGFVLKPWSKKASETEIAA
DGGNENADGNGSSEGVPDVIEVAMNTSRKKKKENAVAMNLTFEVRLEIDAPLTSSLYPLG
HPQCPATYIASNHPYSYSTLQQNIKAWKQQTVGGEKVGTVEESKDNNFSPSCLSSIYFHH
EILCKSLDGRNVDLLTITDRSGICNERFPLCGEGDMPYSSARGETERPHQFIGKQCVVLT
ARVHPGESPSSHLMHGCIEFLLNQADPRAAALRSRFVFFLVPMINPDGVARGHSRADTEG
ANLNRMYKNPCKRRHPAPYSILSMLRSVTSVKGRLALFIDMHAHANKRGVFFYGNSMNAP
ELLQSLLYAKLVSMNTPYFEFQSSNFSEANMFATGKTGEGRDTSSRVTLYQETGLVHSYT
IEASYVIGNTLNPIVGLSSCGVDEPEVIQGTFCPKYSQAVFADIGKGLLVALLDLKGCNP
ISRLSNTQFHSVKGLLAALQRQFQIEIAERLFKIAFMSGGQAAIARDPGADPVYTVMSVL
RSDDIPDAMTIKDGRGLPVTTIRGLLEFVTLEQAIQILAHAPPMFPPRTLLYGAGRRMMN
QVGGGFAGRRSMSNAVPGVTAVPAVSTTGRKSITGSN*
>TCRU_4206 hypothetical protein, conserved
MEFDLSHFLKEIQLQHGLRGEDYARYRRYTTNRLSTLRHQLGLLHDPKRFKQKEITPQNA
TRPEHLQLLVLYAERCWAAAEEMQERRRNVGGGGENKPPGGIPPSDQFRKRLNKSVKWAS
KLHEVARIVAHPRLKQEAEAYALEVKGRAAAAHGAMVEAKKFFSMAREQYYALRKSSTPE
QWMLLLTKVNELDDRVVYCMLRLGEDASKYKPHVDLEDTTERLAATTIEWNGRQLNVASI
KVKDALREVRTLNVESVKTKALELGGPIPLGQQNKVLDLMDRRIGCLNDALAHARQDLRT
LSDDRQKTELQLLVHYLLFHVSQETLHRTLFMAEVYIRRFCATEKSLSGGSSSSSGNNKI
NTHIYSSGFKNKREITPSQYASPLEIVRLYDTALETLGEMELLPGVAGRADLEELTALCR
AGKLLYLGEGWRISLEPTRAQNCYKASLSTLEGVPSTPRVEKLRLVVEKRSLQLASSTLL
TTLQSGVAARRVEEAKEKSTQYLVDAGDQVAVAQNIIKFPPDYQAVPCKPVFVDIALTYV
EYPIHDISSRTKPRDEQPKPSDSAGAKEEKRWKWGWGWRK*
>TCRU_4207 ribosomal protein S19, putative

MVAARTKANSKIRRIGKKKGATMKDVHPWRWVKLCSQHFKQEGKLMVPNCTEIVKSSHGR
ERAPQNPDWYYIRCAAILRAVYMRPGVGYGGLSKRFSSKKNRGSRPEITVRASKGLLHWG
CKSLTKLGLIEKCESSGHRITKNGRKLADAIAFKVAIRKLNTATSKN*
>TCRU_4208 kinetoplastid-specific phospho-protein phosphatase, putative
MNRMHDNQREWDDETVYFYPPRTVPPAINKYTRLISDLLQNIPITDALPGGAPMAIALCE
DAKKVLEKESVVLDIDVTEKDNLIIVGDIHGQFADLLQNVLSMQLVQQEEDCIPSRPLGS
VYKFLFLGDYVDRGPRSVEVITLLLALKIEYPTHVLLLRGNHEEAQTSRMYGFFQECRVK
LEGNGERVGGGCTSMSSSAWLQYNMVFCWLPLAAVVQCPSGMFFCAHGGLSPQTKTIVGL
KSICRNEYGQSLGTSSGFYFPSPTNDNDTELSVADERNIVDGLLWSDPDDDVYGFQVNHR
GCGFIFGPDVTRAFLDRNYGYSFNSRLPGQRREGMQFIVRAHQCVEDGYHWAHGGLVLTL
FSAPNYCGMNNKGAFAVLRGRANVGEDRVLFEYKVYDIAPRSPNEMGTRLHASCDAASSA
ARRVNGSLHGGYFDDSE*
>TCRU_4209 hypothetical protein, conserved
MFAQQRTLEGVTAGVGSRVSSITWEEELLLRGVRPDSGYVPLLHPVFPSPRSKGDGGSSA
SPEVTRGVFAGDDVSGCGLKGERLAGNPGDKPRTLSPPKAISARLQRKELANSPGGESVI
GYSSDGGLSSITQGRVMPPSLVPPRVIVPSLIPMRDEASPPTRERTQPPNTRLKGHSGGF
LPPLNTDASRDVEMAKVSSSKEPVSSQKLNPVGGSAPFSSGANPISDTEATLARLGDFIL
PSSWPSQDNNAKHLGRRCSTSRKTALAPVRSGRKSPVGVVDKRKVLLYENSRKKRESEVH
GVK*
>TCRU_4210 hypothetical protein, conserved
MSDYDRDSDESSVDEMSKRFVPVRCMEEFQASVAAEEECLCALVFTSFLCPFSANVLPFV
KNNFVLSEEPQTRLVRYFHVALVPEEKTDITRLLQKDPVFIATNRQPTGLQKKQLHKQAY
DNLMELLTFLEVCSTPCMMFFVRGQCVRISDDVVDAPRVIATGSSMRKWKAVLQNAVVRR
NELLREYDAEKRREKRRIEREKRREARRRAKAEEEEEDEEDV*
>TCRU_4211 Methyltransferase domain/Methyltransferase involved in Williams-Beuren syndrome, putative
MPPPRPEFENPPDVLYNKTGATRYTSSTRVQTVQRAMTLRALELLGIPSGRQALLLDIGC
GSGISGDVIREVGHTWIGVDISKDMLMLAKELEEKEESEVGKEEDSHSDGQDGLKECGGC
NPGNDLKNVKWGLITESDDDDKDEDEDGNEENTGTMTGPSMVEVLRGDMGQGLPFRPGSF
DGAVSISAVQWLCQSDCRGHVPQRRLRALFQSLYNALHRGAKAALQFYPSNVEQVHMITR
AAMLCGFTGGVVVDFPHSAKAKKHYLVIQAGQVAGGFVPRLPIDVHDSDEEDEASFSDEE
GDEQYMTARVGGRVRVKRSRSHNDGPARKRRRKDNRPVTGTKEWVLLKKSERRKFGLPTT
DDSKYTMRKRRPRF*
>TCRU_4212 GPI transamidase subunit 16, putative
MPFRFSALLCVFLVFLLCPVVIYAHASTVPRTEKKYTIHLQPLTEGLGDVGEEPTLVSVT
ETTSLWLPRGSAEDNDEHLTFNEDLDPFWVHVLRRRRFESLEWSGCGGSWRPDWSVTLHD
TNSSISESTRKLIYDLSHHTVCYFSALSACGWTGQEGTDGYVANKSVSLDVEAQGHHQWL
AQFVSSLLSSPLSWSRVTPRNIRPVGVLHPVTGRFGAAAGLGNRHWCSYHLAQRDTVCTQ
HVSAILSGGRSGKGVEEKIPKGIFRAGLVTMQDFFSSSFHHFNFGVSQSELPAENMNEET
EIQLLFRMAFVARKGDFDLLANHWKRSLPTYSDRLIFFYGPNVNKKFQDAIRSLPSSSHV
EGVSGDKEALKDEKRSFSSELAPTAHYYISSVGHDRGTYRLVIHPPMRRTNTISADEHHE
PGRWNGLRVGDTLDSLLIFPLHVIRPSLYEMHSGPDGSTILENAFFDDNANALLVLLKTV
LTETHVNSLHRSDNNNGTAPYGFVVCEFPFRFGWAALKDMPHDANSHRILPQPVIRVGRR
FGKTELKKFAGPHSANNNGNKRWSERCLASQCASFASMQIDHQASLERLTDSLFRNHSRS
EIGSSCFCYYWLRCSNVAGTTIPTPDPAMVFNVISLGVFFSGVLTAGVSRITRMMFDRKE
GQDFGEEGSTLNRSIDVEGKKQKK*
>TCRU_4213 hypothetical protein
MARSPNVDYLSDRFREMSLNRDRLLNDGKRTEYNLEGHQQAFNFKKKVVDSTHTARNPTY
LNPGRSFPERRSGRCGDVVSDDDRLPSSCTHSFSPFRKNPTNERGKGGYNCRPNCRWITL
PSDEDQSRDSTFGARRRSQPGVTWSSASSNSFSQVQPSLNLIALVNDVARRRGVGSPAIP
PEVIIAFENCVCNGTSMLKFVSHDAPHERFFMIKFLDFKVHGGEAEPVLCWYTKSRSSTM
RHYLPLANLVEVIDGGDGHPAVQKRMVRPGVIKGSAVNLNANYMGADNILQWRFSSSKDE
EKIVAVKLLCKKSYVAWRIVTDFFSKIGSVLMPLM*

>TCRU_4214 RNA-binding protein, putative
MAAWADDFDPTLEDGFADEISASFEGGADAAAAKDDKLAWENAKTVIETVTDSENKRYEI
VKKVRTYHVDRPVTVVDIRAKWKRFGKSGDNNQDLVSRDPPIVLELGEIDPFERVARDEI
VRLMNEVERMKIEVTDPRLARFAKIKEEQEKAALEETTQTDQPKERTWAAARGEKSSAQR
KEDTDRRLRITNISDDITREELYNIFDTNEYKIEKLFLPRDNATGNYRGFAFITFEDHEQ
AERCLKKTKGVARFKNTVMRIVRALPEAEQKRH*
>TCRU_4215 hypothetical protein
MRSMGAAAPPMQHGALLFHGHSRSAEEQLAFHDKYHDRMARFTGGGTGDKYALRGRDESN
GEFRGQAPDYWAEYARKLENLGLPRGGVGVSHVEFEAETKSPPPSGTLDSPPDTRYSHRR
WETYSATKSPARLPEESVLHRLDWLAHERSEPDATDVIDLLRDVEDVLVREESQKHDETH
VEENSQPTGFDSSRWLPASRTSDPGRPMEVPPAPPVPTTTATTANNTNNNVDANLTGNSR
YRTAPPATTPTAAPSFQHVSPGASPAPPSRGADWSQMSRYQQMEWYRTYYAWMMYYAQYY
GSVLAFQQQQQQKMEKVPQKNANNELTSLKELSREYKKLALEVERLNQSFRSHAPVKKSV
STQSALGNELKSKGRRRSSLPHAGEDEYTLYRSEHGHSFLHGAPTHTLSASQDDNDRATT
PERAATAASSGGIRSRAVPHRKSLNERENLTHGTPKSNESENGKAFYGRQSEMPWLLPRR
HSPEEYQTSVAPRPTYRDISWLYKYEESETEEKSQSGTEEGGNWKYDDGERDSDLPVSEG
RRMPPSHNVRGHERRGERRSSVYERKKRELEREKPRWCF*
>TCRU_4216 WD domain, G-beta repeat, putative
MGDNLAASSSAQLVATVRHENMQLQKQLTEACHENRTLRKQLYHLSALLDIAVNKLATKG
ITLETPVGIRELRAAVSRRDLIDTTSEVIDANDLGYENVTKQNSSNRRFQLRRELREHTR
PVQCAAFAPGDRPILATGGLDCHLILQDFLTGEKLCDIKGHEQNIADVAWFEGSGDLLSA
SFDNTVKVWDTRQASGSLAPSYQFTATGFVLAAVPLDKAFVFACTDSKRRTSILDLRVQK
PISWEHDVRANALAFNSYGANLITGHNNGTISVWDLRKIGLALSSTSSMEEGKTTSSVPV
NSSASVEESPAVSVPRVSMIENEPSRSAVTYLGYYHNRDDSRRLLVVSADNMVRLYRGAS
LNASSSDTISLRNIVGGVPTRGFTVKAAFWKGVRKKTNVSAFFDDGERENDPQSRRLTEC
DLLVIPGAENTACIYDVTEEGGAILVEKLEGHRERVVGAAVHHADSKPIIATYSADNTVK
MWAPVKS*
>TCRU_4217 NADPH--cytochrome P450 reductase, putative
MHEGAEAEAEVLTVLYGTQSGCAEHLAFILASLALKRGFKHCRCLPADEFLLESWRDSSP
LVIICSNASQGEAPDSIRASWSRLLEPTAPSMEGLRFAVFGAGDSLYQKFNYMAKMLHNR
LKQLGGEPIINRGLGDESDAKGHDEAFFPWILQLWRALGRLNVDEPGQITEDFFKFPLLT
KYNVSFIEDSVASDAISQKALYNEETFNCVVKQNVRLTAKDHFQAIHHIAFSRVVTFLEG
AVERSDPLSFEVGDALGIYCANSDAVIDSFLAQTQLSGDVVICVTPNISEGLIQQRSQPF
FGRPMRLRFFLMHYFDLEAVASRSFFSMLARFAGDDEEVRERLFELASSDHLDDFMSYSH
REKRNVVEVLSDFRLVRPPLSFLLSFMPPMRPRIFSISSSPTFDVSEIHLTVAQLSWQTP
LKRSRKGVYSSYLAAAVPGDFFTCFLWRGSLPLPSKPVPLICVGTGTGIAPLRSLIRECA
AAGSIWSDVPLLLFFGCRHEGKDYIYSNEWSELSKDRLKKLTVLPAFSRDGDKKFYVQHQ
LGRHARRVAKLLDEGAYIYVCGNSTPMPKDVAMTFDEIGTQCCCCGNELRGQEYMKQLRK
QGRYMVDSWSA*
>TCRU_4218 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MMCCGTAAVNAEELSEPNFEWKGITDGVTVESLGVPGLLKVGNDVFTVAGAQCKNGEGED
NTFTGIASQIITKEAAKKLEEALKETKDKTQFLEEVASSSSRKKVDVSRPTAVVKEREIY
MLVGKYSRNAAAVGQDGGADGWGLLLVKGEVSDAGESKKIDWKDTKRLQWKPLGGTNDSL
TELIGGGGSGVKLTDETLLFPVEATKNDKKTKIFLLVIDPRDIPNWTLSEMSADGCSDPS
VVEWKDKLIMMTACDDGRRRVYESGDKVEWTEALGTLSRVWGNKHDEKVKLVRGGFITAT
IEERDVMLVTLPVYSNEKGNRKGVLHLWLTDNTHIVDIGPVSGDDEDAAASSLLYRSGKS
GEDRKEELIALYEKKKDEDEASLGMVSVLLTAQLQRVKDVLTTWKKVDDLVSKLCPSKSD
VESILPENACRTAMPADGLVGFLSANFSDNTWRDEYLGVNATVKGNDGGAEMTDNGVKFR
GAWAEWPVGAQGENQMYHFANYNFTLVATVSVDKVPEEGTTIPLMGVKMSGDGNPVLLGL
SYDNEKKWMLKCGDGTNEELKSTSETERTRHVVVLLKSGGQGSAYVDGQRVGGNEECALG
EAASKGISHFYIGGDGNSAGGVSGIQDVSVTVTNVLLYNRPLDDTEVVAFNQNKAPIPSP
ADTHIEGSVIQSSGGRQEEPRRLSGSSVAGGLGVSTSAVSSATTSSGKEGPANQLASVKS

SDGTQNLGGASSPDGDPAVGTGARNTVQGDGSPQTPVGTPDAADKKAPNAETMGHDGNAV
NPGASAGSGEHEELTGGTDGQEEEGTQPQVREVNATALSNNVGNLSQGNNSDAGTVRGSG
LLPLLLLLGLWGLAAL*
>TCRU_4219 phosphatase of regenerating liver-type phosphatase, putative
MDVNCTLIECKDRRDTSRTLFNLLILDAPSPSSLHTYIKALQRRHVRHLVRVCGPTYDAT
QLEKDGIDVHSWPFDDGAAPPKSVVESWFQLLDKEKEKLLSGASTQPASIAIHCVAGLGR
APILVALALVEYGGMEPLDAITLVREKRRGAINQTQMQWLAKYKGRSAAGGGSSGGCTVM
*
>TCRU_4220 Concanavalin A-like lectin/glucanases superfamily, putative
MGPNQPYHFADKNFTLMATVSVREVPKAGSSSSIPLTGVKLHDPGHTVLFCLSYTSENKW
EVTINGNTRSLSGDRNRVRGRKYQVALGMDYYVKHLIVCVDGLLMYDSEKDYEDNEDFFG
ELKTVLSSHSTSHSYIGGERAGDSDDVHVTVSNVLLYNRILSNAKLKAVMKKIVVGTPVA
KVPVSKGAPQNNPASETFLQSANEASS*
>TCRU_4221 BNR repeat-like domain/Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MLVTLPVYSKEDGNEKEKGVLHLWLTDNTHIVDIGSVSGDDDDVAASSLLYKSGSNNEEE
LIALYEKNGDGEKPSLGMVSVRLTEQLQRVKDVLATWKKVDERVSKLCPTSNAAKDSSTA
TACTTVKITEGLVGFLSGDFSNGTWKNEYLGVNATVNNKEVVEKKENGVKFTGRGAWAEW
PVGKQEENQLYHFANYNFTLVATVSIDGVPESGTIPLIGAKMDDSENPVLLGLSYNSEKK
WRVLCGGRENKEHSSDWETKKSEHVVILLRNGNQSSAYVDGKLVGSAEFECENTKDKEIS
HFYIGGDGGRAEGQQGVSVTVSNVLLYNRPWTSEEVGALNPNKVPITSPVTENVPKTVLQ
PHPKPQPSEQETLKANVGGIGAGVPSAASTATTPSSDVEKTVVTGGGDMMRGNESPQTPE
VSVSSGEDGETAEGTDVQGEEGIHPQDGGVNNTALNSSLGKLSQGNNIDACIMRGSGLLP
SLLLLGLWGLAAL*
>TCRU_4222 hypothetical protein, conserved
MPRGITSLGSRGHQAVSHGTLAAWRSHSEGHDCGPPVCGAIQLVAGCRCNTFGLLHSVRT
DTCGNVTAAARAVPRCISNHVITVARGVPRAEVEASQSTSRRTTKTCFRRGSMPVVGCRP
PSPRCGMADDGPSPCKRVDVQWETRSTRCAVTSGNETLRPLIHVVRAGSSDSSASMLLEV
AARFSPAVVDG*
>TCRU_4223 hypothetical protein, conserved
MEAGTKGTNVRAHHPTFCTVLPRRLDLIASHIEPSPCGRNVVSKRSRGRRARHLHSFVEV
SRGRNADLSASGVSLLLMPYSVSPWVLSGAPAFYWMIGAAEMWRVFAAPSFSTFFARRVR
DGFRLPHCMGCCKAMHYATRLCCGCRAVEIFDVVEVPLEGGGGDPPARVITDGFTRPFEF
AVPSLYFHELAADIAEYIQFAAVLHKFKVLSSAPSTSEADRPVSLKDSGGGSVQFVPRPE
SIPSFLSARHVHTVTLRSLLSMGGMGDDGIRETVALFVSSPGIGQRQLMHQSFPRVGDTN
SVAETIWMGVHRGKLCALYFRAYADGMQLFALSCDASCVP*
>TCRU_4224 hypothetical protein, conserved
MESTYPVAYRRVVVSGSKDPVEYFVRAKDDGRTVAPAQTETRTGWLMCPVRLRSQLRHWM
RAEQAALRCLFALRPSRWLIVKGIQEHSFSEGVSAVWSAHCSVRSIGLFLW*
>TCRU_4225 hypothetical protein, conserved
MRVASAWAVHSVAEVRSACRPSLSSSLRCWAVLPVGFLAVPTHRENQIPQRLVERVIPWA
LTMCVTTPMQQLQCLPHTGQSAGRRIVAGWVQREEEAFPCKVLCVSAVRHPRRTNGMCVG
WRVAVVVAAIRIVWETPVRRRSSAASSPRVRVASVQLGSQSPDTVERQASGLSCRARIIP
SANATMPVLHVPLSCARSDASSAYASQAYFLVMPQWPKASCNRVCATRCCGREKRVRPQC
ESPGDAEPSTCARVLPRFDEKAHKRTPPWKKSRCRSYSPC*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1 Dispersed gene family protein.1
MCQCAAGGHGDVCVPAPVPAGPPPPPITPPPVLPTPLPPPVGECISDMVYPEVAQAVGGG
LSWLCYRNVTFSGGGMSLTVLVGGMTGDVANVTFDGCTWRDGAVLVLLGNAYAAVGSLNI
LVAGNTFSDALLSPEGVFPPQTNITISGNRFTVTRLVPRSGLKLDCSSCVAMNGLAISNG
SAVVLSGNVFQSVTASSSAIYAFGSALSVSWHSVFAVVGNTFHMGGGDSTLINLEGSSQS

LSLSVLNNSAVVIRGNVVSRPVSYFLLLILALRVESRSAVVFQGNDMQGSSVVFYPSYSS
RIYYNSWLQLSGNLCHASPSEAFAVLSPTVNLRDSTVSLSGNRFMSSRVTPTVLRISTGS
RDNTNGAIVAACNTGSGGEGATYVIPSVYNATFLTCSDPCALAASCFPAYTTTASSDGCA
CTCAEGGHGDACLPVAVPEPPSTDGADLCVRDVRVDVEVDAGLGTSVACYVGVTFAADVV
VDMESMSGSVRNVTLVNCTFVDGASLYVVGWLSDPPAGERADVLISGLESRSGGGVLVAN
RYPPGSRVTVVDSVLIAEKRVAYRDAYGLGDASACLVVHSVNLTGSVLTIARTHVAAVFR
GAVGVLFVGGVALSSRGALYVDGLSVQTALGLCVSVEGGVSASGGSVVAFVDSDFLLCKH
AVSVRGAVSVSGSAVAFVRNEFVSTEDYAVAFYSTVSLAGGSMLLAKSNVHDGVSREMLY
TAGTVTAAGSTLSFVRNRALLPRMLSLSLSLAAGAHLRVACNDAGGRVLSTAEEYAAAGF
GDAGSIDVVGCDDCDRDTHCYAPGTASVSMRNGVCVCLCGSGGHGEACVPVGAPALPPAV
GTAPSVFVREGVTVRSVFVVPAGASEVTLRRVVLDGVSPVLYVPWMARDGVRIVVQNVSL
LNGAVLYVMGGGALHGARAAGSDESGPVELSMCDVEALNGALVLTGTHPAGSVLTVTDSL
LVAARSTPLVYLPGLRSSPYAPVLVLSGLRLVRSVLVVSGVALVTVMTGGRTVVVDGAVL
EVVGGGVALDTVVFGGDVALYASARVVASGGAVLRVSGSQVYAAHGLVFDSGVEANASAV
VVNENAGVLTDGALLELRGSAFFASGSWLSVRGNNISGKILSLPSYPRSADLVQSTLTLY
GNAGSGPVVMDGTVALVGAGRRFVVGCLTLNGQALRPMDYRSAGIIGEFRPVACGVCDAD
VSCFAAATRAMSGSCGCRCAEGGYGRDCLPDLPHVDGCNRTPAMPLLSHTATLTETRSLT
STWTPSQSTEHYSPTQYGPTETLQVTETVALPPTRTPTASVSSTLWWSDVACPTLAVTTT
AAGGSLTQNDIRGGGSAVAIRLMVALPPPFRWARDPRLGTHLSFVSVSTAQPRGFGGPWG
AMLRNATWVRNATNPSTVLELAVPVHRGYFIAADETIVIRCDAAAVSGGCKGVLLGSFTI
SSDTLPAAASALSAITGVVAGAAAVAVVVTGGLGSILEMQALGVFARMPCASAQERASTV
ALPYFLSVFAALDPLWMVVGNALLAAVFGCVHCGVTAAFQRWRGVDAASAWAAMRFPSLT
YVVAHAMHLGIFFGSVLALAMPGARVQHRVIGVVGVLYGAAFPAGVCYLIARHTGASFER
YWQFSRKPLHERLLYPVGYWHPAAQQRMYGGMLTNMRDSHVYWCVFQLSVLCVVCLIAAV
QSPVGGCHVQYFCMAALLLAGAGVVAFMNMMRSAFMTVTRTASFVLLAVLCLVSAANHLA
PSDGGAGAYVAIVLLLTAVPLAVTVYSFVVWYAEDRHWQELREPRRGGLETLLRDDEESD
EETPKPHEMTSSLYATGTTVASSYRPPAPPSQPMAGDTHSNAQSPLDRASSASRMVDYAA
M*
>TCRU_4227 hypothetical protein, conserved
MVDGASATHHDSPVDTCLGWWMRSAVGACPRSRHRVRHRAIAAVRVALLVVLALFAAAAW
MPAVHAVVLRLRGGTVDRAITVGRAMDTVLMDGVYITNGVAVVFDVAAMLPGALRIELRN
CVCDGGAQIYVRGHSGEPASDRSLEVSVSGLSGGYCSLVFVHNLPAHTNVTVRDSTIVTA
GPMRYSQLSGLTDAVASPLVLHATSLLQTQLRVSNTVLRSLQAGGSAVYVGGGVDLLSSA
VVLDGVSLEASGGPTASAMHVASLSCLSLRSHSVFSVTNVSAVSSGGGIVLGERLAVVDS
VLRFVRVEGSVASLLVHCDGGTIGAGGWLELRDVWAVGEASSVASLSGVTLSGGTVSIAR
CAATGATLVSGLAITSGTVTVQCNRAGGRVLQSSGDYRMAGLPSVSVVPCDGCAAALTCF
DALTASFSECVCSCRAGGVGEACLPFDVPVARSGGSGGGAQGCVSGVMLTESVTVGGGRA
TACFDSVVFSGPITVAVDLRLTDAFADALNVTLRHCVLEGGAQLRIGGLSESTARLVPHA
LVNMTNVTSLEGTIVLRGAMPLHSSVLLANSTLRATVGRSQYVPTTPGFEGFRHGPALVL
DGVRLLSTRFVMTRSTLVCGGGSCAAMLVERGLGVNLSSVFFMDNCAVNSQMHVMYALAS
DLRVGGGSVFSIQNSSWSVPSTEYGKAACVFKDVVVDGGSVLQILSSTFRLGFTMLKANT
LTVTGSSWLVHRDNEFHSAYVVYVVMENGVTFCDQSVWSILHNSFAYGLYSFFTYMTTKW
SPPSDSRPIIYGVCNEARGSPVTNYQEDLNIGAPVTVLDCGACTVDAVCFAARTSSISGC
ECVCAAGGYGDTCLPAAVPDCLGPLPPPDARDTEVRCVHGGSIDSVDYPDPGVRGLCLVN
VTFTAAIVLDLSYFDAPQQTLNITLLKCVLMGLSIKGSGARVHVNIVSSMLDSGELEFRG
VFGVSSQILVAGSMLVTTSGHAILFVKFALSANMTLLLLDNYIEGNRYAVYLSGGVVVDG
GGIIVKGNTLSTAEDDEGVESSVCVTSVDVKNGGYFDVENNTMSSVNGVILFGDTTVRSS
GLLRVADCTFVGGTEIFDSALVYLTGSVTLEGGAQWRVEGNNVSAASVLSIPYSWQKLQL
SGSGTTVVLANNRQVERSALFAKLFKSNTIVVLPARFVVGCNLKGNEELLYYYLLPEEVV
LFRCGTCNDDSACYIPGTESVDRGSCSCSCKDGWHGASCLPFEVPDAVVPPEEERAVDGD
TSCVVNETLTNLTLKIWKTHHCYAGVTFSGRRSVLTFFLNSMPLHLPVNITLTGCTFREG
AALQFFGGAEAAESSGVLIRVSRTVLRSSVVAFLLALPQRCDIAVTEVDAVQTFAVELPG
TVNNMWSVLLLDDFVLSASTLLVSNVKAHATKRDALGLYSIGALKLVDGSSLYVRYCSFE
GYTHVFYLHSLSVSDHSVFALLNNTMLFGASLLYQRQGFSVSDHSVLRVVGNSGSVRYAI

YNDELWTVEQSSWLDWRDNKVEVGAMFYDTESAFVSIDGSSAVTLTGCRMGSTGLSVSLL
KRADAGYRFVAGCLMVAGRPT*
>TCRU_4228 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MSRRVFASAVLLLLVTTMCCATCGATPARENDGNSDLKSVEGLQWVDLFVPQTTPVLPEG
GGTPGTKRDAFASPSLVSAGGVIAAFARGKINAQYDNDVLIKPISSDIVAEYIDSSWDWS
TLVEKVSESTWKAHTVLDTTDGTNRVGVVLNPTTTKKGNKVFLLAGSRDILNQSGGSWKR
DSLDLKLVVGDVTKPTASEQSGWIKWGTPTSLSQTTLKTPKAGLNDFASSGGSGVLMEDG
TLVFPVMAESEEIDGFSMIIYSTNNGSTWSLSEGMSPEKCGAPRVTEWEGSLLMIVDCED
GQRVYESRDMGKTWTEAIGTLPGVWVKSRSFLHDLILHVEALITATIEGRKVMLYIQRGY
ALREKNANPLYLWVTDNNRSFYFGPVDVEEAAKWEFASALLYSDGSLHLLQRRGNDKGSV
ISLARLTEELNTIKSVLSTWAQLDASFSASSTPTAGLVGLLSNSANGETWIDDYHSVNAT
VRNAVKVHDGFKFTGFGSGAIWPVNHRESNGPHTFVNYNFTLVATVIVHKVPKISTTLLG
AVLAEPISTLFIGLSYGTDGTWETVFNGETTKSGSAWGPGKEYQVAIMLQDGNKGSVYLD
GVSVGSLATLPTPEVRGAEIADFYFVGGEDEEDKKSSSVTVRNVFLYNRPLGADELRMVK
KIDGSMHGGVSRALLLLLLLGMWGIAALY*
>TCRU_4229 24 kDa calflagin
MGACGSKGSTSDKGLASDKDGKNAKDRKEAWERIRQAIPREKTAEAKQRRIELFKKFDKN
ETGKLCYDEVHSGCLEVLKLDEFTPRVRDITKRAFDKARALGSKLENKGSEDFVEFLEFR
LMLCYIYDFFELTVMFDEIDASGNMLVDEEEFKRAAPKLEAWGAKVEDPAALFKELDKNG
TGSVTFDEFAAWASAVKLDADGDPDNVPESA*
>TCRU_4230 Mucin-like glycoprotein, putative
MTRRLLCALLVLALCCCPSVCAADVNRKAGSSSPTTTTTNKIEPPKEEKEDTSEMQKNAK
NPSSPVLVGAPGKDQSGLPNKESVGKPVTSAGSGNVDGEGQSLAVTGQKINNTSSTSQAE
DNKGTIGLQSDKNISADTQTKSEAPAETTTTTTTTQAPTTTTTSAPEAPSTATTEAPTTT
TTTTRAPSRLREMDGSLSSSAWVCASLLLAASALAYTTVG*
>TCRU_4231 BNR repeat-like domain containing protein, putative
MIAECFEGQSVFESRDMGTTWKKAVSTLSGVWVMSHSGVRWDESLRVGALIAATIEGRKI
MLYTRQGHPFWGTEAKALYLWVTDNSRTFHVGPLFVENAMGETLENALLYSDGALHLSRE
GIVGTRWGISLARLTEELKTINSVLRTWAQLDASFSKSSTPTAGLVGFLSDALSGDGTWI
DDYRCVNASVTKAAKAKDGFKFTGPESGTTWPVNGREDNNQYGFVNHDFTIVATLIVHEV
PKKSTFLLGAGLGDGPGKKVIGLSYGMNKKWETVFNGKKNSTGEHVGAGERIPGGADASG
RQQGLRVHGWCDCGEPRDDTNSWGAGI*
>TCRU_4232 BNR repeat-like domain containing protein, putative
MHVTGGLLLVKGSVSGGNVITWNETHAVTFGNDEYVAKSLTHMVSGGGSGIKTKDGTLMF
PMQAAYEDGKTSLLFMRFDKSEKKWKLSHQTVSDGCRDPTIVEWGGDRFLMMASCEQGYR
DVYGSTESGWSWYPYGETLTRVWGNSHNRKGHGVQNAFIKVTIERKYVMLVTLPVYPKDD
NKQKGRLHLWVTDKARVYDVGPISREDDDAAASSLLMKSGNEKLISLYENKKGDDGSYSL
VAVSLTEKLKRIKSMVKKWKDLDSALQSCHSGSSATVDPRKKVCALVLFPLMGLLASCLV
TSLITNGGTSTSA*
>TCRU_4233 hypothetical protein, conserved
MVILGLQKIAARTETEQTHPSTEEEMDQYIRSRTDWKQRAVVRLAWITASCWSEIAALTP
KNFTLEPDGTFILDWPVVPRTARADPHRAFRFVRIRGQDAFDIIKLCRTLQENEKLTNIT
NAKVERALAP*
>TCRU_4234 hypothetical protein, conserved
MRRVHKYDTTEIATIVVFVGLRAAPQEAGLPSRRCQPRERPCEGGHEVWRAGYAGVGCYR
DQRPEGLRQGPAETHELIAGFPIHLQCASARHQTVDGHLNLRAHLAQTITVCASEVDEDS
GDDVIPYTRGPSVNVQCKEMQ*
>TCRU_4235 Sodium/hydrogen exchanger family, putative
MDEPAKGNDAAEELETLSQNVLFLMMLIFCGGTFFMTNMSKIPLPYTVVLFLYGIFVGFF
AHWITPDVATSLGNIPPELLFYIFLPVLIFEGSYAMNVHALRRVFPQVLILASVGVVVNT
CLLALPVACFFPEWSWYSALLLGSLLSATDPVAVVSLLKGLGVDSRITAMVDGEAIMNDG
TAIIAFKLLLPAARVGCLKDSTWNIILKGVQLAALPIIVGPVFGFIQSYWLRHATGGIVK

TCITVSVTYVCYYVAGNIIGTSGVLTLFFSGTFLSFYCPSLFPGREGNLVYNIWEFLVHL
GNTMLFSLVGLILVADVVPTLNILDLIIIICMYVAVIMARFLMLEILLPILNLFPYRMSQ
REVTLLAHAGLRGGVAVTLALAVLQTGIEAGVNILKVTCGVVLLSLFINATTAEKVVTFL
GHKRKQEHRMIQMEYAMDHLEVVRQKALQKNKNNVSYRSANWAAAEAYVKDHLLNPYKGM
SYLREDEDTVVNRLLMKAFKASLWRQRDENLISETVVLTISRAVARAIDSGELIEVRHLH
RRKPSPHIEMTEELEARLIEENLKPLWVTVSEIFLGKGYLEWAHVRVQQNAFMTLLSFAR
CLDEVNPIKYQYAKNELHGRRIEAWMTSQREEVRRVIRLLYETYPAATMCIATSRAVLRA
VNELRKGVEELHHYHGFGAKPTAALEEMVQHMYEHIPRSWEPPRLDNELVIAALAATPLG
RGLDPEEINTLSAMGSTKNLYEGEEIKLEDKLFHVIVFGSLKPKLNRWTASSEGEYGFGC
VIGLERFVVPPQLRDNQMNRWVVTSTECQVLCIAYRYIEPFLWEKSFASVRAFWRAVAVE
TLLPTLEHMITLPVNLTQSSRDHFTSIMMSGNPLIGPKECNAMDWSLQFQLCFYIRGSDT
TGLFCNGHTAPCYVSAFFARRLKWEDPQVVLYAVPVNVSDSGYVPWSQSANKSPRGSFMP
QRSSAAEADLSSAMMLDYIHHEPSSTYAEAADIFSSILRGIIPGENQPRSFKIDPPVADV
GSFDGVDACILQNPENFVTNVPYLNQLFLRYATVLEGLCIAALRYVRVPTDPLNAKHAQY
ISEQALEFLMVFFNELTILSAALRRLSRRDTTTSSFAHGVKRQEKEEQLQDDELEDIRMI
GKVIMWHRVAEMHGAFQLRTMVLQMKSLANRRFRYLSESLRALAEEQPSLKGADSVEELQ
RILLDLNP*
>TCRU_4236 alkyl-dihydroxyacetone phosphate synthase
MLTDPNKIVSFNRDWMNQVEGECPVVLLPTSTQQVAAILRYCQSEKIGIVPQCGNTGLVY
GSSALHDEVILSLREMNGDPVVSPQTMSTEAEAGVILQQLQEAAKAHDLLVPITMGSKGS
AQIGGAVSTNAGGIHFARYGSMHANVLGLEVVTAQGEVLDMMSTLRKDNAGYDMKHLFIG
SEGTLGVVTRVSLKLYPFPRSTQLALFRLTTFESVLELYRLAQEYLAECLSAFEVVDGES
LSVTPQEELPFTRTSKSDTFRAGQDFTSAYFCVMVETNGSNAEHDMEKLSRFVEAAEYNP
RCVSKGDLGESFEPILSQSLAQTAQLWNLREDTPVRLASAGTIYKFDVSFPLDKFYDIVL
HFRKIIYKNGGFDPDEVLVVGYGHFGDGNIHFNVVDRTRKHSDALDAVLFPAVYEFCAAH
AGSISAEHGVGVQKKAYLGLSRKPEVIALMRTLKRTMDPNGILNPYKVID*
>TCRU_4237 hypothetical protein, conserved
MSPAPSGHQPTIDNSGTVRSNENKTKCPGQRTDSGGASVKYKTSRKPLPTIKVKKRSPWG
MQQLRDSWSADAMTKGERENMSERIHREYRYHPEEFRRHHIKLAAFLAFPAIIVGTFGGY
YHHTGRPLWEGDPQYLLNMIRQMDTSPRSKLCPYILEGKEVLPVHVRAYREKNWEKRLAL
EGVILGRVEKEHQQGVV*
>TCRU_4238 Putative serine esterase (DUF676), putative
MSAGGPGDRRHFVLFQHGVWGTSADFDALIRCVFEENERNCHKTHDEHLREVTLGDFASA
LGPNCKTNEAGGRLFAWRGLTCFAPGSNRWKGTNWRTRTCASRTLKEFLPVFGDWLRTVE
ENEEGGNCPVCFSVVGHSFGGIIVREFLYLLLVAVEGDELDDGPFDEVRCVREKLVQLNV
TFENFITIATPHCGVGQCLLSAMYYGTWFLAVLCAPSLSELLLKDSEAVLSTHLIDRGHL
AALRLFRRRTLFANTQKDMLVGFATSSLLYGGARDDTVRIVGLATEALPCASAFSEENSE
YSAVMHLPRLRERSGSVTPTHTLKDLYHEGVGEERQESESEYAELAAHGSPQSIAEALRQ
ELDWRLVALRYTGRFPVAHVACLGLVPRVASSPAIMRRVAQEIIQLQ*
>TCRU_4239 hypothetical protein, conserved
MLGELPPIVALPSNPADALRPVPVFGHSTGLYETRLARRHHHHHHRDNGVCVGNAGGDAT
AVSPVVHKKVDVSQSHFSNNRGEQKAAPVLPQAAAKGEFNNAQPSVALNGNNMETLTEKD
IDVLLEVLETRYEKYLSAKQQITERYLIRIETDVDRFLTTYHGGGSSSPSRFGGGVASFI
KNTLVSRIPSPQRLRSGGNEGRKAERAGDENYNGGGGTRDDGLPSLQESSYKANAISFNY
LDVRPTNMGSIAANLVVLRHCLAECFSPGSRVKKSLLDPVVRGVWDQSLRPIKNSAMELL
GAAQQNVRPPLDYLFSLGQQGDAALWSQRCARYDRIVKALLDDLKYLHTVEEMDREAIEE
PMRARQAADEGLSDCVPVSGLVLSRLHRLENEHRTAWEFWRNR*
>TCRU_4240 hypothetical protein
MQCLIRGRRRWNLMDIRQRPPTLNRLQGVLRLAQHPGSVAEHRQGRHFDSSAHVGLYSRP
GRVGRLGDPDASWHTRRREKKNTFNVSAFRRYYSDS*
>TCRU_4241 mitochondrial RNA binding protein
MFRRLPLSIEAVGAVRTIVVFSQQHHILESNQKARSSPSNVWIEDWEVENHGLQPEPGAV
PTQLLLDKPLELFNFDQLLSPPEVMEAPRHSSYSSRKMYGEKLQFELNDRAQKHGFQSKW
WLTRAQAIKNSLTFKGGARSSIILTKSSLKLFHSSQLIGGEALMTHPVSGGSRKLYSKKG

EAFQILSDYIRQNKFNSGLYFTNRQLEFFKLAVQPSQTPVSLDVTSGDRYLIYNVEQLED
PELALKTLDRSPVNIPTFLLSGEPIQNESLKKLPKFKSNYWLSGRDAELYQWPIRENEKK
KGVPLKNEGSASLQVELYNVEQLSNPEEAFAKAGLFVQ*
>TCRU_4242 hypothetical protein, conserved
MMRRSRPCGVVFTPAMPHLEGFLSRHVRPDHPLRHHPMWLSESDLSNCPNWKFDATSVQN
SGERRVAKNMPMVVAQVPMSLNLFNMDQLLPESEAHWQLPIATAATSVSSMRPYEGQAQR
QLEHRRMTCGFESNWWGTRNQWRKRGCHLDPKAVPSVLAFHKMTRLVHISMFSGGKELLK
DYFVSGKTGILRQLSVSNDLSQLAVNFCFLVKSHFERHGFESPLYFSRNSLRSARIAIRP
DAEPLDLSPLDEYEYNGPGVMAHTSHDVEVYTQYYHLSQVIFPENYRIPPNVLEAERENP
GVPINGKTGEVLKIPELQYEAILNSPSPELASLIARDHESEPADSFSELESPKTVRGRSL
WYLPHDLLETGGLVDVNSVPVEVMGGQEGQKKLWRLLYNVEQLLLPVEGYKAVGRIGWMA
QSAGKQLSDFSDGNADAVTGVGGEPNFPF*
>TCRU_4243 inositol 1,4,5-trisphosphate receptor
MDRKQRIIKYGSLVHFSCEEGYIAASGLEAEDLFIREKNDTDIDEEPLPLLGFETSVFRI
EAPASSLAAKAQEAVADHFSNNNTLLMEHFSNINTAPELMYGKPFLLLHSVSQMCVAVFP
SKPSKSDPNCVRLVLVKPGEVESDFCEFVVTPRYKIHDDGDPVCRGDEVLLRLAAFPIFV
HVTGRKHPGLNTWGMPSEEDGCDSSINAFEKGLAAGRMVDDLRSEVNGSEERAVGFVVQR
YDIGRDQANYQRALYHIARPYVPSGVPVLFYHRERESFLTTSLTSQPRQQKESEENKKTM
EANVVSGGDNGISGGALLTNKESSFVEGVFVSRSATQLEGSGISTLDTPDANDNTDGDVD
HTGTPFPLLMKDETSTGCVSNEGTALNDVWRSCTALWILENENPTIGGAVRMRSVKYRLR
QACSNMYLAVAGSGVDAFFEGNGESDFSETVDGMGAAALEEGGDAGSNSSRNQLRAASLC
MIPPPRTAKDSQRTLFTLTPMFFTECNFLIENDCLTLQNVLTGMYVCTQEARDRLFLQWQ
PSVSDTITVRSSRQEIVQDVMFLRSHCERLCRYRDAFQALARLKNSRHPSFHRDGGGLEP
YPGKHESSDSCEENLTPTRAAFVQGGALSTDFAVSSLGRQTRTTETPYAAILPVIYASQS
SLEELIRFCSLARVHDALRLDGIPIVRRQRMIFELNIHRLVMDVILTPFSLLQSEETDGM
GDKTMSGMLPWGCSPRLPPLPLMGGFFCMGVALDDAHSEVHLVCRLAFRFLRQMVRKAKM
LKKWLVEFIPYFLELGGYRFRVSDTMTELFSENNSVPRPVVESVADHFIGSLRRGRSAGH
LNLLSSMCTVGFSGIFERQAMVCQKLLVENSELLSRFVLNQNGEWAVVVNEGEAPVECGA
LFELTRPQNSQQQLGSDAKYARFLQSEIQLLGCLCFDGCPSMCCAEVGRVFPPEVLLRAI
QTFVWTGAEVMGSPSPLDLLRGHILRLAVQCYIMPRIDDPAVQLRASTVLFGSSSLRLRE
ETHLPISGKPDDDLISSVKAAALNIIRANPHFVQSDMSRSVLLRVSINAWLRLVKAHQIS
VQEMCDLIPPLLGLLDGTKDIVDDNASRVAAHTLTRLEVSEASVQVMETREMICNTLLQL
LETVSNRVADNIILLLYDAFVKGGSFPRRKMFVLLDFDEEPVLDAKYDLHVWPSEGQALL
CEKGTGLLHRVRGKYQSVDITDEAQEMDSNRIDSKEVVELLGRVCKSIMLRFRVKELVPL
LMDLTRYESQQLTARATELLIRLCVVKRTVAHRVLQVHTLPSSEVVRSFDHLYTVAVNTL
TLERRGCFDEAIAFALSNIEEPEGTHDDSVPSEELEEEYLIEDDGSDDEAGGDDGGAGAD
QAGKEAHGGRHLWGKTAGAVRVLAYHNAVRRRRRSVGLSENSELPLRLIVRMELVCHWGI
HIPLMRMHTSIDPNSRAFFQWMRFFYLFTFVRGNARKLLGSIDLFMRSLTLKKECTVMCL
HIIVAIFASVADPTPYLSNTFLTECVKYLDSEVSTRHADVDFLSRLSNYVFSNPAVGGVP
RRRMMQLLRDYNILRCLPRPGGVQVSPVRCDFIASMVELLCHICNCPTSALAMGQRALPM
QDIFAIILEYGSLYSPLHRKSYHQRDELERKQFQLVGTYLRALVLLYITAEREEGGQGKE
MIKLEWMANREWWAVVEMLTRQLHGITELILTNKGKVVNRGIRVIQRYRHVWLMSLPVAL
LTFFSACFSEAGFYRYQDSVGVTFAVMCSSLMEFSSNLISNSDALELSVQEAVNYRRLLG
LLHMQTANIVGLETLSSQLEIVRDQILHWLLQRERLSKAERQGQGGGWEERARSSDFDEY
SSPHDTLAIGEGVSQRIQDSLGDSFSARLFLSSGVSRCRELEATRSALRTFVKSDVLIPI
EDSLEIGEAANVVNALLCRSSALSGVRGFVWSALDGMRKRYFSPMALVGLLNLFYNALYA
SFYVKESPPLQAAEGAGKNSTEREDTWNLLQLTFTDLGMSNVVASLSVKDDDVITYSSIR
LSVMLLEGGNTRAQYALLKDFGAHQVRFFHNIRELLQKSLQWVRQINLQQQLVILECGGT
PVGSNSTLFTSALFAAVLKSSSYRKKSERNGGKEKHILGWDRVEGCMRLRLLHALFRMLQ
LFCEGHNLGMQNYIRFQHDNMHSVNIVHEVLLLLAELSGMTHGATVDVIRGGFELLTELC
QGPCHENQTALLSYDVCVTMCGLLDVLSKLEIIGTRTAPENNSRNMNTEMGITNTTNTSG
TRLTESFMNGVVSQRGLKLTRKAVDCLRVSLTTFLLSLIEGCRSPETFRRVLAQIPIEII
EHQLSIATPEMCDRILEDETLEDDPTVAALFNWLIFLHIVRPFADGLYLQHIDELLRRTT
RLRERLGRIEIRRDDGLLEKVFFCIPSICRGLSQNIKDDVLWSVNRTSRATKLGDFLHQS

DNLIFEVERAHDFQRWVARWTRFTLTTTDTAVEKENEMDTEGVMEEKKVRFYSLKKCWNR
FMAPFIFSSQLSYYEYASILFAVLINIGLISVEGAKWDWAKVQVSKLAITCLCVLQFVLS
CVTLCMDAVVFFPACLYKEYRRKEHMRLGIAKLNATMREVFDGLTKGEVVYHFLTRFTIQ
FRLFLVVTAALSLLVSRYFAAAHLLFVIYKVPTLCTFINAITQNGKQLLLTAFLGVVVLY
LFAIVGYLLFPRQFDSSDGPENGNCVNLFRCFLFILWQGLRQGGGVGDIMQEESWSSSTL
FPRVSYDLVFFALVNVVFLNIMFGLIIDTFGELRDAKREKELDMKSTCFVCGLEADEFER
AHVGGFRAHVVHEHNMWMYFYFMHYLRRKDPNDFTGQESYVDEKIRRGDLGFFPEEDSLS
LGNGGREEDAAAGAQKDVSGMDEEGCATRPGREKAPAAGSGAANGQEVALTLKELAGVKE
ALSAFVRDVSADAQKVKSLLQQLEIMSRGAHVMSLGGGTANDPGSTSGTRLSRGEGSKSS
LRRSIGEGSKN*
>TCRU_4244 RNA-binding protein RBP10, putative
MDFDVKTPRISSQEAPEQQQHQHQEDPQPLLDQQQQPETQHVKDSSAVNAAPSVKETGNS
LQRRNVYVSGLPETFRAAEFREMCQAFGRVEASKLCIDTKCRPMKGYGFALFFEEEAAVK
CIKHLHGHWLGGRTLQARLADAAATPVPLDPSSAHPPISRARPPSKGHRHLNSSMQLTNG
YADVPLPFTSSISISPSSSQEQTPPLTPPQISLTPTLVSHSDLGGGNSHNGSNNSNASVA
TGAQPIFYHHVPMDQQMGHPMTSFSTQPGYLSVPSTFIPSPMMGMPMYVTVPPSTNMPPG
PQQQFVLPATMMASGGYPQQLYPPVVFSP*
>TCRU_4245 mRNA processing protein, putative
MRALFSSTLACRGGGFSNSIVRRLLLSEASMRSAFRRTCAAEGLGVHEGVAEDVLASAIV
DPGVLSLEDAKAQLRSSPAFRIDAGVVYMATEGDCMRSQVESMLLKVATKIPLSGVSGSQ
LQAILEDEVPHFQPSLVGALSFKDAIQSYPHIFLVESDPTGKWKVKSATSAPPDAPTGKR
GPLGIVDFCRRRALMGHHGAYTPLRLAMQKTGITEKDVLKQLVTNAEVSNVLQVKLSLRL
RPKRLPINAFCFIDGDEIGPNVVESMGKGLTLSSKSTYVVARHPIFPKHSNNDIIVPEDM
PTYAVLESKARELMLRQTVILQDVIYMCSSSQFTLYAEHVAKMNVFPDADVYVCCPSRVK
LVAEKQHVPL*
>TCRU_4246 KREL2
MLRRHCQLFLRRTPLWLADDGSSLFERYTEIENSNERRMSALKACGMFDDEWIATEKVHG
ANFGIYSIEGEKTIRYAKRSGIMPPTEHFFGYHMLVPQLQQYITVTREMLCDKLQKKLHT
VLINGELFGGKYDHPSLQKTRKTVMVAGKPRTISAVQTDSFPQYSPDLHFYAFDIKYKET
NEAEYVTLTFDDATELFKRVPGLLYARAIIRGPMSKVAAFDVEHFVTTIPPLVGMGNYPL
KGNWAEGLVVKHAKRGTPGFDPKGLTILKFKCTAFQEISTDRRQGPRVDEMESVRRDSIS
RSGIQLPALESIIHDPVQLEASKFLLDHICENRLNAVLSKIGTDPFEKQEMTPDDLATLL
AKDALKDFLKEAEPSIVNTPILTRRDMARYVLFESRQLVCSRWKAILQRQTADAVE*
>TCRU_4247 hypothetical protein, conserved
MRVLYGAAYARQRLALARRVQRREVSREVVLARWNARPTDPKDDNATGVVGKGMKFASSI
IGGGGGAWGKPCASVASTIADVSWDLCERLDFYVQYSVPSNWLVAERVGENSIAIQCRPP
LTGCGAEQPTAHGFSLNCFAYKQKVKEPNSEKLLHLFLQRFNASVSNSLEVVSESSGRSG
VAAGADSSARSISESLASRLNCAVAEITFTPAAGEPLAHGLCRAFYNSNHKFHYIAVVAV
PGDEFEVSKDLLTHALLAVVEGRVEAAAKRT*
>TCRU_4248 tRNA (Uracil-5-)-methyltransferase, putative
MGDESSGSKEESSGVPDDRVILHEHSNENLLKFDTHDKYSTISAIKKMIMKSLPPPKTNA
PPQPLFNGLLRMGKNPNTPLLFMAFRTPEDSTAAAELLRGVFFRGRKQWQELPVTQRDLQ
LTHKGSSRKRSRGGEVLGQSKVAQWEGLAMEEQLARKKMHCLRVMEAIAPQGDKYAELFA
GVHVSPELTGYRNHVQLSFGYSETGEPSIGFLKGAMIEGTCAIHSALGKDIVTMNPLARQ
VAEAVMSVCHLFLLPEKGGLMVFDKVKQQGFWRKLQVRHNVLGEVMVDMELDIDSAEASV
VSEVKTHLIKTLFSEGLRAKLRMISGKETASVVSAQYHHGTGISSSSVDEPRHILFGTPT
LTEHLLGLRFELSPTSFFQVNTSGMELLLCETAKVAALGPKTTLLDLCCGTGVIGLTLAK
HVKRVIGIELVESAVSDARQNAKRNDIANVTFCSGRVEHLLPDIINSLPEEDKTDIVAIL
DPPRAGVTPTVLKWIRGTPTIRRVVYISCEQKALERDCPSLTKSTTKAYRGLPFELVASF
AVDLFPHTPHVEMVAVLARLQEESVSGE*
>TCRU_4249 hypothetical protein, conserved
MSAWASGSLAEKLKQQKLAAANGIGTALLPAVPTGSATVSASGQKKNKNAPPPTPPAVQE
VVVPNENRKPIASSDCEKPQLHEAAEPVHLGPISFPHELAKLVSSEFNFVGVVTKAPMAL
GETREPLTPNVPEKKYPPRAFGSRNAYHETPQMGNTGHAHPLQQNHHYYYHHHHEQQQQH

QHQDQAQNQYYFYKYQTPQQQQRSMQQGMTRQAYHSAYSSLPYNMSPHAMPYHPRMYNRY
PGMNMGMVIYGGMQGYGRFSLQGRPAYYPPPQKNVGPYMPPHQQ*
>TCRU_4250 soluble N-ethylmaleimide sensitive factor (NSF) attachment protein, putative
MSAESLYREAESKINKFFFKDPERAMELFESAAARFKTEKDYNRAGEAYMRAGDCAVKCR
DKLSASRAYTNAVNAYKKTDMKMAAKLMEVAVNLQIDNNTLNGAARLEKEFAEALCETGQ
PLDAIPHYEKAIQYFSADDMNSQVKACTSAIARIYGENDIFDKALSLYERLGNMSVDGPL
RYEAKEFFVRAMLCRLAAVTDDNRIEKSAEALEALETYMIRDKYLKNTREAEFLQMCTEA
VEGADLEKFETAISLLDELRMLDEWKTHVLLVVKKNMESIR*
>TCRU_4251 cysteine peptidase, Clan CD, family C50, putative
MRPAAVGEILIQKANCPLSDEAELHAVLTDARAAAAARNVLLSGDAWRTVRLLASAARCT
LQAGRGDFALPLITTAFDLCPEPFRRLASLQNEKKAMEGCALVRPMLTAAKSEGVGQDVP
AVVCTALMVWHGALASTASTSSCPRGFFRFSHVAGEILTELAMDASTLDKLAECWLYNTL
AFADRSKNTKAAAFYLLEELQDEIQTPELRERDEWGLVCSAGRNACVRVGLHGPQVVAKW
DRLCMNLYAEGCALLHASQEEVQRRASGAMSILRKSFATEKTCYLIDFRRPLQMSSQEAT
LLRDAAASTDLCVPREDFTPIRVACFLKQFTGREGCNSSVSFPFASVSSVVSIAQRHRYA
DIAIELIRTGSAPSLGDDSLLLWGTELECLINRAVGSDGAGVECAPRERASTHVHFGVPS
PLLHEIAQEWRATDVLRILASSQTVEDKLPAGLTMIRGDRTIGHQILRDKIVPSFVLDGL
SRLIVCLVDEGDLPLARCFIPLVAGICERMSSQANLLVTLHAIAAFAQGCHYDDTDGYWT
TVTRVLLPVLLPRSSGMSPPYRQTKSVVAGRTFSLRRRVFDAFCGTFHTRENVHSHCQLQ
VLLTSDHEGVQLSRSSGVEGMTVWEKVLPVGRTLLEMVARMREIEAQNRRHLEATLYNKE
VSLLGKEKMEAPSDATEAFSNSEVERQSRKARAEWWEQRQAFDSAIRKVVEKLQSDECFG
CWRVAMCGDLPPSCLLELKRVAAQLIHDIGAPAHHMLDVTLILAGLPFLGTRFCAGGKLL
FSPSHGSAEGKCASCDEVLCNLSGALEIELLKNGIAAPSTGLLSVLRGACLCALATMCKT
ISVACESELGHLDLFSLSRSSLYLVLDNELHALPLEGMDVLLTGNVARVPTSTFISTSKA
ESLDICDGGVYCVIDPAGDMPKTSKRLLPVCQRTGWKTSTQSVPCGKLMHELYSYRAKAY
FYVGHGKGERFLHRGELYERLPDPEEFPAVFLMGCSSAYMEGGASYDSYGMPYAFLHAGC
PLFLGCLWHVTDGEIDRLTKRLLLLLAGEAVNDGDGASLLPPRTVGEALALARRACKLPF
LTGCAAVLYGTNLSLERTFDG*
>TCRU_4252 protein kinase, putative
MERASGFIEFLEKNTLPRRQLLGTQFKVLTTLGRGSFGEVLLVEDRNLIGARAVVKRFRK
REEKEKKGNLAQQQMQAALTEARVMSRFNDDGIVRLLDTWYEDCQGVVCFLMEYCPWGDL
EAYLQQHYPLSEEMLLYLFLQCLLALAHIHTKGVIHRDLKLTNILLGTGSSRIPTLKMAD
FGLSAFFSVNDAVDVSMFVGTPLFMSPETIAEGLCGYGSDVWSLGVVFYRMMTNFQPFVG
DDIAALRVSITNLEPPHPAGKSRVRYSQELGDLVMSMLAKQPFSRPSVRQLISLPLFSDA
LLKCPWRSKPLRGALCLFACHKDYTVSVFAEPRLDAKIVGTFHFGDHVFVSNEVRSKATS
RRRSFSPSVGRRLSLKSPAKTKDCLPDVTTWCRIVGPQQGYCLKYVRGQSVLRHVGDCTP
CGPLFTETAVSDERGSSPEPTYRTVAPSPRSSCSSICEGTRRKTPKNVLSFLLKHRG*
>TCRU_4253 hypothetical protein, conserved
MHVVSDLQRRPNRGRLKSEKRIMFLYDIATVVQIVCFLIYTTNFMIASKRTFVNSVWLRK
PLQLVPALILKTRNCRFDVTKRNLYAFRNVHLVLSINNTDDIFADHAIQMFLAIFFCGFA
LLLGVANRSLVEHNFFSVSWRNFTLRKDILSAFEIVMISLVLRTSLMANVSGGLLKEYLT
HCGLVSDAYLPFCSLVPLFLFASVGYFVYLFGTAVYLCNALPKYGIMSEAEIAEYKVWLW
ERRERVREAKRAAEEAKRANLLLQHVMRSESMPPILRPPLPVPTHHDMSLRHDMEATPPL
ELSASHYTPTVNMPRRRDAASQRQTATGASSKPVHTPMYASYINVQTSHSSRN*
>TCRU_4254 CHORD, putative
MKVYFIYEGKDVNGCVVNDSLTEVFKVKMDIPASWLNGPCEKLRCFITSTYNKKHPDNPL
VAEELSLWCGNVELKPSDVVETRIHEFNDVHIRHLAKSVLHEQKPFSVLCTNFGCGEFFL
QAENHESACHYHAEPPVFHDIEKYWRCCPTQRARDWDDFKAIPPCCVGPHSTEKRPVSFV
SPPPSNTPLSVEQVQALTHRDENTAASRTTGPREFEGAAEAQRQPPQEIVDGKARCRNYG
CQKEFVVSENHPTACRHHTGGPVFWDTYKYWKCCPDKKRYEFDDFVKIPGCTQGPHQL*
>TCRU_4255 40S ribosomal protein S11, putative
MTAPEQYARVHSVDLTLQHEKAYQRQTAVNENSHNPNKKHVNMSGHIRYSKKIGLGFKTP
KSAINGKYIDRKCPFTSDVSIRGRILRGVVHSTKMKRSIVIRRDYLHFIRKYQRYQKRHR

SLTVHCSPCFDPKPGDEVIVGQCRPLSKTIRYNVLEVVSKSAPGKLGRKFSKN*
>TCRU_domain family member 20/GTPase, putative TB.1
MEPLYCCQEEQTSPGPQRLPRVKDLRGSQEEVSYLDKCRRRCMEEGLENNTVRRAVWRHV
VLGLDRPMRVFCVQESRSEGSSQGPSSATSVDTPRLRTTAIEKEECVESGKKTVDLQKSL
DNCDLRVIQVDVQRSLWLLYRDHSKREIMRDVLKNLLQHVLLNNSERHYYQGLHELMGFV
MYVMEGASMNVLAAVCESLLRVQWKSFSDKKLRQSESMLYAVHAVLAEEDVELATTLESC
GVAPESHYIVGWLITWYTHVCEDTKVVARLFDFLIGHADEHTVIFFTAALLLHERERIIG
YVREARAGAEDDDDNLTIMANVYKQLTRLPKEVLTTRNWVAFGEMLRHTVALQGKHLACV
KEAREEFLRGNVKKRGMLADERTRNSALKLLWSFLFREWRKPWKGKHISVPLMGAVLFGV
FAVAVSLTTCDSVQLIMRNYFSFDE*
>TCRU_4257 cell division cycle protein, putative
MRGETGLLVVAAPLTWWPPADELHRHPLDACRTFFSAITNAGVAVGAADRVVALSRVGRS
VMFSGILEGSFVRVYNPFDGVEVTLAVQATLSEQALASGASLQIFAEADRVRVEAAAVET
GVVLRPLAEAGHTLGERHAAAAVLHILHYLQRARKPGVCSVLFTGEHGVGKTYTMRRVAQ
HFPSVVDVQGVQHFLERRDVDIARLLQMSDREALTMIRCMFAVPPVESSNGAHAVLLLLT
FDAVDLLWADANFLVSLVSHQLCAVLEELNEPTLTAQTQFHAVVLATATTTTSLPSALLT
RLSSRVVHVTHPSLQERLSCIEMHSGSSVYSQDVRRKLAELLAGHTAGQLAALQEGDMLP
QMLEREASCGLKQSHVEEHHEVVERLDAYCGLIAMNGVVRDLEEFVVWPLLHLQLLRCCG
VRAPKGVVVCGPSGSGKTALLKALASRLQTEVARGVHVMFVDGLSLIEKEVGRTEKNIAA
LFSNARAMSPTALFLDNIDSLAPPRGRQTSEVSNTADRTLSTLLTEMDGISDSTNNGDVV
FVVASAPCFSALDPAIGRPGRLDLHLEIQLPTAKELRDHVVQRVVACVEDCGGSDAAGDV
GTISTLVEEHVERWMKMRRITVAEANAFVREVVLCMVEESSRNLLDRLREALQRAASS*
>TCRU_4258 Domain of unknown function (DUF4456), putative
MMVLLQRTAAKESRLQTRMAARYQHVLGAFRDGVREFNKQLDEEQMLQLLNLKEFLRRSH
EEWEEKLRAEMQRVECHKIQLAQPTVSDADDVLQPFTDHYHKVEVTIDDSKARLQDERQR
LLHLCVESRNAHQMRVDAIAVSEEALETREKERRERLKKTLVEFVEALTKISYTSIGASH
VMAQRAIHDINEHLCKNQAGRKTLLAQLRCREILRQRRYSRQLADVYGVSLELMMRSSLQ
WAVTLLKTAYFRRPRCRMQALEKISQLVGSIRRDGTQFIGNVATTVQTLRRARDPQPMEC
GQVCGGTLPDGWLRSFDSCLFSPVFPVSPSEVTMEWRVKANVLVRNILVQCATVAEEVRI
EEERLCEEAELILKELHALVQWVCQPEENETEMLERASLHGVDDVYKRFTNANAALHAKF
SGEVDTEVLPLLATIRHESEWFTSAVEVELNGQHGTLEGFLLTGPSNVLLTFEKATNALE
VTVTKAFGFIRSRFIELYEARKDHDDALQRVEAELARKQKELQHSATVEAAERFFVENLA
ILERIAVQQANFHRHTVQSLQRIVQEGQKEMEQHCANLLLLFGLESEEACVRRERELAAA
AAAEAAATKKGRGRGVVVESDSESDEETMPPYPTITAVDGQLYFIIGPLALEDNLPASPE
VASPQSSQQKSRKSGGGDVRRNSLTSGSKKLLSQSKQRGSKKIKDNQSRSESGANSSRRS
PMLSVVLPPAFLQTYEALLKDVLKEDGGTTSLSLSTVEAWREMLRVEVLNWTVHLRHASM
EHLQKQCNAQKSAVDEETNEILRHHRRRPAKMQSEFEGRVREVEAVHLKKENRCARLRES
CLALETAWSSMVAFGDAEALSNQLFEQLQELEKMAPKTNAINALVSQERNFASLVSSSLE
ANTNHHYEILTDFTRQRESLESECRSYLLGCGKIVPDNLDDIHDTSAWDDCNDSSCKEVM
DTLLRLHNAAKAFKEKLNSEREQHVRRLDTMKSNYTAVFEQNAGELKLLARLQEILSRLK
VQVHSLTTLSETSEAEIEEMLKELEEKLSSQSLPYDFSKAVVEMAGREYGVSFSNAEVRS
STATGRASTASSPTVTPTKKVQKMARGTGAGAITLTQDRTREVEAELSGRLADLRIETQR
QIRASDPSKVMRLLDHIREKIYVRGRHLDCLQYGVELFNVPQENYIDPRLGATSDATAEE
AATTAAGTTTPTPSTTSFSSQGRPRSKSKSSAIPSCMMAALYTTTELPEVIPAERQLNEW
LAVTKSQVETLTDHHFSMYPPPLLRRLPGMSGGNLKDVMEMCNRICDQQQRNVSQYMVKA
VQRYREQVQRLSVALQKIPNYLVNSTYTLSSTAMERRVATVFDVFASFYGDSDTLRSMHD
RLAKVTLASNYNRDKLDALCDAENARQTVTHATIEKIWGYALREIEDEATMHAARSLNVS
NNFFALLRGVVLPENLKPADDDGGDGRHRGLRSLLRLKAKENRTKEIQQHSTKRERRLRE
TMNRQFQGSTTSGGKRFDPYSAAEASNVLLPVPALQEVEHGRVPLRAVRPLEMFNAEHPD
AEIAAPNIDIASAFARVSRLSRLYSLAGNRRQKNDASIVSLEEHAPAVAIVAPETPLHME
MAKLTQQSVEHFNNTSSNAVDKASVAFQKWTEKEEEWRENWGKSMKRIMR*
>TCRU_4259 hypothetical protein, conserved
MVSDVSTNWLQLLLKELRRIAAQLQAKPLSVQDQTEYAAAVQFIELRVPVLGNDEWKALV
SSGAVAEVFEFAVGSALEDPLSCIAVQSWAGAMDALLARTKPSVNAAHHIPQLWDAARRL

AKDRSGNNVTLHAALKLLRVFLHRSPVNIDCIPRYHLPHPVKTVSVAPRLAALELVPYII
LQPYKCVQQQQQQQYPQEERTGSPTPLNSLPRRLVLATPWVDYLRKAVGCSIPVVREKAL
ESICVLLKEGVVLDTAQFNVILDMMLRLAESEEISSKIENVLGTVIGFLLNTAQHGSDWT
HFAATNAADAGDMIRRIFHPRAMTHATQRVLSVAIGELLVQTVSSEWMENAVARIFELLQ
PTPHDDRMYMPTIVSRAVLLWASRMGSDMFRGSLVEILVRFLDASCTKSVTHTALLCLTG
VVRMIVATSDFATVLWAQLLQIPVRHPSLMQVTSEAMACLAHQNEVCGRALLRRLYTAIN
EIETDKPLPTSVALHAKALLAMPAEFVQRPCVLETLLALFASFSIGITPPKVEMIFFRRV
EYFNRIALLLLKHQRDQLSPATITNVKMSVRVFLSLLVSNPSGTSLYARAASSACAVLTE
VGASDIELKLVVALLDALEVAGFSSQQSVWSAAYALFTGAPWLVCSDGMGKRGILAKALA
DVSDANRDGVPCAAEEEGEISDMGGTRLVGVAEECLDDYQRLLPNMTQKPQAVATWRAVS
LIVGGCTERAGEECVQRVFVSLREWCAAAEADPVVTAWNVLCCLNGIFARCDSEHEWVKT
SAMEWFMFVEEHWLSSSVWAVRRAAARLLARLAVITGKLDDYTSVVVKNFNDGEDAYRLS
GVLLALGEMHGTGSSVTASMAISFVLRVLRQHGVSGGMAIAAAALVAMIRMTPRHSQLIN
SVLPAALVAQLLLPAMTTIVDPFVFVLLLELFLILLPHEQAMVNKGVNVCVRGVIQILFS
SRALHDEVTSAVLNTVRLAVNDPNHTPTDAMANVSASFLTALNSLALKKEVLGLLEGNGR
FSDSVSRAAAEMLGVCCSVVSTVDFFRAPLLRIAQMLDAAVSTETRNAWINVARIILQNS
DRKHLSVFLEEMELIMRGKPAQLCDEVCTRHEPLMNSNHEEEMGELSSVKKTKMNGKRDD
DEKQVQMVASEVGSKLAVLSLMTEMMRQPDLYVNLEGDALVRHLNLLFWSVSLAEVEPIF
IRPAVNALLIVVEKYGNRVKDISTPFLLSWRVMLVSGMRRVIQSSVFCCEESCLLAESFI
NCNLADDNSVRRVVLALMTLLETLERCDADYEAIVHGGCGRVVLALSACRTRAAAAGWLQ
AEEAALDALASLSGQAAVALISNQLVASMAMVHGFEPTYDMISTTLDECIHADLAAVLSV
LENMCSAVQALGPTVRHAAGCLLCLVICTPGVALRPLRTIVPLLSTKHQELIASTAFGLL
LQEGDEAINDEDATYLLEIAAATTCEKYAAEVEPVLLTLATHHRPCVGSLASLRLAVEAS
CSVACINTVLRSFDVDVLVVGDEPTPATRAYMQHISEEKRREMGLATACGFVLLQLINLA
DEQQQPLFVGSRVMEAALSRLMEALARSADPLALLQRVFPKMHQDVRLCSIIFTACSSAH
QPELRRQWSPCVQHALLCIIHKEMLLQEKHSSLVLERVRLFIRALLILEAESSFYVDATD
TMCSLYPDACAALTQQLMRYHVCELKSVIQSLCSKEAATLRRLVQLQGFGETPHESSLKM
EGGSQHNHTATAVPQRLTINLSSYT*
>TCRU_4260 hypothetical protein, conserved
MLPAATREGPVRWNTLLHDLLHDVGLAPTPAVVTSLNALTSYAASPLTLYSDPVTGSRAV
KLHSSLLLALHMTTSSWPTELVEKLALPSVHIGDRNVSVSGPAMEMFVLFYNAAVTNCNA
GIAFMERVHAHYARSLTPSSCPSASLNGDTRAAFKSFQLGAEIATYGEQALAEESDKLLS
ATDCYLVQTHFDFRTLREMAELCMAVAKYVHAATSGNFSEKHDSLAKLAHKAYTVRLPSA
YTSESLRFLPALLLAAYHRHRAEHYNKAAKVPDMSLVLGHITYARKLVNNVELEFMNSIA
SSSSSNKNMRQSGGWQLLGRLSATILGTRASKNDAEMDDDSSPEQSFRKLAEMLEGSDLL
RVFPLAHILLREIAALYEKYQHENSVVYYMRPAKEKDVIADAPEIEPLDRTATPPNFVPL
AIQLSADVTKFDELPAVEKLREMLLQREAAREMREGVQKQIEEVQELVHKMELALVLPSN
VESDLARLEGLLYKKKGIIMTLDERFEEAYESVSRALGRYDNANEDLSRAKGEYSGKSVS
GVGDSTLLNQRERAWRRKADAVRAAFVKELPFFGDVALRETLLLPGGTGLRLCITQAKLA
VARAKETIAWDATPSDAFAVHLAELKEVRKESVAALEQMVPLCTESRWERVSRALSDAAE
VITAAEEFVETTENEVRMAETLKSRAVPAAQRLPQGACVFSQGLRQQQQMHSTSPSMRAG
RRVKRGLSPELQSDEEEKEEKESGRKLAELPKPPRQRRAEQRRKVSRKTERQTEDEEEDR
SPPLLPRTGKGTARNANATELAGGKEEIRVPEAIASASLLQRLRLRQQELEGEE*
>TCRU_4261 septum formation protein MAF homologue, putative
MVLQHLDLLRRKRIVLASASPRRREIIAGVGLHHIEVCASGFAEDLSKDEFTCGGDYALR
TARRKAEEVVRQLQRQQQQQQELSGRGEKGNASGTPSPFDILIAADTVVTMPAPHGGVVI
IEKPATAEEAAAILRLFSGTQHEVWSGVVLTVRDEESRSSIGGDGGDRLCWREIKVRTTV
KFAPLVEEEIAAYTSERCNWEGKAGGYGIQDTAACLITAIDGDYYNVMGLPLQAVCAELD
RLIHDGIVR*
>TCRU_4262 hypothetical protein, conserved
MGNTCAPQKGPRFKNFVIAVYSDDPHNGPVREALGKLQNYIASNPERIPRVCRKISKLLT
IYLKRQKVHRVMVGVQMLRDLIAQFDDVSGFVPHCISICSMLFSYSTVEYRIGAADVLTI
LCYKLAGRVDGEHSCRLLTDSKGKLLPALETMCLETVSNDDAATLRCRYAAVVALGNVIF
CLHGALANNVNCHIMPFLRNLMNAMRSGEKPEWIEREPFTVLQQHIKSGPFDSVALPAER

KQRDIACISAASWGIGAVVGCVSIAGIHQFLQLVLEFIVSHDGWSLPGFAFITFRSLVRA
LEWRPQQLGFTVCQYLCETVIAPRKKEEEAANVQEGIIRALIVCTNEVRMTGGRPQVLFE
VVRNCMNKGKRTDDFNELLLQLLMTLMYTTHKWRNAPQLHLLLVGLLACAQEAISNNAVW
SLRALAVAAAYVRAVPLVDRGDIDLSGTIEPFLATHNALQAYAAKVLVGLIAGTIPSQDV
DVGSSIPDAETVTAEAPPPLVTNEQDMAVAENWVWSVLASTQPVTPSCVIEVGRVVEAVM
QVRGASSLPFVLSFVSRLQAFVKNEKKTSELHMAWAHLSLAVLANCGAILTLPHLLRYAV
HLFQQRHRGNELARQFELRLTEESVGPLQLARGGNAADELLCAQPANCPPVTVLIAFDTV
AEIIAEDADAEVYTVFRTQRKDELKAVISSACFKMDAADASTPPLTPRARARARRLFSLE
PLGPSRSVSASITVLVVDGGATEATATAGDASVAAASVFKRESLMEKSKNCIADLLARHG
VGATTHLVHASARAATLTTAIEKREMIGKTKKKEEGGNNLSADAAKTSAAYSQNSLGEID
SSWRSHANSNFPSSLSKLDPPVANHAFFAGSDDFYVEERLNFEGTDAVKSRIHVPGAFGT
YSDIHKDAGRTCNGHAVRENILGAASGGNRSVSNYVDLL*
>TCRU_4263 zinc-binding phosphatase, putative
MSKGTSPEHLVGETSFIDICHTAIEGEAAALLYPIDDDRQMLRCALSISNYRVLISPGKK
GSAEDELGFSLPLLSIASWNVQRRALKATTRAVFQWGREQTVADHDTVTRAMDETTPPPL
AQSNFPSAGYTLKISSKHLWEVEVLLQGERVANTVRDLWRYFHTTQLKGMPAFVLYRERY
AALCEDAVCDNDDIHEENHREDKKNNNTSNNDDNNNNDNNRDKNSGELTNGDDGGRCGFE
NHIDMVEFGWNLFDADRELERQLSLYPGTAVPSVSDVSRVGIKRDLRPWFRLTSVKQSKN
SYGKSPTYPFRVVVPNAASDELLEDVMAARSRARFPAISFVHLGSGAVLARSSQPLARSP
ALRQDGELCRMFANSGYHAHNAEPRSEPPAVVSIVPISTRQAPPPSLFDTGSEEPPAQRF
PAATYQETTSTTRSQRTLYVVDCRPSNAAHANLAMGGGYESGATHDFCEVKFHGIENIHS
VSKSFSKLKALIHRFNGKQPKENFLSQLHETGWLYHIQRLLICSSKIADSLDLGDSCLVH
CTDGWDRTPQCTATAMLLLDPFYRTIVGFSVLVEKEFCSFGHKFAERCGHQVQGETSYTS
DAGVSGSDTEAQQSNTKLQPSPIFLQWMDVVFQLVRQFPRHFEFTTRLLEHLSEEVYACL
HGTFLCNGEKERMFEGVRLGTASIWTDVVRAAAKERAGHSSLYFVNENYDSATAWEYISK
QKGSGIQRISPNCSSKRLVLWESFYLRHDGDNYSIDFRDGPQQMTKKVSFHPEWERYFDR
FVRDSCAARRRELPDMRRRLQNLCVGRPAVAVASSSLGKGNSRICSHCHKNLGFFSSRGQ
CVRCGTTLCNNCAVCSDSESKMCLDCYKLCEWNTQ*
>TCRU_4264 hypothetical protein, conserved
MLLAKGNVHDGVSREMLHTAGAVTAAGSTLSFVRNRALLPRMLLLSLSLAAGAHLRVACN
DAGGRVLSTAEEYAAAGFGDAGSIDVAGCDACDRDTYCYAPGTASASMRNGVCVCECGSG
GHGEACVPVEAPVLPPAVGTAPSVFIREGVTVRSVFVVPAGASEVTLRHVVLDGVSPVLY
VPWMAREDGGDACWGALGELT*
>TCRU_4265 hypothetical protein, conserved
MSDATKKDSSESSTTATAALRSDAGTEDTPTIPPVGSEDGAGGDKEGKAREEGAKDVGKE
NRGNATSKEVKKPENHLKSVKSPQSRENEGLQSPSLNGTRGVGTITSTSDSLTVNTNQQD
LSSPLQPPIPNSSPHAIPSSTSAAGPDNEKRHENGNGTKNSQLPVVGEIQEKNGTGVKAV
ASTSGEENSRLSAKRVEEMSDATKKDSSESSTTATAALRSDAGTEDTPTTNHPNQPSTEG
ATPPGTTSDGEAASANKYDTVSQSAGSTTAPTTNAKTNDTAKPGDGDGSTAVSHTTSPLL
LLLLVVACAAAAVVAA*
>TCRU_4266 hypothetical protein, conserved
MADDSENTDVSQGSAKGPPSEPAGRNNGKQESSDQVSQGLQKVGEQLDSKKEAVGNQRKD
PKIETPTADKSMDDKGEAEKEQIRGSAGEESGELLEEREAPLDGQGGEGQARQAGNGSAK
VGGHSSATTPSEGERPGTGESSPPGSLLPPASTQGNGAAIPASLQGAPAATMKTNEKPVE
NPRAEPEKEKLSSEDDVPEQTSQGVNDGVEPNNDSQKKENVSVTLKERNGESDGDSESTQ
TRPLAVGDASNMDAERGTEIGLPKNNPTANNAVTEGAKRGDNKHSTRKETPVKATAITND
TARTGDSDGSTAVPHTTSPLLLLLLVVACAAAAAVVAA*
>TCRU_4267 hypothetical protein, conserved
MEYIIAMIPKLTAVLQVSVVRSVLGSVVAHAAITTQSNLERAIYSGCRDGTASDFTTLRE
CVREFELLCAIQIPFWQRRIEGAISGLSVAQRFPLQPKQIADELILWIRRKEAEVAAEQA
STNQVFAGIEGAGKLVAKGVERGIQVVGQTVKGGANAITGAASAIKGKRET*
>TCRU_4268 myotubularin-associated protein, putative
MSVADRLRAFRYATSAREVPWNHVRSVDVAAHRVQEPDLCLMKNLISLLSDCNLASATSP
TTSSTDAYQLLSAMQLALQFALWSQSILKEQLVEKQSGAAVQQINLQYVEGLEKKLEKSH

QEAIKLREERDNIQIASRSLEHRLTQAEAKIRYLEKDLEFERRRVSETMSLFATRLQKRH
*
>TCRU_4269 ATP-dependent DEAD/H RNA helicase, putative
MKFCGVCRLKYLRASKVAYGGSVASLLNGYLQQGAETHAANLPASQKYFYTPKEQHDLSS
SQKHRMIQLRLGSAQMLTSTVGNIANQNEAHPLYYSQTSPRAAGLCVSLVVALKKLRIHR
LTELQGALIPVLLRGKHIIAHAETGTGKSFGVALACANQIIRQKINYRLHTVIIVPTEEL
ALQYEKWLRHFGGGTSQVVQVAIERVPMETQLARLHNIQPHVLVGTPQRVADILRLSPTI
LGEKLRRKVDCVILDEADIILSAELRFGRQKISGEALVDRLFRSRPEEVPAQLVAASATI
NGRTAQALNTWMRNDKAIRLTTSFVEHTIPQTISFYFFAESMKYSLPYCLELILRLICKQ
ERRARVLLFTTIEAVEGVVKSLGTMQQRCRELHGWLQQDPNRIVAAPLQSLLNSTSGRSR
PIVAGSRDVYVKDDSSLAKLNAGMLLVGVGSHELSRGIHVSGITHVILYGDCPSAASFVH
CAGRTGRMGAEGHVVVLYPPSSGRTVQQVCHAVELPFVPGRMEQVEDLLGNVDFSSAENL
EKLQNANLHAKPDEAGESLAPMIFPNG*
>TCRU_4270 Leucine Rich repeat, putative
MYGRGSELTAYTPRFTEVVHDRIDCFVPPAYTRLPVPLQEARTFYTAPADFGANGFAILP
TERLGVFLDQEEPNTKHALLKELVGQPEHSCSSSSSSLLSVPHIEETIASRLRGLFFDAS
HVKSSELMVELVSHIFLSCTDPKRMSTGCIATVDLSHTVLGTVGLWGPQFHVDTHGNPSW
RHKKDICYFPEKRCGRSKIKWYKLQCMALRSLALAYVAPLLWMPGFGRFQVVELSCHHCC
LGDQDAKALAFILRKRCSSGYVCLLETIDLSFNNITDDGADALKKAIKYNKRIRNLLLAG
NEGIRKTQILVSINKRLKRNKEGRDNWTLLQHLKWLIKGY*
>TCRU_4271 acidocalcisomal pyrophosphatase
MSENKATLIEGMTEKTLHSPNTMAEVASLHVANSYIGTGLDNSVGNVKPLPEACKRNVTE
FDLVAYGKDEFTLSMEKKVMARMFSAFDVTQLGYLEERKIEHMCKYLGRVMNEDDVKQMK
SEINAIDGHITFEKFWGWWCSHPEVPAKKDFFSMVSVDFAVPYHQQQLLTRETGELYTPS
YRVLYYFRDMETGKELQVSPWHDIPLYVRDLVRTKPASLPMNRYNFICEIPKWTRAKFEI
ATGEPFNPIKQDIKNGVPRFYKHGDMMWNYGALPQTWESTDVVFEGGYVGDNDPIDAIEI
GMTQFKVGQVGAVKVLGILGMIDDGQMDWKVICISHNDPICRFLKDIHDVPKFLPGCLDA
IHEWFRVYKICQGGVENKFVFNGEFKDKSFAMKVIDESHYMWGNLRKINKKEEV*
>TCRU_4272 Enriched in surface-labeled proteome protein 7
MCSMRFCLLLFLVTLLLFAGNAIALRVQRPAFLASRKFDAYKLSVGPPNWSGRENKGEVL
LVRGAELCADGAGSNKWKGAVVLALGHECDTVVQALTAQRGGAVGLLVSKSGGYAGSEGE
VRIPVEVLKKEDYDAFAITINQGISIHVSIGNSLNVQRFAD*
>TCRU_4273 Rad51, putative
MQFNDAATTKKRDQDDVTMPGSSVESLTLEEIPVEQAERLRLLLRQQGMMETGLNTHSLL
QRVLLRPECVLAQQMNASLDDVYVLYSHVSAALLRRNNSFLSPTPVAAVLSSHHRHFIST
GQECLDGALRGGLGCGLITEITGATGAGKTAFALNLAMRAASYPKKDDRRSCTLWITTDV
SAFPATVAAAVLKRHFEARSCIDQEDGEGLEDALRNVAVTVHPTLAQLRQYFPVLRSHLA
NRTDVRFVVVDNFSVLVRRSFPGVDEEVTERHEAVAEFMSTLKSIAQEFCVAIAVTTVSG
EELGHSFLHAVNTRLRLTQCLLDCRGAFAFQEESQVRVTHVLELVKSSAAAAWRFECEFE
GMCLKRTRPLGDNEVVLVEDAKLFGADPFGHVTLPTFAFC*
>TCRU_4274 proteasome alpha 7 subunit, putative
MSYDRAITVFSPDGHLFQVEYAQEAVRKGLCAVGVRGKDSIIFAVEKKSVQKLQDSRTIR
KIYKLDEHIYLAFAGLSADARVLVNHAQLECQRFRLNYEDAVDVDLLVRYVAKVQQKSTQ
SSGSRPYGVSTIIGGFNENGQPHLWKTDPSGMSSAWRAVAIGRNDKTVLEFMEKSYQENM
TRDQCVHFAIKALLEAVESGSKNIELVVLENKKALYMGDDELHKFVVEVEKEREEEAARK
RRLAEEE*
>TCRU_4275 serine/threonine protein kinase, putative
MTSHAHRVYNRRGVRAEEEKVREAPTLTAEALLSWYTKAVRDLQRAATRHTRGTTERPPH
PFSLSGLNKWNHCTDEEAECLFSGMSHVELTGFCCRVHCLLSTIAGSICGPSLAFPMQTD
KGEAPESAHSAPWSGMTLHRKDSENMILPRQRTRITTTRERSLSKLDNMMEYEDDADFGT
PTRNNRSFSPLSLDRRIMTTRHASKTHWINGAKILNDYMVLKSIGKGASGKVKLAYSLSR
NETVAIKIIPRPKKKAHFGAGRNASAKGAEALRREIEVMKKMRHQNIVPLYEVIDDPDAE
KLYLVMRYVDNGPLAVVGADGRCPKMMPDELVLYARQILAGLEYIHECGVVHRDIKPENI
IVDRNKHAFLADFGVAAILEEGCEDIFNRFEGTPLFMPPELFVSVSKNDEENDHGDSSPR

GNPFAIDVWSLGVAFYTLLMGRVPFLSVKDIEAVLQSPIVIADEVPQAWRLLLESMLAAD
PRQRPKISDVRIQVEKMPCEKVMRQEEAVSPRLAPCDDDSAFSRAENSNSNACMSSPHIV
PVAQPPWLFLPRMLNRGNRTNTPESTSTLVDTLGFESNTNSALSPMTMDGITRRIKECMS
LNSVTPKVNTATEGSVDLLDSPTAGKATLFMKATQRPLRR*
>TCRU_4276 acyl-CoA binding protein, putative
MPSDSLEEKFQRLAGIVGKKATRPHMSLSKKLELYGLWNQVMHGPNKRPQPSRMNPVAYA
KWKAYKNYEYLSKEEAMKKFNEIAEKAIASSKL*
>TCRU_4277 AP-3 complex subunit mu, putative
MISSVFFLNHHGEVIIEKQFREKLPRTILEDFWSTYMTPLRSVHEAPAVTPYSRFAFVQI
HRNDVVLLAILTNEGFPLLVIEILSLIGWVVQEYLKVFSENTLRENFSVVYQLLEELIDN
GYPLTTEMHVLEELVVPPTLENKFRNVLDAPMKKRRRHLGVRSVPWRDPLTRHTSNEIFF
DVVEKFDCIVDCEGNIVRAVVRGAVHVNCRLTGMPDVVVRMANLDFVDDFAFHRCVRRHR
YETDRTITFIPPDGKFTLLEYLCKPLLGAQAPFYVTPQITFDKSGGRFNCMVGIRGAGSI
GKNRDYGIHKVVIHLPLPPQTESVQVHSSTQGTTNFNKTRGILTWSVGTLFRGTSSLSGE
FTFSTDKGADGVIPCTGDSAIVEFNIPNHLLSSIRMDSVQVLNEIGKPYKGVKYVTHSGR
FVVRTV*
>TCRU_4278 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MLVTLPVYSKEEKNGKGVLHLWLTDNTHIVDIGPVSGEDDVAASSLLYKSGDNNEEKLIA
LYEKKGGEGSSLGMVSVLLTEQLKRVKDVLATWKEVDGRVSKLCPTLLAEKDESTENACS
TTVKITAGLVGFLSGNFSDNTWRDEYFGVNATVTNKDLGVEKTENGITFKGRGAWAEWPV
GSQGENQLYHFANYNFTLLATVSIHGVPESGSHIPLIGAKMNDSEKTVLVGLSYNNKEKK
WILLCDGGENKEHSSHLETENSEHVVILLRNGNQSSAYVGGKRVCGNVQRELKNTDPKEI
SHFYIGGDGGSAEGQEGVSVTVRNVLLYNRPWTEEEVGALNPNKAPITSPVTENAPETVL
QPPAKPQPSEHEPLTTNIGAGGVPSAASTATTPSSDVDPTVATGSGDTMRGDGSPQTPEV
SVSSGEDGETVDGTDEQEEEGTHPLNREVTATALNSSLGNLSQGNNSDAGTMRGSGLLLL
LLGLWRFAAL*
>TCRU_4279 hypothetical protein, conserved
MNRSLPWSVVGSAARGVCDEAVAKAPGPSRVPALLLPACLACRHAWQLRWRPARKAPVKK
TVAPLRHPHGRPSPTIITPGRARRACAIILWTDKRTLPKIGQEDVNPPLAGRQGVAVLTS
GRGSGRGGPVTAVSEGRRHRHRGPLVIRRARAGLSKSGQESHRASARCRHSGRDVRAKTR
NRVLATPTSACHAVCAPSFSSCQPSVITSSLR*
>TCRU_4280 hypothetical protein, conserved
MNEESCAALLMAIDVAPSTRPQYARMLRSMLEMNRTPLDMVILWLKKVAARSETKQACPL
TKDGPIYPQPDRLEVTCCLTTRVDNGEALVRDCGLNSQQFHNGAGRDRNFGLVRGAEDGE
SGSPPRL*
>TCRU_4281 hypothetical protein, conserved
MVLHSADRFRPRCAYQCWQQDYEQVKLAFDNLVECIGVLEGWQDPTDELMDFGRSLLNTF
RMQLTIASDPVIRLSKLRGRLHSAVHQTDTYARAAQPLVDRRETQRTLRCQQCHTYGHEA
STCNVRPRGN*
>TCRU_4282 Sarcalumenin, putative
MSSTEAKTATESVAMEPEGLNELIEVLHTNYLKCVKPVEDMYKYDLFRPSWFEETILNQK
PFVTFFGPWSSGKSTFINHLLQDNYLWTGPQPTTAEFTVVLYGEEVGPVSGHVLASAKNL
PFKGLTEFGESFLGKFQGYRVPHELLKRVTLIDTPGILESVKDIRERQFDYVKVSRWFAE
RSDLIFILFDPSKLDAGIELKMMFKHAFRGMEGKVRIVLNKADSINTQELMRVYGSIFWN
LSNLINCTEPPRVYVGSFWDQPYKKGVFTLLFTEEKTDLLHEIVDVVPQQARDKKVASLI
RRAKEVLVHALIVGGMRSDLPLLFGKEKAKRKAIDNLQKTYEIMAAKYKMNWKDFPPVEE
YRTFLEKFDLEKFPEIEKAEKDGKIGALQKCIETTLPSMLRPVKSTTAADPRDKAQREKL
QQMYLKSIRSQYEGKVGKQGSSDVVQSSHRESAVTSSGEGGNASAAPQQTTGPMTVTNSS
SMPDQAQMFMGMMMQMMQQQQQQQQQQQQQQRQRQQEQLHFVVEPVDEDNVD*
>TCRU_4283 hypothetical protein, conserved
MPNRAWEDPLEACYDTELFDALLGTEESISATIRQEKASSVFSNVFMVGSSLFSRRRAAA
MARSHSTRLRGVFLSWIDYGSIYCPFTREFVSLRSAHWSHLVAAGFGIDSRLRHGRCVVL

VRPEKLERLAYDVQQCQTAPHQPKDKKSSHPLALWSPLLQESLGGLLKTMSVGDTNAVVQ
RVREFLSDANCTWTNRRIPLSFYDLDLDKRRIFRWAPGNEKDPMNSDRGVSTEEVMKFGE
SYLHQCLQWRASVLQKRKKITFLHMETIALTPLAPVTFAISPQKGKAAALIDQHSTVNVA
PFVVPNSRMAYLSLTYNPKMPLLEAAVTTILGARFSEEIFYCPLEHCVDYSTLMDVQAYR
LQWSSFGTVKLEESTPLLHLGMHMDPSKNPPPPTIPLVVISNAHLLSKRAITRLLEQWTR
NGLAWNTESRHLRATGQSKREVLLRTGNLMRTIDAGAPLFGNVYALFIGYSPSCEQTPIF
DEKHVVAEIQGKNARVSVLAPVTGAMFFLEEPLVEALRRVAHRFQESMNATERTIFIEEL
CDAMSRIIVPAVEEVKEHEVTCSDTNHRHGTSGVKLYELEEEDMLFLLKEACEAFLTEPA
GKRDVGLLPYEQLLCRYPRFAAMRVRHNLLCEYPLKIQGTESHSEFLFTGPSKSMEGVCK
ERLFPVKQHSTVVESRRRAVELAGVEHDARKRACVLNRTLRSISHAFTGCSIFPTNSSTS
NHFRMHASDKKHQLIAEQRYDPFFEPPVLLGCWTRTLLFCAPMAADMLPLRCLLYGDLIA
AEEQNKAFVVVDVDVFHVDYVSYPPDRRCRLFGIRLRYNSNLDTDEVCDVREAATRALQD
VLVKSAVEARLFPIWTHDMSSTKRHNPNEKKLSHGYTTEGGRSFLPHFYFEELDECVSAA
IPNLVERRIFALAMAQRGPLLLTIGTPVVALRTFSSHITRGAWCRVVRFVPIKEFLSHGS
LQLPVQVGSSCDCAADLSLARRYFHHQRGSNSVPVLQPILDGAERLTDAMETVVLPAAML
VGGYHSLHYYALPTVQLPLLAPCQYAAASTLFHPLFAHEDSLMEFVSMESRAKAVEMMMS
PLSSLSPQRSGGFLCNDFFEDVEPSTQNTKDEIRQQEEKEGKVRKYRAMQSDVLSALSLF
PSS*
>TCRU_4284 Zinc finger CCCH domain-containing protein 40
MQATTGSVPEHAPPIWGVMKELQEGFNGHQCSLPYLLNIAQNLQRTLEETRHLYNNAIKQ
RDEVRAKLIAVQNSLAAVERVVSQYASVKDPVVASDGFTYENVSIREYLRECASTNTKAY
SQLTKEELLDVVVPNQTLRRLVHMLQSVRTTEVPPITQRRPIPPYTPQQGDANWKSNNMA
NSGSNNGNGLNWADEEANPGSTPIRVAELEATLAKAANAGSLNASQSSNVLPPTVPTNNS
SSNNNNNNTSNNNNSGTPGRRWETRQQQAAGHGSKNSNKKHPCLRVYGHCNFLEDCTFAN
YPYEACLNYIKGKCRFGQHCKELHVTSTHSRYPGQRKGSNNNQQANSGATPAQAEEKETN
VKEKRATKDKDSSKNSSTRGETNSKESVEEQQEAKPTPTMTPKSETDARPAEAPVLVEEK
AS*
>TCRU_4285 intraflagellar transport protein IFT52, putative
MNGAMNSAHPTSNGYAPGFQPKENPPKVLFNVCRKELYHPNKGYKQLARRLKQVGTVDMN
KEDITLDRLLPYDIVVFGSSQEKLTEEDLTVIRDYVEHGGSVIMLFGDGHGGRYSYLNRT
LDEWTGITLNEDCVVRTVMNKYLHPKEVCVAHGVTNRAINKAAGKSVLGAPGHQGDRGGF
MAGGSTFGDRPAPLTLNRTAATGHWGNMMSNAATTAMQQQMAEEAAADGPTSLVFVYPHG
LSFNVNRPAVPILSSGFMAYPLNRPIAAVWECSELVEHNGQKKQGKLLLIGSGLLMEDNW
FGKEENELLTTVLFDYMNHKVKLNQIDADEPDITDYNHVPDTASLSERLRVAVEQQEELP
RDFTKLFQTESFKLDTDIIPEVIEAYNKLNVKQEPLTLIPPEFLTPLPPVKPAVFEPTHR
DPMLPALDLFDLDEEFAPEKVRLSQLTNKCKPEDVQFYILQAAEILGVTKKLRSPRNRDP
RALLDYVFRQVVQYKKVNAGSMHTTSNAGLDSYSMDPNAAAAAAAGSMTRVIRVSTGENG
NRDTTPFDDNVPWTLQLQADFGSGNITGKFILHTSSMHFPAQEASLEGTIKPPGEREYPM
EWGVLVRGANDEQTFFVFLAMLQGNSLRGVCEVASGNGNTRNFLYEIEEL*
>TCRU_4286 intraflagellar transport protein 80
MRLNITTPNERHDDACTCVAVSLMGDVISAGDDFVLRRWSPNGEPLGKVHQFDSCITYIT
WVPLQGGRKGRGAAAGTIEGKDNCLVACADGTFSFLNAASGRVERTVEAHVGSITGLVYS
ADASSIVSSGEDGCVKVWSQAGIPRTTLVSVGKCVYALCWGSETTELGGDCVLYCFGSDV
VIKPLNPTIKRQLKWKAHNGVVLAADWSLMTGFIVTGGEDGTYKVWDPCGRSIYVSAAGG
HPCTAVKFSADGEMFAVGSFMNLRVCDKTGWSHTYERLPEGSALSLQWTADGTQVVAGCG
SGTVCTAQLVDRKLYWGQYCVTLVDGNKLLVQNVLTDTVEELELRDKVIKVELGYGYLVA
CTTTQCACYPIERLSAPVQFDLRDVVITLILGEKQFLLSDCNAGIQVYSYEGRQICLLRL
QASLRPEIMAPDLVALSPDTVAIRNPADPKKIFFFDTNHGKPVDNATITHHLEVLSLELS
QPGSISDRKIAFVDRNRDLYFGSVHQRLGVQKLSTMTSSLAWHDRHEILIAIADGHLTTW
YYPTIVFSDRDLLTTTKTVRDDGVDEFSRNDRIVAFDGTSVGVRRGVDGALLTFNTSPYP
PMVFEHVAQHDWSGAIRLARFLDDKPLWGILTGLALRQGELNVAEVGYGALFELDKVRYI
RHLKSIPTPEGRQAELALFQRRHAEAERILLQAGLTYRCIDMHTRLFNWERALEIATERK
THVDMVLAQRQRYLEAVGKEENIPLFRELAASVEVDWDTVLEKMKQEQLKEAQRPGARPY
Q*

>TCRU_4287 hypothetical protein, conserved
MIGGQHTKERLSERLQDCQNQPKNRGYLPGTKLLTGGYSTRTLQGNWAEERMDAGYYDGE
AVFPTHLARAWTTDYRTMTSNVSGSLTRPVFDQATLMDIVDHKHRSYPAHQPYLDQQRDE
VMQERFKTTTRTSYINPEERKREAQLHIPPVIGRTPTAQARAVILRIQRQLLLSRHGESA
FPGNILRQIRLTLQRNDTAGEGMLTVEEAEKGFEEASLVVSRPECVALVRAFDLKEDGTI
SIAKIMEELRGELRDRRYSLVEKVYEMLKGFSPDGIVRLQRLAELVDVDSMNAVMNGKVT
SSLAHDAFVEQWDLPIDSYISFENFLLYFMDASFEIESDQEFEVFMRNVWHLSGGNGKSM
NTSCRRVRVVHRNGRMSTQEVKNDLCIKDSDPNLQERIIANLASWGIKDVARVEMLPGNL
*
>TCRU_4288 lipoic acid synthetase, mitochondrial precursor, putative
MFHRHLCKLCSKTPSAATLASPLGKLQEERGEGVAKDLKKDKQHRQIFLQKFRERLDSDT
TGKNTLAGFIDLPEGISPTMAAVGPLKRGEEPLPPWLKMKVAKGVSRLPRFNSIRKSMRE
KRLATVCEEAKCPNIGECWGGDEEEGTATATIMVMGSHCTRGCRFCSVLTSRTPPPLDPD
EPQKVANAVAEMGVDYIVMTMVDRDDLNDGGAAHVVRCVNAIKEKNPLLLLEALVGDFHG
DLKLVETVALSPLSVYAHNIECVERITPNVRDRRASYRQSLKVLEHVNSFTKGAMLTKSS
IMLGLGEKEEEVRQTLRDLRTAGVSAVTLGQYLQPARTRLKVSRYAHPKEFQMWEEEAMA
MGFLYCASGPLVRSSYRAGEYYIKSLVKQRGAAATKSNTTTTTTNTASLAAATVTDSATL
QGE*
>TCRU_4289 hypothetical protein, conserved
MEFGLANDPAQATRITHRNVSFPEVAAYRVLRITHWQSTPYMDSDRCLISYSAGMDDGIP
RIANTPPRREKATSAMRKADWPAFTSLCETLLAAASTWLDIRSGILRAAERHIPRGSVTA
QNDLDERNGTSRIRRRSSTQSTHIASPGDSLLRAEFIQKVEEQNQALRRGFTMLLEARVE
KLGASPSPSWRCLRGVAAPHPHPLESVVLRNDPRTASVSCLGNRQTCLFVILCGFHVPHY
LILLLLLHSFGSWWLGNGSAFPAVCT*
>TCRU_4290 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGLSGVAADGAGVVSDGSVDEDLLLQWRALLRRECVEEVSRR
TGGSANASAVEECVHQGMESLRAVVDGRRRWRHQRYAVVVVEGVDDGKRNNGQSNNRPKG
SSPSVQGLQEGSGLPGVEGGSLNPPAREDTLKLSGDAISPEGLKVNAGADPAKITASQRP
KEDSTAAGTRNHPPPGPSPPTSPKEENAVLLTNLKGTKTEIKVEPKDQALPVGEQGLHNQ
EGQSSQGNEHQPTVEPKASDIPTERPLEGGEHDVDSQEEDRKNKVVAGRKQTGDGEHEVS
NENVVRVPVEPKVNLTEIEQEVTRTHTGEHLVEDAEAAEKEKQREQRVDGQNEKNEKGPV
TRTQQREQEENQLPHQQEQQEKQGTLPASPAELETTQRSLSTVQPEGLQEEQQQNHSSYQ
NDFTNDKNIVRTNATANTDATDGSTAVPHTISPLLLLLVVACAAAVVAA*
>TCRU_family, dimerisation domain containing protein, putative Sk.1
MFSSSQMERLELRCTTCVVEGKQQNKMFLDVEVRLGDGAIFRCPSAMLREGSRTVSELLD
KMKEEEEFSTEQVELPLPSVDSTVFETVALYLEHFYGPTDSTHLEEGKKVLNNPQPVRPT
SLSRPVCLQELYHLSEWEHCFVVQRLLMWPQDLWKLCREGQWVDSSAESAGSLQSMGQCD
VQHILSVLEAATMLEMSSLRDLCAAVLANLLMDVDERGILELMGVTEAFGPEEERKLLNE
YPWLKL*
>TCRU_4292 retrotransposon hot spot protein, RHS3, putative
MWRCCGRLQVALLRGRWALTVSPTGVAVRLHGAPTAPPCECHAQSHWDSGTKQPRLSFGA
SDICWPQLGGASGMLHRTGVAMAPRHGSCDVSDAAARNVVGSKQRPQWTMSSYIEDILLE
GSTLSTSIKLKDFLRSKLGDEWVVKRKGDVIMEVFVQKPDAYVKKQQLLELIFNLTEYQV
*
>TCRU_4293 retrotransposon hot spot protein, RHS3, putative
MEFTICTNIVDVLFKGRVCVNEMRLNDFLTREPDGGGIVDTNRDVLLKEFFKDPTRYIRD
QGALKEMQASDHYKRMERAVREEMDLEEDLSRPYKNGMDNLLKWLVAAALFCFSCIGCVG
FILC*
>TCRU_4294 hypothetical protein, conserved
MGGHNPHRTCCESPSILNTKLRDSSALAHRVWAARELGGKQRLTMAERERLSTDYAPAIA
DAQNRSVQPHLQVEEAHNNLSVRESNIARARDHAGQRENALAGRKQQMEAIRTQLQEREA
RVSAREAQQAPWEAATASREEVSTSRRGPTDGPVARQNMAEDGDTKQPH*
>TCRU_4295 RNase H, putative
MQPHDGVPCTAPGHGKAECPSCPAQTKTLLVVTDSHSLLAAVTKGPHSHTDWTEDRIWQR

LLSLTRAGWSVQLHFCYEHRGVHVNEPADQHATQATTTGQHTEHGIAPIRHTDLLTCINT
QLTNKWRSTMHQDTHHYLLGGARPSDLSVKDLITQEALDQQERTNIAREGCGESELWGRL
YWTVRDCTNQRRFRNISPEQSAFMRSNDDPTAPGRKLFPRRQGRPTHRLWRDGPPHAVER
RNARTVTPHWWDTRTTSVTVGAFIRNALHRFPTSTAIAATRSSPHKKSTAQKSPRTKPRR
*
>TCRU_4296 hypothetical protein, conserved
MRAVCQSRLTWECQHRHPLLVSTVPSDDVAPCRGAGLCLRIGTPQQGVAASTTETKVTSF
PEKVPRHARCGEVRRSACRLSDRTARPFRSGHSVDITRGGDVHKNPATEEDGFINIWRLN
IAGLSSVKKSHLLRDWSSVHLTPFFCRK*
>TCRU_4297 hypothetical protein, conserved
MYPKKGRSEIKPYAVAPLCFWKPARKDLEPHPARAGDIFTAWWRRTLIFWNRLCSALNLA
AYAPCLGNRQICLFVILCGFTCHTALYCCCCLLHSFGSWWLGNGSAFPPYELDVTIRDSL
LGSAPGPGDMLSEFLHRLGPVARGTLRTMIHNPFANGSLPGSWKMGDAISIPKPGKDPCC
PESYRPITLLSVLLKLTEGMIHRRLSALLPHHPRQFRICTSAFYVGRGGTCYRHITRGLN
EFGIVEHERPGDDAPTRRPRRHRLWSRLIFRLRSTPLTMGIYSACLTDFRALASNQTLAA
QPPAGPLC*
>TCRU_4298 hypothetical protein, conserved
MAAEGGPVAGGSGRRGNVHSEDNSNQEDEEGGGNTVGEDPNPTSAGALTAPTRQEQSSSD
PLRSGTCNPSGTGSASAARMRASGPESLGGGHAAGTTFPRSDASQQAAGGVHAVGGRTSQ
GSQASEQTVTGQSQVPGTAKEAPQGDEGGEPGAQHEADQTTKMTVVTSCAKTAVEEESRQ
RDRKMHHVSIVAGMLIIIIFPCFYRNV*
>TCRU_4299 RNase H, putative
MQLHDGIPCTAPGHGKAECPSYPAQAKTLLVVTDSQSLLAAVTKGPRSHTDWTEDRLWQR
LLTLTRAGWSVHLLFCYEHCGVHVNEPADQHATQTKATGQYTEHGIAPIRHTDLPSCINT
QLTNKWRSTMHQDTHHYLLGGARPSDLSGKHLITQEFLTVRNWFTSQGQGAGNPSSGVAC
TGL*
>TCRU_4300 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGAADGDVVGPVTSGDPGGGQSPLADGSHGGSGGKKADISHE
SKSEPLVAASGEESPTVRIDPDGVSSLSEEHLRPEKRTSNGKQEESQSPPQDASPTKVNP
AEALDFLPQERLLGTPEKEVITNGGGGGTANGGKEDTDQNAGLSPDSSDSSVPQYHKSIT
YYHQQSHHQR*
>TCRU_4301 BNR repeat-like domain containing protein, putative
MEDGTFVFPLMAKDETEDVCSMIICSTYSGSAWALSEDISPAECLNPRITEWEGSLPMIV
DCENGRRVYESRDMGTAWTEAIGALSAVWVNARSGVPQKENLLVDALTTATIEGRKIMLC
TQRGHASGKERATALCLWVTDSNRTFSVGRVAVDNASKRKTELGDCGM*
>TCRU_4302 Protein of unknown function (DUF3682), putative
MASGVLGENGSHMPDGCNETAITVPLRSVLPITAVEASTGGGSVETRNRSNSSGTSNAGA
NGSVSAGGPGPGGVAGGSAASSGDSSGAVAPPGASAGSSPDGGSGGGVSSGSGGSSGTPT
GDQGTGDVSSAGGGGGGGSGDGSTGGDGTGSVSSAPAAAPAPPPVSPAGPAVALPSDAPP
GVDPPAGSSDGKAGSPGSNLSDTTGDSQTGVQTPAAEANETSPPEAPARTTSGNGHTRQE
EEEEEEEEKQQQSDETQVQQHQRHEHPAESGEESAKDKNALRTNATADTGDSDGSTAVSH
TASPLLPLLVVACAAAAAVVVA*
>TCRU_4303 calmodulin
MADQLSNEQISEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDQDG
SGTIDFPEFLTLMARKMQDSDSEEEIKEAFRVFDKDGNGFISAAELRHVMTNLGEKLTDE
EVDEMIREADVDGDGQINYEEFVKMMMSK*
>TCRU_4304 calmodulin
MADQLSNEQISEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDQDG
SGTIDFPEFLTLMARKMQDSDSEEEIKEAFRVFDKDGNGFISAAELRHVMTNLGEKLTDE
EVDEMIREADVDGDGQINYEEFVKMMMSK*
>TCRU_4305 Phosphatidylinositol-4-phosphate 5-Kinase, putative
MTRDGMLLPLLFGKWEEFFELSSSVYDVASGARSREACLYYDEEARPMSGHAVLLSSHVI
LTESLGGKVLFWVEFASVRGMRCTERLLLPGKSFGCPTSENEPPNFEDESPGTATVAQKI
VSLDIFVEGAAVSLRMKGSEGEQFARAALILWRMNHGEMEAVTAPLYYPGDAVYALAGAP

VRLSATVVQCVTVEKSCPFASGEAVDIVMLNEREICIARRPRTAVTLWRDLNLSGSEEME
LLPVDSLSALVAPWGNTVRLVGRRGDVWLLETSDPAADVTVRYALQRLTELFLLGMLRSQ
RFCAVTAEPCRGLRYFDLTALYHQYCAMDAEGAGYILCSSLEAAMGPLLACDSRLVQAMR
CDDVGDAGADASGKVSLPMYLNHMRVMLQGSVSERAEIAFRSFGGGMCRDATMDPTERNG
EGEGKTQERGLVRLTDFKLIARDILFGLSYKSSIDDESVKDTVDNIVEAVYGNCNKIVET
MSFPDFLQAYTLLMELPGQDKMKGCNMPHVCGTPHPLLGFGSAHWVLLTYVMTGVELSVR
AAAEASECGEKNTFELTKGTPTIAGVSFVSNSSPAGGAPSFFRKHISSFQSDRVAFTDYR
PLLFASVRMRLGIHVDTFLDALGISALRARLLLGHFCAPRFLRSSGRSGALLLRSHDDRF
ILKRVTITESRTLRSLLPVYVDHLDRYPHSLLPRYAGLYALWRGSEKNSFVVTENVFAFA
QFSITEVYDLKGSTTHRTTTAEDRRHGAAGKDNDFLASKKRLRVSSEARKALLAQLEVDT
QLLERANRLDYSLLVGIHSGKGDWASSKEAVELSLRQRRRMADLVATIDAQPERVSTDEF
KENKKSDNVFHAYYGGVSSFDGSEVYYLGIVDCLTTYGLKKVGEHYGKSVLLQDMKEISC
VPPPDYRSRFMNFMRSIIDD*
>TCRU_4306 UDP-glucose/GDP-mannose dehydrogenase family, NAD binding domain/UDP-glucose/GDP-mannose dehydrogenase family, central domain/UDP-glucose/GDP-mannose dehydrogenase family, UDP binding domain containing protein, putative
MPEPRQLKIVCIGAGYVGGPTMAIIAKQCPDFTVYVMDISEERIAAWNAPISSPGENSGL
PIYEPGLAGIVYEVRDKNLFFTCDRNCMKGADVIFVAVNTPTKENGVGEGFAADLTYVEN
CARLIGETVVEGHYVVVEKSTVPVRCSISIRRILSAHRKSDKVSFSIISNPEFLAEGTAV
RDLLEPDRVLIGGDDEASIELISSIYERWVDKSRIICTNLWSSELSKLVANAFLAQRISS
INSITPLCEMTGAEITEVRQAVGGDRRIGDLFLNPSVGFGGSCFQKDILNLVYLCQSLSL
NETAEYWSQVVKMNNYQKERFYHKIVKNSFGTVRTKTMAIMGFAFKKDTGDTRESASIYI
CARLLEEGAMLRIYDPKIKRERVIMELENFFNTEHLLKSCTYDRLKRDAVTHSRESVENM
LKNVVVVDSALEASINASAIVILTEWSEFTTMDYARLYEVMKKPAMVFDGRLVVDEKKLM
SIGFEVYAIGKPQVSSRDSFI*
>TCRU_4307 VRR-NUC domain containing protein, putative
MVEEDTTVARPALWEATPTPMVESFHAAIWYILRYCGNVIDAAELLSWRTMLQIPLRVTA
GMRTSIRMGEELELFLRLALRIPTWMQVRQIEEQYAEQIHVRLALDRLSTVFVEKQNDEE
EISQDDTFLRIMDGKGVAKLLLTNNSEDVKEVLQTARVRELRQLAQLQREDVRRGKQKEE
GEVDTKVCHNDYCDGDTVNIKSAEAGTDDFTTGKSPADVRRSPTGLPSRKEDLIHHILAM
DCSETLFAATWDAVVGPICRVHKRLKESVCRVCELLHVLTCHCGTGGIFSVLGRFHPTRP
LSAALWLLAPRLLLRREVRVVCMPTPPWWQINGVSGEGPFSVLAPLCLFSSSGTLTSYVG
ALRLHQKLIEATVAKGGRGGGLVFAMASHNAVEDALVLLQQQQPLGRKREYPEANNSGGP
SDPVSCGRMCSQEAGAINNEGGILTVEVMLQRGGLLYEHLLPFLPKYAWFACAELLVPLL
QYKKRYDLANQWLQRLLEEPVHIVKSACGAVTFPFYYRPQKRGKWWHRVAQNLALLGNKK
AALEILEKQQRVWRQHSLTTHHRVCVESFKSLPVTLQRRVRLLSAVFPSVKGTSRGAQNS
VALYNAVNEHHRLHSCRRFDRIAIERTLASLHCSLLRWTPLPTSHTCFTNQLLVAKELTI
YATRDAMEPNLWGDPSHSMASCSVEKHALRWFGAGPSQNTGWLGLHCEGRWLACLARLLL
WDAYVFVPTRDGCEGVELETTAAGVPDYIWLSPLQDHPLDLISSTAFCQRRRRIIEERLE
FFEACSRETLIEYVKRRCRLKDTPNSSDSNPVRDGLSGREELQCESVSEVSLLSSEDGEL
VLLGQPNLRQDERQEDLLPSFFFHDNASVSQKVDVEELHLLSLLQAIPQVPLCALLRRIY
LSPPEEGYSICFSGFPDLVLWRETPLSLVETEFKLVEVKSPNDRLSDKQMAAIDALCRCG
FDVTVARVVESDQTAKRKGPSKNHRLVPDRVQDGVLLDAEHVPE*
>TCRU_4308 chromatin binding protein, putative
MRPYFLLDASPSAVSSCERTAAVIGKYIVEGETLLKAVYCSKYYGVALFRSGRLVLLAPD
SPERHGTVIEGGDGHVRDVAAGDTHIVFCKEDGTVYSFGYSNKHGQLGDGTVWRNLPFEQ
ETHATDGSDAGEKRELPRLSSPQMIIGFGGGMDGVEGHVLNGKLLQVPVVAVACGAFHTL
LLTSLRNCVYACGLGVSGQLGGRRRPVLQPTFKSIRLLFGLTIRQIAAAGNHSFVLLQTG
KLFAFGENLCGQLGFGSVKAVHTPRAVAFSGAVPSVEMRRPLDSSVFKSLRAAWGSAESM
YFPLRVERLSPERDPNEPFIVSVWCCPTRTVLLTRTMEWLSCGLAISRGPCDIKAPTMRM
DRYGPLGRWIERKEEATSFRKMQWSESVAAALKGVVPPIPLEESLMDEVLCALHVKCSNN
AVVLLIRSSGESQPSHLFVQGETPGVFLVDEDGRTPLSPAPRADKLLHDHEVDDDAAEFF
LTEAQGIFASEAFMAIM*

>TCRU_4309 retrotransposon hot spot protein, RHS3, putative
MGAKDLLLLILGSRGALASRALEQLGLRVFMYGELVCALVEELKELRPPERNEAQDSVLK
VNHQGHPTRTVGLGKLEGGVTRIPMEYGVLYLPKVENFPLVDGFFFMESPRRTLVGLRMT
TTGDHHTIPSTVRQFNERMESYFNGWEEFSEGLSWDIIYMQHADSTPDDWLAEM*
>TCRU_4310 retrotransposon hot spot protein, RHS3, putative
MIVVSSPEVSNYDEWAKQTKASRIIMNCPDEMDVKAMCAWIKRGLEPDKQAGYWEMVEKH
MEKVGPIPRHIFDEKIYIDRLGAVNGALLAIKDTDVGKNFALGGEEKWYSEDPSHKLVKI
VRVKTVEGAELFLNASICADIGF*
>TCRU_4311 hypothetical protein, conserved
MDGKVCVAVVVYPLLLLLCVDGALVCAEGYTQVTGVMAMMTGRVLLVCALCVLWCGAGGR
CDEEMEAAAGGAGGGIAGKGAVEPAGTSTPAADSSSLTKGLPRVNQSKETPGVKPLEVKE
VNADQQDVVVPGVEDEDGIPSEQLEETVNAGPGKENTKTQLKNVGQEVRQPPEAQFNLPQ
QPQPQTPASEKGEGAGENNAGGAGQPSLGVQDIGNEDSKALGKGDLLKSPSKESENSEQV
QTTAPKTVTPEHKTQNEVLTPEQKTNEGQSTDTSNNLLETQKENKEYLASTEGTAQSTSI
GSQEQEAEPSTSEEPSPFEEQQFTGTNTTEDARTPDAAATEKSQSVNKETAGESDGSTAV
SHTTSPLLLLLFVACAAAAAVVAA*
>TCRU_4312 BNR repeat-like domain containing protein, putative
MPSMSRRVFDPAVLLLLFVMVCCGSGAAPTEASNSGKKIIFQVNESFSDSWNESLVQAFH
SFRAPSLAYVNGVVVATVEAHYTNSTDNKSCVSLAARSMEIDGGEWTNGTAIVFDHYDVK
IDRLLTPTTIVDEIDGATNALVGGYGTSTTPLTEVTDGKYWAPRMANGVVSYGTDDEKKK
EFKWNKVASTSGVPHDLWESERTNPKRFKQFLGGGGAGIRMEDESRYVLPIQALTRDGKN
VSLVILANSTYYSWKFSKHTSDEGCIQPAVLEWKEKNLIMMTSCDDGSRRVYWSSSMGNL
WTEEYDTLSRVWGNSRNRTGHGVQGGFVSATIDGQNVVHFSQPVYSWKGEKKRVE*
>TCRU_4313 CAAX prenyl protease 1, putative
MYLAGRPSFYASALIGTNAVAGWELYLQYRQWRSFFREELPESHAGIVEDEEFQKSQAYG
RDKGAFAICCDVRDLILGNVAILIRLSARTFDWVAKLLPVAAGSFTHCFALTAATDVAST
LMSLPFDYYKTFVIEEKHGFNKTSRKEFFKDAAKGLCLRVFLLHPLTTGLILQVVWRFGD
RFPLYLFLGATGLAMAFTFLYPTLIQPLFNTYTPISEDSALYKKISILAKSHQFPLEKLY
QVDGSRRSSHSNAYVYGFWKSKRIVLYDTLIEQMEGDDDLILSLLCHELGHWKHSHTIIL
LGIGIAQLFCISFGAKAVIFNPEIYEEFGFRQMNPFVGFTLFLSVVAEPLLTLFGYAFSL
LSRQLEFQADKFAVESGYGMSLRKGLLIMQKTNKSEVSPDNLYAAMKYTHPPIAERIAAI
DAEIKKSA*
>TCRU_4314 Transmembrane amino acid transporter protein, putative
MVSLCSKKGPLGAALSLSVATIGAGTLTLPLTFEDCGILPVIAFMVLVGAFTVISIDYLI
LCVDNVQLRSYEEISRQLLGRTFEEVARWMLILYNVGVAAGYIVVIRELFDPLVPIIRGH
FPFLDSSMRIIVIVWAFLMLPLTCIPQITSLHFVSLMAIASTFVVSGLIAYRYFVPFHST
AAQEGHAVKYFSLSRRMVLTLPILMFSFDCQTLVFQIYAGIGEQTPKGMRKVSIISIGIT
GMVYWAVGLFGYLSNTPHVHGNILTNYNPIEDKLFAVGDAMYSFTVIIAYVLVLFPSRDA
VFTLLYGYSSTTCDYFDAAISTKDNLIASFLLSTLSLLLALKASGIVFIIALLGGLCSST
LCFIYPATFRIRLHALGIAPASSWELFIAFVMLGLGFIGGVMGSVVMFTGMS*
>TCRU_4315 Ankyrin repeats (3 copies), putative
MVQGGVVEIPPNFVPLEHVCRALKNADCRTPVIFFYEDGDPFLSLCKIAREMQSAVWHFD
LAVIKSIQNVMDYIDVGTKNGDWVLISHCEEVEQHLFREVALRVFLLKPEPKKYPRREFF
RCLFCVEKAFELEGNAMTPFPPVLLKNSIISRRVDESSSKWCLKLPSDAKYREIEELKRE
RRRAAGRDSDSETDLSEDDRLSGKWFHRSVELNKAADESPVTMAEGEMQAALDEEDVETI
KILIADGKIDVSKVIKFGMTPLQYACSTQKVKAAKCLLECGADPNQPRQSDGRPPIFMAL
EDESLVEALVKHGADLFKTFQGWRLDAHPDTSPPIARMIKKLRQSM*
>TCRU_4316 isopentenyl-diphosphate delta-isomerase (type II)
MTQGSGFNKEDIVRRRKKDHIDICLHKVVEPYKNGPSIWEKYKIPYTALPEISMGKIDTR
CEFMGWTLSFPLIISSMTGGEEHGRIINENLAKACEAEGIPFGLGSMRIVNRYAVAIHTF
DVKKFCPSVPMFANIGLVQLNYGFGVKEVNNLIKCVNADGLFIHLNHTQEACQPEGDTNF
ESLLHKLEELLPHINVPVIVKGVGHGIEKRSVMALQRVGVKYIDVSGCGGTSWAWIEGWR
HPDLPEDQNLGYIFRDVGITTDRSLQECAPLTKASDLRLIAGGGIRTGLDVAKSLMMGAE
CATAALPFLKAALESPERVRGVIQRFKKELIVAMFACGASTIEELRKMSLSVSSSL*

>TCRU_4317 ribosome-interacting GTPase 2, putative
MGLLERRKAIEEEIARTQKNKKTEYHIGRLKGQLARIRTEMLENAARAAGARGGDGFEVR
KSGDVRCALVGFPSVGKSSFLSRVTATVSEAAGYEFTTLTCIPGKLMHKGTEIQILDLPG
IIEGAAEGKGRGRQVIATARTSDMIILMLDAAKAEAQRCKLEAELETVGIRLNQKFPNVT
FKKKPSCSMNAISFTATVKLTQGMSEALAKEILKDYGIHNAEVVIREDITIDQFIDVIEG
NRRYMPCLYVYNKIDTITMEEMDRLSRLPNSVVLSLHWDLNVDEVIEEIWEHLNIIRVYT
KKHGEHPDFTKPFVVKRDADIDHICKRIHKDLSSRFKYALVWGTSTKHQPQRVGIGHRLE
DEDVLQIMLKTSNE*
>TCRU_4318 hypothetical protein, conserved
MSAEESSTVSTASLLADQRNMLEGSTSANAEVIAEVEDAKNDSNRMQRRALREQQRLHRI
QGRLTDISLNDIATLRDGGYDFFIENTIVCIRGSCSQFDARDGRTKLMPPLTHDCCQTFS
TIAAVVLSSLGLAVTMQECSDVSTVNYLLYISAWLHQISAPVWPQRRARPTVGDLNAALR
LREFFPSRVNEGEFEVLFYNQRDRAKELVDQLCSTSRGSRNADGSLSVCGYVIASGDYTV
SIFSLAHDVKGRPNARYSEAWSLYICDSHGTQPWSGGKACLTGITVGVPKAGAEVSNGVV
AKEEGLRYFAMILFALLEDHRRKTTSLQHVPYMTWSPIRRQRATLYTAEELKGIIDDSWI
PSLMKNNVIAREAKKYSFSPLKCFLGLSASKTVVANGVVGSS*
>TCRU_4319 Lsm12 protein, putative
MMPSSLSETQAVGVHVALVLLDGSSVRGTVFTYSPAEELLVLFQGISGNNPNVKIIRTRF
IKEVSVVNDAEAEKLPPQLDLRSRLPSMHAGRERSLFKYANSQLRVAREKRTVLLQTEDK
DTPIAALDTLTKLARIYPDIHWDKEEGVIRFNQEVFVRGTPDWNTPVAVAADGATDNSVS
LVGRIQKTLAKK*
>TCRU_4320 hypothetical protein, conserved
MSLLNTTLQTLVVRLRDMSGNVTQQKLHNRVFDAYEAKSLVFEAISPEQQAVMQQFGTIP
SQHPAGQPVLLDGWADLLTVHREDNLYQLLPRRAKNNASYSTMRAICCSAGSPFTMDHRV
DPIDYKFVFRAADMEVRNKFNATNQDKIPPTIWFDGILSAPNDSGLVSCHNSLSPAHINN
LAGTYQFLKEWSNEPPEGDRHRQLKEMYSSLLSKRTHLFIGSSSVPGREILNYARSKNVF
VYAKRGMHYVFHA*
>TCRU_4321 hypothetical protein, conserved
MSYQSSEAKKEEFRKYLERKQVIDTLTRVLVNLYEEPEKPEDPVDFIKKVLGGASSADYE
ALQQENACLKAEVEALKKRLAEES*
>TCRU_4322 tRNA (guanine-N(7)-)-methyltransferase, putative
MTSAVQPKWTRLPIRTRPHRNPLAENLDAHPDNPLELQARCADFYPAMRNPVVEFVDVGC
AFGGMLFALSQEYPDACMLGLEIRPKVVKFAQEKTLGLREATSDSSHHFCNLWFEQMNVM
KFGSNCFRKGQLRVLFFCYPDPHWKKKNIRRRIISPGLVHEYAYWLKIGGLLFTVSDVEE
LEQWMVSCLDGCPLFRRLSEEELQSDAMTRKVLGYAMNASEDAQRTARKGLQKHYAVYVR
L*
>TCRU_4323 hypothetical protein, conserved
MVDKDAANLMEELHKAKQNLSEVIDECVFVERQRDHIEQELTAEIRERDRIVSDAFTCLV
SLTEYLSLLERRVILPALGTFSAVVSKVQEVNGTRSATIERVEGVFSAHDSTHFRGILAK
MPPIAGSLENEIRQRLLKTAAPFSIEEAYVLLSALLEEKDKLIEKTNEALLHMNNAVLKV
RAPSSVPVSQLDEIRELRQKVTALVQEVKLRDSEKREAARRIAFLQKALDSEQNNVKELY
HLRKTMERQERTIEQLRLSSGSPARPKPDSLAAKNSIGGGGIDEEELIPQIKANEMTIG
ALNKELAILEENYRVLERRSEKEREELQAELASVRSRHQAEQEEYNTVLGRVTMELEQLV
AENAQLKKRLKQMHAKRAL*
>TCRU_4324 GTP-binding protein, putative
MRHGVCCRNVFDPAFMRRVKRTLASYKEAMDHSTRKGISREAFVDIGEKGPAWYLGHMQL
ALRTLTEKVRDADFVLEIRDARLPFSTENPNLRKIISGRPRLIVFNKAEMSNEDCNRNIQ
QYYEKTGNFALFTSAKRSWRDTVEAVQRFVTHILPAQQFKVTAHVGLVVGMPNVGKSTLI
NSLRLAHEYQFHREDFRRPRTPEAVSITPGTTKGVKLVPVCRDPNIVLYDSPGLTLPGCL
SKEASLKLAACGIIPTNDITLPRSIVARYIYDVLTAAGISEHMAECLHLPRAPISFDDCI
AMICERSGTSGQTDLGNIDPVRAQMFLIHDFQMGNMGRITLDRLPNKMRRQMTVSEHHQL
GDGRDKNPESTAENNEFLWTHHVNTSDVVGRYSEDMRDVMEELQGGMSTHNMRFHPRSER
DSTVISRKKGPISRVSLHEECFRQSTRIAPGR*
>TCRU_4325 hypothetical protein

MINLPDMWTPEQRRQHVAEMYRNKGLICPDYFLKNECPRSSSCSYIHIRNGETRKVPLSV
CHFYAKRACLRDKCVFFHGTQAQLDQLHAMGAQTYRPQDYMAFAIPPPELLGTDQNVAPP
VVTMPMPVPAPLVNNTMPISKPATNSPLLLLPIDASAATPFSMYWSSSPCQYRSPLSPAP
IPGLAEPRPPAVSHPYTVFSFFQ*
>TCRU_4326 hypothetical protein, conserved
MSSSETESSWQLRSGDIVLMDRRCMAMRNPIGIAICLLNKTECRFDHVAMIMKLSEEELR
RESQNSILSHTSSISPSGTYVLETNLNGITLRSLEDRVARSSANQISARFLHMGGDRSQL
EARMVDHLRTLFKNPYKTSPFGFLPSFFTTPDKMDRVKAAHKLHLLAREIARIDDLKPDK
CSTEDAAILRRLRKVYVDAAVFLADVYFPHLQRIDGNEVSSLEWNEGHFAVDGSNTEHGL
FCSELIARLWQGSGMLTGFPPASSFRPFDFLDDTRFNFLTTTTLFGEIIPLKGGRGAPVQ
LWRDAEEEPRTVTGCLNFYRHIGGDLSVEGGLKPIYRWLVQSNTNREVNDDLDINLFSTG
LLFALTGLILAPLRMRWIECQLGLLLRRGSMWSLAAGFLVRDILCAMTQTLTACIALRCF
LPSQSMSASTSCLLGPPLFESKLFDTRHPYYYVCAVLLTANAVSHLATTPLLNAVLLHHF
GPVTPRPWPMRSLMRGAISLWPMAILLPYQATWITWYETAGSAFIPTPSSILRRRPDLLD
TDEWRYFRYKAITGSFAATAALDLVLYPLQTFCWRSLLAEVYRPAPSPSYGRRLYAGYGF
RFAGNVMALVTTTLSFSFLGVL*
>TCRU_4327 hypothetical protein, conserved
MPVWRRRKTTAAAVPLGSGSDSESTSDDQHAYSSSVSEFSCSEAPSQCGRQMPPRRPRSV
TSVPTSGAGGPFNLALLPSSRNGTLRSFMLSPCRFARTQSNPLFAGASWEHDSARNASLQ
EIPVSRQLLPRQRQRETMRMLIIGAPQVGKSSLVNSYRAAVTNNTKWPAAPVGICGFCGT
TTVDPFPNHPSEPTWLCIDTPGRFYDAGSQQLLQKLFLGVPWKTRLAGKDALRPEEIERL
PVVSENSAHQCIVVVSAIDLIQDNGWMNVFFWKSRYESAPDAEGVVMNLQGLISSLRSFL
HDASPFVVISKMDLVGGAGNAAARRAISSMLARCIPLNRLYFCASPNDESSYETKHPRTV
DLDTRVSLIRLHEDLSLAFRWRRTIEEDA*
>TCRU_4328 Protein kinase domain/Protein tyrosine kinase/Kinase-like, putative
MMDQTQCVPNDFSRCGPFEEDKGEFASNSFGAGGLILPRPQVPLRVYTPFFATVPFPSVL
NGSHVEYFLVALKQLSHLVHEVAVGLLPGKDDVCDVKRTFLIFHISHFVDVSFADTVFME
SLTPVRPDDTAISEYIGLIQWLGDRFVTRWREATEQKTLCSSMSASNSFRRLWIAVKNTA
DAISSHTVLQGEIFDRICIRLPKRRLLEFYITEGNIPSCFCIGCLVWSSLTAFAFVILVW
MARGSFSQWCSLAITILTVINFSGFLCFLYALVLRQSRLQWFSELLAENHLAGSIASQST
RTSSRVGKDVVFTIRSKEDVAFTLAIKSSVLNRQIILIGIVNTKSLVICSWNRAAHMATG
IAPEQVIGKSLEAVMEAKSIATARRLLMELRDKPRQQQRLLLNNARKNFPVTIKATATIA
NVDGIPIGMFAGTVVDDEQQAMMSYFSRVDTYAALRALRYSGCASSILHTLLLSNEWDAL
KRRTTNAMRSWCLVTLEEFLRPLKEIPESSLKVHVSESTPKQFQCDYNGIKEFLAKLKQW
FFPEEDNRLELMVACVTCGIEGYLALQFDVTVPDDSIVSLRLKDETLELLSLIGCLTLNS
STHFQFFIPIALRPFDMTLDSEGRNGHSGKHPFMCTFLLHEPVVAYRRHFYGICDESRHR
IFPVSSLSSLKNLLSNFLNEVTAVILSAASPDFGSMLSYCREKGQFVLVVREGSERSNDG
TPDPSADGPPSDVVKDGDYILHRPLCEERWGYFLEYLYDTRNPECNVVPHAPMELTVIRQ
IGRGSCSFVDLVQDKLTGGYMACKTVFISHERTLDALREEVDIMRQCSSPFIVKCIVASH
SPCTSEFRMILQFCPDSLERHARRKRIKLSQLPLYAFQLLSAVQHLHENGIAHRDIKPAN
ILMMNEKHLKLADFGSARRKKLKEGSVYGVTAQFMAPERLLFLPEEEEIVWRETPMDGLF
AEDIWSVGLTLLDIIGIYPLVLKNLNNVKDFLGFYMQLRDSGDELPFELPKEDSTDSHER
LCAFYDFIRGMLQLQPKRRPRASELLQHLFLRGAKNECEFNGELVVPGPNLWLDPVSWSS
HHLNDSVFPSQHSFFTASASDEEPEDGFSEEAFRSVVNLDGVCL*
>TCRU_4329 hypothetical protein, conserved
MDHRSALPNESPSDHVRLALQPREVKFCDLAPSLGRRAMDSPPKYEKRGFRPALQKFAHS
HAAKATKTPLTDGMEAESGDEEERRRCRRRGGPLEVGVGHNLKSLKPKTRKSPRACVHAE
PLTEQMQISGNALWGEDCGFSALNSLAVLEKYVKYERRLKEELSRTHAAKMLAFRNVIIV
YLASAKQCGKPILGRRRAGAEVALAQCAVVTQTLIVTIQSYIRAFQSRKHAVVRRHFRRN
GLSPDLWNNSSERALQLKEREPSTGSALSETTSSLQELLDEAEIGRLKQLYFDYYDCDVY
VIPGTRPDSSIPSNALLLDSLSAHDPFLPDTDGGVMRHSLSLSTSSISSVE*
>TCRU_4330 hypothetical protein, conserved
MAGFSALEEQISALNALHIGSAKTLESFADTSKAIADRARRIAADVQPWEVARENIASTI

EEMSRAARCYHPPPALRLVLARKEKNPEVLCKCIDYLVFTDNYIASHPPNPYADQIASSI
ATQLATMVEVAEDNVREAFIKSLQKKELWQSGEGEKRDGVAPPAVPAKASLLIHDVSALR
GVDRIVHRLGENFNRNDAVSLDVKELFAERMLRLVDNLLGSSHREGEMQPHAIMPERHSM
APIRRHYQKGSHHLLGISASARQVVGEAGDCLKHYVLEPLDDSFDVVGMPGELGTLVFDR
IKANCFATVKVEDSVLSDPTLMFVMSRGEGVGGVGETQHYSDFIFIGLDILEELWKWKNL
AENLPGENYSFIDYVDSEVERFLFEVRDLLDGYVACKGALDAKLLKEYTNTLHRTEWAPS
LDCSTHISVTNQVYLHKVLLTNYFGAMKLALHGALLNASSEVEALQEVEDYMMRCVLGTL
RDLEVIAEVALELQSGTMIEGGHRPRHAFSSSLSSVRNEFSKRGHVILPDIFLLNNILFL
LESYRKEECFHLRRIPTDDPEHLKKKRKSEVPSVPIVSNIIAMLEDEKGRFVEDFAASWS
ECFPSVRENPQLASITQESGELRKSQRMAVKRWYKQVADNLTERIYACRAFAVLDISQRN
ILIEASVGAVQDGFTTFETILGGRTWSSRPIKWMVQGVEQWADQLSKAF*
>TCRU_4331 alpha-1,2-mannosyltransferase, putative
MLLAGTIAAVLFLLSLAAAVGMTARRGKRRFVRGTVGFLHPSAAAGGGGERVLWVAMRAI
QLDDMRRGITRRYVLYCSRIGEDGVDDDKRGEKRLLQIVQQQFHILLPMPIEVVFLRPSL
TRLLSGEHYPFLTLLLQAVCGSVVLFYETCIVNSITPIVIESVGIPGIYPLLALLAGTRI
ISYTHYPSITSIMTKRVESGESRYNNRGFLARHHTLRQAKVVYYKLFACFYWWLGQFPVL
TMTNSRWTMRHIEQLWKPVVPALVYPPCAVNQFMPLRKPPEQHVNTIVSVGQFRPEKNHL
LQLRAFAKALPRLPADARLIMVGGARAADDRKRAEDVVEEAKSRGISDRVEVRIGVPFSE
VGELLSTCCMGLHTMEDEHFGIVVVEYMACGCIPLAHNSGGVCLDIITSPDVGFLASSEE
EYASRMVEIFEMKMQRPQMYKSFQEQGLSAIMRFSDESFQENFMTAIRPHLEP*
>TCRU_4332 retrotransposon hot spot protein, RHS3, putative
MVLTSDRGWPYTWKWKENKSTHDCHVNCEVDRVWQIVLGDLTEWSTHHGRTDFEPKQRVL
IGTPGIGKSVAAGSYLLYQLLHCDAEKLQVVAHFMVSGTYLLEETS*
>TCRU_4333 retrotransposon hot spot protein, RHS3, putative
MDHWVLYEPKVQTFPLVDGFYFVDSNPMTLVGLRMTTAGGHHTTASTVRQFTERPAAYFE
GWEELSRDMSWEIIYLQHADERLAEM*
>TCRU_4334 BNR repeat-like domain containing protein, putative
MSRRVFTSAVLFIVAMICCGTCGAVEAVGSKSGEVQLQQWVDIFFPNKTQVLAKNGCASG
VKFAFCSPSLVSAAGVLIAVAEGRVKYNDSYKSGWLDSSDIVAGCINAAGTWPSIVAEIA
KTEWRAQATLGSWCGKDHVSVWYWPTTIAKDNKVFLLVGGYEEKYDDSFEHWAMDDWDIQ
LVVGEVTQATDIQHSKPISWGEPT*
>TCRU_4335 BNR repeat-like domain containing protein, putative
MGKTWTEAIGTLPGVWTKSKPGVSWNRTFCVGALITAIIEGRKVMLYTHKASHPLEASEP
NALYLWVTDNNRTFHVGPLIVEDNVGETLDNTLLYSDGALHLLQAKGDHESTAISLARLT
DELKTIKSVLNTWAQLDASFSESSTPTAGLVGFLSNAASDHK*
>TCRU_4336 BNR repeat-like domain containing protein, putative
MSRRVFTSAVLLLLFVMVCCSGGTSNAVKSNSGNAQLPHAVDLFLPNQTLVVPKDGTSQE
TTREAFASPSLVSAGGVIAAFAEGLMYVEYVVEGGKVIEPISSDVVAEYIDATWDWSTLV
GKVSESKWKAYTVLGPTDGTDNGVGFFYHPTTTTKGNKVFLLAGSLGELKESGGRRTRDN
LGLKLVVGDVREPTSSEPTGSITWGEIKSPLKESNLAAHEGKLTEFVAAGGPGILMENGT
LVFPVMAKSGNGDSYSMIIYSKEDGEKWFLSTGVSPAKCHHPRITEWDAI*
>TCRU_4337 hypothetical protein, conserved
MWSAVGACPRSRHRVRRRAIATVRVALLVLLALVAAAAWMPAVHAVPLRLRGGTVDRAIT
VGRAVDTVLMDGVYVTNGVAVVFDVAAMLPGALRIELRNCVCDGGVQIYVRGYSGEPASD
RSLEVSVSGLSGSYCSLVFVHNLPARTNVTVRDSAIVTPGPMRYSQLSGLTDAVASPLVL
HAISLLQTQLRVSSTVLRSSQAGGSAVYVGGGVDLLSSAVVLDGVSLEASGGPTASAMNV
SSSSRLSLRNHSVFSVTNVSVVSSGGGIVLGERLAVFDSVLRFVGVEGSVASSLVRCDGG
TVGVGGWLELRDVWAVGEASSVASLSGVTLSGGAVSIARCAATGATLVSGLTITSGAVSV
QCNRAGGRVLQSSGDYRMAGLISVSVVPCDGCAAALACFDALTASFSECVCSCRAGGVGD
ACLPFDVPPARAGGGGDTAQDCVSGVTLTESVTVGGGRATACFDSVVFSGPITVAVDLRS
MDAFADALNVTLRHCVLAGGAQLRIGGLSEITAHLVPHALVNMTNVTSMEGTIVLHGTMP
LNSSVLLANSTLRATVGGSQYLPTTPGHEESRYGPALVLDGVRLLSTRFVMTRSTLVCGG
GSGAAILVEHGLGVNLSSVFYMDNCAVNSQTHVMYALASDLRVGGGSVFSIQNNSWSVPS
TEYYKGALVFGDVAVDGGSVLQVVSSEFRLGFAMLMANTLTVTGGSWLVHRDNEFRTAYV

VHVDKYDGVAFRDQSVWSILYNDFGYGSYSSTTAYMTSFWSAQDDTSPTIYGTCNELRGS
PVTDYDEDLYIRTPVTALDCGTCTVGAVCFAARTSSIRGCECVCAAGGYGDTCVPAAVPD
GLGPFPLPDAKDTEVRCVHGGSISSVDYPDPGVRGLCFVNVTFTAAILLDLSYFNAPEQT
LNITLLQCVLMGLSIRGTGARVHVNVTSSMLDSGELEFEGDFGASSQMLVAGSKLVTNLG
YAIHFPRFTLGANSALLLLDNNMEGVSYAVYFPVAVVVDGGGITMKGNTLRSKKKDYGSA
SAVYVHTVDLKNGGYFDVENNTMSAASGIYFYGDTTVSSAGLLRVADCTFTGSTEALNSA
LLYLYGSVALQGGAQWRVEGNNVSAASVLSMPYSWHSIELSGSGTIVSLAHNRQADSSKA
FARIASNSIVTSPARFVVGCNMQGEKEVSYDGVFPEKVVVFGCGTCNDDAACYMPGTESV
DRGLCSCSCKDGWHGASCLPFEVPDTVVPPAPERAVDGDTSCVVNQTLKNLTLNMWKTHH
CYVGVTFSGVGAALTFSLNSMPLHLPINITLTGCTFRDGATLQFVGSTEVAESAGVLIRV
SQTVMRSSVVLFRRALPQHCDIAVTEVDAVQSSDIPLSGTASSRLSVVMLDDVVLTASSL
LVSNVKAHLLDHGGYGLYSTGTLTLVGGSSLYTRYCSFDKYTYMLYM*
>TCRU_4338 hypothetical protein, conserved
MHRQVLADEHTRRGARSGRQRGSSHRHARLAVSAAAHAHAHTVLHARRRRPGRVAVRVPV
AGVAPSNVDAPSVAKTSRCILLRRRQDSATSVVACNPQMRPSRKRQVYRQHPRQQRSVVH
KAQRAPSSGHGASGVEHLPRDAVVHVALHQQHRPAGQAHRRIKRYRVVPRRRKVAPHKRH
SGARHAHSPTHRHRMLAQQEVAVNKRHHGAAAGRDTALHRHAQPQRRLHRQPVHVQRTAR
RQRHAANHQHANSVVEHSRHLRARNRQHAPRQVHVVQHEARGRIAKVVGAAVRNTLLCNQ
HRVHHSDARARRVAVRHHHAAGARLKPADQHIGTLASRRVGQPPDNVQARSAHKRAVHQR
HVAHAP*
>TCRU_4339 hypothetical protein, conserved
MQPRCKPHKVVEAFRFPVAEAPAHLLWQPGELACEPRAERHTAQTVRDDGLLRRTLHCVC
VGPLPPHPHNNPRLVAAVQHRTLTVKTTRHAVSQDCVFVCPQLYCRLRRHSVKTEGLQCR
HAARGIGTEAFMRGRTTAGNDVELQCLTGSVVGEASTFPQNTIKACGAPRSAQIVMQSSG
PSLRQRTQRVSPHVWEPQRVTCPSGIAPSGRSVRYIS*
>TCRU_4340 hypothetical protein, conserved
MHRGRDRTARRLQRHAVKHHSARQQVHTAANVHRRPARLRRPQHGAAHTQLRLQQRRRVQ
HKRRRHRVRQPAQLGVAHRPRRHNRRVTDRHVRVCRQVVHKHERAVAPGQPAHAHLQAPV
TRRLAAVAPHVELRTAVAHAVPQFDAQRAGKHRRNVEHHSHAVRDAHAVHQHRVQGAAHR
DGSLHRTAPQSQRHRMHRGHPRRRRNQRQH*
>TCRU_4341 hypothetical protein, conserved
MQRRHGVLHARDGVGGPQLVLVQLQGRMAWRVVSSLRGARHGCAALAGEICGRRHELRGE
PDADEPRAEHVEDAPLLRGCDIQRRGCCVDIFIQQYAAASPHQHHAHWVHIP*
>TCRU_4342 hypothetical protein, conserved
MTMMMTGRVLLVCALCVLWCAAAAVVSVTDGAVVAGGPVTLGDPGGGGQSPLVNKGDGGS
GGSKSDSSHGSKSEPLVSASGEESPALLLDEDEGRNPAEEHLRPEKEDSKGKQEESQSPP
QGASPADVNPEEALDSLPQERSLDAPEKGVITNGGGGGTANGVKDDTDQNAGLPPNNSDP
TALVEPEVKQVVTPQPITTGPSPAMTVSAEETNPTASTGSQHATESTSTTSPSHSKTAPE
APKKTSGNVEPNQHREETDQPDSMNNATTSHPAETAAPLVSTIGSDGAQKKEDKVDNGAQ
RPNRKEPQDGPEDGNTDDAPTANERAPKKPETATTQKNATSKSEDSDGSTAVFHTTSPLL
LLLVVVACASAVVAA*
>TCRU_4343 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MLVTLPVYPEKAQEENEEKAKGKLHLWLTDNTHIIDIGPVSDDDAAASSLLYKSAEGGTD
KKELIALYEKKKDGEKPSPGMVSVLLTAQLQRVKDVLSKWKKADETVSKLCTSSAVDEST
DNACSATVKVTDGLVGFLSGNFSGNTWMDEYLGVNATVKENDGAEQVDSGMKFTRRGAGA
EWPVGSQGENQLYHFTNYNFTLVATVSIDKVPEEGSIPLMGVKWIDDKNPVLLGLSYNKE
KKWKLLCGKEAPKELSSTSEATTHHMVILLRNGTQGSAYVNGKRVGEDAQCESINTEGKE
ISHFYIGGDGEKKESREEVSVTVTNVLLYNRPLSTAEIGALKPNKASTPSPVDALSKGTA
IKTSPGGQGKEERRQLLGSSGVNGASASTVSSAKNSSGGEESVMQVTSGTSPDGTQTVDG
GSTAVGEPTMETGERNAVQGDGSSQTPVGTPATADTNAPTAEAMAPDGTAVTPEVGGTDG
QKREDIHAQDGEVNAAALSSSLGNVSQGNNSDAGTVCESGLLPLLLLLGLWGFAAL*
>TCRU_4344 hypothetical protein

MVDYFFCFAGFFRADEHAAALMATDESTFVRGPMSVSVGMETVCNLCGGLAADVTPLHVL
SSVDGGEGVTNSRVASTARAVVVKKGNAREMGIAPGVLESDAVANALRRPLVELSGVEEV
AAVEWRKGVSGENRPSVVSLAAPSPSSERRVFTDVYPDRSFIPGSDVRRMVLVGKARVQN
LTSASFERAFDGSARGTRAMEEGVEAPRPLPLLSAVEECVGGGRRAASQSAKQPAAASAP
ADGVPRRGVRFASFALAPTPPPSSEQRRPVRIQRQYDAYQGTVPSWSDPAVLLPRPVLRL
RPERVSPAKMQSSKLPPVRQQQEGSHPYHNNKNVQQHLTPRGAANTLVQRPTGEAAPSVS
HRRLAEVVTRLATSRTSSPQLHAQQSIYSLLPAVRTSPDQRDALYRQRRRRGSVSHARMG
PTAAGPPTHMSFRNAPWGPALVSTWAHPMPRSTNGASQTGRFVGDRNVFYY*
>TCRU_4345 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MVPNASKKRPSFANGPRILVASNASGIMSVTCGGREHVAADNTDEASERNATGHKSLVLE
NGVAVSGFVAEGDAGGLSQRNASGHDNPQLREFTAQYSGSGVSPGDCFALLYDAKLTLLE
LTVEGTVRVCVYWVLLLLLGLCGIATPHGEHLPR*
>TCRU_4346 hypothetical protein
MGILFNPESKQWDIFRPRRSFNGESSGQRVAGISSPYHRFSSSFALMEEELGNNTTIVEP
IDGRDNEAGDDPGLWTTGATTPMDASQLRKDLRQGELPGNPLGVSVFGFYRHVLMNPSPT
LRWQMQLDRASDPHQRWALGVRQAFAQPHRDILSVTENNTHNNHHQKQQQQQLFIGHSLL
GGRSGYGNVRRRRGTPPAPYWLSKKNEACLDLSFELPSSVYPSMMLRELTKSDVNSPETV
DLDGPLLDNRAKSWNDLRADQQATYKKHLAKKRQKIFVSRPRAINVALLHQHIFRSGGMR
RSLLPSMRGYENVSK*
>TCRU_4347 hypothetical protein, conserved
MSTASVREELTGETQRHAGSDLLLRKLPLLAKAYALAQQHPKDPQAECNLLCYGPEVYRI
LSIARRRDDRGFLRPRPCQSLEAEEGDDNDDEKKRESRMDAMVVLPTRIPFLGVIESELC
KSMESVQEARRSKKGSEDDTADARSANGASRRIGGKRRRHGAEVDAQKGNDESDEEENED
AGVKEGDGATRSRIEYDVGGEECVLLRAIREPLAAWGAGDKKNQAGATGASNTRNGHKNS
GFSEGVGGGRMPWEQMLESIMSRYGAADVEKDGEAVQSYLRRVSWIEQQKKLQLGLGAAT
GTRHRSEQPWMSMTDAMRVQKEMQRMRLQRKRFHRPHKPTEG*
>TCRU_4348 retrotransposon hot spot protein, RHS3, putative
MWGKGEPPQSWTYKAVGDTLEKNDGAEQSGEAPPRLMVLVSDKGWPYSWAGTESIRDCYV
NSAVDRVWHIVKGDLTEWSISNGGTEFSPKKRLLIGTPGIGKSMAAGSYLL*
>TCRU_4349 hypothetical protein, conserved
MLAWLTDRRGRTFRTGCYSVWALLPCGAPQGSVLGPWPFEVFLDGPIRSFQQAHLPAAIA
PPIVHLPIIDHTITADIVAYACDVIARSTVPGITHLDEAMQPLFNAISEWTRAKGLPLSD
RTSFMAIRIAGHHKSPVPDFFGINGRRYPCER*
>TCRU_of Trypanosoma cruzi region 5/Dispersed gene family protein.1
Dispersed gene family protein.1
MEYSEVAQAVGGGLSWLCYRNVTFGGGGMILTVLVGAMTGEVANVTFDGCTWRDGAVLLL
LGNAHAAVGSLSIVVTGNTFRDALLSPEGGFPPRTNITISGNRFTVTRLISRSGLDLDSP
SCVAMNELLITKDSAVVLSGNVFQTLRASSRAIYVVRSALSVLWRSVFAVVGNTFHMAGA
NSTLIYLEGSRESTSLDVLNNSAVVIRGNVVSRPVRYFIVFLWASRVESLSAVVFQGNDM
QGSWIAFYPSYTSNIYYNSWLQLSGNLCRVSPSNEFAFFYPTVNLRNSVVSVSGNRFISS
TVPPKVLRIFTWSRDLTNGAIVAACNTVNDMEEAKYVIPFVYNATILTCSDPCALATSCF
PAHTTAATSDGCGCTCAEGGHGDACLPVAVPEPPSTDDADLCVRELSVDEEVSAGFGTSV
VCYVGVTFAADVVVDVESMSGSVRNVTLANCTFVGGASLYVVGWRSDPPAGERADVLISG
LESRSGGGVLVANRFPPGSRVTVVDSVLIAEKRVAYRGAYDLGDASACLVVHSVNLTGSV
LTIARTHVAAVFRDAVGVLVVGGVALSSRGALYVDGLLVQAALGLCVSVEGGVAASGGSV
VAFVDSDFLLCKHAVSVRGAVSVSGSAVALVRSEFLSTEDYAVAFYSTVSLGGGSMLLAK
GNMHDGVSREMFYAAGAVTAVGSTLSFVRNRALLPRMLSLSLSLAAGAHLWVACNDVGGI
VLSTAEEYAAAGFGDAGSIDVAGCDACDRDTHCYAPGTASASMKDGVCVCECGSGGYGEA
CVPVGAFALPPAAGTASSVFFREGVTVRSVFVVPAGASEVTLRHVVLDGVSPVLYVPWMA
RDGVRIVVQNVSLLNGAVLYVMGGGGLRGAVAAGSDEGGPVELSVCEVEALNGALVLTGT
FPAGSVLTVTDSLLVAARSTPLVYLPGSQSSPYAPVLVLSGLRLVRSVLVVSGVALVTVM
TGGRTVVVDGAVLELVGGGVALGAAVFGGEYALYASARVVASGSAVLRVSGSQVYAAHGL
VFESGVEANASAVVVDDNAGVLTDGALLVLRGSASFASGSWLSVRGNSISGRLLSLPSYP

RSAELVRSTLTLYGNAGSGPVVMDGTVALVGAGRNFVVGCLTLNGQALQPMDYRSAGIIG
EFRPVACGVCDADVFCFAAATRAMESVPFLELAVPVHRGYFIAADETIVIRCDAAAVSGG
CKGVLLGSFTISSNTLPAAANALSAITGVVAGAAAVAVVVTGGLGSILELQALGVFARMS
CASAQERASTVALPYFLSVFAARDPLWMVVGNALLAAVFGCVHCGVTAAFQRWRGVDAAS
AWAAMRFPSLTYVVAHAMHLGIFFGSVLSLATPGARVQHYVIGVIGVLYGVVFPAGVCYL
IARHVGASFTRYWQFSRKPLHERLLYPVGYWHPAAQQRMYGGMLTTMRGSRVYWCVFQLS
VLCVVGLIAAVHPPVGGCHAQYFCMAAVLLAGAGVVAFTNMMRSAFLTMMRTASFVLLAA
LCVVSAANHLAPSDGGARAYAAIVLLLTAVLLAVTVYGVVVWYAEDRHWQELREPRRGGL
EALLRDGEDGDEEMQKPHDVTSSSYASGTTAASSYRPPAQPLQPVAGDTRSDALSLLDHA
SSANRMIDHTAM*
>TCRU_4351 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MEHDEEHFNALLYSDGVLHLLQDGTIGRGATISLARLTEEPSTIRLVLSNWAQLDASFSE
SSTPTAGLVGFLSNAASSGDKWMDDDRCVNARVTKAAKVKKGFNFTGPGSGAVWPVNSRE
DRTQKSLVNHDFPLVATVMICQVPSGGSFLQGAGLGNSKSKKFIGLSYSMDKTWKTVFNG
TKTAPGGTWEPGKEYQVALMLQDGHKGSVCVDGRLVGSPETIRTPETRGAEVSYFYIGGD
ERDSGSSATVANVFLYNRPLGADELKLVRKRGDGTMRGDVSWVLLLLGLWGFAAPLMRNR
SEEFLPPL*
>TCRU_4352 RNA-binding protein 42 (RNA-binding motif protein 42)
MLTSQEVACQFIPAFFERLASNPAELAEMYGPNSSLTIVDFVYGTTEVRNEDVPRAVEQW
AQILQGCELCVESYSAVPLYGGVSVYVTMFAESKTTRHYFQFVNILEAYGAGAYGSEAYF
IRHQILIRPGSAETEQPEPEVTPDQEPKLEVSPEAVESSALLTSRSATDEERKEQQQQKK
NTTVVGLQAAAAAAAPDKTAAVEPETAATVQRQQPPVPSKPKTWASLASAQPKGEQRQPL
RVIIPENGVNADATEVHAPAKPTQTEQRHTSSSAGGAGATKPPAKFPRSPAVSIGDRLMF
NIDYEVSDEEIKAAFGPLAANIVSLRNNSANGHVFLDFSDKEKVMDIIKANPPTVGARKT
RVSIYRQRTRQQGENNENRTH*
>TCRU_4353 Nucleoporin
MSAGTLLQQIGSACRDGRLSAAVIAEIKAYLTLSFKQSNVSQATSATATNTAATAPFFGG
AAATSSFGGFSAPTQQQQPFALLGSVGDSPVTQTSSIDFVNEHVGRARVLLSLLLLCGDA
ERLTGVNDTVAIVASTAATNIIQFIKAEISSASLLTSGHSSISSVFSAYGKSNPILLTAQ
CLLLLTRHFQMQESFIKELCGLLELLIEEVRRHIHSAVVSMGTFRQHPSTAGISAVAWLL
TVSLLNSMTAWKHLCNSSGQFKENVLFRSNIATEVEEWLRNLRSKFEHLQMPGSLSFSAS
GYRKAGQTRQPSTHDALGNAGRRQYIQWITIVEGYLSMILLGVGVFLCGKGDERGLDKAV
EAFLGDRCKSSHTLNRGKVMKHFIQLIPMQNLLVIPPENIYIIPYDIIAYMFDEMLLAIK
HVADNDVRSCVRYLESLQAGTDGVQSDEAGAKKSTFSAVAGGGGLQQYSVERAVRDQGEP
FFSEMAHILQALTVCLENLPSDVLTPDMDSDCAVTFFIFKNCVTHMRSVFQTQRPNVMWE
SYTLKILTSFLDILAMIGRNPQYTERVVALFSEMQVDCTELQWSSLIGQAQECAGVSGGV
SSLLSLDVGGSMTALKKPTRSTVLLHRQFTQEYLVEKQQAFVASVFVLLRQMATHPLLRD
EVHHLITLNTALNFLYAPRLSQSVLGKVLFLIGSLITNHEEAARVWTLLEENHLLSPVTE
TGAASSARWKQGNNSDFKRRENGNDDDSIAITVEARSLLGHCQYECHHGTYGITIGFLGL
MTALFKYYAPAMENLPTYTVVIRFIAEEIFRGVLRRFFSSADERYTVAALAAAALNRVLS
LQLAYSGSNSMVPFTVVMACSKAPADVLGEALQIISEASTAPNELLNHQRAAVRQCLILL
KTAITVKEEEGLDSLFTFDARTASNTELAVQLLPLSASVDSLLARKALQLLLLIPQPTLS
QAARHWFIRPDALEAVITPFVTALRLEAVSSPIIHVPPALAVLDHDEVQLMLPHAEVETK
SLILDLLIQNARAPQTSITSWLCGYPLYGSSEELLAGYCLEPVIVGANSREVEVAYPHIA
VKYVKLVYLLRANPSLSTPSLQRLMRRSGNEEMFYFLQTLRPDQCSPLVLNKYAFVMKLL
ALDVFSIGTKKPEELHVSLHSTPNSSLLEVLFLLLHVSPPSMSLKSEEYVSPGVIAGHDQ
SVTVDFAQWPSFCLKSLPLFPTNCVAPGGAEGYIFRANDSTPQYSIPLLYEAFQKESQLN
NKRSLSQKEIRERLSVFVRANECLAAYAGGVQFIDGWCSLAKIAVTVLDKIQQEHIVYLA
QCVLEGVQLTSSLTVAAQEQIVYPLSQTLSTLMAQLKRKATVTHDGPHGFPSKNGAQGTI
LAYGSRFGDETIMDENVSFSRRARPDTTDVLQTSAVSQTAKSSLVENFNRLSRAVKRDLT
GAIIESTQEATEMFDRSLISLENLQLLKSLLVTTVQWGSRVTMARQHFYGAMMAFLGTPG
VSPDDITLQRHYTALFDVLVQDITTSSYGGNKLSALALLGQLLHLSPQLCEMLCISSTSD
GTSPQLMTCIISAFQTIDESISALFAHGGTEAASILWLAQIVFDVLMIISQKHAIRLTQI

NALSYCTAMRAWKMSARVLLGHTTCENDAAAYGLENIDAYREVVKSVLLLATRWFNVVLS
ALDNSEAALLPVAEFVRSNQLLFQSVLSSPYLDFHRRHVDLLTLDLFSEIGGMLYRLSCS
PLVDECRALAHLFALPDLLAVLTKSEFTESPIFITGNTTAPVSVSSQLTVKQTGSLPSPT
QRQQIYVAVQNILQFLLRAENLGALFATWGENGTAVMNAEGAVVEEHPPRLCDEARNRVL
MVTITEQVVVIMEKFHHGEVVQAVDFIPHLVALHSLVLFLHAFLLLDRAAHVKDAKSQWG
SIVHALEEAQRVVNLWRAFHSDYLRGLRVTRVGGDRWSVAAPSVSNQSVFPAISAPPQDD
TSCRTNIYHQHLIDAPMRQSLKQKTDSAMEQSFTNQLSTVTLPAAGSGAMQLGTTVDAAS
LAFDAVTLPPAAGDASIGALTETTRRNEVALIDEVRSVYPGRNDVLIMESLLRQLRVSIS
NALRLASRT*
>TCRU_4354 hypothetical protein, conserved
MNPATQDTIETFRQLQKLSRELQPVKAALETLVKREQANPNPTAAAGSLDKIALRVLNVS
RKYSVFFDRASFLLECELPRLQRMTPLLEIKEEHESILRPNGHKKDDDATNDAFRYVCSP
KVPHILNRENYYIIRGMLRLRMEMVDYLIATERYQLARHVADAYGLPLFWFPTLMSLALP
PLPPIQGGSMSGNKNNSNNSNNSFENQGRKSDSLPTSNFLTADFTVSHPEERGQPSTTVA
PEHIAIQCIEARHSVTEAIAYCEERLLPAVERIDDKRQKKILEMLYDLLVELHATRLLQI
FRDGQTADHVVFQYIATHLLPHATRRPAFVQAIINAVTPQNVSYNSSAITAETSFTSGGD
ERCSASPKARSVLTKKNEESVRLVVCMMSVEGYHKLAVSFHKVAILLGSQLLSVSEALGR
IHGKQKESDEMTNGWKHTLPDLVTRVVATSIFLKDEYFDRMVMERLASASLLNQPIPESH
LNTQSGSVAFDQSMMTLVEETLSSTSILGSKNEEVSTMPLTAAELLEAEDRWSNDVLFIR
RSTRFYCYLTKECLDGGTGGNYPIALPNGTVLSKLAVMQCCMKKTSEGDRSQNIVVCPRT
KEEFSSSSLRRIFVT*
>TCRU_4355 hypothetical protein, conserved
MRRCVSAAATSPTAAIITAWRGSAPATGALATWRSAYFHSSRFLGRKSGGSKKLGAGASI
NTTAGASSSPSSPVTNATTGTSGEFVGAPEGAGGGHDAAGKATAKEHQTTASAVSSPSTG
VSLPTASVDASASINNRNTNDDGRASFPSSATPSGKGSAATMKKPRVPQRRKSMQNSEDC
AAPPEKVNDTMRLSKKEPTHMNRLATDGVVSVEPDEEDVVVERASITKLFMLSDSVASIF
CALPQNQRSIDNYLREVDQAVLPPSASDHRAGGVGTVMHGDDGYTGQSKEAVARSEIAER
VLSEERANHTLCIHVRDMDQLVPPPDLLLNSTADEPTKTATTGGARRRKVLRKEKKSGAV
NKTSLTPIERILALHEWQMKALERARGSQERFKVPDDYHAITRVRFHDPPKADLTVVQGS
GCGKTVADVLATMNRGLNNNDMNADDHREEDIFDGNETLDDESGATLLSKPFALKPLLSV
VASCIPRREPALGSRCGEETFFSSGAPYSSSSFCSSTAVTMARKTKRSKRTDSEAKKTAD
SAKMGVELLGHRVPPMPRFTTRVTVLVEHDELEPVDLLSMAERSTTRKEDVDNKKSASRK
KRVPRIYCHIADGGEY*
>TCRU_4356 hypothetical protein, conserved
MEESTNIPTAPISPLPPEHTAMPTTTGVIDAVSESISRATSRPSLRRQVGVVILPNSYDE
SESTASRVPSASNSAVRGATAAKGGRSSAEVRQSTGKKGTARGKEGTSPVKRPSTRSPVT
TPPVSAAAASPARHASGLNRLASLTRLSSSQKEGDKSASSTGARKGRRSPSKPAGKTRAS
SGSRGRERTLGKDRSGSSARQRRSVDTGKKKFKRNLQALMNTEEKFRAAIEVEYEAGWKE
MMMEIAIDSFEPQRRNILQTQEELCRVRRECDTAMKHAENALKRLIKCNSHFLQKARATG
VDLLREEQILDLDVPRTTPNITNEEEILSCARDPSSYLTESYVPVKRKDAEQEDEIARIG
RFFLELAQQLDGTVSLTEKNFILTVEQTDEVEKHTAMLTSSFSLLIQRVKRLVEQRRQKM
ELMQGVINEQATRMKVADDFLRETTAKHHVEVESAIQVCREFGMELRRRMDALEKDVLDN
LSDLIQRSTEVCIENNAFHDHAQLLLNKESTIQRYMSKMETVIVEQGKLLRDVRLRLLQL
WKERCGEGDEERSTLAHSGLPKIYQTALEACDRDTLLRLLHFVSLNSDDVPALLISALDE
HESFIKGNTEEARAVAERSATEAAVRALLEKLYEEGDIKFNLRPCSASIADAINEMVRRY
NTYMTELDKKERRAARRRDMEKLFSPYPFFDSRTPVPEEYAAEIASRPSVQKKRPAICDG
NANRMQPDITTPNFQGGSIALPGINTKKKEDNSNFAQTLTETCHVLSYLRQSHPSALEPP
GTATVVGFGRWGGKLAQRGADTRAYSAEGGDGGGGDGANASSAQDNAEAIRFAIGSRPHP
PPRVPPRVSIMQHVLEHHCHDVNTLPAPPQSQCKLFPGEDAPFLKQQRFVFEANS*
>TCRU_4357 OsmC-like protein, putative
MRRSFCLLGVWGVLHEELSKIPTILRFYANASVNAATKACQSMKNAYTDESPEMSEKRKR
HREAYEEIMRQQQQQAKDASEDALRGLSFRERLKKRLSAVTEALKEATSTNAGAMALLQH
CAASHAAEVAVEQGIDVKNVTMRLEKNKTGTQVGHETVVVGYIDAPNASEEDVMAFAEKL
QMRCPVANSMRERIEWRSVSSTTLKHDSNNDDKNDSADNIPKGTPGFSRYNSPTAKGSGG

GLQDPDDLHLPRSKPHKEEEREK*
>TCRU_4358 hypothetical protein
MKEKLRKVFCCCDFARSASGAEDKAAFLKKRLQAKCLAFLLKCCTPQETVIPPAEWRRLY
GKWAPIGSEGAEVLCELLLNQRNERGAVDGGRRMLTLDLHGLRIGDDGVQALVPFITCDD
GLVTFTLSGNDITDKGVNILLKALQASPSSVRRLSLIDNPLSADGVLRVINFCATRSLTL
TELSLSRGVGAEGTRHALVHEQLTQKMKDEFIKLLHSSQGNTLVSFHYSGFRGKDFDAAA
FGSILETALCQSKLQHLALSDCYTSFHCDHKKGDLSQSLAEPLCLASAGLCSSKTQLKSL
ELQIPLSEEAVTALAAGISGATFLSKLSLRGCSMSAESLRIIGNALADNNTLLSLDLSHQ
SHEVAHPLCGSHWRSRLSTGRTSSIGLLSRHPLLPVFEALHRNRTLRELIVLGIDIFNSD
VEELCACVERSGNHVICHVRHTGSNSEPLAIKLESLLSQNRSKCRGNLFARTAVVKHSDP
IQLPPSGKDKDARPKTQAQMENKIKECTEPRSKCQTPATPAVLGKVKTPGNGKNNEKNGG
KQDGCVFARVVTTAVSVSSDSIGASFTLATPLPIFYSPCESCPLQCVASL*
>TCRU_4359 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily, putative
MSDDGCSVPSVVEWEKDKKLMMMTACDDGPRRVYESGDKGESWTEALGTLSRVWGSKKRD
KNVKLVRSGFTTATIDGVDSDKRTVMLVTLPVYSKKEKNGNNNGKSVLHLWLTDNTHIVD
IGPVSGDEDAAASSLLYKSGKDGGNNKELIALYEKKGGDGKPSSYGIVSVLLNEQLKRVK
EVLTTWNEVDKRVSKLCPSENAKEDTSPGTACGAVKITEGLVGFLSGNLSDNTWRDEYLG
VNATVKVNDVAEKKENGVTFKGRGAWAEWPVGKQGENQLYHFANYNFTLVATVSTDKVPE
EVTPISLMGVKTNDSAGKTVFLGLSYNNNEKKWMLLCDGRENKGLSNPWQPGKKHQVAIV
LQNGTQGTAYVDGQPVGDAPCELGSTESQEISHFFIGGEERSAGCAGRQEDVSVTVTNVL
LCNRPLSAADIGTLNPNKAPIPPEVPGIVQGA*
>TCRU_4360 hypothetical protein, conserved
MSNDDLFVSRQCWLRYFFGTRTTAAKSTLLTVSASLIFLVVVGRGVAGAISTFVPIADED
PQQAQGVVVQPILLTHVQPQDVDLQKRILALSSATELEELPDGTLRRVPFAVFEARLRQG
LIVGFALVESVSSSRITLPVNAAAVRKYTGLCFILTEERLATQVAPATG*
>TCRU_4361 hypothetical protein, conserved
MHSRNGELVAVCRVAHAVHTCGNCTASCARKEEGATVAFTTNVTTHKYAGPYELLWRQFF
PDETIHPPARSSDADRTGICQLPPPHEGKDDTKSDVTTAPQVNAEPSRQHEDWRRSAATD
GPNTVDLSPASNTATNSSETRPEFASNPNEVMVPNASKKRPSFANGPRKLVASNVFGIMS
VTYGGREDVAADNTDEVSERNATGHKSLVLDDGAAGSEFVA*
>TCRU_4362 hypothetical protein, conserved
MTTCEQYGEAVNGLSPRSPEVHVPANHIKSVYGATHTTPAHRNSFSPMRPLAAEPPGKTA
IDHRSSFNGRPPRVPSASMPTHSLSKNVRNEDNRAVLVSLENFEHVPGVKGVLNSPRSLQ
ACKMEDVLPADLLQRSLTDFMGQGVPEELAQLRYNVFEKRRKDRLERVCRARALLLAEEK
KADELDGGVRDPKTPQENTAKARREAGDANSLPRHSISMSNHHGGNSRSSSLFWRQGRSP
SKTYSSRHRRLLWHKPESRSASMGSMLIYSRAITEHRSPSEKELAMLERIEEREQRLAEA
KQRVELEEKNREQELVQKQLDKMRKIVNNMIQKEITRNAAINSRRMKWEEQMMRIREQKR
RDEEARRSQSVPRGNRASTHQGNGVFRASTSGVYRKEQGDSLRAPKIFS*
>TCRU_4363 hypothetical protein
MRPVWDPSWVQSHALLIPRTAASQVLVVHLLALVLEVSARSLLSLARVVLRLRFVSPSAD
RCEITHCRFARCSGPRCKLTNPQQQVAAESTYSTAANLRRSLLSIGPSDFTAGMLRERES
HARRTTCRLLPSVASSLVRSVRQFHQTWTVAMVALRIPDAVCFAVLSMLASLRGILRS*
>TCRU_4364 hypothetical protein, conserved
MQGPSQVNSTSKKVVRLTRVRRSVDMGDSSNISASTGNSSLHDQPVEMPCASNVNPPMDG
TAASALSTPDVTQVVNSLEEGNALVKRLRQLENENASLATALTKVCDDNANLAKHVVKQE
AKCVALSTSPISATSVLRSLFEPEKVGWFGGSKTAARENLEKMMEELQNEFLEYQASHAS
SNDEVQALIGELQSAHMNAQQLSIILHEQQEVISRGPLSVAVRIFPLETAAERVSLVDLR
HELERRSKRENEFRQELSRAREELQVKMLENARLQRDLQALRLEGNHSNEVERQYMTDEI
SRLKTEVTQLRKTLATEEQLHRLKVGENAALSQRLSETESRLHASNAEMRVQPSEAPCDR
CGELQRECDVANERLQTVTREMQQLGMRLSELKQVNEQEVNELQREKSELEQKLNHSVAR
DTLVAAESQNKHLLQELEFTSARVKELEKLIEREREKTTSDAVKSSDEGRGTLKDSEILE
ALERNRERIARVEFQRDQVIEEAKQLRAVAVTKEEELVRLTRASQEDKQRINFLLKRCVT
LTGDLNNSIAAKDALNEEYENAQLKLKKLLREGEEIVRLQQQVTDLKKENDALQERLSNV

EVLENNLVKAKETIAYMELAKSQTINMSQYAELQSKTSKLENTLEPIKKQLEEARKELGR
IKNENESLHAVLTRQQNTIKSHEEQMEALQANDAKMRDKTNQLTSENTRLRDVNETLEAQ
MNNMQDGIKEMAVKLEQERTRAQVAAEATHKEEIVQLRRKLESANATLATMQSTQENFVP
EAIHKAALAEKGHVSEELRQKTFDLDRLKSEILIYRQTINDLETENEEHVRQIESLQESH
KRDLTAAADRLSAETKKVTEANEALEGLQMQINEFQQREEQLLSRQKEMEEAAQKHRRAF
EDKCRQEEKLLQTVTATNQEMERQNEELTKVKSALLEYQRQNAQLESELKFGAAQGPRQQ
EEMESELEKLRGEIQRVNAEKATLEMELGKLRRTAKNGSWDGNGGGVENSGSNNNTDSNS
NNNAMRGKGVDDHGGHVNMETGMSSDAAVQHARAEQLQMSLIQAQRQLEEQRKVGAEAAE
TFDKALDKADAEAEALRERIQQLESDFHRMSQESDETRSLSSAHPKKQKKKKAVKKSLST
MAKIDDLQETDVLAVAAADEGVRQQQQQQLEQQRESLEKLEQELSTLRDENVRLKENIAT
LTQELLGAHDDLELARKATDSKTAELRGQIQLLEAQLRNCLANTDGDTELHRLAEENRQL
QSEVSLLSDSMNATTGNPDATVQRLKAELQALAKELVPTKNKLVEYMAMADRLGIHYPFS
PDMEGVAVLRLKAMHFDTVTGRVRACSAPRQPYASSFDKNAISSSGAKKKKKVKKRQPQG
SHVDELSDLR*
>TCRU_4365 MORN repeat/PH domain containing protein, putative
MGGGSQERFEGRLSSADGYVTNAQLPGNHIYTGEVSDDTMHGYGVLTTELDVYTGNFYWN
MRHGHGTFCSKVEKHPTGVRIYDGEWNMDERQGIGSIQWCNGDTYNGPFLRGRPHGEMGS
YNFADGRVYKGEYRHGIRHGIGRLTQKNGEYYEGEFKDGAMTGMGKGWYAGGKRVYEGTW
ENGKKVRGKLTFEGSKRMYNGDWKHEKPHGAGEMIFANGDHYIGDFVMGKLHGTGSITYH
SQGGKTYCGFFMENQPHGKGVLTMPDGSSVVGYFKHGIQLSENDSAAIEQVIKETASLPH
LFAHDDACSTRSTPVQVQNTQPPSVASSLWDVTEVTERNNNGGVPPQQCSLVNNKKETRE
EAKKNGTTLSSPFVLLDATRELTMPKLPTVELENPLLEPNGSCSNLSRKKEGEILVVAAS
VLAGTIKDGCKGWLEKFSIGRSLIGRSNWRRRYFVLAPFNKGVSLSYFKDESCHKPVALL
LLNTNDTRIVTRPSVRTHKEATQPEREICVIYVEKEKEYKLLLRAYSEDDREYWVYALSK
LFDIINYPSDFPLLENAQE*
>TCRU_4366 Domain of unknown function (DUF1903), putative
MPMHVPDPAPCAVESTLWRSCLKEFDYGPDRPKGACEKQRAGYYACIRAWRERQNEVYDY
NRFNLVKECAKEAEKLHQCMMVNMFEASRCQETMTQLKRCAARHDPEVRRALADDPTLIM
SEEEEPQGIKRLWYRAIGKL*
>TCRU_4367 NAD dependent epimerase/dehydratase family, putative
MEEGEGKAKVRFLVWGHKGWIGQAFMQLLEASGFEALGAVSRADDVAAVEQEMQRIQPDR
VVSLIGRTRGGSCLTIDYLEQPGKLMENMRDNLWAPVVLAQVCANYGVHFTYLGTGCIFH
YDESAHTVGGEDGFDEAAVPNFFGSSYSTVKGYTDRLMHLLFNSTALNARIRMPISADDN
PMNFITKIANYEKVVSIPNSMTVLPVMLPILMKLSLNKVTGTINLTNPGAISHNEVLELY
KRHVDSEYTYENFSVEEQNKILLSKRSNNLLDTSRLQQMFPQVDDIHTAVEKVCVEIAKN
FPRGIVRRRMETTENDL*
>TCRU_4368 DnaJ domain containing protein, putative
MDTAVLAQSILECDDGAVLQVLSLAPGLPPVTAETPIAEARRNYMRLAGMVHPDKLKGRF
ERSTEAFQKLVRAFELVADPKYRKKLLALHAKEERKKKSVKKEQPQLQLEGTQRVKQITA
SKGTAAVLPSTGASDVKPKRAATKKQKKKQRRASKVQGDDFIDYDDEEELEDEDEDEDEE
EEEEEEKEDESADHDEEDMDLDFGDAEPIVSTSRTLIGTKRTGGIYRDTTVSCPQCQTPW
MPDSKQHYTLFMGPCGKKVHCETCLCRFGCATALHACPHCQHSFHYDATMYDTVMECSGC
HKTFGFPYYPVNQYLIDQVRLEEWRERTEREKAHEREERAARRRITDEGTSDDFHSLVGT
CIVNETCPICNRTITARHRQHVEMCLKNKNTGSIALTTKTTKAAAKKTARKPAAVAKKTS
TRKSAPKQSKKAKKRRRSDDSDSDDEEEFSSSSSEE*
>TCRU_4369 hypothetical protein, conserved
MGRRPVEKFSRALRRRAQVCFGQRLPAGVNSSAVKTAATAAAAGDGGRSVAHSRDAAREN
AATGDAIHPTSTTATTFFPSIMGERDDGIIHANYSLRRALARGAPETRLTRQVRHAIEHS
TGKAEALKAFQVLLQADGEGPTAATFKTLSATLLQHHVEQRVGQAGFQRALMDAVGYEGD
RWQSLSEEERSTFVNYTCRMTERWAERGSSYNKLLGFSQEGADNEIVARVEYQMRKCGVM
VLASSLADLMHLDITWSTALHLFNFAEELQKDIPPPMEMTDRLMGLMTGYKSGLGGSRPW
MRALELYQRALVSGYDTTLTTHTHALDALWRSADNFHRVHTSLSSYHRRWLWEKALKISQ
IVQDTPRLLVTGEEGCAYAESVVKTLTASGRWSEAISFIANLDTSNSDVSFRFLVPTAET
YVFAIAGCHTAGHAAHGEALWTIFKETYTLRSLHSEALLIFLQSLRHVVRTSPFVGPLVE

ELVRDGKGLERQAAVASLQLLSSNHVKTREQRWVLATKLLDMYDANPWPQQPLARKTELQ
TVFRCCHLISAMECPHGKRLLTKLRKQLVDVFGSLSAEVEWLDDTSIYALQMTSNWEEAI
SIYDQAVGRRKPKQVPYLPIPLRQAKMMLVEALVRSCRVMEEDGESFLVDEDTQEAGRDA
AVVLTERALAVTRAVYGSDDTFPHHLYAELLVIQATCAASSSQRKLHALAAMRHFSQASA
ELIGRHLVSQTAMALSLTEVHVENALLAGHATLRYATLSQRKGNRKAAKIRSGLEALVW*
>TCRU_4370 hypothetical protein, conserved
MPAVDVEIHFPLKRIAAEGYAEDELLLNQMGKVNDTPEEEGMPLRAWVIKCAHEALEKNP
KIREVYLKPRAVKNSSVQFHVIFDEE*
>TCRU_4371 D-ala D-ala ligase C-terminus/SET domain containing protein, putative
MSFLPIRVCVLVCSYEGSDSELKEYEGEIVQTPQHYFTEEDSKEFVFTLEFVKKATAYRQ
IRQLVKSGAFDVFYNQCDGAIDEDKAGVEVVQALESFKVPFTGAISKYYELSKPEMKRMA
HYCAVKTAPYAVLEAGDNVRELCAALHFPLIVKHISGYSSVGMDKSCKVYDMDALKERVA
RFIDQYQSALVEEFISGDEATVLVCADASQPGGIRVFPPVMVQFPEGEDFKHFHLKWETY
EGMIWRLVSENDPALPDIIHIARTAFLHMMGGVGYGRVDVRIDREKNSVVFLEINPNCGI
MYPYGQEGSADWILRLTPEFKQKEFAKLQISEAIRIHKCKQPLFRCAYDPVREYYICATR
DIPAGSIIFEGEGRLVRLCTKPYVKANWSEVEYNEFLHDAWPVGAEGHYYALWDLESSDW
RAVNHSCDPNMGFCPNRSLNVHALRDIAKGEELTMDCRLFMDDTMPPFQCHCKTSICAGW
IRGGVMRESHFFESYTERLIHREDKFITQLTRN*
>TCRU_4372 Ciliary rootlet component, centrosome cohesion, putative
MAKHHRPIVCVIAGDPLTSPEALLQHLRAYWRRVGVLELCEDVHKLSLRHICRDVNDEGL
KENETALLHITFELLTSPPQTLVTGVDILLLLFSPAHPLSFLHLWEAATSRASHRELPPI
FLLATHMELLVMPDVQRYMHERGIQPINLQELTCAVQATTLSLGRVIPVSLGDAALLHAN
TLDSSCKSLVYLCNSLMRIFCATPGDGHDDALPLQLRWEATLNEASAVQLEAQLREKWVA
MPSARTGRIFYSNRITGEVTTVQPAIVPNDTSETFEQRRAVAFAAQVRGHKKASNLGSSH
GATVHTDVMKKLQYSVRLLYDKRARLKELQQKTHLLRSVVQKLREETGSLSSDLETLRSE
RASLEEKISITQQEFQSFQTKCELTGSVTESHLVSLYEEINHVKRSYLQQWNCNKLRRSD
VRAMHLRVEEVINTTERLRQQITEGSERTLRLLQKQYLMHHNEIAEIEEKSLLFRRWQAL
RGRERGEEPPNGGGSSCCAGDAPTEWALLLRGLLNALLVVVEPLLCAIDRLQQMSGRLPA
PCSVTVQATHAMRRLLLEERLQRWRIGVECTLDYASCIVSDFLLPMQRRGRLLGEHAAAL
LRLFS*
>TCRU_4373 protein kinase, putative
MERLRERCILGREVVISKLLGAGANGRVYLAAPVSQSDESNQFSYPPHFVVKVMQKDLFP
AGHLETILKEINAVRVLKHPFIVSYVGAWVEAGGGEHDGSVCLAMKYCDGGDLHDLILEY
KKRDEYVPNDLVMMVMLQIFSALNHGHAHHIIHRDIKPANLFLVRGESGCGGVARALVGD
YGLARPVERTVELAKTRVGTPCYCSPEIVAGEAYTTKTDIFSAGVTFFELMTRQRPFWEK
DFTDRQSFYAILHSDPMPRLRRMAEGRYDSCLVRAVGSCLCKREKGRPTAYELLTGFATR
LTTYVRTNGIPVCGEVARVSPVRDDGCSPLRRLSPISPVRRTSPRPQAPSRPRKATPRRN
AVPCAAPIVPASPRAVVEDAAAAPREEEEAPGQKGVTAEHVLQVLEEALGDHAECEGLKQ
LLGGDVEAFLLVRVLLLTRGNDRNAFENGIFKLLLSLKPQISVERVILWMSGRDRTA*
>TCRU_4374 hypothetical protein, conserved
MSVRSIVTKQLLRQSTLQPRLKLPAGRVVSLEEGRRLARLVHEEVEQTDAANLAAVENRS
LNSPVVLEEEVSKRILLLRQRSNKAANIRAAVAYAQRSKVPGAVGKMGTEVREVAVKLLR
KDSSARGALKERHERTKRTRASKKRAVGTRK*
>TCRU_4375 hypothetical protein, conserved
MAMMMTGRVLLVCVLCVLWCGAADGAVGVSGGEDNTMKELFIPVARFQERSEQRAAEATA
DAKATAEMAAKAAAVAEAAAEAATEAAAEAAEKAKIAKEEAKSATAKAEEAKAAAEESPQ
QQKQKQQLKQQQRQ*
>TCRU_4376 BNR repeat-like domain containing protein, putative
MSRRVFASAVLLLVVVMMCCGSGGGAQADVGAAQSQKSSPEKPFHWRDTNLPLRHSSEAQ
GCLVEVNGKVFAVAEAQCTRGENSVFTGIASQLLTNTADSEPEEVLEGAREKTQFLEEVT
SEDPKKRVDVSRPTAVVEGDTIYMLVGKHSSEASDTCKAETEKIKSGILLVKGRVGGDGD
KKIRWNDTDGVPCTLGDQHESWTGLIGGGGSGVMMNDGTLVFPVEGTKNKEKKEEKDVKT
TLLIIYSSDTTNWKQSKGMSADGCSDPSVVEWEDDKLMMMTACDDGRRRVYESDDKGDNV

DGGLRDTLACVEQQTKAT*
>TCRU_4377 BNR repeat-like domain/Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MLVTLPVYSKDEKENEKDKLHLWLTDNTHIADIGPVSGKDEDVAASSLLYKSGDNNEEKL
IALYEKKKGESSSGMVSVLLTEQLKRVEEVVATWNKVDDCASNLCPSENAEKDGSPENDC
SAVNITDGLVGFLSGNFSDDTWKDEYLGVNATVNNEVTSTDNGVTFTGRGAGAEWPVGKQ
GENQLYHFANYNLTLVATVSIHKVPKGDTSIPLMGAKMNDDVKTVLLGLSYNNEKKWILL
CSGGENKEHSSTWEPQTHYQVVLMLRNGTQGSAYVDGQRVGGDARCELENTDSEGISHFY
IGGDGGIADNTESREGVFVTVTNVLLYNRPLTFSGGNAEVEEVTDSPSAEPASPFVARNQ
NAAPPATIPPEAPVEQTTLQQPQQGRETQKNTMVGESATAQELPANTSQGSVEKAAASNS
HAAGEATVDDGTMRESRLLPSLLLLLGLWGFAAL*
>TCRU_4378 BNR repeat-like domain containing protein, putative
MSRRVFASVVLLLLVVTMCCSGAATAQVGSNADASTPGSALTGAIATEGSASGGVEGLQR
VDLFMPQTTQVLAKNGPDSSRRDSFVSPSLVSAGGVIAAFAEGHVNAKYQGAQLTKPLSS
DVVAEYIDSAWEWPTLVGEVTNATGGEPSKRIKWGEIQSLLNESAIAAHKGNLTECLASG
GSGALMEDGTIVFSLMAMNEKNDGVYSMIIYSTNNDSTWSLSEDISSAECLNPASPNGTR
DRFS*
>TCRU_4379 zinc finger protein 1
MQPQTPTFSDARSDNSVGFNTNPRYGRRGVDYSKFRTRVCRNYSMGITCPFGERCAFSHG
EPDKSHVRTEEAELPPPPPYPEGVQAEIMLPPAYPSRFRHDPYSFNGVLFEN*
>TCRU_4380 endosomal trafficking protein RME-8, putative
MDEVVLGVPQLAGCEAARRKPFEEYTSRYTVVKNSWKGKYMRIFCIGPRQVATINPQSIF
RVTNNWEYNSHLVDVVATPGSPTDFTVTIGKIGKPETMSFHCNTAMERAELLTDVQRNRA
KFDARYRQQVFNHVFDARKYSFYEEYRNCRLRITSIAVEQLSPEGNVVGEYLFMHIKGLT
SILANPRTLILLYGPQLKMHLYEMEDCQRVATLIEEFSRRFIGLPPLREVRRLTQQQFDS
DRLGVDRAEMVSLAKFPVSKWSSKHPDTPMRRILATTQKYLLELDAATYNPVSAFFFADI
YALIRSEEDDQRLMIQFKEPAITKVYTSPMRDALLAHLVDCCRASRNLNVCVIANLFDRG
KRAAPCRTPIPEEIESTLLNCLIDPSKGGGPIAMTFPEVVEFFNANIEYSGLRLSENREG
LFAENREKMIFSGLAALLNNFPVTDDPLVVVQQFYALRRLCVARIGFSSVAVVPSFMKNI
EDVSMKALKMNHVAVSHAVVDLLGTLMTPHHDYYELAHEEANKNYILGQEQLVLRLLRML
RDYATTDSAALVVQALLDFFVYALCPPYCESTEAMLFTSVMKDLVDTTGKELFLLMQHGC
NAISYSAGQLIRVIMEEGTGEQFRALQLAALSEGGIIGQLHLAIFSKNRELRDLARQLIA
YWTYENTDMQDLMRTIFPPALLYYLQSSEEPPKDEMEEERQRNVVPMTSAFWESKLGWFK
KRFHPSEVLSRGAAQNLSPSQGDGVFKRPRHVKVKTTLNWPMFFYEIKRDHLRPELIWNH
TTRTELREALETEMRVLRLGMSLRHENPTSWNYREFEVRYPSLDDELRIGQHYPRLLFEM
KDPAISRPKEFFNDMYHRFLLSQEPKTKMSCLHGMTILYEHYAADIGQFNDVEYIVRMLE
TTFDPIFRDRLLIFILQLMRVRYNVKLFLDCDGLKPLVDLFTLAHLHVDRPQLRNATNAI
ENNVDTTDLQDQEKEWYYTRDGAKQGPISYIRLKQLYEEGEIKSDTKVWAQGLSGWKELK
EVPQLRWGIMASKSNKLLTLTEVSCVILDILLLLCACFPSIDEHGAIMQPPPRVKRFLSS
PQVLPHIVQLLLTFDPGLCARVHSLLYLIMEHNPLMSRFFLTGAFFFALMYIGSDVLALC
RLLHLSHRRQAFQFKDENEIVRQSILSTMLPPALVCFLTNHGPEQFADVLLGEYENPEVI
WGKDMRRYLVEKIASHIADFTPRLLGNNRALYQYCPIVGVTYEPLRHELFCFQYYLRHFC
DELRYPNWPVDDPVKFLCEVLAAWRLELNKKSSGLTQEGCLEELEISDRSNLTLQVIRRG
YFKLAAKYHPDKNPDGREKFERIQRAYEFLASETSVSDEPNPHIIALLLRTQSILFRRFS
DVMKGYKYAGYSLLLKLIKMEFSDPEMLKKEVVLMEPATELCYFTVQNLPMNADELQEEG
GIELLSGVTQRCFEILTPNATEELNQAKIVRHCMHTFRVAAGFADCRRHIVEEPVICHLA
AKGIAYEKAVGLSRACIQACQAFCVDEILQERVLKFGAIWHLLPFLFRYDYTVDENGLEL
QEENHTQLFANRAAIYALRAIYALAGICPSDEYLLTKPNDEVICLLQRLLTPYTVRRMQL
LPGDEKELLKLLNSNHNTPYLLWDNSTRQELLEMVKGNSKKCRDAGMFAEDLPVISGSVV
NYSLHADELVIGGVFVRVYNEQPNFAIEEPVAFCAAMIKFLEQQLTSNTTTGVLLTLEAL
KHLLIAYATAGVANTLKHHVGILIKVLLYEDTAITVKLMELLEKVALHHECLEAIGNIDS
AVAYIILALHRGGEVVESRCLTFLRVALADRGVAQQALDRGLYVVLLRILGTSTSPECRE
DVCSSLAKACSDKLCGPKVFLRASKLLPSVMLETMNENTTNACQLFDTWQETPELMWTKE

RRSRFVEICLACQSDIVTTLQQDPTAYWKIPENILIERNKEMQIGGVYLERYMNQSGWIV
RKPKEFLTALLERFVEESGKVTEEKNAEMISLVADAGVRLLQTTPTVADYVVSLGYAQKL
FKLLELGDKVIAENALKWVHEICASRLCVESLGNFDPVFFLLVCLRAQFQQLPLIMDTMN
RLMSHSSERANMIRLALRNQLPQRLLELLEDGITSESCGEQSPAAVRALIIKVLKTMVAV
QDPLHGPQLEAILADSKVWVKYKNQSHDLFLSNTRFGGYLEGAYQQNQMLLSYAAAPLSD
DGSGQEPPPV*
>TCRU_4381 tRNA modification enzyme, putative
MEAADMEDAFNVGAAPVAAAERLAFVNARRRKWSPAQRQDYGDGIPSNATVFIHTFGCSH
NVSDGEYMAGLLAQAGYRVTDVFNDADVYLLNSCTVKNPSEEHFISMMNRVRATGKPLVV
AGCVPQADPRNTQWDDVSVIGVRNIDRVGEVIHEALQGHCVRLIGVNEHANNKQDFNKLP
PLDLPKIRRNRFIEIIPISVGCLNHCTYCKTKQARGDLRSWPIESIVLRVRSVLKEGVKE
IRITSEDVGAYGIDINTDIICLLRAIVKEIQGTEVMMRVGMSNPPYLLRHLDDFAALLRH
PNVYEFVHIPIQSGSNRILNAMQREYTLEEFYECVHRIRSVVPNVTLATDIICAFPGEGE
AEWRETMELCDHVRFPVLNITRFYPRRNTPAASMKQIPTDVAKRRTSELTAFFNSYRTLD
HMVGEVHSVALLETAHDKHHLVGHTKAYVQVLVDPQEARLGETVTVVIMSTTKYSVVGRV
LRRRCERLLAKSTMTARQINWRSLSVVACFVSAFAAATAVAIRKVHAGRR*
>TCRU_4382 Uncharacterised ACR, YagE family COG1723, putative
MDRRRGSDDASDSSGSSQSRSFEHTQQQERTSRVWSQMNSNRGEPGSYSRAGSGEADEAQ
ELMTLVRAEDSFPLLRDSVYSDTSFDGFGRAKRKDLYHNPHVYESVSVTRDFPSETSSPP
SVSLKGWYAHGEQGRLSRIQYRDEYTQLLNPQQQTQRHSGTDADTDADEDRASSSFKTPE
TSTPSANEKSCATPKAEAVEVEMHDQSDVNSDKKQARFVDNNPEPVSTNVERMKYEVPED
PRNLIINVIVNSASASVTLQEIHNALQWEEQFEATNGSVLEYLQGYQSIFAVSPIDDRVT
LRRPLKTAKGRRKVRGQRGHCSIPNKIGSISYSYVASAFDLDALSAIYKRRGYDTALIYE
VLHVSSHRIFDMFLFPNGVVVWWGLNRRDHWLVEDDFLSSVNSFVREGVKERHAQKAIDD
LFPFWCSYELDEHYDSSTPSRREEALERFGTHLCFDHYLIPVVKPLRTQIMLTVSYSLGR
TAVVDFFDNMTHHLQKQVLAIPSDIKSLFDYFSMRHHIAHREGEIQLARSAIMALRDSPE
FLWEMPWLDDYYQLAERQNASGQLLMCFIAKSDALLQQLAYIKTRRFCLFILGSDVFLIL
ILVADVFFIMAGFILKLYFNLGKEETASS*
>TCRU_4383 hypothetical protein, conserved
MCFTLFFTGITWTLDRLRKIERRSAIILTDPYVFLSGGLAGLAGRAAAIPFDHGGIKGPA
QACYRRIPQFGILMWVYVPLASQLLPGTEREPSLKAFTTFIIGVFAGFVMRLICSPVNRV
RDECLRTGDSFLKTCQIFKSKTVLQFFYTTPPLMANAIYFGTLLTVFEGLRRFCERNRLL
SINVEKDKNGKDVFELGNYAAVACVNTVVGGVAAGVASTVCYPLSAHTYKQTVIHDSAIC
RGLLPTLKKEMPMMAVSFGVFSLLQPIIAPHHGIRVGFGY*
>TCRU_4384 zinc-finger protein, conserved
MSVPVPRCGTCNFTFDSVEAVRKHYESDYHLNNVRLRVEGRRPLTAQEHRCVRIAEKDDV
DEDGKPTFACKLCKKTFHSVQTLQAHVRSTAHLMKKEQRIIARDSDALSAITSTSLGSAA
MGLHRRHNAKCAKQPAQATKPKNLLKVGLDEREEDVSEVRCLFCGALSDSVEANLQHMNT
IHEFVVPLKHRCRDVVGLLAYLARKTNGLLCLVCGEKTKMFASLEALRAHMREKNHERII
LGPEYEEFYNTSLGDADCDDLLAPNTANLALRDSGRVVQRRERGVPRPRKKESETQAEKR
RAILAADQEAMAVARKECQEALRVQNKEAQRILRRQNGEYQDHLLKVNLRTNKLHPKGYD
GEGKIN*
>TCRU_4385 hypothetical protein, conserved
MGDNLPPLEFLTEEEAALLAEYGVKGPYDDLLRFPAASTCVFDYGGRDVFLTGTRPDEGD
DDNKRLDKTDAGEINHVDHTWPLDCVLLHHTHMLSYSTAIPLWDGVNGVLNGDTKIVPIM
TPHSPLSVERSDAVGSIDREEGKFEMEDVSPARQFNRYERSDLDLLVTADDLLREADELL
AKRIQYLDPMAEDYLLERERAALEEERRWSPIHGAETTTTALTETDGSSEDEDAAKEKNG
KKELKNLFAYEFGPTTEEQQTLHEWDEAVLRCEQRLELLRNNAVDGETMNASRDEELDVM
AVVFPSLRAEEYHGAPILATHSPSVKQHTGILESIATMEARDSELQAAACQQLEKAREER
RRPRRAPPAEIVFDQFLTRVNQLLPPNEMEVKLEATETLESAEEVKMAPSVSGEKTAVGD
AKSHTQPLSTNQVQRNARREGFRVRCELREAWCMQEEDRRATRLLLWRKEEATRIQNDIQ
GCLSDERSMREILLLEECNVYREISYLERQSAFKAKENEKLRQEEFRSQLVRSITKEHAD
IRHEIMAMEEGTMREILREEQHARDLLLVRQQEHTAHSITAVSRSNFTEWEDSDGNEERI
TEAVPLKKTAQAWKLLKSSGQFPATRTCIDHSPIGNALRLQSLQREEGMRRKWVHECKKG

IIQTASALAELTHGVDERTTNTPLPGVRPGVNSTPTPPTLSNDVSYSSLDNTAIRLDANL
AKQLQPTVFGGVKSSLREVAQLCHRLSFALEQVAAVDFASLATLEVCTNGGVMNCKEKHM
TPAAPLVQELDLGGNALRTLPLDDLLRVFPSIRRLNISDNGLRDVTCHSASLRGVSEAHA
HSLAQSTHLSHLDVSMNKLHSVEVIGKLLPYRLRSLVMYANHVDSLLPLASCTHLESLEA
SRNRISSLSELQHLSLLRTLDLSENCLITWDAFAQHVLLQNLYLSRNQISAFPKTLFLGF
IRQLFMNENQLEVLPSECFCWLPFLSVLHVENNKLRDVSGLAHCPRLTVVGLAFNRLQRV
EDLSPLAACKKLRSLSVNENPFTRGIDCNKFGTSAKVKMTLLAWLPQLSELNNEKLIDAE
RSSAMENEIMWLRPFSMARRLRQQFHESAVYDAWYWPCGSTVEDLQQVCGSREWGLQYMN
IKSGYAALFSALTSDVALTTLQKEQDVLIAFCRRRHHDALRVEEELQKRFRESKQRFNPA
IHLLSNTVDERNGSETNSILRQHLTALQTMPQIMANMHLRSVLYHERMKEHREARAKVFI
CEWMRLRLLGRRAKKELESLKAAYAESQRRRYEAAARVIQPVWRGAAFRSRLQRILHIND
DKDDDEFTHVSLDFIDDLQTKGDGDGVEAVLQRVLQSHVALPNFPVSSSPTRITGTQDSL
VGPLLPRASSVLPDGTSRIGEEERQRPETQPQRGTRRLSQEGRKQQKEEQLPPHSSFSSS
SRVDDEWGALVSSQLRKRQKKMERAQRENMRREFMKDPLKVKRALGGG*
>TCRU_4386 tubulin-tyrosine ligase-like protein, conserved
MRCCRRLRGHQPVVAVATGMEEKQQMKQTSLPPEQAVYLKPSRSRRRKATFLFTRMRDSP
PAYAFRAPPLGTALPLFCITSSSCEYYALRLPLLKAGFKRLPTGTNFSLPSNVLWGRSMP
LYPAVGVYHLPSSSSPSHLSSSCTSPHADGATDNIVFPASSAATNEEAETSSSIRMVCNH
QRFNHFPRSHVNVGCKWGLTRRLRQVSKLIEEVGEDKTLYDFVPRTWVFPDESEVLFKAL
AEAPSTQRFIWKPARGSCGHGIFTCLGGTKNTPRWQRLAAEIKNRILTETPGPGMVGRKY
VVQEYIENPLLLNGRKTDLRLYVAVTSYDPLTVYLHEEGLVRLAAQEYSSVGNGPNFDPF
RDLTNYSVGRRWHTRGKQSHIQGEEDISVVSDISSGEKLSPPSLELKKSLSDLWEHIDAM
HPAVTPINTSLHRHMSERVKEEIARVIVKTLLAVKVPLATATCSLSVPGGFFELYGFDLM
LDSKLKPWLVEVNTLPSLASSSPLDYAVKTNIVADLLNLAMIEPFERPVSCFDELDDELR
LSGILDPLSKEAAETVHRWCGGASRDPRPLNDTEAREEVGLRLQDELVYCGGFQRIFPPL
PSAQRLSIMNEVDVFSRCLCFSKADIWALEV*
>TCRU_4387 ATP-dependent DEAD/H DNA helicase recQ, putative
MQDDGEELFHDDIVSDGTASCEFLAVNTEETVDVEGTACVPYLAPPRLMAFGAASPLLHP
STFKKDESTVRKKFTGDYPAAQNNFYRPETTLSDVVQEAEAEENKTILQVNLEALFEESL
MTSSYSVSSVQTVPVCNYILRTYLGVASGQFRQGQQEVVLSILQGRNTLAVFPTGWGKTL
CFQFPILVYRLIFEAKLRAWQNLQGSDTSGTSSGPPESHFAVIVSPLLSLMADQAGKIAS
GGSLRTAVLSSGTSTSRERTILDELASPLCCIDLLFLSPERLVRHSELQSVLERHAHRIA
FICVDEVHCVSQWAYDFRPSFMYVHRVLERLCGGILAMDGRRHAPPFLCLTATASPSVID
DLKVIFRIERSVIVPYCRENLQLESVSLLDVGCQRPPTQRMLQEKLLQAVLELPKPMLVY
VQTRVDADELATFLISKLGTVQRGTRGNGLDGTSSSIFTSATHVHMEKSGGRRTVEGKER
IIIRSYHAALDRHVRTKTQQEFMQCRIDVLVATVAFGMGIDKADIRSVVHASAPSSLESY
VQETGRAGRDGQKSFCRLLYNPFDYYTLRSRALASCLSPLEVHAIVSSILSSPTTHFGEK
LTMISVSKISEQLAVGEETVETVLFMLVLQESGVLHELHGTAPMGYRVNHAAAEVVVTTE
HSAKRKRGRDAMGSSGVSGVLAQLEVLDGVFELFRQNKRIENVVTAANALNLSLRDFQFR
VNDLIAGGFVSAQPLTPAYVVSLGNNFSEAAAPAGQKAIAERLWQAHHRRLDSLQKALDV
NFAVLQHPTHESVRKGLEWDARHGTDAMSPTLKWQPPPKSLTKLKAVSIANDFVEKNRPR
IRSIYEAARALHGVLPKALTSHGKYAGELPLSASWYVSSPYFGLLKEFDLQWLLKVLAPH
GLDEDDSMERSSRLPTA*
>TCRU_4388 hypothetical protein, conserved
MQEEGSVSDWEAQPFDAVNSKICETIRRLDETIGRPPFPNPSTTQCRLLAVSLVQMLRHV
QNYGRIAALAESPEVNMTLPILCASVTNGSEGRKPCTVLMELLLEALICVHSVSLYPLQT
TLKDAKEVLPNSPVAFKLFVVTGAIDVDAMRFFLGVEPPPKAEQKEKKSLKGGRRAARSN
TNLQMNTNNNFKEGFKFVSTDMLNAALDMVLPSDCMEVLLSLFNSSAKFQKVIGGDSELA
ARVMGVYGDQLLPNLRPSAFICCLDVPVLDTFVDVVQMHGESMALLKDSVLTHIPLVDWT
AERLSGLIRYCVDRKVRHDEALASLAVYVFLCKLLTMWRETHNLALLPIEEEAKMWISVL
NMVHLLPLNAGAIPTDEEEQLLRSLSVLAECVKRRYTLTEVRRATSAVPHASVSSALEML
TALLSAKEAAMSDASAGIGGGGGKKKKKGGRHNNTAVATANDIKLSVLPAQTASMDFFCR
GVADFFALLFWFTPPSTVKMDAYKTESILESLAALLLRLVDEGAGKIPHACTWESYLDLL
LSIISPWGKRSHVSCLRPKTISAVLSAVCVTRRIQCCGVIAQRMPDVYSSPQCSINNYKI

LLEVWLRGGLCVDDFYAPAVPFSSTESIGIILGLLDGDRRCELAQLLLSAERLTRVLIPA
IKEALLEEPLNHPLETTKTKTSLSAAATARKGLLELQNELLGGAEMQRKMVAEQQQKEED
EKTMQLLAEVQKKEELKARNRAFESEQQKRWEMKDEEQKRIRRLREDHEREKEERREKER
RDREERCQRAIAMLKEMAAKTKAERLAEQKERLLRYRECVAMNSRILSFLEHLHLTPSRI
MHLLTTLRPHLPRMTYDDVLEFVVTGNRKVPGDIHAVDERTNNTTTGDNVHAGEVTREVK
EQAVCFVDEGSSFWDSVMQLVAQQSDGQTRKTRVVSAGKEEYEGNLPKEALGFSFHRRMS
AVLDLFDYSMGTNETVPNPLPSLNVRCALRVIEKEVLAGSGVCGVREAFLSCQQRGLCLL
QNNICTLTPLGFRYHYPFHDPEQMLEIQLERRREKARAMMVERQSADLDDYEEEYEEQED
VLVKDGTDDETMPSLADDNTVCFTDELI*
>TCRU_4389 hypothetical protein, conserved
MWSKVFSPLLTNRLAPAQKFPQLKLRPLQHRLLTRERQCIISLTSFDANSVEFARREIAP
GSIVEVRDSERHHLLALGFYEPALLRVDVFHLTPKLISELPTIGEEFFLNRMREAWQKRQ
RVFGNMAVNGDNNTYRVVNGTADGIPSLYVDLYSSSFARIVATSFGAERLVPSVAEFLRC
YGAEQLLLDTPYLKDREKLTLVHPTIPLSAVYIENGTRHLWIPPAETPATRSNRWLLNTA
HRRTRFVLREVCRNKRVLTVNDRSGSAALNALMSAKSVLIAEADAALLDRIRENLVANHA
TTVFNICETVPCTNIEDLEARRQDVVYLEHHPDTLSSEEQWRTTLATLLRRRICGDGTLL
FVAQEAAPLGIPDLQQQHASTEYFVPASRETVATALRLAASEHNLNLRQLRVFGPSVDYP
VLPMAESTCFSQIFFLESNR*
>TCRU_4390 SET domain containing protein, putative
MTLKCALRAWTAPMAQVRRSHDGIRGMIAKSRFHRGDLLICVPLAHCYFPHASRDPHRLR
RWNRSALFPEAQFWLRQLSPDAPDARVSLCASVSTEKNKVLTLTLSPVEAALAVSVALRY
FWRNVVLLKDREGSGRPALGPARFRSADLYLHSLPMEEYISYGLEGPYFSDVEDEANVHS
NIEQIAWNLRDCILSHAPQEEYTFYDAHPSELDATLLAAIYVIRARLLRMTAFFEEEKAP
DRVTSVIAPIVDLLNHSSTDYTCAACMSIPKRAVVVRAVRDIDFGEELTLDYRAAARQRK
NKKQKTLGISDLEEEEDGWEPRYLFSAKDA*
>TCRU_4391 zinc finger protein, putative
MESGRSPLKRKAFEFQLHRPPCDTAFLAVVDAPVLFHADDATSGKVKDATIRHIGWHVLH
LPEEWFFSQKSRELTERVCQSMQCTIQYLAYRMKELQAELKNARQDVEEIKEERNEAFEE
LVELREVVARMKQRYEARGQSRLATKAAAPDRLVVVEKPRRSFMCSLCGNFYPSTSSLES
HMRKRHRRGEHHAAMNTASAAIQKKVGESNNFSNDVLRGEVTSLREEVMSLREAMAAEKE
KRQLDATLSFFSPVSIAAIPAHHLPGPPLHERDISHILPRLQEEEKRKMDALQDELRVTK
SRLQQMEEVIYRQAREIEGGYGRRTHGLESSTLEEILPKNAVPVSTSVKHKGLARFASGS
SLHSTNRYPLRIADTHETVNKEVSIGKEGDLVSRRMEVLEPNHEAKMPLDQHLVVLSGHS
SSASWPAPTPVSPSSRERSVHSPSVDEFRPEISESPRQYSKLTASVGKLSVSPASEASTV
SVVAKNNVPFLEIHPSQVAGYSGSVFTSLNLGSVGVVDDGGLHRILAHQIGPTSHLRAGE
TNIVTKNGEKALDIDNAGLVSDQNKGLGFSSSLRGFSENSVPNFNRLNSLQEINCGYSFD
SYISPLRSSARGEAPFRKTTPSGLTSNSFRSRAEEGAESHVRVFAGEIPRQEEQHAEEER
IAVDPKKTSLESVTSEKGKTWKKLFLSRLFMKRKK*
>TCRU_4392 sphingosine 1-phosphate lyase, putative
MILGFLLMTLSEFIDQTLQGRRPSSIVYASVGTIVAAKLLADIFKDGFLIKRSKFAKWRI
IRTLAAPIIEREVKTAGKAFKMPAKKGEFKAKKLPEKSTTDERVLSLVKTFHEDLDKPYE
TGGFSGSVYHGGESHTQLINRVMELFQWSNPLHVDLFGATRKMEAEVASMVLHMFNGHLL
PDACGTVTSGGTESIMMALKSYRDWGRAKRGIEKPSVIVGVTAHPAFDKGAEYFGINLIK
VPVDPVTQKINVKEVAKHIKYNTVAIVGSAPTFPHGTIDPISELAELAYRHKIGLHVDCC
LGGFIVPFMEKAGFTVPIVDFRLPGVTTISCDTHKYGCAPKGSSTVLYRTKDLRSFQFCC
VADWPGGIYCSPAVSGSKPGNIIAGTWAAMVRMGEEGYVENCRKIVNARIKMTAALSKLP
YITILGDPITSVFAFNSECIDIFILGDRLSERGWALNRLQFPSGLQFSVTLLQTNEGVVD
RFIKDVTSIGEEMYMAVKEAEKEHRVVKKDEAGGSIYASQQRVSDRSIVKDILREFLDQY
YSANH*
>TCRU_4393 zinc finger of C3HC4-type, RING/B-box zinc finger,
putative
MATDTDGRIEEPRGVTCGLCFNVLKLPLTFDCRHSYCTDCVRAKLESQNSDGFACPLCNV
LYAAVSARNLQSFSDARLASHVKMIAEGTDGAPMCQWCEEVPAAVQCHECMFVYCNDCNT
AVHKSAAKRGHVTAKIGSQQKLRGMQKKCLVRGHEEYRAEFYCSQCEEMCCAYCLQVGPH

KNHENMGAARAAADIRQQLSRDMGLITQKKTVLESQASELNRVTAQYFNSYDSVENIITE
RFNHFKQQLMQREVELRKLLATLRESGDASLTSTRKLFLAKLNALNEATLRFQHLRSGGS
DHEVLESRSILYSFLKTETPTVTGSGFKVSNLGDMMISGLELHLDLQTMHGVELHNTDST
ERRPNNGPPSGGMTTRQPSEATNGNRNFVGGSTLPPERPLRLTFPVDDDVEATLKGDGVL
LRCVARGGGGSTQIGVRSRELMETVGTLFPEDGGCVTWRIRLELITESFVGVVEKTDAAA
IPEGFYWCPTKSGVVDGHIGRPTPIVQQLPVCRNGDVLRFTYDIRERTLRFGLNGSDRGV
ILTELHPRVAACFIFYPGEALTVLS*
>TCRU_4394 ADP-ribosylation factor, putative
MLKGLRNRVRRENEPRVLIVGLDNAGKTTLLNTLGESDVNDDENTRKTPAAPEGPTHGFN
IKTLTRGDRRAKLCDLGGQRALREYWQDYYNNTDCIMYVVDSSDHRRLEEAHTSFVDVLN
GIPGVPVLVLANKQDLATAKTPQVIAESLHLQESRDRKWHIQGCSAKSGVGLEEGVAWIL
SVCTS*
>TCRU_4395 hypothetical protein, conserved
MESSVSSLMDHLNGVETRRRVVMMKRKEAETRLAFSTEEQQQLEQQTAQNEVRAVELKKE
LDHLLEEQRQLQLQLMAGMDTVRQSEVEEALLIEHARAKLEKASMLVTTWREHTCDLDEV
QRSWGEDDAAAPLQQSAAELDAELVRLCGEKKRIEQAIKEAMEEHALRAAGLGAGTSPQS
DAAAAHALPGGDDVATVQLKDQLELEQRELAEIQMHHARQMAALDREVADLKSRSMELAQ
WLADTVGSRDQVLLSTQHLQSCLNSGVCALCRPSS*
>TCRU_4396 paraflagellar rod component, putative
MSCAVSPALDTETTQTHSAQQLAFDDSVFRLRLTPAASEAFYLEECRNHSVNPNNTFLKQ
LLAGVTVFDFENGYLGERGIVPILSTLQRLPVVELSMRNCEVTTEDVELIQKTFESHDTF
RKIDLRGITLTVAAARRLLTLAVQNPHVTEILVDEDTPKYLSIQKQCFANAELTVLASRC
LVCNRPVIHSPDQKIEGRLLLSLGEELDTMLPAQTGVALQAMFRCILACCEVDDGVLFLC
SGECRLHLTKDILTAMHVVVGKRFSGEQTAYPANPILRRCVEGILKTPLGKPVKTVNNND
MHVGDNLRTKVTCSDKYDVDEDDEEDEDDSNRRNILEEVEEECSICGVHAVCLPNGGLQA
MRRVCKEIAEGSVLRPSALFRLAKLMMQYTDIRPCSQKCVTHLVRFGIYGYGGVLRPSSK
KNDQYVSLLDIPLTNLPIENFAVLNFSAAYIEELDEEDTTCALTVASAMSDMDGVAIDPY
MVFAFGRHLARLPSHVLGMELRHACEAVQVVGCLPASLGPFDRRKERPPRSRYVSWEKWS
EYADVDNIVRVAFSRRRQGVYLIDGPHGNMFDNTRAALWAFRKQRRAVLVAMKFSLEWLA
FPGGVVKNESPLKRGFLTTFKVVGQTSIDNAFYLICQGNFGPRVGNNGFFYIPRGIFNLY
VIGDAYIFIDAGAYMTLRGHRRSLYAARILPKKVMELAEQIPLLKEVHYLCVEALNWKTR
HRLEVTKIVCEALCRLPPPIFFIYRGCDRDVAETQEELLRTLRKIVFMGNSRSLILFYLH
EVLGLRSVEWVHALVQQISKYPPLSVLLRKHAECLTAADLERRWTRIQWTSLEAEKSLPI
RITAPAPEPSRRGRPSSKRLAKATGGKKSGKEARDAFMNRLENRWKTLRERRELMRGVPS
LSRSTRQSTGQYPFGPGTASVSTARSMALENDSVPLSLVGHPWHSVRLTEADGKLTDYVL
FFIKDHTCCFNTKNHTITEPLHPILENPFTCRFPFANGFDCVLHSPVNPRTAYFFCGEQW
IEWDTYWQTCTGGPFKLQLHQQFAALPQEFFCKIDAAVPVPNTSYAFLFSQLMYILMDLE
QRRPVDTVKRIGDMTKSEKNLPTFNTTLARLFPYGPMTALLWSVEKEFECDKKNEWGGKR
KPPETGGELADVDKMSVMLIGREGRVVIVHSFAPSVSTMKSDEYQTLPSTSFSRLPQALQ
QMTTAALHGVCKHVLDAECNRCGVVLNNLEHGGHLAETITSTLTQKREKLMDLLFLTRQD
GTCNVTSLLCEEVVFVQTEESLLGYLPQVIEVDYGLTYPVAFGALVVVLDTTRLDYRVLR
VAPIRAVVESSDDGIVYVKHTCFVLAPYVTATCWGDAHAARFWRLRFITRLPVGTGVVRL
LWYEVLRVLEAIPLDPSVPLQPHHSIRVNITAPHILCKPTELLSYLAPGAVFASSSSEGW
LEKHCILPLLPDGVFCLFFCGKNFVELDLRSNIVVSHRTIPLASHPGFAHLPYPFLCGFD
AVFYPNLQTPSVVAIVHGKKIILWNLKLGSEELQSSPNDPNLFFKGLPWSMDQIEDIVQI
WDCPGEFFLIRSQQVLRWNIFTAEVVEGPMLLRNCPYLYHKEFDGKTILCVTSFPKEPRC
LYVFCEDRVAFQTVTDGIVSDRVGPICVSQMDLFSSMTWYLNWGKRRRSSVIHIDFMEEH
PLLVGMVIRSSEPCDEDWLIEYSDDGLDWKTVGHHLQSSGLSRTMWGLASVEFTSHRLWR
LTTDATQSYCVRNQPVFYMSVVFYTLPCTPYLQSAHKIALSGTLNGPISELFMKGKTTVA
FESLTEFANEHNPKTHHVTLEYGVLKSPNLMAFTCRCVEGWVNAVWGVWCSDDGSRWEQC
GLWRSRFGHFKASWKPRGPRRYWRIELQTWEPNVLFENFYLFEYSGPSIAVENSTPVGDG
WDPSILWEKNSAGSKVTPMTFLAHVGTALVFENKKDSAHVVGVRLVSHEKQSTSTTFVVE
CSLDAVEWRTLNVFLLLRNGSAQAAWESGDYYQFWRLRIVQHTGPSFLTLRDICFETFKP
TLYRVVEAKKLNTESPGFELFHFGAEPKEMVAVQVVLPPESVYIVEKLSPDGAAWEEVAI

IQNSDTTQSRTVRQGWVPRGSSSCWRLRPAVQNVEEGYVASSPSISTDMSAQWYSFSGKM
LVSSKLSDIPFVGVTTTGFLEVQAPGRLTENKTDTVVLRSIGQQKVMTVTWCFEKGITPL
FHQVFLRGRRFTDVIRSMSLSSLSQHKKSTHTMNSSTKASTRAGTNVLAGASEGEGNGNT
EGEAEEEMQKEEDGSCITIVVETSEDGVNFVPIAERPFSQLGNSLSWPTNVASSYWRIRF
KGIREDENLELRQVTWFQETGATTALAPPILCMASHSMYSKWQDAAFNYEEEFCQNCREG
FDQARSVLSGLREPDDIERHGRLAKGVIRLRARFMNFVAKTSKEATKERNPPLDKFVSIG
QTLSNDIMYLLYKATINYGCNVDELNQLVEHPMLLSRDFVRSADNNSWFYPKFYETGTLV
ESFYGFHNVRASLTVLWSLSVQLQKNTDLLFHPSMTPLSPHLASVIITINIERDNWIAAE
HFPELPLLYYAGFTERPMVIVFALNQVRFTSKYNLTIPGAACFPATFPFRILPGVNFLQR
MPLTACPFPLFDCLQMIYSKEFLGNYETEVVFTSPSMHSSTGLVCFTLPGEGINFSIPGL
KIESIEFEVQLNVERDIGEEGNTAVMEQTGAEDDFSKVTFFTHNSVFKGAAEDPPVQITL
LGAFHQTEDRIAVRGVSPSAHVPVLCRFPDAFITDLNISFDLVAGEAPQSFVEPFFTVAG
TLTTPTCGSYDCQFFQVRLNRGHESIALQVVSLQLAKFIHLGNYMVNSLSQVQNMDWLRN
VPVACSFNLKMCYSELRVFGTGTICILDFRGDAFAIISPDGVGITATLPTLRFGDILLKG
KSDKECVVVNIAAPASAPSVIRIDGYSSLLATQPYPTKIEITQEGVMCISTGVFYDVCIE
EESFFPSGAYAQVTISRGAIADCLSELLQETPMIVAFLATGIPFSLEVEEVVGEECLLER
KLLFLTVRGVLFGCRFDVMTSVLSPDNTIEEARRICQDLIPRIVEQCDESLWASYELLAG
CFLPLGSPERERAAEEGGKGAVDEESGKKDEEAALSPTGQPAPERNSLKAESGQFIGYWI
ECECEALDKEIQEDFETLACENPKWSFV*

>TCRU_4397 Arrestin (or S-antigen), N-terminal domain/Vacuolar protein sorting-associated protein 26, putative

MQAKVQNPLTVQLDRVGGTYFAGEEVTGCVVVNYATSSSFVDINLTVLGVVAIQFPYGEN
ASVFRRVGNIKPLKVMSLQIPLCRRGTQIPAGKTEVPFTFEIRASHPDVPLVQTYTGVHV
TCNYTIVAISTGIMSSDVSEVVPIYVIVPGQGQPPPHVLKEDTGVRFELNEESLEVLCDR
PTPSDRVNPNFLLEGCFDRYYNDIDIPLSGWIVVRRCSAKILSIELQMQRVEQAATPGKV
VREVTELQTIQIADGNVLRNLEIPIYMIFPRWYTCPSLKTPNIRVVFDANVLVKLQGHQL
LRKVVPIHLYSAS*

>TCRU_4398 pre-mRNA cleavage complex II Clp1-like, conserved

MARGIQHAHYELERSELNIHFKGSGCIVLVDGDATVYGAPLKRNVRYNFSRCGIPVVCSL
SCRVHVEGEFTAKISLMSSAIDDIHALLDLARADATIINDVPREFHDKGPRGPRVLVVGN
QNTGKSSLCRALANLATSDKKYGVALVDTDVGQQGIACPGSIATAFIEEYIPVDDGFNTM
MPLIFFFGDKTVTASSRKRYLDLCAFTSQAIASVCMSRPQYAIGGVIVNTMGWTTGIGRD
ILFELISVFSITHVVVCGSDEELAEELRRAAIGHSITLLRYPKQPRLFQRGRSQLCESRT
EQLLTYFKGTLRTPLSPYRGVAFVKDVYFLNALTLEVLSWQEVAPLSVAAVSWSDSLESV
DEANIAGFIVLLEIGKRFFSFLSPASGNLPKPFLLVSSTIKLPWSKVPPFTAPG*

>TCRU_4399 peptidyl-tRNA hydrolase PTH2, putative

MYTSEEAQTTGDVAGTVKHSLFGFFLGCIMVISVDLFLRRLGMSLRGGQIPPCSLERERQ
VLWGSKHQAALPQHTQVPSSTPRDGQEEEWSTEEEEEDTSDCSSEFERIEDLRLKMVLVI
RRDVKEVSPNEIFTLSAGAAVSLVQKVRCDAEHREWRSWYEWWRRVGCAKIALQSPDSRT
LRKVALAAEANGLPWYGATSLSSLLDEADAGEQMGVLVAVGPAPSALLDPITGKLKLLS*

>TCRU_4400 hypothetical protein, conserved

MGSFSLPVLQLRDKAELFPVLTLCNCISDAEESSNGARYSAQDKFTGCVYEVRCLPLKVS
GSKKEIERALGMQQQRLDALVAASQRRNMLPSVLLPIDAYVQELAASKEYFVISVSSFAG
LSLGDMIRSGYRLLEDADFKEILSCVEEYALESVRLPPHRNLTLNAILRQLALRPGTVEM
SHSSRWAIGDWLLFAENTASITHEELVRDLEWLLYSAFSKLNVSCEGNGDVLRKDIVEMR
ISETIERIKRGPMNGVRRDLIATFGDTHVKRQSDRRRSLVEGYAVPAAPVDGGDGANELV
DKVALHRQKLHQEQHILQSFRREKGKEGGSRVVLRHNEVEPDEVEVPRRRVKFMETLYPS
KILRSVTLETEESRRQFVGRKHAIIDVVTETLDICLQRDARNRKMEEEARHMRRDAILSM
LMRSATISSKRAKYPSVDTGSAPHGTPPSLHGTPRFKHYSPSATKGPIPLGDDSMYDPAT
VMHPSPSPRARRPDLQRRAVLPVLPSKRGESERISTPQRDLNGVNEDHLLSSTSSRRKEA
VLPIAKAIAGISTNENITGRTNKRMSSSRRSSVNSTNLTERPTFTGGSPLIKPPQSTRRR
QLSEMGNRRNVRSAPRRLAGNYSTPHVAVGNRAASATNVIRAPVTSHYPSETPSVSEPNW
RGEGDYRLPRRRSKIAADSGAVLRGHVRPVNETSLGITMRRRYAAPGEGIV*

>TCRU_4401 DNA replication licensing factor MCM6, putative

MNVVSLVGDADVPREEPPVVLEVDADGARVRDAMYVFLSRLVDPSLRSSASPPTDLRYIV
RQLERISTCVDWSTCVVRWGDFSHFDEDASTAIEFDYQRFAPFIDFALHQVLSQYYAEDY
ANRGKCSPSLVFSCVPRCLGIRAVRASMVGQLCSIKGVVTRTSQVRPELIVGVFRCNDCG
TESQPVLQPFHYTEPPACRDPQCENKSRFQLVPTHPQTRFGDWQKIRLQEDTNNIPAGCV
PRTMELIARNDGVEVAKPGDRIIAVGCPIVVPEVAKLLGQAHRREVQREMSGVQRAQQEA
QQEMEGATGLRALGVRELKYRMCFLATTITDVNGDDRKMTEAVKDSTDGAAEREYVRLTP
AELEKVRLMRGHDNLLKALTDCVAPNIFKHDVVKLGLLLQMVGGVSKSTLEQIGLRGDIN
VCIVGDPSTAKSQFLKWVASNVSRGVYTSGKASTASGLTATVTRDADTGDRTIEAGALML
SDRGVCCIDEFDKMDVKDQVAIHEAMEQQTISIAKAGIKATLSARTSLLAAMNPIGGKYD
RRKPLQKNVAMTAPIMSRFDLMFVIVDESSDDADYAIADQLLRLHRFGDRAVRPPFSTDD
FQLYLRYTRSLTPRLKEESVQLIVAAYRDMRLQDSLSNRSKVYRVTTRLLESIIRLSEAV
AKLYMSEDVKPAHVEVALELMRQSLSTLDMTEVELVGISDPFEVASEGVKAEPLDQQQRQ
QEQQQQDVPQATAGEQSMTARRKRGKAAAVVSAPAPAPRKTVISADHYFGIVNRIVARL
QSLGESNPPSRAELVTWYMEQVRSLNKSQLEVELRYVNLVIQKMLKDGNLLEVEVHEGEG
EKMFIDPNYNPDVTKQ*
>TCRU_4402 WW domain containing protein, putative
MIYSQKTQDDSEVVVPAAGETFVAEDGTVSVVLADTVDDDYEPTQDEIEDFAEWMGMQLP
EDKEFLYIAREGLKAPLPKNWRPCRTNEDDIYYFNFRTGESTWNHPMDDFFRQKFLKMKE
EKKSSTVTTPVVTKHAAVPTTTTGGVPTLGSSGGGGGPVSILKKSPSDLIGGMPGTATHA
FVPALGASRSMVGSSTTSVRDRVAVDTLKPGTTAVTSFQSGGERRIVSEAEKNLEEKLRL
EREASFKADEEKAEIAHEARLQEMLRTHAAEVEKLQKELEARRAAIESQAVVDEWGPTGK
EREALEKRWRTNIDQALKDEEELQRQLLELRERHGQRLSSEVARVEATVREQHQREEKQM
EGESLASLKRLEDEVSAEFLKKKAELQQKSLADVQRLKEAAEKHHRTEVAAMRENHADRE
KKVTECGKKIASIRAKEREAIAAIELKSKNEQAAFRASMEAKLGRMREEMLCEVEGAFPV
TLGNAYTPPVDDALDAVRQRWQVEERKCMHTLEEERRKKLSSIERPQSLSSSSSKTSSTS
SLPTTASSTTVCAGEAGEELRAANDVVLAEKEKSLQETEKLLRAMLEEELLHKDAPAEVQ
IAEALKHDLNIFVRSTELCRQLEREDIERRGQAALAEHKRARELYEKKVVEQRAKMEAES
RAVMEEMMREVEQREVENALQAMTMEREFAERKLQKRYEDERRLLLAEVDQEASAYERKQ
RGDIVAQEEARLKQREAKMHAAEATEAPAEVRQSGQQPASAPTTSTLGVPLGFLHQRLEF
VEKTYAEKEEKLQAELNSIHADMRRLRGTCTPQGLRPPPGQADGNSMPDVCFTPALAFNK
KETKHSSLFASEALRFLSEQQRELSARRGALSAAREEWKNNFLNASTCARSFLPSGKPFP
KLTEGDAVNSKLLTLVGVLSERLEDLTGCIAKIQTTTGSATPQRHEEQLRPRSDRLHARE
KIAANKTHTGSNQRKGRIPREPHSHGSPARQQDAVGLLQKWSHVLLEFATPSLDQDELTT
SIQRFVVDQ*
>TCRU_4403 conserved protein
MLEARGAVAKEGDTVLLVRGHLNLTPLMLRPGDLLHCKEGKFRHDDIIGRPLGTWVTGQS
NIKGDTSRPPRLLVLQNSADLWTQAVPHRTQIIYDTDIAVIIFNLRLGPGCRVAEAGTGS
GSLTHSIARTVAPNGTVYTFDFHKGRCLEARQEFRRNGLPASLVTCNWRDVCSKSLESDV
SAGVEDEIGEGTDPKHGFGLSRHHVDAVFLDVPAPWLAIENVLHILRPGGMLCAFSPCIE
QSQRTAQRLREEPFEFVDIRTVEALTKYFKPSFKRDREEDGRPSRPKLRPTLVSKGHSAY
LTFARRRLERIPGLDDEDEERNDVSPRSGEEENAAS*
>TCRU_4404 dolichyl-lipid chaperone, putative
MDFKGQLASALVLNVTLKLLSFTLSTLLTRQLAPNENGTNFSNQLYFNTVLFLARDCVRS
VNARHDVRERAEDGRLVLQVMNCAMASLPLGVLVMVVLELLPFCGIHVFPSLAALSRVGD
IATALGEVNNHTVGFPEVLLALSVGVLLMVEPCIALVLCFDYSRFIITSEFWALLARLIT
CLIFVKLCGGLGGDLYTARLCFATGSLTYAIATMMYFLWLWNSNCSPEDRKDKKGEGDDL
LQRARRGAIAARWGVACLTSSSISPSLRLRVSLPWCFLSLRLAGAEVAKETLLLRQFLSE
SCLRLVLTEGERFALATFGSATVMGQYDLIANLGSIMTRLVFRVWENACFVKWSRDAAGG
KPEEAINLLFTMLRVASYFGAAVVLLAPPVAEGFLLRLFSSRWASPVMVQALQLYCYLLP
LLAWFGLLDAFVRATASASMLQLTQRVMLAQAAVYGVACYVVLHLRWLVVEPVPGLIVVN
IISMALRCVTCVCLLVAGPAMTTPRKGHGSSQPLLRLGAFKAVFNRRIVLAWAALFVCTR
CTPWGFLSAFTAAPLFAWAVVKWDTELRQVAWNALRR*
>TCRU_4405 2-oxoglutarate dehydrogenase E2 component, putative
MLRRFSALGLQPRRWGLQKLSARFCLSINVPTIAESISSGKVVGWTKKVGDAVSEDEVIC

QIESDKLNVDVRAPTNGVITKINFEEGAVVEVGAELSTMKAGEAGGAAAAPAMQPPPPPP
QQQQQSSPPPPQQKRSVETPAPAPKPPQVVTTATTGSDPRVRNVRISSMRHRIADRLKAS
QNTCAMLTTFNEIDMTPLIEIRNRYKDDFYKKHNVKLGFMSPFVKACAIALQDVPAVNAS
FGTDFIEYHDFVDISIAVSTPRGLVVPVLRDVQKADFAQIERQIADFGARARVNKLTLAE
MTGGTFTISNGGVFGSWMGTPIINPPQSAILGMHATKKKPWVVGNEIKIRDIMAVALTYD
HRLIDGSDAVTFLVKVKNLIEDPARMVLDLA*
>TCRU_4406 Vacuolar proton pump subunit B, putative
MGVHEAEEVRMLSKQELLAEHIKAIQSGYSVKPHLEYTTIRAVNGPLVILGDVRLPTFAE
IVNIELADGTLRRGQVLEVDGDKAVVQVFEGTSGIDVMRSKCEFTGKVMELGVSEDMLGR
VFNGSGIPIDNGPPVLPEQYRDIQGIPINPRARVYPEEMIQTGISSIDVMTSISRGQKIP
LFSGAGLPHNEIAAQIVRQAGLVRKEGKQEDFCIVFAAMGVNQETARFFRTEFEENGSME
KTVLFMNLANDPTIERIVTPRLALTTAEYLAYDCGKHVLVILTDMSSYADALREVSAARE
EVPGRRGFPGYMYTDLACIYERAGRVLGRAGSITQIPILTMPNDDITHPIPDLTGYITEG
QIYVDRQLHNRQLYPPINILPSLSRLMKNAIGEGMTRKDHGGVSNQMYAAYAISRDILAM
KAVVGEEALSSEDLLHLEFLEKFEKKFICQGFYESRDVFQSLDLCWQLLRTFPKVLLNKI
DVKTRNEFYDRQPERK*
>TCRU_4407 nucleotidyl transferase, putative
MQFKTTVASPSLAASHLFDVVVFAGGTADSLSPLCNNEPKPMLCICNRPMIWYCLYPWYA
AGCRTFFVSVNEDYAALQSYLRREFSDVEFVFVLVPFTQNEAPSTTCDVVKAYLKHKESL
LPNKLGHARDALLLSCDTLLPGLDPEPFIRNFYCSVASVSVLLFRPLKGTRSSTATEASS
SGGAKTNKGHGAGFPVKPYAYRYTCTAYEETDEDDNGASTTNLGEDGEAVGDTKGACSYR
LHFMCPYEERQELRISMGFAGRRPNLTFTSDTMDAHAYLVRHWALNAIAESAGKGMSVQR
DSIPFLARSQHSIVNENKMTFLRPDGKIKYNIPKHWLLESDSSVNFLNASPGPVLPSEAD
NLLVCCTIYEERPEKCMRVYRVRTREDYIAVNQEILAAKCQLLEMNEVNGRNSMRISSRS
TRASQQKERLGQTQRVLRTSMERKSINTAADSAGLPFSAFALSGLVSNAAFTIHKTDASR
QINIIHSFLRTEPTCKATIARSIVGNNVTLGPDVRITNSIILDNAEIGAGAIISNSVIGS
SAMVNSGVRVVSCTVGPQCLVESNETDRVIRA*
>TCRU_4408 Putative serine esterase (DUF676), putative
MKHRLVVLQHGSHGTHRDLGCLARFLRALDSPPIVLEPQVNEGFRTDDGVVVCGARLAKE
VVRFLSGLCSGESLGPATHMTPLVDGKKTVQLSFISHSMGGLIVREALPQLVREVQRHEG
CLRVEWKVFCSIATPHGGTRHMDAFIRSYVGRLIGRVYSTAYHDMFLQSNVLTERLISAE
HLASLGLFEHRLLISSMHDLLVPLMSSGFMLKPSQFCGMSPAAREEREMAMCASSEEEMH
SKRHRIVKLTSEDWPHDHYPVERRIAEAMLEGAGAFDSILVDFSHVQKHCDDPHTRRTAE
QLSHRALVCKEPICQMGLEEVFCFVSRWVANVLAACHC*
>TCRU_4409 FG-GAP repeat protein, putative
MPWLSALLSVIAGLLLSTAQAPVVEAKWTSNTAAYLGDAPIFFRVTATADWDNEMKTGLL
GTWANRSNLLWYCRGNADEHVTGGKDGALYKLCWSSVDFPGPIVSTIFADFNRDGKLDFL
VQCEDGVLYFVNGRHRDDPPTAIPSENVPRFFASTPQMSLVTVFSRCGLPEIALVDVTGS
LVIMQATTQTTLGDHCTGQDVVPTFNPFVLVEGVKGVREVVPLSIISDDMDGDCIVDLLY
TVHEINSDTLHVYAFFPERSKHVLLLTLKPARRYGFPTVADVNGDGAPDIVFPLCVSQKT
SVSFGECTLFDGWIVFYNNLQGSPPCADGGCCNGHPFGFSENASKEFYFHEKNDCGINTS
LQISLAMTSSLASPLLLRTGDYNRDGYMDLLVPSTYGPLLLMAEANSNGISFSCGPLDRD
RASRSADGDPTYTKAVPFFAIIAGDAALDIVLTFHGASAIPLGFYMNHLLSWKQNYFLGS
SALNGAAASHDWGVYQPGAVHRFGWSDFNMRQRWAYATQLSRTQGHALQPSRVLFGLGRT
FSYIQGYAVGIVVNQQGAHHAWSANLVPNSNVFLWLSPLLSQESWRLRLYLVFSTYKRLL
ILVLVTSLALIAIPIIFLKWREVQHDCREWKLR*
>TCRU_4410 MRP protein, putative
MNFSRVAIPGVKQTITLCSAKGGVGKSTCSVNVALALKNMGFSVGIVDADITGPSIPTMM
SVDASQVETYRVAGSDRFAPPTNFGVKVMSMGLVVPYDEAIAVRGPMVNKYIRALLFQTD
WDELDYLVIDMPPGTNDVHLTLTQEVVLTGAVILSTPQRVALVDVRRGIDMFAAVNTPIL
GIVENMSYFACGQCGTRHNLFGTGGVKATAEELGVPFLGEIPFLPRIMQDTDAGYPPALR
GDGTMKAAEPFYKLAERINDAVVALKTNKANKLRGAGPSIQFDG*
>TCRU_4411 hypothetical protein, conserved
MLQSPAKPQPLEEELLKENIGAGVLSSAASTATTVSSDFAQEAATGSGDTMRGNGSPQTP

EVGASSGEDGEMAGGTDGQKREAIHPHNGEVNATALNSSLGNLLQGNNSEGAKKACL*
>TCRU_of Trypanosoma cruzi C-terminus, putative Dispersed gene family protein.1
MVLLLTIVLVAVTVYGVVVWYVEDHHWQELREPRRGVLEALLRDDEENDEETQKLHDMTS
QSYASGTTAASSYRPPAPPLQSVTGDTRSDSLNLFDGASSASRMIDYAAQ*
>TCRU_4413 Protein of unknown function (DUF3682), putative
MMLLQQRTIRIQVGLSTLVALVKEAVLALEAVVEVLLLVLALLMLVEAVEAVLVELLLEV
KAPTAFLLLLLLLEVQGILLLQEVLALEAVLFLEEAVELLLEVMSPVAAFLLVHLKVLQI
LLVLLLLILLPAAVVVQRDPQEVINLTRRENLQQEIGRLQQRLTTPRHPKDRQGRHPALD
TKDRKKKKKKKMKSSSKVMKHKSNNTNSMNTPRNTVPLRSVLPMTAIEASSGKDTSLATQ
NNSNSSETFNAGGSAAAPAVVTGSAGPGAPASGSGGGGGGSSGGTSAGGQGTGSVPPAAA
PTGGPGASVGAGGSGAGGGSVSGGSIGTSTDDHVTGGVSSGPSDAPDPPSGPPGAGAPAA
GSGDGEAGSSGSNSSNTTGESQTGVQTPAAAAAHNSSPPEGPTGTTSGNAHTRKEEEEEE
EENEKQQQSDEAQDQQHQQHEHPAESGEESAKDKNALRTNATANTGDSDSSTAVSHATSP
LLPLLVVACAAAAAVVAA*
>TCRU_4414 hypothetical protein, conserved
MSCPTDCDNAASWCYEVFYRGGIVSSGECGEYSFECTCNNASAIVVMRSKGVCAWEGSFD
TGEPEGNYCFKYTALCPTNCSNIGLWASQCANDVVCEESKNEYHFNCTTCEGRAYSIVGN
GTSCKKQFSSKNHNCDPLITCNGHGCCRKPDDPLNESPCICFKDSQRGYWAPPTCATCDD
DYDPSRGNCTRPRPGIQKILSSIGTTWTMVLPNLAILFLFVVFGVTRAEFESDRRFQSAA
LRKTGLSAVQVARRQQRGLFRSKYIPKRPAQSRCFLNEGETQTQRRGAPAY*
>TCRU_4415 cytochrome oxidase assembly protein, putative
MLRFRPRVFQTNTTRLHWAFLFKRRLQSTVSGFREASWIAPPANKAVAHWLYCSAALVGG
VVVIGGITRLTESGLSIVDWKPVTGVRPPITHKEWEEEFTRYQNFPEFKQKDKMTLDEFK
FIFFWEWAHRVLARSIGLVYGLPMMYFFWKGRFKGQKALTGSIIAILALGGAQGAMGWYM
VRSGLDPRLLEEKRKATVSAYRLAAHLVLAFTIYASMMRIGFGLKLPRPVHFQGNTTVQS
FARLSFAVVFCTVVSGAFVAGLDAGLMYNNEFPWMGGGVVPPRDHLLVVEPWWRNALENP
AAAQTWHRLMAAVSTISILGLNAACVLHSAALPKMLRRSMISVNGVLALQVGLGIWTVIS
YVDIPIATAHQLGSLLLLTTIIRVCAVLGSRGLCLA*
>TCRU_4416 paraflagellar rod component, putative
MPPKGRRKKNAPPPLVAPEPAGDELEVDILWDCVKEVDDKPSFMDGTLLEATRACFEGEK
GQKGTGEAARTAFFGRTRHLLAPRACPQFLASEKELRKTMEKAKNIQEDVSEFELLKENE
REEAQRKRERVTMTARNLMTELSDARLTFLEDMEEIAEGFFSDQKQMLETLCNLAVKDNE
VEAAFLEQQTMQQLYRDVEEKYFRDHGEHVVLIAEMQSETSQQQEEMLQLMLHRLDKGVV
EMTKLSVEELEDKASAQEEMSRLIVELLRVQGQSVVLEKETTSIAEEMAVMQRMIALELQ
KQQFCLRRQKQLREDLQSLSARVRENEMRLIAMMSNQTPSAAYTATLPMVPVSPNTITSL
TETEGKKSVALLSIELQRHLEASSAELANYKDELCALRRQHLVQLSGQYQSFNLNNSFFG
TTKEFFLDADTKAAVRSIVVEALMQVNHILGVIDDTAKVPGNLERLLSVVDLRDQKFIQN
YVANRINTLFSRICPTAPPLLFLREAANVQSEI*
>TCRU_4417 hypothetical protein, conserved
MTELGDVLTCRLVVEDERMRRQREAFEEQRQWLLSKLVSVSHDDGGGDDERAGTRPEKRH
EKRPLRSRSSRCTVGVPVEERLLEYGRQRDERVERARRIRQEEAEMAEAKLLERAEPRMQ
RGTRAISSSTSETLTRRRAQRYERLMEESTAELNFHPRISIESARLARERRVKENIADLS
VQEALLRRKAMADEQLERKRNEMHAIRAAPMITKKAKKLLLPYTAVERLYLHAKEKQSEE
RDTRERLQEVIEENTEFPFHPSISERAEKLHRRPGRHAYEDLYEHGLQQQQQRRLVTSEE
GAEFHPNINRVSELIAARMNESTTERLLKPRQANREETAPRKLLLCRKDLDRRFDQLYMD
GGKRAARRRSFSEGERELGPECTFAPKINGSRTSADGVSGLPLDVRMHLWQERKKQRLML
IRREAEKMEEEEAVAAMPIAFRHGTQSLMERSSTCRPMSVLNGSTTLAQESHSAKSGIKA
PTSVGSMADEETILKALQALENAERVSQYIMRD*
>TCRU_4418 hypothetical protein, conserved
MSDSQTAAFTAPRNAVVDSDACSMQAALSPSSLGGGGEAHTGAFEERPARAFTAARLPTV
RHRPANSKALVPRLSSPERLRMKTCRLQQELQALRLRHESRHERLQTIRARRSVSQSSLF
RGSSQCSGDTNSTVQPSIILTDRSYSQRRRDGGPSLPNLLKCFEEARMKYLLEGERKKKV
MPPIYSSQIPRNSEAARQQQQKQQQDIMKNPDAFGRRFFTRSYSNEAQW*

>TCRU_4419 hypothetical protein, conserved
MNLEIGQLRERNARLREENSKLRVRLNQERQHVASEGMDGGHRELEVGLCKDLIREKEKQ
ATILALHDELTRLNRQCAVYADALEEARGNFVEVKRLYGELNNLLDHFNGPKHP*
>TCRU_4420 calpain-like protein, putative
MSVEALTCVENALLLEQQGKLREAEEWFTLAIHRLRGALQDKSLGNSQSLVLTEHLHDAA
RRLQQIRSVMRAEEERQRQRQQEQPKPGPQDSRRQMPSTPPPVREQKRAEVVPAVRPPSV
PVHAATPKRQQQQRQQQQQRRSDYSLAWASPSRASDTVKKAIDIATTLLQQKKYKQSVDV
LQHAYDVGNKERNKPGNFHRIEEYLVLLRREYYNHFKPRFLQDNPVLPAEMDVLRRSGIT
NTIQLPMWDDVQEGYARENVFMPCEGHWEDPFTPRLSTSQRAEGAKYLRIGEIKPNADLC
IIRSADPLNVKQTVVGDCSMVCSLIICASYQQRFPKGKIISNVIYPQDNNGDPIVNPKGK
YCVKMLINGMTRLIAIDDRFPAAPRTGRLLCTYSKDETELWVSIMEKAFVKLCGGSYEFP
GSSSSSDLYKLSGWLPDSVSFESKEFDPELQWKRLYTRHVNGSVLITASTGTLSEEEEKR
LKLAASHAYAVLMIREVDGERLLQLKNPWSRQSWSGMYSFDDRREKSRALLAQLQYTEAL
ADQGVFWITWKDLCAHFSRCSLSWNPYMLYKMPDGMSQRPTRLSCHRRFLYTMSTGQAPQ
FHIGVINAPRPSRMHLVFARHTSNVESFGVQFVKDDPKVPYVAVKVYDVTQFPSIAQHLG
ASCSFETCYCRRLAHGTELEAGFTPLHDVSYKNMAEHTLSFNCPAGTSNLLVVLSRIEST
VKEEFSFSLTLHTEWPQIKLNGEKRSPSGVYMHFIPQSQLKHCTVRQGKWEKGVSCGGRT
SLQTFAYNPQYLLTLSKPSMLSVRLNVPECEVSAQVHLVRKEQNPAREQVKWSSRVSALN
EECVFFLHAPLYAHGGVVVDTSLWRCVTFDPRRLLGERRKEKEKAVAEPPSPLPAGEYTI
VPALWDKGVPAVFELVVETTEPHELREIPPEGVGFVETTLQGNLMGGATAGLSMLLLPRT
DAYFSSNCKACLVATNPCVLTARLLLLLADDTKNDVSTNLSLFCSKDAATMERIASSGPY
ELCGVALPPVKLDANVTYVLVMSSAKPSHAKYALRLYSSTAIRAWLQ*
>TCRU_4421 hypothetical protein, conserved
MQAQLYVNGRAGLLSPAGIRTYRQMGVVVARGLLSDDLVATLARVCRDVVQTRGARVFPG
IDDEHNGRIEFDARMEPKPTANLGAQTPPPEIQEQLRRQDEAQALERRYRKVLLKCRNTR
EVDRVYAKLAAVRERYMKFKYVKNCVAEEEERSGRMSDERIQELGSKHTYEDVKKSFERY
RDSGKMEMEVRHEYHLDRALEHLQNWSKCWCRVWPDSLELRRLLLPGGGALGAIVGEAAA
ALTGEIVIRLFDDAVHDYHPFLNSTPFHFVGNSTNFRSLSGMTVSVGLAPRATPMLVIPG
SHHVMREFTHDGSDFSHYRTGGVFDMGRAIRKIEPLRTLPVVQLEPLEPGSVMFMNHYTI
TAVQATMCGVAADYIPPSARTVNCPYQYSMNLMPDHCVFDGLRNSWASRDSHGPLHGYEP
GQPLDDDAVFPVIHRALDVE*
>TCRU_4422 Pab1p-dependent poly(A) ribonuclease subunit, putative
MDSKGRSGKSNLLGRGNVLMSGASANSNQHPYGRRHVNSAGGVLTNAFVASPASLYSTPQ
PLDPFCQHLPDAFPSTPYTPVGQLFMSASVRSARPNASLLMHSTTRSITPVTSSKFSHYT
TIYNIENMPAPSVMNSKLMTQMYQTTARYTGKEIALRRLVMTTATAEECSAVNERFRHYR
HPNLVPLTGVILTDEFVMGSKDVIMEYKFISGAKSLHEEFFLSGRATEGLLWSFACQMVG
LLRAFHETSVPLRGLHWSKILYVSVTGRFYFSGIGLVDLQEPKNSNPSIAVMMKQDIQAL
GIMLFQLSTRNLAARVDDTLNQPMPGFSKTFWTLVKACLEGAPDIRDLCCALGERMSMEV
AHQEGHADYLVTQCAKEIHNGRLMRLMVKLNFVLESLNDVPEHSTEAHNRYALRLFSQYV
FNQVDENHRIRLDWGHVFHSLNKLDCGSEELVQLIGNDDGNTILVISYHDLRASLESAFE
QLQLSASEADIQSFSVTVGTTPTTL*
>TCRU_4423 U6 snRNA-associated Sm-like protein LSm4p
MSTKKSVIPLDVLRNCRGKVVSVELANGETINGTVMRVDRLMNLLLKQCIRTGAEGDVFW
KSRESLIRGASVRNVRMDERALVMPEARAAVRNKSRPDTKKQATGGKKRGRGD*
>TCRU_4424 Concanavalin A-like lectin/glucanases superfamily,
putative
MVSVLLTEQLKRVKEVLTTWKEVDKHVSKLCPSESAKKDTSTDTACSTDKITAGLVGFLS
GNFSNDTWKDEYLGVNAKVKGAAELATEATLHADGVTFTGRGAWAEWPVGEQGENQLYHF
ANHNFTLVATVSIHGEPKEGDTPIPLMGAKMDDDGKTVLLGLSYNNNEKKWILLCGGGEN
KDHSSTLELETQYQVAIVLRNGTQGSAYVDGQRVGGNVQIDLKDIEGSKGISHFYI*
>TCRU_4425 hypothetical protein, conserved
MNGCVCYFGRTVCRPSPAFASCAEEGVSLGGKVAVRAWPSSRRVSSLAARVHCDSIFGVV
TLPPSERLCRARHCPPACRSKGIHGVLWSLVPAPVLFWSVRVRVNGMLFQLSFGQLIHRA
CAGTGRMPSDRHIPGNASYLSGELLLVEVPKMNYDPGLRFVRRRA*

>TCRU_4426 Ankyrin repeats (3 copies), putative
MPPKMRRWVLEDPNNTWNHQLMQASLRYSLTDAEALLQNGADPVGACEAVPFYKEPLPPL
IALLLQGRYTAESVAMMKWLLEHGASVSQFIPLEGKDLQTSPGENGTILHLFVQLGQPAF
LLDLLILVGEPRPVPGSIQKRLPRPDRPITPGMSTFTVGTGAKGSATRGTQGSSSGNSGK
RGARLSRMTTDAAALLASNNFVDPAFHLTGNVIDFEARTSVNGWTAMDLALRCGDATMVQ
LLLYYGAPGVFHRLVNGSQTALARACTTGDKELVELLLDAGDAIGQISLDGRYTLIHYAA
GQPAILDVLLARGLSIDAVNALGETALVSLICYGQGNNGEHAIRETPRSSDAAKLAALPT
PALLNYILTPMPPIAAPPIKQVRSASSTSAGIGMDMDFPRMTHEADAWWYFASNCSTWTM
IQNLCDRGADVHGDAPEEEEERLEERSVNNRCKGSGVGRQLYLNPSSSSSQLPSEQSGSS
TNVRFNNSLAGMSAMEIHAEGQMNEKDMTVPGMQFVTHLTPLMHAIVAYHPELIRRLVVE
FHADPMVRDAKGACALHYAAIARNPSVMELFLSPLVIPGHANFDINAQDCLGRTPLHYAA
ACGNSGVVRALLKSSSSLIAGRMDYAGRTPLHLAVLAGEANVVELLLRYGETVATETQST
VSAVSTRKKSVITKRKARQPSINEVNVPDHATVIDVEAEDRLASQTALEMAVYVTRDAEI
ARLLLTLGYASARRPSGLPTGGSLLHRAVVDGTMDILLLLLENYADPNELDNLEQTTLHL
ATQSNLPQACEMVRELLRFGATPEARSGCTLETPILIAARRGDAGMLDLLLHQQEEFSSG
RPLLFHGAKGAQRERMRHSSRSRPNASSPSNRRNGRQQQKQAPTTQSSVRRGRQKQQQPT
VGNTSLSSDLNDNSILGVAANNSNSNINPIGGTDLRGRHSTTPILVPGSTTAEVGESFSG
NIESEGQKIQLLKPQHLLLTDGRVRTTLHYLCAHNEASKQAVLLPIIQEILGCSIAPTLV
LQLDADGRLPLHDACSAGYAAAVFELLKCDDGSCAFQLDSRGCLPLHYAVLANDAASITA
LVQSVGVWLPCTLKGSTCAMDDDRLFPITDRILQQGPHFKNHHEQGDIQMPSQQYPHRHG
VNPLSGVARCNKWINTPWEYLNVPDDMGRTPMLLAAELGHLKASKALMQWMQVCSK*
>TCRU_4427 kinesin, putative
MGKAEGIRIFLRIRPAAGDGLSRPPFNNSGGGVEQGTYAVDHTFDLSTVHFHVDRRLETD
VVNNTREDYRFTFRRAFEPSATQEEVFNVVAKDCVLAALDGYNSTIFAYGQTGSGKTYSI
TGGAESYEDRGIIPRALALIYDEVARRQRECTWSIAVSYLQIYNDKGQDLLNHGRDARRL
EDLPTVTIHDGDEEEMLLKGLAQHGAPNVQEALNLLFLGDTNRLYCETPMNKTSSRSHCV
FTIYLEARAHGSSVVRRSKLNLVDLAGSERVAKSGVSGTVLTEAKHINLSLHYLEQVIMA
LSEQASGRREHVPFRNSFMTMVLRDSLGGNCRTSMLATAHPATEHLPETISTCRFAQRVA
MIRQDAHINEEVDPQLLVRKLKVELQQLRDQLAFYTKDGGGAPDRELSDDERQRCQEMVR
RYVLETSNDGRIEGFEGDLARIYYCFDVMKRMLTTGGHTAGHRSGLTDGGGGSFSESAGA
PPSQQQKQQEEEEEQKRLDVYRARIDALELSLQQKENEMNMLFGVLQKAQRAQFNAETQT
GPTANTSYSLSGNNANTFSNNTSTTNRDSHTSAMLQEGNLFSSPIPQQVLENGIHGAVGL
HRRVLHDRLDAAQATAVDEFFRKQAQLNEVYDLSALTDADLLKDRATAFEAFHRSYRHCA
EMEGNKRELKQRYDTCKATARQLNDAVDRIKHLKANIQRLRAERALQGVEEVDDAERALL
EELTATKAAYNDFATSLRRQKEEIDAMHLFMKRSQEQLTRDFEEWLQIRQQQLAMVRNGD
GNGIPKNGSTKLMTTTSASTPISSSSPASQNLLKHSNSMPIQSSQQQQQQQSLRLVMSLS
NVPSELPPLREEVMSSARGWTGGNWPPTNRATGNNGEANNGGSASPLLAAVSMDLLQPHP
VTAPPSVRPERASPPIPTRRVPLNPLASPSRAPLGTNSWTGRDAFTSSSSSILGQSGSNN
EVPNPYAPEHRSTGDAAADKQLAALYRARDSMRQEFKF*
>TCRU_4428 ATP-dependent DEAD/H RNA helicase, putative
MGDGNTANRVPRLFDGPTGDVNTAFTHKVRQLLLSSSSCGTSSLPAAVRASPLYAAILCF
AEAGTESRQQQQEQQRSGSEAGKPSVGSAPVVPSSLARRGVVPRDPLLQRRMRKQQQQQP
SSSLLLSGTSKAAPSSKTAVDGHEPQVQQRQLFHWSRRPLQEMTSAGWEVFREQMGILME
IVSRRAVGQPEKQQQPRPPRYTADALRPIRCWEEARLPLALGTIVSRRYALPTPIQAQCV
PLVMATAATPSDKIDVLGVAETGSGKTAAYLIPLFADILRRTPRLLGNEALISHGPLALV
MVPTRELAEQVTREAIEIIHGIPEMELRRLIQEEYKNDPGNDNVAAQHNTLDEIRVVKVV
GGEQMEAQYDELSKGAHVVVGTLGQLDALLQQRFLALGNTRLVVMDEADRMIEEHQRETL
VSVLERCPMPRQTVMFTATLSEACEEVALKYFSPDGFIVVRVPHRCSTITQVFEMLPSDA
GAMAPASATVAARSDVNNHDTSQQRSNQPQVERRRHPLLHPMKFARIVTYLAYATAPVVV
FANEKRTCDVLYDELRAEANHLATLEESFSLEALVGESPPVLQGTLPDNNKHRRRPVLNL
ANMRSIALVHSEQSQAERRRLVELFRRGERRVLITTDLLSRGLDVPNVTLVINYDMPRVD
KVGPSMAAASASAGEEAVQKYIHRIGRTGRAGASGVAVSLLCLPSSLIQRAEQHTLRSAD
DRSHAGNAAEKPPKQRIDMAGVSTKTRVQERDRQELTGAKNGEDLDENLLKFNDTDDAMD
NNAEDEDEESDAPPRSRRRMERQQQRGDGGGGGGPPPSFPHDEPLLQPLWAFIVSCAEAN

GGGVRGAELIRQQRCRLVQMSPALAALMMAFTRSSPYGAIMT*
>TCRU_4429 hypothetical protein, conserved
MSTGRAATGVAGRTIKRKVQSNRDAPYNTRLFNTLWTYRSGQLTTSNVRRLKETGIPIDY
GSNGNSNKYDEPGDAPVKSDLQPHAMHKFTGDENWSLLIAVPKNSEHFHNILECSRGSLM
VGHTEPQLFHWFKQLGTLPPRAILSGPLELLSGDMQHEAWEKTFSRHPVIHSIAQDMWTR
KDSKTEEEVVTIERREREEDEKRMRRMSSSDWRAKFRDRERNPTAEEDEERPIYVIKPET
FALLRLQPDVKLWMNVVSQTQRVWEPVIPDPDPLCRCAPRFLRMLNLARQKLVPSLNMNF
ALKLTNAFIFEVDKEGLWAMGTQENLHGSCSPADGAVREEWTELRLEFGKGQVIQTEQEM
EWWVRGLTKLGAPEMSQSNSQVEDAGMNPEDYDYRHI*
>TCRU_4430 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSVCVTATGEEPDNDSSNLPRALPQEAGVPEATKTSVTSSLV
GMTVTLPGTHNSDDKGQASETRSDTAIGTGGVPDTSGIPVPTVTVGSNVQGAGGPATLEN
DAEKPHGTSGLQSVADLAKTVQEQAQITGPGGTGSRSTSSKENTGSGSKTSQGLSSGNGT
AQNPGEKEAVGSNKPDGKEPNLGTTTDTGKGKGTGSPPSASPDSTSPEPITEQQPSGSAN
PVQQVQKANAPTTTSTTTTTTTQAPSTTTTEAPAVSTTRAPSRLREIDGSLSSSTWVCAP
LVLAASALAYTTLG*
>TCRU_4431 hypothetical protein, conserved
MLLPRTDSHDPDTKDADPRSTSSAPSVSAPALSFTTTADALASTPLPNTNPCAAYTWLPD
TRSTAPPDATTRALAYNAYSPPNTAASSATPPPTSSSTAPSTTTVHPPVTTVTRATPDTT
STDRTSRRPDSTSTGAYGEDCEPGRYTSGVGLAATSRESVTVSTDPAGNVPLSTSAPFSA
STSHTDSSTGPLSSLPAAPAPRNVPPPITYSTAPFSSDTFCTTIRTPSRAIHGT*
>TCRU_4432 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGGRCDEEEDTALVVGPPGGLSNDGKGGPGPAPSSLPGT
GTSGPRSILPESEGSQERIAVKSPEGSGEKKNQNEDGVEESVAEDGENSKNQERLSEQST
QQEVSDEETPDEKRLEEEKEKDVHPPGEEEMKGTQQSQSQQPPPQQSQVQITAPAERGGP
TAATGPARPPPPAEPSSMDGSRTTEPTDSRNPSQESHDKSQLQTKTESRAPDPPLKDDFP
EQHGQETTTPASMLNASAGSQARITAPSTSTGGSGEAQIKVDEDDAQRPNPNESHDNSDA
GKTKGPTTLSEATTQATETVAATQTNRTKTIGDSDGSTAISHTTSPLLLLLVACAAAAVV
AA*
>TCRU_4433 hypothetical protein, conserved
MWSGVWRYTYGVGEYNLRPYEVRGRAWGRRFNKAGAIVIDYYYNCGKQKEKTTPPQLLMF
PHTPEHQMHRRFKNPSLPGFRDISALHGKRIFREIQYHLGQGLRFYLVDGVFGSHPETQT
PYRIITDNPTHAYFASLAAIRKFNYVAQQEIMLSKRITQSPIDEWGWRRPGVLVYHAPGW
DFESPRIVEEFGGPRPKDLGLEHPKFIALEPYSIPMKAAIAAEPSCDLLLDVTAFLCARW
GFYADDKGFLTVAAESILSPDAKKLTLVVCGSELEADILRASPYIFGARHHRIAEGWVSR
AWDVVSAKKDKVDVGEHDLVEKSLGRIQKPLSGRIGLYKARSHRHYGRRHVSGFGYKLPH
IYTDDAATKAAAGGHLFSSPKDAFASHPARPNAFKLSSVSIIVVGSGTNAAKVIVDGLGK
KGMMYAETDKLQAAFETTLKEAKSVRVLDPGSATAELQRLAQSGSA*
>TCRU_4434 Protein of unknown function (DUF3682), putative
MPDGCNKTAITVPLRSVLPITAVEAAAEEDNAGGTKNNSNSSENLESGASTASSAVPGAP
AGGGSSGTSAGGSGSGGGGGGGPAGPSAGGQGTGGVSSSSSAASASGSSGNPSDPPAAFP
ASSSGGTAGSSGSNSSNTTGDSPTGNQSSTAAAANDTSLPEIPAGTTSGTGHTRQEEEDH
VIQQQRDEAQVQHQQHEHPAENGEESAKDKNALRTNATADTGDSDGSTAVSHATSPLLLL
LVVACAAAAAVVAA*
>TCRU_4435 cysteine peptidase, Clan CA, family C2, putative
MCLLSVLGEYRQICEELGLQPLLALEKAFAASPEKIDLSLLIVSSKHFESLIKLLERRDD
IERVDLSGIKITMTQLVRLFSVLSDGCVKELILRNVHLGIQGGEAVSKLSIACDDLIYVD
LTGTLLPEYLEASIKTQVEMNNICFQKKMQYWQKAVEPEAPRSWRWRVESWTEENETEPK
KPVVKSMQNDSLWGIARSVMEGGVLFTDKEFPPEEALKNPNVTWIRVSSLLTEAKKRECC
CVGEKPLYHSRYNDTKNFCAALNVVQQFHHLSKQLCVRRLPNLGLFAFCFCIRSSLVTVI
VDDQIPFLNGEPAGIHHGRDSDDYWGCLVEKAFAKLYGGYDNISGVTFGSALSQLTGGIT
FAIDWKFLRQKFTETELFRFLRDLTNSKKILSARLIPRNSMAMLSAKEKGIEPYMSYVVA
ATEAHRDEKPHPSYMVQLSCPNKLECEDTFFISYSKMESVSGLPRYWIGFEDFLTYFDKI
CLLLWPRNDPLTNHKNVVEHICECSGGTDSSSKFATNPSFLLTNMGKPQSEIMIVLRKSD

DYTANRSDWIQLHVHKVNDNGNEIERRYDICSRNALLCTEKLYDEEAAFVIRLRENERLQ
ITASASSRCICTLTATSTDRFQINPFPSFYECTIEGVLTKRDVLNSSLVLTNTSQEKVEK
IVVALSQEPVRKRTHSVGLELWVNPDFCCEDGRPHFVTEFRRDVLVVFCFDLCVKPNDKI
NIIPLTKKHSENVPFAMSVYSSVPLERENKMI*
>TCRU_4436 Vacuolar protein sorting-associated protein 16 homolog, putative
MVYQRGFVRTSRAGVWIALTRETVVRLIDFDDLLWGLKTGLSELKVAYCTAGGPLALYCG
ERFDLNEGGNAICFYNARGAPHPVKSHIQLNGMESVFFMCWNECNDHLIILLNTGEVRFF
NLAGEIVASSIKVPVGLLCVSTANGIALLVDDGEPHVILLEYHSSGEYRKFFLKLPLVFQ
NQKPTVMLAIPKQFSDTGYTELFIPFLSNENVSSFFHCVFYNNPRCFDLRLSVGGGSVVH
MALSPNGQSIAFLVRDGTLCVASRSFEDVTRLINIEMDVMPVQFLWCGDKCITYLHLARQ
FDENAEFPTRLTLVNVDDPDQSEFLNDIPSSPYLFSECDGIRIFSSDAYQFLQVVSAPSR
RIFSVGSRANSALLLLAFDEFMCGGTSSVKMIRDLQRNPAEMNEAVNDCIAAAGFEWNIS
QQKRLMRVAAFGKSFCSMYESDFFVNMTRRLRVLNALRKSKVGMLMSQAQFLSLEGDRLS
ERLLQMCHHQLAYYICDFLGFNTRRVMMEWALAKLTKPFFSVTEEKRTALDVIEKLKELK
QNSFAEIACKLYVKQKKHAALLLLEAEKVALQQIPKLLDINQPELALQKAVTSGDTDLIF
TAMMYLISHQGIEALPLLMSDLTTEKIFLLYATFSEIHRELLMEHHKTHPEHKTYMDILN
YLREEEGVKQSLLKKNSNWEILQQKKLTAIENVAISVKREIPGGFSNSAIVRNALPHAVV
LSGFSTSSQTNENWVRLHMQLLDEQTKLVREYNDKRFLNASVKRMIVLCHEHGCDGVAGR
LKREFGVSDKMHCWSMLDAYTTMSQWGLIDQLGEVKNKNKPVIGASAFINTLLACGRQEQ
AKQYIHKIPQIEQRMEYYLLCSDWEGAGADCRRHGEPDLLTQLKDRVKGDASAVQLIEKG
WNSVQESGAVKLAKLFA*
>TCRU_4437 protein kinase A catalytic subunit
MKAGTTVTKEEVAEWQLHDLELGETIGTGTFGRVRLCKHKTSGKYMALKILKKQEVLRMK
QVEHILAESSILQELNHPFIVNMLKGFMDNDRLYILLEYVVGGELFTHLRKAGKFPNDVA
KFYSAEVILAFEYLHNCNIVYRDLKPENLLLDAQGNIKITDFGFAKRVTERTFTLCGTPE
YLAPEVIQSRGHNKAVDWWALGILLYEMLVGYPPFFDESPFKIYEKILEGKLQFPRWVEA
RAKDLIKGLLVLEPTKRLGSLNRGTQDVKRHKFYSGVDWDILLQKKVTPPIPVRLNKEGD
TRYFDRYPESPRHPLPPLTAKQQEMFAGFCDGEYTKA*
>TCRU_4438 cAMP phosphodiesterase A, putative
MLTELHGCSSLFVTTADRCSIMAKMNEEAECFCVSVVMPSGVCYQDEFDEEGLCNVKETL
GEHVSWARFFSVVREAFNNGQVTVQKATDASVEVMCHADASGEGAGVCGAEFNVSKVDVS
VLPTIEKGLVDLYQFQAHPNTQEQKLKKLTEEVAQLKIKTDQLEKEACFLKEIAHRRRKL
DIYNIQRIKQLREEVTNYEGIYECAHRATKGEATTNMSHRSSTQARHKGRIRQPLGEKEC
AAYDPELLCLIKSRWMTLSGIDAGPSCNRVIVPSPSPGVSNQTPVFGNKQQEVVWEAMNK
LDAWDYNVFEVQQTMSGDDFASLHHQPNGGSLFITMYALLIKYSFLSKFNIDEQIALNWI
SCVEAGYNGNPYHNSMHAADVLHITHYILSKGGMIERCQLSDLQVFAALFAAAIHDYNHP
GVNNNFHIKTQTYSAIVYNDRSVLENAHVSSVFELMKNPRFNILESFSEDQQKEIRETVI
EMVLATDMSLHGKHIAHFNDRLEEHASFTERENQNLALVMALKMADISNCGRPLEIYLKW
SSKLSDEFYLQGDRERNLGVQCSPFMDRMEPALAKGQILFINYIIIPFFEKMAVFLPKMR
LAVECAESCKAYWLKSGQG*
>TCRU_4439 predicted ankyrin repeat family protein
MSSHLSELCKASEVGPIIERLKQVYPERPNLGCDYDDDDAFHLASGFTREVHEQMRYTFE
GIWGYQDDDGRTALHWAVAMRNFSLAGTLMKAPYFSLVFSEDHDGASPFITACMVGAPEE
FLKELLTTAAAQRSWKLTQEQESIDSKQEHVTADVNSGDTKSLDDSLMNHKIAILDQADN
LGNTSLLYAAGRGNIAIVRFLLQLGASIDHQNKRGQSALHRATSRGTNDVVEELVVTSRK
VHSAAEHRRWMNLQDYHGDTALFYASMDNNEELGRYLLRHGADREIRNKEGKAFWEV*
>TCRU_4440 Multisite-specific tRNA:(cytosine-C(5))-methyltransferase, putative
MNRRERRRKRERESLPPALSALITCISPQTDPAAPLRYLKSFSTRESVDVDEEDCVYVLE
GDGLNRLCEGLGNGICAKDLLAVARRAPRSQSTIEKIDVTELCFAIAQVIAPVNVHERRR
NVGSTEPLDENAPLIKYYSKGRFASLLECANTEDAQVEWQRFIACISSPLPMTLRVHRNE
RTLKRIADEFLLHDPMLREVVHSVSPLLPPSIGLYGCSHAVYHTEPRVEYICRTLHAASA
VSFQEAVSVLPVMVADIHPHHAVLDMCAAPGSKTLHVLDEMLQYGWSTYSVSQGVFFVNE

KDRIKATQILPARLKRFHAPNVICTRCDASQWPRLFYSFERGSSLAEKRFDRIICDVPCS
GDGTVRKEPASASSWSPGYVKSLVPTQKALLRRGLDLLKEGGILVYSTCSMNPKEDEEVV
CAGLELFGDTVELLDVNAILREKGALLHSVGGILSPNVDQLQIATLPLTFDGRKVLRVLP
HRDDTGGFFVAAFRKRSLPDWAPPLLLQEKLNHWTKGKFWAPVGRDDPEWCNIVEFYGIN
PNCSDAFQYYNSTLEKKEENVVGSGLVPLYHLNPNGAACRRIVLVTVATARMLFETRPYK
GPGVEIVSVGSRAFEAYDGKFLLNARCRWRVVVESASYLASFMRARKIVLNATHHPELIR
EFLSNGFIWLRDYWHVILRQVSVAASNTTTTANTLTSNNNNNNNNNNNNNNNNNTDGIGN
KGTYLGDAAEDFTSFVRSDGPLYELLRSKGWTESLTQEICPLLAENVLVGGVLVGLVGGK
LAGEEGPWWLSATISSSKLELAVDVSLRTFGLLVFLGFDKNNTMPGVGVPIAK*
>TCRU_4441 AN1-like zinc finger, putative
MQVGVGDDESKRCTFQGCTQVDPLASRCVLCGDMFCAYHTSVAAHMCRTFNAQNVTCPLC
HQAVSLERSGQPIDEAVSRHIDRGCRPAALFSTGIKERTNYCSYTDCRNNAVASIICEDC
GNRYCIEHRAPARHQCRKARTPAVPALSQAMSTKPTLSSGAVSHSHSSPQKNFPRNTPST
AFGTRAEGTVTPLVLFAKEFGVSPFFMHFSRLMVVGRALDLAVGQATLDSAAVGAEKGTW
VLHVVQRPHSADGFSVVAPPFSATLKTAGVVDGSIVYIGKKSVQPDDLFSELAPHLANKF
HRGKEKKCASM*
>TCRU_4442 Ras-related protein Rab5A
MIASATPHAGCETATAKIVLLGESAVGKSSIALRFARNEFCPNQETTVGAAFLSRTVSVP
NSSSTQDSTAFGAVKYEIWDTAGQERYRSLAPIYYRGACGALVVYDITSVDSLKKAQTWL
RELRANADPTLAIFLLGNKKDLESLRQVSHEDGKALAQEEGVNGFFETSAKENENIELVF
VELARTLLEHGLASSSSAGGVGGTRGAKRLEPPSRPSKTSGACFC*
>TCRU_4443 BNR repeat-like domain containing protein, putative
MLVTLPVDPEEKDKKDNGKGVLHLWLTDNAHIVDIGPVSDDDAAAASSLLYKSAGSGDNN
EKELIALYEKKKEDGKKPSPGMVSVLLTAQLQRVKEVVATWKEVDDRVSKLCP*
>TCRU_4444 glucosamine-6-phosphate isomerase, putative
MRIVISQDSDAVADYVASYIIDRIHDFSPSKERPFVLGLPTGGTPVRTYQRLIQAYREGR
VSFRNVVTFNMDEYVGLPREHPQSYFYFMKTNFFDFVDIPEENRNLLDGTVPDLIQECRR
YEDKIRQVGGIHLFLAGIGTDGHIAFNEPGSSLDSVTRVKSLNDETVASNARFFNNDIRK
VPTMALTVGIRTVMQAKSVLVIATGSKKAIAVARCVEGSVSHVHPITALQLHPSAVLCLD
EDATLELKVKTVKYFKGLLKREDELKRRQEQAPNTMSKM*
>TCRU_gamma, conserved domain containing protein, putative
Elongation factor.1
MTANLTGVWLQRMEHVSQYLLGVALIIFEERRHDIVALCVLRGRGIPAIVSDVTDTELLD
WGRKWQTLRRGGSAWRLRVLGGPDDPEACAGGAHAGVSVACL*
>TCRU_4446 BNR repeat-like domain containing protein, putative
MGTAWTEAIGTLSGVWVNARSGVSQKESLRVDALITATIEGRKVMLCTQRGHASGKERAT
ALCLWVTDNNRSFSVGPVAVDNASKWKTELKDCGM*
>TCRU_4447 serine/threonine-protein kinase, putative
MLHSHEPTGTSPNGKANRCRGGEAAPGDVLGELAEKGHGQEEGCHLQQPHSNPTGSETFD
PCGSSGDSRVDAQPAPSSRKTLDSTHDTNWNKGDRDAVGRALHRDPNGNAFENSHPSGKP
DRVWDLVSGTPKKSPPKVKAAAAAVADVDSDAAACPVDVAEMATREVRSSAVPEKTEAEI
RPTMTKGWDACGDECGGCGAAFVNSGGNAEILAESEDDWRQQKEGVPTVSIQQQQKQKQQ
QQQQQTKRHTVVTTTEHTAGVSQGRCVPVVHTTSSTAAVTSASCTRPVTALSVYLVALYK
KVNEAYCRQRRFEAPGPKFNNGFDDKEGHYLVLSGEEILNRYTVQEVLGKGSFGTVVRCY
DEKRRENVALKITRHGLSFRTQAKLELDILLKLNVNPHLNQLVVKLLKVFDWQGHLVLVF
ELLSFNLYHLIKCTRYNGVTLDLVRKFAYQLVQVLYQLEQTKPSPIIHCDVKPENILLKN
QNRSGIRLIDFGSACYSNKVIHKYIQSRYYRSPEVILYLEYGTSIDRWSLGCVLAELHTG
VPLFDGRTEAAQLARFEAMLGPIPVEMLEASPKLAKFYGTTENGYKLKEQPLPKRSLECV
LGVTTGGPRGSRKGTPGHSEESYRQFHDFLSGLLKYRPTERMSCSDALRHPFIEPLWISD
QQQQQISRKPPPPPNPPP*
>TCRU_4448 hypothetical protein, conserved
MVPNSLKLSNDVHAEPRTVKASDICDESPLAGHDGGGSSHPCRNCAHPLPSGAEHKGSEM
DTTMYMSIVHRLQEKVHNLQEALLVSNQCSSLLDSLVRPGETSMTEVSLRQAQNSGEGQV
TRRMRNEWSRAAEVNNDIMSLQRVSSRVGVESVNNWMNGTSLSSWDRRGTIHDEITVPSP

KEEEIEKETVIPSFHPKKENAGDPKSVSASARVVVDPVILVDITAVMNKNMPLHPVTKSE
NAVSRFTVDAEVERLTAENVRLREESAEVRRELQIRGEELRRREVELANLSQVLKQLQEC
NSTLKEEAAAVHRRCDDAMGMARASELKVKELTATIDSLETGDEKRCDSCAAARHEAEDA
WREVRRLDSELRAWGPKERELQRLRVLMRFSELKKDSDRLNVIVGEMESAESELDRLREE
NRRCRKLLAEYRDRLDAAVTNTAMPEPLPVPAAECPSACEESEAWPHSQRPHSAGSRPQA
ADRIRRPQKPAVASNAAGKTRNEPLTHGRQRQLPFGRKKMCLFSCDLSSSSRGLCCLFGS
RGGVLSYHRAIKGSVNSRRFQKTPLQ*
>TCRU_4449 hypothetical protein, conserved
MSVESGLSAGDGGEEKPDSGRLLSWEEYRAQYVMRQRLRYQMQREASDNMVNSTPPAPPA
TAARAAPPQEEWQQRREQAQHPAEEQRGEGALANVWGRIELRPGDFINAARVMGRVILAA
FLVFRTVSLYYVFLTLMTYLGWLAVRFAFASIRIERENVAGARAASHATAARGRRSHLPH
QHQRISLPRKTLYIITRCITSFLLSFSPTYSVEQLEAELLEDGIIGPHPHQD*
>TCRU_4450 60S ribosomal protein L13a, putative
MVLPTRQVVDRRSRKGCKKHRPEIIVVDLKDHVLGRAAAIVAKQLLLGKKITAVRCEQLT
IAGTEIRNKIKYLQFLRKRKLSNPKLGPFHHRSPSDIFLRTVRSMLPRYTKRGQKALRQL
VAYEGIPTNVVRTGGRVVIPKAQRHYCYRSERPYTVLGNMCKHVGWKYSDVVKKLETARV
EKAARHHKKTEKLRAAWKSARKEALSKVSKNNLEVLKKFGYA*
>TCRU_4451 hypothetical protein, conserved
MVLEKGVPFKITLHPSVFEQKSVLGIPLSFTATVVDKELQHRLEFCVPSGPGVAALEITN
VEFLFEAKKLKGGARKSSRSSSLNGGSQSYLFMQMLDSQGRSSSHPFAVVCCDAAMGRGI
HSRVRLPLQSNQRVRFYLVERKNKEDEKMEIKERVVGVRFTGILQLLSGGVHVRSAKTRK
QIQALMEGSLNFEADSCDEKVSTLKRDRDSSYHHRDDEEFAKGSLRSDKARSIPTESIRN
DLDEEPPNLIYAFVSGGDDES*
>TCRU_4452 zinc finger CCCH domain containing protein 12
MPKANKHAEVKPSKYRTALCEFYLRQEECPFGTRCAFAHGEHELQTEERNVELLKATGLQ
RLDAAIFPTPTRCSAMTAESSLNAVFPVTSLSRRHPVIVSLPCWTESRVVGFERSEPTTP
GKRLDEREAAPSFSFPAREVHRARCSSRFSATCSTEAPVMYRHNPYAISTHYE*
>TCRU_4453 ATP-dependent DEAD/H RNA helicase, putative
MRASHQNLRKRSSGEKKNNVCGVSKKIFRIPYVNTGVNSDDATVTSGDAMIEGASEFFFG
LTGVKGTGDIVPIRKEEWKTDMPGETIPVNNSCCGSKQRNGAGNQTQDQVMWIELGLCKA
LVRAVTHIGFLSPTPVQVQAIPAVLGGSDVCARAVTGSGKTAAFLLPLLHILLTRAPQKQ
LHSGGKRRFIRSIILLPTRELGMQCQYMLQQVLTHTTGLTVALAIGGIAQTAQEAALESI
PDILIATPGRLVDLLHNYKGAHGSLDVSGVEMVVLDECDKMLTVTLKDQVVDIIQRVPEE
TRQVLMFSATMTSEVDEFAKEHLFEPKNVDVGHVALQSKLRQQFVRIRLSSDATTTTRTT
APLRGCYNEGNGEMEGDEEEKVDNKKKRIRSKRLRDAAKSEAVDSHETEDALEHLTKIKS
RFLVALCLGYFREKTIVFTRYRTTAHRLHLLFTALGFTSAELQGNQPQEERFASLKKFAS
GEVQYLFSTDVASRGLDIKGVSTVVNFDLPPTLTAYIHRVGRTARIGGSGTAVSLVDESK
DADIMRKIITVSGVVNSHQVSSVKRRDVPDELLSEATRKVNAVFPQVRGQLVAEALEEKI
AQAERRYSRSAEEMFADGVTAQPKKTWCLSRAERKRRDEEARRLYEKEAEVTVHHFQNEL
SNWEREEKEFLQKQKLARRQERDAKARAAERVKNAHRELRRKSEKKLQAGAIKKMKKKKI
REARKQRRAESRERNGKAAYKRRDGLKSKSKSRHRKRMARH*
>TCRU_4454 mitochondrial carrier protein
MSTTAGTSAPRREWEYAVSVFAGCVSGVCSTCITNPLDTIRVRLSASRGATGKPHKSLLY
TVRDLFGMGVGHAFSRGLGANMMASLPSNGIYLPSYRFLQEEMAQLGVDERIRPALCAIG
AVCTTNLTLAPLFLVRTRVQVDDRMTVREVFRDVMRREGFVGFYRGTVTNIGGRFVEEGL
FWSVYELLKRITKEGSFKDSNSFLLTSAAMVSLTMVSKLVAVGVAYPYNVVITHLRTVNL
VTRQCEHTRFFPTIRHIYQADGVVGFYKGLSPHLLRSIISKAAQIYAFEIVMYAYMCFNA
RAKYAAVLSSNSATATSPMAVSEAD*
>TCRU_4455 hypothetical protein, conserved
MNRRTKAPSVSVEETEDTRLENFGRFLYESFVKNVCPSIFEPQLRYYGDYIHHFGFFVEV
NTKGQSVSFLSSTKHPHGRHDGVSFSHDGAACGGDVVVDAGWGIGESEQKEADAQARAVG
PLDGVTKLEEITAKVIAPFQQTTWRQSGTQCLMKKARALYCWLCENITVELPSPSPAVEE
EAAPAVTTAKKVTGRRGAAASRNAKRKLGVDVQSTTAPVEVVDPLEAAMRKRTADPLILA
RLYQKCLYWAQVESKVVEGYVRGRAPEEVMEWAWNIVCIPQGENSMTRYLVDVALSAYTG

PLRHTTRNKDVVEEAEAGREPSSKDLPSVKSKRPAVLQKEKPKQNFLDGPILASSVSAEK
CMESFYFNTKPQEFCFTHLPKESHNTLLLNPPRKSLWEGAPCLTHTFFRFPLALQSHRRR
CLFTVRSTPFYISLINEKPERTELSCFIYKGTLEALPEDLSTATPLGPQWVWHQREEATN
SETFTIMVPEAGYHSIVVGARTIRKDPFTAVVSEELFVPVVAYQVLVTFVPHQLPQFPRQ
YFTPSVCKLLAPLTSHVPEGSTHFVVMPSCPNVAGVAVVSKQPSEGERLLLAFLTFSPQN
VAYTGTVVLTSGSEAEVWILYAAPDHNYVNLTELPRAEPRFQTRLPPLGSDVGVVHGVLP
HISPQKPKRESNLLFFPFVTGIEVKKPGAAVNEGCYIQPQPTLEEENQLTLRRLIGVKPE
LLDEVTAAMLKRSLPVGSYFDKKISLGWRAVGDV*
>TCRU_4456 Flavin-binding monooxygenase-like, putative
MLSCAVIGCGAAGMAACTALRRSGLLVTCFELAADPGGIWNSDPRSPFSSRGLVSPVHPT
MRCVLPKDLISFGDLRFDYTVPQFPHHSSVCRYLEQYAEKMGIRGLVRFNTKVQSVRYEE
RDALWRIITVNVVNGDVFEWSFDKVCVCTGQTQEPRYPDGIRELLEPYLREGGELHHASH
VKDFRQFKGKRVVIVGDGVTACDYCWELLRSGSDVYQSSCQSLYMPQQRQQQQQLENGAN
WSSLKMHEGGAMRDAASAALHLLSCSPGWRKDITKGNRIVSNWIKFRNIACWGGMPGVGH
PLRSEGRGILFAEQPKRIVDIIAEAKTRSMARDRQGGIQSSDDTPGEIFVDNIDAIICAT
GYHTRYPFLHRDMRNVVEESSLLQISKGEGGQSPPSHGDSTGKEMHHHRGLYLGTLYVHR
PSIAFVGIQKELLPPFMLFEAQAKFISYAFTHRVNLPVGVEGLLSRQSELMKRYPLLENL
YHPQGLGLYSALYFNVLQEELQVGSRNTYTASIVERRSWILTTSLLRLVHKLRSVAPLKR
KRQHVLFSNAI*
>TCRU_4457 ATP-dependent protease ATPase subunit HslU1
MRRATVFPLHAGVVIKVTGAARFCSAAATAAAAPSMPPPPVSTTGRTLIRNMRPRELMRE
LDNYIIGQNEAKKAVAVALRNRWRRHHVGPEIREEIAPKNILMIGPTGVGKTEIARRLAK
LVDAPFVKVEATKFTEVGFHGRDVESIIEDLYKASLTQTKQNLMRQNEAVARQKAEDRIL
KALAGVSDGFREHLRSGALDDIEVMVELQEKAPKPKTAAGEGVFIAIDLPGALGAAQTRT
VKKLLKIKDALPAVQQEELEKMVDTEDVSAEALRACEEDGIVVIDEIDKIVTASGGYKGH
QASAEGVQQDLLPLVEGTTVSTKFNVQIKTDKILFICSGAFHNVKPSDMLAELQGRLPIR
VELKPLTSDDFHRIITEPKYNLIKQHIAMMETEGVKLVFTEDALWEIATVAAHINSTVQN
IGARRLITITEKVVEEISFDGPDRKGETFVIDAEYVKKSVENMVKKVDIKKFIL*
>TCRU_4458 hypothetical protein, conserved
MRSTALWLYKMPKNMGVAPRFDVWNESYEPWQHMKRMGRLVGTGFYIPPEWYNHFRMFPP
INHNFQQEKTLNPRNESEPTQDDTGSLSQERAALRDELARKSRLLASEGMRYYNIFWVRK
PLDRMEKEYYELKRKGIAHSEAIKKVLEGFYKELAVKKRVAAVQAEEAKLSGRFITMREA
TVVLNVLAQLHREQLTPHQVALLAREQHQATEKASGLTATVSRVSAPAAGIDADSTASKE
SGSDEALSADSLANMLEDDHASGAGTQYQVEVKHSARDSVRQLHEKSTDDTGSPDWYTGA
SPVYNGAA*
>TCRU_4459 hypothetical protein, conserved
MSLSIDSAPRVPYVVVPEALRTEYGFLDTCALYYCAQVEHFVVSTGDGGDREPAVLFITC
DSLYIGDNQGGIYRRVELKNICCILTNIGFSLSDNPSSSRSLFTAFVLSNPQEPSDIVLA
GKTGYAAAVVAERLLSLCGHPVPMQRCMTDRHDLLPEGVVRLPPRGKPTLTLQEQQALRD
SISSRSGAANAAFLSSANTFGDRLGATLARLVDEKRSRTTAPDTVVADAVPPDVWVPVAI
RRCFPPFNDVSLFWGGSVRFYGKTLKEFSEATLFITPAQVVVVHAQQPVRVLPLQAISKV
LVHSIDSVRKQRFTFFVSSLKDADICIQTVGKDSDLLLKRVQNALCALDPTHVPPINPVA
TTKGLKLRLRPKKGYKLPTIAMPPTSENARYRNFVFERVRDILRACEPLKQDTAAALTEQ
FLGRELELLSLLYNTYPEYAMRQEFSSVPEHRERLLLFCAKYLPDSVGIVDDVLNSYKGR
EEELFHHLVMRYGPEPREKTVGLERYKTTLSPEEIRRTLVNFYRHYEPKKIADVDAIMAL
YQDREQLLFERLTQLYGPMPLDQDSSALSVQPNLLLSPRDASHVSSSPPLPNEDETADRP
SWRQRLEAFLARYIPERTGDADMLLQKYAGQEDALLCGLEKKYGPEPVPVTRRNRARVSA
FFVRAGLPEPDEAQIDETIRSFHGSEEDFFLYLEQRYGAESPLQFPREAEEITAVEFAKV
DLRTEVPFVEVPESLQCLFPSFRGRAALFWFGRVLHWEQPAPPTLRCAYLTSSHIYVGNS
EADTVRCTALERVEAVYMNSKRERRDMPLSMIMCVHEEHDLFFAFASDEEGHQLLSVLTS
TLIQYHFGRQCRVFACANFTDFGIHVNCARPPTYINHVVAVLQRPRTNASLRVGQKNNEA
ASSGIDGDDIHVHRLLKQKECELRSGLHDALILKDDGYQNVELQRDAVLVNQRWATIRQL
ATKERKMFGTVPPRPSAGSVIVSNARSTMNRTNSPPHSFQAVANVPSHIIKANPLQRAQY
GRFSPNGTYGLGVKARLYGGIEGAVKNVSEASEGNFTRLLMYSNERSAAGSVHNASYRPS

ITRGDGGPDE*
>TCRU_4460 hypothetical protein, conserved
MRPNKIERRKELELAVALRQKELEGLRRRKAELEEELSITPQNLTSGDLSAAFPVLDYCG
ARPRKDLRTVPIERVGNMLTQFELASKAISERNQALMHEVNELNRRIKAQGKHYIRVSEQ
TKNLEDATGVRAQGGDQASERRAFLRQNETDVTPQELESRKALILKEIRTGRILLKKKEQ
TIFEMTNAVQLRREILDEIDALNNGIRVTDRDLKCEKEALQALIAEHDDVDAKLNKAMIA
KESSSRLLIQEGIAEMRDEISGTVTESRQRQERVIKTQNYRIEQLEHRLECIEKALQNNN
LLHGVDAALSQSWAAKGDLMTLGDDVDMYDSDKINPSQERCHPAIYNLFLAEKNRLTRCI
SLLNLVAKEKEAVIDALGCKAEALSKECQEAIQELDQVASGAAYEEENQRVKAIEYIEQQ
RLRYSDLFFEKHRLKSLALTTPRTGGRQHAGRG*
>TCRU_4461 hypothetical protein, conserved
MATSQLIAMRYMDLLSEGNVENALVYLSDDAVYNTWMGVVYGKENVAVFLRDNVRFVHHG
RNYNRWRQVQHSLDPSLRQYDRADGSGSGSGIPSRALLQYGGDQAVRRYFNAEGYDSQGY
ATFERDGTIASRAKFSAFNVKVKETVVLRNNKVVLVNVSKRV*
>TCRU_4462 V-type ATPase, C subunit, putative
MPVESEVLPQPSRLPPDDALEVIWGFVRYFLVFLVIVFGIIPALCGTVFPPFSALWDVLS
AVSPYAWGSVGIGIGIALSILGAAWGILTTAASISGAAIRAPEIRSKNLISIIFCEAVAI
YGVILSIIMMGKLEANTSAIDETGKYTYKAAAAGFTLFAAGLAFGVGNMSCGVAVGVVGS
SCAIADAHSSALFVKVLVIEIFASALGIFAVIVGILMSQKAVMV*
>TCRU_4463 C-5 sterol desaturase, putative
MISFISTLSEAQPRLVEDTEGAREGSFGKMSALAFDVVFTGVIYLGFSFYERVVCPLVGS
VVKDRLPDRPQCLRSLTVRDKIYINFAKVVTALFVYHTYQFVVRTDVSGMCVDFMDGPAV
LRSVAWMPLHLVALFIVYDFFYTLFHWALHWPPIYPLVHKHHHRQVTPFRGVDDAINVHP
FEYVTGEYLHLFSLYLLSRVTPVGQMHALTAVVFIFVGGTLAGLNHTRVDLHIPYVFNVR
AHDLHHLQFKYNYCQYITLWDWVFGTFKSAPKVSKAARE*
>TCRU_4464 hypothetical protein, conserved
MAVMMTGRVLLVCVLCVLWCGSSRIAASGVYASGVEDSGRGGCMVSGVLGTNLSYTPSGC
NKTVPMTALRSVFSVVAAEASTEQEDSETDTVPDSPSGDGPDSVSGSPVGSVVIGGSKVV
DSTLGRLNVVPPDTRVAVAPPPPPAPETDASRLPEVSQSTEKHNSSEKLVDLKTKTPAGT
PPLNNQASKESLPTVKPESPTTSDSTVTVKGTDQISEEKLAVLQGPSTVNAGEDGKKAVT
EIKPNTTTNTPDAAPTLSSEGDVTEQHGKDTDSPNFMNNANTGSSAETTASSFSKSGGID
APKNESEDEGDAQRPKSKEPQEKPEDSNTNDAPTENETAPQTEKPFGSAQTNDTSKIGDS
DGSTAVSHTTSPLLLLLLVVACAAAAAVVAA*
>TCRU_4465 hypothetical protein, conserved
MFPNASKKRPSFANGPRILVALNASGIMSVIYGGRERVAADNTYEVGEHNAIGHTSLVLK
NGVAGIGFVAKGDAGGLSQRNASGHENRPQLREFTAQYSGSSGSPDDCFALRNDAKLTLR
ELTVDGTVRVCVLCVWLLLLGFYGIVAVV*
>TCRU_4466 hypothetical protein
MGEIFSSVWASEGNIARQCVELVLVSAIGILLYYVPLFFFKRQRNSRALVVLEPTAKATA
AGVVLYSCFGMAQPHFSDILQTYRTGTPSPDALYFLAGVALGYRLVLQVSHYFDDTGLSA
TTTAMVAHSVAEGAGLGLIVSSPVFPVIFRHQLIHGVSEGMLMAMVALERYGLKQTMRSA
LLGRLAQAIAYYATAICMPSVSGDAMQVAEGVALGSMAAMVWGELAQPAYNALGSIRTLI
ILLATAGVCHHTLV*
>TCRU_4467 protein kinase, putative
MVDTAIACLDQQQVLVSPKQGDSREAKGKMVTGTRKDVREARDVSVEDGQRSALLRPGAE
ASSRNATVAAVRCDVMALPQRAAGAMMLVKKAQTLTTAPVECTVPGLLSEMLSSPKLGFV
AVSDEHKDIQSGDGEGNVNRHVNVRRNGENNFTTTSAVDDHFCRSNVYGDDSRNSSSNEY
VSSHPQREGAGCCGDGGGAVNVASPYSFSLQSLSQVSPHVDGDSNSSRFSRSGNDDILTS
GTSANNYGDAKVPMNCLGILSNGISKQEEFLGQGPRSQRKVTDTITRRGHEGGSHRPAAS
PTWMETGLSSGQKELVSGVAATARQDVRISPKKHTTSTGGRPCEEGTKYLKHSPPLLIAA
ELTMPPCMQTASAIPTDDVEQAKGTVGLETHLFGETNEETISMNSLTALPIYAPSAAPLS
PWLTSAAEASAHSRPFSSTAAPLPRRPTLPRSSGRGVQQSPLRFKRVFSPEVLFATEDSS
QGSILDSFHQRDVERGQSPLRRMSLSPLYTPQDDNPLRHEDKCSTGSTSPTADSVNRSHD
GNEVGFRENSFACGDSRRRTSVDDTDGVYESPVMVCLREETTYDLSEAEGDHVRGGASDD

KDIEAGQQWLQIPVLFYLVFNLIKLHEAGEYRTQRERERELSEIIDDSSTPLVARRSSMT
LSASLQDVYTQLSHTLLEVSGVLLQPRLTVWSDAILRESVAEVVEGWKKGGPHSQEFESA
SLRLLRVVSADRCGKVKPTVLYRVWEFIGAGEHCRHVVIGIFITVFILLASLLSIAFLGG
DQTVARTVLVAWTFIIVLLSAGVCLLLVDHNAVAEEVRDFYFSQLLSRVAAAMRDVDGSR
DDDTNPNARNISFMGFGTQGSRFHENGWNFGGLGIKGHGMDEDAIGRHNGIGSLGTASSR
GGQGSSNRHPLMISTAVGSSRPEIRVVQSFRGNVEKDEDCVVGNEAHGDESAWDGCWEWG
EGIHHPQPHERDDPHGENPQSEDPLYDVPSSPQEEAMLKEDRYNSLLMSRVNFEQTQFAE
EQMKELLLQKHLGVGSQDTPRPNVEDAGTSPVPSDVAIAALPGGTHESSSGGSYGFVSLP
VNSITSASASGGGGGSNGSVSPKSRSIVPVSTRMTRDNLVNSGLDAIAITALVYCRGHAV
TENIFSKLWNRNFLILQRTSLEALDAAFRRGSERFKVFLLHAPDLDAGQLQLALSWLRQE
RRSVFFFASALGTMAKEVPYAFRLELPLTKRDVENLLLSGIGVDEEMNNVSIFRSSKKFK
VPPYTLGRRLGCGAYSNVFEVEMELTGAHCAVKRIYLRGDREAEADEADSQLKEIAREVG
IMSSLSHPNIVQYLFCERDDNCVSIFMELCSGGSLSELIASGGLQHADEIKRVLRDVISA
VAYLHGKHIVHRDLKPENVLFRLGRAKVSDFGTAVFKRGGLTNVKGTFAYMAPEVLLGEK
YGKACDVWSFGCIAADALSVPLGHRSLGLPELCDHYRRMSLDETLEFDCDEPTVREFLQR
CLRRDPKKRSSVEELLAHPMLREEDETALQQWLTMSAERRRTQQVEELRKGSNFTRTKIR
TRSTSAISLRSADVLGAYYSPYQTPLSPSFS*
>TCRU_4468 paraflagellar rod component, putative
MPNVIVNCTFNPPAFSITGTQLRQETLDSLEKALPQCTTTSQNSMGAANGNAPKFMLVNS
QPNTWRMSIGQHYCDQRGRCVVFSTIISTLQTEGWALRTTDSHESDNGKDITRLFFWRSG
*
>TCRU_4469 hypothetical protein, conserved
MTDAEEKEKKAPEIGSSGSGTCHHGSMSPNVRRMYVTLRVAAVLLWVPHSMALMYVVATT
NTANSISTLFYVLTCSLFMIAVTYYFAVYKQCGEYLLIISWLFGVLSEEAWVFMFPDTVA
FAQRSRPTFLAAPVVAGGGGGGGTIVHAGGSGGGGGVEDHDSPRFLWIAVSMLQGIVGGI
LCKMKDIDEDRYYPTHAIGERLYVVVPFCTGQWLSFILQNGWRGIVVENLTILLSLAMVG
YCVIGYKLLQEHTSLKRGDLIGFVEELLTTSFGVVFAVMLFGSIFVTLLAIPFLKSLFSL
NALVSSAGIILEYIVYEVA*
>TCRU_4470 hypothetical protein, conserved
MTYFTVYYGNNEAMMFNAECNTGSLMGRMIELLAPHTTGYTRLELLPMNFVLEHFKPSTG
ISVTTANDVAAGAASFAPQNAIKSPPFTGAIPFVGLATRAVESYADALLGGPAAAAVTAF
PTTTSTSSTSASAAGVSTSAAYFTNNGVGAGPTVPSPALQNCYVLLGCRYHHYHPSPRPR
DQASTAVTTSGMMSPPSAGYKNISMPPRKICSSETAATPQQIASLYRAQLIAAATIVPAP
NSRGNGLSGSFNGWTTTTPQQGGSPNIDPATLLLYKSGTLLYGASTAFWRKNFSQYLTTL
LLPPLTEGNNNNTATITNASPTEQERNPTALTEADSTHDESSSQDNAMLLPSMATGLFKT
PTPPITGYDVLWRGTRDEHIRLQETLDEGVFTDTENNKKKKSKKN*
>TCRU_4471 Mucin-like glycoprotein, putative
MMLRRVLCVLFLALCCACVCATAQEEGQYDVAVVEAGEGQDQTTTTTTTTTTTTTTTTTT
TTNAPAKDTTTTTTTNAPAKDTTTTTTTNAPAKNTTTSKAPTPGDGSGLGGPLWVQVPLL
LLVSAAVATAGAAC*
>TCRU_4472 Mucin-like glycoprotein, putative
MMLRRVLCVLFLALCCACVCATAQEEGQYDVAVVEAGEGQDQTTTTTTTTTTTTTTTTTT
TNAPAKDTTTTTTNAPAKNTTTSKAPTPGDGSGLGGPLWVQVPLLLLVSAAVATAGAAC*
>TCRU_4473 hypothetical protein, conserved
MLRGGRVFRSVGGWRSKPIGEMDRRGRFNFDEAAAALNLDAAYVAALYKPLHYTFAVRGQ
HYPAEQGRVSRPGSLSSSRNRMFPLYRRNNRLDAQLLRLSRRRISTE*
>TCRU_4474 BNR repeat-like domain containing protein, putative
MEVLNGAEDKTQVLEEDASKDPKKVDVSRPTTVVEGSDIYMLVGKYSPTAAGQEDGGADD
GGLLFVKGNISEESGSGKRIKWKDNDGVSRISVGEQRHSWSRLTGSGGSGVKMHDGTLVF
PVEGTKKEGEKNVSLILYWKDTGDAKLSKEVPADGCSDPSVVEWGEKEDKKLIMMTACDD
GRRRVYESGDKGESWTEALGTLSSVWGNKQDEGARGVRSGFITATIDGVEDNNRNVMLVT
LPVYAKEAGKKETGNSKGKLHLWLTDNTHIVDIGPVSDDDAAASSLMYKSGEGETNNEEL
IALYEKKKDGEKTSPGMVSVLLTAQLQRVKDVLATWKKADETVSKLCPSSAEKDESTDNA
CSPTVKVTDGLVGFLSGNFSGDTWRDEYLGVNATVNNKAGAAEGKKGEVTSTEKGVKFRG

AWAEWPVGSRGRISCITLRITTSLLWRRCPSTVCRRAAAKFL*
>TCRU_4475 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MSTAAASSGQESVKQPTSGTSPNGNKNADGTPSPDADPTVTSGTSPDEGQTVDGGSTADS
EPTTGTREGGRDVQEELNSQVGELNATALSSSLGNLSQGNNSDAGTVRGSGLLPLLLLLG
LWVFAAL*
>TCRU_4476 Protein of unknown function (DUF3676)/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MGSDSSLTPSKSDTETTSAENTDDVSRTEGDEFPVENGEEVPQTVDTASGNASTLPGETK
IPSKSNATIPSDAGILLENGHYSELAGMALFAESTVHGFVSRMLLLMLLGLWGTAALC*
>TCRU_4477 inositol-1(or 4)-monophosphatase, putative
MQEQVDLEKALVVAIRAAQSAGNIMLEFYQLRREDTAAKMMRLLKEGGSHTTGEVAASPK
PTPVDLLDIKMKSSSTDLVTHYDKLCDETIMKILQRFNAKVEDEKRKEPSEAFSFQFITE
ELTPNTPLTDEPTWIVDPIDGTMSFVHGGCDCCISIGLAIKKQTVLAVVYCPFLSIVQHS
VEDLRSTSAVAGELYTAIRGKGTFLNGQPIRVSADALPNTALVAFNYPMDARLSAAETPS
DSARVGVLKGQKHRKVVEAAGHIREQLAMHPVQGIRSYGSCALILAQVAAGRIDLYMEPA
GMMWDVCAGSLLITEAGGVVKNMWGGDFGLEGTTTIIAAANETLADYGVQLCTQVNYGDY
WKK*
>TCRU_4478 Ankyrin repeats (many copies)/Alpha/beta hydrolase family, putative
MTELHAAAEVGDVWVLKNLSRRCDIDVNALDDQGRTALHIAAAHGRMTFIKKLLHYFHSV
DACILDKNGKTAVQVAPPDIQSQLALFLSLNEAKTLERSGRDDEERKEEENVYRDNDVES
AEMVNPRVLRKAVICLLIPFVILIFINGSFFALQFITVTLTFYFVSLGYFVSEIAIRPPW
YHHHPKSTKLTMHNCPDYWNGYCHDPKRDFGLEYEDVSFTSTDRYTLRGWYVPPPAANRR
KMGIVLVHGGGRDRRAWLRHVPFLHKEGYGCLLFDFREHGLSDGNMRGFTYGMKERFDVV
AACHFMRHTYKYERICAVGTSVGGSSVIMAAAIDKTIDVIIAENALLTCATLQDQKIVEM
IGGYFSRRTYSKFVLNLFRRTSSLWLNIRIGNKPTKHCQALHCIGKIAPRPILLMHGTAD
ELVPYRHSLQLYEAALEPKELYISEDAFHCGLYNTHKEEYEERVLNFLQRHGG*
>TCRU_4479 hypothetical protein, conserved
MRPRRSKAERTFLAELASQSTGATAISLLSSCTSSNGKNNLRVGLRGSSPMCRSTFAQEG
HRCWLQNRIFDAPNKHLFLDPGGTWCHLCREPLGTSAVGHLSDREHHNHQLFLFLAAAFP
RGVHGEHQRFFYSPLAVLDDAAVLFPKLMQAVGEGNMHTEQDALRRASLESMLIYLSDGG
LCGGKPVLTVFHGSVPPELAHSGERLFKSDVSRLIVEWFPALGPGAITQIAHKCWGRSNL
ESIFDALRMQSLVDRRGREVAGVLSPLARNRAWRTTLQRQLSTKTEKATFVRLLMWELTT
RCEEAAGCDAALPLTETEQLMLELTRRRLAFEMVYLQSMKYMQHADQLLREMLFPSLETL
ISMGAA*
>TCRU_4480 hypothetical protein
MKRHASQRTVNNGEGESSPTVDADSRQKATERRLRDELADVTKQLEQAREIVCELLRFVD
RKRYAAQLSALEKNMMGGGGLFLTTTAAELEKALRTPGSRIVLLENHHYVLETSGPINIS
RTHVSILGNNATIEGSISLTHNATLDACDVTFLGLKNVSDEDEVDGKAWNSTSLLPCIEV
TQNSTVYLRNCRLVGGRDGLYLGIESEVQLRNVAISDCIRGIYEGVGCRAFFSGCTMAGN
CFHLVLLGEDREAHVEALTAPNKSDGTTENSELLVRFSDTSDSGKKRTRADIAVDHNPIT
DVYAKCIHGGKRVELPEELATCGLSDPVY*
>TCRU_4481 tubulin tyrosine ligase, putative
MVRYTPPCRAPYEWSEKPSGWLRFVDCVPVTYNIPNDFQMFTQEFRRQPCSTWIVKPTSR
SQGRGIFLINRITQLKRWIKERKEADEAEGLPASTFVVSKYVANPLLIGGKKFDLRLYVF
VTSFKPLVAYLHEQGFARFCATPYVANALKDDNLCSQLTNVALQKGEDAYNEVHGGKWSL
ANLCLFVQGRYGAVCADGLMRSIEFAIYHSLRAMESAMFNDRHNFELYGYDIPIDDCLRP
HLIEVNSPPSLFTTTLSDRLLKEEVLADVLSIIFPPSFPSPCAMSYWEYRLRTDLTTALE
T*
>TCRU_4482 XRN 5'-3' exonuclease N-terminus, putative
MGVFGLRRFIDASSCTRFLPETVQDAEKPLAARDLDKTHGTAGNSALSSSPAATPHVDHV
LVDLNCIIHSCFGRDAATMRKRDAVQAVLEKLRALLTLVVVPRVSLTICIDGPAPYAKLQ
TQRLRRRRLALLDTGSAQQLTSLAVTPGSLFLVELENALAAQFKLRGGRGFLPHFVPVFL

HGSTAAGEGEAKIARALAHVATASLSRGERYNPNHTVVLIGNDIDLTLTCLGATQYHNLF
VVGPSSMQLISVSEMLYRWLRGGTQGAGEFRLTVQELSSVRVDFVFLFLLNGGDHYVGVG
DVAPILWKRYRTVRAASMRRCLVAPDLMSIDVDFLSDVLQASDYTGDCDAGVGMELLRAS
LWSLYTTVTGVCPDYQYIPAPMSPHLNHLRAAVLHCLKNRRGIRIQPRRDARGPLTPLET
FVALMPTEATLPSSVAQALRSSRKYETIAQQLFTSNDAAMVADAAKQAVEVAGEFLTVSE
QCLRDFTSPVQLNVLQPPRRLSRHEQHRMLASKGRIEREEPLPLVECVTLPESFEYVTAT
YPSYVKDLLFLSPFCRAAEALSSSNRGVTTSMQPFVAGTVREARRRQKCKRGSSDGEVRR
IPVQMQSSEEPSAARQLQKTLEKASSLAMPEGRDKKTLRRLKKKLNAQRQLVEKQSRSEE
SSAEAKRHMLRQNDKAFIAEIRRFLGEEDEDVRQLLRHDGGRAPGNTGQEERPMKKQKSV
SRAGDKVELCGRKRRRESAETLSVTRADEEGDRHESSYGGCKAAKRGRREVSHTENHHHT
TAGAARTCGRDTREAVNGSSSEQPTLKKKKKRASREMGSTSSH*
>TCRU_4483 hypothetical protein, conserved
MNLFDDPTGGLTAGPAEELSTTEIEHQVRLNVSSYSRSIFYLLYTPFVDVISVLLERGLA
PDVAHPGEMMCRWFTDGALTLQNPASVEEGMGAENWRQLCEGLDAFYEEVEPVMPLTAAV
RKHGLPEDLLVPFLRQLSMDLLVPLRKRAVLEILPGLILGLANGRAPTALGFPTDSQRAR
AIMVADLFLGVGQETGNTDLAYLGIQLLRANDIPVPFPKQKQLTNVFSAATRIHTDWQMR
VSGQLVEVLPKWMEYYKKVHLDNLRAMKGLSETDSTSAVKQGDDDGERIDVLKAKRAIHA
IGDGVNAAGKQTDKESNSDGVHGYFSSHRTENLLRLSALESQVLTAVRHRVVAWNDDSNK
LYYRFRRRRSATAEPNAEETDVPKEPTEEEEEDARRVDATEDVALVEDGRRRRRAKTHTQ
ADEKDPKVNPKGHRSRKKRTIAAPVDDDSGSTFTLTV*
>TCRU_4484 hypothetical protein
MLMPCIHASVGFAVRAHQAALRYLERRLRADGRFDCSLHASCFGMVLFRWLTLADEETAG
LMQRWSDVLASSSAMNEAGGHRYPHRVSLGLTQVQRRVYICVALAADGDNGDACVSRCDV
DALVDLLKTAADEWRDMSSSVTSAMSSKSKT*
>TCRU_4485 hypothetical protein, conserved
MAPKKQATKQRVRVTNKAFEARQFSTVRLPRKAEMQAPQVDVERMYEDHDRGYRRGDEKR
GDGGGDAGGVNAQKSVPLIFDPIPNDPLFVVVAKSKYWPPPPLEELRAANGAPIEDGFDA
YDRREDDRAARRERVRVVRGELNHPRGKPRQNTIVKLDGSDEEKDEKG*
>TCRU_4486 GHMP kinases C terminal, putative
MSKLILAEIVRGMFMNSASYLRVLSEMRQQALEMHDAITRGDFERYGRLIGVAWEQNKRL
DSGTCPQAIADIISRVEKDVWGLKLAGAGGGGYLYMVAKDVDAAQRIRHELTQRPPNATA
RFVGMSVSHSGIKVSRS*
>TCRU_4487 hypothetical protein, conserved
MLSRGVLLRSMSGLKLPPSLQRWFHWYPRRGGEFLGDMLAGHNLFIADIPRKFDAQHARH
FSLVESLCITPLFTLTMVHYFSSFFLHPTRWQMIPVLMTELARKTETQQQWMSVMEKKSS
TDVVVWRASMSLMQIVLFPACLLLSSLTPQMMHAMLERTNHIVHQKLACINKDAPPFVQK
YMDEAREAEAFHSQQLCITTDYLAALLIVLLVLYLTS*
>TCRU_4488 hypothetical protein, conserved
MRRFIPTVSGGSSLLLRFVASAAVMRKVPLAKSSAKLGTPVTKEEVSQVFNVPAAILEQL
HRPAEILFTEVDLARVRFAPLIATLGAEEDVTKIEAEVKTAKAAAAAARTPVAGAKEKFK
NTAWKSVTELVTFYEEVMLPARLAHQEYTVYELKNFHIKDDLKRGLSAFKQDHLDKQKAE
LAKVQKQMQECQEFIKGIGKTAFDTAIFNDLANILRVCGECNPYAHRLSMRVLEDMNLLG
VPFNDVTTKLLHAIVFNDGALDDSALMFTLVEYPERGEVSVSREPVDRIADSALKIISVR
HQTPLDDGVKLRQGDTQPCLQRSAE*
>TCRU_4489 dihydroorotate oxidase
MMRLKLNLLDHVFANPFMNAAGVLCSTEEDLRCMTASSSGALVSKSCTSAPRDGNPEPRY
MAVPLGSINSMGLPNLGFDFYLKYASDLHDYSKKPLFLSISGLSVEENVAMVRRLAPVAQ
EKGVLLELNLSCPNVPGKPQVAYDFEAMRTYLQQVSLAYGLPFGVKMPPYFDIAHFDTAA
AVLNEFPLVKFVTCVNSVGNGLVIDAESESVVIKPKQGFGGLGGKYILPTALANVNAFYR
RCPDKLVFGCGGVYSGEDAFLHILAGASMVQVGTALQEEGPGIFTRLEDELLEIMARKGY
KTLEEFRGRVKTIE*
>TCRU_4490 aspartate carbamoyltransferase, putative
MLELPPVASLKGKSITSAEQFSRADIYALIHLASAMQRKIDAGEVLNLLQGRIMTPLFFE
DSSRTFSSFCAAMIRLGGSVVNFKVEASSINKGETLADTIRTLDSYSDVLVMRHPRQDAI

EEALSVAQHPILNAGNGAGEHPTQALLDALTIHSELGSVDGITIALIGDLKMGRTVHSLL
KLLVRNFSIKCVFLVAPDALQMPQDVLESLQHEIATKGVIIHRTHALTDEVMQTSDVLYT
TRLQKERFMASTSDDAAALQSFAAAKADLTIDAARMRLAKEKMIVMHPLPRNDELSTTVD
TDPRAAYFRQMRYGMFMRMAILWSVLA*
>TCRU_4491 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MDEYLGVNATVNNKAGAAAATGPSDGVKFTGRGAGAEWPVGKQGQNQLYHFANYNFTLVA
TVSIDGEPKSNIPVVGVRAGSNGGSKLIELSYDSGKKWQVLCGDGDPKELGSIGKTDTTQ
HVVILLRNGTQCTAYVDGRRVGNAQCELGNGESKEISHFYIGGDGGSADDKESQEDVSVT
VRNVLLYNRPLDDTEIGAFNPNKANIPVEVERPVEGEAIQPSGGRPEEQGQLLGSSGAGG
VSAPTVSSATTSSAGEESVMQMVSEESSDGSENVGGASLSDGDPTVETREEGTDEQEKEI
QAQNADVKAAALSSHLGNVSQGNNSDAGSVCGSGLLPSLLLLLGLWGFAAL*
>TCRU_4492 hypothetical protein, conserved
MRGKTIHNKGEETTPETGLQPTEAREGTDGAPAPPQDPPNTTESHEDKSRRVAAPETIPA
LNTSPGSSQEQTSQSSSPSGSETTGSSDKEDPEKNSKNAQISDTPLKDEEQHRESTAGSK
DATTVESAAEQGNTTTPGDSDSSTAVSHATSPLLLLIVVACAAAAVVAA*
>TCRU_4493 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MVYLPLTEQLQRVKDVLATWKKVDETVSQLCPSSAVDDASPGNVCSTTVKVTGGLVGFLS
GNFSDNTWRDEYLGVNATVTNKDDGETDDTGATKTSDGVKFQGAWAEWPVGSQGENQLFH
FANYNFTLVATVSIDGEPQEEGPPISLMGMKMSDDKNPVLLGLSYENGGKWKLLCGDEQN
TEELSSTSEETTHHVVILLRNGTQGSAYIDGQRVGRDEACTLENKDSEAVSHFYIGGDGG
AGDAGRQGEVSVTVRNVLLYNRPLDDEEIAGLAKNKITNPKPEVPKASAKRPLSPAVSGS
DVQGTVPLSNSAGQLPSEQGQQKGSNGAGAGGASTPATSTAAASSGQEPEKQLTSGTSPS
GNKNADGTPSPDADPTVVTVGGETVQGDRTQQTPEVSVSSGENGETAEGTDAQGKEGIHS
QDSEVNAAALSSSLGNVSQGNNSDAGTMRGSGLLPSLLLLGLWVFAAL*
>TCRU_family, putative Se.1
MRGGLVRSRPSEEGQPREPSNGVRGCVRDYIFHQMLDAVHGSFKVFLCDAHAASVLSCSL
RLHGLMEHGVTLLGDPMTPRQPIMSSPAPYFFAVEDASVSRVVEDWMATVPYRDAHIFSL
GCTPHLIPQQLPRTRIAPMAMRSKDIMLCFAAPEVLVFHPNVPSEFFQLLSPLSPPN*
>TCRU_4495 hypothetical protein, conserved
MALVPYTASEWCDIGARPWDLVRQRGEAQVQITFINGTEMSDETLTVAASSTGLCLILGS
VTRPWEDSSFTGHIANLRVFQVPNFENQLILPIVGAARELGRVATTHHCFKAVLEHEMRP
CRRGREESKRSASFAGGRGA*
>TCRU_4496 Mucin-like glycoprotein, putative
MMTCRLLCTLLVLSLCCCPSVCVTADVDGKADNSGEHSGLKDNQTEEPRQVTDPQSTLSS
LSKVGEVVKLTAESQGDRIQEQEEKPTNEEVDGGETDNAKDQNQKTNAINTTTTTTTTTT
TTQAPTTTTTTTTTTAPEAPSTTATEAPTTTTTRAPSRLREIDGSLSSSAWVCAPLLLAV
SALAYTTLG*
>TCRU_4497 hypothetical protein, conserved
MRAGRSVHRQFCYGHCGVHANEPAAQHATQTMATGQHTEHGIAPIWHTDPPTCFAAQPSN
KWRRTIRQDTHRYSFCGARKRSLLPQDQPTSTGTPVDTQETFRHLLLECPGTSAARQRRG
IQEDPRSEKFSQWQLLHSRKPFPLLNRLLGTQMALYS*
>TCRU_4498 hypothetical protein, conserved
MCSQYGPLRSSSQRGRPIAVSVANSCLRAAATQKFSKPPSAVHPRNIGRQATEDSMNSEL
KGLAGVYQHQRSPMGSAVELASNTALLGKVRLEVIGSVMLHFMYQVCQLHRRGTHTTASM
LVWARRPQPKQSTQCHFLSDLTHDGRKADGSI*
>TCRU_4499 hypothetical protein, conserved
MAALQMTVPSLTPAKLATLMAQGADMIAIRETWKSSEQIASMHTGEYLPHAQSRIRKECV
AAVLVKKNLRSERMPLITPQRDSSLDVVVVQFALGQNRDLIVASTYMRPPPQPTQPLGGC
*
>TCRU_4500 retrotransposon hot spot protein, RHS3, putative
MDMLEGCYESVYNARWHHVVEVPGGEGTGMEVKEGKPPQSWTYKKVGRTLEKDDGVQQSG
EAPPRLMVLTSDKGWPYSW*

>TCRU_4501 retrotransposon hot spot protein, RHS3, putative
MAAGSYLLYQLLHYDAEQLPMVAYVITDRKFLFDKITETVKKYGEASSIVDILDEFSGRG
VKGYIIYDVSMKGHEPSTGLPCEGWGMIVVTSPDKNNYESWAEQMGAERIIINCPDESDV
KAMCVWKKHNRRLAGEQAEEESEEEAEEEADYWKKVKGRMDKVGPILRFIFNEQKSDARF
NECEDAVNDITPSMLRYYAGIGTGESCNGNHVSRKLVKVVRVRRGNNFASPLNVLISPHL
EREILSRLENEMKQSDFIFLFRGSGIMSHHTLLKSTPYPHF*
>TCRU_4502 Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MVSVRLTEQLKRVKDVLATWKKVDERVSQLCATLLAQVTSTDNVCSTTDKITDGLVGFLS
GNFSDNTWKDEYLGVNATVKKGEVTSTENGVTFKGRGAGAEWPVGNQGDNQLYHFANYKF
TLVATVSIDGEPEGDTPIPLMGVRLDGGKKLMELSYEKEKRWILLCGDATTNSGEQSRVS
EPEKAQHVVVLLRNGTHGSAYVDGQPVGGDVQCKLETTNSKEISHFYIGGDEDNAEAQEG
VPVTVRNVLLYNRPLTFEEIAGLAKNTITIPKPEGPKSSAVDARSPTVSALDVERTVLQP
NSAGQLPLEEELLNGGNGADAGGVSSAASIATTPPSDFAQEAATGSGDTMLGTGSTQAPE
VSVSSGEDEETAGRTDEQGEEEEVHPQDREVSGTALSSSLGNVSQGNNTDAGTMCGSGLL
PLLLLLLLGLWGFAALFCDGDECPAVQPSVD*
>TCRU_4503 retrotransposon hot spot protein, RHS3, putative
MDMLKGFYESVYNARWSHVVEVPGGEGTGMEVREGEPPQPWTYRAVDDTFEKDDGVQQSG
AAPPRLMVLTSDKEWPYTWERESKDIRDCYVNSEVERVWRIVKGDLTKWFGTHRGTVFSP
KKRVLIGTPGIGKSMNVGSYLLYQLLHYDVEQLPMVVYFIANLTFLFDKITKWCQCTRVK
AVS*
>TCRU_4504 retrotransposon hot spot protein, RHS3, putative
MKGRQPSTGLPCKGWGMIVVTSPDKNNYESWAEQMGAERIIINCPDESDVRAMCVWKKHN
RRLAEERAEEEEEEEADYWKKVKGRMNKVGPIIRFIFNKMNVSLALGRVNSL*
>TCRU_4505 hypothetical protein, conserved
MISKPPPQSGSALEGSGMENANEQRDDEFLALERRAREALEELAANSEREEVSTAEYTNA
LREYRQACQVRARYVEADLVQQVLRHLRLDEETRHVRGLTEQQMQERQALEDAHREEFQE
FHRVWNARIDEFEERQMEMETALLERQNAELQIFYQEVNALTPRTAKCSRGLLDARAVEQ
ILASQREYARAHRTKMKADRLEARDAERFMQAKIELFERREEVLRQKHQQERDVLNKKIE
RRRMELERLRKRELDVLFQRYMNVRRELELQQNIIRSKTGTILLKHASNTKSDASGSAAL
VESAGSGAFGLTVKRRHFDEAMSHRTSPASHQAPE*
>TCRU_4506 BNR repeat-like domain containing protein, putative
MSRHVFASAALLLVVMMCCSTCGATPARENDGNSDLRSVQELQWIDLFVPNKTQVLPKGG
GTPGTKRDGFVSPSLVSAGGVIAAFARGKINAQYAADGKVIKPISSDVVAGYIDSLWDWS
TLVEKVSESTWRAHNVLGTTDGADNRVGDVFNPTTTTKDNKVFLLATSYDMLNQSGGNWK
RDSLDLKLVVGDATKPTDSEQSGWITWGSPTSLSQTTLKTPKAGLKDFGSSGGLGVLMED
GTLVFPLMAKDEAEDVYSMIIYSKDNGANWMLSNGTSPAKCSHPRVTEWE*
>TCRU_4507 BNR repeat-like domain containing protein, putative
MSRRVFTSAVLLLVVMVCCVTGGAAASDGQSSEPNFEWKDITEDGETVDSLGVPGLLKVG
SDVFAVAEAQCKESPDTVFTGIASQLLTMKKDNKPEEVLKNAKEKTQFLEEVTSTKKKVD
VSRPTTVVEGDNI*
>TCRU_4508 BNR repeat-like domain/Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MNDGTLVFPVEATKKKEKEEKDVKTALLIIYSSDAKNWTLSKGMSDDGCSDPSVVEWEKD
KLMMMTTCDDGRRRVYEIGDKGESWTEAIGTLSRVWGNKQKGNEKCVRSGFITANIYDGV
EDRDVMLVTLPVYAKNAEKGQVNGKGVLHLWLTDNTHIVGIGSVSGDDDVAASSLLYKSG
DNNEELIALYEKKKGDEEKPSSGMVSVLLTEQLQRVKEVLATWKEVDERVSKLCPSSAKK
DTSTDTACSPTVRITDGLVGFLSGNFSNDTWKDEYLGVNATVTKEDGAEKKDNGVTFKGR
GAWAEWPVGKQGDNQLYHFANYNFTLVATVSLDKVPKGDTPIPLMGVKMNGDDNNPVFLG
LSYNNNEKKWILLCDGGENKDHSSTWEPQTQYQVAIVLQNGTQGSVYVDGKRVGGNEACA
LKSKDSKGISHFYIGGDGDNAEGQEGVPVTVTNVMLYNRPWTEEEIAGLAKNTITNPKPE
GPKSSATSPRSPMVNAADVEGTVTQSNSAGQLPSEQETLKENVGAGAGGVSSAASVTTTP
SSDFAQTVVTGSGDKMQGIGSPQTPEVSVSSAEDGETAGGTDAQGEEGIHPHAGEVNATA

LNSSLGNLSQGNNSDAGTLRGSGLLPSLLLLLGLWGFAAL*
>TCRU_4509 hypothetical protein
MDLRVGVLGEKEDMKSSRGGILLETRPSPEASNPAREISLNSDMPPSSRQCDGAKPAFIV
VQEGKSSEVAEQAQFLHVRFFLWPIVRGCRGTPSMEHLTPRLQKIAQSAAAVFPAGTTFE
VRREVRINRCLTLRDRTHCSNVYSKSDISKRRITLCEEHRILRDEYAASFSPCDNLPFDI
AFIFDPTIRAEVTHYTNMRHTLERESSVVPGTYFVAVFNGTEIFSIRELVEAFFRVYLEK
TEGEIEENHPFPLVIPPKKGTYHEVFHSNRAEEFASGQEEYHEEEISIPVELVSPRVFLE
AREHHRLLDGPVQQVLVCDRELGVMVLGHAIDKRILGPPSRPPTGSTRSMDSKEMVQSRS
QIIKKKPHVILEVPSPILPPFKLWHLTGAIVEAVGLFTRPYSSVPEFRVRYSTHDDDDVE
LSQWAQKSKRKREREDAFGTTHNIMTLEDAHQILSGAQEKERSKGDQGTRDISFSFSNNG
NSTSFNGTVDAFRLHDEMGPTLGWLLRFSTAFAFA*
>TCRU_4510 hypothetical protein, conserved
MLQRSFVVRWVPRYIRQAPQVRQKEQRDAVAMGRSKAPSKRRAECSAVSKRDGGVARATQ
EKRLEITEKASTVLESPVSDVSRLLLRKAETLLDSWKKLNMTMAISGSRSDSLRGMKNSS
SNQKRDAVAFMAQTEVFAVVKGMIHLSTPQEGSLNRCEEENKHDGLRQNAFQEYRSTNSI
SGMVVIPDEATNDAVNYLAQIGRHCVGKVQDEVASLDDSSPTSSAIFSLREVVVFLELYN
AMDCEDGELLLRLLEELRRIVFSTEKEIRTENHVLRECEEGVIPRLLLTLSSLGIVEEHV
LQRIVAINDGSVLSRAKIARYPESDLIRLLVALNRFGLHHEPCFHVTAKTLRRNSLRNPL
KSFCRNALNFRVDATPIGDGERSRVPSSMAGLTMNELLEALTAIALSLCREREVVKLLAA
TIVTAVEDEEYMRCSTKEKAKTREEDLGLLRTLQVHRAAKVCEQMDMPQPSLAHLLHRLS
IRYGGLLADGGDVSLSPERVGFYDFITADLVKARCS*
>TCRU_4511 hypothetical protein, conserved
MQDSRSFAQVVAEGASMKPAEVDVATTISDVRVGMNTTAETTVPTGAPTDSVPLGGAGPL
PIVRLPGGESYADAVKSRSVKLNGVPVSAGKVLGYVESLTNSTLQEQESVLSSWADDDQC
FFDSIRIAHEAAKKDGVEQPQQGRDIDQSTGSFRQRRGRRGWRFIGGSEGSRNSGRRRKG
YNNNNNNN*
>TCRU_4512 beta adaptin, putative
MASMSSNTPVELRSEVNELRQGFRDPQIEKNLTRKRELLRKVIALMTMGVDTSSLFTEMI
LACGTTDIVSKKLIYFYLISRSENNAELALLSINTLTKECGEESPLVRGLALRSLASLRL
PQLFVFLIPAVKKGFSDVSAHVRKTACLCALKVFRISPVEFHKQRFFERMLGMLRDSDSL
VCCNALAVLVEVSRDAEANGTTEGVFEVTKPILYYLLNKLRSVPEWHQAQIINLVLRYTP
TSEEEMFDIMNLLEERLQSNNSDLILSASNVFFYLTQNYPAVYRQVFDRLKLPLLSLLSS
CSKMEVSYVVLCHIKLLVQREPRVFQDSYRVFYCLYMEPTYVKAVKIEILSMLATEASST
DILEEFAAYALERDKAVRGAAIEAMGKVALRLPCTAQKVLQHFLLFLESDSDHVRGKSLA
VMQNYLRKYRDIEVVRPFLDALVRVYHEMNFVDEDSRVALVWVLGELGEHIEDAPYILEV
MCNENLLAEPPEFRLQFLTSAVKLFFKRPPEMQPVLGTMFKLLINDFSHADVHDQALLYH
RLLRQNLMAANKIICGPMAEIKYFVEEQNAALRDKLFEEFDTLSVVYYQTSDSFMKPSAA
GGEEEDEEEDEDEEEQNDEEHAVNEGMMSMASASREAQEPNGMGFGWQRPVLGLMDSGFE
LSEDPSIEPHEFQRRWGALGEKATSTLQLQLQKVPDTETFEEGLEECGIITLASGAQGDA
QKYYLYAQEEGDDTTYFMIELFLHKSGSVNITVKSDNPHMPQFLLLVKRIVEQF*
>TCRU_4513 Tir chaperone protein (CesT) family, putative
MDDKQAFFVQSEDGRKFKMVIRGDLGKLSVGKIRRYLKSYGIPDGQLLLHDGVVLEDSAV
GGDFGLKNNSMLQLVSPRRGTVAAEVRSKPTSDPTPHVSGEKRSSSTHRATSADTHAHHS
ERPSSRPPTTATVSHVDPSSMSDGLSQTNVVSSTALGSKMNSKNNGKNIGSSLSATLEVE
NSRLRNEVDRLHQELSELRGRQKCGDGGVRTGPVLVDLLQNAKSNLQELSEELGVSLQFD
MNLTCVIGTDERHTVLVTFDHATERLYVYSTLLTQLPVDAAVRVKLYELLLEGSLLGREV
CGGGIGMSLQSGIVLLSTSIPLRNCSTSALKDIMPSFVETLGRWRSLINELLD*
>TCRU_4514 adenylyl cyclase-associated protein, putative
MPVPPPPPPPPPSKAASGERTTTVGGAASALFAEIQSCGDNIATRLRHVQDHEKAYKQKI
QHGEVDFSDFEVKKAEADARRQEQSKLTAAATVDEPVLQLEGDKRWVVKYQKGTSAEQKK
LTLDKVHMRHAVQICNCEYVMVEIKGKVNSVSVFSCNRIQIVMESVVSSLEVLKSGNVDV
KVHRAVPTASVEKSTSVNLYLMERDEALQTEIVTACSSAVNVNFPSEEDASDIIERPLPE
QFVSKIVRDKKGGFKIATTPCENV*
>TCRU_4515 hypothetical protein, conserved

MASLNTELALVKRFHMLSKNYDNRPVVARRSTLPALVRFLGSKDRETRQYSLDALYLLAQ
HPENVELLAEERALVQEVFKVYKDAQYDDPELYELANQLLDLLEPALQGRDPRREGAPKM
KETGSSGSNDRMDDDAANENSIKRRSRAARVLRGVGLDAIHTVELDIPALDPRNGDDLSL
VEDIFQSTRGVLSFSIFLEQRRARLFITCETRALQQVLSDAGFESIVVRDEVVSQEIFGG
DGGSHLSSNRSYYGGETPSKRPSYLESLTNTIYETALVLAGGGSKDDTLSGRVRRQQDRE
QRGSSAWDHAKKALSKWW*
>TCRU_4516 hypothetical protein, conserved
MVSVPKILQVITRLFESPQPSFRPADAYLVLNFLRGIPLDLRGPTVTMNMFKIVLHCPHA
STLFENNTRLATKVILTFLVERLRDDAEVEEAMRCVIRSVSVNQNLSTPLYLTMTRKLSR
QRRDSSTSDSPAALVQDDALVEDLLERVIRRIPRAGQDIREGVPYGFLSQKEMHKRGGRE
FEKPELIFLISTLRHVTVSRAARCKDGAVETVFNPMPLAAHIVEAVIRGVESLPAFRHED
APPRADDWILISHLMGCLDSRLHEFGKRLWRQKARLYDPTSVKFSEDFNLPIWLAGFLFS
LRGTDKIDAIKLWIDIMTTPQVLSEMPPKMMRVLLVDVTFALRNDSDSNLRERLILGGNR
ILDALDTAYKSSSSSTVSASSESVRTRMSFSRFFPPLENPKELEKTFLLLKDALESDEEV
ACELIGESADFVRYMQRTERIDMQTLSTVLQLLTKRVLRVLDQPFLDEANTEAIIAAIVA
FTALLRDIQPKESNGEEDVTLRNLFHAIAVKFFYHHSLKPTPLIIAVLLQYMELLDFTSN
TQYTTRVRELILTALRSVPDKVQEINSHTAQHCFDMTLRAVRFHVMDEEVLMGASVALRH
ATDTAILREMSWEQRNLMIERGAALYRELSHSFSSLKQARRLGKQVLNVTALAASEKVKP
REPQMHSDGTPRHKDFRCLRRCAQLMWVVAMRATLLPIPRTPVDRYLVSMLRFAKKHWIA
ETLTTSCGFLCLLKDPAVHQVDEKLSHEFLDVLLPLFHPLIVLGVTDKRAFYANFRRNKF
IISTACEILQRNSDFLSPCVWYHVQRTFSNLFSILQGQITPLELKVLRLALKQTLRSVQA
CGNRGTWHLTEQKKSLRQETEDETILTPKWIGDMFSCAEFVDDPDLRLYLISLLTEQLEV
VGNEATNETETSVSEEEKSRLICLKKTMLTLRRGSVLYY*
>TCRU_4517 AAA domain containing protein, putative
MRICLVLLSGLPGAGKTTLSLAIQRLSEQVTTEGERSNSRHGGVVEAVLELDTFISSYEE
REGTQRNGSNFSPEAWRRACDEVREATFQRIRQCLLNPEKKRGRNMSSTTTRFVFLVDTL
PYRSMRASYWKLCRDLGKEQFQHKLERDGVMNKCDGRVPFDAVFVNMVEIRLNTPIEICL
ERNERRTETPQYVPPHVIKNMGGSFDVGVDTSAKFSADDNCWVVSPRQASTPWPVIWLED
VKTNCCLPPAALAQKLLERLHSPEVMGELEKQSASFLEAEVKRRERERCDHDQPQEGDAA
KASRSDWLHQVDLRLRAVVQQYMKEFKKSGKLLPGTGALVSKCREEQYAQVKAMLACRQD
DEAFDARKETLLHDLLLEFERKLLAL*
>TCRU_WW domain containing protein, putative Phosphorylated CTD
interacting factor.1
MSAVEETCASTQAQLRVRLLTEVLRYSSACRLAKTLAALATTEVPCERKESRGLMTAAIF
EGLQSAALHGVAEGDTRHWVHPVLDLHRRAAVCERKEAPGAPSAIYTLEGIVLTKGCVLG
VLHDKNGNEARREVSVDELRLAEESSLFHDNLLPALECIQPQRTSKSAMNWFLEKMCGAS
TKLLTSFNQKRRKAWALTDRLIILFYEERRRLAGLKERMKCEGAAIELRDLTLTEREGCG
MVNLEIQICDKTDEGWFHAACPKELARQDSRDVLITLEVHAEHVTRLRRLAVCTEDGQFL
FSLALVLLRYAGLSGGEWQLESGWHAGVPHSVFDALVSAFRVSVECFASPLNCTLPRYFS
AFPDTDVFFGCRGNFFALQHLPPPEEGLISLEANPPFDHEVIAAGLGRALQWLEDTPSTT
PLSFVFILPDSTQTNGIEVRRKAEQSQFFRGDCVLSPHMSLYVHGARHIGQPMKRKRQCE
DGCPGDEHLIVLSCSTRLLVLQNDAAAAMLSASEGITKVRSAWKALSASVKF*
>TCRU_4519 Haemolysin-III related, putative
MPYNENADLPLYTIDQVPEHLCDNRYILTGYRVGYTARMCISSIIALHNETFNIWTHLVG
FLAFLVVVVCFFVIVLIPSSHQQQHEGNAFSNTASESKGLTYFLFAAYSFGCLMCMLCST
VFHTLLPHKSRKVYSWAHSLDYFGITFLVVGSFLPFCYFSFACEPFWRWTYLSMISFFGV
FGVLGPFFKEWTQQQYARSKILFYVCMVGSGLFPIVHIYLLLPGNVSSSFVEGLLLMMAL
YGVGVFVYAFQIPEFFFPGKFDIYLSSHQIWHVFVLAAAFVHFFNTASIYVNFRQMNLSC
*
>TCRU_4520 hypothetical protein, conserved
MVLAAAPQDAVHRVEGALRRWEQHRQNQQRLLRLLTTIVETLEATKHHSHEKCAAIAPSE
TLPLPVMSPFPSSSSLSLSSSITVDAARNGHGVAIKLDPSTQVALGDVLRTLARSQQFIA
VACSRFSWRVQTINEDVQRLCNVLRDGTSLVRKQLDVQRNGRALEALLLAALATIVRSGY
DDTSDTAEHPGTERPKEQKEEEKVECPLAVPNALFHSISLRPYWRKEERTFSAAIHDVTG

VYDCSACTTCNLLRSSLLETLSAQRCFPSPQVYRTRRAARYAWYREMNEAAARRRAAQKS
QWERHERMTEALSEDEWATLTAEDMK*
>TCRU_C-terminal conserved region containing protein, putative PS.1
MTTTGGEQAVSMTTAVEDESNTRNANANIAAVPMNVADKSSAHVLHCGVRDSKHPPSVVP
SRASFAKDGTHESEDTVFVSTLTVHPRYRRHHSRSQSSFSLQNGSARSPTHSRMSSREQF
SWDSIAWKELGPELGLAADPTKEYLRLGCVSSECFHGQNDARERPPRRHTRSLAAWDRSE
VEAPENGDEKDSDKNETQGYTTPIGKNKSCTESLFETAPLGHQQSFSLLSQREASQQGRE
SVGDEMAVKANREACETDAKCSIMTHILVKFKQLYGVFYVPKSEWGTFAIGDLVSVESHG
GENMGRVVADLTAHMSNESLIPSHLAQLPREVLYPEDASKPLETVEPGNNKEKLLRLPRV
IRRGMNKGKKRVYYARRRDTEAYNVCQRLIRERGYSLNVSGVEYQVDFKRITVFCSGLCP
SANPTELYLFIQQLATLLRGSAVEVLFSMECPASLEVTRDITKGVFNDIYASMAKSQENE
EARACPRTPTSAHHTPNVQRSYLEGAMNPATNPPVVPMFGLPPPVPPTPPVMMPAVNMGA
LYGMPPVPPLGWGWPTPPPFLGLPNVAPGMSGRM*
>TCRU_4522 hypothetical protein, conserved
MALVPYTVSEWCDIGARFWEMVRQRGEAQVQTTYINGTEMSDETLTVAPSSTGLHLILGN
VTRPWEDSSLTGHIANLRAFQVPNFENQLILPIGGAARELGRVARAHHC*
>TCRU_4523 hypothetical protein, conserved
MGDAVVRAGLSCSATSFPEGCSTALDSVSVSDDTFSFFSSFEFCATFGALRPPSPAEKLG
AIDFSSDVAGANRSGNGAAGDCVNSGVVCCTGGLLAADDALEGLPVSTVICTFSFPVVTS
SVSGLSSVSCSVGDCSSAFGCVIAGACDLGSEGVGSVVPECTPVSEKLFF*
>TCRU_4524 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSVCAAGTQEAVQDKGSPSLPPAKPQVASVPDSANPRTGTPE
ITGINAVQPDGTSGLGGAADAVDRDGQEPIKESSAPDSADPTEKVQEPATISETGGTGPS
SQPSSGKKQSGNPTSQGSSAETGVPGSPNTEGPENIPKAKPGVSDESGSSGGSVNPNKSS
SSVTASVPAQSQKENAPTTTTNTTTKAPNTTNKYYNYRGANHDDHPRTVTSSQIRR*
>TCRU_4525 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MEDGTLVFPVRAKSGNDGFCSMIIYSKDDGSNWSLSKGISPANCSNPRITEWDGSLLMIV
DCDDEQKVYESRDMGTTWTGAAGTLPGVWVKSQLFFWDLSLRVEALITATIEGRKVMLYT
QRGTFLGEKRERALYLWVTDNNRSFCFGPLGMDTTVEVEFASSLLYSDGKLHLLQRRDNG
EESALSLSRLTKEVSTIKSVLSTWAQKDAFFSQLTIPTAGLVAVLSNALSGGDTWIDEYL
CVNATVTPNAKKVKDGFQLTEPSSRVSWSVNTQGNNLRHVSLSHNFTLVASVTIEVAPSG
NTPLLGAILGDTNSNHTMGLSYTADKTWGKMFEGKITTESRPWEPKKEYQVALMLQGNKV
SVYVDGQSLGEEEVPLKSETRLGLVRFCFGACDQKEGHEKEPHVTVKNVFLYNRPLNSTE
MRAIKDRIPVPTRGPETQLEDGTERRHIPRIEGVRANAPAGSGLLPLLLLLGLWVFAAA*
>TCRU_4526 retrotransposon hot spot protein, RHS3, putative
MTLVGLRMTTAGGHHTTASTVGQFTECLAAYFNGWEELSRDMSWDIICVQHAASTPMSDW
QGCDVVNSDNVNRAENREIAAFWEEKVHQYIAAISSDDAIRDEAL*
>TCRU_4527 hypothetical protein, conserved
MDRPLTPYELDVTIRDSLLGSAPGHDNMLNEFLHRLGPVACGTLRNMIHNSFANGSLPED
SMSGSDDGDSFLPSEADIFWLPLFFMVKKSDGEDSLGQ*
>TCRU_4528 retrotransposon hot spot protein, RHS3, putative
MWRCFCRSHVVLLRGRWALTASPTGVAVRLHGAPTTPPCECHAQRHWDCGTKQPRVSFGA
SGTCWPQLGGASGMLHRTGVVMAPRRGSCDGSDAATHIRVVETQQPKWTLDSWLDKVLLE
GKERITNMRLNDFLRNYFDGRGVVEFYRNVYMKEFLGSPNEFIKDEVLLDTIKASPSYQE
LEKEREEYYVLLGASQDLEKERIFTLRHWREFERRDTVIPLARAKINKAYSQILREERWE
AEEKARRERQKLGINVSTWIKDTVREGRVRVDKMRLNDFITMELDGRGALDANRDVLLEE
FFKDPKKYICDAGVLNEIQALDRYKRMERAVRDEMDMEEDADKLHKNGVDKLLKWLVAAA
EVKASVHGATKRFLDAAAEEARNPKKSSAPRYLEGCYESVYNARWHHVVEVPGGEGTGME
VHEGKPPQSWTYREFDESLERDDAVQQSGAPRLRLMVLTSDKGWPYSWAGNRRINPLVTA
M*
>TCRU_4529 retrotransposon hot spot protein, RHS3, putative
MAAGSYLLYQLLQYDVEKLPAVAYSFGGNTTYLFDKTIKTVTRYLGRGAFKEFLYDLRHL

KMKGYVIYDVTEKGRPASCFAFFDKWGMIVVASPKVSNYDHWEKQVKAERIIVNCPAEMD
VKAMCAWMKRDETAEKQAECWRMVKERMDKVGPIPRYIFDANKFIAHSAAIEDALDGINS
RDGEKHFTHGGVRLWYSENPSQKLVRVVRARGEVGAEVFLNAPISFCLGRRIPHYFGKRD
E*
>TCRU_4530 hypothetical protein, conserved
MTKIPSKGNACRRLYFLSEDCKRIHSCDLDHQGFPINRKRPSVTVWIRDIEKVLIGPSTA
SFVNYSGEAQLAKTRQEAVFDNGTHRHDATQNITSSSLGTDNRRAFALLLRGGKSLEVVC
ETDGDCEAWLVALKRLLHLRTPAERLLEERRGT*
>TCRU_4531 hypothetical protein, conserved
MTWRRQDVGLRPVLKWRRGCMMPAMREGVDCSWGHSSILVVFALPVACVARCVLKRDGRC
HDGLLRRWQSLCSRHTSTHSSLSLFVGVIAAGHCCGRDGDTTASPLEKVPRTVGCGAARR
FACSPNDVTAQSLHCGHFVGITRCGGVRKSRSPDEDGVVVIWQLSTSGLSPLRIALAA*
>TCRU_4532 Concanavalin A-like lectin/glucanases superfamily,
putative
MVRSHLLQQRTNEKGSVISLARLTEELKTIKSVLSTWAQLDASFSKLTIPTAGLVAVLSD
ALSGGDTWTDDYRCVNASVTKAAMVKNGFKFTGPGSMATWLVNNREDNNQYGFVNRRFTL
VATVIVHEVPKGSTPLLGASLGAPVSTNFIGLSYSMNKTWETVFDGKKTTSNTTWELGRE
HQVALMLQDGNRGSVYVDVLIVGSPENITTLETLGHEITQFYFQGDEGDINSNVTVTNVF
LYDRPLSVGELKMVKESDGKKGNGDGSMRGGVSQLLLLGLSGFVALC*
>TCRU_4533 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MVSVLLTAQLQRVKDVLATWKKADETVSKLCTSESAEESPSPGTPCSPTVKITDGLVGFL
SGNFSDGTWSDDYLGVNATVKGNDDEGKKAKKTSDGVKFKGAWAEWPVGSQGDNQLYHFA
NYNFTLVATVSIDKVPTSGSVPLMGVKMSGDGNSILFGLSYNKEKKWKLLCGSGSPEDQS
RNWEKDTTHQVVLMLQNGNKGSVYVNGERVGGNEACDLINTKDKKISHFYIGGDGNSAGG
AGRQKEVSVTVRNVLLYNRPLSTAEIGALNPNKASTPSPVDALSKGTLSQSSSGGQSPSG
SKSLNENQGADGGSTSPSAPSTVTTSLGKEQSVIQLSSGISSGGSKHVDVASSSDGDPTV
GAEAGGAVQGDTPPQTPVDTTDTADANAPSATKVAQVGPADTTAVGASSDANGETAGGRN
VQEELHARDRGVNAAALSSSLGNVSQGNNSDAGTMCGSGLLPSLLLLLLGTWRFAAL*
>TCRU_C-terminal conserved region, putative PS.1
MRQSHFGPKDQGLPHGLSSGAVNFFMASGDGHLQKYIERMLGWGSGPHQPTSTPVYGPSK
TPRLQQFVDMTTNNSGMTPFFSLNSAAGGCGNNTVEYTEEEAVEREEERTQVYMDPSQRQ
EKWEDHLAQAHITMSTPQQKKRPVQISPGVNTPASTMGMTLSPATAGRSVIQVTPASTAA
RSTIHVESVSHPPPRSAHAVTMIGGSNSFATELESAFAEQTKRKNAVTKQNHQEEAEIST
CRADVDTTQSVADISLDGKSQKTLDTGRVERSTQRRNKEKRHGKLNNCSQQNHQRQNNKT
NANKNNNNRSVLTPLTPHENTSSMENNRKCFLRLQCHGDRPATVFSCIKFHAGDHVIFDA
DRGVDLGEVLHCEELTDESSPNDTEAAAAAAATAGGFGAKGGSRRSLPRVVRRATPEEVE
DWRGALVKREEEAVLECRAACGELKLTIHVAGAAFQFDRQKLIFFYETDGRVDFRSLLQV
MFSKFRCRIWMERINATP*
>TCRU_4535 BNR repeat-like domain containing protein, putative
MSADGCSDPSVVEWEKDKLMMMTACDDGRRRVYESGDKGDSWTEALGTLSRVWGNKHEEN
EKGARSGFITSTIDGVEDKRNVMLVTLPVYSKKDENERENSIFG*
>TCRU_4536 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MVSVLLTEQLKRVKDVLATWKEVDDLVSKLCLTSRAKGDYSTATACTTDKITDGLVGFLS
GNFSGTTWKDEYLGVNATVNNEDGAATTDNGVTFKGRGAGAEWPVGKQGDNQLYHFANYN
FTLVATVSIHGEPKKGSPIPLIGVKVNDGDKKNAVLLGLSYNNKEKNWMLMCDGSENKEL
SSPWQPGKKHHVAIVLQNGTQGSAYVDGQRVGGDEQCKLETTDSKVISQLYIGGDGGSAE
VQEDVSVTVTNVLLYNRPLSSEEIGALNPNKALIPPAVSDNAQGTLSQSPDEQPLSDLKS
LNENKGVGGGSASTSAASTVTTSSGKEQSANQLSSEIFSGGKKNVDGGSSSNDDQTVGAE
AGDSVPGDGPPQTPEVSVSSGEDEETAKGKDEQEGIHPQVRELNATALNSSLVNLSQVNN
SDAGTVRGSGLLPLLLLLGLWGFAAL*
>TCRU_4537 hypothetical protein
MLRGTLNGVGFMLVDVPPVSKVISELRKGFYGGGMVHNAFLITSDEVSMQLISSTRNGAP

DALRETMEAKRVDFVSGVVTEAMLEMEGVAFIDPLLLEPRLNRFRRNVIRLSPTLEQQLF
VLAEYLGNASGGSAHAVIRSGEAAAMADVLRRSLLTFGVSLAATRWWTTCRWRAMCLWWA
FQLGMPVRLRGTCRRTAVCACSSCSWSLRCCMLSLLLRSVTVRVRTVLCLRRACRTGTTG
VQRRRPPGILLLLCRGRKTGRRCH*
>TCRU_4538 hypothetical protein
MYRVSAEKLADFFYNNVAVAVDDMLYGPFADGGACPATESGAGCGRNYGATRISVWPLAR
ALDPAVPELFPAVTPSMKYADPAAGGLTARLLIGVIAG*
>TCRU_4539 hypothetical protein
MPAEAWVGRSLCLLSATSVLTICASSDKEVPSSELAALEDVTDADWFTVSPAVGVVVLDT
AGVDGAPSLGPLLPFEIACSVSCGAAVVGAGAVGCVSVATGVVTVSTDGEVAAAAGSGSL
SGGGMVTLLALRAPISVSFNGRLYRKTFATVA*
>TCRU_4540 signal recognition particle receptor alpha subunit, putative
MIDTLSIISNGGIVLWEQSSDSSGRRLMVNRVIQEVLLEDRAGVPELVIGDYKVCWALEN
DAQFFVMCVYPKFLPYLHMGAFLRGIVRTFAKKYGRIQDSLFDEYDFSAEFAEALSTLDA
GGGGGGPGVAAAEEVADSGSGGSEEGEAAQEAEGEEGDEEKVVQRGGDRIVTKSGQIIGR
KGNKMTVGGKPAASTKVTKKGKPLKKATRWDEPSFDPAVNDQRQQRAPTQEELEAQAEAQ
RASFIKRLPNGNVAPVREKEWENQPRGRLANWLRLYVGRRELDSQDFQRVIPSLREKLIA
KNVAVEVAEHVCKSVETSLEGMKLGTFDSLHQCIEKAMTSALHRILQPKHEVNILRAVAS
AQSRKKPYSIVLCGVNGVGKSTTLAKIAYWLQQNDHSIMIAAGDTFRHGAVEQLEVHGRC
LGVPVFQMGYGTDPSAVAAAAIAQATRQQYDVVMIDTAGRMQDHESRMRALAKLIHDNQP
DLVLFVGEALVGNSGVDQLRRFNQCLVDFSPVGTVPRGIDGIVLTKFDTIDDKVGAALSM
VYELGQPIVFVGSGQTYQDLKVMQPDVVVSALME*
>TCRU_4541 hypothetical protein
MLTSSLCSLNRQMGCATGSSTDSLRYYYEDGRGNKVWVQNLTLDYDARRLDCKSCGNGGL
KDLHKDPCGTFSPPLHKRPLLRQKTSPARKVASLCGRVVFASANTQRVKKKSFLRRAETS
AIRCTCSCPVHSGLAREPADPYVKWNEGLNWTFLPETSFKGVIRTVDDAEFLLEKLRSEE
HILRKAYVR*
>TCRU_4542 Domain of unknown function (DUF3846)/TPR repeat, putative
MNDQSPTVAPFKYVLIPSDDAEMPVEMTFSGGSDEELRASIQQYFRRQLLSQEQRTEMAK
HLTEKAKDGEKQEEDGAAASSVQQSAMIEDYLEQTSFEIVPLLMPGRDNKFIGTSLYIDD
SGRFKDLALNSRASKIAQRDIRGDAFLLCNHDDPALDEWSRVDCTLTHYETLLKNPPMTN
YDTSNRTQMASAAMLRESDTKRISEEDAIKAKKAKDDGNAFFSAGDFKAAVLAYSESIDL
TEGRRDLLPNGAEVTALRLSALLNRSICLHRIGKNDDAAKDARAAIHLDGANIKAHHRLA
VALCGSRDYDAATEALNAFERLGGPASDAAAVRHAIGEGVKALQKEQKQKYSKLFV*
>TCRU_4543 NADH-ubiquinone oxidoreductase complex I subunit, putative
MAVGGGAAHAHNEEAASRQGDRPPFERIPMPSMATEEFGENLPAFDNGKPMPSPRGIFDR
FSRVLQLQYGQDPDIPILGSSLERKYDSWFDYITSPISPMRPRTYVDAYTRPNPCPEEYW
AASWRWPRTKYVNAKVSPPVDGKYNDYYHYLAYKNWFERERDVYIAHANLVNEMTMRCMV
KEGQYNAAKNCRHLYNKEFAMSRMEELNQTLLYMAITGNAAIRETPYPENFVEEKRKIYD
DWLFRTRMKKPGDVV*
>TCRU_4544 hypothetical protein, conserved
MDALEVVRREDGDEEDDNEVTLQECMRIHKLARSVDELVAWSFIMGEKEMILQELENVVT
QTEQELEKAEKALKYQHRRCALIPDDIYMSSERRDQRPHAARGEDRELSALWAEHGNSLT
RQYERHLARYKRLWHELLEEPKVTAENIE*
>TCRU_4545 hypothetical protein, conserved
MSVDPLLPASEERQELERLLKENRKLREANALLRVSADTKRASANNGSAKNASATAEEVR
DNTGPSDESVDVNASSKAANVKRLKEDLQHCRKELEQALCEQKEAKEEYKQLKSIFESFV
VESCEREEACKLLFARVYEEVEEQKKLCEGLQRQLQERRPAVVAPQVATPAAAVVGMDPS
SLYDLVDNLRSSLSELEHRLGYSGDAGSRHTAPAAGVAASRVAREKARSTVVVGTTLRGD
THRQTQEVLGHHHSQEAESAVRLVVPAKGAGALRATAMPGSQSTTTERKKRGRKKLSEIE
TVKRHAGGSVSEASAASLFKGFVPVIAKQKGLVVNFGQEPIADYLGLLEKTDLGNVDVLR
RELMNFCGTDVNTLASYAVEHFLSKSLLKAPLVTLWKNTERVMHIGKDVFSAFMKQAVRK

LVRLLGPECAAEIDHTPQLRCLALVVRMACAISLRDTAQGGDAFFVTFYECTVSALRSWR
LGSSAGEQRHVLGPWMVVVQHLCGFVEEIHEIVRYYANSERVLEELTIPNSLTRYAVQAI
MASCYFTSSPQSPVAPLGSDAHADMDMWINFCDAMDWSHNELPLKMIESAAAKILAHSKD
VLKRGEALLSLRLLVLQKGLGLLQTLTEELRFSGDEVDIDAAFAELFSLAVIDLQLEDPR
DEQWGRAMAFFAEYLSANSVEQSKSNEELLAACKGTHLLVLRAMLQLCHGAGGAISEESA
EQLAKALQWAKALHVGLERSMREKKTSVLVHPFQSTLLGQQLRYLCSQEL*
>TCRU_4546 Protein of unknown function (DUF2870), putative
MVLLTVKGTMFPDEFTFECTASTSISPELARQLCHIQNARHQVKLQLLSARELLEEARRK
RGLDASGSTDDALTSYGGLIEEVSTRLKDKNKPVTLEEFDHVAEKLREMTEKLFPEECSL
SEGGRDAAVERLYALHDNPDIDEDYRLVVYHCRAILDKRWKQQELQREDQAGLWFCGKLM
EGTISKYSGRNEKSRLTVKVHPKDGAAPSIEPRMSYDDQRALFERMRQRREEYKTLEESE
LREKVLAQSRGRVVLDVASVSGGVRVDMSRLRPICPRKEENDVT*
>TCRU_4547 Small acidic protein family, putative
MNSLKGSMKELQATAAQLAESRGLQPDELPCHKDALLILAVAALKNIEKDENIFLSSSEI
VAAAKSARNMLRPYLPCQPREEGKGELRADKKRGRVNAHDNNSDDDENEDLGQYSHTKVF
DGNAKKRAKFARLMGGGKGEGSHHNTFAADASAIKRINGELEDQFNTALSRLGKKGLGA*
>TCRU_component, putative 2-oxoglutarate dehydrogenase .1
MMRWIVPVAAASRVPFLNCRAAATSVLQQRRVQSDIPLRRLLYENDNFLSGSAAMYLDSL
YQCWKEDKTSVDPSWDAIFSAGGLPSYETPLLSSAVRVLPTTSEDAVTVQQSLTDCGRLT
WMIQAFEDRGHLRASIDPLGYECDDSISRSYSRKYKEVLRLDLASFGFTPDDYNRVVRVG
FQDKVGGVLNTNSRPMTIKELHEYLTMRFCGKVGYELSHIADVDVARFLREVVETGDGGY
NPLHRSLSKEERLWAWDLVASSVHFEDFFKRKYSTQKRFGADGAESLVVGLRALMDASSK
QGVEKINIAMAHRGRLNVLYHVIGKPFPVILKEFVGITGKELEPFKIQSDVKYHLGARST
MTMRNGKPMDTELLSNPSHLEAVNPVLQGYTRAAQASLGKDGSSTVLPVEIHGDAAFSGQ
GIVFETMCISEVDEYSTGGTVHVVVNNQIGFTTDPKSSRSSAYCTDLGRVFQCPIFHVNG
DSVEDVVRIFEFAADFRAKFKKSVVIDLVCYRRFGHNENDDPTITQPLIYSRISAMGDLF
NKYSGELIASGVITPQQQTAKSIAEKGRYGNFQAEVPLVHYSSYLKSCIPEMWRSMKYSD
QLGDVKMESTAVSREQLQPVLDALKTLPEGFVVHPKLKNVLDRRNDTLEKGEGIDWGTAE
ALAFGSLVLEGTHVRVMGQDVERGTFSQRHAVLHNQEGIGKYVPLANISKDQAPFIITNG
PLSEYGMLGYASGYSLYDPNSLVMWEAQYGDFANGATIVFDQFISAGESKWNQQQAVIVS
LPHGHDGRGAEHSSGRIERFLQAVAEDVDTPAYSPAERAHRVNMEVVYPSTPAQYFHVLR
RHVRRDFRKPLILFFSKQFIRSPNESSMDDITLGTFCPVIGDASVPPEKARRLVLCTGQL
YHILNACRAKNGNTDVALVRIEELSPFPVAEVQKLLLDYGNAELMWAQEEPRNQGAYYHV
EPRIEFYTGGKRELRYAGREISASPSTGYKSTHDAEERHICGVVFA*
>TCRU_4549 glycosyl transferase-like protein
MRLRGWGHTAFQTSLNGSRCWGSRGASSASHCVALRSASSSFSMSTSRSPFDAVYVINLN
RRPDRWKFILRQLQRAGFREGEYERFTAVDGRAVDIQKAQACGLVSLLGILRLREEESRR
IWGMDLNPAAVGCALSHVLLWATIAARRYHRVLVVEDDSLFPHDFQKKYDERMRHVPQDW
ELVYVSGLDTADQTSQLRVAEGVSRVPQMHRTTNCYVVTHHGARRLLELCLPMTYQLDTM
MTMHAVSDPQSGVPHVTSPVCYTLQPPLVVQATRMGSDIQSSNGRDEQEEERARCRAAGW
TTD*
>TCRU_4550 class-E vacuolar protein-sorting protein 24 (Vps24p),
putative
MLDKLFKRVDPQEQTKLWRRNLSSEMRKIDTQIRKIQREEMKVKQAAKAAARKGDTVAVR
MLSKEIIRARHAVKRLYCARTQMNSVSMHLQQQASQIKLAGNIQKSAAIMTQMNELMRVQ
EVQATMRAMSKEMMKAGLIEETINDTVDNALDEDISNAELDDEVNKVVEEVMHGKMQGAT
VGQAKLPQTQQVTEEVNAADEDEDDLLEKFNVLRGSAT*
>TCRU_4551 CRAL/TRIO domain containing protein, putative
MGNCEELSYEEAHAAQTRSGPTVLSKEHQRKNLELRSRLRDVLPVDDRQKLSDCDLLYRF
LIGRRWVVEAADASLRTYVSLRKKMNLNTIIAEKFSKEVETTASCLYGFDKEGFPVMWNT
PDIPLLVRMLKDGLERDLLRVQMQSMEKARFLAKERHVDRCTLVLDLRHVGISSANSVIL
SFSRELAKIMQAYYPEIMCRMLVFNAGWAVAGAWKMLRPFVDQRVQDKVRFFPGAPTMEA
ILPFIDEDQFPPSFGGKGTRDVAAEMLQAEIEHVQGIPVGESPQGTSNTVVPTTTGPTAT
NVSITAISLPHSVHPGSLRVMGEKMGISTTPPCLPDDTSVRVGSGSADAFSTCVSADNEA

LEVFSFCSSIRSDSDDAVSLPLIQIGSLEALELSDKKRGGPESRAGKERQVQFLVPERTS
MSINLTEYADDKIIGFFGNKFVGEVEHNFVYGASEGFMENVLVPRTSSSFSSSPTAFLSA
PSAVRERVMMGELLNESGHRIHPHVIVCDAQRRARFVLRKSRLRRCVDVFQFLGGANVMT
DSLTRHTVSGERVKLAKCVPHREDTDDPTVWMMNAVTADGSRQLRQQRTSQCLAEKKGQT
LIAYGMLAAMAPIDVFTLLVGVCRVWEAGVRLAPRGCGIPKAKNLFGVQMPLVKPAIFRR
FWRPESSMPATDANQETETHPE*
>TCRU_4552 vacuolar sorting-associated protein-like, putative
MLERERLQEKERNPGLLGRLLRKVDGCDVRFIFDGKMDECMVTVDDPYERKSERLHLFSD
NEPVCGRVVLTPKGAYRHNGVLLELVGVIATFEESEEKVEFMRQDKLFEPDTFRSVTSLE
FNFAAPREYESYRGMNARVSYYVRVTIYRPVKNITELVEVWVSKVDAHMSETQPDASRHR
SYFRETVFGPQSISMDVGVENFLHIEFKYDKKIFHLQERVLGKVTFKIADMDIKYGEVGV
VRKEFIGPGNATDIMQSETLQKFEIMDGTPIVGEVVPIRLYLRSIPHLTPTYPNVHNCFR
VLYFLNLVLITGEGRRYFKQQEITLYRRHGQEAPIGAAMESP*
>TCRU_4553 short-chain dehydrogenase, putative
MFVLERKTLLSSVVAFFLLRWLLYRVFRHRRGEKLVPGSIAVITGGGSGIGLEFAYLFAR
AGCHVVLVGRNAENLHAARASCLSLGAPTAEVVVADLSTVEGTDKVGDALQGRQEPLKYV
VLNAGAGAIVPFSSDPSFNDVCDKMMQINYFSNVRLLQHLLPALEKSNSAACSSRVIVLS
SLAGVLPSVYRSAYTASKHAIQGFMNALRGETAVPITLCCPGYVDTDFHQRAQLTGAFAS
SNTRRGVPAHVCARACLDGALRGDAEVLTTLSGKLGYILRPIFTKFIDARAKKISLHSLQ
K*
>TCRU_4554 60S ribosomal protein L29, putative
MAKSKNHTNHNQSRKNHRNGIKRALPMYLHNSKRGSWLPALINARRVRKNNQKAAVKARR
ERLAAHKAKQN*
>TCRU_4555 60S ribosomal protein L29, putative
MAKSKNHTNHNQSRKNHRNGIKRALPMYLHNSKRGSWLPALINARRVRKNNQKAAVKARR
ERLAAHKAKQN*
>TCRU_4556 hypothetical protein, conserved
MWRRTAHLARTPVSAFLHEPSQRKTFEETLAQCSANGTDMASSLTSDFASLQSKLLKYRI
VRLRDELQYVRHNPLASLPSPGDLLKHTVLLTLVFLFFRNLGRLSFRPLEPVTDPADATT
TETTEMNTKAGNN*
>TCRU_4557 hypothetical protein, conserved
MTLRRLVKRPKITNLQMLLMRRREPYKPTMKDRHEIENREKLERFETKAAEGIMFVPDKV
LPPWQKSLATNAYANASRMNFRGFRVRVADKQDEPGFPTPFR*
>TCRU_4558 Bromodomain, putative
MGSTGRKAVDEINHWIAYIDCALSHPHPLPKGKHVFRSDLSTVPEVRDIYDCLYKLYAEE
SASASFREPVNALELGVFNYYEVVTEPMSLRTVLDRIAEGGHYSQASQVLADVEKIWSNC
EKYNGADSALVKQAKKCQGILTRLRERLAEEQPAPNAELDKIISAFESADESVLGELEAY
FRREDPSLIISNGDVDLTALRVKHLKAMKAILERAMNGGGGRG*
>TCRU_4559 hypothetical protein
MADVGGKSPHTEFLAAMTRLESALKRDLETILKRQARAVAAEQPSSFREFLYPNEEVMVP
QRILALRAKRGAITNTMMPPEEEGFE*
>TCRU_4560 hypothetical protein, conserved
MLRLCKVWLRVQSHQKKRSQHPNAGTRFGRVYNRGFIRYGFGGFGMSVYTPKKDRTFRVQ
PLPCLPGNVFADDTSLVPTTRTLSPNFRAFALQDGGVLFSHPSHEQIMRWGQGVLTEETK
ATGMTSMDNYVNSRIQSIIAENTVENVALSHWRRRHMWNLIKSHGKLQRRWGVSDETKGA
RSNIYGRSG*
>TCRU_4561 Protein of unknown function (DUF3595), putative
MIHPFALVFSGLLTSSAVLGGHLPAAVLLIYMMLLRNPKCATSPIVLVLAFLFAVLQLLS
TLIVNLLVAFSPSTRGGLFVHHRVLIESFGIYEAGPGVKAWILAGACVPSGLICVYIIYF
RKKLLSRISMGRVRPLLTTVSWALMSVTTGLIVPTVLAGVLLVIGMIALSCVALGGARTI
FGAASSRPRRFLLLFLHFCSLCGTFASCIILVASCVSQNAAVACALGNLDPMYGLNKLYE
QPADIAICRFVQLCLMMVTLFLAQMAMECHGKELQQQNAGDPLLREEVSNNNARVVEGTQ
GISVTVVFNHADVPSAPNSASAAVPSHSNHHLSRPLSAPHGLSLAGHSSPNSSAAFGTNY
LERGLFLCGSLGTWMMRKLFASSRMLPLAFMAANMVAFPSVVSLSLLPTMMLGQLVRFHF

FASLLRPTLVLNFFLVNVQYVVLATASIQPPIVRHLFLADEGRWWGLAQVVSSEIIFLAM
LAADAAIRQQHRLTHSEEDHPDEIVVPHPLPLPSIAPSAPTASHVAREFVALSDEKDSSG
ESGGDTSLDFLGIWRHAEFKLGARRVAELLAYVPSEPLESSEAFEQLFSFLVGRRPTAEE
EKCLCKEGIGDALLREKLHDSQSPLLSYYVHWAGILLMRHAVLIALLLLFIVGSFTYQMD
ILHAIVLLLFVLYFFLPDSMDDAWMFVVIYLMLLTSFKLIFTFVSEFVTLPVYIAGSPLQ
YATVGLVPLRSRYEAIPYVVAVFILTFLFLRIRVCRSWGTAVSLHEWDRFCHSNTARQWS
MRVTMTVATTVFVALGVFLHYSFIVEGFLALFLLLTISAAAFSLSDAFLGVLWSVACVYS
GIVVVVTSVCQFTQLADFIWEHVFQRLCGHDGDGSGNSTNARRCEQESGLYPVREDMPLT
LFLAPWFLAFATAMLHRAVKRVRETPPRWARQPDGSGGLVGMTVEQQEEEQPKRGEQSEG
EQRVVPVECVSLPCLESDDQRFIRHMLRLLAVMDKLGDWVAAFGSDYGGILVWVSLFLAA
TYRFTAIGSVYMLFFLLDLTHISVLVYCVLHILVLYTYKFSFVPEITYSIFNVPLASVIG
LDKKGGNTLFEHVIGPVIVFFVMLLRIHTCGANREVRRRQRTEGPESSNWKSVLCTQLFF
YAGYEGLVLTLLLVLACSSHSCIGAFVGLAVLPLLLAMGRQQLHRVSYSFPLLLLLSLMV
LWQYALLLNAAHRLFPAIADYSEAKETDGMWEYWVFTSRYHTLLGCVLGIMLLHTSRQQS
GDTAVSFSMLRSQFNGHVTLVSFVRAASVGSLQLLPRDTFDLVVPSFVESLPPSCLGRVT
TFMVFAVSYLCPVAFLSFAAGVMSQPSVINLLLIIGGLLQVAQLEMLHWTFFSLWPFIAM
AYWFLITLSVVCNAPYVRQFILEHYGLSEVLGLLQAGKPFQLGSLHVLLLFMVMLQTRVY
DEFRYTKLLRHLYDRTATRHTRHEELWAWLRGKQEAEQQLADARSRALHAKLEEIRSTLH
GAHHAWVPEDSSTQKCSANAVTNSQQLKDEKMMMMMARQRIADDDDDTAARLKREEEEEE
ERSAKGSMLTDDKVKGSKKKSEKDGTCAHKFKTGIQRIIHVSATKLANWLAVHTYEPHRH
TAAHYRGLSSRLFWVTIRALERHTVMVVLLATMINFMLSQCVWELLPFCFMLVVAIAYHP
FPPRPIFVFFSFYVALGILLKALIDVVLAQVSYSPRLLKILGWTILHVSEGAYWKQRIGY
SYVMMDFVVFATLLLHQDICLANGVYSRKDILRSREGEQAAGNTKGTNNDPLPPPSPPSS
FPAIYSPSSFGDAAPGTEQLPAGRSPVEDPIGRSRTSCMMGIYRKVCLAVLGFVRNATSI
PGVGRDWYIYYSTVEAIALLVFVFGYNKLSGWVDDTLQESVKRNLLPGPMVTVVLVSILY
MIADRMLYVTQCMKGKLLLNTVTGVAYCILYMLWGNLLTVSSRVVGNLFFTLKILALTIA
VIQVRVGYPRHRRHDPFTWTAGRSRIAGYLYFWYRCLPFLWEIRVVTDWTVEKTSLHLDN
YLKIEDLYDIVFERQCKLYNVCKQRQALGTPIPRSTKVTAGLSRLVLFVGALMTPLVYYS
TFNPSMQSNEVTQLRVGLSFMSSQPFYASTTFTAEEIPNEWFLWLARTRPSLDRNGIMNT
KKTLQLVNASSCSNELWPISPQAYGQLNEQLMEVMENKTTMQLFQTIELSRSGTSNFVSH
TQSWTFSWEAARDIHRMLNNPTTNGTGYVKLQNFYTPFLFSHPDGLAAFDDGGGANVMDC
SILLRQEADSVLNNTVRYWCVECQSLFTHGNIPNSNKTRFPEWGCLSTGEGCSNFNFERR
NGDVNYNPVPMYFVVLSDPSVGGVPFLQGIGIVALYTTFVLALGRIFRGMFANKAKYTIL
SDMADPTPIAQLIEYITVARECGDLPLEQSVYIELVDLLRSPERLLRLTGFNRQMYDAET
DVIQPSHATPSNRMTENLSHRGDALRGPEAGIAPADDAAREVKAAGHDKKE*
>TCRU_4562 hypothetical protein, conserved
MSTPLCTVYENTIGGTRPRRHIAPQIRTAGLVVGRDCGTVAQLTSNYYSSGRVTPDLIKF
HRRGGEVGRTYRHYGIARDPPVDESIRHGIKNDVSESALLCLQPDTNHLSALMNEQLERR
YLSSIRRPLGRAPAPPYEVRVPRDGFGVRSDPSESVKRVMYGGKDVDVLHPVGERKDRGY
DWESIGIDPTQHRFGATFAKDAITAADVMCENRPISTVFPKLVKDHKTAVKTELGRPRTY
GFDNSAFEEKAEKLAVRRSRRGDGDAARELLSSWAQHPATVQAREEQSARVAASKTGLMG
DGTKNTTTTNNNNTDSDGINGGSGRFRSRFTSTFGSKRADGPVSLTELEDEARVPHLLYP
SHYVQLGVKSKYFAGGRPLEDIRRISKQVDFGLTDSQIDDVFASIAQDGVCGIEQFKNKA
VAMGYLA*
>TCRU_4563 actin-like protein, putative
MQHSVVVVDVGSSTTRLGFGGEEAPRVVAPTVVGTPYNSGMLGSLLQHHGDTFSGDAAWE
RRGLLELSYPVQSRRVVSYKALEHILHDALYKWLPLVPHDTPLLWVEPVTTPREDRERIC
EIFFESFDVPLLAMTNAAAATLYSTGRTTGLVVDSGEDCTTVNAVWEGYSLHHTFYSSPI
AGRVLTDRLLEYLRGKGYALSTPQDRCLVDKIKRSLCYVAADAEIELKNLRNKPRPDSYE
LPDEQRIFLHESQFMVPELLFNPSRANDAGFGAGDGEVGWAEAVTQVVRRAPSYAQPRLW
ESIVLGGGNTMLPGIEQRLQREVSARNNGGEQTINCVAFPDRDLATWIGASVVASMPTFS
HLCLAREEYHEKGAAAVHLRA*
>TCRU_4564 hypothetical protein, conserved
MQSEKKVSFYHKVGSNKDRGPTVSIPNIPKVLDERARMRLLCDYEKYEPELLKHHIGTPE

TTQTIGLKLVLTDFDRRLPSSSEPTIAEREYEARRRNRKAKSQLSPAFPASKQLLKRGAA
DSQLAPAAACDRARTTTVPPSTSPSTSAPLPENVLPLRQHRGRSSHASWVAVTTTPSLSP
SEPKSRETSPGRATAATRSPSKQVSMQLAREVSHSLQPEKGEMVKSLVPQKPLYPTSSVK
GGSVTSPTGGGGGALFPQKNDGVLNAELCGKLLRVLLCTPPEYSESFHLNLRNIDLRWMH
GTRYPSLFVTLHTWRPFEIGASVPSINSPRSAIVLLQNGIEVNDLIPPTSIQEDALLPKD
PEMRQMVKSMRAKRRRRYCEELLESMQEKYMELCRRVKLADVVKAFNEDTKQETSVELPA
SLKEDHERRRRALLNERKRIEKQLVFARDVHERQLIAEERQRQVEEEMRAKMEAKKEEER
IAHERAAERMALQRRKLGELEAFYQKRIQERQARAAEKNARRLEAQKRQIEQRQEERQRL
SEERQQRFERVAELQEQQKLMIRQKHKAKEEKLQLLQEGQRRRQEELHVKLLERAAKSEE
LRELARQRAEMREEKVRKAAEEQQQKVEERLSRFYQSRKEARAQRALQEERKRIRMSEAL
VIAANKINVLKEEAALKQLEHEKLFGELQRQREADVLTRSEREHEEMEAKSFAVTRFKRM
TEFGKLQTVLQLLSKREAALALERERELLMQETRKAREAMLTERHALKEEITRQTKTMQS
*
>TCRU_4565 hypothetical protein, conserved
MELANALTAAPTPIVRAIFLMMSAMHGGEAGDRKRWTCCHANGTTAENLSATEGWQTLRK
ESERTPFMVEMHYRVGDTGDNNVKVKWVRMDDTHLVLILQNESGTAELRQPVSISICTEE
EPLVSYLRGSIEWTVEKAETAVTQLRPALYEIIEEQQQRSCSSNKNNNNNGGGGGGNETM
GFTTQTQRQGYESRQEYIPDAPFLAEPRGVTKPLFAEMGPRPPGFRYGEGDLVPGGSLSP
EGVSGGGMKLDPKAFHGTGAIPCRYDPMFPGDVPRGGGMWGPGPGRVFPGEPDPDNFAPP
GNPAFRMGFGPGAAGGRGGFGGGLPPFP*
>TCRU_4566 Macro domain containing protein, putative
MVSYKEGFTRDGRKRAPRVLFGVHTIRPFPWIRVALGVGAMAYVFRQQYLARYYISPEEQ
FLRKIVVAPYGVLGNQMTLQGSMVRAGSEPDENVVVVDSADLRHIFTTADGATGASGAIY
NWLNLRGPFPDEVVKAVWRVCDAKWFRYGEKNVIHVIGPDFREGTWSEREAALELSRAYR
NALHEFVMSEGDVLRMAPISHGVHSGPLYSQLPPITQSALSMAFEQLHIFDREYLLRQDK
SIELCIFMNREWDMYMNVFKNQQKLLAF*
>TCRU_4567 Enoyl-CoA hydratase/isomerase family, putative
MLRRRVLPESHRYASWPPIYETSQHGIKTLDVREYRPLATPIEFRFYQRYANHPNRQSGI
QFLTHYNTHQRFRVNKDYIDYMHWGKEQGQARLPHRHQRVAFDFDDQLHPTRTLDNEGDS
YAWCAEQDPTLGPHPDLDASFDPNRRVFSHPEHWNKMFSKRRPGEGRIDLRVLPSQSLLG
PLMEQSDTQGAAYFRYDNRGHSNGRVPGLNTPFFGEFDRKMMQAMSRPLNADRTITGNDG
RFSKTIMINEPKTHQALSGKTASELSVEIDKATNAVHSKLTVLEAAQSGLTNYYCGGLNF
EMLGFDLHMAEMLREKARAILNGVASVSSTSVMVTTTSVPTKAQEREVGQLLRDALRYED
RVDDAIRQHASLIWRVYTAPRPLMALTNGKCRGTGCGVSLYSKYCALKDASEFIFDGPNL
GITPYGGLTRLLARPETSLKYPGLAEFIMLTGTSLFAGDALRLGWTDLFTTLPDMSYHIK
DWFDTTEHMHNDAVAWQLGHLLETCFKMKEAHSSAMERVAITPVRARWIEDSFADQPSVN
HIINTLSEIERLPITAKQNTCDQTRCTPYTLTSVEAGISKLENHRLRYTHSPWDITPPED
EVSLQHASEIFNAYVLERRGTFNVVVHRDTEKLAAWNRQRQEEYHAYRSLRVAPHPRHVY
ARLEGCEGKLVSFDFVFSLQGKQKDQRSGNKEGEELQQTACLDALKRQVLTSFGMPDGRD
IELGWYLPTLDTCPIHNDVEIMQLLHADPGIEDPMAQLKYPPIYFIVKRNCLYFSEWAYA
VKHQLLLQSPFALRAAYEMLLEVRGDGSAERVMPLAESLATEFKYISRLLRRPDFYRVGV
HTDKSAEAWEEIREERQRNLHKTHQPTRPLPDFEDVFERNVEIDGHRFLLRPRWSPRTLQ
EVLDADVMRLHTSLAYKDEGIAPLHVPTQCAKANRISDMVEDAGGLEVVPGLGELDAKGT
PVVPPLQSNAHVPQNVSFYEMARHPWEDAASSWRRDGFTEGSLANYEAQYRAAERAVYDE
EGRGGHNYWPSREASEGVTSEEKDAALLRERLFKPLEEALSGVEPWARNLRRSASDGKLG
YKTEIATPEEKIYDDEYYRWFIQPGHHPNPTGLTNFHKGSSTLQGSDAAEFERIWRHVVS
GVDGGNASDEAETAAEDGEEEGDTQMNEKNPVVPNDEEEGV*
>TCRU_4568 hypothetical protein, conserved
MRTMAICTERRIICVSWHTNPRRFECRPHNSRPCGTVGFCAVTRRNYCPCVEADPFAVDF
TQQLSSVCAAHPALAHSHVSERCLACDLLCVVEAAASRFLLVPNKKHFALRWIFTCVAVD
ARDDAQRVCLLFGGHEGDFGVCRQHRESIRRRIEAKLTEACPLHLSWQLRGTPSAQSGWM
DAAQLGRPVFFSALRCPGKIDNPQRHCQLHFTAGDRLC*
>TCRU_4569 hypothetical protein, conserved
MDGVRAVVDGRSRWRRQHSAVVAAVDSDDKIGEGSDGTLKGLSSSDQMPQAGEGGEEGQE

HTGSLEVTNKLAGNEDSQITGEQNVSSDADRPKQTGSQVPAGGQPEDEEGTKSPQPPPPP
PPAEPLPQLPRQPPPGTNTLQSEETHPAITAEKHSKPQDGGHSHETKMLQTKGSTKHEEG
ASSLQSPESVSHLSRESTTPLSTSTGSSGVAASTVENSGANNPTPPAASVTQHDSEGDTG
PAALPASNSELQSEEIPNAGIIATTHDDDNDSSPAAPTAERTTAGTRSTQTSGDAGDLEW
ANNDDVNDDVARNGKTAEFEAASGDRNTEADNDERYTTAPENATNKTINTEIPADSDSIT
AVSHSTSPLFLLLVACAAAAAVVAA*
>TCRU_4570 BNR repeat-like domain containing protein, putative
MSRHLFYPAVLLLVVMVCCGSGAAQVVVEEPLSGLQFKWRGINESGGETVESLGAPSLLK
VGNDVFAVAEAQCKKNGDVSFTGVASQPLTTETAKTHRRKF*
>TCRU_4571 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily, putative
MLVGQYSSKDCQNSGAGGCELLLVKGSVSGEGTNNKKIDWKVTENPPQGLCGAQLDSWTR
LIGSGGSGVEMKDETLVFPVEGTKKAEDAEEGVKTVSLIIHSSKDTANWTLSKGMSDGGC
SDPSVVEWEEGKLMMMTACDGGRRRVYESGDKGESWTEALGTLSRVWGNKKGGKAKGVRS
GFITATVGNDGDKRNVMLVTLPVYADNKEKGKLHLWLTDNTHIVDIGPVSGDDDDAAASS
LLYNSGENTNDDELIALYEKKKGNDGKPSPGMVSVFLTEQLQRVKEVLTTWKEVDGRVSQ
LCTSLIAEKERASTGDVCSAVKITAGLVGFLSGNFSGDTWRDEYLGVNATVNNKQGAAAA
TGPSDGVTFTGRGAGAEWPVGKQGENQLYHFANYNFTLVATVSIDKIPEGNTPIPLMGVR
AGSNGDENNVLLGLSYDSEKKWHVLCGDKTPKEPSSTWMTGTPQRVVVLLKNGTQGSVYV
DGQRVGSEECALGNDESKEISHFYIGGDGENAANKEVSVTVTNVLLYNRPWDEAEIAAFS
PNAQENGA*
>TCRU_4572 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MGSSGVNGGGASPSAVPTVSTPSAVKDSLQQVASGKSSDGTQTVDGGSFSDGEPTVETRE
GGTDGREKEEIHAQNGDVKAAALSNSLGNVSQGNNSDACTMCESGLLPSLLLLGLWGFAA
L*
>TCRU_4573 hypothetical protein, conserved
MRRFIPNVSGGSSLLLRFVASAAVMRKVPLAKSSAKLGTPVTKEEVSQVFNVPAAILEQL
HRPAEILFTEVDLARVRFAPLIATLGAEEDVTKIEAEVKTAKAAAAAARTPVAGAKEKFK
NTAWKSVTELVTFYEEVMLPARLAHQEYTVYELKSFHIKDDLKRGLSAFKQDHLDKQKAE
LAKVQKQMQECQEFIKGIGKTAFDTAIFNDLANILRVCGECNPYAHRLSMRVLEDMNLLG
VPFNDVTTKLLHAIVFNDGALDDSALMFTLVEYPERGEVSVSREPVDRIADSALKIISVR
HQTPLDDGVKLRQGDTQPCLQRSAE*
>TCRU_4574 hypothetical protein, conserved
MDFVFPEFVRASNDIAPPAPPQKSLWQLVMESGPNDIIPERDVPRRAATNCAGDYGSGMG
AHHGMSGMDGDTAAAGVTGLNASTNHAAVGLTSRTSWTPAPYMIQHLMSSGFVSQFAMMH
GVECSARLPPPPCLRLQDLQLPPLVLSRLRRQLFFPHGRKPLNLDAPQDTLRPKLRELQE
IVFGTEAVPSSRAGTDGGGREEEEKDGRQDADGDEDDPREVLETMSALQQFAVTSMLLGH
HTLSVGPRGTGKKTAGLLATGALTLARGIQRQEEKAIGGEKKNDPSNDGGAGDEAKVEVK
HEPSDAYKFHPAAPRAMILVSSFHEVQWCNRWLQDVFTAGAFMPMTFRRGTAELTPLPVL
YESSCDWGGKLPPETEARPPPSPLHPPIPPPVALLSLPPSEESHHRQHFSHEERQEERSL
HKRGREHSRGRHHHHRHSHSPAAKERAWSRHRRHRSSSRHYSRERRHRRGRSHDHRRDRK
RRGSRRQHRHRSGDVSSSRSSRHDKKRIRRESSRSCHHHRHDDRHGEDWMQKLSDRKSSV
EKGDCVSLECAAVTAAPPPAAAHDTSMATGPCEEIPQFLQQHVPILIGTHQSLVEALQMV
RGQAEILPLECVRIVCISDADRMAQPNSQMAVPTSWWISLSNAVDVECQYIVSASRMYDE
VDGWLQETLLQETPDVVNRYRQRDDTVWDGVQHIIEEVFVDEAEEYGAQQMFERVEAAKV
RRLLRIVKQHFCSSHVNSGGHSEVAGSHHHTDGSAASNSATPLTSSVGRMVVVVSSRKEQ
ESVFPQLLTGLRESDARVHCTCQIADFQRGEADVLVTYDWMLCVASDDGGMKNRPVDFVV
NFGFPRALMAPGKEESLLECLVIRTRTLLHHTASRDTVDEKDDESFFFERRDAPVVRTQP
TVLTLLTERQIHGRFGRLLTSRAQAMSSM*
>TCRU_4575 hypothetical protein, conserved
MLSRGVLLRSMSGLKLPPSLQRWFHWYPRRGGEFLGDMLAGHNLFIADIPRKFDAQHARH
FSLVESLCITPLFTLTMVHYFSSFFLHPTRWQMIPVLMKELARKTETQQQWMSVMEKKSS
TDVVVWRASMSLMQIVLFPACLLLSSLTPQMMHAMLERTNHIVHQKLACINKDAPPFVQK

YMDEAREAEAFHSQQLCITTDYLAALLIVLLVLYLTS*
>TCRU_4576 hypothetical protein, conserved
MAPKKQATKQRVRVTNKALEARQFSTVRLPRKAEMQAPQVDVERMYEDHDRGYRRGDEKR
GDGGGDAGGVNAQKSVPLIFDPIPNDPLFVVVAKSKYWPPPPLEELRAANGAPIEDGFDA
YDRREDDRAARRERVRVVRGELNHPRGKPRQNTIVKLDGSDEEKDEKG*
>TCRU_4577 Pyridoxal-dependent decarboxylase conserved domain
containing protein, putative
MWGSRPRYRRNVKALLDRSARFLSSLLHGVPNASFLLRLNAPSLWGKSESTPEEWQRCLG
ELLCRGAAANCLLDTKSHVAEVHASLVAAFLPKPHWNNSITHSMDIISLSSLEKEVSDTV
AALLHLPARFLWVRRAEAVMKKAESRMTHSSTELHSASPAALISAVERPVPYVGAGDAGG
GGLLHSTSLESLIVLLTTARAQAHARYLSAHFSSPEEEARLSQRLVLYCSDQCQPMLKKA
ARCIGIRHIRVLKTVYSPHVHNYPMQPDMLKASLAEDVANGLYPLLVCGVFGARTTGAVD
PLEELAEICHRIKVWFHIDASHSGLALAASAASAAYGFRDGAGQSGEFASVDEKDAAAER
MWEQCTSTFHRAALLADSIHFGVSTSFLPTLSANISASLLYVADVAKVKATMQGMNAEDE
AGGNTWCTPGMTDVASLRLDAPEMRSNEIFRLALMLMPCSHVSVGSAVRAHQAALRYLER
RLRADGRFDCSLHASCFGMVLFRWLTLADEETAGLMQRWSDVLASSSAMNEAGGHRYPHR
VSLGLTQVQRRVYICVALAADGDDGDACVSRCDVDALVDLLKTAADEWRDMSSSVTSAMS
SKSKT*
>TCRU_4578 hypothetical protein, conserved
MSRISSPLSSAVFSSAAASSSSFRVATKSAEVSPCALRSRRSFSLSALHDGGGCWRWHLT
SLASIRHLSLRSLCLHHSGGALNKFDAVGFAGRQRNVANAFDSLEMNLFDDPTGGLTAGP
AEELSTTEIEHQVRLNVSSYSRSIFYLLYTPFVDVISVLLERGLAPDVAHPGEMMCRWFT
DGALTLQNPASVEEGMGAENWRQLCEGLDAFYEEVEPVMPLTAAVRKHGLPEDLLVPFLR
QLSMDLLVPLRKRAVLEILPGLILGLANGRAPTALGFPTDSQRARAIMVADLFLGVGQET
GNTDLAYLGIQLLRANDIPVPFPKQKQLTNVFSAATRIHTDWQMRVSGQLVEVLPKWMEY
YKKVHLDNLRAMKGLSETDSTSAVKQEDDDGERIDVLKAKRAIHAIGDGVNAAGKQTDKE
SNSDGVHGYFSSHRTENLLRLSALESQVLTAVRHRVVAWNDDSNKLYYRFRRRRSATEEP
NAEETDVPKEPTEEEEEEDARRVDAAEDVALVEDGRRGRRAKTHTQADEKDPKVNPKGHR
SRKKRTIAAPVDDDSGSTFTLTV*
>TCRU_4579 XRN 5'-3' exonuclease N-terminus, putative
MLYRWLRGGTQGAGEFRLTVQELASVRVDFVFLFLLNGGDHYVGVGDVAPILWKRYRTVR
AASMRRCLVAPDLMSIDVDFLSDVLQASDYTGDCDAGVGMELLRASLWSLYTTVTGVCPD
YQYIPAPMSPHLNHLRAAVLHCLKNRRGIRIQPRRDARGPLTPLETFVALMPTEATLPAS
VAQALRSSRKYETIAQQLFTSNDAAMVADAAKQAVEVAGEFLTVSEQCLRDFTSPVQLNV
LQPPRRLSRHEQHRMLASKGRIEREEPLPLVECVTLPESFEYVTDTYPSYVRDLLFLSPF
CRAAETLSSSNRGVTTTMQPFVAGTVREARRPQKCKRGSSDGEVRRIPVHMQSSEEPSAA
RQLQKTLEKASSLAMPEGRDKKTLRRLKKKLNAQRQLVEKQSRSEESSAEAKRHMLRQND
KAFIAEIRRFLGEEDEDVRQLLRHDGGRAPGNTGQEERPMKKQKSVSRAGDKVELCGRKR
RRESAETLSVTRADEEGDRHESSYGGCKAAKRGRREVSHTENHHHTAAGAARTCGRDTRE
AVNGSSSEQPTLKKKKKRASREMGSTSSH*
>TCRU_4580 hypothetical protein
MRHKEAQSWNEYGTARHTEANGSSKAAQVMSTKKTFTTSSVAAPAVATAGATSTPLSLLE
DRAKGDDTPPLRYRTDLDKHVIHFAFQRFPHSIEILEDEDVMSDDWHFFWMNVGRVRSIF
STAEYRLTDTQIINHFPNHYELTRKDLRYKKHQEVHSRPQQCTADGAVYAAMSGTVRME*
>TCRU_4581 tubulin tyrosine ligase, putative
MFTQEFRRQPCSTWIVKPTSRLQGRGIFLINRITQLKRWIKERKEADEAEGLPASTFVVS
KYVANPLLIGGKKFDLRLYVLVTSFKPLVAYLHEQGFARFCATPYVANALKDDNLCSHLT
NVALQKGEDAYNEVHGGKWSLANLCLFVQGRYGAVCADGLMRSIEFTIYHSLRAMESVMF
NDRHCFELYGYDILIDDCLRPHLIEVNSSPSLSTTTLSDRLLKEEVLADVLSIIFPPSFP
SPCAMSYWEYRLRTDLTTALQTGFHLLQVEA*
>TCRU_4582 Emopamil binding protein, putative
MFLEVFVDPFVYFCVSCIFVPILVDREHLTYADVIGYLTEPAMLFAAALLFIAVAEAKIA
RWRYRSPPLSTFYERMRARWYLLNGVVIHIFMDGLVGVFKASTLLARNYEKFDKRYGAAL
GNFEGSAVHVVSLMELFVKGPLCILLYRAYQTHSRHRDALEFFSCVTQAYGTLVYIGEEI

ISGMPHLDVDYKLEFTPHYLLYFWFAIVFGCLCYLFVPCWWGWEAYKRLVAASSHPARKE
VSARAAHPPPPSSFSFSPPKLKKTK*
>TCRU_4583 KREPB8
MRCGRVTLLLAPKLTPVCTVARTGSCSSASSSKSLRQLVGAATLSTGPSLGQHLGAMDAH
CRLGTRGTSPESTTPMTERSFDIFEGNNKQAWLDLKTGWCHLCQEPLGATMGVHIGDRDH
TNLQYFLFLYAAHARDWSGEEILHSCMMTAPSVHHYATRHTTWDHLHVMDDAMRRAELEA
LLFFLTQPPHQALSHVLQGRSPFGFWYSGERMWKLRISRLVTQLFPPISAGMMTNFTQKC
WGRSNGERMYDALRLQRIKAYFGWQPYESKEKKAFFVRQLLWELLSVETREELDELTKHM
ADLALQRMAFEMIFLQSMEYMHKVQYVYKLMGCPTVHELAAMNLL*
>TCRU_4584 recombination initiation protein NBS1, putative
MRVLEVNCGRGDVRRHFLLAGETYTVGRKECRLPLPNGDPSISRHHATITVRATSPYDVL
DPNTEMDVSVTDRSKHGTLVNKELIGRENGCFVYREDTIKFGRRVTARVLSTALILVASS
KLNEVERLLLLSDAVSLGASILHEPVLPRETFFHMQIDCIGFLYVTQDGYEMTPEVLLAM
THQYHVTTPSYVRSLVEKLREDSAVSPLQFASPTLARSISSKFPVEEHIPPLRSFYNVGE
FLLAPPQPPPRRLLRSYAFFIADTQLNSRYESLLDHSGALVAFMPPEKTTMAWPYTHEKT
TMALVSDDMFTRIAVKFGVNHDHHSKGNGVDESASSPLGSDGDNNHASNGRYRCDVADHG
RGSTPHNDPIESAYITMYNAGICLIPETNVLRAIFIGDTLELNEKPSAFCLRRVDEACTK
AAEANEETAAAAAEVPEAASTETASYDRVSNENCSVTSSTFSPYMAAALQLEKRSNFLSP
PPPTEAHGGGPLRDMMTNRDQHYACKRTSVKAVRGKKESPCAADGDCEGEEPPKTPRERE
ERRPEGVQQQPVASCVGHTHANNSNTTAVTKLRAFESSDVRPATAEVNALERKPVVVHAA
SQMNGSNTGVSLLSRQRVTAHKLFVPPPLFRSPSSVLMSSRSMSYQPSKDSEFAPHAESS
EKQKERCHTSEGVDSGSVVGVPRHEYPASSQPASRNSSIGPHQHSEVSGSTSRRTSFGET
VRAPHPHPAGRTHLKSISSARPLRRQKSCPSSAVCHAWGKRQTPSNGRDASPLASFNTGG
RRFSDSALSARQHRSVAHKKCNNNNNNKEKQQEQTANFNTTGGAPSTVPSSGDIARHQDA
LLGKRCGEFMSGFFDEFSVSVEDTCWHCLKQGQVDAKSREFLEIGAVRVMEFLRCIQRME
RDIPPSYSTETTRGHVYEVRKRALATLRRILSTCESVRSQLLFTLKELCDAVSCRPPSAS
RSLRSRRASVPYERKSSLCGN*
>TCRU_4585 protein kinase, putative
MGNDEIFEDLFISDTEPEELYEELGPIGVGNYGSVIKARNRQTQAIAAIKLVLLVDKDER
DFVQKEISILKKCVHPNIVRYYGAHKSLSKLWIVMEYCEGGSVDMVYKVLRHPLPENLIA
YVCRQVLLGLQYLHANRKIHRDIKGGNILLTRDGDVKLADFGVSTELSHSLSRRNTFVGT
LLWMSPEAILELDYDEKADLWSLGITLIEMAEGAPPYIDTHPARALFMIPKVDPPTLHDK
DRWSPQMALFLKRLLIKDYRLRPTATAMLNDPFVAPEKIGTKEQMKAVIDEVLAKKEAMS
PQRLHGETNSSATFVERTSTDTDGEDGVTNDTCTSGRAPTGAKVPANTSPVAMEAMDITG
AHLFFHDGTLLPLPMLSTHDIGFDELGLGREGIGPFAKPVPDAESLLVPPEQRSTALHGS
GGLAYTMHVTQTLKSMLYYHKQLPFFREVTDAEAIKSKELQLKYGSILKSIYRL*
>TCRU_4586 hypothetical protein, conserved
MNCGGVNFSPDGTIHPPARSSDADRTGIRQLPPPREGKDNTKSGGTTAPQVNAEPSRQNE
DWRQSAAADGPNTVDPSPASNTESNTSETKPEFDYV*
>TCRU_4587 BNR repeat-like domain containing protein, putative
MEDGTLVFPLMAVNEAEDVCSMIVHSTDNGSAWTLCEDISPAKCLNPCVTEWEGSLLMIV
DCGNGQRVYGSRDMGTAWTEAIGTLSGV*
>TCRU_4588 Leishmanolysin, putative
MNGVVSSAHGNAVAEEVVPAAVKLHADRLLVQPLEGSLIVPSLATGSVCSRFTVPAEHCS
AGAANSDTVLYVAAAPGGVWALPCATLEDGRPVAGAMNIARPLCFTDASPPASPRT*
>TCRU_4589 Leishmanolysin, putative
MASRSTVRNVACVRGRALLVVVNSTTAAMAAREPRDCDDIDGVELQDDDGDGRTLESYRS
RCHARDEWMAAIESAGYCTELTLAALAVLGCMRVSREMAEPTRWCSSRAVRCSSRGIAPH
*
>TCRU_4590 Protein of unknown function (DUF2826), putative
MLRLGDPHIVVVLTHSRGTADIDALSGRSEASFEALQGAGCVDAVTTCMECHDGTAGCGW
WNICFSEATEREGERAAAAAGVVAAFCGPHADYFLSADHGWCASTSDVVCRHFTAPTKRT
SCRMLWLWMWCRECSRHYFARLLFAALRQIDASPPESFTAAPCVVPPAQDSRVVWRLADG
RTPLRWDMQGCGLPLTVLGTAVWMRRPHERMYCGTMKCVKYAESQWLQ*

>TCRU_4591 hypothetical protein, conserved
MVCVCCRCWAAAICDCAVAVRGVAAVSLLLLPLCVDGELFCAEGCRQVTGVMAMMMAGHV
LLVCALCVLWCGAGGGYAWLHNYCESGEESCTNSDQYKGLYNSSFRSSFLGETNSASGKT
DSSTGSTGNGGDRAGSGSSGVEDSTGHAPSGGSQSPPTPSQPASNTPGDRSASKEPSDTS
EENPGHTVKSDSGGGGGPNTVDGAQLTVGGDLASDHQTPEDGDTDPDVSHAASEDGEDTH
SPPTSPPDKKTEEPKVTGGGEEAPAVLAKEESEGNPEDEPENEQRSSANGVSEQQPEAAQ
QGETEDGNTTEKTPDEAAAPKNGTAAPDESDGSTAASHTTSPLLLLFLLACAAAAAMVAA
*
>TCRU_4592 Leishmanolysin, putative
MNGALSSAHGNAVAEEVVPAAVKLHADRLLVQPLEGSLIVPSLATGSVCGRFTVPAEHCS
AGAANSDTVLYVAAAPGGVWALPCATLEDGRPVAGAMNIARPPYFTDASPPASPRT*
>TCRU_4593 hypothetical protein, conserved
MSAKRPMDSCPIIDPALDVRDADGVIWRGECLSAVPGDRPSSWCPDTPPTNTTDARDPEE
TYLSAAMHAALGCLVMQVRLRVVEKGGVRWVPCTDGATIAWATRPHDEGSVACRGHARVC
TISAAAGSLFPVALWDGEERVWSRTVPLAVTGQGLRGGVRPRCGEHWSRPRHPPKDVDSA
IPERNLLLQGPWRPSVLLLLLE*
>TCRU_4594 hypothetical protein
MALLSDVPGSRAPVVALLLASLVYVGLPDCEAAPEAPPLPLAGVAEGVCVVPDASVLPTT
SPVGSCEVLPGCGPADVILCSIFSADDEAPLAAELELPAACSAAGASTAVNCAVGVTAAV
S*
>TCRU_4595 BNR repeat-like domain containing protein, putative
MSRHLFYSAVLLLVVMVCCGSGAVGVAGEPSVSTFKWRGINESGGETVDSLGAPSLLKVG
NDVFAVAEAQCKNGGVSFTGVASQLLTKKTAETPEEVLGKTKDGTQVLEEGTSEGQKKKV
DVSRPTTVVEGNDIYMLVGKYGRKAATGVQERDAVDCGFLLVKGEVGGEESGGGKGIQWK
DTKSLPQTPFCGQHEFLTGMVGGGGSGVKMKDGTLVFPVEGTKKKKKDGTEEDGKTVSLL
IIYTLSTASWTCRRGCLTVAAVIPPLWSGRTKNS*
>TCRU_4596 retrotransposon hot spot protein, RHS3, putative
MTTAGEHRTTTRTVRQFTECLAAYFNGWEESSRDMSWEIIYVQHADSTPMTGWQRCDVDN
SNNVSRAENREIAVFWEEEVHQYIAAISSDDARRDEAL*
>TCRU_4597 amastin-like protein
MSKKFSEKIEEFWEFGTQADTHVLVMFVSSVLSFVLTVVAAPLSQLDMVWGACYTYWGYK
ENCDSLIYNNRTPFITCDPVRKRLQAGAAFSMMTVAFLFVAVVCSGLLLRQNLLKLRFFT
LLVLTIALVFQMLSWALVASILGARYCEDRSLPRTTTYGVAFGMSLTSWFFIIIGALACI
VPYFY*
>TCRU_4598 hypothetical protein, conserved
MAIVVIKEPNLRKLLAEQQLLLSTLPQPPSPVSTYLTAPVAPLTSVYHSRGCVELIEDQP
APLCGGGKGDDEDATNQKRSSLLFDLLNAASRVDLDVEKTLSLTCDVLSKARCRSYKLTD
NAQQLLGRIMELSACFKGLSEQQSTTPSSPEK*
>TCRU_4599 Leucine Rich repeat, putative
MAKKEKIPPPGTSKDPTTNFYTRRKWRTALLQATLELQGRKIIPRGVLIIGTALMKNKHV
VRLDLSQNNIGDEGAVTMAEVLRKNETIQYLNLAQNGITDVGGIALASAFIPNVNPNGQP
GQWNRNLFTIILTGNDLGDDTLLAMSKAAACHRDLTSVDLSWNNVGPLGTKCLLRSMQRN
PLCVYHLMANKIGDAGTTCLCEAMQRFAGKGTTTLNLFRNDVRHKGCEAVGRLLENNEFI
LDVSLHSNTLGLKGMQLLRQHFTAAPNRVRSLNLGNCMLGDEGAPEAAALITANPPALER
LNLASNGFSDDGGVIIVKALLKNTFLVMVSCADNTFGTKTVDATAELIGTAKVLKLLDFT
NSIESVEMRRTLAFAASDADGIRVEVGEVQEETLNDRLQHVAEYMQMILDAEAERAKSRK
SKKRPKKE*
>TCRU_4600 Rrp15p, putative
MAGRFRGAVGELSRPRKSRAARKAKKKRTVALVRRAPKLSSECLQQRIAELTGAAANDDE
KANAAKNTRVKILSNATARAAATASQKPVGRAAMEIVGKRTERLVPKTDVAAERTPAEAM
GLKLLHRAVKDQSHNRLLPHQNRHEYEYRLRTVATAGVVRLFNSLAQARKAGAVVEMEEK
HMTAEKVHEKKQVATKEAFLAALRQPRKMDL*
>TCRU_4601 nucleolar RNA helicase II, putative
MPRRTAEEMAARNGGENPSAEKRARYETNESDDKSGGGEAPNNGSALTGRPFSDFDLLPN

TVEALKSQGITTLFPVQALTYEAIMKGSNVLVQARTGSGKTLAFGIPIVEKLARTTKSNE
QPVRGRGPAAVIFCPTRELAIQVRDVIAGISKGFVVTALYGGVAYSTQERALYSGVDVVV
ATPGRAKDFLEKRTLCFDRVKVVCLDEADHMLDIGFKDDIELLLQKVAEQNGSTEGNPTH
QTLLFSATVPEWVHTCSFIPRNKEFIDMVGQGTMRAANTIKFYRRKCHFSEVSCMLADLV
KVYSGRHGRTLVFTNTKKECHDLSINNTKLDSQCLHGDMQQEQRESTMKSFRDNKFSVLI
ATDVAARGLDLPMVDLVIQCAPPTDIDAFIHRAGRTGRAGRKGVCVLLHQPKDEYIVERI
ERHAKIKFEVLPAPTRDEILRAVARDAAEDLARVERSATNLFMEQAAELLKDADATEILA
SAIAVMSGYTSSITRRGLITGAKGSVTIQMLGQRTLPIPVFCSILRNSLGDNLFTRCRDI
TLLQESPGCVFDVPEEVADQILSAPIRGMQLGVIETLPPIIARELNSGNRGGGGQGYFNG
RGGSNGYYRNGGGNGYRSNGYGSGGGRRVQRRY*
>TCRU_4602 protein kinase, putative
MSLFPFREELHINQLYETDDIYDFIGRGTFASVFKAVSLVDGEEVRKGDAVALKVFNKRD
LTSEKMRLDVINEVEVLRRINHKNCVRLLDCFHTPLHVVIVMNHVEGAELFKALRDTVFT
EAQVRFVAQQLLEALDYLHNVVGVVHRDVKPENILVKPFGNDEFHVTLVDFGLARMLARR
GGGHRRLGATRLSLRALPEPTSVESIDSHCDSPLIATPCGTLNYAAPETVKSLTQSGGQL
ATTPDLLARMDVYAVGTILYVMLVGKLPFRHSGNKMQLVKEMEAGPLFAETQWSSVPREA
IDLTKALLFFDPSKRPRAREALQYAWFHPQAAEEEGNGGGGGSSSVGGLDDEGWQLREFM
GDREYMKLAFGAMKPPESSFYDNGNSSVGGRCISVPFGSSRSSVKSYFGFCL*
>TCRU_4603 dynein light chain, putative
MAKLADFNINADMTKEMQEDARNLVIQAFETETLEYAMASFVKREFQKKYRGVWHCVFGK
NFGSFVTHETKGYIYITWGQMSILLWKSVT*
>TCRU_4604 hypothetical protein, conserved
MDAQSSDGSFVDHGQEVERGVGARPEWSVEKPGDVICDDDDDDSDAAVGDDGMRSADDVV
TATSLSRDAFQLAAAMKKATLHTERLLQTNRQLLGENETLAKVNSTLVASNRSLSRQNEV
LTNALTSISRRQEESQHAIVELTRHVREIKTALQSVVDSATKDCKATGPRG*
>TCRU_4605 major vault protein, putative
MGDIIRIKRHHYVHILDYNTNVTRCMVGPLVYTRRENERCLFNPKPCIVVPPRFYCIVQN
PCVRDASGNPVIGENSSVMLRMGEEEICFEQEPFPLQPGEVLKREEGEWLFKMKLIPVNT
GYHVRCLCDFTDKNSVLRRAGTEWLVEGPQTYVPRVEVEVLREVHAHIISPNTALHIRAL
VKFTDRTGVPREAGDLWTVKTVGAYLPAVEEDVIGTFQGITLTDTEAVHLEALSNFTDVY
GKRRRAGERWLVTKEDASIHIPDVHEKVSGKVRAIVLSEKEYCVVQNPLGANGLNEFGRK
EVRKGECRFFLHPQEELLGGMQPINVVSKDQALLLQAVDFFDDNGKIRRPGEKWMLHGPA
EYIPDVNVRILEQRNLIALDKNEGIYVMNTTTGVVRVVIGKPYMLNENEVLWEKEISPKV
EELLAFANGCMSEGERNPGFKSTRVRHRVVRFNVQHNAAVQIYDYKQKKLRVVLGPNLVI
LSPDEEFTVVSLSGGKPKVPNSLHCLQLFLGPRFSSDRIVVETSDHARLELDLSYNWYFD
VNREEPDAKIFSVPDFIGDCCKTIASRIRGAVAAEDFDSFHRNSAKIIRVAVFGRGENGE
INTSLRFSANNLVVTNIDIQSVEPTDAKTRESLQKSVQLAIEITTKSQEAAARHGKERKD
QEARGKLERQKLLDKIEVERTKTKWLQLQAQSEAVQASGQSVAEAKAKAESLLIEVDSEL
KQAEMRAKAYRITAESELKKQKQKLELELEFTKRQNELDIMKARQIAETEAERVQRMVNA
IGRETIVAVAQAGPEMQAKLLGGLGLKGYLITDGKSPVNLFNTAQGLIDAGSSAQEHS*
>TCRU_4606 hypothetical protein, conserved
MENVVPSPNGWETPPTAGSAATTGVYAADHIPGTYLKTLTGVQRGEELFYRPDLERPWRT
TAAQRSAALLALKEKEIEELMRKCSSLRTLLGNAKHDAKYLEFAADERAKEKAAEIQKEV
NRLETALKTVKEEREELKISTEHQLRLLKSQHEKELIQVQTEKRLLNDRCVELTRIYQQQ
VDDVKKAAARELEYVESLCNTRVEQLKSELQAAHSESLAAEERRAEELAQAKNLTHRIET
DYKERLCEAEKRVDEVRERLETANKRLTEERNTAIKEATRSTERLAVTLADHEALLERMK
KWNTYILRLLDQFYTAFVESRPEQAVEPHDPELHESASLYVPRSLMEDPNAKVTAERIVY
RLLQLKHAHLTEEVDRVPRDGNSIEALEELVEKQKRLSQAFQEIEEKCAEARDSLSGVIS
RLCFFSDDLNDAIVNSGYVAPPQSCAIFVCLGVFRGRQLWAEDAERARASVSLMNSVLRP
KMTQYGAYECYSDGTSMLLAFADPVAACRFCVESQWWLMNLPWPQSLLRSVWGKEEYDKA
NKLIYRGLRLSMSIHTGDAFVEPTAIPCGDSYRCHYYGRAVSQVIHVCSLAQGGQVLVTG
PVWDMCAPDLHELGPVGVREIGAVPIVSFNKETNCYEKESLLLRQILPQELLGRPFQNIV
EEDALDLALFGKMRRSMLSDEIQCVEARRAFLKEAVGVAGEELVAVDRAIHALMHRTREA
KSYFHLLPPTEMVELLNDLYGVMEKVASRASHIRGDLRRMDQRQDELVNQTRGLKDYCLQ

HAFTASRVEELQTHSELMQTRYEKEMTEMHRSHAEKVEQLQRELRERDQLIQRLYRKLQS
APLSHS*
>TCRU_4607 paraflagellar rod component par4, putative
MPPKKGKKKGGKKKESAEALRLKQLYALESEAEELQKRENDRRDREEQEERLILWKEEQV
RIIREKDGKVKELMAKVEQLTTSLHDERVASEAQVEQLVLMRDSLLNEVSLLRVELEEKQ
KLLLHEKQSAEMKLYSVREEAEKNIKALSDEMEEMRSEFALFRLEHAEYREKMEETLDNK
EAEIRTQASTIGNLRRELEKALAMNRSLQEVVETREADDRKNVTLMQLLNAQLDENKRRY
EEQYEEQRRCTGIAKEEVLQLETKCMKLQDEIDVLKNENAEFKLKSDVMLREYQQQIEQV
RSDSAYLAAELRALHEKAIQETEATQTAKISLEGELQNTLVELEANQKRMEELELLLRRK
ERETFDKITFLNAQVSNNRTIISQLQQKLIQERKVHETELMRTFDETKDKEKELDAVRNS
FTQNRDAAKEREAQLLSEVAVLKATTFHVQTALQDTQRNLEVVVAAKDEEIKRLCNLLDA
HFIPHRKTIEGEVTTYEGTIAILSEKVGELTREMEIREQLALENETQLKARIANQEEVIE
ALREDLRCSQARRREEVRSVEEEVSRLKKTLEIHFIPYEI*
>TCRU_4608 small GTP-binding protein, putative
MGWFSWFWDMMSYLGFSNKTGKILFLGLDNAGKTTLLGKLATDQVHVHRPTFHPNVEELT
LGGIKLKTIDMGGHLEARRLWKDYFTKVDGVVFIVDAANPERFQEAKQELDMLLQTEELA
RTPFIILGNKIDMPRAVSEEHLIAAMGLTGLSTGKQNKVTDPAVRPLEVFMCSVVKKIGY
GDGFRWLSQYLQNS*
>TCRU_4609 hypothetical protein, conserved
MLRMVKIYYRARIIAFNPWKSRPSGLNLNGRPQMVNPSYFKGAYRRQNPDDPTRLLKIRH
VLLKRCRLCKRTLFVPLSQKDHFHTCCEGVPMKVYANMETVMNSEYKLLAHSRQWDVESD
RPWCNSHKPRPKGRSKFKK*
>TCRU_4610 hypothetical protein, conserved
MDSPAKGDARQGLKGSQKHIEFQLQREKAYTRELQDKIKSQQAHIAKLDQDKAELRRELI
TLTDDEKKKTKLEEKCHALQKELAEKQAALIVEQKRVTSAECEKEQIRRDAHASIAKWCE
AEKQWIAENEALQKELDDAKETLVKLKGESEALANSRDDILKQLQREKERSARLESTAAV
TEKKIASLHSRIESLQNDIYTRDETVFKLDEAGNKWQEICHSKDDEIRSLEVQNKKLSDN
IEQLQTTISTLNQRIEAIKLLGMEEKGRTEKILCDLREFEQENKLLQMELEAVRRDLEHA
SQNASKQQEMITDLRAKLAASAEQLKEKNSEIRKQELTISQLTAAFKQAERERTDNSYLA
SSLQNELQSLRNAFEEAQSLVKSLQEEKALIEVELQRAKLSHEAKDEAVVIMKSELEDRI
EGLFLDIKNLESEVIARQEMINNITKQLGDANTKNEKLHGKVLQGSDLLTQLRNKLEELQ
KEINKNRFENFFHEEAMARSKVQEQYFGGMQDIILLLSGENGALLTRYFNEICRLDNVTR
VLDAEKVAAGQKSDKMKVNLEEELQRLKEREIKQTHAIETRNVEIAALQEKVGKHEESLI
LLRSEVEAQRKRCEEFKNMNTLLSDKIVDAENLLQEMSTASEKQIYFSHYVTRQLDDTAG
LLMFFSEHYVNWIFKKVNIVVMEFDKAYAKENERVLDALNHLRKVQEETKERYTNLQMKL
NDAEFRLGEREKASVEKFENFLSEIRLIEKQRDVAEKMKKDILRKLDSVNDQHLAEINKK
DEQIHELLVNLDAEKHKIQTVETKFQKLQKKFDYEVERKKEYKRALEEVKAKREEAERYR
ATEKDWAMKAIHRANEEVNYWVRSFEKLKSMLDEISRRSGTQVSAVDQAMINSFEEAKKR
IVLRDQVVNIVSSEEEIHKGKRSRIE*
>TCRU_4611 Adenylate and Guanylate cyclase catalytic domain
containing protein, putative
MVTGWAVMMAAARQRPGLHKKTGCCGGIPLLGWRLSTYALYLVLLLLLPRSGVGQAACPE
INVKVLTLNVTDLPIHAHLSEALYYGFVAALWSRNYIVGENVRVTLINKSTTMAESGKAV
EEAFQNNSDIFILAAAMGDTTLRYYLPVIRDRKLISFAPFTGSTVIRGWDPYLYFVRADP
LAELFALIRYALTFLRVRRLGFMYLEGVSFGNEEYEATKNVMTRFGYNLSGVFAVKSSLT
HEAENSVFDAAWEAFANTRPQAVIVFGSPIKDTAKFIQRMLTDNRTAGAYLLAPSAVQDI
TVETWRAAVAGGIKFVSGQVITTGTNPLAKDIQYAAIQRFQGVMRSYMEKFLPESSSLRK
NFPDDDIEGEMMVAGWIAGEILSQTLSSREWAKNRQAYLASLFNQRRYMVDNLVIGDYGG
SCQGVAESEGAMCYCNQGGRTVYMKKFVDGYRADPLVDGKISFWTWQCSPSEAVIVPPLN
GFAIAMRDNPLAIFALRAFGVGARAAVVNNSLIKRFAFTVQVVNSTVDGAAAALVSELKV
KLVDVVTGVVTKGMLEVEDVAFINPMYLQPRIGRFRKNVIRLLPTLEQQFFVIAEYLGNV
SDGSVHAVIRGDDGATMAEVLRLSLETFGGSLLSTKLLAGGDKMADHLPEEGDVFVVGIS
ADDVGAIAQHVVSHDGVRVFVIFLEFSMLYPEFVAAFRDGAGADRVVFATNLPHWNDDKT
TSVTAQKFNAAVPEVNKRTPLAIMGFATGLLLVTVRSRMEKVNVELFENFFFSNVAVRVD

DMLYGPFIDGNACPVTESGAECGSNYGATQISVWPLARALNPAVPALSPAVTPSMEYRMP
VASGLTARQLIGVIVGSVAAALLLIALILLLLHFCRDSRDNENAPKERTDPVTLVFTDIE
SSTALWAACPEVMPDAVATHHRLIRSLIAKYRCYEVKTIGDSFMIACKSVFAAVQLVREL
QQMFLQQDWGTSVIDDAYHKFEEDRAEEDEEYVPPTARLDDAVYRQYWNGLRVRVGVHTG
LCDIRRDEVTKGYDYYGGTSNMAARTESVGNGGQVLLTRAAYMSLSTAEREQVEVTALGG
VALPSPRCVLIVRCLILTMAVISKVVKMFLCTAHGPAPLKPSCLF*
>TCRU_4612 hypothetical protein
MPLCERWNVRLPRRPSFLQDEEYCRLVIDRLAVKMSSVMERKGQLGMDQNMSFTLSATAP
GAHDPASGTWGRRGGEQAHARRFREAASQSDSVEVHPFTADEPRSSMDDSIITVRARRFR
*
>TCRU_4613 ATP-dependent DEAD/H RNA helicase, putative
MNRKKGVNQRQQTAASHAPPTQTIGSELLENEESKCTSFKALGLCEELISACAEAGWQNP
TRIQAATIPVVKEGRDIIGVAQTGSGKTGAYVLPLVNWLLTQSKVPYLSVLVMVPTRELA
QQVTAQFVMLGHSVGLRVATLVGGADMVDQACELSKRPHVVVGTPGRIKDHLQNTKGFQL
VKLHALVLDEADKMLDMDYEKEIDAILEHLPHSRQTMLFSATLNTKIDRLQKASLNDPVL
LEVHRKNTTVDTLKQYYVFCPFAQMLPYLHLYLTRETGNHILVFCRSAALVHRITLTLRI
LGHQALPLMGRMDQTNRNIALTKFKEGKVRILVCTDVAQRGLDISHTDVVVNYALPDRVE
DYIHRVGRTARAGAQGKAVNIISQYDILLLQRIEATTGVKCEEWPVQQGDVAAVLQRVED
AEQETIKEIRENEQESKFEKEVRQLVTAKKGKRERGEGDMGYDDSKHGKVDFATLRLRRE
NEAVFKMTKKEQRKSLWAKRRETQKKIKSQM*
>TCRU_4614 retrotransposon hot spot protein, RHS3, putative
MLRVCAQCEAEPCGGTSGRRGAKENGDGDGVHEGRPEQSWSYREADDAIEENDAVQKFCA
APPVLMVLASEKGWPYSWHTIQDLPKDVFVNREVEQLWQIVKGNATAWSSPHGGTDFKFE
RRVLIGTPGIGRSMAASSYLLYQLLRCDAEQFQVVVHCFGGRDAYVSDKTSRTVTRCSDE
EMCILESRRLRGHGRNVYIICDVAKDGTPPPRNFAPTSGWGVIAVPFPKVTNYDEWAKQL
QAARVIVSCLDEMDVKAVCAWMTRDKTKDKQAERWKEAKKHMYLLGPIPRHVFVEEAFNG
RCGAVKFALQSINEVTVREHFSRGGESPRCSEDPSHRLVKVVREIYAGGVILFNAPLSAC
LEERTLERLPSVAE*
>TCRU_4615 hypothetical protein, conserved
MGCKAGPEILQIIITSAIAGVTTVVHCLWAAPPLVRIDVWIDNIRIAGSKSDVTLWEAQV
LRNADSCHATMEERESGATQYTFLGVQFDHTHRAVSLSEKFVRSVRAMPALNSLTIAEME
VMASRFLYAAAILGTCLCGHYFFIKAVRRRLSALNRGIVLETSPANLPPSAVGLGERLRH
IIGKNRRLIIKPTEKASAAIITDASLHGWGAVFILQTPATLKLPEGNGRGNLFLSCRPRH
ERYAWPYRPFPPSCHPLWTFGWTTLRCKERRIKAAQNHTP*
>TCRU_4616 Protein of unknown function (DUF3676)/Trans-sialidase of
Trypanosoma hydrophobic C-terminal, putative
MDYDEWTVLVDQREIDRNRYNKNLFDLHRISHFYIGGDSKDQSATGGHVTVTNVMLYNDD
LDNNGLYKLKASKVTIPSLGAEKHPTEQVTSTEVSVVPESRSEESTTSHEKLNEDDPEKR
GENSVHILVPAVSSSTVVAGSSVSKPATATESAGNERPYDNAQFHQDKTSQQDTPNEENK
SMQRDSEVQPQELLSAELTEVTDVEMSSGSYDEEMPEEDGGTNDRSGGSTSSVGASSDMD
MATRPVDGEHQVQQSVELATENEGLRSTGTGTTGAKESLSLEAGDRNSERTMSSDSSLTP
SKSDAETTSAEDTDDVLRTEGVQVSSEYGNEVPQTVDTAPGNTNTTPVETEISSEFNATI
PSDTDILPEHGQLGELAAMALIGDSTVHGCVSRVLLLLLGL*
>TCRU_4617 BNR repeat-like domain containing protein, putative
MQLTAQLSMNRGVNWSSYPRPEDLDAFSASPHRMSLPSSFGPFGSLFAFVEGYDLRNGAI
IRFTDGWGGSGLESVIYFLETGPGLSGDLSMNSVSMSFHLPYPYQPGDMIGFLNDASTPI
TKMTDNTLVFPVQFLTRGGETASTIMYWNSVQPHWTFANSATHAGCTNPSILEWEAGKII
MIASCEYGHRRVYESTDKGNTWKEALGTLSRVWSNPLAGSGLHIQSGFITATIGGKKVIL
LTQLEYPRHNQRDEIHLWLTDTNRIYHVGLLPTGNSATSSSLLYADDKLYCLYKTGFGSD
SGAFFLDLTSELYWIRHALSTWAANDIALSRRCSTGAALSRGDCSVPFPTAGLVGHLADR
FSGHKWEDEYLGVNAVVRGAAKKAPSGLTFEGHDAGAEWPVGKQWPTRPLHFANYGFTLA
GNGVDPRGAEGHHSPDGPEENGEDNTPGTVVQ*
>TCRU_4618 Ankyrin repeats (3 copies)/Zinc finger, C3HC4 type (RING
finger), putative

MEFQYAAVGNTAALRAWLQHHPERVNVPSPGSRYTLLTTAVKRGHLDTVHMLVGEFHADL
GIPCGGIDNTCVHAAASNCDVEMLSYLLACRAPLKPNAFMEYPSDIAKVATAASLVKEKC
IAMLRAHEGELNPHGLRQEGKEGGQPQPMQWRSPLESVVSPTSLRDVISDVKLTGDEDGK
EEDVQRRSLQELPMQGAGTATRTAESLKTTTNGVNGNSEDKSRGNASRVQPRNARNIKEE
VTLPLDLHTFRRMYGNGFDFIESTHAYFIRGLLPYSFKGNVYYTPVVLILRKTVDAEQEG
GESSQQAYHISSSSSSGPSRRRRIVSRYGALIDRKRLGDLFINRRATYIDPCTAAIIPSE
ADAYYKNLLSFLRHAVLDNFERIPPLTPSVDENRGVQDNLPLFRLYPREREVSLRILRDL
SRFCDGVFTYDSATLRVEGFLPLFMDLLTPPREGGFFVSDRALAKTASCPNPHPHNSPGT
TLRGGEEEVVATDLIMKLPLRVQFSANSNFEDPPRVYFLSATTSSPETRTNYEFLSKIIA
DSSVGEVRRDTLSSLEKWNQHGSLLSVLSELQQKATSLLMEYCQASALSFAKGGSEVAMT
QKIDSYSSRTPLNPALCGTGSVGSTSVECDMDWLLVGHPTVRNAPDLFRNTSPTSKHNFE
DMSTANVCVICLEAGRNVVLLPCRHLVLCLSCSLRYKDHLADEMLCPTCRIPIVGMLEIF
P*
>TCRU_4619 Vps51/Vps67, putative
MSSEEAVQEVRRIFTNNTVEQVRDYLSTITRGIQESDYRLKQIVGQSYRDLIAACDKVVG
MEQTCRKLLQMQKQLHTEQQLTLSPQSPGDVLERGTFSRRGAHSASSEATPVRCLFEVAV
ERQTQGREAERNEAEALSSAPCDRLVFQQRCVAIEGLLGSQQVQKAATVWHELMDGLECE
KRLAVKSMTTTVEFQASIVSEGQGKQHEQRRLLLESYRNRIRQGVRELLRKDADDAAQRT
VTYAIATKRSVRGGGSMRETQRHATANATADSVTLGDEFLTDVLAHMAEAHAALGIIDTA
PAALALQNLIELVSAMINDELQLILKAINGGNKRKRGSESACGTTNTVKNPSGKMEWLRV
ALPLPMWLLDDAANSPLSTAWIPLSMEAAHSVGNDITTSATTTDSSHPVASVAGRSNCKT
SNGVIALHILQRTQQLFFHLVAYVASVLPRLYEHGRDAEKRPLSQHHGGVDDDDGANDRE
DVDGYGNYKRQQRSLQTLLTLRGRLVAKEQKERQKQQEEDGGKDLLEFSNRMSSRMGGSS
ARGALSSSLLSAPEEIGDASLSESTSAMSILLPGGFNAPKRTHLRTIYIREVMRQVCGMQ
LLDPKLLQGRKPAKRFSGVDSGSDHKNSPAALEWKCEDVSRKLRIVQETVSQLLGCVADA
GLLRSPRLVALQERLALQEATRMQKWLRESHRQNVLLFEDALWTEMVHKTTERALVRAVG
AGLRRADVVWNAILQSIRVEGSCHAHHQSLSPSIRPYVETDAVTTTKPGTSSQLSQRLLS
RSFFASRLIAAVHCSDGCRNESVFSFSNPEGRMRSSGKESATINALLARAVVQCVWSHSK
MASFEGKTQDTCQLYTNNPHNFISAASSKGCVSSDTFTAMMDGEKHVLAFEEEEEMLFVD
DDDENDNDDVDDDGKNEGGKEEEKRGEGNTNVRKGNNGNHLEEKKKAIMCMFPLYSGRME
RKIALNDDQAAVFERSVLLYMLQRIFDSERLCAVAQTPVHNLITAWISGALGRVRDMMRE
EKEAYQQQQQQQQQQEDEGESFERCAAMMVFFHRLSLLVEVLLCVLETTPAVSNTAGALW
EEVRGTVIACHMPWVQLLRREWESGLCAAYREAWAAVRVPTVDAVAPSLAARRYTLGYAA
CWCHDFCRHPHQPQQREEEKGEQPVAYPIHLTPHVAELLFSLQHILYTVGAGQRLRETVL
PIVIRELLDGTSSALLNVVLPSLAEDKRHLNDSANSNAGGGGDFPARSCQAGSVVNSAAS
HDTEGNKDDTDDDDEKDEALLQLYFDVLFITGLFASPDKVSNSSTAAVLQAIESRVDPVT
WSVTAPFVKSASARLLRATTLSFGSWCSAAAAEVWNVAGSNAQSGTENMQPHQSPLFNGA
ITTPKERDRFPLLPLATTAPSIIPSVGGTHPSLKVRGGSEGRGGATSSCGAADVGSGDGS
LPPAASTGGKEPVTPSFTATLLWGDGTTKGWMGSLW*
>TCRU_4620 glycosyltransferase (GlcNAc), putative
MRSLRRFLVGAGLLPRRSAVFWFLLTFVAMALVMSATMFCSIIVEKEPTHELTQEPAPED
MKEPAHSRSHDVQREVASTKKTRESLLLHAGHLLSLLEQFSEESVTHPTAAGPGVEPDVR
PVGKADMTPEFLLSRYYETELVRLNNDYEKEIDSGYTENVVHSENYWSPFHATRRGYGLE
GSIFVGITHSQEEVTSSEMETACAATVRNIYDAARWPLGVFTGIVEITLSKTSPTTHDPT
KSTETPMDSAVPPAEETPAWIPPPPSVCTPRAYLLPSCAERTAFCPTDNIRVRQVRVGPQ
SANGGDGAGISGRRKSHTLLSSAAAQRYATLALYRGETYVMFVRAGLQLVYKWDVLTRLL
WLQLPSRSAVLSQPPVQINRQSVRLVWDRVVVKHVEGIVVASEKQFSTPANNGSLPPQPG
EGQNGNGVDHWIDSIRWALDLGAVRLHSAAAAAEEEGGSVGGRKTHENNEGDPGMMEEEI
VQYVFHHDAEVFREAKKNRFRTDVNTPEWGKEEGKSSSGSRSRRDIQIYWLRQFYVSLRE
ALLKDVVEQETTSCLSGVQMKKMQSGGHLDPIFRLHAASLKRISHAMQDPRYMRPSPFHG
CGGGAKNACPKMSDYKEVCNDDAILPYLQQSWVTPDFLFTRAEAFFDFPRDGIDGYRDRL
NADSVPLDPFLSFLGADEEAVLLSARLWTHGWDFFSSTEPIAFIVSKPPAEGDASGTDTS
TLSPTLTRMRQRSVARLRHVLFGKSRTAGLAPDAKTEALRHVERYGLGRRRSREELFYFS
GLREAMKDEGVIGYKVDAQHNVDPTCPASFCHS*

>TCRU_4621 hypothetical protein, conserved
MVKLELREFAEATRRMVQLSGVKKSRLMLRARPNSGRRTFVLKSTDGRTTLTTRVTHQGE
LKIVEGIVNDFVGSCTAAVASPGGGKPTLPAPSLIPTPAPGKQADGGTGGNSGSNLQPAS
SGGKGGSKQGGKSAGGGTNANQQQQQQQHRSKKRKGGRR*
>TCRU_4622 glycosyltransferase (GlcNAc), putative
MIQRSTNMFRVYWGVAQQHYYSDLPCVSADALKPQPCVAAPTTSGVMIKDANFDGAICFP
SDNIRIRRIRSFTALGPAFGRYMSMLLYGGEDYMLVLDSHNRFVYAWDARIIAMQVALEH
PKAVLSHYPESYAPPEKGEFAWERKTTAYLCQAKFLNTAGYLRLVGIIIGEGDLFTENAR
HLKPYAIPGLRLRPDVVRPLAQPWAAGGFLFANASVMREVPFDPHLPHLFDGEEVMYSVR
LWTHGYDIFSPKRGICYHFYDRPNEPKLWNEAKRWYASQTYTRRRIQYFLRSRLMGVDVL
RVPKNTQDPVVMIDADRYGTGRLRTVDEWYEFAGADPVRYTVDGRWCG*
>TCRU_4623 retrotransposon hot spot protein, RHS3, putative
MYDLLGWPLATPEVKASAHGATKSFLDAAAEEAWNPMTTIAPMYLEGLYESVYNARWHHV
VEVRGGEGTGMRVEVGKPEQSWSSYYDW*
>TCRU_4624 GRAM domain containing protein, putative
MEFNRSQAAGNGKYVELFAQSYSGPVPKPLPPCTEPTPDEQYRQLMEEKKNEIGEREQRH
AENTAGASGSNVDSSNVVGLFSNAATKLRNVAQQVTLKIERASTEVSSATGAAVRQVERQ
LNVDRFLNNFPELGAMGEILLADYACTAINGGQRVSGHMHITKNYLCFSAPGSSVINQLA
TAVLKESGVGSDNNPVLGIRQIIPLTEIACILLSVALETVDHRPPFFLPLPAPYVRPTGL
QIYTTKQQLFQFLAFESIAAKAGSVFTDAVKGLPIQRAYNYLDHAWRASTSVPLPGVNYA
S*
>TCRU_4625 hypothetical protein
MVRIQVARNRRCMTKATNGGRKLGSVSDFQKKAAEVHHVHAGAGRWAHAEGSGLQKVGAT
SSRHSHSKVWRTKRATPPARPLQVCWKSPQPTRRVAGAPCCLHSCRKAVSVRCCASRAAR
AILEGEGLEVPSCQTTTGPSSSGRRLLRTPPQRLMPT*
>TCRU_4626 hypothetical protein, conserved
MLAWLTDRRGRTFRTGCYSVWALLPCGAPQGSVLGPWPFEVFLDDLGHSFHPTHLPAAIV
TPIVHFPIIDHTITAEIVAYACDVIVRATVPGITHLDVAMQPLFNAISEWTRAKALPLSD
RTYFMAIRIAGHHKSPVPDFFGINGRRCPCKG*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MGSTGLSVFLLRWVRAGYRFVAGCLTVAGREVTTAAELELHGITNVTTVAACGECTKDGD
CFAPLTTAVSDCKCQCAAGGHGEVCVPAPVPAGPPPPPLPPLPVSPPLPVPPVGECISDM
VYPEVAQAVGGGLSWLCYRNVTFSGDGMSLTVLVGAMTGDVANITFDGCTWRDGAVLLLL
GNAYATVGALNIVVTGNTFRDALLSPEGVFPPHTNITISGNRFTVTRLIPRSGLDVDSPS
CVVMNGLAISNDSAVVLSGNVFQTVLASSSAIHVVRSALRVSWQSVLAVVGNTFHMDGSN
GTLIYLEGSSQTSSLDVLNKSAVVVRGNLVARPVQYFMHILSTLRVESLSAVVFHGNDMQ
GSLAVFYSTFTANIYYNSWLQLSGNLCRESPLYAFTLFDPKVNLRDSTVSVSGNKFMSST
VTPTVLLILKKSRDLTNGAIVAACNTVNGEGEAKYAIPSVYNATILTCSDPCTLAASCFP
AYTTTASSDGCTCACAEGGHDDACLPVAVPEPPSTDGADLCVRDVCVDVEVNAGFGISVV
CYVGVTFAADVVVDVEPMSGSVRNVTLVNCTFVDGASLYVVGWLSDPPAGQRADVLVSGL
ESRSGGGVLVANRYPPGSRVAVVDSVLIAEKHVAYRGAYGLGDASACLVVHNVNLTGSVL
TIARTHVAAVFRDAVGVLFFGGVALSSRGALYVDGLSVQTALGLCVSVEGGVVAGGGSVV
AFVDSDFLLCKHAVSVRGAVSVSGSAVALVRSEFSSTEDYAVAFYSTVRLAGGSMLLAKG
NVHDGVSREMLYAAGTVTAAGSTLSFVRNRALLPRMLSLSLSLAAGAHLRVACNDAGGRV
LLTAEEYAAAGFGDAGSIEVVGCDACDRDTHCYAPGTASASMKDGVCVCVCGSGGYGEAC
LPVGAPALPPAVGTAPSVFVREGVTVRSVFVVPAGASEVTLRHVVLDGVSSVLYVPWMAR
DGVRIVVQNVSLLNGAVLYVMGGGALRGAVSAGSDEGGPVELSVCDVEALNGALVLTGTF
PAGSVLTVTDSLLVAARPTPLVYLPGSQSSPYAPVLVLSGLRLVRSVLVVSGVALVTVMT
GGRTVVVDGAVLELVGGGVALDAAVFGGEYALYASARVVASGGAVLRVSGSQVYAAHGLV
FGSGVEANASAVVVNDNAGALTDGALLELRGSASFLSGSWLSVRGNSISGRLLSLPSYPR
RAEVMQSTLTLYGNAGSGHVVMDGTVALVGAGRRFFVGCLTLNGRALHPMDYRSAGIVGK
FRPVACGVCDADVSCFAAATRTMSGSFGCRCAEGGYGRDCLPVYLPHVDGCNRTSAMPPL
SRTEMLTETRSPIPTWTLGPIPSATNYSPTQTLQVTETLALSPTRTPTASVSSTLWWSDV

ACPTLAVTTTAAGGSLTQNDIRGGGSAVPTRLMVALPPPFRWARDPQLGTHLSFVPVSTA
QPSGFGGPWGAMLSNATWVRNATNPSTVLELAVPVHRGYFIAADETIVIRCGAAAVSGGC
KGLLLGSFTIRSDTLPVAASALSAITGVVAGAAAVAVVVTGGLGSVLEMQALGVFARMSC
ASAQERASTVALPYFLSVFAALDPLWMVVGNALLAAVFGCVHCGVTAAFQRWRGVDAASA
WAAMRFPSLTYVVAHAMHLGIFFGSVLALVMPGARVQHYVIGVVGVLYGAAFPAGVCYFI
ARHTGASFTRYWQFSRKPLHERLLYPVGYWHPAAQQRMYGGMLTNMRGSRVYWCVFQLSV
LCVVGLIAAVHPPVGGCHVQYFCMAAVLLAGAGVVAFTNMMRSAFLTVMHTASFVLLAAL
CVVSAANHLAPSDGGARAYVATVLLLTTVLLATTVYGVVVWYVEDRHWQELREPRRGGLG
ALLRDDEDGDEETQKLHEMTSLSYASGTTVSSSYRPPAQLQPMAGDTRSEALSPLDRASS
ASHMIGYAAI*
>TCRU_4628 hypothetical protein, conserved
MRSVVGACPRSRHRVQRRAIAAVRVALLVVLALVAAAAWMPAVHAVVLRLRGGTVDRAIT
VGRAVDTVLMDGVYITNGVAVVFDVPAMLPGALRIELRKCVCDGGAQIYVRGCSGEPASD
RSLEVSVSGLSGGYCSLVFVHNLPAHTNVTVRDSTIVTAGPMRYSQLSGLTDAVASPLVL
HATSLLQTQLRVSNTVLRSLQAGGSAVYVGGDVDLLSSAVVLDGVLLEASGGPTASAMRV
ASSSRLSLRVYSVFSVTNVSVVSSSGGIVLGERLAVVDSVLRFVGVEGSVASSLVRCDGG
TIDAGGWLDLHDVWAVGEASSVASLSGVTLGGGAVSIARCAATGATLVSGLTITSGVVSV
QCNRAGGRVLQSSGDYRMAGLSSVSVVPCDGCAAALACFDALTASFSDCVCSCRAGGVGE
ACLPFDVPPARSGGGGGGAQGCVSGVTLTESVTVGGGQATACFDSVVFSGPITVAVDLRS
MDAFADALNVTLRHCVLAGGVRLRIGGLSESTARLMPHALVNMTNVTSLEGTIVLHGAMP
LHSSVLLANSTLRATVGGSRYVPTTRGHEKSRYGPALVLDGVRLLSTRFVMTRSTLVCGG
GSCAAILVERGLDVKLSSVFYIDNCAVVSRVHVMYALALGLRVSGGSVFSIQNSSWSASS
IEYDDGACMFGDVVVDGGSVLQIVSSTFRLGFAMLIATTLTVTDGSWLVHRDNEFRTAYV
VYVESENGVAFRDRSVWSILDNNFTYGSYSSTIVSMTNDWSPPSDSRPTIYGVCNELRGS
PVTNYQDELNIGAPVTALDCGACTVDAVCFAAKTSSIRGCECVCAAGGHGDTCLPAAVPD
GLGPLPLPDARDTEVRCVHGGSISSVDVPDPGVRGLCFVNVTFTDEIVLDLWSFDAPQQT
LNITLLQCGLVGLSIRGCGARVHVSVTSSMLDSGALEFEGDFCASSQILVAGSTLLSTVS
RAIAFSDFFFDANSTLLLLDNYIEGNIYAVYFSIGVVDGGGIIVKGNTLSTTEEDDGMES
CACVYAVDVKNGGYLDVEKNTMSAVSGIYFYEDTTVSSAGLLRVADCDFVGSAEFLDSAL
LYLAGSVALQGGAQWRVEGNNVSAASVISIGHDQHKIQLSGSGTTVALAHNRQVDDIYPF
ADLDQSNLIVVSPAKIVVGCNLQGDEEVSYGGLFPEGVVIFRCGTCNEDAACYMPGTESV
DRVSCSCSCKDGWHGASCLPFEVPDTVVPPVAERAVDGDTSCVVNQALTSLTLKMWKTHH
CYEGVTFSGVGAVLTFFLNSMPLHLPINITLTGCTFREGAALQFVGGAGAAESSGVLIRV
SQTVMLSSAVVFALVGLARQRRGSGCDVLRH*
>TCRU_4629 Concanavalin A-like lectin/glucanases superfamily,
putative
MNKKWETVFDGKKTTTNTTWEPGREYQVALMLQDGKGSVYVDGKIVGSPENITTLGALGY
EITQFYFQGDEGDSGSSDVTVTNVFLYNRPLSVGELKMVKKSDDKKGNSDGSMRGGISRM
LLCGIVALY*
>TCRU_4630 hypothetical protein, conserved
MSRHVFTFAVLLLLLMIMMCCGTCGAAHAVESKSGGLQLPQWVDIFVSNETRVVPKDRTD
ETGVREAFAAPSLVRVGGVMVAFAEGFLEYNGHHEKLFGTRYSDIVAGYIKAAETWPSIV
AEIARKEWRADTVLGGGNGDDRLRVFCRPASIAGDRKVFLLAGIYEEKYDNDDDEMNGIF
SWLRVWPRSPRTASSVH*
>TCRU_4631 hypothetical protein, conserved
MKRSLSWSISSTCVCASCVSCLLACLALSVATCARGACQEDAGTIAASACEDFSNYLNAR
LSTSSMCPRTVDGRAHTAAGWAGGHQSAARWSARSCGAHVGKMFWRRQRRAGLFSKGGTA
SPTQRVICDTEGSRRHVEVWAGVAPCLCAKSRRSGHDVRVVPGIESPPHRQVPAMRCAPS
FSSWTTFRCRRFTAVRKPTCQIGPPSLLEGSCHHGLVVSGLIAWDTAVPGENVEPSV*
>TCRU_4632 Ubiquitin carboxyl-terminal hydrolase, putative
MQEERGRVLARRDKELERRRQVRQKTQFDVTTNAEEVSTGAMAGDAHNIGNKSGYYELCG
VISHKGRSAESGHYVFWGKPEDQWFVYDDEHVASVTEEDVKRLSGVGEAHIAYVLMYRSR
DPRTKATTIPL*
>TCRU_4633 Concanavalin A-like lectin/glucanases superfamily/Trans-

sialidase of Trypanosoma hydrophobic C-terminal, putative
MVSVRLTAQLEKVKEVLKTWKKVDERVSQMCATLLAQKITSTESACSAAMPVDGLVGFLS
GNFSESTWSDEYLGVDATVNNDGGAKKADKGVRFTGRSAGAEWPVGKKGDNQLYHFANYN
FTLVATVSIDGVPKEGNIPLLGVKMDGDGYPILLGLSYDKEKKWILLCGGGQIKEHSRDW
DPETTKEDHVVILLRNGNQGSAYVDGQRVGGNAQCELENTDSKEISHFYIGGDGDKTREQ
EDVSVTVKNVLLYNRPLDSTEIDAYNPNKASIPFLVNTTIEGTVSSSTAGRQQQAGKEPL
LESSIANGETAGGMDGQEEEVNTQDSEVNAAELSSSLGNVLQGNNGDAGTVRESRLLPSL
LLLLGLWGFAAL*
>TCRU_4634 hypothetical protein, conserved
MVAEQTTVEGSHGDQTEPSRQKGQEKRRHWPRTPLSLSPMSLSFLRSVEVGNIVQGQIQQ
NCHVGAVAGSLLREMQGMEEDMTFFHQLESVKSPLSFPLTQSPELPTIIAYEEASSRRQP
ETQQQRESPQTPSCTACAEMGGAFEHPVESCHEVDWFARRLNFTLLRPQSEEKQVVQEAQ
EEMGYVASCESPGSAFEWGLPHIDSYREGQKQQGDPVDVMTVLERTDSLISTPLMNSVTC
FRPFSVAPVSSCEMTCEEERVVLEQVQRAEQQQQQQQQEELRSPFSGLKAKDAQEVITL
RPRVSRFILEGSPTPCPSISPFASTTGTASFVPLGTPVMHIESVPSIFISPLSRPLSAWM
DSPHSIYPPRRESFAPMGVSTPSQLPVQQTTTEASPFSRGAGDGASAGYAWSLSGIFDMS
FNRTPKHSLSSSPLQRAQGWLPTRNGSSNSDGVLTNSWSTESVRQSEQDRCEGGRLPPSR
CVANAGTPTIPAAAAAPSTKATSGEASQDSPPATLRVPPVQTMRRPPTVPQRTIPQEFPM
HEGECNFCDDEEAHTLLSDEEFSKTSGELSGNDDESGFTRTTHHPFRQRLFEPSPSRWRS
SRRHILRGASKRQKRGDDGMWDLSARLRELERIRVSNHEAMEEREMQSIMSTEMVPNPVE
TSWVETGASGISSIVLGQRRRRGRVREELREKRKDGSPAVLDNNDASCQENTSHEHASND
GGRETKESGGQEQLSLEEASHVIQKGKKLKEGERKDMDIQSSRSSGSSSMGNNGYGKDDF
SGMPISSPSSSGLPAKERKRRNSGPFTNVMDPFFDVCSDKGGKVVEESLSHERRGAGGET
SRLEPEAREEGNAMVALLPGVTSTEEYEAVGKEDEKKGHEDDSVDTTKTVTGQTTLGSGL
SSLCIDRHLRLHRKTPVSTPRVLLKRTPRFTALPRRGNNLAAWVRNISLQRREEGMMQFI
GGSKAFKTKGCRGFPPPMDEKNEGRDDNNFSHRRRKVAVRASGKNDESSIQRGCNDNNNN
NNNSGCGGVMGSAGVSFTATTTTTKVATVTKATSWLAQLPVRASNTSFERKACGGETASH
AYPPAQHVKLNRTAITAAGVSASSLMSPLLASNTPVRTPPIATVLAAMHWEKLSHSACFV
PAGGRTERHTIECSIQTRAAKPHLYTAAEVVTLTTSGSSPTKFASRPTKNGNGHAGMNSG
GFSKPRPISQYPNVSQPTISRHPSDLTFATVSLEKRRVRECSRGVSGSPDIAEDHDYAPC
PSRGTSKPTAQVISCDSSISTNELNTSPLGGQPPHGGNSGITDVSHTAPTSRPKSFHVKS
NCKPSSKSSTRFLNHSNYCLPGTGTYDAPHSVDVCTTSGWMGGSRLTQPLERVSPSRAAA
VTSQKQTRHTAVTTTARKGELVKFSRSKTLQGCSAVVAAPMMTGSLHVSKSAKGGANAGN
QHRPHPTSVTPNKTRMTSRYPHGGVKNNPITMTTEPRSRPGFFTRIDIDHRPSQSRFLRL
TTAPS*
>TCRU_4635 Amidohydrolase/Amidohydrolase family, putative
MLRGMLLFHNAEQVVQVVCGGERYLAGREQSNRIAVIPHGSLLVDTTTGNIAAVGTNDEV
QAFVTANKCNVTDTVPCEGKVLLPGFVDAHTHPVWDGDRAHEFTMKLNGASYMDVQRAGG
GIGFTTRCTRAASEAELKALLRRRLQRMLSFGTTTVEGKSGYGLERDTELKMLRVLKQAN
DEGPLTIVSTFCGAHAVPEGKTAEEAVRDVVEVQLPAVMQERAEGRNDVQNIDVFCELGV
FDHDQSRRVLEAGRKSGLIINFHGDELSYVASGELAGELEAQAVSHLEHVSDEGIACMSK
RPTFAVLLPMTAYVLRIAPPPARKLIDGHVPVALGSDFCPNAHSLSMPHTMNVSCVLMHM
TVEEALVAATINAAGSLNMSDRCGSLEVGKWADVVLLHAPRWEHVVYQMVDPPIEAVYKK
GRLVYSKELP*
>TCRU_4636 hypothetical protein, conserved
MYGSRRSLFKNQKGFSVGRESQLHADDVALAERNRKLFGAATAQGEGSAETRADDDGMPT
AFELDRILPSAKQLQDEIPSVAEVRDAMKEGGDAAMWKKTEEDDDE*
>TCRU_4637 hypothetical protein, conserved
MAAAVGAAEDEMPRNKRTKSLDDITMADESFLYGLSSLFFGSAACRRLTGCLHSAHFEAL
RSFLQGDVTIIRAAPSLTGFECDNTNDGKESDEDDDDLHRETDYLRVLAHESWEGLDAVP
TIPGLAEPLAFALSPAVISAHALG*
>TCRU_4638 hypothetical protein, conserved
MTMTGRVLLVCALCVLWCGAGGGGRAEPPQASPGSTPDKNPQNEKDTTGGAGGGDQNGEQ
AAPQVPTSPTKSESQEVPANPPHTIQPGGVSSEKAEAAKDNNNQKEEKTEEKEDKEEDEE

PKEDEEGEEEEEEEENDTEEKEETKKEDAGAGTTEVTSAGGQEQPSLSSAAEGASNITNP
NSTQTTGDDDPAADGAGTAEGKQNENKDANPKETPATATKNTTATTGDSDGSTAVSHTTS
PLLLLVVVACAAAAAAVAA*
>TCRU_4639 retrotransposon hot spot protein, RHS3, putative
MAASLTDGAHLDKEWPYSWKWKENKSARDCHVNCEVDRAWLIVKGDITEWFSTDGGTDFK
PKQHLLIGTPGIGKSMGAGSYLLYQLLHCDVEKLPVVVYSFGGSTTYVCDKAIKTVTRYV
GRGASKEILWDCGIV*
>TCRU_4640 hypothetical protein, conserved
MTASASAVTLRGIPRRHGEHLKPTVRTRSTSESGIKQISPVTSSCAASEPRRSDSIAERE
SVAAGTLVGDGNAAARRGTENCLWPSSVTGHSARQEQARLPAAAR*
>TCRU_4641 hypothetical protein, conserved
MTLVPYTPSEWCDIGARLWDMVSQCGEIQVQLTFINGNQMSDETLTVAPSATGLCLFHGP
ISKAWQDSTLIGHIANLRAPQIPDFETQVLQPAMGAARELGHQQGLITAERERLNFDYAN
AVADVQNRNARLNSRVEEAHINLLVRESNIAGTGNLVLELRQQLEAGRAQLREREFNLGV
LNA*
>TCRU_4642 TAP42-like family, putative
MSTDGTNTTVKGCFNELLRQYEEGILGGMHSGEQSTIARSLIPQFELLWRQMAVMGVVSS
NEQLDDLSTSSLELLWIPYIIADLYQRIQGPIPTLEATSLLSSSAPETRNTSDMTREEAL
TLSKGWYDIFFQWMLDYELVDERTLEKYRNMHPDQRTQRVELSRKRRELEEEKRRYEQQV
QYLLAKRKRMQALAKEDGDELEDTNGDEEDALRNRALSRLRWSIYESCQQLQLSFRELEM
LQALSLEQRQAIAIDHQKTIEAVQRGEKSLGRHTYTILPGGLITPGGPIPTTQVGSVAMS
AIANQQAFRQKVVKDLMVERNPPTMTLQEFAEAEMADVQRRMDASAAAKRQQEEEDERLG
PDGVEERQRQRDTRLADWKEDHPPIGKTAKGNYT*
>TCRU_4643 hypothetical protein, conserved
MYSAMYRRCAALMMALENKMPSELQRRYIFIGQLTPLLRCSFSNELPLSIPQLRERMQRQ
KKEGAPRMQTLDTEGRLVLTLARSPRPEERVEALERGESLWKELQESSSPIPMTSRTGVR
MALCTSLRRCAIVSRRRELADIWTERFSQRHNIRPEDFTTGPDHTLGEVLGWREARPRAR
PGTGIDDEDIAADAEEEEERRREEKRRSQHERELPPIQQFRRDVYMDHPMMQRAFKRGME
GPGPRYTGD*
>TCRU_4644 AAA domain/Conserved hypothetical ATP binding protein,
putative
MGKYAVVVIGPAGSGKSTLCTVVAEHYATKGRSTHICNFDPAAEDLPYDPSIDIRELISL
EDAMEGKGLGPNGGLVFCMEYLLGQGEVWLCDQLGDHEEDFIIVDMPGQLEVLSHIPAVP
GFVRLLERSGFHVVVLFLLDALAATADAGKFVSGCTFALSCMVCFECPFMNVLTKCDLLP
PAIREEALDHFCTCDFDYLNTKPLPERWREMVRTLAAVIFDFNLVTFRPMDNTDVAYVGN
LCYLIDEALQVVDDAEVNDRDLPDASEAGEAVEDTMDWKHY*
>TCRU_4645 Surp module, putative
MATEDDTTPGIIAPGPELRAKIEKSAASLAKRDKRKAEEMMAKVLASQKREEFLYFEMTH
VFYPFFLQKLNEYRAHPELIPTDEKKDPSQGKTTTTAPTTNGNAVTTQGAASTLTTTTTI
KAGGIVRREGGTAARHDPKRDEALRQAEIEAQRYLEDPFPNRYSLDLHHGTINMPALTLS
YMTCTAQYVAKHGERFMKDILTRYRNNAAFRFLNSEDVRHSVFMKLVESYRLILHHDPDE
VEDRLERYRSAREILDTVCEEKVKYAKAAIARRKAALLTDEELRDRLEWNVFTVVHQFSL
SDLGLDGPMPQSAVAHRSALPETSRGAAAATTSSDSGDALGEKTATATELSSVAAAEMSG
AMDAPEAPPRMLRPPQGFMAPPTFTPTFISSHLVSSTDPTAPLNRSKRGYDEMDENHRPR
RHAPMRRGTDRFDDQRGSEHVGSNDVERWGGGSTAVTRDKHGYEGAQADASATDTEFERN
VRPRREKAEGNER*
>TCRU_4646 DNA polymerase delta subunit 2, putative
MTGGLNDEGDEVPRRRAGLSLQRTHQRFLLRRQQFTQQYAAMYQCRERALQPRALRAIRT
KIEVHLSTGSSAPPFARVLDLVPGQRALCVGVIYKQMRLLPRFLDEYQKELIRIDAGEDD
DEESGAADALCDTTPPLASEQVATINGDGEIGGGRHAEWQGGRGESREQHVPLCHSADEV
FMEDGSGRVLLKEVPVDLLCTGLVIGVDGTLRDNGCLFVHSYALTDLREIYVPRLLPCKT
RSLPCYVGIVCGLGLGSPQMQEAEVTRSRTMVELLVDYLSGHVGDDAMITQASRIAHLVI
AGNSIAPTDELRLKKKVKLDPSDHTRLSDEKQEGGAITSAMLMTEFDAVLTRITETIEVD
VMPGDQDVTNAFQPQQPLHPLLLPEAARRSSLKLVTNPYEFHAFPCKKPTATATAERTAT

TTTTTTAEGGTIFFISSGSNLNDVSRETRYRTRLDAMSMLLRCGCACPTAPNTLFSYPFK
ILDPFVFPSAPHCFVCCDQPEMQTRWVPLEGFNPAGDDTTNEEAPVEDSAGVRLICVPPF
SQTGALVLVDVNSPQLDTVVVNFTSASHEMP*
>TCRU_4647 GTP-binding nuclear protein rtb2, putative
MQVPSTSDCVATFKLILVGDGGTGKTTFVKRHLTGEFEKRYVATVGVDVHPLTFHTNRGK
ICFNCWDTAGQEKFGGLRDGYYIEGQCAIIMFDVTSRNTYKNVPNWHRDITRVCDNIPIV
LVGNKVDCADRQVKAKMITFHRKKGLQYYDISAKSNYNFEKPFLWLAKKLANDPNLTLVE
APLLDPNVQPLSAEQLQALQEEARAVENAPLPMGDDE*
>TCRU_4648 Putative intraflagellar transport protein A1
MSFRELRSFVETMRLLGYPNLISMESFRNPNVELVADCLFWLIKRYEPSAEIVYEIEREG
DRIFFFKQICEVALAKGQIKLNIKKLYQSDGNAVQEMLTLASVLKKAMNATEAEEADYTS
VQQMVAQKNVQDAKRVQQLCSDLTSDGSALFFLIEEEISQRGERQRVLSRATEVGEFERR
LRDVLANVGKQIEQLQTTIMNLSADETTLEQKIESKKTQLERAQKRLKSLMAVRPAFMEE
YEKHEGDLQSQFVVYLEQYRNLEYLEHELAKFNAAEDAVLEEHETRLRVMRERLRKEELS
AIRGEAGHKRGGVRANEDFHTLAKKIHHNRNVNITEDGGDESMGVHGSHAQDWARNAAEE
GSSVSDSGPSSRAGDPPRPQAALGRTRPSPLASAEVAMRRNGGGEVNSRINNSGTTDGVH
PDFREVEPSSTDMRKSRLGASSSSSGYAAIALARGADTSEYAIEDSGTDLTGDDSVSDSD
TDIDTSDISTDSDDSEGSSSI*
>TCRU_4649 small nuclear RNA (snRNA) U1
MYQPIGREELERYLPNFDPMRDPQVGEWVLVSPHRRVTLLRPFVQMAVDRGLQPTYPFLV
ANTLTDGASSPSVLTAMEPTCSAQVDPRRIFPTLEEVCRKYRRRRVRNTKPAMFNNKINN
IHDVNTEDGDEEDDDTTLYLNVRALLLTPCAPAVFGGSDFIEGLDKETGRVVFLNWKTGE
VRTDTAALKPRPIPEWAEEVAEKAIMEWENWRREEKKALHPRETDCDAPPLQKARKE*
>TCRU_4650 retrotransposon hot spot protein, RHS3, putative
MPRVAAGWWVLTVLPTGVAVRLHGAPTVPPWECHAQRHWDSGTKQPRVSFGASGNCWPQL
GGVSGMLHHTGVAMAPRRGISDDGFDAAACGGVEETQRPKWTFDSRLDKVLLEGKERTAS
MRPNHFLWNYFDGRGVEEFNENVYMKDFLGSPSKFI*
>TCRU_4651 retrotransposon hot spot protein, RHS3, putative
MKLNDFLAMELDGRGALDANRDVLLEGFFEDHKKYICDAGVLGEIQASDRYVRMERAVRD
EMDMAEDVHKLYKSGVDNLLKWLVAAAEVKANVHDVAKGFLDAALQEARNPTTTIAAMKM
EGFYDSVHNARRSHAVEVPDGVERKKTGTGMEVHEGRPEQSWSYREAGDAIEENDAVRQF
GAAPPVLMVLASEKGWPYS*
>TCRU_4652 Mucin-like glycoprotein, putative
MMMTCRLLCALLVLALCCPSVCAAGSEDETEQETDPKIDEEEEPGQETDSLPTTLEPQTR
EEKKGSEKQKPKTPKRTPQETATVTEKAKSESNSNKVQEQEDGRSNKEEADIEKTNSVTL
NEQNLKPNAPTTSTTTKKPITTTTTTTAPEATSTTTTRAPSLLREIDASLSSSAWVCAPL
LLAASALAYTTVG*
>TCRU_4653 hypothetical protein
MSFLFPFQPSADVERVSENVGGDATVLAALLFNFSTLGTYRIQEHSIHRVKDAIGQGKGI
GRLNSEKYRLLLQDVNLAAQQLHETVEEGRHTLQRMHLCVGRLLVGMPGTERKQILGTPR
EMDSPPLP*
>TCRU_4654 hypothetical protein, conserved
MSRSNVFGPGSQFSFTKFGALNRATTATNFSLNKRVKDIFRLENQKHIRNDLDRERRYRF
CTKCGITSVTINFNAVPSARIGLWGRCVDDRDYTHHKLVELSQREYEQLRELPVKERIHW
WRYDRN*
>TCRU_4655 retrotransposon hot spot protein, RHS3, putative
MLRCCGRLQVVLLRRRWVLTVSPTGVAVRLRGAPTTAPCECHAQRHWDCGTRQPRLSFGA
SDTCWPQLGGASGMLHRTGVVMAPRRGSRDGYDAAARHVAGSKQRPRWTMSSSVKDTLLE
GSTLRTDMKLNDFLRSNLGGKGVVKKNENVAMEAFVQEPDAYVQDQRLLRIIFNLTEYQV
YKLHHEGVFSLEQWKDYEGKDTVTPAARGKLNAALTQILTERLRGTQEMKFTISTTIEDV
LFKGRVRVKEKKLNDFLTMELDGRGVVDTNRNVLLKEFFKNPKKYIRDKGVLKEIQITDA
YVMMERAVREEMDLEEVVRKLYKNGVSNLLGWSEAAAEVKETVHDITKQSLDAALQEARN
RTTIEALKLEGLYESVYNASWHHVVEIPDGDKRKKKKKGTVMKVKEGKPKQSWTYKKAGN
TFEKDDGVQQSGEAPPRLMVLTSEKGWPYTLNAPHGTDNDFFINCEVDRVWRIVKGDLNK

LFSSHGGTDFKPKQRVLIGTPGIGKSMAAGSYFLYRLLHYDVEELQVVVHCFGETAYVFD
KTTKTVTIYEGNITSKNVLRGLWKSGMKGYIIYDVAKKGTPPDTGFAPSTGWGMIVVSSP
KVTNYDEWEKQLQASRIIMNCPDEMDVKAMCAWMKRGLKPNEQAGYWKEVKERMKKVGPI
PRHIFDEEIYIVRLGAVDDALLAIKDTDVEEYFSMGGEKKWYSEDPSHKLVKIVRARTEK
GAEIFLNAPICDNIGFRTADRLAKVIGPKDILLLVLASRGTLASTYLEKLGLCAFMYEEF
ISALVKELKELPPPSPSKPRSSVLKLNHQGHPTRTVGLGELENGVTRIPMEYRVMYKPEA
QNFPLVDGFFFVDSPRKTLVGLQMATAGEHHTTTSTVNLFKNNMAAYFKGWKKLSRDMSW
EMIYVQHENSTMITNWQRCGPVNTKNLSEAEKEIVAFWNGNVHEYQFALTTDFVNKIRAK
*
>TCRU_4656 Glycine cleavage system P-protein, putative
MALQTREQHIKKERATSNICTSQALLANVAAFYAIYHGSEGLKEIASEMHNKAKILSVGL
ESVGHTVVNGTFFDTVTVNLKGITPEDYVTCCVEKGINIFVDYSHGTVSISVDEATTEGH
VVSLLEAAGLQLPVIGVLSKLAEQKRAMPLQMLRKSVFLGHSIFQKYKSESELMRYIHRL
HGKDYGLTHGCVPLGSCTMKLSPAAAMLSLSWPEFTNIHPLAPKEQTRGYSALCLDLEQK
IRDITALDAVSLQPNSGARGEYCWSSCDPLVS*
>TCRU_4657 Glycine cleavage system P-protein, putative
MSQGTPPVILRNVIENPAWHTPYTPFQAEISQGRLESLLNFQSMIIDLTAVNLANASLLD
QATACAEAMYLAFHHGRKERMTFFIFVSRDVLPSCVEMAKTRAEPLKVKVVVGDPNLIDW
SDSSLCGILAQTPDAMGMLHDFTTLFDNAKRHGVVSCCGTDLMASVLLKPPGEMGADVVL
GSAQRFGAPLGFEGFTPHFLLSRRNLSD*
>TCRU_4658 protein kinase, putative
MDRFIVGSPIGEGRFGVVRAAVVKESGVPAAIKFVTTPRLDEGIPHPTARELLVALRLVH
PFVIRTYEVVPCGCSLALVMERCKTDLATVLSGRTASNPLPALEAKSLFKMLLLALAYIH
SEGVLHRDVKPSNCFLTAEGELRLGDLGLSRVWDTEASMTHEIVSRWYRAPELLLGQRHY
GPEIDVWSSGCVFAELLRGYGGAFFAGDGDIWQLSRIFDVLGTPTPTSWPSAVLLPDWGK
AHFEPKRPLPLHEFFPDASECALDLLRILLCLDPQKRLTAAGALRHAYFSEYPT*
>TCRU_4659 hypothetical protein
MDVSVFLKEFKRARKESGGSVPFGGEGSAGAAGVTNAFSQDATTIGRILSPDDSGESEQS
INDLEAEDAPPSYLRSKRQRCDAFWRRTQEGGLGRTRGSFTEIKTYRTNRCPKTDSSIPN
ATVRRATHSIPLRVAAKRGGASTVNKLRDELLRKKNSLSQSLVVREHTGGCCADDSRECA
LSTGAEEFLVCVDDLIAPENTTMDQSPFFG*
>TCRU_4660 retrotransposon hot spot protein, RHS3, putative
MNAGSYLLYQLLHYDVEKLQLVVHCFGETAYVFDKTTKTVTKYMGEIISKNVLYDLRQCG
MKGYIIYDVARKGTPPDTGFAPSTGWGMIVVSSPNLDNYDKWATQVKARRIIMNCPDEVD
VKAMCAWMKRGLEPDEQAGYWKKVKERMDKVGPIPRHIFDEKSYKDRLAAINGALLAIKL
TDVEEYFTLRGGKLWYSEDPSHKLVKVVREITKKGAELFLNATISADIGFRIADRLEKKM
GAKDLLLLILGSRGALASRALEQLGLRVFMYGEFVSALLKGLNELRPPERSEAQDSVLKV
NHQGHPTRTVGLTELEGGVTRIP*
>TCRU_4661 retrotransposon hot spot protein, RHS3, putative
MKFTISTTIEEVLFKGGVRVKEKKLNDFLTMELGGRGVVDTNRSVLLEEFFKDPTKYIRD
KGALKEIQITDAYARMERAVRDEIIFEKDRSKLRDKDVVNLFGWSKAAANVKTSVHCITK
DFLDAAAEEARILTTTIVAIKLEGDATSLCTMRGGIMSWKLLVAMRERKRGREWM*
>TCRU_of Trypanosoma cruzi region 5/Dispersed gene family protein.1
Dispersed gene family protein.1
MLSNATWVRNATNPSTVLELAVPVHRGYFIAADETIVIRCDVAAVSGGCKGVLLGSFTIR
SDTLPAASSALSAITGVVAGAAAVAVVVTGGLGSVLEMQAVGVFARMSCASSQERASTVA
LPYFLSVFAARDPLWMVVGNAVLAAVFGCVHCGVTAAFQRWRGVDAASAWAAMRFPSLTY
VVAHAMHLGIFFGSVLALAMPGARVQHRVIGVVGVLYGVAFPAGVCYLIARHTGASFTRY
WQFSRKPLHERLLYPVGYWYPAAQQRMYGGMLTNMRGSHVYWCVFQLSVLCVVGLIAAVH
PPVGGCDVQYFCMAAVLLAGAGVIAFTNMMRSAFLTVIQTASFLLLAALCVVSAANHLAP
SDGGARAYAAIVLLLSTVMLAVTVYGVVVWHAEDRHWQELREPRRGGLEALLRDDDESDE
VVQKPHDMTSSSYASGTTVASSYQPPAMP*
>TCRU_4663 hypothetical protein, conserved
MRGVHLAPRHAQHSASRPNHARTRVQRIVATEHSRVQRDTATDKLQHRAVHHHRPSTSHH

GHEGHAERNQHGPHKPQARQHQHRCVRRGLRAGKTHKRRRPRGNQQGVRHRQHRPRGIRA
GQHKRTVQRLHVAHGQLHRPALVAPRRPRTAQPSTAHHVQHSTVQQRDVLHNDPHAVSRH
PRHVEHRTHAVQHDVAQHHLARAGRHNEHRPHRHALAEEHTRRSAHSRRQHGSSHRHARL
AVPAAAARAHAHTVPHARRRRPGRVAVRVPVAGVAPSNVDSPSVAKTSRCVLLRHRQDTP
TSVVARHPQMRPSRERQTQRQHPRQQRSVAHKAQRAPSSGHGASGVEHLPRDTVVHVALR
QQHRPAIQAHRRIKRHRVVLRRQKVAPHKRHSGARHAHSPTHRHRVLAQQEAAVNKRHHG
AATGRNTALHRHAQPQLRLHQQPVHVRHTARRQRHAANKQHANSVAEHRRHMRARDGQHA
PSQIHAVQHEARGGVAKVVGAAVRNTILCNQHRVHHSDARARRKSVRHHHAAARARLKPA
DQHIDALASRRVGQPPNNVQARSAQKRAVRQRHVAHAPRHRLHVHHDVRRKGHTNVAQHR
RPETDVHLHVYTHVPHAQVGAVGARWIGDSDRQARIAMAALRARAGAAITRRRRRVRREA
RCRESAWVAAGQKCGIVHGRDAVFRLLLAVHSVARSHNRSFFEVAGN*
>TCRU_4664 BNR repeat-like domain/Concanavalin A-like lectin/ glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MSRRMFTSAALLLLVVIMCCGTGGAAPAGKGSKSDSGSSLDKHIVWRDKKEDETVDSLYA
PSFVEVNGGVFAFAEALLKDGNYFFTGIASELLELSGENQKKMGGSNLKTKTLEKCPSEG
GKRPSQSTNRVGSQSFHRVDVSRPTTVVKGNGIYMLAGKYIRENVAVCQGRADAASWGLL
LVKGNVSDEQDKEIVWEVIDDLPCTSIVKLHESWPLLTGGGGSGITMDDDTLVLPLEAVK
EHGTESEAKEGKNNNVSLILYSSDTKNWKLSKGMSAYGCTDPSVVEWKGKLMMMTACDDG
RRRVYESGDKGASWTEALGTLSRVWGNNQKRHEWGVRSGFITANIDGVGNDKRNVMLVTL
PVFSKKADTRGRGKERGELHLWLTDNTHIVDIGPVSGNDDAAASSLLYKSGTNGNNNNEL
IALYEKKEDGFRQSLGMVSVRLTEQLKRVKDVLATWKEVDDLVSKLCTPSNTEKDRPNST
PCSTTVKITAGLVGFLSGNLSGSTWKDEYLGVNARVTGAVKKAEPSDGVTFKGRGAGAHW
PVGRQGENQLYHFANYNFTLVATVSIHGVPKDGDTPIPLMGAKVNDGDKNTVLLGLSYNK
ERKWQALCCDGTTAEHSSTWDPQRQYQVAIVLQNEKQGSVYVDGQRVCESVQSNLENTES
KGISHFYIGGDGGSAENTVGDEGVSVTVRNVLLYNRPLTFTGGSADLEEDIASPSEDPVE
QAASQQSRKKREAQQVPAALSSNAVGEATGDGSIVRESGLLLLLLLLGLWGFAAL*
>TCRU_4665 hypothetical protein, conserved
MAEAASCLDLKASFFQVSLPRETRHLFRCRVEDGTLVELTRLPMGYKAGPEILQIIITSA
IAVVTTVVHRLWAAPPLARVDVWIDNIRIAGSKSDVTLWEAQVLRNADSCYASLGEERES
GATQYTFLGVQFDHTHRAVSLSDKFVRSVRAMPALNSSTIAEMEVMASRFLYAAAILGTR
LCQYYFFIKAVRRRLSALNRGIVLETSPANLPPSAVGLGERLRHIIENNRKRIIKPTERA
SAAIITDASLHG*
>TCRU_4666 hypothetical protein, conserved
MSGSTPGTDSRHTDRRLSCGVRAFLFLLGILPVPSPDCGEDAHVPGIDAVLREGSCHDGV
SVRCNAAWDSAVSWGKCGVNNVRPRYASESGTVKISSLTPSCTASEPRRSDSIAERESVA
VEIRVGDGMLPPCGELGTVCGHAQWQDTPLGRSMRGCQQLRGEAHRERGCPGSRVAAQRI
*
>TCRU_4667 hypothetical protein, conserved
MGLSCSHNKKWETALGGKTTTRSSNREPRKEHQVALMLQCNKTSVHIDGRSLGEEEVLLA
GERPPEVLRVRFGACGGHESRLTVTDVFLYSRPLNSTAMRALKDSVPAPTREAAPTPPER
IRVVDSVSEHVAGDITEGK*
>TCRU_4668 hypothetical protein, conserved
MPRDGGEVRHEPASEAGSIVAANLTTNTHITRVDSVSPVPSEVYIPNRLGNMKLHLDGEL
RRDRTAVEKIALYKETKYNSINAFNRFVTFLLCLLAPSVFCMAIGMCSTEWIVTLNHLQY
RSMGLIFSCYEGVVGFCMQRGSSRYPRQLRDSLTKAIICESSESFVRAYISAMWSLAIVQ
FFCILLGIIVTLRIASRPTRSHSSLVVLCLLLLALPCGIVNCVLFHFYTRCERRACEALH
SPSPQCRVRYDWGFDVYIASICFNFVACITAIFLCSYPHSIRAQTAQKYDERREQERRRR
ERAQTSHGERSRHMTRFLRPILGEPEEPLYLTAEELEITIDGANDWVYDDKSDLFYSFDL
DMFWDPLTRDYYSRELCSWQATPQGLLELRRAKRSRNDR*
>TCRU_4669 hypothetical protein, conserved
MRPAHRCTAERQEGMDEEKTQPSHPWTREDSLTAQLKIQLYRIYASVSRQREWFKIHESN
VRALTEEAETLRARFFPHERSLLTAVTGDAKNRRETHSSSFCFADTEGMSSDDMTLTTMR
RPCPCSKDASHAMIRDFSSKALTPWCPSSLQADEGWTLPLRPGGDGTGYPSAAVLIPSAN

DVHSCVNAVDFRYVVPEYLLQLSPGWIHERLGTTGGGKGGGIMAEEATSALVALLLPLLR
AFRGVVDTARWLTESCDYATGVPAHDGFLTLKALCAAARHLFYLLHEALCCLSSWATEVA
QSGMATVAHKMSPEERAEATQILLYLLDDRGSGALVLQLLCTDKNTSNTPHHTELGTLEP
ATTGFVPRSVVSEAFSFLAIHFFGICLGE*
>TCRU_4670 dolichyl-P-Man:GDP-Man7GlcNAc2-PP-dolichyl alpha-1,6-
mannosyltransferase, putative
MKGYARLGLVVLFASCVVCEVLCPYTKVEESFGMQAMHDFIFCPAPECWDHHEFPGVVPR
TFVGPWIVVALTLLIVTLVVEPIGTVVKYTFLHAGVLSNIMDNKKWIVEHPFFLEVTAPK
SPMFFSHACRLVLGSMVCGALWYVATGIDEFENKIVKSTARPTRKRCSASFVFFLLCILQ
FHLLFYATRALPNTYALILCSLACGCTLRGMHYHSIALLNVSAAVFRCDTILLLGSSGLF
LLLQRDVTLARSALVSFFSLVLAFGCSVALDSFLWGRWVWPEATVLFFNTVENQSWRWGR
LPWHWYVTYALPRAFLFEYMPLLLLVGLACWDLGRRLIHLMVAFCSRAPAASLFSLSPYS
PSSSFRGALFSLWLDTGVRYRAVLLPAALFVVLYSFLPHKELRFIMVAFPNFLAPVAAAV
SLTWNELIAREGDGSAHVKDGNGKTVLQQPERGNASKQRKCKHVHYEQRMKRVTMAVFLG
LFLLQLMTVVMSVYFSIHNYPGADALKKLHQIIEKDIFDNNSCANRLGVGSADQTVSLTV
FIDAYAGMTGINRFQKAHHLQPPGQFVDGRIGYLPLYPSSLRDRLVAIFALPFVALLHLS
EGITSPLGRFREYHDGDLYGAMGGPSTASDAASVLLSGADRRQLRGVQLRYTKDPTLFDE
ERGVYKSDGLDYLLVRYSQRELHRQHGVFEELFTASPDFCSHVAYWLRGFWPWRCHLFFN
ERAEKPFILALRRRCRE*
>TCRU_4671 ribosomal protein L11, putative
MLRRGTVSLLRARPKTVNVEPGSNRMPDAAVMAKAKDIFAVPEFPGKRVLHNWRFFIKAG
KAATGPPVGQEFSKLGLKAMDFAKSFNDRTKPHFKDDVELIVRIQVYFDKSYLYTIEPPP
TAWFILRALRKRRRETGPVPIRGHYCALMTLEMAYEIAKMKPRSWGRPEYPLIETRVRRV
VGQARRMGVCFVGVDTPHSSPVKGVTEKQYAEESERYRAMHMEQYEALRQRELEEAPLIE
RLHRPNFAPLSEAQIEEGLKEPGLFHALWQASHPKSPYHRDLRQREMARRYLNARGWVKD
MTLDEMQVVFMNYRLPEIERGHQMDEGGMEGQVYWTRDGAQ*
>TCRU_4672 hypothetical protein, conserved
MHGAGVESCLASAYERRADAVLRLAEELECGSPSAGQCSSPHFFRALVTAYLVQNDAVNA
TWALQRWATGPAGAGEQEEEGGVRAMLERVARHCGRCAYGEAFREALGAVGGGTGRDVEH
LERWLLDYLAARHVHQRRTFYGESGGMEKLAVGLGVTVADLEARLQRVREDELRHIGREV
SGGPCEKTRDTLCCMLQVGKAV*
>TCRU_4673 MSP (Major sperm protein) domain containing protein,
putative
MTASLVPLVQFSQESLYFPLPPKDIIIENIVQVKNLLECTEEKTENIIVFKVLCTVRNRY
GVKPSVGFIFPTESVKIKFLLDLPQLRRQGGAEAALVLPNAKTQDNMFVDIAVLPKDQAK
TYMESLNENGNGKKIGRSSSRMYVEQAAAFWKTLGQIKPGNVQVVRRQLSCVYGDKGVPE
SLVMRMGGYGTKLLESPQVVTPSGSDAVSTPSPPAVPKSRFHTVKTDTQRKSPPVAPPRL
SVAGSARNRDMKSPSTESGGVVSSPRAKNNLVPPTVLHNSGAGGGITINSRPAAVIAHPT
PALAQRKQKVWKDCLCFRVSFRLLAALLVLSFLCALFESGTFLSWLLIGR*
>TCRU_4674 retrotransposon hot spot protein, RHS3, putative
MQASDCYKRMERAVRDEMDMEEDADKLREHCMDNLLRWLVAAAEVKASVHGATKRFLDAA
AEEARSPKKSSAPRYLEGCYESVHNARWHHVVEVPGGEGTGLEVREGNHHSLGRTGQLAT
LSKRMTVCSNPVHRVPG*
>TCRU_4675 hypothetical protein, conserved
MERRLGDHQHSARPVTSLHQFCRGKLECVPYGRDNRKIMQIHDVPEELELLLGTRGTKSG
IRERRGFVRRITVAPFDGVLECVMDATPGHSSWMRLGPPLRRRLRQAPACRQL*
>TCRU_4676 hypothetical protein, conserved
MMTMTGRVLLVCALCVLWCGAGGGGRAEAIPDSSDSASSKEKPQKGKEAVGGTGEGDQIG
EQKVTEVPAPTKSEPVFRGRLPRGRFVSGGGALKTISPTKDSRVQNGQEEKEETKEGEAN
QQEEARDEDEDDDDDDEEEEEEEEEREVDAKENEEEVTMKEGAVTSTTEGISAGTEEQRS
LSSGADGASNITNPNSTQTTGDDDPAADGAGAAEGKQNENKESNPKETPVEAWRR*
>TCRU_gamma, conserved domain containing protein, putative
Elongation factor.1
MQCVTANLVRGWLQRMEHVRQYALGVALIIVEERRHDVVALCVLRGRGMPAIERDVEDTE

MLDWEEAVAYVAAQRPQTAKPLVAVSFFGVGAAGFNHARILDSCCVLFPAACRRWRRSAA
NLYALARRSGRNVPNPPITPHPARSAPARDPPARRREGG*
>TCRU_4678 ubiquitin-like protein, putative
MRINVSGVRPEHTISDLEVDLDAGVEGLRRTVAERIGAAPERLRLIHMGRLIDESRPLGS
FLHEGATIHAVITQGAPPPSDSSSRGNNSGNNEQGGIPVMNLLEFANFWRGIPDPLLSFI
QQSVSSMVGPTAGRTPVIIQGGIMGSGMGAHSMDNSQQQQQQQREQEPQSQQQQQQQQQQ
QQQSPMEGQPQQQHRFSFSYAVPTPEALAPSPVHIHVHVSLDELEQLPERLERFRRRMQA
SGSTASVHVERGPLPHGATPSAQPAAPRTAESNNGNRGSDNNAPAGSRNLASNALPETIG
ELTNALIGATEEEEESGLPQLCVIAFSNANVATLFPLLQGDFSFFAASRERLVEAVRQWG
EQPEGEARRTQQENRRRFVEDQVAQAIEALQGNLSFMEFIERARRPQCNFLSELKSYLIL
AHEEIASAILNPTVDIDQWTTGLRVAFVRIAGIAAERASVWFEGGLSVLYELIPLMLQTM
ISQALNARTQWISQVIPMMRLSLTGFIPAWHAEYMSQHRRDTDSILFEEAAAAQEQRKEE
DDLLDDCLDEFCTDRVEGGGNGTAANSHAGANTDEVRSALHAFRGASEEEEEDICRRARR
FRYEERPANAFNASTMWNHLKKQ*
>TCRU_4679 hypothetical protein, conserved
MWRGPQVAPRLRTGVQLWFVACAQKRLCTSSSSSASSAEGEKGGGGSRRAGSDRRGDGEE
AADTTGGKRTSAAAEERRRIARSWENAFFGRVHYEPGMHEKYQAALETEEEEEEQMRRSN
RELFPHWPEDEEAPRHEFHRLPDALKKRYIVNRLTMGERRITYAADYGGLLMMQHLNLGE
LMINEAERLLVECGWCNDDVAAKIEAVRDCAARTKFQFDLD*
>TCRU_4680 hypothetical protein, conserved
MEVLASDEGGLCALSPNKGLYAFVKKGIVVVFMDYIRRTSGMGNDTPSGGEGVDTLFEDA
EFPKHRTGDAVISTHTALDEIHELQWSPDSTLVTLLLAQRRIVEIVSVYGKCCVARIDAG
ISGMRAVLWHPSSRAVYWLGLLQAHVISLVDSQVMRLAGSVKYSTQLAARKLSSKFFSHG
DPNSSLSSRMSDPVSEAALIRFSTCHRFLLYLTPKSLHSPLSKNQEGQAVPSRGLNGDVT
PTPPGEPDDNENCASSRPQRSEWLVVASATTHEELHAFPTGSFVEKVSDFIPLECGIALV
DYIHGSMALIPYNGTAMLHYEPSGVKNVVSSKNGTVLLVIFADACRPVLVQRNRILVLRR
ISFQEDVILPLKLRELHLLKEPSLAEGFPLVTVSRADESCQQDVDILTEPNKCHDWTQGR
GMEAFLHGHAEISASGQIAAVTLARWPSWVLLIDILGQRVTEVLRHNEPVVGLCWSPSPS
SEYWRFQRRYYMGQNGGTVGADGAGDGAVKGKTIIPGQEEPLLVMTDNHQAKVFFWLANY
ATCFVASREGCVDEMDARRRRKQRADASCGCEGGFPALRLNRGMFGESAATAVLVDDVRG
IALTVAFRMNESNQ*
>TCRU_4681 predicted C2 domain protein
MATLKVTVHEAWDLPIMDRTTGLADPYVVLRLNDLEYTTEIVHMSRHPVWNTVFRIDTPD
LFILQEDPLEVRLYDHDIISRDDIVGLTFIDCNSMVLQSNPSMSGWFPLFDTNAKGIRGE
IRLTLKIKFHNAENPLAPRLPIRYAPHFTLPDVDQRSRAEDHQLLLPNPQLDMYLAEGFE
PLRATRMEHPSIAAEEEGILIFSAWRLDPSVYRVESVLTMVEELIVKADPEHSKLTNLRS
TRSTNEARIIQLYKLSGKVRRQLARKVVEMQCNAVLGYVEKFDMESNGIIVRAYGTPCVL
SAVKFVDRERAERLLPDSTRVALRATEISSGSITPAHDPSVTTLHMQAAESAGGLTAAGV
VLGSGMTFASPMQQRTSAPETSFLQLPEAEVPTPPQLASNNPPQTCLLSPAVYPQVTSMP
CDNYPMTLSKADYGFPSLLAQQTATGARSNVLILTLKDLPSGMIEHIGGYISARSVKIVA
KMKSKQMISQERDSWWMELREELKANARAFHCNVILGYEEVVMYHEDVAVLSLSGTAVVL
NSTMLPLRCGPEYLYQTARGRFGAQKNCSMLHLFYPNLRLKDFVGEMECPAVCNLCHRKS
VPDVLLVSCTMPQDLMCEEQPRLVHTVVSKAKSAVRGVDLALAVSQALPYIEYSLHKQLI
FHLRLQKLNAVFGLRITVCIASDTIIGTLTGTGVRLVALPVPSLPRLKFIDPAIQRNKTV
MRLVELVAQHTRLKRHQHRNFPPMGAEHQGSFSSSRSSSAVQMEDSNPFETAGGDGELSS
ESGSDQGPHGIGRVSRACDYVLKIDDEEEAEMMLGMSADLTFEHSLLLTIPYVPEWANTY
GSQKRIVINRRFVFQRIHNESVTTGKINECFANAKKAFVQVACRVAMRCCRCPLERLHVM
GFTFDFFFEPNSCSLQLRLEGCLMLRTTTQRVRLMELEERSFMECMRRIERYPLPGPIVY
GNPSGSADIHPPSQDTSTLPHGSLGSVPTLDGNRSSGFGSFGDGEKVMLRNIERRIFVMS
NAPYALPFVFERHVSPPVLGSSEGTNSAPLTASDVYGYYKDNRARPGMMERQWQALALLA
STAVRNLMEKTGLNSDGKGGVDARHRDGANSLKSTGSGGPILHQPAQRLPMDLKTLEAND
SSIIFTPLDFVAGRSIARYVGRLSQHFIREAYEIDSSEDLGVFFQKTEFEMQCLVQAMVC
LMGGNALLKHCVTYHEVWDSDGSGCAFVFVTVTGDVVQTTTLPLVTLLLSNGGSYEEGSD
D*

>TCRU_4682 kinetoplastid-specific dual specificity phosphatase, putative
MHETSPRLLVRVVGVPLPLFLPPGSNADCATTKAVRETRQEKYRQLILESEHRFLRGLEA
CLLWLLRCRRYEKMQKLLPPRQLSEKHESQISGDRTGHASSFLSSFFHEEPATLSVPLYY
LPMHIDDNVTSRLADIIDVATAFMDWIVDADMSLVKESTALLQELVRLSHLMERGAEYDN
DYSKRNNNKQQNTDEFLYLLHRHVASLLEATHQYGSHVNKENNNTNTTIHSNGRAFTLPI
VCYDDEYGMPLSELVLDDSLIDLFPQPRASDDDYDSNSSDAFSSMETIHDFREPQGQLTL
AKDEYGVVCTAHSLPGVLVHCMKGVSRSPSVIMAYYMQKCCRQFYTLSFTPRHTILEETI
ASNIEDDIEDAYIFSFRQLLRCLQEARPVVNPQICFLAELRAMWTRLSRDMADKEAEELL
*
>TCRU_4683 Protein tyrosine kinase/Protein kinase domain containing protein, putative
MIVFRNEEGEELPEIFELRTRYEAIAPIAKGAYGFVCAATDNDLVENFHMSPPEEYNDPS
LSKEERLDIYESHTTVAVKKLRQLFEQNRPRMWLCATREIQLMMAFKHENVMSALDFFIP
LGDCERMTYESVEYLRHNFDSVYIVMKKMEYTLREVLESSVFTTTDTQDECGKLSNGKIT
SSAGTEKHDDGAHDDINKSTARRNERIARCPQTHLVLHPLARDYRMFILYQLLRGVGYMH
LCLVIHRDIKPENIMLDRNYNTRVCDFGQGRDAVATELDGVLQTFLDNCTQWYAAPETLT
LANVSSPSGFVDQKTLHAADVWSIGCIAAEMVIGRPLFYCRHSGGVGQLNAIMGVLGKIP
EEAAERILQHRDEDTQKLFESVMRREMQQHLHKPSTLRRLLQSPYGDVDEEEIRLIERLL
CYDPSQRITIQEALQSNYFINEGYEPVIDPDDTATHVRAVEAKEVVDAVRGRRFLWSLFL
KHHPEVEELMRVLEIRRNSSSTDSTEVPPPACV*
>TCRU_4684 Protein of unknown function (DUF2392), putative
MAVCFKCKQSQGVFRSRDGATKPYCADCFVEFCTRQIRDNLFKHCGMPCEVPLAVAVSGG
HSSMSILHQLGVLRAQNRMRPECAQVTFTFIPFHLREDELVLPLLAEEAEENAGVDPRQE
ELRCVAASMTEQFEKLETMIRTQCVQWKFASTPLFAEGEVCVVRYSDYLSPGELQAFRGV
LHHSRLSLSDRELLYERLRQRVLTAAALECIHRWHRTRQAPSAVGWYHLLTGENALRCFM
TTLREVMSGNGQNTVHLSGYRGFVGQCLVLRPLRTMLPHELVMYCRTQGIHAAYSPSLST
QTSLRSMNRTLELFFNNMLRTYRTSVFNVLNTVNKLHVETAPELTCMDPQRGASQQQAKR
VLLGKSAQHHYEKLQTMQPPHYSWFGGSGMEPFSPRNDDRTHQLCLLCACLIPVPDGHTV
MPQTGRRQFICKACMTFLQGLPDDFITVVPSEINTRNNRTGEKWARRITELSDSGSLDAF
SSLAARMEALMRTADATAETGREKDIVETRNVRWRLSGHDVSGFLLQEDGEDDNVGE*
>TCRU_4685 Protein of unknown function (DUF3720), putative
MAMMMTGRVLLVFALCTLWCGAGSFGDARDNRGIEGEKNLLTHTHNGGNDRVRLTADCGL
ISTRMGLIKAVEAGDDSEGGTTNAPLNGKEKTSPGAEPAGIGGNETPGPKEVKGAAGAET
PSPSGPGVPGTGAETGS*
>TCRU_4686 hypothetical protein, conserved
MDPGSKEPKESQDRTNDQLPSPSGSPSTRSGEKSSLTGTDDLTPLPNDTETELGADLQDK
DGSDDAIEEEDGEKEKEKKQEKDTLQPEKHEGQNNGGGTPPPPPSGGAAPSSSEGEGGPT
TEKENLQNITEVKNEATPSGPKMESKAPAPPSGDATQGQHTHDTDTEDSARNAATGTPAE
TSSSSTSASGSGDHVRNKADEDDAQRNEGQHDSLETGNTNVVLILSGTASKTPETITANT
TDTTPGDGSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>TCRU_4687 rhomboid-like protein
MLAGGAACKFIAASLCVTTALSQWSTTLLRVFGLIPAHTFSVHSYPWNVLSYIFVESNVI
LCAIGVGYMLSIGAMVEAAVGTVTFLQLILVTGTATAGLLLVLSALLHPLGFSCFLQCFC
GVWPPAAALLVPWVAASPMAGALRGILASHVQRRHLPAILLGFSVVVDILFRERQKISDE
DIDSENIFPGSIFLPAFLALCISWMLQPLFRVEPPVAFRVLLHPIASRLLSCFGVSQRRG
SAEEQKDMGIESAVSVTILRGAANLTPLPGSTEEDAERRRSIALAALNSRLRENTPMAPD
LSKMSDMLA*
>TCRU_4688 hypothetical protein, conserved
MRDGIYEEWDGERGSCQRLWRANLIPKWHELLKNECETEYTKNGTVNAAAVNCCVYDAMR
ELCNDVYARTLKETDDSQVEGICKEYAGKPNDEVKCPKPQTEPLPGTGATVEVSVPEGLG
NEEELKKQSEEAPGAPPEDSDPKPTGIPASPPVEGSPDKAKDVRVPNSEEGSVSMEPTKD
SAEGDIVPIADTDHNEASNAQAESTTTTPADASDNAKNKAENGTGENIPNNTTESDVAGT
EGKTDENKDNNSNEKTLPIVGVKTATTTPGDSDGSTAASHTTSPLLLLLLVVACAAAAVV

AA*
>TCRU_4689 hypothetical protein, conserved
MPSDRHIPGNASYLSGELLLVEVPKIKYGSGLPFVRHRAKTAWEWLRHGLCSLRRRCDRR
AVSRSRPRSSAGRWFRWDFWRLRLTAKAKFPQRLGACNAMGVDHVRHDTSAAAAVLAAHR
AVCRASDRGGVGSSRRRWLFRAKFFACLLCGIRAAPTACAWDGGLQWSQQPSVFVRNTGA
GAGRRSLLPASDSGSRARGFPVACCSGAVSSWPELSDTNNTSGQCDDAGAPCVCELCEVG
RLLGLCITSLFPGHAAVAKDKPHPCARPSVLLARKKGTPTM*
>TCRU_4690 hypothetical protein, conserved
MDAEPEHRALQSAAVRADGDTAGDGDGGVAAHADPDGVGEQHAVVERGGVPDACRDDDGG
WWVPDAERHPRRWERRPDAADGGAAAAVSMGTRPAAQHAPELCAGVDGAAERLRWSVGSD
AEQRDVGAQRDESVHRPGAGCARAPRLLHCCRRDDSHSLRRYGGVRRLQGRAAWVLHDQV
*
>TCRU_4691 hypothetical protein, conserved
MVDGARATQRDSPADTCLSRWMQSSVGACPRSRQRVRRRAILAVRVALLVALVLAAAAAW
MPAVHAVVLRLRGGTVDRAITVGRAVDTVLMDGVSITNGVAVVFDVPAMLPGALRIELRN
CVCDGGAQIYVRGYSGEPVSDRSLVVSVSGLSGSYCSLVFVHNLPAHTNVTVRDSTIVTP
GPMRYSQLSGLTDAVASPLVLYATSLLQSQLRVSNTVLRSSQAGGSAVYVGGGVDLLSSA
VVLDGVLLEASGGLTASAMHVASSSRLSLRSHSMFSVTDVSVVSSGGFVLGERLAVFDSV
LRFVGVEGSVASSLVRCDGGTIGGGGWLDLHDVWAVGEASSVALLSGMTLSGGAVSIARC
AATGATLVSGPAITSGVVSVQCNRAGGRVLQSSGDYRMAGLPSVSVVPCDGCAAALACFD
ALTASFSECVCSCRAGGVGDACLPFDLPPARAGGSGDGAQDCVSGVTLTESVTVGGGRAT
ACFDSVLFSGPIIVAVDLRSMDAFADALNVTLRHCVLAGGAQLRIGGLSESTARLMPHAF
VNMTNVTSLEGTIVLHGAMPLHSSVLLANSALRATVGGSQYVPTTRGHKSFRYVPALVLD
GVRLLSTCFVMTRSTLVCGGGSCAAILVERSLGVNLSSVFYMDNCVIRSRKHVIYALASD
LRVGNGSVFSIQDSSWILPSTEYGKAACVFKDVAVAGGSVLQIVSSTFRLGFAMLMAATL
TVTGGSWLVHRNNEFRTAYVVYVAAHYGMVFRDRSVWSILDNNLTYGSYSTIANMTNNWS
PPSDTRPTIYGMCNEARGSPVTDYQDDLNIGAPVTVLDCGACTVDAVCFAARTSSISGCE
CVCAAGGYGDTCLPAAVPDGLGPLPLPDAKDTEVRCVHGGSISSVDYPDPGVRGLCFVNV
TFTAAIVLDLSYFDAPQQTLNITLLQCVLMGLLIRGSGVRVHVSVTSSILDFGALDFRGD
FGASSQILVVGSTLVTTSGHAISFVKFTLSANMALLLLDNYIEANRYAVYFINGVVVDGG
GIIVKGNTLSTKKDDDSVESSVCVNGVDVKNGGYFDVENNTMSSVNGVIFFWDTTVSSAG
LLRVADCTFGGSEVFDSALLHLSGSVTLEGGAQWRVEGNSVGEASVLTIPYPQYKIQLSG
SGTTVALAHNRQVDNSYPFADLSPPDTIVELPARFVVGCNLQGDEEVSYDGVFPEEVEVF
RCGTCNDDAACYMPGTELVDRGSCSCSCKDGWHGASCLPFEVPDTVVPPAAERAVDGDTS
CVVDQTLTDLALNMWKTHHCYVGVTFSGVGAVLTFSLNSMPLHLPINITLTGCTFRSGAA
LQFVGGAAAVESSGVLIRVSRTVMRSSTVAFIRALPQHCDIAVTEVDAAQFSSSELPDTR
MNTLSVLLLKDAVLSASSLLVSNVRAHAMKRDALGFYSTGTLTLVGGSSLYARYCSFEGY
THMFYLYGLSVRNHSVFALLNNTVFSGVSLLYQHNRFNVSDHSVVRVVGNSGSVRYAIFN
DDIWTVQRSSWLDWRDNDVEVGAMFYDSSSAFVRIDGSSVVTLTGCKMGSTGLSVSLLSR
ADAGYRFVAGCLTVAGREASTAAELELSGITNVTTVTACGECTKEGDCFAPLTTAVIDCR
CQCAAGGHGDVCVPAPVPAGPPPPPPPSSPPPPPPPPVGECISDMVYPEVTQAVGGGLSW
LCYRNVTFNGGGMSMTVLIGGMTGDVVKVTFDGCTWRGGAVLLLLGNAYAAVGSLNIVVT
GNRFIDALLSPEGVFPPHTNITISGNSFTVTRLFHWLGLDLRRPSCVVMNGLAISNDSAV
VLSGNVFQSVTTSSSVVKFVGSALRVSWHSVLAVLGNTFHMGGGDSTLINIEGSGQFSSL
KVLNNSAVVIRGNVVTRPVKYFLLVILALRVESQSAVVFQGNDMQRSSAVFFSSYSSYIY
YNSWLQLSGNLCRESPSAAFLFLNPTVNLRDSTVSVSWTTGPPASSGNFSPWRVACATPT
CTALVLRRGRCRDRAAAAVLNAGTGATACRCTCRTWTGATARLACRR*
>TCRU_4692 hypothetical protein, conserved
MASGVLGANRLRVPSVCDKVGISLPSRMVSFIIAAEASTNDDASGIVGGNPESHSGAAAA
GSVSGGAGGAGGSGGGGVTSGGSGNSAGGSDGNRITSEDPTGGGGGSLQSPPSVDSHSPS
IPNEVDESQNTEISLSTEKIFPEAAAGSGTTASPGDTPPKVETPDKLEPKEEEKELSLTQ
AAAPISVNGKASTGEQNQHNDVGKVDHSSNQTPPPVPPSAVTSPGLSPPSAVTSPGLSQE
LAPPGKEPSPSDVSLPAPNVPQNTKGQEQKTSVLTAKMESKAPEIPSEDNVVQQQDQNTT
TRELMETSSGGSEADTTTSSMYTSGTGEAQSTADADDAQRPNPSESQDNIEGTDINNSPT

ADEAAPQSAITLTIAQKNDTTTTGDSDGSTAASHTTSPLLLLLLVACAAAAAVVAA*
>TCRU_4693 Leishmanolysin, putative
MAVPSLAPCTLPAVLFHGDLATRIAAHLVAHAFGFTHPHMASHGTVRNVAGVRGRALLVV
VHSTTAAMTAREHYNCDDIDGMELQDGDGEGMTLESHWWPRHARDEWKAPIGCAVYCTEL
TLAASADLGCMRVKWEMAEPMRW*
>TCRU_4694 hypothetical protein, conserved
MDRPLTPYELDVAIRDSSLGSAPGPDNMLNEFLHRLGPVAHGTLRTMIYNSFANGILPGS
WNTVDNIRISKPEKDPCRPESHRPIKSLSVLLKLTEGMIHRRLSALLPHHPRQFWICTFA
FYIGRGDTCHR*
>TCRU_4695 hypothetical protein, conserved
MEMDDGILRLANTLPRRKKATFALRKADWPAFASLRETLLATASTWLDIRRGILRAAERH
TQRGSRDSSKKIWKHEMLQAEAAAEAAHEAHTLPFLEKCYILPNVPEKKGGTESSLTPLL
RYASGSPREKTWSLTQPELARSSRRGGAASSSPGIGCAPH*
>TCRU_4696 hypothetical protein
MPSLPPDEDANFESIRRGIVFSLEVLLAKCSIIPSASGLESSGFTGFETLPAHDFSMELS
ALDVASMTSSFSCTRRETNAMSEACSPFGSKVSPSEKRPNGAAKTSPSQSGIWQDICLNL
GQRDGRK*
>TCRU_4697 glucosidase II beta subunit-like protein, putative
MRWIFLLLAVLSVLKPTDATPDPLEHAMGLNYKIAFSQKPPPRGLSKGQYYSMRLRNGSF
FVCLLPEVLLERRSSAALFEANSEVPVKLIERIHERFKKVCINLLEGWWTYRLCWNDAIV
QVHLPTVILSDGVLLTTEPQGPQTQFLLGTSPSKDDLNFRYGVDALGNRYIFTKYPNGEV
CDLTNAPRETEVRLYCARDNEEEKMTLREVEVCRYVVSLTSRHACIQELQQEVTQRTITC
HELV*
>TCRU_4698 hypothetical protein, conserved
MTQRREEKGRYRGRTRGSAKGAGRYRWKLALLASVCLCLVVYLLQGEDDAIASVILANDT
QDLLSALRLAREKTSVNSIHTVTDCMMRVGLTLDGMLATADDKSTATATQKIMTHTVETY
RLATAFVLEILSPLLQEKPRDVVLQNYRAEPKFLWRWIAVAAYALTTVLPEYFLALDDTE
THGEVLVMGLHVLLHASNAASSSYFSPLLPTERAALVDCIHYEKNPRWEKLCSSGFSNLH
GLEVRRAAILEELIALYPEYAPLRLHYVVALSLGRHAAKTEVVFELIERERARLHTRTHV
DPLHGAFLGLCKAFVSSVEKTRRVEATEGVVEGLRQINTCARLLRPFHEDRGNWRRYFRG
QERPDVMDKRQARRLLDAMRELLQEKGILESLPPGLRACGEGD*
>TCRU_4699 hypothetical protein, conserved
MYESAEDELLAIKGELWMCADSEKPYKVGAGRGSKNYVCIEEDRFYVYSTRSSQSRLIKE
VAFRSMKRVAWFTHNPKPPVSGGHYGVSPPHPPPRRGHGVAAPQTQQYYYMVLEFIRDYT
VEESENLAKRERVVLCTENAQDFQIWQQFVESYKCTREPPTAELLQGRSRKKATAAAEYD
HDETTTEEEKDRVAELMNALRLWKHRALQLLNETSQAVDSPTSSGTSGSFGVDHVDANTW
KTRVDALLGKMKKHVERDPVGSDISHSGKESARLVELWNDVYERHVPNSSPRVYDGDNHR
VEEQQRRRVQHIEDILSKSKLPFTVLPVPQKVTNACHVDGLEKTCLAIVSHYESTKGPIE
KSVIREVDDSDDMTLPDKIRHVYETLRQGEENVSQKEDAEDMLAELRAARRALDDSSSTP
QAAIHHVRQGKTIERVAKEALLCFTETAVELFQVCYEEYASIRDHILSAMRGSNVGGDKI
AITSEHFEVVKALEEERRAAKTKQEALEKIMEELEYVRRDRDMEIGMLEQNFSRAKDGWV
NDLSVLQTKLTALQSSMTRTAVVLPDEKATLVSPRQALYGDAKETPDFAPEKNTEDTDDS
IRRWATQLVCNGEKLPGSIVATRLQRFFFWALKSVVPLCAGRDTNCILELVIWAMQNHLA
LLQTAARVFGSQAIGAESDERTDLCTSLQALYDNHVQLEQIIEHYAGVACPSNVKGNADF
TEVSNRLRTLKDNEANLQNIHTILETTNENVEEYILQLISSHKQLQTIRKIAGEPSDIVQ
GIIHQQQLIQQLQNALRQLLDNEKHMHFSTEELLNQIPSLYGVQKELQHTKHLLQQTAQL
VDTMATQLTVQQEELEERIEHTHEYYQQHPIRIQTWSVITETAIAELIECSPNAITKKIR
EILEELKLCKSILGEEKVNTQSLKKDHKLTRAQCLHGIESALAALGVEESEEPAAAAIMR
AAEEARAREEELHDRLDESAARGRALESKLSELTRVADSLQRALDGSVLAVEDEEDASAA
GDRAVEALKRLCEDSVTVSAVMGGAMQRKLEDAEAEPLLLQCRKMASDMEALRRSEQRYR
ALVGDDDAGDRCADREDPSTRAQCLHGIESALAALGVEESEEPAAAAIMRAAEEARAREE
ELHDRLDESAARGRALESKLSELTRVADSLQRALDGSVLAVEDEEDASAAGDRAVEALKR
LCEDSVTVSAVMGGAMQWKLEDAEAEPLLQQCRKMAGDMEALRRSEQRYRALVGDDDAGD
RCADREDPSTRAQCLHGIESALAALGVEESEEPAAAAIMRAAEEARAREEELHDRLDESA

ARGRALESKLSELTRVADSLQRALDGSVLAVEDEEDASAAGDRAVEALKRLCEDSVTVSA
VMGGAMQRKLEDAEAEPLLQQCRKMASDMEALRRSEQRYRALVGDDDAGDRCADREDPST
RAQCLHGIESALAALGVEESEEPAAAAIMRAAEEARARRGRALESKLSELTRVADSLQRA
LDGSVLAVEDEEDASAAGDRAVEALKRLCEDSVAVSAVMGGAMQRKLEDAEAEPLLLQCR
KMASDMEVLRRSERCSVVNLFNQRALFLGSLLVSEELDDRISLLSELSFFPSNLLKILVS
YFTSVSGICALLRCDAGSIVHQVEELLESRDYYCRLVGGGDFILETDDDDVTRAECVHVI
RRAVSRLAPAILDDATLRLPEKLQGAVQGIIRDISHIRASLEEALDSAGRAEKDLETIVS
ASERALLMLRGVDSSSEAVDGVVVARPSVSFLSRSLLSQAGEITGRLRDLSDVCVECNAI
VGQALKRECEQLQVGAEGSLSSTAPIEPDFLFLVDHCRELVAEVFTLREQRRSSLAAIER
NVGDHEVLLGAVRGSVNALLFALDNAASVASQGEEDGDSSESVANLCDRLGSCTRAVTRL
LREKEHAASASVKLLQEALLPEEDRRSSDNDGLFSLASDVVRALEARRVELDSMGKALEQ
SRHFAKEYRRRMEKNFAEQDAAMTAQVQTHAAMEGQLKEATERQVQATANAAKLLRDLSE
FAGSVAAITLYDGDVKVDDGERSEDARVAHKKDVVTYEVSRERLEGILENCSTVMRTLEA
AKAKAKSLSSEADDLRGRLRESENTSRELEYQSRHAETKAAARVAAMTEEMNFLRNALQA
KVTECERIQQQVQDTERRVDRLQAEMADNTKTFGNERDTLSKVHSLLLLENEEMRRQLEE
LRMEQKELQNFLRGCQVTSLDDAAKKMVAFAGDVLLNSLALEEAENRVQLLQNWALSYGV
HTAPLLGICARVANAISASEFEDIPMRVAEMLKREQEFGRLLGVPARTVGPTRAALLKMV
TDWAEKIGVEQQPDAGTFLTELDFALSDLHSGYASLKNKIAAIQNELYQSLSTLETGGKQ
AEQITALLRSAHPTEELTVTTATAGEMSPSAILQVALASLRLEVEWAVEKIVSNTEQTRR
TLEVLEPVCSGRSVLEVCLHAAEELQERRSTEEVLRAELANVQAKAESYRGCIEASMRCL
PDSLIHVKAGDDLQRRCASASAELRRRMEVLSSAQRIIALAGHDNRSGDLCMNVDDMLRK
LRQLKEREKMLEANYESVQQRALKLEKTLRATEERLEETITFQAEKERNAIMQEKEKQNL
LQAQLSESIHEREKLRTTLAACASAVGCSPEGGSGGNDAANNHNNKNGDDKEVADVLRAI
RALASAHDASVNELEELREQHALSRKALASANDIRALAQEEQCRLMEEVERLRAEIIAVT
ASNEEHRAALLHLTEQAEGVVLRLSTAHSPSLFWASSTLTKRAPLVAQCLLDACNVFEEN
RCALEDELSTLKRIHEESQHEMKAVNEVLCEALELTGETNPSDTTQLGAIVKEKLSKALK
EKNAIAVVTGALQSENATLKASCTSTEAKLEETTTALEQVDTQKRALQEELRAFAAFAEN
VAETVGEPLPSGSTDLERLKVAFAAKQASLQHHAEELTRVREELDVATSSSAVMRTTIDE
NAAERERLTEQLLGAEQEREALLKASEQLVERVQSILDDHVEVQRELTFAEGDDDVTVVD
IVQACVEQLDKNRIGVETSNEQLAALQRENAMLMKEIQRLQNSAAVKSGEVTELHEQLRI
LLESRQVAQADQSKLQAEHDSLSRQVQALFTDALRMAADEMGLQLPMFTDTTASGALQGL
RSLFDYIAEKFRSGTLRSDDTEDKIESLKQLLQLQERQNAKENKILYRTFCDHVVVYTGT
NYSRREDGDEDSSNGKPHRLTTDFLVAVGETLHSVHTEFRHAGRLFRRLIGGPAELSSSL
RGMTLPESAAWLGEAANETVERSELLHNAIRAVSQIVEILPIDLASSQEQVTEWVESFSL
WLERAQRGIDSFDRLLEALTSVVHSHGGTVEETLSTNTTITSFNNYNNNSSSNHHHHLDI
VDTSLQDLNNSRTDISFSRYITDPHHRAVFNAVRDLLSQLEGRGRVLTSEWQALMDQNNR
LIHERRQTEEEQARVEDHVQELRRVVQRKIEEDRRVEQSLKELDRHLDMQAKELAMKYRS
DHDIIVRQFTELRGTIRRTIKPPRSHSTAATTFGSASHRTL*
>TCRU_4700 AP-3 complex subunit beta
MSRAIIAEKATLASERAKEFITGGGGNIVSRARSLISGDAQFFSVQPKLEDLRHHLDSDS
LQEKRSAMKRIIAQMCKGNDMSNLFADVVKNIHTSSIELRKLIYLYITHYAEDRPNEALL
SISAFQKDLMDPSMHVRSLALRMLSTIRIPAIQPLVLLAVTKSASDSEPLVRKTAAISLA
QMHAISTNDEDIETVHKLLGQLLADKCPEVTSAAALSFIEICPDKMSLIHAVYRDFCRSL
LDCDEWGQVVLLHVLLRYARTQFMDPNISSKPCLTKHTRKEKKKESLKKQTVDTKRSSTT
SSSSSSSSSLSLTSCTESSSDALSQGNGHGSQKSIDFLLDADHRLLIDSVKPLFMSLNSA
VVVAATSLFYHCAPSVELDVCVRPLLRLLGGPEEQHAIVLSAIYTVVLSRPEPFVPYIKE
FYLLPHDVSDVRELKLRIISKLATKDNFMELFREFRVYVRSFHLDNVVDAVRGLGLIAGR
LPKCAPQVMRLLVPLISHHNAEVVSECISVLRLLVIQGGDKTRTSQLVYRLLQQVVKDEI
TVESAKASILWLVGENIQRHVAIATAAPECFRVFAKRFSQEGLDVKKQVLMLGCKIWLFL
DGSSSMADRFCKLFFYVLELARFDEDYEVRDCGRFIQCAVNRQSDTFAALKHVLLSEKPL
PQSNDPYVERTHYQLGTMSHLFGNSLFGYRKLPPWSEVPTDPMLRGPQAAGYDDDDDDDG
SSRDFDSDASSTLYSSYSETSSPADGESSRDSLQSASSAESCSEKDEEEEWGENTQRSSS
SSSSSPASSVTSGADVAVAAATTVKCDSTKRVSCHVDPVTISVTGEKTMGVCAHCSATPT
GTDGLKQDEGTSTADVLQVTPPRDTAGAVSTEADASHPSPRPEPSMKELRGGEHEEKMSA

DEI*
>TCRU_4701 hypothetical protein, conserved
MQANAVEQVAMWLCENRCPTTLVELYHEWKTVHNEVHARFLELAAACTSFDNLPGGAEDD
TGAALEGAVADMLVAYGKQRGKAALWRTVKKARKQLSSLDTASVGNDEGDLHLLLSPLAP
VATTVGEEKQTLLTETPRHGISVISSHGGSGGGDGMGAPFHPQLQHLEEKLEQTIAVLSK
GLPTLVSAVDPMRKDVLIPIIGLTATLHSTKANKAASRLQLLTLYTRPNREHRAAVAEAW
AVTLRNVPSSVLEYDIVPELYNLANARSTEKHILALDCVICLAPLLGVGYHALRKSICQG
LLRPLSEDEARTVRWHVVRSIAELWPIRSSDMEEKNTSHDTATDSLLCYAELILRLGLYD
SSGTVRRFALQSLRKHLLLPACTPCPVVLTRILPLFLSFLERESAVMGCDETPIRKGSNA
RVSTNVDVVEENVARNTLILARLIEDAIGNALRGTAGGNGGVETFVLNAYLHVVMPSAYA
MVLVSQEQDTLQASICAVASALALLVTALRMDQWVRVRNSLEMFIAERRVRDHGDSDVRR
SAGWRERQLCFLFAFLTSVSGGKETAEKTPQAEFSSIMKDASTWLRELLLLEATEDGRHE
AHEQTRGKRGEAGEFIHAEEAKCDGAKRSEASARLDACANCLLWFATHVDDEGGNAAVVS
SVLWSFAKSHEERQRMLAVALVERMSGLPKNDRARETSIWPPLLLLMSDTVYAVKEAAVK
AALSMVKCLSTPAAHEKVMTAVFTTVETEGCASRLGVAFLRHWCSLMHVMPAEPRESFLY
PQLVTMIGQLTDTIRRMEGKAATVTALGRRGSQPPPTEENKLIEDALESVLAVLAAIPRC
AVVTPQLVNKYLIPSIRLLVSLKSLPASSRSQLLSITKEYTVLLESSKGLRGTPSVFDRM
RSGWKRQF*
>TCRU_4702 hypothetical protein, conserved
MTDAPRTRVLTKEEMERSAVRLSTSRRPEVKLPPLVQQKTRTKEEVEHSIKHLYDDSLAH
RQQRLREIEESVNAEISKFHASKKKLDDGEKESLVHRLYDESVQRKQQNLQGLYERELSH
LASTRRTLGKKEQATVVARLYNEGMENNRKKHIALFERFVLDRQPKTVYRSEEEVLAACE
KLSKGEGVMSA*
>TCRU_4703 hypothetical protein, conserved
MTRHAQVTAAHQMVVLQPKTQPTSQDSSHRRAATRRFAPWRSTNAAGESEHELDAELSCG
LSCGVSCLHPENVERSPRQPSSALFFSPIGRRTALQRRHFVTGGVASKTASAVFCSRRTL
HELGVSVSEENVMAAGDFVSLLDEVVVPAKYAVRLHDVEGRMLVVHGDASVEASPIAPYL
DRSSVNDGKYFYMKPLLERPALFSSSHLWHTGTSDGAGVAVPRWRQYTVAVALYIALADA
GYCDRALPFLSIQWINWRRLLRHQMHLRLDLMKNDVTRELLQPCYKHLHHSRDIKEEEEE
ERKVPVALHLPLSTKGVLHRPCGAKGELPSLSTQPFTDAEVFQLFYLQLVFRAVYDIRFP
GMMAEAEGNPLRSDLVGADNSGVQPLAFEHPTLPDHWLLFPPRSRVLHLVSLEEAIIPHY
ASPQTILDTTRQRLFGATPLLPCQGQLGREVVMKWAVHRVVQSPQEAFIALEELFKFFED
PYGIKQQFIWQASVAPRTYRCGMASLTRLHENNVELSKFFYLLKNFDGAVPRGILPLPAE
KTQVNTGIKEDGIVQLWRQYLQEGSIALFDGNTDAIEIIRFLGSGGSSLVYEGRLGPQSL
PVAVKCLILPNGMDHETYVKESLTNVAFFVLFNQMERCGILGGTHIYEFVVSDTPPKGMP
EEDVLTCSRGAHVNSCTKLCYVVTQLMDGVIGRFVTEEEDAFDPCYDTIVNTPLCDGEVF
QFLYTQLVARALFDYIILDFMLHGQLRGDNVGYAFVSRDEGGTPGRPSYDGIIMMFQTPK
DASPRYLRFPAGISDSSELRPLRFIRFIDLGQGKQPTTERLSQRGLIGETVVDSCITDDG
LGRYWPLDRIYSKYIDTIGTLARTAVEWGANLCVDSPQAAEAALEELFELYAPMYGVATP
KSEELARHAVFEWTPLTVRELRRQSVYRCKDDDSN*
>TCRU_4704 hypothetical protein, conserved
MLEASRVRLLNRQTQKYMTKLRYRFRRPQVLPLRQTAEQRRNTILEILRKRRISSGDHSP
YHYVEQRLYSKSSRLDREGVNLNKTYALQGLGDMEPLRNSANFGLSEKDALKYESWGERA
KYTSPPLPFTPLAARKLASGAFWPSAPEPTGMMSKEVRFLRHASNMSPSARAFCERVAYH
LRRSLKACPAHIGERIDFAQLVIQEVLGSRRSKEIYIVWSTVDPGARFELEPLLHQLNHW
VQRLVISRVKSRPHIPRVSWIYDGGRLEREMPRELMNEMKNFVGEASTTLETRVKYLKEL
DTMNQRMKNIPWFMPYLWNKEEKATRRKLMEADLAEVERRQRNENIVHRSSPPQTSPPPQ
FIR*
>TCRU_4705 Glutathione S-transferase, C-terminal domain containing
protein, putative
MAYRVLGSPYALVLHQHVTYLRLRRQPFKVYCRTLTTTLFYALLFRARNAFCTVAPDGKS
HLQMWQLVDAVERSGIQGVEDPFLVKKRTHPNIHLATWSIFVYASWWLAKTGAMYRWVDG
ESIEVVEGYFRYFLLIPGIGVPRAIVRQFRQAMQRLTSVTGVSKETAPYMHEHFQRLCGA
LEEHFQQHSGTMFLLGTPHPTLADVSMGAAFSANFLMDDPPASFVVQKFPHLNRYLERVT

GWRGGFFVGAEHTEEMNEWVSKASGGYADVIPESLSTFFQLIEEVMPFMLSQCAAFHAFM
AGDGVRQLKREPLEGPWKGCSGYLVPQVTEIKSLMIIDNGVYTVRARAQDLEVALLAARE
VVDDDFNTDDEGLGEVAEASIQKMTSASSNLTHETLRPEAGSKTRAVVSSDTSVDNNVAA
EMDAGDSLAEDADFHRVFTKSNYRQRGVLPMRRGTSNLSSIAVDSRLDALRTMLYKMHHP
HYTLSSVFHGRKMFVAIIPEYEVDRKRKETKGGVV*
>TCRU_4706 COG (conserved oligomeric Golgi) complex component, COG2/
Domain of unknown function (DUF3510), putative
MSTLVEMEHGGVDDGDREDAVNEASVDLEQLQLIQLCFGEHEFGVALDKDVTDERDEKHD
GVGSDLLRQRNKTHQNGVVIAFDFDPIQFVQEKLDHGVPLRSLCRDLEAYATLLDRSILR
HVNMDVHDAFVKVSGHLVGMQDELRCVRQSVLAAVKRVEDAMEKLSRLEETVSGQIRDAT
EVELTRLFDVVFLKILLMFDLLCGRVEALPSCLRCSEMVNKQQAAPPPPQQQQQQQQMKH
MESSSSTVVVMAVGNPHVFEAIFDIAVTVQQWKALYQTLPKLPQRAKEYEEASEILREGT
KLSHQVFAKVYIAFHQAYLQAPREELKQALRDVMGLYRTSGEFQEFCRMYRERILRPLLE
SVLSWRAATQARYNLEETISLLTTLRDQLETKVLCFLPIIWEAFEETVLPIPMIIWPTLC
EALVKKMVALYDIGVADAFQRRYVAAHELLALMMSNCNSSEELRVLMRSPDVALWKHKWN
TDVYGTIRANELSKKIEDAIQIFRATPVEKLAQKSLNQSEEHVTGGARFRMELFTKLKEA
LDWLFSPETYIYILTPKFIREAAVATRRVVQSFLEHTEGAQNGTLMQDWLHFVMGACADL
DVLVAYFEGPFCARLEKESRTPFPVSSPLIQLLTQDTCRGAVLSLQLLVRSRVAEECVVG
LQNIRSVRSAYSHMHKPFPTAPSWYVPSIVEPLQRLDASVRSLMPLETHHVVMTELVKDV
ASRFRALAKETLVTAKKTEQSWEKLRRRKETTSGGRGPDAEAPSGSGHPSSSSAAVRPTQ
ETASDRDKMTLQLYLDAKAFVNEVEKTLGPAVKTEELDAVDALFKLLRRANWIMGEDIPE
PPDIDESDP*
>TCRU_4707 hypothetical protein, conserved
MLRLSFVHRKSRHQNVLRRGRPHMQKYRELNRWQRQAQGISKWDQSQSHRPLPYVERFNP
EGVGVTRGTSAFAWQWWHTQQPWLPNVAPPNHTGRKITNTSGTTEETAKPPAWDEEFTSV
VLSMTDSEIREYLLDKLTDVLFAETQRDGYELRRLDFEGNPLTELPERRIIESFVFEEET
LRERVIYQVVEGVFRLSPTSADRRELRSVETIIDYVLTHVSAARPDSRPRVTPAALAVMQ
QCPLQPELGFVHALPVDSRDEILQEWERMHHLDWQFGKAVYVPRSREETRGNLTWLREER
HNAERVEFMKRVASGEAKAEHMRRIAEAACTERPETMHG*
>TCRU_4708 eukaryotic translation initation factor 4 gamma, putative
MLFKPRGVTSNDPKYAGNSRIMTIPDLLAYRDTWKERLSDDFSLGRILFAARAAKSKPAA
PEKLVMTSNGFKVKDRDAIAPSERGVRMVQSTLNKLTESNFDLIAKAILVPEIILNANVV
ADVVRLIYDKALVEPVFAGLYARLCYMIVRYEYDYRSTQSGEVDAQKSEVRVAIVEKCQQ
MFDGATKAVRETASEEEAEKVRKRNVNNIKFAGELFLKSLITQKIIDRILGEKLFNITPN
DMDLEVVVNLLEVVGKMYEEKHPAAQPALWKLLGELQEERRFSNRIRFLLQNLIERRNGG
WKPREPEQVIVEDPQQQQQQQQQQQQQQQQHQQQRYHFHHHHHQQQQHQQHHQQHHQQQ
QRNSDQLQTPIGKRAKSYQDVSNPYGVGARRSTSHLDLPGYGAYAMPPPPPPPPTLQYA
GVEEQLSVDERKLIVLARPPETLTEEVRRNIFRIARDAVEDGLPNRDWITNDLSRVLGPN
ESSSQSLMTSVYVILLRALMDPKESERTLFCTALESGNWERSILGRGFAWCLTKIIAERD
VADCPRIYSRFVDVVTRVTELNFLCVTKDIIARTARYLDVLQVVYDETEEWEEDFIHVWD
KLLVARQAPNKVTAAESMESMSFTRLGSFLRGILPDFVASMVQAGFFTEDELRQWRQENE
SNPKFRAITEELAQLYP*
>TCRU_4709 hypothetical protein, conserved
MVDHRVAHLLLNLTDCAPVDGECVHSPESVAWSPHNVLLVATHWALYLHIRGLVASDFVL
RPAYQPRGDTSSMMCITGAKWALDLVPEKAYPATCRLCVRTTRDIYIYRVIRSGKGRIRV
SCGICFIPKVASEEGLDSVAGAERKGRKRARSSFGNIAVPDAENGGKGHLRLSDGPGWCV
VSYAWFPLDLLVVVTVGGIYLLNLFDDVSDETELQLRLFPSPAFCFTGSPLASLVASCAT
RVLGCDRNDYRLVVASPCWLRIFTVSTTYVHLTHYVEVPSLYGVPTALCSMMSDASKSTM
RVFVSAPMCILEGNLVVGPSNNVVGEAQQVNWTAVGSWNSEGELGDEVSVRHFLVVPLSS
FVPTEASTTLTKRKSTTGESAMDGRDAHYLVLGVCQRRLLGFVGRRCVELLHCLRMDGSE
FPRDVALEVLGAAIHPSCTLAVIGVRIGMRQYPPFQLLPVSLNTKGGFLLRLLQLLEGFD
SLSDGNGDVATISATAPINTVLPALWNRQHSTSYFVWEDLLPGSAVASAIAHSHHEETKR
VLEFSKIEEEVKDEGGNIHATSSPFFSLYYRVLGAWRRGYLEERQKHGVELFLRFPEANA
AWRWTLLRIWRRFPGDAALMELLLANAVRRMAEEVHYAGVTRSESAALPLEAADTSYLAF

LAAVQFGRLYQQQSVKGGAWVYDGGFVEQVGKFVDTVEAQMWRKQRTLQKEREDQNTLTS
PSRFPCSICGMEEQTLLTMSLTSTTKVGRNMEGKLQDCATGFHLTVFSGSTFTPLSFVKQ
DEVLSRCLSCGTYDYVTGPLCSVCEGLMM*
>TCRU_4710 hypothetical protein, conserved
MPSKKKGGANDSEKAELLRQAELRKLAEEQERLRRLESEARQRLEEEWRRALDNERQRQM
DIHRAITERELKLAFEIREQALNEALECKDRETRELRAKLSGMQLGVDNMMQERESALRR
VAMLGNELELAQMRSVEAENQLEEKMRVSREQLWDVERLREESVNAYRELKLDYARLNRL
HEELQVQFNALQEAQNTDALAIDARLAHAHPQSTDAETALLLKVLNEEVEKYRETARLLQ
SELERKGRDDEKGSVLISLLNSQLEASRDECKRLHEVSTGRRVELEGVQSLLDAEREKTK
SLYRELDTAHAEATVERRQFTLEIGVHKAQVGELTKNLENVSAELAELKTQFDTHRARAA
EREQYDFQVNVSLKGEVEQLKKDLTKMAEELRITGDDAYTKKALLRAEIESLKVRLQKLQ
ENAEKNERESFETIAVLRATNERLKEEKETLVRTTEESTRRMRDDMIEVCAARDAFKALA
DELKAQKEEVERDLFEKLLRMTANHDRLHEELQQTVVKYAAREKEYVENAIFLNAEKETL
KTKVEELSEKLARRAQEHACHVQSISEELNSLKLKSETQIKAHKSARLAEEERASRAEAE
VQSLKQQEKRMERQMAMKQSEREGAERAMKGEIRVLQQELNAAKRTIERFECALGDTSYK
SLCEANERMRRDLEQQREKVAVLNETIASMKVESTIMETYKEKMLADQNEQYARRIQELE
KLRQMMNPLFFELRSIVERNGLAGALRRDLDAFDDHLRRSSATTGQEKRNIASSPSSTGK
AVVATETTGPAPSADDGYRTLPAVGDRRGTHGSDSEGYRLFQRKPVSTVPQKQHHHQQQQ
SSSTHELPTIF*
>TCRU_4711 hypothetical protein
MVAGCVAGKTYLLHVKRGDKIHASSPPLIADDGGKLHVNLSRIFTSTLQRQNDWKYKKKP
LKVRIEELRSHFVTSLSYDLSKNIVEETFPERRVIIRERDGLTEVHLRLRGVKESLYIRQ
QDVQTASNASSSSYMREPSTASLFGPHDPSEEHINHSTTSFVVDDYLSVIDSLTGTASEQ
RSEDIHSETKETQVDKELNKRNFDKCAPAPDTSLHPLVAPMHRRTGGVSNTISKENFKNL
AFARGSDAAILKGKDLSTLKPSWKRNIAFEDPVHGVIRQICDAVRWCGDIGRESQTARDA
SNGAQLALDFYLNQDGETLGRFVVSFLAHVVVEVCRETRHIGNWLILLTHVIYGSILYTR
HQFNPCDVKGMSIRIADLRDLDVDTFTTRGEAIIQDLARDLSVPVATDMFWFAGLDYCAS
TLALLCIHQIQGLCDNFVTLFPFSGRGCISMEEGLVAATAILCSHLHSLLTTLLSQTEQK
ELADIRNAPPLYRIILGEIITMVFDCVVTVIIEYMHKIDCLPDGSAFHIAFKALKLLISW
AKGHFLLSVVSPILMSLVVYCDFVLLPQGLLKNHEYRLYLERFLPSFVDANNSNGKKSRT
MISPCLSSNTSDTVAFSFYSILVEFTERGCRGTPKAERGSWTLVEVLNGDKDDAARVLSA
EEVFPATGFNGTRHSLSDPILVLPLLAQEIKSSFK*
>TCRU_4712 ribosomal P protein AGP2beta-1, putative
MTLQTRRDKYDTSQLTLSSLVALCADCSSFCLERTARVLDNQSRAPKGWENQFAAVAKQR
RQEDCELCERYCHRVSSVCPASKDIELFEALGYKEVARRTSLDGLPTVQQMSRCENAVSE
FSRVLFSLAHKPSKVAFEDVDPKSGLKKSEEGGDGEPTELHKKVLSGGSIDDAILQRWST
ARKGRAEMEEMGVLRSAEETASLRQELGRQRSEEYIKTRGTTPKW*
>TCRU_4713 60S acidic ribosomal protein P2, putative
MKYLAAYALVGLSGGTPSKSAVEAVLKAAGVPVDPSRVDALFAEFAGKDFDTVCTEGKSK
LVGGVTRPNAATASAPTAAAAASSGAAAPAAAAEEEEDDDMGFGLFD*
>TCRU_4714 damage-specific DNA binding protein, putative
MTTIRELSESPFDKSKVTLSLVYVSERNTFVQVTSVGVNFVKGGKGAYIICKNEFGIQHA
SADANLRLLVFSSSRFVSVVDLNTHHTRASLGLDNEVSCLLISSSRGFVIGEWNSGAVCL
YEVQDGEILLKGRIFCSATSCSMCILSHLHTPRLVVGLLNGYIADISLEAVLMGSAAQET
LIRLQPVQLFNLESHNAVLCLGEVPLIIILCDTGFQLTGIDFNDVAACAIIEGSHISSKY
IFLSQSENSLAFGNIVDLKKLNSCFLGLKATVTRVKYIAWWNVFVISVRRSEKDQILLLM
GHELANSWVPQNELFSIELLEKERCVFFETVFLGGSNESPNGNEADKEKAILLGTTFAFP
DEQLPRSSRFIWYSVEQGKLISERPQLRQIGSKDVEGALQCCCIVPNYVGRIALGINGCI
ALYSWNAADSVFVAEETICIGTIVTRVLPIFQGDASYMVAFDARHSCFFIQVDTFQGSLE
IVARDSEPRGVMDGAVFQLGNIYNICFGDDYYNFFSLSRGASTLPSASNATSATVSSGKL
ETSAQYHLGDMVTAMQLGSFAPCSVTNIAVPIPTTLIPGICGPQVVFGISHGAFGTITPV
SNETYLLLKALEVAVSSVVPALGGFEHVTYREVLRAGQERGYSRNASFENANVVSSGVFD
KRRKRYLSRCVCSGDLIESFLTFSQTIQQRILREAESRIKSCYFSMNSTLGEFFEHNDLD
NSFAERSDACLDECKTIGDVNALFSESGLPTLPLTREAVNEFLQNMQRIH*

>TCRU_4715 hypothetical protein, conserved
MTLHLVAVLGLVAYRNSARGRCCEHDGDQDDFTPREVPSHARCGEGRRSARRLLVRTARP
FRSGHSVDVTRGGDVHKNPGTEEDGFITVWQLNIAGLSSVKNIAFAARLEQRPPEIVLLQ
EINNRGGVATRLCGHNDYLRASLGAVVVLPFWCATLYRASACRSLAQTSWRPLLSVYFRR
AVPAFACRISTTLPQQLFNNPHLLISFAAWARRDYRG*
>TCRU_4716 Reverse transcriptase (RNA-dependent DNA polymerase), putative
MEYARPGGGAPTRHPRHHRSLVALIDFSTVFDTIDHGKLSGMLDGLPRLGQRTKQRLHNY
LRGRYVRVCTREQHSRKQLTSAGVLQGGVPGPQLFLHSVDDLLRRMGSIYSASALMHADD
LTLVASGAGNHAFAAAMQPALPLITT*
>TCRU_4717 hypothetical protein, conserved
MGSVPFRGAGLWLRIISPQQGVAASTTETKTTPPLEKVPRHARCGEVRRSACRLSVRTAR
PFRSGHSVDITRGGDVHKNPGTEEDGCITVWRLNIAGLSSVKTIAFAARLEQHQTNIVLF
QEISNRSDVATKVSGCNGFLQACTGRGGGVATLVRHSLPCERLSLPGTDLLETIAVRVFP
PGRPSICVANLYNPPMETVQ*
>TCRU_4718 hypothetical protein, conserved
MGSVPFRGAGLWLRIISPQQGVAASTTETKTTPPLEKVPRHARCGEVRRSACRLSVRTAR
PFRSGHSVDITRGGDVHKNPGTEEDGCITVWRLNIAGLSSVKTIAFAARLEQHQTNIVLF
QEISNRSDVATKVSGCNGFLQACTGRGGGVATLVRHSLPCERLSLPGTDLLETIAVRVFP
PGRPSICVANLYNPPMETVQ*
>TCRU_4719 hypothetical protein, conserved
MARHEDEDTSNDFWWSHRRLSEEEATLTGFSMAAIDISASIDTIRAKARKMLEAVATKNG
SDTIEGSVAEIDEARMAPWHEELAVLRDQLLDALLASQQGRQARTQDEAVRGGGTVVEPD
TSSLRRTSHEMLLHAVFGEWAALCASNKDAHGGLVSESLLDIFLDGIVYTHAAKWSGEEA
DEAAGGTMRDVVWMFVRDTWGMTPIEQEKLLPRLVQHAWEAFIAEMQRLEEEVLRVCTAL
VKSPNAEVAAHERRGEARTLVTNAVRVLRMLASPSAPAEAASMRDTSHAHVLVATSAKAR
RVVQMIGRWLPVCCEFLHALAPRQDNSRKEENEIGKCPAGNNKECSDTPATPEAVEWIRQ
LKGQVERVLRLLAQSDETSPWILILVDIIARVFYVTSKDALQTNGDADAEVRQHIALKSF
LTSYEKSDDVPPAAALTGHWTLAEACNMKISHVLSCALDKTGFPSSLSTRVLRVLLVQRP
IATLRHLLTFLCPGNNVAALCDCEPVITDKGSASDARSMAFMEEPLQENAVARTFFPKFF
SVFRAIEQALGSLCGDLTDHDSDADAVSLILDRFLAAAMDKVFTTGFAQEKGVAASEWLM
FLAFICHDTPLFDVNSLHHVRNAARRFFAPGRPMISYLHEQIVKHGRHGLTAFFLPPLRA
IGVDYSTSSDQEHLGCALRYPLSAEVAYFQELPRGYYCRQPLRLALNAKNDALHFFHDLL
MPPVVDVLSKNSPIVERKLKEEDQVAVRDSFVDMIVHIGIFVLARVRGDADFPPVTDTVT
ADAMSSFFFGILRLCSTVTYWDATRRHEIQRAIVKQLCAKSPAASNPTATSGNKRQNGGS
HRAGERTAPLPMAFLLRGGCTLGDGDAEAGGVSEGETELPQAWHDWFCNVELEDIDARAG
VSAMTLLRICNRGYMKVIPTRTLLERRATLEQHARKQKESGSREKVESAMEAAILRDVKR
LRGQRDGNAGRQTNPQDQPTVKEKVLAGDEMKAENGVEENGKATVVKAEKSDDNKGEKEI
PMPIPDEKPLPIAVVKPYIEAMVVTLMQRARISVVDGAAAGVALKKWLMAVSGRFEPQAL
LEVVRRVVLQANTKLTHATKLECASLSAFLGTVAEDIVLPYKLSFLPCNPTHTKQQRQQG
TAPAETKEKDNSNEWLHKVLPFSEKDAGMLLRVLIADTTRAVTRFLEHATPLGDWKAYIL
TFHMRRIMGLLARYESAYRAALARRLQQLGTTSVVMEGTHPVQLLAAVECPLLEKMTRPA
ADVDHLFTSAMPTAQETPVPLSSSTSGTQMNSTAALGGGNGGNTSRKSWSKSVDASKRKR
QRSSDNSHSHRHGRRRNGPRDQEE*
>TCRU_beta subunit, putative pyruvate dehydrogenase .1
MRRLTVSRLFSAAVTTRALTTLTVREALNKALDEEMERDNKVFILGEEVGQYQGAYKVTK
GLLDKYGTSRVIDMPITEHGFTGMAVGAAMSGMRPVCEFMTMNFAMQAIDQIVNSAAKGH
YMSGGQLLCPVVFRGPNGASAGVAAQHSQCFASWYASVPGLKVFAPYNSEDARGMIKTAI
RDENPVVVLEHELMYGESFSVSDEAMGEDFLIPWGKAKVERVGQHISMIGFSRGVELCLK
AADQLAKEGIEAEVINLRSLRPLDRRTIIESIMKTGHAMTVDESFPVCNIGAEICAVVME
SEAFDYLDAPMERVSCADCPTPYAKDLELASQPQVSDVLAVAHRVLS*
>TCRU_4721 U6 snRNA-associated Sm-like protein LSm8p
MLTHYLRRRVSVITTDGRYLVGVLHAADQLLNVVLTSCVERVFDEARENAGGSQEQQENQ
PMSSNDNSGGGMMQELPMGVMMIRGSDVVCVAAVDTVEEAKLSIKSWRGRNLPAVERVPR

AAAPAVS*
>TCRU_4722 leucine-rich repeat protein (LRRP), putative
MYTSLNRHYPDLLRTFYKKSLQGVARSVPKDKGGASRRFGGAGKMARKTEAGEEEPTVAD
RTSDVESELEEFPPYVDPTEEQEVCLDPIRALRIPRSRFHTVKELTLCRKGITRLHSNVQ
LLKNLDTLIIRHNRLRQIDFLIPPRNSRDVFSDARVYEESALVDIPHGTLRGCRFLRRLY
ASHNCLQTLDGDVPYLRYLEVLFLAHNRLSNLNAVSAQLRPLKCLRELDLRGNPLCDEEG
YRLFLIHEHPHLEVLDRRVVRDEERKEAIAYFASGAGGAGRHRGHGHHATGSVADLAEPA
TGLRLTLTEPFSAGERNEGRNDVNPTKGNKKNSGPSAMEQPLVSALSRQRMSNASGGGGG
GMRQNEKTKFLVAFLRTYTPPVVGEVVASPRQAIFQPSACERLLEEKVWRDKQLKSKRQQ
KKTQELAAEQQELREKHQAFHATWALSRRGMPLSAEKWEMLTKAVESSNNTSLPDTQPAP
QRRVSLRRRSIAVRQPSTEQTGRKTSNPVSFNLENEPVELPRLPSPTVRKSDYSVMYDAL
LGRSKNVEMRIGQNFLCLPEIRRLGRIKNILGQVTEFLRQPAEERGVNPKQFNSIREIQQ
QKDALIPEPWEHTSIEGLTTTMNSAEQLEYLYLMVMSFFLPTEFSALEGHFMTSTGEILP
VQEPPRSKKQTKKDKSRQSDSTQTLTSGSTSLLVSAAAALRQRLPAALTATNIEVGPPER
TTFVQIMNMLDDHSGIWDLDLERVSEAFREEYMSKKKSICTDGFPKDEEKSVVVSSFRRG
RRSVGKSRAKGESRGVSKSSPRCTDIRNVVSNPTPSPAIKASSLKLGNVLLDIVRYLPFV
KNRLAFFQRKCTETASKGVNGPSGEAAREWFAKTQIALMHYERLLKAMKMANLTEESALA
RLVPLESIAVQEVQEVGSFFRSPAASS*
>TCRU_4723 chaperone protein DNAj, putative
MAFRLVSSTPLLAALAPGMATGTNARLLHMTRLARQGVGRGNFFAYLGLPQTPELDAAEV
QRAYHDLQRRVHPDQANVQAREVEEGQEQSKTTLAPVLEREEMGAAGGVADVDESIYANA
SYETLRDPFLRCRYLMRLSRAEKVKGAPLTTAEEEALMHDDDRRSLEENRKLMGDAVDIA
SLGSDFLSDLMAVNETIFSTDLSKEEGVANLRLLVADLEERYEEFYAQAKEYWKQKDTRR
FYHSVLRWTYVRNVLKHAKDRLD*
>TCRU_4724 Mad2-like HORMA domain containing protein
MSQAVQTITFKGSVAMVTEFLGFAIYSILYQRGVYPQEVFEQVKRYGIPLMISTDSDLNA
YLAELLQQVAMWVTADKVRKLVMIVADGAESNVVVERWAFDILAEDTKGVIATTRTDAEL
QREIQAVMRQITASVAYLPLLPEGCVFDLLVYTEMDAELPSNTWELSDPRLIPCSSEVKL
RSFTTNFHRVNASVTYREDAA*
>TCRU_4725 hypothetical protein, conserved
MAKGKKKGPVDVFATLGSSGRIEVAGETESTDMRPAEMLDTALVITPAIPRVEVSLSIQF
RCTVPIVEGDMLQLYLPGFRGKASLFTPEFSPIQATKSLRQFRGYWSGEGAKKGKGPGKQ
LLLLKCVHRVEAQQLVAIVVPRSLRLMSPDKLAQNSSKIKISGVVKHAEGGRILKQVFVS
STEVKKRHVLEEIKDYKLLISELDKISGLEDVDAHVAEELSMEEVDHIWESTYERCPYPI
ALQWHIANSAFRDYESFGPLLKTIVEGAIHLVKRRHQLLGLYREIATNLGVKVGAVIIFQ
DVLNMLYGSLYPHIPGTVLLAVRLFTMEPIDIARTFLISEPPQFSLAQEIYSSFRTGDPE
GLKKWAFTVSTLLLIVGTHANDPEPSVDTPILPLYYAIKEVPHDELQYIREMPPNEWYLF
PFLALVRPRVNWTDEEAFPIPDNAVLFEIHNAADGLDVSDLSMYPYDREWLLPLFSSFRV
NHVKVYDDRNSLTHVVMYMHGCLHGSMKEPMIPEEDRAVTAVMVRKLRTEAEKIIYRAHQ
IAEHAYLNVTLNERLRLHPQTLLRAQYVDHYFEVKRFSQAKTTVEEGLVNWQVCTTPAQL
IDPVEGVIKHAVWEFMPRKFALLAEQYFLSKTRFKKVFEAQGILLDFAGYVCDYGGKGPR
PMRRLLRKRVTHEAPLPVFEELRS*
>TCRU_4726 Elongation factor P (EF-P) KOW-like domain containing
protein, putative
MLRRHLVSFRLGIGVGVGSNKTLSCSTSLFYAQRGVFADKARAGMIIAIDKRYYRVLANT
RSQKGQNAASFNIKLVEVGTGRKKEVTAGQGHDFAQVRAERVRLLFSGFDDDDMACFVYP
EHASDAGKEVNIPGDSLPDVQQKFLCCGMPVDILHIIPDDEDSSDAKDIWAEVVMPSSYN
YTVEKISLKGMYKMASFKECDGVVSVNDSVQINDKVKVTIKPDGTVAFGGRAS*
>TCRU_4727 hypothetical protein
MNGEFPVLVSHHKLLMLPTVGVARYDSGNAGIIGEQTHNFHVIPEIELIVVRVHGKMTEY
QHNHLLLTSVLQLHAKPLHLFLTNASINIQHIFAMTITMLHAIRFCPSGSTGPCCKHRQI
RPIEHNEKEHAALTYLKTIVTGWHPQQTINMIMVLFAQPQEIVVPQ*
>TCRU_4728 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative

MVSVRLTAQLKRVKEVLATWKEVDERVSELCPSEEDTSTENACNTGKITAGLVGFLSGNF
SNGTWRDEYLGVNATVNYKDGAEEKDNGVTFKGRGAWAEWPVGRQGDNQLYHFANHNFTL
VATVSIHDVPKEGSIPLMGATMNDSDNTVILGLSYNNNNENKWILLCGGRENKKYSSDWE
TNTSEHMVVLLRNGNQSSAYVDGQPVGGDEKCNLENTDSKGISHFLIGGDGGSAENTGGR
EGVPVTVSNVLLYNRPLTSQEIAELAKNKVTISKSEGPKTSVVDAQSSATSGSPVQGAVS
LSNSARQLPLEEETLKENIGGAGGVSSAASVTTTPSSDVAQTVATGSGDTMQGIGSPQTP
EVSVSSAEDGETAGRTDAQGEEGIHSHNGEVNATALNSSLGNLSQGNNSDAGTMCGSGLL
PSLLLLGLWGFAAL*
>TCRU_4729 hypothetical protein, conserved
MFLFQAPDSRRESTLSPENLIAVATPRAIDPFRLDSSNVQNNLSLPLVVADDSSDVKLNF
TRSFSRTDNDPAVGRQVNTPNLGCELHRQSGGLRSFGSADEASEDMWQGRGSQMHGPSAI
SRGAMGNVSGSAGECRFGPLFGDNLNGNLFEEGFFLFSSHQVQIPPFRKPVDITPLLERA
DRDLASKTTLLVPVLSSQVPGVEEEGVRSSRDSLTLESISWLNSLVDPHASRRKF*
>TCRU_4730 BNR repeat-like domain containing protein, putative
MSRRVFTSAVLLLLVVMMWICCDTGGAAAVVEGKSGDAQLLQWVDIFVPEKTQVLRKEGS
KSEVKKAFAAPSLVNAGEVMVAFAEGVFEYNVHGRGLIGIRPYEIVAGYIKAAESWPSIV
AEVNAGTWRAHTVIGSRNDVDRLRYLYRPTAVAKDNKLFLLVENDNTRYDNVNNTWVKDG
WDIQLVDGVATQSTNGVQSKLISWAEPKSLLKQIPKQTQDQLMQLFAAGGSGIVMQNDTL
VFPLTANGKNYPFSSITYSTDKATTGCSQRAFLLYDALIPASPNGRRDKFS*
>TCRU_4731 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MMMTACDDGRRRVYESVDKGASWTEALGTLSRVWGNNQKRHEKGVGSGFSTATIGNRDVM
LVTLPVYSNRKGKEKRELHLWLTDNTHIVDIGSVSGDDDAAASSLLYRSAGGGHNTNERL
IALYEKKKGDGESSLGMVSVRLTAQLKRVREVLATWKKVDERASNLCPSTAAKNPSTGNG
CSAVKITDGLVGFLSKNFSGNTWKDEYLGVNATVRKGTNGAATGHADGVTFHGAWAEWPV
GRQGENQLYHFANHNFTLVATLSVHGEPKGDTPIPLMGATMNDDKKTVILGLSHDKEGKW
QLLCGGKTTKELRSNWEPETTHQVAIVLRNGTQGSAYVDGQRVGTEECALGEAESKGISH
FYIGGDGGSAGSKEDAPVTATNVLLYNRPLDDNEIRVLNANKTSIPKLTDLKTLAAGATG
VGTARHFGANGDGSAVCGGGLLPLLLLLGLWGVAAS*
>TCRU_4732 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCYPSVCAEEGPTDKLKTRTTNNTAKAKNGTESQGSDPSGKPSNG
LGMEQGKSPVTGHSGSSGSGSGVGSGIFDGDGKSSTDNLQREGNKGTTGSQSSKKPSTEE
ENKKGEDTSETTATTTKEPTTTTTTAQATTTTTTKKAPTTTTTRAPSRLREVDGDLSSSA
WACAPLLLAVSALVYTTLG*
>TCRU_4733 hypothetical protein
MTFDVVSYTKAQQQRLEEIRRATEKERQLLALYAGKLAHGTHAVPIPPAESAQTTAASSD
GGRWLSLNDRAVELHALDEKLLLEEREVERQTFELDGRLHAAERRKAELLSQLALLQHRE
ALLKKEEELLEGVESGAQRASRDIEALSQEMNEEQRAVEARVGEKRTRLAAAKLAARDQQ
KKRDALEARSRLQLEEVQDRIRGHRMELARLGSAVNDKERWLRQEQSRLREAELAAICRL
KKDIELMAISLDDNTGHH*
>TCRU_4734 hypothetical protein
MNRARLIRMHFFTAVHLTGLAYYFSTYKLISFMCTTLVLFTCFCAIAMGLVFVAGAVIAS
HYLRGGSSTAQDGEPPSEDEEDEAEEGDLIEGKHLLSLHHSATTLLHDEDLASNLAGSRQ
ESLVHLYEANLPLAKEKKSK*
>TCRU_4735 hypothetical protein, conserved
MEEANNHFSARASNTAVADGLLAQRESALAGRERHLETTPGTKGTHRCLGSAAFSLGCGD
SPGQRGVPSSRRGPPDAPARGYEDSATTTPPHHERLIAGGVPASTIPQPIFTGERRRVNT
LASLGIVGDRVSLTP*
>TCRU_4736 hypothetical protein, conserved
MKASLEFYSKSGAHAISGTEGTLTPESPLAFLVSWMRASRLHREPSKQFMDLGGIVLRAF
RMRIVIKSDPSIPIQKLRARLRTAFHEDDTFARVAQSLMDRRGTRPQQ*
>TCRU_4737 hypothetical protein, conserved
MKTAPSIPPPPTISPQKTSHRTAVVPSDPSNRPTSLRSTKELMRQRRSTVVPRLTDIFAL

GQLHEKGERVGSRNVCPPTWKQRVSLAGQFTTFCCTHEQPINTESCAAFLMAILDVAPST
RPQHARMLRSVLRMDRTPLEMMILGLKEIAARSETKQQRQQSRAIYRRCACASSGRNSMA
PPMRTTVNENETARTLRRSCFSATK*
>TCRU_4738 hypothetical protein, conserved
MPGDTPSSWCPDTLPTNTTDARDPEETHLGAAMHAELKCLGMQVYLRVTEKGGVRCVPCA
GGAAITCVTPPYDEGNVVCRDRAEVCTISATGGNIIPVFQWDGEERVWNRTVPPASTEQG
LRGGVRPRCGEH*
>TCRU_4739 Leishmanolysin, putative
MPRWPGEHHDCNDVDGMELQDDDGDGRTLESHWWQCHARDEWMFLIGGAGRSTELTLAAS
AALVCMRVK*
>TCRU_4740 Leishmanolysin, putative
MLCCHFDVLSILWLCDACRRREFDKSCCERRDLFGAEGALQTYTIIGRDLWATIRVYVST
RDLDDARRHRGFSWSHAMNLLNENRRCEDGIPSSVHGNILAEETVPSAVQLHADRPFFRP
LECPLIAPPFAAGSVCSWFTVPAGHCSSGFADSGMVLCVAAALGGVWTLPCATLEDGRPV
AGVMNLAPQFYFMEASSPASPRT*
>TCRU_4741 signal recognition particle receptor beta subunit,
putative
MTGEVPEIRETNAESGGTARFLFFGIVTVIVALFIARFISHYVFGAIGVYSRHRHTLLLI
GLCGSGKTALFAQLVAQKCVSARTSMQPNRAVMTRRQLSSHKEEEESSFSAPSRFSNGAN
ASQVVVDFPGHRRLRDSLLSAIEEAMSVVVVVDAVTIQDDRQEGAQALAELIFSVFTSSA
FYGVQRVLVACTKRDELTSYSAKAVRKLLEAEITRFVTSRRGDLQSLDTILNSARVVVGH
KKSKFAGGGDSSRRDGLAHQLSLDESGKFTFDNFPVPVHFADVSSVVDPARHPFNVEPVW
EFVEGRM*
>TCRU_4742 dynein intermediate chain IC 138, putative
MQKSSSHAEQRKGPQSSLIRASERHSTVISRVSRSRRTKTESRHRSNEVWQELESTVHVL
DNGVDRTPLPLQRRTNANGVPRESHQGMSSISLLLPLESSSIFHSSLLNASSIDALNIAS
NTSPYSPSQTGFVTASSSLTSVSVDRRASVFSSSTFSAPGQTVQYQAGSFQFEDAFSAPK
KRVLTREERHMWFEDKTTVVLCETPTIMLYTHQDEIVPNERKEELQEVQDRNAAYAELVE
AKRVDEGTRFQEKGSWTFIAPKKSIHCSICPPKKKDAGALQVTPWLLRDQFTALLAEDTD
VMKDEEEEVDEEDGELEETGEEQEKEVPSETTGEQSSLSNNRSILSWMFADSLLPTLRVM
ERVVVQNTMEEVQLSYRGITMDPAARRVPRASEKEENPNVEEAEMAVAAEVQDPNDVAPA
VAATPLLKSELPPLRMSEDIKGLWTFRSPQTRDRSVTCMAWNCKENDILAVGYSAVRGQD
ALGVEPANTFQGGIVCCWSLKNPLAPERVIQLNTEAGVSSVAFSYEHPSLLAVGNMEGGI
LIYDIQKDSNVPAIKTTLTSGQHTGAVWEMKWVARGKERGEFLMSISGDGRVVQWAVGKT
IERVAPDLMTLKRQGGAAFEPVVADNGTNGGKRNGDMQQRRRRDALFSRQCGGMCMDVSP
ADGTVYVVGTEDGSVHKCNKSQTENYELDYAPHSELVYRVRWSPYSDEYFLTCSADWSSR
LYRLGQSTQLLKFDSPNQNAVQDIAWSYTNSTAFATVTAQGNVELWTIMDSIHPRSTVQF
LDQRRLACVLFAEQDAAVLVVGDEKGDVTLFRLLSPYYSGMNMLADEQERQLEEAIRKAI
S*
>TCRU_4743 hypothetical protein, conserved
MSTNPEEREAEPQPSPHSVPPQQQLQEEAIVEEMTGVGAADAAVEEVAFVPPPPQQQEEK
QQAEEQQLEVALQEEQRDEERGMQGIVEVEGNIDTKLGTLLAAHPKPHSRKGGSTTKEGD
AESLSTATETRLQMSKTLPPLAALSLLEKGVGSEFRAREASNRSFKMGNYDSSTGNRFYS
AGNYAPFRTVNSMTPNEEYMAFRTRNGVSSNYKGPIFAVEDLYVMCAECGAPVDPVTRVP
AGKLFFHPQCINCKLCGRTDIADAYFRAMGNGAICSECASRGFAWCVPREAAAARGIIPG
AVVGKIDEAVRLYDLKRKLQPINHPTLPGAIPPTLVLGRLFVHRGQSTRKYSLIQRQQYY
TQNDNNIICLPPEGSRAYSRASSASRHRWKKDEMPKLM*
>TCRU_4744 ubiquitin activating enzyme, putative
MNGLKYDRQLRLWSLAGQRSLAEAHVVVLGATATAAEVLKNLILPGIGFYTIVDDAPVDD
GALGNNFFLSVDDYISHRPLSEALLQHLSALNPQSNGMACVESCVSWVEDFLSTGMQARG
TVSLDQQWPPPSLILVTPRLPAFLLRRLSVCLKVQNAPPLLYVQTLGLMGLIHVQEKERL
IIHAEPKSETCVEDLRIFNPFPGLKDWFDAHDPEDDSLFGDDIELHSHIPWIAILYHALQ
RLRRERGTPRLVPRTKVEYDAVRRVVGAFIRRPHPPQEGFMEAMEKCCVILNRPSLLPSK
VQDILQDPRSDAPCLNGQLVNDHRPLYWLVLHGIKRFMEENDGVPPFCGYVPDFTTTTQW

YGELRAIYDKKLRDDCKLVYDYAMEAIGGCSYDSSASVVDANEISELTRALVQNIWTLQL
VRFGPDLDETATDAPLRWQRVCHYFDECESEEERFTVELYMALLAAHQFEEQFGRSPGQL
LHPSAEPDATWVDDSKELLRIIEEAWQGYRCDTDLTAKACMEVARFGGGEPAATACIVGA
AAAQECIKLVQHRRVPIQRPLIFDGYRCCFWLVPPPREEVEGVAPT*
>TCRU_4745 hypothetical protein, conserved
MSHRVARPLRLLQSSWSLGVEREDGHTVPTIAVYKPSGLPYFAASQVAACSSGRHLFSAS
PRDVPAVEPADVSDSLLGRMTDLLPPGSGIPRVALPLIHPALSRYATASQLNALTAQRKG
TSLIACSPHEFMFLRNCHRLHLVRSVYRVLCRLPPCVSVRVRRALRERNAAGRTTESAFK
NPYVQEFLQRSSSISGVAGSIPIVSEVDGSLPPCAYPYPLLQGGFISVKERCLLPHGTVS
GYLSGYQLPPGVQTILKKQQRLKELFLPSTVMNSFSSSSSSSRLAMDAVAEDNNAGGCT
ICRGKMTGQEDVTHPWIGPECRMRVALDVRVTPDRKAVNEINVDCSDVDRALTPHPDGNE
GAPLDQPQWGRRGSRRLVGKPFRFDFRLVTLNDACELALYEVSTNNASDEEIKAAFAAAN
FTVMNDFLNDIALAEAMQTVSQEIHTVSRAKIADLPMAAQHMLREGSPLELVAEPLLSIP
TALSPVDGAIEPQADLLKHMEQVSERSGLRGHRYRLLLETLGNLKDEKTFFHVAQLVFGS
GLECTAIHFPDPRNEANTSAVQHLLLRMEESEFSEAYCNNVAERMSFVSRGAAVDCETYN
TLLQNGSMRCLPPQREVSIAWGGGHSTIVRREECGELGCAYCGARGHVWSTCPGGVPLIS
NEAGSYVEGEKSKKGITKDNSVTESDKSNLERKALDDILLTTVDDVTDALENATRKTDDA
NFISIPNIAPTQDFNPHAWRRHNQRPALHQHRLRCAYCSGKHHITQCPRLSWNEMGAQVG
GQLDKEQLRHNAEKLFCIKCGKFGHLYDRCPAVPQGLHAATHCPICLQPHRKIHHEPLHC
PRRVTPPHDYFPSGVPASFAQVNRSRKKSTRHGGGVLLSDSFFSRP*
>TCRU_4746 GRIP-related Arf-binding domain containing protein,
putative
MWSNWSDVKRKIKDIAAEITQPLDEESEDAHEKEQPSGGGRSRPLQEEPRPMSHATPHGS
RLLTVKNDSIYDHSGSLSTSRLGGYTAPPVRQAAPSDISTTPPSRLNNSSVHEESVERSR
ISSTATVDKTLSTSCKEPEMGTAVATTSPAETKNGGEAKHNKEEYIEELEQQVRRLSEAK
FQIEQQVLAYQEKVRESHKKTVEYYEQKMETLQHGISSEKALKEEFAEKLSQREKDCQEL
QSEVQELREQVKKFDDEATTIKLLHGEMKKTLADREEECLEKRRQIESLQELHDALLERV
EREKQNKDKTPMESVPIAHSDAHVSSHVASGLVVGDSSVAELRRRVEALEEEKVLMLREK
EQMTALLLEERRIHRVTVKEREQILSHDRELAQRLAALVQRLENERQQERQNDREEEEKR
GKMLTQQEEAAPGNGMETERAAARNREKLEKLTSSLEKEIVALRSQLETNKREGEEAVHR
VKAALSEEHARNMAAFVSQEEQRTRETIEKLQRELQDAQQHGIELERRREKLWEEVQQLK
ERLKQAHSDAETLSNKLIVAETQVEELQFSLQEARHATEGNEASLVCALKARKKELETTS
ARQKELLQQLEHTITDCLVRTDTDLPPPREGVGASFSDKVILLVSEFNRLFSENQKAAQL
QKEWERTYEQARGVNGTLSQQVSEAWKTIGVLREDLSIRDQSLARMKQQLQAESQQRHDA
QHTLTVITNELHGLKEEKRAWETRIGLSSDGKANHQEQLNALEADVETLRRNLLDREEEL
SQAQSSLETLQQVLDTFTQNKTRDVEERTADMQIEIDQLRTQLLEAEKRQHHHQADIDAL
AAGHMREIAAKNAEITSLHRKHAEIRKALDETARQLNGTTMIDKRVISHLTVNFIHAFVG
KRREADEMLKVLSGLLNWDEEMQEKAGLLPGPSNPKPGHQRKGGGLIGGLVKTVWGGPGR
GARQEGGDSGTSPSIAELWVEFLMRESEAGIIQGDAASVNTTSNASTLQIEDVIVAEGDD
SGVKSLTV*
>TCRU_4747 hypothetical protein, conserved
MMAMMTGRVLLVCALCVLWCGVCCGGRAEVTPVPSDNASDESTQKEKAVVVAEGSDQNGQ
KAASQALATTAPELPAAAANPSPAPPSGGGASDTPNTTTEKKDQNAQEGEKGENEEKEEE
EEVEGEEVEEKEGDGSKENGETEEETATGTTEETSAGSQEKPSSSSAAEGASAVCCWCVP
SACCGAVSAVVDELK*
>TCRU_4748 hypothetical protein, conserved
MAEAASCLDVKSSFIVSLPRETRHLFRCHVEDGTLVELTRLPVGCKAGPEIFQIITSAIA
GVTTVAHSLRAAPPSVHDDVWIGNIRIAGSKSDATLWEAQVLRNADGCHASMGEDRESGA
MQCTFLVVQFDHGNTVRYP*
>TCRU_4749 hypothetical protein, conserved
MQSEARAVRLASSAFSAILPSTMDVWVDNTSLRGAANKGSSKSHAMTWGLKRIYEFLDSR
GVKASFAYVRSAENPADGMSRGRVFTLQELAKGGTCEGERRGLVVGGPQSLPIIK*
>TCRU_4750 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-

terminal, putative
MLVTLPVYSEKGSKKEKGELHLWLTDNTHIVDIGPVSGEDDAAASSLLYRSGKDGKNKKE
ELIALYEKDGGKPSPGMVSVLLTEQLQRVKDVLATWKKVDDLVSELCPSEKDASTDTACS
PTVKIKDGLVGFLSGNFSGNTWRDEYLGVNATVKNNEGGNKATKAEDGVKFTGAWAEWPV
GSQGVNQLYHFANYNFTLVATVSIHGVPKSGSVPLMGAKKVDDNNPVLFGLSYNKENKWQ
VLCGDGPIKEHSSTLATEKTHQVVLMLRNGTQGSVYVDGRRVGEDEACALENKDSKEISH
FYIGGDGGSAGGEEDVSVTVTNVLLYNRPLNDDEITALNTKLSIPKTRGTKTVDGDTPPP
EAIKQVTLETEIPSSLGGQQQNEQDSLRTSENAGTGVLSTSAVSSATNFPPAKESESQSA
LGTSPEGHTNVDVDSSSEGGQTVDAETGDTVQGDGTQQPSVDTPATADTNAPTAETMSHD
GTAVAPEVGGRSGEDGETAGGTDGQKGEDIHPQDGELKAAALSSSLGNVSQGNNSDGGTV
RGSGLLPSLLLLLGLWGFAAL*
>TCRU_4751 hypothetical protein, conserved
MSRRAFTFAVPLLLVVMMYGSEATYGKEGNSRNGIILEGGDLFNDAENKSMIHTLDSFRA
PFLAYVKVAVVAIVEARYTSTTDSKSCVVGAADSIDSDKRTWTKGSAIVFDHYGISFGPL
LRPTAIVDDGGIKGPLLGVVASQGLH*
>TCRU_4752 small ubiquitin-related modifier
MFFKIKCGTQLKKLFDAYCKKQGISRSSVRFLFDGSPIDESKTPQELGMEDDDVIDAMVE
QTGGNTF*
>TCRU_4753 hypothetical protein, conserved
MSESKLKLSREDVHEFVRAMTAEMQTPSFFEKLREAVKQEPIPTSESELMAVFEGLQVEF
LTRYEATRKCGENEQQEKQDNATIPDGNAILQELREAVLHYPDKETEGMIRQMCMLQESQ
MLSVCASTPSLAPLVQPRGDGCQHAHCHGHGHSHGAPDAQQMMEMQMAIQSLSPQLRQDM
TRIQQTIHSGQQPSGEDVLKMREIQSHIKAFITTLRQFNAGNAATKK*
>TCRU_4754 hypothetical protein, conserved
MRRASGRGGRGVRVADDVVHVAGEVETEGKFVNEAERDSETRNDETLASERGTPSPAQER
SLRAANSVMAPPPRFSEVSPASKEGTHSSRKRFRRADSPQEGEGEEEAEAQEPQMRHTIA
DSCCSATSAITRGRPSGNMMYEDEEFFHDLSAMQPLRIHLGVCPLPGDATTARTTSISSS
LLTEGETSTTALLLEPRKFFTLPEEKGGKDIVGWAAAFPSVAVELPGEGVYNNASVSVTV
MLAP*
>TCRU_4755 hypothetical protein
MLPCGGATATQRDAAMAYHQLIQQQQQALMHRLYQNTPSASDVPNDDNDSNGDVFQVVGD
EMMAALGRRVIVNRTAVTDASGEAGRQMMDRRGEAVRSALLQRYSAIPLRHHARYHRQGQ
PEEDIHSMDHERRRRNRRVEFILQRMPDFWSIITNNAVGGLY*
>TCRU_4756 ribose-phosphate pyrophosphokinase, putative
MRTGKGRSEGQAFHRRLLSEYNTEITLENYVAYFELKPIAKSVEQLRKEIDEHTSLAAAV
AAAAMLSSTSHEGTFGPMATTESDPALEEMMKKRHELEEKFFVELRASFVKVKKYLWQLE
DDLLTRVHELEQLTEEEIRAMPDECIAKLYVKVQTILRYRSLNLAAFRKIMKKFMERCAC
DSLELQQRLMSIDETIFNSAIAQPRLDLRRIALDLIALYGTVYRLTYEETVAHLSHYEYR
AGVNIRRILPHSDTFFFTLNFPHQERQGNFAARILSGSTSLFCEKMICEVLQCPRYPPCC
NQFPNGEINVSLSRTLRGDDVFVLQSLVRCDHLGLSHSGTFMELALMLHTARLSSAARIT
AVIPYLAYADSVSSVAVVAELLEKMGCQHVITVDMSSEQVEGMFSVPLENISARYEFVRF
IAKHLTNEGHDFRNITVVSPSGTSVSRAKYFADALMNYMKLSSAEQFVSVCTAVHRHPNL
PPPPPVKSVSHRPCATDKPTATVTTTAASSATCQTSVPEENSSKQQEAQKSYSHSRAGTV
LDLFSPPPRRVSPTQENASNTVAFVKALRQQEEGVSAICEDRADNPAQTDGVALVGDVKG
RLCIIVDTTIDEAIKICRTAWKLHEAGASRIILIATHLILSAGAEERLVKSPIDLIVVTD
SVNQDVVFKKPLFAQKLRLLPIAPLLARAIEKMHTENTLATLFEK*
>TCRU_4757 protein kinase , putative
MLRYVLLLICYLSTLAEISLCVLDKTEEEYGSLWMPFDSTMTTGRANSAVVYAYASFFIV
GGCGDPICKKRLNVVDIIDPNQINPTRQVTLPISLEVEELGNKNICSKRVPMGVAGPTTM
VRVDPQDGDDVSLYVVGPCGYYFPEHQMTVNSTLIRQQYRSLWRLSNDLTRVVYHFSIPE
NSPGNGESEEGMKTEIPTRANATCISRGDSIFIVGGVDIFTGKALATVDVFDTKSRRYTP
EVVRLETAVQNPLVAEDSAFIYVAGGEVQLNVSIGEIGDACTDNKTQCQSSNHSDNQNII
WRPSATVQAIIFGNLSSQQNDTIHGANDSSLNVYIQNLPANPELLLRGMDKDTFYPSGSG
HLFAFNGKLCLMLNATFVNCFDVDKFLGFISPSSDCNKALKWQPLSGTSNAPPVYGSTPF

AFPLPVGVLGTVLSFFEFGGFDVDGIASERVFYRTSGLSLTSVSKLGMIVPVNKTLSLKL
HPPEEGYLRLSDNLRCIGNTAGTLDVWVVILPHESAVAEFHPITESRHVYVCFSNGPIWL
PKVPTTDSDYPSQTEGYIFTPITFTPFQIRDPRDPSYPQEKKDNSLYGMSVSVSISVGIV
VVAVVAFVFVRLRSPSGYSEDYTMHLLLAGHNNDEPRGGNPTSVAVLAADGQIPYGTPKK
SKKISAETNNFIVEPTTPMSPKSEQDSLVKNTTHWSRYEILQRIGEGAFSSVYMVRRKST
GQKFALKYLVCKDNKERLDAIRECETINSLQGHPNIIRLVDMFMNYEFDGGDMVGLCDVA
NAWTAPIPAVVAASPMKFLPPQWSAVGGKKQVHNPHVVMALASPQRPPQGGASKPQELPQ
PQPPSSVRHIPSKGSHRLEVVSIENAKNTSTAGKQSLSSVAEAEMTGPGTAAYRSFHSPN
GNRGGGDGYDADGTVLGKVNSGMPLGLPPQSLLPTPSLSIPPPAVASPPAVTATMSMASG
GNSRLLQEVSGCGAARGSGLHSPNVNLFGPPMGMLPLPPRNVMHYSNFAQVSHVGAPLPL
LNAQHEVLPAPQKRTSYAPLGGIHYKDFDVSLAFSGNNVPTAMQVPINHKNAAATQNKKY
APLQYVQPTEGRMQYTNFFPPASVSKEASNNLESLTKPRSVADAVRAARTAKANEGTVNA
AKPLPPSNPTTGIHRNGFATAGSPVVTANTPQATILKQPQPQHCQDDALDMICLLPDKVA
DVRLNEGASMARKQQKQPREEGKEFPVKLAVINSPAHIVKSPTGVIHDMARLTTPGTPDS
GPVHTRYLCLVMEYHPMGDLCGYVLRHSAKHNVKLKRQLEEEKARFIKAQEEQAKKLEHD
FPTTWVRIGSEHDSTPSFFRPGKSLMSLSHETQSQSPRDRMNEASNNATAGSRSFSNDDI
LLGMGSMSILERESETEFAMRGNALTEPQILSIAYQLASVLYHLHSQRPPIVHRDLKPEN
ILIRGEPSHGASEKNDDNDEADDGDDDVKMHLHNSEDGGNGKSGADDFLARKKNRNSSRR
GTGCRIKLTEDVIPIVVTDFGLAFMLEDRRRTGRGGGTRPYIAPECWNGRTTTASDMWSL
GCLLYALATARVTLHTVRIMYEEAKNEGFAAKVFNDILAENYSMAFACFVVSLLVVNPNK
RPTAEMALQCFTLDDGVVRFNPNCPFFSNVLDL*
>TCRU_4758 small GTPase
MPLRIKKVVDNKPDEARKPVKLILLGDSAVGKSKLVERFLMQRYIPVQMSTYALTLYRYD
FISEDDEAVDVDIWDTAGQERFSTMHPAYYHEAHACILVFDVTRKATYKNLEKWLSEMRN
YREHIPCIVACNKIDTDPSVVSKAFAFVEKHKLTLHYVSAADGTNVVRLFETAILEAVKY
QKSPKNEDFMAQVLGIIKEGERKDEAATAAPQGGTTAD*
>TCRU_4759 hypothetical protein, conserved
MPCPDPYGAMRLMRHNTQRRAVQQMFAETRRRMTQQGCMARMKCRRRRRASGAWAAKTPD
GARAGNRAQNSGWGPCQQQSGSHEPTPAGHFGGFSPAPRLFSNDPENTRIPEERYGNY*
>TCRU_4760 hypothetical protein, conserved
MNCGGVYFPDGTIHPPAWSSDADRTGICQLPPPREEKDETKSGETTAPQVNAEPSRQNED
WRQSAAADGPNTVDRSPASNTAINTSVTRPSFANGPRIVVVLNASGIMSVTCGGREHAAA
DNTDEVNGHNATGHKSPLFRKWRCGQWICC*
>TCRU_4761 Mucin-like glycoprotein, putative
MMTCRLLCALLVLVLCCCSSVYATESSQDPAKDNPTHSPTQPQETVVSGATNTFTTSSSA
APAAASPGKSEGSDAQGATGAGKAPPEHSSGVAAPAGSRGPTSSVPITKEGSGGSGSSGS
PGPVADTAQKNGDSGTTESKSGNNPSTDQTNTNADDSAKKTTAATTTAPEATTNTQAPTT
TTTRAPSRLREIDGSLSSSAWVRAPLLLAASALAYTTLG*
>TCRU_4762 hypothetical protein, conserved
MHLCVRMRCALRSLSILCLFLVLATATVSAERLMAGWDPFAVAEEEGLLKQLNSLPQFNA
KSWLKEGASSRGGKPTVPVNTQVVVNVPTATGERRFVLYVPDSYMQNGNSTAALQLYFHG
LNDQCDRFLNAINVIEHAKKTGFVLASLCGSEGAIGTAWNAGTCCGFFSEKQPDDFDFAE
KVVESVSASLGVHFTRVMAVGFSNGAMMAEGLGCRKPKLIRAVVSVGGVVVLRPGNEAGL
NECSRALRTDNEEGYRPSVLMVHGNLDVVVPMDGDRFLGFPPLNTNVRSWVESNGCKKAP
KTLNTSNYETRVYTDCTSVSDEFVSRMKSYWIRAKSAIKEGLTGQKISSTRQSIVEFVLA
LQEGHSWPSDKEFSTTEHIFDFAQRVFFSG*
>TCRU_4763 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MSADGCSDPSVVEWKDGKLMMMTACDDGRRRVYESADKGDSWTEALGTLSRVWGNKKKGN
VKGVRSGFSKAKIEDREVMLVTLPVYAKTGSEKNGKEKGVLHLWLTDNTHIVDIGPVSVE
GDDEVAASSLLYKSSKSGNEKEELIALYEKKGGEESLGMVSVRLTEQLERVKDVLATWNK
VDERVSHLCPSESAVQAPSTDTACSTSTITAGLVGFLSGNFSDNTWRDEYLGVDATVKNG
AAAKAEPSDGVTFQGAWAEWPVGAQGQNQLYHFANYNFTLVATVSIDGEPKSGSVPLMGV

RAGSDGVTKLMELSYGSGKKWQALCCDGTTKRLKGTWDPQTQYQVAIVLQSGNQGSVYFD
GQRVCESVQSNLESAESKGISHFYIGGVGGSAKNTAGDEDVSVTVRNVLLYNRPLAFTGG
IADLEEDIASASEAPVEQAASQQSRKKRETQQVPAVTSSHAVGKTAGDGGIVRGSGLLPS
LLLLLGLWGFAAL*
>TCRU_4764 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MSADGCSDPSVVEWEKDKKLIMMTACDDGRRRVYESGDKGASWTEALGTLSRVWGNKHKG
GKVQDATSGFITAKIEGVGDDKRTVMLITLPVYSSKGGKEKENEKGRLRLWLTDNTHIVD
IGPVSEKDEDAAASSLLYKSAGSETNNEKKDELIALYEKKGDETTSPSLWSVRLTDQLER
VKEVLAIWKEVDKRVSNLCTSLIAKKERASTGDVCSAAMPMDGLVGFLSGNFSDNTWRDE
YLGVNATVKGNDGEKKKAEAATVDSEKGVRFQGAWAEWPVGSQGENQLYHFANYNFTLVA
TVSIDGEPKSGSHIPLMGVKKNDEQKKSFGLSYEKGKWKLLCSDGPNSGEQSRVSEPDKT
QHVVILLRNGTQGSAYVDGQRVGDTPCALGNTDSKGISHFYIGGSAVSTEDVPVTATNVL
LYNRPLSSEEIGTFNPNKDSTPPLEENPSKPSPDSSDSIIPPIPSVTPNAQQTETPSTPA
GTQLTEQGQSMGSSGAGSDGASASAVSTVSTSSAEEESLVQVTSGTFPDGSKNVGGGSSS
DGEPKMEEREGGTDAQEEEVQPQNRDVNATALNSSLVNVSHGNNSDAGKMRGSGLLPLLL
LLLLGLWGFAAL*
>TCRU_4765 Sec7 domain containing protein, putative
MQRFSQKLAADLENRTAFLVQLRALLTQAQKILRGNQRGKLQELQVGIEEWVREVDEVRT
PGTSICNPNLEASIELSHNQEQLQEGGPVNTNGGVDDNKKNGTPRSPLNPTLEASPSPLT
TVPPTAQTPHGDELSCSTVGIGNNVSNAAFCGSASSFSALSSDFELRNLEDFAEFLSMFF
PSGLQELVKLRSIGRNAARLVIVRCFSIITCSLQQVLCQVYGEMHHVAESTMATNGEDNG
LPSASFFVPLARDIRVSINAVMKCLELLTAHCDVLSMRFAAQVCVDILKQLRQCVTLFVY
RALRGELRRLRTMGIDAKDRDALLLDASRVRQSAKTRAKELQLLLGPSLLISIEHLMGIV
RPTVRYLMSVVSFKNTVSSQEQQVLKNDVCANLFTLAQWVTPALLLRRRRQQSSSEDNLA
KEREGDFASGRSPKTVFSLSGSLPELDGIEATHTFYYQFVCFVMDSVFPVVFSPEYTACV
AQHCGDQNEGQLLAVRVLNDTIVQLAEREMEEFRHLLGCSAWRKRIAEGILNCLVSLQPV
VLEAGLETLQRIVVGCPESLGSEVGFVYTSGVFGLLESESTPPVMRRSLLRHVISTFFKP
TSVPDEPSLLLRLYRHFDLNVQWHQLNVVQQAVATLSKTVRCAAPEDFADEKEVKNDSQE
ITAPRKSLPFLALQGLSLAVELLAVHIPRDGDAVGGKSYPMLRNRDDKMEEQRAVDIINS
SPLKGIKKLFGVTDDEMNPGGHMNLAGKNWAHQHIPLPASPAIEEKVRRIVQFLMETPSL
NPESVAEFLSHPAVFPLQVCRVFMEALPIAGRSLVEGLRKLFSVVQLPKEGQRIERLIEF
FCSAYFKANSVDGIDIETFPFESENACFIMGVAIIMLNTNLHNPHAASTKMTDSSFCAQL
RGCNEGKDFPERFAKNIFNEIHLHSLSSMKGFWSAGMSSGVRYASVPFPRKMDSIFFSSE
ERRELAFGVVRQRLLSETRELIYRHSNIIQTQLEEMELRDWCCVTRDLFFSTWPSLCAVF
GVAGHGAKVPEEALTLCVMGLRSSFLVATAFGLQTECGVSQLALLRMASFEPMRDVCHKS
ILEVASSPYSVSFSAPCWVPVVELLVAIRKQQQQQVMVVESESVFGRVEEFTRESCENDG
KKANPAVTSVCKNAVREVLQGISTVLQNTSVDGETLSAAFYVLRRFLGYSLISHEQEQGA
VVTNFINVRDFSNFIVPTLVDIVEARNGNGDGYMHLVVGFVVDILNTIWGSCICETKLEG
VGRHSELIKCFTFFQTCYDRYGASAEVRMHVLQGVKELVARTLHKVGSKKKRAMGFPSHT
LFIMALIWAQLLQPVARALSEKDSLGTETCSLAVHILRKLVDLCCGMGGTTIGIHLQKKV
RSVPLLLLMNVAYIGGMCSDVDSAQSCLAQFSTICTSALNQEETVSPEDELPLLDAADVA
EFDPVRESSKFLLQRLIENVRQKPDVLVLHALERMSLLLCCHVQQTRTDVITALRALVVQ
LGPSQLQHLAVHLSDAVLKASLGHATPENTSPMADSSFVAHALFSLKTPFNMRRCSPTSF
RATLPLVLSFMSQEFLTEVPLEYLDSVAAIVMKHCLVPLVVSPRSAFQFRATAVRFLMHC
ALLCVTRQTIDGSDSCGGKTGSSSSSIISISSSSNTIAECVSLLLFALRVPVWFIVPDGA
DHAGRRWVKEEKSAALSEYMRKGADAIQALWTAEAYEVTGSRRSATLSGTGKTEANVEPE
EIARTMRSSWSSPFGEVATDEQLVEYCSLMALLLSPLPKVLGAFPPQVFRAKNGDPTPHH
SQRQQQQEEEKLFDAVVWAPPPADHKLLKELVLETTGIFFSILWRVNNVAEMEKFMTRAT
QKGRDAPSICKSSALLPHAAIRGGLNAFLTLALWVDIPELRDVFVEILRITATVQKMTLS
MREAQKMVEGAAETAAMQRPSPLEQQHIRSCNVGMYQELSSVVAHWIRTVVHQTDEMTSS
LAATQRDELRSVAGDPEVFSGVVQLLTVAAGAVIVAVRDYLVWYIAAQEHETKQTTETFD
PDT*

>TCRU_4766 mitochondrial calcium uptake 1
MSTPIWTLRFIHPQGLSRHYSVRHRVEWWRRHSLVWAACQWRFVYAATRAALALSAGWFA
ATTLGASVAFCRTLDTPEYLIPYYLRDVTTRFKHYASYRKRGSRSKYMTVEDFVRALLAS
KDNDPLDPSVVESMTRLFTELDADGKTYLSLTEFSFLMLLLTAKREDLRVLFFVLDKDRV
GSLSLDEFAGVLRGLGRDMNEAQLLTRGQKNGIVRRLFGDDGQSRCSFSQIAETVDALNE
EVWTAEFRQIDTDHNDRITAEQFGKLIANHMIGRHLPFHIVDNIRKLRGSGETITLEMWI
GFHRVMQYADALSEAVELFTSSGLPLRRNDFNRAIRAAGLPPFADAELDLIMALFDRNAD
GVLEFDEFVSVMRQKLSYHYSYRGDPRKKKNLPVRFFECVGEVLSH*
>TCRU_4767 pitrilysin-like metalloprotease
MLCRSILCRCAAVTAPLHAGKRPLLNTEKKHGFTHKDTRRIDELNLVAYEWRHDATEAVY
YHIDTDDRNCTFCIGFRTPAENNKGASHVLEHTVLCGSKKYPVRDPFFMMMRRSLSTFMN
AMTGADYTLYPFATTNQQDFCNLLDVYLDAVFYPLLREEDFKQEGHRVEVETAGEGMGKR
LVYNGVVFNEMRGVVSEPSQHYAHSLMRLMLPGTHYEHISGGYPPDVLQLTHEELVAFHG
KHYHPSNSITLTYGAQHPENWMEILNNYFSSFSKGGVVTVPTLAPEQRFHQMKKISLQGP
LNSMGNPQRQKRISVSFGVQQEDNRLEDMVDLSVLDSLLSSGPSSPLYQALLESQIGSHY
APMRGYSSYLSSPFVSYGVEGVDEARPNAEEEVLNAVMSTLQKVEKEGFDQRRVQSVIFQ
EELQQRHRAADYGVSLCTGLCSMGLCRAANNPLDFIDWLPHLRRLGERQVAPLLSRISRN
LLKNPHCALVSVSAKKEFLDSLRDSLQCMEEKLNEGVPDARKEEIEAETASWLERVRAPQ
NGDILPGLTVKDIPRQSFLEPTPRQANRGDHASLYTILNPTNGLVYVHGLVPFCSSLMSS
IQGSGSVENLADVPLWHSLLGNLGAGSYSFKELDIATELVCSGFTFSPIINQSYRQKSEY
ILGTTLGFYTTKEKLREALELLKVILLEPRTSSKDDDVCGRVLSLTKARCSKVIQRLQHY
GHRVATTLAVSRLTRCGAVKEEWSGLTQSTHSSLLLEELQNSDEATVRNVIVNILNSHEV
FAQSLASNVRHGTFWATCEEEHRKEVEAMLAAFLQGFPSVSSSASVLVRNSLQVLERSIG
APQIRKPLPIDTSYVGFAAPNELDWHHPQQAPLRVACQLLGNEYLHRRIREEGGAYGSGA
DATLRGEVGGITMSSYRDPTPEQTIRVFQEAADWLGSADNVTQVRVDEAKLRIFASIDAP
YSADSYGESYFLHDVCPTQKQALRDALLSVEPKDVISVARYFNVSGEASAVVSVLCPEVA
VKEH*
>TCRU_4768 Golgi/lysosome glycoprotein 1
MKTSLFLALLLFSVCCPVVQGGNLYPRCQGEELLGTADAGEESIFFKIRRYSKALTLTCL
AYEVISISDVGRGERDPCQVEHQTEYQYRLVIRATMVDEATGKIIETDYDVKGLAGGSLG
DLLIHSAELSKFSLVFMNKATNVRCRLRIRALMSYTERTKPFEREGLPVVIGLEPTSVYR
NRSSTTKLFLSYPSGTNMQEAQSDVVKLTNLEKECADEHSQGHAMRPQPTPQSMEFIDDT
SLVGLRDYYFDSSETLRICYHKKGKSVGAELAIVRVFECNPYGYEVVKGQDDEGRVYVGV
ETTIKFYGYDLDTRDLGDRAKFANDFEDCATAPPAGGVPEGLPLAPAESYGPGTRYTLWT
WVLREGGFFKVCYKTRDGAWVEVPNIIDVAYDAPSTYAPGSSSPPSIPRPRDPITQEECP
MAIERPGEPWTVYKSLKLTFNESKISEEYLLVLSRAFCIPRSALAVTRMTHDGEGHQVIY
LSILCEELGDAAPCDTVERQNYILTLGKSNSTILSDIGILSVEGSRHLFAFGDDTVTMKG
TGGRVMTLLITCATVVLVAAMAVYGVLKYRENRQYFIQFGNDDAEVEDMYAASDPRNTEH
KGPLPVKDAVIEVEE*
>TCRU_4769 hypothetical protein, conserved
MLRTTVIGCLYATLVAMKRSGKPSETPEYKQVYLPYDTAPTPLELERERKKLQQAYYGRM
EHRKLVPVKEVPLNVYTYGKEGMSLPISIFKDQQDPVIGPEWTYPGIYENKVAAQHWYTE
ELFSKEAQNKFDSPWQKQILENQVKRRMAKVAFRMRQVNMKAVDLFQKERGSAKRGAAAA
AAAGGGGGVAAEKGKAAAKKK*
>TCRU_4770 cytochrome c1, heme protein, mitochondrial, putative
MAGKKAHPIKRDWYWNHNDRFEIWHSLDWPSVRRGRQIYTEVFAPCHPLGRMTFTHFQGF
MTREEIKKLASQYEVIDSEPDAEGMLNPRPGKPTDTLPIPFPNQRAAQFANNGSEPPDLQ
HSVFGKEGGPDYIFSLITGYNWGNGELLEVPPFAPELKPGQFWNPYFKDCVLSMPPPLSD
GMVDYEDGTPATTSQMAKDVVNFLRWSAESEYDDRRVMFWKAFTTLGLVNCILLHYGQKN
TNWRIYGRTTFRYWKKTW*
>TCRU_4771 hypothetical protein, conserved
MVMRRVFFVVLVLALLCCCSCVFAVEDEPQVTQVNAVCAGKDKLGRWQLPGRSLWYNCTD
AVPGAGKMICDMGVGNCASEASQSRTKDGVKDAVITINVSTFTPEILENWWVRKVEPKAA
TIESGPTKPPEAGPPGPQEHKAPGYTSTTDSDSPPAGAAGASGDPPPPLPATPGGAVANS

AAVAAATTDPSAAASQASDSALSGELQSPSHSASAASPAPESIPDPEPTEGGDHSSHDPP
VELQEETAAAPPTQLPQTGEDRSAAGGAEEDTAANTTDTASSEGNPTAAGMPAPLSSAPK
TNALENSVGTDACFHGTRLNALPLLVLAALTYGTLG*
>TCRU_4772 pentatricopeptide repeat domain containing protein, putative
MATLSQARLSGWASRWLTDELVALSKAGNWESAMATLAQLQQANIVQSNVFHYTTVISAC
GRSGKWEAAMSVFTHMVKNDVKPNVYTYTALISACAAAQKPDVALRMYAHMRLAEVLPNV
RTMTALANACSRAGQWERAIKILRECEELSIAPNVFTYTAVIEGCRRAGVWKPAVELLKE
MRDPLQVRPNDVTYNTVLGACAAASAHEPALKVYAAMVSDGYMPVLYTRTLLTGLLKNTA
LDGLADELQVRKGTWREAQVPDSDPAAILELTREASAKEEAEEVQETEPKKEAQLRTGVA
GGNGD*
>TCRU_4773 Miro-like protein, putative
MNAACNLNVLRVLVVGDTGVGKTLLLRRLLQAVAPGEASLDTTWSPTTGFHVEVILEKNQ
QFSLRDSIAVPCVAFIELGGNRNFGPSSQFPISLMSFDGVIFVYDRHNANSAIGLSYWYE
DLKNYGVVGIVGGAKVMLLETALSPSVSNSPNANSGLPDELLGAYLQRNIKTPPPWKRRF
NKIKSSIAQGVGSSRLSVRDFLHHQGTLRVRVAVFILQWALKIENLLLFLVAVILFGPHQ
QSVRLRRPSVAEALAMISSDVAGTQTVFSCPLFDQLEFEASALGKLLSFVDSLRRD*
>TCRU_4774 hypothetical protein, conserved
MLYTWKRYALGEKRANVLCLWVTDNNRTFSVGPLAMDNNLELFHALLYSDGALHILQDGI
IKASNTISLVPLTEGLQMINYVLKSWAQLDSSFSESFTPTAGLVVFLFNASSGGDTWIDD
YLCVNAIVTKNAMKVKDGFEFTGLGSGAIWPVSSREHNGPHPFVSCDFTLVATVMIQNFS
KLSPPLLGAGLDAPVSTNFIGLSHDADGRWETVFYGIKTAPGSTWEPWKEYQVALMLPDG
HRGFVYVSAELVGSYAKIRTPETRGLESHSSKLGATREAAAAVRR*
>TCRU_4775 hypothetical protein, conserved
MQLQSYSRCNLFYGREACNVKPPNSDAAFLLGARALVDVTAACDINGVTAAKRSCSFVRQ
SAGRPLHLPAPGMAWNPLEGWSRLGLRRARSNALLRSSYMQPEPQQRDKVRTPSLGPGEA
AVPPAVIRDPR*
>TCRU_4776 hypothetical protein, conserved
MARETAQNDGQADLPVAEAGRIRGQVQCGAQPIPGDEGAAPPRREDLASSGWVRLQVFSR
GLPEAQRSNGVRLDFVPPFFRVHSVKCSAFPGKAMCVLRVLPRHATFRVSIFVLGLSRPP
RGIWRLAARKMPLRMSNHVDRVKRRVSHNQVEAGQPALRRAKMAFFRQGSVLASRGMPSS
ISTK*
>TCRU_4777 hypothetical protein, conserved
MRALKDRVPAPTREAAPTPPEKVRVFDSVREHAAEDITEEEWMGTTPLDMNPHYKQSPRS
VWSGVSTDDRLALSQRREIDTA*
>TCRU_4778 BNR repeat-like domain/Concanavalin A-like lectin/glucanases superfamily, putative
MNLRVGRPTTLVKGSDIYMLVGNYSRTAANNPEKSVGDEWGLLLARGNVSEEGGKRVNWN
DTYRFLWTDLKKQQQSLTGVIGGGGSGVKMKDGPFLFPVEGTKKENGKAVSLIIYFSAND
GWTLSKGMSDDGCSDPSVVEWKGKLMMMTACDDGRRRVYESGDKGESWTEALGTLSCVWG
NKHKGNEKVVRSGFTTANIYDGVEDRDVMLVTLPVYSEKADKKEAGNGKKGVLHLWLTDN
THIVDIGPVSDDDAAASSLLYRSAGSGDNNERKEKLIALYEKKEDGETPLGMVSVLLTEQ
LQRVKDVLATWKKVDERVSKLCTSISEENLSTENVCRAVKITEGLVGFLSGNIFGNTWRN
EYLGVNATIKSGAAVATKNSDGVTFTGRGVWAEWPVGRQEENQLYHFANYNFTLVATVSI
HGVPEGDTSIPLIGARVNNGDNNPVLLGLSYNRERKWELLSSGGNNKDLSSTWDPQTQYQ
VAIVLRSGTQGSVYVDGQPVEGVPFDLKDKGSKVISHFFIGGDGGNAENTGSREGVSVTV
RNVLLYNRPLGDSELTALNANKVPISVPEDRIELAGDAVLPAASGSDLEGTVSLSNSTGQ
KPLEEEPLRRVGGVGGGVSSAASIATTPSSNVDQTVATGGGDTMLGNGSPQTPEVGVSSG
EDKETAGGTDVQEGIHPQAGEVNATSLSSSLGNLSQGNNSDAGTLCGSGLLSSLLLLGLW
MFASLWE*
>TCRU_4779 nucleoside diphosphate kinase, putative
MALSRQDPRLAFYCERQDDISQLVRRFVLFFFYEDRSIEMREIPKNVLYLRRAPFPHLKK
DDFTLGASLTINGGIVKITDYADEVTRVLCEKKSEFTVVLLGDSLFPRLGHYLAILTEEC
DFTISSMQMAWLHEGTSEKYSLPEKLTDPRLVAACCVRADAIQKGLDYVKRIPGAFAASD

ENEAKKWAQLVEHVSRDPVAIRGDSRCSVVIVKPHAVQSHAAGVILQQLVDTGLELTALM
LANLSSRVVDNFLEPYKGVLSDFRESAKALTGLVWILQLVSLDDSVDVVHLVREVCGPFD
PAFAKELRPKSIRARFGVDRANNAVHCCDLPEEGPIYTSFFFDPINVEER*
>TCRU_4780 Leishmanolysin, putative
MNLLNENRHCEDGVLSFANGIILAEDEVVPAAVKLHADRLLVQPMEGLSIVPSFATGSVC
SWFTVPAEHRSTGVAISDMVQCVAAALGGVWALPCATLEDGRPVVGAMHFPGRFISRTHR
HPHRHALVGPCCRVQLSAHGQPQHGEEWCCPWQGVVGGGGLDDCRDGCK*
>TCRU_4781 hypothetical protein, conserved
MEESPHYSRVADAAESINVVTGRSIYYGMRPWRCDDRFHDLLSSFLNMDSLVVQLHLAGL
LWRCSRSKKGSEPIDCYKRLGRGEVMYYVDRYRSGMMRTGYFDKYPYNQNELQRIIEEDG
LKMRVWRHQRELEMESKEGKIDDLLRKNVMKNTERFRAD*
>TCRU_4782 ARP2/3 complex subunit, putative
MHSRWNGYEESSLLGCGVYPLRRTSRLTPPGPAPRMDEMIEEGEEEPQDIVDEALYFFKP
HMFFRNFPIKGAGDRVILYLTIYLHDCLKKIVQLKREEAHSVLLNYTTMPFSSPGEKDFP
FNAFFPAGNEEEQEKWREYAKQLRLEANVRLIEKVFLFPEKDGTGNKFWMAFAKRPFLAS
S*
>TCRU_4783 hypothetical protein, conserved
MSRTYVLFAVLALFVAVGVPAIITNAEEDDGLEKMKGNWSIFWLAGQSPRRTGFVAELSA
ASLVLREEKDAPSAVTAVAESLLRFLRLLGTQDDVQGPLSVPAAWLLGLPRVVNARVSRE
GVHLTDCPTVGVTFARPQHYMEAGLGTVFEAPQTVHLPVDGTCAQAPFTVRGYWLERLGK
DEILMVIMVRVDGEDNSAVFHLCRRLEEGTGVRSFITSAALLVTVALIRFFPSVFWRRKG
GTASATRITPNPLRPALSELRRRELLRRQEEIIRRMKEEDGRS*
>TCRU_4784 PUB domain containing protein, putative
MPGHDEHSPGVKETNVDVASSSSATSNLEERKKYYISQALFETLQGKGFSDNAIKKSIVA
GCVDDGTCTQWITMHEGHPELDTPLEEGVEVVVKFKRVLTEVEREAKVRELREKAKAKVE
EEKRLAAEKERDRIEMGRRAIETKEMLDKLRRESELAAVRKQKEDDAIARRRVRVQLLAD
KYARQGMAMEEAFRVAELEVEETVRQRRREATHVEGRDVQNAREGAPKTSLWDVDGIIAQ
NVSLTDVFDKPLEPPSSLPRLVDELRNHKDAAVACQCIAVLLTILGNVLKSPFDTTKRSL
KTTTSVFCTKIAPVPSAIQILRTCGFQLATDANGNESMVSTIAVIRVIERAIALLKNEV*
>TCRU_4785 DNA damage repair protein, putative
MSGKKNVSVGRKWACDQVNSVRHFQQHSRLHFIGQWKTKAHDLFKDWFAVHPTWNHGVLS
HQALFVHLDMDAFFCSVVLAKEENAHMREKPVCIAAGKGNSDISSSNYIARSFGVRAGMY
VNAAKELCPNLQVLSYDLPRCEEVIKCLYRLFFELCPDKVCIAVEVYSIDEVMIAFDTEN
HDVVKSYCANVLRQLELTTNCTASCGIGPNIMLSRIATQYAKPNGVYSILPQDVPELVGH
MPFSEIHGVGSCTMTKLRPLLRPYLKDADISDDDILCCHVQKLSKQQLQRALGQKSGENF
FHLCRGHDTRQVSRTGDEENQRMLGKKMPTSVSCSMNYAVRPLTLDDVWGILRELLEVVC
GKMDRGGYSSSGLRVTLLERHPLHPKETQKFMGRGRCVEFHVPINFEKPLRSSELELMLS
QVKDVVTPLFVLDRQMSDEERARELGLEDDAESRVIWTVSLKTVKDIVISDIRGMTVQAT
GLHSQGGAVTEWKSTSGGQLSLFNAFSRGNKRKRQSSEVILSPPTGIAQVMENAFEPSVV
EDLMGLDVDEIFIEDWKKAVTEASQRADYTVMKALLRVAAFQCTARLGSCDLAQTIFKDL
VAYANALLPVPVAFT*
>TCRU_4786 hypothetical protein, conserved
MNAALLQGLRRAGHSLKEGSHNEAEYVIRSLQAINDPAAAEETIRILQDSVQELGHDVTY
VHFAAFRLLRFYLTRNGVLWGESTRRLLHFLLDYVESKGEQIVTLAWRPVLSEAALDAAV
MLKLSCAGAEGGVDTTIFLGIVSDMLSLLAERKSEGFIVFVRHVVIHLVEEFGLYHPSSR
GREMPLRFHRACRSVFECHGLVRFLDALLCCAATGLSETSRTVEALFQCLDTILSWSTHC
FFEEEVAEDECSHSFRVSGILWHTLLLEGVTVAGTKITIDSLLRTWYSEGNLCGFFFNPL
SLVELICQFCGITMESWSVSDKMNYGERFLSLTCFVTRKLLAVAGPCEDARTFLPLAISG
VRNIVENLGDIFTVHEILVCYVSELSLFAKTLIEFDSRFPDDDGIMAALDKALSCLFKLV
TMMPWHDVSCTAVAAAGMEVFHTFLSVKLSNAHSSEEAEHFSDTFTMSHISLLGHLARSD
PERAAESLCLSLEALQGRNANLEQHLSGSDRLQVQEGIWLVLKIIDAFLADACEGEEVSI
PSCFTGSFRSGSHPVLKVVSTLMVLMQEVERNLSVASPALVSSLLEVFGTFIGVYVTADD
GGVAGNIFFAQVCIAVVSHVFHALRAFSFDEDVALAGCRVLDISVKIEGVAFLLRSSGIL
HTAEELFTCGQLFYEDVRGRIAGFWIRCISEGTFSEQIVPVLQNFDIHGTDFTSVDVTLC

LERCSSLAGLFVSLQGSERLAWCFASLTSLCDHVLSVSVCRFYEKEVTIRTTELILQLFL
TCSVTLHGEEVLWVLSKVRMTLASVINTIAEDPTWSNEGAEEEQHRLLKLISRLFCEVSR
WVMMECTLPSDLLHPLGTSVISSLSGFLKLFNERSLSFPELRESVFAAFQLCAEAFARDF
VSHTDSQVFLLTILFALDDESVDVQRVGIIVAERVVTCLRDSGLKNHELFAQLLSTILRS
FLRGKIAVSFSSQLARCLTTLCGCLSPEFVESVLGETLRLCPEPKLTDIVRGVMRVVHEC
VVSEESRRQAVLRSLDESIADGLCNIRSVLLA*
>TCRU_4787 stress-inducible protein STI1-like, putative
MSFEELRLKGNEAFKAKKYEDAIDCYTKAIDMSPESEVAAALYSNRAACWQNMGNAANAL
KDAESCILLKPSWLKGYYRKGSALESMQRYDEALEAFQRASKLEPESEEISDKLQKLVLI
LRGRNEKATPEGCRTSDEAKRIGNSMFSAGNFEKAMLFYSRAIELSPDGNGELANYYANR
AACHQQTRNYNLVIRDCDKALEIDSTHVKALMRRAIAYEGLEEWTEALNDYNKANSLFPG
MAAVSQGVLRCRRALMR*
>TCRU_4788 SAP domain containing protein, putative
MRTKRRLLYLPDEEATLLGDLTDSPRPRPSRLSRLAIFSSDDEKKAAPVDDGTETPGAGV
VDRALLVSYNSFALADGSGNFRRPMTAGEAMALYRSLRKCCRFLRTFLQDKSISETSTDS
LSTSTSEPSESSESESESEPRQRWHRRRPKQAENLMKNGENYAGMTVAELRELLRTRNLP
LSGPKALLVSRLQGNDEEASKMEEDGQSTLMVSECGNNESSDANSFFSIESEVAKSSQNV
WSAIVNMGSRLFRKSTGSLPEEKKNLYRKRQRIE*
>TCRU_4789 FGGY family of carbohydrate kinases, C-terminal domain
containing protein, putative
MTRSEFTTMSFPEAFVIGLDFGSDSARAVLVRVCDGKEVAVAVEPYRRWSDGKYCDPSKN
QYRHHPLDYIEALEIVVSRVLDQGPPEVRNHVVGMACDTTGSTPCFVDEKGAPLALQELF
SENPNAMFILWKDHTSVNEAMAINDLCRKSLVDYTMYSGGTYSSEWFWSKALHVLHHDKA
VREKGYALLELCEWIPALLTGVSSYAEVVRSRCACGHKAMWNEEWGGFPPSEFFFQLDPA
LSVIRSRMGGDTFTAEKPVGCLSPDWSRRLGLRENVVVAGGAIDCHMGAVGAGIGEYTLV
RVMGTSTCDVMVSSREDMNKRRINGICGQVDGSVFPGMIGLEAGQAAYGDVFAWFFSLLA
FPLKTVIQNSTLISEKEKVKVWEEYKRGIFGVLTERAEKMEPSPVNALAVDWFNGRRTPD
ANLLLKGAISGLTLGTDAPTIFRALVEATAYGSRAIVERFREEGVRIDRVIAVGGIAKKS
PLVMQVLSDVLNVPIGVCRTDQACALGAAMFAATAAGCYSSIEMAQKKMSSGFVSEYTSC
SARAAVYDTLYGSYQRLGRAIQKESFSHL*
>TCRU_4790 hypothetical protein, conserved
MFVCDAWGQALFVVSGHASHQHDGCEGHGRNIHLGAVMHAALRCLGMQLRLRVTEEGNAR
CAPCTAEAMITWVAPPYGEGKAIFRGHTQVCTISATSGSLLPVVPWGGDVRESVWSRTVS
PASNEQGLLGASVPYPESIGTGRGTPPKDVDLAAPQKHPSPERRNSSGMP*
>TCRU_4791 hypothetical protein, conserved
MAMMMAGRVLLVCALCVLWCGAGGGSVDALDVDGKAGGSSSGGEDTLGSPRPLLPEPNLS
DSERSQPEHQGNASPSRAAGEVVGDDDAEKKKEDNDSNDGDDGSEESGLPPPPAAGASGK
EDTKKSLITLPQVSGVGSSAGGGGGPSGNPNRSGDNVLSSSALISAPPPFISTGGNGSQT
VIGVSSTQQMEYSKESLNLFKKPAQYIPSKEHPQEKPAPNAREVSSTQRVTTKSQFVGED
TTGEDEARNGNVANDPSSKQTEQIALQKT*
>TCRU_4792 hypothetical protein, conserved
MDVFLLGFQCWVQAAQEEAQSPCSATPTTPQIDRVLPRRRQRQAEEAADRDKQQLSHHRD
SEARPACLPSRCFDPCRREKILAVCRSILAGSTSPLATDSSGEQPRLRPSVVCHGRSQRS
LDRGRMPVAKPVQ*
>TCRU_family, putative Se.1
MEHGVTLLEDLMTPRQPIISSPAPYFFAVEDASVSRVVEDWIAKVPYRDAHIFALGCTPH
RSPQQLAWARIAPRAMRFKDIMLDFAAREVLVFHLSMQNGFPQLLSPLSPPN*
>TCRU_4794 cytochrome c oxidase assembly factor, putative
MRLAARRGGLLLRPGGFTRFASSTGQQEQQGGRGFFSVFSHGPRSRAELWGLLLGCSVFP
LSVALMNWYDKQKEVPPPELAPDFQSTHSVRMTPKQQLGGPFRLRESRTGAYITDQELFQ
DHWTLLYFGFSKCAEVCPTTLQFIADVMKACDAATTKSTAPEVAKLQAVFLSIDSFRDTP
EVLEKYVSKFDPRLRALCGSLEEVKQAASAWRVYYSSIEETDEERKLREEKGVPEVFLDD
TYQFDHSSAIYLVGPDGKMKDFFFKEMGLEDAVNRLGVHFEDIYGFKDTRES*
>TCRU_4795 hypothetical protein

MQANGASLSEKTESSGNAATLTYSVAPHPFSYQTLFAIVMVSVSANQGTLGNLKSWMRRV
QDYSKKGRIKWSQVAFTHCFSRQLEVRRSCVVASVSCALLSHGERHWGVLWATSHGLYFR
SVVENEIFGSIFKEKSEKKMTMDKLEDNEKTWGDESLALKEVLSFKDVVSLLPSIALEVV
DDGPPYVMGIPNPIVRPNTLQVFTVSPNQIYQFVHMHDLTVIPPSSSTVMGDTSEKMLLK
HEYDVIRNFPSEFDAVTFCALTERLWEARLKALQIPLCRDGVTYAARH*
>TCRU_4796 vesicular-fusion protein nsf, putative
MSSPLIVCSVLKDEDARTNLLYMNPQDAKIFVDSSGIVMINEFLFTVSANTGIRAGHVGM
NSIQRRLLGLSTTAGSTVILHKPPQRIPSIAKMVLTVEYIVASKRGGTLDCMEFIGYFLK
QFSGQCFRDSQTLAVVLDSGLRLLATVTQLNCDGLGSVGFLANSTSLILLATEKSEIALT
NVPDNQLDAQQPQLMQNFNLENLGIGGLRNEFAQVFRRAFASRLFPASYVKKLGVKHVKG
VLLYGPPGTGKTLIARKIGEILNCHSPKIVNGPEVFNKFVGGTEENVRKLFLDAEAEAAA
KGDLSKLHLIIFDEFDAICKQRGAVRDSTGVNDNVVNQLLAKIDGVNSLNNVLLIGMTNR
MDLIDEAILRPGRFEVHVEISLPNEEGREEIFRIHTRGMRENGIIGKDVNLAELASLTKN
YSGAEIEGVVRSAISNAFNKHIDLDHPTEVVNAQDVFVTRQDFLRAVEEVEPAFGQAKEE
CSNLKGDGIIYYGKPWEGVESCCSRYVELLKGEGKRIHLLSVLIEGLPGSGKSAVAAYLA
EKAEFPYVKVISSEVMVSYGELQKVNIIRKAFEDAYRSPTSVIILDDIERIIEFSHLGGR
YSNAILQALLVLIKRPPPEGRKLLVIGTTALYDVLDSLEMVSCFSVKMTLPRVPPEALSL
VANELELPFATQADLHCCVDLLPMSLPMKQLLLVLEMAAERDTEGRAVITSKTFEQALES
VGVRGG*
>TCRU_4797 tubulin-tyrosine ligase, putative
MDWAHDSTWSAGSPPHGEACMGNGDDDIQKTVQQRLTEAQRQRNELIARGVAHLVAPSVR
HYDEANGSVWRTTTKVHTVVRSAAADACVTLSVSPFRGRKPTIVFLPLDHPWDGDLHSND
NSAYVEPLPLAWLPPARMGEQKKLRRERAYAALHFTMSDNAVRFSSVMCTLERAGFAEER
SLLSTTWSLKWCKRPVRSDFLRLKPFQRINHFPGTWRIGKKDELHKHLVAARERWCEKNN
ENLILVGHAHGNSFGDFFPEAWVLPDEAAALKHVLGSNKEHDHLFIVKPTNSACGRGIYL
LKASEHLRLEHALQQPNACAASETRPLRLLVQRYISDPLLIEGYKFDLRLYVVVTSYSPM
RVYLYEEGLVRFATLPYPAEETLEDHASKESLTAHLTNFTINKKSEDFVPPDGIGDNGGV
TSASKWTLAALQKEFCNSGLDWNGTMARIHDLIMKTLLAVEPHVIYEQEAINDTVGDCCF
EVYGVDVLLRRPYTSESPTPMPVLMEVNIMPSLSTHYSLLDQCVKGNFVADTLTLVGITA
AVGSKKCGKDVVPICEMPEGDRLTFSYGHPFLDALTDALELESCLTSEEEFVRRMHFQRL
CPTPESYSRYRPLFTQVQRGALQRSLNEVLSLWEQAKLDDPPVYS*
>TCRU_4798 Tubulin/FtsZ family, putative
MAAEREVITVALGNYASLVAAQWANGTTEYDTTRRTLYAERRVGAVWGGELTQQRTGATV
RVPRLILLDAPHATRMKFPRRRIHRDTNLKEAQEADRGPTPGAMNCPTTADFFSSDSSNS
HSDDNDNDNNGSEKQERGEVEETPSFSSSTDQRHHGRTFSPSGVAAHETFNSVRQIKREL
FNERDELVPWWQYIRSGVSANCVHVLHPLHPLGGAAADVPLLHSFGFGMSQLSSTHSNDM
AEVMGSIRQQLEEADSLQGVQCFLDGDSAFGGAACNVMEEFWEDAGHKIPAVFFACFQPL
PEETMTPGSDVDFADRRRDELCLNRLLAASHLTRQDRAVYIPLELEYWKTSFAEHTTLGM
NVPSWLQNDIATAQLVAMAADTALYGIRDDGSVNTTRGSGPSFYMHDWQEAVRPTRTLRV
AAALAAVPLRVYDANAPKNDLWDFLHRYPLLTTSPVANNGFFTPLTHPINFEFQTEAGRV
LGHALTMRGAGKLLDLTYPRQEALLRYGLPLRTANYLPLVTGNSYPISSTFPQDFVLPRD
ILASGALDGIDVGSHVVSTFGSAPMIQGILTDAEKVLHCRRHLYEDAYCMEKDEWKEVME
DVLQMRDDYDHRDNEADEEELE*
>TCRU_4799 conserved protein, unknown function
MGAAPSRESTTLYSYFRGTYEIGLIPLTKAFFGLPGDPHSRTTNKTEEGEEEEDVGIGLR
YKQEPHVSQTTSTAAHLSSTMELRRQFVIMRSDPAILYANARGKVSASWPELLSDAFTEE
DLDAFLDKVEERIYNTDAEMFANTKNALIPLPCALCLVCKDGQERSGSFFWRGRSIVVIG
YFACLPEDLRSAFKVAKGKLPEGKKGTTGTDNDAKHTLSSTSQVSLFLNAGVLASAGDRT
LERVLLLAAVMLRNQYLDSFFHVFAPTPIPSSYTGDVFQNIFNTEFDASPFFPHDGMFLD
TAARGKNATAQQTREEALKTLERRLQNITVYVETAVDNYSSLKSLTENAAFLQCQTNLRP
GLCFMDLPQVVLDGFEPAGITEENTEKTADGEQEEAKLHSARASLDDTTTAVENTKQDGE
TSKVGIHEETLEKAKFPETDEKASTKNSASVELVRVCFTPEYVVKATMWASGLLSSPTEL
VGGSWVQYKLKDESDELRQTLHGKDSIVANWREICKDVAGSYMGEGTLSLLRHVKALRDE
VERARAISLNSWSVDKLIQTREGRTCALHHTSFGTMLVGIRSRRDGENIRGLDKKKQSIR

EKAGQGSDNDTSNYAAASRNSRNRAGSHSHASSQFQGLGHGSTSGGMHLDTLSNMSPMLN
ARSMGGVPTGPIYGAAPGGFVAPLPFVPEMQMPSNVAFQGNMMLAPMMVPFMGNGMRDAS
VMERKEQQGAVATPPLFHTVSFSTAPIDARGENLSGVYSNSNNPNRDDGKVVNPCASASQ
NFSAGDANITVPSYPFSVFNLSGTAPAGTAFPSSINMPSQQQQQQFVLLQQGPGGVPVFV
PVTSAVQQSSLPPPYGFSYGVSSGAPQVVVASQQPLVRDSSLSLPQTNAAAAAGAAASSG
GGLVPNYVYYIPAPMGGGGQHAMGSC*
>TCRU_4800 hypothetical protein, conserved
MGLSIKGSGARVHVNIASSMLDSGELEFRGDFGASSQILVAGSKLVTKWSHAIAFLDFAL
GANSTLLLLDNRIAWNMYAVYFANAAVVDGGGIIVRGNTLRAIEKDAYSSRSALYFHSVD
LKNGGYLDVENNTMSAANGVYFFGDTTVSSAGLLRVADCTFVGDKEFLDPTLVYFYGSVT
LEGGAQWRVEGNKVSAASVLTIAHAQHKMKLSGSGTAVVLAHNRQVEDIYPFTDLAMSNT
VVSSPARFVVGCNLQGDEEVLYDGVFPGEVVLFRCGTCNDDAACYMPGTESVDRGSCSCS
CKDGWHGASCLPFEVPDTVVLPVPDRAVDGDTSCVHLVCDCSECDLYTFCVVTMHPHCKS
PHPRHDCKKELSYGDVEG*
>TCRU_4801 hypothetical protein, conserved
MAEAAFCLELKASFFQVSLPRDTRHLFRCRVEDGTLVELTRLPMGYKASPEILQIISSAI
AGMTTVVHPLWAAPPLVRIDVWIDNIRIAGSKSDATLWEAQVLRNADSRCTTMGEDRESG
ATQYTFLGVQFDHTLQTVSLSDKFVRPVCAMPSLKYLTIAEMEVVASRFLYAAAILGTCS
CDYYFFTKAVQQRLSALNRGIVQETSPANVPSAAVGLG*
>TCRU_4802 Mucin-like glycoprotein, putative
MMMTCRLLCALLVLALCCCPSVCAKNTELDQNSGSNGNISSLPSHAPATNSVSVAPGISN
KNVTPGDPANVGPSPSQREAVSQVTAPSGPSSNGLGAEPGKVGGKGSESKDTIDVQQGED
SDDKAGTEIDTNTSADQKDKNARVAAKTTTTTTTTKAPTTTTTTAPETTQAPTTTTEAPT
TTTTRAPSRLREIDGSLSSSAWVCAPLLLAASALVYTAVG*
>TCRU_4803 BNR repeat-like domain/Trans-sialidase of Trypanosoma
hydrophobic C-terminal, putative
MLVTLPVYPKKDDTDDNEKEKGRLHLWLTDNTHIVDIGPVSEEVDAVASSLLYKSGDNTN
ERLIALYEKKKAEADTPSLGMVSVLLTEQLKRVKEVLATWKEVDDRVSKLCASENAEHDS
STANGCSTTVKITDGLVGFLSGNFSDGTWRDEYLGVNATVNYKDGAAKADNGVTFKGRGA
WAEWPVGKQGDNQLYHFANYNFTLVATVTIDGEPKSGSVPLMGVRLDGEKKLMELSYDSE
KKWRVLCGDGTTKRLKSIWEPQTQYKVAIVLQNGTQGSAYVDGQRVCGSAQRGLEAAESQ
EISHFYIGGDGDNTERKDVSVTVTNVLLYNRPFSFSGENADVEEDADSPSVEGEQIVALL
ATKPSEAPEEKTALQRPRQETEAQQITTGGKPATTQQVPTAPGPHAVGGTTGDGGNVYRS
GLLPLLLLLGLWGFAAL*
>TCRU_4804 hypothetical protein, conserved
MAMMMSGRVLLVCALCVLWCGLVSADAGGDDFSGGHGTLGGSGVGADGRPSLPVGGDIST
GGTKDECSLGSGGGSPVSASPACKSLLSDAENPGGKALNDTKKGLSRVEEDPDAEQDPPQ
PGSHVVSTAEVLAPGQPNSEAQEQSSGKLRTEEGRNNGDGGTTVKEEVTGVESSDTADLP
PTRATHHKQHDQ*
>TCRU_4805 hypothetical protein
MQSHPQSLLSRTCLERRLRLLQSHPQSLLSRTCLERRLRLMQSHPQSLLSRACLERRLRL
LQSHPQSLLSRTCLERRLRLLQSHPQSLLSRACLERRLRLLQSHPQSLLSRACLERRLRL
LQSHPRSLLSRTCLERRPRLLQSHPQSLLSRTCLERRLRLLQSHPRRLLSRACLEHRLRM
LRGFRKILH*
>TCRU_4806 hypothetical protein
MPFGVGDGGAVAVIPSGSSFAGRSEVNSDASAFVDPMIPSDDDVNGCNSLVYKEAVGEMN
SGFKFPLISPRGGDKQNVIKRLKEGVEKTSFDGVRNEPLVVGDACVTLKNFEQMLVAFRS
DLVGVIRSEIEGIVFAPQNTEGDNHAALPKTTRDEMTSSGKKGGEVVGFSQALRAHLSNA
FRKYY*
>TCRU_4807 Nucleoporin
MALRPTKLDAVCEEVHGEFASCGIASLQELCQQVRLLRANVQRLASEQIPSLSLDITALQ
EPHLHLPLHTNFHMGMQEKKPTPGSVIFGAESLLSHCKRLTADCTRGSHRLPEKERPTQM
MYAVGYTPHYPNRKMPSYNSTKYTERKKIEEKKDTTSYTPSNPSHPNAQKSFNHCTDQLK
INQQINPHIANNKQKTTLEKTQTEQKTEPFGQAAADDKPSPFGQAAAGDKPSPFGQAAAD

DKPSPFGQAAAGDKPPPFGQAAAGDKPPPFGQAAAGDKPSPFGQAAAGDKPSPFGQAAAG
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DKPSPFGQAAAGDKPPPFGQAAADDKPSPFGQAAAGDKPSPFGQIAAGDRPPLFVPIAAG
DKQPPFGQAAAGDKQPPFGQAAAGDKQPPFGQAAADDKPSPFGQAAAGDKPSPFGQIAAG
DRPPPFGQAAAGDKQPPFGQAAAGDKQPPFGQAAAGDKQPPFGQIAAGDRPPLFVPIAAG
DKPSPFGQIAAGDKPSLFGQAAAGDKPSPFGQVAAGDKQPPFGQAAAGDKQPPFGQAAAG
DKQPPFGQAAAGDKQPPFGQAAAGDKQPPFGQAAAGDKQPPFGQAAAGDKPSPFGQIAAG
DRPPLFVPIAAGDKQPPFGQAAAGDKQPPFGQAAAGDKPSPFGQAAAGDKPSPFGQAAAG
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DKPPPFGQAAAGDKPSPFGQAAAGDKPSPFGQAAAGDKPPPFGQAAAGDKPSPFGQAAAG
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DKPSLFGQVAAGDKPSPFGQAAAGDKPSPFGQVAAGDKPSPFGQVAAGDKPSLFGQGTAF
DASRNTMFANPPGVFQVSFGKPSTTFATTSFAAGGGFGAPSAFGSILQNVHATLPAGSAL
SHIGSAFGSPGTYSGGAFGGAGVSGPAIGGGKLSALEGSGFGQAFSAFGNHASTVLGSFG
RKEGEGTFGAVGAHGTGSATPFSKTSTTFQSSSFSSIAGNYKAAPQFKSVFGPH*
>TCRU_4808 glucosamine 6-phosphate n-acetyltransferase
MSDELGELELRELEEGDVPSLLDLLRHLTDAPAVTTSALRAIAEARRQAGMVTKVFIHRP
TRRVVGTASLFVEPKFSRGGKSVGHIEDVVVDPSYRGKKLGQALIGDLCNIARSRGCYKV
ILDCAEAAIEFYKKLGFEARERQMRLDL*
>TCRU_4809 serine/threonine kinase, putative
MQQQGYIIDGQYRVIKLLGSGAFGDAFLVEHIRLKSLFVLKCSKSAKSNDLVLVEAKNML
LTTSDHVVRCHRAWIEPLDNRCYMLLEYCDGGDLEDYLGLAFPFSEPQLISMFAQLLLGL
DHVHLKHLIHRDIKLQNLLLQRSTGIVKIGDFGLSKALQFTDEVSVTSLGTPLYFSPEVV
SGLEYTRKTDVWSMGVAFYRLMTNELPFPATSVEEVCEYLGKIRAVHPCRLREGCYSEEL
GDLVMKMLTKSRTKRPTARELLALPIFAPVLCSWPWQPPRLKGTSCLFVCRPHSSVNVRS
QPSLKAERIGEFAYGDHIFVSCEHLKNEESTWYRVLYPLEGYCITATNNGKQLFQRVDDP
TRCSPIS*
>TCRU_4810 hypothetical protein, conserved
MCRRWFGLALFPRGLRRLSGFGSVLGTGTVPHELMRTLQEELKEEERRRQGGIGEALRNC
IGQSELDHLESPEADAAQRRKLDLMVESLFSRLPLPEDPMKAALAPTEEELKKREECEVL
KEAVREQYMRQKASNAAEEARLSRAMKRYEVVAERGANSDIPEHMKTPGEMNELRQEIDN
LKHQLAKLEKLLDSKVHGQCT*
>TCRU_4811 hypothetical protein, conserved
MPLFHRLFVSGADLRGCHTAFSSNFTQRRYWAKPKKRPKVGQGFHEKAQKWRDEFLLDRH
RILADSLRAYVEFSASKRTEPWDTRFRPFDRVEKDGVYVLMRHLMEDKFQLCNYHHRPVK
RLFCNVGLLGPQVTTKARWKPYRYATNPANTSKAERIFQKDKTLYTHGHND*
>TCRU_4812 hypothetical protein, conserved
MGGPARKKPRMEEVRPPKAQGCSDDEKGATSSILDDSLCAMEEKGAAVEEAVACPFTESC
ASDEENELLAEGEKLSGAALKRFLQRNFIDYIDQRKPFFAELEEKNTREHSYGEK*
>TCRU_4813 U5 snRNP-specific 40 kDa protein
MSLSLAVKPAGSANGGDSWFLSGHKNDVLGIATDGSGVFATCDVEGVGLFWRHDVSLHDG
GPTHVSRIATDGPAIVDACFFRLTRLCTAQGDGTVGVWNVETGQREHSFCRLSGRGKPMN
WTVLNAVTVANDTSIVFGGDDGFLVLGDFKQKKNGATINLRVPITSIAASGDSIFVGDVL
GNIRCFDARTMRSLYSLKGHSDVVNCVALNVGATSMVSYGMDNSLVLWDVMPFAINTSDR
LLHRIEVQQGESRTLLRCGWSRNDTIVVPAGDGHVVCVSALKFEGARATLPVRHREDSVK
SAVFVGDDLAVSSAGTEVILQRA*
>TCRU_4814 hypothetical protein
MGRRPRAPKHLLSAEDAPLGTFAVIDPFSRMLFVPQASMCDTHAMHRPGVPSLCRLHMEG
RCRQGMSCYQAHADVTVVNQLRMAALREPTCCATHGARSDAEGIATNLAIIVVGNDDPEE
FQRTTLAHIAVTKGFRILLQKQAAEGGVAEPNAVTVTVDSLCRLHYSGPCCRFGHECNYV
HLCRELVAEIHKRRNEKSEPHNRDEVPQPTQPSPTGALTTCYSPPRSNTKLLTLGPEADC
SIGVSPVQFFSCSGNFLTRPMAAGTVSLSGSPKLGTSPVLSRSYNSTSFGIVWRHNPYGG

GSSASSVVET*
>TCRU_4815 hypothetical protein
MASLDSSFRLGCSDPEATPSSPLRLIGGQQRGSVEPPMLFLQLRHLKAHAAVRVIETGNY
NDQELSSPYSSPKKPQKFSLGRSFRSVTSCLVSKVVIPSPEERYVAIEQTSEHTAAFVVR
YPQRRARAGGAAEEIGDVILSYPLTKLVDVSTFFLHEKGFFTFNTQPGAFDSSHAAENTV
RTKKKGSNGAILSSSSSSSSFSPNGDVGLQLVFKEPHVSSPPAKDNFQRVEMQFASSRER
DVWLHCLEEFYASFLLDSVRTGSEVSLTAPEVRGLIEESTRLMQQKPAPAVIERYIDFFL
FSSCPEEADGKQEVRNINPKDVPCGGIIRIDLGDNQFETRRFAYKKITNRSHLSNGNLEE
GEEEYLVICPTTVSQRVRRIRKQKVPTRKLRVVVEEEDFGNTFFLEQTTEATEAHRDSIL
SVCQSKSCKFHSGVVVSAPRGNSDFAITETIELHTSGFSERNRWLRWFELVLGKPVIYLS
RLREEKKTLEMILNPRQRASSLCLEYSSPPFTDDG*
>TCRU_4816 Low-affinity phosphate transporter, putative
MKFGKRFQEEMVEQWRESYVNYKALKQLIYHSELSGVEFSRDFFAMVTEELEKAEGLFQD
LLDELQQSHDELLEQDPDLPVMNPIRTLRFYRKRLHRDTRSTNGSGDSEVFDSSRASSTV
DPEPGRRGCIPSVVKSLFLLIIGDSHKRAFDEHAPRAKFAEWHSSAHKLQHFAELNLEAV
RKAAKKLKKHRRREGDFTIAIEAEINRSRLVTLMPRLRSLMADIDSDYERKFGDSLDQYK
NVAMQQAYHAKWQFVFLSAALFCLLMFLPILSEHPPAHNCVALFGLIVSLWITEAIPFFC
TAMLIPIVAVPLGIIADPHTNEVANSTVASGIILGKVMDHVQILVLGGLTIGKALARTNL
EAYAATALYRLTAHRPPLYLLGVMLWSGVLCAFVSNVAAPLLVLGVIQRTLWEFPEDTEA
PHGILLGLAFACNIGGMLSPIASPQNAVAMNVLRFHSVSFAAWIAVALPIVLFSIVAAWA
IILVVWKPFKDVKGIPLHVVSTESGKDTRVTDRVVVVVVSLITIILWIISPDVLFGDTGV
VALIPIVVFFGTGILAKEDFNTLSWHLMFLLAGGNMLGLCAHDSKMLDILAHSMHGTLVS
QPPYLTFVLVILVVALATTFVSHTVSAMILLPIIAKIGFLLPKQEGIFSVTPATLVMLSA
LMCSGAMAFPISSFPNVNSLLAEDSTGQPYLKAKDFLFCGTLITLLFLFCLGTWMLPLAY
VVLEGFH*
>TCRU_4817 RNA-binding protein, putative
MSVERGSNNAPAEEELQQPPPSALVQMRESRSERSTATTQRTPEQRPKNSEEMFPSNGSS
FSMSWPSCATDPEALRNLIVNYLPPMMDETQLYGLFGQFGPIESVKIIYDKETRESRGYG
FVKYVHYFSASYAANSLNGYCIAGKRLKVAYANVEAAWEAYRALRASSMMFSAQQQAALQ
NVFYQQMLLARQEEGDRR*
>TCRU_4818 Activator of Hsp90 ATPase, N-terminal/Activator of Hsp90
ATPase homolog 1-like protein, putative
MARVGEGDPRWIVDDRKDGHNVNAWHWEERDLSGECHEELKRRLKNFTLLKEDNIELSVE
ELSDISGDVTVAQRKGRMMCYFELKLTLKWSAGGDVSGKLTVPEVDHDNFRDEYDITVSV
TENDAASQKADALMRSKGRAAVRNVITNYFNELFETYQIGKNLKNASSLPPPATKKETTP
VGGNAKSGATATDSKDTEATSFSWKMRWRIPVEELFTILMNEERASVYTRAQAKIDPRSG
GTFEFLGGVISGFFVEVVPNAMIKMQWRLRSWPSGVHSSVVMALKKEEPGVVTLEFAQVG
IPEGELQVVQEGWRANFFDAIKMVFGYSMEYI*
>TCRU_4819 RNA-binding protein 29, putative
MSQVPQQRFGCYIGNIDRSVTLEVLRQVFSQCGVIIDCSLNGRDEDPYRYGFIDFASEDD
RARAMKYNGFTLAGRKIKVGVSKGNVGRPEGFNNTSSGNNNNTHSGGNTNTNNNNQQPQQ
MQQPQQPQIPPVSLAASFLPTVMHQQQQSAQLLMQLIQQGAIDVNNLTPEQQQILMASLL
PQAAPPAPGIPAIPPMAPMGYPPMHQAWGAPRAGAGGGAAGIGVVGVVGGGGGGGMYAGG
VPINRGIPYSRGPANPMPSEETVKLREVQRKQFLDVVRRDAEKYEKKLQERSVKEGRVGS
VSGSDDSSEDEDAEKRHRTQDKRSEDEKEGERNTRTTSRDDSNRHNHHQNTNNDKNNNSD
EHTTEAEKNNDPDNNSNNDNNDDNKADDKKEPECEEGTEEHKGLEEVREAESQEGKDDRE
EI*
>TCRU_4820 60S ribosomal protein L7, putative
MGKNPPKWLPGERVKETILLQRKSVEQLRADRVLRRDKLQERRDRHKAKLDAKRKRKLET
KKFISAQTILKHAQRKERQGSIFRKIGEKVRGRRQRMAPGEYKKSLDDSHLVLIVRARGK
QIPSEVSAAFRHLGLLKLYAARLLCLNPRTDPLVKQLAPFCIIGHPEPVQLEELLRTRGS
LWNEETQTKRFISGNLMLEQALGQYNILCIEDLCDAIVKKTEHVQAALRHIAPFDFHPPR
QLFLERHRSVHQKLEMVNQESFAAYLAQQLKGVAKREKKLSASNKRKAAKKSSTPS*
>TCRU_4821 synaptotagmin, putative

MIYLLINWTNILWVGTLAVALVGLKNYNEMTDSEHEKLVKALDKVRGVAPIPIVIVSVWL
MLRCLYALGAILLLELILVLSVVCYSFRKESRRAVMQTHQLHWLLQNTENLNSILGQDLP
EWLKYPNVNRVQWINTLISGMWSCIASATETSIRQFVGPLIEANKPSFIYEIVLKECFMG
TNPVVVHGIQHFPSEDNNSVIDLTLSWDSDMDVNLQIKMPGPDMHIHVRRFEMNMQVRFI
LSPHIPQWPCFGAISLSIMKIWVLNFDIVAAGISLDVVPAVGEFIDQFIRKTLIGMLQHP
KRITIPMVRGYTVTASREDSALGSLRVRLLRIEEWHQRYVSNREKTPFYVKLIMIGNDEK
NKKRLKSAIYKGLSSELDDVFSFVLYDTNGTLRFWLYFDVPGTDPCVGECEVPVQILMDS
KQTEHSCLLVKSSVTNLEPRAKLIILSEFLSYTGRSRTESTAAPSHAPSRSVSEAFMRKQ
EMCERPLDLPSVRSTANGSMHMSGSGSGTLFVTVERCTGLKNLEYVGVSDPYVHLRLRKQ
TRISPYVKSNLDPKFNFEAELEVYDIQTDVLHIKVVDKNDLGKDRAMGTVNIILNCVARS
PGDRISGEWNLDPQGKIFLTMSLLRH*
>TCRU_4822 hypothetical protein, conserved
MASRLLLHWRYLLDIRSLTVVVLFFMHSFAVYECAMKGHRENREGSRRTGNSLTDTNDDV
LIVGPIYSIRVHFLRHWPTGGETRDCEAVARAVSPADVLILAFPEGISLNQTEVVKHFVL
LQRWPWITPWSPSPGIGFNSTHSLPERILSFAERERSPVPVIFRLREISAFLGAKLTAPF
VYSRSGGDSIAACFLLEKEPLHIPIPSNGTPQKEIMADKNTSRILAMAANWSRAHNASFS
LFISPCRTNQLHVWDKRHFHFMENTTLWWVCAASDTFIELNVAAKSVTAISEV*
>TCRU_4823 hypothetical protein, conserved
MRFRRVLAPLVASPHRWKTQRSPRDEETMGESGAIEPDTSEAWVKNYVARAVREGRQTKE
SAEYFESIMNDQVEFRQYIQEARRLLNNQDPRMLTKYQQRHFAERLSRQMSGVAAERLMR
AHAEESNARRHTQDGTPTGENYWFEAGNTLASPSVPGFVKDEVMREMREDRKKKSAAFQE
SEELQAMADKDEAFAEHLRLQRQHLFRSNDDVN*
>TCRU_4824 hypothetical protein, conserved
MLSCRAALPMGFFDVALTTHVRHLSVRTEDFFSKEAISHARRVSWAPHTTEKKQGAFAKL
ARSNFSDPLPAGFTQEPYYEEEIEAHRLHHRPDVYIYKYNVSPTHMSLRE*
>TCRU_4825 protein kinase, putative
MSLNLAEAADERSQREMEKYLVERVAGQGTFGTVQLAREKNTGVNVAIKKVIQDPRFKNR
ELQIMQDLSRLRHPNIVLLKNYFYTVLGDHRHNDVYLNVVMEFVPDTLHRVCRAYYRRLA
SPPMILVKVFMYQLLRGIACLHLPAVNVCHRDIKPHNVLVDESTGDLKLCDFGSAKKLSP
SEPNVAYICSRYYRAPELIFGNQYYSTAVDVWSVGCIFAEMLLGEPIFCGENTSGQLREI
VRVLGRPSREELHKLSTSNVELNVPTNKSTPWEDVFKRPLPAEVYDLCAKIFKYLPEQRI
TPLEAICHPFFDELHDATVKLPSGNALPAHLFTFLPEEINEMTEAQRSQLVQK*
>TCRU_4826 hypothetical protein, conserved
MSTIEELRLAIEEENRQHQQTMEMILRQRETLQGVLEEQRQCFQELIARVTKLRVLKAEL
LSTSSDAAVQELKFDTGSKGVDELLYTIQDNLEGTALTGDTLLNKFYKAAQQILRTCTSN
KKSVFSSGSSGMRSSDIAFVTRNEIRGTQLWAQKHCKKCFTCDGKRLNLQPGEQVDEKSV
GLARLPDLSRIPGKDFYKSSIRFLRKMSGERMLEVFRFSAVVAMRGKNGIRITDSFATAK
RVTDVITAWVKKALATAEEEAKKAPWNEEATKNLLLSGAVEVFLHSLDANISVTVASSNK
THVMEANCTPMNFTVAILAPTYIPTVATLLELLSDAEQRAYFAKYIVQPLAERIGKFLGM
IDVVTFYTRVAINTVDALFRMTKAKWFADILGKGFQKSEKSVPQEKMAKKVHAVLLALSI
FGTSVEVNCALPPPGDITDTASTKNFLLNIAESFLRLLIAPSPYRIPPMNDPKSANLIVS
LLRAPTVFLEILNSTFSSNRRLPSTARVGVVDYLASPKAKIRHGLRLFSEIIVDVYRPYA
PNTGVVIADDNGKSGKPKATGCTPISDMPRDIVRANVEVADWAESLMKRLLSFRKNSTLE
TELTQGGKELIRRVMEVGDGTVFSAFLKDVEALEVEMVKILDVCVDVWLPFGSGAVDMMD
CPTELLYVRLEWSRHN*
>TCRU_4827 hypothetical protein, conserved
MGDAVVRAGLSCSATSFPEGCSTALDSVSVSDGNFSFFSSFDFCATFGALRLPSPAETLG
AIDFSSNGVGADRSGDGAAGDGANSGVGCCTDGLLAADDDLEGIPFSTVFCTFSFPVVTS
SVSGLSSVPCSVGDCSPAFGCVIVGACDFVFVVLFFEGS*
>TCRU_4828 hypothetical protein, conserved
MGDAVVRAGLSCSATSFPEGCSTALDSVSVSDGNFSFFSSFDFCATFGALRLPSPAETLG
AIDFSSNGVGADRSGDGAAGDGANSGVGCCTDGLLAADDDLEGIPFSTVFCTFSFPVVTS
SVSGLSSVPCSVGDCSPAFGCVIVGACDFVFVIVFFEGS*
>TCRU_4829 hypothetical protein, conserved

MAMTMTGRVLLVCALCVLWCGAGGGGCSETPQGPPDTLSQDDKNIDGDSNKIDVAGGDNQ
TGQTAASRTEAPSMQDAPQAESGAAANLPTAGAGKNSEETGQEKDEEDDKQQEEEKTKED
EIEVAKREEEAEEDDEEDKDDDVIDEEEDEEQKKKLFWYCFFTSGVQVNVRSSAGLLPLF
TVRITV*
>TCRU_4830 hypothetical protein, conserved
MCRRCTASFVRTDGRLSASRRQQGSLMTAGGTAASPGHQRWCPHLVAFLGLWLRIGTPQQ
GVAASTTETKTTPPLERVPRHARCGEVKRSARRLSDKTARPFRCGHSVDIPRCGDVHKSP
GTEEEGCITVWRLNIAGLSSVKKIAFAARLEQRPPDIVLLQELNNRRDVATKLYGHNGFL
QS*
>TCRU_4831 hypothetical protein, conserved
MIVESHLEVDEHHNAPNGPIEESNSKHTPELHDLSKEGSDVPLTGTSGNGGSAPARVLSP
RAQSAESGAGDNGKAIPAPRQPSDDEVQKTPIRKEEAPKKADSSARSFSDCGSDPPEAAA
MAPVPTPQPSVNAAAVTTYKKTFEGSQWASLLSSMHDTIMRTLLNEVSRATGLPDTKIRV
VEMKMEGDSTLVTEISLFHDSTKSAEDMDHALNAYAFEGMKQLLEMRSFSENCQPTSHNV
TLQGKATLSKGKTAASADEDDNVNGVKKDSPSGVHVACLNAADEAATSNEETVAENTHPT
GSPKKTGVVMRGKVHRDEARTKKTPSPTPVKKGLKKQKVAQRGKSPTEKMETSPLKGSTP
RRALTPRGVTTSYTEANTPNGPFTPRGAAKSYARASTPNVRRPGKGFLPFSSKFITTLSP
HAARLQYSPRPVGRPRTAAAAERETPRRRASARASPLRTYSASRGRSSEGPASVSKQVAN
TADSSVIKRPNGVVNRGGVRPIPPQRVIRVGLPTFPRTPRVSAVAVSSLPEAQEYGEAEG
FVGTDHAASTPVEAPPVHENDGEPHEKVAAMTPNSVGFEQ*
>TCRU_4832 hypothetical protein, conserved
MATVDRTPSTKSLTDLPKDADSAVSSLLDDDDDDARTRISPDGQVAPRGSRRSTAASPAS
SGAAQDVFRCPSEAVVSLEQHYLTTVQQLEKIKRMYHRLDTHNDDLEDSFVVLRDRLDAF
RSFVVVRLSRTAKELRGEVRFLRDTVLFLMEDFAENLRRCGRHIISRVKHAGGASEPPSL
PLRPFHLVPASDVHHNHPNSFCVHGNVNTMNTDPEKRKQSGLLSREALVRSPRSPRSAFP
ATPGSMAELRGALDKALRKQEHLEDKFIRQQQSYEKHIQSIKDLHAQKERTLRRRIELLE
RFVRRDVSGENFTDDSTRRDGDDEEFHEAGSNGRSPHSSKLFRRDLFANKNHGVDPRLST
SNAFNCTSRRSRLSIERTPPGEADALGEELCSKREGEKSGGWGAPSSVYAMAAGEHASTA
SDGNGVSRRAHRSPRNEGRPRQRFSAPGEAAAAMEPWTLGHDVERRVRSQMLSGGRKTPY
EGRCCRHFSPTSRREEKELEAAAARLLDVVSDAYTAQNDQHQRQREHPRVKSGVCEDDVV
SRLYYLRRPPPRRPGTKTYLSPVPRSGSVPRPEKFSDVSTVARGLWAEKLLQQRATQRLS
*
>TCRU_4833 hypothetical protein, conserved
MESEAAGLLRTAALERHMQSIQQSAPAARINRAQCVLVASCLRKIFNILSRLPDPSPSLQ
LLTVFSSADMLVQEMSCEGWEQTLQSRFTCSDSFTGLFGRMRKAWRLHSTTTWEWEHKNA
IREDELSNASKYVQLLRSGVLISIFRTAEEKEKGKKRGASVNEPEASEEQVICAFRRHQF
GSWKMSFEELTPPVGSAHDELVKSGNAFLLFDVHSGYRYKGTAVRLHELEENNGRLISPE
THTAFVQDMVVRATWSHPNIVPFIGAFTQKMSTHDGDAFVASVTPTPALGVIMRDVTGFT
VQSVVNDNVNASVASYIVCPSGSRKDVATYVSLHEILFVQRRRFTLREALGITLQVAEAL
QYILMDETQVPSEVAAAWIVVSPSNIFLCPIPPTGETRMAAGPERGRSPSCWEQECTVEN
REMEEGHVRFVHMPATGAFAVMYAPPVYVEGSPFSRWQSHPHAANPVTYALIQLFIALIS
NEPPYRLLGRQKDLAARIFKAAETMDGEHDSTTLDDEAADALPFVKVSIPIGSVIPAGLP
AEMRQLCERGLLLQHPSPESTRNGLTLEEFFGRMHAMWENAADVPVALTEQRCYEITGDS
PGVSQSDEFHSSFEMVSFRTLLDDYGDLSQ*
>TCRU_4834 NAD binding domain of 6-phosphogluconate dehydrogenase/
NAD-binding of NADP-dependent 3-hydroxyisobutyrate dehydrogenase,
putative
MAAIKRSLNVGVVGMGNMGVPIARNLGFKARSAMYLQIHSRTLSKARRVCDDLSVDGASC
AMRIHDRYSTMTKWCDVLLLALADVHAARHALLEDSEALIRNARKGQIIVDHTTVDIDTS
RECAYEAEKRGAYFLDAPMSGSPRACFNAQLVLMVGGHAESFQKMLPIFHMYADNVHHMG
GSGSGSATKMITQALVASHNAAAAEALIMAHRLGVEDQKKLVQVLDASWSSSTMLRRNAA
LLQDLIRNPDKAPPTSTASVDRLLEDLALLDASLPKRTGTTNSSENTDTDEPYPVLDTAL
RSLAAASDAGMGDRDIATVVHYVQAGEVELRNRRVMNFASADSMGRGEAVCGGAAVENAE
TEPVEFGKEDFY*

>TCRU_4835 2OG-Fe(II) oxygenase superfamily, putative
MRRTLSCLSTLVKIGRGAENVTEAASNALLESLQMHGYCYVQHPFIQKEILDQLHRDSRI
FFERYVTDTTAAASRPATMTTRFKQDTHQQPVLPLSPYELESIKSPSGFRGYHRYVGASG
LDDAIECFSVGREVEHPAHLREAYYKLSGWNEEEYKPLISRQTPWQVLLSHPSGNASSPG
TDTFMADYREMMLAYFDLCAEVSIDVLRHISCGLGVRPTIPQGGPDPASGYDLDFFTPFH
NKLDFDLQAKYYPQLGQVTRMNNGVEIKNARSAANPYGAKVLRRKGALAQPLLKEGADEA
KGDVTIRLDTHKDLSTITLLAQDALGGLEVWDDEDEKYVAVPVLNDALLVNAGLFLEKWT
GGLLEATPHRVRNVKDGSSRCSVVFFCLPNHDAKVEPLLQQDENPSLDAQEGFYAGDLMP
VS*
>TCRU_4836 hypothetical protein
MSFLDMSLDDVGSCRNGSGVGDNFNADGSSPHPCDVEKRPSFVLAADSPAKELPRQRDSL
HQEDKGPQEENGGEKAVSPSATWAGTNQECTQTPDICRGLLFHRGLELLQMQAEVDRHTE
ECGGSLEDMLAPVRPHPTVVRATGEVDLVPHTPSLFGSMARGSFLEERRAKEDAAAGRNT
QTHAMTLPPLKQKSQSSSMSRMKASLKVPPHKWTKSFSEQYKNLLLQREEELQKTAEDYE
RYAVELAKQFKRPPVVLPTHLVNSFADTNVIEAKDHKGRRDIFIKPFSASSRSFNRSEDD
FNDGALESLRMHEGEESFLQQRQQKQQQQRKQNPMNAFPQRAVSKVEEEKPSRFTIHSLS
NGDLRERDALRGLRYWDSEAPAVRKRVLPSRLLEERTNKAFHKYRFYSHRFGKLLKELAI
AIGGEEGVELLRRYETREESLPLPPKCRGDFFESVVDYDMLLREQERIMEAAENNLREYY
GYRLDKSPVASQQQSLPLLPH*
>TCRU_protein (LYR family), putative Complex.1
MRACRVCQRALCSKALVAPVAADVIERAGTNLPGIPHTYRVCRAYRQWLKLAVLCPPSAL
CELNEHAQMNERFVIIIRQKFREGAELRDPEQIAVAVQTSERSLAMFRFLAADGAKRRFP
EARPRLNLHKMGFLEMAKINYTQMAKEYWNTYVMRRW*
>TCRU_4838 dynein heavy chain, putative
MEEHHQRVRSDTRHMYIFSRVKDFFACGDGEVADRLTQQLDKKFVDGSPNFMVVHDMLEG
RGANTLIFTYQPDPNDSESTEDVLAVINPLKEKIPCLSKRCVYLLRPNNGKGISAKDPAQ
VVQEITMGSLDANILQSYENLLMEVYTPLFNKLGKWGKNSMAERNQFIVHLLRYADRVSE
LQQLQGESCVLDPVDAETWRLLQSGGVNKRGGINDPVLVHNLATTVEGWIKVVYDVVTRP
PNYENELNDEKAGPKTEISLWKNRLAKLHLLEEQLETVESPRAVQYLREAKSPLLQRWTE
VDLALTDALTEARENVKYLRSLDKYLDVLYSSDISQIINILPALIANIRMMYTIARYYSR
RECMTALFFKVTNAIVLSCKAAINPSGVRSRIWESGQDPEMLKELLRQLQLSVDCNKAYN
EEYKKAQELLARKDGKQFDFDELKFMGHFNLFTKRVDKLISVFSTVDQFMKLKTYHIEQM
EGLIPRFEEYLGHLRGKTTDILDIHDNNKFDVEFKIFEHRIAELETSMQVAINSSFENIT
STDNALQLLAKYQHILKNEAFAADLESKYLVIFHSYGMELENDQKTYERYKTDPPVARNM
TPVVGAITWARQLLRHIKSPMDKFKTNRTIMANTKDSKKVIRTYNKVSIALIEFEAIWVD
AWKRSIESSKAGLNATLLVRHEGRLFVNFDVEIIQLIKETRAIMLLGDIEVPASAKMVLM
QEQRLKTFYNELTYLVKEYERVVGRAGGARSKIVGITRALLQPNLDTLDAVFLPGETTLT
WMSMNVDTYLERVHKAIQELDGIVTKVNDIIHHRIQVNLKLISSTLLVNIFEDHFSLDQF
VQVQEKHIRQQCEVMDVKNREVESAVDDVIACILGSQGLSSDIAALDSATREKVSTLKGH
FNRLMFKAILTSTTRSLNLLKKRVGTRNKVSFLFAEKPFFEVDVQLINAEPYVFLNPSLD
EVQKAINQCATAVLSCSKYMTLWFDLGDDALSFFEEIAKNKEVVKVVLLLTGGIHGLKKQ
VMDYLNHFRKYEHLWKDDKDLTYEAFCAEEPSLDDYERVLREHVALYEEIEGLTPVFNIG
SLALQNKPLKTDLLRKVTEWKELFSNKLHAKAQLELDSLTHKMDEETHQLSAPIPDQEKL
EDLRVLMETLQEIRERESVVEFQFYPVQQAYALLQRFNVNIFKEEIDRVEDIRFKWRKLH
AQAELRSDEINHMQHGFKKGLTQEVQKFGAEVISFRNDYDANGPMVEGLKPQEAMERLKR
YQRQFDDKYRKWLTLMAGEELFGLPVHKYPELVKTKKELELLDKLYTLYINVLQKVDGYN
DVLWCELDFDAIAEEVSVFVNQCKRLPKSLRDWDAYVELKKILDDFMELQPVIQELKNPA
VVERHWQEIMRITGHKWRTDPDLFKLQNLVDANLLRVVDEVIDIASSSVREAEVETKFRA
QEALWKDQELKFSEFKHRGPIILKGDDTSTKREALDESSLAINSMLSSRYCAFMRDTIQG
FLHKLVRVSEIIALWVEVQSTWQYLEAVFAGGDIMKQLSQEAKRFAMIDKAWQKIMNKAN
EMPNVLEFCYENELLQNLPNLKEQLDECQRKLSLYLEQKRNLFPRFYFVSDTVLLEILSQ
ASDPQSIQPHLASIFDGLASVRFERIKPKEAGAQPYFQIVEMISGEGESLMMREPTPCVG
NVEDWLNRLCAGMTATVREVVKASVTELSTLLGNTNYLGSIIERYPAQVSLLMLQFFWTA
DVTECITKGVMRARGKESASSRAKCDSVKNYLVNLTTSAELERQPKRMRTNVETLITIQV

HQQEVFIDLQKASIKELTHFDWLKQARFYYKPERNLTIISIADSDTEYCNEYLGVKERLV
ITPLTDRCYITLSQALAMYMGGAPAGPAGTGKTETTKDLARTYGKFCVVFNCSDQLDRHA
MGKIIRGLSQANAWGCFDEFNRIDLPVLSVVAQQVSCVLQALKQHKEKFIFIDGQVTDLM
PGVGFFITMNPGYAGRQELPENLKILFRGVTMMIPDRQTIMKVKLASQGYSLDDLLSKKF
FTLYKLCEEQLSKQRHYDFGLRNILSVLRTAGAVLRRNPGKDEEDLFMRTLRDMNLSKLV
FDDIELFDSLLRDMFPGRQFVKGTHPEIEGELAKVIQEKGLQQWTPWVSKVLQLYETKLV
RHGIMVVGPAMCGKTRCYEVMTDTLSRISVPHRQLRMNPKAITAPQMFGRIDVSGDWHDG
VFSSLWRTAVRNAKKRNIWIICDGPVDAIWIENLNTVLDDNKLLTLANGDRIQMTDTMKC
CFEVENLANASPATVSRAGIIYISDVILGWKPMLESKLHATTSADGVILPSDVVMTCNPL
LAEKLLALFMPAEGAPLESTMTMKAAEFYQKECAVVMKTSVAHLVMNAFHLAVALGEEVG
DGVAVSNELALQIFWFSISWAFGGMLESKDRVKFDDFVRQQYDGLPPASEGLVFDFSLNC
KTGRWEHWSMFLEKWKYPGDDRLDFSTLFIPTTDSARLHFLANCNFIQKRPTLLIGVSGT
AKTVTMEKLLLKIKTGSETSNFRKLNFSSMTTPQNFYNALDDMTEKRMGSTFGPKNCEML
TVFIDDINMPEINEWGDQITNEIVRQVVESSMVYDLGLAGRRKELRGLVYMAAMSHPSGG
KNDIPNRLKRHFSVFNVPLPEESSVQQIFGVIFESRFCNDNYARGVQDIAKMLTQMSISF
WRAIGKRMLPTPDKFHYFFNLRDLSRITQGVMMAGMFNDPDRPEKRSTSKPWETITDAVS
LVRIWKHECSRVFSDKLNSVQDKRWFDEHLQECVVQHLSQTPYKDVIEQVRDPIYMANYL
RDPIIDPETGEIVEPAPRIYEPAPSMEALQERLLRFMRAHDEQSRVKQLKLVMFEAAVKN
VSRISRVLSMPRGNLLLVGVGGSGKQSLTRLAAYVNSQDYATLVLSKGFGVNQLFDAIRE
QYIFAATKRPVTMLFTDNDIKQEIFLEYINSFLSNGEIAGLFASDQRDSAINDIRPVMKK
DPFVKFDDMNEVLWNYFINRVRERLHFVLCFSPVGDKFRTRARKFPALVSSCVINWFFPW
PKQALLDVSSRTLESFEMATDEKHKKSLVELMAEIHSLMLEKSEEYLTRYRRSVYSTPKS
YLGFIDSYTSVYKKKFDELNEESSKINKGLQKLHQAGEDVRVMRTQLQEKEVLLQNKRKE
TDALVREIEIRTAEAEKKRMEVEIVKETVARDAAIVAEGEAEAKKDLEAAEPALLEAIES
LNSITANDFTTLKKLANPPALIKRIFDAVSVLLHRPLQPPGAEEVKGALWITDSWEFSGR
QLASDSGTLDNLRSFGENQKDYINEETCELLLPYLWMEDFTQERARKASGNIAGLCTWVR
SMYKYINIAKIVAPKREKLRIATIKLRVANKKKEEQEEELARVTAEVERYNQQLAEENAK
KQALEDDATRTKQRMDSANGLIDALSGERERWTRQSNDFKSLIERLIGDVALSCAFISYC
GPFNSEFRHQLLYKNFYVKCRELKIPVTSDINVVKFLVDETTIADWQLEGLPADDHSVQN
AIMITTSAKFPLMIDPQGQALNWIRRRTESMDSKLCQLNDRTFAMNLQEQLDAGRPLIVE
NVPEEIDPMIDPVLEKQVVRSGKSQIIRINGEEMGYNENFSMFLTTKLPNPSFTPEMFAK
SLVIDFTVTMEGLEQQLLSHVIGREKAELNEESAKLSEDINSNEKRRKNLEDRLLKQLSE
SQGNLIDDVGLIQTLQETKDASAEIAEKLTTALETKKRIAGACEEYRPVATRGAVLYFLV
VEMSLVSNMYQTSLMQFDDIFDGSIQRSEHHPVASKRIQCIIEYLTMAVFKYIIRMLFSK
HKVLFVLLMACKIQMKAGQLDSTAFDVFLKGGGAMQVDRSKPFLWIKEKLWANVLALSEN
VPRSFKQLPDLIMRNEQAWRQFIDSDAIENLPVPDINEKLDSFDRLLIVRALREDRTMLA
ANQYVSRTLGKEFAEPQHLDLHDVVEETTGLTPIVFLLSQGSDPTTLIEAAAKSLKKKIF
PISMGQGQEEAAMNIVNNAWTNGDWALLQNCHLGLPFLLQLEEKLRQQLLPGGKKMEIHE
EARLWVTTEPHNAFPIGLLQMSIKLTNEPPQGIRASLVRTYSWLSQDYLEMFRRPEWKPM
LFTQCFLHSVVVERRKFGPIGFSVPYEFNQGDWTASVQFLINHMTTIGENLKNPVNRDTV
CYMVAEIQYGGRITDNNDRALFKAITEFLYDLRITNPDRVRDAKLLGTGNNTNRTSHNAN
TGGERMEFSSGYAIPLFDDINKHREFIRETYPDVDATEVFQMHSNADITYRTRQAQEALT
TILDIQPRDAVVSGGVTREEKVLGMADGFLRQLPENWSVDRKLHIGDRQPLSIFAGQEID
RLSVTIRAIRQTCTNLKLAVAGTIILTPALQDALDYLYAARVPPSWVAVGWPSPNISLWF
TEVLRRHEQLDNWARNGRPPVYWLPGFFNPQGFLTSVRQEITRSHANEAVPWALDKVEAR
TEVRSSEFRPNQEPKAEDLKTERGEVVIYGLFLESAMWDKSNKRLKDPPPGDLFRELPML
LISAYNKDAPQQAAIAPTKPGQMKEKQKKQEYYRCPVYKYPTRSDLHWIFDVNLPVAEDD
AYWRMRGVALLGSTD*

>TCRU_4839 hypothetical protein, conserved

MTVSAEETNSPALTGSQNATETKSTTSPSHAETAPEAPEKPSGNGEPNQNREETDTPDSM
NDATTSHPAETTATSISTSGSGGAQKNENKVGNSDQRSNSKEPQDGLEDRHTDDAPTASE
TEPETAKTATTQKNVTSKPGDSDGGTAVSHTTSSLLLPLVVACAAAAAVVAVRA*

>TCRU_4840 Leishmanolysin, putative

MLTWCCPWQSAVGGGALDDCRDGCEEPRDCDDIDGMELQADDGSGRTLESHWSQRHAKDE

WMAPIGCAVCRTELTLAAPADLGCMRAKWEMAEPMRW*
>TCRU_4841 hypothetical protein, conserved
MRTAVTLRREERESGATHHTFLGVQFDHTHRAVSLSDKFVRSVRAVPSLNSSTIAEMEVV
ASRFLYLAAILGMRLCEYYFFIKAVRRRLSALNRGIVLETSPANLPPSAVGLGERLRHTI
ENNCKRIINSTEKASAAIITDASLHGWGAVFIPDSGDVKIAGGKWWRSPFLSCRPRRARH
AWPYRPFPPSCHAPWTFGRTILRCEERRVKAA*
>TCRU_4842 hypothetical protein
MEMSRSSDTFSASRNRVRADEINDEEDHADAAYVEKHNLQCLFSEMAEQLSEKDPKTEQE
AERILLEFLTHRKAERDRAALRLQFSHSFEVNLDNGRKIMRLQLGQETSTLQLEQKGRVL
KMDEAFSISLEQTEELTEMFYELGRFVVDGTKGEQGGFISIDERDVYLLAAGRECAEAGD
ELFNLAMLFSMDRGKKSEQTSGEA*
>TCRU_4843 40S ribosomal protein S10, putative
MATYVPKRSRDDVYRFFFTEGVISCKKDPLGTWTGSLGGKTFTVPSIQVMQLMRSMKSRG
LIKEQFAWRHFYWFLNDEGVEYLRKYLFLPHDAVPNTHKAEYKVLEREGGRGRGRGEGRG
RGRGEGRGRGRGEGRGRGRGFHSERDAYRTGAAAAPAVEAQ*
>TCRU_4844 ATP-dependent DEAD/H RNA helicase, putative
MTDGWDKCIGESNAWLFSTLQQQLNYEKPLPVQQAVIPVVQRALLSGIPMDFCLTAPTGS
GKTLCYLLPMLHLVTDCKKGVDHTRLRALVLVPTKALGMQVFRELQQLTRGTSIAVESLC
KGDISVKEEAESIVRFVTVVNSMPLPGDAEKPSSGDVYGDCDHDAAVDDSTSDDVARASS
RLHYYYSRVDILVATPQRLLRHLDGTPGLSLADLRFLVIDEADQVLAGNFSNFVAKVVER
FEGEQATRVGSVGGTRRLVQLKYNLHKMLCSATLSSHIARISEVRLRNCRHFALDSFGSD
IHRGDEGEPLPLTNDTRKRGKRRRGAKDGDKGQQDSDEENDDPVAALPISRQQLVRTSFA
LPPKLQEHVVFVEDWYRHAVLLKLVRAIIAKQSTGCAPAGTISPRGNNNKGNDVNSDASA
GGDGHGVNPEEDGILRDEENEVEFRALGYRRHKRRASTVTMSSPSEYPSCSDDAGKRILV
FCRTAEEARVMGHFLLSAGVKATEFTTLSTESERRRALLKSSPDACIVASDALMRGVDVP
NVGHVIMYNPPETLAQYVHRAGRTARAMRAGHLHLLLQKNGPSGTQKDGEVAVFKALSAA
VSRRQPVLYERHFFMFDNPPNAAVPATTAAGGGTREDATTKDRALLLVEEADGYLKKTQA
RLATHWSSAIEGSQKERMAKKRTAATGSESTIHAPSVKKERKS*
>TCRU_homolog transcription elongation factor.1
MGGKKKKTAVPIKKESKYKIPARFDCPLCDAKNSIAVRLVRSSGSARLHCRSCRAGAGKE
FPFLPLEKPVDVFFRFREELMRQDRDFLEEHQIDTNTTTAKTGLVQFMPKGAARTTAVTG
AASTSRSGDVAAMHRIELEEEEEDEENGLHFFAPEEASAEYGEDVEGGIAL*
>TCRU_4846 Mitochondrial protein 90
MRLAGSCVRSRGLLWSEWQVTWRLCRHFSTSTFRLALERVEVAHSQSYTRRGVTIGFTSS
AGSGNSGVSPSSSLSSSSASTGDVLANYVSFLADDTTAPAATKENGAQPLRSLRSVAAAE
ALFFKEEAKNYCRLCMEESQTTPKSHVVLAYRASHTNHACREVVLDSLALLAIRGYPIDD
IYLVWSDILYRESMFQRIPELVSPRWSVNQRSEVLAKLLSLLKKLNVLDLSLAAQAPDTF
DAVSQQMHHRRRVAFERLEYIGDNSWGNHLSNRMMVLFPDRQWAYSQNAYSFNCFRDACE
MNVTLEFMFDTLHVSELLPIGVREKLGTGKIKADVVEALIGELHVTLWGLEPQLYDSSCF
VEINGVGEARLSAVVQHCLTEIYDLILLSYVQELSGSAIPLAKEIAAERIWGQAYPPVRK
TKDRGGAARSGRLSTTTVIGVGEVRQLPALPSLFTVPTPLPDIVPHPLRQLRVVGEIPEE
TVCTHTNTDVFVRFVDSFSRLSLLDDRRVATMDVRRLRDVRFLSLKRELVPALPVNLEDV
AEEDLAADNATAPSLDGMNTTATERVLDLEEVYFRDAYYNLFPSPMSLEKDAELGEESNF
LVAVGTTRGSSGCLMDYEKQLQMATTVIYPPLRATPTVVPGDVTAKGERICSFAQSVYVP
PGTKTPSAGVVTDKNLHFGEFVFLPVQKETTREPQESDETPKKDVGEDASKRDGAVEEKM
LEAVVAGSEHDDSAGGEDEEEGMPGIVSHDLRMQAQSKWHRENPYFAVPSILTHTASCM*
>TCRU_4847 hypothetical protein
MPAKVKDDVIVEIDPATVYFTFSRIRPTFSCGRTIASTLDQFLRCEVTPNDLPLLCVLTD
KAGRCYSLNNRRLYLYKELKERGVLETVPARLRQMPDTRRMREKYTPEKCALRATLKREG
HAATASQEQRDDSGQDEAEERTEGEEGKKDGGKTFTMAPPTLLGWQEAAKARRKRNGGRA
TTLEEELLELGV*
>TCRU_4848 transmembrane protein, conserved
MQLHERVEETLIALLYAEDTVNGTWKSRGRDLAAAFEASLIEITGVPENASRLETLACVR
RSVNSFLADPTPAPLETFFLRVVTILHCYTVVASANVGSSQLPVGVKTAAVAIASAFFSQ

RLRVACVETNNNDDIDTNNNDEDDDSMKSTSGGAGEEDDLLQELHALWFCFLCVFLQQLS
ARGGDFTAWRQFFRACAAQHKKCDIKKENSHGTEDHMSGEDGSREEERIGMAAWGAVSEE
IFNATIARTRFRRTAILCKSFCPHLVAQAPGTTYQLLHTLHSFMSDWMRYKKEKCNDGEA
NEEEDIVGRYSEQMGELLGEGQVHAFLLSTAIGAVLSSTYILSTRGARGAETARWHLTRP
DTAWQTEAQWRQTNFPPIGRLLERLHIRSLLGVHHFAFCMQLCIGLSPTHHTEGRQKLAI
YLYLTEVCSLRVALAIYHFAPLQFPQGMLEEAATVFPGEGIASLTAAVDDYVQKAHCELI
FSAVDAGTTRRRHRHSAHAVNSGQSNEEELIPVNGELTGPRFAKMVFPVSCPTWGQYLAE
AKPTGATTKMASSSSTSAQMTNALSAMATSSRTPVGATGAFVKQTTFAQSVTPCRFVLDL
CEIGLPGLMAETITQMRTEMGMNVCLVPSVALPGVGSIPRKVLQHVQAFLSNKEEEKEKD
EENNNNNNKSTLRRYAFSATLRALETYFPLLSTIYAYVASQAFLCCLVEVITRECGQLLH
FVHEEQEGQYTAMNKHAEDKNYSVACRNALGLAERYLIHVVMPCMRVLAPSPILYGRVQA
LFLLMKEKGPVVKFGMNPAEFLHMNTWLHWLLRPTSISDRAPHDVLRSKELEALFAQSLK
RMTQSNVAHYRNLLQPVIYANPLLVARKLFQQAVGYGNNFLQIHTQLLKGAPAAVLTLVA
HEGLSIMRQYAEEERIGTADANRVGLIATFLSVLWRDNPHSFDGGMLLRAAEYALRREAR
ASIVFGLELLRSILHEMLDLTLEHEEQYSVAQLKALLAPSSTQWFAKGAAESFRRGRWNT
SLTPAILAATTSMFRVALQEECHVPVENEEPEEDEEEGEEEARDMHRANTTATPQQRHDD
EGKGTPTVKFTLGQCLLLHLCRLHSRIYTVQADLAGTMQLVLLTCARDYNVINDLLLCME
TILPQGPPEEEIFMVAMPHVALRITARFAVKEAQRKTSIGKKFSSVDALFNVTPSDIMSC
VERPASVTAIDSVIPFSILRKLSYYSAAHFVFDESVYTAATNEVNQFHNHATALVKRSIH
KDTGIHNNTHGSVHNNNNNNNNNNNNSGAGSSPTTDPTIRWLQEQLRQIRLEKEAHQELYQ
KCEAARAALLEELRCSGVLAEPVVFATSYLLPRALLSLEDTLFVYHFMKWLLNVTKATGN
DKDGCGDYERVVDIVLSLITATMTFFVGFTDGECKRVGFLLALLRAALHETTVEMPPFPS
VNDAIATSTPTSGGAADVSSPPVNFTTEALMALLEPKPRTFMSIFASYAAGMTDAANGVK
DQEEADSSGEKGAIQEAQAALPAFPTQLEAYLCRALVHLLLHQREIPFLHRNALLVLERL
TKNTPSFPSTLCATEWLIKAITPHAVRSSSCYASATAVLKVLKGNRHRMEEMLDSLASQL
VLQTGPPSKNGVEKQIEAWQKLWKSREAYVRLLLLEDIAAAERRGETEAVVSANIGGMGF
QAEKSVEDEVADIEEVEAEAPDDDGYANGIHVENEEEQDARELQEEAEDDDVTDDHSEPR
SFSLTDCCDNEESDVCSEQQDEETVEEENLVTDIPFNDEFSLREHAAMSHGEEMVETRGG
NDRKRSRDEEHDASESPPRTVSRLEMSLKDEEENV*
>TCRU_4849 cyclophilin 15, putative
MQATLHFCFPNRQNPKEPRDVSVRVLLQAAEQRPKATLNFFFMCTGQLPSTDVLNSLGIA
VGELSATSVGGGLRSSGLKPFAESTVVRIEKNVMMEIGSSMTKTIFGGFIEDEPLEGKQS
HPSSSSSISTAARSTHAAGMQQLRAGTILIGNVGSPNTNGSRYYILLQDVVTEKQRQELG
VYQPLGMVVAGLQALCEACGSAAVQPRTLAPLQAVPIWVSEARLQHRAPTPSSCINIQSG
EVAMATQGKGKGRERVVVARMAGHTRRRDEMEAEEEADAGGSGPAARAAQDGFFNLTLTF
PKRSDEEKQGVNGSQAKRMRTERYVTTADGAKALRTTAVEQADGEPFDYFAAQEIAFVND
VDIIAETQAARQQRRRGRQQQQQKRRNVRKFGFGGSMKTSKSNQGTDRTAAPKKKALLRR
Y*
>TCRU_4850 Protein kinase domain/Protein tyrosine kinase, putative
MACNYTPQESNTYFTALAFSSLRRDAIMDSLTTLFFDVQGLRLLAATVESHCVQRPMISM
QQIMARRNGNFVATVLSPQDFFKGIIFFKGRVVFAMRRLHSLYKGSFETTGEDSQLSEQL
LAVLRRWEACAEILISDDAFGTRLSELIAALDDVIAKLEEVILKLRSDEKLISTDNSAVV
AIRKAATDVEGAHIRETTLGSKWHNSYRMCHTAGHFLGPIRRLGFNVNAILSTTGLRCMM
AAFSLIIGLPVVQILFGLHAMRGPSLSMFLEVNRTAVIPSYVDGNSLCMLFSAIQFLVGL
GLGFAFLVIHSTATSNLAYAAVLQALFMQGAVSLRSTGRNTSDADHVDDEEDSDDKENGM
TLALQSSIKFEKDPQSTSPPSLPWRYEGYGGTLCGGTYDGGILEEYQRDHSSLYQAFGAS
LVSLREGHGSKTAVADIVESEEEMQLSSLGPGKDMDIDDDGTSDKDCSIRYLCMQAEREI
QMLFTDAPSGVADKYKDFSPCLHEDRSATICRHITENVQDCVCPLIIVEYVPHTVTLRGS
FKPGDTKELYPIVYCSISALELLQYRWMVDLAGKDFKNLFELHRKLKRSSHKNRVRAGDK
VTSLPALPQKSRGKPPGRLVLVPAPPSKERSHSEKRHMEKVEDMRCLFESGLEELLTLQL
LQKSSCFEVYAMSSNNVALPSSFCEPNQFSSSASMDKKYLVLLFIREVNGEPREISRKLI
GDTVSREEFEPHITLMDNSPMGHAFSTHLQKRPSTTSSGTVSILNAFGSLMKDGAEDDCE
SHASLPRSRRVRTAATGHRRRKRRSTLREYPSPISAERGHAVDYVTAQQLREKLNSLIAV
CGVELTSRVPEKFLINFVALMIFVNRVLKRYKRVNCRVDAENMFILLELKALENVPLMKV

GLRHGDDENSSSSLDFSPSDNGSRVHATNDIGISSILSANLLEYLRVCDATIHLTANGCT
LRFPYTTQERLALMEEAGTLQLSTLRGLSLFGVTATNALTEDAAAQSSGQMIHLHQYAAA
EEAFSEAVRRTKFGSTWRAEEGALSAPTNLKVDPGLKGDCNSSIAGFFGIPLVQPLEELS
GSSSGSVTRLPQVFGGGQSKTTDPNGHPPTLGIAQDSKSGYDVNQAPPNEWPSVSALARV
DNMFGKSWARSGSDAMATSTSCTSPLGGKLGGSYKRYLHVFLYMKEHRQDFLQSLWGRGH
SATVVSDPVVMKRYLSIGMNAFDVLFVEWSEKLVTPDIRDLIASETVKQTTILYLLTDDA
YSLPLPPGTREEAVLRMQEIGEIFTNFTIGQNVSHYIRQRRLKNEMIQIRWRKSYQIVRQ
IGGGAFGDVYEVYLFVSRGRLAMKRLFLNGASHRFLEQLNREVSIMSHMDHPNIVSFSHS
SMEDNAYCIFMELCDGTLDQRLHRGFPATESNQMNKPPLPRLSNGASFPVQPVGTIGDRP
DTNHDEFGKIPEPLTAREIVLLLRDVASGIAYLHSQGIVHRDIKPCNILFSGGVAKIGDF
GSAAEECAAKPLVNMKGTLAYMSPEVLLGEPYGRPCDMWSFGCLLAEVIGLRLGHLQGLH
FPALVELYTSIPKDGSLPITVANHKGGKLQHHFGTTTAQMILGAMKNAYNDARGKQCEGS
VQRRLVASTSPKEKMSSSSRNESFESKLMSSMTCDSSRAITYITTNNTTFLGSEKAELPE
SLVELLENLFCRDPRRRMTAEEVLHHPVTWDVEWMEMVIRAVEEICPLDADDASADASHA
GENSAEREEDLDLSISST*
>TCRU_4851 hypothetical protein
MTSHADKSSVRLFRSDTRESHLRGDEYRASVSESGRNRSRLSPRNTSMTRHAPPECPSEV
TWASKRSSRVTWKQAMNRRPPQDWSNSRPDTFHRDDRVPFKLSEVDESRKLDVCRLDECL
SEPQSARGGVRDSAAPLTRWHLDKHVQRSGMASFHTEEFLHDHDTVEDWELMLVSEGKRS
LLEQFNASKLQHSPEGGEEESSSVCPTKTKTARDTLQSARNTPHAVAPLRRHAAQRDHAA
EEEEEEEIIARFYADQHARRREPQPLMGTDSTPSPSVPDVRYTQPNRQYDDNPHVGNQLT
MASSSTIPQNIHDSHVKKEHARPTEDEPERINWEHEGESTEKKKEPKLSTLEEFRQYVIQ
QKLQSRSKTHTRNAGENATLTHSPALTKNTEKRKQNENLNDISQSMDNTHMPLLKSNTLH
NNNLISSTKLTLDINTTETKNPQDKSFANARQQDRDVVSHAEEAERSAVLAAAHRGATAI
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EAERSAVLAAAHRGATVIAGAEVLSRREQQDRDVVSHAEEAERSAVLAAAHRGATVIAGA
EVLSRREQQDRDVVSHAEEAERSAVLAAAHRGATAIAGAEVLSRREQQDRDVVSHAEEAE
RSAVLAAAHRGATVIAGAEVLSRREQQDRDVVSHAEEAERSAVLAAAHRGATVTAGAEVL
SRREQQDRDVVSHAEEAERSAVLAAAHRGATVIAGAEVLSRREQQDRDVVSHAEEAERSA
VLAAAQSVRFVWGACGFYGGENVLGLREKRDSIASWPLRVGALDPKSVNSVEELAAVSHS
GISLDTGLGVSDEGNACATAVSRVNDAKLDGILLTGGCELTQLNVRGGVLLAEETVSSLR
VEAKETEVQSDMLGKVAVHPALRTGEVRATTIPHGEPLGDDSDDDIPIHPRYTFFGCLLS
PFVCCMSRRQTQISRIEDPLSNE*
>TCRU_4852 hypothetical protein
MADLSTATTVVNTINVAFIVFDDYVVTGGLYKRFKLKASTMQLNLPPPPLINITFSGQPA
ISTGVVNLRVLLGSMDYVLVKHIQGEENHADISDNTDADGVISSGRRQRQLQVCEHAGQP
LGCFLVEAGGSYEVVRHDDLQWGLSSGSLQNGGPAVGKRKKSPEEQRGGKEELADPHRKR
KRERKQQGLEEKAGEVGKEKKRSRISRHREEKKSAMMAVVSAAVEKSNVNEKDDNDGNDA
PLREEKEANGQEMYAVQEGNEVENTAGEDATTPLQRVHLETPPSHSTPVPLEEKLKAREG
LVGKKAVSPLLVESRSPVLKEKRHRHSRESLSSSSACGPDEMKSQNQPLEQQDGEKQEEN
QRKRNHSKSATHRGSGVTGTVLEGVNGAATSPRSRASTADKRKETHPPRVGTTTTTTDPF
GNADENVGRNPPRKRLERGTSATVEAEKEVGNVYTDAHGSSHVSPNGWAPNESPALGFTS
VNNTLSQDFSLDSSSITSSADYVY*
>TCRU_4853 glutaredoxin, putative
MNKALDPAKAPQFLDMMLRRNQIVLISATYCEYCTKLKMLLIEMKHRFVSLEINIIPNGR
EVFAEVVGRTGVHTVPQMFHNGKYLGGYDEIVALYRRGELSATLERR*
>TCRU_4854 hypothetical protein
MSFLTQEKSSNASADSGGSYPPKTEDPLQDDTRESVFVSYEERLPQERKSRWRGAKKRSS
SGKKMSSHVASANESSSRMNRRDNSYNVVAATRGRCSKDKNRILALSPSQSVPSNEVRVP
LTSARVLRGSQFSSIAGGGMPAPSSPPSGNEGNGTARGKDPVRMDSTFSLNPEEPIVNFI
LTEDLPVAPSRR*
>TCRU_4855 hypothetical protein
MDGNMDYSSEGARFNRPNDKELVCYRAGPTWNEGRWAAHPQLPLSVGRVTPAPRHVNAIY
TTVVRRHSDQLQPKSPNVSGSKQGKAMAMNSSRFENASSHARSNNGLYPYPPSINKLPMG

MAAPHWSPVASRIIGWNYGNVSDIHVFPRDNERNGVRMIEAGPGAINNNQKRAIPAVSSV
TGLPVVARGPQPSLVEPTRFKENNYMRLRCCRRPKMRHLGNETWFQGTVHTKRVISPPPS
PKRGSCETSRKQGEIIKKKESNPSAKTSKFLNAFMNLFK*
>TCRU_4856 conserved protein, unknown function
MDIHTRDDPFAYGYGNGYGVVDNVETLDGLFSSTAPEKNSQEVGVLEKKQGFLPLLQYKG
TPGFCSPPRKSSSPKLGGNAKNGEDEDVKNAATTTITVARRPRVSLPNSDATRPLARSPD
GSPQRGQGAAAGNVGQLAIRSRVSLPHTKPNGLRESLSQPRQQSLSKALRDGTNKNDIPV
DAPPNGRRVSTRKIFFNATATKAQNNAVKKRGSEDGRRKIYLSGERARAPTEKTPATAIP
GAPGEAFIRVKHPTVSEAPAPGGKNTLKATSTAPVSVCTPSKSENNKTESIQPLKKTDGW
VEKKQDMMGQHVIAYESPPTEDGKHPPSNVPKIDNYGPPVHPSVNDHQKATKTREKSDSI
DHGYEDERAALHRSFHTEMWDTLIEVSGEKTVTSRSEEYGTERSHRGEVSRESTDDMQEM
HDHIDELVSTSTEAMVRLRLFSSAEKRWPEIEMWATAPLLMFTPPPNPNSSTAGVIEYAG
EQLELDWNLHNVVAQVFHHDRPRNLTYPEKMPLELEKTKTKRRPRTPRSFYGEKGARMPS
DWFRHALGNIKRVNSPDLEAIDAAEVSKKISHSRVR*
>TCRU_4857 cation transporter, putative
MSGQDVPVREAQQLEPIGTQDEAELSLREPGSTLEVVKSIQQFHELFQSGALSEEEFRSA
KARLLRLDGPLLSEASSRVSYFSERPRHRRRIGRGSKDSRFSGASTKHDERGKSHSSSSK
KNNNNTISSSSSSSSSSDSSKSTDFMIAPRAQVWHLLISESDTDNTIGTTSGATGVETSA
VPFLSAGDEKEQPSVLGTVPAWETMQSSSPTLQQRRYGTFHSQWKIQRMSLPLPQGRLRV
PLRSSQEVRVEYFNCLGASGDRFSDVMLREEELRPPYFLRKRGAAPMDTRQSGVDLTVLM
GQEWKAGEELTTSSDSTNSNLEMCLNWYWIDMVGRDASLRKYKSALRFLTKRFNICESFL
IDRDHSIVMPQICASPKVPTQFLVCLRVATPQIALDSDSVLELTNRWIIVVDLSQKLVIT
IHHMDCACLANMRNQWSSVMKGSNIAFQEFLFKLFHDAVNTYESSLEAHANLLDLCESKL
FFSGCVGLCKASREEEHRQDQLSDRKVLSYFANSSHSPFLTQLLDHKSKKPVDKSVMNMF
LYHLHCRTNAQYRTLSITQTVLAESFTKLRLCSKEHANQMCVHCIELINQSLEIRDEAKT
LLNLHISLQSFRSNELMAVLTKFSVFFTPCSFLAAVYGMNFTRIPEFRWDYGYYYFWIAC
LGMCLLIYVYMGRRGLLH*
>TCRU_4858 cysteine peptidase, Clan CA, family C19, putative
MNDPNDKFMAPPIGIEERTGGSCTSTDVSSPGTIPPSTSLESGQDMETALWPVEQQGGNN
NSVIFDVGNSVEARLAQEAVANVPLPSSGLINEGCTCYLNSLLQLLFHLGYFRAAVYRMP
EEGEEEDGSCSISEALKELFFHMQERTTPGHTKKLTAAFGWTERELFIQHDIQEMATLLR
DNLEEKMKGTVTEGAINQLFEGRGEQVVMTLDKTYVSRSRDIFYDIHLPLSPHVTLIESL
RSLTVKEQLVGDNKYRVEELGKEPEYKDAEKSYEFCRFPPVIWFHLKRFEMNLTSPSLEM
KKVNNRLEFPVELCLQEFEKGGENCEVGKRQNEEPKESAGNHAEEMTEKQKQQQQQQQQQ
QQPFSTNSPAIYDLQGVIVHRGSVRSGHYYCYIRQWDPEQESFVRWIEYDDDKVTVVSED
LAVSNNFGGCVTRQGRQSSVMATNNAYILSYVRRADCAKVLASPAADSIPQRVWNAFQRE
VLEDNRRLQMENEQRRKMNLVIFTDELIREHVEQFQSETFPRDIRASAKLGIELGIEKRD
PVRLVYEVIAAHKQLKALQLNPGEFRLWRSIANRSIRPNLPLKTYEACGDTLMAEYLDKG
EELNSPMTSIFVYLQLPTMLPPFPVTDATSFILQSQKSEGVNEIACSMLLRQSVKLDSVN
LYLEYGCYRRSQFFVYLELRSEEGFLLEYKDRGYTNERTVFNFKVNPELQNILGVVYRIE
MPKAAASVRVREIRLSAPATALPTLQPTYHPGEAVLPEANEENVLIFFKYFNYITCRLIY
AGSAIVPLTATIEACGNVLRQLLDEDGATTEPIQMLEEKHATVRPLRNDETIASARITSA
AVLIGQREETPLVCRYPRVEEYLNAILHAILVRIVHIKFEKNTTPHLWMFDSSGTSINGG
SVISNSSSGSSSSSSNINFNTTGRSGSAGGGGGDNNSNSSGILVGSDREGGVVGDSSVVE
FVLCTKDEEKECCDTSFYASRRFDVNEVYMRSMNTQWSYAEVCEVIGAASGFDPNYIRLY
RGDANAREQVSPEADPSPSTMSFGELLGGGRNCVLFFEVLPKPRRVIEAMPRVIVTVRTE
TNEPLYTEKIVMRQNASFGDLVRGTLERCSRMLRRRIPTTAAAAAAKDGNSGRINKNSDG
YDIHSANMGDGVAVPFRIASHYVIVVVDVGVGTIRKIIEAPMTPDGKCNCGLPIKAEREP
LTLSLLPARPLMENEFRLACCHGDWPGDMYGCQPFIFGQPFFVTINNATTVSGAREVLLE
YSGVPPGEVASSRYGVVMYTDIVRHFPNWNERLYLYWKNTENSSGRIPTLLLNHKRPREK
PGSRYVVQNNPALRISKK*
>TCRU_4859 DNA topoisomerase II beta, putative
MAEASKYKKLTPIDHVLIRPEMYVGSVDTSSSSMFVFDHEKGRMVWESLKVNHGLLKIVD
EILLNASDNIANKGGRMTYIRVHITEAGEITIENDGAGIPIVRSKEHKLYIPEMVFGHLL

TSSNYDDTSQNAVAGRHGYGAKLTNILSHRFSVCCRTKGKEFHMSWHDHMRRATAPRVSN
VDPREKNLTRVKFLPDYERFGLDANKISHDMKRVLHKRIMDLAAMFPSIEISLNGVPFAF
KSFADYAMLYSSPTSSGEMPPAPFVYESRNGAIAFIPSLTAGTRRIFGVVNGVVTHNGGT
HCNAAQEVLQSSLENVEKALKKDNKVIDTNRVLRHFTILVFLVQVQPKFDSQNKARLVSV
PTMPRVPRQELMDFLLRMPFLEAHVNTVTGQLADELNKEMGAGRRMSSKSLISSITKLVD
ATTTRRDPRFVRTLIVTEGDSAKALAQNSLSSDQKRYTGVFPLRGKLLNVRNKNLKRLKN
CKELQELFCALGLELGKIYKDAEELRYQRLLVMTDQDADGSHIKGLVINAFEALWPSLLN
RNPGFISIFSTPIVKVRLRDKSTHSFFSLKEFHKWQKTHGNVSYTAKYYKGLGTSTTAEG
KEYFKDMDKHTMRLVVERNDHKLLDSVFDSQEVEWRKDWMTKANAYTGEVDIDRSKKTLT
VPDFVHKEMVHFALAGNARALAHAVDGLKPSQRKILWAIMRRSGNESAKVAQLSGYISEV
SAFHHGEMSLQETIIKMAQNFTGGNNINLLIPEGQFGSRQQLGNDHAAARYIFTKLSSLA
RILFPSEDEPLLDYVTEEGQQVEPNHYVPILPLLLCNGSVGIGFGFASNIPPFHPLDVSA
AVRSMINGEAAKVVVRRLVPWAVGYQGEVRRGPEGEFIAAGSYQYYVDGRVHVTEIPWTL
SIEAFRDHISVLASKDVVQRIADYSGANHVDIDLELTNGAMTTYAECESELSLTQRIYIN
GTVFSPTGVLTPLEGDLAPVLQWHYDRRLDLYKKRRQRNLGLLEAELAREKSTLKFVTHF
REGKIDIVNATDDSLAKTCSKLGMVRVDDSYDYVLRKPITFYTKTSLENLNRKISETEKR
IDKLKKTTPVQMWLDELDRFDRAFEEHEKTAVATILKERRVNPPTGDVSRNLQQPRLELE
EVKVSSSGGKSVPMRVRVRKYVPPPPSKRPHVGQSVGGGGGSVRSSAAAVVAHVKAEKKA
ARARSMQKMLLDVVARQVARVLPRLPWFLF*
>TCRU_4860 IQ calmodulin-binding motif containing protein, putative
MELDSIRMQLRELRRYYEDDTKNDDDIIYSVYNWVKGAHVVAQLLLLEGRFPELRRCLDL
CRYVLHEQHAEEKSSNLGGGGKSPRKVISGAVGEDRLLMDSLLVRTSQLQKQYEEARKKM
KGRDTQYYMNKLLSTDKEAVDFDGTKNKTAAGKRREPSPPERGVSFGRRTRLNRWKVPPV
LPPLVTEVRPFFRHVVDKGPEEVSDARSRRFWTQSRMDITSTSSFAETRTGSAYSVPYED
SLREGPFSGASETTTVQEQPADIAHSDKSTPPPSTVLSASAMKASLQQKVLGRSGPALPG
GHVRPLSAGIATSMLPSGDVEYHLVNNVDAHAIRAAVAIKSASEAQERSVAVMQSLTNSA
RLLLQKEQEKKEQQQDQVTLIKPMNGVGICKKGSEQRGNNDNFSECAHHRTPSCNSFSAV
GRMGRGTVSSRRLRGAVFSPLNSPAASGYSGMRSNDLNVSEITNTSLNVVVETPEESKSA
YFLPLKKESFCLGDLHPQISQDAKRQLEEIYENYMEKNDELLASMRTMCRKVKDHGNLFK
PHEQVVLVEDTAVWKARRRQPATVLDRSVTAGSSISELGLSTIHTLDSKGTSNTSGGIAA
DLLTAPLAVRSITPPGGRMMGCGVAPSTGGSSKLNEWEHVHGSMQEWENADRRPKETCTA
TCDGLVLEESVSRGPGYTGFGEESPITTCSSTKCVSPLLSPAELRLARLKASTHVAFPDV
HEVVVRRTTKLVEQERRFMKVGSVIPQSQATASWSSSSLKPVRGVANGFKASHFLSKNVS
TKTSEKDLVAGQVETSIEPALDTRSGDKDEREKTIQKPLLIEEPYRWMSFVLSDAGTTEM
NLSLILATVRVQCAFRCFLARRERQRRAAALEEHFRSMALRVKSVVAIQRFVRGWLARRQ
MVTILLRLGYQLDQRIAHEVISSDDAGSDGAGNNLGLSTMRQRGASFSNSLLTEKKNSAS
FLSGGEFNDWSNHWRLTRMAAVPTLSSEYKLYSIPDTNLFTQSATRSARLRRIQKNIACR
VILRAFREHFQQVLKRWEREARTYMNYVTGKLDFMEAFGLKGGYPNFHDTVARQPLDSNE
TTNDNNVSQSLSFFLSVFPLPPERVLGDVVAAWESRMEDARCLGDFMTPLHHVKLSELQR
ILRERQEAEGLQRLMEEELRLQKEEEIQQRQRVKVDAVSMIQRCARGYRIRYWFSMQRHK
AEERNSIQHRRAELIDGSSVAFSGSQTCNCGGDFLLSLPALSATIYSEEQPVPPNVARVI
MEGIYRRHPMSFALDDEARRRRLKVVTLLQSFLRCRDSVNCLTDRYVDICATLIQRRWRI
VLKRRRALEKRKRNCMIKVLRAMES*
>TCRU_4861 KREPB7
MHRRTLRRLQQVVQNPPVGSANIPSPYATEGGHVPIWSIVNGFVQKRNWVFRNPEWCDLC
KEPVALWVNHHGRKDHALMDMHYTQMVEFPRRWNPEEILAVFLEELGLSVEAYQKYYGGY
EREHRNELYAMLVALEEAKMLHFGEPRDTYLYRMQGGLRGMDHQGALVLHRYILGPFMRI
YPNGHIQDYSNLVDFVTCAYNMETVYDLCGFYTLDKVALKADYKPSSPAALGLGGIAVHS
SATHGFAQQAMEKPQQSPQPQPQRHMAVGTGGRSAADMEEEAFSRKAVFVRQLLGQLRWL
TLPDEEHPAGHMFPQHLIFLGEICLKSLVAEIVAARLCEYMVRVEPVWRDHGYERVKLDV
DKIMRKENDILPEPVKFFYRPMSPKMDDLYSTNRGNLDEALEKAVVAPLSGKGA*
>TCRU_4862 CorA-like Mg2+ transporter protein, putative
MASTYTITEGSKVSLCQPDWVSRTPADNPGSSSNFFSASSSSVNGGLAAPPRIPPPGRRV
SRWFFPGFTAEEAHREGVETSADKTAVSSSRGEKRTLTSSASPKNTTVLPSLSTESRPMQ

PAGYNLAWRQEDKIERTHVVQGATKKAPATNITTPRGNAAPFSSTSLDDDLPSAFRDYQE
RRNQSIKAFLSTALGSAFTKAGMDSDGLRTSFSAAASEATKEAVGLRRISPKVLISFLPG
PDNAWNWVDISAHPTASLDEYRGALSQVLIDLGTHETLVSDALEPMLLPQTTVMDGCHCL
VVRYAEDVSKTCMDGFQELTNRLTILVTDTRVMTIHRTHCEFVENIKWNWLNLMKEHGMQ
GKTFLLNLLVKESVDTFNTALTCCIVEFDNYEGSLFSSKRQRSTLAREMYHIKRRASVYA
RVLVLTGEAYSQLCGALSIMPNDVQFQDVQQDIAHVRSLSEELHNNAESGLQLLFQLSSF
QLNELMRVLTIFSAFFIPLSFVASIYGMNFEHLPLLEDEYGHMYCIAMMVAVGGGLGVWF
KLRHFI*
>TCRU_4863 E2-like ubiquitin-conjugation enzyme, putative
MEPAVKESVSRIPLLKTKAGPRDNEKWTQRLKEEYMSLIKYVENNKASDNHWFQLESNEA
GTRWYGTCWTYYKNEKYEFKVNFDLAVTYPQAPPEIALPELEGKTVKMYRGGKICMTTHF
FPLWARNVPYFGISHALALGLGPWLSVEVPAMVEEGILKPTNKK*
>TCRU_4864 Nucleoside transporter, putative
MGLGFESWGEAYSYAAAIMCGLSMLLPINAIFSAPLYIMNYYQYVMHDPNAVAKHKNFWD
NALTYYSMLIMLVALIVEPLTLSEAFRRIPIRLRMLSALSMFWLEIIILMSVPAAGSTEA
GAISAIVCASFSSALGKSVFESTAYGLFGAFPSRFITALMGGVGVAGALASILQLIVKAS
LPQDYSGIRTQSKIYYGLMAGIHGITFIMVAGLHWVPFAQRYINALSGGMSSPANNNPDQ
AAENETEAASKANEKSASKATNGGDENADSGRLVNTNVIFVLKCVYPMLSACGFNFFITL
FLFPTIVVSVDPDDYWYGTVAVCIFNVCDVCGRFSPSLKCLWPPRWVVLVGSFSRVVFVP
LLILASYHYIPSHAYNYVMMVIFGLSNGYIGALAITLGPLTRNLETSGQRFVAGTMFGIS
ILIGGTIGSALSILVQTLRG*
>TCRU_4865 DnaJ domain/DnaJ central domain containing protein,
putative
MVVDTSLYDELGILPSAATDEIRAAYRRLALKYHPDKNGGDARAAEKFKKVAEAYEILSD
PTKRRHYDQLGKASAAGQNGPSAANFPFGSVDAEELFRRFFGVSTGGGSAGGPPSARKPP
DIVIELQLSLEELYCGTRKRVAVRRVRRCPHCKGHGTSDQSPLASCQLCGGRGQRVHGMR
VGGLVLQQMQVCSSCNGTGKTALKHPCKHCFMSQHSDNRVAGTVECVKELLLEVDPGTDN
EARFRFHGEGDEMPPPYQEPGDIIITTKALPHPHYRRISKDDLLLLNCVVPLESVFQKDF
FIPIEHLDGRILKIFPAEGTCAKMNILEPLFPHCLYSVANKGMPIRGDPQGRQGKLFVRI
HVVYPRALNVSQLTLLEEAFRYHLSDMTEPPQGKFVCLNHYSGNSAPSQKASSNWEKEEQ
QEAKRNSNSRVSTSSSTCQLQ*
>TCRU_4866 inositol/phosphatidylinositol phosphatase, putative
MIPGLPPAFDVECNRMEDVFASVKSRTVGKDGNLLSPEESWVLRELQYYENLYTEQQELT
VCLVTFNVACKKPPANLAALISLKMAEDTNRPVDLIMVSLQEVDMSASAMLKEETEASTP
WVVGLHAAVGADSRSPSNTPYYAFPPKQLVGLLLCVYLRRQLLPYMQEMSVATVATGALG
SMGNKGAIGLRLVLHRTSLCLINVHLAAGQSNVVKRNADASSIFTGMDFNVQKRQALIAS
VEDGYIISEYMDQNPELRPHDHDIIIVSGDLNYRTKLNYEEALELATRCDIERLLKHDEL
VSELANSHSPWWGFVDLTPTFPPTYRYDIGTNIYDTSEKQRVPSYTDRIVTWTKRKSHQK
LIIVERLQALVDIFSSDHKPVQALLRLPILCEVEEKKKNVTQLLNDRIAQVGLDRSTSAK
TTISPSLLDFGEQRFYECGARRVLSLTNVGECVALVKVFRQRNNDISEGAWLRVYPSNFS
ILPGEKKEVTVECQLHPRCMRWMGSWRPFEGRGRLSLSSMLLVFVNQGSVHLVECLCTFN
PSVFGNSLENISLLGNEACLTAYGIKGDLEKLRKVVRPQLPKELWFLCEAIYARGARQPN
LFTENGSAEACTEVMRHLDTCCEPIPAEFDIQSVATCFITFLQSLQEPVVPFSLYRAAIA
AGKARGRAPLVFVQQQLPPQHANVWIYVCALLNFLLRPVNARSNELTPRILAKLFSEVML
VRPGVLIHDSSGHREGSYNGIAAPPQGVLTSQPLRLQLQQEKEDAMSLIEYFLMPPPESL
R*
>TCRU_4867 hypothetical protein
MSSSSSSSSFLASAAAGAAAPPAAAAGAAAPPAAGAAETATALIFAAPSATRVATLRPAM
DSMTNESASLSTSIPQALQMASTSAAPGVGLFSDARAYAARYFMDMAEVA*
>TCRU_4868 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGGRCEEEVVPVADLPANSVSGSGTPDKDTDHTVHGGAG
VVSGEQSQTQKVEDSALGASQLQAGLPPESTVQQTHFDTEPKDSLSNSQSLQEERQGGSP
DGSSGRPAASHSQEDRKNESIGDQQRNNPPSPSSNNDFVSRNTEERREDTPRRAEILDAA
PSDEGQERENVTRSLEQPRETSTAAPAVTTQTISMTPPKDGESSGVKMSEASPQSTGTAN

TNHTTTPGDSDGSTAASHTTSPLLLQ*
>TCRU_4869 hypothetical protein, conserved
MRFRMFYDFLQLQRWERDVLSRDSRREGFFVRAFRRVPWSGVAMFFFIMVFFGVDLGAGI
KHTASQIREKKEEAMQSVELQKVQARQWSVEQVKNFREGEIPKPSWSEGGPRRASSSV*
>TCRU_4870 hypothetical protein, conserved
MPALKSLTIAEMEFMASRFLYAAAILCTRLCDYYFFIKAVRRRLSALNRGIVLETRDKNR
EDPYEANVPLLHISHYLSPVMAEAASCLDLKAFFFQVFVAAGDSASLSMPRGGRHAGGAH
TAPNGIQGQPRNSPDYYYFGICEDDDGGSPPLGCTSIGACRRLD*
>TCRU_4871 hypothetical protein, conserved
MGYKASPEILQIIITLAIAVVTTVVHSLWAAPPLVRVDVWIDNIRIAGSKSDVTLWEAQV
LRNADGRHATMEDRESGATQYTFLGVQFDHSPGGIPE*
>TCRU_4872 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MMFPNASKKRPSFANGPRILVALNASGIMSVNYGSGEHVAADNTDEASEPDATGHKSLVL
GNGVAVSGFVAEGDAGGLSQRNASGHDNKPQLREFTAQYSGSGVSLQDDCFALLNDAKLT
LRELTVDGTVLVRVYWVLLLLLGLCGVVTDL*
>TCRU_4873 hypothetical protein, conserved
MTNRVDRSRTPSRTSAGPYRNLSWPMVVGTYCDPPTVARSVEFASSTLECCGIAPCSAIV
PSIDVTFVMLTKAWGIRRAVLSLRPPIRSCAPPASTQWRSVTFSASANASIERRFTATMI
GPLNTTESKHAVARQPPTVTDSVSVTPPTQPSAAPPPPPALAGGTSNGRHASPTPPARQL
HTQSENDAVSASKHASAAAQPSHGTTLTEDRPAMR*
>TCRU_4874 hypothetical protein, conserved
MYCSFTNGRTDSRPTIYGVCNELRGSHVTDYQEELNIGAPVTSLDRGACTVDAVCFAART
SSIRGCECECAAGGYGDTCLPAAVPDGLGPLPLSDAKDTEVRCVHGGIISSVDDPDPGVR
GLCFVNVTFTAAIVLDLWGFDASQRTLNITLLQCVLMGLSIKGSGARVHVSVASSLLDSG
ALELEGDFGLSSLILVVGSTLVTTSSHAIAFLDFSFGANSTLLLLDNNIEANMYTVYFTV
AVVVDGGGIILKGNTLRATEDYRSTSAVYYNGVYVRNGGYFDMENNTMSAVNGVYLLGVT
TVSFAGLLRVADCNFICSTKVSTSALVYFDGSVTLEGGAQWRVEGNIVSAASVLIIPYFQ
HNIKLSDSGTTVVLANNRQVGSRVSFAKFLPSSIVVTLPARFVVGCNLRGDEEVSLYEGV
FPEGVEVFRCGTCYDDAACYMPGTESVDRSSCSCSCKDGWHGASCLPFEVPDTVVPPVPE
RAVDGDTSCVVNQTLTNLTLNMWKTHHCYVDVTFSGVGAVLTFFLNSMPLHLPINITFTG
CTFLDEAVLQFVGGAAAAESAGVLIRVSQTVMRSSVVVFALALPQHCDIAVTEVDAVQAF
EVQLPDTRITTLSVVMLRKVVLNASSLLVSNVKAQASSYLAFGLYSIGTLMLVSGSSLYV
RYCSFDGYMHLFYMQRLSVHSHSVFALLNNTMSSGTSLLCQYYAFRVSDHSVLRVVGNSG
SLCYVIRNEELWNVRESSWLDWRDNDVEVGAMLYDTGSAFVNIDGSSVVTLTGCKMGSTG
LSVPLLSQADAGYRFVAGCLTVAGRVVTTAAELALHGITNATTVAGCGECTKDGDCFAPL
TTAVIDCKCQCAAGGHGDVCVPAPVPAGPPPPPPPPVPPPPLPPPVGECISDMVYPEVAQ
AVGSGLSWLCYRNVTFSGGGMSLTVLVGAMAGDVANVTFDGCTWRDGAVLLLLGNAHAAV
GALSIFVTGNTFSDALLSPEGVFPPHTNITISGNRFTVTRLIPRPGLDIRRPSCVATNGL
AISNNSAVVLSGNVFQSVTASSSAIYVVKYALSVSWHSVFAVIGNTFHMDGSNSTLIHLG
GSSESFSLSVLNNSAVVIRGNVVTRPVKHFISFFWALRVESQSAVVFQGNDMQGSLVVFF
PRYSSNIYYNSWLQLSGNLCRVSPVVAFAVFNPRVNLRDSTVSVSGNRFISSTVTPTLIK
VPRRPRDITNGAIVAACNTVNGGDEAKYAIPSVYNATILNCSDPCTLAASCFPAYTTTAS
SDGCACRCAEDGYGDACLPVAVPEPPSTEGVDLCVRDVSVDVEVKVSFGTSVACYVGVTF
AADVVVDVESMSGSVRNVTLSNCTFLGGASLYVVGWLSDPPAGERADVLISGLELRSGGG
VVVANRFPPGSRVTVVDSVLIAEKRVAYRGVYGLGDLSACLVVHNVNLTGSVLTIARTHV
AAVLRDAVGVLFVGGVALSSRGALYVDGLSVQTALGLCVSVEGGFAASGGSVVAFVDSDF
LLCKHAVSVRGAVSVSGSAVAFLRSDFVSTEDYAVAFYSTVGLADGSMLLAKGNVHDGVS
REMLHAAGAVTAAGSTLSFVRNRALLPRMLSASLSLAAGAHLRVACNDAGGSVLSTAEEY
AAAGFGDAGSIDVAGCDACDGNTHCYAPGTASASMKNGVCVCACGSGGYGEACVPVGAPA
LPPAVGTASRAFFREGMTVRSVFVVPAGASEVTLRHVVLDGVSPVLYVPWMARDGVRIVV
QNVSLLNGAVLYVMGGGALRGAGTDGSDESGPVELSVCDVEALNGALVLTGTYPAGSVLT
VTDSLLVAARPTPLVYLPGSPRSPYAPVLVLSGLRLVRSVLVVSGVALVTVMTGGRTVVV
DGAVLELVGGGVALDAAVLGGEYALYASARVVASWSAVLRVSGSQVYAAHGLVFGSGVEA

SASAVVVNDNAGVLTDGALLVLRGSASFASGSWLSVRGNSISGRLLSVPSYPRASLLLGA
*
>TCRU_of Trypanosoma cruzi region 4, putative Dispersed gene family protein.1
MDGTVALVGAGRKFVVGCLTLNGRALRPINYRSAGIIGEFRSVACGVCDADVHCFAAATR
AMSRSCRCRCAEGGYGRDCLPVYLPRVDGCNRTPAMPLLSHTATLTETRSPTTTWTPGMS
TAQ*
>TCRU_4876 retrotransposon hot spot protein, RHS3, putative
MWRCCGWLHVALLRGRWALAASPTGVAVRPHGAPTTEPCGCHAQRHCDCGTKQPRLSFGA
SGTCWPQLGGANGMLHRTGVVMAARRGSCDGSDAAARHVVGSKVWSQWTMSSTNMRLSDF
LWNYVGGRATVDERLKFDGGDVCSGAG*
>TCRU_4877 retrotransposon hot spot protein, RHS3, putative
MKRAVKGEVIFDEDIRKLCDKGVNNLPGWSLAAVKVKTAVHNSNKHFLDAAAEEARNPTT
TSAPKKLEGLYESVHNARWSHVVEEVPGGEGTGMEVREGKPEQSWPYREADDVIEEDDAV
QQFGAAPPVLMVLASEKGWPYSWHTIQDLPKDVFVNREVDRVWRIVKGDVTEWLSPHGGT
DFKFERRVLIGAPGIGKSMAAGSYLLYQLLHCDAEKIQVVVHRFGGGDAYVSDKTARVVT
RCSDEDMCISELRSLRGHGRNVYIIYGVAKEGTPPPRHFAPTSGWGVIAVSSPKVANYDE
WAKQLQAARVIVNCPDETDVKAMCA*
>TCRU_4878 retrotransposon hot spot protein, RHS3, putative
MTVVGLRMIPAGGHHTTASTVRPFTDCLAAYFNGWGKLSRDMSWEFIYVQHEICRPMNDW
RRRDVVDSNNVGEIESREIAAFWKEEVRQYQVSISYRDFCGYAAHRSEEEPLKYENKLGR
ERGSSDFW*
>TCRU_4879 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MVPNASKKRPSFANGPRILVALNVSGIVSVTYGGREHVAADNTDEVSERSATGHKSLVSG
NGVAGSGFVAEGDAGGLPQRNASGHDNKPQLREFTAQYSGSGVSPDDCFALRNDAKLTLR
ELTVDGTVRVCVYWVLLLLLGLCGVVADLWAKECGIAIPHREHVPRSLRVFFYYLRFTLF
FLLLFSWNDKYRCCCFIQWSVAAHSHE*
>TCRU_4880 hypothetical protein, conserved
MAKGLLRVNWRACGGWLVLQWRRPLPGTTERVAVTVLANGTTPLVAGLGSKACQRVRVPY
GRDSMFRLLSGCHGLRRMLSRRLISMHSTMSVTKLPVHGPACTHQCQETLPDPVLVEGRQ
ERLALCRHKRGFYFCGGSEG*
>TCRU_4881 hypothetical protein, conserved
MMNGRVLLVCALCVLWCGVCGGGLAETTQGLLDTASEESESPKKNKDTDGSAGTDGPTAE
TKAPQAADRGSKEQEGTVEQAAASVPGVTGAGAGMETAPQPGREATESAKGTRGNKEETK
KEEESEKELEEGEEEEEDEEEEEEEEEEKEREKEKKEEAVTDAKKGISAESQEEETKKEE
ESEKELEEGEEEEEDEEEEEEEEEEKEREKEKKEEAVTDAKKGISAESQEQRSLPSGAEG
ASNQTKPKSAQTTDVNDPAAEGAGKRKEKQNENKEANPKKTAVEATAMKTTTATPGDSDS
SHAVSHTTTPLLPLLLPVACAAAAAVVAA*
>TCRU_4882 hypothetical protein, conserved
MGITHPVAYRRVVVSGSKDPVEYFVRAKGDGRTVVPAQSETKTGCLMCPVTLRSIASLDT
CRAGGSPVSVGFTANPLAPSEGHSRAFVL*
>TCRU_4883 hypothetical protein
MKHKPETIGAPVFSTTPSLTINTGNNASSATNNCNVLSQRVVCTHGVELPPSTAWQKWHH
SSEASLRHVREDASRHDNGSDNDGHDGKSGGSCLLGLCECQPVAYQRETEATAPEASPFI
APLVLVDQQQHEGGMERENVRRMLGGPDCSEVGLAPQPPIAVSKVSTPRSFAFMQFVVDG
KPYSMPPVYSPRSYKSEVVSMIHAEAEASREYRTVGTSVLVTAGYSGVHPETISHSGQPH
ESGEFLPLPKESMGKTSFKCTPRHWRANPHPSEEAEGNVGENLTPERAACKTSFLSPLSS
VAAFPLGEGACDKLLASRTSPRCVKMHGKGGGKKDTAEMEEKMEKGVFMTTSLLPGTSSD
LFCRGKQRPDKGVECGERILQSCEEAIDTTTKKLSSQLQKETIDSGRNPLEKTWVTSTNE
MDTGNSQCLVDHSVDSSMNMLFHFSVSSMGAMRLATYSMGASQGVVVGGGGGGGHHVCSF
HAQSKSCVLSEEKPCCCLTGKNVSLNGLYMRNTHANNNMEGSVHEEEPAAAVTAAAPANT
SPSLTLDASMDALFQVLDVPPELRLQPEGLMDVARFSLPLPMTPPVATGPLSFTVRSDVF
PAIPARDATRNEDDPLNMTSNIEEGTSICGSGANFRPLWFSPPHGLMERMGNGATGVNSV

SGDEPSSALCLHSPSVLFTERRCGQCGRGVSHWSPRLPEWCARHPHNEPERHEVSDSLKS
PMKTGVMARSNGTVEILLRSSRYAPGGSDTLASNNSLRRQAAYPHSGDGGNFQLPTFRSF
SYE*
>TCRU_4884 hypothetical protein
MIKEDSTSGLSYADVHHRLAEIDRLRKSGGTAEGRRRHLAEAHERMSQLLLLLRQQNQLS
ESPSARITEAQALMHRAVLFRDMGATLEEAISYHDAATLWFCVERERRQLNFPTSDDALA
NGVLCGAMSAAVLLRDASESRGSPMPRHDAALVASASDSSRKSHSGIHAGRGSGVGGCPQ
ETREGDVLLGEEASQMSYSNLLRAWRELMRVGTVLEDFQCLELAANYYELAAVILVKGKG
REILQSPHPSNSFAAAAGGGGDGRAGDDGNNSSTNTNASRRSSVSSSGKHAATSKSIAQV
LWGHVEGALYHMKEGKQQQQQQQSTAASAAGEVLDACGLGMDAAPLEVYSRTHTYEVILA
LHRASMVSALTQDYPRAMLYADTLMQTLTVEAEQQRRFKDDPPLFPHSFIHACNAEEWHA
KEGEDNTRGGNSRPTLKSKGDEKDEKECGTTDPAPEDHHNASLGSHSTLTHMAHPQTTLE
AFSFVATHLSRWVQLIVLKVYMVLIHDDSGAEHVTRTSHRSNPKDNDACGKKNIRSFSVC
SGTAREEKDDVGEAAMMAISTLFDLAGEVRRVERDLIRYSEAAHRASMDTIKIANAYENG
CFLSPSLSFSHCRVATRTEFSCPLAPHCPCDTHHHAEEGEEKKREQQQDGSKFVSCTKTE
DVLGNDDGDRKKKLAAKALAQRLLQSDALRKLRVAAASSKLSDYMQKQQQKQQQQQTTVG
GRNEEASMISNFDSKDEQNSEKNVLRDNSEDESDFEDVRLRRLAASLHVVYTRARNFHSS
EEDALSARTALREAVAIVDEHLAALGMSSRTLTIMGQRLLREVFYPKSATMIGGLRNE*
>TCRU_4885 myotubularin, putative
MSRGVSTLVCTQRNTQGERDEDVRDGLRLQESDMPQPEQTSSAVSCDRFLLLLEVDVLEA
VEGARTDAGYLRHWQQIRGAGLGPFLFLCASCKMKGSDGLQFVVERPVDMSLPHLVKRLI
RQSGGENQDRPSLRLRCVQSIPLRPKQHEPPLRDVVEGPSLFVTKENVVNASPVTVPAET
DSSGEVEEEDGVVKDVEEEAFLLSLLRQTSVWNVALLERCGVLTSSGGSPCPEWSNWSRV
DMAVRAVRYLQQATCTRPQHEGAIDIVGMIVEWASVMHAALVVHPRPESHVSQAGAGAVA
EEVFSRVHPEITPAQKYPTKNEKSPAPHGDSLVTPGRMTPPRPLLPSSLASVQFPASATK
NRSGSRGSGASVETEKTIREAVPLQTHGNTPTPLEMKRRLTTAVKEHDMPFMSVCSEVLE
AAFQLQQGHVQSKRSHFRNSDAGERVDGEDGHSAGADAGVISGRESSPASCGGMFGTVAT
SQMEPSEGCGQPPCSTPGNDASDGGGFLPSLIHRLVSIRHTSSNGRVAGQLSRIAKGDFF
PSRGMLDKEDLLRQRLGKTIIVRFYDLDPQKPQQQHQPCLNENNTAQLGLSASSIAAGFF
NNTGHPCHLFITHTDIILASVFDDNYPPQSWAATNRNNTAVDAFNSESRSSSSGGSSASS
GSSSRRRSMNNSNGNNSTNSGGGGNNRGRDNTLDDGAIYMKHMLVIPRVSLMEIWRPLTA
TDASMATVLRLQTRSCRRVWLAFQEENELRRVCMELNSGLNASFGNLFLASAQRKWRMTA
LALVAGDVLPSPHTPFYQQVLQNLLVAFADVESRREHRSTASSEQPSATDGTEVTPPLEE
EKAEARRGALKTLFHFWWLYSPMREYMRQGIPTRQWRLSCVNSRYDHFSSYPAKFVVPSS
LDDDELVQSADLRARGRVEALSYYYLNTGAGIVRAAQPAAVNICASASKIDVLKSYRRAS
GMRVCTFDLRSRIRAYANTIVGGGFRIMETGRYCSLANIHTVREAYEALSAAVLDNNPTF
LAVMRAAGNMATSRKDNTAPVSSPVGSSTVESPEKAAAAWIEHIHGLLRTATDAARLIAG
VSEEDALPPAATGAAAGGAPLNFMHSLGSVSANGFNSAGVNVGGLNDRFIPRSSTLYVWR
RAFRPIPFRTGNGSIGAATAGAPRWLEQQQQNLQSPPSYTQPDNRKNARLVIVNCSDGWD
RTTQVCALTELLLDPYFRTVEGFITLLEKEFVSFGHPCLLRSSTLGSHSDWSTGATVTDG
GFIDIHDSCRIPTSENCQSSPIILQFLDAVHQLLRLYPHCFEFTEAFLLLIVDLMHAGIL
GTFAVNCEADVYRWGIEQQTLSLSQFFAVLFATTIRTDRHQPLEAANDGENCHDVLEEGE
EQEEQEPTETGFFSSSAVPLHCFYQSCGGGTALGTVGWDSTPGSNPRRMAMTYDAIHHSG
LLNPHFSLADNKLFFGPLLDVVRQPQLQLWERFFLRHNFWCERAAKISQFSEQSASTVHA
RVVESTMAMTMPHSAQSLLETGPMLHPATGERRPCTNSTVLMKPTDLSEFSSLNKAQGTV
TLSLVSNTKRKAIGEGIFTPPARLTPNNTILPGGRSEASRSGNQFAPCTVPRSASHGSLA
AFSSSSSSFVGMQPQEHHQKQSPSSFLQRGASGPVISGGYTMNGHYNSFLGGGMTKRQSP
MKPSNNVEFVASPCVSSTEWTRHAQQKSASSEPSGAQVRTYNTLLSMLDQAFE*
>TCRU_4886 conserved protein
MVYFLARDVALCLLLDQYGDPTVVRKFVEESWRALQESQPPSQLQYALWLCHRVAKEVQA
DGATTLSTCHLNSDDSHHGKGDDEGRLASMALRIQAGTPLSNAVERLTVQNVIQWLKSMP
PSPSSLPRFGGSNNEEKHTDGGVVMRCETVEQLWVSKCLLRLVRRAVGMQLRHVLPPSKS
TDVRPGEKHHGCANNNNKSTEEEDIFRHDFAVLVPVYVCRCIQGLSLRQIVALCSVQIAA
VPRSDNNTTTTTTTSSSSSSGDEKKNFSRSSASSLGLIINPAVSPSDNPHRKEKNRRIEN

IQHAMMSQHYQEMVRTGSRSGSTHGSALQQEKQRESFASFLRDASIGFDMQIMALSGGAA
GYYLAHMRGLPAQVCIVCGAIGLLFMLLVDAVLFTLRIGRMDAQTRKEKSRRWKQLRKQH
NGCTQRREESEKLTGDGGDDVDTVTREKKNN*
>TCRU_4887 BNR repeat-like domain containing protein, putative
MLVTLPVYSEEAEKGGNRKGKLHFWLTDNTHIVDIGPVSGNDDDVTASSLLYKSGKSGDN
NNEQKEELIALYEKKKGEGKPSHSLWSVLLTEQLQRVKDVLATWKKVDGRVSKLCPSESA
VESTSPNTACSPNFKITDGLVGFLSDNFSDGTWRDEYLGVNATVESNEGGKKATLHASGV
TFHGAWAEWPVGKQGVNQLYHFANYNFTLVATVSIDGEPEGDTPIPLIGVKLNDSEKTVL
LGLSYNKEGKRAVLCSGGKTTELSSPWEKDTTHHVVIVDGQYAHC*
>TCRU_4888 hypothetical protein, conserved
MDSCTITGPAVDVRDIDAVILRGEYLSAVPGDKPSSWCLDTLPNNTTDARDPEETHLSAA
LHAALQCLGMQLHLRVTEKGNVRWSHARTERRVLGPLRATMRGNAICRDHAEVCTISATS
GSLLPIVLWVAM*
>TCRU_4889 Protein of unknown function (DUF3676)/Trans-sialidase of
Trypanosoma hydrophobic C-terminal, putative
MLYNELLGIELYELHASKVTIPSLGVEKHPTGQVTGTDVSAAPESNSKESTSYEELNEYD
PDEEEEEIVDDPVLAASPSEAAAGSSVSEPAIATESAGNDRPEDNAQLSEGETFQQATLN
EDNGSMQRGSDLHPQDPQPEELTEVTDVEMSSGSYAEEQPEEEGEANDRSGESTSPVGAS
LSMATAAASVYGEHQVQQSVELSAENNDVRSTGTRTTGTEESLSLEVGDGNFERTMSSDS
SLTPSKSDAETTSAENTDDVSRIEGDEFFFEDSKQVPQTVDTAPGNTNTTPGETAIPSES
NATTPSDTEILLEHAHYGDLAAMALIAESTVHVCVSRVLLLLLGLWGTAALC*
>TCRU_4890 hypothetical protein, conserved
MDRPLTPYEFDVAIRDFSLGSAPGPDDMLNEFPHHLGPVAHGTLRTMIHNSFENGSLPGS
WNTVDTIPIPQPGKGPYRPVSYGPTTLLSFSLNRRIDSPPCISDIAAPPTSIRVHTFAFY
IGLGDTCYW*
>TCRU_4891 hypothetical protein, conserved
MAKGLLRVNWRACGVWLILQWRRPLPGTTERVAVSGLANGTTPLVAGLGSKACQRVRVPY
GRDSMFRVLSGCHGLRRILICKLVNMHSKMSVTKLPVHGPACTHQCQETLPDPVLVEGR*
>TCRU_4892 hypothetical protein, conserved
MVWPFALYALELSFRDSSLVLAPGPGGVLNALLRHLVPAARCSLRAMSGTSLADGSLRSS
WETGDTTRIRRHGKNACRTENCRPLPLLSVLLGVSEGLVHRRLSALPARHRRQPRLTPRR
TVSDVVTPVRDKTARGLSERIAVECGRRRGGVPRCTLTVAALSQSRPASRLRSTPLTMGD
CWLWSAGSRACAVEPNTGCAAALG*
>TCRU_4893 hypothetical protein, conserved
MVCVRCRCWAAAICDCAVAVRGVAAVSPLLFSVLLQVSSTALGNSTVCDDDWPCALRPVG
SCSDVQQLVRVFDGCCDGVCVRPAGDGAVTAEHARAVMAAGGGPWPVALDERGT*
>TCRU_4894 hypothetical protein, conserved
MAEGFLRVNWRACGGWLILRWRRPLPGTTERVAVSGLANGTTPLVAGLGSKACQRVRVPY
GRDSMFRVLSDCHGLRRILICKLVNMHSKMSVTKLPVHGPACTHQCQETLPDPVLVEGR*
>TCRU_4895 hypothetical protein, conserved
MCSQYGPLRNSSQRGRPIAVSVANSCLRVATTQKFSKPPSAVHPRNIGRQATEDSIDSEL
KGLAGVYQHQRSPMGSAVELASNTALLGKVRLEVIGSVMLHFLYQVCQLHRRGTHTTARM
LVGTRRLQTKRSPQCHFLSDLTHDGGKADGSI*
>TCRU_4896 U6 snRNA-associated Sm-like protein LSm6p
MASVNLAERMQKPAVCFTVFGETHRGVLHGVDNNFNAILDKGGEQRELCFVRGETVLYIG
FMDEEEKKEGGGGESTNSV*
>TCRU_4897 hypothetical protein, conserved
MSSLPGVARYERLPTRTKIQFFWCSMLVMGFAYQFLKMTVLRVQPKREEQMYMHIKKIYG
DNLPAELIEIARKQREAQDALTLSNMIRTPTPGETAGALQHELDPRRIAQLKSRNGY*
>TCRU_4898 hypothetical protein, conserved
MRIYVHVREKVIALECGDGTQDVIWLGNAAMVHYDSSFGRKYGSPKCIQKEGGITCDPDA
RVCDLLDDNQHVFAVLDTDDDDENEATP*
>TCRU_4899 hypothetical protein, conserved
MAEGSQVVQVVCAVANGDGDWADVPRCVREAIVLALAGPQSQMAPHFNAAASSSLGGEAA

NRRQCSPWPEPRQEARVVASSLSEEMIQRGVQTFEDAAWVRDQAVRSFAQFHNSIEATRE
AVRHHLRSLWRTAIQLDPSLLRVIQQERRLGPRDEVPEDIIISGGTLRRMQQLEAMVDEI
EGSVDALRWTSVRFAANFLSDEEKRAMGLDPANLRPEDVSLGYTPQRDTSPVHASGQRPV
NTGGSIPQALLDRQQKTCEQENTPETISTPSGHKDDAMFSEMRRRYMNRIALLNEASMHH
VADEVMARRHSSSSKNVSSHHRVASASNQSSLSSMM*
>TCRU_4900 hypothetical protein, conserved
MASSDDDSCRALGTHPHTLPCLTVGVIAAGHCCERDGDTTASSLEKAPRSVGCGEARWFA
CSPTDRTAQSFLCGHSVGITRCGGVRKSRSPDVDGLVVVWQLRTSGPSPLRIALAARLAQ
HHPGMVLLRESRHESAPAARLTGCGDFHQACGGRAGGVAFLVRHTLPCERLLLVAPTAWR
PLPSACAHLPAPACKWWISVTLQDCPRRSLCEQHSSLSPRSGYLLPEFAPWAAGRSLAIH
DGRRGPRRHPKRHGG*
>TCRU_4901 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MAPDGTAVTPEVGGHSGEDGETVGGTDGQKREGEVNAAALSSSLGNISQGNNSDAGTMCG
SGLLPSLLLLGLWGFAAL*
>TCRU_4902 hypothetical protein, conserved
MYGEFVSALVKELNELMSPERDEAQDSVLKVNHQGRPTRTVGLRETGKRCREDSYGVRGA
VHTGGCKLSAGGRLFLFEVTAEDAGGAADDYGGCAPHHRQHCESVQ*
>TCRU_4903 hypothetical protein, conserved
MGEDRESGATQYTFLGVQFDHTLQTVSLSDKFVRSVRAMPSLNSLTIAEMEVMASRFLYA
AAIFGTRLCDYYFFIKAVQQRLSALNRGIVLETSPANVPSAAVGLGEGLRHIIENTIVSE
SSIPRKSHRPPSSRMRRSMDGEPFSFQTPATLKLPEGNGRRSLFLSCRPRRAVRLALSAF
SAILPSTMDVWVDNTSPQGAANKGSPKSHALTWELQRI*
>TCRU_4904 BNR repeat-like domain/Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MNDGTLVFPVEATKTMKEGTGKDGKTVSLILYSSETMNWVLSKEVPADGCGDPSVVEWEK
DKLMMMTACDDGRRRVYESDDKGDSWTEALGTLSRVWGSKQKGGKVEIVGNGFITATLGD
GDGKRNVMLVTLPVYSEDSKKEKGEFHLWLTDNTHIVDIGPVSEEDDVAASSLLYKSGSN
NEEELIALYEKKGGDKDKPSLGMVSVRLTEQLQRVKDVLATWKKVDERVSKLCLTSSAAK
DESTGTACSTDKITDGLVGFLSGNFSENTWRDEYLGVNATVNENGAAKADNGVKFTEAWT
EWPVGKQGDNQLYHFANHNFTLVATVSIDGEPKEGSPIPLMGAKMNDDKTVLLGLSYDKE
KKRAVLCSGGKTGEHSSSWATETQYQVAIVLQNGTQGSAYVDGQRVGNAQLALQDIKGSK
EISHFYIGGDGGSAGSQGDVSVTVTNVLLYNRPLSSEEIGALNPNKAPTSPVVPGIAQGT
LSQSPEEQPLSDLKLLNENEGVGGGSASTSASSTATTSSGKEQSAIQLPSGIFSGGKKDV
DGGSSSDDDPTVVTVGRDTVRGDGPPQTPEVSLSSAEDGETTGEKDGQEEGIHPQAVEVN
ATALNSSLGKLSQGNNSDAGTMRGSGLLPSLLLLLGLWGLAAL*
>TCRU_4905 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MGVREGTSLQEEVPPHLGTEVIPKADVERPIHEEEATSPEGATEWQTQEITAPLVENEDS
EDVSTASGNTSTLPGETKIPSESNATAPSDAGILLENGHFEELAGMALFAESTVHGCVSR
VLLLMLLGLWGTVALC*
>TCRU_4906 hypothetical protein, conserved
MTSNWSPPSDARPTIYGMCNEARGSLVTDYGEDLNIGTPVTVLDCGACTVDAVCFAARTS
SISGCECVCAAGGYGDTCLPAVVPDGLGPLPLPDADDTEVRCVHGGSISSVDYPDPGVRG
LCFVSVTFTAAIVLDLSHFDAPQQTLNITLLQCVLIGLLIKGSGARVHVNVTSSMLDTGD
LELKGDFGSILGRP*
>TCRU_4907 hypothetical protein, conserved
MQHNRALQRRQIRHVDEGVRHQARLALAEAANPQLRTAHKHAVAQRHVQSVSERVHRAQV
HRHSDRPAEHHRVEARRRTPAANRHRLRQRHATHAARRTATTAAGPRRWHVERQACLAQT
ASMAAAHAVRERRSQRIKARQRSRTAVARHHAHGGQAGHAVVAAALQHPAAGTVALHRHN
AARDRQPGDKRRANGSAARNRHGTAAQRHTRQRCHRRRLAHRPHVVQLQPPAGTDCPTVA
AHQRRRNRPLDAHKAQHRVGHREALAKHNAAAAAHNRDVRHGEHRVAPQTEARRGRHMHR
GRGKTARRLQQHAVKHHRARQQIHTAANVHRRPVRLQRPQHCVAHTQLRLQQRRRVQHKR

RRHRVRQPAQLGVAHRSRRHNRRVTDRHVRVCRQVVHKHKRAVAPGQPAHAHLQAPVTRR
LAAVAPHVDLRTAVAHAVPQFDAQRAGKHRRHVEHHSHAVRDGHAVHKHRVHGAANRDGS
VHRAAPQSQHHRMHRGHPRSSSNQRQRHKQRRTHSRNGPAPHTVPAARKRAHRRPHPSTQ
TGTNRALVVCRTRPVNHNSCLANPFLQMGNPDTLFR*
>TCRU_4908 BNR repeat-like domain containing protein, putative
MIKWSDPKLLLKKETLQTEDTVNYFFPGAGSGVLMGNGMLVVPVEGADKDDNSVSMIVHS
TDNGSIWTLCEDISPAKCGAPRVTEWEGSLLMIVDCKDGQRVYESCDMGKKWTEAIGTLP
GVWTKSQPGDYQDVSLRVDALITATIGGRKLMLYTHKASHPLEASEPNALCLWVTDNNRT
FSVWPVAVDNNKNWDLASNLPYSDGALHLLKERANEKGRAISLARLTEELKTIKSVLRTW
AQLDASFSASSTPTAGLVGFLSNTSSGGDTWIDDYHSVNAKVRNAVKVHDGFRFMGFWFR
GDMACEQSGEQWAAHFCKLQFHSCGDGDDPQSSEDQHYFAGRGAGRTHQHALHWAVVRHG
RYVGDSVQRRDNEIRQHLEAGERIPGGDHAVGRRQGLRVRGWCDCGEPGDATDT*
>TCRU_4909 hypothetical protein, conserved
MAVIAEAFVPLDSSSGKKIQVVESDVVAVYLNSLWGLSSLAAEVDNGTLRAHTVFCNMDE
MGSMSTVPSPKSVSRGNKVFLIAGSQKLHCKNATECVPGDLDIFNWL*
>TCRU_4910 hypothetical protein, conserved
MRRQVAFRCAKIEFISPKPEALIPAAEIKSISPTLLYRRLLKLYIRKFDTDHKTIVAAWK
QTKFEFWYHRNDTPEEAELQNIRGQQIFEAIRAGLVPVYRDSKTNETFFKYDADTLKAAH
NHIDPVDAEEFIRRYHDKISPEDVAEMKTMLKKLGRWKGPDELRDEDLHRVKQKVTRKAK
CTDPDD*
>TCRU_4911 hypothetical protein, conserved
MEEDNLRDLMNRLRFATGKAIEAPMPEATTTRIDEQCRLVIQQALCHHPALAMLQQTRDE
LKKHVMEQIQDSLQTEGSPSDDVGRLLGWINETSEALETERLSAVYSDPEEVFNALKRRA
LGDLGIEALPKHLQCGAGDLSPWNVLFTLVFGPLLTLDETRYRRVEMHIPNPTQAMVTDL
TEINKNAYSTPSWISLLNSLASFPIKAVRHVWLAALFFFPTSGPLVAAYLTREIEEAARR
RFLWDEGDEDDAKETYCSYCRVLNCFFRHLPLCFSVDLFCLFMGFLERFIRPDDATLDNV
FRTALQRYIGHCPASAEVWKKYIRWKSEKIRDAHLRREWVRKMYIRVLRTPLNGLNEIKE
DYEFFLKAEYRGRPPTESRLEERLVRARGAAVEINRFIGMHGNVHGGDALPRLLYLPRPV
TLTANNTSRVVASEKEEIMRRLEVELWAHWTSLIDRETGSTAYMGMELFGYERVRFFFAM
RASVFPHQAFSWTSLVDYCLGQQPLLSEAERRAMAREVLEKASFLLKGNFLMQLSYCDYM
LRDLADPDYAHRSMKGLLLQQRQSIVDYIKKEALVSLEGAMVALERIALLSINWMRWGSV
SKEVTNSQYIRLVARFTMHRVEFLSLIMGVIRRASKEERNFVPRRCLLAFNTFCHFWVEL
ELIRNQAKAEAVMILERWKDHLNMFCGSAKDKGWGLVDCGVDEYFISSCANLCRSDPSAV
QKVLGFMDEVRLTAVNSLSFLPEELDSLLNNIRGVRDMFFVVDADAGRVSSSPLPFCLFS
SRLRGATVPLQTYDHHLFSAGEAWHEEEKTYMSRHAEEASEGGSAAMNAPMGSSVELMPD
DARWIPHVPKRAHAAAETSQLAQRANTEQEVKQRRNKRPPNRRSLVAEGVLLHDLPTAIH
AAGCTTASDAVLLRKVEKMLVMYLPSTYETDVLFRDRAVGTEWLLQFMERMPAMQ*
>TCRU_4912 PIN domain containing protein, putative
MQRGSQGAVALPLLVASSGCASWADVLSSYRKTCELLRGVYQPTTEELYHGLSKMETSWS
TSLFYYGVIKGTCGYRQPPTRLVSAALERFKRSGNFYAIKRVMEEDVDTTTNEGARSMLV
YASFTGMWESAMALYASSERMQNNLADTRILVNILAPNGRWDHALQLLYRRSPPPLSSMF
VKPIVRSLGLAEEYDRMFRLVAASLAQGHKMDESLFSALLRSLQKEGRWRAALETAEELG
IFSLSREIAPKHAAVYGGLCDCLYLANPYFNFTLREIVDDITSRMHPRNNFTDATKKNEK
KFRLITTNEMFRSYKRYVSPLSSIYVKLFSLNKAHHRPVSELADEALKHGDTLLVLDTNF
LLQCTAKDLPLSHFYPPIRRQYPHLEGKPLEHLVIPFTTVREIYQIIWSPSTQLKRAVRN
LLWSRVVTFLKQPSVTVLTFASEFPCITFSAISNLAYLRLNEPAKEGDPDLRILNTCLAL
QHTLRLRKAASLQGVSLISEGTMLFSFLKYHVRRHHRDVRGMATESLLLCTLDKRLSAAA
DELGIQTFPQFHISENVASETTGKQR*
>TCRU_4913 SPRY domain/HECT-domain (ubiquitin-transferase), putative
MATLRACDRYPSGRTLQSSAPGTNVNLLSGEAYVNDNDALLLGSTTYEAKYVEPASLLKG
SLYIQDPNELSNTDEHLRIDKLTLSQLYSTAYVPYMQKRQCRPEMEFPLLPSPPDFDGEV
PTDPEAVMQYIKGLSAVYCKELGDPSPFQLYESLVGGLLENVATMTNQSSVENKDGSLNG
DMPLQLSLHDDMPGTIFASGFQSFTPAVEMVALTISMWLSNIRHLDNIGIVLKKVEKASA
ATRALSPSTVKIALETCRQLLVGDKCSQERKGEVCSLLGLVVLPRGEIQEVLEYVGILED

YCSHSRSSIVPIVLPHYEEVLRSFVLTSPMQHVMSSPVDAHHGETTKLPLMLSEGTSVVC
FCVSPCGSMLATATVSGILIFDTTTGELLAESLDAFLPRSLRMMQFSPDSKKLILTMVSG
LRHVVLNTGLLYLCEHNTEYPAIPTAVTSESIEFLFSPRLTSGRKSSLYFTACGKTVLDK
LGPSADRAVDNFVICSHINGDFVGNLVVLEADDDNFTIHVKGGIVTLTQGTHSCSGACPN
SAPWHFIFCKWNKGVWMLGIDNTLVELHGARTAQPKTTRVVRATVFDGIGHVGSLVAWSG
EGHDGRVIRKFSTDRVLESSVRPFFYLPLDEGEGFWLKELATMRALSIPEQSIVWDEAHC
CPCTPPESFDHNVRFPQQLLLQSEVLVSEFQVLIIIPSVHKGGDGIVVAVQNGSKSISRI
YRCPGSYSQSLYFLSRDESFLYSFQQRFSTFSVTSISTAARREHNLQESGILRTDTLRGS
PEWLYNEILKRICIDGVDLLRIPPEISPLRAENLRQLCAVLRGVQRDSSGVKLVAVMTLA
MVHFERLVLEDAESLSEIAASLNRSCKHIMEWFPEGFVRDVAAALVRAGAGQSLSMSDKV
DILMHADDPRTADVIDSCMYKESLYNIISFVINDNPSKVLLIVNGLLRRCRLEEEGLASG
RSLIHFMLWFSIISVQLLHANGQDMLISRLLELYVQHAEQLLAKRSWDDSMQQTVVHTGL
LPMLIGVARLCPAAVTQVVEMALLHLLDTLPREATKSLFPVSFETRQACDVVPTTDDAPF
KFVLDYKRATTVSIGKEPSDSEVTVITSNPSTAKPNKIVLSNETPFVKVCGSTLLLFGNG
ENSLTIVCSYDLCVGTPWSSVLREGILNLLLSAARHLTTTPRPCEVFLAPLLRHGLDTKT
LATHGLDVPGRVNESGFAVDILNDVGEGKAFVDDVWKNMRGSVTPPMRPAIQALLSLLIH
SGLNPQQATDELKLRWFSGEWGSKLQGSGKDAARQSLLGLAKWITSFVYYQRDSSPLYTR
RLSNGRRSTMESPSTTSRSASDPRGFTTSRRSTVRGVMQNQDTLDQVRALLSKGITPQEL
EDILVERTASALSIVRGLQLLSSLLSKLEKEEKRMLHEVLKTLWLFSGEGSGKHMIESLV
GSGTELEMRVRMAFHSVLETCESLLMNNCSREMSAEAMLTSPAENGPSTILLLAIMCHPW
DAVDCEFFKCNGNEDELAGILGHLEEQMNLFTCNVPLMSSWRNHRHQSDATGAAKRPNKW
NEMIGIAEHMSINCILPNGFSIAIPNLQLSLSEEGITFEKAVAGPLTLRADEAWPLPRLM
AWFGGVPRVFYYEVTLTSPCHIFALGLGHCRGGMDRGVDVAYFYENSGDTHDISCPPFEE
GDTIGCGVVATTRRIFLTLNGVFVSFMGTVSDKTEALYPVIRINNRERAGFTVNFGSTAF
CYDFRRLHPALFISGRPTCYNIASTAEIVLHYICARACTMRDSGKSCARTFLINCCELVC
RSINKVASIIMDIGVTKVENCDSRVEQAVVLSIAEASLMKFIAALRHILQIGKPYLLPEV
IGEMLFNAATVLMMLPLHSIQMSTISFFPELLPHIPHVQDMGASTKLVKTLFEHAKVPLD
TRGKIPFVPYWRQCDTRCMTISHVQVASMQPEAQRSIVLGNIIPRTGKVSFTVRVFRKGM
SKGHSLKGGYYIGIAVANLTPLSPSSNSQSWKAVKPPVVWALHDISPQLPHATNPTVKPN
VFHRTFGSGDAIRVVIDCDKQTVSFHRDNEFLKTLFTDIPSNVDLVPFVQLYNDDASVSI
SPGEMTAPISSSTLLSAASVDVLRSMLTLEPFERLVADGLCEELDEAAFPYVTLALFRST
PDPRVLQLCCRNGEKILVTVRRLTQWRVKFSVGNLAYYEHINNLRTASFLGTNGAFDVSD
VSVSLSGIERCISSLVSALRRLVAPLVTTQALSLLETQQRQNILEDENDQWDYLFHGVRV
TQFLSIQRLSQNILLLESPRIPVDYTFSAVLSHPGFYFSPRYCGRLATVPSGAENTTTPF
IAIAEPAVPSTGRFNLRCQLIRGHTGQILGGGYYVGLCVASFDWKRRDLNVGNPEVWAIH
DMDDAPWRLRHLYPGTRFQTIADPSCILVSGDIVRLEIDRDEGTMHAYRKGVNQEEVLVG
LIFDNLPKETELFPFVHLYNTDAVAVLLPSDGDRPATRTTVQQPHFALCFSNVKRNCDGC
VTQHLETRLTSRVWYKCNECVDYNLCHSCFTLCIHSHHSFTEMGPDPLVYSSSPPKFLAL
GMKVVIPGTTALYLKKCGCRVLEKHMNCVAEAKRNNAVAMWGIVFKKIATFTVMVDTSNG
EPLCPETPMFIGLGEAEDVTSVSVEMLRERCISGAASIVSLCSDSSLGRKLNSPSLSPYG
FRRGSTITIEVDTVSGVATIRRDWVTLGTQPFSVSHLDNPINLVGFVLFGRKNVVVSIYP
ETNQTIPAVVEEVTDTFLRVSCQGRVRLLRPEHCRVPLSPSQSPPTVGALGYVFVKKDLV
QCKVVAVEKDEVALHFPLDNVVQWVPYSQFLTGRFDAIAEERLLHREIDEAGVTMSDGFV
ISRLLIILSCLCENEALLPLVLSHSPAILSVLGPMAAVEISNDAPIEFIQEVRTAVDVTC
NCVRVMTGNRRLAGFIPSLSIGSHQCKPKRNMLMCSMEGPHRGKIFKVFSVESANSFRGV
DIADISSTALLNMVDCIPVKQSGGKPWWTIRNGLPCNLLEHTLRVTDLEHRLKNTTLEGE
WQGEIIIPRRSNGSISIRLMADCTGLATVNFPTGSRECVVFGEYMRYSRTVRLCLYHAAG
SKRCSGFLFQKGDKHPTFEAAVEQVESMFSSNKEPVFVVVMDGVIDTEGQRILGEWKPRN
DRAGSFVVNTFRRVTFISPTTELAQIEPLPECKDPVIPPAPQRDMASTMHRLVVLLARHL
YLLILYKGGEVGRDAFQCIIHYHSHPLTDQIISTYADTEQLLRTVYETLHLILDPNTKPW
DSTTLSLLITKSVLLRDGVATHFPSLLWDLFHAVVAATHQCGADYRRHLLKNVIGFVERH
RDGFHDVYTQLLSLLLTWVDRNVPSFSNSSESRQDVAAGVELVMSVEKSLLKDTIRNIPL
APLQCLIDMSNSFTEGVPLPKAVDLVGEEMAIRDVPPVEAHCAFGEFVEGLLKVGKVMSS
CAARTRGKYYYEVTLPDRLTAPFVVGWGTEEHTEVPSLHVGSDTCSFAFTGNELTSKNKK

EEYKPGQEVVPGSVIGCLLDMNEKLVAWSVNGAYGPFVPIPIEHGEMALYAFMSTGFCTG
MRVALDASQFGYVPDGYSDLSGRFTRVQITTYGEQPLQSVLPVRPLSFYEQLASYLSDTE
DSTMLKMQTSNSSFSAFSSVGILSPEAELLSRYPQLSNLSYEERKEHTKVIRVAESCMAT
ARRFIDLDSEVVNGRLSCAFLLMKHIVRRPFGRNLLVSIPPVEKNNNPPGITVRITELYS
TLPRTPEVALQHSVLSQIYKQIGSFTDKQLRQSPLFKVNLYIAGSGHAPHDLGGPYRQLW
TFLSEELMAHPDKCYPHTDYHRNPLCRYLNNSRRIALVPDSSANSAYDLILLNFLGKIMG
HMAAAKTPLALDFSPFVWKYLVEDTLTVKDYYKYVDSVVEKSMEDADFLMSGMAEEIIPN
LSAVLESLENKSESENAMVFKCRRLAEDCLTHSMDLQLNAIREGMWSVLPKRVIRCLSWR
DLERMVCGDSDLTPDLMRQSIEVQLNGIREQAFWRIMDELTVEQRSSFLCFACGQKRLPL
IRKIRVTENAESTEHLPRAQSCSSLVTVPPYDTYELFKEKLLLAITHEMEMELA*
>TCRU_4914 TFIIH basal transcription factor complex helicase XPB subunit, putative
MQCLFLEERVSAEGYVVLLAETFRSSFQRIQFFLTTIAEPTSRPSLMHEYRMTPFSLGAA
VSASIPVSDVICFLDEYVYGFCDEGENSRRARVCAFLEMCMSRYNLARIVIEDARTFVEC
DNVETAETLLLDPVVRSLCAEPPQIVPVVPHSLLVLRSRAVARRVAERCVLLGFPLQQQY
DYERDSGVRNINVMLKTQTKPRPYQIDAVNAAATEGSLRSGCIVLPCGAGKTLVGIMLLC
KVKKPTLILCAGSVSVEQWKNQILEFASICAHDTDDEMAAAEKHRSRLEGAARIACLTGK
QKDPVTEETDIVLTTYSMLVTAHKAQMRQRAAHASGLADNRHQKRRRANPKEKLFQPYGL
LIMDEVHVMPAEAYKESLSLVDAKGVVGLTATYVREDAKIQDLFHLVGPKLYDVSWETLA
SSGYLANVTCIEVLTPLTRQFSLEYMQRSGEDHTLQQRKMPLLVMLAAANPNKMLCVLEL
VRRHVADSSKILVFCDHLLLLREYGILLHAPVICGQTPHRERLMIFSDFQSTSKLNVICL
SRVGDVSVNLPSANVVIQVSSHGGSRRQEAQRLGRILRPKARASNGKMVDAWFYTIISTD
TLEMAYAAHRTAFLVDQGYTCRIIEFQPDELSKDEVDDVAVAAEAGDVVSLKQEKLRSAL
REKKLQCDSLTVPQGSVDARKIEYQLDLLSRVVSNWELEYHIQGLKQASSGHDGFPPDDD
ANASEGRDVMEIVPESDLAAIKREWAGGTRMDHFQLGHSCTSLQGLVSVDENFVYHEL*
>TCRU_4915 hypothetical protein, conserved
MDRCSITDPALDVRDADAVILRGEYLSAMPGDEPSSWCLDTLSNNTTDARDPEEASECCL
ACGIAVPCHAGASGSD*
>TCRU_4916 Leishmanolysin, putative
MHLRAQDALQVWSFVWRKRWVTVRIKALKTDPCDSRRHCDFSWPHAMNSLNENLYFEDHV
LSSAHGNLLAEETVPAAVKLHADRLLFQPLEGPLVVYSFANGSVCSRFTVTAGHRFTGVS
HSDMVLCVAAAPGGVWALRCAALEDGRPAPREG*
>TCRU_family, putative Se.1
MLDAVHGSFKVFFCDAHAASALSSSLRLHDLMEHGVTLLEDLMTPRQPIISSPAPYFFAV
EDASVSRVVEDWMATVPYRDAHIFALWCAPHRSPQQLVWAGIAPRAMRSKDIMLDFAAPE
VLVLHLSMQNRFLSCCRLRIDGPLWTLRRHVLWRLFTP*
>TCRU_4918 hypothetical protein, conserved
MDSCTIIGPALDVRDADAVILRGEYLSAVPGDKPSSWCLDTLPNNTTDARDPEETHLSAA
MHAALRCLGMQLHLEVTEEGNARCAPCTDWATITRVAPRYDEGNAICRDHAQVCTISATS
GSLLPVVPWEGEERACGAGRFHRHLLKKDCEGHPSPLRRASRTAAAPHRRT*
>TCRU_4919 hypothetical protein, conserved
MQCASQRELLTIQAPVKKRQRGCRTPLMNAGDGSPIQSATSGYYAQTLHRAADAPPDLSN
CPTQSSGRAMNLICQRRSTVVRRNTGSSALGQSYEESERGRSRNIRAVNVGAENVPSWAI
QNLMPHARTADERGELCGLLMAIDVAPSTRLQYARMLRSMLEMNRTPLDMMILGLQKIAV
RSVVKQARPVTKEETNQVIRSRSDWKERVVLRLAWITASRWFEIAALTAKNFTLEADGAL
ILDWSVAPKAAGADPHRASRFVKIRGQDAFDIINLRGTPRRSARLTNITNAKVERALAPW
DATAHSIKRGALRHAAPIVETLNLNPHVISQLAKHVDPFELPKNTV*
>TCRU_of Trypanosoma cruzi C-terminus, putative Dispersed gene family protein.1
MRTASLVLLAALCLTSAANHLAPSDGGARAYAAFLMLLTAVLLAATLYCAVLWYVEDHHW
QELREPQRGELDALLHDDEESDEELRKHHDRTSSSYASRTAGASSYRPPAPPQWERIIGS
NERNPDTIDRQPQPLGVDTHSNALSFLDRASTTRGSVNHAIP*
>TCRU_4921 hypothetical protein, conserved
MGCKAGPESLQIITTSAIARATTVVHPLWAAPPMVRVGVWIDKIRIAGSIGDVTLREAQV

LRNSDGRATMGGDRESGATQHTFLGVKFDHTHRAVSLNERFVRSVRAMPALNSPAIAEME
VVASRFLYAAAILCTR*
>TCRU_4922 BNR repeat-like domain containing protein, putative
MSRRAFTSAVLLLLVVMMCCGSGGAAQGDEPEPGRETSPGPRFAWKDGKGETVSSLRVPG
LVEMDGDVFAVAEAQFEDESGFTGIASELLKFNKKQKEELDKTKLKTQVLEECPAENKGN
VLPVKKRNAAAVQRVRMIPKARLKYM*
>TCRU_4923 hypothetical protein, conserved
MSQETLSAKQVNQPGVHAPEVKALLSARARYRTVVVVAVTFLLLACLFVISSSSSEQGEG
RYRPRAIVLIVPHLPPDMLEAAMASNKAPFLGLISAADGVYARPLAKNTELSSSLVTILT
GRVDSSATGLVGATSFLGKMKRAGRKPVVLAAASYWSAQVAAADGNCSRVGLFDSECSGL
RCPAATEAAYCNAAEKLLSCDGKAQLYEEDVLEAFRHLMQHDGDLLYAHANALCGTVSTD
EERMAVLSDISIMDSTLGKLALAVIERSSTTRESWLIMLVGAGGNGLERVPLVMVAYAKG
GLVRFGPIPEEATLADVAPTVLHWFALSSHGDAQRVRGMCSTGVAAISCETTTRWP*
>TCRU_4924 hypothetical protein, conserved
MQCGKVSSLARSSGDAEAGVSTGELVSVPVIDRSLSRAAAVFPASFALSFVAENETTAAG
VNDSALHDTTVFSDLSDEIQRVEARLSAIREEEARLMPKRTVPAVPARESGRFSSALDLK
TGDYAAELTASGSYRPNSLSNADTLSTEPDATFCRNSFPTAAATSTSSSGRQRSPLHRTN
ASLAYANDLTNTVPEKRHYDPLESAPSSIGGMRDSRVESVRPLVEPRDPVYSLVNFLRPL
RVVDIEIDTGVYEKLEVFAGEDMKGVARRFIEKHGLNMERAFRPLYAFLSSLKITELRNS
PLKSPKEKVSPPQGSKTGTATVPSHFGHFPFKGDSGRVKPSCTETLGHSSEAKKKIAACE
RAPGRHTFDHIRQHPTRSVSLDKTRRAAAANGVSQFAKQASDRIVREGRTAISGRSQRKN
TSPQHQTHRTSTPLNGLKSPRAVCQMDKTKECRRGNTPTWLNVEDTNVAPAIPVKNNIPP
EVVAVEVEVNRPTRTRTNNTVKVRSQNGVCNNFYSQRSSSELCRGLGTARSRKSSTLEEE
PVPTFRPSLAPRSKELVAKNPERLQGPTYARLHAHARRFSKSFTNANAECTGKPKILSRK
RENNSRVPVGQRLYDQAVDQQHRMQERQIKEKQRKDDEERFAIAGPQINKIRRPSLKERD
SQSSTFCALRARPSNHSRQNSCVLKSHEERELEACTFVPAVNPASVRIFNMVVRGRDSEE
EWGECEGNSQAHSVNPLPSGGSRSQNSEDVRRTSSVADRLLRHEQNRRKRLEEERLFREN
FDLATGRPLFRPFLGR*
>TCRU_4925 hypothetical protein, conserved
MKAIRFDKPRLALIGCCARVTKGMPRIDGFRAYSMEQGVAVHPRREQVNLTCRSLHSALG
SLLEDRQCLYRDAVLSAKLSPHRHELKSLLQRDSMPIAGSVNETELTKARLLDWREEWVR
EGDGGEDSLLAFYNAFLLSSAIRSDADVRLVLDVMRDHDHLEPNADTYIAIMLSLIAGSN
PSNRTAADVAFYYFGHAFKSRGESFITDKMWGTLFIVCAVLKVAGKIVDQWWDLFVKTCG
DASVPLPYTAVHGALTWCSANRDVERVMRFFHTANSRGVVVVAADDELSLFIGSGGLTEP
SKDKRVQMCQLKLLVKLMVTVKSIRMDGGVRELVVKDIRRLIEADLLKLASWGVINDLLS
GLSMPSAMQLLKFRSMDHPEGDGAIPFALWASLLRRCARDHHIDQAESVFLFIRKRFELT
GEQKAELVEIMMRMFATLPQGDFASAMALFLEHVLRHPSGEPAVRPNATMYNLLIRAGDS
RNAAMMTFLEACAAGVEVNEETFEAVMGCHRHTTLASLTRKLPHDYSASKLDEQLHIPRN
VDAHLRRDEAMKLRGKQLVDSTGEVN*
>TCRU_4926 hypothetical protein, conserved
MRLFYGSSLPPGLEGPTRGELRIRIEKLLLKDDLVTRGMSSDVPHAGSRPYAVPVDHCAV
NPLFWGEQNPTCHCVPATPGKPRGVVTLVYPLKTYEPQFREYLLHMSHSEQKGLQISVFV
PTSYSGRHRSIPVGKSIVALDTLKPSSPVSGWFTIVSDGAFISSTPCDKEMNLPGILLEV
GRLKMTFTMTFFARAPLSPTSHASRSTYKTSYEKNTEKEKIGGSEMMQDEARGEQEVQPA
QAPPIVSSESGVIAPINKQQLQQHQEKQQSHHQGHGGATDQIAKSSMMHENAGPALAFDP
RPSSSLFPPTAASINFNQKMAVGELLQKGISLRDKMARVLSHSTSFEDMAPSSNFLTFQP
LLSVLGGPPSYSLPLTGAEHLHGGLSIPPGSTESSVSSASVETVVSDTNELGIDASPAAG
AGADREKSGEWCDIPTGRRPFRLPFQSPGVSQKEDTYVEVDLSRIAFSSGRATLGMEEMR
VGIRLSRDVKTDEPVESYSSYVHRVPLARGAEHHIIIGFSVRSFSEDRSRMVISFYRVRS
APVANPPGELLLPVPASAQRVLVEEILLGMCIVGLHSQSRDIVLHDPISGEDPTQAHLCV
STRSGKLPLPEDSRPNVGAAKEGDAKNPTLRLEGGEKSQVLVNSAERHSPIETQRGTKTI
RPKVKYSQIKQSDVDLRSSSSSSSSSPSSSPPSSSSIEKIPRKVKVSASGDERIGASSCT
GHGDGRGVAPEPIYAHEQRPSNSLTASIPNTIMTKAAVSSVDQCLSPVELGALMDLHAPG
SCDGKKVPSYASDARMADTYLDQTLKKPTLERFRIHVSIRAGKELPMVTISHEGFTSISP

VAAADQLDIGVRSAVTSDGSLILVDSKHRVFKPPTTFFVVEDLFNGVDSRAASRGIVPDW
FVEAAVRGKFDRTLIVPESQSPQYDYESILSIPREAVFLRHAVSGSHATFRGASTLLSLD
DTISKASNSAFCLRELRLTLWHAVTETSVASSPDWKNDEERFWAQTALLGECRVDLRSLR
FLKVLDGWYRINAIDRVEEVVGYVRVSVRLL*
>TCRU_4927 Protein-tyrosine phosphatase/Dual specificity phosphatase, catalytic domain/C2 domain of PTEN tumour-suppressor protein, putative
MQRYPSENCEAPLLHPDGCNEECPSFVLQQDRGHVDSKSTGERDVFCDSIAEDTPFLREW
NPSLPPELSVVQYLPKSLRNAERAAPPACVASIVCVIEGTFMQLLLLLLFIFHCAITFYG
YFANVGETIIISFVVVFIFNAEHALMILNEGKNHFGPPPFRIVILITECFLLLALVLELF
ALIVWCVTAKTFANLIGLPVAVMTFYPRCRRLQLAFRRRVSSERRRYRENGFDLDLSIVH
STVLAMSWPAENFERCFRNPAEEVEALLDMMYGPHAYLVVNLCSERGYKNPGLFHGNFLR
YIMDDHNPAELDEMLSFVRKAGGFVRKDPEHRAVVVHCKGGKGRTGTMICAYLMYSGLQP
TAGRALEHFRAMRTAPGERFQGVQTPSQERYVRYFEKLLASMRPPFALKKNVHPRRITHM
ELRNIPFLWWEGGIGKLWFVVILKPSTERHVIYISNPTVSFNPHPPDDSVMRVRSSLHDI
CVPTEDSLYRDSQEVNLSTPISPCHDTFFVSVCNQRIESATFDREYSASVLREKKELKVT
LEARQLQSISPVVDDVVVKFYYAQRSPNPLAPPMQFWFHTAMEGNEIHLSKLQLDGPHRD
AKGTCYPNDFSVMLRFKNVVDKD*
>TCRU_4928 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGRCQEALLVSQSDVPGAIEGDRGQPQGSSGFKAPESHA
PGSETSVRDVQEEQDPSPPREETQLGTKGGNKVEKAKEKGAAKDAGKEGEVDGKSIELKK
PEDKLTSVEGQQLNNNEGLQPTTLNGLHGVETTTPSREILSVREDQQDLSSSLLPPLHNT
SPGGTPPSTPAAGRADTKSHENDIGKKNSQQSMVGDIGQNNDTGEKAVASTGEEEGSRFS
VTTIEEMSETTTKGDSGSTATITAMGTEIGTEETSLTNHPSQPSTEGARKPGTTSDGEAA
SANKYDTVSQNAGSTTAQTTNATTGDTAKKGDSDSSRTVSHTTSPLLLLLVASAATAAAV
VAA*
>TCRU_4929 BNR repeat-like domain/Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MLVALPVYAKNGEGKGHEKNENGKLHLWLTDNTHIVDIGPVSGKDDDAAASSLLYKIAGS
KDKNDELIALYEKKGGDKDTASLGMVSVLLTAQLKRVKEVLGTWKKVDGIVSKLCTNSIA
QDVTSPEDACRIAMPTKGLVGFLSGNFSDNTWRDEYLGVNATVKENDVAEQVESGVRFTG
RGAGAEWPVGEQGENQLYHFANYNFTLVATVSIDGEPKGDTPIPLIGVMMNDGDNNPVLL
GLSYNSEGKWRLSCGGETLNELSSTWDPQKQYQLAIVLQNGTQGSVYVDGQRVEGMPFDL
KDKGSKVVSHFYIGGDGGNAENTGSREGVSVTVRNVLLYNRLLGDTELTALNANKVPISV
PEDRNELAGDTVLPAVSGSDLGGTVSLANSAGQKPLEEEPLRRVDGADGGGVSSAASIAT
TPSSDVDQTVATGSGDAMLGDGSPQTPEVGVSSGEDEETAKRTDGQGEEGIHSQDGEANA
TALNSSLGKLSQGNNSDAGTVSESELLPSLLLLLLGLWGFAAL*
>TCRU_4930 BNR repeat-like domain/Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MLYTQRGYASGEKEANALYLWVTDNNRTFSVGPVAMDNNLEHFHALLYSDGALHLLKEGL
NEKGSAISLARLTDELNTIKSILSSWAQLDSSFSESSTPTTGLVAVLSDEANDGMWTDDY
RCVNASVTKAAKVKNGFNFTGPGSMATWPVNSREDNNQYGFVNYDFTLVATVTIHQAPSE
STSLLAAGLEDGAGKKIIGLSYSINKKWETVFYGTTKAQKNTWELGREYQVALMLQDGTK
GFVYVDGELVGSPETITTLETRGAEITHFYFGGDEKDSDSNVTVTNVFLYNRPLNSTEMR
AIKERIPVPTRGPEAQVEDGTERRHIPRIEGVRANAPAGSGLLPLLLLLGLWGFAAA*
>TCRU_4931 BNR repeat-like domain containing protein, putative
MSRRLFNFAALLLLVMLCCGNVAADEKQSEADPTFQWKDVAVAGVTVESLGVPGLLKVGS
DVFAVAEAQCKKGEGTFTGIASQLLTAATAVQPMELLTDPKAKRQVLEEGTSTVVTQVDV
SRPTTAVEGSDIYMLVACPGVCLILRRCSSS*
>TCRU_4932 hypothetical protein, conserved
MPFALSLVATCAAEHSLSIDADRSGAALFCIASHRQSDEDTADHRLGNGNQRVKFHPVRL
LGNAIDRHLNFGLHVTAAAGQTVLLCCQLRLDAGAGASQQHHAVSSGWVRPQCVAPRRRG

SRTASLGPRASTKDASVHLAASQAPLRRIIGFRAPTQHERLTFLWYIEEVRGAVCSETTP
SSILGKAATTIPLPGDAVFNGLRRVCRHMGIFPHHIRAPHAEHRIVVCDTVSRNEVGVFR
PRHANDSLDCVRRSALEAACASLGPCIWISCTATLLPGQRSSLWGLTAQLLTALHAPAER
SVLPLSMASDTSSSPPGSSIPIAHTSSCRHRLPLGDGRAPACPRAAHDDFTEAICTVLLS
LVD*
>TCRU_4933 hypothetical protein, conserved
MPTVSYLWTRRIHVQRTQHGQRELLAAQMPVKNGSGAARRLLGWRTAAPAIYSATSHQTS
QASRRTVDASSDISNCPTQSTRGAMELICQRRSTVSRRNTDIPALGRLREEGERGRSRDV
GAVNAGAENVSDGAIYDLMPHARTADGLGEPCGLFDGTVRRGAIDLTAVRQDAAVHVANG
SNPAGHGDSGVTKNRGAIGDETGAPLDE*
>TCRU_4934 hypothetical protein
MTDAFLNINAHPLDLLGALLRKLLDAHTTLGASNKHWRGCLAVKQKCKVELTLDTRHSLS
DIKQIHPLSLGSRLLRHKRFVQHLLGTIKGLRGVLADMYAALKAIFKCAHATATGEDLRL
DDLLFRLDLPQSGLHLLEGTARDAKLCLAAAFLQNGLRLVLVDVEETALNAHALWDASAA
QTSEHDSHFFYCFRLFVFFCLSAFFRVPPLLFVV*
>TCRU_4935 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MNGGKTVLLGLSYNNKEKKWQLQCGGGTKSEGLSSNWEPGKTKRHVVILQRNGNQGTAYV
DGQRVGVGASCALGGTESQEISHFYIGGDGENTAGDEDVSVTVTNVLLYNRPLDEAVITA
LHTESVTIPKLDHAKPEPRGTPSTPAGQQPSELGHLVGSSKVASGGVEGADPQIRGVNAT
ALSSSLVNVSQENNSDAGTMRGSGLLPSLLLLLGLWGLAAQ*
>TCRU_4936 RNA-binding protein, putative
MEDHRDNGPPPRDRARRGRSSDSSSSSRSTQRWRHRTTRHWRSRSRHRHASRKRRRSSFR
RSSSSRESSCSSDRRGSNSSSSRGRRRSRSRWHRNSGGSRRGGAAAALLSSEPFSVRADQ
GLLERPEADWVCGVCSNPNSVRREECFRCGTRFAVSINATPSEEIRVSGLPDKVVFVDIQ
RALEDRFTEHGDTCRIVAYTIDTKVNRKDNAKEQVAYLLFDSVAEAAKALTYTRSLLAVG
QTMCAMEFSLKRRANRKPTPTRGDTEMKTAVKPVDGLPDHLQPGVWKPVERFSSPTEEKE
YLDLLSRHWEKLSQEQKDYYDEGVRRALAAQRRRQQQGNVSTAMKGTTPNAESTVVVPPS
NGSSLENIKKRLAEKRRAVQGGASEGQTANEHTTSAASLKERLAMKKAQLSSVAKPSSVT
ETETAAVAVPSAQTLTSHKDTAPTPVHLFFGFPIPSRFPTKTDYLTHSKSPSFRAGLMFR
YVPPAVAERILPPSARPPPA*
>TCRU_4937 hypothetical protein, conserved
MSTYDDSFEGSDTSLSPSPRSSLRDESDAAVILPQPSASSVPIPVPVEQELPEATNSPVQ
ALPGDTLADRADAATPTPPFANTAAAAVADPLLASPASVSSLPQRELKSPVVGGAAPASA
DKASVDTNLSHIEVKLGGLNAPSTAKFKALSSYVAFGATPPGSTSVLSATINETRRETQN
SVAAEVKEKKFPTETPAVILPIASETDGSSSRRESSVFSTLSQHLTKRQSREGESNSEKL
RKESAATAVAATHLLVDEKKDEGADGVGLAMAPLPLPQAGESQIQSNVPISFPAPSTDFP
GVQSNPFGVEGALASLPPPLPSRDPRQDPKIVELRETSEAVERLVRAFALLRGHVAAPSS
DPLADAKDFYATKDKEKLSSLRLQRGVGDAGTLRVSQSSSRRPFLPRSKPVDESRDANEK
AALQMSEAAVEEAIMCLVMELMQSDARQPFEENTGRKFIHPSLEFVGMDNFNLFPPSKQR
KFPRFLQKIDTPFSVFDGGMQTFAPGDPDASESLFHSVFQGLQKYVWSHVAATDRHTTNR
FPPVSAHFAWALQLDLLLVCMQTLEGRFAGERAGTKDGSTVWIQYEGSREAEPLARNAAH
CLPFEVLDAKQRDKTVFRLEYWVTKDKMWTVLEALVASIREGIVSRSDGYRAFSSDEEIH
IDPSALLPTRVPLFSLVPQERLGVAHDDERNGIRKEAAQKGQEESRSNFFHIHPNTMESL
AHAVSTAGTELLESDRRISGKNYRQSYQDATTAVAEAVCELLDDAGIRAAIQRRAKAKIA
ALSERREMDNTLNRQEKERFLIETAEAEAERVVRRILHEIRVDEARGA*
>TCRU_4938 hypothetical protein, conserved
MQRVSLVVLPLLLLWMLQATKGVAAEYDERSVAKGSREEQIVFWEKEIDRLRNGELAKAY
QTLYTTQMALNEAKRHSGWLFTSKDVQARIKVLDAEYEKNMAAVVVLKREEEMMLAKLKP
LHGIVSRRFAQEQRNAIVDAVNLVQQASYDQAWYGSLFDIGDAETLTDIIVGFLLRWLIG
YVLLYPFAAIYYALWTAPRNIYAYSSGTSDIPVGVVAWCVSVSVMLLPVMALVGGFWYIR
RHYGDRVTEALRAARERERGRR*
>TCRU_4939 protein transport protein Sec24
MNFALPAEYYVAKQNAAAAAARANGERPPNLYHAFEDSQQIQQWGTAVPQQAPQDVDGQR

QAYYNYPQQQQQQQEVLYAQYPQQAIPPQQPQARGLPHAARGGQRSPIRSPTSQSRSYL
NAQTQPADSVLSWEVQLARSHEKSKFLDHPSIPRFLHPNLAEDMARVPQTIPYILPVSRT
TMRPTFQTLPSTSQLADTLQLPLGITFQPFAETQLPEVDLSSLGGRMIRCRKCSAYINPF
TTFCEQGRRWQCILCRQLNEVFQEYFCPIDPQTGLRTDVLQRPELTYCSVDFYPTSEFLR
RPPQRPAFLLMLDCSYQAIASGQLHAICRGVLSALETMKNEDALYMGVIGFASTVYFFNL
GSALQAPRVIIAPDVVHDVCNVDDNFKFEPIELPCAVNELVVHVKDAYRLLKDLFEKLPE
TFAKTKDVGCAFGPALAAAISMLENSGGKIVASIDAMPSIGEGKLKPRFDMAKLSNQPKE
YTVCSAANEWYKQRALACSNSNISIDLLVSGAQDVDLTTIAPLSRFTSGSIYRSTPLTIN
GMPEQVHRILTRYVAFESILRVRTSNGLVVPNFYGHCHVREPDLLALPVGDEDSSYSVQL
QLGSEIKSGFAYIQVAIVHTNRSRERRIRVHTYQLNVSPSLSAVVNSADSLGVTCFLSKM
AIDFAVNAPFQQAEKRVTDKLVATLRAAKKHNDGLGLRYGHFMLPESLRFVPQLLHGFFR
NAAVGLSTATPILPDERVASMSMVMSTAPHTMVPYYTGWSYEVYSPHAAPENFPMPIFPT
QTYFRSDGIFLVHVGSTLVLWYGRKADAHVVEAFGLTPSAEAPRSSQPPITEEQLAALRG
RFDELVWNLRRDIRGAFTASLEACPQGNSVFEPALTRMMTEDEVRTLPSYTTFLRDLWQK
VSATGK*
>TCRU_4940 hypothetical protein, conserved
MLRCSAQCLLFSRLGRTKLGAEVLMKTRIEMREVSKSENRFIRFFARRRPIDYLALEVDG
PIAKELHPSFRIVKHICTLLLVVPVFVTLVMGKLSPTYYVLVPTGFVTVEQFERMWEFSH
WAVVLVGQLLFFVVFYDLSVYVRYPFFAYVLAPLYRRLGWRRSRLQSSSMTLDELQRRRP
HARPLGVPLGEAKRGSRRAQRPDLHGSREKERK*
>TCRU_4941 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MAPRTLMVSVCENVQSNLENTKSKEISHFFIGGDGGSTDSAEGQGDVSVTVTKVLLYNRP
LSSADITALNTKPSISKQKDPQAVTGDARAPEVREPPAPVTVPQTNLGAQEQGEQELLKT
SKVADSHGVSTSTVLTATTSSGEEGSVNQLSSGTSSEGTQTVHGASSFDFNPTVGTEAGG
KTQEDEPHKTPAGNVNAADANAPTTGGEGQDGPAVNLEASARSGGNGETAEETNGQEEKQ
IHPHDGEANATALSSSLGNVAQGNNSDAGAMRESGMVPSLFLLLLGLWGFAAL*
>TCRU_4942 BNR repeat-like domain containing protein, putative
MGRPQTLSKLISSASHEGDWTEFIASVGSGVVMEDGTLVFPLTAKDEAEDVYSMIISSTD
YGSTWTLSEDISPAKCLNPCVTGWEGSLLMIVDCENGRRVYESRDMGTAWTEAIGTLSAV
WVNARAGVSQKESQRVDALITATIEGRKVMLYTQRGHALGEKRATALCLWVTDNNRTLSV
GPVAVDNAANWMLTSTLLYSGGNLHLLQGRGNSEGSAMSLFRLTEELSTTKSVVSTWA*
>TCRU_4943 Concanavalin A-like lectin/glucanases superfamily, putative
MLADTAFNHTVGPSYSHNKKWETTVKGKTTTRCSTWEPKEECQVALMLQGNNASVDVDGQ
SLGEEEVPLTGERPPDFLRFCIGAYGGHESHVTVTDVFLYNRPLNSTATRALKDRVLVPT
REAAPTPPEKVRVVDSVREHIAGDITEEK*
>TCRU_4944 Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MGMRVGSNGDENNLLLGLSYNKERKWHVLCCDGNIEELSSGWETGKQYQVAIVLQNGTQG
SVYVDGQRVGNGECALGNGESKEISHFYIGGDGENKESREEVSVTVTNVLLYNRPLDEDE
IAAFNPNKDPTPSLVDGSVEGDAIETSPGGGRPEEPRQSMESSGVNGESASTVPSANTSS
GGEGSATQLVSGKSSDGSKTVDGASFSYGEPTVETREGGTDGQKEEEIHAQNGDVKAAAL
SNSLGNVSQGNNTDACTMHENGLLPLLLLLLGLWGLTAL*
>TCRU_4945 BNR repeat-like domain containing protein, putative
MELDKAKLNTQLLEECSSDKGKCAAQIAAHSGTESEKRVDVARPTTVVKGNEIYMLAGIY
NLGDATDTSAYWGLLLSRGNVSVDKESKKRIHWNDVDALQSISNVQKQESLTDLIGGGGS
GAKMRDGTIVFPVEGIKSNGAAGGTDTVSLVIYSLGNEGWKLSKGMSAGGCSVPSVVEWE
KDKLMMMTACDDGRRRVYESGDKGESWTEALGTLSRVWGNTKGEKAELVGSGFTTATIDK
KKVMLVTLPVYSKEKEKEEKEKGSLHLWLTDNTHIVDIGPVSDDDVAASSLLYKSGESGN
DNNGEELIALYEKRER*
>TCRU_4946 hypothetical protein, conserved
MWHRVRACAVGSTAARTEAPKLASSTALMEQKAGLRNLHQYPTARHKSLVKDRIRFARNW
WLTGGNNYELVHEEGHEREATECFAEYAQDSSNDVYLFSTNRLSDLPPRDRLNAIVGIMT

SRWKVRDSNRGFDKARLLLQALECFSEMRLSGQIKEFEELPEADQDTFLQYVEGCSRFAQ
ACSHSHPSAVAILLRVAHICEEMRCSEKRDEIIHVAEGAAERMDRAYAFSRPHDNLKRPP
PSLMENESVLRHKNLEELKRRFRDKAPHVLEKKQQPEYVHIHRNKRLYLRPMDASRKELE
MLRLPARPEFDSWTADQR*
>TCRU_4947 hypothetical protein, conserved
MSGTLKEKFIDPDAAVCSTFFRTTDASEKTWRDVALVAELDNHTFWTVVANHGNLPLVLR
NLITAVDVAHSSAFHRQLKRSDEHALITFIVRLATTTSAVLSVGVSLTSVARHLEEIIPP
DLLMPVSLIILRHCFSIASVTITSLILLNPLYLCAMSATATSWCNATSCLSVQCVREVAR
GRHQRLAGDVVQLFEQVYRHVKQLWALVHCAPFLADYMPLTRVLQYLRVVVDLISPLLQH
FLLTCTTLSKRREQLSKANSAILNAAVNTASILILFRTYQKVTGFDRCHCVERIVVPVYD
ALTSHIVQKVPGPPSLLLSNTRRPLTRIIHELLPPQAGTDELEVGKVILHLSEAVPDSKD
FSDGFLGARSRYLELLLLELIHQGFHIDLLMEEKFITIHEAEELGASERVITQAILGIVE
KTTGDAALPKSDGGNDDVTEFPTSTAAAAVTTTKTTTTTRASSDPLVRIVLDVMPHFNVE
GIKAALCYYNNDVEDFILDASMNNIPPHLLTQLSEPTSSCSVEISGRDETGASAVNAIAT
AVPTSRVTHTLTSNDYDSNFDGINLDLFISRDLCDVINGDDRPFSGDDLSNDLGYTTYHP
DSHRGAAEMFEVDEALREKIRMLTELMYEDEFDDTQEIAGVCGYEAGHDANGSDSSASGD
EKVDAGHISKSGLREESAMTTTTPHRPRTQYDEKRFHDTRSKQREKNLKALKEAQEDAPA
YIKKKKITRKKMQHKMALTRDVKRGKSDL*
>TCRU_4948 hypothetical protein
MPKGHQVRNEEGPSRVFSSFTPLSEQPCSRNDASFSTTFLESGRWKSTLSNFFRRGDEPL
PAPSMIDTITHCKSPSSGSNNKNNNNSSIGSHNDNNSTSRTVARARVGILGDAGSGRTSL
ASAAAKVADRCGSASDFQSLSSGSFVTYIYQSSVSRRKEFLEMSVVDSGPVPLRGGTARH
VLPGCDTIVIAFALTGIKQKYPATRKLLTFMGKNEGNKESSSTVLVHAGDQTLLHDLFAT
IAARISPGGRCPNIILVGTHKDLLTDQTTGAVEVLLKEVRSICNNFLASFRKSLVLNSLF
AVNTVDGSCVSENREGPTTMAGMWSFICDVTLKEILSRHSSRISHQASCSDSFWRPHRSP
LYAVAPSETCNSKEDELSSKWNDTNDNSSSSHPCSVMKVPVNSRIDAANSKLLGLITRAK
AEKKVLFAYRNILWRLLYSSVMVGRRQLTLILEKLQNAGEVVLIRHHPDVLPIRDVCICF
HPHLVERAQATVFLYASYANNHSEAHGNLLKDVNLERCGQCDPNHDVSRGIFSHRLLLEL
SPRLKLACFSTKEVETFAMLLLLSDTAILRRSFLSAAMNTGNTSTTSTVTMEGKFNGVYT
PNADCPDFPVTMCSSWKRNKEDDFETVSELPCGAPTQRCLMVEYLVPSLIRNRCPNEVIE
CVRHFAATTCGAKDEQQNNVMSRVLMLHHCPQDFFPMLTSRLHRYMVPSVPIFSETLWLG
NLTPAGTPLPLLRVCVCHTRDESMDNAVKEGGQISGVSLLEFHAFSDVGYLPLVLLLDDI
TREAARLIRHEFPGMLTEALPNNVPLSWRQLDGNPLLASLTTTSEMGSFTGMTTLRKLDT
LFHSFNS*
>TCRU_4949 Cullin binding, putative
MMRVAKPDGNYAVYEALFCSIIEKSNGGQKNLDIDVLELPQLEILAEMIGVSLDDSSIYR
LAWSWSCQTPLSIKKNEFMKGMRALETSMKKTKPNAITPNLPKNTLRPEFNPYLCAMRSH
VDEIDEVLHKDPDQFRKFYRFIFGWVRSPETTARSLGELGMNIATAVELWQMLFPEYKTF
LKMNDWITFCTTKEIFHREAISRDLWEQLLEFTSLTRYDTYDVNDAWPSAIDDFVEYFKA
QHPNCGEEESPTQIHEDAK*
>TCRU_4950 hypothetical protein, conserved
MCAAFRSLCEELSRLQVRMLRRDGNPSQLVAEATQMIRSRCNDIEIKRQNLPYVPIFLRS
CATLFARADTDPVHEALETVGQLAEAYVDGNHGDVNESATVLQSLVSFARNLANEGDLHK
KNMPSSSPSLALRSLLAPCLEKTLQKWKEQSVRPHTSTLLSLLRGTDIVYGEGFHFTPVS
VDMMGLLPIKGKIQMEAKLQKCPSARHILKSLREMQLSKLDAGICLSSLAELGLYDAELC
NACCEVLFSTHALVTCQQFAQVIYSLGVLQHRHIHQKFFSSMVDFKKCNAAALRKHTMGL
AMLRQPPPNERAFMDGIFLHALRPTDPLEYSYSPEEELSSEWFVSIGHALSCLGIVHYKY
RLMLARRVRRDIIQLTTQQRCQMLYALGGVPIDSVPDELRQSWKNKVERSIEVLTERLRY
NVEPSDGPFVMNALLFAGVREHPMIPQKPDLLSGENPVEVLLRTWSTCPKERVLHLTEQI
RPRHLGEEPTATLSHVFSVIAKNCSASPFDSYRFGPLCDAVRSHGGEMSVEEVLGTIAAI
QRIGIGGRYRETLVVLLENLWRQRHSMTSEQQSRCCRLLERLGHLDTAMELLEYMTTL*
>TCRU_4951 hypothetical protein
MLMETLEREVEALSAEVTRLRFMVYHMKDAVFSSAPPLAAAASSVNCRSGGCGGGGAETT
DSAVKLKANSSSCGTSPPLGLVLQDLTQAVAQLLAASNEVKMASSALRQGREEKNNERPR

RHQGSRTRKKTKKNRRHRRSSSASSSALPALSLSLSSSTHRASKKRRRSHRHADKKKDSK
DLRRLEEKMGDGHNDLPSIKPRNSTSQEKGFHASNAVAQRQLQKEEEGHEFNCSRGEDKE
KRSSLRSSQKGGDPLTRKTPAELESVERSRPPSLGTSYGMLASASVQSAGAGDPRTSIRR
ENRGSSAVAIPVPPRKMDGQRKEDGETPPSTEEDGYSFLTHGTLSLGCFAPEKTKNVTPT
ATKITKTEGYEEKSKEKGNMQFKPLHMFRTPPTQRRNLLDRFRGGSDESSTPDERDSTPA
SIQQAGESAASHSISLHNAVNNAIGFASTDNVSRNSFAIGAIRSSTPDSFGGYGAGMMEE
YGFALNESFHASQSAENINSRGHDEPSAILTRTNARYHLRDGNSTN*
>TCRU_4952 pseudouridine synthase TruD, putative
MVEICSAGGADDREECIGMHFFLTDAILAEKGMNLGFRRPLVSLKTLYSDFVVRELSPLY
NNGEPLVLEQLPTVERLDSKLKAVKRPREEKEEEAMATALDAQPILLLEHVQAQFSSLLG
PEDLSSLLEALRAGADRVMLRDSSLTKAHRTRVHEAVKNTLGPSYLSRTVDGSLVIEKST
SVSRREEMRRSNPLRLQKFLHFTLYKENMDSNRALRAIAGHLCLPVRQLLFSGTKDKRAV
TLQRVAVRGLSCERLSEINDRSFGPDCKLKVCGFQEAESGLRLGDTLGNHFLIALRLLPD
STEPSPDMLKVIQEVIGSVGVVNYYGPQRFGTTEVLTSDVGIKLLSGEFEQALRMIFHSK
AIVEPNLLPSKEAVERRSFDEALKLLPRYCFQERDILKHLVKCPKDFLGALHMIPRTLGM
LYCHAVQSLIWNIMASERLKRGVGPLPGDLLLKNWYTHIKERANRPDDNDEDFTILLKED
GLPEVVRLTEEDVATGLFCLCDVLLTVPGPDEELQYPSIASCTRESYIAALKLRGAEMLL
NAENPLVKVYHYHGAYRPLVVKPRGLKMRLVNTKGPREPIILTDLEKLAMCDTNNNGMMD
NEIEQDACTTTAVSKAIVVEFSLPPGSYATSVLREFSIPNSEGYHSTAAMQCDSSGSH*
>TCRU_4953 Rab3 GTPase-activating protein regulatory subunit N-terminus, putative
MASLSLRQVGVLKHAEAVSQSFPLCVTYVELMKGAYLFASVNAAKNRCTVEFILDTNNNN
TNAAAADSTFTTNTVVMDAKSHSSAASEVVEHETLLENLQSSFRIPKFFQVLEEEGMITA
IELACDYRKVEDSREVLPKKKRALESTYVHLFIGTSNGTVFICNALRGTIMALAQFQYHG
VFTHSQLEKSQGDETPPTCRNESVVRFVLHGTGPDVRFNANIAQSTASLPIGTLHAVCVV
HSRGRVVLLSRNVLDIFLSVAEQRLDGKRPYFLLEWSPDSSISSFPSAGPAAHFASCIES
VFIVSEEERYSAVELRTQPITSNSPMGRSIRDAAFFFGNLSDTAAILRNGPQAMESLILC
GEAPALSMYTFESTRAAFSARKTVRAVVSVLGGMARRIWQRSSENEDKGAMKPQRLAKRH
QQAKDAFFEADIVFNVVQVDPTFQWAACYSESSGRIYLYDLIGGALWRVMKGCRSAKFQW
CVATIAGKRMLLLVVHLLLRYAVEVYSIRLGERLAARHVPQGSILLRPESVSSALSILLL
TPFREVIRVNVELNAKKEEEIPSSFLFADPSALLNEGESSFKTLREKGYQIMPRDIFISA
LRLPLPTPVTDERLFSAYRLQMKKLENTVKSKFSPGVSDERCFPMGMDTTVETVPRNITA
AQCLNYLELRLACVTNYHRAMMLRGLNDGMQQPGMKASKLPNSEALFSEEGESHPSLLQG
VSAASEMLSSGGFPEFVHFLEDILPSMQRLLAMHKDAPPETNFTQIPSIPLDVFLKHFHC
GGYKLEFLRDKMWAFENASDAEEDIWAEIGAVFYSSAGRGLGSLLQQLEVFSALGFQTVD
VAVISLSWLCCSFARRPTLASLGSLSDLVFLLKTCNDAAFLTGVEHVPCFTTGIAGTNYG
GNEACVLLLILCMIIRQHEKPVGHAYYTRYLRLLRQLLAFRVMLHCWKSQLQASITDSGK
KCYQRIRMCGLLPCEGGDTLSAYCFGIFPTSVAQFLCENIMGRDEMKRALGGVDMVELFK
LISIRKETFELNVGTSWYKERTWSHVVFSERVLKPILSVTAALMPKSPQERPWIHTATPQ
EVAGLGLILVVELILLEWELEPLREEPLAFIQKNLAPDANLFEGSDDLVKSLARRPKGSR
STRDYFNSCRELLTLAQGVLADIVGDASNLESCEKVVEAWSSLLSYDNNALFAHVPLLMR
QQLEPLIKLFRTSPEPLVRRIREVSSFLDTIMFFAFTEVGTQLSSVASPSASLSVPWDSM
FDARERMLHLRPDGDFTEFPERQQMETKMQMRSSFLKEFAFMNYRSTYTDGSGERVAQLG
EALGLNRIVGDISQLILFDAAARHLCSNTELHRLRNVVASRHLAARIAAADFRIIVASCL
KYYNELKRGIPKENRFEIQRVALKIKSMDSAMTEECRSWIQMGDAKKGLDTRLGEDVTSR
SPLENEIVACPSWYTLNDIRAVERRVKERLQQPRSPEAFSDFNAVLFTLACVAAEGRTEL
EGVARRVAAELPAVSSRLANLL*
>TCRU_4954 Mechanosensitive ion channel, putative
MKRFFNRFYLDTGIIADPSQRSLASRVSALLVQGAVAFSLLGTIGVDTSPLIAAAGVTGA
TIGFACKDFGTNFVASIVLSGQQSLRTGNQVCIGTGLNVVKGEVVDWDTRYLYLRSSEGH
LLHVPNNMVLNSVVTWEQEKKQSLHETDPPKQDVVKATGDNAAKQ*
>TCRU_4955 Gcd10p family, putative
MTGSGSSDAEEPRTDGRIALGDHVIITGGGVKRMALVQADNKLRLGSSGVVQLEKLVGLR
FGEVLRYDPKDRVLLPTNAYPDLDITSLQQRLEDARDNRHLVDDNRNQILSNVEIAALRQ

EKGVDAFLTTLVQKSTTFHTKTAYSQEKYLRKKKKRYGTLYKVERVTPDAAAEIYLPTIN
PSDVEPEETRSMRLRADTLALILHHSDVHSGSRVLVYEKTNGHLAAALLTRLGNDGVIMQ
VMDKVAQPNVFLAQAMGLTRVRELWKAIPRNDAFLLGREGTEEEQNPGDEKKKTGTGKNN
TNKGNKKRGNGDIEGPSQWIRGIDARRMLKERPADSLIIVNDTESESLINELLPFIALGG
HIVVYSQFLEDLSGAFARLWRECVNICVSETWYRHHQILPNRTHPTVNMSTAGGYLLTAI
KTETNGIPRPRLEEVSKAILLEQAKSTETDGKMPFKRQREEGDERREQE*
>TCRU_4956 leucine-rich repeat protein (LRRP), putative
MPSGTDNTVEEGTLSEECILRVSRQYDVEMVFQISLCSRGLRSLGDGFARCLALVRVDVS
RNCLTSLEGIALLAGSLRYINASENEVEDLAGVDRCSLLEEVRLEGNQLSNEVAIVPLAQ
LPNLRSLFLQREMPLSGDTHETLLLENPICRDKGAYDKILQRHFASVLCVDGRCFRHPSP
REVVAETAVLPSSTPPPSGTALDKKLDTEDDLGERIFANAVAECRAACRKALI*
>TCRU_4957 hypothetical protein
MMRFTRFLAVAAKRSATSAKLGKSVGLTAALSPRQRSLPRVSVTKLMKPSGSGKHALSSF
LLKDKKKVATAKVAVPPKKKRALKVRKGRSSGKKAAALYVRFYYALKKSGLVKGKRRMQK
TGELWRATKKAKDFKKRVEAALRLAKKGQKSRARKLKAQKKAKGKKSAKGVRRVYRRVSR
KKTVTSTVPPLP*
>TCRU_4958 kinetoplast DNA-associated protein, putative
MLRFCRSRLAIGAYALFMMEQKKNPALSGLPVAQRGKVTSKLYKALAPAERAALEKRAKA
TPSPKRNKMKGNDEKEQKPKRKPSKYAQFVKANLPKYSQLPNSERLAAVAKLWRQQQQQQ
QQPKKKMA*
>TCRU_4959 kinetoplast DNA-associated protein, putative
MLRFCRSRLAIGAYALFMMEQKNNPALSGLPISERGKMTSKLYKALAPAERAALEKRAKA
TPSPKRKKLKKNEKKEQKPKRKPSEYAQFVKANLPKYSQLPNKERIAAVAKLWKQQQQKQ
LHL*
>TCRU_4960 hypothetical protein, conserved
MLRTVVPLHNSRKLALRFFQTEQRKNTNLHGLSAVQKKKVILKMFKQLTREDMDALKKRA
AAWEAKKISGETAIPSYRRRNEITPYELFYKEQLSNPSIASIASPGIREKKLFAIFNSLP
DATREALEKRARELSQGMALSDSPPPSGKKPSASKKKKKKRITIKTSSKSRSMTSQGASV
GKKKKRTVTKTKVSPYAAFVKEQMPHMTHLPTKERMKAIAEKWNSMKTENAVEKSKPENT
AAADPAPPS*
>TCRU_4961 kinetoplast DNA-associated protein, putative
MLRFCRSRLAIGAYALFMMEQKNNPALSGLPVAKRGKMTSKLYKALAPAERAALEKRAKA
TPFPKRKKSKANGNGPKPKRKPSKYALFVKANLPKFRKLPNSERIAAVAKLWRQQQQQKQ
QPKKKKT*
>TCRU_4962 BNR repeat-like domain containing protein, putative
MLITAPVYANDSGKGRLHLWVTDKARVYDFGPVSRENDDAAASSLLIKDNNSELISLYEN
KKKDGAYNLVAVRLTEKLKRIKEVVKTWKDLDSALRTCSSGSSATVDPRKKGMCNGRVPT
DGLVGFLSGNSTQTDTALLMEPHLRFHCLPLFSQGLPHSFKGSGAGCGVACWRHGADCAV
LLC*
>TCRU_4963 Nodulin-like, putative
MVQLVDDLFRMRMLIVGVYLALGTSSNYCFSIFTDHLRNKYGYSQSDITTIGTVGDFVSN
FGFHAGVLFDYVGPTVLLPVGGLLGCLGFVLFGMTFDGKINNSSVALFALYQGITSLGLP
MMDVSSVMSLMLQIPLERGYVVLIVKTFSGLGTAVLIAYFNGWFKAANSDQPEENNYSGY
AYFVGVMILLCSLIGACFTRLPMYFPCSWRKKRLSSEEAAEREKTLDLYMSQHAPTRRLR
IGFAIVVATLIFSTAQSITTAYVNTSRAGYLAISIVAVLLMASFSVIAMPFQFLGRYTPV
CPTHMEGIGIGKTTTEPMHERKGETASESAVADGNNLGANGVAVPAPQYSGSFWSHLLTV
ELWAVWLACFGMFGTGSVMQMNAVQIYRSMNNGKLDTRTLTLYVAIISVGSAVGRMAVGY
LDMKLFALQREGKTKTLTTIALPIGSLLLMAACLFFAVLPGSALLPPFLLGAMGNGVGWG
MSVIALRMMYSEDIGKHYNFCFTSGAVASLGLNRFMFGEMYDAEARRRGEFPSCNHPRCV
RSQMFILLAVNVVATLAAAFVHWRFSRFTRARLGCAGNTGLFPRRE*
>TCRU_4964 BNR repeat-like domain containing protein, putative
MLVTLPVYSEKADKKVTDNGKSELHLWLTDNTHIVDIGPVFDDDAAASSLLYKSGDNNEK
EELIALYEKKKAEVDTPSHSLWSVLLTAQLQRVKEVLATWKEVDGRVSKLCTSSSAGELL
STDSACSAVIPTDGLVGFLSGNFSNDTWRDEYLGVNATVNKKEDAGETGATNTSDGVTFR

GAWAEWPVGSQGENQLYHFANYNFTLVATVSIHGVPQEGSPIPRVGQQKGRRSEGR*
>TCRU_4965 hypothetical protein, conserved
MPQLVGYQTHVLICHRQFLRVKVHGRSKWTAIIQQGALNRPRGWTISRKNVGVKNHVGAS
HTHRAVPARDGEFIAQTQTGLWNNDGARHGPHGETLRVQLNCGGESLPQNNVPPLLRQHV
VRLACYCAAFVVNAQIPHRTAVPQRVEHVLRGHLDADRSPAIVPILAGGGVRLHGALSPA
RQLTHHRSRQPAVFLHHRVKPTAVLHGGIGGNANTNATHHHHEPRRQQQRGAAWLAHGSG
TMCLFRRRGQQWY*
>TCRU_4966 dynamin-1-like protein
MNQLIAVVNELHDAFANVKMNIKLNLPQIAVVGSQSSGKSSVLEAIVGKDFLPRGSGIVT
RCPLVLQLVQLPKTSEEEWGEFLHKPNKKYFDFLEINEEIKHRTVEIAGNSAISDRPINL
KVYSKNVLNLTLVDLPGLVMNAVGDQPKDIDRQIKEMVTRYVAPVNTIILAISPANTDLA
TSSSLRLAKQLDPEGIRTVGVLTKLDLMDRGTDALDALTGKLVSLRHGFVGVVNRSQQDI
NDSKGMLAAREDERAFFHNHPSYSAIADRQGTEYLAKKLNQLLLQHIKDVIPELKKHVDK
LLGSTMKQMEKLGMLDQTNIDPSAHMLSLIKRFSDTLNHTIDGGATDATKELMGGARLDY
IFNECFAAYVNGLTAKKELTDEYIRINARNMAGMHSALFPSDQVFVALSRQQIARLEEPS
QKCVQFVFEELIKIVDICASKLDNFPRLKQAVVDICRQSLQEYRAPTMSHVRTIIAAERG
FVNVKHPMMEQLVQRSFLKIFGTENEKSQTSHSQQGGNEGKDKGKKVNSEPTSNGVEKSD
MGDVPVTIMLGNNMSMHEQHINNVIRDMVEGYFGIVKGTVADQVPKAITLLMITKLREDV
YSRLVRSLYSEKKADDLLAEPPEVETQRKATKTMMIALKKAQEALESVREFTL*
>TCRU_4967 leucine-rich repeat-containing protein
MGRITIELLRRRAEHNEGCLSNLKEIALHQQDIEKIEVVGDACRELEILYLCNNYISRIE
GLQHLKRLKYLNLAVNNIACIEGLEGCESLERLDLTLNFVAEMTCVQRLRANVFLDQLHL
TGNPCTKIEGYRAYVIHALPQLRDLDGEEVVRSERIEARQCNSEVAAVVDEAALRVREAE
RIKAEMIAQGIDVFPPRYNEKGERVYGHTPEERLQMLREKEEEEAEREKKLQKERETGHL
ASVSAEVNKRPQRLTAEEEIAKYGRLLLRNEPKFPMRLDQESDETAVILTVDVPKFLSTT
LIDVQIEVNYIRLLVKEKLIQVPLQREISPSAARVQRSVVTGALNITIPYASHVLQEIEE
AKKRRQRLHGTWNDDECSEPLE*
>TCRU_4968 NAD-dependent glycerol-3-phosphate dehydrogenase N-
terminus, putative
MRSRLLVIGAGELGTACALSLLANMRGRDARAGDVVTMCARDREYLQELEHGSQTFRLFG
NNIRVPSQMCFQALGEEMAEEAFHCEASLLCVPVSCFAEGNGDTPREKASAGVCDCLGRH
ADVPIFVFGRGFSRDGLTPVEELNRVIRPRPSKLVVVSGPLFAKEWAAASVQENTTSKSS
SHAASSNSGVSIAFAMDDATDAETLQAVKDISQRLWCRESVTWLTEPKSSGLLSLVNGCF
PLCSMGAGMVSSEYPASVSAMMSYMQHAISATEKLVNEVISRPQGTPLPACAVATLAMAC
TNHASREFIFGRRLNFHFRHRDAIRAVFPGNSHESLDASVAGLHTLLKRRSFSSPFYEVL
MDAFLTVLRASVAGRGLVRTGFYDYRDQLPVEDAPLLRHVLAVDEAMHSGDEDSFNKACH
TLEVEFNNSATPSSGL*
>TCRU_4969 metallo-peptidase, Clan MA(E) Family M1
MSSVTNSVKLHNPFVPSSYDLHVSVDLANWRYEGKEKVVLRRSPGVEVSREVQLHCGNSV
NIQCVTGAAIAGRDEKAGTLLLLLDGEPADGHTVTFAFSHEIREEMRGLYRAVFKTSDGA
EHRMAATHFEPTAARLFYICQDEPSARADFTLHVSLPSSMAGFTVLSNGPLKSKETQGDT
VTHHFETIPAVPPYLTSCFVGELEFVGTTACGIPVKVYTTVGKSYKAAFALKTTAFALEY
FEKFFKCKYPLPKLDVVAVPDFPIGGMENWGCIACVESILLEEQTSSVESLKRAASLICH
EVSHNWFGNLVTINWWEGLWLKEGFASWCGYDAAHHLEPSWKLNEDAAMEVTGALVTDMY
EHSHPVEVPIHDPAEITQIFDDISYSKGMGLVFMLQAFLGEKWAASVAHYIQKHQYSDTR
TIQLWQALEESSGVQITEAMQSFTTQMGYPIIHVSRPTPSTVVLRQEPCQFLTAVKRNTT
LWCVPIVLQGVGGATHRVILRGSEPQQVELPHEVAKSPWINANPSGRGFFRCRYDNEMFS
SLMGAYSSLTIPDRRGLIADTLASIYMGNEDFDRMALFPSLLGKLESDKIVWQEYYKSME
NILAILEDDAEGNELRRKLMHSIDEKATKLLNTEPNTMEERLERALYINAAISTALKLMP
LEVALQCPSVKWAIKQAECYMEGGTPSLDTLAMSLSAYVRLGPNAAAARTDALWERYTRV
HDSDELCRCILRALCWAEDPCYVENTAKKCIYNEGIRAQYGGVIFLGVVSNPSMPKGYAW
SLFKKHFQGVEKQWGSGTFRIQNIVESVARSLTGETQAKEFHEFFQTHPLPHARLAIHRA
VEDIRLRTWLRSKWGVGTRLSSIFFPH*
>TCRU_4970 hypothetical protein, conserved

MSSREEVAALMAHGDDKAKISLLKKAVVSVTKEKQILEQHNKQLQEQMAAIGEELARVQD
ENEALRRKLSAAEAATAAERKRGHFAASMKTTLKGLSSLVTGTDGEEGGTASRRPKASEL
PLKLSQEDQEKLVTQNEAIHMQLFDLKKKYEDEGEMWRKERERRSSECAAMHEEVTELRS
ILESTAHSCDQLNAECTRQAALVQFCHHFFVLSWDNAENAHHHHQQQLHVAMAPSLTTER
GGVPPREVREELATGTLTGVAAFIRTLMSAVSVLVASLRDSFSTQMNGITISEVRCYRER
LSTLLEVHGVQKTTLLFHVKELEDAFTASATPDEKITQIRRLQGVLISAFINWLGMICEN
IRLLVDACKKAGSHDPNEHRKEIQAVVESTTLGAVGTIAAIRGSLEALHQLCENSCSLFK
QQGCESAEWLLALERFWWEGCGASLSMRRAVESLRNQLRDISTSSANSDHVRAALQFMCN
SLENFAARAWCATKDVGLQPTTSVPHVSPSVDLPSNTTNPCDFASADNRELVAALAATDL
AAVCYHTQMNYTLLELAEKQDALADAQREIERLLSLNQQQAEDAERVREVLETQIRLLSD
QIVECANRNGGRNNW*
>TCRU_4971 dna replication complex gins protein sld5
MFFEDHLDEAFSRETSPDGVAGRRTNGNSNNNEASLHKSSAALSELLKSLIQATENERCA
PDILPYPEAIVDGVAAQIAAQNEQIRLLSAEEKQQTAEKDPGASLLPFKPSDIMALEVQR
AQFFLSELLRCRLRKIEALALSLFYEGQLHSDAPTQLRGMLSHNEVIVADRLAELMAKYV
LQAGLQSAPAELQCLIPNLPYAEGVEMLPVPELDQYVFCVVLDDLGVVRLGEDAVQAVHA
GEIFLVPYRAFRPYILDGRVRLV*
>TCRU_4972 hypothetical protein
MDEKTLKRIVKNADAAALQTYIRDCRSPFSQPLEAQARFAYFHLSREGDKRAASGPLAAF
HGEGRTVAPFEEYHGPTTTVVVRSQEKGRVVECHTPHLRHTAPVSGTDGRRQNLSESTRV
VESSGWTEGILRHSRYLYSSSSSHDLLQPQRNTSVRASYHPYDGAARAPRRLSNSSGCGI
KEMGDFGLQCHSSLQEYESKRFFRELQRVEMEERRQRLKLEAAFEGFIMDRHRGWHLLLD
RFAREKGDLITAERIVRFTIKEEEHSHYKEILTKCLEDLMGCRWDGVRMECLRKQMANSL
AMHEWVVLNGMATRPQDSRQDIAVGTEGCASEFGQVETFSPSAQSVDAQRHSLTPNCATL
TPHNVVYSAKASEPFPRAIRSNSRLPSRPRVLPPAVPHEECIVS*
>TCRU_4973 BNR repeat-like domain containing protein, putative
MSADGCGDPSVVEWKDKLMMMTACDDGRRRVYESGDKGTTWTEALGTLSRVWCSKHKGHE
KGVGSGFTTAKIDGFEDDKRNVMLVTLPVYSEEGVMERTYSIFG*
>TCRU_4974 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MVSVRLTAQLEKVKEVLATWKKVDERVSKLCATLLAQVTSTDNACSAGKITEGLVGFLSG
NFSNGTWKDEYLGVNATVKGNDGGAKMTDKGVTFTGRSAGAEWPVGKQGENVPYHFANYN
FTLVATVSIHNVPKSGSVPLMGVRAGSDGGTKLMELSYDSGKKWRVLCGDGTTKRLKSTW
ATETQYQVAIVLQNGKQGSVYVDGQRVCESVQIKWENTESKGISHFYIGGDEGNAENTGD
DEGVSVTVSKVLLYNRPLSSEEIAGLAKINIPKSVAARASSPAVSRPKSSSESLAAGATG
VGTARHFGANGDGSAVCGGGLLPLILLLGLWGFAAL*
>TCRU_4975 retrotransposon hot spot protein, RHS3, putative
MNCPDESDVRGMCVWEQRSKPLQQQAEYWREVKGRMDKVGPILRHIFDEQSYDDRIEKCH
ETVEETISPETQYYTGLGNSTMWGGNSVFHWLARVVRIREGACKGEFSLNLPISGHLCNK
TLCMLAKLMQQDDFNSLIETQA*
>TCRU_4976 terbinafine resistance locus protein (yip1), putative
MAQNTVLTAPLYSTLDEPITTTIVRDAVAIGRKMTIVLAPPLGEDQELRDWDLWGPLLLC
LVLAIILAGSAATHQGGLIFSAVFVLVWVGAAVVTLNAKFLGSKVSFFQTVCVMGYCLAP
LCIGAFLGVFISYFWVMMVISFVVWLWSCWAALRFFRGSVTPEREMLVVYPVALFYSFMT
WMVIVGV*
>TCRU_family, putative CECR6/TMEM1.1
MHRGVDTSVPSGALEAERKVAQRRVYLLTFIVFVVVAGGSFACVFFGIFEIVGHDSMLMN
DGLGEVMTVLGICFTVPCVFCVAVFAALTLDFSCFPSIRFFSEYVVMGLILISFVVQQVL
CDVYLFGVLGFLVMAVAVLDVFVFGLYFFFRLRSFYIPNVLTVVLFVGKTAVLWGMTYIP
HAEGEAEGKQQPIGSNGLFAMLVLTVSTVQLPLYIMETNESSGLQDGIITDNSIVENFNN
NFNLLLLHLLNSLDIFTVYGYIISFNNRGRALRTIPEPFRILIFIIASVAFVGNNVGVIH
LFYARDGVEHAELICLPKKLRDATNQWNSTDVGGSHKRRILQYLLFLVVLCDAPFLAVRT
QLWLRGHQMLSVFLIKNVKSILDIVMVVLRVGRSPGATDRLRRSIFES*
>TCRU_4978 retrotransposon hot spot protein, RHS3, putative

MDNLLRWLVAAAGVKAGVHCITNEFLDAAAEEARSPTTSSAPRYLEGCYESVHNARWSHF
VEFPGGEGTGMYVREGEPPQPWTYREVGDSLEKDDGVEQPVQHVQS*
>TCRU_4979 retrotransposon hot spot protein, RHS3, putative
MDNLLRWLVAAAGVKAGVHCITNEFLDAAAEEARSPTTSSAPRYLEGCYESVHNARWSHF
VEFPGGEGTGMYVREGEPPQPWTYREVGDSLEKDDGVEQPVQHVQS*
>TCRU_4980 hypothetical protein, conserved
MKHIAAQHHRGVFADHQLIHRDTRRPHNFQTRPRDQPRDREAVPVDRDVRARRKHTLRTE
QRVTERVAGDDDVQRPHSGVRVAQQQQHGTVPPRASIERDARHVARHRPYQHRQAHAAPA
ERHVAVAQPRQPAPHCLRHLGVHHVADALTNRRRWRRWRRRQWRHWRRWRASRHRRRDTH
IAVPSSSATALAANDRRRQRGKAVAVLRALTARGNRRHVGDAVQLQFSCRRHHTSRNRQA
PSNETVAGVSLR*
>TCRU_4981 retrotransposon hot spot protein, RHS3, putative
MWRCFCRLHVVLLRGRWALTASPTGVAVRLHGAPTAPPCERHAQRHWDCGTKQPRVSFGA
SGTCWPRLGGASGMLHRTGVAMAPRSGISGDGSDAATRRGVEGMRRPQWTMSSSVKEILL
EGSTLRTDMKLNEFLRNYVGGRTAVGEDHNVTMQVFVQEPDAYVQDQRLLRIIFNLTEYQ
VYKLHHEGVFSLEQWRDYEGKDTVTPIARGKLNAALFQAQASTKVVKSTVLKGVYQSVYN
ARWSHVVEIPDCEEEQTEMGMKVEKGKPKQSWKYKKVGESL*
>TCRU_4982 hypothetical protein, conserved
MPRCIACATTYVRLGKRIAAHALAASTARHRWKAAVTPQCTHPNTAASSALPTTIHSGSR
TANTDRKYGSAAVLARSCDEAHGILANTPTACISRTEPSPPVTTTATAAAPATTPVIAER
ALEAAGSVSDLIVKEPSSTPLQPPDTATASQRMTIVSSATMK*
>TCRU_of Trypanosoma cruzi region 4, putative Dispersed gene family
protein.1
MLMANTLTVTGGSWLVHRDNEFRTAYVVYVTEYYGVAFCDQSVWSILDNKFTYGSYSSTI
AHMTSNWPPPSELRPIIYGMCNELRGSPVTNYGEELNIGAPVTSLDCGACTVDAVCFEAR
TSSISGCECECAAGGYGDTCVPAAVPDGLGPLPLPDAKDTGVRCVYGGSISSVDYPDPGV
RGLCFVNVTFTAAIVLDLWSFDAPQQTLNITLLQCVLVGLSIKGSGARVHVNVTSSMLDA
GELAFEGYFGVSSQILVVGSTFVKTSVHAIGFLEFFPGRNTTLMLLDNYIEGNSYAVYFS
DAVVADGGGIIVKGNTLTTVENNGEESSVYAYAVDVRNGGYIDVENNTMSSANGLYLNGD
TTVSSAGLLRVAVCTFIGRTEFFDPALVYFDGFVTLQGGAQWRVEGNNIRAASLIGMPNS
LYEIQLSGSGTTVALARNRQVDSRMPFFNYFLLSTVVMLPAQFVFGCNLQGEKEVSYDGV
FPEEVVLFRCGTCNDDAACYMPGTESVDRNSCSCNCRDGSHGASCLPFEVPDTVVPPLPE
RAVDGDTSCVVNQTLTSLTLTMWKTHHCYVGVTFSGVGATLTFFLNSMPLHLPINITFTG
CTFCGGAALQFVGGAEVAESAGVLIRVSQTVMRSSVVLVAFAFPQHCDIAVTEVDAVQSS
EVQLLDTRINILSVVILDNVELTASSLLVSNVNAHASKRDAFGLYSTGTLKLVSGSSLYV
RYCSFDGYAHMFDINILSVRDHSVFALLNNTMSSGTSFFFQCLDFSVSDHSVLRVVGNSG
SVCYAIYNDDLWTVERSSWLDWRDNDVGLGAMFYDSGSAFVSIDGSSVVTLTGCKMGSTG
LSVPLLSRVNAGYRFVAGCLTVAGRAVTTAAELELNSITNVTAVAAFGQCTKDGDCFAPL
TTAVIDCECQCAAGGHGDVCVPAPVPAGPLSPPPPPPPPVPPTPPPPPVGGCISDMVYPE
VAQAVGSGLSWLCYRNVTFSGGGMSLTVLVGAMTGDVAHVTFDGCTWRDGAVLVLLGNAY
ATVGVLNIVVTGNTFIDALLSPEGVFPPRTNITISGNRFTVTRLIPRSGLGLGSPSCVAM
NGLAISNDSAVVLSGNVFQSVTASSSAIHVVRSALRVWWRSVFAVLGNTFHMAGSTLIYL
EGSSESLSLSALNNSAVVIRGNLVSSEVQYVIFLISSLSVESQSAVVFQGNEMRRSSVVF
YSRYFSYIYYNSWLQLSSNLCRESPSEAFLFMNPKVNLRDSTVSVSGNRFMSSYGMNKAL
RISTGSRDLTIGAIVAACNTVNGGERVKYSIPSVYNATFLTCEDPCTLAAWCFPAYTTTA
SSDGCACTCAEGGHGDACLPVAVPEPSSTDGADFCVRDVRVDVEVNVSFGTSVACYVGVT
FAADVVVDVGSMSGSVRNVTLANCTFADGASLYVVGWRSDPPAGQRADVLISGLESRSGG
GVVVANRFPPSSRVTVVDSVLIAEKHVAYSGAYDLGDASACLVLHSVNLTGSVLTIARTH
VAAVFDDAVGVLFVGGVALSSRGALYVDGLSVQTALGLCVSVEGGVAASGGSVVAFVDGG
FLLCKHAVSVRGAVSVSGSAVAFVRNDFLSTEDYAVAFYSTVSLAGGSMLLAKGNVHDGV
SREMLYAAGAVTAAGSTLSFVRNRALLPRMLSLSLSLSAGAHLRVACNDAGGRVLSMAEE
YAAAGFGDAGSIDVVGCDACDRDTHCYTPGTASASMRNGVCVCECGSGGYGEACVPVGAP
VLPPAVGTAPSVFVREGVTVRSVFVVPAGASEVTLRHVVLDGVSPVLYVPWMARDGVRIV
VQNVSLLNGAVLYVMGGGALRGAGAAGNDEGGPVELSVCDVEALNGALVLTGTFPAGSVL

TVTDSLLVAARPTPLVYLPGSQSSPYAPVLVLSGLRLVRSVLVVSGVALVTVMTGGRTVV
VDGAVLELVGGGVAVDAAVLGGEYALYASARVVGSGGAVLRVSGSQVYAAHGLVFDSGVV
ANASAVVVNDNVGVLTDGALLVLRGSASFVSGSWLSVRGNSISGRLLSVPSYPRSAELVQ
STLTLHGNAGSGPVVMDGTVALGDAGRRFVVGCLTLNGQALQTMDYRSAGIIGEFRPVAC
GVCDADVSCFAAATRTMSGSCGCRCADGGYGRDCLPVYLPHVDGCNRTPALPPLSHTETR
SLKQHRGGHRRRARRNTVRRSTGRRRPCG*
>TCRU_4984 Concanavalin A-like lectin/glucanases superfamily, putative
MWSMSRWGPNRQYSFVNHRFTLVATVTIHQVAKGSAPLLGANLDAPVSTNFIGLSYSMDK
TWETVFAGKKTTSNTTWEPGKEHQVALMLQDGHKGSVYVDGVIVGSPETIPTLETQGAEV
SFFYIGGGEGDINSSDVAVTNVFLYNRPLSVGELKMAKKSDAKKGRR*
>TCRU_4985 hypothetical protein, conserved
MVAIAEGLFEYNAHENKLFVVRFPDIVAGYIKAAETWPSIVAGITKKEWRAHTTLGSRNG
DNRLRVLHRSTALARDSKVFLLVGIDTVGYGNGDDI*
>TCRU_4986 Mucin-like glycoprotein, putative
MMMTCRLLCALLVLALCCCPSVCTAASDEDQGGSKEVKIPTPSPRVPEEVKVVETEQKLG
TSGEPGERSQNIVDQTPGTTTDTEEPLNQVITPHTEEVRASYSRGTTYN*
>TCRU_4987 BNR repeat-like domain containing protein, putative
MSRPVFTSAMLLLLVMMCCGNGVAAQSEVKESTVSKFEWKNANDDGLSVKSLGAPGLLKV
GIDVFAVAEATCGKEDAEDDTFTGIASQLLTMDKGKESKEEFPKDAKKGTKVLEDVSQGE
KKKVDVSRPTTVVKGSDIYMLVGKYSGKPAAGVSVEGGGDDSGLLLVKGKVGDETKKKID
WKETTDLSRAAFGKELQSLEGLIGSGGSRFEMKGDKLVFPVEGTKSIKEGKKKAVSLIIF
SKNTTSWTLSKEVPDDGCSGPSVVEWGKEDKKLMMMTACVDGRRRVYESADKGESWTEAL
GTLSRVWGSKQGAEAKGVRSGFITATIDGVEDNRNVMLVTLPVYSEEAEKGGNRKQRTSI
LGRTDWKWWIEI*
>TCRU_4988 hypothetical protein, conserved
MSQVIRGRTDWKERVVLRLAWMTARCWSEIAALTPNNFTLEPDGALILDWSVAPKTARAD
PHRALRFVKIRGQDAFDTINLCRTLQENEKLTNITNAKVERVLAPWEATAHSIKQGALRH
AAPIVATYNLDPHVIPQLAKHVDPFDLLQNTVRYLWKYATMLTQVLPLVALM*
>TCRU_4989 retrotransposon hot spot protein, RHS3, putative
MTLVGLRMTTAGGHHTTASTVRQFTECLAAYFNGWEELLRDTSWEIIYVQQADSTPMNDW
RRCDVDNPNSVSDDEGRGIAVFWNEKERQYQVSISSGDF*
>TCRU_4990 retrotransposon hot spot protein, RHS3, putative
MVRTSEKGWPYSWHTIQDLPKDVFVNCEVDRVWQIVKGDITAWFSHHSGTDCKPKRRVLI
GTPGIGKSIAAGSYLLYRLLHYDAEQIQVVVHCFGGGGACVSDKTTRAVTRCSDEDMCIS
ETRSLRGHGRNVYIICDVAREGTPPLRHFAPTSGWGVIAVPSPKVANYDEWAKQLQAVRI
IVNCPDEMGVKAMCAWITRGETKEKQAECWKKVEEHTQLLGPIPRHVFDEEAFNGRCGAV
KFALQSINEVTAKEYFSRGGESPWCSEDPSHKPVKVVREIYAGGVILFNAPISACLEERT
LERLPSVAEYNSF*
>TCRU_4991 hypothetical protein
MTHMMRAEMDVYREILFAGFPQRTQKTSFPSTYVESFFGHYGEVQHFVFDADRGIGSVTF
AKGEVAMNCYLAVHLSLLPPRPNGRGTDDMCDEENTCLIFMEFAQCIPCVNPYLLRTGEL
SRHLMRYKNRMPSLQAAASSPSPCSVANHVVVTWHEATETDLDSNPKRRVVRDGPHFPVT
DTSTVGSTLVKRGNDAIAEAVWSLLRPEKRSPTDGDAVTVLDLWWEYYQRYVLHKTEPAE
GRIKDPYFLFAHKPTVAQEIRRALTSRQTGGSGDVQEDTTVIKRLIHDDVYHSVCNYLGV
KLRFCNDPSWASLARDVASAGTAVGRRTQWKEPEHSRSSKMKGDGDDDEVGTEEDNKALL
RLPILKAAANLMENVRFLQRVRRGEITVDNKPLRPKENEKSRSMNYPASTHQKEGDFYME
VLSTLDGYSPTGTAASLMAMCEDPHTFRHVEGHIGWCELRGMKRSTWWVTCQAVMVVILI
FVFAGWVLGLATSWLGVSWIVGNKTNAAPSRYEMSNPIDRKINIRFAEL*
>TCRU_4992 hypothetical protein, conserved
MPAIYLQTSDGTRIAVPEEAGELSVVVRLALEIWAENHCPQAALTEDDFDNMCTNSRSDS
ERTPDHIMDDDDDEEEEEEEYDYPSTRNCSHGASGNPDNVTAEYKESREYDAGRLREPFI
EASCDLDRTVSVLEDDDVNGNDDRSSSRTPSTCPSIDSAQSPPLRGQRKTPRRRGGSKLN
SCEGNNAIGSLGFSENGKEMREFILAAPAIAADRDDREDSATPSTLEDEEVEKTPNKVIN

EQQRCVSLDAPPIPDLNPPSAHPHPISPNTSAAAPPSPPEEKTATLGSACGTDRNSRAGC
LEPASRNNDKRVVVNRRDSSTVYIEPPPAAGGKEHDGIGERTASTDFISPIPTLFSPRSL
TNEEFLSPSGYHHRTPCMIGDEEEKLLLPDGPFSRLIEEMTMSNKSKDSVSPGSGGSNKN
NNNSIGTPGSVEPSPQSSPSTHRLTENSTNNTRPRSIVQNSSVASSNHTAAAGTGGGPST
EGFSAGHLQCFIISEEEIVIEVHKSLLLATTTRTQINEKEIQDSSVTLPPASQNHMARRQ
SRSACSATTTPVSTMEQSTSAQSQAETVKLVPAPAAVSPDSLGNNSADVSSPILSEALGF
CVAYLRYFASDAEPMERLRPTLIPEPLSAPLLRFLSPWERGFLYREILGQTEEELATALE
ILRIAPTISYIYAAPLLSQPAIRAALTVKVPASDRVNLLAGVIRAAGMLKISSLENMCLA
WCADFIIRASYASMDCFGAAALVRDCFSVRNDWTRKEVDCLKLENEWPGNEEE*
>TCRU_4993 hypothetical protein, conserved
MPLEGQEGTTRRFLQHFFSILDAREQQSASLARGEREELSSLLQLRQRTAIGNLFPEWVR
LLLTQSPDQSKGGVHVDKGRRGGGASAGTTSYYLESNMAERWFAFPHLALLSSVWATQRV
PPPLRATRHRLLHHLQQRYERSTNEGEKCGVFADDFMRSISQHSNSDGRSVEYSSFMNAV
QSLFQHHQSSQCHQHPPVALVAAALFSEWCAVAEGGDSSFASTHVLLKVIADDIAAYNAT
INGPAREPDGGVNTFVVVGTLAGLACAYPMTTATRAGLDKGVSVQQGRKRRRVGDSDDEY
DDDDDDEEEEEEEYEEEEYGSDDNVDGDYGADDEELNKSSTKTDSYGDLWRSQRRQLNSY
IRRNTTAFRVPLASVLLNIFHVRHDGTGDAMMECHVTPAHPSEVHCRRGELRWFIVGESK
RHHNMLESK*
>TCRU_4994 hypothetical protein
MVSRDSDCLDSVKCLLLQGPWASLDRASDVICSLLDDSLKICCCEDDMRHNPVVNAENNT
EKTGLFFAFVKYFATELTLRRIGCVQGTFKRNESTTVHGSVLKETRVGTQEPHNAATYLV
HLQPSVSFPSVQELLRQPSLVAAIELLAEAVWKIQTLLHCGVSDVEVFHVGRCPLCYAAS
IDHVPGTDAMWSLLEFYATYRIARELPLECDGKKNANLNATHSTNESHDDAIVADVDTQR
LLWTHAIAVCRNAIWNGAVQTLRLSVEQWLYAGTHPTLFAVTTPSQGSASAVQVGGDVFS
LWAFLLIQCCLLVQEEVAFEMDTANTTNKTTPVNKKQMNNMRRTPEEASCKDADDDGVFS
QLSSLTPQDRGDVGLHGSLLALYEMSHGAGITAAFVALTTTAPYDATGGLTLLYWVCARG
HEFCVRLLLTAWVAVHRDARLPSNVTRTETYEEKRVRIGFARMQGSDLVTDEKAVPRRTA
KAIRCTALQFDEGILPRAILGGSISILRQLFLCGASRHQWDGGDTKNEEMSALLRDPGFV
LDKAVGSLHERVCDALCATAAADALANAAWKLWKEKVRKLTAGEAGEALYKRSHDGVMRT
ALAALEFDPHNPLARTTLRDLLARKVIDSRTVESLTGEAALHQKRYYQTARRMCEQLFTT
DTELEREIRSLLQSIQIVSGPSSSSLSSSSLRGTATAPVESDNIFLFRNNFEGGDVSGGG
GSSATIAIDEKQRPVYALVNLTDPAASATSKTTAMMHPLWVRLPQGVDVQRSLEIAGGLY
GVVESALPLVAPVERGDLVIFELRQEFFRFDVTRIVRPRDGVVVEVPCVLEGDGEEVKTS
VLRCALVPPPVHELDDDRVKGDPLQWLETTSTQAGDAVEQILNSRQHLQRWLHIAHRCHR
TLWFREVCVTPSAACVWHLFKASNGVHARSAFAVAAFSFVCGVESEEADDPFGITSETIF
LLRSQEKSAVKSNVAFRVAGVFPTWGWR*
>TCRU_4995 AAA ATPase, putative
MAKRQRRQRSPDANLASEAATVAAGNKSQFGEEEKKEMAMNKQLDLFAPILQHYISLLAP
TLTVGPGVGSDDGAQVTNDVKPASRPVLNGNGTGDVASQEQQQPEQNSSEFLLPQRYEVL
NSFVFPSTVNGYLSRVSLLPEDDTSGSEMKRHRVESFPHQKEREEKLLESIRRIADARLP
PFADDSEFIAAHESRYVWNEWVALTSVFANANTQLLRMVTMAKLDLFQQCRPCQKVAIDM
YTSHITTRLQKMRLPPRVVRVAQKLQLQPREMETLTYVLVCHCGSVWPLNCGGNGSLTPS
ALALHNNLNSFQLMHFLADYREHIKQGMLTSDIKLKSSFMDCRLAMPQEVIAALSGDSLS
EEQLIRLEKTALAEILVEEREDTNIAAAAGASGEKAMDKTETTHQPNNEDAEEEMSNCTS
GGSTPNLEALVVDPNILQIGEEGNIETAVTERLQKLLSNLQQPQQGGGTTGRNGSVASST
SCVVTGSTLHVPYASDIDYMDESFKLIANVVRLRGAESEIKDEDEAIFTPKTKMEAMIRE
LRGKVRVATAIHRSRTEATIKAGKFLPRIEALSQRLQLSDLEKRIMLLLIGNVVSNDILI
AINGRYVMREGQRVLTVGYILFVLCDNLKERVAARRSFYQSGPLISNSVLSLSLDGGGRT
CFNTDLMDYVVDIDRKIVDYLMGTETETAEMVPGSRLYMPVVPMEKVVLPKNTTDMVVTT
IQHYTLFEQCKRSCGFHEGLGTSTGGLVFLFYGPSGTGKTMLANAVAHELHKRILLVSLL
QFKNDTKAPEMLRFIFREAKLNDAIVFFDECESIFESRETNPLVTSILAEFEKYDGLIVL
ATNKAQLIDEAMNRRISLMVEFRLPDQQMREKIWRAHLPSNLTLHEDVSIATLALNYELS
GGLIRNATLAALNRAVAREKTSTPTLCMRDFEEGARLQLRGFFLAAEKPPGASTESYITP
KRSLADLVVERQTQKQLDAVARLSKGRSTLFSQWGFNEDDCVDQGALYLFHGPSGTGKSL

AVEGIAYECAATIRLCNVAELLLVGALKVHEVFDEGRKLGAIIVFDEAQVLFNHSEQSLH
VAKLIYYHAVRYPRPVIFIATTGTPEASSIDVRATPLIFQQEILFRLPTQQLRRELWRRA
LPERMPVADDIDLDVLSETPVSAKTIHSAAFNACCSVAMLNSEERRLTMQMLRDELENLR
LKEKHCQPHSVMFA*
>TCRU_4996 hypothetical protein, conserved
MSAAKQPQRVQLVVRGRRFESNVEILSAYCFLFRSFFHEAFAKITTSNGVKGEKDDWWVC
YEVARRTIEVCLQRPVHDDLLVDVTSIELDREASIWRFVYTAETLAPEDVGVIFVYIRKL
FCWSQQQKQKQIQEGQTEWQQEPQLPIRWVEMPYDTQLAMARVVCTFGVEPLVGRFDRPT
ASLNNHGKSTEAGPVSLREKAEVYARQHLQQERSVACGTTQEKSTEETLERGKDRFHYAI
ADEDLVLETKACSRCGITGHADVDCPH*
>TCRU_4997 ATP-dependent helicase, putative
MEDALPQLMGDEILAYVRFLLDWTDAAPRTATGQVHHRLITLGTGDEEDEEKKEEEEEML
SPQTFSYERLPGLVRRISDGIVWGQSRSACSVVIRNAMKHVMSDRCAGKPRGHCTSSMRQ
GTTVERLLAVARSTQYRGPLVLLTFHPNEAVRIWSRETLLHLVKIAASSSSEPSAAAIHV
WLLGMQLLCAIRHLTCVSLDVQEEGTCLLVTDGFCSLLAVLMALDTNLVALERQLLQGTF
AAGDKHLVLFCGVSTATIILLGGSMLLYWLLTMKPAENNNTTMEAPESATGINFKTSSVT
EELAGMLNAKLGTHTTLQPASLASDTKRALVKILVHCLFESSKHAVTSSREDELWYKRRM
RNLWCLASHIDPPSPTNSTKKQSAGGTLSSPPAKSAGWMLRFLMRNASVQLNMQTALRGV
RGEAQDDVTIYTMETAVHALRWLMTALAETLPELATSHYYHEFLLSIQEDCVKLTMAVAM
RTQQPQVTLMLLRHLLLTDIVLFGRGGQPPQPGDCLRRAWETIPTLLRRSVIRQGGKTAS
NSPCSPSLLLRVIEVLDITMEQSSACAWLHLKSLKDGPQPLALVLSKCIQRITEIMEESM
EEMRHQWEEAVMMGGNGNVVSGSGLNLNYNNNSFSSNNNNYFYYHNNHDNTNTSYQGNTS
SAAASRLLSSGSSIPRLAHVFMISKDHVTRRFGEVLSSLFLRSFSLLAQDTFRADAANWL
LKVILNDPVLQENMLKLHDAKVDSTVRENGATWVPVMCSCNWSNLPTEILTMSWWLCALV
TDVCVLEMSLWDRLLDLVVTQLPPLTTEKQMLICSANSTTSSAVTVAEIPASGDEANFSQ
IQNSLRQCAQHLLLVLVQKCSFYSATVFARAVLHVAAMSFPPTRTPSDKCFKSALLKAFL
RVLPKLPAEAKDMLTEYAPAWLAEILRSAQRSIEDSMAKQNRSLQQYEVEEKQIMQLEEE
NRARARQEEVICRSNRERRLKELADERDQATHNAPCVAQMKSAVRRPRDELASLMVAQTG
PCSREGGLLQQQQQATPQLRLEGKDDASLLVSQRQASPPPTALQRHLQKLGEKRVNELFR
VENLNKNLEAIRRIAGNTDFLQRPPNTDDIIGYGRHCLAVDVPVIPYHFSATSNAACDLY
VASFIPHIALELRYELHQKFDEILESCRMREFGKKRRRDHPTTLSAMRARAMDSTINCLP
APSLWTTENGLSVVCTGDVTLNPLDPTCMQFSVVLQSTPSMTTVASLSAGLSEGDVAVLL
LPLRHIFTSLPRLFHDNACSIPEAWRVLGCVPKICLVSSLQPGARTALLTAFTSATKTAS
SFSSSSSSAVAASLGVGGENEVGTISLNFSHVIRAFASSQTHFYIKRLSSIGPSLATVNA
LHDIQRKMFASTLLEPHREAKISRMYYHAIEREIVLSERWEKVSLALVLQHCLNEWQKRA
IMALLFAFAPGWEATALGKPLPLSLLPRPPDLFIIEGPPGTGKTQTIAALTLNLLHYLPR
TARRVLVCAPSNCAVDEVLLRLRGTAKRVPQLGDLQLLRVGVRDSVDREVLESLPPLFFD
DCVRALADVSNTSHSISAGRMTRNGSGDVLKNSNRQNIRDHVLFGAHVVCSTLGSLSQLQ
RADFLFDVVIVDEASQGTEPDVLQALMLAKKRAVLVGDFRQLQPTVLCQVAAARGLKRSL
LQRLLHQGHRSYFLREQYRMHPDICAFPNRYFYGKRLLTHASVMARQRDGSSQALPLPTD
MGRVPRFVFVDVQDGLMEWGRGRSLMNRQEAEAVVLQMRRFRAMLQLTPEEFARRTGIIT
FYQAQKEAILQLLLQEERRSELQVSTVDSFQGKEKDIIFISCVRALHPASRLDGTAALGF
LEDWHRINVSLTRAKEFCVLFGHKKTFRAAAAFKRQQRGVEEHSSCKFEIMVDDDKDEDE
DVVHEVTPPPSKSDEDPFVLDELVQYVVEASHKTPLDKGASAAIFKNHKNLHVLRELLAR
SNEDQEL*
>TCRU_4998 Bromodomain, putative
MEERRQKFYPEEEIVALVRSLDRPQDEGLFSMDVLVAYPHLEQEYTRVCPKRFDLATAAE
KAANEAYSYDVNLTALREDIKLMVNNCYRFNGTKGPLANIAERFEAFAKEQIDAYVTKKA
GGRRLSSLRLSAVTATAAETSRGKRQRVESKDTSGVHGSQKPQQHRGGDKSRSGEMDGPS
ATSAEMVRLVDSLNRREDQGAFAVDVVEKYPELKKSYEEVCPVKMNLTILRERAASGYYL
GIPQPTTTSKNPEPQTQSKRRQLLASDASPSSVFGSTIAESLVLLRNDVELMVSNCVRFN
SNVQSWVELARSFQSFAHKKIDDFVIRHVPALKGTRSGVDAYVTGEKQQSQQQLLSQASK
SQQLHFTSSQDDERMVTSTHSLASPSFSLPSTTTATTYAMKGRAAEAASPPLRAPAVTVA
NYITPTIVPTALQPVFATPDALRRRLVSDHLHRETLRARIIRLSTRSHNDKGENKDTIKN

GTDNNKEEEEEEEEKSVQHTYNSAFSCRAVLCAFAASVREFYRLKRECQNFVTPFEYPRQ
EEQLYMDCIVLIEQQFERLFLHTLLYDKEKADFYDWNAKKAVRKIVGSVEVTSLKEKDHE
GFLCGFGSSWLDDAHLCYLVRFLQHLPQLMGLACATTVHLTGTESKNARPALQITEVAKG
VIEKLARITEELLTFIAQYEQEAMNMESHAEIGKEIS*
>TCRU_4999 hypothetical protein
MYSFGRFSFLAIAVLSGAYSVYAITKYRAACCVSRARLVIPRAVSLFYASLRKNDSARDF
HQHQHRDDDDHTAKDTAKPLAVQPGVARASSSAGTWSGATETSTPSVSCPVVFVDNTNFE
ANVRAVVSLLLKNNKQVRLSTKGVRCPELLERAAALMEKYAVPCPEYDIISPGRPFVSGL
LTSTAAETLLWARRGTFSSLLLGQPILDALSADRYVEAMTLNFSSKVRCLVVVDAVEQLE
LLWNAAKAWISDRGYTRLGFDNAVESLHFELMVRIDFSGDSLKKCFWRSEEPQTLCSPRQ
VTQFCGKVGEFNAKLSKEKLPVGVQFVIRGLWTYENGQLSQMDIAPNVLPNAIGCTPARW
FLRYPLLQWYKQYVSRNLQMRCMSILQRLGYKKKVSPEDLLTSGGSSVSLVYSAQDSTLA
EVCMGAGLLCGHQLDCYVDSPFKPSLYFALSVTRVAPHRIVICSGFGHNLSGAIPVYPPQ
LQSINSHGADIDDDLEVGVMVLDGTPEERLISIGDPIVFRPEYSSVLAELVDSFLLITEE
GEVSAVMHTYRGEGWNIWA*
>TCRU_5000 hypothetical protein
MSGDESAPRTTAERLRAARRQETALLYEQSFDRRRCSFVRGPSCLGSAPTMASSVSSDVP
LVRQNKGTQGQCTSVIAKSESHETVTARDCNVCDSDSLPITLFASPLKVLDRNWSGYNTP
RRPEWCMYGAGTHTPKKKLSMNTVTSTRRQPPLLLRPSSAATTIRSNPTGGLLSNRATSR
LMTTPRDRPYSSSSSLMTHNTTISTAATVMTMAAGTRRADSFRTTPRRLRSQSAARCAGS
TAKGQTGGMGVVVLTKEEVQRLHQLIASS*
>TCRU_5001 PPPDE putative peptidase domain containing protein,
putative
MGLCDSKSKQVLSTSGVAEKRKDSSKGNGPAVSSSSTAAPGFPPSFSSTVPAGSSSNAPT
TTERRREGVAVVLNVYNLQRRSVRESRSLNEWVGLGVYHTGVEVFGTEWSFAGCASCSSH
VCGIFPSRPKTVLPRQMLKESIVLGYLPPDTEPSRIYAVLRKMSPLWSASNYHIFQRNCN
HFSRAFCHAISKEFPEIKLKKFPSYVNRAARVADMILPDVFYRSWARGNSFPKPNSPIPT
AAEKEDTAGASSYGFGSKDEGVATIPIPSTREAMESMTVRELKTMMWVNGISWDGCIEKE
DLIQSVEAHRQRHSRR*
>TCRU_5002 hypothetical protein
MEAYSADELLVRQREKLNANAAWIRRQQMRMQNTDGYDGNAADADENNMDDIVMRGTGAG
VKAQEGMERNLAQEEEFMKTELTPSAGQRRSVGSVSRQIAVRQASANPRSPGDVGNTANQ
GDFFTTVRGGSVLRVQKRNALWQIRRQQKLEEKRTLHAEDYSQYTFSPKIHGYSGNASGS
AFMTAPGVEEFLQRQERAREIARMKEERGRVDGSKWVHRLTVAEPFVFGQRPEIESLRPP
LQNVPGTLREILSEGETEFVRSGKKKISVGSRRELLPDTPAPFETIAEAAGVSLPPPGAF
SSWALLYCGGEAPNDSKTEKDSTPSQ*
>TCRU_5003 mitochondrial carrier protein
MDGEMILTFLPGAAQGLTTVALGHPLDTAKTRMQAVGPRASRSFVCTIWSMARAEGAWSL
YRGVTPPLVMSATKRSLQFAVWDTFRQHDIQRTSHGASPSYVSCTFSKIFAWIGASPFRS
GAIAGGFGTIIGCPMHVIKIQTQFSTRCVTKNAWTCAIDIYRNEGFCGYYRGFRYHVVKD
IFFASCYLGLYDASRRWLCELFSVFSQQKWGPRATVIVGDSTEYFTSQSAFLAGSIASMA
TWTLLYPLDTIKTIVQARNIGFLQVTDIFRREISAMYRGIGVSLVRAGPVSGAAMVVYEL
AKSKTDQLLLQSRRGHTAAG*
>TCRU_5004 hypothetical protein, conserved
MYTALGRGSALRESNNVVTHSNAGTRSIVEGNGKSTLRLPYNKENEATTETSDFSLQGTM
LKTLMKGEEEGEKAGEGEREEEGEQGQRSLGENIFAGSSNRSALSDSLFQTNFRKRIKIS
WKCGMCGYHVLAMDQNGKPLPLSVSSFGQVLPMSCPRCQLEHTSWEQAVPFDEYGDHANI
RSKLSNNYVRTASNVGGTDVEDFRPTATKRATGVGVETPDIPPILQEIGCWRQKEGGGQR
VAQNDPRFCGPRMAYYCGKCGRKLLRIDPYGELVPMVRDEDGSVLPIVCPGCKVEHSQWD
VKPFTVTL*
>TCRU_5005 PPPDE putative peptidase domain containing protein,
putative
MSLQNILAAANSPKLVRIISTVESVLKPLNKSGDTARAPVSATENGRGERNFAENTVFLN
LYDLTEANDVLYHAGIGLHHTGVEVYGMEFAFGRCDEGSGVFEVAPRYSPPHIFREQLVL

GETQLSQQEVLNIVKEFKENDRQWSGRAYHLVQNNCNHFSEAFAKRLLPPEVRAEQQRQG
KLRVYDDGERELVELSNGATAILPPLMPRWINRLARNASRFMPSKLVERIDAMDRGEGGE
*
>TCRU_5006 hypothetical protein, conserved
MEGAGPCRLPEDHGSTSFAVKVAGWLVPDVRRHLFLLVWIFGVPIHLQYVVHLIRMSAVS
LEIGTRVTMTGSEKEQVAHTAMEAGDSPFCPDEASLRDAALDILFVQVLADCRAANERVR
KASLSTDEWSEVQSLSYRVDENGVTRVVAQDVLAKGEVLALLPTGAALLEELEATYFTAV
DQARRFREQYPFPLACWETRCRRNNRTQIKKKEHSRSECASAAIDCEADVILIDSDDDVR
SLRKPDIVILSDDGSGGSSSSGGYQPVKRRRKASPRAVYEVVE*
>TCRU_5007 hypothetical protein, conserved
MKYLVLLGQLPGEGLWATAEDYNGLVSHMKEAFGVDYNPIFKYKLPCNPKMLSPPNGTCH
IIIDDEDDFQIWKNGRVPVNRHRDALDDIHHPPTPLTTTLYVFRKDVHSFSTSKLKDSGR
ASRHVELKSGAERPSPEVLHAEHDVVKMPLYSLLPPLLLLQLGVRVALRHSNAAEAILFS
SRSVSGAGEGHWGLMVRKAQSAWGVLRPSFRYLDLDHGVTAMNIFNVRDYMFWSRGVGRE
RVELVVLEHVYRDASHASPLSGLLTAENEKSRTAETKYASSNTIAARQMDGTLGNRCNYT
VTTEATVRGVHCGLYGPSFTTDALIPPKYSELEAEAANSLEHHRTLVGILTRSGLF*
>TCRU_5008 protein disulfide isomerase
MIHFIFKQREKKTSLRAEGSEVVEATDKDFDDVISSGEIALVKFYAPWCGHCQKLAPEWE
KAAKEIPSGAVMVDVDCTKESNLAQKYSIKGFPTIILFRDGKEVEHYKGGRKSSDIVNYV
KANLGTAVVHVETAEELEKLREEHNAVCVGVTSDMESRLSKTLATSAEGLRMKMKFVVIT
DSNILPDEKPESIIVFRKGGEKEVFDGAMETADLKSFLEVAFIPFMGEINPNTYLDYAGI
SGPVAWVLLKPSEEESKELKSKLLDVGKKMRRLMVLLWVDAEQYGVASSLGLSDDAKYPA
FVIARGEDHFVHPSTEPVTAESIEKFIIEYSEKKLSPEIKSQPVPEIETVEGLTTVVGKT
LDKYLSSGKDMLIEFFAPWCGHCKNLAPIYAKVAKEFESSDVIIAAMDATANQVDNSLFD
VSGFPTIYFVPHGGKPIVYDGGRTFYEIYKFVHEHSSTLKDVPIPEEVKREEEKNGDYDD
L*
>TCRU_5009 hypothetical protein
MSDMEAHRLCADYSGTSAWHDLPEESYERVVALARAYRQRLTETDQNSGTALALDREEYV
DSLPKEEMMRRRRIEKKEQDAMSIVMKLWTQRSIAFANELRTIREEKLRMEKVKKQRILL
EEQLYREQFLDFWQKRKKEQLRNLPVHPDRVLMNAYRHNILPFATDPVDCWERGIVVPPE
LQQTVVLLDSEGSVFLPAFHELSMKLRTAYHRYRAQ*
>TCRU_5010 hypothetical protein, conserved
MSPHPVAPLCRWSYFATHCCVGVVHLPCRGSILGEPLWSCRLLLTECGFSALPPPQQKAV
CSQETLTLKCRGVPFVEFSTSELKEGALVHVVAKMYKKPRFIPIHGTYVEDTELLVSEQF
GSLVLLGTL*
>TCRU_5011 KREPA2
MRRLLLAGALAKFSRRVGARWLACAPKARYAVNRLNDGSYFFLPALNCQERFQSSSDKKF
HCSVCKKAFRLEMAAKLHLQQAHGGDGSVEAGPGPGAETAPTAIPSAPPSSPIERNFTDE
EERRPRRMRPTPKPLHQPDRGVPDADMAELLGVWDKIGLNRLEGSFVHSTMVMKVFAARP
DVTEQPLYEPVTPEGDNPFEKMDQIDARAAPESYVKDHALTEVDLKGPFAPAPDQTLNPF
RAGKVDNPFAKVPTVHREVPRILQPQQQVPKEEPVTAPITPFGQLPMFGKQQQTKETIPA
KPLQQNISVPGEVASPFTAAVANSPFIGQVASPFTSTPDAAATPFEAPPFTVASPFAAPG
MQASSPFTATDALSPFAQNASCQTSAFPMAMGFSNLTPNVQTGQRAHVEEKCPTCGKSFS
TFDGLAMHSKAKHGVLLEREAKKDGKQRGRSVPDLPAYIPSPVDLSSSSPFGTKTAVAAS
WVETELIPHAQCVSNITIVGRVLDVTQAMEGVSHVTVFVQGEEVGEEETVTVHCSGDINI
QVRDSVKRNVTIFLTGTLRLHPVYEASNNKYYVSPVVHVASPTGTLAVIA*
>TCRU_5012 Ribosomal protein L1p/L10e family, putative
MVETPRSKEALTKLCSFLAGDKSSKRENDILGDLFSPSTQTHFRSVDVEVTFLLSPVAHR
VPLYFTVPHEVLPGTVCLVTPPAQRKYKDKILRLSEEGNSVAQRVKKVIDTKKLSTKFVD
PVAVRALANSFDHFILFGVKKYPPQLTGEFLGHQKSPVWVSRRGGLREKLLSAVKTVVFQ
RRGNSAVTCRIGHTGLLLEQLHENLHSFLAQMTSHAQAATPQDILHIRVAGTNTDGRRAG
LPIFSHAFQIPHKMPLDESEGPKTKKLKRK*
>TCRU_5013 nuclear pore complex protein (NUP155), putative
MEPREGVMIKIDDAVKKAVEDTISAEVRSGAVGKYSNPSASGHATSHLLALTTFDTSSTL

PDFIPLVGVSWPEPVKAVWKTFRANSIVGLFPELSRAWITVDNKLLLWNYGTGRDFLVYD
EIPELIVAVGNPVTPVAGVFQLHITLVFPVATPKTIHLLGLCVVGDETAKKAELCVVNLG
FSVLAPTLVIKLVGLRDLGRVFAVGADGCLYELKYTKESTPFIPKVRLINHSIIFAGIPI
LSTVSSLMSTLKQTWAKQRPALRDIAAESKRKLLFTLDAEGKILMWRITEEGLKVLTTVK
CTRSSFEHHRHLESSADDATSFVKIFCVSPYDENFSVVVITSNGEQYRYLCQEGMWDRTD
GNLTLRDWTPSCIPSNREISVCFTSDGVALFCHTEKDDENASSDSVAVTTSPKTVLPPHH
HCRDIVAHFEPSASLMARVDAIGEVPVRESVSPNELCSQVVCSPRQFVFVHRHGISTFMK
LRPVDTLHMILSFSGQQIRDNLLQRFSSVYSASDYCCMLLQIAVGCTNVPAIVEGPYIEN
GIANSPFSQMEKTHVKSKGPLSMDQVGSQLINATSQEAQRLAREILRNAMMPSWHEGPIS
ASGSRQIVVQVSPFALGVAAYIGRALYKVWETPMGNLPLHDLAVIEVVLSSLVRLLNSLK
KDVWSENMVQLSVPFRWDQSKVTLTFPSHGSSVSSYDLKMLQSAFLYSSHSLCERVLQTI
KFAKQTAYIPLSLDDSKITLAQVVGDQSIAHRLARYIGRLVLSTEQRVGFLQQDRIAPMT
QLQLECPYFFSSIDVHEYSARIELDQLLSSSGEGLYAFSESKMTDWESSVSRMAASLWSS
GALQGICQQLKALKKEDTLVRLLLHAASQLDPNNSAFEIYLAERNGNRSQCFSSTLNAVY
NQKVKVLTAVISTLEETWNTHRSVVDDLLGGPLSSGSIWQVEPSDEMAHCFLFDWMCVPR
DDATITSMLKETLVTARSPFLEAYLHQNALTLGEQYAHYLRRTKKNYKKAIEVCAAMAQA
PLADIPREERIPYRLRCWSEARDCAAECNSDQLSLLEERVKLMEGQLQLSKIICEFINSG
LPQLDRQVSVSGRGFLTERQVALEQLELVDNFALSTSQLLEVAGLFYAFGGAEIQLDVLS
AANVTDASLYAACVESAFKRRNTTVEETARRIIGKCRHLIAFPLSHVAKILEAYAFHQSP
DGSTLTVDILTECGVERNIVFSTLATIVEKKDTVGLPCEAFDESGVTDAFLMHSLAVALH
RVVFAPHVGSVQLHFLRNALNTVREGINRVAYFPADEDSCRALTAAERILEQCHLATSRL
TSRPVF*
>TCRU_5014 predicted bromodomain protein
MTDFVSRVKRLRNRIKVKRDEVHRHLENSFYRECRSVLNAVMKQDENGIFASNPAALPEY
VLMISRPIWWKLISRRLDRYEYGTKMEFLHDMRLVIDNCYAYNGEVSPVAALGRRLEVVM
EDLFVTKLAVAPPDAREIITLGKGVNHAQARQLWDIVCRYEGQGQGTSAARRHIVPSQLK
CATQRRVIAFLRQKMGPHEQNVRSGKGSSLRQQQQQQPLSSLPSLPLPAKPQTPKHPAQS
LLKDDTDVAFSTEQKMTPNHLQEPQLERVPQNKRSGFASFCAVSPIHLESSGIEEEEEV*
>TCRU_5015 hypothetical protein
MSRAVTKEQYASLRAIRRTLLGTCSGIPRQEFLDAHSMGLINFLSSKESKLQALVRQMDI
GAHDSMQFVKSLVEFMSFIVGGLTVEADKIEEAVLHTRRAVATLTHEIQRCEMELEHKQQ
YGGTNVTRALAQFYRTKLVISSSKASSNRNEKGCTHELARTIAEDRARLQETKRALRVLI
MVQRILWGSGIVSQEDVKYMLCEFGVALTIRRFNHKLRDLMLPLRHETRDPLGCLLSLEG
FIENVHIGLSAALEDLDACLVSIKKCILLQQEEFRVRRTNALRERSSAEVSSVFHSSRPN
RRVLLTSAKETEELSKLYCS*
>TCRU_5016 EVE domain containing protein, putative
MSRKRVPSSEVGQYWLMKSDFHAFSIDDLKKSGCSPWDGVRNYAARNNMRAMNVGDRILF
YHSCAKPAGVAGLAVVVRTAYPDHTALDPASPYYDVKATKEKNPWEMVDIQFEEKFPSLV
TLERLKAEKELRDMKLFSMARLSVQPVTRSEYEYVVWLGHGGKGGCR*
>TCRU_5017 hypothetical protein, conserved
MNREAVATPLSAVPTSLVSPPLPTPPPLLALEPHTTRQEADKPALPVLLPVESPPRAGIK
DMNAISTPGQKDAVEEKSTVEEQPAFTVYPPSSDKPQTKHVSLFGRVRFPSVFAAPVCVP
AREILSALPQQLPPPYVVFGGARYDQMPFTKKAQRYVDPSRSCQRATAMKRASLDYMKGQ
LKLAREYLDLGTSPVPPDAPKGGQPLPNGVIKPATTLSFEDGAFSQKNIWTVAYTGSAKE
LHGFIESLDVDALNANGFVLYNRRQYGIKKLGEKFVLGLGQKASPLQFAAVAGHLDNVVL
LLHYGAMDNSTPRLKDIVGADVMKMIRGLRAGLRCRRAAPSSKAKVEDDVLLTNAPLPLT
AEEVFPPMGMDSNFSTGISLR*
>TCRU_5018 RNA ligase/AAA domain containing protein, putative
METFLDGCFFKKPWTDGRVEGVVEYAGTGKGRLFCTGAFTSFEVKESHQGDVKCLPTGAR
TLLLDADASKVMVRGVDKFFDLEDDKTEELNKDELWEMGSVWLQRKVAGFTVTLFSLDGG
SVGVTTKHVVEGLHVELARCVLDHLLSAEQQKLLAFDLFSAEAAVSCECVSLKDDLHHPV
LEPVEYDNKLFIFSVHKRNDLREIAVPIEKVQVMSKRWGLPVVPSWRTGDREELQQWLQE
REKWLGVGPDGIPLAEGYVVLVEIPVTQMSSTVVLEEPFTVAPLRLKAKTVRYRVLRSLR
SILTGDSTESQKLFHDVLAVWSEHIGGYKCFKQAVAQRGVCKICSQFETYVSTHSKRRLR

GSHMSIGRAFEKLKNFTEGEALVKRRASLNVIMLCGIPGAGKTTLSLALVAMAERGDSPF
RYLIHLSRDQVARDVAAQEGIDDSSSKHKQRKLRAMVHHALLEAVKQAVLFSLIQEGPGL
LLMDACNAKAETRRVWRGKLPPKVESFRLLHVTCSDHPELLRRLAKRRDHDVIRNNSEAQ
TVLYAVKKVFLEPLEDELCVRLDTASTSAEDIARYVFSLYKGDRQRYATVYDYRGPEEGL
KALRATLVESLLGPVGEGASTLLTSSVKRIKTSNAIFVRLEISSDELLQIASEAIMAVTG
MDCLSLSWWEKFKRALGIEIRPLCSTIEDGHTRWIYGWLFDGRKEGKAFSADAWRHALTE
RFECRASAPHVTFAHDASSVESSSLVPEAGSMAEVNLTSILLDRFAICFGATAVVNGQRY
EKQLGLSETVPLHVTVCHTERVKPSYAGEMFDLFRQWGHHNKELQHMKSGVLVKRSRLKF
FNFLKLRLERSVALRGIVVSET*
>TCRU_5019 hypothetical protein, conserved
MSEALESSAVQRARDDYMQHFSDVFSEELVKVYESDGSATAVEQLTACIEIGVAVWGHPI
VVKNPLKG*
>TCRU_5020 Protein of unknown function (DUF2453), putative
MMRIIRRVSPAVAGNLLGCNRSCSSNKSATLTQGELQQLVKLLEEDPKLLIDLVGRLDAQ
SRRRLIVAGGAMEWFGKESAASEVERADVDKDLLISPKDFDHWLESALRRRVRGKWPQQQ
EDPAAADEEIRVPFLALVRIAFGAGLPFVGFGFLDNAVMILAGDAIDSTLGFYLNCSVMA
CAAMGNIFSGALGMQVHGVIDKAVQKLNFNTPVLTERQMKGRRVFFAGHIGGTIGIMTGL
FLGMFPLLLLDSGEEKADHALFQRLDKHGNGYLELKELGRALTDMGLPASAVENAMEKYE
QNSQLDFKQFQKIRNDARRGEALFA*
>TCRU_5021 hypothetical protein, conserved
MLCEVLERIVTQILRRARIPLTAKRISDALGGVVSVENITAVCLKLVAEGVLAKWGNEAY
SVKFMSRLVPRNLLITEEYQALGMTLLRVAENTLVHYIPQEAEHRFFEVRRSTVSEKAGL
GLFLRSSRALPQGAVICEYVGRMLHRPPKKTNQSVYIVKLRNVPAYVDGVDENGEHLSLA
TFINDNGPAAANVEMREYDMHSGRVFVVASRDLVPGEEVLCTYGSRYWGYSSYDEIVRNL
NGLSRKRKRQRDHEFDEGDEEDFGDFLFPCRRCGEQLPRRLMSLHHRTCGDHLVNQKLLH
LNCLPLNDFTAMENRSKVLPTGRLRALRRAKHFVDLGDPQTFALSHEDVVGDLVFSWCAA
*
>TCRU_5022 hypothetical protein, conserved
MQQGARSLGAAALTYVKKEAARVLAEREGYSAGVMKTVEFAPDKIVERKEGMLSFPWSAR
RGAVNAVKSAHGGALSTLADAFTRVHLGAVTTSAKLTSVSFEISFLSAIAENTECTCLTR
LVSLDVGNLAFMDFSFEDEMSGQVFARGTHVLCWCG*
>TCRU_5023 Uncharacterized conserved protein (DUF2042), putative
MCDTDLSELVKKFQAIQRQTFPDQIGERNVVEIINVLREKQLVDLLYTLDGKEYLTWDQL
RREVVDEIVFNGGRMNVVDLPGSLNVHFTHIERVLQDVLEDPTIRIESGELLTDEYLEST
IQAAADVLKENGFLSIAEFAKTHRFSSVFAQDLLMKAVESQRLRAVAERSAMYTTQFVHS
QKAILRAGLMAATRPVKLTTFFERHNLFVPLMDPVIDAVRAELPGKFVGGVYVPTYFEVT
RAEQVENVYLSNGFIEYASLHQHGISQAKEFLLGKYNPVVEGSAARTATGTEVRKRRGRR
NQNADATVEAAPVARSETHPNAGHALSSCFVSDRFLANLVALEDLAHGDTLALDLSLHLP
SAVSFEKDSNVLLRRLRELHPVIDSCIVLDGGLLVHEAALDKFRARLRVVFEESFKQGGK
RKRSKTSESAASGDEKEQSVLRVLADVTGLSLEEYSTALEDLSSQWREIARDIYDELAAA
LEQQASVDLKRMRSKLQVSLGVSWVDLFVVSKGVLWSKSHMDEAASTAVSRHVLTTRVLP
MVGDIILNESLDVAEVFERVSAVLTPGQPSIVTLQKALQVFPEKHRRPLLPMIEAANGRS
VENFMSILQELCTSGQIAISSFYQPNKKLEREALAALKKRMLERVEKGTFGTDVAQSGVL
FASICSFFLYTHFHVYVELPGRVVGSAVELIAREAAEVGGVLQECYQLITGAISGKELST
ESLVRLEEVRRMALEGALVSL*
>TCRU_5024 ATPase, putative
MRDSRIANNMWRAHVSSRQTVTEMYDALVQKRALRHDPRQRDMAQACTPLLNHIHSLERT
GVVTSSSASSVSTPVSFADAISNKLLRMRSWLRSHAFPDRVTREVAIQWPENVGVERKTG
VYMWGNVGVGKTLILDLFELTETPGWTKRRAHLHSFMSDIVIRLHRAEVAARRTRKFSPI
NCVVEDVLRESPILCLDEFQTFDVTHAALLAAFFSHALPRGLVLFTTSNRPPHELTSIST
AFERFIPVLWRHCDVVHCGDIKDYRENASRSHHDVIFLYPNTKENAKRLIRRVERGFTGK
WAWEQGATIWLYGRELVVPVHCGGVALFEFSHICGLLGPPDFQCIAKSFHTVIITNVPHI
AGVSRNAAQQFIILVDELYQYNVKLLFTSEVPWEKIVDTGTAAGGGGTDLCYSEGEDERS
GYSAHYEFRNAEEVLSFHRIASRLKEMGCQHYLLRDHSHFVISDYNIASLLE*

>TCRU_5025 TFIIF-stimulated CTD phosphatase, putative
MRLQRVRGASFKEEYKYAVFRRPRLEAAMRETVATRTLLAPKASTLADRITVVLDLDETL
VYAREGPLYVRPGIEELFQFLEENCESVVWTAGMKQYAEAVVRLIDTNGSVHHTIYRDST
WFRGRSCRKDLTLLGRDTETTIVFENTPDCIRGFEQNGVLVADYEGGELEDHTLYTILGL
LKDLVRRRKEEHITVPEYIRSSSLLDLRVVPTDNGDEMSCYCLNACFPELEGRKCTPVRI
HKILCRTGDRRNIAVH*
>TCRU_subunit, putative adaptin complex.1
MDAVLRKVQEKIQQNFRRGGKGSRFFSTARRGEGVELHEDLNSNDRERQKNAVKRIIAGM
TMGRDVGFLFMDVVKLGQTPNLELKKLVYLYVLNTAKLQPDKALMVVNTFLQDTTNSSPI
VRALAVRTMLCIRVEAVTEYTLEPLRRAVTDPDPYVRKTAAIALGKLFHQNTQLFMDQGF
GEELLKLLNDVFAVVSANAAAVLTEVNSCSPTPILPTGDYINRLLHHLPECTEWGQLSIL
EVIADARPKDAGTAEDIITRVLPRLSHSNPSVVMGAIKVIVNLANRCNAVAVSHYSARVN
SALVTLSRGDPETQYVVCKNIHAILVIFPNLICNSLDSFYVRFTDPPYVKLEKLRLLLKL
VTPSTACQILKELEEYSSEVDLVFAEEVVKGIATVALKIESVAPSCVELLLRIVGRRPEL
LPQVITSCKNIVRKYPEQLVLETLIIEHGADAVAEEDAKVSLIWMLGEFCDFISDGKSII
TRFIDELMSHEQPVQMAILSAVIKMFLRDPVGMEQTLNVVLDTLTTRSNDPDLRDRAYAY
WRLLSKGVGVAKMKQIVHGHQVPITVESTFSDAMTMADLKKSINTAAVVFGKPFQSFLPP
YGLVNEEASEEEEEEVEETSAVSPAAVASPTSTTLPEYPSLEDNGPPVVKHVDPLKEFFG
GPPVTTTAAQESQTKEQKQQKGELLLNPLDCFGEQRQQQNQQPPLPPLVLPAGSVDVAIH
GQLSEGPALWIALVNHQAVAIDQIVLQINLNMLGYLPGVAISEFMASVPAGETRSVKLPL
RVSQGHFDVARPVLEVGLKGRNLPLLLFHLEVPADKILVHSSPIEKSAFVADWQALNSSV
EVKEPLGEFGENMLASPDRRGILEQNHVFLLTPERDSGDIISYYGKVTTTLGLHGLVEIL
LDKKRPLQSYVCVKSQHVGSIMPILLKVIQSAFPKKTVASVGATAGGTLSDCDAVLDQWF
A*
>TCRU_5027 ATP synthase delta (OSCP) subunit, putative
MFRRLSRSALAAAAVRFYTPSESLKKLYTSDFDKTEFPLSIVPSDSVLFAKFLYKAAEPN
NSFDAILKDFQTIAAASSSLPIFWERTAVVEDVAEFKKLSEPMFFTLVWMQKNGMLDLIP
EVSEIYETYVNAKMKRIVAKIYVAPGKEGEVGEAKRVAQELHKEAKELDGYTLVFKTVVD
RSIVTGFAVELAGQYVNRAEGHKSHAPAADEADYTTIPAPRLPKTVWEDNIETEVLCRYL
ESLAEYDAEEAKHGV*
>TCRU_5028 Aromatic amino acid lyase, putative
MRVILDGCSLTPDVLYALGYEKGATIEISDEAVARITAARAVIDKIVNDRQTVYGINTGF
GKFESTIIPPHQLEELQLNLIRSHSACVGEPLTPERARMMLALRVNVLCKGHSGIRLETV
QKYLKAFNVGVVPYIPEQGTVGASGDLGPLSHLALGMLGEGLLATLNNKKFRDAGSVLRE
LGVEPITLAAKEGLALINGTQFISALGAEAVVRARKIARLADVALAMSHEALRATNSTLN
PDIHRVRPHKGQQLVAQRLRALLHSEEYPSMVNESHANCGRVQDAYSIRCAPQVHGISNE
VIEWVYGILTTELNCATDNPLVFPDGVKKVVSGGNFHGEYPAKALDMLAIGVHELGNISE
RRIERLNNPTLSRLPAFLVKNGGLNSGFMIAHCTAAALVSENKVYCHPASADSISTSAAQ
EDHVSMGGFSARKAIKVVENVERIIAIELLGACQGIDLLRPLRTTEPMEKVWSLVRSVSP
PWEEDRVINTDIDNVTKLLRSGAVWKTVKPYVPEEARFLGVLTVKKPFELKSKM*
>TCRU_5029 serine peptidase clan SC, family S9A, putative
MRSVYPLARRSMAAYTMHNMTVPEPYDYLEDPENPETKTFVSEQNAFFEEYFASEAELRK
KIFESISNSQDYPRTSNPSYINGHYYYYHNSGLQNQSVLMRATSLTDTAPSIFLDPNTMS
SDGTTALKATAWSEDESMLAYSLSDKGSDWQRIHVRRADTVEDTSDVIEWAKFTTIAWWH
NLGFFYTRYPALQGDVDKGAETDAAQDAFICFHRIGRPQDEDVVILSVPEHPQWNMGASV
SDCHSYVIVVLFDGCEPHNLVWVAELPSVEKGLGSEPLVFKKLVNEFAGMYTYLGNEGST
FYFVTTRDAPRKKIVSIDIHTGQETVIVEQQRSVLSQAALVKNTLLLAYLEDVKDVFYYC
RLEDPTLNAIPLPIGTITSFFSDRKKDFVSFKITSFLLPGRSFFLDINDPQSSLRVFKDD
TVEGLLVDDFVTEQKFYNSSDGMRIPMFIVYRKGSVSSKSPLLLYGYGGFNISLTPAFSS
SRMVFLRDLGGVLAVPNIRGGGEYGEEWHDAGRRVCKQNCFTDFIEGAKFLHRQGYGSPQ
TTAIMGGSNGGLLVAAVANQAPELFRCVVCQVGVLDMYKFHKFTIGHAWKSDYGDPEKEE
DFRVLQKYSPLHNIKSGIKYPAILVVTGDHDDRVVPLHSLKYVATLQHMNPTEGGPFLAR
IEVAAGHGAGKPTSKILREAGDIYTFIAKNINASWKE*
>TCRU_5030 hypothetical protein, conserved

MTAERLVTLKGVLLTDLWNGPLGAVSRTRDRLGHIDFAMVVPPLRAFVYCMLCPFLCYPI
AALYLWGYYRCMRTIIFPKSYRRERYASNVMYGVQKRVYDARQRRIHETTVGDADEIRHA
LEVTNGARNHFVDDPKEGGVAYFVVEQKIMRPEALFTGENWAWAFISDSCRFLTPVLLSY
LFVPSCRRLGIDIRLWFQGRLRWWQLRHPVLNFFKSYRDYNNAVKRINITKPPPKGKEPW
TKNL*
>TCRU_5031 hypothetical protein, conserved
MQAAERFVSSLLAARAEEEERREVRRRRRIDFIIAGNKERTRRCKDNLSVFLQRDVHSMS
LVECNFLDSLGDVENWWDLISKHILEEKREREEAVKLQSHLKSMYLETTKRREETEQSSV
VVNDERRLQELEEWCLAEERRTREEVIGEVMHRILAAVDECIGFTEKHALESDSWNTSLG
RIALNAFIRKINMKTWTEEGRAHIAFKEIFNCHPFQMTCDAFVYLLHAIYNSLEPGLPHV
NRFDLSRRPLFLMYGPKFSGKTVVSRNVAAELSLLSLSDRDLIQKALEAYRNERNGLPTL
LTVEDSNALPVLSAYEERNKQNDEIAYYSEAHIEQVVVSFVRLSSWAEVGKTVEEALFRG
ESVDPFLIVQLMQLQMADTELNCDGILFDSTVRGLEQLRLLQSPISKRFHPFEGALRGFP
ACMEEVSLSSKLLLVQREGRPEASNTKSENRSRPPKKGVDLSALPPPVLPEVIRLELSEE
EKEAIKLWEQQGQKHSLFPAVVHINCGTHEIFCRFAGLRVDKETNEIYHMLFDPPPPDRL
PYVVNFDRVKSSTAQLHRVLLNEHRNWEKMRRWMMSEGDGSEVLHEVDGERPLENIIFDV
WHILQEAKNNYEAALRLYDAATAAKKREAYIEASIAEQEEAREAERKRLVALYTEFGAPI
PPELEPRPQWTPFYKMPVNLPEAFMRVFVAFRKHYESAYDWLGTAVEKLASVMLGHRCEA
MGAFHRFWNQPDEKQEKLSRFVENYNRVLVELPGQKSCKEELHLLVDQLREELFRTLDMK
WRETSAKTEQLTKKELFLDPWCVSVCNVGIAAVQAELERFLLTINLVAIYFGAVVNEPCM
FEELDLEIIVLRTTAESAMEQTKGREKKTQSTKKTPRLEEISEKTFEDTFVEAIGKIVTA
MENFVEKISSVIDAPVRTRENTKTSVVAVDNVRVLSVLNRCFPFAKSELAKAQERISCIK
QFFLQIQREGEAYCARMKEDMISYAREKNFSQASAVNTAIYIIRNAIEEEKPLSPMHLGR
DTFHTATAEKEMPRAQQLLSPQHLQMMEPSDEPKIHATLSSSRLVEIILAFRSVAPGYTL
GHAEFFNIVRPDDYAGATASNLGRLKTQEEVFTSFDSLGCGFIDWREFVVHLLLWCAPAP
EVGSDEDAENNFYFPEFSVENLLETRTELGLEAVTEDVFYDVPFFFDDCLNDDRLEAYVR
ALWMTFSTEEGLLEPLALLAFFCSDRQPIRGAQKAFYVFSREQDGKLTPEELDFAFHVQA
TNPRDMRFLDVFSPENIAMLYDGESLLAFQSVCERVIGRTMLNNTKAYQRKLFITDDPHV
E*
>TCRU_5032 Mitochondrial carrier protein, putative
MPENESKKNDGNDAYQVTVLHRFVGGTVGGMLQALSCHPLDTVKSRIQRDLYPGIFSCCR
HTWANEGFRGFYRGLTPPFMMSGVYNSILFSVNQFMTNALTPAGFDSKSKPPLWRTALSA
WLTAPIYALCITPMENVKVRLQLQQSFRTERDFTGPISCIRFIWVREGPRRFFAGYLPTL
LSRLVGLPFYFIVYQVTKQQLENSPIVTNPAGEIFGVMISGCLAGLLFWTIICPFDYMKT
QLQSGGAKRRFLEVALTTYKAAGVRGFYRGLPACLLRAIPANATVWLGVEWTTNIMRKYE
I*
>TCRU_5033 ATPase, putative
MLWVDKYRPKSLVEVELYPELTEVLKRLAESQDLPHLLLYGPSGTGKKTRAMAVLHHVYG
PSVYSLRLEHRSVQVTDSKVVDIATLSSPHHIDINPSDAGNYDRVIVMQMIREIAQTVSL
QSSTSNGVKYKVVLLNEVDKMGRAAQHALRRTMEKYMSTCRLVLICNSTSRLIAPLRSRC
LAVRVPSHSKENLTKVIRVVCERENRPLPSPEFMATVTQRSEGNLRRALLMVEAAAMTKV
DFSGNGADIPQPDWRVFLDEIANDILSEQTPKKLHEIRGKFYNLLGQCVSGELILRLVLE
KLMSAVDPALRRPLVALAAQYDHNMKLGTKTIVHLEAFAAGVMQLLKQK*
>TCRU_5034 hypothetical protein, conserved
MKAHASCQGNGADLRDELDASVECGSGYICIYGPPSSGKTTLLLNYLTAREKHVRNMKRS
FHLEYVSGKALEGDPLQRLTWRLQPHTKRRRTECSLQQFGCLVRQWLESAEEGSELHFVM
DDADMLEEDTIQINHWLSECLTVTQEERNRNIVCLWIVSQMPLHLSNCFRFHFLSKPDAT
ALQTWLNSLFAANHGFFGGDLDVSTQHFTLGQTHTAVVDAVAYYKTHLPMRASIVAQDLR
QLLQRVHQILPLLLPHYTSGRPNAMHHSAAWGKRREFSALGHSSDPLVAALKRIGYSAML
WAVSAFYCGAVPMSKQAYVFDDQELQRRRNSTGTNSTSHRAAVLSSSAHVVHVPRLMLVY
RALLKICVHHIDPLELAPAETAVQHHHTLVSWGLLVSSSQNSKVYHCHIPVTSAIGLSQL
LSLNLYDLIPR*
>TCRU_5035 hypothetical protein, conserved
MPPKKKATDAQVVDEKRQQLDCLRRQCQAVEQLIMLSNEEKRHLEHEKTVLKKKLAELQE

QCETTEKRMEDQLRTMQHLTVTCDEQLWHRLKSLESKVADAEEGNAALHLKIEETTRKRL
EELQRLKDGVAELRQQLESKALACGVQLRDFLLTHS*
>TCRU_5036 Cytochrome b5-like Heme/Steroid binding domain containing protein, putative
MERRLGAVELSNYNGRDEAPIYISVKGVVYDCSAAAEFYGPGASYHVFAGKEVSRCLAKM
LISDEEANAGWCNLTEEHREALDEWSAKYNEKYPVVGHFLPDDQFEERGAAMEP*
>TCRU_5037 methyltransferase, putative
MSEVTDKTVEFLLRHSASRRPPDIGSLKEKAFERVNWRDAFDRFQETERLTLWETKSELD
GVDEGAYRVARDALFPFAVSGSQGAVSFGNRAGHKLREVMEAAGVWEHLQRETSGQKGAV
VFADVCGGPGAFSQALFEMSRQYKLRMRGFGMTLRNVKGLDWYSSLPLGKFLPTYGIDGT
GDIFNLANIEALLSLTIRERLKLVVADGGFNVPFNIANYQETLSGRILFGQWLAALKLLR
PGGCFILKLFDTFSPLSRALLYLSTYLYDRVHVVKPRHSRVVNSERYLVCLGFLGTPGPW
MEYFEQCYQVGFSDNDSIPKIMPISWVMEDKTFMKDLKQMNSTIASNQTLALKMVLAKLQ
PS*
>TCRU_5038 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
MSALSLQLHTALPRRKLLLVVMDGVGIGPGDEYDAVHVAKTPFIDSMCADAKHFRSVCAH
GTAVGLPTDADMGNSEVGHNALGSGRVALQGASLVDDAIKTGEIFTSDGYRYLHGAFSQP
GRTLHLIGLLSDGGVHSRDNQLYEIINHASSNGAKRIRLHVLYDGRDVPDKSSFKFTDDL
ESVLEKARAKGCDARIASGGGRMFVTMDRYEADWSVVERGWRAQVLGEARAFASAGEAIK
TFRKEDPNVSDQYYPPFIISDVDGKAIGPIEDGDAVLCFNFRGDRVIEMSRAFEEEDFDK
FNRVRVPKVRYAGMMRYDGDLGIPNNFLVPPPRLSRTSEEYLVGSGCNIFACSETQKFGH
VTYFWNGNRSGKLDEEHETFFEIPSDRVQFNEKPLMKSKEITEAAIEALKSGKYDVVRIN
FPNGDMVGHTGDLAATVTAVEAVDASLQRLKEAVDAVNGVFLITADHGNSDDMAQRDKKG
KPILGNDGKVLPLTSHTLAPVPVFIGGAGLDARVQMRTGLPKAGLANVTATFLNLMGFTA
PTDYEPSLIEVIPN*
>TCRU_5039 hypothetical protein, conserved
MMGDSLIAQLEQDFRAIEQSDPSLADGFKIVYDREVPCELRPMRGGNAEPGSLEGMKVKV
LSFGDDHSLSTMRVEITSESDLFFHYTCVINHAGFIRLREHQSLVCDFPDFLMTLLKMFN
RCIKEPQRFLVVLLLDENGTANMEFIENLEYKLVGVLTLPFRASPPEVVREQIGYRYSAV
RARLALLTAQLKNSNLVLKPRQ*
>TCRU_5040 hypothetical protein, conserved
MRRGVISYAVTDHATRALTLPLLLDTVRRDPGMTAAYYANRYFGKERQMEVTRVLWGELK
FYGQVTIDRIDGPEEPPRWYPVFSIPRKIHNIRRHCAEEEDLSVLQQDTALAAGGSPVAQ
EASASMAASVENSIIALVQKSPGHDIQFYIGELPAVMQAYAPMAFRRLREAGVIVREQTP
QGTFVWR*
>TCRU_5041 mitochondrial carrier protein
MSVMAPLVDLAGGAVPYVKDTTERVPTSATSAVTRSWSHVDCVTLFATFAATSFAYSLVG
HPLFLAVSRQQCSTTRLTVRQVLQEVYLQHGYRGLFRGAGVAVSGTVISELVYYLIVEYG
KEHLPLPTKEQRCLTGGFAADLISGPIFNPFAVVSQVQMVADCRGGEHKYRNAFSTTKCI
LMEQGWRTLFRGTLLTMVVSPLTGAWWFVYELLKQRAYKIASRSAPLLGAVTPARVRQEL
PVTCTSTTDNLIVNCVVGALSSIIIGILMNPLYVLRLRLQVAKNLGSTRFPAIWMMRNVF
REEGIQAFFKGLRANLFMAVIGGSAFGMTYEGAKQFSDITESGSFTLNTLEIGSR*
>TCRU_5042 chaperone protein DNAj, putative
MRQHRARTQRWVRRAVYPASLHGGVSCGNLRFLVRSDLTAFTPCIAAAADLTGLGVSRRF
SSTNAKKDLYSVLGVARNASQEDIKSAYKKKAKQLHPDVNPNPRAAEDFADVKQAFDVLS
DPQKRSMYDMTGNSGAADRFGSGPGFNPFAQAGGENPFAGANPFGGANPFSSSAGGQGFS
FNDFEEIFQKMSGAGKDKTRKPQGPEPGADIHFKLRLAFLEAVNGCSKEISYNTFRRCGS
CTGSGFQDSGSKAKCVHCGGRGKKVMSTGFFHMQQDCTHCGGTGETGRSSCTHCSGKGIV
KDRSVQTLPVPKGVDNKERLKVSGKGEAGVRNGPPGNLYVEITVDEHPVFHREGCDIHVI
TPISLATAVLGGTVRVPTLTGEVETKVPVGTQQGDKLVLRGRGVHRPNQNKTGDFFIHFA
VLLPKSLTEKQKSLIAEFSKEEKPLELTDPQMQELKGRYKSWFSS*
>TCRU_5043 60S ribosomal protein L10, putative
MARRPSRCYRFCKNKPFPKSRFCRGVPDPKIRNFDIGKRRATVDEFPVCIHVVSRELEQI

SSEALEAARIQANKYMVKRANKEVFHMRIRAHPFHVLRINKMLSCAGADRLQTGMRHSYG
KPNGTCARVRIGQILLSMRTREAYIPQALESLRRAKMKFPGRQIIVMSKYWGFTDILRSK
YEELRDAGKLQQRGTHVKLIVPKGKITQYNLLA*
>TCRU_5044 adenylate kinase
MSESSKPKVFFFLGGPGSGKGTACDYLVKEFGFTHFSAGDLLREASKSNKSDVEKKIAEI
IRMGNIVPSEITVELLSNAIAEHPNPRGYIIDGFPRKMDQALMFEEGIAPAKGIFYFDCH
EETMEARVLHRAKEGSGRDDDDIEVLRRRFRTNVELCMPVVERYKAENRLHTIDANRSRE
EVYGDVKRVMLQLGEVPL*
>TCRU_5045 hypothetical protein, conserved
MTTSVDLRRVALRRHAATTRRRQRLLSANENGAIVEYEPVTSCTAAAPSRRIPLPPRHAL
TRPRLLEYYKIVTGREPSLMRCDTREEDYNYSWFIPVGIEGRKGKEKGGRRLQEALVASR
ISLGAFEEGVRGVFDSGHLYSPICRWLRPNQGDKLITDGSNTMTNRFLGNAENADSNIIF
VRPRKGELPTEAKVSSDELFRVAPKGREWDRQHALRHGIGPTAQEAIIDRRIDSRYRLPG
DYVRRNGRGELVDVRGRPMRAAGAIARKNSEAALFSGI*
>TCRU_5046 hypothetical protein, conserved
MPPGREERLKAYTTALGTKAYILHSTPFDGSYDGNNDGEKEDVPAGGMKCRSSASLGPCR
NFTLRKPKLHGKDVLPPAAQRAFLGVKRKKADDAHFRSPSKNKSNSANTSYPSLSADFAR
FLPTTVVVPPLSTSVLPADARPASVRAVPDAGRASLGAVEVTVPSLLTENIASALRAPEK
FNSADIPLLSFASSPHINYGRVADSFFCSADDHQEMVGNGFVYCPQCGVKLRHGAQVDYL
PADCPVRHEREIGENEEGSNYCFLCGASMGVCPMPPQELREENSKEGNTLGGCWNRQLAE
TGMPKAAFLGPTNTMFEGIQAVKMPSVPTSAATTSTTAANFGERKGDERAIFGTEKLLES
MPVDTTEAKAKKNAEWGGPAAGSLPVVTPPPIPLVTAAATSSKTAGKSMGSSPLHSEGKN
QEKSTQASGPTYASLFDGGEETKMSFLTPQEGMLYTVGVPGVSCGLPHCALCEPFVKPPL
PSVVSTQTHFLRDEAGRRDGANVCVVHNHYYQSISPHLV*
>TCRU_5047 Domain of unknown function (DUF947), putative
MDDDTSDGPPPERSARVRPKHRSALPAVRRQRAVDPRFSDLYGTVDQKQFEVHYKFLREQ
QEEEETHRRNRIRRLKCIARRGELEASGADLEEYDLSETEREVFGEDHLDELSAMKLLPL
QEVQRELQQLQRESQLHVSRTKGRHVQSRRDTLRKEIIKREALAVKEGKKQRPFIPKRAH
LKREILADTFERLERKGGKGAVEKYVGRKSRR*
>TCRU_5048 COPI associated protein, putative
MAAKFDLKKGTLNFATHDSHYQQQISAPEQGPTAAGRNWPRVFLTLSCISMGLVIASSII
SLMTLTVGISAIFLNIYLVVLCFFTLTAELRQINCLRGLIYNWIKYLYFLTTYTGRSFFY
IFLGTLAFGGGILNYVAAGVAVALGVIMLFVNLFVDLPKYVDPEMVREEEAARREAMGGM
DQVIFFPVPRPAAKDNISNAAVASSSAANSGYKPPGINEGPNAL*
>TCRU_5049 hypothetical protein, conserved
MMTMTGRVLLVCALCVLWCGAGGGGRAEAHSSASSGTTSDEESQYKEEEPTAGAGKDVKN
GQQAEPQETSPAPKSPAAPANPPQAPPPEGEAPETASPTTDSKGQNAQEGKKENEEKEDE
DEEDEVEEEEEEEEQEEEDEDEEEEDGAKENGETEEETATGTTEETSAGGEEPPIISYGV
EEAANQTNLKSTQKTGDDDPAADGAGTAAGKQNENKDANPKGTPVTAAAMKTTTATTGDS
DGSTAVSHTTSPLLLLLVFACAAAAAVVAA*
>TCRU_5050 hypothetical protein, conserved
MMMTGRVLLVCALCVLWCGAGGGGRAETTPASPGSSPDKNSQNEKETTGVTGGGDQKSEQ
AVPQETPSPTGSESPEASPPPAPQSVGGASETAITTTDNNNRNTKEKKEEKEVEEDDEED
EGEEEEEEEEKEGKDTKEEEDEEEEEEKEEGDDNGENEKEETKKGEAVTGTTEGTSAGGQE
QRSLSSGAEGASNITNPNSTPTTGNDDSAADVAGTREGKQNENKDANPKETPVEAAAIKN
TTATTGDSDGSTAASHTTSPLLLLLVVACAAAAAVVAA*
>TCRU_5051 hypothetical protein, conserved
MQNTLTDNDGSESRAAQPDSASGNTQNSVDEDTSSPEAAPHVSTAANADSAGSTKTARNN
TNTKKENNGDSDSSLAASPAVGTNTATATTTTTNDASEFNKDGVKLSTEDVEQNASKTNS
DADSGTTETAAANSKVPTAASNATNKTSNTENTADSDSSTAVSHTTSPLLLLLVVACAAA
AAVVAA*
>TCRU_5052 retrotransposon hot spot protein, RHS3, putative
MGDSSNVSVVRSLSWRGVKGYIIYDVAEPDDEPSDDLPPRGWGMVLVTTPNEGIFKEWYN
QGTTVRTVMNCPEEKEVKALCVWMKRDQPFGKQAEYWREVKGCMDRVGLLLCYTFDKR*

>TCRU_5053 retrotransposon hot spot protein, RHS3, putative
MTVLVGGTEPIFDCHVNCEVERVWQIVKGDATECFSGRPEEHFKPHPRVLIATLGIGGSV
NAGPYFIYQLPQYDAEQLQVVLHCLGDTT*
>TCRU_5054 Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MGARWGGQGEKKVFGLSYDSENKRIVFCGGGQDTEDQSVTLATETTHHVVILLRNGTQGS
AYVDGERVGGNDACDLKNANDKKVSHFYIGGDGNSAGGVSEVQDVSVTVTNVLLYNRPLD
DNEIAALNPNKDSISPLVVGSAQGTSLQSLSDGQAPSGPESLNGNEGVGGGRASPSEPST
VTTSGEESVKQSALRASPGGSKHVDVASSSDGDPRVGSEAGGAMQGDTPPQTPVDTPATA
DANALTATDVAQVDPADKTEVGASSGANEEPTEGRNGQGELHAEHSEVKAAALSSSLGNV
SQGNNSDAGTVRGSGLLPSLLLLLLELWVFAAL*
>TCRU_gamma, conserved domain containing protein, putative
Elongation factor.1
MCSNHKDNKMQCMTANLNCGWIRRMEHVREYALDPALMIVEEGRHDIVALCVLRGRGMPA
IVRDVEDTELFD*
>TCRU_5056 myosin IB heavy chain, putative
MACVDFKKSAVVGVEDLVLLPQLSDKAIMENLKLRHSKDIIYTSIGPVLLSVNPFKKIPN
LYGEERIAFFRSGGKSSGGTFGITHGGPHIFGLAEETYRTMVSEEENQCVIISGESGAGK
TEASKQIMQYISAVSGNTVEMQHVKRVILESNSLLEAFGNAKTVRNDNSSRFGKFFEIFF
DRMGGPVGGRMSNFLLEKSRVVSQQLGERSFHVFYQLCHGASPTLRERLRLRPPGEFFYL
NQGGTLDRDGVDDAKEWAETLAAMEAMSISMSDQQSIFDTLALVLHLGQLQFAPSAADRE
DAALMVSNPEELNFCAMLLGVDAAVLEWAFTWKRLEMGTSEVVNVPLDIQQCRNARDALA
KTLYHHLFDFVVESVNVALGKKPYDLMLGVLDIYGFEVFEKNGFEQFCINYVNEKLQQIF
IELTLKVEQEEYVREKIPWEEIKYFNNKIVCELIEGTQPPGLFSVMDDVCATMAKEKESV
ADIKMLDKLDAVHTGNPHFNRTERGFRIKHYAGDVYYNAEGFTTRNKDLLGADIALVLGT
SSNQFLLKILAETIAGAAQGRTVGKKPRVTTAGFKMRQQASYLVKTLMGCNPHYVRTIKS
NDEKRRDFLDEARVLHQVKYLGLLENIRVRRAGYSYRQYFDKFLKRFKYVSSETFPRSFK
GSDRDACAAILRHVGDALPQGSWQLGQQKVFIRQPQHLFTLEDLRENALDNIVFKIQRAW
RRYQQNKDSVLMKSAIGRMYLKAGKTRRADSVFRPFFGDYLDYRNRLKPLHPYVEFNPIG
SAWKEFWTETGRRYYHNAIFQQSQWERPREMSPQKIVFTALVERVVNHQKALLEKNFLII
TDLAVYMIQERLETIVQPAAKPTKKNAHSLPPSNSTMTRYLLQKRLDLRLLSGISLTTHA
DTVLLLHFYQPTVPYRPIVGNTTAKSSKKVYHCECCGGKLLPAATKQNCPGCGRLCCAKK
CLQYNRPLPTLLGHSKPVRVCPNCVHGEPFEPVEDVVLMTPMKSEVVAVLRKLYRQLMGN
KVPVTISDGLTYHLFGENRPWILTATALPSISETALISSCPFTLAVSAPPGISQEIIQAI
ETAREKRRGAAAERRRKEEEEERARELLRERERERREEHRRVVEERKKARAAAEQKQESERL
EREQAARDQREESARIVAERSAWYR*
>TCRU_5057 hypothetical protein
MMLESSSLVERENENATQASVEMLRQELIRKQAEIDSLRLFRKENNYLREKVLALSDRVD
LLTVKWTEPATSGEIALRAQLLAYQRHSRVHQEELDRKEETIVELQGKVEQQEDELLIFK
RRCEILFGRLCTAGAVSPVKNREESTGVGTPGTVFTDEDDPTSFWSLIRKLRGVEMELDT
LRERFVSLQEDYERRGVLVAAMRRENAALRASVSQLIQQVRQSAALQLGGGMENGATKPQ
MEAGEQRNDNAVDAHPKLFALLTQKEEKLNTNKHGDSQGE*
>TCRU_5058 Cell division control protein 14, SIN component, putative
MSNDPSMNTALLNFCTSLSNGSGTGDREQLPRRNPEELQWLKEALASVEAPERQIKRLLE
TVARDGVTEDDCAAALEELSDLVEDINWAVEFSLMNGHRIMLDLLRRGKLTAESEPVRQG
AAMVIAHAAQLNERVQKCFEEAQWEEVLIPLLREEKAPAVFAALLHSCSCLCREYSPNAL
LFKKAGGIEVITRVLRSESLDGCDKKIIKRVLFLVGYLTEVLDIATEDMIRSVSVHAASS
DEEIQMNVAQTLFLVAEKSCAIVRRVLKEVAPGSLVRWRNALLGEEDDPRRRLVNKLDRE
GHDG*
>TCRU_5059 hypothetical protein, conserved
MKPVAAGTLPADLIDAIRGGAVTLNRINDEIVVFRDARGGVEWHCTRHAGRLCSYRHQKT
GANGKAEISRFDAVKRMTVQPEEKSPPNTSVTEETNPPPLTEASRRTATLSEVMQQHRSM
AMKVAHLLAPAPRDQKELRRSFATEDGDALNAVLSTLTVLNHRGQRELLDVGYEIIDIEH
YNSKAVKQQVANLALPKVAHNKAVLDRFAIYADRDVMLAVCSKGIMAGLGSFKRKREEED

DSEDAEGDEGTLGRKAEEAAQGAALTLFTHMDQCGIRWCDGDLTERRWVLSSAAKEALAQ
RKCAHTAVGSGASQRLKPMPIINASQLAAAHGNYVVLHKEYHSLYGLLKRVEEITEAARG
WCQSNATRISEELRQEMQRWFAAQEGPWRTLIALFDVLHKALYELKREIEDYVNLREWGV
LT*
>TCRU_5060 N2227-like protein, putative
MTSPQDVHPLAPPPYPLGAELDPNFIPQHDGNLHWPPLSPCENDDMHEDHISFLRTVNAF
RSYRKQAMGVRDMRLNNFMKFHQQHKQTLCIDLERMFSKYLECIETNSCFFESICNVSSE
LFDTYWPKGTTVRPEDVPEPTPLDIDKVFTTLRQFVRDWSAEGAPERNSVYMPVLTTLEN
SYPDRAARADVKILVPGAGLCRLSVELALRGFAAQANEFSYHMLIAGHYIQNHVVSSCQH
TIYPYVDNTSNLVNREDQFVDVRIPDLCAFEAIDGLNGEEQHFFGELSMVAGDFTEVYTK
EHQRKSWNAVATCFFIDTAHNIVEYIEIIYNLLVPGGYWVNVGPLLYHFADSSDDMSIEL
SLGEVLTVAQRIGFVLLRQPEFIDTTYTNNNRSMKQLVYRCAFFLLQRPLTEEQEREQQD
GKLTVEKI*
>TCRU_5061 EF-hand domain pair, putative
MDSARKLQKSSSHGNSGRNPRGRPSTHVEQNRQYEFRLTRADVEAAFAFFDVQNKKDLKP
RDLKARLTAFYPNMTNKELKFLLESADGNFTVETLWGIIDNYHAMYTSTVTAETLTFDPV
KEAFKIYDPQGRGVVDVEVLADIMKRIGLGELSQEELELLIQTADFDKDGNISLEDFRNL
LKIGR*
>TCRU_5062 uracil phosphoribosyltransferase, putative
MKNCGDGSSLEQSLLKEFPKLHLVPQTNQLIFLFTIIRDKKTTRTDFVFYCERIIRLVVE
AGLDLVPVLPKDVTTPTGAIYKGCMPDPQGIIGISILRAGESMERVLRETCRGIRIGKIL
VQRDEKTVEKCPDERYNYSKVPRDVAGRRVLLLDPMIASGGSAIHATDILIREYKVPEEN
IIFLNLITCPEGIRRYMSRFPKVHVVTAAIDGALDDSKYIVPGLGDFGDRYFGTHD*
>TCRU_5063 TPR repeat/SET domain containing protein, putative
MNGGVPPDVASQAQARREAAANLGTLRGPLLALAKILPPDSGTRPVKELLAHLQREDAPR
LASLLENLKQEVQGASDLNNDGAEKWKEEGHKAYDLGKMAESVLMYTRGVMYASQDDTLA
SLLYHRGKVFLAQARFMEALADTHAAFTFMPTNWEALERRGVCLQKLGFEEEGKKDIHAA
AILNVDSANAATLISNILHADVGRSEDEAVNLIGGGISSSHLNDINYNGKMKGVEAKRHL
EPGEIVTEAPVVHALYDDHWGIRCCYCLRVTQALYPGSAYRERGKLSRGLFCGEVCAHLS
WERYGQHETANPFFQLCPIDALIASRMMCSDCAVSRCHSLRGDFTGELHPAAVIGGYETA
VSLCALVLDAVSLEDVDRLRLAQRKVMLCSFEVKFWTGSQVTINSETREAFIDESRPIPV
GKALYVSASQYRHSCDPNCFASFVGNPLGCSLYLAIRAIRPIPAGEEITISYHNITTYKA
VSAQFRRRALAERCGFICNCRACVDTKEERVTVEKKGYYIQASDLYQKGCRLIREGQYDV
AVTVLSQSYTIAMEHLCPPPRPPQSMIPKTHMALARAFNRLKDNEKCVEHLLAKVELDRQ
IYGENHLEFADDYIRLAYFALSEEERGVFAERAKAHLSRFYAPSRELHAQMSRFNSFVVR
ACF*
>TCRU_5064 mitochondrial ATP-dependent zinc metallopeptidase,
putative
MFRILRVTGASPFVAHALNTRVCFCATGGGKNDNNNNIDGSKSNDVGKEKEGGEEARPFN
NSTSSTEGLLSGKRHPKGFEAFYSKYILGRMPFTRVPAESVKRAYTMSPEERILTMNLAA
KALKWKRIRRIGIVFFLLAGVLMARMYVLRSYMVGDINNYAAIAVDLSKHTAAFLDEKGK
YLGIRNFVDYRAFEATCDKNMDILILFHSYYPWVPMLLLCLLPFLAATNSTFSRSAKMAS
VVAEKSRFNFKREISVSTRLADVAGLTEAKHEVVEVIDFLKNPARYQALGAKLPKGVLLD
GPPGVGKTLLAKAVAGEAMVPFLSCSGSEFEEVYVGVGAQRVRELFRQAHEHKPCVVFVD
EIDAFGRKRKTETGGGSSRGTLNAFLSELDGFKDATGIMVLAATNRVDILDNALTRSGRF
DRKITLEKPSYKDREAIAKVHLSPLKLEASSNIHEYARIVAALTPGCSGADIFNICNEAA
IQAAREKKDHVTQQHFHQAVERVLVGLERSAVKLSETERERIAFHEAGVVILHWFQDKTD
PVVKTTILPRGRHRTGVTQKLPQTTFIFTQEQLMQNLVAQLGGYVAEEYFFQDISTCAAE
DVQSATNKARHFVCTYGMDPETIGHFGYQLDQEDSIQKPFGPLKEDVVDQAVHRLLEVAL
KGARTILNQYLDKTRVVAGLLMRQETLTAHELWLVLGDRPVMTREFRAYLES*
>TCRU_5065 hypothetical protein
MSSESEKWCNLDTPTEASYTPRNSCEWETTGFPVDGCEAPRSLSMVTEDLDGEKKVLQEE
KEQLARELENIKKEVEGFQRAHREQAAALLVENKRLKQQLKNAKYKMNNFQRTHRGREAA
LLAENKRLKQQLKNAKYKMNNFQRAHRGREAALLAKNKRLKQQLETNKK*

>TCRU_5066 protein kinase, putative
MSQKFGPYQVGETIGRGTFGKVKLAVHEPTRKKVALKIISRKLMEQDARSNIKITREIKI
LKVLRHPNVMRLYDVVQTTHDIVLILEYVSGGELFDYICRNGRLTEDVARGIFQQIVAGV
AYCHRYHVAHRDLKPENIMMEQGSTRIKICDFGLSSVFRDGCFLATSCGTPNYASPEVVS
GKLYGGPETDVWSCGVVLYTMVVGALPFDDSNVGNLFKKIQTATYHVPNTLSAGLADLLR
RMLVVNPLERATMEQVMRHPWVFPAYPPYLLALHYETILETVTFGKMALTREEALDEKIL
EIVAARFHISVPEVAAIIASKEKKKSPLFSIQETTHEKGASGKSYPALEFFEKAVNVVDA
KLWPAPLVIPPAEQALRDDEHNLHVSYLILLHNKQDSLFLENLSKVGSSCDAANSLILTL
SASQGYGSLNANSLHQISMGMSAVSRSLQQAQQKGAPQTLRVNKVGGITFCGSLPAHVQS
ENQLTEEVDLYMKGYNDVVEAFIPLCCVRSKHTLLGKLLGVVERPMSAKEPTQSHSQTPP
SKSKGGGTLLQPLLKPMINEGSTSPASMSNEGALLVPASRGKKTKGNTSGKGNVTPHNCE
GGISFSSSMTPDVFQCGTVTRFGNEFIRNGVLFSKSGWVTTLHYVYNAMEEEGFLWKTTQ
PFSFAAVVHPSVKLQLKIYKVNAEEQIVDVKVSSQSGMHACDKAMSLLDRLRRKAVLHTE
RKLRENMAMLEQGGASSLGPDK*
>TCRU_5067 eukaryotic translation initiation factor 6, putative
MTLRTRFESSDDVGVFSRLTNAYCLVTAGGSQNFYSVFEQELANHIPVVYTSIGGSRVIG
RLTCGNRHGLVVPSIATDQELQHLRNSLPDSVKVQRVEERLNALGNCVVCNDHVALIHTD
LSRETEEILRDTLQVQTFRTSIAENALVGSYAVVNNKGCMVHPKTPAQDMDEIASLLQVP
VVAGTINRGNAAIGSGLVVNDWAAFCGLNTTATEITVVERIFQLRRDLGGDEPNLLQQLR
DTLVDELA*
>TCRU_5068 HIRA-interacting protein 5, putative
MFRRSMRLRMMQLHAAPTPNPLCLAFHIPSSTYDGFIPNGQTCEVAHRGLAWVHPLSNGI
FEQYGQEVASVFIAPRHVSITVYPNVDWSTLEWSISSFIGHYLLFVNECVPAAKEYTLME
DDLLIHEEDSEVLQCIKELLREQVRPMVQRDGGDVKLLNFNEETGVVSLAMLGACRTCPS
SSNTLKDGIERVMKHFLPEVTEVVEDKGHAFYEEYELLFHSEEALRREAARIDAVRRRKI
SPKATASLMSFDALHEPDGDE*
>TCRU_5069 pre-mRNA splicing factor ATP-dependent RNA helicase,
putative
MDPDKLRKAQQASRDAYLRKQALKREKAASAVLQEKISEIEAGVLPHSLAEIELLSKRAQ
EVQAAGQLQITAQLRQELLEEDGALASHALDHGGDSSLPLNQVELMEQSSSVGYQEKSHN
FVAMDESVVDESIKKHDFVEDKTEEQIKQQRTEAIQEQHRRLQEQRRSLPIYHSREALLE
IIRKNTVVIIVGETGSGKTTQLLQYLYEENLCRTPPCLTEGGDGGGKGKEEKEGEEGEGT
SEEKRFICTQPRRIAAISVAERVAQEMNTRCGSIVGYKVRFDEKLGPTTRLLFVTDGMML
KELVGDPELRTVSAIMVDEAHERSINTDILLGLLKDITRRNKQLKVIVASATINAEKFSS
FFDGAPIFTIKGRTFPVDVSYLTEPMADYVSATAESVLLLHATKPLPGDILVFLPGQEDI
ENCAAAIREGIANSGGQLRPLMVLPIYASLPPREQRRIYEVPPPTTRKVVIATNIAETSI
TIDGVVYVVDCGLCKQNYYNYQSMVEELRVLPISQASAKQRTGRAGRTQKGECYRLYTAY
TFRNELPQETVPEIQRSCMSSVVLQLKALGIDNLLQFEFIDAPSTASLERALDHLYLLGA
IKPNGRLTLTGRRMAEFPLDPSLSKCILRGSALRCLRHMAIAVAMLTLDSVFVVSRDPKE
RASIASARDVLFSAGNGDVMGYVRLMEEWMRAGPSMHEFCQSHSVNAKALLQARDVLDQI
LNTCERLGLDLLSGEEETSLSMENFTKALLAGFFMNVAKLNADRRTYLIVRPIDASVSRS
GHNHNNYNALDAEETATAELHPSSYLFNAGLEKKDVKSNRNDSMVSTVPTLRERPELVVF
TQLRYTSKRYMMHVTAIPSVDWVLTTAPENYFTREELETKLRKRAHD*
>TCRU_5070 protein kinase, putative
MAGLKINLDDLESDNDDSAQISHEVLRLGELTVSAEGLTTSMGYKYGLSPDDVIVSATGF
LGQGSSGSVRRATHRRTGEVLALKEIKITSHAHLQEIRRELETLHRDGNNSPNLVGFYGA
FCHEGSVFIAMECMDGSLATVKKPVPTEALASISRSILLGLWDLHGNRHLIHRDLKPSNI
LFSRDGHIKISDFGVSSFLECTRGDAHSFVGTLTHMSPERLKGESYSFAADVWSFGLVVA
ELALGRCPFIDKLTRSKSSTEAGFWVLLQHLNSDRPVITLPQTMDPSLADFISMCIQKDP
QSRPTCKELLRHSFIIKGSECDDKHVIREWLLAMPMQAEPSPSTGECGQSLVPPAGPSAS
LNLDDELSRLVR*
>TCRU_5071 C2 domain containing protein, putative
MRGEEENDATTSPTVLLPPGVYATAPTVEDALGDVTVRDGTAMEEMNPHERVEPALMRRF
DRHRRLRRAMAAREATLLEITQLILDKSAPERTVQFSGQRKATGVGSHPLSTTPEKGTGA

ENTTMKLSKVPCPNVPLEAGMRQDINEEKRSKSIDIEHSKERAQLEKLVYDLRRELEAAG
HTLRDQTEALKSVGMGMAQMGPHRMAKTQREQKKKLLTASESSIEGEPGPWREFENICGR
VKTLESLLAAERDRSERAERRCAELQATALRSKAKGTQGDATDVVGAGGVSFSGSSGEKH
GAVLTTETEGRDREVKANEKGLMDKVRDLEDAHRAARRVWGTQEREYRRYIQVLEAAISR
MERRMPVEKPSKATLFNLTLRLVSCERLINRRNNGAGSIDPFVIVYSPIGERVLETLPRE
DTDCPEFSEVDDVVTLKAARGSSWHILFEVYSRGTNNVRLFLGQAKVPVGPLLEDVKLGR
VRRHSTKLRLRDRETDNELLRQTRSLGTIVFDVTTTVVSGGLARVGRWRSPSLCPVGRLI
SPGRDGEEDANPSAGIRRNEGCFASVTGLTLRVAAAKGVLKRGPGVNSCPYVVAYDGCTG
SELMRTPPVLGTSEPSWESETQAGVSLSSLGPRGCIIFHVFDYDENGRSEFLGEARISMH
QLDFGKEWHEVKLCPREDEPIAYIREHRERLGKLVLHCTREIRSSSVGCTEKQYGHPRRP
HNLSRSSRVLCDESVSENGNTLLQPVAVQVHVEGCRGLWDRPGSGNIFVRMVAPNSNAYV
TTVVPHTPNPSWMEEDGSATMTLHPLDPGVIAFHVMMGDGQPGGKEQSLGYAQLAVRDLF
LLGLGKKELQLDVHPQETDSRFRQRSITELGSIVVSFTTPDVIPVNTHREKENSVEKQTT
EITAAETPNQTSAASLPTSSSILKQTEEVLGPTTSSLRIFVKEGQDLLDCDQAMFNVMGV
TDPRVLVWVGPDLAFTVPEKRDTVNPVWTQEEAEFILRVQSTQVIRFEVQDVDVSGFDSM
GCATIHASEVIDSPGVRRLPVMLDGKQYGTLVVVFSRDCEDFSSS*
>TCRU_5072 zinc finger protein family member, putative
MFGSEQFRQRFSVGGGGNPAGAATPFMMMYGVCPKTNGVASTYSNQPQATTNNTAFQRPY
GFHVNGYGANSTAPHEEEDTEGLFEVHDSHWKVPISVHSSVVSPSVGSRLLFSLQHPTVG
PGNRSVVRVCENFQEGHCVLGENCNDIHLHPEYLMAKRQAMILWIHSKEREFQNTLIHDP
RKVFRVFCADLKEVVEVPISALRFTKGLYVDPNLRARRARSGHQNQFAVMASQVPTACGL
FSEDPSQCKWGKWCNQVHIEQGWMQFKKNEFESWSNGLERRFNELPSDHLFSVHDPQLKT
TLSLPKASIAGFSRGLFQGSAKKAPSVCMLFQRSRCTANTCCNQIHVDQSYLQLHRRWVC
NGEQLPEEKRRELWEQMNSVLESLLSRSEREAIATNDMYDPARELNPQAQPFVPSPLSTP
QPTENFVGETGAKRREKRKDDACHVKGEGKGITSFATRQSRSHVSDYPFSTETEIICTPM
KSQGVVSTGTRSNQQHQQQQEGSNKNISANNTNCINSRSRNNNSAGAFLPLGEFVTVVDG
DERSQSSLQASHSNISHAGRSYKHTNNPYTFGGSSSCAASPSFGWVQPIRSAGNSCTTMP
NSCAGAETGGSNGGNGVWGMRTKVDPSPAAPDNRSALFGAHHEFDNSFCALSPSFQWNAS
GSTPAKTIEELQKVSPDMDHANAEENGFL*
>TCRU_5073 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily, putative
MVAFSESLFGYNVHGRGLIGIRPYEIVAGYITAAESWLSIVAEVNAGTWRAHTVFGSRNS
NDRVCFLCRPTAVAKDNKVFLLVGIDTTRYESDVEMWVKNGWDIKLVEGVATHSKDGVQS
TLVSWAEPKSLSQHIPNRTRDQLMGVVTAGGSGIVLQNGTLVFPLMVNGENYPFSSIIYS
TDNGSTWTLSEGMSPADCRYPHITEWEGSILMIVDCENGQRVYESRDMGGSWTEAIGKLL
GVWVNARSGGSWDEGLRVGALITVTIEGRKVMLYTQRGNFWKGQREMFNALYLWVTDNNR
SFHVGPVAMYNNKNWDLASNLLYSDGSLHLLQRSINGEGSAISLSRLTEELSTVKLFLST
WSQKDIFFSSLSIPTAGLVAVLSDAANNDTWIDEYLCLNATVTNAKKVKDGVQLTESNSG
VIWSLNTRDNNVRHVFLNHRFTLVATVSIQKIPSKNASLLAAMLGDAGVAHFMRLSYTKD
KRWETVFKDQTTPKGSTWELKKEHQVALMLQSQKVSVYIDGELLGEEEVLFTIKTPLEFV
DLCFGACGEENPSQESHVTVTNVFLYNRPLNSTEMRAIKDRVPVPTRGPESEVEGGTERR
HIPRIDGVRANAPAGSGLLPLLLLLELWVFAAL*
>TCRU_5074 hypothetical protein, conserved
MDAPETGGNSQSAGSPAPAQNNLDGQEVSITNAEAQSSIKPHAAGNQIVNDDETGGENER
KAAVTGGTPSKQQPTPLQPVQPEQPTTDSHTRQKEERDFEEEQSPPPAPSPTNSREGIPA
TRELEISTEEKRQTSPSETQKGLVGQEKTSMDDAEEHNTEGTTPSDSVKDAVASGS*
>TCRU_5075 hypothetical protein, conserved
MYTTHLRATCAAQPDGITCRADGHQKTAEELLAAHEGERRQPHYLPLFRTDVAQDRRHSI
RPLEWPDAIVERGNGAYPPTTLGCGTTKHRHPALGQSNEESERGGLRNVRAVNVGAENFP
RGAIHNLFPHARTADERGELCGLFDGNRSGDIDPTAVRQDAAVQVGNGWNPAGHGGFEVK
KSCGAIGEETDEAGAPRLSRQRRSAVVRRSTDIPLWASQMRRANEVA*
>TCRU_5076 hypothetical protein, conserved
MSGARLSILLTPLWGIVILNCGRTVLHISLHSHLDPLHCHFTPRTAGLPVGPHRTAAGSL
TCSCRAECPANEHGLGHFPVPRLAAASQSPTRVPVATDCLSAMEALRLGPLAVHDDVSEE

ICTVPLSLADRGHTAGSTFSPSHYGIPRNATADADAVRPRSLPQDCVNAWHVDFLTAVR*
>TCRU_5077 hypothetical protein, conserved
MSGARLSILLTPLWGIVILNCGRTVLHISLHSHLDPLHCHFTPRTAGLPVGPHRTAAGSL
TCSCRAECPANEHGLGHFPVPRLAAASQSPTRVPVATDCLSAMEALRLGPLAVHDDVSEE
ICTVPLSLADRGHTAGSTFSPSHYGIPRNATADADAVRPRSLPQDCVNAWHVDFLTAVR*
>TCRU_5078 hypothetical protein, conserved
MGYRREVIVKSSWSNTTPTERRKRGRPDQSRPAPPNPWRAATHNGSSPQETTHVSPTVFG
APDSSGTFPPERSNVRYGHTADGSGRSRQVVTEKEKKLAPTHSTEQPSKDNEKIKHTVDT
EKAKIADQRPPTAEGGCSHASLQELLRRIIALEFSGRCTQRSMAVLETICDTLCQTPMAV
VKVMEVLDECFAEAVNMRQQQQLLNYWYIVDAVMKLFRDRPSMLNAVVVALPHLLLQYVP
WKKSRLAEEPWVQRESDGHRYEQLFLTWGRAVPKPLLDEIWSLWKNGAPQTETNSLNKP*
>TCRU_5079 hypothetical protein, conserved
MNFGRILLQAFRVRLMPASDPGIPLSDIRALLRTAVHEADAFARATRSLAERRGTQISLR
CQLCHVCGHDTSTRNVRGVARRKPLAAQTAVKKRQRSCPLLMKADDGSPIHSITSRHSTQ
ASHRAADAPSDLSNRLTQSSRRAMELICQ*
>TCRU_5080 hypothetical protein, conserved
MQLVLGHCGVSRNEACDAKSEKASDLSQLTDTWSTGIVALAESINRARQLKPEARRSAVR
GDWEPTRTDPTLTRGEEAALARLRSGVSHTIRMAATTTAARHPTHMLLVRLGCRTADTQR
TLHGSAASSRWTHPATIRRPADCPVCGRHCSYRTGVVAHMVDAQGMTRPQELREFNFPDE
SEPPEIPPEPTPAT*
>TCRU_5081 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MKDETLVFPVEGTKKKAEDAEVDVKTVSLIIQSKEATDWKLSKGMSDGGCSDPSVVEWEE
GKLMMMTACAGGPRRVYESGDKGESWTEALGTLSRVWGNKQGVNVKAVRSGFITATIDGV
EDKKVMLVTLPPVYAEEGNEKGKLHLWLTDNTHVVDIGLVSGEDDDAAASSLLYNSGENT
DDNDEKLIALYEKKKKGGDEGKPSPGMVSVLLTEQLKRVKDVLTTWKEVDGRVSQLCTSL
IAEKDPSTGDACSAVKITAGLVGFLSGNLSGNVWRDEYLGVNATVNNKEGAEQVENGVTF
TGRGAGAEWPVGKQGEGQLYHFANYNFTLVATVSIHKMPEEGNTPIPLVGVKMKNAGNSV
MLGLSYDSGKKWHVLCSDGNPKEPSSTFETETQYQVAIVLRNGTQGSVYVDGQRVGGNGE
CALRNGESKEISHFYIGGDGEKADNKDVSVTVTNVLLYNRPLDEDEIAAFNPNKANIPVQ
VDGSVEGDAIETSPGQGKEEQRQSMESSGVNGVSAPTVPSAKTSSGGEGSATQLVSEESS
DGTQTVDGGSFSDGEPTVGTGEGKNGREEEIHAQNGDVNATALSNSLGNVSQGNNTDAGS
VCGSGLLPSLLLLLGLWGFAAL*
>TCRU_5082 cation transporter, putative
MSENETCDALLSQYELLRGKMAAQHCDDSHDGDKDEHSHGDCGGSNGPYTVGLHVVAIFV
VLLSSFLGTVIPLAGKHVPCLRMNPFLFVLGKCAATGVVLAVSTIHMIHPAAELLEEDCV
PDSWKESYDAYAFLFAMIAAIVMHALETQLVAMFASDESPSSPSGGNGEKGDANGDEERA
DGAPSGDIYQHHHSHALASVEGGRAHRLLSALFMEFGVTLHSVFIGLTVGITSDAETKAL
LVALVFHQMFEGLALGSRLADASMRISLELLLALIFSISAPLGTAVGVGAVVGSKISLTG
VTFIIMQAIFDAVCGGILLYLAFVLMLSDFPTDLRKHAGVGAAHRGWKRLAMFVALWAGA
GIMAGIGKWL*
>TCRU_5083 hypothetical protein, conserved
MMANLIGRVVAAHGARAPVRVGRCAHDCGGEAARRCGAVCVARPGRAGDCEGRGGHGAAG
LREEVADVAAQREGPTIPRPVLEGRVFK*
>TCRU_5084 hypothetical protein, conserved
MGHKAGPEILQIITSAIAGVTTVVHPLWAAPPLVRIDVWIGNIRIAGSKSDVALWEAQVL
RNADSCHATIREERESGATHYTFWGVRFDHTHQAVSLSDEFVRSVRAMPALNSLTNAEMV
VVASRF*
>TCRU_5085 hypothetical protein, conserved
MSRPYNKHRGRDGGRGNPGRGNTGRGAFPQEIASNERFSRWNERGNSGPGDRNNNKSNNS
NKKSGDRDVAAVPVMTTLLDLLFQKSAGAIFDPNTGMLNLSRFKDSPDLLSVQRSVDFNS
VTFCKSLADVIKNKIGTSLRILVLNENNIRKLTVLLTALEGADIHRGVTAISATGNQISD
FAFLGPLKKYEGLGELLLKENTITTRADYRTQMVRSLPKLMMLDGELIHRGLMRLPNPVP

VSLNESQLGVLRFLESNLFAAAASRNYDALVNLYTSGTVFSVSRAEEPIPRRLPFDTAHN
GDLLSESQRNVMTNDFLILRRQVRWRNLQNNLQSLSHVALGRAKSSLALQEVGGGERKFI
SVSHELNGNANVVFLSQNMKVPTCIVTIHGRLFWHWSPKGSNGADLIPREKAPFLTCFFD
RTVSLLLDSVSNVWIIQNEMIFMRPDHTLVHENGSASSPLFFANEATRVESMRRRYLPNA
SLEVMQSVVEHFGSDADVHAFITGHLPTLPADRVEGALKDRSVMLSLLQR*
>TCRU_5086 RasGEF domain containing protein, putative
MNISPAVVVRQVESSPTVEDIGPPPAEDDEGSHVLSPPFSPPPPSTGSFSGSIRTSPVVE
VPRSFENFVRRPVRRPGTTNNLLMAEMQVNTDVLQSATTSAMSTGRVENIIAPGCKKTPR
MSPFSSGSDVENSCTSVSLSRCQYSTSIIPVALTAGASPRNLIRRHQITRDSGSPIIPQT
AADGSREAPFPPLTLVDMNQAIQRSIQEYQRAMSLLNHSMPFTRVQKAEHPEEMDTTTPS
THPKVCLGEFQVRCDVHSFVASFLSAHGYKEAMRSFEMHLPLAEKQLQSCLYHHQKQKQV
QSQHLDTASLVKQGRQDTSFSPNYALTSDDLLLFVMESVRRRQSLNDSLPWRDINCQRKD
YRLEPLEQFHSPQDHNPVSGDGDNAIFYNSAVGGSLELLIEVLIFVETDVPFTTGMPITN
YTNTFILLSSLFVMPEVLIVRLIRLFRHVQKQPRVLLDDSRRVFILRRIVHFMTAYCNYH
EADVTYALLDRLRQFLRSLNATPSVGHSLHDVQSANFSGRGTSTTATQQMGGDFSFVSAE
VTPRLDELRIFVERALEKKYTLLPDRDGRGVCWQRKLTASVRPLGTILKKELKQQDGAVQ
AERVGSSLQGVCLKMEAYYTEVAFTAVAAKTLAIQLCLLSFKLFADIRLRELLNNAWCDS
TMRMSVPFHLSRFVDYSSHVQRWMTALIVSPTRWSECQKVMIHGIRVCRFLYEEQNYEMA
SAVLQGLQHPAVVTLEELYKKHFQCRSILSDAEEREFTALQKIMDPFASHESPSSYSFVS
NQALEETRVPMIPLLAPLLGVLFRTEESKGRTVELSPTTGVPIVNWSKIMAIGRTVFLWL
RCQNTPYEFTPDARLQHYLWQLPGHHFFDSTLMRLARRKRMQ*
>TCRU_5087 molybdopterin synthase sulphurylase protein, putative
MDETTELEAEVEAMRRKLWELERRLSERRRTLLMQATSENGHMKDKYTSDVLAPFVCAAA
SLTKADVERFSRQMMVDGIGARGMERIHRGRVLLVGAGGLGSTIALFLAASGVGELRIVD
FDVVELSNLHRQVIHATDRIGWKKVDSAASACRALNPDTMVYPLDVALDPFNAENLVRDC
DVVVDGTDNVAARYLINDAAVRHEKPVVSGSAMRWDGQLSVYGYDGGPCLRCLFPVPPPR
EAVGSCNDTGVMGPVPGFIGCLQAMEVLKVLAKAGDVLSGRMLIFDGLRFHMRVVNLRGR
QKTCLVCGDASDKSRGLHELVAERPEYIAVSCVSGSALSAQLLPTEARISPKDAFAYLQH
IGHSTTTCMILDVRSKEQYEMAHLPTAVLLPLLQLKKWQLDGVLWNEWERFVSCHIGTTN
DCVTVFVVCRRGIKSTEAVKIFLSTEQRCDTLDDGRTDATKPYTSRRRYRFINMEGGLNR
YHHDVDNKFPFY*
>TCRU_5088 Hereditary spastic paraplegia protein strumpellin,
putative
MNREKWKKHRSEFLNDDCGQNALQLAARGSTIIAEILRLSEHIPLEFIHPEETEYALLIS
DFRYFKAQDGFEKRIQDSYELLQKDEVLATTHMELLDRFFKLFRGVYGYVLELNRFIEEI
REGMYISQTLESILVNLDGKQLLCEILHLYGVMLLLLDYKIGGKTRENLLVSYIRYKGAG
EANMVEVTNLCRATGYEPDQTLPECYPVAYFNRVPIDKEVVGMILGRIRSDDIYQMAYNY
PAPEHRSAALALQGAALYVLLFFRPEILHNEGPVMREIVDKHFADNWVINYYMGFTVDLT
VAWRNFRAASSAISGTVAIENVTYHLERMQSCMKSLNNSIGEVLREGVLTEQYVLDNIHS
SLLPRIREANVVLRWFILHSTRGRPGSRYLEKYRRSYEMIMSSVTEDDIITLLLRTAQLE
FTLRAMFTTLLKQKRSKWESSREEGATKMSKLATFFSGEHVLSDNVRDSQLEAWFSEISE
RIEGLDYTDSITASRKIQKLIKALENVQEFHQIDSNLQVVQFVQDTQFLLRQMIRYINIE
NKVLITIATVGDLSYAWERVSTHGYFVNAIQMKIKQRPDLAVQMRAVFVKLASMLELPCN
RIDQGAQNDARLLAALETTSEYYSGDLVAFARGVLHIIPTSIFDVLREIMEILTNDLREC
PTKLLRKEMKNESQLDIRRRLSAHTADIAKYASGILAMESTLVGVIQVDSHQLLEDGIRK
ELVRQITHELHHSLLFDGNDPISASLFDEELARLARRLNGIRASFEYIQDYVNVHGLCIW
LEEFSRIVHFNVEMECNAFMQKKLYPWKSQYQSDSIPIPYFSRSKEKSAYSFLGRILQHL
LVMTDPMRSVFLSAYGSWYARDSLQEIVGTRTFTSVCDAIGSMGLGALDRLMCFVLAKDL
QLALKSIRAAIEPVEEGVAKIGRELCPASDTPTNGTQIYLKLIGAVDGGSGGGDSHFAEL
TKILVRVGRIQLMRTMIASELRSFCKLNSGSLFAALSTANEALLMDLRHHYHNPDSHPIP
DEVIAVISPFLDSVGISDALSKVYVTSKPIPSLVFYLLALTLRNVPRMRYDESIASMVPN
QPKDLVDPEAFAKGLSLLLKQFHSDQLVLLLNHLSQAVRVYVCAFGQKGSRQQEDILPTE
AETLTQVMHTLAASSGFSAMDFHRTIPATLCGTFRLSTQSKKK*
>TCRU_5089 hypothetical protein, conserved

MYEQDTCFSAANTPLFSQLFGSSYGPGRRSCEKESFILPETCDGPFDGVCHGGTAPPLVS
NMRASEAVVTSGGDAVTDEPHAAPTVNDAAFVEEDEPRTPGRPKVPFCQVMRELERRFQE
QMEVHRGLRASMRQLDLLREEISLFQTERRTAGLASALYQQSMLFMESVGANVTLAAPTP
QQPAKSNSASIASPLLEKVLKSYTEECSNKKALRVEETVPPKSKMMRGTISVDVVRPTEE
PRPYKRVYYVPVVKPLESARGDASLSASVISSLANAVYSTVSYTEDFESSGGVSTDLPVA
NISNSSSVATSSISIKNDSSMKNSSSQSVNVSTSMAESSLIEEVNIDMRVPIGDDISLLS
TLREFYNACGSANRLMQALLGPDGDMRQLRIKNEDEATLEMNSFTKPKNDDERRVWLSSL
RRDIGDVRKLRRFIDQMKRNMKLLDCQRKAQEAKQKLLAKAQRIAKAHQRMRHDKSTLSD
VMNDIIDLMENEAGRSSDRDMVDEVSTVAALSRSSIIDDMVEDNVVGIANGSDLMGNEVF
DELDDQGTWSGGKPDDDDVSIPQEVVSELSWATAESDYANALVGAINVVDMVEDDVPLPS
DEGETREVDEEIPRASLEDSSSVTEVVDDVAGSFLDVSTEEQQRINLASKSYDDVVTDSP
FSDISNSEDADVSSVVPASSASSFSDSVSRQKKDDYDNDETDSAESALDALERDMQETEP
RRVRALLSVYPPLFTPLYATDEMDTMAPGSCQEVPAQTPKCENAVAEQPIVHPTECEMTS
AYAVSPLGDETLEAAIQVPPTNVHSSYAADDLLAQLEWKERQLALFRQLRPKTAWEQERE
KEGIEEKTKMATQAPIAVDEKADYHWGVLETLLQCRFTCAENEPLDDDDDMLDGNANESS
WTDAYDGNSVQTNSDAELSADVEYSSQAI*
>TCRU_5090 eukaryotic peptide chain release factor subunit 1, putative
MGDHELSDSEKAIERYKVKKLIQMLESARGMGTSVISIYMTPKEQVSGMVTKLNNEYGTA
SNIKSHTNKLSVQSAITASLGRLKQYNRLPPNGLLLYCGTVLTADNKEKKLTLDIEPFKP
VSRSLYLCDNKFHTEELHRMLESDEKFGFIVVDGSGTTYATLCGSVKEKLGSFTVELPKK
HGRGGQSKNRFARIRMERRHNYLRKVAEGATQYFITNDRPNVVGLVLAGSAEFKEVLYQS
DLFDPRLKAVVLKVVDVAHPGDVGLNQAIDLAADALTGVKLVQEKKLLQSFFDQIACDTQ
MYCFGVNDTMKCLEAGAVETLIVYEDLEMSRYTIVKNRGTPEEEVTIRIMTDANAAKENI
HAHEAGKTQNEIEEENFVDWLATNYQKFGCTLELVTNRSQEGTQFVRGFGGIGGILRYKL
DLMALRDVEKKDDDDERIAAKNEDYDFDDDFM*
>TCRU_5091 ABC-2 type transporter, putative
MRHFRNQREVQQPNATDDDSTLAVPMGELPAAVLPDALPPLGPMLPESACAVSTSSPDCS
STTKTLEEGSPFLRSRDVLAQAKSGFVIAFENVSLEGRTSIFRSPRLILRNVSGYFLAGS
VVVVLSAKEMCSRKLLEVLAGVEERASGSVMANELPVVSTAFRRRVAFITSTGVCLRDAT
VRRNLLFSVRMRVETLEEDRIVKEVAKAVHLDQLLDVKTEKLSPSQLYQLTLGMELVRNP
MLLALDMPMRSLSSGELHGFVSVLRGLSGSSGRVIVVSATEIHRALFDIADNILLLGAEG
HLLYSGPKAGVEEFLREQSCVQRMGDESLGELLVALDEKGDSARVADVFKSSAVYRRIQR
QVEDHRKSIALNGFDPVLHAAAPSPNYFLQWYLLTAHTCRRATIEHRSFLVSWITLFLLF
FLMASLIAGSGSDQNAMQNKRGVVFFLVSCSMQVNTILIDTEVREFFSAVHLRNNNYFDT
LQYFTATVLRLVLTRAIFAIIAACCTAFILTSSLSLALTMGLTSLAHASLTLLLVYWHPF
EQDLWLFQNIYYVYCIILSGFLICLPTVPRIFPALSLLRYGYGGVVASELRGNPYSCDTK
ANRSYCYTGDQYLVMEGFAHDSWGKSSLVLFIISLVLLALVAVSMNIVWVPHTH*
>TCRU_5092 hypothetical protein, conserved
MNAWFFRVILDRVSFSHSQDAGGDVLHNGTLLFRLLFDGKSVDLSLPSASRNAEKTRPIS
FKYRIQAPSLKDLAATFSQRSVCFQIICLNAVEQQTDMDAHSSHGSLVGVASIDLLSLAR
NVAAQYEFPLRVSDAGSENRILGRVSLCITMDQICDFRMQLSELRASGLESGEYKLRYFL
SSSTVDMRSGMVRSKLGSVTWNNEILPEAFFQGTLQALASREFTLSVLKCGENGRETPIS
LFTLSLFKVQTNSYEGVKEIPFLIEDVDSPTIVSGVLRLSGPPVFQQYIRYVSKPSRPQN
NDEMRNECKESLEVAAVGEPHGVASSNPILTPVSASVETTAGSTGGANPSLPDLSDVPPL
SPSARAEDQTSVRTPLEEAIENEKANLAHSNRHASSDVLFHGTSPIHESEVRSCPNPLLG
STPATASTPTTNEQGTGDWGDSMSSFPLRSVTGGDIEGVCVPSIQASSTKEDDEMAEREK
HRVNALYADTLQGGKQQQKGVESQKLMYREHRLPQELDRLDERIGILQDCLQNACILVKN
KEHDSTVQIADLEQKLSELDVAEAALTRLWDRLHERFRQCAEQYRKSEREFHASMRRLED
YADVLIDIDRRISAEIHEDETEMPAAERTETSCRLPHPPRVPKPTRR*
>TCRU_5093 BRO1-like domain/ALIX V-shaped domain binding to HIV, putative
MAALVHLPDPFVTLPFRRGKDEVPDWELCLKFISVNHSSNNTSAVEATLKRMNTLHKTIV
QTFRTDTKAPPTETFIEHTLKPYCQLVAMAQAHLPLHGAQVHKNMTFVWRDGFDDNQKNE

SMNGNLELISCIYNLAASWAYVGAHQAQTGMVGDVKSAFKSFQNAAGYYEMVENLLKRLP
PEHIKGDLTSEALNLLRRMCLVMAHHSAYLKAENDMKGNHSMLAKIAREGGRQYEEVASS
IKSSAWYTGSKRNSSVVLIEQLFSTMGTVFYARSHLHLATSMADTECIGTAIAHFEKAKS
YLTDVPKLSTNELRNWINGIIANVNKEHEKAIAANESVYFMRVPKEVEAPSGLPRPLGKA
TEHPSFTTFQSKRGDDPFFGIVPAHIASIASKWREKERNLVSVCYKSCVSTRNKLNERWQ
ALGVTAIIEILSGESKSRGQVPRQLREKIQSLHKNDEGVTVSLVESLVSTVKTCEELWVA
ARGKLEQVNSELEAERKEDEAYVTAYGERMWRSVQRPSNEVAEYISIRAALQEHEKGIQQ
WFVDPFTKAKKLLEGSLRNLARLDWPMADLDALMPFEETKEARKQSKRVLEQLEVLKNLT
QRKRTTEETQDLRLRELNELIESDDVTFGLSAVEASQHNAVLDGAAQKISDAIERANETM
REEEQIMAEVEQVVNSIGVLQSSDPMVAEVQKVCNGLENACSVYTDLRQEFRDIMRYASS
TLDGLESTLSSARSLTVCRKLEAEILRATLDAQIAQKISEMQQSKESMDAINESRRRQDE
LRGQIALLEQQQQQSEPQRAERMAEILRRQREMAAAFDAPPSAPTSDSAGVDAPPSYDSV
MGGPRYSPPPPPYYNPL*
>TCRU_5094 dynein intermediate chain IC140 (IDA7), putative
MPNSTNSSDPPPASASLWGPPTGDRPQVSEGGTSSVFLGLTVGGHEKRASVSSADWISDE
LLDLARNLKTIVPKGTWESLGSENEIAEENGYNVKKRPQVRVSFEVRRDVLLLQRMVHTS
YLTKEASEDSRDQRGTTSTMYEVSRNEVETGVQAVLPVVDEASQTSFSRKVDSAIQVQPT
LVDACIHNIAVPKTEDPKMTAFLNKVLPRMLHCLLQNHEVPIYQDDFSLFTEDDAIVGSR
DDTVLIEKGNYTHTTMKDLRVSSISWRSFRPKDDLVCMASISRHNLEERIEAEKRCETVI
NLLWDFADPMHPRAFLEAPVEIQVLHFNPLRPNYIVGGAMNGQIFLWDLNRMDTTTAPNK
KLVVDHADDKNKLLKPVPGAKEIPPMALSVKGVSMERDGDVLVPRLQPVQISRVELSHRR
PVHAIQWMLNGLECGFDGKQTVTHEGRQFVSLSDDGYMCVWDIRPDYLPPDKLRKIKHQS
RVVGEEVPWVPLLRYQLSRPGGGIDLMGFRFYVDGLDFRETPSYVTVCGTTLGEIAMCNT
LIPDERREFSTQAEETRFVRLLNKGHSGPVYSIQRHPTISDIYLSCGDLHFKLWRLGLGH
PIFISSQHDAPVTCACWTPLRSSIVFVGTMDGKILVWDLLDRNREPLLVQQLVQDAITVI
NFKPVPPTIPPHYVQYVAIGTSVGSFHWYALPKVLSRGPSGEKRHFRAMLEREVRRVHYY
EWRWSERVRERDRYGAGAPKMLETPAPAVNPTEEKAVWSNESFDENFYAYDHHRDKEFLD
KVAQPLPEAEEMDMDSMVEEEEEVGRANAN*
>TCRU_5095 hypothetical protein, conserved
MVLALCHRFPRDGVVQVGLFFLLASCILQAILIGSHNKEKDSGSIVPIDGRIGAGQVVYI
GALPAVYLGDGNAICLWSADSDLISVGCARFVEAFHAVIGLFLSCFIVSVLSLLFAVFLI
VPISRTTTFMLAGMLLALFLPIALHTAAIGVFFHQCERYAKEIASQVVFLGAKVEFRRGY
MANVAIGSEACLAAGFLILFFRFLLAVIYRQSVKKRDIVRRDIGKFMRRHLVNDDWERQK
AVLQSHARSVQLEIVRCEGDTEATQEKGGVSDTNKGLLGQDGDSEFTFRPSPAHSSVMIE
VVKGTGVSLMSSEPYHPTTNEQ*
>TCRU_5096 hypothetical protein, conserved
MPLRQPKPPAQGGAEEEAAPDEKRSMGGIAANSSRIRGASRPMRTATETTTTQRTAILNG
SPSDHEANRSSAEKGTEPTADARQNAITEGQAETTSPSSLADAAAAANDADAGNA*
>TCRU_5097 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MISSLGTSPSVGGIPSNSLSEEGDGSHSPGETLTSEDEVSSEVSGPSVQRKTPGQSDSPI
VEAPEKSGPETKTHISDKQGEAGSTEANEDATESEKGQSGVVKRDTSSAPQSPPTPPVPA
FPTKETPLAPADLRNSVEENRNTPPSQTKTDLEAPETSLEDAEAEKHGEGTTTSDSMKDE
AKGRSGDSTPSSISTSDSVDAQRKAEEEDDNEMEFLNPNEASILPLVNKNGQGNVIPSFS
GEQKEQKGQPLGKSSAGGAPTSTLSTVTSSSAGKESVKHLASGTSPDGHQNVDGGSNADG
EPTVDTGYGDKTQEDGPLKTPTGNLATADANGPTTMDVGQDGTTVNTEVSVSSGEDEETA
GEKNVQEEEIQPQSREVNATALNSSLGKLSQGNNSDAGTMRGSGLLPLLLLLGLWGFAAL
*
>TCRU_5098 hypothetical protein, conserved
MTLSCGATWMAVLLRALCGGLFFSMSLPFCVWESCGRECVRESECEWLPAPPSALGASIH
VDLLDGVSRHPGCSEEEDGEGLLWAEGGWMGQSPSVSFPVSLAANAESINLSECGMEGLC
RFVRATQSSSLHAVVTVRCGAVPLDEGRVQCHGRCAPQLFIASASALGFALA*
>TCRU_5099 retrotransposon hot spot protein, RHS3, putative
MEETVKDEIDMEEDVRRLHEAGVYNLLTRSKVAEDVKASFHEITKRFLDAAFDEARDPTK

SSAPRYLEGCYESVYNSRWSHVVELPGGEGMGMYVREGEPPQSWTYKAVGGTLEKDDDVQ
QSGAARLRLMVLTSDKGWPYSWNLKGVESTRDCYVNCEVDRARGIVKKDLTEWFSGRPEE
HFTPHPRVLIGTLGIGKSVAAGLYLLYQPLHCDAEQLPMVAYFIGNQPFLFGKIAKMVSV
YTGEASILRIVDGLPDRGFKGHIIYDVALKGC*
>TCRU_5100 protein phosphatase 2C, putative
MATGGVLHPLSLRSVGVRWLALLCSICAFLASVTVAYCMAVRFGSITALFTLAFFWFIGA
LNLLKFLFRLVVVTRGETDYQDMLRRADVMHQPNVQKSSGSKENAWLSYGFSCMQGWRRS
MEDDHVVLLDDDGGFFGVFDGHSGSNVARFCAGNLFDFVSKTAAFDEGNYAKALYDGFLA
IDKHLYANYSNERSGCAAIVLFIKEDDLYCGNAGDSRCVLCRDGEPLPLSNDHKPFLPTE
LARIERAGGYVWNRRVNGALALSRAIGDFVFKCNMQVSWDQQAVTSAPEVRFIRLNRDHD
EFAVIACDGIWDVLNNDQVVEFVRHRIQSRIPLEKIAEELLERCLSPRPFGVGCDNMSVV
ILQFKRTKSFPSTSQTVEKTKTNDIGNNTAKDGTGIA*
>TCRU_5101 hypothetical protein, conserved
MPALNSSTIAEMEVMASRFLYAAAILGTRLCDYYSSIKAVRRRLSALHRGIVQETFPTNV
PPSAVVLGEGLRHTIENNRKRIIKPTERHRPPSSRMHRSIGGQPFLFHTPATLKLPEGKW
ERKPFLIMQADARAVRLALSAFSAMLPSTMDVWVDNTSLQGGASKGSSKSHAMTWELRRI
YEFLDSRGIQASFAYIRSAHNPADGISRGRVFTLQDLAKGSGGVLWLEDPKVCRLVSLYL
HIPFE*
>TCRU_5102 hypothetical protein, conserved
MQGSKSGATLWEAQVLRNADSCHASLGEDRESGATQYTFLGVQFDYTHRAVSLSEKFVRP
VCAMPVLKYLTIAGMEVVASRFLYAAAILGTRLCDYYFFTKAVQQRLSALNRGIVLETSP
ANLPPSAVDLGERLRHSIENTIVSE*
>TCRU_5103 QA-SNARE protein putative
MASRDRTAEFLQYRSVRPRHPDAQRLLEEEEQLHSVYVTPLWVEKMDDIRAIEKRIQEQM
EILEGLRRNHLKIEFSSTRDEGQEEVRIERAQDVIDSLFKQCEKVVKDLETAYMRDLPDS
GTDLELSILRNVKMCLINELNNISKVYRERQRRYMMDVKKQQAVAQRWAGGEHQRVIEQQ
LETDAVMDQYLQKGMTQEQVETILLNHHMVDERVKEFDRIYASIKSLHEMFKDMNTLVIE
QGAVIDRIDYNMTITHARVQKAKAELQRAAEYQQAGGFKICVLFLVVLIIGLLIALFLKA
VT*
>TCRU_5104 hypothetical protein, conserved
MPSTSLRSHRCAPILWLPFSLCLECALETRVRDLQKGVKSFGPCSSSTSYPAKDGEHSLD
SSSGFERRVFHALLENPFVPMRSLRGVFPAATEYYKEDAVLEMLIHVASNVSAIVASPWA
EMEAHKSVAAVIVVLNCHDYEPCQALTALKLVFQRYFNGCTCRCIVLDPTAEAQAAMSQH
VFLPAHSYSPAEDVARYLLTEIALSIVQQVNAQIVSLSASVENVAPAKWPTTENAGTTNG
GGEVPTARVVNSRLAKKRGDLLLRVGALDAALLAYHDSLPEADALWCSATLESLASLRYL
QRAPLLDFTTAVEGVFSSLESDATVWNEDMNTTLNQLEIIVENVRMDQRKATSLLKHSLP
ATSLNRRLPREVEEPLSTHIENFRRQVAIIRRFFQEDNTEEVGICVEDACKNARGAFKEI
LHVSFVELQIYLQEALQQLRSVPGSVFGLQEREATIQLKRAELFAEEGDKRKFLESLTVL
KAAAKSAPASMQQYLRWRIPYLSSLSGCWRKAIFNVVEAAVSEQQANAHGASVCLLLRAC
RMAGISLPRMEFQDPTTEGYFLSREKIGNSYAVDNEKGETGATGNRAHRAQDVPPLMQLL
YAVTRAGLDTGMQNVVTSLLLFEYYPILRREIQQKLMDILEQSNTLIEPLTLSPPPLLQS
MEVLPLPPHLAPKTVPLSGAHFTFIDTGRLKMTVLTLNGKILPPGQVVWSVGTVGEVQLV
LKNPLRLDVQLTSIALHCRSVEKLDDLGRVSDDTVGHVFGPLAPSSYLVTGVILPSLSQR
QLRLQVQPNMRGYLVVDGVEIRLGQLSLCSTFLMPSPTPTIIPVLQRLPDVSCTLGVNEV
EIFGGQTIHFPLYLTNAGMVTIEKLYLTAHDESCQLESCTGCKERVSTASLYVMLEYDSL
PKKGNSHCLYPGDILPVKVTMVAPADNDHVVFQKVVFRTTIELPYDPPVTPENVPNAVPV
FAVIPRRVQETNLRVFHVPSVAVTSLELSRDRRYVEITVKNKSKLHTIEILCSQLFFASI
PDAMIVAGAEYLIPPIEITKIPSNMRRFPLPWAVRELPECRGELALDFSILENVLVSMEP
LEDVVVCIMVSADDGSGVVSSKGEWRSGPASTSQFPFKLPVMKPATILVHASAPWNRAVP
LRVRLSMENHLDAEILSGPVDTTSIVGGGTKITTDVGNSGGTNGDEQNENDGVRCYEESI
EFFPFKVGEHVLTITLSDLDEREMTYTVKLQVEHL*
>TCRU_5105 btb/poz domain containing protein, putative
MPQRSTVTRERHKRPRHGGEEIRKGSATPHRSDMITDESVSRNDEIDESQESNCLPSAIS
AAAEAADIQNELKRQFDACQLIERDVASLLKQRELSTVGMGSILSLRNISPYDVIRLNVG

DETFTVPLQLLLGKDGQENYFDVLLGFRSSGTSRDNGDEEEEEADKNRQSQVVQPPLLDE
TGALFIDRDPATFRLILNYLRGYRMLTMLNEDQLSMLKTDARYFQIRGLMDELGDQTPES
AVKFRPGPGVNPERNRFRVIYGVAMVGNRFLITGRHRITFQVLNSDYVGIGLVSDSCVST
DQEFHRTSHCCVYYMTGVFYSNFPHHRKEDGLEALEKDDYVSLMVDMNRRVAEYTLKNSA
KMISLGNARKLRFAVAMKLSSSVRIVPEEEARQLPLFQRKAQTDAFLPGNRTPTMGDDRE
ALTQVSQSNGAGLSAPGRMQEQVLLQRPQSATSLFVSRSLDGGSRPGFTDGLGRRARAIV
LSSFASGSLPSDINEIDPLLFIPGNREARDDT*
>TCRU_5106 predicted heat shock factor binding protein
MSKNAASSGKTADGGLPGAYGEQGTQELTGFVQNLLQNMQERFQEMSDTIITRIDEMGTR
IDDLERSISELMQQAGMEEGEISTSKSQPAQSKKR*
>TCRU_5107 ankyrin repeat protein, putative
METGDQRKETIYDACRLGNEARVKEYVRHGGCVTESDANRMTLLHHAAFSGKFCIVDAIL
SAQPTQTVNLDAADAGGWTPLHYAAERGFTAVVERLLDEGANPNARDEMKRTPLHLAAGA
GHVGVLQILLKNGAMPSAKNVAGLTALACAGATGQVEAVSILEQQ*
>TCRU_5108 hypothetical protein, conserved
MTVVQEAIRVTSATPQPYGAAADVLAMKTLSPHDKVRRYMEEQESRHVPPTDATPEVASS
EGEHDAALLGQHEDVSPSPNHKIVPLTGEPGPDARERVPDRQKEKKKQKKQQAPRKRKQR
SESAGREADDPLLLFRRSQKALRTEARHVNMKEVLSRSLSGLFDGPGEASNPFSPAAGSQ
SSSAWSPLVANSITSQFLSNVQQRKKQTFERLLQKEIANSQLSTSRLTPDDGESDDRMPE
LVIGDETAVMEPPSMGHDALLMDAGTTSSQADTLLMGNNTSRGFVELDEEAEQAQSEALM
RKHELWRLRQKHLRERLRAEESVPQLKRGDHQASLRGQPQTTVPMNFVTQSTSSLSTARG
TTADVDGPTETLVLAHCSIIQQSQSLALGLSADHIEMIRRANNFDNTSSQRLVVFETKSR
KKREGLAHLQQ*
>TCRU_5109 hypothetical protein, conserved
MTKDRIKIRNSMKHAHGAAAVEDAVGITELRTIHRCGTGAEEERGLRLTGLMKWSFDDFI
VQEVWPDGFLSQVEEKGVRKKTATAFVLRVISEGIPDTAIAAFIEGRCPHRASLQFLTPL
DFTSSQERFVLLHSPSQEARHVFRHEQKVHLAEGVVCFGKAMEIPVEENAAPSLPIHLLP
DLRYSIVLRGMRGSLADVLPRLEGLKKNGFLNYSHLARHGVGLFRAFESGRHLLQRDYVE
FLRGHVLGLTERSPTLRKEIPSLLEIIADPKSTRRDWASVKQGLEHALKEDDALIHRAQT
GLYYPHHMLLRDFLERASNIAPKSHNSAQLIRECIPRLLLQEKLRSVADAHFNALASLRW
KMHGNQVALGDLVILDEEKGPLDLFEAPADHMNGEMTSVHHPEWLSIAGEKHMNHLRGKI
HVVQTPEEGRRFSLEQVVLPVLGNGAERLVSPDGKMREASERLAQELQIEGLMKMKAAPP
ATYRRLVVRPRDFTYCLFDDERGWCWESNNDAPIRPQLWEDQEGIMRQLSPLSVATGKNI
IARNGIRGAEQRSHFLKAARRSGMTCVLRMTLPRGSAVTSALREAFQFATLDPGAIFHLL
R*
>TCRU_5110 hypothetical protein, conserved
MCVVNLCGLPTVIAHVSHFASDIHRLGLAAPIAVDLNSHHELRDGCSPSTTSGEGLATIS
SGMEIELSDDPAQATRISGCSVSFPNLNAQRVLRVSHWTSTRLHGLGPTSAIPHCRDGGR
PLATGRHAATTETFRLVLRDADCDASI*
>TCRU_5111 hypothetical protein, conserved
MASGVLGENGSHMPDGCNKTAITVPLRSVLPITAVEASTGESVSDSTDIYPDSLSVPPSP
PPVTGLPEALKAPKAPQDPPESDVGQTGVGDRLSLVPNDDSSGAGGGFEENGNSNKIGVS
ASEFSTVVGASRSSIPPEVGGSENKSGAPPNLKLESPETNELRERILVETNKDTQKVSKL
EENPESSRKKEKANIRGTSEEAGKNEAGRSGVEAHGPSSVLSADGQLQRQGTTVTMTQPP
PPSPEQQTSAVSPSPGVDTPAARSREAGDLEEGKGIPPARTASHNSTDEKRKAPPLRSEK
ESAAPKPPSADGVLEQNSEDTTTKEAIKMDAHTDGPAATSEQSTSASESGVVKRNESEDG
DNAQRPEPKGQHNDPDAVNTKAAPTASEAASYTAKTVPARKNDTVTYGDSDSSTAVSHTT
SPLLFLLLLVVACAAAAAVVAA*
>TCRU_5112 retrotransposon hot spot protein, RHS3, putative
MVLTSDNGWPYSWPLGPSIRDCYVNCKVERVWQIVKGDLAEPFSTDGEPYFTPDPRVLIG
TPGIGKSMGAGSYLLYQLLHYDVEKLQFVVYSFGGSTTYVCDKTIKTVTRCVGRGASRNV
LYDLWRLKGHGRNVYIFYDVTEKGTPPAEYFVSSTGWGMSVVSSPNVGNCDEWEKQVKAG
RIIVNCPDEMDVKAMCTWMERDGTAEKKVEYWRMVKERMDKVGLIPRHIFDANKFIAHSA
AIEDALNGINSRDGEKHFTHRE*

>TCRU_5113 retrotransposon hot spot protein, RHS3, putative
MEYHTNTNIKHRLLCIPAVGAFLLVDGFFFVESNPRTLVGLRMARAGEHHTTASTVRQFT
VCPAAYFNGWEELSRDMSWEIIYVQHADSTPLNDWRRCDVVNSDSVSRDEGREIAVFWRK
RCASTKCQYHLGALEETQLSEVRNSHGNRKTN*
>TCRU_5114 hypothetical protein, conserved
MHFLALEVAIWAPRVWNEGIFEVAVDPRSAYSYKCLHQADAQVKPAFDGLVSCRRALEIE
RDPADRFMDLFRALLQTFQLQMMTTESSVPISELRARPRTQQQRSLRCRL*
>TCRU_5115 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGAGSRCENSVTAPSESGVSNPIIAPAPTNRSELPKSNENEG
PKLLGDLTNCDSATVPEKEICKNDSKKSPKCTEGPEVVGASPSHPLGQKEHNKVQNSGIP
APSEKDTTLKDQELQGRLQDVETLSREPAKEKEPKVTIQGEHSSSPSPPNATVTVSSADI
SGVGIGTVQRDNMQNTLTGNDGSKSRAAQPDSDSSNTQTSVDEDTSSNGGAPQVSTAADT
DSAGSTTTALNTTNTKKEDSGDTDGSPAASPAVGNNTATATTTTTHDASEYNKDGVKRST
EDVDQNASKTNSNADSGKTETAAANSEVPTAASNATNETSNTKTTAYSDGRTSVTYFTSP
LLLLLLGVACAAAAGVVAA*
>TCRU_5116 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGCGRCEEEGTAVPESGGGLPLASKQLETSSQDAQELNG
RVPGVKDKVSPASPEPREVEDDVDEEDDIGEDEDEETEDGGTEEEEGKRTAGQSDQGGKA
APDPGSGEKNLSGIEKKTGHPIVSPEGISSSNSLESNAYP*
>TCRU_5117 hypothetical protein, conserved
MAMMVTGRVLLVSALCVLWCGAGGGYAEDDADVVPGGGPGTGKGEKNSEELSSPVPGLQE
RQEEPAGGRGSAGPQGLKDNVVPTTDRRAPNEEQGANLDVDPLNPTTEQNENKDSTKAGA
GTINQTPPPPAGPPPPPPPVPPPDPEAEEVERTNTPEKQDSPVDHHSTQHRTVLQEKELE
QQEEDTKNQIINEKHESEQLPVQQEKEEEKLRSEEQLEQREHLHEEEREGEHLQEEIRDQ
QKKQEQQEEEHEEPQQEHEDSIKQGKEQEQQQQHQKHENASKNSDGPTKNETAVGTNAIA
STGDSDSSTAVSHTTSPLLPLLVVAYAAAAAVVAA*
>TCRU_5118 hypothetical protein, conserved
MGCVEELQVLADVVAGVRAGVSATRSVAVGKTSFTLAAEAGIDEANVRAHHPTFCTVLPR
RLDLIASHVGPSPCGRNVASKRSRGRRARRLYSSVEVSRRGNAGLSASDISLPFDAIFGE
SVGAV*
>TCRU_5119 hypothetical protein, conserved
MPSDRHIPGNDSYLSGELLLVEVPKMKYGSGLPFVQYRAKTAWEWLRPGLCSLRRRCDRC
AVSRSRPRSSAGRWFRWDFWRLRLTAKAKFPQRLGARNAMGVDHVRHDTTAAAAVLAAHR
AVCRASDRGGVGSSRRRWLFRAKFFACLLCGISAAPTACAWDGGLQWSQQPSVFVRNTGA
GAGWRSLLPASDSGSRARGFPVACCSGAVSSWPELSDTNNTSSQCDDAGAPCVCELCEVG
RLLGLCITSLFPGHAAVAKNKPHPCARSSVLLARKKGTPTM*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MLLAKGNVHDGVSREMLYAAGAVTAAGSTLSFVHNRALLPRMLSLSLSLAAGAHVRVACN
DAGGRVLSTAEEYAAAGFGDAGSIDVAGCDDCDRDTHCYAPGTASASMRNGVCVCNCGSG
GYGETCVPAGAPALPPAAGTAPSVFFREGVTVQSVFVVPAGASEVTLRHVVLDGVSPVLY
VPWMARDGVRIVVQNVSLLNGAVLYVMGGGALRGAVSAGSDEGGPVELSVCDVEALNGAL
VLSGTFPAGSVLTVTDSLLVAARPTPLVYLPGSQSSPYAPVLVLSGLRLVRSVLVVSGVA
LVTVMTGGRTVVVDGAVLELVGGGVALDAAVFGGEYALCASARVVALGGAVLRVSGSQVY
AAHGLVFGGGVEANASAVVVNDNVGALTDGALLELRGSASFVSGSWLSVRGNSIRGRLLS
VPSYPRSAELVQSTLTLHGNAGSGPVVMDGTVALGGAGRKFVVGCLALNGQALRPMDYRS
AGIIGEFRPVACGVCDADVHCFGAATRTMSGSCGCRCADGGYGRDCLPVYLPHVDGCNRT
SGMPLLSHTATLTETRSLTSTWTPSLSTERYSPLHYGTTETLQVTETVALLPTRTPTASV
SGTPWWSEVACPTLSVTTTAAGGSLTQNDIRGGGSAVPTRLMVALPPPFRWARDPQPSTH
LSFVPVSTVQPSGFGGPWGAMLSNGTWVRNATNPSTVLELAVPVHRGYFIAADETIVIRC
DAAAVSGGCKGVLLGSFTIRSDTLPAAASALSAITGVVAGAAAVAVVVTGGLGSILEMQA
LGVFARMSCASAQERASTAALPYFLSVFAALDPLWMVVGNALLAAAFGCVHCGVTAAFQR
WRGVDAASAWAAMRFPSLTYVVAHAMHLGIFFGSVLALAMPDARVQHRVVGVVGVLYGVA
FPAGVCYLIARHVGASFTRYWQFSRKPLHERLLYPVGYWHPAAQQRMYGGMLTNMRGSRV

YWCVFQLSVLCVVGLIAAVHPPVGGCHVLYFCMAAVLLAGAGVVAFTNMMRSAFLTVMHT
ASFVLLAALCVISAANHLAPSDGGARAYAAIALLLTTVVLAVTVYGVVVWYAEDRHWQEL
REPRRGGLEALLRDDEESDEETQKPHDRTSLSYASGTTVASSYRPPAPPQPMAGDTRSDA
QSLLECASSARGKIDHALL*
>TCRU_5121 hypothetical protein, conserved
MFYDSSSAFVSIDGSSVVTLTGCKMGSTGLSVSLLSRADAGYRFVAGCLTVAGREASTAA
ELELSGITNVTTVTACGECTKEGDCFAPLTTAVSGCKCRCAAGGHGDVCVPAPVPAGPPP
PPPPSSPPPPPPPPVGECISDMEYPEVTQAVGGGLSWLCYRNVTFSGGGMSLTVLVGAMA
GDVAHVTFDGCTWRDGAVLLLLGNAYAAVGSLNIVVTGNRFIDALLSPEGVFPPHTNITI
SGNSFTVTRLFHWSGLDLRRPSCVAMNGLAISNDSAVVLSGNVFQSVTTSAGAVYVVGSP
LRVLWKSLFAVLGNTFHMGGGDSTLINIEGSGQFSSLKVLNNSAVVIRGNVVARPVKYFL
LVILALRVESRSAVVFQGNDMQRSSAVFFSSYSSYIYYNSWLQLSGNLCRESPSAAFLFL
NPTVNLRDSTVSVSGNRFMSSTGTPTVLRISTVPRDLTNGAIVAACNTVNDKEGVKYSIS
SVYNATILTCSDPCTLAASCFPAYTTTASSDGCACRCAEGGHGDACLPVAVPEPPSTDGA
DLCVRDVRVGVKLSAGFGTSVACYVGVTFAADVLVDVESMSGSVRNVTLANCTFVDGASL
YVVGWRSEPPAGQRADVLISGLESRSGGGVVVANRFPPGSRVTVVDSVLIAEARVAYRGA
YDLGDASACLVVHSVNLTGSVLTIARTHVAAVFRDAVGVLVVGGVALSSRGALYVDGLSV
QTALGLCVSVEGGVAASGGSVAFVDSDFLLCKHAVSCVGL*
>TCRU_5122 hypothetical protein, conserved
MLQGNKASVDVDGESMAEEVPLTGGRPPEVLRFCFGACGGHESHVTVTNVFLYNRPLNST
AMRALKDRDPAPTREAAPTLPEKIRVVDSVREHIAEDITEEK*
>TCRU_5123 hypothetical protein
MAAQGYQNSANEGTALTCSDEHDCNASLQPCELLICSSSSLNASRLALEAQPEPGDSSLW
ACADANAQGHTVGARPASTPPAFVNDTLSPFSHHRECPCVLMAAQGYQNSANEGTALTCS
DEHQTYEGRELPEAHAPGAGNAANEDSSRNLAPVLLGEEGEESLSPQGVDAATANEIGDD
ACLMLASVAPKYDSDDVARTASSFSTETVSLSACEPLPRIICIDIIEYCPHLTFCEFCEY
FSSTESTTSIGESECDTADSQSSLI*
>TCRU_5124 hypothetical protein, conserved
MHADDRTLFALCADIRACAAAMPTAVSVVATWAAEHSLKIDADRSGAALFCIASHRQSEV
DTARPSSGRWEATRQSHPVRLLGSAVDRHLNFGVHVTAAAE*
>TCRU_5125 Leishmanolysin/Trans-sialidase of Trypanosoma hydrophobic
C-terminal, putative
MVAGDHVQAKTKAHFGCETLEGMELEDEGGTREKAIPHWKGRHARDELMAPTVGAGYYTA
LTMAVFADMGYYSVNWSMAEPMGWGNSTGCDFLEKNCNATENLAGKYPHMFCNDSDKETL
RCTSDRRHVGTCTATIVENEGSLAEKDLCPVVSSYFHEKSSGIKYRTCSDENVDYLPGSL
TGGDSWCLDAELLETKDDKNKNVKGVCAQVLCGEGTVKVKYLGSSGFQPCPEDTEISVTL
KDFKKDGKIKCPKYVEVCTIAANGSSLVIPSVLEDDKGEEQEEQVEVSVAAPALSPAEEP
HAEASSPGQPRAESKAQASPAEEPHAEAYSPGQPHEEEPRAAASSTEEPHAQASTAEESH
AEASIAGKTSEAPVVQTTLQQPQKESKAGQNATVGESANTEHVFVGWNSHAVGESTGDAC
TVCRSGLLLLLLLLGLWGFAAL*
>TCRU_5126 hypothetical protein, conserved
MRWWTNAVKNNDGFRFTRLESRAIWTVNTRGDNVCHVFLSHNFTLVASVTIEVTPNGNTP
RLTAVLADTASNHTMGLSYTADKTWGTGPEGKTTKRTSTWEPKKGYQVALMLQGNKASVD
VDDHSLGGGRGAASRWEAT*
>TCRU_5127 hypothetical protein, conserved
MGLSPDPHRRRMPWTAAKECVPGVVHSSKEKMVLDGAQRVDVDCVDRASQVYPLEALRAT
VAKCDYTTCRGKNIFNWFLRRNPMYSGNRFTARIGRRGRTTRTPPASPFISFATAATQPH
ETTRLAGFPGWYALFCLSPLFPIPERRCRRPSSMQVPVDCGHTH*
>TCRU_5128 syntaxin binding protein 1, putative
MPRPVRLRLLLLLVTASSSDELTEAKKQQLIRDGGLTPNAYLFENPEHVTRRVGSVQRYS
TASAQSGRSTSSSASNAATDGDPFLKHACMMMETAGRKRKLRVELSLALVQRDHAMGPNG
ASGGHNSGAAGKNAGSFQGCGGKVGNHPDLGGGGGTIALTTPQRIVLLVLGGVACSERRS
VHEVSKRVWP*
>TCRU_5129 hypothetical protein

MGQTSAFLNAKAFPVKYVYGLLTPISVHFIHGAECLALAIYFIGQWVENVKLDIPTADFV
FVGVNVQGWWQWRRQALIHLDAVTDIVRAYSDAADPLWWCAALAAVLLDLDMDHTMSVGD
FIAAGCGGDVGTQTPCTPVSLNEMIAFLKISPKSCVLVTKKNSDFGDTFGLLMAVSVLEN
EALFYIVRPSGSAGGDEGTTGDSPICSLKGEWRSSRELLSEFDLFQTVRCFSSYTNPEIR
WVDAVQGHFTSVSVLLPEGVLVTRDAIYARLFDVTTSLWWPVEVISREGNTLMFFSPFLE
SATSVIVLLNVDVDTVRRLEFLQIVSEELGIFQRKTAVVVQVDGQEVCTSSLTLNAAVGQ
EPAPREGIASISAHFGEPDPTTDAEYSMKEIRAIDVRRNQSTTAADEARSQNLIVSLEAD
AIFRMVKETLAVHMELMVNYMDRFLELLSFSLWSQPPRLDERGGAVVLSPMLATTIARQH
VELSTMRARKDFLSESLCCAAKELNSTKTKLNCLEEENGVLREELAQQASACEILRQDIV
AKDEKLAGAARYCCAVEEQLRLAMDSFLELRCCAEEMQ*
>TCRU_5130 hypothetical protein, conserved
MDHLRHLAFGLSDSDFRGSREARLELDRFMAPENLLRIWRQGEQETAETLLREAEAVGSP
EVYAALGDGLKRLFDTGTGRAAAENFLRLDTSHIVTRFLVNGVAHEDLSRAASVRPALIG
VMALLPSDLAPPVGEFLSAFLKNERVLRLFDENKPESAENEMVCRFLLSYTDLISFITSS
TVFAFEHDPLLVANYLMISCIISRYVEMPSPLLEKIERALTEYEDEFVFCFVCRACASAL
RNHELNAERYASLWGVKAALSLAQCNDSVRDAIYEFLGGASTTAAGWRGIYSVVPIEDEI
VRALGVAALRPRALGLMDTFVQSPHVPDSFFSSLLLHAAWQFCGDADDVSRENLWCFISD
GLVRKNIMLSMAPLCASFFYSMPQEANVSVRERQLQVATFLVERAGLSQEMVDRLKQFCA
RGLYPPSSVGLESMARH*
>TCRU_5131 mitochondrial structure specific endonuclease I (SSE-1),
putative
MSVRERAVVLVDGPAVVHRWYHRWSYTSKHTPVDVKRFTITNARHIIATAHSFDPSHLAQ
HLLSPQVEYAHTPKHNKIIVCFDQGDGGRRELYPAYKENRAEREHAAELSVIKKVAIKVF
TGEPKNTLIVLPDLDAKLKDVDAEADDIIATLALHNQQLKIPTVVMSHDYDLYQLIDEAN
KCYHYDIRTKHLVSEKGVIERVGVHPKLVRDYKSLAGDSSDNIPGVKGIGKTRALQLLKK
YGDLEGVLTKGKKKQGGHLGDLLRAGAADAELSRKLVELRSCPKVLKACEAFMKL*
>TCRU_5132 protein kinase, putative
MPPVLSPEDHAKAKEFSAFLRHLGLSHCLNLFVEQWQLLVKQQDSAKSHGGKKGQKVSRS
SASSRSRKSSSCAVSNFQILQTMHRVVTSTGVEEELWKLSGEDYLAPEFAGGAGITLEKY
RELQPTEEARLVPTKPYFKEAAPSNLPLDSFHLRVVYEVGKTGFEEEKDFPILADTVVAG
RYQMLQFLDSAAFSRAVRCMDLIEDREVCLKIIRNSKDFFDQSLDEIKLLKLIDSSGSAE
ENCVVKLYDYFYYKEHMFIVTELLRDNLYQFSKFNREEETEFYFTLPRLQAIAKQILTGL
CFLQNLGILHCDLKPENILIHSFSRCEVKIIDFGSSCYLTDNLSSYVQSRCYRAPEVILG
CKYDGRVDIWSLGAILAELATGRVLFENTSLQQMLASICSVCGPLPASLLHEGRNTQHFV
TKTGVFYEYREGKELVFHFPVPQNSLEAIFGYDDPLYIDFVRACLTIDHHQRPTAAELLQ
HPFLQEDYGSACSSPPPLKKKLLDNDEPPVGSVTAEVEFQDAQPTA*
>TCRU_5133 calcineurin B subunit, putative
MGEGSSFTPEEMRQLREATAFSEAQIVRLQKRFATLAQGGRGVLTAEALSSISSVASNPL
LGRVLAVLDTSGDGKIDFMTFAKALAVFSPQADKRERLRFTFKMYDVDGDGKISNKDLFE
TLTIMVGTNLTGVQLQQIVDKTFIEVDLNRDGYITFEEFEKLSLLNNFGDRLSLSI*
>TCRU_subunit mitochondrial RNA binding complex.1
MLHGSRLFFKKGWTHTPGRTRRGGKNLAWRPKISEHVLNQFVPLSLAFPRRHPNSWHELQ
FNLLGYTKWPKEIGFYNAGDNFELTPEAMFRLYVKNRDEAFWTRLHNEKVVIHLMPKIEH
DPKKYMERVNDIFRHHIKRFGSDHYIYNAVMQACAFAKDLSRCEQLLGEMRTIGLEPNAQ
TYVNMMLAVRLSGAPHEKAEAYFKEGVKSGALDAVMRLDTEFKMWMDQLERLGSFTAKTG
YLSVNEEGAKPMPRDMWALWGWHRTEPKFISRKQMIEEQARNRVNSGRELVGTVYSKARR
QPWAKYNGMFPFDYNGPARRRGVSFEDAPPPNLNKEVCETAF*
>TCRU_5135 DUF2407 ubiquitin-like domain containing protein,
putative
MSGEGAVLVRFVLSGACYPAYSGRQLQLEVPLIQENGSSTTTTDLKRQIRREWPSDLSEM
QEIIKTVEMKILRTGKLLADGTPLRSVLSSTEAQECSVNVGAGAKNGDEPRSVLMHLVFQ
RNNTTTRREKGGDKAAPGKRKETGGSDSNCCSTM*
>TCRU_5136 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGGRCDEGLVESRAGVSGSGGEPPLASKQLENSRQDTQG

LHGRVPGVKDKLSPASSRPREKEDDVDEEDDSEDEETEDEGR*
>TCRU_5137 hypothetical protein, conserved
MGPRAAGFLVGAVAATFFSAMLLQYDILRKKDITDREISLLEKEASLIRERFRRAQRALI
DAREEEIETQVH*
>TCRU_5138 hypothetical protein, conserved
MAQWIPKTAWRVSNLNKRYGPSYITSGDVPLSTFGRAPIVYDATMLKKKLSCAEGLVMID
VRDALEQQRYPVPCAVALHHHDLLSGAACPILPREKESSELFIIASNLQRGVNSSTALQR
WGYSNVFLVDYESLVEAGCIGDAEDDEKMKTVATTP*
>TCRU_5139 BNR repeat-like domain containing protein, putative
MLVGQHSSKDSPNSGAGGCELLLVKGSVSGEGTNNKIDWKDNESSPQRLFGAQLDSWTRL
IGSGGSGVKMKDETLVFPVEGTKKAEGGTEVDVKTVSLIIYSKDNTNWTLSKEMSADGCS
DPSVVEWKDKKLMMMTACDDGRRRVYESGDKGDSWTEALGTLSRVWGNKQKRHEKCVRSG
FITATLDGVGNDGDKRNVMLVTLPVYSENGEKEKGVLRLWLTDNTHIVDIGSVSEEDEEE
ITASSLLYKSGKGNNEQNDELIALYEKKKGDGNSSPGMVSVLLTAQLKRVKDVLATWKEV
DERVSKLCPSESALEDTQTDNGRWLQ*
>TCRU_5140 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MPKKEKENVEKGELHLWLTDNTHIVDIGPVSVEGDDAAASSLLYKSADNNGKEELIALYE
KKKGDEETSLGMVSVRLTEKLQRVNDVLTTWKKVDERVSQLCTTLLAQKGFSAGTACGAG
KITDGLVGFLSGNFSDNTWRDEYLGVNATVKNGAAKAAKTSDGVTFHGAWAEWPVGKQGE
NQLYHFANYNFTLVATVSIDKVPEEGDTPIPLIGVKLNDGKTVFLGLSYNNKEKKWQLQC
GGGTKPEELSSPGEPGTKRHVAIVLQNGNQGTAYVDGQRVGNEQCAFGNSESQEISHFYI
GGNAENKKSRGVVPVTVTNVLLYNRPLDEAVITALNTESVTIPKLDHAKPEPRGTPSTPA
GQQPSELGHLVGSSKVASGGVEGADSQIREVNATALSSNLVNVSQENNNDASSMRGSGLL
PSLLLLLGLWGLAAQ*
>TCRU_5141 Protein of unknown function (DUF3676)/Trans-sialidase of
Trypanosoma hydrophobic C-terminal, putative
MDSDSSLTPSKSDAEPTSAEDTDDVSWTEGAEFPVENGKEAPQTIDTAPGNTNTTPGETE
IPSESNATTPSDTDILLENGHLGELAAMALTGDSTVHGCVSRVLLLLLLGLWGTAALR*
>TCRU_5142 oxidoreductase, putative
MEALPASCRKIVAVRISSNFRSAVEIRNSPLPSVLKPTEIFVKNRFVGINASDVNFTAGR
YKPDVEPPFECGFEALGEVVASGEKVKEFFVGDIVVTQAFGAFAEYQVVPSRQAKKVPSK
KKEWLPLDLSGTTASISLGEVVKPLSGEVAIVTAASGGTGQFAVQLLKNVYNCHVIGVTS
SSYKANFLKGLGCDHVIVEERETIDEGIKRIAPTGVNFAYESVGGETFQVIVQNISLRGR
ILSIGGISGYSDGSTWMRRSSMYTPLQTALLSKSATLHTFFLPHYSKYAARHFATLCDYY
KSGIIKSCVDSFEFKGLESVPDAIDYMYSRKNQGKIVVEL*
>TCRU_5143 hypothetical protein
MSFSLPRSSVLVVSVPKTGIVVPEKQKTRKEEEDTFTQQKKELEDIIERQQRRIQELYSN
LTVDAECHERLCRAQLLSEKENLETALAGFTGKLEKLSARRQELLQVNDHAFQWGEMRSK
CVEARSRISDLKDEIEESEKQLETVQTLVNNQQERLHTVRRELRHVRQQVKWMLECQAVD
EQAFKNRIREEEDYLRQLMEARDGMEKESSEMTEMEKLELLPLQDEVNTLEAYLKGIKGY
TQTLQLECYEFQKEMERAKMITIESSENELASLEYQRALEKVDQQMLHFLNEKMEKTRRQ
GVAPIVVHTNKKKWLQNYHIVWDCLSQYCSGMRQEKEKDTERILSEVKQGIETARRELNE
VTGTSDEGKRERQTAFLFIEHLVSLLHRGRKMESQLLKRIDDSAGSIGEMPEAYISLAKM
SGYNDFMDDEEEETVMPMESTEQLFKPIEEESPELAIGEMRSTFDFSPDDRKVEDIFRKM
AHRPRGHLQEFLQQKSLFMSEHAAQAHIPLRRTLTRSSPSTVEASLSLFFEKMIVESIHY
AKSHQQKIMQDTMDLRHGVVQADLQYAIEANDLQTRVHRIFSERHRSFLTSSPASTAPLK
GTHPTRTSSVSKAIQRIVIEGAHLPPDVVRASLALQAKYFLSCAIRGFTAVMLTPGSVIP
TVRHLFLTRDLDRLCARDVSSAEIGKLKQVDFTAKLKDVHDIHLVKDEKLTSSKLKAEIS
FTIVLSTESEHRASWVIQADNPESRTFWAYVFAWVINESAPSNEDAIIVRLKSANKIFVL
DATDATADGFEPNNRCGLYVQVDEK*
>TCRU_5144 WD domain, G-beta repeat, putative
MSSQKAHQPLFVLKQHSSAVMTCAMDEQKVFPRLLLSGDSDGVVKLWDLELRTPLFSFHA

VNRASLDAETNNQNKESPVFLVSSGVMKVGFLTFQGLAATAGEKGENVLFYTQCRNQHVH
IWRVVLECDDDGDDFEELQSNNAGGNSLELLYKISVPQHGFCTVPCAAISCSELQLAIPH
DNDGMISLWSIGLVDKSGKNWEGLRVTCKKTFSASGLGTKCGTIMCINYRDGTHIALAFE
SGHLTLNNFCGERLAIVRAFSETALTCVWSGNMLLASSADGQLHCYAVVSEKNEALDNPP
SEADVTLTLVIQWEASLRKGLGSVALQRHLAVVGSWDHTMRLYDEGSGRVVSILTFHSGP
VNDIALVPASLAQYASFGFDVRRPRWCSAKASKIKQEEDSVYLFASASGDFTIAVWRLDF
KMLRATDVSAI*
>TCRU_5145 serine/threonine kinase, putative
MNGRYVPQEVLGTGTYGRVLRCNDVLTGRQVAVKVSQRDAAYRRSAMNEIRVLQLLSHTD
NALKMFDFFEDSGHLCIASELLCTDFYEVLRKNGFQPLSLDTVRIVGERVLRALAELHKA
GYMHCDIKPANVMLRFNETDRSNLSDFTKTCLIDFGAARQFHENTYYDVQSLWYRAPEVM
LGLPYTSHIDSWSVGCLLFELYTGKPLFAGENPREQMTSIMCTVGMPPMEAFSSGANVEK
LQLPCLAMDVNAEANLRNLIASYRCNNTGFNHSYQLVGEESAFVNLLCALLQPDVRWRLS
CTDALHHAFFTSRCLYHGNIVSANFSVFSPSSNGLQSSIDSNFGAVFSSTGNDARGFGGF
EHLVPQQTQPHPNPHPQPRLKSESSPILPANSNSVPLVGLVGSPPGMVLPGTRPPASSQV
NIPSSRVVLQNVMYPTPPMKIIQPVPFNTQQSQKALQQPQRVSANMLPVMVSAIGNPYSF
PPCVRPECQVQNWEPVIFQPQQQIPPEVTPMFQCKILPGGCQYNYQGGADPSFYGASIKS
DLHSAVYVPS*
>TCRU_5146 hypothetical protein, conserved
MAVEVAPSTRLQYARMLRSMLEMDRTPLDMVILGLQKVAVRSETRQARPLTEEEMNQVIR
SRTEWKERVVVRLAWITASRWFEIAALTPNNFKLKADGAIILDWSVAPKTARADPHRASR
FVKIRGQDAFDNIKLCRTLQENEKLTNITNAKVERALVPWNATAHSTKKGVLRHAAQIVE
THDLNSHVILQLAVHVDPFDLPQNTVRYLWRYTTMLTQVLALVALM*
>TCRU_5147 hypothetical protein, conserved
MESKAPEQPSEDATQEKHSHDTTTEDPTKNAATGSPAEPTTSSTSASGSGDHVQNKADED
DAQSSEEQHDSIETGNTNVAPTLSGAAPKTAKTAATARINGTVTKVGDSDGSTAVSHTTS
PLLLLLVACAAAVVAA*
>TCRU_5148 leucine-rich repeat protein (LRRP), putative
MGCSQSSGRKEVNTNFGATGLHVGRDGDVDLTSRSLDILLPKYIDLIRRDKLHTARRLHL
SENRLYNLGKELTLLPDIEELYIDGNRFDRVPAVLGSMENLRLINASMNPLGQQARALDV
LPRMEKLTNVILRDCSLSVIPESLLRCPFLKELDLSHNLNMQFAGVEFSALPSLQILRIA
NCGIRGEIPTGVRGITTLLTLDISENFFNFDDLDFFGPHLPLTLTELHLRGMHLVAVPQV
VVQLRKLSYLDLAENALETLDVLAGRLVRKLGPSSAFFGGAPNVVTEANEDNVSVVSHGS
TRIGMSQLSRAGRIANVPQPIPLKRLSLRACDLRTLPKYFHKLTNLVDIDLSENEQLNDP
NMTLFSLSNLQVVNIVGCPFAENRNLAHNEWFDIAHLYKLHTINWEVWKGVHNMNPYRTK
VPFEICGLQLQYINGIKLRPKLFVGDAVQTIINLLVDGYLKVDLALDDGLVYSYAEATRA
LNQLESFFFDSSKDDEKHVTGNTQRGRPKMGGNTHFGNGKRSSLPSSLPNKKVRRDALQI
AISRYIFFLTMQAANYDAVIVPPADVMAIHYAQMTQDPISYRKDCEAICGQVLNCNYNLF
FLEQKARPQAVKEALVGSRRVWNMIVHTTQKDLFWLRYEFWERRERDFLEKSSSPQNDKT
NRNVENRNAFAADDAKAPTTPPSSPSPKTPTTKTPPTAFAAVKVPCAPPYNGADLGNLSN
VDAVGDLCSVLDFSITAHFTEQGTDRFVASLVRFFSVNKRFLDCAESIAGQHLDWTRYVK
YLALYAQIQRLKQPKQQEKRVSQLEMASGNNSFVSPDAYLPQPMVTEELLPKVPQRQLTR
LGLRAGLAYARANSVGTSQRGSIEQSRNDSPVTGRNSDAGGRRLQQGMPMSEPVPTIGIS
LLLYSHRTLHAKYYQALALLGIETIDIDWDETYDAVEATMRAWMLLYDELYVKDAEGAFC
LGDGLNCFHGNDDKKETSQSEPRTAIRRPGSKRVSRLLRRTILCSAGGEHVIF*
>TCRU_5149 Domain of unknown function (DUF3883), putative
MLDEHPLQMQKATLFSMEAIDAYVKELQSGHDRTSTAPPLTVENILCRIYARFYSKEGQP
PLPDGLPFSLKQVPSLASTAVLQSRITAMIQSAVATRPVVTLYELEAEVCLTENVEMYAE
LGLGCSLAALPCVRHLFGVSVGTNTAPVTSTEFMHFLLFDTNAQALLSGGGDAGDAVRAF
ACCYKGGKYTSMQLGIHIQHFPWLLRFVRQEVGRTSTFFSDLLNENAWCYKRNKVIYERV
MQSLHTAMMSHKNHAEEPPREVKFVVHASQEEAMGTDFPPEMWGTCNGSDGGLSLHGILS
AESSFLLVDVRHEMHVSETARVEQMPPMPVSSFSSLAFPYAAAATVTATDATKTTPTMVT
SAHTRKRRRGVVVEERTEVFEETLMHPLKQQKEEIQSEDAQTSTTEAAAGVAAGSTPLPT
LLEPPPIPLEKVLSILRSLAVMQSSTVAGVCVAPCGDFAVFRTYASKLLSRLRRVERDAK

EHVGLASISNDPFSVDADTLLRFFSSNETSDVWCAFHNSLASHANAPECGEGMNTSSPGE
LLLHCLELGFADLMFLPLVATKSLLPLLAARSLLFRRVLLSGRHTSTDLLVFHPLQFIFD
ASAEGVDGYPLVTVLDGEILLRGLQDSEFHHKLTSLLGKLEGHGVLTSVPESWLYDGFLL
QAVRSQMRDYFNGAERTDLEACHMALRMLLLYWWLVGMWCHAPPSSRIANGVAEILHGLR
DVVWLPSLSRHGSESDVSDAALRVESWHAPSELFPFVGEFKRHGLQDFLHFAPHEIRDVL
SLSGQNGDISLFQHAHRFLDRWIAVVQSGMEYDNKYLLPSPMGMPEALTAAVALRLLCLL
RVGKRISVFTIRYLLRRIAETDEEEVLIDARRLPIIPLSMTHMGLDENGELVVREMATCG
TVCWEPLPDVDRTHMLDRSINFIGDDFYELAVDVLRVSPVPSLATWLAAAEACRKHIMAG
PEINASLTELFLRVFSYSCTSHYKHLLRRFEQQNPVIPGSAAEAALRGVVDVVSGDSLAG
HMFPFHGRWRSPAEGLFYCGPYYRGFSGLTLKVTTLYGAAVDKNNDDTVGEDMTPSLPVL
IFTEQPHYAVAAVLQRMGVIALEMCTEKIVTFGRMNAVNSTGFHNKIAECAPRVQEFLRT
HYPHYYALVHSQVRHSLEYFSTVLAAEPVLREVLRFQGKTYVMTRTVRCWYVQQHNCLYG
ADEEFFSFLAADAIADLFLPLMDEEVRQGVKKVLQESLRDAELCFNDTRPPPCPPTTTEL
PPPPPSSSSAVLEEVWQISAAPALRFRDHFPLGKDGFGPRGKEGVAQNTSGILGGLKMPQ
MKLLLWGEGGYMARSLPQWKCDLFDSAHDVLHAMEHGRSNAGGDSEDEGCPSTPTAPTPK
KKSSARRRARRGGRSQFVAPAMVVQENRETADYALAAERFVAAKLRAEVPPDVDVVWVNE
NGEYGTPYDILLVRRTVRDAPSSTSTEILAYVEVKSTCTNVRRDFEMSLREFLFAARFGK
AYKIYRVFRASTSATHYMHVEVLEDVVRLWRTGSLTMTGGVKVMLAPGT*
>TCRU_5150 cell cycle associated protein MOB1-B
MKKFRAKLFDSDRTYKPKKKHKEGTERYNLHKFAKSLVRSGDLSKAVRLPQGANLNHWLS
VHTVDFYNITNVLYGSLTEFCTTSSCPVMSSGPRYEYLWKDPPEYPKATKVSAPEYVRLL
MEWIEKQINDERIFPSEDRNPYPPDFVERVKICFKRLFRVYAHVYYSHFAKIRELQEESH
INTALKHFMYFVWEFDLIPREEVSPLQELLINLMGQRAKDKLEAA*
>TCRU_5151 glucosamine-fructose-6-phosphate aminotransferase,
putative
MCGIFAYINYHKRQTVREIFNVLLDGLQRVEYRGYDSAGLCIDGRDADQPPVLIRSVGNI
AQLRKLVFSDETVSLVDLDASFDVHVGIAHTRWATHGMPSVKNCHPQASNDQGFVVVHNG
IMTNFMPVKQMLLGRGYHFSSDTDTEVIAVLLEYLHTQEPKLSLVELATRITSMLEGAYA
LLVKSMFFPNELIACRKSSPLMVGFRRGGPSGAVANGDALPLTELYFASDANSFIAHTRE
VIFLENGDIAHFHDGALALYATSNTTAGLNNSVAVATPVSRAPQIIDATPEGLSKDGYEH
FMLKEIYEQPESVTRTMRGRINFLKGDVNFDGMDASILAALSRAHCLMLISCGTSYHSCL
AVRPIFEELLRNLSVVVENAPYFMDRQPRVHRDDVCVFVSQSGETADTIMALQHSKAAGA
TLIGVTNVPGSTVSRQTDYAISLNAGVEVGVASTKAYTSQIVLLTLLALLMSQTTNSSWN
DKETTKNIRGNTEENKKEVEEGKEENNQYVQKRRAEIISGLAALPAAISQCLKFVSDAVI
SIAEEWHDASTILVIGRGYDYPTALESALKVKEVSYVFTEGIHSGELKHGPLALVDANSR
VIAFCAHDRHFERSKSAIQQVKARGGRVVAVTTQKDAEVENATTLCVEVPKVVDCLQGVV
NVVPLQLLAYYLAVRRGHNVDCPRNLAKSVTVQ*
>TCRU_5152 TLD, putative
MTRRPNSATRRIVPPGVVVRLPSESTLSAFCSCSLNIAALFPDGLPSPPLPLSRCELHEL
LLALPQRLQNSPWRVCYDTEHDGFSLHNFYRKMKQVHDEKELGIGIFVVSEGVSDSVPIS
SVGGLLGPQSRSGVSALPSSVVLGCFTPEVPCLEHSQHAFFGAQETFVFTYADVSRYASE
GSCGEPQHASGVTPAHSSSAASDVIASPKMARNFSTPSLQPSTRLGFNCLPRILSVYPWT
LEEQNKEFIVCTNKFFGIGGGRDGAAIFVDASLSHGTSSVFCGTFASPPLGGRLRATLRQ
SEFTVLRMVWFRVRDRKEVFTCMDLPKREPCDCGRLLESEDGNRLVRVRYSGHKRAWHIC
N*
>TCRU_5153 hypothetical protein, conserved
MTQKLLLAEGLDLLRRTEAREYEVDRIQARMCSSSKYRHELLRLVQAYNTVYHDYLRAVE
IINYVRRTAASNNDPRDEKLIEMCEGKMRVYMDRCELVRKKEDNILLPIEQMNQDWTSDD
FLLGSPVFVLSGVQHAIKRNAPFVREEKLGDGSYLFVVKNLDSYNVAAPELSVTIDILPH
KGQQQRLEKVIPCQCGWRRAIGVVTSTELHVLIRSKGLLRDSHVDVALYRLEPKSATTTQ
APLPGAMSDQRIAKLPKLTDEDLALLSIPNVPTESLAPLPHQGAQPNETGNAMQELQSLR
VPYSQPRTQLAAMVPEPIEVNPANMSCAERMQRLRNTLSAWPNSNVLAVPLDREQQCVLQ
AVFALPFPSDLASD*
>TCRU_5154 peptidyl-tRNA hydrolase, putative

MAPLLDYASFFVSFSTGVILTLLCGRGGGCGNFWPPALFRLKGRQAHAFLAHRHEPLKMT
LVVRKDLKMGTGKIAAQCAHAAVAVVEKVESRRQKGDTTTPTLRAVHDEGVEANEGAHWD
EWVAWYDAWMFAGGTKVVLQCESEEKLMDAFREAKQEGLPHALIRDAGRTQIAPGSKTVL
AVGPAPIKLVDRVTGHFKLL*
>TCRU_5155 Protein phosphatase 2C, putative
MSSGISSPRAALPSGILLFRQQGLQLPLQTQRQVQQEEEEEDSSWLHRNPVGLIAAVPFF
EFLCSSASSPIAGASRECRVSRSKLTCVSKGSLEDDLASFKTPLSPQPPHSAFEVLTSSC
TACTRSSFAIQQNEVSSFSFQRGVDNGVAAGCSMGKRRMTEDSVLHRTSDNSSRASFVPH
SPPTVAAHMSEKTSSCYQNSLSDLLGEKDMQPQFHVPSCIPTSIPLCPPSLSVTRDKNGS
QKVLVEVAHTTLSGHRNSQEDAVCIHERVAFPPDCVAREGMQLSSASTYSLYGVFDGHNG
DHLSNMASLYYLEHFNEALNRVPPSLTSCEATPTTTQDCCHPSDGDADAHPKALLSENVP
PQRFLSNALVQSLIHLDRTLYDTTPFAQRSRSGTTAGVAAFYHGMPMSPHGPVPCYLSIA
NLGDSRAVLARISDGHVIVSTFDHRVPTYPSERVRVERCGGCVEWDRVDGALEVTRSLGD
FIYKLPPEKWLGHPGACDTSASQIGGKTPAVDVTAPMHDIVEIACSQNSNSRIGSVGSLA
EEIPPQLSMSSILSLRATPLNQNDDDIERHHMEMRCSLIDNVVSNVADVYEAELTGDEFL
VLASDGLWDRMSTEGVVEFVRARLLQSGLLHGGNVLQPMPQSLATADLPKTPIHSSSPLV
DFPRRVENTPPPSLFHSGPDTAEVKHIFSMTLLHTDGASRGKQDDGDSSGFATPPPQCAV
GRWEQRESPGDSPYSCGTPRRVLQAVANSLADHVVHHLHSADNVTIFLILFHRGG*
>TCRU_5156 hypothetical protein, conserved
MEGCIGAVFVTIQLSGGPIDVLDFFYRAWNAELLRNVAAETTGCLLRFPLLRVNGIVCSG
VVASVLTGGMVRVVSSGSIEAALAIADFVYTYVIRRLPALPRRTGTKSITSLQVVLSPTP
PLPRGMNLDTSESTAEWLREHIASFTAASKSGGADDESRQSQWWRCLTESSVACRQYRHT
IRIVCHFRQPPPLQVGRELGPALGRGVDDSDADAFFFESELMSVVPLGSVFMAVGRNLDK
GSEDDMRGAGDEGKGAGHKRSRHESEMMTLANSFLERPAKDEMTALVPPPLPSSLATSST
AARASKTGPSAAAAAATEGCSFVMKPLVKVEAMVYPSGRVFTTTDSVEGLFFFVEEVLLP
LMQRQRGT*
>TCRU_5157 hypothetical protein, conserved
MYATRWPRREEEVQGTFQWSTSDDSGVAKVRRRHLTRNRINVALERAKEERKEEYMRKLE
ELRMELDL*
>TCRU_5158 hypothetical protein
MGNCCRRSFPKEGDGDDDAAVLRLTPRQRLLALFGMHAPHLLKDVDDILRDYNNDGMCAV
SYYCAFLGPEPKLHEAKQMYTTHLTEGDIALRKLIYGLLIKYDPTRIVELELIVRAHEEE
AKRGGKETAAGFIQRLEEQYLGGLVGEAPAPPLPLQDFECSTTGACKTPQPPTCYPSAAA
ATDDMSAPFSAATLFSTATAALSMSAHAWRGGKRGGANGSGDGDFLRDFDDILARSRKAD
FSILLPYRPPALLTPWATG*
>TCRU_5159 isovaleryl-coA dehydrogenase, putative
MFRHASHIFMRRTARRLSTAGATGPGICFELSEQQKEVRDLAHRFAKEKIIPVAAKLDQT
MEYPHDLFKEAWELGLINMHIPQEYGGFGASCLEGVIVHEELSWGCSGISTAFEANNLSQ
APVIIAGNDAQKKKFLGRMLEEPLKSAYCVTEPGAGSDVAAIKTFAKKKGDAYVVNGQKM
WITNGGVANWYFLLANSDEGFIGFVVDANTPGITPGKKEINMGQRCSDTRGIVFEDVVIP
EANVLGKPGDGFKIAMRAFDFTRPPVAIGAVAVAQRAMEEARDYANQRKAMGKYVSEHQS
IAFMLADMAAGIEAARLLAYRAAWEVDQGRSNTYYASSAKLFAAEHCERCVTAAVQIFGG
NGFNTGYPVEKLYRDAKIFSIYEGTSQIQRLVISRHVIGRR*
>TCRU_5160 predicted TLD domain protein
MGGLFTRFIPFMCFDRNDDAEGMQATPPPPFDVGVALEEVPPDVYLKRETAIKPSIPITG
KQFLTLQEHIPPRFQGRRWRLLFCSGLHGFSRLALQQNCAEEIRSARGNERPAVLIVSAG
SEGKILLGAYISCIPQTSNKKYVGTEESFLFCVPSPSSSSSALSSSDDLHIFTAPADAAN
RYFMRCDNGAIAFGGGGKGPALFLHSDFASVSCSTFCPTFGIRESLLLLNARPGGDGDAA
VFDLPNDVHLEGGEPTTSVRAVQLWTIGDEYFSLL*
>TCRU_5161 arginine N-methyltransferase, type III
MPARWHNKKKKGSNGHKRPSTGGNGSAARRDIGFIPPGASAIQNSSAHYADTFMYRFPQN
FPVPGRLRHAPTSLVEAVNDFHFAMMNDQPRNEFYYELLKRHVTPETGVLEIGAGSGLLS
LMAAQLGAKWVVAVEGSAEMAKLARANICANKMEHKVTVLHMLSTELTLRHLPDRPDVMV
SEILGTLLLGESALDYIADVRERLLKPTTKIIPQHGTQYAVPIECDTLRDVCAVSGWKGL

DLSHMTALQDTVSIVFAKQYGFRMSSVPFCRLSEPIALFSVDFASAVRRDIPMNLKLDVK
ATSSGTAHAMLYYWKAFDGDLVMSTDPADTLNNFPRDMQWGQALQLLDAANGPFPTPVVF
TEGEELKFQCHFSSDRVTAHIHLCPTAEAAASPAKTTPTDNDAIKTENEAYEKVNKGKK*
>TCRU_5162 Concanavalin A-like lectin/glucanases superfamily, putative
MNKTWETVFDGKKATSSTTWEPGREYQVALMLQDGNKGSVYVEVLIVGSPENIATPETLG
HEITQFYFGGGEGDINSNVTVTSVFLYNRPLSVGELKMVKESDGKKGNGDGSMRGGVSQL
LLLGLSGFVALC*
>TCRU_5163 BNR repeat-like domain containing protein, putative
MPWPRITEWENGQILMIAECFEGQSVFESRDMGTTWKNAARTLSGVWVMSLSGVRWDESL
HVGALITATIEGRKVMLYTQRGDFSGENGANALYLWVTDNIRLFCVGPVAMEEAVNWELA
SSLLYSDGAFASFTTEDQ*
>TCRU_5164 hypothetical protein, conserved
MQLLAKEGTENGTRLLFGGPFLVSAGGVMAVLAEILLPHNSFDDQASQLPFSDIFAGDAN
SVWDFPSLTTEHSKDKWAYTVFNTVVGENHLRSASKNTTIAKSNKMFLLVGSHMLREPIG
PRFAVTNRGVSVVVGVNTQPKDGEPSGMINWEESKYFLQQISKLT*
>TCRU_5165 amino acid permease 24
MSHPNEPNRFCEKTDEKVVNVKKSGIVLFDWEERDGTRSEDYLPSSELDLTPQEDDEASE
EVRIGVIENASLFKCAFNIFKGNVGSAVFLLPTFYKDSGYIISPIIGLLIGSIVVDCSRL
LVRAKTKVNRKSVSNYLELCDFVLGNPFRYVLLLALLLTQFGFCLLYLQLFGGSMAKLVP
SFSGDDYVWMTVMFALVLPVSFFTDNLSFLAIISIIATICVFFALISTAVLSFMTLHEKG
VEPSTTPFGTSVPLGWFNNMANNMMMLEGIGVVLPVENSCKNKPRFSLLLTVVLYLVVGW
YLLYGLSGYLAHGEVLKVSLVDALDVNPFSIAVRVAFTVNIICTYPILFMPGILQLDSLL
GWPPRSWKGILMRIVISLIIYGIAMGAGTGAVNIVVSLIGALPAVVMLIILPSLLSLCLE
NSVEEPHEPRVTWVYWRHNLFGRRCTLIRLRVYIYLCLGIVIMVVGTLSVVKGLVE*
>TCRU_5166 hypothetical protein, conserved
MEQQRLHGFRLSKKEIEERNKMEQRRKWNEKLERVDVVKLRTELESLNRASFLTPQQNER
KRLVSRMVSDLEQRARVTSDMQKESQLDPRCRNLSISTSSSEDYDDLFDRARVDSTVRDS
FPTKAFQLLPRSLRKRNNEGALIAGGDKKRAKMAEDALLSSSTVGDNIEEFFDSL*
>TCRU_5167 RNA polymerase II
MALSSRLRSLLLTRMDHARFIDNGKWLQGLLEGFSVENVLGIPSVGTSPCVMIYGSFVAG
TAFQDGDADYTIAFISKKSHEELSRLEKLKPSSSNFLEVSREHHQYVLSSILRHIKNQDP
YAGLEHERIFMARVPIVRLKRKKNTGDDGMRFDLSLSLDGFRNSLLIRLYMESDPRLRAG
ALCVKRWGLSQRILDARRGWISPYALTVMYIFYMQATGRSRFVINESRVDKMLEAVAAGI
SEEYGINCSQFYENIPCVDVNASDVLADLKGFFCFFSDSRQFDFDADVVDIRTKGKCLSK
ERWLENMRGFSEKERWELLGYELIMVRDPYEPHNLGRSVDFFRAEVIREAFRLASEKCAE
DLLEL*
>TCRU_5168 pseudouridine synthase, Cbf5p
MSNKKIGEIQRNEEFRISLEAQDSESTLPPGQWPLLLKNYDQMNVRSSNFTILECGWSPL
RRPLKEYLKYGMINLDKPSNPSSHEVVSWIKRILKCDKTGHAGTLDPKVTGALIICIDRA
TRLVKSQQNAGKTYIGVLRLHDTVSEKKVLAALQRLTGPCFQRPPLIAAVKRQLRVRNIY
SNQLVEYDKHRHLVVFETHCEAGTYIRTLCVHLGLILGVGGHMEELRRIRTGVISEDDHV
STMHDVLDAQWLYENEKDETYLRRVILPCEYILTNYRRVVVKDSAVNAVCYGAKLMIPGL
SRFDNGIERDDIIVLITTKGEAIALAYAEMSTSQMASVDHGIVARSKRVIMDRDTYPRRW
GLGPVAVKKRSMMKDGLLDKYGRPQGNTPSDWYYVDYGGVKTNAEGVQYGEAPRKSTKRP
RKAEDDSE*
>TCRU_5169 vacuolar ATP synthase, putative
MKPQNAVVLAGAAAIVATGSAAAGTISCADVYPQSAAFFGSMGCASALIFANLGSAYGTA
KSGVGVAHLGILHSERIMRGIVPVVMAGILGIYGLIVSVIINNNIKTETQSYSAFSGYLH
FGAGLAAGLSSLAAGLSIGIAGDAAVRAYGKQEKIFVAMILMLIFAEALGLYGLIIALLM
NNTANKVNYGQCQ*
>TCRU_5170 GPI transamidase component GAA1
MFRKRVASVVKKYASNIAPFLLLAGVLLIVAIPAVKPRRNFIDESAVNVDGIPVLITSSD
ASHHDATIHQYHRIVHGQRSVGSESIAVYVNTVENSSIILANFLIRSLQRKNNMACETHF

YFVNGSTLHWPIPNSFVRAALFINVSSLKTRNLCFSVYGKNGMQPNQDLFNVAVAMAREW
NLNVDILCQNPHIPYSVTRSKYEHYLAALQTAVIAPQNPQPWHFFRPSGISMLAIGTEKS
DGLYELSVAHHIAAMHEQLIGTLSYLDERFHHSTSVWVPLSVTEYVEYDIAQFGIILLVA
SLLSVGYSIYELEGLCLSPRVVLIFLAPILASGANKFFGVWGSFVCSIFLTIAWSVCAWE
LSWLTINAVMLCLLIILQPATGLLVGSGVAVQLVFLHVKCQKPPFLFLGTFFAWAVLYYF
IVMLKIRHDDMNTIGGIYLSFFVYPNALWVTSRLIRSVLPTM*
>TCRU_5171 proteasome subunit alpha type-5, putative
MFSSKTEYDRGVNTFSPEGRIFQIEYAIEAIKLGSTSLGIQTPDAVVIAAEKRVPSVLVD
PSSMNKILEIDYHMGTVLSGMVADARILVEHARVEAQNHRFTYDEPMRVESCALATCDLS
VRFGESGGRKKLMSRPFGVSLLIAGVDENGPQLWQTDPSGTYTRYDAQAIGAGAEAAQTV
FNEIYHRNMTVEEAETLAVRILKQVMEEELTKSNIEIAIVPACTGKLEVYDQTKIQRIID
RLTEE*
>TCRU_5172 hypothetical protein, conserved
MHREIGLLKSNLFSSSNARKNPKIGSSDAVGRIPTREIKHFFAIETDSEGSGSRRVDIEG
SSEPCLKRLGISFSHGLLPASVKDLVIPSSSDSFTSLRVSPKRAEDVHLDDMENTEGEKR
RLPVGDQSNISSLGSGDDAEKTPSRHELQTSLVIPPESTFMNHDGKQQALESRKSLLMAE
NIPVGDFSHRSQPSRQRRKDCLIELYYRGVKTRKQLEEKLESIRAARENEFKAYSFQPKI
TNRAKAIPRSGSVPGCYERDTRLRQRLLLEAWRSESEGQCQSAPKISKGSERIVRRVRGN
SAPVIPVEERLHLDAARRRCRMAEDEEGVKQQISSVKRTAGDIKIHIDRLYMYEEKRQLA
LRKLREETGVGHSQMPLYVSSEDVVRRLSKPLKKSRCDHSVEENLLFAPQLSPVTEELSL
RARRRRIDDWYLFFTHRHGEGVFPPNAVAEKIREALQQAGLLGAFSRRAFGMALDEYEKR
NGLQLWHSTPPPSTPPLNEELTFVPRINSQRNLKAHAQMAHERLFYAAKQQQLAVKEEER
MRQKELLEEEKKRRKRQQRQQQQFRALSREKMKSLEIISSAGDERRSPPSSLVRSKSLQG
IADLSCDSETSVVSPESVSSSPSDPSFMSVAVKSVSSCSNLLAAAEQLRQLIDAPADTER
NNIKPSFFQRDEVPCADNNNKPACVPAGTSELVFASSEPPVLRVHKKKSDTFANTRVSTD
LLLECALSRLIWPADVATRRREWCKGRRRLQRVGKMLYQNM*
>TCRU_5173 BolA-like protein, putative
MVAVAEIEARIRSNLEPTSCEVTAISEEDRKYSVAIVSHIFEGMPLLKRHRMVNDLFKEE
LLSGDIHALTIVANPS*
>TCRU_5174 60S ribosomal protein L32, putative
MVKPFVQKRIVKKRTKRFTRHKCELFPQLSSSWRKPRGEDSPVRRRYKGQKAMPNKGYGS
DRKTKYITPSGFKNFPIHNVQDLYMLLMQNRKYAGVISHTVGAKSRKAIVRKAHELDVRL
INGNAKLRRCESH*
>TCRU_5175 cytochrome oxidase subunit VI
MPFADHKKYKIQREEMPAVPHFSDFSDPRFSYTANKQKNGILAYYQWLHCIGNWGEEHSM
CKKMRWYLERMMQESWLEKWEEKRALGHFDHVILYGVKPWKEFEPLYQPVKKNRKGAYEF
WLDRDFEPLYDADAADFREKAPILHDVFVNGKKPVYD*
>TCRU_5176 Protein of unknown function, DUF607, putative
MIQKTRALWDSSMSIQCLKKKLRARCALDCSGKRIITTEDFIAICTTNLYAPSHERMTKC
EAAQYLEKLQHAREVIVIGGYVYIRPSDVVNAVHLKLELPTLSRGNPMNLQQCPVQQSCA
TLRVEQKGGVRRREFWAIVSLLSGAQMTVLAYLTFIVYGWDVMEPVCYFVTTFTALCVYA
YSLVCRRNCTFHAIDDQIFSPCTPPATQCSPVAREMSVADRTMCAGKDCFDSSSWHDDCE
LLELLESFDFTTIEAASNTKEMK*
>TCRU_5177 pumillio/PUF RNA binding protein 3
MWTVHEDEYKSTEVKFSGVLQGGLNGDDDKTAKPIGVYTKSSQVFATPSMNSTESTPLNG
HKHSSNVSWKRTHTPVSFSIPNGLFSQPQVANSSQPSMMRVDAPPFEPSPKNMAATASYA
ASSPMGKRGVTPTQVSQTNVPENSNLHMIIPMDDVAIREKDRGAAHHMEWNGHAVNPHHS
HVAVRGYSGNITPEGLRGSVYEIAKDQHGCRFLQRLLGGSNGDGEFVRIIMNEVVPHVAE
LMTDQYANFLIQKLFDMMPQDVRYKVACVAAPKIISIALTPHGTFSVQKMVETIASREEM
DILREALSKDVVRLVKDAHGNHVIQKVLQRFSHADKEFIYAAVGSDCISIAKNKQGCCVL
QRCLEYASCSQRATLVNQILRCCLQIAEDPFGNYVLQYVLESNDSKTTDTIAIAFLPHLV
QLCMNKFSSNVIEKVLRGASQPVQEMYVETMCSPDVVSRLIQDDFGNYVLQTALTICSSA
QAESLVSAVRPLMPIIRNAPYAKKLEGKIDGIVHKTAGNDRSSFAEYEKSRQGEMNGQNC
DILLPHHARESSVAPHQQLSS*

>TCRU_5178 hypothetical protein, conserved
MLPIPAIQAEDGLEARESEEGTTLGSVATTGPGSVSDGGHGTVVPGGAGDSGGGPNLKSP
SSVDTTVTHGGGGAGSAGGPSSTSQGNSQEEVLPEVGPKPQQSSLLE*
>TCRU_5179 hypothetical protein
MECNYLPFPVMPRVCHDTTLRRARGAIARAISLDATALFRGVVRLYGRPDEEEEDVDRPS
LPDSSASFLLNALTKLLVSFCSLCQAWRLLEERCDGVDCQAAEEAVAARDVLQTFSAFQD
YCKEVDISYLLYVQESKFSDHDSDISLQDGLRSLIASMVRSVCLRPLPTNPAIFLPVNGK
IHRHAEQVAGDVAATNTLKALQSGSADCEDLAALPFLMRIALFLVSEDGRDVDCVSVLSP
EHSSDEHSDAYMSFWTPIASDEALCASLVKLLRRPWLRGMFCRLFLRSRTTVRKWTFLTC
FTSRRANLAITTVTSHFKMVCAR*
>TCRU_5180 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MLRDNRGSVYLDGVVVASSETMPTLETRFIQLSEFYFGGDEGDRGSSVEVKNVLLYKRIL
TAAELRTIQWSASSSSGSGPDTSMRGTMPWLLLLLLMLWGFAALYGV*
>TCRU_5181 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily, putative
MSRHLFYSAVLLLVVMVCCGSGEAAGVAEPSSVSTFEWRGINESGGETVDSLGAPSLLKV
GNDVFAVAEAQCKKKNGDVSFTGVASQPLTTETAETPVEVLKNPEDETQVLEKGASDDAK
KKVDVSRPTTVLKGNDIYMLVGAYNKVASSGQDGASDAAQLGLLLVKESVDIEDENNKKI
DWEVIESSPQGLFGTQLDSWTRLIGSGGSGVKMKDETLVFPVEGTKKAAEGTEEGVKTVS
LIIYSSTDNKNLKLSKGMSDGGCSDPSVVEWEEGKLMMMTACAGGPRRVYEIGDKGESWT
EALGTLSRVWGNNKKDGQATAVRSGFITATVGNDGDKRNVMLVTLPVYAEEGNEKGKLHL
WLTDNTHIVDIGPVSGEDDDAAASSLLYNSGENTNDEKLIALYEKKKKEGKPSPGMVSVF
LTEQLQRVKEVLATWKEVDGRVSNLCTSLSAEKDPPTGDVCGADKITAGLVGFLSGNFSE
NVWRDEYLGVNATVNNKAGAAAALASTKNGVKFTGRGAGAEWPVGKQGENQLYHFANYNF
TLVATVSIDKMPEEGDTPIPLVGVRAGSNGENKLMELSYDSGKKWHVLCGDKTTTKLSST
WETGTPQHVVVLLKNGTQGSVYVDGQRVGNEECALGNGESNEISHFYIGGDGENAANKEV
SVTVTNVLLYNRPLDEAEITALNPNKDPTPPVTPNAQKTGTSSALDGSHLTERGQSMGSS
GAGSGGASPSAVPTVSTPSAGKDSLQQVASGKSSDGTQTVGGGSFSDGEPTVETREGGAD
GREKKEIHAQNGDVKAAALSSSLGNVSQGNNTDAGTMCGSGLLPSLLLFCWDCGGLRLCE
A*
>TCRU_5182 orotidine-5-phosphate decarboxylase/orotate
phosphoribosyltransferase, putative
MGGDSLSPFLQYASKGVFVLCKTSNKGSNEIQCLRVNGRHLYESVAEHAETVWNYNKNVG
LVVGATDPIALSRVRVRAPTLWFLVPGIGAQGGDLKEALNAGLRADGSGLLINVSRAVAR
AKDPRAAAKKLCEDINLVRFGKACSTDLAAALVASRCVRFGNFTLKSGKNSPIYLDLRRL
VTHPSILRLVAREYANVLRTLQFDRLVGLPYAALPIATAISLEMNIPLVYPRREAKSYGT
KAAIEGDYKKGDRVVVIDDIVTTGGTKLEAIEKLKAAGLEIVSIVVLIDREMGAKQLLGS
LGYELEAVVTLSQLLPLWRQSGAITQQQMKDVQSFMAEASSKL*
>TCRU_5183 ubiquitin carboxyl-terminal hydrolase, putative
MLEADDWVTRLPVPPNSERGADGSSASLSADVLFSAYRLGTPCVCRHTTARNRVLNCVAS
PRCFAGFLELATDASVLSECVADIMGEGPQLLPSKEGDTALEDTLNKLTCAKSHPLRRGI
RNLGNTCYLNAILQLLFNISSVRYEVFSACAEDLSVEEHRVYEICEDSVQKPDDAERGED
EGSQPIKYALQASGLGELFAEMALTRDGNGANAQPFAAFLSLDTKTQQDAQEFFALLISW
LQHHGGEVVERTFEGTLLYDRRCSNCHRVFKRAEPFFFLSLPVKGTVEEALSTFLQPEEV
EGFMCDGCNLTTTASSCQYLRTLPDVLLVHLNRFAFDLQTLQREKVTTSVSFPLEWELAD
YINRWQQQQQRNEENDSATDGAANITATTNTAATTTTHLSKACYTLMGVVNHIGETALSG
HYTFHGKVDEEAGWYLFDDAKVTKLHHRLHGNRVISKEAYMLVYQLRPCESTTVSHDDMI
RASEDVKNERSNSVPLPPRLLKHVQQLNRELEIRRQDWEMRRADFLFFLQQWGEIALNLL
GGRLLCNSVTVETAAREEEEDEGERSSTELADLFAVPSSWLRLFGRGFLPSYVDVREYNE
YEKRKKRLRRNASGRTGLEDMLGGDPPKSSSLVGNETCDNARGATSTEQLDDDATATRIK
EGGGGVDMAKENNILFEGTSWALLLDLMEGLRCPHGKLAPWGPYKLVPSALSARLASLLN
TMPTLHGTFPVAEEMSSSHVGWRVRDYACAVCTRSMAAEVLRLKKSWDEERAALALLSGA
RDALKSKCHGSQTDTSNQTNIYCEELRSEGEAAAATGRTVYVSKALMEFWEKSLAANAKR

KDVVNRQGFTGLFAALRMEEAADRNESNDNNNNNNNNDNDNHSKNNNWHDDVSRLTLPEC
GRLLCDHRLLAPSAVVQVVPAATWRYLRERVAQPLCAGENTSEVLDKFLPYLPTESTPRC
PDCIQNTVSLTAQRHHAKMSKIAESKRFPTLASAAQFLSMPQAEMRKQHPNSYVWKRNLE
RLYRDHYRLWEKEQAAVVAAAETQIATLTREEEERKRAEAAWESMRVRRGGHKKRFKQTN
SSTETRTAPQVTPSMSVATPLQQAEEALKKARAATCPDLCHTYGCIPMWWVTLWRRWFMD
LDGTFSFPPCFDYEALLCPHGGTLVAPHLLNPADPFWEAKSVARHLVQLWHQRSSAISID
DACDVYSLDDDNKLPPFPPLLLLPLTEFVEILETYGKSGMLLPSSPSSGEKNTELIRCRV
DSSKAILFVERNTDRVFDPPTCEECVASLLERIRESSRCFLNGSLRLQLRFRRSRKNFYE
STDVLRELHHTTTLRELKQAISRLVAEHHGFLLPLQEMELLRGRKPLRRHRNHTMKKNES
EVQPSGSGNVASPLVIDTNEMPTSFQGDEDAGTLFDYGLCDGDVLTVNATERVLEKIPGA
MKETEVWEEVPAELLQPVQESSTAFGATRLHGAVGKSRRGGAAEAKAQVACDVCTFINAP
GRARCDMCETPFKQ*
>TCRU_5184 hypothetical protein, conserved
MRRPSRWRHVVRPTLPFEASVITAVVDAAMTRMGMTRSVSTAPPISLLSWSVDGAGHTHR
RCRRRLSIQERIPLICNTIREAAPDIVALQDSLPQVADALCSQLAPRHISKPHDDNTQAE
LLPADAKDGPQYELVGAVRNGRCGCLQLFRRHDSVWGGRLLLSCPSLTAEFVSTAPSVHD
SASRKATESSKVAAATAVGGDGGGVRFVLTNVDLSYRGKSLAVGGMPLVSPDVSANGSPF
TLHVAPGTPARQRVKGQLDPHREVALKFFSRVARPDVLLGNFFMGRDESMPGYEDAWALA
GAPAEHERTINTFYHHKHDAETNFFYFLPQQTKVVGNPVSFPPADAPVGTRIPLNASCLI
DRPTGSNIVDTTTNSSVKSGGERDAVRPRGEVPQVAARIQRCFFRRLPSRHHKRQLPLFS
RYERRQLVVLKPFTHALLTAEEAAAAGRDGGGMQVRCSAADGYPILVLLS*
>TCRU_5185 transaldolase, putative
MSQLEGLKQHTIVVADTADFSLLAKFKPEDATTNPSLVLAGSQLPQYAKLIEDAVKFAKE
NVSRLRDGLTPGADEKAHLLELSVDKLTVNFGSEILKIVPGRVSTEVDARLSYDTARMVA
KARHIVKLYEESGTPRSRLYIKLASTWEGIQAAQKLEAENINCNLTLLFSFGQAVACAQV
GVSLISPFVGRILDWYKEHQPEKAESYVGAQDPGVISVTRIYNYYKQHGYKTIVMGASFR
NTGEVLELAGCDKLTISPKLLESLDSTPGPVPRKLDPAHLTEKTEKLPPFTGPESLFEGE
PNTMAKEKLEEGIRNFSKDTEKLEAQVAALL*
>TCRU_5186 SH3-binding, glutamic acid-rich protein, putative
MTGDRRVRDHCRQIETLLYLKRIQYVSVNVADDPFTQRRLREMYAASTGRNVMPPTPAFF
IGEHFIGDYEVLQELEDDGKLMETLCQCGYRTPQESNKEGGRTEQGDSC*
>TCRU_5187 Nucleolar protein,Nop52, putative
MHVCDVLFDELCRAALSTALFVALSDRIALHAMSRGNCVEKRVLDYFISPLAGGMLSSRR
REQHQQKDGQLTSVGALNKRKRCRNEDKSGSCSGHEESAAHAAADAETRAILLQLAECCR
NYSVARRTVHSVRVMFTEGEMALRQAANPDGYEELTRGDLRRRIEREVAEVRETRHAVVE
ERRNLRRLRQQEKKQLLQRLKKKKKEKKGSIVASAAADNDEDEDEAVQQKLEKMKKKTRR
PQPRDTKRKKHYTLTKEDLYGDE*
>TCRU_5188 hypothetical protein, conserved
MQDTSRKRKAHESDDCPSRTSSGSLERHGAFQRTRCAAARCSNRGDIEFGSTRDLAVSEA
RRHVRPSPEYCSIFGEVHHNADPGVAAGRIDVKEETAEGQELWLRAEERFFHDFYHNHAA
TITRRATRTRLATPQDEHAIPLQQVNVPVLNLEWIKSRLNRLPWRGSCKFGDSSGGPLSL
RLPPAKRAKAHGGFQPLTRVCYEKQELPRTVRPQQQADR*
>TCRU_5189 hypothetical protein, conserved
MFVDSRGVRATFAYAQSSENPADGISRGRVFTLQFVRSVRAMPALNSLTIAEMEVVASRF
LYLAAILGTRLCQYYFFIKAVRRRLSAVNRGIVLEKSPANVPPAAVGLGEGLRHTIENTT
VSESSSPRKRHRLPSSRTHRSMDGEQFLFQTSATLKLPGEMEEEAFSYHAGRGTSGTPSL
IGLFRHLAIHHGRLGGQHFAARSCE*
>TCRU_5190 hypothetical protein, conserved
MGEERESGAAQYTFLGVQFDHTHRAVSLSDKFVRSVRAMPALNSSTIAEMEVVASRFLYL
AAILGTRLCQYYFFIKAVRRRLSAVNRGIVLEKSPANVPPAAVGLGEGLRHTIENTTVSE
SSSPRKRHRLPSSRTHRSMDGEQFLFQTSATLKLPGEMEEEAFSYHAGRGTSGTPSLIGL
FRHLAIHHGRLGGQHFAARSCE*
>TCRU_5191 hypothetical protein
MSHRLLVHKEKQNAKLLMRRQAKKRQKRVPLRGNAFSTCRITPAAHQQDQQYGYQKDRKY

KEIETKEKDFRQKQQNQRLQQDKNTERHSRKTSLEEQNSLQRMKWQ*
>TCRU_5192 hypothetical protein, conserved
MDLFPGLGIGIVSTVFQEPGRLPFAKELWIIVLKVCRTQRARDGAGIHPTCCRGHGLSQA
RSRGWSRQFHTAGKADPFPGHQEAMECGVQQQQHKVMWHVKPAQNDGQADLPVADAERKR
GKYQFGAQPIPEDEGAAPPCRGDIATLGWMRLQVFSRGLPEA*
>TCRU_5193 hypothetical protein, conserved
MAMLTGRVLLVCALCVLWCGAGGVYAEDDAGVTSPGASASDGKSFQEPPPIVHGGSHNSV
LTASDVNEQTDETDKEVLLTKEVAGSDEVPQTSEEIPPPSPSPKKSKGGGGPPQEDDLNL
EKVDENVMQPEKQRRVEEGLETLGDGEAGVTKQNEGIGVQSQDHETPVQEEDTINGEGHQ
QTHGKDQQTNVEDIPPRKSAGDYSSGEHKGNDGSNEKEEKEGEEGVEGRERHRAQEREEA
AHVSGAPKVNSTDIQQEVQRTHAGETPTGIKQKAGEEKDDEAEEEREEQKKQNQENPPGK
VQETITGANATNQINTMPGDNDGSTAVSHATSPLFLHLLVVACAAAAAVVAA*
>TCRU_5194 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MLAGNYSNKGASDGQAGDWGLMLVKGNVSDGEKGKRIYWNDTYGLPWNYKVEQHESLMRL
IGSGGSGVQMEDGTLVFPLEGTKKLNGAAEDGKTTTVSLIIHSLKDIASWKLSKGMSADG
CSDPSVVEWKKDKLMMMTACDDGRRRVYESGDKGDSWTEALGTLSRVWGNKKGEKVELVG
SGFTTAKIGDNRDVMLITLPVYSKKAEKDNDEKGVLHLWLTDNTHIVDIGPVSEKDDDEV
TASSLLYKSAESKEKKDELIALYKKKGVEETSSGMVSVLLTEQLEKVKEVLATWKKADER
VSELCTTSLAQKVTSSENACRADGKITDGLVGFLSGNFSENTWRDEYLGVDATVNNKGGA
TNTSDGVTFKGAWAEWPVGSQGQNQLYHFANYNFTLVATVSIDGEPKGDTPIPLLGVKMN
GDEEGSKLMELSYGSGKKWKLLCSGKTTTEHSSTWDPETTKKDHVVILRRNGNQSSAYVD
GKRLGDKQCEFDNADSKEISHFYIGGDGGSADDTRSQEELPVTVWNVLLYNRPLSSAEIT
ALNKNKPSTPRTVADGKELVVVASPPGVSVPAPRGTVPQSALGGNQPMAQELLKEGTDGG
GASTTALSTVTTSPAGKESVDLLASGTSPDGTQAADGVSSSDGNQTVDTADGGKTQEDEP
HKTPADNANAADAKAPNSEGGLQDGFAVGPERASGEDGETAGGTDGQEEEGIQPRIREVN
AAALSSSLGNVSQGNNSDAGTVRGSGLLPSLLLLGLWGFAAL*
>TCRU_5195 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGAADGDVVVSGGEDNILKELFIPVARLQLRQEQGAAEATAD
AKAAAETAAKEAEAAAEAAEAAAKAAAEAAATAEAAAEAVDTEATAKAAAATESEAAEKA
KAAATKAKSAATKAKAAAEAAATATEAAEAAKAAAEAAEEATEAAEAAKAAAKAAAKAAT
AAKAKAEEAAEAAAATIIATSAKEAAKEAAEKAEKAKAAAEKAKAAAEKAKAAATEADAK
ATAAKTAEAAAEALRGTTVGEKEVKTAIHDQDNSVEHHSGEKQELLHEEGPERQEKEQHE
KQQHRQREHSARNGEEYAKHKTANGTNATAINDDSDGSTAASHTTSPLLLLLLVSCAAAA
AVVAA*
>TCRU_5196 hypothetical protein, conserved
MATDTFQFSAWQRHPNRTHEFLLPQIPSRRWRRYALARWRCTTTPAGRFAPCRFHWRIEV
TQLAPHFPLALRNPTQRDGGRCCRHGTIPPAGLRQCLARGPPHCSQATEPKECPGGSRRR
ARRVTGACRCGEDSIPGVGRRYEVGAFQPRHAKDALDGVRRSAVEAARASLGACVSGSAA
LPLDSPDSGAPCGPHRAAAGSLACSCRAECPATEHGHRHFPVLRLAAASQSHTRVPAATD
TLSAMEALCLGPLAVHDDACGEICTVPLSLAD*
>TCRU_5197 hypothetical protein, conserved
MLDSGALEFEDDFGASSQILVAGSKLLSTSSHAIQFPSFTLGANSTLLLLDNNMEGDMYA
VHFSDAVVVDGGGIIIKGNMLKSAKSGYDSASAVYYNAVDVKNGGYIDVENNTMSAAIGI
YFQSLVSVSSAGLLRVADCTFTGSTETFNSALVYLYGSVALQGGAQWRVEGNNVSAASVF
IMPSFWHSIELSGNGTTVSLAHNRQADSSKSFAKFSGTFVTSPAQFLVGCNMQGEKEVSR
SFFYPSVVLVFGCGTCNDDTACYMPGTESVNRSSCSCSCKNGWHGASCLPFAVPDTVVPP
APEKYVDGDTSCVVNQTLTSLALNMWKTHHCYVGVTFSGVGAALTFSPNSMPLHLPINIT
LTGCTFRDGAALQFVGGTEVAESAGVLIRVSQTVMRSSVVLFRRALPQHCDIAVTEVDAV
QLPNSVNYMLSVVKLLLQHN*
>TCRU_5198 hypothetical protein, conserved
MPALNSSTIAGMVVVASRFLYAAAILGTRLCDYFFIKAVRRRLSALNRGIVLETSPANLP
PAAVGLGERLRHIIENNRKRIIKPTEKASAAIIVDALLLG*

>TCRU_5199 Ribosomal protein S10p/S20e, putative
MAYVKKDQAPAQETQRVLVKMTSRNAKAVENVMTELLLHARNEKVVLRGPVRLPTRTLKV
TTRKTPCGNGTNTWDTYELKIYKRLVELRAPTELVKKITSFPIDAGVDVAITIPHDQ*
>TCRU_5200 PPR repeat, putative
MHKRVGYAELVNSKLRSDKLLARRDAVRLAKLKAFLGQHQHASQWSACVGALTDAARQNI
IPSSEMVCDAIRRCGLKGKLDVARHLYTDFHREINKPRTLQVHVTFMAACAECGDFGEAH
DQFLRLWRRDAALLKNNDKHLPVVGADLTSEYLRAAVVASQRRRGECQFNPFSDEEVAMG
KKGDKKNATQPWEVALKEIQSLQKDHAWFLRHNALTPIMVEHFARLWEIGGKWENCLRFL
RLSGQQNVLIPPEAHDAAIRVCYRHGKYAHVVGQMRQMIATRSPPDERSVRLALLSCEEC
TALERTGLKQQPDSWVLAVSLFDAMRSNGVTMHQQDYESPLRSCAMAGRWEDAMRILDVM
RKDNRPISSQLYRLLLAARIESCNSFEEAQRFAQMPVMQNGGIIVYLALLRCCMTKRDWK
NFDRVNKEMRDREFPETFDKMRLLIEAAYVREQWHSVLMRFARFESISRYEEKRVLEDKV
VRAYPEDFDMPEAILDMVLASYKHMKNHKDPVVHTAYRGALKRKAKGTEQLAFSSDEAVT
VPSEDWMFSQEEREKKIPPKFF*
>TCRU_5201 hypothetical protein, conserved
MESSGKLLAAAAAFVENISAVGVCSNEGCLNAFNPSAFSLPLKFNGGVPVLPPTAARIEA
AIAAEVFPLGLMGRQLCSSVSQLGFTVEEYVAKLFTSAQHQFGCSLETLLHSLWILERIQ
TRNILAHQKGIIALRNGSYCRFIDVDNDMWAGKDTSGLILTETGASLHDGTNAEEICIAA
PLVSSVSSETRSVGPMSDVGDDDSLCSVCTGSRVFSLQPWNVQLFIAASLLLSIKVNEDA
FAEVDGEMLTLQFGTMAGCEFKALLCAERCVCELIWDELRVTRKGIENVIRRLGMRLPVL
*
>TCRU_5202 Vacuolar sorting protein 39 domain 1/Vacuolar sorting
protein 39 domain 2, putative
MERQTLFVTSHEKIRVTAAVVVSVERSSKELLVRDMHLFPNETLRSLLYVGCSDGTLHVC
QCLTCLNQEEVRYEVRTTCLHKRSLSTYGEKKVDEKGTDFVQDGIVFLHVDNRLSNPQLL
VIVDGSLDALHCEGLESSGIFQHLPLPSGAASVCCVARGQDYVLHHAQRLAVLIKRWIVL
VEYTERDSRILQSGTETQEPAAAESLYILAPEDTQTMAWQRDFIVTGSLKEYCVFDVNTH
HLRERMEVVDTLTQGLLCRYVEGFGESSYILIRISDDQLALFDATTETDLETVSPVQFSE
SVVDVAWAPPFFIGIKADGGVLMRSWLDGEDEFPHINASSAYSTSGFDGAPQQVHSTPLG
IYGLCGRSVQFLLLMPRKTIVALYIDAGLYERALRYVDHTHTAEKDVHLRRVYNVCARHA
LMEKKYTEAFHYFELASTPTQELLELVPELRRSPEDTDAWKVKVTPTLSSGEAYQDLYEL
LLRRRSLGLGSNTEEQSAIEFAIFLLYVLECVPYTDDELADMFLLSSTLVPEECLRYVSE
DGIRPKPMIVPLVLACDGRFSEALECCQAQRLVHEAAVVLQMSGEEQLYMQYFPWMLSVD
INAALLAVVRPQLRAPSVSMILPMLLGYGGYPLHDYLHFLIFMEGNTQRELHTLYATNLI
DIVCSLQLFGVEGLKATSVKVRAGEESGIRGAARRALLVFLQLSSHYEADVVLSWLQGAG
LVEEEVLAMKQAGDHIGALTKLVYELNDVAAAVRYCEEQHARELQSRRGNVFKWSLETKE
FNESAALPACDEPLHETFADRDDSVWLAGNRYMVQGSRAFNEYFNILLHVLLVPPAGKKR
LLSEALWVLNEHSPCINPLSVMTTLPSEVCVAEISSYLVRAFQTLCNQVQMAEINANSVA
SMVADAERHHALLIQRCVYVDEKRPCAVCGKALGVGVIAVFPNLKATHFRCFHAQELDPE
RGVPFRPDL*
>TCRU_5203 P27 protein, putative
MSRITNKICGGMARANVVDHGVYMKPISHNPYLSTVHDGVSTGYLAGFSAKPMHWLYRFR
YNTLPQGFATGFFSRNPYGRYVHWLEVSTIEKMRLQAISVEGLPCNVVSVLVTLYSLWYI
YRLCFYHPDLTLYNLGLWTTKPWISAQRFNKKHELDQPIFRWIHRAPEYFITDPYRELNK
LEVAANDTWREYVKSIGREDELLIGPHDKGYGVDGKGMLLPMEIPHEDKSGHSPGPFPTL
R*
>TCRU_5204 hypothetical protein, conserved
MSGNVKLNAIASAATSAAKKKADEKPRAILPHEFLLSLHGRRVTVFLSYQNHELEGTLMA
VDADKGDVFLENVVHFVWSHGVAVGNVKEGRRTELRRCSSAMVNSRYIEIITPA*
>TCRU_5205 40S ribosomal protein S14
MSKKQEVKFYGSSAAKDELVYGVVHIYASFNDTFVHVTDMSGRETFCKITGGMKVKADRD
ESSPYAAMMAAQDVVARCKECGINALHVKMRATGGVGTRSPGPGAQAALRALARAGMKIG
RIEDVTPIPTDSTRRKGSRRGRRL*
>TCRU_5206 dynein light chain, putative

MTNEYCEARRSSITLPLPGTKFRPSVVVGVIEEVCRSLVGDRPYVYDEIQVLIKEICSEI
QQRVVRLGYERYKFVTHVTITEAAHQGMRIASRGLWDPVTDGYAAYTHSTESMHVNVVLY
ALYWE*
>TCRU_5207 hypothetical protein
MSPTISARNEKRRSDIIDGETVQKTTHRDIFPVTFKLKGEDLFFSGCRDERVVFYPGLLK
PGGSWCLNAESMQARGRKTTDHKGIKGCVRTGVVRGWHGEVEFPDSRTRELVPRGWRKIR
CPKHT*
>TCRU_5208 hypothetical protein, conserved
MMHSFPWSVGDQQLTASVMRRRRKSLFHIEFPRLCFLRVLPAGMLGSFGGDLCARHLLGR
RWRHCGIRMRGVLRPLERQAENVRRVPSYCGRTRRRCRRLGRRTSIRRSLVDKELRRSLR
EEVPAEAEPGHSPQCERAAPPTQRVPCDPQGACRSVEERAGVASRLCAVPPLGARCPGQH
QE*
>TCRU_5209 hypothetical protein, conserved
MGYKAGPEILQIITSAIAGMTTVVHSLWAAPPLVRIDVWIDNIRIAGSRSDVTLWEAQVL
RNADGCHASMGEERESGSTQYTFLWVQFDHTRRAVSLSKRFVRSVRAMPALNSLTIAEME
VVASRFLPAAVILCTLLCDYYLFKAVRWRLSALHQGIVQETSTANLPPSALGLGERPQHI
IENNRRRIIEPTEKALAAIITNASLNGWGAVIIPDSGDVKIAGGK*
>TCRU_5210 hypothetical protein, conserved
MQDTSRKRKAHESYDCPSRTSFGSLGYHGAFHKTQCAAARCSNRGDRRFGPTRDLAVGET
RRPVQTSPEYCSIFGEVHHTADPGVGAVRIDVKGETAEEQEPWLKAEERFHDFYHYAATI
TRRATRTRLNTPQDEHAIPLKRVNVPVLNLEWIQSRFNPAILESLMQALGLVGRSPLSPS
SSGKAREGSRRIPTADAGLLQKARIIVDASSTITGGWIIPFSVVDERQPVHDDDGSCGHA
TRTATTLMRLMFLFYIFPIICHL*
>TCRU_5211 hypothetical protein, conserved
MEGSPVAGPQAPTLKVPPPPPPSAAASADGESDVGPVGIGGTGRNVSGGSLVGASDTSRV
TGEATKDPKGSGGPISGPPSGGAS*
>TCRU_5212 Protein of unknown function (DUF2984), putative
MYVVNLCGLFLAIAHAAHFASTIRRLGPAAPIAGYSNSHHELWDGRSPPTTAGEDLAATP
SGMECELPDDPAQATRISGRSFSFPDVTVQRVLRVSHWTSTRLHGVGPPSAIHCRDGGRH
PATGRLAAATEHAALALREADCDASTSACGTSLVTVTTWLETH*
>TCRU_5213 ATPase, putative
MLRCVTAVWRCSFKPSLAYNNLVNAGSISRDTQQLSALPVFDRLYDDLVRYTNSAGRLRP
RQVELRPPNRLGVVPSFFIRREQEDKVRRALQEIGNDANTAYHPLSLVKGLYVYGGVGCG
KTMLMDLLYHHVPTEIKKRRIHFHQFMLDVQRTLHDIQYVSKSNSELQPRRTKEASVDLF
DEVAQRLINDVELLCFDEVVVVDVAHAMIMRRLFNAFYKIGLVVVFTSNRPPDQLYLGGL
NRESFVPFIELVKRQCVVYDMRSETDHRLTGSDAQMYIAPMNEENSARFNNIFLQLCKGM
PPKERILRVFGRDVRVPTACGGVCRFQFTEICNEATSSADYEIIAKTFHTVFIEGVPRFA
YESSDIKSRFLLLVDALYEFRCKVIIYAQVPPRELQESRAEYEASQKHLESGGSSGDVGR
FDLLTEFERESGKRLIDHTDAAFQMERCISRLIEMRSREYLESPHRHEEVSLSTE*
>TCRU_5214 hypothetical protein
MHGGDDDGHNASVIASVFRRHRYPFHPVTVERLLCTFEQLLESLPSSSSSSPSITEKTVE
VEEEYGEKGEKRRSAIPSIGTEVMPPVAAALDSNNNGASHDHPDGGMSDDGNSPFCALYA
KLQALLEQHREMRRLCLEKESQRQIQMYPAPFVISVGAEERAHASSHVSMIISTVGNNLT
PSQRYGSPRKGNRQFMSAQHQREMNYLLHVVHAAYVETQRWQSRCKELQVELDGTKSQCG
ELMAEVDELRVLLAQERMMSQQLLQQQQQQEEEEKLEDEKKEEEKEKEEEGDGGKINVSL
NFAEKTVNDNGSDKSPSVPGRVVLSPLPVSATAHPPLFSPPCDVVTTPSESRLERLARED
FVSPPHSAPDGNDPNDAIAATAAHWRSSLFTSPLPVTFARPSLSSLQAARQAVVATNMGV
KTKGIASAARGRHGGDRRLVHDKGDGDNPDHDAVALRLLRRLVPDVSEGFLNVSVGVYEG
VYKLAARCRRAEEGSRRHLKRLRELEAQAATVSRLEECLQRQTRLSSTLHCRVEEKEDML
RQLKVRLAAADRDIVELKRQLAEHQQREEPNEAGEEEEAGGRGKGADQQPEERSAIERQQ
RCENGDARQHRCRGAGPAPKPAYVNAPHGRMKKRRTDGGKALLSERARADNAEAELSRAQ
QELACAQNELQEGKHLLACLVRDGQRELPEYNNTDIKEEGDEHSSTVPTMTQSQVACGSD
IMDLPEPQPPQFPSPSVPQQETTPAAAVAVAAQPCELSKVHAMGQISGCSSFLLSICPSL
PSGEGEVALLLPITETQCDQKEWEEDQQKPTPNARKPKMRNRSKWETELGEDDTVAPWGD

W*
>TCRU_homolog, putative double-strand-break repair protein rad.1
MFFSTYVLTKRGPLAKIWLAAHWDRRLTRNEVRVVDLRQSVVDIVQPAVPIALRTSGELL
VGVVRIYALKVKHLLKDATDATLILRVAPLPAKSVSSSSVANKNNNNEPDGTGAMAMLDG
VLISGNGDIEAVTFDWSGSAAAEAVATGKSDAEALEARFDDIADLLHGSKQPKSTPGISS
SGSNNNNNNDASAFLASAWYALEPTSQAVEELHSTQQDYDEIAKLRADLVAFGDRVSGSS
SSKKSSNPSIEKARASGVAGVASAVAGLGGDFSGFPIPGEELDIGVPLPEDHALLPDFLM
PAEGIADPFAIAELLQQKQQQQQQTTARKTRSVNILDLAATTVSGETVQRWMDDRSDIV
DAVPRRGPYDVQEARDRATILPESSKSDLWAFVDAAPLSWQPNPSLCAMYTTLLKPFIEQ
AEASAMPPLQQQKHQQQLQLQQQQDENLPAGRMGEEEEMLAAAWNMEEEMHNMNTRKRGR
DDENDDENKSGSGGLSMIAMATLRRIRDEIEMPAQQQQKQSKKSRKEVATREYCFLHDVC
RGMRRREAARTFVSVLALASKQLVSVGQPSRMGDIELGLLPGAEGLMLTS*
>TCRU_5216 methyltransferase domain containing protein, putative
MSKYADPDYWEERYRSNDTTYDWYVPFDSLEPILRPLLQPPEQVRVLMVGCGNSRLSASL
YDELNIRKITNVDVSPTVIAQMERRCKNMTEMQWICCDLVNTSPEKLLALFCPNDYLFDF
IIDKGFIDAILGGHNSFHNVYTVTKNLSRLLKKGGRFLSVSYGSPETRMDHFRRRRLFFD
VEHKAIEKPMFNSTATTTGHYHVYIMTKLGEKQTAAAVGDAGAALDGTTVSGDSDDDEDD
FYDRFMMQTTSPTMAADPSRIHTL*
>TCRU_5217 hypothetical protein, conserved
MPRGGRHAGGADTAPNGIQGRPRNSPDYYYFGNCGGDDGGPLLWAAPPLVRIDVWTDDMR
IAGPKSDAALWEAQVLRNADSCHASMGEERESGAAKYTFLGVRFDHGNTVRYP*
>TCRU_5218 hypothetical protein, conserved
MAAAVGAAENEATREKKLNLLDEITMADESCFVAFASYIAKNAPCRRLTGCLHSAPFEAL
CSFIQCNVTIIMAAPSLTGSECDNTNDGKKSDEDYGDDLHRGADYLRVLAHESREGLNAV
PTIPGLAEPLAFALSPAVISAPCVGADPFAVEFT*
>TCRU_5219 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLCCTVGVVADGNTEEVVESVVPLSGPNGSQQLQEEDSRRKGHS
ENDEQVDETQMQKQRQDGEGHQEGSIQPAEQSVGLQLQSERPRVEEAGRRTEEEQLQQGK
QPNPSVEHQTPSNPADKYQERGGKDDVPKERDKQKENEIISQSRGETESHGKEKENVATD
PGSPEVILTEISQEASRSPPGKPLAENEQIAKENVGKKEEKDKQHEKKGDPHVQQQNGKQ
EKLHGSPAGSGSTQSSLATLPPEELQQKQTSAGSTSHLEGEAPLIGTESTSNGNNDPSLP
SVSTHAAVAATHETDKEDAKDRHSVESTETTVNETDEQHEHLTENDNESAKDKNSVGANS
TANTDDSDGSTAVSHTTSPLLLLLVAACAAAAAVAIM*
>TCRU_5220 hypothetical protein, conserved
MTCLRLISGSIAKQLEGSTVAGHVADRRAFQVPNFDAQVLLPIVWGGPGVGGKQWLVIAE
RQILGSDYTRAVADVQNWTARIYFQTEEALNYRSARETDISVVGGLFAEGGDAVSTRGAH
LSERAARWPHARQWRK*
>TCRU_5221 Leishmanolysin, putative
MLAGKHVQEKAEAHFGCETLSRAWCWRTKMALGKKKSLTGRDATRGTSWGHCSGCDFLEK
KRNTTDNLAAKYPHMFCDAKDTETLRCTSDRRQVGTCTATIVEDKGSLVDKDVCPVVSLE
FHEISSGKTYRTCSDENVDYLRGSLTGGGLWCLDAELLETKDGDGHKSVKGVCAHVSCGE
GTVRVKHLGSRVFQPCPEDTEIPVTFKDCKKDGKIRCPTYGEVCNIAANGSSLVVPGALV
NGQGDEQEKEAEESAVAPGLPSPEETRPQLSPVSSGASIEKEPPGASAAGVAGGGLHAGP
RGDPGVRTESEDNTQRRGRRPGSGSEGANRASGPDAFKRGSGFPALP*
>TCRU_5222 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGVGGVCTEEEERAVAGSDAEPPLASKQLERPPERSQGLHG
RVPGANENVPPASPEPREEEDDVDDDDSEETEAQEEIIEEQSGQGGTTAIGSDSMEENLI
GSEREAGQSIVPAKDIPPSDSQESNANPLQTEVEGKKETDKNTPAVKNALTTRNGENTLP
GGVAGGNLPSPPKDGVDSRKQDGDDTTSEDKKNDPPPETAATPQSHRDEGSGGTGEDTKA
TTVTANTTDTTSTQNSDGSTAVSHATSPLLPLLVVACAAAAAEVAA*
>TCRU_5223 BNR repeat-like domain containing protein, putative
MSRRLLDSTVLLLFVVLMCCSGGAATAQVGNNAVASTPSASALTGAIAAEGSASGGVELP
QGVDLFVPQTTQVLPKKGNNSSRRDSFVSPSLVSAGGVIAAFAEGHINAEYQRGQLIMPF
SSDVVVGYIDCAWEWPTVVDEVNKSSWGAHTVLGKAEGEGSLGVVLRPTTTMKGNKVFLL

AGGTVLSPVNGDRRKARFELKLVVGEVTNATGGKQSGRIEWGDPKPLPKPISSASHKGKL
TECIASGGAAVVMEDGIIVFSLMAMNEENGDIYSMIIYSTDNGSTWAFPEGMSPAKCLNP
RITEWEGSLLMIVDCENAQRVYESRDMGTTWTEAIGTLPGVWVNSQSKEYSDGGLHVEVL
ITATIGGRKVMLYTQRRHALGETERATALYVWVTDNNRSFSIGPVGMYNAGEKGVASSLL
YSDGNLHLLQGRGNGEGRVISLSRLTEELKEIESVLSTWVQKDVFFSSFSIPTAGLVAVF
SNASASDDTWNDEYLCLNATVEERSEGQRWVSVDGV*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MVDGTRATQRDSPADTCLGRWMQSAVGACPRSRHRVRRRAILAVRVALLVVLVLAAAAAW
MPAVHAVVLRLRGGTVDRAITVGRAVDTVLMDGVSITNGVAVVFDVPAMLPGALRIELRN
CVCDGGARIYVRGYSGEPASDRSLEVSVSGLSGSYCSLVFVHNLPAHTNVTVRDSTIVTA
GPMRYSQLSGLTDAVASPLVLHATSLLQSQLRVSNTVLRSLQAGGSAVYVGGGVDLLSGA
VVLDGVSLEASGGLTASAMRVASLSRLSLRSHSVFSVTDVSVVSSGGGIVLGERLAVFDS
VLRFVGVEGSVASSLVLCDGGMIGDGGWLELRDVWAVGEASSVASLSGVMLSGGTVSIAR
CAATGATLVSGPAITSGVVSVQCNRAGGRVLQSSGDYRLAGLPSVSVVPCDGCAAELACF
DALTASFSDCVCGCRAGGVGEACLPFDVPPARTGGGGDGAQGCVSGVTLTESVTVGGGRA
TACFDSVVFSGPITVAVDLRSMDAFADALNVTLRHCVLAGGAQLRIGGLSESTARLMPHA
LVNMTNVTSLEGTIVLHGAMPLRSSVLLANSTLRATVGGSQYVPTTRGREGSRYGPALVL
DGVRLLSTCFVMTRSTLVCGGGSCAAILVERGLGVNLSSVFYMDNCVISSRKHVIYALAS
DLRVSGSVFSIQNSSWSAPSNEYYKGACVFRDVVVAGGSVLQIVSSTFRLGFAMLIANTL
TVTGGSWLVHRDNEFRSAYVVYVAAHHGMVFRDRSVWSILDNNFTYGSYSTFTCMTTKWS
LPSDTRPTIYGMCNEAIGSPVTNYQYDVNIGTPVTVLDCGACTMDAVCFAARTSSISGCE
CVCAAGGHGDTCLPAAVPDGLGPLPLPDAKDTEVRCVHGGSIRSVDYPDPGVRGLCFVNV
TFTAVIVLDLSHFDAPQQTLNITLLQCVLMGLSVRGSGARVHVSVTSSILDSGALDFRGD
FGASSQILVVGSTLVTTSSHAISFVKFTLSANMALLLLDNYIEANRYAVYFSAAVVVDGG
GIIVKGNTLSTKKDDDSVESSVCVNSVDVKNGGYFDVENNTMSSVNGVIFLGDTTVSSAG
LLRVADCTFAGGTEFLDPALVYLSGSVTLEGGAQWRVEGNSVGAASVLIIPHSLQKIKLS
GSGTTVALAHNRQVDNSYPFADLSPPDTIVELPARFVVGCNLQGDEEVLYDGVFPEDVVV
FRCGTCNEDAACYMLGTESVDRGSCSCSCKDGWHGASCLPFEVPDTVVLPAAERAVDGDT
SCVMDQALTDLALNMWKTHHCYVGVIFSGVGAVLTFFLDSMPLHLPINITLTGCTFRGGA
ALQFVGGAAAVESSGVLIRVSRTVMRSSTVAFIRALPQHCDIAVTEVDAAQSSVFELPDT
RMNTLSVLLLKDTVLSASSLLVSNVRAHAMKRDAFVVYSTGTLSLVGGSSLYARYCSFEG
YTHMFYLYGLSVSDHSVVALLNNTMFSGASLLYQRNRFSVSDHSVVRVVGNSGSVRYAIC
NDDMWTVQRSSWLDWRDNDVVVGAMFYDSSSAFVSIDGSSVVTLTGCKMGSTGLSVSLLS
RADAGYRFVAGCLTVAGREVTTAAELELSGITNVTTAAACGECTKDGDCFAPLTTAVSGC
KCRCAAGGHGDVCVPAPVPAGPPPPSPPSPSPSPSPSPPPPPPPPVGECISDMVYPEVAQ
AVGGGLSWLCYRNVTFSGGGMSLTVLVGAMTGDVVKVTFDGCTWRDGAVLLLLGNVHAAV
GSLNIVVTGNRFIDALLSPEGVFPPHTNITISGNRFTVTRAIPRPGLELDCPSCVAMNGL
AISNNSAVVLSGNVFQSVTTSSSVVKFVGSPLRVLWKSLFAVLGNTFHMGGGDSTLINIE
GSGQFSSLRVLNNSAVVIRGNVVTRPVKYFLLVILALRVESRSAAVFQGNDMQRSSAVFF
SSYSSYIYYNSWLQLSGNLCRESPSDAFLFLNPTVNLRDSAVSVSGNRFMFSTGTPTVLR
IPKRSRGLTNGAIVAACNTVNDKEGVKYIISSVYNATILTCSDPCALAASCFPAYTATAS
SDGCACTCAEGGHGDACLPVAVPEPPSTDGADLCVRDVRVGVEVNVSFGTSVACYVGVTF
AADVLVDVESMSGSVRNVTLANCLFVDGASLYVVGWRSDPPAGERVDVLISGLESRFGGG
VVVANRFLPGSRVTVVDSVLVAEARVAYRGDHGLGDASACLVLHSVNLTGSVLTIARTHV
AAVLRDAVGVLLVGGVALSSRGALYVEGLSVQTALGLCVSVEGGVAASGGSVVAFLDSDF
LLCKHAVSVRGAVSVSGSAVAFVRNDFLLAEDYAVAFYSTVSLADGSMLLARGNVHDGVS
REMLYAAGAVTAAGSTLSFVRNRALLPRMLSVSLSLAAGAHVRVACNDAGGRVLSTAEEY
AAAGFGDAGSIDVAGCDACDRDTHCYAPGTASASMRNGVCVCACGSGGYGEACVPVGAPA
LPPAVGTASSVFFREGVTVRSVFVVPAGASEVTLRHVVPDGVSPVLYVPWMARDGVRIVV
QNVSLLNGAVLYVMGGGALRGAVSAGSDEGGPVELSVCDVEALNGALVLTGTFPAGSVLT
VTDSLLVAARPTPLVYLPGSQSSPYAPVLVLSGLRLVRSVLVVSGVALVTVMTGGRTVVV
DGAVLELVGGGVALDAAVFGGEYALYASARVVGSGGAVLRVSGSQVYAAHGLVFESGVEA
NASAVVVNDNTGALTDGALLELRGPASFVSGSWLSVRGNSIRGRILSVPSYPRSAELVQS

TLTLHGNAGSGPVVMDGTVALGGAGRKFVVGCLTLNGQALRPMDYRSAGIIGEFRPVACG
VCDADVHCFAAATRTMSVSCGCRCAEGGYGRDCLPVYLPRVDGCNRTSGMPLLSHTETLT
ETRSLTSTCTPSLSTAHYSPLRYGPTETLQVTETVALPPTRTPTASVSGTLWWSDVACPT
LSVTTTAAGGSLTQNDIRGGGSAVPTRLMVALPPPFRWARDPQPSTHLSFVPVSTAQPSG
FGGPWGAMLRHATWVRNATNPSTVLELAVPVHRGYFIAADETIVIRCDAAAVSGGCKGVL
LGSFTIRSNTLPAAASALSAITGVVAGATAVAVVVTGGLGSILEMQALGVFARMSCASAQ
ERASTAALPYFLSVFAALDPLWMVVGNALLAAVFGCVHCGVTAAFQRWRGVDAASAWAAM
RFPSLTYVVAHAMHLGIFFGSLRALAMPGARVQHRVIGVVGVLYGVAFPAGVCYFIARHV
GASFTRYWQFSRKPLHERLLYPVGYWHPAAQQRMYGGMLTNMRGSRVYWCVFQLSVLCVV
CLIAAVHPPVGGCHVQYFCMAAVLLAGAGVVAFTNMMRSAFLTVMHTASFVLLAALCVVS
AANHFTPSDGGARAYAAIVLLLTTVVLAVTVYSMVVWYAEDRHWQELREPRRGGLEALLR
DDEESDEDAQKPHDMTSSSYASGTTVASSYRPPALPRPMAGDTRSDALSLLECASSANGK
IGHAGM*
>TCRU_5225 hypothetical protein
MALTGDSTAEYRRVSSFLVHVAWPNNKLFVQLDKEFPVGVDHVLQNMPTTATDRAGGCCV
LYDSDNVLADFTMLRANDVTSVLRRVAEA*
>TCRU_5226 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MLVTLPVYSNRKGNEKGVLHLWLTDNTHIVDIGAVSGDDDAAASSLLYKSAGSGNNNERL
IALYEKKKGGGESSLGMVSVRLTAQLRRVKEVLATWREVDKRVSKLCPSPGTAKNPSAGS
GCSTVRITDGLVGFFSGNFSGDTWRDEYLGVNATVKKGTNGVATGYADGVTFRGAWAEWP
VGEQGENQLYHFANYNFTLVAAVSIHEVPTKGDNPIPLVGATMNDDKSTVLLGLSYDKEG
KWQVLCGGKATKELRSNWEPEKTYQVAIVLRNGKQGTAYVDGQRVGDASCELKNVDSKGI
SHFYIGGDGGSAGSKEDVPVTLSNVLLHNRPLDDNEIRVLNANKISIPKLTDLKTLAAGA
TDEGTARGSTVCGGGLLPLLLLLGLWGIAAS*
>TCRU_5227 BNR repeat-like domain containing protein, putative
MMCCKAALAEESNPVTAPKFEWKDVTDGDVTVESLGAPGLLKVGSDVFAVAEAKETKKGG
QDSFTGIASQILTETVKKEGNTPVEIMNDANTRTKVLEKSNSPNRKVDVSRPTTIVKGKD
IYMLVGKYNRNDAQESSGGDSGLLLVKGNVTEEHSKKIDWKNTKSLPRGPFDTEPESLTG
LFGGGGSGIRMEDGTFLFPVGKEERVSRRGPTCRGISSTLRCCSSSSFF*
>TCRU_5228 retrotransposon hot spot protein, RHS3, putative
MIVVSSPKVTNYDEWAKQTKARRIIMNCPDEMDVKAMCTWMKHNETPDEQAGYWKEVKER
MEKVGPIPRHIFDADEYIDRLGAVNGALLSIKDNDAEKYFPLGGEKKWYSEDPSHKLVKI
VRARTEEGAEIFLNAPICDDIGFRTADRLAKVMGAKDFLLLILASRGALASTYVEQLGLR
AFMYGEFVIALLKELKELRPPEREAQESVLNVNHQGYPTRTFGLPLMEKVEKKINIEYRV
LYIPWATNFPLVDGFFFVDSPRKTLVGLQMTTAGAHHTIPSTVRLFKNNMVTYFNGWEEF
SEGLAWDIIYVQHENSTMITNWQRCGPVNTKNLSDAEKKIVAFWDGKVHEYQFVLTTDFV
NKIRAK*
>TCRU_5229 hypothetical protein, conserved
MHGRNGELGAVRHVANAVHTCRNCAASCAVKEEGATVAFTMNVTTHKYAGPYELWWRQFS
PDGTIHPPARSSDADQTVIRQLPPPREGRDDTKSGGTTAPQVNAEPSRQNEDWRRSAAAD
GPNTVDPSPASNTATNTSETRPEFASNPIEVMVPNASTKRPSFANGPRIVAAPNASGIMS
VTCGGREHVAADHIRGE*
>TCRU_5230 hypothetical protein, conserved
MAMMTGRVLLVCVLCALWSVPADGDVVVSGGDDSILKELFIPVARLQLRQEQRAAEAAAD
AKAAAEAAAKAGAAAKAATEAAEKAKAATAAAKAAKAAAKTAAAKAKEAEEAAEAAKAAA
EAVDTEEKAKAEAAKATATSAATKSTTASEAAKEAKAAAEAAKAAAEAAAAKAEEAEAEA
AVKAAAEAVATATEAAEAAKVAAEAAATAANAATAAAAADKDEAEEDDEAAAAAAEAAAT
ATLIATSAAKEAAEKAEKAKAAAETAEAKAAAAEKAKAAATEADAKARAAKTAEAAAEAL
RGTAVGEEGGRTAIHDQDNSVEHHSGEKQELLQEEGPERQEKEQHEEQQHQQHEHSARNG
EESAKDKTANGTNATAITDDSDGSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>TCRU_5231 hypothetical protein
MREKTTSAATPMRCRKELAVTLTRTRNSPRTPVTFELATERGLHNFSRRGPRVRAKSSIA

VHAATALPLSLLEQTLWTEIEQLNAATNRLRERILEVKRDFSADAIAAVTGGEPLPVEAR
TSGLFRNPPKQRGQNSKDEPPYAVTFTPSHSQKKAANVRLQFTSPRKTPMRENDSSVLTS
LAMFEYTPQNDDHREGARPTENRNVLQKLKPDETFEADTPVHLSEAAAMGGPFVVDLQKS
DHGAANNTDAKPTELSTSVDSVRESAKHLLLQANMMGVEQDLNHYMSDLLVIQRDTLDAQ
KRGLIDPNDSSVRELRLGIRDELNACRARILTLESLQSSFSAGIATKKTIP*
>TCRU_5232 hypothetical protein, conserved
MQSGIRGPLLSFLITRRHAGICVNFHILQRPQLWQLRAVYCTPIARFDMKKYEMERRRRR
ELEKAGIDVDEENDEPWIAPEEQQRLDDEEERRRADEAERVKEMLNRRAQEDIEKRKKFK
EFRARQLAMSRRRKEANAATKRHERRDQRLVEEEEEELDETGASDANASDVDPKK*
>TCRU_5233 hypothetical protein, conserved
MKDFLSSFIGFFRSAACCCLTGCLHSAHFEALFCFIQGDVTIIRAAPSLTGSECDNTNDG
KNNYEDYGDDLHRGADYLRVLAHESREGLDAVSTIPGLAEPLAFALSPAVISAPCVGADP
FTVEFTQQLSSCCPAGPALALSHVFQRCLACDLMSVLSGPPTRVFCWCPIRNTLRCGVYL
FAWPSMHVTMLNGCVFCLVGTRETSVCADTFSKFFVDGSRRN*
>TCRU_family, putative Se.1
MLDAVHGLSKVFYCDAHAASVLNCSLRLHDLMKHGVTLLEDLMTPRQPIISSPAPYFFAV
EDASVSRMVEDWIAKVPHRDAHIFSLGCTPHRSPQQLACSDSAEGDALQGHYVRLRRP*
>TCRU_5235 C2 domain containing protein
MLSTEWMQRKNIEYKQKLEELNEVCAQLKEQLATRELNEYEQEVRIRDLKAQLKELSDVE
NNLSLANRNARVLEEENNALLMKLKLGDKMNASAVHGEAVKLIEENNRLRSEIEELRAVN
NKAIQREYQLDQKCKIFAEQQEKADAQILLLKKKNNDMEERLREERHQWTIAKEVWETER
ARYVQDYEELLASIQRFDGATQQRESRDNKERGNEQQLQQTLLKEDIAELEEKMRLAEER
FRKKERGWWQLEAALRSEIELLKNNNEQGGKEVYRAFQDQLASFKQEVTAFRGERRASRA
PFSFPIGETPTDDADVRISELESELQMNTNRIKALEEINRTLSQKNTHLLKENEKLREEI
DNLQDKCSRIEDRTSEREVRIKELEVLLASAQKNNILSGVSSIENETKRDKFSDVESENI
LRASERLRASLPRHEIRTADLKGSHEQQIALQEASQNGQVAQVGDPLRQSDVFRSRPSPW
NSGKLPVADRLQELQDLMFRENENNLRKKIGMDSVVVDRFSKDKIDCIDDVMRALEAAWA
NEEEHKKEIKKLYRENAELACAMGSGEQRGKDDELRRYLQHLADREEERQKDIYRYQIEK
DRLTDQVGALQYDNRLKDDKINDLEARLKELENCLKNDEYHSGSKNEGKKEGEMENRMRR
LEEAVAEKEADLRGVSKSRDKQLQELNDQLTKMRNANDGLWKQLVNFQEKKSPSRGRPSS
GRASRTPRGSARRHSIEHFSYSQPSTQLSEEKRRTVVADGAHLAVTIVELSDVMRNSKPI
TEPGYVIIKVKSVKEKYKTSVKELASVIRFNETFVFYLAQPDEDVITLHVYYKAKNSSRE
YHVGDACFAMASLYRGVPRERLAIVAQNPGTKDARRSAQIEVIMQSDDFGKMTVPTEAEI
EDEKLRFSELLKRMEISSPENLHCADVLMAANNV*
>TCRU_5236 Guanine nucleotide exchange factor in Golgi transport N-terminal/Sec7 domain/Domain of unknown function (DUF1981), putative
MPWRYEEVIDACGKALIEERSARIRSLLNVVVKDLTEIKSIANETSGQKLNEANGEASKK
AENSNGFEESTLSHLGFVTQLVLMENCGNRFSSKGLTAVLEFATVLLNSGLIPTSLVSIP
PEISITKSPSSGAGEFFSKLLGGAAANRHCVQFSSIESPTAQSEFKNGAVNVFSAVVEGV
LAVARHIQGRDVSDQLLFTLVTALQASAVPCSGRARLSEKPRDDYNNYFLAVRGDTLLHV
IEELFGVFKRNNLILPLVEGTKSALNCIAKTLSKAIEYEATEVIEESAVVNTIGGSYQKD
ASRILEYCCSLTRSSESPSTSPRPQGNIVGIISVPNEASIILLTALGIILHLIVNGGPTF
RNSTVILSAVKSTVIRCTLSTALLKDLDAFRLSVNVLLTCAMNFGHLMVNETKTIFRHLF
FRVLESKTSSLTQKSIVVEAFHRYIEEPQNLIALFLNYDCNTSSQSVYEQMIGYLAALSV
PFGMKMDAVCDRNEAVSGVIVLDFPIPESLQRSALSTLLLVAYSNRQWIERFECDQTISF
GNSSNFNSSSGISEFAKHLEKRVEPQGEMLLAGSVGKENDPFIHALRIKDAFRKFMYLMN
DVKDPKAAIEFLIREPLLLPNITEGETKHEESIEGNESAIESGMSKSSETALETHVKNCD
NSEEKVNFKAGLIALFLKEKEDYIDKLVLGEYFAKSFGDPQRRMIFVKWIEQHSFAGMTL
DAALRLFLGGFKLLGEAEVVDKTMEIFAAQYCKENPTAFRSANTAFILSFSICMLNTDAH
SPHVKNKMTLDEFARNNRGIDEGDDVDFPLLKGIYERIVLNEIKLRPSRFVTSITNSVIT
GRNDSLSSNRISSGLFESIPILKRFAPVARRITDTVMIPLDVAGNMLFNTLQRKKEEIYQ
AELRNALKDVIEALDTANALKSKFVEATRIENAIPMWGITVDYLIRCLLCAFESFFSVSE
ATGLPSNAQGCHDPTQRYMDIPENREYFDNLLRGIVNTVRVCCDFGNISQAESLIERLFE
LTQLSNIVVLSQKPIPCVSLSNGISKPRIELLKTILDLFIVNGASLTTRGWCVAYTGISL

LELIFNGLEGIWKIQCRKPPLGGGGKPLPDTRFGKVEDIPTSFDKNSVQKRIAILESLRS
FSSVDVWLERLFDATEYPSQTQVFMSNALVSVCEKELISLRTFSLTKLLDFLTVCASFSS
RMQWRDLWNNANKVFTLAGTMTFEIASLSLGGLRIIALTYLMREELLNYSFQKEVLMPFE
SILMGNQDVNIRQKVIETIAEIIEFRANRLASGWNVVFSILSHCAVIPEVVKSAWDLSEG
VITSHTALMKDCFRDLIFCLTSFACNNVDEEVALLSISYLRVCGHWLQFGLEPPPEDIRD
ASAVAEWASRFKGADNEANAAQLIFGVPRVTLSMVPITSQQTLEKPTTLSVKTNYHLWMS
ILEGMIPIILVHPSVRVRAHVICSLWALIEQYAIAFATNIQESLFTGILRPVLCNLLMHA
PVDQETVIDPVDYKLLTLLSLKSMFLACRLHSHLLKLACETFVKICTTDFSLEHVQAGLV
DVILRICVDLEPRGYVHRLGLPETASDLWVTRLLHELFQIGYIDVIHFKRTTGWTELHHA
IAVTTPRIDFDLNIEEEARSIIINTVLTAVFDGIIVQVFAAMNRCSLQEEYLLLFKAMRR
AYLVIALFCSADSTGKVFPRLLTGLSSSSLVIPEQQLLIPYLCVLIEFVFALRSNTPTIA
ETQALREAIILMCQTIRQSREFCIHSQAEHIAALESDGTKEETTVAFKKHRGRTFVDVFR
SGRAPLNCRAQHISRTVPERVLNEWRYLTHTLGLRYAFTVDGVTARCMPVECLHELILLL
PSELEEQLVEPFICSCWEELDVSMPLLRVSVISQTLGVLERKRGLLHS*
>TCRU_5237 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MQGDGSPQNPEESVSSGEDEETVEGMDAQEEEGIHSQDGELNATALNSSHVNLSQGNNSD
AGTMRGSGLLPSLLLLLGLWGAAAL*
>TCRU_5238 hypothetical protein, conserved
MPLFGCGGETTGLLRRWIAWPRDKNRDDPYEAHAPLLHISRCLPPVLAEAASCLDVKASL
LKFLLPRETRHLFRCRVEDGTLEELARPPVGYKASPEILQITINSAIAAVTTVAHPLWAA
PPLVRVDAWTDNIRIAGPKSGATLWEAKCFVMRPAVTPRWEDRESGAAQYTFLGVQFGHV
HQTVSRSEKFFRSVCAMPALNSLTVAEMEVMASRFLYAAAILGRRLCAYYFLITAVRRR*
>TCRU_5239 deoxyhypusine synthase, putative
METVDALDYSELVALNQEEALRRVLASYPRIGLQATELGRARRIVQRALYHKRAGDAVFL
AYTSNLISSGLRDTFACLARDRLIDGFISTAGGIEEDAIKCLGKTLVGQFSLDGRELRRC
GVNRTGNLLVPNDNYCHFENFFMPVLKHLHELQRESRWETMTAPSEMIAAIGAALECKHP
ETCSDSLLYWCYRNNIPVFSPALTDGSIGDMIYFYNFSKKGLVLDPIVDVVRLRELGCRN
RRCDDSQGGNRSQNNNGRTTCIVLGGGLPKHHLLQNVRADTVVYVSTGLEVDASPSSCNV
AEDRANGVLPDNCEVVRVHGDASFVFPLLLCKAETSADTHKDVAA*
>TCRU_5240 Concanavalin A-like lectin/glucanases superfamily, putative
MLYIQRGYTSGEKEANALYLWVTDNNRTFHVGPLFLEDNVNETLVNALLYSDGSLHLLKE
GGIKTSKAVSLARLTEELNTIRSVLSTWAQLDAFFSKSSTPTAGLVGFLSDAASGDTWTD
DYRCVNASVTKAAKVKNGFNFTGPGSMATWPVNSREDNNQYGFVNYDFTVVATVTIHQVP
KGSTPLLGAGLGDSKGTRFIGLSYSMDKTWETVFDGTTKTQISTWEPGREYQVALMLQDG
NKGSVYVDGELVGSPETIPTPEARGAEISHFYFGGDEGDSDSSVTVTNVFLYNRPLSDDE
LKMVKKSDGKKGNSDGSMRGGISRMLGFCTFVALY*
>TCRU_5241 hypothetical protein, conserved
MAEVASCLDLKAFSSRVSLPRETRHLFRCRVEVGTLVELTRLPMGYKAGPEILQIVITSA
IAVVTTVAHFLWAAPPLVRVGVWISNIRIAESKSDVTLWESQVLRNADGRRATMREDHEY
GAM*
>TCRU_5242 fatty acid desaturase, putative
MTSLNKSETQNISAAEEKVPSNLPQWTKGNYEINWVAVAVLALPPTMVFAAILAGIPLLP
KTFAVAAFFYVFNGMIGITLGYHRLFSHRSFVAHPILQWICVFAGAGAFEGSAKWWGRNH
RIHHRYVDTPKDPYDATRGFFFSHMGWMVMKQNYGLLGKVDVSDFKYNIIIQFQHRYFFR
IAMLSGIILPTLICGLGWGDWLGGYFYAGLAKVVFVHHCTFFINSLAHTSFFGAVQNYSD
RNTSHDSMVCALLTFGEGYHNFHHEFAQDYRNGIKWYHFDPTKWTIRLCEWLRMASHLMR
TPNEVIERNVKNLQYKGVRRQMELLEKRLGELELPTTVEYTWEDVAKYVQQGQKLIVIGD
NVIDLEKSVPTGSGYTHSNEKIVWYEAHPGGKKMLDIYVGKDATEAFQGGIYKHSLGAES
LIPHLRVAKLKRK*
>TCRU_5243 hypothetical protein, conserved
MGSNSRGLGSGAVWLVSSREHNGPHTFVSCEFTIVATVMIQKFSRLSTSLPGAGLDAPVS
TSLIGLSHDADGRWETVFYGIKTASGSTWEPGKEHQVSLMLQDGHRGFVYVSAELVGSYA

TIRTPEMRGLESHASKLGATRETAAAMRR*
>TCRU_5244 retrotransposon hot spot protein, RHS3, putative
MDDPRIEDVVNIFSDRGVKGYCIYDVALASRQPPAGLPCKGWGMIVVTPPDKNEYERWTK
KMDAIEIVIDCPGENDVRAMCIWMRRNRPLQEQAEHWKEVRGRMNNVGPILRFILGKQAY
DDRIKACQQTVDGSTASELERNLGIGCCYSPIDSDLSRKLVRVVRVRRGNSIESPLTVLI
SSHLERETLSRLESEMKQSDFIFFVLRFWDYVPPYLIEKHAVSAFLNEDFLRAIRLKIKE
LRPRGRRESHSCALKEHSDKSFTRKEVLPPPERLSNPVAMDHWVLYEPKVQNFPLVDGFF
FVDSNPKTLVGLRMATAGGHHTNTSTVRQFTECLAAYFEGWEESSRDMSWEMIYVQHADS
TPMNDWQGCDVDNSNNVSRAENREIAAFWEEEVRQYIAAISSEEFRMGEAL*
>TCRU_5245 hypothetical protein
MSRCENAVSEFSRVLFSLAHKPSKVAFEDVDPKSGLKKSEEGGDGEPTELHKKVLSGGSI
DDAILQRWSTARKGRAEMEEMGVLRSVEETASLRQEIGRQRSEEYIKTRGTTPKW*
>TCRU_5246 hypothetical protein, conserved
MSRHVFTSAVLFLVIVMLCCGCGAANAEGQQSGDVRMPQPVDIYVRMKTQVEPKSDSGKS
GRRDSFAAPSLVRAGGVTIAFAEGHAEYKGSHYRLNVRPSDIVAGYINAAETWPLIAAEN
NKDKWRVRTLFSTVSEEDLFVVACNPTAIAKDNKVSLLVGSYNM*
>TCRU_5247 BNR repeat-like domain containing protein, putative
MIVQCKDGQSLFESHDMGAMRTEAIGTLSGVWTKSKLGVFREDNLPVETPITATIEGVKV
MLYTWKRYFSGEKKENVFHLWVTDNNRTFSVGPVAMDNNLELFHALLYSDGALHILQDGI
IKASNNISLVPLTEGLQMINYVLKSWAQLDSSSSESFTPTAGLVVFLFNASSGGDTWIED
YLCVSAIMTKNAMKAKDGLKFTGPWVRGSMAREQPGA*
>TCRU_5248 retrotransposon hot spot protein, RHS3, putative
MFMLEGLYESVYDARWSHVMEVSDDTEMGMKVKEGEPPQSWNYKAVGRTLEKDDGVQQSG
EAPPVLMVLTSDKGWPYTLNAPHGCSNDLCVNCEVERVWQIVKGDLTKWFSNFHLTFNPS
PRRRLLIGTPGIGKSMNAGSYLLYQLLHCDVEKLQVVVHCFGEDAYVFDKTTKTVTQYVG
NKISKSVLGGLRQRGMKGYIIYDVAKEGTPPDTGFAPSTGWGMIAVSSPEVSNYDEWETQ
LKASRIIMNCPDEVDVKAMCAWMKRGLEPDKQVECWKMVEKHMEKVGPIPRHIFDEDDYI
DRMSAVDDALLSIKPTDVGEHFTLRGSKLWYSEDPSHKLLKVVREITEKGAEVFLNASIS
ADIGFRIADRLEKKMCAKDLLLLILGSRGALASRALEQLGLRAFMYGELVIAIVEGLKEL
PPPSPSKPRSSVLKVNHQGYPTRAVGLKELQGGVTRIPMEYRVLYIPKVENFPLVDGFFF
VDSPRRTLVGLQMTTASAHHKITSTVNLFNERMAEYFNGWEELSRDLSWEMIYIQHALSK
EISKWQRCGPVNTENLSDTEKEIVAFWDGTVHQYQFVLTPDFVSKIREMRIQQSWRKRDR
EES*
>TCRU_5249 hypothetical protein, conserved
MRVDGNTVQLNCPQPLRDAGFAVAEASFDVDVALDVPDASTLFRKLFATAAPNFTHERQN
MVAFSYGVRSSPKRQLMYGSAAGEGYAAWVITEVIRLGAKKGIFALSCRVIGSTEHRADL
LNVDNELGVIVDSVKEGPRVRMVARIRVSLAGDVRAAMDTIVKNYEK*
>TCRU_5250 hypothetical protein, conserved
MPYLPDTVVLQLHRDDGEAEFADYMDANSLTFVALGDAERSALCGIDAAAQLHYEGAQRA
LVSAAGIVSNIRRRRLCIPFGISELSELLRRAYNTEKGNRSNSLTGSTETALLAHAFLDA
VWAEESFHCLSTTRRVGNILGSTGIGSTTRDLAVDKWRLDQDIMELRDELMIARTAYDYR
HFSYESNRPFQT*
>TCRU_5251 hypothetical protein, conserved
MIQLDGARGREVIMRERHSIEAVRRTVRKERCRQRRQWIHQIKEMNAEFPEQVRPLAEER
KKKYEQAKAKEDAAERALAADVKMIEEYLPKPISLEDIPVNPEETDIIRHQFDEVFTQ*
>TCRU_5252 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MHDDTLVFPVEGTKKEGEKAVSLLIYTSDNAASWKLSKEVPDGGCSGPSVVEWEKDKKLM
MMTACDDGRRRVYESGDKGDSWTEALGTLSRVWGNKKGAGAKGVRSGFITATIGEVDNNR
NVMLVTLPVYSEKTDKKENGKGKLHLWLTDNTHIVDIGPVSDDDAAASSLLYRSAGSGTN
KEEKELIALYEKKKGAEDKPSHSMVSVRLTAELQRVKDVLATWKEADETVSKLCPSSAEE
DASPEDACSPTVKITDGLVGFLSGNFSNETWRDEYLGVNATVKKKDGETDDAGATKTSDG
VHFHGAWAEWPVGSQGENQLHHFANYNFTLVATVSIDKVPEGDTPIPLMGVKMNGAGKTV

LLGLSYNKERKWQVLCGNGTSTELSSGWEKETQYEVVLMLQNGTQGSVYVNGERVCMGEQ
REMRDAELKEISHFYIGGDGGDGENADNKEGVSVTVTNVLLYNRPWDEAEITALNPNKAP
TPSQVNEPSQGTAIRSSPGGQGKEEQRQSLGSNGVNGASAPTVSSAKTSSGEEGPAIPLA
SEESFDGSKNVGVGSFSDGDPTVETAEGTDAQKEEIHAQVGEMNAAALSSSLGNLSQVNN
SDAGTVCGSGLLPLLLPLGLWVFAAL*
>TCRU_5253 hypothetical protein, conserved
MRTTPPDRQAHENALQQRDVECLLWRVKAPQVKHNRGGEGHVDKAQTTHTGIRIVHGADD
ATVHAADLRVLRFEERERSKAVRNRCWQTCFTVAASSAHTLTAADAARPRCEAHGVHGAR
TTVQHRHGRPNIELFLVIRHR*
>TCRU_5254 retrotransposon hot spot protein, RHS3, putative
MYGELVSALLDGLKELPPPERNEAQDSVLKVNHQGHPTRTVGLAGLEGGVTRTAMEYGVL
YIPAVQNFPLVDGFFFVDSPRKTLVGLQMATASEHHTTTSTVSLFNERLAEYFNGWEELS
RDLSWEIIRVQHAGSKPMNDWRRCNYVNPNNETDAEKEIVAFWDGKGTPIPGYFKG*
>TCRU_5255 dynein heavy chain, putative
MAKGEKEEAPIDKRVQWLEQRIITAIKAKPVDTRKLIDNEESRAQINEFLDTADATHLYV
YQSSGGVLVARIEPPEELRKKGIYFTKTKRERISDDQHMKTKIVFGDLCPDALSGLNSMT
RNVYAQLIKREKKNVSQVPDVAVAELMDDTNGLLAQMLVTLGLSQGKTLLPMPPVQLPSR
VTDGPFEAEFIYCLESSIIAWTAQIRTAIDSTPEEMTESSAGKGIRPGPLDEIAFWKSKA
ENLANLEEQLYSVKAVKIIVILKKAESSYYSSFFELINELKEASAEARDNYRFLKPIEPE
FEAICPSFPGHLEFTQLASSGTFKRLFHYLYLLWTQSGFYNTPTRLVVLLRFICNDLIGL
AAEHVNIEEFAKNIEKKDALTRLGETLAVCGQFKAAYFHYKSYLSTMARPWKFQNTAFFF
RLDVFLERCHDLLDVMETAVLFDKMENIKVGGTKSQMLTKEAEEIKAEFDEAYMNFFGVE
YDMLDVDDPRFDTNYSQFRATIRELERRLGAILVTTIDDAKAISEVFKAVDTFDGFTDHA
VVQLEWSKKQKAVLEAFHEDLLAVQEVFYQGEATGSYPNIPPLAAAVVRCNALLDRINES
HSRVSELSHSLLESEFGKETMELYEKLHNALRDAIRDKYEAWCADVGSISVDKLKLPLLE
VDRNNNLKVNFDPALVKTLREVYYLEVMNSFESRDRQKLEVPVDVQAVFEKRETYRSQTM
KLDYVSSTYNGFMSTLRQEDEKPLIQAELDAFEKIMHQGMNEVCWQDGDGVDSFIDLALQ
KVGAIDRVVLTFHTNVQRMVELMEEYRKGDKFFPLNRSEGAKTMTEHELWKGLDEHIKQR
HRDIEERGKQIHALLHESFLAVNHLKESEGSLPIAEDSEAWVYYVKYVDTTLKKAITDST
LYSLNCLRNQLDPEWITENEGIPLVEVRLCLTRPSAGITPCSRYEPNIRGATEGDHSVQK
LLYNAISNIEAAAGLIKPLFGGQDYATEVCNDNEVKRVKAEIESLLTQNYEDCEEYRCTF
DEFRHLWETDRKKAFTEFLEKDKVPRRRTSYTEEDLAKEPPPTTSGEYFGVSLQEFDRSI
TEYERISTRISNTEERRVVSFVSIDVKPFRAALRDICKKWKEMYSDYLMNKVSADLENLY
EFMKEADKGLDVEVLDGNVDSLKCVMRWIRDCRRKNKEVMGEEENIETGGMFPPIQAAIR
MLKSHANTSSALEVELAKIEKLDELRKPAPDQWVALNKKALNVRAQNSIVQDREAEKVKE
QVMLFEEKLRNEAQEFKQKRLFGYPVDRRTVYDELDDVYKHFLVIEHEAKELQNLQELFD
LNSAQFKEIRECRHELMMLKQVWDLNEHVMSQFSDWMKSTFKSADVSLFEDECKKLSKQL
QQQPMKVKSWDCFKGVDEQVRNMRTSLPLCQSLSSPSMRPRHWQLLVTTTKQPGNIDPEA
SDFTLEKLFALGLHKFSEEVANIVEKADKELRIETNLNKIIDIWETMTFTYTLDKDLDTY
LLGSVDDVVEQLENDNNALSSMLSDRFVEYFYERVILWQKNLGAVDTCTGKWMEIQRQWM
NLFPIFVRSADIKEQLPEEAKNFAEADRVFRDLMSKAHKYTNVIEVICSDTLKNELGRDE
ELDLTLNYIQEILVRCEKALADYLETKRKIFPRFFFVSATDLIDILSKGSDPRAVMVHMS
KIIDSVDTFTFKNDPNSLVGSKDTCEMVSVQGEKVSLAENYTCEGPVEIWLDGLIGAMKK
AVKKQIKEANASYIEKPRNEWIYQYPCQAIIVASRIWFTTEVHQAFIQIEEGNDLGMKDC
LKNQKTQLDSLIKEVLIDRTSNERKMLVHLITIDVHNRDIVQSMVDERVDAVDAFTWQSQ
LRYYWDETKGNEIRIADAEFINGYEYIGLCGCLVITKLTDRCYITLTQALRLKKGGAPAG
PAGTGKTETTKDLARNMGIACYVFNCSDQMNYITLGQIFKGLAMSGSWGCFDEFNRISIE
VLSVVATQVGSILNALKEQKRRFRFMDEEISIIRSVGIWITMNPGYAGRTELPENIKSLF
RPCAMVVPDLKNICEIMLAAEGFGDAKDLALKFVTLYRLNKELLSPQDHYDWGLRAVKSV
LYIAGALKRGDPDIPERNVLMRALRDTNMAKLSKDDVYVFMGLIRSLFPNLDVPKKDKPD
LVAACKEVCQKHGNLPGENDIFILKCVQYEELLHVRHSVFVLGPAGCGKTECWKCLQGAL
TKLHKDEWKAKAVSSCLNPKAITSNELYGYFTPNKEWRDGILSMIFREYALESKKKRNMK
WIVLDGIIDAEWIESMNTVMDDNKMLTLVSNERIPLTDSMRMIFEVSHLRNASPATVSRA
GVVFINESDLGWGPFKDKWIATRDKREGTIFDSLFDKYVPFVFEFWKRSMRPIVSIMDIN

VVQTICFILEGIFTQATQEELSKHPNHFEVYEKYFVFAVIWAFGGPLPGSDGRIDLRLNF
SNQWKKEFSNMKISDLGSVFDFYVEKKKDENGLIQYEWKPWSDLVQPYVPDPDRQLSTVS
VQTADGVRMSHLMSLLVDNAKSVMLVGTAGTGKTNLIMSKLRSLDHEHVLFRVISFNART
SSSGLQAVMEQSLEKRSGRTYGPFNRKKLVFFLDDMNMPAPDKYGTQEAIALLQQHVNYG
FWYDRVKIIQKEVVDLRYVGAMNPKSGTFTILDRLLRHFAVFSTNMPERADLISIYGQIL
QAHTHKFQRDIRDTMTTLITNASIELHYLVSKQFFPTAVKFHYQWNMREMFNIFQGLCKS
HPKIHTTTAQMARLWVHECNRTFRDRMADADDLARYDALLFEVIGRAGFPDVNPKELVQD
SFLWAPFHTSPEGEENVYDEITLDSAQAYLIKKLKEYNENYARMDLVLFNQAVEHLCRIA
RITSNPRGNALLVGVGGSGKQSLARLSSFINGHDIFQILVTSTYGIADFRADMQELYRKC
GLKGYPFAFIITDTQVVSQDMLVYLNDMLSSGNVPELFNQDERDGIVGSITNEVKAAGYT
DYSNPDVCWEYFIGKVRSHLHIILCFSPVSKNFAAWCRQFPALANTTVIDWFLRWPEQAL
RSVARRFLSEIELGSPEMTQNIADFMAFCQKKVTETCEEYFLQEKRRAYTTPKSFLELIA
FYKELLSKKREDLNDRKQRLVSGIDKIKEAGVQVAALQEVLQRESVEVEEARQKTAALME
TVGREKAIVEEQSAIAAKEEEKTNKIVAEVENFESQCAEDLAKAKPLVEEALAALDTLDK
ASIAELKNLGKPPVDVQMVAICVKVLTSNPRAIPSVKNRTWAECKKMMNQVDRFLAELKG
FDVNNIPQVCIDQIQMYITNPAFDPDNIKTKSFAAAGLCKWAIGINKYHLVRCEVRPKEE
RLAEAQERLHQSKTALKKIQDKVADLNAKLSALISQYDEAVESANAIQLKAKKTQLKMDL
AQRLVSGLADESVRWGNTIQELQVASDLLVGDVLLGASFVSYIGPFSKAFRERIVAEDWV
PKVKELGIPMTENLDITMNVLTSEAKVASWNNEGLPSDRISTENGAILTNCTRWPLLIDP
QLQGIKWIRTREEKNGLKVIQTSQKTWQRTLQTCIEQGLPCVIESLGEFIEPVLDGVLSR
QTFKKGGRVYIKLGATEVEYHPSFRLVLQTKLGNPSYGPEVNAQTTLINFMVTEVGLEDQ
LLAVVVNQERPDLENKRGTLLRQMNTMTIELQKCEDGLLFELTNATGDILENVALIENLE
NTKKKAKEINASFAQAVATQKDIAQNRLTYTSVAVRGALLFFQIDQLWKIDHMYQYSLEA
FMVVFNKALKRAVQPEDRKDVHKRVENVLQSIMESVFAYVSRGLFERHKLILSSLLTFAI
LQRRGDIDVKQLDFLLRGKKKLGVPRPETVVEWCPEPNWAAAQALAEVEGSVPPFNLLPS
DMAENNRWRQWTETEKPELEKMPSEWKNLTQFQRLLVLRCLRPDRLTSALETFVSDSIGR
FFVSDQTVDISVSISESTTTTPLFFILSPGVDPVRAVEEAGRKLGFTYDNERLYNVSLGQ
GQEIVADRALEKCFLHGGWALLNNIHLVQKWLQSLERRLDNYAEIYTRVAQLKKERKERR
AAGKKVLEEPEEEREAEGEAFPEEVSKASVDEGELVGGDELEFSAMVEGGEFGEADEDDA
KGKGNRENVEEDEEDDDDDDIPFEGPRGHPEFRVFLSAEPSNLIPIGVLQRSIKLTSEPP
TGIRSNIVRAMTNFSDEPWEKSAKPTEFRCIMFSMCFFHAVVVERKKFGPLGWNRVYPYN
AGDLTTCMEVAANYIEDRPKVPWEDLRYVFGEIMYGGHITDDWDRVLCMAYLRTFVVPEC
CDSLQLAPGLEVPAPMTYNEYMDWLINGEDFPQESPLLFGLHPNAEINYRTVQADVLFRT
INELQPKQHGGGDMLSAQEVVQQKIEEIRERLPEPHNLQDLAERLEDERTPQQHVFYQEC
ERMNLLISVMKSTIEELDLGLKGALSMTTPMQTLFDEIFLDKLPAVWEKVSFLSLRALGS
WMENFLLRNDQLVNWIGELQTPKVTNIALFFNPMSFLTAIMQTTSIINSFDLDQMALVID
VLKKSADQIETSARDGCHVSGLSMEGARWDTSSSCIEESRMKELYPKMPIMTVRSLPLSK
IDRRDQYECPVYKTQQRGPGYVVGFWLKTKQPAKKWTIAGVGLILDVVE*

>TCRU_5256 T-complex protein 1, zeta subunit, putative

MSTSLAYINPGGRQARKANALEINMFASRGLQEVLKTNLGPRGTMKMLVSGAGLIKITKD
GNTLLGEMQIQHPTAALIARAATAIDDIAGDGTTSTVLVIGEMMRQCERCIQDGLHPRIL
TEGFRLARIEALKFLERSILKIPADGQREYLTNVARSVLSTKVGSNMPERLAEAVVDAVL
AIAPVDGKEIDLHMVEVMHMKHRLSTDTSFVNGIVLDHGGRNDDMPKFLENAYILTCNVS
LEYERSELNAGFYFKDPAEKARMVVAERKITDDRVRDIIALKKKVCTKENNRSFVVINQK
GIDGIALEMLAKEGILALRRAKRRNMERLVLACGGEAVNTTENLTPEVLGEAGRVQEYTL
GDDKYTYVEDVRNGQSCTLLVKGPNDHSIAQIKDAIRDGLRSVKNAYESGGVVPGAGAFE
VALHDHLSRFAETVTGKQKIGVRAYADAILVTPKTLAENSGLDVQHCLISLQEASRAARL
QNRWVGLRLDTGGVVDPLAAGILDNVITKKSILEATGDIASQLLLVDEIMKAGRRGAGGP
PPE*

>TCRU_5257 Mucin-like glycoprotein, putative

MMTCRLLCALLVLALCCCPSVCAAESEEAQVSTLGEHSVLMKDRKEDAVENLVLVTSHSS
TSSELGLQPSAPSGPPGPVSEQGTDAGKGRSSTVPRPQSNDADNNLPKEDKKGDTGTHIH
MDLSTEQTDKEAEASTKTTTAAPEAPSSTTTETPTTTTTLAPSRLREVDGSLSSSAWVCA
PLLLAASALA*

>TCRU_5258 syntaxin binding protein 1, putative
MPRPVRLRLLLLLVTASNTDELTEANKQQLIRDGGLTLDAHLFATLEHVTRRSGSVQPES
TASAQSGRSTSDSASNAATDEDPFLKQNCMMMETGRNKTLRVELSLASVERDHVTGPNCA
SGGQNSGDSGKTPGHFKGVVATRRIFLIWVAVVVVGRLPSQLLSALCCLFCVVWPAARGA
RSMRYPKGMAVRWPLGSLAAAS*
>TCRU_5259 hypothetical protein
MAGGLNGIGTVVFVIAKAHVAEVGLGVVDLAVHAVLGVVAAGSADLVLIVVDPHHVAAGK
AHNIARRTPHAAAQIEHRVRRLELSLVRQEELMAGERLKQRLAEIARGEVKALSPAVLEE
VCHDVVVLIHHRCGLRLAPADGRIFSLKPLTESIRRGADVFVLLLRPAAAHEVEWESGRS
SSGHFFLILFFFYLTLLSLKTRVWCYRRRRFFVCPMLPPPTTTGQEEEPKRDMPTKATGN
DDSNGANKMQFKRVSECEWVKASERARMAPH*
>TCRU_5260 LysM domain containing protein, putative
MYDIRHWLHRQTTCEFHTIYRKNVIHDGSVFPTEHDPATPTTHDHHRMFSFALDWQSAPV
NRLSVARVLEGDDWERVAQRLGCSVDDLKEANPAIEGLEAGAVLNVPGGASRRLTSFGAA
PRVLPLQNPNNGKRIRTWEDAATVLDCTVEELQQANGHAALTYKQTGENGEGEFGPSVTE
LNVPLSCWVSTPETEFSPVELVFAGDTFATIAQRLRCSEEALKKANDGQSDLSHARFVRV
PAEAKAPRRLLEPQLRSQAATDVLMTRTIAEEAAYGIKNIPDLPSNANKFPHEYHTPTSR
FPTTPKEKESESDWMAYTARYLDKQFTHTTEPTPIYNVNKLWPMQQVPGKIDQTPFEEDQ
TWLLNPIPVQQLEQHHPEKDLQDLPFVNHEQFPRSLEWTAP*
>TCRU_5261 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily, putative
MSRRLFTSAVLLLIVMMICCGSGAVPTEGTDSENDSGFTIGMILAATGYEYDTTEETLPP
GAPTSAVAVPAEGNKSVHSRVKIPALSVTAISSLSVVDVNGVVAVIAQADYEDGSSTVLA
RIIEPTEEGAVWTLPNSSANNPQTHYAEGTERRKGLPSLFNPTAFFKNGGLYLLLYVGKE
PRSPKGAVPKSEYPYPSLVIGEIKSMNASEKEKSKKITWGDSDLLSSEIAAEFQKRSFEN
FSASGGTGILTQDSSLVLPINGWTKDKEEFSLILSSGGPKKEWKLSKGLPDRYFAPVIVE
WMNGRLLMIISCNDGYRKVYESGDNGESWTEAVGTLSRVWGNSHNRTGKGVQSGFISAKI
EGKNVLLVSLPVYSTDNESGRLNLWLTDGRRIADIGPISSTDEDITESALLYRNTSGEEL
ISVYGSRNATGNLSISSVRLTGQLELIKRVIISWGEMDKRVLQLYRFSIAEDSLSSVGAC
STRMLMNGLVGFLSGSFNGSQWKNEYFGVYAAVHGEVTTNSGGAIFKGVGAGAVWPVGTQ
GQNQIYYFANTQFTLLATVSIQEVPGSGTISIPLMGVKMNDPNGKLSTLLGISYSADKKW
EVTFNGVKATAEGSEWELRREYQLALILEDGEISFVYVNGQLLGSSKTMPTGKERLLDIS
HFYFGGDNGEKKGNRHVKVRNVLLYNRVLSASELQCRLPEEVVQKPRNASPTSSKKHEFG
PKDDDFYTVLFPEKLSVLLSNATGSPKKTAVGAATVPSTGGPNNNLKKNGDSCMLVNVSG
LLLLILLWMCAFAALF*
>TCRU_5262 hypothetical protein, conserved
MQWALTRDRIASSELQQTLHKHQKHIHAQSALWLSRTQALSYYRLQCRGGFPVKADILGE
RSIFYFTEYTLRERRALLNMHSLPMNKMNKWMLLTGAAGGPPAWTAATLEQYTQASLFAS
GENTSETALLVDATVAVPSSPSHTVIIFNAQETSNPFLIDDTLQHTHFVTGASFSHVVGS
SLSTVWSQFGYTSLKWLPASERNDFKHIAVLPGQEPHRVFDLEPVVLVHLSQTSNEHQKT
ILQAVPRWVLLRSLRVPLVFFGGRWLTGRQMNLDEDLKIKRDRATADMLKLPERPFSMNT
LPAELPYELWLWYDDSFPYTGLPQRRHIIHNRFFYNSSQLVG*
>TCRU_5263 hypothetical protein
MIAVRVFDLAAGPRTAKRVQLEKAETIAAQLPAFSEAIGEPLEISSATFYTVRERKIDKQ
PLPTDVPLEAVGVTDGSFIVIVRKGPKLAPKLEVKKGVRESKVDEIAPPQAESNEPASMT
SVPEQNSAAADEQVVPVGDSREYVASPAEIPQPVPTAAPSDAKGPDRESMLSLVREMENV
KREIASSWERWRAELTHDTSKFERECLVEVLGAVTRLTQQQDAVEKALGRLQQHTQDREQ
ATLVLSSIYEVNKNLLNELSTARQKARGTVEESFAAIMNLQERIEENLRTLVPVNSQKDS
IQGTVAAASGVKGTTRHLATSATMPEEAFALHESLIQQFFFAVGQVTVTASEMLNYCDNL
TELYTALSLKYNLRHTPMQEALQGYLHAHLPHLASAAPVICYLHEGREVEYVEIVTLRSL
GLHLSSPHTWLEVALPSTLETPDIRYYYSSLVGLSQRKKPKWLQSVSIELCRISALSSVC
PRLGLRNPQWTEHDSQSLSKWRRSKAAALLLSYRPDLRGNMDLLLGSYAGREETLLKLIS
AREFMR*
>TCRU_5264 hypothetical protein, conserved

MGSLAVESLELEVLRAPAFVKTWLRLVEAIQLSEHESAAAKANATNVAYERAIRANGFSY
KLWVSYIAYRRDNTRELSSLHEWFRALRNIYDRAVEKLPMMPLLWVSFLEFLMDAPVPPR
LTLIRHTIIRALRALPVTQHHRVWKLAKRWTRLPHVPTETAKYLWKLYLLFDSRASNQRD
YFLMLWEKGSTSEFLTECAVFLADGSPHEDLLSDTTLWETVRLALETKDLRFSGDVTKIE
KLLNVAAEHCASPAELKISHAVFLSGHGDFAMAREALWALLETADDATIFSRVFSMAVAF
EDQIIDSLAMDPSIQALSDKGYQQFLEKLCGDTRDPLAHLRRLNHQHALLLNQVQLRENF
RDTTMWLKRVELLREMVCDNRASHNDVVMLYRQAIAQCTSGLKLVDVDAAQLFESYARYL
WDTDCGKEAIAVAKEAAWHISFSSTSSNLFLMGLFVEFMLLSSTRENCLTELLSNLQAVN
IFNGIRSRGMAKGAVLSDVQKDPRSWMLVLDVAFCELPETLGRVIELYNKSSAYSVESAC
YLAGRLWHSGRTHQAFREFERGLVAFKDAHLAMLYALQQYLSCLCLSFGKQLPLHRLREL
TRLGFEVVPFTLRSCPVASVEFLLNCAALESRLGLSGTAVKVAQDCLDVAQRNYGNAENF
LLCLVDTVLDVTLTLQGSQMLREYCAKLLERPHLSSSFIQRVALWWAAVEKRTGNLERAH
MVMEACCKSQDPNSVHGCVFWTLWESICTAVSQFEGVHKRKQQVALQYAGDLAPSAEASV
APKATQGLA*
>TCRU_5265 hypothetical protein, conserved
MESIPPKTRVPEDWIHPALKRQLMDRGRLSSSPKDRLELLERQRIEMESAAVRRKQLLEE
KKRHLEDLDRRRQRIAEEIKEEERRLMNLRHVHERVGDQLIVQKTIGRQEFQTVPGVEGL
QSSSCALRVTGIIGWGEIMSCFTADEETRERFFSKYAPLFTVNEGGSMPLKEVTEPVFFD
EMCLMETEGNRCMNSACPYWHRDQLEHAKLGCMELFARAATCIKGHSSICDAASMFSRFY
VLIEAATDLADVVRIQRDLINHVANLGWAAAILEDEESPTWEAPLLPRPIMSLEHVASLL
RDSREKTLWGHIIHSKTDVVLQATALFKQHADSFSWRCLMRVAGTTIDRLLWLATRGVAL
FPTSPFIRLSYLVALMKSGCSISDCVEVCLSSAQLISDQAAFAIFSPQETEWCEVAARYV
AYMIAISCIHVARTDPEAAVGLLEAVLELPGRICLLPLALQNLNLFLVVLRKTRRLDGAS
ALPLASISDVSFTLGDGFPCFPDNECGQLLSRHLGLIDLCVSAGIDGSLTERMRSSVHLS
LMHALSSDAQLVDQILTRSPMHSALGLAEVWVGYLRLVEQRGGTVSLISLVQSLLESCQS
PLLMVHLVRFLQVHDENVETVIDNFLENFAKSRGILLEKVPLMASTDSPGLPVDEWIPIV
ILYSLRLRLRERLELLLSVPLDLYCDVVELVVLLWLETIQVALLLRDDDVFRQCARQGLL
LLHEPFLHYFSPVDWDFDEMVSYAHVASLMVYRAIPVLLGTSYQFTAHYRGILLELSAEL
HVVHPNLLSTE*
>TCRU_5266 protoheme IX farnesyltransferase, putative
MIRRALLRGACVKCCGAVAFQSNLNSVTKCCPFSGAMDSEQLKPLKTGTETVSCPVLGIT
PELRCPMEFEKDTKTLPMRQIAAQMGKLRLSSFVTATTVTGYVLCGGTSLVAAAALTVGT
LLQSCSANTANQILEMEHDKKMKRTCRRPMPMGYITSKGALTLCGLELVVGSSILWLLSP
PVSALGILNWFIYVAAYTPLKRVSAVNTWVGSIVGGIPPLMGGIAATGTVTNPAWLLGAL
LVAWQIPHFMGLSFHCRRDYEAAGYKMLAFYNPWRASFYAVLMSVVMAGMTLAGPVVIGM
PSEGWYYPAAGIANGVMIYKAWLFHCMPKQHCRGCFVFSYIYLTIVLTALMVNHFGPVKR
CTAACEFVFDYIEGQRQEANSKRPWKLT*
>TCRU_5267 vacuolar proton translocating ATPase subunit A, putative
MPREAASGLWRSEDMTMLQLTMQRETAHDSVLKLGQLAAFQFIDLNGDVNAFQRDFVQEV
RRCDDMERKMRYLHEEIGKAGVTSVPGQVGERETMFSLEQKVDEREAEVRELNEQYQSLI
EERNRSREHLEVLNRDFSASSTHSQGLNLITGVIPKERVPILERLVYRATRGNSVMQTDD
IATPFYNVATNQPIYKCVFGIYFPVPRLRESLGKISEANGATLYAYAENEEQLQGMRESL
QVQVETVTHTLQQSALRQRQLLMGISASVYEWRRAVAVEKAVYSTMNMLRFSGATVVAKG
WAPVRSLDDIRTALQEAEYLSGAQVLTIVEGVTTKETPPTYFRTNKITSSFQGIVDSYGM
ARYKEVNPGVFTIITFPYLFGVMYGDIGHGLILTIFSAFLIFMEKSWEGKPLNEIFAMIF
GGRYLLLFMGFFAVYLGFLYNDMFGFSVEVFTSGYRWPQLPPNGPDGVVRPSLPVGVTPA
HSVIFGVDSAWAETENKLEFYNSIKMKCSVIIGVVQMMVGVILSLMNHLYFGDKLQVWFR
FVPEIVFLSCTFGYMCLLIVIKWCTPWENRTHDAPSLLETMTNFFLQPGTVNLPLYRGQA
VIQVLLLLIAFAMVPVLLFVIPFMEKKHHDEAMKRKALLHEEDEEEKDEFDFSEVMIHQV
IHTIEYVLGCVSNTASYLRLWALSLAHSQLSEVFWNFAFLMTVGLDGGSGIFVFVGFCVW
MCATLGVLLGMESLSAFLHALRLHWVEFNNKFYSADGYAFTPFDVAEVLSKIN*
>TCRU_5268 hypothetical protein, conserved
MSSVAIVFDLRYTDWDLFESARETFVTAVGEMLALSRAASFLRGEPWLRVEIFAANGTCL
VPAWDAAFDANNVADAMRILSTLDPVRSPARDTDHCVVDALQRLLYTAANGGADSFRGLL

FLTTFTTIHDFSRRVHSTKILAIPFMENFWVSLHLDATAMTTTSLALTPAIRLIRCSIGP
LVLRSAIQQALSPFLKLQRHVPVSLRFGRYNVPCAARHSFFSLPTRCCTAGDFDLTRKGC
TEECSGESAILFLSGRHFCTSHFERERWATKEVALTVEGILSSDAVSEELLYGDGWTLCP
KETEPCERRPEEWLYHLSKELQGDVLILTTQQPHLDPPHQIALPASTFVGFFLRPTLLYV
RALIPPELLAEQVGSVGACATRYRHDAALSDDIKRTADNLRSASASTLLRRPVGVCRALA
QLRRSQQFTLKVESSQGPTKRGSAYSLHSLHR*
>TCRU_5269 alanine racemase, putative
MSRYDVLNEPTAGEIAENYKNVLGRMDAASGGRPVTLVAVSKTKSPACVQALYDCGHRCF
GENYVQELVEKAGVLPKDIQWHFIGHLQSNKVKELLEGVDGLYLVQTVDSEKLATKLNNG
CVTYRGGRSLNVYIQVNTSGEESKSGTEPGNQTVELAQYIQEHCKHLNVAGVMTIGMPDY
TSRPENFECLLQVREAVARALSVPADSLALSMGMTGDFENALKMGSTIVRVGTALFGKRY
CPPKSPRKGTTD*
>TCRU_5270 hypothetical protein, conserved
MEILKKTALFRIEQQTKDTPPGEVTNISLSDVPLLPERLKCFSALTHLTLVSMKPRINTL
QAISLASFPSLRMLDVSDNSVTVAEDLPLCPTLRRLFIANNRVRQWAEVERLAASFPGLE
VIDATDNEVDDASRFSDFFELFPNLVALDSKNRDGEEVVVADSDESSSSLDDSEDDSEDS
LISEEEEEEEGETEKKNENKRPRACEGLGGDEDNAAPKKVSRTQ*
>TCRU_5271 Sulfate transporter N-terminal domain with GLY motif/
Sulfate transporter family, putative
MVGFFFRPVDIFGHPKTALGENLDPQRTWLEWVFMPRHKPLFYNFMANIKAGLTVALVNV
PLSIALAIGSGATPAQGIVSCVWAGGVATIYGSSHFNIIGPTGALSGLLASMVVSYGGGV
LAPLALQAGLWMMLFLLLRVNRLLRYVSSGVAHGFGCGVAIVIAVGQIPSALGLKGVAQR
ETIMEKLKEDYRCLGTISVPDTLLFLVTVVPLLILSKRYNKIPWQIIFTLFGILMAQVLP
RGSFVLLNMKYPDLSLNFFAFSSLDLLINPQWFHPRIILYGFGIAIVGLMETLISSVIAN
NHVSDKSYLNYSSARDTFGLALSNIASAFVGGIPSTAALARTALMVHSGAFSRMAGVVSC
VAVGLLCSVLLPLLKELPMATVAAILMVVAYKLVDLNDLHILHVIDTANLYSTIITCAAC
ILTDTFVGLVVGIAISVLLNYADATVSDVVFEEEDEMFASPRTPQPRVFRVLIVQPQESL
LFINSEKIKRTIFERSVAFRESLPPETKKHLVLDMSLVNRVDFDGTKALGEIINAHREKG
WIVDVLNCQHLRNSLVLCTPYQDLQKLEYMELY*
>TCRU_5272 GAF domain/TIP41-like family, putative
MHADNSSVIPPCGSKRELYTRLEAVVRSFVELPSSMLTPHFNLMIGLSNVSALLFYELNR
FANTNAMLSDLPLNWLGFYLLQSPQRLVLGPFQGRPACIEVAMGRGVCGTAAQKGETLIV
PDVHAFPGHIACDSLSNSEIVVPIKTAKGHVVGVLDVDSTQREFFDAEDAQGLQNIATVL
SQNLEFPMACTLARNPLLANAASIPSHNEAPFSLAGKDEDKVPTVEEAAGSKAKGAFPPF
SGTKMTAFVITRAPGTTPAKALTEVGEGASKQQRSQRFTHRVGGWDFSVTELSRILTQEE
LLHYEEALGVSALPEIPFAFNTLRIAPAERADVALVKFSLLEVLRSAAAFYRTDAYCRST
LPQLQIPVADSWKKSPYATVDAKVDWAWRNNYFGVNEWRCKLRPLEPSMPGVNWELLKDQ
TLPIVFFHNFDIFEDDLHDHGIVKSSVRFRVMSLAFFILFRHFVRVDGYRVWMREVRLFH
EFSVKRPDGQPHIVVREEVRILDIADGEKFRNYDPNDCAREATVVEANDFYVSIEDPTYD
DWWSTIGVH*
>TCRU_5273 LicD family, putative
MTCDVLPRLFLLARHRAASLKAAEVRSSLVSADGAKVRSTNCAVGLHRLMDKVLEELHTE
PHRWLPTTAENELVELLDKSDAPDFPSAQSFYSLLAQRRFVLDIATSSAVLNVTLFDEVA
LQCGETCVLREPVSRSSLMRLILVPVDMRVALHGLLRAVLGVLESAGVKCWAIGGTLLGA
MRHGSIIPWDDDVDLGVLAADEAKLRAAFGFPRMDGVETDLLLEYVPMFGYKVYSRSLPP
PSRDGSVTCMKYGYFIDIFILEELQGRVFFARNEAKRTWPNEWWYRDELFPLTRVPFLPT
PSSSRQMLWLPVARSPLQHLQRHHGATCMEEAVVPRELHGRLLSHSLHIPMTLLDDV*
>TCRU_5274 Tumour suppressor, Mitostatin, putative
MPCLNALALIEARQRRECEQRLFNKAHAEDCRLRLTANWERRGDTVIQRKDLMRHLDSVQ
AKHDDALVARRKRLAEMLLQERAEHETMMNNLAETEEQRRERLIQKARELRAQQQEDLRV
DAQKRHERLFREKIDSLRLAESRLKVMQVADARFKQLALAERRREEDKREEEFFAQQRLE
EQRLTNERAQRDLEMVRVGREKTKQALAAQVEGNKMRKAQQQAEKQREDDEFNRVVNEER
AAEAQRRVEARRARAALAKEISAFNEELRQVRRQEYEQLQQEDKEVLDRLLAELAEEERQ
KRQQKEEHREAARAHLAEIREQLNQRKKDEGDLDRLWDEANSKEWAKREAQWRADEDKRE

RLMRNVLIIRRQQVLDKRQQEKDAAEAAAREREEFLRELANTVDLDAQERARRYKLLRED
QKYLIGQMQRRAAQKEAERQAVMNEMTDQQALEAKHAERIKVEMENLERAKPERYKNVPL
LPKKRHQVF*
>TCRU_5275 hypothetical protein, conserved
MSIGDDNIVACSCEAPASSSEEYSDTLESLDARLIAEAHARLQRRMEQGTLTESKELAFP
YCSVFAPCGMFPISTPPLPLFMKDDDVVSKIRARLLKERQDAVAVEDAMEKAELAVLEAK
CMLLESMP*
>TCRU_5276 short-chain dehydrogenase, putative
MKFACSFFAYVGAFSVVLSLYRVVRFLYVNLLASTDLKRKYARAGDWAIVTGATEGIGYA
MAMELARRGFNVCVVARTRSKLDAVVAEIEKKGVQGKAVVFDFSTADAQAYKRLFAELEL
LEVAILVNNVGVNYPYANYFDDADVEEDMKMLKVNCEATLRMTRFIVPRLKAKRSGGIVF
LSSISATMPSPLLSAYAGTKSLSLSFGEGLAYELQQFGVDVLTVTPSLVVSRMTQGVSSR
KPKETLFMVNAATMAHQTLNKLGTVTRTAGHINHALLNSCLRILPESLVANKILTMHQAI
KRRAERSRTQ*
>TCRU_5277 exosome component CSL4
MTVAVCTGRRVVPGDVVYSGSASCGEWDRVAAGEGCCTRIVAGDSSVDSAEVRQIIATRL
GTVQWSESTVSVQRAPKRRHESAHVALISNDPNDVDSPSALARSTAVFGPRLGDTVYMRV
VRVSRAFAYGEIIAVNGVWCSNSSVSVGLAGSFRGVVRVEDIRPFKPTKDQLTPPPPAAA
FHAGDVVMATVLSQSDVRQYQLSTMHEHCGVVEASVVMDRVRVKLQHIPGRRDAMRNPTD
GTVHYRWCPLIHPAAT*
>TCRU_C Terminus (BRCT) domain containing protein, putative BRC.1
MFAPNARMSDAKERNKHAGEGGEKLRGARQKCCIFAVSSHYEWGAKQEILEALTHKLHHT
TVVLQRCEAGKEPSMALQLGCNVLISPFMPTAPCAVAYATKEKVLQYACSCIEDEIDDEL
DALLHALDYTARPSTPLTEAATVKSPTNVAPVVSRTVLQGGIAASPQNATGALGVHESIK
WQRSENNGLQPYTQTIKRSRVDLLSMSPAVLTEPTDFSLQLSQVIQYQRDSPSRTGPVLT
ADHAENSVLDPSQWRFQISNSLRESKDEVVSAICLLGGRVDHSKSYNPQTTHLVVAEGLA
ERTEKYLSCCAARKYIVSPRYVLDSAKRGKWIVDRLHEYDKNPLRHLSNVSSTPPFHGWR
VVLFTSTASVDTGIVTVLKAGGCTDVTSYIFNTVAAPNIDCRCIEQASHLLVECKNVSRT
GRFLTPPWFPDTLKRQDHRLFSLELLLHLLCFCPTSVFDEYGRPIDTLQLPPSCLLEIPL
TDARLSGILDRAVK*
>TCRU_5279 dynein heavy chain, putative
MSISFKELVALRRVHLAQQQQQQQQQNQQQSLDQWYRNHVAMSSISPPPIGREAVETEE
SPINDWDGADDGVSIEQQLPAWLREESPTATTAPLHPWSQPVVGRYTVGEEVPVGKEPKV
MVPREDLKGELPRVEVMRRWRRRYDEVSVETLLKERNIIVDGEFTGNKPGSYQSLLPLHA
FDDRRYEELSPEDWLGKRDGTGGVSCKALHNKGKWRWLPARVTEWNAKTNILTVEIADIK
EDGENLKSPQRENGAVVALPRLYVCFDAENPRNFVDRFAEACRLRTLVESVLRQQLYVES
IPPDEYQVVDPLVLERVHNLSLNTPRLRENEAALSVNRLLEEVRTDYSRVMNFELMRQTT
KNGALTQLFSGSGLPPERPVVKPRECGVYGLRRNCFREVVNTFYRDSFFACNAITISVLQ
RVKEGNDALLSRKVFRVDQSLEDVCPMTMDAFEELQVGFVRQNAQFIREKWVPDITKYIK
NAFSHCMGASDVSLHLPESVYGGSKTQRLMCTITLQMQDALRTFLTRELGKFASFLEMAA
NYTVQVRGISDVKVVPHQDRKNMRITPLFKVTLVEGDSRTLMYTTTATDFSKMLTELINR
CLTLHTGLRSVERQLFSFLYDPGTAFVSSIDGEDPVVQSCLKRLVETLTRAGVPLAEYIA
KYEVFEDLVALDVSQYVESFRVQFTSTKGVEDEIERFIKKRADINAQIPRFMDMGLFQVD
CTDLRRQLANKCTQITNSILEVLLQRVNLKVADVNDGFRAIRESLMKPTETPEEVVERNE
FIRMIPEKVFDLQTTIVEIQQINAILDTFQVPLSEDDFNRKWMAIGWPAQLDDEIIRRQN
ELEQTKRSLIVNMRKSQEAFQEKVSQMQLTVGGFHRRTNVNKINEIVADVHAIQEHIQSL
IGTANTFNTHESLFGLETTDYSVVRELSSDFDSFATLWLAVYDWNVAIRDWYNKPFTDID
AEEMEQRVMKNYQSVSKSTRDPKLTGLLIDIAQKTKTKIQEFKPMLPFVKYLRTEGLKER
HWDQISKEVGHEIRPGKTLISLNDLTALKVTEYEEILSRISEVASREYQIETSLKKMKAD
WENIRLNVQAYKSTDCYVLPKDSVDTIQEELDDQTLITQSLSFSPFKKMFENDIAAWEVS
IRKIQNVMDEWLVCQKAWLYLEPIFQSEDIVRQLPREAKRFQKVHENWHDLTNKANEIGL
VLKFCEPNESLEKFKENNGLLELIQRGLNQYLESKRSSFARFYFLSDDELLTILSEARDP
RKIQPHFRKLFENIMEIEMREPINEMYGMYSQMREYIPFDSSIIPRKNIENWLTEIENMM
QISIRSQLAQGLKNCVEKGRKFFILNSPGQVAIAVNQIMWTHDCEENFKAHGSLEPHLPK

AKANLMELVELVRQPLSNLQRMNLSGLITIEVHARDIVENLAEDKIDSIYAFEWISQLRS
YWENNDCYLRQVEAQFRYGGEYLGNTTRLVVTPLTDRIYLTLTGAMHMFLGGAPAGPAGT
GKTETVKDLAKAVAKQCVVFNCQEGMTYASMGKFFKGLAQAGAWACFDEFNRIDVEVLSV
VAQQVSSLQEAARTKQYRIAFEGTEIIVDPSYSVFITMNPGYAGRTELPDNLKVLFRPVA
CMVPDYAMIAEIRLFSFGYSNSRTLAQKMVATFRLSSEQLSSQDHYDFGMRAVNTVISAA
GLMKRESPDEEEDVLLLRALRDSNMPKFLEEDLLLFSGIISDLFPGVELPPRDYGSLLGV
LRETALEMHLEPTEMFVKKCVQLFEMNVLRHGQMIVGPTMGGKTSSARVLQAALTKLRVE
MNEERFAEVHIHSLNPKSITMSQLYGGFDEATAEWRDGLIGELFRTAARDTTDSKQWIYF
DGPVDALWIESMNTVLDDNKKLCLISGEIIAMTPYMSCWFEVEDLAVASPATVSRAGMIY
MEPVSCIGVEAFIKTWQRHRLPITMDPYKEALGNFCTALFPALIEFVRQDVVEYSPSVWP
NLVVSCFNIFEALLIPFTPTRTMEVPQARLERLKETHMHLFLFAVVWSFGATGDMDSRQR
FDQFIRTQLNNLEVSIKIPVIGCIQDYEFVLDEARWVLWTDRLPAFTAQVTAQNIADIIV
PTADVARYKFINKLLLEKSFHTLCCGPTGTGKTVLLQQLLMHGMPKEFTPIFFTFSARTS
ANQTQDLIFSKFEVRRRASPQIWGAPVNQKFVIFIDDMNMPVKEQYGAQPPIEILRQYMD
YNGWYDRKTREFFQIVDVVFAGAMGPPGGGRTHVSQRFLRHFNQIAFPEMDEDSMKRIFL
SILEIYFKPFGEDLSSKLSSIVNASIGIFYTVTKELRPTPSRPHYLFNLRDVAQVVSGLL
KATPKKTTNLVDLLRLWVHEEMRTFRDRLTTVEDREWFDEQLQRQIEKHIKVPFTEIVPP
ETGTDGLLFVDFLDTKSDQLFYEEVKKPEKLVKVLEDKLVEYNNVSFHKMNIVMFAYAVE
HICRIARVIRRPNGHVLLLGVGGSGRQSLSRVAAFLNDFEVFQVEISKSYSMNTWHEDIK
TALRRVAFHNKQVLFLFTDTQIVKESMLEDVNNLLNLGEVPNLFVGPELDDVFNAMKPVC
IAEGIQLDKVGMYARFVKFCKFNLHVSLCMSPLGEPFRNRLRMFPALVNCCTIDWFTAWP
TQALRSVAHNYFTKLKLVPAEELDKCTDLCVTIHQSVEEISIRFLEETRRHNYVTPTSFL
ELLHTFKRLLESQTEMANMTTHRLQNGLTKLRETENAVAGLQQTLEKNQPILIQKRESIK
KLMEEIVIQTESAEETKREAQTEEAAVAAKQRECAAIEAEAQDQLSEALPELDRALASLA
NLKSSQITEVAGYKAPTPGVVMTMQGISILFQIKPIMRAAGPMEEKKPDYWATAKEQLLN
NPNLLMQRLINYDKEHIPERLIQAVMPLVSSEDFTPKKIAGASQACAAMCQWTHAMVKFH
EVNKKVEPLRQRLAVAQEDNRVFQEKLRIAQAQLEDVARKLEKLQADKTRAEEEMNELEH
VVQLTEIKLGRAAMLIDGLVGEKKNWTSTMQEINENSKYLLGDMIAAAGQIAYVGPFTTL
YRNDLLNGWKNELKNHGILHHAQLSVYHTLQDPIVTQGWNVNGLPTDVLSVENAIIMSNA
RRWPLMIDPQNQANKWIRQTYPEGIEVLKPSQKDVIKRIEYAVRSGRAVLLENVGESIDA
SLAPLLAKQTFKQGGQEMIRLSEHAIPWNQEFKFYMTTKLPNPHYIPEVMVQVTLLNFFI
TPQGLEDQLLGVVVGQERKELEIRRSDLIKGNAAMRAEVANIQKTILRKMEEVTGDILDD
ESLIEYLNQSKATTDEIKIKVEEAEEAEKEINASRELYRPVARHSSCLYFCCATLSNVDP
MYQYSLQWFVRLFINGIESAEESEDLEKRLQNLKDYFTYSFYQNISRSLFEKHKIMFSFF
LCVRILQQAGGIDDDEFRFLLQGPSMTSKTQPNPAHSWLTDSTWAEICYLSANFSCFRGI
SSHIADNLEHYRGIFMSSTAHREKLKGIYEQRLNSLERMMFLRCLRPDKLMAAVQDFVRD
NLGERFIRPPPFDLFTSFKESSPTTPLIFILSQGADPFEDWKKFAESQNMGKKLSDISLG
QGQGPRAERMLQEGMENGTWVLLQNCHLATSWMPTLERLVEAISPGIHPSFRLWLTSMPN
PYFPVSVLQNGVKITNEPPKGMQANVTRSLLSYPEEYFESCRKPKEFRKLFFAMSFFHAL
IQERRKFGPLGWNIPYEYTSGDLGCCVTQIRMFLEKYNEVPYKVIRELSGNIHYGGRVTD
DWDRRTLNTILEVFISPEVMEDGYSFSPSGVYHSIPTGMQKHYLDYIDSWPLNTNPEIFG
LHENADITCARNETFETLEAIVALQGEATRKNALGKSPDEIVVDLAKLIQGKISDSFDLA
KFHKRYPTKYEDSMNTVLVQEAIRFNNLTAVVRETLEALSLAIKGEVLMNRELEEVYRCL
YNNQVPGQWSERAYPSLKPLGSWVDDLAQRLAMIQAWYEGGHPNVYWISGFFFPQAFLTG
ILQNFARRKQISIDTVSYGFEWINTDPGTVTAPPQTGCYVHGIFIEGARIDRQTLQLAES
MPKVLFEQVPMLWLNPIINKEKPKNDVYICPLYKTPRRAGTLSTTGHSTNYVLTMEIPTT
VDPKHWIKRGVACVCALSS*

>TCRU_5280 hypothetical protein

MNGGESPVEFRGLPGSVFFAKWFTICLVLVLLLSTGMTSMLFMTSISASYLRATNSQNVM
YLPPRNGTTELAAVLMIPEYIVEIGMLYFTIGASAFSRRTWNLLPLQPFSSATNPIESIL
SEDLLVAYVKVRKDALQFGYAAAESCGGASATNIMHRSRFVIAAAIIGTLCGMGIVFVAF
IFLFYLRKVYITPCTKFCVEWKDRMVRLTGGKKELGKFIELKKAEEHRERSVIIALIILS
VVGTTFLVTAEVLEHNLRSSTLKCGRSFCGAYEDAMRSLFQSPWTSGGRFSCQVGYSSAL
FLAGTVLNVVLLILIMFLSALHFFMRHVHVTLICEAAGNGIQPEGNGQRNPMEAPYLSLE

QGNGGGDKINSIFSASNRAATVVGSDEEKDLDRLRQVCLMPTGIDAMEVAGSLNDWKRVR
Y*
>TCRU_5281 Reverse transcriptase (RNA-dependent DNA polymerase), putative
MLQEARVEKLGASPSPSWRYLRGVAAPHPHPLESVVLRTDLRTASVLCLGQANLLVPHFV
RFHVPYRLILLRQICLSVILCVFTCHTALYCCCCRRTPLVPGGWEMDRPFLPYELEVAIR
DSSLGSAPGHDNMLNEFLHHLGPVARGTLRTMIHNSFANGSLPGSWNTVDAIPIPKHGKG
PFRPESYRPIKSLSVLFKLTERMIHRRLSALLPHHQRQFGFTPSRSKSDVVTIVIGKITR
KLNEFGIVEYERPGDGAPTRHPRHHRSLVALIDFSTVFDTIDHGKLSGMLDGLPRLCPRT
KQRLHNYMRSRYVRVCTREQHSRKQLASAGAPQGGVPGPQLFLHSVDDLLRRMGSIYSAA
AFMHADDLTLVASGAGNHAFAAAMQPVLPLITT*
>TCRU_5282 hypothetical protein, conserved
MQRRRGVLHARDGVGGPQLVLVQLQGRMAWRVVPSLRGARHGCAALAGKSRGRRRELRGE
PDADEPHAEHVEDATLLRGCDIQRRGCCVDILSQQYAAASPHQRHAHWVHIS*
>TCRU_5283 BNR repeat-like domain/Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MMGGNKATLHEGSVKFQGAWAEWPVGSQGENQLYHFANYNFTLVATVSIDGEPKEGSPTQ
KGELHLWLTDNTHIVDIGPVSDDDAAASSLLYKSAGSGDNKEEKLIALYEKKKDDGKQSH
SLWSVLLTEQLQRVKVVLATWKKVDERVSKLCPSKIAETDESTDNARRDFKITDGLVGFL
SGNFSENTWRDEYLGVNATVKGNDDGGNKATLHEGSVKFQGAWAEWPVGSQGENQLYHFA
NYNFTLVATVSIDGEPKEGSPISLMGMKMIDDNNPVLLGLSYNVGGKWKLLCGGGNPKEL
SSTWEKEATHHVVILLRNGTQGSSYVDGQRVGEDAQCDLKSAKDKRISHFHIGGDGGAKA
DSEVQDVSVTVTNVLLYNRPLDDDEINALNTKLSIPKAEGTKTVKGTPPEASKPVTLETE
TPSILGGQQRTEQGSLRTSEIAGSGVLSTSTVSSVTNSPAAKESENQSASGTFPEGNPNV
DVDPSSEEVQTVDAETGDTVQGDGTQQPSVGAPATADANAPTAEIMAPEGTAVTAEVGAH
SGEDGETRGGTDVQKEGIHAQDKEVNAAALSSSLGNVSQGNNSDAGTVRESGLPSLLLLL
GLWGFAAL*
>TCRU_5284 Leishmanolysin, putative
MLTWCCAWQGAVRGGALDDCRGGSEEPRDSDDIDGMELQDGDGDGRTLESHWSQRHAKDE
WMAPIVCTGCRTELTLAAPADLGCMRAEWEMAEPMRW*
>TCRU_5285 Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MGVKWIDDNNPVLFGLSYDREKKWQLLCGGGTNTEDQSRTSEKEATHHVVILLRNGTQGS
AYVDGRRVGEDAQCDLKSAKDKRISHFHIGGDGGAKADSEVQDVSVTVRNVLLYNRPLDD
NEITALNTKLSIPKARGTKTVKGTPPVVSKQATPEAGTPSILGGQQQTEQDSLRTSKDAG
SGGLSTSAVSSVTNSPAAKESENQSASGTFPEGNSNVDVDSSYEGVQTVDAEAGDTVQGD
GTQQPSVGTPTTADANAPTAEIMAPDGTAVTPEVGAHSGEDGEKVGETDGQKREGEVNAA
ALSSSLGNVSQGNNSDAGTVRESGLPSLLLLLGLWGFAAL*
>TCRU_5286 Leishmanolysin, putative
MWSSPTARSMPGVVGDVPLGALDALHLCSGVWRDPWVPFRIKTSTIGPCVSRRHCDFSWS
HAMNSLNDNRHFQDGVLSFAHGNILAEETVPAAVKLHADRLLVQPLECPLIVYSFATGSV
CSWFTVPAGHRSTRVANAKTVLYVAAVPGGV*
>TCRU_5287 hypothetical protein, conserved
MPSSNFSADNPKYHIARAVRVASSTSSVGRISADKSKFCKRSGSASSATEVRSATSDVIG
SVGRKRIGLSSLDSTRMKNGSADDAIFRSQTRQPYFPPPLHPKQVKEFLARMREDEARCT
KMHEKVCESKGIAFHPTKRLNCRRRSSMIEQPCNTPQRRPVISCSSTPSRNVRSPMLRRS
MGPNEIFRPDPLPVRGKSPTLYGKKSDLQPRAVETATAKIPGARGDKRGENGAGGMPKEA
AARRQRPVISVNSTTSVSRNGITATAANNRRVQQGRSTTRQQVRTQQSPSQGTPLHQGLP
GVRQPPRSSLSGVISPSSVSPCLKNCRTETAPYIETPAGGKSEVCSPVRLVYDTVDDGSL
GLFR*
>TCRU_5288 hypothetical protein, conserved
MGLRNAELHRRTIRDLSDKGFAVLVREAVLSCMGARTPRIPYFSLLSPKVNEAVSTLLSL
TQLVKKSNADFDAALQRTQAALKRLAAESLGDAEILLRGEDVTAALSYTTFLARFRALWV

FLFGFTYPPSSLQVVPPHIFAVRWPEVLCDDTIGWICATREEAGRSFASIQSGTASHLTY
FVFILQHTLSVRTVLLECVAEMMVNSAVRFDVMSVVRSMYRAYETLEEMADLQETWKQEG
LFSDDFITKYTSSCASDAGVGGVFWDDCGLDLVLSPTKAHAKSTFLCPFLWILQHLVWCL
YGRLTLLFQSCFIALPPEISPHQAVKDVGGTGVANNEEGPTVVQRNFPELNRSFGRRQES
RGDLVDSSAIAAEKVSFLHRRTTTTTTSVYVEPMTTGSKLRLSFPSLTRGDSATRLVEDD
SLQASRIEFHSPFDLNFNGAESNERGFLDKVGCHILAQLLWNITHERPRSTFFVVTDCTR
RPGPRAWQRNHCTVTTWADDVSGRQGIEHWVLNFVCPNSRLSENPAKRAQQEIMLLRAVV
FQVLGSTQRRARFTNDGSVFYVVRSDNEMDGGRLYFVLLLQRDTSTTHPSVGVRDITSKK
AVELESCWAFRSLEEVCVAWCMPHLCNLAIRLAALISS*
>TCRU_5289 HD domain containing protein, putative
MAEDTITFLRTVGKLKETDRTGWVEHGIPNPESVSDHMYRVAVMCMMCPDEKLDRNKLIR
MALCHDAGESIVGDISPKMGVSKEDKYNQEKAAVLHLTGLLEKESPLSRELHELWEEYEA
QHTPEAQFLKDIDLLEMVAQAHAYELAHPKKDLSSFFVSGEKIKHPWARNIYETLLRTRS
SEK*
>TCRU_5290 Splicing factor 3B subunit 10 (SF3b10), putative
MGDPFVRPGLTYQPHIEQVLLRNEGTLTLESSKDDWLRYQHRDTLASLILHRDRLEYLSL
VENVAPARMERILLERAVDPIRKRGRSNN*
>TCRU_5291 hypothetical protein, conserved
MSLVTNPRNIIIEKSDLFDDSSDAGSRSEEERILEALREIRGADLKCERNNVDLRAREMS
QRFSEFAQEKQQERGGKDQLRRNKPPRCTPEAVERINHSTVASRARSQRKYVDQLKEIQR
QKSLPSPRAISPTATKAGLRLYAAAVGCQRRLEKMREEREKLKRENEEKIKFQPRISTLA
KRLGSSGYVPPHERFNHTKEKLAQNILLRERERMDRVMAGCTFHPTLAENSAKMAVLQRK
NEPFSDVGERLFFEGGRRLIRQQLRQRILEQKAENGLIGDFQISNEAAKELALRLWKWQE
TSNRNREHMQSEYVQRVTQPFSPRLRFTQQSKQSRRSSGNNNRTRQPLFASSFPSENNVV
GRIPGDEIRKIRCRALFRKYASSENSASVQLQEVKRQVRELFPEDSGIVAALASNFSGTE
EISMPAFVESLMRFELLHGPQRWGNPRWDYVTSVSDEPPVLFSQPPSLALCQEEATDMPF
RKLRRSKSNCAPPLERKNGTVKRDLIPRCRSAYRRSSSASACGHLSGGVRDSSRGYEGCL
QRGERSVTRSTTVQKVGERTAELGAAEKGSRLLGRREAIPRQKPEKSPARDRIAPREVPE
ARHSQERSSSPESVEVSSITEEADSTPDMKHPGEVLAELEALIAKPFESSPAASPMASGI
QRACAPRVGVVSSLPSPLRRSMDKASFPCTTRDECYSTVNEGRAAHQKLLKEVEEVLGVG
TVSVAID*
>TCRU_5292 Tetratricopeptide repeat, putative
MEVNTLLALAQNAVDVGNSKAAEEFFEVALTRSPNNIDVLEAYAELLIHHAQDVPRAKQM
LQHAIELDPQRGYVNYLNLAQLSDADESLECYQRALQIVYGELRSCRKKRKRNTLNETLS
TIYCAIAELYLTDLCYAPDAEQHCEESIVQALKCNGQSVEAHQLQASLRLSQNCPEEALQ
SLRHAVDLTHRLSEAHQPTYDSKVELSRLLMQVSPDDAYRFLLEILQLGDNNPYIWFLLG
ESARLRKRYADSARLLRRARVMLTMTENGVEALKEVDKAIGVLVEEMGGPAAVEQIADLD
HPNPIELLMQEEGEEAEERDDDNEDMDKQEWESCDDED*
>TCRU_5293 Regulatory subunit of type II PKA R-subunit, putative
MYEMETFRERTLANRYQPRQHLPPNFPSVLKEYAREVLRAQPDDVLQWSADYFKRLALET
GTLQAEQSTSAQFTPLVENEEREALNQRLVKIFSELDSDGSGVLPIQTIKKALLETCGLS
PSQALYVLTATALGESDLVDYKTFASESSGALLFFQQTCHEFEVSVVEEATVHGLSRRDV
EQEFLRIFRYADEAETGLLPMDQYYKALANAPYHLTHRDLRLLFIETARNAENEVDYEAE
LAYMFDRLLLAEQFFLFDEDA*
>TCRU_5294 kinetoplastid kinetochore protein 3
MLGSVETISYDGEFVWLVELRLPLRGSTQGQLLSIRTCERIGQGSFGTVYRAVCDGYPKL
ALKIATGKAARLRQELDVLVKVCTKGKLLLPRFEFGAINKTGDLIVVGMELCVPSTLHDL
LLVTRLTNEADMLFLAYQVLQAVACVHEQQCIHRDVKLQNFVFDLDGNLKLIDFGLASSA
WNPPPGDVVAGTVSFMAPEMAHNALHRDQRVSVGAPADVWSAGIVLFSIFTQRNPYPPSI
ASITSPHSDEDEDGDGDGAAVPRKLNRENVRLLRRVATADWRWPVGSSVSNELRQLVEFI
LVTDPVKRPDISTILRKPIWNLRRRAPPTAVTAFLGVQDDLLLSHDETHLLRAVEQRSAD
VTASLMGSRANSLDGDGDEEAERRSSLKFVAREQTAVGGVPTHQVYDIRRESRQKRPLRE
ISVVIAEETAKGLRRRQPKRARGDVSSVSRGNSCASSRINSHANSRATSPARQCGVHDSV
QSLVKAKKNGKMSRTIPQTSSVIFDDEEDEGVQREVEQMVTKKEKPFVATQRIQKKQRNG

GVCSHQCLRSSRIGDEAENTKGLLRGGINGSAVDISSGAVLELPKCQMGLTKAVDGETRT
KKGPIHVHCDRKEQVSVWIDDMQLVAMEKSQRELAEKRIFLELEFLFSAFRLTTEENQAW
FDMVWLAEEQRKSAAHPHRFKETTRVSKKYQYGFICDMCDYEFLPAGKTIHFFHCTCGRD
LCVDCHRVYSKQCTCAECGAIYENIVALRGHHRKGGCKALGKNRRSSVAYEGQVSSNGPL
MRRKTAAQTHDIPRGATVATGPKATTEAAAAAKSFLRSEAVRMGAVNAVKKEAVVKEKTA
SSLFSRPINTPPEGQWKPMERLSVSHKPIHPTPEEREVLLNGDWIRHFHLFPTEEEAEPV
AFTYHIQPGRTGAIFLNHKFSMHSAVISVLERQMLIVDYVDTFENSDAARVVSLGNAKCL
AESAYNLLQRVVAYDCNMMKQHRTPGTISIYRTAQTAIRCQGEPFVYVRWFRFDAERSLC
AFLLSNGAVQVLVGDQYELRWFDENRKFLLRSNGVCEMVDDSTFALAPDVSRLLYDDF*
>TCRU_5295 Mucin-like glycoprotein, putative
MMTYRLLCALLVLALCCCPSVCAAGSEDENEEVTDPKVDASSTTNGTTQAPNNTENTIPK
ADVDVSSRSSNSVSELQVEGESGSPGTGHTAGHSKNNSPGTPGSTGPENQSNEVSNARQS
KVKNGAKEPPSPADPSSEKADQGAEDAAATTTTTQAPTTTTTTTTTTTTAPEAPSTTTTT
ETPTATTTRTTSRLHEMDGSLSSSAWVCAPLLLAVSALAYTALG*
>TCRU_5296 hypothetical protein
MMAAQKDLEERYASDAHAAEGRQAEMQGQIEQLEGQIEQLQADLSEMQAAYENAEIEHEG
AICVLNNFVEGRDHELEEMMAAQKELEERYASDLRAAEERQSEMQDRIEQLKYDLAEGER
RLDEMMTAQRELEERYSSDMRAAEKKQTELQSQLEELEYELQATEKQLQGEIAAYEAELD
DWRGKLDAEQRQSEEQSVLLGNRIKKLNDELGEANGRIKDLRHYLMGVERYTRGAYEATL
EGLGTKQREGLEELSLRMSASMAEYAETTAARLQLVTTVEDLQRILEETKRQANKEIAEL
HKMLRESRSAGRSRLEAVMALVQSAQGALAQAVETDEVYGDGTPRSGSAERSRGVSIALG
DCSNKENDVKRGSSRPMVTHNNNSV*
>TCRU_5297 BNR repeat-like domain containing protein, putative
MLLRRTSTLRGNGPLLLVRSVKEEWRAHTVLGTAEGKESLGGLFNPTTTMKGNKVFLLVG
STDASYVDGSWKEGRLELKLVVGEVTNATGGEPSKRIKWGEIQSPLNESAIAAHKGNLTE
CLASGGSGALMEDGTLVFSLMAMNEKNDGVYSMIIYSTNMLS*
>TCRU_5298 retrotransposon hot spot protein, RHS3, putative
MYESVHNARWSHVVEIPDGVERKKTGTGMEVEKGKPKQSWTYKKVGNTFEKDDAVRKSGA
PPPRLMVLTSDKGWPYTLNVPHGCGNDLCINCEVERAWKIVKGDVTEWFSNFDLALNSSP
LPRVLIGTPGIGKSMAAGLYLLYQLLHCDVEKLPGGCPLFWNHDVRV*
>TCRU_5299 hypothetical protein, conserved
MRRLCAFRTGTPTVPHRRFGNAPNRVRPVETPCVHAWRQTEREVSVAVALAVMFVVPVWV
ILLSGSRAEQKRESVRRWAMGQQRGGE*
>TCRU_5300 hypothetical protein, conserved
MMAGGAVGNGVSWRSFARGRPYTPLGTVQDFTASPHHIRLAEMQRELDEMSGRSPTHLYE
GPTVTTVQGPRPLFEADMRDDPANDDMPEHFIAARQRLMTLNSDSYGESIRGVVSPPPPP
DANAPRAYEQPRVQLGNIWWTAMTLIIVSFFLMARFGR*
>TCRU_5301 UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase,
putative
MLVLYVLGRHPSHGYDYSAALLEEAAQWQDVVALPMNEGRVSSTKKAGVGGAIGTEAEIG
LSQKVYMWFDLALRLFPTARYISKGDDDMFLRVPLFVAHLRLLPRRRIYMGVHCGGNIWA
NGRSVGVHFMVGWCYTMSRDVAEALVSFKPLRRLAHTPYSKEREEEFLSIGMGHEDMMVG
HVLLDEVKYQPLIHVKVLPCHFLQARSDTGESQVVPTAICVHHIREDDYAALMARFGNDT
SPVARVGLYSEDVIYPSCD*
>TCRU_5302 Mucin-like glycoprotein, putative
MMMTCRLLCALLVLALCCCCPSVCASGDTSEVEVVTETTESITATVSPENTKNSEANGKD
ANLLPSASKDKQGKGNSGSSVLGFSADSGKSAVEGDSTVTEPQSNNVPNTIQTEVNNGTT
GPRIGTSYSADQTDNNAKDVSATSTTTTKEPTTTTTTTPEASSTTTTEAPTTTTTRAPSR
LREIDGSLSSSAWVCAPLALAASALAYTTVG*
>TCRU_5303 hypothetical protein, conserved
MRRWRKCLVHLKYPRLCFLRVLPAGMPGNFGGNLRARRLLKRRWSHRGIHMGGLLKLSER
QAEHVGLVPSYCGRTSELCRRLGRRTSIRRSLVDKESRCSRREEAPEEAGHSPQCERAAP
PTQRVACDLQRVQPVEERAGVASRLRAVQPHGDRCPGQHQE*
>TCRU_5304 Calcineurin-like phosphoesterase superfamily domain/

Calcineurin-like phosphoesterase, putative
MVARGRHGAGVRERGSRKLPMVRLAVLLNFYFIFGVAFFCTGEEVKSTRKLLTMGLVADT
HYDTFPAGEKAPWETMHQWLREQRQRTTAWTVRRYDLARDKMDEAIGLFNRVADMDVVVN
LGDLVNNNLMWNLRPILDSFNRAKAPHYSVLGNHDLRAHNDRFGKMNKTQEEWLRKKLGL
PRWYYKIDHPPFCLIFLDSLVNDPQTTNATAKEAQAKWLEEELHAAKVAGRVVILFAHFP
IGFETNRLGPLLKEYDQMPLVFSGHNHKGDYRIQGAYHVHCVALEGQVETLTNAFAVVEV
FEDRAELTGFGRVPSRILRFQPHLIKLLQEYNGSLRTNLSSQGCQPLPPEELWVGEVLQK
PPPLRLNIPHYRKPNLSPTLVRFFPKTRFYNDIIVWFNNEKTHNIRGSEEPVDLTSATGK
RTLLSNGTSVILETPVVPHELYEEMTSGCGKDTAQPKRRTLTEGANTDNSWKKQWLPTIA
LWFFLLAFTIGIFFAARRKKRARHREWVAYTER*
>TCRU_5305 hypothetical protein, conserved
MSLKIRHFAEIVVAVTLGYVAYRGMQSFLRNEVTISITELVHLPPSERLLEVDDVTPLQG
EIRCETYLMRSYRFLMRLSASVKAVSISPPPTSRTRHRVTHAAESGSYRSMFSHGVNKKR
EGLPNVSVHDVHSMVDYWELSPNGNVYFTPPCIGDELLMRYEASVKAGYLVNAAVRNCYL
QTDETPGLKRLSFDLVVYDVLHAAKIHIALPNRYCDVVAIHTGGVGIIQQPNSNKPHHFI
WDIGTVDETTWMKVKTLSPEVLPEGRLARRGFTDDDLATAIERQKSGDNVSVVANSYQLP
NTVDSRFDSRSERCDDDKVFDGGANKGMLCTRTSSGLPEGTQLLIAHFILVFEEPDEMEH
DYVSTDSEMNEGEDEGGECDEVRRRKGTRDSSPGGAGISRKDAKREERARKRRLRRSSAD
LILAAGHGVPTRKPTIELSYSVVGLASGVSVRKLQTVSDLPNWIPRSFFDSWVLQWMVPG
IQQLRLGKYAHYTSWFVQPVPVASL*
>TCRU_5306 cyclophilin type peptidyl-prolyl cis-trans isomerase,
putative
MSQRDIHDDSGRAIDRELEEEEEYEDEDFLPSIPEALLHPPHNDVITPTKTDESLEVERK
KRSRSPREHRDGGASYGASDDVYSDNGGDERSEEGFMELLNLEGFPSTSLYERSYCHGHL
LHDIGVVQDDIGCLIATVDAAGTLRAWRKLPRGVFFLGDFQGLFSRNLAEGDANDMARHF
ILIDSLTSSLLVVRIMPCVETKAGIVTVSVEVRRVNSTLMTVETRLSFIFSVTLSITAES
SSWKDSVTPRPFLLHHDQQPFIVFFTVEKDGTSKSVFLPCVAEKALISGGMATLLTSAPI
STANRVVCCQQHRSSGLVVLVDEKGIIDYARIMVSPSDDGQTVAFLQVISGVPTRNAADP
MMLRKWITFERRQKTGFFTLLREAMNISKTGRLMTPLHVGFCATGKYFVVSSGILRAGHV
CVSVHVFEFASGKFLARGETEEKVAPALDGEKALQAAIRLMRGALYGVIMEDAVRKSPRG
EAGGVWVFVPEILLGGKLFRGRVCGRRIFVFRAAPSPARRMMTADGGEASNRVTETPFHM
EQMWRPIGDLEETVREMALPTSSFLSPGAGLDQHLAAPLAMIRITVPASQALKNLVAQSP
VGSTLLQEDMKRLFFVPSNTALETAVNERFFNASDPTFCTTSLEGTALLLYTKYETQLGE
SAAFQSLKGGATDATDAVGGRTEQTYREKMLYDLHQRRDFDCGELLLVESSPRGVLPHEA
VKADDEENKENDSVAHEKRDEHEIDGDLEEQRVQHIITAATGRVIEWESSVIHVSLFVDV
FGTIIFRLLPNFAPKAVVNFVGLAQEGFYNGLTFHRVVPGFMIQGGCPVGDGSGGKSVFG
ERFEDEGMNAMDFFSYPSVYWLCMANCGPNTNESQFFITVGEVAPWLNGKHTVFGFVVSG
KPVVRAIVQTARDDDDKPIAPVVIRRVVATERTTEK*
>TCRU_5307 dolichyl-P-Man:GDP-ManGlcNAc2-PP-dolichyl beta-1,4-
mannosyltransferase, putative
MFRYDELVWTISFPVFCSIVMWFSMAIALLVRSGRGYYRRETIRKSIAGMESRGETVSGS
LRRSSKAILRRAVVVVGGDFARSPRMQYHAASLLKCGLFDGVVLVGFDMGNALIDDLQQN
NSVGANEEGEFIVDTTYLIPPVTPPSWFRFLFPHPRLYWIVSTIYRACACALVFAWAVIA
ASLMVVSGKGQLLLVDLILVQSPPAIPFVPVIKYIVRPCVLFLNAISYYCFIVPASWMMW
DAFCEICGDLKLQRQLNVNENKIISPSRFVICPAIIVDWHNFGYTILRGDGRPSLAVWVY
RKFECNLCFGNRNLTVSKAMRKALLELQERIKVRGDKSRLSIADDVAVLYDTAPSFFGPV
SRARFVQKVLRPVLQSGGQDAKEVMGLSPPPAWVMETETHDSTENNSSSGMFVIGATSWT
LDDDYSMLVEALVRIDKRLKEQGQDQNSMQAPAVRPIWLLMTGKGVSRERFERAVVAAHL
SPLVTVTTIYFQSYVDYAMALGAADVGLCIHHSSSGLDLPMKAVDMLGSGLPVVALQYEA
LPELLDEKRGWMFSNAEGLEAILWRLAYRHSGNAAGSLEQKRLCVIESRRNTWDERWRAV
VLPLLRDLL*
>TCRU_5308 hypothetical protein, conserved
MSFVHSGRSGLIVLRFFQSHRSYHKTIGYRYRPSQRPGDHRQSRVAGRLVAETARVPLKS
SSSAGRGSDDNNSFARGTSTRDGHEGVDSLAGPSSPQAYLYRLRHGRFDDLIVLLSAPYA

ASPLRILTDVLREVLQLRLRLTSGECGGIEDSADRVDAWESLQRMANALSDPLAVRSVLS
GAIHAVKEATEAASEVGDRISERELQRELGDIESFCSQLRQWNAEMEKNLTFIAQTADDA
RYSHLLDWDLSNVVMAEIWHGLLELCSLTGAFYVAVESLNHLIELSELVECIDAKKKGDK
ALWHGRNDKDKNEHEEAEEEHQQSAFTLDNVVEVVEDEVRKFFPPVLAIDHIRAMRSCEL
ARNFDVAYTLFSRYIQHARSGVFPLTSKDIEAALIALARCCNNTAHFAMLQELFLESEAD
QVVGVSVELYTALIDAVSRANENPQCMAIALALYRRLRDGGLAPTADTYAGLMACCAAKK
DPKQAFAFYHEARHQCGVNCLSPMVYTNLLLAYAQAGYGADARATLEVLVEAGAPLSRGA
FHAVLSGDLTVREAEEVILLMQTKYNISATPQTYAYLHKAVIKRPNGSSTVLQMFDWHEL
ALKSLLKVNDTVNHQMPNTLVDGHSGQAAISTSSIVTPLEKDLLARYPTYAEAVEGVLVR
LRVDPTIDSRLKSYLRPLLRVAQLRMNSFTGMAPQVPTRVPKGAAIAVLAADVLANLEEW
FMPFASYYSAVVIPYSSLVALRNGGGRRVDGTFEKGTQQLLNDPLWREIGSEQQHMLESR
RRVLVKFLETYRDVIHLVSLEEELALSRDCDRYGIAARKTFARCAAFALNLARLDVANGT
KVYAEQTCNIVLVSSSFDGCGRYLVDLKREVLRGKKDIDGLQGLTQGLQRLCYHNPRTSP
QWRPPQVSVASLIHPAVNQQSYEQNL*
>TCRU_5309 actin-related protein 2/3 complex subunit 1, putative
MATPKQKETICEAAIVGFSFNKDRTEAVFSPNNHLLYIVSCKDIKDCSTWEIYATLEHHD
QSVSATAWHGSTNRILSCSQDRTAFVWQRNAKGKWKPQMVMLDAGVKRGLTSCAWNHSGS
KIYVGSAASNIAVGRFDAENEWWICRLLEGHTSTVTALAPHPSDDTLLLSGGTDGRLMLI
STFMKKLDGKKSSSFGHVYLEKCFGAWVHAIAWAPSGQRFAVATHDSRVHVFDIPSVDNL
SESIDEGLAIYSVSLAILPLKSLAFVLEDHLVGGGFDYFPALFQPSKKGTGWTMSGKWTM
TRVKGAKTAQQIAREKFQNEARIGQAELLEEEQTRHKNTINGVLTLIDDGAAFKSAMEGP
VFATASLDGRVEVWTIRDMIPII*
>TCRU_5310 hypothetical protein
MATVRDSVLFYAKVEKIGTDDTILSRNVFVTPSALLVCLPAGGITRTVSLANITEIELSK
QELFGKPCCKIHVRGEVPINLSFADQSDADGFSDAVSKAAINVRVVNVAVASVPEKKIRL
DLSQTAPKGVHFSAPQDPPESSPSSLAAENDKWHRLSSPSFSVGPLSRSGAQTVAKPIEA
LEFTGPTSSVGPKANGERDSIRDSVIPLENHVSPFRREAFHYPHAMGSADGRASTSAGVY
DLGHQTTGSMYTSDITRPVTTLASPTCGQPFQLQERYGETLVDLCAQRDSVANMQQRFSM
ELELQKQAVSRLTGELQEKNAFIDDLKTALRSQEGFFQEMLVSTEQIRSMEKTKSQLEEQ
LDVLQTEVKRLENLNRQKESDHRKELATKLAELHEAHTKEVEELRGAFAQYDVEMTEYVS
GLLKERDREARKGEEQERRLQKQIESQRNEIAELKGALASRQPAPSGVVASSADPTVAAA
SYEAKEEAKRATVVEGADGLNGKLTASSSHHERELPQPSRWPISHAVTMPQLEIRLASLE
EERARLRLREKLRHRIHRRE*
>TCRU_5311 Nrap protein, putative
MSLTPYQLHWSEALIRRVELRLQQVHASLEVFYRKQKYSAVTHTTATAEEDGEQRQQEEG
PISSVGSFLLRTCVHSTPLYETQLEHGVGADIAIKIPAEVCSLKEIHDGHYLERRHVFLL
KVEKFLKKYNEKMMKKKASKSSATAETEEREMTDEHERRSIVPWEVRRVPFGGGSVKTEK
DILRICFLKSRSDKTRREVFHVDVHFQPIALTGRIASVAAVRKHPFYSYLVQEDALMTVH
LRKLHELYLKNHLLSRATVFLKCWAYHVGLMARTSGHPEGLSGFHISALLLRLVEEGVIL
PSMSEENVIRAVWVYLSRGPTHNKINGIWKETPVPAAEERGEVAVLRLAGETMNLFFRSS
AAFFQKVVKRAADEALQLPHFSEVFVKFPFQPLQLVMDTCFVVEGLLAYFAETDSTPVVK
KTGAARSPSVQRVQAIQDLVQEALGSRSSYATVWRRGEDSVHVAVQLTTEVEGRNRLTRG
PPVEDTEAVEHFNAFWGKDITSTRQFPDGSIHRCVLWSFDDDVGANTTIALSAATVIRRV
LEFALRKHLLPTAKVSLLLGGLEGVLAERIGAEWRDAAPMMQKSLMEACRNVETMIGEIP
RTALPCKITSLEIIAPSERHTATFPVRPHLALTYTTDDLTQPNFAGLSTEPTIEPIHGVL
TIDDKNKIPDTIEAIAAIKGAICAQLSKVLHEYYGDDKRHSGARSKKPVKRDFENQQKEP
QCELQRLHIRTSCTSHSVDIIYKGYLFRFYIAHYREVSLLRALQRESEAAMIERKLFWSV
QHAKFLRTIAFGHHSYPMAVRLSKRWLSAMLLLEFVLPEAVELLVAHAYLGSNPPKTFVG
GFVRFLQIIATHDWSNPLLLPYSVDSKLQADTAALLRAMGEQQGMFIATPYAPMESPFTA
HTPRPMIMHRVVQLAKSALAVLLTQIDGRATLQFSEGLIFTTDPAAFDFHMEFHPHLLLQ
PDRLLMPPYSAPDASVSAGTSVANGTAVSPSLGPVSAGGTPATGVLASLPSRIWQLDELE
EDKSRVYLTELIEREPIVHLVRRVRTAMRDVCMIFYDFVAPQGIYVITITSSPMREVCKQ
IHDDIIRVSHGALLPFHCLPAVGATETQAKVERRPFPKTPMKHTGGNVTASAKAEADPIA
ADTSRKVLGRNRERNRHPKRPREFPENEDAGATSRSDCPQKKSRQETAHAVKNRKSEQTA

GSAKKKKKVK*
>TCRU_5312 hypothetical protein, conserved
MRRFTWLLFPQKGLNANTRRLPIKRKIPSRHSLCRGALLAELDRNPNDNDIAAGANDVVE
STAALSTSSLHGDNKYLVPSPFAKKLEETLMAVDLSPGHISSVSAHSREVRDGSQLPSLD
TLKAQERALRTMFADAKCRCIRMQKDREWLREERRAFQLSHGRPPSNREVSPFVDIELSP
VAALKLSKCLSRHSSARDVVVQSILLQQSITRNRIVQSGEKTLFRCLRCFHVYSARPRTL
LSDEVGHSWMQYEAERKKVSVAKELAHCPQLRKRKYSVGKQRKALMEDPHCCPSCGSPKA
QWFMEYVHYRTHA*
>TCRU_5313 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSVCTSESPEKDDASSTKNGTTQPPPSEERADADGSVNSRSP
SESGLRVEVESGLPGTGATAGKSEKNMPGTLGSTGPEKQSDEVSNAGQTKGTNGVIQSQG
GTKPSTEQENQVVEFGAATITTTTSKAPTTTTTTAPETTSTTTTEAPTTTTTRAPSRLRE
VDGSLGSSAWVCAPLLLAVSALAYTTVG*
>TCRU_5314 Concanavalin A-like lectin/glucanases superfamily/SPRY
domain/HECT-domain (ubiquitin-transferase), putative
MDDLSVHYLRMANGPQSQLHDPAAVVNFVEQMQLVVERSSAPRKNFLIDTTTPRGDVIIT
EASAMKPGNGWITLQVTEGIRRGVHEWCVKIEHQGETTDGSGLMLGIVPKSFAKYDSFIS
QGGGWCLSRAGKFYGHWRRQDNNASVVFGAGDRVIFLLDYETARMTVRVGDKSVVGEISN
LAPEVYPAISLHYRHQFVRFEYHKVHDRHAKKLNWIERFAFPHASVYLPLTPDQLEKVPL
DSYVFSSLFNEKEGQNGRWKRRKGSTASSKGLDGIVAVTEEYETARAANARLTVVLRAIQ
AVRRYCGGGVIPAETFLDRNITAETLRKQQHALSSRGAGSRDGMDAALNCGALVLIHMFA
HASMTLAGATMLPLIHNLQEYLRGVALFSLGEASSSPYFVGSSISPEVMLQALDSVARIL
DRTLANNNSTDGISGVVNSATTVHNNYYNNYKGVTSRMTYNNTDGDVAPALLELLVLLSL
QCGSISEVLRTVRYLLRLPSNFVSKGTLEWLKLNESALTPKRYLPSLNEAYDAIEEETEQ
LTPFGRDLNLQILSVGYDHGAVYIHTVDGLSKRSNVVGMYALVCSTNEPLDCCPQCSYSS
IAFGEEGVLLLLTNRMIAAGLAVVTYSTALEIRQKVALTDVPQWPVSSRYMAIASGPESR
LLLVYDVANPPSTAAAASDVNGASSFALEMQVFSACSFPEVQWCRSIQIAPLDRTLAYCL
SLSKGSVIDFGSPEACLTTVGGHVTVEVWIKILEKDDTSVLYQHGDRSTSGEVFIETARL
EGAWRIRGGYRHDSRGMCVVTASVSPASESHFIHIALVFDGNWRLCLDNEEVSCTRQGPQ
VSLENPRQRWTAGNDCVCQIAALRVWKGGRSLREIVRDSRRLLSGNEPGLLCQYFFNEPN
GNVVFNHVRSGAAFGRHAVVRGHFSRVGCFDHPLLPSLRESGASGGNTMPASLEPPQLEH
THVFFNGIHVGLMELKERVFPGFGDWRHVHQVNFFDVKTGRGVYGSYVLRQKSKMGFLGC
DRDGHYWEVFHTGLNSGVPGELQQQVVAVGKLSGLSTAVKENFTCNCLHGSNATNCSPPD
GTHVCVGGNARASCGSSQTETGSRYGQESLIQLDTTNFTFESLAMWLLGLLSSFAEASGT
ELDNHLFNPLLDDVGTRCVHEVQQLLCEHCRAVKAMNARRSANLKDSTSSSVISTTLRVL
VRLIRRVREFKLHPDTIGFSEVNGSDDFHGLLHELSIVQRRRNTSWQECVGSTASSAMST
NKSSTAVTATERTDPRGRALSVTIKRGTNLLGVLADIINEAGLNLPMELAALARVIIQEG
VTLFFPSATVRAKLLQEILSRDQPNALQSPALNVLLDAIVKSFTDMTSAAALVHGVDSTS
DRMNERSKSTDTMEKKLLLVKTTLFTLLTESASQMISQVPNEPRQQQLSLLPTMAEAIGT
LQLLLFSQCNWIGVADVNTAVARRGVENIFSIPLPTDLSPVLKDYYVELFNTAEMIFKTL
IERLSAAASSREPPATKTAATEKAAVVTMVLDMLSSSFLGFPLHTAITALPFMVTRDESE
WFLQKLCLLREHYRSLLQLIRENNSMGLDKTGRWSLLALDNGILLASSWVASFMSLGQLP
AESLEKNTPSQDSFDHSTSIIQEICDHPLLAAGLRSTSTVVNNTHMNIITKLQQQRSSWE
AIARRQDPIASKTPTGLGTVMSLAAVAVVHLSGIQLHRLTDDERHELLAKTLLQLKSARN
ELLNHRSQNPNDFERNVSDVKERCLLLLRIRRLSEADFSKMSSTFLAQSLVDRVVGEKKT
KGSRWRRAVFLLRAQRMYHEVLLNGWQLFQIGPALKLVERVIVSLGVTAANLQAVIQARQ
TTALQRLDGLRRLLHLFETDASSALKVASLLFSGSVGSHRQFEAGISGCLDSTRCAIRRT
MYDILCRLRDATAGSPATGVNDNSTRVEKSSTAAINNDAPFHPTTLSEVLNRKWSSSDFC
YLEHLHFVKVVFEANCSMFEQSDPEKLRQERSTERSHRHEAKDEQKKAATSGCSQDVTEE
DANEVSLQRTPQEYALMESLNTLKSLGQQAARILGDVSLSPCERRGCTLFLDELFGVLEL
ELRCCARYASQKSYPAHDRVLEQISLICTLACTVARTLPEKFLCNRENCFKVALLALRLC
IVAKILLAIITAVVAVTTAPATTTNNSTIKLVEVCIHTSILLLHHCQPATVDLIFLAEEV
MEMTRQAVCVTGTGGETLGFFLAFVLRCVSISSGGLGEMGMRCIDAFHTLVCRTPWDESF
NALCETYQCDLGAVAMAEDEEASRLSGVRLLVWMYAIGGPLTASLSPGKKVHMSVDNMLS

STEEAYIVDCSTQSGAATVISSNLCSLVEEREVSLDSLINSSYEEVTLPRADVLFRFLIP
ALEHFFKPPLKPYLSPLIWAVVAALLRITRAVLKNDPAASRILLERDILSHVDAFAFRLA
AKIPLPLCYLYEVCPTVVQHLLQCTRRILFDAVAPSFSPLTNNNAPNNSSSGTSYGHSSP
RTELHRNITFGPAVPLSTSVFGATALLGNSMVFRSEADNNNNNNNNNNKNNNSSNGVLPS
IARIPHPHSSLCLTPSVLCFCGAKDAPAGTLTIKSTGVRSCMPLWTDGVTLEASVLLYDR
LFPELGEDFVIPVSWQRPEIQFSLFSLYEKPSPGTAALMRVVFNENRIDCAVETARGSTV
IVSSKLLREDWDHWIHIAVVLEGSTVTLYKEGVGTTAVLSKAVASRLETLFREGGADRLV
IGNETRGGINSIKNARASSGNGTAKVRSTGINQRHTNNKTSSSSSNGENIKNQSYHHFSD
GETMDEMLVAIEGVRFWGCARGLKAQRTTADFVTREQTLPLVGVLDRSQTTFRFSESTGN
EMFSENRECVGILCGNARWVPFPVFSGTMNLDKSPRIDPTNQIELPLFIPRSEFECFFAA
LDRSQLVRIGSEYLQTLCAHLSRQCVLAAIRQVVSPGYHVLAIERCDNKQRDTKPSHTGD
DGNENCGDGPPSITGIVNPLHIISSNDFVRHLINLLRYSDTGAVSDETMKAVSEFIKLCF
CSISSEKVLENSFRDAVIAITEALRDEAETFRVELPPLSYVTTDIQLVPIAILNGPGGTV
SFDANSRGIEHMTLLRDRKQKVLLAKYPDAQGGWPELEIPGDSPWFYARPIVSTRAATAS
FTLSARSLKPLVACGIFGAIREVLTSHTKYHCGWKCFLNTPFLSFLTIRAGTTRCSSLPA
CRLLAALLDSWRYIPHFAPHDQSPLKILLAHLNVPLMAILHRGQIAPNSPPLLSPTLGHY
NLRVQGAFELLVAAIRLEAAWKGVSHSHCTRIRWKRLMSLWEGSIGYGTPDSSPSSSIIT
KQDPTVVERGYVRLVPLPSTGSPIQYRPKATIFQRGNGVWYASCDRVSLSARSSVGFKRG
RFYFEVRIPAGGEAISVGVVTERAQQHSVLAPRGLGHDSDSWGFESVQLCRFYHGFRHEF
AVRTKWKALDVIGILLDLEAETLACVHDGRQVSIFDNLRSNRGNDAATSFFPAVSFGTGG
VDVNFGAAPFACSLPVGYLPVDPSNYMASPTSKLWTLLTAVDVGETLAMCSNSPRGGYAK
AFYAEDVTVSKDGTIHLPNLFEKANDVGMAYQTGRSGPYSVSLLPCDTKARTVTVQGSEV
RAEDDPCFVRGSVCVRSGRWYYEVALRGEALVSIGWVTSTATPDWSRTKSLGNDNESWVL
EGSRTTARHNKHQRSVGGQMWKHGDIIGCMVDCDAGTIAYSVNGTPLREMHDTNGDGVLF
SSVNCANGMMPVVGVDPKNAASILFFDEELSFRPRGYRALSTSNPIRIAIELHYCTDDLE
NKDNGDGVAGPTFSPTLARSLLSSLTSLTELNFMNASAYCLEDVLNKNSSTIRYEKFQGR
ENALRLLVTLQNLSGIAECMIPYAHAAFNYGEYDTLLSGPICRSLWQCREYLLPVVVLRI
LHGFFSHTNCLGENVKLTLNRRKALSLVNDADAPVSERLRGSLFGQVYQLLHDKNVSLFC
TNRKLWSVNFIGEGADDIGGPYRESITQLCSELMGPGLPLFIPSPNQANDIGDSRELFVV
RPVMEPPVRIIMYHFFGRLIAGCLRSSEPLPIYLSSRIWKALVGAPVDESDLCVVDKTTA
QSYQCIRQLLLSKRGEGTTDEEITELCPGGFSVVDDAGVEQELFPGGKEISVGRHNVEMF
LDMALHFKLRRMGAMQIEAIAEGFHQVVPITAVSLLKWYELEQVVCGQPDYDADALIDSA
RYEDLDPNDVIVQYLRQVLRQFSRHERALFMRFVSGRERLPSGVRLKLMPDANSRPLRRE
TSQNSGAHSNDGNGGVKALVDTFDDNRLPHASTCFYWLSIPRYSSVEVMRERLLFAIQQC
LDIDADFVVHENGNSEDEVEPTLAVNADEDEEDFEDFSHLR*
>TCRU_5315 EF-hand domain pair, putative
MSYQPPYGYASSPQASPYFPGGNYYSTPPPIPQKQPFQTSPLFGTEQEAAQWFRAVSSSS
GGYISVPQLQSALSQGGMIFSYATTERLISMFDANLDGAIDFTEFQGLHRYILSMRGGFS
QRDTSRDGLLEENEVRMALSANFYQVDDTTFQTLMRKFDRRKRGSLGFDDYIELSLFVGK
AKDAFQAQSQGKADATFSFSSFLSAGASLL*
>TCRU_5316 hypothetical protein, conserved
MRASYSHDRGPSTSLPRSSSAGPKALRRQSTAQSPKSRRRGSRNMSVVDLSRRKSRPLNA
EEPLTESRRPTTARTIEYYLSHRPSRQSCGEATSAGNQHRHIVQIVRSVLPQEIRALDSI
ELGISNPGSLTLMKMLLPLEQANYPFNVHERRKPFLPGDAVAVKMGQLSMRVSFARVEDM
ALIGSRSLKIKNAPVLVNSELIGEVKYSCIQHIDLVVPAGDAQHLMVRLSGVIGFTVHLC
FSERSLCSVFVKLLLSHCNGHVTLSDEAGVFSSMSRSVVFEFPQRGPSFCAVNWRAKSLS
LNGNFVFPENVDQDGDDTENR*
>TCRU_5317 hypothetical protein, conserved
MEQAESAAEAAHEAHTLPHPETACFEPNSSKKWWNKIKHYAVASLCFWKPVWKNLEPHPA
RAGDISEAWRRRTLILWNRLCSALNFGPRLCSALATGKSACSSFCAVSRAIPPCTAAACC
APLVPGGWEMDRPLTPYVLGVAIRDSSLGSAPDHDNVSNEFLHRLGPVAHSKHLER*
>TCRU_5318 RWD domain/Uncharacterized protein family UPF0029,
putative
MAVSDDNAEEVELLLSISPEVVCRDPTHSSTLVFLLPFRFVLHVTLPPRGYPDVSRPSLF

VAAGPNAHLVNQFSSQLNKALREEVPLGGPMLLHIFTLAQDIATELQRTREAEAQEAQAR
REAMESEAQLALAEREASSVEVWASDAITDRKSKFVAHMARVDSEAAVREVVMHLRSQKH
IAEAAHPTIYAYRFTDSSGVVHHDSDDDGETGAASRIMFLLEQMKVDGYVVVVTRWFGGV
LLGPDRFKHIMEVARSILLTIPQREKERGVRDWQDRQ*
>TCRU_5319 Got1/Sft2-like family, putative
MSLRVNVDSLFDTTHTVPLVGSQSNTLGLPVGEEDETGNLCPSLSFQERVIGFAVCLGLG
FLFSIFAWVSIFALDFNTFAVINTVSNVTSIGSTMFLCGPMAQLKRMFDSKRLIATIIYF
TSMALTFIAALVLRIPWLTIITVLVQYVAMLWYCLSYIPFAHTAVLKVLGLG*
>TCRU_5320 translation initiation factor 2 subunit, putative
MARAHNATLESIQYARGTLRLLDQRKLPLETVFDEILTVDDIWTAIKEMRVRGAPAIAVS
AALAIAVAAGNELKKKDGACNSVDGTRLFLLESCDTVMTARPTAVNLSKTLIQLKRDIAD
VTANTAGGLVEACAVLAEKNYAEDVACNEGIMRHGAAHLTQLVKKSKVSVLTICNTGALA
TSRYGTALGVVRQLFYEGKLEQVYACETRPWNQGARLTVYECVQENIPCTLICDSAVSAL
MGSRPIDAVIVGADRICRNGDTANKIGTCNLAVAAAHYGVPFFVAAPSTTLDPMTADGES
VVIEERETMELTHSMATQQRVVAEGPSLRIWNPVFDITPAALVTGGIITERGVLQPSATA
PFFDITRIVGAR*
>TCRU_5321 hypothetical protein, conserved
MPLPPLEEAPRSMTRRNYLVERNRLRVSAYAPTRRELEEEDIRMAQTREERRRNMLNSWK
SQSMYNPDLTRPLPGGGPRSKRMKEAATLKNPNYYKIVKEEEAQLKAERTAMYRADVLQQ
LKDREEYLRKWREDEKAYVSSLVESNKEQARKLEEREREEARAEKEYMNRMRESNLRELE
QKRMKEREREEYELSLIRTVQAREKEKAETEERRARDMKQMMRRENEEYHRSIKKKQKED
KAREEAELKAILEYNATLAERERQEQKQRRDQYKAEFEETIEKQKEFFRTHNYDEPPESI
RERNEKAAAALALIKKEERLRLADRRREYRQELMQQIREKQEWQLTHIDGV*
>TCRU_5322 hypothetical protein, conserved
MESDDEIDALVSAQVGMTRAGATILPASVSDDELDALIHEALTGASAAPKAGENRAMAAA
TNPRQQQRRIQRNRVSFPKASPAVDVRIATGESAAHDPIVGAQRACSSSSSKSSETDSEA
MLQAVLEGYGFPGPKGLETLHLRGKRPKTVLQEHEEITKDECDEQNEEETVLMEALLHLA
QPPRELVSKNHRQSGDSKSHDSSSQIVTTQTKTKKLTASNPFARGNGEHPMLSDTPNRNG
ETPPCEFSSEEAAQWPEHPPVIPKDGKLSSSTGPPPELQDMEDEKQILTAILNAVRDRQS
SVSGDLVYGEDDCNVDAVLQHAEQIAASSLRENKVQLSRILHLHEHIEMREELRKARGSV
GWPTCVCARSAPVVIEGDSPKGSGASSLSLLPAAAAATAKRPALCVGTTLGVVLLFDANK
KICGMCGSVLAFSIEARGAVVSLSMSFDASTVLAGYERGDLVLWDTDTLTPLREIVGEFS
TPATRLRYCCMDPFKIVVLNSSGSVKLLSFTRIMSKLIYRLTHIASSDSEAPFNDMDIAF
VREEGLYLVAAVSADTLLVSALECGLTNVTTPISRRSQPLNSARTHELLKFVPTSVGNRV
LMCVAWSVDLEVFSVSAGGTFSQIERIAVVRLERPLHAMSLIADCCLLLLDQKDVLHLLD
AGVGVIVETRVLHGVEPVVFSSRSCGMRRNAAFAFMGSDVFLLGRRRTFTCTLLSWRARL
DALVEKRRFPEALELAKAFALEVALAVVGLHGDSATRRASIHSYLPHLITSYLEHVTESN
SSQETLVRCITCVIQFCSEVDAMDVFFGPVMEFLRRDSLHYSLALYCLEESIVLGLVTVL
PDMYIQPFFDLFANETLPVITELMHGTGDAVSSCGMLRVERALMCLDGNHELLMRIAKKH
KLVRLAVSILSYRQQRYVDALRFALEEDHEHGVAVCFFECSMEGYTILGDTEISFDQRQK
AKRELWCHLLTVPNDFLALLRMDPERVLFATFSSLQESGPDSPWGEALSKRQCVGELFLQ
LVGTEVSSSDPLRPWELARRKWPPYSVVHQLFTGVTHLLLTEALVLPHMRQFCEHACSHF
IYEFQIAKNEHERRGAQSDMAALMTDFITREVDFSFAEDELRQQRMARALAALHCSRLEY
DEAIDCYLDRENNCADPELSKDVFRVLREEMTRAYHLGDETIAQRLREAVMHRISLLVNV
DATSLAQFVLEHLQGSHEDVMNILRRSSGTFLRYLDELVAKDDPMVSNDVRLQNTYIELL
CAHDPARVYPYLHSRDLIITYDIHLVLDAVKRHNIADAAVFLLEKTLMIDEAMEILLGAV
TGKLRALRQEVLDHVVSVCRKGTRPPRLSLWTLSQQQDTGRTRRMTAAERRRGGREEDGE
KKGEQQPHGEQQQQRAHIWAGEEPLQQVLKVGVNLCNKYNDDCAPQLNQNWFCLLELFTR
PRRLLCDRQNQHNAALRSVQDAVDGFEDDEICATLTPGGSPRNEGRFPLLSGPLSAVGVL
FLENMIAIYTKYVSFLLTHMVEVLDPSAVVCRIVEDHERERFGPFKPVIVDIMSSLNFEL
EVNRLCKSCIDNDIMALGNELHRSLNGGVVSLSDTCYICEGGLGDACEAEGETSVRIFAC
GHGYHDTCAMNFDGGAECAQCCKERMGENYRVALRVPRDGVGDEIKKDGGKNKENGEDLP
QAMAREKEGGKRGEEEVSRVLRRLRYTRARLDGARDYSDLLCRFLCPSESLTPSHELLKG
STEKRLLAPAPPFPISFGEFSAETLDFGPTLTAGLTDEELLDLFGTQEEGSDDDDDDKGV

MSLGDGMEFQFDTTQ*
>TCRU_5323 hypothetical protein, conserved
MAMMTGRVLLACALCVLYCGAAVKAEGDGLGSGGGSLVQSQELEMSPEGSHGLKDEAGGL
QEELLSAPAGDEDDEEDGDGDGAGTDDEEKPIGRQGDQEVAIAPDTGSGEKNLSGSGQET
GQAIVSAEEIPSSGSQEPNANPTQTKIEKKNDTDKDTPAVENALTTGNGENTLPAGIAGG
NPPPSPEDGFDSRKQDGEDTMSEYKKNVPSPETAATPQRHRDEGPEGTGEDTKATTVTAN
TTDTTNTQNNNGSTAVSHTTSHLLLLLLVVACAAAAAVVAA*
>TCRU_5324 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MLVTLPVYPEKADTGGNGKGKLHLWLTDNTHIVDIGPVSGEGDDVAASSLLYKSGDNNEL
IALYEKKKDGGDKPSHSLWSVLLTAQLQRVKEVLATWKKADNLVSRLCPSSAEESASTDN
ACSAVIPTDGLVGFLSGNFSDGTWRDEYLGVNATVKNNEGGNKATKTSDGVKFTGEWAEW
PVGSQGENQLYHFRLNNFTLVVTVSIDKVPTEGTIPLMGVKMAGAGTSVLFGLSYNGGGK
WKLSCGGAADTEDHSITLSTETTHQVVILLQNGTQGSAYVDGQRVGGVVPCALGNKDSEA
VSHFYIGGDGNNTEGQEGVSVTVRNVLLYNRPLTDTEIAALNPNKAFTPPSEDLTAAMVV
DTPSTAVSGPVAQKTVSVSTPGGSTVNHESSASSGEDEGTAGGRDVQEEDIHARDRGVKA
AALSSSLGNVSQGNNSDAGTMRGSGLLPSLLLFGLWGFAAL*
>TCRU_5325 Concanavalin A-like lectin/glucanases superfamily,
putative
MRLTEQLERIKSAVKTWKELDDALRVPTEGLVGFLSSKLDGTAWRDGYLGVTSTESGVAL
KGRGAGAEWPVGDMGQTVPYYFANNKFTLSATVSIHEVPKEDSSPIPLIVARLNDTASTV
LFQLSYTSERNWNFTLHRMEFLVKPSGDVGNWEKNTAIRVTVQKDNDDEWFVYANGRRIY
ETDEKEMAKHRNADQFGSHRISHFFFGAGNKEDEGNSNVTVADVLLYNDALFGDDLGDLN
ARTVPIRHPAAEELHTAVEVTATEEEKQKATQLTTSLADVEEAPIAQPTDSQSVRVLAGS
ESSAENVTDGLRPRNAATNDTSVPETNHSASEGSMSPEDRLALITDAKLILHDLSGDSTA
RACACLVCCCFFWDCVHLWQSCEPESVTLRLLTEIVWRIPRGFFSFSFFF*
>TCRU_5326 RNase H, putative
MQKTYATLARIVSGVPSTVNPESALLEANMPPLHVLCLRARLSIFDNTRACQMDWMRRPP
PEPSPRAGFRISPLSRDELYAFVDAYAKGYGIPRSSPREERFFRSSIPPWSAASAHRVTI
GVELPIDHSITDEEELIREKRRVSEEALALHSHRSWILATDGGVDVPKSAGVGILLSSLN
SSEIIEKASINCGARPCSYRTESRALLLALEKLMIPRIRHRRKTLLVVTDSQSLLAALNK
GPLSQTDWTEDQIWQRLLTLTRAGWSVHLQFCYGHCGVHANELADQYATQTMESGQYTEH
GIAPLWHTDLLTCFTTQLTNKWRSTIRQDTHRYLLCGTRPSDLSGKDLITQEVLHRQELV
HLARARCGESELWGRLYCTVRDCTNQCRFCNISPEQSAYMRSNNDPTAPGTDTVPPSARE
EDVSPVRRRTLTRRRKEKCPHCDSTLTGFSGLVSHCRPFHPEHPPPLPELKCDFCNMVFP
TRRSTAPHRSRCAHNPDATRHRNSSARRRSLLPQDQPASTSTPIGPQETLHHLLLECPGT
LAVRQRLGIEQDLRLGKFSQWQLLHSRKLLSLLDHLFGTQMALYS*
>TCRU_5327 Reverse transcriptase (RNA-dependent DNA polymerase),
putative
MLLGDGQHTYKTARRAANALNRIFLPFHPSHKAVRFSKGINRQSASLNINASFLFGQQNN
NESAATFTSGSSLSSSSEPQDKNDAATTSGLVAHLHSPLDAPFNRTELLAALRNTPYGKA
PGPDEVYSEALRHISSKGLRFLLRCINHSWTTGTIPVEWRRATIVPLLKPGKSPELLESY
RPISLTSIVSKVAEKMVLKRLLWVWTPHPHQYAYRSMRTTTMQLAHLIHEVEHNRNHYFQ
VSLPKKSGIGNQLHYRPHRTLLVLVDFSKAFDSIDHRVLSRLLANIPGVNCRRWLRNFLC
GRYAKTRVGHRHSDRRPMLRGVPQGSVLGPYLFSLYVHPLLNLLNSFAGVTADMYADDLS
IIVKGQSGEDAIPTANMVLQKLHAWSQENGLAINPSKCEAAWFTLSTHTESDYDREGRWP
LVVAGCQIPVMTMGASRTTKLLGMDLDPRLTLNVAATKQCAATSQRISQLRGIAHKEAGP
SPHDLRTFVIGYGAPNYAMAASSYGQ*
>TCRU_5328 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSVCVTAEDDKNEQVTVPKADEEVGAGKGMDPRPTTSQPPTK
EEVEKKQEQNPSTPTSQTMATVTGTPQSQNISKNTQEKDGGDSNGRTEHTNADKENEQKK
AAAPTTTTTTTRAPSRLREIDGSLSSSVWVCAPLLLATSALAYTTVG*
>TCRU_5329 hypothetical protein, conserved

MTSKKKFKCPSVNPQLYEKSMKPSVTIAMGFKTSHGASSCWQAQVEAEERIHSNWSKKYN
KDEEKRRVEALERTLEREADRIEVYRKDNDALQTILFRNDGVNPRGAAAMYLKARNALSP
QEKYKKPQTSAQDIGWSVPLAMKSEGHFAASRLLNSAARMNQLATAYRRPDDADHAELFG
YSFERPY*
>TCRU_5330 hypothetical protein
MRKNPSLGAFLRPQQRRERDERLFDHDSFDERQWSGQHEMGHRGGVASWDRHDSAYTSYA
DYDGGAYEPGAPRVSDTLQPRLVNDIGLQRALKRPSMRSSRVLAHAMDGARRERENVGQP
REEWRETRFSLKPYENFDSRGGRDAVAPQGDIHEEHAEHARHGWEQHTPSVVGETVYSPR
PLVDVSAAFGRMSSSTLDHMSNVGRSQNASATNRAAPSLSPLPSAPSHGTADASIDLSRA
RESINLEGVNATTKTTPPRLHIEQPSAEISTQDRYRGWKASMCENENVLAGSSWTPVYGP
DGFSVIQSTLPDSGAVGQYQNPNAAAERILYALLQQNEELSTVASHQPNKWGGEKLSLSN
GKETSSAITALDPMARQRLSLHVTPQESRLVLSLVREKDREILRLRSSLATSYRFAAYAA
YRQYPSVPSGKSNALFSAMESRFFGALASAVKNRERDPLLLVDRAPPHVHGLPNLPLPLG
LPYSMAQVCGVLSMINVADMLHKKASARFFLSSWRTYFVVADDRGLSVYRSEEDYKRHAF
QRTLLVVPFRDMEYFVPSFRDVSVAGEDLLQAAEALGAARTRQQESGSSNFFSSLINRRK
KLKAETTMKNKKTGGVEAGETEDTSDAVNSQEDEGRESLNVQRKRPDRYDELMACIAMQH
AGDTSHAYFGFIPKQPNTQSGGKVVNPPVLFRTQSTQEHMEWAHYFAQCFNRKLYREMFP
TALAETYAGSLSRETQTVFDTTDTAALEGHDLNECKKREPMVASREVMAMVQSVEAAAQT
TPREKNDEATNTEEEQDVAGLSCIVTPPPPPTSPPRRSVIGTQEASGSVYESVEEEGESE
IKSNAMATMESALTGEVGKDVPWKELVTELRRLLDTKNTERKELQEECEELRLRVRQLMR
ELQQLKDDRESLLKELEEVHVMYDAAARRVEEAERSFQSAQEAAHTAEAAKQEAVTREEE
QAARANKLREEIECMQHEQEILTAELLALKDGYSEGLRCLAKKALGDIDKLHAVCTAGEY
LSALRGGHCDPPRKEDGWLCAERGEGNASRVGSNDHIMSPRQQGPSQPPHAPPPATSLHQ
PLFHPHRKKQQCDPMHVRSASENSNVPQHASAAKKTSDNSAPADAGEGFLGIAMLLISFM
PQHMAIDGCFTVDESQARLLRSGPSPTQRGREWVILHHDTNAVFSVTAELRTEKEPRHTE
PSKSPQRSVLSRRARLGSSQSVHPKSARRSRERIPRVADVEKTAKRAQSTTDK*
>TCRU_5331 hypothetical protein, conserved
MATGEVLRITAQTALLPDGNLEVSVHNAFVPGVNGSAVIFSLRCSHPKFFSPLEPTVPDG
VLLPGERRKVLLSGPPDGAKWSRLRSDSHDVNLRLGSITEVFLRDANSGVRTHKPLALPA
NGEEESAQNPQPLPPQQATSNSFTDAAVSGGDVSTTGNSFTNRYRERGLPKRVQPTTRCR
GSSTSLPRCLHFSYSTESHEEGETPSTPKRLKKREDACTQMSPLMDPKGPLGALDTSEVS
KSSLAKGTVHSNYNSTSDLLLSSQSPSSTVKPYENSLDFLDLDSNSQPPFSISVENTPNS
SSQCPYFFVYYGKLGSGAKYVKNAMTWLNREREKYVIWRQKVLRCLKGRGESESSLPPLL
GEPVRWLKNMDGAVIHDQKSKLYRNPYSRSSAKMFDSHRRGNGCVMVPYRPSHGDPASIR
ERSELSGVELDKDPLSQNSGGTKKETGRQNGSENMAVGHENGGCSTSAADRPTNTATSMN
SPPSHGNNKSGDGVSKTGVWSRKRSLVSPLDTKVPASAQPLEENLGGCGELPSLATFDCP
TNFHARTETEETVEMLDRTVCGEDYGDCWNKRKRKGNYENKRPIDAEPIEANSSDIVTFR
HLRDRRSNSNLEGISGGLSGRCLENNPSIDEVQSSPVLPPTSEKEEGRSPRCRVETREED
EAYVRRKQSSFNAPRRGSLSFIGKLPPGGELSISQVGDALRNIAVKSAPLMQTAMGGTVS
TVATTAQLFFAVIEDSIDILHAICLPVLSLFSLFLLWMAFGSMGDEDGMISTMNLFA*
>TCRU_5332 hypothetical protein, conserved
MAARTTAAADVPAPPACPIEYPIVFARQGEEAGDEVVPAVGIFNALRWLLPVFQLAGWLP
KQVSREKDEANGTPRGSVGEDVSAEVQETRRLLPHFEPFFTRESKVVPNGALLYTVQTFR
FPTPRGPRSITRALVETPGKYFSPLQEEKGGGHFLCCYEDKQLLRCFTYVQLDQLRFAWV
AVKELLEEHKAVQRTDGTLTGLARRDIKKNNTNSNEMANSERANGVGGSTTATTAMGADA
GSSTAATAPAVPPPSMARKPHPSSNVIVGPTAEARKTREELREKKYMSELLKEECAARWP
HTPVHKSVIFLVDEQQLEATGGRKGRKGPRSYLATVELPLLNKKGGVATFKGPQWCTARR
DAENAAAEVALRALRTIKS*
>TCRU_5333 hypothetical protein
MDETSLPSAAIMTVNGHRGQNGTASPPTSRKEEEEGMLQVETDDVVVGKKGGEIASSDAG
VNAPEPMEAKSLSNGSPAGTETKEVAEGPHTPPAVAPQETTPAKEETADRSTGGDDITSS
ANAETSSQPQPRTGGDASSEEGKAAATNEGEVKRRPAMVGVTAHRVFTEEELAAYMEKQR
QREREKEEVRHTKSRRNSGNGGSRSRGSRGNASSMRIPPIDTNAIHLPQLPHALQQFFTA
PAAAALPLSAGAAAHPLAYQLAYAGASVPPAGVELTIPPYSNPFAANNAPPFNDRLRVPL

LPQQQPQQPQQPFQQPPALCAPWGIQLPSQPPFMGLPPPCAAPGIFDPAAVMRFDQQLQH
MNDFGAPFLPSAPIPNPAPGSMTAMNMQELEVLARLIVLARNEQQQQPPFLFSQKQQAQP
PQYCYYPGGRQSDMENVVNSLNAPNATHLGVNASPACNKMHDGAAAVSPPGMLERDPRIV
VLEGKHNGTDS*
>TCRU_5334 Galactose oxidase, central domain/Kelch motif containing protein, putative
MPIPVRNRGLYYEEPPSGTGGFMAEELEAKYHVTFFRLHDDATNNLVSTREPGLSESPGK
GKRMASVQPSSSGATAAAAARRSSSVTASFSLHTSEELRQPLHQVPPPRSGHLLLPCAPR
RSLILHGGLEVGPEGFLNDTWEYLIDEQRWVQLICRGVPGPARRSAASGGGETDADQAVD
DGMPPKAFGQSGTLFGGGRFLFVHGGVKSGDGGTAPAFQLDIERRLWTKINLTTPLPSMW
GSVAQTLFIPVFEDGTTKRLPPSSSSKKAAAAAAARKREQRRVEVVVVFGGMNDTEAYNT
TYFLYLTTPPPSSGKLQYGEGEKRLLQILPSLGATVFPGRRRACSTVCRDFFFFVFGGRD
GIYFYNDMWVLNAYTRQWIMVREETPLRFMREFFLRPYDKKPGARIMEYVESLLLMRRDS
RRCRMPITIPHRCRHFNSSALWRTGAVMVTRGLDIFVLGGFTYDSRGMIETHKDVHVYNY
MRHIWREAFVDVGCLPSSFPLGYFRKTGNKSSQKRECYGEAMKTELWHVNQENNAEGSQN
WRLIKNIVSMLPEGRTMAAMCVDPVMPGFRFFLFGGRTEDEPSGELYDVRIHVDCAAPSD
TTVMRNRGIQHGGDVTVEPSENTPHVSVQGTRLPSMKCFSISSDDAPSTPREVPRWGERT
LREQAGDWVRAVLLEESVLRRTMGLMLCPDDKVVRQEWLEDAHKAGAKMQKKADAIFPEA
VRLVVTCAPPFVRRE*
>TCRU_5335 hypothetical protein
MHHGATLHESLPCPLVSPIVSIDQCPFQPHERSETRPPHGNASLTFYTARSRCRVNFTPG
PNVTYSAENKYSWNPYYRLETENKSQRLKAAQEECNSASVSGPCPIALTPRQGQCMARCS
NTSSSTAQSPMHTFGCETPAIVSRCELSPQFSSVKSESGRALLTASHSIEENSITESTCV
PQFDNMMHGLPMYASIHPVGEVWPLNEMNNEENVVFDAIKPTRNEQLQEQLYPTPLLVSQ
NQPTVSPYPYVMESRTIQPTYVSYNKARVPLLRFSKMLPPPVRCEAMSILENENPQLPLL
MMYNPVLRWYERIKALLNEDYSAWPGGSCAVNISNNKGVRLELEEPCPTLPNKAEQTREN
MSQWLKECNEWWDRQFFEKSRNGDKRRNGTGRGKWRQYSIQYPYNNHNNNNKAHKVNRGM
QFDGEVAFLRRGGLQ*
>TCRU_5336 hypothetical protein, conserved
MHLRAQDALQVCSFVWKDRWVPIGIKASKTDPCDSRSHCVFFWRCTVNSLDGAFGCKNGV
LSSAHGNLLAEETVPAAFKLHADRLLVQALEGPLTVSHLPREAFAVGSRCLLSILPLVFP
ILTRRCAWLLRLLVCGHCGAPR*
>TCRU_5337 Leishmanolysin, putative
MVRNAIGVRGRALLVVVHSANAAMAAREHHDCDDIDCIELQDDDGDGRTLESHWWRCHAR
DEWMAPIGCAGCCTELIHTEHE*
>TCRU_5338 hypothetical protein
MVRSMVSSRSTLICPLQKSWRVGGSVTWSRRRSPLQLFRQNLLQQDLRALKKTRILVNPL
LELILILLLLALLVQLVLLHWLKVRRSPLQLVRQNLRKQNLRALENTRILVKHLPDRILN
LLLLSLRIPRMSLFHLKLQLQAALVLTLLLVLRPRRILLLRPRKRRIPLPLVNLKALHIL
PLLLLLHPNPHQIRTTETVRPRMLRNV*
>TCRU_5339 hypothetical protein, conserved
MAMKMTGRVLLVCALCVLWCGAGGGFANDEKSGPGNRAELPLASQGPETAPQDSQGSQNR
APGEEENLTSVLGEEADGDDVDREKKAEEEEITERQGSEGGTAAVGSDSRETNLSDSEQE
TGQPIVPAGSISPSNSQESNANLTQTEVEGKKEPDKNTTTVEGALTTVNGEHTLPAGIAE
GNLPPPTEDSVDSREQDGEDATSEGKKNASSPETAATPQRDREKGSEGTGGDTKATIVTA
NTTDTTSTQNSDSDSSTAVSHTTSPLLLLLVACAAAVVAA*
>TCRU_5340 RNA polymerase-associated protein CDC73, putative
MSLREQWCHLVEEVAGINSTDPLPREYTPVEYLPGGRDISEAVLQHIRAAATEFDAESRA
LFHPQMTPEEGYHAAPVVAWQGTFSSSLVKPDGNTTNNINSSDDDEKNNSHYNSGDSGKR
PRTSSSEGPNFFEAYRRHVTAAAAATDVKGGSRDTLFSAAITAATGSGASRSLGSASRLA
SGFLLPEYYSQKHRQPDFIPTILVPASVSSLLQLFNIREFLERGVYIDPPTLFVDEETGA
VNVQENKPDTVIVSPGSFLDTEKYTVAYKMFRVVDDPQQVKNWQHVCACIVDGNEWQFRG
WFPNEPAPVPVSELFQRLCGFLPYLEEEKLPKALQQWHVKPLPLTRRVVKSHAHILQASV
FWERLYTFLETHPFFKLFTVPLD*

>TCRU_5341 hypothetical protein, conserved
MPAKDLSDLLNVPVPTHAIQAEKGPGTRRSSTLRSRMHPIAVTDYGMKPTPVARSSRKQQ
LQAEILDEINGRGSQHRMYAVFYWIFFLLLIVGVARAVFLYWPEFW*
>TCRU_5342 hypothetical protein, conserved
MRPLGLSSRHERDLASESPVLVSVGRADFQLRSEMDQTTVALRQREAQQQRVFRRERAAV
RSRVDRDMQVLLEGVEGVLPPCVIDPPVITETRSSVFSLPEKRGAARTAHATGELLPASL
STSSRERRVLVSCGDNRSKLNGAAEEVKSLQVTGVHRGGGGALPRGFPLPFEESGFQCVA
HWADTSFQEVLLAALGPRSQRERREKDAPSSRFLVSVACYLLNELLTREPKMSVIWPELR
DVIFKAVFRPCAPSSAPGTEGADALFYPRFESCHDFTGLQLWSDAFFASRAENARLQRRI
EELKGILQKSRLILRFAQRRVDRMRLWHTFCAWRKTTQRERSFFDSATAYFTRVRQRIRM
EGCFLRWRRIATHSHGLELLRMLKESEVRLAFVESSNTKKVATLMNQLEEERKSNLILEM
KKEALKSQLAEGHVIALRAIDNEIQQHQANVLMTKKQSKRWERLAKTFSYRVNCVMVPPS
LRKYGVALRLIEDKYALNASVPNNLGIEARRALEAFLLDWVNYFMRTTVGGDFWRPVVKI
NTGLNDGDFGCGALLQFVRALESVYIAKGARCAGSAPPVSRWYEGRRSIEGKDSTSLPVE
EQSDVVFTELRRLLYIQTMEGLYPTLLCHCTFLDSFFTPTLFCRAAHPTAMLWVLASLFV
GYTRLACSGSALVENDLDAALRCQEEGALQDRTTGFPSMCNEKAEPVPAVAATTAKEGGF
AKHRSGGRNSRVHVVSKNTAIQKRLRSKQCNMESFRKRHDEEETDEKATGEMERLADTLS
DLEVYLGLDDQEDEESSSSSKSNSRCASSEGGRTIHRNDDYTELSSTVMHSSSDAREESG
SKQSTNVTRGERQRRVNRKAHLIPPMNPSICSFSFRDFVAYHSRETKKRRLWTGFSRVVT
SLVVRLRVLDVEPPTSVEFNPVSDRKKSGPRTKNTFLSASARSASTLQSRKSIRLVPSFS
*
>TCRU_5343 telomerase reverse transcriptase
MSSTFPIVPGYDGPWSLKDFLQRYFFVRLRFDASPPTCFVPPNNERVLFVRPTGGFAVVM
YASLSAPPPPPPPAPLLVTTGEGEFASKGHDLLPRAASLTPHGRPLTSSLLRLPFWNSLF
TQLGPAAVSFILAWCPVVVQFEPNGGGLQVLGPPLKNAVPRAVNRQRGPGWTGSRKMGRY
ERNAQHRILRGSSSESLISSLYRLNVSRLPLIGEAPLCTFAEIDRRVNPRLSKLWREHHG
GMGAAPSSCRCSVTAGAVPMPCADACSVLAVSRELVHLVFPYTLSINVDEDNTVKMASVE
RHLTHVLHCVLSGVCKMNFRGAAIKHTGFLEERSLSFNHVRPRGEAGACAAVPVSELTVP
ETIMTSYLRSLLGGIWWRAPQATERVSFWGEALVLERLCAITLSWLQCGRHENFPLSHFL
HQMPVAKLPWLRGFYTRGSGRRRRSMIQQRVLLQFFFFLFQHVVPFLVRSSFHVTWSSKK
PNAFLFIPKSVWIRLVSRELRQVCLRRRRRTKRERDGDGAPQPMALPPMALERLTSENIV
GLKMPPGKDAVPAVTTAPPLLYSSIRFLLDQRKLRPIARVRFANARWLLKMADGLCSPAT
PSVCNVSGRAVASTNRTKRSSAVSPNATVLRGALRCLLAGLAEQRVGSSLVKFTNNSHQD
EYAEVRSFVEGARRFFHHPLLASTPVPSAAPVESSAVVTMVRGDAARCYDCLPQEAVMNT
VRRLLPHEFYHTLSFTAVAPLTDGRGTATVEGVGVQGWKTAEEDAPSVGVLLHRRVKLQT
VSGKCVQNGTLPGIPKGWIMYEEPIPPSESVMRGDEMRTVLGQHLQKHLVVIEGRLYSQG
VGITQGSAVAMLLCDILLETVDHSLSNILSQHEEPALLLRRVDDVLVVTLSPVAAARCDA
ALRHGWPEVGFFCQDEKLRCTTVALIPWCGLLWNPQTLEFSVEWRRLSSLVPHIASRPMT
GNEPLHCSLRLMSILCLRTPLTVLCRRINTKTRVVQTLCEIGFLWSRFFLKKLLQNAMFI
RPHVRVLLRPLALAIASLCRLIRRQKGYLERLGSFCDVTDEEIRLCVLFTLHHTLQEWLP
RMISQIRRRREGLKQFFLLISALVRRKVRAALLMDGAPCEGDDEHIAASRGGSHGVAAAA
AAINKYDDVGKLLLAEGDDTVIVRALAAVRFPLSRAFTHGGNLWRLSEDSTGKIAK*
>TCRU_5344 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MGILYTANKTWETIFKYEKTTKSDAWESGKEYQVALMLQGNKSSVYIDGKSLGEEETMVT
GETPLELARFCFGACGMKNSPVTVKNVFLYNRPLNPTEMTAIKDRKPVPKRAPEPQARGV
SQTIASAVSAVSGPEKNAAASAVPMTLNPHAVEEVSEGGAARRNTSRTEDVQFVVPEVSL
NSAGSGLLPLFLLLGLWGFAAL*
>TCRU_5345 hypothetical protein, conserved
MSWARALQNYLVSPPHIRYRDGASVFERVCRAHLHGFPGHTIDVRSLPLLRRLRGEMLKS
GTPEQKARTLETILACYSNANCSYTYDPVRSEKENHLLTLEQLQCLVEAQIAGVPVRAAH
YRFLLQSPQLSQLSPNVPRLLFRKVANAEGVLTDDARVDVSVGLASGGHWEEALQLCPRF
RLLDVIERVASSQRHGWRHACNLVSHLKEEAVVQEESYLVSTAAALALRFAATREMAIGR
RMEKLIEAYFLQHRETPPPKRVIDYFISACSPEQWRFATGLVMRYNGRVEDAARIPLGKV

MALMNGALQWERALLLYQAVPSALSSHERQHAAVHNHALVALAKGNLWQQAIRFYASQPA
KNLHTYNVWLRMVVLERRIPFASVWESCIEALQHIENPDHRFAEGLAHLLASIGVWAAAL
NVAKAASEKTPRVLITAISAAAMASNERVAWKAAKELSSYRRGVSAKQFCTSVAIVGCCT
KNVPQDLTDAMADALDSCTISQEQFDDAMCHLGRCMALLGGAARNDTNAEAPSAIRLILR
REGAERNAESWVFALALLKKMSDRGWSLKAVAPAMLSSGLGASIAIRFLPG*
>TCRU_5346 hypothetical protein, conserved
MLRRCGVCRRTAFVTDVEGDLSYFIRYAEQSRVLSWINGRLEFRDETSHFVYGGDAFDHG
DDIAFAKTLLDFRDAYPSRVHLILGNRDINKMTFGAPMAKVFGTSQLSPEAAQRLVFPLT
LTNASGGKEWYSYAGYLEANNLPSVVTKVTFIQWTLAYKMGAPNTFEHRRRELQIMRKGE
GEVTDVEVAQSFLDAACPGGVYYEYLKQGKIAEVLDGVLFVHGSIVDQNFGILPDKEVFV
DGAPLKRCNVSMKDATAEEWLGALNGFKDEEFRQWASGGDGMLLRQYAFPVSIVPHSVVV
HALVETDGPHYLGLDAVEFLNSSGISIVCGGHKPSGDTPSIVQQPGLLRLAADNSYCAGD
GTRGESVVEVLLEEDGALCIHGRRADGTSYGFLATEAPLGRHLGDGWWVKAKVGEDSFEA
QRTRDAYRTRDAQALTAEEVEARLRQWREPPVGGNVPERWSKQRLDQKPRVVKVKRTGGG
LGKSGTVPPPKKTV*
>TCRU_5347 dynein light chain Tctex-type, putative
MTEKLTLADDAKDICEEVVSRHFMPVVRYQHEKIPAMVSAITENVVQRLTLEAALPRKYI
AHCVVFQNNGAGFNAISACSWNPASDACYVHHAENKAMHCVLTVYGVVA*
>TCRU_5348 Anaphase-promoting complex, cyclosome, subunit 3/TPR
repeat, putative
MTYYRERRKTLTVQGLKDAVQESLAKYLYDNAIFCAERLYALAPTHESLHTVAHCYVTSG
DAGTAYRILRAHYPYLLSATPSFATTNSSTSGNGTGVGSNTAADAAARWDCQYLLGVTCG
MTQRYMEGESFLEELERQQSSSEVLYWLGVCRRHLRRGYAEEAFAKSAVLDPLNFVAFEN
HVKMTRTPREEVRCIYTDAAPGVGAEDAVRRSSMSGMGMGGVGGAHRHVKREALRLYLSP
FASVTFLQWTYRCKEARALLQHESFPERDSGWAFGALAMAYFHDGDVENSTVEFANMRRV
APWRLADPALVYYSTALWQRKELGTLGSLSQTLINEMPASPITLCVVANNYSLAKESKES
LCMLNRAIQVDHDFAYAHTLRGYELLYLDLKSEAVDAFHEAILIDGGHYNAYAGLGELYF
RSEDLQKARNYFQQAISINPLPTIMNRYAATYHRRDATRESLNEALRIYESAIRRHPTNL
GARHQRAEVLIRLGRFHEAHDELLGMTKECPDEAMLYVTLAKCVHLMGLTGQAVQYYHTA
MDLDPRRVGYIKSCLERLAMGKPDVAEANA*
>TCRU_5349 structural maintenance of chromosome 2, putative
MRVKSIVIDGFKSYAHRKALEDLSPHFNAITGLNGSGKSNIFDAVCFVMGITNLKRVRAE
DPRELIFRAGTTGVHAARVTIEFINDDPRTAPPGYSCEEYPIITVGRQIRLGGKQQFFLN
NTVSMQSKVKRFFESISLNVDNPHFMVLQGTVHKLIGMRSQDILSLIEEAVGTKAFDHRR
RTAENLIRSKEKKMEEIDNNIETQIGPMLRAMKADQDEYERFVQMSESIEEKRRFRVAFE
YEEQRQRLEERTERRAAVERDVVLSKEQLKLLPASEDASTRRLMELQKSLATPAEAVISL
HEEESLLKKQLARDEAHVEGAEKALRLLEGNFHKLEKEKGKQAARIEQFASKKEQREVLM
ERLRAEKENVAKLKRSLQLQTSGVRAGMSGLSLEEERADIERQLIHHGAEARRCDERIKE
LERQLKHFVQKAATRGETIAKLEKELARARERVDAEAESYAVVAPLESQASALQEDLLRL
RAEYWEANDALQREMGNGGRGFDVEYDRLACPGIEQHIHGRVAELIVPKEEKYAMALMVG
AQTQLLRVVVTNDLVAEKIIRHGLRQRTAFLPLNTLQPSKGVESGRMEEAKRIAARKGGF
LAIAKDLIEIKDEAHCIVAEHVYGQFFVCSSLELAQELAFNPAVRCKAVSLDGDVAEPNG
LMTGGSTQRLRDIFAEIRSYHERKAPVGKLRIKIAQLEAELEAVQEKLRQNAPLIRRYKE
AEEAMGLAEHKLKLEQGETNGPVEELGAVLDEERRKHEAECEALRELKERKVALERHTRE
DPDMVRKEMQEQLSMAQKRCCALAREEEAGSAEFERMEAEIMQLAADLERKISEVQEEIS
QRTAARDEAKAQLDETRAKLGKVVEQLQRMEEQRQCLEKEVEEVQQELQQLLVKKSSLEA
FIKNSEVDLRDAAKAAEELKKSVHEAEHRHPWLVEEQHTFGRSDGPYYFEDKARTAATLQ
ELREAESQAAVMSKRLNRKATILYEERKKEYDELVLQRSALGEDRDAIQQCILGIEEKKW
HALDRMVKVVSSVFSKLFSTCLPGAAAVLREERDDQHHLCGLQVKVMFNGKEKESLSELS
GGQRSLLALCLILAILRVRQAPVYILDEVDAALDPSHTQNIGRMLQTHFPSSQFLLVSLK
DGMFSNADVLYQVSNTQGYSEITRIESGAGRG*
>TCRU_5350 protein kinase, putative
MNLEREDLSYCEHQGVPLQSEPTRIDFDEGYYVGTVDEEGHMAGYGKAFWTSGDTYVGEW
LDDTMNGRGVYTWADGDCYEGEYKNGLQDGFGVLKDATGVYTGEWVDDMRQGIGKMEYVG

GSVYEGEWIANMRHGQGKLTEETGVTYHGEFVQNEKEGKGVMTNAEGDVYEGEFARGKPN
GKGTYIWADGAKYVGSFRDGLKHGQGCEWMANGDWVAGVFVNGEHDQRQAVHKAVVTDDV
HQNDQIDLADVKFLDVNFLRMLSEGKFPVEDKKYSNYSNTTSGVTGSMDDTPRRNGNASG
GLPLAKSLAHLEHGNIGSSPASPVKAPFKQQGRLMLTDADLEGWRQIKIIGKGSFGAVYE
ALLVSGRTVCCKVIELGSLSDREEMDKLRNEIALMKRLHHPNIVQYHGCQEDRSKNTLNI
FMELVSGGSLNTFVKKFKTIPLPTVRQWTYQMVCGVKYLHDCGIVHRDIKGDNVLVSLDG
IIKLADFGCSKAIDDVCSKTHGCQTMVGTPYWMAPEAIKCEAGGYGMKSDIWSIGCTVVE
MITGKPPWPECNSMWAAVYKIAHSTGLPTEIPKDLDPKLMNFLELCFERDPKKRPTAEQL
LRHPFLAI*
>TCRU_5351 hypothetical protein, conserved
MNATDCAHRVVLKVKVAAILHINSVNAKDGLHTVILLRYDQRIFLRNDPATINNNTDGEI
NCVPIRLDEVVKQQQRRVRTKGKFREANGVARPRQELTARHQYLGAYAKITLKLQSTQIQ
NRGEHAHVHTRTTPSDRQAHEDALQQRDVECLLWHVKIRQVQHDRGGEGHVDKAQTTHTG
IRIVHGADAATVHAADLRVGGIGERKRAKTVRNRSWQTRVAVATSSAVCECRRDAARPCC
KAHGVHGARTTVQHRHRCSNIEVFSVIRHERAPCLVAHAVDGRARVG*
>TCRU_5352 retrotransposon hot spot protein, RHS3, putative
MMELEGRGVVATNRNVLLKEFLKDPTGYIRDAGALGEIQATDAYARMEGTVREEMGLEEV
VRRLSEKGVNNLLRWSEAAAEVKATVHDITKNSLNAALEWPRILTKTSAPEKLEGLYESV
YNARWHHVVEVSDGEGTGMEMREGEPPQSWTYKAFG*
>TCRU_5353 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MSRRVFTSAVLLLVVVMMCCGSGAAATEKVVDPKFEWEPITDDKETVESLGAPGLLKVGS
DVFAVAEAQYKKNGDTVFTGIASQLLTMGTDKAKEEVLEDAKKVTQVLEKNVSQGEKKRV
RVSRPTTVVKGSDIYLLLGKYNRNAAGVQDSGEDDSVFLLVKGDVGGESNKQIDWKETTD
LSRTYLGKELQSLEGLIGSGGSGIETEGDTLVFPVEATREEKKDVKTASLIIYSSDTKNW
NLSKGTSADGCSDPSVVEWKDKLMMMTACDDGRRRVYEIGDKGDSWTEALGTLSQVWGNK
KENEKRVRSGFITANIGDGVGGAKRNVMLVTLPVYSKEKADEKEKGVLHLWLTDNTHIVD
IGSVSEKDDAAASSLLYKSVESGDQGNKEEKLIALYEKKADADKPSLGMVSVLLTEQLQR
VKKVLATWKKVDDRVSKLCPTENAEEDESTDTACSTAMPTNGLVGFLSGNFSDDTWKDEY
LGVNATVNKKEAAEKTDNGVTFKLRGSWAEWPVGKQADNQLYHFANYNFTLVATVSIHGV
PKSGSVPLMGAKMSDGKNTVLLGLSYKKEGNWAVLCSGQTTEKLGRTWEPQTTYQVAIVL
HNGSQGSAYVDGKLVGSAQCEYENTKDKEISHFYIGGDGSSAEVQEEVSVTVSNVLLYNR
PLSSEEIAGLAKNTITILKPKDPKTSTTTPRSPAVSAPDVEGTVTQSNSPGQLPLEEETL
KENIGGGAGDVSSAASVTTTPSSDFARTVMTGSGDKTQEDGLPQTPEVSVSSAEDEETAK
RKDVQGEEEEIHSHNREVNATALNNSLGNLSQGNNSDAGTVRGSGLLLLPLLLLGLWGFA
AL*
>TCRU_5354 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGGVYARDGENNAQGGCMVPGGFGKKALYLASGCDKNAP
TLSLRSVLPILVIQAGDSEGVPSKENNGKNSILVGGVAGPDITAVGAGGGSGVNSARQDG
DGSSQTGSVPGAVLLPPAGASGVGGNPSGSVTPGGVLSPDRSVGTGTSASLSSTAQSESE
KKVLQGDEEKDQSHQLPNGRAPDTPVVETQSRGSDTTRGQDVGDTSTLSGKEQHSSEEPE
KKDGDSDIPQTVNSPGDPNKESQEKGKALPELSNAPLPEPKTDHTKMNPEKEKNGRQKTS
ASMDSPAKQEGNSEDPVSTSATAESVLTGNQEQAATTSSNDSFSPFQKEISAEKTTVENS
QPSDTAQTEKRQSGDKEKVGDNDGITAVSHTTSPLLLLLLLVACAAAAAVVAA*
>TCRU_5355 hypothetical protein, conserved
MEEANNHFSARASNTAVADGLFAQRESALAGRKSQLETTPSPTPGTRGTYRFLGSAACSL
GCRYARTAGSSLFQKRAARCARARVRGWRNDTTPPRAFDGWGRVSIHNSPTHFHGRATAG
QHSYVIGHCGQPRFPHPVTSPFRSPDSEEVSVSNEVDLDFLQFDVTTWVPRIWNGGILGI
LFEIRSACDYWHRGDAHTQIAFDILFLWMRVAVTSGTQQAVYGLGQDYTAGLPDADRD*
>TCRU_5356 hypothetical protein, conserved
MGEYLRMLCELGVPVECCASDLYSSGWCLGSIHEMSARRPMDRCPITDPALDLRDAAAVI
WRGEYLSAVPGDKPSSWCLETLPANTTDARDTEETHLGAAMHTELKCLGMRVRLRVTEEG
NARCAPCTTEATIAWAAPRYDEGKAIFRDHAQVCTISATSVSFLPVVPWDGEERVYGAGR

FHRRLLNKTSQGTSVPVAESIDPGRGTPPKDVDSAAPQKSPSPEERQSPQTLRQATVCSR
PTTTPCTISREKKKKQSKKKKEKCEFK*
>TCRU_5357 Rab3 GTPase-activating protein catalytic subunit, putative
MGSRGEDENEEETPLEIEDYSCNTHFEEVVGEIERYLVEEFSKRQELQRFLVNPLHPHHS
HDERDMAARGSSNGVGEIVFGRSFFIFPEGGYGRGTSNTDDEGIAVEIHVQNGLRENGKR
QRQQKLHPIARLFALPLFFLARGTTTAPSYRTSESSFYLSLLTTAVGRVLRGPLSLRFDG
DPSCLPSPFFYVNGMAPCFVSVGDHYQLAFKGVAPPVMVGHAKCSTTEPWTLQQLIAQPV
VKCRFHCSAYPHPPEWCQRISDQLDMFQLQIGPQSRVQTDVFDGICVSLQRTFRLNVPRR
FLENYYAEVEPSSCGDVKARSSTLLWHDILELENETMLLSAGPTNFPFGTGTAPLRGIDF
CFQWNQLLDTEAHDGGRRNSNLNPFAPEGMVLQNKLTIRAMAIPKKECELNHTACKPLSE
YVYMVMEHVSPGESLREVEGYSNILTCIADDIVFGHKISLARQKALIDRLTRHEGQSEKV
KTDIRHIYFPGSLLCRFAYACANQIHNLDDVLPLWLLVVEHLGDLLESKGERRQALEELI
GIIGIPDVEDIDHGLPLLVQKLQLLSYCARRMLCESKSVAVKQPADGWDDDMDDLASHSR
GEASAADGECSADGFLISGKCLITNGEPLVEPKALPTPPCTSDVMMMKAQELQNLGTESA
GRHTRAWIQSEGLFNDMCLFLYFNRAQEGRVVRFPDFVQWHSPRDFIPPLCDSKEKKDDD
DAYLSERMRRHSNAENGLVNIWWPLWERATPRSPEEIIAQSFVPHEQARLIIRWMEKELS
ASELLIETVHANFTNSLHRILSHRCMEGNREIAAYAQCKNESIAKSIKAVMQTDGSAPLD
NEGIRTIYCSAIRQIGEIETCLCAALAIERMLGASHGISDAAPPHTDEPCTSMGQLIATL
ASPIAEKEEEDDHKELALVEASLNWNLWQRGGIANRFNEDDQNPVTMRLRATCMAERPLN
TTACFQQMFAEMDETGVFRVALALADEVL*
>TCRU_5358 PUA domain/NOL1/NOP2/sun family, putative
MISFQAFAESAYVYAAPATQDYVQSTVFTPLGFGPSYSSIFAFPPCTTNLRLVGIGTRSL
ATQAHALAVYLQDDRGFSVKTLHEWGMPYCLSMVPKTEKEGEGKVMAAVTRNLFPGVLGV
GSPVVVVNVGCAEAVLRGSDVFAPGVVSFVGSFVAGQEVFVGVYLQPASASTSAGGGTDR
RTLLLCVGAGTALMDRREIIRGRQNGVAVRTNWTPMAQPSKSLLSSMLDAAVATLLKAGA
TETSSFFLQNYSSMVAVDVLVQQFSSIDIQREGPLAFLDACAAPGGKASLFLSLLHEKVQ
GLDSSLGKKDKSSDSVFPTFTLTCCERSKARYKRLLDLLELHFGISIVKRLVRPFCGDVN
KLQKTQRDEDVDSMWECEFHGILLDPPCTGMGLRPKLNAHLITPQGIRDSADYQRKLFDS
CVKMLRRTGTSVLVYSTCTITLDENEANVLWALNTYPFLRLARAKTNDKKRLCLLGSTNF
ANGRRFLLEEEIQKAQRRNELLESHTASTERGDTDEPENPLMILRFMPGLSTMPEEDGVG
FFLAVFLCQYHADEFPKHAEL*
>TCRU_5359 hypothetical protein, conserved
MESVDTRRYQSFQLLELFIDLIHGDLIRGDVACRRVADAFVSAYEDAIRWLVTEENTFTP
ALKGAINTYCARHVIRTAPELLIVSEKAVAAYKQIADVLFETEELSHMGKAMAYELSHLK
RRLETKRFSRLVDLMADVVVAYMQKAFQQHEEAKASCMHLQKDPAFWVSVEKFCTSSTRI
ENEYITMDKKRQREEKKEEEVLQVDKNRVSKEAPMRGFSEELRLAISSPIKSHTTQAIST
RFIACAQPSPSPPSIAEAEEEAKRSKEPVKCTGRALLQANDSVLAAVEGMGKRDFQTAQD
VSSGFIVADDSGVSLMPAPSTMRKVVMVAGGLNETDASLLSDDVHVRSYVLCAKTNRYEP
QASRRSLP*
>TCRU_5360 hypothetical protein
MVAGRLIGVAFAIPLLGALGWTAYTSRGVRNVVVRNPLDISPYCREAAARTRRNGVPCLI
CAFEVPVVVSTAKMRRELACHPSDGALYALHALLSGCFIRVEVIATAFTSRWRLSDAYIC
WRSVSRSVLSENRRVAIRQKQQWCHDTSGSVDLSSTYGEWEVLCAQNENSDGRKEAVLTH
GPEAIIVSLEPVVEGSRQAVLRLCYLVQPFDGFERNTMAERVALWGAEKYGKLLTAQTAY
ALEQMEAF*
>TCRU_5361 protein kinase, putative
MKKYLHPVPDLEEDRFGVAVSDPMDAPEGLSPMTCGELAIVPSPSEMQIASRSENYTARR
SRSPYGPLSLSGVCPTCHRPLSEGVAESFSLPSNERRFTPQYFRTLVQAHKQHLSICESP
SLHQRLEEKEKTEASQQIRMSAGLRRKRKVHLGNEEAEEEEEEEEKEEARVADRFKEAND
KLMGSPKGEDVTVGSPGDNINNGNTTTTSSSGSSSGYYKCYFREIQKLGNGTFGGVYLCQ
HVMEGVALGYFALKKIPVGDNAEYLQKVLREVRILEEVKRHPNVVEYNHSWVDIAQIADF
GPPVRCLFILMEYATLGSLDSYLERHGMALPTIAVWYFFLSALVGIVHLHQKNILHRDLK
PQNLLLTGAPEKPPRVLVSDFGTATLLNELSYERTGGTGTIEYMAPELFECTPESGGTYI

HPHTKATDVWSLGMILHYLACSGTLPARLPNGEVVLNVEECAPYARPPEMIELIRVMLHR
NPKERPTCKELLNSTVVQTILRSFEKAKLSTDILPTTAVAAAAAATASWRQKKRNQTGEP
MHLDCRGCDPPNPRLQDGGAPNDNEGEGILQYPHSPVVEVPLMLQYKTMELKRNISAGTR
GGNKGRKLTTVDRAVQTDYVKIVYE*
>TCRU_5362 hypothetical protein, conserved
MARTELEEWDAFGIFDGPPPPPTTHLTVRQYVSLVQRIGQCLGISDIFFRFNLPLAGNDD
GDDVALNACGHPPVCAHLAREDGLHAMKHPDLLPTVACDDVNMAVHGPPHVHCLFCLHET
QGTHGPVVIPDLRQNILGHCMYHLRKRNECLALLEGEAVAHMGEIGWGVDLSLEAQRGEL
EKKAECEGRHGCFIASASTAACPIVVTYCVLCDQLAPLATFVTVPKETEHDGNKNYNEQR
QGLEEEEEEEKEEEAKSMEEAELILARILLGCEVLYLLRRERAQAGRVSLPHVQQERYIF
LATPLLFGEDREELTDAFESGAMATYGSVILPMASVSGTPEAPRLCLMNREATVHFLRDQ
LPPYQFTDAVVGFVMEWPTEAETNEKVEWVLRQDGGLNVQRRLVYVEDRDEWVIARVFYH
QETASLESCSESRVERMYGGSLRLRKDCSVVKMLPVSLLQQYTLQDHCGREDMAPCMNND
NNEMENKVDAMVIEEEEPMGCPYSMEARAVHFFVGMTALAKAMKMVADHMKEHQP*
>TCRU_5363 hypothetical protein
MAICTYLLSRIGEDGGEVLLRQSGVITTNLDRITDPVNELVAEETMTQLHHGTYRVVSLL
KDGSGDAIQFVFKAECRPASRWHGQQGWTEVAVYHFQQLFYEGDEWAYPKAELARGVVIA
ITEEQLLRVVHRDRCGVLTEKDMVHLSRNITHGKKFQRRDHIVVTGKSKKATVLMIGVAL
TWRDGFDDNTYPSASVYAPYFLVPPFYNPIKREPIHRFVLHEMSDVMVFDYLLLNPDRAF
GKNWFRDKATHLHSALIDNGWAFAGQKFGSSVCEVESGLLHCPSPLRTWSNQRRSQWRCT
PRDHAMTDFEAEMVMKARRPGLLKWCRFRPETRHALNRTRMQWHNENHASTSLSQRWIEK
MKSDTLVAFLLGAYGEETSKNRFNRALARYVHECPSHPVAKEATGYKMSSLNLLHALEVG
LLARMDRLAAHLEECLQECGETYVYAIDVEN*
>TCRU_subunit mitochondrial RNA binding complex.1
MSYRAYGGGYRGRGGRGGRGGQHWQQTACEEDTFRDPSNFNSGSPYAELRNYFNSVEGVN
YGELKSLTNASFALSESVRCTFLAIQSDPFAPGSQVRMSCPCPFQLQKILQCSELSSCVP
CRRIAAEDYILRSFHDGHRRGVARHHSGALHVMRPSQHVLERSTVVLVNGDRERGGVEVH
LFARVKLPGHGRRIDGHGAIRIFYDELLPIMERCVVGLDEEALYQHVTCVHDQEHLRGEL
RAAGCVAFVANGSVLPRESGNSDRPLGKGAVPFVSPASLERTFHLPHSGATVTGMGLPHG
LILIAGGGFHGKSTLLRALEVGIYNHVPDDGRVYVTVDPTAVKIRAEDRRSINGVDISPF
INNLPFQKTTTSFVTSDASGSTSQAANIMEALELGSRLLLLDEDTCATNLMYRDDLMQQL
VPREQEPITPFVDRVTDLIQNHGVSSIMVIGGSGQYFPHATVTLVMNAYKAFDCSERAKE
ISRTFMSSVQPPKKAISAFVSPMQRQFDGSGTFSTVHCRRGHDSIKVSGVGVDSIRFAEE
TIDLSLVEQIVEEGQVNAIAQCLAMLYDGEENGIRTILAKGKSLKLLYSPSGGSEPRNVP
FYSEFAALIEGCDAALRDARLEARTPSCYLPRGFTSAARRFEIGAALNRLRTLRTLTAAM
K*
>TCRU_5365 Tim10/DDP family zinc finger, putative
MQPPQANPQLAGLPQRDAVVLAEKLQLITYDGFIHCARQCITHYGEDSLPYHPGEKSCLD
RCISKVYNGLELSRQLKKEFEEKVKRGEMPYRWMKEMTAAAT*
>TCRU_5366 ER-golgi trafficking TRAPP I complex 85 kDa subunit,
putative
MEFKQWVENRYRHPVVLVFASPMTEQACRRNGMDLVQMLRPFSVHPTELFAHIGDRADTI
QVRKFGVRFTRLDCVREVEALQSARYFRHLLRDHVAMELAYGEQLDRAMSSLLKENGGVV
EEPRLSAQVASQLLERSHPAWYSQFIRDYAYVVRCSHFDTIDHPVGCIYAASTLEEGGID
GIMREFREQQKQPVDTRRNMPCMDDELHSYFLLVHDITEGPPIEEVRRMLAAVKAQYGHA
HCAVVKINSVVNPQDVKNMDPSLWIDANRLALDVPSRSAVHLAQPSQQTNQMSSPGDGVV
RGNNNNNSSSSSGGGGGGEQKPVSGSSSATVNVVFTAENSSYPNSENSSSTPASLHFPRV
HTMFGKWPNGMAKITGCHMSPEDVEGLRDVVTYYLSRCLFNFLERKLRVLVLTINEKRTT
TFGKVAAWFRNKDEVKPKTDSWVASHDGSPTKYLAGSLEMQMRRAADILLALADYDSAIS
YYRMCRNELLSTVSLREFNKPLIAACQEGIGVCEFLQGRLPLPSLAPWMTGGTSSKNSGD
CRLEVAQNDYVECRVHTYAFRLSLMLYEYSRTRSPPALDRAAASLIHVQRVGIAYRNKLY
SAILHELLASVSLFLNPPQPAGMTIPALLPNNFLLRSHVRQYARQMIIAGSAYLDDNLIE
NALRCYLRALRVCGGVGRRGSWQLIFEHIHTLLAHMYRKIGNQIRGMVMASIAVSMATPM
YSNLRTGLRNFESFWSRQRQVMENLGYKLCPHMVAPCILPESIRVSANAFHCDEVTRQES

QVVSDELAEVEWHKMEDKLRQHYTGYASSSPRHQLNFREEIRKTQRDNAVVCMRRYSMHL
TEPLEITVTLRNPIGGPLTAEKLCLLYVAKQKPDQLWKSASSQTVELQAAESKSVTISFS
PSEEGTYVIIGFCWTLMGLEGYYYFATETYKASDDGGSDNRIGAFEYAVEHPMPNVNSPA
NMEIEVAPPQAWITARLDPELPPFMRDGEYCQTTLVLTNGSSYRTARSITLQRSPKNAHV
VWMEPFGLERNIDAEATFVLEQELAPKTSLTLPMTVQAHHSQDSSSRCKNNVFFLVGYIS
GTAKEEDALPSFSSSSFLASLRFHRFFRRVVVKSAILLSSMVLPPANVTMATAVLITASN
VSEAREPPVRVSRVMVIHRPRWRVVPTSLGNLLAENALDCILSSGGALCVPLSVVSETPS
SKATHTDATVVHSRKLIEEVCIPLSSTLAATSRRIMVEENIGAGVVDSEMNSYFMRCSFR
GPGTIGEVKVPEGLPFYLDKAGAAGKSAGSDEGAAQKQEEQIYHPHHQQTQRHSTTVVPV
VEPFTPICVAVVWAVEERGRMYSGQMFHFVDPVCFLSSCEFSVGEAHDRLQEHLCDSMIK
DHTLHPHHGAMFYHVEVPHTVETTADNPDVAIIPVTVHCRSLAAHPLLVTVKTTMPGSPD
ALPSPMLSPVPLTFVGKTSVGFLLLPHETHLLNFTACAFAPGVAECNHFQVSAVALKPPQ
GETCGSWRTGTSQSALMKLLGENTSCLGRNPSMTAGVRGGEINVSGGDGNKCVSSGGKDH
LGGVEDLLRDGVQTVILGHGMAAITHVLFVSFSVETRRVAAETVAARARAYQEDAKIYEK
QYREFEHRRALLNFSSGTTFQKADDLLVLYPPRARKLVEGTQDTPHGAAIGVSIGSVGQT
DPSPWHGDREILRGIVGSTSAVMLEAVGTTSSLVTDEVVEVVADVEEQENQEGLQNVTVP
LEDTSKSGTDVSCSSTTSTDMSLESTAEQNPNTSSEEVYHTTQQQ*
>TCRU_5367 hypothetical protein, conserved
MTSSLLPFTNVKVLLHVRESIFGDDGDLTKHYAKKALRKLGASLTLSEVTADLIVFHCGS
ESLLENATAHGKTIVTPAYLQECVKRMERLPVEGFLVRPRMAPAQRKKAKKTGCIGGGPQ
EERPTFMTSTGLSTIPYLDDVAEAEVEKDGASRVKGSERQDGATARPTAVSSVIDYDDDA
DSMELVVRENSFSSAGRRREMPLQPDDCNSSGSPLVHVSASTTPFKEAVKSTHRGIMQST
SSKEVNLGVDSTKDPSALPCMGARRKALGGTMPAGRAAVSSSSSLPTATVRRRATNSTEE
IPAVQRKRDRCFTDSASDGHVTGAPSKKRNKAQERKTESGTHEEGATQLTMAFTDTCLIT
PLFASEPVAKCSTRHGVTHLRPPTSPPQLRVAVAGDDDDGIQFLCDIVEQLGGVCVPRVF
GRVRKPTQLVLEGRGELTPMVLLAKALGIPVLTPQWLYDAIGLGAFPKIIRAHLHPIYST
HVTNSDDANCSGGGSGKEENDGKGGRSGAIPMHSLRKDAGVEKGLVGLFEHDVGPYYKPI
FLGMVVALVSHSPLAHADQFMELVRILGGFVSRSALSLNLSVIVDLRCGAAASDAQARKE
EQEDVGIAAEVKGRKPRRRALRRAKAGSASETQSNPMTYRAALSDGRNASRHDSHDVLQR
LLAQRRQHNLPAVPVVSVEWIIQCILLGEVTETAPFEVAVNGRERVGGVETDHSIEKKHT
EENYVIAMTPPRQTMWIESDQRSETARSHVTIPRQPHVVTSPFAKTSEGPSSAMKRAEQQ
LSTQQLLLSLDSEDE*
>TCRU_5368 WD domain, G-beta repeat, putative
MPIFERVLRHTEPEASHESLRLEWAFGLHKDFRSVIHNLSTSPSERVVFYTIGHIGVIYD
AVQNTQRHLMGHRNMIIASACSRNRRFVVTADSGSGQANSSSFSKDSIVQSSIQQQGSTG
VERIEQQEERDVEYDSSLMIIWETQTGTPVRTIPTGLYGGVVACAMSLDGMYIATLNRRI
PQEIMLWGWTAENEVDDEHSVTDTLIEDLALASNIIPEYRQLIPAQDEQTSIRFSEDDPH
LIVTNGLRRVLFWSWAERELKYYSPPILAKNLKVAVGNFTQTMFVPGTSMACSGTVDGDV
ILWEVQPRDRVTKEQDKTMLKMVRIHSTGVSFLTWTSGYIVTGGIDGHVKFLDPKLRLVA
WFEDLNGGAVTSISFDRPPFIALQAMDELRREFKATTQKKAALVGTTAVGEFSAPDFMIS
TAHAMIIDVASKAFHTGNAELLRGKLIVQGQEKGIHCIAAHPKLPQLAIAGHSGDVHIWD
YNSKRVLLLSIFQGSHINCMAYDPQGVYLAIGCTNGLVKFLDATTLEERKSIKPKRTDCV
TRMAFSDAGNRLATGDSAGCVSLYEFDHPQGNTKKPMEWDIVGRHKTHRAAISGLQFGDD
GGLQRLLSVGEDKRLVEYDLIDSEPESGLLVQTAHKITQGSSPTGFLWVRENGLVSDMRR
RMQANKDAPDDLLLVATSDYKMTVFLSDWSRQCIKSVLSPTFGGPVSEMFTVPSLPGSEK
RCLFYATREKVIGLVKLPLLGDPCMSTGVVAHPGNITSVARSYDGAFVFTAGGDDQSVMQ
WRVNGEGIAPPNEIALAESAFIEGGDEVPLDHLIAAVEGGREGQFMREIVDYFYYAQIRL
QGEETTAKRELLGAVPFSQLPNLFRALGYYPSELEIGRLTYEVANIYGPLEELVEECDVG
KIPLKFSQFMRLYVNYRPIYGITRQDIESAFWALGADAETGQIARDVLFKLLATHGEPLQ
QEEISAALRSLLGEGVRLDMLEDTITARAFAENLLGFEDYETVGAEAKVPEELQGNNDDE
LFLDE*
>TCRU_ubiquitin protease, putative JAB1/Mov34/MPN/PAD.1
MAQMMGTLVLPPFVVAAIVEHAKRRRNSAGYLVGSRSGNQITVTDYIPCTHESTSDVRTR
AYAEELKERVSLKKCYTPSITLVGWYAAATPEPGKERAFDLWCQAPGASFSKIRSHNQAV

MLLGRMPTAADLGIRWEAYITSNMNDGDSLQCERMQQLTVSIEAETPSMNVLLAEMISKT
LYNGSMPYPTNRITNLDRVALEAESRETEFGRKDNSRNDAEPRPVEAALLNVQNKLHQAI
SHARAILVAGNKNKSERQNESAAVVENYETILAEKSQQSSRDDFITESYKDALMIKYTAA
LLRRHVMEIERHGRQELKEKTQHGHGHGQNKTSSPRGPRKLGAFR*
>TCRU_5370 hypothetical protein, conserved
MAANNVADRDGYNNNDYGTGEITAMREEEGNAAEQREEMAGDLTGQPEGQASGGQISEET
SAEDVLQYCREMILRRHITPPPQWRRMRVDLPASIAELRLTPSAPEQIQITPPITPSPCV
VLQLDNSVPEGMTTKEYARSLVKYVMDLLAYQRASTAITSLRFVKIGTELSQLVLTFGRD
VQLASLVLGEFAKVGLRAGFGAPVKEHVPNATFRVTDYYMTLHDGTGINTEDITTLLGSK
RSPQDIVVLAGYEPGVFYAAMRRPEAVYAWLWNPFCSFVVQRTLFEQCGVLVTMADCPHE
FAGRSRATFASQQQQTGRGRRELEGDDHNNNDDDMADSGVEEDDDENDDDDVNDNFKKNG
ENDDDAFVDGFGRGGRAAKNDAPAWSRNAKEEIDIFEGVEKQTTRQAAFPGFVDDDITEL
LHQLNAEKHQQQQQQSQKQKQEEEVEGLQQQPAMYAGTAPPVVSYDHSVDGMMASMPYTQ
APAMQQQIQSQYAYYGGGPLLPPWQKQHQQQPQLLGKTVPSMYGTTPASNDIHVPPREQN
VNYPKLVDEDNINNTFSDTGNEEDMESTSRMAQAQQQQQQGQQQQQQQPRPMYWIPGGGS
IPVVGNGGILYPVSSPSPYLTHPFFPSIQLPLQPNPIHDKMNAMPSILGQPVYSTPYNSV
GVRVGIQNNTNQHSNVGILARPPATNAPLPIPRVMTVERAQELASRVVELARIVFTTSSS
SSSPAAAAVVVVGGGGGEETAVTLPSTDKMTELDATVSITSPENEMSSTSEALFPQVPCT
ATVPRMSAEMEDLMSCIREEYVQLKEVIENSSPEMQESHRRIVSALLTHRSHLLEISEAT
DWNPQEESNMDEERTRSLQLPALLPYLLATTEGTELVSAIASNDTEQLLPLLTRYVLPFL
LDVTVVRSVVTVALRAEPTAENPLVKRILRHWEALANWLHEYINCQAAAAEVRAEGEIEH
ASVTLPPSKSTTKSNVVRRLTSHVGNTMDMLLAAMSAEQRTSTKAYLDTTKALDTFVKSL
QTVEQRESVQDIEVEGEKQRTAVVSHKFMTTLWSAEGAIHRSLMRLYLNANLLDGTKLVD
LLFAPQSSLTRDQYYFVLVAFSKSLVSQVLSEETARACGAFLRLMEQKFLNVEPSTTEDN
VSGGGGGGKNNSSSSSSTHVLTEKDAVHLVDTALRAIASAEVYSYLRDAYFTEPPPMRRY
EKVETRLARPTLPVSSFSAPPGPQQHSYQQQQQQQQQQQQGADGQNVSSTSGWQAEWTAA
MRNYPQLGDPFTPLPTGWTSALSRSYGHYYFKNAKGTATYKHPTDAAEFMATPQAFLQEH
GVTITLADVLAYANSKGSSKNDNANNSKKTDEEEEEGEGEVGVAAPSGETATKTHVFDNA
VNITEEQAENWFADQRMRVEALDMATLALLKVKYRVGGGAGRSGGHSRGRSSRHRRDSSE
SHRHHSHYHNHHHQTRKRARGSPLNTLELQRKLVKMSSYPPRGHPFLPLPRGWTCNLSSS
NGLYYFRPPRGNPVYQHPVTRREYRASPQAFVLHHGIYANAIAVEAQKSVEEVEGWLADQ
RQRDEVLDAAVVLMVPIEYALCPDYDEDDAQAESDHHHHKHQKQQQEGERQEYDEEEKQQ
QQQQEDEHDGSNSHRSATSHNPTIN*
>TCRU_5371 hypothetical protein, conserved
MPSATESLRWVKYDDVYYASLIVPDHDAPMPVESGHVFVYFLGTESGAVVPIGDTSPYDP
HDTSRTSHPAAAAGVLVAQQIIAGAEAAAQEELSKGGGEETGGGRRKAKEREIPKKKEKS
GKTKHHRKEDLNALRRRAAEEEEEEMEAEVEEAEEDRVLEKTLSMLNKRSRRNQKERDQE
EEENALLRIDAYRGSKKSHVTVEDEEQDQEQEEEDSKRSNKEVSNEEVEQRNRWDDMAED
LNLTMQSSVGGGRGTHTRSTSKRHADAYPVSLDSGSIVVPFLAEIRHYYRAVLQEAVESD
RIVNLQEAELVRMIESALLQRRGELIYVQQMLQDVEAEYHTVAGGDPSYASDRDTALLEE
AEALRSQLAQLKSSFDIEDMIKKHLHLRDKLPERRERKRPGVAAAGNSTFADASLAFVLD
VQASTAMPRELTQQLAHRYREQRVRRERLLASQHGIGKIGFSAPVTRVMEKWRQSRELMV
LDPRRESQPVSRRYSESLAKVERHAIKCLSAAKGSSNQLFSLYLLQQGQRQPQRASRNLY
NFHEFHEDEEEEARQRQTTAMYQVSSSHPYTPFAGMQNDTDDIAHDTFQAPLISPLRTSF
DPRATFAVDLGEIRQGNTLAEQLAMQSMQYSHSICLPSQESVWENSEVYEGAQRRRTGRP
MSRAGSMSRASSRASSVAREHTDATFKKNSTHRNNNNNSNNNNVKNRNERHSRNDWRASA
KRAILEQLTLYLRGIRGKPTVLNKDQFQFVAKKLLERAVRIESERTGISMSLQANNANAP
FTKDIEARLRKSVDNYVVRHFVTTRTPEPQKRNRGADIGTASMDQWVTSTRDMTRKQEDG
DETRSLMGAYPHSHNSPVYDEW*
>TCRU_5372 hypothetical protein, conserved
MIFCAAIQKLERYGQLGQKRRSVDDFVQSSLKDPKRGNVYALTHMPTWRSCLAALTPDDM
LKMQPAVVDNDDEDDDDERQLHNVGGGKEATVAAPAPVIVISDSLLYAISFATALVAHHL
DEQRYVERKEKEEEKKAQKNKIRRGDNPAVLVGKVFLSRLEEAEELLAVLQAVAEACGRH
AHHRNEGSPVVTQALAHLLSTAADTVLIATILRQTDINNEEAEERRRIGLCRHATALVAV

AATQLRTARARNPLNTLHDVRPCPTLLQQFLAKSKSISSTATRTMKSKDTGIVGVQSEIE
KEDMDAIVILTLVAWAAVAPHGGLIARLAPFTLFQKLSLVDAIVAESPASCCCVEVSRYR
RTLASLVSSTACNRATRLVVYFRGDDIKLMQNNVRDNAEYALHTHVTTPPAEEATLRSVA
QLPEGQQQHAAFLLVQWMASIPFFYHSFCAEQSWTAFAQEQRRMVLLKESQARRERRNQR
RYNKNFGNNPSFSPVSASSRGSSITTNDDNTSNTNTNNNNNSNHDGIVQKNISRSDGNEG
TVEKEYDVDDEDERKSLISNQSALSLASRASMISTMSRSSMTSYRAFLSVIEAARSDGNH
MENALHVHQSEDGNTNLPLILLEEVTLALQRFMGTASDSSVAAMFDRFSLQILAWRTIGE
LYTFIQSTITTAAPSSSLAFSNNMTASIRPMTVAMDEIPAVFHFGQDIRYNRGLGYEVLG
LLFAKVVLPQLLTTCGGPPVAQRRMEPAITYCLSAYEIIAPQVIDQNVSAILRIAARVAM
DVSSQENKSEIRTASTTLAPMSTTNTTTILHEFLISLVTRLGKSNQIPMLLDAIVSHVKK
EGNTIQSADMHGDDAMVAGLHEIFSHPRVRAALVQACGISLDPEELLIHLLQYVSRWASE
ENEDEEAADAEANSGKEPSKVNTTSTTLSHLLPQEVLFILDIVATVAEGIIATSVTAVTL
LERAAELELTLSTFLVNRLHRTFFSDKMEEEKEYGRSRNENKGNAVLKVSSPFAGGEEIV
RPKMQRRLVLYTLHAIYQARELIFGCLQDLGIQNVEAYLQMMEETMWQVQKNIGALVGPL
SIDDLDAAMSLSTQMRHAPYVHRATLLPQFVLQRLTLARSVSVALNVAVKPLTEARRLTT
FVLCHMRLASEGGYLPEGETTRALELADRITEEEWKCIVEFGRPKRVCHALVWLLRTTFA
VSPTAWRSVSWLTRCLNTCAGFLLEALCEVIMGVNDDEVRACFYRHVKRDSNVEDDDGKG
EEMLLQLCLALEDVLRRLGHIPQWPSLLQRAVHWLLLIQREREVLQDAKEEEEKMNKKKK
KRMRTFLLESRVLQLVADFLLCEEGVPSLFRRILLRPEESHSLQRAGRKNGREKYTVINE
AFVRAIRVPFVPSAAILHTDVGAPDNRNVRVDNDSDIEDEETEGETMAKRTASVCNILVR
QIFSRELAILLVHYSERGEMAHCGATILRQVYTIALSACCGEKAATDSPSQAHNFLLAVV
DEMYRLCCEEDNFSALSLFLKTMNNNPVAFASAIPKGTPAEVHRRKRQRHETRAESSLEA
TNDLATLAPDNNEDHEEEEHEGEVTKKNHNNHHDCGETRPLHEIAVRWMDLLGELFLRVL
KSIKIETKEHLLHCFTALCISLKRVRGYAVMPQGSGKRPHQRQEKEGHFDRCLGTSLAFA
AMASPRASGAIEELRQLFAPNDEKMRRNSLVTLVRLLSSGKESALQALWVLFLLHDGRQR
RVAVGEENGITKDYGCWLAAVISNFDPQQDYSTSETAMSELLAATESWATGARRGNHSFS
FVAMQHDAVYRTDAATRWLLDQLRVVPSILHAFPTDSAPVLLQEYMHTLLHEAISTSSFS
FFYAAACPSSSTPTAFISQCLSRHEKLLRAACKALHQLSAVPHMRFSAWRGDVKRLLVVS
GSRVLLNSAAKALWCQVLELCALPLPALHDDDMFIDHELNFIHALLAKSSGTRYLEEEML
LRVLRLLTRTLLPLGVLWRRPHLLPALMSALLTRFLESVSRGHSGQILFNQLSSFFFQLV
RDANHGSKDSNQSGGHVSPSVKMLCLASITSCLFRQSVAYIDVFTTHSSDLDFLAVDFLK
ALQRIHLPPRQTPSVPQQQCPVWSDATLCDLSYACVGHDDAQSLLRQAAERVEEEEGNGD
RQIFMIPN*

>TCRU_5373 signal peptidase type I, putative
MANCDNPLVVVLSGSMEPAYHRGDLLLLHKISKVNIGDVIVFSLPGRTVPIVHRVHGVHE
DGGTLLFLTKGDNNELDDRTLYPEGYHWVRDEDATGKVFAIIPNAGFLTILSEDRPWIKF
LALSVAILWGCIAGG*

>TCRU_5374 hypothetical protein, conserved
MAHKAGPQILQIIITSAIAVVTTVVHRLWAAPPLVRVDVWIDNIRIAGSIGDVTRWEAQV
LRNADGRHATIGEDRESGATPYTFLGVQFGHTHRAVSLSDNFVRSVCAMPALNSLTIAEM
EVVASRFLSAAAILGTRLCDYYFFVKAVRRRLSAINRGLCWRHPRRTFRRQRLAWARPYD
A*

>TCRU_5375 retrotransposon hot spot protein, RHS3, putative
MKEKDTITPLARGKPNGVLTQVLAEARREAEERLRGTQEMKFTISTNIEDVLFKGRARVN
EMRLNEFLTRELDGRGIVDTNRDVMLEEFFKDSTKYIRDKGALNEVQASGRYLSMRRAVK
GEVIFDEDIRRLCDKGVNNLPGWLVAAVEVKAAVHNSTKHFLDAAAEEARKPTTTSAPEK
LEGLYESVHNSGRSHAVELPDGVERKKTGQEWRCMRGGQSSHGRTRKLTTLSKRMTLCSN
LMQHLPC*

>TCRU_5376 hypothetical protein
MSDPNFAELATRHAQEATSGDAAGILRLEQELRDQACRIAREVRVARRLDAVRNEDLHER
YPFLPEEPVRGILLGDVRPVQQPAFRELSNKLDEQRRDPTRNAAAIRATEEQMTALVARL
AEERAEATERAHEQYPFLPRRVLGVRLGDIPLQEDELLSQLARRRVRQQRYTSIAKDVSY
TEKEMMRRAEELARNVKIVDAYRGNGNEYVRARNPFLVYEDRKCVPLSELPLAGDGVYQG
LFRDHLTALEDAEANAPRIAELENALRSRADELALEVCEREARLSHYSFLSAQDVPGWSE

ALLHDAEFKQLRERYDELSKDPQGNAEALRELEDAMEARSRAIAEALRTAEATNAAEQAR
LKTPSQAESGVFAGDRMHGSEHADLAHEEGGTASGTMRGAESVAKSSGKHSQRSVSHASV
VDLGGEAHGTHYAFLPDAINGVAQEELYLEDDAYFQELLARYKELVPVGAESTEPRAKQL
REQMRIRAGQLAVDTRKLHAAEERAASRMATLYPFVGLAPLGVALWSIPVEADEEFRALL
LKREEALAGKSGSVHEVESALSARAEAMAKAVLEERLAAP*
>TCRU_5377 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MGILYTADKEWVTMFSDKITKSGTWEPKKEYQVALMLQGNKASVYVDGKSLGEEELPLQS
ERPLEYLRFCFGACEMHSSSVTVKNVFLYNRPLNSTEMTAIKDRKSDGSMHGGVSRALLL
LGMWGIAALY*
>TCRU_5378 BNR repeat-like domain containing protein, putative
MLVTLPVYAEKDGKKEKGELHLWLTDNTHIVDIGPVSDDDDAAASSLLYKSAASGTNKKE
EELIALYEKKKDDEEKPSPGMVYLPLTEQLQRVKDVLATWKKVDETVSQLCPSSAVDDAS
PGNVCSTTVKVTGGLVGFLSGNFSDNTWRDEYLGVNATVKGNNDGGKKATLHEGRVTFKG
AWAEWPVGSQGENLDMVKRLMLK*
>TCRU_5379 hypothetical protein, conserved
MKPLRHPHGRPSRNIITPGRARRACAVILWTDERTLRQIGQEDVNPPLAGRQGVAVLTSR
RGSGGGRGGPVTSVKKGTAPPTQGVTCDPQGVQACRRAGRSRIAPVRSAATRARCPGQHQ
EWSPRHTDKRLSRGVCAFLFLLGILLAPSPDCGEEAHMSGIDAVLREGSRHDGISLRCNV
AWDSAVSR*
>TCRU_5380 hypothetical protein, conserved
MPISSVTSSCTASDPRRSASIAKRESVAAGTRAGDWDVAARRGTESCLWPCSVAGHSARQ
EHARLPAAARRGPTGSSVVRGIWWQRGGSRRMLNMRRRAVRPAACVIRSLGGARRFKGRS
SDTVQGVLGVPWLEDARLVAAQSVQATIRCSA*
>TCRU_5381 hypothetical protein, conserved
MAPPSSSACDPRVYLHERVRQHYLEVLPSRWRAVLFRLAKNTQLRQKNDVIVETHLLSEM
QADFDLIHALLDEEHRVYREGVTCLCSQASNGKSETERWTASRHLLQGMLSCIAMKEILI
AHWRNDLVDISPNTLRVYCHACISHPHVSETDIERLLALYAVS*
>TCRU_5382 nucleolar protein, putative
MGAKKKAASRSSGKKKEAENDVPSGPISFGEMSHYDEEAIEFDDVLSDENYEEAHDETIN
DDDDFEVKAEKYRRQMLALSREAAEERDADMRTRAVKATPLHDAEVAEEQMQLLGQQHTT
EELRDRIQETIRVLSNFKEEREEERTRGEYVDLLRSDIMALYEYNEFLTDAVLLLFPPAE
AVEFFEAMEKPRPTTIRVNTLKAKRRDLVQALLKRGMHVEPLEKWSKVGLQVFESNVPIA
GTVEYLAGQYMLQSAVSFLPVMALAPQEKERVLDMAAAPGGKTTYIAQLMKNTGVLFAND
VSEPRTKALNANLQRLGVTNTVVTNYDGVGYNKIMKNFDRVLLDAPCTGSGIISRDKSIK
SSKHYEDVQRASQQQRTLLLSAIDAVKVGGYVVYSTCSFLVEENEAVVEFAVRRRHVEIV
EMGLPFGRPGLTKYRHHRFHEKMQCSRRFFPHVHNMDGFFVCKLKKLSDDCRPEAQDIAA
VEETKNGVSRRAKSGMKGAAKRQRDSSADIVATEPRRESRISVPPPTQRGGRKKHRKV*
>TCRU_5383 hypothetical protein
MEDDLFLLIDFDGDGAVTLDETTRYFERHGFMRDKDSALNEKGTPLVFFKETRIDVTTFR
ELVKLLCAHCRVTLGKVWSVCVEQALYSVFRANALVPEMVVSRKAMEQLEQHIMRHGETP
PPDAALFTGNTFSEYLDYGEFIEYFLVRWPNLSRAKVAALLRHAGSEHFHEVPPSGLETE
IIEDGVVDQTQTEEGREDEMEQLLRYTAQLKATLRSREEAVEKADELAAQNTILLETLAV
AEEEHMRSQEQIKNLSRKLQELQSEIEKNVSIPHTSFSPTVSESYACSVGEVSNDDARML
SLVQRFCRKREQAEMSKEFFLQEKALQLEKQREFLLQWEEALHTKEGEMIQRELEIRKRW
SEAFLRKERQLERLQEILELKRLEIAAREAAIEKRRLAQLERDREVGELSLGERRRRMQQ
LQFIEAKLHKREERALAREEEGLRHAVGFGEHHRPRKPVQQLARGHMENIGESQPTDGGA
TDSRVLPPSKCRTPYLSLLS*
>TCRU_5384 NLE (NUC135) domain/WD domain, G-beta repeat, putative
MLHEIPLHDASASAAERQEGAQGGRVVVTFFTTSFPKTMPEQSYSVPLDTLPDGLNTLVQ
SVLAEESQNFDFLLNDEYITTSLQKFLLRRGISYEELLNIEYTPAMQAKEGSLLPHDDWV
SSVRAPFLGCADLLLTGSYDHCVRLWDGENCVALGTYHTECVKEVCLHPVRPMTSSTAAK
ELSRKRKRAAKMEDFMCVSCSKDGSIVAWRFESGVSKFEPLGALNPHMDGVDSVDISPGN
GEYVASASWDCTVKVFEWSQLLSTETPPNSKAPLISFTDHTRPVLACRFSATNGPSLLYS

AGLDGAVKALSVEQAVLLSNYEGDHPIQGIAVKPTGGGGDLIIAACTDNRARLYDTRQKN
TVKAFSGHRQWLYAATWMWRREEGEQGGPHLFATASQDSTVRVWDLRSSSAALLTLDTMH
TDGVLDVTYVGNAQIASGGKDNKTKIFSLSHGDSAMS*
>TCRU_5385 hypothetical protein, conserved
MGSVFSKKSEEPPKAQTGKAKRASLPSPAAPAATAKVPADDAHATGFSAAFEERIRRFYA
HYSPDKVDTVPVILRHWTGTEEELIQTLVRRYGPELNDAAKTPAPPLTENAADDARVWES
RFARQLLAYRPERLSRLRRVLERAKGKEEATLMSFIKQMGPEPQGPLPDPLHDTTRIPTN
EASRKTVQEEVDPQPAVVTKAEQPAEVMETPSTIKDMTAEKVDSVEEKNVVPVLSLKRRM
SSFLGVRVPEKLPALEEYLRRYAEEGEKLFDSLRENYGADPTEEETKEYFVRRLEGLYTC
YKPESVASAASEVAAHYGTEEEYLETRSKELNADPKMMFTMTIGPTEETRAQLFEYGDKG
MQEPTQCDKNNDEEPKTNVHQVEAEALPDVENCLPEKQSNDFQDVPLCDEPILSTTDPLV
ADDEPPTENTPKLLQKTTSDTEEDFKQMTETLSHTVEEQQRQLTALQAEIDRLGSFMEDF
QIFSPKKFSFSPAPVKKQQLDCTSMPSPSSSPQISYKLRRTTEASVANTKSSSFDCHACR
HGSVEDLLPPPPPPRCRPPRNASSASRQLAVKVPSLFVLRTPSPSREVRTLAEMRLEYER
ERENICSAEKRLLACGVVL*
>TCRU_5386 hypothetical protein, conserved
MSNGAVPLLSTVPPSYRDRLVAFFHEHDETKLGYVDDMLEKYAGKEEKLIAALLKKYKSR
LPQPECAVAPAVDLPAGDLQDECHPSSDGKSAYRDAAVAILQKYDPSRLVHVDYLLRKYE
GKEELLVRQLKKKYAEGGIQPAHDDHSPLASTTPVERVDYHQRLTSFFLRYDPEKVPHVE
MILRKYSGKEAKLIKALVRRFGPEPSVIEECSADQEGEKPCLASTEDTAVAPGDSVKDTR
NNLSGSEGLAVARAEGSQRTVDVSSFIRLFSVEWCLTEEQQAENSRRLDAFFHSHPARPS
SQPAPLLPSVQTCGETVDPDIWSLPEVSQEELQRWREEKLSLSDRLVWRRRKPIKQVNMQ
RM*
>TCRU_5387 cysteine peptidase, Clan CA, family C2, putative
MTTENDGCYLLLFPSTSQAMYEDEMRAVSVATPLPDLLPRSFDEIESMRKMRKDAESGKK
YVPPRHDLPPPYVNDDECDEFEDATIDNSLENLSSMTPSRKYQLSGPSVEGEVSSVFENG
MLYKVIVEDGSWYLYNDTEKYEMHVRFRFGSRSELQPGERVEMFVKSNKELEAFLIVYPH
ETMKLISGKVNGFKCMAKAVPLSDEKRTELFSSINNEALNELSLIAKELDVDGVQALEEG
QVLHYCVENEVPYIDCSFPPCDVSLCRQDIDKYKLRSLPWVRPDAFIPPEQLKEVRLFRR
TILPSQVTQGDIGDSYLISAMASLAESRDRVRDIFRHPVSAGHGKVERALSAYWVTLNYN
GWWCPVLIDDYLPGYREGPEFARCAVDLRRMWVGLLEKAYAKVHHSYSNIASGDPLEPLE
DFTGFPITRFDVFWEEAVKGDDEFFKRMVLYDKKDFITMLYTPRNDDSQGQPAHGSNNGA
TTNVENRCNEVGLRLHCGYTVLRVRYFEDFDLRLLQFRNPWGTGEEWTGSWGKKDKRWDK
YPSVKARCFPDGMDATEPDNTFWMEWRDVLTTFVGGGVCHVKRNWYDYRIRGDFNDGYPT
VCLGINVSDPVDAYIVLSQEDERDGDDLEYAAMLISVSRHGGKHEKMDRTSSLDVEMPGC
ELKFNFARDVAMRYTFEPEGNPYFVIPRVHDNSISKPYVLGLLMDTYAGNGIRVEFKGID
RECRVFQNMPTFSVKGMTRDVSTEYQIRNPRQPSECVGAELKDERLKEFGVYEN*
>TCRU_5388 Domain of unknown function (DUF1935)/Calpain family
cysteine protease, putative
MRHPHHTAVSLSPEDSGAKLESLLDGDWSPVALSTMPSIHFSEYSHPTNGDWSNGVSNVG
DSCTPLIPQEMVQNRLSCPRVRDAGGEDAASVNNGGKHTVPPTESFTPTERGPAFSLTRL
SGGRSTRNRMRAPRVVQTEVPLQSRIVKEPQSTRMRNRLEDSGPVSRLLFSPVLENERNL
KAPSSEQPTEEDMRESWEAHSFPVSDLSQHQEPSSLSSIAEKNSNSGNDVNKHLRFVVHR
RSGRGSLPRRSARRCTTTLFSAVEPLEMSDKTSSVSLPPLVETSPSKTLKASECFTATKG
TEAQPILPSETDSDLQFSVSLLEKTSRDHSTAISPFDLCWAQRAESTDTATAETGKSQFN
GSLFSFATSNALGEGSRLNSETMGGDGTEKRECGPLHTALTSDNVTRTELPKNSDSFEQL
SQLVKRTSDPEVLHLIREHFLRNNSDPQRHAFVVLCDKLAKEMEENPGEKNARRAAVTDG
DEEGDDKRMSSIEDFDRHDTEDDEFDDDNIRESAYPKKDPHRKYTFANPSVQGKSTSVFS
SGMLYKILRENGEFFFFNDTLQYVMVVRVQCRLWGDEVIDEKVVQTQMGNGETELTLAIP
PEATCFLMKTVRDLPRVWAKGVAPPKDFVAPSVKRNMHDIDVSINNVRSKLGQWSRAGDQ
KSLLKCCLHNGLRFTDLEFRPSANSLCRPGVDTATFSFLTWRRPVDYLMLTEVGQARLFR
RDISSHLVRQGSLGDHTVIGGIAAVAMFPFHVRWMFRHPVSSAIGKREREVGAYRVTLCV
GGWWTTLLLDDYFPASLKAPLFARCAVDPRRLWVSFLEKAYAKALGSYAALCAADALEVL
TDFTGFPCRNLDVLWSEAANDPEAARNLYKYIHSCARRQFLIMVYTPSFLKPSSAPLMDN

SSCPSTRFVGSGEGVSFFLPGHVYFITETLYCEDLDLRLVRLKNPWTWSAAGRTHRPFGW
KRSKWFEQPENSTTMGASSVIFQSKGEDGRGGGDGNALKQKELGTMWLEWSEAFRSFEGG
GVCYTLWNWKEYRIRGRFCQCIPTVVLEVRVEQKAECILTISQESRLRRLGSARKFRYDA
MLLFVSRHMAASNMESLACTSSGDIESPSDGFTYTAARDVSVRCIFEPEHSPYYVIPRVY
HFSDREETPFVLSFLCDTVIGGDDAQVHFRHLDPSCRVFQDMSSFTVNAELCRPVTATYQ
CRTPAGVSAYEGQCIRQQNWRGMRQMHSDDG*
>TCRU_5389 Domain of unknown function (DUF1935)/Calpain family cysteine protease, putative
MGLGFFCGSGKIRRKYTSEEAEGELDLKQGRQRAWRKSKFKFGGPSQGGDAFPLLQKGDC
FYVENGKRWLIYNDTLDREMHVTMHFDADAYVFACERTQLSREPSGWVAKIVAYPLETVP
FVFFDSRHVVYSEMETVSQPLTEAYLQKVNTAAVARLQQEKEELIGIASRCCTEEEILRI
CRRKGVMYVDLSFFPGPGSLEGTQEVNIVMDAAEITWKRATDYIPHERHDDIQLFRGRID
PKEVDQGQLGNSWLIGALSALALYPSLVKGLFCSPIASRKTRKEQKYGAYRVTLNKHGWW
ENVIVDSYLPTIGCQPVFGRCANDPCRLWVSLVEKAYAKVHGSYATIKEGDPLSALRDFT
GFPFFSFTDSWVAAVASAEAASAFFKSLQSYKKKGYLITLSTPVIEIGAYTNIYDMSGEL
DNGMKEHYRSLGLELGSLYSVVDVRRFRFPDVLLMKIRGVCGECGLKWTGAWSEASEKWK
RHPILRLSCQPSKKDDGTFWMEWSDISRFFSSGGVCMVRRKWFDYRIRGFFQGPTPNFFL
EVVAKREVDAFLTLSQRDNRGLPEGDPDALYKGLLISVSRYHSETDTHVLHANSTLDPEA
PSKDACSFYFTRDVGMWVKFLPEHSPYYVVPRVGENSAEAMKTFTLGLLSRRKVEKGGLQ
VNFRQLSTSEKPLEIGMQAALHAAQPQRMSFQYKKPKRPAVLREGVSIQDSKKVK*
>TCRU_5390 hypothetical protein, conserved
MYVDSFPDAFREVGAWSTPDDVPALLLLDDDSFTDAGDTRRTAQVLSALENVHAWITRCG
RCFNYAFVSNSFPEIWQGAELPFAAFPLVCFLFGSTGSVSVQTTVGDMSEPKPLRLSWHN
GLCMEK*
>TCRU_5391 ALBA-Domain Protein
MPVYPSREEYRRVRKTDGEKEKGQGPENEIRVTAKHGQRSYITYAIALLRGEDGKVQNDT
IKISAMGAAIHNAVNIAEIVKRRVVGLHQTTDVSSEIIHDEYEAIDGKKENMKVERKVST
ILITLSLKPLDRNHVGYQPPLPESEVKEQDDPEPGESAGENRNRGERGERTDRGGRGGGR
GNNSGGRGRGYSRGGQRGGSNIGASRSGRGGNGRGGSRGGSRNGAA*
>TCRU_5392 BNR repeat-like domain containing protein, putative
MFRHLFYSAVLLPLFFVMMCCGSGGAAQAVASPSPQKSSPKPYFDWRDKNEDEKVSSLLV
PSLVELDGDVFAVAEAHCTKEEGGFTGIASEVLELTGQNRKEELDKTKVKTQVLEECSSD
KKVPCRIADQAVSKSQTTVYVSRPTTVVQRSDIYMLAGNYTSEGAAAGAAAKATDGVHWG
LLLVRGNVSGEEGKGKRICWRDTYGLPWGLFGKQDSLTGLIGSGGSGVQMEDGTLVFPLE
GTRKKRNQDDGNEKDGKTTTVSLIIHSVKDIASWKLSKGMSADGCSVPSVVGWEMDKLMM
MTACDGRRRVYESGDKGDSWTEALGTLSRVWGNKKREKVELVGSGFITAKIDDRDVMLVT
LPVYSSKDGNGKGVLHLWLMDNTHIVDIGPVSGEEEDVAASSLLYKGGNGDNKKDELIAL
YEKKKGVEETSSGMVSVRLTAQLEKVKEVLATWKKADERVSQLCTSESVGRDTLPGTACS
ADIKITDGLVGFFSGNFSDKTWRDEYLGVDATVKKEVAAALR*
>TCRU_5393 hypothetical protein, conserved
MAVDVLVKACQDGDAYSGLQTFKAALQRKVRLRDEAAAHAMLLEAFQQAAVPFRSAETAS
ELVSKLFPILKDFGHNGDLWGIEKVRAIISCFMNVPEGEVSVAWCQSHVQFVVSALGWWR
AGKNSQGCVDGETSINFSVFLNEALCHANMRLAHCTENDEEALCEALASAYKASLCCALN
MELILSVVMELRCKLTETERVFLVARTIHGLLSATGEDVGVSPRRALDTARSMLSHEAVP
AEHAALGSFLHDVLFIFDSVLKTPTRPSVEQLGGRVIEALCRAYATALEPVADLDWVALL
HALCTESE*
>TCRU_5394 hypothetical protein, conserved
MREKVVPIPFLSREVSAWLYRTTRRVREHPYRASGIVLGVAVSTILYEANVTHKDRIPSP
NVNNHLEYELRREPKGVKSMGEGALERSQHQLGVSLVNSQTLDDEWRKHNAAVLGRVKEL
EQLIASTSDSEKREELQRLLDEEKESEKKHGGTTMKVTSGQLYVREPHWNIRNNERNWTI
LARDQQQQKDHYWYRLERSREDDFARNTYSRL*
>TCRU_5395 hypothetical protein, conserved
MVSGTPSHCWETSETRCLLFDGEIVRGQLLSELSLLAVAVGDNTRHTAVPPEPFTLRLIM
HFMEVASRYPMVGTLLLDCPRRLDEVMEEELMHWLREESALIFFSGERNDASQSLCHHAF

SGNPAPTDVALGSDSGCPICMWIGQWPHGFWEAVEKGTVKILVRCALSAFPSCLPPHTRR
SPFQRPRDAAIGAGQWIHVNGYVTAVFFLHREFAYPAPVLEFQPLLSNCNGMIGQSPLLL
DLSLLPVAEARAVAVVGERIQVVGLLELACSNMGTVLYSRRRHTAAAATSFSSSLFPSSG
QILIEARAVRTANFASHWSKDPLTATTTSTSSPFFPQEVNGVFSVNEEWEAAAFLQARCS
WETVAGAAAFALAKGTGGILQKQKPNGPCRMEALLAASGAFALPTALWAVVGIALTSATA
NVGSIVASVVGPSDSLSVLQTFLLELAAETNMVVPLVHGLEGALLPAYTSVAASQVNIPI
PVEVGRRIECVRGGLLNMAHQRVLFAPSLHTLTTSALHAVQGVLKQNEHVVVREGGQRVG
CRAAGAFIGITQESMLVQDRQLFCFMERGDVVLHLPTNTTSCSVEDDHVAILELLLNNVE
WGERSEMVAIDHINRCKSQWLMCCEWALHPFVDEPSVPQITTACAALLRSFFFTAKANCA
EAVDAGMMTALAKLTCAHALLRQRAHHGGTCGNIQKTASSACVCGVKMREHSESTALVDA
VVAIALCDASLKFIADVSLMGKSFTFDLMVIDTQFDVLHFSKELYAHLLSHMPTPPM*
>TCRU_5396 DNA mismatch repair protein MSH2, putative
MTDERDVSVLQAFTAVGGDDKACVRLFSRGGSTPGCYVLGSWAGFIAREYIRSTAVLKNW
GGVDVVVVNDSIAKEVIRDCLLRRGASVEYYERPPGGGTYACVQRGSPGNITDFEATLFS
FEEAEIQLMATGAIVLENNNKSGNAGKCMISGGQGIRVGFAALNTTLRTLTYAEYLDTLQ
LTSLDALMAQCNLKELIYLDKSRCRGGSNSDRGGGAAGVAGGSGREEESLRAVKQLCERA
NITYRELGHNGAAPSHDSPQKPLQLQGRREGNVNKGDFLSALEDILRVPEDRLALSNCPL
ASRAIEYLVSNIIDNFDATNHRAFYLKHTIPSTFMKLDTAAIQALHIIHQKPEARGSLPT
SVYSWLNRCVTGMGSRMMRQWLLQPLRNAEDINQRLSLVELMVEDSILRDALLSQVLRCC
GDMDRLNRKLQRRSIALKDLQSILTFVNTIPRAVQVLRTHQGGRNDKLLMDEYIAPLEDI
NEHFSNLRILITATVDLSDENTTRINPEFDDELMELEEQRKSVVKAIESEHQRVMKVYGW
TEKQLKCEYHTTYGYVFRVTRKEDQQVRTSKELITVSTSKDGVRFVSERLSSLSEQYKGI
RKVYDVRQQDLKQKLVSTVVTYLPVLDDAKELIAALDVFVAWATVVRDSPHPMVRPTIRT
PETEEEQEGNKSLITLLNVRHPLVELRQPVYTPNTLRLTDDANALIITGPNMGGKSTFMR
SVGICVVLAQAGCFVPADSADVVTRDAVMCRVGATDHLAQGVSTFMVEMLESAAILNAAT
RDSLAIIDELGRGTSTYDGFGLAWAIAQEVAVKARSALLFSTHFHEMTQLAEHHTNVRNA
HFGAEVNTVEGTLRFSYRLEPGPCGRSYGLYVAQLANLPEEVVQSAKCKAAGLETFEQDE
GQKRDYTTISSASSEITERLAYYAKCIRGLNDTKLAADNEEASRRLRLEIQQDSLISSLL
*
>TCRU_5397 serine peptidase, Clan SC, Family S9D
MCFVEDGDAVIYYLHIRHCTVNGASASSDTRLTILYSHGNAEDLGSCYEGLVALSRAIGA
DIVVYDYCGYGFSKARGQSGPTEERVYKDADAIFAELTGRLNIKPLQVVLMGRSMGGGPA
CYLAAKHHSTIGGLILLSTFTSCLGAVNCSCLRYLCVKDMFPNEEFLESVVDCPVLIMHG
KKDSVVSFSCAERLLKIVEQVQKRFKKEGLVSHHWFANCGHNDIEVVSMEELRENLKTFL
NRLTIHNTERSIHSTQ*
>TCRU_5398 hypothetical protein, conserved
MEKPMKGEKVRPLQVLPRNSLHPAGRTGGRHSVGSSGICSRSGSSYVVDFSASPPTWAAA
GAGCVTVTQPSLPPVDDTEPQHRRMSSGHGATPSRTSLMVVPEGTVGEDDTRDSFSSSSS
AYMRHHRYENPFTAYQPVSDPYDRHREIERQRRFINDSKRLGRPFIPSGGRALEKPTRYL
LGDCVAAIYRTIGRDWPETDPMVISTAEDLVVVYMKRARLRNTDTVLRYMNASLKRNEAV
RAFDLRKVPEGWDLLTDDGHIMYTFKPPWVRQRRFLPDQVVTRKAH*
>TCRU_5399 hypothetical protein, conserved
MNPDAPAFIPTFARDSVHRRVYTRATLRNIELNVIQNISCAPLTGVHLTLRTPKDFAALL
KLPYAIEWLDVAHVVSLVRSGQRVVQKGPLHRDSCDQNHGKIDNKRPRCIQCQQGREMCT
LIGEVVAASVRRAASSRLGAAMLQSGDVVWGLLQLALVFDARQSSLRLRLLAERHPGVVE
CIRQYLCGEGYHLPLPSVTAHEQWQVLNSMLKFDWIRDSRTRIFTEISKRWKKRHTQFEQ
FVHFFEYRDDRPLHPVKNMLTHSAKPVLVSILSGDVLAVVLLARLGFFVPPDYYWEIFPF
FSESLLAGGDGEMYHLMRHLCLYFDGRQRALRRDIFNPIAPPRSISQ*
>TCRU_5400 predicted WD40 repeat protein
MRQWAHTDLDSTPSGRPSGKRRTRTSGTMSLQEVSANTLQILLRSPVEDDAPPVRLSRHI
PQREGVDMAVSAYNLTSTSTNTLIMPPVPKNGSGAGVGGGTGGLSLMHSTVTSHSSVHSE
SFVSDDSSYVTSIYNEVLAEQLSDENTQRHRKIGGGVLRFNSTENIYNRGAPLKPVGIAS
TVNGGCISSSGDAGGGIGRRHAGTGGSRAGSPSLFASSPVRNTRIKRLMPGKPVPQRVLF
TNPERVLDAPNFPLDAKQLLHWGSNNKLIIGLKNSLYGWDSETAQASMMVQLQDSMHIHA

VHWLHKCACVALTLDDGVTAIYDCRNEEFLRTVRTRLSPKEFFTYLAVNGPLLAIGTSTS
CGGVYIFDLRAKHALISVYEGHTSGITSLHYCTEEPFYLASGSADGSVRVWDARHNSSPR
YAFDRIHRGPVNSILWNPDKRSKIYTGGQDGMLCHVDTHAPMRNIPPVLRIDEEGPTTGS
HFITRAINTLHPISGIVSPPGVDEVATTHHGKGHIQIRHANNFHLIGTLNSPNCEAAILC
PTLAPDMQRICAAQEETLKFWRVFDPNPPQRRTKSATPPPPVSQLEKELR*
>TCRU_5401 Heat shock protein 83, putative
MTETFAFQAEINQLMSLIINTFYSNKEIFLRELISNSSDACDKIRYQSLTNQAVLGDESH
LRIRVIPDKANKTLTVEDTGIGMTKAELVNNLGTIARSGTKAFMEALEAGGDMSMIGQFG
VGFYSAYLVADRVTVVSKNNDDEAYTWESSAGGTFTVTPTPDCDLKRGTRIVLHLKEDQQ
EYLEERRLKDLIKKHSEFIGYDIELMVEKATEKEVTDEDEDEAAAAKNEEGEEPKVEEVK
DDAEEGEKKKKTKKVKEVTQEFVVQNKHKPLWTRDPKDVTKEEYAAFYKAISNDWEEPLS
TKHFSVEGQLEFRAILFVPKRAPFDMFEPSKKRNNIKLYVRRVFIMDNCEDLCPEWLAFV
RGVVDSEDLPLNISRENLQQNKILKVIRKNIVKKALELFEEIAENKEDYKKFYEQFGKNV
KLGIHEDSANRKKLMELLRFHSSESGEDMTTLKDYVTRMKEGQKCIYYVTGDSKKKLETS
PFIEQARRRGFEVLFMTEPIDEYVMQQVKDFEDKKFACLTKEGVHFEETEEEKKQREEEK
TAYERLCKAMKDVLGDKVEKVVVSERLATSPCILVTSEFGWSAHMEQIMRNQALRDSSMS
AYMMSKKTMEINPAHPIVKELKRRVEADENDKAVKDLVYLLFDTALLTSGFTLDDPTSYA
ERIHRMIKLGLSLDDEDNGNEEAEPAAAVPAEPVAGTSSMEQVD*
>TCRU_5402 Heat shock protein 83, putative
MVEKATEKEVTDEDEDEAAAAKNEEGEEPKVEEVKDDAEEGEKKKKTKKVKEVTQEFVVQ
NKHKPLWTRDPKDVTKEEYAAFYKAISNDWEEPLSTKHFSVEGQLEFRAILFVPKRAPFD
MFEPSKKRNNIKLYVRRVFIMDNCEDLCPEWLAFVRGVVDSEDLPLNISRENLQQNKILK
VIRKNIVKKALELFEEIAENKEDYKKFYEQFGKNVKLGIHEDSANRKKLMELLRFHSSES
GEDMTTLKDYVTRMKEGQKCIYYVTGDSKKKLETSPFIEQARRRGFEVLFMTEPIDEYVM
QQVKDFEDKKFACLTKEGVHFEETEEEKKQREEEKTAYERLCKAMKDVLGDKVEKVVVSE
RLATSPCILVTSEFGWSAHMEQIMRNQALRDSSMSAYMMSKKTMEINPAHPIVKELKRRV
EADENDKAVKDLVYLLFDTALLTSGFTLDDPTSYAERIHRMIKLGLSLDDEDNGNEEAEP
AAAVPAEPVAGTSSMEQVD*
>TCRU_5403 Heat shock protein 83, putative
MTETFAFQAEINQLMSLIINTFYSNKEIFLRELISNSSDACDKIRYQSLTNQAVLGDESH
LRIRVIPDKANKTLTVEDTGIGMTKAELVNNLGTIARSGTKAFMEALEAGGDMSMIGQFG
VGFYSAYLVADRVTVVSKNNDDEAYTWESSAGGTFTVTPTPDCDLKRGTRIVLHLKEDQQ
EYLEERRLKDLIKKHSEFIGYDIELMVEKATEKEVTDEDEDEAAAAKNEEGEEPKVEEVK
DDAEEGEKKKKTKKVKEVTQEFVVQNKHKPLWTRDPKDVTKEEYAAFYKAISNDWEEPLS
TKHFSVEGQLEFRAILFVPKRAPFDMFEPSKKRNNIKLYVRRVFIMDNCEDLCPEWLAFV
RGVVDSEDLPLNISRENLQQNKILKVIRKNIVKKALELFEEIAENKEDYKKFYEQFGKNV
KLGIHEDSANRKKLMELLRFHSSESGEDMTTLKDYVTRMKEGQKCIYYVTGDSKKKLETS
PFIEQARRRGFEVLFMTEPIDEYVMQQVKDFEDKKFACLTKEGVHFEETEEEKKQREEEK
TAYERLCKAMKDVLGDKVEKVVVSERLATSPCILVTSEFGWSAHMEQIMRNQALRDSSMS
AYMMSKKTMEINPAHPIVKELKRRVEADENDKAVKDLVYLLFDTALLTSGFTLDDPTSYA
ERIHRMIKLGLSLDDEDNGNEEAEPAAAVPAEPVAGTSSMEQVD*
>TCRU_5404 ATP-binding cassette sub-family F member 1, putative
MEEAELLNSSEGVQIAVTRKERKRQERAEKHLEELRVLSERANNVNKEGDNPFSVTWEVE
QMSEGSRNISLKKVSVSVNGKVLFKDTVVKLSAGSRYGLMGPNGRGKSTILRLLSSRELP
VQSNLDLLLVEQEQEFHASDLSAVDAVLESHKKQKEYSSEAATLRGKVELNEVEFARLQF
LEDELEMMGASQAEARARRILFGLGFPTEWHERPTKSFSGGWRKRIALASAVFIEPDVLM
LDEPTNHLDLNAVIWLESYLCEQYSEKVRRPKTLVVVSHDAGFLDEVCTHMVHVENHLLN
YYRGGYSGFDEQLRQRHQELDKKYAAVSKTIKEKKRNGMSNAQVDDWIKDQVRTGRLDPL
YLEKRRDYIVNFPFAEPPELPDACIFKLEDVSFNYPGGPVLFENVNCALWTDSRITLCGP
NGIGKSTLLNIMTGELNPTVGVVTINRKVRVGRYNQHFVDKLPLEKTAVEYIRSLGINEE
DKARRQLGSFGLEGNVHKNQIATLSGGQKARVAFAAISTEKPHFLLFDEPTNHLDVESIE
ALCEAIKAFRGGVLVVTHDARLIEETEMQIWEVGNRTVTSFNGTLSEYKKKVRSIFEREE
AEAMKERKQVLETKLMKNRLVRQGDGRNVEELRREMEEKQQKQQVVDVDNAFDFLEKRGK
KKKEKKEKAAKGG*

>TCRU_5405 protein kinase, putative
MPTPRLVGRYEFVRLVGKGGFGVVEEYHDLLTNEQVAIKTIPARFVDQESKRLIREIDTM
SFLHDAHPHVIGFFSMFVTSCSSVDGRSLLEDGIQCSGSAVSGEAPQSLDVQAPAYAGLS
CGAALFKHQTQLEAEVAKIRGSDKFNLHIVMPLMKGDLLHFINHASSPAGLNLAVTEEFI
EQVCVVVAFQICFGLDYLHKCNIVHRDMKPENILIRLHNTNPYESTALIADLGLARDAQA
SDTFYVCTRYYRPPEIITTVSRGETSIDVWSLGCILFELVTGRALFRVSSALNEHGVWEG
HRASTQLEVILDTIGTPSHDEIKRLMPVGNAQMYLLRSVPRPSRLMEMIRNNWRLHTTRD
RQTKWMDLISRCLVFFPEQRPTCEDLCRHQLFREFNVLYGENVKQYPARAYVPVEVGTLM
VENKQIVLRLVRRALEQCAPLAEDETTDETDGGGEEQEEDGVTLFESECFQNEEESFEEL
NGANSVAVLSVPSCEEDVPSEARAEDDRGPKDFPRLSDPGLLHQYATTTAFTDGDALDDV
ISRLLNDLQYHTHDPERSEQLRALLNYFISLR*
>TCRU_5406 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGGVCTDEVVPVDEPPVISASGGSGAADKDTGRTVPGGA
ENLSAQQSQLKKVGDSSPGISSLEAPSEVESTKQQPVRLVLVFLGHCGSVSGP*
>TCRU_5407 hypothetical protein
MAPTRSSTRLVTAGSPATSDAQAFCHTQKKTPRRMDGRLRGTRRQVWSSGDAVPEWNADQ
HCQGRRRTGAMQPQSLKHRPAPWYKNPLGSIRRTGSAPYSISTLTGSQSLLSALQKRLLS
RF*
>TCRU_5408 retrotransposon hot spot protein, RHS3, putative
MCISELRRLRGHGRNVYIIYDVAKEGTPPPRHFAPYDRWGMIVVPSPNVRNYDEWAKQLQ
AARIIVNFLDEKDVKAICTWMKQGQDPGKQAEYWRIVEERMKRVGPILRYIFDGESYIDP
LGAVNDALLAMKPSDVGEYFTLGGEKKWYSEDPCHKLVKIVRARTDEGAEVFLNASISAD
IGFRTADRLKKEMCARDLLLLILRSHGALASQALEKFGLRAFMYGEPVSALVKGLNELRS
PERDEAQDSVLKVNHQGHPTRAVGLA*
>TCRU_5409 retrotransposon hot spot protein, RHS3, putative
MDLECGVLYLLAVGNFPLVDALFFMESPRKALVGLRTTTANAHHTQTSNVRLFKERVASY
FNGWEEFARELSWEIIYVQHADSTPISDWQRCNDSANVTEAENREITAFWEEKAHQYQVT
VTAEMLWQNRLPEVSDN*
>TCRU_5410 retrotransposon hot spot protein, RHS3, putative
MVLTSDKGWPYSWNRNQSIHDCYVNCEVDRVWQIVSGDLTEWFSPHGGADFKPKKRVLIG
TPGIGKSMNAGSYLLYQLLHYDVEKLQVVI*
>TCRU_5411 hypothetical protein
MQVIPMLLLMEVQVGLEIQLTVMLVAAKLLVVELAALVQVLSVFMVKVPKEVLVVLILTE
VDILLWKLSVGRQVEKGEIKAG*
>TCRU_5412 hypothetical protein, conserved
MEHVCEYAFGVAHDFGAEAPRHCGAVGVVRPGHAGDCEDTELFDWEELAYVAAQRERMTA
ACAGRARRSRGLCWRD*
>TCRU_5413 bilobe protein, conserved
MSLSLRDVVERPFEAEAMEILMDEYNKWCIGRLDDGEDDSGDDEEERNNNNGGGVGVGDE
MYYGLPKVAGAFNVRALSRVEFPRTWIVPLGTIPASCYANAAVNGGSDMSLMVDYSQTRG
VVRVRCELLKPTGDGGLSQKVLAVWPNERRRRSSYPSHHPYQQKEQSELYWPAFVTRVIG
VFEDPLLDGSPASLTELQIYEDFDDVLIRALRSPMRVCVDVTFCIDEISEARRLTIAPAV
RYPPFGASTAYDPEIARVSEQVCAMMKEDQRQDAMVDNEAQCPLLVPEVMPQVVSIRNYS
HAAVVGKVRRVHSPMQNAAGTANDRSSGVVSAITTRSSSLANISRKQSVATAMSAVDEHT
ASHSEKGIVNVCELQGCGPSLQHTGRATAVSKRRASCSITNGTGFASAAGVSKAKLNRNT
LSHAPIAVVDMLAGPICQTGQFVFLRPSAQLVVMAQRAAVEEIYVIWQRLRQALFEPLYA
EEIVLPSLHDESVKEATGPTLCLPDPETYMSPYVQEDHEKTEDGTPLPLPKVSHEPTYAE
LTLRLPILQGHLNCWTREMQCQREQRQSNIPPCFERGMIEFTKREESGRKSARREVSPSL
FRTHDPEGDMGTATTRNTSYYSVPGEGGTDAGSVGGPSRTPKGICDVSVSLMSTTPGRSG
LWCGNSHLTPMGMEDWGTMSPTKETLRFQQSGIRRNSQQQKTPPSLLFTVPSPVARQTPK
ALLKEWVGEKKRYELVAGAVDSKSHEGIVGEGSTKSQCSPTWNVGSERNSSKWEDNDKER
LAFKHNGGEWPREPKQEEQWQMSFRSRTGSVKTVETASNDAGRMSNTHQHDSPKNRDAFH
HVEGRVSVPSEPREDASELSQLGQLDWNAEDATHEAVSRAFDPKPAAEQRSAPKSSRQRN
HTPNLPFHALGFFQLLHGKKGKGGVENGLEEPKGIYMREKTGATARKPNMPTSMMSLDFS

ANSFLHSRGSVRPGLESIAVRQECRRLDASELPREGLGETRGHSRNRSHSTSHICSEALS
RTRSPIKNTSMSQRYTLVSWRDASGVEINLDDAFLLPSAVAAETRAKLGPRPTFHVDLRP
ERGRTKQENTLRRI*
>TCRU_5414 Mono-functional DNA-alkylating methyl methanesulfonate N-term/CPSF A subunit region, putative
MTTRTAPQAAAAVAAAASPRHPPANTDLIYHQTIIPTQKITHCVVGTFTLPGATDFVVVR
HDTLELWTLHVDRNVAECIHSTRLFANIYQIATVPTVAAAGRSSAGHGGSGSAGILDTPS
SDSVAMQRLAVTSETGCLVLLRYDLDEIPVPARLAQDPTSSNPKQDDNEEDEATRMRNTS
MITSLRGKFVRVSEVALGRSGARLTVPSARLAVDPLGRAVFVSALMRLKLLVPLRKHEEY
YAQRGRRGSGSSLQEGAEEELLMLSPRDAEAGPEGAVMSTKRRPAIRDLMSFGSPVEAHR
QTIIFFMCALDGATENATFATLEQEIPEAETLPSSADGSGNAAATSNVGAGQAFLRVNSS
TRQTSHGKSGSSSGRSKQLVVYAFLAGLRQVQRTHLVSVPATAHRLIAVPAAPFGPGGVI
VCTDAELIWYDLLPQLHGGGILGNSMSSSAPPLQTPLLSSGLSSVSLFKTAVPFPRRNDF
REQLYDPMIISHAMTCVRNDFFMLLQDDQGDVFRISLTIMDVQRSYDALRMQQQQRRIGP
PTGSVPPVSVPSPLTVTYFDTIPPTTVMVLFRRGFVFAASESSPTHGLYKIVKDGYRSDE
EYILSRMRMVDQRHDSRRHEDGYDEEAKGIILPTPLNSNPSSNPSAAAVTEEEEEEGTGV
PRGGMMPPPSLPKAGGPAVLLPPPSSLPKTPQQQKGRVVPLFIPHPSLRHMVLLETYPST
PAITSFVVTIPQGEQDVETHQERQQQQQQPHVQIDALVGRGSDSVLFHARYGYAARLESS
FTLPAVFFHLTPLISATAMQQRWREMQMETKKTTNGGRYRSTAKNSSRLASSELWDDKLL
LSTRQGTTVLSLALTGHVEPDTLSGFVTSEHTIAAGTLHYGVGYVQITPSCIVVLPYRTE
QQQGAMGTRPMAESATWMHPHGKRILAAAVSGNTIVVSFAQGGGISSFDMGISGTRLQQL
EAIPSFPHAPAISLLRDPDVEYKQFSASLHPSLATSSVAMLAAIATASHEVYIVNPKKLR
EPLETIHCTADDNNGGIPPAIVSVLLTYLGRTGGVRRLFCFIGHIDGTVTRCELDAATYR
VMDRAVLTCGSAPCQMIAGDGERACYVLCGEFNWRCDVRDGLPKTVPWRFPSPQVMYASF
RRPPTFNASSTGSATTEVEMPTGAREELVLGVAGNTLSLFAAQQSGGTSTAETSLEYSFG
HTPLSVAGRRLLQHPTRAEYLIVIGTEHRGYGVAALRRASAAAVAAAAEQQRRIQSNNMS
NAADDAKNDTNNNKNSHMNSASGGVGIALDKPQRSLNHTDHYVSTLQLYNKRTDRLDPPL
YFQEREAVLSAAVGSFVKDFGKEPVVVAGCAEQYTHGSGCGVGPSWTQGRLRAFRFLVSQ
PAAAGGGGGTASSTLRLEQLHDTLIAAAETSAEGLAEGTLAASYRAAPLLDYPSALHICP
EVGLLFVGLGPENGLQVYAWGQRRFLRKRRLPKVPSRITAIETVFISPPGAASATTATYA
PDLFRCGPSNGNIAREKRLLIVCGTLDQSVFIATVQPGSGVGGSMSFLMLVARDAVPRSV
TSVVCLDERTIAVADRFGSVAFLRLPQNARLGFAEPLHQMSDAELVEAERYAAHEQVLQE
IAVHHTGQLVTALRVHDYDPSGGADPSLALRILFYATSLGTVGAYTPFVREEDAVFAAHL
QPLVAAHIRCPLQEGSGHLPYNAAGRMTATAAAAVSPTPVHNVVEGDQAQLLLHASTSLF
STESKTEVEAELARQERVEAAQRKILGLPPRTWPVLAELVAKHRALVTLPP*
>TCRU_5415 paraflagellar rod protein, putative
MNNNSNGKKSGGGGAAATAAVAAAAAAAVMMTSPAAVPARSQERLVAAQKWFFQREAVLD
TCAVPVGATTSVEGRRRMARESATQILSLLEELQATIGPSANGAAAATSVVPMNKAAGGG
NHNNNSNKNTSNNNHAAREADGLWMSALVEGSGSLFCSECGLEVEAREMRLPDGHAMTAA
TSSSPTATTMTVSSTSPSAEAVSRRLQPLQRLLAGIQDVRHLHPYGKLLSSAGKGDASAE
SISMLIKGLQDAVEESLRTIEHGYATCACSVDDISAWAEWSQPLLRVLGETLRRVTLEHV
MEEPQERLRRAAFDVKEKQREQEDAVTDGDMVRSENLYFEKTALLEGMRPLYDQLEHVIE
TYKKDAAEEPTRKVRALATELVPRLVSPKIAKEQNLKKRCAADIERLASKREEIRSARSA
QRANFSVQMTEWEKLFELNRQQQESCLRAIEELEQRLRHLAEERTFLVEDRLEKMSEERQ
REEDAATFMLFAERQEEALRTTLQYVEQSLHCAQSISDAVQSGYKHLNHHLHNVILQTAE
TQLLNVRKERLEHFRSLYLTLGELQFKKERHMEELDKRIEYYHVQQELAMETFNPKAKEF
SKAKKDLLEVKETMEQQLQLIAKKAAQQLEDFKPTEKLLLASGVQFRHPVDELVEMNAVR
TQKLLEYHSLMSTMRKDDDENKEDEDRNMGQSHSPPR*
>TCRU_5416 non-canonical ubiquiting-conjugating enzyme 1, putative
MAGAAIRRLAKEKQKLDESRVRDFYACPLNDIFEWHFTLQGPPNSPYEGGLYHGAIMFPR
NYPFSPPDIIFLTNSGRFEVGKKICSTISSYHPELWKPVYDIELVLVALRSFMAQEEELG
VGSLQRRYVTSEEKRHLARESHQFSCPTCGMTSAWDVWKTQMEQYPPVSSEVEANVPKSV
VKTRKKEEDIAPPAAATAVEVGKGEEVSMTAATVHQAASNTPAANTTNSAAQIAGHVEEK
EEEGHACGDRVDQNVVQVTPAVAPATVMNKASGVSFGATRVMAAKSGEDETSTTTMKYGD

AAKNASAHTSEPTAATTEGQQQQQGEDVHGGLDTMGSGSLSHSPKASGQGQGQDEEAVSL
VGSAPPVFVRIQLGNWVLFRVQLKQIDVAIVACSFICFAVIFKKWLWS*
>TCRU_5417 hypothetical protein, conserved
MSTYSARPTTQTFSINGSNKKGGLVDGNTGDVTLSLEEKGNVVEINPVTKSLYLTVATSR
AFPYVTNWLREKSSEMRNEANSLEWNCDMELSRQLDQKHKAILTGRVASEKERQKMLHFL
QELYSVRLHQRAAGESWFVAFRDAAAAYMSELHEMEKALLQRVSLAEEWTIGGKREVVVA
GLKRMEKQQQQLKRRAEREVAREKMRRDQTLHSLRAAMEQLVGEVGDALTWELHRCMHGH
VHTSFEGRKTAMNDSVTGALSDTAAAALPAPPEDERELLEQERQLRLELRRFQKRGRKMR
RETRAEEDGGGKNEGRLDRELSGRKQKWPFRQQQQHEVEEKETKRKNKKEEEEEEEEEAS
GATSEAAEEGSIINAMHPVAMSLLSSPHNTTATTTNATKMATTAENAAMQSSSVETGRLP
PSRRRLQLHSGRTWTEVSQSLTLPPLPTVHKGAEQDIGGNIGEGGKDGPTSTSNPPAGDA
GSRMRQLKYHRAPLVVRPPVVQPPNRAGRDAGGRHKSGHIAGLLSVLTEDTAHFAASREK
IRTELKRLRGELRKHKEETERMMQTSTGLERQRTQLLVQCDAQEAKLNAATAEKRSQEKV
RTLDTLLLNDEISHTMELLEEQKKKRSAETEEVRKSIEEFKQRIQEHEQLLHNVREYWCR
SAAALRRTKNPGNCQKMSYSWDSTLPSASGVEGAAFSLETAFCSTAPPSRPFLEGSPLIP
TVQPHLVSSVGSETKLPEEMSEGYQSIPALGLYQPEEVADFICSVFEELTVGSPGECVRS
RSNT*
>TCRU_5418 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGAGGGRCSEPPQDPQDITSGNGNNHQSVNDSTGGAGEVGLS
GKSAESQAAGLSVTELPGAGAATNLPGAQTSPTAGAGKNSEETGQDKEEEEVDIKEEEAE
EDDEEDKDDDVKVEEEEEEQKKKKDDADATKKLSAGSEEQPILSSGAEGASNKKKSKGTQ
TSDDDDPAADGAGTREGKQNENKDANPKETPVTATAMKNTTATTGDSDGSTAVSHTTSPL
LW*
>TCRU_5419 hypothetical protein, conserved
MGAEDGSPIHSTTSHQFPQASHRAADVPPDVLNCPTQSSRRAVELIRQRRSTVLRATDVS
ALGRLREEGERGGPRDVDAVNVGAENVSSWAIYDLFAARTNSRSTRRAVRHFDGTVRRGA
IDPTAARQDAAVHVASEWNPAGHGGFEVTKSCGAIGDEADEAGAPRDRGRDESSYPQSDR
MEGTCCFSTCVDNGESLVWDCGLHSQQFHTGGGRELSFWIGPWHQRRRGRTPTAPCGSSG
CEGRTRSTL*
>TCRU_5420 hypothetical protein, conserved
MRWWRNAVKDNDRLQVTGLESRAIWPVNTRGDEVLHVFLSHESTLVASVTIEETPSGSTP
LLTAVLAHTASNHTMGLSCSHNKKWETAFEGKTTTRSSNRKPRKEYQVGLMLQVNKTSVH
IDGRSLGEEEVLLAGERSPEVLMVLLWCVWWARISCDADGRLSVQPPTELHCDACTQGQR
PRSDKGSGSDTAREDSSG*
>TCRU_5421 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MVTVRLTAQLQRVKEVLTTWKNVDERVSQLCTTLLAEKVALTEIACTTGKITDGLVGFLS
GNFSENTWRDEYLGVNATVNNKGGAKKTTDGVTFRGAWAEWPVGSQGENQLYHFANYNFT
LVATVSVDGEPTEYTPIPLLGAKVAGVENNPVLLGLSYNGGGKWQLLCGDETNKEISSTW
KRGTKHQVAIVLRNGTHGSAYVDGVRVGEDAQCELENTDSEGISHFYIGGDGGIADNTES
REGVFVTVTNVLLYNRPLTFSGGNAEVEEVTDSPSAEPASPFVARNQNAAPPATIPPEAP
VEQMTLQQPQHEGKGQNATAEESATTQEVPATTSQGSVGKAAASNSHAAGEARDDAGIMR
ESGLLPSLLLLLGLWGFAAL*
>TCRU_5422 GPI transamidase component Tta2
MPKTESLTLPLAAALVTLTVRWLTYNFRDFLPLPYHFGITTPNTAAETWKEAVFWKQRFG
AVPEYLLVVVPWYVEHIPLLPSAMYVSILCVCDALTVFLVSQWPSAIPQLVFTLFVLNPA
MILLPALESLAPVEHLILTVVIECCRRPRIRGGLIYVARILAPVLGFSFIAVTVALWFPV
GTKSSKVAIIGVILGELGIGGFSLLYLFQWRNMSTRTSLYAPPDNGVMWYVRLLIIPVFE
RCMEVFQIQLPAMLTVLVAVAVPNEVLAKPLEYASSIPGNRRLFLVLFAVCLSKLCRFHL
ALPDYSLAALFIYSLLNKTGGGGKGGKEETGFSMFDRICSANVFVPVYTLLLAVPLQYSF
YTGWVMWDTANPNWVFFPQVAFAVVGAIFMIIFLRKVFDAITKETVAEDTPKQS*
>TCRU_5423 ribonuclease HII, putative
MAEPRSASSKALSGAKGSRTSVEFDVAEFMRAMDCTENHMVLGIDEAGRGPVIGPMVYTG
AMIALHEHDRLLEYCGVNDSKLLGENQRKDVLCKLQELKTFSTFTVVVTPAEIAAAMTGI

HGKNLNTLSHDTAIAIISKATLEATGMLCGAYIDTVGPPESYQQRLSGRFPHLRITVAKK
AETKFPIVAAASVVAKVERDRHIERLGIDVGSGYPSDPKVMTWVRSHVHRFFVLPREFDF
VRLSWGPVVELAKNKDVCVPILFEEDAKTKAEKKRATSGGSSDGKKQRLLSFVKPPPRRH
TVYTHLLRLKTVATIQDTQHPSLG*
>TCRU_5424 Protein of unknown function (DUF3592), putative
MPWYLSTFRVSFCAIYSYLAYLQLRWIAEAEERYRRSLTWKPAVATIFDHNIVMKRGGSS
HVQYRFVVGGKEYVGDRFRSGGIHKEEMVSNPALLGAGTQLVVYHNPADPNESAIKLQTD
RGAESVFLLGIAVSLLVSYRSVRCETILPNMFYTFLGVNRRLGGITGLKEARTHSKQKMR
YGKETGAI*
>TCRU_5425 chaperone protein DNAj, putative
MGLEDIDECLPPSLGGKGQVLKGRPVNNGDGTSGSCAKVNFGELFGFPVASSGGAVMPSA
SAGVGSVQAGSKTECQEPEEQWIWVSAEGQKSKAFPVDNMAGRSNDPLDAFFTSHTPSFQ
PSSSMKREEKPLTDLLDFSKPAERVRYSDEHSLLEAFENQSKGRRADVRDDPSLEDLSHG
SSNNAVRARLLKIMNYYDILGVTRDATEEQIRQRYKQKALELHPDRVGRDQTPEEVELFK
VMTKANEVLCDPEERAKYDEELRCSNVGADDEAQWLFHLHLR*
>TCRU_5426 ubiquitin/ribosomal protein S27a, putative
MQIFVKSAAGKTSAIQASAQETVASLRLKAGVCYGTLFYGGQCLCDEATLADYGLQREST
IQVMLPVEGGKGKKKKKKVFTKPKKPIHRHKLEKMRALKYFKVTENDDGSFKVERTRDEC
PNPVCGAGVFMAQHKDRKYCGKCHLTYAAR*
>TCRU_5427 Eukaryotic translation initiation factor 4E type 5
MKETAHALKDPWFLSYIPQLTPDTVKYDFKGDWNKAKQALQQPLDYIRTVEEFWSTINSL
PKLHQLGNGSTFIFARNNVDASYEAFPNGTRVLVDLYKASVAEKGMDFVLSSVLGEGLTY
DVFNGKTVCDVVRLSSRPNQESPELVRLEVWLSDQLYAKDVIPYIRKGLNEAGLSFTDFI
MGESTFEKDKKKPSVSGAKS*
>TCRU_5428 Elongation factor G1, mitochondrial, putative
MRRFGIISLRQFNAVRFATPQFAKSIHRLRNVGISAHIDSGKTTLTERILYYTGRIGKIH
EVKGGTEVGATMDSMELEKERGITIRSAATHCKWNDYFINVIDTPGHVDFTIEVERALRV
LDGAIMLMCGVGGVQSQTLTVDRQMKRYGVPRICFINKLDRDNANPQRALKMARERLGIN
AAFIQINMGISQDFEGVVDVIENRAVYFDGANGERIRFEEVPAYLKDELKTARKELIERL
AESDSEMEEVFLNDKEPTTEMIHAAIRRATIANKFIPVLLGSAYRNKGVQLLLDAICRYL
PSPMEKENKGYLLKKVKDEEGNISNVKEEKVDLLTDDEKPLVALLFKLEETKKTGLSNYV
RVYQGKMRKEHLLNVRSGRTFLPPKLVRMHADSAEQVDEVKAGDICAIQGEIDASSGDTI
MRAGPKSGLLISCEDMYIPPRVISSSIKVKDDRDLNRLRDRMAAFMREDPTFFFYRNSET
NEDILEGMGELHLDIYVERLKREHGLEVELGKPTVNYREVITERKEFDFVFKRQSGGAGQ
WAQLKGYIDVFPIDMSIEKGVKNKVTVSCSNGDVRESLQKSVIKQLERKIFVKGELMGAP
VWGVHFHLGGGAMHEVDSTDMAFKNATQELWETLLPKLKPTLVEPYMDVEIVVPAQCMTE
VTTEFSKREGIVTETSINGADAVIRGETALDTMFGFISDLRRLTKGQGDFGMQFKEYRPM
QQYKAQIRMDERNKEIGRKLYKLAGE*
>TCRU_5429 cdc2-related kinase 3, putative
MTTLTTLPSRPLSSNTREQFERYNRMDILGEGTYGVVYRAVDKITGQIVALKKVRLDRTE
EGIPQTALREVSILQEIHHPNVVNLLDVICTDGKLYLIFEYVDYDLKKAIEKRGCTFTGV
TLKKLVYQLLDGLFFCHRHRIVHRDLKPANILITSDNVLKLADFGLARTFQIPMHTYTHE
VVTLWYRAPEILLGEKHYTPAVDIWSVGCIFAELARGKVIFRGDSEIGQLFEIFQILGTP
MDNEGSWPGVSSLPDYRDVFPRWAGKPLAQVIPQLDSEAIDLISRMLKYSPAERISAKEA
LQHSWFSEIRT*
>TCRU_5430 ubiquitin-like protein DSK2, putative
MSVTIKLSNGSQKTVEVPDLNITVAKFKEIASAVTNIPADEQRIVLRGRVLKDGDVLSAM
GMEHGQAVHIVRGQKSTKSDVAPSSAQESASVQETQTNTNPQARAETVNPYAALAANLPA
SGGFSNNIPGNPNPGMQMPPELLSNMLQNPAFMQYFQEMMRNPQFLQQRMQQPQQQSQSQ
SPFGMNEGEMQRLLNNPMFMQFVLQMMSDPSIMQQLTQSLGGGFPASNTPLFGQQNAPAP
NFAQNTGFFQPQGDPRVLYQSQLQQLREMGFTNEQANLAALEQAHGNIDFAIERLLNA*
>TCRU_5431 protein phosphatase 2C, putative
MGETLSKPVTEKHTSTFETSHLRVGCCGMQGWRKSMEDAHVAQLNLEGDKHHAFFGVFDG
HNGYKIAKYCSGHILDELMATPEYREGVYDEAFKKAFISLDRKLSEMPALRSEGGTAIIC

VLLAQGEIVCANAGDSRAVLFRGNRAIPLSTDHKPSVATEKARVEKAGGTVQCQRVNGTL
ALSRAIGDFDFKENPKVSWEEQMVTALPEVNRVKWTSEDAFIVIACDGVWDVLSNEECCD
LVKKGLKETDSDIGLVCEMVLDKCLAPRVQGVGCDNMTIIVAQFKPAFFC*
>TCRU_5432 hypothetical protein, conserved
MNEVDEQLDELRLVAVILDTLSNTEQGLRPDQVVPLTARIRQAVDIIETACAGRKPNLSK
NSGEKDRFKRADGLPELTPQVRKSLISRSLTLPQKPTVTKPSSISVFPVPREKPPQGQLA
VSKEVSRCLACSLYNILEGSTRLLKATSAHIFVRKDDEMVSIANCAARLTFPPELVRHKC
LGSLDADVLASGIALNQQISDGSKTNSSLLIFPVFASDQNSQMAVAVVHVENKFGGSVPF
NSEDEGILLTTTRLIGGLMSRFPQMDWRTKFYDPVTQHILAPFVPRKRIPMTREKTSVGQ
QAFITETSTDTDHSDVMYWRKIEECEFPRLIRRETLPRLDSQKPLAQGLSTTSSLREVGA
YIENMHSCWKRSISSNVRFSEEERSNQIELKVLRRELTRVKVLYAELEEKLRLYQLEGRE
YEEEFRAIKGEIDSYLRRRDNLDVK*
>TCRU_5433 mitochondrial carrier protein
MVGKDTDEAPFNTTTGAAAPFIPTDVIVRQITPLIPLPVERIYDLVERFDQGKIGGLTEA
QWVLFCEENQKRFTLLSEEQFGFERFIECTVPDVPEQPSRTHRFAQSVVRFLEGFAAGGI
AGAVSKTVIAPGDRVKIIFQVDPGRRFTLRNAVVLGVETVHNHGLLGLWIGNGAMMMRVV
PYAAITFASFDYYHSGFLYLANSQGVDGAEDERLAVTARFLGGSLAGATATAFTYPLDLM
RARLAFHSSTGEKPPSYRIAYKMLVGSHGWKSLYSGLVPTLVGIMPYAGCSFAVFETLKS
HIVQWHNLPSEKAIPVYERMVAGGLAGLIAQSATYPLDIVRRRMQVTPGRYRGVFHALWT
IYKEEGVFQGWYKGLQMNWIKGPIAVATAFTVNDIVRRRIREYDEKAAQYSHREYLVTLP
EALVCGGVAAGVAKFWTIPFDHLKIIYQVSMSASDPHTFGRQGFALIGDMLAEKPNMWQS
SGITMMRVIPYGALTYCFFDVFQTAAERLLYSVTPSPATNFLAGGSAASLATAILYPLDL
VRANAATNRLSPVSQSYYWILRDMARKKGLHSLWEGCSLAIMGICPLAGIGFATYEFIKE
RYECETFGQRLLAGMCAGVAGQITTYPLNVAKRQRQVEQIVYSGLGDLKNIFMKPGFYAS
LYRKMPFGWSIGAMTFGISFAVNDLCRDGVVRARKEILHDLFFKSLT*
>TCRU_5434 TPR-repeat-containing chaperone protein DNAJ, putative
MGGITGENSAQWTELREEGNKAFKAGSFDTAVLRYTQAIEVNPQEPALFSNRSAAHFKKG
DFEAAAQDAEAAITVDKTFSKAYSRLHNAYCNLGRFQEVAQRLNEGVEALKSSGASKEEI
RHVHELYLNAEEGSKAIENGQRFLEERDFAAAERCLASTARSFPDCAPVAFIFGEARAPQ
QPEEVNRALLRFAQKHEEDPSYLYVRALSNYYRGQDGFKVAQGILRQALELDPDNRKASA
LLKMIRVMESHKERGNAAYREKRYRDAINAYAAAIELDLTNVRMVATLRANQAAAKMELK
EYSSALLDCEFAIQNGVNSAKLYARRARIHEALNNYDDALRDIQKASEMDGSYQREFQRT
KASSKKAMRKDYYKILDLPPNESDDAQIKRAYKKACLRWHPDKWANAGPEEKTHAEKMFK
DVGEAFSILSDAKKKRMYDNGMIDNAVEGAGESGFSGFPGQDEALMEMMNRMFFTGGGMS
GGFGFNGFPQGRRQQYQQSYTFQFF*
>TCRU_5435 zinc-finger of a C2HC-type, putative
MPPRFRICPICQQGFGTASLPIHIPQCYEKALKRWRLNPVGPMPVMPSLEPASSRGRGTS
TGSSACDNGVTDARPLRRQEGFTGVPEYSEGNMNLHPCSRCGRRFLFDRIAYHESVCKGN
VKRKVFDSSKQRTVADDDGGVGGGFGYSHGKRGKRLKSSTGGFPASGGIPKTRWREQHRE
FMEAIRAARGAAGASRAMWGGNVATSQRVPVESRQRAPPAVMRHQKGMQMRQQRTMQPIE
VPNFRQPLAGRRAPPRRSHGSAFGGGGERFAGGGGLGGGGGKIINDNTTSLGMLQAFGRA
*
>TCRU_5436 hypothetical protein, conserved
MQDTSRKRKAHEYYDCPRRTSSGSLECHAAFHKTRCVETRCSNRGDIQFGSTRDLAVGEA
RRPVRPSPEYCSIFVEVHRNADPGVAAGRIDVKGDTAEGQEPWLRTEERFSHDFNHNKAA
TITRRATRTRLATPQDEHAIPLQQVNVPVLNLEWIKTRLNPATLERLMQVWGLVRRSPLP
PSSSGKAREGSRRIPTADAHLLRKARIIEDASFTVTGGWIITFSVVEEKTTGLRRRWIAW
PRDKNRDDPYEANVPLLRISHYLPPVMAEAASCLDVKASFFQVSLPRDTRHPFRCRVEDG
TLVELTRLPMGYKASPEILRIIIASAIAVVTTVVHPLWAAPPSVRVDVWIDNKRIAGSKS
DVTLWEAQVLCNADSCHASMGEGRESGAAQYTFLGVQFDHTLAGRYP*
>TCRU_5437 retrotransposon hot spot protein, RHS3, putative
MCIWKEHNGQLAVEEEEEEADYWKKVNGRMDKVGPLLRYIFDDRKYIGRIDSCKSKVKTM
NLFATKYYSILGTNEVCDDSHISHKLVKVVRLRGGNNLELPYNALMSPYLGNLVTCKLAE
FMVPNDFNLLVLAIKHNLLSKPLEKHSVFTFLSEAFVNAIIPKLRELKPEKNAPPHLCAL

RVYPHKRPLKPCIFQCLEKFKKKINMKYGVLYKPVAQNFPLVDGFYFVDSNLKTLVGLRM
TTASAHRTIPSTVRQFKERMAAYFNGWEELSRDMSWEIIYVQHADSTPMNEWQRCDVVDT
NKLSDAEKKIAAFWKEEVRQYQVSVSSRDF*
>TCRU_5438 retrotransposon hot spot protein, RHS3, putative
MKYGVLYKPVAQNFPLVDGFYFVDSNLKTLVGLRMTTASAHRTIPSTVRQFKERMAAYFN
GWEELSRDMSWEIIYVQHADSTPMNEWQRCDVVDTNKLSDAEKKIAAFWKEEVRQYQVSV
SSRDFKEKEEAPPTVEEQQQQEAD*
>TCRU_5439 hypothetical protein, conserved
MSRRVFASAVLLLLFVTCCGIGGAVSAGGSNVRGTVDALMWIGWEKLENWEDVPVRPPFI
PSLRVPSLVEVQGHVFAIAEAHCRDGDKCSKFGFTGIASKYLGLSGVSGPTEISTADASI
FGTDSAFPVSLRCRVMYLLLLRPIAEMETSAANSALLGLRQSTLV*
>TCRU_5440 WD domain, G-beta repeat/PDZ domain containing protein,
putative
MAQKEVALAAQFNGSYRCATTVVVRTAATETIHRAMPARTLPKQRGDSASRSGNGSEGTG
TPQKGTRTNGSSPSAHNPSCEGPRCTFWLARSDGDIEIRSVAVPDRVIDLVHRTKKAIVT
SLLQISCNRVVAALSNGLLQVLDAVSLQECRTVQAHKSSITCMVPVTLAKTQRSQEEFGC
SRIPAFVTASSDLTIAKWDGVTLECLGRMKGHSCSVTALAATVSGAFLFSGGEDGSLRMW
SLAEGAQVLRKSTSQKNAKKGTKTKEMAVTPSGQQPQQDTKKKRKQSLLPVQKDGSHTAR
HRAVAQVSAARAIRSLSAQTPSRGGAKKAVTTPRTPSVATREKGSRAMSLVLEGRPPRKK
SIKSSNSKPITPRPGPVHFSGEPEAAMNEEDADEEEEEEKEENDDEEKDRVTGSEKTRAL
LPAEDETGASLRNGLNAGEAGEHKTPRKTSKVKKGKKRLGWNFDTVLKQLLGDSVEDPVV
QHFFAMQHFCWEEDTALLWPMKCEHQKAITGLTLIRDRILVTASQDGVAKMFALPTGRML
RSVHRGRAALTGLVMDELHCRLWIGSADGSLAVYDVLHPDVVPLYSWRDLNTPHPQLVPL
VFHGSLSHLYVFSSFDDKNALSLLSVKDESRGQPAHPCQGNRFFVKDSSHKKPCSEKKSN
LPAKASLTCVWLDGGDGAMLMDIPFLKSLDKQFESTRSFFFGNSVRDAVFRRIIRRPVTE
EGEELPQYLARERAKAASAVQFALTQALRQRAFSRWLMWRARRMARYRCMRAVRFLEAFQ
QERVLESYFKRWQRWRASARRLLLHMDMSSVEKRLKCISTSYRWNEISDVADIAQELGNT
FAAAEHRRLLQRYYRKWVIHIKETRRRIAQSTAFNRLFLSFCDVTFGDKSFIWKRLRDAA
EATQRRRRALWLLEQHMVSSQHKCRRYYMKLWIKYVKRQKEARHSLVLVDTLSSVLADER
ALRSRFYLKWYRFALFEARLLRLDEERTTMQREWIAVQNAVDSTASLTELRQEAEQLEVE
IAEQAFERDEVESRNLALRSDIEYLQVQKSLECLLAGYRDSSDTVRRRRDSGSASRSKMS
CNASRERIALFADDDTFDGEVGTLRQVGAVLRALKATGVRCGRHRALIMASYEKVVQLSI
LEYPLEACDYNSIMSLCSNSDESLLRMRPNALVTEGKTSSEQRRHFTAHANTPLFLSDEF
DRTMQRLQSIIVNAARLTGVNLHEPSNYDSLISIQEESSGNEKRIMNTTDCASLRWLDFV
PPTTRTEALPLIVDLVAMFDSLKAHSDMEVEGGEKKLSTRGAAKVIPLPLRSLCKTQTAV
WLVRHAAVLLELMSPGLWKRHLKLRTLAKGVTEPGTGTLGSDAAESSPARSAGATATSDN
SPGTNQSRTYNNGALEGTPRQSIPQQFPKLSVDELGVCKKQHRSMSWTASETRRGHSQKV
SSPCGRATFQQRVLVHSGGSLTPRPKSSFQFKEEDSDGPRRSLPIPLPFTHSGASTPTKS
MYGSSTTRPYLGFRVAVSRDDAGHTTLTVHEVAESYVGASDGVTREGPAFASGLRAGDQL
VRFAGYAVTELAAFNAVVARHVRPNGTVPVVFSRNGQLMSSTIVVGEKSRNG*
>TCRU_5441 hypothetical protein
MGVALGRSTPRGPCMSLERRGKKGPRATSANSRPPEIQQPQPKSTLLAAEVHVLPAPNGG
QSDHFLPDTQGNGNTGKTSPPRNPIGIETGGVKALRPLSLSNSSNLVSADKSNDASSSRT
PGQKRKKKNLLRSLDGSVSRQKQGPSRESNPEDIAATPPLLRMASLYEGKGSSRGRKTGD
ESQEFGLSGRVGGNSVVSRLHALSAKKSQESIFSDAQSNGESAINLAQTNNTRSKQSMLG
SLESTKTLLHAKAVLRKHVHHSLAIPPLSARPSSCRSTTYSALSEGDAILTRTVNPLNSR
EKYGGNFHLPALHSGEAVDGIGKIGRYHDRSDIVSLLENNTQAELSSSSLYLVKSPLLRE
NGDSWRRQNGLLADKCPNHNIVELVVDSATDEKLNGQSGDRSSRDHLLRSAPPTDCYPLA
DVASRNPTPRIGCGHSSQNEFGCAKRPGKKGDSGRGGGQTGQDAADDAAVGWIAIGGEAG
VGGEDWYARLRARCGLEESGGIAGLTAGSIGDCSDDDVKKTETVTPVGTAEPGTAH*
>TCRU_5442 protein kinase, putative
MLNSDGVERRRLQCTASVACSQSVRSAAGGTEKSCAAPRRKFEGSGAEFQRAIEEVTRDV
VDFNSLSMEDISLMRLRGCRAMASRGSSLFQQEIQKQHSGKGPFPMTSHMSMSSLHSTSF
VPAENLTALFHNVQDADSYPHQGAEGEVKESALGAQLTPGRVDDGEENDDDFLSGIHAAA

DTEAPEVGPRAFQRIVSQRLFSFQLENSESFEVNVSSIQGKRTFPPSASPRQSRSSSHIN
LTPGSQLFSTWKFPVLGKVEGGPPSVFWHGEQKGIEEEERVSAENDGGREEKEEKEGLWT
SAKQNDTAVPAAITENANGGGDELVGKGGKKKVHDDDKMNARSLYFSEEEQERRYMKLLR
FVYALYESMKAKKTTGIAANAPDEFSAASLRDPSQSAVRLLHPRVGILCPSLSSTMIGAP
SGYYSLGTRPSMQHGNKQFVPVLPPPLDSFSIHHNDTQVHGFPCEMDPHIVSLIEQRPLL
QTTVFVEFAYRKCHQRMRGQEQLRGRSESFLGSGPTCVPSNSGKLAREEENLETESKEVT
HLTPNAEETDLPVKLYVADALLRGVSGVGAAGASIPQAAGASVPLMVMDEPPITVHRRLL
TQVRAWKRKVHPIDETSRIVDNEEDNLVVYVGMILMGWLEVVDILGAGTFGQVFLCKDLR
VADGHFLHPSEIEGEDFQYWQCSHEYIPFGDPSMVPTHPPLVAVKVAKSRALFEQQSILE
AEMLVYIGAQTAPQQNRDSGVLEGPTATTSATEPPESDPRCKYVAKVFAHGMCYGHHCIV
MERCGANLFEFLKSHDFRGFPMYQIQAVGRKILLALMLLHEQCHVVHGDIKPENVLLTLD
SCLSAATVHGAGAMNTGSGHGNHISTADGKPSCVFKTPLEASRVLLGESAKINLKNSLLD
APASKNTELALPAPSPFRIHNVVSLKRAQNAFVGKESTVESKQDVEGAATETQKIILSSL
KIKIIDFSSSFYVGAGIYTYLQSRYYRAPEVILGARYGPPIDIWSTGCLLAELLLGLPLL
PGSSDFHQLYLMEEMLGPLPPEILVKGMQTANYYNVEYTEPETGSPTGGGTLPTDGNGER
TPSFTLFREEEYRARHENVPAAEWRCYFQYRTLAELLRNCTLSVEEKQIALGRCPTLAGG
DTPEDMAAAGKQRPIKAIVDEMMQQRFLLYDLLKKMLHGDSSRRLTAREALVHPFFVHTP
NYMQPYHFVTE*
>TCRU_5443 hypothetical protein, conserved
MIAVLPFAVHFSSWQAAAATHSACSIPSVQIPVGMSRLPLVRCLGASPTMCSQWPETLHT
PRWKHHSQLHAGQGDMFPSWQHACLSRDAVLRPCSVEWQMVVRVHVNGWTFSGRHAVRVV
QSRRERYAAAADPRCLCRVVGQFRFHVDWGGGEIISCRRGWRATVPQLMA*
>TCRU_5444 hypothetical protein
MYSVDDPDFWLELNGSLKVTALGGITKLHEAELVGLQSDQTYGILSVISTRNSVNPELSD
LLVMIYNPFVEAAYTGPMNKGDSCWTSELRSSRPCSAIPPHGTGGLCCWRRRAPSSTHCT
RTSRGAHCRSCTTTLLVVP*
>TCRU_5445 hypothetical protein
MLPEFIEGGGVISGARLYGVGKEFISLFEKRSDVVSCILASVRLSEQRNWIIDMVRSRKE
VNTALRKRKPNGKVDLSTKGMLNGPAPTEGLVGCLVT*
>TCRU_5446 hypothetical protein
MNRTSLRHSVAAIIMPRNPESIRASLKRKKHTAVWSKWAALEGRRLALQCPYECAWSQLE
IKNIGVQLRCPRAVPGGAYWIGADAKVAHDNQWNDNLATISAQPGASQVSTASATGSWNA
FHTAETIGRSYKFMTCQRGIRAVTRHTGNQEWNP*
>TCRU_5447 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGGGGCDETPQASPSGSGGMVVGTDAGRSGEADNSVAEE
TVVREEDVQTSVVHTPGSEGQQPQETVGGKPGGVENTENVNSPAEKGTGATPPPVGPGPA
TPPEEPTNLTKPTNPDVSATLGTTTELESA*
>TCRU_5448 aldose 1-epimerase, putative
MAPMSKSVVEAKNEDGSSITVHTQGAHLTSWRTREGEEILYTSPNAVYKQGVPIRGGVPI
IFPQFGNRGPLPAHGFARIREWNVKELRSGMASFTLELPSSELRKQGAELRHNNDTSASG
TVSLLYTITFSNEQLNLQMEVTSHDTEADIRFTFAFHTYFAVGDITKTRVDGVNTTSFIN
NLKEQQALQSPEPLWCIREEVDRIYVDQKSAILLLDQARHRTVHVSGENLPDVVLWNPWV
EKTARLKDLPLDGYNKFVCVEHGSIAKEVILPPKGVWKASQCISSRGVSNL*
>TCRU_5449 hypothetical protein, conserved
MRCSRLTSSHAAAAPVLSGEAAASRELQWTPQQLCYRQLMKSLRAAYFHDRSKLFWSRHR
VLVEFYKYSGETNEEAIRQLVGVGLEVAAFIEHHMRTDVERIIKHNETILMLPPGKAKKF
RADYLLAEKQHDSWCKQKIKAILTRRPPPPYPFF*
>TCRU_5450 D-Tyr-tRNA(Tyr) deacylase, putative
MTIRVVLQSIEKAAILVDNAERYVSVGRGVVIYVAFMGDTDDAALQQAITAIMNGRIFQR
ILQEGSPVTSVASLKDCCDADILVVPQASLAGKLKGRSVQFHGLVDKSRGSLLYDRFCQL
LRAARSIDTSSVDANGVPLDASASTQEAEHVGRVISGTYGNRQGLKMESEGPLTHFFDF*
>TCRU_5451 vacuolar transport protein 4A, putative
MTAALSSKKIDEALQLTSEARELLLFYGHSRKARASSLLRIQTLVRDILECTSLMQAYDQ
TPCHSSIYGHVSRTFMSVLDLQLEGDTSSDGHRGKEATCHTEAMGDSLSCVPCAMGRDSE

TETETVGISPCIQPAGNRGVRWADIVGCEEAIAALKQATTLPLRFPQLFQGRRRPSRRIL
LFGPPGTGKTLLAAATATEYEATLLTISSADILSKWVGESEQHVRRVFERAFRLPRCVLF
FDEVDSICSVRGGAGESEASRRIKTELLLRMQGLNSENVTIIAATNMPWDLDAAFRRRFD
HLIFVGLPSPSARRQLFASELNCVPHSLSEEDFEWLVDSTEGYSASDIQKVAMHAVMGPV
QKIAQSEYVKPMIAMIKSHSTGTCFIPCSKEDENAVPLLGIPAAELRVPDVCRDDCEAAL
REFPPTVSKEEMEKFWQWRSREKKMAA*
>TCRU_5452 Leucine Rich repeat, putative
MGKERHREIKLRRPFDRVKPSLMEMGGDIVGNIMMLELETFSDEEAAYLTSPDAPHSHIV
DEVVEALFENVCTAPRRCSWNTPSARPEWKEEFRLAGEWWLSMRVLPATVNPNEYHPPLI
PFFLRNVQTENQLIADLALHMRQRSSVLSLFHMDHISITPDRASVLLFEGILRNEARNLE
CLSLSFCEVGAATLLLILCGLNQCRSIQPQLRYLNLSYNWIDASCSNMMAMLLERTSIRR
LSLHGNRFGGSDISSFYEFLLQGCSLLEELDLSYTALTCAEVCALISCLPRMRNLEVLLL
DGVEVPENKAAALSTAIRKSNLIHVSLKGIIACNGEAYLHRIHEACQLNRAARDFLKDQS
TLRYFSEGGSFFEAFARRKCEMQCLEDRALPVTYRPFVTNDPSLLPAKKL*
>TCRU_5453 probable rRNA maturation factor YbeY, putative
MPRPFFSHVRVYGATHKLGDAVQRLAEAVLWLEHAPPSVELSIHFIRLSQMQLLNHERRG
IDRPTDVLTVSGSGSGSPDASWVNGVLFPDKSHIVCVSDGLRASEWAAPSRRDLLLDLGE
IYVSVEEMWMRCLRYPHKNLPFHDYLQVALTHALLHALGYDHDTPERWKKMSRREKFMLH
QLAAFRRRWPGCLTELDGIELLASVKA*
>TCRU_5454 Zn-finger in ubiquitin-hydrolases and other protein,
putative
MLRYTLEDPSCNDQLCEFEGNPPVKAVVGRVQLLRRLSFKREFFVPFIPTKHILLLFPTC
HPLEGCTVKKETVEHVSNYLIWLKEKSSGKFIVQEILVCTFSGCTVVIIECYELLLAMSV
LSLSQEGDAPCIGYRRVLAFPCEKDDISDEELAFGYYIVPTCTICAERLEPTLTGYTSRT
CRCAPDRECRCFTEESSCIVCQTAIKMQRGGNEIYCGECHLLGDPWICFVCGFVGCSRYQ
AQHAREHFCQQRHLFSMSLLTQQIWDYDSDAFVHRIVMTLDVDTGMVQRVQYPERDNLPT
TLEEDDAGDVVAEKAKKKHINAKYDSELETSNEKLALMIKHQLDLHRAEYEGGEIKHQQR
EEATPQKNEGSFYEWGESNTMYLTRHHFVNRQRWLSLFLENQRLQSELQMRELEEMTLKE
SLHKLESELREAVEQCVTEDRRLTDDILNLQETIKEIELNISLRQKLAGELEGDDYQFFR
VVGGMEGKPDRKTVKKRENRSMRPKK*
>TCRU_5455 Domain of unknown function (DUF4379), putative
MRRFAFAGASACLCCSPALRAPSTSSSSSLPLSSSLRSEFGTHSGHLVMSRRFKASYIRV
ANRKRVEMFLAKRFHLPTRLKTAAPEIAAEWDHEKNPMHLYPEIVGIGHVTPVWWRCVAC
QHSFLMSVERRVVRGGGCPACAAAKAAGGGRKEESTLEGERNPDLRPKRPVMFNLRTKY*
>TCRU_5456 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MLGNGSPQTPELSVSSGGDKETAEGTDVQEDGIHPRDKEEKAAALSSSLGNVSQGNNSDV
GTVRGSGLLPSLLLLGLWVFASLWE*
>TCRU_5457 Concanavalin A-like lectin/glucanases superfamily,
putative
MGVKTNDSAGKTVFLGLSYNNNEKKWMLLCDGRENKGLSNPWQPGKKHQVAIVLQNGTQG
TAYVDGQPVGDAPCELGSTESQEISHFFIGGEERSAGCAGRQEDVSVTVTNVLLCNRPLS
AADIGTLNPNKAPIPPEVPGIVQGA*
>TCRU_5458 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MTTHSVGSQSAEQLPSGGSHDGNESVNADSSSDGNPAVGTVGGDTTQGNESPQIPVGISD
AADANTSTTEGEGQYGPTVNPEAGVSSGESGEPTEKINGQEEEIHPQDREVNATALSSSL
GNVPQGNNSDAGTVSESGMVPSLFLLLLGLWGLAAL*
>TCRU_5459 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MLVTLPVYSEKESKKENGKLHLWLTDNTHIVDIGPVSEKDDDVTASSLLYKSAGGKDKND
ELIALYEKKSDDKDTASLGMVSVLLTAQLQRVKEVLTTWNEVDDFVSKLCPSENAKEDTS
SGTACSADIKITDGLVGFLSGNFSNKTWRDEYLGVNATVKENGGGAAAATGTSDKGVKFQ

GAWAEWPVGEQGENQLYHFANYNFTLVATVSIDGKPKEDNPIPVMGVKVNDDNNPVLLGL
SYEKEKKKWRIVFCGDGQNKELSSDWEETKKKDHVVILLRNGTQGSAYVDGQPVLGDAQC
DLINEKDKKISHFYIGGDGSSAGGAGIEEDVSVTVTNVLLYNRPLNDAEITAINTNKRFI
QRLTDLKNVARDTLSPDVDTQPTLAAVSETTRHGQQPLKPEPLKGEEGTGSGGASNSAKT
TMTTHSVGSQSAEQLPSGGSHDGNESVNADSSSDGNPAVGTVGGDTTQGNESPQIPVGIS
DAADANTSTTEGEGQDEPTVNPKTGASSGESGEPTEKINGQEEEIHPQDREVNATALSSS
LGNVPQGNNSDAGTVSESGMVPSLFLLLLGLWGLAAL*
>TCRU_5460 Protein of unknown function (DUF3720), putative
MEDYWGEGGGNGLRHTSNGGDDGVSLKADCGLLSTRMALIKAVEAAEAGEELSVPETSQD
TEESSPDNKLNDNTRGTAEPGLGGGGVAGQTAEAAVTLEPGGSGTGGQVTLPNVVEANGK
EGETANDTKNGSASNSEKIKTVESSFPSSGSPGPEEGEELPSKQTSKRNEFSDGTPTQEE
DAENHRITSHSREAGAEEHEVKKENASHEAPTETHGRPANDTEIQTATPSPPPATMNEQS
STVNLPPVQPLQRVQDDNAEFTTPSLMANGGAANNETDNSTDERIPNNDPAADVAGTREG
KQNENKDANPKETPVEAAAMKTTTATTGDSDGSTAVSHTTSPLLLLLLVVACAAAAAVVA
A*
>TCRU_5461 hypothetical protein, conserved
MAMMRTGRVLLVCALCVLWCGSPRIAASGVYASGVEDSGRGGCMVSGVLGTNLSYTPSGC
NKTVPMTALRSVFSVFAAEASTDQEDSETDTVPDSPSGDGPDSVSGSPVGSVVIGGSKVI
DGELGNSAVVPPDTRVAVAPPPPPAPETDDSLLHKVSQSTEKHNSSEKLVDLKTKTPAGT
PLLSNQASKESLPTVKPESPTTSDSTVTVKGTDQISEEKLAVLQGPSTVNAGEDGKKAVT
EIKPNTTTNTPDAAPTLSSEGDVTEQHGKDTDSSNFMNNANTGSSAETTASSFSKSGGID
APKNESEDEGDAQRPKSKEPQEKPEDSNTNDAPTENETAPQTEKPFGSAQTNDTSKSGDS
DGSTAVSHTTSPLLLLLLVVAAAAAAVVAA*
>TCRU_5462 BNR repeat-like domain containing protein, putative
MLITLPVYSSKDGNGKGVLHLWLTDNTHIVDIGPVSEKDDDEVTASSLLYKGGGGANKKD
ELIALYEKKKGVEETSSGMVSVRLTAQLEKVKEVLATWKKADERVSQLCTSESVGRDTLP
GTACSADIKITDGLVGFLSGNFSDKTWSDEYLGVDATVKKEVAAALR*
>TCRU_5463 Cyclin, N-terminal domain/Cyclin, C-terminal domain
containing protein, putative
MKMAETCVFADQTNRLNVARKPLPALVSQPPVGRNGIVSAVSKGVDGNQHCRHNELTMGP
AYVPEYSAEIGDYLLVAERSHYRDPSYMVNQPEVTERMRMILVDWLVDVAIKFKLHPESF
YLAIDIVDRYLCAKKVSRAKLQLVGISAILLSAKHEEIWPPGIKDCVFICANTYSAEEVF
QMERDIALTLRFRFTVPTTYPLACHFLDSGDTEAMVRDATFFFLESASHNYEMLQYLPSR
IAAASVLLGRLLVAWNRSLDRSNISQEKLWDREMIHVSRGITLDEIFSLSEKLLSFTKTL
SSSSSKLQAIRRKYVSQKFASVASLEMPSLSAVFVS*
>TCRU_5464 cAMP response protein, putative
MKNSVVRTQPTRRYENFTLENNLPLCIGANFHDDPICFNTLRKSHNLLLPPKVDYAPHTE
YIYNGGGLTRDGKKRTQTAVDGESDDEDVFNGWTVANFDVPNGGKDYVVRFLAYFIENIP
ESSTETAIVRKVCIRYHLQDNSISIIEAKQDNSGILQSKILSRRQVPKRMDEINELITLD
DFKIGGSIEIFKRKYYILDMDMRSRMYYKKIRGEEVPDSLPWPAELDKFGTGMEAQRSKS
THRLATSDDMDRKRAIEQQLTGIYTKHATEDILAAQKFLKHNINEHLTFFALWDDRENLK
GDLRFCAIRIYLENDTFEIVERRPENSGRDGGTTILGRQRVPRPGVDLQKTRFQEHTFGV
VMKRDFLVADDMQIDETYIIHGRPYYIYDADSFTREYMKNKLGIELAPKVDIDPFVQVDL
KTPVKFYPPPPNGFGSEREKRANWITLTARPQRPDFAKIEKEEGRVLRFLAILSKPLVPG
DEKRKFLVSFHRASDEIEIFEIPERNSGFIAGRFLAKGVHEKRMPDGSSVPYSPEDFEVG
KEVIVLERPFKLIAMTDETERILEDKESSATETRVRDLLLLFKQQIQLKFLRVHEAYCTL
APNGVLGYRQVREFLRSCSCTITDEEAVLLVKNIAPDSTGVISFDQFLKVVNVTFSGDMD
EASLTVRSVKSVNMSKDESLKLVASNAERTKRRQKLAVELRQKLIQRRGNTQEQFRLLGG
YSTTSKMNRDVFRQSLNKIMHFNMSKDDEDMLVSILFDDRADENGDITYKQFQEFTDQDN
TL*
>TCRU_5465 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGCGFGEDVSQDEFCNNTYLEVLTLLANKTDEELKEKYC
NGNDKTECVDTLKKYIADALENEKKMKDNAADRDPNVAHGAGVSVGSSTTKSSTAAGADN
AGMSSPLPLSLKVEGDVDAKVHGPAGGAGPQQHSDDGRSEAERIHHSEAEGSNQHGVGVQ

GKTIHNKDEEAPQTGVNSTEARDGTDGAPAPSQDPPNTTESHEDKSRRVAAPDTIPALNT
SPGSNQEQTSQSSSPSGSETTGSSDNEGQ*
>TCRU_5466 hypothetical protein, conserved
MYVVDLCSLPTAIAHTVLFASTIRRLGPIAVDLNSHHELSDGRSPSTTAGEDLAVIPSGM
DAELSDDPAQTTWISGRSVSSEPHSRFIAVTPSASPAAVVSARAAAPMRMAS*
>TCRU_5467 ATPase subunit 9, putative
MMMRRLMITPPVARRVAAAVPLSTSLVVRRASTVAISVQGLHYVGTGLAAIALAGVGLGI
GTIFGNLLVACARQPNLTKMLFNYAILGFALTEAIGLFALMLAFLMLFS*
>TCRU_5468 hypothetical protein
MSEKAEPQGSDSTGSGMRTATALEGLSFVDENKMHHDFRRLKGNQMYFVDHCTFYEKNGA
RGEKRIFALTPTAFFVLDFAGTMERASPYELITAMYQKKTKDKKILSLNSAEYHLLLKIP
TEIDCHISFVNANSFQNCTHVLATLLQARRGAPFSVKEIPSDKEIEFFCNEVRREGYYTP
REVAEINRQRFHFDAFICSARSHIMELLSRLEATKAQITTHENEVEDLKKQGIDEKSIRQ
RKVKLEEKQVRLHKQMSQKHDECERVLDTVKELQEKLTALSGNKEALVEKGVAEMKAKLN
KKQEGTVALRRSAQQKEKHAVVESVAAYKKELHAAWASVTDEKRRSIVSQIEASFVELER
ELEALYRLEKFLATINGKLQVQNDLISAQNLEKEKFINEREKRVVLSRNAASAGQGGNIL
DDPLINLSAPPAGAAIAVDDLLENVTADEDLL*
>TCRU_5469 hypothetical protein, conserved
MDILLWTIRTSTDSQERKKAEANLRQLQEDSPEEFLSFTWNVISSPTLATEERFFLASTV
QEFVEQSWRNGVPKWLQQLTIDRYTQLVLSETFPTLSLARKVATILSIMSTRTKEKVMPG
TLSSPTKRIVGLLSDASVWNASFVTADSTGFLTQILLTLHVFLKELRRKRSCSIFSKLCA
FLVPAMSKLFAASASWDHGEFYMPLLYLMKCALRIFGYGVFERDFHTYLLKITWELTRAV
TTPEQHQQQDHQLLQCRQRLLEYALKVQLRAVENFASSLSELSPEFFLPRTSTVDDTVSL
FGLLFAIIMTPLEYTASEKMVFRSMDIFSKCAMIEETVPFLNEPLKALVHSPLLHRMLER
ATLLLADDVQESTLREWETNPERFVLGLTELVGADDAAESGAEELLLSLTGSTNFAARCL
EVEWQVVNAFLASNDLARITAALHAVGLCYYTMSVDADPAGYVAFLTEKLLPLIRGEVFS
PNSPFMMRRVVWMIGMWCGSVQDTFLRRQVHAAFGSLLVSSTSTAVLLNLLSTINQFIND
SNFKPEELPVDYVHNLLLTIKHILPQMRTSSGANISAELVQGLVSHEVFNFSNAEVLLDV
VLPAVYRFINEANAIMKAVKKDDDDDDDDSEVDLGSLMVLLQCAAACTKLSTPATENRVW
ALFPDVVVPCTLPGGKLALVVEDNAWELLLEMCITVHAWNPVTRDALAWCFENMKRDVEV
LPMVVRCAYRLLLLCPDLLEFVSAELVDHALELLIRDQCSELLTAVFGLLAVMVRRGNTA
LQCHLLDSAIGLLLSKESVQLDTYCIHLALLVTWCLPPYGEAAVLDALVQDIGRYPNAES
FSERIVLLLDVSPSILVTEELKALLRLLLTERLRPLLTADDLTMVQHALEGTSMSLQHES
QEDDMSETERDPAEMLLELVGDQGEPQGSPHIVRLFTLFGLNLNRPFLPSY*
>TCRU_5470 Conserved hypothetical ATP binding protein, putative
MFGELVCGPPGSGKTTYCEGKRQFLSVYDSTRPVILLNLDPANEDVFPYPCDVDVREIVS
HARVMKEEGLGPNGSYVFCASVMERNMEWITRMIEEAVERRLRDVVSTAAPITTSSGLLS
TRAPYLIVDCPGQVEFYLGSYFMHALFKVLTKQLLCSFCTVHLVDAAVSTRDVATYVSSC
LLSITTMIDHELPHVNVMSKWDTLSAEEAEEGETFLRASHFMAEDFDRLWKKQLRRRRRE
HRRAQMYPTGSTDASRVDTKLMEKDDTDVEAIDLERDGGRLYHYSKAVMDVVDGYGLVGF
QPLDVQSQDMMLRLTRQIDEAIGNFV*
>TCRU_5471 leucine-rich repeat protein (LRRP), putative
MTQHTTNTLTSKESTKGRALLGRAWTGVDDAEELKIEMAWTRITPELCEGICRTIVDRDA
DVPVRVVDLIDNQLGPEQTQKIASMLESSTVRDVLLRYNDIGKEGCDALANVVNVSTKLQ
LLDIRGNGLTAACVRKLLKSISMSTALTRLGLSANKIGHEGAALLFRALEKNVYLKSLDL
SLNEIGPSGAESIAHLLALPASPLKTLQLYGNHLGVAGIALIADAVKGNKCLKDLTLGNN
NATDAAAEALADMLRENSTLETLDLRSNTLTATGVRILARDGLANNIFLVSLSLSANPIG
SVGADEIAKTLIMHQGGALTRLDLSSCELGPTGGMRIASLIAATITLNEVNLSGNQLDNE
AAVVLSRSIVNSISISIVDLSANEIGEWGASNLIDATQLNARISSLLLHGNNINRIVQKK
IDTLLGERISRNRLLNQQASLLQPEQLVN*
>TCRU_5472 Ankyrin repeats (many copies), putative
MQERFDHEVSFSNRRFSFYTRSFRNIRKSIAASIFEYHTHSPRAWRCLSVGCFGEAQRLS
RAKNDLVCLAASLAMCGNTAKALTVLEAYIIATCVLAHEKRLRPYGSEERHVRRLNELIV
GWMSGPNLADQVMGQSAQARNEEEYYAAVLDASSAVDWDTIHRWFIIALFLHEGKGYKPP

NVLWFHYFFGLFMNGTPVVEEESQRSTKPRRRQQIAMDELNNTDVEDILLSQCEPNDIHF
ISAITAWKTRRYRSAIAAATNFLSVEGCGYKITDSNMRVMTLFVRCMSLIEIGERTIAAN
DALELLKNDDHFFSIVGASISAFLMPLPNAVKLVTSYDGETQMQNHVFVLCEYVHALTLA
QLGCMEAAREVLRCAMPFASKYDVGEWMTDLMLVVCTALEDSSTILKIPLSPHRQLYISM
CPVFFGGFGSGCAKLRSNTPAARLLYPKRVPTYVSVRQMLPFHLNRAHHFFVERKYIEAW
SNVCLAVGCAEEVVGSLEMAFTDCSPLNAYYFGCRLGLEVLQTVLGVMSLGENAIPLNYD
RNSAYLLLEEGNLLCEEVIRKCAEWSQRLRQFYPNVRLGCIALSKYFTMSRTDSFISRAI
CLAGRYPRCVLAQNCLTFALYTNHHIPEAVDNATKALQTFPHSSEIVSVYRQIVEKDGVY
VFNYRTLVPVRYAPGSGRLWTKRMFILLLLLVLNFVLFALTVIVNIPGGVAYSESMKEIS
VRFQLPSVFPLFYALLIIVYAVLATVSERNLVQTIMVDLFFRDTRLNRLLYSMRGIALVN
AFNAIQITVFGNNFLFESHWYTFLLYIFLTLVLVPFTSRVWFLPSIDEPKDSVWTWLTLL
SVDTLSAPLLLVPHIALFALEPLMFIAFFFFQPVLRPDRCNMGGNIQRRLRIHNSCLRKC
ISPYVEGNQSQFIHVRLMSLLYYKTHPNPNTKNLMNQQIDEDNYRIFPLIDVYDKISTKP
IERLTHEEIVKQESRHGVMDFLASVRGSFIIGMDEEDEEEEGVEVSNCLPGAVGANYGPD
IPEYPIGNSDAKNGAANAVAGENVVKGETGARDERRGSKGIFGLGSAQTSGKKRAKVAGL
IDVIHGDGEEEKKDGEASRRSREFNSKKTPKEAKLSEDKNSTGDVPSTTNSDEAAFFSPV
NCMTGRVPERMSLRADARECLTLLADTYRASMEEFQNSFVSPCGSMNENVAVSSEQLNYP
GTKGAPELLRTRLSAFSSAARSSRISSAFDGNETSTFYTNPDFVSLEEISLLCALQTLYR
ALDTPLSERDSHSDWACELQEKKKIVEERLLERYELNSRQLTLKSHRCLELCCKIASKIV
EAGDDELSPYAAGNLSLIGAILLLHDASGIFDTLLLNGLLDHCVVCGFTGMLSLIMSPRC
GERMKYTHWESLLRSFGCESSPHRVESLHIVLSAFQQLSEPSLINEIVPLFQRAVEAALS
NQISKTSSTALENLLSRVKRDGNLKVDFWQVEGARGQTIFSNACAVGNLGLVESLRSLGL
VANLNRVQSDGTNALMQAVMHNHNDIVRWFCELPSDLTAESFKHKHPKKGTVLDITKRGA
LHSMLKDAMTKKEREGVAP*
>TCRU_5473 hypothetical protein, conserved
MFEPLRKERVPSRVQGSEGYVAFAIHPDPTSAAFNWGCCIVTSKLDLIFHRARDASMGLS
PPGAREKKKTPYFFRLSCESGSVVPEYPIQPANVIDYMFSEGSSANMEQREKPAVFAEYM
PTVAILLRVSSTEVNLLILRPVLRGKKGKGVVIRYSTLLLPAPGCARYVRMDHRGGAVFL
LGPYVYEYDGRVQCYSLQLDGDKQITSSFRTILLMAFVSPTGNKYTTASTLAGTQLIVWA
SLRRPLCHVSDNSRVLFVDLMFLTDRGTAMVFRVSVDEENRESHATCIWFSHLLQNNFFK
HTHIPLGVIERWKTTSFFAHAIDEVRRAFGKSLEENTTVDLNPVSSAVPIFSESPTGTVL
CVVIPTEKKVCLIALGCNAKASATTSCSSVCVATPPSVTICDVAWVAGSLCGFLLLGVSK
QMEQSKAMLFFLPLTGHMPLRIHLDRAHASFLTSDGGIFSFFSIERSQDVFGTTQLHLSL
YHRSGSHGEENENEVRTGLLSLPTIASFGPMRSPLHVMHIIYFTGLASFAFVHDRTPITS
ALEKAESTATGDEGNAQSRIPHKFAADDEVQVSVEATLESFLDPWLHTGIEGSAFPLCDV
MHEIIPSLLEDMEHSRVASAASQTGDGGNCAALLSVFRAVADVLAAVSVTLTSSILRRYL
AEIHGVVVMLRYVLTVIGQSGAVSACFTAVAFLTPLVDKNAAGELSCPEWCAIIAPLFDD
AFAHVASCPSLAHALLPYCSAPLQRIMSTGESLLRREKKRELKADIPHVSVYHNGEVIRP
LEETLSLARRGNSGLVMLSAADVCWAARRLFFCDGVDAARAFLKTVVDFHLSNPDVRAVC
TEYDVVQKELAAVVNCI*
>TCRU_5474 hypothetical protein, conserved
MSSLNETLDQNTSTVYSDTNDGGQTGDTSRAEEQGSLLTSHRTMSETDLRTGSFLDEEQT
QYEYTTGYDSRTYYSRTFETRTYDDSSFPQSPRSDELSSTFASFYMESEAARKVKSTIFF
LRRPLIFFFMALSGSGGIGTMCRVVHAITVAATQRHARHITSPLNDLNSLPDGYPSVPEW
MRQARLALPSIVEVLVKKLLRTCGVPALADLQKDRWAAALGSLESAREEIISQTTHVVSG
PMVPLVIFLPLFSFSVISIARRIVALRQVRQAEEEEEFQQMGIDEAEKVGIPHSAELSAI
QEAEASNMSVDGAIVHTAKFYENREVTKSAVVTTSEVAATHVSVETNVSSFIKRPTGLHS
PSENQTSPHTVPTSRDLSPVSVVTEDAMKTNQVFGANGPDSPLPQERVPLQGLNVAPYAL
KGDVVAALLGTPTVKEVNVLLIAASRYNCRRVIIPSRVAASSLVSVSPSLSIERTDDVLQ
HVMSVEEPRGLTTVAVFLRPVTDDAVELSAYKHPSAAVYVFLAASGVEEDVVAHLVDQRI
YSASSLDEPMPANACFYDRSVKEREGTVDVY*
>TCRU_5475 spliced leader RNA PSE-promoter transcription factor,
putative
MRRGLAVLRAKATNRAGGAEYRPRFRPRRLVMPVDPNDVHSSLRSNNPLYEKYKEQRRLR

KVAERRGSIVLATVPAERSVGDAFRCMLEVCEKDGLFSESISFTPKHLQPLEQLLKKARV
LSASTFSKLEEPQEVEPCQQESSLYAIGLSAAREMSGCEEHVSTARGGLTVRDIDTIWRL
LDRTPLDSPVHGILSHRGKALVENCIASMAQEAFPRLRSKHLQALLHECCGLLACGRVAL
RLGFADMCNVSGEISMWRELNVLTERFNIARRKAAAHLQRIEKGVPQQRRWYWRGVLRSA
AGRLKLFPVHQEDLIPRMEWIRGSVFAFVAFIEMAEQSGDGVRVEPLIRKLFCSQLGSFL
HVSQILDNAQRLTEELLQYKATSENDKTSSPPGIYSDVHERQTLANCIKEELEKLRHMTE
DELEVLSERTHPLNNRADARRDQFASSGGAHATQSLRDDIFDDYRVTRHHKEAPPAVLHC
IRPQNALKEAQIILRYDPNVPKVLSSAPIDVDQVVRRVTEVHETNPYASLHSRQQFRQVE
YTVCRLYAGTRCIGQGKGETLMEAMNEAAQHTLLNYYLKKGPSIIPEKDSTTVSEGTSVD
AERTEPWGVRVNKSSDEEIFF*
>TCRU_5476 hypothetical protein, conserved
MRGFQQVTREVELLEGRLALTRRERKMTEEGMVLLRRQLDTYNTQLRDFSESYTVEDAEK
MAAQQREQVEARIAQLEEEKREANELRLKFDKELAGWRTALAAAKRELQKAEKARMAAEK
QCRVQQEKSRLKAKT*
>TCRU_5477 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGGRCDEEPGIGVMPGVDEYLVVEWRSQLRRECAEEVSR
RTGGRANVSTVEECLREGMEGLRAVVDGRRRWRHQRYAAAAAAVAAEEGDAIPENDDQAR
NNEELPPEKKDETPVSSGQGIADATSVKERTPHNPAAAPLLTKNGTSEHQQERGKETKNE
ERSEDAEENKDEEEAEDEGEETETRETTPQAGGGIKAPSVSAVPGVIPTSGSSSPSGVDS
SSRIGGKTGPTVSTSSNTVGKTSKEDVALQKRRVNTPS*
>TCRU_5478 Protein of unknown function (DUF3682), putative
MAMMMTGRVLLVCALCVLWCVAGGVYARDVDTNALRGCMASGVLGGNGSHMPDGRNKTAI
TVPLRSMLPIAAVEASAGEGGSAGGRQNSSNSRETSDAGANGSAGGSPGGGPAGGPGGSG
SPAGGSGAEAPASAAGGSGGVDGSGGSGGTPTGGRGTGGIPSGPASGAPPPAPPLAPAAV
VATPASGSGGTAGSSGTNSSNTTGDSSTGDQTPAAAANDTSPPEGPAATTSDTGHTRQEE
EEEEEEEKQQQSDETQVQQHQQHEHPAESGEESAKDKNALRTNATANTGDSDGSTAVSHA
TSTLLSLLLVVACVAATAVVAA*
>TCRU_5479 Tetratricopeptide repeat, putative
MEESEPQKEPVNYIDVKLHGVHNLPPGWFSDGKPPAFVEHPFRYEVSFSVDGENTYTFKH
GRLLQELSQYESYILGATPPPLPSEVNEMLRHIREFPDTSNLLSAAANKRTASKFRKAED
DGTPLATKILWITTPAADTVSTNSEEQGIKRRRRTSPMVEDAPAPAVPTDDDPPPCVIRV
PLTERDVAALDAMVVAGKPLELQFTRVLRGGVPNDWEDTHQWYFRASIPVDLAPFAEPGS
LELTEEIPLLPLNSSARVEEKGRKRNSRRPKSGVPVILFEEIDFEAQHPYVTHNTSAVVS
LHLEKTLTRLASDRVRPLLKPGNLVPQRAPPSKEYQDGTRQFTDVVEAIAKQIMQDYRAA
KAQGGERIDERLFWNFQTTGQLAAYKEQLMPLVIKVVREKFFRSQDASQEAMSELINELY
VYLLDCVHTTLQNLTGNVGRGMRKDGSRASVGLQYSQDGDSSGVTGRIWLERAEEAETLR
EYEQAAKCHQARIASCSSSANFPAVWNDAANFFVRVSDATRAEQCYREAIAHDPMYVDSL
LGYGDLLLAHNRFDEAAVYLHAAADAKPNALCWGHLSLLCDLNMLALEQGPQYETKRAYW
EREGALAMKEAMGATEEVDYNEVSLLVADYLLQLHHPDLANVCLSRCRSGPKTEVLYARL
FMLCEQYEDALTSLKNAEGLELCADEVGILRGECHASLGHNEEAVREYRQVLCHEDVKPN
RRFGPSYIHLGNLLITAGRYSDALGVFTLGIQAWPCSLMWLGAGIAYYRMRQLDAAEECL
SESNALNNINPRTWAYLALVCLHKGRVELEIVMQQAIIQGLSDVALLTELGRDLVRASYL
RLGEGCLRKVIAMERDAGRATSATSCTAMYYLASAIEGTQQHEAKEMYAEVVRHSQNEFM
RKRAEEQILLLSK*
>TCRU_5480 RNA-binding protein, putative
MTISSEVRLKLQRQVEFYFSDVNVQKDVFLKAKMAENAEGFVPLGTLLTFNRVNSTTKEV
AELAEAIRPSEKLVLSEDGLMVRRRDPLPESIQTDEQTVYVKPLPPGATLEELTEFFSQY
GTVQAVWRRYFPGKKDAEPEARTKPSVFVVFGTKEEAEALKASPPMHNGVQLTVEMKKEY
LEKKAEEIAAKNKGRNRQPQTPQEQPVAKEARKTPSMPLKSSYRVTGCGVMEGYSGVKEL
WPAEERAGIRYVFMPDEETALLIFQDPATGEKMVADLKQRGTTLNGKQPEVQKLEDADEK
KLLLDVEKEIADRAKKHQKGRPGGRQGHKRPRE*
>TCRU_5481 SNARE domain containing protein, putative
MNRQIQHDDHITEQNKLLDQLHSSVMNTRHYAVSIGDDLREQDGMLDGLHSGVTLAADES
RRQNSNVMRLLKESEEKGFCVAVIVLVLIMFLLLVI*

>TCRU_5482 hypothetical protein
MMGGIFFVSPVHAQCNGLLAVNNEDYAILGGLLGGLFLVAAYVLTLKLIDICYLQQNCRR
VACEEDPSASGQMRQMTQTQPARHPSVSRQSLPGSVGDGTAWSPYFSTQRRVHFNTDVVD
HVRSPIAFRSRDISHNARQTADEPSVDVSRRDTNNETEWSYARGGMYEEVFSPPPTAPPR
*
>TCRU_5483 hypothetical protein, conserved
MNLELLAQQYLPISPRHVSLLTTDGSGGNPAAVVAVSPAFDPTNRLFFLEWDDPMYAASF
RLTHVSVPGSSVTAIALMLSSEGVVHCVVQSRAGNGPGKAGDGSAVTSYVFRRTENNEED
DDCEEDRTPVTYRKLPKAIEDDGRGWTTALRLYSGSNRFVSGGGGEGRVVVACGGQRGES
NALKLLSLSGTRMSVQQTVELPMLSTFPVLQLREIDGDASSVLALCHHAILEVDTRMKQS
DSIVRAWKWTPHDPLITFAVRDNAVVAGTEEGVLVVWDLRLLAVREKSSGAVDHSPPCGA
PVTGLHMPHSMGILSCHADGSVLTWDKRSTTDGVFRFAPRPTDALPPVFLGTPGCVTLAA
EEHLAVVADDSGTLSVFYVS*
>TCRU_5484 hypothetical protein, conserved
MNHKSRRPLTTSESANELLGKTLAALDTVIQDAQQPDAGNSLQAGRKRQRGGDFFAAMAE
PHLYTLRSLVVTYGVQLAPSLDAIARRVLLAVASPGIASAASWELAALLGTYFRAGAVRV
LEELMELLLNERPPFLLAAPCVVGWTGAATEAPSVGEGDGDVSTPVAEDEKEEENTSKVL
RSLRALEELLFAVGPYMNASMMQRATLRFAQEVVMEGILDAPPSSLPADNRKHLGGKKGN
SNNNNSNDSGLQQQQRTVASSTVFLVEEALQPLFVDLLTSFLLLCRPLPGVVSACVVRVL
KELPARPITMRNCRENQNLLRSISRLSATFAALRHPHALPFYLPPIDIVEKPTRRVAGDI
SSAGGDKTTDVPASLLPSRPSPLPTSSVGMALQPGETQQQQKQVAATDCARPVSSSPPQQ
TISAARQQQSFLGRRENRGQDVLPATVVPQQQQKQQRNTPVKPFPPAGSTADESDEEDEM
PEIDMED*
>TCRU_5485 hypothetical protein
MAASLENVVWAPVMQVFPNYLDIHAQLRGLDNFGFRLLEEQLQMVLQDVFVAVERPPTNS
AQGQKPKFPYAMAWPIRITPAVTEGDGTLSQGAVLAITDMFTSFHAMLALLPSHPGHVSV
SMQCNRMQTIREKDAIIVVTRIDKIGNRLIFTTAEFLRSMSPAVAVLEFSEKGIDAAIRC
HSLCSNVKHVKAVLTPIIETPT*
>TCRU_5486 metacaspase MCA2
MGFDFGCLLKLCSTVLKPGGAPGPINYMEIGLNLIKIAAPYIVQYLGIMERPPRVDVEEF
FQQAEVTEGFKPWETPTHVSGTFRALFIGINYYGTSAELSGCCNDVKQIIATLQRKRIPI
DEMSILVDERGFPGANGLPTRDNIVRYMAWLVGGAKPGDVLFMHYSGHGTHTRATSDTEE
KFDQCLAPVDFSTKGCILDNDIFRILLSGLPQGVRLTVVFDCCHSGSMLDLPYTFVGSRS
LSRSVAGHMQRIRKGNDCAGDVLMISGCADEQTSADVSNAATFGTGASGAGGAATQCLAY
TILKVSNLSYQDMLIATRDMLRRKGFTQVPQLSASKPINLQQKFSLMTTFEVDPAVAT*
>TCRU_5487 cysteinyl-tRNA synthetase, putative
MSTSRHQPQVVGGLKVTEPVRRPRHPPWYPPVQNDAKGLRVLNSLTESVEPFAPREGRLV
RWYACGPTVYELSHMGHARAYLTFDILRRIMEDYFGYQVVYQMNITDIDDKIIKRARISA
LLKRFREDFLQGRDMARLVAFTAEAETAAVEALELARIKFSEPLPDTTPSRIKAEREEKQ
MELALKESQLQKTRERIASATASGNFDELFNAASGINGDLLDEREGQYVTDQSIFEDHAR
LYERLFFEDMRRLGVRDPDVVSRVTEYVPQVVDFIQKIMDNGFAYRGTSSIFFDTAAFLR
AGHDYPKLKPVSERGENDATEAEMAEGEGALTVGVAGEKRNANDFALWKFSKPGEPRWPS
PWGAGRPGWHIECSVMASDILGTNIDVHSGGWDLKFPHHDNECAQSEACHMQHQWINYFL
HCGHLHIKGLKMSKSLKNFITIRQALDELDVTPRVMRLLFLANHWGKPMNFSDQSIEEAK
ERERVLRAFFGSVDIVLRKDNWGETQGLNDHDRRLQETWLTAENAVHGALQNNFDTPAAM
DSVMGLVGATNHYLLSGERPSATLVRKVGRYVTRILQVFGVVEGTDMVGFATQQGSDDRL
LTVMDALLRFRDGVRDAAKVENSTETFLPLCDAVRDEWLVPAGIRIEDNPAGPTTWKSDD
VAVLQREVAERRAQQATERRTRLENQIEAKRKLTEKWRQYTCTPIRYFSTRDTEEKKYAA
FDEATGLPTRRATGEALGEKEQKKLAKELARYAKVHEEFVAKGGEGWLAEQEKELASLCQ
ALESL*
>TCRU_5488 Papain family cysteine protease, putative
MLVSCDKTDSGCGGGLMNNAFEWIVQENNGAVYTEDSYPYASGEGISPPCTTSGRTVGAT
ITGHVELPQDEAQIAAWLAVNGPVAVAVDASSWMTYTGGVMTSCVSEQLDHGVLLVGYND
SAAVPYWIIKNSWTAQWGEDGYIRIAKGSNQCLVKEEASSAAQQGLLLFFVFRFVVFLVL

VFCVCGIVFLVFFTFSWVFFLNYVLCLCFCECAFCCVFFVLLPL*
>TCRU_5489 cysteine peptidase, Clan CA, family C1, Cathepsin L-like
MSGWARALSLAAVLVVMACLVPAATASLHAEETLASQFAEFKQKHGRVYGSAAEEAFRLS
VFRANLFLARLHAAANPHATFGVTPFSDLTREEFRSRYHNGAAHFAAAQERARVPVNVEV
VGAPAAVDWRARGAVTAVKDQGQCGSCWAFSAIGNVECQWFLAGHPLTNLSEQMLVSCDK
TDSGCGGGLMNNAFEWIVQENNGAVYTEDSYPYASGEGISPPCTTSGHTVGATITGHVEL
PQDEAQIAAWLAVNGPVAVAVDASSWMTYTGGVMTSCVSKQLSHAVLLVGYNDSATVPHW
IIKNSWTAQWGEDGYIRIAKGSNQCLVKEEASSAVVGGPGPTPEPTTTTTTSAPGPSPSY
FVQMSCTDAACIVGCENVTLPTGQCLLTTSGVSAIVTCGAETLTEEVFFTSTHCSGPSVR
SSVPLNQCNRLLRGSVEFFCGSSSSGRLADVDRQRRYQPYQSRHRRL*
>TCRU_5490 Beta-lactamase, putative
MPCLLCFVAAVCFICSTASARLEEINAYFAAICGEDARVFGGAVVTWGEDEEGIDAFTTT
ALGSRAVVGKRIPMTLDTSFRTNTLSEVFLVMTVAYLEDRGELPFSRTQPIPRSFLPPPY
GRNVAFQNPLFPAAVVSLDTLLQHTSSLTEVGFDSGAVQTPGKTVNITKFVESVFAKALS
GGLWGTGEPGLGSSYRYSRLNTALTTYILEKVLEKMAPPVSLATFIQNKFISPMGLSGTF
LLDNVGNVPGPTYPKDSDVSLSARAVQDVTGDGSNVALSRTIHAAYASDYMYYTSALDLA
KLAYELFLGGHHTAVGNALKNDPVNINGENVPPGAVSRSLGMYGFDSEILCRELGDTETC
DFGDGANLYGWAFTGAYNQIALLCTSKKCVAAEVSHFQTRSTIKPHALGLAVSSLKQVKV
RPPLQGGKLYPLYVFIGVLATIIISIVGSYVADYIVQPAPAKPTFPVQNARNTPLPMNGS
GTEDVSVPLRVEGAYATQGISSPLRRLDMYD*
>TCRU_5491 hypothetical protein, conserved
MSQVLERLLPVLLRHLSGDITFTTNEHNGDYDDGDSNDENDKSDVVDMAKKRRNKKFGTS
SNNSPVEPERAPRQKDHEFCHLKAEDSNEGRDPCGGGKKIGGGGSGVAGGGMHYKSAQRW
RRCVELWRHLLGSDRLFLALLFHSGTLWAVEWCPSTAFSSPSASGTGTEEARSWSNAVLW
FLQLQEAVATPTKINSCNDANKEATGDGVAPRSYRRKTQFTTHMHSEDEVAVQRVAMNLL
SEWFAIVDSCGKRFARAYYFSCALKIAALVGNMALVEDIPHLHDIVMQEPRSVSQFTAFC
SILCCLLVEEAQQQQPFRLNLPPPFFLMNFNLVGRGSRIGVWLPRGSPRVVSGTLRSAAA
DRGTVTTGGSADCAQEGQFHSCEVCSPGVILRVPSSSSQIDATGDLILGVRLLDEAYVQG
IDVLPLMPHDDNEEDASNNDNTGGGRRGTRGESVSEKRRRVCNRRTKVVSAAAASADVES
SPRRCWSTSSPLTQIYVRVDLLYPRAVSAIVSPLSSFSPASTGGSGRRRGNYQHQHHAQQ
PTNEETIVNTVPLRRSSCIAAQRDPLATIVFSLATTARRLMGCRGLFVEKPREHSLLTAA
AAVENENSQEERAVECRGKPAKGPFDVDGRRARRQAWGTAEGRMHTTANEVPPTALALFP
TVEEELECLVECAIHLFLEALLLCRALSSDVIPQIDAWAMEVTSNTVDLALATPLPVVRH
LHAVGYALCLMPQPHQSLLVTVGLFATLAQRQRESNKNETDRSNSIASYDGGGKTGHLGH
GSVGFTGWWEVFKACVLKDAVIPGQLCGGTWGLVERVERSLCVTPHVRLHRHPRQPQPPQ
RDKEGTPAEGGSTKSTNKEVDKVKKDELASPDDAAPRRRLALLHSRRRMEQDGSVKKLKH
EISVTPPWLRAARAVEVHTCHHHRDQHESSLQEWIMAMWWSLERAATDAA*
>TCRU_5492 glyoxalase II
MEVVVKHMGAAFSVAVIPVLKDNYTYIIHDKTTNTMAAVDVSADTTPIVDYVERIRRSID
ERGAGAMSFSTIFSTHKHWDHAGGNVVLPKALKAAGAFRIIGGVNDNISGVTQTVREGDR
LSLGALQVEVLEAPCHTRGHVLYKVYHPQAEKDGVALFTGDTMFVGGIGAFFEGDAAHMC
RALRKVYNLHHNATDKEEADRHTFVFPGHEYTVNFLQFARDTIPPAHPDATFIASQLERY
KESIAQRKPTVPSTLAEEKRQNLFLRTCDESFVREMKHGDTAETLMQHLYDTCP*
>TCRU_5493 hypothetical protein
MSVHSGFSGASRVGVTYHSIKGYSGAGTPGNPLVDGKKTDDPYVAELQDLQAILRNPSLR
VESDGSAVYDPNYLPKNKKIISMAPYDSSGEYDPVEPIFWLTCACVVGLGAFIAFLILSL
LLLELDVMRGTIIYVAAGSCAGFLFITMFLFYAFSSKDERWFGRLVDGFIGAAPFIVLGA
LIGYTYSGLILMMVQIVNDDRESVQISWWFAIFSSVPPFLLLFMPMFVAAMQVQEASAIS
ARIFRGIPSQPPGYIPRTNNSGQYLFSATRRFIVGFAMGVGLAAYYAITCFALGMAAYGL
YCSTELYFWIPIAVVVPVFLLIIILVALLLYFSPFTLRCVFAPWTEPLLAWSPVALRSAY
FPRYHTGVTVKQMIRQTNNTTRKAGRHHVRGDCARAEELYEDADAQRAEIERRGIKLRER
ECRGWRKLQRRRRSNMIRKDMEKK*
>TCRU_5494 proteasome regulatory ATPase subunit 3
MTYAVAQTAAAGVAASTAVAPQSLYEEHERLVKTIQNLELKTMICKTETHHLQKEETAAK

QEVQRIQAVPLLLGTFVEAVDAGRGIVGGASSSNYYVRILSTLDKERLKPGASVGLHKGS
NACVQLLPNETDSTIHLLQKEEKPSVTYSDVGGLDMQKQEIREAVELPLTHASLYDQIGI
DPPRGVLLYGPPGTGKTMLVKAVAHHTKASFITVAGSEFVQKYLGEGPRKVRDLFRLARE
NAPSIIFIDEVDSIATKRFDAQTGADREVQRVLVELLTQMDGFDQTTNVKVIMATNRWDT
LDPALLRPGRLDRKIEFPFPDRRQKRLVFQVCTGKMNLSPEVDLEEFVTRPEKLSGADIQ
AICQEAGMLAVRKNRYVVLPKDLEGAYRTVIRKTGDERYDFYS*
>TCRU_5495 hypothetical protein, conserved
MSDALAILDGAAACVSALLMPEELGTLIRFLRGESWDEVPPSKTTSSSSALLSTTAKTAT
TTTAAVRDGEDTPRRIPNALTGCYNYIPLAIAAELSLLSMSSSGERSALVHKFERNEFRV
FAVNLLPESRMADYSLHQKGGSSSAIVRLSCMEAVRAWCDAVYAEKDGVSSRSPVMAAKR
HRREETASTADVPSLSSISKGKFKSGPIKRRALFILSCCANESAARRGDINRSRRSCDPL
MMFLHEISAIAALCRAREATHGARIEFSVLLLPDDLAYGGALLEEALREPLCREFCVQLF
HGSITGVTRHDDAEATAFMRRLETWMNVPTAPPRTTEANTHANGKTERVTEEKQRHSQQQ
DQPQQQQQAAAAHVELADKTRQRESSFFFVRRENLPLCCFLREALRRFPVILHPMALRQL
QALWATRRQLGDVVTGLHALLCPFAHSASARDRCASSPFSVRLFSAGASTTNTTANKRNR
GDGMSRHVDTVDILNAILAAAGQLADGQLLNEAVAFAVLYEDIVWKRSMRLQRIPGVVSV
LEQLWRRWGNDTDMIFQEALALCVPVYTPSSTLQNESYQNAQENGAEDTRAVVAIPAAMR
APAAKMPLGAELMHSALLAVLPPEESLEELKGVVGQDGGHGCPSWLKGENCHDKSGAIAM
REFSLSENNFFNPSIPDSVRLLHLLTSHALGQGNSRQKYVSFEVLQRICQISDEALVRAL
KELQLAGMVKLNGREFKARVVLDNS*
>TCRU_5496 hypothetical protein, conserved
MGNESATRYVAAVTIQRWIKRRFEVTRAMRLLSILRVLQDEAKGKRTVTPLLEELWSPTD
VGMATTDGSDGGVSSSQAVKMLLELAVMYAERLHSENYTRRLMFSSHEPQSRGAGEEDKR
AVGQYDTTRRLLILSDEVLGQLVLDVRDKSKQQRLQRGCGLQQCLDAPCITWLSHLFCKS
QEVEEAWRARPFWWSLRHNLLDTCVATNHVGVGKVDDVPPLPQPPILRRGKSLAVEGGAQ
KLNPGGNKEKGDPKFDNSSGTDDDDDDDDDGDKDDDDDDDSEDFYSDEKYYEKKKEQERA
TRARVMSLLQMDDSSAATRGKDAAEEAAARDSYMELFGEVKDVLFPTLNAMKTMSTEVAT
AAVKDASNVSNCCIVCELQDEAGGLVRCPCGSWVHVDCAMSVSSGVPRCSQFCHFSA*
>TCRU_5497 dolichyl-P-Man:GDP-Man5GlcNAc2-PP-dolichyl alpha-1,2-
mannosyltransferase, putative
MMGFVGVLRVLAAFSLLSAGHYFAAVFLPVADCDETFNFVEPIHQLLYGSGLQTWENCPL
YALRSWLFTWIYASPALLMSGMPSPRSVDVYFFNRICYGRMACLSELFLVYSVRKAISGR
AAAVTLALLLFNYPILHAAVSALPTSFTMINYFMALGFWLRSGHRSARDKNTPAAASTGR
HTGTSRRRRSESHHFSVFGTVFFAVFACAVVWPFAGFAVLPMALDLIVRHPKASVVSLLL
AIALIIPLAVGLDTLYYCRVTWSAWNLVRYNLKGGAELYGVEPWYYFIKNLLLNAHVLFL
AGVVAPCVIILRPTLNGSLKHTRDGTKHDYSNRNYKEKGGAREEAATMQRKRAALPLPFT
SFSLVDVKAYMASVPSVLSSSSSSLPPSRSRMLLYISPFFLWFTFWLMVAHKEERFMAPV
YPFLLLAAALSFTLVFFPSGSAFGMTTGTRAAAAPSAKTTDQDSNEKMGRHGFARGTLPR
NSRLLPVTGCILLLLCGLLSLSRSMAVYHFYAGPQRLMYDTYDALQHAAAHKIASKKGRN
NMTSSNDLYTVCVGREWYRFPSSFFLDTQRARVAFIKTDGFSGALPLPFKRDDSYATCRC
GAAGVNDLNQEIAEQYVSDAALECDAILDSHSAYDSSDLKNYPQDVFAYPLVATAKPQQY
RLLDVDRTPMWCRVLYYPFGISERCAVWQRVELLSKHRLHAST*
>TCRU_5498 leucine-rich repeat protein (LRRP), putative
MPVAMVVVDVPTAVCDKTVAQTQSGPWARGADELYSSLHIEGSPWLMEEKNNGEIEHLPV
ARGHVVDGVNAGKKNSFPSSSSHSNRTVPPKTCAFNVVKPPNLKDDSCVVLPVLGRNELL
DLSSRQLTVLPCLHNTAAKTRHGSGARVASQVRTLQLSRNSITSLVAVPEPSLSAQPTAL
AEFTRVVLLDVSRNEITSLAGVENMTSLRVLQASHNKIEDLGPLFTPNSILQKSAALRVL
DVSFNQIRTLLPPSVNVLEKPMRSLHTLTLSYNHLSELNDLDMLFPDVVELRVARNRMTE
LPQVLPKRIYRIELQQNYLDEVAQNNVREIQRRMRCLRDVEMSEQRTRQEDTSETENATS
FEGVHGTENEEDRMDDAVLHRHAFAVDDVESDAENRGMLDVVVPHSIFGGQGKDAGQLKL
REMIISPPHIECASLQKRSVIPTAWARQKNPRWLEKDPLHVTMMLTRVIASASLHSSSKI
SYLWVQPRIIEAGSTGALVLIHEFSHAELVAPSIRLSVGDINRVCVALSHETLAAPCALA
GNLLFSLLTQSTGETHGVADKIRVFKEDEEEKEKTTPLQRQQRMKDFSLQKLTVFYKSIQ
SSMPKRNPFTHGTSGREWLMSELRAPLNWNETRRRPCPFTSCLPLRRTKQERIDRRRKIP

DT*
>TCRU_5499 hypothetical protein, conserved
MSHFSREATKLLRAAEDALSGRRPAALSLPVEQQESWDRRDGALNCRHGDSSVLELQRQL
RVAMTEISNLRNELMAERESRSQTIVSLGRRWKEEMMVELHAADHQSRRAIAELEVNVLQ
RYKEEATARAVMQRQLDEVLRSSKVRDRSQFERQEYIQEQIDSLRERLEAAVAECGLIRV
ESTQQLEKERASLAQRLDVELLRYLDMRRDDQREREKLKQQLKADIAAIGLHVRELMDEA
WRTHATALERTLREPIDTFAQKIARHEELVAGMDAKIHDCTTTCHAEVRLQTASLQERVG
ALESSSAVTASRVDRAERKADTAQEAMSRVDANLGVARDTAERAQAQAQRAMERAQRVED
TVQDRDARLTQIETHLGAAATAEKLRAEIESVRRAALRAESGVDALRQVCERDEQLAEQT
RRVVDGFTDRIEGCEQLVHRLRATVETVEGRVPHLQQRLAALEETRESLFASTTRLDDLA
AQFGQRVQNVEAAVKGVGERLEQSRRDTLGGLQSVNARLEHANDMALRSETSSAAARAEV
DRMDRRLCELESRAGRFAADSTTLRAATEDHAKDVATLSSRLQQAIEWQEQRDARMDAAI
LAAETQNTTATEQVAGRLETKMQRDVRRLQSTFEDRVSALETSMESKVAPLEEAVAKMRT
LRGGEETSQMLSRELRTCKSKIESLEAALAAMSDTVEQGQKEYVLLRDWNVLRKTVASLE
SRLHATNADTTLQQQTCEEFQVKLRQLEGEQRRQRQALHDLQTSVSECREETCAANRSVA
AVISLHAKEAGTTTRVVTGTGDERKQGNFQAPLDNFSELRSSNPRMPSTLASAGGTAMKT
PRTHPQTSITEVVVKDDQNESPDAQAIPFSQKGADVSRRVSSSVVNMTTATTPPMETRRL
KSSAVDTTNRQQAMTWNDTTDSDSGGATPPEKVGVAPRESVFAASDLRPPAATPLVDAAR
TFGVDDDNTEATASVFDAEMKAAPMQPPHELSSSIFLPEEQSRRSRAFSFRQHSSSAESV
IAADSSAGAANVTPVKDTAGTAEKEAPPPKPTTAWYDDWDASTESEKVSSAKEGQKEETA
SAAAPHTGVAPSSHGEGIYSTPRKTFLAFVKEPSEDAAFVPRHGVATTASTSSGESRRKE
TTPVMPASEPKRFTSFDDTTSEDEESEKEF*
>TCRU_5500 FYVE zinc finger containing protein, putative
MNHSLRILPQNEWYKKSEVSACQNPGCGRSFSLFNKPENCHACGMVMCTHCLKRQLTLPG
HPGSAPVPLCHACAICVAKLQADAENAYHQQGQLLNMLNEQREELERLLAISSSLREENQ
RLISLTEVLRAEVEQPMVKSDMGEALLSHSSARARRKSSSQRTPVRPFTGEVNAPADDGD
DVFDGPTAASANSSSRTATVEGAALAEELRAKQRMLSRREEALQASMKKVTSDATRIAAQ
RMQLQEEEKKLRARMAQEFQAIVEEECRRLQNVYMEELTTLGEQFAKWRRNADEMLETVR
LREHRNTSVELSTVLGPENTVQAVKCEHATYMTQQEEAYKAKIAQLEELLRKVQKRFDDD
NFMLQSALGVARREVEMEKRRFEASQRATGVLTLKMQEEQQRYELTCAELRGRLETMHFF
HVKWQQLKPPPPPTPLSSSLVLSRQDDTKDRVATVLCTALSEWRCVAEVLLSQHSASLSA
ATLFACTACSLAASPLPSSPTKKEALAKISALAGEDEQITELRCELGSAQRLSKVLEDRA
NEHALEAVSPARTVAPNTEELQQLREKLSRTERALVRASSIEKQLSQQLQQQRREREKNEG
PCAAQGESSASVLGLAAHMMNHAGLYMDGCFDLLRDALLRRYDAGVQIMHEELLRRRELM
RRNTVALEQTTASMKKFQEGLKRRESAALRTEEALRAWEQDTRLRLIRLMKVSAALRMVA
ERLRVASTNGETNRSRDGNFL*
>TCRU_5501 Plus-3 domain/Zinc finger, C3HC4 type (RING finger),
putative
MAEARQTDFLVDEHTPAPPIEILLKLQLFRTALVNFIEWKNFEEVVRGCFVRVLLEMRSE
DVRRDNSDHYYIACVKGARRGPRYSGFSADMASTEWHIVIELPPCFRATQNGNVVQLNSI
SNSPFRQLEYQQWVEMTREAGLAFMSMPQLHFRLDLLEEQKQQALTVEPRRKRYGEDPQM
AERRERALNALRDQIKAEVVSTHVQMPSISGLQLCPLEQLQEIEREMLEMISRVRMTINE
RSKCMICHRRLCTVICYPCKHQVLCKDCAEHIDGKCPVPNCSIPVRESFEAYTS*
>TCRU_5502 hypothetical protein, conserved
MFNSPLSVDQRSCPSFIKAKKDYNAEFLQDPFNRLPLSLRDVALKTPSLRRDASGSLSPS
PSSPSARRKRRSNREVYEAMLRRDIIAAEKKEEARNMAVQQELSLCRRTPRISEMSHNLP
RGTVIYERLDRLHKEKQKREEFKRRERERERQQVMEGWFVPNITDRGRQSKGRALQETEE
YLNCHRQQEQERTQRAEERRHHRLAEEMAEVYGSPRINLRSADIVQRARERNGFDKKFFI
EAMLEKAAIARLALWERQEEQERAESLPFAPRITAHAATLKRDGDVVDRLISSAKKPSAR
PCGDIMHTRSASRVRSRSEGHLSRRKKDTEPHEQEHSGLNRSSNHWMGDSCMVSMDERRR
RYEIQHEEKMRAIWEAERRLHKPTINPCSGMTVSGLPVKSPGHLTTVRERRENAVLQESG
SSRLASSHGSSWMDAREAIRHSDSNCYHRGPEEYVSPIQTPSWGSGKTSSTRGKDTIYER
MRRWKQLRDEKVQRMRDELQKEKMQRSVEANNTTLNAEKCMEDDLASPEVCPGKTFPEEY
KTPRAPTGGAGSVRTPVVLSLLERPDDEMY*

>TCRU_5503 hypothetical protein, conserved
MRRCFATRLTFQRLLCGDKLPLKDAAAVQETASAFRTRYPLVPIPVPIGAALSRNYVLQG
EPKRAVALLAAHPSAFALAEETKQLLSQDANVDADTLLRLVDAVRPVSSVISCDFLRAFA
GRLSREGKTQEVKQRLMRDIREVPHLAGSLLCPLTEMSDAASSEDKVNVAEALDIALKRS
FVSPKDYGHVLLLLSRGGEHRKVLALWSWMRHSSARWDKTAASAMIISASLSRKMNAAIA
AIQTLAEANEDPTIEAQKYFIRYLASRVPPLSRYADQLVSHWYTETQLWTTEARVVGVEL
LFAHYHGKDYDQLRDGLIRAGREAVTEEAKQAILRVKGIPYIMRHFAYNIAEEPWLQDFY
NSGMQMKDLGEYPQLLGLLASLARHTEAEKKFVDSIRELKITVEAFEEMATFVADDICFK
NAEDTLHFIHSMAEALSQQVPMNLRSWLELLGQK*
>TCRU_5504 hypothetical protein, conserved
MSQHEFSLLSHLGVSVPEVPSQTVQKNNRREGNYRVLAPCMRPPVKGAIAAQVISPRRVP
RVPLADYTGEVVVVKGKAGRPNTEYLIYNARVPCIRAVNLQLMKERRRQREEEAVSRISP
DTFFIQTSEREDLARRRLLEHLQNINREQAQRKVEERERERQRRLEVEVAELKAVKEAAV
NEAAALLIKKQAARQAMQRELLDAMERKRQEAADGNNHLALECAAFPWDNAPPNEAKRRE
ICLSLLDANRKLAEDKKMERQARKIEERAREAAALEVVRAEVEREDRRALEKKRYLCEER
QRSGMGTFVKAAPVVLETSDLGSEWFLRTTREDAGARRERQRELMEANKRLAEETKRRRA
EEVERQIQQEREALREAERAYTQRMECDWAEKRRQQDEFKKEARKTAVERHEKKRISTED
DLCLSLFQDNCRKAEKEKQRREQLYCEELKRGVDMARESRREEKEREAMQEKKYLEMQEI
ETKRALERERAKALEKREAYRKALEEQIQSRKTKPACQAPVTRHGSVLKVLYRCPVTGDL
LPPDQFGIFSVRQRQSGWI*
>TCRU_5505 Mitochondrial SSU ribosomal protein 29
MRSRLVGKSLASLYVRPPVTCYTDACEAPVAMWNGAIPLKEVRVMQKGVPVRYVKKLYSH
PLETSPTRLSFNDINSMYCVGNEELMQFFPEGLGGKVMQLMPPGHPRGFLYRKEAHLLNL
FIDKIQHWQAKRNVLSSLTNNRPGFIIDGPKGCGKSALMCQVVHYARSRNLLTLYVPNAK
EWTHGEWCWPSTILPGFFDAPDAARFFLRYFAKANRSILLSWRLKCTPNDLPVEQGERQP
QNLYELCEWGHQVVAPASIDRQSVCVKFLMDELSAEKKLPIVIVVDGWNLFSHDTHFRYP
HPDFLRTLASLNDDSTDIDLYPQELPRIPASRLGFVRGLNKMILSKDEPNKFFFTCTTRD
FKPFDGISGFPDVETDRFTNSLDEYAPYDAEKDSLFHPIQLGNFDEYEFRAFTRFLVNSG
ELAGLGWGPLWHFSSDFERKLYKIGFLSNRNPQGVIDHYHQELVWRYEYQRTRQKQYLLH
RNMELVVSKRKNRYAEPKGG*
>TCRU_5506 PITH domain-containing protein
MPCNCRHGTGSHEHLRDGFVREGVFGIGSPLNEQVDLPLLQLWNARHSAFEAARLFDPKM
EDNQDAVCSDADPELLFLVPLKQVCRVRGISILGTNDDFAPAQVKLFCNPTDVVGFNSVR
RLQPQEEIQLAQVSSGDRIVYRLNPAKFSACSNLGLFFERSFGEDETHLLRIDLFGESTG
RSVHQEVATNIVYEAQPNPADHKVSDEHLKTFTVL*
>TCRU_5507 translation initiation factor EIF-2b alpha subunit,
putative
MEVPHDDYDISIMIKAVKEVQYLLRSKQFSTYSELDKEITETLRGYESLGDGFERFRVHL
TKDAAISHDLQRSLSDMNARCEARLKDFEWSQKDQINDMLPFVGSTSRILVHGCGGLLAV
AIACAIQERCGVHFYICEGRSASKKYSEGTGVALLERAAQTQEGMRLKDALMKSCTIIPD
AGMGAIMSKVDFVVMGAYCVTEHGGLVHSTGSLQIATVASAMKVPFYVLCETFKFTRIFP
LSTADLKQPEESNDVPLVEFVPPTMITLVFSEQGIMPPSAVTAEMFRFHTARFAPGKRKE
LFF*
>TCRU_5508 hypothetical protein, conserved
MELLPRYLNEISDGVRQKRLAAYEKLLHLCECGSLNNVEEFDLLRCCLRGFEDTSERCRE
YSVKIVTCVLPRQGSSVLDWILPAVVTRIGVLPVVEESEEVRLLLLRLAVLCMETYPNEI
GPRNYIDFLKILLENCLRDSFPQLKKEACCACVRLCEIEPVQVKYIALSLAKVVKCYLLH
KHSVVRAEAVRALTSLIRHGAAQILSDEKEEERNKTTVSILFVLANDHVEAVRVAVLELL
STAFLDIVERLEQHRKYLPHLLLLMTDDFVAVSTKAYEVLENMGKLYMLDNEDNSIDITK
RRVTMKDIEWYGDDEYPDMTLTTVDVNLYRVLQVRPSLGARYVVAESLRGFIEKILTDVT
AIDWIIKFSSNNRRVIALRILWMSIYHAEKSVVQFVEQILGVLYKSLREDNQDVVQESLI
CVEILGKFLTPDQYMPFLTGKGDLKQAEEDNTVLIRLHSKTILVSPADGSLTPAVTVFST
AAMSVKCSILVTFRYLIEGSKHLLSTSQANQIVRAMTSADVLETDSEALICSLLDTLGVL
ARVLGERGFIPTATNPLPREICEDLTRRTLDSILFYALLCLRSSDFPSVQERVSRRIKDL

SSIVTGEADGIYGLHFGRLLFRYGVHMPVSAFSDLVLHCKNIESHAEQVSDVFLVKLNSI
DFSKSIAEELQYLRVLEQLLWQKSSFFTGTQLEEILRLIILPLGTFHPGRQAYLIRKVAI
GCLCAIVEEKHRRPLLTAFEDNNFALSSKTVAIWCNASDADDAEMRLLCMESAANICSLP
MHAGSANDILQSILLRFDDSSDVLRVRAASGFLAVLQKKDSVSCIVIDQIIAQATPLVKK
VLIHLDDAEETVGLRLVIVDVLKCIAILSPSITAELVIAAQRKHHDSIYCESVLRYIDSL
ES*
>TCRU_5509 mitotic cyclin 6
MNSTTLREVSNLSGSIGDVKQRLAQRIGGGWGSYRLGSSTTVSRSSLRDFGSGATERAKE
MLVSPRADRYHAEDPVYCNDLVKDITVMYMEKEKQAEGQLANDQVVVSPKYLTYQPEINE
KMRMILVDWLIDVHLKFKLHSETMYLAVNILDRYLSCVNTKQSSGTYVARSQLQLVGITA
ILLAAKYEEIWPPEVKECVHISANTYTREEVIKMERNVCAALSFRLTVPTPFPFLVRLLS
VMEGLVHSGSLSEDYTLQLPLLRHTALFFLEHGMLDYKCLQFKSSQQANASLFLALVTLR
IKQKGGSCSFAGETIWTRQLQHYSRARVHEFKACAEAILEFVNYVPTTKYQAVRRKYSSA
KYGEVAKLIMPNEVPDY*
>TCRU_5510 dihydrolipoyl dehydrogenase
MFRRCAVKLNPYDVVVIGGGPGGYVASIKAAQLGMKTACVEKRGTLGGTCLNVGCIPSKA
LLHATHLYHDAHANFARYGLMGGEGVTMDSAKMQQQKERAVKGLTGGVEYLFKKNKVTYY
KGEGSFETAHSIRVNGLDGKQEMFETKKTIIATGSEPTELPFLPFDEKVVLSSTGALALP
RVPKTMVVIGGGVIGLELGSVWARLGAKVTVVEFAPRCAPTLDEDVTNALVGALAKNEKM
KFMTSTKVVGGTNNGDSVSLEVEGKNGKRETLTCEALLVSVGRRPFTGGLGLDKINVAKN
ERGFVKIGDHFETSIPDVYAIGDVVDKGPMLAHKAEDEGVACAEILAGKPGHVNYGVIPA
VIYTMPEVASVGKSEEELKKEGVAYKVGKFPFNANSRAKAVSTEDGFVKVLVDKATDRIL
GVHIVCTTAGELIGEACLAMEYGASSEDVGRTCHAHPTMSEALKEACMACFAKTINF*
>TCRU_5511 hypothetical protein, conserved
MALNDVSGRGGGGGVRELGTVTAGMAMMNFDEKTRPYTRADFLRFLQNYEENLSPSEMRL
VEKGMFGTFVGMPLGFFLVYKLSGRLAWHRVVRVFATMDDKEAAAKPSWIVRNIPRVGRT
LFGLTGATIPYMLIQQWFISRVLELDEHDSNLSFHVRRLMITQRSGMMFKRTATREVTRE
EQDRLLRESAEQMEENRSGRRGGAPAGAVDVNLRLGQQVLTPVAQSGYKPMPGKSGS*
>TCRU_5512 hypothetical protein
MTLASKEDVQTPCKSNLTPLREVGEQMTASDEKTVDALSRVLEEVLSVSYLRDHAHEVYD
ADTTDPASPASLLAAMDDGLTVPMSYLVGLPAVREIIPIGLDNERTADLFVSATRMSQKI
VLHNTQRGLSVGPFPQALPRSRCTLHIQGVSSTVTVADVQDLIPRQNIFHFYRLSPESIN
VAFENARSAKEAFVLLQGKPIGGCTSVQVKMRMENEKHPQTILHRRHNWTGAMPKTASTP
NNNSLTANATAAATANTNTVSPVAPIDAFVPFSKMEELSSARSPWVKASRRGSMLRQFPS
MQQQQQQHADIFSHRGGRRGPRAGLMSGFFSDYYSPNMQWLTIQRYMWNNAAAAAANAND
AYQRQWDENECPSINTAFGYMGNGAGMQNPALAPPCPVGDDHSSPEENAWLACGPNLEPE
ILGYNAPYTVEMQPFLNEDNYVNLPTETTQSFVNGPACSARRRRVQRDPYKGGILVDSPE
VSNNVSTVFVSPGSVASYKPRPMDCRILSPRMLHPEDFTEPAEKAKPVSSMTDDESPAQL
TPCETNSQAHSDAESGVRQQVLCEGG*
>TCRU_5513 T-complex protein 1, alpha subunit, putative
MQTKQKQTLGINGSRTSGLSVRRENVTAAMAVANIVKSSLGPIGLDKMLVDDVGDVCVTN
DGATILKSLDVEHPAARLLVDLAQLQDKEIGDGTTSVVILASELLKRAQDLIVQGIHATS
IIAGYKLALREAVRFLKENLSLPVEGLGKDVLLNIARTSMSSKILSSDADLFAKIVVDAI
LSVKTVNELGDVVYPRKAVSVLLQHGKSSRESALMQGFALGLSRAAQGMPTSVQNARIAL
IDFDLRAVKMKLGINITITDPNKAEAIRQRELDITKERIKKMLAAGANVIFTSWGIEDSM
MKYMVDEGVLGVRRVKKDDMRRIAKVTGAQVVHTLSDLEGEEVFDPKWLGKAERVYEQRF
GEDDVIIISGTSNAVCSSIICRGANYLVLEEMERALNDALWAVARTLEASRVLAGGGAVE
VALSVYLENFAHTLGSREQLAIAAFSEALLVIPKTLALNAAMDATDLVARLRVLHNEQQA
AGKSQGVERFFGLELIEGTLRNNVEAGVLEPQPSKIKSLHFATEAAITILRIDDCVRLNP
EEEEERR*
>TCRU_5514 Tetraspanin family, putative
MDAMRSGERENFDDSFVEDILHSRSLRNQLETPLIKNSTKNISAFAAAAPQEAENSPDAA
SSGRQKSPRVSGSGESESSLRGSRRVLQSLFGYALIFINFTFIMASMLLVMSGIVARQNA
AVRLCEPCGQIAMSALVFGIILCLFTILGFMWIRQRQMMFLLVYVGYLVVLFIALFALII

AAAVYDRDTRVSVMDPSKFLDAWKRGVNNTKTGRNHDICLLQERFNCSGFRDGCCVAGVC
YDAIDPPEWVDAVCPLCPSFPPMSPVVCTDVVYSTVRKNLSGFLVISIFSMVLVVVGILF
ALLSRSANRLMMSGGV*
>TCRU_5515 zinc finger ccch domain-containing protein 14
MKEPTVAVDLEAFLRASFPSRCDFFTTEDATRALADYTAASLWEASLAVDMRRSHHTMEQ
MQTYATRIAGGRRGNGEEGPRMTAMLPGIQDSHGGKEAAWESGDGSVRSLPVKPCVERNR
KTCKQFWENGACKFGSRCLYHHLAPSQGHLADPSVTKASVGHCFGIANRCVEELPKPNVS
GGPLDLNSKEGKRELLAALPSSVNNYSSSAPRSHSGALRATTAMPQEPPKPLGGTTCPAF
AAFGGVVVVPVSLPDGSICGYAPFPLQMPLVRFPRP*
>TCRU_5516 hypothetical protein, conserved
MAFSGGDSRCVLGTHPHTLPCLSVGVSAAAAWSTAAAVGAAEDEAPKEQKRPHLLGATTM
ADENCFFAFASYIAKNAPCRCLTGCLHSAHFETLFCFIQCDVKIIMAAPSLNGSECDNTN
DGKESDEDYDDLHRGADYLRVFLHESREGLNAVTTIPGLAEPLAFALSHDVISAPCVEAD
PFTVEFTQQLSSGCAADPALALSHVFQRCLACDLMSVLSGPPPPVFFLCPIRNTLRCGGY
LLAWPSTHVTMLNGCVFCLAGTRETSVCADSTAKVFVDGSRRN*
>TCRU_5517 hypothetical protein, conserved
MMSVSVPTTPHHEKDRVPHLMSDEELRNEYVQLRKKNASLNEECASLQMEINSIYEESVR
LQQSTEIEEEKLANQLLRRLQSEELQKRRFHDLIRREEVARQKIMNQIAQIRTEKTDLAG
QLGKQESLMLQLQKKLMEVVTKKSEVERELLKERRRYLDVLSTQLGLLIEGSINEKKGEK
ASDAGQSVDASEQKPMESSSMDADSKTINCATSIPAFEAATTDTHVAINRLEKQLNRLLC
EHAAAVQNLTSNEVCCAELAKKLDTIQQAAFLDRARASKLKEELKEAKSRLAGLERQMSQ
MSSSAISEESSGIPTPTLCCLRSFSLRGRTRGALSSRQRETSVSVQPSVDASDTGDDSRS
>TCRU_5518 thioredoxin, putative
FLSIPLFFMVLLLTSIVFAEAFPFTKFSGVVELTPATFKNFVSSHKPVYILFYAPWCGHC
RRIHPEWEKFAQSAYGTVRVGAINADEHSQIAGQFGIRGFPTIKYWNVGEKDINKPQEYN
GPRQAKSFQANAMNQITSSGIKTITSSDALREAVQKAPEKKIVVLFSSKPRIPAIFAVLS
HSPRLKSMPFYFVGENAKKEVSEEFGVQERPSIAVLNATEGDIKTVIYPGKQIAYEPIAK
FLLACATDDADNLDAAKENAGEHPQENDSGKGKNTAAAGGGTPTPALPVRPVRLTAQLLA
DFCLPATLRVHERAPLCVLSFTSAFTLERVHEMFHNEPLLFFEADAERDVILSALRNDLG
LEEVANSVEGGASHQMLLLRAAKRDTIRYKLLDGIETVDGANEVLQRVLSGDLQLGKK
>TCRU_5519 dual specificity protein phosphatase, putative
YASLFLAHPDLLFSNRAAVMCTGEFAPGEVVGKYSVLGSLPTGTVGRSFLVKAPPEERGR
GRGGTMGKTGKNVGSENNVSYQLSSSLTSQSPENVFKVVTFVTRMNLAERVLDDHKVLTN
LIHDNVLRCVDVLDDGQHENFVFVSPYIENGSCEALVGKLETKERLLSLLHDVAVGLRVL
HSHRIYHHNLKLDNILIKNSGTACIADAGFGHIFASQSSEGLVFNGELACMPPEVFQTED
VSAINHFKADVWGFGVLMYRLAYGRKPLDVEGKPFGTIRDSVLHGKIECPDADWVSDVSF
QDVVLWCLDRDPNNRPSMIEVLRHPLFGENVRQSISGSTISPPAATNSHYGGKVGSIASL
STIGARFSRSQKRGGLPISEAFVRGRNCETFLVNSARNMTKIVLKVMRRSVMKKLENLSY
AGNILHDLAFCRVARHPNILHLVEIVENKDGCFATQPYAEGEFLSMNFPPLTNIEDPYFT
LKGMLVDVLRGLHFLHTNGVSHLCLTPSNIFYQRGVGFVLADFGPLFLTRDEALTKDDMG
NFWYSFPPWVIEDLKKPLHKTKHAVDTFCVGLLAASVIPVVYKQVWQSFYSGNEGGTIAQ
NVIKKVEEFLDLLTQPVLSFISKAITTKTSAKELLSHPYLADAFDDSQLLGVKPLQLSSA
SIKGAVSLDFSFREERRLMDVVGQDPIIDTEFFGNSNFVDSIVHEESRASVFDPKELDSS
VLLHFKDKIVCGLCHVDLAIVVFRCSVCPSYIRCGKCALNDDHEEGHEMKPYLIHTIEHK
GDGNQEAMLLPPSSIHNAHVLEEVEMQANLPAGSIVDITNCLSSPKGISLSHFKVQCRKN
KSKKKLPKACEIDDLSWEEEINKCRENGNPELLLYRFDLTSVPREVFDPPLLHVVSLDLS
YNKLTSIPHELSFLHKLRSLVIASNELSELPDSLGNLSQLERLDVSHNQLQQLPQSFMYL
YNLATLSMDYNNFAGIPESVLEIVTTAPSMAMLSVIYLAENPRITEFPDQEVLEKFPKLK
LALDNEPNVYRTYISEKLEEKLPNVSIMWNKIYPDRIVEHVYCGSLRSAQSQLVYDKLSI
KSLLTVGRELVPTPPIGGDHLTLSIDDIEGADIRLTFQESVDFIEKSVKKGRGCLVHCFA
GMSRSATTVIAYLMMKRGMRLDEAYLKTKEGRPAIYPNQGFFNQLLQLDAELFPQQRPLN
MAAMERD
>TCRU_5520 8-oxoguanine DNA glycosylase, putative
MHAWYALPSPAAVNLPMTLCGGQCFRWRRTPRGTWVGVVERGAYELSDAAHPPEFQAVYS

RGEEKRGMRPSLSHPSDDLSGDVLWFRCLHREPKNASDLSTEACFLRHYLALDVDLQKLW
RRWTRDNPMRNHPLVRYLTSNAGKGPSVKIRHLRQNIHETLLAFLCSQNNNVQRITGLVE
KLATSYGDHLCDYNLETGDVRNVGYLNHSSTRSTKNAKRADTGDGDWIPLHTIPSMDELA
RRSEDELRALGFGYRSKYIVQCASIIQSSGATRRKKEEGVNCFCSSMQSYKWYDDLLDPC
LSLSDRREKLLSLPGVGRKVADCILLFAVGHHEIVPVDTHMAQVATEYLAGTATCGKKVL
CNGMGEKRKRNSEGKSSLTAVSTDGSCWEKVLADWYRKGKERDMKMPALLHKHHDAIQLG
FWHLFGDYCGWAHSILFYARMR
>TCRU_5521 multicopper oxidase, putative
LLLLGVAMPGSGRELAPLREVFPLHGRTVVDLRVRASEVSVPLRGYGEGAVFTYTGRLYV
YDDVASVPGPVIHVKPGGKLVMRMFNDLGGQTYAHGEDEFYNFHEVNTTNVHFHGVHGDP
RVDDVFKTASPGHFLKYELDIPKKHLPGFHWYHTHAHGSAYLLLMGGLFGPFIIDSTKND
PIASLPSFILMVHLYRLGKSNLCDGMTMEEVDIAIRTNMSSRPRILSKSGKVLPMPLDLF
LVNGQHKPTMNINRGEKTLLRLAFAAGSCHLNISFPKECRFHVAAIDGVPLKCTRELKDN
WLYFTTATRYDVVAVCEDDEKRELPVISGRLEEPIFYIAVRSHRSKQRRPHEITFPLCFP
LTNVSYLTADNPTMWRDISFSQEQIPTPKPYYVIGYGTDCSSPVHSGTCFREHFSGEKGE
LRENYHGFVVPLGATVEARVFGDPTDIVPHPLHLHVNHFVFVSFTPRKGGLHENFSMSEF
GVFSGELRDTIPILDGETIIRWRAATYTGEVVYHCHILTHEDLGMMTSYLVYSSAAGKTR
TETVVAADKIVGEGDAGRFFFLVLAIMFLL
>TCRU_5522 inorganic pyrophosphatase, putative
GLSLALPRWRRQEVGAPSTHAWRMFFTSDSVPVTEARTEPAMPTTGMRSAWHDLSLHPAA
DPSIVTFVCEIPKGTRAKVELQKEEPHNPFAQDVHKKKEGKPLRFYTYGDIPFNYGFAPQ
TWEDPLLVDADTKCTGDGDPIDIVEVSDSPLPMGSIWAVRVLGVLGLIDEGETDWKIIAE
TLRPEGKMYESLEKIPQELRDTIVRWMRDYKTTDGKKRNELAFNGELRGAEEALHVIRAC
SRQYATLIDGNAQNPGYWLR*
>TCRU_5523 hypothetical protein, conserved
MIILERTPMTNGEVFALLRRRRDERNAKAQFPFGMQFVGSSNMSQMQQQRVSASMAANAS
AHTSLFFPPEALVSDAKFFIVNGTISATPLPNANNHLLFSSPAASHLMVLLTEVRALRYL
SRYATISGHNSLNALYGPTSVHTRRYQELGALGSGENLPRAQRQSEENGFDALPPQAGEA
PREINAVTKTQEQALTQLVRRYRPGTVGHVRAVLALLGIWETNGREMERQGSTRVKLVLR
AVRQRLSDSARGNEEIPIVHNNDKDNQNGEQQQQHLPSEQLRPLFTPPSLPLAVFLAEQP
PVVTAADTSTENYQWTEQDVIRLVMARPQSSLDVHRVVENIEEIVGHNEELLNFFEEELV
KVF
>TCRU_5524 Tryptophanyl-tRNA synthetase 2
RKEDVVTPWGVAATGPRGGDDGRVLARFRSEPVDEPLLQRLEETCNGRGEHAQATSTAQE
EAGRMALHHFFRRGIVFSHRDFGAAIDCVRASFATGTHRAYLYTGRGPSARSMHIGHVIP
FLLTRYLQDALGLPLVIQITDDEKHFFRDIPVSGERASGLVVENIKDIIAFGFDPRKTFI
FRNTVYMGDMYPTVVQVQRMLTLSAVKNAFGLKDSDNVGKAAFPAVQAAPCFSSAFPRVL
TASWDPPLKCIIPCAIDQDAFFLLARNVAPRMKCCAPALLHTKFLPALKGAQFKMSSSAG
ENGVITLHDTEQEVRKKVRKAFSGGGGTLEDMRAEGVNLHADVAYRLIRFFCPDDNLLAE
VTSKYSRGEMNSAEVKDLAADVVVRHVLSGWQARRAGVTDADVEHFSGIRSIL
>TCRU_5525 TPR repeat, putative
LEEDFTMATTLVREGSHNDAIGVYAKIVEDARATTPQKVRAYSNMSACLAARDQYAGALD
AAKKALQLDENNSKLHGRMATAYHGLKHYEEAAQHYHRAHTLDPTNALYVEQHQVVLELI
RNGKGIATQETKDAYYYRKGIEQGKEAMGKGEYLSAVRHFSKAIELHARCSTGSDERNKD
NSTDVSSSKSAELAVLFCNRSAAYSRAGRHLESLEDGMKATEVNPMYARAFFRIAHAQHH
LKHPHEAYTALRRCLELNPNHDEARSLMTDVEQLVMDLRKTAEEKQREREEEIQKIREMQ
STERVTDSANVPVGHRSRAHATSYMHCGYCNEAGHTRAECPLLRRKRSRTS*
>TCRU_binding protein C terminal, putative KIF.1
ESVRNAYKESPSQTAMSQICRCYVFIGFNMLETDEETEGVNEICKAYTLTLFGAKKELLD
DVVDIAAHPLEEILRNEVPFVTAEKEYAFVTEFMRVHNALGFYFSNRDVELRINDAKQVL
IVAEKAYRAWNDWFHQSFPGHCLMKDIPVLENGTLDRASISPDALPIYIVRFEMDTAFTS
TLFFLAQVYTACKMTALASRYCHHTLYHQLLNKMEFSKKDWATNALHLSAFYSSCFEYGK
ALHCLRAGEYIMPEENANEETLGIVAWAFGKFYLHRLHYYAEVRRNCAPRGHFPDEFEGW
WVDFPLDIPPPQPLPAIETFEDARECFKEANVWFNKALNYYVYDGCCTEHIDIKKDIAQL

YAALIPFEENRDRIIAMHQRRIALIELFPSDLNFNAYPTLVRQLLFDLGGMHEEMLEVYI
QQKNSPMEGEKPLSDKKINAFTDKVQGFYRRFCDTWKEPQTNKIPETIDIDSRLPFFRSL
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VRQKDLWRVY
>TCRU_5527 hypothetical protein, conserved
MGIFSKKRHGEMLATDDEGRCFTWRLENFSSFKLGTTLDGMNVVAFTKAKFHLHMTIDTN
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GDDVLFVNFCFDNDSLALLRVSPKNLVVTWTVPHLFRQVLNPYSSNGFVHEGVLIGLRLE
IKKEAGANDAFAPYDVRKIKDLVFFLFSRKRDVPPHSIELLDSRGMSIAKLDRKETPGVQ
TLTVSKEVLWDALGDDGDLQVRVEIICRGNPIDALNALSGSQLQQQQQQQQQSELREGG
QAGPPRTVQIGDKKEEYVV
>TCRU_5528 carboxypeptidase, putative
MKPYKELERVFTKLYRYGHMLLLADWDSQTMMPCKGSDARGAAMAELQLHMHDTITAPKM
RALIEEAEKSVGDLEQLQRANLREMRRAWELENLLPEEFVERKTVLTTKAHQLWKTCREK
NDFAGFLPTLKELIALFREEGKLRAGNSGKHPYEALVDIYEPGMTLQRLDEIFGNVRSWL
PGLLKEVQEKQKTLGETVLEPKGPFPVSKQEALCRFFMDVWKFDFDGGRLDISAHPFCGN
SKEDVRITTNYTETQFVTSLLGVIHETGHAKYEQNCGPKGFETQPVCMARSLGVHEGQSL
FAEMQIGRSGAFMEFLAPRLVEYFGDQPAFTSSNMKRVIQRVSPGLIRINADELCYPLHV
MLRYEIERDLMDGNIEAEEVPRVWNEKMKSYLGLETLGNDKEGCLQDVHWSGGMFGYFPT
YSLGAMVAAQLMSCVRRELGEEVVDECIRKGDLGKILAKQNEKIWQHGSSLTTDELLRQA
TGETLNPEHYRRHLERRYRDD
>TCRU_5529 NUC173 domain containing protein, putative
RTLLKHARKSANMSRQKLLELRRQAMAVRRQKAELQKVETKKTALRRIQSAHNKKTHKTF
DRDILRCVQDGLVESIEILGEAVTPLSFFMAAFTALSRSPEKHHISYLLAIVSACAPRLG
QGILMHQLDAAITLTEQIIAENVATNHLVVAKAMKFAQQLMLSLQPPSMRLLSAFSRLEP
SKLQVETMKMYIVAFRKLLERAALCVTSPPPSAHSVRDAKTGAYVLSENQRFFVEALPRF
VKVCVANFTDSPVNVVSTTTSELAGLFQRTISPYIVESLEGREMIEGVVSTHLLELLKPH
CQLYWGYALEIMESLFGRLNYLKRTSSGDAMSFTQRFPSFPFLLRVLNKLRVMDDPKLNG
KIERVMVALGKGMSVQEFVGIISFDPWRAHDAELKAADAVTEEDAWATSYVLGVLRRIAS
HDSLPFFVENFFPPIQFVRNIALDYEKQQRMELANKWTALLQQYWRVGVGFCHYPRIITK
DSFREVAKQLVGLMSHPLFVDTSATALHVLCHGYHELATTESLEDDMDEIVGNNEGNEEE
RLDDDQRETFTQGNRALPQKSGLEEDNYFLALNDPTWNRHIYHGISQERAVDVCKNVIAR
FSSNIMPKLCNTFEGHDSTAILLAIQSFSRVCTPDVMQVILKGILDLGTNIALQTQGKDI
TAVTKSNHTPLTGKRRMVLDISCAVISQLPAVHVETLFNDFIEPVLMDPVPESRLLQKKA
YKLLFAMFEHRMKDIFPLFPRIAGLLTVGRQHITISGIKMRLRCLVWALDACKMYYPEQI
VSMIRAIVGETIMLSRERSSETRATSMDLLEKMQRYLVGAGNPVNMLLRLVLAGFSGKTP
WMVSSTVVAMAKVVYVTHQELPEADLDAAISLGFRMMESALPDVRSAAAMFARMVLKLMK
RCRRVAAAVERSLPKLLLAIALTTSQPSVSSKIRLQMRVLLEKCIKRFSFERLEPIFPVG
SKNFLRYTQKMMRREQKKEERELMKHATEKKNEFDRLFLGAAMKAGTEDDAERDLLQAGA
LTSLVSTYDLPSFGIAEDAEDSGDELDNMHLEFQDGKLHIMSIEEKRQQVERQRRQEMAD
RLLHRGRHLAHADSLNERALGMRGKRFRVEAEDFENDELLLRYGNKISNESARGTIAAAQ
SRVGPGANQIEKLRDQQREKRELKRMRVEEDIRKGEEFKGRGDGDVRRGNMAPYAYIPLN
RQYMNKRHQREAMQRLMTVAHPHMKGNKAKLARRAKNK
>TCRU_5530 hypothetical protein, conserved
PSPPCGSPLPSDVTEDDDPVLPFLLPNSTMPLTQLAKLLPDEVLEKLENGLKSHLENFPA
RYRIFRGTNGLLHAQCVTPAGNNGTKSTEEGKVEETQGKKKVSLSIPIVPGRFLTLESFM
RFNYAARPSGTVDFNASHKEKDENIQMMKHFFHGYVHPVKSAELWLLTAEYKLSKFPSAE
AAVTVTGVEKRTVVDPEMSGVMEGKEVLQAFRWVHLDNREKLNQAVTMLRSEACSDSLGN
DVGEKRASHGEVSSGTTFRRSSTFVRFLVPTAPLPMDATTSSHCLENGIEEYNFYRMCRA
LSTTTFMRLPELQDIVEGWLTQPLAAVLAIAGEESKTTVGLNGVDGKRSLLEFDCDPDDS
TRIVGVRFWLDEERYLPPQYRSMSPAELEKDLSELETITPKDLNQLSNHKRVKIIDRKRL
LKRCIALHELGVSPICHPDVLAYYVFDILPMDGQLILTGHLPKLLPETMRRITDARSRAW
LRGYPHLFRLVETPPEVCVQRMEASAANSDEDDKQDESQKFKEEEQDTATGPLKASCEYQ
QRLLDDPEEQLRVVVSIVAARLGTCGSRKLLPSHIPKFISSDVRRKIFPRGSGGPKEYLM

RYPEVFILTDGIHPHEPVVTLAPKYHPN
>TCRU_5531 hypothetical protein, conserved
MTGVFLKSCDSPPANACGIPMVDVQGGCQLLTNSQVFQQNCISPSFIPILKEMIPRYEAM
LGFGGSWFWNCYLNALHGEDIFLDLKGTGVSLSEDSLEAQVSLRRKLASLDDANMFEVAA
EHCCSKVEALCAMCLSIVLHVSHRPMLESEQGPQALVLCATKDQCDELYVLLDRFGSALH
LVTHNLFGAYPPMPSGKRADIVVGTVPLWESVAKLSLLGTLDGLEEILYQVSHDSRWTAS
STRWRPYSLDFVVQLFFVDLDLQHALGYGPMLQRLFMEHKRPVLPRPKPVRNKILHGTRH
GSISFSGLPQRCQMYCLVGGCGKGKDLFEILLALRDRRGDGRNKNEVVRISMKQPLVHPD
KNGDLVTDAPRKRVRDEHDHGVAIEKESKRECPRLVVHNALSHSRLMLDAAAFEEFAAET
KRRAQNFWSRFEAKSSPNANENHRTFVIDVQLAYLCIGPDQHSVKNERTWFMAETVAIIT
PIGDGAAHPSRTALLMRHLEDELSGQIFDGSVVQCLFQRGSIDRVVSGAVMLNRVFSATA
KSISQEPLFLRFATEDGEEKEEAGEAKKENTDLEMVDTLTNLAHLRQLAQEASSEVEGSS
SFPLHKFLAVSRCQSRRTVLSFRQIAPTISLFCDAQSNSKSMALLYLEECCQYGKVVSYF
IFGQRRGGKDGKGCVHFFVEFAGHEGAAEAVRQFSLRFASEGNETENHMRVKLFPNELYY
EGVTAELQKRRKTGKIDNTSDNSSDSDDDEFMGVSLLGE
>TCRU_5532 protein associated with differentiation 3, putative
ISEPKRFGMLVAGAYGCLCVSLSYGFNIFSGDLQKAYELSQADMSTISTVGIVFAYFGIP
YAFVYDYLGVTPVFVIGLVLITVGSLLMALTFNGTVAASVLRLCIFNGIFNFGTGVYDLA
CVVTVIGLFPTRKGVVVAVMKTYIGLGSAIIGAIQLAYFEGSPTNYFFFLMGFGGVIGVL
ALILIRQPPYLLTDYERSRLTDAEVEKRIMMKAIYLKQQPPSMRFAIGFVIVVFLILFLP
LQSALIAYLNLSWGYRNAFAIVTIVSLGIYPIVAMPFNFLDRSWKIRRSSSCDAVTPVEE
PVSDNDGTAILPTLEMDYVAPQYQTRFLQSLCTVKLWAIFWSLFCTLGTEFVVLTNSRFI
FAAMSGEDVDNSLNTLLTVLNGVGSAAGRLLMSALEVWTQKRKAEDRIPITLSLFLPTIS
VIVMAVLFLTISNKDILPIPYVIGALGNGFIAAVTILVINTIYAKDPGLHYNFCFFATTC
SSVLLNRLLYGEWYTREARRRGVDVCLDRACVQLPLLVMLG
>TCRU_5533 hypothetical protein, conserved
MLRRSFCFMNRPKGPHGLRPGKEYRLTIPYRSEVTMLRCANHRAFNSNIRELFKKPLMQN
NIKAIPRDLGEIPRNYVIKLLFFHQPIRLVDLWSVCKEHDDVPLDSAKHLRLVLKIAKLQ
RWVYAEKNQTNNLYYYYIHQSRVREVQEMVRADEVRKKEKESLEAVEAEKLRREEDENRR
MALDDKILALQSILISNVAQIQQFDPAFVQTKPYVTEGGAVNVAWG
>TCRU_5534 kinesin heavy chain, putative
EQNACLCVAFEGPRHVICRTARSPCWTQQLVASPRGTLTDDASSLSGTVVASDYYKFAFS
RVYEPDTTQKQLYDDVACPIVDDVMHGYNGTLLVYGQTGAGKTHTMFGLHSPLSEESGSL
SFNMHENAAGIVPRAVRQLFYAIHSAEEVVEFEIRVQFVEIYMERVRDLLNPTGCSLHVR
EDPAGFYVENCEMPYVTSTEEVLQLVHSGLRRRVTAATTINDASSRSHCVLNIVVKSVNR
AKHEATIGKLFLVDLAGCEKVSKTLADGLRLEEAKLINKSLTTLGHVIICLAEKRAHVPY
RDSKLTRILKDSLGGNSRTALVLCCSPSQLEAHETLSTLRFGARAQNVCNRAVVNRQFTT
EELKGMLDLAKVEIQRLRCLLRGKACSELTRETYTSRGHLEAQAGGLSRRTKESFELDSV
DALLQQGVREQLSLEDMRAEMERLRDALRDAQYTTDLLYAQSAAQASVVQILQQECVAWE
EEFSNVTRELYAQRRYAEHYRMLFHEAREEAEVVPLQLTSYMEQLHTILGMVEDGSFLPQ
RHVRRSPFSRDLSQNTNKSESPPITPHAGTGILEGSRGNKKSTSDRKSCPVESQPFVIIP
PRYERTGLRRGDNVTAAVFDSIREMEDNDWIGHHSGDGDQNEDMMLNRMEAVMDEVEKLR
NLNGALTLELQLAEKKLVIRHERIETLKHGLRQECAAKQELQRTLEAERVCHQAQLQDAR
NDALHWRQLYDDLLNNSHTRSRKHNGRHRNEHRSSTPTLEAALTSREPSSPADSPVAMGH
GIIVKPIRGGGQK
>TCRU_5535 Sister chromatid cohesion C-terminus, putative
VDPLFEVLAAFPLPQLLTTSAPPELRGVACDTTQVPDDVIKNTVMKSARTLMASSSYMTL
RRSAERCEEDSDDKGTSQLSPLARRVHEGLLRIEIDQIHSISGMRNIEAPSKQARWAHNT
ERRMELRPRSALDSHDQKEGEAEARRVAKVPKLEPKPSLTAPVLSHDAEFSNAERKSELS
CSSTISDIIEKGLQGAHSLESLLGVLSDAPQPFKNIPADRLTAFVSSLVALPEENATSCT
EFVIPVSVMQRALACCACIAHPSFEPSILAEDTVDHLITILAALIRRIKKRHSAHVPDDA
SGETELECLRNMLNCFAVIVSDTRLNICVHGDLLRLEDLCFQCLFVITNACEQQEVTNYA
AYLLSHALYLYSALWNRLEKQRETTWVRFFPRLPHGENILLRLHLLPSGVKTMALTPAVV
AAAQSLPIVTGNNTKSSAEILQQQCCAWSNMFFQQFLLVDREEKKERDMCSTIALQFCED

LANMVGLPEYPVADMLLRSLLVSFAQYCLSSSATEGLRALFLDVVFSVSCVVFSATQQNV
LHSALPDFSVLTDAQLREWRHLTHPGEATIDTELPLPDDEMRRALLYMALSHRVDDPAPH
VAAASLHLRAAHIFTWALQDEARFPHAVLEPLLHRMHVADGGVSVDWGVLHACSAQLCAA
FEKSLLSAMAKERLPSWLISVFQLREEQHIAGLEASRKKALQHMAKLARLHPPLLAKIWP
IARRCVRDDNARVREAIIPLFLTLFSEMCGSGDASSRVEETATEVVSSLLHLISDRSVAV
VTRAITALDTILTDISFRRFLETSARGENLLTFTESKLLAMVASAKENRHQTCVMRLFLH
RWVGQESVDIAAHHTRVRVAKELMRLTVTNMAYPYEVPESLHLVKLLRGMCRLTERREMS
GRTTKNLGVDSLELCAVMIGAAKVLWTEHQRLMPSPEAAAALAAINALAMACSEWIEPLL
EVLAQILLQSITLPSPPSSPSSQAVEREAMGVTLLHVCRIFRTVLLAPRAPPLSLDTLAR
ALTTLLSRYVGPHQQQILLSASGALTATITCGGGKLSKYANTKYLLLCYSLMNTYYVRTM
SLISSLRTDPQSVAYTLRFLFLLSEFLRQYPEWKRHHQELTEETAVRGSGVPNQLALGDG
ICANVYAAVEQVLKECSEEAQKRTTVIALRVFASLCILQPNVFFYRCEPYLRCALDPAGD
MLLQAQGLVLIRDFLKDEDARVEYAASTNAPVPLPSSSSPSSSPPERKRRKRDELHVEIA
PCVDDQNSGMATWVLQKFHVQILQLCEISSVAVRQLAFEVLQLCAEGGLLPPSKYASALI
VLAADPQNEVIRKAAVDCMASQTKRYADIVAANAATGVVKAFDLHDACGVDVLRSAVLSD
TGPEAVECVHAHLFTSFRKRHRDAFLSSLLRYFYQEGRAAQWLREHREKDGESARSPFPF
LGHLAIVMAHVPYTQESDVLHVLDGCRTAVDLVGQSCLDFAEAQRSLLQPEKRSTHLAKR
RKIDRWSEATAKPDISAELWLCFGILCIFQLRAFLCNEYGLHRAKLRRLAMRRSGGDTHQ
AKPLTRREPQSAASVAFRQSIAAALQTVAPLWEGPSASAAATNSRRRALEELCAALS
>TCRU_5536 cholinephosphate cytidylyltransferase A, putative
EHSFFFTPLERDRIAHAETFVDTRPSSFVTVIFSPLWQAMSRHLVPEMVAPNAITLAGLV
SSMQSYQIISDHYDGSESDPNNIEAQTPILLSCLLCLVAIVCGSLDGVHAKRCRSASPLG
DIFSRVCSSISRIFFALTLMEAFSVRDLHTKWYLLMAMQLVELNTVLSRINADNLKPQKA
KNLAYHLTYCFRDSELSFLILCALITRLVYPSTGFYVLFTSNFPKYSFLLLVVVSFVNVA
LLKMKRKYKSGIALCLVARVVPLYKILLFNNYSVLSVISGALVVALLSIEVHVSNVARRR
VHAGVLCISIGSVFNDIFSIVASVLYIIGMLVDLSYSTRIPLFVPVRNVFCDGVFDLCHA
GHKNFMQNALQYGNRLIVGVCGDEDCENYKRRPIMTTEERVNEVRMCKFVSQVISNSPVT
GVTEEMIKRHNIHVVVCGKEYDRPDDTFYAVPRRLGILRTAPRTEGISTSVLIARIRAAT
DADVVAKDKSSGRSVVRDGS*
>TCRU_5537 retrotransposon hot spot protein, RHS3, putative
RREEQINFNLTLSIKDAIFQGRARVYKMKLNRFLKMELDGRGVADTNRRVLLKEFFKDPT
RYVRDAGVLNEIQASDAYSRAERAVREEMDMEEDVRKLHYKHLRTLLGWSIASAEIRASV
REITKGFLDAVLEELRKPTTTCTIKIEGLYESVYNARWHHVVEVVGGERTQTGTGMEAKE
GKPKKSWTYRAVGDTLEKDDAVQQSGAAPPVLMVLTSDRGWPYTLNGLHRCGNDLCVNCE
VERVWQIVLDDLTKWLSNSDLTLNPSPLPRVLIGTPGIGKSMNAGSYLLYQLLHYDVEKL
QVVIHCFGSAMYVFDKTTKTVTKYMGNKTSKSVLGGLWQRGMKGYIIYDVAKKGTPPDPD
FAPSTGWGMIVVSSPNLDNYDKWETQLKASRIIMNCPDEVDVKAMCAWMKRGLEQDKQAG
YWEKVEKRMEKVGPIPRHIFDENEYGRRLAAVDDALSAIKDTDVEEYFSMGGEEKKWYSK
NPCHKLVKIVRERKVEGTEVFLNASICTDIEFRIADRLAKKKGAKDLLLLILASRGTLAS
QLVEQLGLRAFMYGEFVIALLKELKELPPPSPSEPQDSVLKLNHQGYPTRAVGLAGLEGG
VTRIPMEYRVLYIPAVQNFPLVDGLFFVDSPRKTLVGLRMTTAGEH
>TCRU_5538 retrotransposon hot spot protein, RHS3, putative
EGTGMEVHEGEPPQPWTYRAVGRTLEKDDGVQQSGAPRLRLMVLTSERAWPHTWKWNENN
STRDCYVNCEVDRVWQIVSGDLTEWFSPHGGNDFEPKRRVLIGTPGIGKSMAAGSHLLYQ
LLHYDVEKLQVAAYIFGGSTAYVFNKTIMTVTRYVGSQTSRNVLRDLEHLNMKGYVIYDV
TEKGMPASCFAPYGWGMIVLSSPNVRNYAKWETQVRAERIIMNCPDEMDVKAMCAWINRD
GIAEKQAEYWKMVEERMDKVGPIPRHIFDANKFIAHSAAIEDALDGIKSRDGEKHFTHGG
VRLWYSENPSQKLVRVVRGRGEVGAEVFLNAPISFCLGRRIPHYFGERDE*ERYFSFLLL
VLGKRNTLSSECVEMFGLRVFMFGGVFGALVEDIKELRPPTRRGGQRGSECEPLRAPQRS
YGLVSLKNPFEGGNLEYRLLCTPETKNFPLVDFFPFVKLPWKTLVGLRMTTAGAHHTTAS
TVRQFTECLAAYFNGWEELSRDMSWEMIYVQHADSTPLNDWQRCDVVNSDNVSKKESQKI
AAFWEEKVRQYQVSIPSR
>TCRU_5539 Ankyrin repeats (3 copies), putative
PTEEMCGACDGKVSEWGGVEMEQNCMFSLADYDYPDRHLLRSFCTAPAIPWSAFNPIRGN

IALPNEISAKGITENLAKLSGSNCNRSSGAGGNNNNTNAAGAQNSIAEPVKSIAKFFEEL
CPELCGEKKDSMNRGATYLLLAVVTGSVEIARRCLELGADPNNMSFLSDPDVAVNQMQHG
YSPMFIAVIAGRLDVISLLREFGGSINVYDRWGRTPLHAALAIGNAEVVEWLLSEGVSRC
IGSCVTMLPENTTYPGLAPPIPALQNRPKPCSNPAEADLCHCRLKGPKGYCGCVDDMFLR
WSYDRLQASWLSGMDLSALSAKYAS
>TCRU_5540 Enoyl-CoA hydratase/isomerase family, putative
RAAPAAPEPPRAAPAAPEPPRAAPAAPEPPRTAPAAPEPPRAAPAAPEPPRTAPAAPEPP
RAAPAAPEPPRTAPAAPEPPRTAPAAPEPPRTAPAAPVPPRAAPSAPEPPRTAPAAPEPP
RAAPAAPEPPRAAPAAPEPPRTASSSSFVSARKNVRLGTEDNKIRGHRKRGGEREDRHPS
KRGESFQFRGKPTGSGAKVGSKRLSLNDIIDDVGEIKVVFAQRGTDKPSHTASPPSPPIA
PSAPLPPSPTPSLPQQTLPSFSTPIPSTGGTGESLFSAPVGTSQEGEDDIFFTIAPRTSE
EGFQGRTWPKSVGFSVDEEIETARATRPLVPSPDVAQETNAKLRLNVVNGDEQSMTDMEF
DKNKLNPLPHKEAAEIGRHEIPDVVSERADFTPPMPTKDSSKNNEKTEHSTTTASLKPME
ESSSFPLNETATPSPRNAATKMPVERPPLAPWMPSVRPEDGEDASCAKVSFKNDGSPVTT
ILLETQPTNIMSLVKFLHRTITLIENQHIAPGKKTEVLFTTFPTLGFFNAKHGPLELTSG
ERVELLRAKESLFARMENASKQIHFVANVHGGAIEDFGAELFLACHHRVLLDPAQATFGF
PSIKVGDFPAASTVRRLSCFFGSQRTIEMAPRFHEYSVESIMDVGLLEGHSSPPAPSFLL
RLECAMLEFLSRATQKELLLRKLFFTSGFDTSAVLVSPNPLLKAWGRYAMAAIVQGKCAT
NNDGKAVRTQEMRSESIFSEMLYTTPAINAANVCSLGCEMKRRALPSLPSRRFVTFRGEE
MQQWDEKMKALSSAKDDCAAVLLDCSQRFINATAQIVASHQDILVNVNVVLIGEEHVARP
IISTLPCSVVVSCASPYRVSALGRLQEVRVFAQDSCSSEASETALNAALTYLQTQDSPYV
VSRGSSSKRLIAALATEACRLTQHCDVACIERVATDVLGLFVGPFHLIDYFGPAMVIRML
EETNNMNTQGNPLLVDLLPAIAHHALNGMLNDGYLGVDSRRGGFFSYREDGTAIAPNAEV
LRRYFSRPLSDTEVADRLLAVVVNECCEMILSGCVRSATDANVLTIAAIGFRETTGGALA
LADKAGISALVQKMEELSNWHGPHLRPSSLLKCMAHSKVSFASLSDAMIQSARM*
>TCRU_5541 PUB domain containing protein, putative
LSLLLCLMHRQASAECRTKALEILDMIFKNIITHPSVAKYRRINMASVMWERYLTPSFHI
LQFIEWLETLGFVHDTEHSSLHFSGSEVNGLIKAREEVCILLEAYSTPCREKTDDDFKGG
KELLPLLRFIVGLTDDGGPKNDPSLDKEASPTCITGDVWEIVKSPLYLAVLGRVCARRGH
GDLGLERISQPPASLGRSWAWSSLVQVARELSLLQIEEDCAVVEAELFVGYEHIDCGGAE
VKVLRKEIARRRVAEKHKNDFFLQEKKFAKAPAEVMCVATRLIVDIASCMEQIAVLEEEK
GMVRKDRLEARRLLRKFEEDADIAYLHSLKEEWLEWLEAAKQKSGKLLVY
>TCRU_5542 Histone RNA hairpin-binding protein RNA-binding domain
containing protein, putative
MQTPVRPTLGNEKNVPIENAFSEKKMAGKHSSGRRPCQNSLEQERRTAQREKQISYGFVT
EGYRNMVKLVESDPLLKSGGILPLSPPDLNKGSKRTWDVSLRKWRRALHMFDNVFIENED
ASPTTLESVIENQRLQWVSPLFTQEPKERRVRLSTEKIKEARNSIYVPKRLPVEESLKII
LRSEDFYEPVTNVVPPSASSLIRGTDISPLDAGIKIYLTPSGHNQQNSTPEKPEAVFHQE
SPQHFLFNTATPARADTSPSSMHTCSPSGTSCQFYPGYRTPSWNAPSELHHDPIPVPVVG
FSHPQPVMQSVKLFQPPVQQWNSIFAAPACAPQTSNAPVLHSGLNRLRTPATVPRRITVL
RSVREERKLGDAAKSQHNLYTNHNEPSYYSTTKINVFSP
>TCRU_5543 UAA transporter family, putative
MSDAALAICGVLGGCQANVFLLELIIVRSPNTLYAMTFVQYVVVSLLSIFLVSNFFDSSR
GGGWLRIRLRPMRILTSHKLILAFSSWLMSVSSNLVFGLYISVPLHATFRSSSLLLNMLA
GYFFLEKRYTRSQVLCATAISGGLIALAMEKSRKVQNLNAENGMKTSEGNLWWFLGLTVL
ACTTAFSTGLGIFQEYMYAAARRREEETKKRDESVQSSLSPPPMWAEALFFSHIISIPLF
FLQSGRLFREFASISSDSYMHFALNALTQYVCITGVYILNDKTSAFTLILTLTLRKLCTF
SLSVAYFGHYRHFTMMEWVAMVTALAAGALYPLLPKA
>TCRU_5544 cytochrome P450, putative
MDRHLRNIPEAPGRIPVVGHALILMGGSPWRKMADWSLDSFSHADSNKKKDAPRTNRLVR
FNVLYQRVVYINDPLLLKRVLLTNQRNYAKDVETSYKHFLCLLGTGLVTAEGEHWKKGRL
LLSHAMRIDVLEEVPKMTIKAVGRVMDQIAAIDDKNPFVDLNEAFRHMTLQVIGETTLSL
EPEETDRIFPSLYLPVVHECNRRVWQPWRVVMPFLEGFQERRRCLKELNHVICELILKRW
EDRHKPHKRDIISLCLSQIDKMDNAMVVQLRDDVKTILLAGHETSAALLTWATYEVISHP

DACEKIVEEARVLFDPARCEEKVVTPEGKTWGIPTASDVRNTLRWSPACLRETLRKHSVV
PLVMRRALKNDVWPASITGLDGDVTIPAGCSVAVGIQAVHRRPDIWPDPDAFKPERFLDV
KLENNFTTPNHEAYKDTVDPYAFIPFINGPRNCLGQHLSLMETEVALAYLFLNWDLRFYG
ADAGATDVEKRLFQEEVGRPHVFMFPIVPQNGLKVVGTPR
>TCRU_5545 ruvB-like DNA helicase, putative
MTETKIRTEEARDLTRVERIGAHSHIRGLGLDDALEARMSSQGMVGQVEGRRAAGVVVQM
IKEGKIAGRCVLLAGGPGTGKTAIAMGMAQALGAETPFTMIAGSEIFSLEMSKTEALTQA
FRRSIGVRIKEETEIIEGEVVEITIERPSTNPAEAKGRTGQLVLKTSDMESTFDLGSKMI
ESLQKEKVQVGDVITIDKATGKINKLGRSFVRSKDYDAMSSNTRFVQTPEGELSKRKEVV
HTVTLHEVDVINSRQQGFLALFAGKQKDAPVNWC*RHQTWSQRLISDLMIESLQKEKVQV
GDVITIDKATGKINKLGRSFVRSKDYDAMSSNTRFVQTPEGELSKRKEVVHTVTLHEVDV
INSRQQGFLALFAGDTGEIKHEVREQIDQRVAEWREEGKGEIVPGVLFIDEVHMLDIECF
SWLNRALESPLAPVVIMASNRGISRIRGTHYKAPHGIPIDLLDRMVIVTTKPYSEAELSK
IIRIRCEEEDVEMDEDAIALLTMLGKSTSLRYVLQLITTANLVAQKRRASTVSIHDIKKV
YSLFIDLRRSVELLREHEKDFLFGEADENLESGHRTNCRNEEE
>TCRU_5546 hypothetical protein, conserved
LSSMSSIAFEECFLLQHELSSGPNLFFLGGDGSFLAPSNCYYPLIVATLHQSKYSSDTVE
FLWPLLLLTLHTTDVSLSLSEAHLFSGTSVMGYHCVRIVVDRLKRLSSTMSFHEDFTCIR
LVMSLVASPLCLDDSFLVEIRNFHRPIPGYILRLILSLSATPFILDYIMDCELRKYSGKG
IGPGPFVECLSGLLCNDHFFSSVHFQEMHAIAMNIVKNIGPSFDFLSIQWTPLLSKLSRV
YMRQYEGESLAILHFKLLEMVPALETKMPLAYLVRVLGSLVDVCAEREDTRSLWRTIIDV
ASLAVRLHGNSQGGLQSIWKPFFKAAVTSKPTYLNYERVLEAYHVCAFQGNPLTLDRAAF
SQVVRFLVGSINHLSLEETSASMRNFYCFLKEHPSVNFLWVLDSLLSLLSEIWKIHGEIA
SVIVQEFIKALQDDYFPSMRLSGVQLCDNPQIRPLLEKFCVVNKTEFWWECGCGTQIPAC
AKKCLMCLRKRNAAWTCVTCGAEYRGTDVEKSCMCGSENPRRLKAASMGLELCMNCGDVV
LSSSGCIKCGNTYCEEIATRECSFCGKSYSRRAVCCPLCYAANEDKKPLLWRCDECEEYN
HWTWSKCQRCPGRRRVGCIVTPLEPWVCGCRRRNHPCITGCETCSRAIYGAYTCNFCKSV
SSKHSFFYLTLQSIKIRVIACQHCGHIHPRDQNVLCSPYLQRQCHQCGKKYLRSNLPLDS
HCEFCNAFLRYNELNPFKCNSCESKSIQTGFHCVSCLTPRSDLQFDDVYVWKCSQEIVSQ
TALVSSHVCGHWNYSWLSKCRFCGGGRAQSVYESRVRCSSWVCTECLHQNLPTDVFFCSR
CNTGLQLIENCFICGIPHLNLTC
>TCRU_5547 hypothetical protein, conserved
TVANRVPIDGTKILFLDCDGVVSPFGGKMFAPKQMSLLRTIIAETGAKIVLSTSWRMSEF
GREEVARQLATNNMPNYISCTPYFHDKSRAVEILSWIETNKERYNIVNFVALDDINLPAT
APNRAFFARHAITTNAFTGLTEADAKEAIRLLDDSNNI
>TCRU_5548 Calcineurin-like phosphoesterase, putative
MQVTFASDIHYDPFYGGPDAFGTACRSAGLPLVKRGCESSADFVKYWTSDMATRKSACTF
VTGDLQRHDFPSLKTTVTATFGFVIERLAAVSPNKTPSGRPSVLVALGNNDVVPDYYFDV
TRIPSRVILEEASVMQKNGVLMADEAQQFQQCGYYLRVVSPKLRVIVLHTLLWCYTIVPA
IPDGDEDPCSQFKFLTTELENARKANSKVIIMSHIPPMSNIWKVLEGGNFTSVAEDMYWK
PLYQKRFNQLMREYSDTVTVQLYGHTHLFYYQALSGGVPFFIVPAISPLFGNAPSYFIAQ
LDNKSLSLKSLTQRYFDYDWTNGVRVEDLFGDLTDTASLRASAMRLVTDDKLWAKYLRLC
GGGVGSDKLFPGGKCNSWCRKVIACSMVSDAWGDIRACVE
>TCRU_5549 diacylglycerol acyltransferase, putative
LMVVWTLGFVVAMTTGAIADAFQGNAPIFPFIPTACLAVGLNGLCALFSILLGCSLWDSF
SIYQPFAGGERYVLLQVCGWTLVVSCSSFIVLYLIQLEPPMYRYGALTILEGFASIGNIL
LAVSLRYFSPSESRNIVEATPQHPTGQPARESPLKWILHSPNSETALVIIFVLFQLFFCN
IGALFQIISSPAMVVFTIFHLLSGILVHLLIEWRQMEGFKMLRGPVETFFYLLSLLVYFV
ALVGGIALIRTGTEAPQVAFGVTALAAFTGILSMLALVRTARIKESHVSFHFVVARYARF
LLSAMAIALAFIAIGIMYYVQVQKHFLMESRNGRALMDGLLFCQTLSVCFLLALTPVTHL
IGRVIYGAAFSFFQPFRGSVGFVFLQALGWAFFTACILCMTLHMTATNFRWILSAAAAGV
MGQICIQFSIKAFASGFCTEAKQGLGLGKRSESKSEKESIISGELILSLLLQLASIILRL
VVDISLTQDGEFSAVPTHVLMGFSSLASLVSAPLAHYSGKSKDIPFFAPFRGSGTYIALQ
ALGWILYALFVLKNILDSLLALNGLASVYFSSDRPPFLWFTLEGFLQVVPLLLIVLSVVM

EGRFSVSRRRRQGMVVEALERVKRALDERVDAQEESERAALQMSMRILAASTLSAHGMQY
DSSRFCLSVKPKRKCTAIKEVAEEIIDGTQEEDDILPLFSTEAENRHGAATLLVVMMCFS
SVSSYIIAALWANTVPLVGFVFALCGLTVCTISCVSTHCGYGALLHDRTGEYTFFMPFKG
GSVFVALQIAGWVSYACTFVLTVIYTLEDKGGCVQLLTGAFFSVFSQIFILFSIPKFDSR
PKRLTYLDENGEGVVAMLVFLGAFLIGHLYLRAQEFFRVLDDTSGVEEDITASSRRSHVP
FFIMALGIMTAVPFILITLSRSARRLETVAYSPRRDIDTEEDVPLGRRKSLFLNITLRLS
EIMMLMLGMVTPMAFIFVMYYIVNGVHSGLLHIIQYWTPFALMAGTLALLISLVPHVMDI
GMLEQLVSFRECVVTCGLYSLPIISFWIALGPAFFLPFHSVGAYHGIYVLLLGCGCSFSS
VPHVAKVWCVCMLGYASYLEYLRVLDSGTVVAALSTLRYYAVDAVVLLVWLWYLPSYDGE
PEEKGAYHSVEFVKWTQKYIFRDIDRYFNYRIIREDESLNLRDSSHQYIFAFHPHGVYAG
TALCGVFSDAWKQSIGYNSKTHVTIHEASVLFNIPIIRDFNLRLGALSVTRSSIASTLAR
GNSPLIVIGGQAELILTRRSDKVMSLITYHHGFVKLALKHKVPLVPLISFAEQNVLSIVR
APRLHHATLKVLGFPLPILPYGRWLLPLPHRTPLTIVVGSPLPIPAGASADNPKDVADLA
EVYFASLRTLFYKHRAAAGYPEMELDFYTRNRKKVLS
>TCRU_5550 hypothetical protein, conserved
MRRFCFPVATFAQAALRHRGIRWNTTMADNESHTGAKASAFSSTPSEANEISAMERASEA
RREIHDLWMSTETMLDPENRLRSVASLIEKYKLDPSTPRENDVSRGLGDAFDRLLLLCIP
LGKDSSKGTDDLERLMNLAGRNGREISVRTIQHLFARTDSFSEALAVFYAMRRCHVAMNM
EAYYAMLYSLQRLEEEGWAQRFREECEEKGGVSEQAMDFVVKGINNALLPENKPWLGRVM
FGDRDAPAQRREARDYDELSAMWTERYRDGS
>TCRU_5551 hypothetical protein, conserved
MSRAFLERCPRRHLVIHMDINRTIIQVDSAGQRTMEDALNGNIAANVWGRCEEDKWVAVL
GPGEEGDRSGLVTFDKYVDNSYTEPPLMQELPKAERECIWRDISARRRSVVRTFTHAGQP
GENYAQHVEEQRKVLTAASNCSMVPSFFQLVNTLSELNWSFTMIFRTFGHDLANVLQEWR
QFLFGEHAHKPQGALLRRMKEKYVPEMTGCIFRAEDHIFFCVGPDKAAVVHHPEGVEKMS
PSEVLAQLSAMPSCKEVHQTNFMQLHDQILEYTSASNNVGGIVDYYPFWAQGAERRSGGK
VFPVAITSSSCVTAPVTPRFYVFFDDNIFIGEEKSIVDLRDIVTGKSITDAAIERKYCVA
VNPYKATVDKEYFVDCLAGRIRLQLG
>TCRU_5552 ATPase family associated with various cellular activities
(AAA), putative
ERHCPRCPICSARGTPFFLRLRYCVLTSLPAVLVKREFSVEKDEKLRHRVMEDVKELLLT
RLVGQEHLKGVILEAVRRKLIYPRDPLVLHFAGDNGVGKTHTARLLSLATSPHCAPSRPA
CDMGENMLVISGTGFEGMPIEDARTRIIQRVTAHQKVYPHGIVLLDDLAAMHPKLVAALA
PLLGRAERFEEQPEGTPSLAQLIVIVTTDFGKQGRTWGKSMAEIEQLVRDEFAGLYGTLL
SAFTRTMLFLPFSRHDAEEMIRIAVAALPCGTYWNKGAVVTSSIEDLAVTFLVERHRETW
EGKENGHSLRRAVEDTLVSLLLQYFDQHGHDKFVWAHFRLDERAAKIVLSTG
>TCRU_5553 hypothetical protein, conserved
PEEALEGLIDMLGLDAQPEAIVCKSESELIEVSSSTPLLMFLCEFAMNLRNEEPSPMELQ
VLRTRCTFVASLPDRVANAFLGTFGSTKTLETDLDLLATRICQSLCRFLFVIHEAPPSKM
VQATSTMRRYRFKRENALLVCEVLIQNLVRRGFIRTLFQCFISSLKAALPFLAFLEEIVQ
RVFGAVYKCCLKNGEVPRASMRNIVTANLHTNIHWSEWNTWFLRVAERDTGLRPLLISSL
IKMINIPDKNEEAATEALAMSRALMKELFVTETSYLPTERSLLRVIFREVLPGIVSHSSE
RGEIPISEMEMGLFAEAFQRWSTRDLIEKGSVELNTTLANSILYILIHIKEYHVKDTKGH
LPGALLQPLLAGISLRFELVRAESLKTEAITVASVFATFFVGNDEARNAFSSLEQFPSLL
NDWLKGEADSTTIPEMSPITPIGTHRGGNNKVDPFFRRRSIDDEEYPLDPDAAFMFFCRR
DAGTMKKTGTLTTGGTVVFNLDTIVNHGHLPSFGKTRNEQDELEESVTVLVTLRESYNAI
IGVGRSSNAQVHEVQQAVESGLRGFFHALNRLREKLGIWKEQKVHGEVRRLREKVGMELN
PMIPSLLPALMSLTIHAPESRHKELMDLRYSVIVSLVIIAPENALSQLGKMLYSSHYGIF
QRVEMAKAVAEAAKYLSQVEVRVEPEEGGGAAASQKHDIWKERLTKRRIYPPIREGNAKP
MSIVISEGRETRRWGSAVAGRVDRKERIYCSLLTNVVPFFVSALLEKAENDHFSFLSEYD
PYVPTEILRSIGTVVQCMASARHIAPALCEKLMSFAILAAIEHPLSVVRKQGWILIGEIM
RCWCGAGPLVLEDGSSFTSRGVFGGSLSYVFSQEWLDAQRALGTLFVKTKDDPSCAEIAL
LVLADIQDLVTAKKDLEAMENRVVNTKKIT
>TCRU_5554 RNA-binding protein, putative

YRPVSAKVMLDASTGRSKGFGFVLFRTEEEGKRAYDDLNRKSTRACRHNFNLIIYPSQHS
GRAAVSPSNALYIRNIPITVPQAQVERFLSTFGTLAFCAMREDHYGNPVWVVYAEYDCLS
CSKNALQRLHGSSEHFYGPPVMVKYADTDEAKQERRRRREEGKVPRAPPPRSVCVFPPPR
QTAAPEVHQCNCMDVATAFSNNGNITVAACPRELTPSRDSTSCSLGPNLSSDTSSTASSA
HKVPDNVFTPPPPTLLGSAALPPMFSVPPQSQPLPMDTLDASCKVGPPGSPPVRRANSNK
DDPPVMIVLENGQQLMLASNAVNLRPSDFALAAQSSLLWPPEVGYASPLPPPKS
>TCRU_5555 Protein kinase domain containing protein, putative
MSLELRVGNRFRLGQKIGAGSFGEIFRGTNMQTGETVAIKLEQAKTRHPQLAFEARFYRI
LNAGGGVVGIPNILFYGVEGEFNVMVMDLLGPSLEDLFSFCDRKLSLKTXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXTGKKGHHVYVVDFGLAKKYRDPRTHQHIPYK
EGKSLTGTARYCSINTHLGIEQSRRDDLEGIGYILMYFLRGSLPWQGLKAHTKQEKYSRI
SERKQTTPVETLCKGFPAEFAAYLNYTRGLRFEDKPDYSYLKRLFRELFIREGYHVDYVF
DWTLKRIHENLKAEGSGQQEQKQQQQQR
>TCRU_5556 hypothetical protein, conserved
RGKQEEVEPRVSLAAFERLLKVHVAMRNNYECLQRNHQVVKSFSMACAEALLHLGLARCR
AGKNEGKREGTTSDIIVNICNESSAKGEEVSSAPPPLLLSADTPLYTTLISFPPPPVEAL
LHMTGSSKCRKDGDSGELLLAAMEVVDGTNVEGLVEDSETVTKGRAHDTDPTVSWGANPP
GVESLLACLQGVPMTDIIKLMETVAYFKWIKDEEVLEWKKGSAVEQLRREISALYAATTK
KKETTSTPDVSDEANEALCVVEHTSKTLLNRISRVDCVATAAASFATTDSYVHVIDLMLN
VLMRVCLWKWPRMSCVDQMSVVLIATFPWFSRDLSVEAASWMTYYHLLAISDKDVNMNHY
RLFLYMQRIRRLCWPSVQDLSSNIVRKLFFLRETSDSTGNAEKDSNNDTREMQHEEPEEA
ETDAKLIPSLKDVACILYGSQEKQRAAYECLLVWLKQSDQFDLRLASPNGRYVGAIGIAI
VDIDRFAMERFGSEILKGEWVLLRVSGKNVPALKRVTQCTQTPYALTRLFFCGYHNPLSH
IWHGIHAARRDLLWSAWLRSVARPMVEAILPGSASREDKGGEVCASQFIEPLLASLISDV
VFQRLITQLVILSLNKMSAAVNMQPFDIMCVRLIETVYTGALVLYCVSLNKSAVDAPPEA
TPGATKNKSPVEGNAPEQQQTPASVAIRRAFREVISAMVRILSAEHVPLVHRLLDALFGV
WINDTARETPLDGIRKEISTICDEKTYNMLNEWLNRRANLLLVKVALLEDPLLRSWQQAV
QEVDAGLPTTLPTLMECFVGLLGLLEKRGHPILNTEQKKQQQSAVDEAMAVGNAAGSCAT
VFTLPELEVILTVFSRAILYRVSTLKTLGLTSISQEFAALMTSLNGDGGDNRDGGSSSNN
NTNNNTNNNNNMSSSSGSGNTNRNNMEGRNTATSASTAVTACTTTATPMLAADHVMLLEK
ILSAEVESKADGLTWGSLLEAILLHLAPYGILESSYNASSNSEAAGTSGNVAPVKKLEED
MQVCHHKRLVSSVVLFRCYVFATTHDGGWADATLLPQISEQETDVSHASDSGDVAVSHGQ
SAQLREITWLLLEVFVKNWARNSKNTNTKRKTAAGDAGTTEKAEGTMRQGQFEYILACHA
LVVYMRLAPLFSTRSLSLQEAYEQFLHSAEHTTTTFGGNQYNGCDLLFLWLAASANALGV
HFSPAQNYNWSTVGGVTKLGSGSMKTTASLGEGTMRLIQILAPYVQSETLRMNPRVKFLV
NIIVAIHTFGKLGIHMDTGGLNMDQLLLRTSSDRRLLHRHLNLFLVGCSALPSTRHALLN
VASFLREARCLLSAAEIDRALVAVALSANAFAKNHEAQADLQQNGDLMDVTHSTAPTMRV
PPTQLRHAWNALTRSVLERAEGMPTSVFVRGVQCAGAVACVDTILCQQLLSFLVEFRRDE
LSLLDWTAILHTARQSFESRRIFEEYLQEPLTLLLLSMSKENGRGNALESQHVISSGKRL
VDDLSLFVEALPELFTGDAEFWGLVRTALKVQWIAQFNAASSSEQHQQQLTLCLQDLARS
YEWAVRTAG
>TCRU_5557 ADP-ribosylation factor GTPase activating protein,
putative
QKLLLEKLLHLPENRECFECSAKQPRWASTNLGIFLCLRCAGIHRAMGTHVSKVRSTNMD
TWEDPMIECCECIGNKRGRVLYEHGMDPQLRPTAATDNISVDRFIRDKYERKMYYNPQYE
TLLKQFFDAGTSVNEEKCSGLVSSKPSEQTGGTSASMPMLWGGSPATAMEAPASLEGNTN
TKNGIDINELFTTTTSTVTSAPMQHQQQQIFWTQMAGNGMVGYHQYYQQQSQCPSSAPSQ
AGHQVDVKTEIMSLFSTPPNCSPNHVYSAWQP
>TCRU_5558 NOL1/NOP2/sun family, putative
MDVYRQASEIVCAVREGNGTAKALCLRKEMQKKKQTYAVVCETLRHYDLLQDVLDQAEFF
KYYPRANKGFAICMAYDVVLGKGLNTNRDTTAQAIKKSAPYLREAYWHVKKHHVIPSRAH
EPFTEDSNGGSRNDEVDNNEDNYNRRCTLTQQCFSGDSDRAAAVPELQIPRYARVNTLKI
DVVTLVERLHRAAEKRGREDDGSQGKEQQRKEKKTHHMKGFRQLSAFTMDPVVPSLLVFP

AGTDLHAHPAVRSGQLILQDRASCLPACILLDAVEVVRPSSAGAGAPLEYIVDACAAPGN
KTTHLAALGAPHVKIMAVERDEKRADLLFRRVQSLGASDYVNVVNLDFFQMSSADREATE
GILLDPSCSASGVLTRVDVSLMRQRQARVAEVGENNRGEDGAGNNETWAISSEEHGTEFA
SNADRVMGLARLQRKLLAHALLSFDNCRTVVYSTCSVHVEENELVVRQVLEDTRVQARGW
ALSNIMPTTWKTRGQKTEGDTFPLDHTIRCDPVADATNGFYVARFDRAV*KKKKEKKMK
>TCRU_5559 hypothetical protein, conserved
SSSTPASFASRPVISKEDRKVMPWVEGGSPADAAAASKTYRTELTHEASTAAAAADGGDG
FEKTPPRGQPSAELSPTARYAPWEIRALLLPLIPLGGATVALREVIHLLPTAAREEMQRD
GGSPLAYVRQHFSDDVVVRGVELSRRTVELDGVVPHGGARQAAPPPPPPPLPSANSSRAA
AQRPSQAAGGAKTVLEVLDTLVEFIPTFFVQQQMVSDQLPSEVKKQYVDSSFLFYIKRFR
HYIDIRAHHGSTEIRLRPDFAHPKRGAADTRYATGLSNSDMLSQLARGRRPPRNSEANLI
HFIIPRIPSTYTPLATVLQDVSDIVSRHPSFDPRLGVTGLFEKYPEYFQIVDSKLRVRPF
HSAPNSLDDLNATTSPLPTIYAKIKQLVDEYAEGKDYTVEAEKAAAVVPTGKLYALLNNT
EKKEVKTRCRSFPRFLRLHGEEIVVSVDNMKVYKFRPTYERCAETIMDQRLSMGSLSPDD
PVLKIPAAIDDNSSADWAVRELYDALPLMQCAELDEVMSLVPPSVKSALPQEQEKLVEHL
ALYPDYFLTWPYPDDPRVIVVQRAKLEPLPMEGEDIARVVMPMIPQGGIEVSRLLRRVPL
PLQRHFYRHGLKKVLGEMKNYFLIVGEKVMRVG*
>TCRU_5560 tRNA pseudouridine synthase, putative
KSAWIWTVDKATLHAIDFLAYRLGLFHPPPGGTVCGAATLARSKCDRLSILSERSSIHSS
FFPVVRKQQTSCGEIHFFSSLDTMKRMMREWERRQRKRARDEEEVAIKEEADVAAKLQHP
EFLFSDEDSVLLRFGMGSFASPTAPGFSGLFRQHWKDFIVTEMVTDAAGLATAIPREHDW
TIPALPPSLLNATETREKWRGDSDADMNKNDAEDEGRGDVGPSSSFFAVDVEERVAELLK
EGSREENPLASGEPEEGEKEKKEDGNNDCVAGKRDFYLQCYLHKRHIAHSVALANIAQTL
RMHPSGISVAGIKDYIGDTIQRVRLKNITPAAALEANSFFRMKKWSMTLSDFSYQNEPLV
PGRLFGNHFRIVLRDVTAAREDVERALHAFEQNGFPNYYGCQRFSWFGGKNDAAFALLHH
NWLVFAFRFLGYTSCEFTLRELLQREKKYPNPLQDEYRRNVVRRLRRIATEPTELDVAPF
LSCPPLGAPPTSADGGPISDKQELIILQLREAFLDLNVRDRRLTAQRLSSYLWNQVLTLR
LHHFGLKVLVGDVVLPESFRRVAALPVDRTDCYREGIRFIADEEEKSAYTITDVMHPGFS
FNGIQRPMNTVGEYYLQVCGKYHLDWHAHHAQTGIHDFLEPPRPIIRKPINLRHEYNIAE
SKLTLEFVLERGSYANVAISELMKLLRCAGSESILLLPAPEGIWDIGSRDPGYVKSMQDI
YSGFEDGLGFVTDKHDLPLVGEGKVWDHDGPLFLPDSADPVKKAYRWGEQHLLRNMERRE
RDEEAMKMRLFEKPLARTLKDGEVARYAGHTVPMLPNSKAKRVFFTVLRRQQRFPCAPKT
VPRIRRGAEVRNRTPVNVPFKTINRNTWNVTW*
>TCRU_5561 Arv1-like family, putative
MPRCIECSAFVQRIVHPETEMVEKCVSCGRCCDKYYEFADVQKWIDVVLLERRAWMHVLF
NQRGIFSSLFLASLVCCLIEAYVVRTTSVYADIRNRKAFFPATPGGNLSGEDSLQLVRNL
RSDMLPLMMYVDTWPTLFLYASMEYFLCLIAAVWIGVQSLRGVASGQDDAMTTWATSVSL
AYTAKVGYLVFLVWRIPIPLVVVVDFLFLLWMVRGFSITASSHPSRFLAIAALIVSVLSR
ALFRHLTAWSPQVI
>TCRU_5562 mismatch repair protein MSH3, putative
MGKRQRDAEAEAAAVRHAIELICQRPVNDTEVKAVTLTPLEKQVVSLKESLPPDVVLMVA
CGYRVKFYGRDSRVASRRFGIMCVGTTPFESSSVPYVRVNLYVHRLVAMGYRVAFADQEN
ASIRANSGTAKGIFTREITRVCSRGTLLPSEVIGVANPAKTTNSNGVSSVDTADVAEAGA
EDDEAEPEGVNFPMKEESSELFMCFIKAPSPSSLPAAAGAPAMNVTLVSFVTYAVTRHRI
ASEVELLDVLHRYDIVEVILLCEPPQGENANDKLLSPKSSPLRCLPEVYASCLNEVLPLH
FGPTINGEEDDRSISLSVFEGVGSIDETIASYLAPYRLNRVYEKMCLEAGQTLPRNAAID
SVTGKMELPGSTLSALDIFHSSIGAKGSLMALLDHSLTTPGVRRLRLWLSEPPCEMNTIT
ARRKAVSFLLHGKDDNTVTHLLRECARFGDIEATLGKMRAQRCSVGEYIQLLRALETVHT
LAHAVLSRNDGRIDNLILETLQRVTSAETANFIQLCKCEMESHATSPLEYFTSHGVSVPS
AIQTHLTARDEALHALDEELEYIRQTLHMPDLEYRTIAGTPFIVDVPQAKCNRVPKDWLV
LTRTKSHVRFHTPNIVDRNVLLCSARERLLIAAKDSWQQKQDELSNSSLAMNAFQAVIDA
VAVLDAIRCLTVTSSSRGYVAPELSDGATCLKIVGGRHPVLDNILRGGYVSCDFCLAKGG
AWILTGPNMGGKSALMRMVGAFVIMAQLGCYVPATAAQLPLFTAVYCRMGASDSLLEGTS
TFLKEMQETSRILRSPRVSSSLVLLDELGRGTSSFDGIAVAAATLEYLLQRGTTMLFVTH

YSHLCEPYLHNTSEGKQVSCYYMGFSEEQDEDGGDGEPKLVFTYKPTPGVTPSSFGVRVA
RMAGLPHDVVAEAQRLSEMEERENMTRMALMRLRRFV
>TCRU_5563 trypanothione/tryparedoxin dependent peroxidase 1, cytosolic
YDLSQHKGHPLLIYNVASRCGYTKGGYETATTLYNKYKDQGFTVLAFPCNQFAGQEPGTA
LEVKEFACTQFKADFPIMAKIDVNGDKAHPLYSYLKRCLTGSAGVQAIKWNFTSFLIDRH
GVPVARFSPGASVEEIEMQLLPLFE
>TCRU_5564 hypothetical protein, conserved
KKEKRLTDIMAVVQTHCFNWMDHDGTRSETLNLALLRHSDTGNLRYSDYRQRQEVVADIS
MRLKIIKRELGLLPPEEEVEWNENKGQPEDLYVRLDDEESEVFLQIQERRKRLFALMERP
IEGTDESDVYYYPGTPADEMQREAAAPFALCVQSLLVQFGETFVSYLDGSEFLTLSKLVQ
HNEARRGEVEAAAEEAGVLLPSESEFDVTSLHAALENREQARMKLDAVRAASDPSYAAKF
VRAEERDNSGQPITNVSPEDGTEAQLSAKLTAAKAQLESVRMAYNRRAHASARRVQKALA
NRVPPVE
>TCRU_5565 hypothetical protein, conserved
AMLRICLRPLCRPPVFQAGESVGGCLTNSLHCDGKTTPLERLLAPFIPVTFTALTQISRS
VDAELMERVAEAGGLRSFLGRHSDLFAVSKVGGVYVARRLRRRCVGSIPSEGAGLRLSCE
AHGPEPEQQVEDAGVFPRIQSVPLEVFRLFPTFFVPMEALLAHLCKLPSTTLSNSRGEEE
LVSEDHSGRNPEAVAESLVEKYNKFIEVVSLNDNNGNGEKEQLKKFVRLQSKFATRAASY
EEKEVEVTGGREGCISQIMEPYKVEEYEQYRVARLIPVAEEFCPISAEMRQAAAVLLPEG
RSLIHVLLSAPDLFEVRDTPELSVRFILDSRFRPTTTCTKEEIERKLTELKESRVKNGLK
MPIDRKKRRTLSRQLQFFVKPTPYLDERVWAHALLDTLPLDGPVAFAVAMSNLPSECLAC
TPVNLQRLISQYSYLFSLVEGEREKLLQRADIPAVEQRSVSSIDTEEILLTIYNYYPRRR
HPNCGTCLERCIYSMPLLLRTRLRQLDFVEDVLRKHPDKVEVLGMLDEELMMHDRNLAEK
SQMCQVFRFVGEYQAELIKRYEALCVKLGKDPN
>TCRU_5566 ATP-dependent DEAD/H RNA helicase, putative
SDEDSGDDPFGAAASTPSEGEADTGENDGDIEDFRERLLAHVQLTCAAKRVGTVDSTVAG
VTPAHALQHLKEELLKPVMSTALTVVSATDESHDLMAEIVSAKLPPPPPEDVKRLRKLQY
VDHSTIQYPHIRKEFYVAPPDVKDLDADELKRLIAELDGAKLRGRDPPRPMRTWNGSGLP
DSVLDLLAREGFEQPFAVQSLGSPALMSGRDLLITAKTGSGKTLAYLLPLIRHCVGQEPC
GKGEGPIGLIFVPTRELAAQIAQLAEKLCVAAKLRFVSSYGLTPLADNIRHCRAGCEVMV
CTPGRLLDLLTVNGGAVISLRRTSFVVIDEADRMFDSGFMEHVEAFLKNIRPDRQLALIS
ATMPKELKKVIMRHMQDPVEVTVGGKPTPASNVEQRFFFFDEEVYEVEEANRTEDKKFLK
LLQILSDEGGTGQHLIIIFAQRKEECDELFARLSACGYQKRIAVLYSGMDPLDREFALEH
FAPGNQFILIATGVAERGLDIPYLELVINYTLPDHYEAYVHRIGRTGRAGKKGKAVSFFM
RGKDDDLSVELCEGLERAQQQVPEELYERAAKLREKRKEGIVRHNTGFYRGYMKAKKLRF
TDRGQEEQFKAAARAAGLEEYLSASSCTDSDLSEGDEDGKEDGIEIVAVHEDGTRGGGSR
NEEDSCTADLSEGDEDGKEDGIEIVAVHEDGTRGGGSRNEEDSTALMLYRDTSALTLSSQ
QQQEQQERLASALAYARKTTDSIVDPSGTCARFEAEYPINDLPERIRLRMQSANLLRSVQ
EETGTTIIRKGVFFDRKYKHSHRLREGVRPLYLLLIGKTVEAVRAAVKKLNEIKEEAQSR
IQNKVSALGAEL*
>TCRU_5567 hypothetical protein, conserved
RLGVIQFTSRNINDEMSSKVPLFLYFHVPNNPDVVAYTERLSVQVDAANRRLQSSGISDK
YQEFGKDRGLAIKLGLVDCLREVGLTEKFSVDPHMFPIVYFVRNKVYADKMVGIVPESQV
KEAIDAFIDYAVEESKNEMSGTSVFQKVKRSDEDDENAMTLLNVAHTRLKNKEIPKAREL
FKKAYDMAMAETQVARERLGFSRERKVTQEMWGRLKREGCYNVSPQALCGLAMCAMATKD
NAEAQSIVQRVREEFPFATRDLRDVAEAVNRIELLIIADFDVEKDNYVSLLTYDDLTHDP
AALYRQHLKLAVAHFVEKRHHKGIEECLRLIRAEPKLLPALKEAGVVPQDLVLGPHAKTP
ARQVILGIFEALGSSNEQTITGRQLLQRYL*
>TCRU_5568 Meckelin (Transmembrane protein 67), putative
CLPGFSRIVRVETGDTECVDCNLTGGVVGMIPYLNQSERCVQCGGDRTFSELVDPTHDEM
TRKCVCPADYELVEQVGKRLLESQMCVPCGPDGCSGCVFPYSLKETGECVCASGYTTLYD
ASCVPTEVYNGVVVAAVGATTTFQPLNLNNKGILGPSVTSVVVRSYAMDSAVQCMRGMAV
GCSLLFNMCVLMMYDVDSLPCKLYLSVRDKRTSYRRLPPLFDGDNTDTYTSDDGVLLATT

NITAAGDPMTFLVAVYDWRGNLKGLRHVSEVLNLCCISDADMSSFFKVGSNRRLRCFFDW
YKLLQDAGPTYFFELFMRDFTNTSRLVPVPVVMDYTTGNIHPQSLRDGTLRRAMATGYRR
RFYLYDTLTDCKLDVPQVTETTPCYVTALRHVVFALEVVDVYRDHHSLKPVVYLQYASGL
KKAHNGDLTARTANNIVEGGVSVLFIASSSVDKGMMITMIIFCLLCICSAWIRTYGWMRR
RQNVMLSIGAVIRFMVYFCNHIGNLFALVVSLASWYVFVLYRAQKPNLSMFLSDNYVFLE
AMLYAATAAKGIAVVYKIVEQCNADYFVIDWERSKGQLLRENRILPVSMWRSTFVANELN
ELQVLRQWRPLLSMTIVLFFLVGLNYLKYTESVPVTSGADEAGTYSLTVMRIALGTFFWV
SVSLVLNILEFQIYYRFFCVHPLQAFVDLCSVSNISIMILPETQWGYYIHGESIHAHSDV
SMEEFQQNLYLESQGNLPVRGLGGQSKCQTFEVFMGIYMRQYLYMCYAEIEAEYQRSSGK
ALAPIRPGRQWHLLECVLGFSRKSRVYNTEILAIKTRINSVLKQSVRSAEGTLLMKFIFH
RWFDLAPNILYMNGPQSGDKSGKDLFFVDDVLAYGNAFLYGLDVDLFVLYTMLYASVDAS
MHNVWVALVITFALELFIRWYRMSEGVANISSKTLIDDRFFI*
>TCRU_5569 hypothetical protein, conserved
KREREEGDERDETCRVYLSCGGWNTCVRLYRPIAFDTLDEDMFPGLAFFFAPRVVGVINE
CHILSLSEVNRPCDHLIGQRLWLPCKYHGPFRCSCHTLEKIARGVLQLERELLFFPRKLT
VLRNNAEKHENAPFIHIDTLNRTATVYLSGLPLPKSEYGSISLHVLDDERSITRAIAAAF
SDRDQVTNGGTKCVLCGLTTNGNCSVCRCWVCKECDVLCCLCGKNACKACVV
>TCRU_5570 Domain of unknown function (DUF4379), putative
MMDRTRLFLAAEFKQKSRWSSVWPNMHYGAMYLSYSIGRKLPMKGVNWVTRESNRLTNFS
KRYQAVINDIDVKKTEEELGITLQDIRWNDHRRIYWKCSFCGSSYRKSVSVRTKFHAGCN
LCKGRYPSEVLREQHQSLSLAASAPELIKQLKETDKKDNLGSLARTSKFLAEWKCQGCGG
SYRASVRSRTGMVESGQCPLHPNIVDWSAYCPSCSWKPNMEAIAEEVQRTGQFLGLEAES
RKNASAPPARIPRRKKL
>TCRU_5571 hypothetical protein, conserved
LQRTLRRFSAGGGDLFPTSKKAAHLEPSWMMERQVPPPPGRGKCYVDVTRPSVRSKWQAT
QPEVHAVALTQMDAPCSLQDLAIRRPSRRSVAATLAGVNGILNHKPKTAENNIAMANIAE
KNRSESRMKTRDYTGHKQPARFRTGWETKTDVVKLSEWMYTRIHNHRKLHNDNRKGYEKE
KMIWETAPTTSTSKN*W
>TCRU_5572 phosphatidic acid phosphatase protein, putative
LRVVDYLLCVFLCTAALTIGKKVRPHCRQFSWQDATIGHTYAGAGLFPSWSLAPIAILPA
LIYFVVELIRALLWRPDTRPSHGPSTSLDLVTNALETRNSERMNMRRCHTEEADGGTVIN
TSDGEEAGGNARWWLFLENLNHWLLAQAFSVTLSMFIVDITKLYAGRLRPDFLARLENEG
YSEKSTGVDWCKVAREGRLSFPSGHAAISFSSIVTLVLFFVGHLQVFYFASPLRLFLSML
PLILPIVVAVSRTRDNRHHFSDVLAGGIIGTGCALLSVTVLFRVVKRNGMFLPRRLDYAS
KR
>TCRU_5573 C2 domain containing protein, putative
MGKLQVCICAARNLHDSQVFGLPDPYCRVRMGDHEYKTKVINNSLNPVWNETFRFQVADE
STAQLCVELWNKNIISDDLMGTYSLSLGHMTRGVVNDEWYLLGHSKTNSELHLRVLACDF
GINPSPSDVWKVTTDINNDPALGAGKKPPLAAAPVTISSNVNNTPINPNIGPAVVPAAV
>TCRU_5574 protein phosphatase 2B, putative
GKTSVPPPCWDEIKRAVLIDRKGKINLNVMIAHFLRQGRLGKHDALSIIQNASGILRAEP
NVLTIDDDSITVVGDIRGQLYDLTKILRIGGMFDDKKKYLFLGNYTDRSFCGCECILVLL
AAKLNFPKSVFLLRGNHESRLMTDFFEFQEECICKYNEQVYRAIMEAFDCLPLAALVNKR
FFCVHGGLSPDVIKLNHIELIHRFREPPSRGAMCDLLWSDPLWDVENPSSVSGGSKSDYY
TPSAGPSYGSKPVFLVNEQRGCSYLFNFASLKHFLMANSLLCIIRSHELQDEGYKLYRFN
SISNFPCMMSVFSAPNYCDTFDNKGAVLRIEGKKVDVTQFFSSPHPYILPNHLNGFRWSF
PFLMECLHDVFDSLL
>TCRU_5575 2OG-Fe(II) oxygenase superfamily, putative
CCCSGIRFCGRCIESERAQGIIHQNVLLVKSSDVISQQYGAGRTSSCSFTCVELSHYGLC
WQCNTIFLMHHGAFKSCADHEGATPNLDIRIEGLFVIPEFLSLLDEEKLVSFLDEPSSLS
GWKHSQSGRRKQDFGPRANFKKRKLNTSGIRGMPKQLESVMKKVKSFVRDITSKEYHIVE
VSALEYKSENSSSIDPHIDDTWVWGNRVGGLNLLEDTVMTFVNNEGTAVDVFLPRGAFFL
LSNGSRYDWLHGIRLENIKHRRISFTFREFSNDLDIDREIIQNVIKTTSTFV*
>TCRU_5576 hypothetical protein, conserved

RTALTKPFVAFVASMDRRIDLMDEPLKRHIQHHNNSGEDLCASVWHEYWSYQKALLPYRK
TRLLSELSYMAGGKISLASMGVKEIILFSRVLTKCLFLFIIFVIIGRRSVFPSLEPDSVF
VQEIKTNWQPNHKRGLL
>TCRU_5577 protein kinase, putative
MDRFIVGSPIGEGRFGVVRAAVVKESGAPAAIKFVTTPRLDEGIPHPTAREPLVALRLVH
PFFIRTYEVVPCGCSLALVMERCKTDLATVLSGRTASNPLPALEAKSLFKMLLLALAYVH
SEGVLHRDVKPSNCFLTAEGELRLGDLGLSRAWDTEASMTHEVVSRWYRAPELLLGQRHY
GPEIDVWSSGCVFAELLRGYGGAFFAGDGDIWQLSRIFDVLGTPTPTSWPSAVLLPDWGK
VHFEPKRPLPLREFFPDASECALDLLRRLLCLDPQKRLTAAGALRHAYFSEY
>TCRU_5578 hypothetical protein, conserved
WIAAVYMILSLFVCLLTHAVYVAVDPSLPLLNVPFYVTAEFLQQGQNLFLSSSSVCDVEQ
LVDAFCTLQANRTCEFNVTSKSMGVSPHYERYVPPLYICSSAFSQGYIQSLQLHVIDVTP
RFVFLERLSTVTVGDATPVGSIFGFFSDEDCNDVIENMPEKVLRMHRTLSLTAGDVGVIH
LCARIPYGDDGLYSSYIPAATLLPVSPFSVSETKALRYTKQLFKLDSFSQIPFASFSLSP
ICLQLLQEPVGGIKLQNIILTILVPKGDYYFCTGLPYYKNLRVYVPSSNLITVQEYGLQP
HTMYAGLPTTMELTLDAASLETNATVATALFFSPGCKKDPVISWSTSRTWTVTLPGLYYA
CVAVTDSSGSTMALAANITVLDAPIAVVSRSPAIRGIDTIVKLNNREASAPGVITVGLSL
TPNCLQLVSRSATTETGDQATLRVPEDALETIYLCVSTPLFHTGGHLDENIDYGYIYFIE
EVTTRSYTVCYDTLFVGKKGAVTLDKDVQFEAGTKGMFSNDTTCETMVGAEFSMNETVLK
NVLFTDIGEYSLCVKLLYASAYAHIATVVVYGAVELAPTSIVVGTLTNVSVSLVPPYAPV
KIQTSKDCSFAPVAKGVADMNGELKIQVLYARQTNLTVCVGYGGSKDEGNWNIIPVGVLP
IREVHVAPMAVIVSKVNRVNFIVPDATSLTGFQAFVHGAEGSCQSPPTGSVLPVNVPNKG
RAFILFTPPEAGAWEVCLGNEFSTFRSIETIFSVAPLEMTANPPSGAAGLPVKMKFGGSS
WSALKPILFFITDNVKSCALPSDEETLILGEGSINKTNGVAEPFVVARTGALTVCVGWKD
KNQSFFVYGGSVAIVPFRSFSRYAIRARTNSILAFPVLDDGSLFLVSCPSKSMCGVPISV
KVCLQATKRYYTSSLVPLKGAAVGRYVLCQEEANGKGIVASTVPIFVVDPFLVTIYDTMV
RQFGAVRIGLSGGDVETRSEPITLFTMPPGLQCNETDARSEEFIFAAGAFFGNITVTMIN
PFAEEVRLCVKASPRDIFLAEVFDLLSYMTPATVVTDRTTPVLSGLWKENVVAKLTALPD
CAGSVMSVPPALITNYISELRVDGCEGGNADLKTVHYCESLDGGRVFDYRGAMALVRLRS
CDPDHPSEIAPITVPPGRFIFNYGIDRARFNFFALSEKSDCQKLPIGKNFFLPRYDEKLI
FFVCVSVRTDPDYVFTTDSPTLQVDNFKVSPKSVPGILVAGFGAKMRAELSLNYCTGEKM
TFLSDSASCGNVLVSLRGLAVNPSRVLLFLVGASGLSYVCVTPQGDIRRKVALAEILVVN
PPIPSMLDPILVLGAAFHATLQVSTVSGQAQLYSLIPGEDAQYAFASFYTTFFRGIFFSI
DACRSTVNGSDVVYVRDTGRVVLPTKDIPEGTKSLSLCAGTPAGNLSVVADIQISTAVIY
PTQFVLGADADVFIPLTPNGIFHLRQDDNCRGEEVVPSFTTNSEGRGRLLFRRSSGAGLP
SAGRWTLCVENTGHDGAPPFDQEGMAMAAPGVPLQALTTIEAFNPVYYNVRGTDIIVGVS
SILYLLDDLKVTDLRRGFSMDRSCKEQVESYGFWEPLRASTERGLGRIIVYAGEPTPALY
LCAAVSVNRSIVSLPRHGAVRFLTPIFALPSIVPRCEPLQLGKCASLDPSWSGKFFTVIV
GDCCSFADRLNIVGVIERGSRNLCTLRMDHKMLDDDPPQTEYSVCAWDSQDASYCSNLGR
VKVSTDSCTSDIGTSGSPMSEELLILIIVLSVLVGVLLIVFLICVTVRFCRMKEKKKREV
VLAYPQMLEQELNPLTIYGSTTVSPLPMHEDQSLGAANGDRFTGSSQTPISVGTSVDRAM
GQSPVGVGLRGVTLMNVWESIESDERDQVALQEARDRYNYRLAFTDGIERMSLEEKEQAV
PFELSSDWGNPLEAGDENASASFRRASAPREKDAEAWMDPTEVQMESEGGVAAEEGSTVA
ASFLPHNRTDAVQSLRSGSYTTRQRFYDECRYLFEGETVRRQRVANMADEEWHDIVDAEF
NSYVLLQKNFSGATLPEPLPDTTVLPFAAVVDYQTDTESSNRHYDFCCTDEDDIYDAPTF
PAP
>TCRU_5579 hypothetical protein, conserved
VASPDDVDAALGRVADGGSLDVRGFARAMCAEACSSIQRLLRECAEKAGALDEEVRGLVE
RNRAEEDALRGAATGAAHAEMGALRNERYAEFSRRRARVLAERAAEGAVASPTSAGGRSC
VCVGGCGASLCLRPDAVFDLCKFGDVAHVLLGWRTATQTLRAQCDSLSESVPAGVPNVSV
RVLLVNGFRCTPSCTGGACRLAETDVEAGGGGVVAEDLFVQWPGAVDMRSLLTGNRLRCI
CDPACGMARSDLWLVGDGHDTLGIVRHTRLHHSAVFRGFFFSEQLRVECVGAQANLMLPL
FGATGSESQKRVERRAVDVFESLREQEEGPPSARTSAAVLLPVQGDASAAADDSLPLGSV
VLDIRPLAPSLSFARHFRCAETCAL

>TCRU_5580 Protein kinase domain containing protein, putative
SSSLSSRSISPVSPERISLPLHIVSPMESGNNSQVFLARRANEGGFAPAEDREAAPRKKQ
QSRAYSPQQCREADCDGTDAGNTTTAEDTFMALKFVSSSSSHMQREIHCLRYLNRFRGEP
NAEANDEVNEAPNCGRCTASLLLSTRSFPPPCPKLFFTQEVGGHVAIGLELLGPDLFAFT
ERFVLYEEELCVVGIELLRALSAIHQLGVTHRSIKPENFCWNSREILNNAANKDCVSHDK
SGSTNSVEDVPVFIFKIIDYGRGSVNTGDSPPMHSLYERPYRGWWHSLRGLLGKPMGQKD
DLMGVVHTIGYLLDDYESNGGSLSVSSRSSSLKRVDNAKCDPITHTTTTATTNNTINSTN
TSFLAGESSTESCAANDCRSEKNGSLIQRNVRGDSRDSLSVSSLTSDGSALNSRRRSYSS
WRRHFADRIAIAYGAASKSYRRLHGSEQREGTHGRGKKLVCAERKLPDAVDRRNAKRAWI
VRHVETEYLPAMLPDRYYPPTMPQWWAEWFAACNAWCSDDAVTVEEMTAWMMERMQQQIE
KMGDTVERLRQDLKDLY
>TCRU_5581 hypothetical protein, conserved
MPLRPRFPPVGCNMNDMGYPFRGEYKVEPPLNHGHTGVLQKGSTALMLRITGANLLIEKL
QQGKGQVLHCELGVDNGPSRTVVFPFGGGAVPVPGDGHEYHLNAVVQGGGGKHRCKIILS
GSEGKSVLRLRAPPDSRLADGIMLTVDGQRVHPKGGWYEIPIQAKECSLGMAEMEHPRRS
PSSLAVASLPPPATILVQATAGNQDDAVLFCSGSGEAIHLTPNRPFTVAVESGPFTFQLP
RAAATQPFLSSPAFASEHAKPLTEDFSKHRFPELETMLLAAPPGDTSPPKFVATAEGFMV
ELVGDNGSSVSGYGGAQLSLPDRMEHRVRIVIMDTAGRMLLRQNTVVPPTERAPLTFSIA
EGAHGTRVITGKPLSRISVDRLPPVGGDVGVHVDSGSSHVVTVHDDASSAVFEIGPGQST
FSQPTAAVSTGVEPWIPQLAKALQSPDLDSARRGIQSIIPPTPEATTIVGFVSDQLFKKP
PTISFTKSNDTVSDIQCAGYGVTASVDNSPSCAIYGGGGVQLQAGHSVTLSAVTLPMGRV
VASCCLHCPPSDKNLDELLVARLLETFERHGASPEKVLTELTTITSPQSANGQRLLPLMT
ECLRRLTNSISRPIYLSAADFPENMQISLTLDDKRINTLSSHSMLEVPRDTNNIRVSIQR
PPAPGKASRNEFAKALVDAFYLQSTTPLPVRWGAVPTETPEERALLDLLVQLLRDHENEL
ARQRAHGSTSASVDGFQFTCGAGCLKNVRTERPCRLSVDVDGTGFMNLEQGGQVPQGYDF
PAGSVHRVHIIARDPVSGSLCAETRVTLAAPEVADTPLNVTSPVSCFLDASVTQLQEEVQ
LRLVCPPRFCIVCGVDGNSSGNTGKAVFIARMSAACPHNVNVRLLDDAGGVVFEQRLALP
SMIAPLWSVRLENSSLQVDPINGGGKTVVKASLDRSPEMDLIDPLSFDSNYPHTVLLRRY
FLGPDNCNTYVGELSLRIPAFVNPAHVEDVSRLYQTARSSGDDELRSGLVDLRSRMPSKV
VENLITALIESMTPAHSAVLRSSSDTHIHFRLSGDES
>TCRU_5582 glyoxalase II
IKQLMGVSLLLVFFGSLCISGVASLPTTLAMTFLCYLSGIVPENEYFPRVWFKNNIFTWV
YRIYCSDSIGYKYLRPMLHVRHGLPHSDYRHGVRSLSGGHKASSLFPVELKKNPEFYERG
GGLVDLKGLGEEYKKGYRGVAVVPVPLLADNYAYLILSFATKKCAVVDPADPKLVMYMLT
VVRYLTGVEFVLTDILTTHKHWDHAGGNLEFMQHLQNKSDAEITELLDAQLKIYGSAIDN
PHACTNFVEDGNVLTVAGGGVTVAVFSSPGHTVGSVMFLLGDALMDSDVPQRLALFTGDC
IFCGGCGAMFEVTTVDEVIQTRDLFFSHRMRKHPTNNKMFSADDVLVYVGHEYTERLVAE
ILRLHERDSGKEETNVELRNYLQALRAAMRSARMLRSKRQLDEISVSVPFGDNTKSPWSL
PACTVPSTLAIEKRTNPLLTVKRAVLEDLREGEFLPNKLQTIIYASLER
>TCRU_5583 WD domain, G-beta repeat, putative
MLTSFSWVPKGAMRPVPIHSTENLETVRAKLRRQNPGCAAEEAAGVAGETGPPVQGEFCS
SDDDSGDGVDNMQFGGGVDTVLEQVKSDDEDEVNDTTFKETDIVFVTASAEASQPRLELY
VYDEPEDTMYVHHDVEIAAFPLSTTWLTDGTMSLCAVGTMRPFVEVWSLDVIDAVEPVCL
LGGCIHWEDNYRKSIKTRMLKEESHKDAVISVRWNTCAQHMLASGSADSSIKLWDLNTST
CAGTYAEPDKVQSLDWHREEANLLLSGGFDATAVLRDCRSPNQAAIRFATNGVVEHVEFA
PHGGRIIYASTSNGGWMAFEARMNAKPLWQLQVHEADATFAASPHIAGLLAVGGKDGNIS
LWDARDASRPPTQIVSRSYRTGAVLSLAFHPNSPHILGACGSRGEPLVYTTTTDIRDVF
>TCRU_5584 protein kinase, putative
VCGHCGAPFSKVTAKFCSRCGTKKTSSAGRKKATPHVIGGMAPVNSGPQATATLRPGDTS
NDRGSGGKHNSSDVDHRTDALLSTASTQHQLVSTQPTLMKKEEGTHESLDDDGTIRATPE
EEEKYISWSTLGPEGITPEMLQTSDAEELGSWRRGLLIGRGTYGSVYLGLLDDGSFYAVK
CVEIGGKTGVFSVNELVSLSREINMMRRLHHKNLCTFRGVFYDSPNNVVCMFMEYIGGGS
LSSLVKKFKPLPHAVVRSWTRQLLSGLLYLHTQRILHRDIKGDNILVDTSSDPKKESQIK
LVDFGAARRLSDAVAQSRTVIGTPYWMAPEVVDVTGSGTGYSYKADVWSVGCTVAEMLTG

KPPWPVQVNAPAAIMLIAQAEGGPTEIPEAEATPGCLDFMRKCFVRDPGQRPTVEELMQH
PWILGEME*
>TCRU_5585 hypothetical protein, conserved
EEKEFLFDKSVRNAMRPSVTSQFKLMWCWPASSTNQLDVVCERGPRNVGPTSIVELRGEP
FLREENRRVAVVVNCGERFLLPLLPRPREGSTEQENGVFWSTSTRPNQDLPPSFAELLVG
TVQDLERASNIVQNSPSSFHTQADGAGICDGTSAKEEEVDSAGSLRTFFFRSLPYRTLWL
HQFSKCLIISLPCEERLISLNLGRSTHSTEVFPRLVMKSIECTGSFLLPSFMVPLDISEV
YHRPFLAVGTMCHGVLVVLLEKGMCASVVHRLPLSGLSTSMFPVTHICAVFPPLRCENDK
SGGLGVWGAKSAFLSQCLEGAILCASPYENRTVVAKCSSAGGEGCGFEPPPPTRTVARFL
CSTPYSSPEFGPIIATLDGRLLHFGVDDTKLSETEGSPTKSQRKDCRQRYGAFDLVSPEV
FYVNTMRVLLGVTPNHFCEGGPVRQKVSHSSYQASFDRHWLCLTGISHQVILLDRRAANY
VKHSAITLTVPKSPSFVATASTLESRPPEVSNKKQKNVSFCEGNGAQEISGDDSVYPTAI
EDGISGISWVRVTDGMLQLVAAHHQNWLTVVTWEV*
>TCRU_5586 hypothetical protein, conserved
MSLIVAGATGAIGRCVVREALKREEFERVFALTRSSALSDPAALFGLTVVMDASEANVPD
AITKEQLKRLLAVTFDWEKFLLFWQGLKAQKASRAANTSASTVTVGNDGVEATHYKEIFG
GHKYGAMCLGTTRRDAGSAVAFERCDYDYVVAFAEALREFSGSTLVTYAQMSAQFANEDS
WLLYSKTKGRADAAVEKLGFPHLCIYRPGLLDRGAKTRFNEKIAKWFVSGLPVETCGKAI
VSEFLRSGNDALSLSRECAGKRKKQAVKGETKTDAEVFIFANNNIKKEAAYIS*P
>TCRU_5587 carnitine O-palmitoyltransferase, putative
LRGGDGEVPPEWRGIAEYFCFLEQYAREYKRICNNLLRTSHMAALWNSFYLGNRSALPFG
WNYTLYLDGPSLEQPCQQLNISLPALRAAIIGAASFHLRRLVKNPRFFTLEGQSRLPTSC
RVDLKLCRDQLTRLFRTVRIPHLGMDGLRWSCTNKVLILRRGHPFVLDWVSFGAEDEVSG
LGLRWLEEVVANARLINAFICETSTLSLQRENPLVFSSGCRGTWARIFERLWNEGTSKAA
LDDITSCSFSICLDDEMDPALSLHGGKYPENRYPDINVMYMLNPAGGASCNMEHSWGDGS
TMLLVCSMIHHYAVSFCKEYIALDRTAWINSLPDYKSHVRPVQFGSLTEDILDAIAECRQ
AHQRHVDNTELTVRNICAFGRNEIKRHCRVSPEAFVHAAFHLAQRRLFGDQRSTYCALLM
KKYHHGRTETLRTVTQETQALADLVESAENTKVFDQAVAAALQKANEEHCRRIAVCRAGE
GFHRAVTFLRRLHNVAKERFTRATSPPLASDFSKALAFVDALFFDSSSLRELSCDYLSTS
NITGSGIASFCFTATHPDGIGIGYSLFPDHLTFAFSAHKSFARPLKGTWKNKLVDEGVAK
SGGRHICQLYADALEQSLYDLYRLSAVLPTPKL*
>TCRU_5588 hypothetical protein, conserved
MASRGMLGAVCLFGGLTMTGVALAGSRWRRISTRRAQLNNEYASILAELRSLNDARLKEA
EDLRQKKQENALLHETVTTLWADRLARYVQTNKELHSFLKALPEALGALKGLTSHYRYMA
TEMAKFLAFDVSCIKVHNFALLLEHGENVGIPRVIETIRQLLIAEPLVQVVCDSVINIPA
DVSSPRSIGECSSSFVFCMEELDQAIEAAVLRYVDFQSDHGTKAPNAICDGVRKLTSEAK
LNTFSKGDIIMQKEQRALRDLLLRDRRQLHTTEDLRSALKYVETVSDELCYENAKDGGLK
ASVSGDTAVKVAREQLLLWRKSAAVFLVQQQAKEVLGAYQLLLAETLTKT
>TCRU_5589 hypothetical protein, conserved
GDAEGGVSEAWDNMYSGKSVWRWPEEVLCQRHHRLMAIDFGALSFGALRNGATLADQVPL
AIRSLLDMA*ETMRAHAEVGKEVGHYVEMHVDLSDGHNIPQQVWSPRLDDSIFLIKLPGV
EVSALTSVHRIFLHLTGCAADVEGHHAHLFPAGAMPFPTFEGNFPDDALCHPHLFYVTTR
RNAGLVLSDEGFPSRLEPKRRVHEEACCSRLVDAWPGRSLSAAVEHLICLIA*PSTHCRG
LVLLSNADRADRMIVFYCWKASVRRKNIIYCSLFLNETNLFFD*STSALSQFLAAGGFGV
YSNQWLSLAAPRPNIDWCSFLGPRCLVQQLFVQLDNKFPVSVDHVLQNMISTATDRAGGC
CVLYEYGNVLADFTLLRVSDVTSVPLVWQRPSQRRIECCDETQHRQPSCCSSLCSFSLRS
STWE
>TCRU_5590 LMBR1-like membrane protein, putative
MLNWWLIVLLILVILLCVGLSVYLLFYFTSEEDDGEAYGAKVIVVLGMVISMGVVLLLPL
DVSNSVDPTIPNKYINTLNMTLMWQIVLWILFSMTFIIVPFVMFYYEAYDPDYNRIRKQI
IQAILYTIGILSIFFIICGICYTFIGIAIIPVLTYEGLPQIISDMEWISYNGTGKVINIE
IPVHFFTYCVGIMCFLGWIAFLFYGGLGIISFPLDLIFGFIKRTKSIHISRFKEEMNLIA
LKSDILLELSLNLQKKCRGIISISLRNKIHILRNETYLLEAQQEQLIWAYTKAGGSPFII
YGRLLLGIMSLCISILWILHIFIYNTFHKNLFLNQILISINNIFELFGIIIYGIFIFYLI

WISFEGQVRLGMRLIFFQIYPLKPHDTTLNALLFNISISLLISPAIIEFASRSFQEYGPR
TTINALMNIYVLHLKGIGIFIRWADVCFAGISLLAVLWVLLCPVHKRIKDPTK
>TCRU_5591 Ring finger domain containing protein, putative
VSMSTEGCRLPSLGSKLRTRRRKEKIQIWSAVALQQHFARGALLTSELPTLEEAPPPLPG
GRLTLAQKMGLVPLPPPAPTEEDWRRIEGTAVRRNFAMPLGTNVCCICQEPFYATMEQGQ
IVLSCSHVFHEQCFCRFEKLARRSHDKWDAKRLCCPVCRNRHYHKRIFYAGKAMAERAAI
VKIQAFFRRVLARKAYLKLRLENDSDFSGEYARERLTRLSDAYAAYAERREKERSAMLDN
IGLRLQRALAQCTTREEWNSLRERADRAVATGGLDCPICFCAIQRNPHADDVQKGVTGED
VVAAFRREYDARMAQRRNTEIRGERLSKEACRRSNCVNIKAQSKLTECRPSTSAARLSQP
PNPSSKNSNSRAGCMKTTGKTPGEPRYGLLLSCGHCFHDACLSSFEHYTEMRAIEKGDAV
LIPCCPLCRSAYVKVDY*
>TCRU_5592 SET domain containing protein, putative
METSQSLRCAPTRRSLKFHAGAHAQHFILFDPSISKHDRMILYMELFAFIQHFIDTEAIP
HFRPSRYLPEEYVELRVLTDPRHPAYGQIGLFAKNTIPANTVVTPYSGYIEIFSTSCSSR
TYTMGFGSFGDEYALDAEFVGNYGRFANDPRGVEGLVANLTAESRFTPRGEAYTALVSRR
IINKGEEILMSYGKAHSLTPSPWVGLKGELLTRQRAGGIVPFPQLMGKRRNGLIPHLEWA
PVRGNLNSLASLGSHDDTARIYHKWLQKSVDVSGAHSPAENENTEMVLLWECPQCGMWSI
GSPTPVSINHCFLCRSPRLQRARMVAVCCSPSLSREDVLASVIRGVASVPSSPLGEQPPD
LPFSTAIEDGASALGTYIASSSEGICVKSNQKGSGSGDASGSPTKEILTFPFGSEAVSWP
LNVPFLPWQVWDSAVPLSAIRKHSRFETHVSIFLYAVNTASEEDHRPMGSEGKRGREEGE
ARELHQQRTQLHQRGRRPRVRRKKEELWQKEELLPSSVQDHAEAITASNPTRKCLGETKT
AENSNATDYLFYISSSSLCGENQYDATEDNSEDAAVHSASQSLLKGVVRRVFAGKSYQSG
EVVAAVGGLIVPTSDGRRRPDSSVLEIPMKYFLPARVRRKLRGMRNGGRGPTNSEMDVEE
AMTLSDLLRRLEGLSLIVTNELMFCPCLVLRDEEEKDDKHACTDGIEQEGNSFSKRHPLI
GTCNVSFVLTMDALGSPYVAAVALKDINTFEPLLACVG
>TCRU_5593 N-acetyltransferase, putative
DVSDETLDALVEAIEGDSNLNLQKSSKKGMTKKQALALSEKKVDDVICKIKGTKNGMTFN
EEQLRMALFAQRMMQEKAIRDAQYLNVVVPLKEDQIKWQEVAPKRYIRYEQFDGSQNAME
FVVGLFTKELTEPYSSFTYEYFVFGWPDLTVIAYGIESETFPDSSVKGERVGAVVSRVTR
KGPGRPLRGYVAMFAVVPEFRGFRLGGRLVALTINLMREKGCEEVYLETPLMNERALSLY
LGLGFVKTKFLPRYYLDQSDAVRLKLWLND
>TCRU_5594 SET domain containing protein, putative
SKKASVEYMDAQRGRGLVAKTEFGEGDTILLVPYDIAVLYSPFVRNTCYRCFASVTEPQR
SRGGGDTTRRRRELEEIRYECSSCKHLVLCFGCVKDLVEEAWQRSDGTALAMSLEGNERE
AAILRTHPLLEAHQLACEWFCTLPDSVRAGDTDYLRFALQYGSRALLGDTPLLQAVEGLC
MNTSQQLVKAYRFCESFAKLVVDTFAPQGYDVDVARLRDVLLRTKINSIGYPFNESETLG
WALQGELCMINHSCVPNAAVVRPKHRTAAGACSMELVARRPIKTEEEITIAYIDVDSYAD
DANARRQRLLEDYGFLCRCKKCASATKATS
>TCRU_5595 hypothetical protein, conserved
MSLPSLLSSAASLSRMRVVQRGFLTRRGGRHLTRAAVAVEYRPAQQKRISDGSYGRVIDA
EVLHGDEQQFWGERRNYYCKRAPYFPTWDRLAQTLILMTRQVPRVPQEMAFRLMAVFLKL
MLLPRLVMNAELMLPSWVATNAEGVITQAVGDEEDARKKKKESEDTAGEKKEEPTK
>TCRU_5596 dynein light chain Tctex-type, putative
AESQDQMHEDAAINSDMIQEEVSGLLRGKFAQESWNPRKVDVWVDDVVENVLKNLADLKK
PFKYVVNCVVMQRTGAGISTGFISLWDNTLDGVVHVPFENDTLHCFVTVFFLKLD*
>TCRU_5597 hypothetical protein, conserved
LCADDCDLMVSLMQKACPTFPPRAQEATGSEEDEQNETESQIYLKNLTRALDEALTRKRK
LNMKSRSSPKDTATSWVESSHASTTSAPVEAERGALELWMEEQHRGQRITRSAEPFCKSR
SLTNAVSKGRFPDDANAPISEAVRKWEKEQSQPSSNGNQVREGKIMTKKLTVRYPCPLTK
LNGVPTLLGRVKQLPVRSWRMIHHLTRVPEPPVKNDSMPTDERPVDFMVVENWRRNFDYV
GYEEQFNLDGLLSTRDFCRCMVTRHEASTTGQTPLIALADMFKKNRARSAAKKREEQPCP
NKDVLWSSVWMQRANEIALEKERLKLIDGIRAFELRVPAAARSKEAVEELQRDLVELLKK
WPCDSMKRHVFTKINFLEWVRERQKLQPTVGTGALPSLSLAESMASRAEASFVEHVLALL
P

>TCRU_5598 Adenylate and Guanylate cyclase catalytic domain containing protein, putative
LVLLLLLLPQSGVGQAACPEIEVKVLTLNVTDLPIPAYITESLHHGFVAALWSRNYIVGE
NVRVTLINKSTTMTESGKAIEEALNADPSIFILANVIGDTTLHYYLPVITNRKIVSFAPF
TGSTLVRQWNEHLYFVRADPLAELFALIRYALAQLRVRRLGFMYLEDVSFGDEEYDETKK
VMTRFGYNLSGVFAVKSSLTHEAENSVFDAAWEAFANTMPQAVIVFGSPIKDTAKFIQRM
LTDNRTAGAYLLAPSAVQDITVETWRSAVAGGIKFVSGQVIATGTNPLAEDIHYAAIQRF
QGVMRRFMEKFLPESSSIRKKFPDDDIEGEMMVAGWIAGEILSQALNNREWLKDINTFLA
SLFNQRRYMVDNLVIGDYGGSCQGVAESEGAMCYCNQGGRTVYMKKFVEGYRTDSLVDGT
ISFWIWQCIPSEEVIVPPLNGVAFFMSDSPDAILALRVFGVGVRAALSKTTSSKRFEFLL
TLVNTTLDGAAGALASELKVKLLDIVGAVVTKEMLEVEDVAFINPLYLQPRISRFRKNVI
RLSPTLEQQFFVIARYLGNTSDGSAHAVIRSDDGATMAEVLRLSLETFGGSLLSTKLLAG
GDKMADHLPEEGDVFLVGVSAGDVGAIARHVASNDGVRVFVTLFEFSLLYAEFVAAFRDG
AGADRVVFATSLPHWNDDKTTSMTAMIFNALVPDVNQRTPLSMMGFATGQLLLAVRSRME
KVSAELFENFFFSNVVIRVDDMLYGSFIDGNACPVTESGAECGRNYGATQISVWPLARAL
NPAVPVLSHAVTPSMEYRRPVARGLTSRQLIGVIVGSVAAALLLIALILFLLHFCRDSRD
NANAPKERTDPVTLVFTDIESSTALWAACPEVMPDAVATHHRLIRSLITKYRCYEVKTIG
DSFMIACKSVFAAVQLVRELQQVFLQHDWGTSVIDDAYHKFEEGRAGEDEEYVPPTARLD
DAVYRQCWNGLRVRVGVHTGLCDIRRDEVTKGYDYYGGTSNM
>TCRU_5599 protein transport protein SEC23
QQSYGGYDAVTLQKQQQEQQQQQQHAYSTTVGNRDYGSYYNPASIDASQGGMASGVMNSG
YGNQYMQQYQQQQAYDGYRGGGPEQWQQSYSYAQQQYASTMNKTADAHSASLNPYAASNT
AYTNTAAEAADSSLNLGSEQPCAATNATDDNGLRWTWSTYPNTYRDSKQDSISMGSITLP
EMIIPLACMYTPLKPLETSHFIIGDPAARGQQCSNCGAFWNKHCYREEGKFWVCLACLRR
NPTPPNYSIEHPALHYETVEYIIPTEASTTTGGEALTPAKKHTYPTFIFIIDVCIPVEEL
ETLKQNILRCFNWLPPQSLVGLISFGARVTVWELGNTAVTRCYSLRGDKEYDPAELSAML
QVTDTMPAKGRFLSPLEDCEFLLTNLIGELQCDDTVTPGNKRPLRTTGTAVSVAVRLLET
LYEKLSVKESRAAGAAATVSTPVLKAGRVLLFTGGPCTRGPGTVVCTEKEKMMRFHRDII
DGETPYYVDAYNMYNGLQQRLSNVHASLDVFAESFDQTGILEMREAVNQTGGTFICGDTF
NHEMFLKSFQRYFDRYDPRIRGPETPGGESQCAAFSVRSAFGVKFGVHTSVDTLVCGVLG
PCLVDEKANKANPNRVSSPIQIGVGGTTNWCVSTMDQAVTYTFIFDTATLGKKSSSGTTG
SKDPHSNEAKRRFIQFVVRFNTPHGESRVRVTSVVLPIAPSSPVVDPQYFVRHQAFDQTC
AATLLARMVVGILEKHPSKWDDTKRWIDTVLVRFVRRYGTFTPGVPESLRLHACLSLFPS
FLFNLRRSEYFMVLNISPDETTFKRHWLMRETVDNCVLMIQPALYSYDIETPIATPVPLD
SCSLRPDNILLMDAYFNIHIMWGTTIFAWIQAKYQDEPEYAYFAQLLESVENDALGVLST
RYPYPRFSRTDANGSEARHIKTRMNPTTTHHNGAAGGAVAASDRSDVIYTDEASIMKFVE
SLKQAVVS
>TCRU_5600 Sugar (and other) transporter/Major Facilitator Superfamily, putative
GDRQPDETPTFCSLENLKVAQVQVVGGTLNGFSIGFVAVYAYFYLMSTDCSMYKKEVACN
RVLNAECSWSKTRGECGWNGLTCFWGYGKDKDSCLADGRCKWVYSDEECKNPTGYSSSYN
GIFAGAMIVGAMIGSIYAGQFAARFGHKVSFLIVGIVGVVSSVMYHVSSATNEFWVLCVG
RLLIGVVLGLVNVACPMYVDQNAHPKFLHVDGVLFQVFTXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXEIGLGPCFFVLAQELFPRSFRPRGASFVLLTNFIFNVIIN
ICYPIATEGISGGPSGNQDKGQAVAFIFFGCIGLVCFVLQVFFLYPWEESTPQNHGDTNE
ESALPEQQSPIEVATPGN
>TCRU_(CLPTM1), putative Cleft lip and palate transmembrane protein. 1
QYTPFSKRGDLYSIIITSGEDGLFSEDIFSDLVLDDNTQEISRHYTIDLSRCYAENSSAF
LTIKTIIKKREYSQLFPLVRYLPFRSARRKQHLFLYTKTAEGDASNTTDLEPRTVWKAYF
QPLLTLSPIVDFSNPLPSSMIPYYFMDNETQQYLPLVYINNFWVLRDHLLEINATTAASS
LNFTITISPRPLWKLALYVQFEESMKQNQELGLAKPEDLDKTKRIFLETNPYFLGLTLIV
TLLHMLFEYLAFSNDVKFWRSRKDFKGLSVRTIVMNCYFQTIVFLYLLDGDETSWSILVP

NGVGVLIEYWKLAQTVRFFRHDNGWWWFTFNDGYDECTRKHDDRAVRYLMCAMSPVLLLY
TVYLALYDTHRGWYSFIINTQVRFIYFFGFAMLTPQIFINYKMKTVAQLPWRTFVYRALN
TVIDDLFAFIVKMPWLHRLACFRDDVVFVILLYQRWIYPVDKGRSEIPDKESDGDAKRVE
CV
>TCRU_5602 DnaJ domain containing protein, putative
RNALQKNSSFAAFVDRMHAINRVFLVKKKRESEVETVSCPDPVDDDARDEARSAYIDAET
KWLDCCLREFLERKSRYGSRKLFLLRLLGVLIVLMGVLWYFWPLWECLIDVEADAHFRVL
AISPSSQPNEIKRAYREAVKRWHPDRNPNCESCRIQMIKIQQAHDVLLARGSQRFKLAEK
YREELLQLRSLVFFRLYDMAFYAAQELYYFLRGNVMRNNGDEKGFSLSLQVGCRILTMGL
FTMYEFLYISGFNIVVIFQMFYYCVSVTRISVAEREMSRMVKHSYFDFYREAVMFAGMPL
LFHLSQRLMGKVEFFGEDGLEFFFRMSFGILYVLSHLYRMTPNIWDNVSAKKCSIPLNYL
RLPAKSISYQSFLLTELGVILDDLFAFTCRVPSIYRFTVIVVHVIFLCELAWLPSDPPAT
VNLGRQYEKKRLRKKTDIEKGLNSNSEREMMKYFQHHLSPQERILVENLDDETITWIDVV
TTKYKKRMDATVAAYMRQKRGSIRFDLASTLDLQEVVLLSITQSSPGSSIKVDVLFRVKD
EVCSRLLALQRGPLGCVPPETSESEDYLGIIRRYAKITGKEGLYTPSEIWGLKLSNKKIK
>TCRU_5603 Translation initiation factor eIF-2B subunit epsilon,
putative
MDYSASRRGMEVGRKRQNPPFVVIVIGEVFNASSHPLFPVAPAEELPFALLPVCNTPVID
YILENLAGNGANEIYILLNSESVAPVCQHLQGNRTACSRPGMQGSDLKVEVVASTRKMTN
LFDAATQILEQNIVQQNSSFLFVPIDAIASFQNLSDLLETHIQRTMNIKNYAATMLCASV
KSLLEDTLHDVLVGELNKQERAAGSSILERDSTSTVGVNIGAAERRPHTAPEYLPNHLTM
FTLEKSTGVVHNMVRLEQDEKLAEAVTMNFRKNESLSVRTDLGPTGYFFCSAGALSLFTF
HTVDAHSFFVSLLASQELFGNVFGIQAVTPPMGIIQPINSLRAYIQANIDVCFRRMFPLT
RESSFLGDGFRYAVSPHCQSVYLHQKKAEVLSNTCGPSVVVGEQVVVPPNTVIRGTVLGK
GVRIGEGSTIIGCVLLDGAVVGRGCFLIRSLIGYNVVLNDRAEVSNSIIGSGCNIGVVPC
GSCITDSNSPPGGVVVQDKAIINCEVSQTEEGITGHGGRGKALPKRHVNNIIPTRELFVR
DPVPCEASEASDDNDGDDDDDDDSEKTAGFREAVVELVNQALRNPSHIEHCVFQMRNTRL
SFERKNSDLCFIVTERLLTHVLEKHGPSHDPRPVIEAVNGLFGQWCHPFYLEMVTGQDEM
QAIMEATCIAVADRNCLLHLRGPQLLECLYNGCDEELYDERGYCIVSGESLVEFGARVRR
LAREREMYADDNEGDARKEGMLRVAVSCLGFIDGVRAFLEEEED
>TCRU_5604 glycosylphosphatidylinositol-specific phospholipase C
FTNTEWHPQSWMHDLRSFIGEMAITQLCLLGSHDAASYGIRKDSPFGADAPGFLLGDSVL
ASLSRFFFRGICASWSKCQGMSVRAQLDYGVRYLDLRVATNPEDASRLYISHTQISVPLA
DVIEDVKAFLNDPSSANEFIVLDFQHLYLTDDSDGKGKFLGELDRLSDRFIPVDVPLTTP
LEILWRVSSRRRIFLVVSSGENGLPYPAARIRSKCMVSRWVDQGSLSKLLEALDNLLLDD
LKYPQTGVPSKLHVTQAVFTPRKSNIFIGIFPKISRKVASSIYDVATRVNPSMLEWFYLL
NANGLLDGMKVMIPSGINTHGNILMLDCVELGRCQIMDGTTETNAVGMCVYLNILRASR
>TCRU_5605 peptidylprolyl isomerase-like protein, putative
TSMSSVESQSLRDVEYPIREETEVPGTNKGLFKTVLVAGTGMRPVKGAKVKVHYIGKLEA
DGSKFDSSFDRGEYFEFTLGSGQVIKGWDKGVATMQIGETAILKCSPAYGYGAAGSPPKI
PANATLLFEVTLVDWTREEDISEENDKSIMKNLTVEGVGYEKPGYEATVKIDLRVYRGAK
EEGKILCERLGWRLILGDAAVPPHLEQCLSTMRDRETASFRIAGHRITEPCEEFNIASGE
PVTYVVELYGLETVKVWKFEGRERLIECERRRQQGNDAFRAGKLEAAMRKYRRAIEFLET
DSGLKDEEKEEARKARVILFGNLSQVLLSRRKFSECVGYCDKVLEKEPQNPKALYRRAKA
NCLLCEWDEAKRDVERLLAIDAQNTDAKVLLQQLQEKRRAYEKKQQAIYKKMFT
>TCRU_5606 hypothetical protein, conserved
PRPVLQVGTSPRMPLREHLKNFYFLFFGSNFNRCIVAASLMLLLISFVSTASVSTLWYHV
MEGILTFLFAGEIALRLAVMRSNFWESAYNISEVVACVLCITIFFILHFSRQQSSRTEHQ
VLIILRYLGQLLRMIGVVAADTMVSTSGEGGIQLFSANSTKPSSTDLRETYRDVL*
>TCRU_5607 pre-RNA processing PIH1/Nop17, putative
GFCFEALLADNATMVLVNVCGHSSVGMALAKNMEVVPEGYLDKYGVDNLIIPIAVGPAKK
YDGEKCEFTIDVVVHPTLIVRCVRSHPLFDHYVIRLTNLAIEWILQECGMRINPRSCRLI
PNKKYFLNDKDNFYWTLSRIVKAVEKRTTTDPVDEGEDEEISLPSELCLNAPHLQSEIKS
SPLIKEMPVVTGIRKGFLDGVRLYGAGGSGECNRPTADSLLHFPERLRNRCQVIDTRQLV

NGATQVPAAKETDHIKEKPKQTNSNITKKEACQWEVQSVDCNEREIVVRLHPPPNVMSMK
DVELTASLDVIEVDEAVIRLPKAIKVDDVSAKFFKSSRTMVLTCPLA*
>TCRU_5608 WD domain, G-beta repeat, putative
MLFVASEGKSRLIDLETKAVQRTCATTHIERRGLTYCASLKAVIAHQSRGCTSFFSPHTQ
QPVQRSFTMEPIMCSACTADGVFLIGGTAEGNVYVWNILTGQLYHLVRAHRRCVTEITIS
SDQSLLVTASEDSVCKTWSLVSLVARGSKTVAPCSFFHGHTLAVNTCSFMESGFMVVTGS
ADRTCRIFNALTGQQQLVITLDDAPTTVRPSPGDEMLLIGSAKGSLFFVDLYGNASEQNF
PISLHGRNESVIERKSFGDGHSGAILFIWFDPARLGHAIVGSENGALLWWSISTQAVHSE
AFPRFSGGVLSMCYVPRDSLTAVLWPCVGLMKHPLDPSTTDYIISSLPYEGAAEEKKPVA
AGPRRRCRESDGGGDFGDRDTKLRAEDKNDSDCCVSAIRRQREKNDELESLRDQLKVKLQ
ML
>TCRU_5609 MSP-A, putative
GWAPIRFKVFTEDLKNPQKYCTAEGQQRSDLRGIMTICRRENILTEEKKNIFESYVIPKA
LKMHSDRLFVKPLRISLVVPDPVYGICTEFTIPREHHTKGVPNTDMVIYAGAAPVTGAAA
WAGPCLTLRDGRPFVAVLNYDPRTLVRDDATVRQTAHEVAHALGFGYEIMEPLGMVSKIP
NVRGKEFVTVVSSAITKEKTREHYNCPTAPGMELEDEGYGGTAGSHWERRNALDELMAGI
SGASLYTSLTMSAFESMGFYRANWGMEEDMAWGRDAGCALLERKCIENGVSVVPDMFCTN
ATPPGQLLCTASRRGLGSCGLYTYSQSLPIHFQYFSDSKAGGGNDYVDFCPYIHQFSNTG
CIDGDPKVMRGSYVGPNSRCVKGDSLETLQYPVGDICVDTLCENGVVKVRYLGAEAWEPC
PEGGHITPNATFYKGRIICPRHADVCSRRKIK
>TCRU_5610 TPR repeat, putative
LTSFEMGELRYQQGLLLAQQGRLREAINAFGKASFFLPHKPQPLFAAAECFVSLCDFKGA
VKQYRRALWLLRPRDDTESVEHPFGSALHPEKLSRCSDFLGRVSAFSIIEGEKDEGRESD
HNDDFMLSTTDSSGRIATAEATPPPSAFRARAAAAAGDDRAIAGAVKTRLAGILDALSIV
LFNVKDYGQALRFADDSLDLCEHPQVMLHRCAYLVALERSDEAEKALEKHLKEHPCYFIE
SSSLLVHLYCQRQAFRHAKELLESVPLNDRQRAQIVLAQRIFDDAYSVFRQRSIDQSDVQ
GLTRCLGVFPEDPALSFERAKYHISKGMDKKAVPDLFRCIKISDGSYKNAVELMTETLFR
LGAGRDGKDGIKDAIEYYSTSLLWHADNIPVLLARGDCYAKLGDYKNALQDFLCVERIFP
KHSGATERIARLHDVWGTEFHARGKLEEAEQEFSRAIATCETEPLFYYHRARCRFDMGEP
RYALRDVLSCRELNAEDPVIRDFVHAHLSFMTQ
>TCRU_5611 kinetoplastid-specific phospho-protein phosphatase,
putative
IPIEIHRIIAVGDVHGDTENFRQILSMAGIVSYSSNADKQLLWKPMWDEKEIELHKRHHT
KLRSTLIQMGDLIDRGEDDLGVLEMAFSLFEQVKSNHTSDNIVLLLGNHELLNLQEQFYY
VHPETMGGFLSKTLRKRAFEPSGTFGRFLLDKFNVLYFDAETVFVHAGIDQHFASVGVEM
LNKKTMQAIREKDYGNPLLGTSGPLWTRKMITDAANGRCTGIQKMLSFIGAKRIVVGHTP
QRSGHVEVFCNDSVIAIDVGLSRWMYGNLAALELMVTSYKCDLGICRDVVMREITNSDAR
RSQTIDESLKDSLLLEELMHAVEEFYQ
>TCRU_5612 ATP-dependent DEAH-box RNA helicase, putative
KKNLYAMVKAFVDDPNAEEMSFPPTLSAAERHMVHEIALNFNLHHRSAGCKSERVLTLKK
IGSIKNQEKDRENAAFNGDRVKTIDGYQGAQRLPDEYIKSRMNEISLLLGPFLRKMYSQL
KATAAKPLRNRHLVVVQPGLMKAPQGNTQHQRYRELQEFRRSLPSYKRRDEIINALKQNN
VLIVSGDTGCGKTTQIPQILYDSEVFQKDLEIICTQPRRISALSVAQRVAEERGETCGNS
CGYIIRFDNMTSPSTKIVYMTTGILLRRLHTDPQLNGVSCIIVDEVHERDVETDFCLLLL
RDRLIEQQRNNQLYKNHVKVVVMSATVQIEKVASYFVCVCGGRAPPIISIPGTLFPVEEC
FLEEALKWTHLPPSAVPAISMLANVSEKKSKNGNSEDRNDGSIFEKIKATVFGETDNDPE
VLVPYDLVFKLISYIHASSHDLSESILIFLPGWASISRVNTMIQRSPIARELSVLQLHSS
LTAAEQQRVFYRPPKRFRKVVLSTNIAEASVTIDDIVYVIDSCLTKGTSYDARGNTSVLK
ATFISKANGMQRRGRAGRCRAGVCVHLLPRSAYEKLPEFLLPEIMRSPLEDVCLQVKALK
PDEVCAKVLSRAMDPPPADSTEHAVRFLKDMGAFTSEKEQMTNLGRALSKLPIHPLLGKM
LLAAACLGVLEPVVTIAAYLSGKSPFIKPLPHQKNAMRNAVQSIDNGLLSDHLSVMKLFD
EWKKSNCSADYAMQNFADQTVLRSMDRIRKQLLRLVKDSSLLRKVEDPMRMASRHSSNLG
LVRLVALWSLYPRIASVEYRANRSRKRPEIFCWDNKVAQCAMGSALAFKNRDDFRDRAFV
FYHERMYLEANLTVFDASAVTPVEVALCLREFALRPLTDVPPAFLTDDESKMAPAFPFVL

EREEEAKDLAVLFFDGDKKLYVTSLPVGLLLRDVRECMDYYLALSIKEVRADLFPEDLIR
VLAYVVGYPFSDEVSAIDNNTSDKPVVTYGEEESLEPTTIDCRSAQLNDISDDEDDAPEI
FMEDFEDLQMTEEEIQRAIDVFGELAILNR
>TCRU_5613 hypothetical protein, conserved
DAETYKLYINRLVFIDTAEDSSRWLARAKKQWGFDQPIAIRVMNESEHLGTTTPQMIGSH
AGWTGISWTGDANDGVGIDVPNHQGPMLVLEVVGGKSTLSIYGTGLINSSGMATEKRQYA
KYCVHLFPTQTTFDSETVFAVVEAEIRSSAWDGRHGDEFAPLEYNFGSVRVSTLDFYFPS
FMLTGTGEYIVSNLVCAMNMTENSALAMQLVPLMDARDYISVEPAQVITVKPQQRVYFTA
TWSIDERACMKELQVQLVVNGSQPPSAPINISVYNCPPQLKSTDTPYHYWLNTTCVTNRQ
FSLSQEFSLVFALLPVFRFVLNGRVAGLGAEGVIVALDKDKGENVLVRADGVPVVNVLSA
GLSTSLLDSSFESNAWAQAEKKAWSMPDDGRQFALDTLSMNLLEKTCQCTIHLGTIRGFP
MVYEVSTGISPSFQVSITLLDQKGWQVVKGETKARYQSASGSLRWDDQLVLRKWPGASSK
QFARLNLTEVRPRDGDETPIGAALVSLYRLDRTRLHVGIQLAFHVYETYSLYDTLHSSSL
LMTDAFITFSELP
>TCRU_5614 60S ribosomal protein L14, putative
MVKANYIRAGRLVRIIRGPRQDRVGVVVDIIDGNRVLVENPADKKMWRHVQNLKNVEPLK
FSVELSRNCSTRTLKNVLAEKKILEKYAATKSARRIAAKRAFARSTDFERYQLRVAKRSR
AFWTRKVFDENDKKKPVSWHKVALKKLQKNAKKVDSKPAAKKRIEKARAARKAKAAAGKK
*EKTA
>TCRU_5615 hypothetical protein, conserved
MLTTRQLVPSSVAHIVCPLLLQDGTTVFLTAMGSLLKVQQPVWKTDRDGKESCVFVPTRD
ELHVGSVAVALVACAHQCFLVLTQDCEILVGRYQANLPAPPNSWLCNDVLHHSNAWIVLY
RGKFSASQAGGSSIPDARPLFATGMNGTTVQCSILRGVMHTIIIGIPNNAPNTFFREKWL
LSIPQSVGPFSYGVAPFRRDVIEQSDEELLMHCTVAELAERKHLESPPPVTQSYGFPPVS
VTLLHRNSDDRIMSMGPMPAKHSQGPESFAFVFANRSSLSVLGVFSSSSRGKLLKNLTVS
GSPYFALTLPDRMLVLSLLGCVHVLSILAIDATTQGAMLTMVSGHRTVRIARSMQHPFAA
VLLQRCGSWEVLWLLLENGLLTEVPLRSCSRATAIVICDAPNIQSGDCEDGEWPIACIRG
LPHGFRATSILPFNRGHSTNFQPHPVTQRYVLLGDGISDTYIVDLVERCAVGGLLSHGAM
TSACSGPDMDIVVTYSKGMLQRLSPGVVSPLRVHAAFAGVHQMYALPHMNASRSLNLTLY
FLVTTATRTALLRGAAGCMEELQETEEFVLDEPTLAAFSAPPDDEKAELSSPPSLSFAQC
TPTCLNLAGTRNSLREILSRMDCASNACFAGDEFLAVADSQRVTILSIKGRKTPHVILQE
RVSGDVSHLAAWRLPESSKWAVASCLWSQEIVVWLLGEGDVKRHVLPVDAVVLSGFSVMD
GGVGLNFINRTVAVLRYATAEGLPFLTAMEDVDGGAFRAEMCLSVTAVFGLVARPHFNLV
AVNAHVVELLLLGPAAVVEERLRVALFPLPLDCRSGINDNSSGSDERTSADGACVRPRPL
RCGFVLYFSAASFYMLVLSDGMGIAMWSFPDLVPPGSTNATRFRRNGALQRGPVKYQESH
AIQLPFITAYDHRLTKAIYMPLSNTIVALTDRGEDISLVSAVDAEAFRVVDGLPMASKEI
PMCIESLSGPVEDVVVIGTAVQSAGVTTDPASGRLLLVHVKPLRVSSVACIANGGAIDIS
VQGYGGDHLIAVASMDRVLVYRLTGLTLSPVCSAEMKSSCTTVALCYPFLSCGLYTWGTQ
YMQLLPRGRAGGDAEEWETASIDQEDDKRGNSQGFSNSNTWNSRMSALKQADIFSWTRCV
GSGLLLRHALEPTAFAGVHSQAVYGDELVRVDNERNVMTVSFWDPPGLVADEAPDTRVVG
LDGSYSSMITRCLRLPSRPLRVQPSEQWRLPWRYRKTPFLTWCDRLTALWPVGPTLLFPC
ADGSLHCAGEIPSAFASPLLRLEQRITELYDTTLSLSRQGCGAGLRRTYHSLSFEAAGAV
QSATRVLRKQFVLYGDAIEEFFLLTRLTEMPDPRLTAEEHEWVTRKKQLMDAHVKQVWEE
YAGELQEVDVCDILHLW*
>TCRU_5616 retrotransposon hot spot protein, RHS3, putative
TLTTTIRGVLFKGRVRVKDIKLNDFLTLRFGGKGVVATNWDVSLEEFFRQPTEYIHNARV
LNEIQATDAYLSMGRAVMDEVYMEEDVHKLHHEGVFSLEQWRDYEGKDTVTPLARGTLDA
ALSRAQISTSVVTSTVLKGYYESVYNASWSHVVEVPDGVERNKTGTGMDVKKGKPEQSWT
YKKVGETRERDDAAQQSGAERLRLMVLTSDKGWPYSWEEDEFIRDCHVNCEVDRVWRIVE
HYLAEWFSTDGEPYFTPGRLLLIGTPGIGKSMNAGSYLLYQLLQYDIKKLPVVVYVIGNE
TFLFEKTDKTVTKYMGGASIEHVLASLSLRGVNAYIIYDVAKGGCKPYPLPNSRGWGMIV
VTSPNEDNFGAWEKYKSPKRIIMNCPKKDDVKAMCVWMKRNEPSVQAGYWRNINGRMEEV
GPILRYIFDDSKYNGRIQSCKDTVDKLNRIDAEYFLPFGTTQMLGGDKVSHKLVRIVRVR
GVHNIESTFNGLMSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPHERP
LKPLPLPLLENFKKKIEIESRVLYKPVAQNFPLVDAFFFMESNPKTMVGLQITTASAHHT
IPSTVNQFKEKMATYFNGWEEFSEGLSWEIVYIQHADSTPMTGWQRC
>TCRU_5617 hypothetical protein, conserved
MPSCEHIPPDLFHGVESRRHTDACVRQLSRSKEFQRYITHREYSESLQLTWFMALIGLSI
ALYYHLLFVYRDMYVAPFGNFEANTIPSLFSTALLLFYIAPCVLIAPFSGFFETLPSRGA
LRLAVVFTFTNMAVVSFGGRWLHHPPFLITEPPIPWITGKTSEARQLVTITLTRTLPLQG
GVVAGWLVYKWRRMRWKKAWHVPLPLITVPILVGVFSCLWFFLATCFVTSLTTTSFFFPV
GGDTKAVGDDVVSKILSMVLAIKQEFLSVLNWLSLPMSLPDARILYHLWCATLELCVLYF
LGVFLSSFSSVFRGIFWLLPTHPTTWLLSLISCLVGLNALMRSDSGNMLHVLGLLTLACM
LVRNGF
>TCRU_5618 phytanoyl-CoA dioxygenase (PhyH), putative
KESRLTHCWRCGLEFNNRTAQNAIRCRICNLTFHRRCYLAETGINKDEAMSCVCCLSGIL
RMPHSLRVQQNSVATKFLRDGYCVISLATRAKEKKLLSETLEKYRANADHYFKSFMHAYE
AKVEFSTKVPTLESGFSNFRERGSGRFEMISTEIGNEVLSIIGNCNELSNILDLLLTSAR
RGMRVKKRLMSTGCFYSLPGSSKQSIHTDGPPLSSVVNLFPYAINVFIPLVPVDKNNGTE
VFPGSHRIEWDSRSSLKKKPVTPSIPFGNALLFDYRLLHRGLGNRLSSPRPCYYATFVRS
WYKDKFNFSFSRYRTVLHVPSYLLVRRSDENVQKRRRIE*
>TCRU_5619 DNA polymerase alpha/epsilon subunit B, putative
MQHGVRWKAAANLELLLGSEHPPARIVRDVTNASANIDGAAVDARNTVSFKNTLYCNRQD
AGYVGTWQRLAEYYRFMFSKIPLWEKSVQHGEKTKETTEDSVAKNEEEGDVEMPTPHENV
LPPTYRAVGVLTQTNNPGDIGGDLLLPWEFYPVTDINDEDAYAECIKALLREAPVVNGLL
HIGAEEEDELGAAGATMAASNLNAYSRSDGRLSIYTRLVPQFSGIYPGMAVGIVGDPFKR
SSSGMLTGVLVRQFILPSRPTFPWNMQMPLPTPSASTTIPTRVHFCSGPFPRREIVSILN
AVTQNALARGADLLIIGGPLVKEFEEFEKELLTTLQRTFDELLGAYMDGIEDTISNYYAV
NSNPATKHRLKVVLISHRDDVTQIPALPTTMYGVQDGRDVWVRSNPCRISVNGIHFGVCN
EDVVGNMRDKMVERWPTEAGSLRRVVEALVQSRLYAPIYGLPAVMHELKHFQALRMEYLP
EVSNEEVSNNNEDKDDANLRNGKPATSLTWDSLFSIYSAESVAPDEVKNEAKRVKMETQD
SSVPLKNGLNSEATVEWMPHVMFLPSTRPRFVVVTHRSVFDGAKGARRDESELDDVSTAS
GVLVVNQEIWSKRSAPKFELRVAEVTIPDSGLVMRRGASEANGVSCGLIHFVNNA
>TCRU_5620 hypothetical protein, conserved
MIRDQCKAYCQCSYCKQTGEQMRVIPDSIKLASGNGRSRDELYLRTLNQTLRARSLMASS
KNACNFKPDEILQSTRGDMARAALTVPVRRRDRLQELLILENKERIKAERQRRQNLRAMG
LPDDADKTSRDCAVSTRDDFNVARELGKTNEAEVVVPQAHSADEDLRHVLNTVKAITDEH
DARDSSKSLTSDQIHRLRRLVQEHDNKRKSTTADSPLQPHVADHRHQVSQPHIQQKMFPS
IHDRSTRRLKYNSHPYGTGVVWLPLEEDNTDEDGKNATFTAAGRLDNTRLDDKAYAEHQY
PGSTYNKYLNDGPKAAEGTTLNDASPSTADNLAASADLKILGKGNNAENVALSDAERKKS
LKETPSYKSSAAFWRTTNQDRAAQMQRFLEFKKLQADAARVYAESAVRRPADVGTADA
>TCRU_5621 leucine-rich repeat protein (LRRP), putative
LHASVPVARVQNVEFPFSSRFPDCTGNSLLSSVASSSKCRLSPIGTMNGKSDKFVPVGGV
VPQDTTSRRARVKTSEDLLFRQSGRHVPLPEARVVHPQGFRILKGRSAVERSLRSYFRLP
PAPSLRLIQERLRTQRQLLAVETTEDEEEARFFSNLMEAPLRQSHVLLDGYLLLCASGQP
EPEAVEEVTLQHTHLVGVIEDDLTHFQNLRFLDVSENELLLEHLLFLTGLEVLHLPYNKI
DSLAGVARVVMEQRLQSTNSSNAYLNRGGVRGSGVGAMDSAVHGSRSIRSAAAYYAQEKK
TTTIDSNDGVRCPTPIMREQGVNGNFHAAENTGYYSPHQKTAGRPCQPSECSMHDVLLPK
LHALNLSFNKIPSSDILHLAYFPFLEKLDLSGNNLRVLPEDLADLTGVTHFALERNHFRD
GNTVFAALSTMPALIEVNLNHNELRHVPPLSVKNGRGLCFPSIEVIGLGYNRFRGVRDVV
ALTELVRTLQRVMLAGNPIARKSKERGAAHSVFAQAVMNLYWEKAGLQTLNKGEFSTMNR
FSNDVPYEDTSMLHTRQQCKSETDNEKEMTRSEYHGLGSLISSWQRSRMTSGSKVSSRCQ
TENFESEGDAAHLSGSVSDRPYTPFISPSAGGGSTINNLFWYGDAEPPPSRGTATLGHDG
TLPELPTPLLLRFVELIFEDTVMKKQKPGYFCSKWRQTTMEIENQSRMTADGGHLSRLVH
PKTGLVTLPNYNEFMDIYRLLEDPPLSRPGLRRRRYATSRGRRRRQMADIVVPKEAADDT
KEEEMEKKSEEEREEVVTPKPVDMQSTGTEEEYEMDESSSERSVSPQDVVFMTGVPLQEE
RASVPKKWGEIKPKKVVVQEFPVEDFCGGSKEREKPLPDPTEHANKREVKGQRGQQRRKQ

AEHSHERFPRDRKEQKFSSAVPEPPSTNVRILMNELRRMLRRPLPSLPSVSTKKGK*QCP
KG
>TCRU_5622 GTPase activating protein, putative
GELTDRYGFFIDAERKAEESEYIRQHPEMPATQKMWARVLVRWDHTPYKKKKKLAREGIP
QSMRRIVWPLLLNSHESSSLSHEKYHVLKSRPPADPELFAVIERDLGRTFPAHHWFARAD
GVGQTKLRGILRAYANIHPEVGYVQGMAFLASTLLLHIEDEEDAFWAFFSLMRHPKHSIW
KMFTPGFPALYMRFYQLKKLMQRNCMSLFRLLEAFHVEPEVYATHWFLTLFSYCLDFDLL
SRIWDMFLCEGWKIIFRVAIALFLLCEKTLKEAKDECNLLLAL
>TCRU_5623 diacylglycerol acyltransferase, putative
EVSKLRKAYWLATGETERLRSRSGSKSSIFGNADCGSAGIQPLHPGVEGRRRQDGKILAC
DCALRQLEEYVGPRPEAHTFDHDDDSGNEGERSRMRRFFCVPVERRLQTLLVSAFLFFTL
IPVSLALTVALLLNWWTMPFMVAYLVHIFTFGQPRHPLRKHTAFTRLKIWRHYGAYFPVR
LVIPCRVREKFEPQKNYFFVYHPHGIHGFGAIANFTLDATVSSLLPGIIIHAQTLKLNFY
IPFWRELQRLCGNGDASEDCIRRTLRSGPGESVLLVVGGAKESLLASPRTNELSLQSRRG
FVRIALQEGSPLVPVYAFGENDVYRIPRAAGSRWWRRVNAILRKVLSFGFPLFVGRGWFN
YCFGVLPHRRPIYVVVGEPLPVPKIPQPTPEDLQEWHDKYVAALKRLFDGYRAVYDVESS
GLHIH*
>TCRU_5624 diacylglycerol acyltransferase, putative
PTTTEEMHELLDMIVSACDHLQGLIRDRLPVTQREVSKLRKAYWLATGETERLRSRSGSK
SSIFGNADCGSAGIQPLHPGVEGRRRQDGKILACDCALRQLEEYVGPRPEAHTFDHDDDS
GNEGERSRMRRFFCVPVERRLQTLLVSAFLFFTLIPVSLALTVALLLNWWTMPFMVAYLV
HIFTFGQPRHPLRKHTAFTRLKIWRHYGAYFPVRLVIPCRVREKFEPQKNYFVYHPHGIH
GFGAIANFTLDATVSSLLPGIIIHAQTLKLNFYIPFWRELQRLCGNGDASEDCIRRTLRS
GPGESVLLVVGGAKESLLASPRTNELSLQSRRGFVRIALQEGSPLVPVYAFGENDVYRIP
RAAGSRWWRRVNAILRKVLSFGFPLFVGRGWFNYCFGVLPHRRPIYVVVGEPLPVPKIPQ
PTPEDLQEWHDKYVAALKRLFDGYRAVYDVESSGLHIH*
>TCRU_5625 Leishmanolysin, putative
MRPPHHATPRHTALPLPLWCMILVCCASGCLAADAADAAQRQRCGLEGRRRRSGLVPTAV
VREVPRKGQGAMQAHTVSKEDEDDNWAPIRIKVSAREMYDSLRHCTAAEDLRVDHGGRPI
TSESDDVLMEEMRDIILRQMLPAAAKLHSERLSVRPVTDLTVLPRTNLGLCDKFTIPRKH
CTVGVEGADMILYVKAFPTSGELAWTIRCAFLEDGLLFAAAVKFDPKVIETTNIRVLPAA
HVLGHALGLASELFFAFNMISEVPKVRGKLKVAVISSPRVKEMVRS**NCPRIEGMELED
EGGEGTKLSHWKKRNVVNELMSSDGEIGYYSALTLAAFEDMGMYWPKYSMAETLWWGNNS
GCEPLEKKCLIEGTTDHPDSFCNQFPDEDHMLYTHDRLSLGSRNVKMYDELLPVEHRHFS
IPTWGGAFDFMDRCPIVEAYANTGCKNGMSSVMPGSFIGPNSRCVKGKHLQFDDKHVGDL
CVNTQCNDDTLSVQFFLDDTWHVCREGETVAPRGEHWSGGIGCTRYADACTVLPNSSAY
>TCRU_5626 hypothetical protein, conserved
MSGKLLLVCPNTTTTNTTSSSFHHSYSDACYFIVMELPAMCDARMCQEHVRSTPGRGRIS
HTTPYWRRK*AAMHESGVATDLENDKGAAREGNSAGVVVVITVDTVSGQLMHAGVPQKDL
FASVSDAMRAIPTLCSRTSFPFEVRVVCEFVAFAGGCLTEETINLLFIESSTLIMGGNGT
TFHAHALGVEAGLFSFSPMNRCIPPIFSVDKARWVHIPLRIAVSALQQPLTSSGVHSWTL
GDRSSTPYKLFSSVLDEDAITPYLYFSPGVDVTHCCVLKEAVRRLLVPFKAGRDCTNSLN
NNMDLDGNPVLAPPLINEFFPPLPKQAGRGALGQCDCLWNEELIRFCNAFGLGDWCCRLA
LGSCTAITLPPSFRISSVALLVVRLSRLAISGCFYDYKPSSAKVQLDSYVSALETEFQLL
ILHEPLQNQTDEEKLGAISSLTWRRGTDFAGHKNIVEQNERVKECAERFLDPLPPCEDHV
AGIFAAYLERYGSGTKVSLAHAGTVILGGQNSTRDGASQAATNASRPIKTRKSPVKRRGL
PPSSPKGRNSLATNLANAASGRRNDFDVSAVDPVSANKSLQSILQLLAGHVKAHGLRPVV
TVGALFPVFYPCSSRSSLVGINSDAASVNDGGGFLQTFWGRESLHVDRFQMADSWVPRVC
VSDDTQVSIIASIIVSVGWVVSWLFSELDEERDVAQLLLESRAWVRDIILLVANSAAATS
CIRTAFLKQEAMEWVWRCLVEICEGAPVAFSPVVWATAQRIEHMTFQARENGSGSFDKEE
HDDHKSGVIINRTVHKFLMTFFLSEGGFFPRELVQHRIVLLSHPSRLSSIINVQMLVPHS
KMQGSSAETLDEEEPSWNNSREGLFPLTPMRHLNPPVECDGEFPLLSWSGKGPTPTLNML
QGLMHPFSQPLCMPLCFEGVEFTISLPSLSYVTHVALLVANAVQMAPYAAALSISLSTFC
YVGQTHERSVLEDVPLPLCVSSRSSFGRQISPHLIFFELHRPSTEEAPLSFVEEVVAGIG

TSGRSFNQSTPVVARYMRLSIRGSGCNPMALPPILVFGEPVDCIPCEELHAVVGCQTKLS
RMLFAARSLFTWEAGDNLTVEFTDPKSPLSVVTAATQDGDESDKRNSHVEEDQEVGDGEK
QGTAVEKHASAPRLVGTLMATHGRREMYLMKVNSVIPADLFQLNFELTVAMESKRLQSHV
RRFYRDFILYRTGVPRWVMNPAYQVLPRSTFHRSQLPEEAKDTEFIRYRQKKRGEKNGEF
CVATSSSAREKKKCRMKNEERKRCALCLRVFSWFSGVKECDRCQRHVCEKCLSENRVRLP
ELGIHDSTASVCLACLKKVMRLEETLRGFLWSEALGEVESEVEKEESIDFYARCTKPQLE
SVLALYPLPLHSSYAHASVLRNCDKRPYQLTMHPLTRVVNAPGMDDENKTLFEEVLGVMG
FNKNLLRWRCVTEDEWTDSITRVSRHVILLLPHGAAVSHGILRYMLSGNICGNIEVQLYL
GNSLHSLEPFSGADIGSPGVSHDDVDGVSGVGTLREVVLQREEINSFREEEGKVIFSTST
PVTNTISRNTGIGAASTNGTTTHLAALFFIGSVSDLLLLYVDHFSLWGQFTSEVPNVNSS
YYNCTPDLSRYGSLSTNMVHGTSGVLGIACLPRMLPMTRLIPLRNVTVHNCEKVLVEFDF
GVPATVCGFTLELYHPAVMTGGHDGIATALRLIGVTASGYRGNMGIFKLPWPPLPSLSSS
SSLLSDASLLDIFSYAYSLPSTSHSVVSVLVEVVEWRLAPSAVGRDKMRKWGRMGGSSRS
HGGGGGLEKGPEPETSSRRGIYLGRLQFWTSANADTQRMVCSHTY
>TCRU_5627 Long-chain-fatty-acid--CoA ligase 5 (EC 6.2.1.3) (Long-chain acyl-CoA synthetase 5) (LACS 5), putative
EKNNASAIYRVVGMSDEEHKKIVQSYYLSETPTQNVFKMCKERKNNTAMTYRVVENIERI
TSTDHTGKRRRWKCACLNQNVVTTYSQLWTNIEKLGKGLAEIGLQEGEKVAMYEETRWEW
FCSIHAIWSRRMVAATVYANLGDDALAYALKETHCKAVICNGSNVLKLIGVLRKMGILGT
IIIYLGSIPESTDTAGYTLYAWTDVLKKGEDSKVSVVNLPSSENCDDLALIMYTSGTTGN
PKGVMHSHGSISAGFSALAHRVRDVLGEPNELETYCSYLPLAHIMELAVLSILFLRGCTI
CFGSPRTLSSTFAKPRGDFEEYRPVLVVGVPRIFDTVKKGVEAKLPPPGSLKRRVFDCAY
QSRLKALKEGKDTPYYNARVFSQVRKALGGRVRVLLSGGGPMNPSTQEFVNVVFGMIIQG
WGLTETVCCGGIQRTGNLEYVNVGPPLNSLEIRLLDTEEYKHTDKPEPRGEILLRGPFLF
KGYYKQEEQTKEVIDNDGWFHTGDVGAIASNGTISIVGRVKALAKNSNGEYIALETLEAT
YGANGLVTNNGVCVLVHPNRSYTVALGITNKDLVMKFAKENKIPGSFPAILENKEFRRKA
TESFQATARAAGRRSFEIVRHVRLLEEEWTPENDVLTAAMKLKRRVIDERYKELIKELF
>TCRU_5628 hypothetical protein, conserved
KRLRDEERELDNFQARPQGRFATQLVKIYFVRMSKLESENERKSGMEVYSLEDLMPSLAE
QVGSVAHHYQLIEEENVPLSFARTNALLKPPKRAFIATVLAILIQTFVFHECGVYISVSK
FDAWFNGFSRVGGIPISRCWLDTKAYVAKCIAQKTRIAVFGQETIWKYFNNIQELHCLGD
RVLWMILRSANYQHLQLNQNEKLNFVSLVNETSNEEVCNRYCAPKDTFLWRIWYKAFSRL
FSCWANPTENKLLTAEKLFVESIENSKCLILNLTRIINGNANNIESTYLFNELYPLCGGT
SGEFAAICLFLALKSSLVLHFAGEATTKLGVGFSAEVMLRLFNELIRYYLFLSPSSRHHH
LLDICQALWQSPGVSFSKSMFIQSFASQRQKRAPVVYQEDVFKHPTMTTCTLYNEGSEVQ
SKRFSICILDELRSEEGVKKLVKCLEFQRKNITTVCDVSRGKQAKSHEVSVACSSGKLIK
KPFFEENIIDSWCTIELPKESEEESSFIERFLRNDADSLVKKRVHDDMSKL
>TCRU_5629 mitochondrial RNA binding protein 16
MFRVSQISRMTPCGVLYNKGKVISWMSGRGFGFIEDDTDKKQHFVHFSALQTETGGFRSL
TVGQEVEFEVASQDGRTRAENVTAPGGSKLPSGPRPPEGMGRGRGGGGRGRGGGGRGFGG
SGGRGGGENYQGRGNQSLSDDF*
>TCRU_5630 zinc finger CCCH domain containing protein 44
HGADKCMCSCAMCRLTCYISAVYGNQRRASTHVLLARPSPFYAATGGMPPPLQPLDATPH
QHETRVCPVYESYGFCPFVSVCFLPHVAGAEPLVKPATNANEEFDRLVAKVRLEEDQEIW
SCAVCGYDGIDENSQSKVGEMYYYRQCPSCSLMCYFPHIVYLVEAVLQESGDDYQTYKTV
IDRYREAIPDILKIPLTYEAHRIASMAFAWSLVSPKCVKDALDAAYRALPEMSALVSIGS
GTGYIEHIFNRVANGVAAVPKDPDLSLGPSSFEGVHASFYPHKKLPIFAFDEVALNCPYS
VAVSLGGPASLLSLKCSTSVLLLCWPPFGSPQEEQSSMGFEALEYFTQAGGQIVIYIGDV
ASTGDWRFHELLYTHYKLLKDYPVRRELRRWYPQEMGLIYAGNDTIGVYKVRNQPLPSPQ
WQW
>TCRU_5631 40S ribosomal protein S15, putative
MTSNITQERYEQLKKERTFHKFTYRGLEIDPLLALSEEEFKTLVHARARRHMNRHANRRA
PVLLKRLREAKKDVKAGEKPRAVKTHLRDVVITPEMVGSVVGIYNGRQFNAVEIKGEMIG
HYLGEFSMTYKPVIHGRPGVGATHSSRFIPLK*

>TCRU_5632 syntaxin binding protein 1, putative
SNGVCGCVRDYIFHQMLDAVRGLFKVFFCDAHAASALSSSLRLHDLMEHGVTLLENPMTP
RQPIMSSPAPYFVVENASVSRVVEDWMAKVPHRDAHIFALGCTPHRSPQQLECARMAPRA
MRFKDIMLDFAAREVLVLHLSMQNGFPQLLSPLSPPN*ESVVDVAASRPVAAIHAMNNGV
PAIRQQNSGSICHGLAWNFFEGFSDLATTSRISLRGADSRGNPVRIIFDWGCVTVTPLMQ
QRKCRCLLDDLMPLEKKLYEQTRRNRLGEDSKRQIDGEYVYWCSCRHYFLAQWVEELSVA
LKKLHAYHPGLVQDLEPKANLAELSSAVQAPPEFRGRQARLSLHIDICARLVAQYREKRL
AEVREVEQDIAVGHQPFRKNLDGVRRLARDAAMPRPVRLRLLLLLVAASSTDELTEAKRQ
QLIRDGGLTPDAHFFANLEHVTRRAGSVQQYSTASAQSGRSTSSSASNAATDEDTFLKHA
CMMMETADRKRTLRVGLSLALVQRDRAMGPNGASGGQNSGA*GKNAGAFQGCGGKGGIID
LGGGGGTIALTTPQRIVLLVLCGVACSERRSVHEISKRYGREVVIGASLPRP
>TCRU_5633 hypothetical protein, conserved
FDVHHELGSREFILYSNNIHDASVLVHCLVGSSPLRSLDGGCKKDTGKKKLLPKARCQNC
TINVPPVEFSVFVYVFGSGITVEISCSSMLGFLIIDGVTTHDGLITDSLVPREGYPVGEM
LYQGPWLNQRALSESVLSVRSNVNPLDPWRQEQAFFFNRHVRPWISRFLRFGHSPVHTVK
PEFADALFCFLECFYVDDDLAAFVERFAHEVQRKEREMWSKIV
>TCRU_5634 hypothetical protein, conserved
RNPMFRPTGLCFPKVGCEEITRKARRVQLRPMEYMAQHRMQAWQLRFKEMGPPFSRVWVA
LGGKMRRRRIGRHVDVKDLRYYWRPIEPQYQRLYMSRLRAHDHSNKRRQPMRLRATNYEI
GRVTSSIEWERASNRKYGARLAPPKRLDFEFRV
>TCRU_5635 hypothetical protein, conserved
MTARDTSAPVKQDVRVFQSSIDTSSVISTVFNQPSMYMGIVNMLIMYLTQRFPEELMSPK
YMTMTYNGIRAPAMLTIPFCCIAGAYFSVASVISTSTVPLAGHLYGYTLSLGVGLTMLTF
RRVSWYYPLLGVMYLSFGGFHHYRRMMMFGDNAPIYNWGDATEIWNARVEARREARRQKQ
TAA*DTTELR
>TCRU_5636 protein kinase, putative
MRVNDIVKGRYSTYQLQDLIGKGGNAVVYSAIDRSTGLVVAVKKIMASDDTVMATWRKEV
AIISSLENPYIIRYIDHARSGNAFLIVTEYAQGGSLFQQLKRNGRFSEREVARFMFQITA
GLAYIHEKKFLHRDLKCANVLIGAGDVVKLSDFGLAMPRHVVRDDPSGGEEGAELGPPVV
AVNMEEGVVGSVYWMAPETIRGEPQNESSDIWSLGCVCVELLTGNPPFYDRALANAMYHI
AQSDEIPIPHMELSEACESFLTECLNRDPTKRPSAASLQRHAWFGGFVAENILETLATAQ
AAEISAEQAAANSAAIARWVETNLFQEKAEQREQWLKGGCLKKVVAVLPKVTAEASYHII
RSFSFAAQRCRNETSCFLTQLGETDLWDNAQLSVLGKADSLSSLFVCCCERQDSRVSQYA
PTHPGALCFLLQCQEGDVASGCIDALHSLMVGCEDDESSSPFSIPQEISAADVGQITFRR
FVSQNRFVTDHAVYAVQRIIEEACCTAFYEEKEPLIGWQSLDKLFEVLLQVFKKTGDESI
VVGPSMFVAQNGEGGEASNVAAVTAVDAAVAMADSGARGGGESGGRPGVSRGSNVGGSSN
TNAAGGGGERQAEGKWLLALQEASRHLCPNAILLLLQFVHHATRGHLKSLNVGGKSIAGT
FLVVASNASIDATTRIALLRCLPLLQCASQKAASFIRDTRCSVPLLAHAAKSIPVLEESR
EDEVMKVLFNLCEDERMAAALAASDAFLSIAVDRADLAVERHRWTEVVHAIRFIEILLAY
SVDSSRVVESRGLLQLLLRLSDGESFPSSVNSAAQRLLNSVQVQTNV
>TCRU_5637 hypothetical protein, conserved
MLSSTAGYTRRSRVLGRRRDDTTLCSTLCPAMRTRGSCRIYAREASVRASVAAEKEEELL
RSATELFRLQEEVMQDGAAADERQRTAAIESIVAELKCEKSYGNWSLDAAVAERMASLRL
RCCPYSHRRELQMDLRQSKRRDTAKMEEANEKQEANEKRPKKGVIAARQRVFSSLSPLQK
CVACLLWQGSFEVPQRVVCDVRRRLEAEMLLDGCDADGVDVEAEEERVVTVTVFRPSLGV
VDLSSIPQIVAYVSQHPDDAVIRPRTAAYFTGSNTLRFPRGVSEKEIDIGSPACAHELVE
AIVWTFNWMNDEATQQQQKQPVVLRSLTMRRCAMRTADALINALRKHQLDTTLIALDMSD
NRLMSLRFLFLLRTHFSSRLLRLSLENNPITRKPEYREQVRNSLPKLTSLDGRPIRRPPL
STPHPRVVSYTCTATQDTPGRQVISVEELKEVLKGVSRFLYVWETRRVPWTSAELMYQRQ
QQQRQTSDDEQQLRGNNRVKFFRPPEEELDDNNFHHRFLHPSATFSMSLQEGLAFFDPAK
MRLATEVEMDDEYTGMRLSPLDVRDLGVFDVAMKGNSRNLLMGRSVLHRFARGSLNCYTA
YNYSLYPQRLEVCHHLGNAVVSVSKITDTAPSMRENIPTTAVSVEATRVEEESDSPKQKR
RKKRRLEATRPHSPPLSSSRTTARTTTVGAPFSTRNDQRKPTFYIVTIHGMMSWRAPTMK
RSECILAAYDRVMTFVENALPPTNPIEKRRSAPLLLFNDQVHLRNATNGHLAWFVAQTEE

RVARLVVEYGLEACADGEALVRAVVERASSDAAASGAMHILTFGLGSKGAEEEEEESGHE
DSGDANGGCDACMSRHFDIFSLPSVERPSTRRDDGKEKDDDDEETGVVAEEGVPHRVTLA
QVDATVAAMNRRYTAVFA
>TCRU_5638 elongation factor 1-alpha, putative
MGKDKVHMNLVVVGHVDAGKSTATGHLIYKCGGIDKRTIEKFEKEAAEIGKSSFKYAWVL
DKLKAERERGITIDIALWKFESPKSVFTIIDAPGHRDFIKNMITGTSQADAAVLVIASSQ
GEFEAGISKDGQTREHALLAFTLGVKQMVVCCNKMDDKSVNFAQERYDEIVKEVSAYLKK
VGYNVEKVRFIPISGWQGDNMIDKSENMPWYKGPTLLEALDMLEPPVRPSDKPLRLPLQD
VYKIGGIGTVPVGRVETGTMKPGDVVTFAPANVTTEVKSIEMHHEQLAEATPGDNVGFNV
KNVSVKDIRRGNVCGNSKNDPPKEAADFTAQVIILNHPGQIGNGYAPVLDCHTCHIACKF
AEIESKIDRRSGKELEKNPKSIKSG
>TCRU_5639 elongation factor 1-alpha, putative
ALWKFESPKSVFTIIDAPGHRDFIKNMITGTSQADAAVLVIASSQGEFEAGISKDGQTRE
HALLAFTLGVKQMVVCCNKMDDKSVNFAQERYDEIVKEVSAYLKKVGYNVEKVRFIPISG
WQGDNMIDKSENMPWYKGPTLLEALDMLEPPVRPSDKPLRLPLQDVYKIGGIGTVPVGRV
ETGTMKPGDVVTFAPANVTTEVKSIEMHHEQLXEATPGDNVGFNVKNVSVKDIRRGNVCG
NSKNDPPKEAADFTAQVIILNHPGQIGNGYAPVLDCHTCHIACKFAEIESKIDRRSGKEL
EKNPKSIKSGDAAMVRMVPQKPMCVEVFNDYAPLGRFAVRDMRQTVAVGIIKAVTKKEGG
AGKVTKAAAKASKK*
>TCRU_5640 mitochondrial processing peptidase alpha subunit,
putative
RAISQYKFGQPSLTRAFGPVPRERQVAQAGKFMSTKLPNGVRVVSHDLDGAHSVVGVYVE
AGPKYDPLGCPGLSHVMRYAIQTSNMDSSLFQVDRTMRSTGNAYGHGEICKRYIHWKTEG
RRDMWEKPFAMIATGVVAPRFHESDLERFRDTMDNQREELRWQNPREYCVDALETVAFFK
EPLASPRMVPPESNDRCNQKVLLDHWAAYFQPGNITVAAVNIPHDALLAAYTSLPYPHSA
EAPHHARSRPPTLSHASESAQFYPGRQYIVYEDRAKNMGTVPDMKEEVIAALGAPTFGRD
EDVKKYATALVAREVYQASIESVMPAALTTSHGVQSFYRPYSSAGLIGITIRGAPKEIAG
FLDAARGCFPIKVKDDEVAAGRARAAMAFTRNHLDMVRDYCDFIATLSVTPQQLMEAIGA
VSAGEVDAALRTLSAVPPAVFVTGSTFTFPKVPSL
>TCRU_5641 hypothetical protein, conserved
MPFLLQERELLFILVGTLATLALVVLIQAFTHVVCRVGAKLSCIQWHYMGFLCITIFLIV
SLHTGLTLYILTVAVGVAVVNGASSWRRGFAAFLLCFAFMGICLPQFSGHVHLEIPSDTT
TWVSRYYGQVAVWPSHGNAGPHHLFVVYDGVSITQVPCKKQNAGLTAYEVKNGLKSLKKS
FVSLGDHTRIYALEGCVENVSVFRRTMHYITLLGSNGRMEGITIRCRIPTHVGSNVDEFS
VRCLNLASDVLLVNVDLELYDGNGRLISSGRIHRADGCMDFLGQLRQLNWFFSSDTESLL
MCFPKLGGHDMLRLLGDRSVAPPFLKGQVPYSLRWLWQMPKVLQSVHGHMAYVVEYVLIP
SSVVLGAKLSDLFVAARSAFFCAVKKATPYFMARLKDLEVLTTGVYCSARNSSHVSFCEV
SNQKYAEDGRYLLGARIGGGSYEFFLWALDALDFVPGLWEAYNWALQMEWWLTVHCVKGL
GTGAIFLYREAAQPVWRIMNYAARSFATLVGDLAPLLSDLLHLSDFKSFLRKSVLFLWHL
ELHLLAAESKLIWQLLCYFVTCMNMPLGLGFNMARDALGWVRYALGLYTTTTLSAHVFVA
VIQTAFILIALRNELRNIATREREKYPSFVRRYTGGGFVIMLLAFTRVHSMLTIRYVGAH
FMVLLMLIGLSTLPFFVKPYNLALCVGFPCVSSYTCLAFFRKNPERKHVICLSVVKGLFV
IVIDRTIGKFVAQILREMFF
>TCRU_5642 60S ribosomal protein L26, putative
KCGSRRKARRAHFQAPSHVRRILMSAPLSKELRAKYNVRAMPVRKDDEVRVKRGAYKGRE
GKVTACYRLRWVIHIDKVNREKANGTTVPVGVHPSNVEITKLKLNHNRKAILERKDRSTK
SDKGKGKVTAAEKAMQQMD*
>TCRU_5643 hypothetical protein, conserved
MDLFLTSAREADDMKLVNFVAMNDAIAAARTSEEGRELLAALMDAYYAADRSHAVYQPAL
MKAIGCCLRHAGPSSSDNDSMDRWQLTADDYILLALFFNELSTIDDTKLFCIFTEAVTLI
FQQTVPIVYGAVGYDLSVDASTVESLCSELQTLRVMMAKRLAAFPADLSTCEGSVGMQLG
IIDCLRTLLLSLMQAAATRADTKDTLTEASGKEGENVNLAVRQAVEGILSPLRTAVDAVR
SSASGGSSEKASASIRLHAGTTVSPLVLTSALRVLEEIVWRCACHVTPHDVLEKTVAETP
LIAAARLAVTRVLGALQQYLVLLQQHSMESAAGSIEKSSLAVDVLRTAGVQWAVRRLLSV

VRLHLHLFPSMGNAVVAALNAFGGNMEMEDPFQLMRMRRECETALNDENNNDAANNNNGS
GSSNGSIKDAAWRKAWEVADVIIFLIRRLFFSS*GM*ADFRSAA*GNNGGRRRHRRPRRP
RRHDTPAGRRRWRR*QRGPVAKHRRPRVCECACGNGASERECETALNDENNNDAANNNNG
SGSSNGSIKDAAWRKAWEVAAMSSSSSSDAFSFRLRECEQILEAPHEETTADDGVTADLG
DLDDTTLLQGDGGGGGSREALLQSTVGPVSVNALVEMVLLSVRHMDIMTEQAIQALHTQG
LERMQYEAAKRAQREEILRQRRIEQQGVEGIPVGRLLEHLKESTSLYAKGTHLLESESAL
AMVLRSAFFSLLDAYDAFLEETESRVLEAQALIARALVQLPPSMIDAAVDAVCVRLRKEI
SRHVHDKKAPLPLYSAYQLAMQVLFTLFSLQAPVLERGTTAFAFLTATSSVTEAELQLPG
SSMKLRSHAAFTIDTENPVEWLQSTTHDAAGGLNNRKRLRDEETTVQMKDEETGEEGVEN
GVSHFFREDTTQSPCMYSYFLCRVVELVTEAELPALLLDVLLQCPCITRYVWHYIHKQYC
LSTEKARCLLGMWLLKSLAIKRTVYRRYAVNSLLHLAASRNEYQRRLAVTKLGELLSAKG
ADGRRVIDTNAETLLVRYAKRQMAAIPVTKLPSSTTSIAAAVNPVAKMEGANTSHDEGGT
ASLRDKEMRKLADALDRHLGPFLMLCARQPKELFPALLAVFKECVERQNEAMMHLLAEHV
DVRRMCQRLFRMDAMSFMSNVMPYLRRHSSDATVLVQKILCAVCSELRAMGQANESSASQ
LEQTALALLGHARVMYESSEIPQMYHPSSSAGGLGDATVPLHDVRFISPFFSLISAEELR
RTYLRSFLHFVQLQLQLQLQQQQQLGSDAGMNATAEVTRMNSEELDAFIRDVVREVLVRS
PVHFSDGIARGLSRTDLLVYLHSASHESNAADSQVAAGKNSTLSASAGREELRGILGAGL
SSTAATEEAAGTKSIAEYLTISPFTTKRVIAVLLKLTRTFDSTTTEFLYGPEEIKSAVRQ
VMQQLGGVGGSGTGRSGIISNVSSVPPQLMVTLILACKIHAQRPHADLVRFVHHVVLLPL
AKDATWEKDTKLWRGVLLFAEEHYRECSSFLVNLPEKVLIQALRSQPQLREYFREEHGNN
AAFGHILGSL*
>TCRU_5644 Pyridoxal-phosphate dependent enzyme, putative
DRRTCILDTVLDAIGSTPCIRLNHVPKKHGVCCDVVAKCEFLNPGGSVKDRIARQMVLDA
EASGRLRPNQTIIEATSGNTGIGLSMVAAVKKYPMIITMPKKMSHEKEVTLQALGAEVIR
TETALPWDHPDSLIGMARRLEKEKGYVLLDQYRNPSNPKAHYEGTAQEIYDQCGGKVDMA
VFTTGTGGTMAGVARRLKELLPNIVIVGVDPYGSILADPSVPLDPKPYLXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXKYVDRWVKSADKESFALASEVHREEALLVGG
SSGAAMWGVLQAAKDLRPDQRCVVVFPDGIRNYMTKFPDKNWLVENGLEEGEVTRPTYGS
LEAQLEEAKKKLSEYEAKCG
>TCRU_5645 transporter protein, putative
DLPNSISLLSRNLLLFTVLKTIGSFDSGAFSAALGAENGIAEEWGLGTVRQGTLSSSVFL
GNILGCPLSGHMFSHYSAKRVLVCSLILHTAFTFFFATITNYGFALLCRFLIGITLSFVI
VYTPVWVDIFAPRDRQSVWMASHNAGVPLGIMLGYTCGAFLPSYTNINWEWAFYIKCIFT
IPAMAYLMRVDSFSIDRPRRNRTEAAPTFATSPLADMSATERVLNVLHSNFLLIWRSCVP
LFRNREYMCSTLSMCSLYFVVTGLQNFLTQYLRDDPFNASMKTIMLGFGGAVVTAPVLGV
IAGGILLDRIGGYQRNLRRVTTFICAWGFVTAFFSVMCIFVTDTITFLIIMSIVLFCGGA
IIPPGSGMVVTSVPEHLRPAGAAFSQMMYNLLGNFSGPMVCGYVAQWTGQLRYGIYTILC
CSSVGLVPMLVLLFKA
>TCRU_5646 retrotransposon hot spot protein, RHS3, putative
LNDFLTMELDGRGVVATNWDVLLGEFFKNPKKYICDAEALGEMQASDCYVRMEGAVREEM
DMEEDVEKLYKNGVENLLKWLVATAEVKANVHGVNKRFLDAAAEEARNPKKSSAPRYLEG
CYESVYNARWSRVVEVPCGEGTGMDVREGKPPQPWTYRAVGRTLEKDDAVEQSAVPRPRL
MVLASEKGWPYSWKWEENKSTCDCCMNCEVDRVWHTVRNDLTELLSPDPEADFTPKKRVL
IGTPGIGKSMGAGSYLLYQLLHCDVEKLHLVIYSFGGSTTYVFDKTIKTVTRYVGGGASK
EFLRDLCRRGMKGYVIYDVTRQGTPPEEYFLPGHGWGMIVVSSPSVRNYDKWEKKRAARI
IMNCPAEVDVKAMCAWMKRDGTADDQAECWKMVKERMDKVGRRPRYIFDANEFIAHSAAI
EDALDGVKSRDGERHFTHGGVRLWDSEDPSQKLVRIVRARGEVGAEVFLNAPISFCLGRR
IPHYLGNVMSDEDLVLFLVLGKRSTLLSECKEGFGLRAFVFGGVFRCVSRGPQGAEATNT
PWRTVRGAESEP*RALHRVICGLVAMEYHTNNSIKHRLLCIPVGAGLPLVDCFFFSESNP
MTLVGLQMTTAGGHHTTAGTVRQFTECLAAHFNGWEELPRDMSWEIIYLQHADSTPMDDW
QRCGDVNPNNVNDDESREIAAFWKEEVRPYQVSI
>TCRU_5647 hypothetical protein, conserved
RRREQKRRASRDTVSLRDSVGMLIPEACLRRDRLSPDALDRSVEEKAREILGLGADSAHA

WGPYGAQFDRRDIRFQGKNGDMRQFAEMATRAASMEKWRGMSPQGDALLKDAVAFVGGKQ
QRQQLLGTSTDNSKENFKCGSAPMLQRVMKRYGGDFSPLAHAMAAGGVAEANAGNCHDDG
GGDGNSTPISGTNRKPGATTLSPSVTEGKRRVERRQRRLERILNREGNVHPCVYQGGCAS
KGGAAMCPFVLYPATVCVAWLRHGRCDDALRGCCPWWHGCVADTSKREVVGNRLFCDAGD
ADFGERELLRESCTWMGTILQMFLDLVVTTAEHAEFSVSDGVISAETVGRIFEEPPGAVR
RNGKRRITDMPLQYDPARDVLLVERELAVSALMTEEGVTGSMRWNDAQTREEEDEKDSFD
AIFFHELASSRQEVEAPQKKLGKTAEEMHATAQGRLRQVLITFRGYVATVDAIDRSGDRI
ALCTPLTRWLLQKVADDYAYQNNNNNGTIMESTPQSLFEEASTILLHLCLRRCKLGHGND
KNTPAGSHRWSGLLLLQLMSLLTRIPASREASTAVGCTEGSFLYTALLSLHMKRTPSWST
DNIQARYMTCWVFFHSLFSTLALSLVREGIEQFAFARLSLVDVARQIARRVEDHFSMPLL
RASGWSAWTDEQMFASHQKKAYTAVDYARFHMPATAHCFMASVMNTFMLHILREATRLYQ
PRVTPVAAVLFGKNRDLESPQECIRWERCLRGGGGGLTVRRGVQPYACEALAVLSCLHDE
NKAVLARRQELMEEFMTRRVEYRERTAKEIARRRKNSGTNQPNLSNSTQPAEGDEFHVFE
KLLPSASVMVSADVFSFLLPVLFMGGGAYKALRLASSAIHASRMLRHAAKQPMPYLVQGE
KTIHRRVRNGRTGRKQIVRVRVPVLRVVDAEADERERNGAGARPVGIYMQLSEYVLAEIA
RMGMRMGTAGAKLVRGVCEDSVRGMLVDYAAGRCFPSPDAADVHSDGSIAAAFGAKALKA
ILLFAGVNDHVGGGGHDLMQKTSQVTGLAVLERRIPPTALLLEIVVALTPTKNREAHTLY
QRICSMDPRTLVTDRVLLAQHYHAARHHFGRASGVAAAVWLDFIRTDATSLSRPSTIILQ
KEMEQLPAPVEFGEEPLVAEPHHHHRERTPAPRTVKELRDCLEQSGKEGAVVSTTSRYHG
GYITYVAQSLAAHATDTIALRRMRWALLASTLLAVTHDRLTGTQGVWPRLLLRNTFIMAI
QANSFQERERDTQATVRVFLLTDILSPVTAAVEKADEDVLLWCSDNVRNLPQYLAAQIRL
AEELQTNPQDGEFMDKIRLGLQLLPLFKASMGLQEYDTTQTNAWRLLEPFLGHPELAIAW
LHESLFGVSRSLLIWITAHVDTKDQQAAFSLAAWTILLYYNQAVDDAVKHAVLQAVCRKL
TAEKSQRI
>TCRU_5648 hypothetical protein, conserved
VCNNVEEALELSNRWQIPLLIFVQSPPSEVGRHTDAFAFTEMYTTSSRGNRVIKPTFMLG
NGPLASNGGAQRKVLEAVLHQSRLDLVTIVHFMEAGSEAHNLFIAAVPEASNTVPRLHVF
PSSLREQPRIVLHGVALTPGRICDAIRFGLQMPPPTKVARAKEEFMRQVEEMNAAVRREE
VRCCQRGLESLLLVQVERRLALLLGVGVGVSRVFTSLSLTALIRGNLSSHHPAVAYRVGE
GRAGPRPGTAGGRWDGTFTRKPNVRLAHRTTRDGHPKLHQRRKGDWPRGG*FR*GRCQD*
NSHNATQHKSDGGEERAECDGATASGPSCGREPQTENGERENVMRCDGGVCRIGGNFLSG
EPNIEQQKDALPPTASAVEEKQETKPAHNSSINRENARIHVRCSLPSGGAHMVDDLDPAV
ATLSTHLRRPIAGLIGHDAFVFARVYPPHRFSLEEETKPLETLGMRSSSALRVVPTGGPP
NARQEPKLTEVNKIGLFGLVSSLLRRAGASTPFVGTTQTTALPFGDTRAAGTTPQGSRFR
TMAEMRAKEEEEERRLAAESIASADLTKEHRRKKANRYYGGGSTEYAGWDDNGVEKED
>TCRU_5649 Zeta toxin, putative
PPPWLPFIEYVLMALEHPPDMFVSRLAACCTMLFLTRSDPELLRSLCHKWAIRFSRDRAT
LVARIRRRAQEFQSPPIKSLSSNDGFSNLPPGPKLCDPDECVEHFLRLVNTLVPMYFSWN
WHRTEDVININKEYEVYVRQNILPMCMSTDPEEDVSDEDESFSIFPERLSPCSSEHIFGF
TTKAPGGQPDGETKGGSLNFHRLTFTTIGNISERLQKSPNGLVLVFHARFSAKSCEALHI
FEDILKKELLDPVPTVSVVHVVAEPELANMFNISWFPTIIYVPPLERGDPNHSLGKEGRP
PSENNSMELISSLSARSDKSTNNNAFRMAVLRNSGPSISEALYGVPSDPGSPSSTLHGFC
TNEEEISTIIGKGDYRFYPANAVITIPALVEWINNKGLSRPRTKDDEDCVSRIKVLREGQ
KFRKCREMVSAIVMLRQLQCSSVEHCRLVEGEAPVFIFMGGGMAAGKSTAATALSRSLWW
EKNKADIVLVNADDFKVAMTPWSEGAKTMHESSTRAAEKLLVRAINQGRNIVFDSTMMWR
PFIEQVMSMVRNAHTTLYQQGVGYKENGAIEEYFKPLEPRSRPLANPYEVRFLAITVEPE
IAIPRGILRWFSTGRGVPIPMQLRSFRLFAENFERYIELVDSATLFNNNVFAELTKGELP
PVLAEKTEEGMLIHDEEAYALFMRHRHLNEGAENNLELY
>TCRU_5650 Cysteine peptidase, Clan CF, family C15
MRRSNLQLYMTGFGPFKSITVNPSAMIGESVSKKMMEDSELQVHYEKLEVGLEAVSAYFG
GLEGALAKHMEDNPDGCVLLLHIGLHSREEEGKMRLEVCGYNELEGSPIDESIPMDVCSE
SMLVHDGCDESKATAELIEELNAAISKRGRREGDRQQPHWIISHDAGRYYCNYTLYRSLK
LQKKWRGRVFAVFVHVANPFTCNNPSLEEQTAQVLSLVSGLVR
>TCRU_5651 Type III secretion protein YscO, putative

DIDWAALAALPFDEWERTPNIPDLNEWVQRASRIKWSVEDEHFSQPQYTTAIVRLLRLIT
VHFVHKLERLHREKEELERSASAARDAEEAIRARVELLRRENNDLCLLLEQKRITRDGAG
EMLPPYISDSGAEKRRVKEKLEKCARELDRLKQENKELRHIVQRYNEEKRHMASEDRKFR
LEYEHLASKHKRLMEKFKKTDEMLQEFRSSEKARGRDEETELHQLRQKLRTLQQENYDLV
QSRDRAEELCEKREAEALRDMSELQQLHHDIVEEEKQRSQGLAEELQKLRHDSQCRIEKA
VQELQQSVKDLEEENSTLRKRLERRFGVGHLSDRDTTENSESVGKNSLSVGASMSSFPPN
ISPHSKFESDSRTRQRLIADRQRLQQENDRLAAELQQMEIRAESRDAEIIKIQRLLKEYE
RGDEGLHRLRGELADSNRSIELLQDENAQLHERLNAMEDSLTFSNALQELCIRIGVTQEE
IDRLRPKNTPLFSEVETLREEVATLKDEVVWLEKERRHWMDKVRLKPLLDTKLRLKLGLS
TEQLRQLDQMVDQMKSGRLIIEEDAEDNYKEKYFQELQLRRKEMERFNAFVRHRIEEVLR
EVLGITDLKSESEAKSALNALRERFDFITTLPPMDSTEEPPLDAAQLRMQLQSAAQLLEQ
SELTIKEHAASQAVLCEQLAAVTAERDMLIGERDQYRAAVFESLGTTPYAVTKAQRHESN
VGKMEGPSSLAAPVFGGASDAPCLPSLPAVQKENLASPRSPFFASLLQTFEEQLRVKDEL
IASLKGTVEAAKNGAAQHREAKIKATEQLSEACAAQEDLRNQLLAIQQMNEELRGKLDEK
NKIVEDLQEAMQRLESDNTRQIFQKIVVLRQREGKLLERLRRARETQEEALRSERAMREY
VDTTFKSLKEALDNTSTGFVLPRSSGVICVEKDVLEEVQQRFEGALRGKFFKEDSAYLLQ
LHEIYRNMEQMEELNILRVREKDGEKKIEEMKIEMNELRAELECLRKAHEESPDTHRNEA
SEAARWETEATTLRQKCTLYMRRCEDKEREVSTLEAELGEAREELAFLQEHIHNLSCGSR
NDNTTGVTRKLGVVLQEQKEEMSRQQQKQDEEELQIKQQCETKQICHGTTVDNKVRQLER
DVARLKSINLGLLHHSLDLQGEFKRLEIQLEATKQELSLVRDAGDSRKISDFVSAAIQQH
AALRRQSELSLLRAKRTRMQLYASEANLRVAVNEATSYRLSAFRLYRTYVAQMVSVLDYV
RGLQRGVKGSISPHRVAMMHKRFVDAIADVERGKSRQIEMASKLAESDGMVNLLQQQLDL
LKAKDFEERQDALHAKLLTSLSAVREKDMRLVELQEDHQYMQQKLKRAESHIQNLTEELA
RLELRASGGVSLNEDILQNLLQLKETVFAKVESPALIMQSSGGGLCDMDDGGADTAIQEY
KLALDKQAELKRELNLLRKRWENEVSESKKARTETESLKEEMNHLRGRLQYAQRQLEEER
QKGEERERRIIRSHEAQVEVTRRAAEHNSQCLRDMLQNKEACIKQLQEQLQSERRKYLEY
QLEESSRMERLHDHLFKENSAMMERFREAIDGVTENYTYNTTAQGATVCDASPDGVAAQL
ALLTKETLRLKAELKDARMTNIMLEAQLNEQVTKSQNQLLLQQQGPNYSPQQAPQKEATA
EASVVGVIKDQNAIIESLRQREFSLTREMQRYRNERDLLEQQLHEVRHTIVEQGGVLKSV
ATLEMTGSSVEQELRAQLIFVESQLVETRAQLEEERQSARRLQADTSGWRSHLDALREEV
VRQQADVERARHLVAMNEALNVDMRRMEEQNEKLILATKMLKEKLIEQAQQRGDDSRKQQ
HEIALAQRMGSIQLESTEKLRTVNERLHSIQQELEEKVRREEEALKKHEEAQRLAYDLHR
QLQEREEEILRLKRELSGTRPASLHAVRGTHEKGRQLLYTVKEEKQDTYEREEKMPRNFL
KVESAEKREEEKVQKRPAHRSTSSSSAPIRALLADANANVIVKPQIAAMLQREIEKAQRN
NMHEISSLRANVRRLESDLEEARQQLRGERDNSRSLRVMIQNARRELEEKELALARASAS
RQQRAKEHQHVQGNFVTVSSKNPVTDSTAAVSPVPNTAVSGEQDQLQRQREENEQLRRQV
ERLKKRVVTFDNVVSEAESYKKELADLRSQHPESVDSAYMASPLDIRSHKRIVLHLESVI
DSLRRELSVKKEMQMRNLQRRIDELTVENQRLAAELSSRSQFTPNLQPPIAPSRADNGSE
RATLQRELLEKNGIILDLRFEREALQLKVGRLERHIEEIIQVDSTNTKRTGTSQQRSRAE
ALESLVENLKLVVERLQKENNTLKSKTVSMSKHMDLVRELRELRRSEQKLREH
>TCRU_5652 ESCO acetyltransferase domain-containing protein
GDPNEPMRAFCLSEGKLSKGLLCPPCFFMDVCLFQRVGDASADDAGIFSAAPLRYAVIPG
FFAHPSPSPFKQTAKSPRRARDAVCKASLRKLVKKAFDAARHAMGAVDDIPNDSLLIVAF
AFTTGATADAITTRTRVRHPESNRFSSANVAGGLRRWGEVVGLCVARELSRACRVRCELN
FNTKERHGSKEQVEERREPTGTKVGDSWCVGSSFCGVQFFWVAEPHRRRGIGRAMVELAR
KNVSYGFEIPFEQVAFSEPTAHGTLFARRYAGRDDFLVF*
>TCRU_5653 paraflagellar rod component, putative
SRYGQVGAMLTVSHEVVNRVAMTREEDTQAAYHVAKRNYQLTLNRISSCLPPAPATIKSL
AQTLDKKDLSSYCSSTSPSLSATRREKEGRDDELDCTEIDELLYARALKRQEEDAKGGPL
WKRDNQQPLDTFLRREALARSDIEEVEYDFYRRITGALRSHPSIWTVEITDAERRARKEI
EDAWMSASLPFLENCSIKQVEFIEELWRRAFGKNRPTRRAQLAKEEEEEALALDVRLCHP
LLQRCETIRRETESEEEIAYLYLRLGEAAQRDLVARGVMRCNPGTGLLDSVSHPISALHY
DEVDFAFGAEFRYLQSLEETQRMEIID
>TCRU_5654 hypothetical protein, conserved

MPLFPLLREQLSGRGQPHIRRMLPCAHCPKMTTTEKAQLREMNVLSYDQSDLLRQISSAW
ERGDLNALHRCLQECTVYFDPNKPHLLAYFVSLGGIDLFATLLCDVTMPARLSKASTHQF
GFMDTKGHAPWQLVRAIATLMRVLTELLVCHNELGWHYYDSYPGLFFRLLELAKVAELRL
TAVVMLEHLVLSVGPVLEISKVPALQELIRTSDDATLAILCRVIALLIVPGVVLNQRESP
HQSLVYPESLLPLQRIQRVIDSNVLWLIGEKDLVKRLVMLCEVRGAGDLRAMMQTERSVT
SLEGIVFEPVMQELSTTAIAALPSLGGGFPANNPFGGLDFGQLGLVASRALGRNSNGSGT
SNSNNSDPATRFDWVGGRGYGVEELIEDAGGTPPPQALGAMMGMWPEEDTTSAASIATVG
SNVDFSWFVGCADAKQRWRMRDLTLREEVDDNCPLLCGFGPVTDSKSYEAFRKESRFFWQ
FLAPVLKDPSVSYGPQVIVGAQSEILFVLNLMLSTFFFGDVWCKLRDCHWINAASRFYDS
AFDSRAHPHSFLPYMEQLQRSLELRQLPRFLEPAESSEERVSAERGGQERSEEDEEEGEV
KNGEPGEVQQEDTSRNNKSNGSSKNQWEQFLLAAQLGEDTEAFIRHAAYHGVSDDDDGFD
EKNHQHDPNTIRKLELLRGVQEFWNAQDRRECSMLHEGETAKESAPLALKIALTLARQNE
DSCVETSACHALEGYLRCFSFPVRQKSAADAPQTVLGDVLMRSIFEHRVYNATYVPGLSG
SLSPAKRIDSFFALLGELVRYHYGNLTLLQDYVTGSVGLLHLNNPSAASSLHGQLNHATS
EHVEQLLRLPPLDREENEPFARVLLRRMCRHGCDTNLFLRSLLLSLTPGLRSRVNYLWKP
VTSLTVDVKETLDGPARIGDVVTGHPNRLNYIRKYSRRFVAILSERRAAAKKSPSGTDAK
TAERDASTVFLPLSSSADSKLSLWDMLQILLRSPHRLLLEERPFPCFFDDYDRALIVGDI
ELPPIGPPPQFLVPLFPELVDDGGDGGLGSLAGLERALLQEPHKLVYSMLGPLNAERIQN
AGRLCVVTTCVLVFVRAARLGGGDAVHEILRSLKSLAMVSYAKWKKQRNAPNHCNKRWIR
RAKQVGSCVSRLPREGSCYCTANDGSARCSAFLFHGHCAPMSASEQYYYRYGGCFFRNMF
RLMCVWIGHYGACQRYVETIYYCTEVPFAETKCVVLYLMRVLPDYFL
>TCRU_5655 DEAD-box ATP-dependent RNA helicase, mitochondrial
NAESPNVQSLYATQPSEAVPRELTPDVSVIDASGNKVQVTPIQHFSELTHTPDWLIKGLN
DLAYPRVTLIQGYTIPILDQGHDLIGLAPTGSGKTVAFAVPALKRFKPSPDGFPTILVLA
PTRELVQQTAKVFSQLSSGIVRVCEAYGGAPREIQARRLQNGCDVLIACPGRLRDFLRNG
DVTLEHMSFLVFDEADRLLDMGFKIQLDEILSYADPSRPLQTMMWSATWPIGVEELAREY
LSQDRYTIRAGTAGMGLQVNENIKQHILFVDRHQERMETLVSLIQNGTIDENTAKMMIFV
ERQTDTENAAYLLAKMLGIHIRNIGMIHGGMQQRQRDYIMNGFKHSQTRILVATDVASRG
IDFPDVTCVVNFIAPKSIDRYCHRIGRTGRAGRTGDSFTFIGHSDGCLAKDLVGYLKKCG
MEVPQKLLDIAGKYVQYEEQRHLRRSWSGRSGRGFKRQKQDSPAPYQSSSW*
>TCRU_5656 tricarboxylate carrier, putative
MFSYPPFSLTKPMYDTDTYIGRSLYFFFSINPLLCFQTERMLMQKRLLLDRVAAGEKVSV
DDKTLWKARMAIENCVHPTTGEVIFPLFRMCAFLPMNSLIVPFMMTPGTVSSVARTVFIQ
WFNQSYNSAVNYANRSSEKQKLGELSKAYVAAVGISVSGALGATALLKRVPSGTLQATVI
RATLPCLAVSAAAIVNLSLMRKNEWMSSGQGLKVVDEDGEVRGYSLVAGMDSLKKCSVTR
VVWNIPSMFLPTLLMAPLTARFGFARAYPICTETALQIAGLAVGVPAALGAFSTTVSIPA
NRLETSFQDLKRKDGTPVKMYTYYKGL*
>TCRU_5657 Leishmanolysin, putative
VVLLLMYCASGCIAAADPATQYRCGFDVKRRRNGPLPTAVVREVPRKGQGAMQAYIVATQ
DDDSDWRPIRIAVSTEDLERGTNKRKSYCEEGEDECRKALGQKVLCKAEHVLTEENKQLY
TGKIPHGAVKLHTERLLVKPTGGTITVPRAMNGPCSHFTVPTRHKSDGVPDADFIIYAAA
MPSGTKSRAVWAATCSTWSDFRAYIGAMNFDPKYMTEMAWSVRVAAHEIAHALGFSQESM
REKSLVKKRERSMRGTHRRMVAGKHVQKAEAHFGCGSLEGMELEDEGGPREKEIPHWKGR
HARDELMAPTVGAGYYTALTMAVFADMGYCRVNWRMAEPMSWGHRSGCDFLVNKCNTTDN
LAAKYPHMFCDATDTETLRCTSDRRHVGTCTATIVEDKGSLVDKDVCPVVSSYFHEISSG
TTYRTCSDENVDYLRGSLTGGGSWCLDAELLETKDGDGHKSVKGVCAHVSCGEGTVRVKH
LGSSVFQPCTEDTDIPVALKYFQKGGKIKSPTYGEVCTIA
>TCRU_5658 ATP synthase regulation protein NCA2, putative
STFATALATRSCRTFLQFTHSPAVVELLSEWPGIGNDMETYALQLRNLDDLAGLLHCIKF
SQGTTRMGAQVSRTLRGAFAADNMGSLGSDSGANLPSATESNLIGWLQLLVWTRLFAVFS
MRQLAAIHDQISWYLWYWSWAEVHSARASVHLALGRTWWWEGFLRRGWMGQVLLVKSYAI
AHKSALNRVLHGVVRTLGAVYSLVDRMNALLSSMEDTAAGDRLLSQSQAQAFRRRSRQII
ILVSNVCATVVSTMKLMAHTLRPQGTTGFLDAHSRGMPREMPYVGGCAGELMIFEFPTRT
PSEETPERIETCASLKDIFNLLLDTLNFTRNYTKSISEEIHTRHVPPNGRHWRRLLLAGC

TVVPSVILLSSHSVSNLWRVASSARVVLRSLMENYVMYPIKEIYKSLTSSRPGVLERRRT
LEMEMESVANIIRDYHEDYYPNIPHDELQRLRDRTLKHLRSGVIADDEGYCLINKHYENA
IRHPIRSAFFGNLLRLMLIQLTYQQLEVMRVVNSTDEVLEGNDLNFKIMAMVPVFLFLSG
LLFISFQKRRASLRPVNNQLKLYWRSVHRVVTFPEDLHDEFHVSRSGDDVSMDQTKDNDA
WELGSANHLNSHDQGLLLLLTHHM*RLAVEYHMGYSHLQEFLEDLDDLESVQSTRYQRLL
TLERMRHIYYFL
>TCRU_5659 CRAL/TRIO domain containing protein, putative
SLYLHDLGPEAVSYRHLLDEVKRQLDITHDEFDCWIYGFLENKKYNIRETVAKLQRRFAM
EANELATYTLTDYMRESLRSGIVQFIGEDKLGRTVLYVMAQRDHPVSSRREENKRTFDMI
LSYGTRLRADSKRCQMVMLINQEKASLWSNVDMTFQADIALRIAKFFPGAVDKMYICNMN
RTLAAVAKPIFSRLPAIVSDRIIIISDSELKAGRLLEYFDESVLPVALGGSNDCDHQENY
TKRTFDMILSYGTRLR
>TCRU_5660 RNA helicase Prp43
EGRRGAMEAGKNPYNGRVLSPRYYTLLRGREKLPVFAAKEKIQRLVARYQTLLLVGETGS
GKTTQVPQFVLEMNPEHAIACTQPRRVAATSVSERVAEELDVTLGEEVGYTIRFDDMSSE
RTRLKYLTDGMLLREAMSDPLLRRYSVIILDEAHERTVHTDVLIGVVKELLPRRPELRVV
VMSATLEERRFQVYFPEAPLVHIAGRMFGVEVYFSRSPEANYVEAAIRTATQIHLYEGEG
DILIFLTGEDEIEQTVERLQKGICMAEHSSADCHKGPVVVLPLYSALPPQQQRKVFQKVP
PGTRKIVVATNVAETSLTIDGVVFVVDSGFSKQKVFNPKLRVESLLVTPISQASARQRCG
RAGRTKPGKCFRLYTTKAFDTLLQPQTYPEILRCNLGSVVLHMKMMGVEDLVNFDFVEPP
APETLMRALELLNYLGAINDDGDITEIGRQMAEFPLEPEMAAMLLHSPEYGCSDDIARIC
AMLSVQSPFVTPTNDQRGRAMRCREQFSHPTGDHVAFLNAFNAFYDANNKSAAWASENYL
NPRVMRQAVSIYRQLLGVMRRLGRDVCSTYSRPPTRAPRETDVKDEFANEIRRAILRGYF
TKVALSLPTKNQFMTLKDDVKCLLFPSTFLNRRPKFVVFNELVLTSNNYIRTVTAVADEW
LLEASPTYFAREEFDGVSRQVFEELHRRHHRHAENRDGCSEKRPRTFDDDDDSESS*
>TCRU_5661 cysteine peptidase, Clan CA, family C51, putative
RSKESRTSVAKTGDDFLPEGCRKGCDTTFGAILGTVNGVVSYSNCNSSTCTSNLWHPMSS
LLAHGDHNNENRWNTTNRSGLEWQCVEFARRYWMLRGTPVRATFDSVVGAADIWALNFVR
LLDGSKTPLLKYPNGLPRRDGGSAPRAGDLLIYPRQREDFPFGHVAVVVGVTKNSVLVAE
QNWDNKMWPGPYHNHSREIRMLYSPIHDAYNITEEENIIIDGWMRY
>TCRU_5662 GTP-binding protein, putative
PMLRGCSCCLSRRSHPFVDAVKMLVSSGAGGDGASVMSHENGNEFAGPGGGNGGNGGNVM
LRCSKRIADLSHLKEMGSQITASPGSVGFARTAHGKRGKDLLLELPVGTEVVDLDTNEVV
YDVDEDGMELLLLEGGQGGKGNAAFANKWHHSPTESTRGLPGNTMLVQFELKTIADVGLI
GYPNAGKSSLLSAISTSKPMIAPYVFTTLRPYVGVIHDLYGNTCRVADLPGLIEGAYENR
GLGHQFLRHVERTQSLAYVVDMSGSYTPEDNKVPSEPWDIVDALRGELEYYMPGLSDRAV
MVFANKMDLQTDSSGALLTNKLEELRKRVKLPVFPISAALGISLGTWHTEAGLTPALQFM
CEEVFRKKKHQEGIRHAQRQREAFTLEKNFRAKNLGVFAVAEGLEDRDGENLSLVDQQLD
PYGFSGLGEDFDGYQNAASRGKLHDYRDLTMKGRYWSLTRQRGEKLGGEKWR*
>TCRU_5663 hypothetical protein, conserved
MARKPLFEVIWQSMTASNAWLVFAAAVGAVSFYVFLLKSAPRGNGRVTPSISNSKDGKPS
LLNRMRQQQFKGHRVCIAWEVLAEQGQWRDHAKEALVVFAVDMEVYLMCRVNCKQEKNEV
LAMLTGISGLVRHRILFCETAKGYESFCRQIKPALVVIQNEVQASFLSTVLPNVVLVGAN
VPGSTVTCISSIYDLL
>TCRU_5664 glucosidase II beta subunit-like protein, putative
VLLGCVFAEDCELARQLRENEMRLFNNVELSQKLKSSRIGCIAWNMGYWSYELCPGRWVR
QYREVKEVIVEEYILGVQHRWRLVDEIGSQLLQYSDGFYTLPDRLRSAGTTIDAENQLYA
CAKESNNNNNKQVDVVYPDGSPCGKGFRRFSLLHFVCNENVQYPIVKLKEPAICKYDITV
VASTICEAMLGSFQAQIELNDAHMRFAI*
>TCRU_5665 membrane- trafficking protein, putative
PPNLTLAMVEAKEKELEERRESIRRRQRSIAAEVGPPPNFPPAFLCIRPQVYHNIKEQVP
VHLQRFMYTLCALYICLIVMIIYNIACAFVNFLMGGSTMQFALSFLYLLGIPGAFVVWYY
NVYCATKDSSQSRKLMSYFGLLVGLIFDVWMAVGLSGFGGCGWIITLGLTHNAPVFIPFL
ISSILWSLHGAIFFIMLLRFWRYQS

>TCRU_5666 glyceraldehyde-3-phosphate dehydrogenase, putative
RMEDVVLPVCVGINGFGPIGQAVLFSSFTDPLVSVVAINDASMSIDYIAYLLRRESSLSA
GDRASVLVVGEFICIQGSQKIRVSHKHDLVEIAWRDVGVQYVVECTGLSSTRERCWGHVA
GGAKGVIVAGQSADAPTLIAGANDEELKSACSVVCAGSPVAVALAPLIRLLHEQYGLEEC
SYTAIHGMRPVELTAGRSKNPQDWRQTRVSIDNIVPYIDNGKKTMDKIFPGLVGRISGTA
FQVPVKKGCAVDMLVRLSQPVSKEMLDQALKEAASGRLNGVLSYSKEDLISCDCVPNGKL
CYDATGSCSLRDGEAQKLLLWFDIDGGYAKRLLSLV
>TCRU_5667 Hsp70 protein, putative
RKMQIVSFVILAILLSYGASANVLGIDFGSEYIEVAGPHNGNNVDIVLNEQSHRKTDNYI
GFKNGERYIGDQAKALAARFPLNMVTMINQLIGILCDSTEFAMLKDLEFEFETRPEERNT
IGFCFSQDGNYTAEELYAMVLQYCQSISEKDGVVDPKSVVITIPFHSSMGKRQAILEAAR
LVGMNVLGLMHSTTAAAFYYGIRRRGLGNKTMNLLVYDIGSTHTEVGIYKFSPPVAQSGK
KIKNADSFGTLTTMAVVDDTFLGGRAFDLCIAKIFEAEAMNKMKISKVIGGKTIPERKSQ
FSLLRAAKKSREILSANSKTPVTIEGIVPERDFSTEISRKDLEEKCSHLFERVPKLAEEA
LSKAGLSLSDIDAFEMMGGTSRTPKIISDLSAMLGREVDRTLNSDEAAAVGAAYYALRLS
PFYRVRSFRVEEHIPFVFFFSITSSSKNSSQSRRLLAENPALGMRQSITLNRTEDFTVEI
FESNNCVVKIQVMGVKTTLERLGFFAPTIVHPNNSHIVRVQLRINDSGLFEVDEADVIYR
YAANVSSKIKLNTTTKDLNTSDITNTSNITNTSYRTVHNIKMKRTSATVATTVSFTNPSP
LSEEAFRRSKRRIAEILDKERKKHEAAVAKNNLEAYVFWAKSEGILENETALGVISTEKI
EMLRKKLSEVQEWLENEDCGSEPCSKEEYEKKMEEIKQIVRQEPDATNETEVVIESSDDD
RGDL*
>TCRU_5668 hypothetical protein, conserved
SLRMASVNQSIESNTSSLQRSGLSMSVGDTKSIVLALQALQDKIRRLEQDRNHHQDQYER
ALQAHEAYKQDMEHQLERERTHHRQREKDLQEMVQRATTEKTKLQNTLEESRKDLGTFRT
ELEEMLIKECDAAQKRENALASEVDKLRQELEEQQKRYRALLSSIEELRAEKEAALDTNH
HLEQAIQELMRIQSGRGVNRTLLRSGDTSRLTAEGGKRRSRRGRTHSSAAVNLANRTGYS
RRISEPHQMDSRPTSIVRSSSARHTYRDPTYSSIQRDVRKENGTQVVDNSFAGEVARPVS
YATESAARTQPSVPLGGRQNGAMAEVCQELESELKSLHQQYKETVERAAAEEISAEVVAA
ALNRLAKLMDRKKEQIQLIKEAQRDMAAAGTVVDVPTSRPTGASKRRPPPVGSDKVTQRS
LIVNELRSLLSPQH
>TCRU_5669 clathrin heavy chain
EGMVGKTQLYSVENRDGRVVDGHAGTFISTNTPTEPRACNIMCLAWNTPHEGGKVQLMEL
PTSPKMDITMPRRVVDVAFPPGDFPVALTVSPRHKLLTIMTSRGTAILMDIFTGTIIQSQ
QVTPNIVFCGTLYTKTGGLLCVNNQGSVFHVSPNDNGIIPFIKDQMRNPELAVRIASSAN
LGGVDDLYRMQLENGLRVGNIEEAIRACLRAPNNALRVPEVLQRFVHHPSAPGQPPAIST
YFKMVLAETTLNAHESVELARAVVPKGGSAYIKQQYEANKLTPSEELADLLAQAEPEMAM
KMYYKAEAHAKVVNILLQRNETQKAVEYCRRSNFSPDWRVILNNFIRVNPQNAVSLALML
HRDLGDTPVVDPNEVVDMFVTAQQIQQATEFILEVLRGKNDESTKDLQTKLLEINLKHSH
PSVAEKIFARGVCLYYDGMKLAPLCERAGLPQRAIECYVTAQNQDPDLDNLSNIRRCLSH
ARNFNPEWILEFFGKLSQADSMRCLGDLLQNHRENFKVIVQVATKYSDALGADKLIELFL
EQKLYPILYYYLGAIVPYTRDPEVHFRYIEAAAEVGQAQELERMTRESPCYDPERTKNYL
KNKKLTNLWPLINVCDQHGYIDELVRYLIDTDNETLIEQYLQRRSPGKTPEVVAALIDCN
AREDFIKNILNAVGTMCPIAELVQAVEERSRLRLIQGWLEARLAEKKTDPALHNAVGKLY
VDTDQQPDKFLLENAYYEPLVLGKYCENRDPNLSYIAYRKGHLSEELVELTTKNGMWKQL
ARYLVQEKNLQLWASTLKNDTKDRDRLVEAVQQTALPESEVDEEVSTTVRAFMNAGMTHE
LTSILDQIVVRGRFRKNRFLENLLIMTAIRSRKEKVMEYVSTLENYDAKEVASIASNAEL
PEVAFAVYEKNDMKKEAATVLLRDLKDISRGRSYAQKCDIPAVWSVLGEYLLAADEVHEA
IESFIRAKDPDFLEEVTAAAERNNQFGDLIKYLTMARKESRAKDNKIDTALVLTYAKTGR
LMELEEFLKETHNVQIQPVADKCFDEGLYDSARVLYTLASNFSKLAVTLLRMNNLPAAVE
AAQKAQSRKTWTAVNIACIEANEIKLANICAVPLVLEAEMLQSVMDRYESYGLWEELLSL
LKTASSTPGAHMGVFTGMGLLLAKYRPEKLLEHVNMHAKKINTHKMIAACEEYHLWLVLR
VLHVNNEDWLAAATTMMHHHVDAWDHDVFKTVVSHLGSSDLVYNSISFYIQTNPQLLDDF
LTSMFKTLDPERVLLEVKKLAPVHFIRQYLESAQERNSRRVNEAINKLYMEEEDFTALRD
SVERFDNFDSAELSAELEKMELFEFRKIALFLHRRNKRFTHAVAVAKENKLYQDAIETAA

ESANPQIVEDLLDFFVVDHPDCFVACLYTCYDYLTPQVVMEKAWLNKRTDLAMPYFIQVI
QDYTTKLSRMEKSMMDAQQLAKEAARRAGPLHTGANDPLMIQAGPANPMGGAMPMPMPMP
MPMPMMGGVPPGNYGPPPQFDNRRPY*
>TCRU_5670 hypothetical protein, conserved
LAPIETTSRSEILPLVIRPPTSYVPNHETFLEKVDIHRLKPTSDFKATFKDWNDLMSCGK
RQLRVRGIPRMTRIAIRNAVHAFQNGNPPEYFDTKEEWLYYKQFKTIDFSYRVIPELPEK
YRPHQNGIDQAPLPDYREINKMPEWARKEEERLKEKKI*
>TCRU_5671 NOT1
MLYEHTVDISSSRGATVRYLIAAATKSTLQTTLQTLEKLAAQSVELHRFVIMAAVSAMRK
SPQNEEKCALASKLVSTALEKSNALTLVATALEESPTQVTNEVLTNLMVKDLKLSPTQQL
QFAMGLFLGSTKGKEAATAFLNTFGVSPATLKDDNGSMWALGILARQAGGMESLDTQLSS
AFNGVTLFPNSGVADTHVSLSKIIGELGTACVATQADCRELLSFFPHAFTESDVAEVLGF
FASQGSAPSDINTYNTLMSLTGREPTKTQHSATISPIPLLELLQERSSTKMDWDAILRML
DKPGEEAFRQKHVAIVFDAYYKFKGTGTPGTYPPVTIFLGRWNNVGRQRSALEYILKHPE
KVSLQSLSRDQMAAAELIESTSAAATAASPSATTATTGTARISESELWRFFPFVEAAVHV
ASRDRTFDMETLRPAAQRYPLLLFSMLLFGTFPGTVKNFSTAKLILKERWLALDRVAAIV
LPEAEKNGRLNAVIMVLSELTVVDASRTIEVMETVLKSKTAVKAFLASGGNPRLVTAIAM
CMEDSSETGETWISKALEGKLHFRANAAENRFAVAMSIVEVAEQLITKQNYVSNATAALN
TFLASSLNDVLRDVAEQARVLLASSDSLFPSDIENEATEFYKRMYAIGDPTNTASLAFIE
QLLKSSKTRDKQLYACIVSIMFEEHGAIECYPQKELQLFAVLYGQMIARELLPHSQQQHA
WSLLLPVIVKPKGPVMEEYGIIALEQLKPRLAEWPQYGRALRYVKDLDIKIPGIMAAINR
GIKAEEAARQQQNRQPLPEKPPSKEAESLLSDPAVLAVSTERRDSTAAADQQKERSAAAT
LHQHDIGTLLSSKNITAPPRVIQEQINFLIGNTDMHNIENNASDLAKQLRPEYYEYFAEY
LVIKRAALEPNYHSIYLDLLDKLQSKPLEKAIRNATISSIKRLLNSDKIRADPGERSLLK
NLGYWLGLLTLAKNIPITVQDLCFKDLIFMGLREGKLMAVVSCVSRVLHHCMSSHFFCPP
NPWTMRLLCLLWEMYNLKHLRVTLRFEVEVLCKHMNVTLQDIERYYTLHPISTASQLRMV
EIYKEINLHQSGDFRVDEKDLHEPSPLLMQQPKAPPPLQQQQQQQQQQQQQQPQSVQQVQ
QEQQQQQQKQQQQQQQRQTRQLQASAEPFKPKDAMPVANTMPSADVSASGHPAILITPDN
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DVGGMLRAGQAMARSLAANLCTVTVRDSLIEPFNKHVAVLAEHFVEVHLPNVMERRERFR
NKVRENNMELCVRVLEYQAAEEAERRVHDKLMQVVREKLEAINTREFPRIPKEHYEVQDI
LMQMGEVLRPPRNVPPLQRAVYDEYRNNVPIVGLLATYLRTIEDATVAHYSMENCKVLSL
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RIKVINVTRLDEVLSKAILDSSMSGPAIDFAGSVIKKALITEKLVVPKNLKDTLAQLELV
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXQQQQQQQQQQQQQQQQQQQQQQQQQQSHSHQQHQQQQQQHQQQRPEGATTA
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WTSSEPSASATTTTATPSPGTTSSSKNPPQYEYILTLRKQGQLDNHQLGTFLSLCTRFCV
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SLKNDTRQLLSLLRRILDAFQRSLIDHHQNVVLQMQQKQQQQQQLPINKMELPPETAFVP
VFQQQPYVRFFSILFTTLVRADAPNRETTEQITHVFAELLHRLSPMKYPAFAFGWLELVS
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DMHELIIKPDFSESNAMRFYRYLASTLDNKHRYHFICSCANHLRYPNCQTNFFVKVILQL
FLQHPSIRNPTTRLCIQEQITRVAVEKTLIIQPHPWGVLSTFMELMRASEYGFWEKSFIS
STPFLESMFHKLRRSVESRNAQQQQQQQQQQATTT
>TCRU_5672 ras-related protein Rab21, putative
RSMASGYKVVLLGEGRVGKTSLVSRFAHDAFDENQSSTIQASMYTSADVPLLDGSGAKVK
INVWDTAGQERFHALGPIYYRNADGALLVYDITDADTLEKVRLWIRELRAVVGDQIQLVI
CGNKSDREEERDIRKEKAEEFAKSHEALHFVTSAKTGENVAVAFQALATAVATASGGRGS
GGGATNTGGTNNAAVTAARGRRKRRGLLRIEDE

>TCRU_5673 Periplasmic binding protein, putative
IGDTIFASSLTLTMRHGLALFAPFTGSSLVRGRNPKFYFLRADPAAELLALLRYALVHLR
VRRLGFIYMEGEYFGGTEYELAERAISGMGYELSDVFSVESSVNGGAKKEAFDAAWEAFA
DTQLQAVIVFGSPTNDAVRLVRRMLAGKRTAGAYMLASSVLQDLVLRVWRAAVAGGVVFV
PGQVTTTGTNPLAKDTQCEAIRRFQELMREYLEKSGQKYYTDKDSFFYHDDEGDMMVAGW
IFGEVLSQALGGREWVRDRTSFLASLYKQRRVFDDIVIGEYGFECETRAASQGATCLCNQ
GGRTVHKRNYGGFALDVAEGAFTLNLDECGASPIELHAPLNGLAFMMQDVVVAQLAMDST
LACADAAKAPQDDHDGTTVKFRTLSTSAAGAIDALLSEMSARRVHFASGVVTNA
>TCRU_5674 hypothetical protein, conserved
REGRRTDKTWMKNHPMEGDDIVTSFYDVLCKRNPRTMKPCRNVFVPDTVVYERSFPRGWY
TTDVRAREVMRRQGKDLDAATIEASFGRKVSDTCPIVATYLSTLEECMGNGVSETTTQVE
VLNTESVGGFIARKKKREGILQRFVLPKGYHNSVIRAVWSPRVAMVQRRTNRFPIMDRKR
AEKDPFAIAVTYEGPEYLSEEGTVSAHVALGVKSVCAEIVTHFFYTEHKHITRMVLYFKS
DARDRLWLLWCGSLRVADRNSASEMPVNLAPRFGEPAPEGELDEDEVLRTADRAYFLVTR
DEFFHGTYMRGNGPLATDAARPGESRTQASVTSGGRGAGEGGDATMPRGDEDGDYVPAEL
RVSMERLHVQEELVLDAFRDVFYRAYSHFLSGDAVPFELRVPPHVVSVLTEGCVADLMRV
LKLRAVPCAGGESEGAGEGAMVYTIPPLHRTPLTQLGDTAANWIREHFASRWEALRRGVI
AGGVPSCVPSAGAAAEQVERR
>TCRU_5675 Periplasmic binding protein, putative
VDSLEAGLEAALWSRNFTVADAVYGEIIRKVSTMQTSGAVIGKALN*SSYILLVAGAIGD
TIFASSLTLTMRHGLALFAPFTGSSLVRGRNPKFYFLRADPAAELLALLRYALVHLRVRR
LGFIYMEGEYFGGTEYELAERAISGMGYELSDVFSVESSVNGGAKKEAFDAAWEAFADTQ
LQAVIVFGSPTNDAVRLVRRMLAGKRTAGAYMLASSVLQDLVLRVWRAAVAGGVVFVPGQ
VTTTGTNPLAKDTQCEAIRRFQELMREYLEKSGQKYYTDKDSFFYPDDEGDMMVAGWIFG
EVLSQALGGREWVRDRTSFLASLYKQRRVFDDIVIGEYGFECETRAASQGATCLCNQGGG
LYINGIMERFRAEDVAEGAFTLNLDECGASPIELHAPL
>TCRU_5676 DNA polymerase alpha catalytic subunit
MEPWESCRTKDQKRETPAMVSLFSETEEEQWQRLKEEAMIDSDEDDANITDGRALVLPQD
ARKRKPKKSKKSTFFSKATHIQQQKLTQSISTSDMENLLKKYRGAVADEEDEIGIDVTKF
LQDDALESGEEEEGVTADELISSLLTTKNTGASKPVETTPSVPLVSLNDEIFSYEKKSIA
RQAVVNKKQNGHGSEANYVVKDTFSGDLNIVTELPTQAPSKLKQSSDNVNKGTHLVDCFI
GLMRKNSPILYRNLVLYFFLVSFMRKKEKKSVFLLVVFMSKTFTGVHFYFLVRGHLIRKL
SRR*TTCVKNMV*ESDG*GLWKDIMPLKNLVVPLVSLNDEIFSYEKKLIARQAVVNKKQN
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LSEPGTIFLFGKFYEEKREKVGFSSCCVHVKNVYRCTFLLPREGSSDTEIIKEINDVCQK
HGIGERRIRFVERYYAFEEPGIRREKNRWAKLRFPGKYPGFPIMGEFKHIRAVMGASRSL
IELFLIKKKLMGPSYLSMENFFPATERLSHCELEFVVDSPKNIKVDDTARPSPLFTLASI
QLHTQLDSKGVTNEVVAASIAVYRDVNIDSGMKTEVSECFTGIRQISSDAALPLNLEAYC
QSKGLPGVKNFGNERALLTWMASTLGNLDPDIVVGHNFIGYTIDILLNRYHELNIPRWST
IGRLDIKRFPRSQNGNSNLSNEKEACIGRLVVDTYLLSREYYKSTNYKLESLATQMGVAG
ITDGRGSFEPGLTVLGNDIMKSSKDLFHVLLQLLNCAVLSVCVVAFLDAIPLTKRLTTLA
GNLWSRTLYGARSERIEYLLLHAFHDLKFVTPDKKRFDGKRGRQDLEDETKRKTKYQGGM
VLEPKSGLYSDYILLLDFNSLYPSLIQEFNICYTTIERDENTVSAEIPPPERLICTSCAA
AGLPSPCSHKCVLPKVIRGLVESRREIKRLMKTEKDPSNLATLEIRQKSLKLTANSMYGC
LGFEHSRFYAQPLAELVTRQGRIALQNTVELIPQISPLLRVIYGDTDSVMIQTGIKDDIR
KVRELGFEIKNKVNQRYQSLELDIDGVFRAMLLLKKKKYAALSVVDWQNDGKTYKKEVKG
LDMVRRDWCPLSQKVSEAVLSRVLNAEAGEDILDYVMTHMKTVSDHVRAGNYYGLEDFVI
SKSLTKEPESYRGTAFPHAAVALRMKQRKENVRVGDLIPYVICEGEHLNDKAYHVDEVRR
TKGIRIDVEWYLSSQLYPPVMRLCEHIQGFSPEQLSEAMGVACHVRTEREIQETLIVDDF
SHCSLFKSRDLSECFPTAVPLQVQCTRCHQVVPIDPHKYINDMFSASKTSFPNEPFELYN
CVNCGQSLSVTYLANCLTQMCHKIIQQFYISGGNAAAVRAVRAQFTYFRALFDVPHAPGC
SPAIKAAHRNLALRCLGTDQKLYTLSGAARAVDVEPVDHLFFCADSFYRRMDHLFLNVGN
LF
>TCRU_5677 endoplasmic reticulum oxidoreductin, putative

LEESFCCCSLDDISKGTKDIAQLLNNITSRPFFRFFKVNLEKPCPYWAVQLLCTSEENNC
QVCSCDANDVPEALKYSHDMSDPSVVDSRVFYGKSDPPNVDKWGVWRDADSTATYVDLYQ
NPEGNTGYSGPMASRVWQAIYKENCMTEVVEENGLKAETECKEEKVFKSLISGLHTSITM
HVAAFFHKDKDGTSPLKEFGVLRNPSVSYFPNCGMYRRIANNTEFINNLYVLYQFVLRAL
TKTRLVFLSDLNAFNSGTDGTPTSEDTFLHKELRELFNTHLLCSTTFNEAKFLESAKAKQ
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INLARQLAISVENFHVLKDVCRR
>TCRU_5678 retrotransposon hot spot protein, RHS3, putative
VTMGIFVQNPETFIKKKGLLHTITASPSYQVLKMELEERKILLEAIYKLRHEGVYFLRQW
RDYEGKDTVSSLAKGTLDAALSRVQTSTSVVTSTVLKGYYESVYNASWHHVVEFPDGEGT
VMEVREGEPPQSWTYKAVGGTLEEDDSVQQSGAELLRLMVLASDKGWPYSWEEDEFTRDC
YVNCEVDRVWQIVAWFSTYSEADFKPKRRVLIGTPGIGKSMNAGSYLLYQPLRCDAKKLQ
VVVHCFGIKMYVFDKTTKIVTKYVGNKTSKSVLGGLWQSRMKGYIIYDVAKKGTPPDTDF
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AGEEEDYWKKVEVRMDKVRPLLRYVFNRRAYKDRIDSCKSTVNKMVLPDTNYYSVLGTDK
MCEGGHVSHKLVKVVRVRGEDDSEMPYNALISSHLAELTLCKLAELMVPNDFNLLVLAIK
DDLLSKALEDHSLLAFLSAAFVNAIIPKLKELKVERNAPPHLCALRVRPHERPFKPCLLE
CPENFKEKINIESRVLYKPEAKNFPLVDGFFFMDSNPKTLVGLRMATAGGHHTTASTVRQ
FTDCLEAYFDGWEELSRDLSWEMIYVQRADSTPMTGWRRCDVVDSNNVSRAEGREIAAFW
EEEVRQY
>TCRU_5679 hypothetical protein, conserved
IMRSSIIFRRGVYHNAPTVYPFVKPFHDTPYDEDRGKHYVGRKRWLKNSWPEWMDNGADA
FGYGIGLHRVHPLSKLRGNLKTSPSHVPRVLNMMIQGVWHKSGVKLYFRGGKPPNPSKHP
YLTGEPCPVYGWRITDESVIRQFNMPSVDVTKVRYKPYVALQERKIMGLDTHKTVVSQTS
KKDSDAKPLVKRLFFWQ*
>TCRU_5680 hypothetical protein, conserved
YCAEEAHGQGLDGTEVPTRTNPCSSVQGRCDSGRSRGSTQTEDDRVIFAEEIKKGRENVV
AAVLNCTSLVKSRPVFHRFKSESERRALLSSLELLLRLYFLDCENKALLTAIRGLRNQLA
DLRNQDVFGCARGKYPEVYILYEFFSLRKLLLNWGKLGADNQIAAMETALKLVVLVKSLA
YMALEAHLRAAKEKPQLVEKSVTNIIACLDQACCDTPYGFFSICCNVIPAVHPHYKSPVG
KLAPELTLKEEEGETDDDNITSPEDEFVGRVIGLAHPLSKKRMMDRPESRQAQGARQRHT
SKVKKEHDVCCSKYHTQYSTPERHASKECQFC
>TCRU_5681 hypothetical protein, conserved
SSSGMMRSLFHFTADDAVILAMEHNNHNKLLAVSTSNNEVFVTSTREMPLEGIQAENGEQ
SQWDPAEHTVRIDHLRFPCTQLAWAPWQYGIYLACVCRGKQVRLYRFSHGHWSLDEEIAA
QDCNSVAFSVHFTMAFVTSKGKILIFVQTTANEDNTWSLHSTYSEGESYNMTRQLNSRIR
NVKGFTCVSWDETGTWLAVGDDEGEFLIFLVSNEGRSIVEIAYRSEPRSDRRKGVRQVAW
SPGAGRSFLILAVVASYKVTLLFFQRTRVGVNAGGNSTQIQAGMQLQLITKTSVSMEEVT
ELSWNTHGGGFSTAHTDGAICVWTVNISYQKGQGTSLADVENVMGMNSNGGGGTQHVGAG
QPYDDLTLVASVRKVSGVHPYH
>TCRU_5682 hypothetical protein, conserved
VLRRAVVALRDALNGGSPMTLCRKGMERSPDSHRRRMPWTAAKECVPGVVHSSKEKMVLD
DARRVDVDCVDRASQVYPLEALRAAVASYEYNTSTGNIFNASQTESNVLRQWVYCEEWQE
GTHDEDATRTAIHFRRQGSTQPAPIRLADFPGWHALFRLAPLFPPFPSVGADVPVDAISC
RLRTHPLID
>TCRU_5683 paralyzed flagella protein 20
DDESTPKDPELSATLMSKIEDVDFDTFQRTVQMQRERGMPPPPRPVLKRIPESTDDFLRN
FFLRNGMYRTMEAFEIEWYEKYGSKPLSDAPVFADNYLETAALQDRIDVLEHQLRQHAEL
TAKTTKQKPRKYFQTKKERDFHRANHNRVVQEKNRVAKLLRQAQRHAEDITPTLNELRQK
CETLHKGKVLLTIERDKLDAKASRLEKQLESMERMLKSEVEGETRSRATEAAFERKDGHA
AKASDANPNEKKRGGRAVRTTESSSDGFRWPADERSGSKSVNTNYVARTEPFTWVCQSSF
KAHSMPVTRVAMHPEKPAVASSSDDGSWRLSALPQGELVMSGDGHKSWISSVAMHPTGTM
VATASGDKTVKLWDFATNSCKLTLKGHCDSVWCLDFQETGLLLASGALDQTARVWDATTG
KCRQTLRGHVDTVNAVVWKPYTNILCTGSGDKTVSLWDSRMNCCVQTLYGHRNIVQSVAV

LGTTETLASCDADGVVALWDVRRMEQKLTVDCGPYAANHVASDGTGMYLAVSSEDATIKV
IDIPNSTVGVLAGHEDGVQCAVFDPSTNSFIVSGCRDGTIGYWC*
>TCRU_5684 btb/poz domain containing protein, putative
MSVRAMNWIQRNLGFDVTGEWAQQVSLNVGGVTFLTYRATFRSFHEHPIFGPIVNGTGKV
SEDGSFFIDRDGVTFRHVLNFLRTGALLLPESFDEWEQLLSDAQFFQLPELEKAILGRFE
YQRLVFRRALPQAVFVHWPEGNQSKNGVVIEPQLPALKISDDGSGVHYQGELLRSIDELI
TTLLSAYGFVIQHWNKREGKVFLSLG
>TCRU_5685 vacuolar ATP synthase subunit c, putative
MTENFLIFGLPFLPQCNDTLPSSQFKCLVAEMGPLGQALRPFVVPTLKVGTLDSLIEASD
ELAKLDPQLENNVEKLIALMEETSQKPRSVVSALRINQTQEMTPAAYIKNFLWSSAQFDT
REKIQSLIEKISQISASIEERIRVLLSEYNETRNRLTAVNRKTQGNLSVKPIRELVASYN
QKFQCFVDTEMLVTLFVVVPLASQKEWLETYWSLNEFVCPQSNRVIAEDKECVLNSIVTF
RKAMDDVKMICRKKRFTVRDIDGVDDLSVAEVKELNQKAEKERKALYTVLWQQYSLCYVA
WVHVKALRVFVESLLKYGLPPRCISVVLQVDGKKEAEIRKKILQIYPNLISPLTNEPPTD
TGMLQYEYPYVSLKVTNFQK
>TCRU_5686 Poly(A)-specific ribonuclease PARN-2
MDIDKSSLFFIFEDFQNSLEKCDFYAVDQEMTGVDFDGQQRSRFMSLPELYEACRGVVKR
YIAFQFGITLFTRLKSGGYVVKPYNFYLLKEHCDFGVNTDAIKFLVAHKLDFQKWLAFGV
HYCNKEEEGRFTTKKENPSYLELEEKIVFHVVNEIKKWYLDPYKKEEEILSLKTVMTKGI
EAFVISTLKEQDIYVNLEYDEISKLYELPVQLTVHRVDRNKLDLEGEKTAVNSASVFSEK
LGFRQIWKCLTKCKKPIIGHNFWLDIMFMLHMHEAPLPTMYEDFKKQVHELFPCIYDTKT
LSKTMFFSKLNKCYHLDDLYKECCKINKESKDSIVFRFPPGFHFYDEKCLGSEGKAHEAG
YDAYMTGIVFAIMKDVLKNGDGIEFKKWENVISVYGSNYYMNVVGNDFLKSGSIFLIEFE
EDVD
>TCRU_5687 hypothetical protein, conserved
DAVPFYQRCMVICPSMMSSDRENSLLARARDHLPSVRLAPLRRRSWEVSQRAESAASLRE
DGKVAKEVTRGQLPALISPLEKTPPQSLDLVVFAANVFGEEMLHDAPWHLSLAHRCLAPH
GVVAIMGYATRVCVVAPEAARRDADDFMEDLQRTAREAAKMKDSKELRVALGRAIDISSS
LDAGHADMYFPFRSTKRRWFTSEYAATPAQLAASYRALPEYQLLSREMPRYRQALISGRQ
KVQVGEETEKDEPVNVFRRHAGAEPLEVLQGCLQAQVMSLHGRNTPAMPPLRVQVRHFII
TCSSRSVNAASEPFQLRSLGREIPQLK*
>TCRU_5688 protein kinase, putative
MERLRERCILGREVVISKLLGAGANGRVYLAAPVSQSDESNQFSYPPHFVVKVMQKDLFP
AGHLETILKEINAVRVLKHPFIVSYVGAWVEAGGGEHDGSVCLAMKYCDGGDLHDLILEY
KKRDEYVPNDLVMMVMLQIFSALNHGHAHHIIHRDIKPANLFLVRGESGCGGVARALVGD
YGLARPVERTVELAKTRVGTPCYCSPEIVAGEAYSTKTDIFSAGVTFFELMTRQRPFWEK
DFTDRQSFYAILHSDPMPRLRRMAEGRYDSCLVRAVGSCLCKREKGRPTAYELLTGFATR
LTTYVRANGIPVCGEVARVSPVRRWVXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXQVLEEVLGDHAECEGLKQLLGGDVEAFLLVRVLLLTRGNDRNAFENGIFKLLL
SLKPQISVERVILWMS
>TCRU_(Poly(A)-binding protein 1) (PABP 1) Polyadenylate-binding
protein.1
PTVPVTTKALQLASLYVGDLDPVVTEPHLVELFKPFGTILNVRVCRDIITQRSLGYGYVN
FNSHDSAAKAMEALNFKQVGDKCMRIMWQQRDPTLRYSGNGNIFVKNLKNEVDSRELSVI
FRKFGDILSCKVMEDEEGKSRGYGFVHFKNDNAAREAIEKMNGEKDHADEEKKMGLYVAN
FIRRNARLATLVANFTNVYIKQVLPTVDKEVIEKFFSKFGGITSSATCKDKNGRVFAFCN
FEKHEDAVKAIEASHEQFVDGVVPPGEKLYVQRAQPRSERLIALRQKYMQCQTLGNNLYV
RNFDPEFTEENLHELFKEYGVIRSCRVMTDANGNSRGFGFVSFENADQANAALREMNGRM
LNGKPLIVNIAQRRDQRFMMLRLQFQQRLQAMMRRMHSMPFALHGHLPQRRNARGTQRGG
GGGGGGAGRIQAPPPMPPPVQQDMFATPSMAFEPPRTPQPSPGVAPDTPPLPPITAEDLR
SMSVDEQRAALGDRLYIKVFEIAPDHAPKITGMFLEMDLKEAFTLLTNQRLLQEKVIEAL
CVLKAHESSA*
>TCRU_5690 hypothetical protein, conserved

GMDRLSIMFYRINPHDYPLFMQCERSSEQPGAILMESRMLQGIRYTVSLGYLLSILYFYG
YHRPRLPFADRPLARLHHYFYPSAGYSTPIGISVGLAYACFYDGRVACSEENVTREAKRE
RGRAVMAWKQHMQRQREEEEAAQKRRSWRNLLILSKAPASDCRSSYEEFLDRNGVLSVGR
QAAEVEDASFYQLYSKQQVDALVSAAMKLRQSPEEQRWLRTASRLGSYGVLGMLLTWNSG
GMFFRSFMGLGLGVVSGAFISGVKLDS*
>TCRU_5691 hypothetical protein, conserved
SLWALRCIALQPDALTCVALHQLIVVAEERRRQSTSDHDREVEVLLSRLLEWPLPVLTRC
ASTLHVLRGVVRGWISTAQAKAPPPARSQLSASPATPYRRLYNICLWQRRYPLFILTPVL
DAFGERLSCQALNDMLEALSGYISGPLNDIPHLLRCDVLMTYHRLPFHQQLQLMQSFRTG
YALEECEAPPPPELYIGEHVRHVPPRFGSHNISAEQYAELRRAFELHKRAGIRRLLACTP
*
>TCRU_5692 Endonuclease-reverse transcriptase/Reverse transcriptase
(RNA-dependent DNA polymerase), putative
DEKVFCVLSGKRRPRPEATSSSPPGFQHHGTARTCGGGGVFILDREGLQAEAGPALVASV
GLARATIHPEAGMKLTVSPEHFPPSPRCVATEDLDRPLCAGGPQLMSTGGNAHGEVWDRK
IPSDSRGDAVVRPRLGTHCGTSMPDSAHCVMLLDFLIGDEDTPAAVPNPDRASLARKMAD
WNKHGEIASTGSVGKNIVSGTRKATKATVPAWDHQPSPLWTPGLAELDRATAAASHA*RG
QRPELRRRDVARGVQNRRRELRTTPEAAGGRQHAVRTPRPRTPAMKSDGTALSKQQKVGQ
LIKLWAAEATRHPKHRSPPPTLTNARGLVPITMAERDRAPRPLPLGPAPGRDGMHREAWR
RPGRVAERAPRLFGRRLNAGTVSRSWRRGVVIPLNPGKTAYDRDSADPALAGHLSQLM*R
IPAARIRDAIESPSTPQPSGCRPGDFALDRLLHLRAAMHRNTPQHRTAAVFVDRAKALNT
AEYDKIILQMRRMPVRNHTAHWPAAFLNNGSAVFGAGKPTSFPRSPQEAPRGAVLGPVTF
IIVVKSLSGRLSNAPQIFH*FLADACALNTQQSDRGMIGSSWHEGPSVVAEWA*ERFMEA
NTGTTKRGLLLTGGAALLHLKYDGAPATMERTPVLLGANSSYSRGMSAHAGKLREESKQR
LPRLTAIWSFAWGNQRTLLEAFRLALDSAHQKASGIVARTPKSGRMEGAVLVA*PRPLLD
TVLVRGFRCVPRCEKRGGALRPSAPTVSHPQRAA*KPHGSIM
>TCRU_5693 cullin, putative
DEKWEIIRETVLSILNKVMSQYSFQQVHHSVFQMCQQQGSGILFDHLEAILATHVNSVRD
RLLSVTSENFFKSLKTEWDDFSSAVNFISKTLLYLNNNYTCHRQSISQMGESIFCEVVLR
NTQISEMFSICVRRSFTSDQTSKNVLKELASRLSQSYRHNIFEPYIEDPFISALADQYRQ
EMGIKLNELGTKNYLEWVVGVIEESKTNVSNILGESTAQRVEKILGILLIKENTTKLLYN
EAGGGSSMFRGMETQSLHLLAEALGKVNESEAFLDMIVGTAKKMGSELLADVDNASPVSA
VEKILNLRDRIKNLISNLPFISNSNQSPVSQAITEIVKDSAVFAEKLAYYYDAKVKSKIS
EAELERLVADVFGLFRLLRTKEVFDHAFKLLLAARLINSKPEDPLSNETFLIDQIRNECG
ESANHLEIMIKDGRMRREMNKGFIRSLGTGNKLPHEFYVTVITAGVWPEYTDLAPDLPES
MQNCMQLFRSYYLPHHNGRKLSFNTTLGTVFFTLNHGKIYELVAPTAFASTILCFQNSDQ
NNEYLSLQEICDKTKLIERDASFQLESLSQLGLITVDRVDDVLRYAFNQAFDNPRSKLRV
RATSGNRILEKNRETRAHCEPLGASISFSIQAAAIQIIKSKKKIGHTEFCNAITKSLQKA
GFAPSVADIKKGLETLMSKGLLSRKNSNIYIYES*
>TCRU_C-terminal conserved region, putative PS.1
PVSDFSSVRVKTQKITNTLPSHDVPRAPFRSFNGRAYAFPLSIVKRYGNALQCVSNEATP
EEKNRYHAAVKLPGVLWRHDPYSAKVLAATPITPEHKTSFAGGGGSSMCGIMFEENAGSG
GRPLMPR*KVGSHLLHTTVTRGIPCAC*IPHRHRSVQCCTSLQRVGRTLLVHIQLFRSST
TIPCRKHSNTLPNPAPPPPPLMPEAMKYRSGGGLEHCQCAAAGSITPSARPLPSASGSFL
FVRSPPSLPLPAAASDVSNTPRPTDATVVIAGYLGKSERGGSQGHEIPFEARRSRSSRAG
NTHRDYGDKFGECPSTLSMFFSLPTLFTDLTAYTKRRPPRAGKKDDSDSQLRVEDVHYVY
LVGHRCRRTVCAASVLHEVGEMVVLEGDMGIEMGSVQLVLPVEEFEQMETAELARRGFPT
EHDVVTAALILRNATEEETQHYNHTLRQLSKDLLKFLKYGLNPARFLSCEVQHMFFLDCE
FQADCKKIYIYYRASTRVLFRELAQYLYYFYRCRIWLHEVGRCELKASGDFSQD
>TCRU_5695 hypothetical protein
LDVPWELREAFSDPICSYFDFLGTKHFWFLVQFSARVTLIGMLIPAVIIALESHQKEYMS
FTYTLPAVILGTDIYVGGSAVFLVQFLKAGCIWLPLATASAALELHRKFVVWLVVYFLLL
FFIACLTRSVTQRICLLLINISLVGQLNGHTTLMFPLYLLLSWLIGLLFGFAAILLPYPV
LATRSAHSIIRRLFTNAGTAFRGLSTCFWAVSNTERSMGMVRIRHVTRSLDILLDKAESM

EKLALYEFLFFENYERRKVRLEKADLLDNLRLNLRSMTRVIDIVQDNANIIDNSSLCIQF
GEILSQSMEGISRYVEELLDGISEAQTRHDLLNLGPRFEACGRSIKKLQEEFSAGSRRLF
YERGHTEMEEFVPLMTFFVFSVVNFWSALDEFHQQVRMGSKKSDCVSPKRVLDAIKRPFV
NNVVFLKKLFLKRSEAEVRVLVEAGKISVAMLIALLFFYYVQPELLLLSGPTIIAFLSGV
NPVHAVQGSLARLTGTLFGSVVGFFAASLCKTKVDFIISLCVITAVLTFFRTGQKFGLVC
VYANFIAIPSLSIDSQTNTGNVVSRIQQNSFAIMIYCLIAVLVFPISPGKLLMKKRMRIL
QTVADIMANMMDFYREPLHNEPFRFDSQDGEFLQVRKAFSAAHIDGHGEGESTSGKSGNR
LKPAGIVPTFIMMPERDSRISNLFDKVWYLRREMAQTATIMPFAADERGIKPFIYPQKAC
EAVHTALYRIFALVYTMVCSWRLMRDKGYFTPEVRRILLYLYPVASDIKHSLQRFVNLLS
FYVAHPSSSLGSELTKCLLQFRALVSELSVRNHRAILVIIREAVKKQ
>TCRU_5696 hypothetical protein, conserved
LCTSRCGVAYKTDASSFESEVIQSQQAICLVYYRPDSSSCNAYLTHAERLVSRLNREISD
TDKKDGCDGEKEKSVPAQKAWLKLCTINADENRNLASAFSVERAKLPVTYFIMQGTIIDK
VTGHVVESRLEGILRKFLEHYKQQMNVELMGGGSPEHQHPLPAAATADLLHGASTQYLQN
RIMDALVGPERIRLPEESEQLDGLRKTVQQAKKKAFDELQELRRELGVDVRRLSEEELTK
RYHRSSQYIACTVLSALEALFLARVHATIGNIAAENIIFALNAIQRDFSPVLADPTVRRL
MSLCEVLLVRGEVVLLQRRQHHLPSGSDDAVSDKLARTLYWIDNLVDARVVPEQFPSDEV
EAMFTLLRSNLLQSRREASQPKEGEEMAMVEAESARCVRQTKTCLLGLLQLYHGDPKSQD
ARSRLSSLLY*
>TCRU_5697 mitochondrial DNA ligase homolog, LIG k-alpha
LSFLFALSALRMGRVSRTRLPITPPANLATFHPAIASSWMTAASNKLLQPQHVLPTSRKL
AWWRCPHCGHEHHKRIDLHVAAGGVCPRCHRMPTLLHPSDASSAVLTIPLVKHRCRPDNS
LSVLAAANANRVKSSIADDGYLRVVETRNLQPMLARNFEKESDTIDDDAVLFVSPKLDGV
RCIVAWNVRERRPCFFSRSGTLFECCDHRIEPGLRPLFEKDPNLVLDGELYNHNVDDFEQ
LISAIRTTRDRRTPAIAKLQEQLQYHAFDIMYASKFPDMSVVPFSERHKHLGRLIHGLAS
SKGQVQEKAVVLVPAAQVKKADIPRLLRLSLADGYEGIIVRRDGVVSARGENNCSRSGTS
RGVNKSSSRGVVVGYAYGARSPNLLKHKVMQDDEYVIVSGVEGRGKWKGCLGAFVCRTKR
GHQFTVAPATTEQRKKDMWQRLAQYKGKMLTVQYQELSANGVPRFPIGKCVRGAKNGKDW
I*
>TCRU_5698 KREPA6
RLMVRPTALQRCKSVNSVTLVGVVHDIQSGFVYEDAVTQFTLTTTSIDTTHPTQEVVVEK
DHHTIRCFGELFSAEVKQKVKEGNVVCVNGRLRLSPQLEPSCNKHFYFPYIQVQPPHGQV
AVIHGDRRNTPASVNPTAEEIPAESE
>TCRU_5699 MSP-B, putative
LLLCCVSGSVAVAEHRCISEKIEKKVGPRTTAVVLELPTRGGGMIRALTASAPEWAPIRF
QFFTEDLNDPSRYCTAEGQIRPDFTGGTLECKGEDILTEEKKSIISKSLVPRALKMHADR
LLVEPLTGRVIVPRYSSGVCAQFTITSSHHTEGVFGADMYLYVSAGPTQGSTLAWAHFCT
ELPDGRPVVGVMNYGPSFVTDSENSVRVSAHEVAHALGFALEIMRKLNMLKEFEGVRGKA
AVVQASSPKTVEKTREHFNCVSATGMELEDEGGERTASSHWKRRNAKDELMAGIPGIGYY
TALTMAAFEDTGFYRANWGKEEPMSWGNNSGCARLTEKCVINGVTKYPEMFCTARSSPLL
CTSDRLALGRCAMKLYDAPLPPQYQYFSNPKLVGPGFLMDFSPYIRPYVKTWCSNGNATV
MRGSRVGPRSKCLKRDGLADFLGFIGDVCAEVSCDKGEVSVRYLGDDAWHKCPEGSSITP
TGLFMKGRILCPKYDDVC
>TCRU_5700 hypothetical protein, conserved
MWRGVTLRISRRGALLVSKKNLRLKCGACRRLLPAAHFNNTTAPSQSLVCVDCKRLCILC
GLHLTVDRFTDASAELCDNCLAKRHVARENVYFRYPVLKYRACPFSVDQMREEIRRE
>TCRU_5701 palmitoyl acyltransferase 5, putative
ETFACLALVITAVAAFMYIVIMGPSRYHRDGVVGRMYFCLMDCPTACCGCFCGICFGCSY
RRGRQKWTRCSDHTFRERNCFMVIFYILLVWSVEFLYLFIALPELQVSIWSKLISYGLVM
VSEGFYALAVFSDPGIVTSREEKEAQQFAFAAPPARNKKHKKKRGEENVAASGCGHVTKH
TNAHSDTTMGNGEKWRKGKMRQFLLSPEAEARQNRKYIVDGILYAMDGSSVGGNTARNLS
SSSSALSSITTTATGLECSTCHVPRPSRSKHCRLCDYCVRRYDHHCPWINNDVAEGTHRW
FLLFIICHAISCLWAAWDMYALMKAFLVQNRAWGWSITLTNGLPYFLTPIDYLIILVTYQ
TVAACLFFFSSMIGLVLLIFGGYQMSFVFDNLTMNDMGKIDDAITFVLSLPSLDEVYREA

MNVWQCLEVVAARPPRKLRQLKPPPPDFVPGSRGDKSYRKKVQKMLYSDLKGLFDRGVWN
NLVEVFFPYS
>TCRU_5702 hypothetical protein, conserved
MSAVAVAVMETGISSVCTMGTPECDEELYLFLRCLRVHHPDIPVIVGCTSAMLKVGENTK
SKAYAGFCNDSRMVWIPCLDPYVPIQRREMERQPGVWYPSRHTDFMMEKANLMEHAMMLR
EEHGGENMGAVLFLDCDVILLNELPRIPSGTEVALSPHRISPRDEALFGRYNGGFVAAAS
PAPLHEWRRATRHSRFFDQASLENVAKKFASTLYEIPPQHNYGYWRFFQSYRKNPLLEAR
QFSMRRIGAQGEWMLCYEGKPLGSIHTHFLDAINPRARDVSVFNGLMKEWILKCIRPTPH
ATTTALCSGALAAVAAGNRRYKEC
>TCRU_5703 mismatch repair protein, putative
RMRTGATTPSAAKRSGASQGTGDCVMALIHNRANEVGVALCLFSSLAVIITQYGDSVAFA
KTLSFVFSRNPVEVLVPETALDGNFVQTLLRHFRHITFTGVQRGTFDEARGAHRLFELMS
TDEACLEVGNTDRYLCVAAANALVEFLEMNYNCTLLPHTVRVQYLALENYVEVSPIAARG
LHLISSGPPPRAQSGGQRQDDAVGCGHKKRSTRKTLFRGPREQRQSAPMLSLVDVLNHTM
TIVGGRLLRSTILQPLRDPTSIELRYDCVEWLRQEEETLKALRRSLQLLGNNDIERAVSN
FSHEPKVQTLKTMQQRIEAVVTLWQLLGSATQLTTTLRNCLREDEGALKDREHDGPRSHD
RCLSSDSGKYDVNEGDAYCSFRDEQPCPKRRGLEETCQSPQGASPAHNHGVAAEAPAVAL
RTRRGTTTLLCKIIETLTECRMEEICAEIALHLDEGVLRATSGVGPQVGDRVTQRACRPS
SAISQVQHCFAVKPNISGTLDIARQQYSQAIEAIFALAEELKQRYSVWSLHVVYDGVRGY
RFSYDARHERNAPDAVFLQKYSGGSHDSLYHSSRMTMVGEEEKQTNTMEKNGGGCGDGYG
VGRARAVATGGVSPLRDEYSSTCQERFRPTYSHDAATLTPGEQSGCNGEHQLTKHQVRGR
RVTCTTNGLLVLCRNAEDAVAEIFYTQDGHVRFLIEYLRQRLGKLQAVCDAVALLDMLTA
FAVYSRRNGCVRPKLLKPERLLVSGGGTYFLEARHIGGLATANSIQWGDDARVLLVTGPN
AAGKTTILRQVGQLFALAQIGCLVPAKAAAVCPCDRIIAHMLCDDLEDTTTSSFGKEMRE
LSYLCLHATQESVVLVDELGRRTSAREGAAIAWATVEFLVETRCRSVFVTHFGPLTRLEN
RSAGAVKNYHLAVGTESDEEGGALGDATKTSGRPACTPRFEHRLIPGPSQVDHYGLRLAE
RVGFFKPALDLAKELLPLMEGVRGAQQVGNTDHDAAAPEAEEVGRDE
>TCRU_5704 DNA repair protein, putative
AVLTITDRGQWKPAKGNDRVLRYIVQRAPTMRARCRKCSQYIVKGELKWGIPIRHTHGEH
GWITAWQHIGCTRISQIDEAINMIFGFEKLSSEEQNEVLKEVTSSSLPFHLLPLDPDDLV
KRGSLPEMEPSSELLRPLLRYQKEGLSWMVAQERSCIGGGILADEMGMGKTIQMISLLLA
NRVMGPTLIVCPVSSMLQWKAEIKEHVVPGTLSIIVVDRAIHVKKDEMENADVVLTTYPM
MEQSWRTVVNKTKVSCPYCEQLFLPRQLVVHNRYFCGPKARKTAKQRKREKGREDVNVVK
NRRVQSKETIKKGLRTLRVDVDDTVDEGVFVSENENTNERGTVGPMGMYRELMLEAGRTV
RSRWEPAKELSDGTDSTSISVNINTESDETNEEEEIHRDEEAFIAFQCPNCKFQLLRYPF
CPKTGQHHVLSERLKNIIETDNGGDDIDIYESIFHSIKWSRIVLDEAHRIKGRNTSTSRA
AFALQGEYRWCLTGTPLQNRVGDVYSLIRFLRMTPFARYYCGTEGCSCSSFSHPFSGTNL
RQCIFCGHGPVQHYAYFNRYIMNPILRYGYVGDGRQGMMMLANEVLQKCMLRRTKLERAS
DLHLPPLTIEIIKVKLTKEERNFYDSLYKKSAAAFDTFVDKGTVLHNYAHIFQLLSRLRQ
SLDHPLLVVESMNVGRVAHLKGVCGICTEGGNENSLQVNPCRHTFHRVCLAQFIESLPGN
EYRCPTCFVTINIDLRQLRSELEEEEPAPIMPPEIEDELIEEEQAGKLFCDGGTPMGISS
TSEKVVSTQNKRKKDILSRIDFSNPLQGSKLDAIAEYILSVPKDEKIIIFSQFGDMLELI
QIWLQRASVKAVKLTGSLMLSQRQAVLQAFLHDPGVRAILISLKAGGEGLNLQVANHVIL
VDPWWNPAVEMQAAQRAHRIGQTKPVRVVRFVVERSVEERMMDLQDKKMLVIEGTIDGKF
SSLQSLSEDDLQFLFTR*
>TCRU_5705 Leishmanolysin, putative
LHAERLLVKPTADKITVPRSLNEPCDHFNPPSEHIRDGVPDADFIIYAAARPSGTKSRAV
WAATCITWGDSRPSIGAMNFDPKYMTDTAWSVRVAAHELAHALGFSQRNMEEKSMLNSEY
IVRGRSRWMVAGNHVKAMTRAHFGCDSLEGMELEDEDGASSRRIPHWKERHARDELMAPT
VGAGYYTALTMAVFADMGYYRVNWSMAEPMSWGHRSGCDFLEKKCSEITDFPTKYPHMFC
DDSDNETLRCTSDRRHVGTCTAAIVENKGTPAEKDVCPVVSSYFHEISSGTTYNACSDGT
VNSLPGSLTGGDSWCLDAELVETNDNSEHKSVKGVCAQVLCEEGTVKVKYLGSSDFHYCP
EDTQISVTLNGFEQNGKIKCPKYGEVCTIAGNGSSLVVPRALEDDKREEQEEKREESVAA
PALSPGAEARTKASSADLPAAEHSSEEGPSEEASTAEASPPGKNSEA

>TCRU_5706 NOL1/NOP2/sun family, putative
RYDSFKSMHGNITSLFALLKSPESVRREVRQYVCHVPRRYMDSPRQRGSWVRGTLNLVFE
EARRRGSYAVARAAVEVTLEQQQQQKQQQQQQLTMESTWVKNALAACRTPEELREMETLL
TQHRCLLGGMGEAGCGLTPAAQSDDVVLPPSLQDGDNGGSEVHGTPSLVAAGYSTAALAT
LRQGRDHVVTAPNASFSRYFMRQGLVADEVELMELFKAMRGRQPVGFRVHTSQMYGRAVE
CLLRDRPGIKPLSWLPSTCGAFVLLDTPDTPHNILLSNRQLLRALSNERLISFQSTSSML
PVLLLDPRPGEAVLDLCASPGSKTTLIHDYMFGISSSSKSLLATGCIVANDAIFSRRRTL
SQRLQSFSPSIAVTQIQGQTFPAQPIASGGVRYDKVLVDAPCSGEGRMHRDVMSWRMWHP
LKAMEFFTTQVSLLRHAVELCAAGGCVVYSTCTLNPLENEAVISTVLADGEVELIRPPHF
MTADSGWHFSRGLSHWLVPSRAGGFLHTFAEAEAKGEETAVELFPPEGNGEIQKALESCC
LRVLPHRNSGAEGFFLAALRKVQQGSAPFSASSSKDIAREKKVALSSCQLVAESILHACG
TVRLSAGNMLLQRHLGGFFNDSATQMEEFLTKCGLCAAWKETRGLLLISESTWDHIRAIP
STTNLSSSTAALLELGIVVIEAATGSLTESGAFYLRPHATSRVLRIPLSEMQWLLSHQVL
KISQLQEDPKVLARRIVGSTAPMKHETETEERCVPLPWVAQVFDAIGSREGNFIVCGFSS
FVNKDVDHDNNADGLASISIPVILCRSSTGVELRLSLSQDARQRCLAVIGRVIARKRRTG
ATMAAAAALEKEYMQMGTQYNTSRKMDSAGLEGRPLTLQRQYRHLHASN
>TCRU_5707 Histone RNA hairpin-binding protein RNA-binding domain
containing protein, putative
VSMNENNRRPGSRNNMMNGGIGSAVAAPAWEGFVGRGLPKADVATSATPTRNAPALAAAA
AAAVQQMRSPTVTTHQPYRGVPPSMFGVESELEGYTGINMENLVTVKAAYKTGIARSSGP
IASGHASSVLHRFSQRSPIAALDSHDPQVGPIGGLCGTAVASISTQSTMNGNGPTSTVPP
AAAAVSVAAANRNIPARVGINNKRMSNIDLVERSGGDGNNTGADIYRCPVALRIVETEEK
HLNYTGVELYASEINMGETAERERRLQQRQRQVQYGKETLGYSNYLRAVPSRCDREFRNP
MHPITPRPEYDCSKRTFDRYLNVWRRQLHLWDDYDPNNLEPQYVRIGIPTLRALGLELPP
STPEGQQNALISFTSINAVGGASACTPVMLRHTRREQPLSAGPYQRTVGYQQGGNVAAGG
APPASLCAPLHARPLSSGGGASWSITNTPHTPYHGSTHSTSSYPPPLLSVLAQPTIYSPH
WGDSSRHSSPNPHNCQRGSIFAYHNSGGVVAPTTTTTTTTTTAAIAPPTAPGNALYWEG
GTAYHSNTNNNAGYAYRSYSSPYGGHRYTPHSTPNQHHPYYAGSTAAVNVTVGSARTMTS
PLPVCVGQETWGNPPRQ
>TCRU_5708 retrotransposon hot spot protein, RHS3, putative
KDPEKYICDAGVLGEIQASDRYKRMEGAVREEMDMEEDVHKLYDKGVYNLLRWLVAAAEV
TASVHEITKRFLDAAAEEARNPKKSSAPIYLEGVYESVHNARWHHVVEVPGGEGTGMDVR
EGEPPQPWTYRAVGRTLEKDDGVQQSGAPRSRLMVLTSERAWPYTWKWNENNSTRDCYVN
CEVDRVWQIVKGDLTELFSSRPEDHFTPHPRLLTGTPGIGKSMAAGLYLLYQLLHCDAEL
LPVVVFVVCGSEAYVFNKTAETVTRYMDKSMMIKAVKELSRRGMKGYIIYDVGGGLDIPS
PFLPPGGWGMLVVATPEKTSYIHWANEKRAVRIIMNCPDESDVKAMCVWMKRNQPPPQQA
EYWREVKGRMDKLGPILRYIFDEGRYKYWIGDCHGLVDGTTSWGIRSYFVFGTSKLWEGN
KALEYLARIVRARGERNGESPFNAPITAHLASKTLCKLKTLMTQAEFNLFVSRIRDCLMH
ANFGKCAMFAFLNVAFMAAIRRKLKELKPPTRRPSHRCAPDVHSQEGPTSHYFLPSAERI
GKKTCINHRLLYIPEVENFPLVDGFFLMDSNPMTLVGLRMATAGAHHTTASTVRQFTERL
AAYFNGWEELSRDMSWEIIYVQHADSTPLNDWQRCDVVNSDNVSKKESQKIAAFWEEKVR
QYQVSIPSRDA*RDEALRVRNNRRNRKTNWGG
>TCRU_5709 60S ribosomal proteins L37, putative
MAKRTVKMGVMGRYGARYGANPRKRAKKLEVSQHARHFCSFCGKFAFRRKAVGIWRCDGC
SKTMAGGAYTLSTPNNSTVRSTVRRLRELK
>TCRU_5710 tryparedoxin 2, putative
QVMLPRVLGAGTLELLRQDGSNVTASKALQGKKYLLVYLSASWCPPCRFFTPKLAAFYES
FHNSHNFEIVFVSQDRDERSMQAYFHNQKYSKLAVRGGEGSHGDWLAVPYEQAKRLGVTL
MQTYAIRGIPMLLLFDLETGELVTRNARDLVARNLDTAEGFPWAGNTDGEGLRGSYWNQL
FLVFIIASVLYQFWR
>TCRU_5711 hypothetical protein, conserved
EAEYVPATYMHGKYVLLYLTDPTGNNIAAYKPAMEPAATPFSVGYGHNALSTPSPSSSIH
VTGSTVRLPLTTGVPALAYNTQFISSATTVTSKSSRRVKSLISAFYDLLIRQLTVSSSQD
GKPVFPVVILEVRQPIGFDDAPPSNTVLGEQRAVSAIATTTDAARDVPSSSSPQKTEGIR

SVLDFSPTEPRPSLNIAITSSPFFGGWFSLEAPNAYRQVIKTFGVSTWPSVLLFDPNGRL
LTIHALNYIEREMSYGTVDSSQPFSPAGHEAEHQDRYAGFHSDFPWLMEETPEVTDKESE
SSIDAFPFSSLLRRLIPHTRRVGRALDCDFPAEPECMAERDEYVKPDECLDGATHLALYF
SGGWHPSSNKILPRLRSLWSALNGGVEDVDSGRDHHKEERFWNMEREALNVSLSGAGLTS
VPQCILSYRTGAYGGRHYSNSQMDSDTRGFSSNNSPLETPVRMSKEKVFRDASPHVNLGT
EPKPEGTSAKQLSGVPSRSLSPAHSSSQRQPSSPSPQERLEEKVELDRGEEEEEEEKQQQ
QQQQQRRAVHLQVVYLSCDTDKSQLYSVLGDMPSSWLCVSSLFGPNHRKMLEECLDIFDV
RVFPRLVFMEVRSGSEMPGPASGSSLVTLLPNLNFHVLQSHGEGLIFCDNGVKEFPWREE
KRGGLPQLPFRRPVAHEFSLLSGSRGAIKSFLAEGGCLFLLCGTGKVSAELHKMCAAAVN
EASLWWSQEIGLFLERLKSRLTSSSRGTLAPTDCCASEQVPGNPHWSTTSDVWASVTSAA
TLLESSAAATNEQMPYLPVYFFDAVVEETAMGNDLEAESQNGSDGGEGHISSACKEEKAL
LQEYIFSEVLEDAHLLPPVEGEPFLLCVQWPGRRAAVLRQKFEYENGSGPASAISLRSSC
STGTNAP
>TCRU_5712 kinesin-II 85 Kd subunit, putative
RVGRKRGEKMVKKQPGAENIRVVVRCRNLLPYEAERGDKALVRLDLATNQVIVQHPIGDA
DTFAFDAVYNNTYTQRDIFLQEVQPLVEAVLQGYNATVFAYGQSGSGKTHTMTGKLSDPQ
MWGMMPQVVNYLFNEVRKLSTTTKSFKIKVSYVELYNGKSRDLLASKQVNLEIKQNMAKN
FYVKGAEMPEVTSFDEAIRWFNAGTDRRQTASTELNDTSSRSHSLFTLQVEQFDFEQDPS
SPIVLTSKINVVDLAGSEKLSKTNATGETAKEGCNINLSLSALATVIDTIVKGGKHIPYR
GSPLTMLLKDSLGGNAKTVMFANIGPSEKNISETISTLRFALRAKQIENKPIKNMDPKDA
RIQDLLDQIEELKSRLGNVDLNQEDQLRQRIEELEIENADLRGGGVQNNIELEEDIRILQ
AKLEEANGMVAEKQKELEKGIDGRSLLEWNLQSELGRGRELRSLVMNFIKQVCQDEQIQA
IRSKMPQDGSYNTTDDGWDVKEIEFYLREFAAMYESWRQSTYTREDLEKYAHLSVTGALE
QTQRQLDEVARARDELVRLRQEDSVKRAAENELVSQLRVDLNTLKDENTKLREKVERDQE
RMKAKIFKNKEEYKSLAEELERSKALVTEKERDIERLKRISEETGNNAIISASTGGGASW
ANADERTAMLQQLNEEKNIRKALESRIREVNVSLRRYGVCIADAKEVTNESREVSEATDA
FILAALEEKDTMDGDLCAKLQQQLRVKQRLTELRHQHQRKLDDMLRKYELIKTGRTTANS
GAGADNNMLHSGLADEATAQQIKELLHRKDEEIERVIKEKEKTCDRIVKKLNKCELRIKE
LEATLEEERVQSTEERQELDRENRELQRYNQQLSVELETLRGQLSEMKEEMDFMERAKSA
EIERWKEEAANGAGRLEEMRFKMAAYSELQKSYDRLQEQLQRTEVSLKEKSDNLENTRQM
VKWSNSLLATEKQKVEQMEMMLKQQEVEMRRREEQLKSEMMNDINKQVAANNRRMQDQAA
QYQELISQEQDKQKSIMKKVKSSRKETQKAAQRYDEMILENEALLSKLEELKVTSMRIFL
EKQEAQRELEALRPTKHVANRRL*
>TCRU_5713 WD domain, G-beta repeat, putative
MRSCKTAHRTFVHHMALDPSGVLLATCSSDKEVNIFYRNPLGVDSSAWALCSILKDHVAT
VTRVAWYLHREHGPLLATAGADRWFYVYKIIVTMHGGKVACDAVKYSVVRGFEKDVITDV
AFIPFEQHRILRLSTASLDGWIRLYDIQPVQFLCVSKITQETETGRSLDTRRGGITSIAW
FPSSADEGRALAVGCMNGAFYLYRSSKDCEQFELVRRTLPERAESSIHHIVWAPCVGRSF
QLVTICCRSSVYIVRLNCVSPVLESYDCDVFRWPRGAACAAWSRSASLLYLINDDETSEM
TVLQAKDPSDHQSW
>TCRU_5714 hypothetical protein, conserved
ERSAAFDPFDGVEKDEATQVKIKWWASHVNQVLDSHRSPFVAAEILLQQMNEYGTNENIT
EDLLLATVLPVLHRCAFCLGTYGDLLEKALHEVLPAIMFARTYAFPHGEVLQRRPYAECF
ACIRRKFNYHVHLSSILQRKVALEEEVMTRVVCKLDKLWLKMCFRAWCGLCLHVHAKKRR
FQRLAARGAALRVVPGFVRSWRRYAHEVTLREKLLKHDGLTREIEELYHIEQVVKSRHES
ILEEVREKHRLLETTTERFMEVESRLKVLEGILDETVLSLRAHWKSWNETTVSLFSDTNE
FQPPAVGNLRADLQSTIQNITDTATFYLREAQKRACKLGKNTISQFLSRAKMGGEIAERP
GPDDLIAMVTSVCNPVTSPLRLVDVVRDDQRKYDLTLKFLACVNDGGHCSLFTQHEFPSE
DEFSTDFFNEHGKEMVAHVATGVDSLHCCPATNEKYIEAIRNCLTAEELNKVGDYLGRVF
CELAAAGLPLQKAKIEGCICPIVEPHDRQIVRALYPSQGIKSIDDMINYLLSVSHLTSWT
ISSLVEHLENNYDADPKEDLFTALSDEAVINYFNEQARVIDSIFSTFKGKRSQVFFSKEL
IQGFLIAKFGLLSSEVDTLFSLGAVQGKVTKGEFNRFLIVLAAFVNPSPFVSMAEKLAAV
VRLC
>TCRU_5715 cyclophilin, putative

MPSKRAARVQKLHEGTGDDNLPVFSIFIEKEGEGQYGRIDIEIFVNKVPKSCEIFLHSCP
AALTGDKRVSKLSLVRQHRFLRLTNEGLQVGERPVSRLVSLSDIENEIGRVNHGIGVVSL
CRSSNTFDESFFFCLTDNRTELESLDKRHTAFGRVVYGLELLFLIRDALIPYVKEGCVIE
GSPYAISDILPKA
>TCRU_5716 chaperone protein DNAj, putative
LMRRSWRMFQAAERGPFDPYRILGLSPNAGKEEIKKAYHRLALRYHPDGGPEGSTERFQA
VNEAYEALRSGKWRPEKVNKDPMEGKGYGWDPRMGMYVYEQPGSTTENYVDSRTQTILRL
CVLWTAAFVVVRFFLLWIFPFSRELPTVEWVAANNVGGTKDARSQTRGLHGNVGTSPHSV
HANQD
>TCRU_5717 member of the NOL1/NOP2/sun family of proteins
QQEPQKKKKLKSFGKNGRELRRRTKCDNDGNWVAVNHQDALRQMPCPALERYYRDLQLLR
TPAEWDAELSLFRKPLPTTVWINDTDPLAGEVRRYFESMDCSLVEPIPWYPLPGMAWRIL
ADKTEFRKRPEMQALRRFMIEQTALGTISRQEEVSMLPPFLLDIQPTDKCLDMCASPGSK
TAQILVALGRHKVVPVDSDASPFTFDYESEGLVMANEIDTKRANMLVHQVKRLRLLFPFA
LFTNHDARYFPNVKCAASLVGNADEDLRFDKILCDVVCSGDGTIRKAPHIFKIWSPREAI
ILQKTQIQIALRACHLSRVGGRVVYSTCSMNPIENEAVVAQIVHRTRGAMKLVDARSLLP
GLQCAPGLQRWVVTNFKGELVVAPSDEAHEALFPPNTPGAYASAAVNELDLRLCMRLYPS
HCGGGAFFIAVLDKVKEFRLQKREESAAAELDGRNINDCEKGEGSGSDNSSKWATAGERK
RTKVGAVKSVEEEGGVTPEKRVPPTYVTAPAAITDVVRNFYQVKDFPFQQLVVRTATGQR
ELNLSVSSTCSIVSSSALDVLQRNTDSLLVVSAGLRVFAHENLDKGWRIANESSILFAKV
MRQSPRLLRVPVSFVERLLSGGKLKDVLFTDIDDDALRTRLESMDVGTVLLEIDCPAAVG
GVFYSVALRARTRLQMLVDHEDVVGLKLRLGIAA
>TCRU_5718 Leishmanolysin, putative
RCGFDAMMERSGPLSAAVVREVPRKGQGAMQAYTVATQDDDSDWEPIRIAVSTEDLEGGT
GRRKRKYCEKGEDECETVLGEKVSCTPEHVLAEAKKQLYTGKILPGAVKLHAERLLVKPT
GGTITVPRAVNGPCSHFTVPTRHKSDGVPDADFIIYAAAMPSGTNGRAVWAATCDTMSDF
RPSIGAMNFDPNYMTEMAWNVRVAAHEIAHALGFSQESMR*KSLVKKPEISMRGTHRRMV
AGKHIQEKAEAHFGCDSLEGMELEDEGGLREKEVPHWKGRHARDELMAPTVGAGYYTALT
MAVFADMGYYSVNWSMAEPMSWGHRSGCDFLEKKCNTTDNLAAKYPHMFCDAKGTETLRC
TSDRRHVGTCTASIVEDKGNLVDKDVCPVVSLEFHEISSRTTYRTCSDENVDYLRGSLTG
GGSWCLDAELLETKDGDGHKSVKGVCAQVSCEEGTVRVRHLGSSVFQPCPEDTDIPVALK
YFQKGGKIKSPTYGEVCTIA
>TCRU_5719 dynein heavy chain, cytosolic, putative
PLTLRNLSIQAVDMRRPLESLQTLLQTVYEPLLRSQHEVKLRSQLQDFLSSVRSHCQVFA
EVDLKLFVHAELLELCAAHPEADVEQLVEILGFEKCTNTVFLRQVMTLCGQCRSVLDTKF
EGRDIVSARDEVAYWQAVLRWVEQVQKQLHCREWQLVHRLLGNRVETSYEVEFKMHAKLV
RDYLDHLKSVPFQQIDEVEGENYAALVEELFSAMVRPTTYPASQSVRLLESIVRELAERF
LVLVSRNDVLRMETPEAQLQFLRRHIQVLQDMHQRYMDNGVISVRNSHAVTAITHAGRHA
AAEAEVPALVLSRARQLWRFVNEHFHYERAVKRTFADGSLEAGMTCSFHAELTDAYDCFA
TATGATGRLWDVTPAGTSEFHRALAAYKRRLAKIDERLALLVGTMLATAQEMSSSGLSLA
SASYSSESAVAVGTLSGYAANTSCGPSLYRIYSRFRPLRREKVQAVVAGFQMALLEQINR
EMKNVRERYFDAESCRDAVRITVARFGVTPVVARMLWERSVQREIETYLVRRDAIYEHGW
HQLLNLRTIEHCWYLDESLAQFLGAPLDDLMTKELGGDPEVYGTAYALAYLDAVYGKDKP
EWSADPYIHDAQNFVQESDAHAISRAKSRLVILRVGSGRGVEQSEVRDVRNFCDIISQRL
QERVVQWCEDVLRRIAALDLSPGTMTMKGPLWHLVELSGRKGCGNICISGSVNSNNGRST
AVGLRRVVMPHIPRNMSSLLRDLHVLDGMQLLESHVQLVADVRSFFTNNEERFRIANCLS
ELICAFERALNGEDELMVNLATEEYASVHKSFLDGAQLSWSDEGMLQQFAQELSERVYAF
CAAVAQVRGVTADMERGITQLRSHAVQKAEAVVGRVEEMHALVNSLYANCANACWWVRRV
QPCLDAALVWQLEQHLRRWTNEFLSMSRDPRFLDKNAETEEFGLRPLRVRMRVVFKEISL
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DDLEKWGDALQHIREMASRLMDYTQPSTLVGGIVIVADDAQKELGRKLDNMTQYIHSRYR
DVVEKHLDSCYHHVMEVRTAAENCNVINDLEDAARFLCELPDIKADMQATERQLVSLATA
EEYLRRQGFSLPDSWIYVRKVKTEYRAYHDLIERKVKALEFRRPFLREGVKSQEETLFRQ

IDELEESLHTIAIQVQHHEQAQLEEVSDSAQRRFRDMEERATRLKEKRKQLIALQDALGV
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EFPEGVRSHQAYKDLQVCIENRMACRHLMQELRSDAMTPLERAERHWMALKSQLHAPWKL
EELTVGDIWRSDPIEHAKIYHDVLQFAHGELRLESQLGHIVAFWNDFEFDTMVYQHQFVL
IRGWDVIFERLADDLDSFQGLRSSPFFSSQHVIAILTEWDNRLHFLLQSLEVLMVVQRRW
VHLDSIFTGNADIRRQLPNDAIQFDRSSREFMKIMPVKAGTSSVPVLTAQDLIQDKKLLS
SLQRLEGQLSRVQRALSTYLDMQRRQFPRLFFVGDDDLLETLGNSRKPTLVEKHLPKMFA
ALARFIVSSDDTAVGGEAKGSDSSAAIQIVGFSSADGEKVMMVQPVALKDRVLHDWLAEV
EGSMVTSLCQLTVSAVNSLTSAGKVTTAWITSFPLQVVCLAFQVWWVRLQEQTLLTLQKQ
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ILSVDEFEWLRVLRLYLSENGTELHCRMADASFRHGFEYLGWYQRLVQTTLTDRCYLTMT
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AYVIDPKAMSKAELFGVFEATTREWRDGVFTEILRRIVNNEMGGDRSRQQHWIVFDGDVD
PHWVENLNSLLDDNKIYTLPNGERLSLPPSVRIVFEVQDLRYATPATVSRCGMIWFNRGT
VPISSVLSRHFNVFYRAPLIDKHGKKQIASVAYDGEDYKTRSGGNCFMVQRIGVDRGEML
VDTLKETQGIKPEEIERETASPASNIPVAASKEHVTPSDQSSQKETSLWYSSALTDLDRD
LLQLQISMANVWAPAFAKDGLVEIAVRLIHSERYWKQGIMEHDELQMLSSVQSLLLDGVS
RIWRLREKQAKLPTMDILQKYAANVLQYAVLWGFTASLSHELRRRWMEELSLAVGSAFGG
GLADGLSLLDVEPDPITGEWRAFRERVQDTFITADQMGANDVLIPTVDTCRHEGILRAWI
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RGPVMSPTSGKVLLLFCDEINLPALDQYGTQSVVQLLRQIIERRGYYRSCDNAWITVEGV
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AEKLASAMVEMYTATQVHFTSWQQPHYVYSPRDLSRWARAVHSAFLTWEESERHKLRVEG
LVRLSVHEGLRIFQDRLVEREERDWTDSTIDRAFTTHFPEITLASVYPPSLQRPVLYSTI
LRPSYTENARDELRAHIEQKLDAFCEEEVDTALVVYDAMIDHVTRINRVLQQPLGHMLIA
GSSGVGKTIIARLVAWMNGMTAVRLGVHRNYQLDDYERDLRDILRRVGCKLERICFIFDD
SNIMEASFLEYMNALLASGEVPGLFDGEEWGKLMEEIRESVVAQQCLKASNKPQKLPQEE
DDDDSQGRHQQQPQQQKQKQTSMLPSSHSKSEDAASSHGISAPQREALDTMDSAVYVDTK
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KKAQTMLDCIVTDTETTKQEKQAAERLRQQLQEEEEMIVTDKARVQQQLSEVEPALREAE
VALNTIKPEYLREIRAYTTPPQMVKRVLEAVLVVMGEKRADEWDVIKHHIRRDDFLAGVK
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NRIDHLSKVHGAKRAQLQRTEVEIATMEASLLQLKKGYQEVTEEIAAIKNTMNGVAARCE
RATTLLRQLFDERGRWETEAMGFDSEVRTILGDCILAAASLAYFGYFDEHARQSLLFPRW
RQCLQQLQIPFREDFRSVVEYLVTPQERLSWEQCGLLKDHLCVENAMILSRCQRYPLLID
PNGVAVTFLLQRYSKDKINTTSFSKTGYLKHLDMAVRFGYPILMQDAEFIDPALSPLINQ
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CRSRLMLHEHSELDVRRTNILRAQGEYQLRLRVLEQELLTSIAHCEGSLLENDALTVALE
RLKGETESLKAGIAESEASMQAITEVEAQYQPLAEVVAKMYFSLRRFSRLHWLYQFNVDF
VFRLLADALAALPARSTDVSRVDEREDDAARLQVLTRHVFNLAHQRVRRGMFVQDHLVLA
ILLGKLRSGIDDRVGRQITVEEWGWFEDVLHNPAKTNAT*LPSRVAGTLRHTVPVILREC
GVCASSSELALAALLQRPLFAELRASLLNPRHAEAWRRYFEAAAPYTEEMPAFNISEYNR
AGRRDHREYTRRAFTAALLLFYTRRDAFAPAVQEFLRRFFGGDPDEKKDEKINDSSFFTA
EAPDLAVVQAELSDSTPLILVANAGSDPTLTLEALARTLDVPLRVAVMGSSTGLDMAGRY
LKDAMVEGTWVLLKNIHLARAYADVVEKWLHRERSEGRLHRNFRLVLSIEAAPGIPGSSF
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QPVDIQRIYLAAAWLHAVVMERLLYIPMGWSTQYEFNDTEFWRILQTVDSWVGITSRSSG

MDGKKGIDRASVPWPALQTIIGTTLYGGKISNEFDQLLLDFLCSQLMSAAVFDDDRFFAL
TEDDEINSRLRCRSIESLQDVQEWVRALPDAQTPLWARLPASASRVMSAQHAVATIERLA
IVRLIEEGDNDGTNTDNEEEHFVQQAAPRSIGETRWGQKIQRFCKMWRHSLNALGCMRPQ
RTTVTTSFSATAAVETTSSNNTSLEPTVIAIQREYTFALERLGEILDDLEALEDICAGSR
NPTATQRVLIDHVLMDQVPPRWARSYHTFPTTADQWISDFRNRVAQAQFMHEAVENKTLG
KKCLSLGLLFWPGAFLTATKQQAARRQHRSLEQLQLRLELMSEEAAQIHAANNIEESHTW
HIVGLTLFSARLEAKCGTCELLPATSGTSSTPVGALLSWEPIPAATAVEVLLPVSKTSLL
MRLLSQNPTSRCFATPFYVNPRRDSMLEVVELTVDPVHSPMRAWYERGVCLVAWS
>TCRU_5720 Beta-lactamase superfamily domain containing protein, putative
NMDGSTFSLTIVGSGCSTGVPVIGHLSGNCACAVAMRDAEGPNRRNNVSLLITVPSPHGS
SNGDDRGVRRVLIDCGKTFRDAYFRVLAKHQVQTVDALLLTHDHVDAVGGLDDMRDLQRM
SLDGHNNWFVEQYIPTYASAKTMNALRCQFGYIHRNSRVMGPAPRTAEEHESIMQHFAEE
RERAGLTNKIGTRRSTALELFTLPDDTPTPFCIPALGADFKFHAVPVEHGAGYVALGFVF
GRGVAFRSAGATGAIVANHSCVVYLSDVSTVPAAAMMFLQDLVKIDLLIVDLLHGPGYRY
ETHYCMDDVIKLVASLQPTCTYTIGMYCDVEHERGNQQLRERLEELRCSGKCGSNVLSVE
LGFDGLHILLPL
>TCRU_5721 hypothetical protein, conserved
FTSLFNSRPVAERAAAMLIAQRYPSGGVTLKAFVEQLPSLSRDDMFRRSMRVEDWVRACT
LIQLEEDAHGICLVKLAADAKFFLPGDAAEDATEEKEGLPPAKAEKQEVDMNLIEEVLPF
LRQRVLGTRESGGSSYKALNDAYSSFIREALTNATLRGFANTLKYVDFIAILSSPRAREE
VWVLNEKYICTRLPGETQPPRFVSPQPQTIVAHALNAYGGWGAASNVPTRQDVYEILKYV
PVAWGNFGNLNIPAAVKKRHIRIASTLQWFRRQPFYFELRNLAGTTEIRRSILLHPDVHG
LTPEEAHERLQLKIAKGEANSLAPVNAEGEVLAATEASQHTNTLLKFVARVCPGYFVPIS
LLMQRYTKKNLTPGELLACAKGNPDQFEIIQLKYTDIPLLRKRIGADSLRWNDGFVEDFE
RHPEDVRGLIVLMGRVCSTWDRPHYVYVRLTEEEKIIVGGFDGMMKILRRHPMVFRAGEN
FISRVDLSDPLSLRESEPSPEDMATRVPIREENPYLTPRDLAVVFHYLAPDDEPCTAAFF
LQCASPAMRAVLPPRIVTLLQLFPSLFVCKETSPGVFLMRKVKKSARLSAEVFAGDSARE
KREEVFSETPSSPGLSLEQRRRQDLGEEGEADDEAVFEENDVLSREEAIEAVKVLVPAGG
VEASRLLLWASLAVQQAANRHYGGVLKLVEANRDEFRVQESPESKMIYLTK
>TCRU_5722 hypothetical protein, conserved
RSSIYRSYQRGGWCPGSKHQKHMTMNPTLYLYRFPGPRGPGPYTMKYWWTLGCFPTGRET
PFRLQEFLLAYQQEHVPIEVEEWLCCFVKDPLEELCDASKDLFDAVEAFPEMEPTRGYRA
VKPSVTPLLATLKKFERQLGFKISPTGLRAVVSNTVLKERFLDDLFEYRKLIEREGSTPH
RRLARESLEKFLPGREDEESYVTAQKVDMVGNELGKFVGAVASPPDTTAADEKKLICLLT
TISEGCVDLGHYDDASSMLADALLFCHDSDTKAAAHANLAISSFLNGKFRQAEYNGREAA
LLQPEAKSVSGAGAKGHAVWAAAVAYQDDIDKAERIINDALSLYSSNEAIKEMAKQIQKM
RVAQSSFSSNGEVPETLRGSRYYLPSQQSQALARGSGKGFDNEFDWVLFKNKLYPNKMDP
TTNEMGSVFRRVGDMGLFISSSRSMEPL*
>TCRU_5723 Ribosomal protein S19, putative
MTSNITQERYEQLKKERTFHKFTYRGLEIDPLLALSEEEFKTLVHARARRHMNRHANRRA
PVLLKRLREAKKDVKAGEKPRAVKTHLRDVVITPEMVGSVVGIYNGRQFNAVEIKGEMIG
HYLGEF
>TCRU_5724 tyrosyl-tRNA synthetase, putative
HKYILQGNSPLSKAVLCVLRMFSVPMEQIITDGTHFAVNDGSVIHIGLLPILMVLRKSSE
TPELRAFVGAEAEVLPLVNQWISTALLLSADAAGARATACATTPLATHVFAEIERCVESF
KLKNGFLAGTPRATVADLLLYAAIHGHPNGLTEALPSTLAWSHHAQQDAYLEPILSAPTA
KATAAAHNASKVKKTIYVKPSEEEILRRRQEKEKEKEQKAKLAQAANTSTAATSSGTKDG
HTRKGGQKEQSQQAAAPDPNQIDIRVGRFTNIKRHPDADRLYVEEMDLGTETRTIVSGLV
GHYTAEELEGSLCLTVCNMKPKPLKGINSEGMILCASNEAELRLVQPPDGAKPGDRILFA
DAFNAEALKETKQLSSHVMGDLIGFLHTDGEGILRWRDIPAQHAHGVVRVPDITNAIVK*
>TCRU_5725 serine/threonine-protein kinase, putative
MAQVADESKAMASEVFMSKYRNVKSIGKGSFGEAVLVRSKTDGKRYVVKAIESASMTSKE
KRDVQNEIRILSAVNHPNIIRYHEHFEDGTLIFIIMEYADGGDLNSRIKEAKKQDPLRPF

EPKLVMFWFLQICMALKYLHDNHILHRDMKTANIFLTSRNVVKLGDFGISTVLQNTLACA
KTVCGTPYYFSPELCQNRPYNNKSDVWALGVVLYELLTLQRPFNAKSLKELLKKILVGQY
DPIPSSVPGEMRGLCAALLQVNPVQRPSINRILESSFIQESLRSFSVDLEKQAEKDRAEF
EEKRPYLPKTTPKPIQDRPKEVPKPPQMSEREQMAMLRGMKRENMKAMLAKQAEKDSTAP
ECAKEVEKDEGHLDVDDDGDYIEQKKAIVQQTKDIVGNTNLGGHPEEFGDGPSTSLPQVD
MITLSTGESVPASTVRGILEEQMGAELLNKAVELYNQRMMTSGLSNAEIQQELNELVGPE
YAHHSNAITKLCVYEGKE
>TCRU_5726 hypothetical protein, conserved
RDFLCEIRSMDTANVVEDVHNRLLKVLKDESARPTPSTHGLCQCSVLFGAFCRRLAVLDA
SVVKDAIKYVESLRSELIRVVSPVQEASFFAYAMGEIEAFSTMRRVKYRQRLDDLTKSIP
ASRWDVEKITEVMRDLSATWWRPENVRTYHELVKRPRDVLDASSDGVPMAVRWRLPLRDP
ISLGAIMIPARGSLCRHKEVFDMATFVRATQQTVMRRREVVEETANPRWVSGGEEELPSA
ACPICGRAAPLHSVRVDERIMEAIRQHAAKGGTICSDDCVVWDDSRCAYDVVE
>TCRU_5727 60S ribosomal protein L6, putative
IAIILAGRFRGRRVVILKQLPRNGPLVISGPMKYNGVPIRRIDSRYIIATSTKVNIKNVD
VSGITPDIFKRPKQEKRVKSEGEFMGDKAKKAAEQKAKKTAKAAPKGIVSDARAQLQKTV
DAALIEAIRKDPLGKEKAGYLHSVFTIKPGDAPHRMRW*
>TCRU_5728 succinate dehydrogenase, putative
MPSAPLTGEVARYSSPLFMYRRILKNAAPKPETVFTAKDNSKTAFHVLTQRPGFGNNPYA
VSRWYLKEKVHSSNRNRLEGLYECVLCASCTGSCPQYWWNREQFLGPAVLLQSYRWLIEP
LDRDYDSRVKMFEHGPLVNFCHNIYNCSITCPKFLNPAYASKEIKRMSSPVTPRVPPPLD
AKI
>TCRU_5729 hypothetical protein, conserved
RRAMRRGLCSSTMVGRTLVSFGSCFNSRWHGSVGDGGAGRGVLNAVEMTPPPPRPAFYVP
PEERDADDASLQFLHRKKQSADGRCEAKEAGTAVGSGKGGETRLHPGQAFAPELHIRPSR
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CGESIFGVRDTFEGDEKCKKGSVRGESSGDSGGGSAPRKRPLLREMELDLRRLEYYQGTP
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LEAQPIDYLRASKPLKVELSSGPRAYDPVTVMQKLGVMRFQGYAFPPTTELGKLRDSEGR
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DRQTAFHVMMSYPYTDWIHVFYVVLVGLALYELQTRCGAYEFYDEYLGLDLRQVPRLKKP
FLVGVTVMVMVVALFHPLLVASIATTRFYRIFMRRPIGPP*
>TCRU_5730 oxidoreductase, putative
MKSMRAVTMRAFGDVDVMHISEVTGVSLSRPSDVIIRVMAAGVNRADVSQRQGHYPPPKG
SSEILGMEVSGVVEKVGENVKRFKEGDRVMALLTGGGYAEMAVAHEGSVMKIPEGYSFVE
AAAIPEAFLTAWQALKLHGNLQKGQHMLFHAGASGVGTAALQLAEKYFRATAIATCSSGK
VEFCKRFAKFVVDRSPDASGKCFSSKVRDAVKGETVNLIVDPVVGGTYLQEDGEVLAQDG
KVVLLAFMGGAKVSLDVMPFFRKRASVIFSKLRDQTDEYKEALVRSFEEEVIPYMTRREI
VPVVQCTYALEEVAAAHKLMENNKSNGKIILTV
>TCRU_5731 cyclic nucleotide-binding domain containing protein,
putative
DEPVVAGIEVDRLSFINTALCAVPGNTLRAFFAPVMAVRLSLLRRRRLTQRHLSSPPARS
DKMFQEGVRVLTKALVDASLELLETPMPLDEKELATALRGKLTPVCYEPGAVLAYPGEVP
EGLFVHVVLSGSVQVVNYQTQNRKGPIADSSKRQYFFSNDLLRLNGLLGLQPELFRLVSA
PVEIPGDAASDVVSNSTVSTSIQRTLRRASRIIGQPTLLATRTELFRAPYVCCAAEALGL
EPFRLATVTAEAASPDGKRETNCDSRVTVTMRVRANDLHNALIEIALRLRDKSKTPVSQL
GTLRNVPGLLDYIAAARVKSISSHYPLNEILMRQSWLLQDTPAHTIRFLVTHLTPRFYFP
GEVILCPHSMSRQLCFLRRGTLTIEEPPSTGFRGAGNHCCGDYNPKRKILQEVPVGASFG
ELSVLFGEPRQFVLRAQTACDVWCLSCQSFAATVRRDDALRRNLLSKAAALRMRWLGEQR
YTSSLARVLRDSCELFREAPDSFIRLVQERMEPVVYPPGTLLTSISTRCTEMLIILHGRV
TSIVDGVAEYGPGSVIGEPTIIEHRWPLGLVSKSMVEGWKLTRLHLRDALRRIEILRRHS
GEVGTHAPQLMQSIFVPPVPPCELDAVGRSRMPVVDPPPRGRTYMEFARWLAEIQLKAMC
FQFRDFVKWSDISYNTLPGEADERPSTGPPTESTEAANFGFINYKAVAAGNGVKALRCVK
KNASAQPKSGRAVNTGSILPFYVNPAIAHQPFTQPYLRKPPSMFGGEAEPLLARQRALAA

DQNASVRVTSMPQLEKLKKLLENRDKLRRVETKQQELAEMQQERVDLGNVSRFGCPAPVH
IFLRGNKPRVQITVEEAIGVGYVLQFPDTKSIQSCVSNIDSDVTIGLPHHRQRRRDMALT
PNFRHHRRCFLFAASQLKEKSKEEAMLKEAAVRDAEKKENAQHLATLLMNEMSEKQSSLC
ILRSAVVGEGSNTSAPEWQRNSLFKSSSRGTLTPKRQSIASRHCSLPAKEQEEPAFLRQL
RENPERAMNSLRSKLSLPRANTDGEAAENNFSRSISEANNSSNTMAQGNDLMERLRGVSG
MHELKKMEASVNGIPPRRPSDKNGEKETDKTGGEDGSPLASFIADENAPLFVDGYGQLGN
LESGAVEELPAHSKSSVENPPLETNYWDAPSVSNEHTRDDNFASISRSFVMPTVREATLT
MRRMQRNIEGLNAVAEEQKRERLQRLRRRVDCTDFLLEDASILAEYQRIVEDWAANYTQH
ARDPLYVSEIPPLLLPEAGADYLAEEYQHIRRQQLTELIEARGTDGWHGEIEAKDRRAGK
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>TCRU_5732 hypothetical protein, conserved
MEFEQLEMGRNCLTTVIARQDVGDYYDILHPKVIVVSHFEYPPAPPTVADTIPLIARGLR
RATAEKAKTKTAATQKRGTVAGGVARTRESGPLGANRAAGTESMATTTTAATRMGATSDS
TLKSEKTMNVGRGSKSFDDRKQRPKKGGAGKYEVDIVEGPLLATERLYRILYWMSKGKHI
AETNVEMEVRKAILQESEKLPPPPAPKNEAERYAQIGRQYTERNQRLSRFIMTYGRDSLL
FRDECYFEDGLIVTVHRYMLTVQEMFAVLGLSGCEHQPQAQRRMEEILAEREDFYSARKV
RVDMNGHATLPLLDFTFCKIPDSLHLLQVRPVSGTPHLPRKVQPNVEPQFAQGVFLNQQS
DPSRPQKEQRVIIRARNKQGDEEVYEFVESAKSRFGFLQDPKRAVESSLESFAGKLKSVY
ATTSVRVSGCEMESTEHFVPVLRRLVVNAIMTIRALDLSDNHISILPDFSLLPLQRLQLH
QNKISDWSQVESRVCPLPLLQSLTLHGNPIAENEPQYWQKALSRLIRHPNRVVRLRQLDF
VTLTLQDYNMAGAFELFETGNPRVLEASR
>TCRU_5733 Ring finger domain containing protein, putative
MSRSVPWRTNCPQAVKDIFDRLPSCHLLLVRRIGPTSFILSGREGREKFRTSIGDPHECS
CGDGQELCLHILFILCKVFFLPGENPLVWQRSLVAAEIDELLRAEKRVRNVQNQTGATGT
VVPKQVEQGDVCPICFEDLCNDSPLCYCQASCGRHIHAYCFKQYKRHNFGAFLRCPYCRS
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ERHDGRRPSRVQPIQEAPTQIPAEVLPLMYREINPNDYEALLQLDERNIRRVLTLQEFMT
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IVSDVEDHVAQRSSSNLPVLRSYNRRQGNRQVPAVHSAVSRRTVRTISRRIERPRVASTV
SLPPIELQVLSLGHLQRREGNSVRFCYG
>TCRU_5734 KREPB6
RLTSSLLLSRLPVNHQQRHRGTVAARDFMTAGLSCSNSNNSLAYSWVWNETENWCSLCRE
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TQELIGESYVDYVHAPTAGKDNLSALMKYYDRAEHYERRLELYACIQHLIENGILRTDRA
SLSGGSSFHGSLVTFKELFPNLVNIFPYADAKEISALTQMIASTYNSETVFDLCNFRMLV
PWDQGQEAKTTKSNVPPTTGEHRGDFISDSAVGEYSYHWKAVFCRGVMGQLRWALESDSV
ACPLQTGEVKGGDFRDHYLQVLAEHTCRALLAEMVFCRVSEYVVRVEGVWRQRGQEVGHN
PNTAGSPNEEDALLKLTSNWGMLKYMDDHFYEPSFGNSLPNDGIPK
>TCRU_5735 TPR-repeat-containing chaperone protein DNAJ, putative
RRVSTDAMAELPLGVVQAFEELCEAHRRHQKPRVFTSPEAGATKNAGDDSIAGRRTVRVK
RNDAIPGSRVVKSIPSRTNADSINAAKPAAIEQEVRDIGEEEFLQREAIDRMEADERLEL
LKKHSASVRNIKGRNRNSSKALKAEADATYEKAEYTMALELYSKAIEQQPLDRLTRLSAL
HGNRSSAYFMAQRYSDCISDCLKVIALEPGNVRMYTRAAKAAAIMGDIARAVAQMETIPE
NLITDSILAEKKKYKSGLDLFQRAERVFGTAEGDEIWLMLVAQFSDTIPFRLRYAESLFK
QKRYLKAVEALEVVSPSRRSPKLWYMMANCLYLSGFEHFEKARSCLTDVQQLDDNCANLL
KLINLVDEGKQKGNHLFQQKKFAAAVEHYTSAINAAENNNQILRILYCNRAAAHKELGKF
REGVEDCTNAIQLDAEFSKAYARRARCQQQLNNFSAAIRDFKSAIQYDPSDHELVRELRH
CEHGLVKEAEREKDYYYVLGVSRNSSEREIKLKYRELSLRWHPDKCIALPDEERAQAERK
FKIIGEAHTTLIDPVKRREYDLKLDRDRMTRSGAFSGFATYSSDTFRGQASRYRSGTSGF
W*
>TCRU_5736 PHD-finger containing protein, putative
STSSSSSNSQVLVRRNRMVTRALIKGRSPLGPIDGPVGGVLRCVCTAYLVSTQETLLECY
RCRNWCHPACVGVDHAELRRYQAENNYLCPFCTGLHKRFRSESQAPAPRQLPIRLREVPD
RLPFGSVMRLRHLLKVTTRAAHEAGFLVIDLPVVLLTDKMEKECLACCEDAIKEATFSEQ

YPAYCLKEVREQAHSYVQGTLLRCKQSGRIVSMVLSNGMDVYGNLRHTITQLKGGINRGI
IDRRHQTTFMASCTKLTDISDFVHITLSATHREYQKRGLARMLMVLDLLKWALRGRTRAY
LNMALQKRIVDSGTRLECVASPASRRLYESFGFKDVYPRFDRETDEARWTPKEADMGRVM
AHLNFVEDVVQMAMRYDPGSAKECVSNGKAAASTANIGGGVIRKA
>TCRU_5737 Domain of unknown function (DUF4505), putative
MPLARRYFYYLNERGHLFHVFDIKGLVEHTRMPSGPTYLRDRSFLDFFYRRLQHNSLEQC
VADGVMCKNGTDVMCLDDGTCLAPQEFLRHFPYVSLCGVERNFVKVQDSPVVFTDYEFIC
KEEQLSGVLLFAGSLQEPFQPAALTVTREGKLFHPITTLKRLQRGTSIAENKGLVGAQVS
LKLGFDFVCEELDNDGQYVISWGGKRHFIPY
>TCRU_5738 conserved protein
MLSRNTWIRVMTPRVALTTLGLPSSSLSDISHARVKKAYIAQTLRCHPDLHPDDPDATEK
FRRLSEALRVALKSLEMKLHAGMTMKNVPLDDSQSVLDALRHAIAAYHHCRDATRSGGGG
GVEAHHAEERHDSFSSHSLEYVSSVCQREALAMRRVKQFCEELPEVLCGKSCVLFEAVAF
FNARYVEAMSRCVLRFSRNLPIIVNRVVKGRKKTVRYTRNQANSGFGTGSRPCQQRIEDM
AMKPLVLVGALLFSQKPKSKAEVFAAQSRENGQASFDPHEEVKSTCGVMSEKEIKICEEL
KCTIYPSDSIGEITEKIGRWEAASYERLQLELAMVDTTSLLSGMLDLTEHPLTVMHHLHL
PKEVSEKVSLTLQKIVCGFCYHCDEPTHENRDACDSDEGGEEEQADEKRIADGIRRCQHL
ARVTTSYIEGNITLIWDSETPLVESTEEVAVGDGDDLFWRCIKRDEMNQDIVVTRHMSCC
TAEMIRFYVAVKLSKDVGEFLSRLVAAMEIVKEQAEYAHSLLPQLLAIREKVVNEEFIPR
ESNPRCDENTSPLTEGREVEQGKSGTCQAPRKKKGNWASTTELTHSKDSDCFVEHAPCED
NNEEEAKKHMEYLYRGTIHCFPRVFSMNTAQELKYWQMLHENRIYLAQHAPAIHPINVYY
NCLPYKPHPNALHPEKNSFNEELIGGWMGEAGDGADDAVITHKELESGSAFREWLEDVVE
QSSLNSECHRIVDEAGVGYVMRDPALPLPQYLSFVKVFCAAAGVRGILEGKAGKTRTVTP
EDTGLVIVVGTECDVRDGGRLLVPWWMDPSLLLALLQDDCQD
>TCRU_5739 glycerol uptake protein, putative
MRRCFTNTVSVQDFWRDWHASLNLWIVRYMYIPMGGNRMKHFNIFPIFFFIAIWHDVELH
LVKWAVCILTVFVLELVVGSVWHSSRFAWLRRSKYQRFIRSFGGLFTVFGLIVANLIGFS
SPTYKSSERQMDNVISNSLLSAGPLFYVAFVVFLYCAAAAGIITRDAEAAELLRLKKRYG
V
>TCRU_5740 Vacuolar sorting protein 9 (VPS9) domain containing
protein, putative
AKYELQKNVLLKAIRPGGLFYEYVDRGPVEMLCVPHQLFLESSGIAPYLRLPSTHSHNSS
NATTTLRIGERDVALTPEQHQQIACITREAFLDYHLVHFDGVASPAFVTLRGQRGEFSAD
LQSVARYGRIGASKVLCELSPLLEPDDASVSAFHPCKLHILVLAKPLMDDEEVHNLLSAL
QRILPPMEGAGTEQCQNDQKTGVEQTPGPSFLENCFSREAILNYRRTVAKDNDVHSREFQ
EMMKLPVCAPVAKTISNFVETIQQREAPLYDNTDVRRAISFCLDQCRRIPLFARDASKLH
IAAEGFEKYIMTKLYWRAFGVDPEEQERNKELNEKLRRLSPLVNAEELDALKEVEEHHLW
GQAMLDLEGMNFFKTPREKLRCAVRACEGLAKAVSAALVQNKKKCFDGNINNNNDNIGNN
DNSTSMDENPVVFGADEFLPCFMLLVLRASPRDYYLHVHYVKRFRDASLITPHESYCLTN
LESAAEFWRSYTTSLSRQTDTSRPSTPPKTIVEDLFIAPVATSSPVQPADKDELCALTQQ
TESKYGQLSNSSLQHDFFSLTGDVVPEGINVAKLLLEERKPFENLTVAELRGIVEEARRL
LAEK
>TCRU_5741 hypothetical protein, conserved
MKYFSCQPDSHNGFGLLIGHTLMYFTVECDQPETVGANISNSIISSSSSNNNNNNNNNKN
NNNNNNGSDSNAATNSEKGTSRAHIQYTVTLPQEFGLAPQCFSMANRSLYGFDMAFVGAS
TGVMAVVVMATSSAIYVPGRNIASLRTFPTAAATPAAARQGDHRAASHVHPQSNTGTIGA
SAFYSPSLGQMSESDRGVGTITWMRDKPIVFVGFMSGRVEWYYVTIAASTQKAEMGKGHA
GAATTPVTGTATVATSAVEECPSRGNRSVEGQEKAAGWTEAGSVTRFFGDCALPPSIWMH
NSFWQRGTIQKVHENGEGEGVRIRLHLSCAFYDTGGFLTSDWFPATGHVVAGAERAVYVF
STEQPGAPLYSVLCVGCSFLACHPCLPIVGCLSFGRSAETGKQPGACVLHVFEWTTGGTL
FLAAEKRTFHGVPRHDVYYSCSWKFSADRQLAICNVVEGAVHVLHLAKTEEGFETASQEG
TETSLSSSSSLPRPLYTFNREREAPIPLHSLINIEFISAATHALPEVTPPTTSLSLHNTG
GVLVREHMLARRMLHSSGPRRKVCRSHDSRAAARAARIQRGMATVCIIIMVIMITKGQVA
VDVVALAVETFVCTVPLRATIPESRRVRVPFPALLVSITRANSQPFQWTQMQGFPFWDQD

VLLPVSVGQFLSGAAMHQMDTGQRMKRRLVAGFGVPAAANVQALCEFNDPSDEDLRVLFA
YISIMETVGAVGSSGPVPSIIELLSLANAPNTTKLMALNLLPHGITVVCGSSTSPNDSRR
LLLLQLLNWIPSEESFSCGEGNNEVCEYTRCDELERAVAVEVLHNRRPRAVTLLQRHKQL
NSKYTTIAGLLEYPDFILNTLRGGAMEEAQECFLKQWSPWLQVVFLHEMNRTKIYTNVGL
PFWDRIAIAVILESDTSRLISILSSTFARECNMLQRLLLLEGISERTFPLMQMIVDCTGD
FQLAACLFARIGARDARSASVSNTSTPLDASLQGRVDAADRIGAVKSEYLASPWDLWAAA
YRTFLNDEEEFVKRTMFDLACQQLRESHVLQLPPQTTTHQRQHERLRYPEVQFYSRRFFQ
PSLSSLSPFKGALSAKTDPLQHCALSYPLLATGHSHCSVCSSLVYLRSSCAQDSLAWCTA
CLHGGHANHLQEWFSTHRKCPVYGCSCRC
>TCRU_5742 chaperone protein DNAj, putative
AFASAMTHARRWQSSTGAADYYTLLRVRPDASADEIKASYKKLALQYHPDRNSDPGAEEM
FKNISEAYHVIGNKERRKEYDGRRAASSFSGGGSGSGFSTGYAQQRPPGYQHMSKEEADR
LFRELFGGMRVDQIFRDFEEEMRRSSMGVRQGRTSSEFAENEQAFRPFFRGGSTRVFTDA
HGNRMEEREFQDSRGTTFKVRTISSENPNASTNQRVEEFYGAKAEGSRDGRFHYGNSSFN
VNPRGATNDFGQAVFGVRTHGRHPFVGMMIIAAWGVVIGTFFLAVFAFLFSHPIFTMSVL
FLIFLGRMRPF
>TCRU_5743 hypothetical protein, conserved
VLRRAVVALRDALNGGSSMTLCTKGMERSLDSHRRRMSWTA*KECVPGVVHSSKEKMVLD
GARRVDVDCVDRASQVYPLEALRATVASYEYNTSRGKNIFNAPQAESNVLRQWVYREEWQ
EETHDDEVTRVVIHFRRRETTTQPAPIRLADFPVTRTVLFVATVPPFLSVGADVPVDASS
YRLRTHPLIDAAGTP
>TCRU_5744 GTP binding protein, putative
LHACLLLLRRRGAGIIGLPNVGKSTLFNALTCSQQAKTGNFPFCTINANLARVPVVDDRL
RRLAAFVGAQRIVDVEIDLADVAGLIEGASKGAGLGNKFLADIRPCTILLHMVRCFESAR
DGFDAPTPLDDISIIVNELVLADLEAMEKLLHKNRKTRRAGDAALEFCQRVVSWLQDGKP
VSYMKLKTEEERQWLQQYQLLSAKPMLFVLNMDEASVVTGNKFATQVEEKFDTERTCRVS
ASLEEQTSQLASRDERLMFLQEYGIDLPRGELLLRNAYRLLRLQSFFTVGPLMAHGWTTK
VGATAKEASGEIHSDMEKYFRRARVMPYSEFLSKPNLEAAEMQMEFVDAKYIMKDGDVMI
VE
>TCRU_5745 G-patch domain containing protein, putative
MSSIAKRMLERHGWKEGMGLGKNAQGVSTYVKVVRRDPHTTTGLGHAADATQAPQASTFS
VELDAVYADMSRTGKKKEKRQTGAAVSIDVEAEVNSPKDVKREKRGRQHSTGSCNSGRIS
DGNDDRCDRGGSSSDDGSSSDDEIRVDITRLKDDELLRRCGGVRLGRTGRHRFFDGKLRR
IENSQR
>TCRU_5746 hypothetical protein, conserved
MRSVFEIARSHITLPVSRDMNALRRVLRDWHHYTEKLELQKKTTHPAALCVTVHPSRNST
ASPPQGVSLHPSLRVAAGGAYTRRVSLQLWTAVLPWEVQRGLSMSELRLSSTLMDASDSK
QEAKKENENCRYAREMQEEEDDPFGVVTAPSKSANGAMRTPPCGTSAAAVTAPFPGMLFV
MDVDSAAQGVSFWSGAIAQPIDVAFISPIEPAVTNSRSFQELRQRQLAAVEDGGGGGGGG
VDEKRAVHNIARFFPDGELDSPTVTFALQSYSHLDPFPRCDKTGGTRRRQHLAQPAGADR
RDATFAAGGDDHNNRPRYVLETTRYLIRDSVERALQECRQQRATTAGALGGKNKSVHEGN
EEGMEVTITLELSDGLKEELREKARLYTNYVMPLEEHIAYHIRHQNSSVVGDGNNDDVPR
WEMGAEGKTGDDHALVSKFAAASPSFCSPATPVGVTRGPIHPSRPNTTGRRSVMLLRSPK
LAEEHEDVPSHLVPSVKGRHEAPVLQQVEREHGQLISAKALARYPNTSSHMPAIPPIDYE
LFDLCLRLGLCRQDTIYYFYGRIMRAWQKELHRLRKSCDEQNNSEIPDADVRRMFLLVRD
PSLQVPEELSACVEAVARRRNIAEKA*FPV
>TCRU_5747 calpain, putative
LDPAPEGIPIQDMLLMGDSAFAASARERMKLKSNPVANASKISALEEEMDQRAHVLAKQL
RAKERTFLDPEPEGVPLELLSLNENEAFQELERELRALNRKPRKDAKAIVALENDLLDRT
NVLAKELKENERNIFLDPQPEGVPVSELSLDLDEPFHTMEVERLRLRHEDPRANVTKVKE
LENALNDRAQELARLQLRKERAFQDPEPFGFSLEELGLGFDDAVVRGEAQLRELRKEPRK
NAAAIKATEDEISKLVRDIARKKAALDRAFLDPEPEGRLVGELPLDEDKSFVAMDTKRRQ
LLRRDEDPSKVKALEEEMNDVAHEIARALNAKERLDYLGASPCGVPLEDLPLDLDQEFRE
LEAKRQQLKRDPRRKAALEDVEAALNARTEEIARRQLAGDRGYLDPAPAGVPLSLLPVDR

DAPFQALEAKRAQLKKYPQRNAKSIREVEDDLNDRAVVLADELKAVEREKFLNPKPNGVP
IDDVPTNNDGPFRDMEIQRLLLREEPVRNATAISNLEDAMNERALELAANMLADERAFLD
PEPLGIPLDDLPLDKNEEFLAMEAQLRVLRKDLVKNRSAIVSLEREMCDLAKEIAAYELE
KDRDFLDPEPEGRLLQDLSLRKDKEFHGLEKERYRLKKDIKKNAQKIADLEELMNERAHQ
VAKALNASERKDYLDPTPRGVPVDDLPLDTDEEFSKLEADRAQLMRSQKKHAASIMDLED
ALNLRAEELAQEKLQEERSFMNPEPGGIPLKYLPLDEDAAFHEKEVERLALKAENLRRNQ
GKIKIIEEEMNNRANELAKEMKLNGRQSVLEQVPKGVPLDILSLDDDMPFGDLEVEYLKS
VGDGEDNFKARDLADAMRKRAEDMAAKVKADNRMNLEQNPLGIPLEELPLDSNEEFDRQE
RKLFELMKEPSKNAKLINDAMKRLNALVIQMAQEKAQKEREFLDSEPEGRYLSELPLSTD
STFLGLERQRRELKKNPYADEDRVADLEQMLNDRVHELAKKMNATERPNYLAVIAHGLPL
SELPLDGDKEFGRLEAERAYLCHDRKGNASQIAKVEAALKKRAEEMAADAVRQDRMFLGD
EVEGVRVRHLSLDDDPGFTRLETKRAALKNRDPLRNAKAVEDLEGQLLDRASAIAKELKQ
ELRNPLDPRPLGIPLGCLPLDHDERFHALEDGYRELGADPGNRGKKDEIIDQLNERALEL
AQEMHDRERSVLDQYPEGVPLSALPLNNDEEFTALETETRALRSSPISRGRALARLKELE
DAMNRRAAELANDSRKAFCDPEPEGIPLTLLGLGADEEFARMEEELRYLRK
>TCRU_5748 trans-sialidase
EKDGKVTDRVVHSFRLPALVNVDGVMVAIADARYETSNDNSLIDTVAKYSVDDGETWETQ
IAIKNSRVSSVSRVVVPTVIVKGNKLYVLVGSYNVRKATGLGSLMEATGILLAVGEVTKS
TADGKTTANITWGSPVSLKEFFPAYMEGIPTKQFLGGAGVATVASNGNLVYPVQVTDMKK
QVFSKIFYSADEGKTWNFSEGRSDFGCSEPVVLEWKNKFIVNTRVDRARRLVYNSGEMER
PWVEAVGTLSRVWGPSPKSDQPGSQSSFTAVTIEGMRVMLFTHPLNFKGKWLRDRLNLWL
TDNQRIYNVGQVSIGDENSAYSSVLYKDDKLYCLHEINTNEVYSLVFARLVGELMIIKSV
LQSWKNWDSHLSSICTPADPATLSSERVCGPAVTTVGLAGFLSDNATQNVWEDAYRCVNA
STANAEKVPNSFKFAGVGGGALWPVGQQGQNQRYHFANYEFTLVASVTIHEVPRDATPLL
GASLDSSGGKKLLGLSYDEKHQWQPIYGSTPATPTGSWEVNKKYHVVLTMANKMGSVYID
GEPLAGSGQTVVPNEGKPDISHFYIGSYNSSNMPTESHVTAKNVFLYNRQLNAKEIRTLF
L
>TCRU_5749 hypothetical protein, conserved
LCRQWILSHRDEQARARAVVDVARELFYSVMVRCNSSIVEDGYDQMQLLALKTAASCFLL
EEIVKALPRHGILRPCVGFLLRAVYVPDTPEMRDALGGTLAYPFMLQNFPLEPATRTLLA
RYARKTYFIAHHELTQKVIVHAHTNVSRLQHFKRLPRVFALMSVNWVKFLLRIILRAWRH
LCLVRRQNEQKHRARWARRFAAERIRFGVQRWRVYANIRLQGAEAGEVMKARIEALKMST
RSLENEINALSEESARLSAEIESKAELHVLFGKRISEIEQEYKNTLECVREMDRVGSRLL
DSLLLKTPFPAEAETLSPLELLVLWANTTLLEXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXPLGPLFLSSTDEDFVDAIDKIASKETNKQQINVSEVAEEDLPFNPLLT
ETPMVNLPMHCFLALIRAMDYEAGPGKEDLKMVCTSEMRIRSLRSKMENNAEAVDLKDPE
TAAILESEVVVGHTIVEAYEALTGGTCIVTGAQLMTRKRGIQLLFLAALMRHFSNWMENQ
VRKQRSVEDKRPSLATAPTLTTVEMDLLGAPKKEQEEEETPTVDSHLGVRDRKYFEWYHP
PQNHVDWIARVQNQRQWIAASLSALHEALNVALEPNTLVPMEVQGESPEFLENVTLKRLS
DILPKKAITSGTFFLRLARVVENALPKLRALFLQYSLEDRTADGGGDFSSGSNSSNIGSR
YITSIGFWNLLRDCRVVGGPGKINRAILRQILGNVFGTSVAAAGNGRVREGQNLPRAQRR
ILSALLSPVSDVRGSQYRLRFNAAEFIEILLRCAQAWDSLRHRQIENESKAFCKKTSAVD
TNTASLASLPGKGSDVLTDAEADDTVEDAKGEKKEIRYEACDMTWALRPAAVREFFHEWI
VSHGFRGPTLDPFHRALRHPALREHIMANIDILLSLFTIYTTPKEAYGMPTKIPDMETSM
RRLVLDKPGSSIQQKERDSFVAGAMTSVQSGNPGIVRVMTVRDVKRMAKDFDWLSIRRVT
SSVIEDAFFAICPDTEHEFGLIFFTEWLDLLCVIAQYHNPDPTVPLHEKVPPFFKEHVTR
YHR
>TCRU_5750 hypothetical protein, conserved
SSCNSGSEMREAIAPEMVTIEILPAAEEHGSHTAAGVGDSHSDRDGNMDCHRCEVDMSSR
ADGTSTRSTGDELRQKHYWDVTSIDNFAKSRVLNYVRRTGNRSADVFEVSAEQMLGRTVY
RARCKLVLPSPHHFYVAEGIGEDEKDAELLAAMHAERVCDALGVPLFRLPSMQQKHAENA
RRQGRYAPMPGDPIKPENTIAPPPLRMLTALPDCGGASSTDVADGASVFSTTITEAEIIG
DTTSIGKESRCVPNPLTEHVSSLTPPIDPVAATKATPAIQTTDLEGDTLDFSGEPPYHST

VHYPWLSPNTSSNQGGSAAAIGGGGTAISNTVTFDPTEGGIWQMVNANSTRCSPSQDALL
LPCVYETAAYERLKDHFLHQGMALKDRITISHVAVPGHSVRMYVAEIHLFDAIVARGKAQ
TKECAEHMAAMHAELLLDALARPLFPQDNARQARHAMAVERFGRWAPNPLTGDTRHPRPH
DPLPLPLKQQVGGDEVWLDPQMLRRYTYQRSVGERLIAAHNDINNYCGDYIESNPDPALL
AESRKALESWQREVARNPHPDLFVITRMGEQFRASTLLPVPKVFGVRGGNAVGKTMEQAI
DLCALHAVDTLCALGIPLFANPSKQQAFLEQRRRMGLVTMEDMAKLSACKGLVAILAPSF
SELESKSPPTEKAARPPYLPGYMVEGNQPRPLPHICDTLQILQLRIPEDFDVYGENLSDE
AVLEAGNEAKLCVQNYLRYHLPKDSNVNASIYITGFARQVSVHNIAYLPLVLPQKDRNVP
ENTTSTKKKKKKNNNATADVPEGIEKTNKADNAPPSFSSVAASTANDGDNNNNTGSIDHV
AVVTQSQATKGEEGDTARKNAGRLLAVGISLKKKDAERMCYLHAVDILRSLGQDVLSTYR
AGLPRRKQSPTTPQSSTTSTPSQAEDGTNTNGGDSSIAANNAQPDNMKPATPSAPKPYMH
KLMKQFITSGRHYTPPKRRFQPGPNSPF*
>TCRU_5751 WW domain containing protein, putative
IHLFVDGDYFLSGMTPTSEEAVRGGVEDMLDAITTQLFGQKNRGTAAVAVEQRIVFFSSS
ILKALEGQQSQRDVLITALRRLRFQTIVLDSISSRAGSPVDAAICTKTMSILAKAHGALN
VNIGGGGGGGGGGGKFMTLVYFAANAYISSALEWAHDAGCGVCFVVYNGDSVADELMAY
VSPTYGSGGGIATIAKGEGINFIPNTGAASAALAALQHEGKELPLAVLMQLKQLQQRLTG
GDAQVGNTRNAAAMPGTDSSASSLIPSASAGGAASLLSPADASSRPHPPPIAGAPDPFLP
DEDKSAVKKKQHTTAIDATAPSSTSTEEPKLDTLTLGTAKNTGDDAKQTAHVLPAAGTTT
PMRATATPDVAKPAETATTPVSMAMNTATPLPHAPTATTDAQPKSTAVSAFPEPEVSTRL
PAGWTLMYDRQRRRHFFFYTNADRVVKTTWTHPGGLEEQMDLERQVEIWHRKQQECRQAE
ANGNERNDHTKPTTTSTAAEATTGAARDWDECVDPKSGRKYYVNRYTKQTSWTLPTAVAS
VTSNNPAMNAAEVRPNPMAATTKTNTLPPFWEECVDPKSGRKFYVNHQTRETTWTRPQAT
PVTTPQHVPQPHALTPSHAVAPASIITALPPFWEECVDPKSGRKFYVNHQTRETTWTRP*
>TCRU_5752 hypothetical protein, conserved
RCFTPRLSAAGNGVWRGFRQMYEEYALWRDRRDDERYTAVSEEGEEGITLSNRRICANPN
ACPRSVLLVPAECIVEALRRERRGGVTADAVMFDLTCCRGSRGEARDNILRFLQAEEKGE
KRGEDMSGGQCSHDDERGRYLIRVNSPEFDSANGFLDMELAAVLGERIEGVLLPAVTVNT
YSLVEEYIHPSHHLWAFFDTPLSVVQASEICRQGHYRYAVMGSRRLAEDLHLPIGGITYG
DTYRGDNNSENATPAALLGSLPLLNSSLQVLLAARAFNMNILDDAFEDASDTAGFSRDLH
LSRSLGFEGKLVINPAQLASCHAAFAPSAEELSWARGVQQRMARRYAKEESAGKLEAAQW
RRAACLLERH
>TCRU_5753 protein associated with differentiation 3, putative
VEVLATGPQKAIYEPHRFAILLLGSYGCICSSLSYAFNLIAPEMQSRYDLTGRDISTIST
VGLVVGYFLMPYGFIFDHFGPKPIFILSMVLFPLGALLFALSFRGTIEGSVVRLSVFNAI
LTLGCTLYDVVYMMTIMSHFPISKGPVVAILKSYIGLGSAIVGSIQLAFFDGRPDHYFYF
LMVLFFVTGAAGFFLVPLPSYHLTGYEEKHLXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXAYLGWGRTQRIIFASILIAVLVALPLMALPVSCLERRETQREE
DDCGGTERPSAGDEVANERAAAGGPPKKVETDVDYIAPQYQTTFLQNLKTLKLWAFLCSF
FCIAGSGFVIIYNASFLYAALADEEVDNAIKTLLTVLNGVGSAAGRLLMSYFEVWSQKRK
AEDRVSIIVSVYFADVFVILSLVLFLVVPRAALPLPYLLCAIGNGFSSASLVLVSRTVFA
KDPAKHYNFIFLALVCSTIFLNRLLYGEWYTREARRRGVDVCLDCACVQLPLLVMLGFNV
TAFISNAYVHWEYVKFNRQVLDERRRLFEEQQ
>TCRU_5754 CRAL/TRIO domain containing protein, putative
DIGVTAYTHQAEVDELRQRLNIPHNYFDCWLYGFLENKKFNIEEAVSKIRRREAFEREQI
AQHTMTDEMLQNMRKGIAQIIGNDKEGRVVLYVVTARDKPTASRRAECKMNFDMILSYGT
RLRADSKRCQMVMLINQEKASLWSNVDMTFQADIALRIAKFFPGAVDKMYICNMNRTLAA
VAKPIFSRLPAIVSDRIIIISDSELKAGRLLEYFDESVLPVALGGSNDCDHPQHWAEHAA
LVEGYYTQLKEAVLGGGLSVKEWEL
>TCRU_5755 Protein of unknown function (DUF974), putative
DMASPTAGESKTNSGGKQSVHSATSFSPAMLANPLTVRATVLRRPEFFEAASPELVEEGD
VLFDVLSNPLHHPSANCMANDAQTKVRRRSKAAELSVHGIGTVLSLPTSLGKFFVGQPFR
AFLSFHNAATYPLATMVFSIVCLHPTLHRSKIVNYECSHLEGKGNASFTVECLLKEPGQY
TLDVLVTYMDIAKEAKRLTWSFSIQVERAIIEVSRTIHVVPIITRHGKDTHAQLRAAGPT

LEEAMSNITLPTKKYVLSVCLQNVSSVPLFIVSVKLHTGGVFQLLPRPRRPSTKTESSLP
PWWPANVAKPRQDEREFGTHYTGGGADALESVYLRPKDKHCYYFELVLKPDILCSLPLQH
TATGAPAAVVPSNFTDVGYVEWKWCRANGDGGAEHSSRVRVDHLFMQPMLDFFVLNVDPE
TPTAGKPTTFDCVVVNYDSDKQFDLALRVRPDLLAPSFLYAGPLLIPLGLIEPRGTINFP
VSLLPWQPGWLVLQGGLELCDARAPATLLWPLQPGKTQPLPPNSSTILSSAVTDTPEQPY
PPVLCELLV
>TCRU_5756 Protein of unknown function (DUF778), putative
MTGRKGMGENRSVALPLPPRIDPSEEHYPFCIVWTPIPVLSWIFPFIGHVGICDSAGRIH
DFEGPYHIGVDKMLFGNPVKYWNISRMYVPTFYRSQGENPRTTEETCRREVEEYDAAVER
VTKHFRKTQLYNFFTNNCHSYVACVLRDHPLTAAGSFIVFRVAWGLLIHGR
>TCRU_5757 hypothetical protein, conserved
MQPAEGTFRYRLRETRARVWRALLPDDRPTPVFTLLVVILNGAQLVHGFDILLSMPCSAS
TAIWCALGVSNSIVNMIYAIAVMWRMRYRIEEGIPLESSTVRLFLLEPINIAFLVYVVWE
IAWMFSVSSLFMTPLVRDDCGTYLSVQLGCSFFFFVVGGIALGSTFLTELFKTPRWRHHA
DEVWRRKHPV
>TCRU_5758 retrotransposon hot spot protein, RHS3, putative
RHRRAREMKFTISTNIEDVLFKGRVRVKDVKLNDFLLLRFGGKGILVTNRSVSLEEFFKE
PARYIPDAEVLKGMKTTVCYLKMGRAVMKELDMEEVLRMLHEKGVVSLEQWRDYGGKDTV
TPLAKGTLDAALSEAQISTSVVKSTVLKGYYESVYNASWSHVVEVPGGEGTGMEVREGEP
PQSWNYKKVGDTLEKDDSVEQSSAALFRQMVLTSEKGWPYTWNLKGAESACVCYVNSEVE
RVWQIVKGDLTEWFSSQRGTDFTPKKRVLIGTAGIGKSMNAGSYLLYQLLHYDAERLPMV
AYFIGSQSFLFDKITKTVSVYRGDPRIDDVVNISSLRGFKGYIIYDATLASRQPPAGLPC
NGWGMIVVTPPNKNEYERWTKKMDATAIVTNCPEESDVRAMCIWMKRNWPLQEQAEYWKE
VRGRMNKVGPILRSIFGKQACDDRIKACQQAVYGSTASELEHNLGIGCCYSPIDSELSRK
LVRVVRVRRGNSIESPLNLLVSPHLERETLSRLENEMKQSDFIFFVLRFWDYAPPYIIEK
YAVSAFLNEDFLRAIRLKIKELRPPGRREPHSCALKEHSDTSFTRKEVLPPPERLSNPVA
MDHWVLYEPKVQNFPLVDGFFFVDSNPKTLVGLRMATAGAHHTNTSTVRHFTECLAAYFD
GWEELSRDLSWEIIYVQHADSTPMNEWRRCDYVNP
>TCRU_5759 exonuclease, putative
MPHHTKRAMAHRMANKERIACQHGQRLAAAQRGKNKQKSHAQNGHFLGRVPYVSIYDEAD
PLDRQLFDYIIVVDVEATCESNNDNYHHEIIEFPGVLIDVRRGIVDTRRSFRSYVKPWRN
PVLSEFCKKLTGISQEDVDNAPGLPEVVKAFERWYRETIPIGAKVAFAADGPWDFKNFIY
EHSILRDHVSFPGIFYEYLDIRTTFAHHFNRGAPIKLDAMLRRMRLRFEGRPHCGFDDAV
NIARLAVAMMRAGCIFDFLIVIPMDDDYHYHLDTYPLYRREEGSGRLDPDVVDDIAKSCY
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VMLLILVSTRIL
>TCRU_5760 hypothetical protein, conserved
MFTRTFQSSILKSEGHNLPREGVPQEPHKMTFWHSYIDPSNSEKERPVVDVSAPYNPLDE
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ANSFGAVGNPRTKFAWNLALLLGVVRVNIAGLIGIGGYFYSYEWLYTHGPWPFRIRDPSL
NGWKMAWGDGQSCYMARAVASIFPPLGYAFFMGRWKKANFWFTLLLAAGLQYEYARQYIF
SGNRLFYSFEANKEINRQANWGSLMPVLAHRVDPDTNRNASAAQFRYFRITSGTMQDTIW
ENAVHENLPLARFALRLPNPYFNWQKAPQAYNDKPYLRKNDLWEMPQVLN
>TCRU_5761 Nicastrin, putative
ATAERGFSGDVPPAPHDAAYAAYFRNYPIMRPCIMKAVFMAVKSDDQSNNSVAYRGCSIA
DNAVVPHGLLLLHATEVAQASMDGCEDNASSLQEIIRGLSIPDTVSTSGIGLVLSTSEKD
DYEEGGRKNRVKTNTQYDMTCFLAAVQQYNAVANKHTQGLMPPITAVAFSDDNRCCRFSG
DRRSGEELLLPREVRSVYDFVILYFPSAATSSSGPANSDWTALMNAAEFNRIHWAAGRRY
PQNVLETRNGMPLAELLSSPTRVRSCLEGPSPSCVPLSGWTVWTSTADMRWEWNETSLDF
EKKTRKGAVALLVASTAVSLVQDATPGADCPASAIVATLSVLEALRRVGGDDSRDVYAFF
FPGEHVGSIGSARFISDATMLECVHAGLSNCTALAYKENLNFTTVDFNAIDTFLVVDQVA
YQDAPLYYHVDSRVGTTGSAQQQKAELEMEKSGVRRASTTRLPYSPITTLLDLLPAVIAG
EKVFLTLTRYNTTFANPDVFTVVDKTTEHSALRPASVAEAADVMLRVLLPPTQNAAESPP
VTSVNRSLVEQLWGCFTENLQCKFLSAPNDVAEFMAPDYSVGDMANSRITDTQAAIEAAL

HRIGWTDVARSPAVPKSLRIPHGDWGATWEQDKDWMRLHNDSRYELHVMSFWRGNIGARS
TMVGSETVALIFLILSITATISLTLCIHVCVRK
>TCRU_5762 hypothetical protein, conserved
MRRTAAACGGFTMKYKKGTGLWDEDHVNDYKTNRYLSARATMRWYYEMERLQTRNSLNAR
RGTQSHNNNMGLHHSGRGAFEREVERHGLQVEKYALTTTTGATRVAELTLLRRLELEKKA
EEAMAKQRVAARQPAPSAWYDEALGPLNPEFLRLMQPHYEVEIKILPEAPLIREQQQ
>TCRU_5763 hypothetical protein, conserved
AALQLPRARWYARQVQRSLVDFECVRRLCQDTHMRTEHRRVAMALGCIYALNSSSSSGGD
GGGVSVTDVLLCLPITDRAATVAALLRFFSHYAVSSDRLHEALATVLNDRHATKKEAWVL
LQAMMAVSDVSSIVQLWGITEVVRHVFLGEGGSSVVHRERTMTALRFGECVLTAETLAAL
CEESGLWYESAAYHSFASGVLLEVTEEGKKSNRCGFGEEMVVLLRAVRNGEYTAPSSSSS
SPPIGTIEALRKEMSPVVATYTMHRVAAELTRNEWENGYDASNREGSGNRGSRSGSNVTA
LQYMRNAAPLSDDAVCAQAFKLHFDMRLGSLSTSLALLPSCRHDWYRTVRLMQHTHRAGV
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LSAGPWRHLAEAAARHQPHVGQALWSLPVSYIPRVAAAMPHLPSSVLSCWIRLLLRHRRY
DSVDVVLQMAAERGVVPEMMALVEVLESVYGLDRDAAQLQRVVRSVRSFFPDCAPAVFRA
FVERTAAQMHDKPSHSWSTGLKLLSTVSVLGLLHYPRSCLESIAACAPTPVVYAMLQILS
EEGDAAAVEGDGGAAVPCSSPAPLELGALRRLLRSAQMAGLRPKVDVVAVSCATKKTAWW
SSDTAVAGVPMATALYRMQAVGLWRHALQEVSWMKMSCVDGAARCDGVAVHHAVRLASFG
SDSVATLRRGVLAAEEMGRKKVGLVESGRACRLTRVDDAILISTIACVAGALVARGRWES
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FRRRRCGMPAGVRRIVKKMQMSEMFRWWD
>TCRU_5764 ATP-dependent DEAD/H RNA helicase, putative
MDEDRRRAKQKRNQQRWLERQERSRLNRAEIRELRTRIEELRALLDSAEGGDRPGGKQKE
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CFVVPVLERLFVEQWDTAMGVGALVLSPTRELALQIFKVLQLVGYKHTHSAALLTGGRDV
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>TCRU_5765 amino acid transporter, putative
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SLPEFWRSEAGNRAVTSAIWFVGMFSLSLPKEINSLRYASAVGVICIYYFIACIVVHSVQ
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MALCCIAYIVAGFFGYADFGDEVTDTVLVFYDVRRDVLMAIAYAGIVFKLCVGFALCMQP
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>TCRU_5766 hypothetical protein, conserved
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MEILAAFQTIFFSFHVCHTVAELAVLAHPAHRLSSAVDNVLSRTAYEGVRYVHDFILLVS
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXMHENMTEEKRMIAVAMSLVKSPHIVSSTTFYSVNRERAPTFLSSS
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GIHGGGGFTVQLLRMMEADSTRATMSVVPWRRALKFLPDPHEGSKEMVTDIKRFRFYVAL
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DLLLNGHYVDAAALVRRTPTLLRTREFYDACARLMKYAHHRTVVLFYDAYIHPEDELESG
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LHAKVTHDTSQFNNNNDDDDGGTNTKESLINILQRERELACLFVKIFSGTFSGVASELCE
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GSNSHHPIVEWRDRSLFRIGTESHAWVLALAAYATSRSYVGHTYISGAHTARLVKLITAS
GSLRVVIPAARNVFFHLNLSHPKSGEASPFLNAMLLLCQAVCTMKRHTMHRLQNAAEMDS
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MAMGDAVMGLYFARLQDGCLPNTYSIEQSLRLLSVPTVSPLLALQYAQALTLLPPLSNRR
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TLCALRGNAEAALRFVEKQASLHHVMHLSNALLCRMCAAVTAGISPTAKSLQSLSHIMQN
TKFISPPLRYMLTLIVAEQSTFWEIYHTGGSDPKKMTMMEKKMMTIGSPRHVAANEVPTS
VVLRSVSRTYELVRQHFTPPDATMLHGLLLPKHLAAAETKDDHKIAHEDEEDDDGAVRSQ
EKEEEEENEEGASDSVAQNVAWEQALKLFDIFIRNAQPNADLSVPFEALIEIFCRGGQWN
TASRYISLAGTPPTCTLHTSQPARSREVADDAFKKDDASHFFSRHVVVDCFLLKRLLDAM
EAARQRHYRHGEQSPSEGVQHGCGHPGFWRLTLHILQQQQQQMLLLLPSEVTSDGNEKSD
VAISSVTLLAIMQEI
>TCRU_5767 YjeF family N-terminal domain/YjeF family C-terminal domain containing protein, putative
EERLQSCVWSAAWLRQAEEEAAREHKITLYDLMQRAGKAAFGVFRREYPSSRHWLILCGS
GNNGGDGFEVARLAADDKLRVTVLAVKGTKPLPPEASAAHAALLKRGDVKIHDAGQWKET
DLAEDVDLVVDGLLGTGITGAPRADYARLIELANALPVPCVSIDIPSGLNAETGAVEGVC
VRAEHTVTFIALKPGLITGQARNYTGTLHYDCLQLGEWMLDPKRQSQLFCRRIVSSHLKT
IFAQTPSPCAHKGSNGRLLLVGGDHKFGGAIIMAAEAALNTGVGLVRVVTRSAHIGPILS
RCPEVMAYDTEECSLPDLIQWSTCVAVGPGIGQAVWAERVVLQIAHTREYFTEKPFLLDA
DALNLFSKMVSSGNLKKFGLLERKNKKTVITPHPGEAARLLQCTIEEVEKDRFQAAKKLA
DLYGFTVLLKGPGTVICAAEEIDISVDALNTAHGILSSRCVVSDAGNNGMATGGFGDVLT
GVISGFLAQEFSVWQATCGGCLAHSTAADLAAAAQGGVRGLRATSLFEHILTCVNPLTE
>TCRU_5768 UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase, putative
DAALAYIPRRVVDTWSRREYLIVLGIISTDDEARRTRRNLQRTTCWRFPGVATRANDFTG
AMLVLYVLGRHPSHGYDYSAALLEEASQWNDVVALPMNEGRVTTNKTVGQYGSRSDEEEI
GMSRKTYMWFDLAHRLFPTARYIAKGDDDMFLRVPLFVAHLRLLPRRGIYMGYHMLPPSG
PERYIRGYTFMGWCYTLSRDVAEALVSYEPLRRLAYLPYSKERDDEFALLGFLYEDAMVG
LVLEKEVKYQPMLYVKVLGCHFHDARNETGHSQVVPTSICVHHVLEDDYAALMARFGNDT
SPVARVERVSDDVIY
>TCRU_5769 Temperature dependent protein affecting M2 dsRNA replication, putative
MRKMGGNRNNERQGRGQGQQGSPMAPPVSSMGYQQHQHQHHQYHHHHHHQHHHNSSYSNV
YEGSRPPPHSMQQMSPHGYGPGGGGGAPAAAGGNGWNPPQQQQQQMPMYNQGYGHMGPGA
GGGSGGGYGDMGGVYQDMHPGQYPPSPSPSHMGGGSGMPYMRNPPMHGGVPPAGPIPGPY
GGLPGQGAPLPPMGYGRGGHPPMDPMQQGGMYGGPMVRHDGYPDNRISPPPQVGYGPNVG
APPPPPPGIPYGGGNPMPVARSPAGVPTAAGGYPDPRSKGMLNNPMPMLNAPRHPRVGTP
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DPLWFLHSTLPEELLDSVCHHVEWMRSLNLEPIWVFNGLSVSGDVETFLTSEGELRARDI
VWSRLEEGEIPDEADIQTAFD*PLGEDVQMAVSRYLKKELNVMAVTAPFLNWAQMVAFHK
EGLADLLMGPPEVLLLPYDNMKLIVQIDVSNSNVSYFDRERVLRVLFPYHVTETSTRGAG
DRLMDLGLITATHPALSSTSVGLNLTMEEVYEELSSETPKFRSIKDFINAHAYVQDANKK
KAGLIIKHSKGRGYLRYSGVFSSKLQDSPLVYLIRVLEPGLTNADMPTNLIGVLGNLVPL
SLFYLQFVGLLSVRIMTVITQSYIRDECPVSDTKDYHEKLEVLMTMRSQIIAQVFKKISK

DRHPNNTECLSWVRWFKPILAPMQRPRDLINLDEWDISSSEEVLQLDEEHLERYSIASVL
TFSAEAARPIRDQNICSPRETPIRYHGKRETFFTVLLKAFDFLGYFSHSTVSPEMGEDGE
MMAGGVEEGMEAVGQGNNAEGAPILTSDSNSNNYNELHDSLPEEGISEYPTVYFPTYLMN
AIKHNPRSFQNAFVVLTEILRVGIIGSLPCRYIDPADPQLAISMENQESNCDPRVLLASR
IGCLINLPYRRKTEDLPFIWAPVYSRHLCAFTVMVRAMCRCLRELVEVIATTVFLAGNSS
CSLVDFSSFAFLLPFGEIPSAIGGLLLHYVLVFPSDYQVNLTTRQERLEYLQEKFRDIPD
LAVHLRMVMTFTLQALYLINAYKVSDKGTVVPQHLLEDNTVECTIQLLWEKWYDHIDDDP
PQDIHGLY
>TCRU_5770 ATP synthase, putative
TPEATDAICQMREMRVADESTVRLMEHLFSCPPTSDLLHSLLDGKHQAVAVALFKTTQGI
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ALFLAATSLRYGPIEKNEEALRRFFAHVTDVLSAETLQVSAVAFAVQGCSIVARTKALRR
WFFEEQIVQFLPRLLFDIVANDSASIVQLIYETLLVSWLLSYEYRGVVELQKHKMIPHVH
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IAEMVGVGMLKTLAQLSRRKFGDEDISVVINELKNVLEHSMEKLTSFSEYRGEVLSGEME
WTPVHTSNKFWRENVMQFENNDYEVLVALGNTIMTTHQDLTLAVACHDLGEVVRHHPTGK
SLLLLPRMEGVKNRVMALMSHPNPEVAKNALLAVQKIMVQRWEYI
>TCRU_5771 lipid-like atypical dual specificity phosphatase, putative
CKQNMKIVPPNFGYVEERIFRCGAPEPCHYAFLASLRLRTCVLLTESHDEAFVRWLRENN
VHTVCPLYDGSRTNSLGDKMGCVGYHTGSMTLSEPVVVDILHVLVDPINYPLLLTCSVGR
YRTGIVCGCLRKLQGWSLVSILEEYRRYAQDKGRAENEEFIELFDKDLVNLELKDGRRPT
ILY
>TCRU_5772 WW domain containing protein, putative
MAKRDRGMSPPKPTAKRRKRGGKRRRKKQKGEVILPSAPASFVCHICTKNHWTVACPRLE
RNPEQYPLMDRKRGCWKCAQRGHPSAQCPVKKYRCADCGGIHDTRDCEFDHKSEEWHEFY
DPITQHVFYSHSETHEVQWTPPTHRLDVVLWFCPNCNILMPTSVPECVKCHAPRMESKIS
SDSSSSESSSSSSSASSFAAEDDSEEGAS
>TCRU_5773 paraflagellar rod component, putative
GSLLTFYKDPYCKIPVFMMGGCARRCILWIGGQSESFLTFDYFPQLVNFLEGEWQFVQIE
LASSRIGFGAQDHVHDAEDVDDLIDILVMKHEMQEITLFGTGTGAQVVFELLENSRNSKF
ITRVILYGVVCDPETQIFTPEGEAERKEFVAQLIAEGRHEDSRAMVNQYDIPITPARLFS
GGFPTLQEAVWNPCFREDTETLSRSMGVVKVPLLLMLAHHAQYKPTAEEVARVVRLTKEY
AGCTHVTVSYFSDTCDERRRVLKAAEAEHVEAIVQFLFDEEEKRRIQLEQQERKALENEK
KRKSVLQASAFAQ
>TCRU_5774 phosphatidylinositol 3-kinase, putative
SSGSSSGGGATGNGSGLHVLGCGVVGNGGGGAVGRGVSSGPVPDVAASSYVPMSSSTPAG
STDASDEEVNQLLKELECSVNGSNAEAVMRDAVWAIERRALASCDPMSRDLFLEQRIRDV
LSELSRTSNPKLLLLAVEFIDALLAVPYTNPQQKFTRLCRSLFIVLHCGLEKPVMEAQRV
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RRVLDDAIRSLNTSHNNESSIISTLQSIRALISSRGVQFMEKQVPILPQLCVLVTEQHRV
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NVGYEVLDTTNRTNLDSILMRYITRRETQEECWHILAAIFSSHAWSIYKRVLHTSKSGRS
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RCIPHLTNAVLSAELVKYVTMIQEHVLPVSAELQAALENLVDNKLKDNLQDSKRMNFSGG
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PFLLEQRILKTLMSFLHDTSQVREKTVELFVVLTQEPRSTPSVEAVQQSLLILVESYVAV
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DTILGALMKDENLMLRNQDDLAELYAPAVSILRHSTSTSLSHAAISFLVKMHAIGASPRE
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PHCIPVVFPMLMHFVQQLEQLVEVRSLSLCAAIHIVCNLKAVQHLPALLHAIRTLTRHCV
LSEDLGPRLSTAMVLEALKVLAAMCLSGKSTIAALRECLRDTEEMSSLGPTISSVAESGL
DTTAVMGDQPRSPYLSRYHPKHQQELGHGNQYLDQPDDDRYDTYPQGQHDITLFMKHVEF
GLRTKDNKWREWFAEFQKNIIMVSPHPVFRIVVDLFDKHEPLRRKLFYPSFKCFYESLNA
EHMKKVNEVLHLALRSTDSEVISKCLGLADYLDHNPPDIKEPVLQQLRYLESNDSNTRAT
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NNNNNEESNGNTNDFTENGVDTSRYYHQNNNRMRRTMCENSEIAIGFNPLARPITSTNAQ
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VPKEALHSLVLPLAWLYSKREMQDSVVGLFRVIRYKTENEDGLNYELLQWWDVAQRVYAG
KVENNKNFSLVDLEGYVRTLCLCGEWEKALHVVKTASPRLTQSSAAIAQSGAMAAWILGE
WDDVKHLKECIPVKEKVDTALRLFFENAVYLHDEFHSKTDGQAILMCADRLCTTITRAKM
EVDESLKTLLPLSYAHAYENLTLLQHFTEMEEQIVYVQSNSSVFREQLVERWKSRFAALK
PDSLMPSLRSLMLHSLVLKPNDMSEMILNFCERMGANYPQLSMWAMSWLWQGQFPRSSHQ
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IPTDYWVQAIPQLIGHLSDTRHDVREVISMILRQLCEVHSQAVVFPLLVVFMSDDGSGGP
QLRRRELAQSIITVLPKRIRSDAELVAKLLIDVSSIPIEKIREHLSAVATVWNPNAEYEG
DAEEVCRRLQAVLDIFNAHRHHLLYTVGDIGHYVGMVMEDEKRGDREKASSIVSQLVDEI
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RIRLSGSNGFIYTYCLKGNEDIRMDERVMQLFGMVNVLLSDAHTPNSAFIHRFPVIPISN
NVGLLGWVEHANTINNTICIHRNTISNVCTHQESGVLRSYVESFGSWDKLSMIQRTEVLE
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SMSTGKIVHIDFGDSFDVGRLRHVLPETIPFRLTRMLTNAMEVFGVDGIFRSSCTRTQTT
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PLW*
>TCRU_5775 trans-sialidase
VHSFRLPALVNVDGVMVAIADARYETSNDNSLIDTVAKYSVDDGETWETQIAIKNSRASS
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IKWGSPVSLKKFFPAEMEGMHTNQFLGGAGVAIVASNGNLVYPVQVTNKKKQVFSKIFYS
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SRVWGPSPKSDQPGSQSSFTAVTIEGMRVMLFTHPLNFKGRWLRDRLNLWLTDNQRIYNV
GQVSIGDENSAYSSVLYKDDKLYCLHEINTNEVYSLVFARLVGELRIIKSVLQSWKNWDS
HLSSICTPADPAASSSERGCGPAVTTVGLVGFLSGNASQNVWEDAYRCVNASTANAERVP
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KKLLGLSYDEKHQWQPIYGSTPVTPTGSWETGKRYHVVLTMSNKIGSVYIDGEPLEGSGQ
TVVPDGRTPDISHFYVGGYKRSDMPTISHVTVNNVLLYNRQLNAEEIRTLFLSQDLI
>TCRU_5776 Leishmanolysin, putative
HCCGFDAMMKKYGRLPTAVVREVPRRGQGAVQAYTAASEDGDGGWAPIRIKVSAEDMHDP
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VIPQTDLGMCENFTIPHKHHTVGVAGADMILYANIFPISDSTAWAIPCFLLDDGRPVVAA
VNFDPKQIVTTNVYVRVAAHELGHALGFGDTQFLMLHMISEVPNVRGRPKVSVLSTXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXGCGLLEKKCLTDGITEYPDLFCNQFYDYPKFFCTYDRLS
LGYCRLKRHEEALPQEYRYFADPRVGGDDLYMSRCPYVNKYSNGGCTNGDPSVMPGSVVG
PNSRCVKGQDLQFDEEYIGDVCVDTRCSDGKVSVRFLRDDAWHECQEGETVT
>TCRU_5777 Leishmanolysin, putative
HRCGFDAMMKKYGRLPTAVVREVPRRGQGAVQAYTAASEDGDDGWAPIRIKVSAEDMHDP
LRHCTAAGDLRINHFDRAITCETDDVLTEERRNIVLRQILPAAIQLHAERLSVRSVTGPV
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NFDPRQVAVTSRNVRVAAHELGHALGFARVQFLKLRMISEVPNVRGISKVSVLSTPKTKA
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VYVANYSAAELLWWGNNSGCGLLEKKCLTDGITEYPQLFCNEFDDDEKFFCTYDRLSLGY
CRLMRHEEALPQEYRYFADPRVGGDDPCMSRCPYFEAYSNGGCTNGDPSVLPGSVVGPNS
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CPQYADVCTA
>TCRU_5778 aspartyl aminopeptidase, putative
LMSFGSPFSMELAKEFVEFVNKACTPFHAVEVISSWLLEAGYKRLKEDEPWPSILVGDRY
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LIEHIIASKTLRATLVANSFLLSVDGAHALHPNYKDKHEENHRPLLHRGPVIKYNANMRY
ATNGATASIVKSIAKEALVPVQEFCVKNDSSCGSTIGPILSSLSGIRTVDIGNPMLSMHS
VREMCGTTDISYLTNFIEAFFTNYGKHVISS*
>TCRU_5779 ubiquitin hydrolase, putative
MKPPFNITDEACAHCWDESVMLVPNHRSAVHKEECAYCCRTCRHEMGTLVCMCCHMGLCV
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HVLDGPAKYRLHAMISHVGASAKTGHYVCHICDAQTGKWLLFNDEKVAESLNPPFSMAFL
YFYKR
>TCRU_5780 Ras-related protein RAB2B, putative
LMSHKYIFKYIIIGDMGVGKSCLMQRFTEQRFRNDLPHTIGVEFGTITVDINGETVKLQI
WDTAGQERFRSVTRGYYRGAAGALLVYDVSRRETFSRIGTWLQDARGNTNPHTVMMLVGN
KSDLDESREVSYEEAVKFADENNLLFVECSALNGDNVEQAFLSTAHKIHEKVMCGILNPG
>TCRU_5781 ribosomal protein L11, putative
EPGSNRMPDAAVMAKAKDIFAVPEFPGKRVLHNWRFFIKAGKAATGPPVGQEFSKLGLKA
MDFAKSFNDRTKPHFKDDVELIVRIQVYFDKSYLYTIEPPPTAWFILRALRKKRRETGPV
PIRGHYCALMTLEMAYEIAKMKPRSWGRPEYPLIETRVRRVVGQARRMGVCFVGVDTPHS
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KEPGLFHALWQASHPKSPYHRDLRQREMARRYLNARGWVKDMTLDEMQVVFMNYRLPEIE
RGHQMDEGGMEGQVYWTRDGAQ
>TCRU_5782 esterase, putative
MQYALLLGDSLTQQGYESGWASRLSKRYVRRADVINRGLSGYNTRWVLDILKDDTRRQQL
LPTQPGKALFVTLMLGSNDCAGFPQHVSLDEYGANLRAIIDTVRKHVCPVGGIFLLSPPP
LDEKGRLQWLRDVGCDPNSCGRSFESMRRYRDASLRVGAEEYEEHGDVFTVDLYRVFLGR
SADTVPYAEGSWCEYFSDGLHFNENGGRVVFEALWCAIEKSVKASHILPDRLPYVLPPHE
TLV
>TCRU_5783 hypothetical protein, conserved
IVMPQTQETMASATLDALRAALTSGQMSALREVKADAVLLDEVNALPELLRLCGLIEAGH
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KINSDMASRICITIASVPERVHNILERTNSPKSITAVLLIATKVLQKLAEELNTSYAICE
CARFVAAELVAVTGFVLSEDPTFLACIRRLVDISFALTEDGKEVRVDGMLRYHAAVCLRN
FAQRNAVVPLGQLRLLEAVTTALRILLQGGDVADTDVSMRDCEGFLAHRLEEWKSLLSRS
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QPSEEETLVRLEQLVCAAANMTRHALSSNG
>TCRU_5784 acyl-CoA oxidase, putative
CWPVICIQGRLFYRSFPLRMELNPSGNLYSMEHAFEEPTFRFMCEGEDIDYREEVRAALL
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HDKKHTGDAKEEQENMQESEEEWDLFHGLAELPSFAQKK*
>TCRU_5785 protein phosphatase 2C, putative
MRPLASFRGNTQTMLYTPVQDKYSILMEDDKLRVGASSMQGWRSTMEDAHTIHLSLPGLP
SHMASEDGAIAAVFDGHCGSKTSQTSAIRILEWITSMEAFGEGNMEKAIRDGFIAGDLAM
QRSSPNEMSGCTGNCVLIVENHLYCGNVGDSRAVLCRDGTAIPLSEDHKPNLPRERERVL
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DGVWDMVTNEKAVEIVRSEVADHSDLSLACERLMDACLSKVSTGAGTDNMTVIILQFKSF
FLKKVESRF
>TCRU_5786 mitochondrial RNA binding protein
MGGPFEKMARDVAVRMRSKVHKQSFSNAVMRAQERKLTPAGRLAVERVAELVALQKRHQQ
TFDPALRTEAMQILRTLPLLSTDEDPLFVQTQRALRVAAYFDAASLPATYALINQHTKNA
FLLDAVAMSSFFFTLSSLRHPQTADIIAILLPRLKEVAPEIVPREAVYILRVMHRAGVGD
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EVKGIILDVCRVVSLTCSGPRGLFNSIARRSMDLAPQLTPLDMAYILKAFHMGSYRHLRL
MRVLSSSQASHLTESTGPLRDLTPVAVSMTVQALAHFYVVGCEEVVVSLVNAVINSLEGL
NFALTMVSCVRLQCVSPGVKQATDLLCGAPLQRYTQHPHSIQVTSRLIYALSQAGRCVTA
EETSNLQLLLRAVLRFRSPFPDDTRSFLLDAVATLSADSHCVDDNLRKLLSKTRERL
>TCRU_5787 leucine-rich repeat protein (LRRP), putative
MLFEPSGVLRSDYGAYCHALGFTEREEVYRSIFTSEERRQEKEVKYLEAHSPSDADTNAD
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DPAKALENAAPLTLTFIVMRQLKFCLNRRDIKPLALAIPHCVSLVSVEFVGCGLSEESYF
LLVEALYKSRRVASVTIDFNSSSNPGFYVDPVLSPGATFQTANQTTVVSFTDVTPELALS
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NNPRVTLDGAREALRVLSLHEPSDDKEMSALQNCVVQPPELYCASIKLHTFVILHDGDPG
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>TCRU_5788 Flagellar Member 7
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XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTNADDARSPLRRQPANADDTRSP
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RKLLKDMRENRGSNHVLREIGRAMATRKIQRWFRRRLHARWGTRRRVAKREVLASEQHKA
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AVEKERRELAVTVIQSHWRRRKAERETRVERMKARELRRKINEARRRNAAEKIKTWWRLL
VARAELQRLREAQAARETRLREHQRKIDAATKLQAFGRMLIIKREAEPLLTTARLNAARA
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>TCRU_5789 ABC transporter of the mitochondrion, putative
ISALSPSLWTCRRLFHQATRLRLEPSKGVSAAEGTNTFRTECPQGKTKEEKRKTQKQQQP
RRQETAVKEKIQPTEDSIVSAEALSKIPVYRVVSHVMRHLWPPGQPMYRVLVVTSVICVV
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>TCRU_5790 MIZ/SP-RING zinc finger, putative
MPAHSATRGTQRASGPWAGFFSSSFGRAHAQVASMEGAKASKSSALVSQTLLDLRQRILD
EVKGNKSANSKLRQAHRQRAWEMAFGHPGGDEVEVSTIEISLLCPYSRMALRYPVRSREC
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ILDPDGSYRSGDASRKQKKQQVTEIIESTQAQKEEGDDNFLLNSSNGSASPTQWISDIRI
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RCTRTLLKSEGGEVECCTECGLGREDWTLVRSFPGSSLSLELTRDGTLILRGADALAPHL
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>TCRU_5791 autophagy protein APG9, putative
MGFIRVPSFSLRYQGNGRIEDVHLFMRCLYQIWYFRGPWGCCLASCVDFLNSVVLFCAIF
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>TCRU_5792 GDP-mannose 4,6 dehydratase, putative
LSRRRVAIITGITGQDGSYLAELLLSKGYNVHGVIRRSSSFNTGRIDHNYRNEHLTLHYG
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FRPAEVETLLGDASKAERELGWRTTYSFGELVDEMVQQEIRDTETGADAWR*GGTNVSGE
>TCRU_5793 ATP-dependent DEAD/H RNA helicase, putative
MSLKKRTFKQRAHRNEMKERHHVSSELRKRMRAAKRRHNRFDNIDTGSRPLEALIEEIAE
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LVATDIASRGLDVDGLKHVIHFQVPRSTDVYIHRCGRTARCGGTGLSVVMIDAQEHVSFQ
KLMDSLGRGSKEMEVFALQPTIVHQLHSHIKVALQIDKLQKEIDKSRARNNWARRMSREA
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>TCRU_5794 Pre-mRNA-splicing factor 38, putative
MEGQKRMMWNLKGRSAVAALDPSTRHRIMQSHAMASSFHKPLLATLEVLITPQYVGGLTG
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INKNGGSGNLWLGLRLPPIL
>TCRU_5795 Rab-GTPase-TBC domain containing protein, putative
MSVALDVNTVTAALWPTATGKVTRSTGQILEVTLVDRGAARFTHIAFDPSDETKFYASTS
EAVVYVFSIRKNDVKLFAVLEHPVASMACCGNGVNPLFVCATEDLTLIWLDCNTSRILRR
EKTPHRYAIHMMHAPVGFGTPWLATISRDALVLWDATQMVCRVNSHITVVQMVHDFLSVH
AEMSFLVTVEYSGIVKKWDPIALVPIKAVTIAMRPRAATACQTYVAVGMSDAIVGFLNTS
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RSPSSFSVSGPSFGVFLRGNHLSLFHLPTSRQYYLRRTKWNGVDPNPTLPRQVYPFLHRG
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SQSQFVEPLKGRKKSEELEADVMNKEKELSQRPFLDRASRAANMQNLKRLLMRYGAFPDK
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WHVPMFSVIHFLPMIVYPFLQLYGDDIQLTVEVVLVVLSNWGQEFFQYYPKHPVALTSLL
NQLLRTEDLELHSYLEQCGVMVEEWAWEALKSLYTDILTSAAWLQVMDHAFFNRPLWFFL
FYIRWLVNIRERLMKLHEHRELLAAFSEVHPIDINKVIAETYQLHERCPKGELSRPYSVL
HAFVDYAYPVEWKCNEANIARKLEDLQLPFQQEGKEKEICQQIHGIREQMAEAEVQEDVF
FEKKRAEIAAQLNTANDSLINEVAHEKKNQRAREMKNMARIQVVEKHLQQADRLEALREE
LVSARVQIADLAHIREREAQHWRRAESLTDHEVRRLEEAARERLAKAKQAIEEEEKKSSL
QSREGGDFSGHTTPPTKTTRTAATDVARNPLRTSLNVLQTPVEPSVSVQAYRMLQSSVTP
AVKETLRPQKPQGERSTGGQPPNRSY
>TCRU_5796 protein kinase, putative

MDRFIIGSPIGEGRFGVVRAAVVKESGMPAAIKFITTPRLDEGIPHPTARELLVAMRLVH
PFVIRTYEVVPCGCSLALVMERCKTDLATVLSGRTASNPLPALEAKSLFKMLLLALAYIH
SEGVLHRDVKPSNCFLTAEGELRLGDFGLSRVWDTEASMTHEVVSRWYRAPELLLGQRHY
GPEIDVWSSGCVFAELLRGYSGAFFAGDGDIWQLSRIFDVLGTPTPTSWPSAVLLPDWGK
VHF
>TCRU_5797 Tumour suppressor, Mitostatin, putative
MANMMTRLDASVFPPRKPGQTDGDLRKELNERKAPRDSTILTRTELDIVRSMIAGKNVMT
FPLQSTVRTRTAAANERKQRMQEYDALHRLHGDDDKTLEDIEEEQQKRLHLERAKNLIDE
QFEEVRAMNQIVMEAKCVAIRNAQLMEKKRGKEEERAQEKELDQMMLFESKKAQQLYEER
ERQQIEGRKKNLAVIKAQLEEREVDRIRKLEAHQQEQEAMTRHIERLREEEAAEKLRRQE
AARRLMEDAALANAEQIKLKKRQQELELEEDKRVAQYIKEKEERERRFAEEQQRIREEKE
REVARLRAQQQRVQDKQAELDEVRAKRIQEAHAREMRRKEKERKEHERAVLQDLARVREQ
QMEERKRIKEEQRQQEIEELEHIVAVQKLALEQERERKARARQQHEENSLAVLKQIMEVE
ERRRRERQEYVAEGNHVMMLMRDREAAIEAIRQRKLAELGELGVPEEYCQALMKKIKVRG
A
>TCRU_5798 Zinc finger, C3HC4 type (RING finger), putative
SKCTRRPIYYASDCLEMSECAWCCERPIGQQCFDKFDNNSVEPPCSEYAIVTNRDTTCGQ
LCSVKYDDCERCEMRNWCYFCISTSTCQPPYASCRNGEVIQSCKMREKEDGGSNYYFTVT
IGVGGALMVFALIAALILLSLQLRRREQDEQQNFVEEGTPFLRDATTVEENTNVQPVTTT
ATAPTTVITASGIMPSNITTTTNDNNENDNSTNEYNIHDTENSDRDSHDLATNASAAVAS
GEEPPAARDFREEGGAEVRLPTPRSAKFSTGEDDSLCFLCLDASPSVTFLPCYHTCCCET
CSNKLRPTRGDVLTCPFCRTKIVAMVSL
>TCRU_5799 nonspecific lipid-transfer protein, putative
MSSQVVRIVGVGRTAVGRLGKSASVLAVEALRMALRDANLEMRDLDGLVAVPSLASPHFM
QAHYLATVSGLVRENKELVLRTIDTGGAGPITALGTAGNFIRNGWAHNVAVVASDAVLTL
SSSAFAERSDASVAGGELEKPCIPNGYDRYAQWYMKRYGLKREQLAMVPVLMSSMAARHP
DAMCREPYKLDEVLRSRRIAPVTNLLECARRADGAVALILSSESHYARYFALKKLDSSKP
VVVSVGEASGPLFPPAIENITPELFSCERAVKFALGAAQLGIQDIDFFGLYDCFPICLIR
AIEAVGLCPIGKGGEFVEAAYNEMMKNQGVIEPSQLRINTHGGLQCFGAPWEVPAMYNVT
EAIAQMACSAGNRQIWPVPK
>TCRU_5800 hypothetical protein
KMRGFMDQEPEGVPLKEIPLDVDPEFRQAEVARYRMRKDPHHSPEEVAKLEDAMNDRARR
LAKAILAKNRGFLDPEPCGVPLAELPLNTDEEFNKLAAERYRLKRSNKKDNNPEVKGIEN
EMNDRVHALAREHLRKARAFLNPEPEGVPLEDVPLGRDPRFLDMERGLAKLRNDPNASAE
TLSSLEEDLNLRAHEVAREFLKKERAYLDPEPLGVLVEDLPLNHDPILNALERKRRELKK
DPNEMGILFVDVKTTHDRVRAIAKEFLDNERRFLDPEPEGLPFSELPVDTDRQFREMENE
RRALLKQPALNKAAIEGLEERMKTRVNELAKDTLRKCRAFLDPEPLGVPLDDLPLNTDEK
FREMEFRHREMKKKPFVNAVSLEKLEDEMKQRARELAEELLKKERAFIDQEPEGCLLSEL
PLNKDKHFHEME
>TCRU_5801 hypothetical protein, conserved
VEKKSPSLCSRLERAITSFLYGDPAGRSRSWVMGLQVPLWFWTHQITVEAEREGREMQKV
VNLVRWFHDNGVNVTQVAIIVPCEMKSRLRDELVASLQDSTTSEELVLPTILGIHEMTAM
NVRDDVVHRYEVVLYVLALPPVTRSLPLAMQQEQFIGDAIASAKSAFILIADVGWTSPHI
AIQWPQWRTFVMKFEEETPLVSSEVNVKLPGDARFPSLVGSHIPLCCARHAEQRQLEHGV
APIVRTCRRLCLQPFVCQRDGHVCMEPCHPRVSHTNCPYACQTLMPCGHECLQSCSERCN
CFEVHEHPLLCFHKTVIGMDKATMQPIYAEVRHVFKGFCADAELPCAVEYTTECARCLGP
LTTSCSEARQQNHTLEHKTILCPGCVRLEREVRAKVLGEILVKTEEAKRQVKLEMQRSLH
QQRKASSQGLFQEGSRVTICDVLRIVKPLCAEADFPGVKFVDYDAPDFYSSMDGAYGTFV
SRHVDIDDLSEVRNLIRLRDGQHVLVADGGVRLIRALTSNITQQAPALLLTYNSNNNNKE
DDGKGGGRTPLKDGVAFAKSAKMVGRSYYLPVPVPCGESTISDKIVQVTAVDPASPDCVV
VECTRTSVIQHVDDAHDGDENNYHNANKCEASDSLALKRPRLEASQAKNYHLRTSVEVLT
CTVPVALLEPIEGYAVGREVLVIDPTRQVTNPHDVEIFEAVLAQTPGIDLNGAVISTVPV
GKDTSFILLGVLNSPSNLEKRYGPCAVLRRRVRIVTVRSGRQRRGARGRFSAVQHVATVN
GGAGDTVVVLVPFVFTAADELLEAENSLDAAALEKFEQQVRDTIAERSDELAIRHDEEAF

HQQRQMPEVTETALLEKRFAYSIPFPLPTEDSLAGARTRHARLLCASPTSLRLSKQKDAL
VLKQQQLALSKWLESMRTRYAQDKEADVAYCRGLQIK
>TCRU_5802 Selenoprotein T, putative
FLLVMFTTVHGAAGDDDRDTSDTEGDDDSLFKYLEMLEVSDLRQMLHEKKQPFHHLRSKQ
ELIHAIITLEKKEKLVEKLRRRRDTKASRPHVLRVEYCSG*GYRRHYEEMVHHISRSLPP
NKNQEPILKFLPSVYSVGIVRETIGSFLSLLFIASLIIGIGAPYFVGIFPPNVVTWVEQN
RTMIIAAGFVANLICGSILQSGAFEMFMDDTLIFSKLQQNKMLSAVDLAEIVIQALV
>TCRU_5803 solanesyl-diphosphate synthase, putative
TTITSTVPSNLLTEDGRPFAMVAREVRMMQQNMAGLVSNSNNAVLNHIAKYVFSVSGKML
RPTLVAMMAHALLPPHVSEQIRAESIGSIDDNSSGAIRPFLRLGEITELLHTATLVHDDV
MDNSNTRRGQPTVHCLYDAKRAVLAGDFLLARASIWIAALGHSRVVLLMSTALEDLAAGE
MMQMDGCFDIESYEQKSYCKTASLIANSLASTAVLAGFPNTAYEEAAAKFGKHLGIAFQI
VDDCLDITGDDKNLGKPKMADMAEGIATLPVLLAAREETRVHEAVRRRFKNPGDTEMCME
AVERHGCVAEALEHAGEHC
>TCRU_5804 Leishmanolysin, putative
RCGFDAMMKKYGRLPTAVVREVPRRGQGAVQAYTAASEDGDDGWAPIRIKVSAEDMFDPL
RHCSAAGDLRVDHDGRAITCEADDVLTEEKRNIVLRQILPAAIQLHAERLSVRPVTGPVV
IPQTGLGLCGNFTIPRRHHTVGVAGADMILYVKIFPTSGPAAWAAPCFLLDDGRPVAAAV
NFDPKRVAATNVYVRVAAHELGHALGFDVDYFMMLHMISEVPNVRGMSKVSVISTPKAKA
VARQYHNCPTLEGIELEDEGGSESVLSHWKKRNLRDELMTSDLRVGLYSALTLAAFEDMG
VYVANYSAAEMLWWGNNSGCGLLEKKCLTDGISEYPDLFCNQFSRAGYKLCTYNRLSLGS
CDLKRHEEALPEEYQYFADPRVGGDGLYMSRCPYVKTYSNAGCTNGNPSVMPGSVVGPNS
RCVKGQDLQFDDKYIGDVCVDTRCGDGTVSVRFLDDDAWRECQEGETVTPPSGPWRGSIV
CPQYADVC
>TCRU_5805 Leishmanolysin, putative
DSGWEPIRIAVSTEDLERGKNNRKKYCEEGEDECYNALGQRVSCKAEHVLTEAKKKLHTR
MILFGAVKLHAERPLVKPTGGTITVPRAVNGPCNHFTVPARHKSDCVPNADFIIYAAARP
SGTDSRVVWPATCNTWGDFRPYIGAMKFYPKYMTDTAWSVRVAAHEIAHALGFSQESMR*
KSLVKKPEISVRGMRRKMVAGKHVQVKAKAHFGCDSLEGMVLEDEDGPPEKEIPHWKGRH
ARDELMAPTVGAGYYTTLTMAVFVGMGYYRVNWSMAEPMGWGSRSGCDFLVNKCNTTDNL
AAKYPHMFCDAKDTETLRCTSDRRHVDTCTASIVEDKGSLVDKDVCPVVSLEFHGISSGT
TYRTCSDENVDYFRGSLTGGDSWCLDAELVETKDGNGHKSVRGVCAQV*CEEGTVRVKHL
GSSVFQPCTEDTDIPVTLKYFKKDGKIKCPTCGEACTIA
>TCRU_5806 AUT2/APG4/ATG4 cysteine peptidase, putative
VYNCMFRLRAHKLLLADGVETYIIGSGMYNGAETMKWADKATEALLYFSYRNRIVPLMNG
ATTDLFWGCMIRTGQMMLAHAFMRYFNGGGPHIGSERLQELRARTQTLFCDVPSAPFGIH
AVTSEGTKHGVNCGEWFGPTPIAKTLSALMASYLAAGGEGPVVLAFPERQIFLEEVKELL
RQSTHVVLLIPVMLGIRVISEKYSQLMKRCLEMESSIGILGGKSRSALFLFGHQDDDVFF
LDPHCVQPAFTSSGSPGELTCARRVLPTTSYDTSMTLGFYISSLDSLALFERDMASANDG
LTFPLISL
>TCRU_5807 chaperone protein DNAj, putative
MLRFRSLGSSRALPALLTPRRTMMGLFEEEGPSGLGETNVAAFAYSMDQLENRSLRLDRK
AYGIPFHIGEEEAVDAVYRHHGTAVHVHSVERYLMPFWLGNTAASGSFRADVLQKDPAFL
TQQHCLVWVEGPSYEFHYPFGEHHVFNQVSASYLHPLSTVEHCVSGTHVPSMLISRFELL
KELEAMEKPPKVIPFSMSTVTALSILDYRLSRSMVLRRIDEELVKFHGSFVRSCVTLTSV
FKESVSIRPVFLPMMKFTVSTGTNATPVPSFVCGATGKVVGPILHLSQRTKMSAVTLSGA
VTALSILDYRLSRSMVLRRIDEELVKFHGSFVRSCVTLTSVFKESVSIRPVFLPMMKFTV
STGTNATPVPSFVCGATGKVVGPILHLSQRTKMSAVTLSGATALLMLAPVVGPGIATAAA
IASAVVSVYVRRYLLTLRFLRDQARQMTELKTTGMLYFSSDQNGYRWTPEDEERAEYEYR
EELRQRARRKEAFEQRVKEEAARDEARGKRQVDPKNRRRTDLENVDPLGYYQLLGLSGRE
LSATAKEIAKAFREAARHHHPDVAHRNDDDVKNKMQRIINAYKILRDPKTKKAYDSGQL
>TCRU_5808 hypothetical protein, conserved
MVRTRLSFKLHVVRRRLRKRRVIQAVPKLDAKKLRSCSLFAKWPLEALSDLRRRMLWEVH
LKGETILYGGEPCSVSSLFWIASGKLSEVPNRREKSGTRRPSNKEEEGVTSMETVGSAEH

SSVSPHVEFDQTLDTFSAGQFAAGERLFLGATYHRTMRCESDVTGFAVSFRTVQKIQRKW
GVPREASVSAAKEIVKKQMLRRDEKPLLKLALFKNRVLRGLDATTLSIIWVLLSPMVVCA
NELICADIFDAENISFIQSGDVRVGFKRGQQKEIILSCGSAVGLQSFAPSEMPRGRGEGH
TAAVAVTFSQLWSVGRKAFSEMVSEREWGKCAAIALRKIHFHVDDEMLRKVAIFSLLPRS
KIMALAKRAELRFVRGDEYILPPWRRPQEAIVILVGTVYFTQKTPAEEALNNGKTDRIRI
PCGYPVAFAECVAGMPLKSGVFAATGALIVSLTRRAMLESLSENGAGNDIEPVVLEAAMN
QLNVSPSSRSATRNANKAQEEALQDMRNYSRPQNGNLPSWKNELQDLCSPNDDVGEMIEL
HTQVLSTLALQVHNLRPSMWKAGRVGVHYDNASRIAMKKIPTNESPSCHRSRSCFTIDKK
GRVMFCSKGAIAERKKIGRVQPNDVLSGTEGNKEIPRQALPICLPVKNGLSKPSQKLPSS
LALRCAPSEKLAAVVGHSPVSQRVMELRREGKRLKDEAENNYIFPLDCFLP
>TCRU_5809 hypothetical protein, conserved
NPMYSHTDTLIMIPCHGVLRSLNAYDWQKQSLWEFENHQLRDGVNLPFCLASHIRRALQI
LKERFDSSILIFSGGQTKVGAGPRSEALSYYLVAEETNLFGLFNSSVQIRNALESRIFTE
EFARDSLENLLFSIARFYEITGHFPESIIVVGWKHKKERFLKYHRQALRYPAENFFYIGL
AFEDAAPFVRDLEPYRLALPYSDAIALSYVSKDMYLCTAGKETKNKRNPQFRYPPYGITC
PPLLPLLRHCGPHLIDRSLVPWK*
>TCRU_5810 retrotransposon hot spot protein, RHS3, putative
ERLRRAQEMKITMSTNIEDVLFKGGVRVKDIKLNDFLTLRFDGKGIVATNRDVSLEEFFK
EPTEYIHDARVLNEIKKTVPFLKMGRAVMDEVYMEEVVLMLHENGVFSLEQWEEYEGKDT
VTPTERGKINAALSQARISASVVTSTVLKGYYESVYNASWSHVVEVPDGNEEEQTEMGMK
VEKGKPEQSWTYKKVGETLEKNDGAQQSGEAPPRMMVLSSDKGWPYSWEEDEFIRDCHVN
CEVERVWRIVELYLTEWFSTRGEPYFTPGRLLLIGTPGIGKSMNAGSYLLYQLLHCDVEK
LPVVVYVIGNETFLFEKTTKTVTKYMGGASIEHVLASLSLRGVNAYIIYDVAKDGRKPYP
MPNSRGWGMIVVTSPNEDNFGAWEKYRSPKRIIMNCPEKDDVKAMCVWNKRNEPTEQAGY
WRNINRRMEQVGPILRYIFDESKYNGRVQSCKDTVCKLNRIDAEYYLHFGTTQMLGGDKV
SHKLVRIVRVRGVRNIESTFNGLMSPYLGNLTLCKLAELMAPNDFILLVLAIKDDLLSKP
LEKHSVFTFLSEGFVNTIIPKLRELKLEEDAPPHRCALELYPHERPLKPFILERL*NFEE
KINIEYRVLYKPVAQNFPLVDAFFFMESPQKTLVGLQITTASEHHTIPSTVNLFTECLAA
YFKGWKEFSRDMSWEIIYVQHTDSTPMNGWQRCDVV
>TCRU_5811 30S Ribosomal protein S17, putative
MLRRSLVTFPWWNFQTEHRQRCVMMYGGSRAKNTHNANHRVFIKKYKRNAFPNRTRHHWA
VSMTGVLGQRPRRMPWPYDLTSLIFNQPRQGSDKIGYVVGTSMLKTAVVAANHMVYYPKF
NQRVSRTSRFFAHDEDLACVEGDLVHIKQCRKISKYKHYYVFSILEPNIEGRERLKLGLK
AVPPPLFGYPVSRRIVKLNLTNAEGTKEKLAAVIQEHVQDAYRFAGPTPDQPRNRLTDSV
TFDDANNMIAPNAPATPESLEGGESPSLLGDKEEYTEVEQDTRNKKGDEYWMNLQPKEKY
DFKGFKKSP*
>TCRU_5812 unc-50 related protein homolog
FRPSSRWISQLPEFARRAFQVDQMELDSALSQMYSLCLKPSLVSKMSKARKMTKNHYHRD
DPAFIVLQVLALVITVVAYGLTLKGGLLQIFFNVLYEVGVTYLITGLIMATAAWVFANRC
LMSNGGQMHELRREVDWHHSFDIHCNGFFPYFIWTRVIQFILLPLLLRPSFLACLVSNCL
YMIGCVLYAYIVFLGYLELPMLVQQQQLVYPVPAILLFTFFITIFGRWNLTQWTLSQMW
>TCRU_5813 UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase,
putative
YIPRRVVEMWSRREYLIVLGIPSTDDEARRTRRNLQRTTCWRFPGVATRANDFTGAMLVL
YVLGRHPSHGYEYSAALLEEASQWHDVVALPMNEGRVTTNKTISGEGFWGLEADIGMSRK
TYMWFDLALRLFPTAMYIAKGDDDIFLRVPLFVAILRLLPRRGIYMGNHIGTTHFVHKGL
PGSAFMMGWCYTLSRDAAEALASYKPLRRLAYLPYSEELDHEFSLLRFQHEDVMVAWVLE
RVIKYQPMVYVKVLGCHIHDARNVTGHSQVVPTSMCVHHLAEDDYAALMARFGNDTSPVA
>TCRU_5814 small GTP-binding protein Rab18
MSQAVDASIKVFLLGDSGVGKSSLMLSFASGTFDPDISSTIGIDFKVKNVEVMDANGVKR
NVNIHLWDTAGQERFRTLTSSYYRGANAVVLVYDVNEPQTFHGLQRWMEEADVFCRNDDE
DDAVYLLIGNKIDKCIGGSSEGEGVPFMSVPKEQAQQLAQRRRMLLAFTSAKTRAGVEQA
FDELARTVYDKIRVKGSEYSSGINFNKPASEPKSSSCC
>TCRU_5815 hypothetical protein, conserved

MSFRYTNGLVGALKHRMMLESSHRELVRRRFTGHCRGVEVVCSGYGTVLAVRLVDKTAWE
PFYRKGHPSPSGADMDSAPSSSHAESTPVGGESAAPIDFERLAESIKAALWDATRKIRSA
KEAALNRSLSHNQQLRAQAHLEHWYDEDANTLQPLAFEALKHEAATPWMQFVQFGKYKHA
AAVMHSESGGKKSEAFMGETKRASADNEEGPCVTALDEKDVDPTSIPIGSVHPLFLPALI
QFESRVDNSLNDDAIRQEQRREMSRDEQLFWERVELIRKGQVATIKGGHKRDYADEAAVA
SDNAVDKVQLRFTQ*
>TCRU_5816 hypothetical protein, conserved
MFNPTYRCLTAITDTCLPKNFMHATDLAFYFPRFQPRVHLRPNGVPELQDALALLQPAEG
NSQRRWSKPNAMSTQEWGKCCDKAFTLLDRAEEIMKNVGGLKNFSTADVLRSISAVKFEL
LNGVEHLPRSEYAKHVNIYRMILKQAGGLLFFNDYWDKSDVQQIDTACVIVAHFVRAFCA
LHQKPFHTKQEDGIKKKYGNISAWSMVMDEAKESGENILTLPMVMDRVDELLKLSRKAAE
THAEKNPDLRWNVPKLLLIKGILTIPFTGHLGQAQEHINEAAKLVYESLRRKQPILDGLL
ARKQEPELGLFMLAQAEMAARVFDWSVSPNEVDKGVMEMFEAAAKFYSSPYNTALDADGI
MSADGVEERRFETDAYASCLLSYGTFLLCAPRPPGTSRHDTPVFLPNQLFTMSPICTVST
SSDIIFSEVREPASMAIDLIRKRTGETLERALELNRTLYPEHKQNPKAGWTLLAMASLYA
DMRDYLYATGLFSSAEKALVENYGNNSLERLLALKLRYEFLAGVGSEQEAKTAAHEVVQL
LRHMDSLP
>TCRU_5817 hypothetical protein, conserved
RNRHNVILFPNHRDRLACDPLNFFCVYATYEYRWSDTTLEAERNIFALVDSMVAAVRKAF
DDAFERWKNMPAFVQHAHTLRSAVSFSSALSTNTLLHMYSHADNVARHTTLRKTLGSMLP
SLPAANPRQEMNICSASSAGRSTFSKGALPRAAHRERREEEEEAVMKNLAKQWIPPHNGP
KCRLVLDIVASRKTLGDDPVISDPYRLGQKVFSFTRRNYLREVINTFVGISDSGVTLVGR
DILYPFRSTGGGSPKPSVKMNSLSGNRRNLSGSAISGLPIDSGDILGVAASGGVAAKVSG
FEQILANTIPVPRMVPVPPTNTEKVDNIRLLVCFPP
>TCRU_5818 Ubiquitin-like domain containing protein, putative
MVSPVISFMDAIRCRYGSPDDSELYDADALLVGDSSCRRNKKWELVGMEKTRMKQADHTR
LVHVVLRGMNITAAERAEGELAAAALNRLQEVDISENPSLSMREIGIIACHLPALTVLQL
SDNPDLLLFEAASTTVTPIKPLLLSAQLRKLVLHNVGLRSIWQLRVLVDLPALEELHLEK
NNVRSLKLLTEAEEASTPQIQANVESTGNRSDCWFPNVTTLSLAQNELASWGRESGLNET
LTTAFPRLTRLFLTGNRMTNLYDDDITATNSITTAAAGCGEYAYLWPLELLCVNDNKTIN
DPRTLETLRKLCPHLHTFRITYSAMFPQWNESLGRMYVVASLPGITTLNRGQVRPKERLD
SEIFYVQRGLAAKQQEQKQQSEKQEEWVLPHYPLLEILQAKHKDVIMAIYREGETASHDG
ITHMMLHLNICCDGFENVKKTVPSSMTVGKLKALIRAVFGVAPSNQRVSFFSGDDAVIER
ATELDNELQSLAFYGVSDGALVRVVDTSLR
>TCRU_5819 CHAP domain containing protein, putative
MIHTARKKQFGLSALALFVLLLFLLVCVTLGLHWWRDTSGPALHPPRSRFDPLAHCATPH
GTLLGYALDIPAFSNCHRRWNSKSQAFVTLEHPHDVRQEPFLLGTLRSRSTGVRWVAAEF
IARTYYLHRGMSFIYGAPDAPEYWSALEFHGPMVREREYETLELLNSAEATTAKERKRLA
PRVFDVVVWSPMEERDLPEGHIAVVVQVEDDVEAAGGEDRLRELRKLRLQPRLLYIAEQN
FDNTHWGGKNYSRVLRFQWRNGREAVLQDPLGLPIIGRVRPGR
>TCRU_5820 CHAP domain containing protein, putative
LLLFLLVCVTLGLHWWRDTSGPALHPPRSRFDPLAHCATPHGTLLGYALDIPAFSNCHRR
WNSKSQAFVTLEHPHDVRQEPFLLGTLRSRSTGVRWVAAEFIARTYYLHRGMSFIYGAPD
APEYWSALEFHGPMVREREYETLELLNSAEATTAKERKRLAPRVFDVVVWSPMEERDLPE
GHIAVVVQVEDDVEAAGGEDRLRELRKLRLQPRLLYIAEQNFDNTHWGGKNYSRVLRFQW
RNGREAVLQDPLGLPIIGRVRPGR
>TCRU_5821 Protein of unknown function (DUF3808), putative
MTELDGVESLNAVAEEEKHEIYASTKRRHSLTKDGLKALREATVEQIAESDKDVARAISL
FFGNHVYDAEEIFARKAGVDPLYALGAACICTIKAMLSLTKSDMETAVERISFTITFAEE
LVPSEKSLFSKLADAFRRSSNKRRLLPGEFRAKAVLADAYFFRGFILLLQQNSINGILRG
GMALNRSYCLLNSLANELNELKEEKKGSSYDEIGLDCNSVYNALLGFGCVNVVMSMLPPR
ILRVLNFLGFTHDRELGVARVSQCWESKTLFAPLAGLFIVAFNSFPPGFCSLTKPVLLPV
AKATASDAIKQPPTENSVIHLWLTGRISRIELNMDESIAIFSRCLEVADKGQIARSMSQL
RDFAVYDQAWNYAVSMRWEDAIKNHAYLEESSAWSKIFYAYAQACSYEMLLHSTPEGNVS

EALHYKEKATEAYWRAAHYNVTVMGGRTVVIESFVARRLHDIFRQAGVPYPNPGNKSATV
RPLTPPPRNLVLQNIVQLPMLELFVLFELMHQLSPSHLEAFVTIIDRELESKAPAFLQTP
KSDAVSVDQIQPPTKNSGSLEKQQGVVLTTIKAIVLSHIPGKEEFALNLIQQSKKVACEY
KGRSCTVAWMHCWLLYEEATMAFNIGDTKKSVELLSRAEDVNDDHIFRTAIETKLHFARW
>TCRU_5822 electon transport protein SCO1/SCO2, putative
TSGGSSGSKDIDVVDETKPIHIRVAEEKDSQIFTMQDYIEREEAELNASRSLGQRLSDAR
DNPVWMLWALFFLSLGVMTVVVSIRVRREQMRFDPKLRAVKAFDSPDGPSIGGPFSLVGV
DGRRYTEKDFLGKWLYIYFGFTNCPDVCPEEMAKMSRVVQHLDKKVGRDYWQPLFISLDP
RRDTPEKVREYLADFSPRILGLVGTQEEVEAAAREYRVYFAIPDEEGMSEDDYLVDHSII
MYLMDPEGRFCDYTTKEFQWFESYSKLLRRMMDYEREKVRKQRERGGELQPGERAANMKV
ANIATMLDESAAAVPSREEL
>TCRU_5823 Zinc finger CCCH domain-containing protein 47
MSFSVRAGNSPMSQRSSASQAHVSPKMIPQSALRPIAPSFSLQASEDTLNNGNIGISTRK
MGTNPTRYKTTMCRNWEAGTCNFKGCTFAHGVDELRAPVRVDHYGGHNSHLHVSSQGKTP
PQYSTAMGGPLGSPRIEQLLEMLYAEVIRERDLVAVHVEANRTLESLLKKEQTLHEETKA
QLDAERSRVNELARVVLETSEEINTLLESCRINERQRSRVAMLLNKMAFVFPECDGTRDK
EEREGNRVVELLKALQQCQKPAD
>TCRU_5824 glutamate dehydrogenase
MMRRVVIMGLVGRAAFCRSGMNSFRFMASEINASCIINTVKEGGMFDEDSIRKAVQLFTG
GLSDSSYGLCYTEDEVTNHVKGFLCAKAKSTMGDPFEYVHESDDCAFYICLKDHESQLRA
VRRLSRFVSRVREENQCISMRGYTTDDGTTSVYTAKWQPFVNPQPKLGETDIKQLASHVF
LEQRSPELQNRYQELLTRFKGSVGPVFTLVDGKDGETCFSMAIAADRNYYLASLMAIIRE
IPGAVVIRSFSETFSNGVHIYTLYIDGATGTQLQDRVSMVCLLPNRPPNSITRLHEDLIF
NVEQTVFTDAAIVFAFYFTPNPSSDDYHHLRALLLKEPNGVNRLNSLRTSLSLEMMSERY
IGTLISLYPEYMIDIYEDFRRGSTAESRQVIQNKIAARFREDQRTTHDLEIFTSFLRFNE
VIVKHNFFKKEKVALCFRLNPLFLKSLEYPLVPHGLFLLAGGQWRGFHVRFTDIARGGVR
MILSRENAYRHNKRTVFQENYNLAHTQLLKNKDIPEGGSKGTILVSSRFLNRFDQARCQR
LFLQYADALLDTILPGETGIVDNLKQTEILFLGPDENTAGTFPSDGALLGKRRGYPAWKS
FTTGKTPSMGGIPHDVYGMTTRSLRTFVRGVYEKLGLKEEEMTKFQTGGPDGDLGSNEIL
QSKEKMLAISDISASLHDPKGIDREELKRLALGRLQLRHFDKSKLSPQGFLVLTEEKNIT
LPDGTFVADGAPFRDEFHFTKYTEADVFVPCGGRPRSVTMANVGRFLKVPDANGESMLAG
KFESTEALKYKIIVEGANLFISQDARLALERCGVVLFKDASANKGGVTSSSLEVYSGLAL
SDEEHEKYMCATSKENTPEFYKKYVKDIIDRIEDNARREFEAIWRDHESHPGMSKTLISD
TLSEKNVKVRASILASDVFKNKKLVRYILFHYTPKTLLEVVPVDELMNRVPIAYQHAICA
MWLASEYVYSTGIDSNEFDFFLFMSAHIERA
>TCRU_5825 pumilio RNA binding protein, putative
MVQTHTKREEARAERLRKLPQTERLRKSALIKKREGRVLSAAEKHAMKMTSEYGEIIRLW
EVLRVSSDPAAKDAAAKSVGQRRAERYEHKYPTVDLLLKLIEPNFATYVKTPRVSRVIQS
MIKYASLTQLERILVLISNPFVTHATDAYGHFVVTALIRHAPHSFLDKLLALIIPAVPSL
VSHRFGIEVVNAAYSSRLCTSANRHILILAVLKDKIAVMKRWKGYPILEEVLLQEVTQRK
RLLSRLFGLCDTLVSQKCAIGYPFVQRLVAAYLKQGIKDEVMELCDTLRPHLAALCATRE
GAPIVTTVFFLIEPKKSKEVLRALSENLGSLLVDKYAAPIVARLFDLVYDVQLLRKYVVN
ELEAHLVEVINSPFGHQIVLHLLTPHEERKHKFLLPNWFQHNLFSMENNGWNHHTWLTHE
YEEETVEIRSKGAISTHLVVLPSIVRKFIEIASDPDKGLRINKHYVGLIAREVLVVNETE
DAYRAALQLSGEEIKALTRLAPSRDPSKRLREEESG
>TCRU_5826 60S ribosomal protein L19, putative
MVSLKLQARLAADILRCGRHRVWLDPNEASEISNANSRKSVRKLIKDGLIIRKPVKVHSR
SRWRHMKEAKSMGRHEGAGRREGTREARMPSKELWMRRLRILRRLLRKYREEKKIDRHIY
RELYVKAKGNVFRNKRNLMEHIHKVKNEKKKERQLAEQLAAKRLKDEQHRHKARKQELRK
REKDRERARREDAAAAAAAKQKAAAKKAAAPSGKKSAKAAIAPAKAAAAPAKAAAAPAKA
AAAPAKA
>TCRU_5827 hypothetical protein, conserved
QEEMSTEDKTRGCLTKAQTLRASGNYKEAVAALQSLSEHGVQWGPMYIAALDLLAELCFS
QEQGITVDRFFPAFKWNRNKLRGSQHLEEGTKRIVEIAMKHLRALGERAHTNAKATGETP

SEEELILAALSGVSPAQRAKERYLVPAETVAQFLGSELLSFNAIGHSRKLLPIYLDTATE
LIKYCQQHNLKRAIGRIADAYVRFFRRFLLSPIPSIVETDNPHLITMHKELEADREDFYK
EKPNTDRAVRVFCHLLQTLTEMNSWHAAWSTLQCFTRVMQEITQHPDPSRECQIIANSAM
AAVFWKCSHYAFHAHCLGVAAFLTGNGGEAAAAASRAVLATLCVPNTNKERRNFERGSDS
VFEKNARIAQLFGLQSAPAGLALWQRLQRMQVFQKAFPEVQALDGLLRNEMSDENIARQA
IKQLSIIVQKDPSLEMYEKPLRKVVIQRYLECMAVRTTRVEASSLQIGENEASEEVYIHE
IEPYILNESGIAVEIDHKTGFISFSNTTKMRVLEAFDALAERVDFHPPALRRKLDIRPEH
LLRAHDRSSIIHRLQHTCEETAEARRQSAKEREEAERENARLERIQNEEKKKEAVRLAQE
ARGLAEYQEHINQNRRKVVLRRLKEKYKGFDAPPALTLRASTDFVQELTTLLTAHLKKTT
QQKTADVTKMNHFERACRELEIPKRKAIELEELEQHKAERAAARENFLIQHRKEFEKRQL
DNQILKKFIKEAAAFAEQTQMKGKTSKRDEQQMLLQQERERLQG
>TCRU_5828 Long-chain-fatty-acid--CoA ligase 5 (EC 6.2.1.3) (Long-chain acyl-CoA synthetase 5) (LACS 5), putative
EKPDASAIYRIAGYDDAQQKQLSKELYNGPNLTQRFETICLRDPKRHALAYRPIDRVEQE
TMKDVVTGSEKVMDVTYLNETKYMTFEALWECMLSFGRGLVELGIRPNANVAIYEETRWE
WLATIYGIWSQSMVTCTVYATLGEAALAYALRETECSAIVCNAKNVARLVELITHGNIPR
ASIIYNDTLPASFDAKGCRVIPWSEVVEMGRRVAEQVPLRIPTDNDLTALIMYTSGTTGD
PKGVVHTHGSLVAGVSGLNYRVLDNIGPYEEGETYCVYLPLAHIMEFSVMNIFVARGALI
CFGTPRTLTRATARPTGDLEEFNPVFIIGVPRVYESIKKAVQMKLPRAGSMKRRVFDHAY
ETRLRALKDGKDTPYWNQKVFDKPREVLGRNLRIMLSGGGPLSDATQDFVNVVFGLIVQG
WGLTETVCCGGIQRTGDMDVGSVGQTEPTVEFRLLDVDEYKHTDTPEPRGEILLRGPFLF
KGYYKQEKLTREALDEDGWFHTGDVGSIAANGSLRIIGRVKALAKNVLGEYIALEALESM
YVDNALCVPNGVCVLVHPARSYICALVLTDETKAMMFAKEHGIEGSYPDI
>TCRU_5829 cytochrome oxidase subunit X
VMRRVFPNVACLCLAKSKRDLHFPITPPPIEIEYLDEDPLEFAVRTEARKWGFDDMSYMR
ELAFVRINNNPTVGQFRTMTPDERRNLFWGSDRQDFFRHLTFMLTGTPEHLYHRGW*
>TCRU_5830 conserved protein, unknown function
MKGSLSSYEKDLPSDLLELIDHTTRGVQRLYETTRRRETLGESRERKAFVDDGRASACGV
QHTEELAGTARAGGGVAVPPVMGKKRTAGLSSSLLPRTTTAAVHEDRPPHYCYQSENGRP
LQKHRREPNNKDTSAESSGTNGARRWPWSRVQTLSMGVAADGRSGTSTTNTTLSSDAPSR
TLLAHSTQGAARSGQNVSVKGTVNTSTTGTEDNNASQIGQRWKDTFRSLLSGAAANNTNT
PTPAATEASAAPYENTHTEQRGPVTNLPHETSLSLEATETRRQHDAHAFISTQTSAALER
LRRQLAEQEASHREELSRIRMEHNRELSQLRHEALETRQKSEEEVTTQLQASFNVKQKLL
QVAVEEERLRADEARKTVEEREKAIEKLKVELEAATSQRQSLQGDVDAKKRQLADLRESL
KGTRKRLAELEEELAKRKGDLVESRQREKMMTMREKDALDLVSRLELQLREQDQRSREEL
RRLEAEFHLTTKSYQDLIGEATEKLTALEKVERKYHALKEQRRQQKEQQEELALKLTSVQ
EDKKHLTERLEFLQQELEQLRLQIARKEHEMREERAGHQKIVEGITQQLQEEEHKYCREV
EALQQALRHAEDRTVRLEREVEGLSEQLKEEQAHSKQLLLKMEQSALRHQEDLSSTRRAA
SAHQQQTESVLSSLRRQLREKDAKLEALATTASEPIQRLRNQLEDERSKRAHLEEQFNRY
KQRAKVAKEAALREIRREQQRAPFAPRSLSRTSAPPPSTSPSYDGGKGFLGAEPYTVQVS
ETTTRATTPQSSKMAQTGWDSVGSISNISRSSPLCSSRGEVIETVDPPSGDTGNRWDATQ
TTLPTSSQPPQLDNIDERVLQHEQILRDFHQSAAEVFRKITCNRDEFLEKCTSVVRSVSH
RGGDGE
>TCRU_5831 pumilio/PUF RNA binding protein 6
MFSLGVAERSWNEDDERVQKQQQQQQQQQQSMPSMNTSGEYGMGTGSALAFAQHMRGNFA
GTVERQRLQPFIGGLQPGSQQQPSSASWSRYTALDFELLLHEGKQPTDFELLLHEGKQPT
EDMRRSVAYMRWYNSKRLHESQLPPPLTDARQNTTDIIEEPWEGTSTVRMAGRMNLPGGG
VLETGKGAIRLELDAKNLQQSNEQHSFNPYAAGFQHDNMLSPGTQFFGAYAPTPLATMAT
PNTLRAYAHSRMGAQNSSASNNNERDVPQAVPPVATQPLYTEWNSTADFCGGTNALPTLN
QQYYTQEPMNPFDYYTDSAVTGYYNAAVASMPDATHVQPAFVAMGSANNPGMMQGAGGRG
RRGGAGSGGRGRGASSGKWNPAGVKPSGRGVPYSEPLQPRSARLEEFRVDAMNGTISHWR
ISHILGYAVEFAQDQEGSRFIQRAVESATHDEVDALFHEIFESPLVLVTDIFGNYVLQKL
LEVGNARQLAHAATRLQNNVVSLTLQTYGCRVIQKCIEVMPPEGLDIILAELKGNVAKCI
QDQNGNHVVQKCVEVTPQRCGFIVSAFTGRVMELATHAYGCRVIQCIMQHCPDQEEVIFS

EILKCVDTLAKDQYGNYVIQHVLQHMKDENKVTRVFNALKDDFYEFSKQKFASNVMEKIF
VRADPEQRMEIIQKLCAPVEGLETPPVEVLAFKRLPPVKKEEAEKQRNGYAKKGRRDKER
EREKESAGGPVIEVHSDGKEAPSMLCLMMQNPFANYVAQRVLDAADVEQFWCLVDNIQKY
LIPISSYTYGAPIVQRLVRRELVKAPEDLVFNLATAHPGSGGKGNHAHHRKRIAE
>TCRU_5832 NUDIX hydrolase 3, putative
MLKRYERTKLNVLRGERFLRLCEVSYRAVCRDPSLGGAEGIANIEDRTWEMVQRTFQASP
ERCSLKNAPFSVDGVEICALLRRPDNVFLILVAQYRPPVDAVVLEFPAGLVDNGEDVKSA
ALRELKEETGYVATEENIISVTDALCCEPGMTDSCCKFVRLFVDGEKEVNRFPQQELDEG
EDIEVILLPISLKKGVAGGDTPLQSLNKLLHEKNKGQQRNIVDAKLYMFLDGLS
>TCRU_5833 60S ribosomal protein L34, putative
MACPRVQYRRRMHYATRGNRMKLVRTPGNRLVMQKRVKRSQGPHTPWVLGHKRLAGTKAL
RHTEARLASRHEKSTSRPYGGVLSHEQVRDRIVRAFLIEEQRIVKRALKAHAKSQKEKKR
RDSKKKRKEEKKAALTKKIAAKVGARSALTKKTTAKKKAASRVPVGAKV
>TCRU_5834 acetyl-CoA carboxylase
SMDRRSSTQQLPFHNLPEFCTFLGGTKKIERVLIANNGLAAVKGIDSIRSWLYEHIGDSE
AIEFVVMATPEDLNANAEFISLADFHVAVPGGPNSNNYANVDLIMRTALQNSCDAIYPGW
GHASENPILSRECTKLKGKVVFLGPTEEAMFALGDKIASTIVAQSNGVPTVPWSGDEIRL
PPGVFEVDPLVYEMAYITSVEECEEVCARIGFPVMIKASEGGGGKGIRRCLRMEDVSDMF
VAVSEEVKGCHIFVMRMLENVRHLEVQLLADEYGDCIAVHTRDCSVQRRHQKLIEEGPVF
GVDPSIIASMEAAAIRLAKAVGYRGLGTVEYMYDKATDNFFFLELNPRIQVEHPVSELIS
GVNLPAALLCVGMGVPLHRVPEVRSFYGERPYTKTPINFSQRRSLPAKGHTIAVRVTAEN
TEEGFCPTTGRVEEITFKNSKECWGYFSANPGGEIHQFADSQFGHIFSSGETREDARRGM
VMALRNLVIRGEIHTSISYVLELLEREEFIDCDISTAWLDRLITERAMQGPQEQDLHLAL
IAACVFRILRKSEENIGKYVTFLGAGHVPSSDYLTNQLTESYVNRSKKFTVTMGFTSPAE
VAISLNGSVLTVPFRKLKSGALQLRIGGKSFIAYAEKEPASLRISINGKDTTFTGDTDPT
KIFSSVPGRFVRYVVNDGGHVAEGSTIAEVEVMKMILPLRATAAGVLHHRVAPGSTIAVG
TLIGGITLDDPSTVARPQEVWEQWPSSLLIEREKKMERPNGLTRAQLGVESLQYMLRGYH
FSGISLKKRLQEAFDNLSSLCLSSVVLDAVNFPLLSTKVSTAVWDDTKRDTPNEKLRIVL
HALVADYISVEKPFAHCSRQEAIQRLREVKDDPMEVYALDFAHQQPCHHSVIKELLNMLE
SNMLLLRSLQSTLPFLLELDSSTYGSLALQVRYLMRQCSLPSFEERKTTFAKVLEEGRIA
DLIQGSHGDDLMCAVMFDRRTPHLAQLCLELYIRREYFGESHVKNLDIFVQDGCWYAFYE
YEPLEDHDPLLAESFSSEENIIDFVSEYKGAGLCMMFPDDQVLRVKWATALNNFICNVPS
EPSVCTVFFAVSVQSDVEEVARQCQQLLEEHTLALMQHRELQRFTFIVHGISGGPHTFTH
RRCHEWREDKLIRNIAPLSARRLELHRLVNYDVAMYPTPFKDVHVFRATPKKKNASYLES
RIFARVFLSPRDLGVEAWTEANEVDAGHMLTKCFGALEFARNDNAFRYPIYNHVFIKMAE
LTFDIAKMKRLFERVLKSYRQRLTYLGVAEVELSFNLKVSSGCIPFRVMISSPSGYHVVM
RTCYELIENSVICLRRAESSEDVVLTTPSKLNESTNDFSSGSKDKGNGSNGTNNNHNSNL
APRTLLRTLSKLEALRNLLPSRDKMETPGCETSDEIEESLPLGPYPMVSSKQLRRLQARS
LKTVYVHDWPLLLETVLRNQWEKHASGRGLSWKCIPKEVIRAKELFLDASDGKTLCEKKP
LGHIPCGMIVWLVTIVPPTYYDSDTDTAGIRRIVMVANDIAFQSGSFAVPEDDVFSAASE
LARRLRVPFVYISANSGARLGLSVEVKKRFRVALSETNELEYLYLLPEDYEELMRLGVRL
SVEPRQEKDGNGETRYVIRGIVGAPDEYLGVENLRGSGLVAGQMSKNYSEVPTISVVTGR
SVGIGAYLNRIGRRVIQTDDAPLILTGAGALNRLLGKEVYTDNGQLGGKRIMVPNGVTHW
CTKNNYNSAEALLCWLNYVPPTVEPLRCCPRVLALPNYDPVDRDVKFMPKVGEAYDPRHL
VCGVGDRWGLFDRGSWTESLEGWAKSVVTGRATLGGIPCGIILVETRMTRKHDPADPADP
TSASSFIPQAGQVWFPDSARKTADALDDFHHERLPCFILANWRGFSGGMRDMFDEVLKFG
ASIVDNVRVYNCPLFIYIPPCGELRGGAWVVVDPSINHNGVVEMYCDPTSRGGVMEPSGV
VEIKFRENDVRELIRRSNPHLAALDHQRLRDEENRLLPLYRDFAIRFADLHDTHFRMQAT
GAVRGVVPWKDSRRLFHAKLQRKLKELSVAVSMVEAKEVGSISEGVRKIEAAFAQDHPDI
PWGTNDALHMQWLTEKVELNGVFLSGVSLLPPSPLTAVEEVTRLTAQCQGTDALENCFES
LFEDENMLKAAMGAMRR
>TCRU_5835 tousled-like kinase I
HQRKRAREGEVGTEPGDVELPPQLPQEKKGSACQSPPHSRAPPSPEKPTNSCAGEGDSDC
VFVPAPSNSCGGGTSGGGGPHQERKLKQATLVSFGLINDASLFRKEIADRDAQIDELRER

LSSMESRVAEAESALAASEAQLGQVVLRAEHYQRVLREEMLRTARQAKSDARRALHQKHF
ELGQIAMWHSSGREVWVEGNRPKELIMQLEELSSRRDEVEELKKAAEKRVRQLVRSSDED
SMTPELQSALMESQEAMQLYTSEFAALGSSIQAVKQRQLELDHEKKAFLKEIRRVSDEDA
SEFMAVPAIGQGQRYVLMHLLGKGGFSEVWKAFDLQDARYVACKIHRVQREWSAQTRLHY
RRHADRELAIMRTLQHPHLTRLYDEFEHGEAMFVSVMEYSQGADLDTHLKRYGCMREMEA
RLILLQVVSALRYLAAQEQPIIHYDLKPANILFHSSNASSLEIKITDFGLSKLIQSRDGP
HDNPTIELTSQGTGTYWYLPPECFDTVATPRISNKVDVWSCGIIFYQMLFGRRPFAEGES
QRRIWQDKLIVSSARTLRFPDTPRVSQEAKDLIQKCLEYHPSDRYDVHQLSQDSYLQRTS
RRSTRSER
>TCRU_5836 hypothetical protein, conserved
MLRRTLQFLLEQERPFTLRRAVMAKARPSHSSPGTKKGGTPDIRQNGHTGEFHDDAVAMI
AQMVPNAVSPPPPPKSSGALQPSKDQQHGDASEDAYRFLLHHIDSEIAALKRRITTVAKQ
RETVENNQSRRIRELFECIERPWLLLESIHAPQLPNKALEVYAKELYFKQHGADAGNCEQ
DAVFLDACRRNWRGLATAQRKPYEIAARRNEHLRKELKKKISNGCSHFESFCEELKEWTA
AMARNEMKPLSSSQASPRGSTQLAQKATKSPAMTTRKASASTPANVAA
>TCRU_5837 Regulator of chromosome condensation (RCC1) repeat,
putative
MLRRLHTRIIGMGSVCGMAPSPPAEVFLKSLPPPEEVDYAKYLRFEREERELRQSTRMRR
RLVAPEPFYDIHCGAAGHKHVTLMTREGNLITFGDNRYGQTAAPRQEQQERHQREEEVQD
VCNRALRNKAQVSDPRWAPLYIDLNGAFKSGKQSVSCGSNYTIVYQPGGRRVIAFGNNHM
GQLGVGHKAQIDREKGFAEWNPTSAWWGHSGGVIRSIVCGFNHTVLQLTCGSLFAFGSNT
WGELGIGSTVSPMEPTRIQYFEKRGIKIIKVAAGNSFSLFLSNDGRVYGCGATNSGQLPP
NEFEPAPVPLTRSFQHGAHRGGAKLIRIKDIACVGSLAVFLSSKNELLLQGALPDYGFRV
SSPRFETVNQQHALDYFRSRLSDASEDAVGKDGFHIDRLFSGPSTLLAIYRNGCVAGLGA
NTEGQLQSVRKTWKGREFNLAKAFAADGLLPVLLPAKPRAEEGGTVPWLTSGSGFTLLFD
NDEVYGAGAEAKPIELPPPPASRR
>TCRU_5838 cation transporter protein, putative
VGDAFNYFFQGERERRLFSFFLLTVAVMVLELLYGISANSLGLVSDSFHMLLDSVSIAVG
LFAAFVSSLASDKMTHPFGYARYRVLGGFINAVLLLFIALFVVVESVERIMNPPDINAAY
LIHVSVVGLIVNIVGVAFFHGVGSHSHSHDGCSGSVDHNLRGIYLHILADLVGSINVMIS
SIVISLTGMKIVDPICSLLSCVFIAFSAFPLLEETGKVLLLGGYPYDEENFLKKAIAGIK
DIEDVDSVENICAWPHSTAPNESAYCAIRVLARARADHGKIRFSVTHFMRNFFKAETGSH
HLNIIVHVE*
>TCRU_5839 SLACS reverse transcriptase, putative
LVQSLDDLYPQEDTSLYPEPAVSAPLVTFDSKDVAKMIGSRLTRGAAPGLDGWTRELLYP
LTKDKALLMEITAILTDMANGNVAPEVAHRLRATNLTVLRKPNKKFRPIGAECVWAKAIS
LMAVDAVMPALKTCFKNLQYGVGNNIELAIQKIRRDFHLKGSVAMLDGRNAYNAISRTAI
LSAVYGNTT*SPLWRVTRLLLGTEALVGFYEKGQLVHSRKSMRGVRQGMVLGPVFSIGTI
ATLRQLESSFPNASFTAYLDDATVAAPPGMLGKVCEATSRAMRVLSIETNEDKTDVLNKG
GPVDMPAEYIWPFARVMDAGIANDPESELITQFVQLKAEETDRLFRAIVELPFAKHTQWR
LLSVSALPRVKFFLRTHAPVHTRAAAEWFDDRVTGVLGIIMDGPVTKRARDIAALPVRRG
GCGLRRQGEIAEFAYLCLGEKGKQHALTDELDAKHQSDLYETLQGPDRKVFVSNTAAGAG
RLLTDPQVHADDKGFSTYLRERILMRVLPEGQKCVCGANASNGHVHKCTRLQQNLRTTRH
EMINMTFANGLRLCGFQCGMEPRLTEASRRRPDVLIVGLDTYAITDVTVTYAGRVTAYVS
EESMEEADPLRAARDRLTQKRQKYRHWALANGLDFEPFVMLTNGAIHSASRRWLRRILGN
QDHRLTITNAYDLIVADTLAAMLRGNVRVFGAACGR
>TCRU_5840 aldehyde dehydrogenase family, putative
NTPIEKIPLVVSRCRNGFRTGVMRPLEQRKKILLSFLRMLDENEEVFCRAVHSDLRKHPN
ETKFAELSVLRVEAHHFLQHLDEYASPEKPQMEGVFRLEECEIRRDPLGVVLVIGSWNYP
LLLTLLPLVGALAAGNTVVAKPSDLAPASADIMHELLLKYIPDSIVGLVKGGVTETTQLL
EERFDHIFYTGNSRVAKIIMTAAAKQLTPVTLELGGKTPVIVDASCESNLGVVARRIMWG
KVLNAGQTCIAPDYVLVHRQIQTKLIEALKEARDEMMGANPLQNQEDYSAIVNTDHFDRL
VDLFKGGTLAFGGEMDKVNRTIAPAVLTDVQLEHPIMTEEIFGPLLPLLPFDTANDVLQF
LGPREKPLALYIFADDKRFISKVVENTFSGGVLVNDVVVHVAPSGLPFGGVGHSGMGAYR

GKFSFETFSHKKPVMQRKMGLEFLNAPRYPPYTLDKFRVFRHAVELSVGDRSFNQHLRPF
SDPARFVALGGHFIRYLM
>TCRU_5841 protein kinase, putative
LLLLLLDGRICCVSLVDGKVRWETQLPGGPLFHCGPRRQSKKEKRMWAHLPSRSACRSCR
SISTRTMGTEAQQEKELENVITDCSLLVFPHDGTRHGVPLINWHLLIAPDRGDKKVTWWP
VNDVIKCWNESSCSAHKVLELQQQVTSHTELDFSSGKLLISLSSQEDHINTEEETAPDEL
SSVRIILERTDQTRNVIFPPSQPPSHSRVETPSNREGQEEVSQSWYATHSTVTIDLLDTS
LDDGLFFDSGSHVDHRLFHIVQTITGNGFTSCLHISEGSESIGRLELADVNCPLVAAQIV
CRKADAMASNEGKTSRLTCQGIPVVTSWSKMERIYVFNWNLQECGGNVQELSGFLYGNRR
VLFVESVTPKIEFLPVPCDSETPEKRGVDFLPSCTLVGNGYGNGSYVGDDDDSSETESSV
SSGAAENAMVLHKRATSLRNGEEKGALVSGDTEISFFDENFEIVALLGRGASGAALLTRN
RLTGLFYAVKVMLMRDYFSKGNALREVRLHALLHHRYLVRYYACWSEALTPCRIQQLATI
GLCKPMGLQEKAVINGPGCIDCVNQQHGVLLQLKDSTNCLLASEQQGMNRNLLMAPPDTK
AGNSTGTYLAGVDSPESSLDESPQRREEWDDGEESNSSSSVSSNASRNPPMDQVVFLQLE
YCQTTLAHRLGSRICIDRVENIIIALQIFSALHYIHSRDCLHRDVKPTNVFLDYNCQTIG
MDDTSDDVDEDDEDDDSNNNNNNDDDDDASAGDQKEEGGKDADAENTTNPNGGVQDFHFD
SDENACSRMELVQPDLAPAIPTQFLSAFELLRLKASVGLLALYLKRFKSAQDESEKRKVA
RLVRRWLSSRLVQVRLGDLGLAKPLSDQRVEVARYFDRSAINTLGVGSPLYSSPEQLEGA
LCTPASDAFSAGVLLAEMYIEPKTVSERLFELQRVRDGVFPYPALLREYPELQVVQGLTR
SDPKSRMTLRDAGRVLVKTLDKILILFLS
>TCRU_5842 phosphopantothenoylcysteine decarboxylase, putative
MSAAKTPVNVLILVTGSIAAVKVGLLLDQLFNESYQVRIAATKSAFHFLNRAQKPARELP
LHHILTDEDEWREWQGMNDAVMHIELRRWAHLVVIAPLDANSLAKLSNGLCDNLVTCVMR
SWEVKKKPVILCPSMNTAMWTHPVTAMQLKTLQSWYGMTPVGLRLDTDETDGYITALPSN
LDEAMFQIVWPVKKRLACGDVGIGGMASVDAIARVIQHTAELIRAKNPNATT
>TCRU_5843 single strand-specific nuclease, putative
SADAWWCNGHMLVNEIARRRLHPEVALIVEEAAVNLSASGPFPSTTDFVESGCWADDIKK
LGLFVMEDWHYIDTPYNPHNINIKKNSVNTENLKTVIESLKRTLRRQDPLPYIMSFAIVN
IAHFLGDIHQPLHAVELFSPEYPHGDRGGNAEAVIVHGKMMALHSLWDSICQGDVKNPRR
PLDRWHYAKLREFADRLEDTYKFPAEVKSETNTTLMAMESYDIAVQVAYPGVVDGAKITD
EYLEKCRAAAESRVVLAGYRLANVLNQLLDKTQK
>TCRU_5844 hypothetical protein, conserved
GMGGKNDKNNEEKPKKLNAQQVALNKVVEVADRLYKQHEQERVKTETADQISRRGALLDA
ALEKERLRIDKAEHEKIVKEMEEREQLAYRECEKHRIWSRVPHASRLPQVNSESSINTFL
AVWRDEEREYDKHTPLVTVINRRNSVGGGLQNYYFINGEFGVSPAARKKMVESELQQCLE
AYELTEAIRLEADRSLTQLKMEDLTFFSKNIGNVCEQVLHSLDFITIHALLGYDVILEGP
NSEFLTMSVPPTNPVVKYGLWVKVKETTRSFASMVFPNIAIRLDPKSSALPKLPKALGLS
KENVAVRVIQLGFNPHEHHGSIGREFYALNCVIKLDLLNFTERPKHVGDWLYRSETEEAH
ALHLVPYPPQVLESNEEDLSLRVSFEAPNSIVMRHSSLLIGKWLEASKDWEPCSHTSAST
DSTGIEGRRCVFATSEFATFAVLQEKGFDVPYEHWRLHPVSFDQVLMVLEGRRRGEGSDR
EFRILIQDAQCKLLAPEDPELAHLRENWLEPATLIRLLSQTGFNFLLDDEDAKFLENIVP
KTSALEEKAYADIAQFCLFYAIASSRHNKCGEDADLALFRVSKQSRALDNDERLEVQLDE
DSDWHSVRYQTQCCAFAAIRESEEVPDLHILEGHESHFNLYTLLLHEKGEEVRLQAVHHT
NFLLRRCVFQLLRLIRPLTWG*
>TCRU_5845 geranylgeranyl transferase type II beta subunit, putative
LLADLHLKFILGLDEKKDDLRYWMSQHLKVSGAFWGLSAMELLGHLDKINRQDVIEFVVG
CWNSDGGFGGNVGQDSHMLYTLSAVQVLCLLGALNAIDKEKCACWVASMQLPDGSFQGDE
WGEVDTRFVYIAMNCLQLLGRLHLIDLDAAVRWVLQCQNWDGGFGVAPGAESHAGQIFCC
VGALSIANALHCIDKEQLSSWLAMRQLPSGGLNGRPEKKADVCYSWWVVSSLSMLGHTDW
IDRKALFNFILACQDAEDGGISDKPGNMADVYHTFYGLCGLSLLGYEEYPLNEINPVYAM
PYSVLEELGVPEERGLHVGKAR
>TCRU_5846 hypothetical protein, conserved
LLRRMVPRGMALVATTPLLSTSRGYNMFVFRDPKRRPQLTEEERAKVVINQEEWPEEFKE
FDPDDPYKNSPEIIEGMSSWNLFLWGVECAFIYQFYELVFPKSI*

>TCRU_5847 hypothetical protein, conserved
MSIAFTRFKLRCTTYTVDFMRRFCDRCNVVLSALSSPFAQIGQRIGQESPWVVIIFASSI
ISIFPLLFYPLLKPYLMNDVRWQQEEERVRLCLQKGIDPYPYMRHKEYVFGNTVPASQSE
EEVPLEVSWEHRAVVEFQKAKEKLRKEVGGDVTDSVAKLMALRAELRREFGKSRRGVSEE
PENLIFKGQRDV
>TCRU_5848 hypothetical protein, conserved
SPVNISRFIEMSARSISPQREISQMTPQKQFPQNKITREAKGNSTESVKPEDVLHEVSHP
EENMAENTAYLLQCGSPLYDPVKEIWRCWNGHELRIKERSQYGAVDGVSCDFCGFTDWLE
VLEGTGVGMKGKRRGKKTIKRREKEAEPRYFYHCDVCDMDLCTHCAKDLRVDSRYHVPCM
QCRRCLVFMRNEEAALHHCYLKRAREVLNFMTPSTSTSGGASSSSFTESVATLTSFRPRE
SSPPVIPMPPDPTRASTQFPIIAWEVCVKFENATAEAEVRKIGESLSLRGIETPGVPDQL
IFRTPTRLAAEELAQLVHEKGLFASIRR
>TCRU_5849 hypothetical protein, conserved
MNLTSSFLMGGQPDVHRYAQATFHEGTHRQAPGDSTPWRDVSSPLNRLRGWWLAPAAKGS
MIAAWSVTLVLGAYCFFIQQDAKGTYLLNNVLLRTLHEETLRADANQERASELRELMKKR
NVQEEIRNEEHLKAVKGFEEYDKKMKKGIINHELELSRERARADAVHERNRELVSELLGV
RQELTRVKKENKTLSAELANLQKI
>TCRU_5850 hypothetical protein, conserved
ILYAHIFLFFQEFSTLGSWDEGIRAFLQNASQKEPQPWDMGYEERRRATHEPRVIRQLEL
EDEWKGTCMEGIWNGMRRFALPVDDYKVSEACFYEYLASVGINSVFLGNKLYGIFRLDKC
SEVDFLRVCKAIHLGLTDSSTSFNFLEHCYKSLPLSPISEELERNTVIKVSELQRRKKDQ
KTAAAELRLQQLEGILQYYEETGEAIFDIGAFCSLFFDEKWRYWAGSFIKQLLEAAAKYF
SFPYGVFPTIPLRWAKKTEPLPYDRNALHDADSLLLRNIELTERGNADGKRKGRKHHGRS
SKRK
>TCRU_5851 cytosolic coat protein, putative
HNVNIFILSVTVILWMCALRAHAFAFDLPANKQRCFIEEVPSSTELLISFAALPGYAQFV
DVVVTGPVDHVYYKSTAQDRGNFHEFVAEGGDFMVCFYSRLAQGVRQTEGMKRSISVDIR
VGSENNDYSELATKEKLRPIEVELRVLEDAVRSIHSEYLYYKEKEAEMRNANEAMTFKVT
WFTAFIIFIFVVFSVWELRHLKSYFRKKRLID*
>TCRU_5852 3-oxo-5-alpha-steroid 4-dehydrogenase, putative
PANPTLADLKKAYKPKTDVHRKCFKVAAGSGNAENGQLQHVTLVDKQPLREQGVKEGGKI
IYKDLGPQVGYRTVFIVEYAGPLAIMLGYAARPSFIYGSNITRGYGYTQKLFISLFAAHF
VKRELESLFVHKFSHATMPRRNIIRNCVYYWSFALFIGYVLCHPKYTEPSSRVLVNASAA
AMVVFELLNFAVHKQLSGMRRGDGDTARSVPHGVLFSLVSCPNYTFEVLSWVAFSLGTSL
LSSWFFTLAGFVQMAEWAVKKHKGYVNSDPKVKRRKCMVPFLF*
>TCRU_5853 LEM3 (ligand-effect modulator 3) family / CDC50 family,
putative
YTRHSTCPVFLTLILLAVIFIPIGVVVIKASDSVFELSIRYDETNNYQYRVGPDGKYPHK
FRFNNSNFSTGAHVSRNFTLLKSLASPIYLQYALVGFYQNYRRYAFSRNLAQREGNAYPV
SAACEPFRFPGEYHNRRIIGIYFPCGAIAWSLFNDSFSLYRLSDASKSNINSQVFENAKL
ICDGGAFDAAGNSLNEKNLCIKKGIALSSDVRLFHPLTDGKKDSAVWRFGGDPAANDPYQ
KEGYYYEEPGHPIPSNVDEDYIVWSSLSYMKDFTKKYRIITTDLVPGNYLIDIVENFDVF
SFSGEKYVSLVTRSWIGGKNYVLGILFLLMGCISFVLSLSFIIVQYL
>TCRU_5854 Mitochondrial N(5)-glutamine methyltransferase MTQ1,
putative
DGKDETIVEMDEVRMQALPKTYRRSSPKESCLSVEERRQLTRMIFETHYASLGEGKEDRA
MWYQSALEVQWLEEWALAEGGNQKDAARRAVKKAVLQRVDLHKPLAYIIGNQPFYGCNIH
CFPPLLCPRPETEMWTHWFVQRHLSRATADEKSPLRVLDMCCGTGCVGIAIAVHLPHTEV
VAVDVMEEAVKVSEENARRNGIHVSRYRAIKSDMFEAFVELDDTSSSGKNKEGISENKKT
QIADLHVGSFDIIVSNPPYVLPEQYVQLHPGIKLWESKIALVGDAKRENHQYLYFQELCE
MGSVMLKPKVRRNATLASAPNFIVEVGLQAERVASLMERSALWEDVEVHLDYAQQPRWIT
ASSSH*
>TCRU_5855 hypothetical protein, conserved
QRFFEWICGTSCVNSVVVLRTANPHDAVLYHTLLLPLQKKLNYSFILAVEKVTELDKMVV

IELRTREFHREYTRGTMLAFPELPKCSVATAPSIVSSCKAQERLVLCRVPLPDLRVYRDI
PAVISRLIAAHGENRRLFSSYAEEMLFYLPFIEANSRCQNHPQQQSHQIGTTTVTKASSS
TASLSHGEEKNVFSGPDTLTQVEAAFLGNSSPSTGRSDKSAGLALLGDVIDINATMFSTS
WLVGVGDGAVRTAEDVGSMNSRGEDQFIYDAIHEAFFHVVLRTPLARPDFLAAETLKLHP
FKVWRASRRSRRAAAELYVLDVAAAKGDAVISFAHVVDEVVAQAVLVHHRGSLAEFVDAL
FARFALRYTPVIPALREVVERRRGGVQRRRPSGENSERDLRMEGNVNCSPPGAGPSGLAV
GFEDGVVDDEEDIDEVVRELHYTREYILEHRITFYNAVLTTQGSNQLEEVFGVPATVFPF
LPCARESVAFVTHAYECIVAEYGPLDFHNFTKYAHDVFVRDRPEIVRHAPRIFRMLNKTR
SGVISFEELCCWIARKLSSGSRQRPDAHLIAIAMSLRLPMALVFNKRKQWPRM
>TCRU_5856 hypothetical protein, conserved
IMRQSLALLRRGKPRPRAGMFPDKYRRVPALLKPQQGGQQFFNQFLIRFTNDRLMRRDVE
DGEDKKESEIAAQLPQMDWERMSARSSSDAIREEMHRLVEGDAVQHQRVFNERIWYEEEE
RRRLQTGADAAVPTEDAGGAKEHDIPPRVLGNDYFQSRFGYSLVKQSEMPQGVTDYNQLD
MWGEMPKYTRDMVFLYLISRRRNTYAVAYTYEGKRILSTYTAGNRGLKGGDRGFRSDGST
DNGHQVTSMYLNDLLPKVRELRANEGRPIGRGEKIELVVRVMGFYNGRQGAVRAVQDRAN
EFHVRYFEDITPFPLNGPKMPRGVFK*
>TCRU_5857 hypothetical protein, conserved
LMHVEFRISCIERICAFDAESFIRMHQLRDRSLLELEPKRALVTLPEGDRRARRSFQPHL
KIQLVFENLVCIESSVFCGEAERQQHEKQVTTNWDASEIRTKRYCSYTGEVIVASLPISV
AKRHLKIRLVQLVPELSREEYALLKASYPSFFNMQDNSLCIGVAKIGMRELLITNGGVSV
KLQPKQGMMSAVEARNLNTIATNGMFGRDVGGSAVLTLQTASVIFGEKSLLPWFTFSRRS
TGATPACPFSTVAQGVDGTVDVHGSAETNGSEERIAELRQQMSSPVAHFLLVPYMVFIHT
VLCLSDAVSWRHTTRTALLFCIVMFVFLTDVLEMGLMLGFLVEVISITRMAVLFYRMPSR
MDRSVDSVISLAKRGDDFQAVLYGCQNHVINGMVRARLFFSQGLLADCYFELAFLFSRML
RAKRWLLPCVMSTITASLVFSTETLLFLLLLAAFLIHPLTLRVPPSHLRKLWRRQMSLGV
FWQVLTLCRPMRVSRVVLVTEERERKRLRTGSLSTTPFISPSPMRSSSHSLHPPYRNKRH
WRRIGIRTASVNASAERESGQSRQAGDHGSLSRMNPQAARFLGNSAAVDKSSLGTAMNSN
NHLAAHLSSSKVFSRSVGDTLRLDAQTKSLLNFALIVITTEGAPVNGNKMAISSSGGNGL
IVQKFRRILQRARALERPPPPESQREQYQAYFNCVIPFLQFLRRQCTLKVYVTPSSSLSS
LPTLDTGKMLRLDHLANLSHLVDEGEDDGITSTLLAHSSQQVLVGQLPPLEHIDTSARAF
AVLAAYLLQGSRLSIYSRPGNKGCGTIIPLKMGSNDIELAPEPNPCPPSLQKALIDIWKG
WTDEDVSIFINTDVVMNIISTQKEFLGGDGSDGLCSNEDYQNIIMASQDGCKTARETSKR
LFST
>TCRU_5858 endosomal integral membrane protein, putative
FFLLAVAAVLFSPFVADAFYIPGMQPKYYSEGETVPFMVNSLRSLKELFPQGYYNLPFCA
PVFIKTKPEALGEVIWGDRIQNSLYSVDMKKNSTCTKLPDCDVVANNRNIRNNIDKLEKY
IEKGYRGFMNVDNLPVFGDGLPEYLASCRFQSKDTQYNYYRGYPIGVPRQCAGKTLINNH
LDFVIDYNTAPRDNEKFMVVGLRVTPHSIKHDIDGNSCSEALVFRRGEMNFLSTDDVREG
TTVYWTYSVTWQPSNVIWATRWDAYLHSSIADTSASFHWIYVCGSLLIVILCATSVATVL
MRALHKDFNRYNSLDPEDNQEETGWKLVHADVFRPPDRAPLLASLTGTGFQVLSMFTGVL
LFALLGFLSPARRGALLTAIIILFVFMSTVAGYVCGFLLKYFNRREWKHVFICGCAFPGT
VFGVYAFANMINWAHGSTDTVSFSVLFTIFLLWMLISLPLTFLGASFSFRQDPPANPVRV
GRLAREIPPQMWANSPSFLYVIPPIFPLSTIILELNFVLQALWAGQVYYVFGFLALVFLL
WIAITALMTVFHLYYVLCYENHQWWWISFILSGGLGIHVFVYSIYFYCTQLAISSFASSL
LYFMYMGLLSCAYGLAAGAIGLTSGICFVRTIYASIKVD*
>TCRU_5859 nucleolar GTP-binding protein 1
MSTIYNFKAMTVVPTYKDFMDIVLSKTQRKTPTVVHKGYHISRIRQFYMRKVKFTQKTIN
EKLTHVLLEFPRMDDIHPFYGDLMHVLYDRDHYKVALGQVGAVRHMVDNIGRDYVRLLKY
GDSLYRCKQLKRAALGRMATACKKLSSAMVYLEKVRQHMSRLPSIDPNARTLLITGFPNV
GKSSFMNKVTRADVEVQPYAFTTKSLFVGHTDYKYTGWQVIDTPGILDHSLEERNVIEMQ
AITALAHLRACILFFMDLSTQCGYTIAQQLSLFQSIGPLFTGKPVVVVFNKSDVCTIDDV
STEEQSLIMKAIEEAGAKWITTSTLTDFGVGDLKTLACETLLVHRSEQKEGSGRFQAIQN
RLYCALPQKRDNMERPAYVPTSVKKEQEECDASGPARVRRKTERDYEWENGGPGRYQPNE
RKTWDLEDPEWNSDIIPDIMDGHNIYDHIDPDIHDRLLELEAEEDARLQELEMEASKKRP

QYELDDATLEAVRFIKEKVKVLKMERAMKNPAVRRTKQQSDAIKKFNGRTGSQDARSATP
AAPASTAGKKRGRSISVAQEAIIRDRSGSTHVSTKTTRGISSRSASRERSLSVSRGEGYR
DINEKLRAVKLSKVKSRSRNRQGKKGEGDRDTPNLRPKHLFTGKVKVNGKRDRR*
>TCRU_5860 glycosomal transporter (GAT2)
LFSLAVMLFHGIYQRMRSHQESTHPRRLLRRLSEPRKRPGVHFDRTLLRRIIELLRVCFP
RIVSAESGLVLLLTSLLMLRTTLTLTFSQISASNTKALMQKNFGHFIFGLLDVAVYAVPA
TITGVGINYATATLEQCFRGNLQNALHQEYFEGCKMYDLAIKGLVDNPSHRVTHDVQRFC
SELSGLFPAVIKPILDIAIFSSALAGFGGYGVPLVMMLYYAFVALMFRMLLPNFAGWVAR
SREKEGNLRLLHTQLIQHAEEVAFYRGAEIECENAERLLKSFICVERRLKRAKWWSTFIN
GILVKYAATGVGYAVCAVVVAREKGHLDAAALTQLFVRCTQLYIPLSVAMGRLLSLHLKV
SSLCSSAHRVGELRDVLSAMERVDQGALSKIVEIPNGDEIVFRDVVIVSPSDQIVLLDYT
ATFKAGRHLLIMGCNGAGKTALLRTLCGLWPLRSGTVERPAMPELMFLTQRTYLPPGTLR
TQLIYPAVEGEEQARRMPDEMLLQLAAEVGLNGVVEREGGLDAEKEWGEVFSGGERQRIS
IVRAMCHCPTFVFLDECTSAISQDVEPTLYELLQLRGLTLVTVSHREALKALHHETLILD
GMGGHNMSVLG
>TCRU_5861 NADH-ubiquinone oxidoreductase complex I subunit, putative
SAHPILFNVPVMSRTVGRDAELLSLWQNLLSGRHIQAITGPDGIGKSSIAAEFCDRARRS
ERFTCIQWFDARGGSLPSELLQFFHSMRGRKEKDVLLVIDSVDDPHEALRHIPKHTNVYT
LLTTSVPIESSTKVGTINVQSLSPDGVARFSHLTEVEESKTVADVLFALGYVPLLMHVAL
CLMESGSTSPEELKRELLAKGVDGNGTLSVSYAIGVLVEIALAGLETHMPGGIRVLVMTA
LFDIRGVSYAVVDRLVGDESGEAFVMQAARLGLCDQRWDEGSLTMHPSVAQILRTKADST
HVAECTKVLLSLWPRRWRGAGSSVANELARHTRAISEVSDARQIPLNNDLLVCLDRSATL
LAFNEGKDLLTAAELWLRVVRANQNAERRDAEAVRIGRECGRLLHFLRDARAGDVLRYAF
DLACAVRGKQSAEASLILGCYAPYLPASMDAVRMLQVGVASLENRMTSSDTVLGKEEGRM
LQETIFVLLVRQGQMLQEMGETVPASVWAALQELEQ
>TCRU_5862 kelch domain-containing protein
TTYLWSSVIPRGDTPPHGCCHSLVNYKDEFLVLFGGGALHYVYNDVYCFDLKTFTWTYKE
TINGDIVAPRISHSAVVYGDNMYVYGGYHLYMPVLFSEVLVLNLKTFTWSCLHHAPPEPE
GPGERRLHSAHVYRDHMYVLMGEPCSTSTCFWYLDFNTHKWHPVQSFGLFGKPIVPLIGH
SAQVEGDYLYVFGGYHTHTMSQTGSFVYSNSLFYYHFPTNMWREVLPYCGPRPFPRYSSA
MVVLQGRVYIHGGDNDGNVYFEDFWCIHTKTQLPRWIDLTLSCGKAHPSARSGHAYVLAQ
GSLFVYGGELPGDTDVLYYSNRFYRYPLGLFTHLSLTELASRWLAKSNQVNVRVLQECIP
RGPRAALSRNSPEAVTEDVDTLMPCTR
>TCRU_5863 retrotransposon hot spot protein, RHS3, putative
EGCYESVYNARWSHVVEVPGGEGTGMEVKEGEPPQSWTYKEDGNTLEKDDGVEQSGEAPP
VLMVLTSDKGWPYTMNLLHGAGNDLCVNCEVERAWQIVKGDLTKWFSNFDLILNPSPLPR
VLIGTPGIGKSMNAGSYLLYQLLHYDVEKIQVVVHCFGSVMYVFDKTAKTVTKYVGNEIS
IVVLGGLWKSGMKGYIIYDVAKKGTPPDTGFAPSTGWGMIVVSSPKLTNYDEWEKQAKAA
RIIMNCPDEMDVKAMCTWMKRGPDKDKQAGYWKEVKERMKNVGPIPRHIFDEDKYIIRLG
AVNGTLLAIKDIDVGEYFTLGEEKEWYSKDPSHKLVKIVRARTDKGAEVFLNASICSEVG
LRLADRLAKKMATKDILLLILGSRGALASRALEQLGLRAFMYGELVIAIVEGLNELPPPS
PSKPQDSVLKLNHQGYPTRTVGLKELEGGVTRIPMEYGVLYLPAVENFPLVDGFFFVNSP
RKTLVGLQMTTASAHHTITSTVKQFTERLSAYFNDWEELSRDMSWEIIYIQHEISKKITK
WQKCNYVNPKNKTDAEKKIVAFWDGKVHQYQ
>TCRU_5864 Rab-GTPase-TBC domain containing protein, putative
SVDELRGFLSVMINKQNSEWNSRRFVLLERRDREIHRQLRKDDEDAAKQHSESSCPLCIF
LHSLLAESREEWREALSLRVNELKREVRYSAGAALPARRDGNEGEDVEWSVAQLYKTLVT
GLNSTATEELLTSRLFGGDVSLCHDSIDSFGLLTVFRAPIQELLAQHEELAPSLTILRRS
FAALHPSNGCPKTISHTEISAHDAEENTNTFLQFADSPGAVAKALRGRVSPSLRRLLYAR
ALQLSIIVTDGSSLFGGRGELQVNRHCDGVERFLTFATKHGRDKVRRRIYHSYATKEQET
TAKVIQAIVKVDNSQSVGNSDKYFIFSDETEVLVVSLLMDKSLPEVHMKNTLRLMGRSSE
QIESYLVFLEENDEETGPRQRRPPPSGFFPVRCFSLLVAPVCYITGDTVEQYELVSSLFG
QLWGRIQGPTPELAQCCWIFEALVARFAAPACLHATRTLGLPPLRLAIQWMITAFVEVLE

PAELLAFWDLILSYHIEEIFAGRTSLSVHIREGVGSGVEKKKKEMEGEEKEVSPFAPSAL
WLLPLLAASLFVYRAPLVERCATAEEMLVVFKDGHHLRCRPLLQYLLFMAK*
>TCRU_5865 hypothetical protein, conserved
PELSKDSGLSLTRTIFIKNVPPTVDNSHKLLPFVPSVGLVSLRVKRTGGRDVGFAEYNTA
DSAYRALQWFYRLEVTAGIAFNCFPRMLQKWTPIPPRFRYPVPYDEYNHCAGDPTRSTEL
LLNSVILIAEWSVSSPTCRPGSDSSVMSLQPPSPNYYHFFVQKPMEFIPQATLQLPRFVI
QSSPVSHCVGFTAVTTMPQWAKGPVIPSNIIYCKPSGEFIAAGNTNECSGSAAGCPLKSR
RNIQRTASAGNHPRAFENGHFRCQGDAVASPLHVKPQLSQDDKASQRGVLDSTIASAVLD
DKELPSSTLLVRVLSPGERRRREFLLSLRGLGISFLSEPGNIGEASEATEVSSCFQSQES
WEKQQQKDMRQVKYSSEEWSCFHHRHHLCMERKLREEPLTQYTADAKTLKAADLPHFSDK
EEPMCDELVFDGAPILPSLLSSVAYCGDSDTESAIVKLLLRRSFFSERFAGFYSFVPYYK
WAGFVRFEKTADARRCLLWLRRNPDLAPLIDVQFARKDTRRYRSHKGR
>TCRU_5866 60S ribosomal protein L24, putative
MRIEHCSFCGAPIYPGHGQMFVRNDCKVFRFCASKCRKNFGMKRNPMKLKWTKTFRKANG
KELAVDSTMDFEQRRHVPVKYNRELLHDTLKVMKRVEKIKQKRQEAVWNKRMEKTRLQER
RDAAVALKHNIDWIEDSEVKHKARDDLVAVQQEVEAKRQQRREAARKRLQKQREMERAAG
FTSSSSVK
>TCRU_5867 Alpha/beta hydrolase family, putative
RRRTGAATVSSLRNSTVYDSFGLGSYKYYEGPMYSGHVHTILGARRPHCRVEYIREKVIA
GDGNPLFIDCLPPVLSGDAQVRGLVLILPGLLSSSRSVYVQRMANVLSREGFFVGVLNAR
GVGDTPLEKAQIFSAVYTADLRHVLKMHFNPTQVQQRLKSSQPKPFIALGLSLGGVFLCK
YIGEQGLWKETNPLSAAIALTSPFDLNASDDQLSNSLYNRAFLRNLIAYAERHKAVMERL
PGVDTQLLFKGERPLLYRLRSVFQFDQYITAPHFGFRSSEEYYNAGSCFVSLLTSQIPVL
CIATRDDPICGTQKSIRRWERLANTNANVAYVEMPSGGHLGFVGNPIAEFN
>TCRU_5868 Serine incorporator (Serinc), putative
VGTSGGNSQFTPGVLLRVQYACYLFFGLILTMLLRSSLSGIFSHLSILQKGCKLATSALS
EDCTAEVLVYRVSFALALFFFLHLLSVSDLTCCIESETRVEFQKRFFYAKTILLLLVFVA
TFWIPNGFFAIYAYVCLFASAFFLLMNVIFLVDFSYQWSDDFGRRSERSSKWMWYLFAIA
VLSYLGAIGVNIASYIMYVPHSDCNYNAFAITSVLVSALVFTVLSVWIPHGSIVPSGIVF
LYSSGIMFVTLRTGTDEYCNRLAVPEGQTNSIKQMVIASIVSSFALGYSVVSSGGNGSAL
GIGRDEEGEDEDPDEIGHLSQYLFFYTTMMLGSMYLAMLATGWHVSGMGKSTLLGSINIA
FWVRSATVWAAVLLYIWSLLAPYFCCRDRDFGYDLDDW*
>TCRU_5869 BTB/POZ domain/Regulator of chromosome condensation
(RCC1) repeat, putative
RACHMYADPNNLETGHVLYSTDVANCTDSRPDDFQTAADEIVRRRHDWVKLNVGGTYFTT
TFSTLFSDRDSLLALLVQAEMEHMAPVDRDSDCAILLDLDPLYFAPILNYLRHNVLVIPP
GVPAAGVLAVAEYLNLQGVIRQLAPERQKKRQLLYSWGSGASGELGTQRFLDCSTPTLAQ
ITPFGVRVVDVALGANYSCALSEDGNIYTFGNGDWGQLGLGSARELDEHPDDKSAVVTVP
QRIPLFEQDPAVHLAAGYAFAMALTAGHHVYFWGNNNHGQSGLGPRYFDYSLRKVEEPTL
VDTLEGKRIVQLGCGSFFSLALGDDGTLYSWGLLECLGLGTTEEVRAAIDDPFIITESLS
TEKRTVVLVPQVVHVPTEHKLIRVHAGQWHSGVINTAGELFTWGVGYQGRLGHGDKEPAL
VPTKVRGALTGQHVIDVACGSFHTVALTERGAVYCWGDNASGQCGAKSTIDAVTSPYRVV
NLEFVAGGVAKAISCGRQHTVVVMQGPQSWCQRSCCKLDHNGKPRAPHGQVFTFGETSRT
GGGAAISGGPVICGKMQDGKVYRQFRLVPSLKDLNVINVKSGLHHTFVFAEE
>TCRU_5870 NADH-ubiquinone oxidoreductase, mitochondrial, putative
RFIHGEMRHQNTDTNNTRIPWDFSIASYEEINNAILPKFPRSRRRSAVIPLLHLAQRQQG
GYIPVTAMYKIARICEVPPMQVFETVTFYSMFNRQPVGKYHIQFCVTTPCMLCGCDELVH
RTEAYLNVKMHGTTKDGLITLGEMECLGACVNAPMLVVSDYSRPPNFSYDFVEDLTWDAV
KQLIENLREGRPFKVGTQRSDRKWADPAGGRTSIFLKEPPMPYCRDLDAKPDPPAAPAAA
KK*
>TCRU_5871 trans-sialidase
VHSFRLPALVNVDGVMVAIADARYDTSNDNSLIDTVVKYSVDDGETWETQIAIKNSRASS
VSRVVDPTVIVKGNKIYVLVGGYNSSRSYWTSHGDASDWDILLAVGEVTKSTAGGKTTAS
IKWGSPVSLKKFFPAEMEGMHTNQFLGGAGVAIVASNGNLVYPVQVTNKRKQVFSKIFYS

EDEGKTWKFGKGRSDFGCSEPVALEWEGKLIINTRVDRARRLVYESSDMGNTWVEAVGTL
SRVWGPSPKSDQPGSQSSFTAVTIEGMRVMLFTHPLNFKGRWLRDRLNLWLTDNQRIYNV
GQVSIGDENSAYSSVLYKDDKLYCLHEINTNEVYSLVFARLVGELRIIKSVLQSWKNWDS
HLSSICTPADPAASSSERGCGPAVTTVGLVGFLSDNASQNVWEDAYRCVNASTANAERVP
NGLKFAGVGGGALWPVSQQGQNQRYRFANHAFTLVVSVTIHEVPRDASPLLGASLDSSGG
KKLLGLSYDKKHQWQPIYGSTPVTPTGSWETGKRYHVVLTMANKIGSVYIDGEPLEGSGQ
TVVPDGRTPDISHFYVGGYGRSDMPTMSHVTVTNVLLYNRQLDAEEIRTLFLSQDLI
>TCRU_5872 cytidine deaminase, putative
LAQIPVELQRLARCAINAHHNAYCPYSKFAVGAALLHKDLKITAGCNYENCTLKGCCAEV
CAIVKGNSEGRRTATAVAVYGCSKVPDVMNLPPPDTVTPPCGFCRQSLVEVADLSNNYED
FLVVLVTLDKERVKLVKLCDIIPLKFGPSNIGMD
>TCRU_5873 NAD dependent epimerase/dehydratase family, putative
MLRAFSGSCLSLEDMEIVRRPNLVKQPHILGPGVDFFTEDGQPVRPQPGAHTLQKVFSGS
ALDLNAMNGDILSEEEMPQPNAFPPNPQEQYVLPGATVSTILNQLSSETEKGRAKSVKNK
TNVLVIGGIGYISSHVVAKLLDAGYTVRVTVADTLSEQQQMDFYSMDQGPERRLTIFEAD
MTNSSALRDAMRGCKYVIHCGCPTSPGNKDPVALHTSAIRTLFDAIRSTGKSTVKRVLIT
GAASSVFHITDPDPPSGAFDESCWNTVATAATDPIPYARICFEKEAWRMKQMIGVELVVI
LPSITIGPSRTEEISNAMMQIQGLATASPSFPYAPNLYWNYVDVRDVADAHVRALECQEV
KDQRVIVSNGCFSYAEIAEMIKEAYPHLTPPTRTANTLMTLLIGATQSQVKMGFLWRFVG
VRKRLQTHRATVDLDIKFTPMKETIRVCIDQLIRAGEVPAPNASRATCTRKLFAAKKRVG
LLLFAAAAAIWIVARTR
>TCRU_5874 hypothetical protein, conserved
GLFSPTSSPLRSGYKYFEDMFPKHEPAPRYATYEEQSLGATVKSLEPKKQLTESEKLHQL
HEWKKEEDGLTPPPEFGWPEEWGPEPGEEGHSEWYKKNRMYMSYEEKSKYDLRIGVPVEK
NSMRHQEMPYHKRMKAAYHNLQEEKPQWFDPRQRKYWARYSYEDQRDSVAKSRDEYLKEW
LEQPDVTHENVAKKIGDYNGTAKNQSVKPVQRRPEWELAPMKG
>TCRU_5875 short-chain dehydrogenase, putative
RHHSTAAAARQPQKQKIHALSENKSDASAYVDADDFADFSSLRHMGYMLLHARRMWVPMM
MAAAYYASAPLFTASSITKGVYWSLCVILQRLSIRGRMNTVYKDLNGFTCVVTGGTSGIG
LYTAMQLIDMGAHVVIASRPGREEATREFMKANCQCSKGSNEDVIQERLTFVSLDLSDQL
DVMACAARIKGRFNDRIDLLVNCAGVWREEPTVTKQGFEEHIGVNFLGPFHLTEALLPSL
RRSGKGGRVVYVTCLSHNGVHKANVVRERMLLKPSPDEAQVTARCYSASKLGNLYHAQYI
ATRRYEGIPLNQPTELRPVDVCVADPEFCATSLTCRDAPPLLGTNFLARTLRSLWIRDAY
EGSQTVVNCCVRDDIENGGYYAECMLMPGGISRRAHDPKSRKDVMQWAMANTIAKYYTMR
PSASDRHTAATAASGAGSGAAS
>TCRU_5876 Leishmanolysin, putative
LLPWLMMVVCCAGVCVAADPAVKHRCGFDAMMKKYGRLPTAVVREVPRRGQGAVQAYTAA
SEDGDDGWAPIRIKVSAEDMYNPLRHCTAAGDLRIDHFRRAITCEADDVLTEERRSIILR
QTLPAAIQLHAERLSVRPVTRPVLIPRTGLGMCDNFTIPHKHHTVGVAGTDLILYANGFP
TSESRAWAIPCFLLDDGRPFAAAVNFDPSQIAVTNGDVRVAAHELGHALGFVREMFLMLN
MISEVPNVRGMSKVLVISTPKTKAMARQYHNCPTLEGIELEDEGGSDTLLSHWKSNSVRD
EMMTSIVEVGLYSALTLAAFEDMGVYVANYSAAELLWWGNNSGCGLLEKKCLTDGISEYP
DLFCNQVDVYDFCTYDRLSLGRCDLKRHEEALPQEYQYFADPRVGGDDPFMSRCPYVEAY
SNTECTNGDPSVLPGSVVGPNSRCVKGQDLQFDDKYIGDVCVETRCGDGKVSVRFLDDDA
WHECQAGETVTPPSGPWRGSIVCPQ
>TCRU_5877 hypothetical protein, conserved
AAGRLAAPRPVPSFKPVPFKQEKFLSMKSRTAETYFNTRKHILKRAADVQLQVRKRQQEQ
SGKEGDACCDRILRGNPLTPHVADEIDAWNRSLKGLEALQGFVLTDELIYGAISKNIRLG
AFPYALDWLRKCARERRIPFPTAVLHDVRLFIDFLQSVLPSSNLSLTRAHEALLGGTFVR
AGPTALATTEAKTAASIGSSDAEGGEETHAVQLVNSSPYVRYLFKELYIPLWECLVELGL
LPLERSHEAETGWEQSLREARHDEMVLDLFGRLCCCPCSDAASFSSSTPSPLSSLSSSRD
TTLDGRDKSTAAVLEEYTGLLLALVQCAAEAKEVKLLIELQLMFCMLFVAPSTAGESTSG
WKLKKTFWCHSQSDEELLCRFSNEFISALYYGRLAYQSEMLLHRHICSSFNVAHDNEDGD
DADSSNIDSNNNVEDNDDGDDNDEREGGMNCKEHDGDEDKLPSSFSNDKLRALDSMDVSS

STSWPESRRQKTLDDILRNLLQNEASTLADASVYAALVLEDPALIPKDDNSTGNHRFSKV
EVEWMRVHLDICRRCHHGENVASELEEFFLLGGVVAQGLETSISNMEDQQCFLALVMETI
VGVVAASTAPATERYTLMVRVMTELLIRMEEAQKKQPKEQREEATLLQLPLYSAASAMVL
LSPLLRTISSPEGVNGDAMDLNDAAALQKDALRLLQEMVRSVLNQPTGFGNAYSVVLMLL
PQVEMWEEVQRLLHKLDESDEEGGTAHGFSSVILDQRVWAWLFRRARDAGRADICLFLRQ
RREKLFY*
>TCRU_5878 Arrestin (or S-antigen), N-terminal domain containing protein, putative
STKHTSSFFVFLERMQHYPGDTLRGVVEIAVEAPLYFTTLQACVLGEETTRFGTSLTKRI
DTETRYTTFYRQNVILAGDPPNPETRSASEEDFSDVWSDNGGNFMEGSGAKTVVTKGLMP
GTYSFPFSVRLPDVLPPSYVDHRNTGSSKLSYEVRAKLFAGSRVLAKHRVYFSLKMPPLN
PKRWIKAHMDRGFFFITPSKSAVATDDRTEASESNTGSKTVLIDHQVSLESAMEPGRQGG
EGSSCSNNFLGSTFQDATAKAFLKNTMNNWPSPVSAHENSRSEGTDGNSGIIIPGGNEHI
AGKRTCEHFLERTEGNPGAHPSPSAFLKETSSWEHHLEVPVYGVFKRGVVDVFLIVHQII
GTRGSQIRFRAIVDNTRGGSCVTKVKFQIVSHITMRSHAEEQDYRSVLTEKVLHENISRE
ENHGIAEMELVLPGNTPLTLFTPGYSCRTFLEVKLSYSQGLLTQSGSAGVEIAIVDRFTD
SDSSRLLKHWTNRF
>TCRU_5879 Leishmanolysin, putative
DSDWRPIRIAVSTGDLEKKRNKKKTFCEEAGETCETVLGKVDCEARDIFSQEKKQLYIQK
IIPGAVKLHAERLLVKPTADKVEVPRSLNEPCNHFNSPSEHIRDGVPDADFIIYAAARPS
GAKSRAVWAATCITWGNSRPSIGAMNFYPNYMTDTAWSVRVAAHELAHALGFSQRNMEEK
SMLNSEYIVRGKHRRMVAGYHVKAKTRAHFGCNSLEGMELEYEDGASARKIPHWKGRHAR
DELMAPTVGAGYYTALTMAVFADMEYYRVNWSMAEPMSWGHRTGCDFLEKKCKEAKDFPT
KYPHMFCDANDNETLSCTSDRLHVGTCTATIVENKGTPAHEDVCPVFSSYFHETNSGTTY
NACSDGTVTSLPGSPTGGDSWCLDAELLETNDNSESKSVKGVCAQVSCEEGTVKVKYLGS
SDFHYCPEGSVISVTLNGFEQDGKIKCPKYGEVCTIA
>TCRU_5880 Cell division control protein 48, putative
SSFLFAEELLCGVLLHWPHRSQPASLLLCGPPGNGKSHVVCRALQRARSATSRRRVLAVT
PQLALSLSRRHVDGSTALREFVRHSIRGAVVCPGSHHSGDEDGDAAVIVVLDHMELFITA
SDNAAGWIRGDRSSSEQSHSTAPHHPVVLAELYDIIRGRELFDKDELRFMHLNTVLFVTL
FSGAWEDIDPFARAKLFDAYVPLETPLEEERFAFFRTHTKYPLLWCRAIAARSGGIPYRG
LKEIVEHMEDVVHNATPAEHYNQMSVRRDEAFDDAAHNSDSETEAVAAIFSLRAVRAFGT
SGSIAAQEYRQSAGYVDVQETRWQDIAGLESVKETLHRLVLRPLHSSTLHRRFGIRPSTG
VLLYGPPGTGKTMLARAMATELNASFIYIDLPQLIQAEVGQSERRLRGFFDAARERSPSV
MFIDELQAAFGTRRAPQGFLGSTHDMRLVTQFLHLLDKAQEDEEHFTLFVGATNVKEMLD
EAVLRAGRLDTLVEH*EGLLCRAARYLQRAVYGEWAAWFPANEVASQQALVCAFIKGTAG
FSGAELRHAMNVFSLQFIRLASTTTRSGSAEFFQKLQDMMIQKETHSLSTYAQDALTRAL
TRAAR
>TCRU_5881 hypothetical protein, conserved
GMGRSRSAEQMARVLLSSAIRHDTWECKASSDAVGGRLFTARFVWEEWPMVPELQYAIAL
QMTFYDRVACAFVGATYTVLKDAPTEPLIFQNRGENMLLVVEVVARDERHNALPEERRVL
MWGYVPLTEVCTLRSIDLLPGSAQLLLLNSTSWPSNNRSETYSLKYTCVEVEDVVLTQLM
SRLVPPGVIVTQSFTENRPQSSTHSFRCTVRDIQLFPTTENPEWRDKGAEWRVAAVSHNG
YQQLGQGAEVPLVFDEEIVSSVSTTSNSSSGSGSCESSNEFSHTSTSAYVSVEKKKQQST
SLVHSVVPLEMDLLPVHSATSLVLAIRRRGKESQRFEVIGFCVFPLCVMPMKDRDLRVEN
LPILHGPFSCRDPRMLMLESSSPYGKQPFTVTLTVEYHDTLVVDTFPVSAPTSRYPVDKR
ELAKTADKGAGGKKFLAEVYDITQTFPSSTAVPGKIMGIVSTEELEEGKKVAAAPAVSRV
TTTERTAEATPPLKLTYPSPDELVAGKWATEDNSSAGVFKMLCAVMEELRRLREMQESAM
RRRDQKGGLVGREDEIGKRLGDAAGVEVVDLSPMPLAISWETRCLIEEGLQPILHPVHGT
RLEDHALASSHDMTASLVGIRFEGLTADASIHVPEDVCFIFSFGSLPLQTIGPIRTVCID
KNNQLRTFKLYEGVERGGMVWCEPLEAVEDPFMQKYRQVTDATLHIHVYDALTMFYVSSV
DVQLAHFRRPYNAESARIPMDIPLYRDLSLTERSIPPKVFPILRNAGQLHVTLFCVAAKG
GSVAQSRNKVLIPPSGSRVIVAKKLPHAKIIETHLLEGEKTDAGVKMPVESSAAHPSDTV
VTSKGPPQLSSSSSQQQQQLVPATSSANEETTGIHWRRAQHIKQIYCNRTILPGVPNEH

RLQEGDLEFRLRYLEKQRDEMKSRKIAEALMERLTAHHYVYVSSCRPEVTRTPFQNPFCS
VMEFNVEVDTPAKGALEIVSSPTFYLGPRECTEVILVVRLNAMAKTRDAESKHLRARLLT
DGREVVRIVDVHVTLGPTFVDRRFEIYGPAGTEVSKKFFSRVFSSALFPITSDRVKLLSR
MRDMCARTTITSETTTAEVNAVLDPITQSFVTAWEEVTVRTTIPRDERGQRVEYLVLYKD
DAMSHVIETWELCIFACQSVTSRELLFGQTTTVALPASGIEALYCSHSHVKVERGEGCYL
LHVRPTEVGTQQVLLHALTDHHLAKTLLTIPTVYPTPTYTQTLEFSLADTTAPIFRRLQF
LHRGTKEEVFTVRHNYKYQLRVTPKQFSLAPSDTQFITLQIDMLSLPEGQMEGRWPMWIF
INNADDKTIESYLLNVVLRAHRVL
>TCRU_5882 proline dehydrogenase
MFRGYARLASKCARNVSPPSRTIQPVNFNDDTVFRKKSFWWLVRALVVLRICQISFFSRN
AVYLMKKSESVLGPFLIYNIIVKMTAYGHFCAGEDERGLKSTVKALERQGIGSVLDYAAE
ADVAGFAPPPGLEEAPNLSMASLVHKTTVNYSSHEELYDENMKLYVMCVMHASLNQPVNG
VGLAAVKVTGMCDPQLLARVSAILHSVHAGWVQNFTNEKPPPIEECRVVMGTNKEYQLYI
TYDQLRKGLTAYGSARKYTEEEAEAVIKALDEKNEGKVNYYQFKKVVSEAVLSMEPTPVQ
KLIVEKLPKLTEEERELWRALHRRLSVIVRTAKDLRVRVLFDAEQTFYQVAIDNIVLQFQ
RQFNLEEPTVYNTYQCYLTYTEDRVFNDLTRSELEGWVWGGKVVRGAYMVQERETASKYS
YKSPVWPTYEETSACYQACARRILREFTRLPNTPFEVLFGTHNKESLKEISEAILKLPPV
KGLAVFAQLYGMADHLTIPLQKAGFRVFKYLPYGPVKETIHYLGRRATENASVLVNGGSE
EVELMRKELRRRLF
>TCRU_5883 hypothetical protein, conserved
IPMDWSSSSSDEELRTALRHNARNMQAEGRAVPTSGPPITFYNGEAVKVQYGTIYCPFRR
KYFHIHPVKRNPAEFFGDVNVRRNKRRCLSPSSVQLLDASFFDETPPEFKEITLKEINDN
GFYLFNGIRKSSSSSLTTLYPPLLQDFRYSRVVLKNRFKEYLLSPVCLRSEKDGWKRTTY
QLPPKGIVSSLFDGRFAFCGMDSQSELFIVENHRLLPHSIKIPGGTDDIIGMHCVGRNAM
FIVRKNRLQHLSWDSDTPSNTAVWDFSPEVNASFSCSCTNAFSENQSAYCVILACGRSLF
TAAMHENTIHKPQKMCTFRTTPILSVDTFSLGPLANQVVVCGMRNGTIQAQSLQDMRTHR
SFNSGIQLKAACIPYVHCVENSFNFVSVSIIGEIKLWDIRYMNKKEAVFEMVMDTAGGRF
HDIQAAFVDDIACFTNSTGCISCINTRRWLGLGQYQRAGGNEGRIHLVRGTFGYQILDAG
ICNTMAYLLHVVYS
>TCRU_5884 hypothetical protein
RNYLDDHPEGVPLELLPLNTDQLFQELEKERASILSTYPVSASKLSEKEKALNNRAHELA
AEYKKSARTQYIREEEIPFSAENLSLEYDIPFQELEARRFQLLTGKEEHRDHLLTEIEEA
LTNRAKEIANIRQEEQRNLLDQYPLGVQLTSTTPNKNAEFLQKEEELRQLRGKPQKQEEL
ASKGEELRANLNAMPAKKTEESYPYIEANPKGIHIQHLQLNTDQKFIAMEQERRQLLEKD
PRRNAKEIAALEESMNARAQELAREKKLADRAFLDQKPEGVPLRELPLDDDSDFVAMEQE
RRQLLEKDPRRNAKEIAALEESMNARAQELAREKKLADRAFLDQKPEGVPLRELPLDDDS
DFVAMEQERRQLLEKDPRRNAREIAALEESMNARAQELAREKKLADRAFLDQKPEGVPLR
ELPLDDDSDFVAME
>TCRU_5885 hypothetical protein, conserved
GQRPRRQYINKVTEFFFRELDRGISSPYVVLSTGVLLALVGWKVMVYYVEPNRKIDAVWR
RPQSRVPMSDSHNVFWGFNIGSDGWRGLPTGRHLAETMTESAEGALRRPRLVYSEDSEVL
GPRGESLSVACMELPEYDTRIGNDVMYRSVHYVHGATREKVMTPTNVETGEVAAADLSAQ
AKNGEVRAAGGQPVPAPAKTPLEEKATEEDNSLYFSRMPTRGLSTIHGMTKCRAITSLNN
CVPYAGHIESEYARKMMLTLGPVHILRDIAKTTFPLRFTTAKEAPVSALVCGLHSGEIPR
WLSTAFPNFQVDVVERDGTLARICRRFLGFQESNNLHLYLAEPVEFLRRTAVPKIGRRYD
LIMLDLMDGAGRLNTQYGRLEFINSVRNSLSGSGCVVVSLPNRDGAFLYNIVQNWRLAFA
GRTVILVHCVTSPQTLLMTFQDDATRGKANFGTVANVDEFKDLLRTSLAHYGSWRVPFDL
TGEVSEGTFRVLRPGTVYSVVAYLPAGHPQIKDMAAAETAAGRGGWGAWLRRWTATWLTP
SQ
>TCRU_5886 emp24/gp25L/p24 family/GOLD, putative
CHVVFVGVVVPMVAEGFRFTARPGRKCFTEELPEAGRYELHYKMSRSLTPFVSVGVSAPN
GRVVVEHEMAQADAKEIVTVDSRGEIAICFTVAEKARHSATSFNVTLELMDAEDAELTRQ
KRQVYSTSSAIAVGVGKASGAIQQMDYIFHTTMRIRLAFVSLTRMEDDVRYFFKEMKAVS
WNYVYIFAAVATLIFVITYFRLRHYFQVRKYI*

>TCRU_5887 hypothetical protein, conserved
CSSLLIPSRCYFWPFNEDFVPRGATTSGFQSSASPNTRQRILQEYALSPLFGARVPCCTL
GSMRSPREMVSRKKEISLFLCELVRMRAGSITLGPLIQTTDMMLFRHAHVRSEADCSTNS
DGCVSAGGYCAGRGLGPLIQTTDMMLFKPDTPLSPRLGDDRKSGMHTYARKPIAARTLMD
VFLPEDIALDEVVAIGHLVQEKLLLARSDQNGMSSDASGSAAPVVTSGMDDVARMLVGRM
DIVYCEVPPLDESGFIFDAVCGFNIDADEAERVVRRWQER
>TCRU_5888 hypothetical protein, conserved
MATALRHGRKGGKVTSSPAIAPKVLTPGSAMSPASLQAFGEGTTIISDPNAAHPFDPDAI
TNVVKKPTTTEANVLQFDMEAIQHIGKGIMVGRTKQVRTTTRQPQVSNVEALLKLGNAFT
AQKDMLVSPKNPVGLEKITDNNVVVVHRPQEALTLAVALSTLVPQAKVLVVVPKYFEVSS
VKTYLSSLVVDGEKAATGEFCGQTFEGTESTPLWVTSAEMALLYLTKLQSMAPFSHVVVP
GFFNTTQLLSFFVKAFGQWLRSRTDSSCSVRLVLTPERTDRSEIEGIFQDLKVAFIEKAV
EHVTEFSYGETCALVEKEMMEMEKDGSGIFPPPTRRLIDYTAKVSAEVVSCIVRENEKPQ
AIVVFTAEAREVLVALQEAHIENCAIYSGLQGTEETEKTKHRVYVMNHVRHALDMDNEYT
MVLDIGTIRRPAAQHRSESFMAASTTEWETKVERAERLSLLEGKKGCCYFSLYPEDVSAA
FHEDAKSFPDVFSVEDAFVHCARLNLPMGEVAALLPAIPTETAEQVMHNLAEKCVIASPQ
SLAMTFLGEMTARLPVDLDIASFIIGGCNVGLGEAAVAIGSVAALPFRSITPLTYSSVPW
NEATTWSREKYAGDIARHSDLLADTLVFIEWLKLRARGESTAEFLNTILVQEFKFVKIEG
LMKYIREQLTNYLFLDRFDTLELLEEVSTSVQENSTIFLFLQAVALARRAAFIRDAGHLN
EKDRYASMAFVRTSKRLMPHNYIPSSIKWDTGRILIPVILKNSTNILAGLFSLIHTPYFF
ASLLLLYPYVEYSKPVITDKGRVVYFGVSCNRQMKRFMVSIEEAAQILDFREKINLALSC
MQALRTLSHPISKTKFLLILKKHDRLFDVERLHKNIRSQLLEIVTELNVTEHQGSFETFA
THCTAPKELLPMTDTPAMDVSVLRRFVDGTLWDSLPTPGSVVKPRAASFAGTPSTLPSAP
LISTNDEDDDEEVEIIQDSYFMRHGPLIEDDDDD*
>TCRU_5889 Putative death-receptor fusion protein (DUF2428), putative
EYSTAMRMQQHRVRTTEYIPLPECVLAELTRGIPIICKASTSLQPFAPKAASIVCREVEN
MTSVTSSEHRVRCISQITGVLRENTFMSQRSVTECRVFLKKLAAYFVFPLMLHCAVRYLH
RALATLLRTVYVIDDDLETCFCAAFTAAHIRCWGSGTSERRPTIFGDNAAARLESEATLL
GFKDSVMSWINCIDSTTVVAMPIFPRVFASTFFDVLPLLGESLQWMVLNASVKCREVGIG
NAANGTILGEDLAYVRYGIRVITTYTHKFLHLLQDVWNNGDRTTHCHLKEDVGKLFSSAV
LMLSSPVFPKDVLNGAGLLVSSLLTLRTCVPWLLLEVCRQCGALDPPTDAAAAKPGVTRI
AYTLESLLQSDVRECVELICSDDHHRRARERPQALCALRNILGALTNNGRFALLKGLLAH
LSTPIHGNVDSLGILLKPITPLAGAGPSVEALEVVHDIIMPAAEAYCSALQAPDTRFMAI
QTIDSVVRHISSVLNCIAEVLEHPPSENETRRGNVRERNVQWPHGGKLLTEPQKWGLMAL
CTRNAKLTRTLNHATEIIMGMWDDNTLQVTGPLYDAYNEILSVHAALRRCAALFPSTFET
HALDEEIFDTAEALRRILCIPNERRGKYHALLGILSVLPVPQFLSVLKKNFSQETASISE
VQGLRCFSRMLLSGACNHKVGNIAGDVFAKAASLIRHSDNADAHREVLFMQGIIDPLVKS
LLVSGYAAPPHLSEAACVSNIVTHMIMPCLKSEEVFIPILLSQLTQALEGKHNSSRVNQS
VVEIIHRARVVGKDIGAYLQPKSQTFQAILASLQVHETELRYTALGLCVLSTKKAETVKA
WQCRMMEWYISTNMYCGGDSVAMRNLLEVYKKWMRRLVDSYGNQNNKQKKGMAGSETAEQ
YKELVVDHCVRMVGCLVPQIGENANWCRNLSLERRVAAMSTYSCLLRNALEFLSEEDVRK
LKEQLFPVALIEGLLECLSEGWEKARLSAYSILIIYCNHVPDAIFSHRHLGNPTAASAAK
AELLRARTFRKSEGEVLWYVLATHFTPAAKQAAAENPSHECEKRVRDVECEMKLLKEKLS
ELRALGAKGACEFLQLYPLHGIISLCAALLSNAWEIKRDVHLLYEAFNNLLLCCSAVLQT
CSSLVGGEPVNSVDDGDVEVDCRGHVFEKDGSYTEDKMRTVVNNTWLSIRTAASAVERVM
NLAKVEDLSLPVVREICYVLIESLLRTKHNGVMRKVREALKTVAAALLRSRDVAFHSLPR
EMLDFLLGPDGVTSRSVARMLRRSQGLPHAILAVLEAEDPTVPVFLFPRAMKLLLHVAKG
AHFGGDDCQHLLTEEKCRSQRSNALNVLKFIFENKIFASRSVADLEEAFWIAAEGFDDPS
WGIRNSSLMLFSAVLPRFVGEHPSTGSVGVNTSLHDIAVRAPRGVAFAYEELVKSSTTPV
PSLGVFPLLQMLSMVTPDPPHLFTNATTSQQIADADVDSSRIVRAIMLCGSSKNLMVRAA
SAVALTSLVPTSHLETLLAEIISNLFQPKNGLNAVHGALLHLQQFHTFYVGTLRRNMRKK
AMNSSATATVAFLVNRLVVEGLGAPNLAVSSSKLYQACVHCPTIAATFLSLASDALYYIQ
SFGLCADNTAPIVNLMRFGVAVVYWAVCAPTRSFELARHDHAAVCENGALFALLVVRLLS

LSKEEAEGTEEENDKLVSFNGNDQVWDTLSQVFTSESGEYLISCLMDHVSHHTAEKRWPR
EESERTMRQFTLRLHCDPVNAALRMLLRDLSEDSLLQRLPCTRILHMSVHLEYLVFLGND
GGPRSETCEALCKALEENLLCRMDPQSKRPLQNTEVQSWAIRFLGRCCVRHGASSVTLLR
ILEHYSRPFFDVRNRAAVVSALKDGLLCLEDDTAETAVKHRCAFLLILLRLLFDDAYDVR
LESCRVVSQLTSPANFLLDHMTCVLSLVFLIRQSGECRVFDAEFLQQYLLGADVSRNSPL
GHNDENNDGVEADDSDSEESDVLFEKEAENMFAENTLLAYLVGAVMHEAEVSSPTFGVYD
ELLRVAERRGSVAAVYATL
>TCRU_5890 Tetrapyrrole (Corrin/Porphyrin) Methylases, putative
PRWGSFKYRHTRTIPDDAVNPLTTPTKIDAGTLHIVSVPIGNLKDFSIRALDVLKQVDYI
VTTDRPATKTLLELVHIEAQGRLIHYSRSNRAASKDKLVELLRGGRSMALVCTSGTPCVG
DVGSELVREMQSEGVRVSAVPGPCALTCALAVSGVTFSPYESDKSSSTAMQAESPSLSSL
RSLRDGSFFFGNMLPESHGARLRILRNTVRQANYPCLFYEIPRRLLLVLQDIALVLPRRR
VVVAHELTKMNESLHADTAVKLLAFYSRQEANMMLKKGQLVLIIDGPDADETQEYLQREA
EKRRRLRREVTELVGERCDEKDSCNRIAQPKVRSRRELIRRKRRKRLIAKIEKEQEKIRM
IMKINQTDASR
>TCRU_5891 6-phosphogluconate dehydrogenase, decarboxylating
VSMDVGIVGLGVMGANLALNIAEKGFHVAVFNRTYSKAESFIKEHASAPFAANLKAYETM
KSFIMAIKKPRKIFILVQAGAATDATIEQLKGVLEKDDIIVDTGNAHFKDQTRRAEQLEA
AGLRFLGMGISGGEEGARKGPAFFPGGTLSVWKEIQPVVEAAAAKADDGRPCVTMNGRGG
AGSCVKMYHNAGEYAVLQVWGEAFDVLRAMGLSNDEVAAVFEDWKAKGFLTSYMLDISIV
AARAKVADGSHLSEHVKDCIGSKGTGLWSAQEALEVGVPAPSLNMAVLSRQMTMYKSERE
LNAKTLPFVLKVPGYAIKDKSPNAPEIRQLYHAVSIAIIACYAQMFQCLRALDKVYDFGL
DLPATIATFRAGCILKGYLLQPMTEAFAKNVKLSNLLCAFEKEIREGLQSYRDILGFITS
KTALTLPVLSASLVYVNGMFTPTLRYGQLVSLQRDVFGRHGYERLDKEGRESHQWPELQ*
>TCRU_5892 mitochondrial carrier protein
MAATLQTRENGINATYTSLHTPVRPWAHGVAGVIGASISMALFYPLDFLRTRMHVYKGGN
KFPLRSARQIIREEGLRAMYNGITMSIFAHSVGWGLYLLTFRAAQQKLFLAAEETACSSD
DHRSSGRHTLQDFLSACIAAVTTGVVITPLNVLKTRRQLYDVKSYGEPRGFVCGTRAILK
REGFFSLLRGVGPQILLTGSTTIQVTLYEGIKRGAFHDKDNPSFMEVIIASAISKAAASI
LCNPIEVVRTRLQDKRHGSLKEYRSMRGALCAIWRSEGVLGLYRGLPVNICRVVPTTVMT
VVLYEKLLLAISSANS
>TCRU_5893 hypothetical protein, conserved
TEAHLRREVQEAVSCLGTSASPPWVAISRVSSILSDEAREALAELGGLAGFCRRPEESGE
KKFAVKMVNGVLCVRLLDVQKTPEKPCVGVGRRNESIAPNELSQACSILPGKPVPLTSCQ
RAWKLPTMEATEEYLASLMKRVELILKRHTSKAELSLYVQVGYHGKEALIVACGPQAESI
VNQSFNEEAPHWEAEDTSPQYDLWRLSRYLRTDGFVPIGELKSFTNDILQTPLLQVALSY
PQRISLWLGPSMCLEAADADRFYVNGASCDEIREVLGMKFVLSEEEVQRHLTSKSEKLSG
LTDAELQEERLKLRNLPPLRRQKLRRSIVREEFRRCFPLGNAFLNPDVVAFHIYDQMSPG
VWVNNAMVRETMLPDGGKGAMHVGVDFFDQFPHLFITQSITTTSLNVMRREQGMEDVPSD
GESWRNNAFSDEEILLLLLPRLSNKKEDWGDNKAIDVLTTLLPRHLFKYLQNNGGARSRL
TAILKRYPEAFEVVETDEKGNGEEWKRVHLHYDGIAKLGSRLVNQLQEKERSKTLANNQE
>TCRU_5894 Ribosomal protein L31e, putative
KVLGKERKQALLDARKKAVASRKARDDRRWKRVLAKMDSEKRKKYHGVGNTAEHSRVRGI
TRAALRKRTGRKPDNITMEATIHLSKLLKRKTFHKRAPIAIKRIKAFVARLMKTKDNRID
ASLNTYVWHKGVKGVPGRVRVHVERKSETLEGGKRKHFYTVISNVPVASFKNLTTKVTEQ
*
>TCRU_5895 hypothetical protein, conserved
IFLLIFAAYRQMRRVPSLKEKGASKTQSPKDFSSSTPRAAQAVPVEVVVEKLPDGWSAAP
PIYYPPYLAAIPFLHCNSFKEGVVSEKNNFIVCDGSRLHVVQEPRGTEELVAFYTQYIQD
MPILKSIDTNGAAVRPVKEVGFSCESGCFTHAVVIPEEEIVIAFGQNGPYILSFVFTKYL
TSPLMAENEKETVEKLNSGDLQMLLDACRLVPLVDGVRLPGTPVGSQRGCLRLKYQYGGH
MLVFSLPSSVSVRTNEEKNQKGNKGASDALFVLEGDVLPGNKIVVGSAALDAIVKGTSID
ALFPLSTPGFPPLSSLLSLDAVEESASPIADGATDHATRPREEEAMNIVFSHEYLGVSFS
VNPKNGFVHEPILTEDLLLLYYPLGDEAHYAPPPGQMRNVAPPRFSVRRVTQLSPLWEKF

VSTEDELKHNVLFHFTDWAKEQVPCSLCDISGFKGIQLFESKEGHSCRSYVIPRADSILV
VRWETETKDWDMHLPLLQKFLDTLHLADPLA*
>TCRU_5896 DnaJ domain containing protein, putative
CRVMILRMAASSSSSTDASSKYTRSKSPYEVLGVTASVSFDEIKARYHELTRYYHPDMPH
GDPARFREINAAYRVLRAAEREKKSEKIDPGSFRAERSHKNGDYQTDGHARYQDCRYGPA
ERPQRHGLLREIFWLYECYELAIVVGAAVAVLIIATERYLLVRRMTLEKRARIRAMDEGL
PPSMPLVLEDGMLQKYNVRVPKEEIEIDNAMVKEEAYHRRATQRRFEDFREFLFVYDPDG
VTSRRVTTKRFSIQYIDEALIPARCSHVWEFNSEMKNKQYDSIVSGVVEALAATSWATPD
VQYIAPLMARGLATIPMNSPETAKWTFVEYKDIDKKGEPACVLALKNNRFGRLGMCQRVT
VTGSNSLSPRLVIKQEADLKSGTLSAKSLVRGGTLPVKDLSIPLEQMKL*
>TCRU_5897 hypothetical protein, conserved
PQVQFLSNMEAKYPEYAKAIQFTESMMVKGLSVLDKFYPVGERIYKSGAEWFSTAKKHQL
AHVWPIFFGFCVCFFGGCFAMLIAVVEVVYLTTWDSIKKSIGTIYENYLLAREASLKDDM
LDEDGNGIPDVQEISGKELFSRKLSLFLCSVDPVSLREAFNNLLLAFFAILAALKNNIAN
TLVFACGLADIIERNFTIREFIDDVLPPEYKKLSSIITMMVLNFISLTIATVLKRYVMTL
QCALLGATMLVGNAIKLGKKAHLVEEDLDIKCERSKRLITLLACFGFLWQASNGFSVPFP
LNILLFPVSLLEWLLDVVFAVS
>TCRU_5898 atypical dual specificity phosphatase, putative
RAGHQAWTPPPNFAMVEAGVYRSAYPTLASVPYLKHIGIKTVVLLSIELLPASVARALAS
TETTTRATGNSEGNPTFKRETSTTDSICVVCTADLTEWVNEYSWTKGDFAESDVRHALNF
AFETDFQPVLFTCPTGDIQTSVVIGCMRRYQGWTLAAVLAECELFVNVSTCVRPSVMSFI
ERWDVHEQPLREAAIASWKRELLLQESQQEHFQGRNFRGLMYGSIDSGNDDVITSNDNKT
GGKRGLENYPTHNGDNVAERGSSHARKGGEGAAVSSSASAVTVALPPWYTAGLARRTAYA
EEILAARAKALSSSEGRMAEPHERYFGVRNPPALDERSTFTKESVLEEDD
>TCRU_5899 NAD(p)-dependent steroid dehydrogenase-like protein
ELSPALSPLQRQAASKEHPMVPQVCVVTGGTGFVGMRLVEMLVERGAERVVSFDIVPVEK
TAGAWRHPSIQYVVGDIADYEDVSKAVKGADCVWHLAAAVGPFHPRQLYYKVNYEGTKNV
IRACKEWGVHKLVMSSSPSTRLKGSLFHRPCLDGLTEDEMPKLPLDAYMQMYAETKAKAE
MAVSAACCDDLLVVSVAPHQVYGPRDNLFLPNMLEAAGTGKLRIFGQGKNRICFTHVDNY
AHALIIAERQLFKGSPVLGKFYIVTDGRTHPEPDAYCIFWKELNKAVVAMGFSSIEEKMH
YSFWFLYIVAIFAEALGWLLGRVFKLNVFNVFVLTMHRWFRITAAEKDLEYQPIIPFVEG
WADTILWFKEHWLPTFEQKDRSWFGLARRSQQKIDIQARKTR*
>TCRU_5900 Leishmanolysin, putative
PRHTALLPLLPWLMMVVCCAGVCVAADRSVKHRCGFDAMMKKYGRLPTAVVREVPRRGQG
AVQAYTAASEDGDDGWAPIRIKVSAEDMHDPLRHCTAAGDLRIDHDGRAITCGADDVLTE
ERRSIILRQTLPAAIQLHAERLSVRPVTRPVVIPHTGLGMCENFTIPHKHHMVGVAGTDL
IIYANGFPSSDSKAWAIPCFLLDDGRPFAAAVNFDPKQIAVTNGDVRVAAHELGHALGFV
REMFLMLNMISEVPNVRGMSKVSVISTPKTKAMARQYHNCPTLEGIELEDEGGSETVLSH
WRKRNMKDELMTSDVGVGLYSALTLAAFEDMGVYVANYSAAELLWWGNNSGCGLLEKKCL
TDGITEYPDLFCNEFYDDPKFFCTYERLSLGYCRLMRHEEALPQEYRYFADPRVGGDDLF
MSRCPYVKAYSDTGCTNGNTSAMPGSIVGPNSRCVKGQDLQFDEEYIGDVCVDTRCSDG
>TCRU_5901 hypothetical protein, conserved
VLRRAFVALRDALNGGSSMTLCTKGMGLSPDSHRRRMPWTAEKECVPGVVHSSKEKMVLD
GAQRVDVDCVDRASQVYPLEALRAAVASYEYNTFRQKNIKLVSQAESMYSGNGFREDWQE
GTHDEDATRTAIHFRRHGSNTAHETTRLADFPGWHALFVWRLCFPIPSVGADSLVDASSY
RLRTHPLIDAPTP
>TCRU_5902 orotidine-5-phosphate decarboxylase/orotate
phosphoribosyltransferase, putative
ECIRLIDATAEYAAAYKPNAAFFEFFGEEGWKALQQVIAHVPANIPVVLDAKRGDIADTA
EAYAKSAFEHLKAHAITTSPYMGGDSLSPFLQYASKGVFVLCKTSNKGSNEIQCLRVNGR
HLYESVAEHAETVWNYNKNVGLVVGATDPIALSRVRVRAPTLWFLVPGIGAQGGDLKEAL
NAGLRADGSGLLINVSRAVARAKDPRAAAKKFCEDINLVRFGKACSTDLAAALVASRCVR
FGNFTLKSGKNSPIYLDLRRLVTHPSILRLVAREYANVLRTLQFDRLVGLPYAALPIATA
ISLEMNIPLVYPRREAKSYGTKAAIEGDYKKGDRVVVIDDIVTTGGTKLEAIEKLKAAGL

EIVSIVVLIDREMGAKQLLGSLGYELEAVVTLSQLLPLWRQAGAITQQQMKDVQSFMAEA
SSKL*
>TCRU_5903 Autophagy protein Apg6, putative
ERETLRRQKLHPAIKGSLLTAAGKYAPLSPSPLSPWLKERYAVLRKNMSLVRSGEPQTVT
SNNKRTTIAQDRMVTRLAPFFIYQYEWFAPEEPVVYMQELWRMFHNGPVPPPQPSSKLSA
QQTEFRSEQPLPRATATPDASAMQMSATHRRASTQTASELPVPHADVLVSPLCPFTCVEP
SSVASGEETFAFSPQLSVAAGHVLPPRISQITAQATANLPHSARILNMHKIKSMVPHAGG
KYASMIPTAAQKAGTTSVASSLTTASSPGQPCVPTFSRETFLFEFSRHLMRLVVHKSRTN
VPLCVRCWKDSLEAQQKETTRIMEDIIALSAVSASPDAKSFVLCFCPRRKRDVASDEPHF
GITGGVGITDRNEKTSDRRQLSDSDNRYTNADTTENDVISQESLYRLQIEVWEVEANSRL
MAKACQALHDELTVLSKQRTAVKLEWDEAIARYNARKVASFFDIEDAASGVSLRMQLAAC
SCTWMSKLHAMSLAFPIDTSGTVATIAGFRLGKCPTTAPSRRRSFAAQQRRAASAPPSKN
IFAAEMSRSLESTMLMNQLHMQKEYARSLLGSRNDTVSIAEINQACGYLLRLLETIIGHH
RISLPTFVLRPNGEQSTVEFVPARGSSMQVTRRSSDFFISEKFFSWRTFGAACVIVASCV
REIATWMKERLISLREAVYRRFIVEQGTMHSSWVSSATAVLESIESVDAPYDIVHDKVDG
FPVRHGDVSENLWTLGMKKLLEVVQWCVMVSTNVDELQRLLEE
>TCRU_5904 Leucine Rich Repeat, putative
KAMTSSNNSLATMKRIVEMIPLDIDIEKARQITLNGKKLTALPPNLGVLLREVRRLDISD
NDIHDVTPLASFPHLTSVKLSKNKRLSSIAPLSTLHLTVCVVDHCALSSLVGLEGSASTL
KTLIANDNNLLLQSPVGEAVEGATADHIAIALRNYEILGMLSACETVVLSRNPHLCALYA
GHKPDEEGCITGDVKKNSGGDTPHHEADWPHPLSVLEKMTHLKKLSLSGCGLVSLPLHWF
LPMVTELRLSHNALSSLVPEGVIFRSVKILDVSHNALIDVSTLRRCRFVRQLSISGNPFL
RVDEASSAKKDEEVRRGVYLPPEVIRFLTRKMPHLEVVDSTLLSSIQLGDDAGENRLESC
DAAEDESFQKKDKNNPMEANVEENVDVVVEPPEVVPESIRAPIVRRERTNLLAQRKRELI
ADGAVVAQLVKKQKIERAGW*
>TCRU_5905 mitochondrial carrier protein
RQKPASAFKHTLATQAAGALSTTILFPIDVVKMRFLSQDGTTYRQHNGQTYHSIRRALVT
IYREEGPRALFRGCHVAVLGSVAAWGIYMYTYRSLHNLSIAATAQTSRGRVEDFLLSLLP
SAFASCFSACICNPIWLIKTRMQLEEVSAHRTTRSGLAHYGSFTRGLVYTVRSTGFLSLW
RGLSAQILLGLPNSLNFPLYEALKSYLLLWKSCDTLNTIDICFCSTLAKTLVTLSSQPIY
LIKTRLQDHRSRCGPLQYVSFLQSFSLTWNKDGLRGMYRGIVPSLLLTVPRSVLTLVFYE
YFMHR
>TCRU_5906 retrotransposon hot spot protein, RHS3, putative
YESVYNASWHHVVEVPDGEGMRLEVKEGRPEQSWTYKKFGQTFERVDDVEQSGAERLRLM
VLTSDKKWPYSWKWKEKESIHDCYVNCEVERVWQIVKKDLSEFLSPDDEPGFVPGRRVLI
GTPGIGKSMAAGSYLLYQLLHYDVGKLPVVVYVIGSKSFLFDKTIKAVTQYHTDEMSRSV
ISSLWQSGMKGYIIYDVAKEGTPPETNFAPPEWGMIVLTSPNVNNFEDWREHKTAVPLII
NCPDRIDVKAMCFWRKHFQPTGEQAEEQAMNPAQYWETVEERMDEVGPIPRCIFNELEYR
IQLTAIGTAVKNINASNATDYMGVGGDKIWIDEYVSQTIVKFVRVRAVPGIEVGCNAPVS
RSAMATITQHLTHMTPPVDVFNLLLRNFGCFLWVVFEFAGTAAFMNPHAVDIIQRKLTEL
QKDE*RQFSVLSNKPRGHPTRSETLKKLRGNPDRMDLECGVLYLLAVGNFPLVDALFFME
SPRKALVGLRTTTANAHHTQTSNVRLFKERVASYFNGWEEFARDLSWKIIYAQHADSKMI
IDWQKCNDSANVTEARIVK*RRAGGEKVHQYQVTITAEM
>TCRU_5907 mitochondrial carrier protein
MSTSSEKKHTPWVNAVAGGLGGAAAKSLLSPFQRVVVMQQLGEHKEYSTLQLARHIREQD
GWKGFWKGNLTSMIIRVPYSGIQFVLYSQLKFFFQDICERYVRPRKGSAGDAHHRGETLE
LFLMKCGAGGISATIAGVAVYPGEVVRLRLMSGERQFNGIFNTIRCIYAETHSLRNFYRG
LGASLMQRVPDILVSFAVYETMKYRLIEKDFLSSHPSYKNIVSTVAGGGAAALASILVAF
PLDVAKRRIGMSGKGKSGVVYAGVRDCLRQVYAQEGIRGLYAGARVEAIRCVPQVVLMWF
FIEGFQSFLT
>TCRU_5908 exportin-T, putative
RMTSPLSTNYFTRAMELAHMCIPDVTPQERLEAERYLMSLRATADGLNLSFHIISNEPVH
DLRCFWAFNTIMHHLPAIAGSINDAQAEELYRTLFSFIYRYFFSSSTLQRQPMDFLANKH
AQLMVAGLQEFFPSRWTLFFDDAFELFERRGILPHVGDAVTVYVLRLFEYIDERVVSVRA

QTNRCRELRARDMELKDAMRENVMPRAVTTWYVILCDCRIRAPEIAKLCLTVVQTYIEWV
DFTLFITAEWINLLYFLVTAPAVRGAACECIFSLVEKKQLPVAKLESLRTLNIVDALPRI
VSLLQVPPKTEEDVNFLEVVARLTRAVAEQFLFLFENISAATADGGNPNRLYNSDETPFC
PCIREGRSFLMAGPSWVHVTLRQEQQQQQRGGTATIIGCSRDCIDNVRAALDTILTYLLR
LLSINHSDVSNTLLPFVQAYLKSAALHEERAGEILLRLYDHSLIQGLAEEEDQMWLDDII
DQRKQIHNLIRLLFRRYPTIVLQHLRLCVAQASTPVSVEECFRNKMDDQNRGDHQEYHLH
VENASVMGGGGAKNRHAEEIEATLRYLYEVGESVRMERLRNAEDEFSQLVCTVLSSECIA
QCPCAVVHLSYFEVLDRYYAFFIYHSEWIPLLLQRLLLLPYGVTNRHPRVRARVCYLFGH
LVQLLKTHLSPHKKSIVNALQDIFSSGVLQPSDCCELYEATGNVLSSMSRTSTSGMDEGA
MVVRFIEIMLKGLRDASSLVSSHQVMTGDSSACSEAVADQISFLTALAKGLRGGGGGGVA
GPNDTMTHQGGGSSGEGVDVVIVKTFHSVTNDVMRTLIAWHASASVRDRAAQYFTQMIHI
LPFECMDAYFTAYITNWLAWMEAIPELTKLLRLLFHFIHRSGSCVGALLTTTLPVVLHKV
TAVGDLLISPEEMELVSESTREKREVYRQLFAVLQGATQAGCVSIILSLPSANLMPLLSQ
LLAAMHLPVETELPKLALQIITKITTTGWAEGVGPPKDYATKDRPYNHHPHGGTNKSDNS
TMDMGNNLYDGGGDGAWTLFVLNEVVPTLLQRFLLPEFDVKDAKNFLLIGEFGLLLKALM
NRLGPSDPSLYMFLYNMLQPLVGEEEVTGLVTALQKEPNFSTEMRMRFRNMLQAAKE
>TCRU_5909 hypothetical protein, conserved
MWRKGAATMIRLRQPLCYHNGMRAAVMATRALSSGDVQDEATRWARGMEDKYGPGAYKLF
RPLYKDLSDEMRREVNVRPPPPMDGWTTRHDEATNLAVFERAADETTRVGRVVAYSPIEM
ANPPKLNALLYFLDWFPVEVLVARNGVILHFSMAVNEGGMHMRNVRAYKEEEHLLSTTDD
AAWVRRHLYYDGPCLWHLELDVQNELYDTMQDHGITLDWMRWAAGWVYYLEHVAYVQWSV
GMLEQLIPSVLRGPEEDFLTAEEREELSKPTEEWLDEHY
>TCRU_5910 nucleic acid binding protein, putative
CSNCSATDHLRRDCPLVTCRACGRLGHFKEDCPSEKKRARAEEDGEVSVCRSCGSSRHVK
ASCPLRSQSVECFQCHQRGHMAPTCPLTRCFNCGSYGHSSQLCYSRPLCFHCSLAGHRST
DCPMKPKGRVCYRCKEPGHEMAECTQTALCHMCNQAGHLIAQCPEAVCNLCHERGHTASA
CLKSRFINYKAPHSIESCEGTFLFKEHADGSSAGEASLNDSEGEHEKRCQLNPTSTSPSE
VVPAFVSSNLKRDGRVAVIVDGGYFERILKGHDRRDEEQYKLTVEVLRYTLDFIGEIFQK
DPVAYWFDTDPAAMTEYIENSMPLPHREKAFRESHLRKRLLLDEMNSGRQLGNVVSRLIG
RMKRQKGYTRDGPRHVWVQTGVDVAMATCVIEIFLHRQFEQVVLLCGDADLYPAIQYCHT
QRRSSPVLEKSNPVRVCGTSKSMSKLYGKDQDLSDFLPRILLDAPSHTEKEREIVFPTYS
VF
>TCRU_5911 Metallo-dependent phosphatase-like domain-containing
protein
DNIVSYLQLVRPGGTWAVAHADSLFWMSLSHAPLLVHRNCRTGRHTQPTKVLQTRFCSAL
LVSHAGPSLLLPRRPSVAALEVNDEATVTTVFLREFCATTVIILCI*KKWRDWGLGPAYG
STVAMVPLTALLAVFFFFSVDHYHCEPLQRHDRQLWLLRVMDLACPAPTKNAFSLALLPM
SILRVPFMALDHRYRGLRGYDSEREERYGALSLMCGWDGAGVPYFLGSGVEWRGLQPRPW
RANWPGMVPWFPTFIAGTADSDAMLNLFAVGRRGVEQNATPNVFCLLSEHRGGAATRPES
DASALRSAVGAAVGGSMRRVELSADGSRREV*LPLGVGDGEQLGAHAGRPWVDELTISST
CAVRVLIGGELVYPNLTDVTH*ARLWWVRLRRRGHAAMCVVPLPIPQSYGWLDGPLRSNK
WIAAGNRLGRWPVPQRSPFPISDAPYDGHVFCGNTETADVDCERRRCLLKRIEAKPKDGA
RVIATCRKSVWVCEATGRTCTSPMQPRLSRAIEVLVTRLRRKCEDIRRHPRHAPCTFCTQ
*AECGRISLLPLRNVLASMPSRRVGLCLVH*RFGFIAESLCFGLILSALPLKAQDEHTRD
ATGLPQHAASVASLTLGLSLCILDRALVPLILFSFLIVVLFLAAERPGVVFHPF*GSHWT
VLMRQSTTSGLAVVETTSVCMTGRRMLLSTGHWGDMMVAQGRGAADTELNRTREMLWEAY
VVVSANRKRRSAAHGAGLLSAAVSCLRGLGVAENLAYH*HHIGLHVGGTCLSWAGRPHVF
AQHLHLLLVYWLLATPLLLVISLFLFASDHCFWPLHDGV*STFRMEDYKHLIRSRIEKQR
RVHGHFLAERRVLGLWKRDARHFAEVESREGPSLPHLRRRQRRGAPCGGSGANF
>TCRU_5912 dynein light chain 1, putative
LMSDRKPNVKFADISEEMQNDAMTVATKAIKEHQMEKDIAAHIKKEFDKRYNPTWQCIAG
RSFAADVVHESKHLIYFYVGQMSILLWKTG*
>TCRU_5913 hypothetical protein, conserved
LSSLSSDLDTLQKRWMRCFRVCITSTPRVVIEAKSMDSDVWTQVVTMKTTQLPRGLIKTV

EDVLSLPTEAENRRVTVIDLRDRPEDIAVAQQILAKRFPGLRLQIDHSKGTDLQGTVTHT
VSVSLRDHGFVDGSPSKEEKSVKETFFGEAIGASFASTARRALREAFEAARIPPPPRHFE
RDQGESEMEIYLETIRNATNETIEIMTSLVGDDHVQVIVQSSNGRRLGLLKGRRDDALSI
VLACVERAAECTNRIATEEARKRIADHPVVLALPPKGLRPKEILHRLLFHTFGLTNERIR
VLTSQGDGGTFVTTVDAELHWSVTVNTECPVFSTLSRAVGVSKKAAEELACVKAIQRCFP
RVFEDQLSFHADVREIINSTKATDKDSICPHISKGLLAQLRWAAQCHKKEVLIEAVQLLP
NSENESLGIRTTRALWATQLFLVDQQGTRDFICLALDPKKSASEQKAIAAAIWKIFREEC
SEGVTYAIDRGLIDKEGNATSCEGISTSEPLPKNDYELAAESDPFIQKLQIVPSQSISVP
HRQSLLSVFRRGVQLYIDLLNERSGGGGVYGTSIGQLIEFTDRNLMDGSFKAQILVQFSG
DGVEITKETLGEAFHPSSAIIALFSAFKGLFEEGGIIAKAAREDKQVESIYRDTCQRAEE
IPPLPLEISTSNPLETVAQCIMLKYGLGIELRISGGGNVVQVQFFGQSPAHLGSDHLVTS
SQFFLGHGRGNSLLKAVVSCCKNVFYAHVCSKSEALGGARLSALNSGTVQVLFQGKSILA
SRVEDVMKEILENKAVSSAASIHVKVSIHSVAEGTMYQAHLCVVDGARVVELERTSLVAD
LLLSLRQLTENIIREMGGPTVDIDAIKRQCTGPLRYGTLQQLLEVFYGFPLLVETSLKDH
QWHCRLSVHLFEDFYYALAYSVNLKKKEAVENAAKKALEHCFGAAS
>TCRU_5914 2,3-bisphosphoglycerate-independent phosphoglycerate mutase-like protein, putative
GPFVLLFVYGTLQRGENNYAWWMADPKHATFVATARTVKRYPLFVKLLPGSDGCSPCLLN
QPAAGDVGDVSNCNERNNDAGGVTPQFVVGELFLVTPTLKSCLDVIEDVEEGVYTVGEID
VLPLDNEQVVERTLHVGKGEAVRALVYFRTKNYPPDWNCPSAANSTCLMQRFSAMECLRL
YGSRFAGFPAHLRYAAELRDGLQRHTRWPFDDVCGVPLRPKPIVLFIIDGVGDATYSELG
HRTPLEVVAGVPPRRFEGEATAKSQCTADRYASSAMNLVTKNGVSGLMDVFESGVSCGSD
TAHLALLGYPPKQYYRGRGAYEALGAGLALDDADIAFKSNFSVLNESTGIVTHRRCDRDF
TQEGPVLCAHIDGTVIAGDDAGLFESVHTLRARYATEHRCGIAITGKGLSCFITGTDPLA
DNRPLLHCRPTVPPEHAEYEAALYTSRVVNAASRCITELLRHHPINEARRREGKEAANVV
LLRGAADKGWVPPFAVRHGLFGFIVAPTCIIKGLGICCGLKSVGAAGATGDYQTNVNAKV
DAALSELGLAGAVDGATREEGMVRSVFAVIHVKGVDDAGHDRSLEKKLMMLQRCGEALQR
LWTALPDGSTVAVLSDHSTPVSIGDHSCEPVPVSVATKGCGFHDDVEHYSEVECGYGALG
RFRGEELLGIVKRAHYWYHYR
>TCRU_5915 hd phosphohydrolase family protein
LTFACWGQRVGCLLQRSSSDSAAVAAAATDLYEKYIVARYTEPQRHYHTMTHLEEMLGCL
ARFQSEAPVAHRLPAEGARRLVVELAIFFHDAVYDPRRSDNEERSAAWFQSFWGEVRRCA
TLHTTALDDGETRGRVGPLLWDDLDAARGVEEEVVNFILQTKHHMAVEPCYMHRASQSGG
TDDAPQPTPPPPPLHIFLDLDLAILGSAAERYRRYALDIRREYSWHSEADFCRGRAAFLR
GFLNHPQWYKTKFFFDALESSARANVEAEVAALEARL
>TCRU_5916 Leucine Rich repeat/Leucine Rich Repeat, putative
VISYMGHHVPLALVAVSPSARFEAELVGYAIGNVYVSCRCVDEGNSQDQEPGDVVLTMSA
PQSLEVLVLNLWWFARYQAVTLLLDHIGREHFPLFQDLKKRLKLRELKLLHSVVGCDMMH
VMSTCRELRALTVQNCFSESEVILRGVTSILSNRISEKREFSTFYISGVTNLGVLSNLRN
LTLCNTPLSEVMMLYLSECVSLERVVVNSCRGLRSLECLSSLRRLTELSLLNMGITEEGL
AFISNCNSLRHIQLDNCMKLQGINCLGSLIGLRTLSVSRNRVSDDGIRSLSNLRNLEQLR
LVSFNRLSSVEPVLCLDKLLELDLTENWVTDEGCAALANCGQIQKLKLASCRCVSDVRWI
CALTSLRFLDLSKTHVRSADLQLLTMCQRLEELHVASCSGVKDASFVEGLLSLGHLDLTD
TSIKDAGTQSLRKCTALTFLSLQDCRFLTDIQFVEPLRNLLNLNLEGTEVVDANIIPLMH
CTKLEVLSLRHCLFLTDVRCLRELKALKSLDLSGTYVTDEGVSDVSQCISLERIDLSECC
LITHFEFLRPLTALRHVIADRMNVLDVTGLGGSGSVERVSIADCKRLGSMGMLEAPRLLD
LSLKKSAITDSGIHSVLLRCHSLRRLNLQNCTSITELSAVAQLPSLTELLVRNMKITNKS
VAFVARCATLEKLQMVECVEITDVNSLKYLHRLVELDLSRTSVTSGGIVGLARCYNLKKL
NLSGCRYLTEVNCLGELRLLRELHLGRTTVSDSGIVGLCRCMQLETLILTNCSQIREVEK
LQNCLPCLVKFDVYGTSVEDSRRYLGVGQRVQHACVLL*
>TCRU_5917 hypothetical protein, conserved
MSISLMTIANTLSSECTYYAGDPDLLKSERYAERISKMLQSEKADLLAARVAIHAQLRDA
FKDDSVQKLLKPYLREDETFQALIDDAKSRAKFFSRKQQELQAAVMASEEQVALRDAHRE
LAAWERENAVLLRHQMFMSYKPAMSLLLESAATVALYRQYAALEDGGDTSESSSGEVPEQ

LVKMGGVPLFTTQAPNKEFEVDEHTKMFSQQVLQNKRVEYEEKRALVVKQRKRLEDCPSL
QRLHDFINTRNDIFRKYGIDLLVSLRVRRDKALAEPFEGGEDATVSGLPHTNEIMKSRRV
AQYSLAKIVEQCHQNYLSILHGGSGCLDAVQVLKIVRRYRAKPLKDMETFRYWLLASITA
DTPQIGPNKLVGKNPTPVDEYKKLWQPQKSSYVPSLNTSHRQQFKIMAERRGFPHIIILS
PVTYTYMQNNDPKTIMKGEMDLMVYDQTNEKVLLMIANSKDERRPRGAFLLGQEERYRFA
AVIRAAIANDNELFDFQCQGTLAEYFFDTEAGSEENYYCIMAPFKVSQKVSPVIHVPVSA
LRPFATCPPRYFLLGSNWGASSGNAKNPYAISHVHSELNEDAIVLQQNISEGFIQKNVMP
HLITRSEGIEIMKREREQRAREQRESMSARSGTLLSSARGTRSLGQTPRDSARTPRHTTT
YPSDVASTPLEEAEREDGILPEEEDPLAPELPGDVLRPVREALLNRRFLQPGYLQRRLKD
QEIKKLPAVKDGRLRTPLMVFHEIMKVKHGEEEPPLSQPQSARGRLNSIS
>TCRU_5918 CorA-like Mg2+ transporter protein, putative
PMQVHLMVQFNDGTTREWGPIAFMNEVVQTLRAVMMGSLGGNRQNNGSIRLFDQDSVAVS
VDADLHDVTAQKVPKMHPPVSFFWIDITGSPEPKDLNVLFGLLKVNARTQRKWGVEATGG
PAGDSLNCTNGSVFEDDSDPFWGSNEERGGREPDEMHVFVEEQYVQLQLAVIRASSPPCA
HDATQSTYAASRKEHATHQPDRLHANLFDVDVEEDLGRVELLCFSDGIVTWRPVPEVEGW
GYIAQAVERRLADPSSTKRILTTSKLLHIILDELCEAFLPDPTLVLNEADAIDSMLPFVR
QRESEQVDVLRRSLRLRRRLAVHRRLLLSKVNLLEQLGRPVMRTLLAFITADLGNTGNVL
QRPNAVVASKPLTKEPMHTDAKSVAVKNLRGLPHTSIIHRILYLLRQLDGAHTILSNATI
VYTSTVAMRNNNVSTEADYRMVVLHYVTLIILPLTIVASQWGMNCYVPWKDLDSTTPFWT
ITGLSVLYAAALLSYPLYYYFTGRPEKLV
>TCRU_5919 syntaxin binding protein 1, putative
SNGVCACVRDHMFHQMLDAVHGLSKVFFCDAHANSALSRSLRLHDLIEHGVTLLEDPMTP
RQPVISSPARYFFVVEDASVSRVVEDWMAKVPHRDAHIFSLGCTPHRHPQQLVRARIAPR
AMRSKDIMLDFAAPEVLVFHLSMQNGFPQLLSPPTRESVLNVVDVAASRPVAAFHAMKNS
VPGIRHQNSGSICHGVARTFFELSKLCYDEPDFTSGADSRGNPVRIIVDWGCATVTPLMH
QRKCQFLLDDLMPLQNNLYEQTCRNRLGEGSKRQIDEEDVYRRSYRH*FLAQCVEELSAA
LKPHAYHPGLAQDVEPKANLAELSSAVRAPPEFRERQARPSLHIDFCARLVAQYWEKRLV
EVWEVEQDIAVGHKLLRKYLDGVRRLTRDAAMPRPVRLRLLLLFVTASSTDELKEAKKQQ
LIRDGGLTPDAHLFANLEHLTRRAGNVQRYSTASAQGGRSTSDSTGNAATDGDPFLNQAC
MIMETANRKRTLRVGLSLASIQRDHAMRPNGESCAQNSGAAGNNAGPFQECGGKWENHPD
LCGGGGGETIALTTPQRIVLPVLGGVACSGRRSVHEISKRYGREVVIGASMPRP
>TCRU_5920 UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase,
putative
YIPRSVVDTWSRREYLVVLGIPSTDVEERRTRRNLQRTTCWRSPGAATRANDFTGAMLVL
YVLGRHPSHGYDYSAALLEEAAQWQDVVALPMNEGRVTTKKAIGCYGTWGEEADAGMSRK
TYMWFDLAHRLFPTARYISKGDDDMFLRVPLFVAHLRLLPRRRVYMGVHCGGNIWANGRS
VGVHFMVGWCYTMSRDVAEALVSFKPLRRLAHTPYSEKREEEFLSIGMGHEDMMVGHVLL
DEVKYQPLIHVKVLPCHFLQARSDTGESQVVPTSMCVHHVREDDYAALMARF
>TCRU_5921 ABC transporter, mitochondrial, putative
VTQAMRSSQYIWRPYHPEALCDLRRFASTIRLQTNFGEATPAQRPKNSFSPLYVTEPASK
KGSFWRYMRSARDEAPYIALAVAGVGFYSMATLAIPAGFGQLIDYASKGELPLGTSAQLL
GWFTLSGVANFLRLACIGYAGERVIARLRSRLYNGFLAQPTTFFDSSENATGSLLQRLSM
DCNVVGSSLTEAVTQGSKNLLQTVGSIGIMLYYSPILTGVICGMVPPLAVFAGFYGRYVR
RLQQQMQDALAVKGTVAAERLGNIRTVKAFARESEELKWYEKKVDAVFQISKRMLFYNAS
YMASLQFVGYGALYCIIWAGSLLVASNNLSPGVLFSFVLYTVYCGIGLMGLTNLATEINK
GYGASLRIYDVLEEEELLQKAQDKTKATIPLECKWNIKLSNVSFAYPTRLEAPVYENLNL
EIAPSRCTCVVGSSGSGKSSLALLLLKLYSPTRGTITIDGHDLSSLDTRWLRGKIGYVSQ
EPVLFGGSIAQNIAYGAPDYKWDDPIDRWLYSSIVDASMRANVHDFVSALPQGYDTFVGE
GGRSLSGGQKQRIAIARALLRAPNILILDEATSSLDTESEVVVHEAISRLIEDARRGKEK
RTVLMFAHKLSMIRQADHIVLIDKGKVAVQGSFEEVQNNPLFCQLVGL
>TCRU_5922 CorA-like Mg2+ transporter protein, putative
VWVDMQGCTDEQNRNVLRLLFPDLQQSQIEGVLSPEKYDAVELQPVKGEYLIGSLACACE
RQRCAVEMEDEENTVICSFVCNDRFLVTMHAAPFLGLKELLHHVKVGGGLLIQETTSEFC
DSEGTDIFTMKGSAVLCALVCFTCETYLPNLTGLISEVDCIDEMVLLVAPGKRDQTDLLR

RVSVLRRRMSTENARLYLKEKLLQELMGPTMRTTFVSRDSELVKAYREVFMELSQVLERM
EVARDTLNHVNLNFVNAVFMRMSQASAGFDYRMMVISQISTICLPLNLLASFYGMNCKVP
WSADDYDNLNCFWAIMGIMLAWTIICMFQPVR
>TCRU_5923 hypothetical protein, conserved
RMVIAQVEVRRVSFLACKEGEEVGAVDALRRCTDAEGDEDTVQCFLSLIAPSGIELSCHA
ALPHETYTGEAKELRVCCATNEDLQDIWFSVREICGTRAELDGDNVTLPCRLWCLKSTAR
RQCQRDTASDASSCSHHTFSFLNSSGSEEGEENGEDADAFPTSNWQLLAEGRLSFMEYGL
QNVELEMDSVAMDRSGAFVSVLFFVAPRLQCTLEETGANLLEQEDDNPPMWMRLEAHESC
DPTSLRGIFFSDDDEDEEEEKEKDDADNEEEEEEDLKSFVDSHAAAPSEEDLVNVSDVSE
AFDVEGAANASAEPLCATGKRSGERDEAVAAAVAVRESDTHAEPQRTKMMVLSSTSDLRE
RTAARWVLFVDMAPWNLHMPADEESIEYASTGETGNDFCDAAERLWRLTCCKADGHVLAC
GSSFYESVCSHHGWSDVIVAIDDDILAVAVLSLQLQALLSVEVGDDVNKNKKDAFLPLEN
NVPLPNCLMRWVPVAVSTQIPVADLLVSSADACMYSVPLYVTTTGNTFAPSSFFPFRKGK
ALSVQAILDRLPEVVGTSDTTGWMKAQQRVAAQFHEEMSGQVRGRYLPEEQLTVPRCIDA
VYSVALHVCFAVSQQLCPHVDMGVAYPFVALTISGGCELLLHASGERKEKDRDDLRRAPV
VRFDARVQTTLDKAHSVLLLTLHSPVAPEVVFGRAVLSIFELSPKSTGRLWLPLRSGREL
DCETCDGCDPSPLLDPPPVGWIHCSYEYIILSEERANSAAFLANQELLQQPLLLAAPLFV
PKYFSSSSLGAPLRWNCLRLCIVEAVDFCGVLVRSGRWKQKRGVYARADVLPPPHSASYA
DSSTVTAAFTTPALVSHNPRWVCCGSLTIAADTTHLIIRLFDELDGGDGLLDGDTAGIGV
IDIPRVTNSRFWTTPTGEAWLPLIAPRRGASPCYHGAVFLRWTFSSRDDPHMDVLHGTRT
SLCPTWSLSAQTQPHGTYWVHLSCIELLWTWLLHHVAWKASFASSSLQRRPVFFLWLRAG
YFMHELPLEPPSEGDCYINVHGAVCLPLTDHVEVAVCCRHDFNFLPCASSNAPLPILSAE
DGSKAVSVVGVGELLLSKEDRDDIVAYHRLHRVVIMIEPHVMYPPCSVQAGLLTAQLHIA
QIAQQESDALCRHAATRWTWPPPHHSTLVELRLGRVFMLHARTTLLQSSHTPSPPRRWIV
GVREKAGGSDKSNSHDTASASHADIIHPPVTLNATAASNVSQGEGSDALYLRWPASPFVI
GLRQRPSPPMIELLLSRELANSEAVGVAVTTEQVGSVTLDLPYCFERQKGTQLYAIRHPC
ASQAISGSGGVIGFVELHFDHNFVQEDVGVEAKVMEAPEKVVGRERVLVITVVKARYRQR
MCLPPSLQKEDTEETLTSFVVGVGETSWRTTTQKGMTPQFDCQMLFDLPRKNKNEAEMGS
DDVVEIRMQMLPELSISDTDPTRTVGMMLSPPFVTAFAFLRLCYDDVVSAGEMNSGQWVP
LYTFDDHMSVVRILVGEVLVRWSWMNQFSWGCVTPMSVCRAPSSANQPDNDVPTPPSTRG
GDESLSLPPPVYLSLQVCDFVYFNISLLETAQKERSELFLMVSMSESPNYLKPTTSFQCP
GDDHHRHHHLQQQQETHPWDGFGVRYGDRTGGAAFDPVSKRCVWREYCLLPLFMDEGLNL
CFEVYCCSEEGSATVVGSGYLNNWDVVGRGITAVAIFALGDMQPCGALTVALMQAPLYRD
LMVVSTSQPQERVTESPARDKDKVKPQPQLAGDLKGVKFFQSSSSSPSGIDVPQSALLRI
TVHSVEVYGQSVSLSDVCWELKLRSDATYAPQGKKYQWTSLDAANSLLGEGHGEEWVGWM
CAQNMSTIEISLLRRDVAGGRRMALTGMRDVHGWFVVNFPTHPSGEDSRRSVHVDLLRGA
PFGPFNDDSVPVGRLYMSYSPLLYSGVLYDPFTVFFKRTLRLVVTELLGVVRSRHLRSSR
LQRMLHETRGVGETEKEEVKDGEHNHDTSEKDARVCMRLQCGTATAVSSLFSPPIMKVSK
RNGMWQLDGEQHCETLQFSLLLDCIPVDCEEVADVRLSLHLATRLRSRSKQTGPTHCLGA
Y*LGKVSHICHGQAKRKARGCQRQP*LLEEGRQNQQVMPHLWVPISAVGEKSARTAYAHL
HYAWSHEVSLGSWLVCIRIRSLGQQFTLYRPFLFFRVRFPNGAELCLPLDLFCAFSTSNP
SNDEGHSAAVATPLRSTWSFSHVQLPVIWPLGAQIESVELHDCVAAGLTIHVGTHRWSSS
DTPLLALLVDQNETQEPRSTGSVLFSSERWLQFKGVDTGEQRGEAGTSECVHEVLLARSA
CPPRGVDATRCLHVPFHWWPLQASLRFTTSGSDLVALGAGRLAVSCRLCIGRWQLDSTTA
TAGWVWERNDDDNEVKADEMFASYVEVEPSTASVTATWGTPANKNSAAAVATGGGGLRRH
FSVEELRDGLTRYAVRVSVICRTRCASKFGSESTTPPPASAAWNAGMNTVYTYEGVLIVD
DDCTSTCGETRLVLVEGSGVSARAPKDSGREENSIAMAWLIAHEEMKLFATEREDSHAAR
LCRPSLDAVGKMRRWRQRRTNDVHQKPEMLSWLVTSIEVKKLPVVLTSMPNATVTASNGF
PATGFIPQDLPVLIHLGLKRLRRCHSHKTSASLNGERVVMVGGGEGGFRARFSPVSLHAR
SVNTQRIRPLCTLHVEPMWCISPQHWMDHRRPLNLMLWQELSSSEELSCILGTLRLDVLL
RDAAAQRPTRSGGDFGGEVVTDWQPLHGSELSAQCAGIVRVRFRPVMHLPREERTKDRQV
PVCVEVLEVTAQSFKGIFCSRHGGRLGLMFSPAENAGFSSCSSTFLRRGGEEAKFATDET
GSRGRQMKDAAVTSGMITEAADFLPNDDEHFSFEEAARENKEMNIDRSGPSETDDHVSVH
GNEGTTPEELVALSTFHTILLEGREMDLDTGQKTWFGMDVILVECGIDGHQQEGSSIDCE

DIVRVLAAERLDLRLHSFMSCGSTERENPQSLQTSSRAGVAPSLYSAANFTVALSCVSSG
IVTVRLHVVILESSPPFIHEGNDTNRNDDYDGEDVETRCIAPRFFFAADGHGKDRISSFG
DRVSAVGGKVYRMGRKVYEWDAQELQRVRSSSSSSTAGAVAFSIPRLRCFKWKTVKTKSG
NVSHPTALPWQWRYRLGHTTWVYDNRYIMLHGGICVSQVGGRKPPPLFKRGDGRGRRHRG
CRFTSCIFNHAAESLVHDASSAVFCYDTKEHSWAVMETEEGDMGKASVNGEMVPCQHVFH
SNVLIQEKVWCFGGCRVAGKMREDGDEFGDAKDAAWMTQKTVNACRGILSNALKCLDLPT
RQWSIVKPVAQMTSRAICPDRTIPFFSAVKTPLMSSSPLPVMCHTAVGWKDQMFVFGGLQ
EVVEGEGTVLRPSNALYMFHTIRLSWWLLSPANALDVVAVVADDGGVGGGGLNRSNDDTG
RRRNWPSARYGHAAAIVPEHPHGAFIVLGGATCLPMNGKKSGKLTFDCALDELLWVYYAA
FGYWQRIEVPSFVPLTRRVFSSLQIVRLTTGEPWISYLIVIAGGCDASSLEKQQRQEPHA
EEEAIDKKQDTGL
>TCRU_5924 hypothetical protein, conserved
LDGMSSSVSSFSCAVITTRHTKRFEGDNWKCVLENHMEALRSTFVLEAAIACHRELEDIT
DLEFRIGSLYVTFHVSHDADVGESEIQERVDLYPFREVLRLYANRDAPPSGLDAALKRIS
ELEEEMKEKLEKLQDENLRKLAELEEAKRAMEETLMRQLHDREREFCEALGKSQDELRAS
EAENKRLEEEWKRALEAMKRERRRLDKHAMRQNELIAAIIQGNKKEMEAKEREFEENLLE
KDVIIENLRVRLRSKSEPANGEMVSRAASVDADRAEEFAKLMGRMEEMAILLEKTQESES
EARGEIQRLSEALKLSEEARQSDAVIYENNFLAIKQQLQAFRDTKLAEDLQKRQEESRSR
RGANLSNEERTNETIVRQYETALENIIGTLQDRLTILREEYASFLKVSEEETANEKEVLN
EHEQDSQRVRQTFRTAALTLQRVFWSTREKEVPEVISELDNAAAAAEKSRAAVKVTLALL
DSRLQSFSEQKEWMETHQQSLEDLLVSLRQLNKRAFERQLSLMNERVARPSSTP*
>TCRU_5925 Triose-phosphate Transporter family, putative
SLLLNIVSSVGVVIINKRLVYMEAGFRFGIVLTVIHFIVTFLGCLLFAWLKFFEVSSIPI
LKVIPISLAFCGYVVFNNLSLLTNTVSVYQTSKIACTPLIVWIEYTLYHRRESRRTLLSL
IPICVGAALTVYSDASLNLMGTLWALLAILSNSLYTVWGKTKQLELEVTSMQLLMYQAPL
SALLLVFAVPIDGLGELVSFEMTFKAVWAIALSCLLAFGVNFSFFLFVGRTSPLTMNVVG
YFKTALVFVGGFMFLSSEMNAKTFSGVALTLVGLLFYTHSKMNGLSAPSYSRE
>TCRU_5926 Autophagy-related protein 27, putative
LLFVVFFFLPCRAYAGEEVLAPMCTEVIGFAGEYNSHIRIGAPVSPAENEAIVLVLRAFP
LNLGELSQRWIQMNVTYRLREGSTVFLQSDNDGIAVIQNVEAGTNMDIEVKRVRKDGPVP
FRFWSFHANRPSCHIDVSPTNSFLAPIPARFGKVATPVRVYFKSIAPQGAKGFILDITYG
FFSTSPVKYEVMQSPTSAAGLTRTSGEVVPWSEGVAYMTFSPSISTETLQLLQVKILWVD
DITTAGGTAEGVDPAVPPEEFAKKNATPSEGTSKEPSSQQSKAGDKKRGSVLGLLFILLF
SLAVFMLVMSFVNYRLKGATEFPEMIPFVGVFRSCGQYVSLATEAFMRGRGNHRGGYSDL
>TCRU_5927 chaperone protein DNAj, putative
SSSCPFAVLGISQSSSMETVKEAYRAKCQTEHPDVGGTGAKFLFIKDAYEKCTRRVHERE
EMCHGMYSKTTVDSAAPERAEEKEEGRSGRYHRQSDVWYESLAKRLGEQRQMFYGAFPRA
KTSNEMDELFCSALHCHCFDTIDVAEPLVLALSHYHRVTGYGAPHLCSCFGTIDRWEEFT
ESRAGATMYHILLQLYTDGPKQGLTPTIITESVEAIMERMSAKGLEYDDWTLTLAHKAYR
ISPYPS
>TCRU_5928 reticulon domain protein
RGMSLWDMLAWHRPKVTGVLLGTVLSVLTFFCLMKYTMVTFLCRILQLVLLAGVLLGFTN
RWHLTSDDIHEAVNRLVDCATPRLVTALESMHQLVTWRDYRRSGLVTLASFVVALLGNLV
SDAALLTFFLLLAFTVPAVYEKKKDLIDKWISAATAQVEKYMGKIKTKVEEATKK
>TCRU_5929 hypothetical protein, conserved
GVMDARVVCVSRGSNDVENAFKRLDDTQVQLLYTKFPVGMGTFRRNKFIYVIFVGPNCGV
VKRGKGIAEINLFKNVLHGAAGISTTDRSSLSLPFLVQQMRSVFVTDAGNFSLEKIQEEY
KRCIKEQQWTMHRDSIPPSRPHSISRALSRHSSDDEVYEMPSFTSFQIQNVPCDIDDNTR
SVLEALHMKLGPLNWATFEANPLHLTLAGAGNGGIFELVKQLPAAKWLFGLFRITLGAAE
ERQSLLIFFQWIGSRLRVVRQGPTTHIFPKMASILAPYEYEVYLVGTQDLNTQKIINKCR
LAFLDYRVQGKPEVTENTLRDLKKKLRPVNSTFTEEEYRVILEEERAKMDLNFDFIRPRK
NHAVRSFSEINNDNGVGQSRVFDIKETLDLINQSEGGLVWGIFEAR
>TCRU_5930 hypothetical protein, conserved
SRTLPLKGVQHITSPSVPSVVLGNKHLPQLPYKPIVCGEDGSIFTASLREIGPSACTLIT

SRKKGATQKFMTKSNSSKMSKNRREGGMEACVASKAATVGHSKARASPLMDASGDDLQRP
RSPLLHSKQFEKLYKNVAVNALSLSKKMNRSYSGTMDMLNSMTLRSTSRDSLPPLVNTLE
RYIYREMDATLSRGSPLTVQDRLQPFREAFFAIIDALPAYGNILNDIMSVYDGVIQEQAK
LLADVITEHSQRNAFEQQNAMELAELRSTVSNLMKELEKAQNAAKEETLLVPSNDWNTTL
EPRLQRTPRTRHENEKELQDAQKKIKEMGEVIKNELEKQLVLINSLRESDKRTKSLEVQL
SCVNSQIDELSEFKVMAGEAQKQLEEFKLKYQNFISVQDHEIIRDYLKGELQAAQNMARQ
YRRAAAVRGTQVDVIDRKLKAIQKENKELLEAVEYERKEILTPRPDWKKIHLALPELKDI
AAPVKSISLEGDEAITSNVGGLTETRLQVEFLVESVNSLSRELQRRKMVLMPTVAPTLPL
IGQGVESHVPLHLRACGIIPRVSLDPVEILLLVHDFFGDVLQPHPDVLLHTLDVPALYKE
FLRERIKKREALNGFVGAEHLAINIADFIRDKERARPSFLLLDGILSGIFPARIACDVMM
IVENVRFELTSLSKGQKKTRLRRVAISDCIAPVLQLKTMEEITALKDTMGSDTTHDVESL
CATEGKFMSTLFDQECASGMKFYVGLLEKLTSYSHYRSPESTELVISLESVGRAIAEMEP
LTPKVIIKEITEKPKEGSKEDGETIIGLSDAIHLLAAAPVIRRS
>TCRU_5931 hypothetical protein, conserved
GDMSYIEPSPKKLSRGEEHQLNVGTHSTFKLIVRTTICATLFAIPFCVSIPSSPLLKLSQ
TQDTKKSLIPRMMSDFFYVNFIASWCAYFFLIEPRITNEKAKKGFMPYLGPVTAQVPGLS
CLLLSHLFYPGMWAVFNERRWRERRREFIRLNTKCFLAYAPIHIPTAVAIGAGVGIVLYP
FKFFKKR
>TCRU_5932 hypothetical protein, conserved
DNCPLFLSEYIRSNPSSAISARWVSKLTDEEQGDCIAKMVESAVYQETWLSYFEYAEKKE
ISVTDEISLEAIRAVGLDPYSASLWLKVIELCSNEEKKRELFQLALRVPLYQQGLVYKAY
KNFESEVAKQSGHSISSFPSLSEVMQYSKILETEPVWPDRFVDVQTANRARKDAVIAQWN
NLLNFMFEKYEECLLSKDLYLRRIELAFRQLCSQFSHEDICWYAYACFVAVDLKDEIQAR
EIVEKGRFLIGDNSIALRSLDALLSNSDLESVNSFNDILNKGIFLQRLYANAANASLQNR
KRFRDVGKIATANSLSDWRIYHQWAFAEQCVLNDIQMAARVYERGISCAANSLKDAVLLS
NEAVNYHLWQQNEREVLGYAERQIELLSSTQHEGFIRASWNQLVHAESILGLPSLTKTIR
RRAERCVDFARKSIIERYRVGNYIPCSDEELDWLEYVDDLFKARKEEQEPVFEGVTPLKH
LTLSTDLNFYPDPVLPDVSLWTTFEMCPNREHSSGAEDSDEVVGSRTLRGRLVYKLKIDE
KTVARLKREAQLRQEENKGVGSKALKDPHTALQALVEKLESKKWNASQLKMCRILNAEWL
MNTLTHGELDLRKRR
>TCRU_5933 RNA-binding protein, putative
QLITMSFDSPYNRNVYIASLPANYTEEELHALFAPFGRIVSTALVKDKNKGRCKGYGFVL
MERYQDAYNAVIALQGHTIAHTRVQVRLARPEASAKRIYPLYCQQATISNTVSPTYVLLV
P
>TCRU_5934 hypothetical protein, conserved
KNGSRGRKKDGSRRKSRSASRRRSRSASRRRSRSASRRRSRSASRRRSRSLSSRGRSTEK
SGGNSAAESKRNLDKSADKFPLRLLVEGESCLIDPHISEMEITLYRAVPEEGNTPLFFDT
TACLFSDHGGQTDYVGVGRETTNNKGLSHIPHAVLKFEADSVGSRNFLEPAGGPSVIAGD
GVSVNLKRLVMWGGFSLCATLFTKNTSFTEVTDAYYAVKVPKAQVPLAVVPVTPTSSHNS
CIALMVRKMKGNTKAVWELVRIGELCAQQDVKGVLVALQNRGLVCPADYRLLSYQGLDYS
CEGCDEESFAFDDDDEDDDEGDNAVDNSIVDENARFENLLANVPRVAREGRRQYSVGRSI
LNTVLDTADGSDDDEVMRDALRAVVPRYTSLRPVRYEDKTYNVGSRDEVLASHYVSHREE
YGLHSAESQSGKGFCLPPIFSPSSGKLSRLSFGRTGFVRPSAPNELLATIPSALSRRSGT
GRRGGRSSIGLPRLSLLRGRSKSRRGRKGKKKSRRSRSKRSRSRRSSSKRRKRLGSR
>TCRU_5935 hypothetical protein, conserved
VVALLLLFVPQVVVPKPVVCETNVKVLTLNVTDTPNDRNFADSFGAGLEAALWWRNFTVA
DGVHVEIVRKVTTMLTSGTVIEEALKADSNILLVAGVIGDMTAAISLPVLVRHGLVSFAP
FTGSSLVRGWNPNMYFLRAEPAAELLALLRYALAHLRVHRLGFMYLKGVFFGEREYAQAQ
RVMSGMGYNLSGVFGLKSSMSHGAKKEVFDAAWEVFANTRPQAVIVFGSPIKDTKKFVER
MLTDKRTAGTYLLAPSALQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
VTKYKAIQRFQEVMRAYLAHRNDTQSGVGKDFPDDDNEGEVMVAGWVTGELLSQALGNRE
WVKDRTSFLASLYNQRRYVVDDIVIGDYGGECDYTAALKGASFHCNDGGRTVYIKRFVEG
FRAEDVAAGAFTLRLWECGAADTMLHAPLNGLAVTMQDSVDAALAMSSILAGVDAAKKPQ

GQYDGNTVTFLTLNTSTAGASDTLLTEMKARRVQFVSGVVTDAMLEVESVTFIDPLLLGS
RLNRFRRNVIRLMPTLEQQFFVLANYLGDTS
>TCRU_5936 hypothetical protein, conserved
PTGVGALHHSKRFASTKLARIYTMELNKARSDYRRTPTRTQQEECLRNVTGTPLHLIQGL
DGKTVAHCLSTLVVLDAPRDLALLHDCAVWLSVHPDSFSPHSFAQSLYSLVCLEYPDTAT
VVRSVQDRLLAAANEMAPSSLCMILASVLTATAGADCVTQGPVDLSNKLSDRLLRVVNDG
LGLTEKVMIAVALGKLSGRASTSSVLSSHVVSQLSAAVWVSIPGAELAVVSLADLVGLLS
AAHTAPNSIREVVERALLDELKVRVEKEPLVSARSAILMARALKLFLKNENPSAKPLCGK
MQVAIEAYIGSEAATLDTATKLLTELVDMEEGPFDSIPSSLLRYLVKAINERREKWSSES
VHVVLRVLNKIDLFRADAQALATQCVDFIQAKFTTGAPVDAGEVAALLVEGIVDPHAEVL
ASVVAGNISRWSVPSVLTFLRAASEVSGKPTRAIMRDVASKLVPYIEKATAAQVAAVISS
FGRARVRNDVFCAAITNRATALSSELTLHQVSTILGGLASVEYRDTKLFVDLAPLVIAQA
PTADATLTANLLAAYSKMLIWNFRVIWSLAERAVVIYEQFSIPQTLAVVMSLNRMDVQHQ
ELMNALLQQVMRHASDNAKLSLTETVMILSAFSRSGVWDAVFFENLGKRIVKDQQQLTPD
ELAETLMSFARVGLTQYNIFEELTLRALAMAPASPLMPLAHIAVAYAIVGCRHEELFSII
ADRFVNQKADVPAVTIASLLSAFASIGIRNDRLFIESIPRVRHVGQYGTPKDITNVVYAY
AKVGLWHYKLFVRLADRAIQLRGEFRCDHVARLLEAYARVEMRYEKLFVEFSPRIQTIAH
LLTAGEVTKIVSAYAKVRIPDVGVFNACGDRAVTVVDTFELDEAQQVLAAFRKTRNNHDG
LMASFTKRFPEAVATIPPMEEEE
>TCRU_5937 hypothetical protein, conserved
SLAIVLRACPPPSFHFFKRWGMHDFHTSKWTRLNPSAKTKRTLLGRSCIDKPSMDMVSVS
RYGGNTRRETLATAFRLYRSMDQSEKAREAGQEALRAIRFTDFSVDEEEEEDLAVDFACL
YLNACVLFGVAPTQEMMSQLLSWLPKSLYSSFHWECVLCALAVYLRPSEKTATAAATAAA
FVCMIRGAEVGTVPGSLSRDGKTLLLIVINRAIDVLLRANGRAEDRQHLLEVQLQTMELL
CPTTPTPTAPSPTSSREERLTLVDTICWRYAAGVSLPIAAKLVPLLQVKTHAELEELSVS
QCVRLFCALCIALATQDSSGTEWTLERHSHVLDPIVRHLDERVRVHSVDDVVILLVGLQA
NRMARSRYKKLPSSLLVHLREQQQQQRSRQNQEADQVSTSLKSDDSLLALSHVLSQLAMD
AEDALADAAETFLTDL
>TCRU_5938 ADP-ribosylation factor-like protein, putative
MGALFSSFWSLFVPSRNYKLVILGLNNAGKTSILYHLQLGHAITTQPTLGGNMEQLSVAH
GPNNNTIQFTCWDLGGQEQLRDSWALYYEQTDAVIFVVDATDVGRFAVARKVLQGLLNNE
PCLRKAVLLVLANKQDLRGAVSPVEMIEALGLGAVRDHTWTLMGCSAATGASLREAMAWV
AQKVTDQAVAAA
>TCRU_5939 phytanoyl-CoA dioxygenase (PhyH), putative
THLSLPCRLKSYVLKFLRGQLPEDLKDLNGALGCLYGTLPDVDEFGQFVIAPEIVERFHQ
LGYIKLPRPVLDAQQVDKLADEVNELANNVEHHPKTEKLYATSLANLTEGPLFYCQGQWR
AAWGMHDLIYLPTITVAASQILGNSIVRLWYDEVFMKEARKGPCVPWQQNYARWQHTTPV
NHVTVMIALDTMNKDRGAPCLVPGSHRWREGGLLPSVPYDPAKDEAQQLNTIWEITNEEE
SEMLMDTPPATVDMKRGEALLIHPLTLFATHGNRSLDAVRCCFIHYMGGKTYATQNGPLL
PHTTQFQAGAMIQGPFYPVVFDPAMTEELAMLP
>TCRU_5940 hypothetical protein, conserved
DHAMALCPSNGNTHVIYVTSNMGDNIWAFDTSGQYIGLVINVSTIPFRVAKLREMTFGPG
NHLYIASARGKYSRIFAVSGNGLLNHTLGEKCTRNYLFTATAQSNANPFLDHPYSMAFHP
QDGSLFVANQNSVTITRYERVQDDKDAPPRWEPVKNVAHAVSNASGLVDIPDKAGLFASA
WSNEYSMRSVRGLTISPPLPRALVEQAAPQGWYSTERGLAYYIVVCDIAADQVHVFLAKT
GEHVFSIPVSSPVQVLFPSRYQKPISTPTSYFETPYMYVTSKEDALTFLVPLLTPSHSGD
ATSITNPQRRLKTHAMTKRVPNHSFSGIFENPSHEMLLIADRLERRISIFASPFLANNSG
ETESSPFLGHFASKLPDQPEFILTTAVEEQSAIPLCYELGEDGSFRYVALCTAGYIW
>TCRU_5941 hypothetical protein, conserved
MQQKCEVHISGVTFSYLVSSVLSLCGATKRNYNLFGHYEVREGDTDNTENLSLLEAIVTT
VLPLGVLPPEGATFLGYASARRSGPHKLSFEDTRFLLGKKILFDTQSESFSSSYPLLLLL
VTSHPDASPSTGTNTLEYSVIQSVYPFDSAKYSFTNKNFVPLKVDNMVDSLSGFISISSL
GCHNPSDKLRLPFFVNRPRVAEITFEHSVSEMEDASRKIQVLFQRLTDLKRILSEKK
>TCRU_5942 hypothetical protein, conserved

MKLSLPLANYEITSYVTVTREGWKFPKRRVFSSVVVSPSGEWFVANDELQAVICSFEAGD
KYRLDGTLLFRQYGFDSSMLCLLGVNGTVSDFNSPRPSLPCPISLKNLHLTYGSEMVHVS
FSSFDEVVLVSSNCCIGCVQPEKQRRAFMGHFISYGKLSGVVCCGIVPNSALMVILTGEG
LCGVVNFRDSALLSISRQGIFSELGLPSSSTAIWGVKADTIRVVVTFPLSRKVHVFVTST
LPEENEDEHEKSSMNVSLESPLWNLGAHSYVRNYGTSFAVASVWQNLVQFSVWQGTTLSD
AVFLENEMSVPYVSGCWVDEVFVVTRADGMALPFSICLNGEGKGGINIVSNKHIDLTSCC
SAILFGQSKYFMFLTVTCMESLCNGIPEAIFVTDSNSHRRFLQMCENKMEKPDVFLIDIV
PFENGIAVINVKCSGECIAFLTSASQVKSQFLAYEEKTDQVTCCLLYKRQDIIFVMGYQH
GGINVWLSGAPKCVIPMVHAGAVDRIILLPGEKGRLEADFVSVCTERGTVVIHHSETFEC
TRIFQSPCGPLTSLIWDSQTDYVYTVSGSAGNLWHIPTCRLERVIHDVSAISEGPERRNL
LTSPKIGPVIIDRIAICGRIHFSLIVNVLPLIDTLTQRDAYGAPLACRLALSILFSGFNC
LDSKIHDLLGLPERGFNGGSFSVCTVSAEQSAKYLLAVVLLTKALKPSTGLKYLISTSEV
KALSDTLVRSGLIEQSPIPERLIIQALSLLLEVSDPAKKAIRLCIKAASEEMTSQQLIKL
FKNLLSMSSEELSIRHWFSVSTRLSEIDVWCYGFFVRMAFLGDMPRSDGIIWKCVLESFG
SDTSRLTEVLNMQGNKKCVLLLLQTLREYYQELSKTLVIDSTPVVDAVASLAFEGEKNNG
ALAIKTLMSIASVEGNDFIESRLKGWYEQKRSWRPRIIAFFGALIEFAPLQSYHSLPTIM
EFLLRALDPHNPNKDERKSCLLPVTQVVRRAVDYLPNVSFQQHLQYLAVGYNDGIVRVIN
MKTTGIVASFVSHPEKILCVAYSSNHSGHDIAVLSEKMKNIKIWHASRPVGLMGIIFAGQ
MPEFRLKFVVDIPEIDSAESRERPDLFSMITKCRLRWLSPHCVELSSPWHDRIQLTV
>TCRU_5943 transmembrane protein, putative
SEVYELQRRVGVAGDWESISSMTISRGPVGATAKLKQNKDAQDSGKDIDLTKEKKTALAK
AQFVYYRLVRKGDKDGINAVSVVLTPCSLVRDFDALDSRTVVLRESLRVAVGPDATVVGL
QATSGTNTFHAKMLNGDECDLSILSLFPNVRMRVSVGLVEPTAPRSLPDYAELDTIARLS
DSKSTGSKDRKGKKSGAAPSSYGDHPSEQQQAGVLGEKDEGEEPEEDNRTFLQKYWTFLV
IPFLVSVIQGLLSKRQ*
>TCRU_5944 hypothetical protein, conserved
FSSAAFTGDDCGEHARREFARTQHVADTTDTFSSSSTVKSRPTIDTYRSMSSEELETLLR
TREKQVQQLRAIYENFHYEADKRFRTMVFDYHEKAMNLSQVHGKMQLGSLQISREALVKL
REQQEMYSRDHRLMVAICTLFTFVFWVWVRRHYVRHEDLFGDDSQLRIPKNQRSVTGMGS
YNENLFGSAKRSARNMETSWEREVRE
>TCRU_5945 hypothetical protein, conserved
LPPWPVDAIEFNTRLPNGGHDKRRAHEEQMARIACPKELPLDSEPVHSGEIPPPQLPTER
QWCEVHRVEKTEEGIRTLASGGWVCGSCFRCMPHRSRSVCDFCQTIRHDAVRAVAGWRED
PTTWFCSRCREFNFERDLACRSCSLRRDEQIELRVTHHERVGDEIQRAPVGSVIVTRNRI
VRWRCPSCQESNALQSSICRNCNKGRFEFAVFCSNCKASQMLSNKQMYGSEPADYIHVSR
PFGLHNCFPRLAPEQRCKACKSPLHGATASSRSDAWLCACGQVGNPATLSCPRCRFPRRL
PQTAILGELLRVWDFAGTTNWFCESCNHVNKASRHIVALERHDPSSPVDRNATKEKAAAW
KVDRILHGFSHCERCEVPWHHQPLNDGQHWLCACHKVNRNEDAHCQVCRLPAVDGIRSDV
LSFWSRGDWYCVECHRQNYREKVVCNCGKKRPKE*RAKN
>TCRU_5946 Domain of unknown function (DUF4042), putative
PFSLGETESAVCRSIWTFCNTLIRDAQALVCGCGELTKMEAEASVIMQRTFPQVSTTEAA
TTADSTAVQSWEKTPIPTPSLYLGAVSKLNSFMHSLKMSAAAGNNDERVMTERILLLLRV
MALYCFATARPSAGSPGEFSSQESSGRTTPVTRPFRRHDQNNRQSTENENPGLEMQTAEE
TFRVAVDAVVRLSTYGAAQRGKGGKKLLKGPTISLDLYAELNMAALYLLTAALTRFSNVP
FNAMRYLPALFPEVDARDPHFIHPLLTPFLWSPEQRVRAAAAALVSSLLRNLQHNFKYAE
EPHQNRQSFSSLASQSGRTLSFLHDVLIYALQLPNKLPAVGDMSAATATTSHFFKDLVLS
SFGVLVSTTPYRRCPHAFDVIKEALELPLLRDILLDASCDEFAPAAAFLISVFKADSLTK
MLQSYLFCEGGDTSAKIKGPSNRPVDRHVGGGALLLEALLTHAASRVEVWRCVVQLSRIH
PLIVGAHFTILLEASLAVLRAASQKIEEEEAAENKKQHESAEMAVGNTLGECLRAWLHFM
GYVWQSFDGHSADPALRQEHLPHRATPHQKKQLLTELVLPVLQMTSDGLRYNEARRTALR
CLAQVGDEYFSSISATVREGIVVHVINSTTAHESSVRSESFTTIGVWAWQYSTFGEWLSD
FVERSVSALCDDAEPAVRFKAAFALSNITSRLGEENDSSLLRQSPYHMQLLCDVAMYATQ
VREDPAVVSHGIRMMSHLLHSLSFEELIGELSEKREGVAEGYFNALLRFLLPSYRDAKLR
WNAACALGLGLSREVVFEAEPQAATRAVERLCVIVCHDRIFKVRTQAAMALAKVPMTCLA

AGRYAVEDLSPKVARALCESLQVSGSSLENFAQYKEQDALRAALRQALGVMITSASPSAM
LQRVFAEYRVLLEAEGLL
>TCRU_5947 hypothetical protein, conserved
IAAVGNFLFGDTSVQNVLFGMGISWLILALYGLYYLFKRSREVMASTMAPFIIFMDYLTD
GATAGYDKPLMSLLHPELLENVVERGLIRAMARCLCKQFGKVEHIPRDTVMMRSRCDDVN
FVALVDFQHAKRVKCRMSWRWRSSGDVFFQKAGLVRSFYITGFLVEPRPEEQFDVLNFLH
TEDFVPFAESFVEKLFEQSPKAAVMMMVPALQERYMTDLEKLQRSIERVCGISQGSKREV
DAKLVSEVILRAPALSKPPGENTDRESGDRDGGVVGGGSATAAAAANDDSGDMNEKEAAK
TAVRGIEMRFVVNGVGRREMEVTVVLSFSGLRCYVSRYEVRARSDPRTQVLLDHDTGERT
IV
>TCRU_5948 aminopeptidase P1, putative
MMSTASKILAILREAMRKRSLSALIIPSSDPHNSEYVKDEYKCRAYITNFKGSAGTCLIT
MNEAYLWTDGRYWLEASQSLYPEWTLMKDGHPDVPKLENWIQLNLGSDVLVGMNNHLSTV
AEWERRRKMFNLVPVPEMVQPLMPLVENPVSKLYARPEEFCGMRCGEKAAALIEEMEQQK
CDALVLSALDEVAWLTNLRGSDVPFNPVFYAYGVLRRCSPPKVHLFVDAVMSEEQGPSLE
LHPYTALESYLRTIPAGTTFLVDEHQTSQWLFTLLESLGMRIKRVACGPAQKLKAVKNAV
EIEGFRRCHVRDGVALTRYLAWLHDTVAVKGDTSVTEYSAAQRLEDFRREGEHFVQLSFS
TISSVGPNAAIVHYVAPREGSATIVPDQLYLVDSGAQYLDGTTDVTRTVCFREPGDKERE
AYTLVLKGNLALHSAVWPTGTSGHSLDVLARAALWKCGLNYAHGTGHGVGSFLNVHEGPQ
GIGLRPTPTEATLAAGMVMSNEPGYYKDGEFGIRIENLELVVDVATKHSKKGFLTFDTLT
MVPLCHELIDVSALTEAERQQVNAYHQTVRETLLPHLRRCNDSCAIAYLEHHTKKL
>TCRU_5949 retrotransposon hot spot protein, RHS3, putative
FFKNPNKYIRDKGALKEIQISDAYARMEGTVRDEMDLEEVVRRLHDKGVYNLLGWSEAAA
EVKASVHNSTKHSLDSALQEASKPTTTIEALKMEGLYESVYSASWSHVVEVPGGEGTGMK
VKEGKPIHSWSYKKVGETFEKDDGVRKSGEAPPRLMVLTSDKGWPYTWGQGLNERIHDCY
VNFEVERVWRIVNGDLTKWFSSHGKNKLSPQRRVLVGKPGIGKSMNAGSYLLYQLLHCDA
EQLQMVAYIIAEQKISFDKTAQTVEKYSGASSIVDILDGLFDRGVKGYIIHDVALKGRQP
PAGLPCRGWGMIVVTSPNTNNYESWAEQTGAEQIIINCPDESDVRTMCIWKEHNGQVEEE
EEEEADYWKKVKDRMDKVGPLLRYVFKQRKYKDRIYSCESKVKKMTLQDTNYYSVLGTNE
VCDDSHISDKL*GVRLRGGNNLELPYNALISSYLGNLVTCKLA*LMAPNNFILLVLAIKH
NLLSKLLEAFRVYIFERGFVSAIIPKLTELKLEENAPPHLCALRVCPHERPFKPLVLPLL
ENFKEKIKIKYGVLYKPEAQNFPLVDGFLMDSKPKTLVGLQITTADEHHTIPSTVNLFKE
NMAKYFNGWEEFSRDMLWEIIYIRHADE*LAEMRCVNSDNVSRAENREIAAFWEEKVHQY
MAAI
>TCRU_5950 MSP-A, putative
HKCVHDEVAIPYNALPYTDAKYRSGIRNMKVFSVFMTAVREDIRFHVIFLLNKSCSGVGQ
FVPNFLGDEVRCTADDILTPKKIRMIKIMVKRACNFLEQAILVDPLDELSVMAESCPFLG
HSSLRVTEKDYVLFVTANPRSSARGVIAWARSCERISTGRPSVGHANFIPSFFGEYATEN
DIHVAMHEITHALGFTDLATNAKSHVGPGGKVVPGFARVLRPKLGKVVTLVTSPKVVEVA
RKHFGCPTLDGVEIEDGGKSGTAGSHWKKRILYEEALVGSITSANLFYSSFTLAYLEDLG
YYSINYSMAEDNFRWGRNRSCRFLYNKCNDQDEDVDEFCFGNGNAMKTSCTNDFLGMGSC
DIMRHNAVLPVDYRYFTDPRMGGSIPLMDYCPSVQVYSNWNCISEVTAEVPNFLGNEMGQ
HSRCFSSNLVTGASPFFSTGFRCFPMVCTKSGQILLRVQGQTVPCPLNGTAGEADTSHLR
GVQGKIICPAAILLCRDKERNISSESFHYSSNMIEEPVTAETKRSASEFTKNSSRLCEER
VKCAENITSFFPACRVSAQRILDCFGRDCPLAMRMWIDRTALLEQCRHPKLIAELCLDGW
MGAHRLC
>TCRU_5951 Putative methyltransferase, putative
PVYSLTAQLLENWAECYPTHPRDRMELPRDAAGMNTLPLVYQRAPDVSELTTEGDKLERR
DIIPGKYYGGLKVWSCAPYLVAYMFGNRDMFRRLFEITDSPIESTTARKVLPDGQFAGTS
LVHPIVAEVGCGQGLPGIAALLLGARRVIFQDYNEEVLEICVKSNIGANLLRHAEVVALR
ENLLPSCLPVVQMVSGDWSRLQWQDCDDGTGKKAHDVRCKVVLGSDVTFDDEACEKLAEM
LERCLSPTAGVAYIASKQYYFGTNGGALEFQKCAEGRGLQVEEVSRMDEAGGMQRLIMRV
E
>TCRU_5952 hypothetical protein, conserved

IPIDVLRLVLSFLPAPVTLNTVAVVSSLFSAVTRSGTYWQNVWIERVSAFFRSYAQVANL
PSSSNGFSYASSSHALLGDHRILLASVPSLSLPRLCAHGYNGDLSVTEEHDDKESRITQM
RLRVGSMVLLSAPSVDAYTLAQNLISSSSREERCNQHHYHNHRHDGDEGRNELGATNELR
RKNGVKDHLRLRKALYFLDDEKALDLATKRRPMIDSLYAIRLFMLHLALPPPHRREGTPL
EREAVLAEFISALVYAWECCHPSMRPDMSTMRRLLPQMELMSTTLFVGGSEEEEAVETGD
GHTDLFFPVADPLSSLPFSTPFQSLPLSVSSNGVLIAGSDAGTACRLRHSLADTLVYLFL
LHHVTFSDIHQHVWDDERKCAICSRLLSPTGHAVEFRFFMSSLWGSYPRFFVKMAFAEGE
LPHTCIRETFDNESSRNVTSLLGSSSSDDVVPKILTLFYGGFGRVEVDIPPTVSCDGFLR
LRESLGLAPTFPMQLLWNVVVLATGVGGALLRAQGPYFKLYYQTSFTAAFEKTF
>TCRU_5953 acyl-CoA dehydrogenase, putative
SMRSLHYTPRVRDVQFLMEDVFEMYPHYEKMGRSDVNKELFESLLEEASKLATRTLLPLY
TSSDDEGCHLLKDGTVKTPKGFKEAYESYKNGGWVGMSLPEEYGGQGLPGSVGFILRELM
ATANWSFAMYPGLSMGAANTLLAWGSKEQNEVYLTKLVSGEWTGTMCLTEPQCGTDLAQV
KTKAEPCADGSYKLNGTKIFISAGDHDMTENIVHIVLARLPDSVPTTKGISLFLVPRHVV
KPDGSLETNKNVKCVGLESKMGIKGSATAQLSFENSVGYLIGAPNEGMKQMFTFMNTARV
GTSLEGVCHAELAFQNALKYARERGSQRSLSGTKCPDRPNDPLVWHPNVRQNILFAKAVA
EGGRAFLTDMGRLLDIQGEAKDASLRDALEHEIGFYTPIAKGCLTEWGLEASSRCLQVWG
GHGYIKGNGMEQILRDARISTLYEGTTGIQSLDFIGRKVLKSRTDEVARFGAKVNALVRS
HFFSRGVVGKSSRRLWTLQKQWRLAITKVKMGAMSDIDSVGTASEDLLMCTGYLVLGYYW
LRMAIAAEKKVAAGQDPDGFYQCKVDLCHFVFQNILPRADAHFHILQAGSEIVRSNEAAW
DL
>TCRU_5954 Domain of unknown function DUF21, putative
EVQWAYLVFADSILLLFAALFAGLTLAIMGLDTLSLEIIADSGSEPDKTYAGKILPIRRL
GNQLLCTLIFGNVMVNTLIAQITDSHIHGWVATVVSTALTTVGGEVIPQALMSAHALQVG
AKSVYLVNLFVVLFYPVCKPLSIFLDHFIGTDPGQIYERNELKKLMFMHAAHGSESGLGE
REVDLMVGAMELHEKTVMDVVTPISDVLMLEASEPLNEETIQLISERGHSRIPVYQRNKN
NIIGVLFAKDLLMIDPRENTPVLLLVKFYNRRCHIVPSETKLISMLKYFQTGRSHIALVQ
EVQQRSYGDPYYEVKGLVTMEDVIEELIHSEIFDEYDIDPHHSFAGSQLTSKRQVGLNPR
CSRRVNLSANQLKASALFLCESIPDLNFYARDVSSFLPQAISIHGTVYKVRPPADARGLE
QDDKANVWLYRSGVPSDTFTLIITGRVEVFAGKEEIRLELPSWSLVAAEALTMESYVPNF
SCRVVKDSTLMQITHAAFQKILSMLSD
>TCRU_5955 mitochondrial carrier protein, putative
MAGINEPVKEGFFHTACPALLSGAAQAILFNPFDRALYVRVKFRRQHFLDRRNFGQPFQG
FMNAAVYRTLVGASYMFWQDSARIFIESKTPEYFHASQSPNLNAFLIGAIAGSVNGAVLN
GMQVVKYRTWNVDGNVSFLRVALEVYKESGVRIFFRGIGTTALRDCVFGIVYELFRRSTF
IKDVFDPYVISAERASHFLRGDEVPPNSCRVSAGATLPNKNYNHKHTTTTTTNTNTTNSN
NNNTDSKGRVALWNQEKCGACAFISNLVAALLASIVSSPFNYARSVIYGAPSGSVPMRCT
SLLQSFCYQVRFIYVCGESFTDAKAIAAESARKAPLQTSSSSACSQNRLLGRSKYLWRSL
LTGAYWRNRHPVAAWRWVNSRLNIGWGSLRVGLGMAVGQSLFHFLQ
>TCRU_5956 Protein of unknown function (DUF778), putative
MTGRKGMGENRSVALPLPPRIDPSEEHYPFCIVWTPIPVLSWIFPFIGHVGICDSAGRIH
DFEGPYHIGVDKMLFGNPVKYWNISRMYVPTFYRSQGENPRTTEETCRREVEEYDAAVER
VTKHFRKTQLYNFFTNNCHSYVACVLRDHPLTAAGSFSVFRVAWGLLIHGR
>TCRU_5957 dual specificity protein phosphatase, putative
MQELIAVRVKDGIFAGNLTASQDRDFIAMNKITHIINCAGGELPDLFVNDGVKYLTFPWR
DTTGSICTAVMFDSADENIEKTVRFIDEALDAGDCVLVHSHFGLSRSPALIAAYFIVKYG
WKLDNALSFLEMAHKDMCIRPHFLRQLRMFAKRNSVDRDVFDPDVDDSEFGLDNDQWMLR
NTLLNGLTFEVQGHNGLYRLCTSKVELGNPIELRKKTPARKSKRIVFIDTKQGTHVDSES
GTPVVNVQSLQQLDSSNHFLGYHGSVSLRSWHRCSSIMSRCITPCSRRAESDPRTNPRGR
QELIVRSESKIGRSASMLDGTSSSAAARTASGHSTLEGGMYGGMDSRHIAPPNTVHAPGR
SPFAALTSSHKYRKGSPLPASTHDKKPSRLSQRPSSASASEANSRMRATSNLVASRAPRT
FVTRTSSPNALGGSLTSASPAASARLSSYKNITPHRSQPGNGVASAWDSNKSRESPSVVQ
RSSLRNSPQGSRRGSPAGRPNSAIVRVASPS
>TCRU_5958 glycosylphosphatidylinositol-specific phospholipase C

WHPQSWMHDLRSFIGEMAITQLCLLGSHNAASYGIRKDSPFAKDAPGVLYENSFRGSLAR
LFSYRISASWAKCQGMSVRAQLNHGVRYLDLRVATNPKDAGRLYISHTQISVPLADVLED
VKAFLNDPSSANEFIVLDFHHLFLTDDSDGQGKFFRELDRLSDRFIPVDVPLTTPLEILW
GTSREKRIFLVVAARRNMMPYPAARIRSKFMVSRWVNKCSLRELLQALTNLLLDDLNHAP
SGSSSRLYVTQAVYTVCSCGVFRGIFPKVSSKVVSSIYDVAKRINSSLLEWFYSLNAHGL
LDGAKVKIPPGINTHGNILMLDYVELGRCQIMDGTRETNAVGMCVYLNILRASR
>TCRU_5959 translation initiation factor SUI1, putative
MFHKRHSTKEQLVVGKKESKKLRDRFVAILERDHLDSLESFWKKSDSITRITWEFSTGGV
AAFYVVNGIPLLFSVISLPDDSQGMFAGNDVALIPTLFFFLLMRNYYKKEDMEVVSLFGS
KVWCKGATSHYILSGAHLMMPGVVDIGEVNNKKLLVGETVFIHSIGTSCPYAVGLSTEGL
VNRAKIGKGVYVLHCYKDLLWDSYFAVFNAFCGSVYPVLPSTFRANEVVEILLPKLDTAN
EISEEKGDQGNLENGDDEVLRKNVFFNQSRVIQTTLKMIEGEDALIDFALCETVRALSHS
MLPMPLTEFSPLLISNAPRIPGAKLQIDFKRTKYKKVLPYLLMRSDLITVSEEKKGNHFI
VQINKSSELLRRHRRNYAEFLQLIHEPAKEEEALEAEQKMIREGAKGGIKRRIVSIETLY
SPKNGSAIELTRILCTGMYLDNMKQKILGETLPQNLLLASYGDNNDFLDELYSRKHLCDN
LRKYIRGKGLLETEGHSDGIPFVKLDDTLLPIASELDKSMRITEVEDRVIDRMFAPVHQI
LMETNQFINGVATSVSFITKTTKKGKLPKILVFTEKRKGNKIVTIVRGLDAYGFDLDSLA
TEWKHQFSTFCTIYDPSKEMTKVKQGTQVPLELQLGGDWLSKLKAVLQEEFGFPQH
>TCRU_5960 ribosomal protein L22p/L17e, putative
MPKPAPRFAMGHILPRRTNVGSQFLYTQKHGARNVWYKKQYFSIRPFAIQRHRGTTPRIL
LDRSLWKSVWLTKVNLPDVNRWERVVNSQRITEDRYALVEEEGVMHKVNWGLYCERLETE
LKASLERLPQYTLLMKAVPSSWKKLDIEISVVRGLSLREAMAQCKLSMRKGHQIVFRALE
IAQQGAEAKGLEKDNLRIAHISCFPGPTDKQIDIRSRGYYAWKTKRSSHLILTLAEDPEM
VLPDRTSIPYASLLSMKRAGLSTEPTVLDVPAISADGI*
>TCRU_5961 retrotransposon hot spot protein, RHS3, putative
LMVLTSDKAWPYSWAGSEHICDCYVDCEVDRVWQIVKGDLTKWFSSHGKAVFSPKRRLVI
GTPGIGKSMNAGSYLLYQLLHCDVEKLPMVAYIIKNSVYLFDNTKKTVSDCGSEEVFVDL
LKDFTLRGVKGYIIYDVAKQGRGPHLGLPFTLWGMIVVTSPNANNFKRWMGQNGAMGIVM
NCPDESDVRALCVWMKRNEQGEQNGYWKQVKERMDEVGPILRVIFDGNKFTDRKTDIDQV
INDVDSSNAKHYVGVMSDKLWNAANPSHKLVQIVRVRKDLPTEIYLNSPASRVIASKIYI
HLSTKMHFMEIFKLLMHPDVILLSIVLEMSGTVTFMCRGAVNIIIGKLKAETTRRTRSPA
SALQRNPEGHPTEAVGLPTKQGLPLEKNFARYKVMYKPAYPTFPLVDAFFFMESPRRTLV
GLQMTTAHDHHTKTSTVKQFTEYLSWFFTNWEEFAQGLSWDIIYVQHADSKPMENWQRCD
YVNPRSREEKKIVAFWDKKVRQYQ
>TCRU_5962 hypothetical protein, conserved
KMELPFQWDDGNFISPFLTSGDDTLRVLAAWLNDSPLLRFQHGGALRLTDLGCGDGSALL
SLSAGLFTLRGASGCRDVSPLQLTAVGLDLDEELILAARRRAEAIIVPPPHRLHCVFETV
DVRQLDAAQYFPLSESSRHVLFVYLLPEGLEAIREKLLEIISRVALLVSNRWEVPFLDRW
KRVKLQNLHLYQYVGDGAN
>TCRU_5963 hypothetical protein, conserved
MKRQLPLFLQPRRPSSARIQLLTYPMAFAQPQATVPLLRAGTDATDGEKSAPSSSTTSKR
VTTSLHVRLRDVTKEFHCPQSDGKAIVNPRRWVRDPDELCVASLRRSKNINRINTYVATY
KFDDPQWAPLLLPRVRLRPRQNPVRDSKNEMSEAAASSTPPNVPPTSSGSSSALLDDKND
GGSRVVIDHNKLLTLECMSRHVNFSLRHIVQKGHAVYLLHHAQHSILRPKGIIEQSFVTC
SFGIRGERLRTEIVHVGPLDAMDVLDIEEGPPGHTRCIFNFQKLDIPRGVIAVSQVEGYG
TWFQRKPMLWQRSRRIGALQSQLGAFTYDLLAPHEVGKERECEVSLLAPHMRFFGNGTGG
SEAVGIIASSQVAQQDRLYLGEFEAPAMTALDAVQQLAHATALRCRLVRPLRINTDGCDD
RNGESEGKDDDDVLEKLVPLSWATRTPPPYVPLEADLPFKLQMSKPAVFGSETQPEQQHG
VYPTGATVGSPFVRGAPIMLFEYNLHQGVDHYVFDNAPSARPMKWWSQKSNLPYSGYMFF
ARSGLIDRLSPSEEIPSPVEQTSRRKPLHKIVPPTKRVQRRVSQYKKRLWEEAERGKATR
EESTG
>TCRU_5964 40S ribosomal protein S3A, putative
GKRGKKKTQETMSRKEWYDVVAPKNFEVRQFGKTICNKTQGTKIAADYLRGRVYESNLAD
LNKTQGDDDAYRKVKFVVQEVQGRNLLTQFHSMEMTSDRVYFLLRKWCTTIEAAVETKTA

DGYTLRLFVIAFTKKQSNQLSKNCYAKTRLVKWVRHRITNLIRQRLSKVNINEAVTLLTR
NILRDRLAKRCNPIVPLRDLRIRKVKVVRTPRFDAQALLNAHGEIPASAEGEARVVEEAQ
EAPA
>TCRU_5965 hypothetical protein, conserved
RTTLWYICFPEEVTVYIDPIIRFIFTVYHLPPIALVLALTHSGLERIVWVLIVPVAQQME
KQPYDSSCMTTFMLGMYHIFLLILPYSTLGVAVATLGHKVLHCFLETMVDAHSTHQGKDY
PLFAARLRFIMQDRQRYYVFLVVLFFLVSVALSGLHTDLLVAWPAREPWVVTGAWCIIAL
QVSFVWGSAISHPELPPHPFIWRRIVGIGDGEFARFFCGTWWKSYIHYMRYIAIEMVALI
AFVALFFRGPLYVLSSSVELVMYLNMPHLVGHTVVSISVSIINIQCSLNWLRRHSDAVLP
VIFIASPFQLLLFRAMFYFRHHRMTVLLLIGVNVLFIQRVIDLVREFDVTEAGSVYWKYV
DKDEPIPPYLSVILENAYETKSSHIDVASLDYLIDIKAMKIHRDGEEVDLERKQITEYGN
AHSFIWDGRFYAYTVPRMISVQSSRHFGGKHFRRVYVLLRMITSCCLMAFTALVMGLLFQ
AAFPQLHPLPVRVSVSADGNALTVDHIVLRMHLLSGQADVTPTLPIASSAMGSASAAFKW
HNATSLGEDWYSSLCARTFHDISIWEISLLALASYLSNDDEVKEMLDFMSMHMGSDWVVR
ERHGTDCISIDSSTQPTGWDGYYDFYSAKHDMSIIAVSGTDMTSFRDFLIDVNLFFEVVL
YHLLSNIIPGAVILPSELIADLIRLASLPAAKNRESETWETLISSRNTNLRVCENNNYRR
DYFADVYNHLAFVGSRPNPPKHVLLTGHSLGGAVASVIGSRMGIHAVGFSAPGISLSRKK
FGIDLESIHKFVTRVISSHDIFPMIGGSGGEEHHVECLAKTRELCHAMEFLVGTLWRSCG
SIRARYPSIHSVV*
>TCRU_5966 hypothetical protein, conserved
MHTFYTIRYPPPNSQKGGEDSQPIRVTNKAMESLLFCIVHSIEFQSPLQPSRPQLGSSIG
SSGKDSITDDEAYVRPVENSSMLLGNVTYVSRSKHKPSVLASLHTAVEAARAIQIPDKSS
QVPFELRVRLLRRHRGWLWHDSRPLVEWVFRMAKTREEFSFSTTHGDASERPRPRTSPRA
TNAHANVVRATGGGGAHSRSREEGLVCSNDPEQIRQVLQFILKHSYDAIDLNTYADFRSG
ELIFDVSVQE
>TCRU_5967 RNA guanylyltransferase
VMSAFNPDAPAFIPTFLRRTGSNAVGEEELSNEASSTSAKRPLVFLIFGCRGAGKTTQSE
LLAKEYNLLHISSGNIYRQGKQPFVELRRVLLEEFGEGGKRRYNGLVLDRFVVNSEFDAF
YIQSALDAVKLPVPFVFMLAIDAKLASKRAESREDNKTAHQYWRVVEQKAQAVTLNTIYA
PIGCLKTIRVTEDATIEDVFGEIKATIGTQLSANPEGIKICPAARHEAKGMKLIDDYETY
MELVCCVHAAVGNVSGRKDTAPLSGIGAYLDREYFSFGHKNLRSLLSTFHVTLKADGQRY
LLVKHKRYGYIGFPAAFTHCYDFNKLFDGVEMSCGFPPETQKFITDNKHDNSVEVLLDTE
LVIHDGNPVFYVLDYLYLGGLEGKKMRFVARLKILREFFGRLASVTQAVVLKDYVPINML
RTLLPKWKEAKMPIDGLVFQHSGVYKIGRDRFLVKWKPIEHCTVDFRLANGILKGDSWTF
ELMVTDDISENGGFGEIPYEGALAIIPSTVVQENGLCNGIIVELALKDRKETNEGVSSPQ
TTTWWSFRCLRNDKPSPNKHSIVKKIVDLRHLSLEELVDLCEKVPFYGNT*
>TCRU_5968 pteridine reductase
ECPAAIITGGARRIGHSIAVRLHQQGFRVVVHYRHSEGAAQRLVAELNAARAGSAVLCKG
DLSLSSSLLDCCEDIIDCSFRAFGRCDVLVNNASAYYPTPLLPGDDTNGAADAKPIDAQV
AELFGSNAVAPLFLIRAFARRQGEGGAWRSRNLSVVNLCDAMTDLPLPGFCVYTMAKHAL
GGLTRAAALELAPRHIRVNAVAPGLSLLPPAMPQETREEYRRKVPLGQSEASAAQIADAI
AFLVSKDAGYITGTTLKVDGGLSLARA*
>TCRU_5969 hypothetical protein, conserved
VLRRAVVALRDALNCGSPMTLCRKGMGLSSDSHRRRMPWTAAKECVPGVFHSSKEKMVLD
GAQRVDVDCVDRASQVYLLEALRAAVAS*EYNTFRGKNIFNASQAESNVLRQWVYREEWQ
EVTHDEDVTRVAIHFRRQGSTQPAPIRLADFTGWHALFRLAPLFPPFPSVGADVPVDARF
YRLRTHPLID
>TCRU_5970 PA26 p53-induced protein (sestrin), putative
YSSSSGVDVSGRAEHFGVRRHSTPSENVLHFQSAHVPVYSSEDGTCAITGDPARRNGVCM
DECAVSNLQEARMMLQTIVGTAFSCPSEPLAKAFQLVIARELGLSLRPFEACCGLLKFLS
FLDPTLRVANEERIQGEKIGYLYYLNGVQTSASLTDALFSSSEATDSIQWFTAPSPAAVL
PNLTRSLTGSLLEVMEELQQATDGIAAAEALATTSLSANPTMSVTIPSFSRRRGGGCSNN
RIIRSTGAEKELLNAEWGKAGYASRQTVWDALCRCSLTIPKSVLSDRSDLLYRIFFKMGE
VPQYYQILSIYPDVLRAHHATFQYIFFEEGPLPICERLMIALMAASRQKCEYLFSRFAAL

LLHFEEKQPSSDVVAENWLLQGPPPKLQALQRFIAIATHVPWQMKLNDIRGAMNAGWSIP
GLIQASCIVAETLSLCSFVMGLFVPNDMWVSITLPTSLSAVLSSCPVLGEVIDHQSCVDF
TRYTGIDNIVSENRVKGSSSNVFTLSCGKFNWHEHGGTLMEQYYPGAATLINNELDAFSA
VARKLTHLDCVGLTTPDYSPSNAFWFLRLYVQNIMGLMPDDYPYNSINKVLRRPAKLIAQ
SCTMRPETLSSSQMRLWVQMSSDSAAAPGDLHSAKKFSTEKLEEHQHLEVDMTEQKRQLI
ESLTAHKAPFTLSMPGTEAGRRPQPREDVLEAALGLHEERLIFLVVLATMEARKEGLFAL
LLYPMWGLLNNM*
>TCRU_5971 lathosterol oxidase, putative
MDVAFDLYTAVIPVDRNALSHQLFVFWLILTTGGIFLYLLCASISTFIFFVLFEETYFPL
TMDKKNQKHELQRQMLHEIFIAVLSIPFMAILMAPSSTLAYRGYSKIYYNVSDYGWSYLF
FSILMFFIFTDFMVYWFHRGLHHPTLYRYLHKLHHTYKYTTPFSSHAFNPCDGFGQGSPY
YAFIFLFPMHNYLFVILFFAVNLWTISIHDQVDFGGHFVNTTGHHTIHHVLFNYDYGQYF
TVWDRIGGTYKPAQQTHHFPLFTKGGR
>TCRU_5972 retrotransposon hot spot protein, RHS3, putative
EASKPTTTSAAMKLEGLYESVYNARWHHVVEVPDGEGAGMYVREGKPKQSWTYKAVGETF
EKDDAVQQSGEAPPVLMVLTSDRGWPYTLNGPHRCGNDLCVNCEVERVWQIVKGDLTKWF
SNFHLTLNSSPVPHVLIGTPGIGKSMAAGSYLLYQLLQYDVEKLPAVVHCFGTAMYVFDK
TAKTVKKYNGEITSRNLLYGLRRSGMKGYIIYDVETQGTQPDPGFAPSTGWGMILVSSPE
VSNYDGWEEQLKVSRIIMNCPDETDVKAMCAWMKRDETKKKQAECWKMVEERMEKVGPII
RHIFDAVEYEKRTKDVLRTLRWFNMGDRGKYFTQGGENEWHSEGPSQKLLKVVRVREYGP
IEDFANAPICEYLGVLTVSRLAKVLSPHDILFLVLGMKNAVQSADLKKYALSVFLNEGFV
TSMVKDLKELPPPSPSKPRPSVLTLNPHGYPTEAAAITELNLIDGLQKLKRRLLYIPTSP
TFPLVDCFFFMESPRRTLVGLRMTTASAHHTTASTVRQFTERLAAYFEGWEEFSQGLSWE
MIYVQHADSTPMNDWQGCDCVNPNNKIDAEKKIVAFWDGKVHQY
>TCRU_protein (LYR family), putative Complex.1
TPLRWMTPAGAGEIFLRHNPYRSEVISWYRKFLKASFSVPWETDEDALYVLEEARRLFRK
NARINDIETIERKLREAEMRYEIGVHYRIPYPRAFHKTQGSLQESGVAYAADLDSMYDHP
VSPRIGWIMEGSVNGGTMGGSEHLTQYLEDGPGVENDNLSE
>TCRU_5974 hypothetical protein, conserved
LTVQASNAMTNPDLRKVSLSLLGNLHYDVLFGKPGGYGVCNQGQPSIATPGCDSPLKLIR
SVMRDVSKWKESFTLITGGLLRHGTDTIATTEIESMMKDVVVEIANSSRESYLKKEGATY
TVALSFGGTDFIPANSFTPEGKQPHFTRLLNLLELYELLNSQESKKLGNCGYFFRDLNGT
KLRVISLNTLLWSNALRPGFGVGDVDPCGQFPFLQGAIEQAKQRGRSVIILGDTPPVINV
ADALRKSSVQEAESYWREDFTEAYFRIIATYRFSIAAQFFGHTNSFAFVDSPEVGPPLYI
VPPISPVTGSNPSYLRATLDTNTGRVVTLKQRYLSENGKWVEGESLEDAIGAPLREMGES
LPKDLLLITESEKKWEKLAAMRVGGRFLTERGACSLWCRRVIACASLYYSKTAIERCASI
DLPSQRLGLILAIVFTCFGMLMITFSFGYMISHYKIIFHPP
>TCRU_5975 Calcineurin-like phosphoesterase, putative
MQVTFASDIHYDPFYGGPDAFGTACRSAGLPLVRRGCESSADFVKYWASDMATRKSACTF
VTGDLQRHDFPSLKTTVTATFGFVIERLAAVSPNKTPSGRPSVLVALGNNDVVPDYYFDV
TRIPSRVILEEASVMQKNGVLMADEAQQFQQCGYYLRVVSPKLRVIVLHTLLWCYTIVPA
IPDGEEDPCSQFKFLTTELENARKANSKVIIMSHIPPMSNIWKVLEGGNFTSVAEDMYWK
PLYQKRFNQLMREYSDTVTVQLYGHTHLFYYQALSGGVPFFIVPAISPLYGNAPSYFIAQ
LDNKSLSLKSLTQRYFDYDWTNGVLVEDLFGDLTDTASLRASAMRLVTDDKLWAKYVRLC
GGGVGSDKLFPGGKCNSWCRKVIACSMVSDAWGDI
>TCRU_5976 radial spoke protein RSP11, putative
RSPLVVMESIFCVEQVNVPPELGTIMKQYTKAVLRDRPQDLYKYSANFFAALCGQSAPFD
KDGHFVEARELEPMEHLVDSEKESGEAVSPTPLVDNEGKDVIRGIFNDYDVNGNGRLYKE
TVPALLADLQQALGLNKLKNIRAEELLDVLHTDENGTVDLLELRELVF
>TCRU_5977 Leucine Rich repeat, putative
MSTKRQAPKEKLKAVVNTPAQVLNVDVDLRRLHEACGSLGEYIVPFMRRLKMELQRLKDG
EQADVPTIPLFVHGEIPYAEIKQLFLDVLSTYPFLRVMQLHHCAIGDEGILTIVDFIRSY
RPSPDRNPFGIQCIELLECLIGPTGAKYFAKLLSENETLTRCLLDFNPLGDAGAEAIGKA
MLWNGTLEDLSLQYCSIGASGANALAEGVLRCSNVRVFSLRGNPVGPEGIKAIGAALSIG

NRINSLDIAGTGFGGSFPALESFCQGAECSPSLTSVDMDYNLLAPEAGSLIASLISKNKR
LVQFRVNERMEVSEFLTIQNALEQNMRNAKKKKKK
>TCRU_5978 hypothetical protein, conserved
SMVTGHAVRSPSLVSVGGDGKWLAYGCAPDMMVVCALQDDSTEQRSLREEEFIAAMRIVF
LGAEEELSVIVLHQTKELLCIGTAHDGLYLTTASNPTLSSKTTRLPRQITGENVFSACFI
DGYEKISDVLVVSCGSQDLSKERFKLSMWDANARTLLWRGSADALDAIVALPGIFGFASC
TQREVTLWTVKPHGEGGVNANGHPSAGGGRENTRTEKGETAVFTVLSKNCSVVNELRDAE
FVAIVPPRGAEDSLTVVTTVGFLVSFDCRNGAPVKWMDCKVCPATAAYRIADNIIVCGSL
VRFFSSDKWEFHGKIKQNGPSTVVSSSLLTRLMDSLCTGAAVCGKDRAVFFFSGGDMSRY
RVIRPISGNSRLSFHRVDQYTPVLPDEGPLRWIPLTVDTLCLWSPQRLRLFDTRHWRNSD
MTIESTCAVHHRSLGVLLVYDSSAYEIVAVMPNLERELCRLGVDEPLTSLAIHEEDQFVS
LSLDNSLFYFKGQWKAKDEFILQGLQVTRLTGFKTPLAKLVSVAGAVCAASARLVVNLKT
GKNVSMAEDIISFEVTGSMLLVVHRHSCVMLDPATMQRVGEPLRVTALKEVVASPNGDLV
ALRSEGTLSVVSLKDRQSVAQLPLQRDASTLHSANIISVGFTADGGSLVTCESRGLVSVY
RLSKLESALKADVKRVPRQQTEHGGVRRSLSCDVPTNTELQSRFQELHGYYETTRRTHKE
REKGHKKTNTAMLTSLRQNSITTTSSSGVLILARGNSILQIPSGSADQKIPSLRGWENDG
APTELPYVVSAVEAPDVAVTASMVELSALTSMDTTMNFNMRTVAESEATLTPSITANLLE
NEREKVKFADAPTYGVRSPARKGQPSISPTKTPEDDVVNIDSNENEELRQHLHQDPVALN
GAPAKFPSVASSSSSCVRVRSCEIRDALMDLAEAYEQQDQEGVVNGAENIDVETVEEMFN
TLSRLYARVQSRQSRRPDSAGSIASSDISSASFNVILSDLERLRQQNSRIEAQNEEILSR
L
>TCRU_5979 ras-like small GTPase, putative
VMQDQIQKLLLMGPGGAGKTCMRSIIFDNYLPRDVLRLGISISLDQSQVRMFNNLYLNLW
DCGGQHRYVAEYLNRQKEYIFRSVSVMLFVFDINSMSRESNDTYGGMSTDWSRPEMLEYF
QSAMHYIRQYSPHAKIFVLLHKMDLIAKELRESIFESRKAEILSRIEGDECTCNIQFFAT
SIWSDSLYFAYSSVVRSLIPHRDVLMEEMKKLLIGCNAMEVALYERSTFLCLTHVSRTDA
DEIFAGDAGSSKKNKNKDTYVDTDGNAFCSPGCEFRTTEVSETVKHFKLSCMNNSTSLDG
FQITTDTFTALLHPFTNCTCVLLVSTDPSVSVELHKRNVCSAQRAFELFLQSGDPVAEEM
RQIL*
>TCRU_5980 DNA repair and recombination helicase protein PIF1
MYTARRFVAEKRPKSSPSNTKNAARRAVKNPPAGETVADASVDPLTKHTLHPPQPTLHTV
APPPSQPKQKRLAGKKEETMNSAALHLAPKQELESLPPLSNATSQLLHSTLVYNALTGRM
TSETSQSMNCLKSIGFGINDKSQVYLEKPDVLREFAQKMRNGTATLPSHWPVSIIRALGV
ILRNRAIMDPAEAIQQMIQVKINNLAHNRYASIINAVGTGVIDDALDQSLDDLQAVELND
EQKKVIELALKGHLLYIGGSAGTGKTVLLRALNHRLQAERLRVAMTATTGVAGCHIGGST
FHHALGVSSQGEFLRKIHLLDYDVIVVDEVSMLSKRMFEEFDRVLREEAGTPDLPFGGVQ
IILCGDFLQLGVINESSIITSKLFQDVFVKLRLETQVRHVPESKFAEALQDMRLGVVSDS
LLQSVQQLPPGTMVQSAVNLLPTNKEVHAANERELQRLPGDAVMLVPETGITALRCGATA
TLLLRTKPDFNEEEFSKHVRSLLRATLDLPKASLLCLYRVYEDGHAMRVCLPQGESAAWH
DAMRERFLEVAGLINDLELGATVTEILPNGDGMHTPEIEEYLQKLMQKHPIAQPITFKKG
CRVLLRANLSSRLVNGSIGTVVDFVECSHENIPAFLRGDRVDNCVERYRIFCMTECGMQV
PLLPVVRFHSGDTIVVPPWEFNVGGGPLTYYYSLSSVALPLSLAYAFTVHKVQGLTLVGR
VHLELSRMWPCEHLLYVAMSRVRNPEQLSMSSFQSSMVIANKECVEFDRRLPVVHELSST
EKFPVSSWKRCNDTIYHLRCRGASLSHLLRGAALKEGFGNNGGVGGEANFTKPMKGTLEH
SVIVARRLRKLIKCTERAARVQENRRKSSTAPAADDTN
>TCRU_5981 protein kinase, putative
MDSLAGNLGAARTGIQQYTVGQANVASGNGGKALNSARSTMTTSQSTNSARRSGSKRDRE
TATSTDITRTKSQYGEVTKKQATATTTTTSTNTTTTTTTTTTATAGGANRIVEVLPLPKK
KKVTYALPNQSREEGHFYVVLGEDIDVSTQRFKILSMLGEGTFGKVVEAWDRKRKEYCAV
KIVRNVPKYTRDAKIEIQFMEKVRQADADDRFSLMKIQRYFQNETGHMCIVMPKYGPCLL
DWIMKHGALSHRHLAQIIFQAGTALDYFHTELRLMHTDLKPENMLLETSETVIDPVTRKA
TPPDPCRIRICDLGGCCDERHSRTAIVSTRHYRSPEVVLGLGWMYSTDMWSMGCIIYELY
TGKLLYDTHDNLEHLHLMEKTLGRLPQEWAGRCGTEEARQLYNSVAQLRP
>TCRU_5982 hypothetical protein, conserved

MEAKAVCSHQTTTPFSQLPAAMRVDGNTVRLNCPQPLRDAGFPVAEVLFDVDLALDVPGA
STLFRKLCATAAPNFTQERKNMVAFSYGVRSSPKRQLMYGSAAGEGYAACVITEFIRLGA
KKGIFVLSCHVIGSTEHRADLLDADNELGAIFGSVKEGPHVRMVARICVLLAGDVRAAMD
TIVKNYEKCFFPVLCEKQPTPELEAMPSYLPDTVVLQLYRDVGEAEFADYMDANSLAFVA
LGDAERPALCGIDAAAQLHYEGAQRALVSGAGIVSSIRRRLLRVPFGMSELSQLLRRAYN
TEKDNRNNSLTGSTETVLLAHAFSDAVWAEESFHCFSMTRRVGNILVSTGIGSTTGDLAV
YKWRLDQDIMELRDELMIARTVYDHRHCGYESNKPFQTWREGMKRINAIESNREEARERQ
LSVFCERPKHEAEKMAKELERRGGTTLDELERTLEAKKRESIALQADRESRIWECEHTLE
KIRTRKEDGESASERLRQAMQQLEQGLSLRQSAIWAKERQLEMVHLDRARGREAIMRERH
SIEAMRRTVREERCRQRRQWIHQVKEMNKKVPEQVRPLAEERKKKYEQATANEDAAERAL
VADIKTIEEYLPKLISLEDIPVNPEEMDIIRRQFDEVFAQEKQTYLARLEEEKSRKEKLE
RGLEVYRQCMLDDYVGKKNENLHDAEATEHHLSSVVDQVLNYLRNGVRMKKISSKGNARR
RLYFLSEDCKRIHSCELDHQGFPLNRKRPPVTIWIRDIKKVLIGLSTTSFVNYSGEAQLA
KTRQEAVSDNGTYRHDPTQNITPSSLGTNNHRAFALLLCGGKLLEVVCETDSDCEAWLVA
LKRPLHLRTPAERLLEERRGT*RDARAQPSDSDVEMRWGGPPDIRNMRGFVSLAPDAAAL
CGEDHIPPALFLRVEQELAEKSQRSTITACGVRVCSGLDLFCSGRLYDYLCEKRVVPPPY
*
>TCRU_5983 R3H domain containing protein, putative
RSKQIIEQLLLLRYECASCLCNIRHDVAVWSCNDCFRIFHLYCIKKWAKQNESGIGTSFR
CPHCQATQEPVSKYYCFCGKLRDPPYDPHITPHSCGQTCGKTRHLCHHPCPVQCHPGPCP
ECSSFTGPKSCPCGTTTYTWRCGQPDPQKLCDNTCLKTLNCLIHKCKAKCHIGACEPCPE
KSLATCYCGLETRELPCGFSSFSCGSVCGKTLRCGVHVCGLICHLGNCPPCDRDPSIIVT
CPCGLVPLTVTRKHCSDPIPTCGNICGRVLDCQRHTCQALCHEGECKPCEKRVLTKCVCG
ATQQLVPCAKQDGFRCNMVCKTKLSCGKHECRVTCCSYRKQHNSVVHQCNRKCNRKLPCG
HACLELCHRGMCPSCVHVVSERLVCRCGAEFLMPPQPCGTSPPKCTRPCTLTLSCNHPPV
KHDCHYGDCPPCVFPVEKLCAGGHTLLKNVSCSASFVCCGSKCGKMLSCGHECSRVCHPG
LCVDERHPCVQPCGKVHAECGHACRAKCHPSKKCPQCLETVECRCQCGRNTQHFTCKKLL
SYMHEHSGEKMNVECNANCLFEQRLEVLAGLSKIAPSSAPTTTVKYSLFLWDFGSTHLTW
IRTIEEELERFVLSNVTLSSLKPMPPEKRAAIHSLCQYYHIHSEAVDAGPNRSCLLTKTT
RTSIPVPLLSDALADPERNNPLTFINEICDRKEVVCGRVILMDGENVNAIVVSRALQDFA
GEFVCGAEETIANGKKRIKVYFTHPSGQQRAYRHLRCVTPPFEFFLPS
>TCRU_5984 DNA repair protein, putative
MPPLPRGTVMVSEACKGGKIIRLMQRHRHVVEGMDNDVCDFVCGRTCVLYVNELNRLCDE
SYRAAVSQRISFANAQVITAGSRTVLLLLVDSTDPRPDVLAWLNLHCSVELRCAVMLCWT
EEECASYLEGLAVFSVGSVDYRLSNKKESAPIPVLIEAFTQTPQLMTRNDVVRAAHRYGS
VAELLTASLEDLASLPGFGPKRAGRLHTVLHAGFHASRRLVSDLLTESNELCGVDEMRSA
PDRVSAREKMLQVLNQLRCREMED
>TCRU_5985 hypothetical protein, conserved
ERYVVVITNVENDFAQVHQKALPQYCCLNEQHHHGPQQQALSATVKGMDKEASTALGKEA
KRRQCRYTVTARTETRSVEVAVYGRADGDVSSVYLPHRAGMREKKQGHQTNKEKVVGRGN
GKEEKKGVGVSGGSPIKCVAAPVGNNPVFASLEDMVMALRHAPYFTHPPKFLLNVPGKED
GEVLRGVKPRKRRRNATTDEEKEEEHQSGEPTPGDAKNFSPLLQSTVRQAEMITAVATTS
TRMHTKELCDQLKEIPGFITCWMLYPQHFRVLFASRKTLFRAKELLDQFEVDGHVRVTLT
LSDGAAKAFAEHLASVENTV*
>TCRU_5986 serine peptidase, clan SB, family S8-like protein
KETQRWWKWRQADKTCGCLSIAPHVSKGGGWQDFVVVRVLSPQRNRSMRCVQTELRDVRF
VFPCVGQISVLRVVENTFLWGNRTLASVAQQTGFATARPLYPRRYFGLSSTLKWTGRGVR
IALLDTGLDSHLLLSESSSLEQQRDSKGTGGTRKPLLMCTSFVPGFSCENNQDGHGTFSV
SLMAGNISLLEWNRNKCFGGKTHEVRDKFIAEKTGLLSARSQYLGMAPGADVHMLRVFDD
NRVTRTAWCIAALNFALQWGANIINLSFGGIDYYDAVFTEKITEVATKGVVVVAATGNEG
PRMGSVHNPADQNEVISVGSLGTRGRRLISRRDYYEDGDDNTEMNKSSIRLPVRWVSTFS
GRGPSTWEMPYGTGRPRPDLVALGEHVLGVGRDEGSGTLSLRVSHGTSVAAPIVAGIVAL
CIDALQRLHGNWKANMNVAVIKRVLMETAVEIHPRLSALRFMEAALHKEEKELLAQRKSD
WWRRGRNTFHRRDGIAITRTLFHYRNVLQYSRMSQGAGEVCPMCALSWIAEEGQSRKLLS

GFAFPREIEATGEHQLPYGEASPSSLPLCLLNWPYCEQPLFPSATPVEYNINIYYPQCPA
ARLAQATPWIRMTSARGICSAHRREQCQASIVDLTTAKQLLFLRAHAPQILEAYSGVISL
FALSPSNASNVRLKSSPTEILEADDRERVLGHFDLIEVSGNVNVVYTCNASFHGILRRTK
EDETRFASEWVTIPFKISIVPRPSRAQRMAFDISHQWFYPPDFIPGDDSRPEPMHGKEQQ
HKKRRALRESHGVFECDGDHPHTNMAPLLLYLRREMKLFVELPLLSYFSFGLHRNETIPT
PSLHWRNASRSYYSSIGTLLLVDPELPLLKEERAVFSDAVLLYQLNVVIISEWYSEQVAR
GLSFYDFTRNHTWSPLFLTKRGEMVESTIVDEEHERNSHGLKGACHVPSLNKFLCEISEG
SLQLDEERVVDGELVLATSSSFSRRHTGWGEQTVYRHFPRMNSAGMLRWPPAGSGCFARA
SPCGEIVRTTMVCGMERAWANELHEFTKSEGRTRGDEASSEAADVWRQVDPGVFIPLFGF
VGVGNSDTDKECGRSSADGMKRCGRGRGRVAVFTDTSGFGSSSASLQASLRVLDKLFYDV
SSQLSGNTGVEVVVPPRVREAIKNLVIHESEAPSFTFSIIRDFFHFVYTGDVPEFTNGAE
CKRSGGHMHAVTTPVEVNVREYEENEYEELLSALFASAPRRVAVARRLREVFSGWETAVT
VAED
>TCRU_5987 UEV domain/Zinc finger, C3HC4 type (RING finger), putative
TRFFSCSSHCKPEVLGRILHDVENLCNTFHFYCRDATGVTQQEKLCIYGGLPITIKKSNS
DHTSLTPDSREQAPPDRYVLPLQIWLTRLYPIEPPLVFLLSAEQGCRIASNHKYVDATGR
CHTPELAAWHPVSSSLCDVVKKLCQLLSAEGLIPLCFGEEGVSSPSKGHATAVSQRLRHG
LENGDDDKQTDEHERCVVCFSPKETVLVPCGHYCLCDACATNVTHCPLCRGSVKFRQRVF
S*
>TCRU_5988 hypothetical protein, conserved
MAYRRKSPPVAQLSLFRQLQLMCNATSFGLSFQVHNAQKILDQLKINNATAYTQFTKNAT
RQDFFSSRVVTGSGSGAIIRDAPKFTLPLPNYFINPSEKAEDFVPRVFYHASMVKRAAEL
REQSYMPRCGLTGLFFSREEVVDNLQAAAAELGFKSPFWIRNDHPALGNFLELKDGSEAI
CLSLTAAITGMDNVESFCEDLWHPDLRRAVVSKGRAFGKDVPLGMNALSGFVTKNPFVQS
LPNRGVWISQEQVLQNNLQLKKEKSALSNDPFVLVEVEQWEMHNADQLSVPGRLALDRST
TKS
>TCRU_5989 ADP-ribosylation factor-like 2, arl2
MGLLSIIRKTKRKEREMRILMLGLDNAGKTTCIKKFCGKDTSSISPTLGFQITAFSLHGC
TLNIWDVGGQQSLRSYWRNYFESTDGLIWVVDSNDLARLEDCRKELHALLQEERLAGASL
LVFLNKQDLPAAISPVEIAQHLDIDTIKKGKRHVQLCACSAKTGDGLLEGMEWIVRDVSS
RMYFA
>TCRU_5990 Trk system potassium uptake protein
SQLLEYAGPVVLPLSTTQDSIARRINFFKKWYLLMHVTYIFSIACVGSILFYVMEDELAY
IDAFFIAISSVCCCGLQTVDVATWKKSTNILRHFLMIGGGMVFTSAHQPLLRIWMLNKMW
PLLEPHRDDLFLEGRLRASRRKYAQRLWHTSVICLLTPLLYFGIVNVTLIFLLAVFNQSN
LSFLEIVEMAIASFHGSVFLPMEQYVRDPAVVLTVTIGCGLGFTLFPVILRGFLYAEWFT
FRLVRRVRRRLLPSPHTDLESPLAAPLSEDFPLLFSLQEREGDVLPHEFDAVDDMLHVNA
WDKGFRDILKNKHPVSFHAFLFVRSETFYLGVAWCVITLAQSIPFWVQQWSGDGLLAPFP
TAYKIFLSVCQAAVVRFAAASFISCLDYSNAHIAITIFCMFLPALPIPTDRTYRKWKQVF
SASMVRLFTSRLFCLFLAILCLLFGEEGWLTQELKDSRFDVMTRSFFEVISAFAGCGLSL
SLPGTRVSFVGSLGMFSKLVVAAVMLGGRHRTVDLGIDLGFSVL
>TCRU_5991 hypothetical protein, conserved
MKPRDIWKLMTEMVSRSLQDSLINSPELILKETLENCTALDEEERVLVRETVLGTLHFEK
VCEGILKGYGDCLRRILRDKISMYIAAYLMVFQYTVLGGHRIRELLYHCTTTPRLVEYLE
YMLNPQNLKEYSSPYWKKHYDMNFITSTILRPLLEITPHVRKDVIQWLLDKTAARVLRDD
ETEDVNIPTTRTVAAHPPRVKNDLEERPGKVPPAEVRAMLHTIPEKRPPRIDFTKAPDIV
AKSGCSPTEPIGFSFLTRERRHKTKAEEQPACQTESPKSTREEWRQMLYKPVTVHMTAGA
IRREAQTYLKRMEEREKSLGEMEAVLRNSQEFEVWQRQEKAREIQQREVELLNRKAQIEF
ASHNAVQKRKAVEEMKRMVSSQVRADIASQLESFSAERDREAARQRNQTAKMRRELEGNR
RKAVEQAQRDRLTAAANVKAENMRLREDALEEEERIKTQRIILIQEIRQLRERNLQRQAE
IQERNIRLQKENLEDSMYGGMGISMLREKLRQAKEESAQLEEERRAHFGALRQKEREKVE
ALSVLCANWRQSTRRARDEEMKSKQQEAARLKSNKNEEDARRALLLCDALKQKRKDRRTE
FFALKAEERRRNNELLLLAKGTSDMEEKHWSQQELGAINRLTVRQNK

>TCRU_5992 retrotransposon hot spot protein, RHS3, putative
EGLYESVYSARWYHVVEVSGGEGTGMKVKGGKPKHSWTYKKVGDTFEKDDAVRKSGEVPP
RLMVLTSDKGWPYTLNLLRGGGNDFFINCEVDRVWQIVERDLTEWFSNFDLTLNSSPLPR
VLIGTPGIGKSMAAGSYLLYQLLHYDVEKIQLVVHCFGGRDAYVFDKTTKIVTRYSDEHV
HLGVEKLRERGMKGYIIYDVAKKGTPPLRHFAPSTGWGMIVVSSPKASNYDEWEKQTKAS
RIIMNCPDEMDVKAMCTWMKRGLEPYKQAEYWRMVEKHMDNVGPIPRHILDADEYERRTK
DVERALRWINIGDQGKYFTLGGEKKWYSEDPSHKLVKIVRVREKSAFEDFANAPICEYLG
VLTLSLLARVLSPHDIFFLVLGMKNVLESEALEKYSLSVFLIENFLTSIAEDLKELPPPS
PSEPRPSVLTLNPHGHPTEATAISKLKSVGHQQELKYRVLYIPTFPTFPLVDGFFFMESP
RRTLVGLQMTTASAHHTIPSTVNQFTEHLSRFFNGWEEFAKGLSWDIIYIQHADSTPMEN
WQRCGPVNTENLSDAEKEIVAFWNGKVHQYQ
>TCRU_5993 calcium uniporter protein, mitochondrial
LCKNSPQPLPLLTPVEFAQIAPMVLLCQALKQHAAMDSAVGINGNSNVISRAVFNHYCFE
SHVENSDEALRLLEESGSVVSLSNGEGVHLRPLQFAHMYEDLTGEGEEKGSTLAFFLEEA
TKRLKAAQAEEAAMRSELQPALMRAAKWRRVVWGGALCFSGAQMAIISRLTFFDFDWDTM
EPVSYFLGTGTSLLFFLYFLRHGRSHTYEDYDRTTLPTKLRKYAPPGFDWEKYEAICKNV
DVERRMLSRIKEWMKRH*
>TCRU_5994 NADH-ubiquinone oxidoreductase 20 kDa subunit,
mitochondrial precursor
MLRFTRCSLTGRAMISRGSPEWSHRLDLKKGKKTILMHKLGTSKPNNALQYAQMTLHDLT
EWCLTYSLWPLTFGLACCAVEMMHAYAARYDLDRFGIVPRPTPRQAEIIIVSGTVTNKMA
PLLRNIYVQMVNPKWVISMGSCANGGGYYHFSYAVLRGCERAIPVDFWIPGCPPSAESLV
FCLHTLQKKIRWHEIQKYSVR
>TCRU_5995 hypothetical protein, conserved
HAEALRLLVTAIFPSASIVFSIPKGSQMYAGGAVVEGALFEKLHQKLLRAEPSSDVAEEY
CDQKRRPSEDLPVSPHGGCLQARNGPLSTPCSPDVADVWRTLYLKWPPQPVAGRPLWRYD
SEESSLPGIPCWTPHAVAYIGGFEAPDLRQVVAPQLFAQVPPFSSDTEVDRTFGGRTFDY
RRQKVPKFASRVLDREFLLREKGCAIHEPDLLEMALPVTFPSNSSLKENSTETRRVRTFV
CFAGSEPSLRALQVAVDPMHRRALRPAFGYSIATLKFALPPPLVNATRLLRQWNESWSPT
PLSTAFWLSAVGHAVERRLPMDKTAAFILHENACSLAEASKSIAFLTASLVSSSPQECWN
NFFLPVERFEAERGVRELMDTINLLPVGQLQ
>TCRU_5996 UDP-galactose transporter, putative
AAEVLASVVAYCVCSMSMIILNKLVIFTYGLNFPMGLLFVQNFGALLLVSVGKCMHWVWY
PDFSMEVARKWLPLTILFVAMLWTSMKGLYTMSVSMHTIIKNLAVIFTAIGDSKLYGRRV
TGMMYLSFCLMICGSYLGAKGDRWVTAWGMFWTISNIASTVSYTLYMKYLLSDVSKQIGR
CGPVFYNNLLSLPFLFMASFSSFPKLLSEVSTASFGAIFAIFLMVVAGSLMTFGVFWCMN
ETSPTTFSVIGAVNKAPLAIMGMVVFNQYPTTTGYIGIFLAIGGGLVY
>TCRU_5997 hypothetical protein, conserved
AVVALRRDALNGGSSMTLGSKGMKLSPDPHRRRMPWTAAKEYVPGVVLNAKEKMVLDGVQ
LVDVECVDRASQVDPLEALRATVATYEYNTSTGKNIFQLASQVEFDGRGQRFYRKEWQEG
TYDKYVTLSAIDFNRDGNKGTAYGYVTFHGEXTTRPVQIDFADVPGWHMEFRVERAVPFN
AIVPPPPSIGTDVPVDPRSYRLRAYPFYDAPNPPEFVERLLKDRGVIPDSPVETTELPNE
SEGS
>TCRU_5998 helicase, putative
AASAAVVTSTLLEKLRRNVLRKRLDWQQMPSRYPLVQRLPVWRQRFAWSALFASSALPLP
SGGSVTDTFVCSAPTGSGKSSLVPLFLLDCHWTRLLERIDASSGRLHRDGPRVRDGATSV
PSPMPFFVTGSSREFVAEFGASSRLCIVVSQPTRLACVELAKFTAAILLSSTTTTDSSPP
DDVAQVGGRVGYAVGGDKCFSPATEIIYATPGYILNAVLHKGGLLAPTTLIIDEAHCRDM
ETDLLLAWAKQQLREKGERQLQLRQLVLMSATLPVEEMVALFTSRIPAINAETPSGENAG
AFNPHILLVDAEERQQTGCGDAANVAISTQPYCVEEYFIDDLSDTIGASQVLCGSIEKNP
FLEAPARRVVASLGHFFSYTRFGADVNTPQARVLAQFLLFVLQSFALNSSSSGVGDQRKP
RPLQSSSSVPDQQPESILVFLPGFAEISLVLQSLEMLCRAVSVEVGPDSPPTLTCGVSHG
GTSSQRGNVTFLRYEQWCFSVALLHATAIGSPQQQLHDSAGPFPYRIILATTVAESSVTI
PNVRCVVDSCLERRFFTDPLTGVMLRSTALASASSLRQRGGRTGRTCDGAVIHLAPRRLF

LQPEKKKTARQIEMPVFTAGGLSSLRRGTLSGFVAPAQTLPESLTANAAAVLLRVKYLFP
SLPSALVQNLPSPPSSDAIARGVEQLVELGLLQLDTSGDGGSFNDAGASSDPQCRTGETE
DLHAVLCRYDHATLTAMGEFVAYLP
>TCRU_5999 hypothetical protein, conserved
LIYYALQFACIEEALIIACAMTVPSLLMFPRMTAQDDQSQAGTPAMQYLYSLEIQRELAG
VLKAGAAKSSGDERGDCHLSEPLLLCSLLREWYACNNSNDVVAFHTKYRVNRSAIRLVDD
CVAQCASRLYHLVAVDAKAQDGTEGLYGEHDTAVRRPSTQAVEQLITSAFPRSYRALLAG
SLQRLHRCAMEHATHRFSRRVATMTHWYPHDEQLIRLLQPSARVGDGNVRKRRWGENHKD
GLTMTFGAVQHRLSAAFVAAFARNTMRGEDGSHRVHHRRLVRNLGALQEDADSTCSFSIE
LHTQQQQVGLTRAAPYDRMTLEELHRVLAPYLAGTHLRQLELFVGGRSAVACFGVNETKE
REEETGAAAQQEKQKQKDELLLAPHVLPFEGMAKSNSPAVTLAHIGISLLVSIQSALTRL
TVLLPPSTTPNESNKRSNDNISGINSNGNNNNNNNNGGSNEEKDPGETPACPVSIKTAST
ATSSVYRGICFDSVNEDEEPANVCVTWHDSYGHKCSLLLSDVRRAGYEELFPTPSVTALP
AASAAPEAAVVFHGDECRTTSAGMFSNPSSCTKDQVRSKEEEDDDEETVTLSVQRVVYTR
AVYWKVTLPTVRFAYKRRPLESASTSLTTGEKTTPTPLPGGECHYCWVCHSAWMRKDAFL
AHCRSVTHLTRLAFAVQHGMRHEWVEAFSSGTLSDLLLRQKDRDGSGMYMELRHCNLSPT
SFMNALQWQPRRDEAVVTMPIAIAGSLLMHTTAVPASTMPPHGGGTNLQALHVWVLNTES
EACVFKKATNDMQAATSLPPSVFVLAGYLAAASSGFDVALLMNKNHTRAYAVMLYDWGVW
RLPAPLTQTRLRSVLDVFAGKPWRGVPVTREDHEVDDDCKRDVTPAAAGDEDDVGAGDLH
WCIVSDVCPQCTYCGSGGVSDENRATPVQQRLQHLPIDNMPSAAEVVEGTILLVLHEYQN
SQRTVISFADYLQRVVAKIDVWSAAQEKQQGSTTNSLNRQLAWKRVATTTKATAERRGGA
ELLARFVASRYNQPLESLLRDIGCQFLTPPGSLLQTATKQSASPTTGSGNTSLARTVTFS
ASAMAAEGTTTEKLFLLPTVLPSYLPSPEFAALLRSHRQRMR
>TCRU_6000 Putative S-adenosyl-L-methionine-dependent
methyltransferase, putative
MLQKSFFLFFRCTRITHATLHASEISTPERSTVNSKNRKELKTPLCIELISKMSSQGYFP
MSQFVKECLTHPQHGYYTAKKHVIGSEKADFITAAEIPFFADVISAWIMDAWQKMGTPRA
FHLIELGPGRGTLMKNILKQTKYSNPHLLHFLQIHLVEVGAARMEEQKSALAEFQTAQGK
IKWWMDLESIPFSLEPTIFIANEYFDALPVAQFRYTERGWVETCLEVDEDPANESHFRMV
HAPSGSFSAYLIPNDIRSRGKLGDCIEVNAVGMQTMELIMKKMVDCQKAACLIIDYGKDE
HMHSTLRGIRGHRFVDPLLSPGEVDLSSWVSFKQLRWALERLETARRHLKWFPLMTQREF
LQWGGIDVRLAHVIKDEETKTAMKILQNYRRLMDVDEMGNSYKVFVAQTRSFPNVSPFFQ
ELPLP
>TCRU_6001 hypothetical protein, conserved
MVQQRRYVKRSTKLDFRNITENTLADTPSGYIQDPANHPKQMVTYRKIAPEEHALLEEME
IEYDLMHREELAYNGYTTIAIQKWKEIVLKSNSTPEDLESACTYLQETLNEMQNMIGYTV
KKNPSTRLLQSSVLQGEKDTTDEHLNVVVISENDCNHVRYIIALAMRRLQDYEKAEQICM
EILSSDHSNCDALESLIELYTGTEQPRGLCELFDKIQTWDNEEETKSNRTENTVKLSNKE
RNGNGSHMLEVAMVLLSDMIVEAGSLHYMENGEGSTSRFFLEAIFPIIRTIGSQYTSLFL
ESVFRSMDEQHFAARLESSSKNASEQTVGVVISFLKTLLARNLYELVRDPLRFEFHILSK
LHSALRYVGRKHESYKICERLIKLYREKSGKYELPSGRRKQEIEQGFLDDLEPSYRLALF
QFVEDRAMDSVIVGKRLCIQAVEEFPEEASPWETLALLIHKEDPIKGLDDAVVAAKKAFS
LDPKNLSVVLLLANFYKAQKRYQLYDTMMDRYRLLKYLIESGVSDEDMKATLDEIENLDE
LNPREMEPDDFSVQFAELREHNDRMDMVNSYSMPIDKEPRTFGNQPLSAPILDPSINADK
PNRLTD
>TCRU_6002 SET domain containing protein, putative
MDPVGEAVLYLTRTFEKMSVPCRVHNTSEKGKHVIATAEIPAQSDLFEEAPIVSWPAQGY
VALDIPFCSHCLRQQANSDAANTQNDSLWRTCDGCGSYFCSDNCEFSSKMAHHILCGALR
QLREEEDVGSFDTDAGKRFDLTITKESLARCVAWVVARIATSIKQQRFSGEFLERHHTEN
EESISRQLFHIACAPFNRLIDAPKGTEFGDVDALSWYRTVDRLLREPCRIALLEATLPPR
SENDAWALEIVDALLRHDTLETFLGQMSLNSQAINGFIVQSSSGEKAFSAIPLVEWVLKG
GAVYALQSAFNHSCDPNVSVSNVDGTHDITLRTLRPVKSGEELTITYIPLENTTPEQRNE
KLKGYFFTCRCLRCQEE
>TCRU_6003 SET domain containing protein, putative

ATVTVMPAAPQDRLVECVHSSDPNSDAGRYAVAKADISPGELVLIAAPYAVAMNPNEMPS
AMSIATKVDEWVAATGSTNTASNLMTKRTRKNGSFPASIPNGYLPLLPHSTLCCNCLQLI
PEGTLFLNYETIRWVSGCIAAEHANYEMERWLNEDTEISQAKAVDVDADMEVSGEIDAGD
DRQLKKLQKTVKSGRMRSKLYVNLKKKLSEASARRHEKAMHEYHVKAMQMDNAQEVMWPE
RVVEGEHSLPEGVTNQGVCGCAGCGVIVYCSRACWTEHHNLHRASGTCQTLRRVYPVLMK
TFMVRAGDNANSTDKKRFSPDSWSTKHWLRRTGEEAAWEMQTLLLNALLVAHCAREGFAG
HMAEETEAMPATVNLSKSSEGEREVVCVVSSKNKTPLNLTNGRKLSGATTDAESQLSGAA
ALIATDCAVPQKVEILRMARLQCGGVVEVLDPKALEGGNEFRDPETASQLYFSLRSNMSL
GVCEEKEETHAVRPPRWSDTARLVTNLSMLSKDSRSKFRCAYRRFTKLILPWLGEGGSTE
ANLTVTATFFNRLCAALQCNSFGLFNADGNCIGVALYPEASYFNHSCCPNICRVTYRGIL
AAFHALREIRKGEPLTICYVDVQETSTAERRRTLFSSYRFFCECARCSGANTAAMEIRLC
DSCAIRGYILPVPPSSAFRWGMDAVQEGICSVCRKCVPW
>TCRU_6004 50S ribosome-binding GTPase, putative
FAPTALASYTHLFCTTRVMRHPGKIIIPRLPGGRPTHVEGAAPSGLPSSSSFTAASPYRN
EYRESKRLNLGVAQFLDTEAADTLRRQQQLHQFRTATEEALTKVWRDSKSHLRRQENLVK
EIGVEGAVKEILQPTRTSFRQELRQRPLDRGILEEIYKGLHGRRIERRLKKGVSWEHWIT
KGDGTAPIFTASHKAQQTFAFGGAVRLEAKATHIKQFPVLLASGKRAVGGGDGGPTSRSD
SIESGETQRCVPEVAFVGRTSSGKSSLINAILNALIAPYGHLQGTTSSVNFYNVANKVML
VDCPGYGYYNPMETPALDAENAVAVMRAYIKTCAQHSTEKKRNSEGTKTKRDVGHRASYS
KRPIKRVFVCVPSRGVQKADTEYLDYLESLAVPFSVVLTKTDAAPIRFLARLADHTRCQL
VHYKHCKELMLTSSLRLAGIDKVQNLIGSMALGEDRLHGATADFSSIV*
>TCRU_6005 Suppressor of G2 allele of SKP1, putative
DITMSVATKPFEGTVRCEWFQCPARINFCFYVRERQENDVRVETSARSLTVTIRLDASGR
EYQYNIDRLYAPLAGEAPTVTVRATKVEVSFQKACEMQWPTLESVDNGAHTVPDLDAPAP
VATASLPASAEQLKYPNSRGKDWSSVKIDDEDVKPEGDQALNALFQQIYRNGTDEQRRAM
MKSFLESNGTVLSTNWEDVGKREVKTEPPTGMVAKPY
>TCRU_6006 hypothetical protein, conserved
RRAAMVLSLLVFLLVVPCGVFSQYSLECQNVWEGPNAENDIIACLSNKDRLKGQWRLFIL
PALNVIILAMLLLSFPLLFLCALCCRCCCTPGTAGSTKRARCCMWLWILYAVIWSGVMFY
LVFFGAGLLIATAPRLLEDFVSGPLDYFNSTAERVLDFASDWSTGERKPLDAIPLDLSDF
TTVHEQAMGFIALARRYYFNYLDKVSIATFCVSSVGLVLIILILPFACCHCCIPCFPLIL
SCLYWVTGVLFAVLGTVVSVLAYATTVGCGELELQYTRQPGVFQWYAVPYCQRQFNFSNI
NKMIREKELELSREACIQLLGVCESVTPGETAAEPMKLLAAGVIPSAIPGVIPAAVPVAV
PGVVPGAVPGGVVPGAAPEGVLPGGAPGAVPGAATGDGDSAAIAALAQSGALSGNDGAPL
DISSLAGSDGVGLAGGASSIESFEGLPPGIDLASIKDMPGASESIKKALESRNMSEDILR
MAPGGLNAELLQMLSNATALSNLFARPLVCGKGLLNASECGDFGTMASILFRMAPGGLNA
DLLKMLSNATALSNLFARPLVCGKGLLNASECGDFGTMASILLDTKLQKNIPGCVSKNGD
CTLTDCAATCTIDFLKDASTMILSKGEMARNASNALSYARPLLECNFVIDKVATGLAKCD
DLRKGTIMLGMGFLVGGMIFGLAIYIALRGACVWGE
>TCRU_6007 cytoplasmic translation machinery associated protein,
putative
ESFSMSSADLFKKFTLQNVAQIANSSHKEQMQVRHDLAEQYPQLAEFWEDIMPRKSDIML
VRCHDQVHCVTLVSAQPEVLFFNHHNGPYIPHLKLLHKYPFILQRHQVDVGACKHVLSGA
NIMCPGLTSKGGYITPEIPAGQLVAVYVETKEHAVAIGKTLMSSEEIKKVNSGPCIENIH
HVGDGLWMNRVLSASHIGAR*
>TCRU_6008 Peptidase family M20/M25/M40/Peptidase dimerisation
domain containing protein, putative
LGVKCTLIHNAERNKANLWATLPGDGGVTKGGIILSGHTDVVPVDGQKWDSDPFTLTERD
GKLYGRGTSDMKGFVAVCMSLAPELLKMRRAKPIHFAWSYDEEVSCLGGMELAEFARDHD
VRAEGCIIGEPTGMTVVIAHKGTSHFWVRVRGKAAHSSLALTGESCNAIDYATKLITKLR
EIAEEYRRNGTRHDFQVPFSTLSTNLISGGNASNTVPAECEFLFEFRALPNETVSKMMQQ
VRSYVETQLLPAMKAEFEDAEIVITPRDETPSFEGSEEAPLTKLVCAINNDYKVWKKNFS
TEASHYSGIAGAPTVVCGPHGGAIHCANEYVTPAQLDKCREFVLKVAE
>TCRU_6009 Zinc finger CCCH domain-containing protein 39

QSDARLMVPPVAYRTAYESIGELQNSLQGYDQQVAKVIQHINTLASVVDSLQQHYDSVVE
EKEYIIRSLDVAEGRMQDVQRIVQRYAAVTDPVVASDGFTYERDVITNYFNECQAQKNIP
MSQQTHTELTMMLFPNRSFKRFLEQLMETKPAEMRAEASSSSHGNHGGNANASSRSAGNA
QNTHKADVSNKSGNTGANGERLHPCVRVYGYCNYKDACAYALYPYDACLSHLKGKCRFRS
QCHERHVDFHGPRNHGPANGG*RRG
>TCRU_6010 Periplasmic binding protein, putative
LLLFVPQVVVPKPVVCETNVKVLTLNVTDIPNDRNFADSFGAGLEAALWWRNFTVADGVH
VEIVRKVTTMLTSGTVIEEALKADSNILLVAGVIGDMTAAISLPVLVRHGLVSFAPFTGS
SLVRGWNPNMYFLRAEPAAELLALLRYALAHLRVHRLGFMYLKGVFFGEREYAQAQRVMS
GMGYNLSGVFGLKSSMSHGAKKEVFDAAWEVFANTRPQAVIVFGSPIKDTKKFVERMLTD
KRTAGTYLLAPSALQGLVLGVWRAAVTSGVEFEPGQVLTTGTNPLAKVTKYKAIQRFQEV
MRAYLAHRNDTQSGVGKDFPDDDNEGEMMVAGWIAGELLSQALGNREWVKDRTSFLASLY
NQRRYVVDDIVIGDYGGEYDYTAASQGATFHCNQGGRTVYI
>TCRU_6011 folylpolyglutamate synthase, putative
SSHNNLETTRLFIDRLNMQGYLDKLRFVHVAGTKGKGTTAAYTAALLQAYGLRVGLFTSP
HLVDVRERILVNNAFLPKDVFARQFFKLVDRIADLSNSESQISRDLSKRTSFFRFLFLLS
LYIFAEELVDVVVVEVGVGGRIDATNIISPEVTVITSLGLDHTEVLGNTIEEIALEKAGI
MKPGVICYTSPQEWHPSTLTVMEKHARGQQTPFVVVDEKTLPIFNWPPLAIGGNHVIEDS
KLALLAARYMAGIPPTLPLSGAERQVLQTMTLPGRSQVLSIHGGTGATLYLDCAHTYESL
TCATRWFMEESRSLTGDANPRRVLVFYSTRDATHVLKSFMPFIHCFSKMIAAFVVNPRKA
TGNTADGRYDYARGEVAAVTSCWKEMYREVPCIPCKAPFSSLEELIDVAVPAATEREDTL
KPVQVFVTGSFFLLSDIMGLLQAHES
>TCRU_6012 isocitrate dehydrogenase, putative
MFRRVACRVPFTAAAVCYMSTTRPRLERIKVSGKVVDMDGDEMTRIIWSLIKEKLILPYV
DVPIEYYDLSITNRDATNDKVTEQAAEAILRHNVGIKCATITPDEARVKEFNLKKMWKSP
NGTIRNIVGGTVFREPIIIKNIPRVVPQWREPIIVGRHAFGDQYAATDAVFPAGRLELVH
TPPGGSPQVLDVYTFKGEGVGLAMYNTLESIEAFAVSCFEYALLRKLPLVLSTKNTILKK
YDGLFLETFQRLYDNNYKDQFEQLKLTYSHRLIDDQVAQMIKGNGGFVWACKNYDGDVQS
DIVAQGFGSLGLMTSVLLRPDGKTIEAEAAHGTVTRHYREYQKGKETSTNSVASIFAWTR
GLSHRGKLDGNTALTNFAAALELAVIRTIEAGRMTKDLAICIYGQEKLQRSHYETTHEFL
ESVAAELART
>TCRU_6013 SAC3/GANP/Nin1/mts3/eIF-3 p25 family, putative
RMKPASYLSCDFFTSHGVPMTKPLRDWLNRASYLSKTRTTEADRRKYERWAVGVVEDALR
APGGIEGKDWTRVSPVMPANAEDREPTFLRDGNVASREGNSVTQPGVDHRTLLFTECMRR
APSELRSFVVQAINMIDVEVASGRRRYDALTFMELIQAAQELQRVYQTQMEAQRRMTSPF
SQVVVAPSSTESVHRKPLAPGKVSRPHPEGEERDMERERPSKTRRGELYSQRADGVGPAS
VESERTRVFFRDLVSCNNSTPSSRPFIGKSQELERMYSRYEPTPVDIRPRDVLVKALAFV
LAKAKDKLGKENALASAQYLNEQLKGLRQDLRVQNIVDGFAVDVYERHALICLELGDIGE
FNQCQASLKKLYEGLSDVKETSISDFFCYRLAYLSLGGQHDALATELIIYTNTITKSTKT
SENASPRVKKTDLRWTIKLCTACEDGDCGTICRALMALPRGMHLLLKIYLQKCRLRWLRE
ALNCIRGMVSMRLVMASMGSTPVERHKGEVAPGAEGEDTHFWLDGSFAEAEEALRQFFEM
IKFPLPQRFSFAEEIRRDMKKRHPHCGEEALKIEEDITVVDAAALFKCVDGYIAFLSTRS
D
>TCRU_6014 WD domain, G-beta repeat, putative
QQQQQQRPSILSYSTGWVANGLSWSTRENSPFRFAVSSYIQEYKNHVDIVQKNEEGELVC
RATWEHCYPPTKVMFAPQKTMTDLIITTADYLRLWEVKEGPPERNSDERHRENDDPRKVP
SKRDHIDSHVVFKTVFDSGKQQNEFCFPVTSCDWNSDDPNIVGCCSVDTTVTIWDIESGK
NTRLIAHDKDVYDIAFAKGTHTFASCGADGSVRIFDLREIEHCTILYESHSLSPLLRVAW
DKLDQTYLSTFGVEGTEVIVLDTRFPAVPVGVLRNVRPQPINSVCWAPNSVTNLCSAGED
GTAYIWDINGLPNVAPKCIMNYKGEHPINNISWSSQNEQWIAITTGKEAQLLHV*
>TCRU_6015 hypothetical protein, conserved
MNKDNMYRGGCMVLLQAILTQACRTIIAFCVVADNGIPANRRLIAMASSYVTASEAASLI
EGMGKHVLLTAVHLLCCEKHSYRACRHYHGEFAAAVGAILQESSLRSNILAALTEFITRK
WKGDEDSIHPLLQRAFSVIPVEYPSTPSASGSLAAPLMLLLQVYPELERGGTSAEVDCGC

PHPWFRENLPIALLTLSMEQHAQMWRRTSLLRMAFLRWQQRHGMYLLRRLAADTSFPPIE
MTAQTPRTVPSEQAEWPTPPRPQEAELKQDPTCGHINSNKKSGDNSNKSMFKNSVKFLEK
EITSSQAAAGLTEAPESKVNMFAATITNDPCNVKLIRSLLSECDKLASARLKRQAFQTWR
DVRLVERRGLQRISDQCMWRRKQLCWGRWKHKMERHRIAKRQQCTEEQCQSLMERKKERL
MQETWTCWKKSFLVRRFRTHTCGRRFFGMWRRAYIFMIHAQGNIFPRIAEPALAARCLEQ
WRDSYHFRIADRMFMRRIFLHMKNCFRRRLEIFQLNEIAKACARRALQQRCLKKWCKTCR
LFRLFVQFTRTLGRRFLCQALLTWRLRWVRRTSGGDRLRAFLEMKQQRLIVCTFMHWKRK
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RWRCMRREHDRYAMGKAALNFRAKTLREKQLLARVWFTWKGKTHLLRHRRPIGIFSSSKS
NAYIGVNRSFPRANMSTSSSPSRRGANIQGLSVSFAERRFSPPRRDPLALLRAERVLLRG
IDSPQWQSMVHSRLFNASGSKGR
>TCRU_6016 protein kinase, putative
MRHMRELVIPGATWRDDNSTDACENRLCRKKFSMLFSKHHCRWCGRIFCSDCAPLTALYH
GELLRRCNACRLPFIFRSIYDPLSGRRDGAIAEFIFSFLDSTSLNAFLQSCHTALSEFHV
SGYEYYECIHERFPSFFEGARIGKGVTGTVYKCEDRSRFENPRVALKVITKSSTVTITAW
RKITTELEILKEIDHPNVARLLEVFQTPLCLVIVMEAGDGGALKQVWEFVRTRHCDLEVF
TASVVAQIAEGLDYLYRVKHIVHRDIKHDNIIFSRDFSKVMIIDFGLAEYIKNEKCQLFV
PCGTYGFASPENILAVVDHLQLFEASGATMHRADMFSLGVVAYMLLSGVRPLRGRRFLDL
YREVRGGIRCVGPCWTNISDSAKSLVEWLLKTSTNERATPEDVRNHPFIVNKASLITEIV
KKRKQELLITEQLEGNEWVYVVPSDRHWD
>TCRU_6017 phospholipid-translocating P-type ATPase (flippase),
putative
MRTVRPLDPAVAAAYPDNTVINSHYTFYNFLFLSLYEQFRRPLNFYFLLVACLQFISVIA
PVSPFSTLLPLLFAFTLTSLKEGYDDIKRHQQDDKYNNKARTVLDPVSVSWQSRPNYRIR
VGDVILLKGDEEIPCDVVVVAATASTVYIRTDNLDGELDLKPREIVFPHSVSSNNATKDD
TTTSSDLNLICVDDTCETIINKVGNIKLVVPPPSAIIESFDGVAEFTCASGSSEDATTIS
VSISHHHLLPQSCLLKKTKAALCVAVYTGEETKCGMNKSPPPVKWAKIDQDVSRYSIFVF
FCQLASALTFGLLGYFLNSRVEEDYWYLKLPSNELDASLIIYPLRFFLLTAVMIPVSFKF
VVDMSKYYMALAVEWDEAMKPDGPNSEGCRVKNSDILEDLGQLDYVLSDKTGTMTQNVME
LIYVTIGDERLCLHQEIKELVNKSELGIPNNERVLHFGRILSLCNTVETLGKSGSSSSEG
AFVLPQYQASSPDEEAICRGCVSLHVQLLYRDANKAVLEVNGVKETWIIHHVFPFSSELK
SMGVIVEEKSTGTLYFFVKGADDRIMEMAAPTSTPLFSTLRSRESQVDLLTSHLNSYARK
GLRTLLVAEKKLSESDLNTFMEEMRVAELSLQNRREQVQKVRLKMEKGVTIAGITAIEDK
LQEGVQDTVRDFIRAGIKVWMLTGDKVQTAVQIGLSCSLYAPGNRLIYIVSGNSTDGVGW
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TPAASFQKDNSVLVVEGGRVLERILSTSELRTRFAALSDNCICVICARVTPSQKAALTSF
VRSRGFMTLAIGDGGNDVAMLQEAHVGVGIVGKEGQQASRAADFSINRFSDLRALVFVHG
QQAYIRTAFVIKYSFYKSMLISFIQVAYNVVGTYFSGGTFWNSFGLTVWNGVYTLPQTMF
YCLDRIAPRVVLERHTFLYKRTRRASDMNIKEFFIVFIARGIVQSVLTLFLVTGVFNLSF
AFSETGWAATHDITFSVAYSALIISQMLTMLLESHSITFLNAIGIFGMPAFYVVMTAIYS
SFQRFQYFGVWNNTMNVISFLTAFAVAFVLVLPVIGMLSLRRALTPNARDVLRTAAVQNQ
MRRKIRWGRGDCCSRFFRWISCVSEEAS
>TCRU_6018 hypothetical protein, conserved
MDYLRPINTRVETARLLCGSIMRLCLCSFSHYVGCGLFSRYVLRREGSLAMWERESVPYV
ASLGMEIGVSALICPVRYLAAVTTPRFILDYTMTGWSDTLSLLDRFSPANFAAYAMYAFS
SDSDWNLDFFAWQAPSVVLTLVKLYYRRRKLGSESCRTKRVLAMIPFQMFLRAYIAGFSV
MIPENSAEAVSAVVVTVVESMVTSYLARHTWPF
>TCRU_6019 Transmembrane amino acid transporter protein/Tryptophan/
tyrosine permease family/Amino acid permease, putative
ISHGGMLSGAYNLASVTLGSGIITLPSAFNSTGIVLSVVVLLVISLATVFSTYLLTLAVD
KTGYRGYEKLARGLLGRGWDYWAAFNMWMFCFGSCVSYVISVGDMLRPILDDSSVNPFLQ
TVWGNRCLVIVIWSCVMLPLSIPKEINSLRYASVVGVSFIMYFVVAIVVHAVRGFEHGKP
RHDLKLFRSGNGAIIGFSLFIFAFLCQTNCLEVYAEMRKPTPRRMTRDTTLSMVICCFLY
IISGFFGYADFGDAITDSVLLYYNVRDDPMIAVAYAGLAFKLCVGFAICMQPSRDSMYYC

IGWNVTTMPFWKNALFCTALAIVALVLGLFIPSITIVFGLVGSLCGGFLGFIFPSLFYMY
TGNWSLRTVGFFHYFCTYLLLISGVVAVVFGTTAAVFGEV
>TCRU_6020 mitochondrial DNA polymerase I protein B
MRRLFRVVGTRCDMRCAFSFLSLINTQTALQNAAPLTDDAEGFTEFFRLPVSLDAGVAES
VRQHYKRVVKGMETQQDSHAVRVQEEEQRRCEDLPVFLVSYDLRSRCFHFFSIERDRVVV
VGSPLPDSAETSHNGGGDNHGDGGGIDLSTVADELMQHTHGLTQVILLPLVEHKKERDVL
APYFKRLLVTLRQSGIIPVLHVDNLEMAEALDPNPPPLRELVTNYAVITPKPLSEPWFRA
HWVYLRTLACRMNEEDPIRTINFLIVPRFDVFVIHLVRSGSRGLNVVLWDPVHRRRYAAR
GMLSDILACMLERHQKRIILLPTNRTDRPTLLRCRVAMTKAGRQCHLVFASELGEKYRGV
YQSEPSRFWTLLREVSGGLDMDLLFEIYITAGNNFRRYHSKRLREGGVEARIPHRTAEAA
VSLTNAEVEKWLGVLSLSRRVAREKAEMRKYKKHLFIAYVTTEFAAYTRPANPHASVNFV
VAASLMDAQHRVVEPWTKYAARGDFKLPSLNEFDVIVCHDAKQLLLFLWDDPELHRFFKR
GGRVWCTMLAEYILEAQRCQTGSNNFRDVALKYGVMTPPSSVLGVATVDLPLTFLRHYLI
AAVDALSTVFREQLLKSCERSQVICIAHRMDSLLSMAAIENAGIQIDVEEAARQAQAVRN
RLLATDKALSLYVPNEVPVDLQKLFDWNSLQHLGALFFGGSITLGYTDSSLESSTWTSHL
IHFCHRYGNLSLLSADVHLQRFASEKGLRTAGRLSQRVSQYLSKDESAGMRTYRLVVFDI
ESTGLNTATDAIIEIAAWDPVEATSFSSLVDPERAIPQETMAIHHITDGMVRGAPRLPEV
TRALARYLRLDEAQIDPNEVVVLIGHNVFALDEPLLRRAFEREGVCMDNILFCDSLVLLK
ALKRELQGSTENPRVDRGVLETLTTSLRLSSLVEGLHVEADGLLHRADTDAKTLWFVLVN
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LASLRSKPINENTLQVLHRNQVTVAGLLLQKQQLERNAARFLHSDPSGRLSVLHSDGKVR
QLIDLTATSTSRTTSSYPSCQNIPKDDKSPIRRLFVSRFGEKGRCVELDYSQLEIVVLAL
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TGIRMSFKTRDVVLNLPPVKNYPIQGFGAELAQMMVGRVFRHFVRRDFYGQKAFMVNFVH
DSLWLDCHLDVLEECVRETRDILTEVHTYVAKAFPGVELKVPLNITTQCGVDMCSMETIT
DDFSCVALQGRSAVGAEAEEPLPSLEADAADIIE
>TCRU_family, putative SUR.1
MRPDYMGFMFLTSAVVSFNAGIWQIFRRSEKKRLLENHKNLMKPALKELPASDKTVDEFE
FLPVQLEGVLDNEGSVLVGPRTIPSYKGGATQEESKGGFLVMTPFEIAGTKQFVMINRGW
VPIDAGKHRTLLAQYIGEGFALTTVRGIFRREEYLTASLFWGKNVLNEGPAAADLSWLAL
RPWNMALDYYKRRWGTNNVDARVSQHGLHHYYVEMLEDYSGDDQRIVRGHAWPWRRSTEE
VTYVHLMPIVHTMYVLFWFSVTIGSLYGMGRCYQRQKELFALRRHMTAQSTLLEKKRQEE
ARAYMEAVQEVERMKKLGTASAARIPAQ
>TCRU_6022 hypothetical protein, conserved
ASSWLLRHARHNPRRWEQPSVISSRAAAETIVTMLSVGGDNCWEVATGLYAEALATHSIG
RRGEVALRERHMAIARVLTALTQAATVGMLHGRVARRMARDVKPPRDDASNKEHEAMAMA
CEAILRVLLASGDFEKAQLCAEGWVRTNTSQTVVRRVIHTLVSEAAGGGRKEEGSREEEG
DSDKSAVRRTSLFRCGFLQFLEAATGIPALPALLSLRTEGLTDRCVARWYADAAMHINAS
LWTLCIAHVPPMSASSEPFYRELLVYCCSHRQWPLPVAALDAMPRSVLQENLADAMRCCQ
EELGEAERRRLQDAVSTVVVSSRPRREAILCLDLFSRQFSGGNISQEDVGWWCNHLRRCS
LDSVDSATVWMALCQRIGVEDLMMHSMPSDSSVFPLLVVQASRSTTAAEALFAAVQQGGR
SPPVVDDLPCATAKNLLVLCKDDTSALVVDWVLRHCKDRDYLVQFVMEPPAGHGAAALQV
LRVMMQPEHADVFVLLSSWLQRRSSTWLSSIASLAPRNMQWVVALRCLSGMAAPSIAHVH
VAFLTLAEPCVTPLSVGVDFLWTDDSVTSLQAEVNPSLWQIEAEKWEAALSFLSFGAKNM
NARSDLLRCYAHVVSRAAAFSCQERIRVEDLLAQMKMEEASSTALSAREKLAVLVRRKKW
MEACSLVAQVGGGATRGLMGLLAHHGRWVEALRVVVKEHKEAWVPLIIRATRNAGHWQAA
LWTVEKAVSKRISLHYASIAELLACCAAADVPLEAIQLWLRAQAGETAAHGLIGFGRKNT
GAVTEGSLSKTHAELLFVLLDSPRSVDRQWHYALQLLTSHVLQCNVYPSSRLFHTTFSIL
RRAGRWQESLRLLRLQHLIGVPVTAKMTRLVADALPPTRWRLALICLQGDLRGDAGLLRR
VLPKVLPVSWEYALGLISGQGEATTTAMECVVGCEHVPLQVRLQTWMRILPSLPVSMRHQ
AAPVYLRLSLAVSDHGSCLLVGVDGLTVIERSIRGLRHDFQNYAAFVYHRAVVHRNWCYA
SLDPAVGVMAFRALSEIAGRDEQCEVSEAALEQLTDLVERRAHGKLKMALGDLPCFHLHH
LFLFICLTLTIKNTAWTAMQRSLFV*RRTWW*WRGCRLMPMVQSRHCRALSFFFFCFFVA

FCSVGSPL*NTMRLRTVRCPAAVSTAATVKMTRAFSEARSNYDGTAAPPWPAPGEKPKYP
SALSEFPLQRPRMRKTHTEWMFFHGHGGRPGVYGQTREIADFEFADGTPASMSGRRFAFK
HHQDHLLVQLIRAGAAVERKAARGLLPRVPGTPEQRNWDPAIPLFLEDVDEQGRPPPSVD
RSICSRLIDERMASSTQTPNELANRHEGETLEANTMFESYDPQAFVSDHIKLRDEKRPYW
SRRRWALTDNFLVPKSPKPKNTIKDE*
>TCRU_6023 RNA-binding protein, putative
SSNHMSYHRSNSGSNQNSNRGGAGLRRQRSPSPDAHPQHASYNSGSGSGGGGSYGLSQSY
RSQPQQRRHSPPHRPPFRRRREDMPYTIPDIAPRLHVPHELPVDVTAFLDLIAFYVVQGG
PTAEEEIMKREENNSHFAFLHAPWNDPMQLYYRWRLYSLLQGDTLLKWRTEPYQIERGNE
AYVWVPPPAIPSGPECLLDAFQAHKSVYKGSDKNRDLKVKESPQPVPSASWLSRMSVSEG
AFFVTLEKPAAAEWQQLLRMKHHVTELAAPHGMPLEERVKALTAILLDGELIAQRMVFAI
EHQKAALHLLSLVLDEVVRLAYDSAKPLRPTDGHDDEASRGTCSPMNRSHSGDVDSSPCG
DEAFYAAARCCMCLSYLFTLNDIGKNGGAAPLTEEEIVAIAPSYEKRCSGTSATHNATTT
TGNDNNNSNSNSNSTGGGTGGLTLATGSEAPHAAASIGMSTHTLPLNIPLPASAAPGTMM
PSSFSSLRLLNRALEKIMPTLIEATLFVALCTVQQYGSLLVDNARETSRSSAKPPGAEEL
EGILPLDIDQAAYVHVQVKLSAARATTSGTNNSTSGTGTATNSSLSMSAAPTKCTPASAV
THLKKEERDAVCMIAMLLISWLKQLCSSWADADVIGNRCWSTLLTKYVYLLSQPIETT*
>TCRU_6024 COG4 transport protein, putative
VVANSLQEMRHTVASVNETMHSGDLERIVELIRKYEEANVNLGGRAPPSLLQDYDDDDDD
NGGMKENVKGKEADYANGEEVAPKQQQQQQQLMMVEDGNRDATYPSHSAANKSRENKNRD
GDNDASHPRNHHFEAASIIASARESAREKLLEKFRVASRSNDKLTIMQATRLLTQLGFSE
EGCSLYCTWLCEHTIAALKKMVDRELRKMDDPTEAGMSHLGLVSTVLDAVVAAFENEEEF
IRETFGDAGLLKLLTELHCKSTSQCVPVLKDFLKKRQEVLSSVTSAGGINTNSNSSSSGN
ARGQFPAGSVEAAAGSPVFPTTSSAVAATVDPRRTDQILEEMSHLVSCCHLYWTFAQSKQ
QEYMHGVEATGKQHEQQEVMVSVDSLWSSRDNPLMNTVQEILGVFVPLQTLYFEAAFEQA
LRLQMDALHAAAREALISGTEGGGDLSARKRTGVIVHSSSHHHHHHQSSKKNETYSSPSA
KKTANFMTGLAALYTSTAAASGGEDEEMPDAAMDQVSITLPDDVFFFLRIALHRAVNTKS
TQIISAVFIACIELVQSKLLPVLQLQTTLPPAAQLQQLQQQRQDFTVPSRVLRWTVAAHC
TATYARKLAEELRQLARENFSGKDLLRFTEQAEDMDALSRELTTSVEQWVARFAEVCYQV
HLTSHLERFSTLSYNLTEEMFYHYELSDPWVQVCVAAADVVLRPLDAHLDTHCFDLFLLA
LVRRVVKTLWQAILQKSFSGYGALQVDRDVRTLRTFFLGRAHELQLREPFLLLTSATSLL
LLDSPKDAEQDVYEGLTADDKRRLLGCRLEFKNAEIERLRL*
>TCRU_6025 hypothetical protein, conserved
PQQQQQQPQPQPQLPMQPQMQPQMTVGPQWQSMNGAPPSMGFHPSYPRSYITPQSPQMQP
STPPQTPPQTPSYNLQPPQMYPQPPMGQPPFWGVPPYQQGYAQQGCFDQMCYTIPGQPGP
CDGCGSQAVGSGCCCCNNGPMDPYCCGQPTTPGCMDCLTSHCEYTYCAMIFFTILSAVGF
IVVLVYADNDNLFKRFRANNTIELQESIEEHIIMSTSCEASNLIGLAGRVCMEGNLNANT
FVVQLSEWNIQRYTLYFIAMLFSIVTLLYATIVHFQRQKVGGEPKAVWSSQQQQQTGKQR
PENTAQDAAHGANAKEQQQKQQQQQQQQQQQQQRQQQQSLSPSINRPIEVYGTPFYEFMR
IAWFVMGVAVVFWVANLLYSFWAFYSFYHRSTTGPLRNFFEEYNTRFSASVICVGIYLAW
PVVNIFVELVLWIVFFLPWLIFRTLFKPGIGKLRPALPLDKMPGCIRCDMFFMDFNEVQR
AGFSEPAWKLITGSTTPLFPCCEDPAVDRDPTMAAWHQYQYEWYMRMQGVYPVPGMQAIG
PQMLPSPTTSVSVDMREGESRHRTRSGSARHHRRHHRNEAGGAADENATSPAGGSSPRRA
SGAQTQDVEEGRHRRRRHSRSKRGEEDGGETNGGAAEGRHRRHRHHSRGEGDQSNTMTGV
TAVRSTQKHNADLDRMLEEL*
>TCRU_6026 chaperonin HSP60, mitochondrial precursor
MFRSAARFAGKEIRFGTEARQSMQKGVQRAVSAVATTLGPKGRNVIIEQSYGAPKITKDG
VTVAKAIEFKDPFENMGAQLVRQVCNKTNDLAGDGTTTAAVLVASVFSESLRCIATGTNP
IDMKRGMDRAVGVILQSVAEQSRKVTSTENIVQVATISANGDEELGRLIGQAMEKVGKDG
VITTQDGKTMTTELEVVEGMSIDRGYISPYFVTDAKAQKAELEDAFVLVSAKKVSSXHTI
LPALNHVVRTGRPLLIIADDVESEALTTMIFNKLQGKLKIACVKAPGFGDNKTAMMQDIA
IFAGARLVGEEGSGLELDAENFDPAILGTVKKATITKDDTVLLNGGGESSMVKERVELLR
GLIDGETSDYNREKLQERLAKLSGGVAVIKVGGGSEVEVNEKKDRITDALCSTRAAVQEG
IVPGGGVALLRASKALDSLLGDSSLTADQRTGVQIIRNAVRLPAHTIVLNAGKEGAVVVE

KVLENNDVTVGYDAQRDRYVNMFEAGIIDPARVVRVAITDAVSVASLMMTAEAAIVDLPK
EETPAAGGMGGMGGMGGMGGMY*
>TCRU_6027 Cytochrome b5-like Heme/Steroid binding domain containing protein, putative
LLSFIVGTMTFMFFLFFLRKRQRLFEVAPRNIFVPRAYTLEELSEYDGIKKPLAFVGVRG
VIYSCSMDFYGPKGPYNAFSGRDSSRHLGKVTVGQEESNADWTTLSASHIATLNGWDELL
RSKYVPVGWIIPSEDFTKRAE
>TCRU_6028 hypothetical protein, conserved
LQEVLVPRNSGCLKTAIVQNESSCAIQYDRTLRAPVLVLRSGLSHARVEIPCEDYKFLLK
KFPQLLIILQTYLSSFDSFSLEVTMHTRTSLRVDLTIGTQFSKATVADLSTGVVVSKMPL
IIPRNRWVQVVFHVSGILTHLFDLPPIQSLDSISLTGTCKTSRLMVCNDEEEAINAAPGD
MALFAVPAYAPPIWQTAAGIATPVLTSVSRTTSGATTTTLKSVGNYLPVVGEAGNEKRRN
PFRQPEGTLKSNLQSPPPPPIERNSPKLEGISTVKPPSPCEPLQDKQGSALQRDFLGNLT
LSLSSPSKSLQLQQQKQQPQLASLSTKSIQTQQNQQNAESHSTNRTVSYIRLVNPTNRLP
QRNSNAISRIRPGAVTRSESSASGSLTPASAPAAPTLSNTADTWCGITGWEEAVDFMSGT
NAALLCTADYAIKGSLHSIQGSLGERGATGVNNKIQKGSETQNLKTQQTKKSMELRRRPI
FFPSKRRKGIGGGTESQNFMDDDTGNGVTHSIRRRGHLSRRSRIRERIRLLKEAQSSARR
THEMKKLTASELPIDPLEEAQMMVNEEIVDVMNEPRCGYGFGYLGVLRERGGFETDEGVD
TNLKGALTLDISELSEDEED
>TCRU_6029 Calcineurin-like phosphoesterase, putative
LLELLPEKYMSTSPHEQRLPEALIVRVLREAYPIIASDPIVVYVESPVCVCGDLHGQYYD
LLNIFSRRPPLGGGVLGLSNHALPVQRHKRSRIYSEDSSVSHQDEFKASDAPYDKYLFLG
DYVDRGSRSIEVVITLLALKIIEPSKITLLRGNHEDEQIMLLYGFFDECKRRYGVKLFRI
FTDLFRVLPVAAVVNGTIFCMHGGLSPELKRVNEVPDMRPCNVPHSGIICDLLWADPEAE
LSPNVDWAPSTRRISFVFSAKALEKFLKENDLDMVCRAHQVVEEGFQFFPSNTKRHLLTI
FSATNYCNEFGNRGGVLCVDKEGVCSLLIL
>TCRU_6030 WD domain, G-beta repeat, putative
MDLDNTDTTTSGENDFLFGDGSAAAVPPSLLTSAAVIDLAMHPQLPIFAAGLVTGEVEVH
EYRATETRRRPITQQYFKGDGFQETNPYNIRMHPRGCVSAMEFTEDGNYLVTASSDRTIS
VLDCVAEQIALHIGDGTATKKMTPGTNQRKNVNSSSSKRETMKIKKRNKNPHKFGISAIN
VCDVNLLASGDDDGMIAIWDMRQRTPAFRYHEHGDYVSQMIYFSDIRELVSSSGDTCLGV
FDLRGGKIRDYSEKRKDELSCFAFVNNTGNNTSSFIPSIVCGTPNGGLPVWKFGSWRRPY
DILDRHPAECESIISFNNPDSTFNHNIILTGACDGLVRVIQMYPVRRNLCQLSARDFNYS
HNNSIGGKSSGSYANVAVRRQRGNEGISRMRLSHDSAMLAVCGTDNIIDFVDVRFLSNER
ELDQLRSQVEKGHLAVLREMEREREKEEETERSESETDDDEDDEEGVEKEPGRCMKNAKT
AKRGREEEEVGDHSDEE
>TCRU_6031 trans-sialidase
VHSFRLPALVNVDGVMVAIADARYETSNDNSLIDTVAKYSVDDGETWETQIAIKNSRVSS
VSRVVVPTVIVKGNKLYVLVGSYNSSKSYWTWQPDGSDWDILLAVGEVTKSTAGGKTTAS
IKWGSPVSLKKFFPAEMEGMHTNQFLGGAGVAIVASNGNLVYPVQVTNKRKQVFSKIFYS
EDEGKTWKFGKGRSDFGCSEPVALEWEGKLIINTRVDRARRLVYESSDMGNTWVEAVGTL
SRVWGPSPKSDQPGSQSSFTAVTIEGMRVMLFTHPLNFKGRWLRDRLNLWLTDNQRIYNV
GQVSIGDENAAYSSVLYKDDKLYCLHEINTNEVYSLVFARLVGELRIIKSVLQSWKNWDS
HLSSICTPADPAASSSERGCGPAVTTVGLVGFLSGNASQNVWEDAYRCVNASTANAERVP
NGLKFAGVGGGALWPVSQQGQNQRYRFANHAFTLVASVTIHEVPSVASPLLGASLDSSGG
KKLLGLSYDKKHQWQPIYGSTPVTPTGSWETGKRYHVVLTMANKIGSVYIDGEPLEGSGQ
TVVPDGRTPDISHFYVGGYKRSDMPTISHVTVNNVLLYNRQLNAEEIRTLFLSQDLI
>TCRU_6032 isoleucyl-tRNA synthetase, putative
GKRASLARRTVIHSRVPSIGPSSASLSSLGGTTNHGELSKCFSSSKAAKGTTEGKMSGNK
SVSGGGPLENFDEELNFSKMEEEVLQHWERVDAFRETLKQSKGKKPYNFYDGPPFATGLP
HYGHLLAGTIKDIVCRYAHQTGHHVERRFGWDCHGLPIEFEIDKTLGIKSSHDVKAYGIA
KYNDTCKNIVMRYSEEWRRTVNRMGRWIDFDNDYKTMYLSYMESVWWVFKELWNKNLVYR
GFKVMPFSTGCTTPLSNFEANSNYKDVSDPSVMVTFQTRDDPNTYLIAWTTTPWTLPSNL
ALCVHPNLDYVKVLDTKTKRHYIVGELRLGEVFPSKKKGAHKGDEAPPYVIVTRMKGTEL

VGTKYEPLFPYFKSTYGETAFRVISDTYVTTDSGTCVVHQAPGFGEEDYRICISNGILKK
EEVLCPVDENGVFHPDVTDFSGRYVKEADSDILKHLESRGLVHSKGSVVHSYPFCWRSEL
PLIYKAVDCWFVNVESLRDRLLAANDKTNWVPEFVKTRRFSNWLADAKDWNLSRNRYWGT
PLPIWHSEDWEEMVCVGSVRELEELSGVTGITDIHRQFVDNITIPSKRPGMPPLRRVEEV
FDCWFESGSMPYAQSHYPFENQKDFETHRFPADFVAEGLDQTRGWFYTLLVLGVALFDVS
PFKNVVVNGLILSEDGKKMSKRLKNYPEPNIIIDTYGADALRMYMINSPVVRAEPLRFRE
QGVRGIVKDVLLPLFHATKFFIANANYCVLSGGTVSLDVVSTNEMDRWILASTQTLQQYV
RREMERYHLYNVIPGVFRFVVDLSNWYVRMNRRRMKNAVDQEDRSQALSTMLTVLFSVSR
ILSPIVPFVAEMLYQRIKPLLPTSEQVDSVHYLMFPEDDKGKHDELLERAMTRMITIVDL
ARVLRDRMVISMKRPVRQVIIVHPDQSYLDDVRKVAEYIKDEINTFDVVLSSGEEYVSTH
LDANMEALGKLYRKDAPQIRKAIQQLTPEEVARFIQSGKMEVCGKLITVDDVKVVRKIKD
GFTDFESNTDNDVVVLLDKREEQALVDSWRAREFVNRVQQLRKKVKLVVTDMVDVYFESE
DVELTNSILNCAEQVNKTIRGKWETMDKLPADAKFVAEEDNSISGVGIKIVFTEVSA
>TCRU_6033 Nuclease-related domain containing protein, putative
VANVLYWLPTALMTLVTCVTIFIAVGLAQGFFRNSLLSLSWRNILFFTAMSSRQKQLLAS
MQAEELVEAALRSAGWKHVFLRRRVPVQRLGHNREIDVVAVGPVVLVVEVKHWRGQVWSN
GSRWFQLPDNSKRALEFEDILEDNLVKAAALRRFIENDRRIPLSDHHMTGNHRSPTEEGD
ITQDKSRGHGTWYTDRRVHKQCGEFFLPVVVFTNPAVVLDPSTVKQKERVFNLASFQLFA
EQLMQEMRGPWCVVEGLGGRLAQRLRSILLGSVQRPSAISIHVEERVAAAVETMRTWDMI
YLHSGRLIHGDVTELHLPSIKLWIERKHILDVEVWWFDGFIGLLRGLWEGSGGMVRVRFD
AAQRLLMRRDEIAIPIAPRNLKHMTANDRLVVKTAGSRVTVTVALADVCRLRFSHHME
>TCRU_6034 emp24/gp25L/p24 family/GOLD, putative
VYIRLFPGKELCFNYEGYRDPEDDPPTVDIRHRGIDPRNVNIRTRLYAPSGAQVTLDERI
DSFGSPSSLFFKVTETGTYRFCMRTPLSQPSLRFEMRFLGEKDLIDPITTAEGMPAVDKP
VDAKDYEARLNMLDICVQVALDEVRIIENRLHMFDEVTQSTYYITVGMLFLNVILSIVLT
VWSEKYLERYFTKKKIV*
>TCRU_6035 adiponectin receptor protein 1
CGRCVLPFYNRDDVCVPEYIKGNPYIFTGYRARYTTSMCFRSLFALHNETINVWSHGVGL
ILFGVLSIVVFDALLFTHAEFAHYFIYGTFCFACMMCMGCSSIYHLFLGHENSLLSSLME
QLDYYGISVLIVASFLPPLYIGFYCEPLFQVLYMGCACVFGGLCLAMAALPSLRDAKFHW
LRIMTYVATVICGLVPTVHYVFSTPHNTETMQTFVGVFLMFLFYGMGVLFYCLRIPERFY
PGEFDFFLNSHQIWHVFVLVAACVHFFTCISIYQKWVLSRGAC*
>TCRU_6036 50S ribosomal protein L17, putative
PKFRERSPFHRQQIARRMVTEMIRKDYCIVGGARAPVLRILADHVVDLAKAGDTDSRQHL
AYFLHDPLMVDKAFDEYPRRFKDMYGKYAMMTRLKSRRRTDGVAMYFVEYKNRDMSDNHK
GEDYTTGPERFFLPPRIVETEKGIQRPPHMQMAFDRWASKFKTEEFHHWWRLRHAKMRFW
GVRNVPHPSDVDPLWTEKEEEEWHNEMLANTGDFEDLDLEDDNFSATGEGGEPSADDGAA
PE
>TCRU_6037 pyridoxal phosphate containing glycine decarboxylase,
putative
FVRRTATNSYVNRHIAPSAAESISMPRIIGKEILSDRMTAVIPENILRSPLKEVPAMSEQ
DALSLLHSLGSRNKVLKSMIGQGYYESITPPVILRNVIENPAWYTPYTPYQAEISQGRLE
SLLNFQSMIIDLTAMNLANASLLDQATACAEAMYLAFHHGRKERMTFFVSRDVFPSCVEM
VKTRAEPLKIKVVVGDPNLIDWSDSSLCGILVQTPDAMGMLHDFTTLFEKAKQHGVVSCC
GTDLMASVLLKPPGEMGADVVLGSAQRFGAPLGFGGPHAAFFAVKEEFKRLIPGRVIGIS
KDSTGCPAIRMALQTREQHIKKERATSNICTSQALLANAAAFYAIYHGSEGLKEIASEMH
SKAKILSVGLESVGHTVVNGTFFDTITVNLKGITPEDYATCCVEKGINIFVDYSHGTVSI
SVDEATTEGHVVSLLEAAGLKLPVIGVLSKLAEQKRAMPLQMLRKSVFLGHSIFQKYKSE
TELMRYIHRLHRKDYGLTHGCVPLGSCTMKLNPAAAMLSLSWSEFTNLHPLAPKEQTRGY
SALCLDLEQKIRDITALDAVSLQPNSGAQGEYAGLRVVRSYHNSKKESHRNVCLIPESAH
GTNFASALLAGMVIVKIKCLANGRIDMKDLENSCQKHTKNLSCIMITYPSTYGLFDREIL
AITSMVHYHGGQCYIDGANMNAMVGYTAPGCIGGDVCQINLHKTFSIPHGGGGPGMGPIA
VRQHLASFLPDSVFIQNVGGSQPFGQVSQAAYGSASILPVSYLLMLMLGSRGLKTCTEYA
ILNANYLKKRLDGHYPVLFLGENDFCAHEFIIDLRPFKKTAQIEAEDVAKRLMDYGLHSP

TLAFPVAGTLMIEPTESESKRELDRLADALISIRTEIASIEKGEQSTTNNVLKNAPHTAK
CVTSDDWDRPYTRKTAAFPSSHSYTEKFWPSVGRIDGTYGDRNLMCSC
>TCRU_6038 phytoene synthase, putative
GGGMRLPQDDGISEGLLGFTEYGGSISAFMKPAGERQAAHDDKSEGTSLPCGKEGPFIQT
IKAQHMADIALGGKLPSPREFQVGPIMRNEEPQPSLQSPTTKSSSSLPRRISTPPRKMKD
KKASAAPKGQAGTPVGATAAEGGASAKEELRAREAEDYYRSVPRNALSKEEMWKRITAAS
ADKAERFSSALQASEVDYLKMEEDLKENDLFHYRMGELAYPDADIRRNYYAMWQLATSLN
KARWTMLDVISQRGVKTTGAGMKLLFWKESVNQIVEKRQMAAGQFTDSHPVLRPFAAVVE
QNPHLTKAFIRGFTDARLRVLQQPGNMKQLFDHFDRYYGYFFNSLLEVTHVKDSTAEHML
QHIGRAIGLTQHCVMLWKKYANIGFTMLPADLCADNHVNIALLKNISLASRDRAVRKLLY
DVMCITKMEMLHAKQLAPSCSPTAWPVVMECVYANYYLGFLQRRDFNVSAMFADHNIENA
GFAWYRVKKRWEWERHRSIERLVAEEAPLPFIGISLGHRGSSYKMASGIGR
>TCRU_6039 Biotin--acetyl-CoA-carboxylase ligase, putative
PNIHHVGEVTSTMDAARQMLTAANGVPFAVLAESQVRGRGTGERVWISPKGNMYFTLCIP
EKNVTPEITPVLPLLTGLVCRAAIMSVIKGAVLHVKWPNDIIYAGKKIGGSLVESEGESL
IIGIGMNVELAPPVTDSGRASTTVNEIAAALGQPKVTPAQLAELVWKHFFQMISDTALTR
KILVSRFDAAMDKSLSLHRRTPTGRDPEELRALRLNEWGHLIVSRPDGTEETLMAEYLF*
>TCRU_6040 hypothetical protein, conserved
MLRRTLWNGMKPYLHAFSPGARASEKGMLYRNNNMNAHARVASIQQAQRTHREGKIFLML
LVPDQIFLSATLVGVTLVVVFMYFRQQPFSFNTNKQRWILGALNEHEFYQRNREMSLVLE
AHKSAIEGTREVIGKKPAVFDPPGGGLYVSRSGEFSPQ
>TCRU_6041 aspartate carbamoyltransferase, putative
MLELPPVASLKGKSITSAEQFSRADIYALIHLAGAMQRKIDAGEVLNLLQGRIMTPLFFE
DSSRTFSSFCAAMIRLGGSVVNFKVEASSISKGETLADTIRTLDSYSDVLVMRHPRQDAI
EEALSVAQHPILNAGNGSGEHPTQALLDTLTIHSELGSVDGITIALIGDLKMGRTVHSLL
KLLVRNFSIKCVFLVAPDALQMPKDVLESLQHEIATKGVIIHRAHALTDEVMQTSDVLYT
TRLQKERFMASTSDDAAALQSFAAAKADI
>TCRU_6042 dihydroorotate oxidase
LNLLDHVFANPFMNAAGVLCSTEEDLRCMTASSSGALVSKSCTSAPRDGNPEPRYMAVPL
GSINSMGLPNLGFDFYLKYASDLHDYSKKPLFLSISGLSVEENVAMVRRLAPVAQEKGVL
LELNLSCPNVPGKPQVAYDFEAMRTYLQQVSLAYGLPFGVKMPPYFDIAHFDTAAAVLNE
FPLVKFVTCVNSVGNGLVIDAESESVVIKPKQGFGGLAGKYIFPTALANVNAFYRRCPDK
LVFGCGGVYSGEDAFLHILAGASMVQVGTALQEEGPGIFTRLEDELLEIMARKGYKTLEE
FRGRVKTIE*
>TCRU_6043 Met-10+ like-protein, putative
RVEASVELMALRVKPVHLLGEVLKALRGCLYDMRGVRNVMDAPQPTSDPGEAHKLLLLDP
QVIPPPSPAAKNASTAPTQPLWVEANHASVPPVVRERLQSFLLGKRSVAQSLRVAVAQHI
VRLSHRNFTMPELLQRILPPGTIPLSGFEQVGHIAHVNLSAAHLPYRADIGAVILDCNPT
VRVVVNKVDNIASVFREFKMEVIARRTTHSDMKGSPAEENSGDEEKLHRLLLATVRQHGC
IFRVPYDRVYWNSRLSHEHARVVGMMQSGDMLYDAMAGVGPFAIPAAVAGVKTYANDLNP
VAAEYLRINAELNHINKDTFHVFNMDGHEFLNTVLYRDVVSGAAVCGRRHVTMNLPAMAV
EFLDVFTKPPWSQPLVSLSLLEEKEKAKEGKEKEEHVEMHPDKRVLFHVYCFSKNMDDFL
GDAVKQVERWLAFSLAGENLEAVHMVRDVAPLKRMVCVSFTLPEAFWLHREAKGMSPLKR
AR
>TCRU_6044 proteasome 26S non-ATPase subunit 9, putative
REELLRLDEQRAAVMRQIEEAMAFLNTTPVGLNGPLVDGEGFPRNDCDLYAVRRARQAVI
CGRNDLKALENSMHEKLALLHEENQEEATKQMERDNEARRKGKSDALQREQRMRLVREMS
KKSPFVRVLTTSANSPGAQAGLTAGDLIVQYGEIDAATVAAKGFGEMARVTASHEGKMIS
VWLKRKGEAEDEAVEILLVPTRWAGSGLI
>TCRU_6045 elongation of very long chain fatty acids protein,
putative
DATECYLKNSLCFYPSLNIFVSWSVLIGAHVGYIVLVIILRKWMQRRAALNMNKIMMIYN
VTQIYISAIMAISLAPHLKKGLFNLNGRFSANIEFWIFVHYCSKFLDMFDTVLMIFRKKN
EQLSFLHIYHHATIGFIWGLLLRNGIGNGTAFFGAWVNSAVHFLMYSHYLWTSLGFRNPL

KSILTKIQMFQFFLCIVQASLAPFFDNQFALQWSFLQLTYHITLFILFLDFHRKS
>TCRU_6046 retrotransposon hot spot protein, RHS3, putative
KKYIRDAGVLGEMQASDRYKRMERAVRDEMDMVEDVHKLYKNGMYYLLNWLAASAEVKAS
VHAVTKRFLDAAAEEARKTKKSSAPRYLEGCYESVYNARWHHVVEIPGGEGTGMEVREGE
PPQSWNYKAVGDTLEKDDGVQQSGAARPRLMVLTSDKGWPYSWKWKENKSTHDCYVNCEV
ERVWQIVKGDLTELLSTHGRTDFEPNWRLLIGTPGIGKSMNAGSYLLYQLLHCDVEKLQV
VAYSFGGSTMYVFDKTIKTVTKYVGRGASRNALYDLRALEMKGYVIYDVTEKGKPASWLA
PCNEWGMIVVASPKVGNYDKWETQVRAERIIVNCPDEMDMKAMCAWMKRGLDPDKQAEYW
KEVKERMEKLGPILRYIFDANKFIAHSAAIEDALDGINSLDGEKHFTHGGVRLWYSENPS
QKLVRVARARGEVGAEVFLNAPISLCLGRRIPHYFVKSDE*EGYIYIPVAIIGKRNTLLS
ECMGGLGLRAFVLVELVAALVEDLKELRPPARRGGQHAVLKADPKGTPPSLMWSVAMKYH
TNTNIKHRLLCIPAVENFPLEDPFFFVKLPRKTLVGLRMTTTGEHHTTTSTVRQFTERLA
AYFNGWEELSRDMSWEIIYVQHADSTPMNDWQRCDVVNSNNVSDDKGREIAGLWREKVRQ
YQV
>TCRU_6047 MSP-B, putative
LTASAPEWAPIRFQFFTEDLKDPSRYCTVEGQIRPDFTGGTLECNREDILTKEKKSIILK
SLVPRALKIHTDRLLVEPLTGRVIVPEFLSGACAQFTIPSSHRTVGVFGADMYLYVAAAP
IKASALAWATTCLKLPDGRPVFGVVNYGPSSVTDSEDGVRVVVHEIAHALGFAVGIMRKL
NMLKEVKGVRGKAKVPQVSSPKTAEKTREHFNCVSATSVELEDEGGEGTALSHWKRRNAK
DELMAGHSGIGYYTSLTMAALEDTGLYKANWGMEEPMSWGNNSGCALLKEKSVMNGVTKY
PEMFCTAETTLISCTSDRLELGHCTIELCDAPLPPQYQYFS
>TCRU_6048 Glycerophosphoryl diester phosphodiesterase family,
putative
IVLHVFGLRAEIISAEFVRFSMPRPRGKCPYLTPQFIREGEQEQQRYIPPSVDQLRLALV
SDAEEMGEWGTTAPLLLEKTRPSLSGNEMRNGNDVNDNLLYFTASVQVPASSVKEHTLRF
RLVIVDEPLLSAIAAMSTTATSSSGMGLCVAKGIRPGAAIVAVENAYWQPETVTLVPSDS
HDGKTWHAYIDLRDRVVHFSRASKQFPFLSQLCKADKTNCAPKAGPLLSLTLYANDPRTR
FERKAWLESLPPQLRDAMMYLENEHRRQLNEDNTSGGEPLSPSTSFEVEDIYPVRCDGSC
WCEGHLPTPAPMEKQNKFLKQATKRRQRRKEPENGNEVLLHSPHRHIPCREPMKLESSPV
EAVADYASRNCLQCKRQLSLSSENTSSFREDAITAVMRRGWCVEPLHSSDPVRPFSPGDP
QFTMRVWHSTVNVAPLKERGLQIEAMMPIPIYDTNRRKDSMISNKVAFSLTPTDSSSTIL
FSESHQYDNTNDGERVEWSASHNSNETSNFTPSGYSTTVVGVRWVKGVAVLQPPLFKHHT
SGTLAIPLCFMEITEAGGSPVAHWHTIYVQYLFVFPFHYQQRCTLEVVRSLSSLGRLATK
KLVGHRGLGKTYTRSIPIEASDETSSSSTATKRMKPNRLTVKLAENSLESINAAHRRGCD
MVEFDVMLTRDRIPVIFHDPLIQLQASKKRGAGTRNGRVERKVSSGLPPLDFGCSPVFMD
NLPLNPQIQLSAHSPAFLAPASPSFATFSERRPSQLLQLCMHSLPNFTSVPIALHQLTKR
QLDVVTTETFTHMKDTNTLRNLILRHWNQILRVYRNRTRRKYLQIHKIRPPEGEDEFSGC
LPNELDASCHEHQKDDEYNKFLHHRQRILAQQEDVTNHICTLEDLFEGTPASLRFDLEVK
FPFQPIGDKNLFFQIDAFEVNAFVDDILRVVFAYADQRQSVQDERGCVTDRPRDVIFSSF
EPDICLALKMKQSRFDVVFLCDTEMSEDFKDYRCFGLVEGALQFSVFMHLSGVSILAASL
CTKEQMKIPSTRSVSRLPRQPTSLEVEIQQRPASKKHNGHSNGNYDPYTNTHTIDDVPDG
RSSLVQREAEWASFDCSRGKAIAAYAHAHKQLIWTWGEMNNDGQFTYVQSKVFKIDAIIT
DNVPLWTS
>TCRU_6049 hypothetical protein, conserved
NRNVVLVIAFCFVDGACFSVWIAQLFPVFVHRIEGDEAVGWSAAASGMAQIAGAAFAGYV
GDKIPRKECIRIAAFCGVVAVAATLVAINLMVMPAIYITQAVWGVYLGVASTSIEALFAD
SVLSGHRAFIYNFKWIVQTVCYCVGYVVALVMLLQMGNDWSMDSIKFVMTVGLAAHPLAH
FILLFMRDEDALQHGEADAYFIATVKVGKEQKHTEEKDRKTVALSDLPEAPLLNEGYVAD
EDSKAATISIWRGGPHNLKPQHAREIKPPLEQRETEKETEESNGIYDGSRHVDEEETGAN
CFNCFCSSCHCSLSAVPYLVCMADFWMAVGSGMTVQYMTLFLVNDLHMAPTWLMSSYIAI
SFGAALCSTVLRYVGDHYVGRLPAVITVRLIGTTLLLLLALLDGPKTGLGAVIALVITRN
ALMNCTIGVSRSVIMDCVPKSSRAKWSAFESFASFTWAGSAVIGGYIAGAKGYQFTFFIT
SMLHYVGICVLVPAAIVSQNMERAKRARWR
>TCRU_6050 exonuclease, putative

MRRSILWRAYPMKTMQNLTHLEVFTQLQLGIHPPLSVQRQFIQQNFEEEMERRGITETKL
MAMEGRLCTRLLRQLLFERYLSVPFRLFTFDLEFSGPPVFGPDGPTEDIIEFGFYSPAKD
TVFSCLVNPTNGRRVSQEVTALTNITQEMLEKEGLPFPEAWEKVMETLMTPEPQELPGAE
NRLLVLSHGGKLADVSLIKWTLEAHGLELPTALVFGDTFHFIRDAHRRRPVTPDKHPPSW
ALADLVQWLKIPPTLPAHRAGNDAKMTWDALYHTLERYGDEDLTPREQLVSRFFDEEARE
VMGQKNKRHFIESDGTLATENAKTEASMGLSLDLDFDEIFSPGGKRK
>TCRU_6051 hypothetical protein, conserved
MTGKGGTILVSDLPMMYPSDLLRFEREGGVWGRQWQVRRKQLTFAVATATFSTVLGSYYV
VSRCNTGFVLFSTFSGFTVLGFCVGSALSSAFYPNVASNRETSMMRRVWWAKECAKNWDY
SQVNEGIWKAKYPHVPVPRK
>TCRU_6052 RNA-binding protein, putative
YTIQVRGLPEDTREDAVRDFFSRVGDVTHCTLERNAATLSFENEEDFNEALNMDGMEFEN
GAFIQVEKKRHENDSYHGRSDNNMDDNQKNGATDGERGGDGRDASPRDNRKRFREEFKVA
VRNIAENTTEQQLRELFEPLGTIADLFLEPRRRYAFVGFDNTDSLEAALQMTGRELNGVA
IEVEKKRTGPRENVLPTKVVVKGMPPNTNEDDLRAFFLSAGEPVDVFIHEKKHFAFVGFP
NEETCVAALRLHGTELNGSRVDVERRQRQRCFKCDREGHVALQCRAVEPYCRNCGRNGHL
SRDCRSGPRDNRRNQNDRREFVRRDYNDRRDYGDRRDYNDRRDYGDRREFVDRRDFNDRR
DVDRREDRRRARSRSDSYERHRRRHSHSRSRSPKRFARERDRDRDRSRSRSPPRRRY*KR
VREKKGPHTR
>TCRU_6053 esterase, putative
MQYALLLGDSLTQQGYESGWASRLSKRYVRRADVINRGLSGYNTRWVLDILKDDTRRQQL
LPTQPGKALFVTLMLGSNDCAGFPQHVSLDEYGANLRAIIDTVRKHVCPVGGIFLLSPPP
LDEKGRLQWLRDVGCDPNSCGRSFESMRRYRDASLRVGAEEYEEHGDVFTVDLYRVFLGR
SADTVPYAEGSWCEYFSDGLHFNENGGRVVFEALWCAIEKSVKASHILPDRLPYVLPPHE
TLV
>TCRU_6054 protein associated with differentiation 3, putative
VEVLATGPQKAIYEPHRFAILLLGSYGCICSSLSYAFNLIAPEMQSRYDLTGRDISTIST
VGLVVGYFLMPYGFIFDHFGPKPIFILSMVLFPLGALLFALSFRGTIEGSVVRLSVFNAI
LTLGCTLYDVVYMMTIMSHFPNSKGPVVAILKSYIGLGSAIVGSIQLAFFDGRPDHYFYF
LMVLFFVTGAAGFFLVPLPSYHLTGYEEKHLGIEEKERRLARKSVYLRQQPPTIRFAIGI
AFVVLLVIYLPLQSALVAYLGWGRTQRIIFASILIAVLVALPLMALPVSCLERRETQREE
GDCGGTERPSAGDEVANEPAAAGGPPKKVETDVDYIAPQYQTTFLQNLKTLKLWAFLWSI
FSMGGTTFVIIYNASFIYAALADEEVDNAIKTLLTVLNGVGSAAGRLLMSYFXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLPYVLAALGNGFGSAAIVLVTRTVFA
KDPAKHYNFIFLASVCSTIFLNRLLYGEWYTREAEKQGGSVCLGRNCVMMPLIFLMVLSF
TGILSAAYFDWDYRRFSRLVLEERRRLKE
>TCRU_6055 translation initiation factor eIF2B delta subunit,
putative
SASTMADSALMGQENDDAKEVVRQQRTLKRKKDGLRKLDKKMRSVKADSPEYSALVEESK
ALAAEVAAMEATLGVSTVVVRDASTAPPDAPTISGGAPAEKTSATGLAQSAASARSPSGA
VSHAKVRSGVGPSQENQRSEPKDASAKTGTEGERTATRAKKLQSQPNTSSPANKRTSDAV
DVVQPGESVIESTLSGTQFPLFPEMPFQPPCSSELVHYQVAELALMMESMVIVGGNARTL
AMIQAFKSLLQTTPVLSGPSLRDVNSKVFEELIDENFNFLRRGREPSTGMTYVKEVLVRR
VAALLSSGGDFRVSEDGSFIPLEKEKKQGVLEVTESPLTLSSDMENSLLAGDPREVSLKV
LAGIEKELRLSIKSIVEDRSIPLISSNDTIMVFGRSSTVELILLGAANNPRLGVKPRVIV
VDAAPLYEGRALAKRLTTSGLSVTYGLITSCCTLMPHCTRVFIGAAAVLQNGDVFSRCGT
AVVVASAKQYRKPVLCFSESFKFISEVWLGNLGQNTQLQFSQSLPGDHRIRSPGGMSPPR
HQNREINEQPFGRSNDGLPMQSSASSASGYLYDLTPAAFIDMIICEMGCLDTSAIVAALR
DREDRDACLMSVA*
>TCRU_6056 glycosyl hydrolase, putative
RLICEPWEFIETALPQGENIPISESLFSVSNGHVRVRGYAEGANMAAPYGRHANNEHTVG
RRSSNRAEPTTLGVKAQTPEEEARGTFVNGIYEERLLSRSHRVFTVGTCARECFLICVPD
AFCVDVFVGSEHVSVSTGTILSHRRVLDLCTGELRRRLVWQSKNHGREVTIEASRFVSLA
RKNIAALKLSVSVKNVLNTDIRIVSRTMVPVNAQRHLKVENIVSRHTLIDASSAVCVRTR

NSCKRLVVAATEACCTATTDHNSPPLATFSNIGGASPTGVTPAESSVTSGGRGGTSPPSA
AAA*STTTTTTTATAAATTQQQQQQQQQQKQAVTFLASKSAETMESAETIYTSVISESTR
LELTKYIAFLGDEDATPEDMCDLAIHNSREAAGVTYDAMVSENRNILAKFWEVADLRVKT
NNPFVQGALRFNLLHLYMSLCRAYVKESPPRGLMSETSNGLHHWDVDAIAIPFFSHIDPK
TARAFLQFRIDTLPQARNIAADMDLPRGALYPLRTVGGGENRPLPFCAAFLYGNAVVAYA
MRRYIMATKDTALLLCGGADVLFSTVLIWLIWGTWDKGQFHIRSVGGFDEYSGLSDNNLF
TNLMAQNHMQWAVQVASHFQKKHPQEWETLKERCQFTDEDLLMIERAASKMVILFDAKNR
VHPVDQFFMRKKKWEFGDLKATKGFLIHTFDPSVIYRHQVCRAPDVVLASMLLPEKFTTD
EVRANYNFYEPITTNDSPLSSVMFTVMASQLGMIDRAMYHFNRTIFVDIENVIDSTGRGL
HSVAAAAGSWWCLAAGFGGMRVIQGVLHFNPVLPDEWEEYEFAVRHHGCLVCIIVRRRTV
TYEVVECTSDANELLIIHSDTHRIHLGLGVPQSVRLYRDIHVFDFDCVIFDMDSVIEDVE
DYHYEAWKKTLEPFLRENGMHSFKFTGELYLAYLKHDRPIPALQRFLIKQGVKELSLGTS
EDNMECDTVYGIFRRKQYYFRKCVTYRGLRPREGILEILSELRQSGISVGCVTVSKNGHW
MLNEASQVLMLLDGCLDGGDGESMSLRWRPEMDYFSAMCRQLNASTSRTIIVMDGIDGFS
KSALEQFKMIVDIQKVPEDVTLAIPRVNISSLSDLTLALLD
>TCRU_6057 DNA-(apurinic or apyrimidinic site) lyase, putative
MFIISWNVAGWSSTSRMIREDFGSIASFLQRTQADIVCLQEVKGSWAKLEADPCGMGASD
GGRTLAIDGWESFWSFSGKAHRGFNGVVSFVRKDLTWWCDSRPFSEEDLNDEGRVIVTCH
SAFVVVNTYVVNARHGQRMAFKMRFLSSLKNLLTQLKKQTGKPVILLGDLNQTYRAEDAC
WSLRRLSLPALRNLVHVCQAGGEEAEKTWAQQFPWLPMPTLQRLQGIITEQVSCMLLAGD
DNEGVVDSNKSISVDSAVLDETRNDTEDGKNGNTGAHKSLTLLKQLIRERREQRRRNGSS
DPLATLEELCRAGLQDVPVESFMRRQPSTHNRELFALTQYCGLPPHEDVGVQFMKRLLDE
LHLCDTLLVTSSSAENKAERQEGGEASMRVVCPYTCWDQSRNRRQRNEGTRIDYILIDEM
LLPALVPCGMTENNVGVFSPMMGEANSLFAAKKEASSAFFDEFDGRSALVGARRAMADGM
YPAAPLDGSGLPPLSTEARDVQFRGLPSTGLFVTPPQYSDHSGVCAHFDGISLAPRPGKL
EERHRCQYRPPVSLHAFFAKRLRDE
>TCRU_6058 rhodanese-like domain containing protein, putative
EERESPEDLASEVKATRNESQLMAADMQQPGSEHRAEAGRRDWTEPSLEELDRSIPQVDC
AFIANLIRARTERRKEFLHKKAKVKAKVVSLSKRQASSVLEAARFPILGFNGSGSSSNNS
NNVGGDGITAMNNGSGVDDEYSSFAASPAVLSQLTDDERDVFLSSRPEYDDGFVLLDCRT
VNEVTSWGMIEGAKLLPAHEMFEGFHLTPEEFEVEFGFAKPRPEQKIICYCQYGPRALMA
AQILSWMGYTNVLHFRDGYYEWGKQYNLLLRRWMLHDKESGNEIKRQVAFQAGLELQREI
APEFNALPMQEAARYKIDTTRSRGKILVGDGVREEACKQVAELVSGMQPPLLPGVLDDAD
RAAGQTDGGAVGKREEHLQRFLQQTTGLDSREDTRPSMSVAEAQQKVMDAFTRRD
>TCRU_6059 protein kinase, putative
TTVTFTGWSATEVKMNKTGIFPATVALGRYLVIFGGSAIVPPYIPTSVFLSQYALPTINV
LDMTTGKLVLPLMLVNSEPAAASHKVRRHRDPPPAPPKTVFRVPAQLTFPAVGTKNTVQL
GLAAYIVGFCTMIPRNVIVEDDDEFHAFLRSVQEVRLYQEEFPPVDDVTMDIRNKSLPED
AMLRFNASCVGSGEDIIYIVGGISLEKMAPLASVSQYNVVTGKFIEAGLLLDDPLVAPGV
FEGSSLVFIAGGYRETKTWTSYQPHLTVIDPSLVKTNIGTYDYLWQLNWLSPQIMMYNHT
LAVMGATNDRSFDQQQVWPDLMRLYGAVETVPIRFPPLRSNAAVFSVTTVDGVTVYLVGG
QIPPPDGTGISFDIFTGKMLVDDGHVVVSIIGFHYISLVEDVLEEVEEAAMEMHPTGKWT
DMKGEATSLHGFKAHVRQEDEEAEIEEEQGEKEVVNLHSPMQEDFQGGSTHSLFSSDNTP
TVSPSITPTPPLPPPPAPPTPPPKDLPNNDGHFTVLVNGYEPLWYNFTFNILLSESLAQA
CPGIVNSSKHVVNTDLDEVSSCLLRLSDSPTCNSVLLDIGNLSRVNTQPYVVDIVDPVTN
NISKKKTMAVGPITLVGSLADGILNLTGNGTPYGDPHDSFFFQDSYYHHRRRPRSQPKYD
NDTTKVYYEQVFLYVCFSSGAFVLPQCKSGVKETRWDESKAGRKPCTTAFYKALNAERPF
VLSPVMKWVPSTTTTMAPSPSPNNKLSYGTIATLALFTLIVTILVSFGLFHIVRCCRLRK
FEKGERQHLLLGNDEDEGDENRGVGRGAALPAHQKQSLLDGKYKVLHRLGRGSFSVVYLV
ERVEDGQRFALKYVQCADDVDRQEAMRECEVAYTLQGHPNVIRLVDMFMSYRFDTNLHAG
GARHQQHSEHQLGSLSGSVMICVDEGSDIYPVPPQRGAVAAATSGERYLSLVMAYHEKGD
LGKWIRQQKSEPMIPETTIMSIAFQILTVMQFMHHHDPPIVHRDLKPENILLDSDFACGR
RWKARRGRNGGAEPLRIVITDFGLSRVMDKTFCETGVGSLPYVAPECWQRHYSTKVDIWA
TGCILYAACAKRVESDNVKVMFSECGRPDFKKKLIEELTQVYGYSLALAAFIVYLLEPDP

ARRPSAEEALRLIRKRRKDAVDVNETTVMVSLYKDDGEDEEEEEEKEKEDVDNKNNNNDV
DDGGGVKNNDDSGDGREKSEGEKREISSENNNKSKKGHFSHRQQLRDNSSSKQFLNSTAP
PHDGSGAQTIEKVAPSTMKTHAPLLKDDAYMSESSDHAKTEVHGGGGVMAATRVDYDGSM
RHTAEAVTSRGALQTNSLAHHSQPGSYKEYPPQQKQHFFDTSEVLLREDSATRPSHSSSA
AVKKKELRCRKLEKYFESVAEDSEKCEFFVARESPSLIALSL
>TCRU_6060 predicted WD40 repeat protein
AATTAEVVEGGNGGALMVLPSKKLPGKVGGINDQKRLRGEDAIISVDPKVLKSRITAIST
TVEGSVHDETHVPPPTWKMSKVLVGHRGWVWCAAVDPSNSWFVTGGGDGVVKVWDLTTGA
LKLNLTGHKEAVRAVSLSTLSPYMFSGSDDHSVKCWDLERNEIIRDFHGHKGSVHCVSAH
PSLDIVLGAGRDKTVRVWDIRTRSCVHLLVGHTDSVMSLVVQQANPQVISGGSDGMIYLW
DIASGRAFTRLTRHKKPVRGLAVNRQGTLASCGADNIRVWSLPKGEFLFNASTTATGNSK
GDEEDICYRWSCCAFSPRNVLAVGSQEGRLALYDWEHPRRPPYQLTRTKSIPGTLPGEGG
INSVVFDASGSRMITAESDKSVKVWRAKE*
>TCRU_6061 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatas,
putative
IPLQSSISVDDSFLENSIDFCRFEGAGNPSKGPVLTPPLQLKIVNETGISTNDWNSSTSA
VFLVVSSSPRCGLVARFFCTRLLRYLRWCGESAVFFLSGPNERDIEVQRFEDDVGAWEKY
VESCLEKSLLYLASNPCLGFSAIPVIILLTDCESVDAYDRLHGMLDSRGNFLVRHIWFDE
DWKERASPKGGYINVCLKQPALRMTRSQWSIVCSRAAGYLNSCLPVLHRVYLDEPLVGSP
EETLRSFSPLFFTRHGQSEYNLQDRLGGDPDLTSLGRDDALTIAEFFKRQVVGNSRLFAL
RNAVWDKEEGFEVWCSQLKRTRRTAEPSAQVLTRGELKTFKTLNEIHAGVCEDMTNEEIK
ALYPPISSFRHTDKVGFRYPNGESYQDLMRRLEPILLDLDVTRKCVLVVAHQAVLRTALS
FFDGPAVEEAVHTPCPHRSVWCCTYNRLGEPRLTTITLKPRKKNPEE
>TCRU_6062 mRNA capping methyltransferase, putative
KTSEGRRMAESQRTAASYDEIARRRAGDWKSKESPFRFFNNYVKKSIIQFALDHLKYKEG
CSEVKVLDLASGRGGDVGKWLHCQSPELSFATAKLPRQRLTKAVFLDCYDVSSECIAEAR
KRYEALGSGVTCKCVFTVRDCFSEEFLCGQLPLSENYGKFHVVSIQFAFHYACDTRRRID
MLMAAIAGALASNGVFIATTVDDEVLAERVREKRTESTGLYALHFDSEPVWEGDRLAVGT
KYLFELEGFVDCEEYVVPASYVRERAYYYGLEEVTEYSKTFRSFYEEYKKDSTKNKGFYL
FRGYLELVTLYRTFCFRK
>TCRU_6063 hypothetical protein, conserved
AMYATAATAAGENPLHAVLTEMISGMCGGSVKHRSVTASDGNWRTRQVIRELRGVKSVEV
FFSTEEQIRGVVMSQETRCRVKLLNAFLSGQYLLEEQASVREEEESCRRELTLVALSELH
SEASLLTVVGEEMYDRHSLENACWKGWMNLRRCQNLAFLVLREQISRRFLIKREAMNRVE
AERRRFLAVGREIDMELLSQEFYRTTSMARFKSSKLTLDLALLLAEEERERCSLERIYLL
KLSLMANDQENAAARLVVTSVMRASLMRRKLRDDACWRERSLMLLLVPSKELDIRYMIER
KEMEERQALRVSFLTTWRSVFKRTMNPDEGTVIIERLELYERRCVFDQWRFGFNALNDRQ
ERERCILASREATYDVFYHSVIDSLTSLWKQESVQFNALRKRYSEFVWSTRMIEATMILA
AEEFAARQRIIESEVREAIKLNSSFYIRRCEEAALEGAASIMEMEHKRRISLMQSNIKFV
RDVYFCHLLYEEAWRRIDIESEARTAWSDIVVLQESAPRGCSLGSADRLKEVQRTLLVGD
GHHHFIRHNFTLVIFTEKSNREILEKKELEDRVSAYAAVLGQVEEWNRLELQTEGQHEFL
RILLDAVDHREYVERTILEEFERERREFLFGSFDYSLPHLRACEVDELTARLDIINEAEL
TVGALACSWGMHCHVAYCSEELRLSQCALRFMSSKELFQDREVALVRTVEPMSRREIINR
EISGRLLLLMDAQEQRGRIRIENAATDAYNGAQELFDRVLSRADDWRTRGVLREPVVLTG
REALIDYFRRQEASVAVRLRAQQEKMRELLGVFFADFYWGRDSIVVEEFVGRESIMGTFL
CPHPALRVVGEEPESKLTVRFYSLALMTKDALQSLSIRVHDSLDDVGVTCELLEAQAVTT
AGRFFRVCFPVRVMRWVRPLTEESNVLHFEVRNCEGNLFATASILLRSEELKKTNGATVL
SLPTDDKHGKMNVVL
>TCRU_6064 leucine carboxyl methyltransferase, putative
QMALQQTAYSACSRKVHCVSKHYLDDPFVHFFSRDMTIVNSPLMNRGTWLRTVAIERSVL
SFARNWSADGPLQVISFGSGVDTLYFRLKKDHSEVNIVRYIELDFPDLVAEKQRVIEKTE
RLNQLVGPEYELVPCDLQKPDELREILKRVARNDVPTVLLAEMVFVYLEERTTTAILELT
LNDVLKRDMCVLLIAYDAIRPNDRFGEVMVNSLASSGVPLRGIKELPTPEAHAERCKRVG
LKSVMATSMRQLYLSVPQETQEWLKKLEMVDDWDEWCIMHDHYCFVLATNKAEALPT

>TCRU_6065 pumillo RNA binding protein PUF1, putative
MSSDEEALAAQYARRQELLKQLNEVNSAIRSLEQKISEKTAQNVEKKSMDAATGGDTEME
KLDCLLDRCVRDSNGLRDAMKFVDACKALRENAAEEESSKEKHLFCNRFVHKVIARSPVL
ATDPNGSELIQNTLGLLKNGGSVSPALHSTDYIADRASDLSEILLLLGEIKGHIPRICYD
TNGTRFTQKLFDYVKSVEELEFCAECFSDSIIPLCKDINGSHSVARLLAAARQSNFSDEN
GKVDAATEEKLSGIHKMLYKNFAENCVDVCRNRQGCCIIQKCLQWTPEPYFSMIIDTVLQ
NTLKLVNDPFGNYVVQFILDNEKELSQRGQSGQEATNYTNRTIRQMLHNVASLSCDKFSS
NVIEKCLRTVSSDVRQLLVDELTDPQVLPKLLTDSYANYVIQTAIVTSSVESQFEQLRDS
IMPLQNLLKNSPYGVKVEAKLARRQRASLRKQEHQKEQSRRGTAPSHFPEKNGAENVLTP
QLLPGMHRIPALVGSEPLQQNTVAFSGITEEMTSVMTQPHYMPLMLQGQQALIGLQQGHS
HQPFQVNIMKETAMWGPQHSFTLFQQPKQRK
>TCRU_6066 tRNA pseudouridine synthase D (TruD), putative
MRSTLSWRRRLILGMSIEDARSKFDSPESRVALRLAHERYNQGLYHELTLAQRRRNQLPS
ERRCHLVRHTKPSVKGFQSYIKSCPDDYVVREIWRDDDKETAGPMLDARAAVVAQNSEAA
ISSAEGGSLKKRSKGHDANAEQTPPQEEHVVNSRKEAASDVLNVTPGKEDVVSAPAETLT
PPSLPSHVGLQVTADVQMYKQHRAVVLQELARVANKLGSDARQQLAERRENGTLLAIRQG
SVVDRLVDNVKEAQEKGYTSLSSSSHLLETINLSMNLCSKKDKELIEAFRSPFIFFPAEE
HHISLSLWVAGNLIEHEELGMEFPYHLAKHMESEAGGDGAAPPPTTRLPKASIEIYFSPE
LYQLKQTLGMDGILALRRFIGRAMKRQHDPLPTTPSIVLNMRRDQQEACGICRGEATQVP
WLHLIKAKVSTVTGTVLGISSDEAPTISAMREAIQLVWRIWGHLVKDLRVHGDLDYMYLS
VWPQMETNVDMSQSSITCDERPGKALEGIVHPQDTKQGVPQQKKQQAVNSIRCIGDAVNG
LMEGDSSIWKGFNSRKLQTKSIIVPTDFVVVECTLEKKGLPHRIVVEDVVESLTELQRQA
MEMQRIAIVQARDAEEKVEPQTDAGSGGLRPVLYAPKVFVSHAGVIDAAAHSFQRIRIRG
SCIAHVESLARALETGEHFTEREGLEPMYDNNPGSLISARNMHDAENASLLLPPNLSFCP
RHHVNSTHATDSQLLGHRVPSNYSAQRAASGQFHRYQTLRPLQSMVVDKEEREFWGTHYY
RLSDIRLVFHDRVSTADVENPKGWSPSLKERLLAISQSRNNKQSPQEGDEKMDAAGTDSV
EDAEDTTARGKKSRKKKSKTKRAPSVTLDEVAAKMSPEKLFEFLCVDMEVESASYDFRVG
DNDGYAYRVRLRCIPQNHIPLVKPAMQSLEEKGFINYFGPQRFASYTKQNMHPGLHLLKG
EFRAAANIIVQQFYMDSDIAAEKRRRGAGFFKMYHSKAMGFRIPDHIKLDARRRSIAEHG
TALQSILDSALQAAALLGEDEEKGSSIDPCEEAFLRVVGPNACLMLVHEFLAFVWNDIVN
QRFQRYGTFAVLPGDLVRRNPLASPHSKEYQNVVFASKSGIDKGKYTFSDVVLPLPGVGI
RLPENHTTDLYIVTLQRMGILFNPESKQWDIFRPRRSFNGESSGQRVAGISSPYHRFSSS
FALMEEELGNNTTI
>TCRU_6067 protein kinase, putative
ENPRKYDARRRMATIKECEQMVANMCGTLSFHTTRFPLSLNTLSIELPLLPVPWVEEEED
KENVDPPITTHPFTVIVADRDAKQRNILCRLMWSRRHAVVPVTSLREAMINVEAGGADVL
VIDPLYLEATEEEYAAFRDGTAPFEALRQQTQLVVVLYADDFNDWRVKKLMGYSHVIELP
KPASGALLHLAMHEAERLVMCMREDEEKIALLRMAFTEFQPDRHKLGRLLGRGAYGEVFE
VEDLLTGGKLAVKRMYLEDGVLADDAIQELVATTSLRHENIIHYFYCQKESDTQLRLYME
LASGGTLRDKIRRQGGPLPLEEIVRHLKDLCRGLAYLHSKNYVHRDIKTANALIDHHGRT
KIGDFGTAKCLKRSSEKLYTVAGTPQFMAPEVMNADSTKGIGYNQKADIWSLGCVALELA
TGKSPFSYLNFTSGMGIFVYVSKLTDTPDLSVIKDENPLLYAFIESCLCIDPDKRPTAQE
LIHHELLQEAEHGSRNKQLARRVEMVEKLKRYAAIDAEGEEDEEEEEEEEDEVND
>TCRU_6068 40S ribosomal protein S15, putative
NITQERYEQLKKERTFHKFTYRGLEIDPLLALSEEEFKTLVHARARRHMNRHANRRAPVL
LKRLREAKKDVKAGEKPRAVKTHLRDVVITPEMVGSVVGIYNGRQFNAVEIKGEMIGHYL
GEFSMTYKPVIHGRPGVGATHSSRFIPLK*
>TCRU_6069 N-acetyltransferase, putative
MPKKTGKKGGYDVSDETLDALVEAIEGDSNLNLQKSSKKGMTKKQALALSEKKVDDVICK
IKGTKNGMTFNEEQLRMALFAQRMMQEKAIRDAQYLNVVVPLKEDQIKWQEVAPKRYIRY
EQFDGSQNAMEFVVGLFTKELTEPYSSFTYEYFVFGWPDLTVIAYGIESETFPDSSVKGE
RVGAVVSRVTRKGPGRPLRGYVAMFAVVPEFRGFRLGGRLVALTINLMREKGCEEVYLET
PLMNERALSLYLGLGFVKTKFLPRYYLDQSDAVRLKLWLND
>TCRU_6070 hypothetical protein, conserved

MQRDVYASLIKKRHKHMIPLLIHQVSGDVTRENVFDEVFSGYKLRRIVLMTHMAATSSLS
SRLPRDVIVTDFEKLKAIHQPHFHYKLLPLLCTDIEAFAAMQGICASANSPFTIEDRRDP
QGLTHRLANGCADRQAVCEFFAEHISPEERDVPVFSRKLPISAVVFDGLLLSRKANDVGA
RVAALLTVHETATGKTITERALMRDFFSSPLYTKMCGNSDVGQAVRLAHQRLHFMAVKRP
VGTDDGCRRTLLRLASEKNLFVFEKLADEYHFAH
>TCRU_6071 AATF protein, putative
SLSGRRKKMSISDIVNEQIGGGDAERYEVDAWDEFGGDNPKIDDYHEGDEHDDDDDVVGS
VKRRSGTERRLREPTSRPQQERKQLRRRGPLDASLSTGAYAATPVDVEAAMDDIFGALEM
NDGDEDEMNFLDFYKDGAGGDKINEDDESSAAVASTAIKDNSLGKKRKRVGGKPETEEAY
IAWLEAQQAKKRARRHDIAGGDEDGILEQLESLRNAQMEVVAKEVQEGEDDSEDPRAKQR
RRAQAALRHYVMVYSQLLRVRIKLQPSIARAVAFPQYYSLPDYLNSDEAQIRQGTEEVVR
RLRELXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXVLLSFKDINTSHRRM
MRDVDACVEYWGAKLVQPNSAKLRTVSQPLLQQIHSVLKSKTRLRTKVQKNRSHVTILGH
PEHYKMSQTAEGKAARALHISEGDMDEEIYDDAEFLREVVKRGGVAKLEQQLQEIQRSLK
SNDVPAKRGFHRLTKGKAVCYEPRPKLVGFLLPVPYVLSGQHEVMVKSLFQ*
>TCRU_6072 conserved protein, unknown function
GRNIGKREPQLRRLAVVRPDLVDEWVPELNDADVSSVPCTSQMSVWWRCTACGENYQASV
RDRAVADKGCPRCSLLHQPQSPQHTNGSENGAVGDATTSSGGLPSLAETHPLLASRWDYE
KNGLLRPTDVTSTSELNVWWRPAEGRPAHEPSFRRPVYAFVEVPYSKEEQKESLAKMELD
ILQQVRQAAKIAEARELDTFPAAATMLDDIVSNSPEYAASMPMTREKQGQELEGEDLYKA
IELWERGVDAKSDATYQPLFQFTEACDWGEVSREEVLTVYDQFVMGHKLHKQAKEGNNAD
ANNSVESSSVPSVITDPDWVQHFTLSVDDVSKDCFASSARLVLPDVLFSLKSPRPQEGGK
SEEKTDEATVISRRVDTLPPPPEEYETEIRTSFAPRKRFYPRPPPMPPSREDDLTDSVAM
ATEETRHQATSHEGKTGNGRSSLSRNAPSEASFEVLSLADSQSLLREYALSGDKTLPFDA
DEKDLQKQSLVGPVAVQSMTREDAQALQYNRGAPRPRRTVRFRLRPPVDADIRQAGGLGT
ALGASLSSTANKAEARAQSVIQAPGAPRKVARPKKKHQE
>TCRU_6073 UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase,
putative
AAADDAALAYIPRSVVDKWSRREYLIVLGIPSTDDEARRTRRNLQRTTCWRFPGVATRAN
GFTGAMLVLYVLGRHPSHGYEYSAALLEEAAQWHDVVALPMKEGRVTTKKKIGGSGSWGD
EAEIGMTRKTYMWFDLALRLFPTAGYIAKGDDDIFLRVPLFVAHLRLLPRRGIYMGIHGG
SALWVNKRSAGAKFMIGWCYTLSRDVAEALVSYK
>TCRU_6074 cAMP response protein 1, putative
DHDWLITRTVLPSFESVFDELEPISEFVCPPFVPPCRSSRQYSLMADALTIGGVISEWEK
KMILARLRQTPPLVEEEFQRRLSTVHTRNTREYIREIQIRASTQVEAEREGRRLEYEGGI
SRREAVFARHKNLATILRGEVKTVRARRWCTIIFSHVFLMALMKERRIHEAYEKITWMLL
PIIKRRAAVSVKRKEAEKLTRMNLENIPFPSPSIIRSMYGTFFKGWPSPLLEMLARKAKP
LFFQSGKFLMHEGDLDRCMYMITTGSVSVILNDRSKGKKRTKECSKACFALTPPCYVGEF
ALVCKEPRSASIQCETDVGAWTVSPEDYEEVAQHLSPEVASQQREATDVRRRANLQKFFP
LRVELLSQFPYFEKFSVEALNKIISAVEPIVLHDGDPLFSKSDMDSSAYFIQDGVAILLE
EDGTRRTIPRGSCVGIFECACSVNERKRYSIISKNYCDIWRMRREVLIDVGMSEPAAFLY
CRSAAKSQRANEVVKPTNPSIFVRKDPYLTFCFTRQLIGRLWEAALPVIYLNDEKLVAQG
QLFKQFIILHNGVFETTIIAGNGEHHTVRITVNGEVTAMEVISGSNDNSLYKGREPMTKA
FFSLVLGAYEYASSMPQYSSTVTSYGLSEAFVVDRANFDALVPPELREIMEEDKDARKLV
>TCRU_6075 R3H-associated N-terminal domain containing protein,
putative
TAAPRVNVVPLIKPRHQRRQRGYHHMEVTDSSGDRLSATTALQQHTREVLTVRNGPMTYE
QEMYFHPHELYKHGKYQIHTSSVGYSSGGDLVITRECVSEPSDVDMGFLRYRSEIDRAIC
LDPKARRPFSEDEAKKKLRFNVPRYRKYPGIRAPRNRKVRNRLLNDYFATEYARKIMEKY
RERQANGEEESDASPPVRPVFGNLPPFFLKMLDLDEDAQTRALERCGVQMRPPFVSGPKD
PDSGEARFQSMNARLRSELVHALSSEFLTRQIFDLERAFAAFIVEGNVNKPLEYKFRDGY
GRLVCHGVAAYYNLFSESQQQPDGSKVTIVSWPKKKIHSSVPLTLPRTSLMYILRKKRGD
TSSCSSTSTPQTTPFAHAEDPELLPLPFNLEAASTD

>TCRU_6076 hypothetical protein, conserved
MTCRKHVVWDESNLEDNEEYRRLHPVTMRITEPKTPYEYAEFDEEGNFDDYSEATDGNNK
SEDQGSSTWDPQINALARELKEEFLKDVNKQVAPISPSGRPMLLATVTNGEELERQHEEK
FKRMRRAVYADEGANYKALLGKKHDGDDDGEEEEEEEEEK*REAE
>TCRU_6077 SNF2 DNA repair protein, putative
PSTSGLLVPPSLAAVLRPHQIDALHFLWRKLVEEGIQRVIQASPLAPLPERVRLYQEVFG
CIVGHSMGLGKTVTILSFLLLLQQHYTVSSRSAPALRAIVLTPRSCTYHWQCTAKEWMLP
ALFNDTLLPIYVPLGSRGTETMVLDFYRKGGILFLGYEEYQKLLRWAKETATKSQGYTRV
KSVFDYFRPPLPLSGKLSLLEVLESPDVVILDESHRLKRVNSKLVGELMEHLRGVQLRVA
LTGTPLQNHLEEYNVMYSVVTGTMMQSGSFRRLFTIPIERGQCVDSTFQEFVEMQKCVAS
LRRFFAKTMHHCGPEVLEQELPPRREYVILVGLSPTQEAAYRAMLKHYIKEEKTRIILPL
HHEASHVCFHPSLTSKRVREATHSFRERLVSQLSLNNDVDDCKNNGGRRSFSLTSSDEVS
SHDFNDADIDLTLEHFNVAESPKLLLTVSLVWHIIEGLHEKVVLFSTYRSHLFLLKQLLR
KRGLLADVMHGGLDVKDRQRIIERFTEDASVSVLLCSTKASGVGINLVAANHCILFDVSW
NPADDTQATYRLYRYGQQRPVTVYRIATDGTFEHVVFFYALSKTWLHKKIVDVADPTRYE
RHMKENFFIYPCRVSIDFERSGNSEEKRSPLPNNDAVQKNWREYATSHCPALALTEPDGT
FAWIRSISEHSFLLRDDTDEVIREMGKRFETQKQGLNLPIVMETTQNEDRLLEDVHHSLL
ERCEGALHDCLCDGAARLLSTVQRQSDAFVEDKAMDSAESEKLLCGLFATLVGVDEPAEG
LTEIFAVLFHRGVEEVMRTVLSRPSYTNLRVAFSSRLVGDNLAKDSLLDSLRFRPYTLFS
RMNPVEATYVLTEMGFVRPFVPHCILLGVSLAFHGVRGPRGVLQALCRIFASSDGRDDDE
KTTEILAVEAEKAVTRCIEGIWPPCEGMTIPEAPTDLEVRRCLTERAYRTARERTSGFFS
LKEAAKYLGLRAVHGRRDLYHCKRCSDGLLDRTPPDAVLRCGRCHYNAEFDLQTCVDTRH
ACALYQLSVLFGLLDAFSVSRSFTTAFVPSACRDVLQVLRQLRHSHTVEMSNNFVSDAVS
MGIDVLISGLPEKTVSLLCLQCGVTDMTALKSFLVADSSRVWSAVLRSHVRQLVMDWFKA
TTAMGPKAQAMAMPEMTVVLALQSLARKYGGGGAYAKDLLLGSTQGQEALKLRFICDGLV
KLIYAERLLANPLTRATLDAFMMEYATPSESSDGSGSENSGHNSSGGRRSRRSSTRGRRR
GEFESCSNASCSSNSLSIASVSRRVCARKRRRHTSQSSSSYSNASVASSSFSSCYSDDDD
GENTASDSKSVAERARRELIESEEVLRLRSVQYWAAYCEVYGTCSIESLTVMVEDEENGM
TILPPPPNSFWVSEMKRVTREGMRLDSVVNEFLAKIMTLSTAMRVIK*
>TCRU_6078 hypothetical protein, conserved
TFICISVNKIPFVLCGSRYAPILNQMGAQGRDIKREFLQASLSSPIVGVEEDSLALSNVG
LRKRQKKKAFDALVHWCATHQQSAAKAFLLEDASDKTVPSVCSSPSLESNKAALQWLQES
SDSLTCGQSLLVCSFVSEVLLCRLDAAAAVGRRGEGTVTETNPLIQEQVRAFTNRIVTLL
RRAIESDKLEMQPLAILMGCAYGLHRLSCVESPFLGEAEKVLLKIPPALMFAILRQLRGD
ELRKLFQLDEQVAVNVCLTFLLLANEERRQAFLSGGDTVIVNAVLRRLLRSIVPLLKQLD
GTDEESLLGLANDVSSKGSSSLPSDLQGEVAYSPSMEECAVIMQNIAFSSMTSRLEMLSY
LLRIRRKPAHYTRQELQMLPVLLQTASNIRTAEARSLCTKIIAEVPIPADDPVLVAHLLS
FASSNRVRYLNCLETVATENLSEEDALHIIFWAGAHLRLETLQRLTAFILGKETGAKSSS
TSSSKLVLNGAIECIVRAFLTRLMDSTPGAERDVIQNYLTELVDRVDWAGSTLPTSVKLA
LERLTLLKELSNCGFSIHAPEVVMALGEKALDLESGCSMASTLKCVTEALPLLPDVERRR
KLVECMISYSGTRSTSSIIRFVAFLAPLSVEHGLSNSELVQLLLKLQTLNPLKLRQNFIE
GLPRGGGDAFTLFVLNAMNYLLASGEWRTSTDRIRETVTPWIHEYLNHVMNLSRRQKMKS
ELIHVECKEENSALHEGDLEATIPDGPTPERLEEVFSCLLRAGVKLPDFFAPELTARVRT
TEGEGTPPSGETGRKPHFPPPGHFVFCTKLDIAMESPLSVELLEYLLTTCDCRILNFVIT
AFLVSAKAKSLESQLIVLTNLRLVCRALNLLLQRIDEIGYELSTAFYPSSVSSVVANTVR
FVVGFLTKQERNQRTIESLRKLHSEEEKASMAGNDGKLLIEVTNVENLLLRLLTYLSSAH
TKDIGLLLLDRLTLLAPAAADYLMLRLQNQLGNFTQVELFYLVRKYPPAQDLVMNELQKY
DIALSVDLNDFVRVARSLPVAVSTMVIEAHLPNLNFQWCTRLLSALAVRHESLPINLLVS
MLGKLEEEAGNATVMDRNVALVVLQKYLHYENLPTDDKELPHRRRRVEHCCDRLLVLEEI
ESLDSLSGFLLDFPGVLLDVVGDAIKERVFSSVLPGLLADLEGLLTLCRLLQKHKLLNDK
MKLEITESFFGKLSRAENNDEKLLSSPVSYPLGNVLALALLLSEGASQKASLCSKERLGT
DGAIHHQIAPRVLQVVRERYSSLPERLVILSTLVEQKDMAGFAHTHAVVAEEVCTELIKE
CDKMTSSEFSKLLQCISRLKFWHLVKLDSSQFGNVFQRTCREADAHSRCVAFRALSSDLE
LFCHYESFMMSLLGEVVNVMSHEDMEMVLSAVLALQLTEALESLLDAIGTRVLSMVDQCR

RSTLIRVLQCHAAFGLRDDVLVLRLLTTLEEQCSREIRLDISQVLTLLQATVDLDVPIPS
KLAVNCFVCLEHHVDRMTMAQLGHAARLAVEVEMGYTASVHAVAMRALEHREALRTNATF
RESVELLCDEFSVEIPWHMRPTVLRRRYQEERLNDYINKRRLA
>TCRU_6079 hypothetical protein, conserved
RLATILHGVFLITMTTKAQIGIFDVGEGITAAVDDRWLEAIVRYCGFTVVLNDIIETAAA
FNDWLKVFVSLKQNGEMEQNPLNTVGKAAGLAAGVPKDIIVVRLKLLHSSVPSVQEAEAF
LRKRWGQSSGWRRNTISCFEFSKHAETVSTEKFEGNSTQSEAGGPNSDVSSSVIIDRIAS
DSDGLSDEELLAQISRELRASLSEKKLRYLVAQMRREAIGLDAKEQELVTRRQQRERLLA
TYDLVRVILGERRSVCSIKQLVQQMVAQNRFCDGEESILKQLASLARYSESGIAIFAFNG
DSDGQHPGGVVEGESSSFYSREVDVSQCNMQELEAVLLRLDRHVASRTKLYAALQQ
>TCRU_6080 acyltransferase, putative
GMMLFLFLFIIFMWLLYTRRCPVMVARLWFSLCLVLLAVMCFALCTPLRILASKKIINKR
RSERMSCRITGALLGKALWWLSPHIHVRFLEGSLDWRAIENRGVVCACHTSFFDTLLFLW
LCPLSFVSNCKAFAKKALWRMPIMGEVIRACGHLPVYFNSTDVNSFSVDREKQAVVMTEA
EGFVDGGGVICFFPEGVLNRTPETLKDFRIGTFNILMKHKLPIHYVVYYGSHEVWDPVMK
GIPGFPADVHFFIGNYEYDAGATGADVAKGVREAMQKQLDRMLAKRKK
>TCRU_6081 hypothetical protein, conserved
VTACDIILCSQDGMSFTIPAKIAWEHIGLLNALALLDEGGCAEMPPLELDYPELVVKYVS
EYLMNTDRRLVDIPKPLTAPVSHFAKAWEMVLVRDIEKHQLLIPVLECSTYLRIDVLHDL
LAAFLAERIQEISKAAPSIMEGAESLRQYLQLENEWTPEEMVHLEEEMRYAKEMNPGAY*
>TCRU_6082 hypothetical protein, conserved
DTDGFTATEAVATAAVRSEHQRAAVLSTTTTESYVYTCRMCRRVLFMHHEILPHYPEPVG
SGSKGFKYRGGGHASSQQQQGLHAAQEGGDVCTSYFLDPDISPWVAEESREVHQVSGGLD
VMPDTIYCPNRKCNAKIGTQSWVGSQCSCGTWVAPAFKIHSRVVDKM
>TCRU_6083 Galactose oxidase, central domain/Kelch motif containing protein, putative
MPPKKGKGRDATDDKTPPMALRAQVEYCVSVNAPLRRRMGHLSYVHPKNGLLYVVGGCDL
DTLPKAVKTAHLEETLEPMPLAECWDETTRTWGVECASLREKTPQSEVEELVSSKIDMNR
QDDVDAGEDKKERTPSEGEAFAPSEPVFIHRPLRVPDGFSWPTLAATVVQWCSVRKDDYT
ALSTAVSNVDSECLHEAANEGVDAGNDADGSGKTGEPDASAAREHPVVFFIGGWKRNGRT
SHTVGVDMDKGSLLHIRGGMAVSSLPSTCMTGCVAQDCVYVFGGNTAGGAVGCNLSVMRT
LDLRSRKWVERTGVEMSTSSPFPRSSHVAGVLLDRYIVIHGGRRLAPVPTGRRPEKGKKV
DPKVVQPIEKLVLDFCNDVAVYNLEKKQWVATAINVGPLGPPARYAHAACVLSPNELLFH
GGIGVGGKVLSDAWILRLLEKNENNVSISWVKVVANETKKLPFPSRCYHSLAAAAGRRVF
ITGGTCPSEDVEDVCIMEI
>TCRU_6084 T-complex protein 1, theta subunit, putative
NIEACREIAKITRSSMGPYGLCKMVVNHLNKLFVTHDAATILREIEVEHPAAKLLVQASE
AMQQEVGDGTNLVVALAGELLSQAESLVRMGLHPSEVVEGYKKAGNRSLETLQTLVIQKV
DDVLLKEQVLAPIRTAIASKQYGYENFLADIVAEACINACPSNVRSFNVENVRVAKLDGD
SVLASKNVRGFVIARSPEGSVRHQKRARIAVYGCAVDVPSTETKGTALIESAEGLISFSR
KEEEVMEEIITNIHKTGVNVVVSNSTFGDLALHFLNRYGIMAVKVSSKFELRRLCTAVGA
RVLARLDTPTVEDIGSCDNVDVSDVGGKNITSFVQDRDDSKLSTIVVRGATKNVLDDVER
AIDDGVNVFKALTKDKRLVAGAGAVEMELQKDLTRYAEASPGLDQYAIRKYASSFEVVPR
TLAEVSGFNGTDVVTQLEVDHNADKIHQGVCVEDGTTINAVELGIVEPYLTKYWAISLAT
EAVLTILQVNQIIVA
>TCRU_6085 SET domain containing protein, putative
PSWSYDDVYYRALTDGGNYCIKTNPLKGKGLFSTRRINEGDVVHEETALCCSQNLDDVLG
GIPACGNCLLSLESSRRCVARVTGSKTLAMKLPYAKLEKHSRPVRCVHAEYGCTMLFCSV
RCRQAGWSRFHFAGCPGAMMSDQRDAYDEFIHHDWEYRGVDYSDTVFLAFRFVCMAVTNI
RLHRQSLELAYRPIAQLIKAPLSFFHFTYLFYREGADSTEKKGRGEKQIEKLRLIRWEAF
RKFRATHMSTTENDTTDDFLATGMTLLGRILRFTQEECTLFTVARWSELLGAVLLNGQER
SPPSNYDRLKELVRRLPCGESTMDAFEQEVQMAGNELQHLLQSSRGQGVYTVGCLFNHSC
EPNLQVVYSESGDETLSVVALRDIEPGEELCISYIDESLSYPERQQELYEHYLFVCQCPK
CEREAAAWE

>TCRU_6086 Organic solute transporter Ostalpha, putative
VQRHERRRMYYWVGTFVCVLGVLLLVVLLLKNVMRDQKVVPSFIGGYCAIFATILSLFQI
LEHLTCFSDPECQTKIVRILFMVPLYAMISWICILAPSAAEYLNLIRDAYESYAIYAFFQ
LMIALMGGMDTVYRALMLEERPPITHFFPFCWMEPLKVSPTFVRNCRLCLFQFMVVKPLV
TVVVIILTAKDEMGSILDVRKGYFWTTLVYNISITTAFTALVYFYTGLKEFMEGTDAFMK
FLCVKVVIFLSFWQGILIQLLSATHLLPSFQYWSKDRVPQGLQDLLICIEMMFVSFAHRY
CFGSDSYASDVIVGPENGADDVEDTAVVFPHRNIPPIRYSVSANLRYTLKHEDIMHDLKA
IMQNR*
>TCRU_6087 hypothetical protein, conserved
FHQQRYDYFLQAYFGYGAEQRLKCIRQATQMCMIGLGIQKKSQTRNGDMVHAMRRFLRHS
VLAVEGDAVFVKLVQKARLRWCDEGNIHFDDPRHWPNARCIAIHYGLPSLATTADSCCTA
VDTKEPVGVKAEPEIKGKKFPPATLIAVVATTPIEEGESVRLCLRSYHRCLDEATWYEQL
FGSRFNEGNAETSSVTRGQKRFDMWPEGLAFFHGVGSGHAGTEPVAGFPFTLLELAEARE
IGNGEKGLFAAHPVPYATCFLYAGPAVATKVLEEKRAVAAVKNGITTTNNPAATVAPASS
DITNSSTTTTTCRDNMNTDNINSGSIDDEDDDMLNEIPIHDATYALGLGRHGMCFGQGLM
RYANHRYNISKFGNVELCSVMLSVTSEFSSLAAELERRRNHAFRRRRNPRGAPGRKPEKS
TVISHAKKGVEVVGAKKRRYRPLTGRRIFLEEYSHFVMIPFFIATTDIEEGQQLLAWTYG
EEYDARLERQVVCDGNLVPYGDAVVLDTRIPVGRWQSYKGDYRHGMGVSDIVWCRHFSSN
GLHDPVDELYIILEMPFHGMGYLLLRPLVRSRSAQRQELLEPYQGSPDEMILLDVCESKV
LEQCIIAHMDTVALLLVDMDYWSLRKAKRTPASSPLAWSSCICGGGSSCLIRHIVVNGTS
LRAATRLVRESEHNFTTTTRVEILSGSVWPFLQGRG
>TCRU_6088 hypothetical protein, conserved
MAASTTDEKDAKLTDLVKTMFERVPKEKRLTAEVVMQLLKAKYLSTFPAEYLTNRAEFVA
SLIDSLYRKRSGDKKESDANGNGQDNDNDDGDEDDDDEDDDSSEGDEEEDGEEEEEEEEE
EEEESESEETDETGGENDDADGAPVEKRQRLEEGASDVARRCHEMAECLRRLSYRLRKRE
DGESYESYLEQYLVPFFREKGLDPERYGKEDVRRYRVKRELEQLQSDGADVNLDRAARAG
RGLNRLALNNDATVSIKTSKFLDEE*
>TCRU_6089 chloride channel protein, putative
LHTSFNIMLRKLLDEFWRIANPFTQNSEDMTTEEMEKQASFESFDYYKPYPSMYMKHLRK
HYAMRTSAAFAMDGTSTTTTNTTMNNTVSPAVEELVVDNSDVSHHNIDGTSVNVLSMVKK
YDADERNEALRWILHVLIAISVGILATIISYTVEIVDDYRAAQLYKLITEHSVIGRIIGY
VFSIAVSMALVVVATAVVVFFEPAAAGGGIPDVIAYLNGVHVPHAMNFRTFVAKSISCMC
AVAGGLPVGLEAPLIHLGAITGAGVTQGRSRTLGFQTKLFQAFRNNKDRRDFITAGAACG
VSAAFGAPIGGLLFVMEEVSSFWDHSASGQIFLATMICFTTISMIRSVLEDQRLLGWVSN
AVSVLFEVNLTIPLNLLSIVPSFFLGIFCGAFAAVFTKVNLMLLKYRRRRLRPFVLCRFL
EPLIIVLLYGTLSYMLALVPDCRPMYEMNSKNGTFFWGTENRTRLFTATCAKADEYAPLA
TLTMGNGKDIIRHLLSRQTIGEFPAAYILLFLIIYTVFACLSSGMAVSGGLVVPSLVIGA
AFGRLYGQLIWFMAVSGNESERSYRASQAWLDPGVFALIGAGAFFSGTSRMTMSICVIMV
ELSSELHYLLPVMVAIIMSKTVADLISEPLYQYMLRLDSVPYLQAHLLRPGFEQLTAADV
MASNVLTLRLREKTPVVLNALRNTTHHAFPVVEEVREEKTDEDSFREAETRGKRAKFREE
EERRVRHKFVGLVTREDVQIYLTLPALQIPNQTSDHSGVCSHGSNAELAPSVLAVNKMTW
TEWLTHKTSLFFVFGGARWSEMWTKNNSKDGIAEDNQIHANENNSHNSSGDTPNPFFVDV
RRLPPVLDFSLIVNRSPWVIPPFFNLQMAYHTFRMMGLRHMVVVDGDAVVGIITRKDLLV
DTLLRRLRGLQ
>TCRU_6090 hypothetical protein, conserved
PHNSSTQRVVRPSDIASTVSPLYRYFSFPVCHSNYDKEPYLPPCVRCPNCKCCQLHMQFC
SGAYGMRHVLAWVVRRQPPKVGEGRTIRLRGDTGKGEEKLFFRLPVCRFEVGPVVITRHL
IYCSREQTIETADRGGRTGTFAGMACPRPLNFLDVFFSVFLSTTHRGREMKNYRVLQRTA
MRAIAAQARALWEKLTFSPARECKLRSDKSKAKAGDSSGPRRVPIDWRSPPFFVSLLPCA
PVGNSGLTFVLWLGEPARHIITSYIIEDGEFWRSKHTCIYGGKDNLERADNSDPASGLKW
EGEVRCRRCYGPGSCWGLIFRRHREERDAMLTILRVRRGCTRRRITRRAIQRRYGGDWGP
GTNDVAWVNKHKTRAQFMALLVAYMMRTTLCGPYRQRHIDPPPS
>TCRU_6091 G10 protein homologue, putative
MPKIRPGMRRPPPGFELINDKLDEYDAEMRLVMADDPQQAQLPARSRGAKRGGVAKGSTK

EDVKEGKGASEAELGNSEKPVPPLWRVARINRERTRYVFDACYHEKTVSTDVLNYCCEMN
FIDAGLVRRWKLPGYEQLCCTACCVPGTASAAARTVNKHTNRHSHGRREGNGGEERAEGT
CICRVPAEQRRVKRLEGCTVCGCTGCGSGEKRKRD
>TCRU_6092 Ribosomal protein L44, putative
MVNYPKKKTMHCPDARCNAHKSFKVVQYKAGKARLYARGKRRYDRKQSGYGGQTKPIFHK
KAKTTKKIVLKLQCSNCKSIIQNVLK
>TCRU_6093 lipase, putative
ATTALYHAKAAYCKAEAISS*TCASCARNPGLQRVRVFTNAEHSTQAFVGVNESMIVVSF
RGTRDVTNWLHNLDFIFAPYTHDGCVGCLVHAGFNCELKSLWAEMWGYLQELVAGKGIEG
ILITGHSLGGAMANIAAANLMSQNSLFTSALKVLLYTFGQPRVGNEAFVNWLLASFCRGG
HESYRVTHKRDVVPHVPPMFVGYLHLPNEVWYDNDGDTVHKNCNDVFGTPCSALTTKEDP
NCSGSVLPIKVEDHLKYLGVCTRCSCDPGEAMSDEELRLPPELEWIVAMDYVYQQSR
>TCRU_6094 eukaryotic translation initiation factor 4E, putative
LMSDVKSKEAGANPAASKSGSGEDVAETKLAVPRSLDTGSKKHPLNSSWTLWYDSLSTYD
SERWELSLVEVITVRTVEEFFTMLHYCKPPHVLRVSAQYHFFREGVKPMWEDPSNKSGGK
LWISLDDKPVGDVGGRKWENANTGGAAGGEKDNASAATNNSNSNQNAKAKKEEQETEKKP
ELDTMWENLLMAMVGEYLDPEPDGDHIMGLVLSRRKYHNRIALWLRDASASEAVARIEKK
LVKEAGLPPAMKFIFTPHSTGK
>TCRU_6095 hypothetical protein, conserved
MSLLPLYRSLLRRIHAAQRLPHHLQDIRFILSYPLVEAASRTVTSSGEVCGSGLLRQHRV
DPSHVVRACCDDLHRALLSYSHVCDTPSTSRPLPPVAQRFIHMRELAWLKARLEKVLSES
TQTILKEAEMVASELNETDFLDDAFFVEKDPTKDGETEKEWRSHNNTEEDMCATGVASAG
ELGLRREMFVLRHIAPFPLAAYYLSSFNMDSRAIVAAAGNSERLLDFVQQHVPRRVVCQN
ADLTLTVSVRLFDEAMEGKRVEKGSPFSQAHRSFMLRFELQPRDPTTRIDVVNSYFLRLD
VASSELIEDVGYVHAAHVWKLAQYPYRGNGTHCDSIDNNDDDGRSDGVASGDHHRHCHEG
VDDDVASQFELSFINPSDNPMVMKGQLYYILRAENDNSPACELPVRVISFGQLLLFN
>TCRU_6096 hypothetical protein, conserved
MTDLDATKISIITGKKADPRLLVEVGIHSDEVPEAVKKRNAQEKRCNLCCMSYGFLLSSA
MVLMVSCIGTAACIFTEKRVNYTLNGTMRQVAWIAIPGVLAGTTLHYFLSEAMWSSKRNT
WGQAWMKAISFNSLTWCTAISVGTLFWRKGLLMSSAGRRLYYRYPIPTVSLDSRVLRSDV
EFFTGMGWTYWLSGVVSGQVGYLSCVGFCLWNDRPYFMMNPHGGYAFRCMPRWRREAFAK
QANVRLSD
>TCRU_6097 hypothetical protein, conserved
VLRRAVVALRDALNGGSSMTLCTKGMGLSPDSHCRRMPWTAEKECVPGVVHSSKEKMVLD
GAQRVDVDCVDRASQVYPLEALRATVAS*EYNTSRGKNIF*LASQAESNVLRQWVYRKDW
QEGTYDEDATRTAIHFRRREATTQPAPIRLADFPG*HVCPLGVIVPSPSVGASVPVNACS
CCLRAHPLID
>TCRU_6098 hypothetical protein, conserved
MFVQQPPPPRYVLQVSTGNWQKKSILKSAAPMKEAKQLQNSVEYFLKRAMCASVPTSKNE
DGSLCESTKIMKELDLFETRHFGSKSRYSLFLPTSLQVNPIIGLLCGLPLYQICDALIQR
KDAEWQARKEENCSVGALRLSFEELYDVCTQLVPNMVSEDYLHRMFIVLLPSEEEDSLLL
SSFFSFLVENAFHPALDRNVNALFSAFDPDGTGVISAATLTSKVLLAWAELHLFGNLRGE
WEKMAAALELTNGVDLRIVDGARLLTPAATRAVFCALNTLYVAMESIDMDGRHLNSPS
>TCRU_6099 paraflagellar rod component, putative
FDDLLILVSRKGTKSVQWCGEKMGDAQLETLIAAMEISPIPIQHIDLSRNEITSKGAMLL
ARFIRITPTVEEVEIRENNIDNAGAEAFIQLYFDVRYPKLFDMDGNPCSKAYVHNLSLLA
QGSSYSNEVRRGLLTREADELNVSGIDYNKLDPRLVTFYVQNVDGLERLILSGCSLGDAG
AGVIGALISQSTLTHLDLSNNGISDVGLSQFVEYSNLQNHPTISSLSFAQNIRIGNFSAQ
NLTKTLFEKNGKITFFDLSETSVTSRVRSIINHECELNKQPHSLKEAVIGIRTNDPSCTS
VNLQWEDDMEKAAFFISPILRDNTNLLELNLGNCGFGDKGVELLAEALRLNNTIRVIAFP
NNNITSRGAKKLFQCIIQHVSLEEINLAGNRINDEAALSLLNTIRLNGNLKNVNITNNFI
GIDYINEVEGLLLINQSPKMIRRLVVEIEANEPNLASLSLSGGTGEEYYNDASVRLLCQA
LLLNATVTSLDLSKNIVGDIGVASIAEMLMTNNVITHLNLSDNSISNRGPQRLCVALRTN
TSLQELDLSNNAIYDEGVEDFPEMLKYNDRLIRIVLDKTGVSKEMYSKIIKAADLNKEPK

NIKDLVYRLQSGDDTLRKVDLRRENCSRPLDDESIGTLCVHLKGKSFVESLLLQGNMIGT
KGCQALGELLAEEGCGILSLNLSSNPVDDEGLQELSKSFLSPHIKLETLVLSETEVTSAG
INSLIELLKINTSLQQVFPPERVSADVFCAMNYELMVNAQPKLLKPLLARIDANENIPEV
VLKDSQVPFTDSACQLLCASLVKNTHIVSLDLSHNRLTCECVPFLVEALSRSPAIRNVDL
SYNHIGVKGGMDLMLFLQENDHVLSLDLKGNEISFATANAITELLSLNAGSIKLKRILLR
HRSGNFYDEMINLNGQDETYKLNDNDIRLLCDVMTESSTLRAVDLGLNSITDLGCEMIAD
VLRQNQKIEALYLDYNPIGEAGGEALYNALKVNHQLHTLFLEGSNVPEEIWEEILGLLHV
NETPFKEKINMRAVRLDEVDDDTQFKSTDYANAQKEKVGKDALYLYE
>TCRU_6100 WD domain, G-beta repeat, putative
TKTQSKADVGQYNVPFTIKGPYVRVAVVRASASIWAANGETGTIDVYSSVSGLLSTRLPA
RTTAGGEIIKPTALKETPTHLWVGYDDGSVVVHDHLCLVPLTMGCFHKAPVIAFCVLSNG
ITVSGSSDMAFVRWDKEEKNFEAISRIFGVSELHQGLTCMAAFGANIVLCGSMSGAIVAV
DCASGLQIATLRGHANRVNALTLMGNLIFSASEDGYVNVWNVKVDETFPEVMLQKNFYLL
KCIPLQVAVRDLVIHEGSRSLWVAYADGLVERWSANPDDDFGVEQVVRGAFVDVDESQEH
QKQRQEVISLDCIRNVDTMRVLALGSNGISKVWCGLRNTVEESLQQAINDMNAIITQDTT
EAAAWEQKALILREKEVQRKEKYGGLLTRLHARRLLLAYYTKWRARINFHRLRGRQQEEI
CLTLEERHQFRLVRRYFSIWCEFYDREQRRFRRQLTAAALERLSHQTWVVRLLFRWRGVV
SRRKALRRQGEIVKAFARVSNGLILGEFFTRWKCYDAMRRGVLPEEKLALLVGKSRQRVL
RQAYEDWKMSYASRGQIAVGASVAPAATGAVTKSSNRAACAAGFAEAYAKVTIERGRRRV
FSAWRRWHEYRCGIVSLRALAIVREKQCQRNILYRALLFWQLFCRKRRFEKLSQDVEEVE
KRLRHAEETHVDIFDKLQLQKRLEQLRRQQEEDQRLLHEEITRTEELNADREVLRRLLDR
SGCIDEDATARASSALFSPAVLKQLPIGEAMAFVMARMKGMVLNIYTDIQLFRQIKDRLR
CGTTAAVIFLEGFQEVKRLVVTFSKKQSVNVWRSGERWPLTTEILENLPLHPCATVVQGI
KTMVVAYDMVGAADIETVSGTRAEIVTNADLLFMLWRACYTARKPPLPVNNRVSSR
>TCRU_6101 2,4-dienoyl-coa reductase-like protein
KISPLFLPICIGAKRHLELPNRFLMLPMYLNMEQELDVWSDAHMDAMGSFYAERARHGAK
LIVCGGLGVSRLGKWRIDSMALGTYDAAKAFSRVTHAVHREGGAILAQAFHPGRAARRRW
FISATSTPSSVQPFRDAHPWRIPGLLVEYIVSEHARFARLAEAAGFDGIEIPVSEGGLLH
NFLSTAVNDRSDYYGRSLEGRLEATLRVLDAVRRSLVEPEKFLLSVRLCLHDLKVGGTPM
TETLVAAEAIARFGGVDILSTSVGMHDSPVQTMASYVPQAAFARCVQKVRERLQSHGLNV
PVVATHRVHSIAVAERLVREGVCDIVGLARPLLSDPQMIRKAEEGHEDAIIPCIACNHCV
NRLYKHQRITCALNPTSGYERERQWAATRYKKNVAVIGAGAAGVTCALTLWRRGHDVTLF
EKSNFIGGQLNLAKVVPGKESYQEVLEYWTRQLRQSSINVRLGVEFVREDMSRNHQFFHA
LVLCCGSVPRPATSHQIPGTSECPMVVPFEKILNGSVKAGRRVVIIGNGAISHDVASYLL
HDPRVSRSVEAYCDEWGVNLEDGTLDPHAAERAPRNNRDVVLFNKADKDADLSRGKGWTQ
KLWIRNHGGTIIKHGLIENIDRNGVHISMVAPDSRKYFVECDTIVWAYGMLPNISVGTWI
YEWMKDGAKERGEMISDFSIYTAGSCRDSYTGEGHGEQDLLQAVHEGYEIGYKI*
>TCRU_6102 dihydrofolate reductase-thymidylate synthase
KIRMPETVAEGTRLALRAFSLVVAVDEHGGIGDGRSIPWNVPEDMKFFRDVTTKLRGKNV
KPSPAKRNAVVMGRKTWDSIPPKFRPLPGRLNVVLSSTLTTQHLLDGLPDEEKRNLHADS
IVAVNGGLEQALQLLASPNYTPSIETVYCIGGGSVYAEALRPPCVHLLQAIYRTTIRASE
SSCSVFFRVPESGTEAAAGIEWQRETISEELTSANGNETKYYFEKLIPRNREEEQYLSLV
DRIIREGNVKHDRTGVGTLSIFGAQMRFSLRNNRLPLLTTKRVFWRGVCEELLWFLRGET
YAKKLSDKGVHIWDDNGSRAFLDSRGLTEYEEMDLGPVYGFQWRHFGAAYTHHDANYDGQ
GVDQIKAIVEALKTNPDDRRMLFTAWNPSALPRMALPPCHLLAQFYVSNGELSCMLYQRS
CDMGLGVPFNIASYALLTILIAKATGLRPGELVHTLGDAHVYSNHVEPCNEQLKRVPRAF
PYLVFRREREFLEDYEEGDMEVIDYAPYPPISMKMAV*
>TCRU_subunit gamma protein, putative ATP synthase .1
MSGKLRLYKEKLEGYNRFYSIVKTIKMVTLAKYRTAQGRVKTRDFTLRYTEKAFSKPHAS
EKEAVASAKNALVYIPITTNRGSCGALNSNTIRCIDLVASNKMVLMPIGKRGIDSLSKLY
PNEFKYGIINDMREPMHFAYATYILENAFNVSEEADRYQVIFHRFVSAGVQKHAVYNIPS
FEKWKEDLADAASTENQKSRYLFANALQNEEEQFIRDFYDFHASLAILNAVGENELSEQA
ARLVAVEGQLTNISTLKQRTSSLYNKTRQSGITAALIEILSAMSSLEGSTTKGVQRNKFW
EGS

>TCRU_6104 60S ribosomal proteins L37, putative
MAKRTVKMGVMGRYGARYGANPRKRAKKLEVSQHARHFCSFCGKFAFRRKAVGIWRCDGC
SKTMAGGAYTLSTPNNSTVRSTVRRLRELK
>TCRU_6105 peroxin 14, putative
GVTGDGDARQRISPEESEKRKRVSSAVQFLHDSRVKITPAANKIQFLKSKGLTTEEVCEA
FEKAGQTIPLDEIKKIMNKPSFVSGVTNNNLAPGHVGNDAAYVLRQHPFMPHAGPLYTQQ
PPPFPQTAQGAKETDWRDVIIGVGAALISGFAAFKAFQIYSPYEIRRKDESAKKGSRMES
QRRGKRHEGSVSPDRGAERPVTSLHTMAPPMPAMPTPLPTATAANAAESTEREIQKLQSE
LKETQEALEKEKRSKAEISVSLGKLRGQINALSRTNDNLESRIKLLQEEVDKANSEANKR
KE
>TCRU_6106 proteasome alpha 2 subunit, putative
VFCTMSESAYGLTTFSPSGRLVQIEYATTAASKGTTALGVKAMDGVVIAAEKKTTSPLAA
SLTVQKVFVLDDHVGCTYSGIGPDCRVLVDAARKACQKYRLTYHEPMPVSQLVRHISSLY
QEFTQSGGVRPFGCSLLVAGADSQGNHLYQVDPSGTFWAWKATSIGKGSTDAKTFLEKRY
TNEMEIEDAVHTALLTLKEGFDGTMTAENTQVGRVSEGKFELFTVDQLKDYLDQ
>TCRU_6107 TFIIF-stimulated CTD phosphatase, putative
MTTPPRQRIRGASFKQEYQSAVARRPRQRAPSMNQELNSKWVLPEQDPRYRGKLTLALDL
DETLVYAREGPLYARPGLDEFFKLCREKCVEVVVWTAGLRAYAQAIIRNIDKGRVICHCI
YRHSKWFTGYAGYQKDLSALGRPLDRVLIIENTPDCIRGYQQNGILVEDYEGGEAPDNTI
PALIDLVRNLCDSSMTVPQFIVSCPMLKHASIQTDLGDFINVYKLDVAVWKPGEHVRINR
DL
>TCRU_6108 Ribosomal protein S10p/S20e, putative
KMTSRNAKAVENVMTELLLHARNEKVVLRGPVRLPTRTLKVTTRKTPCGNGTNTWDTYEL
KIYKRLVELRAPTELVKKITSFPIDAGVDVAITIPHDQ
>TCRU_6109 Ribosomal protein S10p/S20e, putative
MAYVKKDQAPAQETQRVLVKMTSRNAKAVENVMTELLLHARNEKVVLRGPVRLPTRTLKV
TTRKTPCGNGTNTWDTYELKIYKRLVELRAPTELVKKITSFPIDAGVDVAI
>TCRU_6110 hypothetical protein, conserved
ATRAVSHALMCCRRANQTGIPTATPAEADSMKCEDTEDQNPAQEVCVLKKLDVFAKSRIL
NYLSRHLPAGDEITRRASPFLITKTSDNALYQAEMLLPVEALISGAMQRTEIRAVGYAQR
EKEAIIAACVHAERCLDALGIPLFTSDRLQRKRVEEAKRDGRYAPMPGDPLREVHLSELP
FPVWFKAEAGGDEETGEDAKCASAQRKSGSYYPTLRSYQPDYHTTKRRYNDFSRRCGSDP
FLRGMAGELAYLQARIFRHNTQLSGMDDGDDEGTSITIDPAEVEVLQPSHVSPDPVIRSD
TAPFFHCPAMRLAVINSRPLNEHRIAGFIDESEGGVFDLVEGEKGTWWIHEELPGLVSLF
DPFARKRIDGLYKSQLKVPFDACVETRVDEELTQVEIGFGPNCRKHVKWYTATAPVPHYP
SLRAVGKALTVDHAVSLCAMHAELVLGFLGIPLSSDVMEQTKHYDACLRHGRLVSPLPRE
LDSEVQALLPKPLKQWHRIKKSRKRGAPMSVSEKLVALNRRVVADLRQHLMEVDICGQPL
YQQLLESSMSALRQFMVEQRHPYESAYVNFVYAENGQYRCSIYLPLPEAYGVRGGNAIGA
TPETARKLSALHAIDTLCALNVPITKNKERMEHLLDIRRQFGLILPRDANDTCARDSISF
NIRSPPGYREVPGGATTRIPPHQDVWNLIMADASDFDVVKDVEPEKCYKLGLPETGSMLR
ELFQTYLQTVGWTAGEQWSYIKHYQGSQHWNGRLRVPCNNYWMELPLDEKLYGRRIALGR
CVFRKGAEKAFLIHVFRILYSLRLAPWDMYSDGALQSFLCHSQKKNIERERVWWAFVVRQ
FLTSSGDEGDTATHGPSFVPDAEVCIPTSADLKRILSPNPVMTHELAKKTFV*
>TCRU_6111 glutaminyl cyclase, putative
EEEAVFSALSFFLPASQRRVRLMQRIQKMLQFGTRVAGSFSPGHRKMLEFIAAEGQWQPQ
LTTLFNPTVIQPSPRSHWRLEWDNFTSETPLGARWFFNLAFHFEGGHAFRQQSSKETKKK
EATTVKRSRRSFAAAAGGRNGEGRSSMAGEKLRHVVLAAHWDSKYFAEFDFLGACDSAVS
VVYLLETMRMITVLSETSEILQSLTENAEKKDFCTQLRHALSPAYRKILLYYYADDDDVI
HCLSGNTTTRMAGNGTEDENVSNREENFGDGDGGGGVAWQRLLRHVSHLPAITVIFFDGE
EAFVRWYDDDHTYGSRHLAQQWKKKKMQPVVTDAYNVADTTLSYFDSIDLFVLYDLMGPA
ETQFHNYFPDQSGMAFALLVDVEEAHRLRAERLSCIVQQFMREKENCSSYLPEIWCQHGT
PHEMYTLSDAPCLMAPLRPHIDNAEKSFPSNDTSQAHSIGLRVRNLFFPMEEKLAQGSQL
DNTFAMEDDHIHWMDTQRVLHLIPWPFPPSWHTVRDDGREIDEGTVMDLLRVLEEFVLYL
GEGWI

>TCRU_6112 Legume-like lectin family, putative
LPEGVVRGPLLHEHAFSAPIVTDWWDEGVPHFMIGGSAVANEKFIRLTTNNLGDHGFAFN
TAPCDHPSWEVRLRFSIRAPLPVVRARARQAEQEAVPYEGGEGMALWYLEQPLGDDHQHV
PKYSKQLDPDAAQEEKLSRDPSRVADLLLNHNDELDEDEDDDDEEEEEEEKEEEMNEKAR
EKRRMARLLKQKEREELYRRVFKRGTSIDNSEYEPRIFGLKFSEFKGFGVLLDSVGHREG
TDSHPHHHRSSNNKNNNNSSSGRGSAKNAPHDPRITLLFNLPAKERGGAKPAVNNFNPRE
PDFHKSPVRLQCQYDFRQLPTERAVRMSAQTTHKDEQEARESGGEALLHRTPEDPVELVV
RYHRRRLSVIITREDVSRRRIVAVNPAEMVQKRPMKGGNTYRVEKMYVDTLCGEIDNVDL
PLNYHFGVSASTGPRNKRHTERKGAGTANLPSSPGGNPLRAFIKDLYTVKQMDMHVDVHD
VISFELRELGKDAKAMGYSKSIPIEHFDYEVDRRERQHFSRQL
>TCRU_6113 Phosphatidylinositol 4-phosphate 5-kinase, putative
ELTMELPPIWQFVHPEYARGDGSSKGDGNDEADEDEEDDEVARMKKAPKLSKLLRFINDV
DDDEELERMLQERDPVTQQTLLQWATRQQHFTLAEYLLKRAKRAAFGFPMESTEMAVYTR
WEEMRPELPTPAELQARQQERDKQRTERLASKLQQEKERADGNDEEEEEEEEEEEEEEEN
EALPEELVYESLSEYHDEWGDHGVGIVKQIGELGVYIGARLRDGTKQGLGQSIFPNGDVY
TGEYENNQRHGLGLYWWAKQGVFYVGRWYRSVRHGHGRIVYPDGSRYLGAWSRDEKHGNG
RYVYADGSSYDGAWEHNKKHGYGVYRFTDGSSFHGSFVDNEFVSGEWRLASGITRYIGNF
SKDAPVGAGVFLHRLGSSSHDAFQQEGFYVNGEWHPGVLHGTTRVPPRLEVFAPQQEEPK
RVPVTFAPECSGGKMVDLVKAVNFPPVQRWIKSLASVSEHGKLGVVLMSIEICSVKYDSE
DANLVVEVRLRPVLYDADKKRLRLSSIGDETIILKENTTRLILIVERPGTTEVERQPMVI
LERSAQMTCAGENHMQHRLPTVQVSMEGEIEGAFARAIQPALRVTLNRHTTTKQLLRPIH
SNPMLGNAAEDVIMYVQEWHPDAHAKLNEKLEVASRVPPEPEEKDKKPKDAKPLEQAVAA
EAAPVVPATEGCSYVAVPLEKVAEVSNEALTVIAATAVLQRRKKSELPLATAPKQRPPTP
LPPAPEPRPELQPLYDARAVLKRAEEGSDNEDDDDKDTAGAEE*
>TCRU_6114 UEV domain/Zinc finger, C3HC4 type (RING finger), putative
TRFFGCSSHCKPEVMGRILHDVENLCNTFHFYCRDATWGVTQQEKLCINGGLPITIKKSN
SDHTSLTPDSREQAPPHRYVLPLQIWLTRLYPIEPPLVFLLSAEQGCRIASNHKYVDATG
RCHTPELAAWHPVSSSLCDVVKKLCQLLSAEGLIPLCFGEEGVSSPSKGHATAVSQRLCH
GLENGDDDKQTDEHERCVVCFSPKETVLVPCGHYCLCDACATNVTHCPLCRGSVKFRQRV
FS*
>TCRU_6115 protein phosphatase 2C, putative
THSRSKRFFTQSLWRMFEYGVTSEQGTRKTMEDQHAMVPEAIPFFAVYDGHGGTQCAEFL
RDNLHTLILSHPDVMTNPEKALRDGIANAEAEFLKKCANGKCESGSTCAVAIIVDDTLVT
GNVGDTEIVLCRAGSPLVLSTKHSLQSNGAENERVKACGGRIISNRVGHPKFNPQVLSLG
ITRAIGDAGFKLDEYTDGKPSGIIAEAETRTTKLTDDDEFFVIGCDGLWDVMSYDRVVQF
CSRLAAEGVPPQDITDRLCQEALRQGSTDNVTCIYINIKAK
>TCRU_6116 60S ribosomal protein L44
DARCNAHKSFKVVQYKAGKARLYARGKRRYDRKQSGYGGQTKPIFHKKAKTTKKIVLKLQ
CSNCKSIIQNVLKRTKHFELNDKKKTGNKDPTW*
>TCRU_6117 hypothetical protein, conserved
AFQMREPVVCAVYPTCVLICWDPPRPANSPTEVDHTLFWTYEVEWTTSHSPSKERFSGTT
KYCHAVIEIFYPNEVINLRIFAHASISVDAFACGSTSCTIDAAETIAMPWLHKRSMECRC
IFDGLLFSTNGVQCIEAIPDGSDYMRATISSVCMLESSFACIIVRAIYNDPPLPISSSTV
YYFVVCSKILVKQRERMRHSGIVEFLEKEEACAVFCGIGEMGSSAALAAHLFIASVPESI
TGLRERVFCIAYGSPRRMFFEDSLVLASTLAFSGNFLYYTGLLDAPDPSSGYKTTPPATQ
EGKGKATSDTALLLNTPLGVRCGLLLDVQEGRHYLRTRCSGVETLCEEECHESLDVSEQL
RVLSRLLLTRGDTLLLPVIEAMEHTVEDGIMVCLRIAGANLQYRPQICVSSHGGWPTAIS
VTNMAPRRIDATFSLLEMVSMESATRRKPLQRLQVDFALLTDMGYTSHMNYTIDVPEDVA
ELLFLENRNKLPYAWIFSKPINLIDSAIVIEPFFTTSVAKEPRRFEPGRQFSTELIEALA
SISEIAHHFATKKQSVNLLSFVANVAAKVSNSGVSSQAMNPIPIEAPPAREGVFGKILGE
YVNNKKRAVSSLLSNLATWKQKLQQGLPWLNDTKYREKLCSLLGVFGKTAPASDVSLVSL
EMSLFTHVLRYLRNTCGVSNLQHLRSLHQCMEFEKFYQLVHPLFSVSTPTLENAAILIIL
ESAALWAVCLVFHLRCSYLFTHLIAVTGCAGSGCKTMCNAITRLGLEQDYRLRGSQRVRN

VLIRRAAEYELDDLKEILLLGFGVTVIVVGEFADIKGMGYKAIWSSIRRSMRSADRQRIY
TFLSKADELVGLCGGNVAAGDVDPVKVLRDTAVTSVCAGSAVGDVPQHLVAVSFSPSVAF
LKTSVFVLQSGMSAEDFAERLLTASLGEVQRIL
>TCRU_6118 Ribosomal protein S13/S18, putative
FALRMVKGVGIRFAYMVCKKAGIDVERRAGTLTAEELERISEVIADPAKFKIPDWFLNRQ
RDPKTGKTEHLTSAMVDTRLREDLERLRKNRVHRGVRHAYGLRVRGQHTCTSGRHGKTVG
VSRTK*
>TCRU_6119 hypothetical protein, conserved
AAASTQRRFQGRIPSKGYRMQPTVPDRLKDAVSLFGADAHNVTPDDPPYVPEEQRMHMTK
EIMGSNQNMKNHGKLDRLRAALDTVHNEGPEHEGWKEVYLFLRTTEMCCELEKDPTDLFP
KGKKLWINLDECEERRRPVLMQMPNGMLVLPVFSMEEYLDHYFCRVDAFESCWFPIPRMG
TRFEEFCHLPFPVTAVGSMQHFSALATVALRSSQFGILVNPGQRTSKFITYPEMVELAKQ
RSMRPKERNTDLKRKSNGVEEDIFDRSFRCGFDTRKLAMRRVEPVELEELLRHRPKIPPV
AQLELHLLLFEYESISKVFVSTVDRPRWRRVFSASEKMTRIDVVVEGGRPDRAIFERIKK
WSYMGEFLSDVHVEFTAVSPEASNGDEMQLFYDSSDGKLLRGMKAFRGITIRRAIGYDDP
LLDAHGNPVAFT
>TCRU_6120 UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase,
putative
YLVVLGIPSTDVEERRTRRNLQRTTCWRSPGAATRANDFTGAMLVLYVLGRHPSHGYDYS
AVLLEEAAQWQDVVALPMNEGRVTMKKAIGGGGTWGEEAEIGLSRKTYMWFDLAHRLFPT
ARYISKGDDDMFLRVPLFVAHLRLLPRRGVYMGVHIGSSHFGKKGLPGSTFMVGWCYTLS
RDVAEALVSYKPLRRLAYLPYSEDRYDEFALLRFQHEDVMVAWVLERAVNYKPLVYVKVL
PCHFHDARNSTGESQVVPTSMCVHHVREDDYAL
>TCRU_6121 hypothetical protein, conserved
LAMEIAKLMEERAYRRHMLPCLSLRQRSHLWALRCQALFGDAPSDLDVPAPNEKEKVNET
AQKQLTPMESSLAGLPKLPQRPLHWYQFTMRFYYSAWVALRGKMTPQLAAEALCTEFLYL
LKVHSSPAMLPLMEAASNTARAKAMAFNLDKREKGSAGGSTINKTAGSSEGFYVRGLHGD
PVVIAFLWFCRAQSIPCEVDFEPLSSELPKGEEDLFLVKSLSQNTVVTEPLAAFVLCVDL
YLPQCGHWLGELPPCSSSSLHTTRALRKSAWIEYMHHILVDLRAPLLRFMREVTSQMRNC
GKSQESQFSQPRSIGQADASCGDSSEVLRRRIREMSDVAMKSLAHYERFSHHYYATIPQV
TVSVAELCVAAYSFVICTTSLCKDFFPPLEAVPSALGKIGVHAAVPWGHRVSLYRDGESK
EPLSESLQDTTALLSGVPKAYQEIATRILRSATSAYSPSVKVLICENDGRNKITDKGTKK
IAFLSSGLLCLESAWDGLTPGANEAAMLVVDRWIWITCSPHRRTLAEVLSYAWCTANEQC
IGFPFLVLDKEQRDFVTTLNAHPTSLARHEAPWKEGKAAAVARTFRLKLRTALGASPPSS
ERRTYRSYAAKL*
>TCRU_6122 exosome-associated protein 4
PVMKQNGGRETPDGVRYPHIALDVLGQCHSSACVELGNTRVICAVHHPQQLVDEYRGSRG
RVACTVRRSASAGSHAAGSAQPSVVTPEKDMSLALEGVAEEVVILEKIPQLLVEVVVEIL
AEDGGVWDAVATSMSAALVSGGFEMYDLFSACGSALLSDGAVVLDPDAAEESNAQASALV
CVMLNSGDICYARHQGSCEPGTVLELVSSAMKGCLSRKSAITTQL
>TCRU_6123 hypothetical protein, conserved
MSTGSTEDVHMTEETIIRRCRMHQGYTTPELNEKLYLNHVGFRTISSLDAFHQCTVLYLN
DNAISSLEGLCPLQRLHSLYLNNNVLQECCTLPVLPSLRLLDISNNSIGSFAGISNAPGL
ETLLAASNRVTNLQGLEPLGHLVTVDVSQNCISQADHALPLLFQKKTVRTCMLQGNQFVR
TTPSYRKVVIAQMPSLRFLDQYPVSPEERSCAEAHAIGGVEMEKAKRMENERREEEERKK
QFLFFSEARATVRERRLTEGPRVGSTAYFENNKCDDIYVPN
>TCRU_6124 hslVU complex proteolytic subunit, threonine peptidase,
Clan T(1), family T1B
MFRRIARHTSFITACQSRQTTILSVRKGDTVVLIGDRQVTLGERIVAKSSACKLRKINDD
IVIGFAGSTADAIALMEKLENKVGEFPQQLTRAAVELAKDWRTDRALRRLEASLIVCGRE
ETLEIDGQGNVITPESDGIVAIGSGGTFAKAAARALIDVDGYDAEKIARKAMRIATEIDV
FSNEHWDVEILTR
>TCRU_6125 hypothetical protein, conserved
KGMEDSGVIAQWTNNRSHSGGRKELSGRGFTTHAGGSSSMNTKSGASIDSRRQRSLSSSG

PKRGSSPTQQQGKGKKAEKLPPIASKHQGRNNTSKGAAGAASGGSPTLKKKRKATGSRTP
TPRGSSGGKRKGSPSSASKLGSRASSFGKPSAPLGSGRHRKLSRASSGFSRTHGSSGAST
SRRRKSLKKRGGSSRSGSKKRLTKGKKGRMRSASSRGASKEDMGMAYMASLFATEAAQRV
GIEEEEDTTRELFMPDYNLLVMNMVRAQLAVVNDRQQYLNDAFKALRAHGIQLGSGQDPN
AAIEMLRLQVQAEMQKQVDDVRVENGTLRGLLEEKKTELEEKTAEMQGLRDKVNRKLMRF
EVESESLKAEVQSALQTSQLDVDRMKRDLGHRIDVASASFRTPKYDTALRSMQDMVRTVQ
EEIQEHHDKLTKLIVSIGAQDTFLREKSDSMHSNFPTRYRDELRKLDNDRLLNILDVLSF
HDAVVETVGKALYVLQKSEHSTNVF*
>TCRU_6126 Fungal domain of unknown function (DUF1712), putative
CLRSLCVYCPTLSEGREERAMDNILFYYPPHVAANAQMNQVGFCIGAACLVERFGATRPP
DRIQTSHGTTTLCNPFPNLWIAVETTAVYESFAVLPVIRRGFEVFVFRHGWKTISALVSP
DVGSAEVLEARKALENFYGNFAVFLETRILVVDIHESIRTARSMTPSFPSAFGTTGTTVG
SERVSTERWKRRWAVLAFTESLLAFSVFMRSTPRAVQSTCHGLAYRYLSFLSAGRVRNSL
QGSRCSNNNNKNKNHVIGHFYNHSSRTVGWGEEYKGIASTTVSAATLTKNAEESLLWTCC
QYIVFVSETLKVVVFNAAPVVVSRLLCLLLMEPGLTDFDIFTESGHSRCCISHASGITVV
FLINADVYRSMHQTILEVCKALAVDIAEYLTTGTCTLTRGGLVDQSEMQQLALTPLNPSH
RTAAEFFSTVSHLPKLREMNLTFQWTVWHNGLIIGSQMHEYPRGVRTLLSGMLTALTREL
SRKTGGVKGICDVDSANNHHVCSCGIFEEGDALSSCMQLPSAATELWMPLSDASWLCVSR
RYHHVGGVVFYNSASLKSCFEATSELFPCMSSLL*
>TCRU_6127 CAAX amino terminal protease, putative
MTDIALCTFISGSFIGSIYAWPKEHRFACLCIRNLKEASRDGPHRVIRDDPSTIRRRMVS
FVGATGMSMMLLEKLLRKEPGDCQALLGSSLLRYIICSERSISQSMVEVAETGVATLLLF
SGPFLEGVRFPRWSDTDHIIFFRNYILAPFGEEIFFRALLLHLLRRRPVASSIVISSIFF
ALCHTHHIFTIAAEECQIATELDEPDTGVLIYWKRAAGNLTGVLGCTFVYGLLGGYCYTI
VCAKNILATILFHSICNMLGPPPLRFISEGSLRKRALQAIVYVAGAVGWAVVLSKMRRR
>TCRU_6128 protein kinase, putative
RREASRSSRSSSGSSRHSTYSSSSSLRGSDERKHYPLFTAEYARRFGRSNIPFLRLDSGD
MHQKQQQQFTSPLLRLKHLSPTPWTRVRPRWILYNEYVLLRELGKGTYSKVVLCRSLRTG
DLCALKIFRNEQTYKEAYWNEVGTLEALCRPLPEEVERQQQQYNIGVSSGGHGGGGTGVC
NGEGSLTATVTGRYDAFGGSAVCQGQAGRFIVPISHLPHPIHHAIVLPPLGFSLFDVLRH
IREESMKAAGNLASGSQKSTLPNGVDEETVLRQRGVIEVHYRGLPLELVRSVLYQILLFL
RHAHRRGIAHTDIKPENVLFESNDTLMTQLCIRTHRHSNNSFEPFGSHEQTQKIGLGGIG
TFTSSSSSPNSMQKGMRVSETVLNVRLPAMNAVRVIDVGAAEFLSECRKLSVLDGKTPVF
YHRIQTTHYCSIEVLLGLGWTSSADMWSLGCMIPELLTGDCIFMPQDDLEHIALMQHIIG
PFDIPESNGQSETIVRRVFAKGRYFESYFDTHTMQLEWPYRFNRSSSQRRRRIISLEDIH
YVVSRPTLQEVLEPFPQLYDLCRRLLDYDPLRRITAAEALQHPFFT
>TCRU_6129 casein kinase 1, putative
QMNIAEGRFLISQRIGSGAFGELFQGLDIRTNSRVAVKFEKRQIAYPQLSYENKVYRVLH
NGQYETIGIPRVHYFGVEGEYGVLVMDLCGPSLEDLFNYCGRRFSVKTVCMLADQMLQRI
EFLHGKGFIHRDLKPENFVLGTGRRGHVLHLIDFGLSKLYWNKRKQLHIPFCEGKTLTGT
ARYCSTWTHRGFEQSRRDDLESIGFILVYFLVGSLPWQGITVRDVQQKTARIGEKKLDTS
LESLCSGLPGEILQYCSYCRELRFTDTPDYNYMRELFLTLAKRRGCVRLPLEKANGVWWN
GSNSGSDTRSSPYDWMFDWCLKRGAEV
>TCRU_6130 hypothetical protein, conserved
MVLMSTYRNSRFVSKDFLHGPVMRFRALGEYYFQRAWNGTLNWTLPGEYRLYAVMIPFIY
FYHRWHQEHKLDIDHVEKAMIMRWGGTLEEVRKLSAKDQLRVRCFTDIEKLYSAYGPKDV
NVQPEGDSLPGKDLYKKAGEGHHH
>TCRU_6131 hypothetical protein, conserved
IALRIFKSTFLASAAIFFVVLVVFVTLIGCVAFSLVGSVTIRHYILSHAPGNQLMSLTFN
TMPFETELWRLRKVDAIVSHLTSQPESLLQRSDDSLVASTKETTDKQLTSSVAWQAASLK
MSLIEQYVKNTLATSTLIIPSLAQKEVFPPGGGISIEALFEQKKPMFNAKGVYDAKMQFV
FMKEDAGRDVSMVLESAVLFAEDPDVPQSLAALDVLLKTTTSFTVTTGEKESHVFIRLIK
MSLRFVFFVPLWMYETFFFSLRYDVFPGVDPLTEVAVVSDVYTGFEPPLALQPRLRAINF
TLYQQGGHVMNRARLIRMHFFTAVHLTGLAYYFSTYKLISFMCTTLVL

>TCRU_6132 calpain, putative
MGCCASKEKQPRPGAAASPPRSPLPPPKGRRQRPPPAPTEDVVKVEGVVQKQATVPEEVL
ERLRRVMEARQATYKYGKCTVEGGEGSSFFPPRGLCHLIKKGDTWFLHNDTMNYEMHVNC
KFSPDSSVIPLGSSIKKDEEDDSAIVSAVVYPLDTVEFLCGEKGMYRSDVFAQALSEEYR
QGLQVLTQAATEELQRVIELADGSVDEEGILCKCIETSTPYVDLSFQPSEKMLYRPDVDG
RPIAAVEIRRSTECHGVNRRKVDAICGTVIPQCIDPGHLCDNWLMCAAAALAEDEERVKE
MFALCNPEETRLGAYRVSLNKNGWWKTVLLDDFLPTVNEVPCFARVLDDPSELWVSLLQK
AYAKLHGSYSSITGGDASHALRDFTGAPSYRFDEAWVNAAKGYGGVNELLGKLTRYLEAG
NIVLLNTPAGKSTKQNAKAGLRDGYTYCLKEVRQFQNFGITMLKIQNPWEPTEPWTGAWC
AGSSNWDKYEEVRLVCNPDFSINDGSFWMEWSDATKQFDGCSVVLLSRDPVYDYRVRGEF
SYVEPNVVLMVRAAEPVEVMLTLTQLDKRGVPLDMPDARHSPLMISVSRAEGNKQLVHKN
SSGDPESPSDAFTFVVAREVAMNYKFEPSEGPYFVLPRIHRKGTLEGRQKDFVIGIRSST
PLDGKLDIQFTKLSATNPALHNRVLFVVEDAAEVIRPLQKKMPGEAAVTSAGSKLSTATI
PERQEEDEEKEEEEEQQEEE
>TCRU_6133 hypothetical protein, conserved
LATSRQIHGRSGRGDLFFVNSDARRHDMRALVQLRGPRQSSQATCPESGQLYYKKLMLHA
VSEGANSGSEQYRHAASTWAYLLPSLLRCAELAVAETLWAKLCRIELEGNKGEGTLLTER
EKKSLRDGQELFRYELHQRIPLLEESVTSAGLRELTSWFTVARRSWVRLPTTSSSPKTPS
IDIATNHLVSMEGSLLPSRDIFSSFAAPNVFRDTTPGSCQTYNMAMRVARLTEVVVLSVH
DEMARLGNDENIGKGKPKSARLLEKEEKMRQCLLDEFRWHNIS
>TCRU_6134 hypothetical protein, conserved
LVYAEVVVSFATAIGLFVFTVVQLLYRTTRRARRLWRAENQIRFDGAHFLSKPEGNVGRK
IIEIGLKEHENKEVKPPSFVLPAVVANDRDVRADCLSMLAETRQIFRKQYGDSACLMSMR
CCLSCVENALPSSQTEDFLRLYENVLFGQHRVDGISDSLTNDDIKFLYAFFHNTILKEIQ
>TCRU_6135 Nuclear Dbf2-related kinase
GIREGNMTEEGKSKVCTDAKVVVAKKYTGEYYVRGMMGDRKSFAIEHSHARQKKHSVDEF
CVGDVIGRGSFAEVYQCWRPDDPEVVYAMKKIRKDLIIQRQQSLNIHTERDLLSDAKLRQ
RRAGCPWITDLVVTFQDPEYLYIITEYCSGGDMISWLIRHDIFSENTAKFYIAELVLALN
SLHKMGYVHRDVKPDNILIDRDGHIKLADFGLSKRDPEWLETLCRSNLDEIFDDGADTQS
RFKDRKERRAIFFSTVGSPAYIAPEVLLGRGYTYSCDWWSVGIILYEMLCGYPPFFSDSK
NVTAKKIVCFKEYLGFPQEPDALSSEAVDLISHLIADPEERYGFEEILRHPFFNGVTVTD
SIRHETAPFYVELSHAKDRQYFEPAPDNAAIQQQPLVTVSREDQAVFVGFTSKLTDRGQS
TTLSGALGRFHELQDFSDED*
>TCRU_6136 calpain, putative
DLKLAKSAMYSVDDPDFWLELNGSLKVTALGGITKLHEAELVGLQSDQTYGILSVISTRN
SVNPELSDLLVMIYNPFVEAAYTGPMNKGDSCWTSELRSILAPERQDVIYMPVSVFCSAF
LSIQQVHIKGLLVPSWHFNSEWGEGTNGGNPTLVTWRENPLYVVRNNSEEPLQIMAMIGQ
PDQRHKLHLLPQQELDYIQCGLVLSQNTDKTMIPTYLLTANNHQMIHKGLYMDFREVANR
IVIPPNFFGYLVPGAMFHEQGRFLLSYWYTNVDDEKRLSITRLKVDVARHLPAIAHVTLE
SQQRKRVDFIVDTPTDAHILLRQEKPYRTANCSDAMTEDFLGMYLYDEHDEYLSGVASAT
NFRETGIVHHLPAPGRYVLSITCPHANGPVPVRVEIVATEEAHVRTTEPPINAVKLKDVN
GELNEENITLPVPQTLVGLTSRKASTRTTSISSRIPSIPVEIDIRNQDFSFLDPAPEGIP
IQDIHLMGDSAFAASARERMKLKRNPVANASKISALEEEMDQRAHVLAKQLRAKERTFLD
PEPEGVPLELLSLNENEAFQELERELRALNRKPRKD
>TCRU_6137 hypothetical protein, conserved
GPMPDTIELAESALAPFMAFDGGHLYLSKGQQDIPVVCGSESSAKSRIVLPVTLNDLDRL
HGTLPVQRLNQTSTASEAQLDIVEGCYVLPEGKDRPCVASLNSTPEQCNMNIRDSTAYWT
HRERLRMTQNSSQILGGGADLLVNHVLWVHGLRARLRRSIRRTRKVAETGKTLWKVVVLG
WDKNTIREDKQAFVEAVSARGRELVNGAYAEVMDKWMVVRQWMKTSVGEVEDAVNTFSTE
NGGSLLGPHAYCNPSTYFVKWLNYFDETLLGDFIASSVKQELDSLFNGFKFFYDNTLKNL
DPVGRLPCITTCFALAMMLFEDFPIRLAYRNMMNGIGSTNALWSLEQFKALGDPNEIVTR
NRNYMLDFYERSLVHLSTEPHVKKVFDGNVSLAECVAQAIQRAPGLNGSLPPSSLYECFS
TVSNSFRDKVCGRGTQNATDASVDVGTYVELPTPPCPWGYTRRSGNNWNAREECVMCPPG
SFDDGNGDCRCSAGSVPGENGCKATEDKYAVPPSWKWVVNSLEGLVASDGPGNRKPVLVV

NPQNNPKEDEKTVLEIRCTRGLTRFVVEMIMPDNSTTPSLQRFTLPPQNSITVASASTIS
LSLAGSAAFGGEQCEFGVWTKSSRSQSSQVLRAGSAFIVPSISKLNVSVYTPASTAHQTT
FPAPGRNLPLCDALPKADPETATLAACSTSTGNFAISLLLQAYKPLTASTFGILKQRLWD
DGKQAAALGRSLRPVLERMHLAVRIKVGRKNSRQPLGEVFIGSFPLSEVINRRFLMPKNI
ERVVVEVQVLDRCTFSASAHNPVCAKAKILFAPGEVKRITF
>TCRU_6138 hypothetical protein, conserved
GVTHVPPVAAPVARASSSLMATVSFSPGGGCGMLVIATLSADDTRRGELTFMTVAADLSA
MVLARCAFSFNTEPPYGIAKVVWAGVSVVGVMSSSGEVVCVRSGLVEKDDNNDDDVDDHA
TDNEEGNEALFVGVVAHALDICGITVGGCPFVVTSGHQKLQCFAFQKQCAGGGMKHKRRE
LNFGPFHSIAGVADHRNGPAILLGCTLGSIVVLEWTSALDAPVVIRSIIMGPSTRYIGIA
VNASDHCESERQVTFCVFGDRTLEGKEELEDVELQRADGSLFDIPKLTGSFVSSLPSWNT
VLHNAPSRPHAEGFSLMVTRPQLHRSSSVNCHALLINVTQSVLNAAGSCVNGTCCDKVER
LPSNVNIKVMDAASTDCKKALARLNSAVSVLPILRCTKSQDSHEYGELCLCDGRCAIFFG
FTEKGQMMPRSVLCLESRHDRLLGCSWFPEARGVMVLSGTLLNDFEEASESTIMKKGEKE
ADLSANVVSQIVLSSREPLPWECADASAPLTLEQVQEVVRTIVQGENEKMWARLEGRLDS
LERAMSLL
>TCRU_6139 hypothetical protein, conserved
MLRRTLRVMSTPKTTHTNAQQEVLEISSAYSLLRMCYRSIDIKVKSRHARQFLQKRLIEQ
WREHCQETDPEKQRFLMDHAGAFLQALHSSRNPKPGEVVKFQLSRRVAYEEAQRAKAERA
KTVHKLPSGAKL
>TCRU_6140 hypothetical protein, conserved
SYLLQRVRSAMGPQYRSKNAFETACRSMITLWSALNCSMLENDVYEALLLLWPIFLKQGV
VFLASDSPILCARSLLEPLVMSASSTSVKDVASISEANTACIGEIMQLLISELRQRTMTF
SSLIPPLGLLQELTGIIELLQEYHLTGSNTTFSSAKIELVDAYNSLIERYSLRFVEDVAF
PSYWNLNWSASSSCFLLNGVHPTIYFCFNSLVGLVEWCGYPIQMVDYMPFRQIVAHVWER
SALAIAVVAEEKEISEVRKKQLQVDTMHLVLFARMFRKFLGERLSGVVSSALVRLLETVA
RHVSLETRKGSSSQSVAAAFETNIWNVPPIEPAEWIQCVRARGGKKTTNAFIPWSEDFIR
ASHVKAAQKPPEGWQSISFQQL
>TCRU_6141 Peptide chain release factor 1, mitochondrial, putative
MRKALFFLFGAGGTQGGVKKLTHENPIPYNKWFLEESTRALLNPIHHPLVTEYFLRLNQR
RLELEMLQEQGQTDALRSLRNKVDGKPFDHVLWNIQYREEIDVAEEISGYLVKLNENVKL
RDQILLEKDPVGEDRDLLSMLEEDMESLLNQVRNMDDCVNGVMARRLESGDTLGSSSRAW
VLEVTGKAGGEEASLFAAELAEMYREYSTGVRNWRIEEAENGAGGGGAAGGGGGDASALS
APALASTGVKFKAIGDSVYRNLRHEIGVHKVQRVPLTDQDGKMQTSTAVVTLMPVLDPVS
VNVHENDCKIEFVRGSGPGGQGMQSSSNAVCLTHIPSGISVKCHQSRSALGNKETALQLV
AQQLLAQRVKDQNSSFHEAWRNQWSSGERSDKMRTYNFPQNRVTDHRLGKDFPLNTFMEG
GNGLKGLHDDLNASEDRKQLVTVLLRHIEGEF
>TCRU_6142 Protein of unknown function (DUF1295), putative
PYLLGKWLSLIDYISEDYLGGPHFIKLAHVINFQKGASLIVCLLMMKKSGNYSATATTYT
ALHGGYGLCWLLKELIFPDAKWQKKITLGSAITIFLSILGPYWYIAYNAIMKHPEHSNIS
LCVAIIVFQIGLSLMMGSDCQKYFLLKKEKGLITDGFFSRIRHPNYLGEMLIYGSFAFVS
KDIRSFGVLAWVWVGIFVPYILRKEHRMSRHKGWHAYTLRSGLLLPRLFPSKE
>TCRU_6143 hypothetical protein, conserved
TMEGPVTAVEQYFNQLINMRLLTQVVVSDRQGNTIMACFGSSKQPEGQEGAANDGTSGVD
DDLTIESNVVLSGAHCFQNLEQLQLGIPSYISLQYHDATVVQSLDGCCMLTLIGYRSQGH
FVGGLLVLLPQIRATPAYRELLEKTQECFQ*
>TCRU_6144 pyruvate dehydrogenase complex E3 binding protein, putative
MRRSFLFLVNFSPLFMPALSPSMETGTIVEWKKKVGDLVNENEVFCTVQTDKAVVDYTNT
FDAGYLAKILCHSGETVPVAKTIAVMVEDEADIPKIADYRPEGEAPGEAVKSDAPAVPSP
AAPAPAPPPSGGKRYGESLEDTIAASGPAVLRIAARLDRKTLESLPFTGKGGRFAKCDFV
GQPGFNDDDVPPPPAPSPPSSAASAAVSAKNSGATRVNKATAGAAPGGSVVGKAFPVCNL
KVSDTTLLQQLIRTMPLPKKTASA
>TCRU_6145 Thioesterase superfamily, putative

MFARQPLWVPLLTHAPVFLERYLSLTQASPHTKLLLDSINYSPEDTRVLLVPDARAKGRH
VTYAMAFPFTVTAAVCDAGIPGGADGGVMSSGAFTSLLDVTTTIHVMERIMPSRDAHVSV
SMQTNCLHPIQLGEKVLLISRADKMGSRLAFMSAELLRDNCGGNTALDGEPPAATVEEME
RLLRRFEILANGKHVKCFIRPK
>TCRU_protein, putative Aph.1
MHLTGMLGCGLLLYAPLLIASFAAIATHPQLLLLALSVVLVALVGPFISGVLYLVMKPVA
LLPLLILVDVTVTEFLRVWLLFTLYRVESVTRSYGQLLVASPMRFALVSAAVGCGFGTIS
FLRGAGTLFDSTQRMTFYTRGTTAYDLNVCPRLPLLMHSTLQAFLLLLCQVAWAVMTGQA
VTALQKLQQPQKAWRRLLLFYRVNTSKKKLPAVDELEVAWLSGHANKRRNTAPAEEEGRG
TTACNSYQEDEEPHRVCPREWVDNTEQREKEGDGDGEERGEFVCFIKTPQVAMKDDGGSQ
PLLPPREQEETQLPEPTLLRSKPLLAVASLLAPFLLHLLFAMFSLFNSGAYNKATQKEVP
RRGCVISLPLQASVTAISLLWMAGIIHVE
>TCRU_6147 kinetoplastid kinetochore protein 6
MQSVLPYTLNPQCMVGCEKMKILNPNTAALTGPMITAREPNLVSGGLLHNWDANAASAHL
STVKTVHTWDLSWTEKEAYWEKNVGKCTAPEEVEGLLPSKWIGYNVSSDVDETLALVCKL
CTALVDKFVSLSRGDNANVSTAKWRQRQVLYDRLGAVVELLEASIGEAIPILRLRDPEFV
RDCWQQLQDEERMDIMSALNA
>TCRU_subunit, putative proteasome beta.1
MIKRPEGALLHEPSCPMEIKHELTFNGPAQSAKKLFEPEAAVLDPQLNEAVSLGTTIMAV
SFKGGVVLAADSRTSTGTYVVNRASNKLTKLAEKIYCCRSGSAADTQALAEQTANYLESY
EIDTSKPVNVTTAANIFKKLCYMNKWNISAGIIVAGYDPLNGGSVYSIPSGGSCVKLDYA
LGGSGSIFLYSFFDANYKTGMSKEECVCFCQRAVAHAYSRDGSSGGLIRTIALHQGEPED
MTIPWTKTPYCMEKDPKYRDLAVQNPPFSSSAKITVNQSRSE
>TCRU_6149 chaperone protein DNAj, putative
EEVDYYAVLGLTENATEKEVRQKFRELSRKYHPDVAKTEEAKAMYGKINRANEVLTDKKK
RRMYDMRGEEGLRQLERALAQNEQGHSMDPFARLFGMGSGGNLRGSDSQSTLHVELEDVY
KGTQRSVVLEKQKVCTKCKGTGASRGSGVTTCSHCRGHGVVIQRLQLGPGMYQDIQQACP
HCQGQGRIAKHRCPACNGKKVVRGEVTLTIDIEQGIPEGHKVTFEMESDESPDLVPGDLI
MAVLTKPHPRFSRRPNGLDLDMSLTVTLKEALLGFERRVEHLDGTEFLVEATGVTPYGEV
LKVRGKGMPRHHMPSEKGDLYVKVMFELPSFLTEAQRKEIEEHF*
>TCRU_6150 hypothetical protein, conserved
MSFRPSCIICCSDCDTDGLFTSCQHFLCTRCTARYPPGQCPRCRKPCKAVKAGAALPKEV
QERMARDPQRLLTFATQTLEFQRRQEQQTLQRLREIVTTLNQSNRSMASQISAAKTEREN
LLNRIKRLQGQIYAQQQQQQQQMTQRTADSHIAGDKSGVTYGSGGQGMSSRAMPVFLQNG
VVPSPNNAAICGWLSSPAMGSRATTPLGWSQSKRPRDDGHHTPNSSNNNNNNNNNNHNSD
DVSGAGSGELARFRLATPAITLRNALPGMRDAAPVHQMDCAAVMSAPKQLKSLLSRGP*
>TCRU_6151 fumarate hydratase, class I
MLRRSAAALGKKAPVPFKYVPLIPHVSHDDTPFRLLTKDYVSVVRPGCGLPEILQVDVEG
LAKLASEAFGDVQHLLRPSHLASLRRIFDDPEASDNDRFVALQLLKNANIAAARVLPGCQ
DTGTAIVAGYKGEQVFTNGDECEALSRGVYKIYTTTNLRYSQNVPLTMFDEKNTGSNLPA
QIDLYATKGQEYNFMFVAKGGGSANKAYLFQETKSVLNPKSLRKFLEEKIGAIGTAACPP
YHMAVVVGGTSAEMTLKTVKYASCKYYDNLPTKPDESKGYAYRDTEMENVVMDICYNMGM
GAQFGGKYFAHDARVIRLPRHGASCPIGIGVSCSADRQALAKINKDGIWLEQLETDPAKY
LPEITEDQLLKTPPVNIDLSMPMEKIRAELSKYPVKTRLSLSGTIIVARDMAHARMREML
EAGKPLPEYIKNHPVYYAGPAKCPEGMPSGSFGPTTAGRMDPFVDLFQANGGSFVMLAKG
NRSRAVTQACKKHGGFYLGSIGGPAALLAKDSIRKVEVLDMAELGMEAVWKIEVENFPAF
IVLDDKGNDFFQQLK*
>TCRU_6152 leucine-rich repeat protein (LRRP), putative
MEACSVALQRCVRNIVNEGGYGNDMSTASLLEEPRENEKALTGMALLNGTHNEKQITQAE
TLCMMGGKFDDDVADYVASTVFPKAGRLRVVEIASTKISPLGVITLLRSLYQSPNDVLEQ
LLFCDTRLHSDECAVIYNLMVKHTSHLQRLELQRCHMDDTAAQAVAEGIAQAKALVEVKI
ADSDIIPAFAIPLEDSQWLLFPSSLKVLDVSGNRIESVHHRGLAIALRRCIASLEEIYMS
RCCVTESFLTTLLKAGLHSSHCLRVINVSSGRLLHTAGKVLSSFLTECPNLERLYAQDNL
IEADGAARMAIGIPCAKKLKVLGLGSCHLNGEGARVIAEAVRQTPSVRELDLSNNSLSDA

DVFQICACEDGSSLQLSFLDLSSNPLTDRCRPFIQALLRSKKNGTCTVLVRNTNVAAEFS
YLQCGDLSGLS*
>TCRU_6153 hypothetical protein, conserved
MEPVIQPLPHDESSFTSRRAAFERTRRLHAGTLNIFTEEDPTTATTVTPHVARRPHHNDE
SHETREFLWARLRRVTPPRHPETPRGIHHVENAAGKQQNIQVVGITDAYKNPKNMPLPRS
GLRCVARSNSSSVRDIISRPESVENKRGDSRTPSRVVSYSQQERFCQAVRDHVQHRRGGV
TAFYVSLARGLVGRVAAEAPLGTPRHWHLEDLPPTHTLTLGSCRDQLQSLTGISISLGDL
AEMLWNPKENIAPSVDDDPSEGQLRHMKVTYRDFSAAFGDNAENNKLAALKI*
>TCRU_6154 TFIIF-stimulated CTD phosphatase, putative
MSDYSSIEGRLMDTLHRRQNTSMIKSYWYSQLRSSGALLDAKAVSSPKDRAATASSQYTP
STGNSSGLTESSTRGPNTMTLSRSASFRSPSSPSTRRRRLHAAALSAELRCALDLRERFG
TLAKPLFQSFLLPQFEAHETCPTLTVVLDLDETLVSNRNGALSAAILRPYCLHFLNALRH
MKGLEVVLWTASKKETALPVVEQLNERGPVFDEVIYRNDMWFTEPLHTKDLRLLGREMDR
LLIVDNAANCCKLNPRNSLLADDFYGSRSEEDATLVNVYYIIERLLKGCQEDIPVKDALY
RLATDGQLCSPLVLTLPDAWKTLPLRDIAPLKIPPHGRFTRVHREPLDKSIMRHWTI*
>TCRU_6155 Dynein intermediate chain 1, axonemal
MDGNQTNARRASHNPNESHPNNSQTSAGPPDATGGQQPGEDRDAVVERILKGTDPSVMST
PVYFDYKKDARAYRFFPSVGQTARHFSQDGSTVRKDDPEAVQQAEDRQRREHDTELAARA
ELNPDLVDEGVSTSILKNQFNYRDRGNQTMNNCLREQCVMTDPPPSTNFSAMATAWEIYD
AYEEDRIQNEKAAAAHKKATAHRTGKDEEKITLPEDTGGSKTSEEILSSSEYREALKIIE
RMVNQNDCHDIIEDFKYWEDESDLYKEDGNLLPLWQFFTTKVKHRAVTSISLNNRYKDLF
AVGFGSYDFQRQGKGSIHCFTLKNTVPTLSGVQIPAHPEFSFNLESGVMCLAFHPEETAL
LACGLHDGSVCVFDLRIISKDGKESVKPICQSDVRSGKHMDPVWEIHWCNGTMNLQFYSI
STDGRITSWSLHKKELVFKDVMTLTTGACASDPEAILLSRLGGTCFDFSVAYDGLFIAGT
QEGSVMLCSKGYNGQCLVRYEGHTMPVYTCRWNPFHPDIFITCSADWTVKLWLKNSTKPL
LTFDAADSVGDIAWAPYSSTVFAAVTSNGKVFVFDLNKNKREPLCTQTVVKNAKLTHVAF
HKNEPVLLVGDSRGSVLILKLSPNLRILCKPKKGEPDDPKSLRKLEVEKLDRLIDITLRD
RVLLGQL*
>TCRU_6156 kinetoplastid-specific phospho-protein phosphatase,
putative
MWDNRCVVVESGRELSIGLDVSCDIVVQQPQSRAAGAHIVASRHPVLARISCTAEEELLL
SIPAASIAVYVNNIKLGMLSRPLRLPPGSFVSFIKCCKQTTFRFFTISTYSVAVPTPEST
SKVLTPKPLVESLRNKPLLLLPLAPTGEVEEINSPRSPRVVQIMGSSKENKAELLMASYE
SKPLEETEKSSCQGLTDPGSSGFAHNMPPYIGKADTYLPPSPHAIVPYVVELLGERAALH
TIMDQSSLSASEIGQLSDPKSTKTKLSHHVLDDPYMTCHGYEVLKGVRYMRFETPVRSAA
ANVLECVEDAYEPEEGTFLKFTESSRKMLLEQFFLLAEHAIMTMSFSPLTIRRRSPIFCC
GDIHGSFADLKFIADSVVPFRHWSLMTTPVLFLGDYVDRGLHDVEVVLYLLSWQALCPEN
VIILRGNHEDEEINGDVETYGDLSFRKKCWDFFGNKDGEMFWRRVNDVFATLPLMAIVDD
TIFACHGGIPLLHVNLDEPAPRGREEQPPQEGQQRREKEGEERDKYPSSPREITAGNDGV
PHEDLLKLLMDGTPSELSDLRFRCLMPVDNEEGRIAQFRRLVRELLWNDPVSSSVTCDTP
LLRSGEGIFGQASDEHAFRHDTFDAHGFRSNMGRGDDRNIIREFTAFALESFMQRWGFTL
LIRAHQQKMSGLEMGFSGRILTLFSCCNYLEDMNRAGACIILNQEVRPISWRRSAGRRVA
EDKFEPLQRRAGPAIWSSGSLPESFCSIKERPMKRPIVPSYVGSSVVSFG*
>TCRU_6157 ATP-dependent DEAD/H RNA helicase, putative
MSGTPSNAICTAWPEMALDSRILEAIKRVKWNSPTPVQGACIPLALKGRDLAIQSRTGSG
KTGAFVIPILQRVITETEKMCNRRTAKNPVALILLPSVELCEQTVEVVTALAKYVRPRVV
VDNLTSRGVVTKARVAAAPILVTTAALLGKHCRSGTVTAEDLATLRCVVIDEVDFLISIA
EGSLRAVQSVLPPSVQTILSSATLTDGVVHIKSQLLHNPVTITLSTDDENEMTPTEGENI
VVESRITKKGINSEERLRHYYLVATDECHHHTLLYALYRLGHIKGKTLIFVNEEEKTYKV
QGFLAQLGVEALVYDSNLPLNVRVDTLHRFQVGSVGTLVCTDGTLESVDNLQESIPGTEA
QTTRMHSKKGKRTEDRHDGALQRGIDFSDVRNVVLFDGIAHPTTSAFSRYTHRVGRAGRA
GKGGMAITLFTLQQAQRVTRHLRRHLGATHDTFEPFKQLRRQEAAKLQYRVDNVLFSITR
SSTRRQRISSVAAELTRSAYLKSHMSQKDEAVLQRILSRSKKTTKCDTTLLDVPHYMHIE
GVDSAEKYRKRVRACTSSKSSSASQQPRTRSRDPLSRVASAVKMGKAKKRRL*

>TCRU_6158 predicted WD40 repeat protein
MDSLGNRETPQESEGNSQREASSRSSPKSSDVPYQEKKEFCTWRKHVRDLYQYLVHIDLV
WESPSARLMPYMTAKNGLATQTVLCCSRTGGLEQQYIQLLSVTTPNTVESLDRTYDTYCD
ATGEVGGYGMAPSQVDMKVERRMLHDGDPLIVRYMHANPLIIASGSSDGNAYVFDWSRIS
LNKFPNDPARPRAPLPPNELSSNPTDEERMTYHRRMQALNAVVTEQDRWDKRRGEGQHLL
KLSGGSGSCEALDWSVTSDGTLASGSVGVVCYWHVGNTAKDDDRTLTPSHTYKLEDGEAR
VSEISFSWKDPHAFVVSCETGTVLYGDVRTPDLMELFSLPNGVTSISLSPLDGNSFLVGA
ENGEVLYYDLRKSTDAVTLFGRMHNGPVSVVQWCPHSRHLFSSGGGDGKCCIYNATSNRL
LFKHAGHTENVTDLSWNWQEGFEGHLISVDSNSVMLWRPRDMFFVS*
>TCRU_6159 hypothetical protein
METIEELRLKLTEAQEECRQLKAENEELRRKLGLSPQLAGACLPGGIFSSCSETTKSTDR
LIIELQRRLWDALQRNSFLEQESHAGHSALIQTYEGFIERLEKELHRCQELLRQQTSDSP
PAKKPGGEIG*
>TCRU_6160 transcription elongation factor s-II, putative
MSEENADEAVGVKRPRPVSFTTTTTPLEDSVDVIPRVSPRTPLPLARKSVMGSPVGSFGN
STQSATPIKPKEEPMIGGVQGSSRVAKWSALIGSALMQGRAKEEEEQINALALRIVTAIP
GDRSLAADGFRVLLVNLRDDKNTKLREDIIEGRLPVEVLVHMSERDLLNPEARKNQEEEF
LKRSRDTDLSEIRRAMATKSTLFPCPSCKARDCSWTQKQTRSADEPMTVFCICNVCDHKW
RRY*
>TCRU_6161 Transcription factor S-II (TFIIS), central domain
containing protein, putative
MSGAVEGSWCDSGSDWSASSASPELRSLINAAFLRFISTSHGRLKRPTHRRDEVPSTHSR
RCGLRQRLEESLQISAGTTGVPSALLDGIVSAIRQQSDRVHAAALIVHHLSDPENSALRQ
ALLESRLSPTALTSMAESELVNPKLREKWENQRLKNLEQKTVIFVGQLTAMVTSIYTCPA
CGGQRCTLRRRQADKQKWAGDDEAPNLLTCCACSHAFRR*
>TCRU_6162 Enriched in surface-labeled proteome protein 1
MPNISRHLFCSAVLLLVLAMMCCNAGGAAEAAGKPSGSRFEWKDITEGGVTVESLGAPGL
LQVRSDVFAVAEAQCKKSGANTFTGVASQLLTTQTPDTPVEVLNGAEDKTQFLEDGSEDS
KKKVDVSRPTTVVKGNDIYMLVGKYSSTDVGENSGAKDGGLLLVQGQVNADESGGQKRIK
WRDNDGVSRISVGERQSWSRLTGSGGSGIETEDGTLVFPVAGTKKKGESNDGKTVSLLLY
SSDTKNWKLSKGMSADDCSDPSAVEWGEKEKEKLIMMTACDDGRRRVYESADKGESWTEA
LGTLSRVWSNKKGEVGVRSGFITAM*
>TCRU_6163 hypothetical protein, conserved
MVEAISCLDVKASFSKVSLPRDTRHLFRCRVEDGTLVELTRLPMGYKASPEILQIITSAI
AVVTTVVHRLWAAPPSVCDDVWIDNMRIAESKSDATLWEAQVLRNADGRRATIGKNANRA
PRNTPSCGAV*
>TCRU_6164 hypothetical protein, conserved
MFRGITGRCSMRVLCLTVVPDGGAMTLALRRLGYMPYTLRSAFQHGRATRHPAEWSRILD
GERPVDMRLFNDHDAVIGPPATLIYDRLLRECPEYTKVILVEETDKKRWVQEYEAHVGPL
LQDDTDKKYICRCRSRRRVGRSRIAKAFDNMIHKMTPRCEAAGPVAALEGYESQVRSNVD
RSRLLVYRYGDGWEPLCAFLEKDLPDEPFPPYDSGVRVIGNLQERIERTEKLTYLLAALA
CCGVAYVVYPVFGSLQTYVSELYRDYQTAYATK*
>TCRU_6165 hypothetical protein, conserved
MSLKVWVKRGGMGDEEALGIHVPVDGTAQSVVDACRGVFRHLQPARAALCTEDGIIVARA
SPVIALRNHTLELIELPPEEAPKRRVANTTTINRNSAAAAASSAVKSENFVRQTSAEKET
RRTPPVPSAAKKSFPTKSSMAAATQAKKTDRTGVGAKETCAASQRLAALWDGLPVFVSPL
SIKRSTPAVAGILRSARRAYAEAVGSQFGISNNSSCDRVPSLGGGQSLLIGDGAVAVLRQ
SEPAGLAECLDATKDNSVRHDNGFWEAAGENGTDGLKDRERGAPSQCELIALEEVQADRL
DNFSPRGTLPCSETVATAVTAAVSAETELETSHGSEGAAGEAMTTKVAGAVEITKTFMQT
LGPEEEQNRTAAGNFVGCGEKIGTAAADRKETDGVSPNTDELSKKAPAYFEEW*
>TCRU_6166 hypothetical protein, conserved
MNLDICVTLSELAKLPRGVPHGGKTLMCRAERVFASRPREFCAGRVFNLSCRLLDGDYKE
HCEEEYAHLYFYDDWAFAASFIEEGDIVILKGFTVHDIPCIGGEDPKFPFFVAPISTSST
LRVLQNGLNDDVMEVMVKADRLDVPCVRVLPKTLRAPFIANDVD*

>TCRU_6167 hypothetical protein, conserved
MAMMMAGRVLLVCALCVLWCGAGGGVFADQAEELSTESPGGRLSGGDPLETEELAKPVLG
GADSEIQSPVVEQPQLNHPQDLRGTATGSLGEGEGEGEVEEDDEKGRGKGKDGKDTRITE
KTEKQKSLTKDRGTLQLPPQPERGKTPAPPGEALQVEEEGPPPSGGDARPRQPAATPSAP
ELLLTLTSIEGQGQGTPSENPPGPKTTTTNGKSAGEASPTASTGSQTATETTSTTSPSNA
KVALGAAEKPLGNRVPNQQKEKTDTPDLMKDAPTRHPAEKKSTFISASGSDGAQKKEDKV
DNSDQRPNSKEPQYGHEDGNNEDAPTANETAPQTAKTITTQKNITSKPGDSDGSTAVSHT
TSPLLLLLVVACAAAAAVVAA*
>TCRU_6168 retrotransposon hot spot protein, RHS3, putative
MLGGDNVSHKLLKIVRVRGECNSELTFNGLISLGLGNLTLCELAEFMMPNNFNLLVLAIK
DDLLSEPLEKYSVFAFSSEAFVGAIIPKLRELKIEEDAPPHRCALELCPHERSLKPCLLP
LLENFKKKINIEYRVLYKPVTQNFFLVDGFFFSDSNPMTLVGLRITTASEHHTIPSTVNL
FKENMAKYFNGWEKFSRDLSWEIIYIQHADSTPMKGWQRCGPLKTDNLSRAENKIVAFWN
EKVRQYQVSVSSRDFK*
>TCRU_6169 hypothetical protein
MVIFCANLTVSAVQLVEKFEFARVHEGHLTPLEMKFRDVRADVVEDAMLRGEEWTSLKDV
YHYLPRVQPKFVFFFLPMNLTFPRCIEESRSLLEDCTWFLCGCSPYFPARRASPDDVQGT
RWCSHALFDQPIVWRYSFWVKLDGDAAFFRSLRDNLLQRLLSSGPVSGHTG*
>TCRU_6170 prostaglandin f synthase
MNCNYNCVTLHNSARMPQLGLGVWRAQDGAETANAVRWAIEAGYRHIDTACIYNNEKGVG
QGIRESGVPREEVWVTTKVWNSDQGYEKTLAAFERSRELLGLEYIDLYLIHWPGKKKFVD
TWKALEKLYEEKKVRAIGVSNFEPHHLTELFKSSKIRPMVNQVELHPLFQQRTLREFCKQ
HNIAITAWSPLGSGDRTGFLKNHVLGEIAKKHNKSPAQVVIRWDIQHGIVTIPKSTNKGR
IQENFNVWDFKLTEEEMRQIDELNEDKRIGGHPDNFFPGGEE*
>TCRU_6171 leucine-rich repeat protein (LRRP), putative
MSRTWCPALTADSSLQFDTKHLRRKSGQDGCHALLSSMGRTKETAAVAAECDASVKELST
DLTERVNSSISKFSAYVVASRTNMAQWPSFADPSVVAFCEAAIPLIAQTEDEAEAIESNE
MPVTAYHLSHILKMQLELERLPDVKLPSDQVVDFIAHVMRLEAQRKNSSISESMRRVTLM
PSPSAKVFLAGVIEALNINRRMMQQLRFLALAGEFEESTEETVLQEFLQATQRLVTLEVP
YTALSHVSGILIPLLKDSMIRVVNMEGNDLGLSSNEADVIPLLAEYIKENKFLLKLNLSY
NNISGTSAVLLLEALATSDTRFTPQYLPESENDGKDEEAEDGVLNDIGFFLPHLHEEEEE
EEEEEEEEEEEEEEAVNLAQAKNLGKSKKKRSAEEEEEEEGEEEEEEEEDEELQQSQDS
DDDEEGEEGEEDEEEKYKLPPHLVKKFARIFRRLLRDEREARVDFVGEYMNEAGELVKEL
DAIQAEIAEEKRIRIEKYCQRRSGWSHLQVLRLRGNPIGNKGATGVAAVLRHEVQLEDEE
IERIQTELSDGADKLLSELLSNRRNCVVEEVSKRRQLINEHRSAWSLMKAARAEKARTEK
RSSVVFPAVKTSSRSVTGVTVVGDDEDVDDEEALENSMDEDGEDSRKTAMVRSTTDVGFV
DDVEEFAEEEEVTELEEARGNWETPFPRTKRGLQSLRLLDLCSCQIGSAGLKRIGDALRE
NESLEVLLLRHNHFARKRVALLATEEDAEEEAGSTTRVDVPHYVSPGCLSLFGTLTTNST
LKTLDLAYNNMYPESIRALARALSSNTTLSSLSLEGNCMGFNESPYQMDPAVIKATGYPV
DAAIFSRSSCFLELLKALLGSGVTTLLLGYNDLAQCWFAEEIEWLTRLCCRLHVLYLNGN
GLLSEHLTQWANAIQTDMKFTLRELKLSRNDLQGESGGAALGRILSRCQENLENLVLDGT
QLGSSGTVSAFASFESSALRSLSLQRVGITSAHVLPCAVLTPLRRLIISDNPFSLSELLD
FMDVLRGSASELMCLSIWSREVMMEKHLPELQLKVCLMPRLLFADFGIMKRFDDVVDADD
PLGQIEAIFVHRHLSRMADGVSTCNTP*
>TCRU_6172 Rtf2 RING-finger, putative
MGGDGQALSNKRKHLEESRAFVTAEQLRKGAGKEVDVTRKEKEQIAQRWAHCALSLEPLE
TPVVFDLCGRLYSKRAIVNELLERRHRPKCNKEGFDGGNCAIAKLSDVCEVKNVEEGERV
CIRCPLSGFEASSGLHKFVGFWGCGHVVCTSSCSDSVMKKGEARDAAPGAEPATTSCLLC
GEDSFQVPLILESEDDEVAQLQRLRPLQRLACKRKRLKN*
>TCRU_6173 hypothetical protein, conserved
MVHEATVYYRVDLYCTDECQRSGQHERWRLSMYSSEVISLNLFRVVWDPVISFEPLPVTR
SAVSVHSSEQVSLMGSSASHPRSRIVGLEQPQQPPVGATLASIVATLERLEDKLCTRLDA
LEAKLSFLELKLSAGNDATSNNNNS*
>TCRU_6174 ribosome biogenesis protein, putative

MVRARKRQRGECDEKEKETNKFPSTGGEGGESMIGEMQLKRATTDKRMTNRQKCLVLGSR
SISSKDRHLLTDIRGLMPHSREHPKIGRTHKLGDDLVELCSLHQCNSSLLIEAHRHDISY
MWIAQAPHGPSVKLQLTNVHTADELRMAGNCLKYSRPLLHFDREFETHPHLRVVRSLLQM
AFNTPRYHPKSKPFIDHIICFFYLDHHIWFRHYQITDGEPRALMEIGPRFTLEPAAILNG
CCKGTVVWKSDMAKSPTEQRRDRKTRRLEKTQINEGIKTKSEMHKALNPPPEQNPLDLVF
KEF*
>TCRU_6175 syntaxin, putative
MAEYLPSSDGLMRSTLRETIKRIRRIRSRAGREDEKEEESTGDPLRDLSLAFIRCVTRTK
EAIKSRNEGLKQHGQDRIAIEESYAIRKDIRTMETLVEEIKKFVDATETALAQENKKTKP
NRRKVTLLEKQLNERRAQYNECLSTLELVRDLDQRRSSVDEKGLDIGEEMQFGRKAQLRQ
QLLMLRRTQTGEGGHVDPNEGIELHDNTVGGGRLEEHEDTKETMKVIAAKDAKIDEGLDR
LKAGVGRLHNLAIEIGAQIDMQNRMLDKTEQHMSTQVERLRNVNRRIGKFMREKKPLNTF
MNVCCCVLIISLVGFFLVQFNVV*
>TCRU_6176 hypothetical protein, conserved
MNFKNRVSETKGEVKGPSRQRPLKENKRKFAAGDAIKKASVGRRADETHPKRVQAANGPS
QQQKVQVATTTSWVKGGSSLSFADVVRRKTENVVMNIQPEESHEDIAEVVHVENDAVDLM
HDIQEDSINVHNMNNESEDIAYPTMQQDTAIVQAVIPPLPEEELMEVPSIKYYVLEIDRI
VEESVNLPPRTMATAADYMGVYTFSGQAGKPPTPPTATQLQQQFYRPETTTARPFGGMSG
TSEISRGQHWGSQQGHTVDYTNANWSLQERGQRMFHQGMQYSSYAPPPPVQQQQPQRNFM
PQTVNRMLQSDSADAPLRHLRESGTFNRHPGNGGGVW*
>TCRU_6177 retrotransposon hot spot protein, RHS3, putative
MVLASEKGWPYSWNTIQDLPKDVFVICAVDRAWQIVKGDVTAWFSPHGGTDFTPRRRVLI
GTPGIGKSVAAGSYLLYQLLHCDAEELPVVVHCFGGGDAYVSDKTTRALTRCSDEGMCIS
ELRSLRGHGRNVYIIHDVAKEGTPPPRHFAPTSGWGMIAVSFPKVIKYGEWAKQLQAARI
IVNCPNETDVKAMCAWMTRDETKEKQAECWKEVKKHMYLLGPIPRHVFDEEAFNERCGAV
KFALQSINEGTVKEYFSRGGESPRYSEDPSHKPVEVVREIYAGGVILFNAPISACLEERT
LERLPSVTK*
>TCRU_6178 hypothetical protein, conserved
MVGDAPRHRTSGSRDSSTGIWTDGMEHAESTAAAAWDAHTASPGGGLPRAEVHRKREDRN
HALRGGFSMLLEVRAKQLGALSSPGL*
>TCRU_6179 hypothetical protein, conserved
MQDSAASAMGNTTASPLERVPRSVGCGVARRFACSLTDRTAPLFHCGHSIGIARCGGVRK
SRSPDVDGLVVIWQPIPLGPSLFRIALAARLAQHRPDMFLLQVCRHQSAPATRLVGCSDF
HQACSGRAGGVALLVRHTLPCERLSLLAPTAWRPPPCPSMYVVNLCKLPSAIAHAAHFAS
TIRRPGSAAPIAGDLNLHHELRDGRSPSTAAGEDLAATPSGMESQLSDDPAQAARIGGHS
VFFPDVTAQRVLRVSHWTSTCLHGVGSTSAIPHCEDGGRHPATGRPSATTETCCPCAACS
*
>TCRU_6180 Enriched in surface-labeled proteome protein 1
MSADGCNVPSVVEWKDTKLMMMTACDDGRRRVYEIDDRGESWTEALGTLSRVWGNKHEGK
AKAVRSGFITATIDERKVMLVTLPVYSKENQKENEKENGKLHLWLTDNTHIVDIGSVSDD
GDEEVAASSLLYKSGTGDNKKEELIALYEKKKGSEKTSPGMVSVLLTEQLERVKKVLATW
KEVDDCVSLLCARH*
>TCRU_6181 Protein of unknown function (DUF2838), putative
MDHRFSKHEYFISCSFTILFSGFVAASYFDISTCPYRYDRVASTSKWTGDGDGACESHTP
GRGGVESSHSLFTSIAQGGDLTCHMADLVIWVYIIALLLFMSHKYYYYRVMGLHYFLLDY
CYFHNACLVLFLLWCLVDVQWSNEPLISWEVYLPQTWLKERQLALSGIQSGGFGRSIKDI
AAKSTPLVNRTWTDWAQQLIPSTARQMILVAGIYQPVSVNVRTIGYAAAEVSSTDEVLLN
FLSFFALVAGSFGPILGAILVWSNSLLFHSFDRMSSSYLHLAPAVTQLLLLHRLFTSAKK
ELASFETSPSGTAAAAAAGGDNDVGTLKHRVDALCVTGTLCHDLRHAVSYWTMLKLHFVM
FIAWQIFYHTFSESRRRRRTRKYQKKLKEIALRHEEFCRLTGTTLEEAQLLRPIFVLSEG
IVGDPTQRVTAYTWLMEHPPLGKEGVLYRFVTIFGTGYLPTVVLFQVAQWLLHMCFFTLA
YPIMYYSFHVALSAWPLALYLTFFLLYTVYNAAAVNKRWIQKLQRLAMIGMEVQRNHGEN
YFPRLDGNVKNT*
>TCRU_6182 nuclear transmembrane protein, putative

MQPAVLQCLFFLLWNVTAAKCALGSAVIVAPFWAMIIKPLLQRLCVPAKRKQQQQQQHAT
PPPPPTVPSQTSGAAGQRTSASRKSSSPRRGGKASGARKKQASREEPREKDPSSFEAAAA
TAAAVLQPSTSHTAPITNEALASLFRSPEFTSWYSGHRDILLERVHVRCAQRLWESLAVM
VALLMGMFLLPFFVLNDGGATLWALLQRRSDSKGYVTTNNGLWNLFFTTVSVHGEPLLIL
VAVLTLLTTAFMPVDAKQTASTALVAFLVLLVEAAMVEHMALGAGLLMLLGVVAWRVSCT
MV*
>TCRU_6183 aspartate aminotransferase
MAIRCLWNNIAALPADPIFSASLVAKNAPEPKVDLIIGAYRDAEGHPYPLHVVRKAEQRL
LEMNVDKEYLPMSGYAPFIEESLKIAYGDSVARENVVGVQGLSGTGSLSIGACFLARVLS
PKTPVYISDPTWPNHYAVMAAANLTDLRKYRYYDSAKRCIDFDGLLEDLNVAPEGSIVIL
HACAHNPTGMDPTHEQWAKILEVFQARRLIPFFDSAYQGYATGSLDNDAYSIRLFARQGM
EMLLAQSYSKNMGLYAERVGVCSVVTADPKKAPLIKSQLETIVRSQYSTPPAHGARVAYL
VLSDSELRAGWEQELRVMSTRVLEMRQALYDGLKRLGTPGSWEHIIQQVGMFSYLGLTKT
QCEKLIERRVFVLPSGRANMAGLTKRTVELLVKGIDDVVRTVME*
>TCRU_6184 hypothetical protein, conserved
MAWVTATSSEEGKSKAPVSGATLSPTPLDRNEAADHNAGPRMSHNIHGSMASEGAPQSSH
RAGEEEDHAILLPKPPLKPAPRQMENHESDTCATHGDSGVKLPEKKCNEMGSNGRLQSAN
NTLTATLRLNEGDLKAENNNDDDDDDEFGDFVGVTSRPVSEPVAIPEEPMLRRNEPLHAF
INQQEKEHGHGIGGGKSESGQLNALTFHTVACASAEPRATTMGSSGCVCVDADRLDMINA
SPVVVKDEGAEEAEEYKHRETHVVEGRDDEGAENEREHHHNNQQQEEEDDEEEEWAAFTD
AAVPPNPPLQKQLVTAGEATGISDMCVEEDTHATSSGRQFVFRRDMDIARIIRQLRELSG
CVLDTEECNGCHDGGIEQQQSDTGSSSGEDRKGKQSRRELLLAVMDALSFRRRDSVNRVG
ETPPVGGGPCVTSGSLAFHCNPLGTPPCIGEGCEKRHDTPQPQPQLPDQASATLDGIIDP
FAPLRLAERHTTQRREQLESVLLQASRVRQRAIPVCEAITKVRNLAMEYEQEKQKEQQTS
DKEKESTWHIHPTLPTPCIGGNLFPAFSLRLPF*
>TCRU_6185 hypothetical protein
MSFQRFHKVLQANEEENEHAREAFLASWRSEYQQFLQSKLAALVWHVEHHCRSHVTPQTA
TSMACGEVPRMKVATTAPNSTTTASTNSNSAMMAEDAEQHDACNVLAHKQNRRTTLPSHF
FLEQTPTSMPFYPREFIVEKEAQMFRQTNSPFTVGETPYDSQHSRTEINASTATVVPLPS
VHKKETADRNSEKDDDRTAILAVSPSPRQISMHSPSQIEDDGSLDASLSPAATVAVTNVL
TRTPGPAVQLQKMLPTEEVSKANLRKTIARLYSESVDTRSSWSDTWSQKKQRAASLLPPP
SSASHMMHLKTMHVSHGTPCENMEASRNDMLSKKQLICELRRLYGLEDER*
>TCRU_6186 Actin, putative
MATATPKKHRLPDGTELTLGYELLQAPEVLFNPALLGKEHPGLAGIVSNAVRVADIELRT
ELCEHIYLTGGSTLLSGFGQRFLSELLQLTPRNCRVRISAPAERSHTAWLGASLLTRLST
FPQQILVSRADFLEEGERALHNRRVG*
>TCRU_6187 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MGTAWTAAAGTLPGVWVNSRSGFRWDESLRVEALISATIGGRKVMLYTQRGDFSGEKSER
ALYLWVTDNNRSFYFGPLGMSSAVEREFAGSLMYSDGKLHLLQQRDNGENSVMSLSCLTD
EMSAINFVLKTWAKKDAFFSSLSIPTAGLVAVLSDAASDDTWIDEYLCLNATVTPNAKKV
KDGFQLTGHSSGVSWSANIPDDNVRHVSLSHNFTLVASVIIEKSPSRNTPLLTAKLANNN
SNHTVGLSYAADKRWGKMFEDKITTESRPWVPRKEYQVALMLQGNKVSVHIDGQSLGKEE
VPLKSETPLGLVRFCFGACDQKEGHEQEPHVTVKNVFLYNRPLNSTEMRAIKERIPVPTR
GPEAQVEDGTERRHIPRIEGVRANAPAGSGLLPLLLLLGLWGFAAA*
>TCRU_6188 Enriched in surface-labeled proteome protein 1
MKKVVAAWKEKDAYIAREYGCRNEKNNWRSDCGEALAEGLVGFLSNTSTDSTWADEYLCV
NATITKGTKGKVASTENFVTFEGFGAGAEWPVGSQGQNVPYHFANDKFTLVATVSIHKEP
KGSSSIPLMGVRMNDARGTVLFGLSYTHEKKWEVTFSDGLRKPLAHDDGAGWETNKKYQV
TLHMDYNDGVSVYVDGSPIYDTEDYEDEEDYNFTQKLRTLLGSHGISHFYIGGDTKNNSD
DINVTVSNVLLYNRALNEAKLKALMKRNAVAAAAAKVPAQEVAAQTTNVSEPSRHPAIAP
VVTPEAQQDATSSPRSQHTPAQKSESKSGPVISKQTSSDVIVPPTSADMEKVEEESPDSG
ALAPASTPTQSAGSRELLGTEMPVSGEHFPPSMASPLMGQVDKADEDSPRNGNTDDRAPH

SISPDVLESVGTNSGPDSFISTNVSGGADRDEDTHAHTAVGTNSSTDPATAHRNGNVSGG
ADAAQTSSSTAPGETKIPSEFNATIPLDNVILLEHGQFGDLAAMALSGALAPASTPTQSA
GSRELLGTEMPVSGEHFPPSMASPLMGQVDKADEDSPRNGNTDDRAPHSISPDVLESVGT
NSGPDSFISTNVSGGADRDEDTHAHTAVGTNSSTDPATAHRNGNVSGGADAAQTSSSTAP
GETKIPSEFNATIPLDNVILLEHGQFGDLAAMALIGDSTVHGCVSGVLLLLLGLWGTAAL
C*
>TCRU_6189 glycosyltransferase (GlcNAc), putative
MSAWLLLHGPENEVPHVRDEKFFDNDAIMDIWRLYEMAMRTKDAYHEAALHDYLIRYKTK
VNEKKETWKREHNVETIDVHEIQDDEPPVLAPYTSSPKVGFSTLMASLRRVLNRIELQGP
KDGLERAANFVEKKMKETSLAESHKRKIFEEGEASEPFDDILYLQLHRLYESEKENTASI
PEHKRAWWQRVKKIVPSIYTKRFY*
>TCRU_6190 hypothetical protein
MVSPVTREASLAPTRLPPPTFRPVPSIPTRPTSASPTTDACDGDFAGGTFSVGDCPVDFC
EFSFGCPGVLCDPCISAGVGGGDCGTVPLSFAVVDTPEKAFVPTALCPAAL*
>TCRU_6191 hypothetical protein, conserved
MLFAWILTILALFFSWLWNVRLRSSNSHRPYKVLHKPIQYLQADFVVVGAGPGGLAASKC
LIEHEKECLVLVIERGMDPSPAGPFPRITGLAHRHNLLSYAVESVGSKLDSGWYVEYPLR
YGRNEDDDDVPCSVAPYPRGCAVGGTSNMDWALYFPPVPAKVGLKPIEAVIVPHAFAVSR
NPLSWGFAESAGAVLKRKHLSSFSEPYMRNSVFPGLLRIDKYGCRLSLSHHLMSQQSPSF
SILEGCEVTGFSFDDKGTVTSVQCRSVDSQIFKVIVRKGVILSAGVIGTARIIRQVFPKL
QEHFFVRDAIALPLIFRARPGISDDRRNLRSFMAHIMWWVARRGPFLNSVSDTLAVVDLP
SLGSRAELVVFLLPFGGRDPTLYRRLGLDRILGMFAEGFMMFLTLRGVDGACFELSAESP
GKEVERRKEFHPLFDRVISFPASKMSRSMLTNVVAAFMDGIQLCRKIVAEPPLAHFSTGQ
EAVDVTLCADPTRAVQYVQLMRKPPSKLKESQRASAPALLAWAKESSRTPAYMEAYIRRH
ALWFGFGSGSCAASLANGDESFRVSGTQNMFIGDCSGVTEKMWRAGGSDTLSAGSVSTAM
ALGNAAAMELLSL*
>TCRU_6192 Staphylococcal nuclease homologue/Tudor domain containing
protein, putative
MSYIVFAVDNADRLTLLGPPTPEGPNLKQIALSFIQAPKLARRSSTGEFGPEEPFAFEAV
ELMRTTFIGKPVKFTEDYVIDVLQRHAGRLELSSGEDASVLLLQNGFATVSEHIPARMEK
TLFAKYSALMNEAKMAKKGIFAPDAANHTRVLRDLTAEEKSKLGEKLKGKVVLVRVEQVL
SPTICMVSAEKFPRTQISVRMPGVTINDSDCLAVSTAARFHTERYLLHRKVKIAFEGVDS
FGNILGSVTSSKGVFQTELLLHGFVKINVSTLAFTSHADALRAAEKEAREKRQGLWKNWE
ESGESGTLQVKYGTAAAEAPGLAVNNANRNDGPEYKGPLSFSAVVVQIVNGDTITVRSDE
KGELIRVSLAGVRSSKNVTREQDGRSPETRVSYTDYEWEAREFLRTHYIGKRVIVQVEYA
RQIFETKEVRPVVLVKIPETGANIGLSLLETGYATFLLGKNDVCSEASLLQIAAEKAREK
GLGTYGKGKPPVQKIVELHHLGNARGKYYLSFLQRGMQGNRPPLLKGVVDAVLGGGSLRV
YIPKENFQIPVKVAGIITPMGAANSSETADPFAEESKDFAVTRLQQFNVEIQVHTVDRAG
NFISTVFLPDGTNFSIATVEAGLGTVANADRLPYYQQLIDAEKKAQKEGKYIWSNQSSIP
QRVAKLMAERNANGVNCYSRSFGPKSEFIPYVLSEVGEDGYSVYLQEQGDENEERLETLQ
DLANKVSSLNGEYQPKRGELVVAQYRKDKSWHRAKVLHAKKGEQIVTVLFVDFGTVSETS
VKSVRAIPRGPEFALLRDLEPLARLVRLAFLKSKVPSPEANAGYACDVAYEYTDGAVIAK
EVYQDGQGNVYYTVTVNENVPSLSETLLQRGVALLDRIAESVDPSEYQRHEAAQAIARRS
HKGMWQYGDIDDESDGEI*
>TCRU_6193 ubiquitin-conjugating enzyme E2, putative
MSAIPHLQKQLRELTTSPPAGFRVESEDLFTWTVWFAGPEGTPYAPGIYRAELRFPKEFP
MEPPMFKVLSSFWHPNVYADGKVCISILHPPGEDEMNKEETAMMRWTPIQTISSVLLSVV
SLLSDPDPKDAGAPANVSALVQYRKDRAAFNSYCHQLAQKSLSELPPNFIPPQKEDRVER
TVNYVSTVEMDYEDDSETDTRSASNRFGDELRQLREMGVAPEKSDAELLGLLVEVRGDVA
TLMERFM*
>TCRU_6194 conserved protein
MASKSKKEPQVVGVLVPSSISGLPLWDDAQIQQENWGGSLGLPTRHTGAVVEFRNMEGKI
VVAHDEAQREAFKEALTHVLVSTAADIIVDWKRPVDIFAPFRPMVHRNITPFLFPYDTER
TLFDGKAAEEAARLSATPTGKKGDSKNAVPPTPLHVQFPEIVHVLDPQAVDGAAGEWEGL

PDERVVARYRELQPLMQAYNPKLELGCAAKPLEACESQYTTVQRHRLQEVDAISKLVEPP
PFLMDAFNSAVTFIEHAQSYVKHGEYLWELVYPHASVTCHPVYNPHGKYAVRLFIDGAFR
RVTIDDYLPVDALGRPFFSLTSQKEIWPALLAKAIFVALGPNCHLLFTDPETIITCLWGE
WVPQRVDPRSQPTAACAFLIAYQKELVKGDGNATHFSFSNTEETAMAMAAGEEAPGKQKK
SSVVEDAFSKKEAPIMVSSPNSPSVSPAGEDVTDVLTTFPVCAISPVEDGKRKLLVIHEI
LFFRDTLAIHISTTSPLKNFESKILTEISDDEVVQDLLHFKTLNEHKCKIPGAVSSSQFT
LWTTFEELAAHMEIVVWRYLGEKTPFHFSSRLVGIEEGSPVPATGKKKSAAPAAVKPFSG
GGKRNIVRWMHLKSDRPEQIAFVSLAAFALPDNSLKLPRAYQRSISSGSLVASAQSPGRS
NGSRTPRDIVRGVSLDLYAWERGGTLSRVGFFPYESGKLQCMVHPLPPGSHVLRLTAVEL
EPQHVLSILSTKEFFIGDEKDAIHSANIFRMTDAGSHMGVERASEEVMWLKRRISVKEPT
VISFVVSTLDPGEDLAAHRDIPVALLKEVKGTKSRAASTKGSQKESVEENQVRVGEVSII
PHCHLLLMNVDNGAVRTGVAGRLICQRLEPNQHGYLLMVYVLIDSLSAASFIEIGMGMPL
ENQAKSREGSNFYLLDEKGNTAAREKALPLYGRGSWKLTISADRGLELYKSIPQNVFSFA
DKGKLRRGSHALLFAYTCAVVEKTSFTLILDLDSHDPIPFHVKVARNGVDAPPVFVSETC
TTHLFLPHVTLELGEKPRSTSYVIEAWLDEEKVQQWEERCRVAQETKFRTLREDAERRAM
ERRQNDLDEYHADPRAFRGRLEQLNAAQMEPVHPSSLRESLLASNKKGRLYSDKRKHPVG
GVMPEKEKVASGPSSPTLPSNPVIFLLDTTDSELTVSFSLRLQFSSKVDIKNGVPPKDPL
ATLRAGWVPPIDHVMVDQGTGYTQRGGGIKGKQRETQVSAEELLKADQGRLSRQRFLENP
RNILLPYLAASDDGSLPSKESARTGLSKDQGVMPVNPSRVVLDVSEEANYLHAPILNESE
YSIQVIPLRAVEIMPPCDQTPPTSASGFMQQRARSPGEKVSPRLAAFPQPTFMPNAAADE
DADVNELRVPIQEVYRGLNEKLKKQQDERIQWRECTREVLREFWGAQKPGASLLSLLGSK
EELPVRQRKSRQK*
>TCRU_6195 Enriched in surface-labeled proteome protein 1
MVSVLLTEQLQRVKEVLETWKEVDGRVSNLCTSLIAEKERASTDDACSAVKITDGLVGFL
SGSLSENIWRDEYLGVNATVNNEAGAAAATLHAGGVKFTGRGAGAEWPVGKQGENQLYHF
ANYNFTLVATVSIHNVPQEGNTPIPLMGVKMNGNENNVLLELSYDGGKKWHVLCGDKTPK
ELSSGWETGTQYQVAIVLQNGTQGSVYVDGQRVGGNGECALRNDESNEISHFYIGGDGEN
ADNKEEVSVTVTNVLLYNRPLDEAEIAAFNPNKDPTPPVTPNAQETGTSSALDGSHLTER
GQSLGSSGVNGGGASPSAVPTVSTPSAGKDSLQQVASGKSSDGTQTVDGGSFSGGEPAVE
TREGETNRRKEEGIHAQNGDVKAAALSNSLGNVSQGNNTDAGTVRESGLLPLLLLLGLWG
FAAL*
>TCRU_6196 fatty acid desaturase, putative
MELLEKRLGELELPTTVEYTWEDVAKYVQQGQKLIVIGDNVIDLEKSVPTGSGYTHSNEK
IVWYEAHPGGKKMLDIYVGKDATEAFQGGIYKHSLGAESLIPHLRVAKLKRK*
>TCRU_6197 ribosomal P protein AGP2beta-1, putative
MTLQTRRDKYDTSQLTLSSLVALCADCSSFCLERTARVLDNQSRAPKGWENQFAAVAKQR
RQEDCELCERYCHRVSSVCPASKDIELFEALGYKEVARRTSLDGLPTVQQMSRCENAVSE
FSRVLFSLAHKPSKVAFEDVDPKSGLKKSEEGGDGEPTELHKKVLSGGSIDDAILQRWST
ARKGRAEMEEMGVLRSAEETASLRQELGRQRSEEYIKTRGTTPKW*
>TCRU_6198 hypothetical protein, conserved
MWKTRHCYVGVTFSGVGAVLTFSLNSMPLHLPINVTLTGCTFLEGAVLRFVGGAEAVESA
GVLIRVSQTVIRSSVVVFALALPQHCDIAVTEVDAVQFSVVDIPDITSKTLSVLLLKNVV
LSASSLLVSNVKAYGSDYRGFGLHSVGTLTLVGGSSLYARYFSFDGYKHLFYVYRLSVSD
HSVFALLNNTMSSGAGLLVQQHGFSVSDHSVLRVVGNRGSVSYAIYANKLWTVEQSSWLD
WRDNDVGLGTVFYDSGSPFVDMDSSSGVTLTGCKMGSTGLSVSLLKRVGAGYRFVAGCLI
VAGREVTAVAELELNGITNVTTVAGCGECTKDGNCFAPLTTAVIGCKCQCAAGGHGDVCV
PAPVPAGPPPPPPLPAPATPPPPPVGECISDMVYPEVAQAVGSGLSWLCYRNVTFSGGGM
SLTVLVGAMTGDVANVMFDGCTWRDGAVLLLLGNAYAAVGSLNIVVTGNTFRDALLSPEG
GFPPHTNITISGNRFTVTRLVPRSGLDLRRPSCVAMNGLVISNNSAVVLSGNVFHAVAAS
SSAIYVVRSSLRVSWHSVFAVMGNTFHMDGGDSNLICLEGSRHSSSLSVLNNSAVVIRGN
LVTRPVRYFMYFFLALFVESQSAVVFQGNDMQGSWFVFFPSHSSNIYYNSWLQLSDNLCR
ESPSEAFLFINPKVNLRGSTVSVSGNRFMSNTVTPTVLRISSASGDLTNGAIVAACNTVN
GEEGVQYVIPSVYNATILTCSDPCALAASCFPAYTTTASSDGCACNCAEGGHGDACLPVA
VPEPPSTDGVDLCVRDVSVDVEVNAGLGTSVVCYVGVTFAADVVVDVESMSGSVRNVTLA

NCAFVDGASLYVVGWLSDPPAGERADVLISGLESRSGGGVLVANRYPPGSRVTVVDSVLI
AEKRVAYRGAYFLGDASACLLVHSMNLTGSVLTIARTHVAAVFRDAAGVLFVGGVALSSR
GALYVDGLSVQTALGLCVSVEGGVAASGGSVVAFVDSDFLLCKHAVSVRGAVSVSGSAVA
LVRSGFVLTEDYAVAFYSTVSLDDGSMLLVKGNVHDGVSREMLYAAGAVTAAGSTLSFVR
NRALLPRMLSLSLSLADGAHLRVACNDAGGRVLSTAEEYAAAGFGDAGSIDVVGCDDCDR
ETYCYAPGTASASMTDGVCVCVCGSGGYGEACVPVGVPVLPPAAVTASSVFFREGVTVRS
VFVVPAGAGEVTLRHVVLDGVSPVLYVPWMARDGVRIVVQNVSLLNGAVLYVMGGGVLRG
AVAAGSDESGPVELSVCDVEALNGALVLTGTFPAGSVLTVTDSLLVAARPTPLVYLPGSQ
SSPYAPVLVLSGLRLVRSVLVVSGVALVTVVTGGRTVAVDGAVLELVGGGVALDSAVFGG
EYALYASARVVASGGAVLRVSGSQVYAAHGLVFGSGVVANASAVVVNDNAGALTDGGQRV
RRCSE*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MDGTVALGGAGGRFVVGCLTLNGQALQPMDYRSAGIIGEFRPVACGVCDADVFCFAAATR
AMSASCRCRCAEGGYGRDCLPVYLPHVDGCNRTLFRPPLSHTATLTETRSPTPTPTPSLS
TTHYSPTQYSQTETPRVTETVALSPTRTPTASVSSTLWWNDVACPTLAVTTTAAGGSLTQ
NDIRGGGSAVPTRLMVALPPPFQWARDPQLGTQLSFVPVATAQPRGFGGPWGAMLRNATW
VRNATNPSTVLELAVPVHRGYFIAADETIVIRCDAVAVFGGCRGVLLGSFTIRSDTLPAA
SALSAITGVVAGAAAVAVLVTGGLGSILEMQALGVFARMPCASAQERASTVALPYFLSVF
AALDPLWMVVGNALLAAVFGCVHCGVTAAFQRWRGVDAATAWAAMRFPSLTYVVAHAMHL
GIFFGSVLALAMPGARVQHRVVGVVGVLYGAAFPAGVCYLIARHVGASFERYWQFSRKPL
HERLLYPVGYWHPAAQQRMYGGMLTNMRDSRVYWCVFQLSVLCVVCLIAAVHSPVGGCHV
QYFCMAAVLLAGAGVVAFTNMMRSAFLTVMRTAGFALLAALCVISAANHLAPSDGGARAY
ADIVLLLTTVLLAATVYSVVVWYAEDRYWQELREPRRGGLEALLRDDEESDETQKLHDLN
SSSYASGTTAALSYRPPAPPLQSVTGDTRSDALSLFDGASIAS*
>TCRU_6200 N-terminal region of Chorein, a TM vesicle-mediated
sorter, putative
MIRDDEESSVLFTVESSEFWMVQHSMKLTAQYTMSNASIQSTYKSKNCHVLKPFCFDMTV
RDVELLINAISACSAQVNATRLELELSDILLYQSYQPAAHCQDNSWKTMKEKGSKGGDAS
PAIAVPFISPFSRNRRIEINSVVICEICVILTYDRRVRPPEDVLFRGSPVGTFVPSLHRA
TIRLPTVRFRDVSRKTLMEVCNTVQEVLFLSF*
>TCRU_6201 Protein of unknown function (DUF423), putative
MAKFYDPCIVAVGVSGFVGVVAGAYGAHALHGRLTPKQQSAWTTAVNINLIHTAGCLSVL
ALRKCVDPNGPAAKHLNRAFHLLLLGTTLFAGTIYATSLGVPGKVIGRLTPVGGVTLMLG
WLTVALAGL*
>TCRU_6202 hypothetical protein, conserved
MMVHAETVEEAPAKTLHKVRHFTPSVVMADVATALVVGAAAAVPISIVDYSIMARVAGVT
DSSLRELWRGTKTLFLRPHRFFLPCAENKCSLVFAVCFVVYTSTYIGSNTMKSYCEAKGC
TPESANFAAGIMSGVANTITTVWKDGIILRSLPPVNAEMLANSKKPVPWLTRGLFCTRDT
LTCLAAFTIAPMVANWLSRHCWNPAENAKKKLPEPVEGKVKIPLPTADMAQLLTPAALQF
ATTLLHITAIRYHQTYPKFSMGDLQSSLRDTYLSSTMLRVVRILPSFGVGAILNRELRSD
LLDRAEGPTA*
>TCRU_6203 hypothetical protein, conserved
MLRRCTSPVFHGGELSRCRGNFRRSKPKFASLAADAESVTEGTQYGGGLPAEPRVVARIS
LIGGVTAEPSNQLDSDILLRLMGHFIAMAERPSDSLDDIMAWRVGVSLPLYPTEPALARC
CCVDDDAVTEGIAVVYSR*
>TCRU_6204 pumilio/PUF RNA binding protein 10, putative
MGKKANFERAHQRQVQHTREQRKRKVAAARALRIGEDTNGRRIQRYSLPKVRLSDEKKKM
LVEQFTQACRLPATSEDLCMLLRSACGEKTQDDASRKRRREETTMDESNLGTIVDAFLQW
GHQAAITTDESDEDEPMTLLEDVLQDECGGRVVCALIAALDTSKNDKKPMVLDAVTKLFE
ENETLHEHYVACKVMSSLVQYGDRETQERVLHVLQQHAKTVDQLQAQLRNRHSAVTIQHL
IEHFPTETLAWLGETLGVTELLVGKKMAKKKRMKKTNHDECDRRDTLLLLILDPVASPII
RALISRSVNTSAFLENMDLVMLLETKRGCKFLQDILSPALPKWNSEGEATVTLDVVMKSC
ETKLLEMCTSIDANFVVQAIIGLIPRTEKASTDRYFKQLLKVLGPHLSSLATHYIGVHVV

VALVVSSHLTPMEDMAEEIAGTIITGNNVADMLCDSNGSLVVRKLLPLCTRKGSKVGQML
LKAINQDMSSLMYDAIGNLTLQEYIKVCGGEEIARKLCKSDELLSMCQHTYASHVVGSLF
ENVGATTHTNLCHALRPHVLTLSRHLNGRFIVEKAIHANRDICDLLLRHFMELACEKGTQ
HVLCTLMLNSDQRGREWVVNTVISGLVDLATQQCGSIVLQKLMLADALLLAAVKKELAQK
PRLRNNLAQNFFGKFVVQITDAAGEQGSPSSPKA*
>TCRU_6205 DNA ligase, putative
MMKLHRILRSLPFVPMALSTFDTIERSAASSTATGSTSHSFVSDGPPYFISPKHDGVRIL
SYVSEHTESLKSTCFSRFGRPVHGMFWIEEELRLLRWLCGDPRLVLDGELYVHKEPHARS
TGDDGARTGFFSVSALVHRLRGPKSACSSEEEVLSYVASLPRLCVFDIVSFQPSDKTNLS
EESSGRGLSRIEKERVSLLREVMKANGVRDLEMLRVIPNYSVFSQRLKVMHFLMCVLHRA
RASSILFPGRAVSVTTSKKNEIKSRNGNSSDMAVGVTNVGGEYLQLVKYSLLRSLDDAKK
MYLKKYLSCGYEGAVIRSASNVYELKEKERGVLLGLLDPLISVGERPFVNKQAACWPKRS
VLVAEAPPLLRTYAKNGLLASIGSGEYDWTDFVADENEAEEANHQAVVGAAVRRAKQNAR
RSTTAVKLLPFCDKEYAILKPLLKIPSANPRARKLVSVPLKLLHGGRDAISVPRTAFGKA
ASKKNEKSKVVVFYGLQCLSETGRVFNVSLPKMDVAKQRALLDHLLEVTGVSRKMGGKRN
TGGVGCRSLTGLYATVKYSSLTEYGIPRFGQVKAIRGGKGWFL*
>TCRU_6206 WD domain, G-beta repeat, putative
MSRSCSPQRVKNGLGQKGRHRGPQSPTRCLLLHSFEECGDLPVTCVTDGSISPGPYGKLQ
DVIPFYGNKKGNVKAFQFWNGRAIATAGQGKMASVTALLLIPGRSLLWCGDENGVVTVFR
LPAKEGWIHGELFFWDGTLCGTDHPASVTCFAADGNNFVYSGSADGTIFSWSMGDSFKFA
GKVGQHTGELAQMVLVCDDYLVSVGSASAMVHVWPLGNKRVGQEPFALKGHLGGVLSCLY
VGKWCGGGGLLWSAGEDCFIHVWDVNNPVHFGCRINCRDVENGEMMDDHTLFGVREEEEE
VRAGLAESLGREDDSLQVNSLRLLVGHKEPVVTLSAASGILFSCDSSGLILAWNPERYWL
LHAFTVPRGESLIHPPSNVLADRGKSVLVEAVRGAHCLGFIEGFCWIIDTARGPRCIYMP
SHTSMKKLLCNGNTDASPFSGERAVSTAFMHLKETFMHDTVSLFVQYIEFHAEIFVHAAA
VLLQWDMPPQCGFCSLGSIAQTFLPGGPNKRCGQTDSALMPRLPCERCAEMHDLQTARRA
VEDERGLFAARRQEEEERWRMERQSLNEEAIRLAERAEALDRLQTTLLEKERRQEYIVKE
NEELLRCLKKRDRDRERQLARVSTELAFLRLKYADWGGVKESGV*
>TCRU_6207 leucine-rich repeat protein (LRRP), putative
MAVTGRGEPRKTTRRVQKRGPHLQQEKKTRMRIDLSRRNLIDFDSAAFSTDDDRELLISI
TRLDISYNSISSLYGLRCLSTLGSLDVSNNNVTSLRGLPPPLRQLNASFNALTDVEGLSP
LLHLEVLVVSHNKITSLEGIPASVRIIDASSNRIASLGGIEGCILLEELHVRQNIIQNVE
GIAMIKSLHSLKAVTLAENPVTSSKRSAAAVYAILPPTLQFVDLPSESWMNHTSAASSFS
HTASVNTATVRDTINISCFSPDSTVRTSKGASTRGSSSPSASSSSHVSLHTKDENEKRKQ
PLSEDNMTSFIAVNDIKADAPSFHLHREVSSFSDTDQHSTFYDSRDATHMQGLKRQQALS
DVNISAPNIHAQHMTSSLEHLQFELDECQRTCLFYKMENEELKLHIQQLQSKNEYQERMN
TILLERNQKLQLLCAGSSPLQQGEIPSAPTDMKHHVEGGGAVQSKSLLMGPLIGPCNKRS
GNLRREASGDDSQHSKVEELSGEVSSLEARAELRRGARSLARLFMSLVLKPELRQPRCSS
PSTADAAASNDNTNNNNNNNSHHHLISPQTEGGANNINVKERSGLRDTNAVDKGRKRSVS
FGGFAYYSPPPW*
>TCRU_6208 hypothetical protein, conserved
MLRYPFVRCVRGCGVSVTTDIFYSPFWRNCSTLTNASSDSSVHPDLIEEIKELLERVPAE
KWIPVGTLYNDLSLDSRRRHVRPHKTLAAALSKATGLGVHLNQTGLMFCKGIPPKEIDVP
SRETTDQTSNATPCSGDKEGAGVCGSSGSGATSEQAAGVFMRPTERVTVDTSSDIPPVDF
YYDVGLRDYPPPPPDFDVTASTLPSPTMMGNGAILSLSSFVSYIPPFFVPLGEVLEEMPG
YTEEHIERYFKHRASEVVTVAGRKYIRLYGGYAKFPLDGCEVAEERFERYRPDPLALKPF
IDSFGGITGRWMPLRILLDRAGHAAVAKLPFKGPASIIYFAQMQHVFAFAVDRDGGSVLL
RPPGYDGLECETTPTPKSCNCILRLVPQDGQVDIRHIEESIPVSVQEEVKIFYGTLLQFF
RFHAAVFSLSADGSVVMRRRFKDRIDKDQLSLEEQLAIAISERNKKKIRSLRRRIAFRND
PSNPFHDPDNLARELHRYLPKKGHVPLKTFLKKNVPEELLNYLPRRFWNFFNNYPQYFQH
FEYQVAGQWCICQPGLPLPRGVIRQEFSEEDLVRLVAEFLQQRGPKACSTIILHLPRGAQ
EAVRKRYGGVFYLVQAFPQYFNVVLPAETGNVVSMAMVHLVELPGAEFTGRSGPLNAVVD
KEGGKWDENEDIDDEEEDEDGALATSR*
>TCRU_6209 regulator of chromatin condensation, putative

MEETSRNHHDHPVRDPSSRVTIAVCGCGNDGRLGLGECESQSRITLLPFFLESALHKENG
TEELIGGIRAVRVGGYHNFVITTTGVYGWGLNENGQLGLGSHSAACVPLPTRIPFFNEMT
VIDIQCGAYHTFAWTTNGLFVCGKNTDGQLGLPGEEDHFSFTMLLTAAQANNSSVREDEE
SGGCRLIKRGQLTHMSCGTHHTLLAFRDVFVVNEFQDETQQQHYQLLIAAAGKGDFGELG
YDGDMWSILEAKTKAMQSALCHGLRRQQEEKDSDAAMPISLEKRWKPLKPRRAVFSSWRF
QPVRLPILLDPIEAPSDKPSCEIVSLHAMHLHSAVVLRDNSVESRSGGVGRKRTFHWGCY
YLNVLEDDASSIPREEEREEVSLHAGNESLFRYSTSASTSHAAVEVMGSGVLGLGEEDSF
VKSWTPLPLPQEAKNLCVRAITGREHYLILLEDTLVVGFGDNMHGQLGAGCVEDVVLDPT
VVLRAGDAVRSPASLAGEGLWRVEAIHDAACGLRHSVYLLKISPVTSAESSSTPRG*
>TCRU_6210 predicted WD40 repeat protein
MAHRLQRRYKAPGGITTCLSVHTEGDNFLVGDTTSHTQWYDCDFSDKPYKRMRSHKGVVN
AVAFHNNTNAYPLFASGASDGQVHVFHGMVYDDYNKNPLLVPVKILKHRRAVYSIAWHPT
LPWVFTSTEDGIVSAWTE*
>TCRU_6211 Paraflagellar rod protein 2-5
MSYKEASGAVGPADQQQPAVPEVTDVTLEAARKQKIHNLKLKTSCLSNEEFIQDLHVSDW
SETQKQKLLAAHEKAQELLASVEGGTKWNLTEAYDIKKLMRVCGLQLSVRELYKPEDKPH
FMEVVALKKTLNELKQHHNKTRTVSFTGTIDNAIAKLEKIEDELRRSQLDASEMAQVPVA
VLKNLEECMNVTVVQTALLGNEEQIKAQLAAIEKAKEIRNVAIADGEMAIAEEQYYIKAQ
LLEHLVELVADKFRIIGQTEDENKPFGRIQDVQKKSFQETSAIKDAKRRLKQRCEDDLKN
LHDAIQKADMEDAEAMKRFATQKEKSEKFIQENLDRQDEAWRRIQELERVLQRLGTERFE
EVKRRIEENDREEKRKVEYQQFLDVCGQHKKLLELSVYNCDLAMRCIGMMEELVAEGCSA
IKSRHDKTNEELADLRLQVHQEYLEAFRRLYKTLGQLVYKKEKRLEEIDRNIRTTHIQLE
FAIETFDPNAKKHSDAKKELYKLRAQVEEELEMLKDKMAQALEMFGPTEDALNQAGIEFV
HPAEEVEDGNLTRRSKMVEYRAHLAKQEEVKIAAEREELKRSKTLQSQQYRGKTVQQITQ
*
>TCRU_6212 hypothetical protein, conserved
MPFLIPNIELFPGTPWAAITWDFISHPLPKTPLTMSGARLLIQFTFSKEIKILNYGRTVL
HHSLNSHLDPLRHYTAPQRQMVSLWRSIVQQLAYSHAHRERSALPLKIGFRHLIPPRSET
SQSSTQTPVATGSLSAIEALRVAPLAVRECVAEEIWAMLLSLVKRGHPAHLIFPPSHCSA
PRNEAAEEEATIAQSLQQ*
>TCRU_6213 Leishmanolysin, putative
MKTVAGGRSAWRFTRRIWRGTNKRKKYCEEGEDECHNALGQKVSCKAEHVLTEAKKQLHT
RKILFGAVKLHTERLLVKPTGGTITVPRAVNGPCSHFTVPSRHKSDGVPNADFIIYAAAG
PSDTKSRAVWAATCNTMSDLRPYIGAMNFDPKYMTDTAWSVRVAAHEIAHALGFSQENMR
EKSLEKKRERSLRGTHRRMVAGKHFQEKAKAHFGFDSLEGMVLEDEDGPREKEIPHWKGR
HAWDELMAPTVGAGYYTALTMAVFADMGYYSVNWSMAEPMSWGHRSGCDFLEEEAQYNR*
>TCRU_6214 40S ribosomal protein S10, putative
MATYVPKRSRDDVYRFFFTEGVISCKKDPLGTWTGSLGGKTFTVPSIQVMQLMRSMKSRG
LIKEQFAWRHFYWFLNDEGVEYLRKYLFLPHDAVPNTHKAEYKVLEREGGRGRGRGEGRG
RGRGEGRGRGRGEGRGRGRGFHSERDAYRTGAAAAPAVEAQ*
>TCRU_6215 intraflagellar transport protein 122
MHTSVKWSEKSPGRDGVRPPIYSLCYSPAADTIVAACGVRVLMYDATTGSVLNSLKGHTD
TVYCVSCSQDGKNIASGGADKTVILWNNKGEGVLKYQHKESIQALAYNSSTGQLASVASS
DYGVFTPESAKVGKNALPSKGLCVSWSRGGQTLAIGLYDGTVLLFSPNSSEKVLVQRNAP
VWALAFSPMTEDGLDVLVVGSWDRRLSFYNTQGKPVSKEKELPCDPCCISFYGNGSYLLV
GGSDHKLALYTKDGNLLVSVIEANDWVWSAQQRPSSSQICCGTNDGCISVIELTLTTVHS
IFHDQYVYRDKMTDIVLHQLTLDKKIRIPCNDYIRKLAMYRDRLAVHLQNRIVVFELFYD
DERQLRFQDIAHIRKKLECNLLCVTFNAVLLCLERRLTMFDFQGNKCREWAFESPVRYIK
LVGGAEGKEALLLGLKNGAGLRIFVDNPFPTTLVKINNPIRCLDLSCMRGKLAVVDDTEL
LQVFDLRKKNEVLFTATGVLAVAWNTEYDDMISYTTSLKTLNIKTGSLPPYQQKMPGFVL
GFKANRVFNINNTVVDVVEVPHSHALYRYVEKKDLDSAYRIACLGVTEGDWKMLGMHAMT
QLRLDIARKAFIRIREVRFVELLNRLELEQRQGSSKENPENDALLMGDIMAYQGKFQDAA
RCFLKSGHENRAIEMFCDLKMWMEAKKVCSNETHLKELILQQARWAEDSQNYVEAASLYQ
ACGDVGKAIAMMRSAGMVDKMVDMCRALPKSDVALITECADYFKKHGAKQYALEAYEKVG

DIRSVIALHVGMQEWREAFALLERYPSYIREVYIPWAKWLTDNGKFEEALEAYRLAKWPR
EAVRMMESLAANSVVCRKYCDAAFYYIHLAREYGVLEDGQHLTEAQWATRMKLSAECVRR
ADIYYAYNFVYAHATQPFPYNEVVLFNLSKYVVSMLSGAVVPLNVGKGEVLYTLARVANQ
LNMTRIARAALEQLQSVVLPIKITEQVDVDSLLIRSKAYADKEELQDVCFRCKQTVPQLT
NSGDRCPNCAHPFVRSFVSFHALPLVEFTLSNDISDAEAERIILAGFGRKAAESNNENGD
TKYSGWKTETGADVITFSEKEDNIDAMIDQQMAAMGRGPATGRDPFQAQLAYVTRPGRPN
AEYQPFVVNAEMLRRMRRDEVFIVKAGFGTLPAQNKYYRVMDHSVGIVLCPVCQHFFKDE
EYEYECMKGNGCPLCRQKMGRRQERSMQKILNDVLSNEQ*
>TCRU_6216 hypothetical protein, conserved
MLLRVLLIVAAWLPVIFCAGDGEPHKEEDAYRVYYEPDNTTLSEQLLSSHRVPLRVRLAS
PIDVESLIWAIRLLDAKRGQCPRLGLWEMLRVAFEKLSLEDIYGVERLETLQRLLSDAES
NDGTDGTESWGQVELELPEGGGVLMVHLGDIVLQHPPGWKEIVQVNMVTASLRHMRGEKR
RQMKDYTKKVWENHQRLRRLQQLDIQRARQRRIEVARERSERLALMKQGSEWRRNITEHV
KRERSVILLLDTKKQDGPSFAQRAGRCENILHAIHTLQSQRVLPTERRMRYLREKEKKVC
GDVFYSMEDLARHEEHEMCHSRCSSYCEGVEALENWTRYTGSAASVVQLHALYHNVLLST
TDFNDTAVNYLSLLFETVLDDVDRGVFSTCAELCIPSKKLVAEMKFFAGVLGILDHTPEA
NAGVNKLSAVWWDRARHAYLHIWGASRAGSRRATAALATMKEHGILAQQQHRVAAVLLST
LLLEKHAYFWRQVMSVRAQSSGEAVPSSQRLLRFERFFAEENGWRLVNEPFLTRNRIKAF
RSEIDEEDDTESSVPPDEVPLTILQNIFLAQLHIAGIKGVPRDLKRAECLLLLLLRKLRY
TCDAPHLEELDKKYFSEAGGGGACEEHLQKLCLLRRSGISMGPCGLLNATSGLKLHPSLR
LIRSSKKIHEVVHRILVLLAYVHLLNGLQYDMAAKYAFLALEVSAAVFFSATAELPKDVK
HNFVVGNISHNEKLVMLKNKNWPAKDLLMNALRRGDPLDSLFDFTRSGFLSSESLVLLAM
SAFRGGVAAQRYICFTTERFFGARSCVEKNGRAPCRTQWTFFLLREASRLWEDEAKIPGI
LDRSYPSPRLVDAFFLMASLLKRGKITVDDIREGELFTSPRYASGASPPFQPFGSDTSES
YRNRLLRFARRVSPFALPGRRVMVYAKNWQYFITRATPPRKLRVLRAAVQSFLEEHDINP
LLAVSDMHDYLDGTRWSWLQSLFGTLWDAVLYPFAQTRAEAIEDQLVREVLPKKALDAEP
VNITERFAASVLSSRHIREATIALQLLTTALVSGEPDGFTLILLEEMERGNGHLRSFAHF
ISEHVWGESLANVWMEEHKAAQWHHAKPKTRGRGPVFAADSRIPFYYALPDSRLELFAQI
ALKLVETRKQYAMSSGCVTAHSNCTAFPEINQEIIRTMALCSGVLIETAVRKGRSFMPRK
PYEGMYFPVGSLRCLQGLLQYVQSTGISPFSGLSAKAAELLLLDLLVELAKAQAQYYDLS
LDALGSSSRTGSDAADANQEDAKKNYRKYLVEPWRRFFNEGVEDIPLPGLGEGAYYNKRL
HRVTGTYYAARMLRWYARTKIWLEQFFGVA*
>TCRU_6217 hypothetical protein, conserved
MRASWVLTDVLSIPLSRSCINVARATYSSRHARQMERLFGPAWHHADFSRTAVGKVSGAV
RDHLRTSLGPKKSAELRAKAVELGLVSDEHDTPSVEFGGEGSSSSSDPLLEFLEKNEDEA
ALLLAMWTSLRRSCLHASEISESISLTARWFLHHLIRMRAIAAAAHFYQRLLALGLQLQK
WDVVLLLSNLPYDRCTTVAASQSDEWMREKRLSQWAARWERERRKGGEEIKAKPKKGANN
ARYEKLGDEAGERRGPEAGAAASISAFSPQPTDSAHADAPSRDSGETVKNALGTVKKTPL
RHPDWVRRWLLYEASMGNIEFPDGEECLPATRTEKLDEICCTDALGAHEELLQDSLEANC
LMGLTAQLKHLMVLQDAGIFLETKKKRDSQKSATNVWRCTPARRHRRYWAEALHIASIYM
DSRPATKHVTSLPDELRDVIRRAVMCSGSWKVCLHYLEANQRHKIKLSRKDYAKFVLMAA
EEEPWRKNPSIEQYMLHHFIPHFSDLTAASYAVQAMWLAYACSVKLDRPESYVELIGTRA
MNLPSAIKGAIMFAKLAVSHLHIEVERYRTEAAAEQLLATSIRLGLFSHVGESMSENAPS
SLTEPTERPASAPLTGVILPEWLRDSFLLVCICLPRVLALAPILVVSQDDAVQINSFLLD
ALYSRIGVWGIFSRLYLVEPFAPARRTQETSFMAASMALCVLRAALALCVAHGEFSLQNR
GVALFTPKQLKLFLGMGLEALTAISSHASGSAELRSFMLILVRTASRLTTEVCRFFSLNP
GSERVLFGVTSEETVGSLSLMVQILLLLHADTPGRRFPVATQFRLRSLLRPNSGLGKQVR
RSLRQKEARQLDALLCRRGRGKARNSDVSPIAQRLRVFSPEDVARIDATAKMHKLVYFAA
ISHENDITAIEDVLISRLQSMQSDDAFLLLRVALHHLRLRPGTFGMPFFVKVLQRLCIGA
TSEAQGKSLWLRAISVYWDAVEHTACHSISINGAQVNKNQSFRNYERDVLSALLLPMLQL
SMAMKRRDMGWVWLNHWVSLHTPAERDTYWDMRNVQARSTLLDRRALHMSLKLILNAQRR
EAVEGPSVELTPAPFISLHCEVAVRHANWRVALDILLQPFVRSLNCGSSVTPLPNIVAGS
ALRILCRAPTNMSNTALRLREIQGDQWDLQSANALLLLLVRQRRWKIALQHVKEMLPALD
RASTATGSSSNRTEKSEEQLKMNQAFFLLYGLRACAIGGCGEEAAELYDRVKVLLTETRP

DTALKNAVTHDRGKHLEELLFASFEPDEVATTMSSAGDGNDQLRIVSGQARRYFLRAMTK
KCLFSQGLHK*
>TCRU_6218 hypothetical protein, conserved
MALGASSRTAQRTPARERRQVIPPDVSGQFWVTTFPSLDAFALQHFSLDDHSAAEEEGRM
FRAFGVTTWAPRVWNAGISGVFLGLRGAYNYWQQADDQAQLVVDSLVAWMCALEAERDPT
EHFINFGKIVLQAFRMQLMMASDPGIPLFNILVRLCTPVHEADTFARAIQVPLERRGTRI
SLRCQMCHVYGNVISKSNVRDATEGSYSQRGRPSRNGEGLLAASYEC*
>TCRU_6219 hypothetical protein
MDAAGSPYSRDAFFLTRSSRACGSVGDKVWVRLVGRTTPCGNSIKVASAWAVQSVAEVRS
ACRLSLSSSLKCWAVVPVGFLVAPTHREKLNSRSALEHLMPQTLAMCVRIRVRHPRRTPT
ECARDSGLQWS*
>TCRU_6220 solanesyl-diphosphate synthase, putative
MRNFSGFGTKGENGGNSVELVGEPLLKPSMMDMISHEAFIQWWYFNAHLRDVDSEKEFSF
FTSFFAFKDPKNEHKDDFYDACTWALIDVTEKKYYPDSLLDRRAAEFIMGKIEANEPKYN
INEYPVEIVKELLKQGKVPLPDRLMEKTAVYDKDSLKINFNDEFFLEGEGDDAERRYKLH
HHNPLRNITVELEFTARTIPSFHGDNGFIKQMFYYYYPSMSVEGKLTIGDSTINVKGDGW
YDREYGSPVDDNKENHGIWNWFGLQLSNGYQLNLFELFDEITGKKEEQLAVLTSGEKRYT
CRDFIIEPVECWTSLVTFQDYNVAFHIELPSFQLSFDLRASFNHQEFQTILTFFGFYEGR
VTGEGSHEGTPVSIIGFYEQKNAISRVSTSSIINKLGEKTRGILSEVYPLHASVEWIEKN
VLGRFCTCKGVLPQHICDTLFLPVRFLIDRGGKYWRTFFLFACSNALSRDYADTSKCVII
TELGHVGSLIIDDIEDGSSVRRGGKAAHVEFGTPTAINAGTACFFMSVPFAGVNSLPAEK
AKRFYELYFEMMKAAHAGQGLDIRGLGYLMPDVVRTGETKALEDAVKAIHTCKTGAICGA
ICSFACVLTDTSEEVTQAMEEFGKAIGLAYQIIDDVLGVKGFEGNLKEAGEDIRDGKITY
PVAKAMGKLELPQRERIWSILNERTSDREKIEEALSLINSANVVDECVADALQLVEEEWK
VVDPLIPDTVSKVMLRALCFYIIRRNH*
>TCRU_6221 Mitochondrial ADP/ATP carrier protein 5a, putative
MSTKREKLPKLGFFEEFMVGGVAAGVSKTVAAPIERVKLLVQNQGEMIKQGRLDRPYTGV
TDCFVHTMKTEGLYSLWRGNLSNVLRYFPTQALNFAFKDTFKRMFNFKKEKDGYAKWFMG
NMASGGLAGAASLCFVYSLDYVRTRLANDTKSAKKGGERQFNGLVDCYVKTWKSDGIVGL
YRGFMVSCVGIVVYRGFYFGLYDTLQPMLPVDTFVVNFILGWAVTIVAGLLSYPLDTVRR
RMMMTSGASVKYKNSMDCMMQVIKAEGAAALMRGAGANILRGIAGAGVLSGVDALKPMYV
RWRMADKLKQQQKA*
>TCRU_6222 Multiprotein-bridging factor 1, putative
MPRGQIMTGQDWEPQVFNFQNRNNTNKKPGRVSEAEANRVLQRGGNVDVVKREHFHANAQ
KTDLGANAKRIDEDNETLKVKRIDNNLRINIQKARQAKGWTQQDLARNIAERAGVVTEYE
NGKAVPEERVLVKMEKALGVHLRGVKAGQPFGGIHQQPQQMKKAAK*
>TCRU_6223 protein kinase, putative
MNRYLIVGQLGDGSFGVVSKAQHASSGEIVAVKKMKQRFSSWEECLQLREVQSLRKLQHP
NIVKLKEVVRENTELFLIFEYMEMNLFSIQRMRTEQMSGTQGLFNDREIRSIMCQTLLAV
QAIHKGGFMHRDLKPENLLTKGDIVKVADFGLAKEIRSRPPFTEYVSTRWYRAPEIILRS
THYNSPIDIWACGVIFAELYLNRPLFPGSSDSDQLFKICSIMGSPSPSEWDEGYQLSRRL
NMRFPTVVPTPLRQLLPNAPPAAIDLIEQMLRFNPSDRPTATQCLKHSYFTETNNVAEAG
GTTTALYAGISTGQPHNPFQLVSMQVSMPNGSFQGGVGLRANGGSPPPTLCSSSRVFSPN
SSVPGINPYANVVRSVPQGVSRATDNDDEFSF*
>TCRU_6224 hypothetical protein
MLLTKFFLFTVLLLVHTCHTEGTLYAVRGGCAGDPAKWTARIGSMAENEVIVAFLRAQGI
AFAGIAGYVQNGKAYWEDGSPVRWMPPGSGPFSTADVGFLVVQSDGSWGSMLYDVFPDTL
FVCTDGELIPSTTNTTSTQAPTARPHPIPTEAPAETTASASEVLDALATALSEVGSFDIV
PGTTNSVEVPVPKTVLFQQLAVLCENHNYFFGVAFVDKEDAVKVQGVSTLIRGSGSTLGF
VVPLDLMESGAKHYMMRVVAVKKFGTFIYRKTSAMIIIHSIHEVLMKVKDTVEINEEDMM
DCKDVIRPLRIIGPGTVAPHALEVAPLTFMGLSLTLINNRNVGKTCAPSVLPVNFVFVNG
KLELFLTKEYVARVKTASRSLCASIDGRHIVIAAVEGRRWTFTTANSQYAYGESIKVVAS
GASMVAVATNMYLAFLSRSARCSSLDDTFLSLELETSVIPAKTSVSYTLKENQQKVTLYL
KALSTEKRVRYLCVQHKPTAKKVRVVSLGGSGVKVAVDPFALPSPGWISIFNGSIGSIAL

KNVLLPAQSEEDLEHFNKISRLIMQNSLFVRFVSLPRGAEWTRKLQGCRGGTAGTELEFG
VNGGVLQVNIPLFFLNSSGILCSGKEYLRVDYIIYEPSQWLQRFGNTDAAAVFAVIPSLP
SSAIRVAVTNWNESAHYAIRLAVDGQCRVGFTANIWQASDATHAVSFPMTVHGDFTLCVG
IYTDFGSTSMFVATDRRVSFIPYETGVKTWEKEHEMLSGTWSLCGASSVCGYVSSQPFFE
VCRSQAVMREWPIIVKEKFYSLGSFIVKLRGKDRSYPGALVDGRVFVKRDHFTCQSPKLL
EMSWDGGVYSTSAVIDRGHSVVTLKPNVQLAGVVLGFASWDTGCVADSIWQKVLVSSLAF
ATATVSVLDLFSLLGGSEDDYFVVCILQDSSWGTVSHTYFHTVTGSEDNKSVRADAIATL
NPSENEELIYLWQTGTVEWNILGLFLPNVTISLALVWDNSFCHASPAYISPMRYVSATKS
RVHVDSSFIAAAPTPTSLLYSCYYVEGAPAMPLRIEQLRNRPITIQDLSLSSINYVPHFA
IRYNTTQNTTIIFSDYLKPPITQLELFLQSSPEEEDVAAGCSLNSPRHFLSLMVQLNEFG
LRYVSIPPSVPAMLGSAGREVYLRACATASKSVSPHFVQVSAYLVVNSIGTVTELNPLSL
DLFFVVANKTASLLSLDKCKDSVKRYVADVTNRNSDEKGILLTAKGNNHFVLFIEPTLGV
SGEDAAKQLRAVYKAILSGGRLPLRVGSADGLLFVLHSVEGVHLLNQSSYDGFPLVFLTA
AGGVEQAPAQEMVTQSVKVFCVVILPGVVGFVVFSLQRTLPRLNRPRLGKDRMKKGNGAS
GSRSAKADRESCATVPNCQDDKSPSPRIPQSMDTDMQVITITAEKTTTDPLYDSDAGEAP
TSLGRTPPAVGNNTFCMYEGGSRDVGSERRGDGEG*
>TCRU_6225 metallo-peptidase, Clan MG, Family M24
MSRNVAAEEEWEDVDAPNEEDEEEEDTTINNSDVMMRYKKAALWCNETLQLLLDATKPGA
KVHELCKLGDETVAKKLKTMFKGTEKGLAFPTCISVNSCVAHNSPSADDEVASQEIQLGD
VVHIDLGIHVDGYCAQVAHTVQVRENNELAADDDASKVISATYGILNTAMRKMRPGVSVY
EVTEVIEKAAAHYGVTPVDGVLSHMLKRYIVDSFRCVPQRKVAEHLVHDYTLEAGQVWTL
DIVMSSGKGKLKERDVRPTVYKVALDSNYTMKMESARELQREIEAKYQTFPFALRNLETK
RARLGLSEMLKHGAVVPYPVLYERDGEVVGHFKITLLITAKKIEPVTGLKPQKAPTLPAY
TDELLLEASRLPLTLEKKRKN*
>TCRU_6226 mitogen-activated protein kinase kinase kinase, putative
MSGVDVEELRQVTLGKKLGAGSFGSVYAGILPSGRFVAVKELELAEDAPTNTEVEIHKKL
AHENIIRYFHSHVDTESTPKRLFVYLEFVTGGSVTSLMKTLPNGHLPGSVVRVYARHMFS
GLEYLHKNQVAHRDIKGDNLLISMDTGIAKLADFDQAKIMTTHGTLRKAATATLAGTPYW
MAPEVITDESGYDPFKADIWSAGCTVAEMITGRPPWMPMANVMHIMNKLAMSSGWPDAVP
KDPAALGSQHAYDFLDLCFKRNVAERPDATTLLKHPFLQA*
>TCRU_6227 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAWLCDATQTSSSAPHRGNAEETMTPEEVTKAIEKLTEEV
LESIRLSCRMSFITSVNATLPAHNDTEVEKCVNKTAVEISGVTSRGRPAAATTDANFASP
LPSSSSAASALQGQAQGSPGAAPEPVKPPQTDPVNNEQLSEAPASTGGGAGGGGELADRS
SRTPTDDARTHEARPAGNATSTPTATQGDSEKSPVNTTPTRETNETDDTDGSTAVSHTTF
PLLLLLVVVACAAAAAVVAA*
>TCRU_6228 hypothetical protein, conserved
MAIAHAAHFASTIRRLGPAAPIAGYSNSHHELWDGRSPPTTAGEDLAATPSGMEIELCDD
LAQATWISGRSVSFPDVTAQRVLRVSHWKSTCLHGLGPPSAMPHCRDGGRHPATGRHAAT
TEACLRCPA*
>TCRU_6229 U3 small nucleolar RNA-associated protein 6, putative
MARARAVETRLEKLLPSLEEYFTSGLLTHDETQDVARQRTHWEYRLIAKPLLLLDVQNAV
AYELGLEKRIEEYCGTTKLVLKHRWAVLERIETIYRIGIKHIKDRDELELLRREFVQFLK
AHNRHSSLSALYGELMVRYPTRSSLWVEAALYEGIEMGNTDNGRAIVQQVVLTAGAQPEV
WNAAFLLELYFADRLLQKLLEEGSKKEQKSPPKDIVKELREENAALASVVVDLALVKAVV
EEALESPACGPNLVQLLLESAMRFSFTKSVVETLMASAFSKMLSALTSHDGPARTASNNW
SGAGLSRFVTDFLRIDVIMLDRGVMGDAASFLRSQGRFHASTPAERRAVLVKAFAASLTL
AQTERISSFLALGGLRETAVAEVEPLLEALRESTSASGVSALCRRLLSNQHISITDTVNC
LCGRKDASFLQRLASAAAERVQAALQTVPEELPVKVKRARNEGKSSKSITWRIWRFLLPD
DRKAVESSVSQAVTRFVSGDDVERLVLSQCDVKDVSAVEHALTLFLREFHLIGESEGIEG
LHRLRFHKSKTPIALWKVFHLLELRCKPRVKPSRTPSSVSSESDIDDDVVDKKRSKTTNN
ASYASAGLKFLAGVPHGSLDQVAEEERLEGCWGLLSVRVQTLTGLKDTTTRADFIACLQR
NSSDIWVEGVRSVLCVARLCEPLPRQTHTEITIPFLEAVALERGGRDGGALQEARDAHER
LLGMYALSKHPNSFLPLVHQVPRRAETRARILPAELNAADWARLVAFEREVAKDLPRAKE

AAVRARRLSLAPQRLLAMLSTY*
>TCRU_6230 40S ribosomal protein S6, putative
MKLNIAYPRNGTVKQFEITEEVLRRVSLTDYRLGNEVDGAIFGDAFRGYTFKLQGGSDKQ
GFPMVQGVMAPSRVSLLVKRGAVGFNTFRGYQGERRRKSLRGCILASDIAVLNVVIVKTG
EQPIEGVTDVSVPRRLGPKRANKIRKLFNLSRGDDVRKYVIRRKVVKEGKKDRFKAPKIQ
RLITTAVKARRAKKAKVAIEKVRKSAEERRAYLHLVGTRRRAARQRNSARRHAHKVAAQK
QALALFKGRK*
>TCRU_6231 NADH-ubiquinone oxidoreductase complex I subunit, putative
MSRRVFARNMGGEISSTWRGGGSEANTMGVNVVTFGATGILGMHVHHLCCYHGFTSILPF
RFRAGLASGVRVLRMAGDGTVGQNFDTDYEIDKEFVVKSILEKVDNVINVVGAWQEPAVY
ENSQSWFSMEAINVEWPRMLARWCREMGILRLTHMSMVGADLNSPSKLLRQKREAEIAVL
EEFPTATIIRGTDIFSENDFSYSKYLKAERYLKIVPVPNRGQRIHQPVFAGDLAEAACRS
LLLDHTEGRIAELGGPVRFTTNDLLRWCSECNGHLHLTWHMPTWMWRIGCALNERLPVHQ
GFALGTRAPAWNKDWLDRQFVDNCATPERDPEMLDWEDFGIPREDLYRMEEKYFITSTMW
SMDSPYLDLATRM*
>TCRU_6232 EF-hand domain pair/EF hand/EF-hand domain containing protein, putative
MRYTLAPGALACDCLSSEELRLLRDSFVHLDTDGDGVVRLQDLKNAFREEMTELGLPCTT
ETLDLASYLELFARHVDVVRRLATSVSVELSDDEMRLLEVVFDNMDTNGDGFIDEEELCS
ALSESLGKCKASYAIIWLTGLIMARVGRNADRRLYASDFIRALQENNGVIPRQLIGLPLK
SLGERSRLRRTVSGGYGGMLTPLRRSFSPYGVLLVLRVAESILCNKQTLTAAQFSASLTD
GFLTLERLLGCDPEELASHICRRALLLSPHEETIGGINCGHFLSLVLDDPGSMLLNVPTP
FSRLESSMRHFADLSYDFGRHLALSLLSSGPDSYTLQQLDELPQRLRATFPALKEVALWD
IVRCCTAAAEVKSEGFFSLQRLVRRLTIRFCVLPCDYSGKLWRRLSPLERCRIRSHLGRM
HIEELYTMSRQRARELVRMSLLSSEDFWDQEHVALTVALCVESMIFLQKMPPEEVRRAMA
QEGWPPSDDLVGDDCRTDIAVRMMAVNLGREGLSAVTESIVCLDTSCDCVINEELLLSTL
RGVVRQLRPRWSNAQVDRAVCDVVLGCALVEDGGCVSCGGLLERLRHIQ*
>TCRU_6233 ankyrin-repeat protein, putative
MRSAEANGTPLGAPILCQVRTGGATGSRLVGTIHIRLNSSLRDVRLLLKSLASRARGDAA
GPSGLEVHGAPVNVTQGEWKKAMSYPLHPFDLSLAFSFVKCGGCLPIQQHHEEKLLLVDV
FPRLPRAWGMSTVAGWMMEPTPPMVKVLARPGEYVPYRDALAVVFIAQGEPENLMPEDVL
VERQMLQQCSYGRPYQLRELFTLLNQWNGNVKDCFGRTVLHECVYQGHFEAVVSLLSFSF
IRVNEQDIQGKTPLHIAVRVGNEFVVSRLLEAGADILLADNGGDTALHVALRLRNDRIVE
LLCKRLRATGIEAKRLYFCKNGVGMSPMDMFQLHSPTFIQLCEEGDVAAIKSLYDHYLFS
RDSIKGCDELLHQSALHVAAACGHVNVLKFLLDELKFGLLTDKQMLNSRSQTPMHLAAER
DQISAVRILHERYPWFISVRDITGATPLVAALRRRQHSVAVVDYLISILPRGSGAINACD
NSGMGALHLLCELGMTLAANSLIVDHGADVTLSCSCGIVSSRYLKKTRILPRLSKRAGEA
STRQVVGEQQGLTPLLCTLRGGRGHVSTIEMLLSHGAGTRGDEVVELLFYLITKGHYEFA
DRVVASGVGKLTSSNDLLSRFCHLNHGVGIRWCIERGCCSLNSPEGGYPLLVSSALGDVE
AVSFFLSRGADPNVTADGKTPLLASINGGHHAVVEHLVRAGARLVASDGSWTALRAAAER
GAESVVRALLGLHVLSPLVVSQTLVHAMESVRGRKSITCERVCVHLAGFLDLASREIMHP
TELLHLAASRSLFAVVRVLVDKLLALPALVLRGILNDAPPPPNRMFVLIEPTVAPLRVKA
SRLVSVKGRRGLYTPPKPFKRLVIQRREAGVLFHRLRLRDVYSYCAEANEGELLEKLLLD
VGLKPWAGPDYRGWNAADYAADKQLANALRMFLVVGLAPCRRHVVCSGTRMGALCRSITC
ANVNVDEAGLLSSALCDLAAAQETTLVRQILTDTCRFHNVSDLSGAGAWLDELILCCVRT
RCLDVLGILEGEFQVPLKKRLSLSVQPLLSAVACRDVKLLAYLILHGTPVDLIGSIPAVG
GNELRSLAREEREVSPLWLAARLGDITAMELLLSVGPLSPAQCTDSTDFRRDALKALVDG
APRRPSKAQDTLIAQGVVMLARAGHVYTLPSIMRVAAGKGLVRTVESLIDCYGPRTVTED
IVSSGLCSLHYLVGRPALSRLLRSSLLLVADVGSVYVEASQNLLATIQTTKFTVNPVDYA
LRAGCSEGALLLLGLGLCGGGGRKENCDPKISRIVRLCAARRAAQGEGGYTVLHAAMELQ
YHEIAYKILNERVLLQHVDRSSMEEKRTDNTPSFASLMNFYLDRAHRHLLLSPGVPAPMK
ISPCDMPYLVFSESFDDEGYREIVRLSALDGGLEQTLDLLHGGLPMAFVWHLFSRHRHSF
YFGSRFFGTMELTPMGCAVAAGNLPWVRLLAYTGVSTSNCNSIVAGIKRGKAYSLVQVPI

PPVHRKVGVQAEARRHVCRKEESYPVNFTDERHHVSPLLLSMAIIVETSWAGDAEGLLRQ
SQVMRFLLSCDQCLRREELNPLAIALAKLMLWDLLEALVAAARKLIDNPSEGRLFCTIHE
AEVPPIIKRAIGTSRHVMHVAARCAPREILMLVAKHSQRADIEEACDAKGKTVLFYALHH
PCRFAFDVLGGLRVPTNVQCCRRTGRTLLMLACQRGQLPLVMALLKKAEMNTRDRDGNTA
LLLAAAAGRAEIVEHLLANGADPSVKNRKGMTAVMAAAFAGHDDIAVPLAENFSTLDDFF
SPQTTLLHCAAVGGCHRVASTLVDMVEKINIWAEDVGGFTAVYLAYAFGNALVLRTLLSA
ALKYGVEPAPSLHLERQIFICSSTLPRYGWLRRVLRVGEVVLDESRQRLLCQSATRPGEM
TYGNPTSFRCFRTSLLLWCVCNNNAVGVRVLGEMKSADDCGALHEAAKRGHMGVVELLLK
LEMSDPNVLDGTGRLPFEVAAAHRHVACASLLLARTRLDMMHLKAPAAGGTQSALHRLAS
SGGAETLFVLVEAFQGMNRPDWSVVASQLLDALDIPDSSGMTAFESAVAMGNPAGVLRVA
QVIRRLALASGRKKALSVSNSILSHLPCMSPAVRVLLYDVFGILEVAMCVGFEQEKRVGR
LAFADVRLIGANALRENAFCASEVAAAFTLEHEISVASSLLKGLPFRIRYIPRSLETRSA
SQQVQLLQWLESSLILSNYENWGVEKPLETIELELVPHRTDEFLEISNMYLRHSVYMDSR
RLLTPNLHAKLRFASRSEALRLRTVAEERCRLLTLKMRQLPHPLMSMGRVMVEWGDGNDE
VTVETVTRLMDDGLARVDAFFSGKLKDALIGVSMADVVSVTAATDRTMNAFYISFRYTRE
TIRRRHYTSSEGGLVIMFNDNAMQDVDRVLHLALYRQVVADVNLVGVSYVRDAFLADVRR
LAGMQMGDDATSFKLEVEGGTLDELPLHLLEAMMSDAAEALASLITESLANMWNFHSSKI
VSDFLKLSLHSVVVLFSPERRPVAEFSERKLMLCLNLQLAPTRCEICEGLRRGALAGEIE
RLRGELPRVIATVGQRLQMRLPTTTFVLDSASLLEGEDDEYVVSALSLLCYNCGALVLQP
LIDGVSMGWDTRLGSVVRRHVRQLTLVLELFGGGNCVLYDSGNFVYNCPLFSLERGVYAT
SSWYLLSSQQIASLLLMQLSLVDPSIFGLVNTSKPLACWSQAHGVCTRLLSAGCQRNVVR
MTTRNIFNLRLGHAVSESSLAFIGCWRSIKVHEATGRVHFIAPTKAGYYEQQILMGGQPI
LKSPLRIRVRPLAVHLPSTKVLSNFNTVVVGRPFDIVLLLRDKYGNRIEAPEKIVVSPVT
AGAARIMSWRRSRVDMIEVRVVVADVCDKCAVPIRLRAADEGDFELLFPVESVSEQTYHW
VCLLRGGYTLDWEKRCRASKTKATKTLSMAGKASDRVKYFFRRTVRDAERRRLVRDAKLI
GGLLNRVFPPRRPNDGKNGNSKKREKATRDEYPSRKRRVCVVMGGESEAKEEEVSK*
>TCRU_6234 60S ribosomal protein L32, putative
MVKPFVQKRIVKKRTKRFTRHKCELFPQLSSSWRKPRGEDSPVRRRYKGQKAMPNKGYGS
DRKTKYITPSGFKNFPIHNVQDLYMLLMQNRKYAGVISHTVGAKSRKAIVRKAHELDVRL
INGNAKLRKVLQ*
>TCRU_6235 Variant SH3 domain/SH3 domain containing protein, putative
MEQCVAIADYEAGDSDEISFRCGDVIAVTAKGSTSGFWEGFVVTPGHGHDAAKGSRGLFP
NCFVSSNMRPQEVPTFCNRALCLHDYKARDESEMFFKKGDLLQLIRPGASSGWWFGVNES
EMERLGKQKETGSEIARACGSMAEPRLLPSNFVTCNIVFAAFSFEARQRHELMFEVGDVI
QVYRRWNDGWWEGTLRGRRGIFPSNYTLPNVATTTPPFFCNTCKSVFVDDSLHCETCAKA
ENVTRSMITALDDYALGKMSKLDLFAYVDVVGAEAPARGACSAGE*
>TCRU_6236 Domain of unknown function (DUF4205), putative
MASKKSVSFSPVHTMPHERQVELLSEALLREYMHKRKFKETLETFDVEHPRDGDTIASRA
LMSDLMALSPETQRALKVEGVETIMEMLCFLRVQRRMKLEDLKQRASIEVPTTPEKLKRS
RKDKKSSLDKSLHESSLSEKRSKRERSDASRGKRLTDSNFGSNSTRSSSRSSGGSSSGGN
NSSDHSNGRKGSNKRNSIGLGIEGETASEQRRREEWMNDEIGATLGKGAARSIMELMCSG
IAFPSSLVEFGFVFGEEVEYGLLQENKGPEGLLAVVQAFICAYFFRGGYIDVQRHQQYCL
LKALATILSIAQPNPRRVCLVDGSVKADSAEVDMTHLNVQRNFSTGQQVEDALFSLLDVW
TQPRGSGVFCFLLSVLLSRGLKKVSSAVGRAATLIDREGRCSATLTRLLLLGEEDAATPG
DVLSSLMMDASKGRLACGYASSGPDDTALDDEGAKTPQHPVWVVHHEGRFVVLFLKKDDR
SQFEKKKEAGMAAASDVFFYEPSAEHRGEKFLTVSFNIAPVTGRRKEGDSSFLQDAVRKI
TIWHDGDIDWNGFEPAF*
>TCRU_6237 calcium motive p-type ATPase, putative
MSDLKELSIKEPLDGNEVPAEEREALPEKYSPSKNWWTFDIPHTLSLVQLDDMCNGVSYD
DIPRRARELGGNKIPISGGPSAIWILCRQFMNSITFILAIVIVISAVFRDWAEFGVVLFI
LLFNALLGFYQEYGAEKSLHSLKEMTAGSAKVLRDGAAEVIFIDEVVVGDIVILEQGASV
PADCRLVENIGLEVDEALLTGEALPVVKHTNVIPDPDGLCALGDRKNMVYRNTLVTQGRG
KAVVVAAGLHTEVGKLAERLVDNSGSEKTALMKKLDYLMYFLFGCCFLLALVVFAANKFK

YNPSTLSYATAVAIAILPESLVAVVTVSMTVSVKIMAKQKCIVRKLAVLEVLGNVTDICS
DKTGTLTENKMVVKKAVIGINEELIVTGAPYERHGLFLDRDYEQMELVQAYRTNKLLYEF
MRCAALCSTTVLQVDADDVDRLTGAGNPTEVAIQVMSWKAELYRDRLEKEGWECIAEYPF
DSKIKRMSTVWYNDKKGEFYICTKGAPERVIDLCTTRLLESGKLVALTDADRQTVGEKIQ
SLASDGLRTICFSMRPCTVEQFPIPTEGTFLATHSREVIEQDLAFLGIVGIYDPPRPESH
PSVVACQHAGIVVRMLTGDHVKTAGSIAIMLNIINRRDIDSGTKLLNGPDFDRIEMEAID
GWDDLPLVVGRCSPESKVKMIECLHKRNRVVAMTGDGFNDSPSIKISDVGCAMGSGTDVT
KGVADLIITDDNFATIVKAVAEGRRISQNIRKFVVHLLSSNVAEVIALICGLPIRSEGAS
LFVLSPIEILWLNMFTSAPPAIGLSLDAASADVLLLPPNTAGLFTFELVSDTVVYGFWLG
VCSLCGFVFIVYGVHDGPSGNNCNSPNGVGCNDIWRARATAFGILYFGLLLHSYTVRHSR
LSVFLMKWFDNFWIWGSFAVGVILFFPIVYVKPVANGLFVHDMLTWHWGVLAVLIIFFMA
MCEVYKVLKNCFFPLKKVSVAPDEEAMQEYRRFAVAGEDSRDVESIAEEQLRMSFASYAG
SIVSGGTHNMMSERKKKRR*
>TCRU_6238 kinesin, putative
MDGNKKVTVAVRVRPILRDATSHAHMQEKFELEAVRRTGDTSLKVELQRQGEPTRSSVFN
FDHIFDQESTQLEVYEDAVVDLVDAALSGANVTILAYGQTGSGKTFTVLGDVKPNPLEND
LLTHESGIFLRVLSDLTEYRARQAKRGFHVVIGLSCVEIYNENIRDLFGGGPGTSPPPLK
AVMIGDEVLLPSLITKEVTSLQAVFNEIQLAISRRKSRSTESNSTSSRSHCLFLIDILQR
AATAPPPSLSMLETKKGGKEKEGKRTVTNGSGPGEIPFDGTVYRINGEREPVYGSKIMLA
DLAGSEKIAKSGVSGEGLAEATAINSSLTALGNVVHSLYEGGYVSYRTSNLTRLLKPTFA
HQNSRVLLLSQVSPTQFTFDETISTLYFANKVKAMKVTTTTGAEAERLLFDYMDSGKICD
TLLADLHIFEAETQSKSAVIRRNCRQNDGLYYSTATNAKAKASMKERRTSIENTGALRFA
SEERDALIRKAQQEEMQKEEEIQKRAQELANESVLEYSNLVAETKESIANEEAASQRISL
QTLQVASAGEASAIQTEEAAMFLALSARFAKEHVAICKKQMAAIEGEQEAISKQLNAMSL
SSVEVPEIAEDNLKYAQACWGHTTAKRFFARCMELREIQGQYALLQKVCFSLGKWREKNK
ELMPRVQERAAQAAE*
>TCRU_6239 ADP-ribosylation factor GTPase activating protein,
putative
MTLTLPKDSEEAKALVGSLRSHADNRVCFDCLQKNPSWCSVTYGIFLCMDCCGRHRGMGV
HISFIRSADLDSWRPEEALRMALGGNAAAREFFKQHGCNDSKMRYTSPAAQLYRRRIDRL
MAEYMGGRRMEPPAEGPNTMSAESSPVENRKDLEPTTTGSPVAQPSVISMAPKTGKKPGA
AKRKGFGGAQKVEGNIKESSDPVPHSLLHDESKLEDEDDAERKTFVPGAFSPVNPADRFR
GVGNPAFQAEAPSCDRMNGPDFTGLGSRPYQPQATRTEAGGFQDTLWQVTEAWDSFKESA
NRSRKEWGNRVREFLDDL*
>TCRU_6240 hypothetical protein
MQRVKNVVGCFSGPFSAVINFQKQFVDDVIVNVKKQSEEISRHNHELQNRRVRLHLDHLE
EEYLCCVCGRPGEERDADDVVSDEFSIVHMPSKERIEQAIVASGQLNQGGSACGEDGFQA
LGPQVYALLGVLSTSAGQNTSEMVAKVQHCILNQEAARRQKRRSAHRDKGLMKIEESDIE
IFQQFFKRPVHGYLCSDCHNSAKRRLDALTSQIQMILFKGKTPFLRSGRAAAQCQRPEAT
TSPTWPVSTVVISNFCARTREHNSTYLSDASITRLRESFHCAVCKRRQASFFLRQSATFL
CQFCCSRDRFYRDNATCINDELMPKETAHLLESLARCQEKKKDREEHNALLGSGEERDFG
LFREHNAVDLFATQLPPHASIDVKAVLPHSPSLSDRRSVAGNLSVSLFSGKKFLLNLSSP
GGF*
>TCRU_6241 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily, putative
MSRRVFTSAILLLLLVVMWMCCGPCEAAAVSTGENSVNARLPRRFDLFVPQTTVLLPRGG
GNSEKKWSSFASPSLVSAGGVIAAFAEGYRSTKEPANASSEYSSDAVAWYIDSAWDWSAL
VAEVKKSTWQAHTVLGKAEEKGSLDVVLRPTTTMKGNKVFLLVGSSVSSNVSESWSHGGL
KLKLVVGDVTKPSADSEQSEWIKWGKAQSPLNETSEAVQGRKLTGFVASGGAGVLMEDGT
LVFSLMAKSEEEDVYSMIIYSKDDGSTWALSNSVSSAKCVNPRITEWEGSVLMIVDCKSG
QRVYESRDMGRSWTEAIGKLLGVWVNSQPGVYPDLSLHVEALITVTVEGRKVMLYTQRGY
ASGERVTALYVWVTDNNRSFHVGPVGMDNAEKEELASSLLYSDGALHLLQRRGNDKGSVI
SLSCLTEELKEIESVLSTWSQNDVFFSSFSIPTAGLVAVLSDAVGDDTWNDEYRCLNATV
KNAVKVKEGLQLTESNSGALWSVNTRDDNLRHVFLSHDFTLVATVSIENVPTEKTPLMTA

TLANTESNHTMGLSYTADKKMETVFNNKITPKSSNWEPKKEYQVALMLQDKKASVYIDGR
SLGEGEALLTGEKSLELVQFCFGACDQESSPTAAGQKTNAKVKNVFLYNRPLNSTEMRAI
KDRIPIPKRGPGSQVEGGTERRHIPRIEGVRANAPAGSELLSLLLLLELWVFAAL*
>TCRU_6242 hypothetical protein, conserved
MQHNRALHRRHIRHVDEGVGHQARRALAEAANPQLRPARKHAVAQRHVQHVSERVHQAQV
HRHSDRPAEHHRVEARRRTPTANRHGLRQRHATHAVLRTTTGPRNRHVERQARLAHAAGT
AAARTVGERRRQRIKARQRSRTAVARHHAHGGQAGQAVVAAALQHPAAGTVALHRHDAAR
DRRPGDKRRAGGSAARNRHGAAAQLHPRQRRHRRRLAHRPHVAQLQPPAATDRPTVAAHQ
RRRN*
>TCRU_6243 hypothetical protein, conserved
MPWASTMCATTPVQHPQCLPHTGQSAGRRIVAGWCPAGGEGVSVRSSLRVCCAASAPHQR
HVRGMAGCSGRSSHPYCVQNSAAEAGQCSLYPTSEGGVRARGFPVAYYGGAASFWLELSG
TNNTLGQCDDAGAPCACQLCEVGRLLGLCITCFVLGYVAVAKDKLHPCALLSAAGEKKGY
IHNVSRQVMQNRRRVLACFHDSTRRRINARCRGNSLGEYCTLRANAALLCVCCGAWTLQS
RREI*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MARDGVRIVVQNVSLLNGAVLYVMGGGSLRGAVSAGGDESGPVELSVCDVEALNGALVLT
GTFPAGSVLTVTDSLLVAARPTPLVYLPGSQSSPYAPVLVLSGLRLVRSVLVVFGVALVT
VLTGGRTVVVDGAVLELFGGGVAVDAGVFGGEYALYASARVVASGGAVLRVSGSQVYAAH
GLVFGSGVVTNASAVVVSDNVGALTDGALLVLRGSASFASGSWLSVRGNSISGRLLSVPS
YPRRADLVQSTLTIHGNAGSGPVVMDGTVALGRASGKFVVGCLTLNGQALRPMGYRSAGI
IGEFRPVACGVCDADVRCFAAATRAMSGSCRCRCAEGGYGHDCLPVYLPRVDGCNRTPAM
PLVSHTATLTETRSLSSTWMPSLSATQYSLTPYRPMETLQVTETVALSPTLTHTASVSST
PWWSDVACPTLTVTTTAAGGSLTQNDIRGGGSAVPTLLMVTLPSPFRWASDPQLGTHLSF
VPVATAQPTGFGGPWGAMLSNATWVRNATNPSTVLELAVPVHRGYFIAADETIVIRCDAA
AVSGGCRGVLLGSFTISSDTLPAAASALSAITGVVAGAAAVAVVVTGGLGSILEMQALGV
FARMPCASAQERASTVALPYFLSVFAALDPLWMVVGNALLAAVFGCVHCGVTAAFQRWRG
VDAASAWAAMRFPSLTYVVAHAMHLGILFDSVLALAMHGSHVWHRVIGVVGILYGVAFPA
GVCCFIARHTGASFTRYWQFLRKPLHERLLYPVGYWHPAAQQRMYGGMLTNMRGSHVYWC
VFQLLVLCVVCLIAAVHPPVGGCHVQYFCMAAVLIAGAGVVAFTNMMRSVFLTVMQTASF
VLLAALCVVSAANHIAPSDGGAKAYAAIALLLTTVVLAVTVYGVVVWYAEDRHWQELREP
RRGVLEALLRDDEHGDEGTQNPHDTTSSSYASGTTVASSYRPPAVLLQPMAGDIRSDVLS
LLDRALSAIGKIDHAGM*
>TCRU_6245 hypothetical protein, conserved
MGLSVKGSGARVHVNMTSSLLDSGALEFRGDFGASSQILVVGSAIVTTWSHAILFLNFYP
SENLTLLLLDNRIEGSSYAVYFTNDVFVDGGGIIVKGNTLGTTEKDEGMGSAVYVYAVDV
KNGGYLDVENNTMSAAIGICLFEDTAVGSSGLLRVADCTFIGRAGGLNSALLYLSGSVTF
QGGAQWRVTGNNVSAASVLTIPYSQHKIRLSGRGTTVALAHNRQVDDSYSFADLALSSIV
VASPARLVVGCNLQGGEELSYAGVFPGEVVVFRCGTCNDDAACYLPGTESVERGSCSCSC
KDGWHGASCLPFEVPDTVVPPVAERAVDGDTSCVVNQTLTSLTLNMWKTHHCYVGVTFSG
VGAVLKFFFDSMPLHLPINITLTGCTFREGAALQFVGGAEATESAGVLIRVGRTVMRSSV
VVFMGALPQHCDIAITEIDAVQSSAVQTLENGINKLSVVVLREVLLSASSLLLGNVKANA
LSYGLFGFYSTGTLTLVRGSSLYTRYCSFDGYTHLFHVYGLVVSDHSVFALLNNAMSSGT
SFLLQYQDFSVLDHSVLRVVGNSGSVCYAIFADDSWTVQESSWLDWRDNDVGLGAMLCDT
ESAFVNIDGSSVVTLTGCTMGSTGLSRPLLSQADAGYRFVAGCLTVAGRKVTTAAELALH
GITNVTTVAACGECTKDGDCFAALTTAVIGCKCQCAAEGHGDECVPAPVPAGPPPPPPPP
LPATPTPPPPPVGECISHMVYPEVAQAVGGGLSWLCYRNVTFSGGGMSLTVLIGAMMGDV
ANVTFDGCTWRDGAVLVLLGNAHAAVGSLNIVVTGNTFSDALLSPEGVFPPHTNITISGN
RFTVTRLICRSGLDIGSPSCVAMNELAISNDSAVVFSGNVFQSVRVSLSAIYFVGSALRV
SWHSVFAVIGNTFHMYGGDSTLIHLEGSRRSSSLSVLNDSAVVIRGNVVVGGLKYFMLLL
WASRVESQSAVVFQGNEMRGGLAVFLLGSSFQIYYNSWLQLSGNLCRESPSEAFAYISPT
VSLRDSMVSVSGNQLMSSTVTPTVLRIPKRSRDLTNGAIVAACNTVNGEEGAKYSIPSVY
NATILTCSDPCTLAASCFPAYTTTASSDGCACTCAEDGHGDACLPVAVAEPPSTDGADLC

VRDVHVDEEVSAGFGTSVACYVGVTFAADVVVDVASMSGSVRNVTLANCTFVDGASLYVV
GWRSDPPAGERADVLISGLESRSGGGVLVSNRYPSGSRVTVVDSVLIAEKRVAYRGAYGL
GDASACLVLHNVNLTGSVLTIARTHVAAVFGDAVGVLVVGGVALSSRGALYVDGLSVQTA
LGLCVSVEGGVAASGGSVVAFVDSDFLLCKHAVSVRGAVSVSGSAVAFLRSEFLSTEDHA
VAFYSTVGLGGGSMLLAKGNVHDGVSREMLYAAGAVTAAESTLSFVRNRALLPRMVSLSL
ALSAGAHLRVACNDAGGRVLSTSEEYAAAGFGDAGRIDVAGCDDCDRDTHCYAPGTASRA
*
>TCRU_6246 hypothetical protein, conserved
MQHDRSLQRRHIRHVDEGVRHRERRALAEAANPQLCAARKHAVAQRHVQRVSERVHQAQV
HRHSHRPSEHHQVEARSRPPTANRHGLRQRHATHAVPRTTTGPRRRHVERQARLAHTAGT
AAAHAVGERSRQRIEARQRSHTAVARHHAHGGQAGHAVVAAAPQHPAAGTVALHRHDAAR
DRRPGDKRRAGGSAARNRHGAAAQRHTRQRRHRRRLAHRPHVVQVQPPAATHRPTVAAHQ
RGRGRPLDAHEAQHRVRHREALAKRKAAAAAHNRHVRHGEHRVAPQTETRRGRHTHRGSG
RTARRLQQHAVKHHRARQQVHAANVHRRPARVQRPQHSVAHTQLRPQQRRRVQHKRRRHR
VRQPAQLRVAHRSRRHNRRVTDRHVRVCRQVVHKHKRAVAPGQPAHAHLQAPVTRRLAAV
APHVELRTAVTHAVPQFNAQYAGKHRRYVEHHSHAVRDGHAVHQHRVHGVANRDGSVHRA
APQSQHHRMHRGHPRSSRSQHQHHKQHRTHSRNGPVPLAVPAARTRTHRRPHPPTHTGIN
KAFLVYRSRPVDRNSCFANPFPTNGESSDTIPPDR*
>TCRU_6247 Retrotransposon hot spot protein, putative
MGAGPHPLYQLLHYGEEQIPVVAYFIAEQTFLFDNTTKTMSEDVVEPDTLNIVDGLLDRG
FKGCLIYDVAMKGCQPSTALSCKGWGMILVTSPHAS*
>TCRU_6248 hypothetical protein, conserved
MSGLKPGTETCHPVKRLACGVRAFLFLLRFPPVQSPDCGEEAHVPGIDAVLREGSRHDST
SVRCHAAWDSAVSWGNVESTARPRSTSESGIMQISSVMPSCTAREPRRSASIAERQSVAA
GTRVGDWDAAARRELGTVCGHAQWQDTPHGRSTQGCQQLRGEAPQGARLSGESGGSATNP
DTC*
>TCRU_6249 hypothetical protein, conserved
MAMMMAGRVLLVCALCVLWCGAGGVYAWDLNNSALNEYYYGAYGVYCNASLNATFCKEKR
NASKGEETALPKSTVQSEEVSDLSNAGGSSGGHEQNLEENGSDRSIGASGTKELKNYGEG
ETTPTQQSPSPTEPSTGAEDLPKPAAPGEPEAPGTTTELQPPQQSPQQSPLPAGGTPTPT
TATPTADGPSGGRDNSSEKNDTDESEETDEGPQESQPAAVSLLLLPLCVDVLLVCA*
>TCRU_6250 hypothetical protein, conserved
MEGVRAVVDGRSRWRRQQFAVAAAADGVSGEVDINSGSSREDQSVNAAGSRAESQVQSPL
VPEPGQADAKSGGENPPKPAGSLETTKGESGGKSKEEEKEENPTVETKGPDSTNGENQVG
NAATGNSNGGREEKNEVTPQIKEEVVEPKEEQEPQKELEEKKKQRAEENKQDDPGKDAED
TEDSADGTDREEGEGQKEGDAGSSKKGKEVNGGGGADGTPLTHL*
>TCRU_6251 hypothetical protein
MKDVDTARVLSELVNALQRVTAQPAWNTVQEPKAITFRLEDLFSTPNSVLASAATEGDSP
EHGGNASEMNSPDMAAASFVNSGVGDGLGETATPLAPLREMSDHFSSNKKYAEEGLQDVF
TMLQRLIDGTYSTAGCAALACMGQEIDKMITLMKPVALIDMRAAVYMNSLCSNIAAAKES
RMQLNAPLVWDFVTNTVQTYITDHPVLYTALVAISNLSYLKDLKLTREDCGVLSRLIYPV
YTEVHIVEVWAAMICNLTAHHPETVQVFLELGVVEVLERLVLYFGEEGRTVIRCLQCLSN
LSMGFITGHSPVLAE*
>TCRU_6252 chaperone protein DNAj, putative
MDIMDDAAIVRHVLNNRSNYYRILFLERAATTEQIRVAYKKMALKCHPDKNKHAGASEAF
KLVGIANATLSDATKRHIYDTRGVQGVQQHESAEGSRGGAAAARRAYHRPNDIFEELFGR
HAGMHAAGGHVYETEFHPNILMAAPLLIFLFLAILLQSSLTEISEYHDPRAGRRDNGANT
FSLTPDPLHGHVVERMTSQNGLRVKYYVHRAWADRAERGYADVRRMEREVLKQQQESLAR
RCEAESLSYRARGKKETPPICVDYETFRRAAR*
>TCRU_6253 hypothetical protein, conserved
MVCVATIKAHHYDTHRFVEVPLFATGVGYKKIGFGRLLNAALQKWCAEAGFEFMMISADV
QAIPFWSHLGYATMSKSELTRIAFYYEHNCYKFKGAEAMIRYCKKQPTHSVQAALERMSK
IVVVGPLALPNP*
>TCRU_6254 hypothetical protein, conserved

MSSSAWVICFISIRFDLDLGPLVECVAPPDALDDEGKRAITRMAFPDCNPKGNHDLIFFF
QMKDCTTASGCHRAETVAAPGKEKSGSTIYGATHYRQKKDVSVPRGYVQQAIVLLSQLPY
LAVHELILRVVVPRFCQCCSLSPDIEKVPVLSALSPQPTTFFEVDSSFNPSQYSQKEVLE
RALEEIEGWPSPHPHVQYNLTLLHQPITFVTPKRFLFPTNMEGTNKRRTLNRLDERVAFL
GSKRQSSSVHDVIPLYALLNEHLRHLTQLWELILCHESLFIWSNTPSMASAAAFAVASLV
QPLNFNGVLRSYLTVQDESFCRYSRMGKAIPFSELECIIAAGTNPFFLRAFDGWPNLLTV
IDRQGLSPERPATPSECCAANVSDGTPFVSAHGLSSMPNSFSRRDSDSATSLNGNGIAPT
SPRLFTYSSFFFALAAAKKTTPLQPDVASAGPGGDSPLYSQEPFNTLKSSFPFLVDHKEQ
TSILLHQLEQASHLNAEAQLASLSAHVWNSCGKLEETSVDRTDATERSGTSSGTQPFFQF
SIADDIVRKFFATLTMEFLMPLSAWFQSMVSTLTLFHLCDPAVMTALTPDSFLSFLKDNR
DSVPSFLSRRPHKAYSVMYRRFARGPLFNAVVWQLMDKRIRQGLENMRVDEWAAAHPTEV
ERVEMFFKLYKLVEREAVQSIDPDVVFVTMAISILAEMVVYIREPLRDELLLKIRDLRI*
>TCRU_6255 TPR repeat, putative
MSRSKEPPLPEELRTRLGQMDGCATAEAWESVGNECFSHGCHLSAIRCYTKALEKGSDTA
NLRSSRSAAYMKSSMFAGPSLALKDAERAAELEPGRCEAHLRVGDAQLARKKYAEAKAAY
QKAIELDGSCTSAMHALRLVERELFLRSLDEQEKFSPATEKPSGENTGTTSTGSNAEGPL
NMEEEIKKRIQLWTEDTTVREDRTAMRAFSARLDEADRQAGRTYKSELLLKFRGKMAAQE
PFRRMVEERRDQEMRMGEGIDYRNADSYRAILTKGTDGVGLGISTDAYKSYKYESKMW*
>TCRU_6256 Ethylene-responsive protein kinase Le-CTR1/Protein
tyrosine kinase/Protein kinase domain containing protein, putative
MFDAVVLEYDRSAGEAVVETTDAASRRYRVPMSSLSWSFRSKVVTSDAAVGEGKQEPPID
KMKKRRMNYLDNLFHSTPVGRCVTIGPVEEMNTGSGEDNRSSALPLARLVHLHEAGSLTS
RSMLPGTITRVSGRFVFIFCSFLPYEAVATRDMFSMGGFFLDTTSAPNTLLKDWEETPRP
VNDEDEWVGRSVHFALHPMSFLVMEAFFTRNEGIQERRGAPKTLAACRKNNNNRWSHPTR
DQRRDVNDLASVQHEAADELNDGHLGTWKFTGVNPCRFFHPELSVQFVHGSSSLPWNAMP
PMMHQKSVFTLKLFSFWMLPGTRISLRALDEDRSDVTDRVLCVEQEELEGMNAVTLDHLE
SREVVLFRCQIKSFEMQDVVCEITLLFCMEHMGYETQLESRPILIRQGLKGRAVVELMGR
SQPCSKKDNLSRKFWTSDVLGPEDKITTGFTDPGRSNQLLTEDCYEELPMVQREIIVVDP
EDARLQMFAALARRVVKGIVDTVVCAQVLAWLVASAYGGESGGINAEDEIVSLRLRSGLS
KRRRGRPKLKEGANVVRLGDVRSGVCRHRVLLFKYLCDVVKLPCYLVRGEHQGPDDAIAE
RHSWNIVPLEGSRHLLVDTTLSPHKLEMWPAPAYRCVPVKLSSNWSDCHCLLSNRSASNI
HLLEECGRGVTAVVRRGVLAGGLTCAVKVPRTNTDLGSLVHEYEVLRNFCVSSHVVRCLG
WSGGIVMEYFPSNLLSFMNHLIICGNRMSLSQQKEVLIGLLLALKEVHDCGYVHRDIKAE
NVLLVVIRCNTCHSVGTVCHLCDVRVKLGDFADSVAVDPTTHMHKASPRVGTPPYTAPEI
DSEASFSFAADIWSCGILAIEMASMQLPETGVQEGCVKESYERSMDRRNTEEEFNYQEDG
DEARIVVSAVVDDGVLVGPVRLPRLPRNPPPPRWQQRFVDGALQVNWKRRCRAGELLNIL
GGASC*
>TCRU_6257 Poly(ADP-ribose) polymerase and DNA-Ligase Zn-finger
region/Zinc-finger (CX5CX6HX5H) motif containing protein, putative
MPKLRVEYAKSGRGKCSSSGCSQEIVKNEVRIGTAFLFPAPGGEQNEAGNERLCYKWRHL
CCFTDIQLENARASGEINDIDGYSDLAPADQELVEKLKRGELVQKKSLKGRIGDFANSPL
AAGLLQKGKGFAKGSTNASSSSPRKAAVKRGQIAKRPREEKEVAVKEEDDSDATEEYEVV
VEKSKPHCPYGSNCFRTGAEHIAEYFHGTEADKASPPRLRAVIKGKKRAT*
>TCRU_6258 kinetoplastid-specific phospho-protein phosphatase,
putative
MNCFPKWDKKKKRKDEKTSYCEEPAKKNGGGKGDMENAISVHIPFENNELKNECAIGEVT
ELPLSDIITLSREFRGLLRECSDFQSKKHLVTTLKSLASEIMQKNFSANSVDSAIGELVF
VQNLLSKIPPVRMRLALAVLRFCGVVELEMENEELMRSTGFLEALRGRGATQESQPPPTV
GNSELINPISPTAGLNVAKIYHQLITKNELPTVEEMSELISRATRLLREESNIVTISIPC
IVVGDIHGQWRDLVDSIIAAGGSLDVGNHTSTHPEEDDMEVVGRRNYLFLGDYVDRGPHS
LHCLALLFASKLLAPDRVFLIRGNHESSETNRKYGFLQECLDQYPLPSGSNRGDEEPVDI
GWGLPEHPLWILANEAFISLPLCAIVTGPNSVRVQEMDSLRGSGKERVAICAMHGGLSPF
ISNSLDGILAIDRFHEIEDGPLADLTWADPIVTVPSDVSLEKNGENGSSKSERQAQRLVR
HRVAFNYDAPVPDPSSTKGYIFSSRGRGHNFGEDVTLRFLKENGLSFIIRAHQCVWEGYQ

WQHQNRLLTVFSAPNYCGLGNKGAILIIHASGEPELVQFEAVGSEVSPANIPEPSPPKTF
*
>TCRU_6259 dolichyl-P-Man:GDP-Man5GlcNAc2-PP-dolichyl alpha-1,3-mannosyltransferase, putative
MGYRWVNALLAAEVLISLIVVLFVPYTEIDWNAYMQEVKGFLEGELDYRKLRGDTGPLVY
PAGFVWIYSALYFITKEGKDIEMAQWLYAGIYIMLFACVTQLYVRCKIRGRLLIRLLLSK
RIRSLFMLRLFNDCVAMLLLYFAVVVLAKGRRWKLGCLLYSMAVSVKMNILLFAPGLLLI
LCRSLPWYRVILCLVVCALWQVGVALPFLLHELQAYMLKAFELGRVFTYRWTVNFKCIPE
EIFISKEFGQVLLLFTVVSWFLLWRRRWSRRLFQRAQVATIKSVEYGAVRGADVFDTDSE
VYRNVVLTMMESNLIGVIFARSLHYQFLVWFFHSMPMVLSVTRLPFPLQIASVVAVQYGF
EAYPSTTQSSFVLICGFALAWVGIVCMDHDSGGAAPRRHKREAAPDAAKRLAPAAPPVKQ
*
>TCRU_6260 WD domain, G-beta repeat, putative
MSGGDIWVRRAPIGHPREMTVSTSVNNGPGPQGRHLFAELPINAGGGEVVLGECGTSGPS
RSCNAMFSFKPPRHEPLWQPTRLTSPYCVLSANGVQDDFYTSCLSWGKGNIALALRDEVL
LFQPSRPLVRLAVLNVQERPRSIISRVTSVAVSRFSDSSCFMGELDGSVGVYASRGDGRL
SQTSVFSKPPPPLENTPLAGEAAMTATASVRCLATTDVHPWLVAAGTAAQGLFIFDSRCE
KPSAQMVECDTFIALDSKRARKPLSPEDCVSLLSSAEGICGVSWNVSGSLVATGGSGGVV
NIWSLSQTRAPVQQIKLPNAHTTVKAIAFNPTLPYELAVGGGTNDGMLRLYDVSSSVSYL
AWGVSTGCQVTQALYSPDGAFIISAQGLRHAKSTADGSAHSTALRMPYSNGAGVDVHRDS
MDALERLTEEFERGMTRNGRTQEELQEPAPSHSETAINWAGDTPRTDDSPAFSLVMWRRG
TQHRHSVPLGFSNTKPRDRPRSQYIQESERTPLPLFSICMMTGHRSRPLHLAAPFSSTAD
RGSVASFAGGVDNTIRFWKCFCPRSEAVNWEQRTRASMRAAVTEEDVEGMMAVPLR*
>TCRU_6261 Leishmanolysin, putative
MTCKKENVLTDAKKQLYTEKILPGAVKLHAERLLVRPASEKITVPRTIGGLCDRLTVPIE
HKKNGGVPNFDFIIYAAAGPSNTESMAVWAATCNTWEDSRPSIGAMNFDPKYMTDTAWSV
RVAAHEIAHALGFSQESMREKSLVKKPERSVRGKHRKMVAGKHIQVKAKAHFGCKTLEGM
ELEDEGGPREKEIPYWKGRHARDELGPPQWLRLTDQQVQCNR*
>TCRU_6262 hypothetical protein
MFCDAKDTETLRCTSDRRHVGTCTATIVEGKGSLVDKDVCPFLSSEFHEISSGTTYSTCS
DENVKNLRGSLTGSGSWCLDAELLETKDGDGHKSVKGVCAQV*
>TCRU_6263 Mucin-like glycoprotein, putative
MSPTVQISSTPLNGHTHDDDVPSAVRPAGARPVLPLFRVCARGFDGFLKTTTTNNTTKAQ
NGTESQGSDLSGSPTNESVVEQGKSPVTGHLGSSGSGFGVGSGIVDGDEKSSTGILTQSD
DATDNLQREGNKGTTGSQSSKKTSTEEENKKGEDTSETTATTTKEPTTTTTTEQATTTTT
TTTTKKAPSTTTTTTQAPNTTTTEVPTTTTTTTTRTPSRLREIDGSLSSSAWVCAPLLLAV
SALAYTTLG*
>TCRU_6264 TPR repeat, putative
MSDTDCLELPSFEAFDTEDRPPPPSIEDYPIGCEVELVDIGPAKIAQTNELWEPFMDELF
GQCRRSVRVVRHQGDYTFVVCETDPELIIGCTLYRACLSEPKVRFKKYIPTHHAEGAIVK
MSVNTREGNDKGLFELYSSATEDDSHDLEGVAIIGNSIRGNDPASAKIKGTQRSLTAAEA
TRRSRCNEVENKHEAPIPEKADAVRCKYNYATRKAYEALSKENYREAVRYYTKALKYSSD
GGARCLSNRSVAYLGMRNLEAAFKDATRVIELIPQSFLGYVRAGNTLRGMKRFEEARTYY
EKALSLDPGNETLKYLLLSNFIMMLYASKYEHRKAASIALDRRTLNVILQAKKDLRAGEL
AWVESSGAVVSLKQYDYLSGGGGVGPSGNHGNNTTPQFCSQCFRPLTKIEEFCERLSDVE
PSILKRLYNEHHIVQCNGHCGVLYCSDSCRSKAWAAHHWVECVTQGKWSEAYRQLPGLLR
DFVAFCNGAANSNCQGGNEYFHGQETRLPSFTEEKVNVIVACVRLACRMFSKILSNGRPL
EDAVNIFEWMLPRECTYNSNLDCHPTNVEQKIVIKKILTPVYNIFQQCFTSEEKHYLSFI
VFFHSYERARFNCVKLRVSAWPAIQAKAGSYIDLMKMRRSNSGSTSMLSSASRDSMPEGP
SEPQISQLERIVATPAESMPGYFECLGVFKVFAATFSPLCAQQEKQAYYNVRVRPIIEPG
AIIHIDVTENIQRNEQLVSDRSIYEAIA*
>TCRU_6265 hypothetical protein, conserved
MEFSGSTLSVSEVEIMVRQLKPMSIEKVGTTEWKDQREMVERLNMCSHSNAVLKKDDTVK
AFLIEHEKLSVLLHELLVMEAWRHRVLPLVKDMMAGNPTAMYMFPYYEMVLVNLFECICF

HEEVVVALDDDVLELLDYCWRQTSRLFAEKGINDIPARPTLQEISEEDSLRHMERQLSHG
MVQRALTSLSILWFIIDRLEQLPLSVSNSVFNKNDLVLGLSEIMMLQPWLRRGSGATQKY
VNGEFKDVPQGDALLVCVPEAHTWFSLHKMLCDPECRRRYPYTQSKKELILRIRRFLNDT
LVDQIPALASVQRALEELSFMQPPSDTEAKFKSSLTIEQVPRIMAAVEASRTHSWEDVAN
TFAAMLKDPRIKNEDAMRMARIFDEMFAENERPK*
>TCRU_6266 aurora B kinase
MSAAEGGQVVASYIALPKAPRSDWKASDFEMLHKLGGGNYGDVYLASVRDCNFVCAIKKL
SIKKLAEFDIVAQLRREIEIAFHTRHRYLLRTYGYFFDDTDIYLILEPCSNGMLYTELNR
VKCFPPPTAARYVAQLAEALLYLHQHHILHRDIKPENILLDHNQNIKLADFGWSVHDPHN
RRKTSCGTPEYFPPEIVGRQPYDTSADLWCLGIFCYELLVGKTPFVSKDTENICKKIHAM
QYTIPDTVPPEAKELISSLLLRDGGKRLALHRVVNHPFLLKYYYLPNGIQPPRGKRMRGA
TDFSGGKEN*
>TCRU_6267 RAD50 DNA repair-like protein
MTSIEQIQISGVRSFDPNPAHRQTIVFQKPLTVILGKNGAGKTTIIEALLNACTGQMPPG
SGSEKSSFVYDPKVMGETDVKAQIRLLFTGRGGKVMQVIRSFQALRTRTKTTFTTLDSTV
AFQDTATGKVLSSTYRANDVDRAVPEMLGVSPAVLEHVIFCHQEDANWPLLPPKEVKKIF
DEIFAATRYVLALDRLRENSKEFRRQQKEHEANLMALREHREQAQQLTGDIAAKEELVRT
IQQRSKSLEPQLKELHAVTAALSAVEQGAEGLAREAAMIQGRIDEKQESLSRMTLPPTTL
TIEEMLEFKQGFAERIKGLEADASDKANLLEKAEAKKQQCEETALRLRSTTEFLEQQERQ
YKENRVELQGIVKNLSTGLVLCDDDMCEEDLQRVSDHLNAELQLARAERDKALKEFDDEK
KLLEDQRNMLLRSMDADNKEKDMKEDQLKHLHQRVVSTEEALGKLKPYVGATYLESLKKT
ISELEQRLEVMEELKKKGENYKQRQDILQRIDAQNRIVAGLRQELARHKECLGGEAEMNL
LRTQITEKERFLEAEMRETLVPELSNFGHEMTEGSSLSQISLLIEQLREQKLGVLRAIQT
EHGELDRQIAVLQQNRAQRMEEIMRENSELQRKRTNCVKALDGLGEIDHFEAVLEKARDL
LEAARNRHHALEAMSTCYANFVQVARVEGKCPVCDRGFTDELSLANFVELNERHHGASPE
MIEKAHLEAKEAEERVRILETLEADVHDVRRLASSVPHLELLVTRTNEELANKSALLEDA
ERKREDVEHQLKRVQDLMRTAIDLNAVACDVRALRQQLSRREAAIKELQAEVVTAAGGGA
DGGARTYEEVSAEYESANTELHRLNVMLNEAQRREDGESDQAAASELNARRAEYYQLEMK
WMRQGELEEVLARYKGEENGYRERIAAINAGQEGVREELLRLQSRIDTLQRARQDAECAA
QQGRIGKIEESTQMLAGIVPKMRDYFASKHGEQLFRAREQMQLAEASRLRAVDEVRQLRE
AIQESRRVVDEQYRQAVEVGKHIEAFKKRQSIDEDQARLQEVERSLTEMKSREIRGVAAI
LGADVIAGETVSRIRELIREKVSELERSRAQQEGNVEAMMQDITNLRSQLAREKYHDIEK
RYRSTFLKVQTTEIAVADIEKYYRALEKAVQSYHQEKIAQINQILADLWRQTYKGSDIDT
VELRSEDDVTSTTARRSYSYRVVMKRGNSEMDMRGRCSAGQKVLASVLIRLALSEAFCCD
CGILALDEPTTNLDEDNARSLAESLRLLIENHRAVKHFQLIVITHDEQFVRALGGQALDT
FYYIRKDRDGAFSVIEERTFDQLFAA*
>TCRU_6268 ribosomal protein S26, putative
MTTKRRNHGRAKPPCSRGRTRPVHCFNCGRLAPKDKAVGRFVVRRMLDQASARDVAEASN
VYGAGFPMPKLYMKQRFCIACAIHSRTVRARPTDMRKRRFTTKVPFRPTGAK*
>TCRU_6269 hypothetical protein, conserved
MAMMTGRVLLVCALCMLWCCLCGGYGRCTVGHCALAELDDAKFAKGMDGEVVLMKRDCVP
TTALRGVVTAVPAAGDSDELGSPDAGVGTSGKQKVDADESAVVFAGSEPTPGGCGAVSTA
SSPASADTIAASSTPVSGAGGAVGPKQQPAVVSGCQYDFSFGGREGKEGEEAGSAGRGEE
PSVSSVCSQPPLVAVDLTICTLDQNKEQNDNASFDTDHQMATQHEEGVPHVPGKRASVQT
LPVPTPAGGQPGHATQPSEELEEHATAPNSGPTRDALNGDSQEQTPQPQTPTDNKQSLPV
LQGLSEGVQENQNNMENIRKGNQVDSTGNTHNKEHDSAAATHELLTASINTRLSGAPGNE
SNTTLLSGTLRSSTAGTEEQAKAGSMPLRQPKPPEEKLISEELPPTATEVEAPGGPSAPP
PKSLPQSALPSSKKVPDTTQSTEAPQSKGVEPTTDARQNAITEGQAETTSPSSPADDAAA
NDADESNVEIANDGSAVNAGVPEEEPNQEQVDGSEKQTSFTSTAKKHNATIEDSDSSTAV
SHTTSPLLPLLLLVVVACAAAAAVVAA*
>TCRU_6270 hypothetical protein
MTVHVHWLNGVPACEGWIEKYSVGRSFFSRKSWQMRYVVVTSEGIGYTHKTPNRCMKPSS
ARCFVPFEGPPRSNGGIHLRPVYLLRHVPPSMHPEVPDGCQKALSCTFSGSDVSCEHHYF
AISFEERKKRLFLLLRTKSLEDYNVWTLVLSVYVPAGSIKTVVPVPHPLENYRHGSAYFF

NSKKGFFKIWDNVINVATAGFYMVDPDPCTAAELGRIKKLVLGWDEGEAFRWQSLRSGET
STSHLTTILQEENEEEWRKLLSVAAELDAVCGPTEESTEYTE*
>TCRU_6271 Mucin-like glycoprotein, putative
MMTTCRLLCALLVLALYCCSSVCVARSTDETIVVREVDDVKEPTSSSTLSSESQVEDDFD
EERGSGTGSSEDRGTKVPVTPGSSGAVVQSNEAEMPVQTGEKKGTTEDESGTTAPKSQSK
GSTVEQGEADVGGGKSLTAPKRQSGDAIGTVHEEDGSTTGPQSRTTKSAEQTDRETKDAA
ATTTTTTTTEAPTTTTTEVPAVSTTHAPSRLREVDGSLSSSAWVCAPLVLAASALAYTAL
G*
>TCRU_6272 kinetoplast polyadenylation/uridylation factor 1
MFTCRLLLRRHAAIGLTCLRFSQRTASFQPFSQKDEEDLVRVVRTKPRHVLKHVRQQVWR
SRKRELHFRNTVTHLMIVLQEFLRKQLIDPASASQIMEGIMEECVKYSQHDMAHLLFRAF
LRFRKYGCVISVDALRYLFESYKENDSSELMIQLANEMRSDPAMRPLCIAAYLFANHPEE
ADALHEGLSFSDLTREDIVALIDGYDKLRRTEKIMEVLQKVTQLNIDPADLTDIFRALFR
VFYQRDDEASFAAVFQASREKSVALDAATFAIILRQRMRHVTSVEEIAAVEAELQEIGYV
PDVTGNSIIIAAYARLIHFGDRGSEELMLSKVDTLLSSIESRLKQGDPDMDISAAHIRAV
IRGYGAAGRPDSLKTAWTRMQYNGLTNDVRVYNELLKWFALMGNVKDVIALKEEMDAAGV
HPDSQTYAWTLRALGKYYPRHVEKLYEEMVEKHVRPDVQLYNTMIGIFGDLGDLERVETI
VEEMKRREGFGTLQLTPVTFAVLIRIYANDLAKAEAAYAEAKKRGLTDHPHVQTSMLHVY
ANHAEGSEKLEELLKEISSWSTDIFNVLLNKYGKSGQREKVTELIEKMKAEGTAMNDVTF
GTLITAFARWGDAEKVRDVIQLLKEHEGEVSAAFYSVLASSLSRMGDVDGVSNAWDDLLS
SKLFPDTEVYNQFLLLYSRQHNAGKMQAVLNSMMKQVPPNPVTATTVLDMLGKSGRVAEM
ESLFDDMKQSPDTMPTSVTYHQMMNTYAKTGDVAKMEKLHAEFLEKGYTNNAVTHNILAD
GYGRARRFERMEEIVQQRKSSGIPMDDLIYCIMATSYGRARLKKEVHRLYTEVTSPTSRH
LFTRKVIWSFIDAFCRCAAPDDMEKCVEELKKTDENNTLTASDVLTLIPYYCRLGDMSRV
DELREKANSMNADLSYTSLNAIARGYARAGRFDKTVETLHLLRDRNWVPDAATALSLSSS
FLKAGLHEQAQQVVQWRRQYAKHAGEEVSPASDI*
>TCRU_6273 hypothetical protein
MERTRGLNCSLGLSGTCKEDVDPRNAWQRTVEANQKMLDIVRGRETRSSAAAELFRSRYF
ALLHELAAEEEEVKALNARSRDLVAALRDAQLHGCGQGQRIDKIHKISAVTPTAGEDTNA
IYKQLLQRLTHTSRLRDELRDEVQRLQSTCKEALHERAALMQSVDAQREALEPLLKEADD
VARAVEMVRATLRTYGSHKDDKEREKAASLSLADLLHGVDAWSFEEKRAMRRVTALLSSC
IGVEDDCIKTADCGRLRSVEEAVRFYQTWNDALMRSLGDFSREMNGRREGLYARIDELKR
FRTTQQMNGAEGN*
>TCRU_RNA binding region, putative Gar1/Na.1
MDASSAGSSCELAEDVRGVRRQRVSLSSVDSEPIIRRHRPDASPRYDDAAAADDDDADDD
AGDDDRNTNGIRERDEGKGSDVLSEGQMTAAHREGSPSALVQAALRDANGEPLLQIPMER
VSEATVASVTGLIARSSTVVADNVSGAFVMDAGTRLCLGDGFVVGVITTVMGPVSCCAYA
IVCLPAVFDALCDGGKLTVGVGLCYDLGEQSVIYDPVSQCDMRRGTDASYINDEELPPHA
RPDFSDDEAERQWKMSRRMSADGEPISSDDDPVDVDWEKIDVLEACLRDERREGAPGMDT
AAPRHNPRLVVPPWVATTRAPNGAP*
>TCRU_6275 hypothetical protein
MFAATPGLRVWDALKSRGRSLCRSRSDIVMVASTALCVSTYCMMANWIYGGYVDLWYGVY
GLEDDDDDEDAA*
>TCRU_6276 fatty acid desaturase, putative
MSRVDNLTVAPGSPDVMKAVLKSGRKKEHNVIVPSSALTIREIQEKIPVKYFERNTTRSV
MFLLRDLAQVALTYAIMHAVVLPFATSMEVSAARTVADGGALSLMTGTAMTTAAWLLKGV
LWAVFWFVQGLNGTALWVLAHECGHQAFSPMKGLNDAVGMILHSALLVPYHSWRITHGGH
HKHTNHLTKDLVFVPEKRNSVVELVEDAPLVSLIQTLIIFLFGWPAHLLFNASGQEFGRL
ACHFDPGAPFFRSEDRHDVVLSNVGIVSALFVIFSSVYRFGFTNVFYWYIVPYLWVNFWL
VYITYLQHTDIRIPHYTHEHWTFVRGALAAVDRDYGFVLNTWLHHINDSHVVHHLFSKIP
HYNAIQVTRKYIREILGATYITDERSLWKMLWEQRRECRYVVPAEGVCVFHG*
>TCRU_6277 Glycosyl transferases group 1, putative
MNYSRFRSRGARGRARTRRKYRAVISLLVLLFCFYLFLRILPPRALATIRDDSGFLIPGG
NTSSVTVVITELRVSAPFSAANLAGSRLKQALSRRAWCTSSSPMSLVSLVMLFYAPPDNA

SWSGGIPVSIQPYGDSGSWNLWSVDLAKRGIREKYNVAPCVMEARVLFAASAAEVESDSY
GMDLAAVRMALRAVRRTDYFVLLADFVRPKSDDFMQKLFLPSRRNGGKVLAVQCTLLEKK
STNTQGIDKGQEVVLDALHVVSDRGVFVGLAALKRLELLLPYLSRRYNGIFATDKRLLEP
ELVDAVSPFCTLFHRQAFDAFKGFDSLFFSENTTLSQAPDIAGWEYSIFLQREYKEWQVW
SSAAFGIIDEGTSPSSSLLQLLRQPAFPAADNWGAEHFDTLQRLHNRRFATPYQKRGEEG
TVDKPLSPLLFFARDYNCSCCGLMREVIGYLRPLTERYAVSFLRGLRHSFCSDAVGSELV
SLELTDESRAEKFFTSFSNSVKWQIAYKNRPKIVIMHLRAPSYKQVHASLPHKMDYFIGR
SLSEFSLIPRDWVNGMHLYADEVWATGEFFRTVYRRSGVAAEKIHVVPESVNIHRYNPRN
CRPASFPLSLPTAYTNRPELSPEDLRRRFRFLSIMKWEMRKGWDVLLKAYWKAFGPSSPL
HNNVSLYLKVKWIQLYSGGAGNHNINELIRNWSKKNLPGFTSMEDMPHIVFLSGLGYVGE
QSLLQLYCSVDAFVFPTRAEGWGLPATEAMAMGIPVIITNWGGTTTFMPPNATFGIRVDG
LEEVPSGAGYHVFRANKWALPSVQDTAELMRYVVDHPEHARRVGKRGRRHMEEYFSEEII
ADLFDMRLEAAVRKLRGNS*
>TCRU_6278 chaperone protein ClpB1, putative
MMRRLALRCGVAATTATAALVRCCGRAAVISPPLVTACGMQRRLQSSVAPWSSNNNNNNN
NNRNNNDNQQQGRTWVNPQAVPPGEFLNKYARNLTDEARMGRLDPIIGREEIIRRTIQVL
SRRTKNNPVLIGEPGVGKTAIVEGLAQRIVSGEVPESIKGKKVFALDMGSLVAGAKYRGE
FEERLKGVLKDTIEAQGKIILFIDELHTLVGAGASGDGSMDAANLLKPSLARGELHCVGA
TTLDEYRRHIEKDAALARRFQSVLVTEPTVEETISVLRGIKEKYEAHHGCLIKDEALVYA
AVNSHRYLSDRRLPDKAIDLIDEAASRLRLQQESKPEQLDSVERELVRLKIEVEAVKKDK
DELGKAKLEHLYARIAERQDEYDALEARWKKEKAMFERIKQRTEDLDVLRHQYEQARTEG
DFAKASEILHGRIPTLKKEIEADKLATRADSFLTHDSVTASDIAQVIARATGIPVQKLMT
GERDKLIHMDTELRRRILGQDEAIESITNVVRISRAALHSHKRPLGSFLFLGPTGVGKTE
VCKQLAKFLFDDESFICRIDMSEYMERHSVHRLIGAPPGYVGYEEGGELTESVRRRPYQI
VLFDEFEKAHPSVSNILLQVLDEGHLTDSHGRRVDFKNTIIILTSNIGAEVIAALPEGVP
SSKAMPEVMRQVQQRMTPEFINRLDDIIMFNRLGRKETRKIVELLFDQLRAMLREQDITL
ETTSDVYDWFGENGYSAVYGARPLKRLVQSVLLNRLALMLLDGRVREKETVKVEMRAGEV
YVVPNHEAVNTTNNAAEDIGLIA*
>TCRU_6279 hypothetical protein, conserved
MSDLSSVEGDEVIMLGAETPADVTAFKEISAENRNFEYYERQFQEVLMSLENDEVLEAFR
VEYAALHHSFLKSHDGETRLLKKCARLQSDIESCTMKVQAAEELTRGDKSTIELLKAEIE
KTRKKSVATKEREAVLKDKVNDLKRDLQDIEERASRPVELTAQEAALQSLIRAHETVLKE
KEAMEYQLAELRQECAGNARRLERLLEVKRSRDDEVRVVVKAIEAKLHDAEAHKSVRLRK
EEELRLTREEIARRAAAAQERQAVIEQLTDENARHDVEIKLTLEETARVTESYQQLSRQL
QNVNRTSQACNEENDALQRRMNELMEELKIKESAVESVSRAHRREKKLLEASTRRHAVME
GRRAEAEATLSGLQSELGLLEEEVAAALRAVDMEERRIATQVRELDVLHGNVLTAAEKTQ
QQSIWLSEQRTEAHHLEHELRSYEEQAQRQNEVIYKLTRECTEYEEQIKVATIQCARIMA
EAQEREVQLAVALDEVKDVESRLHQQQTLLETILNERKAYAKHYGQVRGELAEMVRGFKV
MLAQIKQMQEEVQRRERRLAAEDGVIKTLTRQRRELEVQIAALHTRLDKRSRSVQQYALE
VRRLGDVFAEGEEELGRQRRRLCDVQKERDFFDNEVYFSSEELARLYEKARVQQSLLQRG
ESMYMERLRTINELHDGIARLTEEVRQLRLFAERLPDLRRLVNVASRELVREQNRVRALL
HECERPMNLHPNHQLSSSDPEAYALTEKVNALQRELVSRRQELAEKEQRIKQQEESYLQC
KAAVARQLGPEMAEQITLYQGNLAKKAGQMRAMMASLKYFREQTELYQARYSELRDTLDG
LAQKYAETRQIRDRDAQREARKRQGDGKGDSSRQNDQPGVYVGFFAPPRGGGPATSVSDG
GSVSGERNDSQKEDEGDDIGGDDLKMHEGNEWEEPSL*
>TCRU_6280 hypothetical protein, conserved
MWTPEPPPSKDAVRNSILAQLNTIRTAGRGHHESSEHLQSQSQHSPSFPSSPSHISTGNG
RRANMGSLSSSASPRTRRLPPIFAEQRQNTARIRHVCGGLNEILQKLDLDFAHVGGKIRA
AINTDGVLGRPDMPGAATMRLLQLRSRRQFLAKLRRTPPREQISTEEETRKGAVSEELHD
EIHRARLAAADEGLSDEQSVSDYAEEPDVPRFAPASRLRDEVEAMEASLRKISECVTAMS
VIENCDAGQPWWESAMRTREMKALGIRANYHARSIIKWNQRAREHFLVEAVTSNEQMERC
RTDMLYLREQQDLFQKRIELCHEEQASTAEEMKTVQELLYDINRFKSDLQQQLLGVAHER
RLLPDECEDARLAELVLLLEHVNWPASLRPDVECVKEWVRENVIPFDV*
>TCRU_6281 hypothetical protein, conserved

MRNTSRKRRAHESYDCPSETSSGFLECHGVFHKTGCAAEIVESHTWMTASFWSDIAVLTP
KTFYTGVGRDHNSGLARGSKDGEGGSPPRPAVRPDARAGCVQHYKVMRNTSRKRRAHESY
DCPSETSSGFLECHGVFHKTGCAAEIVESLLNLSVH*
>TCRU_6282 hypothetical protein
MTHYTCIRVREIRQPEFLQWRRHIHENPYLAYEEQPTADYVASVLTAMPAPLEIRRLTPN
SVIADLRGGAGEGPIYALRADMDALPLQEESGEPFSSKRPGWTKGR*
>TCRU_6283 amidohydrolase, putative
MEEIVAGIAKAHGAQHEISWLEPNIVTYNDPAAYEIVRNVAQRVIDGVSFIDLSTAMMGV
ADFAEYGSVVPGCLFWLGVGDSSRSSTSNHNYSSRYCMSETAMEGGVKMHVGLVAALSMS
DGTFAG*
>TCRU_6284 hypothetical protein, conserved
MAEAVSCLDVKSSFIVSLPRETRHLFRCRVEDGTLVELTRHPVGYKAGPEILQIITSAIA
VVTTVAHPLWAAPPLVRDDVWVGNIRIAGSKSDVTLWEDRESGAMQCTFLGVRFDHGNTV
RYP*
>TCRU_6285 hypothetical protein
MGAPDNAVALRKDGRVPSSPGASCAPSTVARRANSFPPTVSTARRLGEVAHGITTSAALR
GTHAARPHPDIADDVPPVPGQKSLLPGPKVLFVCVYRPPFAASLGTSCCIVPSSHVCGVV
LHWAGARHAISLLSEPPGGMGGPISGRLDGTLNVLDPHSGIVIHCPEDPCD*
>TCRU_6286 cation transporter, putative
MSENETCDALLSQYELLRGKMATQHCDDSHDGDKDEHSHGDCGGSNGPYTVGLHVVAIFV
VLLSSFLGTVIPLAGKHVPCLRMNPFLFVLGKCAATGVVLAVSTIHMIHPAAELLEEDCV
PDSWKESYDAYAFLFAMIAAIVMHALETQLVAMFASDESPSSPSGGNGEKGDANGDEERA
DGAPSGDIYQHHHSHALASVEGGRAHRLLSALFMEFGVTLHSVFIGLTVGITSDAETKAL
LVALVFHQMFEGLALGSRLADASMRISLELLLALIFSISAPLGTAVGVGAVVGSKISLTG
VTFIIMQAIFDAVCGGILLYLAFVLMLSDFPTDLRKHAGVGAAHRGWKRLAMFVALWAGA
GIMAGIGKWL*
>TCRU_6287 endonuclease/exonuclease/phosphatase, putative
MDANSIGAGFTQRVHDEEVGERESERVCEENKGPLTCCFKELHEITKSEVSVLGPATPFE
VTHSVSSSFFAVSHNEGECNLHDRIDQYYDDRHTVPFSIEEETFPVPVSLPEEKWIPGKP
LRISYVSWNMAHRRPNFEDVAGHCIHPNAHIIAVCTQENGSYVRVKKEQRQWERHVRHNC
LHGEYVLVGRKELWYIQLLVYARKKDVASYVGYSDASSVKTGIANGLGGNKGGVAVALSI
AMTVSPLQMVPGRRKGENTSHTEGSTSSVFSPREGSPCSVHVGDDVNFEASAPPRITLLF
VGAHLSAHQKGVHMRNKDYISIVRSLRVGSQGRHKALFRERFLHECPFNEELKDVDGGDN
NEVLVSGCGNGVGDECGDVECSSDLSLMRLPVAQSNFDSRLYRDVTDEFDLVFFGGDLNY
RINGTRKAIEYIIKNHKDVRSILVHNDQLNLERAKGLVFRRFYEGNLLFRPTYKYEIAHD
AYNYTKKKDRMPAYCDRVLYKRGQGSRAGRVRIRLYTDVQHLRTSDHRPVVAIFDLATCA
HLPSFPR*
>TCRU_6288 60S ribosomal protein L24, putative
MRTIDCEFSHFAVHPGHGRRYVPFAFLSTKPVLTFARPKCFAMYMRKKNPRFVPWTRTYR
RINRKMTTDRVGRRRAARTVKVERGIVGADLSYIQEVRAKTKKVDRSAKGKAVRAEMAER
KAAKK*
>TCRU_6289 hypothetical protein, conserved
MCRADGKQVVKRNLVVAVLALVFSFVAVDVYLASEDVRLSAEPAPRVSELARSSGVRLAM
LPSPLNEVTLLVAKPFGAADVSHKLARFFTKNVKPAASEENTRALNFRSESEIMKELLSS
ASANMGDEAKVLHLCSANSCVGPYLSQLHAKRAKQSLGRSIKVYALVYGDFFVGRGVEND
LQNLGVLISTVGYPSKAESAMPLIGVIDEKKPNIAADAICSVIENSCQYRIWDKGTQPQI
PVSLIPFSSVSFGNSPLLRTRFDVVHIDVNWDEALASICFLRGVLSSSFRPSHIYLAVYA
SPLLEDTLLLVNTLREQAHYHVFLAGGRCMAAHGASDVLSHEKLSKLLRFESPQLPSKLN
SRGYAMEPLCMLFLSQSLESLPQLLQRVMPIDGAHAMANFIFEFSSGSGPVVTDSESIGV
WSALNYLMLAVPFVVAGLLIWSFVRGQCRLRTVGSNAQ*
>TCRU_6290 60S ribosomal protein L24, putative
MRTIDCEFSHFAVHPGHGRRYVPFAFLSTKPVLTFARPKCFAMYMRKKNPRFVPWTRTYR
RINRKMTTDRVGRRRAARTVKVERGIVGADLSYIQEVRAKTKKVDRSAKGKAVRAEMAER
KAAKK*

>TCRU_6291 nucleoplasmin-like protein (NLP)
MSRSQNQDGEEATGRVSARAVLRTKTAFQIYKDDGAQGNVSDFSTLPNDEVLPYKIQADE
MTLMGALEIVEADPADRRMYGPATLHLVVNYLSDILSFIPLGGRSHELPTVAINYNALQR
VVALYGVPESVKDALAQLAASYLSASEVPIRDISSLLDKFSDTEKALRHELRDAGEKVGI
FTRSTVPVSTLATTGETTINDVVAPAATSQKLPRKRRASSRDEILPARKTEEADTAPQIK
VMKMEGHEKAPSNAKNNNSQLTLQRLTYGRLRTLTSQEKKVVTLLNQMTQVLGQVYAVRY
NNLLPIFELLENRVKQAQEIIDAERANIQSKSENTELSPEPFLEVTLDGILRAIQNASYR
FKTDEECRYELDEDLLHPIAHACMTEVNRIEGFTTLPFEGPSNQAIKAKAKAREAARAKR
EEQRAKALERAKAKEELQAKREEERKLLRAHLGELDPTSLVEDMSIKNPIQTGYVRYGKL
PLEPPEDYERALFIWVMITSLPRPLHLSQMPFSLFLKGLLSDEGCDNGLMEEVVLALLNL
AMEELRSSNGPKVLTRGKDWFGSMVEFVAVCSGNKKTRPPRRPKVVSYEEEEEEEEEEEE
EEEEEEEDDSDETGDEEEEDSRNTEWEEEGDDNDDEAESAESNGEEEGKVQTEGEEKKES
LKKKKTPENETDNLDAGIKATLEKVAELRQMAAWGNVDIEDRLNLLRYMVLAALSSPVAR
EGAEKIRKMHEDMQVTMEKRTKEIREGVHKELTSFFRHFSSSKSAKGNSETYESKRKKLI
EEMEQKLQNIVNEHLGMQDGKDIGALIRPLGMDRYRRMFWRFPFDRHVLVQSTAATDPNF
PILPEPRELLTESVKDLKPKLLDDSDEDNFSNGNGNGHTNHREDVTQRVWGTVPPEYLGH
FIEGLDQRGVREAALRRTLESIQPYLLNLKEPPVSRVTRTRSHSFGYFNKLKIEP*
>TCRU_6292 RNA editing endoribonuclease
MLKRGCCHVALGAVWEVTSLLISRRSHAATAPQSGANFNPRRVRLVSSTSTLGAGAESLP
VDVSPLSSDPNDPYRHVCIYRKDMVSDVGGRAFQLSVDVPLKKFVDLFSDFDAKRCKLCN
ESYMQWHSHSGVIPHSGREALMLEMVRAYCGTPEEIAKMWWHRLHTSPVFNRIPSLSHEN
SHIRKRRLQYLLQFLKERDVIRDTFNVQQSAGGAGRSWEFERLEWIGDNVVKYVFNDRFN
VIFPVREGGIRGRLGYAQFMIDGNDGLARAYDHLELQKLTLSDRVVSKFKSDVVETLFGE
LQLFLWSSETDVGTTYFELPFTPEMFSLRALVWHVMEELAHVMFMYHVEHILGAIQRIVR
EHQLQFIRADPSLRGHTDLQNELASTLYAKKSLTGSGKLTPTKMSPSLRFKDGFAALYHE
SSNYDGFKRVYALGGLLPRPFSREELSATPSFLPHLQEDGVMASRVPSDWWSKLMDTTEE
DAAVRQGVVSTLSLSSLHAAVTPTPHPRSDAAVTPHLSVPELKDNLLVAELV*
>TCRU_6293 Flagellar C1a complex subunit C1a-32, putative
MAHSLTWKLLGPEQTHECLTAPDVPSIRSVLKKIDEACDGKLIGAAKYNEGKVMIVLDML
AHLILFCKSRSMSPEKVSTLVGIVIKIHEESMSGGYTRAKSYHLMRDLMIKHSVPRPPFS
CGVFTVRDAQEIDEYMLRSYYRHYKMYFYAFVPRQVMNVRCLDVTHIHQIPPVGLPSLSA
AVVESEWRTKVEEQRREAEEQAMQEGEIASDAYEEERMRNRLLADPHYSDGIREQLECIK
KEVSSKAVDRLDEIEMRLQEIEKKVAESLAWSDSKQGRRKK*
>TCRU_6294 hypothetical protein, conserved
MAEAASCLDLKASFFQASLPRETRHLFRCQLEDGTPVELTRLPMGYKTSPEILQIIITST
IAVVKTVVHRLWAAPPLVRVDVWIDNIRIAGSKSDVTLWEAQVLRNADGRATMGGDRESG
ATQHTFLGVQFDHTHQAVSLSEKFFRSVRNMPVLNSLTIAEMEVVASRFLYLAAILGMRL
CDHHSFIRAVRRRL*
>TCRU_6295 retrotransposon hot spot protein, RHS3, putative
MVLTSEKGWPYTWNLKGVESTRECYVNCEVDWARGIVKKDLTEWFSGRPEEHFTPHPRLL
IGTLGIGKSVAAGSYLLYQLLHYDAEQLPMVVHCFGSQSFLFDKTTKTVSVYMDEFSIDG
VLASLFLRGVEAYIIYDVALACRQPPAGLPCKGWGMIVVTPPEKKEYERWTKKMDATAIV
TNCPEENDVRAMRIWMKRNWPLQEQAEYWKKVRGRMNNVGPILRFIFGKQACDDRIKACQ
QAVDGSTASELERNLGIGCCYSSNDNDLSRKLVRVVRVRRGNN*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MFYDSGSPFVSVDDNSVVTLTGCKMGSTGLSVPLLSLVDAGYRFVAGCLTVAGRVVTTAA
ELELHGITDVTTVAMCGECTKDGDCFAPLTTAVIDCKCQCAAGGHGDVCVPAPVPAGPPP
PPPLPAPATPPPPPVGECISDMVYPEVAQAVGGGLSWLCYRNVTFSGGRMSLTVLIGAMN
GDVANVTFDGCTWRDGAVLLLLGNAYAAVGSLNIVVTGNTFSDALLSPEGVLPPRTNITI
SGNRFTVTRLVPRSGLGLGRPSCVSTNGLVISNDSAVVLSGNVFQSVTASSSAIYVVRSS
LSVSWHSVFAVMGNTFHMDGGDSNLICLEGSRHSSSLSVLNNSAVVIRGNLVTRPVRYFM
YFFLALLVESQSAVVFQGNDMQGSWFVFFPSHSSNIYYNSWLQVSGNLCRESPSEAFLFI
NPKVNLRGSTVSVSGNRFMSNTVTPTVLRISSVSGDLTNGAIVAACNTVNGEEEANYVIP

SVYNATILTCSDPCALAASCFPAYTTTASSDGCACTCAEGGHGDACLPVAVPEPPSTDGV
DLCVRDVSVDVEVNVGFGTSVVCYVGVTFAADVVVDVESMSGSVRNVTLANCAFVDGASL
YVVGWRSDPPAGERADVLISGLESCSGGGVLLANRFPPGSRVTVVDSVLIAEKRVAYRGA
YFLGDASACLVVHSVNLTGSVLTIARTHVAAVFRDAAGVLFVGGVALSSRGALYVDGLSV
QTALGLCVSVEGGVAASGGSVVEFVDSDFLLCKHAVSVRGAVSVSGSAVALVRSDFSSTE
DYAVAFYSTVSLDDGSMLLVKGNVHDGVSREMLYAAGAVTAAGSTLSFVRNRALLPRMLS
LSLSLAAGAHLRVACNDAGGRVLSTAEEYAAAGFGDAGSIDVVGCDVCDRETYCYAPGTA
SASMRNGVCVCVCGSGGYGEACVPVGAPVLPPAAVTASSVFFREGVTVRSVFVVPAGAGE
VTLRHVVLDGVSPVLYVPWMARDGVRIVVQNVSLLNGAVLYVMGGGVLRGAVAAGSDESG
PVELSVCDVEALNGALVLTGTFPAGSVLTVTDSLLVAARPTPLVYLPGSQSSPYAPVLVL
SDLRLVRSVLVVSGVALVTVVTGGRTVAVDGAVLELVGGGVAVDAAVFGGEYALYASARV
VASEGAVLRVSGSQVYAAHGLVFESGVEANASAVVVNDNAGALTDGALLVLRGPASFASG
SWLSVRGNSISGRLLSVPSYPRSAELVQSTLTLHGNAGSGPVVMDGTVALGGAGRKFFVG
CLTLNGQALQPMDYRSAGIIGEFRPVACGVCDADVLCFAAATRAMSASCRCRCAEGGYGR
DCLPVYLPHVDGCNRTLFRPPLSHTATLTETRSPTPTPTPSLSTTHYSPTRYGTTETLHV
AETVVLPPTRTPTTSVSSTLWWSDVACPTLTVTTTAAGGSLTQNDIRGGGSAVPTRLMVA
LPPPFQWARDPQLGTHLSFVPVTTAQPRGFGGPWGAMLRNATWVRNATNRFTVLELAVPV
HRGYFIAADETIVIRCDAVAVSGGTSPQGVLLGSFTIRSDTLPAASALSAITGVVAGAAA
VAVLVTGGLGSILEMQALGVFARMPCASAQERASTVALPYFLSVFAALDPLWMVVGNALL
AAVFGCVHCGVTAAFQRWRGVDAASAWAAMRFPSLTYVVAHAMHLGIFFGSVFALAMPDA
RVQHRVIGVVGVLYGVAFPAGVCYLIARHVGASFTRYWQFSRKPLHERLLYPVGYWYPAA
QQRMYGGMLTNMRGSRVYWCVFQLSVLCVVCLIAAVHPPVGGCHVQYFCMAAVLLAGAGV
VAFTNMMCSAFLTVMRTAGFALLAALCVISAANHLAPSDGGARAYVAIVLLLTTVLLATT
VYSVVVWYAEDRYWKELREPRRGGLEALLRDDEDGDEDAQKLHDMTSSSYASGTTVTSYQ
PPAMP*
>TCRU_6297 hypothetical protein, conserved
MSVHYVRLRRKDTVVHVEDAGQVHAEAALHEDSNARAPATRQHRPRHDKPRRQQPDTVQN
KRGAVPGSRMATGRRHVLRTANRRAQRRVRQQHTRVRRHRAMQHNRALQRRHIRHVDEGV
GHQARRALAEATNPQLRATRKHAVAQRHVQRVSERVHQAQVHRHSDRPAEHHRVEARRRP
PAANRHGLRQRHATHAILPTATTAAGPRKRHVERQARLAQAADAAAAHAVGERSRQCIKA
RQRSRTAVARHHAHGGQAGHAVVAAAPQHPAAGTVALHRHNAARDRQSGDKRRAGGSAAR
NRHGTAAQRHPRQRRHRRRLAHRPHVAQLHPPAGTDRPTVATYQQRRNRPLDAHEAQHRI
KHREALAKHNAAAAAHNRHVRHGEHRVAPQTEARRGRHMHRGRGRTAQRLQQHAVKHHRA
RQQVHAAASVHRRPARLQRPQHSVAHTQLRLQQRRRVQHKRRSHRVRQSAQLEVAHRSRR
NNRRVTDRHVRVCRQVVHKHKRAVAPGQPAHAHLQAPVTRRLAAVAPHVDLRTAVAHAVP
QFDAQRAGKHCRHVEHNSHAVRDGHAVHQHRVHGAANRDGSVHRTAPQSQHHRMHRGHTR
RRRNQRQQHKQRHTHSRNGPAPHTVPAVQTRTHRRPHPQTQTGINRVLVVCYTRPVDHNF
SFQNPFLQMANLMTRFRQIVILMMLILKPQVIPNTLKR*
>TCRU_6298 Leishmanolysin, putative
MAGRGMVRNAACVRGGALLVVMHSTTAAMAAREHHDCDDVDGVEQQDDDGDGRTLESHRS
RCHARDVWMAAIGVPATARR*
>TCRU_6299 BNR repeat-like domain containing protein, putative
MLYTQRGYASGKKRATALYLWVTDNNRTFSVRPVAVENNKNWDLASNLLYSDGALHLLKE
RANEKGRAISLARQTEELKEIESTLITWAQLDTSFSESFTPTAGLVGLLSNSASDDTWID
GYRCVNAKVRNDTKVHDGFRFTGFWFRGDMACEQSGA*
>TCRU_6300 Enriched in surface-labeled proteome protein 1
MSRRVFTFAVLLLVVLMCCGTCGAAQADEDLSAVPKYQLEDIADVNLESFGIPGLLKVGS
DVFAVAEAQCKKNDENNVFTGIASQLLTIKGDNTPEEALKNARVIRVLEKSTSAKEGKKV
NLSRPTTVVKESEIYMLVGKYSQNAAAVGQESGAGDWGLLLVKGTVSDKESNKQIDWKDT
NAVPTTPFGEQPSSE*
>TCRU_6301 Right handed beta helix region containing protein,
putative
MSSANGVYLFGDTTVRSAGLLRVADCAFVGRTEIFDSALVYLSGSVTLEGSAQWRVEGNN
VGAASVLTIPYSWQKLQLSGSGTTVALAHNRQVEGSALFAKLSKSNTIVALPARFVVGCN

LQGNEEVSYDYVFPEDVVLFRCGTCNDDAACYMPGTESVDRSSCSCSCKDGWHGASCLPL
EVPDAVVPPVTERAVDGDTSCVVNQTLTSLALKMWKTHHCYVGVTFSGRRSVLTFFLNSM
PLHLPINITLTGCTFREGAALQFVGGVEAVESSGVLIRVSQTVMRSSAVAFIHALPQHCD
IAITEVDAVQSSTVQFLDTVNNMLSVVMLRNVVLSASTLLVSNVKAHATRYGAFGLYSTV
AIKLVGGSSLYVRYCSFEGYIHVFYLQSLSVSDHSVFALLNNAMSSGTSFLLQYQDFSVS
DYSVLRVVGNSGSARYAIYNDDLWTVQQSSWLDWRDNDVEVGAMFYDTESAFVTIDSSSS
VTLTGCRMGSTGLSVSLLKRIEAGYRFVAGCLTVAGREVTTAAELELHGINNVTTVAACG
ECTKEGDCFAPLTTAAIDCKCQCAAGGHGDVCVPAPVPAGPPPPPLPPVPPTPLPPPVGE
CISDMVYPEVAQAVGGGLSWLCYRNVTFSGGGMSLTVLIGAMTGDVANVTFDGCTWRDGA
VLLLLGNAYAAVGSLNIVVTGSTFSDALLSPEGVFPPRTNITISGNRFTVTRLIPRPCLD
IWNQSCVAMNGLAISNNSAVVFSGNVFQSVTASSIAIYVVRSALSVSWHSVFAMVGNTFH
MAGGDSTLINIEGSSQSSSLSVLNNSAVVIRGNVVSRPVRYFLLLILALRVESRSAVVFQ
GNDMQGSSVVFFLSEFSYIYYNSWLQVSGNLCHMSPSEALTVFDPTVNLRDSTVSVSGNR
FMSRTVTPTVLRISTGSRDNTNGAIVAACNTVNGEEEAKYVIPSVYNATILTCSDPCTLA
ASCFPSYTTTASSDGCACACAEGGHGDACLPVAVPEPPSTDGADLCVRDVRVDEVVNAGF
GTSVVCYVGVTFAADVVVDVASMSGSVRNVTLANCTFVGGASLYVVGWLSDPPAGERADV
LISGLESRSGGGVLVANRFPPGSRITVVDSVLIAEKRVAYRGAYDLGAASACLVLHSVNL
TGSVLTIARTHVAAVFRDAVGVLVVGGVALSSRGALYVDGLSVQTALGLCVSVEGGVAAS
GGSVVAFVDSGFLLCKHAVSVRGAVSVSGSAVALVRSEFLSTEEYAVAFYSTVSLVGGSM
LLAKGNVHDGVSREMLYAAGAVTAAGSTLSFVRNRALLPRMVSLSLSLAAGAHVRVACND
AGGRVLSTAEEYAAAGFGDAGSIDVVGCDDCDRDTHCYAPRTASASMTNGLCVCACGSGG
YGEACVPVGAPTLPPAVGTASSVLFRECSSCLLERAR*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MARDGVRIVVQNVSLRNGAVLYVMGGGALCGAGAAGSDESGPVELSVCDVEALNGALVLT
GTFPAGSVLTVTDSLLVAATSTPLVYLPGSRSSSYAPVLVLSGLRLVRSVLVVSGVALVT
VMTGGRTVAVDGAVLELVGGGVALDAAVLGGDVGLYATARVVASGGAVLRVSGSQVYAAH
GLVFDSGVEANASAVVVNENAGALTDGALLVLRGSASFVSGSWLSVRGNSISGRLLSVPS
YPRSAELVQSTLTLHGNTGSGPVVMDGTVALGGAGRRFVVGCLTLNGQVLRPMDYRSAGI
IGEFRPVACGVCDADVHCFAAATRAMSASCGCRCAEGGYGRDCLPVYLPHVDGCNRTLFR
PPLSHTATLTETRSLTPTWTPSLSATRYSPTQYGPTETLQVTETVALSPTRTPTASVSST
LWWSDVACPTLAVTTTADGGSLTQNDIRGGGSAVAIRLMVALPPPFRWASDPQLGTHLSF
VPVSTAQPSGFGGPWGAMLRNATWVRNATNPSTVLELTVPVHRGYFIAFDETIVIRCDAA
AVSGGCKGVLLGSFTIRSDTLPAAASALSAITGVVACAAAVAVVVTGGLGSILEMQALGV
FARMPCASAQERASTVALPYFLSVFAARDPLWMVVGNALLAAVFGCVHCGVTAAFQRWRG
VDAASAWAAMRFPSLTYVVAHAMHLGIFFGSVLSLAMPGARVQHRVIGVVGVLYGAAFPA
GVCYLIARHTGASFERYWQFSRKPLHGRLLYPVGYWYPAAQQRMYGGMLTNMRGSHVYWC
VFQLSVLCVVCLIAAVHSPVGGCHVQYFCMAAVLLAGAGVVAFMNVMRSAFLTVMHTASF
VLLAVLCLVSAANHLAPSDGGAGAYAAIVLLLTAVLLAVTVYSVVVWYMEDRHWQELREP
RRGGLEALLRDDEESDEETQKPHEMASSSYASGTTVASSYQPPAPPSQPMAGDTRSDALS
LFDRSSSASRMIDYAAM*
>TCRU_6303 hypothetical protein, conserved
MEAGTKGANVRAHHPNFCTVLPRRLDLIASHIEPSPCGRNVVSKRSRGRRARHLHSFVEV
SRGRNADLSASGISLLFDAIFGESVGTVWCFCLLLDDWSCRDVEGICCAFFQYLFRTPCS
RRLSIAALHGVLQGDALCHAIVLWVTCGGNI*
>TCRU_6304 Enriched in surface-labeled proteome protein 1
MDDDGKTVLLGLSYNKKKKWILLCDGGENKEHSSTWEPQTQYQVAIVLENGNQSSAYVDG
QRVGGDEQCKLETTDSKEISHFYIGGDEGSAEGQEGVSVTVRNVLLYNRPLSSEEIGALK
PNKAPIPPLVEVPTKPLTVSSASVVPPIPTVTANAQIAGTSSTPTGTQLREREQSMGISG
ADSGGASTSAVSTVSTPSAGKDSVKQVASGKSSDGAQTVDGGSTADGEPTMETREGTDGQ
KEEVQPLNRDVNVTALNSSLGKMSQGNNSDAATVRGNGLLPSLLLLLLGLWGFAAL*
>TCRU_6305 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MPLDGTTATPGPVTVLANVERVVTCRVALTPHRIICAQTSGKSEIPSEHNAASLVSNGFC

EQGHLTDLLAMAEIGDSIVHGCASRVMLLLILGLWGTAAFC*
>TCRU_6306 hypothetical protein, conserved
MICGMGDGNCAPEDVRRRINGGAKDGVFTINVTSPTPSAVKDWWERKVESKAVTVANVPA
KPPEGPPSPPDDKISREKSSRADSESPADAADSAGALLHLKLQLQAALVLTLLLALRPCK
HRIPPPLVSFKALHILPLLPLLHPNPYQIRSLQKAAAIPPMTLQ*
>TCRU_6307 hypothetical protein, conserved
MELIRQRCSTVVRRTSDIPALGQLHEESERGGSISVCAVNVGAENFPGGAIYNLLLDART
ADQRGELRGLLAAIFVAPSTRRQHARMLRSMLEMNRTPLDMMVLGLKEIAARTETRQTHP
LTEDEMNRYICGRTDWRERVVFRLAWITASRWSDIAALTPNNFTLERDGTVILDWSVAPK
TARADPHRASRFVRIRE*
>TCRU_6308 hypothetical protein, conserved
MEEEGFSYHAGLGARGTLSLIGLSRRLATHHGHWVDNTSPQGAANKGGSQSHAMTWEPQR
IYEFLDSRGVQASVAYVRSAEGNPADGISRGRVFALQDVARG*
>TCRU_6309 hypothetical protein, conserved
MFCYHLELLGCEWSSGQPLGLISAACFEVHCRRRGARCRVAHFPAEFTVRSAPETDNLSL
SVLCGETVVASSNVIDIGGVSRRVGVRTVALKAGEEVICKVRIMWCVEAEDGTVFSRCVE
DYEESERSAALDVGKHVFSTSPEGPPVVERTPSTEKTSVVSGATPIRCEVWEPTAKPHQT
AQGVVTVQRNFRPPGPQEKGAEWSVGSPQYAPKGILDYYVTSTQVIDRPRAWRNLYTSSA
PLLATNGLIREETESTATRSCEKHCGNSSFFSIQRGLALEDIRLHPTKAPETTDADFRRA
LYRKKMNVKWRGFISPSHASLRATTHEGS*
>TCRU_6310 hypothetical protein, conserved
MRRRFWVLLHSLQWAGRCSSCKGKSSADNSDGAGEEEAGAKDEALQRLVHSLGFEMQEME
RLVRGFATGEKKSTVAAHKKDSASCNSLADVCTKHSVFLLPFCKVAMAYKGLRATSAKYR
GTAGTVTTSEYGETEATALLHRCARRIGAKVNIREVKDLSEIQLLGGALATLFAALWDSM
RGFRREGKHRWQELLNGDAEKVKQLHTWRYEVIKMHVEAFVSLQDACRSVFGMALKDVPS
RQGDAAFRQTLCLCISTINSMTLAISDELHWHLSRPSVKKNDEEERRLLERRITDCVSSM
RNLTNTFLAGMVEENVTVIEDAEGGVQILSVICAIEDILAVMENSVNLPVGVDGFDDSRF
FTLLIMWLLQTASSLFHAPSLNEERRFVSCLQKLWQKLAPPLEQRSSDKVMTHRTIHASL
NLRYARLRSEPQGGEGDKSFVSNPATSALLLRMLERTVSTFLSWQLKRDAVKPSMVLPYA
VLCRTVLEVEVEIYFLACKKTGRELTTPTDLFHTGVDNRKEGTPTDLEWEEILKATSSLR
VAVSSLVHAYMRAFVSQDLSAFALMEGKKGDFSFVKRSVYRFMSGISTSFFPLLRRHYID
SAGKEVLTSSLRSFLALKQVSDIMDGDGEERRHGVNSTFRVCGVSLSQATEVAFFLSLYR
RDHLSLITGSSDPADAIDGHAISSYVKEVLFALDHSTAKQLWHLRSTKVLRCFTGVSYEG
EVTDERQQRRQAQSILSVVHAHVVHPSFLWMPLFQLQEVLLVLAQNRELIEGLQPYLKSP
KADDSATLAVFHVGSAGGTLRHFAKVLGYVALRLYVVSNVLRCYRELLPTEECPSRLALR
DSTSGAKKRREWAKNMALTLQKSFPGLAAEVEGLDPKRRTHRKRANRRVLARLETACIFA
VDQKLLFHVKKQRRKWRAKRAMQRLLDGSDGDGGGNNTVSAIALSETVAQDEILTIFLKR
TDARAPLGFSLYGERPRIRRIAGSEHKDDNEGRSVDENMKDTPFSAALRAAGVVEPRSVV
GWCVVQIDGADVESSKAVITLVRGKHEFSMSLSPPA*
>TCRU_6311 Cation efflux family, putative
MLWRVICLLAADFSPEAGRLRKISAVFLMLWILDLVMSIYFDCLILKVNGLVVLNISVAL
VAAALSCQYDHDCAVFPCSKGKNGLSAAPSDNNSVKRERNWLQNDTKVTSVFSFGLKRLF
VLISFGSSVFVMFGCLTVIGEGLQHAFHSSDMPYSLLFFIGFCHIVLFTAYAEEINAYDC
ISGRGFENRDVHNLSNGKMTHLPHHLQEPVNDSVSILPFGSVILRATSCAYAPLTCIAVS
LMTMLRRTFLWEMAGALLLASYTFVIATRKVKDMAWLLTNNSVCHPSFVAARDRAIRSVK
LVEGVLQVKFSVFWEVKKDEIMAIMCLRIMSSADPSAVTVAVRKILEGVATYVFVEARFP
NDEDDDTNILKVDHLSHHHSHGHGCCDHSNHFHDSAGERNEEGEREGHERGTEKRREHDH
FFPALGSASSSSIYFSSLSQPPDASVVELAERQARRGPSFSSANYSVSTPLQSLTLVPPP
FPRPRS*
>TCRU_6312 hypothetical protein
MAAMGSRSPVEDNVGLLALDAIDALSREYMACFVVDHVTPHIMRCLMEVVCPEAASEAKD
TATEKVRELHVNAQPRQVSYLLRTLFSASGVNVGDVVSRCAEERHRLTVQMARHHSSVIS
VRSRLLNQVKNFETEGLSAVKDLQESQALLDAFAPRIQTLETELRAVLPDYGRPDEMFSS
GMRQIMDATAAIDAKGTVSSKCGYAPSRDFVLQAARQIFAESHASWSREVNGGRRQEQQQ

VRPSGGRPKEKDAHSGVMTPFKGTAHATTSLSGFSLTSSTHFPLQALECHSGKEFCDALP
PTTVAISAEALSARMADKRPLRVQEEERTAREKEWSPLGKNRLACKDIPTGPSAYTRLAG
VRHALELEQQNS*
>TCRU_6313 hypothetical protein
MSTPLGGRFYHVFTKKSTDHVIELHIPRGYKVLSGGVRAYGATGILSSFYDAERGRWFLQ
HDPIDDGASVLLQVVTLVDPDDWYDVTVSFVSLRNTVGPEEREKLVQLEECQYPARLFES
KDEAGSAQAVWEKQRQRRRCRMSGRDTVTLHCPVVDGYTLTGGGFISGYPVLASSAETCE
EWDQRELLTRSGESSFADSNGVPNKMMAFSTASTRSGVLCDSFPDPPHSSVSSTLLKNTR
KDKGPTAWFVMAAENLSLSCYAIGIRLRTARREEILRGMMSKTLLNRGKCDVPSEKTVAV
KVHHQSGGNWAIELPPPHGIFFFRFGVSRTPNPIVLSAFYR*
>TCRU_6314 chaperonin HSP60, mitochondrial precursor
MWQRTFTRRMQYGSTPKDIRYSMEARKALLIGVENLVKAVGVTLGPKGRNVVLEMPYASP
KITKDGVTVAKHIEFENSFENLGANLVRQVAGLTNDNAGDGTTTATILSGAIFREGYRSV
ATGTNPMDLKRGIDLACREVLASLAEQAKPVTSKSEITQVAMISANMDNEIGALIGDAMQ
QVGKDGIITTQEGRSLNTELELVEGMSFERGYTSPYFVTNTKSQKCELDNALVFVANRKL
TAVAHILPALNYAIQQKRPLLVISEDLEGEAMHTFLYNKMQGRISGCAVKAPGFGDMRIN
QLQDIAVFTGAQMISEDLGLSLDHNDFSDRLLGSCRKATISRDECILMEGGGSAIAVEER
VQMIRDMIAAEDHEYNRERLVERLAKLSGGVAVVKVGGASEVEINEKKDRIIDALNATRA
AVAEGVLAGGGTALIIASVRLDSIAKDRRLPGDIRTGVNIVKKAIRLPCRYIASNAGVEG
SVVVGKIMKRNDPAFGYNAQTGEYVDMFAAGIIDPMKVVKSAVVNACSVAGMMITTEAAV
VEKDMFAKEKRAEDKGLEDKEKLEGLNTMRKRVNESQAPLPALSPPMKFPMKGI*
>TCRU_6315 hypothetical protein, conserved
MTSLKKKTQSVWPAPSTTTTTRRKSPFELAYEESLAQLELLQQKLEQQALVSLHLERNTL
EYYYTNTICFEGYDGESVPQQNSGFHHYYFTSVVSMARRERRERRAREERQLQEERRRVQ
LLEDDVRERIINGVLAEQRDVVRKSEEENAALQQHLAQKLAEAETCGKRLQEHEQRQRMI
QQERVESVRRTMQLEEGKLKQMENVDATRLVLSKEREELAAVQAELKKREAVVNNLRETI
ARLSRKRRQRE*
>TCRU_6316 hypothetical protein, conserved
MVLPNVMKETMRKEEEEAAQFFPRLLSSSILQEPFVQEIIQENEAMLGEIARLRCLRQGH
AKERFQHMQTAETAARQLLATSEAEVRFELCVAWHACIIGGLRDTLEELEAVREENTALQ
KVMLKVQEELGALESHSTPVSSEGDITPARVITAIDPGCKLHAHYIVSPNIRANYHSPRV
SFGPSRKRGRSSGDSWHFSPSEKTVEKRGVSQQLT*
>TCRU_6317 hypothetical protein, conserved
MFSRDDVSSLFNNASRTLQRSQLLLEERTRGAPLEKPSVMPKSPSFEAALRALRSFMEFT
AFLDASERVGERLEEESRRPSTVMVKERSNGSMCPLLRRVVDGLTGVQAMWTGDGGAATS
LMAGGASVTSQLVLAGLFADWKHGASRAAEQRDTVLQQMLQLDRVPPLDKPRKDDFLELL
SRAKAGMPEEIAADLDAQVMRVACSLTCDLNVPKTTAPLNALLLFPTLIPHIVQNAPPLL
AVEYILNPLERAAAGLLPIYLSESPSEFIQVSRQLVHHVVLVGMYAAFGLELSSAGDVQR
VARFTKRLFDALLMPVEGAFAAALPRAGMTFALHQGLAESLCRLVRSWTKQEEGRRSVNA
TEATTATKLSSSTLSVAGTQQLMPVWCTASYRALLVVEAVANAELGVVTGRGNAASQQKK
YYSMLQQSNGRVTATILSTVTEDRQLLFEETTTRSAQGHKVYRIHEGGTGPVVYVYLDNG
IVYMKVGRERVFRRAKGVEDVFRVFPDSSS*
>TCRU_6318 hypothetical protein, conserved
MDYWTRSANRNSLENIGVTYDERETSPVINGNVGERAGHVQVATPDMSSPPFQSRSNQDR
DWSSFTDELTTTDTTGFTSSSRQLGGLSVHHRDRNLLGFTFSGIPADVVCFRSCISYHSH
RSSKNFVAPEQTGPFAADVLCIILLYIVVDMREILQVSHTCRYWRFYANYAPHWTYYRRI
DWGRRIKDLPRYIRKVVVKPKIVTQEEYFRERSKVQRAQRREEIMSTARHVRWCVAIALL
SASACTTNFVVAYFLGFLPTVLRNDRSLGTVTFLLMVILVVLEVTVVIVPLGGATSPSEK
QNMMRLIAWGLFLLFAACIFGTISSLAMARVQSTGHVISGTVLDFTKDRECGVMEAHHNP
SFVLLPTKIADIRWRPITMDDTERKFIPYCISHFNETICYVFLYFDGFYRSNIFNNASAV
VTKDIGTRTALGFDPMDNSTDHRCTNESRPHVIALTESVYTHVREEANRYFPDEVYTNPI
LRPQERGKISYICSMDYARAATEDSPGSTRMWYKHGHPWRRHHIPLSTDITGVSKEFEET
HDHYLHYAFGCYIITSVLWAVMLIMQCFTREQALMVLGVTTTVTLALMNPIIMVLAGALC
VKVPDRYFMCNVSSGGSLIGGGLFISAVLAALYVCFS*

>TCRU_6319 SET domain containing protein, putative
MQCSRPALSIAAWSGGLVGFSDAVAQAVQRKKKAGREGGGNVTPVRCMLATRAICRGEKL
CVVPESHILHGENAARLLQRAAAERLLSDYATTQRCLANVTGDTSIISTRDALLILLAVH
VLRQGRMTHPLTPWSACLPPRVPPMGVLLQQSHQHHAGTASFEPLQRRLRMGEQMIVLHP
GEDDTKKASTELILQAAEQYGIGCVGKPQTEVIPSQTLMTSFYRGTRHPLTRRQHEAYAA
QRRHVLSAETQQLLQLEESLHRIVIEPLLPCLLSESSECRNNDTGDGTLLPEECDSEKKM
AMIEQLRWSHFMVRSRAVNLQLQRHYQPQIALVPFLDMLNHSVRDANVAYQYRSGVGVVV
VASRPIKATEELTINYGDYRQRGCLFSYAQEHKTGGEEISAAMRRIESRQMREWDDSPND
DNADDLVEAPFGHGMQQQQHASDVDSNEEARTEATWLWRFGFSRTDDEKAYIASRLWSKG
LRRRIAQLTDVRRKGRPGEFVIGVPEGLQQLREQRERLERERFGGAAVFPPQNV*
>TCRU_6320 hypothetical protein, conserved
MHSERLKALRELSSLLKEKKNVPQELWGMAGMKVGARLKDVEKEIVAMKKNVSKDIKSQM
MEEQQTMLEDEAKRHGVTVEELVGKTQEEREFNMQLKRNRERARDGDRVKKEVQRQTDLG
EYDMAVDYV*
>TCRU_6321 ubiquinone biosynthesis protein-like protein
MLKSGFYLLGGVVGAASSLPAFVAATTRSIWDPVNADDVAAVGEITALTALGHMKQSMMS
DRTGRMILRTQPRVTDETLEFASRQPPGTFGHRYAQFMKFNRFTPNGRTPVAHIADPTLA
YVMQRQRETHDFLHTCIGCGRTVEEEIIVKLLEWRHTGLPIGLLAVIGSLPWLSRQQIRN
MELYFEWAEVNAPNQRHGEVNIPYITNVWWEYYLDKPYEQLLADTGITPIDVFLQQKKGK
TALANGEAIDGK*
>TCRU_6322 hypothetical protein, conserved
MLRQTPFRFVKELVYFEVWEHFKRFGDARGTDSATCRVLCADDVAERLNGRVKMRYLLEQ
FLAKNTSTGGARGEQQRWWTGDFSRSVNSDRRVVAEMLLEDGWVLVQINNAVSEREWLVT
TMTFLRERS*
>TCRU_6323 hypothetical protein
MLLEARVEKLGASPSPSWRYLRGVAAPHPHPLELVVLRTDPRTTSVLCLGRNLFQTKPPQ
ILADQRAADGRPPAQSAAERACLTTILGHILDALSLAF*
>TCRU_6324 hypothetical protein, conserved
MQHNRALQRRHIRHVDEGVRHQAHRALAEAANPQLRAAHKHTVAQRHVQRVSGQVHRAQV
HRHSDWPAEHHRVEARRRTPAANRHGLRQRHATHAALRTTAAGPRRRHVERQACLAHAAG
TAAAHAVGERRRQRIEARQRSRTAVARHHAHGGQAGQAVVAAALQHPAAGTVALHGHDAA
RDRQPGDKRRAGGSAARNRHGAAAQRHTRQRRH*
>TCRU_6325 hypothetical protein, conserved
MHQPAATSHSQRGCHEHGEAETELAGHNLQHAAAIHCNVPKHKRAFVVLGARRTPRAVLY
GEHGAAADTQVRRKGVHHVRLRQDSAVVHVEDAGQVHAKAVLHKDRSARAPAAHHRRPRH
DKPRRQKPDTVQDKRGAVPGPRMATGRRHVLRPANRRAQR*
>TCRU_of Trypanosoma cruzi C-terminus, putative Dispersed gene
family protein.1
MMRSSFLTVMQTASFVLLAVLCVVSAANHLAPSDGGARAYAAIVLLLTAVVLAITVYSVV
VWHAEDRHWQELREPQRGGLEALLRDDEESDEETQKLHDMTASSYAPGTTVGSSYRPPAP
SLLSVACDIRSDALSLLDRASSASRID*
>TCRU_6327 hypothetical protein, conserved
MHRGRGRTARRLQQHAVKHHRARQQVHAAANVHRRPARLQRPQHSAAHTQLRLQQRRRVQ
HKRRRHRVRQPAQLGVAHRPRRHNRRVTDRHVRACRQVVHKHERAVAPRQLAHAHLQAPV
TRRLTAVAPHVDLRTAVAHTVPHFDAQRAGKHRRNVEHNSHAVRDVHAVHQHRVHGAAHR
DGSVHRAAPQSQRHRMHCGHPRRRRNQRQQNKQRRTHSRNGPAPHAVPAVRTRTHRRPHP
PTQTGTNKAVVMCRTRLVDHNSCLASPFLQLANPFLQMANPGTQFRQIVIPPLNLILQVA
PNTLKR*
>TCRU_6328 hypothetical protein, conserved
MQHNRALQRRHIRHVDEGVRHQAHRALAEAANPQLRAAHKHTVAQRHVQRVSGQVHRAQV
HRHSDWPAEHHRVEARRRTPAANRHGLRQRHATHAALRTTAAGPRRRHVERQACLAHAAG
TAAAHAVGERRRQRIEARQRSRTAVARHHAHGGQAGQAVVAAALQHPAAGTVALHGHDAA
RDRQPGDKRRAGGSAARNRHGAAAQRHTRQRRH*
>TCRU_6329 hypothetical protein, conserved

MHQPAATSHSQRGCHEHGKAETELAGHNLQHAAAIHCNVPKHKRAFVVLGARRTPRAVLY
GEHGAAADTQVRRKGVHHVRLRQDSAVVHVEDAGQVHAKAVLHKDRSARAPAAHHRRPRH
DKPRRQKPDTVQDKRGAVPGPRMATGRRHVLRPANRRAQR*
>TCRU_6330 Mucin-like glycoprotein, putative
MTTCRLLCALLVLALCCCPSVCAAGSGDKPDKAGETPTPQDSVVSNDSDNTRANVTELNG
QTSDKEADSSERPSKTVSASPTPSPTGTGEEGPSGAPTLQDGRGASGQSGALEENIISPG
STGDSDKSDVNNREHNKEVALAGKEVKEQAPTTTTTTTTTTTTTTTTAPEAPSGTAGNAE
APTTTTTRAPSRLREIDGSLSSSAWVCAPLLLAASALAYTTVG*
>TCRU_6331 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGTVVGTGAGPSGGADNGVTEETVEREEDDQTSDGGHAG
SEGQEPKGGVGKPGGIENTNNVNSPAEKGTGETANPPPPPLAGPVPATPPEEPDNLPKPT
NPDVSATLGTTTGLESAQQSQSPAGEEPTATGDSSPGPQTAAASDATRSKTAGGDAEPTS
PSPGGQADASGPGENSAAEGTPVPARLLVLMLAEVVKVTILSQKKLLRERRMIKRVTVVM
LGVRAKSRREVLENREELKIQTM*
>TCRU_6332 retrotransposon hot spot protein, RHS3, putative
MELDGRGALDANRDVLLEEFLKDPKKHICGAGVLGEMQASDRYKRMERAVREEMDMVEDV
HKLYEKGVDNLLKWLVAAAEVKASVHGATKRFLDAAAEEARNPKKSSAPR*
>TCRU_6333 retrotransposon hot spot protein, RHS3, putative
MDVREGKPPQPWTYKAVGDSLEKDDDVLQSGAERLRLMVLTSDEGWPYTWKWKENKSTHD
CYVNCEVGRVWQIVLGDLTVWSTHHGRTDFEPKQRLLIGTPGIGNSVAAGSYLLYQLLHC
DAEKLQVVAYFPWE*
>TCRU_6334 IQ calmodulin-binding motif containing protein, putative
MSVVAGDPLQAKCDAMRAIPPQERPPDALRVFSQSVHEIQRAAKEKIRTYYAITKRNSQG
MVVNAEHEMGEQRQQQEEQASELRMQAMILLQRAVEVGREIRAACLVEAHHRRSHDGTEG
PNARDTTQRRETDALQLLQPPLIAAQMLLLVRETHVMMQKLLVSGAGVEAASQRTNRMAV
EHAKHAYELTRLVAVIVQRQREAVATSTSTENGAAMRQIETMEKECNILQFAKSEMQLAS
LRDRAGQREGAVKHNREAVRILTSLSAHGTNTGKDHSRMATEATQLLPVALFNLGCQLEQ
IASTENDPERRQDLFNEARVFLERAREVGVKILEPSHPLLRKLQRHAGDSRSFVQAGGRA
AMRGSGVDAAFTDALGTAAYVFSQVPAPDSSTPGMMNEPHFTRGAIQNSLHYLPRLPIGI
KNNERTHPIDHFANLSLHSASIVSDPQRRSTMIRNSVRARKLNLQLKSTQGFLHSKRKLR
EVDQSLLQCHRLRHPSDALRLGGVAVIDTVLDTRHAEAEKEKKRKEEEKKILRRKRRQRS
FLPEDWNPEEDAPVVSKEKKRRKKKKEQEGKTQQDEKKQREEKMKKILFGGGRGGVFEDN
DVLNLHEEEDKEEGEKFSKRRRKHKRRQKSEGSEGEVSVDTYGDHKENEEGHDDAGIAMK
RKKDTREKRAFAGDPLLQSVLSSYSYPMDETTPLEGRRKSSKYDADDASPESEDSRKEKK
STDISKQPFGREKIESDAGREELGGSIASFPTGVVNFQRGKSIFLHSEEETGKQKEKEEE
EEDEEEEEEDEAEEDQEEEEEEEEERETVEEAKERCETELIIYFNVTRVRRMKAACCIQC
AWRCSRARRALWRRQQVLYQEVYRRQKSAAMCIEGIFSSVLERRQLRQNQLRYAAAVEER
IAWEENLFKQALVIARYAKVFLLRRRREKELCRILALRSVEELKLRAVAAAIVGRWWRII
VPRKAYWRRRTQEVEEQRRQEEIFRRQSYAATQIQRIVRGILGRREAQATRQRRVEDHRL
RQRRLQDCTDLVRLCLQEYMRRCHRLKREEEQRALQRNEAAAVIQHGWKAALKRQILHNV
LARCRRIVRAVLMIQRAYRRFCAGREIRYMRRVQLAMNQERLDNEYRVFRATMTLQTFGR
MVIAKREARHRRAAIGRGFFFAAVTIQNVCRGGTTRAQLRCALQLQREAAAQLEAQIQMR
KDRMVSFTNAFVRARESCFLTERRRCCRLAEKLYIRRCVRRELLRDKSATVIQRAVRHWL
ARRRQREEEALALRTHVIAHIVRIQSAMRRFLAQKQYRLLRYLSQRQARKREEMEEVMVQ
LWIDEWRAAILQAEHDRRRIETREAEHRRDLQFRHKVRMLNVAEAAAAGIKCIEEKKEEE
DDDKSERSLSTYRDDL*
>TCRU_6335 hypothetical protein, conserved
MLQRHGSQKEKLEAERRERLRVDRYGTMRDASHDTTERNSSTGRPSTPQAPLNDRWPRPL
PEKEERQRQMAETCVPAPSAREPVTQSFALSGANRSASSSTPSSVESCTTSDFRLVEQEL
KELLSGYHRLVNTARGYRQSKEENIKASFPLDEAAQKAGGSSVVGKGVSNIATRNNNNDG
DVHDSLQVHHSVSSLPVSSVHGERSTDVNTPTSFVHLPQHISSTRNTVGESENAVRIAAS
YATNPSARVTSPVDLFADALTEDQLSRSLEMQLQREQQMQLLCQHLQPNLLSREVTPNNP
NTAIRVFSTPTVDDDTGYLAMRREAGSPVPPFMNRDCVNLDSARDVMTAYRGSYDSRVYA
AYRYQDRLGAHGKPSTADVSRSKEITEVGLGDTRNTSCLLGSDQRNEESGGGLHPKDEFT

SLDHLLVHSKGKSTKKMQTRRVTSRRRREVVDSTTPEIATSARHTEDPSMRSGATGGNRA
QKLGATKKSATFWHASVNMKHTPVEHRRELEVTGDGYGTGGGEKRASTDLSPEAALGGVM
ITNGMDRKQGQKQQQQKEHQQQQKLRSRHRYRHDYKTNENYSLNRHANAATRFHEMVERH
VAAFEGDSQSSSSLPAFVDSLVGAAITDFCPAVKRRQARLKESQHAEAAAAAAADASLTR
NTYRGSIGTVTPTSSIAHTPNTNVRGSWDSQGHRNPHPNARLYQSVGRDEPALGATCVKQ
QQVQRCERLSRRAGHAAQYIQ*
>TCRU_6336 Ribosome biogenesis protein Nop16, putative
MGRLRVTPKGKVKKNIPVTRVGKKQYLKRRFAHVRRVDVAGANNHFTQKYFDGSNTAAQN
FTRLGLTTDPSAPKSVVELRKKQVRPKSRRRLEEEDTIAEQKALRQKSRIARPISEAEAT
TIVSLIKKHGTDFRAMSFDRKLNPFQLNPRQLQRQVVNYLRWEQAAFPEAFMEAEAKGWF
SIAEYSDPKNRLGKK*
>TCRU_6337 nuclear transport factor 2, putative
MSFQEIGVAFVRQYYEFFSKSRDQLAGVYRSNSLMTWMGEQLQGGANIMARFANLGFNEA
IFKAEDIDCHPSLSNGVLVVVNGEVLLKDERHPLKFNDVFHLAQDNGQWYISNQIFRIVG
GGGQ*
>TCRU_6338 hypothetical protein, conserved
MDSDSVAQSDGMSFLENNENCSSLMLFEQAWAKYYTRQGGEAPDLCFLPKLDLHCHLNGS
ISAPLLLHMEHLTQRQRQTSIATNKVHAKTGELFCKSIGQMDNVLEKFTDPAERMKYCFR
VFENIYNIMNNAAFTRMAVQDLLIHSAAENIFLLEIRTSLREGLYENPHVAACGDEAGRI
TKKTYVETVIHTVEHLMNGGLVDFETGELLPRNAPVPAKWWSQFQKLYASLASTAMECSH
DNDAKSETSGATSGATQELAENLLESLRDWLMHRMHIRLLLSINRGHNAEAAWEVVMLAK
KIQHEQIKRFYASLQAEVALFQGTSNLSMTRQGERIRRTCWVTGVDFSGYCGKNHFLDFL
PALTEARRGGDGISTSPLYASLGVTLHAGEKDDPEELAEMVKFAPERWGHLVYTDSTNLS
AILARHDAIELCITSNAVTGGYTEVTQHHIGDILHRQRGSQGDGVNPALLSLLTNESSLS
MAMRCRVQRRLARWCPSPALGREVTAIPNVSFHTDDRGVFFTSVTDELELLLQHECLKDE
TASRVLWVKAIWALQRLSLPHVFELPLEIVYSCIYPWKECCRLCAGDELAAHINAHVAAL
SDTARAELSLTELGWLLNGFDDA*
>TCRU_6339 hypothetical protein, conserved
MLPRRIAVPELSFAGLQAVKVSRRYTQHSGRLQQFAYLPPGSHAPRMPWLRDAVSQDSTV
KMAPYDGTAPLYANSTVAAAVKPPPSASITAAAPSFIADPSELDGILENSLEPPDQVAAR
AAWVAAESVGLMQTSAAQGGPLRATAACRMSALAEPTLDTHIGDILNVSDSLAGEMLPDV
VRLLIEPSADGVENVSLSDFAAMQPKRQLAALGGRKQWHEWLIESTHYKQVARLELESPY
YDLRALRQAGVTTLYQWAEQPDLVKVSSCTRSLLDAAVEKSVEAYVEEVVRVVNTSNRLS
IMLISWAADTVSKFILETLHITVEQAALQRQSTGVGKPVLGTENANEAIAEQAAAIAAMD
TTSSSMSPGHVCTLEHYYSLARKVLASVRKEYIAQRHADHGGNTTGKVVLDSQAEAEIRE
KAYATLNEAILKVLEARAPSMPKELHSLRDHGFLALERIPGLLRQAASVLQLRNLPVRYF
VFHSTGEQEADDLDRNDLDILSSGGPDAHTPGTTPNSSMNVAAPTLTSGVFLAGTANYNV
KLGEWPGHPQPPPPPSSTSWTEDTVQNEYFSLLHRLKRHTIRVARTTLFDTFRGADEFRH
GFNAAEALGLQQLFGTAKLVEDRLTSVLNCYSIPPSAVKPVHFVEAGHSCGKTSVLERLY
KRMSENGKKAIIVRYTGATMPFTPGLDDNPLAFPSRFWFRVALASCPYLIRTEELFTRAP
KSVMWWANRLNWSWELYQKRIQLYACSAGVPSLLHAILVDDMDRVLDAMEARLVATAGST
CSMTINGVSGLFPQAGYMDAMGEGSTEAAVGKTATTAALISANQNYVSRTHNNENSSSNS
KKKKEDVATSPLKSLMHFKHQIPFQLDTVEAALAKVTVAVGQIDMVFTGHCASKLLLTHA
DAPVRRYFIPLSNGIGLQQRLRVLPLVSVLYALHQRSRLEFSGLMYEVLKNCPGLLGYTM
NVFWSGQAALMDLRGGTPRLMQWSGTHPLLRSYVPTELFSELPQRNYLLHNLPEARLRLV
ELLQRQLSSPTGYLTTGVDTTVQDERDGFVVPYNHTTCQVHPFALFTIFTHQDMLESPRE
TMVVRAWGEVWAEYCAVVNSMGTTNERKRDALRVILHGALLLRVVAVSGAQMDLNMKIPP
YGFPLLASPTRVKQKGGAEPIVMKATPDTVRKAMGAYKNFFSQTEQTHIPFRPSVGINGG
CDVVCIAGTTLALYDLVTTPEALQEISYRFAEALLGVLHCLGKNVLPQNKIRQIHYVSVV
SIDQTMTMLSHSSKLSLTGGTASPMTTDDVFAAPPTPVVPYLLDLSAVFEDDVIDRLRAL
QETLGISKDFRTLNDLLDELESAHQVNVHQDVVASQEELESLLSPTLMQLVPDATVLPAY
RAEVVSPDTLLMDLLVDEEEEGFRGAEVEEVRHDSALAKEVSMTESYADAEHVQESAELL
EALLNDSLTDPRQLSASERVTNATTHAALLTDMATEDAINNNMPVAAGLLATRKTNSSSS
SPPTTPGPAQEDALAWLHDIVTPATIATDGADGKLDQVTVRTTFSGNPSSGAVGSGAFVS

LNNEEDVDVDSNEEEEEEEEEGEGEEDEEAEDEEANHLGRQAVQPKGNKKSSNHGGSTRQ
RSRSQRSKSQKLNAKKLKNSPSSLSVARKKSGGNASSAAAAAAAATAAAAESAAAAQARR
KGGKLKKRSSKTAPSSPSRSAAAAGGEKKQKKKKR*
>TCRU_6340 hypothetical protein
MLRRRITVGFVPQTTFTSGVVAATWSHATYSTDAIGTFKPLSTSFRRIGASCRYAAGSHT
GLYVGSRAQSTSTPSLCTLTTRPLPASPHQCSIEKVLLPSVQASGSGIRTDTLRGMVQLL
LDPDATDVEDVFMLDFVVMVPKRQMAALHGRKEWLDVVLSSERYQACKDARALRLAGITT
VGRWDENRERVPISAYSRGILEEAYAAMARQPVESQKNQVITWLTKTIQKAVIEEFAANK
SNRQFLAPLITGMQALPETADAASNAANAAAMKEGDETYPQGEADVPRKKRAEDAAAEDG
NGGNNTAKPNKPARVRGRKHAKHPEPVEEVTEHAGDGAAKSAASATSTTEDVKKNDKPHS
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TSVATARAEAEDVKPSKLKKKKSADAANKLAEPEHHNQQQEENATAVTDAGKTLPDSKQN
KSLARLAELMLIQFNSADGYLHLPDIKDDEKKGFVIALDGDSAQVDPFALYSTFGAAKLA
GGESPAITALYQVWSAYSAYTEAHEAAEDDATAKFFKEKGVEALVHGAVLLRAISREQAV
TLEPQDIPAYGFPLLSSDRRPHRTRRSKVATDMTAEKVADAVKAYTAFFSTKGKKFTPIR
PTIDYNSGCSVAALMGTTLHLYETSLKETVREEDIRCRFGEAMLGVLHVVEKKVMTRINV
VHYHILATSISGGSGGSNSMESMTTSIVSIDITGSFTTAEKTRLLQLAEPLGMAGAIADC
TCVSDIVDSIEALGVSVVHDILTNRDDLEALLTPTLVQLLPEAEEEEEEEEEEAEKQPST
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EENEEEEEEEVKPARGGKQKSAAAKHKTDTVNEDEENEEVEEEEEEEEEDEEQKAGNGEE
EDDEEEEEEEEAPREPPTISGNSRRHSSPAPVKGRSARGRAHPAEDAKKMREKDEEYDGEG
DGDEPPRQHVQHVQQRAPPLRKTSHAGKRAPPPPPPAASGDDNDDDDDASDADDNKEEEV
HAQPQSQQHTAVSKKGHATKKSPPPPPSTAVTDNDEDEEEEEVVRRPTKKGVSSKRAPPP
PVAAQNDDSKEEEEEVVVAPRVRNRGRRMGRALPQSSSDSNDEDRWFQRARR*
>TCRU_6341 hypothetical protein, conserved
MGKKAEQKKKDKIVEDKTFGLKNKNRSAKVQSYIQSVSKSVNQGNPNERKRTEELEAKRR
AREEKKAFEAEMAKLFRDVGKASKPAKHQPPEDDGDHEAGEVDKNLGCAPEDYLFQPEDF
DEVRYDERRLEEQLEAEREALKDRTDLTPVTEESFQAWKTMKRAQAAELELARVRKAKAG
EGKLRGWDLWQMDKELFVDDDDADEQYEREESPDDEEEEAAYDLS*
>TCRU_6342 WD domain, G-beta repeat, putative
MRLRSFLLRYYPPGITLEYETSGGEVREKTIDLLTLTTQTNLDRLAAEIIKEEPLLSEKY
TPQLLSYLRRLVEKLKAGYNNKQTFYLFKTLRAHMLPLTNCAFNKGGDSFITGSYDRTCK
VWDTASGNEVVSLEGHRNVVYSVSFNNPYGNRVATGSFDKTCKIWDAATGQCYHTLSGHM
AEVVCMSFNPQSTHLSSGSMDYTAKVWDLETGQETFTLLGHTAEIVSLNFNTSGNLILTG
SFDTSAKLWDVRTGKCVHTLSAHRAEISSTQFDYPGNLCITGCIDRNCKLWDVGSGQCVA
TLRGHTDEILDVAFNATGSSFVTASADATARVYDTATCNCVASLVGHEGEISKVQFNPQG
TKVISAANDKTCRVWSVETGQVLQCLTGHNDEIFSCAFNYEGDTILTGSKDNTCGIWKS*
>TCRU_6343 hypothetical protein
MKTEEDGAMRNWQRTLHSRMSSPLVGEGFTFGVELLSPRDPSLSSTFCDAVALVRPYRPA
YYILPMKAPYFTASGCSGLQTAVDCVRQIGGRVILTVTATMSADDNNNMAATYEGVRRIL
HDFVVKRGGDSLLLLRGDAMLQRQGDQASSQTKKRHGDFQDSVELLQFVAREVKGLADAP
VSLFSSGYSQGHPMDRIWNGDRQASLSFMEELSNGINERGVDTTGHLPTRTWDAACVNVR
KLIHRVEQVLSLRDVPSDLPHDARQRAVQTLVREKILRHGVRGIITQMLTSADEFNAYVN
DVRRELRHADTGELVDEVVVWPTIMAPLAAEEYTRLLLFTKTIPSAAVQQALRAYRDGLK
AAVASATRLGTSDEEKVCALMSTKTALEETFRRRLEDETLAMCRTLFLSGHRHLNCSAFK
STHLPLLLRLLDRLQEEANGHCGASPARGSCPSFL*
>TCRU_6344 hypothetical protein, conserved
MLALFAERVEKHPSCRASRRYHWPGPHHHSHVKDDSQRQRRGWTLTDVTGQSLCDIYGPT
PRHSVSVTILTGSAVNSTRTSRNANSMMPHVASLAEPFLATETVTSRCHRHGPPNVTIHL
RRNGSYPVSRIRRDAGGANGDNTEYSGKKDSVQPSASTLSRLADQSNITNAPLDSVRHNE
SDDATIVFGVSHTGAPAAFFSPYSTAQSGTADALTSTGTWLNPTARTTPVGVAELPRKAL
EDDSVPTTYSNGMKSVKSSLPFKADFEQERPSKCDGRVEEDTGAMKKHLQRHAVMRDTNH
GHPDDASRGGVNKINSEFPLRELRGVAAGVEEVRHQGQHSHEGVYDFDVSERASQLDIPF
CLYERKQKSSRLAALFAKAYLCCVEGKNPLTDEEPSSLEFYCHEEDHYNSLDDSYHNDKE

VFDALSITTTSSCAFGAGLASFRLRNHPRQSFDVDDNKNNNNNGNNNGNSDENIQPSLWT
HCSTCVDGGRTMEISAYAAEEAIYELKVQAKRRNAALLAKYVASCRQVVPDSFPAVANRS
RRGDGVDDHQQMEGLKNDAPAAMAGAGFPQVTVDTPVCVRHSNDDRKEHQLPGGAVSRFR
GIEAWLSAVELANESKLEMKTRIQGKCHVKNKKKKSGCKKEKGVA*
>TCRU_6345 hypothetical protein, conserved
MPGHQHLDNPSLTQNQGNLLGDRPCVRQSRLYREHVGGNTMKELMGQDGLKWNTTHTEGV
YAGGRAFDHNDKQHVAGVPTNAKNNKKRNEGDLTNEAAAGEERELVITIDAEESRSRKSP
SPQKSQQEKQPPPPPPQQQQQQGPAVTPVASRAFRPGAGYANRQTYNIFTGE*
>TCRU_6346 tRNA-specific adenosine deaminase
MGEGINDDKVVYCDAFMLAAFEEARTALAEGEVPVGCVLVPAEASCPANAGRLDDNNPNN
SGASLGSLIAARGRNATNKEHHALAHAEFVAVEALLRDAAEKGRKPPASLAGYVLYVVVE
PCIMCAAMLLYNRIKKVYFGCGNPRFGGNGTVLAVHAAKSTSAPAYESCGGHRAEEAIAL
LQEFYSRENSAAPDHKRRRKDI*
>TCRU_6347 RNA-binding protein, putative
MSRVRVLNLPRDCTEEQLRRHLLASLPPSGPQLEITDCVIKRSQSTGKGKGVVRMAFMGF
RNAASGNFVVRHFNGTYFGSAKLRVEVAKGLADVGVTTNMRKKMEGTEERPQRSATAGKR
DGEGTAGSSGGAMKRPRDGGQKMVAEQGDGGGMEMEEDAQLRKKNERKKEFIAERLKATS
GPTWTSEVLLPESAEFNARTVKDGTVMGGAHGNEYDVHINEESDSLDDEENERRALERQQ
ALGKVSDLDFLASIATKTEATIRKSSSVKGNGVVDEEDGKIGDDDEDDAGGEQQEDVGSE
TRQQPSCVDDSSKKDDQEAIVQESRRIRLGNIPYIATEDDVKQFASSLVGSVEAVHIPLT
KDTRQSKGAAFVKFVRVEDAVRALSLCRGAVFMGRLLRVSAAEDDPYTKKLESHGDAAAM
AGNSAFKRLKEQERRNENGSTMGWNTMYMNSHAAVELVAKRIGVTSDAVISVNARGAAVR
AAIAEAYLTTEIQQVLGDEGIEFGLLESARQNLLKTRSNTTILVKNIQTTDPDDAAQLSK
MFLRYGTLEATAFPSAGGFALFRYTHQQDARVAFQRLSYKLFKNAPLFLEWAPIGAIVTN
DDEDGRDDDDKTKTPVKDNSSATDGAKPQDVEKADLDAPSGNAAFAPVFTLFITNIPFTS
NEEEFYVFLLDTCPRLAKVPEKHIERLAFEQDKGRAFLTLKEQSTFKYVQQRLNGKSFAK
RTLACVPSKQTTAMLATATATMSGSSKLGLAATASPVEEGEEDDIAKASAVVARRGAAAR
QGSHVPPGCDALKLVVKNVPFEATERDIRDLFSAFSEIRSVRLPRKSHQFSSHRENNHRG
FAFVEFLSEEEAKRALETLKATHLYGRHLVLQYAKIDGQ*
>TCRU_6348 hypothetical protein, conserved
MDNNTVVLSVLEDLIHWPIPPADPFSVDPATFGAGGADADADAIWREEAPLTAGGAEDLD
EEPGERQRSRYDAVLRLPALAQALGSRWAKVEVIPYLLRCIEEEDAELSFVTGMALIDFA
TSTFTYQRQPGSFLSSSNVRPVTLFLDNGRPLSLENLLPVVVSMGASNDAGVRRFLVEVV
IPMLFFGVPLERNPDLCDWKTKYLKVWPDGGDGAELGDEPKITFDTNGGSSSSGGGGSMN
YSSYTTNGGHSGRRERARNRVEMRHSTGCNGGGGNMGKYHAGKSALGSTTEVWDPFQINL
YANRLRSSVATFLRDVSKEKAEAEGPIMASSGNAIEAHDYTENSCRREAFRSRWTLFVGL
MESMLKSEYAAAVSSAVECISNVFSCIAWFERMERRQELRPSSSPSLLRSIEELVTFVFT
TTRTHVGRSISSGAERPCEDLMMLLSEHRLIVTRNPATSSTIAECRGPIALGCGGLGAAE
REVWNLFMGGNAPVMHRVVRTSLLSSLPQLIQWTNSAARSQFAGALDWLGGLSFFSVSDV
FLQAIAAPVPTLFASEEGGSGDDKKDLNEDCSVKAKTTTIKEKVKKKGMDIPHAMWPPLE
SEVSHDSGIAEAVIDGVQHLLDELLRPHTIKDFLQVKGDCSSELTLVEKMDRLLQLCRIY
RDCVVGLAALPSWRTRWLATQRLPHITAAVVEVLRRVGDDDPKDGPALVEACTEFLCQLH
VEQWSSVEGRDRHMREIVRDKEEEVRCVISVCAAGVFRALGQGMFCLVFPRGVVVDMKSK
SLVVSETREGGSVSRARHADPTKLDTVCNKAGNNGGNGHGGLLSVSILMRLLPKLFDVVF
SCCACVLHDPEERVRAGAAAGLSALARTLSAMVMACDLHVDELGKSTWLQYLDGTTMSLM
MLLTDKSPTVQIALVTELAALLVSSAVETGRLAATIGSHRKDGAAQLRREALIACLQSLS
RHEVWRYRERYARILSEMCVKFLAPNSLAAVEAVSLPPGGETHILEDGLRESSVAAGRPS
GVVVAEDGVNPLHGFAKEALLPLLVEVLFDKVKAVRDSALESLEKMCDQLSAARSQLQAA
SSSDGTSSGVGGVGMAAGGGGGGGSRGGISRGTTSSSKSNRQKPHHNQQQHDDDVFINDT
LWPLIVRSPKAMATYLSRSSLLRIAVRLGVDKESILLPLLDHLGHDAVLNVRLVVAKELY
GILAGSSTSASTPAARTSKVTFTDQEKNGVVLQLLRLLVEDKSGDVRDEAAKALKICF*
>TCRU_6349 hypothetical protein
MLEQRIVSVERRSAAMERAIIAAMEEVDELRSLFLTRIDGIQRVDALENTAKEGRDATPA
KSKKGDLASVPKKPRVGAVGERKEKGKSGRGGEWYNTPCSELTLRHLEEVMQLATEAIAA

SAAQKEKSHLHEVRQSALEKEVEALHSQLERRTQGVEQQTSQQVQEMEMKLRKLETKMQQ
QREELIEEVLKRLHGFREAPPLEGGGGEELIQRLQERVSQLELKQEALRSLVATELDAVM
EDRVKSIAESHLQQLLREQQQQQQWLKGGSTVNTSTQETTAKNGVASAAAIEPLPAAAGP
LDFRSLRLDVDVLRQDLVRCIVEIEKVMDQQQRLGVRVHSCVSTVQRHQTDIDGLSDQQK
TLIQSHMARLETQQATATARQEKHLAAELDLLHAKVLSEVRRVHEQQTDMIVRSENQRLD
DLAAAQERLRDELRVAVEKQREEVRMAIEQVSETGRRLERELASQLRGETARQIDAARQA
QEVFTDETQRLLQDTQEELRRMQNNLKDSAILMQERSRRFEESMENRLNDEARRIKTFTN
DATLRLQKQVEDEVRRIVHITEQESLSSMQHEMQRVNVTLQALEEEQRALREGMLMLSAP
SRTMASLDHRMNVLQEDVRNMFAQIEHVQDIGAPGLTKHVLAKQQRMLQDDILEVKSRLR
RCEECCGYTNVVPQTQEMELSHTLSGKAFPHITVMQPTKLTTESLTPGKPTLGQASDVAA
GVVQSPGVSYGLNQSKLMKGTSEINPFSNTFYDPLAGVFD*
>TCRU_6350 hypothetical protein, conserved
MITEELFCAFVHQALSDPAAARADSHVNVNGGSHNDNTQQMQQHRQQQLPQRCYNPSTVS
RAALTASSCSPLDHPDLLMAYYNASRNALLRYHCDMPFLQPRTTYTMHQRVSPAFVGHSR
TRQPRHYARSHAPPASRRNSSSYAYRHHEDEAPSTSADATYRTERYTDLLGTTAMTNTVA
EQPRGSWRAFAEDDGDIMLEEGRPSWSPRQLRYRQTPGSSAGGPREGSGVSFDALNYGGF
GEDDNDVEEEAEMRGRPTVRLDSRRIGRHEEVFLPRGSHSSNARARVHFHEQHSYHTEPF
TRPSEGASTWVQGRGGSTTTSNEEGEEENEACEWQDPDADGEHSDPHSPLLGTLRRKRDM
*
>TCRU_6351 zinc finger protein family member, putative
MASVAGGVAAGPAPPPYHSTGAVKTNYVVEHAAPSAVCLVRKIQTSPYQPLPSEQVQSVT
LPNLLSLRSPPHVAHQALMDFYFAMNGHCGINCSDPSSLDLITVAVHARNAGGSGSNTEI
HSKETPRPHAGTTPPYYHAAGSLSTTPLTSAMPNNDSKNSNMLFLSNETPPVIDGGMYTH
SQQQQQQQSNSAPSVLGTSIIPPSFTSSSSEDYRLSQIRRNERHVNNALYGKVCAFFNTR
EGCRRGPYCHFLHIGKGGGGSAGNGGGAAPQQFY*
>TCRU_6352 Mitochondrial carrier protein, putative
MSVMAGSTADVPLVPVHTFPSSKGRGLPTCDVNYDYYALFWSFLAGALTGGIEAIVTYPI
EYVKTHLQLQQLSHLHLSSSSSSSAHVYSGMWDCVKRTVRQHSPLGLYRGFVPVLLGSMP
KQASRWAAYEWATETAKRITSRDGSVHNEVILSLPVLSVCGFFAGFVETLCAVGPTESVK
TQLIHDSKQPFPRYHSFGTVGAVRLMLREKGFRRTFYSGVSATMVKQGLNQSLRFPVQKF
VMDAFCSDAVIGLWHDRKGVRGEAEKEWMRRLREERRKNPFWNGLAGFFAGVLSVLITQP
VDVIKTQVQSGTLHDTVIYNNRKNTSNRGRKVTWMMLNECGSPHRMGYMSYFRSIYHQRG
VAGFYAGVIARSVHVGTHVALTFTIFPVIRRMADGNAGNKK*
>TCRU_6353 flagellum-adhesion glycoprotein, putative
MLSKRTSPAPFRALLLPVVVVVVVASVALPAGAQFDLRQQLVIQDFFISRSCAGCSQGQT
DGPSGVGTLFTAAGGSLGSDASTLLLCDHGGGGSSVRLVNKSGIFTLAGSKTTRGNQNGP
AATALFNIPRAVVLEDGALYVADSANNLVREISNGIVTSFITEGLLGPSYIKPYSRPNGA
HDLFVSDTGKSRIIFAPIQKQTFITVFITGFQPDVLQISENSRFMFAICNSTKILAINMQ
GATTPRDYWQVGDADCMGYQSSLMLTAEEDKLLYYGVLKGIPSIMSLPTTKTKTEAPKIC
PDVLLQWPHGPIVSLVNINKHAFYVVTASNVYIVHDGSYHPTVTPTPPLTPTPTPEVTPT
PPVTPTPTPEVTPTPPVTPSPTITIHRGFAVAAFSARSLPIEDPRLMHELLSWIMKDVGI
AFESTDFFAVFPPDREVLVPGDVNVSTWNNLTVLFNFDQTILITEYYTPEGMSSEEGQAR
LFASPWYWTRKLLDSLRETVAWKDLEAFCMVNCVEHCETMTFHKSECVGYVRPPVCNDVC
VGAVVSSAVLGATGIALIALMVGSSANVRSAVILVPPM*
>TCRU_6354 vacuolar type h+ ATPase subunit, putative
MRFSAPVTLGAAIGVCMLSAMGVFAATRREACLARMYPQSAGFYGALGAAVALVFANLGS
AYGAAKAGVGVAHLGLSAPEKIMRGIVPVVMAGILGIYGLIVAVIINNNIKTEPHSYSIF
SGNLHLGAGLAAGLAALAAGLSIGVVGDTAVRAYGKQDQVFVAMVLMLIFSEALGLYGLI
IALLMNNQANRYGALCEVE*
>TCRU_6355 monothiol glutaredoxin, putative
MRSVSSLKEYSSLKEEAGNGLGLVVHFSASWCEPCKNVRSMLEGYLSQYNQKVLFAEVDA
DLVTDVCEAENVECVPFIAFFRTSLRERAQERVADVVGGKLDHLEMNLVSLYGNGHDTRE
SFPDLNEYLKYLTSRKGVVAFITGTPSRPRCGFTGRLVEIFYELGIKFIYYDVWASDEVC
EGLKKYSEWPTYPQVYVDGELIGGYDICSQLKESGELKAILKH*

>TCRU_6356 class I transcription factor A, subunit 6
MASGKVLADQFRRQGIRYEEASGILWCSLCTNAKGLEIIEVESKDSVLEHCALKRHLIFM
EKQLAMDQYCPVEINGCCMLLDHHCVYPAVMFGRGRLLLDDTLGCLIPEDVCGGVKLFPR
HKYTVVELIIPHSTVPLPHKPDYFVEREVRSRKCRLGMDICIAYYNKSVEGETAVMKRRR
TVFGRVNMQGI*
>TCRU_6357 2OG-Fe(II) oxygenase superfamily, putative
MKRLWNGAKHLLNGGSLGYLAAGEPYQPFGEDFGLTIFPDYVQLVEKITLRKGYVDVYTQ
KSASIRLSDGRFQLPPLPPRSFLSLISRIEQDGIVPDGWLNNQTANLYEPGDFIRAHIDN
LFVYDDIFAIVSLGSNALLRFVHVQNGEELDAVVPDGSLYIMSGPARYVYFHMVLPVEEQ
RFSIVFRRSILNSDGGFRPVTTPLGDLMPYRSTQILNTLYTKQIGGVRVTVDDNYLEKEG
IGAFDTAKWVKGLHPLRDWSLLSQLNEDEARIQELKDKRYLDIDLSWRFAELRRRYKELE
ELLSV*
>TCRU_6358 Alanine racemase, N-terminal domain/Alanine racemase, C-terminal domain containing protein, putative
MRHSTYVEVCLRNIAYNVECIRRIAGKAELIPMVKGNAYGHGMGKVSEYLHNVCGVHTFG
VASLGEALELIESQPSIAEKAQNEIFVFSDTEVLNEGCQSYYQPCGRWAVRLTPILGTLP
QLKAFCASNAFNNTKLCLKLETGMNRLGLRFDELEEAVPILKQRGGVDLLLQHFGIAGSV
ERLAETLNHYEAFKNAKKFLHDSGVEVRATSVSNSGAVEQRIGLEETYIRPGIMLYGPRS
VTSKNLWNGKFASCFYTKVLHHFPLRKGEGVGYDLTPVKADSVIVMLPIGYADGFLCTYK
GMPIKVTPEDAAEPIIGTVHGRINMDMAAVVVYPEEVGKNIGNIMAAVKKESRIHVWGDD
IEEKAVSVGAIPHQLTCGLSIRVPRIYM*
>TCRU_6359 ubiquitin-conjugating enzyme E2, putative
MALRRIQKELKDLERDPPANTSGGPISESDLFNWKATIIGPEDSPYAGGLFFLNIHFPSD
YPFKPPKLQFTTRIYHPNINNNGGICLDILKDQWSPALTISKVLLSVCSLLTDPNPDDPL
VPDIARQYKSDRNAFNKTAMEWTRQYAM*
>TCRU_6360 Enriched in surface-labeled proteome protein 1
MRGNGSPQNPEESVSPGEDGETAEGTDGQEGIHPQAGEVKAAALSSSIGNLSQGNNSDAG
TTRESGLLPSLLLLLLGLWGFAAL*
>TCRU_6361 Enriched in surface-labeled proteome protein 1
MLVTLPVYAEEHNKKGKLHLWLTDNTHIVDIGSVSSDDAAASSLLYKSAESGDNEKDELI
ALYEKKKGSEETSLGMVCASD*
>TCRU_6362 Enriched in surface-labeled proteome protein 1
MLVTLPVYAEEHNKKGKLHLWLTDNTHIVDIGSVSDDDAAASSLLYKSAESGDNEKDELI
ALYEKKKGSEETSLGMVCASD*
>TCRU_6363 hypothetical protein, conserved
MAEAASCLDVKSSFIISLPRETRHPFRCRVEDGTLVELTRLPMGYKASPETLQIIIITSA
IAGVTTVVHRLWAAPPLLRVDVWIGNIRIAGSKSDATLWEAQVLRNAAGCHATMEEDRKS
CATQYTFLWVQFDHTRRAAFLSDKFVWSVRAMPALNSLTIAETEVVASRFLHAAAILCKR
LCDHYFFIKAVRRRLSAVNRGIVRETSPANLPPGAAGLGERLRHIIENIIVGECSSSGRR
HQPPSSRMRRSRDGEPFSFQIQAMLKPPEESGGEVLFLSCRPR*
>TCRU_6364 hypothetical protein, conserved
MATPQDELTIQLQQVNVPVLNLEWIKSRLNPATLESLMQVLGLVGRSPLPLPFSGKAREG
SRRIPTADARLLRKAGIIEDASSTITSGWIIPFSVVEEKTTGLRRWIAWPRDRNSDDAYE
ANVPLLHISHYLPPVMAEAASRLDLKSSFIVSLPRETRHLFRCRVEDGTLVELTRHPVGY
KAGPEILQITLAIARVTTVVHPLWAAPPLVRIDVWIDNIRIAGSKSDVTLWEAQVLRNAD
SCHASLGEDRESGATHCNFLGCSLVTLTRRYP*
>TCRU_6365 hypothetical protein, conserved
MDEHRPLDVVVTVAATMAVRRWISWDIAKHWGDSTLVGHFANLRVPQVPIFETQLLLQFV
ADVQNRNAQLYLQVEEAYNYLLACESHIAVAGGLFAGRGDAVSTGSVHLSERAAR*
>TCRU_6366 hypothetical protein, conserved
MVGDLSVRRAMSRLHHKTAEQRRVVEEMRQRAEALTASGRASAKAKQVKPPPLCFLEVAG
EGDLGRSFFSDGMLSGVAIGVSDALDVREFRTRYGTESQLLHQMPHTEFAFVSWLRRHGA
QFIGKLACQTPLSMGEASVLVPECPAAVAVYQNACNYAIGSALMGPAAMTSPIHYDVAAF
KPTAQSFATFTDGYKLGIPSMSVGVTAARLDDIFYLWEVFTSAIQPSYLQEENRRESNTG

NSKNIGGSTDTEHDNNASSVNSRGSNNSKKITSNRSNSTSSNSGGSSGIGGGGGRGSARQ
SRLTDYKSWDTINTFASNEELRGRHIELSVGYPADWIDTLCKERLLSADEFRRRILRLAA
TQNAMRKNELLEVIPVTLNIDIEVVVNAIQTIFFYEISRAFDTLFTPASHNRNRASSPSH
ANTMSQFGLLDELPEGLVTAIFNGRALTNLDYQRALQTRDNVVRATEEQFLDVDLIVTPI
LSEPYVNGSLRSIGPLLPFSLGGNPMVSLQLEAGFSVALIGELGRDTGLFEDCTKFLEFV
RGTSPPWWRRKFMR*
>TCRU_6367 hypothetical protein, conserved
MAARLDALARVFFTPSSLCSPRQSRCHDLSCGSNSTEAVEVGARETDGSAAPNSFLWEAL
TEAHDNMNTTSSSSHRRRPMQSMPYEEEHFFPPLLQYFSELAMGSATMSSATHALLVAPS
GMASTTVTPTARTAATGGYTSMRRQTQRRFVEGASSVLRARRSFAHKQCQSDCHTKGAAC
KAFGHAHSLHGLRASSSLRHSGVHADPLSPDRIDVFANYPQPPLTDGGDSYEALERNYQR
GLNALVGLVEHFNRFFMHERGSAANASNSLGKRAANAETVSAPASSASAGPSDHRDAILN
RLNILLRDLAGHGERALALHVILRAISWRFASKNERVTILFNHLRTCLPTARMSIVTLAM
EVWGQLHVIEASSSVYLKITSELISLACDFLLYDNTLAEQLTGLVIIRHVALWPTSLYRA
LLSNERDSLFLATWTAITNDGSPAFIRELAAEALRALFVIALEQRNYRSVNSVLQHAISL
LLVPEIKAELPGSFSLLPSPQYPPGDEGLRDATSAPAGKRPHVTSMPALTKHRRGDEKGA
DGATNKKGSGAGASSKLFAQLKRRIVTIGRSLFGISERRRWASQGLRSSSVNTVVSVRDT
AAASVERDSAISVGSCVTFPVFSGTRSGASFVTQRKLQKRLSQVPPPQDRETALHAGTLV
VGAFVSAVRSCFPNWEPSVVDFSEGQLTATDLATPPHPTRRTTGVAATTSTTTTTTTAVR
NAGEIGPSQQRLCGSSSFCFANVCGGRKETPSGRHASDLPLASEDDHMENMSHSSETDDF
AGYARRHQAEEEEEDDAEDGEDDDYNEDNGVEWLSLRSSASMGHRSLTAPVLLRNRHSLL
SSPGNKTVPMHRSFSNPRKGSATTVAAAAPETVMVPAPLAGGDEGIAKGEVLSSPSDDAL
GQHPVQQNRQYHHYHHSHHKPRRTDSGERHTRQLSPQMCVGGRKMAELENFITPHTLRKL
LALCYSHATHEAALPSTPPSYPFSSLYTERLLPILALYNPFILSNEDVGMALRLLIGRAV
VAFCDPVQGPPCVAGGEELHRGTAFSATYRGNELRSLALINIGLFLAAIASSHPDIFQAT
VMRQFYPLLFSALQHDTPKYCPAAFPVLALLVHNIPEVFLERFHPIVKQLTELALSAPFT
TEMTGIAAKVCDIYQELRPRCQTALLQRIAEVLTECGARQGSRVDGGSDTKRDGKKAKTK
TSSESFDDSTTLLAKSFFNLEEKITCFRVLQGFCMEWEGTAFFFLEVCMPYMSHRHAPLR
RECVLSCVNLLLSDCFHAIPQETGTRSFLGGRIHRATCRPRRLFLTGINNSTEHATIHSA
KAMMNTRGVGPEPDYRSALTGSLHRRQNSSPVAVAAATRRRRKSDTTTMMASHGERNSNP
VFSPEPDVAVTCDRHTGRSHINTLREVLHRLVEVAVCDPEESIRHVALKNLTVETDQFLC
TDAAILDLLFAAFNDAYLPNRLEVVRILRRIAQCTYSVVYPRLRKLFLQMLRHFQDRIFL
SYSQHEGKVNTTVNITAEELQLLFELVQAVPHSISLHLDSILRLLREILLPHHTAERGTV
IIALHMLSYFMDESTREEWTKFELLLELLAGQLLLRDGDAERLHAAIGTLQKVVQYFVVT
KSFYNTSHLQTIIGSLHSLLHQKPSIGSELSLSVLKLLGTISSIEPYYNQREDGHDTAML
LGRPEYKRRLPSLFHTNVEAVILDNRSCEKPRTRFTESMWPDIILRVLLRTFFEALNGVL
TFTNEELGACLQATVAILRDIGTLRTLEHYMPSLLSALAGLFSRDGADSPLRVSTMENLA
ELVQVAGRTIAPMYALLVAFLEQHWVFSWYALPSCCKLLMALCKAVPDLAQEHCERFLSL
LLGELMRLLGEISSASRSSKEQQRHCNVCSIKHTTAVEMNTATSVIREVLKAIHSLLPIA
DQSAVQSACLALAQLLRNPAITSATLDLAGYNGALHVSTSSLSFSAATTSVFDADVSHDI
AQVLVDFLNDCDMTTKATAVVESVLLQLWHYAQAHKAMLQVLAEKQQEQQKLNYVQQQQQ
QQQQKQRRYDLDFHWRRQFSWSRRQVSDVQLASVMNRSSLEQELRRRRGDQKVWFNCSSL
ARVVIMQETTGDDPEVNYTRSFPFRETNTSWESPVEMDLLACVLVVAGRCRLPAVSYDLM
IGEYLKERFDPDSPVVNFFRNVTSPHYRLCLLPLGAQKPQASLQPPQPPPPPPPSRYSKE
EEERGGGSAHHLQGHVNLDAVAIESAVSLGIHADGLRDDISPLGRREALPHSTPIPVRTR
KQPLRSSRSASFSSHPIVSSSLATLTTSGVNSVTHILLAREVTPESGRGSVRGTNSSLLG
CGTYSASRPTSNFLPAVSVGSGSFVKQRGLKRQPDVLSSGNNSIVNFAIEGVASPGEERP
LPPMEREDNNKGQDAAAADMNDHDDDNDDGGYETEEQRFFLQHENLSASEWRPWFELFCT
MLVESSDHVCVSICSTLVRRHFTIFSSDLLPIAFLSHLTKCDDRVVRRWMRLICDFVHMH
DYLPQIIAAELARLAHHIRLYSSSLFSRPLARAIEQNYITLDLLVVLAERALNPPLLLLY
TQQQILSGFSWEALARLLMALGDVKYDNDPRCFSQDPRIRHAAYQLLHATRSKYRKGITN
TDEKTGVGKCNHSTEKLPWEMRQNLDSDKGDVLSACVALEPVAERDEEECMPSPLFLELG
WFEAASRQYLRSIWTTIRILSGGERGTTSASSTRPILSPNDVVGAMRCYMRVYDFESIIN
MWRRIKGFPLAPEEEWASALTVEEEQRQQSLQRALLGTAWAPSTGGPVIPHIKRYVVSAA

QALSRWDFVEDIDYNHLFADKRDERDRYAPSFGDFSFYKQMEIFRAAALTASKEYEEAKG
VLSALRAALRESYAVFHTENARMKFELNIMFQQISDLEEGIDAIELKTALGDGAGKVVGT
AASMANLAGSTTVVGDVAGGDSSGGAAENRRENSIATGANGVRESVELQQSRWRGRVAYS
EATVRRLKNIAGRPLPAHSTVLQRFEIIALRSTLVSPDWQLRNILELSERIVREGMPKRA
VRTINHFYSLPIDNNDTREERKYRDTLLLEKYRIELQHLFCTKDLECLHNEIADGLMLRC
SRGLMHAHGFMRGKEFEEMPVDAFFGSGPVSEEQAELLLLHIECQRKLKAVYERRRHISL
EPAPFFVPNPHMGAGSLGDLEMILRARFHTSSSHDANMPDGEEDEYNPADVLLREYRIME
HIIGSSVTLASVWREFGLLLFDVCMAIYAEWNNTKEPETLRNFCVQSQKAISALQKSVQF
WNSAASTSVSGIGPFTTASTRRSRHARSAIPAVHLLLKALHLALKLEEVGMDSTYVGDKN
KNIRNTFGDDAGRAASVAAAPERSETWERGAGFAHLDFSPAMYLHWGYILPFLVNAAARH
SELHDAVRDMCAHSRAMLYQCVFHLVSTFEHRYSSILALEAAKGDQTLQYEENYPCGSSS
SPLIAPHAKTAPTSTAYGAEEAAVDDAMRRRTPCHARMTSTESTYTVHQQQPQLQGTVVE
WMPAAGNSERREEGRRAQSPSGTHDHPQRQQQQQQQSRYHRDIHSSHQQQQQWHSAMLLK
LAENGPEHKAIISQTMQLCDFVRSGKGNSLSLGACALPVPTWFLQHRMVEVDKNELELQK
GQPKSVRSFLNTSDKHVQTEREIGSKSHDNTNATTTTINNTTTPFTTTAQESGSKALQRV
LHVRRKLCSLPSERRREEIFLFFISDGSVLRFHSIGMEEDSAASAISMPCSLTEPHDAHS
RLAEAAPATCTATHAVPSSRFTVNGGSDMASGGAQPNPFPATTGGNRTPLMDLVENSAFI
RPLAAMETAVCCLLGHIPIRHARRPLVLPVGIQEFITQLPDRAAYSSSWQLTLPPSLQFN
CTASMLRQPSSLLHIISKYKANFQNRNPIQAEKSHEPHHQQEHQEQQQQQQQQHQEGVFQ
SGKIYNNDTSSQPPQEEKVKERIGARRASRSHRNRRELLTRYESLLEIAFDHGKTGPLCS
FLHRVLSSNKLSEAEYPRPASQMVKLLEEITEAVQQHLREVEEVPKGPVSAEKEAAPLFS
LETGNEENRLGERRGSFLISSSTKGWKAMQLQAKPLTKVRMAIFRAEAPRYAPLLRLAFQ
AASADAAEWLDAVHLFTHELAEWSMLQYLFDATHRESTTFFVDVTSGHVASHHIGVHALQ
PLPRALVPRHHPSFSTGGCSRVDEQVEEATPNKSPFPCTDPTIFRLTGCLISPLPLRCPY
SVFLGAATQFLYSTLRYSRDLAGIAKFGLQDMKCFAWRGALFLQPPPGDGMDMDIMPESG
SVTILPEVPNREIGRLVTTAFVLQSSDISTNLSVVAMSLGEFPGTPPVEGAAQTVGLNVM
VERLSLISSPTKVSETTVTIPGGGVVQEPLMQPAKSEANCELERKRTSAVATTATDIGAT
VAVTKRKATAATTISAMEAARKMSFSTINTAALYTWGARRMTLHHLSFTPRIFDVSSILL
KLMDDRIPMLDEPIVTVFDDPQFARSEELIQLYPSENSTIKFHEPPSKEADDTMADQYHC
DVVENIEERVKQLIRSAVSQENLLGTPEAPHRWSSWAPQW*
>TCRU_6368 hypothetical protein, conserved
MSGVRLACFSKYFAVGMTVTVMCCARHYNWLQSQVSGDLQEHYASVARYADQVADLEASF
KRTKASTKSLPQLQGIRAGDDYNR*
>TCRU_6369 hypothetical protein, conserved
MKSLRRNAAKSADDEKTCVNTLKNNISDALENEKKMKDNAADRDPKAAHGAEVSVGSSTT
ISSTAAGADNAGVSPTTPPLNVEGGVGAQIHSPAGGAGPQPHSDGGRSEAEPSHHSEAEG
SNQNSVGVQGKTIHKKDEKAPKTGLQPTEARDGTDGAPAPSQDPPNTTESHEDKSRRVAS
PDTTPALNTSPGSNQEQTSQSSSPSGSETTGSSDNEGPEKNSKNSQISDAQLEDEDQHRE
STAGNEEGTTVESAAVQSNTTTTGDSDSSTAVSHTTSPLLLLPLVAAAAAVVAA*
>TCRU_6370 Enriched in surface-labeled proteome protein 1
MGSSKGAGSGAGSGGASPSAVPTVSTPSAGKDSLQQVASGKSSDGTQTVDGGSFSDGDPT
VETRGGTYGQEEEIHAQNGDVKAAALSSSLGNVSQGNNTDAGTKRESGLLPLLLLLGLWG
LTAL*
>TCRU_6371 hypothetical protein, conserved
MGLSCSHNNRWETVCEGKTTTRSSTWEPKKECQVALMLQGNKASAHIDDHSLGEEEVPLT
GERPPEVLRFCFGACGGHESHVTVENVFPYSRPLNFTAMRALKDRVPVPTREATPTPPEK
VRVVDSVREHIAGDITEEK*
>TCRU_6372 hypothetical protein, conserved
MPAGLPLPNVNALKGPESKAGSLPPNTQEKSKFSDASGGAAGNKAKQSDVETDDPSSSFA
NTGDQTVEKTLLLPQTPAVLLPVPSAELSPEVPPVTPVQANPDEEGSLPTAPRASEASQR
ELQNKASSPNKTGSESPDRPSKDGMQEQKDKVTTQLNTTKKASAGGLAETTATSISANGN
GDVQNKEDEDDARQPKPNRVQDDAEAGNTNFAPTVSEAAPQTVETVTTRKRETNETGDSD
GSTAVSHTTSPLLLLLLVACAAAAAVVAA*
>TCRU_6373 Enriched in surface-labeled proteome protein 1

MSRHLFYSAVLLLVVMVCCGSGAAGVAGEPAVSTFKWRGINESGGETVDSLGAPSLLKVG
NDVFAVAEAQCKKKAGDVSFTGVASQLLTKKTADTPEELSSDALKKTQVLEEGAPGGQKK
KLDVSRPTTAVKGDDIYMLVGQHSSKDCQNSGAGGCELLLVKGSVSGGDANNKKIDWKVT
ENPPQRLFGAQLDSWTRLIGSGGSGVKMKDETLVFPVEGTKKQAEGTEEGVKTVSLIIQS
KDNTDWTLSKGMSDGGCSDPSVVEWEEGKNS*
>TCRU_6374 Enriched in surface-labeled proteome protein 1
MGESWTEALGTLSRVWGNKKDGQAKAVGSGFITATFGNDGDNKKVMLVTLPVYADNDNEK
RKLHLWLTDNTHIVDIGPVSGEDDAAASSLLYNSGKTDDNDEELIALYERQKKEGKPSPG
MVSVFLTEKLKRVKEVLTTWKEVDGRVSQLCTSLSAEKERTSTGDVCNAVKITAGLVGFL
SGNLSENIWRDEYLGVNATVNNKEGAAASTVASTKNGVKFTGRGAGAEWPVGKQGENQLY
HFANYNFTLVATVSIDNVPQEGTIPLMGVRADKEGKNTKLMELSYDGGKKWHVLCGDKTP
KEPSSGWETETQYQVAIVLKNGTQGSVYVDGQRVENGECALGNGASNEISHFYIGGDGEN
ADNKEGVSVTVTNVLLYNRPLDDTEIGAFSPNKAPTPSLVDEPSQGGAIETFPGGGRPEE
PRESMESSGVNGVSASTVPSAKTSSGGEGSATQLVSEKSSDGGKTVDGASFSDGEPTVET
REGGKNGQEKEEIHAQNGDVKAAALSSSLGNVSQGNNSDACSVCGSGLLPLLLLLGLWGF
AAL*
>TCRU_6375 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGVSVVAADVAGGADGSAGEYFVLRDGALSCGRDARRRSAGG
REAVRIFLPWRNACVGGWTVCVPLWMAVAVGGVNTPLWSLLLILMTKVARAAMAH*
>TCRU_6376 hypothetical protein, conserved
MPQTKGSTKHGEGASSLQSPESVSHLSRESTTPLSTSTDSSGVAGSTVENSGANNPTPPA
ASVTQHDSEGDTGPAAPPASNTELQSEEIPNAGIIATTHDDDDSSRAAPTAERTTAGTRS
TQTSGDASDLERANNDDVNDDVARNGKTAEFEGASGDRNTEADNDERYTTVPETATNKTI
NTEIPADSDSITAVSHTTSPLLLLLVACAAAAAVVAA*
>TCRU_family, putative Se.1
MEELSAALKKLHAYHPGLAQDVEPKANLAELSSAVRAPPEFRERQARLSLHIDICARLVA
QYWGKRRAEVWEVEREIVVGHQPSGKTWMACGT*
>TCRU_6378 hypothetical protein, conserved
MAMTMTGRVLLVCALCVLWCGAWLCDAAEKAGRVSGAELLPESKGLESSSQGSKGLKNRA
SGVKENITPVPREEADEEEADEEEDDEEEADDDERKAEEEESTEGQSVQEGKVALGSDSR
EENLFGSENETGQAIVSAGGISPSGSLKSNANPTQPEAEEKKEPGKNTPVEKTLAPVNGE
NTLLEGTAGGKPSPPPEDGVDSRKQDGDDAMSEDKKKVPSPETAATTQSHRDKGSEGTGG
DTKETTVTANTTDTTNTQNSDSSTAAFHTTSPLLLLLLVVYAAAAAVVAA*
>TCRU_6379 Mucin-like glycoprotein, putative
MTTCRLLCALLVLALCCCPSVCAKGSEDKDEEGRSEEGSDSTKSTPGKLNQEMELPDTTS
SSPEAREENEVTKPVENTALHTSHTTDTIKETPQSQNAFKNTQDQDGGKSNGQTEHTNAD
TTNEQKKAAAPTTTTSTTTNAQTTTQAPTTTTTTTTTTAPEAPSTTTTEAPTTTTTRAPS
RLREIDGSLSSSAWVCAPLLLAVSTLAYTTVG*
>TCRU_6380 hypothetical protein, conserved
MTNRVDRSRTPSRTSAGPYRDFSCPRVVGTYCDPPTVTRSVEFASSTLECSGIAPCSTIV
PSSDVTFVMLTRACGTRRAVISLRPPIRSSAPPASTQWRSVTFSASANASIERRSTATVI
GPLNTTESKHAVARPPPAVTDSVSVTPLTQPCAVSPPALVGGTSNGRHASPTPPARQPHT
QSENDAVSASKHASAAAQPSHGTTLTEGRPAMR*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MVYPEVAQAVGGGLSWLCYRNVTFSGGGMSLTVLIGAMTGDVAHVTFDGCTWRDGAVLLL
LGNAYAAVGSLNIVVTGSKFRDALLCPEGVFPPRTNITISGNRFTVTRLIPRPGLCFRRP
SCVAMNGLVISNDSAVVLSGNVFQSVTASSSAIYVFRSALRVSWHSVFAVIGNTFHMDGG
DGTLIHLEGPSQSLSLSVLNDSAVVVRGNVVVGGLKHFMLFLWALRVESQSAVVFQGNEM
QGSLSVFISRSIFQIYYNSWLQVSGNLCRESPSEAFAVFNPTVNLRDSTVSVSGNQFISR
TGTLKVLLIRTGPRDLTNGTVVAACNTVNGKEGAEYAIPSVYNATVLTCSDPCALAASCF
PAYTTTASSEVCACACAEGGYGDACLPVAVPEPPSTDGADLCVRDVRVNVEVKVRFGTSV
VCYVGVTFAADVVVDVESMSGSVRNVTLANCTFWGGASLYVVGWLSDTTAGERADVLVRG
LESRSSGGVLLANRYPPGSRVTVADSVLIAEKRVAYRGAYDLGDLSACLVLHNVNLTGSV

LTIARTHVAAVFRDAVGVLVVGGVALSSRGALYVDGLLVQSALGLCVSVEGGVAASGGSV
VAFVDSDFLLCKHAVSVRGAVSVSGSAVAFLRSDFLSTEDYAVAFYSTVSLDGGSMLLAK
GNVHDGVSREMLHAAGTVTAAGSTLSFVRNRVLLPRMLSLSLSLSAGAHVRVACNDAGGR
VLSTAEEYAAAGFGDAGSIDVAGCDACDRDTHCYAPGTASASMRNGVCVCNCGSGGYGEA
CVPVGAPALPPAVGTAPSVFFREGVTVRSVFVVPAGASEVTLRHVVLDGVSPVLYVPWMA
RDGVRIVVQNVSLLNGAVLYVMGGGGLRGAMAAGSDEGGPVELSVCDVEALNGALVLTGT
YPAGSVLTVTDSLLVAARPTPLVYLPGSQSSPYAPVLVLSGLRLVRSVLVVSGVALVTVV
TGGRTVVVDGAVLELVGGGVALDAAVLGGEYALYASARVVALEGAVLRVSGSQVYAAHGL
VFDSGVEASASAVVVNDNAGVLTDGALLALRETASFVSGSWLSVRGNSISGRLLSVPSYP
RSADLVRSTLTLHGNAGSGPVVMDGTVALGDAGRRFVVGCLTLNGRALRPMDYRSAGIIG
EFRPVACGVCDAEVRCFAAATRAMSESCRCRCSEGGYGRDCLPVYLPHVDGCNRTLFRPL
LSHTATLTETRSPIPTWTPSLSATHYSPTQYSPTETLRVTETVALLPTRTSTASMSSTLW
WSDVACPTLAVTTTAAGGSLTQNDIRGSGSAVPTRLMVALPPPFRWARDPQLGTHLSFVP
VSTAQPRGFGGPWGAMLSNAAWVRNATNPSTVVELAVPVHRGYFIAADETIVIRCDAAAV
FGGCKGVLLGSFTIRSATLPAAASALSAITGVVAGAAAVAVVVTGGLGSVLEMQALGVFA
RMSCASAQERASTVALPYFLSVFAALDPLWMVVGNAVLAAVFGCVHCGVTAAFQRWRGVD
AASAWAAMRFPSLTYVVVHAMHLGIFFGSVLALATPGARVQHRVIGVVGVLYGVAFPAGV
CYLIARHVGASFTRYWQFSRKPLHERLLYPIGYWHPAAQQRMYGGMLTNMRGSHVYWCVF
QLSVLCVVCLIAAVQSPVGGCHVQYFCMAAVLLAGAGVVAFTNMMRSSFLTVMRTASFVL
LAVLCLVSAANHLAPSDGGARAYTAIVLLQTTVVLAATVYSVVVWYAEDRHWQELREPRR
GGLEALLRDDEESDDESQKLHDMTPSSYASGTTGASSYRPPAMPLQFVTGDTRSDSLSLF
DGASIAS*
>TCRU_6382 retrotransposon hot spot protein, RHS3, putative
MKRAVKGEVIFDEDIRRLCDKGVNNLPGWSLAAAELKAAVHNSTKHFLDAAAEEARNPTT
TSAPKKLEGCYESVHNAR*
>TCRU_6383 retrotransposon hot spot protein, RHS3, putative
MTVVGLRMATAGGHHTITGTVRQFTECLAAYCNDWEEFSRDMSWEIICVQQAGSMPMNGW
QRCDVVNTDNVSDESRENSAFWEEEVRQYQVSISYRGFRREEAVRSVQKK*
>TCRU_6384 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MWPVNIPDYNKRHVFLNHNFTLVASVTIEEAPSGNTPLLIAVLANTEPTHTMRILYTADN
KWMTMLKDEKKPTTESGTWEPKKEHQVALMLQGNKASVYVDGELLGEEEVPLTGEKPLEL
FAFCFGACDEENPSQESHVTVTNVFLYNRPLNSTERTAIQERKPIPTITPEPQVKIAPKP
VVPAAPVAPAAPVAPAVPAGNEGTARETGDGGANGDAGSAYGMVLLPLLLLLGLWGFATA
*
>TCRU_6385 expression site-associated gene 3 (ESAG3)-like protein
MRSYASLAALLRALNKHHCQVLLWTAVVLVMLLNFVSLAIDTNVWQVPSISVYCRDSAPS
PTREPRVALIVVQTDYSPGWCRMQVSSILSRASVTTIGMGANYTHTSRPSLLLDCITDEG
LRDEDVVVVFDGGDTMFTGPLGIKQAVEDFVAKTAPTADAFNATAVHRGEATAPLLFESD
PVCYAPQMELMVPWGPQENFAKCGWYYERVWEAAKSSADQRMVRFLASGYRYLAGGGMVG
RVWAFREAYKAYASLLATSDKWWCDQSIWSLLHVWSVTRDTNVTADFRIRYGLLSLDYNN
SFFLTPRSGAFGSPALYHFPGPPYFWDKMPTLLNRTTWVDWLRYSPDVMNETRDFVQNAT
VKIYDADRKAKTIPFPEVCSLNDVLNPEWLALQLSK*
>TCRU_6386 hypothetical protein, conserved
MLRSALSVTPCQSKYAKRRQLRRATHHAMSSTKLGKGRFDLAEALYRDRQRVENNRTLPW
RARIKQLRSFPWKFFLAFMLLWSWLGTYVVPYVKGMHSRELPALGEGIRIPEELQQRATP
MPAFMHRANGYKLHK*
>TCRU_6387 hypothetical protein, conserved
MNQLIRSRTDWKERVVLRLAWITASRWCEIEALTPKNFTLVPDGSLNFGLVRGAEDGEGG
PPPRLAVCEDTRAGRLRHYKVMQDTSRKRKAHKYY*
>TCRU_6388 Endonuclease/Exonuclease/phosphatase family/Endonuclease-
reverse transcriptase/Reverse transcriptase (RNA-dependent DNA
polymerase)/RNase H, putative
MEPFTWLPAERYFYPLLNSIGAYQRYTYRLRAVCDAQRQKLLLSGDIEQNPGPIAVHQMN

VSCLTPSKLATLMAQGADIIAIQETWKSSEQIASMHTGDYVLHAQSRIGKGGGVAVLVRT
TLRSKRIPLTIPQHDTSLEVVVVQVALDQNRDLIVAGAYMRPPPQVTQSFRRLVNCLPAS
SPLLLCGDFNMHHPQWEPFLETSPSEVAAEFLELCTDAGLTLVNTPGEVTYARGTRKRSC
IDLTWSKHLTVSDWSASVSPLSDHYMLTFTLHQAFKDTIPSAPPSAPKFFYSWGKCKWDL
FIKDFDAQLPAYDYKKQSTGIKAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERIAT
DSKARYLQLPTPDREAEMQRTRSQFFLLLRERLRNTYPRRISKLNPGEPLAWKYISGRKK
ASLPSPTSMLLGDGQHTYKTARRAANALNRIFLPFHPSHKAVRFSKGINRQSASLNINAS
SIFGPQNSNELISTFTSGFCHCPLDAPFNRTELLAALRNTPYGKAPGPDEVYSEALRHIS
SKGLRFLLRCINHSWTTGAIPVEWRRATIVPLLKPGKSPELLESYRPISLTSIVSKVAEK
MVLKGLLWVWTPYPHQYAYRSMRNTTMQLAHLIHEVEHNRNHYFQVSLPKKSGIGNQLHY
RPHRTLLVLVDFSKAFDSIDHRVLSRLLANIPGVNCRRWLRNFLCGRYAKTRVGHRHSDR
RPMLRGVPQGSVLGPYLFSLYVHPLLNLLNSFAGVTADMYADDLSIIVKGQSREDAIPTA
NMVLKKLHAWSQENGLAINPSMCEAAWFTLSTHTESDYDREGRWPLVVAGCQIPVMTMGA
SRTTKLFGMDLDPRLTLNVSATKQCAATSQRISQLRCIAHKEAGPSPHDLRTFVIGYGAS
KLRYGSELIWAVATDSAKNEMQKTYATLARIVSGVPSTVDPESALLEANMPPLHVLCLRA
RLSIFENTRACQTDWMRRPPPEPPPRAGFRISPLSRDELYAFVDAYTKDYGITESSPREE
RFFRSSIPPWFAASAHRVTIGVELPIDHSITDEEELIREKRRVSEEALALHSHRSWILAT
DGGVDVRKSAGVGILLPSLNSSEITEKASINCGARPCSYRTESRALLLALEKLMIPRIRH
RRKTLLVVTDSQSLLAALNKGPLSQTDWTEDQIWQRLLTLTCAGWSVHLQFCYGHCGVHA
NELADQYATQTMETGQYTEHGIAPLWHTDLLTCFTTQLTNKWRSTIRQDTYRYLLCGTRP
SDLSGKDLITQEVLHRQELVYLARARCGESELWGRLYWAVRDCTNQCRFCDISPEQSAYM
RSNNDPTAPGTDTVSRRQGRKTSLQQGDGPSHAVGRRNVRTVILH*
>TCRU_6389 hypothetical protein, conserved
MTASASAVTLRGIPRRHGKMWSQQCELDPPVKAARYKSPRWRRRAPPTGQGGATPSPRGS
LWRQELEWAIGMLLPGGELGTVCGHAQWQDAPHGRSRQGCQQLRGEAPQGEERAGVASRL
GGDPPLGHDVRANTRNGVPPHRQAPVMRCVRLPFPPALPSDSVASLQ*
>TCRU_6390 hypothetical protein, conserved
MTASASAVTLRGIPRRHGKMWSQQCELDPPVKAARYKSPRWRRRAPPTGQGGATPSPRGS
LWRQELEWAIGMLLPGGELGTVCGHAQWQDAPHGRSRQGCRQLRGEAPQGARLSGESSGS
AVDPEACSARDDKPSTANTVSSD*
>TCRU_6391 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGTAGAAADGSEERAVVSGAGGGSLPGSKGVVKFPEGPQGL
KNEAGDVKGKKTPTPSEDEADDDDAGIDEEERTEGQSDQEVKVTSDPGSGEKNFIGSRRE
THQSILSPGDISHSGSREPNSNPTRPEFEGTNTDENTPEAQNPLTPVNGEQTLPEGVAGG
NLPPPPEDSVDSRKQDGEETRSEDEKNVPSPETAATPKATEKKAQKGLGKIQKQRQ*
>TCRU_6392 hypothetical protein, conserved
MWSRTVSLASTEQGLPGASVPVAESIETGRGTPPKDVDTAAPQKHPSPEEKWIRPGCPDR
PRESSLGGRDRSSDTEGTQASPPTPGDDTVAACPCPLLLLLISAAVAVPTLYGLRCGRRC
AARRLRFLMRGLHSALDVQ*
>TCRU_6393 Enriched in surface-labeled proteome protein 1
MVSVPLTEQLERVKKVLATWKEVDDRVSLLCTSLIALEDRPTDTDCGAVKITEGLVGFLS
GNFSDGTWRDEYLGVNATAKSGAAAVTGPSNGVTFTGRGAGAEWPVGSQGENQLYHFANH
NFTLVATVSIHGTTRT*
>TCRU_6394 Enriched in surface-labeled proteome protein 1
MCKGRVPTERLVGLLSGNSTVTEWRDEYLGVNAKVTNGERRVPNGVTFKGSRAGAEWPVG
DMGQTVPYYFTNNEFTLVATVSIHEVPEAGSIPFIGVRMNDTSSTVLFGLSYTHDRKWLT
TPGNRAASKRVDDIVKWEPNKTYQVVLRMDYDEWTVLVDQREIDRNRYNKNLFDLHRISH
FYIGGDSKDQSATGGHVTVTNVMLYNDDLYNNELYKLNASKVTIPSLGVEEHPTGQVTSK
EVSFASESKSEEIVTSHEELNEDDPDKQEEEAASMIRCLQRPLPRLTRDHLFLSLPSQRR
AQGMTVQRTMPSFTRAKRPSKPRRMKRINRCNGARTCSHKTHSQRN*
>TCRU_6395 hypothetical protein, conserved
MAAATATNNNSDGHTDGVWPEFSQELCEELNEKRCLVLAVDAEKAAAVCRCVDGVIAKLG
SGAERNGKPNKGSDDMLPSLQRSPRVRFTTGDNIARLQRCTAVYGRFPMLLVLEMYEDRS
FVLDLDPDITITKETEKKIELFLRGVAAGDVPRALQGAVPPANDCIDSAHNIPLKHGLCA

VTSTLERLKRKESGGAVCLFWSEHCAMCSVVLMMVDRLVGVILEASEARGVARPFSYIAC
NIDHNDFPEEDWPQKSERQIVPTIAAYNGDGERFVYGGRRMASPIISFICTHCLPSGLPN
AAQIASDALAVAEKMKEEELWGGGVYSTAEKDAVKEIKPRENDHFDTNEASDVNLEEAGQ
KRLRRCGHDAQEEESPESERGEATKEQQKQPKKERSEVN*
>TCRU_6396 Elongator-like Protein 3b
MTSKRPREEECGMEGGVEKTSWRGEQPPKAVQQSNLHRSLKEARFAGRSMEEGFHRQLGP
YEAPDEAVDVEDLVQGHEDFGDLPEGRRRALLESVRVLAQKVAATKSKNQLEHLRVKASC
LVGFKDTARKSELTAAYRQLVRAGELQASPVMEELLVRKRGKSHSGVLVVTVFMGPGQFS
CPKDCHYCPNQPGIARSYLLKEPGVLRGYRNGWDPISQFYDRASALENNGHVVDKIELII
LGGTFSFYPKKYAEEFIAGSFYAANTYYDSAPLRPMQSLQEEITFNEDARCRVIGVTVET
RPDYINASELRRFRCLGVTRVQLGVQHLDDDILTIVNRECPTAKTILGIKRLLDAGFKVD
AHWMPDLPGSSYKKDREMFEYLFSPDNENFQVDQWKVYPTATVPYTKIEEWYRKGLYKPY
AEVDDGAWMVKLLVYIMEQCPYRIRLNRIVRDIPTTYIMGGERRCNLRQVIEAEMKAKGI
CCKDIRERECKGKPVDRDHTKIFVDEFRASDGTEFYISVEDPERTTLYGHLRLRLRDNSG
AENSIFKALEGCALIRELHTYGRLVAVSRPNSGNAAQHMGVGTQLMREAERISLSRGFSR
LAVIAGVGVRRYYGKLGYHLEETYMVKGLAVNGENAITEEQVVQDDDNDNLGFFSKLKSL
IFRK*
>TCRU_6397 hypothetical protein, conserved
MRRVVRRAAPLLCRSHQFLARRNAAHEGKALSHAPPAVDTAELDSPFLSSLLEPPVTVAL
HDATRTYSTMDVVEPPVRYDPRCPNVYSEHQGMENGGESEGLVMRAHRAGKLWSAFAAAK
GNDPPEWFYKLCEDLYYRRHSEDEMDATALSSDVDFQDHNTLMDAWKVEEKTSESNKNNN
DDRNNNNNKENDDKDDEEGVDPYLWLPFDLLNEEEYRVGPYVFPSTATYTHEQRTLLCLG
DTRREYVHFCNTYAFPERVQIPTSVGTQPAKLYVDPLQETPVVYIQLSDDFPPAMWLPVK
GTAAAVRRVLAEFASISALHRDWHHEGFEERFRTAQRMLELQRMPSSEGDILRYMSYDAR
NEQFVFAPIREFPNQQEFFLGEHDDPERLLEHVDLCPFLFSIPHLRTVVDPHAEHMTPTI
EGPGVATSLYRCVFSKTLLFVQVQLSAEVKLPPQDPEAFRFMWKDSQVVPKMHIPVFVRV
VWPDNERMCGGGQLVRRFNRFFKTEFASDIPVDAVMALLYIMQWAKQLPNFLGVRGMRER
LAELEAAAQMPEPAKLYPATREIPNPEYTVMERIGMHVQYLAQLGDPEIALTIQRLLPEA
SAPVRMGCAKAALIAGERELFRHIVSSEPPGRMQVYMTKLVRKRKSRDLIDSEPRLLEEQ
YEFAAPLWTKRGTRIDKNTLEGAVDMQGRIGG*
>TCRU_6398 DNA polymerase zeta catalytic subunit, putative
MNLHVVSVENSLTKPNPLLGDELMSPLFHRVSDRCPVLHLFGYVYTSNEGSGPQGDIDAT
VAAGGASDSIQQRSVCAHIHGVYPYFMVLRHDSRVSVMQFGAQLEAVALRVLRPFSSSTS
APPRQLLHHVELVRRLPFYGYHERFRSFFRVSVIDPAMVGRLVHLLGHTTEVGGRRWQTY
ESHAPYHFQFMVDYGMKGMAPFFIPTCTARSPIAKELQHMQAQARLKITAVTSKGEPMRL
THAELEIDVRASALRRRESSIETGENLLSVRRSVRQYFAECGVDDALRCGAASDTSDRNC
TVCDVQNSDLAVSTMRQRALTYLRARADTATAEPLSHMTSTPRDELEKTTNFSLSAGTLS
ENLTTRLMEEMHGDRAESAPFSFSVSGTSFSSPSVSVQSLEDMIGDKGGGLLLSSEDDCV
QGSTLINDNSLAVGDSIVLFDGQADGSAPRGPLIAKITGMEAQTVRLRWYMTIRETHLAD
TQAELERNGRWLARGVPDAGGSAAGVGEELLLGDVEDDNPIDVLKQSVRVVVCHSYRAYK
SPALLCRYNYHVLEQRLSAIEPARDEDFVALPAVLSLPTADGLRAGVVAEDEELLASLSS
SAFSSSSPLCAKAAAVAPETHFVASHSPSIPSMKDGKYIPVPLRRSVSSVVQQAAQSQLS
MLLSRIGKSPSSTAVVHSVASLSGTSVARAPSGPSSSSSSSIECVNSRHAVLFQECGENT
SCLHPCYFMGDIPRNFRWKYDKHKKSVVVSAATWPLATPAVPVDKVAPADASKGRGTLRA
TAGPIETRPSVPLLSQVAPSQWGSPDHQPASGVEPKWQPHPSSNASRSVDRGAYMTCDLR
VMCVEVLIHRRRGTQNVAQEELLAVALGRTSSFTESVGVRLFCVGPSKTPIRRLQQPFSG
VVDVFFLPSEFHLLRQVRKELCFYDPDIILSWDGSRYGVGPLERRYRIVLQRSFAQDFSR
LSGGYGMADGKGEEAVETDALGDCASDGDASFSSLSPPSSLFSVPSVDGVAELPANKKTS
RAAAPAAPLLGVEEMVRRLSRRFGGSDCVPGRVVVDLGRQLRKEMKLPSQTLQMVYQKLF
HSSLPYFTDAALTEMYTSRSDDMRRVALSVLLTRAVTPHRIAQHLRFYTRVVEFSRMYGI
LFYEVLSRGSQYRVEATLYSMTKPMGYVMLSPSPEEVHHQPSLLSMPLIMQPRSDFYKDD
PIVVLDFRSLYPSIIIAYNLCYSTCLGKVSKHRRGRLGVLTSYKQVDPLLLRLLAEDDMC
PKSHRVTFAPNGCMFLSPEVRKGVLPQMLQALLDTRLEVLAALKHVAQPSGDKYMQRILQ
EQQTAIKMLANTTYGYTAASFTGRMPCVDVADATVMLGRQTLERAMRLINIHPGWDAEVV

YGDTDSLFVRLPGRTKEEAFLCGEQMAREVSRINPTPIQLQLEKVLSPCLLLAKKRYVGY
AYYKPDQTQPQFFARGIETVRRDQCPATSRLAECMIHLLFSGGSTDELRARFYEEVGKLQ
RGACNPADCIFRKSVKLGRYHDETRLPPGAQLAMRLMEKDFTRTPYWGERLPYVVVQPMA
SVRLCDRVIHPQRLLNLKENLRIDHEYYITRHIIPTLDRMFYLIGVSFANWYALMPKRRS
YHSYFELGLTRLPLSGRKTARTRHAAIVLEEGTEAGMEHRDQPFHVVNPACFAKKGTLDA
YYQQTLCAVCLEKFSETTPPDPPVCGDCLRIHAVSVVSVIRRRCSVERHLRLLETACRRC
IGSCGEAGGPNFLAGKERDMEDMHFAVPHQLAAASSAVNGEESTCCLSVDCHLSFEKRQI
FLLYSQLMTLENFLTSL*
>TCRU_6399 Beta-lactamase superfamily domain containing protein, putative
MSTELSFVRGLIVGSGSSTATPMLSCITGASPCSTCTEALKDPQHSKNHRLNVSFLIQLR
HPADYSLHNVLIDCGKTFRESAMKVFPAVGVSDLSAVLLTHDHADAIFGIDELREFNRPD
IPLDVYADERTDSSIRRVYPYLFPKDGSPGVGEWRKKKTGYVASISGHVFKPLEKLVLNI
CCRTPPPSGGDEPAMGFWSVVPIAVPHGVNYDANAFLLPMHTSGNKPRLLLYVSDISKLE
EKFFTDLARAKELLGVPDSVPIEVLVLDMLSRKPYFSHLNVDASIAAACKIQAGKTYFVG
MSHSLNHDELKKELQELGLSNRMWVGFDGCVVSIGDADDAESPQF*
>TCRU_6400 YceI-like domain containing protein, putative
MLGWGASERRVTSSKELRDVEMYVYTLPAGLLGRYIGRALRFRVERFAYDIDAATRSLKR
VEVEADSLLPQCEVDRCKFERLLLNFSEVERLSRRVRSYVLDAPRYPRIFYDVEQETKDH
IDGSLQLHGETHPVRCSKTMEGPELVVRCPIDSRAFNVPRYSILFGLFSVSQHVEVETRL
PLKAMNL*
>TCRU_6401 Enriched in surface-labeled proteome protein 1
MIFCGTGGATQGEEDLPAVPKFEWKGISEGDGNLVSLGFPRLLNVGSDVFAVAEAQCKKK
VGEDTFTGIASQLLTNTADKKPEEVLKNARVTQVLEEGAPTEGKKRVDVSRPTAFVKESD
IYMLVGKYGRNAAADARESAAAQSGILLVKGTVSGEESNKQIEWKDTNAVPTTTLGEQPS
SLTGLIGVGGSGVKMKDGTLVFPLEGTKKKDDKTEEDEKTTTVSLVLLKDTASWKLSKGM
SADGCSDPSVVEREKDKLMMMTACVDGRRRVYESGDNGESWTEALGTLSRVWGNNKKEGE
GKGVGNGFTTATFGVGRDARYSAGVSQKGEKWKGRTPPLADGQYAHC*
>TCRU_6402 40S ribosomal protein S25, putative
MPPKKNAKPTKPAPKKGKMENMNKGAKKAAKKWSKGRTREALQNAVVFDKETMDKLLSEV
PKYKVITPSIISDRLKISVALAAKGLQHLCRQKLIKLVSCSSKFRLYSRV*
>TCRU_6403 hypothetical protein, conserved
MVALPFHISQYLSALWDEAAALLDVDASFYRRLSWRICTGEFPLSSEICGSFGIDSPPHW
PRVLCGSSPHHREGLGGRPRDGKTAVCGAARGKETSVWISSIRTSGRRRSVVQRDQCVAK
KWLQQENRRPFPSGVKPSAYPSFSCATKSAALRHDAKTRVEGGRASPKAYS*
>TCRU_6404 mevalonate diphosphate decarboxylase
MANLQVTVEAPINIAFIKYWGKRAGGEKLILPANDSFSITLSTHPFRTKTSVVLRDDLEE
DTLILNGEKSDVRSTPRIQSVLDYVRSTCPDELKNKRVYIVSENNFPTAAGMASSASGYC
ALAAALVRVFNSTANVSMLARMGSGSACRSTLGGFVIWHKGEKEDGSDCVATQFVDENYW
PEMQVLCAVLQGGKKNTSSTAGMQQSLQTSPLMPKRIATTVSERMRTVSEAIKARDFYTF
AQIAMSESDDLQAICATTQPQIQYATEDSYAMIRLVKTYNAKKGHPTLAYTFDAGANCFL
FVLEKDLPEAVAMLMQHFPTPSERFYFHDAMLLQKIQETTVPHEFENIIDYPKKPFVMLL
QSPVGPGVRYLSEGESLISL*
>TCRU_6405 RNA-binding protein 27, putative
MATREDARVVHVFVEDPSVVLIEDVHDWLRIIDDVEEAKVQYDTARRCRFYWLRFKHGFA
AQLAVNYLDGEKLKNNVVRIFSSVYTKRTPMEADAEETTHPEGEKEEQQAVENPNLPFNH
RMPSDLRMDTPLVDRIPTLLSAAAEGSEQHDLVQQLCQLQKSYCQVQEMIQAAELNIQKA
DEEVKQLLWGNNKSSGSVVNGSNDKAENDRSPELRRSRRLANTVQIPMTLLDPASLIVKF
TRHIGPVTDYSFSVSPDGHFFRTVVEFFHEDDVIYALQILNGGGSSKAATHSTKRTRLEC
DAEEALSPLSVYNWGEDASADLLLPPDLSLFYNPAHIQAMNVLQSCLN*
>TCRU_6406 major facilitator superfamily protein (MFS), putative
MFFTLVGVVKEMLNETFPRQKEEERSFNVPVNSSEQDQAECADAALVEEQRPRLERILTP
RFVLAIFTALNFIIYYDRGALSGSLASIKGDKSIAGDSKTLTDTKVGFIVSGFMIGYMTT
SPLFAAFGGIVPSKWIIVGGMVVWAIACVGTGSATTYAALLVCRIFVGVGEAAFVGFTVT

TIDRIAPSGSRTLWIGTFYSMIPVGTAVGMVVGGSVGSLGTIGPTQGWRIVFFTEVLASI
PIVLANAFLPSIYNLRSDSDETEYYSLHKATWILIKNLNYLLIVFGYAMYSFVVGAFAVW
GIPMLIQGKMRLSYINASLILGGVTALTGVLGSVAGGFVLDKIGGTSGSLNLIRGQLLLI
LLILLSVALGIAAFFLENIVGFTFLLTLSVFALFMVTAPVNAAIMNVVPPELKAYAVSYS
VFLIHALGDFPSPTFAGFLSDHVFSKGCPLHNISLCDLDTGNHCRWVNNTDDASSGHCVN
EYQLRNALLVVFSMMFLSVPCWLVVYFRLWRAYRRAESLSDSSGLSLVG*
>TCRU_6407 hypothetical protein, conserved
MMDPAHAMMDAQSLGLRLDEVLHKFATREEDNSDDARLLADIAGLTEVIDKMISPSLSAA
SEAAENEAMVSLPVKTLEELRFLGCACWNMTVRHVSREDSREEQTLKASLREFATKAFLL
GNYAYASSDVSHSYFTQHPREAEQCVLMCLKTSRDLSLCGVAGSAKRLLSLGESVASYIQ
TGVQNSLAYIKHRNMRWEFAYTAMDINWNVTHYKESCEAAKKLTQMLLQDRDLRRDHREA
FFRFVFTIGNGGVLTSDEQYIRDMLHSSMEMQNHFQRAGTNDPSYHVMILRGATMEQMAL
SWLREEKATEALSWAVEADTTLHSNTSALLRLTATAKAGMEPEAIVLLHQYVQRSDVSVD
DAVAACFELHNLLVSRKDGSIEGMRLLYKKTKGNTCSETVLFRFVQLLLHNGSLASCKEA
LQILQNEGIDFEETRYRRYCFVWLWELADMAGFSPSQIVECLESALRFKDCASEAEVDAI
YLRLCTEYITQSEGGGQTSVVLMKAKNILVDYASHRNPKCVFAHSLLIKIAVLESNEAEL
EKELNLLLLCEPAELVMPALCTAINYSLRIGYLPGVSLVITRAVFFSAPVPDPSTELELL
RVYVASLLGKACNCTDDQLRVVTERFRSLLSDECATISLSHEEVSWWAQAFLVLGLEFTV
GPGPTSVYLFRAATFIALQDPVPGEVPSRTFLISGLLCTLEDEFQLFSTGIPQIDSCELE
EHLRLCKEFVPSLPEVNYRLTVLLSQAERHLRQPSSETPEQIQRILDELSSISVTFEDYE
AIANGASFIALKYASEHPFLHGVTIKLYMQAVSVAMNEISTSMKDADNNAEKCLEYITDA
FSCLYKCFTLAFDRTEQLTVVQRLMEILSLAVEDVTVASLIKDYHSNTVRTVNNHPLSFA
RLFLEYFTVEAWNNSVFYLHLTETVKQTQWVHVAWTLVDILPETSSVASALHALKAITSV
*
>TCRU_6408 zinc-finger of a C2HC-type/Double zinc ribbon, putative
MLSASRRGPAFKPQLRVCYLCGQQFGSASIGIHIPQCYAKKVAQWEIADPVTRGKRPKHP
DTVNWRGEGVSMDKLNDEQFHEFTANLVPCRNCGRKFLPDRLVVHLRSCKGDSKRGSTLK
TSGKDDGSSFNGTLGSGPSSTRRSTQSALGSRSPRKSAGHSPSLMSGGRPQLPICYLCGQ
QFGSSSIAIHIPQCYGKKLAQWEAADVQTRGKPPKHPDTVNWKGEGTHMDEHNDAQFAEF
VSNLEPCPNCGRKFLADRLVVHLRSCKPGSRAKPPPRSCSPSTKMPVSARKLDLGASRVG
QNTGVVGSRVANGGNEDQGAAGGPVSEEDISTKDAGKINPKLNRLKKGGKVDPEGRACPR
CGVVEYDMSAKFCRDCGASLVAKNLFDPCEHCGEQIPEGSRFCGTCGAPINGASAIERKA
GAENVNASTIRVVACPACKAVCDADGNFCDNCGAALGDEEPATAAPSTTEVMFCKKCGES
FEDQTARFCEECGEILEKITVSSKDKGPRGQVSTLPPEVVTSHAPLKETRALPALTAVGG
TTVAAGIPSPPKLREARNERKVTITNDAREVRNMPEDMKGPGAPTLPVLSKSSTARNIPE
IPEEEEGNDIGEKGECSNCGRTFALNVLSRHERVCTTQKKRRVFNMRAMRLSGTGADQVA
KSGSSGASAAAVAPAPKRDWRAESEAFRRSMRDARQVDKVLKSGGNVKDLPPPTYSENSH
YTPCPHCGRKFAPDVAERHIPRCATTINKPKPPPRRR*
>TCRU_6409 NADH-ubiquinone oxidoreductase complex I subunit,FT
putative
MRRWGGCGTCRLAAAAGRCFWDPYGHQPESMFLDRKDLEQMYPTRKPKTTGGEFGYERGP
YWNAMLVPNPAVRLPHERRRLNPKPAKRVTVFGASGYLGAEIVREFCEHPDIEKVRATTR
YPTLIPAGSELDMLLQKYPEKIELHECDVTDRIQVNVASNGSDTLVFAVDYHAEYANNSH
HDVFLTGSTNVSWTARSVRAERVIFCNGLDATFASESNYCDFRARAEDAVGANHPDATII
RFGPLFGKRYRYRGLGRYVYPACFPNSLVQPTWVVDAARAVVRCSMAHRAVRYKFDLGGP
QTLKHVEAFRQIAAHFDSRLVVPCYRGIGRFFGKLLPWVVPNPWFDDNWIVTYELDQVNR
RSTLFDRLASWERIAYKPHSISEASAIERGQVPLPPLHELDVAYKALEAADKAAFELEEE
NAKKYGIHRAKAEPGFGRTDGLEALAQEIYPGQQFRMRPLEGAKYPSTVKNPGPVAIQ*
>TCRU_6410 19S proteasome non-atpase subunit 8
MPKDKPQQNPASVDDNRIDDSIARGDGDNARDSGDGPGDNFLFTPTAARVDVHPLVLLSL
VDHYARVNTKVTQKRRVAGLLLGRYKRLPDGTQLLDINNSFAVPFDEDPHNSDVWFVDTN
YADEMFHMFRRVLPRVQVVGWYSAGPSFSVQPNDMLLHLLVADRFTANPVYCIVNTDPGN
KGVPVLAYTTVQGREGVRSLEFRNIPTHLGAEEAEEIGIEHLLRDLTDSTITTLSTQIQE
RELSLAHLSCVLQSIEDYLQDVAEGLMPISEDVLSVLQELISLQPHIYHLKRSTEMIRHS

NDQAIAMFIAAIGRCVGALYDVIANRRRINSEMVEVRARREQALKEKLEHEQHKAKEVVT
TEKDENNNAK*
>TCRU_6411 ATP-dependent DEAD/H RNA helicase, putative
MHFNTYGQKDVPPPFTPQFQWGGRPGAFGNGSPQSAYNSYQPRAGGGFDGGHFRGGRGRG
GGGYSRGGGFGQENGFNRPLQYQGESPSHAYHREEKPEEEIFKEHTPGINFDQYEAIKVH
ISPNDIPPMESFASMNTPLALKENVARCRYQKPTPVQKYGIPVVLCGHDLMACAQTGSGK
TAAYLIPLVSSILSNVTPNHQGQGSRSSPAALVMAPTRELSIQIHEEGRKFTYRTGIRCV
VVYGGADPRHQVHELSRGCGLLVATPGRLWDVFTRGYVTFSSIRFMVLDEADRMLDMGFE
PQIRMIVQGQESDMPPPGQRQTLLYSATFPTEIQQLAREFLHRHYFLQVGRVGSTTENIT
QDVRWVEDNDKREHLLRLLHENQNQLILVFVEKKRDADYLERFLRNNRVACASIHGDRVQ
REREEALKMFKSASCQVLVATDVASRGLDIPDVSIVIQYDMPSNIDDYVHRIGRTGRAGK
VGRAISFFNEKNRNIVDDLVPLLNETHQNVLQQIMDLTKRPNVNNGRGGNAGGGFRGFHG
GGFFGGSGFRGPRGGYRGGNNRGGYGGGYGGGYGGGYGDGFGYGSGYGANMGGGGRGGGS
RGYGGSSAGGGAFGGPAGNVRSMFADGLNS*
>TCRU_6412 hypothetical protein
MSSQFIDSQVEDEEGVRRRLISFYERHNPRQLEYIENIIFAYKGHWDELFVDLAAKYEHE
FWPTDTANESCSCPSNRGRSAGIDSSPGSLSCQPSDRSVGFSSFKLLDPMEVVQRRRSDG
RRDDIQNGSLAMINENPSNNKKKNNNDSLKERKLTLLRQSLSGDAQEDITRRLRLQQLFT
RFAPREVLRMEEFMAQYREAYMMDIISASGHHDVVTEKEWQEAMIHDLLREFDPNKNGNR
VGYKTNTIQREVYLKKSPSSFDSHVLFPFTPADPLDTKPYLGSRLLQEFCATEPSTLKVQ
RMKEKNKRMTSLPFISQLPLTPNKEERTCFHVETSVDEWCEPPKEHLFANTNKDLVASEP
VKFYCDNTTPIRSMSDAEKMRESEELNGNGDPPLLSIILNQHTHGKRVCILFSQTLEERK
AEEFLLRPAVRRALACPLLHYRLFLLLCISMEAAQGGGLTPQGDPILAWSGEETRIPYWE
PSLAHRVLWRGLPSQQVDHTFFLQNEKITGTLPYDLLDTLHASRSLVRTVGLESLWRDEV
TFADVVAVRMRYFARRYPTLRWLVLRPFACLRNNQECTQHFSPDEPQWQGWKKLSSLLFV
DAVTELIRVFGGFSEHCWVEFIEVWKKDRNLLMAIAALQDEFCSHNGLDDIGEVCSDEIG
GTEKEDVCDWEIGKACRSGIPRSVSMLLSCTAFLCLHFGRPFGGISCVDIFATYHCLRVA
AIAEEENYRRLTILRKWGEECDVLRHLEVHCAARVSLQERERCQRGKLEVQESSTRMELF
QSVLSWLARRSHDCCGSLVAQSLFSTTTVTAVGAYFSQPILHWRRDTMRQRIQAFFRSAS
EYQQRLNDS*
>TCRU_6413 TPR repeat, putative
MGGKGNSACAETVRREPTPTLSNLTGSGPITRRLIENYWRSVMDSGWKPIVETPSRALLE
RCGSLKTASLAMRSEGSQKMLLTALSSSSDPVQWCIDNAETAELTGQFAVAENYLQAAIE
QLYRSDSIALGAINTVAFHDDAKLERDCARTADILRRFGKLSLRKSAHGEALAFLNLSSR
IDPLTPVTYALRGACHEHLGNNAEAYEEYKKYLSLSPPTLAVVAHTGQCAIKAGKYEAAE
RHLFELLQMTKVTASPSAVPSGTGFALFESSDFYEAHAYYCLGLVKEKQAEQAAATLSED
SVSNSAETLAQEARAFYELAVANSAYVAALEDSSESAILARDAPLALENLRHLQRLRRSC
AHYYSRAADVCAMINDTASEMEELSKALDQRQPVTIRRKTLLRRAAVYASKLHNVDKAIV
DLSLLLSLPGNDSCTAMAYLQRAKAFEQRSCERPRTSREDVGAALRDYNSFVETALMHPH
ELDVPPECITVAMLILANGAFKEKNYGRAARFFARAVARGWRPLEDLPRERREKKKNVSS
ISLTGVDLLTKMYLAIARTVVSKIPIAEDMFRVPYEQREKPPAQVVTELKKSKAAERKEA
EKPVVAVHAVGYQVVEEHYQRLRALEPTFFSALQYELLELWEPYRTEVERLREDLMLTRN
GKKVKRR*
>TCRU_6414 kinesin motor domain containing protein, putative
MEDPFSFQRLRVAVRERAIMEEDGPNVRLCLRTDEGKVIAHAPGVTEGLMYDCDYYFSCA
ATQEDIYSSIGSQMVDLAIQGLSCNAVVFGFADTGKTHTLYGDGDGDGLLLSTVRDFYSR
LEAQSDEYEAKVLMRYWEMSRDAVEDNLRENDEGKKAISYAVSRDHLDRLTIPNLTAVEV
PTVEEFLMQLGRGNRTRMSRCEERMFRWHGFVQLIIVTTDKPEGTKNYIRTMTFVHMKGT
DRVGEKGIRGEQLREGSCINVGVTLLRAAAIHSLEYREKRRAFSTTPEKHRELIRRSQSF
FMECNFSRMMSQFICGFEACFVIGCTSPLQYNESIETLESLQLFRQLRCVLKPIVVISDR
GMLIRQLLRQEALLGGEVVSELYDSDTAGRPLTEAEEKLLLTYKKIYGTVPRRGLDTTLG
FDREAELIERCKTRAQQQIGKVETHGMRTRIFLNPGKTASYEGQWEDGKFGGFGELLRRR
SRYRGEFRNGLREGEGTLWIRADEKSPWIRVYRGEWLAGKRDGFGTSWDENGDVYEGEWA
DDKRNGFGRLFMANGDHLKGEFRKGLCDGRALLLLTNGDWYDGYWAMGLREGPGMWCYVN

RQQCLCGEWTKGIFKCGTMYDLPHKKTNENSRFIPRLGLLRHVEVLELEQRKLYDRRVQE
FGALGYKWTEPVIFPPLGAAVSFDDDGEKCHVEVTDVETADISWGLNVE*
>TCRU_6415 60S ribosomal protein L17, putative
MVHYSRKPQVSSKSAKAKVSDLRCHFKNTFETANVINGMPLRKAQQLYRQVLAKTRCIPF
KRYNGKIGRTSQAKEWGQTKGRWPRKSVVAMLSLLKNAEANAIEKGLDPNKMVIKHVQVD
QAARMRRRTYRAHGRITPYMCSPCHVQLFMTQPQERVPVPKSKPKK*
>TCRU_6416 Protein of unknown function (DUF1279), putative
MRRVVSFYFSRKSIRWIGCVRNVNVDAGDGSRERGDGSISDVVVDSYTLLPAVSRALPLF
NPCQEFPATAVGMELPDPRDPCVVWREYYSFEHRRPYYHNLLTNLTTFEVPSGFRTCFSL
FHRRQGLYVDTENRVHRQATVQGGGTPDKGAPGASDGEGGSPASPGGGGTLTTKQKLAAY
GGGGLLLYLIVHNILLAAIFFSLYFLHVDLVGIARSYGFSVGDDPIGSGNGADAAVTKKK
DPSFWATLGVSILLNKLLVPLELAATLMMAPVLVPRLQPFATRLIPRVKTFMKG*
>TCRU_6417 Mucin-like glycoprotein, putative
MMKCRLLCGLLVLALCCCPSACVTAQDPDSPSPSTEVKGVAGAGGEAGTGGSIIAPGTSG
AQNQDDKSREESDVGHTSESSSERSTQSDRQEATATGKTPHTSNSADSTGPGPGAPLVTV
ERPSASEAPSNSEHKPNTTTTTTTTTTTTTTAPEAPSSTAMNAEAPTTTTTRAPSLLREI
DGSFRSSAWVCAPLLLAVSALAYTTLG*
>TCRU_6418 hypothetical protein, conserved
MESKAPAPPSGDATQGQHSHDTDTENSTKNAATGSPVEPTTSSTSASGSGDHVHNKADED
DTQISEEQHDSPETGNTNVVPTLSGTAPKTEKTAATARINVTTTSSEGEGGPTTEKENLQ
NITEVKNEATPSGSKMESKAPAPPSGDATQGQHSHDTDTENSTKNAAAGSPAATTTPSTS
ASGSGDHVHNKADEDDTQISEEQHDSPETGNTNVVPTLSGTAPKTEKTAATARINVTTTP
GDSDSSTSVSHPTSPLLLLLLVACAAAATVVAA*
>TCRU_6419 hypothetical protein, conserved
MPSRTSLDAHSGTEDQVLHFVAFGVATWALRIWNEGISVVIAYLLSAYSYYWHQADAQGG
AIDPTAARQDAAVHVGNESNPAGHGDSGVTNNSVAIGDETGAPPDKGRDESTYPQPDRLE
GTCCFSTRVDNGESLVRDCGLDSQKFHAGAERDLNFGLVRRAEDGESGSPLRFAVRGDAR
AGRLRHYKALYDTLKQRKAHEPDDCPGGTSSGSLDATAHSTKRGVSRHAAQVVETHNLDP
QLISQLAKHVDPFDLPQNTVRYLGKCTTILTQVSSLAALM*
>TCRU_6420 retrotransposon hot spot protein, RHS3, putative
MGEAIKSQADHRELPDEMDVKAMCAWMERDGTTDGQAESWKMVEERMEKVGPIPRHIFDA
SKFIAHSAAIEDALDGINSRDGERHFTHRGVRLWYSGDPPQKLVSVVRAGGEVGAGGFLN
AAISVCLGRRIAHYFGGRDE*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MPGTESVDRVSCLCSCKDGWHGASCLPFEVPDTVVLPAPERAVDGDTSCVVNQTLTSLTL
NMWKTHHCYVSVTFSGVGAALTFSFNSMPLHLPINITLTGCTFLDGAVLQFVGGVEAAES
VGVLIRVSRTVMRSSVAAFALALPQHCDIAVTEVDAAQSSAVHLPDTVNNKLSVVMLYEV
LLTASSLLVSNVNAHASKRDAFGLYSIGTLTLVSGSSLYTRYCGFDGYTHLFYLDILSVS
DRSVFALLNNTVFFGTSLLYQYRGFSVSDHSVLRVVGNSGSVSCAIYSLNSWTVQRSSWL
DWRDNDVGVGAMLHDSESVFVGIDGSSVVTLTGCKMGSTGLSRPLLSQSDAGYQFVAGCL
TVAGREVTTAAELELHCITNVTTVAVCAECTKDGDCFAPLTKAVIDCRCQCAAGGHGDVC
VPAPVPAGPPPLPPPPVSPTPPPPPVGECISDMVYPEVAHAVGGGLSWLCYRNVTFSGDG
MCLTVLVGAMTGDVANVTFDGCTWRDGAVLLLLGNAHAAVGSLNIVVTGNTFRDALLRPE
GVFPPRTNITISGNRFTVTRLIPRPGLGLRKPSCIAMNELAISNDSAVVLSGNVFQSVTA
SSSAIHVVESSLRVSWHSVFAVVGNTFHMAGGDGTLIHLEGSSESSSLSVLNNSAVVIRG
NLVSRPVKHFILFFWASRVESLSAVVFQGNDMQGSLVVFYSAFSSHIYYTSWLQLSGNLC
RESPSEAFAVFNPTVNLRDSTLTASGNQFMSNNGVTKALWIFSESTDPTNGAIVAACNSV
NGGEGANYAIPSVYNATILTCIDPCTLATSCFPAYTTTVSSDGCACRCAEGGHGDACLPV
AVPEPPSTDGADLCVRDVRVDVEVNVSFGTSVACYVGVNFAVDVVVDMESMTGTVRNVTL
ANCTLVGGASLYVLGWLSGPPAGQRAEVLISGLESRSGGGVVVANRFPPGSRVTVVDSVL
IAENRVAYRGAYDLGDASACLVVHNVNLTGSVLTIARTHVAAVFGDAVGVLVVGGVALSS
RGALYVDGLLVQTALGLCVSVEGGVAASGGSVVAFFDSVFLLCKHAVSVRGAVSVSSSIV
ALVRSDFLSTEDYAVAFYSTVSLAGGSMLLAKGNVHDGVSREMLYAAGAVTAAGSTLSFV

RNRALLPRMVSVSLSLAAGAHLRVACNDAGGRYLSTAEEYAAAGFGDAGSIDVAGCDACD
RDTHCYAPGTASASMTDGVCVCACGSGGYGEACVPVGAPALPPAVGTASSVFVREGVTVQ
SVFVVPAGASEVTLRHVVLDGVSPVLYVPWMARDGVRIVVQNVSLLNGAVLYVMGGGALR
GAVAAGSDESGPVELSVCDVEALNGAIVLTGTFPAGSVLTVTDSLLVAARPTPLVYLPGS
QSSPYAPVLVLSGLRLVRSVLVVSGVALVTVMTGGRTVVVDGAVLELVGGGVALDAAVLG
GEYALYASARVVASGGAVLRVSGSQVYAAHGLVFDSGVVANASAVVVNDNAGALTDGALL
VLRGSASFLSGSWLSVRGNSISGRLLSVPSYPRSADLVQSTLTLYGNAGSGPVVMDGTVA
LGATGRRFVVGCLTLNGQVLQPMDYRSAGIIGEFRPVACSVCDADVHCFAAATMSMSGSC
GCRCAEGGYGRDCLPVYLPHVDGCNRTPAMPLLSRTETLTETCSLTSTWTATPKPNLSRT
QYGPTETLQVTETVAPPPTRTPTASVSSTLWWSDVACPTLTVTTTTAGGGLTQNDIRGGG
SAVPTLLMVALPPPFRWARDPQLGTHLSFVPVSTAQPRGFGGPWGAMLRNATWVRNATNP
SAVLELAVLVHRGYFIAADETIVIRCDAVAVFGGCKGVLLGSFTIRSDTLPAAANALSAI
TGVVAGAAAVAVVVTGGLGSILEMQALGVFARMSCTSAQERASTVALPYFLSVFAARDPL
WMVVGNALLAAVFGCVHCGVTVVFQRWRGVDAASAWAAMRFPSLTYVVAHAMHLGISFGS
VLALAMPGARVQHRVIGVVGVLYGAAFPAGVCYFIARHTGASFTRYWQFSRKPLHERLLY
PVGYWHPAAQQRMYGGMLTNMRGSRVYWCVFQLLVLCVVCLIAAVHPPVGGCHVQYFCMA
AVLVAGAGVVAFTNMMRSSFLTVMRTASFVLLALLCVVSASNHLAPSDGGARAYAAIVLL
LTTVLLAVAVYGVVVWYAEDRHWQELREPRRGGLEALLRDDEESDESQKPHEMTSSSYAS
GTTVASSYRPPAPPRPVAGDIRSDALSLFDRASSASCSINYAPLDR*
>TCRU_6422 hypothetical protein, conserved
MRKGRVQAVREFVVKYRPHTPIAKRHAVLLGHVHNVGGAELVVAVRQPAAASHGQRFCNE
HGEAETEITGHNLQHAAASHHNILEHTRAFVHVNARRNPRAVLYGEHGAAADTQVRRKSV
HHVCPRHNSAVVHVEDAGQVHVKAALHEDRSAQAPATHHRRPRHDKPRRQQPDAVQNKRG
AVPGSCVARSHRHVLRPANRRAQRRVRQQHTRVQRHRAMQHNRALQRRHIRHVDEGVGHQ
ARRALAETTNPQLRAAHKHAVAQRHVQRVSGQVHRTQVHRHSDRSAEHHRVEARRRTPTA
NRHGLRQRHATHAALRTATAVTGPRRRHVERQARVAHTAGTAAAHAVRERRSQRIKARQR
SRTAVARHHAHGGQAGHAVVAAALQHPAAGTVALHGHSAARDRQPGDKRRAGGNAARNRH
GATVQRHPRQRRHRRRLAHRPHVAQLQPPAGTDRPTAAAHQRRRNRPLDAHEAQHRIKHR
ETLSKHNAAAAAHNRHVRHGEHRVAPQTENRRRRHMHRRRGRTARSLQRHAIKHHRARQQ
IHAAANVHRRPARVQRPQHSVAHTQLRLQQRRRVQHKRRRHRVRQPAQLRVAHRPRRHNR
RVTDRHVRVCRQVVHKRERAVVAGQPAHAHLQAPVTRRLAAVAPHVDLRTAVAHAVPQFD
AQRAGKHRRHVEHHSHAVRDGHAVHQHRVHGAANRDGSVHRAAPQPQHHRMHRGHKRRSS
SQRQQKEQRHTHSRNGHAPHTVTAARTRTHHRPHPMNQSDTNRVVVVCRTRTVDRTFCLA
NPLYRWKIQ*
>TCRU_6423 Enriched in surface-labeled proteome protein 1
MLVTLPVYPKEDGKKETGNGKGELHLWLTDNTHIVDIGPVSYDDAAASSLLYKSAGSGDN
EQKEELIALYEKKKDGEKPSHSLWSVLLTEQLQRVKDVLSKWKKVDERVSKLCPSSAEKD
ASSEDACSTTFKITDGLVGFLSGNFSNDTWMDEYLGVNATVKENVGGKKATLHEGSVKFT
GAWAEWPVGSQGENQLYHFANYNFTLVATVSIHGVPQEEGPIPLMGAKMSDDGNTVLLGL
SYDKEKKWKLLCGKEAPKELSSTSEETTHHVVILLLNGTQGSAYVDGQRVLGDAQCDLKN
AKDKKISHFYIGGDGNSAGGAGSEEEVSVTVTNVLLYNRPLSSEEIIALNAKLSIPKQAS
IKTVKEVTRSPEVRKPPALETVPQNNLGGDQLTAQQSLKTSEDAGGAGASTTAVSTVTNS
PAGKESVNKSTSGTSPDGHQTVVARDGDKAQQDEPQKTPAGNPDTADANTPTTEGEGQDG
PTVNPEAGASSGESGEPTEETDGQEEEIQPQDGEVKAAALSSSLGNVSRGNNSDAGTVCE
SRLLPLLLLLGLWWFAAL*
>TCRU_6424 hypothetical protein, conserved
MHGRNGELGAVCHVASAVHTCSNCAVSCATREEGATVAFTMNVTTHKYPGPYELWWRQFY
PDGTIHPPARSSDADRTASVSCRHPVKGRMTQNLARQLRRKLMLSRHVNTRIGDSLRRLT
DPTPSIGVPHPTRRPTRPRRGLSLPVIRAE*
>TCRU_6425 hypothetical protein, conserved
MAMVTGRVLLVCALCVLWCGAGGGGRAEATSESQDITPGKDNVPKSEKETVVVAVEGDEN
GKPAASQETSSPVQIVTGAGAGAATNPEAQVPPGTQQASAIIKQKAENKNEKTKAGMREE
EDEIEEEEEIDKNGENKEVMKTKGEKEADDKAEKHGEEKHQDAGAGATKKLSAGSEEQPI
LTSGAEGASNITNPNSTQTTGEDDPAADGAGTGEEKQNENKDANPKETPVEATAMKTATA

TTGDSDGSTAVSHTTSPLLLLLVVACAAAAVVAA*
>TCRU_6426 hypothetical protein, conserved
MHRGKPVVIALDSEFLKTHGHVLTRAVAFVPFSSRKGTSGSEHQVDGNVAATSTSLHSSL
SPSLPVPKRQAFRRATVFGVPIILNLDPAEVMRRADVLPCGHSLALEMRTGLVSGERLRT
LQERHARSDSKAFLKRTEEATTTTTTTTTTTTFSGNRAWHLEFNSLCPYSIPNIRRADHS
WFKAIYSASVHSSEFRGAAMCLDHLKAYGKGRRQERSLSFLLRHHPTLLQEILRVSFSSA
EAWCAWLVMCGDLVEKELRQLAEKYRQMSSSPFSPSIWMEYDPSYKGVQYKECGNMEEFS
YELSRLWYILLRHGGEVGTKLYTYGDMDAKAIQNTLRLSCCMKTRYSPRASQSARLRSSP
SQLTGADEASNNKSDSQDVLTPLQPESGQILTSPYEAKVVDVTRHTLFAASGFRTSPRVI
PPLGDALEKAAIVDEAAVRLRSQSDPHNPVWDAKALACITVACGICLG*
>TCRU_6427 hypothetical protein, conserved
MGSPKFIFAAAAGAAVVGAAVYFVVRRGRMDKDGEDDDAFDGPVVRNGEVAVASKADNGS
TKLHGNAATATTPGSNERKEEPQVRVKAGDVSSVENKLLAEALNEIDMHDAADRTTNYGT
GTKSFTINKAGDKEKEFPLLGLSVKLPNDWEIREDLSPFPNVAMLVVFNKDMNPEDAQQQ
QQHQEAGSVPMIVISVEDVRGDNVDLVEFKERCKELAMNQMLMMTGGAIQPIITKDSAVQ
EGPFRYALEYAQSLPPLYEIKVLNLMEVRDSIAYTFQIMCAPNIMPKFKPTFMKMAQGMR
IKENIETSLGYVELHTGEVKVDIDTTWGWEYPGKNGSLATFTTSSNFKKEEISLYKQDAV
PDSAYKPRDEKTVNGVVIVSAFDGAQQQKMFTYNGYTLVVKPLQKSNSHLAEKDLVAVLK
SVTLSSLPPKPKKGGTFVNAEHGYKVDILSGSRLVASRIGGGSVAYAPHSIGEGTASEEQ
PPAVTIRVGTPEGDPDCMGSLDEWMARMKREAADSDIREIKKTTINDEPCLTFVSQNMEE
IAPGQRMEVRGKVFIFVRDGKTTLVRWEMAVGLWRKFEREMNAFVESLRFI*
>TCRU_gamma, putative elongation factor.1
MRSMTANLIRGWFQRMEHVRKYAFGVALIIGEKRRHDIVALWVFRGRGMPAIVEDVEDTE
LFDWEEVADVAAQRERITDYLCWEGPTIPRPVLEGRVFK*
>TCRU_gamma, conserved domain containing protein, putative
Elongation factor.1
MAASDDDSRCALDTHPHTLSCLSVGVMAVRPRSTAVNNGAAENEDEAPREKKKPNPLDEL
PPSPFVLDAFKREYSNTDTRTVAAPYFF*
>TCRU_6430 Enriched in surface-labeled proteome protein 1
MEKKGVLHLWLTDNTHIVDIGSVSGDDDVAASSLLYKSGNNNNEKLIALYEKKKGDGDSS
LGMVSVRLTAQLKRVKEVLATWKKVDDRASKLCPSTAAKNPSTGNGCSAVKTTDGLVGFL
SKNFSGNTWRDEYLGVNATVKKGTNGVATGYPDGVTFQGAWAEWPVGAQGQNQLYHFANH
NFTLVATVSIHGEPKGDTPIPLMGATMNDNKKTVLLGLSHDKEGKWQLLCGGKKTKELRS
NWEPETTHQVAIVLRNGTQGSAYVDGQRVGDASCELNNTDSKGISHFYIGGDGGSAGSKE
DVPVTATNVLLYNRPLDDNEIRVLNASKISIPKLTDLKTLAAGATGVGAARHFGANGDGS
NVCGGGLLPLLLLLGLWGIAAS*
>TCRU_6431 hypothetical protein
MPCNCRGAALPGCGGEWGPDTERLPRHRGATHCGRTRPEGPHGVLERPSLCTQPQLMAAW
RKLLCSGDDVHTKIEVSINRTAEQAHGVGLDAWLPTAQTMVGRVLVRPSA*
>TCRU_6432 Enriched in surface-labeled proteome protein 1
MVSVLLTAQLKRVKDVLTTWKEVDERVSKLCLSEKDASPANACSNTVKITAGLVGFLSGN
FSGDTWKDEYLGVNATVKGAEEGAAEEKAEKAESSDGVNFQGAWAEWPVGRQGDNQLYHF
ANHNFTLVATVSIHKVPQEGPIPLMGAKMNEDGKTVLLGLSYNKEGKWQLLCGGTVTKDL
SSTWESQTQYQLAIVLQNGNQSSAYVDGQRVGDAQCNLENTDSKGISHFYIGGD*
>TCRU_6433 Enriched in surface-labeled proteome protein 1
MVSVLLTAQLKRVKDVLTTWKEVDERVSKLCLSEKDASPANACSNTVKITAGLVGFLSGN
FSGDTWKDEYLGVNATVKGAEEGAAEEKAEKAESSDGVNFQGAWAEWPVGRQGDNQLYHF
ANHNFTLVATVSIHKVPQEGPIPLMGAKMNEDGKTVLLGLSYNKEGKWQLLCGGTVTKDL
SSTWESQTQYQLAIVLQNGNQSSAYVDGQRVGDAQCNLENTDSKGISHFYIGGD*
>TCRU_6434 hypothetical protein, conserved
MRLLPTLRHACTRPADHKAPPVSVVPSLPDCGDRPAAASAGTSSRREHRNSLSTSERRID
VLLPNLRQSAFFCQQYDGTCPTFSAWRSDSLRRPHMRMSQWRRRLPNRRLKRRSSPKIQA
CQQARHAGSTNAGTRDGPGSYATASSQTPRAADPRRTTGDSASSTVVMPRH*
>TCRU_6435 Mucin-like glycoprotein, putative

MMTCRLLCTLLVLALCCCPSVCAAESTEQPEVKAAVAASPHSPSSVTLTQGKGEPGSPSN
GSGAELGITAVEGPASTAADPELVGVSNTLQNHDTDGNPGPEIGTRQSAEEANQEAEDPA
ETTTTTTTTKTPTTITTTTTQAPTTNTEAPTTMTTTHAPSRLREVDGSLISSAWVCAPLL
LAASALAYTTVG*
>TCRU_6436 hypothetical protein, conserved
MVALPFHISQYLSALWDEAAALLDVDAPFYGQLSWRMCTGEFRLSSGICGSCGIDSPPHG
PRMLSGSSPHHREGLGGRPRDGKTAVCGAVRGKGSCLDLRYPNQRAAEERGSAGPMCGQE
VAPTGEQEVLAKRCEAIGVSFSRETKSVALRHVAKTRIEGGRVSPKACS*
>TCRU_6437 Protein of unknown function (DUF1479), putative
MPPNYLPMPTDVRATIRDTKRMLREHLPTYKEVFDEIEEFISAQVEIIKKEQAAGIASVP
EVQAQDIFDGSVSESLKNKIRQRGCAVIHGVFPRDVASKWNEDVKAYLDENNFEERLNHA
AVDKYFSELAKGKPQIYGVYWSKPQVEARQSERMKAVQVFMNSFWKSESNGKQHFDPKNI
VTYADRLRRRPPHSPPLGLSPHVDSGTIERWLDYKFRHVYRNVFSGNWEAHNPYDAEGRT
EVREIKSPAMCSAFRTFQGWTALSPQRKNGGTLRLVPIINAIPYMLLRSLQDDVPEDDFC
GAQPGRALGLSPEWHGLLLEAECPIPEMEPGDCVFWHCDLVHSVEAEHEGEFDSNVIYIA
CVPRCAKNVEYARAQWEAFLRGGSPPDFAADDFEVNFKGRARPEDLTPIGRAQMDPSYLA
SNKL*
>TCRU_6438 deoxyhypusine synthase, putative
MAELAQKAVLIQSSDTNFQFHALGTVSGPAGDQLQSIAASLEHYAALGFQASHFSQAVAI
CKRMLQPQLPSVAVKQLTGSNDANGKDASLTQVLVQPTIFLGATANLFGTGCREAIRFLC
KESVSLPHGVLPAVMPDEMSMPSCDIDDETIPLNPPFYSNALIHALVVSGGAMEHDIRRA
CEPYRITNYGGFDGTPSHQQRQESATAGEDVARFGNISYGGSGTGPTSSIFTSVMRRLVS
RLQAAQKRRKDASTAKPIPAAHDDVCEWAFSPSTVWYMTGRWLPELFTEVLRERSGGNME
AVAEEAQRRAESTVLYWASMNGVPIFSPSFSDGDIMKFILDTEDLTTAKLKLDLVVDIYR
LNKFAMRSQRSGMIILGGGVVKHHVCNANLMRNGADGAVFINNGQEFDGSDSGARPDEAV
SWGKIRLDGESVKVYAEVSLVFPLLVAQVFLPFLRAARGVSPAEESEFL*
>TCRU_6439 ATPase family associated with various cellular activities
(AAA), putative
MGGERLVGHMHAWGSFPLSTATTVFNVLQALTNNTSISGGGNPHPHGVLLDAAMAILFLA
LGKYVHRFLTETWPRWNLAQLRKLLSLDTAEDAAAVDVFINQPEEFVFDNELLVLALERY
VSHLLHSGNQARQGDSIRENASNKSPANLSSRLFYEAEYCYGPIALLKSSHRMSAAEMLR
KHYFLFTLPADGDPTEVEPGLTIWFQKQLVNVSALREGRILPRRGGKPVMEAFIPLNFDA
SPVVNAFTDIRTAAENAVSNVRGTDNEVGGRDDDSESLSEEDDDSSTKSAWQNMKKVFVH
QAILQCTDKSKKGKERIMDFARRAYAWYTKNAVEPVERYYFLSSTSELHRALGLCPKLPS
GALQRWPMRQFVLPSAGFSFRNLFFEQKAQLLALLEEFKQKQGKFALPGVAHQLVILLHG
MPGTGKSAIVRNIASFLDRHIVALPIEHIQTDSALRGVLSGAVVITEEAVWKKETRGGSM
RYEGSAYLLSQSQRLDVSKVVYLFEDVEAISDLLSFQLPVKHQQLLSDPKDADEGKEGVE
EMEMKVRTKREETTTENVSHNKAGNSSSKKQNKLRKKTPDLGVAADSTEKCGQLLVADFL
SPEGVLTALNATLAPPGRVIVFTTSHPEKLPALFWKPGVVTLTVRLGILNASSAMDLVNR
YCGASFTPSLRKRLEVLFARCEANAVAEVMNPASLLHVLTICDDAEEVLRELERFC*
>TCRU_6440 eukaryotic translation initiation factor 5, putative
MSVPMIPIDPDKRDDLYYRYKMPTIQTKVEGSGNGIKTVFPNIHDVCLAINRPEEVLMKF
FQSEIGAQRTVLEKDDKFLIMGSHTEERVQEKIYDFIRKFVLCRSCRNPETQLFVERNKK
DVPHISMSCGACGKVMKLSDLDARYVTAIVTYFAKNPQVAMKKGAGTAEARSSQKNQQAA
AAAAAAAVAPPAEPEKKQIQRSDLEDTREPPQKILARCMQQYPDESEEVMRRCIELMTTY
NLKEKMGPLLVLDGIELAEKEFMAGLRRHSRLLKRFCRVTGTALLDAATDEATKSDLLRR
EKRLQSATIEESARICARRFEPEQMVVILFVLFIEGVLKSATIEEWCGDEKPISKVDPAV
DKKMKQAAAPLVEWLVGST*
>TCRU_6441 RNA polymerase IIA largest subunit, putative
MPGEGAAAPLLLPQQFVEPLPNAPVEIRALHYGLLSRSDIHRLSVLPCRRVIGAVKEYGV
NDPRLGVCDRVSFCATCGLRSIDCVGHPGHIDLETPVFHLGFFTTILRICRTICKRCSHL
LLDDAEIEYYKRRLSSTKLEPLQRAALVKTIQREAYKTRVCLKCGGLNGDVRRVRPLRLV
HEKYRVEPRRGEESVEGVETFFDYELRAACAYNKVVEESKENVHEFLDPARVRQMFLAVP
PDEVLLLGLLPGTSPVDLLVTTLLVPPVSVRPRGSSGTANIRDDDLTGQYNDILISSDTL

QDGSIDASKYTETWEMLQMRAARLLDSALPGFPPHMRTADVKSYAQRLKGKHGRFRGNLS
GKRVDFSGRSVISPDPNLDVDELAVPLRVARVLTYPQRVFKSNLELMRRLVRNGPNVHPG
AVAVYLAQEGSKKSLNHERDRESLSARLSIGDVVERHVMNGDVVLFNRQPSLHRISMMAH
RARVLPFRTFRFNECCCAPYNADFDGDEMNVHLVQTEEARAEAFELMSTAKNIINAKNGE
PIIACTQDFLVAAYLVTSRDVFFDRSQMSWMVSHWLGPVTQFRLPIPTILKPTELWTGKQ
VFELILRPSPEVNVLLNLEAATKFYTKKGRHDCAAEGYVAFLDSRFISGRLDKKLLGGGA
KDGLFARLHTLSGGGYTARIMSRIAQFTSRYLTNYGFSLGLGDVAPTPLLNEQKAAVLAR
SFATCDSLIESAKTGRMEPLPGLTVRQSLEARLNAELSKVRDECGTAAVETLSVDTNTPL
MMVQSGSKGSALNIAQMMACVGQQTVSGKRILNAFQDRSLPHFYRFEEAPSARGFVANSF
YSGLTPTEFFFHTMAGREGLVDTAVKTAETGYIYRRLMKAMENLSVRYDGTARNTRGDVV
QFRFGEDGLDPQLMEGVGGTPLNLDQEWLSARAAYARWIVERCNTLNDASRNDNHTDGSS
RRDRRRNERDVKKTFDPDDDDEFISLLPTEVPAFVMACLSGDSGALEVCERLERLDEEKN
VNVREMDGKSSDEGMRQQERTRRAGLISRLASMSSSKFKEDVANFFQKKVKEQKRIRALL
EISSTSREGKSRKTLCNSLQTAHVENHAELRILEKLQTELLPLTYGMITRFLAQCASKYI
LKACEPGTPCGAIAAQSVGEPSTQMTLRTFHFAGVASMSITQGVPRLVEIINANRNIATP
VVTAPVRRHRRGKSLSIKQEVVGESCEEDSQEEFEKRVRRVKSQVERVLLKEVASEIVEV
CTSTEFYLRVHLNMSLIAKLWLPINAITVRQRILAAAARPMSPLRLLREECVEVVSLDTL
AVRPYFLEAHRVHFNLRHVLALLPDVVVGGIAGINRAMISSNGAEVLAEGAELRAVMNLP
EVESTRVVCNHVAVVERVLGIEAARQVIVNEIQGILKAYSLSIDIRHIYLLADLMTQRGV
VLGITRYGIQKMNFNVLTMASFERTTDHLYNAAATQRVDENLSVSESIIIGKPVPLGTTS
FSLLLDCCEAGARSLQFAGSRTRRGTGRSFHHVRRPRTLLLAAEDTFHLDLF*
>TCRU_6442 Conserved oligomeric complex COG6, putative
MVEEMTVTAPAAATTGGERAVNAHSSGAIPHVESTTTTTTTRNGGDPAGAAGGFAAEGHL
SVTRNFTTSRKVQKLLDITVNDNFRELVLYMNDAVPDFLEKFLPPLPDVSTTEGEKFVLQ
KRLPQQQQQQHHIASISSSTALRTALEGRVVDLHRYFLQEWSALNEVFEEVSEMVSRVHQ
ESELLENTLNSHAALTKDFVALMTTLQVELSLVQQREKEMQEFQKKYHFSAEEQKILEES
PVDVTYLDVLQRAQTTHRKCRELLLSREYYQSAGSMMDITYSAIMKGTEKVARYLVSTSA
VMPGAAGFGSDSPEMTSFCLRCVTFLRDENLSQWAAVVEEVARLRRAAVLRQYFHLMTTG
SATTSAGTYRAGGKSNETSNNSGGTRPLEAEIGNPIFFFSSLFAWLHQVIVDEEDFMGAF
FPPAPPQGTSTTAPKSGNSALTATSGGPVHAEKDTSETHPNKDDNLAQEEVLGHAENFGL
PVNKLSVLGSIFEVLCKHIQSVLDGVLERFLRHASSLQDGDTPNVGGVSTGGGVGGGGVL
SSPAGPIGLTGGITRLLSAATGRVSSLTPNSAGGAQRYQHVLNRSQQEALVAATLMGLTN
GLRTAHALLQLFTYYGHSTFIALLGREAALTRLVVDDAKLQLLRVYHTLAKQILEHALDS
VASVVSRCTVLRRLASTEAMTSTEEEKKDGDASACFVTNFLFEYASGEDLDVDVVAPHDD
YSKSQLFQDQQRQHSSIAGTSITSTGSRSLTSNPYHLIGLSKRQAQAADLLRVLYSMVLP
TPPEVESCLRVLQSTMVEAEKHVEIMESVRTMLSKSSTHVDSTSADFSVHHEQFFTVLVQ
HILSFSLVLARQPTVKNALDEPCRLALQLNTISSLQETLAPHPGLLALANASAGHTTPIL
NVVPERVQQITKQLTAVLSQCALRHYFCRRPQNSLTPVVAGGDDLASSCSITSVAAREAF
DVNCEKMDVSTICAQLNAFYSIVAASGRVYIPIVAAVRSPRIREQVSQGVLRTLCDVYEL
RYKRLLELQKQPSSEGSEVTGATLPMPVTDLDPKKLRILLEVAPSSSVSF*
>TCRU_6443 hypothetical protein, conserved
MVFYAFVLVMKPRQRRFTSQALREIAVAIYNNGGLIRKLSNEGVMRPYSRFRDADNTPLT
YARYVTLQLDMGEEQMRNVEKIMKEHQDVFITLNLNNLERPVGIRRGRKDLQSAYFPLDT
FTRLEEEINWPPQTSADIYKQLEMNWKEFSRTRWSNFLRN*
>TCRU_6444 hypothetical protein, conserved
MVATPAPVRGPASMLTEKQLTTLLSIEGDVQLKAAQLSMLCCEYRTNLTRILLHYEPLMA
PLRSVTFAGLQKVKYIETQLTWLERVIVLQERRGGSKMLPPRELQAIENDLMINVRKEMQ
ESYQQLDVTTKEELAVLRNYEFPPKQALVTMAMAMRVRGEEDTRWSNVQVVLSDNYFFTF
FISRAQALLLRPLADDLLEELEVYCSSPDHAPESLALVSVPLAAIGRWLWAVRDHYRVKK
IVSLPDPPMTVDERRQMVKRLRNELQIIKENMSSASDELNKLQEQAVRRTVEVRNEYDDT
MCPLHDSFEKKTAEFIKVLEGKDVAAEEKANEPRQEEAEEVEL*
>TCRU_6445 hypothetical protein, conserved
MPGARSAVATATVSTFTTTADVFEADIVRLVRLHHIHTVELLSAAEETHVGEAASFSPSL
PALIVVEARLTSTLTWQPDLRNRFQCEKNSKGDGSVFTYHITFLHPTDAVPEASPSLSFN

LPRNSLSARWCTELQRRLAVCSALTGFPTRLCVSLLPYVPNLIWDRGRDGLLGATHSTTM
MSSPAEGSVVYSDGDFAAEQLVRVAILLNANIPLGPRGGRNTAVLLLHATDGDICSLTPS
SFSRLLTSEEGRKRRRQSTLKSERLKTDRLVEKESFFPLLSRFSEAYILPRISWEAVWSR
PMQMEKDSSHDVCGLREQLGSSFYLEGSLDARSAQSITVIVDAPFELWCRAVYGDTLIGS
SVDNGFLQGFPSCVAKTVMGALSRLAAENIDCFRRRLTSMSGGVEGVTDEEEGEEEGAST
LSAAAVSNPVHQSWSLLAQSIADSLAHIVRTSRNRVFVAEVHRLLANHQGDEKPQTACSD
AKGNPAVDLGSGAECSPPPLAKTIALLRWAVETRLMEQ*
>TCRU_6446 40S ribosomal protein S25, putative
MPPKKNAKPTKPAPKKGKMENMNKGAKKAAKKWSKGRTREALQNAVVFDKETMDKLLSEV
PKYKVITPSIISDRLKISVALAAKGLQHLCRQKLIKLVSCSSKFRLYSRV*
>TCRU_6447 hypothetical protein
MERTRSRPPQDAQRVFLRELLGDFSAAKTGTEMPAKQSPSLSLQLESNAMPLKKSNSPSV
STQEGCGLSPPALFSRRPQLNDGQQDPVLLSGANYSPRISLDVAKGPQDLRQRRYNDVSS
VQPVEEVVLPNVQLAPHMPKTPPKSTATLSPQHSFSLSSMTLQGAGNGRRIFKRFGMHTV
CDMRADDAGSSEGTGGISKKSSNGLTPNVMEESIIAPYVRPWLRPQQLSSFSSPTNGLEE
MALMNLKSMPLRENTRDASLDKRSKPRSMDENKLRYNCPNYRAENEGDARVVELPRTDSS
HYIRSYALTSTRTTVNATENPNEEQNLLERQQSARGTVAESFVTTPGRKSSAMLTRTLSE
LRSKSKRGSTVVSSPGLHCSVQDLPTTGKGQGSLLKRNSSFTCDSRINCEKWDGNISPNG
SSSSCSNSSDKKNSDDANCRSSSLRSCVNNSKRGKVPVNGGRLEKYSPDFNAAGCAYCVT
YNNFFEEGDIPSLSVESFRRSSDLSGKVIRGLGARSNSPL*
>TCRU_6448 WD domain, G-beta repeat, putative
MLSAKRSSDSVARQSGTLVEATDPLNLQPFRPSLVLTFRGHRSGVLAAGFQPSASSLLER
RGDTSDVIPTYAFSSGADGLVFLWSAKPTVRALRFTGHRGPVYDCAWSPHAHLIASAGHD
GFVRLWLPSLRRSGGLTAPFTNDNSPENCCHWRAHGGPVRSIAIAPHDDHLYTAGDDKSV
KCWDLNYASSATCVKGGGNKFVCGFTGGHQNWVRTVAVSGGGAHDNGVLPTHISLVASGG
DDRTVQVWDPRSRRPTHTFYEHTGSVRSVDFHPDGCSLATGSADHTINVFDLRRNQLLQH
YDAHDGGVNEVCFAPTGSWLLSASADGAVKMWDLKEGYLYCTLNAHEGAVSTARFSDDGT
CFTTAGQDGIVMVWRSGLPRVSPAYANYPNIHLYAPESVRGGPQISKRPVETTRVAASTS
NPAGIIPETTPRDVPGFSGLCSLMESSENREHVSPSSLPNQSSTQALSKPQRHMPSSIVH
SQFSSSSSSRKPPLFQPSSRPAATPAAAAVASSYSEDNVRTRSEREVDNRNHHHHHQQWT
THDEQESEVRKSLAFTREEGERRYPLSKPPQLSDDEEEDNKERRGKGKAGEKGSYQKSNA
SELPPMESVRGRDCGAAARSSEIDDEMSVVEYVGRTCDEEYEEYCTNGSAPSNCHVVSSP
SHRRQVEQRTNDRLSHLEETCARLAAEVQLAHEHSVVLTQELQKQWDAQQQQQRNQIEQL
RQMMEGFVAQQGALLQALRRE*
>TCRU_6449 hypothetical protein, conserved
MDRSLFKRAVVDSEEPTPGYIYREMAQWTFKDYNTQMKFIDALFDKLKPNTGVHALYKVL
RIIKTMCETGHSDFQRELKKNSRTETLKTFANYRGKPDLKYGDSLNEKVRQSAREAIEAI
FTNRKEGQQIEMGYGNNGNGKGSTTTGQSSFTTGYAVTRGMVERPMGMYGGNIAPMPMTN
KWAEHMAKQMMDANTSKTRRVLSSLSEKAKSGFGLLYNTEPNMMYKSAKDQLYENALRLS
TTGASVVSSSEVDAGGFQPVELGTNVPFPLSRGSGSGDFKFVENVQKDEEKPTSSEKNEG
NSHSQFLPPQQQLTPFQATVQRLCQMKSTPQRVELHAFVEECRRIGTEMIQGRGAYEEKG
ELEECWEELAEALDSQLAQKHPWQRRLNALVALEALLQPHVDDAETAATMRQGVLRYFLE
NPEDVQRNVFVVQATLRERAQRVLGILGLPGTDVSGGAFVAPSTGGASTLLPFTEAQQFK
SEGSTTQSFLWSAPVSTVKTTAAESEVAGSAMVNMSGMSVRVGHRSAKDKTTLRKRAPMS
LHEESQKSTDKNSFVDNSHTGNMGKEASSFGFLKASPVMSSNGNGHKTAGAGNALDDLFG
GPATDKSTTALEFYRTKTPPLSHAFTDTGTVNTQNSNATAFDFLMEDRPRDAAQFTSPPI
QQQQREPSFPFLAKQDAPTAHTNSTSAERPLSPLFGATSTAGESGMVQSERGGIVLPNDF
SALSLPLSSADNNSLPAMLLETQQQLQAFMSNMQNNPNPERLSQLQLLLAQQQQLMALYS
QQQQQEQHGPWIASSSDPACSFNMDSTPLHTHFAMGMSPSSASLSTIKPNTFAKIQEEMM
AKLAATGLQ*
>TCRU_6450 Voltage-dependent calcium channel subunit, putative
MSGVPPAYPVDSNIGVPNAHTQQRLPASGSQSNTSSRVIIGGVAPPTSTGRPHLPLPLPP
VKGAASQPPLTGTGSVPAPGHPPMGRLTPLQHRTLDGAEAQPGARPSPPPRLPMNSSTTQ
PTEASGAAENGDGQSSAAGGLPTFHAPINPLSPISQQEQLRQQRQHTPSRKTTDRAGTSS

ARSRKTMTPASQQGTRPQSAISGEETVEVLCPLPTQTRPVERFFVEFNPGAIVGNGRDDN
AMYEEALLFDRLAEYTEDDSFFSSGSSVLEEDPRRLQKDIFRERAVRSVYDTLNLRALTG
GRTPQELEDKNRENAGWMYQVHRRAIALHHSSFFVFPAGMKARVVTYNVLHHWLMELMIL
LIILGYSIFTASWSRYGAPEFEKPDFMVFADFLYTILYGIEIIARLFASGCILHSRAYFR
SPWHWLDTAVFVLMIMNCTQWRDLWNFTAFRLIRIIKACTYLPLPIRMKIIAKSVLRSTC
KLFQTSIILVYALFFFALLGLQLFRGVLHYRCVNSLTGAATSQLCRPEATGHYWFYWGHV
CDPGYICISDGFPNPNYDFRSFDDVGHALLSTFQIMTFQGWTSLLQETNDAVTTLAFLYY
FFTILLCAWLIPGLFIGVFIEKIEKTSRLFEQKQLELFDAMLLEQRQRLTEAIKLRDFVE
RDECGRLRGHLAEAAPEDTSYPTLRVNSASSNGKFPESGSFNSRNSERNTSVVTGSSGTA
KKRTKWTDEQRVQLHLSLTRQRDIAEQGERRRRVIFKVDKKETDHTNGNFEMSSVSTNTT
NNMGGGDFALGGRVGTVQHHPLTYTIGAAHGTRLPLAVRLENEQERLQFLKYYQQAEEAD
DTTLQGGLTRGSRGVDGSTNNNMNSSHLSHSHPMRRGVGHGDEMGSDIITIRESAGVIPN
RRSATKRGNTSGASTSLRTSTAAAAALNGSAGGVAQSQEILIHDPEGGDFRYAKTFGQSW
GIIRNILHMFTEGCPRILTQYLWEHRRMQTRFGLLPLNYVNKYEEAALRKLRQKRARRGK
LILKNNRIEDDGTDDYSEPEEPANEDQEYLGKLSPIRMAKNIVENAPVTLFSGIMLFLVF
ANGVFNASRHYGQPVYWEDGLFIAGVCFTSLFMLELIIRFIVLGPGPFVCDFINVICVIV
TVIGFFELGFGHSNTITVLNWVRFLRLFRIAPFAPMRRVTRVFLLGFQDIVYALILFPVY
MFMWILTGMSFFGGRFGRLTTQNDDYATIGFFDTFSHATFAVAQAFSYVRDEWLYLSWDG
MRVRGGYTIIYFLAVVFVAFIFRYLFIAVFAWAWQQQEEREDYVLHTTSKGGHQNRGGPR
LHWFDFTVWRSFKHIHGGFERRDVAPDEVFHLNQDMRRQLRIAEAKERFTRESMTRRGFS
ADPQTIFSDSFSTNGNVASYGMPSSAPPLMLAPQFVNVGGQLQRQMSMPSTFDELPPHPV
QAPISRFQAENAQLRFARRYSAVPATPYRGVAEELNGAHFLPVTSTPSDQALHNSNGSVA
DTATETEGLSHQIGGRASGLYGVHGSSNLPNEHHSSVTGYFTTLGYDKSGEKKNGEAMEN
YQQSSENEENGDPENSVVDGGGGGGSGGVVYEHVLLPGPRLRYKHIMVGRHRRVFERCLD
CNVHKQIPLRAPPNVQQRTADELHAEHCHMAAVRSSRQLVLNTIIGYVRLQKELGGPPTR
EAVETVLGQAWSCGMLLFESIEYLSCADIELREYRTWDRTLEALQLQQWLIGLHLGEEQV
GRATLAYILAHQKTQERVATHSSFHRSWRDRSFFIFSPSHPARRFLTAIVESKWFEWFIL
AVIFAASICLCFYSPEDEDRTSKKYLALHILDDIFAIIFAVEMVLKWISMGVVLDCHVAY
FWHRWNTFDCFITIISLIAIAPKYSHFRFLKVMRCFRILGPMRYCRFNKELSKLALTMWD
SVPTLVNVLLLFLLNYIVWSILALRLFMGLTHSCTSHAFSNKTSCEEAGAMWLGPQRNFD
NFYESLLTMFEVSTGSRWLDVIYTGVDGWSMEFEPIYNRHPSKGLFFVAYYYISHFVLFS
LFVASLIYCYLLAKNAAEGVTDITFEHQLWLRMQRMILRLTPRVELVPLGNCLSRFLHRI
VIHPAFELVMAGILLCNMITMSLYWYGNSSRQEKALDILEHLWVAFFTLEILMKLTAHGL
RAFSRYSFCFQVFVTSLSYLQIGLNTTVGNHVPFNVNTLRLLHLGRMLKLVDFLVPVRHH
LHLLHEALLLSASSLVNVTLILALAVFVFAVLGMHFIGPVVPVAGQYIDDTYNNFRTFPN
ALMMIFRLATLEDWVSMLRSSMSDGNNCPISDCKTTNWAPVFYVPIVICFALMIVNLYLA
VVVDHYVTVVRMKASVARINDLRRFRDLWSARDPNATLLLRTRKLPELLEALRPPLGLSS
RKNRAELLRLLREYDIPDHGGKVHYYEVLLPLARRVLAMAFSEDEIDDGVKFEAVWRLSE
SSLRALPTVLVHHSSATAAQHFAASYVQAAYRRDKACRKLHEMRANCWREARRICDELGL
PYKDYGFGDVSLEDEDPRNEAARRGLLNESTNEEKKQKNAADVTAAAAFAAAGRSESMTT
DSNESSGKPAPAARLPGLYQPAIDEKEKRFGPDVPHAVRRHETRSDKLRRKEEERQQQQQ
QDPMDRQPSVPPAPRSTAQRNQSIDYQPPLGTDPSEWLQNEMGRRMSGAGAGTLSSANHT
GAGGGASPTKATAPPSSEGLDGNV*
>TCRU_6451 enolase
MTIQKVHGREILDSRGNPTVEVEVTTELGVFRSAVPSGASTGIHEACELRDDDKRRYLGK
GCLNAVKNVNDVLAPALVGKDELQQSTLDKLMRDLDGTPNKSKLGANAILGCSMAISKAA
AARKGVPLYRYLAELAGTKEVRLPVPCFNVINGGKHAGNALPFQEFMIAPVKAGSFNEAL
RMGAEVYHSLKSIIKKKYGQDAVNVGDEGGFAPPITDINEPLPILMEAIEQAGHKGRFAI
CMDSAASETYDENKKQYNLTFKSPEATWVTAKQLAETYAKWVSEYPIVSLEDPYDQDDFD
GFAGITETLKGKAQVVGDDLTVTNVSRIKMAIEKKACNSLLLKINQIGTITEAIEASKFC
MSNGWSVMVSHRSGETEDTYIADLVVGLGTGQIKTGAPCRGERTAKLNQLLRIEEELGAH
AKFGFPAWS*
>TCRU_subunit, putative importin beta.1
MSSLTELLLALGNVDPSVRVPAEQQMNQARQSDLSGFLFALLEEFCEESKPPFARHMAGT

LLKNSIAPNIRETAARRALEKEWMALAPEVRVRVKQGVLLALGSPQKEVRNVAANIVGNL
SRIELPAGEWPDLLNILLGAAESNNEQHQEAALTAVGYVCEEGREYDTVEAALVPFTNRI
LSAVIHGMSGGHEDVCYYATNALCNAMEFIHDNMNQQEQRDRLVDALCSTAKTSQSSRTR
EKAMETLVKVADMYYSTLPNYIEILHAITTNAIFHDEEPVGLQAMLFWISICETEQDMKT
DGDGRCLDYALKGASMITNIALQALLQQEEHQEEGDWNISIAGGKLLQSLALCIGDPVVE
LVMPFVYSKVESSNWREKEAAVMAFGCILNGPQANTIQDTVAQSLPGLLQYVRDEHPMLA
DTSGWVLAVVCELFSDVFLKQPAYLQQLINIITPMISSGGDMAVRACHILHNLGLFYSEE
EDQDNNELSVYFPDLLNVLLVAIDNGGNQNIKSVAQEALNVLIDAAAIDCCEYLHVLVPE
LQNRMRLMMQLQMQGQISNADAMTMLGLLCGSLGSVAKKVQAGFSGHIRSSMEVLFEILQ
NQSDTVLDEALTMLGSFAHAVKRLLGPYMPNLVPFLLKALMRVDEPDLAVVAVGALGDLS
LCLREDIAPYIDAFLRVIHQNLQNPEVDRNLKCTFLNCLGDIALNVGDSHFAQYLDTFMQ
IARAFYEQSATLNIAEDQENEEYVMTLWESIAVFYTSVCQSFKSVETQLEPYLQQMLLFA
LNASQTAMSLDYVEVFAAAVSLIGDMACVLKGVSSPQLRDQGKSALLAAPVWEVVGRAVN
MENDAETKGQMNWVKKQLELLQAS*
>TCRU_interacting protein splicing factor PTS.1
MEAIPPEYDKETKERIYRQEWLEYFNFIGWDAAMRDHPEQFYAIFPNNSGGSSFAANNGS
GGGPDAMLAHDMLGALGPPPFSGGQQQHHHNHHRPVAGATYNNSVLAAPSITTAAAAAQM
FLDDSGSSTGSDRSSSSSLSSFTGSSSSASVASARPQQRHRRDVGDAEGDGRKRKTSSHR
RRRSRSGSNNSRHRTHRRHKSHRRSPRRDETSRKRRDEEPSGRRKRERGDEKEARRHQRR
PRGSHHPEEDEERRRRHRRHEDSSYHRQLSDRERERERRSERGHGRERTTAANVSSVSND
AYRGRYVLKEERERRRGRGGGIGSSGLGNTDRYEDRREDARQRRQREMEGRRKR*
>TCRU_6454 hypothetical protein
MGNCCGLRKASLDKVATTGRKRSGLEKYQKSSLKLKAQDVEKPFSKSPHGSLYNSADPEE
RGDKFALAPLPPLKMNNDEGEDRKKVAGEKNKETRSPAIALDTGTENQREVANCEELGEA
DIYSNPEEVRDNAVEELPHSSSPVIDCDPIQPGKFITSFKKVSLALNDKHASESGSIGSS
PDEAQEEEYSEKTETGFTSSVVVTVPPPSPPMRLRRSDSDSEDEGEDDESAADKEARDGH
EGLVSSTIVLPTVVAPKTLWATDEKPSHTPSNQQSDGEGPKSITNPVLEANEEQKDAPSD
DSAKNKKPEAVQPDIVITNKSCSDDSSSIGGGDGCSSGGNALANIVRQSLKREQQQVVAR
ATGQVGGECTLNAHGNVVEYDLVFTDDQIVDGEDAGDNYLWDGDAEANGKGTPDATAHRE
PPMKIVTWSDEEDNGRGGGWVDARTKQENTGASAPNKGVNAVECVDSGSSDDDGDGKSLV
TVLYRSQPGREDGEKELEKNEAKMLPYDGFVVAKRKIQLVAVGKNSFLQDHSPVFVAEEA
LPPVRFRPAMIISPPPVTPNDRDANDKENGHLLF*
>TCRU_6455 Soluble NSF attachment protein, SNAP, putative
MAAGSAEEAVALMKSAEKHSQKKFFKRPDWDTAASEYERAARIYTYLEDTNRATDAWRKA
SGAYQNAENNFFAARAMESLAVFLTEQSRKGMADDTSLLNNAVEAYCDASKLYAFNEMFD
RQADCLKKAAQIINPTKTIVTGLPATEAGSSQVKKRMQQVVGLFREGVSVLEEHIEDKPV
VAVQLPELYRNWMLTHLHSGDVKGAVEVLEEQLGIRADPHKKGVFEWLAQPHNSAKAGLE
IIVLCLSCGDDVWARQEMNKLRGVPGFSTSKEEATANALISSFEERDEEQLRAAIKNQTL
QFITIDISRMSRKLKIQFSAPQRTNMTSSSLPNPSLPNVQQQGEEQQEADIDPEEDIR*
>TCRU_6456 hypothetical protein, conserved
MRAVRDEEKRHTAEVPAPLRICEIGSEVLVTALTKQQLQSPKCRSDNAELTVSCAISEVL
NSGVQSSRPTLDAHLYLRRRVSEIVHQIRGASSAHHFYRHVVEIDELLRCDAPMGFTPSM
VLAGVPDILYLLSDAVKKGYLPYPMESSTSTVRALAPVRRGPVATETIRRGLNAVPPATT
MGAAASSFTPPMEEIEERKKPRSCIASKSAARARGKNDTGGGEMAADDLLPFLPPLLHRS
ASPKPMAALPGSTEDEVAISAGTDGRRRPTVRLQSQQSKVRPCDKVARSRKRIGTRMSTT
SSAVVGATQSLTCLSLLPEKQQQQEQTERSEHELSHGSLAPHIPILRDIPSALQALLYHC
ALPLVCLTPEDQRQRATAVHTLASAMASMLRVKLEPVNANLSVYPTVTAEVNKSVDEVDH
NKGCEQKMNASEINFQEISLGIRRAALSSLNALMTHLDAEELTCVNQHFASRDKKRYETT
DAARLLHATSGGKRYQVGVTNGQAFENTSIPKNSQGPGSGSSMDQIIRSVDSYVKPPRES
SGKGRVQRTEPMSVYNGAVALDVFLPLLERWTIILRDDVPENALLDSSRLFYHHPALVQA
GGMEKREEEEEKNNMVVALTTAFDDGISPSLQRNSEGFFVFVSKTRMADVDAEEIYLLLR
VCFHLSTYKQHALYLIAPDKSSNATYTSLAVLLCLTMARCAEGDKCLSLCVEFLWNLLEV
VPEETVSAILQHGIQSEESKRYEKGRPLSSLSACESLLYCFIQILLTGYRIRQRELRNDM
VLLFTMILKTDTAVLIKKKETLQKSAGAAAYTPLPRSTIYAINAFATTIFDLVCGPELGV

NGKTAQMTQRPAETFLRYHTALSPTTRVENLQFRLLGWRMLETFHEWQKARLILEYLCCG
NACETRDVVVDDNANGHDGVGEQGNADDTLVFDVCRHGFINVLLLYVDLMCSEEAVVTWT
REELLTLQKEAWFVLLGLMESAVLSSLSFSHDDKERSNMSLLALPASAVNSMREEEVVAK
LPLVKADTQFIAAGGIQCALHYIRDVTTRDAEEMMCLAVGVLSVLSRHPEHRSKMLAATT
VTSPSTSSPTESDPLLLLVILHVIEKAFQRGSPVEVLPSTLALTKADTNSKRLMHSSNTH
HLGGIGSTRSGAGNGHSLMRRKGKSEHSQHRVETAMKPSFTVAESKIISESNGNGKHCCT
AFETDVVTQCLSLLSNVVVGKKSEISMTQQAFLSLGGVPLILSLVRNLLAAFCSNSFFSS
NGSGGRNELLLAVLGCFRAFILGNEVAQRQFVHEDGVHVLLSLIAVFVGWWQGNSMKIHD
ASAADDISLLAPTLTILADLLHESKEAQEAFLQWSTYNMQSPKDMEDSGCTNATQLLLRL
WEEEEEEENLAQITMDTPPKGFVNWGDNIEDNDPFNMGDSEKGVVTDVPEEKKKRLSNDR
AEPVAGRRDLLAKEVDKSYGDCNEPVVLPILHSDRWGLGLIGIHDRNSVKTELQNRHKEL
EDVDLEEVHSGTAPNAMTQRARRRLAASLHGVLGMHAKVYACLAAVGFVRLIHVKTSAVE
RVKLLHAAALPSLCEDEVWGAIAELVDLHNDAVVLPLQKDGNDQGDGETETPPRRDFLVN
PIIPDSYQLVKVLLDVEARATELKHLSKVCIHTHIAQWDEATQRFLLSRLRQGTESVNLT
TLVQQARTRDNPSSLGRTGSILDHVMSRVGQHETRHVEPLAASSSLPMGTVTGSGKFSTS
RLTLLEKRRKRDSMIRNSFRRSQFAGLEGKLPADKEM*

>TCRU_6457 Translation factor GUF1, mitochondrial, putative
MRVGCCLLLKPLRQRLCTASISSRHIMRWCATSSSNINSTETAAKMPDDDVSGSLSAPSL
LKYKIEPSTATMGAPRPPHDDDRAFCTLASFPPSHIRNVAVVAHVDHGKTTLSDAILRRT
GVLSGSQVGTYTDRLLVERERGITIKAQTCSIFVVWDGEEFLLNLIDTPGHVDFQYEVSR
SLSASDAALLLVDAAQGIEAQTMAHFHMALDRGLTILPVLTKMDAVLSDAPVDRALQDLE
DSTGLLRREVLFTSAKEQLGIEALLHAIIERVPPPTGLLGLSDLQQLPPLLPGSAERVAM
EEKMVPLRALLFDSWTSECGGGLRRPAPRGGEKVNSGNDNDRNLICLVRIIDGTLTAKTV
VTFYQSQRRCEALEVGIIHPELRPTAALTAGMVGYVVFSQVRGEEFLVGETLYTLPTRKF
ARENIVPVPGFRRVQPVVFAGFYPDEGEYITQLREAVEKLRVNEPAVTMEPLDCPALGSG
LQLGFLGMLHMQVFQERLLAEFGQRVLVTPPLVQYKYREAGSDEEEPLKPLTVHTWKWIH
EGAACYLEPYVTATIITRREHFQAIDGEALRRFRGEQLDMRVLDDARVLVRYKMPLADLA
RGFFAVVKSLSHGYASLDYGDPVYEEADLVKVDVLVQKSRISALSVICLRSEAPSIGKRI
VSSLKSNLTRTAVDIPLQAMVGSKIVARETVKAYRKDVTAKIHAGDISRKQKKWNDQKKG
KERMARRTVGAVTLDQSILAAAMGAISL*

>TCRU_6458 hypothetical protein, conserved
MQRLATARFLPVSTSLYFSRRAVSDEVGGEKKRKVNLDDDDRWLEAEFDEKIRTPEERYA
FQRQRELMKSIINKMRNEHDEKLGAAVAKHNEKIDAIKAQMASLEEKLKEISKED*

>TCRU_6459 hypothetical protein, conserved
MSGTSLADGSLRSSRETGDTTRIRRHGKNACRTESCRPLPLLSVLLGVSEGLVHRRLSAL
LARHRRQPRLTPRRTVSDVVTPVRDETARGLSERIAVECGRRRGGVPRCTLTVAALSQSR
PASRLRSTPLTMGECWLRPAASRACAVEPNTGCAATWEAAALG*

>TCRU_6460 hypothetical protein, conserved
MAQQRIQYTAGARGQDKRRVAKGQFKRIQREGPNHIPATRGHASTKCADSSGDRSKWDSD
DATDERVSLLPDFVGAYQRYTCRLRAVSDAQRQKLLRGGDVERSPSPIAALQMTVPSLTP
AKLATLMAQGADMIAIRETWKSSEQIASMHTGECVPHAQSRIRKECVAAVLVKKNHRSKR
MPLITPQRDSSLEVVVVQFALGQNRDLIVASTYMRPPPQPTQPLGGC*

>TCRU_6461 hypothetical protein, conserved
MCSQYGPLRNSSQRGRPIAVSVANSCLRVATTQKFSKPPSAVHPRNIGRQATEDSIASEL
KGLAGVYQHQRSPMGSAVELASSTALLGKVRLEVIGSVMLHFVYQVCQLHRRGTHTTARM
LVRTRRPQPKQSPQCHFLSNLTHDGGKADGSI*

>TCRU_6462 hypothetical protein, conserved
MGCCCCCGKKVLAGTEFDRGELDNEDDGTNCPLLLGVESAAGEEEKQNPPKALSPSEMTA
TTAAVTTSAQCVEPQKCGTCENELSDTIICSSTAVDDAFSDRFRLHRRVETAASWTWPEV
SMPTASVLYEHPRTISEFDTEEDFSQVEQSTGSLRERRLLFIARAREKAVIREMMLTESE
KRHAIIDFCNTGRRAMAFRLYRGILAIERRVMLIGYLTERAALLMRVTEAQEMIGRRLTE
NDWKTGLLDKMRQHRVGRRRSVAVSVESSGSNNNNGSSSSTEPVEASPAVFSEEEKALMP
GAVAAASTTTVGRSLSAPSSFWRRSLQQNRLRLSLSPSLPPRPYQRHSGNCPAHVTVAEV
IKPFQPEQKEVPHRQQRFGACHVTNRNASGTEKFMNCKSNTFSAAGVGAGGLH*

>TCRU_6463 Voltage gated chloride channel/CBS domain containing protein, putative
MAWKSRDNNMQQQQQRQPGEFTGIVNAPTESDWATIDWVSSQHEANERRTAMYHRSHGSS
ITAHTRNALTQNEGFLAAFVTGLLLGILGVFCDACSHWVSAFRLGICANFFWLGRNLCCV
EQEECTGYYTWGEFFLGRGDRVAPFADFCFYVLISTFAAMIASFFCKVYAPYAAGGGINE
VKTIVSGHHVRRYLGGLTLITKAIGMSFSTGSGLVVGKEGPFVHIGACAGGIIASVFPSY
RLEAKKRELITAGAAGGVAVAFGAPVGGVIFALEEISSFYNFKALMAALICGVTAVLFQS
RIDLWHTGRIVQFSVNYKHNWHFFQLPLFALLGVVGGFVGSLFNVVNIRIIRWRKLRFKM
WRVTEVAVVAAITAVFNFVTPYSSGNLLELLGDAFQDCTPQSTIELCHDGNVQTLIYLLI
AATVKLLLCMYTMGTFLPSGILVPSLAIGALYGRAFGIMCRALQESYASYYIFSECYDQD
LCVIPGMYAIVGAAAVLTGVTRMTICLAIIMFELTGSLDYLVPVIIGILCAKAAAEAVGV
EGTYELGIAENNLPFLDPKKECHVDAVAEDVYAQRQFTVLTAYGFTVGQLNQLLQEMDVS
GFPVVNTLSDMTLMGYAPTKNIVRAIQVAAAKDSRVHFDTAVRFSAAPSTNLREGQLEID
ITSVVESPMLQVEPECPVSRMLYFFKSLGVRHIMVCRRSRFVGYISKKDFVKFLREAERE
EHLRNM*
>TCRU_small nuclear ribonucleoprotein U5Cwc.1
MYNGIESVSVKGTGLSGYVQRSRAAISQLSKFTPVDYTDDVPTAAVNPLEALRSAKENRE
LAARLQRHEALRSIKLKVFLYREERTASGVAVDVVDRECQTLRDSLMRNYMEEVGEARRV
EKEAAQKTAEKFAAAFRVKQGAVGDAFDRAQREAERRAAEEERRRVMEQKIAERVKRIKG
EKERDGH*
>TCRU_6465 low molecular weight protein tyrosine phosphatase, putative
MASCSRGILIAGVTNRARTQMAEGILRHLTANTVFIKSGGVHHEATVHPLAVKVMQEIGI
DISGQSVSSLESARRQRDTYDGYISIDCGYDCRMTDKTQRPSAGLRGQVRDAPGINMDAA
SVKDDQGNYVVASSSCEEENVMGYGPMLVPSMPSHWEYGVDATDAQRHWKIWSPRDPSIF
HENSTRKFQDHLYEGEPLFMQLHTSFMRVRMKVSERWEMDEISTRYVLERRSEHEVRFLR
AREELLRRCAAFLSRLEKHYGESLLLDGEVLKKAPVVS*
>TCRU_6466 zinc finger protein family member, putative
MRHLQENIGRLQSCGFSKTKSTQALKDAGNNFDVALRILKKQQEQQKQRQRLQSNVARPP
DEKPAPDDSEMEMAIAPPKEKKHPCIVQYKKCRYGEFCLLRDLPGDVCINHFMGNCAFAD
SCKRRHHVDGVDIRAARRPEVREERITLQTGVIIKLDKVNGHHLLVGRPVERDAEPNADV
TGLVGEPPPPSRFNLIQGSEPTHTDPYPLGWQMQSTSCASVVQAPRPFLEAVRRQPSEQN
TTSSTLVQGPNGPSSALSSASKAATTAFSPSHKGKHPCIFQFGSCKYGKNCNHADRDEDV
CVLFLNGRCNRGSTCPYRHENNAEFLRRAKPQVFGKVLSDEIALGDTNMKPEEMQKNYGE
TLQIRQQHQQRKQEEGEQESWMQAPWERQQAMHLSSFLPDLGSDVDCCSGDGKRTPQDND
DGRLDDMELNALVALIEAFPATEPRLLLHALRSANGDVDLVADTMSKLDGFETVEDVVAY
LWKERTEEEASLEQTKTQSADESLLTLCSLFPALDVPSIAAVLGKCNGDYAEAYGILLCS
TENITQQAFGNCWNGSLKQSDEFRLQKVCKMFPAVPKEVVRSTFGAAGGDAEETISALNA
MTKEMLNLETETVPAFALAAASKKTTSGEPPSYFLRPTATRDEIQRFYEEVDDELRKLGD
WRRVREQAYIVNSCRIRVMSQATQAYKRGDGKTAKTLSRHGKQLGAEYVHLNRIAMIALE
RERLAKDPASTLDLHGFHVDEAVEVLRRRVKLCVQKGIRRLTIVIGSGRHSRCGHSTIYP
VVLRQLKEDPELERFVKLKSVKPAYIEVDIVLRDR*
>TCRU_6467 cyclophilin type peptidyl-prolyl cis-trans isomerase, putative
MSSTRHSFTVCGLINHPVFQKCSEAAEYLQKEYRDEFYVEIFREVPRDFYSRRKKMFDEK
SVADTNMDVFVLRDGGVAMSGEAFLQMLQEQTRFRLLPVPADDAHSYEKMAYASWKKFLQ
ERGNRYCWMSVSIDNVPCGRITFELYSQVVPKTCNNFWHLCHGDLGSVSVVPDGESEAQP
LELTYRGSTFFRILRGAWVMGGDISRDHNGNGGYSCYGRYFPNESYAIPHDAPGVIGMCN
DNEDTNASSFYITMKAMSWMNGRYVAFGRVIDGMNVVEAIHDVDVKHNQSPCKEITISDC
GVIDLTDD*
>TCRU_6468 hypothetical protein, conserved
MLGARRALFGFAGGFAITDMYVNSLCLSDIYTEPPSRASSTGTDFIGNIVKNVSGVFSMP
PPPLPLTSLREDIESALCRNRIAGTMCVCLLLSFGGLWPLIGSGAAVLFDGEDGTERYTA
VKRWLRQ*

>TCRU_6469 endo-beta-N-acetylglucosaminidase, putative
MRQSLVQLYCYDLSGGMAENMSKMLIGEQLDAIWHTAIVVYQKEFYFDGGTGIVHESPGK
TRFGQPRRVEVLGETTKTEAEFLMWTQQQRGSGFGPNDYSLLYRNCNHFTQEAARFLVNR
DIPDEIRNMIPKVLGTPLGRMLRPLLESVTAAGNSAPPSTLQGGAPPAAEEVGLHSTRTQ
LTEAEEEDLMVALAMLQSNEFLSSGSEEGFDITRGAIALLRTSLLNILEQPTEPKYRGLL
TTSQSYKTKLLPLEKFGVVEIFRLSGFRLRQHPSGTGQQWYLSDADGSEEILSIMIAYLN
ELMDAVDREAPVSVSVDKNPTCHEVPHDVQGIDPPEGVTEQDPGDTALQIIQHDAGQPLS
SLKELGDWSATKPGIITPAVACRRRVVGNPLKATRLLVCHDMRGGYNPSDYARFALCDAS
SSVNPVVDTSYTVSYWNLVDYFVYFSHHRVSIPPKEWINTAHREGVPMLGTFLTEWDASD
ICMMLDNVEEMDKVIYQLVEVCNAYNFDGYLINVENRLDPILACRLVPFLAKLLHALNKN
RPLSSSERTVFWYDAVTIKGKLRYQNGLTPENKPFFDVASGLFTNYGWRPGQLPVSAALA
GDRARAVYVGVDVFGRSNMYGGGGYDSGKAAECAENAKLSVALFAPGWTLEMEGNANRET
FLRADAKMWFGLQEIFERKCIEYDTLPVWSCFRSGVGKQFYLNGKRVVDGSTHVVEWCQL
SRTHFIPCYQFSLSSSEEHSWCVLPQKSDDGKLRSVLPVEWITDPVWMGDRSMRFNLPSA
SAVTLMRSKISLAGCSNINGVLAFVDAAWWRGSNEDKFFLPYLLIEGSFGDSTSQIVFDE
ENVPDGTGVVASVGGWYVFRYAIPARTNWSHITSISVLNNSPDHPLGCTLGGLGFLSSGE
REKTKSALLVGQPHRLSAEKFSVHLTKQPTVRVVELRLDEEEEEEEEEKLINFVLLANVV
TEDGASVRLYMGEHEKKPTLWVELRIAANVTVKELLLYPVSPGS*
>TCRU_6470 DEAD/DEAH box helicase/SNF2 family N-terminal domain/
Helicase conserved C-terminal domain containing protein, putative
MNDEELEELFSISHYTTITPTPTAKLRENDSINTIRIDSSRKKTASSAAIPLPETLPISP
EIELKLFDYQREGVQWLYERHRKGRGCLLADEMGLGKTVQIASFVGALYMSQLVTSTIIV
VPPTLLPIWGLALQQWGRLGPPVVEVIHNDAKNKRLQRWQRLKHGTPCLFLTTYGVLRQD
SSAMGVRMVDYVIMDEAHLIKDASTHVFQSAMALSARHRIAITGTPLMNNFEDLWSIFHF
IDGSILGTTRADFRSINAVLLRGNERDALENERGDAGRQLALIQAAIRPFMLRRDKRQLQ
MLRVGKRDLIIWLRLNDTQEQQYFSFLKTERVDVTLRSADTSQPLVLLTSLMRTCDHPWL
SLSDEAYREAMQNPLASPEANRSCGDALNSSKISSALALVVKCIGEQRKTLVFSRSKRLL
DLLAVALRCWLIDFARLDGDVPAEERLKTVQGFNQSERLLVCLLTTQVGGVGLTVEAASA
VIIMDPSWNPSSDAQAIDRVHRIGQTRDVVVYRLITCGTVEEKVYRNQVFKVMAAKQGTS
VREQTGRGSAEFYRYFTRLQLRSMFDVGTLDQSETAAQLESLHPNAVCPEERAALTSLPF
VCDVSDNSCVHVEAVVETERGSDTSLTMSASRRCGAKRRRPSSLSPSTSNECRHELLSQE
EMSEILLQLEEENTESQSTTVQLVLTSEDTTTVTASPVDNSEV*
>TCRU_6471 Right handed beta helix region/Periplasmic copper-binding
protein (NosD), putative
MGIRERLVAFYQKHNPAKLCEVDSLLEAFAGREETMFAALRMKYEESDVTDGVEATSRAR
NVNIEPGISETESNTVCAEMQDLLRDMESVDLRRLLDQLSGRAIVEGDLLVHAMRFMQHF
TTCAHRFQDLSGTILNRTATATQNTTAGAAVPLKRTAGESVATQTESTSPGRCDAAVHAV
RVETVSTGTQTDMDGERLRDVSFKDLNPTSNSHFLRAQMPPTECSSVRPNDEVRAAVAPA
ALKMDKQLNQHRSIGMVHKLKPDKHKRAAVIGALLTKGGLADTDSVTLEPGVYHENLCFL
NSGDVELVAVFPGAPVIIRPLSNLEPIIRAAGRKTRLRLSGVVLVENDTLGKMHVNVSAP
NCPLVAVADGAHVEFHGCHFYQGSCAVEAVGLQTDIRLHLSLISSCTFAGVFLRHGAKAV
MTQCKVTLCEAGVRVASKSSMHARETVLEENTTDGIVGYEGAEGTLERSSVLRNGGNGIF
LSPGSNFMVTESTVELNGLYGIQRLQSSVLRLRDSVVRDNGLLPINHTDEKVSL*
>TCRU_6472 Calmodulin-binding, putative
MSCNAARQNYLQIREQQQLNRERAREAEVEERRAQELIQRQKARYNHVSSHGYGQLRGGG
DDVEIKVFIRECEKGRAQEFSFMESDALRRRGDTKQPPKPQPEQLLPRVPVQPKKEQAPV
SAVNVPRGVVPKYIIQRKAELAAEKVAVLREMERQKEIAKYPPGHRPVTEEERKETLAKL
ASRRKELEYELHKIPIRYDTQSIKARRNRIESELKEIDESERKFSAAKQLFVPI*
>TCRU_6473 thioredoxin
MPVVDVYSVEQFREIVNEDLLTVAWFTAVWCGPCKTIERAMEKITFEFPTVRFAKVDADN
NSEIVSKCKVLQLPTFMLVKNGKLIGYVIGANLDTLKRKIREIISNR*
>TCRU_6474 N-acetyltransferase, putative
MSSFVSVPPHLYHLATGEEITIRHVLERSVYSNERSKVRELLLSSGAHSIPGLLEVASDP
SSSVIFIALKEDKYSERGFIGFVVVNTSFLAQQRVVAISWVYVLSRFRGINVGRSLLQHV

EAFSRVNCVDIIEAMLTDDCTRLFKRHGFRATSCPIVFKNKALQKRVVLHPVPSVPSCVT
SGALILRHARQESKKQWIFCVLEACGYNFGGCDLIRHIFAAEFRIEVVNEKDGRIVAILS
MDSTGWIPIIACTKEYQGRGLGSFLLFFAMEWMRRQGGNSVSLSPLNKSVAHFYKRWSFR
VLSKGSRKRGRCSDDHSVLIREIDPNGRYLPGGYSLEDFLSSSTPPTSSSAHQQEGEGAE
KKSS*
>TCRU_6475 pseudouridylate synthase, putative
MLRVIVRRLAWRPAAIQHLPDLGSKDAPKKTEDTQRQYRPLSLRARQALAEKSDEVQYHV
ITQDWFGQRVDTFLTQHHPEWSYEAMKTLVQQGHIYRYRKNGKKRFTRITDRLEFDELLV
VPTPVFYERQLAPPTGVLQESKKPTHFKLSSQVREMAHNMVLFKNEHVIVINKPHGVPMM
PTSDPQEMNIAAMLSAWKYTNSTKPIVCHNLDKETSGCVVLARSKNAHRMLARMFVKRVV
PNSVYWGFCVGKPSVNFGRIRMHFEMTRGTKGDIIVARPSPTKTSKVGIAEFVVNASALE
FGSFISFYPLTTRRHQERIMAAHALRSPLLGDAKYGGESAFPSSMSLFWDPEDKGLPLHL
HHRKIQLPYKNSTGEFVCVTAPLPIHMEKTFKKLGWPCDVDDPLIPG*
>TCRU_6476 hypothetical protein, conserved
MSYYDKSGSVGYDERDKELNEELEAMLARTPPHIQRHLQQRIHDGILQRMKEETTRKCWE
FVKKYEGCVNSVQPYNIRECLPHRDALNDCAHEINCEDNYQKYRLLYLHGELLKLHEHRT
GQKMEALKSRVPDSIRTWKSDYAPKYADMMSEVGAKPFTGEGENLDDE*
>TCRU_6477 acidocalcisomal exopolyphosphatase
MAAVINDFLRGGAGILAARKPFTLVLGNDGGDMDSIIGSIYLSLYLEKNADLGGGSYIPA
LNFEKEDLPLRNDVIKLFSKHGIATDYLLSVKGKPGISGFLDLKSSQPNVVLYDHNKLIP
EQRSLCERVVGVIDHHFDEKLYLDSSSQFRRIEPTGSACTLVAELFQEAELTVPCPELLL
APIVLDTVNFDPSQKKVTEKDIMLSQWLIKQASVLIDPKKMFLELSTWKNDILALTFPQH
FRRDYKDFEFSFGKNEDKQLQIGISSIACRFDEFLGSSGMMHLASNCLDFLLPKKLDAFL
LAFAGERGYKNYCRQLAFIARGILLEALKEFAESSPEGICFTIIDRAELKGWRLMCYDLS
DPSVSRKRLVPSLMKFFASWPKL*
>TCRU_6478 thioredoxin
MPVVDVYSVEQFREIVNEDLLTVAWFTAVWCGPCKTIERAMEKITFEFPTVRFAKVDADN
NSEIVSKCKVLQLPTFMLVKNGKLIGYVIGANLDTLKRKIREIISNR*
>TCRU_6479 Calmodulin-binding, putative
MSCNAARQNYLQIREQQQLNRERAREAEVEERRAQELIQRQKARYNHVSSHGYGQLRGGG
DDVEIKVFIRECEKGRAQEFSFMESDALRRRGDTKQPPKPQPEQLLPRVPVQPKKEQAPV
SAVNVPRGVVPKYIIQRKAELAAEKVAVLREMERQKEIAKYPPGHRPVTEEERKETLAKL
ASRRKELEYELHKIPIRYDTQSIKARRNRIESELKEIDESERKFSAAKQLFVPI*
>TCRU_6480 Right handed beta helix region/Periplasmic copper-binding
protein (NosD), putative
MGIRERLVAFYQKHNPAKLCEVDSLLEAFAGREETMFAALRMKYEESDVTDGVEATSRAR
NVNIEPGISETESNTVCAEMQDLLRDMESVDLRRLLDQLSGRAIVEGDLLVHAMRFMQHF
TTCAHRFQDLSGTILNRTATATQNTTAGAAVPLKRTAGESVATQTESTSPGRCDAAVHAV
RVETVSTGTQTDMDGERLRDVSFKDLNPTSNSHFLRAQMPPTECSSVRPNDEVRAAVAPA
ALKMDKQLNQHRSIGMVHKLKPDKHKRAAVIGALLTKGGLADTDSVTLEPGVYHENLCFL
NSGDVELVAVFPGAPVIIRPLSNLEPIIRAAGRKTRLRLSGVVLVENDTLGKMHVNVSAP
NCPLVAVADGAHVEFHGCHFYQGSCAVEAVGLQTDIRLHLSLISSCTFAGVFLRHGAKAV
MTQCKVTLCEAGVRVASKSSMHARETVLEENTTDGIVGYEGAEGTLERSSVLRNGGNGIF
LSPGSNFMVTESTVELNGLYGIQRLQSSVLRLRDSVVRDNGLLPINHTDEKVSL*
>TCRU_6481 hypothetical protein
MYWLHSRDEVSRRMMHHSLEQHCQRIREMERCNAAGNAAIETPVVTEFKSSVYHVHPDCH
GRIGQMPLTHNRGILRARGQCGSDVGGPQQKFCARRYKALFPRGWELHQPPRASVC*
>TCRU_6482 hypothetical protein, conserved
MPALNSLTIAEMEVVASRFLYAAAILGTCLCVYCFLIKAVQRRLSALDRGIVQETSPTKI
QPAAVGLGERLRHIIEDTTVRESSSPRKRRRPPSSGTHRSMDGEPSSFQIQAMLKLPEEN
GRRCLFASCRPRRAVRLALLAFSAILPRTIDVWMSNTSPQGAANKGSSKPHAMTRELQRI
YGFLDPRGIKAFFA*
>TCRU_6483 hypothetical protein, conserved
MGTRRAVPFPSALLRQGARKLTEDSSRRRAIAEGSGNNRGRFFCKNRRIDNTLLVVEEKP

TGLRRRWIAWPRDRNRHDAYEADAPLLHISHYLPPVMAEAASCLDLKASFLQVPLPRETR
HLFRCRVEDGTLVELTRLPMAYKAGPEILQIIITSAIAVVTTVVRPLWAAPPLVRVDVWI
GNIRIAGSIGDVTR*
>TCRU_6484 hypothetical protein
MPLAVFPSHQCEQRRHLGQHCGVPPQISNSILGKVERVNVHRQLQDHVWVKIACLHDWSC
VPQRTLFCGVRRGIPRSQRSLHVSSRKIRKLSLRRSVLHNVIVSNASCPRILTNRKARRE
SALAVIDATDQSKIMLPSGSSVKLLGVKAAISERQLAVIHAGQKTTRCFQSVRLWIYPST
HSLVKGRACFLSNRAATPCNPRITMSSGVRSICNTDRSILACRTLDYGAASNISAKRARS
PPR*
>TCRU_6485 Acyl CoA binding protein, putative
MGRAFPGNHFKAAPFFDHEFGDIEGAARLDDKQKLLFYALRRQAEHGPCTGAAPSIWWTR
KRMKCDAWNQLGEMSVYEAMVNFVRLLGGV*
>TCRU_6486 guanylate kinase, putative
MQHQTDILIFIGPSGGGKSTLIAYLMQTWPQQFSFCTSHTTRKPRWGEVEGKDYHFVSRN
EFKLMIHGDMFVEYNRVFSSSRQEDGASSCAGGSGGSSPIASAEDDGDYYGTSKEELHRI
LSEKKVVVLDTDITGAINVKKYCSRLINSGNGAQAAPLRVKVILVKIPSLDVLKHRLRLR
GSESDASLQKRLHAGQRCLEWCAAHPEFFQCVLVNNSLDACQKELRSFVMRSVLKVDSML
*
>TCRU_6487 retrotransposon hot spot protein, RHS3, putative
MDNLLRWLVAAAEVKASVHEITKSFLDAAAEEARNPAKTSAPRYLEGYYESVYNARWSNV
VEFSDGEGMRMEAKEGEPPQSWNYKKVDDTLEKDDGVEQSGAPRPRLLVLTSDKGWPYTW
NLKGVESACDCYVNCEVD*
>TCRU_6488 hypothetical protein, conserved
MLQRRGFLLGRVLDDTNVGSVLRTVKHVERRRVARAQAKKAAEGTNPYNKAQYINAFVEA
QSARMTHEQILKEGAVEEQSLMAVVNAARPSVVVGSHNDVLPGGAAADGVAFGSWREGNP
ALERVCMSMDRNLHCILRGAMTPPAFSPEALQRNAPTRLESVQRLLRLLHAEEHERWSKV
RLNAFSNRMESCLKSVCGEDFGMRQRLMAVLLQSAAMQSWELAFQLYHDYFLPSLKEQRR
RVEEDGRMTGIEAATSALVAVLCETIRCHHQAGTRAIGSGPSFNTVAGLASSSTFILLPV
AAAPLFSVLQPSGNATWQSVLELTQRFQPHGSKRMYLPSIAWGEMLRAMHRMGASLAEVQ
GVVDIITDPSRTKNAEKHMRDTRLWNAYISVSDWQHALDVYSNNLPHYGVKETAATNAAL
METLLRDGRWGQALDVFRRLQKKEGQLIIGTSSVFTAVFRALEQQGDWHAVTSLVMDFDH
FLVHFGVSHDHWLASPLREALQRPQHLRDDSCMTWVAWVRELPEWSHVTRELAHAMEAAL
ITCDTRKSRDNEQREQQVGQESTAGMGAIPDDIMTAEGLHDLM*
>TCRU_6489 hypothetical protein, conserved
MTEVTNENLQILLTKLMTDRFCSGETSDLDACIQNYVPQQTDNSWVNQSLQRRGIKRCQP
YQDVARRCLEDEKKHAAVFKAAANAPVCKDEMRVLNQCRRVRGRNCEQEALEMLYCGMVY
LVQRQKEKH*
>TCRU_6490 MIZ/SP-RING zinc finger, putative
MAREGGRRGCGCGRSVREMAVVPALIPRSIQSPLYPIHAVLRRFDLLAGSHSSVVLQCIG
PLPPKSLLYPPSMSAERMELVLFPCQLGEPTRPIGWPPATSHECTVMVNQTYVTDEFPRC
PTRSASHRTLAGLPLSLYLRLREDGCIDTGAPLKLVVTSKAKWAATFLLAWCGANDICTL
VTDVVARLQRSESTCSWSNLPSSFSSLSSPEDDGSEGGSDSDVDVDSGWVEEMDCGDTKA
NFNNNESKRRGDNKKTSSSASLGAMIVVDDDDEEEGLMNDGEAIVTLRCPLSYQRIRVAG
KGKHCVHLACFDVVTYLESSLRSSTWNCPICDGPVFIYDVRSDRTMQSALDALDADEDTV
VLFGPGHCQWRAARQQKFAPVSATDNNDSCKGMCVTRETKCNGEKGRQRQPQLRVVDENG
ETEEMGDDAEFVGTAMMNSGQKRPRHEKVLRPSL*
>TCRU_6491 Eukaryotic protein of unknown function (DUF846), putative
MLEPNKPKFDFDSFSPSQPSVQQPPPPPPSSQYTPAPYIVTGESAPPLPPAFDSNGVLLQ
QAGQQSDDRIYKGVHPFVAFFHVAFKAGAILTFILGSLFSSSYVTIFVVTILFLAADFWM
TKNVSGRMLVRLRWWNDVKEDGSSQWVFESAPDADTRVNAFDKWLFWITTGGNFGVWLLL
ALFNVMSSRLPMALIGAVLGGANFIGFLKCSRDAKKRVAQFMLARAAQEQELVRQAASVL
*
>TCRU_6492 hypothetical protein, conserved
MIRRRLCFVSRPTKAASISVTLFSVQRQKGGLHTFIRDARSSSFTTPHQASHAEGEHTSS

SLNSTDWATQMQRELFGETDPLGGQAHKDYYRDPARGYSPQYAPRNFAEGGAISYHHAQS
PMEYAEATHRRSWLDHDVSRMEAAFQEQRALLRGMESATERDELARRYAAEHHVADILVE
NQSLLPSTQVHHSTSTSGSALRQQAVVDRFQIADQQSPLATSDGMGREELAHTYRMRSET
VHNDWIEENLRIVHGLREKEKYDFTVLQRATRIPFQGYDMDRFLAQQKGTPYGAQALPPN
TASSTMEEAQRTLRDPTATVPSFEAISLKAFARNTVRDHPTTGEELTQEVVDTIRTSREA
SEWQREQERAQRFGLGRQGALVQDGGPDKRTLKKHVNDERIMDAMFFRSDAYRKTQTDEH
WNPYIRRDTTHGVAHLLNNKFDIARREDRLSKGEQDLTERSVMHFGVPIQQTIDEFVFRH
RNARGERPLDYFKPFPGFRDFRLNRMYRDVEGFSLMKQRPEFLEWELFTRYRAHHQQRRQ
IALLHGLEPVANETAQERDARREKLDEICERTPFDERELHTNDDEMQVSGETLRSWFGVY
MLPSPTVVEAVVGASASVNLHLFPLADEMGTADTRENVLSSRYFNRLLLMEGFQNRISRA
FMGNVSGKAPEPVVQYMQPPGVLRHFTAEERAMYEQYVKEQTSKQLGEWATAMRRRRWIP
DRQQYGHVVAQGYGVSVVDLEHADTAAVLTVSAKAFERELAAAKGNTSHIIMVEGQAYKL
RPDSERFVVPLSVRLESGEVLDMTDEAFGRYELELLPRNVNHALNYGIGDYAYNRGNYIE
TQDVIWEEQTASGEEGWSPATHADGLRVGLPVRARRHVGMNANGSRIVSTPQRAVIVAYD
RQPFFNPEPRLVRVAFQSDGAVEEVPLANIMIWQRRYHGPERTVGDESRRFSPASLRRYI
DVSDPFNEKTSKGEHFLDKYEAARTSEVAAGKYRTTKQITEIDQWTRFDVSRADNFRPLS
ISHRRDYIRLGYMHRYTPWEWIAVQEADQPLIAEQIRQDNIGTSYFFSLNRYWRYKARPH
GYIRHFDNEVRDLFQFVDGVTPWKQAQKIRTYWEVRAHHPMPQFNRPEVAMHRNTVGLLP
AHMWETDKKTGKVKAVKDSVRDYQTKTPLPKWVQL*
>TCRU_6493 endo/exonuclease Mre11
MASAGNAASSSSTFKFLITTDNHLGFQERDSRRGNDSFTTFEECLRAARVEHDVDAILLG
GDLFHDNKPSLGCFARTTSLLRTYVLGDKPIAFSLLSDPKRNFPTHPVPLANFQDPNINV
AIPIFMIHGNHDDPVGGTSSIDILAANGLVNYFGQVFSLDDIVVEPILLKKGHTYVALYG
LGNVRDERLHRCFRMKKLRFVHPKPVKGRLWFKILLLHQNRGVRGGSGEKNGIFENMLAG
FGLDLVIWGNEHEQQMVPTPSEGFDVIQPGSTILTSLSGQECNPKQYGVLEVREGSYRLT
PFPLRSVRPVVRRTVELWRENPTGRTLDAVEDFLRRVIEEMIEEAEEQISRIPDDVLAFH
PSIKFPLMRLSVDFTDPESTNFPQPNINRFGQQYMDVVVNPGDLLRPLKPKPVIRRLPSA
PGGDGTMVVPVPLVNTSDIRTKVAEVFNANARDACSLLSEPEVSAAVYAFAEKGERDAID
ERINELLNKCQKSVWKAMGRGDAEGILMPDSIYTEVIRYKQDMNKRYAEATRAADASEQG
QKGQLQESHGKADRAQTGFGRTDFMIVDAFDEGGVPLGAPAASASLTLNAADCTVQGVCE
EEEDDALPETGLERGTLSALIASAVKQDQETTAGPALHAVAASRNGGGKRHRDEVEVIDD
DEVVDKPHSVQPSVKKGVRRKAASGAAAPAPKPTRGKRGKQAAASLIPTPTLQLTHELVP
EELASQRPATKQGMPQGALNFLSKWAGQS*
>TCRU_6494 hypothetical protein, conserved
MLSRLGARKSSLRCHAVTVPRCFFYAGLDESRVRRLRRASTTFNKPRGRDDLSLAFERRV
RVLPLLEMGDLYALPTTTSGSARSNASGPTTRPWRVLVVELLSLGDVDAPVPYPAAHPAY
YDGWSDGSEEDSQEKRYGTPPFLLREGRRVLLPGNQRQLRQNGDTSLLRGTFTKRSASHG
TAEYAVALCIDPFLELERFRREEAQVELICGYRNVLYEAVELPDGPADVVRVPALSCDTC
GAHLRHEIGKLSQQALIKGFHRISNEAKEALILNPLFRVEVYVPPALLENFERVFLEDAW
ETPESTINPGRTALYPGLPPPRTLLEADGWIGKRRELVEAIETEGRSLMRGTQRALDGTA
ITPREVLTNIRIFGRERELKKMLEGERATAAQEGYDTTGGSSNPSANASLRPGINQL*
>TCRU_6495 trypanothione synthetase, putative
MPTLQSLAVPFGCVQGYAPGGIPAYSNKHESYFSGERSIDGNLFCGFKYQCVEFARRWLF
ERKSLVLPDVDWAVHIFNLKEVSDARTGKPVRCVAIRNGTAAKPVVDSLLIYPSDDYSPV
GHVAAITEVGDKWVRIADQNHRFHKWDANYAAELPLIHEKGVWTILDPLEDEVLKPLGWV
TFPDTPDRNPNEPLVLHESLHFKRGELPTLRRLTFTPTSREKDWLDLTNEAEAYFADVCG
IDVKNPKLEKASYYQMNRELYLDCAKYGNQLHQMFLEATKFVLGSDELLRLFRIPEEYWP
RLRHSWETQPHAITGRFDFAFDEDTQQFKCFEYNADSASTLLECGVIQQKWARSVGLDDG
TTYSSGSLVSSRLQLAWEMAEVTGRVHFLIDNDDEEHYTALYVMQHASAAGLETKLCVLF
DEFHFDENGVVVDSDGVAVTTVWKTWMWETAIADHQKARVQRGNDWRPTPKDEVRLCDIL
LGPNWDLRVFEPMWKIIPSNKAILPIIYNKHPDHPALLRASYELTVELQRTGYVRKPIVG
RVGRNVTVTEASGDIAAKSDGDFSDRDMVYQELFRLPERDGYYAILGGWVIGDVYCGTGV
REDKTIITGLESPFSALRVYQGAQRRPLTHEDLDKAEAAAVGGGLKT*
>TCRU_6496 hypothetical protein

MLENNGTHHAEALFAQLERISRNPVRLYRHLLQRAVAQLDAVAADAETLRATVRLLQKQR
RQQEKCISHLQRQLMDTQEERGRAASRHRRTGTAKNGHTHTTPLLSTSSLSSPSLYCVHG
GHLQPRRQKQQGQREQCSCGRHSTLRELRGNGKKRHTSHSAVERTRNNCRSLSHSPSPTS
LERTAPLSPSQQYDGKVPWRTVGNDGALIERVLGDVLLLLLDDEVPTNADADRTAGGPGR
LLLGNAKTMYDSVMSSIRILKKREGALKCHLRELEETLRRDKKLRLKPNLAEEQHVSFGV
LPSGHDSQNIGNNNNNSNSNIIIGDDDDDDDYSCRQDASMMNTAPPAYMDGVMDSQHTAT
HPINFSSLFSVGRVDSKSSDTTTRVINACMYSSADADNISHNTQTNFFQTYEKEKDGDDD
DGDRLDDLAGEEELLEYAKWKDSFLRQYLPSK*
>TCRU_6497 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MGVVYTADKEWVTIFNDKRTKSGTWEPKKEYQVALMLQGNKASVYVDGKLLGEEETMLTG
ETPLELVRFCFGACETHNFPVTVKNVFLYNRPLNSTEMRAIKERRHIPRIEGVRAKAPAG
SGLLPLLLLLGLWVFAAL*
>TCRU_6498 Complex1 LYR-like, putative
MYWFHSRDEVSREMMHHSLERDRQRIREMERCNAVGNAEIKTPEVTEFKSSMYHVHPDYH
GKIGQMPLTHSRDIWRARGQYGSDVGGPRQKFYVRRFKALFPQGW*
>TCRU_6499 40S ribosomal protein S10, putative
MATYVPKRSRDDVYRFFFTEGVISCKKDPLGTWTGSLGGKTFTVPSIQVMQLMRSMKSRG
LIKEQFAWRHFYWFLNDEGVEYLRKYLFLPHDAVPNTHKAEYKVLEREGGRGRGRGEGRG
RGRGEGRGRGRGEGRGRGRGFHSERDAYRTGAAAAPAVEAQ*
>TCRU_6500 hypothetical protein, conserved
MRILSTVFQEPGRLPFAKELWIIVLRVPHATGPGWCMNSFNILSGPGAEPSKESRMATPI
SYGVKGRSISQSPGTNGVQQQQYKAVWHVRHAQNEGRSDLPFAEAGRKRGPKISSEHNRF
QGMRMRRRHAAKISPPRAG*
>TCRU_6501 E2-like ubiquitin-conjugation enzyme
MNKRGLYEKYKKLYNCLNGVKTVSNFQVTGTLTPLEFVEAGDELVQKMPVWAWAEGEEGI
QPFLPPRKKYLVYHGAPCYQRAPDADSLGENEMEGEDGWVTTHAERQPSKNVVMAPAKTI
NWDDEDDEDQDNAEDIGERKCRLYDVYMVYDQYYQTPRIFLIGYAEDHTTLLTKDEMMQD
VYASNREKTVSIDPHPFLKAACISIHPCRHAETMKRLIQHMKTRYEAEGANEAEKDAFVF
PTHMAFFLFLKFISSVVPTIEYDLSTSIDI*
>TCRU_subunit mitochondrial RNA binding complex.1
MLPTKLGLLVERCGKPIFSNKDDVRRTMAALLEISAFVDRKCLKLIATPFKRFCRKDPDT
IASVMEMVPIDPAELSHGRRAALLLQCLPKQGCDDVIWEQAVQVFLSGMQGKNWDLHDYR
IALAHASRWSRHPTALAVATEELVNATVRSASQSDLPVIFVILTSLPELNRSPCLQAAAD
RVMSLAEVLTPAAIGQICTCLNKFQFKHNSLAIALQEEAIRFAEESDLFSAVQLFSFICQ
QQNDAISPDAVKCLAERVTEGKDLDQETVITLCRALKALPRQARPELLREIAEMIAFLSV
EVKGILLLSVEEGGLKGETSVDNIQSFISRFLALDSLLPPDHERPGELTEAIKLCVEYIT
EKLEEIVADENPPFSIIPNLLNVNMEETRQCGLAIIREAAEQGIHFPTLQAFRFLLILGD
HNMKDRRVYRHLRNEFAKTASGIPMIQLCAALRCFVRGLIRDPEPDSLEDKVEHELEKED
MDMFLRFCVENLQRGFADGMEIKCVLAATESLYQLGYTDPAFLEKVARYLDSKCASASPS
VNSSETANIVCLALGEDILDKYPAVHTFLLAVEKDGVKMEAALPPTEWMNKNDPANFIVP
LTEVQQEGWNIINRMVETRSADTETLRKLAKEYISILKDTRVDDLKYFFGVFEEKVLKED
KLLKECLDYLLDSNMVSKLSATSIGAMLHSLASLRFNFHRSVKRLVLAISAEQWNEMDAA
PLVQIVSGMAKLSLRVPQVLNHVGDRLVQVHTFLSPMDTGVLINALQSLGYGNDEVMMML
MRHASSSACRWDEVSLTLLFGSSSIHRLLRDVEVATPLLEQAAGKTSSPHLRQRIAASIK
RSALPRELIQSSTAALTGVEGQDARKPLQLT*
>TCRU_6503 Tetratricopeptide repeat, putative
MSQIVASSAQIDSGGGGEEPRQQTRGNQLLDEEKTIISSTRKKYTILPAASHSLMTTNNL
RAVERYIALNRAHRFSERDRSPARVIPELPFQRRYDGDEVLQAAVKTARAQESALDVPLR
FITPEEFHAPPLEDPPTNLPLARRVAALLKGMESVPVHWMEQRPGAMTAAGADDSVVQLK
VMRDAISRAQCAVRGGNTREGAHLFCTVASLHYNSGNMELARSFFAKALSAFELISDLRG
IAFCHNILGVCYFRLREFKASLLHHKRQESLGGCYSRAVAQINMGVSYAALGELEFAESA
LEDALTNARTCESSLLETIALGNQGLVHLRMGNMRAAQTDLEQCLEKCSIGGDKSGAAIC
LLLLGELYSLIHDHQHALFYYEHAYRVGGEANCSDVVDVARVSIGIARGNAALRDAVILQ

AKRMGQQIDLKDVVTLLPP*
>TCRU_6504 protein kinase, putative
MGPNTAPPLVGGNVELGQLLGTGGFGKVYCAYDRKRQMNVAVKVIDKRLVMLNDLKSYVE
REIEVMRKIKHPHVVKLFDAIESTSAYNLVMELAQNGELFDKIVHSERFDEKTARFYFQQ
LISAVHYCHGINIAHRDLKAENLLVGKNNELKICDWGLSRYTKEGLLSNEQVVLFRSLAG
SIDYQAPEVLRGGGYEGDACDMWSCGAILFFMLCGYLPFTDTSDIQTKRRILTCQYNAKN
RYLSPGASDLIAHLLELDPAVRYSTLDVIGHPWFQVNLDLGLFPEAQLSGEHSPLSPLAG
EFIRRVLTPSGGFDDTYSSGIELFDEIHRAFVSCNVNGSGFLSREEVRDALIKLKNHQPV
SEEEVNSFMSNFSLDKDGRISEEEFLIGCTTKQDVGKKYNISRMADLFHYDLEKEYLEEV
RRAFDSFDVKHTGLITPESLKQLNLHYSEEEIKKFFDNIDPNNHGNGTLSFEQFVTMCSR
YDTFKEHPITQRLRRFEKFFNVTDIKSLNNCLATGFTVAGRKENIILRLRSKETTLSTKF
ENSVGGFLYGTYRKSNKRILEVGIRLIPSAAGYTKVAPYRIAGKTKEFHNWFLELRKALR
EEILRCEEDTIVKGEPELI*
>TCRU_6505 transcription silencer
MMTTMHPSRTARQRQDLHTASDIDRRMNDLAAAELYEQILLGCVRAGMNPNDKSDAEEYE
GYIAPIYDPLHAARVAAEKRSQLVEIYHERENIIRTLRSSPQHQQLSAFDRLLVETEYWT
GVREWGGDTEGGNKSRLRRHHRDTTDAESLGFDVLHLTETPSYIRGKLRPYQIEGVNWLL
GLFSRNINGILADEMGLGKTLQTIATLAYLKFTYGLPGPHLVVCPKSVMGNWYRELKQWC
PALNAFKFHGTSEIRPQLIKSHLQPHDKLKYDIIVTTFEMVIEELPTFKRIHWQYLVVDE
AHKLKNEEGRVHTALDSLNTNHRLIITGTPLQNNLKELWALLHFLAPRLFENAESFEAWF
DTASGQQDSNAMSNMHKILAPLMIRRIKSEVSTGIPPKKEIYVACKLTKTQRKWYMHVLA
KDAEALNKASGGSMSSLTNIMMNLRKVINHPYMMDGGEEGPPFITDERIVKHSGKMMILD
KLLYRLRREKEEKHKVLIFSQFTTMLDILEDYCGMRGFRVCRIDGNTSGYDRDAQMAAFN
SPNSDYFIFLLSTRAGGLGINLQAANHVVIYDSDWNPQMDLQAQDRAHRIGQKRVVRVYR
FITEGTVEEKIYRRALKKLYLDAMVVQHGRMQGRGGNNVSKEELLSMIKFGAEEIFKTKD
EDITEADIDQLFDGEEKSKQLTSAIKEQIQMSLASFQLGAEEANVYDFEGVRFKDGVESR
MLHLSLTTPVSQDELQRQCSEHGEVTKVVLHPSLSEALVFFRSTSGAIEARDNLPYKCQF
AAKDSQMVVPTEMITEYLSLGEKLGRGHRVREALHHYTQEDVERIQSSVTKAPPLRLPKC
PKFPPHQLYNVKRLRELHATEVALMVQNWKRKYEPSDGVDGDQQKQQVGVEGEATDRNVG
NEDLVEDETLTLVEQEERERLLNEGFASWSFQEYRRLVAALTSGAYDVTDYPRIANAVGS
DKTVGEVRDYVTALLERGMQCITGFAHIEQRIRKSQEKRKRRDDELRAATWKVESYDHPE
SQLTFRGRGTNEFDRRLFLMAYDTGFRMKNIGRVVKEMPEYRFDVWCQSRSDDYFERRVG
ILMKAVKRECEKPNGNTMEPALRRPKLDSLTTD*
>TCRU_6506 DNA polymerase delta catalytic subunit, putative
MSQWESLYRPHLPPEYLQRDLLFQLLDCCQTKGSAHPTVSRVRHAENPVVRLYGVTKEGH
SVLVHCYNYEPYLWIKAPKGWLPAYSQLLKAELNAQLDSLTHASDTIVRIEVHKRQSIMY
YQGEGLTEHLKIVVQLPQHIPRLRTLLSDRGVACAGAWDGVRVFPTYESNVIFPLRFIVD
NGISGCNWLTIPVGSFCTATERTSTCQIELCCSHEAVQNHDAVGQYLSIAPFRILSIDIE
CQGKKGLFPDPEEDPVIQIANHCINYGNEAEPLTRTIFTLKSCGPIAGARVCSYETEEEM
LLEWVRFVKAIDPDIFTGYNISNFDFPYLLNRGAALKTNDAFHYWGRQINERTVPREKKF
QSKQMGNREYTELTLEGRVILDVMVVIQRDYKLRSYSLNAVSQHFLGEQKEDVHHSIIAD
LQQGSEETRRRLAVYCLKDALLPVKLLERLMVVVNNVEMARVTGVPIEWLLERGQQIKVF
SMMLRKAKAKDLLVPAVEYSGGGGDQRGYEGATVIEPLKGFYNCPIVTLDFASLYPSIII
AHNLCYSTLVRPSDIVRYPAEMLSRTPTGDTFVKKELFPGILPEVLQDLLAARKRAKSLM
KDVPMESLEYKVLNGRQLALKISANSVYGFTGAQVGKLPCLEVSSSVTAYGRLMIDQTKF
LVESLYPGVKVVYGDTDSVMIKCLTDEKGTEKERLEYAMTFGKGAAEEVSSHFLNPIKLE
FEKVYFPYLLMNKKRYAGLLWTNTERYDKLDAKGIETVRRDNCPLVASVISGVLNRILIQ
RSVDSAVEFVKGTIRDLLLNRLDISHLVITKTFSKAENEYAGAQAHVALVERMRKRDPAS
APNIGDRVAYVIVRAAKGAKAYERSEDPIYVLENNIPIDTQYYLEHQLAPPLLRVFEGVL
DDPSVLIKGDHTRHILVSAPSKNAGGLMKFVKIQLQCISCRAIIKEGALCDNCRHKEADV
YGKIVAKRNHYEAIYSQVWTQCQQCQGSLNQEVICTSKDCPVFYMRKKVQKDVKEQQTLL
DRFGVVDDW*
>TCRU_6507 hypothetical protein, conserved
MKRLPVREIGLLCERLQSVQGSDAKLQGAIAEGIRTRVVDKNTLPFIVQRLALSGNWQLA

VKVMESECLDRRQIRRDQNAWPILERVAPCGESRDAIRRALVRLYGVACRPKTK*
>TCRU_6508 N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein, putative
MGRHRVALVSDFFFPGFGGVEVHIYNVAQCLMRRGHKVVVITRAYGDRCGVRYFTNGMKV
YYLPLLAVKLPPGSVTLPTWFLSFPLLRSVFIRERITVVHGHQTTSNLCHEALFHAGTLG
LKTCFTDHSLFGFADAASIHINKVLEWSLRNVDQVICVSNTSKENTVLRARIEPERVSVI
PNATDTSVFAPPEDMKYKSWASKVDKEGLTIVVIARLVYRKGSDLFVDVIPEICKRHPEI
KWIIGGDGPRKSQIQQMIERHNLMDRVKMLGSLAHSEVRSVLNQGQIFLNCSLTEAFCIA
LIEAASCGMLGVSTRVGGVPEVLPPNMLLLAEPDPASITAALEEAIVRVPYLSPWEIHES
VRRFYSWDWVAERTERVYDRIFNTTTPSMYERLMNYASVGLLYGVICWLLCVTDWILRRF
LDYWFPEDMIDVAPDFPLELYSRNREKLNALEKGV*
>TCRU_6509 hypothetical protein, conserved
MFSLERSLAPSHSLLIHHLKTLTPQQLRGIVECYGILDDMLSYHLKENLDYVSVVQHRDL
ASRELCYCSLRALISSQESPIKKVAWIHEEAVALLKQKNYIQSNCSNAQDTEISPPKGCL
VLYLLGIPTTIRQEILASVASQKGFLDCFVDAVNGGRCFLCYPTVEAAEHMRRTIAHLHP
EYKNDVHYCDYNDLLLAKEKEKQI*
>TCRU_6510 hypothetical protein, conserved
MNCDAARGAILEHTVEELAEAKQYLIDLDRRQHQYREAKRVLRNYNASDDVWLLCSGRVF
VKSNLGHKGTVTYLSWKISTGEKEIKNGREELKAKVAFLAEIEGPDQALSKLLKGFELRS
AI*
>TCRU_6511 Reverse transcriptase (RNA-dependent DNA polymerase), putative
MERTPAARIRDVIESQLALQPSGFLPGNSTPDQLLHLRAAMHRNAPQHRTAAYFVDRADA
FGTVGPDAVILEVRRLYISNRIVRWSEACLNSTSAVVCIDKLTPSSRTLTRGAPQGTVLA
PIMFVVVMQSRCSCPSNVPYFAEGSLLTPPPPSHSIATGMRPTRPQKKA*
>TCRU_6512 hypothetical protein
MYRDRCRERTRFRSAARREREPVKVDTIHGALPVRRMLLNGFLVPRCGAMHSALRRHGVR
SAPAPGNVDRRSIQVQHRRCSQLDAEFHEAACPSFAAFSSGCGERPVRQMWRASQRSQAW
CWTSSGPSAAAPPREARKRTRAAVRGGGRCEGRAASFCPKRRAQRHDEVVRFSGGVLRVA
DDGGTKTQSITTRLASGRGCSFASNTASSSLPPLGFTQLFCSPATLRDPACSGTSGRHPN
TMR*
>TCRU_6513 Mucin-like glycoprotein, putative
MSLTVQISSTPPNDHTHDDDVPSALRPVGACPVLLSVCAAEANDTGGNTGQGSDPTDSNP
DGQALVTDSPNAAHPPPQSKYKEGTAESESNLNQALDQERDGKSTEEEADRDETDNANDN
NNKSNASSTNTTTTTNRPTTTTTTTTTTTTTTQAPTTTTAPEAPSTANTKAPTTTTTHAP
SLLREVDGSPHHRTTTLTMMTCRLLCALLVLALCCCPCARQRLMIQVAIRDKVPIQRTLI
LTDKLW*
>TCRU_6514 hypothetical protein, conserved
MTASASAVTLRGIPQCHGENVEPTARSRSASESSTVQISSVMPSCTAREPRRSDSIAERE
SVAAGIRVGDWDAARWGTENCPRPCSVTGHSARQEHARLPAAAR*
>TCRU_6515 Enriched in surface-labeled proteome protein 1
MVSVRLTEQLKRVREVVATWKNVDGSVSKLCPSESAPEDTQTHNACSAGKITEGLVGFLS
GNFSNGTWKDEYLGVNATVTKEEGAEKKDNGVTFKGRGAWAEWPVGRQGENQLYHFANHN
FTLVATVSIDGVPKEEVTPIPLIGAKMNDSEKTVLVGLSYNNKEKKWLLLCDGGKNKKYS
SDWETKTSEHVVVLLRNGNQSSAYVDGQRVGGDEKCNLENTDSKGISHFYIGGDEGSAEN
TGGREGVPVTVTNVLLYNRPLSSAEIAGLAKKKITILKPEDPKTSVVDAQSSPTSGSPVQ
GAVSLSNSARQLPSEQETLKANIGGAGGVSSAASVTTTPSSDVDPTVVTRGGDTMLGNGS
PQTPEVSVSSAEDGETAGGTDVQGEEGIHPHAGEVKSAALNSSLGNLSQGNNSDFCTMCG
SGLLPSLLLLLGLWGFAAL*
>TCRU_6516 Ras-related protein Rab1A
MSAEYDHLFKLLLIGDSGVGKSCLLLRFADDSYTESYISTIGVDFKIRTLNLDGKVVKLQ
IWDTAGQERFRTITSSYYRGAHGIIIVYDTTDLESFNNVKTWLSEIDKFASENVNKLLVG
NKCDLVLKKAVDTQMAKDFADNLGIPFLETSAKEASNVEEAFTRMAMDIKKRLAAQGGGA
GGAANSKPLLSGSNRNTGSGSGSGRNSSTCC*

>TCRU_6517 Protein tyrosine kinase/Protein kinase domain containing protein, putative
MDSANSHVETNSLVGPSVSESMMLEARTFCVVCGHFGSDFVLRKSGLKCSGCVGKTAKKS
WSRLQQRQANELLSQATTRARMGSISSVVSGLGEPFHWANFSAMDSEEADSVPPEQFRNN
GSSFDVPMSSLPHPPRGRPLTPRVEGAKVTSSPSRQPHIMDYISNTACYQAAAAGIIVKD
AMCLVSNPTDSSTQGTNEDSYVSATNNSLLASAVASAPRRKAPAVPPRAKVKKPGPPSTE
EVGESGVTEVQETKGDGEQKVTTLHLGKLDPAAAPISLPSSAKKACEGTSSREKRVKARE
TVVVDASYAVESSSAEGNGAGSDEKYANAVGPIALPPLLQSDSCYVPPKTPRADDFILLA
DASSDTMANDETYELQRSAAPLHTGSNDGKLKASISSQSFRTTSSMARKETVKTKATQSS
ASQPASAPPLNSVQSSTDGTRSPAMHASAASKNGGDVPRGCPARKGSSLTSTPGNSKTKA
QRIQGQKQEQGLQVQQAPTSHVDPTSRSFGRCEITTCDTLRTFSLSSSSSSSSSLSSLER
GSSRAGASSQEKELAAEVTSQRQPFLDNASGLPTLHVNIDRLYIEVEEPQYASPDESLLS
PATQCFSSSLSTSTVNQTAVPVPSVSGSKFTVTRHFSSSNPRQENAASLMTSRFSLDQNP
GLATEGGEGTSQRTSGLRRSSASADRVEARKIAFILSLRDRDSREEFYSVRCRYFSDLVP
LFQELKSLMHTLPQISVFRIPSVRYVPESFVAERRAECQTFLDAVVQNHFLVRHPKMVGL
LRLEPYLNQNASSARTIHMSGSLCGESAAHNATKIGRRNTVTLFTQLNKDALDQLRAMSS
RNFLGRQMSTSSCLSTTSSVSRRGAIDAIIKEDLEKVQLGNLIGRGTFGAVYLGLLPGHS
TVVAVKIVKVNENVDEDFLHSMRKELDVLRAARHNNIIRFLGSTYLERERELRVFTEYVE
CGNISTMVKKFGSLPLVVIQKYMIQILRGLQYLHNMAIVHRDIKGENILITKKGRCKLAD
FGCSGTLHEVEGREEMQGSPLWMAPEIIHGAPPATAGDIWALGCVGIEMLQRPIWNVAGD
LNPYIFLYRIGKVNGPPHGLPTEEEVEQFAGREETREEYTCFGLYREFLSSCLRMQPEER
WSADELLKHPFLQKAFSRHLRWMPPKVGEEKSTRATA*
>TCRU_6518 serine/threonine kinase, putative
MAGSKRIGKYELGKTLGSGNFSKVKLGRDIETGKEWAIKIIDKEQLVRERMEEQLKREIA
VMKMLHQPNIIELREVMQTTNHIYLVLELVTGGELFDKIAAAKRFDEPTARHYFHQLIAG
IHYCHTHGIAHRDLKPENLLLDANDTLKISDFGLSNLHYGNSPGKGTMLQTVCGTPNYVA
PEVLKERGYDGVKADIWSCGVVLFVMLAGYLPFDDENVNALFTKIERGEYRMARHFSAES
RDLISKMLAVDPSKRATVEEIMHHPWFVIDWDPNVLRTENKMQLSEDQLRNAIQELR*
>TCRU_6519 Leishmanolysin, putative
MHLRVQDALQVWNFVWKDRWVPIGIKALTTDPCDSRSHCVFFWRCTVNSLDGVFGCEDDV
VSSAHGNILAEETVPAAVKLHADRLLVQALEGPLIAPPFATGSVCSWFTVPAEHPSTGVA
NADMVLSVVVCSTTSAMAARSPATAAALMAWSCRMAMGTGGRWSRTGRSATRRMSGWHRW
GRRLLHGADAGRTG*
>TCRU_6520 hypothetical protein, conserved
MAMMMAGRVLLVCALCVLWCDFGAVGVSFGDSVGELQDEPSRSSQSLSKGGHEEELDIRT
PVGRVLNTSEKPLDSQDITKVSPQTSVKQPPRDNGGAARKEEKVEAKKADDEETRSDGEE
QPKDHSEGTQQRDGPKENERSPSPTPADKMLTSEDPAAEHAGQAGQAIRTPQSPESDGTR
PGGSSVGGSKGGEGSNLDNSASYGGKQSAVDGSGSGGGTVLDLNGDGGSSGGGGGSS*
>TCRU_6521 Enriched in surface-labeled proteome protein 1
MDSKAVSHFYIGGNGGDKGDSGIEEDVSVTVTNVLLYNRPLSSEEIAGISKNKITHPKRE
FPKTSTTSSLSPAVSRSDVQGTVPLSNSAGQPPSEQGQPKGSIAAGAGGASTPATSTAAA
SSGQEPVKQLTSRTPPSGNKNADGTHSSDVAQTAATGSGDTMLGNGSPQTPEVSVSSGVD
EETAGGTDVQKDGIHAQDREVNAAALSSLGNVSQGNNSDAGTVPGSGLLPSLLLLLGLWV
FAAL*
>TCRU_6522 hypothetical protein, conserved
MAMMMTGRVLLLCALCVLWCGAAGRCDGEETAAHGGELLVRSQEIVTSPEGSQELKDGPT
DVNVQVPPAPSPPLEEEVDDDNEEEELEKGKKENKAPTQAQGDKKNEGASLLPPPPIPSG
GQTADQENLHKVTKVKNENTPSESKTDLEASAPTSEDATQGQHSHDKDTEDSTKNEAAGS
PAETTTPSTSTSGSGDHVQNKADEDDTQSSEEQHDSLQNGNTNVVPTLSEEASKTAETIT
AARINDTTTKVGDSDGSTVVSHTTSPLLLLLLLVACAAAAAVVAA*
>TCRU_6523 Enriched in surface-labeled proteome protein 1
MDPKEISHFYIGGDGDSAEGQEGFSVTVTNVLLYNRPLDGTEITALAKNKITIPKPEGPS
TLVVDAQSQAVSATDVEGTVTQSNSARQLPSEEKPLTANIGGGAGGVSSAASVATTPSSD
VEQTVVTVGGDTMRGDGSPQTPEMSVSSGEDGETVGGTDLQEEEGIHSQTGEVNATALNN

SLGNLSQGNNSDAGTVRGSGLLPSLLLLLLGLWGFAAL*
>TCRU_6524 retrotransposon hot spot protein, RHS3, putative
MDAKDLLLLILGSRGALASRALEQLGLRAFMYGELVSALVEGLKELPPPEREAQDSVLKV
NHQGHPTRTVGLTELEGGVTRIPMEYGVLYIPKVENFPLVDGFFFMESPRRTHSKDKSHK
LVKIVREITDEGAEVFLNASISADIGFRIADRLEKEMDAKDLLLLILGSRGALASRALEQ
LGLRAFMYGELVSALVEGLKELPPPEREAQDSVLKVNHQGHPTRTVGLTELEGGVTRIPM
EYGVLYIPKVENFPLVDGFFFMESPRRTLVGLQMATASAHRTTTSAVRQFTECLAAYFEG
WDELSRDLSWDIIYVQHADRKKISKWHECDRVNPNNKTDAEKEIVAFWNGKVHQYQFVLT
PDFVNKITEMRIQ*
>TCRU_6525 hypothetical protein, conserved
MRVDGNTVQFNCPQALRDAGFEVAEALFDVDKALDVPDASTLFRKLCAIAAPNFPQERKK
MVAFSYGVRSSPRRQLLYGSAAGEGYAA*
>TCRU_6526 hypothetical protein, conserved
MPSYLPDTVVLQLYRDDGEAEFADYMDANSLTFVALGDAERPVLCGIDATAQPHHEGAQR
ALVSAAGIVSGIRRRRLRIPFGMSELSQLLRRAYNTEKGNRNNSLTGSTETALLTHAFLD
AVWAEESFHCLSTTRRVGNILGSTGIGSATRDLAVDKWRLDQDIIELQDELMITRTVYDH
RHCGYESNRPFQT*
>TCRU_6527 hypothetical protein, conserved
MIKELEQRGGATLDELEGTLEAKKRESIALQADRESRIWEYEHTVEKIRTRKQTEESASE
RLRQAMQQPEQELSLRQSAIETKEQQLEMVQLGGARGREAIMRERHSIEAVRRTVREERC
RQRRQWIHQVKEMNAKFPEQVRPLAEERKKKYEQATAREDAAETALAADIKMIEEYLPRL
ISLEDIPVNPEETDIIRRQFDEVFTQEEQTYLASAEEEQARKERLGRGLEVY*
>TCRU_6528 hypothetical protein, conserved
MPGGGGGERRQEEEQGGNLSPQESTKVAAEKDVVAPRSVPEAEVARLLQEYDGTPLTGPD
VRKMSEWSQSRSTSVPARFSTLTTNSVGAGHVDSEARLRMKWGTIQKDCPFCLRSPTLQL
GSPSVKNRTESSTNSFTRLGTPTSLRASAAAFLFTLNAQEGLRKSPPLEVIAFSPTAEEE
GGMAVFSSAIAVEGRSKSLTDTQGEPMRITSVATQAAEPIDLNASGVSFGASRYAHAVND
FGGRYTPLRESVGTSVTGNSGQRMSRNHSTKGDDIVSNNPNSDRSFALLSNRNNEDVDSA
KKEVRYELMRLREHPDNEGSHEDNRIDAEDESGLCCRCCGVFSCFSGGMDLRTTSLLAYR
NVGQREEEEEEEEYTGRHSGLQCKPCGAVIRSFNFMNVFVGNLPVASKLFCIMNYIASTL
VALALSLILICLWDKPVTRVSDDSACRGIIVPGIFTPEISFSIAFFLFNVLLAVCFSIRA
VRYENSGLLVCHFITVLLQFCRTIHFVFFTSIDRLSGQVFLYIQFLFGVSAFLFLASCGT
YPWVHMSFGWRTFMKGITRSVLLRRHRRKMFIESFVQLDIFSTISSAFTVVYMLDSDLEQ
MIGLTVAVLSCATAMLYLVMLRRRSMWFLSFFSVIFAVSFVFYCYVISSAVEPYLLRGAG
AHFEVSQCYSPKLFYCLKDLDAEIISKRDLTKYVENKSNGSSDGCSSFVVYRSEYFKTHP
RENKNCQLTWQDNFNDGFTHCCEVYGHCRLKDAVRSYTVVHLLVLAIILWTVRVILVWLW
ARSMKEDEEDATRIWQHPNSDTFVPPGLTFPSFAVNGPVST*
>TCRU_6529 hypothetical protein, conserved
MIFGSEPPLYLKPVGRRGLRRHEADVLQHYPGYSHPVVQLRGSEGYIDDSHRLHPRLTAA
EELRHERELGAERRQRVVEVRRRRHCEREANLAQRREDEFQREQRHKAQLAGLCIRNEPG
DGRDTITQQYRTEDARRHYEYKHELEKHRYFARQQRLREKTHPHGYNILTGEALPSTVVP
PKPSIPSDTQLFAVQHGD*
>TCRU_6530 cdc2-related kinase, putative
MAEHFRNRIKELRSRKVATEDAATGSKTTVASAATAVSSVTSPLLSSAVSSKTVSSVANL
PPPFVSPHGAVVNYRDTVRDPLCARFTTGHALSLFWVTLQALGDKARRKRARSPDNEEPA
EEPQQHCGFQKHQPQQQHASREGEGGGEEQASPRQIDPEQPMVREGCDNEKKVVTNPPFD
TSFSNVVSYFLPEIDGRCFSNNDELEETNGLVKGQAQLEHSKASIGAGIGVGSRDDKKRC
ILVTGKQCLPCRSVNEYIPKARIAQGVYGVVISAIRAASEVPHHDQEVKRMVKKYALKQV
KEQWLVDSQVGFPPYLLREFDLLLRMRHPNIVRAREVVILDKRLGGTGHSRGDAGGDGVG
AENNIKRSHPDVAGEFLQGVKGVAPNGNVATQNQEKSGSDGVLRGERSRSHVKDVYLVMD
YCPYDLKSFLSLHNEKGVYMHLSSYNTHPDAPNNFLSRVKCIMQQLFRALNFLHDHRILH
RDIKTSNILISHEGVVKLCDFGLGRLYREGEELTANVVTLMYRAPELHFGVRDYSHKMDV
WSLGCIMAELFLKMPLFRAEEEVKHFAAICDIIGIPTEETFSGLYKMPELLRIMRSLTKY
NRENNLSRVFAKSHHAGASTLPASGLDLLQCIFRWNPLDRLSARDALNHVFFHEAPLPCE

PAELLRPIPTSNVQSRRYDGKATAKRNETDGVGGTPPPKPRPVRTDAVLRAEEKLTSPRM
GGMKAVEPERTCTTTGTGEMKMTVTDAISSPSEDDAEHVLLRELESLNDIPSPGDEDEAQ
RVANQARLRANQDRDCASSPGF*
>TCRU_6531 Dpy-30 motif containing protein, putative
MKRVLVLNVDSFVGREVCRCFFDAKEYLVDGTLYHFQSTRENPEAKESLRTDGLDSAGKM
KPHCATASTSSVRLDVPPDMRPFLNSVMPRHGDISDEQFRVRVLTYDIIIAILEEDAFEA
DCAIKVLRGTHYEVEKTFVLVSNVFTWTQTDAHERELRRAARRAEREAARAQRYEDDVIE
EEEEEEEEMEQKVWTEEDYRQRYPDLRYHLWKDLEHAVKHANSETLHTYVLWAGLPYGRG
EDLLVSHFNAAWRHQEMLQYGDGSNYIPTIHVKDLARIIYLVGSSYDTLEDRYMFAVDQG
NNTQSDILQGIKDFIGGVVSVTAPEIDRKNQVVIPGNQKKGGREADVKENELAEEIQHEH
DVLVGLGMREAQVLDEEKEEMLRIKEISQREKLLRLGLGVQEIENDDDTNHALRPEAASK
VGASLTIAPPHGLANWFSAVDMRCEPGAVLALLEEEEWVSLGGFFANVDKIVQEFKAARQ
LRPMRLVLSGPPLSKVGEVAGVLAELFDIPHLTLANVTAAYEEHVRSLREELIGILVLRQ
LRRHTAREERRRREKERAKEARRKAREEEGEEGEEGEEGEEEEEEEEGEEEGEEGAEEEE
EKGEEGTPAAQDLDPAERIRAAITEAMLLRVPEDEEEEEEDDSHYNADDEEEVDEKAAAM
AQQVDEAERRRIATLREEYRFATQLLSLRLLNGEFPRRPKSADEEEEGEEEEEYDEYDDE
EEYMNRKKRREQKKDVKKDVTEEPPPTIRYFDEVMAVMVRWRLRQEDCKNQGYILEAFPE
TVRQAWLTFLADTEEQKEMQRPKLQKVRDEEAVPQPLLDANFPLPVLADLEEDRKQEIME
LMTGRRFASAEEVLVPTHDTFFPDCCIALTGNEVTLRSQIYAAIATATPGDTTPDFSEQF
TRYMTHNRPGAPPTESLICWFQTVVAERVDEDGDVAVATEGGELREKVPRKACVLFVPVF
STFPQAVLPKFFNHEEISGMRAYCTFIRSEILKNIGLDSCGSVIDSMRAEAEANKSRVQE
LASEREKLEKLSASDKLFAAAAQKLEDDFLENERRALRFYQAKEELASIVGIDSIPVDVY
LMRYVMPSLTPLMAEVVRMRPEDPVTVLADALFHHKRQVSL*
>TCRU_6532 Intraflagellar transport protein 43, putative
MPPKFGRRAGEGQSKKDGSVDSATPQETNAAAFDSKRYLDVVVHKDDLRSLEDGVDEQTR
EQAAKKAAEEKEKLVKRVAEAPVGYVATMPKLAELDLSNVWSDFLSAVHHELDISALTAS
LSQQLDDEDVAWNPDMLLVQLTSDMLDAAEVGESGLPAPDPAALEAVGKARRRRNELLEN
ADEMQVTTRDRRRRPGGEGEEQAASESPESHQKPEESSSRKSSETKKKSRERSPGKGGHP
GARAAQPPESPTASPANPASRKK*
>TCRU_6533 Small nuclear ribonucleoprotein-associated protein B
(snRNP-B) (Sm protein B) (Sm-B) (SmB), putative
MGRESMLHNINRTLRIVLIDGRELTGKLLVYDRHMNVVLGDATESREETKKMKEAGISPQ
RSLGLVLLRGVHVISVNVLGASENNGDGEGTTKGQPANFEKAPRAKVAGAKRKR*
>TCRU_6534 FtsJ cell division protein, putative
MGTKSKKKAKTRLDAYYRLAKDQGFRARSAFKLIQLNRKYDFLAKSRVLVDLCAAPGGWC
QVAAKHMPVGSKIVGVDLVPIAPIRGVKTFVGDITDDKTRKMIVTYLKKEPVDCVIHDGA
PNVGGVWSRDLFEQNALVLHAAKMAASMLKPSGWFVTKVFRSQDFHKLMWVLKQLFDKVE
ATKPLASRMESAEIFVVCAGFKAPKQLDPSMFNAQKVFSDVGEEKILTPSGALVVPKSNV
PTGYSEFATVSHHVASFSEFLHCSDPKGFLRSHHELRFSAAEDKVYLKSKHSKKELVYLC
GDLQQVGDADLRRMLRWREQLLREQAAMAKEEDGEEDADDEEMGEYEGTGDDDDGGSVGK
GSDDEGIDLDSAEGVAKIARELLELRKRQSKLLKKKQRKIVDRKLKQIKGLINFDPNTSA
EDMTETDGLMEDTEGNMQGEGDNDDDDPDGNDDEGFTVEKLAAVDEARLAKMFDKHGEEL
DERPNDPLNPVMNANLNAEQDWDLGQESDGNSDASEGGNGPLQLVEGEEDGVDVDNYGNY
IPAKRSARVALYDAGLGEEEDDEDTHNEEDVALQKRKARDQQDLEDAGKQSKWLRHHVNI
EKVLNQTFPRPHDNNRRKKRLLEEDRVELTASSPLHDGDLNGRVDATRKRMRFDDRAEDD
DDDDGDQSLSSLSEGRFSDDNCDLDVSEGRMDSRRKRAIVPDMGKLTTQELVRQQRKQTL
KENAATRKQNVRNKSSARKDETGFEEIPVALTDPQIRARTLAIATKMLDPKSRRDILDAS
INRYTFNDDDDLPDWFIKDEQRNCKVILPVTAEEIEVQRQRFREMNARPGKKVMEAVQRK
RRRAQRMLRSMIEKGKTDPRAREKANNASVRKLMRSQAVKGDAKRKKKGPMDRKKMGEMR
RAKQKLKRRR*
>TCRU_6535 Rab-GTPase-TBC domain containing protein, putative
MRPKETEESRQDCGAAASRVPARRMRVVKGPGVAVRAPPGTKYLIYGLMVLSGNSPHKNS
STTEKRAVYICDTDIEEETADRTSITPVSTATGASNGMTSVREYNRMMDMLVSLPLGDSP
EERSTVRGYTWGGNVPNHVRPHLWRLLCGYIPSGPASFSRQQAELRRKREEYDSFVSKYY

KITITDFIQPNTLQDLGTRSGRRGVGTNSKLVGASAGTMAMTTPMGTSTELMAISSDDRA
ILLQIALDLPRHSYALFHFSRTASALARCLFLWSRRYPAVGYVQGIDDIIAVFFFVFLEG
AFNERNMRHRQHVREGAAEPGDGDGARASEHAWIPAKVVYSRDMSELGAAMEQLPADLFQ
AAEADTYFCGGFFLSWLQDNFVHGQPGILRSIGLMEALLKAVDFVLLDSILSNEIRLMDC
CFQWVHCLLARELPLELLVLLWEKYMAIGNSEAVLDFHSYVCAALMMQLRQKIVGQSVDV
IIHLLKDPLEKRARPPQGSRNKDVYDCAWLEGLISRASQLLREYPASSLT*
>TCRU_6536 hypothetical protein, conserved
MVGDAPRHRTSGSRDTPKGMWTDRMEHAECVVVAVWDEHTASPGGSLPRAEVARKREDRN
HALRGGFSMLLEVRAKQLGALSSPGL*
>TCRU_6537 hypothetical protein, conserved
MDSATPKQSSKNDVAEQQNQERDRKDLMKNAATGHPAGTAALPISTDGNGDAHGTASENG
DDTGRHSTKKTHDDPEADNTNVGITASEAEPEAVNSSQTNNTATPGDSDSSTVVPHATSP
LLLVVVACAAAAAAVVAA*
>TCRU_6538 hypothetical protein, conserved
MPRGGRHAGGADTAPSGIQGRPRNSPDYYYLGNCGAKTVVHCLWAAPPLVRIDVWIGNMR
IAGSIGDVTRWEAQVLRNADSRCTTMGEDRESGATHYIFLGVQFDHTHRAVSLSDKLVRS
VRAMPAVNSSTIAEMEVVASRFLYAAAILCTRLCEYYFFIKAVRRRLSALNRGIVPETSP
ANLPPAAVGLGESLRQMIENNRKRNNKPTETASAVIITDASLRGWGAVFIPDSGDVKIAG
GKWKRKPFLIMQAEARAVRLALSAFSAILPSTMDVWVDNTSLQGAANKGSSKSHAMTWDL
QRIYEFLDSRGVQASFAYVRYPENPTDGISRGRVFTLQELAKGSGGVLWLEDPKVCHFVS
NNISNPN*
>TCRU_6539 hypothetical protein, conserved
MAIEVAPSTRLQYARMLRSMLEMNRTPLGMMILGLQKIAARSETKQARPLTEEEMNQVIR
SRTDWKERVVLRLAWITASRWSEIAALTAKNFTLEADGALIFDWSVAPKTAKADPHRASR
FFRIRGQDAFDTIKLCRTLQENEKRTNITNAEVERALAPWDATAHSIERGALRHAAQIVE
KYNLNPHVISRLAKHVDPFDLPQNTVRYLGKYTTLLTQVLSLVALM*
>TCRU_6540 retrotransposon hot spot protein, RHS3, putative
MELDGRGALDANQDVLLEEFFKDPKKYICDAGVLGEMQASDRYKRMERAVRDEMDMVEDV
HKLYKNGMYYLLNWLAASAEVKASVHAVTKRFLDAAAEEARKTKKSSAPRYLEGCYESVY
NARWHHVVEVSGGEGTGMEVREGEPPQSWNYKAVGDTLEKDDGVQQSGAARPRLMVLTSD
KGWPYSWKWKENKSTHDCYVNCEVERVWQIVKGDLTELLSTHGRKDFEPNWRLLIGTPGI
GKSMNAGSYLLYQLLHCDVEKLQVVAYSFGGSTMYVFDKTIKTVTRYVGRGASRNALYDL
RALEMKGYVIYDVTEKGKPASWLAPCGEWGMIVVASPKVGNYDKWETQARAERIIMNCPD
GMDVKAMCAWMKRDETAEKKVEYWRMVKERMDKVGPIPGYIFDANEFIAHSAAIEDALDG
INSRDGEKHFIPRGVRLWYSEDPSQKLVRIVRARGEVGTEGFLNAPISVCLGRRIPHYFG
KRDE*
>TCRU_6541 hypothetical protein, conserved
MWRCCGWLHVALLRGLWALTASPTGVAVRLHGAATTEPCECHAQRHWDCGTKQPRLSFGA
SGTCWPQLGGASGMPHRTGVVMASRRGISGDGSDAAACGGVEETQLPEWTLDSRLHQVLL
EEKERTMKMRLNDFLRNYFDGRGVVECYRNAYMEDFLISPNEFIKDEVLLDTIKASPPYQ
ELKKEREEFYMLLGASNELSHEHLFTLRQWRE*
>TCRU_6542 retrotransposon hot spot protein, RHS3, putative
MTLVGLRMTTASGHHTTASTVRQFTECVAAYFNGWEESSREMSWEMIYVQHADSTPMNDW
RRCGVVNPNRVRDVENREIARCSGTKRYANTSSC*
>TCRU_6543 Acyl carrier protein, mitochondrial
MQRSQLLRKFICRAGALGIFSAQRQILPASNNYYLSSISIPLAISARFQTEGQGGGDEAT
RTGQYLLNKDDVLTRVLEVVKNFEKVDASKVTPESHFVNDLGLNSLDVVEVVFAIEQEFI
LDIPDHDAEKIQSIPDAVEYISQNPMAK*
>TCRU_6544 hypothetical protein, conserved
MRKCTVPRGSRDRPEESRRTECSRPSLLRRQHATSVLSYREAACPVLNCSWFLHAARGPC
ETAWCSLEPKPVMLRGMAAPRLCPLGSAVLRYSRDRVRALPLQQAHPLVRHTVRVALAAI
PTVVRTPCASVPSGG*
>TCRU_6545 BNR repeat-like domain containing protein, putative
MSRHLFYSAVLLFLVVMKCCGSWEAEAAQENNLMTTLLRKGDSFDDSENKSMSQAFDSFR

APSLLVVNGLAVAIVEAHCTNSTDKELCVGLVAKSMTVNEKKWANGTAIVFDHYDIKVYR
LLSPTSIVDNGEIKAVLGGHGKSGDPLTELVGDGKYWTSRYASGQIFVGGVVRKRSLDGI
KVPPRNFFLTF*
>TCRU_6546 Enriched in surface-labeled proteome protein 1
MGSKMDGDDKNPVLLGLSYNNKEKKWILLCGDGQNKGQSSNWETHTDRTRYQVAIVLQNG
TQGSAYVDGKRVGEPCKVESKEDKKISHFYIGGDGSNKGSQEGVSVTVTNVLLYNRPLDD
SEITALNAIKVPITPPKETSAQEVVLPSPGRTPHAGQEPLNGGEGADGGSASPSAVSAST
TSSGSGQSVNQLAPGKPPDGNEDVDVFSSSSGNPTVGEGSADTTQGDGPHTPSVGNTAAA
ADTNVLAAKGEGHDGPALTADVSVSSGADGETAGGTDAQEEQEIHPQDREVKSAALSSSL
GNLSQGNNTDACTVSESGLLQLPLLLLLGLWGFATA*
>TCRU_6547 hypothetical protein, conserved
MRVRLRWWLVWWCSSVCVTAAGSAGDVSGDADAVVVPVDVSCAPSDGSLSYRVCVWAWTK
CSAASAEAQHENYIFSGFGVRMHGRDGELGAVCHVANAVHTCSNCAVSCATEEEGATVAF
TMNVTAHKYAGPYELLWRQFSPDGTIHPPARSGDADRTGICQLPPPREGKDETKSGETTA
PQVNAEPSRQNEDWRRSAAADGPNTVDRSPASNTATNTSETRPEFVFVRNIKVVPTPPKR
KPSIAMSRNIEMDLNAFVTKTALATALRKAVGSRDARKSEAVDGSGEHVPGKIAGGMNGH
NVPGTPKRHQEMCPCAIWSGVSPDGRLVLFDDVELIPRDSTGGRTARVCVSLALLLLLLE
LCGVVVVFRAKEGGIVTPHGGYLPHTLRFLCHFFFSSFLMIYGSLFKPFFLLCNVLFDAF
PLE*
>TCRU_6548 hypothetical protein, conserved
MQDNHRSVMQGAGLKLSGSGAAPMASSSSAADTDAASSTPVSGAGGGVGPKQQPAVVSGV
QDDPPAGGSEAGEREEAGSACCGEEPSMSSVCSQPPQFSAGSATLTVEERDGKKGSASVT
NIQSEWAQQEREGPHVLRTGESARRTPAPAPAEGQTAHATQPSEDSAEHAAAPSSGLTRG
ASNGDSQEQTPQPQTATDAEQSVSVVQGVPEWAREDQGMW*
>TCRU_6549 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSVCVGRSTEETIVVREVDDVKEPTSSSTLSSESQVEDNSHE
ERGSGTGSSEEGKTKVPVTPGSSGAVTQSNEAKMPVQTGEKKGTTEDENGTTAPKSQSKG
STVEQGEADVGGVKSLTAPKRQSGDAIDTVHEEDGSTTGPQSRTTKSADQTDRETKDAAA
TTTTTTTTTEAPTTTTTAPTAMTTRAPSRLREIDGSLSSSAWVCAPLVLAASALAYTTLG
*
>TCRU_6550 hypothetical protein, conserved
MHASGPESLGGGHAAGTTSPRSDASQQAAGGVHAGGGRTSQGSRASEQTVTGQSQVPGTA
KEAPQGDEGGEPGAQHEADQTTKMTVVTSCAKTAVEEESRQRDRKMHHVSIVAGMLIVII
FPCSYRHV*
>TCRU_6551 hypothetical protein, conserved
MEGCPGGKGRRAHRVTDACRCGEDSVPGVDPDIGPRVAALRTGAMRLLPTLRQACTRPAD
HKEPSVSVVPSLPHCGDRPTSASAGTSSRREHRDSLSTSERRIDVLLPNLRQSALVRPQY
EGTCRTCSAWRYNSSRGPPMRMPQWRHRLLNRCLARRSPPKLPSMPAGETRRKHNRGHSR
WTRLFRHRLITDATGC*
>TCRU_6552 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSVCVTTTGGDPGNGGSSLSPSQSKEAGAQGTPGGSESQIPS
SKGQASGPKNPDSKEAAPAEETDKATPEPIPKEGADGSDGSGSSDGSVNPAAASSSSVTG
TVSVQSQKENAPTTTTTTTTSTTTTTTQAPSTTTTTTTEAPTTTTTRAPSLLRESDGSFS
SSAWVCAPLLLAVSALAYTTLG*
>TCRU_6553 Mucin-like glycoprotein, putative
MTTCRLLCALLVLALCCFPSVCAEESTEHTEVKAPVATSPQSPSSVTLTQGTSQSGLLGN
GSGADQGRNGGAGPSSTGVLPQSKDAKNAVQIKDGDNTTGSQNSRSTPAEEANQEAEDRA
KTTTTTTTTHAPTTITTTTTKAPTTNTEAPTTTTEAPTTTTTHTPSRLREVDGSLSSSAW
VCAPLLLAVSALAYTTVG*
>TCRU_6554 Protein of unknown function (DUF3720), putative
MAMMMTGRVLLVCALCVLWCLTAFGDATDNRCIEGDGNVLTHTHNGGNEGLRLKADFGLI
STRIGLIKAVEAGNDGRDENGSDSLKNKDKSQQGSVLAGPGENETPGPNEVKGAAGAATT
SPSGPGVPGTGDETRQSVVAGQKVNETKSVDTGSKEPKESQDQHTDQLPSPSGSSSTRSG
EKSSSKGSSEITQLPKETVTKGDVDPRNNSGDDEEREDEETRRENEEEKHKPGLAKVKIM

EKKHHHYYHHQRVKKAHYQKKKAHRK*
>TCRU_6555 hypothetical protein, conserved
MESKAPEPPSGDATQGQHTHDTDTGDSTKNAATGSPAETTSSTSTSRSGDHVQNNADEDD
TQSHEGQHDSLETGNTNVVPTLSGTASQTPETITANTTDTATKFGDSDGSTALSHTNSPL
LLLLVVACAAAAAVAA*
>TCRU_6556 hypothetical protein
MHTPGRRHSLIGAVRQTSRAQSVTTPKTESQRMRAAKLETRREEGQARTATSPPRETPSS
AQEANAGEGRHTVRPKQQTHPFINVALLPIPRRQNAGPPIKCTLPGDGATMGSPPLGFCR
PAYGFWRRSNDGLTRHRTACHGRRPDVVKTGRCELCEERSPHLLRCPARQAPGQKRGVDT
GEVRNPCFTRELARFPLDAERRQARRGCGRTPMLVAGSSSPLFLVVRWCC*
>TCRU_6557 hypothetical protein, conserved
MCVTTPVQQLKCSPHTGQSVGRRIVAGWGQREEEAFPCEVHCVPAVRHPSCTNSMCPGWR
AAVAVAAIRIVWETPVRMRAGAAPSPRVRVASVRVSPSRLIEWSGEPLA*
>TCRU_6558 hypothetical protein
MAPTRSSTRLVTAGSPATSDAQARRHTQKKTPRMMDRRLCGTRHQVGSSSDAVPEWNADQ
HCRGRRRTDTMPPQSRKHRPTPWYKKAIEQNAADRQCTV*
>TCRU_6559 TFIID-like protein, putative
MDDDFDNFGGDFDLDENEFLEDAANDPSDAAEFDYTLFSSAHNVSRPNDDNDNTNSEEVR
AATPPNIQELFPNAAPDTMPVIVGIIAQAKLGVGVDLCALSCATRNVEFVPRNRTPAATM
RLHEPTAVVLVRTSGFMSIIGAASVGEAKQATELAARIIRKALSLDITTVQFRVRSVTAR
FDVGHPIRLEELAQHEGIFCSYEPDRFSGCIVRLAGKSHDNQWQVSCTVFVTGKVSILGA
RSQKELQDAFYTLLPILAQYAKK*
>TCRU_6560 cation transporter, putative
MRRRLGNFIAPLTVNSVRAHVVEERSDHHHHDHGHHHRQLESAVKGHQLQQCQIVTVVGG
ATNVFFSLTKMWVGMRGGSVALVADGFHALVDLLADVISYVTLTLSVKRLPRCRFPFGIG
RIETAGAVVVAFTLLLGGLTLLFQSLGECQREFLYRIPGNNNANYPHEHVHHDYGHSDDD
EKQPDVVGVQNHHGHSHFQVTQLDEDGRVTVLWTMVLVSIVSIIAKEFLFQWTKRVGERA
GSRVVVANAYHHRADAWSGAVALVGVGGHCFGMPGIDGLAGLCVSYSICRMGYGLLRSSL
LEFFDFQCANEVASVRHALKQYKKTPFVNAFLIRHGHSYALHVTLLVEAEMTASSVVAVA
SELTALAKQSVAVRDTYATLFIYEKDKEASLHEALEMVREFHGLEPIKCRWEAKEIITQQ
SLCGECIEDINTVASAFSAVVIRSEGNSQSSKRNGTCHR*
>TCRU_6561 pdz domain containing protein, putative
MLFAVESRPSTGAVDSLTTADELNTTGNTLTQLQNFFEQHAFDTCGPYSDLFSVLLSCCK
HLVDTNLHHHAALLKQRREVTRLASETEALYDVTARCQEGIHELKLSSLEPHFLGQKKKS
PLRSEVVSPHASRERDEKIIWDRLEELHGHIHETRAAVVELRRRQKEIEGRLLEERRQKE
EGCERVRNLEEIVDGMMRGISAHSERVDREFATLKDLLAAAASSSCPVEQVSEIKQYTDK
KVGSLRNELFTALQETYLENDMIDAKLPTSQSSKGCAPVVASNAIRIRDSSDGKTDARHD
TFASGSRRLVPRTSRSIFTRIEELESRLEAIEVYAPHRCAMAARPPLLGVELRDEKGVGV
RIVKVFHGFGGEAAGMMPGDVVVAVSGQEVLTRAEMYAVMTEFVREHQSRCRLLKELYFK
QHVQLKKNASGLMSTHHDSSLPVIGEEARANSDLDSCWEILRLELKFHLKRGDLLCEVGV
AVEANEDGILKKHERRKVAVVGEVMPKGVR*
>TCRU_6562 phosphatidic acid phosphatase, putative
MDINRLVLYWKTYQLIDFVLGLFLLIFSSILVFVVPPYCRPFSWNDPTINYPYVTNVAFP
AWSLLLLFVLALIFYVAVLTFLGGPIWVWLKAQTLAVISQLVVVNLLKIYAGRIRPDYLE
RLRSLGIDENTYAKIDLKYMASAEFYCKLGVEHRVLREGRLSFPSGHSSTSFSVLTFMSL
FLFAYTQPSSRGGSFLRLILSLSPLAIAFLCAVSRTRDYWHHFDDIVAGALIGIVSALMC
FYNAFYITEDGRCVARVIELAQQEERAGEISNGRPLSVVVA*
>TCRU_6563 hypothetical protein, conserved
MEEDRESGATQYTFLGVQFDHTHRAVSLSDKFVLFVCAMPALNPLTIAEMEVVASRFLYL
AAILCTRLCQYYYFFIKAVRRRLSALHRGIVQETSPANVPPSAVGLGEGLRHTIGNNRKR
IINSTEKASAAIITDASLHG*
>TCRU_6564 Enriched in surface-labeled proteome protein 1
MLVGKYSPTAVVGAPKNDAEDCGLLLLKGKAGGGSSDSIIWGDTAGVPCISTVEKEKVAL
TRLTGGGGSGIKMKDGTLVFPVEGMKKEGGKTVSLLIYTFKDTNTWKLSKGMSDGGCGDP

SVVEWKDKLMMMTACDGRRRVYESGERGNRGRRHSGHSRACGATNTRNRRNVLRAGALQR
LLKMEMPTKKWCSLLCRCIPRRNAAKRRKRVNSIFG*
>TCRU_6565 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWSVPADGAVVFSGGEDNILKEVFIPVARLRSTQEQRAAATADA
KAAAEKAKAEATAASEAADKAVAKARAASEAADKAKAAAAEAAAKTAAAAEKAKESAEKA
KAAKAIEKEEAATAAVEAAAEAKEAAETAAAQAATASEAAEKAKAAAEEAKTATAKAAKE
EAATAAAAAAATAAAEAVEKAKASAEAAIAAATKAKVAAEATAAAEAVTATVAAKEEAEK
AVTAAEAAKEEAEKAKTAAEAAKEEAIKLAAAAHAAKEEAEAAAEEAAAAEKTGEKPAAE
KAKAAKTAETKATAAKTAKAAEEAAEALRGTTVGEEELKTAMNDQDNSVEHHSGEKQEIL
KEEEPERQEKEQHEKQQHQQREHSARNGEEYAKQKTANGTNATAIKDDSDGSTAVSHTTS
PLLLFLLVFACAAAAVVAA*
>TCRU_6566 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MGLSYTADKKMETVFNNKITPKSSTWEPKKEYQVALMLQDKKASAYIDGRSLGEGEVLLT
GEKSLELVQFCFGACVQESSPTAAGQHSPVTVKNVFLYNRPLNSTEMRAIKDRVPVPTRG
PESRVEGGTERRHIPRIEGVRANAPAGSGLLSLLLLLGLWVFAAL*
>TCRU_6567 hypothetical protein, conserved
MPSDRHIPGNASYLSGELLLVEVPKIKYGSGLPFLRHRAKLHGSGFGMGSVVCGGGAIGV
PSLALVLAQVLGGGSGGIPGGSDSLRKPNSRSAWERVTPWALAMCVTTLVRQLQCLPHTV
QSVGHRIVAVWGPAGGDGFSVRSSLRVCCAASAPRQRHVRGMAGCNGRSSHPYS*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MVDGARATQRDSPADTCLGRWMQSSVGACPRSRHRVRRRAIAAVRAALLVALALAAAACM
PAVHAVVLRLRGGTVDRAITVGRAVDTVLMDGVSITNGVAVVFDVAAMLPGALRIELRNC
VCDGGAQIYVRGYSGEPASDRSLEVSVSGLSGSYCSLVFVHNLPAHTNVTVRDSTIVTAG
PMRYSQLSGLTDAVASPLVLYATSLLQSQLRVSNTVLRSSQAGGSAVYVGGGVDLLSGAV
VLDGVLLEASGGPTASAMRVASSSRLSLRSHSVFSVTNVSVVSSGGGFVLGERLAVLDSV
LRFVGVEGSVASSLVRCDGGTIGGGGWLDLHDVWAVGEASSVALLSGVMLSGGTVSIARC
AATGATLVSGPTITSGVVSVQCNRAGGRVLQSSGDYRMAGLPSVSVVPCDGCAAALACFD
ALTASFSDCVCSCRAGGVGEACLPFDVPPARASGGGDGGAQGCVSGVTLTESVTAGGGRA
TACFDSVLFSGTITVAVDLRSMDAFADALNVTLRHCVLAGGAQLRIGGLSESTARLMPHA
FVNMTNVTSLEGTIVLHGAMPLHSSVLLANSTLRATVGGSQYVPTTPGYEGFRYGPALVL
DSVRLLSTRFVMTRSTLVCGGGSCAAILVERGLGVNLSSVFYMDNCVIRSRTHVIYALAS
DLRVGNGSVFSIQDSLWSAPSNEYYKGACVFRDVVVAGGSVLQIVSSTFRLGFAMLMANT
LTVTGGSWLVHRDNEFRTAYVVYVAKENGVAFRDRSVWSILDNNFTYGSYSSTIANMTTN
WSPPSDTRPTIYGMCNEARGSPVTNYQDDLNIGAPVTVLDCGACTMDAVCFAARTSSIRG
CVCECAAGGYGDTCLPAAVPDGLGPLPLPDAKDTEVRCVHGGSISSVDYPDPGVRGLCFV
NVTFTAAIVLDLSYFDAPEQTLNITLLQCVLMGLLIRGSGARVHVSVTSSILDFGALDFR
GDFGASSQLLVVGSTLVTTSSHAISFVKFTLSANMALLLLDNYIEANRYAVYFFNGVVVD
GGGIIVKGNTLSTTKDDDGVESSVCVNGVGVKSGGYFDVENNTMSSVNGVIFFGDTTVSS
AGLLRVADCTFGGSEVFDSALLHLSGSVTLEGGAQWRVEGNSVGEASVLTIPYPQYKIQL
SGSGTTVALANNRQVDNSYPFADLSPPDTIVEFPARFVVGCNLQGDEEVSYDGVFPDEVE
VFRCGTCNDDAACYMPGTESVDRGSCSCSCKDGWHGASCLPFEVPDTVVPPVAERAVDGD
TSCVVDQTLTDLALNMWKTHHCYVGVIFSGVGAALAFFLNSMPLHLPINITLTGCTFRSG
AALQFVGGAAAVESSGVLIRVSRTVMRSSTVAFIRALPQHCDIAVTEVDAAQFSSSELPD
TRMNTLSVVMLKDAVLSASSLLVSNVRAHATKRDAFVVYSTGTLTLVGGSSLYARYCSFD
GYTHMFYLYGLSVSDHSVIALLNNTMFSGVSLLYQHNRFNLSDHSVVRVVGNSGSVRYAI
YNDDMWTVQRSSWLDWRDNDVEVGAMFYDSSSAFVSIDGSSVVTLTGCKMGSTGLSVSLL
SRADAGYRFVAGCLTVAGREVMTAAELALNGITSVTTVTACGECTKEGDCFAPLTTAVID
CKCRCAAGGHGDVCVPAPVPAGPPPPPPPSSPPPPPPPPVGECISDMVYPEVAQAVGGGL
SWLCYRNVMFSGGGMSLTVLIGAMTGDVANVTFDGCTWRDGAVLLLLGNAYAAVGSLNIV
VTGNRFIDALLSPEGVFPPHTNITMSGNSFTVTRLFHWLGLDLRRPSCVVMNGLAISNDS
AVVLSGNVFRSVSTSSSVVKFVGSALRVSWHSVLAVLGNTFHMGGGDSTLINIEGSGQFS
SLKVLNNSAVVIRGNVVTRPVKYFLLVILALRVESQSAVVFQGNDMQRSSAVFFSSYSSY

IYYNSWLQLSGNLCRESPSDAFLFLNPTVNLRDSTVSVSGNRFMSSTGTPTVLRISTVPR
DLTNGAIVAACNTVNDKERVKYAIPSVYKATILTCSDPCALAASCFPAYTTTASSDGCAC
TCSVYKATILTCGDPCALVASCFPAYTTTASSDGCACTCAEGGYGDACLPVAVPEPPSTD
GADLCVRDVRVGVKLSAGFGTSVACYVGVTFAADVVVDVESMSGSVRNVTLANCTFVDGA
SLYVVGWRSDPPAGQRADVLISGLESRSGGGVLVANRFPPGSRVTVVDSVLIAEKRVAYR
GAYGLGDASACLVVHNVNLTGSVLTIARTHMAAVFRDAVGVLFVGGVALSSRGALYVDGL
SVQTALGLCVSVEGGVAASGGSVVAFVDSDFLLCKHVVSVRGAVSVSGSAVALVRNDFLS
AEDYAVAFYSTVSLDGGSMLLAKGNAHDGVSREMLYTAGTVTAVGSTLSFVRNRALLPRM
VSLSLSLSAGAHSRVACNDAGDRVLSTAEEYAAAGFGDAGSIDVAGCDDCDRDTHCYAPG
TASASMKDGVCVCLCGSGGHGEACVPVGAPALPPAAGTAPSVFFREGVTVRSVFVVPAGA
SEVTLRHVVLDGVSPVLYVPWMARDGVRIVVQNVSLLNGAVLYVMGGGALRGAVSAGSDE
GGPVELSVCEVEALNGALVLTGTFPARSVLTVTDSLLVATRPTPLVYLPGSQSSPYAPVL
VLSGLRLVRSVLVLFGVALVTVMTGGRTVVVDGAVLELVGGGVALDAAVFGGEYALYASA
RVVASEGAVLRVSGSQVYAAHGLVFESGVEANASAVVVNDNAGALTDGALLELRGSASFV
SGSWLSVRGNSISGRLLSVPSYPRSAELVQSTLTLHGNAGSGPVVMDGTVALGGAGQKFV
MGCLTLNGQALQPMDYRSAGIIGEFRPVACGVCDADVSCFTAATRAMSGSCRCRCADGGY
GRDCLPVYLPHVDGCNRTLYRPLLSHTASLTETRSLTSTCTPSLSTAHYSPLRYGPTETL
QVTETVALPPTRTPTASVSGTLWRSDVACPTLSVTTTAAGGSLTQNDIRGGGSTVPTRLM
VALPPPFRWARDPRLGTHLSFVPVATVQPSGFGGPWGAMLSNATWVRNATNPSTVLELAV
PVHRGYFIAADETIVIRCDAAAVSGGCKGVLLGSFTIRSDTLPAAASALSAITGVAAGAA
AVAVVVTGGLGSVLEMQALGVFARMSCASAQERASTVALPYFLSVFAALDPLWMVVGNAL
LAAVFGCVHCGVTAAFQRWRGVDAASAWAAMRFPSLTYVVAHAMHLGVFFGSVLALATPD
ARVQHRVVGVVGVLYGVAFPAGVCYLIARHTGASFTRYWQFSRKPLHERLLYPVGYWHPA
AQRRMYGSMLTNMRGSRVYWCVFQLSVLCVVCLIAAVHPPVGGCHVQYFCMATVLVAGAG
VVALTNMMRSAFLTVMHTASFVLLAALCVVSAANHLAPSDGGTRAYAAIVLLLTTVVLAV
TVYSVVVWYAEDRHWQELREPRRGGLEALLRDDEESDEETQKPHDRTSSSYASGTTVTSS
YRPPAAPLQPMAGDTRSDAQSLLECASSARGKIDHALL*
>TCRU_6569 hypothetical protein, conserved
MAAPSLTDSECDNTNDGKGSDEDYGDDLHRGADYLRVLAHESQEGLDAVPTIPGLGLGNR
KRDSGRQFSAPCVEADPFAVEFMQQLSSVCAAIPALALSHVSQCCLADDLMSVVQAAASS
FLLVPNKKHFALRWVFICVAVDARDDAQRVCLLFGGHEGDFGVCRRLRESLR*
>TCRU_6570 Mucin-like glycoprotein, putative
MMMTCRLLCALLVLALCCCPSVCGTAAVVERDDSGTDLTLQEGVSKTKGKQNEADVKPAL
TPKELADENENGTQDIQDPSTDVISNSNGASGKPGKTSTVNQSAANPKLEVPVEKTKTTT
TTNAPSTITTTTTTTKALTTTTTTTTMAPTNTTTAPTTTTTRAPSRLREVDGSLSSSAWV
CAPLLLAVSELAYTTVG*
>TCRU_6571 hypothetical protein, conserved
MYADDPSIIVKGQSREDAIPTANMVLKKLHAWSQENGLANNPSKCEAAWFTLSTHTESDY
DREGKWPLVVAGCQTPVMTMGASRTTKLLGMDLDPQLTLNVAATKQCAATSQRISQLRCI
AHKEAGPSPHDLRTFVIGYGASKLRYGSERIWAVATDSAKNEMQKTYATLARIVSGVPST
VDPESALLEANMPPLRVLCLRARLSIFENTRACQTDWMRRPPPEPPPRAGFRISPLPRDE
LYAFVDAYTKDYGISESSPREERFFRSSIPPWFAASAHRVIIGVELPMDHSITKRS*
>TCRU_6572 protein phosphatase 1, regulatory subunit, putative
MPHTAEHGTEEADMKAEKREKLRKGLQALFAAKNTCVHKDSDEESAEEDPLSVGQGSREC
HTTPEAALTIDTKGKIIEINNVRLFSLDEVELEKFTDCISLSLRKNLIHELSPFPEDLAA
RLEELDLFDNKIRKLRDFFSTVRCMGESTLKENVTGAFGHLTKLDLSYNQIRNIGGLEPL
ASTLRELYLVENKIKEIKNLDSLLNLELLELGGNRIREIGPGLAKLTKLKQLWLGKNKIA
SIGTSLQTLVSLEILSLQANRLTSVEPDNFLGPDANPHLRELYLSENGLKCIQNLGHLPM
LQLIDLSFNPISVINEDVINPRNMPQLIEFWLTDGKIEKWDELGKLSGFKNTLRTVYLER
NPIEEDKRYRDKVYMQLPFLEQIDSWPIVNKGDLEADRKRRA*
>TCRU_6573 hypothetical protein, conserved
MEGQKHDWSSAHAQLWTSFKKSQKGNNLCESNTIVSMDTVTPVSSVFEQNPTIGRDLTSS
ILDEVKTRTRLDEPVLSNKLEDQIIGLVEDVRTDASVRELLSAIIHLKNRVEKANNEAVY
RQDSLLQVADETLFHLNGQKNAAIAPEEMVTEGTGALGVIESRFFAVLIQVEKCKKAIMA

LAEKNGLNKTLSGNSSMREVLEFLTSSKMPVSEGAEFDNEENAMLHQVMDILGFPSGTSL
DQAPDLALKVMKELEFLREENHTNSLLILQYERTVMAKFASCGVVSPPTVEQERAALLSE
SEVLYPHSDNQWIKDHLRSLVSVMTEVNKNYQLDVVPNWLLGGPQEASAEAFLNYMRTSI
GGARELLILLARDLMEAKHSLLEVPQNEETLNMMMRIVSCLPEGDQIKIREMKSDLDSLA
DYVEDAVKSLVMASSVQEHMYSQVKTLISQIAYLKDIADGRGHNALDQATLSSIVGAAED
LRVWVTERYGVDRRPEDAIIQESLHELAQLVPTGLAPSCTVGEVRIDPPVNNILDMVRLL
KSRIERWIQEQQKQQLSGARSRLGKARVEEIVRERSKKLVRITKEILLSSGNSSETEDIL
GALSAELMDGPTTAVNGGNDGSNNNSNNNTGGEMVSVATVFDDLEERLKLVKVRHHRLFQ
SCAADKVRLENLIQSSNAHNKRFSRICTSVGAICRTVGLEQIGSRLERDSKAETVSSSSQ
LVLRPEQRRESVVQPVNDAEIIEALRLIEERLVKNEAIVDSAQQKSELLRLKEEEKHWQE
ETGTFRQAMQMILVRLAEAGRRIKCTLFMLGTDESAEDEVVESVIRQQQRSLEEEGAENN
YDSAGQQRQHEVSEESLAVLLQKFGRWATRLQEATEDHLYTQQKLNKYFADVHRLFCPTG
DAAVAQQNTTDENLIDIDTTLMHFADGILPVIDRALADAEASSNKNDAGGKGAGCEDGVR
SKAISILLQDAPQNRVSHMDHRLVRLYEFVGKLRTIVDGLLSVRYLSIPLSSRRRGGNAA
DELIFEDAWGDSYVELDVGKMKCATTTDKGDTDALNMSDDMLFRTVESNIRSVHQALSKF
STNYKLAVILVQKDTDMMQQFIASMLEPYVELDLERVFRQDPVVLKEMFALLNERTARQR
GCYFFNRVGGEGPCLWATALEQLSLGFLGIIEKLRKRTQVAMELRDIVDDAVDFCAMYVN
WVELNGEAILSLCPLPQEVVEACVREDNDAEVEGHLGQLKQQRGEKKLPKPPLPPNHPRS
KVSHFVEDTIILRVIAHMFQVAQTASKNKEGQGDNDSGKMVVGNSDGIDATDEKTQEKQK
RKQNQQEEEIQQLEEQLQLLRESAAVAEQRANSALESCKRMEQERDRALSEAAVSRAELR
RWRRFYGIAEDKVPPLSQQHLHNHQVIYPAALTGTTSSVDTPEQNAPPSSPEMDSNSSLP
GYPAKDVLSQLAYSMKELTEELRGAFQRGAVLSHQGTAGTNSATVETHPDGLPRAAGNSR
ERMTARKQSQRNTASRSSGLVRSPKEGMEVASQSRCMSPLSASSSLLPSSTRDSRSPLGN
NTCSHKMQNKRQQRDVRQGPLLAPCASVVVTPKKPTYLSLARAHSNTTLGATRAPSAPRY
QPNLHRSEYFNECDACCRHHRSGRSTKIGVDTVPLASSLSRSPNLQLTASASRGSHLAGP
STRHLKQNEEKVTARQYQHDRSSSARRSARLSRSSTGKISLYNAANDTMRTSSAVREHPA
AASASSSLAATAHGEKHNRDHHVRAGPKQPSHFSLSPSTSTVLSPESTFSPTDAGAEQYQ
QQYNYSQHQQCSQKQQQEDHHQHRMTSRPLKEFQGIGGASLGTSLETIGQHTGPKTSPHP
GLHKETVRRTARDTEQQTRQLNYFNSRDRIKAPQSANLRSDAVRKLADIVSRTKVSGDEE
L*
>TCRU_6574 hypothetical protein
MTPEHSVSVSQSSHPQITPVHVTALDLETDLKTYSRLIETISESTWISHNNIMVISYDLS
LQFADDDSDEIDGEEGVYRRVILGFWKREDASTTKRALLKGSIPNVRLYTRTKTDETGGL
TKTQKVILGCALGVGLPLILAIVGATYFLIRYHSHADKEVGDLRTGKKGNTVIDLDYNAV
RMAPVNTTAPTVPIKQKNSSKPLEDIL*
>TCRU_6575 V-type proton ATPase subunit D, putative
MSRGILGFNVHDGCIEAMVHGYKDGFLRPEEYSSLAQCDSLSDMKSQLQVTDYGNFLQQD
GQLTSRVIVNRAQEHLVRQLRDLREWATPPLSQFLDFIVYEHMISNVLKLVIAKRSGRES
LELLTKCHPLGWFPELVSLTAAADVQEMFHVVLIDSPVGRFFSADGDFARDLDELSVEYI
RGVLMRNYLEQFYDFCCELGGETASVMCPLLDFEADRTVLTFAANTMGMQEMHAADRRRL
FPNIGTLVDIHDEIAEVESMEQLRERLRRFAEMHEIFDDGRGGAGGGVDADRHSVEKRFV
ERSVVIYKDAMTRQFQYGVFYAWVKLRELEVNNLQWIADCIMQRMMHRVHEYVNIV*
>TCRU_6576 hypothetical protein, conserved
MKSFFSRVVNSWKRQRLPRSDVDCSDFVRVRPDAPCVARLRQVVQERRFGAENGGAPSPA
ANSSEALHREASVRSTVFDLRYRCGGAGRCVENDYRCRFPCCFAMRPVTKGAEVLAERLA
YEVDDAPTPQIRALVQMARDEKLEAVIQGIQALVNAQIREVAGGRELLAALQPSQREQQE
QQLGVDDFNPAAPKYGRGSVAEGVNPLLEDASLRREVVALYLWRAALLVNVREDERAVSS
LLNLAALVPQEDRERLYTSAAAWAALNDMEIVYYRSLLQQYEAFPEAMTFAHDRPLLLKR
VFEACGETAYFLECATHIVFSKEVTATVSRAQGAQMYGDFTEDPMKSLCIPLSLQYYRFC
VSDAFWEHFMRLLCMPPIPAPNTPEERARDPGEQLGLTPNYMLDAIGRSMMLHHLVMLHE
ARERREIASGAIVDVVKQKKAQGGEGSVVHPLHYEHVLNDRERGIAITRLRELLFLARSYR
NPQRPLDGDDSDGVGEKGQIAPKADSAAAAAAAVTDNGQ*
>TCRU_6577 stomatin-like protein, putative
MLRRSLRLLQYNAPLSYPYAPPNPAGGPYDASTVSAASTAGANNSGGYNYSGSSGSGGSP

NMGGGNLMQRGNRIHLNPASFVESVPRNTILNIVPQGRQYVVERLGRYHRTLESGWWFVV
PVLDKIRYCYSVKEQGVEIPNQSAITSDNVMVEIDGVLFLRIVDAEKASYNIENPVYNLL
NLAQTTMRSEIGRLDLDTLFRERTLLNKNIVEVLRREAHDWGIECKRYEIRDITVSELVR
RSMDLQADAERRKRQLILQSEGEAQAEVNRAEGLKRAQRCAAEAQKYTVLQRAEAEAEAT
GVMAAAISKSVTVVAASLEKTPRSSDAVALRVAEKYIEKFGEIAKTTNTVVLGKNVGDPA
EFSAQALSIFNTINNAYTDGKGSNSIGCIGSGNTLASSSSSTSGN*
>TCRU_6578 hypothetical protein, conserved
MMQRSFFRLAGRSGAFALCATLRSPPFTGTAAVQENNPKAFKMQPMQPHSRSTHMYETSA
KGGEVGARNEAACMNYEAFQPTDLNGMLAMPHTINLLTITPIYCFLVCLASVAWGIFYWD
LYCRRTYETVLIARPESLR*
>TCRU_6579 hypothetical protein, conserved
MHEGDGAAYNATRAERFERFLPAETFPPSYTQVATSAGEKELLAATELFRAEYHEYYPDR
APLLLTPLNECHARKMICTFIKPTVFPFEELFDLGPCARYFAGYMRYEPLEDLEKLPEVV
VSPATALQWRVGNCFELSLLLASVLAGAGYNVYVVVGYARRFVCYNDSSKRMWNDSEGLF
HEVESNDEQEVEPELDAEYAQLVTGRPVLRGVHDPEPAALQPKEVAPREKQITNTTGIGM
GIAGDEGETAKSVRSADSQPFDDGKQEEVEQQPQPQQKQHMPQKNLHSWLLVLPGGRKSQ
KEALFVEPSTGDLIPHNTADAFYTGIEAVFNRRNYQVNLAPNAPVSALTLDLDDGTQWEG
MLFDLDAEEERDLNLQTTTSGTGDRFNYTTTPGVRWRTHGGDISTQNLASTTFVGAATIS
GSIPSLAAAATVNVLTHSARDKGPRRGFISWVKDLTLNREQYEGRYPGGKKSIKYANAEV
RCFAPYAMPDLRVMEVRLPDTTYRHQKQVHTLFKHRADRLRRRSVYPSKGEEYGDNAGKD
GDMDDDGRNFYGNATARVGEAASFRLVKEWYERGRMREASVEGLRLFTHEPGVERTMNFY
WDARDDGLWRRQEFFYEGCMLRKVKEFYRQRDDRLWYRSASFERITSVLRVSRNRGSLFC
DRPNDEKQRLEPVRMSEKYHRNEAIPPDEDVAKYTFVRFTGGNGGEMWVYFHYRPDSMIR
PYRMYTKGPRGEEYLASTVVGNAPAALPSTVVLMPNAEEPSELEQYNERKRLAWWESFCL
GKVYSMMAECNGILSAMRDARVPEVRSVLSVFDTLRNRPHETEADRARKLAEEASREASR
KDYLAPYIAKLALPSSFDGDYLNVSLSIEQARKVRDEALQELKERLIQRGHIMQSQMDAE
KRDFNERQAAYQSKLDAAGLDAGREEEEFAQYCKEATWRMKTLDERLSKHIDQSSERYAQ
LAQRLSEDPRLKALYKVQQYSS*
>TCRU_6580 methyltransferase, putative
MLFFGWFACNSSLAAFCLEELRAAAATLGVDIHVQECLPWLRADSSQTAFCVFDAASVAV
ARQLAGRCVLLRAVHLLIAAAASVEDLLACIAGTSDGGIGEAKWLRGMAWPDDTILRPAD
CTVQVETIGRHYTLEEKTALATRVSVAMRILPDASRPRATEQRPHRLSFVVEHAIENAPT
GALASWLPCGRVLRVFCGALVSESNRQHLLATYDLKRRPYIGTTSMPSEPAFVMVHLAHV
RRGNYVFDPFCGTGSILIAAAHYGAVTLGADADARVMRGGSLRCKASKQQQQQREVAVRS
YTQDTLERAGITAAEAEAPSMWTNFKLYGLTPPDRVRMNFANWHAALRPCNMHGREKGPT
DRGDRGFLDAIVTDPPYGIREPRKKATRLTGEKVEMEEGTDIPACYPVSSIVLDLMLFAA
ESLVLGGRLVFWYPTTTTTTRYTDDELPTHPSLRLVCDIPQRVSLKIVRHLIVMEKTRPV
PFPPPSRASCAATRQAPDLRALMDATDLPDNADYMHYRSKLLRKRDSTRRYFATTTSSSL
STHGDDRPGEAKGERRKLSRAERQDIIVANRERNLQQKRQQQKQQQLTWREENRQSENEG
EGERGRHSSK*
>TCRU_6581 monocarboxylate transporter-like protein
MLPCFTRKPVDHPLGFLVALSGLLMQLMSYGIDNSYSIFSDDMHKDPSLGYPSVTTISLG
NSVSLGLSPAFGVLCGFLVDRVPPRLMMAVSTLMLFAGLWLSSTFAHNVTAVTFSYCLLA
SISSACMLSPGAAATSSWFNRYQGLAMGINFSGGGVGSAIIPSLAGKWVVAYGWRKTFRL
MSAFCAIGVVATLLSARRAPPKKGGEGPSEYDEGQERQEQGEEEQAHTEEENRNNNNSNG
ETTPAQRGLHTHKLNPWELFLSMFSRAFLGNFFCWLIFSWAFYSLIYVAVPYVSSMGKAG
TVYADISPIPTDIASTLFTFYGVFQIVGSILVGWLATGTTNEFAYVLCATIGGIFCAFLG
FCRSYVAFALLLCVIGFCMAGMFAVMPALIAERLYGPNLGFYMGAVFLAGVVGGFSAPPI
QAELQQRHYGNYTYVCVFMSACMTLAAAVCYITMWRDKRVRIVSAAAEAKLA*
>TCRU_6582 hypothetical protein, conserved
MVVVKGGGTPYTIGNGRQMPWEEVPEKFKEKLREQTEVEKCVGMRAEAQACIEERGFWDP
ACVDLTERFHLCQSMELSRGINKWQEKGGVTEKEA*
>TCRU_6583 NADH-ubiquinone oxidoreductase, mitochondrial, putative
MLRRAAGFFSLTVSLLEKTHGGLKDQDRIFLNLYNDFGTNIASAERRGDWYRTKDILLKG

HDWVIAEMKASGLRGRGGAGFPSGLKWSFMPKVKPDGRPSYLVVNGDESEPGTCKDREIM
RHEPHKLVEGALIAGFAMRARYGFIYIRGEFYNEWRSVERAIQEAYAKGYLGRNACGSGY
DFDLYTYRGAGAYICGEETAMISSLEGGPGKPRLKPPFPANVGLYGCPTTVTNVETVSVS
PTILRRGPQWFSSFGRKNNAGVKLFCICGHVNRPCTVEDEMSIPLRDLIERHAGGVRGGW
DNLLAVIPGGSSCPLIPKSICDNVLMDYDSLKEVQTGLGTAAVIVMDKTTDLIAAIHRIS
KFYANESCGQCTPCREGSPWLEKMMRRFVHGNAKKEEIGTMLDVSKQLEGRTICALATAA
AWPVQGLARHFTPMLEERIERYWEANPHWGKSGSPWRRWKTHRYYTMQKGDKLNWDGKIV
RNWN*
>TCRU_6584 Enriched in surface-labeled proteome protein 1
MGIGWEKLDNWEDVPDAGGKYGSLRGPSLVDLQGHVFAIAEVHCKDGGDCSDVGFTGIAS
KYLDLSGVADPTEILTADASIFGADLLKEGSEFISARNGITRPTTLVLGDSVYVLPGNYS
HTGPQVGGTNERGLLLLKGTLTDEGGRKKIKWNETHVVEPQGRGDSRSLTELVVGGGGSG
AVLRDGTPVFPMQAKDKDETSVLLSMRLSKSGNKWELSLATPGNGCGDPTLAKWEEDEDD
ERLFMMAHCAGGYYDVYRSTENGDNWYPLGEPINRVWGNSHNRTGDGVKSGFTTAIIEEK
EVMLITAPVYPKEENKGGKGRLHLWVTDNARVYDVGPVSREDDDAAASSLLIKDKNKELI
SLYENRKKSDGAYNLVAVRLTEKLERVKEVVKTWKDLDSALQ*
>TCRU_6585 Protein of unknown function (DUF3676), putative
MSSGSYAEEMPEEEGEADGRSGGSTSSVGASSDMDTATETVDSERQLQQSTELSAENEGL
RSTGTGTTGAERSLGLEAGDRNPERTMGSDSSLTPSGIDVEPTSAEDTDDVSRTEGTEVS
FEDGKEVPQTVDTKPENTNTTPGGEGIPSTKGAARHSDNDTFTGEIAELLSMGLSRDSTV
HVCVYFVCCCCFFYRGCGALWLFEE*
>TCRU_6586 hypothetical protein, conserved
MGFWVFDRVADGFLFPGRRQLSRLHQRNAMLDANGMPLTGDLAAEATTWRSHHAFSGRCG
LSVKRSPEPHDKRDEARRNGGGDVPHPEKMLPSHECIISRSPNDYRAWAVDFHLQSTSEE
PHVLLSVAPYYAPLQSNLVEGGRSWRPPTTEEQEMYDKRMLETPLIWEEPMTLSLDCTNN
GMFLWSEEWKIFGEKIADNCFSRRSQSRGGDDSVDQMGGVSGVREGPYEAFVRLSWRMMS
AGENDMYGGEKRSLSDASVRNIIVGPCQGEMTVFLRTSSSDQKEGDVSVPRQINGTGNVG
AHGGESVSSGVQVWKRAGGRAVLGDDIPNEIYFTPYVTLMDAGDEATLL*
>TCRU_6587 Protein of unknown function (DUF3595), putative
MSFSISSFPVLRVRLLEVATKGCTVVSLLLLAGGLLAQSPVVQQIVLEHGEPIDVWSIMR
YECDWAKIFKSSAVFRRGAQFLLLSYTIVASRYVHGSWRRISRRELEEHREYFYEPPFLL
WQLFSVRYPARLRKIQQFMGYYLPLAVFPLMIIMSFMVMDLVSILMVITTLFGFLLPSDT
YVVLLPFCYGAIALGIVLEFVATVDSRLQQPFFMVYAATGVTAFMIRLAQCFVNSLLILA
VCMFRVNPIQGQYRSLAEKKAQIRMAFNHLQNRLDEIQCIFKRVCNGTTGTVNRDGFPEL
LKQVLPTSRIREKEIDSLWRFLTEGEPVLLQTTPQVTPRINKATLEFAGNADAVRNALSH
LSSALHGGRRASTSREESNGNRDDNDEKGEDMDLEAWKEIKNGLDSSSCMGALEIKSPSR
EEEKSLEAASTTISFWDVSSGEDQFRRGEHKNGLEDKVQHQQCSGRNSDALSRTISAVGS
PGGTVAYLDFLVLVSKIESYRMQHRNGVYVAASMIKQIICLNTSTLSLVAMFAISMAVKR
LDILNGMYLLFFIGLACVPWYMLYCWFIIVAYTALHVAVRFTVMVYNASYHPNDTPSYWT
EIIGIDIGKDPFALLVYFLLLILAVFQLRISRHEASGKITIQEILQRMEWCRYTSCDFFP
QFYRHFLELSTSLVLVMMALFIPHNVFIAGFALLFLLYFSLGAYSKLAESVTLIALGAYN
VAVLLISALYHVPAISNSFAERLSNITVCQKITVERCALDVGVSQNNQFGSMSLNLLPWY
LAAALSVALCRHYFGVLGRGINRREEGNDDEGASVRMEEMQKMPDPSIPNRRGAREEEEE
EVARERNHAMREERDFLENDGRQRMGLFFCSYTATRGTFIGRCVPMAFAISRYLYLAVTF
IREAGTAQGKLMVWVSLAYASLSNFSVLGAAFMTLFLLDSRGMPVVAVAVAQMALNYVYP
FFFIPEAPLSVSSKRFFGLQKTQNGERPSILPPILACAMAVFYMHTEKDRTARHQEDALR
QAHRRNNPPYHIPSARDGMRAFVRSEEIQTPYVPFVASRENRERTREVYEPPAKFVTLKQ
HLIFMWNYFRTRFFLDLNFELTVLVASLGLALTPDRVTGLVFFVELLLMWLIGRVRSTIE
IRYAVLQESLIVIVLGGLYFIRLGLPKGLVGVSILHPEECNAWDHYCGCGLPLHHFVLMF
ALVVMRRCMRQNVAKVRATILCVEGAFELGELLCRKEKEVEDCRRLLRSDIESVLPAPSR
DIIRNPRTLFDLLIAVSCACLPAAVFAFVQGVLMASLLGVVEIAASLWILAFKRYLAWRW
HKVWPFFILFLFLTFVPQLVARLPLSPPLTTHAENLMLALGFSPWTRGTTVGQAMVLFSA
VVQQRIFSEFFFAAYLIGLCRGSLAAVERNREMLEYFRRKDEELQSQVVKEEEALKRRLE
QLFSERNMCACQDEIEIGALMPPQRVNEKETREEREFSSGVAPHSPMMGSVSKVPLSVSA

QSDTYFSVLDSPKQLTKAGAAVDCPATTFDGRLSGVCSEEHVPPAREDDRKGGICSKISN
AIECWSEQLVQYFSFRTYRGKAPPRTYSQGYRVLFAFTQFLLRKYAYVCYFLFMLNYALS
GTIVDMVLSLSAALYGMLILPWSGKIYWRNALIYNVFSILVKCVIQLIVKWFAMNQMALK
IVSACVLDIGLDRTEPSFSAMNLDIIMDFVLFVSIIIHRQFCFDYGVFAKEHEEPFIPHR
METEKGEVHRKEKHHRNEESTAGRRELPEEDMDRIDVQCVVGVANEGRPSRQAPLSASSS
SSSSSSTLELLANKHDDNNVNNSKHDGIGEYNNSMRQKWQKRVFKKGGVLQKYWSNICER
YGTGSDYYTLQFWADGLSLIVFTVVYFLLAGDFRGSILYSVQQDLLPWQLVLILFAGVML
MAAERIVYVLHSVQLKFVLHVVTILAYHAIFMLWRLTLAHRSTTVAVIILLMRFFSGSVS
ALQLQKGYPLHRKHDPFTTHTDIFHWLGHVVYRAIPFLFELRLLLDWSVSCTALKLQDWM
LLEDVHHTVYMRYVDINDLAWTSPRKGRQFPFFVRMYQGILGFAACLLVLFFPLMLYSTF
NPNVGVNLVASWQTKIAFGTTSNFYTATATEVSVSQNLVSILWDLLPSLQHDEFGSQGLL
QLLMFPRCSAEVWSATPETRLLLLSQLNAAVNNETTFFIHKEDHVVRMEVSAPATRRVCS
YQRYMVPWSTVVRLRDALEGAHLWYTSRHLEKHQGGVHSASTLVYESGDWIPLPQFYSPF
VNNIQNDLVMKNYVRTDCAVQLNGVGNSDGKTPPVLYWCVRCNSFANLTDGSTTRTWSMN
GANEPLDMADSDNDNVEVMQSKETLESGTDAGNITSIFEIVASSYVALNPSLVFLPNMGI
IALYTTFILAIGTFLRNTVMDRAHRVVLMQVANPDPIAELLRYIYMARSSAINGYVDGLL
LEQQLFFELVDMLRSPERVLALSGRRVDDYDNCGRFCKYLKKSSYHPF*
>TCRU_6588 hypothetical protein, conserved
MSARDELIGRLKVALAEIQQRDSYSSNASLDSELLGVVADYIEQGMERETALQRLRGALL
RSEVALGGFAPAVEEGGDEGPREAASLGVSAEEMGRRRAERLLAQALTLRFR*
>TCRU_6589 chaperone protein DNAj, putative
MVVSVHKHDRVRWAWHVLGIDTNPSYDDIRAAYCRLAVTTHPDRCTDPSAKEKFQMLHAA
YETALKNNAEAKEKKRRTKSGEVSDFDWRAEVARVRAAYSSTFKCPRASDASRTPWQNAN
PNPSCSVPQRTNKRRCADQKPQAGAHMVEVRRATAARGGASGSSSGQEEEERRLQAIRVR
RRGYLSPSLNLMRRIVTREASRRHAIVRLEQKELRCIYLSSLEERIRRAIENWADAFWVD
MSEQWTELISFTTCSHNRSV*
>TCRU_6590 Enriched in surface-labeled proteome protein 1
MEAAQRSKEGLSVTVSNFLLYNRPWTSEEIAWLAKNKVTISKSKGPTTLVDTQSSATSGS
PVQGAVSLSNSARQLPSEQETLKANIGGAGGVSGAASVTTPSADANTPASNGEGKVEPTA
KKEMSVSSAEDEETVEGTDAQKEEVQPLVREVNATALNSSLGNLSQGNNSDGGTVRGSGL
LSFLLLLGLWGFAAL*
>TCRU_6591 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGVSVSNGDTGDDAGGLGEDENTELKEATSNVLQRDSLDSE
TVKKQLAEPKAAEEPLTAPEGDHTDRQGSSAVQVKADRDGRREAVEAKGSVNGSQKNPKD
ALDTHQTEITEVRTKVEGTPPSPPEGGGGPTQPKSPEVSRAPVQSPEQLLPPAAHAGEKG
LAAPTALSPMTSLQPPLLPKGKGETDGVQPGPEDKSNEPTVRVEPQGHANEGQHHSTQHS
EVPQEKELETQEQNTQGQIINEQHESERLQVQQEKEKQRSEEQLEQREHLHEEIRDQQKK
QEQQEEEHEEPQEEHGDSIKQGKEQEQQQQHQQHENFAKNGEEPTKNETAVGTNATASTG
DSDSSTAVSHTTSPLLLLLLACAAAAVVAA*
>TCRU_6592 hypothetical protein, conserved
MQPLTIVLVRRRQRQVEETADRDKQLPHCYRRGSEAESLSGLSPNPRAPPPLHPPLEGPR
RPAQHQRYQSSWGQWFWQRHRPCRWRPHLLPVLPQQTSHHRRPHRRCTEDRSPSKPPAAH
PRCRWARAPRCLSEHLGLTQVDILRCGVPRPGSMLSATGTDARGKACSVDAGETVLLHSL
SPRRPTEPLQEGYRWWRISCTPPRGHGK*
>TCRU_6593 Leishmanolysin, putative
MVTKLSKIRGKSNVLVVSSEKTREVTRKHFNCDRAPGMELEDEGGAGTAQSHWERRNAKD
EIMAGVAGIGYYSAMTMAAFEDLGYYRANWGMEEVMGWGRNTGCDFLEEKCVNNGTTKYP
DMFCVDGSFLFQCTSDHLALGVCGLFHFGRDLHPVYRYFKYPFMGGSPNELTDYCPVIMP
SGEGACTNTLNNFTGCRVGPNSRCVESDLLRFNSVTIGAICVEVSCEHKGVASIRYVGDD
TWYPCPEGHRLKPGPPFTRGHIICPRYTDICTTLASAVLKPTLDNNTFQNLLTPVEGPVQ
RSLSKPLEMKKTDARKKHFGVDAGSVAVTPSLPWLLLCSLLGALLGI*
>TCRU_6594 histone acetyltransferase subunit NuA4, putative
MPPKGYVRRAVAAAARRDFGVTTAFTPTAEEEEAIGLPAQLQQLQKRREALESHLETLDL
RVYDLETVYLRQYVELGGCLFDGFGLERQQQWGGVTAAAAAGSQAAAYRARLHSFSPSDR

VFTASSVGALGTVERLKTMEATGEGKRGGRRKRSRTDI*
>TCRU_6595 hypothetical protein, conserved
MASQLASQLQKLQQRPVGDKRLSQSFLFDASEARSFSREQIHQLAVHGLQTLVAIDNRFH
PFIEELFHPYKTRVERKLLSLEENRALDATLEQFLTLLSPHMFLTAAHQVFEYLVRVHEV
HVHNVEAVLRTFLPYHDHSLFARAVMLLDLRDTGFAFLEINQEHGAPLLREHLILACAES
RKALRIVCLTLAMSVRMKVHNSAANALFSGVAVRLASHPDAEALWRVLLPFIVEFLSGAV
SGSEEGGAQQELRLQEDTQGGNAALLLPSREVVCSALVVLAAWSNEVQLSVPTLATVVKP
IARFLTRAADHMVAASLSSSSSAVAAAVVPTSDLLAVLDLLFYTQRTAVTQVTFVPHVQL
LLALPWKQWAPWITAAAEEAANAGGGMYDSLIAVLLRQCLQRLCVAHSLESVAPDVLHFV
HCAVNDLPLTEELVAEVIEAMMACHVRYSASGNRDPEKTNKEEEEDEENTAAEAHGSRSK
GDSVVTTWIRALERRFGHVFDATLSRLLNGVTTQAATTAFLAQHLSGTRYELLEVQGSSG
RTERLPLFSCLLHPLPEVRLLAAKAMDSMTVQQLIKSSSAPGSGGGGNSLLELLEHVVQY
ERFRIVAEQFLRTAATTMEKLLALLVNGEAEELTVTMMAAPDRGFSCTEQDVIIQHLRNI
LRSLWLMATQHGVSVQKDFLGLALQPLWRFVEARRLKSSSGKRRKHENKSSSETDAFHDF
IRGLALYYVTLQYVDAVHQESTGEFTNETSEERSEAARQLRELIVELERRLTAVVPEMCR
TSDFYTVVAEGAALNAEKNEAASDVSNDEANGEQDGKKAVKRTEGPKQVTSSPTATGGVV
KSGYLSVFECVPLLELLRAEAHAQLRAALSRLQGKAGRGEHRFSRESRSTMMECCLVCAS
HLATSEASEADAVIRMLLVFFVGENNTTTGSGTKADDSYLARLREAQRAALRQVREQVGR
GAKNSLVAPYLPKDELTAAMGTAVRCSLEARLRNDSCTCDGVAVWERMTRLLGYLSTPLP
ALALSPMRLPPVYLRLLEPTDAAREEERFPVDWFSLVYTSVFRTRGCVSATETQQFSLSA
LSLTLLCPLAAPTSRRESLLQEIQNIVLTATREKGDVSGVNGATTTAAQISVELALRVEH
ISATTLSAIIESMACEESRRPLTRGAAELLCRMMARMCGKQKELEPIVPFCLSCRAVEHF
FPLRGKAARGEGATSGIAMDILLPALKSILTTGGSISNTTASSSNNNETAANDIPAAAVA
VSSAAADFLHAAFLRAELGTPSDDGEDACLQLCLALIQHPFLHVVGGRARPVYRHALTAF
ANALSRGLEGRKSNPVLFIPQGRKGESSSTSIAPSRGGKKASNSEENYAQHLAATVSHAL
LSNPASLNRLGGDATLLLAGTLGGYHRLFLPWVSRLLQQPSPELSVVVDVMETLAAPATE
MADAWEPPSWCALYNPLSYADVQRLLQLCGKVWNSSLGGKEGWCPRNKDALLALRLFCSL
ITVSPSVHFDDNDDDDSSPSLFTVIDGMLETFPLSGLLPLLAEADDLDEPQFRRQVFVYI
RSLVNLCVSSPQALNEGQSHGAARITRTLVRECVTLMAALLVPDVAAAGDEEGREGEEAT
TLSRHRIDVITELLRVVSPLFVPAPSIPVSGPGGSRVAGRTALHIPVVALLIRLEAVDFA
SAHHRYESAMDVCSSLLEGFDVHTQLSCLTQMMHLLIDPHEQLSLAAARRNGEEEEEEEE
TAVIKLFRKFVKPNQVINRQEMILHLINTTVKSEAFLSGFLELQHHQHASRSSHAKLDGE
ENEKEERAAVLTGSRTNDECMAMLVATLELFAHYAELNAATENDIMVPVSVNGAKKGTEM
QEGLPEYGEKKAFTVLLELLAGNTLACVLAGINEATFVACLERLLTDQRAALQQKGLEVL
LDRLHHALPTVENTLSESEVEEHRKRLRDPKQKLTLMDLVRVKARPLATKRSFALFSHLF
SLMRASVDCASTHSAGVDYLHPLPLIVGCMEELVRIISSGGSLQAEKTLLNVHRANRVTE
ATLSKLFGNKARVQSVHRWVEEIVTVLPLILSRAGTGMPAERTVATGGDTFASSRKEHAL
LATAALLTALGTVCQVMGTAFTTPHSNNILQAVVEVAVFAVVRVAPVVSRSETGSLLRQA
SLGCLLRVFPSCWLMCQPYLSRIVFAATHLHNVDDTETNYRSAETLAMLEAVLEPHLFIE
ACTECLSGVTVDTDTNLGRRPIRVRVDSHSFFLFYTSVRRRVEGLKREELMHLHVLVDGA
TIKENFWLASLHALATAPSLPSGDIVQPVLEAYMAFFLKFKAKQCVRYLSTVAEWAFGGA
AEHFLNRVEKQQQQKDEMEAEGDTRERDDTALVPRTTVHGWVLFYALCNHMLEKLGSIMD
FGFPVLLPYVVGTLTGYCSATQHAMQHAAGLIALTLEGALDCVRRMALAQTAGPDHDHSV
PMDNYLETPEVFTSVMPAVVRQLSNLSYLADATHDYAFRAEHHVVPAVRALFQSLTSSKL
QSRTQNELLKALRHPSRHVRRMTLLCLDGIYADGGDELAARLMAEMLPAVVEMTEDRDDD
VVEQARTLCNNLSAITGQDVLYAMSS*
>TCRU_6596 hypothetical protein, conserved
MAMTMTDRVLLVCALCVLWCVAGGICEEQVKVVDGGAPGGGSVVLVKANGVTATPMPSEQ
TGVLQVAEEAPNKRAADPSSEEEAKEEDGGDEPEEGSKEEAEEIIMEEGKGGKETDKENQ
SQREGAAGHPVAAKGIAGNSNQQTLHTPLSTEHNPSPDSPRLNLESPQNNLSKNNDSAKN
QQTEGSRPGEEDKSKLSEGVPEPGPGKGNSGPEPGKQTEIHEPTGLSSASSGDAQETKHA
VNGPPNASPGPVGGVTTGSHTDVKTGTEVHPPPPQEHPSPAVAAEKEDSIMEDVAIQRGG
NERPQEKLPEAATAAPPEGLRTSAVRSSEKTEDVTDENEEIGEENAEDETKQRQEQLQLP
QQPQQSGEKGQQQQQQQQQEDQSHGYSTDDGEVPKKDKNDVGTNNSDGSTAVSHATSPLL

PLLLVVACAAAAAVVAV*
>TCRU_6597 hypothetical protein, conserved
MEAFAITPLAEDDTTFVKDAQQFLAVIADMQREAEQRRCLLDDLRQKEAAAEMELEKCLA
VREAMVARMAHTKAEGLGLQSEYKALTTQQRAVEAEVLELRRQKSHWKKVLQEFQGSSSS
SHLLGSGDTDGATVKSASPLDRALHAWSQLPHGSMFLKELKKTLTEFIAELAVNAGSNTD
DNSNTTHNGTATEYTTAFLDPSSVFPHLPPLSKVEEAIILLIPFSA*
>TCRU_6598 hypothetical protein, conserved
MNASNANENNRLTLWIRECFADGIKQIIREEWETRRSIVSYEWRLREAKRRVEWLTGAKM
RFEREMKLLLHAEECLRKYIERAELRDAWNIPALCPFVVVFENLGVLGPCPFVSVEDCPF
YCRGEGYRSPHYEFTMKGKPQAVIHSIAP*
>TCRU_6599 phenylalanyl-tRNA synthetase alpha chain, putative
MSTVEDFVLQALASTDAVESDKLAETLRVSHQDVVGAIKSLEADGYVVSEIKPKPTWKLT
SEAENICESGSPEFLLWELLAGGAMTQEEIAEKFGKDVAAVAVANGMKAKIFALNKSEGK
VIVTRSPSVSSFHDGIRVSLMRALKGEHVDPKEAETLKKRKLATLDNMKVFFVTKGPNYA
TQRRAKAVGDLTKEMLQDGSWKTAHFKEYNLGAAGREVGCGQLHPLLKVRQEFREIFMEL
GFREMETDRWVESSFWNFDALFIAQNHPARDVQDTFFVSKPSTHKLDHREVVDRVREMHE
KNFNYTWKEEEARRNVLRTHTTCCSGYWLHHIAKSSPLLPNGRRDFCPGRYYSIDRVFRN
EEMDRTHLCEFHQVEGCVIDRNISLSNMMHTFQLFFSRIGVEKLRFKPVFNPYTEPSMEI
FGWHKQLKRWIEVGNSGLFRPEMLVPLGFDEDVTVMAWGLSLERPTMIKYGLSSIHELFG
HKVDLRFIKQSKLMRF*
>TCRU_6600 ribosomal protein L18, putative
MVKPHLRHYCVVGRETPSEKNPAPTVYKFEVFAPNFVVAKSRFWRMMREKNKVKSTHGDV
LSCKVVKDRKLVARNYSVDIAYYSQRCGYTHMVKEFRDVSKAGAVSQAYHDLASRHRARY
HNIEVLGVKSIPNHQVKRLSISEYHASNLSFPLLHRRVKAPRKDRVVFVKKNTKRAVVA*
>TCRU_6601 ethanolamine-phosphate cytidylyltransferase
MSSGKWHLNPDDPSNAYPLYATTPVPPKKPGTVRIWVDGCFDMLHFGHANALRQAAALGD
ELFVGCHSDAEIMQYKGPPIMHEEERYEALRACKWVDFVVEGYPYVTRLADMDRLEVDYV
VHGDDISVDLNGHNSYQEIIDAGRFKVIKRTESISTTDIVGRMLLCNHSGALTAAENKLL
EDEAKRHAAFHYLTTSRKIAQFSNNRGPNPGDRIVYVDGSFDLFHYGHIRVLQKARELGD
YVIAGVHEESAIRKAKGSDFPIMSLNERVLGVLSCKYVDEVVLGAPYEVTREVIESLGIT
VVVGGKKCDECNYEDGRDAYAVPKEMGCFYEVDSECDLTTRAIVDRVFKNQVAFLKRQSE
KRLKEITDFECKPALYKNVREL*
>TCRU_6602 Alpha/beta hydrolase family, putative
MASYTIAPHEDHDITFSSGDKFHVVVFGGIDAEYTRRGETPPPVLFCLHGAGMSCSSYFS
LSTHLIHPQHDETDGVGMHPDESTDVVRVVAYDMRCHGESTFTGGEANLTLELLMDDFSA
VLRAVKDTLFPDTARLYVVGHSLGGSVAVNALSKEKELMNMVAGVVLLDVVEGTAKLSLK
HMDKFLQNRPHKFAGVEEAERWFLQRGGMTTPAAAAVTVPPLLKRVGDHYEWKTNLEAMA
PVWSGWFNGLDDAFVGLPCPKILCLATAERLDTALTVAQMQGKFQFEILGGGCGHYVMDD
QPAVLALKLRRFIKRIETLSEKLQISLKKQP*
>TCRU_6603 vacuolar proton translocating ATPase subunit A, putative
MPREGASGLWRSEDMIRLDVITQREVLYETVVCIGLLGKAKFVDVNNDVTAFSRHFTTEI
RRYDEMERKLSIINGELARERELVEACSPSLDAHDDVKRILCSTMIEEDEEKVDSLVEEL
KRVNASLQGLRSEMNFRLELSLLHTRLQDLVSSQFSQPSVAFLQTSHLLGMVDAARAEAM
YAMAYRATKGNVLIELDNKPAMLLDPITGERCIAKTPFAIFAPSPGLLKRVERLVLTLGA
TVHSLRDVSQAKMEGQHREMEELQEMYDRMHVRKLELIRQHARIYHELLRIVRMKKKVFT
IMNLCVVSGSTCTASVWIPKKHEHTLRAAIREAVHASAGEVFSVVTLHSSQRNPPTFFDT
NKFTQCFQSIVDSYGAARYKEINPGVFTIVTFPYLFGIMYGDIGHGMLLLLFAFYLILME
NRWNRCQLNEILAMLFGGRYLLLLMGVFSIYMGALYNDFFGFSVGLFSSAYAWPPIGEQN
GTVHPLGEKNRTGIYPMGLDVAWAETENKLEFYNSVKMKCAVIVGVVQMLTGNVLSLFNH
IYNRELHKAIFLFIPEILFLLCTFGYMSLLIVVKWCTRWENTSEAPSILETMTNFFLQPG
IVSQPLYNGQKWVQILLLLTAFAMVPVMLLVMPLIEARKHREEYLGYRLFFDSVSLPAMN
GSDSKTSEDSIVNVSTARRNDFPVANLENTLGSHLGMGWENNHTEDTPLGHASYGTGAAP
ADYDGYEGGNRLDSSEVFIHYVIHTIEYVLGCVSNTASYLRLWALSLAHAQLSEVFFNFA
VVKVLGMDTTGVFIAAGIAIWLAVTLAVLVGMEALSAFLHALRLHWVEFNNKFYVGDGVA

HEPFDLLDHLEY*
>TCRU_6604 hypothetical protein, conserved
MQPLTIVLVRRRQRQVEETADRDKQLPHCYRRGSEAESLSGLPPNPRAPPPLHPPLEGPR
RPAQHQRYQSSWGQWFWQRHRPCRWRPHLLPVLPQQTSHHRRPHRRCTEDRSPSKPPAAH
PRCRWARAPRCLSEHLGLTQVDILRCGVPRPGSMLSATGTDARGKACSVDAGETVLLHSL
SPRRPTEPLQEGYRWWRISCTPPRGHGK*
>TCRU_6605 retrotransposon hot spot protein, RHS3, putative
MLRVCVQCEVASCRGSSWRRGDGNGSERWEPQQSWTYGEVGYTREKDGGVQQSSAARLRL
MVLTSDKEWPYSWAGSEHIFDCCVNCEVDRVWQIVKGGLTELLSSHGGNNFRLIRLC*
>TCRU_6606 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSVGATESSQVPVKDSPTPSVTQSQETGVSGPKNTSTTSVSA
VPAAASPGKGERPDTQGVSGVEQALPETPILVAAPAGSRGPTIPVSITKEGPGGSGISGS
PGPVADTVQENGDNDTKESKSDNNPSTNQTDQEAEAPAETTTTTTTNAPTTTTTITTAPS
STKTTEAPTTTTTRAPSRLREIDGSLSSSAWVCAPCRSPQLSR*
>TCRU_6607 retrotransposon hot spot protein, RHS3, putative
MVPVYMGNKTSKSVLGGLWQSGMNVYIIYDVARKGTPPETGFLPPTGWGMIVVSSPKASN
YDEWEKQTKAARIIMNCPDEVDVKAMCVCITRGLESDKQAGYLEMVEKRMDKVGMLLCYT
FDKL*
>TCRU_6608 hypothetical protein, conserved
MPAGRPESVQGGNVESRVPTVPQGDCRKRTRSDFHTDTDQPAATCRGVGKRQQTNWTLLS
QVEDVLLEGKDRITSMRLNEFLRIFLGGRGVVDANEDVSMERFLMNPMRFSPTAKRHCAQ
*
>TCRU_6609 retrotransposon hot spot protein, RHS3, putative
MTEFPLCRETKILLESAYTLKEEGVFLLEHWRDFEGKDTVIPIAKGALDTALLYVRREET
RREAEETARRDEEERARREQQIKFTLSTKIEDVLLRGRVHANNMKLNDFLTAELGGRGVV
EANRNVLLEEFFGALREYIGDERLLNETKKLYNYVRMEIAARKEMSFCEDLRSLYNKGVH
NLMKWSELAAEVKAGVHGITRDTLDAALVDVRNRTTTSAPMKPEGCYESVYNSRWHHVVE
VSGGEGMGMGVHEVKPQQSWTYMAVGQTVEKDDGVQQSGAPRLRLMVLTSDKGWPYSWAG
NKLIHDCYVNFEVDRVWQIVKGDVTEWFSPGPGTYFTPHPRVMIGTPGIGKSVAAGSYLL
YQLLHCDAEQLQVVFHCLGDVRV*
>TCRU_6610 hypothetical protein, conserved
MTAPASAVTLRGIPRCRGENVESTARPRYTSESGTVQISSVTPSCTASRPRRSDSIADRE
SVAAGTRVGDRDAAARRGTENCLWPCSVAGHSAQQVHARLPEAAR*
>TCRU_6611 hypothetical protein, conserved
MVPNASKKRPSFANGPKILAASNASGNMSVTYGGREHVAADNTDEASEPDATGHKSLVLE
NGVAGSGFVAGGDADGLSQRNASGHESKPNYENSPRSIP*
>TCRU_6612 Acyl CoA binding protein, putative
MTQVQFEAAVNYVRSLPKDGPVQLSNAVKLEFYALFKQATEGPVTGAQPWAVQFEARAKW
DARNAIVDMSKEEAMQKYVTRLVEVTKETGHPWTPPQ*
>TCRU_6613 vacuolar-type Ca2+-ATPase, putative
MRVAPAARVTVVCAWAVLEKTDKELLVGDLLAVSGGDFLTVDGIIAYSNALKVDEASAKG
ENSDVAKDSLTSPIFFSGSDVVEGDATVLVTGVGVDSFAGRIAMQIRKEKEEAPSQEKLA
LLADQIENGGMMDAALMFILPSLRGSFQAVVLGQHPLHDKRFLNNLTTAVTIVVVAAVPG
GLPLSVTIALAYSVKQMFK*
>TCRU_6614 hypothetical protein, conserved
MRPAMGGNDGGGGHVTVALNLSAGRCTAAENNQQRSTICVVHSDPTTGDPGGLAMRMPCV
WAKTGGEEEEAEGGNNSLAVRTPFLTAEGGEAGALPYAAYTWELARHVATALMQNGGAEL
LTVTHGASGSGKSIQLFGPTVGDGVAGIEKGRCIHGNGSGLFAAVLQEIFAAADFDPCVA
LSVVECRPSSDGDDDSHPCNGTMGHMNGDDDDDGDDERMMSIEAIDLLARATDTRSPTGC
FMEDYADIPATRYVRCGSVTETLAVLRAALSHSLAWQSVSTALSQGHADVFGMPDTRSNA
ERRRRAAEAIAAEERQRKEFFGASCTLSGAEFLRPTAGASSHVLLTLLLRYGDGVTSIWR
VWDLSGPTVWVDDGSPALRMAFKTHVALSLMAHRYMHRDRLQGGWWNAIPPPEQIEEIIP
LFSTSRPGRKGVDGVVAMIEASIQHSCSAVVWIASLRFDACYDDINWEVLEAAASLLAGS
DETNGKVIAELRRRRRQENLDAAARVLDMFAIPFSPPAWRLQGPAGRTLLNLSTSSPNAS

PPMTRTTIATAASRELRLISPKREPEKGVIPAPEKKINSIVSSAGAALIETSATVHNSSV
LPLSLPLGTTTVAAADVGISPWASFVDKVPCLEAQCLHRGQRPQNELRERRRECEGQGCS
SQSALPLPSPSLLSPPMPSYVSSLGDEAGVRTKSSCGVSPLSPPSVAGTEHPVEPVTTAH
ELKWKIFSWDTSADEDAAETSSIAGRASQEDGVDSEDVRQWGVGAASLPSNGLTDLASTV
RLLLEEPLAKLREISTQYEEEFKLHHRRVIAQLHELLSSDAATLEELQRRVKALVEAEEE
VAARALNGGRDAVDQQQRHRYFRRRRETTSVEAFGPSVSLQTTLDREAAGCTSSNGGSDR
SNNKNNGESARSCGCENGRHRKCTAAASTRELLVAERKIRFLERQLLRLEGENIRLRAEL
PSRRVGGGAVANVRSLEGVFNDILQRCNALYAKKAAEVNRIQRRYDTLLDAFRHLQRQQQ
QQQEEGPTTMMPVAANAALQDAEVMRSEAAKPHFAVAKNRCHSHRVDCSPQVWNNTSPPV
DLVAPPPMEHVGDVSAIDHLRRLLLRATKFATPSTGSPPPQDTSNGFALSIDRGSNASCQ
LHEKEETGDDIFTGLHAFREAAETARNSALRALFVAKRAVQKPQSPLPTSQLLPYAPSSV
DSVGGGYTLVTDVHTLPFDAGAALEREEANVYRAVGSLQREAAELEHAAIEAISRERQLL
SRVLLT*
>TCRU_6615 hypothetical protein, conserved
MSSYCEVCRGLYEIPHYHGDGDTPVRVPDALSPLRAATAAASSTAAPVCGRSSSSYRSSP
AFAVRSRGSSSQQRRQGSLSRRRRPSASSSHFSPAAGRERGGSRRGSPRTPSAVGVERET
ASTLLRMSSPARASALVRTPSPGLFLRNCSGKTSTSRRHARSWRNILTPQSKERVRSLSA
GHVAKEHMKRRLDHLHETLERIREAVRRDNAAAGSRGPSSTLHPAAAVFASGGVGGDATA
KSWHLDDDDDNNKSSSSGSSGQSNSDGVGVGVASSQPVFCGSAGGTNDGLPNLCPCRSSS
CSRGLSFATSRGSPSETIFPREVTETHAYDGKDAAALRPFSSSCEKSSSLREGLTPFMAS
PSSSSPGTTSAAAAPTTGPQRHLSTVVAAISAGTQTSELPAATLPRGEFPSSPSSASRGT
GANSNAAFTHLEALREGFVELCSAVREDLQALHIRVNAIQRPQAQQQQKEPSTSESVPPQ
HVEGGAHENAAAGLLQTSTSYEKLLAELQQYTVLTVHKALEQQKQQQQQQQQQEPKERYG
GHYGFAPTLSEAMPFTSLHLQSIKPSLPQWNSLATDDMYAWSSETFNAHVRSAVRAILHE
DSFRYDARELLAEQQAQRSEMKALRHEWKRRCKELEEQLNALTDATESMRLDVEELRLQA
VGPPTPPPPPAKISSVAPTSTLLPQHTLMPPSSGVDPPLPARAATLADAVPEVWEDRLVK
RVQQLIADSEERWLQRVQGEIVQPVLEHVRRLMSAHQSMIETVVESRCAQFETYVDRGRH
GWEVQVAELRSRVSSLRGDTHRALKDLCQNLNMACPGL*
>TCRU_6616 hypothetical protein
MPLAAPIFFARRPGQTSWLSLSSSSVGSAVRRRSSPPPSPSLVSVSAAVMLVNCGTALGS
LCCQRRGQSALHKLLQDPSDPYLRPIQDLDMPQIAAIAKNGKKEAQHLLDGLIAITVSLS
VQLGGNGVTEEDIDAAFSVYTEVLRHAPGTAGAAGIGDDAGSVSEDVWRMEWERPLEEFR
VVFRLTGDTRLS*
>TCRU_6617 hypothetical protein
MRGREKRNREEEEEEEEEKEKTASVKKAMKTSHTAASTPPGVPEAASVPKPRPPAGKRDF
FGRLIPEVAEKLSPSTKCKKPTAAATANVTVQYIYHDGSTNAVRIPAVFEDF*
>TCRU_6618 hypothetical protein, conserved
MALVPYTATEWSDIGARLSEWVRQHGATEVQLTFLDEDEPSDATLIVANSTTGLRLVSGN
IAKPWGDSSLTGHVANLRAPRVPNFEAQVILPIIGATRELRAQQGPTIAERERLSADYAH
AVADSQNPNARLHSRVGGSHNSLSAREPGIAVADGLLAERECALARSEQQVEATRARIQE
RGYQLRAANAQLHEREARVYAREAQQAARVAETAGQDEAPATRRGPTGGPATRQNTAEDD
VTTQPHQTNILMAGGVPSRAAGISLARERRQAIPRTSQGNFGGPHIHSFMPLPPHNFSLD
AHSDSPTEEERKFLPFDVTTWPPRVWNKGVSGVVFDLRCAYQCWHQAEDQVLLAFDNLVE
WIGVLEDCRDPTDRIMNLGRSLLNTFRMQLTIASDPGIPLSTLRARLYTAVNKADTFARA
ALPLVERQVTQRSVRRQFCHVYRHDASTCNVRPRGNYSQYRRPSKNGRGAAARRS*
>TCRU_6619 hypothetical protein, conserved
MQDTSRKRKAHGSYDCPSRTSSGSLECHGALQKTRCIEARCSNRGDIQFESTRDLAVGEA
RRPVRPSPEYCSIFVEVHHSADPGVAAGHIDVKGEAAEGQEPWLRAAERFSMIFIIMPLQ
*
>TCRU_6620 hypothetical protein, conserved
MASSAASTRRLTSSSSPLASTPPVTTTTTTTTTGTLSASDPRQQRQSTSSQSPTGAPANI
STSNDAPGPLYSEDGELPEEVLSYFEHWASPTEVLQLRTLCGDIVNKYKNETAKLLRELE
EVKRGRDALQREAQETRRLRELYSKAEAEYEKVRKERSQWSEERELLRLRLQQLSVENQR
LQQIVASRGRSPNPNQLRGRTVAAPLSLGDGSGAAFTSTTTPLFTGSSIPTPTPSSSSAA

RQPHGGSATQQRKKQQQQLPVEHDAASGGNYSSGMGGDDYYYSGSHNNNSSSSSSGDING
ALREQLRLIEEIHRCSTEYAELEARFYFAQTLWDITATRGEQRSMLLVAENEKLKGQLRH
WRSVAEDNAGRLDTTKVQLRDRCNDVEEARRALQAAHAARQTAVAAERSAAEESMSYIKA
AHAEELARVQQQLQVALDDSSRTRDKLQGALEVAQRRADAQREELLADVGAAEQKYADAL
RTQQELEATLAEATSQNERQQAQMERELRLLRSAQETAVKKRDELSGVLEKTLDENTGLT
ARLLEAEEELRTVNAQLNVALEKLQHAGELEEALVSARARAEELELEVQTQQSYYAEQLR
MHQTALGELQKQRDDEVRRLGRAVERLQRRYASNKMRLVAAVKGIGRAADAGPISPPPMM
CGKEEQPAAQPSTVRAFPLAEETTGSDAVLLLQQSTAIVAALARTLNRETHAA*
>TCRU_6621 hypothetical protein
MERCLLLSAWPTLHEREVKEASEFVRSSSVSRRDSMALSLNHADAFPTASHSGSHRGSFA
TILATGSRAASPHPHDPRATPPPGIRCLDLPEHYHTRDTRKKKSAVNEYDEDEDDGAYRS
GSCSRCLSRASSFSLGAGGMTPLAWKMSSSVNGESPSCRATESPCSAFAQEHLVATAVME
RRVNRMAGSISFQGMTPMDALLAGRLAPPDRREEQQELDEGGDARGASPPFRERSMAPAE
LVAERTGRRQPR*
>TCRU_6622 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGAGCGFCEDVSQDEFCNKSYVEALSLLANKTDDEIKMKYCK
KDDEKATCLKTLRSNIADALKKEKTKEDNAAQRESDVSKDTGASVGSQRAKSSKAAGANT
AVLSSPLPLNVIGGFNAQIHGSAGGAGHQQHSDDVRSEEEQRNHPESGRCSEGQAALGEC
SHVPAGDTAAEGSHQHSADVQDKMIHNKGEETTPETGLQSTEAREGTDGASAPPQDPPNT
TQSHEGKSRRVAAPDTIPAENTSSGSNEEQTSQSSSPNGSETTGSSDNEGPEKKFKMRKY
PIPH*
>TCRU_6623 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWSVPADGAVGVSGGDDSILKELFIPVARLQLRQEQGAAEAAA
DAKAAAETAAKAAAAATEAAEKAKAAAEATKTAAAKAEESEAAATAAAAAAAEAKTAATA
AKAVDTAAKAAAEAAESNYLFQLRDCS*
>TCRU_6624 hypothetical protein, conserved
MAMMMAGRVLLVCALCVLWCGAGGRCDEEERAVAGSAAEPPPAPTQLVTSPESSQDLHSG
VTVVTENVIPAFPTTTEEDDDEDEETDETEEKSIEGQSVEGGTAAQDSGSREKNLSGSGR
EKNQSIVSTQDISHFDSRESNANPTQPEIEEKKDSDENTPAAGNALTTVNGEQTLPAEGN
PPSSPEDGVDSREHDDEDTTSEEGEKNVPSSETAATPQSHRDKGSEGTGEDTKATTVTAN
TTDTKTKIADSDGSTAASHTTSPLLFLLVVVCAAAAAVVAA*
>TCRU_6625 RNase H, putative
MQPHDGVPRTAPGHGKAECPSYPAQTKTLLVVTDSQSLLVAVTKGPHSHTDWTEDRLWQR
LLSLTPAGRSVQLQFCYEHRGVHVNELADHASQTMATGQYTEHGIAPIRHTDLLSCINTQ
LTNKWRSTMHQDTHHYLLGGARPSDPGGKHLITQEALDQQERTNIAREGCGESELWGRLY
*
>TCRU_6626 hypothetical protein, conserved
MNAGMRAVCQFRLTWECRHRHPLRVSTVPGDDAAPCRGVGALVAYRNSAAGRCREHDGDQ
GDFTPEKVPRHARCGEVRRSACRLSVRTARPFRSGHSVDITRGGDVHKNPGTEEDGYITI
WQLNIAGLSSVKKLHLLRDWSSVHLTSFFCRK*
>TCRU_6627 hypothetical protein, conserved
MEGCPGGKGGRAHRVTGACWCGEDSIPGVDPDIGPRVAALRTGAMRLLPTLRQACTRPAD
HKEPSVSVVPSLPHCGDRPASASAGTSSRREHRNSLSTSERRIDVLLPNLRQSALVRPQY
EGTCRTCSAWRYNSLRGPPMRMPQWCHRLLNRCLARRSPPKLPSMPAGETCRKHKRGYSR
WTRLFRHRLITDATGC*
>TCRU_6628 Endonuclease/Exonuclease/phosphatase family/Endonuclease-
reverse transcriptase/Reverse transcriptase (RNA-dependent DNA
polymerase)/RNase H, putative
MEPFTWLPAERYFYPLLNSIGAYQRYTYRLRAVCDAQRQKLLLSGDIEQHPGPIAVLQMN
VSCLTPSKLATLMAQGADIIAIQETWKSSEQIASMHTGDYVLYAQSRIGKGGGVAVLVRK
TLRSKRIPLTIPQHDTSLEVVVVQVALDQNRDLIVASAYMRPPPQVTQSFRRLANCLPAS
SPLLLCGDFNMHHPQWEPFLETSPSEVAAEFLELCTDAGLTLVNTPGEITYARGTRERSC
IGLTWSKHLTVPDWSASVSPLSDHYMLTFTLHQAFKDTIPSAPPSAPKFFYSWGKCKWDL
FIKDFDAQLPVYDYKKQSTGIKAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERMAT

DSKARYLQSPTPDREAEMQRTRSQFFLLLRERLRNTYLRRISKLNTGEPLAWKYISGRKK
ASLPSPTSILLGDGQRTYKTARRAANALNRIFLPLHPSHKAVRFSKGINRQSASLNINAS
SIFGPQNSNKSIFTFTSGFCHCPLDAPFNRTELLAALRNTPYGKAPGPDEVYSEALRHIS
SKGLRFLLRCINHSWTTGTIPVEWRRATIVPLLKPGKSPELLESYRPISLTSIVSKVAEK
MVLKRLLWVWTPHPHQYAYRSMRTTTMQLAHLIHEVEHNRNHYFQVSLPKKSGIGNQLHY
RPHRTLLVLVDFSKAFDSIDHRVLSRLLANIPGVNCRRWLRNFLCGRYAKTRVGHRHSDR
RPMQRGVPQGSVLGPYLLSLYVHPLLNLLNSFAGVTADMYADDLSIIVKGQSREDAIPTA
NMVLQKLHAWSQENGLAINPSKCEAAWFTLSTHTESDYDREGRWPLVVAGCQILVMTMGA
SRTTKLLGMDLDPRLTLNVAATKQCAATLQRISQLRCIAHKEAGPSPHDLRTFVIGYGAS
KLRYGSELIWAVATDSAKNEMQKTYATLARIVSGVPSTVDPESALLETNMPPLHVLCLRA
RLSIFENTRACQMDWMRRPPPEPPPRAGFRISPLSRDELYAFVDAYTKEYGITESSPREE
RFFRSSIPPWFAASAHRVTIGVELPIDHSITDEEELIREKRRVSEETLALHSHRSWILAT
NGGVDVPKSAGVGILLSSLNSSEIIEKASINCGARPCSYRTESRALLLALEKLMIPRIRH
RRKTLLVVTDSQSLLAALNKGPLSHTDWTEDQIWQRLLTLMRAGWSVQLQFCYEHRGVHA
NEPADQHATQNTATGQHTEHGIAPIRHTDLLSCINTKLTNNWRSTMHQDTHHYLLGGTRP
SDPGGKHIITQEALDQQERIHTAREGCGESELWGRLYWTVRDCTNQRRFRNISPEQSAFM
RSNDPTAPGRKLFPRRQGRPTHRLWRDGPPHSVERRNARTVTPHWWDTRTTSVTVGAFIR
NILHRFPTSTAIAATRSSPHKKGTAPHRNRRAHNPDADRHRSSTARRQSLLPQDQPASTS
ATISPQKTLHHLLLECTDALAVRQRLGIKKDLRTESFSQWQLPHSRKLMSLLDHLLGTLM
TSCG*
>TCRU_6629 DNA / pantothenate metabolism flavoprotein, putative
MSGENLSRFLMENMTTASMAKLQQWSTKLLEFAHYVSEKPCKGMALVTSGGTAVPIEVNS
VRYLSNFSSGGRGAGMVEALLQRGWACVFLYHEHSSRPFRRNLDHLSTEQLFAELAAPVR
SPNIVAAMQAYERLGDRILYVPFNTVTEYLFLLQLLSEAMSHRAECLKSLPMMLIAAAAV
SDYFIPLSRMSTHKISGGDGLQVHFENVPKALDFISERWHLSSATVPRYLITFKLETEEE
TLKKKALENLFKYKCDAVVANMLQNYRERVVLYWKREEHQPVPLLRPEGGSFEALIVDAF
LERIEKETSKNADSIQ*
>TCRU_6630 hypothetical protein, conserved
MTVEGGPLVTFRQRTFTHGNGEPSSSLSCVHVSQQCFSDCVWVLVTEDDTCAPGVVLRHD
PHEMGLGSHWENPNALPSTPCECLLGMRDHPLTNVVAGVIAHAIHSDGEQRPLLLCISLT
KTAKRLENSTERMAFVRKVRDEVMLLATGKS*
>TCRU_6631 Chitobiase/beta-hexosaminidase C-terminal domain/Fn3
associated, putative
MALHHLSDMTFEELEHFVRTNGESMQLSPADVVALHLHRQRRGYLSGRERPLWLHDSIKR
GDERPSCHALRLLILGEETDAKLGLAALLLHGGGRPRHETLLLGLGPVEGEETESGGGDG
NSRGDAALPRIEVLVPAVADVTASLRGELCIASDVVLLCFSVNEHATFDALRQRWWKDEV
GRAFAVLAQDLAEAHHTTPWPATPVIVVGLAAEKRQALAGKNTIPVSHTEAVQLAQKMGA
SKYMEIFSDNLHHVHSLVTQCMQVTNAFRQSLLKEVGAEALSFLTAAKQQMLRYHLRAPK
PDGEIDSQAMQLRLQMTPGITYFMTFDGTDPRHHVSPAQVPHDGVVDLRPYSKQPGTVLR
ICGMARCAYSSILLEIEVPSRLKPPSGYFDIAWRRFVLTKTPDDALCASREVRYTLDGTQ
PTRASMLYTHPIELDVKSSANFPWGLWRSSVTPPRVIRLAAFAEGEFTSPTVTYEVPAVL
KTPQIEYSPQESTVFLNSMQPMVEYRYTLDGTMPTLTSPLYTGPFSLAADVTQQVRVVAF
PRVFFPSREAVFYVPKVKTSSSGSGICGGDSNGTTAAATSRINSAFHITRTTIMRGQHSA
QKLRSSSLNSLIGSTSGRRRKRMSNVNSSNEEENVQSQTLVRSSTSFSSSYASSPKLRTA
ARAALNRCHNSSSSSCGIATMTSKTCNLKDTPRKRRVCSSSLSPLAPQNPRIRSKSHTYD
GDGDDDENFLQVTMATTTMGNYEVMKGKKRGDDKNCGRRGLKDDMKSNCGAPQCTADDNI
VVFDFPEPISLSYISVMTPGEGAGPKSYEVEVKHAYGTDFLSVGSGELKDIKGVQKLQVI
ENACLFPIDKVRCIFDGAASGFCVKDLKVHGKPFN*
>TCRU_6632 WD domain, G-beta repeat, putative
MYYELAPSVREDVLQRVTRQLGGVAASGAPPPCQEWGDELPLHLAATPEDVMRAYPPPPA
HLAPDAGAAETPEQQQQGKVKENGARAAHKRPRIISPELRQEMTGREGNSDGGENASVSS
SFTPHVHFDPSFIRTDYLGRSFLQPPPALLSGLDSRELECHPPRQMKGGWGKHAAGIQQL
QWVPPVGHLLFAADLKGEVRLYEAMASRKCIATFVAHTQPVKSLEVTPDASIMSTGSVDG
TVALWDVERGVCSNVLTNTEGLPCVQHLHHPFDTSSLILAALGRKIVLYDVRVSSHKYQR

EYTGHMGTIFNLTLLSGGKKLLTTSEDKTLRTWDFRVPVQIKQIADVSMHAITHVARHPT
EDMLVAQSLNNQALVFADSGGGQVKLLRHRVFSGHTISGTRCQLAFSPDGRYLSSGDIHG
KLFIWSWATCELVRSFPAHTQTLASHRWHPIESSRVVTSAWDGTIKNWS*
>TCRU_6633 NOT5 protein
MANSKKVQQDIDRLLRRTQDGIEGYEELYNKFLKAATQTQKERLEGDLKKEIKKLQRFRD
GIKALIVNPEVKDTKALESYQKNIEEKMEVFKTCERETKTKAFSKEGLAATSPHETPQAH
TEAWMKSAMEDARKQIEIIEYDVERNTRGHHGRGKNTASADATRLQKLKFHLGKLEQLLK
AVTNGDADLDEVGDIEERVQRFLQNETNSDDDDDEEALYSGFDLEDNHCEKQRGSGTEGE
DAAGAQDAMKKSVTSSPATTRASSQSAVKKTTPSTVVGKAEATKRQTGTTQAVSRTGNAS
PTGVAKLTASRDIASDTWDDTAGLLDDEMDKANTDTFGDDAMDIKGPGSLADMAKATSNF
PRLGDLEKGRPAALTTPAAAPDAPVSPVTATAATAASSIAPSTASKAQAAEQPAAPAPTT
NTTTTAAATPAAAAAQLSSSSSQPQRTAEHKQSGASAAASSHIIVNYDKAMMLQLVDMSL
ANLPHTQDIDRQRPFEPSNPTTCPLYYPQQVLPALASPDIYREFELETLFFIFYYHQNTY
QQYYAAKQIKAQSFRYHTQLNTWFKRNGHMKESQEGSERGSFIFFNYEDTWSIEEKEDFT
FDYQYLEDQLR*
>TCRU_6634 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGAGGVCTEEEERAVAGSAAEPPLGSAEHGTPRKETQELKVG
APGVIETVSPPSLKPTGEDKDDDDEDDAGGDEDDNETDETKEKRREGQSNKGGTVVPDTD
SGERNLGSSRQEKNQLVTSAGGISPSDSQLSNAILTQAEFEKKESDKNLPAVKNPLTTVN
GENTLPGGIAGGNPPSPPEDGVDSREQDGKDTTSVGKKNIPSPETAATPQSHREKGSEGS
GEDTNATTVTANTTDTTNKQNSDGSTAVSHTTSPLLLLLVVACAAAAAVVAVLA*
>TCRU_6635 hypothetical protein
MQFSFSFLKQTRNVVGDRGLEVLGQYCKRLKRLRIERGADDQEMEDEQGAVTHRGLTDLA
KGCLELEYMAVYVSDITNEAFENIGTYLKNLCDFRLVLLDREERITDLPLDNGVRALLRG
CYKLRRFALYVRPGGLTDVGLSYVGRYSPNAASERYHSNI*
>TCRU_6636 hypothetical protein, conserved
MESSPSSLNYLRAVQQLQKKTEELEHVLDETHRLERENAALVEEKAALMQEVAQLEAQNR
DWRAEFGVLEDQVKRQQRHLQEHIEREAKRLQESSAKSRESGAEMGRLQERLRAAEEARE
EGAEMAAQCRRLSREVAALKRELKSAKAKATHYHSSHTRTAADSAAMEQIESNALEGVRS
EIVSFAAENERLINELEAERKARVVAEEGVVNLQQLLQRQREVSDQQQQLAKEELRALNA
QNDALLEDVKILMEREAAGRSDVFASGTDAAPHRRVSTVDRGSMTTQVPYAPLWSPSTQR
AGAIQPVKQYPATVDDGISTTTAQAQVRELMEKVRDLESKTAEQAFLLREKEANERLLEE
RAALHAEERRHLRSLLEKAATPEKASERYESSHIVRAEADTELSAVLESIIELLRTFVDC
AARLRTRLLLQTSNTDSTVLPIVPCREHSSPHLNAIFSHLGGLRYVATIIDEIGEAASKR
PQKQKEEQQWEALTKKQTPSQTPEKNSDKTHAQITEGPASATHNTTRSPQTGFTRYDIDK
WLMERKENLKRQLQHANTTNKKNSSTSSHSNPDYQSGETLEEAAKELKKPHYRQQYR*
>TCRU_6637 Protein of unknown function (DUF2804), putative
MWKGFVVIGCVVVAAAAAVPWLQKDKEVPNFVELKEVRTLFFSFALQEANSSYDAATGGY
VWGRTLKPSYSVQLHPLNAVQSYTQKKEFVWVGITAGPWLVGVAVLQFNYISVFTVSLYN
VDSEESWKAMTIVPLLAPWFGGRWIPNEKGKMGPTSAGHRVEFHPPFSSQRASLRFEDRS
IKVDVTGTVWQQTGNGTRTASQRYEVHAVATLPEEFLGIVFPLGPRRAALVNKLAAAPLQ
TPLNMRLNGKEWSGEGYFSMDYTRGLLRRETHWHWASATAPAGYGFHLSEGTYDVDNKSV
ENTFYTGRKAVVLDTRVEFRRVTIANTAANTAEIWDVTGNGIHLRFRRADAHDGAFHLGV
VNGNLDHAWGIFDGLIFVDGTKYTFDNVAGVLEAHYALW*
>TCRU_6638 hypothetical protein, conserved
MAEEVQQQQQQRKEGDGGREGEKKSRRIGMEFPPVKSREEILNSQRAAVTQEEIRQGMQD
DIPPVVRSVLELAHLMVSGHSQKLRASPGYQGGLFYGGSPFCFASGYRDGTRPRDMDDKG
NHMKLRDPLTYGVLSLPVTAGYLCEMHGKGVFDLQAPLAHYLPELEDKLDPSVTARSILA
FDTVVDDKQVLKDAEAHCFRPLFAWNICAATQRCVYKPISRFFQGGSANALTGQQQRENY
VQYLRSSSRIRVGLRSRRWLSSPKVSHFSVALLIAAVERQLGGISFEESIRQTVFEPAQS
HGAGYGPPMLWRDPNEMFYQPRGLSLQHQRFFHPIKTGALENCGPPLLNASMNLYAPVED
YGKLLLLSLDAIRHARTTLGVAGITKAGPHFDFGVEWLGRKQERCQRIQLTRHVMGMEYV
PAASSFRYNCEHDLGCFGVTNCGTRNACVLANTLSRMIQHLFLKHVIRKGVDVMRGPDLD
NPAQEQSETETKFRKIIKKQEYTSYFRKHDTHKRF*

>TCRU_6639 heat shock 70 kDa protein, putative
MEEFDGTIGIDLGTTYSCVAVFRSDAVEVIPNDQGNRTTPSCVAFHNGDVLVGDSAKQLA
SRGVTGVVYDAKRMIGRKFGEKTIHDDVKRWPFAVEKGENDGVLIRVEHNGETLRLEPEQ
ISARVLAYLKLCAEQFIGKRVKKAVITVPAYFNDAQRERTRAAARIAGLEVLRIVNEPTA
AALCYGLGLGSGAGAQGADCPVNVLVFDFGGGTFDVSIIAIDNGSFAVRSTAGDTHLGGQ
DVDTELLRYVLNDLKNRHGVDATSQPRLLAKLLARCEQAKRVLSHATTEEIVMDGILTGG
EEYALSLSRAKLEELCANIFARCMTVVQKAMKDAAVTPDEIDDVILVGGSSRIPALRVML
QEMFKGKRLCSSVHPDEAVAIGAAVQASIISTSAEQQSEKTANVVLMDVVPLSIGVEVDD
GKFDVIIRRNTTIPYCATKEYSTVEDNQEEVEVQVFEGERPLTRHNHKLGAFILDGISRA
KKGDPTITVTFSVDADGILTITASEELANVKKTLIVENTERLSDEAVQKMIEVAQNFSAK
DAVAVSIMDATQRLTSGFTELETALATMPLPLSKKLRRHVAFLTHGKQWLEQQLPNYTET
HAVDVKTTKIMKLVQKAMKTLQRESRKGTENNNESDSGSDDDDDTNENDGDAVGGSGGST
PRDSSAGRKRPRSNPRNDEG*
>TCRU_6640 conserved protein
MFEVPVECCECAVPIGDEGPLRAVLLLPCQHLLHAGCVEYVRKRRKLQQLIARGDAGGVG
AALPTPFELGSESIDKKNSNGGCSRDSRLVACPACMVPIQRLIPLFPSGGDTRCGSKFGG
GEAASCFKKTHHAQKTHIAQLRTLYEQRERVTQLTRTCALMHARLSETQAELDRLSKTLP
IGAPAAHVPQLAGERLCVENMTATELEMYIMHSSATLEELEHDVSEQRRLAEKKRKKLGQ
LQSRYQALREMERRPRNTHKREKDADSSSSESLCRSSSRGKRPRAPPVVDVEEEATSKAQ
AMIVSSDNGSSDEEGESRKGDKNNPDNNVDDQEDDDVLYIDQTTPQFSSSGGSRSPAAPD
ASSHAWQPHMSAGVRRDRRSLDENNDTSNGGNADAVIDDADDAMMCYNPMRRVLTKQQSG
IHAPNATRLLPRREDRLWQPSLEGIL*
>TCRU_6641 hypothetical protein, conserved
MVAALNEGTSRRSCNRAVASVTAVDTALFDSALITGGLTARRPLPFRAMPIVRYANMSSL
IQEQLKPDPHREAREALHALQTVPVPHDEFALMDDATLRCICAFLGNCSRELLQIGSVCR
RLRELVIALTPPNATVVPDMIPLASLSSHTAVDSLCSFFASYKRGQLVKQLNLVDSKYAS
SLPVSTSLPLCSHHVYPSLVKSLLSLIYLDLRGVQWDCNSNPHIPQYFFSDLYLVAPKLQ
TLKIGVDLFSQWSPGWWQRLPALEQIVVGSRRDQAAVPGSELRPPLNIHDEFFDMLRAPR
RPWRVKLWCPLQLSALTRLLLPAQAFPELRELTVNLSNMNIFEEFRRPTLKSPRENRPRK
GTKNVTVHSVDETAGRLVFVSLQSLTLANVEQCASLPVELIARILPCAPRLSYFSVVNTA
RVPPPPPPSKLRRRV*
>TCRU_6642 cytosolic malate dehydrogenase
MFFEGACAKVVVSGAAGKVGYALLPLIAGGRMLGPNQHLQLNLLDIEAAMKCLEGIRAEL
MDCAFPLLDRVVITHQPAVAFENVDIAILCGSFPAKPGTLRRDLLQKNAAIFSEHGRLLG
ELASKDCHVCVVGNPVNTNALVLLNASNGKIKPKNVSALTRLDHNRSLALVAERANAHVR
DVKNCIIWGNHSGTQVPDVNSATVKGVPVREAIKDDAYLDGEFMTTVQQRGYEIIRWRGN
SSALSAANAAVDQVHDWVLGTPTGTHVSMAVYSDGNPYGVPPGLVFSFPVTCSGGEWHFV
ENACITPSVAKHLAATTKELEEERAESLSLAL*
>TCRU_6643 hypothetical protein, conserved
MEKATFDDMVLQWVESLQGISRASRCRVLQRTCDSLALAHGTGEVKAKAQALLEAVQALP
DPEEMRQTALFVVQARSASSVEERLSPYCRLVLRYGNDRAVKRLASAQVVASEISAQNAT
VTERWTCVGQPQVWSVFNSPRVIGVRSVFAANGKDVSFSFYDEVEFDVCGRIECVARTLL
VDCPSNAEEVRSLLHFGDVRAS*
>TCRU_6644 60S ribosomal protein L14, putative
MVKANYIRAGRLVRIIRGPRQDRVGVVVDIIDGNRVLVENPADKKMWRHVQNLKNVEPLK
FSVELSRNCSTRTLKNVLAEKKILEKYAATKSARRIAAKRAFARSTDFERYQLRVAKRSR
AFWTRKVFDENDKKKPVSWHKVALKKLQKNAKKVDSKPAAKKRIEKARAARKAKAAAGKK
*
>TCRU_6645 dynein heavy chain, putative
MPDPQGESVLPFDSKIFKERNELCGLLFAFSFVWSVGGNVEPAAMDQFDTLVRTLLETVV
RFPNSGSVYDCTIDFSTRLFVSWGTRMEEFRYDLAVPYFDILVPTIDTVRYSTLAKLLIQ
YGKPLLFNGQTGVGKSVIMMDYLRRHKEEQQLSVIVFQFSAQTSSERTQELIESKLKHKR
KNILGAPPGRKVVLFIDDLNMPALETFGASPPIELLRQMMGNGGFYDRKVAGFWKHVQDV
TVVAACGPPEGGRNPVTARLTRLFHLLHIPTLSDESMKRIFHSILQGFFQAKNFSGEVRD

MAKSLVNASVEIFNKTRDKMRPKPTTPHYTFNLRDLAKVFQGITQVTPRVCKLKRSVTRL
WIHELLRCFYDRLATQEDRSYFTEDLMMDALTRFVSGQHSHADYFEGDPLVWADFLRIGA
VDRVYEELTEFKKLPGILSDYQDDYNAYMSGGTGREDDDGSGGAKSVLNLVFFKDHCEHL
VRIIRILRQPRGNALLVGVGGSGKRSLTRLAASIAERQTLEIAVGKGYSMNEFHEFLLDL
YTTTGVQCKPCVFLISDNQIVHEGMLEDVNNILNSGEVPSLFTPDEREKRVSACLEAALE
RGISDRDDVYNFFISRVRDNMHIVLCMSPVGDTFRTRCRQFPSLTNCCVIDWFDEWPKEA
LLGVAQRLFEDADGGGSNQLLPILAPLCVDIHTTVIRVAHEYWEELRRRYYITPTSYLEF
IELYKALYSEQRAVLEEQLSRVVNGKQKMKETDETIAKMKEEIETKRPLLEKASKDTEEV
VADLTVRQAKASEVQIQVRAQQESAADQQKQASRIANEANARLLEAKPIIDKAKAALDTI
QASDLNELRSFANPPSAVLKTTQACMVMFDPKDFGGAWSGNTDWKGAREFLSYRQLLDMI
RGYPTDNVKPSILNKIQKYVNDEEFTVEICSLKGSQTCGSLCAWVHAVNEYSKVVKEVAP
MREAAAVAERHLAETNAKLHEAQEQLLIVEQELVELQKNYETSFKRKQDLEEGLKVCIRR
LENAESLSSSLKSEGVRWEENIHQLQERIELLPLQSFMASACAAYFGAFTPRFRKHLVGL
WLEKLKEHELDVTKFSLTETLGDPMDILTWQINGLPTDESSTENAIVASLSTAPRRWPLF
IDPQEQGLKWLLQQYAGVGGAVAAKNLTRNAVTAAVKVIKLTEPTWIRTLETQIRLGGVV
ILDDVGETLDPALEPLLSRRIFVAEGASPQIKLTAQSGAIDYNPNFRFFMCTKLPNPSYL
PDISTKVTLLNFTVTLDGLEEQLLGEVVAIEKRELEEEKNRIIQSISIGQKKLKVIEETI
LGKLKNTKGNILDDSDLIAELKSAQSNARVLSENQKEANEKMKIITSTRDRYRDVAVRAS
VIFFVLADISRIDPMYQYSLQFFVKLVQHEVLATEKPADYSEENPVMLQRHLGNIILRLT
LSTYEQVCRGLFNKDKTILSLLICTAIERHSRRLMEDEWQYFIRASALVPNELPPLPPGL
SFLSRQQWELTVALFRSVFCFRNLEGHLVDDTDSWREFIQSDAPQDAELPGNWSEKLNAF
QRILLIRCFREEKLFFALTDYVRCTMGPRFVEPPPFSLEVALSDSSPTVPIVFILSQGAD
PMGALQNFAQSQGRSLQYVSLGQGQGENAKRLIATCRKNGSWALLQNCHLSKTFMPELEL
QVAALQQHGANINADFRLWLTSMPTDFFPIFVLQNSIKLTNEPPTGLKANMVRCFSEITE
EEFEFFGEEQRMGKHSKRTAFKKLLYGLCFFHSVVLERKKFGPLGWNVRYEWNDTDFHVS
KQWLRLFFEEQDVIPWESLEYIIGQINYGGRVTDPQDRGILQTILRAYLRPDIMKNDFKF
SSSGNYYAPPAGSLSSFMEHIQQMSLVDEPEVFGMHTNANLRYQLQVSQYLLSTVVSTQP
RIGSGGGGSTGAEVGAATTPEEEVKRKCEEFEASLPEVLLREEAGPKSFTTLESGLPNSM
STVLAHEMVKYNKLITAMRKSIHDLQKALRGLTLLSADLDAMYESFLTDQVPRLWSAVGY
TSLKPLGSWYRDFLQRVQFIRTWVQNGEPACFWIGGFFNPSAFMTGVFQAFSRAEGVSVD
KLGFSFQVMDEEVARIEAGPERGCYVYGIFTDSWRWDGTRGVMADSLPGEPYASLPVVHF
LPEPHHKMGPGWHCVPLYRTVVRAGVISSLGASSNYVLSIEVPTDKESDYWQLMGAACVC
ALAI*

>TCRU_6646 oligosaccharyl transferase subunit, putative

MLTKGSAGNKGSAGKTPPKSTKSARAAMTEKEATAVDDSSVENVYFLNAFPIPNSVLRTS
RVCVLSLLMVTGTLEAYTLRLIPIHIYGKVIHEFDPWFNFRASEYLDEHGWDAFFHWYDY
MSWYPLGRPVGTTIFPGLQITSVLIRRALSMLGMSMTMNDVCCLIPAWFGSVATVLAALL
AYETWGSFSGAAMTAGLFAILPAHLMRSMAGEYDNECIAMAAMLLTFYLWVRSLRNAGSW
PIGVLTGLAYGYMVSTWGGFIFVLNMVALHAAVCVFADWMRGRYDASLLWAYSLFFLVGT
AIATCVPPVGWTPFKSLEQLMALLVFIFMWALHFSEILRRRADVPIRSTKALRIRARVFM
ITCGVLVLAAALLAPQGYFGPLSSRVRALFVQHTRTGNPLVDSVAEHMPTSADAFWSYFH
ICLPGSLLGFFVTLFLCSARYHHGKSFILLYYLVAYYFSTKMSRLMLLSGPAAVVLTGNM
LGGVMDLSVDSLFLPPGVCEDGKKRQMKGRHKQKDLVERAETRISTAWKKMCRRRPFFAA
ALVGALLVLGGHALLTSGYREHCHQFAEAVSGPQIIMRAQLRTGEIVMLDDYYVSYLWLR
NNTPADARILAWWDYGYQITGIGNRTSLADGNTWNHEHIATIGKLLTSPVAKAHLLIRHL
ADYVLIWTGSRAEDLMKSPHMARIGNSVYRDICPEEDPLCSNFGFEDYDLSRPTPMMRMS
LLYNLHVSGESPSPAIDNMFRLAYRSRHGLVKIYKVMNVSAESKAWVADPKNRKCDAPGS
WLCTGQYPPAKEIQEMLARRIDYGQLEDFNRGKRDDAYYRAYMRRIRNEGRG*

>TCRU_6647 hypothetical protein

MLLRDVLRQHHDAARANTPCGFSGVTRTVLFGATVPPPPSVGVHSPVDARSYRLRTHPFN
DVADTPAHCWCFWHDCRTAPNSGCSGTGDEHTAEQVQSDVAGSPVSVSPTPTTSPANTDM
DGAEKASTDYQESSCPDTSLAAKQPEELQ*

>TCRU_6648 hypothetical protein, conserved

MANHKAGNKKNSKGEVELAPQQGRSLQQRGGQKPPEPSKAAEKALTHPFLGRELRVELVD

RRILVGTLIAYMGLGDLLLQNAVEQRRYADGELSWRPLNLVAIPLKHVTAMHRRLPDCEP
ITFVEG*
>TCRU_6649 DNA-directed rna polymerase I largest subunit, putative
MSLITAFPFHAYVGDLKTRRVVQEKVAVSLSLLTPEDMARMAFVEVRTRCGQEDKTAPWR
PVLRNGEEHATFYDTRMGNFDVRTFPPHSCQTCAASLTGKYGNERCQGHFGFIGMPRLHP
GDALRGEERMSVMNPHLVEEAEQLLQAKCFFCHRFRAPSLDVERFRQALRLVDRGLIGEA
LHLLDVVSNARGYDTRHRRLHTANEEVINDVTLLQEHTERILSRHAHTSAAAGEASAEAE
HGMKGAIDVRNGIARQALRELKEHVGVCSHCNGISPRITKRNGHFFFFRKNSASVNVAN
ALLTQTQLQEWEENNKLHKRTHTYFRNQDIREHLKQLCQREELLLGMLFPHLGEPSVITP
HTTPLPARDMYKAFFIDRILVPPLPLRISSGVQVQDGGAISPDPQTRALSSVLGFVEQIE
CYQVLQNNSTPDRNLLSTAQEIANEINLRNLQVKVNEVYQEIMGTFAKKEGLFRMNMMGK
RVNQACRSVISPDLMVEPNEVLLPRPFARNLSFPEQVTFYASARMNLLKRCVINGPRRYP
GATHLEIRQTNGEIRFIELDVPEQTRRQHAARYFAMAQSGVTLIVYRHILDGDRVVFNRQ
PTLHKPSMMGYQVKVLSGHKTLRFHYVNGNSFNADFDGDEMNIHVPQSLEAKVELDVLMD
ANLNYLVPTSGKPIRGLIQDHIAAGVLLTLRDKFLEHATFVQLAYYGLAPYLRQQHEITL
SELIPLPAILWPRPLWTGKQLISVVIRYVSGVGRRPDWMRINSGGASLRGVSLIHPGVYN
HTIPGSDVVQTVTRQTMDDDALMFMNSELLMGLMCKNQLGASSMSIAHIVHELYGPHKVG
QLFGALGRILSQSLQREGFSIGMDDMCLVQEERRYRQLRQLDEAPLYLPDDEAAVMTKIM
EYATKLQQEFIPGRMMVPFPRNHLLMMTASGAKGSNANATQMALGLGQQLFDGRRVKRMN
SGKTLPAFFAHERRARSFGYAIGRFTSGIRPPEYTIHAMAGRDGLIDTAVKTSRSGHLQR
CLIKGLESLVVHWDHSVRDSNGSIVQFTYGGDGLDPCKASTLTSWEMSKENLVDFGKRFG
VDTGEATSETRRPENWEQGVRNNSVKRGKRPRTSMNNDKKNNTNKNNDKDEEEEEKEEEE
EDGDDEHKRSSNCNHNENARQRHKEQQLRENPLPRHMHDGLEDYLRTKATFPLFQRVSQL
ARWKAQGQVQEKLAEKRRESIAYYRDVLSELATSRRVKAFCDPGEPVGLLAAQAAGEPST
QMTLNTFHSAGSTVTHVTEGIPRLRELLIHASVQKAAVIVPVEKATPVDESAIARILHAG
VAIRLRDCLARGGASGKGYHYHVARRKDASVLTIALLFSQSYLDDSRARMCMSPSEHLES
FTDALRQFGKRIIKALRGRTREERNVGDAAALILNQHDPMDAAAAADGDDYDDSDRGSGV
DKDDALSDGGSEDSNSATVGGVSPALRSQRSVNDVPDASEDDNEDEDDDNAEEEEEGEKA
ARLLRGQNGRRHSENEDEDDQCDDENKGDSIKGTVAPQEAVSYDGFAPLHATSGSKEFIL
DVAPLSKLAAERDGVAALPDGLFFVNVVVCMPPDIIAVIPDVVDGALEQQTLPSWLPQFD
SVNFTRNADDATSGELLFQGANATMRHVLSFLSLFTLGTRAIKLRQARSTDIRDMANWFG
VESAYRTLYDELFKLFKRYSVDHRHLTLIADAATHRGTWENFNFTGVISQSASPLFQMTF
ASSKRWLHTAVSRGLSDELQSISSAIMVGERPKVGTACVKLAPDAAVLRDVLEHTFE*
>TCRU_6650 hypothetical protein, conserved
MANTYISAQLLGNLVRFIEQYLRAQERLSRVPLEGSSSPTANAMQRENAMASLTRVETAP
LVLLDYIGYLSSVGSWTMVWWAFNLAETALKIQRKHQLATTTSMGDVATRAVLSQLRSLS
NPATPRLTHTLMRSVLCLSDIMSESPITLLGFDRVTPLHGLLKHATRGEYRAMLFAMKQA
VILVQRASAAYRETRSQSSTDDPLRRHGAGNDLEEEARKIEEEEDDDDDEKEAIGYKGNR
EYEEQDGGRRRNYFALSAVTRTPEAEREFILFFGCLVACFDNVLDVIRGCALQQDILGDE
LRDVLLLALQTLIHVLQGCIRSVLALPDELWELFRAERAHMLWISLCVAGLLGRVAAVDY
GRLCFNGTLRRSTDSLLGEIGELVEACIKRGGDDGDQRDKGTGKQKGGNHERSKRPLLDT
LTEGLRGILSDVQLSYRLAIRLGVAMRQRTDLTAIITSLRAFAAASARYQPAGVVIHRVW
RVLCMEVGESKKPSGRKQKRLPSGETPATALRVPSIDELQLLLESFRDLENELTSVAATR
KTQRRHAEFVVDWTCEKPLLMLESVTEDLTLVQSDQKRNVALENKGDDGDEALLDMGVDA
GESQALLTTGTLGGMDAAILLQEEEEEGKAKETIPNGELIEALIRQCGRVQTSSAVLPIV
DAALSIPQTNKVLGTHFNCVKAVFTRCTLAEIVALPHAELIFGSLELFVRRRSPVPLEER
RNLWLQLTQKWKREFLEPYSLRFEELQREFLLLVRQRRSSVRLGEGRAAVNSGTPLFSSC
GNVMAQIAKQGVIPVACDVEISPHDDIGGLLVEKKGKNSLGMGRCDYEQLLKQQRYEQQR
KPSVSLDILFTILTDLSRGPRGEAGLEDFARVFTTYIAREYFLLRQRMDGNAMNVMRFMQ
NPHQLGPRIYQRRRLPVSCAYATDVAGWFLTPADRQSVMTSLSHISEGVEMEAFNSAEHG
VFEYMRSLCVYLHLLALTVHVFHRFRMHGDSEMRDGVRQRRQQQQQQHGRCGCEEDLEEE
GGDAAQWSEHRSQDAEARLAERQLHADTRQTDPDSVNMNLLESSLLHFLNVSLVLVDHTD
LMIHRATSIATAPDSDHEHARKALLYADELRLMVAVALQDTIRVLLRDAPLRASFARRVV
HRIICSFSCEIPPEASWNGAAAGKQKEHSSQEPSVNMMALDAWRSKRPELFVRSPTLLCL

LSPSFFNEVLSQNIRNALSLTLTQVVASLHFYLRRTDAHLSPLMTATTSILSNTYVRNAA
LRLFCEELCGQIVERTSFREALAPPTVASVQQGVAGSVPDEVLIPFLASICREDAFVSKN
ALASVLYHSMSLRPDVFGQPPIVDRFARFAIARRGSSSSHNNNNNNNSGSVSPLERGGVH
GNDKSPAAAPVAAGVGSKAGVRESSAKSRLSLGVSNTDVVLESPISSNAAEATSEVMDVT
STAQADDEEEDEVETLNRFMADQSDETATRTHKRTLFSLNLTLAEVMETAMHFSQMRPTS
PEEYKKAMAMIRAADDARHERIAAFRSATPTTGSHNGMGSSPSSSLTTTPTVGYPDAALH
IEEPMHFGVVMLHIRFALRKIIHASMRRLAAQQGPKTLSMMVEMLREVDPKWHQNQNNNS
GELRRQSDSMLAGTLRVLVARSVVCVDLVGEAGDLLGGGAGGLAISAVGLQRTERALHLV
QRAKRSATGSGGNTGDHVSRRRPQRHRGDGGARTSSSGEKRSIS*
>TCRU_6651 hypothetical protein, conserved
MHERDASLLALPTQDSRAQVGRGKPQTIRPHAPLVDVCFPAFTRRRVNESRIHSLPKQPP
LDWNNVLGRRANTTPPKKDVFFSDPPKNSTSTLTQVGKSDESKTFSPRPVGGSLVTSHEG
TAPSLGVSDDTAPGKSGSNSEQGAGEKSAKDETQLSSVPCSRLEEETIAEGGLRLPETIP
VSPRYRNSAMASSLPTLNLKGCLASDRKTEQHQQLTPSSSHSLPMSITSENVAITARFDK
QTARSMMHDMFPAFSRTNSNTSSTPVPHDRTMSFSPKSPTLPESPNFLFMRTTPMGQTPP
SNISTSAVAPPSAFFGYNDDQFVDNVKKKKRRTTLGTPIKRAYASIVRIFGGEKSSQNAA
SVDVSATSSGSPSRSTIQRTKKKKKGKKRNIKNKENAPNTLRMDQSGKNSLEAVSVSTMK
HETPPGTTTVSTTVGGDSTLPSMRNSLCGNSAAIKSMILMPPSFLLLEDDVVESATAAIS
TSTSSQKNVTSYITLDKGSGTDLEGVSAAPDTPQTPGTTSTGSSGTKGGDENSATAMAAF
SANGNLSLSLLSLEPTLVAFENNTTITTNANLRNTLHDTSNVDAGGSVGVSPPEEPKPLC
RISFSSAGSGGTEPAKALNKPKSANDPKNSIETSPAYFRSSEKKREKTFNEQEQQLKQIP
RLSAIEEQVRSCNNLLSVTNNNMPSNMPIADDEKRGAVQQKKGKTVETERMNEKMATYSS
PRPTSTVGQNGRSMEDLFPHNLSNNVSTGSNNASPRGADWPTDSFSTQLPLAGSTPTLSG
DTSTKDVQLATLSQYAHRTEADLSRSTFGSIGACLAVSQTLRVINLKGCMIDEEGLRGLA
EIFTLKVVCVSHIRQLKSLRSLIECRNGRFAEIEEIDAQCTAIQNEGIVGLEKMRRLRRL
CLSMTCVTDVTRLSASRSLEELFLTSTPVTSEGILGLERIPTLKTLNISRTKVQSLPRLY
KSGSLEKLILYSCKVTNEDLRRLAQMPRLEVLDVSTTKVTDLSTLRGSLSLKSLTAQWLQ
LINCEDILFDRLSSRNGEAHAKSRRKDGAHSKKNSCMPTYLSKYPIENDAEAGFCGLADI
PTLEHVDLSHCAIRSVKSLFVSKSIKSLVLRRTRVDSNGIKGIGSMRSLQALVISNVADS
FLAEDASEWSSASGVLVSITELPNVLNLSVLDLSFTDVYDLRMLSALPLLRELRLVETLI
TVDGIRGIEKLPSLHTLDISQTSVTSLQFLSSGCQSLKRLFVRANRNTRGFCIGNLHKLH
SLELLDVSDTVVEDIKMLFRLSCHLKQLIWRWGERRDVRGLIEPLPCWVNTPVLKGIESM
PFLELLDITNTAVSSVSFLAQSASLRWLKLSRCKALDNDGIVGLQSIRTLEELDLSHATG
ITDVSCLATSPTLRGLRLGWTGVTLEGLHGIKTIPTLTSLDITSAPAECEMKGEEKGNTV
VTTDGGKNSHLNRNTPCTVNPLLGGIAGHVLLGKRQSRRVSFIL*
>TCRU_6652 hypothetical protein, conserved
MTAAKRSCSSDRQSAGRPLHLPAPGMAWNLLEGWSRLVLRRASSNAAQRSSYTQPGTQHR
DKVQHHRWGTWIVATDGGVDVPKSAGVGILLSSLNSSEIIEKVSINCGARPCSYRTESRA
LLLA*
>TCRU_6653 hypothetical protein, conserved
MNEESCVAFLMALLDAAPSTRRQHARMLWSVLEMGRTPLDMVIQGLQKTAARSETKQARP
FTKEEMDQVIRSRTDWRERVVFRLAWITANRWCEIAALTAKNFTLEPDWTIILYWSVAPK
TAKADPHCASRFVRTRGQDAFNVIQLCRTLWQNEKPTNLTTAHVGRVLASWGAMAHSIKR
GALRHAAQIVETCNLNPHVIS*
>TCRU_6654 MSP-B, putative
MRQTLLFLMLLLCCVSGSVAVAEHHCISDEIEKKVGPRTTAVVLELPTRESGMMRALTAS
APEWAPIRFQFFTEDLNDPSKYCTAEGQIRPDFTGGTLECDREDILTEEKNSIILNSLIP
RALKIHTDRLLVETLTGRVVVPEFLSGACAQFTIPSPHHTVGVFGADMYLYFSAAPLKAS
ALAWATKCLKLPDGRPVFGVVNYGPSSVTDSEDGVRVVAHEIAHALGLAVEIMRKLNMLK
EVKGVRGKAKVPQVSSPKTAEKTREHFDCMTATGMELEDEGGEGTASSHWERRNAKDELM
AGHSGIGYYTALTMAAFEDTGFYRANWGKEEPMPWGNNSGCALLTEKCVINGVTKYPEMF
CTAETTLILCTSDRLGLGHCAMELYDAPLPPQYQYFSNPKLGGVPDLLMDFCPYIENCVK
TRCSNGNKALMRGSRVGPRSKCLKGDGLADSEGFIGDVCAELSCEKGEVSVRYLGGDAWH
KRPEGSSITPAGLFTGGRILCPKHDDVCIVIDTINGTGDVSSLLSAFPPIPLVTLVLIIS

MC*
>TCRU_6655 hypothetical protein, conserved
MPSCTASEPRRSDSIAERESVTTGTRVGDGDDAAARRGTENSLWPCSVAGHSARQEHARL
PAAARWTSAGSAAVRGVKWQRGGSRRMLSERQRAVRPAACVIRPQKSAGRFKADRLTPSR
ASLACRGCKTPNPLQLTVSRRQSGAQHEGRGCGPGRSPCGCKSAVIP*
>TCRU_6656 60S ribosomal protein L12, putative
MPPKFDPNQELIVIVRAVGGEVPATASLAPKVGPLGLNAKKIGEDIAKSTKDWKGLKVTC
ELRVKNRVATVRVTPSVASRLIRALKEPPRDRKKVKNIKHSGNIPFSEILKIAKEAAPNS
MGANMKSVVMEVLGTALSVGCTIDGENPREIQDKVRNGKLKVPN*
>TCRU_6657 protein phosphatase 2B, putative
MYSERGLPSVEPPPLFPLEKDRLFPCELAGNAGVNGSVDGDIRVPDTTVLQRHFKAGGVL
QEADAIWLIETASALFAQEPNVLRLEDPVTVCGDIHGQYYDLLTLLELGGDPGETQYLFL
GDYVDRGIFSCEVTLLLFAFKIRYPKSFWILRGNHECRHLSCCFTFRDECLRKYGEAVYD
AFQLAFDRLPLAALVAAAFFCVHGGISPYIKTIREIDDIERVREPPMFGPMCDLLWSDPM
EEEEEQMCPDALFLHNALRGCSFLYSSSAVEEFLTLNGLLSVIRAHEAQNEGFRFFRKVG
STGFPSVICIFSAPNYCDAYDNRASILKIERKTLRVIQFMAAPHPYLLPNFMNAFTWSLP
FLYERLVGIIRFLTAGEEEEMS*
>TCRU_6658 hypothetical protein, conserved
MSSPELKHRRMEGHMSFVPPQFQLPARPPASGFPCETDILVPGARGKSSMDGKALLLNAS
PTLELPKEEAVSLFTALRQHPKCASIREQLNIINEAYLEEIFCEDDAREDDTRRRVDYNA
ACALLKSNSSKRLSACVSCLTRGQHRQYRSHMLRYMQTGVVPKNTEEYPDMGIVIDLVQR
EQSSYLHKFMEETLSCEACKIEAGYKKRSGKAVEISTLHRSCWNHNYMDEHVERFAKRWW
LYRLESRLLRCFSDEEASKKESNGGDGGDAFSEIVFDLKRAEAAARAAENAKRTEMVVKP
VAKLTSRARQLAAQCVAATVTQRVSRGEARCLPGVSIPPTLPLAVQQLDTREARLYPLAP
PEQQRNDGDEEVAIQEEVLSLTRPVNSVAGVSFSLRLCKSALVELSAAHLSSCRAEFQLP
VRCVWHPTERRVDICMEKPLPGSRETRRNVNAAAFKRLVDNEPRLPSNGRCSERGLYKSK
CIAEVSFGNDIAFYCVSNCVYDVTHQHPVFRMIKMEYNCKGYNTVPDDEKTFNYESFSKR
EVVRMWTLLHCNPTAVLYVYRINAYSNAVIGIEQFSSVSFMTQVIGAFSSDAEIKRAWSS
LRDVLQSTVSAIAQRMQLSECSKSARSVTFLLSKKKEDGVVSLCSVKACYPQQTAPLDEA
VECFIEPSSRMVCRREYLPPSVWPFPDRIPYTYGPAPRACYVINRTTETRHDSAHYAKHD
VWHHEPRYYTVGDDGVVRELRPADP*
>TCRU_6659 Lipase (class 3), putative
MSISGAVRANTCAAYRRLLSAVKQVTRDCPLHREDGLTRYVAFRFFDAAEQNRRRYLKLR
EGDAAQINKGRRKKLREMEVQYERFIAKELQRVREVAGQILLAPGNRALTSMLQVLAAGV
GNSHYQQTIERNYLRYCQFENKKVERNEAEEEATAERQNRIMQHALIPYGERLLFLHRLD
VKNDTGDVQEPGSLTSWQVTEAIVGTRSGVSAHYMSHGREDVVVEVDETYNKQIVYVRCE
KYDWSREVERVEIIESEEVRGTIFHAEYSSVAQRLCDALLAETPLHAYRSTVVVGHGVGG
AVAFCLALLLHVRGFDVKNCVTFGAPKAVQQTLERYIHAINPIRIVLEGDPLIDLPVTGA
EGDPFVHYGEILLMASAVVPPHAEEGEPRRRQVSKDDETEEGGQQEMNAAAVTDVLTAEA
LGDLLESAENLPLPCEAGDFQMDDEETQAEVEKEEEEGDELGFRRIAAERYAAGFLPEDY
IGRLLDTTVPLTYAEGEEVWDEGEYAQMRRESALRLHTSGLHE*
>TCRU_6660 short-chain dehydrogenase, putative
MRSCTAIRFGYKSELGAICTAFAAAVSFFVLPRSFLTVAVPAWLVVQRLVARGSRNGARP
PHEGATHNGGKEGKKDVSPKECQLAFVISRNMNEEERPVAIVTGTNSGIGYYTAVGLAVE
GYRVVCTCRNPALSESTAAKIRREAEDHRRGRNGDSMYMEVPETVLVDGRFFLECDDFAS
VRRFVDQFQATYKRLDVLVNNAGMMRKRLEFSRHNPQLELHTAVNFLGPLMLTELLVPLL
QRSQGRVVYVSSAAHRFPQMVLEPGLWKTPSKAGLNGRLLDAVKQINQGELGSTGPLKRK
TLGCAFVRYGTSKLLNIYHAHHIARHHKIPACSLHPGCVGTNFSRDLMTREWVQRIYQYA
SLLFLKSWEEGAQTTLHCAMCDVEELRLVKPLNKTNRTEPVSPYFVECGNQTIESLLPYG
WDVEEADRIVEWGKKLVGLAPK*
>TCRU_6661 hypothetical protein, conserved
MGYKAGPGNFQIITSAIAVVTTVVHRLWAAPPLVRIDVWVGNIRIAGSKSDVTLWEALVL
RNADSCHASLGEERESGATQYTFCRCNLITHQTVSLSEKFVRSVRAMPTLNSLTILEMEF
MASYFLYAAAILCTRLCDYYLFHQGSATTIIRT*

>TCRU_6662 vesicle-associated membrane protein, putative
MKLYSLSIVRPFPAGVEKEPVICSQAIDVSSFGFFQRNSAREFIVFLTRTVARRVSKGSK
IQITENGNVVFAHATLDGIVAIAISDIEYNSRVAFTLLGELAQQFQTTFHGKYDIVDGKD
DNFLNWPYLEEMLLKYQKPEEQDKILKIKRDIEDTKVIMYNAIDQIIERGQKIDELVSKS
EDLGMASKTFYKQARKTNSACCTFM*
>TCRU_6663 hypothetical protein
MARRRAEQEEMARRSAEQEEMARRRAEQEEMARRRAEQEEMARRRAEQEEMARRPLVYVP
SGGAGESSMRLFNNLLENGVCQLDNTQSMGIEHRVQLNLVPDVIRVAAEEERVLDVGCDV
PEETALQLAAVANDRPVHHAVILRLAKLVLSRRPGKPHIFLWSHLQSKLGGHEVNAHIQK
KEVYRRTPSTTLTFAPVGDTAEERLVSGAPAGPARTAMRYWARLLIESKPDNPELFMWSK
LEARMERDSLGIPQSRTSNAASARDSTRISLLRGIPRGTPAYTVMRNLVDLTFEKKPDQP
EMWMLYHFIARHKSSAAPSGRSSVTPVRFLEEDIGGDGSRTPSSKDVFFSADASMPRPVA
MLSGQWADRAATWSTQKNSMRSRTREVSTQTFHDSQGTALANSTRVAVIPRARVGSPLQA
TSFLRNLSPRELLQPPPCDMSFLRRRRYGAMASDLEEPPVSPFYYEKYSLLSDPLQHPSG
PLLRRGRSSRGFRRPSQENERNLLGCWGHSDERSDGNRAEQNEFTSLPPCEKFLLHSPVS
LRRLSSSESPESQYAMRRRETDRAEILYEYNWLLQREALRKEQLRKELELLRYEREVRER
MMCRGPTAQMTLTADSAASSQLEAEARLQDLNCGGSLQFPSEPDAIRKKLKFLDVEGDRL
RQLSFARNRFTAPTEREPISDAALRDTYDSPALHRANDRVGISPHFNPTI*
>TCRU_6664 hypothetical protein, conserved
MPWPVRLRLLLLLVTASSTDELTEAKKQQPIRDGGLTSDTHLAANFEHLTRRAGSVQPES
TASAQGERSTSASASNAATDEDPFLNQNCMIMETCRNRTLRVELSLASMERDHAMRPNGA
SGGQSSGA*
>TCRU_6665 Enriched in surface-labeled proteome protein 1
MEHSSTWEKKIPYRVAIVLQNGSQGSAYVDGQRVGDAPCELKVTDSNEISHFFIGGDGGS
AGRQDDVSVTVSNVLLYNRPLDNNEMEALKPNEASILPLVNKHDQGNVIPSFSGGNADLE
KDVASSAEPASPFVARNQNAATSAGELPDAPVEQTASQQLRTSGTLVRKRW*
>TCRU_6666 retrotransposon hot spot protein, RHS3, putative
MKLNDFLRSKLGDEWVVERNGNVIMEAFVQEPDAYVQDQRLLRIIFNLTEYQEMERELDE
MKILLEAITKLHHEGVVSLEQWRDYEGKDTVTPIARGKLNAALTQILREAWRKAEERVRR
AQEMKFTFSTTIEDVLFKGVRVKEKKLNDFLARELDGRGIAATNRDVSLKEVFKNPTKYI
RDKGVLKEIQITDAYARMERAVREEMDLDEDVRKLYKNGFNNLLGWSEATANVKTSVHCI
TKDFLDAAAEEARILTTTIVAIKLEGVYESVHNARWHHVVEIPDGDGMGLKVEEGKPEKP
WTYKEVGYSLEKDDSVEQSGAGRLRLVVLTSDKGWPYTLNVLHGAGNDLCVNCEVD*
>TCRU_6667 hypothetical protein, conserved
MAEPGERHGGVPGTAALRAVETVPRHLESNSETFSFAPPVSAQQWMEVSMFCLQNRHVPL
KRLLQMLEDTAKALMDEKPLNGHSSPLPRGKWYEGDDDDSHRTCETSDAVSTEASSTVSS
ISTPQRQLAARFFMLASHLGIKRGTVSSLRAGVRLAEMAVDAHRCALTTTHLAWACYYLG
SVVQEREGRSTLETMAGKLVRGTLEIIAREANALPTDFVQLVKLAWLMALLGEIQSALTL
AQRLVGQNRADANALVLLSLLFSATGEYDKALEVANHTEHVHPQYILGGIVLTMMRYVTN
DVHLHKRVGCEELLAILVARVQATTQYTSERADSDEFRLVPDIGTTVIADGCWSSRFRGA
SRVAGHWALLAYVAVEVGCTSIAEIAVRAGLEFVGEAREEHRKAYADLICCSVRIKIDRM
EKIVETVRQRHMTAGVGDVVSVLREFEDEQLIREQGTLLDEQEVRSLHSLLFTALEVCTA
HADSYVQLGRLYLLEALKANQPQSLRTTHLVEASHYFQLAIDSTSTHTAAYEGMGRVREA
QGAMEMSLDFLSSAAELAARQPVIPFERFLYIFP*
>TCRU_6668 exosome-associated protein 2
MSLPPATGAVELGSFKQHVIRLLTQSKRLDGRPFDSIRVPHILYENRQDTKINRVLASTL
YTDDTGTCVNCIVTGVFGPPPPQHPEEGRLTVEVTAPFFPGYSAFQIEGTLHELARFVRS
TIISCLDLTELCVISGEACWVLRVELIVMNADGGLRAATLHAAVAALHNLTLPKARLPSG
DVVESRCLCFHRIPVAATIGLCGTAGSMQFLLDTNAAEESVADVLLTVVIDETDGIVSFL
HHGRFPLLLPHLTDAIDMVASHGAALRSAILKSSNLPQ*
>TCRU_6669 Protein of unknown function (DUF2638), putative
MRVSCVLRHHPLIQFKYAVKNGASSVGGVKAAVASDKSSSNVLAGTFVETFEELPKKFQP
HLFTEEEMELIMMGGATPYVPKSLQRRKEK*
>TCRU_6670 hypothetical protein, conserved

MSLKKSLEELTRRSSLRRSSGLRASHVIIVGKRMVEDGCDSIVSLASPRLEERRQRRVVL
HGVGTGDVIRAPSRFFDQIVEERRLPKSAHCYLWRGRGGCGPAWVRPRAIPCVHHAEARS
CTRCPWMGLATAASREIKSERLRRTIESSLLPLASSSPAGGGQPELARSPPSVRFFEPFD
VPVAAHSMREMEFYFRRLSSEESLSSGQGMGSPAVTGEFCFSPNLKGAPECLLSTLEQQR
LLLFLNRWAERLPPPVQQCLSAVFILQHSREGVTRLWERDLHVTLLLRQDVSNFGEQGPL
CSPSQPEGILSLAEQQLVDTVLSAVPLTKRLGIATVCSDGSMACLYPRPQRVECTMAADV
AELVGVVPCVAVHGPSGKKAAANLPFMHSTVAFILGARDVARLEVSPPSLWRHAMSLEAV
GSVLLSILGDFLRGGVLLLLPDPGGSLSFEEASTLSQSSGTHLLATAVSQWLGSMSTMSV
VYIAREDRENGRGKWNLKGFDAAFSSTEEGPAMLFCLLDSVTDVEATVHVLRHGMTSLEQ
DWPLLVLKRIVFLQLTADGDFYLLANALCSVTAFMERRFKLGVDCGIVDIDPWTAATVGY
VVLEISPFTTS*
>TCRU_6671 major facilitator superfamily, putative
MAASIQQAALLCNTEGLEEMMEDDDETSSLLNHDLDEEEEVVDGRASGSSLHARLLGPEL
PVESVHLKGDMGPEDVCGEGNGIVAAGGGEVGRRSWRSFNRRLPPLSEPRRFWQLVVGAL
CCVAVSSSYTFNLYNGRIQSKYNFTQSQMTTISTIGDIVGVLILPLGAIYDHYGAQPIFL
IALVLFPLGGILFGLTFANAIEGSMAAFSLYVCMQSLGSSLLDLGSVMTMLSIFPANKGA
VVAVMKTFCGMGSAILGAIHLAFFPSENDSDTSSFFYFLSVLVMVASFFGVVFVEVPPYM
IRGCEKRVLTEAQRKERYRIRRQFLRQKAPTTRFAIGFAIVLILVFFLPVQGAISAYMEL
NNSYRVTFACVSVGLCAFYPMMALPWKVLDRKLPLPHTGSFSFGSGRASRLSRFSLLSRG
TMDSTAAMRELDYIAPQYQTTLVQNLRTLRFWALLWLLFATSGAQIIIMGNMRFLFGALA
GKPLGESFVALLVVITGVGSGLGRILLSVLEMMTQGRSAEERTPITFTLFVPSVLSVATL
LLVLILPTNALPLPCFTIALVNGSAAAAIVIVLRTIFATDVAKHYNVCSFAGIAASLLMN
RLVYGEWYTREANKQGGTLCYGRQCVLMPIIFSLVTNISGVLAAIYIHWDYSSYCRRMLE
MRAQRLPNRVPHVADNSNSNVVDIQYDDGKGSLTEVKTVVESPVEK*
>TCRU_6672 hypothetical protein
MRPSAALSPFKGVAAVHCCEDAQFRLQSGRLGLFLKLRGDVMRHARLAGGNGGQKRTRDC
RETTVAVEEKPGDVASAVLFGVRGVTTRLFQGVELRHAELRAIHVAREAEDANRKLGERG
EDPITLTSIFSLDSFASLHTLDLECNCLGDEGITKLCLWCLPQLCFLKRLFVASNGFGVS
GLRAIVKYTEGDASGTDGRMPSAFSPNNSTETKLHPLEAVGLTNNPLFSNDKDEEVTDLL
SCLLHACGPLLRRLHLNHVGMPTSSAVAMVQVCFAGDKVRPQGFPDTQRTVYLKQNYIDK
EQFYSTLRDLEMGAAARMFLV*
>TCRU_6673 Uncharacterised protein family UPF0564, putative
MEELLEREIEDLKQQQQKLEQELMAIDELSCCMQQSGQGDVNNSHSIPAVLETGGGKDAI
GDGVSLRERMAQLDELRLRYQRESSRALRRYFDVVSGFPQYQAKRERLLCNPRPFSFESR
ELQKEQRIRTRRMESEQRQKEQALQQILNYRFKANPVPPSTYMNKYDLMVEEWRQRRAAV
EALAIEKAERMKAETELVRLSAESMRQVREIMGVRHDAKAKRAQSADFEGRDRRRVEELR
EIPLEVKMKLWPALEEHEQVRVERIKQRAAERFNLLKEEEARRLAPVGATSQVKEQQQHF
PAGPMPLPAVPVGGPIEAVAASPTAPQMILVGNAPAATPGPTTTQPLAQTSLPATGEVAG
EKRATSATQPPLKRRSQSGDKRAYNRNMTFKPRIHGGVPDFKSMWADERLTLAERKRKTQ
PTEVKSFNLTVSPKETVIRGRPALPTKRFVSATHSRQRSRSAASGVKPTQPTSQPVEKDK
KLVPKGTRAHAIRTRAVFIKYLRAAETDASRESNRDDLKAIREGHERQKVVNARLKEYLR
GTSTNTDAIIKKKVRALRQRSREMEKEAFERLVEMRMRVAQIPPIFVEPTHLHDIAKTRA
ETEKEIIHMLEETGMNVGTLATILTAGGNEASSSSNVNAVEAATSTPDTGAVTAVETKTE
EKSKLDVTSTREERVRSVGDSSVSDSPSDGSTDFSRSDSSSSSRTGAPKEKSDYDDDFEA
STNSSTISL*
>TCRU_6674 hypothetical protein, conserved
MDSRKGATGDSLTGSNTNGSSVGRAPTPTAQQPWRHDTAAAERCGDEGSDNEPEQPLFYQ
VNMREITNALLVPADMVSAKLRPLSPSTVAERPAIQVTSGVLAEGGTDYSSNASSNSGRF
LDVPPANLPVRHGRHHSTVRAAVLPSPENTYYVEDTLVIGSVGRRGGLVERGNTSSNECQ
RQGDATTPARPIASSSLLPVPGPPGFAARSSSPPLSKPFNDALQSSSLRSVTFLVQKPTR
IERCVDTISEESVGLEQPLITEGMNVTKKSASKKKRVHFPEDVIKSVSVVQADDQLRLLV
EYYRPWYAHLVLLVASAFFVFHWGFVVLAMRPSEVSQRFAASVVISFVAFGFASAYLLAF
LALTWRPGSEELGFLMDFSRNRPVIYVLLAGVVSQLSLVASFMFRCDVGSLVCFCCIPLV
VTYLYEEYKKHAVSVLDCIGCILVVGSIVVFYVGAEIDDDSKLYYRVVPVCISVVGGVSM

AYFLFQVRTVSRCVSNFFIMSSTTTLVTLLLAFVGYVMDAFASPIGASQKKLTEISSEDF
FKIIVSALFLFFAWFTYHWSSLFFDRMTLSGSFSLGGPISLLVFNLLSLPTASLPYEIVG
GVAMMIGCALVLFSGFRFRQNVEVRIELERE*
>TCRU_6675 tRNA pseudouridine synthase D (TruD), putative
MLRACGITDFFLPVEKPATARIKERPEDFIVVEVDPTGARTDAEDYQLSIAAAPLSSEIH
PHNATTSAAAAVDGDYGDINDDAELTASLTGSDIFTDATREKLLAVFGSKRDAILQYASG
TFENDPHGGAGEYLVAVLNYKGDRRRLHHALKRAFPHLRTETRRVSSSCGSSDSVDHHVV
AMYDTGYLLLAHLLGESAAESVEAWSDSVPRSDTFCIAVNLPPETTKEKRRALHELISRR
YPGLVCLVANGQVTLKVSSTRHREKRALDDADDASSGLFTHLVVRKRDLDMMKLRLLLSR
QFDVSENAVCTAGLKDKCAVTYQRCSVPLSTQNSKSRVQHGETVRLVWPGDPSSYAEILQ
LLEPCSTPVGIGQLNGNWFSVRLVDVRGMTFCELVQRVRHIESNGFLNYFGQQRFSEHVS
STKDHVGVHLMAGRWAEAVQSILSCVPGIYASFPERMKVRYVQTSARDAVYVVKALQRLH
RTQYASSSNPLCMDDVANCTSRWQQLCHDALLSVPYNIRVLWVNAAQSLIFNIMLSKLHG
MDSTMGAVEVLPLLGHQVTIEEPVRQVFEQTLTELEIKEADVLEQKKVLGVPIPGAVRQT
VVRPTGCRLTLEGNDEGDAKNGFDATVEFFLPPSSYATIFLREALGFDRCW*
>TCRU_6676 chloride channel protein, putative
MSFESTGHRSTVGSLVNSFRGRGNILQSLRGIQRDRGTSAWFQELAQEAEEEGDAAFFRL
RTPLFEKSARPHVFSAEERRRMDKYESIDYSEAQSLTYKARKLHLEKERRWLKWMMFILV
GVGVGLWSVLLLQTLDFLSAQKRSLLERFVGSPVGNKTLGNSTQSIGLTPGGMHWKDVGR
GYLVYILWSVLAAMLSSLCCAIVPSAAGSGVPEVMAYLNGIMFPRIFNIQNLVTKSLSCI
LAVSSGLPVGAEGPLIHIGSLIAAGLPTGRSRTLRCGAGSLLSTFRNPRDMRDFISAGAA
CGMTSAFSAPIGGMLFVMEEMATFFSVRLACFVFVSCLSCMCVIQIINTYLIGWQIPVRQ
PVSIGPGEFRPHAISMFIVDVVKGNRVPMNLFTFVSTMVGAIVLGLLAVSYTVSSVKFTR
WRSKRLFPSPLLRVLEPCICALVYATACYTLPLAFDCVEVPDYVKKHKEELRIELFTAFC
ADRENTFSPLATLALTSPYNGIRLLFSRHTAAATPWYACLLHLLLYTLGSSYAGGMFISC
GTVIPSLFIGAIGGRLIGVIFNNSVWADPGVIALIGSASYFSGISRLSFSLIVIMMELTS
DLTHITCLMVGVILARAVADCFCHSLYHSLLEVKAAPFLEIQAGVHKLDMFCAKDIMTYP
AVTFEMIEKMSHIIQILQSTPHNSFPVMLTSSGTYEGVISRSQLELLLWFIYFRDVEGEG
GSEIQKISKSRTLNSDVHKKNRGLRQEGRMAVYDENDGGEKNASTIPPNANGNAEASRQR
LERQGHATYLELAEVRERIFWRRLPSLPPVELLPTATMQCYVDLSPYVDLNTYYVRDVMC
ISRTYHIFRHLGLRQLPVVDQNHRVIGVISRKNFVGDRMHERLQVAEEAAKQTAHEKAQQ
LYRKGF*
>TCRU_6677 Lipase (class 3), putative
MSGGNVWRLLFKSSSRSRRAFRWAWLWQSPVSRDHTPLWCICDGPVFVRSVGEVYQCELC
GGKQRGVECGPTSLFFGFKNGGCVSVTPGLGHGEGVRRVFGEIHSHVRATGTTYTDLVKR
IPTAWKSSGRSLESYREWCDHVILEKENSCHGTTHTQSALIQRQHVSPDDVQLAVYALRF
ALAVYALPYELGYFNTPARSLWLWTPWYNRYTIASTADQVSSIRRILFGDKCDPLLEVAY
ARYSAALQQPCFAIFLDHRTRRVVVAFRGTVSLTDIITDVAGGYTNVCLGTYRSAVTGGT
EELRTNVPRGFYMNVMEAGGHIMSALSVIRERYPDYALLSVGHSLGAIEAILFHLLFFSP
TTRQGADLRTIAFAPAPCVEQAVMTRVNELLGEEAMTSWVYGLDGVARLQTSSVRDLFFP
SSSAGSSKTKKEGNEAQQPQLPQLSIPGRVLHLTEEGTVVLDVPANVPWREKLFFGKEAL
LHHLPSMYGVALHKALLAREASTRVSVEMRP*
>TCRU_6678 hypothetical protein, conserved
MLSRVIKDLYYLKRIHSVVLDEKLGRALKAKLSALDLRDGPSPGPTALRQLMECLVHFQL
ESSLVTVNAIALVREELPRMTGSQLSLTIAACCALGQHDVSVSAVSLLVEALPSIECAGT
VQLIQSLAAAGVRHEDTWSVIAEHCVRRIDSFTGRQLYRIIECFYERKVQYPDFYVVAER
HICSQPSTYISMEHLTGVIECYRGLGLPVVSLLAASSTRSAEGFDSGLVAVAPTRTRRSH
REGGSLTPAGGDGPSNHAVMATFLESALKAMKVADDPQLSDMLQKCEAKHVMHAEIMEAA
ALRLSELHASSPNFSRTTALIRLMMRFHKKEWFVSASQPLSRLLDECAESAIPVLGHRML
LLADGALKLFPAEVQPTQFYAALVRDLKFDDVAASMNAKRLPIVAGVMISLRAYGGHALL
EQHMSMMSVAAANAPLRVQVELAAMLAPLPAARKAFLSDLFQSLSSQKNWVRLLTAREAT
LLLEGLAQSRLPFNDLLLVVVEYTRENPGRFDTPDLVNVLLRCATLGFSDIEFYSTTATH
ILEKKSRTTVHDLCLLMYVFTFVLKGVIRVVQQMLPRLRVSASHTSPRDITLVLYSTVKL
GIARHTEVTTPFCDRAVNIITSFKGEELASCMTSLRALRFDHEAFLSASAELLGAELSRR

EGTVRDKEGVPLNDTQVISITSAIVHLRRTLLRTEWHVPLQRICFGCLSTASATQTHQIA
VVTAALDEAPCYPEQWDKLLQHANEVCRRFQNGTITAEVLLAIHDLIPLDGADDRKDALV
SSPLFTCSQRNLADIMANTDLRDRLRSKGLLALIAGVSAPFHVDEAERTLSCGVPLRESM
LLHHKQMRQVAATGGSKRSKSRALKPTSIKASAKSKSARKKKEKDETDTRTHTRRRGVPS
GKMSAGITTSNGDTSMDDDDGEAVGAKSSTQTKKRDGVKKHFIDFGVDSEANVEEFRI*
>TCRU_6679 retrotransposon hot spot protein, RHS3, putative
MSGRPSKGIHGNEEGQASTVPQGDSLKRAMSDLEGDTAQPAATPIRVEEAQLQWTMCSTV
WDILLDGETDISDMKLNAFLREHFGSRAAVEEEQNVDMWDFLRSPDAFIKDQQLLEEISN
LKDYQLLRDRRKLADGHLNYLEDWIEFEEKDTVTPLTRKKLNDALTQIQKEVARWEAEER
AKRMAEEDVRQNTEEKTTKLEGFYESVYGAKWGHVLGFYDDKICEDRMEVHEGKPPQSWT
YKKEGLTFEKDDGVEQFRPPRPRLMVLTSDKGWPYSWRENKPIVDCYVNCEVDRVWQIVE
RDLKDSSSPGKRLLVGTPGIGKSMNAGSYLLYQLLHCDAEKIQVVVHCFGEGEAYVFDKT
TKTVTKYVGIGESVSVVLSLSQRGMKGYIIYDVPTNGPQLPVSFAPSTGWGTIGLASPKV
RDIQEFARQRDPHRIIMNYPEEMDVKAMCAWMKRDGTPQEQEKYWWMVCHQMLFLGPIPR
YIFDANGFSKRYNELDRVLKSIKNRDDVRYVTRGGTAVWCTENPFYKLMCVDRKRGVFGI
EDLKTDISSGHLAYRLSPLIDKIIPAVEFFGLQ*
>TCRU_6680 isovaleryl-coA dehydrogenase, putative
MFLGRRVLLPRLGGVPNGAIAARPFASANSSMDFLFNPTPEHKMLRNTIAKFAAERIEPQ
ARQNDIEMRFNTELMRELGDLGVLGVTVSDEDGGAGMDATASVIVHHEISKCDPGFCLAY
LAHSVLFVNNFYNSATREQRERWLPKVLTGEHIGAMCMSEPGAGTDVLGMSTAAKKLGDE
KYVLNGCKTWITNGTVADVLLVYAKVDGKITAFVVEKGTPGFTCGAKIDKCGMRSSQMCQ
LFFDNVELDKTNILGEEGKGMVGMMRNLEIERLTLSAMAIGIADRCVELMTRYASERQAF
GKPIWNYGQIQRLIAESYAETEAAKALTYSVSRSVSPTSNNRLGSDAAKLFAAPIAKRVA
DNTMQVMGGMGYSREMPVERLWRDAKLLEIGGGTIEAHQKNITKDLMKDL*
>TCRU_6681 XRN 5'-3' exonuclease N-terminus, putative
MGTQGLWNYLNKHGLCSAPPSVTGDTSIITPDHLLLDMNGIVHGAIEGPHFLSMQTIQDV
LLSVKRLLRLFPPKKTLVLVFDGVAPTAKLKLQKERRATMRAPQNALKPPSSATQLKYNY
DYEGTPIRLFREEVVSGSEFLLACEDALRKALMSSDGDDADRLPGTFLGEYAVIISGCED
AGEGELKISSMIRTLWIEQKRTETYTGDDVIVVVSNDSDLALIGIACTPYRQYYMVDPVD
YCVTAIAELFEHWRKGAANGLLPLELLPSYRIDFVFLMLLSGGDWYQGVAGRSILLWRRY
RELRLNGGYFRRSIIHGEDFNVDVEFLRSVMSVKDSIHQKVRQSKIKQATIRGDSSLSKQ
SVETGVDLLKGAMWALKSIVLGHCFDYEFRVSTIFPTLGMLKAASFVKGVEKRIRPESKA
PLPLLSPLEQCVAVMGMRGRYSEEILRALTTVCPDGGKKLTNSQSVPYLLSQVRLLMASV
DRDKLTAAERELLKVQHADVLEKGGVLQDAVTFMSYAYSSPSCE*
>TCRU_6682 1,2-Dihydroxy-3-keto-5-methylthiopentene dioxygenase,
putative
MPGAWLLNSQEGNFTLPSHCSPDVSVPINLLEAYGVYSRTVDPATLHERHPSDDEGRTRA
QRLAWNLGYQGQEEVTLTADSQEELREHLNLDEQMRIVESGVLYIDFRDAEERWIRVEAK
SGDLVVLPRGLYHRLVPAADSSPVKLLRLFRKSAVFQPIPRNGELSVEAAAEARAAHEDH
KFYVSHPPTETILGPANTEDNVLVKSPRDFDATLDKVRAQLTPGDILVLLFKGASDRRTH
QSWCPPCATAEPIVRRAVEAAKQKRRVVYVQCNVERSVYLGNPDYAYRKHPLLNIASIPF
FLVLEQREKEVFELCRESDPGEGYNSWVEKI*
>TCRU_6683 hypothetical protein, conserved
MEPSAMKASNELSMAEEARLMSALFPYVSSKCLWECVKATKSVEETIFNVNATVNPDLYS
ASYLINAMRNFATSTEVTTKRTPRNADSGVIAVDSDGNEIVDPLEDPFVSVGSLLHSRSS
LFDGEMNILEVDQQQEYNATVAVFPIDTAKWDEHFITSATLTDVVGAQPLVLPTPAEKTP
LHKDFGGSDDAIQAPIVRWAPTAASLKMKLDESKCISSCEAPSPLACILNCEEGRGETNA
RDEGGLGTKKEKKMADRAMNTVGHVEPVLLTPLQFCTQRECELRERLEELERNGAAAFAK
TEETDFCREIAEHCKTFTSALPEYFQKFLSVVAKEFEGKEIVPPLHNIRLKSFSGGILNT
EEVRIRGIVLGRSYARFSEDGEHILFRVKLKHLALSPVSFSLAREESRGDATKGTVKAKA
KNLKVKAKLELKLHLTGRLIARCGNIHFSIGSLQTKCSVFGLNAVAFFLRPFLKQKLTSF
VVKALSDEMFLDLA*
>TCRU_6684 hypothetical protein, conserved
MVVLGVVTRSPRALLSLVREAYRSLFFYDARTASDVIFALGDLHEPPLNVHALVLSVLTT

LPNFSCGYHVARLFHGLSELHVRHTMLTAHLLKYYLRCCFGKSCTVTPVKCFSRDPLWFV
SSFAIILQTLHRFHSTETLEAFLDSVEELLRADPACFPPCHHRHHERRDGLHEVHAESDV
EKVGNVAEDTFLVMQRFVLIHRRNLYGCRFICTEKLLASFTDHLHCRHLTSLLCLMEDVG
GESHGSEYPRLKKKEMAELQRQLLCHFLYRFCAAALRPGVLSNAEIVVLLRHVNHYNISG
LPPDVRNGLYFLADALCIILENSSLTLDAIRLLVASDLYPEDEEPHEKKGNSADVLQLRQ
KPRLEPFLDGLQHIVLGMESRRFCKREDWLTAEVLLILCHRLLLAHVVHAKKEAGPRLLR
TCHLVCDALKGLECHLGTEDPSVEFRILLATEPVRALLLQGASLLGQELASTLTEAITRH
VLQSAFHLATTHNTDDLDIQSLSFLMREFHLTVEIVARIDIILRLICHQRRFTQHTVKHI
AKALSILGSEKWVVFCGNNKRWIMLATSVRLSNAVNFLISSMKALEQSVAPQHTFEMLLN
LLAVLSPVKLRGKEDRRCRYLAGQIPDSNAIMLLINTVLQGCIDCIPPIALCNDDWDGHK
FFALKATDVAERCSLQSRSSNAWNAPESFLGNVWRSENKSNCEGDTRSLHMKQPSADLVV
GFALWMGAFRFGIKIKDANGRDPSLSKMRMNELRKMHKGILQSAIHVVLQDKALGGYFLR
QRLLRAFYLYLKIEGPYSRGESEPIFISNEGFKHVVPLLIAEVYRVVKDPFFYEGSTMTS
GDLLFSTETWTIFGHCGMDAVELITFLENVTEEFQMHGDPKMPLLLLHDIIWGSLTCIAS
LSAALEEWIDGFRHGDSFHVKNLFNAGICHQVREEGDAVIITNRRNTLLWSLLLLACFMR
NRGAMVRTGHAKELTAALGAVARLVRLVSHQFPVFRRSRPAPECLLALNLRELVEEESAA
GVINGANNCVSDVLDDVLRREQQHFSCWECNFESVAARMRRYV*
>TCRU_6685 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGAGCGFGEKVSQDEFCNNTYLGVLNLLANKTDEELKEKYCN
GNDTTKCVDTLKKDIADAPENEKTKKDSATDRDPNVAHGAAVSVGSPTTKPSTAAGVNNA
GVSSPITPTLRMEGGVDANVHSPAGGAGHQQHSDDVRSEEEQRNHSEAGGSNQHGVGVQG
KTIHIFLLLCGLCPDFSWSLRRNTATGMIQQSVWIR*
>TCRU_6686 Leishmanolysin, putative
MAGSFVSRVAGVVGARFVCVVWAATCNTSTDLRHYIGAMNFDPKYMTDTAWSVRVAAHEI
AHALGFSQESTREKSLVKKRERSVRGTHRRMLQGSTFRRRQKRTLVVTLSRAWCWRTKVA
LGKRKSLSGRDAMRGTS*
>TCRU_6687 Leishmanolysin, putative
MAGSFVSRVAGVVGARFVCVVWAATCNTSTDLRHYIGAMNFDPKYMTDTAWSVRVAAHEI
AHALGFSQESTREKSLVKKRERSVRGTHRRMLQGSTFRRRQKRTLVVTLSRAWCWRTKVA
LGKRKSLSGRDAMRGTS*
>TCRU_6688 inositol polyphosphate kinase-like protein, putative
MVGEKEGQHHHQQQQQKEGVGGMLRAFVPLIPEAQNANPTPESPFLLSPEKDRRGEFAA
AGVDDDDDGYKSSAEQTPRHGRTGGGDGGDDDSHSSICSQSRSFGALKESTRSADDGDDS
MKEGIKKKSVIGNGMDGKKRWTSEMEATDLIRDDDEDDISTEVTRNGNIHAVRGDFQSIK
SKMTSPVRGGTSQREAMSRPDLWHFDGGVKDLSSSREEVGGGCPCADHHPLPMYNSDCFL
RTSGKDEEEDEEKKEEEEEEQPVVKKRNKKCAFRSFQNCDKNEGGGRGEVRRWRTMNSRP
TTASGLLGAGGSGATTVKVDRRMDSSTGGMGSIGGHHLTILEGGVFMKESCSHREERFYE
MLKPVQDYVWRHPELLETFYPLSSSSSSSECSNDAMENSDEQQHGNGKKGEEGKKLERQH
SASAQWNWWRRRRRPSEITRGTHDMHSDSTPSPEGGSSRERDTVTAVSEGRHWDVLIPLV
PFVPRYIGLRRVLLETDGVSTKKSEWVPSSAGAQDGTPMQRCSSTLATSRAFEKEGKTEE
GNFCQMIVLEDLCKGFMHPCILDIKMGSRQYGMNPSEAKLRSKERKAMLSTSMQYGVRLA
GMKRWCPDTQQYETRSKVAGRNLTLEELRETISRFTQCSKRLRYKFRKQVRRLRCAFMNQ
NVFRFFTSSLLFVYDADRPLLSSRVVMVDFAFTYEREELQRGGDPEATYERDFGYIKALD
TMLTILA*
>TCRU_6689 hypothetical protein, conserved
MRTPCGNAPPSLVTRKIKQTHAYTIRGPTTNTYFTLRVSADTAAVPPLPRVAAAVSPSAS
TSRARARGQKPHQTLPSQTSSNSSPLSVFPQLSSPPTSTLWQPPCVALEHRWRFIRKEEF
CLVRSPLGTETTAINHASRNEPSALRRLAEEHSLPSMHPLCRRQPQSSSTDRPEEELATQ
QIQDMRLRTWGLRRGWLEEMLQDDDGVGDAGTEETSPATDPSPLGNADGTVRPTPPVFLG
IKSAPAMNAASEGTEATTTTGAMILAADGDGDGDGDDVSGKKAARGGNIPGGRRLSIPAP
PPPHSTATEKADGKIPRPVSTIAVAAQRLRDKLLTASFQRMVNDLVETHAYTPEEQVALF
RHAHIFRELPLQSRYHEMHPICDLRPASEDFLPVKDFNAAARENKSTTFRQRRQRRQQQN
ECATTGLLG*
>TCRU_6690 Amino acid permease, putative

MNPGGESNFQTLVRRRNHVGPVFHPTLRRTQEVIRRPEWVRRAGEAVAHRGSVGIVGLFA
LMFANCFGGGYGFEDTVGAAGPLVTLVVCLILPWVWSLPTGLVVAELSTAVPSNSGVLMW
VNAAFPPYVSFFCIITTVFITFVGNATYPSLASAYVTGLVSLNKGAEIGVKIGVVVFCCV
LNCSGIELVGSACVVVCVVAMMPFLILSFQQIFTHGLDGQAIAHVNASSIDWASFLSMVT
WNYANIENAGAMVEEVSNPKKTFPIMMVPLMFSSYIAYLLPMLAGVSALGPHQNWADWQA
GRWPQIAHIISGDWLKYYLFSGSIVSGVGFTLTSMCCTSRLLAGMGTMEMFPKRISRIIG
YYHPTIGTPIPAIVLNATVTLIFCISFDFGDVVAMCQSLYCLRMLLIYASLIKLRIDHPD
LPRPYALPCNTVAAALCLVPSAIFCFAAAIVSSMVSLAIGLSLVAFLILVGIGSYLYCRY
VARNGFQGVIVQCETSDGDDIPAEDDREGPPLSRGVFYNDGYDERQGKLILGIFPTGQCP
SPIGNGSGTATDVTGEPEKTFSGRGFGRTSPTGMMSSLSAQREMTGLYDLPTTNGNDGEK
PADPNGEGRGFTNKNAGTSCTEVNAHT*
>TCRU_6691 proteasome alpha 3 subunit, putative
MSSRYDSRTTTFSPEGRLYQVEYAEEAISQAGTVIGILTTGGVVLGAEKGVQNSLFDSEN
MEDKNISGEKMYKIASHIGCSVAGVTSDAYALLNYARLSASRHHYTYQEPMAAEDLCRLL
CDEKQLYTQYGGVRPFGVSFLLAGWDRHHGYQLYHTDTSGNYNAWRAYAIGQNDQVAQSL
LKRDWRPELTLDEGIVLCLRVLGKTMDTVKLSAERLEVAVLHKVPAPATQKLLEPYGVLP
KTVPEFKILRETDLKPLIAEADRQREAEEAAEAEKEKKKEQKLTSS*
>TCRU_6692 hypothetical protein, conserved
MRRLSRMKVFLSPTLFVRHGSSSWWLSRLLYGANASPLLGEWDTANSKEKGKLDDAVRVL
YCKALVHASGGGRLARDWVAGCSALVGASEKLLGIALKHDGTEQDVERYRDYLLTTLCKR
MQEASNDGNGTGNSSMNSSSGGKGTVSASSEAGSLDARELGNLPEVRCFVYDAMRAASFH
RYHKVPEEDRQRLYAVAERLGVEEEVTRGIWQLVEKEGAVQREKQRALDYPWSE*
>TCRU_6693 NAD dependent epimerase/dehydratase family, putative
MASRKLLLFGGTGFVGSRVLYKALQRGWKVTCASRGGLPPVGSPLLDEAVLRHHHPPEEN
STDVAEDATRQITPFHSPLEFVSLDATSRSQVFHFIEDNPDATAVVSCIGLLTRDHNEAR
RVCGDANVNIAAALYERGKGVRRMVLVSAEPYHEALPVLGSRWLLKGYFYGKKIAERAVL
ENLGDRGVVLRPGFIYGTRYVPLGEGFVPLPLWLLGRPLEAVLRPLHRGGILLPPVDVDV
VAEAAVRAIDADAPVGVMDYAKMQELCAESQPRENTTKAEQN*
>TCRU_6694 hypothetical protein, conserved
MPEVGLDRAFLHRCCVQVSSALADDAAVAAEIQHTLRFVRDHACKYPGEITRALIWRVVD
TDNNEVQDRLGAWSVLNAVLAECADIKQPLSSTAIAEKISLFLPYLITYRWYSIHSVSSM
NRARSLSAVALLSEYDKVVPASVLTGDDSRLGDAQKEGEIRAKYREFLTTWKAVWRHDVY
QRFKEAVRRTEGSGNSLSSKERPYLDIPATFRDSLRRLRRRNPRPSIAFHVLSCYGWVPP
TEAETAPTEPMRGLNGTNEGQISSNNDYAKRCPVVPKSITEIEKLDPAAHPRVRQWLRKL
VEEGGGCRLCDVWNHTETRCPCELPFIKVPPPEGSLHLQYRRRRTERTNMSYLEAVEKLF
RYGIRLPLSVEKTLDRIVSLIKDEASYEELLEAFDTVRGAITGPLERHALWLHASYMLMP
SRTVFDKPSDDALSPAMEKAEKHFKVHRRFREWDQLLQSVEVLDSQYRRAELSPALRRNI
EEVRETKSFFFCLIDGSQSAEYVPQSYARVPEEVLQLRPVKDVLCTVCLEPFHVAARCSK
GTEPWDLSVARVLLEEHNLLNMKFPEERHMFDKVLRTIDEDDRKAKEFRKKELCLAVKLV
HEGRVPYCRLCNIMGHSIRRCEEAARRTLHRHKIKDVDMRLNPHLVQRKIKQLRDANDER
EERWLTEAWELLGKGRTYPDSFLSAIRELEDARIPLAAARYSTDAVQGFLLFIKSNDLLQ
HLQPLRDERFPEVCLFCDSYHHGSELCDRANAEERGFLSELRRYGLTLWQYLRAPERYDE
RFPTDYPKGRETVLGLARQFEEDYSPGGIARVRFVENNGLDGDVTSPVAAGGMLSFGSSQ
RSFYGGSSYGIPFSQLVLRPGENYGNNNNNDSNKNTIEATAVAMSVHDSSSSTNGITMRS
SFGWPIGGETPTEMVMEPAATVEPFLDMAGGHGGKRGREADDDSVTKSGSGDDDDNEEDD
DDINAKPHANSGEEEIPMSMMLQSSCGEADGLGHVGRRFRLETRRKEEE*
>TCRU_6695 von Willebrand factor type A domain containing protein,
putative
MTIQHFAYSTSPNRDHGVLAASTFAPLTLRGCVVEADVRGNCARVNLRYEYENKTGMDQR
VIAAYPLPIAWDLMSCRADYFGDCVLTEYSGTVPLRSSADAGAAGLPGPMSDHSVWTVAS
QQLPWVIDVGSTVLIAATYHVPLDVTRWRGVVRIHLPAELFPDFKKPPQPTLDYASLFDM
KLQAKLPSGWKIQAKCDMFVPLAGAVRLRPAEEETLVRVDYIGDSGFSLEYTAPLTKRLP
DGFEIECVVQGTAEPLRFFLAKDVGTLVQDVDRHAFTLSFTPQLEGRPGCITNAELILVV
DSHSRQSCEAMANGILVGMRGLPESVFLNVVVVGAKKDVSPWQCGAVALCDVQLEQLFAF

IAESKPQEANSGASNFHRTLREVMSQEALSLCGSVPTGYVRHVIVMSDEGGMRYATETIE
AVTRHRRNMCFSAIGLLASGTLDAPTLRLLAEEGGGLYRDVADAKTFPEILVDMLSHLAV
PTLTDIVLCFDEPEVRLSIGQTMPAVAQGTQRFVHGLAPASLETLGAYATGRIGQTVVEY
VGKGNVQDLIFTSEVEPRNALSVGLFHLAAASARVRYLIDERALSALSVAEMEEVARLSK
TFSLPSPYTEMLQRRPATAANAQAREVRNVVAVRYVPRSWTYARTMTRYRQRRLAEGLID
GRPKVQQGITQQPEQEQKQPGLFKTSGTFAALVPPPTCREFIRAIVVDVAESVVAEPSLK
RLTALQTADGSFPLNSILGISVGVSLDRLEREFPLTGFGISEDLTAGREYLRNHERFWAT
AIAVAAMELQSFATTAMAYRRALTYMKTHDSEGKLLRRAREIIGKSPQESST*
>TCRU_6696 hypothetical protein, conserved
MQNAKGKSRVAGGVKLTKQDDILLDERINANTLVYSKKSLVAVALIAAFQPVYLSHAVNG
LDWFSPANTFLYIAVMVFTVCMLTQAYITMVESEFWRRQRHYHEVRECDEKLLHKLRLQV
AVGYTLFFINSVFSVFCTGLHMYIFRHSDPRASFILSPTLTAALLWLVAQKNEESRRRLM
AQHK*
>TCRU_6697 adenosine 5'-monophosphoramidase, putative
MSSCIFCKIVEGSIPCHRVAETARVLAFVDINPLSRGHLLIVPKAHAEFLHQVEPETAAD
LGVMMAKIARVVAGEGEPKTQYNVLQNNGKLAHQEVPHVHFHIIPKRNKDEGLAMGWKTL
PTDHAAFAEDAAKYKKALENM*
>TCRU_6698 hypothetical protein
MEAEARTILGVADTLADSVVRSSGVSAVIPELNVARELLRGTVTALQRQGNTVCEALAAR
KTQVQENDSHSGGISGARGGGETMTVQQREARCEEMVQSAMRRLRSVVQAIVTHVDDAKI
TAAFKPVVGSVTENVAERLAKRREGYRVAHAVRSQAEEKKVKVVKPVRDATAEAGTDKEK
ETTTAAAAPARPRQLTRRKTRQVTIKDKVESDVPMTPRGVEHASVLQRAAEQEERCLIAL
TEMPSNKGSELKDAADDSQPRVGAGAMERSVRRRRVTGNEKVTEPSATAVRGSRGAHGKR
FKRTLAL*
>TCRU_6699 hypothetical protein, conserved
MAGRAPDTEAALQLDPTSRTFDPKAYIRQAHVHATHVDIENTLLQTVGREVDFTEEALKE
LIRDNIGTFIGCKEAMDVMYANDTLLFTGEAIDPIADAFQTTLEAGEALVAPTVELFEEL
RSCRLTKEMLEKLMVVWNVPGVIYEYCGARVPQRRSDVQPSQRRGPHRRTKESDAGKSED
GSDAHSSSGRVEDKTSNVVRERGDITFSASEDVVMPRSVRGALEEFADSAEAYGNYILRP
GEELIYWHGTPLARCPCSPQIPRSEGAAGGRSNYEAAVLSLRRAMIYLEENYDLENATVL
GVEARDDTEEEGVHSALKVQKKKQQQQQGGLTLTYQYALSLLRAALYLNEMMAQEIRHAS
AADTVLIEDTLSSMMDCAIAAVKLRHFCFTASNKLQLNATEAAALLGLRQELQDDKSIKE
EDEEDVGESSVMTPTLGSFSATESNFSAEAVKVPPSSLSTEPSTRGHGSEHQRKGNSKGS
LLHPVEYYVHITRDQHTRMMENTALNISCEANEWQIKFMPSATAEENSSVRDNRNEPRRM
WFGSFAATGDLFGTANDSFVQHNNAGFHTLDSLAFAEGSVTDRIKVGGFGVDEAESNEQQ
YADAILEAFRTPEGNFSRFTTFSIGQVEMSGVLECSAQQIAMCSASLLHQLMNCADIQID
ISANAAAVDTFFGRLFAACMNHLELVVVSYWGGIAAAVHAGMFDFSLDPGSALYRMIHGP
AVLGSNDEGEAASATAAKQPDASVNRNRHADDLPHLTYIPIVREGSPTLRQLSVALVRRG
VKAAGEILYALFLSSVNRTLLRGFVRVMAAYRVSDVMGKNREDEEEHIELHAAILVEVIL
AQWEKAMTHVSDSVWRMKIVIGESCTSVTVASEEQAHEVGGLLEDLEQLRSSVFRCYTHG
VGMLAKAYVTLLPSLRQTKPKMNLNKTVSARLSREFVSSVLVNKLLNLISVVIDRTAPFL
QRFDEVYEGIDLFAAKAERDTEDDANQKHGHSTRVLRRKNKEDLEASAQLDTVTAFMAHR
NSKMVLEHVEEQEEVLLALVTNIMLLFVDALHQSCQRASLITGAAPETREVVHIDSLADA
LCLPAAVVPIVIGELVSPCILQVVASLKPDAKTSQEVEALLSRKEEHFRVDFISQVEDHC
QLVVDAMLSMLLVTPQQRITREVRAPGFMMPMMDWQRVSVHTAGAVRPYIADSILLIVQA
HEELQYLRQPCWRRR*
>TCRU_6700 PX domain containing protein, putative
MLLSTADSTMGPSSAGSEKMFQERQQEQSTVSQTQCTSPMPADTTPLARFVVEAAVLGTG
LVRPITFFPIMMTIRSTSSSKYTVPDVPRGPHEKHMDTGIQRGQWAVSSSAQVDRRYSEL
VEFRTLLAYQFPTMIVPPLPPKSKLENFGTFLTNGNILLTQQRTLVRFLREVAMSPELMY
FSMYTPNFFQLPRESFEDWIGIMRAALAEFRRCNSSIDAHSMRKGGLLGSESVAAFTGGS
TTVVRKLVGMLHSWMGSGGESPKAPPKQQQSQRQSVSAVVGAGVLNATEDLNYWTGQMRF
LEEYREALLGAARPYLTVMEQSLEIVVATKEVAEALEKYADALGTSSVNKELARVTLEAS
RFIGEGAIAMDRHQAKKKNEVYERLLFEVSYIDAAMDAIDHVICLWRHRNEVAGEQVGAE

FTIYTSEVSNKLRNFYKNRFLRNFKLRMQSMLHRMTDAECRFAEEVEESMKGTTFARRIQ
NPKYSEYVHGPSSSSSTS*
>TCRU_6701 hypothetical protein, conserved
MAEAASCLDLKASFFQVPLPREARHLFRCRVEDGTLVELTRHPVGHKASPEILQIIITSA
IAGLTTVVHLLWAAPPLVRVEVWIDNIRIAGPKSDATLWEAQVLRNADSCHASMGEERES
GAAQYTFLGVQFDHTHRAVSLSDKFVRSVRAMPALNSLTIAEMEVVASRFLYLAAILGTR
LCQYYFFIKAVRRRLSAVNRGIVLEKSPANVPSAAVGLGERLRHTIENNRKRIIKSSEKA
SAAIIADASLH*
>TCRU_6702 hypothetical protein, conserved
MQAEARAVRLALSVFSAILPSTMDVWVDNTLLQGAVNKGSSKSHAMTWELQRIKEFLDSR
GVQANFAYVRSADNPADGLSRGRVFTLQDLAEGVELAKGSGGVLWSEDPKVRES*
>TCRU_6703 retrotransposon hot spot protein, RHS3, putative
MKDFLISPNEFIEDEVLLSTIKTSPPYQELKKEREEFYMLLGVSHKLSKEYIVTLRQWRD
FERKDKVIPLARAQINTAYSYVLSEERRKAEERERRERQELVIDVSTGIKYAVFKGRVRV
DKTRLNDFLTMELDGRGVVATNWDVLLGEFFKNPKKYICDAEALGEMQASDCYKKMEGAV
REEMDMEEDVDKLYKNGVDNLLKWLVATAEVKANVHGVTKRFLDAAAEEARNPKKSSAPR
YLEGCYESVYNARWSRVVEVPGSEGTVMEVREGKPPQSWTYRAVGRTIERDDGVEQSGAA
RPRLMVLTSEKGWPYSWEEDESTRDCHVNCEVERVWQTVKGDLTEWFNSLPEEHFTRIPH
ALIGTPGVGNLMAAGSYLLYQLLHYDVEQLPMVVCFVGGVKA*
>TCRU_6704 hypothetical protein, conserved
MERQRALHKLRTARVRRHRQNSAADAVAAHRQPRPGRERRRPPQHQQRAIGQRTGVVVHH
DGGRVGLHTALEHQPMRGVHLAPRHAQHSAPRRNHARTRAQRIFATEHSRVQRDTATDKL
QHSAVNHHRPPTSHHGHHGHEGNAGHNQHGPHEPQARQHKHRCVRRGLRAGKIHKRRRPR
GDQQGVRHRQHRPRGKRAGQHKRTVQRLHIAHGQLHRPALVAPRRPRTAQRSTAHHVQHG
AVQQRHVLHNDPHAVPRHPRHVEHRAHAVQHNVAQRHLARAGRHNEHRPHRHALAEEHTR
RSAHSGRQRGSSHRHARLAVPTAAAARAHAHTVPHARRRRPGRVAVRVPVAGVAPNNVDA
PSVAKSSRCVLLRRRQDSPTGVVARHPHMRPSYKRQAHRQHPRQQRSVAHKAQRAPSSGH
GASGVEHLPRDAVVHVALRQQHRPVGQAHRRIKRHRVVLRRQKFAPHKRHSRARHAHSPT
HRHRVLAQQEVTVNKRHHGAATGRNTALHRHAQPQRRLHRQSLHVQRTERRQRHTANKQH
ANSVAENRRHVRARNGQHAPRQIHVVHHEARGGVAKAVGATVRNTRLRNQHRVHHSDARA
RRKSVRHHHAAGARLKPADQHINALASRRVGPPPNNVQARSVHKQAVRQRHVAHAPRHRL
HVHQDVRRKGHANVARHRRPETDVHLHTHTHVPHAQIGAVSARWLGDSNGQARIAVAALS
TRAGAAITRGRRRVRREARSREGAWVAAGQDGGVVHGRYAVFHSLTAVHGVARSHNRSVC
EIAGPWISAELSACPCWT*
>TCRU_6705 hypothetical protein
MDAEPEHRALQSAALRDDGDPAGDGDGGAVAHADPDGVGERHVVVERGGVPDARCDDDGG
WWEPDAERHPRRWERRPDAADGGAAVAVSMGTRPAAQHAPELCAGGDGAAEWVWWSVGSD
AAQRDVGTQRDESVHRPGAGCARVPRLLHCSRRDDSHSLRRCGGVRRLQGCAAWVLHDQV
*
>TCRU_6706 hypothetical protein
MGCHGGAGGRYDDATVVPEAYDDDIMSWGFCVSSSLSSSSRSSASSPPRRGSRSSCQWRS
SAYHTTTLYTVTASSTVVSSSTIAAYALAPPSLGASWLAALTTHSAARSTKLAVCITVRK
AERIMFVKATTPAPASSTAAMQKYWTWQPPTGGCTAAIRHTTHSTDSWNTHQYTRLPLMF
VSMLPYIRCCAAGCQYPTGYSRRSCSGFLENCQYLVKLAPVWRAIK*
>TCRU_6707 Enriched in surface-labeled proteome protein 1
MLVTLPVYPKEEDNGKGKLHLWLTDNTHIVDIGPVSDDDVAASSLLYRSAGSGTGEANNE
DELIALYEKKKEDGKPSPGMVFVLLTEQLQRVKVVLANWRKVDDRVSKLCPSEKDTSTDT
ACSPTVKITEGLVGFLSGNFSNDTWRDEYLGVNATVKNNGDGETGATKTSDGVQFHGAWV
EWPVGSQGENQLYHFANYNFTLVATVSIDGVPESGSVPLMGVRLNDEKKTKLMELSYNKE
KKWKLLQSGGKAEELSSAWETDARYQVAIVLQNGTLGSFYVNGKLVGSAECECENTKDKE
ISHFYIGGDGSSAEGQGGQEGVSVTVTNVLLYNRPWTEEEVGALNPNKVLITSPVTENVP
ETMLQSSAKPQPSEQEPLKANIGGVGGGVSRAASIATTPSSDVAQTVATGSGDTMRRDGS
PQTPELSVNSRESEETAEGRDGQEEEIHARVRDVNAAALSSSLGNVSQGNNSDAGTVRGS
GLLPLLPLLLGLWWFASL*

>TCRU_6708 hypothetical protein, conserved
MNRLNVEEATREELIAVVKQLYQQLRQQRTSSERVKELEKQVEQLKQKLREKESAVQDLA
KQNAIFSEKSVADEETISVLIKQLEEMNVGDNNQAFSDDIVEARAVPAKAAPSSPREKWT
TGGKVVQALVKGSGGGGSGVTEGARGDSSTAFNAATIIAQKNNELAILEKKVRELTEVNT
FYTAIVLRHDEEQIQGVLKDSLSKKEPSAVTDIEITSLHERIGFLENERDNLQRVVRQQN
QEKQVLMKELQEHREELSRLELDLVAAERWKVSLATPSETVEGMPSVHISSSVQSEEFSP
LRASAQLVDQIQHKNKRGKSTLNIPTRPRATDSPDDTHTPPRNLAIGRSPHYLDTLPEIR
LWNPSKQEKILLERVELYRKCIDEMQAFELDRQRGFDEIERARAELFTEMNTKLEEQRRE
IYRLNKRIAESVSVCRKEEEKKNLEQRPVNDVVTSPIVDSLQDEHVSMPSCEAFSSVSAG
VNRMLRKEGAEYDHAEKKAREGNDYIDGEDVNVVEEVLLEFLGAAAASSEMSVPGKEEVE
MAEEKQLTKFGGDDEDVNKQDSPLEAETDGLQEIYDSSLPKVDWAWKLMDMAEEIGRLGI
YCEEGEEAVGMSLRSRSATAALVAGLTVQVAESSKKMEVLETALVEMRVSVSSLEGRERE
LVAEVGRLQEEMTSMMEADKVKKKLTAKREVFTPSLTDVACTEEPWEPLQCVCQAYSEVV
NAQIALLRAASAIVAVPKISDEEFENFCKALDAIVTKDDRVNNGINEKDGRGIPSSFKFV
EEEGSEKQLGRKSSPLKTAPLQSSETSTFYIKHSPGLFSAPMATSGSGKKNAQTGNHYLF
SEFPSTQAADPQSETSGFCLDKSPAAFYFTLESENENDKRSPPPADAAGSSPQETYPAFF
AEKHSHKASNAAPNRSIASPLGSESPGRFAPDPLDYFVKSREMGKDTQRDGSVHGNATNV
KNFLDLFGAAPSEESHSKQGGDNNAFVAEFDPFA*
>TCRU_6709 conserved protein
MGEDPVEDVRRYLARDESREKEQFTASLEGKSSEELLALLKSRRNVDAGESSAYCTGSSI
RSEYGSGVAVKSESDVKNTPPVKKKRQAEDAVSSMTSTEKLVEISRVETSRDEPLPLRNE
SPKSIQGEHTAAWQAVRSGVIVTEEELEEVRQEMLMQERLLKALEKDNANLHEEQRVLRA
KLNEMEQKAVSVEAKYSILASGRGPNSRVGQPVPPIAIVSTEREQKCSQDELRMELEHQK
TVVRELQLELELIRREKKDLETRLAALDIKKFEEMELEVRNLRVDLKRKETEHNETVKDM
ARKIAWYVEHQEFNHSQEELLKEQQDTIHRLRARLHETGAIDDEGKRKRVGKDARVKYLT
KRVVELEEALNQKHPNSIAQLIRSCQPSVQDSKQFKQLNLKIKELEEALVEKDRCAEAAV
TRLRVETDRIKIQYQEKIEKLEDELKLRLMHAQTRRVRELEKQLAEVREALRERDQEKTS
PVPEVEKSASAGACLLENSAAAPALPEKTKLFMGAAQKGVSSQVEEAISSLRKENDTLKS
QLSQVTHEATQKPIAVSPPLEKGEDTFSSHVISSMQAQISTLTAELAVYKRLLMESQESL
RDSNTRWEERLGTARQEYQQQIQHIRQEHNDDIKRIQENHQREMRTIAEQQQNLQEASWA
CQKAAQIPLENPRQGTAFLQSVAERLAYLELRQLQKEREAAHEILEVKRVADFELTLAKQ
KTEMLIEQKNQQIQEFRLQLDQLLASLALLHSHV*
>TCRU_6710 hypothetical protein
MNLDNETGCNVDQLVETLQFYEQQISNLTESIESRNEGHARMETMLMNLISEKIGGVPPP
LMPENATAKAKDDDFILTVGRMQDEIESTRQTLQTAQRNEELTGTALARIAAFITHHDEK
YKYHLDGLREAVKNFQNVWKMSEEHNKQLKLKLKMPPNENPVNATTLMPGKTQLHKSLTE
KMAPCYFEATRIVVPLLNCMTAILDSLKMKGELRLNNRKQLEDAHQTARSKLFKQRDVLK
DVRQMVDSMEGAILKLQAANNEKKDIWDKLQEDLMELENSPKLTDSVATTNETILELSME
IVVLKQALEEASKLTQKAQFEEKKNVDTLRSQTLELDHAKNEVAHTRRALTALEEEKVEI
QGQIEASRENKRKQLQETENEIQKVKDFYEEEHEIKETQKLFEMETQSFRVSLDEARKRL
NILKTQLESKASQKAVLQEKKLATEENVKNLKVDWAHTRNKIIEIRKSISGLQQQEEEAS
KNLQYINLLGSDTVFSSFPSDFNPQQEAGGRIADENLRQMFILQNKNLVTKARREHRCSN
VAAGVSCISSKNLDTVHEFGENKGLERPRSSSTTTQEPLHSTSIPAPVAHIPSSKYYFDD
HFSTHATGRESREKSPFISAEEPPIGTTTHILPDEKSDLFFCSRKIDIRLPDLGSRGNSP
EKRKSALLPTQEAAVKHFSESPTRFNGSGNIRSPPVIERVNLRLQEILNRNL*
>TCRU_6711 Ammonium Transporter Family, putative
MSSGSSTEGKCLPEDSDISWVLISSVLVLGMMPGLGFFEAGLLRSKNTTSVFAQIFSGCA
VLSVLWVCAGYSLTMGRSAGGKGIIGTFRRAFMMNVDYNTCYGGTVIPEALFAFFQMMFA
TITPLLMTGAYAERLAFRPFLFFTILWEIIVYFFVAHWVWAPEGWMRGMGVQDFAGGIVI
HVTAGVSSLVCAVVLGRRRDFHIHRGEAPYSSLPLTCIGATMLWTGWFGFNGGSALQSGK
GAVYAVINSQVAAAVCSCCFLFFHMLRTKKASLIAMINGAIAGLAGITPTSGYITVPSSI
VCAFIIAVFATVSVYLIKHKLRIDDALDVSSIHGVPGLVGAVFIGFSGSSAVGGADGLLY
GGGIRLLGLQCLGCIVAATWAGFWTFVILLIIGRFYRLRVTDEQEHHGLDHGQHSEVAWI
LQGSNVGGDALPIKNRKHVKQVRNSSLFIGETGTYIVEKERGDSILVVERVNNDEVDIDD

DPREEGFNTMTLAVNADARNEIATDIDERLINRS*
>TCRU_6712 Enriched in surface-labeled proteome protein 1
MSRRVFTSAVLLLVLMMCCNTGGAATAEEPSQGASSVKYYFWRDVEGGEETVSSLRVPSL
VEVNGEVFAVAEAQCKEGIENAFTGIASELLALTGEQASKELNKSKLKTQVLEKCSSEGE
KVTWRIADRADS*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MSSRVTPTVLRISTGSRDNTNGAIVAACNTGSGGEGATYVIPSVYNATFLTCSDPCTLAA
SCFLAYTATATSDGCACACAEGGHGDACLPAAVPEPPSTDGADLCVRDVRVDEVVNAGLG
TSVVCYVGVTFAADVVVDMESMSGSVRNVTLVNCTFVGEASLYVVGWRSDPPAGERADVL
ISGLESRSGGGVLVANRFPPGSRVTVVDSVLIAEKRVAYHDAYDLGDASACLVLHSVNLT
GSVLTIARTHVAAVFRGAVGVLFVGGVALSSRGALYVDGLSVQTALGLCVSVEGGVAASG
GSVVAFVDSDFLLCKHAVSVRGAVSVSGSAVALVRSEFLSTEDYAVAFYSTVSLDDGSML
LAKSNVHDGVSREMLYTAGAVTAAGSTLSFVRNRALLPRMLSLSLLLAAGAHLRVACNDA
GGRVLSTAEEYAAAGFGDAGSIDVVGCDACDRDTHCYAPGTASVSMRNGVCVCDCGSGGY
GEACVPVGAPALPPAVGTVSSVFVRESVTVRSVFVVPVGASEVTLRHVVLDGVSPVLYVP
WMARDGVRIVVQNVSLLNGAVLYVMGGGGLRGAVAAGSDESGPVELSMCDVEALNGALVL
TGTHPAGSVLTVTDSLLVAARSTPLVYLPGLRSSSYAPVLVLSGLRLVRSVLVVSGVALV
TVMTGGRTVAVDGAVLELVGGGVALDAAVLGGEYALYASARVVASGGAVLRVSGSQVYAA
HGLVFDSGVVANASAVVVNDNAGALTDGALLVLRGPASFGSGSWLSVRGNSISGKILSLP
SYPRSADLVQSTLTLYGNAGSGPVVMDGTVALVGAGRRFVVGCLTLNGQTLRPMDYRSAG
IIGEFRPVACGVCDADVRCFAAATRAMSGSCGCRCAEGGYGRDCLPVYLPRVDGCNRTPA
MPPLSHTATLTETRSPAPTWTPTPSLSATRYSPTQYSQTETLQVTETVALPPTRTPTASV
SSTLWWSDVACPTLAVTTTADGGSLTQNDVRGGGSAVPTLLMVALPPPFRWACDPQLGTH
LSFVPVSTAQPSGFGGPWGAMLRNATWVRNATNPSTVLELAVPVHRGYFIAADETIVIRC
DAAAVSGGCKGVLLGSFTIRFDTLPAAASVLSAITGVVACATAVAVVVTGGLGSILEMQA
LGVFARMPCASAQERASTVALPYFLSVFAALDPLWMVVGNALLAAVFGCVHCGVTAAFQR
WRGVDAASAWAAMRFPSLTYVVAHAMHPGIFFGSVLSLAMPGARVQHRVIGVVGVLYGAA
FPAGVCYLIARHTGASFERYWQFSRKPLHERLLYPVGYWHPAAQQRMYGGMLTNMRGSHV
YWCVFQLSVLCVVCLIAAVHSPVGGCHVQYFCMAAVLLAGAGMVAFMNMMRSAFLTAMRT
ASFVLLAALCVVSAANHLAPSDGGARAYAAIVLLLTAVLLAVTVYSVVVWYMEDRHWQEL
REPQRGGLEALLRDDEESDEETPKPHEMASSSYASGTTVASSYQPPAPPSQPMAGDTRSN
AQSPLDRSSSASRMIDYAAM*
>TCRU_6714 hypothetical protein, conserved
MRAFRHLTSRCLLMPYSVSPWVLSGAPAFYWMIGTAEMWRVFAAPSFSTFFARRVRDGFR
LPHCMGCCKAMLCATRLSCECRAVEVFDVFEVPLEGGGGDPPARVITDGFTRPFEFAVPS
LYFHELAADIAEYIQVAAVLHTFKVLSSAPSTSAAERPVPLKDSGGGSVQFVPRLESLPS
FLSARHAHTVTLRSLPSMGGMGDDGIRETVALFVASLSDRSAAVDASALPEGRRHKLSGR
DDLDGSSQGQIMRALLPCLCRWNATICPSCDASCVP*
>TCRU_6715 casein kinase I, isoform 2
MSLEFRVGNRFRLGKKIGAGSFGEIFRGTNIQTGETVAIKLEQAKTRHPQLAFEARFYRI
LNAGGGVVGIPNILFFGVEGEFNVMVMDLLGPSLEDLFSFCDRKLSLKTTLMLAEQMIAR
IEFVHSKSVIHRDMKPDNFLMGTGKKGHHVYVVDFGLAKKYRDPRTHQHIPYKEGKSLTG
TARYCSINTHLGIEQSRRDDLEGIGYILMYFLRGSLPWQGLKAHTKQEKYSRISERKQTT
PVETLCKGFPAEFAAYLNYTRGLRFEDKPDYSYLKRLFRELFIREGYHVDYVFDWTLKRI
HENLKAEGSGQQEQKQQQQQQRERGDVEQA*
>TCRU_6716 SUMO1/Ulp2, putative
MASALLGTAGWVHKTLFSSLRLLGRQQQQQEEEEEEEERVTHEWNELPSPAVRPPAGSVE
VVRAGRTAGGDSRWRRDISSPFVFPVARRSRRRIRSPDSGVCAVRGSRDMTHRFTEIFRR
WSSRSREGRTFVDMEEGTEEEVATVSPSTSWASTTISASASTARLNASRGTAGGSVAGRS
RSRALLVPQKKQKQPISADEMRRRVMSAPLSMWEVPLLEEMGPREQLNSREATGMEHDNL
EGKVLFAPIDPPQETPSVEGAFLSQKDSPGATVASPSFPHTTANRPSTVRERDAHQLALH
IREMRALLPRGYGWREPPVGDASHELNELKFPEGKPPPPSSAYAIKNSVVFDDLSCGLLL
LAVTEDDRRVRVVYEDMMHTVCKGIVEDEIHKYIQLMEGVAERALDYWVIDIVLKDTADA

MKRVFPAWSLSRGIQRHIRERKAVILTALVEDEEDEEVYGRVLHRGGRDSSQANGVAVSF
QSGLSLSYQQIATLGPGQWLNDQVINAYLSMICDERNNTSGKEEAVSLGTHFFARVEQEL
KGDLSKVVQLPSLQKDSGILRWLRRRRNILQPGATRVILIPVNLSQTHWALAVFNWEVHT
WFYYDSYIRGKAAMTRGILVLQQLSHVFLESWRILCDSEGGNACHLADCKLVVAEPLRGN
ERSYDGGFAFAPQQSNLYDCGVFVCHMAWCAVHGVATVFTQEDVTAHRRALLHELLCQKS
LLQFPVSAFLTP*
>TCRU_6717 Calcineurin-like phosphoesterase, putative
MNPTLRKSNGGASADEPSAEGVSLSSHTNGKSHSGGSRHGHGGGGNIRGCRMCHGGGGGG
GMASSATANVPPMQQQQPRLAPSHPQCLSRVFMAGVSEDEGPPTVVAVSDNANPTNTTGR
VDSLMDAAANAHDGQNVVCENEDASHAASIIPMKSSTDADPQRGDGRRRRRQWWWWRQQQ
RRRRRRSQSRMEQRLLVTKCDVGNQGKFYPWPYRSTLYLNPHVRCVESSGFSYNRTFKEL
LLAQDAEPPEADTPCLGPTAAPLCVPQLPELNLATGLESEEDSELNAGCGKEGSTASSPT
ITFTLDGVATPKTFAAIKLQGKDVGNISLPASCLLGGGTDGRQIRSSLRRPPPAIRIKEP
PHQKILRSYVNGCFSFYQTEEAKQEFLELCREILAQARPIFESEPLFPRLVAPTFVFGDI
HGNFEDLAFFLRNVLVFSDLQLTPANILCLGDYVDRGPYSLECLILLLSLKISHPSKVVM
LRGNHEDRVVCGDLLTYGSTSFLAQCEALYGVDEGRKLFKELTALFRHFPLAAELIIPAV
ANNGGNNSNTTSSSNNNNNNNNNHNHHYHNNNTNSPGDLAAASVSRSLAPQGRRRTHEER
VLCTHGGIPRFFSPPKEDDSLAFLRHEDFPRMLTLFPNNPFVRDDPEAQVELLGAVGQTG
VSHASSTTAISEAMLRKAWFVAFDLMWSDPTIHDPGDDDNESSATALSGNGHASINEWGF
GVNKRGSNVLTFSAKALETFLQAHQYSMLFRAHQEKAHGLRLSKSTKVLTIFSSSNYLGH
GNGAGCVLVTADGEIQLVEKLSE*
>TCRU_6718 protein kinase, putative
MLPGLRTLHFVEDVVVDRLRWWRSQHEAMMATTMRSTAHGQRLSSSLSVATEAPRPRAHS
ALPHGFSTHRRERLLTTLPPRDVLALRHPPMLLFLRGEATAEQRDSVQMALREVEGAVWI
ARLLPMERVFYSTQIRPEHRDETSGFSPRRKWPRQRASSSPPLPSSSRDFYRVRNKRRGK
GGPHNCREDGTAELPNNKEGLALHLASPSTHVCRKVSCLQDEYVFNPDADFVGDGAFSRV
FRAVPLFRGNTSVSFFAIKVIPCRRKKGALMASDAKWRGEKKEQVSKEGAAHEVTVHCKM
HGRDVEVSIHGGGGVDYHDALHRELVEIEREISIIRSLRHTGCSQFVEALRTPDEFVIVM
NMGRGCMDARRYLQLNGPPSEARVALIIYQLVRTVKYLQYTYGIIHRDIKLENLLLSQID
ASQDCIRQVLGTGFATRSRETESTMQDEDEEESIETLEYKENKKDVQKPRNRLASVWGSI
SSEQSSENFERLLKVTLIDFGLARRTTKLGEKCRSRGFSEGNVGKSQMNSSCSNRFPRVG
MPTPLPSAANMFMSVDIESGSGASSSDETPSETTSSSANDDEDDDRNVSYGRINVDDDVD
KNEDDGGEEDTEKIHMEVGGDVSKCTTSMTSLLVSTAEPLALADGAGIAMAEGPGESTLT
EFQQKGELETATILNSKEQFITRSCGDPLYRFAPTMPLTAAALQGAGATPSAPFTERGEP
NARAWREEGQDDGEMLLFLTPCGTDKYLPPEMLSWIVSYGWKRKLTTLRMARQLDAYAIG
IVAYVLLSGCFPFNGASRASMAQQQQRCTPKCNSDHWKHISLEAISFVQSLLEPNPELRS
TVAEALKQPWLRRAAKLAEKLSLVPESLEEMPIGGNPSAETCKRQEETPNHLLHLHQQED
ATHPGRRSCDISSAVDSGCNSQRSARHDSLIHQSSTTCAAPPFLASRADHAGTRTAVAAK
NSKEKLHGSSTATAMSDKETGHVAHAFSPPTWSSQVSLSATSPRETAASLLAQISATRKA
LHGDGDAAGGPSNISIGKTEWTEDSEEESDLFQRIFKTVMSEH*
>TCRU_6719 Complex1 LYR-like, putative
MFRRGPCGGAALLLLPQRKPQTEKREPWEYIPTPEHKNLVLLLYRNILKGLMNFKSIRRR
SMIAYCRFAFRRRAMATEKLLIDECIEEARRAVYVLGKHHNFTITRSYEFDNMGIPKDTG
QDVQRYMEEVYDPELSRQQFQHFQDVQPGKEYLHQQRGLGPTGGKHHWKGQTSSTEYKVE
IREEDKVLRPPPPPPME*
>TCRU_6720 Enriched in surface-labeled proteome protein 1
MSSSDTTNWNLSKGTSADGCSDPSVVEWEKDKLMMMTACDDGRRRVYESGDKGDSWTEAL
GTLSRVWASKQKGKVEIVGSGFITAALGDGDDMRNVMLVTLPVYSKEKDKENVEKGVLHL
WLTDNTHIVDIGSVSEKDEDVAASTLLYKSGNNKEKLIALYEKKKGGGETPSPGMVSVRL
TAQLQRVKEVLTTWKEVDGSVSKLCPSSIAEEDGSTENVCRAVKITDGLVGFLSGNFSNG
TWKDEYLGVNVTVTKEEGATEATENPDGVTFRGAWAEWPVGSQGQNQLYHFANYNFTLVA
TVSIDGEPKGDTPIPFMGAKIGDENTVLLGLSYDSGKKRAVLCSGQTTTEHISTWELDTA
HQVAIVLQNGTQGSAYVDGQRVGNAQLALQDIKGSKWITHFYIGGDGSSAGSKEGFSVTV
TNVLLYNRPLTSQEIAELAKKKITNLKAEGQKTSTTRPRLSAVSALDVERTVTQSPPSGP

RQMKQETLKANVGGGGGGVSSAASVTTTPSSDFAQTVVTGSGDTMRGNGSPQNPEVSVSS
AEDVETAEGKDVQGEEGIHSRHGEVNATALNSSLVKLSQGNNSDGGTMRGSGLPSLLLLL
GLWVFAAL*
>TCRU_6721 hypothetical protein, conserved
MSESQSMLEPMEAAAGAGTSTDCLLTGAMPSSTAVICMPSVGEEPGDASGMTAGDDSFPS
VAQTSKGLDLFSTNWATASLRSGSSPSPNMAQFLKLPKNELTKECFAMPEAATQRAGFHG
GIWRRIQSFSPRQGRSRDLNALSVLDLATMDLERLKKSFLAHAQLFSRSDLLEMYKVTRN
VAREMRHAERQAERQQRKKQIHRTSPRRTTDSAKLSATALSDLEEGLGGESVASIAEEST
TNGLLTESVLFRKEYSSKKTRLLCIWLYDRLMEQQLCDFRNSSSSRQCDTLGGHTNLVAR
SFLGSGTKMMMLKLRGPPTPQKLFGFDIFDELSDRLRERDPSSLMLAANMSMDNLPLPLP
VFVYVFSRAVFRACYLDRFPKGSFNFSSSSSVSPLLTAVNNTSQPGTGTADAARKESRTL
AFSAGYSRDDMVQEVSVLLEECRHVVMRFFELFDREQRGFITWSSFTDLLMERVEVQHRL
MVVKENSEADVQSDAKVFDEYVLEPFPSVIRQLGYLGAVTEVRHSHSAIIVEGQHDFAVW
DSFYSGLIWRKLLVRSADVLFSHRQGAPDEWDAERWDAAADSARNLQQQRKFSRRILRHE
EGYNHKDESQLKTMKKSRGTEKRVNAAEDNNLSGGTGDGRIDRRAKPSIESALQLYNVSP
ELPKTYVTLHNDLLLRFFNIEQHIWVIPESITVSCTETITSMEWCPSSPEGDPTMNWYMF
LGTRSGVVFKVDLREILRKLPLLKNVGGDFMTTGVAATSTVCEKLGPYILQRNKIHEEFI
TSLSLTPLGILLSASLDGNVVLSRASNMTSLRSFRLMDDSGVRYACMTPLRNIIVTLSAT
NRLSIWGNTNQVSYLDLYDPISPHYFPIISVKVDESLGQLISVDSSGYAKVWSLRTNVTK
MSFYAVSGAVFSAFRHMYTVENAVQQNGYRLFDVDEKEKKRFRPQGDANAQHGTPAILQT
TLSTVEAAMNAKSFYPARYVAYDSLSKRLFVSGAKNNVVCVFVSGLGALKAHSSPICHVS
VCERNRWVLSASIADCRLWSYEKGALCLGLKANSLEFAMVRMAPVFDDASTKFSTSAELE
AVSGETDCHKLDACKKPLPTVSEVINAVGARAVAQRMERSAKCLSKRMASPDEMRRTAML
SRLDKNVNGGTLSNTIGDTAIGTATTVSTVSGSTGGAGSGSGGGVGGMGFSGGSTTENDL
VKSQGTLYRILCVHIDIQEHFIFYALNNGDIRVHRTNSGQLSKTLVTMPPSTDLILAAVV
QYRHIFTSNRRPTDRGYSNITEGIETASGVAGAQIRVHEIAFILHRLLHHERKIKLQEEE
STSIHKEAIGMMTTRDVKELGVMYADGVIRFFPLIGGSVHAHRIIIPEFLVSRATSYMQL
ERNLQRRMATPSHEFSQASDMEETHKRQLNFIVEADAVSFVAVSETLEFICLVQVNGRIS
IMDMKTQTGAVVQVFTVSGELSAVSFLGAYPCLVVAETQGTVSFFLVKGAAMLNLLEDFY
KSLVLHRRHQRGRNSLLFVDKHPMNDIDKYSNGSTLRMWWFCVPGTPTALHFDPIYGALY
IGTRQGYFSSYLVRNLIVAFDLHPIINVSRAGKSLDPPMTSTRQFHDSNEPRLLNVLLVF
FGITPDRVMRYLETERPSSATLGRELKHTANSTGYSVSWRGADSPLLSSAPRAKPNISSP
ADNVRSDRGAAMARFRKGSLSWIFEACKPLFFPASSNMSARQFPETANLPFDILTVTLSE
LLVGAAILRHALLIMSMMSDFSSMRKPSMANAGESFTSFASSACHHYAAVSLTLSDIRHI
RQCIVEEIRYRNGSVGTGTERQDSPTSDGLPGGFCEVEEEFDFDMVRDNSYVIPGTIADN
WVEFLFRRHVVHSVNDSPLTLLSPSATLERARCERYERCKLLQLQYDLEREAQKEFVGTS
WMNTTTPGQATAITVDWNAFMEGTGTHLLEEAFRRRRGEGAGEEDFLNPLDDFGGVRCIK
TRRNGLLFVGSANGSVAVWTTYGGARIQELCPSMLLKESLRCLGGKLKMRLAQEVSRVRR
RRQREAYATSSHNAKDHDTMLRNLNVKYKAAMMRNEMVREGILGNSITEFGGSSNETMSS
LSTNERQQKIQRTFPKKTSSVQLTTDIERTRSRLVKEKEVLLALLNTTPSEASERGILME
DLYFLPMHTTMLSELEEFDLVAYDLAVDIAVRRLEQELCPGAFADDAGNVSMAGSRHGSV
SDTHPTGLGDEANFNTMQMGSAQWGGSFFGGEFGGESMQEDLHSFLIAAHEKLQSAFYAE
ELSYMRWKAAASYSNLPKLGTRRRRMNGGGSLTCMEWQRSIFNQYTADLSQTSSMSWNLP
HERNLPSYARPGRCLGPGVITVGLSTRQERRLKGCFGLELERMAKESRWHTADEAIESIS
GQIKGLLPVESLAGLSRSLAQRPSRNTRVNCPVETFPTGKKEKKWEAQQQKTTRAVLEPV
LLLVTSRENDSSRDSNSNDYSRRQSGDLRSPAEVSLVLSGVDKKRRPDEESGGTKERYFF
FLTEENAGLSSVEGSSLTPPAVLSPAGSGFRQAFRPAPRRTSTSIFSARTEDDDSSDAAP
GVLMQWQLHKKDHSHRAKLSRTGRVAATQSGCQPIVKLGKKSFFASRDGADLHVGTSQGA
SCSRSPIGVRLDLSDPLMFPISFQGGSSQTKVGLGPHSDRAQTPESFLLPLLSSGGGRDS
PATQRAESPLSQRRQKNGVANKRKSRRG*
>TCRU_6722 hypothetical protein
MYVASEKVSWFDPALLTSEHVASDIDDSLEIKEVVMEVTRRRFEEQTLADCAQNSRSVHA
AVRAFYCDAEKKGVAAAIPSIGYRMERPACPIDHNVEPFAHVVVAGGIYAVVTEQVPQHL
YFFDQEKDIAISRLKLASDAKMSDESPAAVKFFIDEKDAVSALFLDPRGNFCVVRWRSGK

AAYYHIPHRRCHRSHHTEGWPTEGMEAGGDEERSEEDMTPRRFPLQFSSNVTGMLQPFYL
ECVAWDPNNKSDTTTGDIILGSSSGGVLLACRLETHGIFEARKLYQFPQPYSTHPIDSVA
YMVDSQSPEHTRHHVVFIAQNSRLFVFSSLWGQGGRLEAAFDTNLMNCKNVVPRSNSATL
YPGLSLSCAGLSGGSLMNYISINKEASTKTMTTTANITTATTTNAATPSPVLSSSSIGCR
HRALSSTVAHVDTKVTHASPDASMPRLFSQVAILDPRELIPTKSSSLRVPTAEGGGEANK
DHDAKRNSVPGGDADKLPHVFFWQYGDTLTHGVIMLTDPVSTLTEEASLAALSPSLLQKN
KGFGSSALRPTGLPPPPNARLPLNLWQSLLPIGILSVVDLGRLLREFSALLQPQKGGATQ
RPPMFRFMSARREKNLTTENLPPRPLGVGDIERLLLIRHGVQYGCGGRFILPRLPASRLA
AGELILPKAVEIRTREKEPQSAESLVSFAMGYGHLLLTTTRAVYAFCHLAALPLPQESFQ
WKNSLVFTRGLATPTVGNTAAGACENHAMMAFCSHDSGRSQVFHLFATSYIVELRLRRRR
RAQYVAQLMDAVNSINVVAMNKITSENTETEGTQGGEARTMELNSQQMTLPQYVSWRPRV
PLQPVSLRTPPGPESPLSPMSVIPSRSSESLSSFFTTSYKLPLGCTNDELQFEEWIRNHK
DKVVNIPHMGTLGGHVEAGLRTMLNYDTDFLYGMALRIAACSSLERERCDLLPRVRHVYA
KRLFRQGRFLEAAAQHGLAMEGPPYLNTLLLEFSRVATDDMEPLILFLILRLRGYEGQKS
NGETCSLELTCLTTWLVSLLLERCNQIRKERQGNGECSGLPASVTVSVANPAIVTSSMGA
EKVVGENRRSLEMTAYLRRKYNLNNPRQLLDQIFVRYGAFVQWKAICAAVFGIASAELAI
LICERLGHHGEVLSRLFLQQERQLDGLVCLERNGTGVCASALTKTTTSATTLLKEDQLNQ
LNQSLKTYWLKYASILMRFCPCRFVRRGIIPFGSDLGLNPMQLFPALLLYDPRRNERTFE
VDGAIEVVLQRHMIEESLLEEERARATYHAAQLYLEHVIYTEGYTNECLLNLLMYFTARD
GDDAALTRFFTELCANQMSHRLEVSYAYRVCLRFGRHVGCAWTCFITGRYEEAIQLAMKI
RNEELAIHFIRSIRGNNEKEIRHMLWNRLATATAKNGGGGSRRALQLIAESEGDLNVSDV
LPHLSGDVMMQEFREELLASVSIFSNTLVSIKQAIEVSLKDVEAIKRDMENIQRRPLKLP
STQRCAVCGKAALTRPFVAFNGCRHVYHKRCFDACRAKMEEQLRSLKDLSTSLPVHTEEE
IECMPLANVELECVFCSRRYLRLFLTVPLSNNITSSSLRLP*
>TCRU_6723 hypothetical protein, conserved
MAMMAGRVLLVCALCVLWCGAGFVSSAGVDGDGRGVDSGGLPESAERAVLLASSPESRVE
SKAVSNPLKEHVEEAPTPAKESSEDEEAGEDEVTLQGEERQQQQEENAL*
>TCRU_6724 hypothetical protein, conserved
MEEGRGFCAFDVTTWPSRVWNEGASGVVIDLRCVYQCWQQESEQVKLAFDNLLEWIGVLE
VLQVPPDRIMNMGRSLLNTFRMQLTIASDPGIRLSKLRARLYTAVHQTDAYAGAAQPLVD
RRETQRTLRCQRCHTYGHEASTCDVRPRGNYLQYRRPSKNGRGAAARRS*
>TCRU_6725 hypothetical protein, conserved
MGAARELGHQQGLITAERERLNFDYANAVADVQNWNAQLNSQVEEAHINLSVRESTIAGA
GNQVLELRQQLEVTRTQLQEREARVSAKEA*
>TCRU_6726 hypothetical protein, conserved
MEEDRSFCAFDVTTWPSRVWNEGASGVIIDLRCAYQCWQQDNEQVKLAFDNLVEWISALE
VLQDPTDRFMNLGRSLLNTFRMQLTIASDPGIRLSKLRARLHTAVHQTDAYARAAQLFVD
RQETQRTVRCQRCHIFGHEASTCNVRPRGNYSQYRRPSKNGRGAAARRS*
>TCRU_6727 Enriched in surface-labeled proteome protein 1
MAHDGTAVTPEVGGHSAASGEKVGETDGQKGEDLHARDGEVKAAALSSSLGNVSQGNNSD
AGTVRGSGLLPLLLLLGLWGFSGSVRSDWLPRGTLATSLHRHTR*
>TCRU_6728 MRB1-associated protein
MLRVRHYILGTPAVALRQRFGALLFGLRRQATSAPSGDFSHVTHNTVWGLWNEGNLFSLS
VPELAFFLQEHCNVANVDPRAKKSALVRQVEEILSAEQANMTVQQEDNPHAVVVTDYDKA
EEGLDEADEYGDWGAEPGFEDRRELDFMELSPGRMGERYEALTPRAYQLMHSEISSDVGI
ACIDPSKLPGHSKVKSCLTPVDVKPNDANKMHFRNAFEWCLMNIWNMNMPGELNIGAGKV
LYYRQVAKQNRNVMPLWTLQKHLYAQHPYAWFAIASESNVAAMEGLAAKLGMTLVQEPTT
SYKVNIRRMNEFFDCELNGQLKCTMLNKPWDRFLVSHYVRSKMPDLRYIVRARHPIKKRV
SDAYLEADILRSTRESVQSVLSPELGDVVYCCERVIRKWAMRTATGATLQLVETKRTPLI
ITRAGDEGERLEYEWIVPLPQQAERIDVASLTDELWEYGNKLAEALEEGMEELMAHTMSA
VSAY*
>TCRU_6729 heterogeneous nuclear ribonucleoprotein H/F, putative
MERPPQQQQQEQQQEEQQYGTEELGAMNPDSIADAYQGEPQTGEEDIPVMIETRVVRLHG
LPYSVSEETIRAFFAEFELDEKDPILHFTEGLHRGTGFVRLKRPEDVEESIKKLHRQHID

ANRYVELTASTEEERQRILEQQEQGCKTHVLRLRGLPFTSTEEDLREFVRSVPGVTRVDI
CRDMEGRNTGDAFIQLATEEDVEEAKQLHNKTMGSRYIEVLPSTMYDRDAIMRAASLRAR
RDRRGTRAGDSPLVGPRNHGNGVSPGAMQMLAPNFFDPFIAAACMGYMPHVSFGNELSQN
PYERSGMPQGAPYGVPGGPQPLFPMFPGHAPMVAPRAPSPHVVRIRGVPYAATEESIAEF
FAGVKIPPQGVHMVYNEQNRPTGEAFVELENDSDLVAALERNGGAMGNRYIEVFQSSVAA
MQRLGSPLTGMMNMMQYSMPGLGVVPQPHC*
>TCRU_6730 beta-ketoacyl synthase family protein, putative
MPMPFGEFPPFIRRRVVVTGLGAVTPLGLDVASTWAALCQGRSATRPLKEVPFFFPACID
SDRRLTPAARQKSHEQLLAKMPCQVAAPVLAPSGRPNFTPTLRETRATLFAYYAAEEALT
HARLLEFPAKRILASFAKERIGVNIGVGMPSLADVGDVSYSLYADPENVNYNRVNPLFVP
KILGNMVTGLTAMKYGIMGPVGSSVAACATGAHCIGEAAEWIRGGRADIVVCGGTEACIT
PVSIAGFSRMRALCTKYNDMPQEASRPFDKDRGGFVMGEGSGIIVLEHLEHAMQRGAQIF
AEIRGFGISSDAHDLAAPHPEGRGAQLCLRSALEDGGNISIDDVAYVNAHATGTIGDDME
LHALEKVLGGDGTSSHRRPVYVSSVKGGLGHLLGAAGSVEAIVAIMSLYHQQAPPNINLH
APSAEGLERLQLVRGNAPLPFQGDAVISTSFGFGGVNTALLLTRVEKA*
>TCRU_protein (LYR family), putative Complex.1
MLRVGICHFSRQEPQVIGTSVPSFRHFPYRAQDVLHLYRDFLRLIHQHPPQERADLLFRL
HNEFYRRRHLTSPKMITGAIKRGEGILNVQRSMLESKTLRARGVSSREQGAQNVDGLWDQ
LQMLSGHVLPGLRNFRPSRNVLKGSYTQQATTQAVYSRRRL*
>TCRU_6732 minichromosome maintenance (MCM) complex subunit, putative
MLGNRSLTEEQTLIRRHFIDFFESERYEEKYHDRIHEMMSAARSRLLLDMGDLLDFVPAS
AGLDGSGTAAGAVPASLGVGIVREPGKFVPLLELALHDVVLRQQPEYLKVDYRSRAVHVG
FEGPVGTVLSPRELYARHLNTMVALEGIITRQSSNRPRVLESVHYCPETNKFTRKEFRDQ
FTPMIDSTHLPTVNVMPKMDMEGHLLRTELGLSTFMDSQCAILQEAPERAPTGQLPRTVE
LRFDDDLVDVVKPGDRVMLVGVYMAYTTADSKSFQSIVLVNHVVSVQAFTMYRRVMAVEE
KLLSFAKKCTQTDGPAGVLETLSKAVAPTIYGMTNEKKAVLLLMVGGVERQAHQSRVRGD
INVLLVGEPSTAKSQLLRFVIGVAPLALSTTGKGSSGVGLTAAVSVDSYTGERSLSAGAM
VLADRGILCIDEFDKMSPQDRVAMHEAMEQQTVTIAKAGIHASLNARCSVLAAANPIYGF
YSVHHRLAFNVGLPESLLSRFDLTFIVLDKHSSEYNRRIGRHILRNHMTAAPVGIDQSVT
KTVVDSVDSVWAQSAKNGGGGSGGMDLRMTTTSTGEPIVGVDFLRAYVQLAKEGRPLLTE
TSQQLVSQHYVQLRAEQQEGSKDGFYVTARTLEAIVRLSTAHAKLRLSSTVDEEDVKNAM
ELLRASVHAASTASLQRREDNQAAAVESRPGQKRPADMIRDGANGRTPEETKDGATPSAM
MEEDITTQLLEKRVTEAIRAMQREQRPSVRLAELHEKIGGGVSLENLRQMVFQLQDENFV
FEGSANDGWIQFI*
>TCRU_6733 chaperone protein DNAj, putative
MSTSTTHVQKETILSLNYYEIFSLDPSARDVDFGSVHRAYRRFALLFHPDKDPSPAARAA
FERVKLAAETLTDPQMRREYDEELLQKLQRSTGTGATSAWQRQQRDVMEEEALAADMILR
QKEAATAAKAAAKREEELEKEAAAKQMLHELTNALTTPFKRMEEELVHEWEIDEDLLSMK
EKEVESLLQKLREYNEGQGRHGRSVDAHACGTKRRRSEEETASKV*
>TCRU_6734 hypothetical protein, conserved
MVCVRCRCWAAAICDCAVAVRGVAAVSLFLLPLCVDGELVCAEGCRQVTGVMAMMMAGRV
LLVCALCVLWCGAWLCDAAETSSSALHRDNAEETMTPEEVTEAIEKLAEGVLYMIRESCR
MSFLTSKNATLPAHNDTEVEKCVNKTAVDISGVTPRGRPRPVTTDATFASPLPSSSSATS
ALQGQAQGSPGAAPEPVKPPQTDPVNSEQLSETPASTGGGAGGGGELADRSSRTPTDDAK
THEARPARNATSTPTATQGYSEKSPANTTRTRETNETDDTDGSTAVSHTTSPLLLLLVAC
AAAAAVVAA*
>TCRU_6735 hypothetical protein, conserved
MDNNLELFHALLYSDGALHILQDGIMKASNTISLVPPTEGLQMINYVLKSWAQLDSSFSG
SFTPTAGLVGFIFNASSDGDTWIDDYLCVNARVKNAMKVKNGFQFTGLGPGQYGS*
>TCRU_6736 retrotransposon hot spot protein, RHS3, putative
MTLIGLRVTTAGGHHITASTVRQFTECLAAYFNGWEELSRDMSWEIIYVQHADSTPMDGW
ERRGVVNLDSVSDDESREIAGLWREEMHQYQVSISSGGFGGDAALRGEE*
>TCRU_6737 retrotransposon hot spot protein, RHS3, putative

MGDASKSRADHRELPDEMDVKAMCAWMERDGTTDGQAECWKMVEERMDKVGPIPRHIFDA
SKFIAHSAAIEDALDGIKSRDGEKHFKHRGVRLWYSGDPPQKVVSVFRARGEFGAGGFLN
APISVCLGRRIAHYFGGRDE*
>TCRU_of Trypanosoma cruzi region 5/Dispersed gene family protein.1
Dispersed gene family protein.1
MRFPSLTYVVAHAMHLGIFFGSVLALAMPGARVQHSVVGVVGVLYGAAFPAGVCYFIARH
VGASFTKYWQFSRKPLHERLLYPVGYWYPAAQQRMYGGMLTNMNGSHVYWCVFQLSVLCV
VGLIAAVHPPVGGCHVQYFCMAAVLLAGAGVVAFTNMMRSAFLTVMHTAGFALLALLCLV
SAANHLAPSDGGARAYAAIVLLLTTVLLAVAVYGVVVWYAEDRHWQELREPRRGGLEALL
RDDEESGDETQKPHDVTSSSYASGTTVASSYRPPAPPRPVAGDIRSDALSLFDRAPGASC
SINYVPLDR*
>TCRU_6739 hypothetical protein
MSFCVRPPPAVVVVTASVGHATSLHHSVPLTDAVGVRVGDSSTVSFTCRVSVGPYCVLPR
LGVHVEVHVGVGLRVSVSVAVWLSSGMPDVRLHPSTRGSCTGRQSRPYPPSPQRQPHDPD
IALVEAAKQLTSASHTLHATGWNSPMMPADLYSIGCSACPFSVRHPTTNLRPVPPSATVP
SITTGPLPAFP*
>TCRU_6740 hypothetical protein, conserved
MWSAVGACLRSCHCVRCRAIAAVRVTLLALLALAAAAAFMPAVHAVVLRLRGGTVDRAIT
VGRAVDTVLMDGVYITNGVAVVFDVAAMLPGALRIELRNCVCDGGAQIYVRGYSGEPASD
RSLEVSVSGLSGGYCSLVFVHNLPAHTNVTVRDSTIVTPGPMRYSQLSGLTDAVASPLVL
HATSLLRTQLRVSNTVLRSLHAGGSAVYVGGGVDLLSSAVVLDGVLLEASGGPTASAMRV
ASSSRLSLRGHSVFSVTNVSVVSSGGGFVLGERLAVSDSVLRFLRVEGSVASSLVRCDGG
TVGAGGWLELRDVWAVGEASSVASLSGVTLDGGAVSIARCVATGATLVSGLTITSGAVSV
QCNRAGGRVLQSSGDYRMAGLPSVSVVPCDGCAAALACFDALTASFSDCVCGCRAGGVGE
ACLPFDVPPARFGGGAQGCVSGVTLTESVTVGGVRATACFDSVVFSGPITVAVDLRSMDA
FADSLNVTLRHCVLAGGAQLRIGGFSESTARLMPHALVNMTNVTSLEGTIVLHGAMPLHS
SVLLANSTLRATVGGSQYVPMTPGHAGSRYGPALVLDGVRLLSTRLS*
>TCRU_6741 hypothetical protein, conserved
MTLVPYTPSEWCDIGARLWEMVSQCGETQVQMTFINGNQMSDETLIVAPSATGLCLFHGP
VSKAWQDSTLIGHIANLRAPQIPNFETHVFLPAMGAARELGHQQGLITAERERLNFDYAN
AVADVQNRNAQLNSEFQEAQINLSVRESTIAGAGNLVLELRQQLEADRAQLREREFNLGV
LTGQFQEREARLNALQTARDAETAGRGKAPAT*
>TCRU_6742 peptidase M20/M25/M40, putative
MSVDWNAVSQTISAEWDETVLPALSAYIEVPNQSPHFDAEWATNGLMGKAMDVIVEWVKN
QPIKGLKYEVLEEKGRTPFLIVEVDGTEPTANTLLLYGHMDKQPPLPPWDEGLHPQKAVY
RDGKLYGRGAADDGYAIFSTLTALAAVQKHGLPHGHIVVIIEAGEESGSEDLPYYIDRLS
DRIGNVDLLICLDSGAMTYDKLWLTTALRGVACGILTVQTMSESMHSGISGGVVPDPFRI
ARILLNRVEDQTTGEVKVPEAHCAIPEAVVKNMEIMNEVNFMEHFALLPGVSPASGDNVE
LALRNSWKPALTVTGADLPDPATAGNVIRAKSTLRISLRLPPSANADDAANSLKKMLEAD
PPYGAKVHFEPDSVGYGFSTPELEPWLAKALNEGSTTVFGKPFASQGLGGSIPFIAMLLK
RFPKAQFVVTGTLGPKSNAHGPNEFLHVPFTKGLTTCVARVMADHFHATPKLKT*
>TCRU_6743 hypothetical protein, conserved
MSPRSPTVQAAMAAVSRRIRVPRATSRLSATTTASTPCTSLFVSSILSDLHTELTSSSSS
SASQGFSKDATDLSCTLRSLLQMTRALASPAAITHEMKRTDTILGKNKKASDSRVGDALP
LYNPTLDPTILQRVAVAIDIDGAIERAREFVRAIRDGGNFCRILSGLRELQSRPTMQELE
LQAGIAARLHHGRNGERVPRLRGFRMYTSDMQVAEVLPSGKIVTFISPTLPDAVDTCHYK
SAGPEQRYLHFVLYKEGLSLSKAFRLLSEACEGMCLPEHFSANVALEESAVTVQVCSLCL
LLADSTSYETHQASVVKKLLRVNLRPLQINIQLLGWRFFPCDPVNSSRCQMQYSMLLRGI
TTPTTTGQTQLEKRVLGWLAVFPNFFGPCHFGMRSPSSLFRSYHAAAAWEKDMPAEALLI
AACLSDDARTMAGDDWVSEMVRLFQSGEDRPAVLKEWYHLHVPCGLRAQIERSKSALLWN
VLASCRIHELGGGAVEGSPEAGEFVLHNGDGILPANVVAKPELFPDASLLGLTRGGDGLH
GAHFVLTREEAASYTLRDVVIPLNVEGNEVISHASRLLGFAPSSRGHNRLSCHPVYFRPL
FSAGSGHPRTTLPWVKVLPELSELIGENGDGFYKLLTDMELRQRASYTATSRGQPRTLWP
IGKYGFRLAERLPAGAVALAASDTARQKGTKSLALHFTLPAHTYSMASFREFMTIEEHTT

LSHTTIENHRSVERKGRADAKKKNAFVVGVTSSDGEVVDGDILGKMGRKQA*
>TCRU_6744 3-ketoacyl-CoA reductase, putative
MNIIFGALWWVLSTVSLLVGLFSMVTYLVAAAAQQLAMRIPQDLKKKYDAEWAVVTGASS
GIGKAITEKLAQQEINVVLVALEDPGLHSTFAELQKKYPKRSFRKLAVDLGGEGMRYMAP
IIEATQDLDVGLLFNNAGYLHTGLFTDTEVDRLRANLECNAGCAIPITHHFLRKMLERQR
RGLVAFTSSSAGYLPGPTATLYSPSKAFLTNFAATIAAEVRHAGIHVVVIHPSPVNTNFF
KYKGPKLSTIEATRRLVAPPSYIADQLFASAGRLTVWDQGMTSAAFRLLNKIIDFQFLTE
FIVRIASLCGDQKRLVEASKTHRGKRA*
>TCRU_6745 hypothetical protein, conserved
MTVEQLEQRVTCLSWNNEGTNLAVGLTHGFIIYSTELLLSEEGWLSEVIRRPVLGGVSIV
ALHGQGNLVVLVGWDSAHRDTVTILDLSADDTVNEDLSVLARVKLSSVVYAVCFHPRMLL
VGIQTGLIYLFDHALQMIESFQASTPASTSRQKGDTLALGTMLVEKMACGICYSQLYGVI
LGPTTGTVRCICYASERHVQSSLLQEPFSDLGKKLTPQLTVNVVEVHRNEVGCITITPDG
VRALTVSERGTSVKLLDVENHVVICQFSRGTTPNAVHALGLLVSSTETIAACISGAGTFH
LFHIRTADTLDARAVGVANTDPWVSGHSFMRAWTDYRNSVCPKTRLVIPEDELYDTLCRE
EDCGKSIYSMVLRHAAKKDSCVALVVQRCMSPQGITRKARLLSVQVELSAKDSMKILRSF
YFPRDEL*
>TCRU_6746 hypothetical protein, conserved
MQGNIFARLFERVASVPHRNITFVPYGEWFGLYVQALKGAQKSAVTSGGKEELRLARRAL
DVALLSSVFSQKWTDVMLPNGSSSTTTTAWCQESTEAGWLLPSSTIHRRELLMTSFLVEP
LLAGRAIASWTAAVRKGDAFPATAGEGAAAHGEAPAPTGMVVIPFTALFQLRWEAYLCHS
TFSAGGEGKKIPQNSFSLQERSARLTALQSLHHLMELQSDSKRKSRVQFVVWSPVNEFDA
VMRVSQVRAGLPEALRSLFSLTHVCEQELVRVAYLAHYLNFATKRTPLTVLAPQMQTAKL
HLLGLKNCCAKSQLRFVEEGEQHRTCGDPNGVSLHQQAVSRCGRLARRMSTREENLRNIL
IP*
>TCRU_6747 ribulose-5-phosphate 3-epimerase, putative
MFDHQDRGTWLSADRPDTLRPIIAPSILASDFARLLDECKDVLSVEGGASEWLHVDVMDG
HFVPNISIGMCVVEALRKHLQHTFLDVHCMVSHPDRWVDEMAKAGASQMTFHVEAAECPK
AVARHIRAAGMQCGVALKPKTPASAVTELIEEKLVDMVLVMTVEPGFGGQSFMHDMMPKV
AELRRAYPHLNIQVDGGLGEKTIDAAAEAGANIIVAGTSIFKAAVRRQVTETMRNAVKKS
LTPK*
>TCRU_6748 hypothetical protein, conserved
MAALVVVQRFRECQNLLDTIVANLSAISNLTSQRIVVEEAIRRTGCSAASATANDNALRC
CTDPLGMLLAFPESAVELIIAQHTEDVSALLRSLGKLQQMWCSKLQQAKEASQQRQQQGA
SMTKAAASALFQVGGRECKEKSTQSPQVMLGMHALLAVLARMHGWLQELILALRADLANP
PRAVQLSQCLTRYFSQMEGAGCCTAILALETALEQLPERVQREWEVCKARHMVDEAWILL
AS*
>TCRU_6749 RAB-interacting protein, putative
MMPNVPPQRSNMAFVDGTADAVEVGVNVPVGTAVPSSLIGKLQYYYTYAVNGGRRQLAMV
RPWKEFFDRECFLPPSGLSESLSRLNRNINHYYHNYMIMAMLCSSYVLLLNPAFSLCVAL
TLAMWWFVGTKRVEALETNSNHFIVLNRKITFSQAYLFIAIFAGISFFITNGSSVVFWLV
LSSVGVVVVHAVLRKPQIEEQPFSFV*
>TCRU_6750 hypothetical protein, conserved
MSKSRPRKHRCVAQMEDGLTASQRLQQWGAAAELLYAPNSPINQPPSPKEPHTFLVARRI
ATVMARLNDLCQKESEVLLTPRDALLELADIVRFALVSFHKEVVTGQLDRAQVASVLAEY
VAHRTAPQAGMVEGLHVIAWVSIKLRVELFLEQLRRRLNMELESSHNNQRTAQQVGALRT
TLTLLNDFESFYDNILVTFPCVQLMDTTPDAAEQMMPILSRQYYQLADWVVLVEVSTTQP
PITETWVQSVDREASTVVLRRTDIASPWGLIFNQCGQIVDIDTSLRSVSEEGEELHRLLC
CTTEGAKIVAVNSTTIPDISSVGAEEVLEIFKNATKSNKRIAIQLANGALKQPSVQQLAF
LLPNQGGEGSSGQRATLVLHRPDRSMPWGCELTEELIVSGLPKRCTSVRARNFLADYRGR
VALMAVNGVEVTTVAQAEALCAHTETIVMNFVVVAPSMAERSKGSLSEKVSLALTQDQIE
KVREKPLLGEKSAKQSGERKKKTKSQQQRKQHENAEDLDAKADDVYTADANEAEELTAEP
EKHAEEDDVKETYPMVADDEATPDDTSGMGGKLREGSKEAERLPAAGETPEPLVLPNNVT
IELLTPEEMVIRRDSNEVKWGLSLESSGEGAERIMRIRALPDLPSKRDARRKHPFYKNFM

KPPVKTEWRVQSVNGVPSLRAAEIFDIMRRALRMRIQFFKGR*
>TCRU_6751 RAB-interacting protein, putative
MEKDNTGGVGGPVDTPHGRDSSGSSSEPRSFASSSTADFSARGRLPGSPTATFASTEEQE
PEQGHQPQSAVDLSSLRDVLQQVWRIRKELQKEELPWIRDFFDREQFCFPKNFGEVASRL
NLNIPFFAANYAVIFYTVTLPFLIFYDPLFFVLLCVSALLVHSIQLSRKKRSRYGTTMRI
GGISVHYQRLADIYFIALLLLFVFGNGLRTVGLVLLINTVLIIPHALLRRPTYFDDEELE
KMRPKVVQYIITLVLLLLAYLECKGSGGGFKGHHRKKGGKKKKPN*
>TCRU_6752 hypothetical protein, conserved
MRDVLMKFLEASAASGAWESALAVWRTTAVEDVAVSGSHTLLLTRMLVQAGKWREAKHVV
MSDAASVCPQRLSARLLAMLAAMTDANGWSEACQLLQDGQICLEKHGSEQRSTLQSEVVR
LAESFERCVVPHIPASQQEPWVRLACEMRRDDLQNRQRPSLEETRGGDTAADAAALTNNE
ELLHIYRSPKSRSSWTRALQTLLSMHHPNAASVNITLGILSRQGRQREAVDVITKFMVSR
EIHPTAVTVKTITEAANTMRSGKLCHLILSTPALRDQITSSSAVPLVRTLQRIGDWRSCL
SWWDSLLPTTESSVPPSNHGGKAELRRNLRLSSYVAVCVAQGGRWSEALAAMRDASAHDP
SLAVLFALRALRVAGAWKAALSVFHCKKHVWENSSVDLQVREVMTRQNAESWVPLDKLQT
LRSLYGA*
>TCRU_6753 hypothetical protein, conserved
MLPFCNQTELMFRASGGIPGMLGSYSGCPDENGVQYCVLFPTRFRWGNSRLLGYCLPSTC
TLLDIARQVVLDPMLNGTFNYSELMHGDGMNTSQVMDRLEQYINCAPRSSSFLELHVHNI
VSWAIMGFIILLVVLATLYDYYWSITARSIPFEVVMMGADGAVVRVLQPPNVVLLENQSK
TNESSPRRHGADLRCTTENKLTEKQKGSFSASVTAITQPLLVAVEQSEADEAGKQIEPAH
SPRMGEREDESATSPRKKTHFGSFVRYKEARTGEEVVSVKKGTRSGERDSLRGAGILPEF
NTELLWSHRRVQKFLAEIPDVPNFRSFLNRTVLCLSLINSFRKWRYYPKSEVNLNLFNSW
RVIAWMWIMMFSSFWYSQQIPTMNNIGSPPVNFIYAFLGKEAFSAFAVGTFLTIAGFLAL
HRLHVSEELLMSSPTARVRASKRTCRQVLAECMLWYAKYLIARFVRVIPISFAIFMLLPN
AVSGFGNGPFWRLFSQSPAFYGNCMKYWWTNLLLVNNILPVEENERCFPWSYYVALEFQL
VALAPMIYFLGKHLHHRLFFSLLALAMAGSAVLRYFEISRRKSVLLGTGAVSHHALSVGS
VYQHPHLMFIPFCVGAMLYYLYKALRQRAEMLRMFGPGILLMMHRIQEEAVAEDRVSYWL
LERLQMRHMRVLIVWSGLAITFSCVISVWFIHRDDEIGGNMGVDVKVYESLILFPWSIAL
CLLALPLLFGYGGIIRGVLTHRLWCGPSRLVLVAYLAAPVVIGFGNASSYDVITMSFSLF
IVQGFGYMGLTLLVAFFFHMLVERPCLHISSRGEY*
>TCRU_6754 Ubiquitin family, putative
MNAAAAEEEHPPLKIEFDSNVELTIHGAFLPTARLLQCDPVAHVSVSTLRKTISVRGASC
VSVGGKAVATNTVATEHHVASTRRQYFTSKPAFNEMVRFVVPGTRVHLPVERLSRVGVQK
QPGVSTDDMDGEQSVEQRVLITLEDAHGGAYGQAVCPFFLHAPSSSTQPVRIMLQPRNAH
DKFDLLFKKDVATLAEHGVDDFGFVTISWKISLSPHGGALITASPTSVDQPTFPVGLVLR
ATWLVPGHTYQRGTQYTTSVEFGSQDRFVFDGANPLFLTIQNATQLERAIFHCTIQNVMN
HANSHDVVTALPIQPMASFAMERDVWWTTAVRAASGTDLGLLIASIRLVRRPLGGETPMC
TEERCSLINDPAHQAQYAHVARDWGRPPPDVPSGAYQPIFWESDQHIARANERRWRRDRI
VEANPSMEHVRHLLDVIMGRATLDPGVARVVSVFFNQKSSGFSPQELMQFLITCAFHVKG
MTPLEAARFCFFALRRDMEHAIARDDVIFMLEHSLIEHTIEMPEMELRRRVVEIFGDTTY
VIFDDFVRYFIHNYAMWYAFGVPVTVSGERSGRGGDVAPQLNPTLTLLKADGEPNAKARA
PTAATTVSISGAAPVSASTSTTAATPAAAITTATTQKTVPHDESVWRTFIARVQHSNKAF
SVTAHVNDTIFDVMVMVQNSTGIRAACQEWRAGNVALDPKCRLGSTELGLGGNEVAAPEV
IIIARDEAVRLVMVYKEKGFRWEVRLPSSERVLKLRALVQHKTMIPLTRCVLRAHGSCLM
DRHPLAHYNLQDGDVVTITQE*
>TCRU_6755 hypothetical protein, conserved
MNFRTLTRFWRKGGKKGAGDGAHGNSSSVHSVSSQQQQQQQQGQRAIGPFENKQAALHYI
FQILESFERNGLALSPFNLEQDPACSRATCAATAASSLSLHSNRTCNPVKENMHALRQER
EELVAALDLCLLAIPEEVAGTNGNCDKKGDAENVQATAVDCPNGQAADGEAPEPSPELPD
ARHSTRIITQEEWRWLLCRLVNLLIETDHAIYTDAMMRSRMPYSFITPFQSPPSSPGKAP
SIPHGVSRSPTIDGRESPTILALQQAAPSKRATPLPSSKSVGEASNDARFNDFRKAEERM
GFVNSLITWTIMRCILSQQLGQERPFGISTSEFPPPQTTRQTTYGVPVQWEEVIEELTNF
LGGTQRKAAEVAIALWILRDATGHELVQCILQKPQCSFGSVMEGKPHGSLDAASTNKSPQ

GPSLFQYTVLLMESSDNTVSMDDILEEVEKVYEQNVLRTWAAYLEEQSSTSMFPKAEHQD
LSSPPLDLFHCHTMATYAVCSPYWSEEKRQQFFRLIQKTWDEMNELALGTETGKEVHAVA
TGVFGSQCTSVDAYGGNASAFSATGAAADAGDALLEEQRMVTHMSHCTPEKPTTGIDDEI
RSFRSLSAQSINGGMSQTGLSIAEAQHAMFDDDFLLFMTQILSAVVLHLRVEQCLSTSPP
RLEEAECFVNSEDELSITSCFFSCRQGARESLVKLRIATGNYPEALKSANAHFFNAKKKW
SFGSNGRSCGLNYLASMMLLVQAQEVSRMDTSIVETVQLALQQADLCEQAFVDSYPATGT
YLVRYAAVRHGVYSARLFHLRAIWRAYYRMYDSINTSKYFNQYLEFVRHCRRSRRNEEMY
AALKERGEQLEVEKEYGSAVLVFKQAVEYAKVTSQAAAAEAEAAATRKTKDLAMGSDVSV
TENADLEILILKERELKLFRCEAESERNLALAYVLQAEHEVNVRCRRQQLSNAVNSAYAA
QNVLQRCILKAKPPSSGTMFDVTSSLVVAAKALLRLGQPKKAALLLEPLIEDKVNSASVR
PPLWSDALPDPTRPIPARELEERVQTLQLKFNVYEVHTQCLSKFDGARASRETARAREFL
DQVKNWASALLSNDQNSGNSSEGESQSMLFANRRLLTDISQKANALRPIITITCGDAWSM
LGNWENALQEYSNALAMYADREGESNSNDISSTRSSFMDAGKERERNNRGLGESVVFSKL
AEVYSALNKPKTAIHYNHQVLECASEVGDALLLYNARIRLARLYTATGDTWEAEEQWAKV
SELAKEYEDQEISRETTRNIIAAQRAKGIYMDVLITAKELDTLASAAEGVDAAADKRFAL
EALADAHLQLGQYKECINALDELEKVQYKCSEWKGTLFRMRARALLGDGEVQEAIKVLMI
WESEARQLRNWVEVGHANAVLAIAYATSHQVFKAKRNHEIVLSAFSEASSVSREDCNAAL
DSARWLVHNFYLNDEEVPLVEKAVRHSGSTPTHGTSPSGGNDRTGSVHDANEFQILTVSG
DLNVLMREDEKRLRKSQELAHAGGGGGTDTVREEEDDNDICFNGGDDGEMLSSNSFRDGD
AAAIPDNGPAPTTGSGSGGGKKFASARKDDPAVSFESTSKKPPPVTAASTTPPRWSSTSS
VSKVLAGRRLINLEGEIAALPEPVQWDALYGAQDPPPRPCTRVRTACFTRALEAIERAAQ
ISLMPLVMRQRLVPRNPADAVDLALLAFPRCTFVFYFAEFATQYVAIVRPAGRSFFLRRL
VQAYSLKEFYNKRHVSQPSTRETASSALAESLSHAPVERKEKRLSVIASSIGSLTRRSRA
GSVDRSPVLPGPIAGHAVMNEELQQGLQDLYADLWTPVRDSLRMARCFNDEAECFAFILD
PALLHVPLPSLYESGANCEPLGQQLTMVVAPSVAKFLGGMQHEEQPSFFNAPSKDLCVFL
PERTSNASAANSMSLGNIAADKVSGKQSLTTALSSTTASLEDTHLFPTPVLQGPAKWLFG
NLHPWSVFTGCTRKEIISAFALPSCRALIVLCDPVKHMFKVADGMVRLEDLTRGHSCLSE
SLSLVVVTNDASTATSVEEPGVAARLCLEHGCRRVLRMDLPPGTSITAEHHRLVQIYLEK
LLLAFEWRMRYPYALALRMAQEEALRCHFPPVVWASLTLLGAP*
>TCRU_6756 hypothetical protein, conserved
MSRRGFPAHRERSPENVDGRSIRPRTENRMPLAELGAPVVQCVDGMSEEALYAAMCPSDG
EPLPPGWEKVVYHGTIVYLDHVAREAHEVRPWEVWQRRSEAAK*
>TCRU_6757 hypothetical protein, conserved
MLTRLAISTVGYFDENFYPAYVEDVEYSLRLRLLGIQERNVLCGKFVHRGSSSIRFSNEM
EPPDALWYRRVGSLMTNQPYAMMKWGPQRACSGCKKPYDGMVPLDV*
>TCRU_6758 predicted zinc finger protein
MVATITFRLRSSNHVGVIDVPHRMISCREIKEAIATQLSGSPEEIEIFISGSSDYLHPEE
ELPAYTVLEVVRHVASGRPPPRREREAPAGNSSHQRSLTRMGAKEGTASAPLTEEERLAQ
LSEAVAAETGIDEVGGWRTRQTRNRPMGNAIGGRESSFLPPPPNYICHNCGKRGHLIQHC
PAAKGTKGLKLLSLPTGIPETMLVECTMDDPAAKFVTRDGRLVKRRLDNASFTGVVTAAA
DVADLQRESVTRLKSSKEGHSKGLVDGEDAKATEESKLLCGWDKLLAKNAMKAPCCATLL
CETCFNERVEELIGREDAEGTPLLCPGCNKPLSVCDVTPAVEERKIIESLYSRKRGRK*
>TCRU_6759 NADH ubiquinone oxidoreductase subunit NDUFA12, putative
MTSIFTYGGIGTNPMAQKYGQMAAAASLCGTKNFVYTKCHDDPHPFPRHHHRQSDVPWKD
SFTWNRLRWIIHDFRMFGLWGALRRHYYIGEQWRRKDEKIFVGKDENGNKYWLARRSQGN
FTVRMVEPVDPHWFRGQAPHTASPMWLKWMQGNAAHTPAQVKARGEWGHNSRLGMALPFN
IKYDEFSPINAGEVFSRDPMWVSAPGLLVNPERRALEEAGYSRWVINKGMPLYMPFCGVH
DYSDELVEEYYRGQWAFGRASKGNDHDEWRN*
>TCRU_6760 prenyl protein specific carboxyl methyltransferase
MSTERGPERNLMRETALIGFFLGACFMFALALICHSLWYTGSVEEYAAGVYILCIPVLFH
MSEFLVVASLGRHDTHPDTFLLIHSREYTAATSAAWIEFFLEWLLVPERWKVPRGTFAGW
LLRLNYSTVTVAAVMAVAFYLVRVVGMLHCGRNFSLLIETERRASHVLVDNGIYAVLRHP
AYFGFFWRTLCSQLVLANPLCLVLYAVVMWHFFSCRIAYEESVLEGEEFFGERYKAYKAK
TMAGIPFIYSRRPECVCMCVSLFA*

>TCRU_6761 Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily/Glyoxalase-like domain containing protein, putative
MSTRRLMHTMIRVGDLDRSIKFYTEALGMRLLRKWDCPEDKFTLVFLGYGTESETAVLEL
TYNYGQSEYKHGDAYGHIAIGVEDVNEEIARLKKMNVPIDYESEDGFMAFIVDPDGYYIE
LLNTERMLEKSREQMNEQGTA*
>TCRU_6762 hypothetical protein, conserved
MLGAGTWFVGLTIPTVVVVGFFASRKRLAYQWREELMDPTGNIYPPVTAAEMEFFCRILP
PYRRERKGEPLSVSENIGLYVSPDAFSGEESHVLLDEVVRWASLFGQGIDPKKLVTLEER
AKAERVDMSFCRDVVIISDHAEDIQLMKAPWGTGDRIKFDMMPASLRYMVNKTQRSFRGI
GRLRHVYVEYSPSGKFYHEPRPTKAFDGHDYVIIPLRRDENAAVVTFSPLLRSKFSFVRE
VLESSWTSRDIDAIVPPGGALRVYGAARYEWGWCIRPHNVWFGHRDNSLEKFSASPVQCG
MIQAITRRLFHSLAEQPKNKEAGLVVLHFEGPRDSKKVRSLLLHPESLIFGRPPKPETFE
QWTEERPTKDAVREEGVFLFMLKNYMEMFRVS*
>TCRU_6763 predicted zinc finger protein
MLRRAGVIRLWRPSRPLATPAAGSSLSKGTPSSASSSASISPSSLAILKYPYEVVDTPGK
LDEAVGSLLKARSIALDIEAFCTTEQAKQLGRISLLQACSDAKPVVFLFDVLTLTAPTFV
KSVEPFLRNRGIRKLLFDCRRDVEALSSQLGLKPEGVLDLQVFFTAIQWKLRSVNRRSGM
TYVLKSVAGLTRQDGDSAVQAAMTLGNRPVWDIRPLPDHFLEYAADDVRHILLLANHLVE
KREFPVDLVSVERLTAQYVEHYAVGKPVTEEADATPAEVNVAWLERYIGPGGVCHFCGAK
GHTEAECFKKQNGKAKCSFCGESGHTARNCFKKHPQLLKCEKCGQLGHTSANCFRTNPCI
HCGGPHNSANCHKMLRQRNFFDERSSS*
>TCRU_6764 chaperone protein DNAj, putative
MLRFTPPFMLWRRWAPAAVAAALPGLSLRLSSSEKDYYKILGVSRTASVSDIKKAYRKRA
LETHPDQGGKKEEFAEVAEAYECLSNEEKRRVYDQYGSEAAANMNAANGMGGFGAHSAND
IFAEFFKSRMGGFGDDMRRGPAQVQPIEVKLRMTLEEIYKGVTKKPRVNRPVKCADCRGF
GTKSQTKKPKCAHCDGSGHVVHQHRMGPGMVQQTVTQCPRCGGSGTMAKSDDQCPKCHGM
GYRHLSQEVNIDIPPGVPSNVTLVVRGEGGTLPDAEPGDLHVHVEVAPHKIFTRRGDDLL
MKKEISLSEALLGTQFSVKMLDGRHVTVKVPHENVLRPDSVLKVSGEGMPSADGGRGDLY
VITHLKMPAKLTAQQREAIIQAFGKPNEEKHTSADKTTTARVMRESAQELEDAMRDQWDA
QEGGGFRSGAGGQGRGRQSSQQAECVHQ*
>TCRU_6765 hypothetical protein
MMQRLKAVAEVQNQWFADRGSGSGGGGMERCWICGERSGNSKLAQTSACDGKEMCVRGAE
ASLSPPPSAASSSAVELPEGAEETVHVHFVNCSVETPLETSDVMQELVLERIMLELRQRK
SLL*
>TCRU_6766 hypothetical protein, conserved
MRRTLRFRAGFLQNLNSGKNNFFTSLWNKPQTRDERVKEYVPEVLAESLEEQRAVLEEST
SRDVIVELGHKVLREIENKSPTPSIAPHLNKIIQEYGSKDLIAQRPLSYLLYPSSTLIGG
QLPNELVANFSDNLRSLVEEVERNGCSARHKSVKGEKKEKDKTKKEEDVSHETSSSGANG
ENLSSALKSGPVVMASKEEHEPMDITLFVRIISAMALANVQHGDWNNAVRCVDVAIAHVV
EQSRLGGLLGMKAGILVYQKKYEEAVECANLAVEASGNIQGYIHGAFALRILKRPAEAVQ
LLERGREQHPMNTQLLAQMEGAQKDLEHMAKVAKTMIST*
>TCRU_6767 DENN (AEX-3) domain/Stabilization of polarity axis, putative
MTAEGAERHQDAGNSNGLYAVSKTLTKRRESCARHSSLVSLNCHDGSDESCLKFFIIFRM
EQHEVEVVWSYPLPFAAVEARHPKFLEFVYSNSGNSYSVEDLSHTFVMTDGHGVRMYGHC
TAFVNGEAAVSLSPYPWCRFFAQLATLFRTNGYDHGKAIVEALCRSPTPPSGSNFVLSTS
IPIVFQRPYDRLCSFIDTSPIDLINIFPETETLFSVLADLLLEKRVIVVGPNFGLVSHVV
MSLQSLISPFDWMHILAPILPSSLMDVLAAPTPYLVGILNSQIPLLERVPIENCVLIHLG
STGICEGVRYHNEEKHSLPNSGTFSALWIGYTTFKMRDPHERTARDLCSLFLTYYAALLG
GIGICGAGAHTLSNASPKDVPFYKSLMNTQCYSALTETVQEALADKNHAWMNNEFCVALV
RGHAKIYPQHYQQLIFEENKGVGYTTRYENCFGSREELTALSAAIHGCGGHQMGAGRLFC
QCLRGLMKHLVCLKHHSVLVTLEASSFARGYGDYDSDPRYSPDFVEMMVVQPSNDTK*
>TCRU_6768 hypothetical protein, conserved
MDGRGNNFAERDDGSVKATIATRSSGMKQRMGQDAKETHGKVLSVLPSIPAATQASQKGR

PQKYSEAEKNPLALLSSESRATAARNTLQEHWRSALLEYEVALRELVTNSINEPPSDVRL
TKTLQVYDAVARVVADQSPELADIMKMFRVEFCRATFSNRSLSDLIPFQDTDGVEEEVDD
LGRAYFDQVSVLLRENAALRVEVTLGNTRDNLAQMKQKIEHLVEMNSHYENELNRLVREN
ELLAENYRKAREELRKEKERNQIMIDTFDDEKERILQENKDMQLRLCRLRKYLGDRESTV
VKDAYKQLKEKKMEVMTQLFDEGDERVSILVMLSQLESRVNEELDNYDRESLLCEESELA
ERQQRMLSSVSVLLEEMHLSEVRYLRLVPNTHLLVGEEQDETDGYVSLLSDKGLYEALVA
RAEARERTLAVTESDAGESKDIMAAMVANTSMDFLRSVSGTVVDDTSFQMSLRESRDPTP
YKMGSPDGMSLPRPDSEDAKHERRNEEVTEDEKEEREGGKGKEKEGRRFAQLTGATPKEA
CVESLMLIRRKQEEWVANIFGSAVEKKDFLKRVLNRDSYQGTMTEQEQLMRYFILRPMLD
VSDNKFRCGIDIFTGPGPLTQSFLCTVMHVDPVEPLHVPQGSNFMHLKYRNPLRIEAVSK
DPSEGALVAPNTDAVEEWGGKTPYVREVTEAVVPELAVSSNVFAELRRPSVLKAAASGVN
VASSSTPSATVFQRLNPLSPNRSPEWLLYQSMFGGYRPLAPRLIDISYIDHILLNSCERH
FDRSEERYSRCFKQARGRATNSQKALNMAERFFKDTYALTDFQESIIRELESRYCYPELV
AKSLYEILCFLDATMASQPLVDLYLSCIRGFESPTRIHYITYVLHQISVNWPSSNPEEPV
LKEDVLTLLEYIYKKVSGITSMEASEILTEYHMATRSAPITLNSLRSYLVTAMMHFEDPL
LLYFNGLLSYNATSSAVVEMNYEQFELALKSKWEEKIEGKLLIRYLAASCGFNKKAELTT
KELACVATSMWSSQLWSNM*
>TCRU_6769 poly(ADP-ribose) glycohydrolase, putative
MAASTVSREDRYIRLPWSRENQCTGKPAQLRGNWDVIVAILSADTSKNMENFRVLLKRLY
FYGSSRFISCLPCFGTLCLVIDSMTPSERVAFFHVTLPWMKRRVIDGPVVLPRDLHALSQ
GESRRLILTNEEAATLLTCGFFSLFPGRCSNSRSKSKSSDKTASFDFADLFSLAPPGRIE
SQVAKIRCLLQYFIYCSHHADALGTCLEFYRVSFLSFPDLGKSLNPMQSVTMLEEGLIED
NYGSLQVDFANKYVGGGVLRTGCVQEEIRFMMCPELLLSCLFTEPLLDNEVLFMSGAGQY
SVSVGYASGFRFICGHSPHFAKLGAATSTPREIWVELVPTSLRNEKDCTAVMLRNSCVVA
MDAINYCGCEEKQYLTSSIIRETRKAFAAFKGTPDSILTSVHSGPVATGNWGCGAFSGDR
ELKTMIQWCAASEAKRPLIYSSINDSDLCYRFGLVYKKLQEEEWTVGDVFTALLLFSQRY
TTNPTSLEEGSLFQYILSLKNPRCASSHSGTEFE*
>TCRU_6770 dynein light chain, putative
MHAEDIDPATFSLRPEHRQKFRPNDIRPIVRSIIESRLENEPYRADEIQSISKEIADTVR
DRIRTMDLERYKIMVHCMIGEQRGQGLRAGCKMFWDSDTDDYFEEVYINEYLFAVVTVFG
LYQY*
>TCRU_6771 hypothetical protein, conserved
MFRASTTSLGAASKRSVSNWSSLPFDRRDKSFWLAFNEYLAPSMKSEFPLASDEFRKPML
SGLTVPGESALLNGAIIKAANDLRDYYDNISLWNPLSLAFQLGIEVSVVIEQLLLAKEYG
LVSMLFVVSCRSCGCDMLRVDAVREICFRATYHKTNIIRCPMCTDCTEVTDLTHVGVFFQ
DFSPPEFLRRKYHRLFYSDEAIRRQLEAYFCPPGAAFAFHMRLPEGRYLIVASGMGILVE
IQVGTGAEFLGKDCPFHAVTLSLGKLLNENSVDSEGNGRRRRVIRVNHGKLVFRVFNATP
YGSYLDFCVAFDERLEFLAPQTPLVATVPMVLHTASRGLRSPLFHFFIPRPPGTRTSGVY
VLHSFALPSEEFDEPITAGTESVLAVIREVHRYSLEDHHGLLISVGHGGSVFESSFFSVT
AALASSLCLAQRVVTRLGEEVAASFTCTITKGTMYMASFQGQYDDDENLRSSYPDVHVVG
PVVYAATHPPVVLTNDRDGKDSVQPVVRCARIELRSVSEEHMGVCLEPAAADAMFPFFLS
YLGDQLKALQVLSEPQALVLLVPLSTLNATVTLPSLLNPVMYTKELRGPFG*
>TCRU_6772 SpoU rRNA Methylase family, putative
MRRVFDGRGGTRAIPSPWTMMATKPTNCTQSRWQSFFGEHRATARQSRQAYSHPLAPKDP
AARNIVIPDAVHAKTRSPMALPAEVLQKRAQRALLMQLQQNIVWEGTVIDDERHELIQHF
VRLRQNPKYRSSKQMMILGGREVLRELFEEGHTPRHLLIRGSQEVPSWAKKKGVETEIVR
VDRHVAEVCAPGNDGYIGDFDIPPPPAKENLIANKQRFDRILVLDNVDDPGLLGTLLRAA
AGFHYDAIITTNHCADIYDHRVVRSARGAHFQKAVPIYTLKEEDGDNVYGMLNHIVQRNN
MSTVCFTPIDDDTEKTNTGKAPNVVLSSSVAHAGTFEREALSEYCHRCFTTEETKGQLLI
AGPNHKRNSLRRWSKRITGPVTQLLLDEVTQTDSLVALSVVIHALRPHGNWDYLPTSEPH
DSNTATLELQTMKARVDIGADRLELRETDLNLDEEEQVEKARFKNEWMKWKRLQRGKMGD
YERWMEAETQRVREMAANERRRQIMPWVRLRWRHQKGAAGLPPSVPNIIDEYRMPLDRDA
LREERETSTGYVRPENYDR*
>TCRU_6773 Sybindin-like family, putative

MTLYSIYIFNRYGDNIFYMQWNRTSAVQEGEASLVAGFIYTLQHLSSQLSSTGTSGLRAV
QTPFYKLHYAETMTGYRVALLTCRNVSTALVQGIFIEMFRDVFHKTLTRDLNYRHKPGCM
ITNPDFAEGLEALFRSKQLLE*
>TCRU_6774 protein kinase, putative
MDDGTGHLIRPFSVIGMGAYGTVFKAFRLPKEYGDEEEMWRSHAQAVAVKETVFTEVADD
ITVVLKEVSYLSNLQHPNIVSYFTAFTNSGVTPVAPSPASTNSKGNEGMKASPSFSAAPS
LCIVEELVEGASVAKVLKMTAEGQLSNVMSEVDIAAVLYDVLQALLYIHEECRLVHRDIK
PLNMLMDCKTASVKLCDFGTCADVSQQAGRYTVIGTIGWIAPEVLDSGMMDCRSGHVTSH
SFPSDVWSLGVSALEMALPNIRKTALSEYIKDVSASSCSAQRTLESSRKSVLPMKISSER
LRDFIACCLRKDPLVRSTVRQLLAHPLIVGSGVASAQKRQKRIGAILDAVKAANKSNQEL
NEKMNDDAIVLPQYAHSTLKKNRCMEAIAAIKREFFAAQAPLSEKSRVSHYAWCLPEHIA
RMSSSDEYRYMPTPLRQQGLGQVPSVHNPQGNARSTAPLKPIFDSVVLPATVDSQRVVLS
LIRKYRKLAGANTADGWTEVDRRNEACYALDELACQNLKHERFIRLHDDLLRTFKATCMA
IPDFAASFLSNFTQSLTVSDDDTQNLRQFIAYIFQLQKENLMHTHRTQLETPDFKATAFK
SSADAFARSLQPMNFVSAEDLLRFPHMPQSAGFMNASNLGDDAATGTMRQQQPLVNPSAY
LFNTWLRRKRADILGPS*
>TCRU_6775 RNA polymerase-associated protein LEO1, putative
MDLPLDIDQLTAPPQLDEPPLSPLAAANSPAVPRFSPIPPPSSAAHADKVQSPTEEGDGY
QFPALDENDEHLAIEDLFGDLFEVGDHRPVDPALVDTRRMLLRFFGDYVREEDVDFEDEK
HVKLAKEMADNKAAARFAAAEKCFGEAGAAALEDQRVEPFGCLQSSLPDAPDLGPRDELW
LTDMPKIAPNRQTLHMEPQPFIPSQCMPLNSTERMLFTTQNVVRWAYHKGTNTFMSNARI
VRWSDGSVTLHVGSDLFTLQTSKENTVTMLARPVVVQKGAVGVPAMVSAVNPTKHLVVEG
ATAASVEEAVIAESARFRSVSKQHNLAYSTPTLPNVNWKKMTKARTPIEEYVMKEYDRRQ
KLIEQRKKEGRPMTLTEQMEMEDELLQKLKTISAEELLEQQQEQQREAVLRSTVRPQPLS
RGRFNRNTNLEGGADMAFANDGSDGIWKGYEEQEDGDDDTYETTLEIMRTKRQRENDADN
AERLRRIHQRENEQVARYKPLMEALRGLVPCLPSGSNALGAVQGTLDFLETGAFSAGVVE
KEVPLMMEEVADECPDIDLGAVRNELRKLFP*
>TCRU_6776 selenocysteine lyase
MCNVEGLPLRQGKPRPLPSTDPLPIYLDYNATTPLCDEAWEAMVSVRSSWGNPSSSHPYG
LAAKFALEEARRKISDAIHAETPESIVFTSGGTEANNLAIIGGTSAVHERDPTRFRVIAT
TVEHPAVEEVVKFLQLSNPLQKEESGLVTHRFPVDVTTGCVNPDQWRQLLLQLPGGPRSV
ALVSVMHANNEIGSVNPIRELVQLVKELCGAEVLFHTDAAQSIGKVPVDVSSLRVDFLSI
CSHKFYGPKGVGALYVREGVPLQNILFGAGHERGIRPGTENVMQVTGMAVALHIACNNLS
ENANRMQATRDELLHVIEEELVKVGMRYVANSDIRYSLPNTLNIALYKEDRAGHPRYISA
QRLIYSVGNQVCMSAGSACHSSAQEVEVSTPLKSVGVDLPRAIGTLRLSTGRGTSVEEVR
RAARIIVRHAAQQFGDV*
>TCRU_6777 hypothetical protein, conserved
MSVGGAPSDGVGVVWCANQHLSAGTGFPFLLQVEDAQVCIDYPAKHHRCCWTRAMLQPVW
ENFSASPVGRNDLKKEESLFQEQYTQRDAFSSSFFSLRTRRTLAELSQSIQLLFKRQQQK
RPPCRNVNRLRYIHLLPSVVRVGRGITGKLSLTFSLRRCGDTKEAKVSLFPTFIAVEVFG
FMTSFVTITLCEARQRSSRKTALLLLQSISHEGNVAKYSVFNADLHLDSPQSFSSLPLPC
ELTWSFRVYAACYSSMETQIRLEEPFMHLREWKSRTTQEERFAIVNPSMDPEITFSIEKR
NRANMERRIHAAIAQMDSPGEMESLNSPSTSSSSLVRATLCHIATVETSRGIMMEPCVQP
GNGTLAAVMPRDISWPLHLLVADASGKTWRSPPIAGSSSLGRLACEMNYLEGRRSAEDGN
ENPELKIKGE*
>TCRU_6778 hypothetical protein, conserved
MTVVTQQQECPRQSDETASGDSVDVRNAQPDLEGAFKDVVTRSLDEILQKRPKDPIRLLA
DRLLEKSDSHEVEQHECLVGNAIRCTLKKACTRKKGADLCQVPGLPLLQLTVPTAFELDA
ALRHLETLTPSNTKVIIFVEPPNPPTDLFFVKGVPYFTDITEKLLLQRRRGATDDILLDE
GDDVRVGSSKKMTSLLQKALLLDVKTLQEELADLATPLSRFCIVQLPEVQSNFLEVFDII
DKAFGVRKHYWNVRTTAPAEVPSALLASFNPRMSNMTFSRIIAAILPLYEQLQRRKIAAT
LERNKARVQQLNYSYITQYWTEVLQRRDKRDQERAKLNALSPQGKASNQALSSGAKSSPG
RKRRKQPNALCMSRSQRRENEDATFLRVSQRLQSQAATRIQALYRGYRCRITMVKLRSQR
EMVPDTACWVENIPTSLPILLQRCLERLSVSHGELFGNYVVSCPPSPRCVTILKPLRRVL

KKQEEDDVDSETESWEEETVILPLKRQTKPIPHFNALRRLMECELLGRCNTIDYATSIQR
DCSGLSVLQRHAYDCYKSLVLNLMHIAFLELYYRERLPAVVATFPEYMYRFHREVFGWLS
APHLFSRTALRVLGGDAPLLPILCERKVMETERVLLTGGSRRGSTFEFSPRYQSEKQELP
SQDDQSSQEMSLPVLSMALGGFASEWTCQGVHATPAFPTEAVWEMTLREVSLTSQEGKVA
WWSLPPYPAAYLNGEALVLVPRHELQEVHGRPRFDDYVVPIEEATKESPVLPQTLFDNVA
VETSRVERSRCGYSGVIDGLSITNFEEKVPVEAMTREDPPVLDEVSCFSTFGLSLRGEDF
HLARLINRERKLHPLGNLKLYSTVNLAGPYGIPMAHASQQPFVLAQQSDIRKLDESFLHE
SIYLAGVSGSISRSNRRFRSRQRGSWCKTLEAVKKNFSSSERLQASWETSKYALSKRNFL
VSPEVINRPRREAPTNPNSLIEVETVDVMARRLAQRVLKGMDFVHERPWITPVCGRAWLL
VFEQFASKCYSQICEGYSIVISMGDPFQVMLFNAVCLLKYARQSKGRNSDEAIESSIFGA
SLHDHATSPSFSLLSDETASCLAFMDGFYECVGGLLKQSDVSVPEVVYVVHKIMHENSPG
GMMFLNEIPALMKSAERETDPRLLVDGILAIVQRIELYCWLVLFQAFLASLAAEGVVDER
GDVVLSSFSAFVDDTALMTWMEQFDPWKNTPGKSPDPFHLRYSNGLRRWDDRNYIFSGAL
*
>TCRU_6779 Microtubule-associated protein Bicaudal-D, putative
MQDPMEFMRRIESISEYGHLFQFMLDGVTPDDPELTRTRHYYVVSKDQSYARAYCYLVLS
LCELKEGRNLSRWLALYSHIFGTITSERFLELLLSIARGCFGQYAFFVDEYVARLAFCAL
TTCDSLKLCERADGESHKHLLQTPRDAGTAEPKEFFFDVDRQRHFEADWPKGTASPSMSF
AERIQLEKQLQESQLLLQVKTSQHEREVSALRDAMVKMEQKLIWYERAHQQRIHHHFFEH
QDEMQRLENEMRQRETELLRAMDTILRDQESLLQQLSEENASLKQRHHEAKIETERWRME
CQELKHRLNSTAMTAVCPLNSVSREQYRDLDRRHQLLHKEFDELSLERSEMEQQLQQARQ
EAHQRRVELDSALEVLNSLRKGLDYVGRELPLMRETPVTYTA*
>TCRU_6780 galactokinase-like protein, putative
MNPLSYTDERLDKTLRQLKPLFMKAFSAHDDSDVEWVLFAFAPGRVNFIGEHVDYMGGYV
CPAAVGDGCHILVGRVKHITDHKLRFSTTRDEYFELGHLGEKDHNKAWTTFIRGATSIRL
SHHGVKLGAEPLKGICMMILGTLEMGAGMSASASFGIALLNALSTTITGRYKNPQLTPGR
RYAILPRESHDEMIDLVKQGRRIETEFCGVQVGIMDQFASAFSVSNKFMVLDCTALTHKL
CDITPVTGDDACFLLIDSMIKHDLLGATSGTYNTVRSDQEQAQEKISKQILGGKPFTFTE
LVRDPHKYTTTGDAVHFIKSCQKQLTRGEFERGYYNVTEQIRTRDFIALTDASTGLTHEE
RFREAGRILNEAHEGMRTLMKITTAELDFIHETINQEPGVAGGRMMGGGFGGCIILLLKK
NVVDSVVCRVREKFKARFGVENKVYPVVMGDGAFVVSLANKSGPDSNL*
>TCRU_6781 hypothetical protein
MDNCSRESRVLLLRLCSIWGFIIGSWAVLQVATPLVLKDIVGKDVAPTWQGLFSATTAVS
GMIFCALTGHFSDRIGRLEFLTPWVIFFFFTTILVVFADITGSIYMLWVARIAAISIPST
IMHAFLSDYLSGNALLESFGYVGATFGTSMLTSSLLCGLISRYYSRVVALTFGSSLAAVG
VIFTLALKPPSKLRLNSPTAFVNTEGTNLFHSAGGVMNSMRIISSDALLRNLICAMALLR
VGNVNTHMMLVLFVDFRLGWGLPEMSVLAGFSALLTVIFQLIGVRFLISSDIVLPVLFVL
LAVVPIVAMGYALAMTGAQMYLISILTSMMTIASTICNAKITAIASENGVAGLALGCVGT
LQNILEVFASLFLGRLLSWSFENQPRTHVLSGLPFIVNGAFLTLVVMIVFYSHKRHGAGR
ASWTEGVHAG*
>TCRU_6782 Acyl-CoA dehydrogenase, N-terminal domain/Acyl-CoA
dehydrogenase, middle domain/Acyl-CoA dehydrogenase, C-terminal
domain containing protein, putative
MFRFTSALGLRCCGIARCAALQTPTPVTLLSESEKMLLDSVRQFTDRVLKPRARRMDEAS
AMEKEVINELFEAGLMSIEIPAEHGGGDMSFFSSILAIEEISRVDPSVSVLVDVHNTLVN
NIFIRFANSEQNAKFLPDLASSCVGCFCLTEAESGSDAFALRTRAEKKGDRWVINGSKIF
ITNGGYADIFLVMANVDPSKGYKGITCFVVDKRKSSGIHVGRPLDKLGLRASSTVEINFE
NCEVPEENLIGEVGKGYQIAIATLNEGRIGIGAQMVGIAQGAMDIVMPYLFQRKQFNTPV
GDFQALQMQYAECATNIHAARLMVYNAARKKLMGESFVKEAAMAKLFGSQVAEKTASKAI
EWAGGIGFTRDFGLERLYRDAKIGAIYEGTSIIQLQTIAKLIKKEYN*
>TCRU_6783 hypothetical protein, conserved
MNQLIRSRTEWKERVVFRLAWITASRLFEIAALTANNFTLERDGALILDWSVAPKTARAD
SHRASRFVRIREQDAFDTIKLCRTLQENERLTNLTTAKVERALAPWDATAHSIKRGALRH
AAQIVETYNLNPHVISQLARHVDPFDLPQNTV*

>TCRU_6784 hypothetical protein, conserved
MQAEARAVRLALSAFPAILPSTMDVWVDSTLLQGAANKGSSKSNALTREPQRKNEFLESR
GIQATFAYVVSAENPADGISRGRVFTLQDLAKGRNMRREAAGSCGRRSPKSATS*
>TCRU_6785 Nin one binding (NOB1) Zn-ribbon like, putative
MSWAAVAQKAKDATATNKEPKRVVFAPAVESVGDGGNEREHIDVSRTSCHGVGTPIPAYQ
KGLLILDANAFIKGMDNFSDVADVLVTTPQVVAEVRDRAARELLSRFSQVLHVLEPSKEA
IAAVVSVAEKTGDLGAMSRTDIRLCALALYCCKATNSLQPPIEPRQAVINPDGDHGTEIV
TDAVPDEGNDDSEAASNGSEDGEDENDGDDEGWITPENIHQHLRGAADAVGERFDGGVAC
VTSDYAMQNTLKHLGVSIVGPHGMRIQELRQWLLRCTSCFALTNDTTRQFCGTCGSGNTL
RRVQYVVTREGKKQLFINFCKPISTRGTVYNLPKPRGGKRGTNRCLVLREDQMAHVIRGT
TSAKLREKHVVRGSGNDEELAAFGEVPKPHKRDVNQPRMFSSYHKYNVNEKKKSRASRRK
*
>TCRU_6786 Bacterial transferase hexapeptide (six repeats), putative
MLRRTVARFMASEAIGPAHPDILWGFMDGRYAGPGWVSWIKQLPVETLTMQGGTSMTNMN
DRAGVILDPEDPRHPMALIQWGPMNHYDGAFMQLSYGDYGKIKKGSRLMQVLYDNYLEPF
SMNRVCAQLYFYQKVPNNYHASVEASAEYIGQTASLVGQVVVGMGSVIMEGVTVKGDTNC
VYIAEGVQVMENTCIVSDAPTDLLAYQRHEAINPYQQWDGMDGVCRIMQNTMIEPNCFLD
SCSIGPFNRIGHNTKILKGVTTGTMVHILPGSVVTADTRIGDGELWGGAPAVKLGKVSKF
EWKRPYYASLLHKECVVESYRNMSRYGDQVVYFQDEMGKLDTLMLQFESDITPSVKAKIK
EFVQGREPFHHMLTRITQGWSPANRPDDKNYNLCPPLPAVKLFAEHNNDSSDSSLHGTYM
NITNIFNDFRW*
>TCRU_6787 hypothetical protein, conserved
MGKMEFHTLDPRRKSPYEEHVVWEELDALRDTVAFLRQRQEQQAAQWRVMSEEQQKHCTD
LASIYQQLQELLLSGSDAEGKKQSGDAVTASQELLRSEVCDLLQNFKHHIELHTAETTRR
LDGFQTSLEEIKKKVEHDNCRAARQEERLTQLEEQQRDMLRRMSFVSTLEDLEQLRVTFT
QQLHSLQEDTATTIQRHIASVDERCATHEVQCREEQLSFQRETHQSIEQVTHLLHDRIEA
LCSELKTHASSIDVKTSNFEEQTRCEMKGMLQTHLEKTCEQVQEVHQELSSKHLQLVEDT
MEAVEKIAHLSGDLPRRVSLLQDDIANIHETLHRHGDILNEQCLQGSLQGAFDEVKDWLQ
DLECRVLSRGEFDEVLASVDRKLAALKREFILYIPAKHPADQSIEGEGVSFVSTTAGGSG
SGGGRQPSEQGSERQGGRI*
>TCRU_6788 MENG
MASQKPEDVTVSDGMLANLEREFNEAMRALEGHVKFVCFREEYEKLHRALLNSHESEKRL
VRRCQQLTQELMSNAAKMQAAVKLAQDDHTTIEALKKETEKAWRMVDVANEKDARAKETI
KKLREEVFSLQEIVENGTELTPTQTATLEELKLEKKRMQSEYDELVKQMETLTRETFELG
HKMKEAEEEMMKHQEELRRVTDREKTVRQEYEKELKARDRSNLQLREQLLLVQQREKELK
SHEQLHSKLSSAVNLLRLQLQEDQNRRQALAQKIESAERQLYHTQQSYDDAVDTREALNE
RHREVRKEITEAEKKAVDITAEKQRTHRVRDNDYKELCRLVQQNEDIRRDQTNLERQRLN
VEKRIEMARREKEDLCRAFEMMQREKDSLKKVSEKEREKMQIIEKLIANEVESQAEIEDA
IARERE IGTRLRQTVARLESEREKYVHEVSQVSLHHTQAQEELKIASITCEETQKAIDDS
EQKLKKQQSRYEQVRSERNLYSKKLIESQDEVVELKQKFRMMDHQILQLKEELAMKEKKF
QEESSAQKTSKDKLTKVRKVVNERTAALDEANQRCENVGQKIKQLVKIISRCDKELSEHQ
QRFLAVSGERDLLGTQLIRRNDELALLYDKVRMQQELLTHGEAACRARVEDMRLLRLKIE
DLKRKASIAQKRAFHTECLKEEINQLQYELQAQRAKVQALTEEAENPKNTLRWENISGRD
PTPEEIEKKIALLQRRLITKSEECVEKDMEVQEKQRLVTELQNIFARQPGNEVARQLNVM
HKELGHKNAVMKQKASELNMTSTHISELKYEAERLRRELHETKRKYYEIQMSNDKLAEYL
SHAKNTSTFSGF*
>TCRU_6789 40S ribosomal protein SA, putative
MTSVESGAKVLRMKEGDVQKLVAMHCHLGTKNRSNAMKKYIHSRTKEGTNIIDLHMTWEK
LILAARVIAAVENPQDVTVCSTRLFGQRAIFKFSQLVGTSFLAGRFIPGTFTNQIQKKFM
QPRVLLVTDPRTDHQALREASLVNIPVIAFCDTDAPLEFVDIAIPCNNRGRYSISMMYWL
LAREVLRLRGTIPRSVPWDVKVDLFFYRDPEEALKHEEVNQAAAPVAEADEGFGWVERDN
NAWEQ*
>TCRU_6790 hypothetical protein, conserved
MIDISRLLSKTEDCERCGEVLRSLDAFQLSRSTLLMRATEGYDKPHSSFIRACEENPNNL

GCDTALDRDRTERVKRASLIISQVKKLYEPKDEGVSLLLNNRYNDFMKYLLDEKEQESCL
TCVVEDGRLARLMTEPVADAVLGYTWYHLYPINERHQAFCWRHCEGLLTYLERIYLYFLR
FYVTQAVRFRLMALQHEYATIVLIMLQLALLVIILQRYVADGRGGTGSGANVGGNAHTEN
NPAGGLRGNARRAALGRGKGGGGGGGKKD*
>TCRU_6791 hypothetical protein, conserved
MDCVLSDVPAQATRISGRSVSFPNLLRNALCVSPIGRPPVYIDSDQHLPSHTAGTEDGLS
RQAGMLPQRKHVAIALREADCDSSISACGTPLASVTTWLEMRKYTIPRGSRDSPQKSRRT
ECIRPSLLRRQHATSVLSYREAACPVLKCSANGRTAIMPSAVFSPCC*
>TCRU_6792 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCAAGSFAYEEKASLRSGGGSLVQSQGIEKFPEGTQGLKDQA
GGLKGKKPHTSSEDEAVEDEEEDNDDDDDEPEEEKERSKEKEDAENPGKSESSSKEMAAT
MPTASGLSEAGGGSPSGVDGVGSSGSSDGSEDSNLEAPGPAVKSPPPLPNAAAGGLQDAD
GALSPQKNNFSETGVHSGTTPLAPSLPKSQAPTITQPKAEEQSPTEQDTEGSPDTEEVTT
GKENVQNTVETVRPSRALSAASKPPVQQPTPLLTQSPAAPLPERLAPSEEKSIAPSFSAG
EGSRRAPNVARNSKEEKNEKIPSETETESKAVEQP*
>TCRU_6793 acetyltransferase, putative
MASVTASGLFLAVALTVASVSAFFFTIWPAAVLVLVRLTAGFIPTNFMRLCTVWYDGVQE
KWLAFVVIFLECVLKLRLAYTIVSTSATTPSGIADVFAPPQPGNFKLIILNHRSRIDWLM
MFPFLARANVLRTLRIVLKAGLSRIPVFGWSMQLFRYIFLSRKWSSDEAKMHDVIVHYRE
NGGATILLFPEGTDLSESNVEKSHAYAAQNGLPRFHHVLNPRVKGFVAMKNMIGAANIEE
IVDVTMGYTDFVPGERPAECSVVNGRMPKKVHILCMRHRMAENTPSVGEERRALDVVPTD
DDGLSLWLNDCFAKKEFLLSQFYASNPVGFEPHHVRSVFGENCTVFTYDEDEEMARHPNS
TKFSLFVRDVGIWRGFVGIIVLWTIPVLYWVFCGGLLSLLLYGLLAAMCVWINREKGGLD
VWLFLQPQPKRPARKEELKTHKKE*
>TCRU_6794 Leucine Rich repeat, putative
MKSKKTVQKSEFHHVRVQGRQREVEFPVSPLSAGPQQGRWGKDSYFVPKLVTLCAEIIAA
NFAQLPEADGLREEHPKLYNVVIERLSTDLPFSVTVPRVRSDEYWRRCCEARWSFGQLGE
RSCGKLLPPKREGWKQFFLERVLSDFLTALRLPEMTTEEAEALDNLCLVCREYVYTLDLA
CQVTRFALYESLLSRMPHLEDIRLTIGVKNAGTNFEWEMMGFGESDALNLRRALMRYPPL
RYLRLPNNRLNSSLLKGILGGLVHNTSIVVLDFSSNRIDDEGARQLALLLCKPELPLEEL
YLNDNHIRSEGATALGEALTMNKRLRVLNLRLNRIPDETGGVAIFNGLATHTTLEVLDLA
HNLLGDETARTLAEVLPKQESLLSLNIAGNKALGLETSQLLLQAVKKNTTLCFFDTRGSG
VAEECMAAMEGKVRDVVRAIKRQELAMKEELQREKIRQEVEAKLAKTLCA*
>TCRU_6795 membrane-bound acid phosphatase, putative
MRAKMLPVGDANRNTKIMMQYAHRVPIQTALGHDPSDATPLGETFLVDLLRDDATNAYFV
RLRYAAAKNGAPAAAFFPFRCLSAADVPTDATTADGVICPFDDFTRFVESSSGTSAAGAA
CYLDEETRKKFGCSVEGAAPSPECARYRAMCPAQACPGGQVYDVSSESCWPLELNRRMLS
ADNMVGLFFVLVFGGFVLSIVIVEICPVFLHWVKTVAKKRTTSDSE*
>TCRU_6796 hypothetical protein, conserved
MYNRFSYPSRLQYRTYSELPPTSVSVPVEYKPDPPYLNACALALLTNSEDAVNTTFCSII
TLHMLLTDSSNWTSENCTASTSVTAMSQCCGRASANTTTEDRITVRLTRIRTPDDSAASA
PPTNCSAAPSRNVHPVNVMLMGRCSGMLLRENVNAAPTPLNITPT*
>TCRU_6797 hypothetical protein, conserved
MHSRTALPETTRLSWSTTSQRPGTQLFLHCVDDLLRRLGNSYSAAAFMYTDDLTLVASGA
DIHACAAAMQPAPPPITAWAAEHNLKINVDKSEAALFHISSHTRSEEDMVDLLPGNGNLR
IQSRPVHLLDTTFDRLLNFGSHASTTAKQTTPRRYQLRPVAQAGASQHNTQSFSIGYGHG
VPLYSDESILPCFAYICLYNTDVLYRDGRKHSWH*
>TCRU_6798 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily, putative
MITYSTDSGNTWVFPEGISSADCVNPRITEWETGQILMVTDCKDGQMVYDSRDMGTTWTE
AVGTLSGVWVNSGSGDSQKKSLRVDALITATIEGRKVMVYTRNRYLSRENKANALCLWVT
DNNRSFSVGPISLGSAVNGGFGSTLLYSDGALHLSRESIVGTRRGISLARLTEKLKTIRS
VLSTWAQIDAFFSNSSTPTAGLVGLLSNAASDRKWIDEYRCVNATVMEAARVKSGYDFTG
PGSRAIWPFDSWEHGKNHGFVDHNFALVATVTVRLVPYVSTPLLAVCLGDSKSTKIIGLS

YGMNKRWETVFNGTKTSQNGTWEPEREYQVALMLQDGKKGTVYVNGQLVGSPENTPTPEM
RGG*
>TCRU_6799 hypothetical protein
MSLELSLAVLSNLNAAIWNAINRFAKTRVGHNVNFGVHSQDTPAVTLLVSWAAFHVTKTN
ILEEVAAEGKTGVPSSFIPGADPRSTFHARMTTIKSRHRKIVVKRMNLVTWIRVNFRLTV
LPSIANNVIKGTLFELVHRAAALKMFQIEIARCLIPVHLILPNIPIPQKQPLCLRQHADI
LSPFFTFKPAKGMCFKVI*
>TCRU_6800 ABC-2 type transporter, putative
MHGGSACGLDENTPLVSSEARSRWSNSTCSVFSKSGGNIGKLCDAAQQYLRSVFCVGGLT
ICVLEVSIVKEFRLSRCFPSFFHPKRYCDAAVALMREGGLHVIADVDGIAGSSLLRVITG
DALCSSGTVLANGVPVEAGVFRKAVGIFTNVEAYMPNLTVEENINFVVSMRTRVAGESRE
ELVEATCVLTELDRYKPAKLLSPSEAFRLRLAMEIARDPPIIVAYYPFYRLGIADASECS
LILKRLSTVLGKTVIISTTTLFSQLFEVTDTILLFGREGCVLYSGEAATMPSYFTGLHVS
SNLSSTHDSGVSKGVSAGYNLPLTTYRAADSTLARESSRNEDYESHSVPLLSFFSQEPGA
AASTNLVSCGDDVLDLAVLWAESETITKYYSSKFYNSYMRRRVVQFIAHFSGPPQNLDDV
APFMSTAPPQYAVLKPFLLCWYDAMQTWRSSEVYVHLACLSLGLFLISLLMNLQNDDQGG
MYNIRGIQFVLFLLTMLTNTTTMGDVDHQLRLFFHQRNNGLYGTACFMIAFVFRTVLVRV
VYLTLFVPVVIYVLKMSSAFLLLVGALSVTQALLIVTVHAFVPHNRWAVIILWLYLGYCV
IFCGFLLNLKAMPLLVGKMSILRWGYGAALAQSLQDMPFSCDGAGNTSYCYSGNTYLDIE
GFLRESTQRSLLVFGGVCGVLIILTGINLACRG*
>TCRU_and EF-hand domain-containing protein 1, putative LET.1
MLRASRIHFCAINSSKATAHSGVAYYANVAWEGIRHVYHGFRLFFMNTSLAWKYSRQLKA
GVALTRRERLLLESATKDLVRLVPFSFFIVVPFAELLLPVALKMFPDLIPSTFETKSQGR
SRAFSAALGTLRARQRVMEYLSTTAFVSFTKEQQEVVRSCALGGSVNASQIKLIAPHFGR
DGPLSVYKCPDSVALGLARTVGVFKSYHGFFPTKVIAPYMRRKVIRHYHKTREDDRLLRL
EGLDDLTDEELIKANLVRGMRWTEDAETLRIQLEWWVSLGRDPDVPYNTLFWVKPTRFSL
KESMRRLPLEQRRQMLGIQYLPEGVRGNLETLCETVDTVPTLGDDRIDADRILEKLEDLS
AKTKSSDRDISFHDIQVSFGAYLTEANVKMMFERIRKGKTANESVTVSDVIDFIGSETHN
SSHVVSTVFDAFDQGQGAKPITEATLISIGARCRGASKSSTDDASQKPTDSSSDGVKRK*
>TCRU_6802 tRNA isopentenyltransferase, putative
MSTEGEGFTNPVFFVLGATGSGKSLAAVNVAKALQRRCGFEHVVIVNCDVMQFYADLPIA
TNKISSSEMEGIPHCFVGFLSPSGMKIRDPTLIYKGRDKEETVTVNSLKEKEAYNIHSYV
RDVVGFIESFFRDHSSAAVIVCGGTCYYAQALLFDNTLTLEDEKDLVDHEKGLSSSVSLE
KYEGKGLWQELNRVDPAVAVRYHPNDTRRLCRLLEIYKKTNRLPSEIYSTRPDPCFRFCP
QKCFVLWINVPYEKLRKILEERVDKMLERGILNEFVEFAERQVKDSFDFALAKAIGFKEF
IPAVDIIDGQIKVKGECELKNSLDLLKSNTKRYARQQDQWIRNRFLGRFRSVFNSFQGTR
NFVSIDASKIFSEFIETVQNATEFLVKPGSQQLQGVTFPLNQIMEPQSEVKQEWCQVCEM
FFCGGKQMNIHLTSRRHRGAAKHAALVKEQEEKYGRLISFKRKRLS*
>TCRU_6803 Enriched in surface-labeled proteome protein 1
MVSVRLTAQLEKVKEVLATWEKVDERVSQLCPSESAVQAPSTDTACGAGKITDGLVGFSS
GSLSDNTWNDEYLGVDATVKNGAAKAAKTSDGVTFRGAWAEWPVGEQGENQLYHFANYNF
TLVATVSIDGEPEEGSHIPVMGLRAGSDDENTENSVLFGLSYNNKKKWKLLCGGATTKEL
SSIGEPETTHHVVFLPRNGNQSSAYVDGQRVGVGASCALGSTESQEISHFYIGGDGGSAE
NTAGDEDVSVTVSNVLLYNRPLAFTGGIADLEEDIASASEAPVAQATSQQPPQEREAQKN
TTVGESATTQQVPANTSQGSVEKAAASNSHAVGEATGDAGTMRGSGLLPSLLLLLGLWGF
ATL*
>TCRU_6804 Enriched in surface-labeled proteome protein 1
MGVGQDGTAVNTEVSASSAEDEETAGEKNGQDGINSQVREVNATALNSSLGNLSQGNNTD
AGTMRESGLLSSLLLLGLWGLAAL*
>TCRU_of Trypanosoma cruzi region 5/Dispersed gene family protein.1
Dispersed gene family protein.1
MLSNATWVRNATNPSTVLELAVPVHRGYFIAADETIVIRCDAAAVSGGCRGVLLGSFTIR
SDMLPAAASALSAITGVVAGAAAVAVVVTGGLGSVLEIQGLGVFARMPCASAQERASTVA
LPYFLSVFAALDPLWMVVGNALLAAVFGCVHCGVTAAFQRWRGVDAASAWAAMRFPSLTY

VVAHAMHLGIFFGSVLALAMPGARGHHRVIGVVGVLYGVAFPAGVCYLIARHAGASFTRY
WQFLRKPLHERLLYPVGYWHPAAQQRMYGGMLTNVRGSRVYWCVFQLSVLCVVCLIAAVQ
SPVGGCHVQYFCMAAVLLACAGVFAFTNMMRSSFLTVVHTASFVLLAALCVVSAANHLAP
SDGGARAYAAIVLLLATVVLAVTVYGMVVWYAEDRHWQELREPRRGGLEALLRDDEEGEE
TQKPHDRTSLSYA*
>TCRU_6806 retrotransposon hot spot protein, RHS3, putative
MRLNDFLTMELDGRGALDANQDVLLEEFFKDPKKYICDAGVLNEMQASDRYKRMERAVRD
EMDMEEDADKLRENGVDKLLKWLVATAEVKATVHGATKRFLDAAAEEARKPKKSSAPRYL
EGCYESVHNARWHHVVEVPGGEGTGMEVGKPEQSWTYRAVGDSLEKDDGVQQSGAPRPRL
MVLTSEKGWTYSWKWKENNSTRDCHVNCEVDRVWQIVKGDLTEWFSSHGRTDFRPKRRLL
IGTPGIGKSMAASSYLLYQLLQYDVEKLPAVAYSFGGNTTYVFDKTIKTVTRYLGRGAFE
DFLYDLRHLKMKGYVIYDLTEKGRPASCFAFFDEWGMIVLSSPKVSNYDNWEKQEGAERI
IMNCPEEMDVKAMCAWMKRDETAGKKAECWRMVKERMEKVGPIPRYIFDANEFIAHSAAI
EDALDGVNSRDGEKHFTHGGVRLWYSENASQKLVRVVRGRGEVGAEVFLNAPISVCLERR
VPHYFGKRDE*
>TCRU_6807 hypothetical protein, conserved
MHVRLPCGCGVRDPYFTLFGAAEVDGEVMQSRAARAWWKRLREPVDDPSKSKCTMRFGST
GKEETVGGLGELQCTRLQKMACVAEFTLTATLGAFSRGRESFLIYLVVLDDTRRGRHFHF
IRGWRTGDKDERERRLAKSAAAGTLTRHGIVCTTSCISSAGCSLRRSLARV*
>TCRU_6808 Enriched in surface-labeled proteome protein 1
MEETVHRPNSAGQLPSEHEPLTNIGAGGGGVSSAASTATTPSSDFAQTVATVGGDTVRRN
GSPQTPEVSVSSGEDGETVEGTDLQEGILSQAGEVNSTALNSSLRKLSQGNNTDAGTMHG
SGLPSLLLLLLGLWGYAAQ*
>TCRU_6809 Enriched in surface-labeled proteome protein 1
MVFGLSYDSEKKLIVFSGGGTNTEDQSVTLATETTHHLAIVLQNKKQGSAYVDGQRVGGD
EQFDLKDIERSRGISHFYIGGDGNSAGDAGSEEGVSVTVTNVLLYNRPLSSAEIGALNPN
KAFIPSLVKEPTKPLTVSSASVVTPIPPVAATAQITGTSSTPAGTPLTEKGQSMGSSGAD
SGDASASAVSTVSIPSAENDSVKKVASGTSPDGTQTVGGGSTADGEPKMEKREGGTDAQE
KEVQPLNRDVNATALNNSLGNVSQGNNSDAGTMCRSGLPSLLLLLLGLWVFAAL*
>TCRU_6810 hypothetical protein, conserved
MQRGRGVLHARDGVGGPRLVLVQLQGRMAWRVVSSLRGARHGCAARSGESRGRRHELRGG
PDAEDPHAEHVEDAPLLRGCDVQRRGCCADVFPQQHAAASPHQHHAHWMHIPRRGRAAVC
WGC*
>TCRU_6811 hypothetical protein, conserved
MQHDRALQRRHVRHVDEGVGHQARRALAEATNPQLRATRKHAVAQRHAQRVGKRVHQAQV
HRHSDRPAEHHRVEARRRTPAANRHRLRQRHATHAALRTATTTTGPRNRHVERQARLAHA
AGTAAAHAVGERRRQRIKARQRGRTAVARHHAHGGQAGHAVVAAALQHPAAGTVALHRHD
TARDRQPGDKRRASGSAARNRHDTAAQRHPRQRRHRRRLAHRPHVVQLQPPADTDRPTVA
AHQRRRNRPLDTHEAQHRVGHREALAKHNAAAAAHNRHVRHGEHRVAPQTETRRGRHMHR
GRGRTARRLQRHAVKHHRARQQVHAAANVHRRPARVQRPQHSVAHTQLRLQQRRRVQHKR
RRHRVRQPAQLRVAHWSRRHNRRVADRHVRVCRQVVHKHERAVAAGQPAHAHLQAPVTRR
LAAVAPHVDLRTAVAHTIPQLDAQRAGKHRRHVKHNSHAVRDVNAVHQHRVHGAANRDGS
VHRAAPQSQHHRMRRRHPRSSSSQRQHKKKRHTHSRNDHAPHTVPAARTRTHRTPHPQTN
QIPIELSWCVALAPSTVAPVQQIPSYKWQIKRHYSDRSLSHY*
>TCRU_6812 Enriched in surface-labeled proteome protein 1
MAKHRNTDQFGTHRISHFFFGAGNKEDEGNSHVTVADVLLYNDALFGDDLKNLNARTVPI
RHPAAEELDTAVKVTGTEEEKQKVRQLTTSLADVEDPRIAQPTNSQSVRVLAGSESSAEN
FTDGLRPRTAASNGTSVPETNHPASDGSMSLDDRLALVTDAKLILHDLRGDSTARVRVSR
ALLLILGLCALVVVL*
>TCRU_6813 Enriched in surface-labeled proteome protein 1
MRLTEQLERIKCAVKTWKELDDALGVPTEGLVGFLSSTLDGTAWRDEYLGVNATVGGGVT
STESGVALKGSEAKWPVGDMGQTVPYYFTNNKFTLSATVVIHEVPEAGSSPVPLIGARLN
DTASTVLFQLSYTSERNWNLTLHKMDFLVKPSGDVGN*
>TCRU_6814 hypothetical protein, conserved

MLRSTVKDSRLSTSALLPDRIRYASVKEREKAFSKHYGHFCAYYKSSCFGSVMLTRLAIS
TVGYFGENFYPAYVEDVDHSLRLRLLGFQERNVLCGKFVHRGSSSIRSSNEMELPDALWY
RRVKSLMTNQPYAMMKWNRPRACSGRYKGPYDGMVPLDVWVKDEARIQRIRAHWHDEEQG
VLEVECDRILLHPFTTKGRWTGASRKFCVFIILFYFLLQILKVSFFIYIYTNDI*
>TCRU_6815 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGAGGGCEEGEVAVVAGSPGNVSVVTPNSQLELPLLEGQASN
IQSPKVGKELPTVAGVSSEITEKNNAGGGGGENEELQERQRQGQAGGIRHDGQDGAHKEE
DRQEEQEETKKKRVKDQNSHESDPVKLAELPLNQIKDSPSHSSNDVEKSDKKISGIATPL
GNGDQLQDALRPLPNASTTLSTEENTSFYSTGSGGDDNSHEKNNDANNAPQSSSTGIEQQ
DTEPHGKSITFTDSGEASKLPVTTVTKTSDTVAAGGTPSAAMALQHNTGMEDIPATPDSS
QPSTGGAEQPSATPDREEASDSTENGISQSAGSATEAMTTAKTNDTTTPVDSDSSTAVSH
TTSSLLLLLHAAAAAVVAA*
>TCRU_6816 BNR repeat-like domain containing protein, putative
MSRRVFDSTVLLLFVVMMCCGSGGAVEAVESKSGEVQLQQWVDIFLLNKTEVVAKNGSAG
GVKFAFISPSLVSAGGVMIAVAEGRAKYNEPHKSGWFDSSDIVTGYINATWDWSTLFGKV
SESTWEAHTVLGTTDGTNRVCVVLCPTTTMKGNKMFLLVGSSAVFYESGGNWS*
>TCRU_6817 retrotransposon hot spot protein, RHS3, putative
MIVVSSPNLDNYDEWETQVQASRIIMNCSDEMDVKAMCAWMKRGLKPDKQAGYWRMVKER
MDKVGPILRYIFDEGSYKDRLGAVNGALLAIKDTDVGEHFTLRGSRLWYFEDPSQKLVKV
VREITKKGVEVFLNASISADIGFRIADRLEKKTGAKNLLLIILGSHGALASRALEQLGLR
AFMYGELVSALVKGLNELRPPERNEARDSVLKVNHQGHPTRAVGLEELQGGVTRIPMEYG
VLYLPKVENFPLVDGFFFVDSPWRTLVGLQMTTASAHHTTTSTVRQFTECLAAYFEGWDE
LSRDMSWEMIYIKNAFSKKISKWQRCDVVNPNNETDAEKKIVAFWNKEVHQYQFMLTRDF
LSKITEM*
>TCRU_6818 zinc finger protein, putative
MDDGQHTGGLALFAAPQDSIRYSEGSDVIHVLIYLPAARCQVILVAVSGGETVLVLAKRL
VDVHFRLGRGSLKSIRTAAREILLRKLRVSSESIVVENEANASDVASHCKHLVLSTLSAS
ELQHAHDGDPMEDFFL*
>TCRU_6819 Glycine cleavage system P-protein, putative
MAKTRAEPLKIKVVVGDPNLIDWSDSSLCGILVQTPDAMGMLHDFTTLFEKAKQHGVVSC
CGADLMASVLLKPPGEMGADVVLGSAQRFGAPLGFGGPHAAFFAVKEEFKRLIPGRVIGI
SKDSTGCPATRMALQTREQRIKRERATSNICTSQAFLANVAAFYAIYHGSEGLKEIASEM
LSKAKILSVGLESVGHTVVNGAFFDTITVNLKGITPEEYVTCCV*
>TCRU_6820 Retrotransposon hot spot protein, putative
MGAGSHLLYQLLHCDAEQLPVVAYFIAEQTFLFDNTTKTMSEDVVEPDTLNIVDGLLDRG
FKGCLIYDVAMKGCQPSTALSCKGWGMIFVTSPHAS*
>TCRU_6821 hypothetical protein, conserved
MITMTGRVLLVCALCVLWCGACGGGRAETIPPAPPGSASDGNPQKEGKATDVAGEGVQSS
QQAELQETPVPPASGSQELPVRPSPAPKSGGGAPDSANTTTEKNNPNTESKKEEKDRKKE
EEDNEAEEEED*
>TCRU_6822 Mucin-like glycoprotein, putative
MMSCRVLCVLLEPSLMCCFLCVCATAAATEVRVRSAGDGPVTAGHMWAVMAAESDHVADD
SGRNVNVNSEGSNTQEDEEGGRDKAGDGSTTTPLVPPTATTGQDQSSTDPPRSNTSDPSD
TGNASDSQTHASGQESLGGGTAAGKTSPLPNSSQQAADGVHAGGGSSSQGSQAPGQTFTG
KPQVSETAKATAQGGGGGGPEAQHEAEHTKKDGGGNDLGKNGNEKGEPPAGSQTAPRPSS
GGNANVAPNPAFSIPLPPEPKSTSEANGTGESPHPTDNEQTQSTRTDTAPSTAQTKNSPN
SKAQEPESEITTTEGPSDTAKNTEAPTTTTTNAPSRLREVDGSLSS*
>TCRU_6823 hypothetical protein, conserved
MVAPRSWREEGGENTLHSGVPLSLLNTMVHELTDDDKTRVAAQQDPPSVLQEELAKRAAR
FGLAVGGHNGNGGDAAAGDDSMRKRMERFGTTDPPPLPVLVVDEATLKSREARFKSEEEK
KMDEAMQKRLARFGAAPAVVELKLSEADREAMARRESRFASC*
>TCRU_6824 lipase-like protein, putative
MRSSVFCLRTHTQLLWRARSLASCVGDKVRVFPSDFIWPLFLLTGNYVHVGVIAYRTFIH
FRLRQALRITIGVPVSAIMLYMVYASWAWYPEPVAAIDTSSVAGCRPVFSSTAELLDFAG

TCSRRYHRLSEKGEDMNSACRNELLGDMLAILRSIAAIEGSFEERELVTASLTVMDPSRG
VEQEASPAEVILRTVLFVSLDQGWFDIVEEARKMYGNLVRERPVPPQANVTSAVADLCAL
SYELERCTSPAEVTMPQRQRVARAIDAFRPGKSVRERCTIAAEIDVLPLVDLDKTTRCLM
LTRHSPGRRPQLIITFVGTNSVRNWWTNLWCTMRELPPVFGVQAYVHRGFLELLESIAFE
EVAKDFDQIILIGHSMGGALAQLAGLYLANERPERRVTVLTVASPRVFASRQWFWQRIAG
WVFILNGKGNDAAIALPSNCRHIRTFMCADVVPRLPPAFLGYQHVGTPLPLHTGCPTRMS
YLGWGLWSCLFHTADMYKAVLERPAVAQLHRYEAMSTSCAR*
>TCRU_6825 hypothetical protein, conserved
MLKLCFIIRAAAASSSSRAAVGCSGGYERRHETFMRFLTANKAKFDGVDVRPSAEQSRGL
IATRKFREGTTVLSVPMHIFAISAERLLEGEHLRSLHPPTLDEVQSFLTACSIKDPVLCE
QVFLALLVAGERLDPKSFFTPYFDSLPYPAVNDEAVMSLHKDVLDPMQLVEWDDHQREWV
TVFRTLARRWGDKAPPVELCYWAWRTVLSRMHLLPDRGLAPAELGSTLNYFALSTFERAE
RQTRLLKRIRAMVGAVFGNGNAADEYRLVPTLVPLLDMTNHLPSGNVSVEVQPRPEVGSC
AELQAVREIQAGEEIGLCFNRSHRPAFTLYRFGFLPI*
>TCRU_6826 hypothetical protein, conserved
MRWPCECLKKSFASKKPPVTPVPLKVIACGREFIISVDPATSLNSVLHGVAERAVPNASR
NSAAPALFLDDKPLEGDMRVEQLPNGAVLHLHFGADAARQFQDDGAKGRSASSSISPPSV
AANSNRTSLLFSNLAVMRLVATPLSASVALISPELSKHRDVSFLRTSPDFSHVMQQWSLV
LPHNGVRTTVPAAAVTVLSSSPSPDPVEIRSQRLLREGRSIPSLERPDPRAVSDDYVVIV
VGDQTAAAIPGEKKDKEEKVGDAVTCAASYLASSETTASFRRLRVCRGYPVGTLRELFAP
HPSQRIFMGDTAIDDERLTFEALGAGPLQRFSFRTELPRKKKLSEESAVKTSKKDEMKKN
KGADDAAALLRVGTLTECSGGGIECDRIPVAADKERSVSTTRGGEREERSSTDADKKRAA
RKKRGGNGSRKPRPASKVHSLDMGVDGEGARLPIKYPVLVGHIDAADGRMNMTGPGWGSG
SRGRDLSPSPQSLRGYGSNKEEEVGTVRLAENESARSPNCFVPLKAGPLNDDKVREEIYR
QRLPTPPPSISPPLQLPNVVLMHEGDDAKRPVLKSILCNVTRAPHGGRKFVVEGHFQRKE
SLWSAAGSENSPPFAQRPPHKWEGTEPNGRGAFPSGVDYAGGIPAAGGNLPFRPASILLT
GSFLKRSRGPASLPGGATGGYCRHRQGSDPTAGVRGGEGDRVF*
>TCRU_6827 hypothetical protein, conserved
MDNAVSNCCDWKTPFYPVSADNAGAVAGDAALGASSVASSCRKRSRMEMSAFAYWMQNIR
HTVESLVSKESGDEEFSWKRVVLETFRVLRGCWLFHGLPQDTFEPAHSLSQVAQHLLIAY
GGYGLTDDRQFIFLQGEQRMPYVGFLLVALQQLLAEHGDSQWDLQPAAVWPRSSPRPFKD
CDMRLVMVGRGGFDRSNGRVDAEGTADGDFSASGFLCGDHELMSMQAVLHEAMGASNDIS
VVLLANCLLTEDGSFSLVRGLHANCFSAVCDGDGLMCLVSGADVGTVAAAAAAGKPDLES
FLSHSASCGCFRTRSVYAHALLLGPMGPLFIHLRQNGHHHNQSGKSTTGHFSGLKDELDE
AHLCEWLQCFLWVPQPTIIVLWDDSDRLTKTGALVSRLVGLSDGGSSLWSGYRRFLLEAD
NNNNDACNSSSCGKPPTVYVRDATLTMERATSLRVDAGVCQVWHVHISPHC*
>TCRU_6828 axoneme central apparatus protein
MPNRQIIQVFEEYQRARVKFVQTIADLASKPQHIEALQQAGVMQLLRPLLLDSVPSIQQS
AALALGRLANYSEELAENVVSGDILAQLVYSLSDQSRFYKKSAAFVLRSVARHSPQLAQA
VVDSQAVEALVGCLEEFDPTVKESAAWALGYVARHNAPLAQEVVDKGAIPPLVLCVQEPE
LSLKRTAASTLSDIAKHLPELAQAVVDQDAVTHLAPLIMSNDSKLRRQVCQCLAQISKHS
VELAELVVEGEIFPKIFTLLKDSDEVVRKNAATCIREIAKHTPELAQLVVNAGGVGALVD
YTSESRDSARLPGIMTLGFISAFSETLALAVIVSHGIVPLADALEKEPEDHIKAAAAWSL
GQIGRHSADHAKAVADCNVLPRLLDVYLNPKSSEDLRMKSKRALKNIIQRCLQLPALEPL
LHPDAPQKVLKYVCGQFAKVLPTDIAAKREFVANRGLATVQRIRPEPGSKLAEYIQSINN
CYPPEIVQYYSPQYAQTFLEKIENYHVQQVQQS*
>TCRU_6829 hypothetical protein, conserved
MRPNKVDEALQLFAALQDTLQIETRQRDANRVVRAVSAEPSLRGLQRRRRSGRETRAPAS
SRPSSLVQSASSATDLQRRLEVADGIMRRLHAKNQLLLQRLTALQRDEGEGNEATVRRLR
DKLQQREEEVRRLRHRLREFEKRAEDSSRGTSGGVRGGSGGDAAVSLLNLRVKQLEEQYN
RLLGRRVADALRTESAGKHDAELRELFSLMKSKIIADARHHEAEVLLLNEALLESERRLA
TIPSGGTGLDV*
>TCRU_6830 hypothetical protein
MPRSRAPLWRRSEASSYLVRSPSTASGVENMDNIVSGGYSKRRKRSKDAPALDVLSLVPS

DDSSVVTATPVTSAGVFVTPSPILATLSTSEWLMLSRNHCESSHPSSMEKPLSGVIITAE
VGGWLRVRDQRNGTIRYQRRLRYVSNPSCLCWSLSFCCIFFVGQQCGLLTMLQLKNESII
EVADCVLHEAPIVAMVRVFLNVHGGAKGSVAVEKASGTARELLLTLDANGVLAAWKTADL
CCLQTVQLSHPPFRCLTSDESLPGCVFVPGGIEGALAADGGSGVFDIMLLEYPHEVGAAW
RSLMTYGGIKAAVISMTLAPRHISSGTAQQLTLWGGTETGAIYMWDVGSGTLLRRVDEVT
PSCSPIHYLYCALHMDPRHMWVCTRGGSVTLWDTSRLMMLSELPVSYPKGPAVSRPSSRS
RHLHSGGSGTDADTCFLRHLVSDASEAPSHFTLFVRPIEPVVTLRLWAAATDGTVRSWLC
QTTLSGLSAGEKSSTLGASHSTSHAAGAVPASVMDRVSNVIEKETVRVFIEGKARLFVEE
TTALRNDVSRLMREVAALQARNRVLADALKKAIGRIASRTDDDNDVSKKKPHVDSPLSEA
SPPRVTGETPHTDSIRVVLKELHSRLQDAFDESEKLAAEKMALRLQLTDKTQRPESSQEG
PAALTSVKSSQQEAVIRGNQLTMGCLQEELAICQETSTSYMHHWQEEQVRREAAERECEL
CKQRLLTLEKELDRARTLLSLHAMDASGGQNNTRQAVQNEGIDGGRELEKLAFCSGALSG
RIDASIDAAAAMHELESAQAELLRRERRLAEAQERLQEMRRDVQRSREEVDAKAAELHHT
QQRLVEKESILLEHAERLCALEEELRRKERCLLLWRGYSR*
>TCRU_6831 pumilio/PUF RNA binding protein 9
MEIREVNFNARVLRGKTDPPMATYISPPRPNKQKLPPPTPPQSQSIDTEKNMYDASSMFS
YATAADSLRMMKIDGRNYAQCPCATCTQYRVYYAMRMAGNPELHFDDSYASSTMCVPTMY
SRKASQLPPPPPPQQQPSTVSTTMPRRDVAPVLTIGTQRPTARPAPHACVFNQSIPQQQQ
QEQTLKQHSEAAVSGLTTHGAIFPLDTAEEFEHKCMGRVVELACAVEGRSMLLAAMRSQD
AMVISTMVNEIIADVETVALDNHGCHVLRALMDYMDAEKTALLVSSFNETLVLNLCTVSQ
YTRRILQALFEKPLIDLQPIVNVLASNAQYLAATQQGCISLMRVFELCNAEHKAQLMAPL
VPLFTHISLDPFGNYVVQCAIERSEKTVAAQYTVSCFAGELLNMSCNKYASNAVEKIIKV
CGDVPAVRRLLMDELIFNPAALLQMVQDSFGNFVVQSIIEHTDSPTELKRICDRLRPALP
SSPYAAKIEAKIRAKAPTSQLLQQHHQRRQQTPRQSQTRRPRQEPQQRR*
>TCRU_6832 RNasePH-like protein
MLFSPAISEAEIRAVQDGIANDVRGDGRTLTQRRPFTIRTNYSAGASIVDVEYDGSCVEV
QCGATTVLAAATPSIIELSESGEAASRKRMRGPLFISIDAVPAVVDYYAQALRNRGGRYR
LAFLSFVATTISQTFGAEGVTVREQLGLAEAEIIDDGDDDDAATTAGGVNEEGADEGLRQ
GRFPAEEEGDSGGGFPGEELYIGGGYAFRIDVDVHVLQTNDGNLPSIISLAVHAALKAVK
LPSVTLHEASGGVSLEVDRSKPFCRPVDWSRLPVLTVLLISPTRHYVVDPTPLEELALPQ
QLHLAMNAAGHVCYMRYQQLPSRRGNAWRQEKGCRARGELDDTAGSFLPAGMNVPDLAAM
LHDVSYICQAIISECDEALHNSR*
>TCRU_6833 coatomer beta subunit
MNVGSNQEVACTLLVGFDGSSVNTKDLKAALEKGDINARAEALETMIRLHLNGEPQNHMI
MSVIKYITPLEDHLIKKLVLYFWEVVEKTDKNGKLLSEMILICSFLREDLLHPNEYVRGL
TLRFLCKVKEKELIEPLISSVVQNLTHRVTYVRRSAVAAVHAIYKRFPDLLPDAPELVEK
FIGDENDVSARRNAFDMLVECAPERAVRFLTGFRESTNMADAGAAFQMSVVDFARQMIRA
NPYDKAKYVAILFNVLQSKNPAVRYQCASTLLSLSSSPTAIRQAALTFIDLLKTHSDNSV
RLIVVDQLDGMRIRFGDILQESLLDVMSVLANSTTEICKKVVTLAVELVSNKNVEVFLQA
IKKELLRSQSEEDVLDKSSIQEYRQLLIRAIHTAVIRQPQMAATVLPMMMDYICDSSNGS
QEVISFIREVLQVQPSLRAGTLKQLLEVFPMVTSPGVVRTVLWLFGAHVSSADEVLRVLA
LLANSLKPLPLTPPVPPAASVNGDANGVESPVMRAVTTVREDGTYVTSYTTVPTGTMAAV
AAVTDTTEDAGVVPAGLRLLITKGDYFVASALASTLSKLLIRLFTNYGSAVDMAVKSKAQ
DDALMLLHEIIRYGTAPDAACAMDEDSHEHIRLSIITIANPQSPFLQAFVDDSYKALNAV
ESTVVGTAVGETLPSDWSKAKEPTAFCSIDTPIIFTQLAQGKDAFLELEATDDLGSAIAN
ASIDKTEEFLKRLEKTIPLSGFCDPVYCEASVTVHQFDVSVDWYLVNKTSNLMQELTIEL
ASLGGMKLCERPQVHSLPPHGSLKLRTALKVSSTETGVIYASVLYDAPNGERCCVILNDI
HVDIMDYIKPASCLTTEFREKWGTFDWENTIAVNTDKTDLRDYVEFVMKETNMQLLEPYQ
DVDEEELQGLSPTDEDGGYGYVSCSLYARTVFGEDALANVSIERDAQGRISGVVRIRSNT
QSIAYGIGEKLSLLDKGGIK*
>TCRU_6834 beta tubulin
MREIVCVQAGQCGNQIGSKFWEVISDEHGVDPTGTYQGDSDLQLERINVYFDEATGGRYV
PRAVLIDLEPGTMDSVRAGPYGQIFRPDNFIFGQSGAGNNWAKGHYTEGAELIDSVLDVC
RKEAESCDCLQGFQICHSLGGGTGSGMGTLLISKLREEYPDRIMMTFSIIPSPKVSDTVV

EPYNTTLSVHQLVENSDESMCIDNEALYDICFRTLKLTTPTFGDLNHLVSAVVSGVTCCL
RFPGQLNSDLRKLAVNLVPFPRLHFFMMGFAPLTSRGSQQYRGLSVPELTQQMFDAKNMM
QAADPRHGRYLTASALFRGRMSTKEVDEQMLNVQNKNSSYFIEWIPNNIKSSICDIPPKG
LKMAVTFVGNNTCIQEMFRRVGEQFTAMFRRKAFLHWYTGEGMDEMEFTEAESNMNDLVS
EYQQYQDATIEEEGEFDEEEQY*
>TCRU_6835 alpha tubulin
MREAICIHIGQAGCQVGNACWELFCLEHGIQPDGAMPSDKTIGVEDDAFNTFFSETGAGK
HVPRAVFLDLEPTVVDEIRTGTYRQLFHPEQLISGKEDAANNYARGHYTIGKEIVDLCLD
RIRKLADNCTGLQGFLVYHAVGGGTGSGLGALLLERLSVDYGKKSKLGYTVYPSPQVSTA
VVEPYNSVLSTHSLLEHTDVAAMLDNEAIYDLTRRNLDIERPTYTNLNRLIGQVVSALTA
SLRFDGALNVDLTEFQTNLVPYPRIHFVLTSYAPVISAEKAYHEQLSVSEISNAVFEPAS
MMTKCDPRHGKYMACCLMYRGDVVPKDVNAAVATIKTKRTIQFVDWSPTGFKCGINYQPP
TVVPGGDLAKVQRAVCMIANSTAIAEVFARIDHKFDLMYSKRAFVHWYVGEGMEEGEFSE
AREDLAALEKDYEEVGAESADMEGEEDVEEY*
>TCRU_6836 Enriched in surface-labeled proteome protein 1
MGAKMSDDDKNPVLLGLSYNNKEKKWTLLCGDGKNTEHSSTWETQKDTTRYQVAIVLQNG
TQGSAYVDGKRVGEPCKVESKEDKKISHFYIGGDGSKKGSQGGVSVTVRNVLLYNRPLDD
NEITALNTIKVPITPPKETSAQEIVVPSSGRTPQAGQEPLNGDEGVGGGSASPSAVSAST
ASSGSGQSVNQLAPGKPPDGNADVDGAPSSSGNPTVGEGSADTIQGDGPHTSSVGNTPAA
ADTNFLTAETVGHDGPALTRDVSVSSGADGETAGGTDAQEEEGIHPQDRDVNATALSSSL
GNLSQGNNSDAGTVCGRRVPPLLLLLLGLWGFAAA*
>TCRU_6837 hypothetical protein
MNYFPRQQQKQRQPKQQPQKQNQQQQQQQKQKQRQKQQKKLHQEQKKRQQKQQKQQRKQK
KRQQKQQQQQQKQPNQKKQQKQLIQQHQEQQKQKQQQQKQQKQQRKQKQQQQKQKQQQKQ
QKQREQQKQQVQRQKQQQRQKRMQQQRQKQQRKQNQRQQQLKQQ*
>TCRU_6838 BNR repeat-like domain containing protein, putative
MPGAAEGKGSLGVVLRRTTTTKGHGVFPLAGGSDVSYEGVRWREGGLELKLVVGDVTNPT
GGKRSGRIEWGDPKPLPKLISSPSHEGEWTEFIASGGAGVVMEDGALVFPLMAKDEAEDV
CSMIIYSTYNGSAWAPSEDISPA*
>TCRU_6839 hypothetical protein, conserved
MAEAASCLDLKASFFQVPSPRETRHLFRCRVENGTLVELTRLPMGYKAGPEILQIITSAI
AVVTTVVHRLWAAPPSVRVGVWIDNIRIAGSKSDATLWEAQVLRNADSSNATIGKNGNRA
LRITPFWGCNLITLTGRYP*
>TCRU_6840 hypothetical protein, conserved
MMILGLQKIAARSETKQARPLTEEEMNQVIRSRTDWKERVVLRLAWITASRWSEIAALTA
KNFTLEPDGALILYWPVAPKTAKADPHRASRFVKIRGQDAFDIIKLCRTLQENEKLTNLT
TAQVERALAPWDATAHSIKRGALRHAAQIVETYNLNPHVISQLAKHVDPFDLPQNTVRYL
GRYTTMLTQVSSLVALM*
>TCRU_6841 hypothetical protein, conserved
MRAWLWGSASSSLSSSTMPEANGSSLSLEDRLHRVTANDIARVTPSDVEQLKQKMSLEDL
HRAMRVLLEDNRYAEVLDRATPSSLRRAAHGLSATQRSFLLTISKSNLLALYNVLPHVTE
SHLAEMNAIFRGAS*
>TCRU_6842 Transcriptional repressor TCF25, putative
MSARQLRRLQNLVRASTGADEDAETECPSKMRMPKGAKRSGRHQKLTSQKVQDENDAHKQ
QHPQMEEKALTASPVDKQDRQERTGNGSERVAFAVEGRPGAAKRANRAVEVEVGAVVVGV
QEKEELADERRKKKQRNKNARAKRRKEEREDELLLEEALRQREEDAFAEGGRFGTGSGRS
EEVDLLELLSVCDAKKLDTREERIRCFGARAVEDIGDGRVPQRRAESRPTSLLFAEHAQF
VPRFFHSLLATPNRYCWPQYDGLGVTLVAKGTQSARNNETKVNDGNTNDGGPLLYYLDDS
SAETRRAEAALAVCGSMHAGVEGIMTCLAAAPYHIPTLIIASNLFETMGNIPRAQEAIDI
ALYHVGVLLSRFPVRQTVRRRSLPFGVTSNRQLFQVLRCGVHQALRKAATRTAWEIAKLI
YSLDDTDPLGMLLQLDYLALRAKQWAWLVQVSFIVARELERHAEGKVDDTNDAWSNRKLA
LALSTLPGFFFSAALAKYFLEREETTSAISGVSNKGKPSKVLRELTPTQLHAFRNTPPAS
VMLAHAIGRFPSAAVLIVEKIGGQSVVSSVPVSWQDIVKAHELNTEENSLHVASMWVARN
AEIWKAADPCAFLRRVITEDDGLWLKSHRADIGANLSASAAVVTADSPHLPTPWRHASLT

EEDILCQTLTTIPAHLLDPNEITEEDLRDEVRRATRRELTPLEQLTLLRFESLYGPLSPS
AISPSERLSRYNAMFEEEGRVRQIGEDHNPLSLFFRMFLPWNSTREMALRAALDTAGIPD
PVASLNHQLRMEEELSWQIEMEEEEEEEEGEDWETEDSWYADEYMEDTDDEDA*
>TCRU_6843 hypothetical protein, conserved
MTEYVTPGRRTHTTAARANAGGGGSAGRRVVRSALELLAETASPEILRGKTSSSNTVAPA
KFTVTYATAPALSLGATAQQLQKEQQLRRSLPAGNDVVTTEEPSTLLFLSPSSAAGGGDS
AVKKRLFKKKKKTVRLSDSAKKTAKAVAKEMWDLEKSAGPGTASDGEKEKQEIGGEPIAV
GVSENELHKKGRQLTKNEPLFTEEEVQERILEALKAYEVRRDAEEESVLQEVGHEIESQN
ERYEKLLREKQASAEECDALKLKMEQLALHCEALQGTIAELQQELQETRDRASRTEVELC
HAKDEKRLKSAELQQELNFEKAQWKLAQEEMQRQITEFEAQLRSRTFEWHELQETTRAKE
NKQAWLSEQLEACRTELEEWRQRNSETQATTVELKELIEAKEALIRQLQLKVQEAEKSAK
RATTSSRDEQTQLESRLRSVEEALQQQTDEVRRKMHRVHVLETELARVEEAKKTQQRLIH
EATNRFFALHSTLETFVGMFRNGCSTRASPRGLRDKLFPASEWCDAHSGAVEDLSATEND
ALCYGQKDDDEEGCVEDANGSFFELITCKELRDDLRQVRFRLGGNKVLTQHQRQNAQRLR
GNTHPTASKKFSNNNGDEVDESGRLQRCHRLCERLLETLRRLYLQHRKEMQRRLQHMEAR
QAEQSKSELKHCQDALAACQRSLEESKQRERLLGEECCQRKSEVKRLEAALVELQAAEQE
VRVQQKRSTDRMEELQRERGILRIQLDASQRDCVELRERYELVREEAEEVRERVRLLEKS
QRLQEEAMEAKAKVLARLARCTEKLKKTEEECKSLRDENEVLSNKMKSMLLQLQTSRVEQ
RNKSTTASVRQQQQQQQQEELNKLKKEMGELRTLQESTAALHAKESAEAELSVKKLTAQ
NEELREELAKRQRALADALSDVELQKRAEATTLRTLVSIHQAGSEGSNETCADGNSPRGV
QQRLFDASLIIQSEDGVTENRGEISIFDLRGRVVSLAQRAALELARLREAIPPGPHAERC
ETLESFRAAEKVAWEAAQRSAARRQPCIEENGEPVPLAQPPSRRTAPLLRSSFQRQQQQL
QQQNKKNLPCHMLGTPCRRSPAQNSPSPKKVGKDVLPIGFFPRSHSMFAVGPDAMKRTAG
NERSLPCRGASSSSLTSAGGVSRSRSARGVLDGSSSPVRPPMLRATSVR*
>TCRU_6844 hypothetical protein, conserved
MSRGNATSSALQQQAKTERIVRLEVQRRHAKGTLRVIDAMIRDVDDQLLYVAQFKKEWLQ
HRKELEAARQELLAEELTRRQQFEKHCLHTLHQLACGKNTTLRAKILQQNGGVTDS*
>TCRU_6845 ankyrin, putative
MASMKYGEVALNSAFREACQHGDLPAVKDYVSRGCDLESASSDGCTGLWLAAEAGHTEVV
DFLCSIGANTNVARSPGGATALFLASQNGHIAVARLLLQFGADPNACRETGATPIFIAAQ
QGHLEMIQLLIHSGGTPTAPNHQGVSPIMVAAHQGHVGCVQLLLEKGCDPYEVAMGRNTI
EWAEASGNGKEIAQAVMQGAVTQLSVEKQEDIASPSATGGTGSNEGGRKEQGNGISSRPE
LMRPETGGTEGRQQDVSVVSFSMINSVSSYEPQYLLRGRHTAGALSTVPQGTAREAGKSE
RGRSKASDLYSHDGFTFRTSASRQKVLMKRENEANASFMAMQRSMFQKHHARRVVGEPRP
IDVQETQARWDIWKRTLYEQIRQLERSGKTSSGDFL*
>TCRU_6846 P-type H+-ATPase, putative
MSKELADMMQQEEEEDVPLLPPSKGLASAEADRLLDHHGRNELPHKTTPGWLIFVRCLWG
PMPMAIWIAVIIEFSLKNFPDGSILLFIQFANATIGWYETTKAGDAVAALRNSLKPLATV
MRDGMWQNIDAALVVPGDLVKLAAGSAVPADCTINEGTIDVDEAALTGESLPVTMGVDQM
PKMGSTVVRGEVDGTVQFTGQKTFFGKTALLLQSVEADLGNIHYVLVRVMFVLTSLSLGL
CIICFGYLMGHYKMNFRDSLEFTVVLLVVSIPIAIEIVVTTTLALGSKELSKKKVIVTRL
SSIEMMAAVNMLCSDKTGTLTLNKMEIQEQCHVFSKEYSRESVLVLAALAAKWREPPRDA
LDKMVLGVADLDECDKYTQLEFVPFDPRIKRTEATLRGPDGLVFKVTKGAPNVVLQLVHN
RDEIKAQVEGIIEDLGRRGIRCLTVARTKEDQQWHMAGILTFLDPPRPDTKETIRRSREY
GVDVKMITGDHQLIAKEMARMLNMDTNILTAEGLPKFPATGDPKDIPSTLGDSHGDMMLA
CGGFAHVYPEHKYLIVETLRQRGYTVAMTGDGVNDAPALKRSDVGVAVDGATDAARAASD
MVLTEPGLSVVVDAMLIARGVFQRMLSFLTYRISATLQLVFFFFIGVFALPCQDYGIDDP
DFRFFRIPVLLFMLITLLNDGTLMTIGYDNVVPEQRPLRWNLPVVFTIASVLAGVACVSS
LLLLWMALDSHDTSSWFYNLGIPPVSEGQIVTMLYLKVSISDFLTLFSSRTGPNWFWSFR
PSLVLFLGAVVSLATSSCVASFWPDRKMDNITVIGLSHGDGTAHRLLPLWVWIWCIGWWF
IQEIVKVLACKVLERFDIFSYRTISEGKWQPSSKKRWRRRSRGMSLGATDNVEQPLLS*
>TCRU_6847 Enriched in surface-labeled proteome protein 1
MLLVVMMCCAICGAVQADEDLSAVPKYQLEDIADGNLVSFGIPGLLKVGSGVFAVAEAQC
KKKDGETVFTGIASQLLTIKDDNTPEEVLKNARVIRVLEKGAPTSKRVDVSRPTAAVKGN

DIYMLVGKYSRNGGQESDAGDWGLLLVKGTVSDKESNKQIDWKDTNAVPKTPLGEQPSSL
TGLIGGGGSGVKMEDGTLVFPVEGTKERDDAEEDGKTTTVSLLLYSSDAESWTLSKGMSS
DGCSDPSVVEWEDKLMMMTACDDGRRRVYDSADKGNSWTEALGTLSRVWGNKKGNEKGVG
NGFTTATFGAGGEQKNVMLVTLPVYPKENKRANSIFG*
>TCRU_6848 hypothetical protein
MFQKRILVRRGVARRGTRAPSALRRRRAVSLHAPGPPRHMLKVRKKMGVGRQSTVSDQLL
LLGLRQLVGAARSHKQQEKTQTHWPGHCGIPHQLPHAIQVFPEVFVPNGDVLFHLPHLHQ
SLLPVLCHKPRANIDVQRQSGLPLPKLRRSPHRTAQLREIGLRLHALRQSRVIRVEFFQR
HRKLLHALRKESVTARAPVHIFLINNCRFESAPDDSYGSAHTISSPAASDHQADTDMCVG
ASAASPWHSPNQR*
>TCRU_6849 hypothetical protein, conserved
MVRFQPWCMAVQTRFKWRHKETDRWRRLMDATCIPLDWCGQTRGPTFSQYGGHWTHLLTC
AHVICPWDYPNYYPTEGPTRFVSRITLADTMTQVRLVSMQGTAVYRHFTSNQHVYVHANP
RLDLCVVHPEQNLKRSGEMKMLWMQNEGYVIRPRLELVEPLAVGDHVWIYGMTAHESLFD
EEKAPEPLMVPTGIRAKVHTLTREHFFLDTTSLEGADKGRIGMGMCGSVVMRNGRCVGML
TATVHEESKCKELAGTAMCAYASDIFDFLLEVERQMKEPNPSAQREETVFQQRRREEGRG
QKEWKDWELDHSRLARHIPVPVSMWHMEEKWMTEEDQMTSTVFGRSGVFNQETQENVFGY
DMNSAKTHGDRPGDIAAFSTASQEGKPVMQGERKDYSPTGIYADHEDFKTRDVWDYSISS
EMRSLFDTSVDAKDAHSLNMMRKSLENIRAQRAMEKMKETVLKNPGRSEDPLNVGGMGHY
KGGNDGAAFDPAAAEENTAAAKRKREEAEYHEALRRQHGMKARPFGDEDLSGLWEKH*
>TCRU_6850 ubx domain containing protein, putative
MLGTSFSNNIFREYGVELPMVHDSMDEARREAQRRGLYLLVYIHSPTHEDTHEFLTKVLS
APQVRELFGTRFVLFGASVLELEGRRLEGEMQVTTFPFLAVMLKRSTVLKVKGLLPAEDL
VRNFQMAFEHWDGRLAEEVHQRLEREEKERARREEEQRAHEMRAIDLERIRRYEEKVRER
REREERLQREREAAERQRREEEEMRRRQQQEEARRRSRVEELRAAATARLPVEPPADADA
STVAFISLKSLRGKQYHRRFYRTEKLRHMRDYAMSLEDYDGDGFQLVAGYPPRPLDLDGD
RTFGDVPVLLPRAVVLMRAE*
>TCRU_protein, putative ATP.1
MLRKSWALYGFYKLPGRKSLDEICKLSLLEATPTAQVATIWNEHHKQFVQYWGRVISADA
YDALRPRLQKCSYFVIPVFRMKGLFNVVTNWDKDLVGVAPLAEWQKKQDHAQIDMTIQFF
TEFSRTKRIVLVRCEIKDKIFVRQDCVFITQMLLKYYTLPHLYETWVEVFNKRPHMFDYH
MYLRHMKEEAQRDDIHIEDKKTQMKLDAYGPVIDTPPDAIAQQILGSVDTGVLQGGGTTT
P*
>TCRU_6852 hypothetical protein, conserved
MECCVHSPCGRYLVRYKNYGESMSIDVIPKTSAFEPSSDVHYVAVLRESHVLEITTAAGV
RKEFAGFADMTYNAMIGRSPSVKFFVETCEEMKSRITAEVAQRGHGTSDSIIDESDASQL
SEASRMQRFFTLDYDVDFTRAVFPVPLVQMTTAEMNGTMDLRRMPSVPPTEQQQQRTTPR
HSGLIELGTDNASKPSNAQLQTENEKLRRENEALARLSREKMLEMQRLCEDFQQRVDGAC
EVERLKKKLAGLRARLRQAEAERDEAHAAFMRLKQRTLRSPPRPDRNLHSEKVKRRSRFD
TPSPAPRRSSSRFLVDSPAPRGRTGGRQGRSAVASSRARSLSNGDRNGATLTKKRLWGDR
GSSRCSSTSGSRCSSRGSCERLYRTPTASSRMHQRELPTHAPRRAVFR*
>TCRU_6853 hypothetical protein
MLDDRVEEFAAALSRVCVMRAMDGITLGSGMCTLEELHACGRREMWRERREAEILEQLGA
WQAKIVSDWDARHAEWRRGGNAFREVEDKCWVLTCHFTLMDFVSSPFAKFDGCARLFSPL
GPCGGLFRAIMQMDEGGAERRGQTMALVHQACPATTPEMRRTRQLLVESRRAWRLLFFVW
MRFLLTQKGPPSRENCLVLSSAAEQFLRMQQREFQKTLMAAKRRSGGSLPHN*
>TCRU_6854 ribosomal protein L36, putative
MPARKKEVPKAEAPAPRTGIIAGFNKGHKTTRRARAPSSNDRYALPHKKLRAVKAIITDL
VGLSPMERRVQELLRVGKDKRALKFCKKRLGNFKAAKKRRAKMEEALRHQTKKK*
>TCRU_6855 hypothetical protein, conserved
MVDLHLVSGNLRIQSCPVRFPGTTMDQLLNFGTHASTAAKRTMPRRYKLRLIAQIGAPHH
TMRSFLFGYVHSVSLYCGDAIVPCLVPTYLHNMEVRYRKGCKTSLGINAPTEDASVYLKA
NPPPLRKIFWPFALTQYERLMRLRYIEDVRGAI*
>TCRU_6856 Glycine cleavage system P-protein, putative

MVETKAEPLKVKVVVGDPNLIDWSDSSLCGILIQTPDAMGMLHDFTTLFEKAKRHGVVSC
CGTDLMASVLLKPPGEMGADVVLGSAHRFGAPLGFGGLHAAFFAVKEEFKRLIPGRVIGI
SKDSTGCPAIRMALQTREQRIKRERATSNICTSQALLANVAAFYAIYHGSEG*
>TCRU_6857 zinc finger protein, putative
MDDGQHTGGLAFLAAPQDNLRYSEGSDVIHVLIYVSAARCQVILVTVSDGETVLMLAKCL
VDVRFRLGRGSLKSIRTAAREILLRKLRFSSESIVVENEANASGVASHCKHLVLSTLSAS
ELQHAHDGDPMEGLFFVANSAMKIRTV*
>TCRU_6858 Concanavalin A-like lectin/glucanases superfamily, putative
MATWLVNSREDNRQYGFVNHSFTLVATVTIHQVPKGSTPLLGAGLGDSKGTRFIGLSYSM
NKTWDTVFYGKKTTSNTTWELGKEYQVALMLQDGNKGSVYVDGVIVGSPENITKLGALGH
EIAHFYFGGGEGYINSSVTVTNVFLYNRPLSVGELKMVRKSDDKKGNGDGKKGNGDGSMR
GGVSRLLLLGFCAFVALY*
>TCRU_6859 Enriched in surface-labeled proteome protein 1
MSTESGYNWNPDGEPITRVWGNSYNRKGYGVQSGFTTATIEGKEVMLITAPVYAREENEG
GKGRLHLWVTDKARVYDVGPISREDDDAAASSLLIKSGNERLISLYENKKGDDGSYSLVA
VSLREQLERFKSVVKKWKDLDGALQSCRSGSSGTVDARKGVCALVLFPPKGLLASCLVTS
LITNGGTSTSA*
>TCRU_6860 hypothetical protein, conserved
MMVTGRVLLVCALCVLWCGLSGIAADEVVIVGPGGDIGTGEDNHNSKELCTPVSKLQDAQ
EQRVGGGRSPDLQGVKENLKSDTGLQVSPEGKVKFGVSPSKTTEDRYQSQVFTEDGVVKR
NQTATTSTPQLPAVPPPLSFPRRETKTEETEEVAGATHEDELKEAPEKEDSPIQHQSTQH
HEVLKEEELEKEQNTQNQLLQEQQESEQIQVQTEKEKENQRSEEQPQREEEPKQREHQEE
LRGQQQKQERHEEPHKEKIKQEEGQQQQQKLESHERQQPKDEIKGQQHQQDEHPTENEES
TKDKNAVGANSTANTGDSDCSTAVLHSTSPLLLFVACAAAAVVVAA*
>TCRU_6861 TPR repeat/SET domain containing protein, putative
MQVAGALKQKGNACFNNGDIDGAAAAYQEAIGLLLQEKKGKKMPEEKNGVTHDIVGGAGE
LLAVLYSNLSNLYNIKGDYEVSWKAAQQATIYDPTFAKGWLRYIQGRRMDGYPFEAFVTL
LRRLRPLLRNSAPSTLPKQIAGDVALVEAPLYDDLGLSRVLPHIELDEYEGGVGIVARRA
VKPNEIILVEKRFETSFAEMDLGAQSDLTTMGIVTHFAKKMYPHQCSHSETWVRFNKQFK
GCWPRRPEEISADVRSELSHALRSQLPEMGDDDFESLFTLAVICRYNCFHSGFFRACALA
NHSCHANAAMKYNPEDETVTLIAVRPISAGDFVNVKYLSDAHFLMGVGKRREYLRSWLFW
CKCDRCSMDSENSATQEQIKCPHCLQYTHLPLTNENTGTKDHDPLLLPEKPCMHCGASVK
WSEDSRAMVSQLVVSFNNITGHVTYERLMTWLLEGMREISVIRVHPDHWLYRILFYFFCV
PMTSIVNEGFDQFMAMGWHSSLVEMLMRNVGIRRLYMETIHARKNEGECSKKKCGHVSEG
CSEIVGCGGAAINSALDQLSSEVMGGGDVLCTLCFLWRLISPFYPEYEGWTLHRAICRLV
LFSHTNPNESAALNESQALVLLRRHGKYVGDAEASLWLHAYNKFKPTPHRKGLLSLKQVK
NAFQL*
>TCRU_6862 actin A
MIIVDFGSSLVKAGTVTESLPSLIFPAVVGVPAKKNGLLKRNKIALDEAPLAPFLVGAEA
IHEMHRATLHHPILHGIVKDWPRMEQVIHHTFVEFGMNSEETSIVCTEPLFTPKQNSEQL
AEVLFEAFGVPSIALIPSGMCALYSSGRTTGVVLDSGDGVTQVTPVYDSYIIRNAASRFN
LGGHEVTEHLRTLLFERGLNFTSPQDRLTVQSIKESLCYVSTNYEVELQEGDEKRRLFSL
PDGQEIYVGKEAFRAPEILFSPFITFSENPSMSEFVVKAVKSCGIDIRKDLLSSIILSGG
NTMFDGFASRLAGEVLKEFPGLFGSAKVIDAVDRQYSVWSGASVLAGLSTFSDHLLTRDI
FEEHGPSIVHNYSRSAVLGDDCSDVAEGGE*
>TCRU_6863 hypothetical protein, conserved
MTELVVFENHDVCLQHVTRVRVPREVNTLELFLGVVSAHIAAFSGDATAAGRYRFVYSLK
GKPLWHVSDCLEAGEVVVSCTPGFLERKRSTAEVSASTPRFDAFSSATAASLFSPSCAAA
ATPAIAFYSHNVSGSGKNLSERAAKNVGGGRSGKGIELDATVFNINGHRLVLPPPPRFVD
PALGAVTEVQHSEKVAAVRTLLSLKLLGRPFLVNELLFCEELRLRLEPIVATAISRNEEA
AARVVVEGPPKSGVSTTLAYCCHMVASAPVSRFHGCLFLPLNFELLFDTAWLQLSNGGKP
DEKRVPPVDVENQQALLLDVPFFFLTLVRLVVDSAVAQRPSLRDDSKVLVEAWEQLVTRR
DLDAPQFGGSRLAQVVGHRALYEWDAFAVAAVQVLRAVEDSPRDMVLRDALIETVLVGFV

SHLASALRFSGVVYIIDGLRCLASVLRHRVRRPLGDAGVFLRCLTKYQWAHVIAGVDKLA
FPPPAVLLPGPVQCLGLLHLLSPELLTRHYGYPAAIYCGDKRFPLQVLMGAPGYLRALHA
LLDAHAWTTMEKGEGMSYVLRVEDDGVLHALQNLTKTLKIESDFGLDCSC*
>TCRU_6864 cysteine peptidase, Clan CA, family C12, putative
MPSWCLIESDPAVFTELIERFGARGVAVEEILGLEPEFLRQYTNVYGLILLFKWKSGKTP
TSDGVVVPDAPVYFARQTVNNACATLAMVNTLLNYSESIQLGDELSNLLEFTREMNAYLR
GTQVAESDVLREAHNSFAPTEFFVLHDETPDASDVYHFVSFVYKNGAVWELDGLQKGPIL
AADATDGNYKEKLVEVVQKRVIDKSAADNTGTGQGISFSLMAVVDDRLLQLEKEIEEAKA
REEPTAYLAEQLEELRLQREKGRAENQRRRHNYVPMIVELLKALAEKGKLEGIVEEALAK
KAASASSDRS*
>TCRU_6865 hypothetical protein, conserved
MGDLSRFGNEDLTCGKRAREDTIAAALTAENSHTGVAEGEGKKDEIRNSLQMATPKDPSA
YYLNVRQVVFCVLQEHASEAALLTREKLVSSLCDACDAVAHQEPFEAPLDIEMLRKSVQK
CLQGANWVELDHTRLDVIAENLTSRLAKVVPKLPLPILAEEEEAQANSSRPAKRPRKGMS
LNAVLQTYRFGGDEPQENHVKKWRGGIFPTPPSLPSVFPESAVCCVNCVTFENLPTKYYE
PEGMRRQLDKICKRIPNAFFLNVHCIPGEGTAVVSFNSKETAAAVMFMVNSANVVSTPGN
GVNLPKVNVIAATESHQRLLWGPLVEQVKKLEEQWRVWHAKYAANPPHMIRQAWSSANSR
RLQLELELLQLTSNEKSGIGEETVGVTAAPQSEEQLRRKLKILQDRLDCKKIIDQAEGQM
RELYGDACTQYLTAGSMEATYSTSKANVSNHRRLLFITNLPCKLDDAEVLQFIQIVGLRP
VHIWRDPTNETTICVELPSMGHVFAVLRQLDGSGMRFCGALFSRDRVVDAERLR*
>TCRU_6866 hypothetical protein
MNLVPLLDAWNGSEEKQEEHLPQNQRSIWGRLIIAEVPYPVIAADGVVISLYFNRLLFRV
SSSAFTVTVFLRDIVRIVLFAEKNSIEMEVDREGGGKRAYIVVFRENDAALMLYDVVLPL
LPVGVKDSSVGHPLSQSTYNTDYSFSLMSPNMMAESGFYELYPRRELTSNETCMKKKERE
DSTPLGLLSALHSLPSPPGESPFLTTTPAPQGQQAQQQNTGETSQASGKSSFLPAILSVE
VEETLLDPNALSQAVSDAQKPPASSEGGVGGAEEENDLQDGPHLMKYMIVNEAHTHGEGN
GRAADAASASVVSTTPLSWKAREVPEMLTPFPHDSQALSSENRSPSAARLNATPGAFRIG
SGVAALSSRSMSSYSYWSCKEGKSFVSMPRPRQSSSAVSSKDV*
>TCRU_6867 hypothetical protein, conserved
MSEQQQPKQRTAVSVTAASKAEVTVEENFAAMRHAAMSMFKQRTKDLTMVSALTTEAEVV
EKLNCQVQSTINSLQEQKAILEARIEAEERRVKEREEQLRGVHTMLAQMKEDQGVFSGVR
RSSEKIAMTLHQFVTQYTAKGGNVVHLLERCHERTHGRAPNEWRTATNDLRRRQSVLEEH
IKHIETHQTTPSGFADILLEWSRGVWKQQHECATALHVCEQLLSHDALGAIRELLPPPTL
VYGYDSLDEDCDIYADACMREIDNLVGVGKTIEGEGENVGLCCAVVPSERVEMARSRWIS
VHRLRLSLREVVAASCDLSKELEEQLMLVKLLSDRVVVLDAQIEDAQSNLQQDSITIQRE
REMHENLFSSWQKALQTSIVHMQCEATCRSAVESKETDMARQEVELEAKTAEMEAQWTTL
HTQAMQLYTTLLVEEQQRAEALCHLTSATDEQRTQETRLVALHEVCEKFEGAVRQECDEM
DRCALAIVNHASHGMGAGAAGQGNGKDENNEAVEKEDSTRASAINDLLEQLLQCQRNEEK
EEAQRESVALSSLMASTGLDAELLQRAADSLAGLQQKVDREMGIHLQWRQETEKELLTFA
VE*
>TCRU_6868 hypothetical protein, conserved
MPQWHPSMRAPGTGADAIYTSAEAAKRSLLKLQPIPSFELYKGAREEELLCYRSVCRVIC
MRSGGRLTKQQTRILEDLREELCIPTQRADAEMLEALEDVLVSSVAASGVLKRREDFFDG
VADVPLEAIHEGERAHDDHSSLYAPPAKVPRKENATAGAAATATTTASSSWRRGVTSKNS
QALLLKTIDKIGHEVNTISGKFLSAVSVADQEAFRRELLMRRERLLLLLKEAEGNAIDVS
GSSSAIPSEHGF*
>TCRU_6869 Methyltransferase TRM13, putative
MHCSLRVCSHTSVRCRRKQYHGTRAALQFVTPLLVDALHAASSSPLDVRRKELASALVGV
PPSLSHEGPLACSHLQALAGLCEGDLLRLLSETFSDVLEAPQTSHVAEMWSSSLQETYVR
ELARARAAECNRSFPRRFEAGMTAHNVFGGAIKDACAFGREEHIRREEDVEQVGAGRWSQ
LIDDYTLMLPDRSPLHELENLPQEIGIGELLASLFSWMGDEKEEIQTIMDVGGGNGFLAA
QLAEIFRCESIVVDPFTPKHAIDNGDFPHWVEPSRRRPRVPRQHPLCRIRQRLTDVNWKS
TPLNFNRCTMIAKHLCGTAIDTCIHHLQFVDRLPRIMVLVPCCFNKGNFVEYCNPVYLHS
AAGVKTEMAWNRWTRLTDWNRSSYQQFTASTRPVKCCSDPVKMGHQKMKKLQHFLPCMDD

IAFMAEAVINHGRVLWLRQLGYHALTVSYVPRCVTPKNRAIVAIRDVKPVAQHLQKGV*
>TCRU_6870 hypothetical protein
MRNSTPCMGNLAVRDNTTAANTVSGPSSHEYRIFVFAYARPDGLRKTLYSLLESDYSKAP
VGSLTLEVFVDFRKHESLQMQQKQSGILQFLRTFKWPYGQYKIHQRLTNVGLRISIMEAW
QPTSDREVAAFFEDDVVVSPYWFSWVYDALAHYAPVGAQGAIETESRFIGFGLFRPIFDE
LSRRRVHVKNDYAPFLLQQPCSWGAVYLPGPWRRFRELFEKDKNRDPTVKRPEGALTPVS
NSWKYNSSWKKYLIYYMCLNGWYMMYPNLPEKLVLSTSLLLPGEHPTPPKKLFLLDVLRK
EHLEKDCVKESLSKFTNMKGMQVYDLMFDKARTVDDLMPKADEA*
>TCRU_6871 Ribosome 60S biogenesis N-terminal, putative
MALVEPLVGYLLSKYAATVTEGLEKIRHHAKTDGTFASAFLLHPQGLLALQELMQKRELC
ALALQTVTQLVESSDNAGVRSGALREMCRGKSLWVLRKGLASLSDAMLPVTMAALQFLVV
VAGSLPKLVLSRFGNTVPLHLSCFSLQLPYSLRRVRVARAQFLISLVASPHANTVEIVVC
AHGYLTHLLEDAAELLQEGTEKGLDIARAALRVFGEHFVEGNIPATRKRSVLLAQKNIIR
LLVKALDHALVSEYAYGILCRIVLELLESPCDYQVMRLEAEDRGMPNYLLFFILRQLRPK
SSPASARLVIFILHQAPDLIRPFFTRVSSHLGEEGGTSRISSTTATVATLNLMTRAMLTP
IPYHLAAGKARLVQVEASATRFFSMSSEHVADEICPSWVAEYVHRLINGSSDLLLLLFSI
QLTCAILTRAKAIQRLVAKLQDVQSNDEKNKGNRQEWETFDAKLQSALLKAIPRREEFWH
RMTQQLHPMMISSSNANGNTTRGPEEKAFFLSQRMFLLMELYGEVFQLRISWLSAVPSFL
PTFCACANPIEDALRRGEGAVTTWPAVSVSALCSLLVSALSHGVSMTKLHHVTMSGAKKG
VLEWPLLLSVMLWAVKHRSPRDEEGQLAWAWVARLMQWTVHGVTVSFVCELEEAFLWLAA
MDESTIPCFVHLINYLLQRSLSKAADRIAHELMLGDAGIIVCAARTFVAKAEVKSASNGG
SAVGMKDNTNNKSNSEGTVVVRRGNDGRQQQQQQKENKRSWHECNNKRDDREPTGAATGG
GNDFWTVDLQEHVAAFKKVTERVACEWSDRGERMRETLPIVFKNARNDESGKRRIALTML
QAEKDHCSLRPIHDQLLEFCRTLRSPMPATDVEEEEMMLLTIARTGDVHALRRHFGEDKM
SPPSVWCLSASLGWELAGLFLRCLHELSGEIISEPESANEAYCSVLDCSQYLLKNIANDA
TDVTRVLLDRSLQESKIAGFFLLLLAATRLLLYGHAKRAVIGSALQVHLESETFEAISRL
LLRTYSGTVSTMDRIRYTTLLTLCYLQQAQRGAVTHPYGDNTGEMRLAMEGEDDAEKEDH
DRSLVELQTATSLRVFSGILVPQQMLDQRFLIMDHQNTPHVAPEVDMLSLLVDMWTDEEV
VTAALQCPARLHNTILVNAKVDAGWEVLRSLFPEFSVQDDIMLASFDALTATTVMDPRYL
LPLLHTVLSLPVEQLPRTNIGTKCIPFLLRSLSFTDPQLRRLGAAALSAVWTPSGPTRIV
VGFARLKLTQLASKKGRAKYPQGKEGEFTWNCPRLPAPISAFLVMVLHPLSNADYPLHND
IMRFLLETQEAFSNPVPLHHFLTSFPLACITTPLMIKRQEKTQNRTSGHVAAAFAEVARE
LQSEAPTHLNFILRLIQFGCQTNGDMMALLGSESLQAMMVIVSMVAASAEIRLEFLQCIH
FACTTSSAVAKQAMEKGHVLSWLFGFAFQLIREYGECVYMYGEPLFMEVLTLLRKLSPLS
LVSPLHAQQVQQQLELIRDGLLANHVTTKDVLDGVEEILKGMRSREGASAGTAPMRKRQT
LHNNARPTPRTKRR*
>TCRU_6872 SNF2 family protein
MNCYCEIPVKCAAGKDGNLSYVCAMSKCRFFALCPLHADGWRRVVAPPAVAGEFIAVRFE
AVLHPEKKTPHVAATVSPPEVEAVIAVLEDAQFQPMWYVAKKAYLYPMESYSHLLVALRK
LLVRVHIEEIPSFFFRCLEAVQEIQLKHERNIDGNASQPADVDDVVYSQLRPFQKKGVDF
IIARGGRGMIADDMGLGKTVQALAVAHHYRSEWPVLIVCPLSLVENWTKELMRFCSIPIG
RIAIFQNSKVRVTDVHSAVIVPYSSLKSLDTQSTTFQVVILDESHYIKTVDSKRTVAALK
LCRVARRVLLLSGTPTLSRPIELYPQLQTIMHPSWTPSKSLFAARYCNAFVGRFGVDYLG
HSHMSELHVLLQQFVIRRTKRELGNELPSKIRQLLYVYITPKEKKALEKSVLALRNSFRD
GATLPTLGAAVGTTNMTQGTGGNLTTCTPGGATATRNMTAFDLKIATARAKIAAVQDYVK
STTEQMVESGQKVIIFAHHQCMMEAIREAVESVQPKQPLDYIYITGETPAAQREALTTHF
RTSTNCHVAVLSMHSCGVGHNLTCATMVVFAELDWNPSTHLQCEDRVHRMGQSSACVIKY
LLAEGTSDSVIWPMLQTKLNVTHAVLEDSQAGGEGWSAGADTRRILRSDVPLTPSSPEKK
QVTLEGFLSHSGSRPSRPLTQGSDSNAEVLKTSDESPRADTSPDTPFQSPSAVAPAENAL
LDIAKLRQQREARKVVHSTPVLGTVGAGSSPVAAVTVTPSPPPIQRQVTLHEVLTNHPAN
SPTPKNSPQQRTKFHVAVASKSFNERSGAAHTSSCSSETTVCAPIVSHPVKTLFLARPAS
ATSSSAASSVKPHAGASAADLSVVSTVSKEGSICLAPSPRSEEIRRYNARRTPFILGSTL
GKRSRPDDMEDQVL*
>TCRU_6873 ubiquitin carboxyl-terminal hydrolase, putative

MEFMNGSNGFVGRDVIFRPIQFERYRKPSVVSYPRHAIVLNPHHTREVAHDGRAKDNADE
ASSNESEQSERSDIDEDDPLHIEEEQMLCRNEQLRQLLHLRWRHVGPAGCGLENMGNTCF
VNSVLQAIAYTPALAQYFAGTFKAPCSHVVGAPYDYAYALGETIRNIHTPSNRARRAALL
VSNLKGLFPHFQLGRQGDAHEFAVQLLHACHRSILFRQIGSRKVSSCIEQTSTLQRVIGG
YLCSVVAWSRQEEIHRLIKAGKIQEAADLKLSSRGSSSDVLVSNTYDPFVTLSVEVVGQT
LDHCLAKLCQEEKLCRHSYVSPRGVAVQATKRFQLHKLPPVLIIHMKRFNCMGGKVTKYI
QYPKKLNLAPFCTDKAMKANAAVRRNAGGDEKDSSCLYELNAICIHEGNLLVYGHYYSVV
RARNGMWLLCNDERVSYCDEERALRQQAYMLFYSRVEPSSLGAKYTQKKETRTPQPLDRR
PVGEAATGRMTTSMLPGSVREGAEEDMGRPLSEEEVRRMMRKKAAAKQPSPDEGKKEEGV
HRGQLNGQREMSSAHASSSSSDEADEHPSLMSGGVLKNVVSSAPVNGKRETSALQNGHLN
SRYCGIVKAIRQRTAPPALVTTATTTTRAQTMDEMTMAKEAKREAIVGGHVMEVLEEMKQ
QSVPITVARPRHAPKFCQRVRDPMWEMEMDRGRVKRVRAKREEHVGENKFQKAEIAFDSR
GRRHRNA*
>TCRU_6874 ATPase subunit 9, putative
MMRRLMITPPVARRVAAAVPSSTSLVVRRASTVAISVQGLHYVGTGLAAIALAGVGLGIG
TIFGNLLVACARQPNLTKMLFNYAILGFALTEAIGLFALMLAFLMLFS*
>TCRU_6875 mitochondrial carrier protein
MDLLTSFISGWMGGVGLLLVGHPFDTVKTLLQDAKGKHKNALSCVASILKKDGPLALYKG
VLAPMTGVGVVFAFYFVAYDSCEKFIRWMKALDASKPLQITDVMICGGSTGVLGSLVLGP
AELLKIRQQTALNSGTDSSLRGVISFIYRREGFRGFFRGTGMTMVRDVPGSMAWFGAYEY
TKLLICSNPKIPSVSESLFAGGMGGIGMWSFAVPLDVIKTRVQASHEKLTLVGAVRGIFK
ERGLRGFYRGLGPALLRAFPANAACFATKEMTQRALNNLTGSATGVQKSIDQK*
>TCRU_6876 SET domain containing protein, putative
MGRLRSSWVARDAFRELNLFLLQRAWHFTALGNYAIAADYVIRMLNRCPRDPVCLLLGEI
VAKFTQQDAFLAKCREAQRRLCVQNNVVDALQLVSEETAREKLRMWLEMARDAPAIEGPI
EEQMIVQESEPFTDTRSSVRMMAQRVSTLPLVELQEPKQSVYGRGIYALARINSSTPVML
DQPFLVQRMRDDACVHCLATIGRSGASAGGVRCAHCDRETYCSVACRDAAWREYHVCACV
SRNEMYAFWEGAMRERLLSDKMEESRAALACLAVAKLCVLSTVQQMHPLALPRICSLRGR
ADYDASTALSEVGALAVTLATALRQTHLYMEELLSLFAIVQTNEFLLPSGMALYHGYSFL
NHSCEPNCALLGSGAANRRLVTLRDVREGEQLFINYNASLTTRVSYADRRALCQQRHFEC
FCPKCVRQE*
>TCRU_6877 hypothetical protein, conserved
MHLSAVARCAPSSGTLSSRLAHLVQRVEEHIASRGTAATVRDDGLWEQVLATAHCARALK
ETDTTLAIVFRLLRCGCYPSRSAVWPGLIRDLAPYSDIEANAVLSYPGVPEGPESQSEAG
PWRCARVPEDILAAGRESEVADMPPLLRPTRETLLMTGGVVPLSARIPCSDGGALSVLLE
SFCSVCEASHGGDGDGEMTVNFLQDVTAAVVSALQPITATIVLTESSPLARALVRFFRLL
FNFSARQSGGQLHLAENFAKGLTKLLPENALGGRMVLLFLAEHHAEYGDEMVHIPLVRIA
AGAIWRQYEKHERFFCLRQLQHVNDAVDVTLQRNANNGNPLALDDSDEAALRLLLSLALL
RAMRVEAVSPDVFLRDAVDIVDRSPMTLSIEYELIVAKVELLDLFLDDESSSNAIYDDLL
HSLRAIVELRPRDGVDGDTSAVPDATHNSIKEDEEEVRELARQHFQEAHRLVLTVFARSQ
LDERLNQAYTVLVTHKYHGLVITRDVANPLLDALSRRGDCRVFNIVDLCVLYSGSHIDYD
TLTYLFRACRVAGDFYRARTLYQLLREMIPGFLLRAPEAIKDALQELKILQPEPAHLFPA
SLAVDGDEAAAAVNYEGVVDDEALTVRQRGPIRELPTKRTHTPS*
>TCRU_6878 kinesin, putative
MTEKVRVAARIRPLPTAGSVLAVAPLDERRVCVANRRVYHVDRVYGRHDSTELIFFESVV
ALVDRFLAGYNATVLAYGQTGTGKTYTMDGLTPLVVRYIVENMSNSTSKLSFQCIEVYGE
TLRDLLTDDPVGSTKHLQLHESDGSGSGGGGVVVVGAARVKARSIAEVQDIINHGARMRT
TGATNMSEHSSRSHSIFTIFNHERESKLNLVDLAGSERNKKTQNVGQRFRESIAINGGLL
ALGNVIRALSRNHFQSPESPRHVPYRSSKLTRLLRDALGGNSTTLLIACVASDASNSDET
TRTLQYAAFAMHILNEPLPQFDDQVAAAEVVRYADAGHDQEFVARKNADNISSEAAAEVG
RLRQRVAGLEEQVQRCRDELKNDEAVFAQQIKEMRLLLEENESLRRRVAFLEGCPTATPR
STPDMRQANWQQQQQQHQEQQQWNSVPIPPNVNYVQDTLQLYGITHRQNDQSFFSHPSSQ
PRPAVWGEERAVRSHERHLPSDSLKRPIVAARWGGAAAAVNAAGECTHVNKIEGGWGDGG
QQLTAREEQLGLLAKEALYYQNSNSELRRRLRTVLAMYEAQQHEAAMLRLEVKQIHDLLD

GPPHS*
>TCRU_6879 hypothetical protein, conserved
MEEAGGGRPTGPSATKRNDATLSVPRGAGITLVESLRRRQVQAELQLRETEDRFRRDCAR
QEQELDLLRIENSKYKAKIEELRMAQTAPRETSMYTFARGGESNLLRASSHKYCMAREAV
EKAREVLSEIKARVVALRQRIHDMQRQCGNARSRVDHSNRQSRRSCIEIELQTRASRLQL
RGLEAHVEFETDRRSGIIEEVKALRRDIDVLLTAQRRGDEIFQERENEMLEIMKETSFLI
EVCNVLCEERDAYRQQLLELQRASEADHEAYENAFSDLVGVEERDKVLKAKLREGVAKLE
DELRSVTREREAAERLVREDEAASRAIRHGENGNDDDSEPENNDLSRQVAEFERYIGRLA
EMAGSESLPDIERYICEGGEERFQLYSLLHRTQDDLAALEKEKEALQEARWIATEGSEVE
HHAREELEELQAKLRQIQIDTLDHEQQAECVRAQIDASLPDVQSIFDALGCDDSMIIAQH
GVSVLSRGTVKLFLASIEQRLEEYVAAWMQRQQPSHVLSPTVGYNASGFGITAQMETSKT
MPAASPHVLPSTNEPEAMEHEKGVTGELLRSEWAHVLVKGQVENGGIDVNDAGGTRDIKL
SV*
>TCRU_6880 hypothetical protein, conserved
MTEGESQKWKSPLLQKRLVTRSAFCNEASQCAASILRSEAARVDGQLCDDVRAVLAGNAV
YIRRFVCDEADMRLYERLRAELVAATGANMSRDGGRIDWSRHEIFENPTGISAMFNEIIE
MLAEYFDLDVYATRLNYYRDGHQWKPQHHDSHAYGGTSTHAGERLREDFTVGITLGATRS
LLFVHEASGQQFDFPQRNGDCFAFTSEVNNAFTHGVPRVNTPIGDRFSIIAWGRRRAMNE
RNSDRAVTSFEGSDLRSVDDAIQAAHQLVSRASASTRPTVAPTLSTRMERNDGNSHRNES
SAGSSVPAKKKKKNRLQ*
>TCRU_6881 hypothetical protein, conserved
MVLTWYPEAEKDCEEKNTKEGKLDVLGFKMCKHESMKEICGNGDDETPSKSRGPRAEEIC
KKYTGDPNKAVDSSTELPEASPDAEKQVAAATRETPKGGAAEMGSTPGAPAGDSPANPTE
GPESTSAATDTSNNEAQKGAAVAMPRNAPESDATRKDEGEEGEVKHSNTKETPAKTETLK
NVTKTPGPWLSRPPQRGARA*
>TCRU_6882 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MAVNEKKDGVFSLIIYSKDNGSTWSLSEGISPAKCGAPRITEWEGSLLMIVDCENDQRVY
VSRDMGTTWTEAIGTLSGVWVNSQLGDYPDGGLPVEALITVTIEGRKVMLYTQRGYALGE
TETTSALYLWVTDNNRSFFVGPVGMDNAVKGELAGALLYSDGKLHLLQRRDSGEDSVMSL
SRLTEELKEIKSVLSTWSQKDVFFSSLSIPTVGLVAVLSDAAGDGRWYDEYLCLNATVTN
ATKVKDGFQLTEPDSRAVWSVNIPDGNVRHISLSHNFTLVASVIIEEAPSGNTPLLTAVL
VDAGPEYFMRLSYTADNKWMTMLKDEKKPTTESRPWEAGKEHQVALMLQGNKASVYVDGE
LLGEEEVPLTGEKPLELFAFCFGACKIDGDEEESSPKEIGKKPRVTVTNVFLYNRPLNST
EMRAIKDRIPVPTRAPEPQVKIAPKPAAPAAPAGNEETARETGDGGANGDAVSAYGRVLL
PLLFLLGLWGLATA*
>TCRU_6883 hypothetical protein, conserved
MGYKASPEILQIIIASAIAGVTTVVHRLWAAPPSVRIDVWIDNIRIAGSKSDATLWEAQV
LRNADSCHASMGEERESGATHYTFLGVQFHHTHRAVSLSERFVRSVCAMPALNSSTIAGM
EVVASRFLYAVAILCARLCDYHFFIRAVRRRLSALDRGIVLETSPATIRPAAVGLGERLR
HIIENTTVSESSIPRKRHRPPSSRMHRSMDGEPFSF*
>TCRU_6884 AKAP7 2'5' RNA ligase-like domain containing protein,
putative
MDDSMTQGRPVVTDGGVATAEGRGMARKGKDGVRVRDCGGSRRGLIGAGQERLHGWRCPI
CMRDSVDPRRVCGFCLAVEPGVVEFNPRRGAAVACSQACLGFSEDPTVRLLSLPHGRCYR
IAAQSTTAALPTRQHLSLEATVTFGNTQAGKREGITVERQADEAVHGGSSPHRTTSYTHF
VSLPIGSLSAVRLNATRLLEEMKTRCVDPAAMVTEDIFTTAPRMHITLLMLSLPTPEAIT
LAKACMRVLEEKLKLWQETQHSNTDNGDCGSLKIHLGGLHVMHGRGRNEKKADVLYMGLM
DAASSAVVKTLQQLVYECFSELIANDPRGRATGRLLHMTLLNTKWRGEKNPRDTHEEATR
TSSRVPFDATCIRQEFGHVSLRGGGTDGAIVLERVDLNALNYDSECECYNCECSVPL*
>TCRU_6885 hypothetical protein, conserved
MFGDPVRPAPAFAVAAVPNAQENMRTKLQRMEGTPLAGSMPTTTWATAIPPLPGNCPAAT
NAAGQKKEFLGANINSCPQFQRLRGTAREDRHEKIFRRTQEAKRAEELRQRQALLSQSVT

MNDYYNTLFRPLQKRDFATTLDSAWSATGNLPAPVGKSLRTRDVVLIDLEESFIACYYKM
NPAALQRKKELEEAEEQRRRSVRAAAQISSFSGGLPRSRSTTLPRGQKSSPTKKKQKGKK
EEQPKEGAPAANLRILLEALLEASDDRGMITFDAFIAVLKRPPFDVKDEEALEAFFFLVQ
TSSTAEVGGSETERRLDGSFSVSAVLPRARRRSASQHTSHVLVTGTSATLGPPSPLTSTG
TLPASLRRSATGPGASQSIIRRAAFASRANKGATTSMTTITLGTAAASEVICSPSVRVRE
ILAAIDAIINGPEIREAVRSVCFGVLESDGFIHKTTLHTIRLFRRENCEGKHAVVTPSIV
KALGDAMELMLQEEEAEYLRSQMKGKRRAKAGKAPALLAHQKSAIPLHMMRRSHINFKEF
SRFFDELPMIAAAFTNVWLPAIFASSWPSVKRSFTSESNDDGMPGDDEENRNNNAEDGVV
DESHAWRRNTARRVVTERLEYMKPASIIESDVVSQR*
>TCRU_6886 ATP-dependent chaperone, putative
MNQLTAAASPTASAESRISDFTALLPEGWGENGGVVIRTLKGLLQNPFFSAGAGLYLLTF
AGAAARSFSTVMQTAMRRRFVVSMEVTSQDESYVWMVRWLAQNPAFYVQQMSVTTRNTTI
FSNDESSHECLYAPCTNVRHWFWYNGRPMMLQRRRVETQAMGNDVLETMQLSTIGLTSTI
MKEILEDARRLTSMRNSDHTVIYQNSGGRWTRQEPRRRRPLHSVVLDGNTSAEILKDVKL
FLQSSKYYEDLGVPYRRGYLLHGPPGCGKSSFVMALAGELRLSICPLSLSSRGLSDEALV
GLLNSAPLRSIVLLEDIDRAFSADSHITMSGLLNALDGVAAQEGRIVFMTTNHVERLDDA
LIRPGRCDVKLEIGLLSRDQAQQLFRKFFPDADDKLRAEFAEQIPLNVLSVAQIQSHLFL
HRDSATEAVWTLREFLHTVKSFETQLRQAREREKCVERMKRAPLLHNL*
>TCRU_6887 Isochorismatase family, putative
MSRLLKHYGSCKTAFLCCDIQEKLAGRVVNFDNCVFVANRFAALHTALGTAHSVYVVTEQ
YPKGVGPTSADIRLPPDAHVFSKMQSPMLLPEVMALVDLPEVEQFVLWGLETHVCVLQTA
AALLDMKKKVAIAVDGCGSQSQGDHCTAIQLMQSWSGDGCYVSTSESILMQLLKDASDPV
FKTVAPLMKQTHPIRI*
>TCRU_6888 Isochorismatase family, putative
MSRLLKHYGSCKTAFLCCDIQEKFMGRVANSANCVFVANRFAALHTALGTAHSVYVVTEQ
YPKGLGATSADIRLPPDAHVFSKKRFSMLVPEVMSVVDLPEVEQFVLWGFETHVCVLQTA
AALLDMKKKVAIAVDGCGSQSQGDHCTAIQLMQSWSGDGCYVSTSESILMQLLKDASDPV
FKTVAPLMKQTHPIRI*
>TCRU_6889 DNA repair and recombination helicase protein PIF5
MFTRLSASVRQTHAVLATRHTALLTCWRHASRGEGGKRHPRRTSQPRQSRAAAAATPSDV
SVREAERLLTSAVAPPSLAPFLVPPPATRRKKSQVTSGSPTFSSTVEEAKVNSRAPVEES
GSYDTVPERIGQVAMKDKKNKATSVVTTTEKRKKNKVSEGAQRQNSTPVARGIDEQIEKE
ETKRKDAVSVSDDEAILDEESEQFMQLLVDETMRRKQQRRGVSLEGRENDNNVAGEEEEE
YPARLEFVHRSDVGKDTVDDADEEGANRAAERTAQRTEETAKDDDAANCIDELSDDQRRA
VELALQRRNLFVTGGAGTGKSLVIREIVRQMREGGRRSVFVTATTGVAALNVRGSTINSF
AGVKFGDGEARELLKWVRRNRRAAGRWKYCQTLIIDEISMMDPELLDKLDYIARAIRRRA
DEPFGGIHVILCGDFLQLPPIPPRRTQWSQQRQPEDEAVRDEDGEEEEAMPDRPKKRYCF
EGDAWKALGLTTVVLQQKFRQNEDAKFQRVLDDVRIGVLSGETYEMLMSRAALKTTKAKS
RKGRQPADNSDNRAMIEGEEGEDVEGGRYVRLCATNKEVEARNAKHFAALEPQGLGDFSR
QTAATSSFYSSRLQDREKNNNNNEGEEEEEEDVMREMEETEDDIRPLQIYRAHDTYDEDD
AASAGPPSWVKFDDSTLPTELALKVGTRVMLLQNISLRLGLVNGSVGEVVGFLHPLELVE
LVLRAPRERYHVSARGQELLRRGGFPTINDAFRCVDTSLGQSLFWSLRQRGLRQPAEVSY
GSVYGNAHCRDVQQLVGISPSTSVHPLELYIGGIPPQQLRLTRLPVVKLDLQPQHLTLRT
DKVDGANGKRSRSVQLPRHVYAFVSPYSHQWYMGDQVVATRTQIPLRQAWAITVHKAQGL
TISHVEVAMHRFFSPGQAYVALSRGTQLEKIRLLNFNEKSIRACPIAKGFYSMLESAEKE
TGDEADA*
>TCRU_6890 mitogen-activated protein kinase 3, putative
MHDSNQELCEPTIVGDFKLYNVSGSQFEVPRKYTLLKILGTGAYGIACSCLNEETKEKVS
VKKCRDVFRDLEDGKRVLREIAMMRFFQHENLLHIMDILPPMKSYTEFRDVYIVTPLKDV
DMNVVLRSRQELTGAHVRYFVYQILRGLKYLHSAGVAHRDLKPANLVTDITCELKIIDFG
LSRNVTMPYYELTDYVITRWYRPPELLLENNYYTTAVDIWSVGCIMAEMYTRKPVLRGRN
TLDQLRLICTHIGKPPSEMVNNPEALDKLHGLPDGSLEVTELVPGLTDPEAIDILTKMWE
LDPAKRQSAAELLQHPFLAALHDEQDEPECPTLFSWPYEQKEMNDSLLRRAFWEEICAFN
PQLKSQMPPASP*

>TCRU_6891 hypothetical protein, conserved
MSRFVHHRNGENATRKFPRLAITHVKSNHVANRRKQHPIPQHFVDPDRRLPRGAQDGVEC
RKPTRGKHEQRQQRNRQLTKRASPPLRKSEAIGNIILASLEIMGLYPVQEEQQQHR*
>TCRU_6892 hypothetical protein, conserved
MSRFVHHRNGENATRKFPRLAITHVKSNHVANRRKQHPIPQHFVDPDRRLPRGAQDGVEC
RKPTRGKHEQRQQRNRQLTKRASPPLRKSEAIGNIILASLEIMGLYPVQEEQQQHR*
>TCRU_6893 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWWSLSGIAADGAVDITRESDESLEGPLRGSRENEDGPQKPLGS
VMQRSNTANQALNPENGVMVSQPEDPAKKQLKDEVETQKESEGTDEEDYGVDDDDDDLE*
>TCRU_6894 hypothetical protein, conserved
MYQLDAVPGRTFAALRLDREMPDLDDGSDFEGEDVSVYSARTGTAQSVVSMLTVAYGIFA
ARQRLKALMPLCERWNVRLPRRPSFVQDEEYCRLVIDRLAVKMSSVMERKGQLGIDQNMS
FTLSATAPGAHDPASGTWGRRSGGQSRGRHSNVTVSQSNSVDLHNFTVDEPRFSTDDSVF
TVRARRFR*
>TCRU_6895 Enriched in surface-labeled proteome protein 1
MVYLPLTAQLQHVKDVLATWKKVDDRVSKLCPSKSAESPSPGNACSPTFKITDGLVGFLS
GNFSENTWRDEYLGVNATVKNNDVGGKKAKLHEGSVQFQGAWAEWPVGEQGENQLYHFAN
YNFTLLATVSIHGEPKEGSIPLMGVKMGRPRRKQSFWTVVQQQKRELGSVVQWPKDHGAQ
QPFGARDNTPSGHCATERKTVLGLRP*
>TCRU_6896 retrotransposon hot spot protein, RHS3, putative
MERCTVFAFLDADFITAIRHKVRELKRTARRQPHRSALEVYSQDRSTRHHVLPPPHYFSE
KVGVDCCVLYLPEVEDFPLLDAFFFVNSNPMTLVGLRMSTANEHHTTASTVRQFTECLAA
YFEGWEEFSQELSWEIIYVQHADSTPMSDWQRCDVVNTDVVSEEEDQRIATFWKGKVRQY
QASISSREFRRDEALRSVEGPSK*
>TCRU_6897 Enriched in surface-labeled proteome protein 1
MAPDGAAVTPEVGIHSGASGETVGETDGQKREDIHAQDGEAKAAALNSSLGNVSQGNNTD
AGTVRESGLLPLLLLLLGLWVFAAL*
>TCRU_6898 hypothetical protein, conserved
MVQQLPCKHLLLMPLAHPPQVVRGSERGGTQQRWNGACIVSSVERGQPSAANTLASDKQD
AGPEWDTHAHTAVGTNSGPDSLSTTDATPADGATEIPEPRTDPATVQRNDSVLDGVGTAP
THPSTAPAESKIPSEFNAAPPLGNDLFDLENITELVSMGLRADSNVHGCESLVCYYCCCF
RGCGPLRALC*
>TCRU_6899 Enriched in surface-labeled proteome protein 1
MGPNQPYHFADKNFTLMATVSVREVPKAGSSSSIPLTGVKLHDPGHTVLFCLSYTSENKW
EVTINGNTRSLSGDRNRVRGRKYQVALGMEYYFKHLIVYVDGSMICDSEKEYEDYEDFFG
ELKTVLSSHSTSHSYIGGERAGDSDDVHVTVSNVLLYNRILSNAKLKAVMKKIVVGTPVA
KVPVSKGAPQTNPASETFLQSANEASS*
>TCRU_6900 BNR repeat-like domain containing protein, putative
MAEGDVPHDDEDEGKKEFAWHGSGTSNLDGLLKDFKPIPEQFKPFVGGGGAVIRLEAKSR
YVLPIHALKDDGKVVLLIIVAKGFAYGWEFSRDTRPAGCIRPAVLAWKDRDLVTMTSSAD
GSCGAYWADEKGESVDGGIRHSFARVGQLTDTCGARRAGWLRQRDGRWTESHSRQPAGMF
RDGR*
>TCRU_6901 hypothetical protein, conserved
MAMMMTGRVLLACALCVLWCGAASANGSDAAETHEDPSRGLQSAPQLGPAKQPEETKPIE
GVSNTAEQSLDAQEVKNGNPPKGSVKQTPTQNGGMEENLKKGEGKKSEKDEKAEQELEGD
QEQPLTRKDTTEDEKETTPALPENKEPPPPPPAGAATPPASDGNHPGDSSKLRNSASDGD
IQPAADRMHSGGGAGSIRNGGGGKQSGQSGVSGGDHLPNPSSSSGSFPRPPTHDGKGAPQ
DPGEDSSPQNKKSLEKVVQSGASVDSALPKVDEVQKSEPDPQQIRPEALVTVGGTGKEAR
REAEGMNEASSGKQVTNEKEVLSPPAGGSAPDPNGTHNSPETNAVNSASENEPESNSLER
PSGDGEAGQQDKEADTQGTQETEVTQGTAASPVSTSGSGGAQSEADADGDDPQRPNPEGP
QNDGTEAGDTHGPTAASDAAPQAAKAITAQTNGTVTPADSDGSTAVSHTTSPLLLLLVVA
CAAAAVVAA*
>TCRU_6902 Enriched in surface-labeled proteome protein 1
MGVKTNGQGNPVLLGLSYDSGGKWKLLCGGGTSKEHSSTWEKETQYQVAIVLENGSQGSA

YVDGKQLDGNEACALGNRGSNEISHFYIGGDGSGAGSQDDVSVTVSNALLHNRPLTFSGR
NADLEKDVAAPAEAASHTVAGGQMTTAGESATAQQLLPSPSQGSVGRTASSSHAVGGATG
DGGTVRGSGLLPSLLLLLGLWGFTAL*
>TCRU_6903 Enriched in surface-labeled proteome protein 1
MSRRVFTFAVLLLLVVMMCCGSGGATADEAASGEASSPETYFDWRDVKKEETVGLLRVPS
LVEVNGDVFAVSEAQCTKGDSVCDFNAR*
>TCRU_6904 hypothetical protein, conserved
MGFKASPEILQIIITSAIAVVTTVVHPLWAAPPSVRVDVWIDNIRIAGSKSEVTLWEAQV
LRNADSCHASMGKGCESGATQYTFLGVQFGHTHRAVSLSDKFVRSVCAMPSLNSSTIAEM
EVVASRFLYAAAVLDTRLCGYYFFIKAVRRRLFALGRWIVADGCYVYINISDVCMCTYLV
*
>TCRU_6905 Mucin-like glycoprotein, putative
MTTCRLLCALLVLVLCCCPCVCGTASEGEVGESVSKVEKEGGPGQETNLQSTSSRPPTKE
EVEEEARGRNEVQGPNPSTPMSQLTAALTGTPQSQNISNNTQEKDGGDSNGRTEHTNADK
ENEQKKAAAPTTNTSTTRAPTTTTTTTTTTTSTTTTTEAPSTTTTRAPSRLREIDGSLSS
SAWVCAPLLLASSALAYTTLG*
>TCRU_6906 hypothetical protein
MNQLNRRIQQEETSHEYKQQRQKGQKLKKKQNPHPQEKLRKREKKVLKRSKKKGMKKNMN
KLKRNSKNNCSLNGEKKHHRLPHLWGGEATQRSLSTVRSQELQQEHLTAGATEHLEKGFP
SVSAQSTSNGKTNSPSQSATPITDVTAVTNEVDKERAKSRNDTESPEAAVIKRGEKHEKP
TENDKTLATDAKAVGRNDTGTHDDTDSSTAATTAVGTDIGTEETPPTNHPNKPSTEGARK
PETTSDGEATSTNKYDTVSQNAESKTPPTTNATTSDTAKKDNSDGSTAVSHTTSPLLLLL
VACAAAAVVAA*
>TCRU_6907 hypothetical protein, conserved
MAEAASCLDLKAFLFQVPLPRETRHLFRCRVEDGTLVELTRLPMGYKAGPEILQIIITSA
IAVVTTVVHRLWAAPPLVRVGVWIDNMRIAGLKSDVTLWEAQVLRNADSCHATIGRNANR
ALRSTPSCGCSLITLTRRYP*
>TCRU_6908 hypothetical protein
MRVDGNTAQFNCPQPLRDAGFAVAEALFDVDVALDVPDASTLFRKLCATAAPNFTQERQN
MVAFSYGVCSSPKRQLIYGSAAGEVYAARVITQFIRLGAKKGIFALSCHVIGSKEHRADL
LDADKELGVIVGSVKEGPRVRMAARICVSLAGDVRAAMDTIVKNYEKYFFPVLCEKQPMP
ELEAMPSYLPDTVVFQLYHDDGEAEFADYMDANSLTFVALGDAERLVLCGIDATARPHHE
GGPTSTGVGSRNCLRHSPPSSVHSLRHVRTQSVVAPSVQHGKRQPQQ*
>TCRU_6909 hypothetical protein, conserved
MKRVNAIESNREEARKWQLSVFCGRSKHEAEKMIKELERRDGATLDEIKRALEAKKRESS
ALQADRESRNWECEHTVEKIRTRKQDEESASERLRQAMQQPEQELGLRQSAIETKEQQLE
MVQLDRARGRETVMRERHSIEAV*
>TCRU_6910 hypothetical protein
MNAKFPEEVRPLAEERKKKREQATAKEDAAERALAADVTMIEGYLPKLISLEDIPVSPEE
TDIIRRQFDEVFAQEEQTYLASAEEEKAREERLGRGLEVYRQRMLDDYVAKKNGKLHDAE
ATEHHLNSVVDQVLNYLRNGVRITKIPSKGNACRRLYFLLEDCKRIHSCDLDHQGFPLNR
KRPPVTMWIRDIEKVLIGLSTASFVNYSGEAQLAKTSQEAVSDNGTHRHDLTQNITLFSL
GTNNHRAFALLLRGGKSLEVVCEAGSDCEAWLVALKRLLHLRTPAERLLEERRGT*
>TCRU_6911 retrotransposon hot spot protein, RHS3, putative
MDMKLNDFLMMELEGRGILRANRNVLLRVFFSDPTSYIRDAGVLNEIQASGAYLRMEMAV
REEMGLEEVARSLCENGVFYLEQWRDYEGKDTVTPLARRKLNRVLTQLLREERREAEERA
VREGHVGFTLTTTIRDVLFRGRVRVMDVKLNDFLMMELEGRGILRANRNVLLRVFISDPT
SYIRDAGVLNEIRASGAYLRMEGTVREEMGLEEVARSLCENGVDFLEQWRDYEGKDTVTP
LARRNLNRVLTQLLRAERREAEERAVREGHVGFALTTTIT*
>TCRU_6912 retrotransposon hot spot protein, RHS3, putative
MDIKLNDFLTMELEGKGILRANRNVLLKGFFKNPTSYIRDAGILGEIQATDAYLSMERTV
REEMDLEEDVSKLHDNGVNSLAAWSLAADLHFRTQALL*
>TCRU_6913 retrotransposon hot spot protein, RHS3, putative
MKVEEGKPEQQWTYKAAGRTFEKDDGAQQSGAPRLRLMVLTSDKGWPYSWKWKEKESIHD

CYVNCEVERVWQIVKKDLSEFLSPDDEPGFVPGRRVLIGTPGIGKSMNAGSYLLYQLLHY
DAEQLPMVAYFIADRTFLFDKTAKMVSLYTNEASILGILGTFSRRGVKGYVIYDVAMKGK
QPQIALPCEGWGMILLTSPNVKNFEWWASRRYAARIVINCPEESDVRAICAWMKHNRSPQ
EQAKYWKEVKEQMEKVGPILRFILNKTAYNDRFSEGESAVNKITASKAEHYANIGELNAF
NDSEVSHKLVKVVRVRRDNIEWPLNVPISHHFESKIFSKLESEMRQFDFIFLVLSIWDYV
IPYLLEKCAVSAFLNEDFLRAIRLKINELKLTGRPEPQECALLRYSNKTLTRKEEPPENP
SNRIAIEYWVLYRPAAKNFPLVDGFFFVDSNPKIMVGLQITTASEHHTLTSTVKLFTEQL
AAYFNDWEELSRDMSWEIVYVQHKDNKPLTDWQRCGPANPNNETNAEKEIAEFWKKKVHQ
YRVGVSADDIKQRVSSVENDQQDTSTN*
>TCRU_6914 hypothetical protein, conserved
MLDLVRQHGDAQVQLTFIAEHGPLDAVVTVAATMTCLRLISAKIAKQWEGSTVAGHFANR
RAFQVPNFDVQVLLPIVWGQPGSWGASKGS*
>TCRU_6915 hypothetical protein, conserved
MADRAVVIFLFAQEKLLFRYPICNPFTLDANSQNTTVPGTHTKTHGKSSAVAVDTTTDNT
ITATAALHAKATKTEASQQQKQQKQQPSTAAPAGVGVRHKPRNTKRLHPTPKTTTADSKE
LSDNDGDGAAKSSITTPTALFLTDKPPRAGRRSSNNKKGISSRSSSSSASGAKEDDGTCV
GVQTPVLVHLLRARFSSCTTIQFAGGTFLIYPLLPSSVNSRRLEASEAMRSHNFAAEDIL
VDMAHNDGDDENNEEDEGGKEEDEEEEGKRRKVRANDPSVSLSQGVVLVVAMSQPDREDG
AIANLLQIFMNILVREELRSKYVTDQVLRMEHRIHAWEMGSDGDGNDAGAVKHDASPCHG
LRGGKRLSTSNMFAALLKDAELSLCKEISLLAQHITAAKINGKKDDGTVVPAFFPVTHPP
HAQRGGVGNTGSNKQKNISNIGNSNSSGGGSNNSSGNVSSAASNQGGAPELLVRGLYSVP
VASILGHRRPVPYHASAYVRQNPNYIMTLEDPCFVERLAKPYIEAVGWRASQLLPLSTIH
TVLGTLPLPWRVGGLYRALELSLTGAIHQRQGMKQQQQLSLSAGSNSNLRLGWVRTEESF
TMEGSNAFSLEDQNSRLDCDALIVEAVEFLRLSGVLAIDAEISVVFTHGDLLPEAGIARW
SGQKKCRADASCPLPAMKIPPTTTNMPSHQDHSLLKPKPPLPVAPASMIGLLVFEAMQSS
GITAPGSSGDLKSPLFSSDDFAEASVSVQTLTMMASTSSSPPVFPSNNMGGSDIPQLEVY
CAWGNACTICEELASTPYAWRVGNSPVRLSFPFLAPAVADAAARRGRQGARLIDPECCRL
MADQRPWFTRPSKFATPAALADDSPVQVYRHLTRGYGEGAGRKVKGAMEDNDGRSIVCCA
AELGGYTKQNIPTNNEKFTAITPGGIPAMAREWLAKNCSAIGSRLAEALKQRQDLEEHAK
KLTEQRRAAVAAAAGGETTAVFTSASGSNSRAQYSLSATQRYHKRVSCSPKSVPGITGVV
LPLSPISLTPSHESSSSFRHHRLAGDGHVCTVTRLISTERVVPFEALMQFVFHHAVALLW
GKPGIGVETLLYLLECNLRRLRPFLVHYAYIQQLTNATGISSDTASCSSAQLVRSVSTHS
GLNSLNAFQAHPSSLSKSNIRDREKGKIKSKKEEEALSDLEQQLLDSYAVFTELSLMDLL
KKLNGMTVEVVPTRLLLHTVVNAFADVLLIGRGHNAGSSSSSSNSNSDDDDDDDDDDDAV
G*
>TCRU_6916 hypothetical protein, conserved
MSSNYTLASQCQLRRDEMHELLVLATAVATTLDTASENGVGPKECSKLALWRMLLSEAHV
RTLMVHALVRVSVPKSKQQLLIHGNKYMKASCPAKGSTEGQQHNYRVGKVVALIPRPRAS
SDVTKTTSDAPPAGSLLSDWLLGVDFGEATELLGAKYVSNEPFSPEEHAVFVRSCLSTHT
DTTTASAPMTAPEADVVVRNLHDIRKYVTAVVEERSGKAAAAVSAVGGIKRPRDEAAAAL
GKEEDGNRHKKEDDEDEEETLTRAQLLAERARHREERHRWEALLDEQQRHLSGLRQLLNS
KNGEIQRVLHAQRQAEAAHRAEMEQWKVKMEEQGQTIRRSERMLADEREVQKENREKTEK
LVAQLKKLAEQTRRFKEVSDTVADWLRLGTKQPEEVLVALKRKLAESPN*
>TCRU_6917 hypothetical protein, conserved
MSVVVTAARWLPFRQFRQFPSVSCTSRSVWGCSIRLFGYSAYDSIRKPPKRRKGPHALFA
STAATVRSKNDNVHEGGVHGSGVGRTRPTQPESQRLQEAKRTFPETLRSGRYKQQNTKSQ
RLYQGAASASESAPDRRFYRKVEDYREVQDDDPYAGVFREHVGVERRRLREWQRQFEEEN
AHVELPYERTNVIARIAPNWFVRYFLNLRDKGGVEHTGFLWACAFVTLSLLWLVGYFFYT
PPSKARPIAELR*
>TCRU_6918 hypothetical protein, conserved
MEGNFYVSGSVIKRELRSNYGKNYAKCREEAVAYGRCIEAGQINRNLTQGLCHEERRALR
VCVDMHGTAMKQQRLTKQ*
>TCRU_6919 ankyrin repeat protein, putative
MPYPYILQCRESSPEDVIVKYDVAATTGGDLTSVFSLTSKPGNHNIFVAACDGDVPALRM

FLGLGVDINEMGQPNPQYGPQFDRRTLFRAPPLCYAAGYGREKAVAALLEDGADALKTSS
TGFKAVDYARHRGYTAIVQMLESAEERKRSDQQEGKE*
>TCRU_6920 DNA photolyase, putative
MYSQRLSRVSPYLSNGSLSPRRFYEMLRRYATENLRDNFVQMQYREALLRLSRRDYWHWM
GLRYGTLLFFPYGPRPEQTDNIPDWRHDEKIVQKWCAGLTGVPFADAAMRELLTTGFVAH
EGRQALAWLLTRGYGQDWRLGAEWLERCSLDYDPFLCYGNFAYFSELILDDFGEPVRSVH
WLAHHHDQTGIYVKKWLPLLSKIPPVYIHRPHVLTPRMQAMHGVRLGKTYPYPLKLWDGA
QYMLGSDELTTYFDDSSAWHRKTKSGAGGPGHAEALRHGKAIMKVREWNAAILPEEVAQR
PWAHHLPASAFESSEDEVETLQMRQRNQNQPKRHGQLSL*
>TCRU_6921 FAD binding domain of DNA photolyase, putative
MTTQYAPHEKNVHDTIVESIKRRKWVSRDVVSGLKLTTHDAAVSHPYGNCNGDREAVTAA
VSPVPHSVWQTTLVHIDDLPVPVAAMAEGERWYHDDVTVASIRPTAPYDRYIARISSLPT
RHELLPTAAERSGLAHPPLYRGSIPTLDQLGYGNQEAFAVEEVIATQSSHPPGEHAAIER
VEDWLAGGGVTSLLRHGREHRTNVKMYSQRLSRVSPYLSNGSLSPRRFYEMLRRYATENL
RDNFVQMQYREALLRLSRLTRLCTAAAFQLWINLATATRKPLRWRRSLRHSPHTHLGNTR
QLNEWRIGLPVGV*
>TCRU_6922 dynamin-1-like protein
MVEGYFGIVKGTVADQVPKAITLLMITKLREDVYSRLVRSLYSEKKADDLLAEPPEVETQ
RKATKTMMIALKKAQEALESVREFTL*
>TCRU_6923 hypothetical protein, conserved
MSCGTVAHHERRQEKASPPPQAAWSASFLTTRHRQRRSAAAVSRFPNLLRNAYCVSSTGR
PPVYMDSDHHLPSHTAGTEDGISRQAGMLPRRKHVAFVLRDADCDASTTACETPLATVIT
WLGMRKYTVPRGSRDRPEESRRTECSRPSLLRRQHATSVLSYREAACLELKCSANGRTAI
MPFAVFSSCR*
>TCRU_6924 dynein regulatory complex subunit
MPAETEGKKKGKKRGKKVLDPIALERARIEEAEKQRREEAMLLARLRELKEEEEAMTLKA
SNTVEARWMVFLRECKQKELIAEIEIVRRAFESAIDRKNAVIEMLFNDLEEVEEQHRLVF
HSNMTTVDALIEMQTRRMADLEAEFEADLLEMKADYEKEMLELVRKHEHEVADLKLILDN
MASEADLLEKKLQEETSEARDTALEKMEGERKQMQNDLVKISESIRVELDARYKEFMTTA
QVNMKDYMDKSKEDAETTERIASQLKRIEKLQESVTSWRTNLARNAREWEEKNNAIQQER
DATIRHLKALKSKMESWRSKEASRLAEFIKNAKDCEYQLRDTVRRAEKILCLVELGKPLE
TEREQVLSFESNIATSEIEQEVKRLMANSDAAEAQDESAAPDGAAFSEEWRLLERFWTKH
NKVVLDNAALSQEKYHLEEENKKLQVLLKQYLEELSVSDAVMQGPNTLLLMSRAPNVVEA
AKRAKREAGAYNTVVEGNKYVSDVTKQQVLR*
>TCRU_6925 DHHC palmitoyltransferase, putative
MSLLSRWGNRVSIFAQEDMERSAPSRVAAASKTASFGALYFIVAIQFVAAVVLFFWAPMD
LESGIILLALAFSFNAAMVWNWAPNPGFVRDSVELSCEEDRSLFHWCRTCRLWQPLRAKH
CDRCERCVRKYDHHCFWIGGCVGEANHPRFFFLLTVAVAYLVCLWPKFLRCFNFFDAATL
DSALLRNVVPFVLLVVCSVMFLLVFLLWVMHVVLIARNQTTWEFASSHHITYLHSRRDNP
FDRGVFLNVLFLFRPGPIDWHLVMRRDDADLV*
>TCRU_subunit, putative mitochondrial edited mRNA stability factor.1
MVSPHGGAGGSHFATAARILFDSAKKVGAVEPLGETSKRYAQQLKRIQSQSQKKGGSLGS
VSYKVAEFLATQRTPKPNIIRNSTSIAKRVPLIDIPRQPPKKKDVSIAVKPHTENVPPLD
FITNEGKTPGVQPARPKETVAHTKTSHSESLISNRVVPTLDFVTELRKTKVSSPDASAMP
LVVMKMEAADTEKQEEIRDVATIVKPPKATIVEEKPLFETTVVSAQKPSFLAEHDLATLF
EKVVHVPEKIVKPKITVPISAKEPSAKVPHVEPVKSGAMSVDAWELQREREIEQLRKSQE
NAEKERLAMKREEEHKTLGDEWVQHRTTVAKKTVGQTDLTACMIEKMYFSNQWEACFKSF
GQLVSISGASSSALKQAVRIMESRLRYVPLEQREIVRSALLKELKQRRLHDEVVKFELRH
CVGEAFLQLYHSAPSSVKDTLDFYTVAKAISLLVSAGSWQEAVELVGNSQKRFNDKTGLH
ELRLLFSASFLDKDAAKSVKEFVSGTLAAFERFGKVHKLQLAKMEKGAHRRQMILQLIAS
NHVDEAIYAELLRITPTENIKDVLDEIRKRGLNPEDPAILAAVCWKTFDPENPQVLFREI
EKQEKKTGIRPAHLLAAVAMARASKTRETLRSTVSIVKKAPIFKARFTLRKLLPLLHENN
MQKEIVELADFYKDHVPVATALPQAVAFVNDALQAEGRPPLSEQTVSKLQLGDKTSGSGV
GSTKATAPTEATGALTAGSEISSEAMLQCAKDRNWMKALMLINSSFPALAKTADADTLTL

FYNCALSASVEKVEVVQSIYSSMKQRGVQVNATTNNAVLSSLMRCGRSQEAIEFYSQTEI
SARDSNTHSVMLSLYGKIGMWEEALELIKCARGGSKKLPPMIYTLGINAVHSHSWSATLA
LFQTLRKEHGDVAIKQAVVDKVVRCLSQNKRTAEIQKLELELAKKKKKQ*
>TCRU_(ORC1), putative origin recognition complex subunit.1
MKRRRADETKKIIAALRAGVAALSVSSTAAAKELTCRDAHLSAIVEFLNDSVHPVMQIFG
MPGTGKTASVNHALTLLAQSAPPGRKPTAVFLNGYVIQKNSDIYWTLNSHLSKARLGHTE
NCLPDQCAALIEKRFRQGWGGASTPLCVIVIDEVDKVLKRHNKAFFRIVDWLSFPFAFCK
LVTISNSMDLAADAKTRSRLDITKRLVFEPYSFSELKEILLRRVGKIKPTLFAEKAINYL
CNQTASHYGDVRRLLQSASSAVCGLMMKLEEGYRVPEAQDVLLTVKDVHAVVRQIFHDRF
VEFIQTIRLPILFISVAVVAHETNKLFRSSPSDCRLSLDSLFLSTKRAQQIYSASLGEPH
TVDLTYGAYLDIVEMLREVALIDVSIGEERIPVKTAQNLLEATEKAYVSMLQPFPTVLDA
CQLHDVFGEGINPLFKT*
>TCRU_6928 hypothetical protein, conserved
MEVVEQFLSLRRDGHGEEAYEMLAPGAALGCPWGGMHHGENVLELLRDEARFVKKGYLDP
VPIEKIDENTFQRKFKWDRGMFEHGNSGFKGLGILPTWREIYFVDNGKIRLVTSDKQLKN
RSLWHTFGLSKFF*
>TCRU_6929 hypothetical protein, conserved
MKRLRILKLAGYGRKLILRPEATKDPYRYPLGYVPLDGSEPLDSIWALVKNGFFVAPLNK
IETIHRAHLGIRYLTQSEYPAISATDLVGLQLRLKELCSRLLIRRDFWVLEDFNDPELNT
SFGIQNVFFDNFKWSQVLWKRFQVFVEEYFPVMDHTHLTYDEYIQLLRSFSHFEQGATLA
PLLPRRHKVHPPFGVSAPSKLDMEPLLLYMQWLRNFRGPLMLNKALIVWSGCGSAAFATR
YCGVPIVRGVDPNPRAVSSSRKDAQLMGKQFDSISFRVSEMLPDINVYEESSKLRKCDLI
FFYPDQGSLNSFFAEADNGYAPGMNGFAGQLEQFFDEADKHLAESGVIAICCTNLYSILK
PHEPNPIEYEIKVNRRWILLDYYDLPIRSKGIFSHIPSDHRFRFPRELKKHFRSELWILH
KVESLSHFAYIHQIPGAQPPSSVASYWRNKGINKLRRAAMKNQVELMGGDWGDYKNRMMQ
MLQEQSGDDEDDVAQAVRMALDPTYPLELAERARVAVEKNKEIERAFHAEVANRFIEVSP
RDCFDAKSAKLKP*
>TCRU_methyltransferase (PrmA)/Met-10+ like-protein/Putative RNA
methylase family UPF0020/tRNA (Uracil-5-)-methyltransferase/
Methyltransferase small domain/Conserved hypothetical protein 95/
Methyltransferase domain/RNA cap guanine-N2 methyltransferase,
putative Ribosomal protein L.1
MARVGDAFSDDPSVEKYYGQRHRLWSRFDDGVWMTQKGWCEVTPEAIACFSSELHKGLEK
KSCVLDLFCGCGGDTVQLARVYEKVVAVDIDPDAIEAAKKNVEVYGVGDRVSFYCCDFRT
LKLDNMEFDALHCSPPWGGPLYAAAPSFDMENSLRASIGMDFLELLGFITKFSRNITIFL
PRNVLLYSTIPSGFTGNFAIYRHYVNDRCKAVTLLLGGLVNCSSLRPPAAPVYSLKEKIF
PRIEKRNRAS*
>TCRU_6931 hypothetical protein, conserved
MEDDQFRRRLVRFYEVHNPSCLSSVDAIWQTYRGREEDIFRVLTDKYGPEPVLEEDNGES
LRTRVCGSNSSIDGLSIPQKNLHLQNQFKERPESPQNLKDFALPKAESPLALNLMDVNEA
KGVHYPRPTTAKTEKSRNLREKLIEFYQQYNKSMVPFVDEVIENYNDNEVHMFEDLKRQY
KDPMDLVLPVSSSSLEDLNAVMKRLSDALETKTAETLALKKDKEHLVKELTAANKLLEAT
QLNEKHLKTQLLAAKEQLRGCHGSAELEVKNAEVVALQKDKENLAKELAMTNKLLESSQE
KEKLLRSQLLATEEILRSREEIFSNDARQRDKEQIRENSLQAELSSLRKECSGLRSSVFS
SGNRIRVLEVEKQQLLEELKEAEKRIIDVGDMLSKEHQKNLSLLEEVGRLRLTTGGALSE
AAFTSIVNDIEKQFSEHYEKKLGQYREEMNDYYVYAENQLRRRDALIAELSNNL*
>TCRU_6932 Endoplasmic Reticulum-Golgi Intermediate Compartment
(ERGIC)/Endoplasmic reticulum vesicle transporter, putative
MSNLRQRSLLVIKENNERPLLKKVAAVDLFPKPKEDYSRSQTYRGALVSLVTVVVIGLLV
FWEVYSYIFGRDAYTTELSVDTSLSTEVEFNLDITFPRVPCHEVSLDVLDVTGTVNLNVT
RNIFKTPVDAQGNFAFIGTRQGVGEYGSFREQSKDDPSSPQFCGRCFINEHQVSMMENKN
RCCNTCNDVLNAYDQQGLPRPQKNEVEQCIYELSRINPGCNYKGTLIVKKFGGRLVFAPK
RVPGGFLIRDVMRFDSSHIINKLSIGDEHVTRFSRRGVQHPLNGHEFDAQRRFTEIRYFL
KVVPTMYLSGKNSASFNATYEYSVQWSHRLTPIGFGHFPSVSLGFDFHPMQVNNYFRRSS

FPHFIVQLCGIVGGLFVVLGLIDGLVVWVGKFF*
>TCRU_6933 Bacterial transferase hexapeptide (six repeats), putative
MKRCLVLTSDAQMPAVLPDWAIKRKTRLATALDGLGFRLSILAKKVIGVSDRMMGIQPKE
ALYRIPRLLTVYGVRPTVMDNVFIAPSAFVSGDVRIGRKNYIGYNAILRAERNETIYLGE
SCNVQEKAVVTGNTTVGKWTTIEPMAIVESADIASCSFVGANAIVMRGAKIESGSMLCAA
SVLQSGAVLPSGEMWSGNPAEKVRDLTEKEQEDIVKAAKHMVLLAIEHRDSWELTWEELE
DQREAREQFARYAENNREVRTKPMYIKEPPRPSRKAMGRKTPQEMLDGGEHKPPLSDSIH
QGY*
>TCRU_6934 ABC transporter, putative
MGSTEDALVISCENVHKTYLLGSEGVPALRGVAVGVKRGEFVLLYGTSGGGKSTLLNVLG
TIDLPTKGNLYLFGQRITEQTPDSVLARLRCLRMGFVFQSFNLLPSMSALENVALSMTIA
GTRSAAEIRERARDLLISVGLGDRLHHFPSMLSGGEQQRVTIARALANDPEVLLLDEPTG
DLDSRNTTLVMDILMKLNRDNGLTMVMVTHDVYMKPYAHRVLYLRDGKLQNVQTVEPRVR
EMALRKLEKDAEKARRGKTDDKGLTVVSVVRNPTDYVTADAQAQISFEDDPGMQQVVNVL
FSV*
>TCRU_6935 cystathionine beta-synthase, putative
MAQNPSAVNNKKEVPDRRKCILDTVLDAIGSTPCIRLNHVPKKHGVCCDVVAKCEFLNPG
GSVKDRIARQMVLDAEASGRLRPNQTIIEATSGNTGIGLSLVAAVKKYPMIITMPKKMSH
EKEVTLQALGAEVIRTETALPWDHPDSLIGMARRLEKEKGYVLLDQYRNPSNPKAHYEGT
AQEIYDQCGGKVDMAVFTTGTGGTMAGVARRLKELLPNIVIVGVDPYGSILADPSVPLDP
KPYLVEGIGYDFVPDVCERKYVDRWVKSADKESFALASEVHREEALLVGGSSGAAMWGVL
QAAKDLRPDQRCVVVFPDGIRNYMTKFPDKNWLVENGLEEGEVTRPTYGSLEAQLEEAKK
KLSEYEAKCGGSVEEGKRCCEKAK*
>TCRU_6936 protein kinase, putative
MVFTEECSNTSFIFDIIAEGQTEVSDVIEDEIEFLKQNYDGIEVVKLEGFYPKVLLTLEA
ESNPRHRVVLEVAIVAGYPFVAPRVRLRIPEGVTPGSIGALDESGAHQIQADIREAISPC
LLVGAPCIMQIISVVERVLSNGIQRSCTPTHVKSADTVEHPPSQTTMKTREVIKLCVLLL
HLLNKCCHLRDPESMEEAKSNFHILGHYLINDVKVIPKKLQKCIPWKYDYTQRAFSEEVR
ESMDGSDIITKWFWSHEERSGTFQNILPGRYKNEFIQQRMLGSGGFAPVFVCRKKVDGRL
YAVKKILTKKDQSEKVLREVQSLAALSHKNIVRYYDAWMEPGCDEDLINYAATLSEEETE
SSEAGNFELSGTKAISPCFWDDCSDTCSEEDSSSDKSCSSTSLDDNSPPGVLCTPYIAHS
DDYHTLYIQMELCSKHTLRHMIEESDRGEKSLFLSENGEKMAARIFRQLLTVVAHFHRER
IVHRDLKPDNILFEMEGSASGGEIEAIRVADFGLARTMMHATVKRNQSSFEMDDPNAFSG
FEAGGCPTGNLGSVLYCAPEQERGEDYDFKVDEYSLGMIALEMWLAVAGKGFRERFNIMT
EVSRGNKLPEWFCKWNPRMANAIASLVERDPSSRRSCEELLMTADLPGDPADIVEALETI
ERHGERITSRVLHCIQKTMMTNYRKPPSQEKESVKIIANTVSCDLMQTINLIGYLHGALP
AASCDSMVPMNPSLSDLDVPFTLDMRSRAWAIPFQPQLATAYFVCHMTNPIIGSFYQFFC
RKRPYAIFTTPLGSSGTVDEAVLDPLLSFFHLLSVFNLTSKLDIIISHAHWLNAAHPRDA
GSKVPFDEILEMNRPIESSDLILPLVSRMDGVFVDAGLLRPSWDRLELIRSFASLLLEVL
PLFGKQVASNISLSIDPTLKPSETSVDRFFLEHGLILECRTQGEGRPVAFFCNLENFASK
CLARGSDMSAVSLSIDLTELGLVGKHLYFQKKSLLLSGAAISRQDVYSPNQMSAVLMAAV
KVWTGNVRACLRVHHDTRTFCKAMKMRNLPVVLLDGVRFASLESVQHGKVRTRKDVVSGD
LCVAIRKLNGVELMDDVQPRDPAIFLRDEKSKTFSAEEAREIYSIIVKSLSHILVVDSEV
KTVECGIKRIMGNSTATEPETPKLTDLIRWLKSNMSTHDVLPIFSTQDRTVTFFVNQKIF
RRIGHSDNGRRKK*
>TCRU_6937 GRIP domain containing protein, putative
MANFFRKTAPTAPLPDTEEVEMLRQKVGTLEELVKRAEEELREEKEKLSTLQNKTAQWKE
KVKELNAKDRACIKQLEEELKVIKAMHGDAPIPITAEIQSLVEKGLATLRYEHEGELGAK
QRELEKALATASDRASELEKSQRKLEALQKQHMEMQQRFTRQMESLSKHHEMEITQLSER
LSEADSIHELKNHISKQEDEIKAMESHSTQQAVLAGELQKEIAELTTKNNELQGKLNESL
DKMSVMQEKQRNWKESVKNMKMQDMNTIQELREELERQKREASTESGLHPSHEEKLHQWK
ERVKHEKLKDMETIKDLTNKLSKSQQQIDEAQKLINNVAIFLEEIPPKVSHSIEFINKYR
SLLSENFVATKKTASANSSTSTPLTARKDEKADQDTVRASQNLRAQLDEALQQREEVRRE
LKRTSEELAALREQSGADTVNLRAQLDEALQQREEVHRELKRTSEELAALREQSGADTVN

LRAQLDEALQQREEVHRELKRTSEELAALREQSGADTVNLRAQLDEALQQREEVHRELKR
TSEELAALREQSGADTVNLRAQLDEALQQREEARQSFRNIQIRLNEIERECEVAVKEKES
GIRLVEEKLVLWKEKVVAAKARDDARIGSLEITVSSLRDNLSKLVNFLVNFLNVLGETVA
CDVYEHGDDDLDLSLLFSCVDNFQRRLEQTMKALDVSEATMSLIELLVSLNGKVSEGQKA
FVEISAELQRCQHELQEANSRLSEAETKADSLPSPELVAELEAKNSQLEEKCDLLRKEIK
RQREAFQRDRALQGLSSTSATQEDGGINLRSAAGVVFERDMLSLANQQSQRDNEIRRLRV
QLQSLEKENAEMKRECEHNNSVVAKYTKDIEVLKAKERVQQSIEYVRNVILRFLCCTNEE
LRLQMLPAISTVLEFSSKEKLDVQRANPSCPRFQ*
>TCRU_6938 hypothetical protein, conserved
MFCPCYPTVWRGTKEERRRSVEGLTPSFVALEFVPMVKRDLEKERQLELAAIWGSETDGD
LRYPKRRRNTARQPTTTAAAAAADADGASDVLSSLGSDAVGESGGSDRGAPKKREKKGKK
ALSAYRLHCFVAPGTERNAVRTVFDAYEPKVEIRVSQKGNLLNKTHYAVLTFRNKAMALH
SVKMLDGTDQRELLGVKELKLGLMLSRKEQNASRRSMRKRLHEERERKMVKETEEDVTFI
KNFMNLYAPSG*
>TCRU_6939 MORN repeat, putative
MATENPVAQVYEYLKHVVGAGGMTGAVPAATVRNYFGALDGNRMFHGEGVLYSAMGFCYK
GDFVHGSMEGHGQISWNNGISYQGDFYNNAPNGRGIFIWSNGNRYIGEVKNGVCHGNGEM
ETNRGVYSGGWASGKRHGMGRQTYDVDSFYEGEWAEDKRHGRGKLVYPNGDVYDGMWEKG
RRHGLGVMGWKFGTRHYVEVYEGQWSEGVPHGHGRSTYVLYLDADNTPKDVDTPSKFSPP
VLSVVNVYEGEYVQGIRHGFGVFYYADGSTYEGEWHRGNKEGRGKCTTSVGASYYGVFRC
NEAEELLKDSENAGTLPTVAVADFFGVSDNSLEEAKSSINMLLLRFNNMLKTLFDSYSGK
FEDIKLITTNPNWWRHRFPGHLCIPQYLRMLNDAHVINGCVSIHDVINCVLLTIERELES
EREASCNWWIERKCALYHAIENFEGCLNYRQFVESLVRLSTIACVGFKATELPKHFTALM
EGPLTKEHLTNEPLCPLTRQHESLLLPLLPSLEALFLRIGVESNLQPCSTISALPVREFI
GFFRDMFVERGISLVDVLNSLFPFDRFKIPGVVPVAICPPRNALGFSMYEKSCGPQEELA
AVFVASERKLTFVEFVEAVLGAVRLVGVLDENDMLEKLREIIATKSP*
>TCRU_6940 syntaxin binding protein 1, putative
MLDAVHGSFKFFFCDAHAVSALSCSLRLHDLMEHGVTLLEDPMTPRQPIMSSPARYFFAV
EDASVSRVVEDWMATVPYRDIHIFALGCTPHRSPQQLARARIAPRAMRFKDIMLDFAAPE
VLVFHLSMQNGFPQLLSPLSSPN*
>TCRU_6941 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSVCAAEEENKTEKEPDLKDDEEGEPGQETDPLPKNSPSPET
KEEEEGKEKQEPNTPTHTSRETATLKGTAKSESNSNKVEEQEGKSTKEETENTNTSTSNE
QHNELNAPTTTTTKTPTTTTTTTTTAPQAPSTTTTEAPAVSTTRAPSRLREIDGSLSSSA
WVCAPLLLAASALAYTTVG*
>TCRU_6942 Mucin-like glycoprotein, putative
MKTCRLLCALLVLALCCCPSVCVAQDTEKVEESAKTTTTTTTTMQPPDPKTNPKAGAQAN
LGVTISSSSSTEGIEGKDQPSPHAPPVNKPAEKPGEDAVAGKSLTGTTELQSDTNKSADH
TDKEDEEPAKTTTTITAPEAQSTTTTEAPTTTTTRRGSAEALWLPSESSRRTDTRGDDER
RTRDRYTAVG*
>TCRU_6943 Leishmanolysin, putative
MLTWCCPWQSAVGGGAIEDCRDGCEEPRDCDDIDGMELQDGDGDGRTLESHWSQRHAKDE
WMAPIVCAGCCTELTLAAPADLGCMRVKWEMAEPMRW*
>TCRU_6944 TatD related DNase, putative
MAAQASGRVLRLLPVTDSHCHVRTAASFPEETPTDDAKKLPFMCHIVRAVVCGTHPDVDW
DTVAASVAVAHSSQLRMSPTFDTTTEPTASPTVIPGFGIHPWFVPNDPACMVADSAVAPE
GTDAAVGCPHDKKEGERSAEELLCLLEAALKRHPSAIVGEIGLDKLRGPPESAQLPLFMA
QLKLAAKYDRPVSVHCVRSFGRMLQTLQELPAEDTPPAIVLHGFTGSMDFARSAMMIRKR
RPTSTGGGQLATKREPLRIFFGVGASTSLRVKDFAEKTLPFLLRERRMLLETDAYHTLLL
PPPPQRDSYGVAAQSPAREMRSGEGGTMSTKWTASLTAAAGCELVWNAASCEQLAHLITQ
VCGYNGGDGDISMVEGLLSESEEAYTKVFIASTPIPAVATQ*
>TCRU_6945 Tetratricopeptide repeat, putative
MESSGQTDRSSRERREDEATPSASDVRAGREADFLLQRQQQQQQEEEEKPRDRHETDAP
GSDEEGEDSSSCEDECKENNDDASVVDGEDEEEEETTPFATDEEANEARAVGIAHYNNHR

YEDALDIQYRVVRHFEKKYGATAPICGVYFLDYGLSQLRVLQSKSTVEAALQPLDQDALE
ACFINLDVARVCFQKQEQERGEEDIEVQLHLAEVHNSIAQLQVEREDFDSALKEYESELM
TYRFIQEEAPQMLPYRRLAAVLYGIADCYMKEGDFEGAEERFQAALDELASFPADAIPAE
LVKELEELREDAREMKGGKYKELQECIQAQFAVKEAEELPTVQEFYGEDAGNEEGGRKTH
PYVSRLPGEPEYSALSMPQSLTNPVQWNEHSNSMSLSLFPPQVNGRGSETSNSQPVHHVV
ARRKPKQPMSQQQQQPGERGGASSIGEPEAKRARTESCS*
>TCRU_6946 zinc carboxypeptidase, putative
MPVKLEKSSTVKGARRAQKDEAKMEVFDPFTSQLGMIPSRILTTMDTASKKLRHTNTNSS
NASNQNRRNPSANAMASSPVVLKSHSVTRKKNELHASLFAEGRRRRSSGLLRRPFFESSS
VAEETPGKTGPASEPSYDLAFSAVDETTIAVAAAPGEAAATPRRTRNNNGMRDASQQHVE
GKAPSPQPVKIDAGIGMDGNQPSNQRVPSECSSLNSSIAHTPCNKEKRGIKKQTLEENRD
REQSLGNNNAFLFSFEGNDLERYTPYDEETEEKAVHRYMEKTQTTDTPWEGRKSEVSTCD
SILHSSPKKALDAEVISIDNSRSSLRSRSVRRRLLRGQTFMKAKTRGGTVHRRSIRRTIA
EGISDATCRSMSLYNAFFLDDAKKVWLVDDFVLARCLDYVGLMGYEQLMPNGDQASQDLL
SGMTVGQMRSPIIHAQQELNRGNGGANRVRSSRWVLNGEPCNKYARTGGSTLFLHPLESE
RWLSEQEYVLAVVFSCCAWADVHRRFSANKSNNNKNKNKNSSGNDGNDNVEPYFSPDWHP
IRQTAALVLERFPHFGDAAEFVENWERQVSVVLGTASLSHQRVFQFPGEGLVFSSDLEGG
NLARVERLKGTPCQPAFTLWLGPEFGCAQRLWFRFAILGVRPQCAISLRIVNIQPNTKLY
ARNGMRPVWRAGNSPRLWTPVGACVYRTINNDEDGELSFVLLPRSSDVVHVAFCVPYTYA
DLLCHITHWHQLVKMSISGIRFEERVLCHTRDGRKLHLLIITSANNKKLLRRNSRHEKEG
NNFSRPSILGPYGRFETGKKVVLLSGRVHPGEVTASHGIHGVISFLLSRDPRAALVREYF
IFYIVPMLNPDGVARGHSRLDQNGFNLNRCYKNPDPQIQPTVAALRKVFDYLQKTYLDRF
FMYMDFHSHASQSSGFMFGNCLPDTVQHWNMIFPKIVSLHAKGVFSYQLCRFGRGHMTSK
EGSSRVLFGERLIHSYTVELTHFSNNRMYIDGACGDDENNVNDRNYSIASCYGDNDTWEA
RYANIRGARLRWATRSQSEKGTWPLPGAVKTRSRSKRGRKQASSRQGISKRTGQSDGKAG
KRGSKNAASKDEPFCFIETPCILSQSAEVGRACVLALLDYCGVGNEASAQLIDYGGIERT
LREVRRSIHSTVTPRPPANRVQLNIRQH*
>TCRU_6947 Golgi SNAP receptor complex member 1, putative
MESKLRVWESLRNDARQADSVIERQLNVLEGISRLGGNSGVYESRATADGAASSVARIEV
AQREFDRKRSDVEMALQQFESLLETMAETARALPPESTAHSHTERFLQLAAEKRRAVTRL
TADFKRRREWAELLPSVTHDLEAHREGEGVRFLMEEQDSLRHTQRRLNNILSQAESSRDQ
LRGQRDAFARMEDRLVQIALRVPVLKRVLGRISSKRRRDALVLGVVIGICMLLMILFW*
>TCRU_6948 hypothetical protein, conserved
MSSSEFFTDIFEEEARYVGKALLAVTAVGYLASQADGSTLFGRDDVQYAIDAYLPQGYDR
GIMASRANQRLAKNLIVKRLQINTVKEQVRVAAGREAKLSGLFELFTLSLAGILSAAHVH
SLIITLHVIKNMTLVLVYVLRKREAKQGSRGGTVVSTLRSWWSGGTQNFIMKAFVEKLQQ
HLEKSPFAENMDEDTMGVGDGPRCLSVEAILKLTIPRCVDAAIQAVRTALNHRAPHVFSV
TGIVTGRDVRELLDELSQDFESHLMWSDWLTPKPSSPSSSALLFSTQEQLPSLGTSNGGI
QHKDAVSSDSDADDDVFNFPAGSTAVLPDGFSASKRMQRDRAFLETVFGPSSEEGPEARA
AREEELRCEQLARDQSAGFFFELIHSDSFSAMCVAHAAEVLEEIRKLAADLRRVGSYDVA
TDSAKTVHVITSFEHYRLQLLDRDFNVPPYLRLFCEETVRATCGKP*
>TCRU_6949 hypothetical protein, conserved
MVRKNMYDGWSYERLRQQRNRAHFLLEDPYRFVTVLLHNGKLYAIDSPCYHASGPLGEGE
LMDLEDSHTAASVACLRCPWHNILVAIDTGEIVEVHPDTSAVRGKDDGGRELAAPSYPLR
PHWEASAGSVRLSRGNVVQRTHKVSLDESNGIMTIEIEDEATMRRHPLPSDAAAGILESG
ALTMQIFDIKSKGMS*
>TCRU_6950 hypothetical protein
MIRGLWLVMIGLLRFFFEVLLFLPRYVFIERHDRSSPFWGVRAEAVVCFVPASSLNVVNR
IGCLNCPESAKRVFSATRYCGNSVKITPSEDEHEAVMKEDLNSFSISSTHASVSMWWLLA
THAVFILLRRW*
>TCRU_6951 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MATWPVNSREDNNQYGFVNYDFTLVATVSIHQAPSESTPLLAAGLEDGAGKKIIRLSYSM
NKKWETVFYGKTKAQKNTWELGREYQVALMLQDGNKGSVYVDGVIVGSPETITTLETRGA

EITHFYFGGDEGDSDSNVTLTNVFLYNRPLNSTEMRAIKERIPVPTRGPETQVEDGTERR
HIPRIEGVQSNAPAGSGVLPLLLLLGLWGFAAA*
>TCRU_6952 BNR repeat-like domain containing protein, putative
MQLLTAGGLGILMQNGTLVFPLVVNGKNYPFSSITYSTDNGDNWVFPESLSPVGCLDPRI
TEWENGQILMIVYCVNAQNVCESCDMGATWTEAVRTLPGIWVRPQPGVRLYKIFRVGALI
TATIEGVKVMLYTQRGYASGEKKENALYLWVTDNNRTFSVGPVAMDNNLERFHALLYSDG
ALHLLKEGRNEKGSAISLARLTDELNTIKSVLSTWAQLDSSFSELSTPTAGLVAVLSDEA
NIRRTTATTGCSQRAFLL*
>TCRU_6953 Enriched in surface-labeled proteome protein 1
MLVGQYGSKVAVPGQDDAAQLGLLLVKGSVSGGGDANNKKIDWEVTESSLQGLFDKLPDS
WTRLIGSGGSGVKMKDETLVFPVEGTKKAAGTEVDVKTVSLIIQSKDTTNWTLSKGMSDG
GCTDPSVVEWEEGKLMMMTACAGGPRRVYESR*
>TCRU_6954 Enriched in surface-labeled proteome protein 1
MANRNGSVYIDGELLKGSGQTVVPDERTPDISHFYVGGYGRSDMPTMSHVTVTNVLLYNR
QLDAEEIRTLFLSQDLIGTEGNLDSSDDDDNSR*
>TCRU_6955 O-sialoglycoprotein endopeptidase, putative
MIRTGTRRILALGIEGSANKIGVGIVDEAGNVLSNERETYITPAGTGFLPRETAQHHTTH
ILRLVQAAFETAQVRPSDISVICYTKGPGMGAPLAVCCTVAKTLSLLWSVPLVGVNHCIG
HIEMGRVVTGSNNPVVLYVSGGNTQVIACAEHRYRIFGETIDIAVGNCLDRAARFLGLPN
DPAPGYNIEQCAKRGRLFIELPYVVKGMDMSFSGLLSFMEALLQHPQFKDRDKCSSALAS
SVSLSTQRRTLPNGVLCAVDEPFGIDDICYSLQETMFAVLAEVTERAMSQCESNEVLIVG
GVGCNLRLQEMMRQMATSRGGRCFDMDARYCIDNGCMIAYAGLLEYKAGGFTSLPNATIT
QRFRTDEVNVSWR*
>TCRU_6956 tRNA-dihydrouridine synthase 3, putative
MSELSAGGSAPPGVCRVKAEYLRPAPIRVTLDAEGRTRGMNKGMERQHSCFVEGTQRPQF
EGESNFFYGETLQRIKAVVRQGNAAAKRSRDGGRQEKEISTPQANVDGAPLNEEDAAAAN
SIDGHADEIVLQKNEEDERDATRNSELARTKQSEENVRENAARRRALFKNKLVLAPLTTV
GNLPFRRVCKSYGADITVSSMSLVHNLNRLQKGEWSLLRRHESEDVFGLQIAVSQPQSAQ
TWAKAIEASGYSYDFIDINCGCPVQMIMSAGCGCGLWERRDNRLRDIVSSLVQHQSKPVS
IKCRIGAGANSNASLHEKIGDYEGWGADAVTIHGRFRAQRYTKLANWEYIDSCAARTSLP
VIGNGDIFSYEDIIDHRERYPHVSSYMIGRGALIKPWIFEEIKQEQPRDISSQERFEMLR
SFCNYGLSHWGSDERGVLTTRRFLCEWLSFLCRYVPLGLLECPPQRINERPPHYEGRDEL
ETLMASDNVNDWVRISEMLLGPAGEKFRFTPKHRSNSYTTTATTGEAEI*
>TCRU_6957 retrotransposon hot spot protein, RHS3, putative
MAAGSYLLYQLLHCDVDKLQVVVHCFGETAYVFDKTAKTVTKYMGNLTSKSVLYGLWKSG
MKGYIIYDVAKKGTPPDTDIAPCTGWGMIVVSSPNLDNYDKWTTQVSASQIIMNCPDKDD
VKAMCVWMKQNRQLAEEEAEEEAEGRMDKVGPVIRYIFDQRAYKGRIVSCESTVDKMTLQ
DTNYYTVLGTGKMCGNYVSDKLVKVVRVRGNEGSELPLNALISSHLAELTLCKLATLMQQ
RDFNLLILAIEDDLISKALEDHSSFAFLSAAFVKAIIPKLRELKITANAPPHRCALRVCP
HERPFKPCLLECLEKFKKKINIECRVLYKPEAQNFPLVDGFFFSDSNPKTLVGLRMATAG
EHHTTTSTVRQFKERMESYFNGWEEFSEGLSWEMIYVQHADSTPMIEWQRCGPVVTDNLS
DAENREIAAFWKEEVRQYQVSVSSRDF*
>TCRU_6958 Cytochrome P450, putative
MVSPVEAIVGLVTLTLLFYFIRTKKSQKPSKPLPPKIPGGWPVIGHLFYFDDDSDDRPLA
RKLGDLADKYGPVFTFRLGLPLVLVVSSYEAIKDCFSTNDAIFSNRPAFLYGEYLGYNNA
MLFLTKYGPYWRKNRKLVIQEVLCASRLEKLKHVRFGEIQTSIKNLYTRIDGNSSTINLT
DWLEELNFGLIVKMIAGKNYESGKGDEQVERFRKAFKDFIILSMEFVLWDAFPIPLFKWV
DFQGHVKAMKRTFKDIDSVFQNWLEEHVKKKEKMEVNAEGNEQDFIDVVLSKMSNEYLDE
GYSRDTVIKATVFVSSSHFSFIL*
>TCRU_6959 hypothetical protein, conserved
MQHDRALQRRHIRHVDEGVRHQARRALAEAANPQPHTARKHAVVQRHVQRVSKRVHRAQV
HRHSDRPAEHHRVEARRRTPAANRHRLRQRHATHAARRTATTAAGPRRRHVERQARLAQA
ASKAAAHAVRERRRQRIKARQHCRTAAARHHAHGGQAGHAVVAAAPQHPAAGTVALHGHD
AARDRRSGDKRRASGSAARNRHGAAAQRHPRQRCHGRRLAHRPHVVQVQPPAATDRSTVA

AHQRRRDRPLDAHEAQHRINHLEALAKHKAAAAAHNRDVRHGEHRVAPQTETRRGRHTHR
GRGQTARRLQRHAVKHHSARQQVHAAANVHRRPARLQRPQQSVAHTQLRLQQRRRVQHKR
RRHSVRQSAQLGVAHRPRRHNRRVTDRHVRVCRQVVHKHKRAVAAGQPAHTHLQAPVTRR
LAAVAPHVDLRTAVAHAVPQFDAQRAGKHRSHVEHHSHAVRDGHAVHQHRVHGAANRDGS
VHRAAPQSQHHRMHRGHPRRCSNQRQQNKQRRTHSRNGPAPHTVPAARTRTHRRPHPQTQ
TDINRAAVVCCTRPVNHNSCPTNPVLQMANPMTQFRQIVNPLLLIFLIVQLIPNSLKR*
>TCRU_6960 hypothetical protein, conserved
MALKLQRSGIQHRGDNAHVHMRTIPLDRQAHENALQQRDVECLLWRVEIRQVQHNRGGEG
HVDEAQTTHTGIRIVHGADDATVHAADLRVVRFGERERPKTVRNSSRQTRVAVATSSAHA
PAAADAARPRCKAHGVHGARTTVQHPHGRHNIEVISVIRQRRAPCLVADAVDGRARVGWW
*
>TCRU_6961 hypothetical protein, conserved
MRGVHLAPRHAQHSAPRRNHARTRVQRNFATEHSRVQRDTATDKLQHRAVHHHRPPTSHH
GHEGHAGHNQHGPHKTQARQHQHRCVRRGLRAGKIHKRRRPRGNQHGVRHRQHRPRRKRA
GQHKRTVQRLHIAHRQLHRPALVAPRRHRTAQRSTAHHVQHGAVQQRHVLHNDPHAVPRH
PRHVEHRTHAVQHNVAQRHLARTGRHNEHRLHRHALADKNTRRSAHSGRQRGSFHRHARL
AVPAAAAHAHAHTVLHPCRRRPGRVAVNIPVAVVAPSNVDAPSVAKTSRCVLLRRRQDTA
TRVVARHPQMRPSRKRQAQRQHPRQQRSVAHKAQRAPSSGHGASRVEHLPRGAVVHVVLR
QQHRPTGQAHRRIKRHRVVLRQQEFASHKRHCGARHAHSPTHRHRVLAQQKVAVNERHHG
AAAGRNTALHRHAQPQRRLHRQPVQVQRSARRQRHAANNQHANSVAEHRRHMRARNGQHA
PSQIHAVQHEARGGVAKAVGAAIRNTRLCDQH*
>TCRU_of Trypanosoma cruzi region 5/Dispersed gene family protein.1
Dispersed gene family protein.1
MRFPSLTYVVAHAMHLGIFFGSVLALAMPGARGHHRVVGVVGVLYGVAFPAGVCYLIARH
VGASFTRYWQFSRKPLHERLLYPVGYWHPAAQQRMYGGLLTNMRGSRVYWCVFQLSVLCV
VGLIAAVHPPVGDCHVLYFCMAAVLVAGAGVIAFTNMMRSAFLTVMHTAGFVLLAALCVV
SAANHLAPSDGGARAYAATVLLLTTVLLAVTVYGVVVWYAEDRHWQELREPRRGGLEALL
CDDEEGDEETQKPHEMTLSSYASGTTGASSYRPPAPPLQPMAGDTRSDTLSLLDRALSAN
GKIGHAGM*
>TCRU_6963 hypothetical protein
MHEVAEEEAARRMYEVEGSRSVVVAEEEMSGAGIQMAEEVAWRTCGWESVVDVEEISTSD
DEVFSLEGIEQVDALGSVVGMEQNWRVCIEAEDRGLGSDAVECKTVYEPRSTVCSLSFWE
AMPVDEEEEALQGPVEAEGSQRDVMVDAREEWRFLAKSRFGTTEEERILSASRSYSDEYK
WRMLKMVKPPPDTQPPKPFIGFSLAEFLVESFLKVDGLYVNGPAYQVGIRIDDILLSIEG
DRVTSITEARRAVSRHCRVGCLTDLTLQRSDGAVYTVSLWVMTAEPRFKEEPYFFDVSQH
NRFQRHRETTVIEGTSRK*
>TCRU_6964 retrotransposon hot spot protein, RHS3, putative
MEGTVRDEMYLEEAVRRLHHEGVFFLEQWREYQGRDTLTLHVCGKLDGVLTQVERAEKAR
RDAEEEKARREKEERARLDQQRIKFNLTLSIKDAIFQGRARVHKMKLNKFLMRELDGRGV
VDANRNVLLKEFFKDPARYFRDAGVLGEIQATDAYAEMEGAVREEMDMEKDLRKLYKNGV
SNLFGWSVASAEIRASVRDITKSFLDAALEEARKPTTTIAPIKMEGLYESVYNARWHHVV
EVPGGEGTGMK*
>TCRU_6965 Enriched in surface-labeled proteome protein 1
MLVTLPAHSRRKGKEKRELHLWLTDNTHIVDIGSVSGDDDAAASSLLYKSAGSGHNNNEE
LIALYEKKGDGEPSLGVVSVRLTAQLKRVKEVLATWKKVDERVSKLCLTSRAAKNPSAGN
GCSAVKTADGLVGFLSGKFSGNTWMDEYLGVDATVRKGTNGVATGYADGVTFHGAWAEWP
VGRQGENQLYHFANHNFTLVATLSVHGEPKGDTPIPLMGATMNDNKKTVLLGLSYDKEGK
WQVLCGGKTTKELRINWEPETTHQVAIVLRNGTQGSVYVDGQRVGDASCELRNADSKGIS
HFYIGGDGGSAGSKEDVPVTATNFLLYNRPLDDNEIRVLNANKISIPKLTDLKTLAAGAT
GVGTARDGGAHGGSTVCGDGLLPLLLLLGLWGIAAS*
>TCRU_6966 hypothetical protein
MLRHAESVVLIQEARTRGHCIVEQRKNRVITHTEPVHVKQVFVPIKAAVTRVQRAATLQR
QRPNRVQTIRITLRCMRIDVADQQRGRTQHDVVQQQYAQHLSHSIQKLNCRGLYRINLRD
GDVAALREGK*

>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MLLAKGNVHDGVSREMLYAAGAVTAAGSTLSFVRNRALLSRMLSLSLSLAAGAHVRVACN
DAGGRVLSTAEEYAAAGFGDAGRIDVAGCDDCDRDTYCYAPGTASASMRNGVCVCACGSG
GYGEACVPVGAPALSPAVGTASSLFVREGVTVRSVFVVPAGVSEVTLRHVVLDGVSPVLY
VPWMARDGVRIVVQNVSLLNGAVLYVMGGGALRDADGAGSDESGPVELSVCDVEALNGAL
VLTGTFPAGSVLTVTDSLLVAARPTPLVYLPGSQSSPYAPVLVLSGLRLVRSVLVVSGVA
LVTVMTGGRTVVVDGVVLELVGGGVALDSAVLGGEYALYASARVVASGGAVLRVSGSQVY
AAHGLVFGSGVEANASAIVVNDNTGALTDGALLVLRGSASFASGSWLSVRGNSISGRLLS
VPSYPRSAELVQSTLTLYGNAGRGPVVMDGTVALGGAGRNFVVGCLTLNGQALQPMDYRS
TGIIGEFRSVACGVCDADVRCFAATTRAMSRSCRCRCAEGGYGRDCLPVYLPHVDGCNRT
HGIPLLSHTATLTETRSLTPTWTPGMSTAQYSPTQYSQTETPQLTETVAPPPTRTPTASV
SGTLWWSDVACPTLAVTTTAAGGSLTQNDIRGGGSAVPTRLMVALPPPFRWARDPQPGTH
LSFVPVSTAQPSGFGGPWGAMLSNATWVRNATNPSTVLELAVPVHRGYFIAADETIVIRC
DAAAVFGGCKGVLLGSFTISSNTLPAAASALSAITGVVAGATAVAVLVTGGLGSVLELQA
LGVFARMPCASAQERASTVALPYFLSVFAALDPLWIVVGNALLAAVFGCVHYGVTAAFQR
WRGVDAASAWAAMRFPSLTYVVAHAMHLGIFFGSVLALAMPGARVLHRVIGVVGVLYGVA
FPAGVCYLIARHTGASFTRYWQFSRKPLHERLLYPVGYWHPAAQQRMYGGMLTNMRGSYV
YWCVFQLSVLCVVCLIAAVHPPVGGCHVQYFCMAAVLLAGAGVVAFTNMMRSAFLTMTHT
ASFVLLALLCLVSAANHLAPSDGGARAYVAIVLLLTTVLLAVTVYSVVVWYAEDRHWQEL
REPWRGGLEALLRDDEESDEETQKLHEMTFLSYASGTTVGSSYRPPAPPLQEPLAGDTRS
DAPSPLDRVSSASCSINYALLDR*
>TCRU_6968 hypothetical protein, conserved
MESLRLGSLAAHDDVAEANCTVPHSLADRGHAVGSVFSPWRCGIPRDVIADADAVIARSL
PQDCVNAWHVDFLTAVKRRDWKDAQEEKEGAYTAWQAPVGVARTLFLVLTRTSCPEWRHS
AQARCDSCPLFAAERCVLPLSMATESFQFPAWQQYPNRSH*
>TCRU_6969 retrotransposon hot spot protein, RHS3, putative
MDHWVLYEPKVQNFPLVDGFFFVDSNPMTLVGLRMIPAGGHHTTTSTVRQFTECLAAYFN
GWEELSRDMSWEIIYVQHADSTPMDGWRRCDVVDSNNVSRAENREVAAFWEEEVRQYVAA
ISSGELRMGEAL*
>TCRU_6970 choline/ethanolamine kinase
MPPTADGRACPLGDVPLRAVLRRSLEEPPGSPLTTCGAGVVQTSPTLSWVSAESLDSIIS
LANRTEEQLELDGLIYRLCHSLYCVAKSKSARMHRRPANDGYASVGDNASRFHNMRGHED
WCPLRHLFDPSSYYHSVGKSSNPHVGCRCLEESHGPLDGPAGVSQWLADELDVTRLSGGN
SNHVYRLGHASYPGKAVLLRVYGDRGGEAIDRARDIKAMRLMSNAEMSPAVLHSFHWGRV
EEFMDGVYTCTTDMLLASPSLLGDIYEGLCRMHQLDATPFLPENVKGAKFVGRVVTPSMS
VDELASLMEGATGYYGSLVREKALESVCPTSFERASFRLLRLLSSHVVEPHRQSLVDWLA
GEIMFLRGELLLRGVPVVFSHNDLNPGNILLSRRQVPAAFRRSDSLTSLDDAESTAESTR
HVVRRCGSKNLVERRGYLFIDFEYTDANYRCFDLGNTLCELDYDYTRGTEAGGRGFIKFL
SVFPPAAKADAWRGLGEEYPRLPELIVDAWRRGDVDGEAGDVGTAALQAVRRYFATSSGV
PVSEVSVSEAHLVELLLGMLASHLHWTLWAIVMGCVPDECADCAVDTEAFALGGSGLDYV
CYGECRLREYMALRHWLVSNAFI*
>TCRU_6971 hypothetical protein, conserved
MGVPDFLKFAARTSPTALCRIKKGVTAAPLCFDFVLIDVTNVCQTIGLETLAEFLMQPHL
KVRQAVVFAMDAQRHRAGTSRSQRTHATVLDADVAVQRLCIALQQHYNKISTADAPRPQI
LISGRQVAGEADYKILDLQRQLVTQAFAAKEKLPTFCFVSEDSDVLCGALCGPAPHTVTI
ATKLHDTMLEMCVLRVAHVLAYIARCVDAFAGGDEGAEVSPQTQQQQRQLNLERESVKNE
GGEEEKIVRRQKQDGPMVATGSCVVLSDSDGDPSDVDEEGPGNCVPSPMPAITAQNTAEA
EILQNSCIDMVFLFVVVMGNGSSVPPLVRGATKVDNQSCWKAYCRMKYDTAELGHEKVMG
RSLLSLHDVLAHPEKQSNEIAAIAVDCSFLRGILETAHYADAQSRPPVEEEKERALLFLS
QAVYTTFHYIIACNLHPGSTVEDTFLDTRSLLEKEFVVPSLAAFLWVLGLTRKRTLYFPL
AGLANEAVLLNATKGISAVGEAVAAACSRRKHAGQNVVLEWDVANTLVTCGSAGSRRVRL
QSLLPRSKPDAHKGMVACINECAEGLARNSSDAAGNVVPQRNKTALFSRLLIAWRSTMTS
FMPALEVIARKEDFTLLPKNKDSYEGGGVLATQANNVKYSYSFELRRMAPLLTSCERKHQ

ISTATSAALLRALRVSHDYEKAPSVSGISSEVTEGRDRKRGQFAKSNAPSTQKGSKTEGA
TEGLTNAERREGQSGKYRRPGKKERERAKRARENN*
>TCRU_6972 hypothetical protein
MARPTGVTGSALTAHSLGGETRNASTAGNTSFLPSQPSHTEAQPREDEEDFFSPSDLIIP
FHLDIASRLMGLQHSSPLERNGEPLQKSDVLELQMALDDYAEGLVYSTRQLFMHDNRNMV
QQLQQGKDVSTVLLFLQMQREMRQLNGDDSAAKERELIQRLSDHLEA*
>TCRU_6973 hypothetical protein, conserved
MNLTDEDSSTYHSHGACTPISPSRTPEWQPVAPEQNLDVFPSSASPVRSLSSSVSSTAET
QRKKQESPSVRSNDGEIHQLEFTMYPLPDLSTQGRESRKAGHLGLSNGERTDEHPHSGGN
DDGTSSIEFAIDDESFRESKSPILSGFQFVQNPSVTFREGSVPPQCSGGDGDAKRTAEPT
NKHGTNLANVYENNKYTQRRGTETKKKAEEVLKISPWHLEEKTMNTSLHTGQSSVESGSL
RHSGETEGDIQGGNRLRRKERVEPRSQWSGRGSYASRKGERRSSHDEKSNSSLPAMSTRS
ASDDNRPRRRQVSNGTSSVRSHSSDFTPKRSLRASPRRGRAFLYPCRVQNSASMPRTQSA
PLRAVVANSPALDRLRRRRTLESPQRGRIKEKEEILAMLDDEMENICNQVREYDMITEYE
MLRSPFERLYHMNNRRDRDERRCRIYHYMKLEEAKKRLMAETEESAARRRERLLKREQRR
EELFDRLYCTTPNRVNNSQLNSFQTTRSGATAVNNALFQRLYNEGVQSMAEKREKARRAE
LNREQKELEEALHARILARLELNTPQGRLLTPREREVEAEKIKHKLIQDPNQLREYLKTS
RLSKKEEDAMAWRLSRQGYNSASKLAKQKEEKELRGCTFHPTTNKNFIIRGGWAAARYSK
ATVASLSRVKKDESKPSPANSPQRSGSRVQKMACEQLYMKALKQRERQKTLAEEADKQKR
LSLLKAKLKEDHHFRRRVELDPSLAQRFMASLVV*
>TCRU_6974 hypothetical protein, conserved
MRSWSGLHAFILPAQCCRARRNGATLSQRYGCCGQRETVPTTTASTTVSRTHRDPMATLT
DILRAHPSALRLHRELTICVANGEAERAADLAYVLAETVKRVCNQMGSGAEQNTKLTSSP
TPADSSAAEAGIVAKEYMPPMGPEDVELSMETTRRRVLEENSGDVAEAFIKGESENTSSG
NAHPALCDNPLFWKQPTALRVTLLEAAFELTLPDGGDADNPLSPRSTEVEEHEKRNMMLL
DEYLTREKKRWEMQKGAIGRAVLTTAQQLGVTPEDLHSVLEETDSTRHVSGQDGCLRVLK
HCNLIIRGEAPEVELMAKNTAGSLRAAAEEELEVLVSRMERSGSPLTPQERELALFELVM
TKSKMRYVVGLHRDLQMALDASENLRRAASQKQLPSGSEVFTQKVVERLNKVAADGSETS
AEDVELIESLSAPVLPFTFMLKMCLWFDVPRDG*
>TCRU_6975 Galactose oxidase, central domain containing protein,
putative
MLHRRRTSVGTRRGNTADEVKIAALRGAILPEMNNGLQRVGHTIVVYKQDLYLYGGYGPK
NTYSSCIFCNVKMTLQWKEIRGVGVVPSGRANHSAIMHEKRMIIFGGHRNLEVFDDMYLV
NLETMRWEKVNYERAQGPGPVFSHAAVYVPPTQTMIVIGGFHQRQHNMYIAHSFDIRHRV
WTGIRGPDSVDPLHVQMCCAAYNTSSSSIIVVGLVERDVLLSSSREIPSVFKMNVHSGVW
VEVNTPVSLDSPIPFRISGVWDYFLREMISMGGVYEDLCEEWFFPLVLAPIENFIFRKKL
ERISSGAATDTKTRSRTRMASYGFFRLQLCDMTWSIIPVNFPRRVVSELTARRASRSGSL
ANPQPFSRRPKKVPLRENKRTIPFFSVGGVSRFQRKYAFAVTDASDTREGRTGSKLIAMH
GGVTTEDYVMFLFTPILKKRTTSVPTSSDSFFTISEADSCTYSQYSRCGGSTDQSSMGWD
DDQSFSGSDIFRIISGEKKVEKLSSRDDIADSNIMVGRAHRIGSDPTLLPLLPSIRDYKN
SQRFALLYHPLSAVHSEKLLPDPTCPVAVLSNESEVKTWAENFYAGTRQWIAAKLDVTRR
EEKGARRKKKGKESSRTAMEESDEISSSSESEKTKDSGGTQLSIMPSPLYSTTVQSSVTK
PKDFFLDKNLEVFDFNNLEVRRTSYNKNSPFLLPGEMPEKFSRLRMSARRRQAVQRTPST
VFQRFSLGHITDDGGTTAFLLMTSALARFNDGSYESARQRALIRWRYLRVMVLNGEAYFI
MHRVNQEETRVRGVDVSTTSMLTLAPELRTKGLNSNKVFTRPIPYTVPAKSSIALRSSEV
TPSGLVAYHCINNIK*
>TCRU_6976 hypothetical protein
MAAMAHNRLSLESEKVNAPLANRLPKLNPERQETPEPIEEPVTPVRSARRGLRLDFPTNS
HPFSDSPMRESMRAARGSHVIQADRIGISEDYHFPFYRGSYRRSGLLSKSHSNSSTPHRR
PSRAVSFSSRRRETIDTFENASRSPYVAPLIISDNEWPFKISSSRKTPHRKHEETLESMR
MRTNSVPISSFRDSPHGSGNFSSSHRHSFFVYTEADERKEVGTEWRTFVSNVFPPRDSSE
SASGARRSQVFRRTPSRSRETGRHATPERVLFRLNESEAIRVLDHAEILTGKSEMPTPDL
SVPNAWGSGLVPLRTHEVILPERTKKKTVGEKMASTVNENVRSQAEINVGTSAPTGDDSP
PPVEIDRGGKNADNTTYPNVSGHSPNTAPIPITGLRADGGASGRGSLDGKSDPKGRSDKL

SPNSTVPTKAGTKEMEAVGSTTAGASKPARQGVSSFSLPKMNELHSKVMEKLSDKMNELR
GENAAPGREILATHIHSKEKVPTSALPDGEERLDPSMAIGFVAGDSAVSGITVTAGEGEE
HLVGLTLEEPLEAAVSSVSTFLRTLLSSSSDNKRELFELPTADIMVSCLLEF*
>TCRU_6977 hypothetical protein
MRNTAGALPLETRAAAALMDARGRLAPATPSNTKPNATMPAATAAARQVSTDGGVGAAGA
AAQGDPPISRWRLARDAAKKGLSSTETRGSSPPAAQNKSDQVLPSDKNAATRQFPSKPTG
TSRGNYTSAAVPSTQPTAVAGAAAQEGDPPISRWRLARDALGGKFSPHTGTLPPKGVSMA
SGVESAASRPVEPRKLVGEKSGTDRREDRTSPPSVRAPASNPSEEKKGNFSSTQLSRQRI
SAGGNAENLRPSRVATTSTPEEEKMPVKCFGVKEGNPTYVSASGNKDNERPFSVSPARGK
PSSWTGPRENTSVNNTVGNPFTMDPSMGKNPAPQASNDEQVEWRKDAVSGLRHGRMSPWR
SSIGTPYAAPRSNATRARSQPVSISRSRPPENEELMRFLGAYGTPPRRSTGVFPPQQMDE
HPIELRGPLIPTSPYAVARRSLRTTTPPNKYRLLDGGEDDYDESSKVIEEELSSLLNGLE
AYQKRLERAALVVSLERQRRRRH*
>TCRU_6978 hypothetical protein, conserved
MSGMGTALDASDQAALTRMYVKQHKLNEIFAHFLQLLIYHKPENPRAFLQREIRLMIATK
TSTPLFGEQDLETMFDLIDVTKQRWVTVSQLRNTCKNLATAAGEGSIGLSPAQEEAIEHA
ADEEGHVSVEKFKEVLAMQLLTRDIWKD*
>TCRU_6979 N-terminal region of Chorein, a TM vesicle-mediated
sorter, putative
MLEKQLSVLLATYLNRFICDLNEEQLRVSLWSGDLVLRDLELRTNIIDQIILFLFQGRQE
GGGHEEAAGGDAAKAVAQALMTPFTVVKGLVKKLTISVPWSAIDREPISVEVHGVEILFG
LLRGRPHNADEDAARVMVVKQKQLHMFELGRLDGRTEGHAVATGAALKSDTGGGTKKNLS
YVEKLIETIKRNIHVVMRDVSLNYVVSYHGLAPCFKCALRVSLDYMCVTATDEEWEDRFV
MDLSMPYRKKLVMTGLRVSVHAIEKQHAEEAETPGDESSKWQREMDIVEVEDLTMCLQLS
GGKESADIELDAAEQSVISVKTTAPIRLRASFGVIGFLAIINDSLKNGLLGLNYRQHLHF
LAKGNEENLKWTQRRWKFALCCVMDDVRRSKNKTKGHQRFIEGVVLFGKRRREYCALWKR
CQGVEWLPPLTSDEKDNLDTLEEILTVEQIVFLRCLAYADLSRERQSMRQQKLYIEDVKK
RREIKKQSVESAGSRWWWWWRLRQGKVHESATVSEANETEGVAGGFEAEWEFGYNFLQYI
ATRHVVGNSMKSSLSSCSASTATMASTKPVLIDAQFPQVDVEFEPHAWRSDLTEKKPLLS
YLENLQQNLNARLNSVVFKYTLTSTPQEQLVGFSLSVESASVGFTGSLPSAVLYTREVCE
GKKRGKDVGDRNFVREPWLSISVNETHSMLSAFITSTSLTLQPWCELQWWMAGVQHFLAV
LPEYTKQEFSSPCEVPNSHSRLSSLPTMDINFAEVFLTVPLFSAYGNERKLVVHAPDIHL
STVSEKKEGQNDQHRLIREPPPIVGLHFFVGEEEPVRLYCEGIGDILVLSYVRVDVASAE
QLSAEVSTRAKLAIAPSVLGLINNHMEFFEVSQGDVGESLLCEVMNNNGKWCLESNNALS
VGGTIMTFPGARCRSFLRLLHQSAFARGVDHRERTAPSAAEATSPLLHRLVLRIDFAHAT
LRNTNNEDVVEVELPGVENSGYEEASSFGSLPSKDAFVLDMTYSVMNGYNSLICLPDVHV
TAPSGQHVFVLEGLRVMYSTTTLLASVEAEVLDIRVCQSLVDCVELLLMSCASWQTTPSS
DLLTRPSLEENPGVTVLSGSAANTGQVIEMSIKRLSLCFQFHQTEECVAVHLNELLLRAD
SSCGGQNLKLQGSLDRVEYIAEDAEGVKTFTLLASSTGLLGSVEAPSFTCTVESTTVAGG
GVGGQTRVSFCMRGGRVGVFYAYWMRLLSVRRDPTVVSLLNLFGSDDCRCGLPDTPKAPQ
EISHKSTSASAAKVAPGSVVISGEVKALELLLATDATREVDWLDSKTYCYLFVDGVSLLA
ETPGDNGNSRHGSRIAVEAPPSLRGQLKLFGISQFSPGGSEGVLLPFITQVSLIFENYTR
LVPNAEKSGYEYVKGGSEDMAVHVLIGPSDRDDKAKEVPAEAAMDVKLTMPMLNAFLWVF
SANIFNASPLADGMQESDEMTMPTVGGGRLVSGTGSSSPPPTLSLLVTIASVRFVLIKEP
DIFVMRAQFQVYLFDGGESEDAVTQMIHINALTIDDISPNRRVMRREVPQWQQQQHGITR
ESHTSQKKRMLELESGCITTLRLLEGMNNTMLAMTTNVLLNGVHFSTARCSWTTLMGMLL
LDVSSAAWAALTNGSSKVQGESKSKPLTLEVTVHQIHVQLELPWEEPLAELSIRSVSAQL
HECDGNKIAEFSLDDPISFTPYLNHAPQANILEWGEMSEEKTHTTASRPFLHVIFTESHE
NWKEYDFHTSYEEKPQVFYPNRVEVTLQSPRLVADVNFMMRLLRFASDEADAYSLLLGAS
TSVKAAPMTFVTVMDISVKDLRVLFSTSEATPAPRWYLTVEGVKLTNECVETTVSDKPLG
VMECMNCFSNVYTVNVHGAFLSCQQLYPLRLPNTVVRAQIPIPQSLFTEWKSTVSVTPDD
RAHVRSTFNFVSPSSLNDPQSVPSFCKLVHIQTEDDASLSFSALHVRDALRALLLQAPSE
DVPPYYVPPVKLAHAPVCATSSVSVTLPRVSVRLTESGHVNATADACADGEKGASGNGLT
KSAAAAAAILAEIRFLEVVALSASLFPHDEITMRARLSIQGAFELLDGNGVVVLYRRGSA

TLAHEKQQPSRRLRDADDAGLQVDVSDTQTERRICLESNGIIISLRPHTVDFVLRMHNVI
GLMHREGLFVVEGKHSTSNSWGNNEGDADTAEIPVSQNEKQTVLIIRVAHFLLMMENTAL
LEARNVESRLGWKDGSTAGIDTYIPYNIFIGDLLLRETDSHHIFVSISAIELSLGVGEVS
IRANPFIINNYDVLFYARLWNSAEALYLYVLQNVTFSKKHEDGFQQTVMVTLTDVRVCFF
LSREHPASGETAGRMEIVFPVVILKQKASTVENRVTFETEKGIIRYRRPEGRLPPFVKNI
CFSCFVENGLVTQSSSVMIRLSGIEAFIPLGDTLQCCAEAVAQAFLPLLSVFSTVYRNVD
VGPSPTIDLPATPLFCDRLVFNVPLVSLNVCASQSDEEELVERPAVLFGVSFRQIVYERS
RTGGNETTLAQIQSVTSTVDATLQKEFVSAKSPNGVLDEPSQWALYFCKKISSGERKAFL
PSSSHTDVEKEQGEGGYALRHEQLPRRLVSVIFRAHAVKLTVSPKLLSTLNEHVLLHVAS
GVHRIRSMTASLFSSRHMGDSGSSWSHSSVRDPNDRVIIITSDCFLSNDLTLGGKSGSCL
RFSKGAIESNPHNKITVKGINHAKVFVSIFVTPDGTLKPPIVVDPGLTVIVEGVPFFTER
GKLTDYVDLGARSLFLAPTEMPKANSHGYSVNLLDTPTAIVPLNTVSWYNLEVVIDASID
VALCLWSVHQSIEVSGEAYARYKLEKNCYEGNRGVRDFIDESGEVALSNVSILCDSGPIT
KNPAGLMVYVKHHKLKEDHTNAGMTVVRAIFPNISFTLSLGNLRLLYDTLDQLQQGLNHI
ASTMEMTTTRESGQNRDENGKLGKGGKTFSGGMTYSPHAEPSLLWSRDGEVAPLIEFGAS
AAWMELILTNDFYRPEVSIVLSSSALMAKGTRSFNRMTWTASTTVHVTDYPQLQPSRDLL
LVSPEVAVEYARYAGGGFSLQGALTCPELSVTLPLVTALRLLRFRFDLQRTGAYSFRNCT
GIPLILLAVKVNKKNTGEGTPFCRLPPGKLVKASIFHYNQTRFRIIADNKEDMDECDGNL
SMSGAEVDLSALQRGATCRFPLVGPSLGALDVVMRLDEMGRIVDITTSVEIKNELATLAV
CLPGTPFDPCTVKPKETCYATLPCLRHPFSLSVGEWRLKTRNVLVTLETLINAFTLLSHE
QNGTVASSLSDAAVVAPRRAYMEDDDTLVFPLTLSKGHDDDDEGRAEAGEKNKEKMRVLL
VLTRRIALENEPRTSHLLPRYEVELRVCPMVAVFNETGMALAVTMVSSSVVDAAARKLTF
LRGEEEFNYFSQGREGETLMMELACEFAEGVRLCSAEPLPLTFTGTTTAVMKDPVGGRMA
ALLVERAAHSKFIVRAAAILVNALPFPVRVYDGSNALILGQNGEVGLCSGGELPLTLPII
REQLPRPDTAVSVRVVAGGFTAKSSQQFTCNAPTVSGIIHSVDGGVVRIFRAQRSGGIKK
MFAPTPVVRLEPMWVFRNQCDVLPLTVCPVGMTESVVIEPHSKKEWTTFSLSSASDPLIQ
VRYGRNEEELFMWSEPFKLVTLVGTNVSIVMRHRMREKPAETGESVLSSSVFKAGVAIFT
SMRIPIMAGDSPTCEHFACLSITPWRRNGIFYVDFFLDAKVPVVVENRTERLLQYEHVRK
SSSAPTQFLCAYIIQPFTDGVTCLDSGDTVHVMRITLFDEKKPPQQCVIDLSKAAATHEA
VRASQGMFVLCTYDYRLQRYYVSVTTDRSLESRLLFQSRYIFHVEMFIRSLSLYIASICV
PKDENTLLKSPLAVLVTRNQLQLGRVITPEDSANAEVLAALKCRELDIVLIQALGIYSAL
SVNEKHYFGHLDVGRLAFIDCTNPRPTHPVIIGLNSGETRRSTSNDKVEKPSLTVNVHAL
VPDESTAVNVGRASVKDVLLPLQHLRVDVAPVTVKLADSFLFILRQAGICILETTQQTVP
TRTMQELEEDCHSHVDHLASPSSFEEIPVYNCHITQLNISRIDLDLTITRRSDGKFDPFS
GITLGSRFIPSVERAPLSISEVERRDVSQRGSSPYSALLSLLWPSYRNQLMLQFYKIIGS
LEILGNPLALISGFQRGVHSFVVEVADMNPAKGAREFLLATTSSALHTVGLLSRVGSRTA
ATLSWDNEWLETRGEDARISDPMNRSGVLLGMAQGLLDGIEGALSRPLSGARATGFTGFC
TGIATGAVGLLTRPVAGALDGFGNTAEFYSKLLQEPDEIPKAHLSYLESERNFIAAAVRN
PSNFSATGRTSSSDSMKNSASSTASGSTAGPSSNFTELLTRLGPSKKWNTDGCEFVSRIT
YDWIRRNARCEDSHGEDATRALKRCAGVHNYALYADWNSFVANATPEEFYNWVHVALAAA
LGKEVEAVLSSGDFSGGGRAPSKLQRTREFLPDNQELAVALERAEVIKSTLGTRDLLKYV
SLEHIFLVCSLDEVKVHFSPGMIYKELPQLILSGARESLIYILCGGVEE*
>TCRU_6980 Protein of unknown function (DUF563), putative
MTNSLRVAALIYLFFLLFVFFLTRGEAAALEELVLPYCVRGWRWKDVPEEAENPDVQPGG
IGTVRTYKGCFQKVRDRFVVVTPTRTKPSPRSLPPCQHFLQRNETLQFHYLSSDICRMGH
TTKDAPHLMTFLMDYFAPCSTPCQRASQGESASKRLRVELTVLYGNVCTSYPAPKLDEAF
QKVILGWFHAVFRGDSPFIELMGSWGIDFVPPAGASGSGALLIKEVSYKMAMSYGGFFCT
RDEGTVPTTYTPASMVSERCTSGLWIITRWERFRWFRTRAQASLFRRCLLHYYKVPPRTG
DHSLLLHRRLNERHFDELHWQKKLQARLEPRGVSVMLQTFISMEYHRQASFMHNSSIFIA
AHGAGMVNIMSMSPGSVVVELFPHGFRYAMYQELAELLGLHYIAYESPSVWPPRCCIQRE
KGSAAQHTPPLHGTPPRTSFGMRSCKGCDINVLEEDMEAILFDALGIVSADICLHSASI*
>TCRU_6981 Zn-finger in Ran binding protein and others, putative
MKRFMCGPKAVFVSIFRWHHLGGGAVVAPIASHDKQVMYETTCCMSRFGFATQSPLLLQS
WAQRASRVWMCVKEGCRHVNAPSATECEACGAEKPNLRGWVCVECGARNHKGVKTCHKCT

ASAENSNGFWMCAACEKNNRVDDLDDNSRCGFCGYDMAPMTMTEAEAIRIQQERSQRLRE
EQERFDSISAREADEQFGDEAAGASALPMSLKQAPSAALRNFPSVPEVKPFTPSPIETAH
SRISRKPKRSLPTGIPPGPPGFDWMCREASCGTINAGDEESCTSCGKHIAPAEWECCHCG
AMNHLSRSRCFNCRIIIPVSWMCSSCKAATSIYDHSCRQCGEPRPVTEPKDPRDVQFSTH
TRGSAFAGGGRRNMPRPQDWSCVECHGMNFASRTTCYQCGASRGASEVDAPAGASSVSAS
PDMAVGHNNWFCRHCQASNFRTRSSCWQCGHPSSESGATSWSDDASAPHFEKEGFQPESD
GAVAEGQVNVWDKKSDDWTCGKCFSKNFKNRQECHKCGAAKTVAVAPRRAVVRKPVKI*
>TCRU_6982 The ARF-like 2 binding protein BART, putative
MSDDSWIIESIVQFTRSPLWRTPIDNFVDDNCSMFSDDGEMKVEQTEVHLAFRKLADDLI
TSFVGELGVPLETVLAVVYKCVNGQSPMRQPAEQFLHNIFYMDDFCSFHKMMLRRNIQLD
ILAARALQRQQEGLPAQASVEEEAAMDEEEALRLAIKLSLQDEETARRMMKLEDMQIQEA
LALSIAAEEARVRREGETVNDGATGTAAEAGGVATGQDAKEKLSFLKEEKEQVIGKLEAR
ALEVRKETMMRGINATQNVPPSSSDVSSAKSTPVVGDESKQQKEGPPALASAAEKLPAKA
ALPPCAPPGKGFGFKALPSIQPSFKQLESLVLQTVTPPPPQPAKRTDDTPKTALPPPTLE
EMEERARHMREQREKILMQNKANREKELKDYSVSGGKTSVKPSGLRESEKQMTLELARRL
REDIVHEATK*
>TCRU_6983 hypothetical protein, conserved
MAVLFPSEGYIASVELICAEHLQRTLLACDEATAFQRIVAQAVVLHGGHWGFEQHHALGG
EGHRGFPLQTIISKRDGWRVSRRTQKIDPVLERREEFMQNEGTLLRRMAAASRGIRQRGA
ALYAFGGSSY*
>TCRU_6984 hypothetical protein, conserved
MKLIILGGPVVGKVNVDVTPDKPFGEVFALIRAAVDKGALWDKFQLNVAEVRDRKVRATT
RVIQSTDTAESLGLSSDAAVLILRPLDRNMSGGPTVADRVTDTNSTPPKSTQCDYRSRMI
AIYQKYEPSKVGTVDASLQKFKGKEEAVIRQLVKRYGPEPPVSANTPSGNTPGPQSALSP
VSPLPPAAVPEVAAASPVVESSSEPAEKSYRSRMIAIYQKYEPSKVGTVDASLQKFKGKE
EAVIRQLVKKYGPEPDAANTDFPQSPPNNDVTSPIRSIKPQTFQGAETREETPVSPPSNP
QSAGVIHTSASPLAPTNSSKTVGDVLLEPSRETLASIPSTALKDAKKTQVESYGFQSFIS
PTDHEPLVEPLSEADGNSTVVEEEQGEGTTKADENKGLRIPKNLSFGTAAAIIGKDVFDT
TKPMLRDLARSLPSRRRGQNDILEGRCVSIITNNRLQGVVKRAVETLSETAANMLRRVYW
RIWQYKVARKLANNLIEERVWMRTRGGARLVDSVPHTLDVPNLEDYVYEKRVCRRERNAE
FSDDLQRALRELLYTAKHHLVEANDPEDTPFIFDKDLCPVRDTKELAAALCLLKNMIIDF
SETKSIVNLRERELSKLRDTNEVLRRRLGEAETSLSHLTQVGEEMAIVQAQCDKLKEELG
QAEEGWKNAKYQLQFLQRELKKERNQPPSNAEQLLQRKDNEVVSLQRELSKLRTKLHREV
KEKESLRSQLKEVKAEAVCAAQKLEKWVSSGALASRGRSAGALASQLNLPRGFFSSGFLQ
TMKTEKIRDEEYLPLGVAEDAREVTSLVGRTSQDIVRENLRLEVELRQNEAAPEEIEFGN
CPHCRRRLTSCSATPTGPPGKKAAFCFSCRRSYTFGDLTTRGNLSAVPLVKRWKDPSPRS
FVKY*
>TCRU_6985 hypothetical protein, conserved
MTTALTSSNRSNIPAVCRIRGRGTAILVSPGILLTSRHVVSSPEVAAQLTAVFFEGSKKK
TVEVKLLPQKLFFAAFYPAYMDYCLVACEEYGIFNVTPVSLPLTQNDWSPVREGDIILVV
QHPTCKDDDGEAETNTGDSDDGEDLPSVEIKRFEEVLRCRNDLYYLKANGNLRTAGCPAF
NDCGQLIGMQSQLRSEGGGVVNRVVSIASIVKHLFANKQLQRIQQKSVFNDVWNTWYVKD
DISRILLILENFSDCEIARATAEKLCEHTCFPNLIESIVASGGVEWILSSLHQFKEDMAM
VCTCIRAMWNVSFGETNAQRLLIDGGGVELVLNSMERYPENEEIAEFSVVLLHNLSTGSC
RPDFTGPLGHRALLLVHAALQRFKETIVLQKFGFSFFTTLLYVDVEYAETLVKLNIVEHT
VYLAERKQDQVFLMEALMNFVGELAQHRKAIDLCFVAGGLASSAGQHVLEVLTSLLIDIM
FKYQEMDTILLQGNRALWGIGNDLSCRAMILQNPRSYEALRLSLAALMARARVT*
>TCRU_6986 amino acid tansporter, putative
MTSREEKSLSSDEGAEVVAEKTPREPKDVQQRINVESPMRLQRESTRASVHEPHLPVSCA
SGLSTSSRWRSAASLRSEGKQTPSLSECSRTLTPVPATHRLDGVNVAVLDSNPRTAMLQR
CGHQAAANYHTSLEFVSNAVETKKVDATYESDEDIDIHSLGERLTDVLESSLRGAASVSQ
RGEANSTLGRAAFHIFKGNVGAGVFLLSTYYKDAGYGVGFLLVFLLGVLMIDCALALVRS
KQKIDLLIVRTYPAVVGHILGSTLMHFTNFSLIFTQFGFCVVYIQYASSMFTALLSATQF
YQLLVFLSVLMVMPMSLFSHNMRMLAYASMIAAVFVALVLAGAVGEELDYLSTRGVSQGT

VFFEPTMRILVFISGHMFSLEGIGVVLPVENSMAAEDRPQFSTLVKYTLASIVTIYVVFG
LLGYLAFGEALQTSVVLAIPPSTTRTMLQVLLGFSLIFSYPIQFLPAIQLVDRALGISVH
KEPWNAYIVRVVLNIFFGALAASIGADTINVFASFLGAFTGVHLMITMPVLLALFTDRVL
NCAQEDAEISFCDYVNFFFTMPDTIVECRWYLYLFIAMLVWIGGTYYTFDSVFG*
>TCRU_6987 Transitional endoplasmic reticulum ATPase, putative
MPPPQSQQVLKPNKLVTDDFQSDDNSLVMMNPKRMEELNIFRGDTVTIKGKKHRSTICIA
MEDEECPEAKIKINKVTRRNIRCHLGDTVHVSSCTNVPYGNRVHILPIDDTVKNLTGDLF
ETFLKPYFLEAYRPVKKGDLFVCRGAMRSVEFKVVEVDPGEFCIVSPDTVIHCEGDPIRR
EDEERLDDVGYDDIGGCRKQLVQIREMVELPIRHPELFKNIGIKPPRGILLYGPPGSGKT
LIARAVANETGAFFFLINGPEIMSKMAGESEGNLRKAFEEAEKNAPSIVFIDEIDSIAPK
REKAQGEVEKRIVSQLLTLMDGLKTRSQVIVMAATNRPNSIDPALRRFGRFDREIDIGVP
DDIGRLEILRIHTKNMKLDPGVDVEKIAKDSHGYVGADLAQLCTEAAMQCVREKMSVIDW
DDDTIDAEVLDSMAVTNEHFRDALTKTNPSALRETHVETPHVTWSDVGGLLDVKRELQEL
VQYPVEFPWKFEKYGMSPPKGVLFYGPPGCGKTLLAKAIATECQANFISIKGPELLTMWF
GESEANVRDVFDKARAAAPCVLFFDELDSVARARGSHGDGGASDRVINQILTEMDGMNSK
KNVFIIGATNRPDVLDPAIMRPGRLDQLIYIPLPDKASRVAIIKANFRKSPLSADVDVDK
IAAATHGFSGADLAGICQRACKMAIRESIVKEIQIEQMKRDGTLDSDQDIDPVPEITRLH
VEEAMRGARRSVSDADIRKYELFATSIHQSRALGDNPIAGADGGGGGAGNAGDDDLYS*
>TCRU_6988 adenylate kinase, putative
MNLLIFGAPGCGKGSVSEALERDFGLLHISAGELMREEVEKGTPVGRRVAALMNEGSLIP
DKVIVDIMVKRLREPDAREKGVVLDGFPRTLSQAQALTENGFEIDAMVFINVDVKLLEER
CLQRRMDPVTGRIYNLKSDPPPESIMGRLLIRSDDTLEKHQRRMRIYREQKSALMKHYEK
LIIEVDGNPPLPVVYAALHAKIDQLRKAKRKSKL*
>TCRU_6989 leucine-rich repeat protein (LRRP), putative
MVTRTARLGGKTNGAKPSGLMLNKKGLHSVHEVTLANYSAEYLYLRENELTEFDAEVTME
NLKVLDLSINEIGGTVDFLSKTPFLRHLYMTGNRVESLHGIANFSSLETLCLSDNAINSF
EGLERLPNLRVLSLNFNNISSFEHYPNLPSLHTLNLVGNPVTEIPSYRSMAIAINNPNLV
TIDGNPVQGEERAALEHYQGKVAYCICEGFIVEGDNVEEATDAFLLKLQRAREKSKHLQL
CSIRLTPEDETRNVLTEGIPVRLTCCMQDIRTFEQRGTDIFFSRYLYPVTFRVSGEATEV
FVVGSMNNWTDPIELERCGDEGEIYFHTILYLPAGDYEYRYIVDGVEIDPEANGVLSKYK
QGFCYIYKVTELERTEDEKDTVLHIRWMKSAPGSCYEIIEDNNTLTYTPTVADVGCCLRA
EVLAYVNGMFSFLYFDISTPIVAGPPTCPHLEVKGKAVEGHVLVAEAEYVGGVEGNSYLS
WFRITPDGQEIAIDINDPWSGYKLTSNDIDCRIKVEFTPMRNDWVAGEPKSVVTAPVVAG
APECESIKIIGSLIEGSELEVEVVYSGGEEGESYYQWLRKDEGSEEYFPIEGENATRYVP
TLEDVGKCLAVEYTPVSKQGEEGETCRCVLEKPIEPSTPEIHDLKIMGELTEQHVLTVEY
EYTGGHFGPHVIQWFRRDRYKRLTKTGRPNSSTLALTKREVDCTIEVSVTPVRSDGVQGR
TVTTRSDGVVSAGIPQTNFLNVVGEPLVGNTLELEVEYFGGEPGEPIIEWEREVPGTENF
EVVETGVRNYTVQKEDQGRLIRVTYTPVRVDGTPGEAKSRIVQVPDDGADEKEEEKEIRK
TSEEPVVTRHVDPGFATATRELEEAAANVASEEETESMKKDEETKDGPEKEAEDAVASNQ
NADEGSQLNSAQAK*
>TCRU_6990 Domain of unknown function DUF21, putative
MTNSTFFGLHIDVSGEVLGGIIVVLTIIGGLASGLLLCLFSLDKKRLNALIQVGNTKDAR
RARRVMMLLHKSNWLLVTLLLVEDLVVEMMPLVFDTFLNSVAAIFVSVGIILVFAEIIPQ
ALFVRFALQISAALTYGVLFVMCLTSPLTWSIGKLLDFFVGDKESFFLGRCELLELIRLQ
EEMRSEKRVRNMSSLAVEDASALEDQDQDFSPVESSIMLGALSMSENTAGDVLKRGIASV
YSLQCGACLTKEITEDIFSRGLQFVLVYNDPNDPTNVTSVLETKVLILLIYCQGNDSVSL
GELPLHPLPRFPETTLCSELFEALQHMVIQVVAISDVRGRVIGVLTMQDIVEFVHKTSFQ
AEMDPRAKVPFQIMVHSWKRLCGVRGDYVASGRYSLTVGGGRGGRTPSTSSSRCSTPLLQ
RPTSRQDMLQSNFTQIKVSDENKQSDEKRTK*
>TCRU_6991 Rab5-interacting protein (Rab5ip), putative
MSLGKTIYVDDDLGENMRSVSQIRTMSALIAGVGAGVMGLTGIAGAVFFFFCAIISSLII
LNVGCEGTPERYFPSGKKQFFSLGNLVTGAMTYILAWTVAYDAIYIF*
>TCRU_6992 hypothetical protein, conserved
MGLRKASSGFYGDLPYCSPVESSVFFDAVAASRMHRISESMISRADSISYFMKENTPFYD

LFLRLRKGFDENDSKLKHGGVLEFLDIIPSLFHSSSAHRLVRESKEGNCFVVIESKEPSD
MCGIFDVAKQDDLSVYFFVSLDLRGMDCMWQSLLTFLLGGASTEKNMVYVLPIIDFYLQK
GNTYGEFLFSLWAIGVSSILHHFALIAVDSVRERLHKVSIRIGALKGHEGDSILDDVQLF
FEDRLRVCVYRVLNTEVLPNDPFAVETECAITAGDREEWLEKVTELILGVHEELCDIGEE
KPKKDDAKLRCVLFIIPDIISLQNDLQKHLSDSYASTPIIVATKESQIYELLALHNRSAP
IVFFCSPQNLREQLLKPEHERYLNRLCVEVFFYSEINRYVCDIALIRMLFPGRQPFYLLP
YPLFDATNSDERNEKANELEESFLEEAINIVLWLFRRFKLEKCRKGIQPVLRISEMFFIS
RGAALIFEKVMNAMKSSGLVSSLNISDESYSFRLEVLGRAVSYRFCLPYESKFPEFTSFD
VKCIFWCHAFRQPKGTALKLISSAHHFPTWVEAAINNFCLQHRIKLENDIVTEREALVKG
LSLIPKFDGINSRIKAFLTYPSGKRIPILGSFVSASSTRSRGWFEQAPVSKSAESVTRPH
VNVYCYPSHNELCEICFGDHTIQCPLDLSYPLIVTHIVLHTTLWNNAIILESGNDNGLAV
PLPIPLALLHSPTLNSILEDVDDGKVGFWLDNCMDSTPPLSDPLELASLMAKTPSLLGLC
DHEALRRKRAQVDLIMKRQKCEVKEVSAPPSEAEAATIREFANAAIKLGRENAEKRFKGM
RGFAFLNSSNENHAYYLHVLGQSKP*
>TCRU_6993 hypothetical protein, conserved
MPLGVATRSSPAVLDGERPSRSSWCEFRSQITAAGLNDEWCSQGEQREQLPWEGCRDSPR
TCWGRPVGTRGRRWSPGSWCHGLQALAWQGVAHQEGHATGTPTAGLVEVTAANEPRRWGT
LVSALLQKSHAGLLLRQSSSKGNPEGRRALRYELPGNYDAILIGAAALADTTAAGDAGKV
TAMKRLCGSVSRAAGKPPRRSTTNRAWDLLEG*
>TCRU_6994 hypothetical protein, conserved
MSVHVSCSRTDGRLGWRLPNETGWRKCANKPAEGGGGEDECALVCIAAGYVYKDAENPRP
CAPGGGPSVVWTGIGMRLSENVKNCSSAAAPTAAVAGQAQSGVGSPPGEAAEAPQKSPEH
TDEGGSYPSLSEHVASAPEASSQTPSSPSGGTATGVRDPGGADSSDAATVWVRTSLLLVT
ALICAAVR*
>TCRU_6995 Mucin-like glycoprotein, putative
MMMTCRLLCALLVLALCCCPYVCAAGNEDKTDKAAETPTPQDSVVLNDSDNTRAKGTELN
GQTSDKEAGSSERPSKTVSASATPSPTGTGERSSGAPTLQDGRDASGQQGASEGNNLSPG
STGDSDMSDVNREHNKEVALTGKEVKEQAPTTSTTTTTTTTTTTTTAPNAPSGTAMNAEA
PTTTTTRAPSRLREIDGSLSSSACLCASLLLAVSAMVYTTVG*
>TCRU_6996 Eukaryotic protein of unknown function (DUF866), putative
MPFFRVCLRAETEGVLSIRPARPRVWGMKFECDSCRETSPHFVYVDEAEERDSGGGGTRN
AVFKCAFCKGVLTASIDPESYGRFTPDGDNGLLLVEVRGGSPKELELDGNWVVEAEGSSF
DGVDLSEDWMEYDEASGAVVSVSGVSVVFERAKKKKQHEGNA*
>TCRU_6997 hypothetical protein, conserved
MRREELLQVLLVRFVDPNREEQDWLMIAALFYSLTRLFLSAQRVERLYYKYLQMHGSCAA
MKAACKGYEAEVEERLRQRVAGGNSLVASMAMGGRHLSISSPTTSRGAGMLTPSAPAGVA
VHSSSGSAECGSLANLFLPSPKGGGRNVDDGSFAGGAALRHLTPEQREHWHRLRQEPISP
DVLIALVQRFSLVEGAGVFLAPVHPSTIMEFNGARSGPYGTVVMHPLSLMCIKRRILASR
RDYEPRQPEKRASVTEMIVDGGNVTTRKRGRVTAASVVERNESMRKKLSRESGDDDAGVI
RTLQELEQAVWHIAANCVAFNAPESYYPFTARTFALACTGIIEEYCMQHLRGA*
>TCRU_6998 hypothetical protein, conserved
MKRRVLRAHANKSRLRLLSAENGLRLDSYNILCDASFMRAFLLAEGSSEGSPAQALRALI
YDTFSAATSHVSREEDGSRSSGSARIKKPNELNLSVYYLLETATTLRRMFQQRLEEEQED
AATRRKRKRNEKELTSLEINKKGRHFISVVESLLEGLECIRGEDVSANKNEAKAIARFLA
AAGSKEGPPTRTAQGRKNAHFFFVATQSHDVRRLLPGNAALIRLTTLPTALWIEKNGDAF
HYGVDGAKNTPLHDASVPTRGKTLSAADVAFMRHLSAELVPAGVGANKSPWVGSKGGTSK
TLNATLAMQNKATPDTGSKNGVRGENASRSRRKSARGPNPLAVKKKRVREVFRVDLGASK
KQD*
>TCRU_6999 COG4 transport protein, putative
MHGWSSPAPSLWGDLRVDGPPSLVAQPAKPPNESTGFGTVRLAFPFAQGEDTPALGSAGG
EADRRRRMSTMTTAAGEKGELSLHGCGAAALPMGMNSMSPAGASSMASQFSLDSWVDAFR
VYISAAFVFPEEKMAISSMMEALAKYTQARLRTQQHFSECEACLNQFTQLQNGVVAAAAK
GSVPLSSGNTKDTFTFQSQANAVSPTFNMANMQRGRAKVDMDLAECRQTLQKVEAFASTF
QDFQRRRTRLLEVLEEEKQQFLLPPLPQRHSGGAFVPIVTAPVFQLQTTLEDGISELYKQ

WDMHIATKAESIICRLNGTHSQEDGDVSGSKEGGELVDSTHLITLLLKMCDDTLGRVETM
RSRISRLGSIRIDEAESIEKLLANMDNYDPTAEEHMGRRKQIDAELEELRSWLTHIGQLR
QRAMNTKELLQQCLTSGNRSTAGSKQTSPCVHLRSEGGGAPSSLRPSLGGPTSLDEWRQA
LVMPDAGAANKMDANPVVNATTAGITTATSNGNSNNNDHAAPVFTQEDGTLTVCNQRPSS
STASDNVKNEENATEINSMNFSLAEPPVSALSVEGNGGNTIAEDACRGGLAVSFPAYGAE
DRQTETGVPFRNSKKNSDEDDDVASSFHASAFDEDDLCGNGKRWRRRRKRSAARGYLGGI
AAFARAVVQRATQFSDSECSSPSDSERVTEVRRRRRLE*
>TCRU_7000 hypothetical protein
MDLSASPLRMDARVKEEFLLHFLNLISSSPLSSSSEVGASFQSDRDAATETKLVTVFVRG
EDAGVDADTKTGRRRRREASCKNPDAIQLEESMAMTTQTSGNTERAQLGRYRQLPGYREA
RRMAQRMALEKVRKQFCCSAE*
>TCRU_7001 hypothetical protein, conserved
MHGRNGELGAVCHVAHAVHTCSNCAASFATEEEVVTVAFTTNVTTHKYAGPYELWRRQFS
PDVTIHPPARSSDADRTGICHLPPPHEKDDTESGGTTAPQVNAEPSRQHEDWRCSVAADG
PNTVDPSPASNTATNTSETRPEFATNPNEMMVPNASTKRPSFANGPRILVALNASGIMSV
TYGGREHVAADNTDEVNEHNATGHKSLVLENGVAGSGFVAGG*
>TCRU_7002 PPR repeat family, putative
MRVFRGAYCWPRVSRFVHAVRWSSTSGVGGATPASRAEMSHVKPASSSSELWRSGEDSRT
VTIGRPHVEATTPEQVEMTFRLSVLARTASNVQLRRYLEQLQPKDHALALAAVQGAEAGG
LRVDAKTNEVHLMKLMDGGQLRASMELYRRMIDSRMTPTANTYATLMHMCIQREMPETCQ
KMFEEMVKRGQSPNTKNYELYITSLAMENPPKWEKAVEVFDHISRDRRGKHLTAMTYNSL
MRVYLNMTPFDWRVVYNCYHELRNRKPPILLQWESYLLVAEALRRGRVGYIRRFITYLDA
WFCVTPIRSVEFLFGMALYVGAMLVLKAIISWLVVIYYERVIAAKKGVSESIL*
>TCRU_7003 10 kDa heat shock protein, putative
MFRTTVSALKKLQPLGQRVLVKRTLAAKQTKAGVLIPEQVAGKVNEGTVVAVAAATKDWT
PTVKVDDTVLLPEFGGSSVKVEGEEFFLYNEDSLLGVLQG*
>TCRU_7004 hypothetical protein
MGWRGNLVSGLRDVDDPRLVKHYQGPLLSMSAASDDGVVLADASKEGSVAIGRRSNGEVG
RGVAGNQPVLCAFVRQVLGGVEETVCEDGEITLDFDSLRIVLKADSTKDGGSDVRCVEHS
SRRRPLHESTTSSYTPQRHIFAPQRRRRNTISSPITSSVNIPLSEQRAKENVRGQLPTLT
MPTEYMNKENVSSVPSRVGHTDSTARAGREIASLWECIRRARSYLSVNLPLLHRERDMDV
LEKEMLQMEEADISVSSITGGKVGDSSVVGSNKTLTVASGSSSFLCRPFQEMEADSHRLA
PRLKGQKLREAWRRDATLPARLHGVADIEGTGSVSLSRLLTVLREHRYLDWTEEEVKGTV
AALANNRYTMNEASDSMIQEGNFETLICINEENETFYLNSGAFFSLLRALLLL*
>TCRU_7005 10 kDa heat shock protein, putative
MFRTTVSALKKLQPLGQRVLVKRTLAAKQTKAGVLIPEQVAGKVNEGTVVAVAAATKDWT
PTVKVDDTVLLPEFGGSSVKVEGEEFFLYNEDSLLGVLQG*
>TCRU_7006 Acyl-ACP thioesterase, putative
MFMVDTDGSAISYHIPVSPFVPLQHDKIDVTTVNRLANFGMRFAMEHGWCYNRHSGDAHS
KYASEAVEEGYVESGEDVTVFFAGVDVELVGEFPKFDGKITPASVFFLGQFWISHVGKSS
FGVYGKIFRYEAADEKNKFPIGVFKLTGVNVSKKSRRPVPIPKERAEMLLETMRRHQLNT
SLPLVVRIDVADFLARSGLFTDTTYCKLVDKMATHASVTPLTVTYRREFHIRQSDIDFNK
HVNQMALIQFVINTFRSALLDQTTVFPRLLDVGVDAIVGDLLLRRLHIDYIRETPMGHQS
LAVALFFAEDSSRDAVIASTPESRGNQLAELCFLAQGIPGDGSPSYIAAVGKLYFFC*
>TCRU_7007 10 kDa heat shock protein, putative
MFRTTVSALKKLQPLGQRVLVKRTLAAKQTKAGVLIPEQVAGKVNEGTVVAVAAATKDWT
PTVKVDDTVLLPEFGGSSVKVEGEEFFLYNEDSLLGVLQG*
>TCRU_7008 protein disulfide isomerase, putative
MFRLSSVRTSFLVLLLAVATLAFVARADDPSVSLEGIVDLTASNFDEHVGKGVPALVEFY
APWCGYCKKMVPEFEKVGQAVKTARDKVLVGKVDATQNRDLAERFGVNGYPTILFFPADS
QTKQQYSEAREAPAFLSFLNRQVPGLNIGTPHEHTYAVELTKRNFDAVVMDETKDALVMF
YAPWCGHCKKLHPVFELLAKAFKEEADIVIGKLNADDASNGAVRNRYKVDGYPTLVFFQK
KSKSEPQYYSGGRSLEELVDYVNERTGKNRLPSGDLSEKVGVNDELSKVLRDMMLKEKSV
DEKKQCLEKVKKAAADLTGVEAVQYPRIAEKILQLGAEYVEMELGRIARLKQGDVKGEKR

DMLTIRNNILASLKGE*
>TCRU_7009 Enriched in surface-labeled proteome protein 1
MSRRVFTPAVLLLVLVMMCCGRGAAANNKGASGQESSPGNCIDWRDVKTGEKVGALHAPS
LVEVNGKVFAVAEAQCTKKERCVFTGIASELLEFNGETQKMELDESKLKTQVLDECSASE
ERQCLSQPVKPDSSQRVMNIHVGRPTTIVTTSQIYMLVGNYSRTAAAGTQKSEAHEWGLL
LARGNVSEEQGKKINWNDTYRFLWTDLKKQHESWVRSMLPVLLR*
>TCRU_7010 BNR repeat-like domain/BNR/Asp-box repeat, putative
MQLLTAGGSGIVMQNDTLVFPLTANGKNYPFSIITYSTDNGNTWVFPESISPWECSDPRI
TEWETGQILMIVQCKDDQSVLESRDMGATWTEAVRTLSGVWVRPQPGVRLYEIFRVGALI
TATIEGRKVMLYIQRGYTSGEKEANALYLWVTDNNRTFHVGPLFLEDNVNETLVNALLYS
DGSLHLLKEGGIKTSKAVSLARLTEELNTIRSHLGTA*
>TCRU_7011 retrotransposon hot spot protein, RHS3, putative
MRGELVSALVEELKELRSAKRNEAQDSVLKVNHQGYPTRTVGLGKLQGGVTRIPMEYRVL
YIPAVQNFPLVDGLFFVDSPQKMLVGLRMATAGEHHTTR*
>TCRU_7012 hypothetical protein, conserved
MRIFPHHIRAPHAEPRIFFCDNVSCSGVGVLQPRHAQDAPDGVRRSAVEAACASLGPYDA
GRWTDGFSSLAEHASGSAALPLDSPDSRAPCRPHRAAAGSLACSCRAECPATEHGHRQFP
VPCLAAASQSPTRVPVATESLSAMESLRLGPLAVHDNVTEEICTVPLSLVD*
>TCRU_7013 glucosidase, putative
MLLSFQYLLRKLILPLLLLPTLLSGTAVRVRAVEVVKLGSDVFLDVSDYGSGVLRLSLKP
LTKSFYEVKDVVVREPEAGNIGSTCEGVSCTINSGQCVMKTSVTEEVFHASYECHGSVLS
SMEMPLSLFEEPSVAFKFPSARRLYGIPEHATDLSLHGNATYAMYNNDAFQYAINDPQAL
YGTIPFLLAHSSKISTGVLFLNSAGMRVEVQEGELIGCQWTVECGLVDVFFFPGPTPSMV
QKQHASITGNTMLPPYFSLGYHQCRWNYRSTNDCLNVDQGFDRHNLPYDCLWLDIEHTDG
KKYFTWDKHNFPEPKLLVNALASKGRKLVTIKDPHVKRESGYFVHEEALKGNHYVKNADG
TDAYEGKCWPGASSWIDFYNKRTRDWYATFFHHDRYEGGTHDVHSWVDMNEPSVFELKDK
TIHRDAKHTSDTGDLLDNKYLHNMYSLYSLMSVYQGHIESSKGLDHVKRPFILTRSFFSG
AQRYAAMWTGDNMAKWDHLQNSIPEMLSLSVSNYVFCGADIGGFFFEPDEELFVRWFQAG
VFYPFMRAHAHLETKRREPWMFGDIATDRIRTALALRYSLLPYLYTQFFVSHKTGSTILR
PLFYEFPHDEKLYDEQYTFMFGPSLLASPVLHQGATEKNVTVPSGSIWYSYATGEVVHPG
VFHMNVDMDSIPLFIRGGHIVPAKLRMRRNTFSARHDPFTLYVALNEHGNSDGELFVDDG
ESFNYELGAYARRQFSFTENRLSCTAHPETMSHTSSLPGVRNTVERIVIFGYSGRLKRVI
LQEAGAEIGVGREMDYEIQGATLVLRKPDVLIRDDWTIILER*
>TCRU_7014 Protein of unknown function (DUF726), putative
MLFKDFTFPWEPYRAARDEDELQAVLSSTTKKFSEEERLSPECRFAARRLMYACVGDQKL
LNLLDGILAPPPYRLEDLQDRQITRKEIEAAMDVIPLELDPVIVLFPFNLAMSTGAYDAH
LRAAVRRLCWLFAIPFNIIEARERALMDALLLSHDGGDESLKKKQNVVRSHKKSKKRSIS
RAATVGAFAAVGGAALAITGGLAAPLIGPAMGSLASATAATLFTLESVGEAMLGGTAVAA
FVSGMVGVATEAAALITLITPVLTVTNLTAIFGIGGASLAGYKAYRRTAESDVFMIRSIT
EIEKLPALAQGDDVLLSVLTKGQIAQCRDAAQRLAVKEGEQEVDMNLQEILEEAGKGGIV
VPAHTRAVTMCNVAAKDHFKQRMRCLTFALQCSLNGYRLELKALKLTVGKWGIVPPKLIP
EENCGIFLCLNRFARPTGAGCVVCYNVRPITSLSSPTLRLWVLAELSLMGNVSIAVSVTK
CDEAFQPKKMLKKLRKMKIESDETFISHNVVVGCFFSPLPFVMLSNLTDGGNTLSQHHSN
AVIPVKELTQRIVETMKLVRERRRIGVSIVNNSKHLIHVLTCEVMNGVQSHRTSNLPTII
SSREALFAVFTNSELSLKGAEAFIIIEVVNSGANADARIICESCYMKLQFEVNALNSISA
FCVAAPSLGELAEHHVHLRSPSEKKFKPILMPESFVWADMTADTKKFLLNLCIEDFVERV
EQMEVQKCPSLTIAVGGFVSIFDERRPQQDQQLALWANHLSGSCLFGMTEGYVVHWEDKN
QTKFGRTIDAGLAKTLTKELGGKAFEKATSVARSQLLRGGVFVGIQALDAVKGSLSLPMY
AIWFTGAIDNSFAKLLNRAEYTGKDLAHALLDPQKGRRPVSLIGFSFGSRVIVECLNELH
RVEAFGVIENVYLMGSIVSSSRTVWGKLRSVVAGRLVNIYSRGDWFLWLMYKANKATLRP
MAGIGHINVPGVENLDVSYLVDNHFDYAEKLKEIIDAIPGRPRRQMYEKSSGSPGAVVGP
DDISLVSKGMMSSMESFLGDSQCATLAITNRLASDIKGFNTELHSLVHVVNGGYFDFEPP
DVIPFSRSAVCGLVVDGESTGGGSVTGMVSYVVSLDSASADLLLSVFFLLQSSRKGGLVV
AADVRILRRTQETLETESERQRRLEEFCRNESEDPKRIQIKCESSERARHEGPFTPSFTV

DLDGVFDDGSREAVFHVTTKYEDHDDKRSGCRIDIVALLTQSSNLTQRKKFTAELFDSIY
QTAVEPKSAIPVPLKEMRLAMKDFNDSFAPKLKGSRGGAAIPQPIVLANCGDLPLIYAGL
GGAGALPMENMGIEWIRYPPREIPPNNCVLTVVRRCLSSSSSSLNSVNGAVLDVFSLISD
TGRCDVQLLGSSACGDGNDAAGGGIGVACQCEVDPSADGTGSASVMTTELEDVSFTLVSI
SWSSEKDAGESKQSQSSDADALMGWIVID*
>TCRU_7015 ARF-like 2-binding protein, putative
MDTEDGEFMVCGSGGTVEDAQLDDLVGVIEDFMAHFDPDAVFRQLPPFSSVASDHERHRL
YREAVLQTEADLDAYVLEHCGSIESLKDATSLILDRSDEIAEEVRDFINEGCFNYTTFVE
LWKQNKK*
>TCRU_7016 Domain of unknown function DUF21, putative
MIRGQLGVCIPFFWRCVLAAGEAAVGSQGTVRSEKNPNGYASWPLVLLLIIFFINVALAA
MFAGLTIGLFGMNFITLEIISSAGKEPDSAYARKIIPIRRYGHQLLATLLIGNMLTMVII
SQMVTAIIQSTEFVNFIVATAVVFVFSEIIPMAVCNKGPYALWIGAKSATIVSIALFLLY
PVAKPLGMFLECIVTHDEGLVYDRNELKKLIRIHYEKYGNESGLGDDETRMIIGALEMHE
ANLTSILKPLDRAVKLPGSIAITRKLVEQLWACGRSRLPVYSNDTYTYITGILFVRSLIN
ITSEQMENGITVQDVVNTNPHDIFIVPETMSLNELLKIFLSSTSQLVFVERDCKFEALNG
SLAANSKMTTNPVSHREGIEKERQKLMGTTRELKNTRVTVLTPQLALERGTAFSIVGIVT
LEDVIERFIKSDIYDEYDRTEEVEEDEVGEEWGGELQGKERSNAQETRLSVRDRCGEIWE
SGLGYSRSEGAPRANFYSYTVNDREANDAMTEEQKWTLANFIINSYPAFAMWTRRQVKCF
IDRIGDCVVRLEEGEHEGTLLYQAGERSDAFTLLLSGGVRVSVCGGNFSTEKRSFSAFGE
EIFLHEGGFVPEYTAVISRTSRYLRFTIKQFLEEEQRVRSGNGPRSVTGLIIDDSGAEEK
RCIDCEELSLL*
>TCRU_7017 serine/threonine protein phosphatase 5
MTSAEEADRLKNKGNEAFQEGKWHHAIELYTEALALHKTPVILCNRAFAYLKTELAGAAL
TDADEALRLDPGYVKAYYRKASAHLYLGKHKEALKDFKTVVQLIPGDKDARNKLDFCEKE
VRRIRFENAIDTPDAEPVSKTIKLGSVHSDYVGPRIEGDTITVEFVDAMQERFRVEKLID
RRDVVYILLEVLKLFKSYPNFVSINVPTGEDITVCGDTHGQYYDLLNIFKLNGCPSRTNR
YLFNGDFVDRGSYSFENVMTLFAYKLLYPEHMFLSRGNHECLAMNRVYGFEGEVTQKYSK
EVFYLFSEVFNALPTGHVINNEVFVVHGGLYSRDDVTLDELQKPNRFREIPENGLICESL
WADPQPMPGRTPSKRGVDCPSFGPDVTEKFLKNNNLKLVVRSHEVREEGYEVEHGGKCIT
VFSAPNYCDQMGNKGAFIRFTGGVMKPKFTVFAHVTHPGKPPMHYAMGIGLL*
>TCRU_7018 lipase domain protein, putative
MPALSWCGRKWRTSTDDFTFSGFFYFVFFLANATLALSRFRFGEDALVLGCPDASRTFQW
VFLALGVTDLVGAVAFLVTAWLSLQGAPFQVSKRRYVPLLLFLTSFTILVMLALSAVVTK
YAVYDKEGRNCTSPTRHFLYAVIVFNFLLPVVYIITFAFVFDPEGRQVWRDSVEYESLWY
KRCRLLCCCCLHTHRNKDAFEEISKTVAGLFCGYDLVPSDVAAGLLLVHKRQKRESRLRG
IHVRYPSAEDERNERISLQARRFSLLTPQQRNYLADIRIYSVFYLSAYGWPLYQYMHCCT
GLIRLYCFDPLMCCREHPGSHRGTKCYCDLTALLAITRIHEDNVILTRWGNSPFRPVFFV
VIDQSTDAVVVTIRGTMSFADCITDMVVNPVLLEVPDAEREANTTPADYYVHGGMQRGAL
YVLQELRESGVLDRILHEDFKKLNVVVLGHSLGAGVASILSIMLWSTEPTLRGRLRCIAY
APPGGLLSPALVAYSERFIVGCLVGNDIVPRLATHTLAELRESILDELMNTSRSKFSLFM
NCLSSDREIESLSSSVSFSSERFTLRAKFRNSPCTSLMESKKLYPPATLVHYCKAVVREP
QYCCCSGNRSCSCRHEEVFVPVFASPKDMQYVVCSASMLKDHLPDRLFDVIEKADVRLNN
GELDRFFSETEDVGGNWGDYGGIACE*
>TCRU_7019 hypothetical protein, conserved
MLRRTSLACSYRASLELDRIRSMLRGRARLERKVGLKRLFFLMRTQTRYRVEQQSHWNRA
IVRKNVDSAAREHGTGWAQLRNEFGRQNILLLPRSQQMLAQYEPLAFRAVVELCASRIPP
PPPPVFTKVPEEAYMPRSNNPQESHPAARVELRRGVERVLQCGPSKLREAVHGDADRLME
AWKEFDVAAGGGKK*
>TCRU_7020 hypothetical protein, conserved
MRPQCVAPRRQRHRSVFGPRSPPQPGSAAPRQLHGIARPTRIIEGYFCPPGRQSSTAAED
RRFPGTTEHERLTRLRYIEDVRGAVCSETTPSSILGKAATSILLPGDAVLKESRRVCGNM
GISRATSAPSCWAARCYLDTVRRNEASVLRPRHAKDALDGVRRSALEAACVSLGPYDAGR
WTDGSSSLVEHASGSAALPLGSPDSRAACGASPRSCWQPCVLLPSGVSCHRSWPQTVPSS

PPGSSIPIAHTSSCCHRLPLGDGGAPPWLADGARRRHRGDLYRAAFTGGLRSRSWLHIFP
MILRNPTQRDSGG*
>TCRU_7021 hypothetical protein, conserved
MMTMTGRVLLVCALCVLWCGVFGGGCSEAPSPALPGSASDGNPQKEGKATDVAGGVQSSQ
QAELQETPVPPASGSQELPARPSPAPQPGGGAPDSANTTTEKNNPNTESKKEEKDRKKEE
EDNEAKGEEDEEEEEEEEEEGEVEVEVEKEEDDTKEKEETGKEKEAVTSTTEVISAGTEE
QPILSSGAAGASNITNPNSIQTTGDDDPAADGAGTAEGKQNENKDANPKETPVTANTTDT
TNTQNSDGSTTVSHTTSPLLLLVVACAAAAAVVAA*
>TCRU_7022 hypothetical protein, conserved
MDNTKNGKLNESAVNCCVYDAMRELCNIVYGKGLKETDDSQVEGICKEYSGKPNDADKCP
KPQTEPSPAAGATVGVSVPEGLRSEEELGKKSEEAPGAPPEDSDPKPTGIPASPPAGGSP
DNAKDVRVPNSEEGSVSMKPTKDLAGDIVPIADTDHNEASNGQAESTTTTPPDASDNANN
KTEKGTGENIPKNTTESDVAGTEGKTDENKDNNPNETTLPVAGIKTVTTTPGNSDGSTAV
SHTTSPLLLLVVACAAAAAVVAA*
>TCRU_7023 RNase H, putative
MIPRIQHRRKTLLVVTDSQSLLAALNNGPHSQTDWTEDQIWQRLLTLTCAGWSVHLQFCY
GHCGVHADEPADQHATQTMATGQYTEQGIAHLWHTDLLTCSTTQLTDKWRSTIRQDTHRY
LLCGTRPSDLSGKDLITQEFLHRQELVHLAGARCGESELWGRLYWAVRDCTNQCRFCNIS
PEQSAYMRSNNDPTAPGTDTVPPWAREEDVSPVRRRTVTRRRKEKCPHCDSTLTGFSNLV
SHCRSFHPEHPPPLPELKCDFCDMVFPTRRSTAPHRSRCAHNPDATRHRNSSARRRSLLP
QDQPASTSTPIGPQETLHHLLLECPGTLAVRQRLGIEQDLRLGKFSQWQLLHSRKLILLL
DHLFGTQMALYS*
>TCRU_7024 hypothetical protein, conserved
MTMGASRTTKLLGMDLDPRLTLNVAASKQCAATSQRISQLRCIAHKEAGPSPHDLRTFVI
GYGASKLRYGSELIWAVATDSAENEMQKTYATLARIVSGVPSTVDPESALLEANMPPLHV
LCLRARLSIFENTRACQTDWMRRPPPEPPPRAGFRISPLSRDELYAFVDAYTKDYGITES
SPREERFFRSSIPPWFAASAHRVTIGVELPIDHSITDEEGLIREKRRVSEEALALHSHRS
WILATDGGVDVPKSAGVGILLSSLNSSEIIEKASIN*
>TCRU_7025 WD domain, G-beta repeat, putative
MCAAFLISASYDKQIRFWDGASGRTVRCFSFQDSQVNALLLIPDTTYLVVAGFGVVRVYD
IGAPSAAAAASVGGGGVSSQAPPLLSSYENQSAMNVTSLGSFPLNLHKGVITLFGSSNDN
SNSSLFNATADFVSTQQPYQENPSGELSTALYATSEDGHIRFFNAASPTTLQLIWDIPTG
AAITCSALSPDRQTLFTGSQIGRVSVWHLPTIIEVATLQAKSTIGIPFGQAPLQVISFDT
DYTAIRSIAIEPLARWAVAATNAGKLHFMRFTREVNASESLADLSCGNANKPECGEKNET
EQPVGESGIPESREVSGNGGTKAPRDASVIQLENVHQLPNVGKDVDANELKSAELSPNFT
HRENLTPALAHSPDPQGILAVASPSEQDAHTNYHSNAPSLQTSLLPEQFLLEVFYSFQAH
YKYILKVAISPSTDLLVTCCADYTVGRFLIPKELQNGTAFAKKSTGHEASSSCESVPAMS
ATAAMGSDGEGLQARRMAQQGAPEVALAVASLLQPMAGGEEAPNSSADKREGADVKALET
PQNGNERRILVDVGDGTAAQPAAKKEEKGGASPGDFPDASSLQFSVVPSLTMEGNTQLHS
TGVLQFIALKPLTGHLRWVWDCVFSDCGRFLFTASSDHYLRMWTGLLTDRVQSTCFVGHT
KPVVCCILYYEKRCQ*
>TCRU_7026 tRNA pseudouridine synthase A-like protein
MWAVVACIRTPPRLVSPSLVRRAVSAGTTSHDVPSLFRGVAGIVGTRRFFGHNLRDGEEG
NDLAQNTVERVEGEAVPVKGAWSNRHWSNEQHREQQSLAEEAIAQLFQDTTQRRRFQQEA
GRTHSAQTTTTVTTTVSEEEERNSLSNLYGGEGESFSPVGVEAVEQELLDDAFLYFPPVH
HAEEHAGTLPAGERYVPGQQIIPPGSTRYRVDVQYQGSDFDGWWKSTSRQLYRRETLPDG
TVRRVPLTPDTTDQEGSSAKKTMSSRYHARTVLEEALAVALDVHTVKVVAGVIPEVGVSV
RRLCCHFDVPSHIELQPRTIIQRATMWLEKRQQPLAVLSCQRCKNQDFHARHSGLRRVYV
YRILNRVAPPLFDAGLQWHVDRHLDVPRMQRFAKALEGTKDFGYFADPKMANALRRAALS
PCGLSTGAALDEHQQPTATGESPRDTHGKAPKVIIEKGSSNLERAAALPTFNEYGQRIVQ
PGAHSREYYRASTNLPTIRTIDRLEVVRQDDEVLIWFVGKSFLRHQIRNMVSLLKAAGHG
LWNELELQQALQSGFEPSRRRFKRERFPPAPVYGLTLWDVEYPTQHRDDFVPFVDSGPYE
EVNIAREI*
>TCRU_7027 hypothetical protein, conserved

MFRCFFWLSSKPTATRRRASQTAMRTAVHSTRETNRREAHADGGNALLASMYPAFKTKDL
AQLLEKPLPSTANVLTIDGTAGVANSSASSILRFVITHDEEVSKLQNNPEHPHPLLLLVQ
TSLDKDDADTNEFVLTSALQQRDRLKDATAIVLDAAQSAAAKSVLKLVEGNKLEERREGE
PADATGGGDADAPLKKVPQEDVTVENHEGEAEQQPPEAEDVLKSSNTKKTSTVAKNTAFT
TTKTETKTSTSSNKGKKNANVSKKTNKDGSLKLSYTPPPGAVKPRSTSVPPTRDDMRESL
QKMFCSSLAAPFQPPKQVERALFAGYVDRVRVADMMNLPIYGGGEVYTLYYRLTGAGACR
TPLITITHILEGECRKKKGKEANVVDVITKNRVPILLLLGAPFLIAEDAQLICEEYQKAL
QESFSSKADVTVLTVPNCFTERNVLFALRSASIDEGADATKGHQQYKKERGKWSELLTPS
SVRHCGQDAVQRPSESLSENVLRSVVSNALEEVALRHEKSTDHLVSTLNKLVEYWSRERV
IELMEGLQGEREVLVDATKEFGNVQQQLRNTRSAMEALQRDMKSVNDKIERFQRGAGGVP
SGDTSAILESTRALEARLAESLCALPSKQQISLDLREELEDVQRNLQRHLDQTLSKKLKT
MHEDQQHDLQQLLKESSGGNGNDQLTQIILQELPQRIQTAMERALSSFSQNSDERTRSLL
ESQQKAAQRQISALCDRLCDTVEAGQGRVVRTVSELLSTKLDGHGTNNADDKKLHAADND
NTI*

>TCRU_7028 Diacylglycerol kinase catalytic domain containing protein, putative

MFFGNDTMHENNTMPRLQVWVIINPTSGHGQGKVLLHSIQKALWREFRDCVTRVHAASEF
MSGSDAEDSVTRDGEALQGIPLSAARPPEFSDGQPEQAGSNTDEELMRYNRGGGMQVDII
VTEHNTRGQEIAEHLTKTAVASRLRRCLEKKTAADASTLAVINNEKKQLNLLHVFVAVGG
DGSLNDVVNGLCRGTLGAFREIIPTCVKTGTTFTGELDSVRHYWQFLEDRSILRHFLPPL
IYILAGTGTDFARLNLCCRDEQEFVNLLRGLWGHPTPCSSPALSDNVVNGAYRSTTTSNR
NNHGSNSTREQYSRIHEKNALNSLGFDVYDVDVGRVSFPRSGRSYFFINECSCGLSCDVI
EKCENYKRSKILSLAGGRIMFAVASIVSVFQIRPKPFRFVPLPEVASLPSNRLIPRRIAS
EMLHPHILMNDAAIQGVQRDLQWVKTSVGVEALPAMEPLRFGANYYAYDAKMVRVAPDHA
APANTGEAVINPFYSDQCCRDAKTPDEIISAINDTDVPGRWICLKSSVLAFANGRWFGGG
LQVAPHANPTDGQLSVTSWFAGFVKFVSRIPSLYSGNHTHWPFTTIWNTTRTIIDVDTRS
YHHSAANNSASRTELLLASCETDGEIRERLPAVIEMCSVVTMLVPRGRATRTMCNKNYGT
GVNGWAR*

>TCRU_7029 hypothetical protein

MATPPRRAVTFAGCSSFPNVMATPPRRAVTFAGCSSFPNVMATPPRRAVTFAGCSSFPNV
MATPPRRAVTFAGCSSFPNVMATPPRRAVTFAGCSSFPNVMATPPRRAVTFAGCSSFPNV
MATPPRRAVTFAGCSSFPNVMATPPRRAVTLAGCSSFPNVMATPPRRAVTFAGCSSFPNV
MATPPRRAVTLAGCSSFPNVMATPPRRAVTLAGCSSFPNVMATPPRRAVTFAGCSSFPNV
MATPPRRAVTLAGCSSFPNVMATPPRRAVTFAGCSLFASGVSFLNTDDKATSLRHCLFCC
LVGSKLGSRGANALFFSWAAASELLASSKVGRTPLVICWMEKLRVVVSVLFGKKPICMAV
RYPTSLIHSVLPKTTGIHCTSSCIAGRGCTGIEYHVWSRSP*

>TCRU_7030 hypothetical protein, conserved

MHSRTALPETTHLNWSTKRQRPGTQLFLHCVDDLPHRLDNRYSAAAFMYTDEHTLVASGA
GIHACAAAMQPALSPITTWAAEHNLKINVAKSEAALFHISSHTLSDEEVVDLHLVSGTIS
IQSRPVRLLDTTVERLLNFRTYASTAAKRTMPRRYQLRPVAKAGTSHHNTQSFSIGYGHG
VSLYYGDAIVPCLAYICLHNMEVLYRNGSKTHLGISAPTEDTSV*

>TCRU_7031 retrotransposon hot spot protein, RHS3, putative

MTLQDTNYYTVLGTGKMCGNYVSDKLVKVVRVRGNEGSELPLNALISSHLAELTLCKLAT
LMQQRDFNLLILAIEDDLISKALEDHSSFAFLSAAFVKAIIPKLRELKITANAPPHRCAL
RVRPHERPLKPFLLECLENFKEKINIECRVLYKPEAKNFPLVDGFFFVKSNPMTLVGLRM
AAAGGHHTTTSTVRQFTESLAAYFDGWEELSRDLSWEMIYVQHADSTPMTGWQRCDVVNS
NNVSRAENREIAAFWEEEVRQYQVSVSSRDF*

>TCRU_7032 hypothetical protein, conserved

MVRATWRAWRVLRGVLSSLGFFWLLVLLLAPHVCGVALGHGDSSKFEAAAIEQEYRCRTC
VALATLFREDVMLPAVGGLHTLSSQTGRKDSDAVRAGARQRLVVKMHDAVDGLCRRVHEI
HRVENNRLGLVTAETDSAEEKGKQLRLHEDDLFGSRRAVRDAVDALCDAVLEEVNEPLAQ
RAFAALLPSSKNSDEESWTEGKETHQLGEAGAFCEHQRICTPSAVQSIVQEEEMRRQAIE
RLAKKQQTGEKQHHFLSFESWRASNVTLMVPVILLVMLTSGFLLRRRRKGKTAAMCDGHT
KSE*

>TCRU_7033 hypothetical protein, conserved
MVTLAQLLFSWRGARKRLSTDTPQEDGDTTLSPCLPKADSFAGYLPFWRLLLCAPELPDK
DPQAFSVRKKGAADASSSGALSNLRSGAELSNAPTPVVSSGKGGSLTITKSVFAGPLQRT
EHVDKDVALQLGSLIPASDGATSSVRWTVTDTRRMNTNPEAALGVSLSTISSSLPVDSFP
DRQKLKQTKAEQMKMEARQKKELQRDEEALLEEEQRRLSALSPDATSHVLSSPSQSVTFG
RDVLAYHEAEPEEGVDICGLANTLGISEEETEDDSSFIEGDDAIDIQDMNFLYAYYRRRD
KTLVSLVQEGTVVDTSAVVASENTNQRRARCYELNSRKYIERVVLAQRSQQKIALLWLLA
ESMRHAWKLYFRLAQLYVNYVPLYLQAAGVTMGNGDDNDLMDITKNRYYAYFSFGTFDYE
YYTYEFIHKWETLFGNVQNYLCDGGTGSVGSVGFAATLLHSMELFERQHELQMGVREVEQ
WLHLCWKRMNTAAVLMSSPVPTVTATNTMTMTSSSSISDSGTPDTAAGMQHDDTANGDET
TEHNGKECEQQLVLTNPVDATLTSVNIRRDAMTHVPIDWWGAQDADVRAHVSWNRKKRKL
LQICLGRAALRQTVPAEGPDNIASSPKGTSPQLQAWMPGALEPIMEDNGDEETQPYRVVN
VGCFGFSFFSRWD*
>TCRU_7034 hypothetical protein, conserved
MIKIRILHLSVLSEDAGDFRHAGLYVVMRVGNEAQRTSVLVEGERKSWDEVFLFRLPPSL
PAVDVGMSLGAPFIASGPLARDTPHYLSSFHHHHHPLTTHDSIAAGSGMDAMALAPPWVG
DPYGLPTVALELWRHSATSDDCLAKYQFCLPHDKCGGVLDRCVRLMSASSYSVEFALRVR
VALSHSDSTHAIRRPPAQNTIPLETPVSWGP*
>TCRU_7035 hypothetical protein, conserved
MSATEYQGEEIERPLPAWLRDQDHPEATGDFFLAEGSAKTVGPKDDPKVMGSRDTSEVLS
LILSELQRQSLRINDVKATLARNVAYRTCFDVLTMNNVTLDAVCESSVSHLRSTVRYTGL
NSTVTISFTPGEVSILLDDPADDVDFMGVSFTSDCILNCQLFAGIKVCSVVLNIDTQKIT
DLTQLTLVARSEEATKELCQALMTLCGRDPVNPGAHLHTPPSLPRARLASAAASAVASDL
SSQLSAQSPTECRVNSRCVTDAVRTPTMRRCKGAKRPSLSEQVP*
>TCRU_7036 Ring finger domain containing protein, putative
MDPPFKETQFSYFPSSDSLSSPAGPLPNSGSFSSYSDTGKTGKSEDTFVVGEYRLSSCPI
CLERFTLDNPAIVVLCGHGFHLQCLESWRQRASICPVCMKLMQGEGIPMMSARDTRRRRR
YKGVNSTVTAAATARSSCDHRSVCVEPAVGDPMMAPPQCTPPLGEEHIANTNRDGGVVWS
VLSVLWSLSRWCSRGGE*
>TCRU_7037 chaperone protein DNAj, putative
MPAVRGGAARVGILASCSLTPMRHATTGEHHSYRPGRFAQLFRRLYVAVTPRSLHRSLAI
NLQAGMERVQELEKEQLWLRLHGSPLRVMGLPEHAELAEVRSRYRDLVFATHPDTAQGDA
KAQYDTIQTAYKMATTPTSLWHQNGSAPALYRSLLSTSRGITRHVDRVTLFALFSYFVMG
VVGIIFSVVVVRQALELALRFFDPEFYEFMVSQEKEEARQKLAGLPVDTDPKRFAPTVVK
RLLFPGRFVHKEDTGSDGAGRA*
>TCRU_7038 hypothetical protein, conserved
MDSYASTALVIWGSTGKRLQFTRQDLQMPESVKERPNHHFFEKQWDSVAGFWMNRVLKEA
ALQQMTVQDIVQCIVSDIERRWEQRKKEKSLYKKRKRLLDSSNITAAGAPSPHVLITNIV
SLEAYRQLVAEDSLQQFVTAVLEKVEEVAKEKVAHHAILVDDDDKSDTESPAKDKVKEKQ
GEDGDGTGPGKAKKRARHEEGDSVSFDDHVAFVCTFSSEAKAARVVSELHGSTFDSRAVL
CRFYAL*
>TCRU_7039 protein kinase, putative
MDFQALQSTLTEVCKGTSLKRGVSFDQRYELEVEIGKGAYGTVWRCHRRFDSMRRPYGVK
IINKKKAGAKGLKWVMGEVETMSLLIHPNIVRLEETFQDEENLWIVMEYMPGGELRSAVL
RDGIFSEAQARRITTQLLLALEFIHQNGIVHRDMKPENCLLSEGDLVCKISDFGFSVLVG
SDQCLMSFCGTTVFMAPEIFGDTSYGKPVDMWAIGVMVYFMVTGTYPFTGRSHRELTDAI
CGGRCNLKSGRIAEGSASLRDFISMLLVVDPNRRLSAREALKHPWIKLGMNMGNSIRDET
ELKRHGLRPRSIFRAAIIALMAAHRLCYLRYCRMLENNFCSAFTILRNFRFAVSGAYEPP
CPTLDCSGVFAKHPRGVRFLLPMLEVSRTIEALDLSSNNIDNLTLFQQLAKTVGQHPTLV
SLNLSFNPIPLLAGRGLLRLARSPQSKLLHLGLDGTLLPSETIAQISAALKEKAVVSSAA
AFTPQLTPATRSLEISTSLSRNNLSVSSPRQRFGVLHSPFTRQPVRKTTEPRLPPLSNTK
RRAGK*
>TCRU_7040 ADP-ribosylation factor, putative
MGAWISQIKAALGFLPADKKIRVLILGLDNAGKTSILYRLQLGNVVSTVPTVGFNLETMN

YKNISFEVWDLGGQANIRPFWRCYFTDTDAIIYVVDSSDKDRMGVAKHELYNLLDEDELR
ESLLLIFANKQDAMGAASETEVAQLLGVASLTNRTWTIVRSSAKTGEGLIEGMDWLCDKL
RERGTVSSTS*
>TCRU_7041 hypothetical protein
MTHVPFLLLLWFFCGAPLLAVARTHIIMDVDGSVDDYASLTTIMQSPHLRSQLSLITISG
MTWGHAATVARNICRFFLLSQLKGVTVSIGALRATADDYNTVLSRGGCRHSQGFPSTPHD
ALRRGMPYSRADVTSSFGAAYSFPPNSFDVRVNASEALHALLNGMSVDDSVKYFAFASLT
NLASALNYLGRHDPDRLQRFKQSAVVHIFEKGYSLAVDNVSTSQVLAEPELRFVLYMPSF
YDPAAAFSFSSWSEFGNLAKDAGASKAVAWLFSAWEAKKALVESRSDDPLTAFFKERGPA
SSLVTLCALDATVRASCTLYHAALSSVSLHLEQPTVSAPGTATYGITGNNVTWPSYLLTT
AGDTPAAKKFIVVQSADSLVPSATASLASVFWSVWLDLLRS*
>TCRU_7042 hypothetical protein, conserved
MPSTTSHPPFKSAAIRRGVLGDAEKTAKGDRQNIDGGDERRPFISIAQPSAAPALAPQRG
KEWRAYPKVPFYAVMQGLQLVINVAGPEEDAGDGLNDAGLLRGLSMLQEMLQASATKYGG
VYYISALPASRNTLLYPAHATRSYTGASALSSVATTAELDYWKYLQALQDVFYRFAELRD
LCCTGFSKEHCTHHVFFLRITEHPRLKDLMAMLAIENSRLCFCLCASSRVTQQYFTQRAQ
DVGVELEWVLGSTLVTEPERLTMTEVNPVFALWDVFVNLPLHTTFAAQEASGAAAMTLSP
DGVTAERFLQNINVTLVSSLRFAGSEWSSHTVRLCEVGQLSEFGRRRLVWSLMATPCVVL
PQLVSGLVRCLVEESPVDYFEMRFTHDMATATGREGAENAGRGVAYVTGARRGVVQRKSA
SSTSNKNFFAFSRLSAEAWLSDDDRRYYGLFLKDDPVPLECEFTVESLRYRRQADQNEPT
TGDDVFHPQCWGCGFQMENHVERILVDEEE*
>TCRU_7043 hypothetical protein, conserved
MSGGSASASEAYVRPSPTPAPSVNFTSGDTPPTPTRSTPAAAAAANFTAWAASKNGRGEE
RKAVAAAVAADVRGTVEYRAAWDVELWKAIQAARLRRQLEEQKKRALAALAKFVKLREQQ
ATERCELREREIGRREQRLVEEEKQMEKRKWRLAEMEKDMQHMRQQLADARRRAEAEAQA
EVKRAKEDAAHAVALQEQRIQAAEAQTKRAEERLQQAQRDYLALSEEFHRFRTRELAGPS
EKATSVETRLRREFAVEQQALQDRLERRHMEREEQLTRRCRELEEENKRLTALATKRKEQ
MRRTAEEVEQLISAKKKIEHRLRRKSAIDATAGVTDTLKKKKELAVGDVISKVPAADAAP
VAKEVERLRSERRIILEGSAGALDQDSDVVRCLDARINELLERLQSRGYAL*
>TCRU_7044 TPR repeat, putative
MTEAPVSLQSLTPLDVKQLSRDQKRQLLRQHRENPSRSANVVLLLGTDLLAGGTGGIGST
ELSCIYEQILIAALDCGRVDMARQYLSVLYKWFGKQSVRVRHLEGLCLEAEAKLVEAERL
YRAILKEHPTDQFAVLRLSTMLKSEGKYQKAIELLEKQQVYTDENGEKHTFLEVHRGDSL
SVYRELSNLYYLCEDYRMALHYADEAMLFNSNEYLSHTRLAELYYIVGDYKRCLVEYAQS
LRLNGHANNCRAAYGLWLTANEVVRQAKAAPKSSDGERTKDEAVELRAWAEKKLLEIYKG
SPTLSAVEAMLQRVA*
>TCRU_7045 peptidase t, putative
MAVKSLEDRLVERFMRYSAISSQSNPANVGKCLPTSPGQQELAELLAAELRASGLEDVVC
DDHATVTAVKRGRRKDCPTIGFIVHLDTVDVGLSPVVKAQKLRYEGGDICLNKEQDIWLR
VAEHPEIERYVGENILFSDGTSVLGADDKAAVTTVMEMITSLRPDEEHGDIIVCCVPDEE
VGLLGAKNLDIKSRFNVDFAYTLDCCELGEVLYENFNAAKTTITFTGVTAHPMTAKGVLV
NPLLMAVDFISRFDRKETPECTEGKEGYQWFAEMTATQNEAVLHAMIREFDLNKFKERKQ
KMIEVANEIQQLHPTGRVHVHTEDVYRNISDFLGEDRTALDIIFEALSILGVEPKVIAMR
GGTDGAVLSSKGIVTPNYFTGAHNFHSKFEFLPLSSLAKSYELTRQIVFLAAKRVKPRL*
>TCRU_7046 Domain of unknown function (DUF3508), putative
MNVIPALAKEVVRRLMKRTDEAAALRVTEDLAAFVVRLSLFDSPHIDEKGNVAETPEGIE
AMAEEISKYFVKCSPHVLATLSLQCQTAGLRGSFTNKRRNEQVKQEAITLRLLGSLCENS
TSQPEEMLSEIAFFILHRYRQLNAAQGNVESRKETVAVLNAVLPRSQVRSFANQPAEEKR
RQLEELHRIVWGIRLYNKAEGRTAGAGLLSLHETAEHLMTQLDSCISQEIHAATAVCSDY
VKFFHSPSSPLGSPEKQAFREEYHRQLQFLLNLRAAKERLDLLSARIRTNLLPAYEKTLV
EVKAALGVGAMRSDGVTLRSSVPKRVAYPKFIALAEAYEDVEQSFEGFEEIEALVDISIS
LGKISKMSLPPTLLEEALATSKSEKAADCAAIAAYVATRTESCPLFYAKNATELKQHASL
RAMNGLCPVSFVEDGICVEGRTSEEDSACAGFVVRPAPAGSLGEWYAFCSEYALRRFVAS
PFWFIEAVKRMVREDFVLISLLGFLDRLPHELYIKGTRKYEAREGLVAAEARQDVCTQTG

QIDPYMDHNYRWNEWDLRRQALKLVNLFDMRTHSTQTIASHFRRDDTTQIRPPRDDETQT
MQDAAVQPPRTVQYLKGLRGTKTSAIETVQRTFLY*
>TCRU_7047 kinesin, putative
MSSLPSHVRIVVRTRPTDFIADDVNIQPNGTLYITRRMKAGITAAQHTHTKNGTSSSSAF
AGGDGDGTLSSLTSEAAGASSQEKLAFTFDAVLHNASQEAVYDATASELVESLLQGLNCT
LLCYGQSGSGKTYTLFGGNTYTTRGCVPRAVHSMFESMAESTDHEFKVHLTFVEVHGDQL
FDLLGKGPAASVRPGGKNNAAEKVVVTLDSNGDVVLRGVEERQCANEGEALAAMFEGLQR
RMSRPNSFSPQSSYSHAVLTFHVLSKSLVDSDALVHHSRFNFVDLAGIQRPVPLADEAAR
QEAKIINRSIMMFEQVVLALSGPQPRHVPYRQSKLTMLLKDSIGGTSRTTLIANIWPEDR
HKELTLATLNFAKRLVRIESHPAVNTSTDPEAQIRMLRRQVTSLKSELRMQDQLAGREAV
PTAPLEADEIQNARELVMAFVSGSTPQVRVGSVREMHACFLVFKNLLGECEAQLRESQVQ
RELSPRQGSATSIKSVKRKGGLRQHGSSEYKENTRYVSSVEDAAAGVGMGTIERLSPVIR
EVFFQRQRSCSNAGPTGLLGARDMGGDGQTPGHTPTPPVATNTTAPNNITAAGVAASTFP
TAGATTRAKAAALPLPDGEKMKIQAHSKRQSSSPPTEKLKTSLPPLECEKATTTVSSSRF
LGMQDNAIRDRRTAFEAYKRTSGGACQLEAIENARKLVAEKKENILQLQKRVKEIRLSME
ESKKSEGSQTPVMEENAIARHASVDATHSSYALFEGSHSATENNVNFSEYFSTSPVENLP
HMTLAERKAFLNLSKNALTRAVMESGVLERRFNRLCDAFMSNFQFWHQSQLQPQFLTPEE
GAAAETTNLNANYSSRENNSFQISIPRVVAKGEGETRFVDAAERLETQNMQQQQQQQQQ
EEEALESAVFYAAKRLARRGFQLRE*
>TCRU_7048 WD domain, G-beta repeat, putative
MGCGASRNVKADADVSLPVFDPLHHGVRGRGLMDSTQRLLGNGERVSLLHGGGDDDDEEN
EVLSDITIELSTRSCRSGVTCGSFLFRENELVRQCQEVPLSIEEDLFVYDDVVVSKNEAQ
TKHWRIEGRRPLASRRVSTRLKGGGPSDNLFHFTDFNICVDEVDLAADQQTGDGVLRQLS
IQEGAQQAILLGATVVRTFSAAPNTVAAMLRTSEPMSRKEFSRLLREIQVETFIGHASRV
KCISVFPTERSFVSCSSEEASVTLRSLVTGKEEGIFTGHRDLVICTAVSPDGKYLATTSK
DQTMLIWDAIITKVLHILRHGMVVICCCFSPDSNTVVSGCQDRVCRLWGVRKGKERVAYS
KHAGIIVSVAFSPDGNYVCSTSADRTLHVWSATTGNTYLKLNGHVGIVLACSYTSDGKYI
ISNDETHLCVWSAADGSCQLRLAVTELAGKPRGTSRAGKLAWTSSCAAPGAFTRYMAVAC
TNRFVYILDICNGSEQSSVFCKAPVYCLAGGYKEKIAFGDNFGNLYVKTLL*
>TCRU_7049 polo-like protein kinase
MHQPQAQQPVMPARRFPSAQQPLSEKPEFREGSTLKEFDKQGRVVGRFRCGRLLGRGGFA
KCYEVERDGESYALKVIDRSILQKTKTLQKLHSEISIHRRMKHKNIVNFIRTFQDDWNVY
MLLEKCSNQTLMEISKRRTRFTVPETQHIMLQALAAIHYMHDQCVIHRDLKLGNMMMDAE
MNVKIGDFGLAAELQYDGERKRTICGTPNYIAPEIIDSAHEGHSYEVDIWSLGVILYTLL
VGEPPFQTSDVKATYRRIKQCRYEFPSRLDIPESGKELIHRILQSRPDHRPTLVEIRTHP
FFRFPTPPSSAPLSLFPSSRRRMEVEGQQQPQKTWKGSETAPAAKTQREVLRPLNTNTVA
PGRQPAQPGAASQALLYGGTVPNACNQGKVEEAGEPPCVDSARPLPGGVPKGERHVTAPR
STYYVLDDEERNHLTAVHDHLQKTLLGEVDHYGSEKPLMSLPPNNTGKVSKPLTMTTTTK
AGGGGIETAEEDKGAKNEFPLPSVWVTDYADFSAKYGLCYRLSTSHTGVHFNDSTKMVWE
PITGRVEYYARVKEVVSHNNAGVMHARDQRQAFHMETFPESLNKKVTLIKYFKSYLSRAR
NGREGVEVVRCSPYMDPTPVLLSEPHMIEDIVYVKRWLLTPHAMIFRLSNKTIQVCFHDK
AEVILSSESRVVTYTDASGHRITVPLYSATSHSNEIASRLRYTKDILCELIQNREL*
>TCRU_7050 hypothetical protein, conserved
MMRRVFCVLLVLALLCCCSCVFAVKGGEEQEQEVTQVNAVCVGKDKLGRWQLPGRSLWYN
CTDAASGAGKMICGMGVGNCASEASQSRTKDGVKDAVFKINVTSPTPNILEIWWKRKVEP
KAATIESGPTTRPEAEPLGPQEHKAPGYTSTTDSDSPPAGAAGASGDPPPPLPQTATPGG
AVASTAADAAAKTDPSAAALGALDSAPSGELQGPSHSASAASPAPESPPDLEPTEGGDHS
SHEPPVELQEETAAAPPTQLPQTGEDGGAAEGTEEDTATNTTDTASSEGNSTAASMPAPL
SSAPTTNALENSVGTDACFHDTRLHALPPLVLAALTYGTLG*
>TCRU_7051 syntaxin binding protein 1, putative
MLDAVHGSFKVFFCDAHAASVLSCSLRLHDLTEHGVTLLEDPMTPRQPIMSSPARYFFAV
EDASVGRVVEDWTAKVPHRDAHIFALGCTPHRSPQQLAWARIAPRAMRLKDIMLDFAARE
VLVLHLSMQNGFPQLLSPLSPPN*
>TCRU_7052 Spinocerebellar ataxia type 10 protein domain containing

protein, putative
MSGCDVSIKDADTEVLRLISAKVDSLLILCETDSELRNYALKFKLEQAVDKTAFQAKREE
GEEMLHFQRVLQRMADLALSIAPHIVRRTGRHLKAKYASGNDKTCSEASSTCAEFMDTDG
IPRNSSVEEFRDGSEAWLETGAHLSHVAVELLCLILVSHPRLVKALQMYLMERDVLSYIE
DALSIPREHEIAFFQEGHRTEHMRLMANLTLDNVEACSFIVSNSALLSAVLTSTRFDEEN
PGMVEWAEFCIRNLCCCTKEAHEKIRRLMPVGISDESKELLSSGRVDCHLNSEGKLVLSN
PCTTTE*
>TCRU_7053 hypothetical protein, conserved
MAIMMTGRVLLVCALCVLWCGAGCGCDEGEATIVVSPVISASGVVVTDNATGRTATGGAE
NLSAQQSQLNKVGDLPPEISSLETASGIESTKQQTQSDHEHKNPVTPSQSSGEQRQDEQH
EDPPGKPAALPSQEDGRHPSVEGPERNGPPSSPSSNNSVSRKSEERTEDTPRCTEIIVAA
PSEEGQESENVTSLEQPLKTSTAAPAITTQTISMTPTDDGAAVAVKMSDATPKSTRTANT
NNSTTTGDSDGSTAVSHTSTPLLLFLLVAAAAAVVAA*
>TCRU_7054 hypothetical protein, conserved
MLFRDCGGGAHSSADSDEYSSSGGSLASSESYATRAFENRMKVILGSVPTQEFEAQDGCD
LLSCMRPMKDGNSHEGGERTCAFAEGTGDDHVLCLTSEEEEYFGALMQGIDKMAKLDTEF
YEYPSPEYFKAHPPKQGLTEEESAESGSTSTHHGTKIFIGGLRFEVVQVGRHMISWIFEV
ACGVRLSLSSILVHRRSKGGRSGSPTGCASVFVPTEQEVERLLAMNQRIFCGEKGVHVAA
SAERMSELILSKAVVDFTDGRARGPTHPVIIERAYGTSGQHGARSSTNATPRSEKLPSCP
PPPYDIVPLGPSSVKSALQPCSNASSMRSNFSAPAVTNTVTVGGEQPGKTRLLAPANEPI
YHLYPGAAEVNKLMLHTSAELQRAAALFVGGFSAETEREFVAWVFSLMCVPVHPTNVLPY
VDSQSGASAGCVLVRVEEQDVAKAMSWNKRVVCDARGAYFMASQRAVVALLAARDKASGP
ARPLAIRRKDGGRGVPNTTVPGPMAPPPPLPPPFPGAWDPTQSAVTSWRRTGSSPRPPPP
PYMQSVIIGNQTYQLPPGASIQLQVVPVITGPNISAGSVPLQSTALSMYQPMPPPPPPPL
R*
>TCRU_7055 HIT zinc finger, putative
MVLCVVCERENARYRCRNCRAAYCCSACHKTHRDPERPNHCESLQPPSNETGGKNEVEES
TDRTDAKEFQTLGSNNGNTALGGHDARLKRGREGETNFIEGERDEDGELVVLGEAHLSEL
AHDTNIRKKLLSSELQQLLRVIDASRSRIDALEAAMANTPEFKEFCDEVLGVVSAAERGL
RPGMKLS*
>TCRU_7056 phosphoglycerate mutase, putative
MIRRTLRRFVKKSNLSNLGTPLASKDSEHLAGVSSTPSTSVPEGAEKPAVLTHTEGEGKM
SITIRSDGFRRSSKVPTAIAEPVKRIIFVRSGKSLADLDINTYVTTPDWRISIVPEGEEE
SYQAGRHVAEMVGDEPVYFYFSPYLRSRQSFRHVLRGYDDYRSEQKMDGDSIIGVREDVR
LRDVDIGRYRSKEELLHHLREREVYGRFYYRFPYGESGADVCDRVTSFLDAFQRERLDFP
MDTNVVIVTHGQTIRMFVKRWFHLTVETYHLMESPPTGSVSTLTRLHHRSCFRLDGRCVE
WMNLPLSLNEYNGYKYRNKQLLGSMSTGAPFM*
>TCRU_7057 glycerolphosphate mutase, putative
MRRQTRLFSRLAVEIPNSHWLPRRLLLVRHGESEANVDRSQYSRIPDWKIPLTERGRAQA
LDCGRRLRNIIKNEKLYIYYSPYVRTQQTLAEVRKSLEESQVQGEREDERLREQEIGNFQ
PLDKMDRTWNERSNFGRSYYRFPDGESSVDVGDRVSTFFDSLFRERLELYSLSAGDPEDE
DGPLNVPGEDDQNVLIISHGLLIRLFIARWFRVPLEAFETMRNPPNCSIVVLERQESARM
VMTDISKKLFGSDPLLEMMKFDGKDSTKRYRHMFFSDHSGSFTPAEGV*
>TCRU_7058 hypothetical protein
MSCIFSELRRSERLLPVEDNASFQRISSWRPLFVDPQEHPALYEHVAFFRSDAEQNSKWM
HTVRSARVSTRQVPFITLTGPDSSAKATVTAGKVPTIVHENHDSEDKLPTHVFQQHVAAL
APYECFMCPTLLFSPFRPLFTKRMVPIALKLSLPVQEVLLFLSMMFVYLDVVIAVSVPKP
LCFQELADLLEQRRVQLVESSVNSACDPHRRAFTTVLNAVIELWKEQREATVSALFPLGT
LTTSVCLRDIDDKAYRAFVPSASRDTKREDHPFQLPPLAADALVSHFVPTWERILEAMSR
DVSVLATLHDYLVRQGAGMTRMRQPGTGNSFASIHALPHNKEELADFVCRLGSSLWTSSN
MAKSIVLSKPQLQSVSKIFQKEFFATLLRLRHRGVQELRVRRVTLGDLALTVIQDDGREA
EVGRPAGFLVGRTAMGDNKPDSDSDSRGGDGNKKSNLPLWLVAEGGVDVVQTFLEHLIRD
TRATTFLPATLPCRNGDGRGSTVAGVSKEDEKGTPTVEEQQFVLLTRMEEGVLHRIFQSH
PNALQLTGCGIRQMLVRREDGQPFLQRVCGAVVAWDIWECYDSEQASKLRRPRRIITADA

PFPLPEGIAPSRLNLKAVRGMVQHYWKALILEQGRAAGSKRSEMTSTTLFPIDRAVAFYV
LRHHPQYYVRVRGCGIVDVCVQRQMRSASSGRPFHFLDSEATGEESQAVTDDTCEYVPAL
AVTHPCGTSTVISYEDCYSPVTNRLNRPQLLENDAGGTNDPACLPTPPLRKRSFSMMRE*
>TCRU_7059 hypothetical protein, conserved
MFRRIIASAGVYPRAMGARTYFYASPGESGISAETMKGLLKATLCFIMLEAFVINRAVFQ
GLSTKNQYVEDFTDLWEDDGTVMEGEEAVANLRIQRERIMPFMNDIKEKLDAAGVETDA*
>TCRU_7060 hypothetical protein, conserved
MSEEEFAEVFGFLLNNREDVRKMAVKGIAQQSKDNSALFAFLASPTHGPRSFDALLQFFH
AGGFQLLGDILTILINCSVDSRCAEMLVSRRVVRKAMRLLEGIEASDHANSLKRSLEEMT
LMLLSNLTASHIIAVDDLLQIEDEDLRGFYLGKLHAYYSRFFSNGVKEEGEDDVDDGGSE
GKELGTTRAEKLPARDLQKWILQILLNLTRSSEGQMLLTEDEDWDRTLTECLGSSNMRHR
LLAAQCYRNCSLQSEHHAAILRGNSLRVCVERLCDGGEQVPGVELILAEIVAEMMRSEAG
MQYLEEVNAKKHLQAAVAGKKVDDGTAEFIERHVLPFLDDVVDAYVVHGGDTVD*
>TCRU_7061 hypothetical protein, conserved
MGETLENALLYSDGALHLSRESIVGTRRGISLARLTEELKTINSVQRTWAQLDASFSESS
TPTTGLVGFLSDAFSGDARGLTITVE*
>TCRU_7062 hypothetical protein, conserved
MMRRVFCVVLAFALLCCCSCVFAVEEEEEQEPQVTQVNAVCAGKDKLGRWQLPGRSLWYN
CTEAAPGAGKMICDMGVGNCAPEDVQRRIKDGAEHGVFTINVSTFTPSAVKSWWERNVEP
KAVTAAIVPAELPEGTPSPPDDRISRETSSRADSESPAVVENSADVPPPPQTASPGGAVA
NSVAGAAVTTDPSAAASQASDSALSGELQSPSHSASAASPSPESIPDPEPTEGGDHSSHE
PPVELQEETAAAPPTQLSKTGEDRGAAGGAEEDTAANTTTETASGEGNSTAASMPAPLSS
APPKNALENSVGTDACFHDTHLHALPPLVLAALTYGTLG*
>TCRU_7063 SPRY domain/HECT-domain (ubiquitin-transferase), putative
MIGFRIRRRQQEGRGVGAPLGGCYYVGLTHGHPPVSNMTSLISRDDVYVLQDTDDQDQVP
HLLLRRHCIPRSSQRRIYGNDEIVWLELNADVGEITYYRDKMVLIGLAFANISRVDDLYP
FVFHFNEDASCELIQAPTPIEDNCELFLSGLRRSVAIHTLQQLHVVPYFGDVVSQWIHRF
LSRSHQDIDNSFLALAVLGGEKSCEFCLHETHGAVVVDSIFDVASKAIVYLEADGDMRVF
STDLLDIKPSFVKPPLFSLLETESLRCCGWLLAELSRILFEASMIVPLMKYEEEKRGEIE
SQFFEVTREAMNLDFVRGLNNLLQENMDTIAMDLNSTDMPLSLLQSTSSSFIMVDGRQPV
SGTPVTIDQRLSTSSLYTPNPSIGVTSGSGYSVIRGNVLLESFFTFTVSLTTKASNDTLL
YVGVSSETELFTDPQKVAHCKKTWALCSHDAEESNSINCSVEPGMIFSSGYILFGSGDLI
ILQVDRREGTASFSRIRSGKCVDFGVLFERIPEREKLRPFVLAGSDTVVVFSFLNCRVFP
ARNIFPLGMIAAWENHSSWVHCTSCEMELSKFWYESEGGMYLCQECFNSWRFPKIMFHLF
QVEEPLLDYLVSRHSPKELIVGDVVEFVENTVLTWLDDKGVNVNIEGGICMASDDLAFAT
LEPLNTFSNQRIDISLGHVAGVDGFPFGGLQPYSVQWRVGNILKSSRRVESDMLLVSSTV
IPHGTRVVIELNFGASEEGRSLNKAGLFLGVTKLASDYRAINMSELERLIADHNIWGTWC
DAKAKLSSSTTLYLLVDTNRVSVLVSSSLSGLHMHPVVVSCNGLAEEETTLRFAIYSRDL
CVVTSMSGFLSANNSVVEPSISPLAVGFIQKGAIGPETDIMNSSFFLFDSVAQTLAHSGT
FWQLMPIVTEEGSGVLFAIGDTLTITLDQSMLAVYRNGLPLAMCKVKKHQNFKPEQLVVY
FSTRGMFATIVPPLYGKSHLGRVVRTYGNDVGVVECLCPCPGRRQYAVRAKDVRFCALAA
DSTRLKVDARVAFKAGSLNVPKRGTVVSIENNSANVRDDEEKRIWFSLQLSSLYLVDNEG
PHQVPQGLYSLPTLPTSTVLRVFEVGKTKYRPQRNGSYNGIMFDLLAHDTIVLTGLSVMT
HTTGRHRVEVFFKKGSHHMHEREATAWTKVFSNFVEMRSEHQFSVKFSGIHIESNATFAL
YINATHNCGVGHYSKEDGCSGAISSKMDSDGILTVFVGRTSESSSPFLETVSTPRGFCGS
IMYMQTKDTRPPLIERTSSSLGCLQNKNERYGDAIFLRSIPVSTRVVSNAEFFLEVFEGS
ILIQKVTFPILIGAGVRHAMGSTHLSLSLFYSSLDGISGVKNAERDWVWAYNAMLPLRND
ICEFCMDGLSLLLKRGKYLFVAICSKLKGVLEDGKGVKLSCFVQSSDESYVVKNSFYGVQ
GFAGDIVATTTSNIMTCNEICSIFTGGRLNQNNSASYNGIMFDVRSKRDVLLEEVFCVAQ
TTTDNVNVRVFWKEGSMEGAEKTASQWQEVISKDLHLSDKQSFSPGLLNLHLRANQMYAL
YINTTSSCGVRFYNSSDGHLGEVGDEFEDDGMLTIFVGKKSESPLPFAEIPAEPRALRGR
ITYRAFMEKVFLAPNQAVFPALKGLLVTRILAALIAYVGGASFAATLFEDKSVIDLLAKI
ATSSTTAFCDAEAAGNLLSSMMRGNFVEELRDGMVTLPLFTKKPTTFNVFGKGDLALVAN
ATETDLSGQMVRIVDDPNENWHVLARCEAIPNHHVTLSVDHLIPIIICPDCNLPFSSEGI

CQKTGKGHVPFLREEDQLISIFTRYIFHQSRLSLVASAVCARSLLLDPTTHTFCIDPKTH
ATRIENCIDMSCCDRCNLEYTISPEVLLEGTEELKSPGFVCPFRYHDTMGAFVSISFSRI
SDSWKIMFLSDLPLRVEKDTPLKVFAVSLEVILRDGTRQDLLSSPQMYYAVKGGPIHCEL
PTLASSLHHLCIFSDDRIHLCLVVKKMNLPSSIPLTLKSVDGWMWEGGRDTAQLQPNKRC
IFQGSFDFEKWPREKPRFWQFSVTSETNEKIFFLEVHVIVPKSMTTVFLDKIQNHVIRCS
FSLSRNEVLSLAFTVDGDFLIYDEDDNIRCHVASDDLRLSSARGLPPKIAVMNVGANPVI
VHLHPPSAARNTRSVTCFNDDATDPGSYLPEWVLYEPHNVSVSRNGLTARCCNEGGQAVI
GSPLSMTGLSAFVIQMDRSDRTRGDSLGSGHFAGIVVSTFQELAPHFGAMCKHVDSVWAV
QDVYDADSLPTQETIPPLGASTNQMFLVGTHLHFLLDREDGTLSLARDNESPRVVFRNIP
SNLPLSPFVRLDHATASATLAAFSCKAWGNGGILTSPSMILSSQPITPTILRRLPYHVVF
SMFSVFRHVVNYLPSQQVTLVEKAWSDRFNCSRFAYRLTCAVQILVELGAFSRCMAYAEE
EEAERFCSRDEVQNVIHTLSESEKRAAVVYSDGNGEDNISLLLPEGYEIIGYMKDDSMIR
LLYFDGYGPSERTLHLFRFDDSEICINSCNLVTKHVCVMHQEDIIPSLGDSSWCGIITSG
WFDCTLDSVSVDILNEHQQRVIAMSILGALEHWHLHSLPHGNVNFKNVYLRIIGETVVAC
TLWNVHCLLRHHTCASPGLRIHGKRDMEGDRWSCAYILNRLSSLLKADVKFGNAVKLLMN
ENLKISDAIDQTEIFAEELRKTADGQVFCLRTGDHLGVGAGSYNGIMFDLVAKHVKVKVT
RVSFVPDTTTLARVTLFVRDGTFMGVESERTEWRLIMDQEMKLVDKRETELTEFDPVIIP
AGERVALFLHTTSGSGVLFYSETDGVRANMAAVEEENDHIGITVGKKSENVMPFVGIQNQ
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EDDYLVFMGEHCEWFHKDLIRNACFTESSNLEELDLTLQKILCKRRKPPWGISHQYLCYR
QLVFHKRIQSNTETDPSRPSVVWWISDPITSSCIVSVWQVIAMADTSFLLLLTSQDLSLS
QSSNQETLLSQGQAFFYIDEWARSVILSGNTGPKVVKQLQNSLSENHLYLAFSSMDLEAM
NAPVAAFLNRFTEDITVRSASDTTALVSIRPGACLQEHIFLNGIVLKCSAEGGKTTTLSR
ATSLTSQRDVRVTQMPCLHIPNETSGNFGSTLTETGVVEQSHPSHFFLEMELRELCISHD
VILHTQSEFLDVSCRCVRQIAHGGSFLCTVTKPVFCGEKVHEIELLIVSTNRHSVQLSFQ
DVTTNWFLRVPLPLFKHYENFYFSSSETVQCIHLRLCVFPQAKRAFVSVNGGMFYEVIPG
YDCPSEFRLAISLSGIASSVRFLHWRVFDRHSPVITREMLETIWSRLRVGCISPNVSQSV
GVLTRHSRTPANLVSSRKTDVGLVSQIEAAMVSYARQLLGTVILSLKSPCLHKGLHILLP
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KVLPFLSTAFGPTLTLLLLRTATVYTRSIRHMALRCVLQLLKTDQCALPSHEALCASFDP
LLGMMNGLCWKGRTSSVVVQLGISLICELIRRYQLERSALTPPGKKSTVPYAIAASTKIV
LAAITSNPPVPLPDAFTEEPKEAHRIEYELRTSTTSNEGIRSCYGVFSEKFRSTFGSKRF
EVVLNPSRKGNVVVGWDMNAALPGSLVSKPSQGDEMSRRIRLPSCGYFIDSSGKVYVCLS
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EREEDATFNGEHLSDVSTGMDIAQLYNTIQEFPDRLDTAVVPQGYDFYAELAHFCQTVMN
SEKICALLENDAGTTVRSHDLASFPLLSSFLGVGAFTNEIPLDPLIPYMRRLQVFDVITS
VFSAVVDLRRKTELFELWKKLKFLCSAESSEKIQNETMRPFRNRPGLKANVIIHTMQARP
SMRLGPYPTLMRSVFGQLFVQLQKSPISTFYASPMFTVKLAGFGSTDAGGPYRDILSQLA
TEIMTTHPNGTFQLNPLFAQCGRGGQSAVMPNVSMALNSQSSFMFEFFGKLIASCFLTKD
LLAVEFPPLFWKCLLSEETTSQDLLAIDPDIMRQLTPEDLMDRTADELEERFPGIFESWS
TFVTENSQMNLGAEIPPSTIRSAKILGEHISTLELHKYDVAISYIQRGFDEVVPLYTLNA
FRWQQVELIICGAPKLSYDALREVCQVSLPANDARMFLDVIASMTDEDRMLLLRFTTGQT
RLPLKEAIKVQRNGAHDSLPTSSTCFFTLRLPSYSSYESMREKILYAIRQCKAIDTDGQA
REHIVLDH*

>TCRU_7064 hypothetical protein

MKQQQKQKKQQQKQQKQRKQRKQQLKQKKQQKQLIQQHHEQKKQQQKQQKQRKQHQEQKQ
QQQKRKQKQQKQQKQREQQKQQMQRQKQQQRQKRMQRQQQKQQRKQNQRQQQLKQQQRKQ
KQQQQKQQQQQKKRKQKQQKKQKQQQQ*

>TCRU_7065 C-1-tetrahydrofolate synthase, cytoplasmic, putative

MSGAVVIDGKGIAETIRAEMKSEVEQLWAKYGRRPGISAIICGERKDSQTYVRLKKKAAE
ECGFVTFNVELPADVTQEELQAEVEKLDQNADCHGIIVQLPLPDHIDQDAVLKKISPEKD
SDALLPVNVGLLHTKGCEPLFVPCTPAGVIELLKRSGVTMAGKRAVVLGRSNIVGAPVAA
LLTANNATVTVVHSATPLADLIDVVRSSHIVVAAMGKPGFVRGEWIREGAAVIDVGTTPV
DDPSKKAGYRIAGDVCFEEAQKRAGWITPVPGGVGPMTIAMLLKNTLAGFKRSLSQA*

>TCRU_7066 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase, putative
MPVMPATLGTRGGGEQTAKPSSFERMAAIQEEIAKIETRLRSLQSTEDADDTPWTSAPQE
DMDPAVAKMLSVELCHLAASGDSVGVRLLLESGADTDCRDYDEQTPLHIASALGHVQVVR
LLLEFGADPTLLDKDDKTPFRLAGENNRREVVQLLLRHSQEHGHELDACGKPDSFLLDSP
IMSAHPDFSQIPQPMMGSLIVIMVGLPGRGKTYIARQIQRYFKWNGLQSRIFIRSTYKEK
LEEGGVVSTALSAAEVERRIAAAIAKDMTQFIDETDGVAVLNGTNCSPLRRMALMSAIRE
TGLIRPNRVIFVEVVNNNSEIVRLNVNRKKEINPGATQSFVDQYYARIERLNALYKSLSP
TTDRDLTYILIEDQTTFALNNISGWMPSRLSYMLHNLNHAPSNLYLTRAGEYVDLIAGRI
GGNSRLTERGQAYSEALFEYFQGELQMKSFTVMSSCALRCIETVQYFEEQSVLQRSSASA
AQIKEPKLNCRVAYFPTLDSLNHGDCDGQLLSDVRKAMPSTLLHMQADPYHTAWPNGECV
HQLYNARLEPHIHDIQASTEPVLVVSHLQLLQGLYSYFVSENDDFVAPQDAYKIDIPFES
VIKIRLVGFNRVAETIDLSKEVDRIQHRRTGKVTKATQQSSLNIFCRSGKK*
>TCRU_7067 nucleotide hydrolase, putative
MSLKAKIDVFPFGAYLLQDPSLMRVMQAVVRGANNTNSSGNMNENSGGGGGAANKRRDAG
GNTSQSVERRLKTPLEKLMSLKARCREEQCVHSVEGVLLVHVHDHPHVLLLRHANTKASA
HSRVLPATNTNNLAVFSLPGGRCRKGEPEEICLLRKLGRDLLNEKKSLMASRTAESESSE
MVVEVGASHSLAVAPSSSSFRVGEALGRWYRPHFDPFMYPYVPAHVAESDVKEVRTVFLV
HLPPQMLLTVAQRDVELVAAPLFDLYENSAKYGPLIASIPTLLSRVNINYCK*
>TCRU_7068 hypothetical protein, conserved
MGQKQSLNASLHRYIYNHDTDGLMGFLDAHEAELNNACMDENIYVELVERQWDTATIYRF
AKFANDQQLAVLIATAVLCSHLIPIVPIFELMQDCKRTIEQYHLKHLFLIACERENVDAV
RAFIANKCYDPTDRRPVRAVLRAQLNKSVVNEELVKMVLEAHPLQTDNVEYIRNKCLSTA
KNEGVRKMVDDLLVEYVS*
>TCRU_7069 ras-like small GTPase, putative
MRRFCIVNALRSSGVVFLTTATPPSTNSTAAANNAMKSSQFALPLNRQIRHGLSSDWREQ
VRRSGGVLNDISPALPDSNRTDDQRKRVAGWQPVVKLLGDQRLRVAIVGRMNSGKSSLFN
LLSEDPTMPHRKNIVRDFDGITRDSVEGHAQLEGMHFTIIDTPGMVNGKLVEEAFRTVET
ADAAIFVTSVDEDLHSAEFDLIHYLQLKCMPTFVLVNKMDLVPLDEEDRVLERYNELGLG
NAIPFSARRKSGMEMLAAVLEPLYHIHSMQKVENDWDIEDLAMQGDESAMEEIRDRNCAD
RFIRIALVGRTNSGKSSLINRLVGFERSRAVDEKNSTRDPVELPCIYKGRKVKLIDTAGL
TRNRFRADRDFIGRIHDLSVNEIRYAHVVIVVFDATEGHPNKYDMAVLHSVAAEGRPFLL
CANKWDAVLDQSATAEAIDFKIKRQVREVKYSNAVVVSAHTGLNLTLLMDQALLLYDTWN
KRVRRAELTRLWRKMEKSVIIPYHVARVGRITQVNTRPPTFLLHLQTKNDENTLPRALQE
MMKNTIVEEFDFRGVPIRLIQEVKDSNPDYI*
>TCRU_7070 hypothetical protein, conserved
MRKRKRTRSISSTEDVGNTTNDDNKKVVENGARDVSSIESEASCEPTRPLGVFIWSDVSV
VLYACMLKQLHYTCGVLAIERSRDVRQNMIYALKSRLVSFWEAETATLSAIEQEKLGRVF
HSHVNAMLERFSSLVAADMTGRDLCHAFLQVLDVFGFPEEESAEESLLVANMRKNADPHA
YSYQERTSHKLSVLPRYEGDRRTEEQHRLPRLGSVVQLPSPHPHSEINTDVQLIEPRKRR
PPLDENRIFSHPKKATSSGMEDILVDEELRYRSLVVLGRHLDTFGSLQNLSPFVRFSLWD
ILGRDDEVFERLTTSPAQDDELLEWQKKQLESLRRLVAEKRAVFDATRAEARETALRVGW
CAVSAHWRDQVLRVVDVGEDADWFLLRDSAKNGFKAIFPNYALFTVIKDIALKALRRVRD
GHVDCGVEDAVECYEVVTHVLFPLLEGKAPSLPGLEAMIEQNTSSDGEDGSGGERQSQQK
EDEEEALRKCVSALMLEKTGNACGDADVARGVRLCFDCGSFLPREGSKCAFVSNMFVWPL
QCLAALLELISVARYSVDGMKKFAAAFLPSNWGDQESLLEFLLRREPTNIPLASLVGFPR
LVRDVFVSAQWLRNDKYFRAVVECRRQGCALPPGGVANNYLQWRALLTILSRLEYGEEVF
ALTVHEMPPDAANEGKMWSVAELECTPKTWAEGLALMMTTAAVSEENRT*
>TCRU_7071 hypothetical protein, conserved
MLSLSRLEEVAGKAEKLRCLLRSAFFDDAPRIEAAIFEQLLQLLEHWFPATSSSNTTPAP
QLDGDNDNDARLLIEQYYLQEVFAALLFLSDESFFLNRAVSVVLLPRLEKCNVLKSEFYV
DLHVRRFCTELLLYFCFSQVCQTPRIVQALYPLLLHGNHALVNGASQNQVGEGLFDTPRF
LQKKTLVSSLLNGVMLTLHDGVVGVFRVLLLDDRVEDGMTVDAARHIASLFSTPLRRAWL
LKEGSVTYTKCLGLDEQALLLSVQLVDLMASDTETSLTPDEERVQIRSSHFLQQQKINQE

KRFLKRETIQERLHLGIATIFNATLHLMPRSEDKSLFVRSYKCFCLYNRHLLTPAFCVLT
LRVAAKADTDEILFALRRLSVLARGSTLGPSPRALLLTLEPLSPGILELLALADTLPVQH
SALLQKVLGALWELSAQFETLAHMFVRGAFMPVRGSYSVDRVQAKVIVDFEHASSSVMRI
RGLQRLLLHGSIPKDAICKLLMAMATMCQQRAAMATAAHVEEKKCSKSAAFLFAENELEM
NSDNDNEDIMLAHMVEEMCLSLTSDELFGTCVTLDRICEVLSTVVTISYACWHWAMLLIP
RILSVNVIHSVFAQYTTNIERQKAARLFISQAQRLLSLVNALHDAVVNTEATTTLENCIA
AVQQYNSDADVDDATFVECRGIVRLLEESLDMKSTASLVVHLLALARIAEQAASCLHRKL
LTADKKNLNENPFSDSVEGRDVVQTALWLLFRVLIEVDDACAAVAACKTVVWWSLARLDS
VDSSFVARLVVGLLGVEENSPMALCSVLPGVTNAVTPPQIGRMKVRLLDILLGLCDYDEE
GRTLRNIDDYCKLERKCTLYDILVELCGPQHGPVVQVAALHLIGHYAIATYPRVSLAATC
ALCVDVFRHTPHEMAKAACASMLSNVAGTLEAMGILAALSEVDVELLQRMAEAMCSYRGA
AGADDDHEAVIHHHGRCIRKVLQHLFYGLREA*
>TCRU_7072 Eukaryotic translation initiation factor 4E type 6
MSAQTSSQPHPLKDRWFVTYFPFVRQKKKGKDFDEQQKPKELDWVTTAEELYATINSFPS
LVLLPSDDNLVFARNKVEPYFENFPEGDRVCVFTRTKAQSEQAVVLVLAAVMGEHLRSVT
DSECVADVVRIAHKPGNVYPESLRVEVWLHKSDFCEKVVQYFVDLFKTYPGIRVARRPIS
SEVTAD*
>TCRU_7073 hypothetical protein
MSSDDGVMRVDEYFPITERSFSVIIRQYEIEAAAARADAVTREEESPENSRELTLMAQYL
EDLANDARRLHRKLQASGGGPVATTNWSAEDVSTLRLLGFDVSRINVAAAEEQRPQVPNL
DKLLAMEREIQKLQTRVDDLTAANAALREKVAEQNCTGLQFQVEENDMSDELEALTEGLK
SLKAAYLSKHGDCFAAQDMQKGSTLAFNDIYLGGHKSHKTAVEFQQYPSSGLAEAFRILR
GVVACHRVRYHVTGDSSGKVDAIDMAVVRLLNDLEFPFPVTIRRLGARGDYFIDRRVEIK
LIGEQLVVRPWPATGVHQGFSADRKCPPRYEHLAKYLIHLYSPALDLYRAAKGGRRDGAG
VNSAEGRPNNDIAALKRQQRELQRALEDRHEQLHEYQKQLVAGLSPLANECTLRDDATGL
SVELRVEERNRKVDESISDSESYPSAGTSDRVAHILRLMETNGRIPDPSRLSESGLQHLK
YVALQRQTHALQ*
>TCRU_7074 Uncharacterised conserved protein (DUF2305), putative
MSLPNAIVTWQCPNRPFSVVEVLQSCPNLLDYLCETSCTEAMRRPPSPHRKLFILFPGNP
GLVHFYERFVELMTLRRLDVLVMGFAGHSFVDQNNGRVFDLQDQVETAEHFLRAVLTPYT
QKWYGKHIYIGGHSIGAFVAMQMLTRFPCIKRCFSLCGLLSNAQNSPNGKRLFFLCSHAV
IYGLFTYCVMLLLLMPKAVVSMFLRWYAPSVSPPLRRLMTRHLNPNILWNCFFMARQELR
QVREIDRPLMKAVEDRMVFFYVTSDRWAPPQHAQEVKVACEGHAGFVMETDPNVPHSWCL
DHNELVVERGVMPFL*
>TCRU_7075 Silent information regulator 2 related protein 1
MNQDNANFLHVVGEPTFEALARYIERNNVTKILVMAGAGISVAAGIPDFRSPHTGIYARL
GKYNLNSPTDAFSITLLRERPDVFYSIVREMDLWPGHFWPTLVHHFIKLLADEGRLLRCC
TQNIDGLERASGLPMSFLVEAHGSFSTASCIECRSPYDIELASRESREGKVPHCDRCGGV
VKPDVVFFGESLPDAFFNVFAEITEVELLLIMGTSLQVHPFAELAVRVRPDVPRVLFNLE
RVGGAMFRFPTDEPTLNSFSRNHTGNSHSSSNSSSSSSSSSDGYSQFANHAADAGGICR
DIFFPGDCQLSVRRLAEAMGLGERLALAVREGEKKRESYGACESGNTHHTHMYTLTDRK*
>TCRU_7076 eukaryotic peptide chain release factor subunit 1,
putative
MRLLRKGVRLDGGVEVKVTVGTSEDLWHLYNFVLCGDRVRARTRRKVAKETSIGTKAAEV
RFITLEVEVQQVEFSPEELRIHGINISENEHVKLGAHHTLSVITFPPQDITIIKKEWDDI
AEERLKEACDNEAKADTAAVIMDNGTANLLLVTPSFMHPKARVEVNIAKKHKNDGTARDK
SIQRFFKQVLDAVCTHVDFEKVKILLICSPGHIREEFFKYMESTTVNAEAGPLRVMYKNL
SKVVLLKITDCTNDALRKAFADPAIANEMSSTRAREDINVWQSFHSTISSDPDRCVYTPQ
IVYQAAMLGAIGRLMVSDNVFRSSSPVERRFYLSLVQFVKKGGGKVSVFSSNHITGEQLI
QLGSVAAILLFPCPELDDVAVVKDFIYGEEATAFIRENAPTRVTF*
>TCRU_7077 HIRA-interacting protein 5, putative
MLRPSLVCLLGAISAARLFVQRRALSSSFRVMRGLGNPNGCHQVERVVGGANCSTWTSKR
FLLVETSETPNPDCLRFYSMELSFLKPGFSMDFPNAGHAYKSPLAEILFSIDGVEAVYIA
DEYITVRKGHLVDWDSILPMIKESIAEFAESKVNILSEEGEELLSGHNEDTEPKDDDDEV

ILAVKELLATRIRPMLQADGGNVRYLDMDDGTVFVLLEGACKSCPSASVTLKNGIERMLM
HWIPEVVEVQECTEEMADDILAEKALRKKMKDDGVTISAK*
>TCRU_7078 60S ribosomal protein L7, putative
MPAKSVPAPESAIKRAAFKRQQTENFKKAIAANKAARVALKKAAYARGLRYSREYRSAEK
KLVHLRRQAKSCGNYYLEAKPKVAVVTRIRGIAKVAPKQRKILQLLRLRQIFNTVFVRLN
KPMENMLRAVEPYIAYGYPSLRTVRMMVYKRGHLKINGQRVKIVNNQMIESKYNNENIVC
AEDIVNQIYTGGKHFREVTNGLWPFKLSPPAGGMRQKRRHFVEGGDYGNRDALINRFLAR
MI*
>TCRU_7079 Mini-chromosome maintenance complex-binding protein
MEFSCCQAEIGKLIREKTEELNDIGAALSFVHHHVLSMVHKSEPGLSMPDVFPSCALQST
SGKLCRCRGMIQEVEPNISFYRASRSDFFGAAEEENMALLEATLLYVIPVPGNSHFYRVP
QETMSEERAAMNNVPAVGQVFGDRKRRERSDGPLQSSALEREMKQFRQEVVFQSDGASQP
MRQLSLYQKLNLPHPPLSGFLHTACVVTVIQHPAVERDRLRINDVVDFFGFLDEDSAMTG
DRMAAFPLDEFGTFASWHAEQIPPSLLSRMTCISWKEVFSTPIRPVLKNYFETKRPLVLL
YLANTICQGDALLAEYILLHLSARVITHESATPVGDIPLRVEAQAIDPEMWSSFMRSISP
VGEVLLDASLLSSVDLRIVPRQDHMANVLRTGVLQLANGTHVTLDCQAVSKASNALHEAL
FAVMHKQVLPLEYPYQLHELPIDLSFLALSTARISEEMELLRLAVSVRWQPELPMAAMDL
TNLSAEDVQDYFSHVRCVCRRFVSEDNSQAHRLAEKLVCFSQSEPSWNNHDPFIHNNSFS
MAAALMRACAASFGRETISDGDIDHILFLERDRVARRC*
>TCRU_7080 Adenine phosphoribosyltransferase, putative
MAIAECSPNHLVLKESHPLSKDLYANVFGETSSFPGDNATRLFDVSSITENPLLFRKVIH
FLAQRYRDMGDAGPTHVLCVESRGYVLGSPLALELGVPLVLASATKRFPSTFLSEGQGPM
VLPKSYSVRNGSISSDSRVLIVDDFIATGRSLVSILRLMAIVDAKVIEAVAVCNVPSLDG
IGAIHKSDGCRFGQTPIFTLMQLKASQETVKEQIAYITLVGMSHM*
>TCRU_7081 hypothetical protein, conserved
MPGRHGKQRVKRKKSKRQKPSEMERVLVDSIHGRKRRERDILKKHLPPPVKLRSTKVALN
TTLPMFNPLPPTTVGAAAESRAKNNKGKKPPKSRKA*
>TCRU_7082 hypothetical protein, conserved
MVRENLDDESLMVSGDAERMYLFGRIQKQKRMEKQQGVKFVSRKGLPTPSVEELQSIRDR
RGKQADMMRMKRHVEAVERRKVMWRDYVSYEPRGCGVEQTHSTHVATTSLEGRAVVLSPL
LALFRMLVCNNRAKKRLERLREGRSLLLPEVMFGCNEGKTVAEVASIVDEHMTVVPACVN
RGGPLPKLFLVTGSFDAKPLRSPFVFLSKQYRTERLPEFSLNLSQAVSKEYAAYVKRDYK
EYSAVTLSDFAQPPIAIEAFDVNKRAYDVAHRRNFVLGYDNFSTAARQSQPFPRGEKREE
VNKTDDVMNGIGLSQELSHLGIPSELAGPLPEDSMSGSDDGNFSSPFQVDISWLPLSSMV
KKSDGEDSLGS*
>TCRU_7083 zinc finger protein, putative
MSIRLSVLGEWKSDSSVQKCEICEVKFNFGCRRHHCRYCGGIFCASCSSFFVKSQKLHVN
KRRRVCRKCFEFLSKTPQATNPSCASVQSHHKELNSVNACNCESDPLTTESAQATTVVSW
TPRRGEDRNTAGTFPDEENADDTDLDDDDDDVSAAVAGVYSSMDDGQHTGSLAFLAALQD
NLRYSEGSDVIHVLIYVSATRYQVILVTVSDGETMLMLARRLVDVYFRLDSGSFKSISTV
EREILLQKLRFSSESIVIENEANASDVASHCKHLVLSTLSVSELQHAHGGDPIEGFFRSE
LCNENKDGMIC*
>TCRU_7084 hypothetical protein
MGMTPLRRLLHKEGDAPLWFISAPAELQPHDMACGNGTPTSGAGGGTDSPTSCMSPPVHC
QLRLVPLIKRYFPSSRSVLFQQLVEARKRQHPRYHFHCTQHLPPTAYLDPTVHYFDLELG
GREVRESEGAEGYSEAIPALSAPFLSPDTLYSLLVEGTEVNLFDSEDALKAVMQAELEGG
GKSAWKDRVGEGIGEGENGGGHNGKSNMGHTKQQRVRPVPCAILLLRYHDVVPDISEKNN
TAFGLAAAVETVSVSPQKGDATASVMVEEDGRSWLMWETGGVSLSARVGGFYGCWTVDEL
FGHMQDAETVRSNLPNVPSSIPHSLMGPFGLSGDSLVVTGFVERDVGEREQPHAWMAACR
AFASSMMDISSHFMGKDGTQQPCGGDMEHHLPSYPLCLLRHLDLAFIPQLSNIPQLQLCR
QIHLFMDTLEELAPAVPTLAKLHVLQRQRNKRPTNGETRGSMPPTSTTCGSAFPVKNALT
GTAYGNCGGSSIMVVGDATNGLGPIADPQNAARKSHLSPLKRLQEKGLCSYFLDGAVVLR
ISNAKVVEALQKLWCVPLSDTTEALMMALTSRVPPPLVFRGELRPPNPSDSWNVELHGVV
PRNGLELSGGCLLPCGFAQAHDVFSVGREFDGAPFRCLVSSAAKNALVGSGMHSKVQGAV

GGKLPANCNSAATLRVPNKSVSFGDLIRFDPVEGCWYIDSSLRAEDVALSWMRRLTGKAR
EAKDVDARWLLYPNPANQDPTEHGSRVGEIMPGAGSAFVRLGRLRPWHIKHDGYSYFHCV
AVRNGGVGGVAAEADGEAAVISSTKEVPGKKKSGESLSVPLPKENAACQKTTHSEMVGES
REAAPQSVAWRQSASSHQLSTTNSQPTFRLPIFNYGAPGRAGGPASYEANGGGCGSAAVE
ARDDSSPAISKIVDAWGAVGVGQIPSTCSSNINASFGALGGHNNSSKNRAGVVWEQTGHI
HCADLHVLDQENSMAHLGMSMHGNNNGIVAASKLGALRRPPTKWTPQSPLRLPFTPATGN
SSLFVLSSKSPTVVSRGSPASQTSSLVVQGGPAPFSTAKVPVPNNTCAPNDDNHVLVGSM
DSFSPCSFDGGLRNGNCSNFLLTPPSVGSLPHVDVIHLNHGVARTARPSDDRKNHMERAH
HEMEAAVLLPECGHDDVQGSDPFLYEMQGSVSLESSPSISSLQVSSVRIYKEDRHCYHWN
PYGTS*
>TCRU_7085 hypothetical protein, conserved
MEPAGDRPVLAEIVERHTGGNSNIATTTATSGDDSNGVLCTLRPIQAVVGRPFPRFHPDR
FYGRQTMDERSRIGLTGTAGGATTAGPAHGFTAHVQPTTSNGAGNITGYIGMGSYDGTGV
IASMARQHQWEAQEFEGLERGYYTVPLHPPSADGTTTAQELSEFVQGEAYVELLLRFLCS
TVRKHRECATSALKARLMCDSKLRERCAFGPGCAQFVRLIITELSSGHKVPCGTAAECLV
LLFYDATAEMVEVVGEIGVPPTDPAACMEEDTTAATNNEATFADLSEWMRGGEDKARALD
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TPTGEIVEELLLLRRVLHVKQACSVLLPLLHESLVLFLRHMCTTPAEEMRSVSEVVASLA
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LALARGAVQTLVTCAQAIEDCAVDEASAGYCASLLAAATSMHYLATYFTIAGETEETSLL
LGSAGETLHRVQEMLAKFVLSSEGLRHAFIRLNNSRVVGSSFTVHTQPLIAFHPQPFVES
CWASLTHARVRLLASTHIAFSAVRPESSMGYAAALAIKFEQNCMGLSKLMGHLLPDEICT
MIEVANFMRRHAHTLSVDQQQQYKRSTYIAEIFILHGIALTKHCLDAAQKIINSILGLPD
DIELGATVQSSTSLPPTTLLRIELGKSLRRAVEQTQWTWFLFPLYDGELLSKSAWCAWLQ
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LYIGVLPRSGGVITASASDTLKALTAYASPHAEESMNRRLFEALAVTATACPPSVSVVMV
RLMAHTILEGDDTQHRTSFQTAVADTTTAMDTNTRDDGDRVSTPSVSAESLLQRWAATGR
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>TCRU_7086 hypothetical protein, conserved
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RMGGMSSPGHADVKKRVLPILCAVAFRYDPNKVAQQTGHTGNFNSQQLHSAMEQGVYLCG
SIVNIVGCFGFVPMEVEGVPVAAAGLGSASGGSQTYPSRQTPPRPSLPDGSIVSGRRSRM
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CDQLIDAGLLQRPAAQTTHSPYHLKPSMPPMDTFSFSSLMTNVPVLSFLHEMRCRLGQLG
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DGFDEGDVLRFDFDRCVWVADRSIPLDAVVLAAMRPHCKAAREAPPDDPCWVTVMQECDD
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STRGKAGNGERSSPGLSITSALFSLAPDSANNETEEGGVSYLPTRVTSTAITTAKRWMGA
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VAGTREEKQNENKDANPKETPVTAAAMKTATATTGDSDGNTAASHTTSPLLLLLVACAAA
AAVVAA*
>TCRU_7088 Nodulin-like, putative
MAYFNGWFKAANSDQPEENNYSGYAYFTGGQILLCSLIGACFTRLPTYFPCSWTKKRLSS
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>TCRU_7089 asparagine synthase, putative
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GRVQRVRAEEELVSRMRSKNSLCGRHKFYRVSTEEKKPCELEGIIPTCGDAADETKFVPL
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RRDEAPSKAVRLVRPADMGKVQRVVPAKWLVSDCDFSPLGSCADNYTCEARVLLLGMGAD
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LATLSSIAAEAYRCAIDTTHRTTAIPVDEDRALQEALAPACCFTAEDGAPGVGDKKILRQ
CASMLGLGDVVRLQKRAIQFGSRVAQAPS*
>TCRU_7090 Ankyrin repeats (3 copies), putative
MRRPLSDEERAAKEARLAELRRRVNARDGDSSSSAAVPDQPHNTYASEDAQDSDDYDDDD
EFFQEAERAQKGTAGVCMYAKPMGELMGETVETGPNARRCTVGDFELLRLAKMGDLLSFK
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PDFYLYDEILRADIIAKHALTKAFGDKKASHSVGWCTVDRSNSDQMEMLHGFIVEQVPKL
FDLTYIPETSEDTLRAVIAEGLFPFVYVSPATGAITDLVVLRLRNPEWRVGEGQGAAMCV
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>TCRU_7091 hypothetical protein, conserved
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DLLVSERIGGEDEGALVVLCSVLRAATNRFAGDKGEQLWTEYECHAPPPVSTSRELALYM
FNAFFGASSAGIMDTTDSSNSAEQQAIDVETRELGGYWFVTLSLSRVGGLAVARAIATAK
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GFGSALTRTQALHIASLCALENLFEGDLAEALSRSAGYRDLPPPE*
>TCRU_7092 phosphatidylinositol 4-kinase alpha, putative
MDEIPFPTWVRRSPVFAMTRVLGQHLLQQLQPTRVEPTGPVVVETTTTNITTKRAATASS
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SFPAFATSSTALPLLWAVINVLEVGNATEVERFCEHLQFPEAPAVATDPDSLERRNRLQD
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FVQTYGHPESVTFHRARECFIRSMASYSVASFVLNVKDRHNGNLMIDAHGHLVHIDFGFL
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SRGNLRTVLYDRYQNFAEGIEM*
>TCRU_7093 hypothetical protein, conserved
MAMMADRVLLVCALCVLWCGAGGICDEKAVGGCMASEVLGENGSNMPNGCDRTALMLSLR
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GSPHHPGAGTVTSGNLLSRPQNASQTEVLRMLKAARK*
>TCRU_7094 Reverse transcriptase (RNA-dependent DNA polymerase),
putative
MLDRLPRLGPRTKRWPHNYLRGRYVRVCTREQHSRKQLASAVVPQGSVLPLKLFLYCVDD
LLRRLENIYSASAFMHADALTLVASGADIHACAAAMQPALSLTTAWAAEQKLKINVAKSE
AALFHISSHTLSEEEMVDLHLGSENICIQSRPVRLLGTTINRLLLARTPPPLQSRPRHAA
ISCGWVQRLGRPSTPCDPF*
>TCRU_7095 hypothetical protein, conserved
MVMMTGRVLLVCALCVLWCGAGGGGCSETTQVPPVPPGTPPGKGGGSESDNNSTGGAGGS
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EGEREEEEEDDTKEEETKKEEAATDTTEGISAGGEEQPNLSSAAEGASNKTNPNSTPTTG
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LLVACAAAAAVVTA*
>TCRU_7096 hypothetical protein
MKFVRIYKKGNRFPLLRCEFGKELERKTAPLYGMHGKRRVGTETHECPVWARVLHTPVLF
GGTGEDVMKIRVEREWSGILNEHNGAVSSNKFIRLLLENPAIKSHLLAQLGKIIFLHCLQ
FGSGGYWAVSLRKSRMQMMPPHFPMTKLVPAVKAVAAGAGAWCGENRTWNKCLHNSELTS
QFCVGVLNVSHFGNPRPFPDITLVILATQLKL*
>TCRU_7097 hypothetical protein, conserved
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DGVSRTLYMVSGKRKAIGHIPNVSETEVLFPAFSMYYLNQKLSFV*
>TCRU_7098 hypothetical protein
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TLKPLKSLVSNESDVHDQVVISNRTLFNWALIEGVQPVVFSDNPLDHELIERVNSDLAAR
RVGQRIDVIKDFEIHQKFGLPTYRGLFSRVLADYPDVHYFVYSNMDILYTRSALETIRAV
HRYYSAMEGSERKFNVKGWFAVGRRTNVEVPLHWSLGTNWEKDVEVVFGAAGTLFQSFSE
DYFAMSRNTFDWKGIPDFVVGGTAFDNWLTTQAVMLARAGLALTVEATLTLMAIHQNHGE
NLKASHMHPKSRYNNKLARISGGWALGHTTDAPFLTVRHFGGEVLVVGKNSVLLH*
>TCRU_7099 RIC1, putative
MHLVYGCPAVYSWDPQPNDYDGRSLAVLSGSVGNYIVVLSSTQLHFWTGTSEIIYLGSVR
INGATVDDDPATHFLLHARGDYLVVTTLQRRILFFNISLELKNTEVLAPLYHDNLLRTGS
FASRVRFLKEERLEFGIVTSLASGGSNCFFVCTTAGVVCVMGWFQQKLLHTWSCRSLGRD
ALSFVPLDEMGEEHADSSMRVSRGDILSGSILDVCHSSQIKLTVFLLSNGYVVLAQSNVG
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SFLWASHGHRLFVVEPLSDGFTEYSFGQIISSPCGETTGCFTPIVAFNNDSMRLAGNFPA
GGGPTFNDVVSVRSQYAIENYPLTQGAVSPDGGSVVLAGKNGFVLFDCLSHRWSALREKK
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ECHEEFNDMFILLLDSSNALLLWRCVIAHDGHSYLPDVKIYLEFIKRTQLPDGLVYPVGM
AGIHPARKGPKRTSFLSFSSQRNGYENALPYALFILRGSHALVSFDLGAAATNTSETSSA
IKILISDGVCRIWIDYSVPMDGSVVIVFGVHGINFLHLLGGEDDTEIFPVVHEYAVSEFD
AESIPVGLSTYDGCLFTAFSTREVIGSIGGTSPTVSLRISLKPLLYNFCVLKALTCMGLP
SLDTVNNKTPSNVNPFPLLMWNDRLLYWLESMRRNGTFIPNADYFLHTLISESIPCSLDH
DSRRAAIQATVSLLRRYSEFYSVVVSCMRMLDVSQWRNLLDVLGSPLEFFRECIENRRFE
ESAQLLRVIMLDGNFPDDGASVKSLEATMLCAVHLFVLALWRRNVPLVHDLLRFMALLHT
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LQRRSVVEFVLRKYPKVRQAVHDVFSESLFAGHLMVLRDISHELFIALRHFVTNKTRPTM
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TEGTGSNVAVWTTAQSYVYTTPRMVETILGIRDLYSIWDECVLAVNVILMIEDAVIQQIQ
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MDVVATPLWSSPPCGSPMAGTVSSGNPLFHVGRSYYRSAAKAYNMTRYVVESLKLDETVL
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GWRRMLLEMELLVCHTLGFNFQIIHPMKRIVELVPEDHTQVLECAHRLFLLSFMTPLCVR
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AIDLFNGKEFMGNVLSVVPAKTTPKPDPHANSSVVFVSPIFRASTTKKQILELFSGMKVL

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AAQKFNKRRNHTK*
>TCRU_7102 hypothetical protein, conserved
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SLSLKAPFLFVGSREEARKYGANLSLSHEDAVGGAVAWCDNVPFVFGIDVVDVKQLARVR
RRFPHFAARCMPCCQPSMLDAVELLKVQTMYDDCIDPSDVVLAQHWGLRECCVKLVGILG
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IIVAACPKFHQHCL*
>TCRU_7103 RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)/
RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain), putative
MGNVLSVVPAKTTPKPDPHANSSVVFVSPIFRASTTKKQILELFSGMKVLRLRTYRNNYA
YVYLDTPAAAQRAVKEKNGAEFRGKQLRVALSTRSLAKDRARAERARLLMAAQKFNKRKN
HTK*
>TCRU_7104 GDP-L-fucose synthetase, putative
MSVRSVVLVTGGSGLVGRALEAVQKRNPSADEKWVFLSSRDADLTSMEATKAVFEKYRPD
LVIHLAARVGGLFKNMRQPVEMWHENVAINNNVLECCRIYGVKKMVSCLSTCIFPDKTTY
PINENMLHDGPPHCSNEAYSYAKRMMDVMNRAYRSEYACNFTSVIPTNIYGPHDNYNLQD
SHVVPGLIHRFYLAKQAGMPVTVMGTGKPLRQFIYSEDLAELLIWVMREYTEGSPIILSV
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IKRSVEWFVQNYDVARK*
>TCRU_7105 hypothetical protein
MAVCLRHPRACVGGAPSCGSLRNVGASRRHGAPAFRGRAAKHRSVGLKRRAVAERLRRLG
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APRKGRISPLFGAASRGQA*
>TCRU_7106 hypothetical protein
MRHNRHCGIRCFCVRGRTRSAESGTLGSVVITIRNRKPCIGAPPIAMKPAVGSRSIPSAR
VHKTKLSEASRTRESIRRQQQMHALRRAAKNPETPSFHTCGPEQRRRMQRNAVPLLLNRG
IFQAGGAGRQGHRARELCSPRTAPRPSVVDLPSAAREIGLGRGY*
>TCRU_7107 hypothetical protein, conserved
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RLARRRLLFARERAYSSSDGGEVFRSIDAAQRAAELASRRATDGLHARGRGGGGSPPLLG
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GRTVR*
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MAEAASCLDFKASFFQVSLPRETRHLFRCRVEDGTLVELTRLPMGYKASPEILQIITSAI
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PRNTPSCGAV*
>TCRU_7109 hypothetical protein, conserved
MEPDGALILDWSVAPKTARAHPHRASRFVRIREQDAFDTIKLCRTLQEKEKLTNITNAKV
ERALAPWDATAYSIERGALRHAAQIVETYNFDPHVIPQLAKHVDPFDLPQNTVRYLWRYT
TMLTQVSSLVALM*
>TCRU_7110 Tubulin-tyrosine ligase family, putative
MNTFEEFSRLLSTWFEAHGLTEHLQRRLDEKLRNDIFDAGEFFSLAAVADGDSEGDADSL
QEAEASASNEYVLVATRDLRAKEDIWLVDHCCTFRLREFCEHLEANATLRERLGRILSLK
LSHTSAKEDTQTVFDHMWTKVGSYRLPNEVFEEDSQYENTWFIHDEVGSAIKVVTGEPGN
MKLEPIPLCFPEKGGVFSAMWCVEDMEEGTIATQKAASVLESAGGKEVVELLYGPAGGES
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RKFDLRFIVAVRSFVSEETPMEAYVYNVFWTRFALEDYALNEFDRYEKHWTVMNYANPEK
LIQLHHSEFIEEFNAEYAGKGYGDSLWARDVYPKVLKMLRAAFGIVKVSGADRRRCRAIY
GVDVMLRETLDDTRGTKSLEPTLLEITYGPDCQRACKYHPNFLNEVFRTLFLGTPANMTR

L*
>TCRU_7111 dynein heavy chain, putative
MERVGLVAVEAQLFSAAQRHLQVIFGAANATRVDDCALFEFSPFGEKEENRLGDEVQRLF
TALVREVTGRTSLRLTGEDDETDVTLLRENTVNFGNFMADFVEMDALPGALDSLPSNPHV
YEMLEMLYMDVVGEVEKGARLVTEFPKVLCPTGTRWDILLAKSVCIQVFSGTEKELIPNK
TVKNLDASMLSASMSTTRCLPDGPLMKVWMDLRVLGNAISSYATAPIESELPSQWRLKSF
TLLEASEVLNLVHESLRLYWNCNPRNERTKVNANSLLCIVSGDLREYIKGQILLESSDWR
GPWRMNLEHLEKALALITEWKGITHKLLKEEWAGWDGGKFHDETLEKFFGRLRDVVHIRQ
LLASASKLTNGAVENTIVPEVIFKEESLTDSKSTSDERWAKCRGKFEKEFLFLEDNLRGR
VKQLFATQQQGSDASLRLLQQHRILLQREGVRSGITGELEAVRGVLIQHIEQARGRYENK
KRRATTELQMLRLLKSCQAECAQVLETAAKLFGSSADLEKVLGPARALMHETQEGEQEAL
TSWKQSMETQCKKVVNLQDVFVISGVDKDYIACTLHASVKQLIQDFHSVRGWWGCGGGHE
EGGNTEKKSNGRQGINKDSARSSSSDDNNDNNHQNFTDVQNTRRGGKGLRLSREVEHTID
LCERFMNAATRTMQIVSNYNIVQRQMLRCTRPVLDAASTRVRAQIFYGDTDSRIIPLANY
HELEGINMRFQNAVEALSNDNRSIRRFHGDFISQVIALHNVDLTRHMDQWRSAVDGMRSA
FVEFLHTHRFGNYENWRQHLDAQIYKALEYQYQRGLETLHEKMEEFKVELVFKQGQVHFK
PSFEAVREAYYVKLREFVSVPLRFRGLQEKRESGGPYEMYEMMPLVNKDLLVTVQLKALD
LFAKLSRLRKVFQAQMVVGACGVNGAPDIDTVVEEVCRTLPQFVDGFNTVKEQAQKLQRI
ENNMKVDCFTLSTIPAKASMEEQLHRLEESLLNAMRKKMQKSLADIDDFVFNASNIITRQ
PITMDEVGQANKAYYEFVETMPSYEAKFTEVEKMNRVLRQQCGTAIDLSATKSRWEHLSE
AVASHHKIIDASVSKMRVSLDGMIQKHLKDGQRFTNKWEKQKQHLVLAFKENKMELINKT
LATLKDEFQELEDLRAQGRDLESKCEYFKSPPPNFHQITLTVEDVMETAAMWELYETFRE
SLHELRKEDWLTFRGHTYLFEDFIKEWRKKLSGGDVSKSNSTVGRVIVEYLEALLHEWST
VFPLLRFVRGEGMMNEHWNEMFRLLGIEKGMRTAELTFGDILDHYKQIIAEEAELKQLHA
RAQGEVQIRDALQDLRAWALEATFTLANPSDLSMPEKVKLITEWKETLTQVSDNQALINS
LKDSPFFPHFADEISGWEVKLATLSESLALMNTIQRKWTYLEPVFARGALPEEQARFKRV
DKEFVFIMREVEADPRVMSIGSQTDIVDRLKSILEQIERCQKSLMEFLEAKRESFPRFYF
ISDEDMLEILGHSKNPSVIQTHLKKLFMGIHSVVFSEDRKAITHMVSAEKEEVQLSGRIS
IEDDDVEKWLCRLDAQMRETLRGLLVKCLRAEDVSAPTVMDAFPSQILQVAQQVQFTMDV
ENAIPSGGLSKLANSLRGKLNRLTEVSSGADHVLRLKVKSLILDVIHSIEIVDLLQEKCV
RSLDSWWWQKQLRYYVSDGSRCVVSMMDTTFLYSYEYQGNAPKLVQTPLTDKCYLVLTKG
MGLGYGGNPYGPAGTGKTESVKALGSALGRQVLVFNCGEGIDFKAMGRIFIGIVKCGAWG
CFDEFNRLKIDQLSALSQMIQVIQEALKNREPTCILLHRFIQVNENAGIFVTLNPAGKGY
GGRNKLPDNLKQLFREVAMSAPDNELITSTMLFSEGFTHAKPLSKKIVELYRLCEQLMTK
QQHYDWGLRSLKTVLCLAGTLMHTWKMENEGKEPTEAEEAELILQSLNTNTLSKLTFDDA
KLFQGLMADMFPRVSAREVTYGELQSAIEKAVQELGLQLISAQVSKVLQLQEAMNQRMGV
VLVGPSGSGKSTLLRILRRALQILHIEVPLHTMNPKAVPRHQLLGYMDLDTREWHDGVLS
AAAREVVKCPKDHRPWILCDGDIDPEWIESLNSVLDDNKLLTLPTGVRIQFSNNVNFIFE
THSLAYASPATVSRMGVILFSSKDISLECAVDSFLGKQTAERREFLGPLTKKYVIPAVEE
VLELGALVLPTTPLGIINSCLAHVLHTISEEDFVFSLMRGLCGMLHAYGAQQISITLYKL
SKLSPISSKRPFDTFYDREKKHLAEFSADLRLDVSPETLLNTGAVIHTTDLQRLLTTLEP
LVDDPLCRPFFLVGQEACGKSIALQQCFSRYPGIKITVIHCCAQTTSLHLIQKLEQTCTL
SSTNTGHVYRPKDAERLVVILKNVNLPKPDKYGTVELHAFLLQLIMYHGFYNSDLEWIGV
EKVQFVASMNPTTSAGRYEVSPRLLASVCIVSMSYPSRASLVQIYTAYFSLLMKNAAIGD
GAESNDGSGFAKFLINVFERIQRRFEGEEYAHCLFSPRSITNCVTNLLMYAMDSQTTTLP
AALAHECICIFADCLSRTDDRRRAEKIISDLLATIGYSMPSKDEPNPIMFVSWFSEVDER
GVKPLKGVPYEMIAAEVERALVKYGREFRELNVHIIPEALAWISRIDRILARPVGHLILV
GRPGVGRRNAVHLAAYMLRMQVVTLNMVQGYSVKNFRNDVRQFVQRATTQNERLVLLLDE
HNIVDESFLEVVNSLVSSGDIPGLFTPEELETMFTSLREDAACSGYIGSIYAYFLMRLRR
NLRLALTMDSHHALFLVRLQSNPGLLSNCDLLWMGNWSNDATRTICKKRLKNIMKFIEAE
PANKGFHLHRELFAVHEAFGNDATPGRFQVFMETYEKILLGKSQNSEADLKRLEAGLSKL
NEAEQNVEKIRKDVTHKKEEVEAMQREADGALTEIQKKMEESKEQRDNAQELQERLKEEH
EEILVKRQKVEDELSGIKPSLEAAREAVSSIRSEQLNEIRSLKAPPEPVRDVLEGVLALL
GVTDVSWQSMRKFLGERGAKERILEFDAQKVTRGIRENVGRLLHQKANSFKPEVIHRASV

AAAPMAAWVKATVDYSTILDSISPLNSQLQQLEKNQREGEERLHALKKKLKQIDVAVEKL
REEFSKKCKEAERLKDVLEKAEKELSKACELLEKLGSEKTRWAQDAEKIETDNRLLPRRA
LLSAAFMTYIAKETEDVRQRYFKQWSDRLNFPSAVTVTGFMRSESDLLQWKSEGLPRDDL
SQENAIAMLDAVQTPLVIDPANQAIEWVKTHLKNNNVVTEITSVHDERFAHTLELAVRFG
KTLLVVDVDGIEPILYPLLRRDLLSAGAKRVVQVGNKQVDWQDTFRIMLFTRRTDLALPP
GAAALVLEVNFSVTRFGLENQLLGVTIQHERPELEQQRVELLQKEENLKLELVKLEERLL
NDLASSHGNLLENAALIGALNDVKMQASSITEALQQSHSLQVELDEKRNVYRPFASKGAT
IFFLVKDVERMNRMYHFGLSDFIDLFVECLNTYNGDSDLDLKIKRLTLSFAQKCFFHVSL
GLLKSDRLMFGMHLVQGFFPEEFPPSLWNVFIGVSTTPSHAEADESRNEGFPSWAPATAR
RKFILMAADEVMAGHMQKWQLHDNGRWSKWMMESFPEESLEQDASLTLMDKLLLINTFRP
DRLTDFMHHVIMNLLKLDTLMPVTSLEETLTHGKATTPIILITSRGADPSLEIQDIALRI
VGKGSFTQIALGGGQTEDAMLHLHRCAAQGDWLFLKNLHLVLDWASVLEKELCAMPIPSA
EFRLIITTEAHDSFPVVLLRMSAKVTIEAPPGMKQNLLQSYTTWDEAFLQGKTKTTSQVL
FGLAWFHALLQERRGYIPQGWVKFYEFSSADLKSAADVLCTLSRDKMDWTTVRGLLQECI
YGGRLENSHDERVLERLISRIFNDETLVSCDRRLYDDMRVPATNVHRAVVQFIREHLPDA
DSPSILSLPDNADRAVKEQFALKLTEDLHTLSHLAQVCVSATEAWRTLLAPVLELWKNSA
LEPEGNAATVSPGETKEDPMSIFFMRELELLVGIVSNLTETFYDLRCVVEGTLIPSPELR
EEGTELIGGRVPPRWLDLMDGPKDVKLWFALLRRRRDTMMENAKRPFSPSTPFDLIDFLR
PQTFLNALRLYTVRVSNEALVELMLVATPVGRTADRFGVGFTLKGNSIHLQGALLDAQGV
VSLPSASSPSSTPLSCDVWAAWMSKHNTEGLTRIPIYTNAGRTAAIMDLFLSCDSDMAEK
LLLGGVAAFLVSV*
>TCRU_7112 ADP-ribosylation factor family/Miro-like protein/Gtr1/
RagA G protein conserved region/Ras family/Elongation factor Tu GTP
binding domain containing protein, putative
MSYSKSSELLFKVLIIGEGGTGKTCLIRRYVHGIFLATNKATIGVDFALKDVVHAATNRN
ITLQLWDIAGQERYGQMTRVYYQAAAGAIIVADITRPETLDLAVKWKQDVDSKVFLGSSG
KSIPCILLINKVDLLPHGVLAASVAEDGTGHLGFADERGIQKTKEEMNAFCTEHGFEAWF
VTSAKENKNVDVAFQKLVDCVLKATEALGGTETAQEVAKERNTSGKVLHGNRTRREEKSG
CSC*
>TCRU_7113 Enriched in surface-labeled proteome protein 1
MGGKLNDGDKTVILELSYHSEKKWILLCSDGKNKDHSSNWETEKSEHVLILLRNGNQGSA
YVDGQRVGNAQLALQDIEGSKEISHFYIGGDGGSAENTGSREGVSVTVKNVLLYNRPLSS
AEIAGLAKNTITIPKPEVPKTLVVDARSPTVSAPDMEETVHRPNSAGQLPSEHEPLTNIG
GGAGGVPSAASTATTPSSDFAQTVATVGGDTLRRNGSPQTPEVSVSSGEDGETVEGTDGQ
GEKGIHPQDGEVNATALNSSLGNVSQGNNSDAGTMRGSGLLPSLLLLLLGLWGLRLTEE*
>TCRU_7114 tubulin delta chain
MACVHVLVGQCGNQLGTQFLDNLVAEAYTSDGDDGFAAQVSSLHFRPSPVLRGREFSHGA
TMPPLPRCVMIDMEPKVIEGILKNTKNGGAYRPHVRQCITRDEGSANNWACGYFQQGSSR
KEEILDSLRRESESSGTVGTFHVVHSIAGGTGSGVGCLVAEAIREEFPCALLLHSVVWPF
STGEVVTQWYNCVMAMSALRDTADAVFMAHNDDFGDAAFANKKVLSGVFRGEVSFARIND
EISRLLVDMHLPQNIYRVTRRPTTASTATSSMNRNRFMRPQALQEAEEVCSHTSIAGILR
RGRVADLVESVALDPALKFFSGVSLPNDAAIPSRGGGGGDNGDGVGVNDNSVSWGSVMRH
AARKSAELFPPFAGRCAGGVLQQRPFIWSLRGSAACSEGLTALQEVTSSSSYAGIALLHE
KRYRGYAAHVSLFGPTFKIGVRLSKALERTEQLLSVRAFTHHFSRYGVGVDDVRDAVVRL
WDTATIYTST*
>TCRU_7115 hypothetical protein, conserved
MSMVSAAVSRRCIQHNPYNTQVLDVRTDGISVAAIEFFKSASKMEESTLSPSQKSLEMMD
VNERMTCTEGGGGISDNGTDEVSRTISLSQTPAIAFAMQPTPVLPLVRYASVNFRFGSAW
FVAPFRTAVGEMVVVEYPHNKSLHMGLVSCISTRVPSTFSAMANSDGVISKDDIQQCPRL
LRHARDIDKQTKMELRSHDFASLENAQALALEMGTPVTFLDAEWLLDLTAVTFLVNVWGD
MSLVDRLADELAAFEGSEVVFTYPAVN*
>TCRU_7116 DnaJ domain containing protein, putative
MLRACRRFCAAGAAAAPTSADIAAAFRVLGLDAGNPQHATSERVRAQYLHLARLHHPDLS
SGDDQKMKVVNTAYEMLQRSGVLNAPLSKRRSEQSAEEKREGGGTGETRFAAKAKLRRRR

VPDDFADGDTWSMKSTLEWETWMNSTFGLNSVSDEELRNPANHPFSHSKFFTFEDDTAIY
RMLRGGATVRQVARTLGKSPTFVERRLHNAQFKQRIQYVLRHERRLRQQPQQGAHSGGKT
KTTAAAATAGGDGRRKKEWEPTIPNFDSPTFFEEMSLEEKGIHAGLLREEERQQHVPLSW
MRVASKVGQSYANYARFAGKPRSKP*
>TCRU_7117 hypothetical protein, conserved
MKKMDDDWALREALLLCVEGSQQSSPIRHATNGFCPWGVQKTTHKFPAAAYGETDCKSIC
CTVTKVEGILRCTLETFVAFISTPKNAQYHDDGVVSNDVINEKGDAVLVRTVYRHRPPVE
VITRHASKMYHIPEAVGTNEALQRFCAHAVGISHDKKISENSNVNSNNGTSLSLSSKVYV
YAIHSVQDEGSVHVSSNNIRGWVYLSAFIAYEMPGPCVHLTFVNAPNKHVAAVMESCEKK
IPRIRSFCEMLQEMMSRGKLALMQRKRSGVKAFGGVGSPEQRNPLGLVQNEPFVFGPPTT
AQLRVLCPLLKLHAGKMWRYRGRQEGCDVEECDANLFIAAPPFLKAYRISTFIACSLANF
FSFVGDPLQTHRYDPFLESSMKISTQPEGEVFYLRYKRLATYSSLRDYCVLVNSILLQPD
MERGSTKLLSAFNSTAMVYIENAIHCNYRPHCEGYEREIVYAFGYIATSNAGDNCVQVHH
IVCVDSKDKSNQRLELAMIQEHITRMAWVRQICEDTQSTSIGMRPSQAPHMYGEERTGNP
NHDDEEEAASFVEVETLEDVTSCVFTQDSADCMSHPTSLNGSVEELEGIFDRDSSGAGTS
FQSASPVRHPQVSDAETHKSHLTPAITTDWNSLVTPTEEVEKQDGWRTTPHAQTELSPSK
EYFVFQDGSKQRLSPPQRDFLQVEIVSYRNFLTWSMAKNRVIFFIFRTSAKSAQTARVTF
KENSLFQHERLLFEGPQGDAMTLIVVVRTSSGRMKRLGKAVMSLRNIRESEPQTRWVALV
RNSGKSDACVCGEVCLTLRGGGLNAQASATPFSEEAEESLRKRIRHVLMTFGRRHLHRLE
WIVGYCCDKSPSEVDLLLARYKKREHRDMVVLTVFDVQGLITEKGVPFLNGPACQVWVEA
NSVRHCSRTVPLQQVAVFKESFQLLVGVAEAIRLTVAVGGFIVGKVLISASPERFGGVRT
HTLFRAAGTKKAMPSGVVTIALSGDMNQHSSHRDGGGGSFDPLGEAARTACLRLVLWKYA
RHVIHRLDVISSSLCDVDHYIKTLGPCPPRCDVRVSVKRWEPSVPMWDSPAAAASMGASE
TEDKDGNEEGRHSASYRNIFKRQTVYAVIHAGLHYYKSSTVRVGEDETAYFNDPVTFHDL
LPERDEVLVSIVGKGISGTETTDLGTTVFTLRTLVRKQTMSFTVPLVRRAGSDDAYFKGC
VQVELCAVNFGSDSIADTGPTSSRLQLQRLLYHYAPQKLHRVEPLLLDHAGREGRLVRSL
LEKYGPDVYSSPMEIRLIGIRHLTPANSCYVKVYLNGEPVLRSSQQSGSANIAFSPSDVK
NAAVVMLDDPHHARVRFKVAQQRYLQSTTISFAELRLGKMVAGSLNECWIPLFDSHGGEI
GRLGVTLRCNGFICRKKEPAKCEEAERDVVSLLRKYKPEALPFLQPLITEAGSAAKAHAE
IRRRVAKRPVAATVYVCVESLSIMELDFSHPSQLHGISPTRLALLQQENEGMEYAVTASC
DHEEGSVIWSEQVKGSGAVIRLDIPEFSRCEDHRLTIAVRQAQGACFLSRSGSRQRSSSR
GGRSSFSQRKASQQLLPPTELGRVVVSLRGLLTGSLYDAAERVTLPLVSFTQGPAARRKL
QQERIQQRRQPSSSSSAFLPPCNVVGNITFSVRLPAFERAPSWLQLNLFEIEKHLAIDRA
CIRYYEERIRDILAKHEPQGLLALHYTLYECDVAHGTWSLSLCDRVRALLQRLGVVEEAA
TTVPIDRSM*
>TCRU_7118 Checkpoint protein HUS1, putative
MKFKATVRDQRTLASVCQACRGIQRRCVIKLHPTRIRFFTSTQSADGMQVWAGCRTQAIF
SDFQSQSQLQENAIFCEVADLSQLFHIMRQAERCPNVTIKLTKNAARRPALRVSMQGVRP
HLDISHDVPVRVLSELEVRNISAPPLESEVVQIVLPCLAELSKFVDKVRSTSCDRMTFTV
RDNERADGAAATSCTLVVLAECFLASFALKYSSVQKCEREGENDADFDGEGDGNGGDKPK
HRDDTSMAYASVSVEVRRFARFLAIKEATPLQVVLHLVDGKAVVLSVFASGGTTLVGYMP
AVAQ*
>TCRU_7119 hypothetical protein, conserved
MGFHASLELESTCKRCFYIFESPCTLWPCGHTFCQQCLPFMFTEQGELICEECGSLCEVG
YTPNLALELVASYQVMQHTDYDDDDDGDGEIGCVVQRRSIEEVLTAMLKDLMSTQTTIAD
APRKTAGKAAPHPLELVM*
>TCRU_7120 Enriched in surface-labeled proteome protein 1
MLQSPAKPQPLEEEPLKENIGGSDGVSRAASVATTPSSDFAQTVGSEVGDTMRGNGSPQT
PEVGASSGEDGEMAGGTDGQKREAIHPHNGEVNATAINSSLGNVSQVNNTDAGTMRGSGL
LPSLLLLGLWVFVAL*
>TCRU_7121 retrotransposon hot spot protein, RHS3, putative
MEYHTNTKIKYGVLCIPAGASFPLVDCFFFVELPRKTLVGLRMATASGRHTTASTVRQFT
ECLAAYFNGWEELSQEFSWGIIYVQHADSMPMNDWRRCDVDNPNSVSRAESREIAAFWRK
RCASTKYQYHPETLEETKLSEVC*

>TCRU_7122 retrotransposon hot spot protein, RHS3, putative
MKGYVIYDVTEKGAPPASYFSPCNEWGMIVVASPKVSNYDHWETQLKAERITMKSTDEMD
VKAMCAWMNRDGTAEKQAESWKMVKERMDKVGPIPRHIFDANKFVAHSAASEDALDGINS
RDGEKHFTHGGVRLWDSGDPSQKLVRVVRGRGEVGAEGFLNAPISLCLGRRISHYFGKRN
E*
>TCRU_7123 Enriched in surface-labeled proteome protein 1
MPRRVFTSAVLLLVVMVCCGSGAANVDVVEPSEPRFQWKDMKSEGAGVTVDSLSVPGLLK
VGSGVFVVAEAQCKKDGNSGFSGIVSQLLTKTEDNLPKEVLKDAKKDTQVLEEVTSAKEE
KRVDVSRPTADMEGSNIYMLVGKHSHGDLAECQAGTEKIKSGILLVKG*
>TCRU_7124 retrotransposon hot spot protein, RHS3, putative
MNCPDESDVRRMRVWEQRSKPPQQQAEYWREVRGRMDKVGPILRHIFDEQSYDDRIEKCH
ETVEETISPETQYYTGLGNSTMWGGNSVFHWLAKVARIRVEVCKGGFSLNLPISDHLCNK
TLCMLAKLMQQDDFNSLILRLKHNLVSKNMERCTVFAFLDADFITAIRHKVRELKRAARR
QPHRSALEVYSQERPTRHHVLPPPHYFSEKVGVDCCVLYVPEVEDFPLLDAFFCGLKSED
AGWAADVCGG*
>TCRU_7125 hypothetical protein, conserved
MSPSRGSYDAVQRLHGSGLDLDCAVCGGGAIGVPSLALVLDKLVGGYSGSLGKLTFHSAR
ERATPLELNPCVTTLTRQLQCLPHTGRYAGASDRVGVVSSGRLRSFRAKFFACLRWGIRD
AATAFARDGELQWPQQPSVFVRNPAAEADQCGLFPLVRWSPCAWLPSRLSRWCGEVRA*
>TCRU_of Trypanosoma cruzi region 5/Dispersed gene family protein.1
Dispersed gene family protein.1
MVALPPPFRWASDPQLGTHLSFVPVSTAQLSGFGGPWGAMLRNATNPSTVLELAVPVHRG
YFVAADETLVIRCDAAAVSGGCKGVLLGFFTIRSDTLPAAASALSAITGVVAGAAAVAAV
VTGGPGSILEMQALGVFARMSCASAQERGSTVALPYFLSVFAALDPLWMVVGMRDDRRHK
PCVHCGVTAAFQRWRGVDAASAWAAMRFPSLTYFVAHAMHLGIFFGSVLALAIPDARVQH
RVIGVVGVLYGVAFPAGVCYLIARHTGASFTRYWQFSRKPLHERQLYPVGYWCPAAQQRM
YGGMLTNMRGSHVYWCVFQLLVLCVVCLIAAVHSPVGGCYVQYFCMAAVLLAGAGVVAFT
NMMRSAFLTVMHTAGFLLLATLCVVSAANHLAPSDGGARAYAAIVLLLTTVLLAVTVYGV
VVWYAEDRHWQELREPRRGGLEALLRNDEESDEETQKLHDIKLLSYASGTTVASSYRPPA
LP*
>TCRU_7127 hypothetical protein, conserved
MWKTHHCYVDVTFSGVGAVLKFFFDSMPLHLPINITLTGCTFREGAALQFVGGAEAAESA
GVLIRVGRTVMRSSVVVFMGALPQHCDIAITEIDAVQSSAVQTLENGINKLSVVVLREVL
LSASSLLLSNVKANASSYGLFGFYSTGTLTLVRGSSLYARYYSFDGYTHLFHVYGLIVSD
HSVFALLNNTMSSGTSFLLQYQDFSVSDYSVLRVVGNSGSVSYAIFADDSWTVQDSSWLD
WRDNDVGLGAMLCDTESAFVNIDGSSVVTLTGCKMGSTGLSRPLLLRTETGYRFVAGCLT
VAGRKVTTAAELELNSIFNVTTVAACGECTKEGDCFAPLTTAVSDSKCQCAAGGHGDVCV
PAPVPAGPPPPSPPLPPVRPTPPTVGECISDMVYPEVAQAVGGGLSWLCYRNVTFSGGGM
SLTVLVGAMMGDVVNVTFDGCTWRDGAVLVLLGNAHAAVGSLNIVVTGNTFSDALLSPEG
VFPPHTNITVSGNRFTVTRLIPRSGLDIGSPSCVAMNGLAISNDSAVVFSGNVFHTVTAL
SSDIYVVGSALRVSCHPLFAVIGNTFHMAGGDSTVIHLEGSRRSSSLSVLNDSAVVIRGN
VVVGGLKYFMLLFWASRVESQSAVVFQGNEMWGSSTVFLLGSSFQI*
>TCRU_7128 hypothetical protein, conserved
MDNCAVMSQAHVMYALASDLRVGGGSVFSIQNSSWSAPSNDFYRGACVFGDVAVAGGSVL
QIVSSTFRLGFAMLMANTLTVTGGSWLVHRNNEFRTAYVVHVANENGVAFRDQSVWSILD
NKLTHGSYSLTIAHMTNDWSQPSDTRPTIYGMCNEARGSPVTNYQDDLNIGAPVAALDCG
ACTVDAVCFAAGTSSISGCECECAAGGHGDTCVPAAVPDGLGPLPLPDANDTEVRCVHGG
IISSVDDPDPGVRGLCFVNVTFTAAIVLDLWSFDAPQQTLNITLLQCVLMGLSVKGSGTR
VHVTSSMLDSGALEFRGDFGASSQILVVGSTLATTSSHAILFVKFTLGANSTLLLLDNNI
EGNSYAVYFFNAVVVDGGGIIVKGNTLGTTEKDEGMEAPVYFCAVDLKNGGYIDVENNTM
SAANGVHFFLGYCRGLFGAAESGGLHLYWRSGGFEFCAGVFVWLCDFPGWCAVACGGQQR
KCSLDNKYIAFQAQYSAVGQRHHRGACTQPSGGGKRLLCWSGSVKHGCVITRAVCGWVQP
SGR*
>TCRU_7129 hypothetical protein, conserved

MGRWRKSLVHIECPRLCFLRALPVGMLGDFSGDQRARHLLGRQWRHCGIRMGGPRELSER
QAEHVRHVPPYCGRTSALCGILGRRTSIRRSLVGKMLRRSRREEVPAEAEAGRSPQ*
>TCRU_7130 hypothetical protein, conserved
MGRWRKSLVHIECPRLCFLRALPVGMLGDFSGDQRARHLLGRQWRHCGIRMGGPRELSER
QAEHVRHVPPYCGRTSALCGILGRRTSIRRSLVGKMLRRSRREEVPAEAEAGRSPQ*
>TCRU_7131 hypothetical protein
MRIVRLEQDDYLILFRGLMLASAHFSDLREATEPVKAETDSGWNDDDFDEDEMQFSNPCG
ANLAASMSVGRVQMEEADDDEWGDW*
>TCRU_7132 Enriched in surface-labeled proteome protein 1
MELSYDGGKKWILLCGDGTPKEHSSTWEKRKTQHVVLLIRNGSQGSAYVDGQRVGGDEQC
KLETKASKVISHFYIGGDGGSAGSTGVEEDVSVTVTNVLLYNRPLNSEEIDAFDPNKAPI
PLLVNTTIEGANSSSTAGRQQQAGKEPLLESSIANGETAGGTNGQEEEVHPQVGDVNAAA
LNSSLGNVSQGNNSDAGTLCEGGLLPSLLLLLGLWGFAAL*
>TCRU_7133 hypothetical protein, conserved
MKRVNAIESNREEARKWQLSVFCGRSKHEAEKMAKELERRDGATLDEIKRALEAEKRESS
ALQADRESRNWECEHTVERIRTRKQDEESASERLRQAMQQPEQGLSLRQSAIETKEQQLE
MVQLDGARGREAVMWERHSIEAVRRTVREERCRQRRQWIHQIKEMNAKFPEPVRPLAEER
KKKREQATANEDAAERALAADIKMIEEYLPRLISLEDIPVNPEETGIIRRQFDEVFSQEE
QTYLASAEEERARKERLGRGLEVYRQRMLDDYVAKKKWKTA*
>TCRU_7134 hypothetical protein
MWIRDIEKVLIGLSTASFVNYSGEAQLAKTRQEAVSDNGTHRHDPTQNITLFSLGTNNHR
AFALLLRGGKSLEVVCEAGSDCEAWLVALKRLLHLRTPAERLLEERRGT*
>TCRU_7135 retrotransposon hot spot protein, RHS3, putative
MDMKLNDFLMMELEGRGILRANRNVLLRVFISDPTSHIRDAGVLGEIQTTGAYLRMEGTV
REEMGLEEVARSLCENGVFSLEEWRDYEGKDTVTPLARRKLNRVLTQLLREERREAEERA
VRGHVGFTLTTTIRDVLFRGRVRVMDMKLNDFLMMELEGRGILRANRNVLLRVFISDPTS
HIRDAGVLGEIQTTDAYLRMEGTVREEMGLEEVARSLCENGVFSLEEWRDYEGKDTVTPL
ARRKLNRVLTQLLREESREAEERAVRGHVGFTLTTTIRDVLFRGRVRVMDMKLNDFLMME
LEGRGILRANRNVLLRVFISDPTSYIRDAGVLGEIQTTDAYAEMEMAVREEMGLEEVARR
LSENGVNSLAAWSLAAEEVKACVRDDTKISLNAALEEVRNPTTSSAPIYLEGEYESVYNA
RWHHVVEVPDGEGMRLEVKEGKPEQQWTYKAAGRTFEKDDGAQQSGAERLRLMVLTSDKK
WPYSWKWKEKESIHDCYVNCEVERVWQIVKKDLSEFLSPDDEPGFVPGRRVLIGTPGIGK
SMNAGSYLLYQLLHYDAEQLPMVAYFIADRTFLFDKTTQVASVYKGDDSIFRIVSSFSGR
GVKGYVIYDVAMKGKQPQIALPCEGWGMILLTSPNVKNFEWWASRRYAARIVINCPEESD
VRAICAWMKHNRSPQEQAKYWKEVKEQMEKVGPILRFILNKTAYNDRFSEGESAVNKITA
SKAEHYANIGELNAFNDSEVSHKLVKVVRVRRDNIEWPLNVPISHHFESKIFSKLESEMR
QFDFIFLVLSIWDYVIPYLLEKCAVSAFLNEDFLRAIKT*
>TCRU_7136 retrotransposon hot spot protein, RHS3, putative
MVGLQITTASEHHTLTSTVKLFNECLAAYFNDWEELSRDMSWEIVYVQHKDNKPLTDWQR
CGPANPNNETDAEKEIAEFWKKKVYQYRVGVSADDIKQRVSSVENDQQGTGTN*
>TCRU_7137 hypothetical protein
MTDLVQVRAEDLELMARNCKSLVSMKISECELANLLGFFRAAVALEEFGGGSFNDQPEPV
AENGYNEQLEKYAAVVSPPRLCQLGLTYLGKYEMPILFPIASRLTKLDLLYALLDTAAHC
FLLQRCPNLVILEVNSHTLRSFPNPLFFMPIAIYT*
>TCRU_7138 hypothetical protein, conserved
MAAPSLNGFECDNTNGDKNSDEDGDGLHRGADYLRVLVHEFQEGLNVNITIPGLAEPLAF
ALLPAVISAPCVGADPFTVEFTQQLSSVCAAGPALALSHVSQRCLACDLMCVVQAAASSF
LFVPNKKHIALWWVFICVAVDACDDSQRVCLLFGGHEGDFGVCRQHRESLR*
>TCRU_7139 hypothetical protein, conserved
MQLRPQQRRRVQHKRRRHRVRQPAQLGVAHRSRRHNRRVTDRHVRVCRQVVHKHKRAVAP
GQPAHAHLQAPVSRRLAAVAPHVDLRTAVAHAVPQFDAQRAGKHRRHVEHHSHAVRDGHA
VHQHCVHGAAHRDGSVHRTAPQSQYHRMHSRHPHSSSNQRQHKKKRHTHSRNGPVPLAVT
AVRTRTHRTPHPPTQTRTNRAAVVRRSRPVNHNSCPTNPFLQMANPMTQFRQVVNPLLLI
LLQLIPNTLKR*

>TCRU_7140 hypothetical protein, conserved
MAGGVSAEKDLYLGSIYHSLEHLPQWYQVFALSGLFFLFPLREITLVGWLAVSLHRSFGT
EIVWSEEYQRILEQMSFNERICLTLYGVALSVLAFFSYRLFARGALHAGLHESGLSGGRK
WWPAAVVCLLLGCEAMAALKEIVARILSDPTSLGCLALEVFQGVENKTFDPFLMKTNPHL
IIQLEILRAMLLSFLERVVPAVVIGCCYRLLRDVPRRAQAALRWYIVTIMISRCLVEIYL
MYWHNEWGQLSSWILFLSTLVLLGMVNYAFGPSKRGGWTATTSVVSSINQTIRGTVKCAA
ILFVIFLCALALVVSVHVVELLLIWLIFFLMTVWIPAIIDSCSTEYSLCIVTAISFIAHQ
MEYLTDVGSFRLWGILFLWWLNLCLLYNFATNACRSRYGGIVAVSISIMGIWRMTDHDGK
TGDIVSFLENSAAKLRDVVEGFSAVNETELIVDNAGLAVYNSLLYSGFTACVILVLCIGL
IAFCEAQEARSRLLGKNIVIVTPGVLFRKLVKTLILGVCFFIFMLTGMLLYRFLPQLAMF
TPDLFALGTAVGLACTILGGLMDMQEFLYLSFMRVIGFMDPPVANEDDRDAERNPFFSVF
NSASSKR*
>TCRU_7141 ATP-dependent DEAH-box RNA helicase, putative
MWSQRLLSAFRLSNRVKICASSAFVASSRWIHAQEINPGEISLIEAVEESHASVGNASHG
SGVFDGSHELPQHFFDAKHVDTFSRARVVNFIKRFSQGAVTGSNDVFQVQEVKGNDGSQL
YHCRVRLPFQSQTGEVWAHGMACNGKDAEMLAAMHAEYIIDEFGYHIYTLPSMQRKHAEA
ARKAGRWAPMPDDGDRAQTHIRIPLPLRRIVDRDETEGGKWLLIELRPNYYISPAHTLLS
PCLFDTTAVYRIKSFLAEHNLSFTQLCTSEAEEPLEKGGPTYYIATVLLPGEVTTFNEIK
AQGKALSREAAVTLACMHAELLLDAHSIALFPSDSVKQKQHALTAWSYGRPAPIPGEDQK
DPSHVACPLPLKELAVRREDRVSYMSYEEDLVRRHRALTEQTCEFIETPVLDDAAVDLLK
GFLRREKTPRTDPFFIEEVQGFFKATVVLPLSDVFGIRGGVGIAMNAADAATLAAMHAID
VINMLGVHIIAESTARNDWIATRRSRGMSTPAEAQDPSLTSPPGRRRIVRQTIFSELNND
KTDDNINQNAEPADPALPQASKRRVPKRAKAINSSEEGEKTALNKIPEMDYIKMRENIPK
ELWELEPDSPDGYIMVSPTDPETRTQYEHALYSPREIDPCAKVRVKNYLAAMGRRAEEVF
FIQRIEAEDNCGQSICRCALNLPVPRRYGDRIALGEAVDPKDAENLAAMHAELILDTLGI
PLYTDGILQRRHAELCMKNGRYAPVDESSNISPSTKSPPPLRREVVGSIHWENKTKRRTP
ISVSKSENTEKTPLLPEKEEAEPVTAPKEARNYTFIVEKDVDLVSRPRVQYYLRRQGKPK
LEPEFRMELRGLGNVLHIAEFTVPVPESFGQRIAHGSALTKRDAELLCWMHAERIIDALG
LCLFDNLPGLQRKHAERVKRLGRWAPLVGEDVSKPPDTPSPIPLTLGTAPEKPPYPIPPS
NVAHEWDKYIGECRRFIEVNTMREENIFYELEKVPRTGDAVYDAALEEVESAPIDVDAKQ
FLQRYCTAANVDYPVFWRSRTVGPVSRRVCLTTIEVPGHEHVTASGVAVNKDASQRRAAM
HALALLRRIEPDYYETEKNVKSDTVERVAFIDPFAMLEDEPPAVKRPAKPGKKRTGSWDP
VAKDFSDEGKVRIIELFTLCFGLHPPIVRHMNRREGTLIHHTTTVEVTDEDGKLWVGEGM
DAGPRFNEATAYENLFSKLSRGVSGFQALMDLIRTHPHLDPEHIANVSLTEAQKERIHRV
IDDLPDMEGEEVAKPQEWGATKVEPVGLLSRVAMDVSEREQVSQHLREKLTEKLTNEEYL
SKYASKRHGLSIYGKREEILNALEKSQIVIVCGTTGCGKTTQVPQYILDHMTEKGEGGNC
SIVITQPRRLSAVSIAQRVAAERLEGIGETCGYSIRLDSQPGRNINFCTSGILLRILHAT
PLLNGINYLIIDEIHERDINSDFLLILLRQLLQTRKDLHVILMSATFQAEQFGNYFDGAP
IITVEGYVHPVQELYVEDLVPIAAQQKVLPPLLKEVAATLEREREFSASGDSLDNAAASA
NSLTTTIPATAKYGFMEATAEIDYVTIQFAIDHAVRTLDLTNSSVLVFLPGWDEINKACE
ILERNTKFYIICLHSSVGSEEQMRCFLPPPEGKVKLILSTNIAESGVTIDDVAVVIDVGR
AKEKSYIMQKGTTAVGRNEMGSMSQLVTVYASRANCVQRRGRVGRTRPGICIRLYSKKHF
QTVHDFQTPEMLRTPLDALCLQILALDLGEPANFLQQAIEPPSTEHIEAAMRRLEELGAT
TSTRQLTPLGLRLARLPVAPKVGKMVIMGAILRCLDTALTIAAVTDTDVFNSARDQREAV
RLHKEDLSLNTQSDVIASVNAFNFWVVAHYEKPPAEVVYDLHERMLSVPQLLTVSRYKRQ
FFDIVMNSGFLGDGIAFERERDHTRADIFVDRSEWSTDALNVGLVKCVVASGLFPNVVMN
RGKRLMRNKLANRLSPSSSSVVHRTSQEDITQPFFVYDELVKSSESDRLQVRGLTNVPLW
TILLMGTSSMPVVYRDDLNLAVVDEWIMFRASFGTLELIRKFKRAMNTCLGRKFLDPSDE
KNNEKLEELRSIIKELVSTPFKPNDLSDKVWEEKGTIIEPRKAPKQEESPPETGRSLSSS
SSENKEVPIETTRVEVEATV*
>TCRU_7142 Endonuclease-reverse transcriptase, putative
MRPAFLLLYLPPSSAKSVSAEEFDGPFCADGPNLTGAGANAHTEAWDCSIPSDSRGDTVA
QRCVQNALQVVHTGGRTRYIERRGGSALDTALSKDHAATHWAAKLSPGSDHYIVLLGALI
GVDDAPVAVPRPDRTLLKWKEADWNKHREVTNQLRRIPRELTSTDSTGRHVTSEIQNAVT

ATVPARKRQPSPFWTSGLAELDRTTVAALHADRCERLRIRRGELLRKASKSRWHTVP*
>TCRU_7143 hypothetical protein, conserved
MDSEPFALDGEGSRARQSEYVDMTLVHVGMKLRDMGIAFEDMELATVPTQFAEQLLSYIE
AFEERESAIRATTTEHRAQLEQEQKRLESLQEATEKARGEVAILSERISSALSACRREEK
LEAQHRRERQRDVQDIVRQIEKKELELRRETMERDRLSKMLKKVKK*
>TCRU_7144 hypothetical protein, conserved
MAQVTLGCGQQSISRLKYAPLSCLVTLKAFEKGLLNVLTLAVGFMEGYDSEDLTPLLGLT
NNDAPRTLAFVPYRAGTEKEGNASYLLSVKPPDIQSSKKPTSSTFSHVTRVSDTKIQFPI
SCMDSSACFYNIGNFSNDFFLKEELAYGVLNSTNSYHVAIKVITLLLASGVHVPRKIILD
LCDRLAVEDPEAAWTIASLLEAELSLSEYMFSLGINLPGRRSPSFSEVKNFIGNVSLDNK
TEQSVHQKEFKNSRLSRLQSVRLKRG*
>TCRU_7145 syntaxin binding protein 1, putative
MEHGVTLLEDPMTPRQPIMSSPAPYFFAVEDASVSRVAEDWMATVPHRDAHIFSLGYTPH
RSPQQLEWARIAPRAMRLKDIMLDFAAPEVLVFHPNVPNEFFQLLSPLSPLSPPN*
>TCRU_7146 BNR repeat-like domain containing protein, putative
MSRHLFTSAVLLLLVVMMCCATCGATPARENDGNSDLRSVEGLQWVDLFVPQTTPVLPEG
GGTPGTKRDSFASPSLVSAGGVIAAFARGKINAQYAVDVLMKHYSSDVLAEYIDSSWDWS
TLVEKVSEGTWKAHTVLGTTDGANDRVGDVLNPTTTTKGNKVFLLAVSYDMLNESGGSWK
RDSLDLKLVVGDVTKPSASEQSGWITWGTPTSLGQTTLKTPKAGLKNFASGGSGVVLEDG
TIVFPVSAFNTENDGFSMIIYSTDNGST*
>TCRU_homolog pre-rrna-processing protein ts.1
MPRNKAHKQRFSSKRAFAGNAKGRFFNSNATGVKTFLPMETKERIRKSVILQRKRSASAL
KTNQLGSLGGAPRVIGVIPANESGNTDLVVQGICRAMGGVKPDKCFPFSMTSKEKKANFT
FIWENQYNDQDCIDIAKVADFLVFTLDASQSVQQTIREMQDAPPIEYDHDEGCSVASGKT
WFGDIGLCITDFTRSMITALNAQGVPSIVVVLQNLETFAEKQRQQVLRVHQRYFTSVLPD
TTKTFAIVEDNEYDSLLRHLQVTKLRSLLWREQHPYLVVEQGSYLSDTQKLIIGGYLRGM
SISSKQLIHLTNYGTYQIEGISFNDPTSGDPHYADYSQVDQREPLEHVQANATLEDAEGP
TEEDLAYHHSLDTKKIRVPEGVSDYQAAWYDLEENEILEETPMPINLMGEEEDASVGAEF
LSHYTSKTDVDFLKVRHIIRLERVTDEEREAEIERIREESEGDAWNPDMVNTPLNLPARE
RFAKYRGLKSFPTGKWDITENLPPHYAYIYKLQGITRIRKAALTKCAEGPVVINQFVYIT
IVGVPKSVWENAMTSGYIIASGQLEHEQKWSVLHFQVQRNLEWEEPIKSKTPMLAHIGFR
KFYVSPLFSDITASDRTKFARFFHPSESFCMASFFGPISYQPCPILLFEVPSLEEQKSGD
SLRLACFGGALPPNPDLLILKRAVLTGRVATIHKKQIVVKYMFFNDNDVRWFQPVDLHTR
MGRRGKITKAVGTHGLFKASLNDQVMQHDLVCMDLYKRVFPKWTTLPFNIADLKNHSNEE
VQY*
>TCRU_7148 hypothetical protein, conserved
MLRLSVGFLMRHIGQDVPKRHTHFVLESRLMYEKSFRDSWLHSVCRAVSQIDEPLSKTIS
GTRQKMLQRKVTCFQYNQYGLFKVPYYRLANVDRYHAVQGVPGTREWVPYANVSYWTMNK
MVRSGNLLVHRVHYTGWGTDPHLKKGGWEHRWNKVMQRNALQYSRI*
>TCRU_7149 hypothetical protein, conserved
MIRWAVDLAGVDADADLQRDDRMKLYVGPSSGRKENWKPTFTTFTDPSSLGPVGTVVTLT
MRDLIQLQQERLEQALAVNPFGQAGISTFQPKNDTEFLKGLEVRVFSTFTNAQGKRTVCT
VQPRRTPFRGVDVVHAFLQQTVVSDDRLSARFSANPRLYKLYIADEFTGEEEMVIQLDGA
AQNFTCFAVQPLPAAKLFLFPQRTQLLPSVAEDINLAVEISPLDPQAKTVKSQVRVPADM
LAESLEQAIVNLLPGRGLVPGSLRIKYGPVELNINEYYNFGSGCGHMDVPIAERTILSLY
RFGVTEVLLQGRIPDENTDVSLLVEDIVVNIDAEEAQAFQQFDVIRINRYGARQQRILCV
DGERLYTVRPNVDGSGAAQVNEEKLIKDIEEVVTSPTKSKYLEIRYSRASNHENDHIECT
TAYNRALLDEKLRVLQRELRKKRDEERQLKGNDTVFSRLFHRFRLGFHKN*
>TCRU_7150 hypothetical protein, conserved
MDLVERKVEGLLCGALLAPLGWTARVHHDVLEDSSLNVAHFERLDISRDFFCVAEYFAPL
GAVSEELFLEQQLQQRLFAFFAHDAKPVRRPAFVVCKLEKPDGNTSHTSLAALLDQYTLL
TCVALWVADMEFGDMEKIIRNISNDLRERYMHRLDGSVPDASAHNCGVGVVYTMRGRSVV
HITRQAMGAVKWNPTLCERVDGMLRNLKEELGLVSENLSLAVRGVNSVVLVVLLPMSPGV
SLMKHHAIERVWAQHVKRSGWHSELLQRVNPSILELAAFSSFCGVSPRSTFYFLSKEKGD

VEGVVAWIAEPRVGSDSCVVLLAPASNERLDFNNTNQNTHPCQAQCEWLQRTFRLCIASA
ASWTPLGVGKEPGFLFRDGSLVVRIPSMSMTYKNVTSVATAAISAVSLGSITVTAEDVSL
TFRRQVTFTLLNELRCSEDYIDYVITEYLYDAPLEKRTAIFRKGRRQQKIPPAIKRNFGK
GEEHSVWIRLKEDGAVYCVARECGVGRLLLTQACVFGHALDDAAAERWEKWISGIDVMAV
VQ*
>TCRU_7151 Protein of unknown function (DUF1674), putative
MLRRGLALWIGVESDIFMSVVNDKKYLEHRLALLGKEDPVLKPKPLSDEEIQRFTTSVGS
AESLFNKASGAKPSDVVDETTGTPIGSTQLSPTRYGDWESNGRCHDF*
>TCRU_7152 hypothetical protein, conserved
MVSNRRPQAVGGNSTPRAVSTRNKDSSSTSPAKQQPLVQESPQRQIPPPPPPQPVVGISR
VAQQVQQIPPRHYEPIRTDQPLPNVVLFGGLFGLTPQSASWALLGRASCFNSGSAASNAP
VLAAPSCGLSFVEAAGEADDKVLRFMPTSAPGYNFFSGIDGLPADQQGMKVIYDD*
>TCRU_7153 ATP-dependent DEAD/H RNA helicase, putative
MSYGEAYSTGDRMGALGANLHDVNWNEVQVVASQWNYYKPQQQRSDAEVAQWLRENRITI
YGDRVPQPMLLFSDLVAPDSIHQSFIDLGYKEPTPIQSIAWPILLNSRDLVGVAKTGSGK
TMAFMVPAALHIMAQPPVRPGDGPIALVLAPTRELAVQIEEETRKVLRRIPTIATTCLYG
GAPKGPQIRTLRAGVHVAIATPGRLIDLLEMRATNLLRVTYLVLDEADRMLDMGFEIQIR
KICSQIRSDRQTLMFSATWPQEIRNLAASFQRDFIRVHVGSEDLVANNDVCQHVIVVEEY
DKQRRLEEILQKLGRQRVLIFVKTKRTADSLHGSLRRILGGAVMAIHGDKEQSQRDYVLD
RFRRDDRSVLVATDVAARGLDIKNLDVVINFDMPTNIEDYVHRIGM*
>TCRU_7154 hypothetical protein
MMGRGGGGGGYRGGGGGGGYRRGGSGGYRMGGGGGGYRVGYDARLYAPYGSAAAAPVPS
APLLHAGGYPAAPRLPAGVGGGGGGMYGVPPPPPPPPPRVPMSMPSAAPQWSQGPTSLAG
EKRARLSPERRRSDSREKYRRHSPSDSRQRYRDSDDNYHRRHDSHERR*
>TCRU_7155 NUDIX family hydrolase, putative
MALPAADVKFLLSIAQRMGERHLHVYVPGARRSAIAIVLRFGDAEQQRAAHRLLACRDAG
LSSLQLLQPLTSAANTAVPSSLCILFVRRADLAADRWSGNVTFPGGRRDAGDASDLRAVQ
REVGQMLGIPLHSKEFILLGRLRDYPIRSRHVQAVRVVQSRFVFLHTGDMTPTVRFARHE
VDAVQWVPINALTVEHVDEGSLCHPIGCFVHASNADARLLLAEAFSHTHLAFPSVQLPGQ
WRVWGLALRSASELLSLDDRASIDWPLVSSNNLWLQHLIIDAFHGYYEALYTFYRVRARV
RFTDTAVKTKYMVLPPTADSILWGVPERVVLRHFFFFCFDVALLFFAIYFVAAMIFTASI
VFRTALGWIDVDGGKERSTAYYAENAHSLVDSMQMMHQRRGGRVNDAAAIRRNTTLPSME
STGPSPPSPHPTTVPLEDGDLMTETATADGETEHRVLGSDIGSSDERGKSDGGEPLPSSL
LNTDDRDAFRHTVEAVEERKSCR*
>TCRU_7156 Protein of unknown function (DUF3735), putative
MAVLEAFFALLLFILLCYLGILFGRLVFVYTIERRTTHFCFVVIFALSTLIFSLVLLDAS
KLGVLIFSVSFSTRALRLALVADLAVISVLCPFCIACLLLHKLHFRRSYSLLMCCGLFVF
ICRDRVLLVEWIRRLSRFSLPWDSAMTVWNAVTTGTALMGVLAVGVLSGYAAVTTPAAFL
RPLVVKDSGERARAALGVLAKRQRHLLSLWVKKQCQIAETWRGGAPLTSSADSGGRVWSW
MAKSVRGRTLVEKGDDIVRLRAENDGIQAVSMAVFLQMSEMDSLVRLAESGATWRGWVNA
LIGVVLLLHAFLKLLFTTINLRWFIFPVSSAPPLSEDTATRVVRLFETYGLATPTGGESD
QRIVWVSVFLNAWMIVNSVRGLLLTVFRLVTTYTTFLSVDTTVLGITVGMGAYFVGQLLL
LRLSPTVESESVLSTVLEEQLPRSDMYCHLNDLVFVMTSIVTLVAQRCMVPLQAATLHSI
AE*
>TCRU_7157 hypothetical protein, conserved
MSFSVSETHEVPGRRETVVGMRREWNFSLTFVHQAARVVMQLSPQWESTFIDPRDFEQLN
RLDRDVKHCPMMPALRYTDLSAVMKPKNELWTEIPKRVSIMYSHIPPDMTLAAYCIRSVQ
HVLSDPHVVSVDGSTDLLHLRVGGKLRCPHRLGGRRSFQFRYHVSVKSKLIKDMVYAIGT
IINQRGYLCTVQCSEEEELEGYLQKNFLPQFTNPDKFAVDQDVEYEEMTSTILKEQQELF
GELHYFDADAAVAFSIPMHPMRIRPDFSPTQTVGVGSVACMTLELYVHQKLIDDLAEADI
MGMPKYKVSPVILFLDVEDVARMGYPRIMSTEQYSHLKTKRLLEIFADAKLVGTPVTNQM
GIRAGRSRTVTLTYEPLNTVVKVMTVSTIVGSHGVSAVFLTKLGGGLFDAHLYLYQQLLK
GIKFCERSAAKIHLSRSRTVSVRLLEQNIPRVYADAPADERQAMERHLKFLRESSDGRVE
GGIVIVVPPEEGGLEKRDEQKSRSTSSYRRQLQSQPSNVNDSTTGRHSAGSNNSQMLIFR

GSGSCVDRGPSEVLCEEYEETSVDEEGASLSNIELSFHSNSVISASSIAHLGDAVPDDSV
VDADAEGTAIRRGSAAASPTDSGECGGELLATSSPLMQAPAYNSAELSALMVAEAAEREA
LCPSSATTPERPNLPHSSTVSGFVDGTEGGLAETPHATQQQQQEERDDEQRHQQQLREVL
KDNEADVYFGPSLHDIYVRSCDMQRCKPNSYLLKKLPTDPRFTNGVLELDLSSNYLGRGG
FVALLNLMEHLPQLRTVYFNDMSLDNVDAENLCEALIGNKSLRAVYLRNNSKITLPSTRF
FTRLLRANTNIVVLDLKGTRLGHNVIKKLEEDAKKNAVKRGVEQA*
>TCRU_7158 paraflagellar rod component, putative
MYPERRPYATAVRHSGYLSKPLLPPVEALRILNSAVGMDIPRSLRRECASTAADDSARKA
YLRPRTAGGPLSSLGAQRRGSPTLESAKPFAFREKQYHNSQQVALNAQLSNAVEELFKLW
HRKVRDLLNYLDAYPPQCATSSTMMEDAMEHYFQGYRFTQAPPVTMEQLAQDFKLGTTPD
MLNEIQKSPALNTERIRRSLDSLLNARHFLAPLEQYVQELEDLASLALKDESCKVVDGVL
RGAVWLSKAAVALHEKFHYDPFEYALKELRKSDLPIERLERRVLEKKEQKERAINEELPG
EALNFLTSQVDLSNDLLLMNKARLDLVQLLSNDVREMKPLIDAVIKDARRSVELLKGRIE
RDLPLVKKDLESLSHDTQNTEEHIKYLQQVDSDANKNAHQEFCKIEDDEKDLWALLLETM
QKLVNISEEKDEFVKLQMRLREQRSRDMALALELLKAQNQYHECLRSCEESLWRWSSVAE
VYETYVEAYVPKLLKKLNDAEEAEQLLYNHEAQEYVRRYEMFEYAVEEGRATRQVHADRL
RALQRSKRLDLERALATLDPHAEKYNKEVEDAQSQVEETEAYISLVGDLERERRSEVEPI
LQHVLSHNRTMLTQREALSSIEQTLRLRDKSSEKNDASPADEMDVEEAGDVVGSTVTTAA
AAALGSDGEPLVTDTDFVGTSSFAFARPPTGTVGMHTGTDSMMLATVAHPHVQARTIGIN
HEEAFLERYRRFTDDEQRAVEASEAKIRQFRQDMDKLGLKYNNTDYVRMKFGSTERNYIN
SRGGGAGEVNAQ*
>TCRU_7159 mitotic cyclin
MNLSSNGNNSLRTIDINLEFFSNGKGFYLPRPQQNLGGKTEQQMARQVASGRSDTSTQLN
YDEVRRGLQNALSRVELLCGNSAEGRRQLLQHELLRLFLSASEETRERLEFVLSDAPLSY
RVLEVLYLRRRELCTGFEYALSDFKCWLSLAMLLDEPDFIQFMMQYAQELGPCSRQRLED
VMFVHESSSKSLCHAVLGIRAPGEGAVPFDFRYYNFMLDDLIAMGDEPPHASLISSVQRE
VTLSMRELHAEWLLQVTMAVNLKLETFFLAVAIVDRYLAKVAVKRERLHLVGCAALLLAS
KQEEIFPASLHALVRYGADHFTVEMLVATECQLFAQVGFDVVLPTLSAVGMGILLQQDTA
PSEAQRSCLLYVLATLAIRTHYRQYKLSSLAAAAVYMSRVCFDIPTGRPCEEVLSHLPLI
RAALSRNPAVGSGGVHDIFSRGVFHEVSKLKLSELIGTEDCEGN*
>TCRU_7160 Vps52 / Sac2 family, putative
MATKFTTEELEDLAHVDLDEALVEANICNNTFDAELSRRVSQELCDDFVQTFLGDDAVPS
LHLQMQDCDESLAGIEHILERFIVNLESIQHDIGDVRERLKRIGVSLTHARKAEQAVWNV
ASRLIVPPDVVRIIIHSNDEELGPQFKLSMQQLLMFLRYRKEGSCQIESGAKTLIFFAAC
RIYAEQVEILDRLTVHACVKTKRFLSKKLTYLSVRNTNVYVQQEHVLKPHAFYVHFLRAA
VPLLRHPHQNGEMDPESPVLLPYRIAKALYDELRGEYTEIMSQLYLDRFRHYVMSLNAME
KSTQTVNAGVSPVAYVLPLLIESQGVTPSTVFELGERAAILNEVLSPPLVPLLERAKRRL
HFYEETFRSLNVLLCDAVTHEFLFTFAFFSGDMSIFVDVFKPTIQFIVDYVSEVMLGQTG
GSVTRAMRDQFPHTSVNPNCLYDCYGLLLLIRLCHDFRSLMKDVRRLSCLEGFYDSLLLL
LWPAFQRNYERQMLSLRSADVMSLSRVLLRRQGSTECEWVRCIHPLSQQYAAFALSLVTI
SSGCGFDEKTDESKLSLRSNSVDEVNGSAESMNNADEINFSELQRIAWRAIEAERVSDAA
DSASRFAVLTGNLNFMRVEVLRLLRDVGQQLAERGATHPETREMYVLAFLLNNIRCIMFR
WSDFLLSSGSSSLEEDYRALEEVERTQRSGYVDALLRMYFPFLYHVVQQEETAERDPAKF
LESADAFAHNWKRELDDVCGAVRSMVADSGHEGELLAEVCMEVLLRNTRLHGCVSRVFAA
ASSSSLDADGASRPMRSFIVTNQQMLQHMRTLATIPEDQEEVMPSV*
>TCRU_7161 hypothetical protein, conserved
MLRCCSSLFFAAVSTDAIFRRAFGSQSILIDLIPVKKPMIEGSLSWFVEENIEIVLVSGV
RGTCSDAVTENVKRTAVHLLQQCGDGDAVKGCHTVRRCIEGARATRNLLHRLDLQVRLRI
WGPMVMMMMMEESSSSSLPTKAAVAAKVRSEGERKGELHCSVYEADAWDPYRNERHIMDV
SKSPSVQSLCDLLREALRILRRDAEVKGQQFALASFQEAKLLFTTAMPVASIYSGICFPQ
GTIWGETGGAFSKDPVLRNLLCPTTYAVDMEFLRYEREDASAFGVIAGKWAIHDDAGNTE
RCDVPLMTLRDRGGLMHQGRCHELVCQENEILDDSAINSLEDAGSFVRTKNLRDPEVVST
LLCSICSQPLLQILLFHVSCDILCGQLAPTKAEDFVASCGRVGIDAWLSEWGHPVTVPMA
PRCLKYPNPFLFLQECLPLEFGTRAMMLASVGSLHFGYHLAVTAGGRVSTIVGGFSSAAT

ALSTLFPWHVATPQRSSAVAEPTDHGQKNTQNSSNSQAKKEEKGPSKSRKTSNEHAEATP
SFVVEVIDMEATLRAMGVASGKFSQDVVEYSDASGRTLFRFEQMDSLQGIERFVKRLRRS
QSPCFASIFVHNNKRASALLLWRAFAGISAHKAPHYIKRIRIPIPLVSDEFFSIRFSGLL
EMEQKDYALLSILERYSKDPKQWPLKRLSPCFFNLWRLTRGIIEAILRHDPLFCYTIKSA
SVEVQNNEFVLSFYSGDEKTHETHIKEKCFLQEVRRCFAQYAARWDIEVPSIETMAFAFM
EIKKSLSISFRAFVTAFLQNSVMLLQKESKASLKLQIVDGVRINLCSATFAQNEPVKEML
SKTFLAEQFPEALPLVHLLQRAHTFLLLITGEGETFFRCQDTTERLGFRWELQKISGGVE
NVTVLDAAVGSSRFEALKALLEKITGEGEGESFRAALGKGKAVPTSLAFARTIEDYQEVL
AQKLGMKKIIHEYDVKRKLLIVRGVHDKELATGTKESIIRVISLGKLCSVGDIIHRYYRR
ELHLADPPLLEDHEQLRTASLEWIYKLCQTHFALPLPPLEKSIVIQPENKGWRVVLRLPA
RLFALEISNYVEYAFWGRGKSEGKRGVLCVFYKAIYGEAREEVERVLSQAHCGEPFSRDG
FSTFTKGSSTAENRNNTVIPQQLQKSNNGSRGIIAADGKSSSVKNGSGTAGIGAVSNLGA
NCMYAELMGLISSQFRPHVGYDGVVECHLSHITGFTGRYVCSPVQEGKLVGLFGVPLRAT
MWLPFQILAVLLSCARRLVPDEKLEALILRNAASWPSLFLDTVQSERLFCTTFLRRYLGL
CIFEENDLDERAAVPGTLYLVERTKQIRVDCFEASLSLLQTPLPPSLTTFSKIIASHKAA
TISRAESTMWGIVLQQLPRLDAVQAEDFDKAVLQAVMRSANEIAC*
>TCRU_7162 hypothetical protein, conserved
MLRDVSLLLFSLCVDGELLFAEGYTQLTGVMAMMTGRVLLVCALCVLWCGAGGRCDEKDT
AVPAGDGGSPLRSAELETSRQESQDVQNGVSDVNVKVPPAPFPSLEEEVHDDDEGDDDDD
GIDDNEEEGLEKGKKEKNKAPTQAQGDKNNEGPSLLPSPPIPSGGPTADQENFQKVNKVT
KENTPSGAKMESKATEQPSGDATQAQHSHDTDTEDSTKNAATGSPVEPKTSSTSTSDSGH
HVQNKADEDDTQSHEGQHDSLETGNTNVVPTLSERAPQTAETATQTNHTKTIGDSDGSTA
ASHTTSPLLLLLVVACAAAAAVVAA*
>TCRU_7163 profilin
MSWQAYIDDSLIGSGHMHSAAIVGLSDGSYWGYGGTYIPQPDEVAHILKCLGNFSLVQSS
GVTIYGVKFFGLQSGEEGEMKYIFFKKGAAGGCIYTSKQTAIIAVYGNPGTSSSLQQDLE
KKEGAEIAVNPADCNSTVKRIAEYLISLDY*
>TCRU_7164 Enriched in surface-labeled proteome protein 1
MGAKLNDDDKTVLLGLSYDSGKKRAVLCSGQTTTEHSSNWEPQTQYQVAIVLRNGSQGSM
YVGGKHVGDASCKLGEAESKGSKGISHFYIGGDEESVEGREGFSVTVSNVLLYNRPLISE
EIAGLAKKKITILKPEDPKTSMDTQSSATSGSPVQGAVSKSNSARQLPSEQEPLTANIGG
GSGGASGAASVTTPSADANTPASNGEGKVEPAVKKEMSVSSGEDEETAEGTDGQKEEVQP
LVKEVNATALNSSLGHLSQGNNSDGGTVRGSGLLPSLLLLLGLWVFAAL*
>TCRU_7165 hypothetical protein, conserved
MTFLDESGAEEAVIAPIRAAEAAISTRAAVVKEETEKKEQSKTSKALVAEVGFSLTVLRE
RMAKKKEELRRQREEATVTVEQMPRGDASTMTASVALSSLPGETSRSSVAAADEPPTRKC
KTEANTSLPLPSLQEVDLYADLEGPPCGWRTQLQPISM*
>TCRU_7166 hypothetical protein
MAERRSPTLLCWDACLQYELSQAEVWAELRTGASTMSNWLGRAAMPSITDETAMVALRHV
ACDYLAATREELAETLYNFKREITKMNTDVGAERLSLQEFMLLLGPLTLVANAESVLQTF
WNEMLQRDKLCARCVSEAYDACAALQLQEQTAREELLSSCRRWQHTRQLQDRLRQQREHL
STLHSLDEEGVADRVKISSIRRAVRVEEERQQQQFAEKALEMDRIACLTDTLETLHNQLR
VAEEYEALTVDSLLREQSDRVADVALEASRKMRWDSRLSHMERQVGILGRFAVGLSLVRL
GRHEHDAILRRMEGTSTCSATTTTTAMGVAASPAAGDLTWLVGDDADATSSYYATTAAAA
TMPGVSDTGNPSSLPVLLQQCLFDPSYYKAKSDVSSERGRQYPSADDYSEVEDILRQVFG
SLTQLIYVAIPFLQEFAATIDTVVLFPSFELFLNTCEMNVLGSSKLAFLRHCSHRLDADI
VNYLKLLVRAEGSWVVEHGMRFEDFVAFLVDQAALEYVRHAYFLTTKKLLTKIVLDIVLP
RWVRRLKKGKTPPFMSLSSNWSKNEDRIDNMNRVLLEKENIDDLCLLLDTALAWLGIARR
SLKQFAQAYRKHVLEYAFAMKPETKATGITTTQALMALLFPKKGESLQLRCHPTRWDALQ
RTQSFCFAQMNALVGEDGSLDSVTAWLTLGLAGINREELMRRIVEAIESILRANLKEDIN
VHVPNDQFSVSMSYNTPVSWILTLAVCVHLSFNSNLVTCGLDKLFQLLTVST*
>TCRU_7167 hypothetical protein, conserved
MNGGEYVRYRCVPPHHNGRVSSTRSRTTSFSSTTPTDNPYIQSFQQKATVDVCRSPAVVR
RKGLRTAPTVERQKEHREKDLEIHSLRTNNHHHRQHQGTELSGEGGITTLAMEPTVVAEL

KRLLRAERVMRLAAERRTLEEAEQGARAAIAIEANYGSRFLHSIFLENIMSISSTRTDMM
PWGRTGGSQSPFSASSLHGKGALSVPSASATVSDANTYRRLVEENRQLREEVSRYKSIDT
EDRREMNELHRNMQVVIERLTLERDMLHAELTGGKSWHSAAISGTTEHGRIPPTTTVDRS
LWHYAHVVDPTAVNGEEPPEYASRLRVLPLS*
>TCRU_7168 methyltransferase domain containing protein, putative
MAHRLLLPLPPAFSPPDSDVEGYSVFTYDDHDTDAEHPALKAYIDQLSAFLCKTRLIQYH
PEDFFLIFLLHDEKEAAGKAEALKYPDGSAVREEEVAYMRDLCGAFTTLMSDSNTLVVEL
HAMIRDGPPVGSAACLHSFFLETRALQMNRQRRPRNDAASVTLRTPQENMSIATPSFASS
LPQNGQEGDELKKRLRRDRVMKVVLGHGMGRKKQHEVGVVRDTIVDLVACCNATRTGSGM
LPPDPVETVLNVGEGKGYVSRALALCDGLQVVGLDCNPAHKERAMERVEFLLQGRLGVDA
ASGESRGRDMLNLMYEPRGHMATVACRVGPCMDWVDVLRGHVRLSDGASLEGCDIFAGTI
ASEQQKIEEAEAPRTLKGANDGTKIQCRICCHITRRSAVNKIIRHVRRHLQSDDMKNFSG
ILSKETIDGWNRELSVEAFNRKIITTFFTDEVYYKSNAAVEDEASAKWTRFGSEGSCFSD
GMMREKLRDTLNTYDCLVNVQMPRGTRAEVLLPMRQPKQQSILPLSQLGDEIDGTDTPDN
VLYRYVHTSLTVVGYDCAPNRHFVITDDGSQKEAFALLQYLHGSNQVDGKFIDERCVPPA
EDAWSMKIALLLRVIPPATPHMPIVHVPDLRNVVMMGLHPCGDLGSNVCRLFVESASRGL
LLVSCCWHALTSAGFPLSYELQRRGWRTEQLSLLLATQPFDMWSTVSAEGHRESVCVLFY
RSLLKLFWSRLRDRWQNSTATSMAAIRCCPFAEVPHLEPAFLRRIAKIKSTITMEVFYVE
VCREYFLDGTTAARKPPYTWQSHVCSSCREAQTKYLFSDTNIALAAEVGREFFATHFAPF
LGMTVLRMWMCHLVETMLLLDRTLFLSEMLRRDRRCRGSVVSLVPLFDGAVSPRMYGVLA
RRIPN*
>TCRU_7169 Macro domain containing protein, putative
MKESTPPVEGTPEQTTAATTPSTGKDCNRAMEEVGKEGQSAKFVTYSTSEPAKLFGEAGR
RSHFRARVLEATLSPLEKAIFDVPIEDWLTVDRSKFSGWRCAVPHPVTADELKPVDSSHD
ILRHIALYNGPVTDLQLDAIVNAANKTCLGGKGVDGAIHAAAGPLLVRECATFKGCDTGQ
CRLTKGYNLPARYVLHTVGPIGERPEELRSCYRSILSLAHRNRLRSIGFCCVSTGVYGYP
LIPATRIAVDETIEYLKQHFSAFDLCCFACFKLEEYNAYTDCLRAWLGTAPNASTDQ*
>TCRU_7170 carnitine O-acetyltransferase, putative
MYQSDCDHVFTESLIAELSTDESRRTRASVLITDLGWVLDSTVNEIMKKAFRDYKQMIEV
NETAVLRFRHFGGAQIKHVKASPDAFVQIAFQLTYYRLFGRACGTYEAASTRTFLHGRTE
CVRSATRAALDFCRASSDPIFGQSTGSALPTQRELMREAMRQHSENMLLAKKAQGIDRHL
FGLRLQAVKHGIPLPDIFENPVFKRSAHWNMSTSHCGSSSLSLFGFGSVVGDGFGIGYMI
KNDHIDVCITSKYTHPYTSSKVFATILQASLLHMMGIVESESSHQRAEARTLLFTHPTGF
NDFKYDPEEGFVYEAFKE*
>TCRU_7171 hypothetical protein, conserved
MTRRAKRTRPATPQDEHAIPLQQQVNVPVLNLEWIKSRLNPATLERLMQVWGLVGRLTFP
PSSSGKAREGSRRIPTADAHLLRKAGIIEDASSTITGGWIIPFSVVEEKTNGLRRRWIAW
PRDKNRDDPYKANAPLLHISHYLPPAMAEAASCLDLKASFFRVSLPRETRHLFRCRVEDG
TLVELTRHPVGYKAGPEILQIIITSAIAGVTTVVHRLWAAPPSVRIDVWIGNIRIAGSKS
DATLWEAQVLRNADSCHATIGRTANRAPRSTPSWGCSLVTHTGRYP*
>TCRU_7172 hypothetical protein
MDEAFEGEERLVSNDDKNFPQYQTGFFHNVLHSIPLWCVWLNAVILSGGVHIVMLNSRQL
FVAISEDPSSEQLPALYVALTSVGNAISRLGVSFFEAWNASRPLEKRTPITITYCIPSLM
MCLSCIFFLIVPARALIVPMLLGGFANGSYAATLVLTVRTIFSIDVAKHYNSIFVFDLIG
VIVFNRFMFGELMTRNSVRASDGRVHCLGRSKCVRTSFTVLACLCTLAFTASLLMHFVYM
RFVRSRRAQEEAGRNVPLEMAGVTSEEVQ*
>TCRU_7173 hypothetical protein, conserved
MAMMRTGRVLLVCALCVLWRGVCAVEVSKADVSENANVFHVPAEVPQPESADRNTGQQES
LEHVSQERQNAGKPLDPKIEAADDQKRDLKIEKPTADELRGETEEAHKDQIEGGAGREER
EDVLEERKVPPDGRGSEGEARQAGNDLSKVGSHSSATTPSGGERPGTSEPSPPGSSLPGA
STQEPGAAIPASLQVAPAATMKKNEKTVENPRAEPGKEKLSSEDDVSEQTSQRVNDGVEP
SNDLTNEENVSVVLIEQNGESDGNFESTQTRP*
>TCRU_7174 1,2-Dihydroxy-3-keto-5-methylthiopentene dioxygenase, putative

MDAFNPISEAQRLQEEQEILERDRKRQQEKEERERRAAQEKEAEERRKREEMERLIEAEK
RRIKQEEEWRKLGTDIIQNLPPVPPSVVSEGLVQAWYLDDETSKPTLRTASLKKGKKRDT
PPVTLQQLKDLGVIYYDINLNDFSIVRQLVKERLYKHTDEVHISQTCKDESFLERWFQEH
FNEDEQIRIVIDGSCYFDVRSKQDKWIRIYAKAGDLFIFAPGLYHRGTLDEDDYVALYRL
FRDSPRFAPFFRSDARAESQKVRLNYLMSLKKGNVAAEIGFR*
>TCRU_7175 hypothetical protein, conserved
MTTINEEALDRLLHENRRLQSYVRSLIEAIEVRRVLTDNVLFALVRREAAQRQPNRKELL
GADVDLWFKFCCGSQMYAPASLMRPPWYCHAFAPNFRWSHRAKRLMKRQVELLGLDNWEE
GNSTQWQIVADAVNYDSSSTRRVDGFQCFLQYYQEVIASPDPFSSTEDNLIDMHDPVSGR
WGKLVDDILQRVGRRRTVFQVAERYRKLKRELYEYNCLLYNTDWVKIEALLRSNATPEAE
FFLECSCRLNMARKIPWLTEDSIRRTFLWYQATRVSGDALMLRNIYAVLLSNGDYFSSRE
AREIGVRLLGCDPLDLREAIARARWRYAQISEEVAAARLSSSVLEIKERVLAKVLRWHDS
VYASDFFRLSINVFGQRDGALACFRISRDYERRRRKTAPHGRLQLL*
>TCRU_7176 WD domain, G-beta repeat, putative
MGFVTQVEGECMFGSLVKVSESSDHVYSTPFSPDGKYLACVLGDGSLLILDPKTLHVRHR
TQMGKSYDGLPSTGVCWFTQKEDDVYDLVSVSSAGGVFVWRWDGEQIERTAKAHEVDNEI
TCVEVSSDAGDFLTAGSDRILRQYDSTGKLKDILCKGFDDDGYLRATHTNRIFSVRFVTP
TIAVSGGWGSPIQVWDMRSLESRKQILGTQIAADSIEPLPNTTCIIVTSKKPERQIQVFD
CLSGEEMEEVSTRLSSEMGDNVPLVSRYCEKTGLLWTITSKSHKVLVTSFSTGKLLASCE
LPVSLMNIHVSHHYPFQAIVSCANGKIFLATVKV*
>TCRU_7177 Double RNA binding domain protein 7
MDGAPPNEVLEPLEEVYKPSLRVDVTAEPPEENENSTGTTPVTSVTPHVSTNIFVAGLPP
SWDENDLRKKFQEFGEIISTKLVRQRHFAFVMFRRPESAHAANNATHLTHPTPNSSMFLH
VSIAMHDEGVDEIPNDRVFIRGLPQWANKDHLRHCFSRFGSIVDSAVLMNPLGQCKGSGF
VQFSSIDEATEAIKARKTIRIENWDAELEIKYSETAEVRQQRQERNKNRQRHSPKYGQHQ
LQYQLFNSSASVVSPIPAFPVLGMSAPFPFFYPRPALSPAASPHIIYSPMVPSPVVPVYP
SPPVVFKSKLDLFPSSGDLLFTGVSLTESTLLSLLQCYGKVDSKDIFDDAGAAVRMVDRG
LHLIIVQQLNGTIFPDGKVMSVVLYP*
>TCRU_7178 phosphatidylinositol 3-kinase tor, putative
MSTSSGRDGLASTIRRIANDPEKRAVMVEDEIKRIKELQRKNLQEYENTISSLLVCLESF
DVVQSVAPEIKCALTVLDILLGLGLTTIQMSQCNSYARLCLCALNDTSLAPAAAQTFAKT
LVDGMASDFARGEIDESLSWIELSDVTMRARRMCGLLVLREVALRIPMLILSKLNILFEK
LWSGLASSDEMIRDTSTQLFKVCGKLLSSRSPTLRAKTVDALLHQLKSNLAAKSRDCNLA
GLLAFETVVMSSMGCPSQPRYEDLSIMLLPYVMSGGSSTNSEIVRKLLFHCLVVLCRYST
TLFIANQLKDTVSFALKSIRNLFQHCAAFDMLSEIIPMVGKGAFTPFAKETCEAVRFISE
RSPTPCWESLKCFSVIFRECPFADVESYIESCIENIFNWGLSSQLIECMRDIISSSSTKC
RTKLEEALLDMISVTLCGLPFRQVTGTRTKNVIYPELEPTESQIVVALNALIQFGFSDSE
LMGDFLRDSVLPLIDNPSASVRNAAISTIVSLLIPPGIKGELTMARRICVDMIVSRMLVV
GLANPDPVIRATILSSFTPSFYPYLSELQFLTQLFSALGDEDIRCRIAATELLCRMVSHD
PSHILPVFRKEVLHILYALSRDDNKNTVLNGLLLLDAVASNAPQFVVNLTDGIVKALGLH
FTSLEIHSQKLQPLLRCCTSVARAVRFFGHNKPVFTNEVERVCELLDMLPLDTEFATSRL
WCLRFLGAALGPQIGGRSPYDVYPHLYRRLSGILKNSDDDLNLRLEALRCAGTIGALDTS
VFQSLGLGHSTHQIKLERGTSHALSHAMCCRYVLRAIASLLDPNEKRVSVNKDTLLRIGI
QTILQIGESCPCSRAEMTVVIHPVVRAASELSAGRLLGVVLYELTQIIKYVGAAALSEVN
VLYTFFDVVWDRCPAYRFLIVRLASTIASFRDKGDQKYRQSDARVIPIKFDALNDADSSE
FLRYAILEYIVKHTETLRFCAEIVVLNLLRATQRSSVDFVVYVVTALRVVCWRLNADELA
GVIVRGLLSALKLHSSALTRVTEYTSFTDRIMSVFCVLIVQLQGEFIKYSSEVIQTLKTL
RISNSEFTTLQGLLIKGFRCALSETSLKEHHDQVVSLLKKCKSMAVRGISRLGEVWSARS
NTEDTTAAFGDDERPLPVAEQRIINTIKTVSLTKEEWLRWIDHFSISVMQESPYRVFRCV
SLPIGTNATSLVERSPEFTQDILRLAFRALWNFGSASIRSSIVDFFRQTLQQPIWTSAVP
DDVITGMLSLIEYMDIVGMTLPIAANDLSECAWRRGMLAKALYWREAAYREDPASTVESL
IILYSELHQRDSAVSILSQANESQKRNLLQQSGLLKLAGYTEFLQLTQREIDRDFVGSET
SSESLARPLPYRSKNFRRIRGVAGRSLSDVNGSFRSEDATLDLHLEREVRQMVSLSEFGE
YDEVIRQWEAVFKRHKEKKVENEDNILFYVSQYAADASIRLQSWSTLEDTLLWMPRDSVQ

YHIARAAFFIHKGQYDEAFLAVDEGRKLLLDDLSGLLHESYIRAYEILVIAQELSELEEV
MTAKRAKETSSMEHFRRISRLWDQRIEMMSPTVPVWKQVLSVRGLLIPPSEDVTTQLRFV
KLCRRENAKQLERFTLFQLLGHRCPTYEQLMSCNANPRVVMQYISFLSANGELGPKSPYG
LESDLLKKLIDTHSKVENTILLSRAYARLGTKTELKEAIECYKAATLYDPNWFHAWRMCA
EANVELLNTSYSDAAYAAAIEGYIQSIKLGNSDSTMIQDVLKLLTLLSRHSDSDKGLIKL
REKVLDVSSRAWYLVVPQLIARLDSGSDDSCQLIADILTSVVFDYPLSLIYPLNLCAMSD
SERRKKLATMILEKLKSKFPVIVLQGRILIDELLRISDLVYEKWYDRLDTAATAFFGRRN
CHEMVETLLPMHEELNRAPETIVEAEFTCKYSSRLQEAREWLKSYTRTESIADLHSAWHI
YHGVYRQIDEQIKSQNRLQLPFCSPKLFEARNLSVGIPDAMPTDDGNVSCIASFNDTLVV
IASKQRPKRLSVITTEGKKQKYLLKGREDLRLDERVMQLFRLVNTLMMSDSRTCKNFGFQ
IQRYSVTPLKDTVGIIGWVGGCDTFHELVKKYRTSRGVPCELELRMLNQIIVFDQPKAYD
FLTIMSKVEVMEFLADHTTGHDIRKAMWASAASCETWLEQRQVFTTSLATTSVVGYILGL
GDRHPNNMMIQRTSGLVVHIDFGDCFEVAMTRDKFPEKVPFRLTRMLRNALDVSGVDGAF
RTIAETAMWVLRDGSHSVLAILEAFIQDPLISWRLMNRPGEEPQASADHQAFEQMGARKL
YSPAAFTGDPPRDSVSTLAIKTAYVASVGEEIDMVHKGVTIFERVRSKLKGEDFLQKKGG
TASMDPKVQVARLIAEATDITNVAQSWSGWYPFW*
>TCRU_7179 proteasome beta 7 subunit
MASGGSVIGVKYNGGVLLACDTLLSYGSLAKWPNIPRMKLVGAYTVMCATGDYADFQEMT
TMIENHVNRQQMYGGGALTPNEVFCYLQRHVYHKRSQFEPCLCRFVVAGCHGGEPFLGGV
DDVGTRWTDDCVAAGYGAYIALPLLRQALEKPGGLTREEAIRVIKDCLRVLFYRECRAIN
KFQIADATSDMVSIGEPFEVETNWEYDGFCFEKTAIIR*
>TCRU_7180 short chain dehydrogenase, putative
MAPKSGLVLGACGALGEAVTKLLLEKKWNVIGVDIVSKNLLTDSYTHVVLDNMASAEAQQ
GVMLEAVDKSTLLDAVINVAGGWAAGSAADSSASCAMESLIRQSLFSSMAAAHVVSQRGG
KNCFHLLPGAAAALGPTPEMLGYGVAKAGVHQLTKSLAASNSKLPEGACVVALLPTILDT
PANRKAMPNADRSCWTPLGTVAEFIVDWANGVNRPPSGSLALVTTKDGGTKITFQY*
>TCRU_7181 coatomer alpha subunit, putative
MLTKFDVRSCRVKGISFHKSRPWVLCGLHNGTVQIWDYRTNTSIDTYTEHSGSVRGVDFH
ISQPLFVSGADDYLIKVWNYKLRRCLFTLRGHMDYIRVTFFHHEQPWILSCSDDFTVRIW
NWQSRSSVACLPGHNHYVMCAQFHPREDLVVSASLDRTIRVWDISSLRLRKQEVGIAQDL
LGTTDVTLKYLLEGHEKGVNWVCFHPTKPYIASAADDRTVRVWRMMESSCHEELQLRGHT
NNVCCVTYMKDFLISDSEDRTIRVWDVKSRNPVMVFRRDTDRYWILATLPEKNLIAAGHD
SGMQVFKLFRERPAWVVNGKLLHYIYEDTLYSHDFESRAEYKFNLAHHLHPPCTISCNPV
DNMTVLWYDTDGGMTETFTIPKPGYAVDADIKKRLNVTDAVFFAPSKYVFVDKSNKLVVC
NCQGEREKVVSPEHSCKRVFPGPMGYVLCQTDAGVELYHMAQHTVTAEAAVCGIRHVAWD
KEFNKVAFISKNTITVMTKRLKLITTIVVSTVRMKSAAFDEQRNILYYTTANHLKYCNLR
TGECSTIQSMKNPAYLVRASGDTIWMITREGKVTVQELDNLELNFKLKLQQQAYREVIKI
IHRKQLQGQALVGYLHKHGHSEIALHFVTEPFTRFNLAVECGALEIAKSTAMELNQASVW
RRLAEAAKTNGDIQLAQFANSKALNFHGGALLSLITGNMAALGHLVDTTNDDNFKLHYGL
YLGDAQKRVQILANAGQLPLAYLTAKSNGLDDLASAIFDKMDPDVSERMLKAKVHPISEI
PKPVAVTENWPMLQVEESMFARLLKEPGQLNAAQAVLGDDEEEEDHAGAGWDEDDYDDTN
NNAGMSMDGEREEREVEGEGWDDDLEIQVPPDYGADGAQKGAYVVPVEHPPLPQHWVEMY
SLPAFHVAAGSFATAFDLLRRQIGLCDPEPLKPYMMNLWTSANASRPSWIVTSVVFPLTK
YPSGEQRGAHHAPLLPEYIPVLTEKLRAGYTAFVEGRFADAQAHFVGIMHQAVFATYEDE
KQRASLLELITIASEYARALSVQLHCRSIDGNSKEALELSLYFTHFKLQRSHLTLALSQA
MSKAYKMKNIKTAAAVARRLLDQDPPKTKANQALAIVAEGERNPTDSEKLEYDERNPFSL
CSFSHRPMYKGTIDPIRCSYCHSPAHPEHKGKACPVCKIALLGAETAGLVNRA*
>TCRU_7182 Alkylated DNA repair protein (alkB homolog), putative
MEERDSTSPQYVGGENLALTPFRLAEKRYKLYRFDRRAARRQQLPETDFSDVVDFRCPDA
NTDQNRSLIRGVSTLYDSQVRCFEFVTVPGLLFFPDAISEEEQQALCRDAILRYGDSSQH
PNHLSTHASKPKCTKRYEAPMRWATLGFSYDWNSKTYTREHYSAFPPALKRRIEEILHLC
SSTPDLKDVNPSIYEPQTAIVNYFSVGSMMMAHQDVSEESMQHPLISISLGCSCVFLMGT
SSRDDAPYAFWLRSGDVAVFSGPSRVAFHSIPRIMDDCPPHLCTISGENNEDEVYWRTQM
RHMRININVRQVYSESCAFLFES*

>TCRU_7183 snoRNP protein GAR1, putative
MTRGGGGGFGRGGGGGRGFGGPRGGRGGGGRGGREAEPDPPESLELIGTFMNAAEGYLVY
KVTIPEVVPRFNAFVYTENRAKIGKIDEVMGNTTDVMFSVMPMPGVQAGSISEGDNIFVS
PTQLTPVRVFTDPPKPRGRGGRGGGGRGGRSANGGGSSRGNFGGGGRGNFGGGSSRGSFG
GGGRGNFGGGSSRGNFGGGGRGNFGGGGRGNYGGGGRGNYGGGGRGNYGGGGRGNGRGY*
>TCRU_7184 Cullin binding, putative
MPPKGQRSLNIAQPLSSSRAQSANAILRSAASAMATSGPAASKSSPRTSCFPRAFMSTGN
ARNEMEAYYEQLLSQDRVDGVDAFGKNGIHLLCKGLGIKPESFEMYTLIWKMGVTRGCCI
PRADWLKTMYTYKIEQPMDLKLVLVEWVKESRGDSFTEFYNDLYDYIRGEEARLMPYGTA
VEAWAVLFQNEPRIIPWIKWYSDIYRREVTRDVWRQIGIFLSAVPNIEAYNVEDRWSCAI
DSYVEWCKVSG*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MTRSTLVCGGGSCAAILVEHGLGANLSSVFYMDNCAVLSQAHVMYALASDLRVGGGSVFS
IQNSSWSAPSIEYYEGACVFGDVVVAGGSVLQIVSSTFRLGFAMLMANTLNVAGGSWLVH
RDNEFRTAYVVYVAKENGVAFRDRSVWSILDNNFTYGSYSLTIAQMTSNWSLPSDSRPTI
YGVCNKARGSPVTDYREDLNIGSPVMVLDCGVCTMDAVCFAARTSSISGCECVCAAGGYG
DTCLPAAVPDGLGPLPLPDARDTEVRCVHGGSISSVDYPDPGVRGLCFVNVTFTAAIVLD
LWSFDAPQQTLNITLLQCVLVGLSVKGSGARVHVNVTSSMLDSGALEFEGHFCTSSQILV
VGSTLVKTSVHAIGFLEFFPGRNTTLLLLDNRIEGNSYAVYFSDAVVVDGGGIVVKGNTL
STMEDEGVESSVYAYAVDVRNGGYIDVENNTMSAANGLYLNGDTTVSFAGLLRVVDCTFV
GGTKIFESSLVYFDGFVTLQGGAQWRVEGNNMSGTSLIGMPKSLFEIQLSGSGTTVVLAH
NRQMDSRMPFFNYLLVSTVVTSPARFVFGCNLQDDEEVSYDGVFPEEVVMFGCGACNDDA
ACYMPGTESVDRSSCSCSCKDGWHGASCLPFEVPDTVVPPVAERAVDGDTSCVVDQTLTN
LTLNMWKTHHCYVGVIFSGVGAALAFFLNSMPLHLPINITLIGCTFRDGAALEFVGGAEA
AESAGVLIRVSQTVMRSSVVVFALVLPQHCDIAVTEVDAVQSSIVFWPNSVNKMMSVVTL
HDVVLTASSLLVSNVKAHASKYGGFGLYSTGALKLVGGSSLYARYCSLDGYTHMFHVNIL
GVRDHSVFALLNLCYKRPCSNLFQCLDFSVSDHSVLRVVGNSGSVSFAIFADDSWAVLES
SWLDWRDNDVEVGAMFHESESDFVIIDDSSAVTLTGCKMGLTGLSGPLLTRADAGYRFVA
GCLTVAGRVVTTAAELALNGITNVTTVAACGECTKDGDCFAPLTTAVIDCKCQCAAGGHG
DVCVPAPVPAGPPLPSPPLLPIPPLPLVGECISDMLYPEVAQAVGGGLSWLCYRNVTFSG
GGMSLTVLVGAMAGDVANVTFDGCTWRDGAVLLLLGNVHAAVGSLNIVVTGNTFYDALLS
PEGVFPPRTNITISGNRFTVARLIPRFCLVLRRPSCVAMNGLAISNDSAVVLSGNVFQSV
TTSSSAIHVVGSALSVSWHSVFALVGNTFHMAGANGSLMYIGGSRDSLSLSVLNNSAVVI
RGNAVTRPVKYFIVFLWSLRVESQSAIVFQGNEMQGSSVVFYSSYSPNIYYNSWLQLSGN
FCRESPSDAFLFLNPTVNLRDSTVSVVNLRDSTVSVSGNQFISGTFTPTVLWISLGSRDL
TNGAIVAACNTVNGEEEANYAIPSVYNTTFLTCSDPCTLAASCFPAYTTTASSDGCACRC
AEGGHGDACLPVAVPEPPSTDGADLCVRDMRVDEEVNAGLGTSVACYVGVTFAVDVVVEI
ESMSGSMRNVTLSNCAFVGGASLYVVGWRSDPPAGLRADVLISGLESRSGGGVLVANRFP
PGSRVAVVDSVLIAEARVAYRDAYGLGDASACLVVHSVNLAGSVLTIARTHVAAVFRDAV
GVLFVGGVALSSRGALYVDGLLVQTALGLCVSVGGGVAASGGSVVAFVDSDFLLCKHAVS
VRGSVSVSGSAVALVRNDFLSTADYAVAFYSTVSLDGGSMLLVKDNVHDGVSREMLYAAG
AVTAAGSTLSFVRNRALLPRMLSLSLSLASGAHLRVACNDAGGRFLSTAEEYAAAGFGDA
GSIDVAGCGDCDRDTYCYAPGTATASMKDGVCVCACGSGGYGEACVPVGAPALPPAVGTA
SSVFVREGVTVQSVFVVPAGASEVTLRHVVLDGVSPVLYVPWMARDGVRIVVQNVSLRNG
AVLYVMGGGALRGAVAAGSYESGPVELSVCDVEALNGALVLTGTYPAGSVLTVTDSLLVA
TRPTPLVYLPGSQSSPYAPVLVLSGLRLVRSVLIVSGVALVTVVTGGRTVVVDGAVLELV
GGGVALDAAVLGGEYALYASARVVASGGAVLRVSGSQVYAAHGLVFESGVEANASAVVVN
DNAGALTDGALLVLRGSVSFVSGSWLSVRGNSISGRLLSLPSYPRSADLVQSTLTLHGNA
GSGPVVMDGTVALGGAGGKFVVGCLTLNGQALRPMDYRSAGIIGEFRPVACGVCDADVRC
FAAATRAMSGSCGCRCAEGGYGRDCLPVYLPYVDGCNRTPALPLLSHTETLTETRSLTPG
MSTTHYSPTETPQVTETVALPPTRTPTASVSSTLWWSDVACPTLAVTTTAAGGSLTQNDI
RGGGSAVPTRLMVALPPPFRWAREPQLGTHLSFVPVSTAQPSGFGGPWGAMLRNATWVHN
ATNPSTVVELAVPVHRGYFIAADETIVIRCDAAAVSGGCKGVLLGSFTIRSDTLPAAASA

LSAITGVVAGAAAVAVVMTGGLGSILEMQALGVFARMSCASAQERASTVALPYFLSVFAA
LDPLWMVVGNALLAAVFGCVHCGVTAAFQRWRGVDAATAWAAMRFPSLTYVVAHAMHLGI
FFGSVLALAMPGARVQHRVIGVVGVLYGVAFPAGVCYFIARHAGASFTRYWQFLRKPLHE
RLLYPVGYWHPAAQQRMYGGMLTNMRGSYVYWCVFQLSVLCVVGLIAAVQSPVGDCHVLY
FCMAAVLFAGAGVVAFTNMMRSAFMTVMRTASFVLLAALCVVSAANQLAPSDGGAGAYAA
TVLLLTAVLLAVTVYGVVVWYVEDRHWQVLREPRRGGLEALLRDDEDGDEETQKLVIVVR
LRHHRCVVVPTTRTAAAHGL*
>TCRU_7186 hypothetical protein, conserved
MAMMRTGRVLLVCALCVLWCGVCAMEVSKAEVSENANVFHVPAEVPQPESADRNTGQQES
LENVSQERQNAGKPLDPKIEAADDQKRDLKIEKPTADELRGETEETHKDQIEGGAEREER
EDVIEERKAPLDGQGGEGQARQAGNDLSKVGGHSSATTPSGGERKGTGEPSPPGSSLPEA
STQGNGAAPPASLQEAPAATMKKNEKTVENPRAEPGKEKLSSEDDVSEQTSQGVNDGVEP
SNDLTNEENVSVVLIEQNGESDGNFESTQTRP*
>TCRU_7187 retrotransposon hot spot protein, RHS3, putative
MEYGVLYLLAAENFPLVDGFFFVDLPRNTLVGLQMTTASAHHTTTSTMREFTECLAAYFE
GWEELSRDMSWEVIYVQHAGIVLMGDWQRCGVVNIDNLSDDEKEIVAFWNGKGTPIPVYF
NTVFCK*
>TCRU_7188 Phosphotransferase enzyme family, putative
MPAEVIFMFDVAGVLTTSPYPATRRLAETLMRCVFERARAHFMSLVGDESPALLAQNYSN
LFSLIHSFTEKVRGIRCAFERLELGEINRNEFVPLYHAEMDFMLTALVKKNKEELEFMHI
AHPSRVASIKERYPLLAVPVVQELLRELMDPEAYLCTMEKVTPRRNVLNLLHYLRMKSQQ
EIRLVVVTNTWEVEGQYARMSKALSNNMSETKWSNFPTACPIDYGDAGGRSSFVINSLFD
SFVQSYTFHKRKPFPDIFHHAIEEAKKTRVTSQDSLMYGVKPHIFLFDDVLENCETARNL
SDSPFDKVYYIENGAYDVYEDVLSALNTVGAADPFWADVAAGVKKEISPFFKPPIDANGK
PTSWINEEMHDYNSNLLILPPPPCEACEPRGFFEPKKFLDEDDKDAILFYCAQNLPHLFP
IEIPSRHSQNLQLARKPGFATSSGPIVFEPMRGIGFFKTYRITLRTGSYVLRLQPHGPVP
HGTLDIRTEYEMMRYLAQNSTVPIAKCLLYCESYAACGYRFSLRRFVEGEVIADMRKLIQ
PRIQRPYSVRRRHIHVELDPYLFFKKAVETLSQIHDVPPPRFLSRTRMERNPNGTAVISV
GNAVHPLLEMINNLIARYKAVVNTAKLPDGSYLFQFKTLERLSQALIERFDATRLGVQSI
PFPEQLVMIHGDYKLRDLLFSYRSFEGRHKYPANIIGVMNFTSVSTGDPLVDVASLALVA
LLPRPFGIYDMPMEMQVLFPTPQWILERYCDSRGYMRTMTGKKREAIFKVYLSAACLRYA
VKTLSDLAEVFEVFNSLPLEEARKLSLVEHALQQGLALMGKFPSRL*
>TCRU_7189 hypothetical protein
MSTDDAHDALALLEANLKSHPANEREDDEETGIVRVEELQQKHEEEEEEVLVLEENEEEE
EEEEEEEAEEKEKQQQLTPWDRLYEEGLKREARRLEVFEKATADRVARALFDQQCNTAGR
SNTQIWNKDFADRQQRWLDTKEERVRRLREEAEIAELRKLQPPAINEASQQMAEKAGYEG
PIRGWESHFARYALRFAENSFVPTHMFRPNININAHHSEETVRDIGERLYKEDVQRRQGR
LRELMMKYQRSELIDGCTGKPYFTPCISWKTEMTRKRRSEQRTRSAARATEMLYIKARER
YNKVAEPPVDSNSFTPEICRLSRKMAERRKARSEKRPDVVPKTLTPPEKKSKLKLGEFLS
REEACLARRRQKMERVERQLLERQEEECTFIPRINKRSVEIFEGSQQRYGSSSPPMEMTH
PGAIQLTPPTEGAETYERDHFISDAISPLLYESSAASTSPLIRIDNDGSRLINEFEHKMK
ELLNEWRSIERV*
>TCRU_7190 hypothetical protein, conserved
MTEPASTVTLSLFLDERGGSLDFFVKLFLGQPLGPFQGTNAFVPGPILFTICARKMQLEC
QAKLEVKSFEMFLPEAVTCVALRRRKHVWELTNVYIHTPSDVSGGVDLEVTVRAPHLSQL
FIVQELWHKALLDSLQSIRQMFTRSASIIKENVRKSVVICRGLEAMRRGQVEEVLVVVVT
ASHIKLRLDLSSGNAQQSTLGGVSLILLRTRSPARVCYKTCFDLAVRSFILRSEGVLSGV
ANLDSVLIKAFLIENADNARNLVCSPTGRTFRELLCVQKLHAMFKERQLKDVFECQATEI
FLGCMDGVGEEERRTVEAELSLYRSSVFVTPSTVPAIFNSLNSVGEVVSMQREVSLLRLR
DGGIKTSRASFTRKVKEAFYGIEWVLDRHKASGKSKRILSSSDSNFLSSGDNNNNRKGST
SIQEIKGGDKPSVASDEAEKSLIIPCMGNPLTRIPCGKLTMKLEQTTLLLGTASAGATSS
GSLIASFPKARLSFAECPGDGNTTVKKVLEINTENVELFRPGAVKVVILGFRGTNNFEFY
SRQGIGDAEVGFMLTLLQSNPWTGNPRFQDFQELIQLVRSFTAKSNAEVFHRFGRIDQEY
PGDSSDTKSSSNAKSSGDATAAAAGAVFAPTAEETVQQNAEKRSRDDRYLKALRHVKFSP

QLRFGGDVAVNVDVILNWLGVSEKMLPQILHMQACDRLEGLLNRVSEGMSKRLIKKRVND
*
>TCRU_7191 Enriched in surface-labeled proteome protein 1
MGGDKIQGDGSLQTPEVSMSSGEDGETAEGTDAQGEEGIHPQNGEVKSAALNSSLGNLSQ
GNNSDACNVRERRVLQLPSLLLLGLWGFATQ*
>TCRU_7192 Enriched in surface-labeled proteome protein 1
MLVTLPVYSNRKGNEKGVLHLWLTDNTHIVDIGPVSEDDDAAASSLLYKSGDNKEELIAL
YEKKKAEGDTQSSLGMVSVRLTAQLKRVKEVLATWKEVDKRVSKLCPSTAPKDPSTGNAC
GAVKITEGLVGFLSGNLSDGTWKDEYLGVNATVKNKEGAEKTDNGVKFTGRGAGAEWPVG
KQGDNQLYHFANHNFTLVATVSIDKLPKEGSIPLMGAKIGDENKNTVLLGLSYNNERKWL
LLCDGGKNKDHSSNWETEKSEHVVVLLRNGNQSSAYVDGQRVGDALCELGEAESKGSKGI
FHFYIGGDEDKTREQEGVSVTVTNVLLYNRPLSSEEIDALNPNKAPITSPVAEITPESVL
QPPAKPQPSEHEPLTTNIGAGADGVSSAASVTTTPSSDFTQEAATGSGDTLRGNGSPQTP
EVSASSGEDAETAKRTDGQEEEVHSQAGEVNATALNSSLANLSQGNNSDAGTVRGSGLLP
SLLLLLGLWGFAAL*
>TCRU_7193 Flagellar Member 3
MDRAFVNASAEYSPLHGRDWNAEFQLAWEMDDSTISQAEARMEQLCRVEREFVAEATRTV
KQIVMLDDDGPRELPKFLQCYRVDNIFFRVLPDSRSGRNYVASLRGVLQSRTRLLTVPLS
CMFFYRGMPVLAQALVPMPREPTRLYGAGSTNNQEVVAEILHIAEALNIPLPKSILCEVY
EGLDARWYCTLTNITTMYFAGSFSLSHTLKRNEMLVFSSFVTSGPEDVFSVMHAPPFLDA
LAKLKGVVQAEAQNKLCDILHFYGINFRFLKEVLQAFLLRRGADTEGVKALENCVIIEMF
ARAIKQELYLRVQANRTAYDGLMLQNDVARYISCGLDAGHFKQEFLPVLARKYNIGASDK
SIIAICDNVRQLKRHDIFARLAVLIGARLRAEETSLGEKFTWLPEVHARVLPPTVNPKIV
QALALQYNVTKTTKKHLYAFCLPLQSKSARWEGDLKTALRYALEVAAAEKARHGEVGLPY
LYALREVCELLLSEDKIEWISDGCKHIDTLLDGFDKQSGALTRMRRHIECACWFLGISGI
VDLRKKALHQFCIASRLAPAEIRRDFGAWLYTRPFLGILRCKQVMRPERFVDVSDIARDA
EQLARIVTPVDYFVEYLWELGMELQCDEKYEMASEILQIAFNMLRKVPRSALDSGILMYD
LINVCRAYDPARYGTYCDVLLNSLSESHSKETFRPGNPLRPSLMRT*
>TCRU_7194 Putative snoRNA binding domain containing protein,
putative
MAKDSVAASPNLFALVGRDVAKQLLEKASGLVGLARLSDAAIRHLGLDDATQFQRARHLH
AGCIVETPIFVEFFGSDEVRADDLQAAKKAIAVLARKCSIVAKADLAGGSASGALGEAEL
EKVRHSFELLLAEGKVNATDTQALPVPHVFVRGEEAKKKRGGRREFRKQRAQMDAPSALE
RAVSHVKMGVSEEEQLQTLMQRSDVRAQVLKGLTKAPEQRKRPRDANDDEYDDLLQIRL*
>TCRU_7195 WD domain, G-beta repeat, putative
MPTLEVATLLGQHLGDKLRVTSAMVVMDRIVVVGTDAGCVLAFSQPSSGAEVGTVGVCVY
ARALHHGPVHCMCASASHLVASAGHDAAPVVQPVLNLLTNGVAQTDRLSGHTLPLTAMTF
FSSGNWLATCGLGGRLIVFDTTTRSSLCDVSVGFSVRCLALSPDETTCFLGGTRIARVDL
YQNTRPVEPLIRREHPLWLQHYSWSSNGDEFVAEAPDDLFIARLTVTEDRLTAVFRPRGW
SGADYAIATWRLGAVDFWLSRDFCRPADKMQVGDGEERLQCSSFRDIFFEELKEDAAPVL
QANGGWDTWRRARVRLECGPPLLTLKRDEGLADCLFSALNDTPAGRLAYEEERGRILQVE
CDEVVRLLKAAMRRDGRKRGRSSAAA*
>TCRU_7196 prohibitin 1
MSLKFLRHLMTGVVAASVGIYSCCFVVRPGEAAILYNKITGLKDSVYGEGMQFRILGLDD
IKMFNVRVRPRLLQTMTGTKDLQMVNIRLRVLFRPQIERLPQIYRTFGMDYDERILPSIS
NEILKAVVAEYKAEELIQKRDAVSARIYQLMQEKVAQFGLVLEDLSLVDIQFGKEFMIAV
EQKQVAQQEAERFRYVVQENEQKKRAAIVRAEGEAESARLISEAIKRSGQGLLELRRIEA
VVDIASQLVPMKNVIFVPTDANLLLNMKNLGG*
>TCRU_7197 MIF4G domain containing protein, putative
MHVYSIQQILEVRSMYKDAPYPGFSLEEACRRKKMTQTKLVRGANAWVARGSAKTTEEWV
ERLVQGSLNKLSTANFDDMVAKLQTEVIFSTKETLNIAVRIIFKKALDEPECSKSYAGVC
YKLAEFEVGITAAKQKAEGKKYSKLRNAVVSIAQEEFLSRRKMPSMEGLTEEEMELRRTT
FMRRKRANMKFIGELFMHKVLSCNTMMNIIQTIMQEAERGGYPTSEDIEFLTELFLTIGE
SLDAVPELRVRLNGYFELLGKLKDQKEVYPPRIRFKMLDLIELRSKFNWERRATAAPKTS

SQTQREPPRVTDKVVATRSSMNASSTGSKKGRQDSVSDPASQQAAAAAAAKTAMGEAGGR
SWSNVVKSPQSPRDATVARAVETVNFEARVRSLFQEWVAECSNDFIPEWMNEFRHCQRHF
DSEDALCKAAAEVVVREACMTTKKEAQREASSFLIVGLFLEDDEVLDGFAMALVSAIEEG
ILEDVPKFSERFINMLRITSGENTVADVYYDTARVLCTAYGLMREPDEMVLDTMMEFWEK
IPRPATDENAVLPLQVVQSLVEMSTRGQAPLTGRIIASLHSIGLVHDETVREWLATPHEE
TSVEVVEAFKKANK*
>TCRU_small nuclear ribonucleoprotein, putative .1
MQAPSEDDVARKEALKRRVEEHMLWKTTFFQSRPPPPFIPKCRRRPEPIANAPVHSFYKR
ALEIVSAEKEHVSSSCSSASPPTMTKTDPPEGDGAKSKQDVWKHKMMLEMERRNPYTDIN
IRTDPRSTVVVSSLHPKSLEEDIRLFGEQFGRVVSVRLICDHNGKSRRYGFVQFGLEAEA
RKAVAHSRKRRLHGHAVVMEMERGRLDRDFLPKRLAEAKRQIEGSSSLCSDKRQRMEGSV
KCPPAVAAGRSSPIPVSDTRDEVDAFLDDIMNLT*
>TCRU_7199 kinesin, putative
MPPGFNRVTVGVRVRPKLDDTVNALQRSERYEPMACSRYSDTTLRVWDGRPAIDSRTFFF
SYDAVFDEDTLQEEIYEELAMDVVDDVLRGTNATILTYGQTGSGKTHTVLGRVQKSSVGD
DIITSDTGILLRALQDILHHAEINRNKFHIVVGLSAVEIYLDEVRDLLSDEQQPTAVQMS
LVRDVVRFGKLTYVSVCCLEDGLRVFQRATARRMQRMTSANDTSSRSHAVFTIEVFQQPI
TSSSAQPLDLLKYISMREEAQLAQLEGKAPRMHSNPMFPTASQQLFGEEYSPVMHSKLSL
VDLAGSEKVRNANVKGDGFDELKKINASLSALGNVVHSLHEGSRHIPYRDSKLTTILRDS
FATASARVVLIVNVSPTTLTVDETLSSLYFADKVKAMKPDPRSGGSDENDMVCEYLSLLR
KYEALIADVHIAGEIHMFTAPQIIPLVADDQYNVLYDPAFHLRRPECEIRRMAASMMCEA
FKASASGKNQSLVEQQQMEAERRLLRKEIVTDWKKRWNSVCTQIENFSTQTEGQGDAKER
ALMDEVNMSLAQVEDARVMRCGMQKKHQKIAECLEEAGHTLRALEEKLMCADDAAVDPVA
ADSTALEPREAHLLNQGEESWPRLSEFAACAVYSATLRDELCRLMCETQRLSGELARQEQ
RHQWQWGAAPQPQSNYDWLHHVVCDMAGNAVGTSLKPEEELRHGDPMPLGSHLAFNDDSV
PRPHQYWKSQSVEGSDAGKKCRGTRFDTAELLEDIYSFVKMGGKVMKYSRGGLPHRRLLY
VDGKAGNEQLSWSVAGMLGREDRIPLRSVRQILLGRPCAPTGSSLYYTSWGVVSQQENKT
KITGFACDTVAEFEAWVLGISQLTGVKPTFGEPMKIQSETEAKWDALSEKKRAFCAEWHI
PPPVFIEAEGQITSRGKRSRHSGLRLTPGELRNLVKLDIFRASAMWLHFFAEGLVVNATN
TLYCHVELRGMPKVMPKRMKSATNAESCDGTSLKSMPFSSDRRETE*
>TCRU_7200 hypothetical protein, conserved
MLQWEWPKTWPTQSKEVIRISIERAIRKAMSGGKNAQIRGVVSVDELNLGCIPPEISLNG
IRELSVEHTAIMVKVHYHGDFSMRLRGLEINLDTVGASAEEADANFALPFFCPFEMTLRD
IQIDGMVSIEIFHELEENPQWEQNSSLIFHTEMKPRVVKNNVRRPSRSVRPSGTNTCLGY
GALLAGGGRRGMRPPGVLETTEASLPLLDADGATDGVLKSSAPARNSVPSFADILEKKVI
VKRRMMKLQLFGDPLKKFRVVSNFGTVPGANSKVEGTVRMLIKPAIEALMEEGIIFTL*
>TCRU_7201 hypothetical protein, conserved
MFFYSGLRCCFAAMAVDAARRYAAEHHDERENHAADTALWLDDTAAERRAMEEHIRSPAY
KELHRPALTNAAMGLYGGEPGFEKAHRVWVDPDRPHMKHIYNQTALAKNLRYARYGYFKR
DMHILDIDKLVRHARMLPTPGRLLTDFLYQRVPLPDKSCAALIRFQRQQIEMLEEWERHA
SFQCAAEMFERLIVTNIPPVEVGVETHAEMVLCAAASGKWEEGWEVYTLRAREMEAESPG
SFTLNTYFFDAVLTLCVAASRVDEGISIMEEVITRNLRPRATMLDKAMLLCAMGAESISK
REETEGGTEQRLQLERKKFEQRGLELWALFDFYQLPRSTASVLSYMRMCCAIEKPTLVLE
AQSFADTAGIPLSLECFYWLVYALRGVTDFGDYIMDVFSQLTPRGLTPDFVLFTLAFMHC
ALQRDGELALAVYDQHFIHMNINPTPEMTLLFIQSCAHCEEPRVAMLERCEKMLLRLEEV
GSSVDYIVLIYDQFLELCGHLGAVASGFSMLKKLVGLGKPLTTRMLNSLLLANAYATPPN
GSIAMTEEIVRLFSLLKLPPNKDTSICLGFCIEAFGDSPSLNAFSAIVHAKCESGDDASL
YDEDIPILQVPPNELRQLRTEWKLRPRDMVLRRFGQHTKFKGKGALDVGSMHGSVVPFGR
TPGERLV*
>TCRU_7202 Enriched in surface-labeled proteome protein 1
MESSKGAGSGGASPSAVPTVSTPSAGKDSLQQLVSEKSSDGTQTVDGGSFSDGDAAVETR
EEGTDGQEEEIHAQNGDVKAAALSSSLGNVSQGNNTDAGTMRGSGLLPSLLLLLGLWGSR
LCEE*
>TCRU_7203 60S ribosomal protein L27a

MPTRFKKTRHQRGSTFCGYGRVGKHRKHPSGRGNAGGQHHHRINFDKYHPGYFGKCGMNH
YHLKKNPLWKPTINLNNLTKLIAKDEALKAKKGETLPVVDLLANGYSKLLGNGHLQTPCI
VKARWVSKLADKKIRKAGGAVVLQA*
>TCRU_7204 60S ribosomal protein L27a
MPTRFKKTRHQRGSTFCGYGRVGKHRKHPSGRGNAGGQHHHRINFDKYHPGYFGKCGMNH
YHLKKNPLWKPTINLNNLTKLIAKDEALKAKKGETLPVVDLLANGYSKLLGNGHLQTPCI
VKARWVSKLADKKIRKAGGAVVLQA*
>TCRU_7205 60S ribosomal protein L27a
MPTRFKKTRHQRGSTFCGYGRVGKHRKHPSGRGNAGGQHHHRINFDKYHPGYFGKCGMNH
YHLKKNPLWKPTINLNNLTKLIAKDEALKAKKGETLPVVDLLANGYSKLLGNGHLQTPCI
VKARWVSKLADKKIRKAGGAVVLQA*
>TCRU_7206 hypothetical protein
MADDVMLAIAMLFAFFVLLFFLLTANVYKRHLQDKKRRRRQERLRDCPQAEPFAPPVSLP
VVVDAVVVFPSHEEAQHRIEEDGAPITRVPSELPGDGLTTSHEYFASAEPVEEGNALPRA
RSGDVLQGVPVDRSLRLPDVNAASRSLNTLSGATYRLRPASAVYGSASYLPHGSSSGSGM
TAGDVPGVSQQSDAASCPETASPVHVCEAPPRAAAAVNAEGRTVPTTTARRPPVEEGQRT
*
>TCRU_7207 hypothetical protein
MTRMQHLDGARPAVSPLFVLPQAFLCSNDGGADLLASLSLYFVDNLAQPAVAESFLLLNA
AEKLATLIRRCIVADGVMPTDTITGRVTRTMGIVGTDVKNNDGASSEV*
>TCRU_7208 hypothetical protein, conserved
MDSAGVNATQATCGAQSKGYHVCGCYGHTQDLPDYKKITVPRTLQGFHAKEGGGCPCIPK
TKTKNMGALYCSRNPMTRDRVMPVNTYRAYGPGEHKVHPADEIAAENTAVRDPETGTRLL
FPNSRNYGGTAKQHEFPAIGKPRRKTREEREYERMQDRKEFLKAVLRDEMRDRLSAEDQL
EELENKLNLRGSRHAEMLLAAAARRDAERQGGEDEAKTVGEQYEKVMEELRFVTRQPVGS
KVNIIRLYYLLEEQERLKYLREKGKKQETWSTTRNR*
>TCRU_7209 hypothetical protein, conserved
MADLNTKTKPHDDGVPMQGSYTVAARHQKKYHQCDCYGHPQGLPNYKILAQPRTNNYYLA
TGGCPCIPRAVAHPGSWRLKAAQLRSATQTHAVSCTKSRPDATCCVHAGETYGWKPGPHR
VLAKNTAASGLCDTFGNMAFKKPTGVRDKDSDVSSVCQQKLEDLEALILDEHEARRNVEM
DVDELKDIQQRGTHEDYRLDYFNEMKRKEASAASEAQLHDLLREVRAIVKRPLNQTNMDI
LRRVVDRQEYLMQLRARKASEDYPQIVYP*
>TCRU_7210 DNA replication complex GINS protein PSF3
MIKSYFDLFDILVNEETVPVTFLVSSFSLGRDIHARTTDGEALEEVRAGSVATVPLWAAV
ALRQEGYLVPQVPSRYTTSVFREFKTDPLAVSLHKKSPYYYEAGLLLCAMLPINEGNRLA
AQLFRLYQLRYLKVIHAASKKGFDLSDVREKLCESERELLDALIGGLEDERQWHHSAF*
>TCRU_7211 Enriched in surface-labeled proteome protein 1
MELSYNKEKKWQLLCGGETYSKDLSVFWGPETKEDHVVILLRNGNHGSAYVDGQPLGGDE
VCELKNTDSKGISHFYIGGDGDKTRNQGDVSVTVTNVLLYNRPLNEAEIVALNPNKVSTS
PLEKNPSEHSTVSSTSIITSISPVSPNAQKTETPSTPVGTQLTEQEQSMGIRKGAGSGAA
SASAVSTVSTSSAGKESVVQVTSGTSPDGTQTVGGGSTAVGEPTMETREGGTNGQEEEVN
QQVMEVNATALNSSLGNVSQGNNSDAGTMRESGLLPSLLLLLGLWGFAAL*
>TCRU_7212 hypothetical protein
MSLEPRLYHVEQQIQHLSKQVGLLKQLITTEVTDLRKNMEQQVAEVKQVVMYQDRLYQER
MSKLEVRIQQLSEFCLHLARSTGHVSPSVALIPTGMVAAPAEVRTLEQFTASETINGRTP
DGDENEEENQNEEMKDVNGIIETYQDRINTIYDFYTVSTIDIFHPTMTLSHFSRMVKDCQ
LCGLSQGTSTELLWMAVMRSLNKRHHKQLDNVQNRGITLGNQVSNEQRKKLFAFQRLEAI
PKEWFGEALYILAMEKRRLRLLPDGSTIIDTVSSLDEKPKDIFLSFLLYHIFPYVDAAIE
EKQRSQGLVFHLGLGINGEDNSGFFSTVSNLIQSYKTDAVASVVKEFIGRIKESYNSAIR
TAQGYHSTMMNLDGFVEVARRHLLLPLIHKPDLRHIFLYCCAVEKEKHPETEEGNISVGT
FLLALYQLADRIYGDSLMRKKFPTPEARMKRLLAKMFFLS*
>TCRU_7213 hypothetical protein, conserved
MMRRVLRAKVLHLPGVSRHAASSFTAGGSNEGSRRQNRERTLETKSSAFHVGSRVAKSEM
HRTPSSDVTRKSHLRAEEKTGVLFPDAQTHELDEMEVADEKETPLMENIRQQKRQEYDDG

DDDGEEVRAPPNLKRRYDCYIRPKRETVVLTSSFANRVSAGADMDEDDEMEDDVTKIYMS
PALSKGCCGEGRVTGARVTEADERDVLRTVGTHDENAIDGMEAGQDNGNEVEKEATENSE
EKDEFKNVKNHSFYADLFRRMEKNATRHRPQIKSAGRYNLEAVNLCLRPLLQLTDYPLTI
GQLQQMAPFIYSNLLRRSLPDLKACRRLHIYRSAETDVILDWSMEDFLRRRYESIHLSWE
PVKIVMMRFGWNQELMTDRDCLLYFSKFRDYIELAELELSAGDDKPKALPIDDAERTAEQ
RPIPVSKLLIRRKATEKTEPSVTEAIRLMGTPALSKPAKSRKAHVPEKDSVEGAFELIQR
EASSVDGDEKTKLQHAINAAPSLRQASHPSGRCVKEFSIGKEKHTVISEGSPAAPARIES
HPFDEGRRAYTPESYEALANAYHKRRVEASQIRRRILNTDSIDHASELQEKLAAAQRDLP
RLREQLEKMRQLRRSEKTDSPGRSHNSFSNSEKHTNENGPSDEFENMEYVDDKISREMQK
GQNASMTSRTFTELNSVKQQQQRQRQQEKGQTEKNLDAAEDKMKIEPVDNADGCEAENNS
SGNRGNASPSGEIESLSSAALMLRQEIESLQEKRRHEEEVLLKKMEEALGTLLKIEDTMK
RVSQREANEIERKKLEMQKKEEAEKRMRREQAEARARALEEELLRKHEERVKILSQQREE
ARKAQREAELALERQKQAEQAAFEAEAELERKLQEAKSKIWNEEENEELTCGGSRTPQAK
TAGPPTIHAERSTECGASSKPVQSDTSTHNANGSSEPSCTPEQYDGLCLGAERLRKEITE
LERQMENEGDEDDMTLMAVLATSRSDLEELEDFIRVVRRREAWAAERDQARKEEMERQER
ERGKHPNDLQEKIAAIRFQIHLMEKRLQHATERNIITKLEQGIINSRREISRLRVEQDRL
RRSGHHADAGGICIPSSISIAETLAQEEAKNAEVISEESEHIAEEVNAAHTQGTGDAYEN
RTTNVEDEDEADQPESVNDTDDAVTGEEYDENEYAEDNSLNGQVKTLEDGQKELQRLTGR
MESILDDIKHLEENIALQEGAEDAEVTAASLSELQKKLQQLLEMRDAIKIRTEQLALEDS
APKSISVSRAPAAIETEAANKLKKTTTMTAATRRPKVLAPLSNRPVSSHASRAEEEVLRF
EHHTRENYQHASQRGTPAARRMRKVAKGKKARR*
>TCRU_7214 hypothetical protein, conserved
MFHLSFTRRKNPVIFKQGQGMFSHQLKRLLQKKAIHRYNWDPLPMYDPRKLVHANRRVDP
ETWQEVYDPHWDERAHLVPDQVYYHIPVPPEYKDAYWWRDLQARRVQCPVEWVSHRMYNK
GDRQRYDFQDLSFRKKFEYSYEEVVKNAKDMRS*
>TCRU_7215 protein phosphatase 2A regulatory subunit, putative
MIPSVNLDSAIARLKEKKLPDSRVGDGVPGCFSPRPTHTRSCSVTSVPQELDKNVTELHG
QVVDTAETQPEWKPERFSSSNVDKSCSVLKKQGLVPDDFYRTTASPSMLSAFADSEGHEH
HPCHSLPKATLIAHQKARSSSATLRHVYATAIFDDEGTGRTSSTGSSGATDVASTSEKFA
LREIYVSGKPWRRVADAYPKYFRRAALNISALVTSSSGEHVAIGDCSGRVLLMRRKNQQR
QQQLEGDKRASDEGKRGRLQYTNKNNSHIQGSYEFSVGRKAYTSVIDPLNSVEVTPCIQA
LCFLPQVGPTTYLLMANEKMPKLFKVVEVRESPLPFSAVNHIGEKNFASLTLNPLDVRRT
TAMKQVTRYALNHEYNINSLCPLVDSAQFYSADDLTVKLWCIEHPDTSIETYSIKPPFEE
EVQETIFCIRCFPHEPFLLFIATTAGTVRVLDIRQRLKLFHQTPLVFKNTYFDEDTSFSS
PLTDCALSPCGRFVVGRDVMSVCLWDVRRDSHYGRFAKSVTSPLHEEEEQDVLQRWELYP
HLRRDMEQLLQGDIIEKFSVQFLNGREVCTGGFAKTLYVLDILKDSVAPSDKRKRTPRCS
NGQAFQLPQLDGANADALFGSLRPIAMDDVRFSANEDTDALFSNTVTQLSQPLTSMNGDC
SLLTSSGQAIFQLAYRNVYL*
>TCRU_7216 C-14 sterol reductase, putative
MNTGTRRTSSRRRSGTPKRDTETAREKISPEESYNLVVERKFTPEKDKWDGQYEFCGPWG
ALGIMLLSHVLIFYFFVCIEKFQGTMIYPGHPLLQGENMLNVFWEYLSVHATPTWETFGV
FTGFFLLEYILAALLPGVYVKGLPIPSENDYRYVYRCNAVHAWYCVILFVGALHFTELFP
LWKLREEYGRYLSTATIWADAISIWVYISGLRKQIRMSHNVFYDFFMGSGLNFRLPGNVD
VKLFAECRNSWVLLMIITLSNAAAMYREIGYVTGNMCFLVFAQLLYVNAIQKGEECIITT
WDIFYEKFGWMLAYWNTCGVPFLYSIQALYIQTILKDYSYKPWQLALMVSTLIPAYYIWD
NANSQKNRFRMMRHGVPKYIIQRRAFPQLPWGHIENPRTLKSERGELFVDGWYRYGRKLH
YTADLVMAFLWGASCGFDSFIPFFYFFFFISHLLDRERRDDHRCRRKYGELWERYLKLVP
YKLIPGIY*
>TCRU_7217 Enriched in surface-labeled proteome protein 1
MATSSVGSQSVEQLASGGSHDGNKNVNVDSSSDGNPAVGTVGGDTTQGNESPQITVGISD
AADANSPTTEGEEQDEPTVNPEAGVSSGANGEPTEGRDGQEEEIHPQDGEVNAAALSSSL
GNLSQVNNSDGGTVSGSGLLPSLLLPLGLWVFAAL*
>TCRU_7218 hypothetical protein
MGALRYRRHKAGRVRAQLVRADRQCIASIGIAAAERQVVVLLSVQGAKRTASHLAVRRYG

RRDAHLHSFVHQLRVRRHARGHHELMGELILAILLSHSLHLVALEEVRRRQVDIAGAGLK
RRLQCGAAPWSVLHIHAELAIGRCHGVHKELVLWALEFTLQLPLLSIAVALREHVLHILV
EVLVESQGLGGGEHGRHILLEFAEL*
>TCRU_7219 hypothetical protein, conserved
MLSGRTLRSAGARKAAGSCAVRPHRERGFPGNQVEAQRIQTHAQHETTSRPSSGLGHTVP
WRRRPLQGPAVWHRPGRPWRAVAGRRPPRCGSQFPGDNSLLSMRGVDVVRGDPHVAADAS
QFLEDGISRQRNGRRGPPKY*
>TCRU_7220 Fusaric acid resistance protein-like, putative
MSEKSQLEIEAGGSQTLPISYQENALGGHSLGSSGMGLSGRPHRDTARSVAIEQFLLDGH
LNDLIGGGGGGGSGPGLANSLASTMAPGSDNIRGPGSITENPSFFSTKMNDGPDGQVADN
LRRRPSAIELEKQPMASAKASRPMPQFLFPQNVSGGTEGQLKNASAAAPRSSRPHSSVTV
FLPKEAPTSGNFSSRGFPLVSSPLEGDALPMGGNKKAKGSPSSPPPLGATGSAEADGKRS
GPRRTKSVGDILALMNGSSGSHPGQAQLPSRPVSPTTGRVISSSGSFRTPHAVSTAGQRR
NTQIWGHAGAETGARMNRPNWLSAAERLQRDHALGISERRLDSFYYPDSNRSAWQWKPQT
GRLRAADVKALGQSGPPGQGHIVNPQSVNFLLSPNGTRTTDRGSESPVTPRAGHNPSSWG
AMSEQFSGRHVHVRARTSARRGSTQKLALGTSCAHSNRPYENKSSTGGVASLGSTNTKPS
KVENHAENMFMSLFSGAKHEKSRHPPLFANDFALPSLGLDSPGSKKGSPQLSRGSAGGAS
GGAGGGAGGGAGGGAGGGAGGGAGGGAGGDNNRKEKKVGELIQGDEEEHEERHFKEQNST
ALHAIPWDQRAFIPISGFGTKTFSIFSAPLFWEKLDWTVRASLFTVLPTMILTLEPKTEG
IFPLPSSVAFLAFWITMPTFGSGLREFIIALKGYALSLAILMIVILIGPRSSWLILLLLF
LLVLMTSFFAEQVKKTTAYCLAVFLMQLQSNPDGTGRKFVWDYFTTLLIALAFGLAAFFI
PNIRWSSDLSKTYVSILGNSLSIYVQGTCSSFWTRSPLERELHILRLRQLSATASKAITK
AASFFEEAGYEPHSGSFMSAISVRHEFLVNIYQILSSMVQVVELINENPQRIETPLCISF
GNAIVEDLAIISSAMDSMILKISDFKHPVQEEDIQMFREARERFQDRLSEVRQDVILDNE
MYETDESDVLIGFFMFSVDELCEEISNFSTKKSANSTFLEWLKAPINDCKSSFNALRLLI
ATMIHGRSLTRRAKEAIKLALCMTVPSIFQVYALHNSDTSPVAGASIIAFVYSQTGAQSF
TYAVNRVLGTVLGSLTAFLGVQIADSRRLILYIAVAILSFLGAYIQTSPEYFAAGNAICN
SVISVITQYRNPAAAIVRIQQNMFAILIYFCISMVLWPMRARAKVQMAFDVSLRCFREAT
CRLLRNLDLPEDVCEVNTAVTDVLKEWNKKIDRQANFLNGAVTEPTLVGAGFPEISWKKL
IDAQRSLWSIMSMMRFAYFTFMSSKADDVTELSVHWVVLRRISPHAKDLSDLVYATVDLY
LLSIGKTTVVPTSHLTRLRHGILEAEQNISEVYIQTICRKLGGDVSDEEDEEDDGKGSGM
SNMNVSSNSGSSGSGKKGQTLRGPGKNEPGGGKGDLGGTIPTAHSAEPPPQENQKKKKGG
YLMYNLTKEEEGELKRYLASRSLANRQKSVVDENAEDNIKRDRKNTLRDSFVNNRSFLGL
FNRTIRPGERELESNLSEEENERLKKKGKKHRYGELEGSMIELDADVSTPQQKGAAGKRR
SRQDNSNAEEGTTDGGSQVELREKSFGSPKGKKKGDDGDEKLKVPVEYPEASAVLQPKFS
KAQENGSFSAIAPTQYSGDCTSTDPSQHTSQLLQNLTFFNNKRKEFVLSNQDIHSLEAFL
FGVRALTVQLGELQKALLEMQHAEELAKKV*
>TCRU_7221 Tetratricopeptide repeat, putative
MTSTQDDSFTGVIERHTEPKRRRRSRKSAFASAELHERFEKHVAKAQNLFLGNDKDGAER
EATLALRIHPTDHLFALLAVIADSKGQRDRASDFRLLQAFLANDTVLWEELLHEFLQEEL
YYKSAVCLQRLSALETKDKIRYRTLQLQLADLYIGLGEFKRAANILVPLWNGSRCRDFEV
FSLLSSLFFQLGRWNSLHRLIESSLKNTFRPNMVVNAEETRLGFSGAASDTAKMSTDGGG
EAPPPVKRRISKRVRFFGVDDNNDTNNNENFTGSVETEKVRGDEEQHRQERQQRIETDAA
PFFVPTTPLPPTEDEDEDKDFDFSNLTSSGDGVPSKTAGSMPSTVVNSLYGDTIELRTPA
SKRNFLTLVNVHAELLNEEGKFFDTIRLLEFTAGCLQVPLLELPPDLLVRLGIAYAFLGG
LEQQCREVFQHLIDTCSMAEYGDVLYDAANALQRVGLHAEARMLFQTLRRYHEFFLSRFT
GIADADNGNGDNTDNNNNNNVSKGERKMLDDEEAAEVKTVFAATLFAEGQCEASLGNSEA
AYNAFCRVLEIDPRHLQARLALGRMYIYEMKDADRAVMVITPREDEQPIERIQLGAELVR
IFARVEKYVEAIALGVSIFELILSGEEDGDTDSVAPGSSRRTTTTLFMPTLSRASSAIIP
PSAISDIVNGPCLGTATSSAGRLSHTLATSIKASSAVFRTNLAKRGNAPLTTSFYGASAA
ASTAAGWFCFDEERSKDSSTIFRFNRTKKGLKRARLESGKENTHYTNDNDNNDLEGTKNN
IEEEEQIREARRRQRVGEVTRRCADSFWKDEKDDNDSGGDESNNVINNENVHLGKMGDAE
KLRRGEVRQIKEEFCEERDLEELEEEAMLNDNDEGDATTQYELPSLEEVSKQFSDPVMQQ
LFMKASSNDTAIAPRNPWEKNVAIPSPMNAAAAAASGGDLGVGQFSSSTLRVTFRDALGV

LGRVGFVELAVTVISCYTAIGKFTEAKEFAFLVLTRCPRKMMFRHFGVLERPLRLAVLRA
ALASKESEDAYRVGVRLLQEQCSEEERNQVVELLYGLLNRVENGSAILLRLVADRNQAGP
ETLVLLGNRYFLRRSFVRALNLYLAALQKRPNDILLCFLVGLSYMLISHQKRIRAREACV
IAGWHYLSLYQELVRAVDIGRMGEAVYNCARALQYLGLHHLAVPLYEQVAYEFKVPEQCT
LALQRAARFNMYFTYQWRTGNTALAMAALQQKQILK*
>TCRU_7222 hypothetical protein, conserved
MGTTTASPLEKVPRSVGCGAARRFACSPTDRTAQSFHCGNSVGITRCGGVRKSRSPDEDG
LVVVWQLRTSGPSPLRIALAARLAQQQPGIVLLQECRQQSAPATRLTGCGDFHQACSGRA
GGVALLVRHTLPCERLLLLAPTAWRPPPSACANLPAQACKW*
>TCRU_7223 hypothetical protein, conserved
MRRVLLFRNRVDFVATLLQQGRLADMLMLQHFTSRTPQKPPAGNAAERNSGGTKVSVGET
SRRALLTRCEAVKAKAMSTPCTDWLADAYGSGEWCALSESRDMVRVVASDNDPTRVKLRG
TFPVLVQEGSSPASVRLAASKESGEALIVTVPLVQSGEKVRSSAIGGGIRAVTLKEADGS
VVSDAATSVDAFAAEQNILSAAVCSGILGKLEEICALHATHTVRYDALLVRNPAVQKRLS
QLACARFSLDALSSFIASAAVDEPMPLVESVALRMHAKHALAIAMGSARDIIHGTAMLKA
SPHRSKPERLIDYPYAQQLFASERYVLSSLGASSAAETMRHFTPLLMQPQTHVPAGVQGP
LASLLLGGKGGNVNLAAPHANLRVSAAFLEKDIAAMLQRIQQQKKRADPLFVMAIAQYAA
ELFANTAVVYRTTASLTHEDDSAPRDWLLTQAFCADSSARRATILCEWDLSSAARKAIGK
AADLNGCTTHPVELMNAEPARKPKVPSKSAAASVTQEAN*
>TCRU_7224 hypothetical protein, conserved
MREAKIESFVREVPSLSSSPCSGGDGGGYTAAEELAAQIVDCASLLTCVNAEDAVRSIQP
LSPRGRTVTACVSWHTTAAAPDDVCSVKVRFSYSEAFTCRTNSGSDHAYESLMALLVANG
CGAADAVRGLVL*
>TCRU_7225 phosphatidylglycerolphosphate synthase, mitochondrial
MVVLVAYLLVLAVAAFVTFRVFGSNRSGLAPGGRGCGVDFFFPEGRQRRRPLEALLPSVD
AQQAEMLSFLQETCCALPVRAESVRILPSPKHFFEELQKRVHAAKRRIIISALYIGDGPL
ARQFVACLEEKVAEMARSGQPLDVCLLLDYNRMHDRHNLLTLKQLLTLAHSTSGSATGID
NQAMVRVRLFLFQTPCRWNRLFAPFGRAKEALGVQHTKIFCFDDCDTILSGANLSDDYFS
TRMDRYVVIEDNVHVTAWFSDLAHTLCRMSHCVVCHGEALTGHNATNNNNNNNNNNNNSN
IGDVNSNSRNLRNRSNGYTVHKKSELVILPNALGIDPSLESAAFSARAKQLLEEFAARAV
AASELFSPEEEKEEYDTFLFPTLQFARANIFHDSLVVQQLLHKAPASTRIFFTSPYLNMY
APFVDEMLASETTYDFITASVNTNGWRGAKGLAGYIPYFYLQLERAFYFLMREYGCSDRV
RVREFSVDGLTFHAKGVWFVESKDGTSEHTEMPTKGGRSGMHAASDACANTREAEEKGIK
APYLVAYGSTNYGYRSVHKDVEAEVFLFTANKALREALRDELLFILHQSTLVTEERFVRG
AQGRFQPVVSLLAQMGQDFL*
>TCRU_7226 hypothetical protein
MTSVYRDPVSQLAIVPPEAMEREARDALHRLLSLSLNANGVIPVIVYYAHVTRRTRRGKS
IPCYLLLSRSHWYIFKPRGKISRCCRIDCIAKVIICRENYVVWKILEGRDVVMRLGDAKE
MAFVTNILRILSVSVAGRHLLVVENNGEDHTKLHGADKPRLERTGHEEGEWPLPVVSAVE
AQQQCTVENFLMMMPPPPSSQPSQSRSELDAEGTRRNSRVDAIISYMDGHVEIPPVPVAP
EAVDAHAGESYSNAGFPDARQAEAVIPPSVNSPTAPSTAVSSTIRRIQPVSNGNTEKQQL
ISPSPHDSSGEFMQEAVASRPPPPALPPPFIHLLDTEGGGSPEVRLALEKLRDMESRVTS
LERENASLRRSRAHGDLESQPPQRILKEANDPLRTPSPLPSSSFIRLAPPPRISSQQENF
SASAADFERCVAAKTVEERLLLRGYEIELKLQQVSSYMQAADAQHLTHVTSLQEDLLLLL
RAQRADEELGMTKRKGPNSVDIARPKAQTTSRDLLDEDDNVDHEEKEEEGVGLDDYDVWA
ATDEGKEWYNDYFGEHLAACRGKMVRNAFRHNKTYL*
>TCRU_7227 hypothetical protein, conserved
MPLKFAPKALNPEDSMRLAVVHMLRHDNAVILQTFTGNRGSSATRRGRLLRFMPHFPFCP
TERTGETAEEAPHVVEIAPLQLPYWARGSSRETMWPAARTPGAVHPSPPHSPHFLAEGSS
SLFFSISLPHFDLPLVFASPRRERRCSRACRAEWSPRAVMDRDVAATWDEMLSAFCAAWS
AAVRIEKTPFALLPPSLSHPLLAEQPLGEGRVPLQDEPAASFRMDPIVVPRRKLDRQRSE
RMLPPILAVDVAGKWNDTPSAFKSQEAVLQRRFLAVARTLERTTAAPSPPLIVASVDTPL
TSDAAGECERLELASVAVPPLMCTQRMKAGRPWREGGHAGARNTLVHEHSESLFSRMPSC
MTRATELRFPDGKHMRQTLTLRNTAKERLQKLFGLRPPRRHRQKMTEWFSTSKFSIARSR

ELAAAALLPSTVLSAASRVKPPHCSERKRRRGDFPPSPQPLQLLPHVRATAVFAFSSWQP
LTLEEEEEENNDTCCEEDLKIAPWRVFPREVELQSFQQLLERGIERNGKAMRVGNYDEEE
EWYHAAFVHDVNTMPLPYREVSNLVEDARLHYCYRLALHREKRRLGL*
>TCRU_7228 kinetoplastid kinetochore protein 12
MTDFAAFREFQARSSIIAERERAVDLRRKLLQELTQNVQQLTEECKRRDEQLQQERLRFA
QRKAAQDEKVNAKEAQGQAQRERVAALDVEETRLRTAIAEREEKMQRVHEELAQRQSLTS
KLREAKEGLTNLKCQLEEWDAKVMKLETRIAKMEMVVEKRHNVIAERLPKYDMPRIEADR
GNNLEETAGESILLIDEFNP*
>TCRU_7229 hypothetical protein
MARPEADEPPPLGPTVFAVTVLSDDMPGVFQLRLVDNRGDHKTTVAQVQRRWQDFVQLDQ
LVRSMAPKFDAPPPDAWKRSSQEKDTDEKEKGRQKQQQEYMQEYLSTAIAFPTLSLLKDL
QNFIGYSDFVRQVRQQVADRQTTSVKLRHVSPSSPSLSVAVSKKSPHRRPLSSPTSDGNG
GASNMDGRINKRDVTDDARRAENKPEHSDRYFLSPEGHHMLEECFRIMDAGAAGYITPED
MKEFFMCVDAGGVDILRLGKDEACNCEHFIATVESALCNGGPTHTVEEWVDRYWLLQYRK
IFMAVAGLFSWRGEATPPDFEPTHPFDKFELASLMYILTEAGLRLVSAEEVVNWVRCGRH
QRGCALTMEELSALLDTLTKAMPFSEVWLALMPHHGSQQKILRITATYASVADNTVVEEI
REHVIRLRRAAPTEELCVNCHRLEESLQQQAARLTESEAARENLLVHVRYLEKRLEERQE
AFAQLQQEYQHAQTLLDDAELRDVELSVAAEEARRDCLANAPRGEAGSSLVAASPPLLQL
MPCGSVAQHATPLMPSCSSSPPPILSICGAVTYTLPAELSLPSEWSVDVFWCDTTCGGRN
KTERLVFRDADGQRSCAFLFKNNELHVMAQRKGTTSDDNDVSSFRLAPRRWYRLRCFLDW
REKTFSVTLLEGGGNNAGCLKKTVPPLLSCGPFAMVDEHVRGVTVVDIFPRTVLLVSYCN
FFLRYFG*
>TCRU_7230 serine/threonine-protein kinase, putative
MGMDHYRIVRQLGGTTATYLAVDKQDEGKKVVIKRLMDGTQGVQELNVSLRVQHPNIIPF
LESFVHDRALYVVLAYAEGGDLEAYLEELQREKKPLQQVLLLRWFEQLLRALQCCHGQNI
MHRDVKPSNIFLNADATELYLGDFGSAKALLRSASLTSTFVGTPFWISPELLMGTPYSFP
SDVWSLGCVFYEMVALRRPFAPTSFASLVQQITSGDIAPLPASTPEDIRAIVVSMLNVNP
ARRCGLEKALEMTERAIQARTCAAAKSATERVRIERPPPPNIPRRAAGASPNKHQPPQPP
RRPSPVEETSPTEIRRGMMDVVVVERKLADWIHARNHDVNIIERYLTKFRQSDEQVLATT
TTNSSLVDAQRDRQRDRDRGRCVAVSPPKITTPPRRETQEDDPHSKPGPEREVRAQEATQ
LPAQSKPAVRPRRRIMSTKINAAKREQNGNHVNRNVSPLAREPSILHSLNGNVSQAFRRL
RSAASVARWNSPPAPSPQQEEERQLNREKRERERAKMLEMIRERKAKAIQERKAKGKSEG
RDAVAVEIVLPDNVRYVGSPV*
>TCRU_7231 hypothetical protein, conserved
MNRSGDAIALRDTAAYKDFYRSQLHDMSTMSGPLKVAAMTSSMSMGAAGAAAAHPTAGSV
VSEDTVLLELLIPVYLKLEDREEVCRELGVFVQTGRGGVNGLSRKVCVRLTDPADPFFLF
ELELLEDDYGSFKQRLELLVDFSGFPRYLVSMLNGIVNGITPYAVCFVVDNRDTLRGTLR
VLERTEFRTVEHISLLLLRQGDAGQKRYLAERFQHFERAYMREVEEHRSDSAAATANIES
LKSEVAAFQEKCDTLREQLREEVAKSEKNQLASVSQLRGEHASEVLQLRNSLESELRRIT
CKAEEVQAQLMEDVRTKDRGLQEANQRVALLESSVAKLQSQLRVAGDKCDAQAKELEELR
SSNHELRDFRSNATRSISDNELNCVKLQERLRGLVLTLKSRDEEAQSLRDQYQKQDSYIH
ILTSQNDQLTEQNKKNEVSLKKAHHIISTQLRHIKGARERERMMRDQLRSQEALLQEKVD
AIARLRDELASSAERGRVLLNKNTELRDQLEKTDAAREKLAQELKQSQDALIHLQRSTSI
NGRHWSIMSNNNTGNNVNSALGVGTINGFGSTSHDIYHELNKNAITTVRNAGWLPSHGYT
DASSLPEVHSQRGVNGNASNPQGALVGETKNLSKASHDLPHPVNNKTANNFETEAESFSV
NSLAKLPTTSGSQMVNGKSTRHPLDTTAVNVALNSRNQAFVTKSFFNDGGDNANSTANTA
SFMEKPTTNLTKTATVPSAYF*
>TCRU_7232 hypothetical protein, conserved
MKQDAYHSPASIHAALRNRRQEYGWTKKETRGLGASPSSWSRDAHETLSKGSGGGSGGEK
RFFSGLFGNDKRAINDDASFRVERIDSASCLALGDVVGYEFVSEDGRWTWSIGTVIASGD
GSDDTIGHVDRNSTVSEDPILVSLACWKIAPDTQGDPPTWASKHEDHEQIDVRRRMEEIE
EEKAELSRRPCMEKVMEAERIAETARETLRLAVRGERNVLRQMTRPPNELRLAVNAAFSL
LRIELLVEKTEDEWDHMRRVLCSDSFDENLSEADASRLDETQCEFIKQRFLNNPLFTYLH
MNATSHIAALMQKWVTCELQLYECRKELQSTEMRLAELSQEAMQNERELRLHPNSKELTR

TASNPYDEENVRYALQSFQDLGQVSFSRGDEATIVVRSSVFCKFVASTSSPISALDSMTI
HRDRLACIRSAASGKQRRLPFGSSFSEADYPERRHNQSRDAVYQTKLLYEQSIERERILV
RELEQLYEKHVRYTMAQHKILLRSTDFAASSYRYSKRDATRLTAAEDRVRELEEALRQEG
GKLRTLQMNHEKEIWRMQEEAKRQSLEAAQYISDEVSTIRLQQVSLQSDEELGRLQLAAN
EARRWSALLLLEMRKSKDLVIADMRQDYIREMNLLRDDLSNRERRQVKAITILEDLLAYN
GEEREYQQQEMQRRAIKRALKTLRGSMSTELSSDSSPRHFSRNPTSSQGATSYRLPVRSS
TLARGISNLEATVESRELEEDNVVILKDRLVEAVRDRDLIHEMLMQEQRKNHSLEEENAV
LRSELDREMQERVEVEKTAQKLQDEIAAISGSVRSTPNGYIKSGSDNEELGLREEIARLQ
GVIATYDGQLDELLEAEGIENKEAPFHSLREYIAEIKASCVAMQEERDAQAADAKMLESC
LKTAANALEDALIHDERWRPRITDSHHTTWHWKKFDGSGWDRVIAETPEALEKALVHGIA
AACHLPEEYVLNLTYHDEATCLYASFDLRHDPAISDEDIMCRLEECNYYELERLYTHRFS
PEEGIDSLRRKMREKEEELQELRATIAHMRGDSKPPGSGRSKRHLLGV*
>TCRU_7233 hypothetical protein, conserved
MRRCVFFGRGLRTTTSAALALVDSFAPSFRMQSSYAQSAEGAASSSEEENTSQEKEKTHA
ETDALGAPRTPGKRRNIVVLSNTTKAVYIHPMNHIASWYWFITDFHKWFVGIVFLFVGSQ
VLARYRISKLQTVVQAQLGENLLDQRTRDLLSDIEVLRRKDPVRLEQEANVYHEQFWKRR
AIAVSESRNEVRRVELQRGMLQGQARGTDMTEWLGAKAKDDEEREVARRTQDYIQGFHQH
LKSKRLI*
>TCRU_7234 hypothetical protein, conserved
MVKLPGAASIVATAGGLIAGVIVLAVFLFTCWGSLVSAILAFLPEGFLASLPPSSNFFFD
TIRLVSFVETVKYMSLANYVCFAVFVILVLLLSAVEEAMITVKEAIEEKAKLPSTELVRQ
MNGKYDHALAVSGNAYKVKQVRGGRQHERKM*
>TCRU_7235 HAD hydrolase, TIGR01456 family/HAD hydrolase, family
IIA, putative
MQRLATKGFIRPTEVLRRRFVPPWELDGKSADEFFSGLMQSTNPIQTHRKEKERHEEVEK
KSVEEAPSPAELHRIKAIHAHNELVLNQRRNFLPYGANPVVYFDRSQMAALGEYEMMLQS
SGVSANNASYSPEVREMLRADLHQKLPYRYESYVEPRGGQAQWPLHGSAGIVLDIDGVVY
RSHKLIEGSDTAIRKMTELRIPLLFMTNGGGISEEEKARELSQLVGCEIDSSQILLAHTP
MQLLAPMYKNQNVLVVGNPRSAEVAKMYGFDHAISVLQFQAEHPELLPYKKWGDLKKCEP
CSVAFPEIAAIFEFTDPEDVFSDVQIMLDVLLSPRGQVGRYISSTQSVPYFLSADDLLWA
TEAPLPRLGQGAFREMLSAVFESVTGNGLQVTTFGKPRTIAYAFAERRMEEVSAKLGWDP
KALRAIFMVGDNLETDILGANARGGRWTSVHVLSGIGLAPAARRTLSENDVELEWLEEHV
TKTPHYVAPTVDHFFRELLAFPESAVLQNKKPFYGMPNPVDLRETYNFPTIN*
>TCRU_7236 pre-RNA processing PIH1/Nop17, putative
MADAQSAGEALFKNPQFMELFQRALGGEENIRDMPPEGDPRREKWLREIQMRIQEESRNA
MKSKLEEIQSDENGQWMYVLPEPGFCVKCTTSGGGKIFLNVCQHERIAEPIPMEEDEKTD
EIKFKIPLSCGQARPGTDKSGKPCKVYDVIVNPSTVQRCSKDHEFRCFVVSLCIHWIKQK
CEPTLNHEEYRGMNFKVKGDLEPQRIRLSTAPKGANAMGDEIRLPKDNSAALPPTKVGGR
SGTGKLIQEVTNPAIASDAVPSPQAAVPATSKTTTAAAAAASSAASKEERIVPSLVKLQG
EGIYDWSRHAKPVLNPYFRENIPATYAVEVCIPTVTSIAEVEVRITPRSIEISYVDAEDG
APFLSIPLDYPIDEDAPNAKFVRKTHMLKMQLLVKLPDETSEPATKADRDVTEIEEEENR
LAREKREKELEEHRIRMERMREEDEHVMRERKSYVENLVAVQEGMMPPSLKEELEKLPPE
QLRAMLQRLENKTRMGDSIDEMLEKFPDSMIDAISRYIRDKLGIEQRPLPSESNKMLKAV
NSGAASPPQTVKDEAGVKTNNPELEEGRVEYSFAKSSERLFGVAFHNRYLFALD*
>TCRU_7237 hypothetical protein, conserved
MLRRTPLCHVHLFTALVPVNSVKAPQLVSGEHLETAKKAVMEAEPLIGRAPLETAFDLLA
DISNFHKQRELDRVLEECITSYRAELYKPLVTDPFQRLQLHEAIMAAGYYQRSSRTSVLK
GESVRFVLHHYNFDVRRDTSITRTVHNTLYESRTSTSESDKLLGDLLLLERRLFGRMRFA
PTSGRQWFVLGLSLDDIKTEADVHRVLDIPVVKEHGNFEMREEDSGKLWKKIIVFPGPEP
ISSFSEDGDFAMSVSEKDLRLECRIQKPAPPMEFWDRVKDTLLRYWVIWFSLWIMFFMVD
EEIITVTALIFLKWRQTRILEEEAQKTGGKVYIASASGRSRDSL*
>TCRU_7238 Zinc-binding domain containing protein, putative
MLAVTWLLYMRPRHIMFTPPPLARRRGFFRCRVCQNSWGSSNVWVTKTTQRVYQGESCEK
CGTTTKPYYVGRSAETVFNRVKTPHPVKAEASSSRHGKKLRHLRYDWRVQRGRR*

>TCRU_7239 hypothetical protein
MDTMVLVTVVAVASVIVVAVASVIVVAVASVIVVAVVSVIVVAVVSVIVVAVVSVIVVAV
ASVIVVAVVSVIVVAVASVIVVAVASVIVVAVASVIVVAVASVIVVAVASVIVVAVVSVI
VVAMVSVIVVAVASGVLLQILITIVKALSLKKATRQLTTITNPYGHN*
>TCRU_7240 TAX-1
MPGPSTRGRPSVLHGAGTLDGDPFDISGAGWASLENKFNELLRLMDAPANGINALAARSA
HGDRVASVIVQLLDRAQEESRRLLVEGDGEGAAEAGVKTLRLKERFYGKTSVKLLPAYFH
LARTNQFLERYGNAEEMLSLAHSIVLNHPQDVETAMKAELHQAFGLLYAADNKLEAAVQH
LTAATYYLSVMNGPENILTAFGYFDLANVFATKASMEGAMALYDTVKNIWLEHLRGLLKA
IVEETLAARSVKRYEDDEVVQDTGYSSAKAFGKENLADVSKMLHAIYNIQKDRFTPLHPT
TARAEFVLGLFLLWVSKKGEAAHHLQTARATSQHFYGERHPVVQEIEEWCEWFEIPLTES
K*
>TCRU_7241 Snf7, putative
MSLNQLQDLQFQLKFVAKQFGKNSTRCEKEQKQEMQKCKKAMEKGNMDGARIFAQNSIRK
KNEALNHLRLAARMDAVVSRLDTAVKMKMVTKGMGQMVRGMDKVLQSMNPEAISVLMDKF
EKQFETMDVASEYMENAIGQTTATSMPEDEVSTLMAQVADEHGLDIKQHLDDKIRISKTN
PMAVETVDSEKDDLEEQFARLRGK*
>TCRU_7242 protein kinase, putative
MLTLNRRDKEICQELIRKNFTLSQIQSYNEPEYSGWVSRRRRVSNIFVWELNWLATSGNY
LLCFSQKKDSCHPIKIMYLPEAIIRRCSMKEECCVGHPFVLEIVPCLHFVREEKGLFPVK
PHEVHFSFENVEDLCGTIAFLAKISARHVRTASITFGPPTRVNHRIHLRAARGKNDFGLE
LLPLPMREWLLRQGITCAEMAGNETTALNCATTLYEVQMQRGMLEDLPPISEEGVTEKRY
EDKAGVPPFPLPSENEGGALEPLLSAGDPESLFSDWERLDGGSQGEVFKAVRVVDGRKVA
IKRITVRGDHKVPQSLVKEMSLLKALHHPNIVTLYDCYRKGKHLFLAMELMDGGKLTDLL
IPSEGEPVEFTEAQLATLIREVLRALRCLHNARCVHRDVKSDNVLLSSNGEVKLGDFGFA
TLLTSPGGMRRTLVGTPYWMAPEVAGGKAYNDKADVWSAGILFLEMCDGQPPLMGMNPMR
ALLTVSTGPPPVMRTANRWSSLCREFASFLLVKDPARRPSVDDALRHPFIVKKAEPTCRF
VATILQRRK*
>TCRU_7243 mitochondrial carrier protein
MTAKKPWDARYLNPDIPHTNSYYLKCLGGGVISCGLTHTLVCPLDVVKCNMQVSPEKFKG
IFSGFKVVLSEDGCGSKGIWKGWLPTLFGYSIQGAFKFGLYEVFKDLYANLAGEQAAKQY
EGLIWLAGSASAEFFADIGLCPMEMVKVKVQTSPSGTFPTAFGAAVAAMRADPKSGFPFK
SLVPLWSRQVPYTMAKFYFFEKVVRLFYTYVFTKPKNEYSKATQLSITFASGYVAGIVCA
IVSHPADSLVSARGKAANAGKGYGQIAAEMGYVNLCTKGLVARILMIGTLTGLQWWIYDT
YKSTLGLGTSGGTGKK*
>TCRU_7244 hypothetical protein, conserved
MRLSDTALSDAERYAVWCEQIRALFGVSGREEEGREMLEDDDRLFAGGVRSGISDTGANK
HPTRGRRDADGGEFPYCFYMRMLSSGKGERAPKEVNAAAQRYCGDTVGCGSDSDGVSFFS
RQQRREVFVDEDALAARIASNLNAYARRLRREHYEDAPELPVVEVNQWTFRDGRVEALSA
KVNEELHELLMYVRRRNLLAEQLRRQLVHTKQLLLFQKEATS*
>TCRU_7245 hypothetical protein
MEYPGSAFVAAQAEERRMAQVSRRSYMPSWMADPSWLKSIEVPREYATGLSFEELRESVR
LTFASRLSVIQKAARQATTSVLAESARRTMSSWAENDRKNEIASSQSSLMSLLADAIKAV
TQRTPWDPVDCGTEMRKEMLAVLLKRFLDRSLDPGAVGIFAKNVLRRASTTDVAEELQYL
YVAFTHDKTWNGEDPYRRLENFIHFADNEKFQEHCLEEVRRRLHMLNVELNGKNNKEMHA
KKVWEDIHGPQRGECFGGSITLFLTRVNLSGISGSDASKNVGGAKKILPKRIKAIWTLQQ
EGHRVASAVVPGKSTLKNGTYTWQPNSRATLMVPKGAREHFRNYAIVLELFLSQTSCLCS
PSRGKPLASTTITVDDALYVSVARPNSPLRTSAASSLNDAPSRSGGCENEPFSDWNVGIR
GYHFSSVLLSQPTTSHKNEYPYSIESATTLCNMCCLNNDHNARPPPINIEGEENVTVRKV
GSGKIFQDAWSKDHHNMFLRLVDILGDIDDMGVAIIKAYCRRYLIHGELETVALLSAVCT
HSNLADQNSRDLCTNSVALLVKYRGNMTTHVTKQLVKESLDTTYSNVIDTLLSLEEMSSG
SLTSSSVFNPREAGRVVEDLKNILLLIDKGMKINDVILQEAQRDTKPLVEALEKLDGRVL
REHRRGVVRETATDLFLPDLEKREDAAQLTGKAHCLYTLITDVTERCKRAFSFAKMSGSS
SVMAVTMCRIESIVNAMSVPLRNVVTRILACLIRAPEPDPLGDTLGFLVSTYGLVMDLVG

VLDPEDGTASICRTLASCFTDFLSSWFPLCESHISAWMSSIVTNEALEPLMRNTVHFNHS
PGLFQDLLQALFAVFLRVFAWSEPRQHEMYAVHFFRLVQTLGEAFVDAVVARGRTSSQLE
EWLVCLSNLNRYQKMVREFGEKDVTQQLIPLLCDTENLMEHQRRVIAEQARASTMETKEE
FERNIGRVLEQSVLSFLSDLTNAKTLEKMPVTPSVMKDSAHRFKIYLGMQFRTAKNNLDD
ELFVEFLNEVVLRSYYGAFHSLALREGKRPLPETHVAYLLHLMQVLDQEIELLGGNLLHT
EPLTSRQRSGRILTALLGQSSQVLVQMAKTERLDRTERVQVMLLLRSRTDGIAKQYFTTS
SDK*
>TCRU_7246 hypothetical protein
MTSALGLFSNELNGTVYDTNHHCYMQKLDLAPNRFSGSLPKSLPTVRSLVALLLENNQFS
GETPDLSSLQNLRHFARAQQLLRPSRRMGFTNDEFGIAGAAIQSLGRSSSRAARENYACK
LFRKQLLRRCSQELRSTEVPEVLQLYRLQFDLPATLFSSVISASRHTERQLKEQT*
>TCRU_7247 CS domain containing protein, putative
MAHIPTKWAERKDKLYVTLQVSGASDVDVKFTENTISITGKGITPKASEPHELNDKITLL
KEIIPEKSSFKVLGVAIQVCAVKKEEGYWNKLVNQSSSSTANWLSVDWNLWKDEDEDDDG
PAGFGDYGDLSNMMNMGGMGGMDGMGGMGGMDDSDDDDEDEAPAQAADLQDLDAK*
>TCRU_7248 The ARF-like 2 binding protein BART, putative
MDGYSLLERLDAFFSEGENTDAIGNFLSEEQGVMQLLGQPTDSQEALEFYSLFKRYAVVV
DNLLNAFIERESKLGYVIDLEQLAAAVMNEWHQEQDFCRYVCTAYIAGALDFDSFKQLVA
DVNAITAYPFGDESSDADSVTETNTQEEEI*
>TCRU_7249 hypothetical protein, conserved
MDPLHCSFANGGGFAVEFNPIICLRLYRRRDIAALATEITDAFDLNGVVVPFRPVTDTYL
EQLGTSQELARCLSEHEEPHLVRSLQPTDFISSLLRVENVVVATSLGLWKTTRYTNEVIE
AARTRFLRGVEEKRRSKKSKLPIRLFFKFLNEMLIDVLVMSTDRKSVVLSCASTTRRLAM
GAVAGEKVTSVPSFRTLLALEFSPSEGYWSPLLLPVQLQSPKLKLDIPEIRDDTGSCSNS
DFLKPQTLTSIFGETAQSCNLETMMLDRTFYNPQRISAKTSRDLQTLEGKGDGESTSTHS
PFTGMRYPNISQTDLQLIEVLQRGLHPVFRRNRVRFFVTFFVAIAAFIVGLVLIIYASVT
LETCCHHVSSRACLNGAEDPPRDNRSNLFCSAAKNPALTEANQSFFFGHLTSPGGFLVAA
ICCMFVSSLLAGAVSYFTTRAIAQKNSRPFFYKLMVAFHVILGAFACAFSAYTLSIFSHT
VHEVPCSLFSGTVAASCSRFQALYPEFTIDVRARHPVHAVFALSFIFLFFCAVEFFASLM
SPMVDDDILHALQKAKPETNVFYPSVYAPDGITDVEKRKLRGHIGHLLHMQLQKQMQQQD
TLLTRNLTIGEMILAKREKSLMVRPSQGSFVMNSRHWNEETPQNPLHYMAYSDNTSGGSS
TDREEERKELDEREEKRGLPPRLLAEVEKISRRVKTSMDGRTDLVKPQLLSESPK*
>TCRU_7250 predicted zinc finger protein
MDVKIKGAHLVGRWLWDCRNDTCGICRQHFEACCPQCRFPGDDCPILTGRCTHTFHIHCI
ERWAEREQGNAACPMCRQPWEF*
>TCRU_7251 hypothetical protein, conserved
MMQRSSVALVALVTRAKSSSGALKGEVVGGTESEQLSAYVPSSSEAPELLQPYVEPTPFV
SARRLQVFFASMGIGATTICVVYYLLSKSMSNNHEEEQRYLQRVVESNRLAMMEPQSLVP
EFTAPSSFNELKEKMQQHERELERKQAQINRNTILLHKEVVFRLKVWWNASLTHIQEAFD
RLGTVIQRRKERAAEAHIKRILEEEGYDLVKLRSGKTHIW*
>TCRU_7252 hypothetical protein, conserved
MDATSLPPTCGEVMDIPGIPSVGCVAVLQYEMGTAAGFSCCVVASREEVYILGPELLVRD
GSLISVRIWRPHVEKKLTRVMSLVAFLLHPAADEVSNVFQKHKVEAEIDEVCAVVAWEDD
DGQQQQHITTLFFSLLQALSTPQNVSVKSFETSFFYERNQQRVLRLFYSPSFSSEFRKGK
HVVLCSGYDETVRKHACLTPSEERNRHILTPGDPRGVLSGIFSFVLCNSVVENDVCRWDV
TWTTHAPAWVASWILQSPFDGVVCSLAVQKEEASSVVAAIGKTNGQLILFNADGTHVSHR
FGGPIADLAFVSTRCIRGDERYRVCAVTELIDQQKENAFSSLNRIPELEVADDGRRSLVL
LDSLGRVIVLRDVTEGMASAQIVSDIQQFITLAENRASHPSSGSVAGESAAGRPVTVSSK
RFFDISSLRQFFYRGKTKRIQKDRQDDKVDSISTQESDPIRQPEQENGMFAGHILSRGLL
SLASLPGPRGCTELVVSTMGQSIVSIPFDKNEGVFSIAGFIEASEAMFFIDFVDFFNTGV
TELVMAGMHQVLVARRSRCQQKRRAALLLRLLARQKMQDATSGDALLGGKV*
>TCRU_7253 Protein of unknown function (DUF563), putative
MYVPFSGGAATAGLCDTHAGGTERKTAAFVSNQTRAQRRKTKCVQLRFLILASCVFVAIT
LVLVALVLGDAKSIPEKADVRKNARANKKQIAPDCWARPAWNVSLEMDRARMKIKAGTGF

FAKSIDELTQQVPNITKLNKSCHFAYPLKRHITLFEYASKSARGKYGRTPVTFFDALQQE
VEGRVVRFSESLPRIVKQTPVVLSPFFDIGKGFGLWGSFFLGHLPAETGDQADVGSHGVD
WCLPLEGGYSGSQVFGPQPPLYAAVFPNAVVSNSHVITCNGNVYTSGGCLRRWYLPKIQS
TKEIDWRGVVVGLCDEWCKGYYHFTHEHLPRLALVHKILLEREDAILALYAPIKKFQLQW
LTDVLGIPSYRILRKPGPVHGHLVLYPIPGGCGTLFTHLTYALRDIVFERLQLVPPIPSK
KRKLRLLLAERERLSRMPSNYRQLKKMLFEEYKTFFDFGVFSGKLHIRQQVRYFYDADVV
IGPHGSNLANAMWMRHGTHLMEFVSYKYANMCYHTTANTINVTYHAIFHNAEKEGSYVLS
YDEVKRHMDHAVEKLLKSP*
>TCRU_7254 Uncharacterised conserved protein, putative
MKRVSGSKYKKFSQENADYLCQEVQRMEESQVFYPGAFVEALRELTEVLIWGDKNAESVF
DNFLERSMMSTLERVVTNAEFPSAVKVQAIQCITMMLQNLTRKSSIYFVCSNNHLNRIIS
IFIDDNDEELFSIYVSFLKSLALRLNEDTVQFFFERETRAFPLFDRASKLLAAPDPMVRA
AARQVVISVAQLNEPAIKNFLRDALQEVFKLISTLLWSQIKNLAEAAAEYGNVERHNANE
LHLMGISTLSDRLEDIVDDMFYINDLFLVPHDFAPFYLECVLEEVVIQPLLMLLENLPCD
ICCFSTNSSFTPCVSASVALSVLTRWILLNKSERLQRLFKEGLLNPSASHDGVMKRLLKS
ECAEVLSGVVVLLKAMLTSGLLENEKKGGGNGPTPDGDETDNEDISEEALDEKEMHVMTD
IFNVNWSIEPEHEDSFPPLQPLSMISCEIFLGRMSQQVENAVRCPWFHGLMSAIYFFITH
PAYTRFSVFELALSVLMDFVKCRQECVVLFRGLLFLCLFIVRRRAVTCAESSALRQDGTV
TSASIPAAAAASTTPNSVHTTTAAGNKNNKSAGAWLRTPYEVVFIKLEHVSHEFGLREEK
LRGNLSNEASFLLPLLPSLDFIRSERERGSNSPHVDCWDVVLRNFREYIAVQKSVAAVVP
LRNRAAHDQSEEEKSEFLMWLTIRHYAHRMLNREDGFLLRLRDYGVRHHVGTNVSLSQSN
TVYFRCEFVKGRFLFGASSPMVAAGTPMYMLLSETEVLFLCAGDALRPVTDRGVTLCVMF
ALQMIYVQALVSHSPFSVIVTHVHPASPLQLHIVFRHRKAAASAVNMITELSSLCRFSGA
ALVCRALNQDGALHVTNEGVSKAPMNSFNNA*
>TCRU_7255 SET domain containing protein, putative
MKTTASFKRGEIISPVPADYIVEQDALVLSDGCRLRHETGFNATIISRFLIATKDLQMGE
EVLVNLNVFFYDVGDEKAFLFSGFKNLAEEEKQEVYMYADENVRQQAIADGFVPNRKESG
IDVVRTRNSQLVTVSRGRHEVNNIVFSSTGVLLPFPVRSTVELPGDQHLRLTGGSEFIRH
ACQPNLRLAIEGDSIHGIALRPIEGGEQLTYNYLCTEWDIAEPFHCACNTDSCYRFIRGF
YYLNAEEKALLFPIVTAAIQEKYHAALPQTASLASLEKTTVIAVTLEGKVAAQRYVASGT
VLMNVNRFCVRSREVVLDSSHIPHSCDANTALLEGRLVASKPLLSGDPLTLNLCTLFYEL
PLPFECHCGSSNCARLVKGFSTLSEGDKSGLIPLAERSVLLEAARHGLNVESSSPLVKIR
RYPPMGEVTFAADFIPKGTRIFHMRGLVIPFPTVYTVYLGDGKHLLFADGAHCLAHSCDP
NTRLSIDASNGTASCFAMRDIEPGEIVSFNYLTSEWDMASPFKCGCGSASCFSMIKGFRH
LDEESQLRLWPHATSGVKSLFAQHRRSALPNLDNSLVYLHENLSELRLARDLSSGVVLFT
ATTFCIAAGEVVLDDVRLKHSCSPTAVFLEGRVVLSRASLRGDAVTLNINHLVYNSPVFA
CHCGSANCVGEVRGFAGLTDEQKNTEMVYVDPRVRAAAVENGYRIQSSCPLVEVKPNGFM
GQATFAKSDIREGTRFFEVSGLVLPFATIYTILLVDEQHLLFADGAQCLAHSCDPNVRII
TDNTRKRIGCIALRDIKKGELISFNYLTTEWDMQTPFTCLCGAPLCYREIRGFKYLGDEA
RQKIWCMATPGIKSMVIATKAEDTWAQIASTRFFVSNDGLLHASEDMKDGTVLMKVSCME
IVREFLSLDGIRIRHHCSPNVAVIENRVVVIFPVSAGEEINVDLNCLSYLLLEAFECNCS
QFKSPHLIQGFKWLNEEKKHACMIFTEPSVRAAALKDGYKMKCDSSLIKICEGRTGLEAH
ATANIPAGTRFMTIQGLCLPFSTACTVQLAEGKHLLLFGGAQFLSHSCDANIRLRVDAVN
NTIECEALRDISVEELVSVNYVAVEWDLSAPFHCLCHSPKCLHEIRGFKYLSNAQRLAFQ
GQVTPAIRQLAASHAIVNLPPNVKGNTAGMLQVTSPVTRGTVLVECTDMDIQPTQVSLGG
DSYIIRHKEDANTVFVEGRFVTKRNMEEGEFLTVDMNFFIYDTSSLFPLAFAEGCQGFFH
LPEVTKQSQLYLCEPSVRAQAMQDGWIVKSSSPLVEVRRNGEMGQTAYAAANIALGEVLF
HSTGLVVPFPTMYTICVGENKHLLFGDAAECIAHHCDPNLQVVVHEENGTFDFVALRSIT
VGEMLNFNYCTTEWTMNSPFVCLCESVHCAGTIRGFLHLKETDRQRLWPITSPVVKRYAS
RESY*
>TCRU_7256 hypothetical protein, conserved
MLSAAPPAYDVEANVLYHKIEKLDKDLKKRELHLAELIDEVVYAEDRKDKAVRRAESARY
LVNQLEGMVQNLLGYLKLIEGDILLPAFLELS*
>TCRU_7257 hypothetical protein, conserved

MVQNLLGYLKLIEGDILLPAFLELSCVMPQEPLKSREVIAQTLEKIVEDSLSSRTKKLIA
AVREIPSETKNLATREVFMRTVAKESVSVEDAIVLSGLLLERKEELTAFMDDLRDRVQYI
LQGNRSESPGEGMNRSVGTIKNACFDHEELQEKLRRVENERDELRQQILSRGENTLRMNP
AFQEETEALGKQLLDSSYLLSKAQSNSQAMRVRVEALEREIEEMCREKKMLQNEVQFLKR
DQISRSRFYVEERRVEEGSKQLRAELDRIISEHAVIIAATESKMADLRAQNTILLTEKQE
YKQHMDDKNHQIANLQRTNDLLRRELFELQQKILSSSPSSIKNEHSESVQGLESTVAGLT
AELNALERRLADVSARNQEERKQIVAQYEEERSRYKAERQECDALVERMANELEKLAMEN
RSLRAAATLQQL*
>TCRU_7258 hypothetical protein, conserved
MASVGPRLAWRQKIRIHLKAICQAVPISILIVAEGRDLYYRATWQVTELPPSELQTGDVI
VICNRWYTLPRLDHMLYSLLSKVLLKSTWDDVGFIWVQDGVPHICFCDFEGAKVLSMESF
VESRMPRGMAVRKLTVDDPHAGRTLISSVAAFFAVEAQKLTPHPWYLFSASMRHGQENKY
YEFMVEMWRQRRKIYEMGKRNASSLAIKGQTEKLREMELMQKHLATFQKQETSFRLFNGS
LVASFLATFDLLDRNLPSPSRYVPQDFAHDLPFKRVAMLEEPVVFFRN*
>TCRU_7259 PHD-zinc-finger like domain/PHD-like zinc-binding domain
containing protein, putative
MVLKPDGGFSQRKVKHVTFGSVTILQVPRRQEFTLPTPVESQASRELPLLASPTLEEVKE
SQGMGIMTQDSESSLLLTQAASIYSLDSQNDLSPVPFGRRDGEDDDQYSPPAACTHALIS
PTQAMLSLGTGTQCACDTLPDPSLNCSAPIDKASEILGGSPLSLSPDFSFISLKRNKRNE
DDAMAAAGFTRCRPEKDAAPSATCAFCHGANGVLNHYEDHYVHLGCALWCPEVYYDTQEA
TLKNIDAVLKRCRDIKCAYCRQLGAPIGCVNSQCQRSYHLRCAVGAGAFLDEKKFELFCP
KHRNRRDRT*
>TCRU_7260 hypothetical protein, conserved
MLDASFINSSLKSALGNGVEAVILLDGNGVLLSSASLNPEYVCQKEHSMIVAATGNVWRA
CARNDLTKNKLTNEMEPEALEQVLIDFGCRKICAMSVGGSAILCMVGTELEMGFLKLRTA
ALQRRLDGHLRPVLLLPS*
>TCRU_7261 60Kd inner membrane protein, putative
MQHLGRCISLQRAMLCPFLVTSRRTFSVAGGDGVVGGEPQNYFEYLDRFWNRQWFGATEN
LLPLPDASPFADLFVTCQETLGLEPAIAILLFGALSRLCTLCFSLYGERASERMRNAMRR
LKAPHEAFQRVYYREGSAALDIQLAATTLKGERRRVFLEEKTSNLQCFSSLLGTPVVFFG
IVQTTAMCGDPRLDFGTSSFLWCPALTMPDPYGVLPLVFCVLTLMNFELSISKELKKGWM
SNLIWGGRLACFCILPAVAQIRAGVALYFLGMSLVGLIQPLLLRSSKFRTWFNFPLQQPE
LDNAKTAEKVDDLHARMCVQFPYLTHLFSPESEENTGLLRDTGATSPNSSHSRCTAGVST
RGMNPIMRGETARPMGRWSSISSSAGVVKPATLPSRRGANFAAGGWKATQTEFCEEDFIP
EVAGVGRNSGKEKQ*
>TCRU_7262 protein kinase, putative
MLDIQIGKYAIFVDKVEAVRRRIDLLAQWPASPLLVEYKDARLLPRHLIIRAESPIEVPL
EPLQHPINEEEARWVVRGVLRALYALHSRRLVHGHLRLEVLRMHHPSRRIVLTQHVLPID
LFTPSSDVGREVWRGCAPEIKRNSVFSYSADIWALGAIFLQLLAPAGKVLETEDLLAVDV
LSPDVNSLSPSAVSFVVQCLQEEAGGRPTIAELLMHPFLIDKDDEFDSYESEEESTDE*
>TCRU_7263 chaperone protein DNAj, putative
MVDGGGIGGSDESFISFAFAIVSVVMIILYIPWLIRHVRSAVEYYGSSKKKRSGMMSPIE
GMWDSLTYIPRVLTMLAMNPDMLATGARVCWDEKIFFLRCVMPKFLKFTFRPKILVLWLW
AILFSSAMYVTLTFDAHAILGVAPSATTSEIKKAYRALSKRYHPDHNKTDEARVIYVQVR
RAYKALVDREAFEEEESKNTHEFSVGIALPRFLTSREHDGLVLFGLLGILIGVPIIVWYK
FRGTQKIPHLLWRVYFDKERVTSFMKHFGIPEDAKYVERRDSRRCTLQVLISLGILPPNT
RESVLVNFPPFPDFITRCVEVDKNMAYLQNFLDPTAIEILHEYMVSNGIRLLDEFEAAHV
EANPSESLDFKAISLAKYKTIRYLFLQHLVQVDEALEELLEAMGGNLPSARKLLNLHVEL
LDLLRLVFECEGKPLKQHVQKLIAIPQRVSDIVDSLEPEIETIYKRLYRNSLQQQLGNKY
ERRLFKASMRRV*
>TCRU_7264 hypothetical protein, conserved
MWSAVGACPRSRHRVRRRAIAAALLALLVALALVAAAAWMPAVHAVVLRLRGGTVDRAIT
VGRAVDTVMMDGVSITNGVAVVLDVPAMLPGALHIELRKCVCDGGAQIYVRGYSGEPASD
RSLVVSVSGLSGSYCSLVFVHNLPAHTNVTVRDSKIVTAGPMRYSQLSGLTDAVASPFVL

HATSLLQSQLRVSNTVLRSTEAGGSAVYVGGDVDLLSSAVLLDGVLLEASGGPTASAMRV
AFSSRLSLRGHSVFSVTNVSVVSSGGGLVLGERLAVFDSVLRFVGVEGSVTSSLVRCDGG
TVGGGGWLELHDVWAVGEASSVASLSGVTLSGGAVSIARCAATGATLVSGPTITSGAVSV
QCNRAGGRVLRSSGDYRMAGLLSVSVVPCDGCAAALACFDALTASFSDCACSCLAGGVGE
ACLPFDVPPARAGGGGGAQGCVSGVTLTESVTVGGGRATACFDSVVFGGPITMAVDLRSM
DAFADALNVTLRHCVLEGGAQLRIGGLSESTAHLMPHALVNITNVTSLEGTIVLHGAMPL
HSSVLLANSTLRATVGGSQYVTTTRGYEGLRYGPALVLDGVRLLSTRFVMTRSTLFCGGE
SCAAILLERGLGVNLSSVFYMDNCVIRSRTHVMYALASDLRVSGGSVFSIQNSSWIAPST
EYYKGACVFKDVAVTGGSALQIVSSTFRLGFAMLMANTLTVTGGSWLVHRNNEFRTAYVV
YIVKESSVAFRDRSVWSIIYNDFTYGSYSSTIAHMTSKWSPPSDARPIICGVCNEAMGSP
VTDYQEELNIGTPVTALDCGACTVEAVCFAARTSSISGCECVCAAGGYGDTCLPAAVPDG
LGPLPLPDAKDTEVRCVHGGSISSVDDPDPGVRGLCFVNVTFTAAILLDLSHFDAPEQTL
NITLLQCVLMDLSIKGSGARVHVNVTSSMLDSGALEFESDFGVSSQILVVGSTLVTTSSH
AVAFLDFVFGANSTLLLLENNVEGNDCAVYFADDLVVDGGGIIVKGNTLSTMETNGMGSS
VYVYVVDMKNGGYLDVENNTMGAVNGIYFSDETTVSSAGLLRVADCDFAGSTKVSNSALL
YLDGSLILEGGAQWRVEGNDVSAASVLSMTYSQSTIQLSDRGTTVVLAHNRQVNRGMAFS
SFAPSTTILASPAKFVVGCNLQDGEEVLYDDVFPEGVVVFWCGTCNDDAACYMPGTESVD
RSSCSCSCKDGWHGASCLPFEVPDTVVPPVAERAVDGDTSCVVNQTLNNLTLNMWKTHHC
YVGVTFSGVGAALTFSLNSMPLHLPINITLTGCTFRGGAAMRFVGGAESAESSGVLIRVS
QTVMRSSVVAFIRALPQHCDIAVTEVDAVQSPAVYLPDTVNNKLSVVTLHDVVLTTSSLL
VSNVKAHAMRYDAFGLYSTGTLTLLHGSSLYARYCSFDGYTHLFYLNILGVCDHSVFALL
NNTMSSGRSLLYQCLDFSVSDHSVLRVVGNSGSVSYAIFAEELWTVERSSWLDWRDNDVG
LGAMFHESESTSFTIDSSSVVTLTGCRMGSTGLSWLQDGLDGVVGVPFISG*
>TCRU_7265 hypothetical protein, conserved
MVYPEVAQAVGSGLSWLCYRNVTFSGGGMILTVLIGAMNDDVANVTFDGCTWRDGAVLLL
LGNAYAAVGSLNIVVTGNTFRDALLSPEGVFPPHTNITVSGNHFAVTRLISRSGLVLRRP
SCVSMNELAISNDSAVVLSGNVFHSVTASSNAIHVVECALRVSWHSVFAVVGNTFHMAGA
NSTLIYLEGPSQSSSLSVLNNSAVVIRGNLVTSQVQYAIFFRWALIVESKSSFLFQGNDI
QGSSVVFYSNFLSYIYYNSWLQLSGNLCRESPLDAFAVLRAMLSPRDSTVSVSGNRFMSS
TGTPTVLWIPAAPRELTNGAIVAACNTVNGEERVKYIIPSVYNATILTCGDPCAFAASCF
PAYTTTVSSDGCACTCTEGGYGDACLPVAVPEPPSTDGADLCVRDVRVDVEVGAGFGTSV
VCYVGVTFAADVVVDVESMSGGVRNVTLANCTFVGRASLYVVGCRSDPPAGERVDVLISG
LESRSGGGVVVANRFPPGSRVTVVDSVLIAEKRVAYRGAYDLGDASACLVVHSVDLTGSV
LTIARTHVAAVFRGAVGVLVVGGVALSSRGALYVDGLLVQTALGLCVSVEGGIAASGGSV
VAFVDSDFLLCKHAVSVRGAVSVSSSAVAFMRNEFLLTEDYAVAFYSTVRLADGSMLLAK
GNVHDGVSREMLHAAGAVTAAGSTLSFVRNRALLPRMLSLSLLLAAGAHLRVACNGAGGR
VLSTAEEYAAAGFGDAGSIDVAGCDACDWDTHCYAPGTASARMENGVCVCVCGSGGHGEA
CVPVGAPALPPAAGTALSVFVREGVAVQSVFVVPAGASEVTLRHFVLDGVSPVLYVPWMA
RDGVRIVVQNVSLLNGAVLYVMGGRSLRGAGAEGSDEGGPVELSVCDVEALNGALVLTGT
YPAGSVLTVTDSLLVAARPTPLVYLPGSQSSPYAPVLVLSGLRLVRSVLVVSGVALVTVV
TGGRTVVVDGAVLELVGGGVALDAAVFGGEYALYASARVVASGGAVLRVSGSQVYAAHGL
VFGGGVEANASAVVVNDNAGALTDGALLVLRGLASFASGSWLSVRGNSISGRLLSVPSYP
RSADLVQSTLTLHGNTGSGPVVMDGTVALVGAGRRFVVGCLTLNGQALQPMDYRSAGIIG
EFRPVACGVCDADVRCFAAATRTMSRSCGCRCAERGRRV*
>TCRU_7266 hypothetical protein, conserved
MDSEATEQPPRDATQGQHSHDTETEDLTKNAATGSPAETKTSSTSTTGSGDHVQNRADED
DAQSSKGKNDSLEADKTNVVPTLSEEAPQTAETINAARINHTVTPVDSDGSTAVSHTTSP
LLLLVVVACAAAAAVVAA*
>TCRU_7267 Protein of unknown function (DUF3676)/Trans-sialidase of
Trypanosoma hydrophobic C-terminal, putative
MQRGSDLQPQDPQPAELTEVTDVEMSSGSYDEEMPEEEGEADGRSGGSTSSVGASSDMDT
ATETVDSEHQVQQCIEPYAENDDLRSTGTGTTGAEESLILEAGGSNSERAMGSDSSLTPS
GIDAEPTSAEDTDNVSRTDGAQFSSENGEEVPQTVDTAPCNTNTAPGETEIPSESNATSL
SDTEILPENGQLGELLSMGLSRDSTVHVCVFRVLLLLLLPGLWGIVAL*

>TCRU_7268 Enriched in surface-labeled proteome protein 1
MGQIVPYYFANNKFTLVATVSVHEVPQSGSSPIPLMGVRMNDTSSTVLFGLSYTHDRKWL
AIPEKRAISKSVGAWEPNKTYQVVLQMNSEYWTVFVDRKEIDRKSYNEDLFNSHRISHFY
IGGDSNDRSATDGHVTVTNVML*
>TCRU_7269 Enriched in surface-labeled proteome protein 1
MLITAPVYPKDDNGEGRLHLWVTDNARVHDVGPVSREGDDAAASSLLMKENNKELISLYE
KKKSDGAYNLVAVRLTDKLERIKEVVKKWKDLDGALKKCSSGSSGNVDALRKGHVQWSCS
HGWACWLLVW*
>TCRU_7270 Enriched in surface-labeled proteome protein 1
MFRRVFTSAVLLLLVVMMCCSTCGASHAVESNVRDTVDALRGIGWEKLDNWEDVPDAGGK
YGLLLGPSLVDLQGHVFAIAEAHCRDGGDCSNVSFTGIASKYLDLSGVAGLTEISKADAS
IFGAGLLKEGSEGINTTNGITRPTTLVLGESVYMLLGNYSHTEQQVEGKNERGLLLLKGT
LTDEGGRKKIKWNETHAVEPQGKRESGSLTELIGGGGSGVLMRDGTLLFPMQAKDKKGTS
VLLSMRLPKSENKWELSSETPGNGCRDPTLVKWEKYEDDERLFMMAHCAGGYYDFYSSTL
DGVNWNTLGEPINRVWGNSQNRKGIRRPEWIYHRNH*
>TCRU_7271 calcium/potassium channel (CAKC), putative
MFEPRSQMAYRQDTFRNIRSLRKLFEVMDQKYSSISITFLIIHLIMELASVVFYVWTAVV
SEATSVSEFHWNGTMFNIEFGLNIVFFLEWVALFFGEDDKIGYCLSWLSIVNAMTSIPMI
VIGIGGLTEPSWRSYWVPMYLRVWWLRDCVVVLLDYPQVERWMKDVTREVCRFVATLFAG
LCTCAGTLQIVESTTGSYMNPFNAFYCMVVTFSTIGYGDIVPGSTPSRLLMTVFIVFAVS
HFMPLFQRLVSISRQRLHYNVYNSRGGRKAHVILAGIFTKLGVKIILQDFYGGWRRYVDL
RIVLLSPVEHPLEVKLLVNLPWFKDRVLLMIGDPQKEADLKRADARHADAIFLFGDTFPA
TFHTDYTLIQQSLSINNHDSELAQYLYLRSERNTKHVASYAAGVVEGERLLHHLLGLGVV
VPGAIPLIVNLLRTYDPFTLDMKRTLHWVEQYELSLQHNIFCIDVPDAYRGRDFHRLARL
FFDHDVTLIGVITTGGMVQLNPSRVATLVGKIIFIAKSPEEVKNAMTEVEETRFSTIDPE
ADDQPCYPTLVLSNERNGSTSWAGEFSGHFGSIQQINDAYDFENHFVVIDLSIANDRAAE
TEGAHEGTLTSAAVNIFHIMQSIRQSYPQNDIVLLTKDTSFSVYFDRYWHGVKGAIPIKY
VDGCGLNTNDLRRCNLKQSAGIVIFVFGDTSGKSTSGVSMLVNLSIASILPSSHNIPVVV
ELDSLQHLSLFPPYAEHSRLRQKAEVDFVFEPNYIIGNAISRHMLFPLVHATYFMPEFID
IIDMIVSGVDEETPSLGRLSLSLSHEVIETYKDVVDYCLSLRYLPIALHICISDTRNLSL
NGKRFVMTNPPKDLPVDREKDGVFYLLPT*
>TCRU_7272 Protein of unknown function (DUF3128), putative
MTALVDAREVAEVRRVLLSLGYQNPSADDIALTLQQVKEARRREAEVQQQRSFSPMKQNE
SFRQVSASPPRGANDVTMAPDENENVEVESEEGNPRRTSTSQKQWPGLSSHSIRGGRTTP
MNSTGTGRHPGRGRVAGTQPHREYCYREPYHSDGSVVVERNAQSMRRDRSGRRRMETSET
FHLGVSNNAGTKETIMVPTAVGTGRFIDAGGLHYPDTGYLNPQARLGRHMRRYEKGLKAA
YTSKYNDDLQDETGEESDSYDEEEESYEEGYTEFGSHEGRGRNLAMCYERRPRQPPVTPE
IPLRPSRVLLNQRNANIIYSFTGDIRYKYRGGLGAPLCAVLGPNGSTLRNRSDPVRRGQQ
MREIWKKDKFLAQQGRKEDRWRVRQSMLSWDPS*
>TCRU_7273 ATP-dependent DEAD box helicase, putative
MAQQGKVEPQDQDSFLDDQPGIRPIPSFDDMPLHQNLLRGIYSHGFEKPSSIQQRAIVPF
TRGGDIIAQAQSGTGKTGAFSIGLLQRLDFRHNVLQGLVLSPTRELALQTAEVITRIGEF
LAEGNSSFCATFVGGTRVQDDYRKLQAGSIVAVGTPGRVVDVTKRGAMRTEQLRVLVLDE
ADEMLSQGFAEQIYEIFRYLPKEIQVALFSATMPDDVLELTKKFMRDPTRILVKRESLTL
EGIKQYFIAVEEEHKLDTLMDLYETVSIAQSVIFANTRRKVDWLAQQLNQSNHTVSCMHS
EMPKQDREKVMSTFRNGSSRVLVTTDLVARGIDVHHVNIVINFDLPTNKESYLHRIGRGG
RYGRKGVAINFVTQKDVEVLREIESHYHTQIDELPVDFAAYLGE*
>TCRU_7274 hypothetical protein
MPTVTGEGRYDSCVSVLALVEGPYPVHFSIGCVVHPFALIVAQRGPIYFGAYCIVEEHAC
IINGERGCEDVTESAPSAVPMTIGPYNHFKSFSRIANLHRIGHGNRFEPHCKLEFLSESP
EVVSVEDYCVFGPFVCLCGPWRGNDKKVDAAVTIASRRVYLCPTDPKGEEKCGCFASALP
LTDSTHSSCCCFCSSACWVLPRGEPFDEEEAEDALRQKCLFFCRLSAQ*
>TCRU_7275 mitochondrial DNA polymerase I protein C
MDGLLAATEMELRGLQISSQEEVTKFSNHLKTSHEKLEKLVNDKIMEFTRGMDDEVRKRI

NFRSPQDISTIIYGGALCRHLGARYVPVETAKTPVTALFPHAVCRVTGTPIPVAYTQPES
LLAPKGPGSNSGSRRGKITIKESKVKTALEAIEGYTTRNTNIFARGSD*
>TCRU_7276 hypothetical protein
MVQMSIGRLAELSWILPNGNQWNNDPTRCVWQKRPLRKACGDIHSCSVRSASSAAAGAHN
RCHPLIPRVALRPVRLQRPPAPIAILQLHASNVVAVVGLLAAIAAVVESTTTNSALPRTQ
ATFLTMLRLAMCGQSNPRAWAIKCAAMRVAMHP*
>TCRU_7277 RNA-binding protein, UBP2
MSQIPLVSQYDPYGQTAQLQQLQQQQQQHIPPAQMNPEPDVLRNLMVNYIPTTVDEVQLR
QLFERYGPIESVKIVCDRETRQSRGYGFVKFQSGSSAQQAIAGLNGFNILNKRLKVALAA
SGHQRPGIAGAVGDGNGYLGAYGGYGAYPSAANPYAQQQMMAMYQQYMMQAPQQTPHQGQ
QQQMPLPSHPQQQSPPQQQQQSPSSPQQQPQSQQQSQAARPVRR*
>TCRU_7278 hypothetical protein, conserved
MLCRSRVRLSGFDVNALYPHGVPKRTFPYREHPKQISTAPMAGGFYMTKYALGWPFQIPF
EWLFYRTSIFLFVACVVYDLFFGFPLPFMKEIPPGKPKHFFFNNAGGSPHHFWQYQDGWK
VPNMSGARRWVD*
>TCRU_7279 protein kinase, putative
MNRDVEWRTLAFQEAMEFLCRLRHQLESGISSKTRSQEDACNSPVKQTDAELAELALSDD
ADEAVSLFSFVKCKDGMNSSTAEEFDVCYDFFEFTDQESTVTLTHRYESLGKGARSNVYR
GTLCVTTMDGVKKYDVAVKMSRLCVGSLHEIDRWMRVVQLWRNLKHPRFHCCYYVGFSPI
EGEELVINMYSAHELALGGTLDASLKKEERFTEDVVRTILFDLLHFLCYLHDEIGVVHND
IKPQNILLVIDNATQQLRYNLSDFDCVYPITPSRGGILVNGMATSDGTEHDSDLLIYGTP
PYMSPESCRGLPFLPSNDVWSLGILTYQLSTGRLPWNPLELSVPSMILNGYRRNASNGFG
PTLHEFEEGFCHVYSDDLKNFVKICLAEEASKRPTASELLRHPFLLFPEGCTR*
>TCRU_7280 amino acid permease/transporter, putative
MSERQYFEHPRWHLLRRKNAAVGGTTSDVPTENLPSEQGTGVSDDKKNVPKRTLSSLMLV
GIMYTYTTSGAYAIEETVMGGGPLLTLAVITLIPVLMAMPTALVVAELATAIPSNAGFLM
WVSVSFHRVVYFSMVIQSLLLIFIDNALYPVLFSEYVCTTISCTTVANRGFRAGMLFVTY
ILNLTGVRAVGMVSVMLTVATIVPFVLMFSMHLFKNNFYLNWPAISFIPADIDWSTFIST
ASWNLCGLEQVATVTEDVKTPHRTIIRALVPLLGLCYLTYIPPILTGSSSKKGPPDISEW
KTGYWSYVAYSVGGSPLQVLLIMGSFFSAFGMMISSLCTTSQVIAGVAYTEVFPGPVNRI
LYQRNKRFGTYHWTLTINALITGLFSVFLDFGPLVKSDQVLYGIRVVVIFLSFLIIRHRY
PHLSRPFRLPLEGYKLGVMIFPLLLFMALTVVAMMEDMQTVTVNLSIIGGTLVLSFIYCF
FIRKGEFFGRVVTETVEEREGD*
>TCRU_7281 hypothetical protein, conserved
MEFTPNTVFSEQSFPFLELQFPSSPLSQKKDQHNFIVDALDKDQSHTLVENASEKFSRES
GEAVCCAKEDAGKADNSVSNFNGTHPAEHKCTNLDHPVLESAVLPTNRTRSSTVFHTISD
EINPSCVYDTAYPCLYQVIEGNKENFIYGLDALLHGVHFGFVPQPPFRVALPGSFGGATH
KSQDVDYDFEVLENATVPAEVYFPRSAAPVSSLGGPRRKFGSGHGNSCKGKASLSNTPSA
EIGVSSVRTPLLSTQFLRKEALVREARSYMQEAEFIINQLFGEDDNGDTLASGSPSSNTP
GKVNAADLEALMTESLVPHSMPPSTPISTRSGEPRFLPLATETGGFKRCQQIDKGPQFSS
EKKGNADMEYPAFDDVSFREPFFWPESSPQPLRTAISSTRGQKSLPKSSIVSQESRPSSL
KTPPPRDTLRQELPLNEFLGSMEYPSAVDYQNDTGSAMTKLQPIFSQFNCPIARGGQVAL
PKTPPRKLEGNEEGLRNEEQRIKDARRQASDKSALRASRMVVMDNRFAPKTTKVSDFPHS
GQVERQEAQERENEERRARVKAYLEKRRAERTRHEEVKQRRSDEEKVERLSKLPKHSFSS
SIGPEQTSTQGANPVHRTSQRRIVSAKGATHSAAAPHPKRLTADASLTPESLKTSGLPEN
QNTKTENHIHSLVIIHRSQEDSNTPAKIKLVGDTKLEIHQGIESPLFFEVDECLESYDGS
IFCSTTLSKLRQMFLSGLNVSMCLAGSESVELLSWRPLREVMQGVFQDLGEDSQLFLSVA
LVQQGLTQDLLSESGRMVRTTFKQFALLDVTIENVGYVKLRDLRHFSKVLARGWEVARVD
HTRGCGFFVVSVVLKQIREDDVILSSMLAICGNKSVTHLNNLLKKENHESSNLISAALGF
SCFTVAVLTLSEGDRSATQLMNTQDKLASIVNSHGNVGSVKKFLEEAERELAATESDDPS
AQKIREVLQEKIAVAKRALMDPQKFFPREAAEEPKVPHEPICKANPETAAKATDEALYDA
AGAEKSSANSQSAEKQQPQKDDSKSVREEPDVSKQVERPPSMHVRKMLLPPPPDPRAAGT
GEITLNTTQEGHVSEVPHPPETVSVVKAPPNNATKDADSAVAPNTCHSTTGSQQEKKANT
PVTLPVIPLAKLCMGRRQTNFPKPPDENGREVPAKRVSSFSSGLGRGVMKDIEKGPIDSQ

DPTPAGVYSSTQTHLLVNANAGAHTEQQLEKNTDTTIALPQGILRASSREDSRPLSASTT
AGTTASTRYINREDVALKKPVFHHIEAHFKSILPVVDKKSTAKLPPIKKKSSERLICSSV
ELPRDADTARKNSLLTLISEQEEYVEEEEEGREKSEFVEDNSIGNERRLGKSNRRDDRTE
MDASLSSNVRTLVVLDPRCKETVNVTHDGTVVIVMTDDDFEEYEVDEVIERPDGCEVVNS
KMLDKLLDKFMLGCNVAILAADSRSSSLSSFVLKGVVHDVLNEIREKTMSHGPKYKGIFS
VSIVQVRGETVVDLLKENISPRKLVIAISPIFGPCVHNVTRLPVENAVVFDSMLTAALTR
ASVKEREYGMVFISFVLKQKIEVEKDVIVSSLVFNLVGENVGLYLTVLDRSPLVSRPLFH
YALGGPCFTLAVLGFSGDETRMHDMLAVQRRLGEMTNRPTHRGSINKFINGIRTDLAPAL
SEKLRDSDDRESTEKILRRLEEMAQDAEKLLENFEDNDPKAYLNDADENQTDENRYNRMS
LSETVPRAEAQGRVRSLVCFEQRLPGNGCIAVENNSLLFHNGEFVCRYDVDEVVVRDSSG
SVPSSQLIDDLVAKFLMGHNTALLAAESRSSAVTPLILRKIAYLIVYNINLESPSTTMKG
DLLVSIALVKDDVTVDLLAVHEGLAFHRFEVEVSSLFSRRLRGVSYHIVTSAEGFDHLLA
FAVDRAEPALRSEDPGVMVVALSLTQYVESPARDVLVSSFIATTVFDSVSHYTGVLHKRP
NEPTGLFKLALGGPCYTIAMLGLCDDEDNAGEFLTVQMELAHVHNRLSRPVSVVKHVNEL
KKGIAKLFELQQTAEDVRQQEYISARITQLKAYLHDAELLLELPVRERGFVPLGSES*
>TCRU_7282 hypothetical protein, conserved
MDFGTHRQALGGFEPYRTRRESPGAPNTKFREPIAPAHRAGAARELGVHRGLIIAERERL
GTDHAYAIAGARNRNTELHSQAEEAHNSLSAREAGIAVADGLVAGSPRPTTGTRGTR*
>TCRU_7283 hypothetical protein, conserved
MDFGRTLLPAFRTRLMTASDPNAPLSKQRARLHTAVREADAFARAARPLAERGGAQRPRD
VSGVTFVGARRPHAKPEARPEGINRDADGRQQRRRPHPCRHRSPSRTGGAPNLHLIFKLP
DAIAEKGEGACSPTEPDCGATVLRHPRCGPATRGGRARRLGDCLRRRRGSGEGRRRAPHS
LPPHTRTAEQRGEPRGLFDGNRRGATDPTAGRQDAAAHVANESDSAGRGGSGVAKTRGAI
GDEADAPFKKEEADPFIRSRAERK*
>TCRU_7284 retrotransposon hot spot protein, RHS3, putative
MKFTISTNIEEVLFKGRARVNEMKLNDFLTRELDGRGVVDTNRSVLLKEFFRDPTRYIRD
KGALNEIQASDRYLSMKRAVKGEVIFDEDIRKLYKNGVDNLPGWSLAAAGVKATVHNSNK
HFLDAAAKEARKPTTTSVPKKLEGLYESVHNARWSHAVELPDGVELRKRGRLTSTSSPLA
LSVPACSKLATPSKGMTLCSNSVQHLPC*
>TCRU_7285 hypothetical protein
MPPQTSQLRDAHVLIAASCHRSGGLVRHVRISSTKTVDYHLESLDIVLQQLVEEVRTGIH
RFPDPGRPNQHTSLGLTVGPTVRAGPRGYIALDGDGVSQVECQMFLQESF*
>TCRU_7286 hypothetical protein, conserved
MMTTGRVLLVCALCVLWCGVCGGEPPETTEVPPVPPVTPPVKDNGSEIDNNPSGGAGGGG
QSGQSKALKEKSSSVQDATGVAAEKAIETEAQVSSTADAEKKKEDKMQGVEDIGEKKSKE
QEPKKEEEDDDEIEQEEERKRKKKNVTIRKKTLVPAPRR*
>TCRU_7287 protein kinase, putative
MHTDLKPENMLLETSETVIDPVTRKATPPDPCRIRICDLGGCCDERHSRTAIVSTRHYRS
PEVVLGLGWMYSTDMWSMGCIIYELYTGKLLYDTHDNLEHLHLMEKTLGRLPQEWAGRCG
TEEARQLYNSVAQLRPCTDPKHLARIARARPVREVISDKLLCDLIYGLLHYDRQKRLTAR
QMTTHQYVLKYYPECRQHPNYPDNRPSLRPTPLM*
>TCRU_7288 cell division cycle phosphatase 14, putative
MPKPLQELLETRRAIEIIPGVLYFASMGEKLLPIGESVVFTSPLRSASARSMNIPKEDHI
EASAASAALAASTVDSLEDRPPSQGEGRESKTTSRRRTPSPIINISHLRSNVAQAVILRR
LILLGNNGDESFGGEVEHGAFYFSVNESPLFQYYPFFADFGPLGLDAVTRLSRCLMGLLE
HCVAYGWGTDSNGRENFGPRGRLEKITAGHSEAEAAMSLLHPNIPLVFCSGLSSHDRANA
VCLLACFCVATLGWSASATWQAFQSAYPPLLPFRDAGNTASAFSLLIFDVISGLEKAVTL
GWYNVRTFDIAEYERLRRHDCSWVVPNALLALSSPNSHVPGRSAEVYVKLFHQLKVTHLV
RLNESLYRREIFLANGVQHFELEFPDGSAPNDDIIKRFFKIVEPILLPSSRATNKEEEKG
RPSLLQLHQHQSGSPRCGQQRVKKVKSGGGAVALHCRAGLGRTGTLICVYMMRHFGMTAR
ESIGWIRLCRPGSVIGVQQEFLERIERRFSHMANAVEIFRAGRSIRVIGSRSMDPSSNYT
SQIRARRHVSSAPGWRRKGPAEGEGVKMEEREGTMVCDMATTLPGPLWNWHSNRPSSDIL
ALEKMDPLVVFPLEAKMPNKSRGAWISSEEGAPLPLPFSPSSISTPSRMVQMRQQNRENS
TGEQTFDGEHAKKRDYTIHVATTSFPSLLPSALPSASSKPLSLTPTTEACFSTPQTRAFT

PSSRIRKERHGSLRDMPTSVKNNDNNKYKYKENSNLTVKEAQLSCCLNDSSNLQRDGFIL
AAASVDSNATPFLRVSASSAPLVGITTLLKGPQPRNKRAVMLTKQLELAAAAAVFADPGW
GAAMVRLEP*
>TCRU_7289 Plus-3 domain/Zinc finger, C3HC4 type (RING finger), putative
MLSEEDQLLFVAAKEAQLTRNEAVHIIMSDVSHSVFYGAFIRVLLELQDHREDYIVARVG
AIATGEVYGGFSNNANIRTDNYLVLQLPPHLAKINGTQYQLNSISNSPMTEGEFSRWLEV
ARSGAHALSSLYALEGVAPVALPVPTREELAAVAWRLRGVIGNLARHGHGAHRQRRCSQV
QPSQAQEQGPATPPPDNLLQALSGCPSRHAPPSEGNFSAPILHSACAADNAYNHDDVSNF
ARQITTASLGPANSNISQQQQQQQPYNPLYLQQAGNINGSVEGSGPSENPPLFQGALSP
IPVSTSPPTAIEISVAERELELPTRRQIRQDIINKMNQSGVLFPTNINGLKVSQLRLAER
DMIEYLEQVREAISSKQENCVVCMDHVPTVISLPCRHKVLCRLCAPSVSTCPVCRSQLFE
LFEPKEI*
>TCRU_7290 hypothetical protein, conserved
MAALSAPAGAAITRGRRRVRGEARRRKGAWVAAGQNGGVVHGRDGVVRFLLAVHGVARSH
NRSVCDIAGPCGYPQRFGHSIAGHELVAGRRHRGVTETHRWAYVGKGFRWGHAAKVAA*
>TCRU_7291 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MGAIKDRIPVLARGSESQADDVPQTIAPAVPAAPGPREIPAAQGKTTVGKTANTQNAPAG
HLTSAGNEGTARETGDGGANGDAGSAYGRELLPLLLLLGLWGFANA*
>TCRU_gamma, conserved domain containing protein, putative Elongation factor.1
MCSKHKDNKMQCMTANLNCGWIRRMEHVREYALDPALMIEEEGRHDIVALCVLRGRGMPA
IVRDVEDTELFD*
>TCRU_7293 hypothetical protein, conserved
MRVDGNTAQFNCPQPLRDAGFPVAEALFDVDVALDGPDASALFRKLCATAAPNFTQDRNN
MVAFSYGVRSSPRRQLMYGSAAGEGYAA*
>TCRU_7294 hypothetical protein
MQILPGDVLKRVDVDGVVNAAKRRHLAVVVLVDEGVNGRPVQRPVEEGVEEVVDNKQRHE
VQRHPRHGAKNCRPVHKVHAHAAHVGADNKLVCVVHKEGRDDLGEVDVNFVPHRERPEAL
RAVR*
>TCRU_7295 hypothetical protein, conserved
MSLRPSIFRLSKTLTKAQQLLLSATADRAGACGLEEEKRAEFLRYIRRLGVLLSSVELQM
TALDDDGGRDEAVARLVSAAKKFLSDVLLSAHGRQGGIPLSCVGLLCRERSPKHPFAVSE
PFLVQEDLRGMSETAYVFPCMYHHHNEASNPQEISTCLRLNDANTHAHSVPTATGEEAAH
AKVMEDIREAIKGMKEGVTRMSDMMQQERLRLDANSELLQRGVDGTSTQSRHMDQLGYAF
GGGPSLPRCLSCIPGAKIFWQTVVAPMWVVIRQAIFLFMIVAITCSVLLLMVTAPKTYVY
VR*
>TCRU_7296 hypothetical protein, conserved
MPSIRDREARESTPLEQTFQGEERRRRGKKGRAVVYVSDFMPPPPSSPSVVPRRSQNCPR
QGKEDEEKLLRASGSGRAEVPNRERKGRRAQLVSGALTAFPSGACLKKPTEASSRTWQLH
RKGKRRNPDTPFNHRAQFSKLKRTICEVRKAVFESLGKSQDAVSFCGKCVNMERNSTERE
TLVEDASATSVDASACFSSKQRQLLRMRCLVTDMERVYGQIHKTMRQKHYARARQHMNQI
RQLKKRLNTAALKWRLSTVAEVEADAAIHTPRPLHHAVDLSGRVAAVSAAFNDLQHDEDV
DGAADLTDEPNYVNFYPSLAQMGVGCHPLAEWIDRRSQKYPRRLGKEEIPRLIEGGYEND
EEKRIFSTGPAVPSPVKYVATCCKNIITDALDDLVFTILQKQYHLQRRMKKEKPLQFKAR
RFYSTGLRETLRGLRAAATRIPVVLIASDIEVHASWNSEGRCDEKKVAEADSHEVRCGKK
KTVQEMGMDGTLEEIRAHCESHGIPLITCMSRHRLAYALFAKGCTVSAVLLHSAEGVHEE
VRALRHYAQHLFEAFAAISATHQNIPPAS*
>TCRU_7297 hypothetical protein
MWRAAVAGGVEFVPGQVITTGTNPLAKDTQYEAIQRFQEVMRAYLTHSGQKYYADKDHFL
KDDVDGGMMVAGWIAGEVLSQALGSREWVKDRKSFLASLYNQRRYVVDDIVIGDYGGECK
AGVLSNLCIHFLGPFFFCVFIDFFCVGFYKVSFFCMCCLVILCREG*
>TCRU_7298 hypothetical protein

MRLGAVLSVLFLLVLVAFYGVGVLAQRMSVVPIQSNFTAVISGLQWPRVLFRLGEKCSSH
PSSTSVPTECTVVGDELTRLLVKALRPSVHTAIHPSPTGITAVFLTLQPHSLQQSLQAEF
AVVRMLGAGSLAPDDLQLVEQVRRADVAGLRLIYDSNGGSITDNVSVKTVRRVEERASPC
GDSCEWAVSIVAPLFATALLLIPVFMSVVHLERAVAVRDYFLVASHDIDDEPQHVNEFAN
CEDWGPVEFVDPDMLPRENVAGHEPHMDGIVVLQHFVEEDAVAVGKTRRRK*
>TCRU_7299 hypothetical protein, conserved
MLHSVRTDSCGNVTAAAFTVPQCVSNHVITAARGAPNAEVEAFQSASRRARAACSVAAAS
LPVAGCRPPSLQWIAEGGPTPCKLVDVQWEAHSARCAVTSGNETMRPLIRAGCAGSSNSS
HSMPLGVAARSSPAVVGGERPSHSSWREFG*
>TCRU_7300 hypothetical protein, conserved
MNQVIRSRTDWKERVVFRLAWITASRWSEIAALTPKNFTLETDEALILDWSVAPKTARAD
PHRAFNFVRIRGQDAFGIIKLCRTLQENEELTNRTTAQAKRALAPWDATAHSIKRGALRH
AAPIVETYNLDPHVISQLAKHVNPFEFPQDTVRYLGNYTTVLTQVSSLVALM*
>TCRU_7301 hypothetical protein, conserved
MAGGNSTLIHLEGNSQSSSLSVLNNSAVVIRGNVVSRQLEYFMFFLWALRVESFSAVVFR
GNDMQGSLAVFYSRSSFPIYYNSWLQVSGNLCRESPSAAFLFLNPTVNLRDSTVSVSGNR
FMSSAGTPTVLRIFTGPRDITNGAIVAACNTVNGEEGASYDIPPVYNATILTCSDPCALA
ASCFPAYTTTASSDGCACTCAEGGYGDACLPVAVPEPPSTDGVDLCVRDVRVGVEVNAVF
GTSVLCYVGVTFAADVLVDVESMSGSVRNVTLANCTFVMEQACTLLGGCPTRLLAGALMC
*
>TCRU_7302 hypothetical protein
MLLPRTDSHDPETKNADPRSTSSAPSVSAPALSFTTTADALAITPLSNTNPCAAYAWLPD
TRSTAPPDATTRALAYNATSPPSTAASSATPPPTSSSTAPSTTTVRPPVITVTRATPDTT
STDRTSRRPDSTSTGAYGEDCEPGRYTSGVGLAATSRESVTVSTDPAGYVPVSTSAPFSA
STSHTDSSTGPLSSLPAAPAPRNAPPPITYSTAPFSSDTFCTTIRTPSRAIHGT*
>TCRU_7303 hypothetical protein, conserved
MPAGAGHRQCTHRAEEDAEVHRVRHNVRQAREAHRRPRTRRVHAAPPLEGRRHTAVHAPK
HSGQQRVAHHHPQRVKGSEHRQEVRQRNGARTLLRRGARHPRKHAERLHLQDGAQPAGHH
HGNSRRTRNNAGDRREGAGSGGQRVRPDSEGPKQHTLAAAGHRRSVAANDYRLVGSNEVT
AVHGHSQLQDGGRIRRVEHPRRVAQHRSPRTAKPARLRRRHRHEAQVRAELRVACPPKRR
RQRHHQPRRDDAPTAANVVLRQTPTSRRRRHGERRARHVAPPQRAAHRRRRTPRGGQRHR
LRHLQCLRRTVRRRTVARRAHARRRCRRRAVRLRQRRRVAQQRHSGRAVASVHVRQVHRQ
AVAPVPALSTAAAARPRHRPRRSCKAVHVGVAHATRHGAEFPDDAGGPVVDRLQHLPVER
*
>TCRU_7304 hypothetical protein, conserved
MQQTHSAAFNVIFFQWRRKPFPLPLNHDAVLAAPATVRVDGNTVQLNCPQALRDAGLAVA
EAAFDVDVALDVPDASTLFRKLCATAAPNFTQERKNMVTISYGVRSSPRRQHMYGSAAGE
GCAA*
>TCRU_7305 hypothetical protein, conserved
MPSYLPNTVVLQLYRDDGEAEFADYMDANSMTFVALGDAERPALCGIDAAAQLQYEGAQR
ALVSAVGIVSSIRRRRLCIPFGMSELSELLRRAYNTEKGNRNNSLTGSTETALLTQAFSD
AVWAEESFHCLDRNWIRHKGSCR*
>TCRU_7306 hypothetical protein, conserved
MELRDELMIARTAYDHRPCIYESNRPISSIKEEEMKRVNAIQSKREEARERQLSVFCERA
KHEAEKMAKELEQRGGATLDEIERALEAKKRESSALQADRESRIWECEHTVEKIRTRKRD
EESASERLRQATQQLEQELGLRQSAIETKKKQLEMVQLDGARGERPSCGSGILLRRCEGP
SGRSGVASGGSGSIRLRK*
>TCRU_7307 heat shock 70 kDa protein, putative
MTYEGAIGIDLGTTYSCVGVWQNERVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA
MNPTNTVFDAKRLIGRKFSDPVVQSDMKHWPFKVITKGDDKPVIQVQFRGETKTFNPEEV
SSMVLSKMKEIAESYLGKQVKKAVVTVPAYFNDSQRQATKDAGTIAGMEVLRIINEPTAA
AIAYGLDKVEDGKERNVLIFDLGGGTFDVTLLTIDGGIFEVKATNGDTHLGGEDFDNRLV
SHFTDEFKRKNKGKDLTTSQRALRRLRTACERAKRTLSSAAQATIEIDALFDNVDFQATI
TRARFEELCGDLFRGTLQPVERVLQDAKMDKRAVHDVVLVGGSTRIPKVMQLVSDFFGGK

ELNKSINPDEAVAYGAAVQAFILTGGKSKQTEGLLLLDVTPLTLGIETAGGVMTSLIKRN
TTIPTKKSQIFSTYADNQPGVHIQVFEGERAMTKDCHLLGTFDLSGIPPAPRGVPQIEVT
FDLDANGILNVSAEEKGTGKRNQIVITNDKGRLSKADIERMVSEAAKYEAQDKEQRERID
AKNGLENYAFSMKNTVNEPNVAGKIEEADKNTITSAVEEALQWLNNNQEASKEEYEHRQK
ELENLCTPIMTKMYQGMGAGGGMPGGMPGGMPGGMPGGMPGGMPGGANPSSSSGPKVEEV
D*
>TCRU_7308 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGGGGCNDTAQDPSGGASQDGKNLEGKKNTTNGAGGGVN
SSAPAESQLSAKSVTDTNGAGAGADVSATQQREKQASETEEKGKDDVEDDEDEDEDEDED
EDDKNKEESETKEEKKDKEKEEKKIKEDDADATKGMPAGGEEQRSSSSGAEEAANQTNLK
STQTTGDGDPAADVAKTRDEKQNENKDANPKETPFEAAATKNTTATNGDIDSSTAASHAT
SPLLLLLLLVACAAAAAAVAA*
>TCRU_7309 hypothetical protein, conserved
MLFLALSCCCCSSVCVTVAGSPGHVSGAADTVVVPVDVSCAPSDGGLSYRVRVWAWKRCS
AASAEAQRENYTFIGFDVRMHGRNGELGAVCHVANAVHTCSNCAASCAAEEEGATVASTM
NVTTHTRALMNCGDANFLPMEPSIRSHGAAMLTGRASVTYHHPMKRRTTQNLVGQLHRKL
MLSRDVNTRIGDVLRWLTDPTPSIRVPHPTRRPTRPRRGLCLPPIRTK*
>TCRU_7310 Enriched in surface-labeled proteome protein 1
MLVTLPVYANTESEENGKGVLHLWLTDNTHIVDIGPVSGEDDAAASSLLYRSGKSETNGK
EELIALYEKKTAEGEKPSSGMVSVRLTAQLKRVKEVLATWNKVDGTVSQLCTTLLAQKGL
STDNACGADKITAGLVGFLSGSFSGDTWRDEYLGVNATIKGNDGGATKTSDVVTFHGAWA
EWPVGAQGENQLYHFANYNFTLVATVSIHKVPEGGTPIPLMGVKKKKNGAGSSVFLGLSY
NNKNKWQLRCGDEKTTEHSSSWKPETTHHVAIVLRNGNQSSAYVDGQRVGGDAPCTLGST
DLREISHFYIGGDGGSTENKESRGVVPVTVANVLLYNRPLDDSEIAGLAKNKINIPTPVA
ARTSSPAVSRPKPSSESLARGTTGAGTARHFGANGDGSTVCGSGLLLLLLLLGLWGFAAL
*
>TCRU_7311 hypothetical protein, conserved
MVRNCVTCLSFLLSLYVDGELVCAEGCTQVTGVMAMMMTDRVLLVCALCVLWCGAGGVYA
EGLDNNAVGGCMASGVVVKNCSQMPSGCDKTAITAPLRSALPITVVEASTENNVSSSTDG
NQDSTSGINPGVVVGTDGEGTVQAGGSKTAGDSKGGGDAGSSGSSKGSEGLDSEPLPSGG
GDTGDSPPSSPTDVTSSTRSGGGMDSTGNALSSVGNKTPEEVQPEKAANAALPQHPTSQE
QETMKSTPGTQSQTPSLAAGQDVGDGVTDGEGQGSSREKTKENEDLKAPGTEVIFESPGP
KLHGSGGNESEVSNATLQETKTQKQGKTLEKENNDSQSGGAPKNSSNKHERNDRREGSSK
APTSTAGTAQSTSTGSQEQAAASSSVGTPTPDQEEKFTGKKRTESTQPPDAAGTGKPSSG
DKANIADSDGSTAVYHTTSPLLLLLVFACAAAAAVVAA*
>TCRU_7312 Mucin-like glycoprotein, putative
MTTCRLLCALLVLALCCCPSVCAAEAVGVKPADSGLLPLESQEAGLRTDTSNPNTHKESD
LDTPGAPNTPVNAVAGVKSDVLSATQDEETEPGDPVPDGGDADSPVSRDKPNNTVEIVTE
HDTEKSETNKEVKMQTPTTTTTTTTKAPSTTTTTTTTLAPILTATEAPANKTKLKQSLLR
EVDGSLSSSAWAFAPLVLAASALAYTAVG*
>TCRU_7313 hypothetical protein, conserved
MASEVLGENGSHMPNGCDRTALMLSLRSVLPIIVAEVSGEEDGPSKGESGGGGGVNPGGK
DGAAGAPASGGGGNSSGSVSPGGGSPHHLGAGTVTSGNLLSRPQNASQTEVLRRDETENQ
SLSSPKGKAADTPVNGAQTKNPDNTVIALPDNLASKELSNNVKSESLIAPGAAPKPSPEG
PNTELQGKGKASPELSDAKLPEPKTEHQTTTSEEGKNRSQNTSASTDSPAKQGRNNEDPV
SASGTAESTSTGSQEQAAATSSNESFSPLQEETSTETTNVENSRPSDTAQTEKRQNGGKE
KAGDGDGSTAVSHTTSPLLLLLVVACAAAAAVAA*
>TCRU_7314 Protein of unknown function (DUF3676), putative
MQRDSDVQPQDPQPAELTEVTDVEMSPESNDTEQPEEEGEANDRSDGTTSPVGASLSMAT
ATASVYGEHQVQQSTELSAENDDVRSTGTGTTGAEQSLSLEAGDGSSERTMGSGSSLTPS
KSAPHKTAESKKLPKHCHHHPDEEIVLSPNRHKESTLKRHASTAKKRLLGL*
>TCRU_7315 BNR repeat-like domain containing protein, putative
MAHTVPGAAEGEESLGVVLRLTTITKGNGVFPLAGGSDVSYEVGCWREGGLELKLFVGDV
TNPTGGKRSEWIEWGDPKPLPKRISSASHEGDWTEFTASGGAGVVMEDGTLVFPLNKENE

VDVCSMIIYSTDSGSALALSEDMSSAECLNPRVTEWEGSLLMIVDCENDQRVCESRDMGT
AWTEAIGTLSAVCVNARSGVPQKESLRVDALITATIEGRRVMLYTQRGHASGKQRATALY
LWVTDNNRTFSVGLVAVENASKWKTELKDCGM*
>TCRU_7316 Leishmanolysin, putative
MHLRAQDALRMCSGIRKDRQVPFRIKKSKKDSCDIRKDCGFFWRCAVNSLDDAFGCKNGA
LTPAHENILAEETVPAAVNPHADRLLFQPLEGPLTVSSFATGSVCSCFTVTSGHRSAGVF
NAVMVLYVAAAFGGVWVLPCATLEDGRPVAGAMHFFCQFYFTDASPPASPRTCWPMLSGS
PARRWQAAAR*
>TCRU_7317 hypothetical protein, conserved
MWSRTVSPASTEQGLPGASVTVAGSIETDHGTPPKDVDTAVPQKNPLKEEKWIRPGYPDR
PRESSLGGRDRSSETDGEQARPRLPVMTLLLLLVPVRCFFCLSLLPPWQHSIDLRCGRRC
AARGLRFLLRGLQSALEAQ*
>TCRU_7318 syntaxin binding protein 1, putative
MFHHMLDAVHGLSKVFYCDAHAASALSCSLRHHDLMEHGVTLLGDLMTPRQPVISSPARY
FFAVEDSSVSRVAEDWMAKVPYRDAHIFALWCTPHRRLQQLVRARIAPRAMRLKDSMLDF
AATEVLVFHPSMQNEFFQLLSPLSPPTRESVLNVAESLIVAAFHAMNNGVPVICQKKQRQ
HLPWVCQDLF*
>TCRU_7319 hypothetical protein, conserved
MPWPVRLCLLLLLVTASSTDELTEANKQQLIRDGGLTLDAHLFANLEHVTRRAGSVQPES
TASAQGKRSTSASASNAATDEDPFLKQSCMIMETGRNKTLRVGLSLASVERDHAMRPNGA
SCGQNSGA*
>TCRU_7320 Mucin-like glycoprotein, putative
MMMCRLLCALLVLALCCCSSNASDTELAEQDSSQKTMTTTATQATTLTLGQSGPKGEESG
GEKGNTAVLGDGGVTTVPGPQLNVTSNVLATEVKNGMTGTTSDTSTAAEKAGQNAEASAK
TTTTTTQTPTKTTTTTTAPEAPSTTTQATTTTTTSAPSRLREVDGSLGSSAWVCAPLLLA
ASALAYTTVG*
>TCRU_7321 hypothetical protein, conserved
MALKLQCSGVQHRGCHVHVHARTTPLDQQAHEDALQQRDVECLLWCVKAPQVQHNRGGEG
HVDEAKNTHTGTRTVHGADAATVHAADLRVLRIGERERPKAVWNSSRQTRVTVAASSAHT
STAADAARPR*
>TCRU_7322 hypothetical protein, conserved
MQGIVITNHWAAALPVAVMTHRRLYFLARAAVEAEGDGVTELQGEPSRASQSASKGGHDE
EPDVRKPVGGVLNSSEEPSDARELTTVIPQKTSVKQTPRDNGGAAGKEEPLEAKKAGDEE
KRSDGEEQPKDHSEGTHERDGPKEDERNPSPTPPDKMLTSEDKTPEHAGQAGQAIRPPPS
PVPDVTRPSGSSRGDSSVSPLSTAGISSSSALDAPLVQSTQPSEKGLRSETMYLGTALPN
EQPKERTESKAKQGFSTSEAAESPDDSGDAVEKKKDKGDVRPKATTSLSSTTSNPPVTQT
TPRSPSAEPSPTDTELQAGEETSTENVTITKRNDTTTPADSDVSTAVSHSTSPLLLLLVV
ACAAAAAVVAA*
>TCRU_7323 retrotransposon hot spot protein, RHS3, putative
MKNVLQSEALEKYSLSVFLIENFVTSMAEDLKELPPPSPSEPRPSVLTLNPHGYPTEATA
ISKLKSVGCQQELKYRVLYIPTFQTFPLVDGFFFMESPRRTLVGLQMTTASAHHTIPSTV
NQFTEHLSRFFNGWEEFAKGLSWDIIYIQHADSTPMEKWQRCGPVITENLSDAENKIVAF
WNGKVHQYQFILEGKFPEAIEFSHDGLPKGDKKGKEIGTTYSL*
>TCRU_7324 methionyl-tRNA formyltransferase
MQNRCHQSLSLHVQRCLLKHCPSLALGRLPLVRRCVFAPHCCSFVSLRHCYTTPVTAATG
CRGGSNSTCHAAESGVPKTPSIIFFGGDIVSLVALKMLREQLECIWAADASTTPNVRSSP
AGKPCLTKTAEGKQQLVVVCPFLPADPSDIFQHHHRQYPVARYCVEHAIPLLPVDHPTSL
ARSGTLRHILCPWNAGEQSTGAAKDKKGEAEGEYILGQPLEAFDVAVVVSFRYFLPKKLL
ERLPRTVNLHPSLLPRYRGASPIFAPLLRGDDVGGTSLIKLSLDRPLMDSGDILWQQSVP
IPNDMTIREYLPLVTKLGATGLCECLFGGPSASAPAPDLHRVGSAADAVTEASVTRACDW
PRTFDARWASAWPQNYDVHFTRDPYHAPVLTKDRVIIRWHAMTAEEAYGTWRAFVGGEYH
TPTVNATLDKGATPVREQLLERLRTRAAREMKKKSRIHQQCDDGVATIRGTDERDSDLGI
LFEKFGATKEKFVGTEKPEVMTSAAEVFHHHSLQQHLLVGCTFTDALHPRDIPTAVVKEL
QQLEEGRVAVRVQARSQQHQQQQQHCVDVRIEPGSAYFPKKVEDMCAVKCREGWFVWRAA

ALRGSTAQSAGLLRKGMAMKTGVLYAAIFVESATGEKERPAVQG*
>TCRU_7325 ATP-dependent DEAD/H RNA helicase, putative
MGIKGRRKRLRERELRADAQDSQHDEMGNVGYHGNGEDADGGSEDVAMMADGVLQPPMDY
NGGLRMKKTEFFNMQDMEYLDRIAEEHANRRTSHMRKRRREEDVEAAVAQTEELMQHHYE
TEDALQALFRRPNSGEMKGGEEGLLERRRRVGRGARFGHPLIGIDPQIVRGLEAEGFYRM
TTIQERVIPYALEGYDLLGQAKTGSGKTLAFCVPVLHATLNLVHKRPNATYTLLLAPTKE
LCVQTHDVLKSICQHISNDVAAFSVQLITGGTKLTEERRLLVAGASIVVGTPGRVHDHVQ
HCAQWNLGRLRFLVLDEADRMLADGFQRDLDAIVQRLPKSRQTFLFSATNSKSVRELARL
SLYRTPLFIATTDNAPIPVQMKTEHGTSDATAMNPASFPPYNSYADPFSDCEREEASTSR
ESSSKPHHMGGDAEPIPSTLRQFCHITPVDKRLICLYVFVKRIARTSKAMVFCSTIASTT
FHFQMMGSVGFHNEVMMLHGHMKHRQRVAAFKVFNEWKTGVLFCTDVAARGLDIPNVEWI
LQYDPPLDPTEYIHRIGRTARAGSVGNALLFLAPEEAGFVRYLSKFDITLEKYPMPAKIP
PIQMKLEQVLQLDPIVAKSAVSAYRAHVGAYMNHLLRETFNIQRLNLAELARCFALTSLP
SVSLPKNTAEGKRQEYVKGKLKSLNRRRLEAKKYYEAQKTKTQWTPDGHFVGAVPPKF*
>TCRU_7326 hypothetical protein, conserved
MGDDESRRRDILARIGASIRDAQYALTVNSPKRVQNAVSETQMAIIALSEYLALPNGVPK
AAAVAKRIAKVLGSVISLLRHSDSGAGSTTQCELEPADKPPSHESSFPNLFDEDSDVNEL
SQLREKLASTQEERDSFVALLRDAQQEVASLKESVADPTQGLSLHTAEIERVNSENKALK
ELLQEEILKSKALAETVRVSNEQLQKISHENATTQTLLEQHRRELKEKEQEIAAKVRAAS
KAAIMNPKPIDNEEIEALKLQVKLMRQALRECINNSSAAEIKAGKKTLVDIENEHQDQLL
AMKITLETQCKRENNYIQQIDDLKNLIDEIEKELERERQRAEDAERCAHDTAGTVEQRHR
EQLATLEAALEQQRAQHASEVDDLCVALERERQRAEDAERCAHDTAGTVEQRHREQLATL
EAALEQQRAQHASEVDDLRVALERERQRAEDAERCAHDTAGTVEQRHREQLATLEAALEQ
QRAQHASEVDDLRVALERERQRAEDAERCAHDTAGTVEQRHREQLATLEAALEQQRAQHA
SEADDLRVALERERQRAEDAERCAHDTAGTVEQRHREQLATLEAALEQQRAQHASEVDDL
RVALERERQRAEDAERCAHDTAGTVEQRHREQLATLEAALEQQRAQHASEVDDLCVALER
ERQRAEERVVVVEKQLEDAVIFYRGEVEKVKSLYAADRCRMNDKLSSVSQFLDEATKEAD
GLRNKVKIFEEENRQLRLKCESTRDALTESEVALREERRSLMGEVSLLRSRCLALEQEVA
AAVELSSERAESVNRLMQQLAEAKSMVANSLNSDSAKIAGTSVSLEEWVHFLRGVAVADL
KRAARGVVVVNEETQDIVNLARDLRRVIDHTAGLSVQVLGRQRQLTQILNVVAAKQCVAL
RKIQQCLLGSVSLQETDVAILEACLLLFNDVESALSEVAEPELKDTDNSASLTPVKDERD
ALLQRTLRRARNRVNENTSSPLSSHGVQPVSGSMITPVKTRGTPSGMRPSSERKFLSSPE
RGHTSVSRTKASPHNSRGPPEHLSKMDVGQCSEDPFDYAVATLSAQEKQYDRRQHSMPPR
RWLTPGKKGTTTRAGL*
>TCRU_7327 NADH-ubiquinone oxidoreductase complex I subunit,
putative
MSALLPAEAVTLLYRRYLKSANRIPNVTIRMLLLQQIRSGFRRNQGVTSPSAQRELINQA
HKDLQVLEDDRLSRTLYINRLGLVSCLDWEVRRTEYNFKPETQYFLSFYLFFGFLFFLAV
IWSAKPLEARHPEISAMVGAMAMRLEADSPEELRDMRERQIRSGLERQGHQMSLEHRVLA
TFHEAPNVKVLPPSLHNPDGAVRYEE*
>TCRU_7328 U5 small nuclear ribonucleoprotein component, putative
MDFGYDEQGNRLNHNDSSSNYDDSDREVASVSDDDAWKRAGGGSGDDDDDDDDDSSLRQ
RHGRSNGGGTDDSSSSFSEDVELIIGEAGNQSIAEPLVDEKDVVSYFRADGARGKFLVED
RRAAPLLIQDTHAAPSSEREFLDLLRGIPSRQRNVALVGHLHHGKTSLLTMLLGGRAYRQ
REDEVERKISLKSSVVTEVVSGAHYQQASHLVSFCDTPGHPDFVAETAAALRLADAAIFC
VDAVESITRNAIRLLRQTVLQENLPLMLVITKVDRLIMDLKLPPLDAYRKLRTVVDAVNN
EIAGFGSPFLVSPQNGTVCFSSSRLGFCFTTETFALKYSREYPSVDPVALSQQLWGQVAF
EKGQFVKITNFTQRPAFVTLILEPLYKIVAHALTGKGHEVLSSRLHPHPRDPVAAAREAV
QLFFGDAATEGIDALLNVMPKADVRLNWLRLRYGLTCETQNSVLAIAPLLRSQNNGEDNF
AIVRVLHGVLKRSMQLVVVDEHSSDAEPFYTFVVKELLLKMLNGLVEVDAAHAGQVVFLT
GFGTRPGSHLVLVGGAIADPFLMEDDAADVGDTASGDWLDDVRVYPLKCGDPMVHVGVEL
KDPKKSAQLQRGLQILLRTTPGLDAHKEETGEFTLTGYGELHLDTALHELRCGLCKGVKI
GISQPFVSFSETVLEKNGVLAVSGSKRAQIGCTSGAMNHQLVEHVEYEQIDLFPSDGSGV
VKLWTTLRQYGMDALDAQHVMAAGPHATKGPSLLINDTIEEEQQEFAPLTQQRLQAIAVG

FRSAVASGPITGDVVRGAAVRIVFADVEAETKDAAIISTARTTVKQALLGGLPRLLEPVL
AVDITCPPECVGKISEILQMRRGSVLSEEPIAATTLVCVRALVPAMDSFGLETQMRMLTQ
GEAFPLFSFDRWDLVPGDPFDASIHVAPLQPARGYQLARDFTLKTRFRKGLPPLLAEFQA
*
>TCRU_7329 COP9 signalosome, subunit CSN8, putative
MSRDLAKEVDEALQQDKYDIQLFLRFLKSYVMAGTQPDKRLLLGILLQTLPRFHSNDFLA
CISLVPGHVQDAPYVEKELGTIYDLENYLSCGRFVQFWEVWNQSKSLPAASPSFESQVRA
GILIVVSSTLEKVPVAKMAAYLGVNSDQLQSTLTEAASIAGEAVSIVSCDAETVTFAKSI
FNAPESDSNQQPLRFSDIVSIVS*
>TCRU_7330 hypothetical protein, conserved
MRQSFPSCVFHRHEVMEKSEYMCKCTQLTEVYDLFCQQAKQVDAFASADSRPNVNPTSLA
LHESISMTASHADYDSLTRCHILETLTEDQVTFFWEHAVMFAAEHILNSFPVSSRRGKAV
MGVFITRNAVAEFSVGLITQGTWRDQRLQEAVSQFSGPHTLNKVYAELPLCAAYRTAKVR
LWWEPRVERVTPHRVMPPVKVILEQQQQEQVDKTQLCGYAAVNVFLCRPAASKLCGTTRK
LLNGADGGVAGKAVIPATEKRNGEINLKTAAFSIDDSNGAARCREQAPWRRSVVLHFDDL
FVLEEGEHLVGVEVERLPSYKAFIPALYGHLAPFLVVTHENA*
>TCRU_7331 hypothetical protein
MSRLFQRLMELGEERSDAVTLSTSLEIHANATREELVAELTQLRTQLAEQKTKHDELFAD
AIALRSEYDTFRRTAGKEKHLLLEQQANDQRMLEELRRAGATGKMDEVYMMETEVKMEQL
QAELQRAVEEAERAYKRQIEAERAQLAAETSKKEDLQELYQQFDRFKEAMRHRNEELERE
ICEARAAAVGIVEETSLEKEGVSLAKDGVDGNSHDDNKIPGTTIKETSQMQGSLVAALQR
EKQARAELLAENGRNQRQLEDLKWKQMEAERKIAELKKEIDTWRSKVAHLEKTLNTRGEE
HGLREKDFRLVIRQKEDNFARLERELQAVKQLAGEARQEVERGLLREREMEARNTVIVSE
AESLKMTANAALEEQRVHFERLLQESEGLLEEQQGVCRTLEATLRQMREDKSNQADRIES
LWHELDHAQQVIGEMELMQAQSQRLIELREEELLSKEEDRQKLRQLLREEEEAHECTHER
MRELGTQRSEAGVRSSRHMDVSEEAACRLATLEREGSLTETRLSAQQTELQRRDQTIQQL
QIQLDDLITQNARFALYREEQVAKTCQFEARIRELEAERSAAIIQRLQTENASAPERPQN
SHSVVFESVSRITSAPTSEVLYATNSERARQQFFSQVIMSARKLRLSAFARFRRLILASS
ACIVLVILASTFVAVFPNTQTLEAGERAMESLRRQYTVASAALARCQAILSECRCQ*
>TCRU_7332 Mucin-like glycoprotein, putative
MMTTCRLLCALLVLALCCCPSVCAAESTQHTVVKAAVATSPQSPSSVTRTQGKSEPGSPS
NVSGADLGITAVEGPASTAEGPESVGVSNTLQNHGTDGTPGREISTRQSAEKANQEAEDP
AETTTTTTTTYAPTTITTTTTKAPTTTTEAPTTTTTSAPSRLREIDGSLSSSAWVCAPLL
LAASALAYTTVG*
>TCRU_7333 Serine carboxypeptidase S28, putative
MFFFLSIVLLFLASCGASGLLPLDVIPERLNRGEFFCSPVGEDGGNLFDEEYFNKTPATF
RQLVDHSKNGGSTFDQRYWVDYSAWNKSELAMLYIRIGPGDFTSPRGYPGIYGHERNMLL
FTLEGRYYGKSLPFPLTETEKLKKYLNVDIALEDIRGFQKFVEEKLLQKKLRWLIVGGSY
AGALAVWFKAKYPTAALAVWSSSAIVEAQFDFYGFDGRVKSAISPECVREIYAVQSLFSE
LWENETARVSFLNRFNIPHYFDKSGILYMMADAVAGAVQYGKKWKMCDLITQKNDMDIMG
RFFNMINLIYGQSFTTSCIYSTECLSNSTMSNQWVGTGYAWFYQSCSELAFFQVGYYNGL
RSLELNTEYFVNQCRSAFGDSVFPDVFRFNAKWGGKYPKASNVVATHGSSDPWIDSGVTT
TNGPGYRVLIANCADCGRSGDLATPRPTDSEALQLQRDELALLLDTWMTSERVSYKFVLG
GSFISQALLEKEKLMKAIQSDLHDFFDHSAEIHDFEFDRTSEKLTITFVFYANRMNKERI
SSFSRNIRKNSSFLLATKKTLSHFRVEDEALVIAFEQISTPIIDENPMNENEVIYLLRYM
GFFLLFLISFAVIACKYRIQKNKNKQTILIP*
>TCRU_7334 hypothetical protein, conserved
MEQPEHVLYPSEEMMVRLIEEQLWCGYEGIESSVGLHLDDENATYLRESLFPTLIPALHD
LVRREQHRISEPLAFQERFQATGNTHPVTWLAQYLLRNNTHHSTNLRSHPYVLVNNEVLR
KQKETIKVRDFRDI*
>TCRU_7335 hypothetical protein
MELDLDAVSQVLERFLGTSSSQRGSLPASKVKASKRTPSQPHGGPHGDSFHRDDGKRELK
AGTETNQENFIEKDCGTQEMLFLPREKKQRQKQQEQHCKHHKPSTNFVISSNQVLCRVVE
ASGLGASAVLLSTATTGKRREDRAWTSNLNQNPHPFVVLKSLSKNYLRKEIFSHVTPTTN

STATRIERVRDIALSIVFDDVVDAAGEAESPIERLVVSCSNHPRTGYVSVLRVKEIEGFF
IRAVIQGSLMGPFMKLTLFPRDAIRVKVLRVRAIELAFADSWTERRIIEEPLSFLSEEEN
EEEARPMDPISFPQEVHEREKVGEYYPGSVPTPQSVKDLVEMVESSLASSTVPISSVETA
LGDGESVLDAYDLQKQFERTKSVKLAPVLQATREKAGASEMQPQNGARGAYNMAPIKSSD
FKAMNSRVGSVKGSNEILPVASNTFLAHDLGLIRRNKNSEERKTAPHFVSIGEGDCTASK
AHCTETEIGRKNMSKALIAWSIKRRLLQDKKIMSSLQAERDTPYDVASFDFVGQQEIRGT
HKIKFDSQSHGVCGSQESVQARCTWDAVIHRSRQDALWELMTNSKTFIVTIARTSDEVVA
SLSQSCALQMLFILFCEAQGSASSSVDCFNLMITIAHAERRRGRETELIFRTKDGFACLL
HPHRDSDMKRQWLMVSVQNHPDSVNDWLLESLDLYEKNGGLQKFQELRSENSITPFNATE
GRIPLCKTAVLHSVVDFACLFELLLPTLRAWLTVCDLRYYGDIHPLLHPFIDECGVIHPT
NWFQCVLHGTVRSVLLSLPNAECGATSCDDPRGMLSTARRRLACITLRRHVFFSAVWQPN
LHAVKVVLSNEHVLHHIELLDGVLLDRHGLAVTEFLSPDSLSKIELLDEDSTQNRCRFSR
GTCATAGGSVAAAAGFSGNTDTTSSLAFQVLSTALQRSWVVVGMALSLRISFDEDAFMDT
VLRWAYALPRTIVLFYMDYPPGQEPSIHLSTGFLEAFAPVTGLKNAIEGVSANP*
>TCRU_7336 hypothetical protein, conserved
MDAYETAERAQVAVSVMSPLLNQFAEEDDLEASSAMSVVISRCIDDAPTLVSIETVDSIS
EKILGVLRRAMESRTESLQSQQEENDDDELDKLKEEEEEAEALIRDTCDLLDKMLERAGA
VFAPVFNNKFIPVLQRMLQGNEKEFMVARGLALLCSLVEHAPDHVAGLISTIVQSVINFA
QRHEDADVLQSSFYLMNLLLQYFERHEYPAIRQFVQQVYGIFSRYMAVAHKEEYEDTTCN
AISMAVTLLSLYYQLLPEHELAQSLDCVVNSLPAGGDKTEACRVHERVMMWVVQRHSLLQ
GNEARVKAIVARLKSAKEDVTNESTRAQLAHM*
>TCRU_7337 RNA-binding protein, putative
MASAHSTSVFFTSVPLFVEARSLRKHFESVGHVTDFRLLGPTPGRDFRYGFADYLDFASA
EEAIKRLDGTSFGERKMKVTSAANSRSRKRNRHYTHTNEPPVRGGMVFPRGYVDPLLGRD
DTSVLECLQRMPVADAYEAVEQLRVLVLERKDEARKLLDSCPALRLAVVMILQHAGRLPY
GPLPLDAVRHTEARPVSATPTAVEEETTQKKADHTEEERDEVIEILTKLSEEDVERIVTM
SDEDLDRIPDLAQREQISVLRARLLDMAGDLE*
>TCRU_7338 hypothetical protein, conserved
MSQAAYCVKFYDSSDDEHNLQVAQVEPVFEETQSLPEESPGTDNREQQQQPSWLRRAIGG
TVAFVTSSLSPQLGAPAGGQLDIAKSSLSASTGSDDWRYREHRRLPFHEESPSQSDSRVL
SEDIAVDLCEVILQYRRTPNDVYKRIILAALEFGEVQINGDVLRAAAGNRELIEMLLRSG
RVNVDDRDVQEVIQEEINSVLLADELQRGRIYSDRIGYLTLLCRVPSATLTKEQARQCRQ
GGFEFAKLLYENPHVLRNILPPSWILARILDLCFFLGMLITWLGLAAIVLNLVSVAWLAS
IWFGRSHSSFGYWTILCYVAGYVGSIVVVMISEEGRIRDYDDRLWDYPDNSLKVVPCIPI
FEIALMYVTLRYELRRDKAKYLVIRHDLYNGFSNLLIINTFLFATPQLLLQYYLSTLYDP
MTKKLSAYKLLLSVNYTLYGMSMSLFMCNVFFQYSCNSFGFAVMAVKQAIMLPINITTRV
LIITAIFYLECNIIGSVMSLTEIDACSRGTIFFTSIAVALTVLETIGLVILITFELTRHI
WAVCVPLILLPVILSIYGSVGIGRKDAEVCRLLALSTSINPPFVYVAFVFLCATFFAWSG
FALYGKLTGKHLYLRLDSHFYWSWRR*
>TCRU_7339 hypothetical protein, conserved
MEAALRTICIIPHEARGDEFFDAVFEDGVRALSQGRLHSLFFSHVLSPAHDIAGHVVGPL
LNKVRQGGNAALIVALPEGETDDMSADGAGATSGEKLEVSLELYGHLLPLLFRSAERCCF
ARVSAVTFSIGDKNVHDLLQRCDVRGEKDVQYQLIEREGSSSRWGTIMNLLHERHAHLEQ
GGILPLESLLVVRVELEGYGTVVLAEVGCGRKTLDQLTLFLRSGGACGAKTYPPRGLLSS
SLRDMTPPAALVHLVGIPDPSQAPRSTMRLLRFMSAMFRASSEKPAEAPLLTRDAPQQRK
PQRGDTTSISMLCRSDLRESEATPEAAGPASPRKPHRAYPWAGELFVDPSQCAHLLPTRE
SATNMPTWDWGTARPEQPFRDTVRSNLPRAPTTPLDGVLSEGSGPRASREQALVNRTTTL
DRTNRELSEALSAAKAEIKHLQGLQQSFQEVLRKKQDAILSLTASSEKTMKENADYAKLV
PRLLRKVKGLEQERDKLQQTSKEWENQTSEMHGINRRLRAELQKLQKEMKCMAKKETQRL
REHALIRIGTGKGAKRIARRVGGLNSPKRVHSVPASPVSDASRQSRSSGVAKKGESGSTV
LGAIEELRQRNTALEAEIEKFRRRQPVADNHVEDDAKEVTVARGEQGALCSNCETMRRHI
LRLTEELDRSYKENKKLRSLVAVPPVVSSHTPATVRDDFVSVVAASLMTGCESMCAQLKH
TEAEFRRKEEQGVKTLFSGSVFREHMEAVAALETAVRDISSRRYRGAECYESIVPASATA
ADAEHLSSLLSFELERGTHLRAFVPTFAQLSVATEHLKMRVFPSES*

>TCRU_7340 hypothetical protein, conserved
MWSVVEAKQKPSRRRREKSAAKRKQTDAIFTLAPTVSSRMISALVRDLRRTSEALRGLTF
ACRDILSPVRRFLETRVDVLTRVHLIALGIGPFSRQESRSGFLQMAFLLALKNECENVIQ
KQSKPLAPAAVGARVDTFPGAGATCLSCEGSPGLFTSFFDPVAGDLYACCCEKLGVVMEK
ENRYGAYTPNDLNALLIAYLPHCPWALLRNLFVSNLLPCREFAGAGHVGQLGSVLVVGND
LRGRACRENDFLEALIPFLRFDTVRAEQKKGNPRVVDRVEDVDNSIPSGLRGISRNDISC
AFSDTAVMQTNTEREAEFLEALPRLRLPPLVRDGPDLL*
>TCRU_methyltransferase catalytic subunit, putative eR.1
MVITPDYFHCITDPRFRRSVYEPEADTFLLLETLDRDADMLRSMQPRRCLEIGCGSGTVI
THLQLVLSGISGNTNNTKEVRHVSGRTWQSEFHAVDINPVALEATGVTWSNTLRRLWGDE
APHLHLHHGDLFGPFQHEGAEGPQEAGAGEFDVILFNPPYVPTTMDELEGAGKQGDFITA
AWCGGPRGRVLVDRFILCLPRFLSARGVCYIVAIAQNDVPELMEKIRNVFKETGQDDVRV
PVDVMVVSERYTGEYLKVIRVRRGPRGDPHGS*
>TCRU_7342 tRNA-sepcific adenosine deaminase
MEEVVAPEEPPKLVCGVAIRIPRPTLSGAFLRIANNSFPLQPNARHLKRIRKAPRAEALL
PYNECPCTLSDCVSRCDNGAKEAGTLATTAEASLELLLGVGCSIDVDRLKEFDELSGNAA
PLTIITVSVPDRAPRTSVVEWKKWCALWPFAVPKPRPASPLLLDEMKKIKSVFNEAVMPL
VKEGHNKGTLGIAALLVDSSQDWRVLTKSDGADLMHRSNAAACFGYVPAVESSENQILLD
HPVTDVLKKLARVQQAQRWTKDNVPYLANEIDLFVSHEPCVMCSMALVHSRVRRVFYCFA
NPTHGGLGSVFSIHAIPSLNHHFRVFRCSASWLFDESNSPPDSSAAPGGSSSEFLREP*
>TCRU_7343 hypothetical protein
MNFSTVVGADGVPQEALLVRERSLLQEAEAWVTSLRARLGALESRASDYGVSPPHSAGSY
SAENVRLTNGGAAACGVSPPSPVIFREVEEPRQPHATLQQQQQACASPGAAAMGECRFSG
SDEDEELCAAKSENAALLAAVEECQLRLSEWRQRRREQQRQPPGLKKTSRGDDGECVGGA
LSLLARCSFAEAKRNRLHREVQELSTACDNERAVHASIADELHHVSAWAERVHRKRLLLM
TERAVTMDLAREEHANASITATLQAVLSKRSSTNGTL*
>TCRU_7344 hypothetical protein, conserved
MAHLLSSHDRQANHHFTSWGEDAQSALDETALNEAFMYRLRRMEAASRLTDEMMAQVRAI
VDTEENPSYTRTTEEIPPFANNALRRPPKGGADAKLDAGRTMVLDGVTMPHSPEVVLQDE
INRKIQKIQEMRMEQQSAAESQVKPTFQLVENSMELPAPPEVFTSTSLAFALEALATSVS
KIITATDKILVHLALLSRNNSPSVFKEMNVFLLYSKHAWRCYKSVLQHLKQHEVCAKALQ
DATFQELSSMREQFLVRKEMLTAQEQKLKVSEEHLRAMRLRLNNLDAQCHMWSGVLLNIP
TPPLLAPSPTASRRISVTRERESPSLIRSLTNRSQSFAPRVSTVGNFPAQRRSSVRVYTP
LVLPNIESSSSVSSTEEELESRLDNMEVKVARFWSNPYVMKAQQCAGRIWRQRHQAQQER
TPTLIEVMGLPTPSRKESIHHLGSSLLVASDLNRLSVHGSLYKGGHTTEGVDKATAEARL
ISLLRSLLRLASSVTGQTEATASSSTAKPEEGDDSMELRMENGDAPKVTNSIEDAGALAA
QSVVVDAAGAMSESVRNLLKFLEEASVTTT*
>TCRU_7345 Ras-related protein RAB2B, putative
MSQHHYVFKYIIIGDSGVGKSCLLLQFTDKRFEPLHDLTIGVEFGARVVTIQQKNVKLQI
WDTAGQESFRSITRSYYRGACGALLVYDVTRRETFTHLQTWLEDAKANANTAIVIMLIGN
KCDLEAKRQVSREEGESFARKNNLVFMETSAKTAQNVDDAFMKTAMMIYENVQSGVVDLS
VVSGKPSPAAAAVTPATRGGSSNQCPC*
>TCRU_7346 protein kinase, putative
MENYEVLNQLGDGAFGQVVKALHRKTGQIVAIKKMKQKYHSWEECVKLPEVTVMRRIHGH
PNIVKMREVIREKNELFFVFEYMDGDLLGVICKAKQMQGHTTAGNAPPIPYPKIRSYIFQ
LLQSLAFLHQRGYFHRDIKPENLLVKKDPTTAAQDVVKLADFGLVKEIRARPPFTDYVST
RWYRAPELLLQDRAYSSPVDIWAAGCILAELITTRPLFAGSNEVDQLHKIMGVLGSPNEK
IWPECFALAKKIRYSFPAVKGVGLERVLPPHLPPQALDLMKQMLSYDPKKRPTAQQCLQH
PYFSVGLDEENFSPSNVSKQLANAVKKYVSGPQTAPSRNTLVPIDLNAKRSNVGATTAIS
KQAGVGNPPPLSPLQALCSPTATGLSPVLLGEKGDHHLPVSKLTPAVGSEGHKKRKVLSP
KLPSLSCEKLKGVVTDVLNGGDGGNNNGDVDLDALTKEFENELETLKVLPQQKKQVSLCT
LGDSAANKVFHSPIFGKSLLVPGATRASPKVNEDVVDFLNSTRYKRSSFSLMENGGPLHT
TRKASLKKQDPLPSLPPALDSCHHAVSPSIKALLAKHMKKRNDSNS*
>TCRU_7347 RING-variant domain containing protein, putative

MHAKTRYLFWLGLIVLLWTFTAGREAAQQPTVALFNGEHGTIMSVATWSDIDFGRRSAMG
GGKRPARVFALEATLPVVGQEKSSKDDERVNRDLYFFPYCSATKNSADKEDSNAPCSLSH
FEGYILLRFRGGWEENFAVSLWQDSAPSIDVEVAERVFRDLINDSSATFPFAIDGSSDKD
STFSGIMRRYELIESCNDFTDECFQARLMTYTTSFKEIPLGRYTGRVIFSVGLPGAWNRP
WVLRLKSTMPHDSLTGIDIVLLLVDKKGSFNWELWLTSSGFGQLFLAVLCVLVTMCFILV
TKEVGMRLSEPTALNGRRTTVLYEETESNNGHCLSLYRIMLATQETCMKIFSWLFVAKRA
MHRYFHSWPRRRWEGAASNVVISAEMREVASNVEEDSQHMEPQSDCVEMNGSSEESDGDE
YLCRICRSKKPVDDLFAPCACDGSAKYVHKKCLEKWRAMTLNTEHRSVCAECKTPYNLVV
ERVPISPDEFLHSPVCVPACRLMVKRAVGPLFLIFLLWIGGYYLKFCMYLVTGLDEGVVW
SAANFYHWVLGIYSVVALCLNLWALEYVLIDFDESWQQLLLLIISLCTVEIPLNYVGQIT
LSWLLNRHWSLEVSYGLGIIVTAVSSITLLPHLYVFLQSLSTEREVVLPRVEGAGNRIIL
*
>TCRU_7348 hypothetical protein
MIPKSPPERKDSGNGNERTALFSCDVCDDMLSCFMAARKADRLCWEQNCLLPSYDNDVLI
ATFLTYRLRLAMLEAKAEYIQRRLEDTVPSRVAFASKESEEEMRCALRKHTEAAIERLAE
VSVSCWVEEDVHSELCAFCAGLLGDENQTTLRGIVEEILLEATTYN*
>TCRU_7349 hypothetical protein, conserved
MERRESEVDPLERPGNKLYVSGQCNEIVLNCWTESARRQCLPSLMRVDSPDRKRTPSPLY
HPLSLSTNTEKQQQQPLPCINLSGSAGSFLNTSEDEVLMAWNVSPDTQPQADPAQARGRR
PQSSELHQAIKVALGKRWRPYANGAIRRYNVPSRLRGGSVNHDGRQESPFKFIEEMAQRH
AEAQAEKRLPHDVFAPQQLPPRQFVVRLPDVDPRRVADEVNAKPKTLSNAEIPTELLHRK
VLFDATLGAVKPYALRERGDQGKLQRGRRRKRPGEVPPSMPLTALSRDPLEVFVEAMRYQ
RPALGVYTFDVY*
>TCRU_7350 hypothetical protein, conserved
MYVVNLCGLPATAHFASDIRRLGPAAPIAVDLNSHHELRDDCSPSTTAGEDLATTPSGME
CELPDDTAQATQISGRSVSFPNVNAQRVLRVFHWTSTRLHGLGPSSAIPHCRDGGRHPTT
GRHAATTETCRRCPA*
>TCRU_7351 RNA-binding protein
MYGQQFPQNSLYGTPNMMSYHGVMQPPISPQGTAPGMLSNYNNNPNRGGYDASQANRNMG
QRQPPRQRNNEIGEVSRVIHMRNITPNVTQLSIQNLVQNFGNIKHIVMLRQMNQALVEME
STKSAQQLVDFFRQTGYAEIDGRRVYIRYSNHQELTATQHTSKTLLVSMFNTQYDVSAAA
QITPMIVYQIFGNYGSVQKIVVLPKNESSQRNHNRVQALVQFDSKVTAENVKSILQGQPV
TIGDTVTFTLDIQFSRMDDIKTSNPAISLVINEDGVPQPPQPPQPPMAPPPPPPPAPQQ
QPHPSPQQQQMQGGNMYPVIPQQWS*
>TCRU_7352 hypothetical protein
MAEQGLLLRQRNTVVDFDLHPLAIPVKLEGVATILSHLLCHKHVAEYIGVVIHKCREGRQ
AAALEVLALLKLVTAKFIGKKRQCLALRIQVTNVDPWIIRDNLVVDHKPLVLKRRCAVRK
LRNL*
>TCRU_7353 radial spoke protein 3
MEQMHGRAVGEGGAMAYTFQHPPQGFIRPQYRDPAGSRGRKQYANIMHDRRVYRGNTYAA
TPISTHAMEEQAREARELVRRKKEMAMRAASIKRRKEMDLAQRRLATPPPVDGRQHIEVQ
TEEFLEELKDEVEVVTQETQTDPMLDRPATPKYVPVKSGRDAESQINEGDLFHFDDAVDP
ILDVMVGKTLEQAMLEVLQEEELELLRQQQLDFEQRRKEELLEAQRLEAREKRLFEEKER
RKKQEIERIKREKETREKLQARQFAKVYLMNLENRVFARLQDEGWFRDRVVHEVEFDFFP
WLMEEVEEVLAKKRQARVLVDDLIRQVVTMQLES*
>TCRU_7354 Region in Clathrin and VPS, putative
MAFSSGRSSSTDSSSSSLLYRHGEEGETEALAPHFELTTIMHELEEPILSMDSQCDVMAL
LGEKGRLVVRDTVQDITPLTAAIRNPYRVFLDPTGSHTLVAATDGEMYYFSSRQRKVSGH
FLLQHRAGARDGAMTVTSAPLLTTSNNVAECVCWLPVKKTKEPNLTTTKVHCLVGTKLGG
FVFEVKIDVGGDGAVKASCRQCLQLPAGEFQSSLASIQVERVNSLWLIFFSTAARLYRAE
GEASCPMDLIEKVAKEPEILHIRESSANSDVSARGAVVLYQPGVGMPAQSYAWTSTSGIV
HGLMNRSIHHDLSKDEAAIFGWSGATAVVNEQLLALTKVKQPPHDAGAFSSSSSSSHALP
QTKMPMEVALTAFHMILLYNDRLVVLNHPAGLTWRGSSSTLHGDCPYACEIEERIRFDPF
RATRKLPELRGIVRDTAARKIYIFGKNILWELQVEQEHRQQWWLFLYRAVNRNESLPLRK

RFFQAAYNISKYRASSKNIVQLLRGKFLLQIGAIQYATDILADCDRFEDIYDLLVSLRNY
KVLQLYVEKRYKLLSKYALDTPVMQTQLACLFALIVMQRLNGTTRSEVSEKTSVEATASL
NAFIEQTIKEKPALFKSRSYNDLIARLLEGQGRPELALCFAERIKKAHYLLTYYVSHGNY
IQAADVLSTLARRTETLELWYEFSPVLMKKCPIRLTTAMLRVGTRDSQGGAYMLLQLERL
IPIFIQYSPEMNEDPSNGEHQVIIFLERCINKFDCVSTVVHDYYLSLLAQHDGERLEEFL
ESSLFYSVDFALRRCLEARRYRQCVGLYRRLHLYEDAIRTALECSDPTHGTDEEWPALRV
AKDVLRSLPNSMESSKVKKLWLIVAQSVLEKGNARMALSVVEDSGGVLKLEDILGDISDS
LVVQEFKDSICKSLDAYTSSIAALRDQQLEASQISENLKQEIAQLQDRFGYITTRQRCML
CHRLLLRGSAPYFIYPDCQHAVHEACAVSKLEEIGGLEAFLADEGLPRQFLEGVTSTSDL
AQMECVLCGEASIIEIDIPLFVEHHSWSVE*
>TCRU_7355 hypothetical protein, conserved
MKFWVKAITDDNFQEQLLVKASNLPELTKELSRLLHTHVTWMSVSDFQTQVVEKLKSGVE
ILPVKILTSKMAGQPHDGETSFVCSEPHTQHATPAQVDISQTSSKEDEAWPFSSRSPSLS
EAGVVARPSSASWALLDIPQVDRICLFRKDIELLLHPSFGGTYVDIVAGCFVRIRERQDY
GLYQIIRLINNMEVLLDIIHYEETRSIEVVSNAPPVPQEVSTWGKKMVSAHRCFMAPGFI
EDKLGDIDSAMRAARATLQDQYFQMGITPPLTPPAHARDSSGQHRRRTLLARTRMYPFIS
LGQLVLETNDVLLHAQVSVIEEPETDAFDLVLFATRHANSGKEKIRPSDFAGCMLTINKS
GEPPVILSDRDVTVKGYEVFCPPQKWDCQYVTLGQIQPSVDSILYFDDEKKYTQEFTVLS
GDLFGGLFNSPTTTMLPIPVWAKTEGVSAHIIRPHLVVHREKLHAFYIVRMLGPHPPHRS
SLFRVKGCGGLGAQVGGEESSIANVASDEKKAVDTSPTSVGNASCDGSFCENAMVGVCRY
SLAHAVCLDPELHSWKLVTEKGPLFSCFYSMPIFTVASTFYAKQDSDEACSTPLKNKQKV
LQILWYEEDSILRQPSSLTYRPSRLSLPSSSTISNRASLPFERLVNSHEELLPEHWVQEP
CYSPVRVDVESLKVAVASLSLFECYSTTFAACLQRDDKQRSVLTVLPLTNEP*
>TCRU_7356 hypothetical protein, conserved
MMTTAMTATALRREVCALLSLALLCCCASVCVAATAGTIIKTENLYSGAPAVNVSVEISC
ADSENKSQWRFPGQTNWTKCAFAQGAHEYVVLPSSADQKNNVDQGSTGYYTVDTSEGDDA
FVEVVLLEPTSADSGRVDESLCLLAEQMYSAAKCNKSCTSSNSDAIAFTMEFPTNKESGV
YKEWLEYNKSSNPPKDTTISTSGVCPLKTTVEGATEEVDGEPQETAAVTPTAQLTAVEAP
AAEQAAGSSSSAASGASSSAENIEQRITPADPQPGNTSQLPTGEVVGRTDASGTTQTPSA
TPASGNGGASGAATGAQDPGTSDGSAIATAWVHTPLLLLLLTALACAAGQRCGAATHE*
>TCRU_7357 kinesin, putative
MSSTPERKGRGNAARPSRKSPRIQRQPPPPPPPAPGPASPSSSSSSQVKGKGEQQKRFSS
SARSSHMTPHRNGHDSKTPTVSSRTGILKRSPPLQWESSAPSRSPMSSRGIFFNEHQRIG
SSIANTVGGPKKSNPHVNHAGSPNATTVSRSLYEVSPLLGTINSDNLAVSKDVVTPSSRP
VEPGSVSVVVRIRPQFSRKTTQPCCRVLGAPGIVEYTVSMREPSALGNGVQMSSSSAVFS
RQLATGAASQETRKILFSFDATLGESANQADTMACVGTKMLQYLLNGYNATILCYGQSGS
GKTHSMLGPAGGIPDRIQKREDFGLVPRMLEQLFTRLQEKFPREQEGGEKLSHVVHPNAV
GADGENKGMTKSFWQLEIGVLELYQEELRDLMADSPPLFSPSRADSLFSVSNGVGTGRTS
FVPEFDEENGSDALDIMETVDKSPSASRSFPTFTSRLRNMRSVPPTARELKIREDPDWGV
VVSGLSWHPVNSFEEAMPVLLRAERMRRVESTALNERSSRSHFFVFLSLQQWGVVATKQS
GERSTAVVSNRTRSLLTLVDLAGSERVSATGAEGQRLKEAQNINLSLSLLGNVIRKLTAN
ERERGQFAHIPYRDSKLTRLLQESIGGNAFTTLLCTVSPDISDAAESLSTLQFAQRAKGL
CNRPVVNHTETKEDLKSRLNVAQSRITWLENQLAILMNKPTEHQSVMEREEKNVNARGNS
ELDICKMNGNPAGQASMGPACIVHPPIFYDIPGETEESNFDLQYIPGTDIAQILRDELYR
REEEYSRVQNEIDMYTRLLREEREEHERMHASFLEERRRRLEMENQLRRVAPSEYGFAFS
RDNMEVEGNGDDHDRVGTSSRVLMHRHPERETRCRTLWRHQVTDSPWHRPRLASESLHRM
LNLMPFIGQQPGNAVESISSLGLPGGESKSPSFLHTPPDVSLTCYSPGRPEGEEEEEEGR
SDAENAFRDSTHTIMMDSSSMVGMLMQYGVDDMIQS*
>TCRU_7358 hypothetical protein
MPAHCMDPTTSGCDGNVAVEPNTYGGVSANGRHTAGCHRHDATKASRKETHCTASFISHT
SERPQTRMHEARVRSGEDSSAALVSPQPQPRPFSKPIMTTHGAMNSNGRGNHGVVEKNGT
RGRTYPLHRTLSLQQRRKNSAATLEERENCHDDTTHSSSWKRRPMQTTTRRLYRSATTLV
TALYSSYTAGNESQSWQHTHHRVHSFTFNTAPSMHHMKATVDSSPGKNGRQSRRQHELVC
LPHRQSNETLVRHATPMTRTATALSPLSKKAALRPKPDARNMNTTKKQTNHDSPDKMSRV

LLRPPSLKPTSHGGSTTASGGNTASLQPWYARPTRSSAHSFTTTQPRERSVATKASSTLT
GKIEPAVRMASAPCFPKSTKATRRTHSSDSLLGNQKRTFSSFLNIASDSIRQKTAVKPAL
WKRSPSGIGGTSNGRGIIGAFCKVSVQNNRKKTLSTPKSIYKPAAVRRTGEVSAIRVFAS
PFLRSAFRGNDPMRRNSLIPSSAHKEEDESRRRPNGIVDGHDALNKNGTSQSKPALRAAS
MTIRATNSTLCKEAFTREKERQQIRQKHEQLAAEVRHLPRALWLATRRELGRLAEIRSKR
TSGVVVDGDVMTPRTPTMHVFDDSHGDKEGNAREMQRQRHDASKAAVGTQQPNCLEVPTE
RGKQFQDHMCGMHLNHEMRGNGLNSPYRGPMRLASGRQQGTHFLFSPDCRQRFTAGNDND
VEVEHKGEVLLSSTLMLRGDVEGREGDGDNNHCRQCRNGGGGRGNDNNNRSGEGGMLMES
SSHGSDCSPSIRPPSEIFDYIPSPPSASAPQPLNGGSIDSEFDSPLVVPPPNKRSPLPAT
RRPRGREKKTPELNFHRTRSSLHLSYSVTPNRRQLQQDSRFNSNMLHASRGGSILHAYNQ
LKKNTKAVGRSMRGDGTVVLTSDMLVALYATIHGTAELSRGNNITRSYRTHSMNNTRSDS
LTGHLAQRRGRRRLQDFRMVRTLSYSENKKTRAVGGSF*
>TCRU_7359 hypothetical protein, conserved
MLASVLRRGGHEASSSASHHIIAPVAALERAAPYTRFNTLRMHAHREGNFRARPAGWRAW
RDPALQDPYAPFVMQSPTRHVDRQGAGMWFGMGHFAMKNFFGILHWRLAMRLSIWGILGF
VIPGATYALRMHRNGWEWKNRGAVFAMD*
>TCRU_7360 hypothetical protein, conserved
MLASVLRRGGHEASSSASHHIIAPVAALERAAPYTRFNTLRMHAHREGNFRARPAGWRAW
RDPALQDPYAPFVMQSPTRHVDRAASGMWFGMGHFAMKDFFGILHWRLALRLSIWGFGGM
GYAFSSYAHRMRRNGWEWKNRGAVFAMD*
>TCRU_7361 hypothetical protein, conserved
MMMMTMMTGRVLLVCALCVLWCGAGGGGQAEPIPDSSDSASSKEKPQKTRKATDVAGEGV
QSGEQEVTEVPAPTKSEPEKAPAEGATAPQSGGGALGTASPTKDSGVQNAKEEKEETNEG
EAKQQEEARDEDEDDDDEEEEEEEEEEEEQEKEGEGEVDAKENEEEVTMKEGADTGTTEG
ISAGSQEQPSLPSGAERASNITNPNSTPTTGDDDPAADVAGTAEEKNKMKIKMPIRKKHQ
*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MVYPEVAQAVGGGLSWLCYRNVTFSGGGMILTVLVGAMAGDVVNVTFDGCTWRDGAVLLL
LGNAYAAVGSLNIVVTGNNFIDALLSPEGVFPPHTNITISRNRFTVTRLIPWSGLDVDSP
SCVAMNELVISNDSAVVLSGNVLQTVMASSSAIRVVGSALSVLWHSVFAVIGNTFHMDGS
NSTLIHLGGSSESFSLSVLNNSAVVIRGNVVTRPVKYFISFFWALRVESQSAVVFQGNDM
QGSLVVFFPRYSSNIYYNSWLQLSGNFCRVSPVVAFAVFNPRVNLRDSTVSVSGNRFISS
TVTPTLIKVPKRPRDITNGVVVAACNTVNGGDEAKYAIPSVYNATILNCSDPCTLATSCF
PAYTTTASSDGCACRCAEGGHGDACLPVAVPEPPSTDGADLCVRDVRVGVEVNVSFGTSV
ACYVGVTFAADVVVDVESMSGSVRNVTLANCTFVGGASLYVVGWLSDPPAGERADVLISG
LELRSGGGVLVASRFPPGSRVTVVDSVLIAEKRVAYRDAYDLGDASACLVVHNVNLTGSV
LTIARTQVAAVFGDAVGVLVVGGVALSSRGALYVDGLSVQTALGLCVSVEGGVAASGGSV
VAFVDSDFLLCKHALSVRGAVSVSGSAVALVRSDFVSTEDYAVAFYSTVSLADGSMLLAK
GNVHDGVSREMLHAAGAVTAAGSTLSFVRNRALLPRMLSASLSLAAGAHLRVACNDAGGR
VLSTAEEYAAAGFGDAGSIDVVGCGDCDGNTHCYAPGTASASMRNGVCVCACGSGGHGEA
CVPVGAPALPSAVGTASRAFFREGVTVRSVFVVPAGASEVTLRHVVLDGVSPVLYVPWMA
RDGVRIVVQNVSLLKGAVLYVMGGGALRGAVSAGSDESGPVELSVCDVEALNGALVLTGT
YPAGSVLTVTDSLLVATRPTPLVYLPGSQSSPYAPVLVLSGLRLVRSVLVVSGVALVTVM
TGGRTVAVDGAVLELVGGGVALDAAVLGGEYALYASARVVASWSAVLRVSGSQVYAAHGL
VFGSGVEASASAVVVNDNAGVLTDGALLVLRGSASFVSGSWLSVRGNSISGRLLSVPSYP
RSADLVRSTLTLHGNAGSGPVVMDGTVALGGAGRRFVVGCLTLNGRALRPMDYRSAGIIG
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LWWSDVACPTLAVTTTAAGGSLTQSDIRGGGSAVPTRLMVALPPPFRWARDPQLGTHLSF
VPVSTAQPRGFGGPWGAMLSNATWVRNATNPSTVLELAVPVYRGYFVAADETIFIRCDAA
AVSGGCKGVLLGSFTIRSDTLPAAASALSAITGVVAGAAAVAVVVTGGLGSILEMQALGV
FARMSCASAQERASTVALPYFLSVFAARDPLWMVVGNALLAAVFGCVHCGVTAAFQRWRG
VDAASAWAAMRFPSLTYVVAHAMHLGVFFGSVLALAMPGARVHHRVIGVVGVLYGVAFPA

GVCYFIARHTGASFTRYWQFSRKPLHERLLYPVGYWFPAAQQRMYGGMLTSMRGSRVYWC
VFQLSVLCVVCLIAAVHPPVGGCHVQYFCMAAVLLAGAGVVAFTNMMRSAFLTVMHAAGF
VLLAALCLVSAANHLAPSDGGARAYAAIVLLLTAVPLAVTVYSVVVWYVEDRHWQELREP
QRGGLEALLRDDGDGGEETQKHDMAPSSYATGTTVASSYRPPAPPLQTMAVTPAPTL*
>TCRU_7363 hypothetical protein, conserved
MESGQYTEQGIAPLWHTDLLTCFTTQLTNKWRSTIRQDTHRYLLCGTRPSDLSGKDLITQ
EVLHRQELVHLARARCGESELWGRLYWAVRDCTNQCRFCNISPEQSAYMRSNNDPTAPGT
DTVPPSAREEDVSPVRRRTLTRRRKEKCPHCDSILTGFSNLVSHCRSFHPEHPPPLPELK
CDFCDMVFPTRRSTAQHRSRCAHNPDATRHRNSSARRRSLLPQDQPASTSTPIGPQETLH
HLLLECPGTLAVRQRLGIKQDLGTESFSQWQLPHSRKPLSLLDHLFGTQMALYS*
>TCRU_7364 Domain of unknown function (DUF4486), putative
MQATGWVGSQQRNKKEEITEGGGGKLEKKQRREGISVLDECKKKFKLELRRLVSLHFSAA
DSADIQRQRGKLRQLITDVRCGAAAMSCTGTLPSLPATLSPSIIAERRQRTGKETEKRTA
GVLRPKNIPFMSDSAPFTQTNSAITSQKTAMADVAADFHTGTSALTSPTHPSIELDVVVV
MTEECLAAGQYLLARGLYEEVIDVCLDPLEKDIQQVLRGAAEKVEAAWLAARTSTTRGAF
NVMGLLDADDTQVLRFGAEKVTAQPKEILYPWRLLAQYDIMRYTCQFYCVYSGGDGFPKG
ELETMKLAASYIDAVTSCLLGIARLNADDSYHILFNGTITVYEMCLHMLRQAGERVGDAA
SHVTRHIALCLEICESATLKLATVRYLPWRLRLYDLIAACYEKQAMYSEALSVAQRAARK
VQELIHLEFLDTVPPPEASQEILMQAMDHVLLTVMRYKWYVKSTTIGGSATGNTASIGVT
ENVPLPKQGQSGSTTTLSALAEQELIMEEMPSNCLEMIDRAWQVLLKVELPKRPAPTTPA
AASTSKGNEGKSKVQGKQQSKSKQKQPQKQEVFNKDIVARRVWGRLVQFLLSLATGSTLP
LGAGDHVTSDPLISSQHASLTSMSSIKQLRIWAVEALEFLARFAICSYVQANPDVVQQGS
PEDFAALELMCKQQQEQRQQTSAANETTSRRKTDRGLRRSNRTQVVVQSSTPAAEDEIFL
ASITLERLLYSISTYNVTTLGGAGADAEKIPTTLTLHTEGMMNEEVLLLTLLMHRVLYNG
NDAKLYDCLCHCSISSLLQRYGEKEDDVKQRNITKPTNNKKMVPPSKKMLQMHLLDTVCV
SLHLLQRMRRVGLGKRVRLKELASVAQELERLIELSAGSTTSSAISILQQSKKDIVATTA
LPSTLPSPPLHCTSTALSGSFAAIYKGLMNECASLLQQHAFAFAPSSLHSNYALNTPSPT
YNVAANKMMFRDDGGEEGEEGKEKKEEEEEAEEGEGCDATDMYHRVVCAYLGAKLSSGVS
DGVGIGHLVLAYLQEMELEMSTNQMDTADKSDRNQSGGGESRGGSASTRRGNVIFGPRAV
LARVSNGKMGDGVTDQRFYALDSSMNAIRRNCNRARMAIASIRMALGSLALHSKQTHTGR
RGVKGGSSLLNLSPKRSPVQETFVGSHENEEELERIRLHHEISDMRTELTRWLIEMRWTL
AILRQHYAALEKHKSNVKLVMERQANTKVYGAPTVKEANVLESFLQSQPEISHVSEDEKG
RLLAWARDEGDDLLHALILICLAPHQPQMKTQREMLEEAFHLLHRHADNRGQTQPLGLHT
KQQGESAYSAFMISCYAVSTCGKLGFNQMTERAKDVLYSIFAKSDKDDKTHEEPDIGMET
SKNKTASESRYISASTFLLRTNEEVLAVSSKLKLQTIVSALLWVSTVEASRIPYQNFERT
GLMSFIGKSVMLDVPFEQRYGLKKVQLWHMRIAYQLQFAMDLAGRVQDSGLMLQCAFELF
NSLLPSLTDENYYPLLLLPLATLCEALMRQPTSVWSDAYVQLLAARTIDALLKTVRKMAA
AGPDVESAVHDAFDSAKGGLAVMPVSIQGWYELLLRLFMHVWGNIYNHPNPRQIRYQESV
RRGATTVQKVLCPDQGGVDERISPSPARNNVSRATTKKANSVSGGVAAATRPTTGNLTAP
AFPGGAYAVPDTILDDCVPIEFMELLGEILFTVPGVNAFLTHLFGPKVDEISDRVQSVLM
AENLVGVPLWLLSVVKGLTDRTPSVVFDCLQQAADDPLYARTAVYVVEHLLRLGDIAAAR
RVATDALQVIQKLKQSVQEHQQSVMEHMNDWLENEGYMLVTPSRIKRKAVEEETLLKGKR
QKGRLAAKGGAAGTTTSTPEEKKAHHFADTDERQWTLSEQQMLRQLTRGLAYVRRRQAFR
WLRGRILQFNAPYQAQLHFYLSVIAQKLLEQRQQRPAQEGDQTATPVTNARPGQKSKGRS
EEAALTRAEELKAEEKEDEERFIQHAVRSAVLFNRCGFPSRAFATVSQAIDGLRMLVCEE
PPDTTLRDEELLSPKQNQQEASGEEDLPMTPKTARVSFDCADLGKECSHAMEMLISHEKL
IQWGPRILPLARALLRVFFLLWNGFVDYRRDVDFLHPAAVKVGRNVELEEQLHFQGRVPS
LHSYATAAGQYEEARLVHLANVKRARLIRWLEWRIREVQTAEQKGRRVVHLQWLTEMRAF
LADQVSVGMSSLRPHVTDVEKRIANTMEQEKTDGGKQALAVSPKKKKMKKNLQPRQGVMP
EPIRIDGADATALIALRFGSAIPAEKIIDQLMFLLRSTQFSCQFASLELCLEVHKLTGGF
FADDLLPFALSMRRNIVISQEDELIKEYGMLRQNEPLQKQLVRNARLSWEKYTTTEAYQR
VTQRLSRTQLPSKRNVREGSIGKTSFVETESASRMSLEMASGVKLVGRGGNLRQPPPRDV
IFRFGAATTYLQRRRLFGPLSEQLYELGWIYLLHRQRLEAERCWIEAVDAALEIPDSLKR
PPETWAQLQIPKIGLPRLLLAVISITSLAMYIYREQQGKAVNCYLLAARILERFLEQGTT

SNFPQYLRDFGGFMLEDLVVLPRLGDTMPTLIPQLAHHMLFLAWELLRFKFYFYAAMVAS
LTEYFARIHMRHVAFTAEARLVQAMAASKFGSYRASMKILRDVCQGVRIPRGALDGTALR
VRALIEGVETSKIGKNTKRGDGGSNSPSRHVEPQAEQQQQQQQQQYQSQEGLYNDAELPL
TSDNVACIQTFLTQCLGVGVANAVTSNPMTSTPSPLSNATSGSGGGSLLQEAVAACYGPF
LSQRVELAIADFLVTLGSKESAYVWCVFATQQTSFMGERRSARSRSLQRISLHGFGDSAC
IEALNAAEQILQLLIARQQEKGHTSTGDTTRRKSPVRDRITSPVQGDVQIKRGQELEETY
VRLTSMLLLAKIYTARGEPSKALATLRALVTNFNAHVESNSTAPTATSAPSYLWTVATHI
FWCDVYELMVVNHVRIREYMAAQQVIRDALALCEQCGDPFSGRVFSLYSSAINARTGSLT
DAIETLCVLQKASHSLSSDNRIDMFHAWTSLAAGSLKRLLHHEENEKGETSSSPSSFSIS
SVEMFEFAVKALQEYCETYGLLLGTGSLLERKQLSLFPENSLPRRFFVAWNVEAVFLHRA
VNLLAEEYMRIGKLELAERVLQHAISALTPRYDTSAHPTPLIESQFILARVLCLLKPHLL
NEQQNSVDHVRDAIYSEELNEEDVLLLLDLPRQQPVRLLIDVIRGVVACGTHDYNILRLA
LLNLAALLSRADRAFHIMAATCVILAKFVEDMRFHVFSGMSIFSLYGEEVIHIGTELVVP
ENITAVIRSTQRSLGNVSEKDMNGSGVGSGRAVTPVFSQEPRRPPSRSREDREEAALKNT
VTLPILVAAFASLHMERSLQYVFPPRELLDLETALQLIRAYLQLRTAPLSGYYLWYDDVT
REAQMKQQQQQQQQQQQQQQQQQQGQGQGRLGEGIRARYSSFAGMDATGGTMSLLPPIV
MDRPPSLLSTTTLMNLGIPKVNTVICQSFMRDVDRNLSSNANGPLPRGGESYARAAGGFA
CTPPTRATHAPAMMTFVLFVSPVHDPNATQHSPINEKNSQSQSKKSNRSTTKSTVSMMEA
KILSGSPLIAHTWNGTRCVMFELPLEEVQILFSEAVKTLQLMQNLLSFPVMTSLGAGIGS
GGSGIGGGGEAEVSVETALSQQLSEALVLLTAKTAPSTTKKGVRAGTTVEFLLNGTLGAS
PGNNSIASTKQGEIAGQLEGDMHSALRTATADGVGDVPAVDEAKSKIIMGFIELFVRSVV
SSTVTDDELMERCIESLLPRCAVSAEVVCFLKSMLAGDGGGVALFHPGIHEWFARMAKFV
MEHTEVMRPEAHATRTRTEGR*
>TCRU_7365 hypothetical protein, conserved
MQGCLQLCGEAPQGAPLSGESSGSAADPEACAARDNVPSVQRPASYGPRGAGHFKERSSD
TVQGVLGVPLPEDAHPAAAHSVPSENSAINKRDADVVRGDPHVAADASQFLEDGISRQRN
GRRRLPRYWRRCGFRAYCATHVLNITETCEAFVPCGCATPNDPPQRC*
>TCRU_7366 hypothetical protein, conserved
MRIAGPKSDATLWEAQVLRNAAGRHASMGEERESGATQYTFLAVQFDHTRQTVSLSEKFF
RSVCAMLTLNSSTIAEMEVVASRFLYVAAILGTRLCDY*
>TCRU_7367 RNase H, putative
MIPRIRHRRKTLLVVTDSQSLLAALNKGPLSQTDWTEDQIWQRLLTLTCAGWSVHLQFCY
GHCGVHANELADQYATQTMESGQYTEQGIAPLWHTDLLTCFTTQLTNKWRSTIRQDTHRY
LLCGTRPSDLSGKDLITQEVLHRQELVHLARARCGESELWGRLYWAVRDCTNQCRFCNIS
PEQSAYMRSNNDPTAPGTDTVPPSAREEDVAPVRRRTLTRRRKEKCPHCDSTLTGFSDLV
SHCRSFHPEHPPPLPELKCDFCDMVFPTRRSTAPHRNRRAHNPDAKRHRNSSARRRSLLP
QDRPAGKPAHSASRMPRRLCRALTAGH*
>TCRU_7368 hypothetical protein
MLNMSSTIRGEFIFCYKLAADTVWTRVYGELFIGSRDPAEVVQTPGNAVEGELFTLNFTA
SEDSPSLSEGDRVAFYTGDLSCLVPGHDADVIITSPSRTDLLPRNLLFQLAAGTIGNHTL
CYWKSNGNVIVWGFETVVIGRNPWNYTTHPAATFLRANQLVSAIFWGFGLIADPVAEKSD
QVKFIPTRNPQTDAACQTIAQETSVVNYPLTANGTLSVQVVRFTPPAVGFYWVCYKLNGG
QFKVMGGDALVVGAANPCGAIPAKNVKTLWDGEMNIWTIDARTAPVEGGIVFYSVHQCNN
FPYYVTPEPSITQFPHGVAVVRNGVALLRTGSPTGDGVIVSLCYYAEGVITMLSESVMQV
VEGVPPVLKEPVPAMALQLFRFGLAVIPTPLDYVVLVANSDDCVGLTAPASSSEIFISFV
TEGDQIVVTTAVELEGTFYICYSHRVGPCGENATEECARIVGTVLASAPNPSDWFMTPNT
VYTSEEAEIHLVRRLGNVAGAMEELWLTPINITQDTTMKEVALACIATMTGGDRIVLQPQ
VNQSNVWKTRLNVVASYALCYLSEGAALPTIFPPLSRAGPVVQLTNVASVVFPVAPVVGT
AAAVILQGRGLSQDDQLVAVGAPATGSIPADICTNSTYTPRVTAEASKSGYGLRDMVYHL
VFESPGSYVLCFQAVASTGPMVLITPNSFEVDLTVLSFTVVSVALTDTPIELEFRGSGLR
ASDEAALVFLHPDTVAESDICAHGKYTAVSSASPDGTTSLYVTVVTNPGTYAVCYTKPGF
TPILLPNYLSVSVRTATGARFTVRPSCSALSACSPQPVVALINASGEPTSDPGATVVMHL
NLENGTAADELLSGGAVYTQEEFSVFYFFEITISTVGTYVMEAEFTLRGGVRLVASLPNL
VVTKDGRKEVMAVVTCVPVGIIERSLLSPGQSNPNVNITCVIETKSPLAPKAYTVQLNAG

KSTDVVLDGDSTAGLPRYNFTVNPPYDQPLIQFVSIVTEAAPPFQSWPVMNSPVIVRIGS
IPEENSTLFCASNSMGLPSKTMVRLNDNLTCQAQGKRMINGVEVNIVALPKYIRIFSEYD
DDVRTDKAINIGAYPENLDGNYIFYVNVSEVSSNVSIIGNVPMSQTSIVYVPMKGSPSRF
TVIGEPQSGESRISCVSESSGSMLWFTPVERFQCTLSLRAGGMPINGVSQDFLITMPEGG
STEPMPVHAWGPTLFIQGATPPIINNVSSPRTSNQLFSVLVTFTPLSRSIASTSGTLVYA
DIVELKKESGGEVSLTLMGSGLSPSNKYGVRSTPECAEGVDSEARVTSSKMSTTELQLSA
NVAEGPFYLCFAPSDQPERWQSLSSEALDYISSGGLDKWKTLLIVGVILLLLLLILLVVV
VWRVCMFKRREESQYVQKAVYMPPRANYRFLRRDRTETQTTEKLPPSAPTTTFKPLAERK
EMVSSPMRRSNHKVRINIHDHDAYSDVEVEGDGETKLRPMAPGGLKKRESNGEMKKDSHK
FAELDSSEDEPSRFIPSVPPPKPPRDDDVIPLIGAVEQATEARLVAGEETSRSGPYQHLH
RQPQERPPMEAQFSPSSNVAAAAASTTTTTAMGEDADRDQQWVGPFLVRGHTSRPMVNQN
SPSNGTVRNGDRRNGN*
>TCRU_7369 Enriched in surface-labeled proteome protein 1
MKDDTLVFPVEGTKKKENDGAGRDVKTVSLVLCLQGTESWTLSKEVPDDGCSDPSVVEWR
DGKLMMMTACDDGRRRVYEIGDKGGSWTEALGTLSRVWGNKQKGM*
>TCRU_7370 Enriched in surface-labeled proteome protein 1
MLAGNYSRTAATGHEEGGTDRWGLLLVKGQVSGAGEEEKRICWNDTHAIPLTLGDQHKSL
TALIGGGGSGVKMKDDTLVFPVEGTKKKENDGAGRDVKTVSLVLCLQGTESWTLSKEVPD
DGCSDPSVVEWRDGKLMMMTACDDGRRRVYEIGDKGGSWTEALGTLSRVWGNKQKGM*
>TCRU_7371 hypothetical protein, conserved
MSVFPILFKPPNVFCYVQHASVDSRRPTVCSAAGASGCDDVCDVLCWRVLCCQPDVLLLL
GQGDACRQGEVDPGCGEGRVLFGAEGASQTCTVIGMNGWAPIRIDVSTRDLDDARKYCSS
ERY*
>TCRU_7372 hypothetical protein
MERSSDSHRRRMPWTAAKECVPGVVHSSKEKMVLDGAQRVDVDCVDRASQVYPLEALRAT
VASYEYNTSTGRTF*
>TCRU_7373 hypothetical protein, conserved
MFHEKPPLVEQPECLLPDVWPDQFHQSHPQLQPVKGHQLHPQRQQEENQNLLWKRRHENP
CLLESPEYVLQEV*
>TCRU_7374 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MGEEEQSAPEEGANPTTLQSRETNGDGDAQPVQESVAPLAGSEGLLPKQSEAPVPENNHS
ESGSGASQEDRLALLNDAKLMLHDWNVDSTARVCVSRVSMLLLLGLCGAVAVL*
>TCRU_7375 hypothetical protein, conserved
MHRRSGRTARRLQRHAVKHHRARQQVHTAANVHRRPARVQRPQHSVAHTQLRLQQRHRVQ
HKRRRHRVRQPAQLRVAHRPRRHNRRVTDRHVRVCRQVVHKHKRAVAAGQPAHAHLQAPV
TRRLAAVAPHVDLRTAVAHAVTQFDAQCAGKHRRNVEHHSHAVRDGHAVHQHRVHGAANR
DGSVHRAAPQSQHHRMHSSHPRSSSNQRQRHKQRHTHSRNGTVPLAVPAARKRTHRTPHP
PTQTSINRSVVVCRSRPVDHSSCLANPFMQMENPATRFRQIVIPILILLIQQLIPNALKR
*
>TCRU_7376 hypothetical protein, conserved
MQHNRALQRRHVRHVDESVRHQARRALAEAANPQLRTARKQAVAQRHVQRVSERVHQAQV
HRHSDRPAEHHRVEARRRTPATNLHRLRQRHATHAVRRTATAAGPRNRQVERQARVAHAA
GKAAANAVGERRRQRIKARQRSRTAVARHHAHGGQAGHAVVAAALQHPAAGTVALHRHDA
ARDRQPGDKCRAGGSAACNRHGAAAQRHPRQRRHRRSLAHRPHVVQLQPPAATDRPTVAA
HQ*
>TCRU_7377 hypothetical protein, conserved
MSRRVQAVRKFVVKYRPHTPIAERHAALLFHVHNVGSAELVVAVHQPAAVSHGKRFCNEH
GEAKTESAGHNLQHATTIQNNIPEHTRAFVHVNARRNPRAVLYGEHGAAADTQVRRKSVH
YVCPRHNDAVVHVEGAGQVHAEAALHEDRSARGTATHQRRPRHDKPRRQKPDAVQDKRGA
VPGFLVARGRRHVLRPANSRVQR*
>TCRU_7378 hypothetical protein, conserved
MCTTPPDQQAREDALQQRDVECLFWRVEAPQVQHNRGGEGHADEAQTTHTGIRIVHGADA
ATVHAADLRVLRVRERKRPKAVRNSSWQTRVAVAASSALTLTAADAARPRCEAHGVHGAR

TAVQHRHGYSNIELFSVIRHRRAPYLVAHAVDDRARVG*
>TCRU_7379 hypothetical protein, conserved
MKHIAAQHHRGVIADRQLIHRNTRRLPNVQTRPRDQPRDSEAIPADRDVRARWKHTLRAE
QRVTERVAGDDNVQRPHSGVRVAQQQQHGAVPPSASIEPDIRHVARHRPYQHRQAHAAPA
ERHVAVAQPRHPAAHSLRNLGVHHVADALTNRRWWRHWRWWRCGRHWRRWRWWRPSRHRR
RDTHIAVPSSSALALAVNDRRRQRSKADAVLRALTAHCNRRHVGDAVELQFSCRRHLPSR
DRQAPSNEPVAGVSLR*
>TCRU_7380 hypothetical protein, conserved
MRPSHKRQAQRQHPRQQRSVAHKAQRAPSSGHGTSRVEHPPRDAVVHVALRQQHRPAIQA
HCRIKRHRVVPRRRKVAPHKRHNGARKAHSPTHRHRVLAQQEVAVNKRHHGAAAGSNTAL
HRHTQPQRRLHQKFVHVQRTARRQRHAANKQHANSVAENRLHLRARNGQHAPSQTHVVQH
EARGRVAKVVGAAVCNTILCDQHRVHHSDARARRKSVRHHHAAAGARLKPADQHISTLAS
RRVGTPPNNVQARSTHKSAVRQRHVAHAP*
>TCRU_7381 hypothetical protein, conserved
MVGRADHAQHSKEHKARSMHHRQEGRAHHVREGNHARTRKQHSRHAEVLDVAASHGRVHS
RNQAHHTQHRQLENAPVHVAAPHVRQHAAVHPLLRRGVPIPDGVQLTLVQRLPRKLPVPR
KARARVAGNQVAHASRKRRTVQHANDTDHAVPHAGVGHRQCKHGAEEDAEMHRVRHNVRQ
TREAHRSPRTRRVHAAPPLEGRRHTAVHAPEHSGKQRVAHHHPQRVKGSEHRQEVRQRNG
ARTLLRRGT*
>TCRU_7382 Mucin-like glycoprotein, putative
MTTCRLLCALLVLALCCCLSVCVTANGNSSSNTTTTTTTTKAPTTTTTTTTKAPTTTTTT
TTKAPNTTTTTTTKAPTTTTTTTTKAPTTTTTTTTKAPNTTTTTTTKAPTTTTTTTTEAP
TTTEAPTITTTEAPTTTEAPTITTTEAPTTKTTHAPSRIRKIDGSFGNAAWVCAPLVLAV
SALAYTTLG*
>TCRU_7383 hypothetical protein, conserved
MAPPRQPISLWGSIVQQLAGSHAHRAECLATEDGIGHLIPFCLETSQSPTRILVATNSLS
RTKALRVVPLAVRGYVTEESWIMLLSSIQRGHPVDFMFSPSHCGTPRNEATDDEAMIARS
LPQEGGPIWHVYILAAVG*
>TCRU_7384 hypothetical protein
MGGSKNTPEDVTEVKKCLHHVLESRKQLKELENKLKETITVTTKMLSSLDAVGNGFVNTT
RAMTQQLEGQPCSATSHRSSVPVGTLHGATKLMSTMLRELREGATIANYKDKLQKSIFDK
LDTLRWSTKKVLDAGNESHALLVKYHKKEGAVNAKEQKYKKKGRDLSTSKRYTKQVTERD
KAKRMAELKTSYFKDMYDIHVASMDQNEGEFFDCFIDANCHLVRKLHDTLSSVGSCALRE
YPLLASVLVRSASHEMPPLVSDDSPVTRTSRMKMGSGNGHVRAEHDTAQKPGVEANPSDG
LHAEGSPYLISHADIDSSPSRPSGVLQEPLTQLRPPTARDAPDEPVHFEDALKATPADIQ
DHHM*
>TCRU_7385 hypothetical protein, conserved
MLRLSRGLCGLYVPVVGCIFLVDTLYGCKYSPHIGVCNLPYVYVKALLFCASGQDKWEPK
RKYVHGLIEYLVPFNREQDSLTKLELMQFVDTVPPRAIKIHTASTVLGSAQLSLTHSTSA
LQQSASTSGAILRSSGGGPSSVTENVTSFLSGALLPAALARVLLYDAVCTCADDDEYNET
ERHRVSQVAAKLGIPQRVRDAIEKVVVQERLLAMRKRRLLLLTDTPPTR*
>TCRU_7386 Chitobiase/beta-hexosaminidase C-terminal domain
containing protein, putative
MASVGAAVVVPILVICALLLLLILAVIFYYFYHTRFRNVNTKYYMYPGFARRRKFELSCI
PAPGLYQPPLEVRLQCSQQEPCDILLDVNYVPASKISTMDDTTADAVRLLGTDDCYSDHF
MLYTEPLEFIEAGRYMLYAYTVYPTLRVVGSVHQFCFDIVSVNRDTRSGEMQQPPHVSIN
VNRDSRRHVSMSAVGNRARPIPPRIIPEKGEVTTFTPINIALSESSTTPDQIRYSVDGSP
PSLLYTGPFTLSLPPFNTDGGSSRIPVVIRALTVSTQDGLLTSETTEAHLTVYKAGHSFF
DPNIPPPVARVRALEAELYFDESRRPPNTSIIYQIVYVGEARQKPKFSHRKGILYEGKPV
PLKEDVAFVYAWTFREDTHGGQCIEPHMDERGHGKARSSAAVYDCNLAMTWNREPRGEDV
GGRGNALPPPCICIRCKEMDVFFEDPPVGGIICYTLDGTEPAQPDSTITAKHLAGIGRND
TVLLPRDHEKILELGTHVYRENQPIHVTLMRTEQVVLTARTFIPVVDLAANSAVTGYRFG
ECFNRSFSTL*
>TCRU_7387 hypothetical protein, conserved

MAYESPARVKWATAIFWNVLDPAFRMHFKYYRRKVAVDRYLERKGVVFNVAVGVTFGLTL
YFTLVSKFLLPAPVASEYSMEDNAKEILRAMKCDTTKELPAFLLMRAKREIIGKLHVAAD
RAEVKHQREEVERLLKTLNQQQDSPPPQ*
>TCRU_7388 hypothetical protein, conserved
MLTPSWGPVASDTPCFGFVPHALAGDILITSRRLQVLSYVLAELSSSAMLLDDYVRGILN
IPHRLLVAWQSIAVAARARQATQRSGESGALRETPKFGGRREPLAPRTPVGRRDHNNASI
GGASPQLSQQNTNNNREVDDNRTAKLHACRLMEDNAARHVEFIRRTVVMALFQQYLQVVV
EKSVDDLLLRGWLGSGFETNTRGSRRGDVARHEGAESSFLDLKDDEGGEVGGNEEVGNPA
NGNKRPRDVSVFPLRQLLPLNVSSDHDDHDDDDKYVRSPVSLQAFMRAAIAFNPTVCALR
LMSRCILYARHVRNVDDEAAASAGTTEGEKGVFYVVVASRAVGTCEHSEPCFGNRKFFFV
RCQESEVRCKRDGSPSTQWAEAAAMSPTWRGPNSRQDANRHKSSAVPRGREAWHWMMCLM
TQTMTGQQSGQGNTLVRDCGGNQTRPCVPWRRSAQHSSERRTREGMSQLGLPYVVTLAAR
GGGGGAATMKSGTRPKGGRVFVPSFQLHRKSGKRGARDYFPNRHYHYAEDEYEEDSIESW
LVMHSNRCSATGTFFGPATARPGRLITDAGKPLGGLSFGSSVACSANNFVVPFDQAISAP
PNAGHDTNYREQQSTEQFSATTEVVSAGQLAFAEELLARLNFWCARGQPRRCYYDPALSD
GCQTATVNPTAEMRMDRGHGIAGSNHTDVDCKGEMPLRLLFTQVGVIRFRPVEASVYRSG
RGQELLLQALADSTEVVICSVLESRSHYGWQNHSSGGTEGRVDGCYAFDTYAVSDDGNDP
FLWGRYDDIAMEASVSWAQGEVTTDGADDVCDTDGNGVSTAGNSSNSHVATRRSLSMREK
HQRKNERLKIEFHLAHSQRLDALLVHQQAAKPVAALILRQLPRKLHHTTGNGRQLVQETT
FVVQSFSHYVVHLLRQIREENVLMVDMDRTLVDNAILAGEDSTPMACQKVSGAKGGSQLH
FEVRKEVRYLVTDTPFQGMRTETIYVRHGVRRLLRYFAIEWGIPVVLVTKSSRRRTEAIL
SQALDPEEELFPPGCGRVFTAELLLDKLSDDLPSDGPFSSSALPPHVASEKDHARWRSHE
SLVNSRKCTTAVLQELDRAHRKRHGTRHFSPKARSVAVLDDAPQVWVEADWPCTVSVVPY
TLGRVDPREYFTPNGLIPSMLLSVLYRGKCVRYPTPHREGNESTYGIGAVKKGIGRNDTI
GMDFTIPALERCVFFCDCDPNNDVNQNNLLEMPRVKDPCLPEDHLLSAASSGYNASAEDE
VASGEETVVEEVNERREGSSPWATADVEDVTPL*
>TCRU_7389 coronin, putative
MSISRFRHTQSVPARHDRHFINVNPSGAIWDCSNMIACNDRFLAVPWAQLGSTAVLLHTD
YGKVASSPPILLGQEGPVIDVAFNPFDPTKLFTASEDGTIMGWDIPEEGLTQSTSDHIVH
LQGHTKKVGIVNFHPSAMNVLASAGADMVVNVWDVNTGKAGEVLKCHTDQIMSLEWNLDG
SLLCSTSKDKKVNIMDPRIGDIVASGSAHQGGKTQRCLWAKRQNLIVTVGFSKAQSRQVM
LWDARDMASPVHTEDIDQFSSLILPFFDEDTNILYIGGRGDGIIRFFELADGRLVPCSSY
DSVEAHKGLCMFPKWSLDTRQCEIARFYALTPRSIYPIQMLLPRRLADSELQVDVYPPTF
ADVPAITAEAYFSGGNSEPLVTDMHAVFNGTEREVKRAVALTPSGKKRHQGVTSAMTHSF
DTNSSKYTDPMTMGVEYTEKRRDEGILDERLGKLAALSLELQKQEEDLKRCQEEVEKKTR
IVMETVEKIRDIALGHAL*
>TCRU_7390 ribosomal protein S9/S16, putative
MYQLLSPRTARHARLFRLANSLASSPSGTAGVPKTDGERLLWVNSHVKRNKDIEMSIEEE
SLRERQLPLKLGENAFTSSAQATHGSLFHFREYPMYPGEYVPAGHNTLSSLRHELRLELT
AQSLKEAWMRISGGMYFQSADDYYASVDGLDAEQLGEVLAALFPYLSTYEAQALVQCTLD
SISKPMNTASRQLSRTITAEAVGLDNAPGHYTNFLDWMGRLTETRGFKTEHALFQFSRRK
FNRDDVRVMFENYKLMSRATLLADSADSYSHFYTVLKDFARKVAGEDSRHQIGVRIDEPE
VDAETGIAVGRGCADGEKYQFTALLRENRDHNGAITIMGKPMALVLDNKAWLMEMLLMPF
DEANLDYRDFDVHIVLEGHAMPSIANEIAAFALRMSIANALVKLLPLTRIPLKKSGLLSV
DRRRERGQFPGYLDGKKVKRKFAKR*
>TCRU_7391 Uncharacterised protein family UPF0546, putative
MLLLLLAAIIWGITNPLLKRYSSGMAVSSSFLEDLRFLVSRPKYMATQLLNLSGSVLFFL
GLRHVDVAVGSMVANALAFVITVLVSALVLREGVLRPATLLGCGLVVAGTTLCGIASSSR
D*
>TCRU_7392 S-adenosyl-methyltransferase mraW-like protein, putative
MKRIVAPRRWSQLNRVEHPPLMMKQLFQGVCGGLRWLELKELAEHLATRAIEDGYPSTSS
VRQALQAKRAPRSRRRQVREEMRRNVAASLPLTSSQNALTVTGGLSTCLAKPKRLVLYDV
LDCTLGGGYHAGAVLENGGPYTRVVALDCDHDVMQTAMELVDEFGADRFKFFCRQMSEAK
SLFGERSFDAVMIDPGPSETQLENPERGFLLDDENSHHLDMRYGPQLGIGALAYLNTVPQ

HALSGALSAYGLLTPEQSMKMAREVRCRRPFTSSRDVIGCVEAAGDMLPEEVWSTQSSRR
KTPMSWKFFTSLRCILNNEMYELREALENALLLLRDDGRLVVFSRLMWEERLIQSTVESH
PHALLCYTEDVPMEEVCEHGFTRHTKMWVASRVAKSSYALKNTVSLTEEKVRESSLRWLS
GMYAGQTYGFPANNFTFENLEPKERRTRRRNGKPPPPDYGLDDR*
>TCRU_7393 T-complex protein 1, gamma subunit, putative
MYSQKQPVLVLNQKTERQTGRKAQMNNIEVAKTVASLISSTLGPCAMLKMILDPMGGTVL
TNDGNCILREIDVVHPAAKHMLELARAQDEEVGDGTTSVIVLTGEILSLAQPLLERNIHP
LKIVKGFSLALTDALAAIEMIGTTIDPNDTRQLESVVRACLGTKFNSREDDIMCKMAVAA
TQRVVVENKTTGQKEVDIKRYAKIEKIPGGSVTDSVVLDGVMFNKDHIHAKMRRYIENPR
IILLDCPLEYKKPETTINVEVGQATDWESLLKQEEDYVRSLCNVIISFKPDVVITEKGAS
DLAAHFLYKANITCIRRLRKTDNNRIARATGAKVVSRIEELTKDHIGQAGLMEIKKIGDE
YFTFITGCSSGKACSVVLRGASKDTLNEMERNLHDAMCVARNIILDPRVVYGAAAVEMYV
SSYLMNRSKSITGVQQAAYQAVAMALEVVPRILTSNCGANVIRTVTELRARHSMPDGNFW
GVDGTTGEIVDVRVLQVMEPAAVKVQALKTAVEAASMILRVDDVVSGTKLRHGNEKPAPA
AAKDDDDHGDAAAAE*
>TCRU_7394 hypothetical protein, conserved
MWRLLISRESRRAVALGAATTLLPFRCVHERPFLDLPTDVSQGEAYDMARDALVQLNVMV
RRGIEPDALMYTSLIATMSRAKLEWQAYKLFSRMLEQGVRPLPETYVALRDATSPSRRRL
RQDLQLKIEESLESLPSELAEEELARRQEQDRLCVEKFEDYMRGVLPTPPPCASYTQTTV
MPAVQEEGGRNDDGDVQKERNGASAAATKRDGGGQEEPRPVATMHIRNPTDAWSTARMME
EQRGIRIQRAQGSDTIALSDELHRLHEEELRIFLAAQRQLRHGTKDELVRRVLDNVPERS
IRDMLGRRKHYFRSVAHILENDIHALRRENIGENKDVLQNSVQEQFSAADRTLTAAEKET
VAPEVLHTPWGILRKPMKRKPDPSASRSMERLQRISLSLEELQLIRCKGETGDLDELPES
LLRRYAFEFNLKWKRRFPLSLLEAVQWHCTTFLPEQLDGKVVVRPTPALRRQQEEEGMHK
TLENYEAFRIISQRTNNLQVVDHKEINLHLKKIQKTMLQKERHTEETLRRERNLLDAATL
AASAKSFTPPDGTSTTVSRVLGVNEASDSNTAKIPPPASTSNTRDDSSVQEECHELPPWA
IFSGAEEFDISTGRFGDPDVGRYQELSDGRFKVLPSREAQDKWAVDRQLLPGPLQDKLQR
AELQQKLHHEAIERRYQQKLQYNRYRKWDSFLRKAQEKGQREKSSEEEEEVDAVRPLPPK
RRLSQLLRKGRDKAPVEGSVKAKYTRSL*
>TCRU_7395 hypothetical protein
MRGGCRWTLLLLLFLFLVSTVASAQVPGDALSTVKVDMGFNGKWTAAFVAAAEFSDAVQS
DVSDALGIQRAAAWFDAAPAVAADPGTVAVSFVVWSDPGIVANFLLRDAEWTATKAYYTE
ATTESVATPFVAHAFRVEAITVRFTGNGWGDTSALPEAKLSEGIITDVKAVKDVTGTPAN
LDAVLIGTVDRTSGATFHLEVVSAGIQNVTTLLSPASTYATLLEYYKHQTTLTDGALRDV
SRTPASPIQQQYRTQMQMIFGGSWQLVLQSKELEVASTIQLILSGALAFQPSRVIIGNIS
KTVYPFNLNVSTYVLHSRGFNASTIPNLAAAANYSSLVRLYMTNGGDPGITPVLLFSDLV
PSRPPTGTSAVSLVSTHKLVFSGTRWPTVLSSVTADVFKDALAGDLTKLVPYGPTTVNVL
GYTVGAKNGCNARVMVDQQGDVQLIPVALNAFFKLAPSLPNTEELYNKHAGAGGHEAINV
FSSLEKQPKRGSACTSRCVGISIMGGCLLVFSIVASIIFCVWRVFSRYVSPPKINSDLVR
IPPEKNPFVSTVTLRGVAETAPSFTRNLSPTGADGPMYPPLTAGVAPFGPMMSTSTASAP
ESRMTSYVAEQPNSSVVRQGNIIIPSSSGEKEFELIVMPRSEFERSHGSEP*
>TCRU_7396 Protein of unknown function (DUF3250), putative
MAQRVSARRTTEEWQDAFYSLEERHRQLQKKFNEKEQELKLLKVSQRRESAAPLFARGVP
SRSAPLMSGRASSMRAPLPSAKANERTLETRVGGEGTAHEGKHDSFPERNAGLVSVPSAA
RKADAGAAAAELRSAWSASPSPDPSMVWGMENSIQNYVTANALYHANEELRHRLDDAVTL
VKTLQHELASSRSLVINTQKRLEETTQQMHQLVRERDLASQKLSVSQQAVAELERTLKNH
NTEEERIRFSLETQITELRSRLVVGADSNELLTRDVRTLLLEVKEKSLEVQSLRSKIALA
EAALSSQKQNNENLLVELRGLNNQLINERKRLLSMTREAQLASLRADEAKDFESRLAEAI
ESRSALEREHVRLMESLVGVTESALRQAREEVRQDIADWRASASHWEEVSQLLYKDIAQR
TQAHIQCRGECEEAKRDRDEASIALRDAWEELKLCRAKLDIVWPTHRADTGNLTPTEILS
TFGNYKAIFRHNRHRKTGRAEGASVSHEENERDDGEITVQLCDGSMEEQVRELHEANGAL
LAELEQLRITNEMQAERLRKMERQVRREREEVQASAEALEQREEATQQFLQTQLDRVAFL
EAQVRSLRGYDVSPNVSLREVGPGETVFELFLGQIFSTETPEGVGLRDTFPPIFCSVDFL
LHETVTTPIVTGLNGFLDTTVSFCVAMDALLQYYLRSRSLLVQLHRVRSQDEIHKIVSAK

SDTHEPLYAERLCATLAEGSISLSAFVLDEKCRQAQRPTVRGHIPLRTTNGHHIASVEFT
VTVRTPFSDSFRALAAEASREWGPKLTETNTPAEVNIPRGEGRMQLVPTTHPSEAFGSVS
TTSSSSMSLLDSKIQDRPSGFTLVPRAAVMASVPSSSSSSTIRLLIVDVHRLHLPHNLAP
VPRLSCYYALTPLGRDVYLPAPPTPRYEYEYLQEGGHGGTLFPVVSVRELLAVTREPFML
FFFDESSPAAHSSERQGECPYWAMARAEWRLALERPEEYVSLELPLMDPQGCHVQGAFLQ
IRLLATKNTQATEAGSAVALQTARRQL*
>TCRU_7397 hypothetical protein, conserved
MPTTPPTRTSTDTTHDITRIQGKDNTGETMALMVIDDRRHPLVSSRTPPQSVGSSSREKA
EGEENARCKGRAIQRKILPQPSKLPTPLPTPAKGPFPLPLPPRTAATKPGASSSKIAVTS
TSKNKVQPASSRQTQELPPSIFDDAPVQASLEYLTRPHRSWDSAFRIWERRGRRQESEKN
RRTWSNSGLSNSVAGSTRLSCASSNKAASSSSISICSAPPTVGRLRTQMSSGNSPGCGVL
RRGRFGLLPSLQADPEGLAVGGSRLSPPAHFSTMSRFKPLPQGGAFSPATTNKFGISDSE
RRGVSTPLLGKVREFTFTMQ*
>TCRU_7398 Rapamycin-insensitive companion of mTOR, N-term/
Rapamycin-insensitive companion of mTOR, middle domain/Rapamycin-
insensitive companion of mTOR RasGEF N domain containing protein,
putative
MVASGLSAASAELLQQFGIDQKDFSKARVRYEKVQEELREEGLEAKGETTDAAAKAEETL
QRLTGAWNEYLCLTQKYFIKITSTVIDDLMNKIREKASAAERAEKLNELCAIGEKWYVRN
EAYFEFEDPEKLALLAKGALDSSSRVMRLLGLQLVRICAASVRFTQCLLKNVGCGLISLC
FDREIATELEYALNVCTRLIELHESNPTAYPDFPYGWICRISSLLDPQDPVPNLQPKRKS
QALRIAIKLLRRFPAMSTAASLHTILLRYCIQKGAATMDEIKNILHVILDLFDCAETRQY
LRYNDLDVLYVPFLYTTDKSTEANINLMNGAKDVLAMVMRTWVGVLWTCSETKGLRAVID
VLHLPGDLDRKMVLLTLFNKVLCQLAPHRGLTALKTWQGVEKNKRETLNSDTISSELTSS
FMEFSSSRISGEYAKTQTFSEGGIFMDQSEVQDNFVPTTKAIGYHVLDPLLGRVLLMLFH
HGLPLALVSMIGDGASSRLLASTASSLLQDIFVLMDTVLPVRPAGRLHTALNEAVGRLIQ
QGDLSFRSGPTASLFQYHRMIKDVSLATTVAGTNAISGGRAIIPSATTISAYGLGTMGVD
DAGFEALLRQTGVDRADGFVGWNQDLLLLLVHGPLRSMPRFQWVLKETRFFHKLIAFYQP
SLQAQSRTFVSLRTEECTPQLCNFGLALLDMFLSTRVGTEVLDQFGFTSAIVRNLQEVVD
GTPQVLNRERLGTRVGQTVLQMVGRYSLSANGLMAMREHNMFGIINNMFDELSGERAAAP
SPNDTLQDVCQLILQSLYIGAVPNYGVCEEIRHAIRSALCNDVNSVRLYAATQLHKALWR
DLSTSMRWGIETLVQALHDEFYSVVESAFKLLLSICLCSEEALDYLISLSPAVLMESEVI
RQHSKDLDLNKLLYCIVGRTSGLRFLQFYGWVDEELRRWEESESANHVRLVERMQSGEAV
EASVEFIQSMVSQRRQFHDRTISDPIYTLYRPTVLSRSIPTYSPPSESVSGFFPSHFAAF
LCKSNEGCTLFKHSVLWQRSVQRILQQPLPPDIVYDGSDARNGGSDDDIDDDERVLNEED
PSFWGQLGAKTEMAETTRSVEGCDLRLLRAGCLPCSRDAQLLSAARGYKTPGRSYLLKSV
GDVAELKDAILCVCHASSSDTGFALMRSVPGLHKRLNALMVFGATVSVRSICFVGECIQA
RSRRCAEQLSDMSRYVLHECNAYTSADGVPYSVAFSHIKPSRWTPIGRPTNQWGVSSLYF
IYRQECSGKADESPYFTLEGARSIEALGQSARRVFDQVCTLSNPVSREGAKKKLCQVLKH
QPNIFLEPHMRKLIIDATQMFRMQHAERKFIADLLENAPLAKPVPSARRSTIVVPSLTRL
N*
>TCRU_7399 hypothetical protein, conserved
MTDNSSAVAAGAVGGTVCAGRSKSLFLKDDERFLFDFGGESAVDGATMKGRDSTSPASCA
FACPHEGEGDDADRQVLRDDVDAGLGVRGKVAVASLSAAEVRRCFHAALNAGSDVFLNMP
LNEAVEKFQFGLQRYSEALSRHTRQEKQRRTVPRKRTRISSDDDDINNNNNNTSSPKNAG
GSFEGKRRTHK*
>TCRU_7400 exonuclease, putative
MGIKGLWSEVRPVCRQSHLSNFRGQRVAVDMYVWLHRSILGSVQLGTRADAEAFIECAEM
TSEAVDAGSSILLSNKFLQFVMGRVDLMLRCGVHPVLVFDGAPIPMKQGTEAERQMLRAA
RLAEALQVLKQGGPSNPRARQEAAQLLEKGMDITTELAHAVIQVLKERRLECIVAPYEAD
AQLAYLCKEGYVQAVVSEDSDLIAYHCPCLIAKLDAHGGCEVLFAQDLPRCPSFYGLSYE
SFLVGCILSGCDYLPSLRHIGVKKAFRLVAQATSVPSIMRSLEVKFGFSKEELDAYEAKL
QQAFYCFAHHFVFDPVRKEVMHLTPLPRGIPLKTNLLGEALRKDIAEKVCAECLYDPVTK
ALYRGSYLYCVQEYWKHTRGGQTPLNSYSGFRDMQSPRVTILLSSSGTDTTGRRASPTTT

FFSSPLQKVSEAKGFCEKVTRNVALVRSKYFTQGRWKVEDWESEDSETTATTTTTTQTTP
ITTTVESAASTTTTATTTAAAGCVEERGEGASWCLSSLRFVVKDDPMRGSSLTASVSSTN
QTQDDGFATQEQGSFVQAKAPCFSSPSVLPPLTTVPTREGTKTLDANESQQQHETSGCPF
GYVQCGRRHSIFELCFQGRNWSKDSNPVAYEGRANQVVDETQNIGAGSSSDTNCLGVSSH
SSLRTGAGEKRQRESALPPSFRPVFRPPASTSGRSTVASSHADKMPPAAKRRVLSSTEQA
KQLMRRFTPGSSAASTVDSEADNSSRMNGGAAELFKKLTFARQ*
>TCRU_7401 hypothetical protein, conserved
MGSKGGLDEVPRQLRQLLRRIPVGYSSVYLNELQPSSQHLFLAACMTKARQKLNGSAENM
LGISVSRQNFSFNPSVRASRLNGVEAKQQGGNSSPSTSVPMLQRMVSELRLPKGSSGRLE
AYRTSHPTLLTNPHLFLLSVPRWMFDDEGGENEGQRTVESVLQRHLVKVNKTLYWREGEP
SHGDKDAATDTPDVMLENIWGCTTLQLCQAAKAAASRGCRLFLLSYPRQRMLSNEGLLVR
ELGGWCPSAFCNFKLDVLSVDLEDASRRSSSLSLLEEAQRGFGANIGVEKADMQGSCDSD
STKYGLENMAQLEYKFPLAVAEAVVDAKRDAPVPWAQVCDDPLTASLFEALYDRRHFCVT
DAVLYASRRVVLPFLLGLSPSSSSSSNTLKGTGGGDGASSAGLMRWSEIHAVLRWRLFES
AFGSLSQLVRTEDVAAVGGGLDPFILPLHETFLTRILIPRMSEYYDATCKGAEASARQNA
VTPGDARVHNKSSTPATVTVDILECFNSLASRRRHGGSGTSVADHNGNEVCDANGDGAVK
KKKKKERKPKKMTDEHSSFDVGDVHFTVADLPGLVKYLLYFSQQFEVHGGGTTLKFTPHR
G*
>TCRU_7402 hypothetical protein, conserved
MELIRERRSTVVRRITDIPALEKLHEGSERGGARTVCAANVGAENVPCGAIHNLLPHART
HDERGELRGLFGGNRCSAIDPTAVRQDAAVHVGNESNPAGHGDSGVTKNCGVIRGEAGAP
LDKGRDGSIYPQPNRLEGTCCLTTRVDNGELLVRDCGLNPNNSTLEADGTLILDWSVAPR
TARADPHRAFRFVRIRGQDALDTITLCRTLQENEKLTNLTTAR*
>TCRU_7403 hypothetical protein
MHKLNAGLVQRVLGRAKHLQRLRHLVLQHLQLLLHLCAELVQLLLGVRVLLRVRVKRLDG
KLQLNVRRADVAVNLLQALLLLVHQLAQRLVQAAERLQVLLMHLQPQVRQLLVRLVVARL
DCAAALRHQLLHHPDASHRQVAVVHRQFQQLLVLPTYIQELLVLHLALLLAVVLLDAALH
LLKSLRPQALQDTLELLDAAPRLVLPVEVLLDELFRLLLLRRKALHRLRVLHVRLLDRVV
*
>TCRU_7404 hypothetical protein, conserved
MVPNASKKRPSFANGPRILVALNASGIMSVNCGGREHVAADSTDEVNEHDATGSKSLVLE
TGVAGSGFVAEGDAGGLSQSNASGHENKPQ*
>TCRU_7405 Enriched in surface-labeled proteome protein 1
MNDSGKTVLLELSYNKEKKWQVLCSGGKTTEHSSTWEKDTTHQVVLMLRNGTQGSAYVDG
HRVGGDVSCALGNKDSKEISHFYIGGDGEKAANKEGVSVTVTNVLLYNRPLDGNEINALN
PNKASTPILEEQQTAVLDTRLTPASGSVAQQTVSLPTPAGPLRTEQESSMMSSGVGGVGV
SNSGETTVTNPLPGLDSVQQLASVKSSDGTQSVNAASSSVGDKRVGRGAGDETQNDETHQ
PSMGTPATADANAPTAKGVGHDGPAVDQEMNASIREDEEAAGGINGQEDNHAQHGEVKAA
ALSSSLGNVSQGNNSDAGTVRGSGLLPLLLLLGLWGFAAL*
>TCRU_7406 Endonuclease/Exonuclease/phosphatase family/Endonuclease-
reverse transcriptase, putative
MHTGDYVLQGQSRIGKGGGVAVLVRTTLRSKRIPLTIPQHDTSLEVVVVQVALDQNRDLI
VAGAYVRPPPQVTQSFRRLVNCLPASTPLLLCGDFNMHHPQWEPFLETSPSEVAAEFLEL
CTDAGLTLVNTPGEITYARGTRERSCIDLTWSKHLTVSDWSASVSPLSDHYMLTFTLHQA
FKDTIPSAPRIFHSWGKCKWDLFVKDLDAQLPAYDYRKQSTGIKAFTRALITSYRRHCPA
ACTRTVPGFGTTLSWRQSGLLPTARPAIYSHRRPTVRQKCNGQGVNSSSYSESACATRIH
VASAS*
>TCRU_7407 Reverse transcriptase (RNA-dependent DNA polymerase)/
RNase H, putative
MVLKRLLWVWTPHPHQYAYRSVRTTTMQLAHLTHEVEHNRNHYFQVSLPKKSGIGNQLHY
RPHRTLLVLVDFSKAFDSIDHRVLSRLLANIPGVNCRRWLRNFLCGRYAKTRVGHRHSDR
RPMLRGVPQGSVLGPYLFSLYAHPLLSLLNSFAGVTADMYADDLSIIVRGQSREYAIPTA
NMVPKRLHAWSQENGLAINPSKREAAWFTLSTHTESDYDREGRWPLVVAGCQIPVMTMGA
SRTTKLLGMDLDPRLTLNVAASKQCAATSQRISQLRCIAHKEAGPSPHDLRTFVIGYSAS

KLRYGSELIWAVATDSAKNEMQKTYATLARIVSGVPSTVDPESALLEANMPPLHVLCLRA
RLSIFENTRACQMDWMRRPPPEPPPRAGFRISPLSRDELYAFVDAYTKDYGITESSPREE
RFFRSSIPPWFAAPAHRVTIGVELPIDLSITDEEELIREKRRVSEEAPALHSHRSWILAT
DGGVHVPKSAGVGILLSSLNSSEIIEKASINCGTRPCSYRTESRALLLALEKLIIPRIRH
RRKTLLVVTDSQSLLAALNKGPLSQTDWTEDRIWQRLLTLTRAGWSVRLQFCYGNCGVHA
NELADQHATQTMATGQYTEHGIAPLWHTDLPTCFTTQLTNKWRSTICQDTHRYLLCGTRP
SDLSGKDLITQEVLHRQELVHLARARCGESELWGRLYWAVRDCTNQCRFCNISPEQSAYM
RSNNDPTAPGTDTVPPSARGEDVSPVRGRTLTRRRKEKCPHCDSTLTGFSGLVSHCRSFH
PEHPPPLPELKYDFCDMVFPTRRSTAQHRIRCAHNPDATRHRNSSARRRSLLPQDQPAST
STPIGPQETLHHLLLECPGTLAVRRRLGIEQDLRLGKFSQWQLLHSRKLILLLDHLFGTQ
MALYS*
>TCRU_7408 hypothetical protein, conserved
MKKKNERTDEKEKKEDGEEDNDQEGEEEYEDEEIDEGEDDAKKEESETKEEKKDEKEEEK
IKDDDADATKGMSAGSEEQPIISSGAEEAANQTNLKSTQTTGDGDPAADVAKTRDEKQNE
NKDANPKETPIKTTAIANGTAPTGDSDGSTAVSHTTSPLLLLLVVACAAAVVVA*
>TCRU_7409 BNR repeat-like domain containing protein, putative
MEDGTLVFPLMAKNEAEDVCSMIICSMDSGSIWTLCEDMSPAECLNPASPSGRDQFTWLL
TARVARGCTSRVTWGQRGRRPSGHTQACGPSQNRSGVSQKENLRVDAFITATIEEGKEVM
LCIQRRYAMGKKRATAHCLWVTDNNRTFSAGPVAVDNAQKWKTELKDCGM*
>TCRU_7410 Enriched in surface-labeled proteome protein 1
MGARWEGQGENKVFGLSYDSGKKRAVFCGDGQNKDHSSNWEPEKTHQVAIVLQNGTQGSA
YVDGKSVCGNAQFDLKDNERSKGISHFFIGGDGSNTGSQGGFSVTVSNVLLYNRPLDDDE
IAGLAKNKITIPKPEDPKTSTTLPRSPEASGLPVEETVTQSNSAGQLPSEQGQPKGSNDA
GAGGASTPATSTAATSSGKEPVNQLTSGTSPSGNKNVDVSSSSDADPTVVKGSGETVQGD
GSPQTPEVSVSSGEDGETTGGTDAQGEEGIHPQNRDVKSAALNSSLGNLSQGNNTDAGTV
RESGLLPSLLLLLGLWGFAAA*
>TCRU_7411 hypothetical protein, conserved
MLDLLRQHGAVQVPLALVDENGPSDATLTVATPMTGLRLVSGKIAKLWDDSSLTGHVTNL
RAPQIPKLRDPIDPSHTRAARVVTSKARNLRSSSSLPEWSSKGKCGKAKATRNKNVVTQI
APRRLEE*
>TCRU_7412 Mucin-like glycoprotein, putative
MMMTCRLLCALLVLALCCCPSVCASDSTGEIIVFDLEDEEQGGGMSPPPPQPPNAKPVEA
NGSALSRPLRATGTPPVPGHSDLSTTGSVAKPGNDGGGGRGSTSTGTNPNVVPNTLQADS
ESEDAAKTTATTKTKVPTTTSTTTPEAPGTTTTEAPTTTTTRAPSRLREIDGSLSSSAWV
CAPLVLAASALAYTALG*
>TCRU_7413 hypothetical protein, conserved
MTTNAVRDDSDRTPPLLGLVPSDHGAAKDGASGVNLERNRRSITAWHQTRLNNIILEEIR
KACVSRDDHRLMLKQLISTAYHKDPQRKANIDKWKGIMLAVEKEYAGANALFSISPDPYQ
RVLAKISSMMIWDGEVRHWEYSYCTEEIARRHSRHIEVLTQLQRAGKHFLNV*
>TCRU_7414 Tumour suppressor, Mitostatin, putative
MDMNSARVERLRRVNRYKAVQAELALQREEEEIRASRERKMNAAARDEALAKQLAEEQRL
ELLDTKMLQLARDFPELRNLEAQLKHALMKQGRKDQVEEIRQLKEKKLQEEKNYIAYLNE
QEELAKAKEEERRRKEVEAFQRHQAAQMDLIEERKTVAEKEAADRRKERIAVDAVVARAQ
EKDFLDALEKREKQRQLQAEQDEFYRLRAEVKEAERRRALQEEEAINAYHAEQSRRKETN
EKLAREREAIKARILEEQSRKIAEEQAKREELETLLNDYYEAERLAKERKAMKDEKEARE
RFAEEVKQENWRLIQDRLKEKEAERAEEIRLRQLMMEDLARKAKLERFSRQRQMQIKREH
ILEAEKMLEARRELKREEERQSALVEEREKKRQEELLEYVRRARAQLLADYLPKLGEFVP
AHVLTVDEKRQYGIIK*
>TCRU_7415 hypothetical protein
MSNGSNDHTGASHDLNGEYKALLEELHVLQAEWHSTASRKAELEASVTSATAQSDAVEPI
RCRLFELRKECALLNQRNEFLQLQIDEAKELYKRACGESSALVGDALEKENLEEEYMQVM
RFVDQFDPNLQEDAALLRAALAEQRVEIRVLQEMLDAVKESVVPDYFSEPLQNSGALFSS
HPNPCVEIQMDDVFIPVPHGRLRLLTGPRGDGLQQLRDRHKVTASVVCFNDMVAVRLRGH
KAGVENCGNDIRRVLSLQEERHEILKGKGEKQKKKEAKNTHTHTSRKTFPTSFVSS*

>TCRU_7416 Amino acid permease, putative
MTDDPASTVPLLNPDEKAMAYGLRGFEISRRPYKAATPEGCIPKQRWGSAPRGAVVYLKP
GSGSFQDVLAPSPRGSLLLYPKRELGSEEETKVNGDVPGIPGAKKPSLGQLRATAIAGNE
IASSCIYATGIVVSAAGRLACFSSLLVSVVLYIFRWIYTEMFGPQPTNGGTYNALRKAFD
KNWASLAAILSTLSYVATAVTSAASAGDYLQFQWNAMPSKSISIGILIFFAVVNLFGMRE
SSHAASLIFLLHLLLLCVLVVSALVYVCRDGGKVLRDSWNSPSLAANPYDQWITCIFFGY
SSALLGATGFESSSNYIEEQGEGVYPKTLRNMWFLVTVINPTLMILAIGVIPIEVLVKNA
DFSLALLAQIAVGDWLKMIVVFDAAFSLSSAVLSAYVGIQGLHRQLARDHVMPAFFLSVN
RWGGSNHFIIVGFCLVSCSLRLLVDDMSSLGGVCAVAFLSVLMLLCLSSLFLKYKRGRLR
GTLMIHPFVVLLALFLVTAGFVGNVIRAPRNAMYFAIYFFIFLFVVSVTRLRVSLSRVLH
DLIPSNCHWAKEKMGDIVASMRHCPVVYFAKHADINVLNKAIQYIVDNEDTHMVKVIHMV
GRSLPPTASSASLKKYGSERDVHQDKEESAESFLRLEDENELTTMRELEQSCAIIDQLYP
KLTIELLFVLAPFTPRVFYEISTELNVPRELMFMGCRGDCFSQILDQFDGVRVINY*
>TCRU_7417 RNA-binding protein, putative
MSSSAILFVGNLPAVTNAQYLERLFYAYGEVKNVKMHQEGIHPYAEVTYGAVDDGDSAIA
ALHGNYCASKDLPLVVLYHRSSPVVSQYGLKVGKEYAAAFAENRDPLPIPLEAFDEKFER
TDVPPPPSEREIFEGSNWSSYNNASHDVGGNV*
>TCRU_7418 hypothetical protein, conserved
MLRRCMRSLYRYQEFEMSKNAKYPFHYAREAPNTSVFPQHQLNFWMFWGWGRQELWIDRD
TRKYETTWEMLRRLLLWLFPCYFIFPFGLPKWIATNYHGEYGEKPFLDYTMHYPMDNHYI
EFGGSVLDAEWLRHIHSKESY*
>TCRU_7419 hypothetical protein, conserved
MITELRTKGATRTPAIRYSYPAPPPSKNAAPQQPRGTPRPRTAKTNVRKPKRSDARRRAR
AGSGFGVVSPVRARRRRVVGPPFADFFGAFFPATRGIAFLSDLPTHIFSSFLLSFLAGRG
VAMLRMCRRLAMKYADLELTTRGEFPHGMKEPGFVKKLDQNIPWYFSTYRSMYHWPITGD
NWSDLNEAEKHHDLHMFYTLAWWKLGEGIFDANDEDN*
>TCRU_7420 Enriched in surface-labeled proteome protein 1
MQGDTPPQTPVDTPDKAVANAPIATDVAQVDPADTTEVGASSGANGETAEGTNGQGELHA
RDGEVKAAALSSSLGNVSQGNNSDAGTVCGSGLLPSLLLLLGLWVFAAL*
>TCRU_7421 hypothetical protein, conserved
MCAYPSRLQYRAYSELPPTSFSVPIEYKPSASRLVAYASTLLTNSVDAANTTSSSNNTLH
MLFTVPDNSNSKDCTASTSVTAMSQCCGRARKKATAENHNTAWLTRIRTPADSVAPAPPT
NCSAAPSRNVHPVSVMLMERCSGILSRKNVNTAPMPLNVTPT*
>TCRU_7422 hypothetical protein, conserved
MLAHGPVSKAWQDSTLIGHIANLRAPQIPNFEKQALLPAMGAARELGHQQGLITAERERL
NFDYANAVADVQNRNARLNSQFQEAQINLSVRESNIAGAGNQVLELRQQLEADRAQLRER
EFYLGVLTAQLQEREARLNALQTAQDAETAGRDAAPATRHVANDGVSTLTHQTDILMAGG
VPSSAARHSSAAYRPPHGNAARPHFHPSTPLPSRTSPLDARLPMEEDRSFCAFDVTTWPS
RVWNEGASGVIIDLRCAYQCWRQDDEQVKLAFDNLVEWISALEVLQDPTDRIMNLGRSLL
NTFRMQLTIASDPGIRLSKLRARPYTAVHQTDAYARTTQTLVDRRETQRTVRCQRCHIFG
HEASTCNVRPRGNYSQHRRPSKNGRGAACCFL*
>TCRU_7423 Peroxidase, putative
MVFCFGSFFSKYASSKSGFRARYRFLHSSAKIAAGATGALLLGGATVALCYFPSGQKVTE
APPFDVNSLRRDIEEILSEDMSKGPLFVRLAWHEAGSWDCRKKDGSPNSASMRFHPECSY
AGNKGLDKGRNALESLKKKYPKISYADLWSFAAVVSIEAMGGPEIPWRWGRVDAKDGSVC
GPDGRLPDASRMQDHVRDVFSRLGFNDEETVALIGAHTCGECHLENTGYVGPWTHDKYGF
DNSFFTELFGNEWMLNPNVKKMQFMDKTTNRLMMLPADVSILLDDKYRSIAKKYADDNDY
FCNAFSKAYQKLLEVGTTNLKSLPAESK*
>TCRU_7424 Glucose-6-phosphate dehydrogenase, NAD binding domain
containing protein, putative
MSTSENRCRFQKEVDKFFDPLRERTLRDHPQELCEYLMENAKKVAAELRGEVCERIPDAI
SPELRGRALTIVVLGASGDLAKKKAFPALFQLYCNGMLPRDVNILG*
>TCRU_7425 glucose-6-phosphate 1-dehydrogenase
MTGGTVSHFIIRAGKALEERLLDIRIQFKDEIRPFGESTQRNELVIRAQPSEAMYLKLTA

KTPGLLNDTHQTELDLTHERRYDVTLPDAYESLIYEALLGNSTNFVRVDELDAAWRIYTP
LLHAIDRGEVKVLPYAAGSCGPEEAQEFIRSSGYKTTNGNAYKCSNA*
>TCRU_7426 HPP family, putative
MRGIGSSRNDGDLGVDSLNPHGSDGRPSMQSRHSLLPNEVTFLSRANSTLISLNAQDAGL
RENVSHAGGDALYGAPANERSSSSCSLKAILGLWPPIRRFPRWYWSRLTGYDQSKSVYGF
FPSWDLLITFVFICVSMLVMALIEFYFLHKYAIHLILFIPTFGASATILFAVPGAHLAQP
RALFFSHISAAILGVSAVNAFQFVPEKTFGLKCVAALVVGVHLVLMCLTNTAHPPASGTC
ISAVLAPLNGYYHYQGFLFVVFPVLAGCVLLFLCSWVLNNMLESRSPYPKYWF*
>TCRU_7427 PCI domain containing protein, putative
MELSVRLFLESAPKRQRYLRAAHILFGLSESGKFSPETRRQLLSAAVEYLKNGLSVYDIQ
LFRRSCEEHSDWLPEDLMVYEEEEAAVGARAEVALQSALSCLERLHVEDRVGKSNSNRLL
ATKRGRLESTELRGLRDQMRVAEVYADIRNYEAMSKAVNRLLALAHSMQQTAAISNRADS
VFVQLEVNRRVVELWLGAGNLDAVRSLVGTSTATLMTQAAECLMQIQFCSPSRLVPQQRT
VEDLISELEEYALFFSIVRGLCMFEDQNFSGFARVFTGSGLRGAGWIPAVVELNTKRNSL
QVPASLGGDVNASGRSSVIHHLRHIVEASITSGPQLGVMVLFSAIAALPRAEAMVLITRV
DIMSLWEDVSDAHVLVQAFQLAKWGEFFCAASVLNSLFLKTDIFAHKHSDLLYRLVIQSV
VLGYANAFMRLELRKAAAKLSIPLGELQEILQELILEGRLQARMDFVSQVLTNAKFNRVT
DGYSPQSLVLMDCICRSDMAMANVEQSLRILSLHRHHA*
>TCRU_7428 PrimPol-like protein 2
MEPCTKAPRYETRGTSVNAIFALTGPSAGVLHVRPDSFLSQTKKVDDALVPVLNGCYLQV
AVPADQYWRAASQHHTLFQSSCSHEQVTGQQAAPSTSLLLATGVLKRPDPNSIPRSFYGT
RLDAISNRHYAVDRGALVIAADNQNGLGGKLFNTLPRQELPSFVGAIPMCHHRNLYVLVD
EHAAVDPFFDIDCPVPLQWLEKDKRDEMGFAGEAQVTNSSSLASPEVMVASVEHWLGKIL
HFLRDKVEAATGAELQECVVLTSSVVVYNDVNVSRTAGHGDKEREEGKQKEGIDHLLSSR
DSKLSFHVHFRLNNMAFANVRELHRFMWQLRDELDVSLSTHENSDLACLYRMLRQCIDFG
VYTRWRAFRLPYNVKAPVSTGFCPSDAAALDLIISALSQSSLLSFSVPDVDVGAVAPSVV
HLIDLSFLEHVALPLHCQQQHRMITKIFFLFRFLLPVIPGGTAIGDKDLNDFLSRYLPCP
PCNGEVNAKYRQDLARAVFDIGVIQRESNSSGLDQESNGDLLRLIVLDEKVSEQRNQEAF
CDPFVVPRPPHRDGVRIHVYDKYVKNLVAEVFRCLCAAYDGCVGGGFMVEDADENGSSRC
GATSPVVGDRVVVQYQDNIRAYYAQQKLSRYCLNQGREHRGTYPQLYLTYGSIKLRCYSN
DCHNRCLAVRWSNDEDEQMTGSTAIALPVDERGYPKYERLTEIRHLLFPPLPPEELLRRY
GSLALEGKQ*
>TCRU_7429 adenylate kinase, putative
MHLFVLGPPGSGKTSISTVLKERYGVCHVTPSDAVSHAVEYIGSTFGDQLRLLEEGKPIP
DWLLTRVVAEATRGPDCSNGFLLDDFPKTAEQARLLNEEGVKPDAIVLLNFADNLLIERF
CGRWVHPVSGRMYHTLYDPPKVKGRDDVTGQPLVQRPEDSEDAVRERLANFRQNLNALRL
VYSDERLWHTVDGYAAVDTVQRSICRVLDPILASRKRRWWPWFFSH*
>TCRU_7430 lysosomal alpha-mannosidase precursor, putative
MRLLTALFAYFIVALILAFSVSAKHTVHLVAHTHDDMGWLKTVEQYQYGLNNTIQVADVN
GIISSVIAGLLLNPRRKFTYVEIGFFSRWWKEQGEEMRNTVRNLVAKGQLQFANGGWCMH
DEATTHFIDMIDQTTIGHRWLWRELKVVPRVGWQVDPFGHSATQAAMLTARAGLVGTFFA
RVDYRDFEYRASTGRRQFWWQPSPSLPELQTFAEINLHQTYCPPSKFSWDVVDYWMSAVR
NTDPLNFVEDKSSENYNIPFILELFKEEVRRNVEQTRGKNIMWTMGCDFNYFASELWFGK
MDRLIEIVNADGEFEVRYSTPYEYAMAKREEHSKGIVYDTKKGDFFPYASAPHEYWTGYF
SSRPALKRLVRRLSSYWTAARQVEFLAGVPTGEVPMLSDALAIAQHHDAITGTAKQHVAF
DYAKRLTEAYKEDLSVRLRPALSGFPFGFENAQHCLLSNVSVCSATAKAFEKEGAVVNVL
VWNPNAHSVQRTIVHIPVPRSDVIISGEGVLRYSVFESPVQISDYANENKEWQPYTLGVE
LQLVKLTILNLFTPQLKFATKKHTSRLVSLVRPSEDDLEISNEALVLKFGRNGLIESVTV
RSSGQTVAVKQDWCYYISNNGDTVSSSPGGAYIMRPVSNATCNPITDSPVELRLVDRRMG
VVEQRFGKDLVQRVILRGDLVDVEFTSFGIPIHDNFGRELVARFRTSVESGDVFYTDSNG
REMQRRRVDHRSDYPFTQTEPVAGNFYPVTSVFFINDTQTQFNVFPDAPMGGTSLQSGEV
LFVVHRRLLRDDFKGVGEPLNETAFVTSYADCVMTNTSNCGHHYGPPLRVRGTLSFSVSR
SGPTAMRRVREQQDENYYTPLVMFSSSSTDAASAIARYNTSFGFSLPPSLQVVTLQLIDQ
QNLLLRLGHRYAVSEDPERSLPVEVDLMTIFKEFHWITILSIDEVSLTAVEIVQRQIQKV

TVRPMDIRTFIFYIKAH*
>TCRU_7431 Nucleolar protein 12 (25kDa), putative
MMKRGTAFDEDGGKNKKGREKKGFKVDRFESFQRRRLKKSGAKDAHRNTGGGNSGRVRAI
KFDENARREYLLTMHKCKNERRVKAFVDARQKTRRENARARRAQREEARQAYNRFAAVPI
LPNFTYQLPQDDGDAEGESESEHDTREENNVADVTVNRRHSAIAAGKRVHVIPTAMRGGG
SEEATSGRKSHLDDEFVTVEVKPLFGGLAAASGSGGTTTTPKLPANDFSDLPAVVEQELL
RLRKETKGPSKTKPRLRMLKELAKIRKIKKHSQKGHGKKTAKGKRKNRR*
>TCRU_7432 methyltransferase domain containing protein, putative
MQLLTCLGRQDAAKAAMYTMSGADGGVTFSASSYSFRRASTAAATTSGPVVYRSLHDCQN
HVRCLIQEISLGFAPTAQAGLQEGEALRKSHRGARTLMELQELAEQFVVKLQSTVFLPSD
VVQEVDDFPMFLLRYFHRAVGRAKEGRPRSEEEIIEGFMEWMDMALPASPSSGREEEFVS
FVELMRLVQSFVRYHRGVRWGGGITSAEWHRNGYLLHPWHGTYCPSSHTEQMPYVHLLQW
LLRRRPVQEGKRRLGDADKRNTSNDDSSMRDDTMRWWSATEPFAPPSWRDERTSSNTVGF
AALDCGCHSGYMTDLLLKAGAQHVIAVDVSAHALGSAEATLREHLRERRSATSVAKRVQF
IRCDLLPELGSVAKQREGEMASPLMEERSTLAAAAARRRLLARKRFMRDNPQFSVSSFSE
VTAAPESEFGPFDLLVFHPPVKPIFPSWPLLQESLNVIEYSPPIAEDHHSHSSLSALHEF
LQRLLYSSKDHTESSTQPQRQAKSLLKDGGYVAFIIPVAFDPKDILQHISLSQLRSYSRR
GDSGVVPFTSLSDAVTGLLEGPYELVVRRRHSLAGMCNTGEEFPLCDMAYLREFADPQCR
DRIKQELNAFYRTYQAVDLLVLRKKPSSNESNKYKKNGGNSRNENHTKDHSPADPKENPI
TYEESFEHTEYIPADGPPLRHHWTEMTPSYSYLEDEFFGSNTGKTKRNFPESNFLAVGHT
PSLVREEVKAERTDDEWSHANLQTVRRSLRNYRSLFTGELKMRRKKRLRKMALQSLENQE
WYIDEKLVKSEGAKIDLLNELSRFDLKDWD*
>TCRU_7433 hypothetical protein, conserved
MIAGEGSGLTLRLQRLYELIATSIENDTGNDARRVPHPNFLVDAAQEYSNILDEAASLPA
MQDSPAVIYEALRVVTLLLAFEGHGSSGMSINTGLATKITNCVLEGIERLNILFAMKQPF
SLPQLLREELLTVVRLLICPVVQQQSESDQNSLSNSHSSGVINAMAEMARLQNALIDRRL
LCARLLIERGLGCCRDMEELLSSSFAYGSVLQQFLLQTLQEEFTTMRRHASGSTTALNGV
TDEFTGDIEEGGGGSSSCGENCFCYYALFFLSENGVSTRSRRSPSTTSNYSTGCNTPSYR
YTSDDHGRQLLVGNRRSNTARRLVCKKGPAVLCSLAVLASLGTGTACQGETASQEHCDKT
SDFVDFVGDLVSVCAVVVRPFLMEQLELMEQMRQETPSLSPKPQSLRGIQSRINEDLVRY
RRYSDVVERFLFCWDSSFIRKPFPPKSPKCAPLPLLGGTELLEERTKKKEEETILQDSVP
TAGSEREEKRKPPWVPVVPALAAHLALPISDDDEVKLLEVVSLFTEVKQFREAEREALWN
QWTRLREKTTTLAADVARMQQRLNSILEFKVLLSSFHAVSMDDLEWEWETRISQRLQELR
EEMRRVQEELVEKQEQGLQLSRVEK*
>TCRU_7434 Domain of unknown function (DUF1935), putative
MTDLVDDISGLFERGTPGFAFTKVFRCFSGKGNGLLFRLVNDKKQWAFYNDTEDMIFRVV
ARLGKESKVRSLGRAKITEREEGENKEWGYDATVVVDPGRTERFLEGNVEGFEIDFFSEA
APADEVEFKNGRPAVQYDSVYKCLKDHDNGLLFRLVSTNMETGESTWSYYNDTKDFTMGV
EVTFADKSCVRPLGMTRVERDPENEGRVVYKVSVAPLRTQTFLIGNPREYRQLFVANPLD
NVPPEDLSDICFENGRPNPDVIAYPCSKILKGFKAKGNGLVFLLIDDDEKKWAFYNDTTD
YNITVTVKFPPKSVYKASRKTTVTKDPDVVDGTICVMTVPPVTTELFLTDGNPTVYQMTF
SAVGLEKTESDELPEYENSGPDKYIIPHYDKVYRCFKDRGNGLLFRLVDEERGRWGFYND
TKNFVFNVRVSFEQDSSVRVLGKTRREEDAELGPVYVLDVPPLATELFVKGDLSGFSTKF
SGKRHVHA*
>TCRU_7435 CS domain containing protein, putative
MSAGKEVVFPNILWAQRSEHVFVSIPLQDAANVAVEIRSGRLLHFSATAGGQDYGCVLEL
FREISSEESSHVTLPRQIELKLKKKWPNDASDEKEVALCRAWPRLTKEKTRNCHIQVDWS
RWKDDDADSENDGGLGFDYNNMMSEMMLQKGLEKKEPTPFSSVLEGKGENDNQEKNDAMG
TGNNDDDYEDLPPLEE*
>TCRU_7436 Regulator of Vps4 activity in the MVB pathway, putative
MKSFFSKKPEFDAVKVKANIRMAVTRVRMQQNKLVNGVKIQRRQIAELLALQKYDSARIK
VEQVIRDDVSIEGLEALSLFLELIANRVQMIADVKGTKGNAAGIHCPPELKESVTSVLWA
SARLGDIAPELQNIKNFFEMKFGKAFVMMSVNNTEFSVNQTIIDRLGIFTPSNERCLQYL
TMIATEYSIEGYDEQKLRDPNTLVASAAAASGAAILSVVDEKKKSGGAAAVRSVTSGTIK

TPSGLIIPALTTPRDELEWRLLQLKRE*
>TCRU_7437 intraflagellar transport protein 81
MNITGKPGSPGPGPTPAFSMAPGNSSTYGNAFAGEGTGAYGGNKPRPAADLTEEEVLQYI
VDNVNKVLSRQYSLVEFDAIQGVPLLQIVNDVFGTLAQSQQMDLEEVPIGEAAPRMIEFL
TKTLGYRIPALLADNFASGFAQAEPTVVYPTLYWVLSNMPQNEKRVYLARFLQRLDIPEA
MRAQDEDVRALYQQYENLRLMFVQTHRRVDALRAAHADPAEARRKVTALEEERDRLQDYI
QVAEKKLGGVPDKESLVNASKSLRAALEEESKLAEKRVELQQSLISAQQRSTEMQNRLQN
LRRDAADGRVDVIVRRMRDEIQTNKMILEEHLPKELEQKRRENEELDKLISEPLDMQALT
TENQKLDEALKKLQHQVKERQKPGEDGSTISTIKQQVERVTKRKEEVLEMLTSLQADNSR
TLNEIRDRENRINQLREAHQMLKGDEFLTFSNQVRAKKAASEGMRAKLSELRVEWGVVTF
TENVLKAQFNDLDAEIGDLERKLGLQGYSRTVEALTKLTREKDTIEELKGKTLEELSRVV
QDFTMAIRERRTKLAPLITELREVRQTAAEVDQEWLSKKSNYEYQESLFMEDISKMERDV
QALRDETNMNESIYHRLQAQGALITAQWDRIEAEREFTGILRSGAEIPTEDERAQEATVV
VGGLKCTYCGKANPTRGWLLYHLNKDHGVTVLAEKGFERAIEDLQVRLRETQQRHLDIQE
NYEGSVQQVEWFNHLKRILEAKLHSIHTEEPQGPNALEKDIQQVMGTASAGVNGVDMLVL
TGN*
>TCRU_7438 hypothetical protein, conserved
MKSGLRPIHRPARDTGLNSSDLTADAEGLHMSSRKVQLLTPLASFSSEELARLRRTSPDA
YQALLQYEQLCRHDTAVIAAKETELQRCIEVGQEVLGQLDQLKGRCSQLAGERDKATARI
RELQQHLKRLEATRNHGADDHPSPVIQGGSRKMDVSLREQLHQQEEERQKSHVYAKKLER
ELQEQKLLHDTLKRDLESAVQTARIAGAGSEAAEAARRSAEASLEEMRLRVEEKDRELLR
AHAAQREAEENLREQQQELAKTSALYRDSQKPSVEMVTAASILVTLHNQLQELILDAGRS
HNTKRELSPVAVSQLTRLRLPTAATVGATADSSFTPGQLGQWFAHSLEETSHLVIELSRA
LQQLEERLRRCDSDLERATAELQLALDKATNLGRENEQLRLSLVALKEEVQTLDAQTDRL
REFDTLEVQRQTNLRIAAIEEEKRAEKVALQCELEQTRRQGALELANLHEDLENERRTME
REIRSLRSEINRWREEEKSAVSAAGRLAAALSSPSGEEQLQAVRQQQLAFQGRVEELEAE
NQRLRAKNSQEIAELRAENTRLEQVVQNSRSRYQRQLQQHEDEMEKMIQSKQELQRRLCE
HDSNDIHRIKELQDEMKCMRDVECKLRGELLKARTELESNTAETEKTMSWLRERHEAELA
QVTHELETLRRGMEEKNASFIAENTKLREKLEQAQCSKETELGAKDSTIATLNRQLCDAE
IEAAKMQDALHRSSQKAKGLAAETVPVDRYEEIETELMQEREHVQALVGSLNAAQTNIEE
LRGKLEEQKQCVQDCLGQLPPSPAQQFARIALLLQATAKRATTRLLAILDEPRSVSVPSL
SPPREELDAMTFRIEPDDAAEISGVIKPLELSPVIRLPTTPRENFPKLPPQKSHGEPSSS
RTLSPPTSTLEDDLSPPSRPGVWKNCELAAAFSSALHTFLSDLTSSVEQVSLRPYAFFWE
SLERLQRLFIASSPMAANTKTTPATTTNTNNNTADTTSEAQLVATDGSNVNIRDIGADND
NVNDSGEETANVHHEETNDDVMWTAIAGGIVDAYVDECAAVFKRLYHSTTIYLREREETF
KKSSHHLNMSCEERVRRMTRGMTEREQGLATQLATAQSKAAAAQRFSDEAYTKLEDVTSR
YNEVCARVEHLEEQLAAKKRELETERRQWQETVAKLQLERAARRQGEEERQEQLLRQVEE
LRAELQNVQARLNSAREEEQGIRRDADNTKELLQRDIHRLERELLEARNSQNKTGQALHE
IREQLAASNLTLQQRQNDEMSRARQAERTIEALQQEISEAHTAHQSIQRLLQAEKFRSEA
AEEHSKDLSRQLAEKQVQIETLEQRVAELQEACWLQEKAFDAMTEENGALQKVNRVLEGR
LAKVESEREPLRQQLQSLLLLEPR*
>TCRU_7439 hypothetical protein, conserved
MCNNGEKSVFSETGAKENSTNHASGRRGPRTTCEYKLVHSEFGITPAIGVCGREARPHVH
PQRFARGKEEEYRGKKHIDPHYISLSDDAKRQEGRYGKRRVQGVTGAGKDTVSSILAPRE
SFTTTERRCVKPLNRNTCTSVQIAEARALNIAENPSYREAAQKVLRHAGNSSIVREEERL
ARRIASVEYAKGSHERCANLKEKKNAMDLGKPGEAIQVHVPFALDDSAPRPDNLTEHRGA
HYRNAESKPTPENPPRRSNGAGEHRGLRDNVLLSKNDYPDPPAVGVRVMPRVAVRPSSSQ
HESKDCFDEDMLRRSRARCHQSANQKMPDFIFGQPPPPKAPQKTLRGITEERWRAEEKRA
AERHTGRAMTHQSHKPTALW*
>TCRU_7440 hypothetical protein, conserved
MERVGGAVTSSRHDPASECFPTLTEAATAIMTPEELQNMRRNLTEEKIAHAKYLREHPEI
DAIMRCAMRKLLMQRPEDPVGVLLEFFAYGNLQVELQSQGDKKGELERFLSMQKERGMMP
VWPP*
>TCRU_7441 pyridine nucleotide-disulphide oxidoreductase, putative

MYLPRNKEKPKENPFAVQKSRRFIVASCGLAFLTTVAALYLALEKARGRQRRPDGVLSQQ
RTGRRVVIVGAGAAGSALSASLTTASPDLHVTVIEREKKHVFHAMVPLAHVGHRSYDLNT
TGKVDFLRSPATWNVTRDASLVRGEVVLVDTARNEVVVLEDSPNSSATQSSLPPTPPPPS
SSSSSLSRWVAPLKSWWAWSSSIFGAAPLERRYPYDALVIACGAERTLGPLKRFISPSQV
DRYRIAVNPGITRDSLVHLFQGTVLHVKVPPTSFVTNGKMRYTSRQHDGTFIGSVNTIWR
YMYYFNKLLLCPYIAVTADRQPSDAFPLILNDRILSLWRNRGVDFITCSYISHLDPLRSE
ATLYNYVTKEKRVVPYKLLVLDLPLVAPAFIAKSGLSGGAAAEGFVDVHPETLQHRVHAN
VFALGDCAALPTVKSYGAAFAQVPVVSHNVRQLLRQLDQVKDKEEGSLRSHAGFARYDGY
SSFHVVMTTWRAMWPELKYGKSKYEIGESGSYTLDGAPVVLTNNHLWDNLAWIDVRGFLN
AVYYQLFLYEVMFYFLFTRAAWYPPSWFSVPTFSEETGEPLRGGML*
>TCRU_7442 Trafficking protein Mon1, putative
MDSSANGSLGDEKGEEGRGTPVGASGGVAVGFAGPPSRMEELSEEEEEDETVATARNMEL
KLSAMRDVTLTDTAGDAGHMEEAQTPPQAAVASQVSGPSSLVMASQCVSPDDIFCRHSKH
VFVFTSAGKPVFTRHGDEEEFTELFGIFRVLMAMAQQRHGDAAAVRQRQKENLHCITAGD
LYLYFCVHGELFYVLVTRANESMRSCMRQLRQIHLQLVSLVPNVSSILSRHPSYDLRRLI
SSTDASVIRQLIRCNSQEECYLFRCLAAAPLSVRRRRSLEFLLTQHHGTAFSTTNSIGGG
EENSTENTGHRAINKEAEAKDHLYSFLFFRGRVVCAVGPADSDAPLHVDDALLLLNFTRC
LANSQAGEIWAPVCLPMYNNTGYLWCYCANMNVMARDSRRGRAGLTSFGDLGNLALGQEE
IQGRITGGHETEGSLCDPAYSGSRVKKDVAALDLPSDETPAAFLKSEGLLLVHIAASQEA
FVALAEQTYRVASQLMSEIVQLEEELSRYERIALSLVTSEARVKKQAQQQRWLSCETTPP
LAAHPDSSNVTSKIFLSPFIHPDGLQWFAAVLRGKPHKGGFLTLVYSEPSPAMRFSAHER
KRLLRLVVEQRERLVHCSCLPEPLVLMRMNDVNLVVMRTTSTFIASLMEQFFKTRTDISS
PSSAASAGDGDDFITSQEALVASSRVKELMLLFSPHVSNPQMLRCALRVLVRLAARESEL
SFYQLRGVRR*
>TCRU_7443 predicted WD40 repeat protein
MLAKKKAERRHAIAVIASAERQRKLRRMRPDAKGEKEKMRKVGKRHRTSEEEDHTVDPMA
VSAENPADVLRAIGDHVNTRLQKLEFDDDLDADLFDEQQRQLREEAAIAAGTKSRVLSTA
ISGFFRQQEEQNKSLKMLRVGHNSNALTAVCGLGSELVVFGDKSGSVYMAELRGSPSLPL
SSNSSQKTLLRPCLPAAVLSIAVSDTSGLRPSQRALFERSTVDTSVTSYIAAGGADGTIS
IWVTRTRMHMGFLSMHRSAVTGLAFRHDTLYSCSSDETLRVWSVPQMICQDKLFGHQGSV
LGIHCLKRERCATVGEDGTMRFWKVDAATQQEFTTHSYFGVKVVLECVTMVNENVVLCGA
SNGALLLYDLNKRKPLAVQEAAHGYGFVGDGTGLEKVILAAQLEKASSNGEEQREECRRN
ANPITAVASIPYSDVAASASYDGNVRLWRIATPETGKKSGPTVDQAQTGAVAKTTFECLA
SIPISAIVTSLYFTSSGDALFLGCGKEPRLGRWVVQRSALNAAYVVPLDDARLRAFTACA
DVEHIPAMLYGFDDEEDDNHREEKEDGGENDVPGSIDLTERNGALQANEGSDNDSEVGSG
LFTLGEDGQMQFLVPPEADATDETAVVKKKKKAMKAKREKNVPSRGAGGNNEKKFSRIKR
AAENRQTHQPTGDSPRPQRRKRKKANPKEAKE*
>TCRU_7444 hypothetical protein
MGESHFSEDGVWLRDAVTSMHSAATQRMNLLEDLARLCKALASDVKHICLREKVKGLEEE
LNFEEYSLSALETLRQLKQKSFQKGVDGDRRHAIFSRYDTSSTSECVGSSPESAGFPLAG
GNSRSDGNCLTEVSRANVDSYLNKEPFLCLSGQVSSSKGEKNDLLIDVIHRRDALRDEVA
SLKTENERLALYQDHLKRSVHFSAHAAAVVGMERDVFTALSELFSALLETSEDWLTSLRT
SEISPETRHENNDAFSDTVSLQSTEEEELRGKIRQHWEAQREAVMARRAATMWAQSTRVV
MATLRQELHEMQMNYKRQRDEGYQQQLLWLRLEAAVMNAESKYLNLRLQYVRRFMSVFHH
ASSDGNDDDDDFARELPSDAASQRDRMNRAFMRLRSIVVNYEMDLCKLKQIKRLLKRSTP
AGSFSRGEQMFKEKHQEIKTAILPCLASSEGKDAFHSGVQRIMPWPLKMSRLKSSFPSHC
VESVHSALLALIVLWEHFTPVEQQRVCAAIGDMAVNAHLLLMIAKYVKSRRRRR*
>TCRU_7445 tRNA pseudouridine synthase, putative
MSCRMNAAAAVESENVGNRREEKDEREAVDEQARKLPKRKVAIIFGYVGERYCGLQWNHL
PGYPTVEEELLRALHRTGMISKENYEQEKVQQKLNWERASRTDKGVHALRNVISLNVMLP
YAKGSTTEYDPQEARRILMTVLPHDIVVYEIVPVTRSFNAYMLCGARTYEYYLPTFALMS
LDEYSRDYFPPSLAPARPTLEEVGFTGVASEGPRATEDETPSFAPLGTKRPREVEENGES
TGDGNDNANTVGGGKVTCEEHEREEVVEERDGQQCIGGRNSNETVQKFHEGRFEKLLIFR
TIPADAMRHVSQYRLSSEQLEHARNIFRLYEGTYSYHNFTPGGRASDPSCMRYVTSVTVG

DPFLVEPTDAAVISALQEWTPSRCYSPDDEQVSLQGQNDENSIEEKREKMREHMQHVYGD
FSSGGVEGSVKTGLEVVRIELHGQSFMLNQIRKMIGAVISICAAGLSPQYLRDHLLNKAV
RCGVPMAPANGLFLSYLDFQRYNYRLDRIQSQGGNGSGKGGVYVDRVSSDAVEAFRHKIV
AVILRNEMVGDVMGRWMRSLRHVLRLACGLEIP*
>TCRU_7446 START domain containing protein, putative
MWNVVSQVGKVAYRTAAKTGLAAGTEQPPYPCALPLQSLEDPEDTAQVQELLDNIFVAAK
DLLENDAEHQWRLVDYQDPDKGGDLHLFTRPHIGPFNFAKATVSFMGVTPQQVLDTMHSD
EEASRKKYSANISHFEILARPTPTSNVQYHEYWAPPPVSGREFIFLAEKKYVEEDDVYYV
YGCSIDYAPLNKKSSGHVRASCLWAWELTPIGNNTMATYVSCMNPRGWTPTFIMGWLKSE
IGKELVACRRVLYGETVQLERASLVSMGLKDEDVLLMRNQAGEEEPLSC*
>TCRU_7447 hypothetical protein, conserved
MYGCGRAAWVPLSAALVVMPWATSPTRRAAVTVGGNELAHRATVLWAQLAPGENGTRPYF
LRARALFGAPIAVGLRCGRRRRIACPGEEWTCAPLLPEVDPMADESNGTRPCVDDSWRDT
VLRSVTSTSDGKELNLRISVQHALLVKRAGSIYEALEGACRGVGRRCWTSRQCGDGGSSH
GQRQATPMRALRQRLLCHFTFHSILARCETKPPLWWNWSRLFTGSSFGGCARTSFGCRVG
FVDLVELTRLHTGHECCPEVPRTTARVLAEGPEMVRPQSVAPRVVRRLLFGFAVSEPAGC
GGAWFGGANVRPRSGANGRTGSPFQVV*
>TCRU_7448 Diacylglycerol kinase catalytic domain containing protein, putative
MSRFKGCVAIINTRSGAREGASVFASALQRYLDGAGISHHDVRVPGRDILHSIKLHADAA
DAIVVCGGDGTLSSVANALAAARHELLLKVPIVPVPCGLQNSIATSLGVLSAERSVSAFV
LGRVEPIPLWELRVNGRFLRYFVSYISIGAYAMCVRHLHYLDAVGENYVALPTVRNKYKL
GAFYTAMRNEVVPCTTVMTVSNSRVEVEASMKLFVASQMPLQHNRYSLTPNATFKHGTLG
VTYATEEASRLRLWHLLSREAAEGAIINEDGVCECLCVSELDLFIKDVPNITEGGVSPGA
LLMADGEGVHLASGSTVSVRRAPFQAFFASC*
>TCRU_7449 WD domain, G-beta repeat, putative
MEQNGEGGRGGHYQSRFRQRGQDYDEYVPRRKIHGQRSVDFYSSAIRHVTTRLLHRNTPY
GFHVEPHPYYSKDMLPAAQTPFNPSTALCTQWVNTSFHPDSRAGHTRVPLMNLKWAPNGR
RLLCSTGRGEFLLFNGHSFGVEVKTVAHEDHRPCRAITWGNNSDLIISGDDAGIIKLWLS
NFVLVAVYNSHHRAVREVTWAPLEGKFCTCGQDGSARVWDTNAVGTDPQQAREEVKLEGH
GGDVVTVDWHPFYSLILTGSQDRDCRLWDPRTASRGSIAALQGHAQSVNCVRWNPNGTTL
LSASKDCTVKLWDIRMVQEIASYEAHSKSVERVEWHPHVPDLFVSAGADGSLMYWLVDAY
EVTQGQGGFLHIIHETAMVENAHDRFRDVANPVNAIAWNPLGSLLASCSAEVKYWHRNKP
GAMEEKERGEEDDVFEMTEQL*
>TCRU_7450 Alpha/beta hydrolase family, putative
MFSAVDAVKYLASGRGVFDSICDLIIRPPRAEYDLEMDLGPTLFRISDDSELFTRTELTL
TNMRGLGVECSWFRPRARRRQPCVIYLHGNCGSRYDALEALFILRHNFSLFAFDATGSGK
SEGEYISLGFYERQDLAAVVDYLLGQNDVEGIGLWGRSMGAVTSIMYAAKDASIKCIVCD
SPFSTLRLLIKDLVKRYGSKRFPARLVDGIVDRIRKRIAKRAAFNIDELDALKYASECVV
PTFIFHGDTDDFVVPSHSIAVSNAFKGSCLHHLVAGGHNDERGEDVREIIVQFLTLYLIH
KPQGERDRKMGPQPVFIKGIQTEAAEKKKAEESSTPSCRDEDDDNDDIDDASVANENYAP
LAPISFTRPLLCAASPLPTPGDETIAADEEEGKEEEATA*
>TCRU_7451 protein phosphatase 2C, putative
MGSMLPKPILSKIVDRAGNYRIGAACVSVNGYRPSMEDAHVMVADGDVNLFGVFDGHNGG
ECSEYIAKHIPEKVRAMNGNYEPEDFERLCVSLDNDFMRDVGDASGTTGTFCLIMRDYTT
IVCNVGDSRTILTRGGKMLFATEDHKPNNPDERDRIEANGGCVVSSRVDGDLAVSRSFGD
SSFKRKDVGGDYMKQKVIAVPDVTRLACQQGDIIILACDGVFEGAFSNEEVVGFVHEQVA
KCTDLAVAAARVCDEAIRRGSKDNISCMIVRLSDGMSSTRLYGANSFVPGPPYPRTHDAS
RVAYAAMAQRMGLTVADALMKRYALLKAYENKTILTMSPVEQTAFEMSDETDIETEKNFF
GRGPAPGNEAAFFSSLAEQGGR*
>TCRU_7452 hypothetical protein
MHRPKSDDDTFADDLPADIAVQYRILRKLLPGRWRECQEAVGAMGPRGRELLSTRSIGRK
DARQFASNGPVQVETASLASSSSCFGGNTWHDNNKLKTLREIELGGPILDQLLAIHAAHS
RLRTALDESWQEKWRTFSEFESMQRHLIETMMGWFFETFSALLFGRVLGQLVDKAQRATV

AERRVRELERNAEELWKYNKILEESHGDALQTRPLEREEMKREAEELHRPLEIRQEELRE
AHQTIVALRRQLRQAETVSRKPLCALMGEFEELKSQYQELVAAHGGTQTCIERKIEGREA
ADEEEGGGGESVTLLRRQLNELQHQLSLKDATIGLLRRELCGLRDLARELGASQAELQKL
EGRLKAAMVPHSHYSNGMVAWWQPFGLSSVSLKKNHNNIE*
>TCRU_7453 mitogen-activated protein kinase, putative
MLTHVSAPDPEGRVTYTFNTQSRVEVPQRYEVRSIVGRGAYGIVCSAVDTATGDTVAVKK
ISNIFGDVVDGKRILREVKLLGFLKHPNLLSLKDLYRPSDPGFSDVYIVTELMSSDLQAI
LRSKSVKLAEVHCQYFTYQLLCALRYIHSANVIHRDLKPANILTNSECDLKLCDFGLARG
GGPNMTHYVVTRWYRPPELLLLSDEYDGAVDLWGMACLAVEMFTRKPLFPGRDYIHQLNL
ITDLLGLPDIVRDLSQIRSPEAISYVRSLPVKERRPLESVCPEVRERYMASICYTMEGRD
DENSDEREGVEEGGEETEREEIYGDANTTTTQAKQDGRNGEERYALFKDFLFRLLMYNPK
ERMTAREALAHPWLREVRANCGGKEFETEAGEQFFWEFDSTELSAVQLRQLLMNEIIKYN
E*
>TCRU_7454 kinesin, putative
MKGQAGTRTAPKNISVFLRVRPTIARESKASCNNLKFDPSDPQRVTVTRKSGSRPISKSF
VFNKVFTPTTGQKEVYEDFARGAVDAAFDGQHGVLFVYGQTGSGKTYTMSNDDPKNLGMM
QQGLHDVWNRIRNDTEHDYSCSVSYVQLYNEILTDLLDAQKGRVRIQLGPEGCGDVVLVS
DSSGMPIEKKVQNYEETMELFCVGMGRKEMTSTMMNEVSSRSHTIFNFNITRSEKTRTVV
VKEGELNDAPTMALEGRLVICDLAGSERVSKSHAEGKTLDEATHINGSLLVLGKVVAALT
DKSSQHVPFRESKLTRILQYSLLGNGNTSIVVNCSPSDESTEETLSAIMFGQRAIQIKQD
ARRHEVLDYKALYLQLMAELDSKNDGTLADALKEERRVYEDRVSALEDRVRILTTENDLL
RQEITELQRGGDGTATDGAAAAGWQAVSKQMRDKLAERDAEIKVVTEERFKLAILLAEEK
RTAFRLAEKLRATMMRYQMDSKQWTQQQEMLAIELAQLKGTDYISLTGGIKECGSSGGST
NQSVFTDSVSMPPQPSPSTGQDDSYMQEQLEKAYNRIRELNQERLERIVYQSKAEKAIRV
LYAEKTALEKQLLQQHVVSKEKTTTMGSRSSH*
>TCRU_7455 KU80 protein
MTLRSALVFALDLNCPSASLALAAEFCRRSAETTMMFAPHDEMALVLAGTCDPHNPPQNG
QKGGERFKHISVPCALAAPTVEFLEPLAHITPPPPPCERHEVDFLETLFVCDHVLRERTA
NKCYQRVVYLITDAHTDVARKDDMNTLLESFQQHGVSLVVIGIDFTETSVDATDDEERDD
KSLTELSLKAQNERVLHVMCSLLGEESMVVSLEEALQEVQELRRRKITQRALLRVVLSIG
DVRLATQMFTKTQEERLPTMKRTTANGEEVYMKTIFQDLSEDAAPLRKEDLLKGYHYGRS
LVPCAREDVGAMKIKGPRAMDAVGFVPIKQVPAYVLLGGVKVIMPLADDMVGAKAFRSIV
RAIAADNRAMIVRFVRTRDADPVLGLCVPSTNERRDVLFFSPLPYAEDVRFFEFSDYKGM
WGTSSDDDDDGEEARLLAAIVEDMTVGKSVLRPRETFNPVIQQYYATLRAKLRLFCDGRE
GVGGNGSCGADELRGGKNGEKNTNGEVLLPLVGAIKATSAAFGVPGNQLESVLSSVREKL
EACARSFVYVSNRENCVAEERQSYRFYSPAASHDVDASDASTRAPSTVATPCIISDASQI
TTVDPVYFFKAIVQAREGVNVRLAMDKLGDIVFTLLRCSLGDAQYAKCTGCVLVLRQHCV
REGEAAYFNDFLLKLMLMARELDHESFWKNGIMARGIAPITKRECPNSTMDDEEAAHRFL
TQDRTLPAPLLEDPTDEGVLNMIT*
>TCRU_7456 Rab-GTPase-TBC domain containing protein, putative
MSEAEIRLFELLDKAAASDSGTVPLSALQEACTEVPYVSSRLTGRRRYQLYSGLLLDKPP
TVVPDTFREHAGEAGEIHKNVAARLKEVLSEDELLEDADLQGFVCYFATKTGCQFDDEMT
GITLALATVIAAAELPPGTEKLFRLYQLLEVLRKDFVVPAASRAFDGSLASLLHLLLQYH
DPCFSRHLDQRVVNIGVILLDWVRRLFVVGDNFQEALRVWDWLLIMGDPTMTVYFALSYL
VAHRQRFLAMETKEELTEALRSLVFVLPTRKEDAVNPALHDGRPISFLSLRSGKSLAQNA
DIAYRSTPHSTRRVIDALLFHDEGGLSKSPDALEGYYTAYTALPLERSDFAESFAPQAAP
SALSYVVLDCRSRKSFEFARLPTAICVGDDVGFDNEKFDRVALTLKDIKGNHICVFGTGR
PITEEFNLLKMLSLHLVQCGFPYVSMGGFRALIPLIKAKVITIKGAPAADRARGDFADSV
AALKDSLTDLLPHLEFDKEEARRKAEAFGNKAKEGVQAAKSWGWSVVQSVGKRLVSSSAP
SLAADSTAGKWANRTTGTGGTLVGAGNGRDDLRPTRATAAQHTFSLSVNDDDDDEGDLDL
ITSVPQYTGNVVEYREGEQLVRGKLLAEGSSPPPGENVEASPTAFSPEHSKASKGILLEI
DEEFNRLFGDSVSPRDLSSERTPEGDARKD*
>TCRU_/ UNC-like C-terminal, putative Sa.1
MKTDRLITLLVLALMAVTCGFLLLNARKRGGLEENPPWKSLSFTTNYASAYLGATLTDFS

RACKGASSVLNEDKTKYMICNCEASRKLFTVQLIREIEVRSVMLVNLEHFSSGVKKFMLL
GSKKYPTSEWRVLGEFEASPWRGTQHFDVPTQEPVRFLRFLWVTSHGDDSWCTLTVFKVF
GVDVLETLTEDYGGDLDNLLHSLPEKALPAPPVVVMPSPPFFTEVDARTDKAADWLHPLK
EKEKLNGGAEIENLFRQVDAIIAVGSNSSGSGGTDDMCTDGDSSGCCDHNEVVENNSTTC
TLHEKEAHLSRSRCKCFSRTNLFSRMALSPRPFQGGAALQIIMQMSKHLKVLQQELEETF
ARQRDTERRLEKAETALGNVGKNFRDALRLSCNYRERLIDMKKEMDVMNSRLLIALESIN
QKGSDVTLRIWVVCFNVVALIALFASCVAPYSSISSRARRFTQRG*
>TCRU_7458 hypothetical protein, conserved
MQQKVLIVTPVALFELLDGKTVERGNCACAIVGLPSDRPKYSLVCYNDRRETLCVGAMSS
NNEHGLRFELQTGMYASFCDSTGKRWSCMFLKESQVEPFLAVLGIALYALAGQPAHTTVV
SDFAPPAGEVRLGLQHRVKMRYSAFAVRKGDVLQLGEVLETNGDRPYNFQPVQSALALLP
EAKGFESSVLGMMEDSWRTVVVPAMLPRSGGRHLYGGDTVAFVLQAVRILHDDSPMAADA
KVPVVFADCDNASALVPVPAHTKDANGTKIVVLHSEHREGTTGTDGMFFTTSAFGEEGGG
VSAEHMALIQKLGAQISRATTDARDVRDIAVGVTGEWKQAVSRPKPSALTNAALEQSVKQ
LIMENERVMEDIARRDELLRSLDQRNRELQKRVDAAALVSQQLMDEKNDSMRTASDMKLE
KERVIMKLQEQINQAVQERDDTQRHLQTVKKLLGVSDEELRQIRGKADVHAIQAQSIVAK
LDTIHDALAEERSRRKGLEAKVMSLQEEIRDAEAELHLKNAQLEELRRTADMERAHYAQI
MEDERQRRGFEAQQLRSEIVSDLQSREAKYQADRARVEEDNFRRGQAEGKEIGRREARVH
VETQLEELQLEAQRAMTELDASKTDLRRVIEDGMAQNRTLGAKVAELKKQMYEETGKKVR
LEFQLQGMRTKLRCARDLPMAAFTSVVYRLSRPAEVADLLQILDALKKRQKLDFSFEKRN
QEAEELQSMQRRLEWIESSMLSLYCDRSEAIYRAWVEPLLAEQKATVEAVRRLWLERDGM
AHYEINAAETRSRFDIGQEMESFFTELSKVFNNQMMQRCECLNEAERAFKGIFDEYLAAT
DAINAYRIAELQARRALSEECMAARTVTEEEEAVAFRLLLTEALTGVTAADQNAFMEAEE
GERALIDADQCAEFSGMLFDCGEGLAALQRLAAAVEVRHKLMAEEAQLRAVIVAEEQEAL
GDITEEQPRQQAPPPTPQSTLLEDGTDERVSGAHSSFYPAEEEEETAEEKATPFSDEPQA
EAPRVELDEASLLRTATKNDSFDANDTATPPPPPAARVFLPSTQAAVAKSNLFGSSSDDD
DDDRNERRVPSMQRPTVTKSRMPPPKSKLFESSDSD*
>TCRU_7459 hypothetical protein, conserved
MQYLYDDVIPPFRFFTKIVLKCVNDALDEAAAIRRPDQGSMYAPYTTIAKDNPILVEIPT
GLVMHIAVTRPRRRSAEERANAPARSILSAVFLCYDVTLCGFTDGRVELMYSGQEGGAVE
SIEIPPLKRNLIHVVALNCVPLSEGKWAVAIGYKGFFVVRKVELGRSAHLPILLRKRAQQ
RVIEMCTAEWYPSGSLSSLQLSPCLKYLAVGFDNDALVAVAALPSLEVPCHELSDGSERV
TMDVTCRLVEDGYLNGSHQGRVFFMPERLPGGMRSVFSAGMNLSDSEMAMGTHHPLCLLV
WVNGNSYTRCPLKSISRSAVARLNSFLFPIPSIGECSTTKSLDDAATAASGAAASAAYKL
GRKSRAGAKGSKRRPLDVSPDAATASQTQSSFTGVYRGLLSDRIVAAALASADGNVVAVG
CAGGCVYLINGHGITSMFFATMFRTKAMRLNSLYPSTGLQCGMVLQAVDTSKKADASVTL
AHARGIPSAAFINQATVHCLREVEGLQAVLPLRELPWVLLFCTHGMYLWDVHYNSVVASL
TGLPPLESISICETVVRRSVIGAQRQSSSFKTRQELHPPFCTESAIVWWTSSETLARLLI
SDLIAQVYPLLETYFRGLPMRSLAYLVARIPPTQRHIPEYMATVEVPTEQQLMMDSYDIN
TPAVFAGAGGSRGSFPGMKAFLKDAEPSRFFELSCTPLYPETLAACFLETTFSSASARSE
ELFLMLGSPLSRVS*
>TCRU_7460 LIM domain containing protein, putative
MQRRWLNCAAVFLAATAVHTTQRGMHGKPTQSHKVRTQHSRRWWTQSKARHLTAMPHDEC
KSRPHFPAYNEDVDRPMLVPAGAICFNCEKPIDDRDVNSYVWIPAGNATVPTTQGYFFHF
KCFKCWKCKYRLIHNKFYSKDGKAWCVACALGRDIRVPTRRWHTSYVNTHRTGSRMSGHF
FPRHQHQMAFLLDPNE*
>TCRU_7461 AUT2/APG4/ATG4 cysteine peptidase, putative
MEWLKIALVAFSGRGNDVDYPCSILGRVANNDKELVNILRNGFFLLTYRMNFSPLPHSSV
TSDKGWGCLVRSSQMLLAHALWRYSANDCRLDHFCDMDTEDSTPFSLHKMVRAVMKKADV
FRPEYWTPSQGCEAIRCCVNNAVDRKLIPPIRVVVCSQGCLLAREICSNLEFGTVLILAP
MRCGASRRMTQMMFFSLEHLLHSSACIGVVGGVPQRSYYILGTSGQRLLYLDPHCMTQEA
LVSGHAEKAGVVTVTASLVKSVRWDCVDTSCFLGFLVDSFAEWLELRTCLEELQRRGMEQ
LLCVDDGDAVGLVDEEIAGWPSEEDVAE*
>TCRU_7462 mitochondrial RNA binding protein 1

MRRCVALSWLQYRGSVRDSRVSCGCVKTIRRWCLSLRIPSVQFAAPRSQTHEDLAYAACP
ICGRLTHMCDMFTHLTTAHRELNPAHCKKICGERLELYQQVIGVPLKKMELTTSGRRVLD
FLPTVLPSGYICNWCDMKNDVYPTRDKFLKHVADVHMEIDLEDVEQHVPLLPRGVVEEKS
STREEMRPTRRLAGVEAVAETFTIPFVATRQVAVSIPRVIDKKVTQQPVVFSDTEFPCEL
CNKVFQSEMDLLQHLETRHPDGSAGASTDVGQSAIAEVAEFTAKEATMGISQRVHVVCDL
CLTSSKVYTMPSALFSHIRFKHPGEDAAYHVERLIRTQKGQSFVCKVCNKAFATAAALEG
HFSNKHGEQAGALLGQGRVAMNNCWWCHDCERGFSSAKGLHGHMQNKHGLSTQVHPCPAC
KRVFSDVYSLEEHITLVHKTIHLTDIGLQTHAKCNTCDRCFLSHEDLHRHAVKHHKKDPR
APIRPFESSSFSSTEGKGAAKTDASSSSLSSSPAAATPQAPRKVKKRKKTAVEEETSS*
>TCRU_7463 hypothetical protein
MGEWGDCGEEAAHLCAVQQLLQAFLETPSRVVLLSAALGEMLGVVVRQQKAINKIVASLQ
IAGEERMQELTALSQSFADILQDTIKRTALAISELRGQIPKQQCMSGAGLFYEEKCVELK
REIGDLRRLVIERLQHDSMGADMNGQSSAIQSELVVTGEKVRNLGAQQSLLLELLDLRKM
LLHHGYTGDASVDLRQLRLLDTTAKVKLMHQLPCFHVLVRALVSTERHLLAGASSMSSID
*
>TCRU_7464 ubiquitin hydrolase, putative
MNVHWKPRGGAQASVGIINAVEFDPDVELLWVSDSFGRLMSFTTQSQTNTLTWTTYSSFL
ASTRPISGIFFLPLGGEKIVTVADHNVIRGYKRGGALFMCRSLPPQSQDYIELFQAHGET
GVVSFTGNAGLTRFSIGNEGNDGVVTVPLGESKVVALHQTEKWVVTGSISGSIVVRDSSD
LQLVGAVPSSRRRVLAMDAYDNTVVAAMVERSMTSSVRVYDLRKLSEPVITIGGIPSDSV
SQLRRYRDSFGISADRAFVLTPCGFHILQMDQTSPVFNSNGMVGDFCTSVSISPNGMCAA
IGNDKGYFIALAHPATREDYVMSRFEQPRRPVNPVFTQSWAEKKEGDTFAFFDESVPPAE
LASNWPPDNYMILSVPAPTRCLSVESRTILQNRWGFLRADSYLPDPKDKMALNLPDPFPF
NLELGDDPAAVQGLLQEMKKNQKRRYFEFRDVAAGEYAPLEPASHVCYSSHHRFDWENYN
AIPQEVVGLDNSFPECWITTLLQSLYLCHLPECPVRKVLLHHLCTREYCVACETSFIFAN
MMMTSAAGLNPIVQVANLIRTMYKVPATASLFEPVKSRDEAIKRMHTAQLTLLEALHRGL
QDEKAYPFMDHKPPCNDFEHSIAYLFGTEFSSGGRVHLEPQFYWDVPSSALKVNEGLQHL
LKQIESYRDQVQIKRLPPIIVLRLNPEGGTLKPPRCLHISREAQEDSNYVLCSNIIHLSD
DADDPGSFVSHQRILDDRFSLVNDYRVTAPMEEEELEESMPAFHSHRAVVAYYALDKLTA
PPYSLHDGNRPPNMFEVLGPLLVNDVLAKPLQRDPSAQRFKSPLASFYEIKPNDLIAIDA
EYVVLSWNSRCIDAGMEVKLSHKTHMALARLSCVLSSAPGDERTIVDDYVHTPEVIEDYV
TQYSGIHPGDLDPLKSTKCLTSRKATYLKLRALVDRGVIFVGHGLYQDFRVCNIAVPPEQ
IIDTLMMFHKPGGRYLSLRFLAYHVLGERVQEDEHDSVEDARTSLRLYRKYQQLVSEGTF
DAVLDKLLATGAETSWYVPEGRDAFGASPALFASIPGSLLFPESPSTLVPAEAAKDDEFP
SAS*
>TCRU_7465 hypothetical protein, conserved
MSAGILGKTHAGVPSYRSGYVSPSGIKIQYSNDWVKHHPLEGDGLRTLLYLHLWKKNKGS
ESRLKDIRLPDTVVYEHNFPRAWYTYDGEAKEINKHPGKMLDAQSIYEHFSRSTPDCDVV
AQFLTTCAQDNPAISSEGGLLTYVKFFTAESLREFLFSPERKPDGILQKFVVPKGETTMR
KNSQLQVMWSPLVTVVYKRTNKQRLGDLHLPVHLRSATFDGDSHLSELSLIAGESKARLE
SLCREVVDHFYFTDLKLITRMVLNFKIDDANRPWLLWCSSLRVSGDRLNPRNVRVPVALS
MPIEVLNDGSSTRDRIIKSRDRQQQLLLLDKQLFELSRDYDFGHNCNDSHVREAKRLGLQ
PLSEKSSPNGQGKSFSRRNPPHPLHDAMRYLRVLSTEPQGVDLSNCSLSSAAQQQDQQRR
SRNDSVRQSQATIDEAEDRVKSELTAMALDAWYTVYSSALSKNPTYMPTKDVFLAEPLVV
SLQPPELERLVVILGLERNPVSEDPRSFMVNSGLIGPGRRLDRPFINAERDVREFFDELF
ASRGGEITQQCLANDRWIW*
>TCRU_7466 hypothetical protein
MLSGPVELPGNIIRGSTTFCLTRVGDRAYYVPRGCTLEDKLHCWRVKADHETGRIFFVNC
GGLGPRWTLPDTLASIDLLNTAGPDGSRHRRSSLPGSSPTAKHAAADAVAAEARSLVELS
SGRKKGNSSDTKSFWDLSLPGKSFLCSGKQPLRVHSNGKRVADIYVNDIAYLRSFDEEGK
SPASFETALHGEFENARTPLECRCAETSLLEAQLRRRIEDYAEEVTTLRRRLEDQERLFM
EKELALVELEERIVSMRLHMVEAVSAYRQNTYSWQS*
>TCRU_7467 Mitochondrial carrier protein, putative
MPMSSGTTGYHPVFAPRFAGEFEEPLVRVQGYTEPRLTFVQHAAVVLGVSATTAFLRHPI

VKFDSFYFLSDVPGESNRIYASDKRAQLFRTLFSVRWFSGPSVLWSMSEYVFLLAVFTWL
REVLSWGSNTPRGFAAGSLTGVAYAAVRHPYDVLRATSEATGGPKKFRGVGDVFRTALRE
KPSALLGLYRGFASAACGRLLQFGAQFGVYNATRYDGVYRQTCVLFFYCHLGAILGLFLQ
YPLLSVKYQLHMRNQFTKGRPHTYRSYILEVRARHGISKIYDGFFTSRPILNAVPAALLM
TLYDVCARRYTEFLHPELQKVHGEVDQPIFGVRSAPYVSSLPKYEFARKYDL*
>TCRU_7468 Zn-finger in Ran binding protein and others, putative
MDFLKRTFADTRLRYHVSKVLFAASTSSAKLSTECLLLAEQHPTLVLAVLRENLQPGSHQ
SYAYLLLLEKIVDACSFSFHAAMALDCTLHDKLVKLATTRAEGEENRKVRRLARLTLLEY
SRMFVDVPELKSLSRLAGCVEKITGKNLMRSIEVESKKVTFVDPRPEDIILISPTEVSAK
ASLPPSRKSAVWSCHVCTYINRPHATVCVVCRTPNATRPTSPPVHKASNGKTVPAAEILN
GTVCHEERSGVEKTATSPDRNGFFAPAPIQKGEGSGTTGNTLVGIVAPHPRA*
>TCRU_7469 ribosomal RNA adenine dimethylase family protein, conserved
MPKETRTVPMGVITAEPIHTTSKKLKFATRVSTLGKPAARKASKKSAMVGLKTGGSQSGM
VFNKGFGQHILKNPLVIAAIVEKAAIKPTDVVLEIGPGTGNLTEKLLQASKKVIAFEVDS
RMVAELNKRFQNTPLASKLQVIRGNCLDHEFPYFDKCVANVPYAISSALVFKLLRKPTFK
CAVLMFQREFALRVCAQPGAEAYCRLSVNSQLLARCSHLMKISKNSFNPPPKVESSVIRL
DPKHPAPEVDFEEWDGLVKFIFNRKNKKVSSIFRTKNAVQTLYEKYCSYQKMEGKASVKS
LAEFKEHLETVMQDPVFESRARLLDQDSITKLLCHFTENGIHFV*
>TCRU_7470 hypothetical protein, conserved
MLRRGWVAPVVGQRFSPLRLQNRRFGDKIVVGSCAALSTSVTILGIFHLIVTPVSPAIAA
ATLSAAAVSGALVVFEGGKNEGGTTFGAVIGVFFGAMGGYYAKSSKEPWRK*
>TCRU_7471 conserved protein
MLRLSCLRKTALPTIINKVCRTPAYLRHAPPGVYVTCDFEKSARHTTLLVDASVEGEPPM
TNGAYLLSSTGGDDLAFQQAHSVLVGLPFAQDASQASRFLDTVLRPALARNGMSIPFDGI
HTIILLELHPFAAHAVQEIVSRLPQVKVACSPLTAAFLSDADFFSGMRKSLCENDAHLPA
KSITFAGVPQSNLSLLEDGSAVPVFGECRHLLVATGDLSDARERWRRERRNKLKHFESYA
LFLYDSSFYAMLAPPSAGAHFDWLPFVVHEADAAALLPLPDFLSLQKSTGSSLLEVWRLR
EHAHRVITALEKFPETQRVLTACYGEVSGGADGYVERLEQTVRKLEELRSRLGRRLATDT
ARDVAKWSVVMEEKILKEIVFTKKAEKKTSEEVLLEYKQWASASYLGRLSRSLALAGATL
PPDIPSEPAQEASPSPSPSSSSSKDTEGAAGVQLLKSHFERRGMASLTPVLEREEIDVVV
FLAMGQDDFKKVFKATFGVAKKMELLQQELRSSH*
>TCRU_7472 polynucleotide kinase 3'-phosphatase, putative
MKRARSPSPQALRNKILPASLFAEWKLIHGSVLALPPSADVVRRSLVGIPGKSLRLKVAA
FDLDDTLIVPRSGAVFPRDDPSDWKWLLPVVPQYLRLLYDEGFMVVILSNQSGIGGKGWN
VKKAESIKRKIVAMSEALQMPLTAFLSTKEDVWRKPNVGMWRLLEEHASAVAAAKIVVAG
DPSGHVFYVGDAAGRKTATLAGRKKDFSCSDRKFALNIDVPFLTPEQFYHCPKAELFCSD
GHSTQRGVEKFISKRLLAAADAPCEVDWDGLGPGELQSLQSSYDNLTINCINADGKRCTL
QTSSPAAFHRTAQEMVIFVGYPGCGKTTFFNRFLKPAGYVHINRDILKKKEKCLSEAEKW
WNSGKSIVVDNTNPSHSDCMPFITMVRQSRPGITPLPVRVFVFQASKGLSMHMSNVRARL
GLSPRISRIAYNVFQSKHEVWSSTSVKTANVGEVLEIPPVACFEGLQEGIRREFFLLS*
>TCRU_7473 2-hydroxy-3-oxopropionate reductase, putative
MSLKVGYIGLGLMGKSMAANILKAGFPLVVFNRTTSKMEELVQQGAQAAVSPADLASKVD
IVLTNVSDSQDVLDVVFGKEGVYSGISPGAIFIDNSTIKASTAREIAERMWKDKKVRCLD
APVSGGDIGAKNGTLTIMVGGDEEAMKKALPVLRAMGKTITYIGESGAGQVCKAVNQIMV
AAQMVAMGEMLVLAKKCNVDAERVIEAVKGGAAQCWTLDVKPQRLFAGNREPGFKAALQN
KDLSIVMDTAREFGALLPSTAINAQLFQSMVQNGEGDKDNSAVVGVLECLANCRITETNN
AN*
>TCRU_7474 Rubisco LSMT substrate-binding, putative
MDAGTRGWFQEALDASECASVKRLFLDRRTLEQDEGSEFPRLLWICRIIAADHRVLWEHL
SSSFMEDFKQPVDPWNEQLAVKLLRLRIDVMSDAVAASRLREELDEHLTTTLKPATATPH
VGSQIVAKGADMYSYVVCPAAPGVEGSLVCNAPLPAFGDLLRVPRERMFFIDTVVQYCDL
GRVVHASGELSSMISGDEPLLVLSLIYERYVAETSHWNELLFSCPGEYPNVPSFWDWEDL
AELEGLDVLDDVLAKKAQLAQFQTETMAVLPFIHEALAGGCRFGKDEFLECFSIEAMMWA

RATFDSRAFNLNVDGRVVIALVPVADMINHHNRSDVLVRKVEPNGGDFVMQIGASLTAQD
IGREIWMSYGPLQNWELLQFYGFVLEGNEHDRLPFPFDFPEGVVGDEWDGRRAALVATYG
LHLAGRCWICHDGRPPPALVALLRVHLAEAEEFDTMERKGPFASLGAGTEARVVATIADT
IRCILDLFSTSLEEDERLLENGSGPVATHSGDDGNTQPLSCNKRLAILLRMGMKRIAHRS
LEWCSAAATAIVARTEAAAGSALNE*
>TCRU_7475 leucine-rich repeat protein (LRRP), putative
MMDVNLSYGDLGTQPLASVVKNPALVRSLNLSGNNIDKELSIEIANTYISCMVNLEELDL
KDNKIGPQGAKHLCDTLLKHCPELKYLDLNENGILDESLLYVAYLLQEKRMESLFLVSNH
LTQRGMPTLCDGILSSRNIRELTLAFNVLGDGGASVVAKALRGHPSLRSLDISDNRIGDA
GAVDVAAHLILPRESRLESLNLSVNCIRDVGFSAISEAVRNTQSRRLIHLDLGGNHEVGS
DGRGALIKCVESMRHLQSLDLCSCGLSDEEGWGLVGAVSSRNCGITAIEWFNNPKMRPET
EKALYEALKAKRAAARDAEQHWRQLKILSSVLLGATLLTGLTVAFHQRRHR*
>TCRU_domain containing protein, putative Yi.1
MANPHEQREDPFREKMFDSPRATTVPQADVAGQTMITPFAEPQTTYTTSEQPERFGQPQG
HTTSNQMFNLQQPFYESPKSPGLSGPLPPQPPLSLTMEKFVPGTGEQTQEQRQEQPTSNS
RFWTIEFYQRFFDVDTRLVLLRMSNVLAPVNAPDFLMHREWRNDALQTPSYEFQEAGVTL
SQKPDLYGPFWICTTLWMALGVVSNVMSRIAFGHQSSDDKKKWEYDFTMASIASVVIYSY
CFGLGCVVWGVMKYKELPVTLLETLCLYGYSMFLFLPVTILCAIPVSALQWVIVMVGGAW
STAFLLINFWRLWEATLNRVWFLGIVAVVSVFHMLLTMSFKFYFLNYKF*
>TCRU_7477 Glutamine amidotransferase class-I, putative
MRPVVVILLHEPSDTPAYMEVYLTKRGIDYVTYEFWKDEMANLVPASVKNCIRCVKRDGE
ACRFTPVSETSVEGEYCCIRGVASFGGSMSVNDELPHYAPILSLMRSCIETRTPVIGHCL
GGQLLSVSLGGRVGPSEHVEVGWIDQEVVNTDACGIKDWFGGRKVINVFEIHTESFSIPR
GARRIVRGKYCANQAYQVGDQYALGLQFHPEVDEEKVRSLTAPSFPSLYTREEIMAMDEE
ESTRLSPAAMTRDDIELCLRDGRIERNLPIADSIYDTWCSGFIL*
>TCRU_7478 lysyl-tRNA synthetase, putative
MRRWGLYSFQCLCACRLTAARQAVKGPLLPPALSSSSSPLETKKPGSKASSTKTVTQEAS
RAPRTKLDLPAAYSSFRGITPISEVRERYGYLSSGDRAAQATVRVAGRVTSVRDIGKIIF
VTIRSNGNELQVVGQVGEHFTREDLKKLKVSLRVGDIIGADGVPCRMQRGELSVAASRML
ILSPYVCTDQVVCPNLRGFTVLQDNDVKYRYRFTDMMTNPCVIETIKKRHVMLQALRDYF
NERNFVEVETPVLHTVASGANAKSFVTHHNANAMDLFLRVAPELHLKQCIVGGMERIYEI
GKVFRNEDADRSHNPEFTSCEFYAAYHTYEDLMPMTEDIFRQLATRVNGTTVVQIYPENA
HGNPVTVDLGKPFRRVSVYDEIQRVSGVEFPPPNELNTPKGIAYMSVVMLRYNIPLPPVR
TAPKMFEKLIDFFITDRIVEPTFVMDHPLFMSPLAKEQVSRPGLAERFELFVNGIEYCNA
YSELNDPHEQYHRFQQQLVDRQGGDEEAMPLDETFLKSLQVGLPPTAGWGMGIDRALMLL
TNSSNIRDGIIFPLLRQDISSHDSKRRHKTASFFDFNKQMTLFCLSSLEQEFRRNGLSED
SCANVRELRRVIMELGQHGGANGLPTAGGRLSGWRITLMFAIIRFICGTPRR*
>TCRU_7479 alkyl-dihydroxyacetone phosphate synthase
MLGGRQADVYERIKWDGWGLRDVALWYDEEKNLVFHLNGKPMKGLLPFIQEKVVQGSGEL
RLIKSPGISVEEAVKRLQQPFINQTFLEELRQALQKDQIRLDGESRLTHMVGKNYRDLWR
ARNGLFDRAPDAICLPNRHEDCAKIMELAHKHNVVLIPFGGGTSVTGGVEPTPFGTKRMI
VSVDMRRMGRMLSIDKESGLAVFEAGVLGPDMDEQLRPHGFMFGHDPDSYTYSTLGGWIG
ARGSGAMSNKYGDIENMLLAMKVATPIGVVETPVTSRPCGVDLNAMFTGSEGAFGIITEA
TVKIERIPEVRHFEGWMFPSFEVAFSAFHTCTRKGVHPCTMRLYDEEETRFSFAASTDDS
LIGSLISKGLKKYLEKIKQWDLRKLSLVIVGFEGTKAQTRCQRSELSIIFKEFGAVSLGS
KPGESWMEKKYDLPYLRDFALSHSLWADVFETSVLYCDAIRCWRAVKESFASVMKENGRT
GWIGCHSAHQYRFGCCLYFTFIGAQHDENDMKFFLQIKQRAMEEMLSHTGNLTHHHGIGY
EHVPWMQRYNGKIGVEAIMRFKNALDPRNICNPGKLLPSPRAEDETLEAAEARQRREMMF
DKMGVPGAVQSHL*
>TCRU_7480 WD domain, G-beta repeat, putative
MFLFTASDLYGECCALYGVKPNRDVAGQLAGSNFLTIRRIDASRTFLGELGVRALLEFVG
SHSGIRQLVLKKNGVDAACVEHLCGVLRESPSLSFVDLSDNPISTPSVRLLSETARAVPH
IREINVENCGVSDDWMNRLERCCNANSELQRLGFYPYGPVRGLRSWETVFVLVLGPESLV
QTYCTEILPYVGSFVSRLRLRIAPLTIDKADTDDVVKNKVWRCSSMHNYALSWCVVLIGE

KAQWPDADISALMAVMRQEEPVVPPLRNKFGVLRDPMYRHAKHLFVYTLTSFHEEGPYKG
NVSTVPSSVWLPALGITVPNGMNAPPAVAVRSGNCWKVRCLTDLSVSLCSVFSERPRSMA
LLEEDEGSDKNLWETIEREKLVGSLHPRCKDIVHYVESPAGQSSVPLILYGAADIGKSKI
LSWAAANYSAVESLRVVPYHVSHENQSLVVLLFHLLRVFLKKPKRMYRSVEELAVDAREV
ISKYDGEMVLLLISRIDLLDSCGGRESLVLEWLPSCLPPSVRVIASLNTESPLLTAFRKR
MPQPYETLITSFPRQVRADLFLKEVLRRDVRKTSEDGGAMNDGGTFRPFEPNKSLEGAFL
QKDGSQTTSFGVYTASFLQRMPNNLAERDMAFILAEDVPDTLDEILTVLLRRYETISDPL
TVQYLTMSLVAAPLPISEVIYICEELGPCRRHKTLPVLLMMSDDGLLTVTSGSIVHLSGP
DVRRVVIKLYADIQDLLSVLVETHLVRLIKTRSPDMCFYFGHLAPIMIANGSVDVACSFI
LDPTHMDALLSRDPDSCTHAIDLIFRLLNTRQFILELGEDISPLMDQTTRRRNREALRSA
LEFLQLDNGFFFQSSLLASDVSPYYLQAMEAEEVPYTVLVPLNRGDEDDATYTLDCKHLP
VYCHLRGEYLVVTTTQEVIVYSATDFQNELMRSFVPFELNQNLRGALVAAGTRVVVIGDE
QLLLWDFGRQSFTMFEDTTASLSENALDPCFLNLVVCHHSKEQLSVIDVSKNKVVLELPT
LEAASVREAFFCGGGILAHTLYDLFLIRGEEVVKLAHTGPIRRVSFSNDGCLIASCVRED
IWIWSGTGELLHLIDAGVTPVEDLCFNASGTLLLTWQTEGVKLWHSLSGKHVGAVEPCFD
ERASFVSFTEDGNNIIGRCGSHIYLWNVHTRQPVGVLTADTGCFTFVQARNQMMIGTTSR
NEVKIWRLGDAPLPSIQSVREKKPTTMWRKNGRLSSAPIVRVDVNLNGSLITVVDGNGSV
ILQPMYGTARLDCEISHVESTAILNDMIFFTMKGEGRQYFWKRLSEDDTVTKVSLPRNAV
MHARLELVKSEDEGSMAVISNSEEGSVIYVYNTSDWTLTNQFLGHSGRIIQAIFAGDFLI
SWGDDRTVRLWSLLRHAERAIYSHDCSIVAATSGPLMTLFLVDDRSRLYHLHVENIASSV
DARFVADPVELSLTIPPTSRVRAMIHTSDLLVMSTEDGSVYLVDLRQGGTVSRLSGYKCL
SLASASSGGDVYVVTGHWTGEVLLHLVRFTEQM*
>TCRU_7481 hypothetical protein, conserved
MRRGDFERRRLRDLYERNVRRVRALADARDGRRSGRDDDIAAPRRYVVSERRTRLEGFGR
GGYQVQRSRRFGRDPRIRRFSDRGVYRRGALDRFEREEDFERKLRRERFRERRLNEGGLR
FGRLRLRRSERRELRQLRELRELRELRALRSAQRNQGNGDRRGKLDKELDRYRKDQRGGR
RGGGGRGRGAPNSVTKEGLDAELDRFRGGN*
>TCRU_7482 hypothetical protein, conserved
MRPRRPGVLGAFSCGISTFHAGRPPRAFRPDYTPLSTTHTVFGQKQATVPALPRHRRLLS
TDHPAFGTNRAFPPGRPFKGPISVSGFFLAVDPNFAAGTQNRMNPNAQITVRDSEGNMSR
VRYRCHLESYTGLKLEALIRLQVGWISPKVTFSCIPYVIYLGKGFDLSIPFLIHFTMVSV
LDEHGDRTGSFLYFSGTPMLGFSAGLTQIRRGKLVLNPAKEVDPVEESKQFVGKIHVRQL
GFVLLKCLGYALCFLACVPASQRFLQYMLPDPFHRHSESAV*
>TCRU_7483 hypothetical protein, conserved
MSVQRVSECSWMEDMEFYKNTLYQRVQECPISITPGTEMIRFLRNELIRAEKNDESAEYR
LVVGDMFKVVTDSLVSAVHRSAPYTHIDSSAPRDYHVTKDEDELLMVDGIFDSDEEGDAD
SETVTKPSIKEKEQKQRKREELRKRREEEEEMLVKQNKVPDDKGGLLNTLGPYAAPRLTV
RASTFTFPSRKSLEQRTALPSPGSSSEEDDNDDEEENVGGGVSSSFSSGGGEAVAHLTAF
MKPLSMDSLKKVSESAKVKIKPSSSNREYITQIVKTAVRLGCEKACVLMDKHKIIEEMTN
HVQAGPLHTAASIDFLQSLPDQLKHALGHILGVWEESPQVEAMWERMVAMGFLAVLTNLR
LKPLKKIATELGVSMPDTHSTEKCCETIMFAAFPRERLRAKNSRSKRQKTLNFTVPPSGM
RCKGHMGFITFQVENVSILPKDNERRYSPEFEFGKLKWSLLCMANKEFLALYLCQTGSVF
CKFLITVLNHVNVDDSICNEGTQRFSTRSQENDWGFNTVIKFEELLNPKRGFWQEEGDSV
TIEVGIVLVETPKPLSLAKNASNKDKQTGPKVDEKAMRQLIEDEKMAQMKKRIKQEMAKL
TRDGEKARKDIAQRAAKGFHDLMERFKAEKQRIAKELAERERREQQERQRELEIIRQAQE
QNAEMRRRIEELKKESVNLSREKKELTHATKELKKAGEKYAQELNAINEMKASLQQKVKH
QEKRIAAVQKQIGDLRQEEPLNPLSSDDEANVSDDSEIMSRLKESFEQYIGLDGKGV*
>TCRU_7484 Uncharacterised protein family (UPF0220), putative
MFLGRPKIAPSAVAGAIFGLAVMLLVDGIITAQHEANVAHHVTFTMFMPALLSVVGFFVM
ILISPVEVKNDVPRAKAGLFISWILCFGSSVAALVLCKLKFAGLQERERSVPGVAVVGFT
SLMPLAGAILWWGKQSLLDDY*
>TCRU_7485 hypothetical protein, conserved
MRAMRSAGALLSFCRGFDSSARFGKELGFGHKMRDIPVLTGNPRPVAREEEWRCAYKLTE
RMEDVVRDVLRKDGWSEVEVQREMEQMFERKVHNTRSSLNTWTTVEEFQRTPWYRRYKPT

DTCAAKFISYEVIKLLEQALIPPSLRTDPYAHLRKRHMEDNWMNDRFSEESAKYITREQL
AKQTKGLSGYGQVTRRKFLEFDQKFKASYNGKQRVNESYSAWLQSLNDK*
>TCRU_7486 cyclophilin-type peptidyl-prolyl cis-trans isomerase, putative
MTSRRPDSGKQLRKEKVEHSNVRADTEDDVSPLNKRYQDVEERRLKEWENYQRSHRSTEE
QQSSRAFLDISIGDFLAGRLVLELFEDTVPNTVLNFRSLITGSCGVDPVTGVRLDYLYTP
VHRVDRARKLILLGELESLNVSSTGTPIQDEGYGKCHSERGLLTMVSDGPHTSGSVFGIT
LGPSRSLDFKQVVFGKAVDDLTLLEKLESLPLDAVGHPLVAAVVTFCGALTGPKPSGRFV
CTREVNGNTAGDGAAAAAEEEEEG*
>TCRU_7487 hypothetical protein, conserved
MDRPLTPYVPDVAIRDSSLGSAPGHDNMLNEFLHHLGPVAHGTLRTMIHNSFANGSLPGS
WNTVDTIPIPQPGKGPCRPESYRPITLLSVLLNRKNDSPPSISVIAAPPTSIRVHTFAFN
IGRDNNC*
>TCRU_7488 Enriched in surface-labeled proteome protein 1
MSRRAFTSAMLLLLVVMMCCDTGGATATNNGTSRKAVLGSLPKTYFFWRDKNEGETVSSL
RVPVLVEMNDDVFAVAEAQCTEASNSGFAGIASELLEWTDKESKELDTTKLRTQVLEKFQ
VEQGKFPSLEVTQNAAASQNRTKVRVSRPTTVVNGSVIYMFAGTYSFEVTEAAGSTAAAV
KWGLLVAVGNVSNDGSSGKKKIYWKDASVIPWTEFENQHESLTGLIGGGGSGVQMKDGTF
VFPMEGTKDGKAVSLIIYSSDNASGNLSKGMSADGCSDPSVVEWKGKLMMMTACDDGRRR
VYESGDKGESWTEALGTLSRVWGNNQKRHEKGVGSGFSTATIEDRDVMLVTLPVYSNRKG
KEKGVLHLWLTDNTHIVDIGPVSGETEDAAASSLLYKSAGSGNNNERLIALYEKKKGDGE
SSLGMVSVRLTAQLKRVKEVLATWKEVDGRVSKLCPSTAAKNPSTGNGCSAVKITDGLVG
FLSKNFSGNTWRDEYLGVDATVKKGTNGVATGYADGVTFHGAWAEWPVGRQGENQLYKFA
NHNFTLVATLSVHGEPKGDTPIPLMGATMDDNKKTVLLGLSHDKEGKWQLLCGGKTTKEL
RSNWEPETTHQVAIVLRNGTQGSAYVDGQRVGDAPCELNNTDSKGISHFYIGGDGGSAGS
KEDVPVTATNVLLYNRPLDDNEIRVLNANKISIPKLTDLKTLAAGATGVGAARHFGANGD
GSAVCGGGLLPLLLLLGLWGIAAS*
>TCRU_7489 retrotransposon hot spot protein, RHS3, putative
MKDFLISPNGFIQDEVLLSTIKASPSHQELKKEREESYMLLEALHKLKKGHIFTLSHWSY
FEKKDTVIPLARAQINKAFSQVLREERRKAEERERRERQELGIDVSTRLKYAVFKGRVRV
DKMKLNDFLTMELDGRGALDSNRNVLLEAFFKDPKKYICDAGVLDEMQASDRYKRMERTV
RDEMDMEEDLHRLYKNGVNNLLRWLVAAAEVKANVHETTKRFLDAAAEEARSPKKSSAPI
YLEGCYESVYNARWHHVVEIPGGEGTGMEVREGEPPQSWTYKTVGDTLEKDDGVEQSGAP
RPRLMVLTSDKGWPCSWKWKEDE*
>TCRU_7490 hypothetical protein, conserved
MLQTKGSTKHEEGASSLHSSESVSHLSRESTAPLSTSTESSDIAASTVEKSGAKTSKTPA
ASVTQHDSKGIAGSAAPPASTSELRTEEISNAGIIATTHDDGDDDSSPAASIAGRPTAGT
RSTKASGDASDLDQSNNDDVNDDVAHNGKSAEFEAASGDMNTEADNDERYTTVPVTATNK
TSITETIADSDGSTTVSHTSSPLLLLLVVACAAAAL*
>TCRU_7491 hypothetical protein, conserved
MGTTTASPLEKVPRSVGCGAARRFACSLTERTAWSFHCGHSVGITRCGGVRKSRSPDEDV
LVVVWQLIPLGPSPLRIALAARLAQHHPGMVLLQEYRHESAPATRLIGCGDFHQTCSGRA
GGVAFVVRHTFPCERLLLVAPTAWRPPPSACAHLPAPACT*
>TCRU_7492 UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase, putative
MQFSDKWMASVVGVWFLLVLFAVSRTQEIETNVDAYLEDDFAANSSQQPQLLPRTTDWEA
LRYVPRDVVDAWKKRDFLIVLGIPTVDVEARQRRRHLQRSTCWRFPGVATRANNFTGAML
VLYVLARHPSHGHNYSATLLEEAAQWHDVLTTSIDEGRVTTNKTVGGSGFWGLEAEIGMS
RKTYFLFDFALRLFPTVPYIAKGDDDMFLRVPQYLADLRTLPRRKTYWGFFLRYYRRRFL
KYIGGMCATLARDVAEKFVSYKPLQRLVRLPYSKEREPEFLSLNMDHEDVMVGRVLHEMR
YKNVVFFSERPCRFHDVREGLWAKNVTESSVVVHHVWESEYETLMQRFGNDTSPAPKRFR
CSKGWYIFDC*
>TCRU_7493 CCCH zinc finger in TRM13 protein/U11-48K-like CHHC zinc finger/Methyltransferase TRM13, putative

MTSQANPDDALCDHYLPRKKRFCRSEKREGSRFCHTHDTFTSSAGPHGGECVRAEECEGR
TRRVPCPINPNHTVYAARLQHHIQVCPDLRYVTRKLPYYKADANALRGKVYCREDDTPHE
RMTHHHLDADNLRQLIERVRYCYFSVIQPQIVLMAEEISNNNEETSKSTCNMSAKHGPQH
RALLRCLQKAIEGFFKAQTPTESAGMAVKGFVEFGAGKGGLSVALQDALLSHAFDLSGST
VEKKELAPAQVHRKPLLVVVDVGNFRRKGDARVSRTSLPLVRLRLDIKDLELAKALRDPS
VFKRARDEEKVNVSTLLDNIHAEGIPEERWVALGKHLCGACTDFALSCITSPNLCTEGRA
SVIAVVFATCCHHLCELRHLNALASTEDDQQAILLLPGTEYTISTAEFAAIASMSSWAVS
GTAVDKERQTTGVCCKRVIDALRIQYLKQNGYRSAYLCQYIEKGITEENVTIVAFR*
>TCRU_7494 3'5'-cyclic nucleotide phosphodiesterase, putative
MQPGLQKRTFARGPAVAEADTFAKDFNAIFRIQNIRQTLCSIVSSRAASSQRDSTPRDET
PHNLRGLSTEGTLMSPRGPPASAAGRFLVSSQRRVEELMRENHRLELLCITQEEAMNQLR
EEPVPVGREQSSEVAGGSAKLGRLGRCKTPSLSRRSQATRSVAEGGDATGTVDASQSLPI
SSRVVEAVQHLVDTAICVFPRLLSNAEAPGDDAGGELDTTCAVFEFVVSHLSDWERLTRE
SAEMRRVNAILSRTIADLEEKQEAWRAKLLSIVKRLQATEAEQRRSIQVRDCRIDALQAQ
VDSLTADVTCAVEQRDQYMLRCGDLERSICCRLEEQLTERQEADRVQREYEALRSELNSL
CKSLPKEVAAPVTAEEGNEGEQQARTGLDVLKLQATIDSLMDERRAMQKRLDTLASSLAE
VNERVLLLEEEKRELSQQLRSKQNEVEHAHQELEELKRFPSPSAAAAAAALSDETPVAAE
KVYHAEGSHQRWFLRPVEYCQFDGKELSTPVVDVSSILRALDTDIIAFSNRNEHVRKPGL
FFQIGCGIAKELELFNNLSSTSLGKWKLFLLQIQDGFRDPEFYTADHAAECAQFFYALLF
HSGMIPHMSHAELLAAVTAALCMEYGHPGVSGCLLSAAQDPAAAGIHSCLLLEHRRLESL
GEIFSQEQFFFCDHRLATVSLLDDVKALLLPDGWHGECSGVMHSCLKLLSSGPLRMESES
VRCQLVQLLLRLAKYAFCMRVFDVNDRYSGKWFQMMQRQAQFAAEIGIYGFDLPHNAPTI
ADTQLLLMERTVLPLCRIVVQAFPSLYPCEEALRANYATWVLRAGQHPTEGAVAEVRDSF
SFSAADLPHVEGITQDAAAADSIDSRGFDAAHRNVSQQLESGSLLVSTALFLSSQKEMLS
VYEENVVLRGMLETLLVPVETLPASQGAVP*
>TCRU_7495 mevalonate kinase, putative
MRRAVVERTEKNHIGFGKIILFGEHFVVHGAEALVAGIDEYTSCRLELTKGQPGICVVDG
RPAVPGYIVEKAEEQRLAHRLVFRHLNIDTSVDGVRIHLGGPLVPTSGIGASASDVVSLS
RALSEMYGLDLTEDEVNLSAFVGEGGYHGTPSGADNTAATFGGLISYRRVNGVSNFCRVL
ITRPLFLVVCSTGITTSTTKVVGEIRELKENNPTWFNALLERYNACVGEAKAAMEVGNLF
RMGELMNENHKLCQELTVSCAELDTIVNFCCENGALGAKMSGTGRGGLVVALAADEAQRD
GIADAVRQRCPAAKFVWKYTVCPRSAKI*
>TCRU_7496 hypothetical protein, conserved
MTQAAGRTARLLLLTMRLDPPRCHLTPRIAALPVGPHRTAAGSLACSCRAEFPATEHGHR
HFSVTRLAAASQSPTLVPVATDSLSAMESLRLGSLAVRDDVTEEICTCRIHWRIEVALLA
SNVHHDTAESHAT*
>TCRU_7497 sterol 14-alpha-demethylase
MTVISNVLGVQIPYLAEVAAIMLIAHGLAYLLTMFYFARKHKFSIPGPKFVTPLLGGLVM
MMKDPYTFWEKQRRYCPSGYSWLSILNQFTVFVTRADLCHKIFATNSENTLTLQLHPNGR
IILGDNNIAFQCGPRHKALRASFLNLFATKALSLYLPIQERLIREHLAEWIKKYPFEGKP
EEMRGHIRELNCKTSQTVFVGEHLLDPEEFTRNYNIITVGFLSLPLYFPGTALYKAVQAR
KKVVDELKAAVIRSKARMSLPDAEAHCVLDFWSATILETLKACEDEGVDPPPFASDDAMA
ETLLDFLFASQDASTASLVMITATMADRPDVLERVRQEQTKLCAGDEPLTFDLVQEMTFT
RQCVLEQLRLFPPAPMVPMKAHSDFVIDGHYTVPKGSLIIPSLVGACREGFPNPDVYDPD
RMGSERQEDRKFAKQFIPFGVGPHRCVGYNYAINHLTVYLALVARLAEWRRTRTPNSDKV
IYLPTLYPHDCLCTWRHREGLKAGK*
>TCRU_7498 thiosulfate sulfurtransferase, mitochondrial, putative
MLVSCIRRQADRRTRHHMMLDGQINPREWMNWHPKEYQPWYFDRHKFLYERQQYAHFHHL
LCHQVFLKDMLHLVQHPEPYTHIVDCRTSPLKMHRWVPHSWWLPRDEVEYALQLTPDEFA
DMYGFHKPRKSDDVILVSHNGLYSEQAGWEWKKQFYQHVYNYRGGTNELFGEQYNDVALK
DSLPPWKGPFPQSGIFVDKWSKRKVLTRTGPFDRQYEMQDFALPDLELERPRHPEEGPRQ
NMPYGLQ*
>TCRU_7499 S-adenosylmethionine synthetase, putative
MSVRQILFSSEHVSEGHPDKLCDQVSDAVLDACLASDPLSRVACETCSKTGMIMIFGEIT

TNAVLDYQKVVRDAVKEIGFDDGEKGLDYRSCNLLIAIEHQSPEILQSLGDFDGEGLGAG
DQGMMFGYATDETETFMPLTYELSRGLAVKYSELRRNGTLPWARPDAKTQVTVQYEYDSR
EGRQLLTPKRVAVVLISAQHDADVKNETLRKDLMEKVIKAVIPAHMLDADTKYHLNPSGR
FVIGGPHGDAGLTGRKIIVDTYGGWGAHGGGAFSGKDPSKVDRSAAYAARWIAKSLVAGG
LARRCLVQLAYAIGVAEPLNIHIETYGTGKYDDGRILEIVTKNFRLRPYDIIKELDLRRP
IYHMTSRFGHFGREDKSGRGGFTWEIPKKLDESC*
>TCRU_7500 MIZ/SP-RING zinc finger, putative
MKYPPGTLVWINCDDGEWWPAVVRETDKELLLVVGGGYDMCVEFYHDPGNLYPVESGSTG
VRMFHRAEDERDTAEKNFFRVTATHEAVQRALLDSTRCEVPTVEPPPYTPEELRCMSALL
KSVNHTTASHLRKTLLSQDGIDFSSRGVRKLMTEREPKRRKRPTRSLEEIVPPSHVVKVI
HEVDSNPRPTELLVVPQASRPQWTFQEAFDSSALDIVRKEVFENKERFVLSPLYRYLDLL
GAVSVDGVPVETTLPSPIALHEVPEGGLLASRRVLLVPLSASLFEHTIGWMVPFEYEGAT
IAMKLFVNGAVVETPCNCSLPSGKEAVAVKTVAGADITKHVLHKELFSLAVGFTGVIEDM
ALWKGVIAAVYVDRIDMDALVDRVVLNYKMPPRRKRRDDVVGVQVKINCPITTLPLSIPV
RGYLCEHMQCVELRSLLMQCARTNVWNCPLCWAPTTPDTIVVNYRLKEWLETHQSQLEKV
DFVLETPAGVPLRPIWKREIFRNVADVIALE*
>TCRU_7501 chromosomal passenger protein
MTATWSPQLVEELLFRQYIKGEDVSMLLPPPPALAVDQYMEKYEQSTKMMSSYVRNGLTA
TLTSQNVNTASRIYGATPVKGHASFSRAANAPLTATDSSVDPRAQLKCTPSAKELPSSVL
DSPVPAAANAAARQANASPSAYVRRNRVEWPSSVPSNASLKSSSRSKVAHLTAKRVAAQE
TVDPDLVFAQNPGELPLHAIFASFPKALDSLAAIRGASGDWRNDTFNTEEESQYKRDLGF
VHLGPSQCLLSRSNLLHK*
>TCRU_7502 Protein kinase domain/Protein tyrosine kinase, putative
MSKVSLRKEDGKSVLNGTLIGGRFRLIERLGGGSFGEVYTGVHVHSGTHVAVKIEAPRKH
SRAMLEYRIYSEFNECAVAVGFPQVYFGGRVGGYNVIVMDLLGPNLEQLFSICGRDFGVK
TVCMIGIQIIQRIQCMHSMSYIHRDIKPENFVMGVGGHSQTVYVIDMGLSKRYRDSFTMR
HIPWEDNKSLTGTARYVSINAHRGIQQSRRDDLESVAYLLFYFLRGSLPWQGLKSQPNDY
RYTRICDMKAKTSSETLADGHPKEFAKLLDYVRALKFEETPNYSFCLQLLNDVLTSRGET
YDYQYSWLAKLDPRWAEKTNDVESMEEEFLDVNASSMARYYHRPSSANASQYQTMTDEEF
DRPFGQKGADNSWRLCDLYNIDLSF*
>TCRU_7503 zinc-binding protein (Yippee), putative
MARRLRVRFTAKDGYGCGRCSAYLCDTGDVISRTFHGKHGKAYLVSRCFNYYFGPQEEKE
LITGAHIVRDVFCSCCDRYIGWTYDFAHVEKERYKVNRFVLERQLLRAIKADATTGLSAP
SDQN*
>TCRU_7504 hypothetical protein, conserved
MDDKTIVELERRLDELKKVKVFDEKVREGVGSLIASMPNPDEEKDPEKKVRLLLLRCKAL
TLLPTYSMEAEQGCGAALKLCHDRPDLWVLLSECLTRRKATREACDALDNALRIDDQNMD
ALCQYSRLLRSLSSDSKLTPAERLRHLNESVSCAKAAAAACPTSTDGWHCYSIALLSKAL
SNGVEIAGAQRALQAMRQAALISPEDPDVRFNKGAIEGLLGHFGNAACDFLAAYEVDQKR
LKGTRQMLENHLTVLRRAESQIKTSRQTGKRPFASLLAKLPSFPDAVTINAILNGSVTSP
CHVTVGVVDILSENSMEPLVVLAAEKSGEFLLLLFYGLVRGAIKVNNSIISLSFPECTPV
RVMHEVPDIPFLEARAHKSTYTQIFVDLKTTLLNGEPIPSRMLVSPKLSSRLFV*
>TCRU_7505 hypothetical protein, conserved
MGGSLRVLKEHLACDEGWGQTFWLRRRRKRRRVSNVGDDCGVTTVGMDEEGEEDRTMVDP
EAQSLFRLRVVGTDGVASVPLFRSALCGPAVEDTYACHYHLYPSVSPGDAHGTALCWSLR
RSSLKIHALMCLGRVANSCRKEIVLFYDDIGVLLSYTTTP*
>TCRU_7506 DNA ligase I, putative
MGAEAQEGNSVRLKRAREDFDCDKGVVDDLALEDIFAGPTSMAKVFLKASFDPYVNYESV
WPRPLPGVREIVPYAAVADTLADISAESSRLECIKCLTNLFLAVIQRSPSDLVSVIYLVI
NKQGPAHEGIELGVGDALLVKVIAECCGVTEAYIKDAYRQTGDLAEVAQNKKRQQSTLVK
PKRLSAADVFKALRDIALMSGKEASRRRADVMKRLLRDAVGPEVNLIVRALQQKMRVGLA
ESSALAAIGYAFALHHIGLTEVVKFTPEQLQRELNIGSENFARIYHEVPSFEIVVGAMLK
HGLNVIVPSSPEGRAHAAELSIRPGIPVKPQLAHPTSGINAILERFQGKAFTSEYKYDGE
RAQIHYSKEKGYQIFSRNAETHTGKYPDIIAMLPRVFSTEAVESFIIDSEVVAVNKETGA

LQAFQVLQHRGRKNVSFESVTIPVCVFAFDILYFNGSPQMTKPLLERRQVLYSYFTPVHA
AFQFAEHLDGTDVEEIQSFLDRSIKDGCEGLMVKTLKEEAAYTPAKRSYCWLKLKKDYMD
GVTDTLDLVPIGAYYGKGKRTGVFGGFLLACYNSDSDEFQSICKIGSGFLDEQLESLTQA
LQSCVLMEQPRYYRAEEKPDVWLEASNVWEVKAADLSISPVHFAAYGLVDPSKGIALRFP
RFVRVREDKKANEATFATQIAAMYTAQSLSRKNYEEYDEET*
>TCRU_7507 protein mkt1, putative
MYPRQDDVSLLQRYINDNKLEEKGVPLTELRRLEGTGQVMLGVDGTKIIDLITQAVREKE
KMAIYTYTTPFTVYDKITDVCKTLRSLKNCTPVLVFNGIPFYPDPSDDNCREKNMVPPDV
AALNGTDSSRLCNMHSMRAVDIQKKSSSRFFVEEDVENQIVKLFRSEFKDTMRAPYLAWA
QLSAFCHPKNRHISEVYGCLELLAFPGIDRVITNINVMKGTVDMVRKSRLLELLRISEDD
LGSLIVVDSRNRVMRTVGPKFSSFDDMCKKITRVNDLSLGASYVHQLHQEAMHLSEQARN
RTLNLKSAVLRNLAALGCPVLTLVPPYCTLLTRLYESRRQLPIDPKMVMGCPLPPVMYYM
FTAGLLSPSLFGALCQGSLVDDWPLVDSIKYRDVAETVLPLRVQTLHQLAASLRMSDFGM
TWFRRYNAFLSRVSKVHAPPEIGLDSWNLAGETISENLFLVDVMEFSHLAVSSRHIIYET
AEETCAAVLLQSLDLLGYLTHETRDDGEDVQVSEPSPFGRALKLCGVPTLSEYVVLLIEL
SRTGAITTEQFRMTSEEIIPRDIPPEIVLASRILSIIPLNVSSSWSGPIDPELAAFSMIS
RMISRSIRHLLEAMLAIIFYQGRTLVPLHRICAIQQALPFSTPVEFGGGVLIEYVLMKEK
CTLSDIEAAFPECNYLRHDLATLFYFWELAVCVLNSIACKDVPLDVGCLHKANERMKELQ
RNLDINTGVRETYY*
>TCRU_7508 T-complex protein 11, putative
MLEAAPSTHEAVGTAAACVQKISNYLKQLEEMGLQYNSTHPMTAETVEHILITDKWCCKT
CGMTELRTCPDTGKPHRRRMVRVAQEILRLIGSRTGQLVVRPPNLSASLNGRSRLRSLRR
VTMNPQALLLAYYYALLPSNEVDGLVSECAQQLVELLEQLKVSGAQTNVDEEYATALLSS
ASLTWQEYNKKFTEDLRSLRGADRRACQEVIVNGTKEAYVAAARELRKTPSNEELQAFVG
MLRDRLSRLMPREGLEEMEATMKEEQQEQEETQEEKGKEEKKEGEREENVKFQSSKPQLT
APTLLSEGNTSGSETEAPPPTIMGPEIPPDWYVDEHGRSRPIQEDSIRKRREMYLRLEFR
AVKAYETVITVPEPKSDPLQEQLISSMNEAQLAILAEQCNQHPPDLQNVPRFLKLIIEGL
LNALPRRLRSRAEQEIRDVLDWRIVRRSVMGSPGNIAALMRYVMGKVAEYGAPAKAEETL
KLAEDMRKDLETCTPDLGTAVANAFRLMFTSIRQLHEDIAQYSLLFISQQLRGNAVTYIR
EFITECLPKVDQWESSLTFIRRYLNDERVKAWANSSVAISATAVTEAERKLRGALLYGFL
DIMRSGGLQVNDRWHDYPTECFYFEKKVVFFAANTVQENSLLLLLSGSIATVLRDKGVDS
RVVSDILKELHDKFRLLFSEQLTLSSLKCSVTSLVNEALTQRQTLSALTESEVTQLDGIV
EKMTNTTGSLYVVFEKRVLSFIEGILAHGQSDPAPLGLVTDSLSRLTALLQHVLAFNWEL
YQPFYREMLSLITQEDAVSS*
>TCRU_7509 hypothetical protein, conserved
MQRRRGVLHAWDGVGGPRLVLVQLQGRMAGRVVSSLRGARQGCAALAGESRRRRHELRGE
PDADEPRAEHVEDAPLLHGCDIQRRGCCADVFLRQYAVASPHQHHAHWVHVP*
>TCRU_7510 hypothetical protein, conserved
MAALRARAGAAITRGRRRVRGEARRRESAWVAAGQNGGIVHGRDAVFRPLTAVHSVARSH
NLSVCDIAAPGEYPQNCRRARAGHESVAGHRHHGVAETHRWAYVGKGFRWGHAAEVAAQL
QPGVVVDRETGS*
>TCRU_7511 hypothetical protein, conserved
MAFYSTVRLADGSMLLAKGNVHDGVSREMLYAAGAVTAAGSTLSFVRNRALLPRMLSLSL
SLVAGAHLRVACNDAGGRVLSTAEEYAAAGFGDAGSIDVVGCDDCDRDTYCYAPGTATAR
MRNGVCVCVCGSGGYGEACVPVGAPALPPAVGTASSVFVREGMTVQSAFVVPAGASEVTL
RHVVLDGVSPVLYVPWMARDGVRIVVQNVSLRNGAVLYVMGGGTLRGAVAAGSDESGPVE
LSVCDVEALNGALVLTGTYPAGSVLTVTDSLLVAARPTPLVYLPGSQSSPYAPVLVLSGL
RLVRSVLVVSGVALVTVMTGGRTVVADGAVLEVVGGGVALDAAVLGGDVALYASARVVAS
GGAVLRVSGSQVYAAHGLVFESGVEANASAVVVNDNAGALTDGALLVLRGSASFVSGSWL
SVRGNSISGRLLSVPSYPRRAELVQSTLTLHGNAGSGPVVMDGTVALGGTGRRFVVGCLT
LNGQALRPFDYRSAGIIGEFRPVACSVLRRRRALLCCCDEGDVGVVWVPLC*
>TCRU_of Trypanosoma cruzi region 5/Dispersed gene family protein.1
Dispersed gene family protein.1
MVALPPPFRWARDPQLGTHLSFVPVSTAQPSGFGGPWGAMLSNATWVRNATNPSTVLELA

VPMHRGYFIAFDETIVIRCDAAAVSGGCKGVLLGSFTIRSNTLPAAASALSAITGVVAGA
VAVAVVATGGLGSILEMQALGVFARMSCASAQERASTVALPYFLSVFAALDPLWMVVGNA
LLAAVFGCVHCGVTAAFQRWRGVDAASAWAAMRFPSLTYVVAHAMHLGIFFCSVLSLAMP
DARVQHRVIGVVGVLYGVAFPAGVCYLIARHVGASFTRYWQFLRKPLHERLLYPVGYWHP
AAQQRMYGGMLTNMRGSRVYWCVFQLLVLCVVGLIAAVHPPVGGCHVQYFCMAAVLLAGA
GVVAFTNMMRSAFLTVMRTASLVLLAALCVVSAANHLAPSDGGARAYAAIVLLLTTVVLA
VTVYGVVVWYAEDRHWQELREPQRGGLEALLRDDEESDEAQKLHDRTLSSYASGTTAASS
YRPPAPPLQFVTGDTHSDSLSLFDGASIAS*
>TCRU_7513 hypothetical protein, conserved
MRLLLFYQGSATAMIRTSPRDCAGDIHGERSVGSGWLGREIATHHRKYNRKRNNKPTEKA
SAAIITDASLHGWGAVFIPDSGDVKIAGGKWERNSFLIMQAEARAVRLALSAFSAILPST
MDVCVDNTSLQGAANKGSSKSHALMWELQRIYEFLDSRGIQATFAYVRSAENPGDGISRG
RVFTLQDLVKGSGGVVWLEDPKLCQFVSNKCFRSYLSSKCHVSGSRLLQTDDMYIHLIGV
KL*
>TCRU_7514 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGVGGRCDVEDTAVPGSGGGSPPESKQLVTSPEESQGLKGG
VTGVKGNVPPAPSPPTEDEEDDDEEDDIGDDEESDESAGTEEDEESIEGQSDQEGTAAPD
PGSGERNLSGSGQETGQAIVSAEDIPPSNSRESKANSTQTEVEGKKDTDKRPSAENALTT
VNGEHTLPGGVAEGTLPPSPEDGVDSRKQDGEDTTSVGEKNVPSPETAATTKNHRDEGSE
GTGEDTKATTVTANTTDTTNTKNSDSSTAVSHATSRLLPLLVVACAAAAAVVAA*
>TCRU_7515 Fructose-bisphosphate aldolase class-I, putative
MIDGTHSIETCQRVSQHVWAEVVTALHRHGVMWEGCLLKPNMVVPGAESGVRATPGQVAQ
YTVSTLARVLPPALPGVTFLSGGLSEVQASEYLNAMNLCNLPRPWKLTFSYARALQSSAL
KAWGGKDSGIAAGRRAFMHRAKMNSLAQLGRYNRAEDDKESHSLYVAGNSY*
>TCRU_7516 fructose-bisphosphate aldolase, glycosomal, putative
MAQRVEVLQTQLPAYNRLKTPHEAELIATAKKMTAPGKGLLAADESIGSCAKRFAPLGLS
NTEEHRRQYRALMLECEGMEQYISGVILHDETVYQKASTGETFVQLLQRKGVVPGIKTDM
GLNPLVEGAEGEQMTGGLDGYVERARKYYSLGCRFCKWRNVYKIQNGTVSEAAVRFNAET
LARYAVLSQLSGLVPIVEPEVMIDGTHSIETCQRVSQHVWAEVVTALHRHGVMWEGCLLK
PNMVVPGAESGVRATPGQVAQYTVSTLARVLPPALPGVTFLSGGLSEVQASEYLNAMNLC
NLPRPWKLTFSYARALQSSALKAWGGKDSGIAAGRRAFMHRAKMNSLAQLGRYNRAEDDK
ESHSLYVAGNSY*
>TCRU_7517 hypothetical protein, conserved
MVEKDPSRRPSPRLTAEQLQDQIRRLTYRPPPPVVRDPFPVCPSVKRSKDEIDAVTQRVF
YEQCQRHERALIEAREKWEKEWGLLSKEVPSEYVEDMVKRLYYDTIERIHASRKSAEERL
LFKSNKKVPVVPLKKFVEDMYLKGMQRERDKEKKLYEKYILPTEIKRTLISREDAEASGT
RLSARTGAN*
>TCRU_7518 hypothetical protein, conserved
MEDDAESYLRLASKLKWKHFARGHNSVSQKQGEVVGENPANCPLKPPMRLPMKKPRRIHD
SDSDDERGTAPRRDAAEAPSIFSFSSSPSFARKPCNGAPITLMEKWFPGSTLGNATLDAA
EAPTPEYTDLTMARMNAVRERFLTLRGGVEDVLKYAVANGDGEFTEDRADWDWRALRDTL
SQLTSRDVFRTKKRVVRAVQWLLANKPSSISIPKRPTVRLWERYLNEHGPECGHMPPLSL
LVWLDSARTTALFAALVDRTLRFYKQGMKATMHTSQKVDETIFEVSENTNVNDDRKDEEE
EDEEDEEEEDLQPHDARDGNIHGTNEDGKQLLFFTQLTPLYGGGAREEIISLLSFLRVFM
PVDAVDASGNVVGRSVGYGIWLYACLSAVDTPLEPDLDRLVHEFFRICCQQIRTLGDVHG
IRGGNRGAIVHAFSPRSGDTTTRREYNSIDDVRKEDVLALHTIIIILAKLFRQNQNRLIP
L*
>TCRU_7519 hypothetical protein, conserved
MYTLLVCADLYGDKCNLELGFPSMPTMTELQEKVLQVFEAESNIRRPSGYPVMDFTIARI
QIYDDALLKWVDLVSQTQMHEYDQLYVFQPQTAWHTDVQKDLPPPCPPSKSLAASVVHSM
VNSPYKSAVITGHTSYRNDTPCASTTGSMALSPTRMRLEEQRRRERALQEELNRIRDESA
RLERELIMEEEDNRARDQEQKNRILRQKEEEVCRQREILMRSEEEFRRLQSETTQY*
>TCRU_7520 hypothetical protein
MRPSSHRRPKSSAASDVGRRIRYSDAPPWDRSIRVNGDRALSAGRASRRGPEMMNTKLQG

TPARPSHCNLATTQAATLVATVPPVNEPQVELMSQLQDVVVRLSQSAVGEKQRLAHMQQR
LDAYAALMREQDRMIDELRGMNIRLQKERDALILFRQQSLNHDLHLMNNLENDGGIDEEA
RRAYAKYEGQKNSYGTPCNGSLGAMTPRSRGFVRSLVAQLRDERRKRLEVEEQSSRMIGE
QQLTIQRLEDRLRPQVVAPRSVLVSRLESPQVSSHQRASNEEKDAVNTPLQCPCVDSVSA
PMSSPTFSVVNQEKRLTEVNPMAPVVPPIPLPERNKEAVITEQVHQSPAVSMDQQITPPL
EVPLKIHSTSYDDAAAILFDIRKRHGL*
>TCRU_7521 N-acetyltransferase subunit Nat1, putative
MTVVLPPAQKKIFEKLGCEFDAREYAKALRCADAILAVIPSHADTIAMRGLTLHHLDRRE
EGHLAIKEAIELNINSTMAWHSLGMCHRAEKNYPEAIKAFKKAHQTDPTNANVLRDLSSV
CVQVRDWEQFVETRQKMVTLKAGVRANWIALSCGHRMMGHTELAAAVIDVMTSIMDAGEN
VVEKSEVFLYLVELELSHNAPARALELLKKHDAEIVDEEEKILLRAKAHALLGQKTEAEK
RYMELIGRGLSEADCIAAIAQLRKIPIDAHRCPKRDEGKYLEILQQVLNAYPKCDYARRR
ILDFIPIEEFKKRLCEYASTFIIKMIPSLFSVLKSLYKDPKRAKQIGEVFLEWESEIQRN
DFSSFGGKANPSFLLWIWMYLSSHHCRLRDFDQALHYINLAIDHTPTVELLYLMKAKILE
RNQQFDEAAMNADKARQLDLQDKYLNSKAAKYFFRANRIEEAEARMQMFYKASAVPGDTY
LTALDSQCAWYEREVGDAFFRRGDYISALANYLMYEEHHMRNHVELLDFHNYVFRRCTMR
SWFDVLARDDDLNGNIFFLKLCPRIVRTYMKIHEEGDESVRTKHIPRPELELCSDVEENK
HLKQLRKEYYLDTIDISNPLQKAERYLLPYLSHNLFSTEAHLLAFEFYTMLRKPLLVARE
VLALAKLKCALTADRIAQFERQLFSEIAPQMDPRVKKVIDEALASAWEKIGE*
>TCRU_7522 hypothetical protein, conserved
MPPSMHGKAATSIPLPRVVVINGLQRVCNIIGIPRNHLRAPPLTQRRIIPWDTVSCNKVG
FYQPIFAQGVSDDVKRTAFDSIYSSLGDYDFELWADGSSSLAELASGHAALLYGSTTANY
LPVEVHRAAAGRLACSYRAECIATENGFRHLIPPRLDTSQSPTRILVATDSLPAIEALRV
APMVMRDCATEEIWINLPSLIKRGYSVEFIFSP*
>TCRU_7523 hypothetical protein, conserved
MSPKQRLPVVLWFLPKIAARFRGRATITLNHSPEDEIEVALCGESFSPELVVEDSSMIVL
RPTCVTGEARRPLRIFNPTCIPITFYVEPSTELADVLQVDPASGVLAAGQQMHLTLLFTP
SEGMMYEGRINFFISHTENKRMISSRGSVNRAEEDQKNLISCPCTAEGQYAVVEVEPVVM
QHEGPAMQEKTFEWTIYNSSLCDVCYEVRWLSKTAPTHHHDHRAPSVQLSHNKCGTLSAR
SHTVVLVTLRPQTGFSEYILYIIVAGSGVPLGTIPHPTTLEEVRQHPHCEVQLIGTRPAV
QITDVGSLEQHRSQLWCQLAINSVNEVLAAPVQSTDLETDSFAFLRYIRGLEPIFMDLGV
GNVLDARKEVLLCFENAGSGPALFRFWDPTEHEGGNETWFLDDEELEDVQQILCDRLLEI
SPREGTIPVGSRKVITITYRHTVVGEHSLPVLLRLDEGKKALLVLEGRTVSPDANALAFH
HPSVYNLHPVALGDLEPPLQITTIENVAPHPVKYILQEDLEQRVAEKNCGFPVFQCLNPS
GVIPAGGSAQLKWYFRPLEARTYSVKVSLRTAGGEDYCLQFVGAGYHPKKVPPETVRAMT
NDAFLPIPVSSALRLPVEKCPLTLSMNVMRVGAAPSFSLHRRLCYLENEHPTHTYSFLWK
THLEPGSSIMKVTPHSGVLGPGQKVRCCLSLYCGSLSQILETPIFCYFSNEATSTAAGKG
ARTLEFSAAEGKFAESEAAEEDAFDDPLLDAKTPPGKTFERSTCTKPRPPGNNRKRLPVN
FLPSEDQSVRAVAPAASAAAAAVLTPTITNTQIHASLGLPEPKDTSVMVGHSLEVLVQAR
IMPIEEYEDLYGKRALQQMHFPTLCQNYVDPANLSLSRRNQLDGIGVYSSDEASVALRVL
DGMLRATITRPQVYASFTEPVREDIPYYREMVHADFGPVAGPGGAVSALLFNQSESIPSG
VVRSCVSLAEKADGRQTDDAHSAVSAMKPGETVRSRGAVVNFLEEVLADVTLQAVGSVAE
RLQVSSRKNPKRVES*
>TCRU_7524 40S ribosomal protein S24E, putative
MVFQKKKAEVTVRTSQFKVNKLLNRKQFIVEVNHPGWCGTVPAKLIRSRLASLYKVADEN
QISVFGFKTKFGGGKTTGFGLIYDDLAALKRIEPNYRKARLGMGKKKQPARKSVKERRNR
NKKIRGKAKGKMQTKKK*
>TCRU_7525 40S ribosomal protein S24E, putative
MVFQKKKAEVTVRTSQFKVNKLLNRKQFIVEVNHPGWCGTVPAKLIRSRLASLYKVADEN
QISVFGFKTKFGGGKTTGFGLIYDDLAALKRIEPNYRKARLGMGKKKQPARKSVKERRNR
NKKIRGKAKGKMQTKKK*
>TCRU_7526 hypothetical protein, conserved
MEIVTHDESITTVTFGWARAGDGYIVQGPQVLHKGGGVSPYRPVIGGLALPPGKGKFFYE
ITTNTDACKLGLCTEEAFRTDGDLQEVELGKRCNFSAQGEIPSSDNCWVFNCQTSTVEIN

GREQKKLWRLFVPVSGARFGFLVDTNVGLVQLFVNGEYQGIVFDSCLGLMDKTLCPCIGL
EGMDMNNLSIGVGSKSAFVSPLKESPAYLSFREGKDATL*
>TCRU_7527 terminal uridylyltransferase 3, putative
MEEEKKGGWQAMKIRASPAVEATETRDELKRNHEDDALNVEAGVGCGGVEDLALAEEQEE
EGWCMPHGTAEDKKAGQGYLRCDLCSEFLFEDEDLHQQRHHAELANWCGKVLSVEAKEMC
MRPVPLEQIGNLGLFVIESVTELDMGREAFAVIQRASKQLNEIIGSFMRNAQVFLFGGCV
ACGSWDGVGDADFTVLESSHGWRLKEGVWENPDETRCIFQIAGALRNAGFLYSELEPIVR
TRVPVLKRKQNVRAPLRIPMRHDGFKLVYVFSEPPPRNAYNDFLREARDRQIKVEENCPN
EVTLHLNTAHDALRYYQARERGLGNVTKRWKSDHQLPDIFSLDFDISCRPLGVRNSWFMR
QYFSQHPVARAGLAFLKRWSKQSGINNALRGYLTSYAIMVLWAYYLLRRGLVEYVDPASF
SLTPSIAQLEVSYLPLLRDDGDGGESMRSVSQSPKLEPIRGELGSCVAGFFSFYACFPWE
ELVVSLRARDGDVTRESLGWVEASEVKSIKLRDRVWYRMCIEDPYEDNLNLGRHLSPKKF
AFVQSQFVVAHSLLMRGRPERLLEDARALASITLRALLHRIVYEEGTTELSPSEARDFIL
SRLDEEKLGYYEVQYSLESLCNMLLQICNNNSNSKRSHPSNTEEENTHDSTCPHAEDGGI
DGDAHQMGAGRVDGTERPPSPRSCLHEIDEKMRTACRLGIPDEEVPASVRGAYFFACGRA
FRTAAERDVLQVHVNALSHVWRDASMEIEEVRVKLEDALPTAVRDPALIDVLLQYPGVHD
ILRVEDRQQGEAERPVVREKLPPRKSSLAFTVRRAYNSFVGKCSDCGQENVSVWRTNNRR
RDPGNYCDACWKLYEEAYRK*
>TCRU_7528 hypothetical protein, conserved
MATAQELQQQLEDLRSRHEEEVKRETAVFEEINKEMMEMQEVTERLEKEERQLEGRLGTG
DRGAGESQGEVSSLLSNIALGLVDPDDSNSRRR*
>TCRU_7529 PS-10 peptidase S37/Serine carboxypeptidase S28/Prolyl
oligopeptidase family, putative
MKYCLGAHALMVVLGLLAVAFSGPVTALHPSVIPSRARHGEVYRAALRRSLKEGSGGQEK
QRHDVHNNAARYYNQRVDHADVTLGTFRQRWWVDRSSWDVNSGPAILLVNGEGTAPGLPD
GGFVGEYSKSVKAIIFSLEHRYYGESMPAPLTNRSMLKYLTVENALADLQAFKRYAEKKV
VKKKVKWLIVGGSYAGALSAWARAKYPGDFDAAWSSSGVVNVIFDYEAFDGHLLKVLPSS
CAAAVRTVFGKFSKAYDDPNRRAKMMKIFGTPNYFTKSDMAWMLADGAAMAIQYGYKDKL
CSSIEFTEERGLFKRYAEIMKLLWGEEFTRSCYYSTECLSNPSYSESWKEGYAWAYQCCS
QLAYWQTGFPGGLRLREVNTSYFMYQCRAAFGEAILPDTYAFNKKHGGAHPDATRVVATQ
ALDDPWLTAGAKKALSEDYPVITAQCNGCGHCGELAATNPLDHPSLKAQRRAVKFYLKQW
LGI*
>TCRU_7530 Phytochelatin synthase, putative
MGGGQSSSDVAVETHIKKWESALKELEQVARTNRGMMDQDRIYSNAGGLTDQRPSTGEDG
LDPSARGMRRSSQVSFGASASASALVAGASQQQVPQVVLPQASQQRPNQTSTEASPRTLA
IGVSYAAAANNNSITDASKMASSTGQHTKHKRQQVLGIRKARMNFFKSYEIERPEEDASL
MECSHFGATAVALSYLLGGEKGCKDRKKRVTVEDIFFAAHVPLHYLHGGVQGLPVMSDII
RDFISVDNRFKNEYGLSVMHFDISPTLGQVELGNNDVGDRQRRMQLPEFSKVITHDCEEE
TQLIRIVSYDPYVLQQETLVDAFDDEDEGHSALAASALINARHAAPLYGRNNRGAYAVIV
DVRNVVQLMVTLAEGVVGESLHVKLMEVSAAALYKAMTIVNSGGRSRGFIRIFRKDSVPV
MTNDEVQSMFAPELSSGKVIGSTLQGIHASVVSTHISPHIVAVAWAMHLLGGVRPNSHGY
GNSLPVSDIIRQMRFPADVFIDGSLPLGEVFRYAREYVRITNRNYNVAVYPVLTKISRDD
AVPTISVFELESIIIDVQNANEDPEVPEHVMAIMYNANVAHNVLNISKDPQWCLLAGYDL
ETQMVLLIDAHSKKFMQTWTCPLDRLHKAMTSNGYIIFSKSREAASRNKSSESSTCGGSQ
VLGFVPEPALVGAPRRIASTVQSRLELLQEQESLGGGRTEVVKTFHFPSLPLSSTMIALA
LTKLGVPTTFEDVIMALPFEISSLMLRYFTVESLAVCLTTYIATVGLSMDVQTYHTDHCC
GGDPRILWEDFRNLVVESVKNTNRVLFVLFNKEKIEIFGASHPFGSTGIVVDYNSATESL
TMMDSNPNSYFRTWPVSLKTLYEVLLDEDAKHRRSGCVTLTLREGRCKSCFPLQYTREFP
LHILPVQNIFHVSPSPHFQALSFAFAQLGFFYSPEEIFYEAYLKTMADQRRRGSQAFAWR
DVDVSLTVINKQIDARFLAQVCRMFIESRNPKKSSKPGTLRRTSGGGGNASNGKSDADTI
QVELLDDVELDDLPTILMDATRREDNRSVLLLNYDTTKAHDVDRWGRSVALVKSYNPETE
MVELWEGEHAVFGLNFIVSLAKLIEIGDLQNEGRSAYGFVKLERVKERAVPKRLTLMKGP
DPDDEDPVTSTTSPSASQGNNNVARRNRGMVTTFLGEKPHEEI*
>TCRU_7531 pre-mRNA splicing factor ATP-dependent RNA helicase,

putative
MQEEVPFLWKLQLIYSRNELYRQLEHLLGRPESVEQAEGYYDDVEELVGLFLREGGNAGG
EESLLAALNSAINAAGDDEPPIPLEQLRGLVRLMQTNLRGVDWPKCLEAGALAIAEKERS
EAEAALRLKLLQQEEEEAAQRDERGRRALESLATDAAERRAAMKVRAEEKMQLAQLVRSG
LLDESELLQLRTDDEEVEQVELNEEEPRFLRGLVRHRPINYRALLPSEQLMRASTPAQRE
AIIARRAMQQTTADEIETNSMKRAAISQQIRNKDRQILRAKERRLQRLTEHARGGVDDGF
ARRNRGANDGEGEEEEEEGGWEAKGNGQYNGNADDNGILGHELLERPEDRAGGFRSSRDL
PSRLPPWMKHSFGEKPRFGPTFTSQSITEQRQSLPIYAYRERFLEHVDKHIVTVLVGETG
SGKTTQIPQYLAEHGYSKRGVVCCTQPRRVAAETLAIRVAEEYGCRLGEEVGYTVRFRDV
TSSLTKIKYMTDGMLLREALLDDTFQRYSVIILDEAHERSVNTDLLFAIVRNATHKRPTL
KVIVTSATLEREKFCNYFNVADVFFIEGRTFPVEVNFLREPTEDYLDCALRTVMKLHLQE
PPGDVLVFLTGQEEIELGGERLFRWMEKLREYSERPVPDMLVLPLTASLPQEVQSRVFEP
TPPRCRKVVLATNVAETSITITNLYFVVDSGFCKQNVFDPKTGMEQLKIVPISQAQAQQR
AGRAGRIGPGKCFRMYTELQFQMDMEPATVPDIQRSNLFHVVLQLKAMGINDLFALDLMD
PPPQETLVSALQKLRYLEALDDDGLLTPLGGRMAQLPIDPSQSKTLLTAVDMGCCEPVLT
IVSMLAVQKRGVFYRPRDQHEASDAAKRQFHQPEGDQITLLAVYDAWVANGLSEEWCKRN
FLKHRILMEARDTREQLSDMLRKRHASIPHHNDDALTEVRRAITAGYFFNVAKRITDVAY
ATLAERREVYVHPSSCLRDAPPKYVLYNELQLTNREYMRELLVIEPQWLVELAPAFYSRP
RKGKLTKEQRAERLNPILRAWENGSSWRISKLRRRK*
>TCRU_7532 hypothetical protein, conserved
MFFVFPSVIYPRRTEERIFKGLYHICNAAHFISLVVLLTEFYVRQTSVFPGYFGGGEVSL
SPGLEAASENCNYSKDIRIGEIRTVIRVNSETLPLPLRVMAECIIAVLVVQFLAVLNNFL
SLLNYSAGRRHLRICGVHVPFYHILSTFSIIYCVVLVAMVWITYPMRNFYREAILACAAE
VFAKNPTTLAESEFDGYDTFSTPIEWAFSAAVINLFICFLGVGVLIWKSYKPEIRLFSEA
TVPWEGRGLSCKPNKAALRIHTMARDRILSEAREALDQGQKVRIMCSYALMTEAEYDAQV
QEMQQLFATQLKEQQFEHLHTHFDRESELEGNGLLWRRQTSPPPPPPDDADEFFNMEDIS
PVNDDGIKIGGGDEFCEILDEPDIEERFWSECEGSGYEAENADDGGELARGPLQRGTQDH
RLRKKRRRHRHQLGVESESATQRERASIAQPDLGEALYDGEAAGQEGLQGDSEESLQGHR
HHHARRRRRRRHHSHAVAERDGESEGQIAAAEVRFEDADEL*
>TCRU_7533 hypothetical protein, conserved
MRLSINQCFPDPLARQWPATHHPVLCECRQLYVLVSICCCVPSAHLLVLHDGMSNSTVTS
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QVLSALMDVLAFGLLRVGNTVKRVPSLRIVAFCDARTYAIALPEHVRNAFALSTYMSALA
MESAAVIQSADTQSSNVVNKRHMLEAMLSADGEDLIETVTLSGEVSRYLRHLLVILRGVM
LVHSAPGCYVPTCISRMLRLLKVFALLFAPAAHDRVGKLHLSLRSTSPPSHRGTDLAPIT
NFSHVVVSPAHVMCLLCPMVAHLFSIRRAMVASTFGLDSECRKNSLPMANGEGARAAFTL
WDARALHWISAAGNTHADATFNGDETARLGLSSTRDIARVLRGMQEEWLSYLECRELIRV
TVMQHSAPPKG*
>TCRU_7534 kinetoplastid kinetochore protein 14
MHSPYEAVYGFDRTHIRRMTLQEYMSEEDAPTAGSSLRRDDGCRLLISRDPNVEFCTKYP
VHDRFGRELCVLYQILEMELQQEIRRVEQGGDGTRKSGVRLSTEITLDDDPVDEPFKPRQ
REERGSAYHPTPFVHTALADFNCGDGGRDDDNSNVDVSASSYRFSSTTALSPGGKGSCKG
VCDARGSSFSIYRESGLNVTAGLLQQPQGTNRQQLLQQQGLGVASDGHTSALTTRLGVGC
VALQPLPPQRSNTASPPRAVDGGGNEEEQEEEGGCGGLCVTRETLDTTLGTDPLRFTTTR
PSELRTTKQLFLPGRATVTVRRTIKHSNPIPRQAYGLQSEFISAALVAPLVAANLEAISS
AGEFRNIDGVIPQLFTGATVTLEKCRYRIHRYYASSDVYEAREGEASDDSPQILLYCWSV
HAVQLGENESHRAALGLSLVAASVSVKGYRYRDGGLTVITMPLGYYAVPLSTVPISARSF
PTCIKLLLRMLSDLVVKRTVHGDLRGLNRIFIAFRSGNDAQEMPLTLLVPVHWEGLVDFS
MFVDRNAGRTIPMVYDESGSRRGERIYHGQDVSMVINMLLENELAEQLQPEQLTEVQRLM
IMTTEPTQVANYLIQLKNGMTVIPSDMASLRQEYEVALQCQ*
>TCRU_7535 Flagellar Member 1
MQELREANKVESVLLSLGSLQITEGMMNTTLVLIKPHACREKFLDVAREHFDQYGVRTDD
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RVMTPEDAMTILGLSSEELNARWCASKSCARLEYGFYVSYLEEERVYVVNGFYPSLLGSF

TATDSQTCLFVLSWPESMYTWKQFNLEVLGAANPSEAAPTSLRRLLFENWREYGLSEQPS
LMHNGLDASSGPLEALAHRSVWMHRRATEDDFGRALLQEGVSLEFLEQLLKNPTITYGGE
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EERRNRALVFVKPHANTPETRALVEERLMQTRGMQIVSQRHVFGGEIAAQQLMYKHYRTI
ARYAVKVSPMSINVSTQNRALFKEVFGIAWKEAVCSGRVWNAETAIHTLGEISAVELYGM
WGSCTKTMKLASGAYVAQFLNEKVFVINGFYPYLRDTYGAQNAKVTCYLVSWPEACMTWR
AFREELIGSTNPGNAPPNSLRGLIRDRWQELGLQYPPTTTDNGVHASAGPFEALLERHLW
MHLPLSHDPLTLRLQECGLTGALLYRWASNPEVMLRGKKLSGCVFDILENMQTSEMVDIM
REAEQQTMALYKETPMNRAVLILKPFAVNERTIAAVKKTLESVGLLVTREMSVFSARIVK
CYLNSAAFCAATRLAEINSSTPQEVVSPAIKDRFCEIFHSTWDYCVVDGSLMGATTACEN
LGLTPKELLQLWEASSPKKVGRACYIAFLKAQGIFVINGFVPFTRECYGRPGSRVYLFEL
EWKESAWTWRDFCEVLIGDSSSPQNAAQGSLHRTFADEWSKFGLQQQPVSRATSALYASE
GPLEAAADREMWLDVDLPEDSFVQQLLLDGVPLSLLLPYVRNEHHGGSIPQGPQQQEHEG
NGLLAGAIPEYTRSMLSKHQQSSEVVRRMKVLTSRFLRAIKMNYAFIWVKPHAGTPEVLK
WIPSALQEHRLEVVASGHLMMEEVIEKHLVDQQYNALYRNAMGRSAAEVPISAKQKVEFE
RTFGITWSTVLKLHMIINAAAAEEIMGVVELLEAWNRATRKVCLSADLYVAYLEVEGLYV
INGFYPYLRSRMYTGSRIYWYVVMWDGEIMTWDEFQRYVIGGDVPATAESASLRNLLWAS
WVELGLPQQPDGVDNGFHASASPIEGLADRVAWLGTSVEDDVFGRLLIQGGVSAEYLRTL
LRNPLVRHRDEPVDAVGDVFEKLCTENPLLIAQLVGLQSTGGMHLISNRACSGAAFSRPS
LSRQGTPIEKTSTNKNTNEPAVEMVWQTNEAAGVVSPPSPPAAATATKTPRRNYAFLLVN
PKCLSTEGEELTTAYITDFLQRHKVRVEAGGRVRAIAPALRHVWEELQADTFRYAVKQTP
SQYAIGGDAISAFEAAFGESWDPEKIWNALDTALEFNLSALRLKELWDGCALRKRIAPFL
YIGKMRDRGLYVVNGFALHSTEVFNLSSSIKRYFLLSWDDADADYAQYLRHFIGDPYVEQ
AEPGSLQRMLCDDWKNAGLKCPPDPFEGAVMTSTSSLEAIQQRQLWLSLGLLRDPVGCFA
VRQLDVSPYVLRWAVSNPRSRRGDGLYLFETVRGQGSADALQLLKAEDTRHRAAPLRNSA
FVLVKSHALCRSFAMTIEMVLSNANVRIDEEGDLSGLVVRGRGLVQHLYATASRYAVREV
STIRLTEVERERVRRELGADWKELLRGGVIVNAYQALEVLGGVTPQYLYGCWKRSSRKLV
IRPNFVVAELSEYGIFVVNGFFPELKNSLESTTALLHWYVVSWCEEEMSWPAFLDQVIGD
DCPSVAVPQSIRGQLFQRWREYGLSMEPDLLHNGIHVSEGALQAMRDRTKSLNCPLSEDY
LGDAMLRHGVPERILRVWLDNPDVTSGGVEAGVFEHLRHCDTSRLLMLLTALTEELRCEE
SDGTTVQAARIPLVENNDGLTAPLQDGSQEGHTRGIENDNNKNESVLGKFLDEAEGALLF
RNTAVIILKPHASENLGVMALLERILTGNNIRVRRELRKRINPRIVDQHFSSPMYYAMQK
YHTAFPEVTEEGRVRFYEAFGEEWEHAIASQRVMGAFNALKLFSMTPSQLYVKWSLSEQG
HVQLAFDMEVVKFYAEGVYVVNATIPLERERMIQVGQVTQDVHCYLVSWDQRECSWQKFL
YEVIGNTDPATAAEISLRGQLYNDWEKFGLPSRPNRIDNIVLASSGPLQAFMERELWCST
ADLVPDPLVRALCYVDYDSSQLFEWKENPLVQYTGKKLGKHSVAMRMFGFTHEMDTREFL
ELMAEHDGFFVPTVPPCEMEDAQDQSYESFEMKADRTVKGSGKRQAHRSAKTLPFRMRDK
RSVDWLQEALLKADEDDVVRLWEYYGGIADREEEEEEEEGAAGAYADELVSTTGLHRRLR
GTINGEAFRRDIEALDCFGLPLSRYKVKKLFEGMAWRGDGRITHEEFRVAMAVLQQM*

>TCRU_7536 Mucin-like glycoprotein, putative
MMTTCRLLCALLVLALCCCLSVCAAPDTPEKPPNTTTTTTPQAPDPTKSGLGDDVSTTSL
SLPLPGLPIKEPVVEIEESVGGGEVWTVQEPPTVTEDTKEVKNGMTGPINGNNISTEQTN
KKSEASAQKTTATTTTTTTQAPTTTTTEAPTTTTTHAPSRLREIDGSLSSSAWVCAPLVL
AASALAYTTAG*

>TCRU_7537 Concanavalin A-like lectin/glucanases superfamily, putative
MLQDGNKGSVYVDGVIVGSPENIATLETQGAEASFFYIGGDEGDISSDVTVTNVFLYDRP
LSVGELKMVKKSDAKKGNSDGSMREGISRLLGFCTFVALY*

>TCRU_7538 Sodium/hydrogen exchanger family, putative
MSDPIHKEKDRVPSAFELQERGHSDEGDGRDAVGMAEFQRESARDNLQDEAASPEIEINT
VSLSAVPEHLHSLACRINDLNETDLVMIADFTENSAKRDVYSLLPYTGSNWFLPQIKEVE
EGECYWGIRCDTYGRLSVTIWGRCLVLPVINIFLRIAVIVLCWFALWNILPHWLVEPGGY
VWDPAVIVIVSAVVGGLICRVLQIPPLVGVLWIAIMWNNIPYEHYLTTGIVLPLKDISSK
MGLTVIMARAGFSLTIKGIQSHWKQSIMLATLPFACEAVAHSLIANKLFNYNGDYKWAFL

QGIISSIVSPAVVVPGTLYLHEMGYGHSSKPISLMLSAVGMEIVLGVWAANFIMGLLFHD
QKLAVAIVLGPVQFIGGIIIGIFIGVLFMYFVEILKREAERLPNGRYQKEHFYGTLDFAA
FVFLLLCFAMVFFGYALNLAAGGCTMCVFFASTVTHLCLKDGNSELEEQKKYIGSWLAFV
WDQVMMPFLFALMGSKIRILSIFNGDFFPMAVVCLVCSTAVRLLVTFAAQLGAGMTFKEK
LLVCAGYSGKASAQASLGALAATLVAEEFEKLAPGELPSAELLKRKEYASNVQQISAMYV
MFMAAFASISLVRGGVAILPRVKPGKRKQYRRSSTEEVSLPAEDNEKSQLPTGSDTAPFG
ESKKCEPHATPEMKTA*
>TCRU_7539 AAA domain containing protein, putative
MTNRGVVNAEELRGAVCAIVSRYQKTPQRRLLVCVAGRPGSGKTTIANILAEEARELLRK
VSSDPRDHAENAVVVMPMDGYHLYRKTLHAMPNREEAIARRGAEWTFDARKLCRDLQAIR
LPSETADKKGAPLYDDVFVPSFDHSVGDPKERDICVSGSAAIVIVEGNYLLYRGTPTWAE
VNRCFDMGVFQACPAATCARRLCRRHMAAWGISEAEAMVRATGSDAMNGDLVETTGKNAD
IVLHSIESSM*
>TCRU_7540 hypothetical protein, conserved
MSRRSQWESMRQEARNRVQNMDATPILENTPGSSNLPNTPGGSGERTRVKSRHSGHLEGR
GASLHQHEGSGQEKDGDAVRTKAGAEEGVEGADHENAVCRLYNAENAAVSLVPILDLHAT
RPLGNSISADTAAANSLVVSNPPSWNVLDEGHGVPKAGSAAFFEETVRELSTAGSENGVA
TLQLELAREKRKNIFVEQRLVSLEEEVKVLRAENMRLASITARDAAATRRDSAAGIPRGE
ELLRYDVPRGGPMHMEQLVTELKEELDLLKEYTRELEERLAERSNALERCSREVEQKESR
IRQLERIMADEMIRRSKLESAEESTGGTIHAPTTTNTIAPAADKHHFYTSKSNTEKGNNE
GGSGKNHEPNSRMREKPISKVEAPSVVYRVTSLTRARSETEHPPGGAGSEPLAQKNRASV
PQETTPSSLSLKQEKSSKSDLSLSPHNPRKSGPSTTKNSNALEHIHSHAFLQNEEQQNHH
HYHRLGVSSVNATPRRASLITRKTGASVAIPSVKTSSRRGGKEMSAPSSARQGSATRRKS
VSKNVNRDRQSTPKRNNTSSISNAQYADESTQRDSNPALLLASRRSVSRPPPLENSTIST
SVMNLNTTTLQHMDTRSVASTVRSRPRIIHEDSGNVVIQASTTTVVTRSAKKRESLIPQP
QPRADAVEPVPSDHPFVSEKFSTTTYRPNRLLRYHKDDSNTRSLTPPPL*
>TCRU_7541 hypothetical protein
MEYNCVVAGDAAGGVDGLVYLLADAPPSHVQRAQQQEEEQQHQFLLKSLSSTLPATGSVP
PRRVLELPHPSLPELKIRVVLQAAYAPSEMMGEEEAPTVVVFVFLMSSVDFMQSIQAEWA
PKLVNLNRAPTVILVGLTHVDKSGAAMSIQPGEIAIVARMLQAKAFFLVDGSSSEPNICI
TQITEIRDAIARACIGEFCELGHVTEANIYERQKCSSFISPLRSPLESPSLHKVYDSSIA
SPISGRSGGHAAGAHGAVWGFKRHPRTGRIFYVNRMTKKSQYKRPPGYDGEEPELTLEER
VEAERERQERLQREADLRREHEEIARFNAKMEENQQRVKVLQSGVRQLETAVERLRMQAG
ALAFKREGNKASREHVATLRAEVSAKEQGFLQESFQFHSRHEVQIALVQQALKEAEEEGD
EEKDEKGSARHENEGMNCSVFASPRRGKTMRAIHTIQAEMQSTVDSTRVIISALRGLLEK
SVKQRERNAIVHAELSSALRLTERLMQRTSAVEAEGRRVRAALMTERASMETEENVLQPL
LAAKEARLQRDRARRQSSEVDGLNEMMMMDEVHLLEEKIAAVKESLRPLKRVTSVANTHE
LAYLHRTRNIRACVIAFSKWANHVFFISRLKRGLYLRMERYADLSRYRQFLLGGLRERYV
QERLFLLHDWYALEAEGNHSGGGGHRGSNRTDTASHMRLVEERMDQLDTVIDRLKTHAAI
IEHNTSIHEMKLQRCRGVLEKLPLCELGDPSPLSGDAVVSCWLLLADRLLEVVARLQSVV
FSMEAPSDTDGIGMDAMRVMGEEKGAIYVEHMKLLWQELWRLSGRSLLRHFRLEELRETA
RRLSRQHGLTLNGCDNNNSSRVSNGNAPKRIMANSMSVADASDSHGNADEDGVMPENTDE
LSLLQPAVDLTSASKDTIWMEKLLLSILAPVTGNRNFDVDEAVVMTDKSAAVCSPVSYNA
LRERLQKEYA*
>TCRU_7542 hypothetical protein, conserved
MRGKKREFVVEANAPERYPQEEEEEEIQRPLQRIAHVDTSLPSSAYEQRIVDQLQGLLDA
SQVNLQESVKMGRIAAAALFFHQGAPVAITFVMLIISCVIDPSAQNITCTVLFSVLYAFC
MVVQVYLLWARITEKKMRTAYIMGDVLVRWRRRIMGMMKMPRQSPHERRAAFLESTAILP
AKAFRMVAVIDVATGRLKHVLKSLLMRGTKRLDGSKLCTWPYTEPVGPCKLVDVMDMTLK
SDAIVLRPLQDKGRPPRRPNSQILENSLEEEEDNTTEDSDHERVPRMDTSDADTKSVSQR
MEFLVHRIFLLVWMFGMLLTFVAGFVFHAFLDAPIGQRVFLYPSVALLGLLPVNAILLNR
ALVLYANVYLERLFSHLVSRPVNALDDRIPRFSFVSIWKALWHVVRQRPGRQLLCFSSSI
VEVLGMATVVSLLDATGVVTDMVPLPVVMLMCKPDEHPDVSSSSEDDGGNTGSGGPRPVH
DDDVAAVADSTANERKRERKKLAGRKRFQDRLFFELRLTPSQRDDLAVQFADEKESNARQ

MNISPVALCLLLHALLPEPENLETWTERFRFCDRTVRWARSTHWIARASGFIDSVVDSFR
ILARIFQINTETRTGYRNDYPEQASTLLVAGEDGTVHAFTMGSAYMVAHNCSFYFTGVSI
EELDPEARDELVHIGKMVWEECMGLETVAVSHRILPERYRSVLENNFKWDSDGYSEYFFS
NGVQVRATETKNDLEMEGFNGGVQPTSPQAKEETRRQLEDAEELPILKSDQPNQEDEDIL
NTGLGSTAVQATHDNPSLNLADEGKKPSVKDDDDTPASLDSLLDLLVGDLYVFLALVGLR
DSIRPNVESAMTLLDEAGIRCMYFCAENERRTKSLGNRLGLETDWNCCISLKKGAVELDH
HSIRAQLPVGIDAIRKHILHVDPIPLQVKMFSHAHSVSTRAMLSILQDNHEVVVSIGSTF
NHGNVRSFIQSDLSIGVLPTRRGPVAEKEEVCLRRHGRIVEPSEFSAKKSFNRDLPLYQN
VTELLSCSCNLSASPTPSILPIVTTLIRQARLRLSGIGNCVEFTLHANFFVTLVNVFALM
TGLPLLISPTATVFELNVIIPILALSCTYTAYADVDPMKTISSRHNYFVRLAIFRHSVLV
WCLRYVPSLVALLVLGITCGKHLCQRSVEELALSASDFCMTSTRGYIALTMNYWLIIHSW
THISRHYPLAPNLSFKTRYGKRSSYLFKSFRLVSACVLTSALSILFVVINTLSDGVTVRA
FYPSLVHFLTSLLFPVLLLLLDVPIKAWRLRRFTLMQKFRRLSFGTRLGMHSPRGDYEPE
GVTYTSTSEELERHEDRVPALKQRLHDVFYRFTTMRRGKIELNCVCCDHIGGNYATYHIH
GNDM*

>TCRU_7543 TPR repeat, putative

MQQSIPELLLLLPTVVIDERYVQDGRVTMSMDDASTIANAYFQIVEDYLQQRELHRGQLE
LEKEVIPAIEFALRLFNAENFSGELVPTERERLASVLQRFTMADVPHERCVQRLLVSDGE
MPHPFLRLGGLLLCVLAVVCSKVRGTKQPLVPYYSVWRLRVHMRHQLVLQHRAHSVFLHL
SACVDAALSLPDEDLSVEHLLEVGHVHNYYHRRDIAAETFWRAVRKSGLSVSESAMMGVR
TRWQGHQLVQMVMNAQSALPFTPQLVTDAPRVVMGEKDGHDLLDRPRETPESPAPPLQSL
HPVDKAIILALCLDIRNTNPYHGLTQHHMQTYVERLLVDPAPTPFMIQSQMLLIRSRLER
RRNRVQERAFMQITELVDQFSAARDPTRETFHRTESDYFYSVAYPSIWHLKSEYADFCYE
ERLFKTALDAYEQVLDWENIIKCCKALDKRKRAESLARELLETDPCNPFLWVALGEATRD
ASHLWKAWDLSNHRSAAPMRALAKLALEREEYSKVVEYFDEAVRLNPVFGGDWFSLGYAA
MRLEQWGRSGEAFTRVCQIQPNDAYAWNNLASVLLRDGRLRPAFNAMSQALRNNRRDWRM
WQNYFSIGCELKEVTETTNALNVLLEIAKRNTQLERESLHRFVDNAIAYMEGRIPASSKD
QMEGVEESHLFASLMEDEEEQNMCDIVPIAGDVEMPEAFLESGRRAASVKEAEGVREGIV
ERYKQRMRETFKRITDLFVTDPDIYACGAKLLRYMDGPLRAYEMRLKELRCCQQKDQWER
DEARFARTCECLRDMTTDVLAALDDAISASNTLGGRDDVQEAVISALDDARNNTTAVIEA
AQDYMGDAADYAQLRSVLLPQIRGGLQKAKSAFNSD*

>TCRU_7544 hypothetical protein

MNGGNGKDCNQPDAAVASSAFGDALRPVELRHCVSLNKYSRMPADEICEEEVVRSEVAVQ
LAEKVVVLRRKLQRREAEIQTLKSGIGTDTSAATHTTAAATSTTVADGSTVESCNDVCAA
SSVTRESSAAEQAVDCNSQGNSAEWQEKLAEMEAQSVLWRQRVKEALRTSQKREQALLAE
NIALQKRLQELQGRLNEAVFCIEASALKNARQTTKVSRYCQTNESSEDAESGDESYADDA
TGMSNVSSNPRPLRRRRRQSVQISALRTPLRVVASSENLEKTARATPLMTPTQTEISDSS
SKSPSRFPYPPQPLVPMRRGNPNTDGGSNMGSPNYPVEICSSDPASQAQTPPFIVAVHYN
NSDGWSVQTKLCVKPGMTVAQLKEHCCSQFYDRYQMRLDDSTLCVRYYHEKARRHVVLSS
YRELHSFACFQRCERENIPITLQLTREDNLSKFVHDTMNVANMSRVNFSQDRAD*

>TCRU_7545 Domain of unknown function (DUF1726)/Helicase/GNAT acetyltransferase 2/Possible tRNA binding domain containing protein, putative

MPSPASVASTTRSSATGGVTIKRKVDDRVRHIIENAVHKKHRALLLLVGDRGKDQIVNLH
QMVSHANHSAKVSVLWCMKKEPDFGSTSSKKQEKRARLEVKGGMSTEATKEAFQTFLSQT
SIRFCQYKETHKILGQTFGMAVLQDFEAITPNTLARTIETVKGGGIIVIMFRAMRSLKQL
YTIAMDVHARYRTEALRDVVPRFNERFLLSLVDCETALCVDDELNVLPITTKMQSVENAR
ATSYEAELVLQGHQKHEADLIALKDRLSGSNEVGPLVAICQTIDQGKTVLSLMQTVVEKS
LNTTCVVTAGRGRGKSAALGLAAAGALAQGYSNIFCTAPSPENLQTFFEFVIRGLKELGY
TERTEFEAMQSTNIEFSKCIVRINLFREHRQTVQYISPHDASKFAQAELAIIDEAAAIPL
PVVKQMLGPYLVFLSSTVSGYEGTGRSLSMKLVADMRKHCGSDGGVAAAAGNSDDRRFLR
EIALTDAIRYGPNDPVELWLHKLLCLDTTVRPTGVKTCPHPSKCELYYVNRDALFSYHPF
AEQLLQTIVSLLVAAHYKNQPNDLQLMSDAPGHHLFLLCPVSVDAKGGLPDVFCVIHACE
EGQVTSEAIKSNLSRGVRPAGDLIPYTLSQCYLEEGFAKLAGLRIVRIATNPELQRAGYG

SRALMLLYEYYSGSISLRPAPALSSPSLAQGVNDGAGALEDDASSTIILPRKRIPTLLTP
LIDRPYEVIEYLGVSFGVTTALFNFWRRAGYEPLYLRHAANELTGEHSCVMVRPIGLDLA
LLRAEFRRRFIPLLAMPFRHLSTELALSILKDIDVNDPQKLAAATDLSQASAHVVRVGGQ
VQCTWSDLEKIFSGNDMKRLKLNATMFVDGGQVLDLIPAIAKLYFEYRLHRLPDGSEGVV
LSHAQAALLLAVGLQCQTVEQVAQQTAFAGVPIQQLRAFLQKAVSRIVEHFSRLEKLKSP
GTNGTETTREEGAGETEEDAREIYDKDGKLVGLSVEKKLRRLINVDSTLLRDAKSSLQGM
KNEAASATGLQRAFKRTKKTRRS*
>TCRU_7546 Organic solute transport protein 1, putative
MAIGSLAFLVLNYGAEMIFILHTRLIAQNVEKEMAETVMNDMVRHMFSPEFLAELFRPQP
LYSYSAVKEIFKSLTEMSVMRLSPLSMNKLFELMAMGVKYQLFTLRHPLELVEMTWTHLE
ELKRLITPEAQAKVTPVFVMLEGLCSRLTHGDLAEIRKELLNFIVGRSTVISVLFEEGMQ
SDRGSFVLPVDRVLPPLSICEPPGSIRYFKNGKLDASTAFEHRDAVLRHPPSVPLDKWDP
KNAGTRMTKNGTNIYAPSRQEASTRAEANGPTSLLPSMPSMSRLSTVPTAVPSEIANVVT
GELNYLSRFVGCGQNAPQKMFKLKFFDDVEEEMDEHCVGGGEKGSKIGGATDRVGDRTAA
STIPLVRMTKADVESQNKELFKIMDGLRVDETRAGPPERGNDLLDIMDED*
>TCRU_7547 hypothetical protein, conserved
MLRRPLTFTTASAAVAFSAVRLYRIVPHVYNEIEELAETQQAGRWYISHRNCLQQPLKRA
EIMCDKLNYREKRRMGKLPEKSVARRLSQTYAVDGKVHESKYKTKLINITVVGFDGHPYH
FRMYPMPDVTLNTLIDGSGMCHGYAHYWGKCNNPDCADWNHGDGCMVNVDIETLDKLLPP
NRWEYTSLTNWRSMDRPDITYNTRFSCQIPVTEELDGGLFALKQYWTRALRESVSDWGLV
DDMGTIHGARSKKIEPWAPIIEEPTKVDFPITFDMLWAQSYQDIMKAKYPDIKRKDGYHT
KPEMWAAYV*
>TCRU_7548 hypothetical protein, conserved
MVILGLKKLAARTETEQTHPSTEEEMDQYIRSRTDWRERVFLRLAWITASCWSEIADLTP
SNSTLEAEGTLILDWPVVPKTARADPHRAFRFVRIRGQDAFDIIKLCRTLQENEKLTNIT
NAKVERALAP*
>TCRU_7549 hypothetical protein
MEDCGLMEGSLGDALGGAMASNRTVQQLFLRSNGLARKTGFLPPLLTEAVGTHSVLCVLD
LSDNGISHAGCMRLFAALVRSNSMCKLYLDGNHLGAAEESASYAELVVFLENSVSLSVLS
LCNTEMHDAALEKVGEGLSRNTALHTFVASGNAFTASGIAAFARLIQQNVTLKNLDLSTE
ALYHDEAVYADTHRLLSGVGRLDSVQL*
>TCRU_7550 hypothetical protein, conserved
MAAEWIYSVTKEPRRRLDDPATHRDIKALLEKQPSVSLAVARVLHEPAPLRRTAVNVDGR
VEEQVVPHPEAPTLLLPSGWRSCA*
>TCRU_7551 hypothetical protein, conserved
MARIQVVEKHLQQADRLEALREELVSARVQIADLAHIREREAQHWRRAESLTDHEVRRLE
EAARERLAKAKQAIEEEEKKSSLQSREGGDFSGHTTPPTKTTRTAATDVARNPLRTSLNV
LQTPVEPSVSVQAYRMLQSSVTPAVKETLRPQKPQGERSTGGQPPNRSYSPGVASCGPLY
DNLLGGGVPKCHSEKKRTRSVDIQSQNLRPLSDRDERSSAGTVLLRSRDPMAYKIPRPLQ
EKLDK*
>TCRU_7552 hypothetical protein, conserved
MNIVSAHASNHDGITHASRTDAVSRVVFSATEIKGETSAVSFLTQEGGKEPTGTRKKSTD
TSVNNHSSNNNGAVSISIKSNSNTNNMSGLPLRPKSFVPLASPRLAKMSFTRSHERAGSK
VRSLASIAVCKTERGFGKETAHSGNEQARKEQRRRELYAWNKELRLRQQTTVAVDAV*
>TCRU_7553 SET domain containing protein, putative
MEELRVRGNALFSSDPRAAANLYQEALGVYEKLKDKSGALEEYTKCAGNALTCLFKVQEY
DACLTLAEKVLQCNPLIAKAYAVIGRCLLLRPAFTLPLHGDPLQYLCRAVHLSPSMCETI
IPFMDEALERLLHECDTLHDEEPCIEVQQGECGRCVVAASHLPPLLVVSSTLHPFSVCSY
EETGSVGLCAHCGVVFMPDDGEEPTAALRTCRRCQFVSYCSDRCASCHGRQHEEYECRLL
FRLREMLGSMRSCEAAVPDDFFTMATHCITTMSGVKMRKEGHEAVLRLESHEVEVSQGLT
PLVRLVQDLFSGEDPTFVTRILGVVRCNALAVCDASGLPVGQALHAASVTSYFNHSCLPN
CAIEAGAIVTTRAIRPGEELTISYLPQLYWPAWLRREELAERYFFDCRCVRCDDGDRSPF
ESALSATLRLGGSREKEREYISSVQILCGRVRAKDVGDVDVGDRDALLHLLQECRQHLFP
FHYLCHELHNTLSFVYAVLGDTRACLCSCLRELVMWEAIVPGAHPVKRRKVQNALRCCAD

EVADKSDTVKNGPSSNSKNDTHEESLLPLRSLLMKFATLYDVAC*
>TCRU_7554 Ribonuclease H2 non-catalytic subunit (Ylr154p-like), putative
MVAEKTRQERDACVVHSLPFKTTFRGTTDIEENFSRHIEHTENGGLRNTLRGRTLIGREV
VLPPSYVLAVTSFMPRQQHPLGTGAAGCVTSSAPSLAQVEAVASDVRITATEDRFCVWEH
DKQPERVDALAHWLELSRVLHSAP*
>TCRU_N-terminus/FAM.1 FAM.1
MAGQHHARDLQQALESRLPYEALSGPLRQRVSLQAYKLHSVHFAALRYHSYQRLPKFLRV
SMTEQSYYEVLIAYLQENLQLYPYLHIRKIAQYTKETPLSYYTTMISELLKAERSYDTLP
NFTAVDVLNIIGIGRNQYLELTKEVRSKLRWHINRRFVKNYLPSEMLPSVTLPPFWGVFA
VDMPAEAIKRANLSNEEATLHRQLLKLSAENESHNRGSDGCHFACEFPREPLHALYRKGL
VCATFSVGPEDQITVPPLERFVMNRTSDDPTEVMLYKVLSTIDNRTSLSLLAQLLMLDEL
DVCAAAQVYIRLGLAQLKTVHIPEEILNFTERVHETWRDVVEERMSEASAVSLTGSAPCT
SAEAGASEADADTKDTCPNNGSHPPRRIALLYDASLTGFLMMTNLSADPTFKQHAVTLFE
LGKLSEEMIGSFIEKLEQVDIKTEHDLGDEAVKYICSVLSLREVLKALRRVVGPDKESGV
DMLKVESMNELEPTTRYSVLGRNYWAYFVTSPVSYAPLIDVALNGVYGSTVSLMPSPWMT
LYLYNKMGTGPPSLLLPVGARLAAWPPLLQDTEKSVAKLRLQPFTMDAEITYVEAATSIV
LLNEMTVMAPLFVQRVEDVPLERDTEGRFLVESTKYTSLDVVVPFTASDTEAVALFSSAV
MQHSHATSVHFVSADVVDEMVGLRRFLDLFHLAVEAMHLKDSLGCFTFHVSLHEVVKEEG
WGKETAPTPTPTVTHVDPTKGMGFKKEMSRFYSLADAHITDLGFGIPLTHPDCCSVMVRH
LEDLLGETRSECHNNAMRDLANDFGLFLGSHSPLTSSAREKMALQSTAVVGPSTQMHIRR
LGEGGNGGAPFPSAMIFFDGAHLAVMDDWNPLVELWPV*
>TCRU_7556 Vacuolar sorting protein 39 domain 1/Vacuolar sorting protein 39 domain 2, putative
MSHEVFCLRELKQKLSCKIDSIATARNLFFLGTSDGKVMVYEVSLQNRDAQCVYIHNSKH
KLPIRMIIPIVEKGILLVLAGDVIAVHQLSHITHAPLDSLPEDRLPEMNTVKGTKDIVTL
HVKRQRGIFSMAVLQRKKITLYEYRDHLSEFVMVNDGFLLPDGAKTLLWVGKNIILGFRR
EYVIMNVLSGATDYLYPTGKSGIPLLLSLDPVPEVLVGDENKGMRALHDGSLVPGRSGMS
WSSIPTNATYIHPFLLTVHDNNCMEVRLPFFTAHAEASDLSPWQTLSLKGADRISQRPFA
DFDASLPKEATPSDALRKDISILVSSNNTVYLLELLPVREQVLALASLNCVEAGLILCQL
CANEVDQATVDSLKTQFALWSFHAKKDFKTAMLRFRDANVDPRLVIDLFPGFLTKRARET
WHPPKEYTRSLDTTDLAMDMRSAITAFLDYALPLRREYATEEKTVLAEAIDTAIMKAYVV
MGQEQQLLSFLAEENFCSLAESEVFLVDSEQWVALITLWYFYKQNHKSLALLYTLGTTRE
RVLLESLLTTSFSRGNLPFDTEFLHILHLLLANSLGKSSSNRVLSDRRDRRANFIPQSVM
MRILDEIAVNADPSHQLGLLRRCVSVVTTITYISLLSWDEQEERALVEQYSRWILANVSP
RWSVKMFPVTEIQPKHCTTVLRLLSSDMSDMGDTQPHERRAEWLSLVFDNACNVKIDASI
HDAYFQSLVHLLLSTFSQEGDGGNNEEKKERSRISELHQRLENFLRLSEHIDISNARNLL
EQPNLRSHMYAERAIIYRRLELHEEAICMFLYEAKELQAAQEYAKHVGHDGQDAFQVLLR
LLLHPSDGCTSPRLDDVIEMLNTCEGVNLLTALPMLPDDTPILPIAGFIKRSIRDASTRS
RSAAMNASILEARIRQAELKIALERSRQVVMDLGTCCAVCEKKLRPDVVFARFPNGVVVH
QACMEDEHICPITYKDFRLGIEPFARGAL*
>TCRU_7557 serine peptidase, Clan SC, Family S9D
MTSFFGAIVKSIILPKPSPSYGTSDHLGKLLHIPRVEWRTRKENGSFTYGLLLLDPTAKY
IVIYAHTNAVDMAMMVEELSYFSKRASTSVLLFEYTGYGISHGDTTEHSMNEDMLSAYCY
ALRHLHVPPNRIVLMGRSIGTGPAAQLCASLQDECETPALLVLQSPFTSLKGCANEITRN
VGSIVSFLGYDWFRTIDVIPQVRCPIIIQHGVLDDVVPFEHAERLKRAIEEASPPGFVEL
YVEKICKHNDLPIASVARIVDKKLREFGQERCLQIKCRTYLTVNPPIYEYLFCLDGKRIK
TVDALLRHWNEHLSIGSFAYKREKLYILLVASVALFAMRCARVWQCYTGSWKRQHSEEGI
GEGSHCGKEEIINRYLACRGSPLGVFLGLEGKPVLHKFFGVHVAAGAAQGVDGGGPPCIV
YEDRATYLSVAELEFTSGLMKSVVAAVSTAPTLTEAEESGNHVFLQQCIVTRIQTECERL
VAFLDDNEWNNLLFLLLNFDETATTFISSKALHFYNEYTSLAGDGGEGRRHKKKESIVDV
EEWLRPWITSPNAQTCLGGEVPWDYYLFKARVCVQEEYELRASTSWTEARRIVDAWLVVA
EIHRLFKTYSGRCLHPAFTAA*
>TCRU_7558 hypothetical protein, conserved

MQIPEGCRGRSPPSPSSSASLQTEPASMRLVPAQVVELISEAREKGGFAGALRYCDLGPL
LQRLGCAWDMERLDDCWYDMVRGRPTSFVDDLPWAAQCLYEHLRGDSVVIPKPAPRRHLH
GGKDTLTPQQHETDGLARAPCDSTSEARETQPPQPQELKQHSGQEKESRPAPKAAISSRR
PRDLSAGKSHAATPRNVRFASPTLSSLRRSRSNSLPQRRNNALERSPKRGRSLSPKTTTG
GVFRRLIEDAERRRKRASPPPTSNLETRTTTGGEGGGTVVLTKASMKPEDGVPLTKPISR
HMSFTAQSWNKPTKSYTAKLGPEPASVDRLEAAAPTPHVERQEPTGPSAYVPTGYVEAVA
RLRRFAASRNHFQFVDSLRSKTPVSASTGILLERAPILRLPVSDPIEGNSAVDVRLATPA
RSHCLLVPQDVPYDDPSRVLIQDLLRGTRVRRRE*
>TCRU_7559 SpoU rRNA Methylase family, putative
MKWSAVCLLKRDFDAWAYSINWPQRKSLLPLLGSVSLTVEDIKFAYNAWCLLRLAMFFGT
GHPKILSPLVNTTPSMDIIYGGNRLFYMHAEVGASLSRYKPKVALTPSHPDAQPVQSFPW
RNVIREAGERRTDNEDCDGGVEIVLGMENGLSENVVSQCDYCLYIPQYGSIGSLSMISAM
AIALHSAASAHVEQCMRDDDRVSPCSSRGHMPLSNGSLKVTKGNNLPHETNLLSLSNAEI
AEILRARRMSYPMQLSVMVYNEFGDRNIGAIMRNANVFNCEQMIVLHRRKFNRRGALGTQ
HLIKTLFYSGVDDAQCQKSLEGYTIWLLYQYYPYLKIYEDPNGDEDATFIRPESSLFQEW
LQCSHGMNPDHPMMTFHASHLIGTDVYLDDSDSVHAAVQHAANEGYRGIVLVVPEEGASF
QREIVKKARRIAYVVHPDRLARKVQRGLNGALSSAIALERLRTAIDGLQ*
>TCRU_7560 Leishmanolysin, putative
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>TCRU_7561 hypothetical protein, conserved
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RVLCRHRKELLRIQRVLRRLGIEGQVADPAAAPRSQGIQQSLRPLSSSQEQQQDVEDTKD
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SSSGVFIPRPIQIIS*
>TCRU_7562 hypothetical protein
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LALSFPERTALATSFPQYLLE*
>TCRU_7563 deoxyribose-phosphate aldolase, putative
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KTMVQEGAEDMDMVLNVGALKDKDYRYVLEDIKAVLAVCPPHVTTKVIFETCLLTEEEII
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>TCRU_7564 hypothetical protein, conserved
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>TCRU_7565 retrotransposon hot spot protein, RHS3, putative
MKQSDFILLVLRFWDYAPPYLIEKYAVSAFLNEDFLRAIRLKIKELRPPGRGEPHNCALK
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NVGDDENREIAAFWNEKVRQYIAAVSSADARRDEAL*
>TCRU_7566 hypothetical protein, conserved
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SGGHNSGA*
>TCRU_7567 dynein heavy chain, putative
MASRVKFDLGDEGVPLESHPECTAWVLQRIKEELCYDVDGVTDKQLRLINEFLVGDEELR
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FDSLSTTEMGAECIEAFYLVAKGEELLLQLDRGKDRVFRLVGSCVSLVQGKLQRHFNKPP
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NNVLAEHLAMLSSMKMSRFVESFRPKVVQWEQTLSIATDTIEALLLVQTKWMYLENIFIG
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WSVDLVERIDQMKQWGQRTPNVFWLSGFTYPTGFLKSLQQQQARHDHISIDQYTWEFIVH
PSDERTVVHRAKKGAYVRGIYLEGAGWNAEMNTLCEPRPLELIVPMPIIHFKPKLRDGKP
RSSSIYECPLYMYPIRTGTRERPSFVVAVDLPSGEAVPEHYTKRGTALLLSTDE*
>TCRU_7568 retrotransposon hot spot protein, RHS3, putative
MKQSDFIFFVLRFWDYAPPYLIGKCAASAFLNEDFLRAIRIKIKELRPPGRREPHRCTER
ALRHELHQKEVLPPPERLSNPVAMDHWVLYEPKVQNFPLVDGFFFVDSNPKTLVALRMTT
TGGHHTRASTARQFTECLAAYFNGWEELSRDMLWEIIYVQHADSTPMDGWRRCDVDNSNN
VSRAENREVAAFWEDEVRQYIAAVPSRDF*
>TCRU_7569 Protein of unknown function (DUF3720), putative
MGLIKAVEASDAGPELSVVPEQVEKSQDTENSSKDKTSRSGASGPDGDGFAGQPAPPKPG
ESGPGGQEREPGVLDPNVIKEAEERNGSLSESQKLRSDQSSTTGGPGTEDSEEPALEDTS
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TTQVDEHSSPGDTVAKQQLQKPQSEMGPNENSQSKSVATITANQHNEPSADHAGSRPPSP
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>TCRU_7570 hypothetical protein, conserved
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>TCRU_7571 ATP-dependent DNA DEAD/DEAH box helicase, putative
MSTARECLGPLISYLPYPNFTRVQENVIPTLLQCDANVVVAAPTGSGKTALLEVAMLRLF
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ALEAVVSRMKAIKASMSSRGPRFYSTRFVATSGTLPNIEDFAEWLQVESGGAFSFTSADR
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FREHYISVICTTTTLALGVNLPAHLVIIKGTTFFKSGRREDLPLSEVAQMSGRAGRPGLD
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GSDASLGVSGEKALKPPKESNTLEKMTGAPVIFTLPQILGILSRAAEFEELHLRQGDRKH
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FADVLKSDPRKLEVLCGKNIPFGNKLQDRCRAIPQCVLCLEPCEGSESLRAVITLTTTPR
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RGWW*
>TCRU_7572 hypothetical protein, conserved
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AIQTLLLAGKTQRAVQCYLAHAREVLLSDGVLVALFDACRHDEKDSLALYHAVKPFYAEW
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RSLKSQKLQFLYHVILPLVADRRAERLQECYDHMLLHEPDSVVDVLLRCLHTPCGRELAA
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>TCRU_7573 hypothetical protein, conserved
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QIQWMAIPGCRGTCVLDVPIHELIAHGDGKKNIWTKPKCLQWALRVEDPGEWVGIGVGVG
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>TCRU_7574 hypothetical protein, conserved
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LFNEHLSHIEGISTFEEEPLVEDEN*
>TCRU_7575 hypothetical protein, conserved
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>TCRU_7576 hypothetical protein, conserved
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>TCRU_7577 rRNA processing, putative
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NGRVKLLLDKLQHEQTKN*
>TCRU_7578 hypothetical protein, conserved
MTEAAGTSPAKIRQPQRLRDSFDGDFCLSDLDEGCEWQEWKRDGEKSERMDGDLMERHKA
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>TCRU_7579 ATP-dependent zinc metallopeptidase, putative
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FEFYLNRIITGDPNCKPKVQRFRTRKEGEAGATDSSTTAGDGTNNEKKEEVTNSMMEEIP
AAVKIIPGVSNKAYALELAERTPGVSPAQIATIVNEAALTSAMLEEEVVPLKTLQDSIDD
VLIGRKHRQRMSDTSLQRTAYHEVGHAIMAWISPLQKDVVKISIIPRGRAGGYTQQVQDE
ALEPRTDVFLFSQLCVLMGGRVAEKIFMKDISTGAMDDLQRATRIAMEKLLMYGMSKSIG
QLAFKPNDRNEGRAWMNFSEDLHAKVEQEARDLVAAAYKHTEKTLLEKRELHEKLAKLLL
EKKELMREDIESVLGPRPVLTA*
>TCRU_7580 hypothetical protein
MSVSTRTSVTQWGNGSYSEALIPPYRSERHHIPRLIPVLDSGSDEVRDCSVILPPLGPSL

AYVAAAPVKHARRDPVGKGPTHTGDAEFVVKWKGLSAEQVERNLTPLVYHYRQQLLLLEE
RRRRRIIFTEEFTQRIDLGIHSRYSAPFRERLLSWDILDTLSRRLEAACDRSCHSSRMIS
PSSSYIRRSRGDDPFYTSSWYTSVTHGSPRTRDSATARSVQRPVFGFMVSAFGQKLEEHL
RNASTPEHVVQPRVGLKSSGQLKASKFLTVSSRLEASEEMGGSQKNCTPLTKESKCDDSL
TMSPLEKSLSTISGEGSLDRSVASCKSHC*
>TCRU_7581 YqaJ-like viral recombinase domain containing protein, putative
MAQHPKKLQWKEGFPFGLSASQFGMALGFCGRVVDFVDYLRNVVGTELEFKCNASTVHGN
KTEPKARALYELLTGTTVSDGGFFVTDDRLLGCSPDGRIFYDVNLSLPSSSDCVKSDIEH
TSPDTPVSVPIPFCSKWSRQGKRTVAPARVATQRACRLLEIKSPYYSLYDGSKPEYQPFG
IPLHYLCQMQGQMAIANADECDFFVYLDRCVCQVVAWRVRRSSEFWKWAKPKLLQVVEWV
RDGPPASLDRRFEFEAFDFDKIVVEPLIFPYDITANLPILDARRFPFFQRHPNPYLGTVC
GTNQEGILRGLTSAVTRFLFHVDVDENPVGTTNKHHNDDAVIWCRSTDSVVYGAALALSW
NAVAVVRSPIIGKKLAVVRPHDFNDDRIICRIYAAEEKQEGNDYDTIYVHFFQRDFFHSL
EPLECARGFESAPGVGYGGNGVAGYVNLPMSERHRL*
>TCRU_7582 hypothetical protein
MDDECCAHAPRPPRFPVSKILVLCGFVVLFFVESCTVGSWPMPGAPAPTSSPAAGGPEMP
GGRMSDTVLQYTMRQMNAISSRQTAPFLFPWGEERLAILKEWKQIYYSIRGDLARWARSN
AKDGKAKDTQTEPEPGNRLQMLVYDVNDGYMTLSLASFFPDLFVTGVVLSGCPQTVAEGN
ECPSLLQILKGIENRWNTIQSQNNLENPRLFLCLSPPMSLIRLGNMAGRQTMAEYQVAVS
LFENFAHTPTKRTFQRSLISFLKSASVATFITLPVFGKGPNKPKNVLHWYNQPHDPEQLM
REAAELFSVQLSIVHLVSVRWGDEDRALFRVEVLRDSNWTEQGTMQCEVRKDLLRCDPRG
QFVNCSA*
>TCRU_C-terminal conserved region, putative PS.1
MESTSFQDVTNAASGKRRVLPQSESHKSKESSVVTGAAIEELSRKVDALSHKLDTIYDLL
SALVPQQGRLSLLRLRTESPEAVHLDLHNKERNVTALFNNALRERQSHLPRSDASRDTQQ
PDATTSEMPNSEVPGTLEAKITDHKKSPSLGATVSAGGGVADQHSWPKYNCFILLVEFKC
QRVKRCESNFFIVPGQYAIVQGDRGYDCGVVNQCSEWNAEKGCFVREESLDGTMVNVARM
KSDMSRVLRVASEEEVERLFGEIARNENLALRTCREIVARLGLEMDVVDCEYQFDQQKIS
FYYESSRSIDFRHLNSELYRIFGVRIWLQNVNNAVKNVVPAGAMSKEDKAQYRKSGLRTR
LR*
>TCRU_7584 Clustered mitochondria/Translation initiation factor eIF3 subunit 135, putative
MVRLPPQQQGCGRRATAARVSNASAPLQPPIVAAAQVAASASSEASVVYWQLLGASASLH
QGPLGDVVGVVPCGTVIREVRRYMDPFGSWWVALKASEGDILWALLSTEREMEISEEHAR
WQKVYNERLLPQGFSETDRQEEARVLRRAVIPVEMNSKAAPSKDFAVHNVRVFEECWHNF
SAVTNRGRDWNAEYQRLVELVLFEKWEKSVSASEELQRFMGQFLTAAEEAALSVIADMLR
PSSDRVAKGPIFGSVGSFLYNNLLVKLAIDDGSGNTRGDTHAWRQASQTLQAMRLIALEG
PRRLLYSPPSALITFTGFRCSVMAIPPVEVKNIVYLSLEERGSTLDAPEFVRSQLMDLGQ
ALNLKQHHLRPATGDVVTLTTPLGMAVVAGRDKRLYLINASRLIPACAFVTSTEADANEA
VMPRFRPEFLLSYGKPLSSDSFVKDAATPEDNADVVEATEWIRDEVIPAVSAMIGFLRAV
DVPRQDPVECRLCSHTMENELRFVVCHSIDMCCCICSHCYTQRLSEDKKDNLLFCDAVKC
DTAARGPKGLLIEPPINSIFHANGLNMRFLPFVYYCLPHVSRFAVAHYLEIEMIARTAVR
LLRDKLRRTAQSVDEVKIVCHEFLLGLLQSSGAKAKHFWAHELGPALESLYGVQMPFDTS
EIDVELLYHRVAQLSGVHLRMASVASLHTEKPYLQLAEVRPLIKVIHPPLLVDEASHEKR
RAALLQCLEGILLFWISFSANGNDDGDFDSVQPFYMTERESWM*
>TCRU_7585 hypothetical protein, conserved
MEDAAQTNSQSQEQQQLQQRPSALGRKRKPSPFLNKQQHLQNTLRCDYVLLWYERDPKSP
PGQCPNFLTVGDPIPVSLSHHVFMQMAFGILKDRLMSAPSRNKSVEVEKGVGKGDVALES
PSRESETQTSGIHDAAGSRNKKTPTLHEQDVVALFCFLWQYVSSMLQSQAEALHAFRRKN
KNAPAPKTTVHMTKQQLRLQMVLEHGVDVRQFLGDGLLTSNAVSEAYCKRLMTGKVMEEE
FLNQLSKPAGMAQTCSMM*
>TCRU_7586 phosphomannose isomerase, putative
MVGLVKLDCGVQHYDWGKVAAESFVAKMKHETDGTRKYAELWVGTHMNCPSRLLSGQLLG

EYLRDPGIANSFFSPEHQSNVELRSNVPFLLKVLSVQTALSIQAHPNKKLAEKLHLENPS
KYKDNNHKPELIVALTPFEALCCFRPLQEILSLVESTKPLKTLLGNTAVVSAKESEGDLI
EGMMRVLYSLNPEVHTKALREHAAAVSAKGEAASTEDRLFLRLMSQYPDDIGCWMLYFLN
YVQMEPGQGLFLSDSEPHAYLYGDGVEIMANSDNVVRAGLTPKWKDVPTLLEMLHYNTNG
LERAKYERYRAAEGEAWEVQCYSPPRRFTEFSLYRLEHVAQKASETCVNLPNIGLGFCLG
GEGVVNGTHVAEGDCFAVPHGPLKCEANGRCVLFVASTNDGLPEQAHI*
>TCRU_7587 DNA repair and recombination helicase protein PIF4
MLFGTTGALLLRSSVPLKNLLQEPFLRGVRKAVISRNTSQESKGHDGPHARAVGREGPSY
LIHNKNQLSQLPYGSQFSGGKNSSTRCSSLVNELPDFMEIPKPHQHDELKESGQKVCAEE
NKKPEKKWLSVEKQIVRQLALDGASLFIGGDAGTGKSFLLRCIAESLEAKGLTVLVTAST
GIAAVGIGGNTFHSTFGVPVTSDDERDASTAGAAPHIWYDTESLAVPDVIIVDEVSLLHA
GYIEALDLAARMAPGRSQNKPFGGIQVILSGDFLQLMPCRLWSRGNSERLFCAGVEKKGV
IPTGVTPEMEKLTVSQEENCALGVSSQHPQRESTLFSVKRRHQLLRFYCDRPVYESATFE
HCLLHLQLSEPARQREDPEYLEDLNKLRRGILTHRLSRSAVHNPEDPDAIRLFPVKRAVT
AFNASKMLELTGEERCFKSEFHVTSGNGATSSARRSTSGDCRTCPDMLVVHFRNKPMRSA
NWRRKAEELIRQFCSQCKLNGAVRILIPPVSSRYSHHLSVYVCFLGPTRSVASSSMAALR
SAFDDNFLAKSKEAAAARKHWGTILWEVRKVDFLKRFLLFSLERRYAKVIQRDQVLQHKR
LKVGCRVMLLRNLNRNYVNGSLGTVVGFQPLHQVEHLLPTGLKVLLPAGQYTALSHLKRH
SSHRHTAAQKKKGTCNEGHGGTIVPVVRMDSDGKEVAIPWVSLPLPWEQREGFYAVRIVA
MPLTPAYAYTVHKVQGLTFDHSVLFDGSGFFPCDHLIYVAASRVKRFSQFRMINVSPRMV
SVHRGALRFTSGIPSVSEAAKKWAAWKRTEKGMVTSQSSKEAATLSTPPSDLSLFCAEWK
LRPYGRAKQK*
>TCRU_7588 hypothetical protein, conserved
MSSTRLTEVESKINEVRHRLANLNLSFQLDEDAARPCEVHAVKDDKQNSPVLVERDLNRS
VTAKSAMPASTGDMNRLVELARREAAQRDGNHQTPQPNGRKERRRTTHFSTENLQIGLQG
HTYYDPTPAAPTTKYHVSTWAPTASFQQQPAGSAGRASLYSSHVPTSTLSCAGHRSNVPA
AAAPTPRPTSGLVGGFDPLQAVQARLREKLRKSAASRSPLSSPGSTEQSPSPKPQELWQT
GHSGALTCAPDDASNEVLPSTKQTGLKKTKGEQQEQQNVEASTPKIKGATDFIRNAKQRF
ASPGSPGVASLSQSFLDGKGHCQNRVASKPLPKDVYSRSSSAFRSESFTNPSSQKKSVQT
PRRPSSVASRQRSPCQVAQPALPRKSTPQRTVLDVLTGAEVFALMRLRGIIVSRGETGEC
TLPETRCHSIYLSPDEHKQLLDLRANLRLRHFSVKKKGDKSQPSAPRSVSRKSSSKPLPV
RRSSSALHDAPKW*
>TCRU_7589 hypothetical protein, conserved
MFAEVEFENEGGVICSAEKNGPHDSSDESRDNMTAGVVRMHRPGEVGFSCVAGTADDVES
IHDARLMNGDSWLGNECHCVRCETVRVSTQLAKLRQRSSKKAMVVVLLDLDNYGFNQFRS
VPTNVPANGGFDLIEHMYVWCFFGSCFSRYHGEFPSAESVCRSIPREGTDTKFKQLVGRR
PSVWQRLVSEGRCHFTPCGGQRQGADGVILQIARAMTHMPVIVLSGDREMLQKVCVKRRL
VGKKAKREVVERDSPGNVDIINVLEHGKRFLPVWRELESKIRCVACQ*
>TCRU_7590 hypothetical protein, conserved
MAALRSILSRREVNQFCSIGSELLSGPLSLSLEKWEAALEALEKAKNDSSILPAVASLSI
DSASTSVRHYHNVYSKCVRLMVIPLRRWQQWREGLCFFMGESSGEEAAPLATLCRQCLVS
QQECFAVAFWGCWSSVVIRLELHMTSLAAAAASEVGVEKSSENGDGDVSFEEGEEKDEEE
EGVNTEDVDLSILRLRRRCYTELYQFQRLAHDAAHLFGSYAMVGRAERQWLTDTYLLGRD
EKAAEALVRRSFKRDFGVPSADLDSGVLLDEYHSFEVNEGKEKAIAKRAQDTLKGAWCLK
ARDVFEHEMRAQNERPSKECGSDNSGNNSCELLVRCLREKVGRPDLAFAVTMRRILENEP
FPAKVDLARVEFALSLFLQWFEKYTHERHHGEIPLFTTADLWSFVLERHTELLKWVVFHY
CHDEVVADLSSALEAVKAVGFSARHCLDVYLAAMASRRLSNDVRKQFEEEARRKVCNWME
HTVVNTFLSAIQSICSEAAARAAATAATTPSFAFSPEIISVHIDVAKAQLLLLCDAAFYA
MDARRILLPVVDAGFKKMSALSVDTDLSGLSCWTFCILGVLSCLRRSVCCLRDGTLATDD
LFTALHLHYRTLQRLSPSSTADLVTDAWIDFLSGEGRGAVVGARQGGIFDITRVRHALIN
NDDIVEGFGKEKGGKRLRDE*
>TCRU_7591 hypothetical protein, conserved
MGLLLEDEDYTPPIKANRVESHTPPTTTTTKAARKGEKRDVSLSEREKRHVSGSYTNNSG
DLSAKIGIRLRGGNGIEKMDAFAFGLGRSPVTFADASPLRVRGRSSTKVLQGSLNLSDTQ

RDPPPTVAKCVMASSQDILNTVETTPNASSNSTTTQMTSSTPFDTSDGTTGSAASGNPVS
RSLFSDGAAINPDIALSAVQTGVEGNEAAPKPKVQMKLSDFFNRMACTKKSE*
>TCRU_7592 chromosomal passenger protein
MLSKNVDYFDGLRTFPRDANALRHHSARLNYTLQKRYNIPSEVADLALQPQNTEDFDRYY
RKQVMRIMAHFNAMTQRQVKVKVDPRLPRGMQIIRGSNATVPLKSGKTEKTTSDWRAAVA
SPSAKVNKAVSDHHKDLDGMEANRMITHLQPEGQQTPQGVSPVLAAMMCGYTVTDGKGTV
SSDDRSTVIQSSTKKSCREVLFGTPPEFKGFTALMEASPADSLMSKSPLLF*
>TCRU_7593 hypothetical protein, conserved
MAEQDGTSSPSPDFQVEALSSCCLSRAGSEAPHRTRESLVPSPRSCHSSCTGSEAPQRRR
RGHSLRNPPGATPRGDDRTAEFDDAVGEGVAGVSDNNGRVKKFGGWVNNTSSFYIGNDGG
KMNVISKADGHFARSKEASEMEMALYHSVPFAGGSFTLLQKLHYPFDVPETLINLRARSS
VQEGVVENAEYEATGELQATNGVENGATRSVVRNDIETIESCVSAMTMCMMPDPVYGAPV
LALCVGDANGRVNYSELDVCHTRSAQSLSLNAQKSKSNATIGSSSQTDPDLISYDASLPS
DHSFLYHDSAGFHRPPLRSHGHQAYVREMDCLTSVTISQAVKSVCFLTTQDSPHTVSYLT
ANERDIKLFRVQREGFTPFHAFPSMEAVVGRRHIQARYFPPFSPPSIILPVRVFSGCHLN
VIQDLCVCPDVHSFLSADDLQVFLWNLESCDLSKGMCVTDCRPLSGRMDEVEELVTSIAF
SPTHSSIFLVSRSSGFLGIGDLRQSISGSQCQYTTSIRVTEDAAFPIPEQYSDILCSISG
AKFLGPQHVVTRDYLSLKLWDLRRPDVPCSVAHVMSYVSPYLDVLYENDAIFDRFPIAVD
HVSGTVVTGLYDGAAAVWQPLHKGRAAEKDLLAYYRVDPQALLCEVENGGRTNVEELSAS
LERDWKTPAARGIGEMPSLNVLPTPVAKKVTCASVADGGERFALTCKDGRCLFIFERKAF
CDVS*
>TCRU_7594 hypothetical protein, conserved
MELEKGNVFGRLYPKELRDQAAKARDAQMREELESLERDEIESLRERCGGLTAACPAEDN
FGLFLSNVLGRSVVHGAVSIKTDYKSPLAQKMHADASIGDSDGSEMVKKTTREERRYRIA
CFDEFLQRQNEHKRSRSRSVRNMEKALTPSFKPEISVHSVQIAKELMARSSTTPSGSNNA
SALASAVKKHRSPYVDPCTFKPRITAVSRAMEPRGVKSMANDGVRLREWRKRQQERAAKE
EIRYPFRPTLNDAHNKRIESVLTLKNYSRYEQGLRRRKEQMARMKEEQDAIKENEEVERS
TFCPKTTRKPEYVTRMASSFALVRQQYGEL*
>TCRU_7595 hypothetical protein, conserved
MLRRSALVADSFKEHYHRVHLPRRLALQRYIRQQTLRKQAKAEPEVPYKYNRWWVNADHE
FVHQHAFVEDPEVTRAKRELLPPVTKENIWKDPQKTFFMPFAPYIRVVDYPKDPDSKFMK
PVNVPRWKDYMQRTKPVVPRTWY*
>TCRU_7596 hypothetical protein, conserved
MDAQVQVAFDGLVSCRRALEIARDPTDQLMDFGRALLRSFRMQIMMASDPGIPLPKLRDR
LHMAVHGADTFARATQPLV*
>TCRU_7597 retrotransposon hot spot protein, RHS3, putative
MPSKRNRVQGGNAKGRASVVPQGDSLKRARSDLEGDTAQLAATPIRVEEAQLRWTMCSYV
SDILLDGETDISDMKLNAFLREHFGSRAAVRKRKVDMWDFLRSPDAYIKDQQLLEEISNL
KDYQLLTDRRKLTEGSVNFLEDWIEFKEKATVTPLTRKKLTDALTQIKKEVAKWEEEERA
KRMAEENVRQDTEEKTTKLEGFYESVYGAKWGHVLGFYDDKIRKTRMEVHEGKPPQSWKY
EKKGLTFEKDDGVEQFSPPRPRLMVLTSDKGWPYSWRENKPIVDCYVNCEVDRVWRIVKD
DLKDLSGPHGVYRPTLRHRLLIGTPGIGKSMNAGSYLLYQLLHCDAEEIKLVVHCFGEGE
AYVFDKTAKKVTKYVGSKASESVVSSLPQCGVKGYIIYDVPTNEVQLPIIFEPHTGWGTI
VLASPKVRNINEFARQRVSHLIIMNYPDEMDMKAMCAWMTHDETPQEQEKYWWMVRQQMG
FLGPILRYIFDAKEFSKRYNELDRVLRSVKSRDDAKRITHGGMTAWFTENSFCKLMCVKR
ERGVFGTEDFRTDLLSRHVGRRVFFFAQRIAPLNEICSLQ*
>TCRU_7598 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MSVREGTSLQEEVPPPLGTEDIPKADVERPIYEEEATSPEWATERQTQETNAPLVENGDG
EDVGTAPGNASILPGETKIPSESNATPLSDHGILPEHGHLSDLSGMALFAESTVHGCVSR
VLLLLLLGLWGTAALC*
>TCRU_7599 Protein of unknown function (DUF3676)/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MLYNEELSEDDFLDELHDSKVTIPSLGAEKQPTELVASTGASVASESNSKESVTSHEELT

ENDTDKQEKESADAVVPAASSSTVVAESSVSKPATATESAGNSRSDDNTQLSEGEKSQQF
TPHEENGSMQRYSEVQTQDLQSEESTEATDFETSPESNDAQPPEEEEEADDGSGESTSQV
ASSLSMDTATETVYGEHQVQQSTELSTENDGLRSTGTVTTGAKESLSLEAGGRNSERKMG
SDSTLTPSKSDAEPTSAEDTDNTSRTERAEFSVENGNEVPQTVDTAPENTSTAPGETVIP
SESSATTPSDHDILPENGQLGELAAMYLLGDSTVHGCVSRVLLLLLLGLWGTAALC*
>TCRU_7600 hypothetical protein, conserved
MVGWCYTLSRDVAEALVSYKPLRRLAYLPYSKERDHEFAPLLFYEEDVMVGWVLGSVLKY
KPMVYVEMQDCHFHDARNGTGHSQVVPTSICVHHVREDDYAALMARFGNDTSLVARVEWL
SEDTIYPSCD*
>TCRU_7601 hypothetical protein, conserved
MCRHIVDKRAPSVADWAGRRQSAARWSTRSCGARVGKSFRRRQRRADHLGEERDGTTDTW
FLVIRRVRAGLAKSGQESHRACARGRHSGHDVRVNTRNRVLATPTSTCHAVCAPSFSSWN
FFRYSRFTAVRTPTCQALTQSRGRDRAMTAPASAVTLRGIPQCHGEHLKTTVRTQSASEC
GTVQISSVTPSCTASKPSGVTPSPRGSLWRQELVWAIGMLLPGGELGTVCGHAQWHDTPL
GRCMQGCQQLRGEAPQGARLSGESSGSAADPNACSARDDKPSTAKIVASD*
>TCRU_7602 hypothetical protein, conserved
MTGRVLLVCALCVLWCGVVVPAVCGLVSDRSVVEEDMVLTWYPEAEEGCEEKNTKKGKLD
VLGFKMCMHESMKEICGNGDDETPSKCRGPKTEEICKKYTGDPNKAVDSSTELPEASPDA
EKQVAAATRETPKGGEAEMGLTPGAPAGDSPANPTEGPESTSAATDTSNNEAQKGAAVAM
PVRTLSSFFLHCASATTNMPLPNFKRPGAPNDFTVTSPSSSLMPFH*
>TCRU_7603 Protein Associated with Differentiation, putative
MPTTANSEDIVQGYVEKLVSVEGQKPLTEWRRFAALVAGSFAAICASTAASFNLFSGALQ
QKYSFRQRDISAINTVGMVFCFFLLPYGVIYDHFGPRPIYVLACVLLATGALLFGLSFGD
HIEGSTVRFCVYNAMLSLGSELLDMACGLTLLSIFPTNRGGVVAFLKTLLGLGSAILGSF
YLGFFNGHPDHYFYFIIVVVLCVCSVVVPVVRLPSYHLTGYEQRHLDAEEKERRLARKSV
YLRQKAPFWRFLYGLVIVFVLIVYLPTQSALVAYLKLDRTYQLSFAIVAAVMTLMLPLMA
VPCGYLERKQMDNEGALEPRKQDETRSTEGTLPNRDDAEGKEEEKRTSLEEGRLKTPVET
DIDYIAPQYQTTFMQSICTLKLWAFFWTFFCGVGSEFVIIYNARFILGAISGERVDDAMG
ALLTVLNGVGSAAGRLLMSYFEVWSQKRKAEDRIPITISLFVPTMCIILSLLLFLVLPVN
ALLVAFAIAALGNGFCASVSILVVRTIYAKDPAKHYNFALNSLWLAAIILNRFLYGEWYA
REAERHGEILCYGKSCVLMPMLVMLGLNVTGMISTIYVHLMYSRFSRMVVAERRLLRMDS
VEPLGGEMTEVEEPRKS*
>TCRU_7604 Ankyrin repeats (3 copies)/Ankyrin repeats (many copies)/
Ankyrin repeat, putative
MRQVGAEADFFRAVATKDLTLLRRLIAAKKDVNIRGERNRTPLHMCVWDNYVDGARVLLE
AGADINVYDDLHDTPFLLAGAEGRVEIMKYMLKYAKPDLTLCNRYGGSALIPACERGHVE
MVNLLIKAGVNVDHVNDFGWTGLLEVLELGGDDLDHVEITKALIAAGVDVNLADREGRTP
LYLAKKHNLKRITKLLEEAGGRV*
>TCRU_7605 hypothetical protein
MSVVRPDIYVDVELRGTRVHPRVIIMLVAVLLVVILVVVLVYFLCRFFVRAQYSQQKRVN
ADSTNVGGRRSFQLNCDDTDIWKRTFFGIVCDNKKYVHNAAALHAVYCVPLDLRLCDPLS
NDELFMDKNCFSRACERRRMLNDVFGTFVHDVRRSSNAETVSPGPKCREASATLQSGPKS
QLINKI*
>TCRU_7606 Anion-transporting ATPase/CobQ/CobB/MinD/ParA nucleotide
binding domain containing protein, putative
MSLEPTLRDLLHSKLQWIFVGGKGGVGKTTTSCALATLFASTHVHDAVTNTTRPRRVLLI
STDPAHNLSDAFSQKFGKTPVPVNGMEETLFAMEVDPTTFTHGGFGAMLGFPGHIATDAD
APSPFAALGNILKEAAGTLPGIDELSVFAEILRGVQQLSYDVVIFDTAPTGHTLRLLALP
HTLNSTMEKLLSVEGLNTLIQAASAVLSSTTNLGDMSSLMPAFKQWRENVQEVQRQFTDA
EKTAFICVCIPEFLSVYETERLVQELMKYDISCDSIVVNQLVLKPSSEPDCRMCNARQKI
QSKYLAQIDSLYEDFHVVKMPLLSDEVRGVPALQRFAQFLLEPYDADRHGYIDVCGAAS*
>TCRU_7607 hypothetical protein, conserved
MKAKDGSEFTGPWSGAVWPVSSREHNGPHNFVSCDFTIVARVMIQNFSKLSTSLPGAGLD
APVSTSLIGLSHNADSRWETVFYGIKTASGSIWESGKAYQVALMLQDGHRGPAYMNADLV

GSPEMLRTPETRGLKSHASKLGATRETAAAVRR*
>TCRU_7608 retrotransposon hot spot protein, RHS3, putative
MELDGRGIVATNRNVLLKEFFKEPARYIRDKGELDEIQATDAYARMERAVREEMEMEEDA
DDLCEKGVDNLLRWSLAAEEVKANVHNLTKRFLDAAFIELMSSMTMSAPMKLEGCYESVY
NARWHHVVEVCDGEETGLEVREGEAPQSWNYRQLAKLSKRMTVCSNPVHCVPD*
>TCRU_7609 RNase H, putative
MQPHDGILCAAPGHGKAECPSYPAQAKTLLVVTDSHFLLAAVTKGPHSHTDWTEDQIWER
LLTLTCAGWSVQLQFCYEHCGVHVNEPADHATQTMATGQYTEHGIAPIQRTDLLTCINTQ
LTNKWRSTMHQDTHRYLPCGARPSDPGGKHIITQEALDQQEQIHTAREGCGESELWGRLY
WTVRDCTNQRRLRNISPEHSQRIRSGSVS*
>TCRU_7610 hypothetical protein, conserved
MSFVQLSSTGRVACGGSFMDIYGRRPPATIQAVYPTGLLSPPSLMSWSAFPTPKKVRARH
ASHGDTNEIAAGEHVALAFSHVADASSQELFFAVGVFRCDTWALQWAVRSDSLGDGRRVC
DVCCLSAHTVVFLLESKAGGKRGSRKQLHVASRAEVPRVARRENRQWRSFLTKAHRVEKK
FESEDVHSIQALSATSCLLLTGAGRLIRVTVSFAPHLEATSEEVEVEGGRIAPRANNTCT
LVLSSATGKEMESSCCYAAVFAAGSPTCRVMKLVSTDTAMKASNPQSISLPTGATVERVE
FAGPHILVLILALDNKTAFALHMTCLVPSESSSSSSSESLFNCVSFAPLRMTAQRVPLAT
MYCSEKETHVVLVSRRRRDDYFDGQHEHNVKNNGIIKNNESLWWRFFEYAELPLQNGPYT
EEEFRSATWCSLPEPCHTVLPSVVSRIANGDDNDDDNKENTAAHFQQDLALLTHSQSEGN
WEPIRLHYALAATFSQETASGGKNNKVAVNVFAIETAPFVHTRLVKQWHNATRGLKFLLD
GANNTVGGSEPFAVSWNPRHIRRALQLFSQEGLRVLFGRLANALRVSTETSNAASLFYGA
AATAVTDVALQAVTLSRQVGAILSPEDVTVVALLLRASRETGHLIVNSTTRGRLLLESAV
RSRLANHVLGGGEKCQKRSHGGKNTNANEEGEEDEVGAEFVHVPTELRVERALRTKYALN
AWTQHLLRKNNEYSAVVTGALQHLNAVASLQQQQQQQQKQEEQQEEEHAGRSGDGTLRPH
QDEEMTATPALLPDWMTLGRRAHANAAFAEYESALLHSTAKAR*
>TCRU_7611 proteasome regulatory non-ATP-ase subunit 5
MADVDEWRGASFKQEEDHSEATTSLLEKINATTIPVLLRSTNKSLQDLVDELLTLEKIAR
LGGDALSTQRLAVEVIRVYRVQGDYAKMLLVLEMLMRKRGQTKMTQSAMIAECAVMISDA
SLPKESRREVLERVVHLTDSRIHVELEHARFAIDLAKLMESEGQKRAACDLLSGLHVETI
TNMPRAEKLDALNCLIRLCLELEDYEHTPLVSRRINHRALARAESREAKLTYFELMRHYY
TQRKSYFNVARCWYETYLTETEEGAKLAALSSMAVHYLIAEHATPKALEDLAECTAFSPA
TYFAERNAAIQGITTKLQKQLEDIPQLQYLLQRFTSIELIREKVAREVETLCANHPQLAG
HEDRQLLLRSRCSEHDLLVVSRFYRRLRLDRLAQLVGLTPEHTEEFLMMMVASKTLYAKM
DRVDGLVVFEAKKNATEVINGWNEAVERSVALLDKASHLIVKERMLHNISAARAQQAVTL
*
>TCRU_7612 hypothetical protein, conserved
MPFRNAVSGHAGIKAASTRNEGRASSSGSVCTRTRGAILRKQTGKKIQRKLSTSPSPPPQ
KPLEMDGDNFNGGAQTKEKRLKSVPELNSHLLEECFSLNARENHSPPRLLQAQDLRGEKA
MQTQLQISLSPRTRKAVYPTGRRAVSPNALFVDNINSKGNTSPTSPLSRTWNVGAIPSTE
FSVASSYHDSYRDISPSVSKYRTAGPVVTEEWSRSIVRPQDEHLLYEGHVSWKKRHEEQV
RRIQVVWLREQARMASRRDEEHVGGMRPVAATVPLLSVSRARSMRQQHSQQQRMSSQESV
SLENEDIERERTVWMNERHILARGTPLLFTRPRSRPFESNRNSHSEWQKNRIEIPTKLTA
MATSGVGFDVDATSSLKRHFNSNIMITSILHHHSLNSSQNFLPNVSGNSDTQSPSLSAKN
KRPVLLSVDTLPPTQRSAGGTSGGEKRLSQDEDAIARPQTNFTSSSLFSDAAAQEMTRLF
DNPFFILCSDENHERLLIAQEEHETRDQLMQLHTTSVQSGHSLLTTEKTREESRAPSKHE
FSVGVFIPQGNSTRGSAAMPNEPDPMGNARKGNNHKGKNTVREAAGDIAASHFFASTVME
GERENKREEGEARYVVLDIPSRKKTAVAGRMNEHSHHRLAVMEEVIGHRSAADPGKGEAR
QDGTAAATKTRKKHQGRKETQKPKRKAAPLTTSPRNTEVPHSGKETVDTFSPPPKTQQQQ
QEQQQQEQQQQQQREAVEAMALENSPPEHKEQHQQLQNPMFRVNPSPVISPVKLSRLPGS
PSSPRTSKGAENGRARDAVGVWDITYPSTESLSRATSASRSPVRQLMLDEPMPKTTLDLE
SVNASMKSCIKTADSGVGGAAVQTSPMKRSHHVLSTGSTASKSSETEFSYQGDEQDAELQ
EYVRFALREEEGNQTKSGKGAEEDIAGLPGVLWLKQHRRLLPEGKADMQSVQNTLENVES
DREKENVRVGTDVVLGSDEDGISQSLEEIGHYALNVKSVLTAFGNLWQAPFQDTNQRDNL
PPTVQAQLLFLNQWSHEDKKDTDDVSDGEIDSKNGCSKSQNGRPLSVGAEE*

>TCRU_7613 predicted TPR repeat protein
MSGRTTRVAFNGVVCRRSVGWRAFSGNFALYRTGCRSPTDSLQQQKFALCCQHRAIGPRQ
YAPKGFREAAGRAPMTFEFGEECNELAKVAHQTKNYGDAISLYDRALTMRRERYGPIHEK
CAATLHNIGRVFLEMREPGAAENALTEAAAIYEQVEGQNSIRYAESLALLALSYTHLNFL
EEAEKAFRESIKVFRDVSYNHATNSWLPDDRSTAATITEPQKHPLASAAHALADCAQLFL
LQNQEHRAIAFLEEALEIRRYLYIRHNKYRPIIAQTLNKLCELKKSINDATGAEMCINEC
LEICIATLGRDSPATAQATSSKASLLAARRQFREARRLYEESTTTYAVALGKDSALFGLE
LVKLGRIQELCDDYITAEKTYERGVDVIKKALGPEALQLAEAYTFLGSLLVKRQELTRAI
DLFRDAVRLRKTKNRKDPQLAYLYQKLGDAYAMRRESHAEAYFLLAIEQFRENAKVEPLQ
RTFLTDVLDDLGLFYLDFHHYEKAERCLKEALDTRIEMLGESHATVAYSYSNFALLYLHR
EDTDNCEKMCKAALDMYAKTARSNVLAQADVYTTYGQCCHLQRRLQDALSWHEKALNVRR
TRGESSELSTAESLNHIARVYVSMKQYASATKYLAEAKKIAYQFTAEFAQYLRQEVAKTE
QQIPPMEEWSAEDRIAATPTLPVDNNEPREEEMTSH*
>TCRU_7614 vacuolar ATP synthase subunit d, putative
MSSNRYPALPSRMSLISFKTRLKGAQKGHSLLKKKADALAIRYRAIMGDLRNAKMEMVEQ
IRGAYFTVSKAQFIAGDIGLAVQESLKLPTYAMRLRVENIAGVRVPSFHEREEHSGDLVT
LDEKGRRIGTAGIGRGGEQLREASEKFRETLRLLVKIASLQVSWVTLDLAQKVTNRRVNA
LEKVVIPRVQNTLSYITSELDEQEREEFFRLKMVQKKKRQIQANKAREALARQANASKGP
STVQNALKMMNGNDDLGIDEADLVV*
>TCRU_7615 hypothetical protein, conserved
MENEMPRLPVWFGGAALLGGGYYAFYYHFYTPRHTTRSEIETAIEAEKLKWQSVMQRYAI
LHHMVQKLRDGGTDATNRERLYIYCELQKLREAFYNLSIRAQSASEKQTVLRDLDEVETA
NCTVLNFREEALTVGQIITCQLCFSLYVLCFCLIDPVLRRVHCEAVERVRRRGLHIVSWW
MMRLLRIPVTMTLENTLPPPDGDVNEVTREDEEYIVFSPQHWIEVVGFWACPTNPLLTNI
RVRWLLPCDAVPFEIHWRGRWQQMQQELRDPILVVKKEEENRRPVVQSSFGYPLASRLTC
GGGMQDDSNSDHVLATTDVYTPRFFPVVSTGMPRVLFVSDAVARRDVRTRRTLHEVYTNV
KHRQFPVTHNVVKNNKADDCVKGYDATYEQLHAWRKHGGVPVWHRVEWGSVYGDVGSGGN
RNRRELTFRMGRPCSANELMVRQLELLQNLLLQTESNGEEVSLL*
>TCRU_7616 SET domain containing protein, putative
MRGMPRLCLRCTRRGSLCRLTADAIGVVSVTTVTPSRYRSAHERGNLDSAKKFGKEWGIG
KARTAWYPRVRAAIDGHPGEEVVDMDRPCPDEEVYRKEAKGSSTESAAVVDEALDGQAEI
GRVDQAVDEVQAFLREKQLEVAEAQLERNVAIPYPTHPDDMTPEFRRIKRHQSIVVVATD
PDYPVFVRRDQFVQLPLPKNHPWVKNTPIGPFIQHGDGQLGVVGSGEVGFDDEHVAKALP
HSFRGLRHRSVMQQRLPEKNGKVLQDAVVKNSFSLTGRGVFATRDIAAGESIMIVRNTAC
NLGVKGEVERLVEMCGDVLLTVYEGTEADLDYLHDWVLTGQPSSLLEFWPKSATERVLER
IGGVEVLHALELHEIHIARIAAIIDMNSFLVDAVVKNSFSLTGRGVFATRDIAAGESIMI
VRNTACNLGVKGEVERLVEMCGDVLLTVYEGTEADLDYLHDWVLTGQPSSLLEFWPKSAT
ERVLERIGGVEVLHALELHEIHIARIAAIIDMNSFLVESSYAVRKGMAYFPEAGFLNHSC
APNATYDVMPEHTFHESEYYLDEALQAEASDATDPTPSAAAIEEKDETVVMDEKFSPSRR
THPSNRVEEKENGEDGNNSTASRELTVGAPVQYLFCCRATANIPAGSEILISYVPPEWSF
DNRQYVIHDRYRFWCKCPKCAPTLDAKYARVPKLIVFLLVFSVFLQLLVLHKRDVEQTAA
RENLVTEEDSTFYRDDNDEDDAPMEQRRAPRKRPRGLFELLEEERLQEMYATDRRPLPAV
LANDQWARPPR*
>TCRU_7617 proteasome activator protein pa26, putative
MPPKRLVHAQDLRDAFPEEESCGVVERWATNLVSHVAKIAEQAGSQCASIQGTKYTCDNA
EKVPEEVMSMLFNYQSACRRIYCDAELIRTVISVRIPELKEEDNLGVAVQHAVLKMLEEI
QNKTLGAGGAGGAGEKTSSVKAQAGVFSLREYFGARGAVEEKILGKPDDDKNNSKGGSKS
PSVLLELRQVDVDALQKVELSALQLVTAMRSFVNAYALNWKKLIEPRSGGGRMVS*
>TCRU_7618 AMP-activated protein kinase, gamma regulatory subunit
MRRTSAFALRSSYTVASGVSRRGGNALRVNDETQQIQDHDVFLEAEYYLNDEECQLLAAP
IADFLSRCTSYDMLGTSTQVVVLDVDVALTVAFIAAQETRLNACVLWDPTARAFCGMLSS
TDYIDILLYCHDHPDEAEQVARYTIREWREKKRDASDIRNKQILSSLSPTSAFVTCAPDT
TLIKCLQLILRHHVRRITVLANKEANDVSVVAILDLQQILLYLGAVFLSIEAVGNGRRGV
GVAAGVDDVNSLVGVSGGVNAGISPDGVDPADTDLLFAEGVLPPHVRNLLFAPNEGEGEN

PLMEFGKEPRVGPYRTIFDIPFCYVPQLGRHRAHAISVTLESPLLEALRLMLQHDIESIA
VVSEEYIIVDVINRSDIVRIEDQGVYDTELTVREAIGSTVSAKICVFHAKDALRDIFFHF
ARQRVKELFLVDPDTDKLLGQLNIAEMVFFLVFGVTTTSATGDVRGCVQTTFSSSPLLAP
TPNPARAVAAANDNDGNTQK*
>TCRU_7619 rRNA dimethyltransferase, putative
MVRVRCCNTTPTCIFSFSAGLFRCGWRSQSSSSSSSSLFSPRPGSRSRSASGGGGVAITP
LRCPGGPRVKAEGLKHLFKVPHAGYLAKYDQRFILNLKLTHQIVSHLSRTTLKTHDKLLV
ELGPGTGALTRSLLTRPCVAVLGIEADERFNAHLEQIRQYTDGKFHWVNADVLRVNELDV
LCSVFPRFIEQHRRRRSDARADETREKMGAEGNNDGDGEGYEGAPLRNSQRERILRRRFG
RSAGFNHGTASDNNRNPVNSQSTGIAAAFAVTDRWWSDGDAKVEVVANLPFDVITELLMR
YAVDCSRKQNLFVFGRVPLHVFTQKEIAERIIAPAGSIHFSRLSVLCQCFFHVQVRQTFR
EMTYYPKTEVLGAMLTLQPRSVPLVPGMDAATLIHFTDLLMKPGQRGMTVHKALMKCVPA
EVAQYMLQELRVDGALTVLDLTAEEICKLAMLWQRFLEASSQQQTNPRGEAKKGGKSAGN
DE*
>TCRU_7620 Mucin-like glycoprotein, putative
MMMTCRLLCALLVLALCCCPSVCVSDKSAASSKATTTPTSTDPVANGSVTSQSNSATGVA
PPDPGHSDLSTTGSVANPGSGGGEGPGSNSTAVLEPKVSTEPNTSMTDGTKEQQSRTETS
AEQQNKESEASAQTTTTTTTTTTTTTTEAPSTTTTEAPTTTTTRAPSRLREISWS*
>TCRU_7621 Calmodulin-binding, putative
MSGESVFNLIEPEVEVPPPPPRHYSKYSGNRAAPPTASTFGIHGTSAVVANMGGEVTEPS
IHPAKKPTGIFGRVTGPMVKPSEFLKKNEGPLTASRGAPIVNKTKFLKSAKDATKSKDNI
PSRYDKPVMGLKTEKNYVVANAVESVLAIPSKCIPPPENRAVDRVDFGKVPVYLEEVKEE
IKERHALVERLKAAQREAEERWSELSAEELEGLRQGLQRRWDALNSEYQSRGFSKIQTPL
QKAHHEALGKELNAVEFAMHKLSRSHVFVYDDQR*
>TCRU_7622 poly A polymerase regulatory subunit, putative
MKFPASRLLTDKSPRRAYVPSRADSLESVVVKGLHFGQRKLLLSEIEFLSAYLEPQKKSA
KPLLVVYAGAARGTHLPFLFKLFEKVKFVLIDPAPFCASVQELAKDEKGPILELLERYCT
DELCLRLSRSYCSNYDIILISDIRSGEPVNQSSKENTVMIMRDNEMQRSWCWSLKAKAAL
LKFHPPYPRCKDTASRYYDASDDTPDSVDYFDGNRLFGVWAPKSSSEVRLCVAGPFIPGA
KVPMRKYDCTVHEEQCYFYNTEDRYARDCEAEKEILERYLKLNYGTFSGGVISLSKEISK
FLNFPLFAPLEPSFTENDARWLTLIYSTRDPKCEEWFEPLRGLMTLEVVQNLIKTYRNES
SVPLNVTVGPITLTRDFWKVMCTGNLVEAYGLPRLHWRFFSQIVSRKSKRTSL*
>TCRU_7623 guanine nucleotide-binding beta subunit-like protein
MRIRVDIELQEPELQSIDHIKHVLKSFPEGVNIGFSTNKEALARLVNNALMKRNFESIIP
ELKDRLCHPSLYEDCLDVLCEAIFDSQRGEKGDPLDGFISLLSQLPESKQNTVKSDIVQR
AMIFLSRHRRLDCSRVPLLPYAEVLAALTKAEMLNVRSVVVALMQMIRLDNTRSAGITCL
GKMVEVAHELLLERLDQHTLETLRSTVAFAQQDDTFLYDVEYIMEPFGWSQSEKFINFAV
RLSGAHHTSAILSLAYGGGANSREAVVTSSVDGTIGTWDQSGVLTENLVLSRHYASSMDF
ANSGRILIVGTVGRHASVAPAIVLYSTDPTYNEESNWQESGGAEPRGARFITTVRSLRGT
GTLRYCCGVTTSSANSVLLYDGTQMIQEYNDHNDIVSAMHVIPDREHILVSGSRDCSVMI
YDLRMAQNTTTPSAYRHYSTVTSIGSCGDYLFTSGLDRRVVVHDFRMMGQGVATRELDSA
VLSLSVNPNMVCAASTMTGIHLINFANNAMPTCRADGGRMSPRYNAIAWNAQGNVLYAGG
DSNTLDLFTRSYPDTEAYIA*
>TCRU_7624 predicted ankyrin repeat family protein
MDDGTRIPEDVEVFLRAARARDTFKCAELLKETPSLINSVEAGGFSALHFAAFNGDLEMI
RILLEFKPNLELRNYDNNTPLIMAAKGHQNSAIKLLVDAGAEVNLRTPTGGTAAHFAASM
GYVDTVRCLVELGADVMHENSETGTLLHWAAHSGDINCIGEMIYGFKIPINVKDAHGGTA
LFTALFMKKFEAVEFLLEHGADPRVMIGGDKSTPLHIAVEHANTECVKVLLVFGADPHVA
NTSGETPISLAEKAKNNSALRELMKPMLSEEKRKEEAARFKAQGNKVFEGGENVKAAKFY
TLAIHLDSTNHVFFSNRAAAYFNQRYYNGAYWDSLRCISLAPDWPKGYFRKAATELAMKK
ADEALQTCERGLRLDPKNKDLLTTKEEARRQRNK*
>TCRU_7625 hypothetical protein, conserved
MSTICQAVDGSTLQEKCRIDLLDTVAQLTRHCETLPKKGVTVAASNLPSCTFAKTVSHSV
KKHHSQDESAVQKYIAEKEGTRERTLQASCQTYFKKHNPKFEGALPRTEPFRNTRNRNEL

TGRERDFVHRYAEAAAKKSLERKVNDDVTTQCATEAYQKAFRAYTGRDPNKKELEEVERM
WFAVSEDGTVGVIQKTHFYGPHSHVSICNRRHVRCPNQVYNAELPPVRGARTRFPGPIPV
WSSTQNTHTLVSADTYVPGLHNVSKFGSA*
>TCRU_7626 Phosducin, putative
MVERTADQRIRTTEWEDIQYRHGNRVGNYATNELEIIAQKIADENVNACLKVYDPNEERV
RDKMERGGYEKELQLGESNTGGDTADNVMDDDDEDEVLLAFRRKRMAELRQQQESQRFGV
LRHISGSDYMSEVTESSAANWVIALLVKPGNSDSEKLLSVMRVVAQRNREVKFLSMISTE
AIKNFPDRHLPCVLFYKEKKLQQQLTELTPWMSKDKQISLNSVERVLHRYGVIRNEEFEA
EEEED*
>TCRU_7627 AAA ATPase, putative
MSVDGLILSDLRRVLSEARPSPFFFLVCGPSGSGKTFVLHAVRQGAGAYGMSVSHGVPLM
DDGMEPEKTEWNDSKARIFYVDYNALRSNDSRASSISEKYPAGTVVLLDDIEAVDYLLRL
NASLHRLEDMVCRLLRSPRCALVTSATDVLHVPRWLLAMWTPFTYKMHELTSSAARRLIR
SFPDAEDLLAFVSGENGEELVSYLRTRRALTLMLCHARCEKNKSWVPTSQTALHFLGHAS
TAPQLPSSSRGKLFGLGPALERVETLVRLFMERENLAGRKLLATVAPTTGILLHGPSGSG
KTAIASRISASYPGKCFLVSCAALFSKYLGESEERLREAFRKARLCAPSVLVLDDVDVIG
TSRGAFLNGGTGDGLNVTKRMLAALLCELDGLIDNKRVLVIATTNVPGTLDVALLRQGRF
ETVVYVPPLSFEAAEEMALEFFGAFDGAAMKAREELSRLVAGRAEGCAAASLKAFLREVF
EQQQQHQEMEVNKTTRVEAGERETALFLPSEALVRATLAKTTVLQRVNYEYSFL*
>TCRU_7628 HEAT repeats/HEAT repeat, putative
MEYKSTFELRQQVLDLPTHLTSRARTGKKNSSSNPPCLPHPLNANNNGAVMDSDPDDPTA
LVRELPALDKLNALSASLKNEEEVQNYVEARNLSLEDTAKYIMANGSTGQKMSLFQRLKE
TLVGLDMSSISQVLMIAVDSMWVQEPELQCFAPGALIEVLPLLNNTVTRDLLMVTSTMLS
VKTAEVRIAWNKLFSAFIDYLNNKQLDNDVVPLALKKTEHVEPQDQRELSCDLIGAVCRY
LPHDIVERKLMNKVLALCQDTNVGVRQHMCQQLGIVARALGVDMAKEKIAPELFELLNDE
DQTVSRAAFSCLVDLVEFFGPAYRREHLYPIIKNFISHPPEEVVSLIVGEYGRFLWEIRA
DIQTSEDVTLFAGFYQNAALKGDDATRHRCAYNLPSVTASLPISVFALHLAPCCEALATD
TSEPVRRSIAAGLHELVVLLGEKAALYLPKPFLWLLDDSQKSVLNALSTHSHVLMDAFVK
QLKPTERTAFFSSVEDVLLRLVARAEREWRIMDHVLDILSTYCKEFQETNLYEKFIPLLL
KYGRNGAFCLKNRCAEMCIKIVANMSNVNSKVQFFSKLNNEYAHGSSCLGRKDYLRFVRA
ACSLFSRRFIRERMLECCFELQHDQMDMVRLELARTLPYLRRVLELSTSGSAFEEYQDMI
HRLQMDESSEVRALTQSGLEIIELRDRGLKRDAGRIKFEEENREDRRREQAEGQLLDVAK
EYDKAERRSKLRDLLKTEREKEQAELVRKSGTVRRLVKGATVQATPTKLSRPIPKTQTTY
SGGATFQKKVQR*
>TCRU_7629 hypothetical protein, conserved
MTQAAGRTAFRLLLSMRLGLLRCHSTPRTAALPVGPHRAAAGSLACFCRAECPVTEHGHR
QFSVPRRAAASRSPTRVPAAAHSLSAMEALRLHPLAVYDGVTEEICTVPLSLVYRGHAVD
STFSPRHRGIPRNVTAEADAVMVRSLPQDCVNPWHVGFLTAVRRPY*
>TCRU_7630 Concanavalin A-like lectin/glucanases superfamily,
putative
MRPVMTRGTTSTVACMRWWRNAVKDSDGLQLTGLECRAIWPVNTRSDEVRHVSLSHDFTL
VASVTIEETPSGSTPLLTAMLAITESNHTMGLSCSHNKKWETAFGGKTTTRSSNREPRKE
HQLALMLQGNKASVHIDGRSLGEEEVPLTGERPPDFLRFCIGAYGGHESHVTVTDVFLYN
RPLNSTATRALKDRVLVPTREAAPTPPEKILVVDSIREHIAEDITEEK*
>TCRU_7631 hypothetical protein, conserved
MHRGRGRTGRRLQQHAVKHHRARQQVHAAANVHRRPARVQRPQHSAAHTQLRLQQRRRVQ
HKRRRHRVRQPAQLRVAHRPRRHNRRVTDRHVRVCRQVVHKHERAVVAGQPAHAHLQAPV
TRRLAAVAPHVDLRTAVAHAVPQFDAQRAGKHRRHVEHHSHAVRNGHAVHQHRVHGVANR
DGSVHRAAPQSQHHRVRRGHPRSSCCQRQHHKQRHTHSRNDPAPHTVPAARTRAHRRPHP
PTQTGTNRAVVVCRTRPVDHNSCPTNPFLQMANPVTRFRQIVIPLLLNLTLQVIPNTLKR
*
>TCRU_7632 hypothetical protein, conserved
MACLDSVVLSGPITVAVDLRSMDAFADALNVTLCHCVLAGGAQLRIGGLSESTAHLFPHA
LVNMTNVTSLEGTIVLHGAMPLHSSVLLANSTLRATVGGSQYVPTTPGFEGFRYGPALVL

DGVRLLSTRFVMTRSSLACGGGSCAAMLVERGFVANLSSVFYMDNCVVSRTHVMYALASD
LRVVGGSVFSIQNSSWSAPSTEYGKGACVFRDVAVDGGSVLQIVSSTFRLGFVMLIAETL
TVTGGSWLVHRNNEFRSAYVVYVAAYYGMVFRDRSVWSILDNNFTYGSYSSTIAQMTSNW
SPPSDARPIIYGMCNEAKGSPVTNYQEELNIRVPVMVLDCGACTMDSVCFAARTSSISGC
ECVCAAGGYGDTCLPAAVPDGLGPLPLPDAKDTEVRCVHGGSISSVDDPDPGVHVLCFVN
VTFTAAIVLDLSHFDAPQQTLNITLLQCVLVGLSIKGSGTRVHVSVTSSMLDSGELEFRG
DFGASSQILVVGCTLVTTSDHAILFVKFTLSAKMTLLLLENYIEANRYAVYFISAVVVDG
GGIIVKGNTLSTTKDDDGVESSVCVNAVDLKNGGYFDVENNTMRSVNGIYIFGDTTVSSA
GLLRVADCTFAGGTEIFDPALVYLSASVTIEGGAQWRVEGNSVGAASVLTIQYSWQRIYF
SGSSTTAVLANNRQVEGSALFAKLFKLSIVATSPERFVVGCNLQGDEEVSYAGVFPEEVV
VFGCGTCNDDAACFKPGTELVDRGSCSCSCKDGWHGASCLPFEVPTTVVPPVPERAVDDD
TSCVVNQTLTSLTLNMWKTHHCYAGVTFSGVGAVLTFSLNRMPLHLPINITLTGCTFREG
AALQFVGGNEAAESSGVLIRVSQAVMRSSVVVFSLALPQRCEIAITEVDAVQNFEFELSG
TVYNMWNVVVLHDVVLNASTLLVSNVKAHATKHDAFGLYSTGTLALVGGSSLYVRYCSFE
GYKYLFYVYRLSVSGHSVFALLNNTMFSGVSLLYQHHGFSVSDHSVLRVVGNSGSARYAI
YNDDLWTVQQSSWLDWRDNDVEMGAMFYDSGSAFVTIDSSSVVTLTGCRMGSTGLSVPLL
SQAGAGYRFVAGCLTVAGRVVTTAAELDLNGITNVTAVAVCGECTKDGDCFAPLTTAVID
CKCQCAAGGHGDVCVPAPVPAGPPPLPPSSPPPLPSPPAPPPPPVGECISDMAYPEVAQA
VGGGLSWLCYRNVTFSGGGMSLTVLIGGMKGDVANVTFDGCTWRDGALLLLLGNANAAVG
SLNIVVTGNTFIDALLSPKGGFPPHTNITISGNRFTVTRLIPRPGLGLRRPSCVVMNGLA
ISNGSAAVFSGNVFQSVTASSSAIYVVRSALSVLWHSVFAVVGNTFHMAGGDSTLIYLEG
SRQSLSLRVLNNSAVVIRGNLVTRPVKYFMLFLWTSRVESRSAVVFHGNDMQGNLAVFYS
TFAANIYYNSWLQLNGNLCRVSPRDAFAVLSPTVNLRDSTMSVSGNRFMSNTVSPTMLLI
PQSSRDLTNGAIVAACNTVSGEEGVEYSVPSVYNVTILNCSDPCTLAAWCFPAHTTTASS
DGCACTCAEGGHGDACLPVAAPEPPSTDGSDLCVRDVRVDELVNAGLGTSVVCYVGVTFA
ADVVVDVESMSGSVRNVTLANCTFLRGASLYVVGWRSDPPAGERVDVLVFAGLARHCGGL
GADSRGACCVPRRLRPWRRVCVPRGAQRESDGERADNCANAGGGCVPRRCWRVGGWRRGA
VVARCAVRGRTVGADGAGAVRVGGGRRCGQRRLRGGVC*

>TCRU_of Trypanosoma cruzi region 5/Dispersed gene family protein.1
Dispersed gene family protein.1
MSGGLGSILEMQALGVFARMSCASAQERASTVALPYFLSLFAALDPLWMVVGNALLAAVF
GCVHCGVTAAFQRWRGVDAASAWAAMRFPSLTYVVAHAMHLGIFFGSVLSLAMPGARVLH
RVIGVVGVLYGVAFPTGVCYLIARHTGASFERYWQFSRKPLPERLLYPVGYWHPAAQQRM
YGGMLTNMRGSHVYWCVFQLSVLCVVCLIAAVHPPLGGCHVQYFCMAAVLLVGAGVVAFT
NMMRSAFLTVMRTASFVLLAALCVISAANHLAPSDGGARAYAAIVLLLTAVLLAITVYGV
VVWYAEDRHWQELREPRRGGLEALLRDDEESDEDTRKPHEMKSSSYATGTTVAFSYRPTA
QQELMAGDTRSDAQSLFDRSSSASRMINYAAM*

>TCRU_7634 hypothetical protein
MTDQTIPVTFHTYPRAHHRHGRIPQVRTWNVGALDDAALGFVARYGPQLLCVQEVCGVSM
ESTIFTGTFYTVACIYAPSRRTVEAREHMSTVLDHLVTHIVDVTFRLARSTEERAHGCSS
SLATAAYPRTKHVMHRPRRRSTSHSSQAHGAPASFSLAEHVICVRQLKPEARRSAVRGDW
EPTRTDSTLTRGEEAALACLRTGVLHKY*

>TCRU_7635 cAMP-specific phosphodiesterase
MAKHGKSLETFLSVLGNPETSEQRIAELTMQIVLKAGDVSNVTKPFDISRLWAMAVTEEF
YRQGDMEKEKGVEVLPMFDRSKNTELAKGQIGFIDFVAGPFFKKIVSASLTGMQWTVERV
ESNRLEWQRTLDAK*

>TCRU_7636 Concanavalin A-like lectin/glucanases superfamily,
putative
MWPVNTRDNNVRHVFLSHDFTLVASVTIEEAPSWNTPLLTAVLVDTWIPYIMRLSYTADN
KWETMFKYEKITKSGTWVPKKEHQVALMLQGNKVSVYIDGESLGEEEALSTDERPPDVLR
FCFGACDFDDGGEEAQSEGDWQKTSCDGDERLSVQPATEFH*

>TCRU_7637 hypothetical protein, conserved
MNQVIRSRTDWRERVVLRLAWITASRWSGIAALTPKNFTLKADGALILDWSVVPKTAKAD
PHRASRFVRIRGQDVLDIIKLCRTLQENEELTNLTTAQVTRALAPWGATAHSIERGALRH

AAQIVEVYNLDPHVISQLAMHVDPFDLPQNTVRYLGRYTTMLTQASSLIALM*
>TCRU_7638 hypothetical protein, conserved
MPGDKPSSWNLDTLPNNTTDARDPEETHLSAAMHATLRCLGMQLHLEVTEEGNVRWSHAR
TERRLCGPLRPTMREAVFAVTTRRCARYLSPAAGCFQWFRGVARREHVEQDGFTGIY*
>TCRU_7639 hypothetical protein
MESLRAVVDGRRRWRRQQFAVVAAAENTEERVNVNASNEGEGSSGGNGVESEQAQLQVED
LRTASGDGGVQPEGASLEGLKANSVPQTKASPAKEAKKVIPASSSSMRLPSDQQVEEEVE
EEEEEE*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MSGSVRNVTLANCTILGGASLYVVGWRSDPPAGERVDVLISGLESRSGGGVLVANRYPPG
SRVTVVDSVLIAEARVAYRGAYDLGAASACLVLHSVNLTGSVLTIARAHVAAVFDDAVGV
LVVGGVALSSRGALYVDGLSVQTALGLCVSVEGGVAASGGSVVAFVDSGFLLCKHAVSVR
GAVSVSGSAVALVRSEFLSTEDYAVAFYSTVSLDGGSMLLAKGNVHDGVSREMLYAAGAV
TAAGSTLSFVRNRALLPRMLSASLSLSAGAHLRVACNDAGGRVLSTAEEYAAAGFGDAGS
IDVAGCDACDRDTHCYTPGTASASMRNGVCVCACGSGGYGEACVPVGASALPPAVGTAPS
VFFREGVTVRSVFVVPAGASEVTLRHVVLDGVSPVLYVPWMARDGVRIVVQNVSLLNGAV
LYVMGSGALRGAGAAGSDEGGPVELSVCDVEALNGALVLTGTFPAGSVLTVTDSLLVAAR
PTPLVYPPGSQSSPYAPVLVLSGLRLVRSVLVVSGVALVTVMTGGRTVVVDGAVLELVGG
GVALDAAVFGGDYALYASARVVASWGAVLRVSGSQVYATHGLVFDSGVVANASAVVVNDN
AGALTDGALLVLRGSASFVSGSWLSVRGNSISGRLLSVPSYPQSAEFVQSTLTLHGNAGS
GPVVMDGTVALGDAGRRFVVGCLTLNGQALQPMEYRSAGIIGEFRPVACGVCDADVSCFG
AATRAMSGSCVCRCADGGYGRDCLPVYLPHVDGCNRTPALPPLSHTATRSPTPTWTTTWT
PTPSATQYSPTQHGPTETLQVTGTVALSPTRTPTASVSSTLWWSDVACPTLAVTTTVAGG
SLTQNDIRGGGSVVPTRLMVSLPPPFRWARDPQLGTHLSFVPVSTAQPSGFGGPWGAMLS
NATWVRNATNPSTVLELAVPVHRGYFIAADETIVIRCDAAAVSGGCKGVLLGSFTIRSDT
LPAASSALSAITGVVAGAAAVAVVVTGGLGSVLEMQAVGVFARMPCASAQERASTAALPY
FLSVFAALDPLWMVVGNALLAAVFGCVHCGVTAAFQRWRGVDAASAWAAMRFPSLTYVVA
HAMHLGIFFGSVLALAMPGARVQHRVVGVVGVLYGVAFPAGVCYLIARHTGASFTRYWQF
LRKPLHERLLYPVGYWHPAAQQRMYGGMLTNMRGSHVYWCVFQLSVLCVVCLIAAVHPPV
GGCHVQYFCMAAVLLAGAGVVAFTNMMRSAFLTVMHAASFVLLAVLCVVSAANHLAPSDG
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>TCRU_7641 hypothetical protein, conserved
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AARDRQPGDKRRASGSAARNRHGTAAQRHPRQRRHRRRLAHRPHVAQLQPPADTDRPTVA
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VHRAAPQSQHHRMHSGHPRRRRNQCQRNEQRHTHSRNGHAPHTVPAARTRTHRTPHPQTN
QISIELSWCVALAPSTVAPVQQIPSYKWQIKRHYSDRSISHYY*
>TCRU_7642 Enriched in surface-labeled proteome protein 1
MSRRVFTSAVLLLLVVTMCYGTGGAVGVAGQSDEPKFEWKGITEGDVTVELLGAPSLLNV
GSDVFAVAEAQWKKKDEKIFTGVASQPLTPETADTPEEVLKKPEDGTQVLEENASEEQRK
KVDVSRPTTAVKGSDIYMLVGQYDSKGCPNSGAGGCELLLVKGSVSSVDASKKKN*
>TCRU_7643 hypothetical protein, conserved
MCCDSEAKNPDNWRLYHLLGLEQPVTAKQVQWTFRKVTLRHHFYQAYLVLSDTDRKSLYD
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LVVSAVGNDHVDLSGKFAAYFSLPIIADVVYYLSSLVWRWPRRIRLQMEIGLNNPSCFLC
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IGVKTVMGITFDTLGAFFFNGMLLVSLYFVAVRITRGKEEVQMPLALIPVYAALLYLLCA
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SSSPTSSAFFTSSNHSAGR*
>TCRU_7644 bilobe protein, conserved
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KPAKNYAIKLREAAGQVIGKLLFALEAREPEPENKGVPAKELRLRGIKRAASVNKSKSPP
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GLRVRAGEAVTKGRTERDGETNSDNRMQSFLDQIASSDLRSFSATRQAAQGMELPRASLS
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TNGRPPLPIR*
>TCRU_7645 hypothetical protein, conserved
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ERRTELEMFFHDALAQVRREMLEERRRGTRYIGHQHSNSSSFQRTTPRLKEGEGELMLIS
NRRLRLPLPPPLQIGGSGSNTTWHSKESPAGDGNMGGPSLPLITLPKEELAVTRSSRLIP
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ILFKQLQGKSNSSKAEQCKSTGDTGDLVGSVVVNSETHTFLTE*
>TCRU_7646 OTU-like cysteine protease, putative
MKFRLRLPNSSQPVTFDVEETTPWIAFLHGVESRSGIVKERLRILSGYPPRVVDAADADL
VGSLFRQGDTLIVQEGEATVVRGLTRGRYVPPAHDKWHFIRRICPSDNSCLFHAAAYVLR
EKSRTDGPKLREECAAVVLANPDYFNELLLERPNSEYVQWIRQPTSWGGAIELIILSFLA
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DEGVIARAERFVLEEAERMKH*
>TCRU_7647 AAA domain containing protein, putative
MALPVSADYEETLEGVQEKLWYALPSIAKMRADMAAAAEKNADDAARDAPQEALVEKDPA
TSAVRKASVPFADMRQLVESLFMACHTNPIADDVEKSVKALLGDAEGGMYTWDDFLQVLR
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KTIITPFEEFVEFVKPREFPEIYDTLWGLLVPGVEESGSSGILPVEQFTVFFKWFYLQVF
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IVYGRRGVGKTAVGKALAKRLNCVHVSLEDLALEAIARAGEGDALGAELLDCVDREAKIP
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LMLQPCVLPQDLTAESRLPPITPKPEEQQGEEDSILILERENEMKRAVEKAAAELGVAFS
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QYERPSEEHSNAASPSAEEDGGTSETGKEEVPMPQQILLEKLENRMRAGSGDKDESTPTQ
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SVD*
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>TCRU_7649 hypothetical protein, conserved
MHIHQTIPVTIVDPVTSAPSPALKHIEDRTLYAYRNMGFALTHFHPALVGADCHPVVIEN
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DQDIIKSFCRQLESPFAPATHLRLDAVAVSPHASALITSCDTLTDAFLLNFVRTAHYTYY
LYQRTTNPRYLEAWGSVYGSPKLPLKRPLLLYIGVGPQEFTEGQMEESMRRSLQSLVAIA
TKRIEAPPTEPSAELMPASVRRLAEKYGVRLLQRWQMRYFMVRR*
>TCRU_7650 hypothetical protein, conserved
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>TCRU_7651 40S ribosomal protein S27, putative
MGFFDSDLSYPTVRSERMKHKRRRLVQGPNSYFMDVKCPGCNAITIVYSHATSEVQCNGC
ATKLCRPTGGKAMLTTGCGFRKKADH*
>TCRU_7652 retrotransposon hot spot protein, RHS3, putative
MVLTSDKGWPYSWHTIQDLPKDVFVNCGVERVWQIVKGDVTAWSSTHGGTDFKFERRVLI
GTPGIGKSMAAGSYLLYQLLHYDVEKLQVVVHCFGGGDAYVSDKTTRAVTRCSDEEMCVS
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IVNCPDEMDVKAMCAWMTRDETAEKQVECWKMVEKHMYLLGPIPRHIFDGGV*
>TCRU_7653 hypothetical protein, conserved
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AVRIDRRLSPEYHSPQAEPFACVRSGVRGDGAGNARLSTAEVDRILASARSLLKSVGSAR
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TLEDDLL*
>TCRU_7654 epsilon tubulin
MPREIVSIQVGQCGNQLGLKWWDVMMQEQKANPQYPDARDALFISEPVGKDGSVTLKARC
VAIDMEEGVLRSMLRGPLQGLFDATFFVSDVSGAGNNWAVGHMEYGDKYIDSISDSVRGQ
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ARNIPRIRERQKLVYWNEDGFKTALCSVSPLGHRDSVLMLANHTSIAQKLETIYERFTRL
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>TCRU_7655 hypothetical protein, conserved
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ALPPLHATPWLHSSTVVNRPPPHIPSTLDAAIFAPALPSVPGTYKAVPGVQQTLPPMPSA
SPPLLPPVLKDSPSRAVLSSRDRQYDFNTNLRSQFDKDNIDQRPKSQSSMGFITAYPQPK
EDELLARNRERQKAIEIQNENARLCEERRLQREREKQLEIAEQRQQEEAARRERQRVAQQ
ERLAMERERQESGEIMRGGNKRVLSGKSRGAQLQEDLKKQMDENQRRKDEGEERLPAIGR
KWTERATSESPPCSNGGGVNPAIVAAEREGLEISSKKSPERFPSSVGPSTNGGAANVSAL
LFQAPPPFSFGPSLYDPTRAVGAFSLAPNFSFPSATPISVPNVETKVEHTAAPSALDVPV
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GILKKSSEPSSRITVLGVSPPSRSLGAGSIGAVAAPFSGKADPDELSAEPSFFVTALP*
>TCRU_7656 kinesin, putative
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HAVVQFRVTQWRTNRITKESVELNATINLVDLAGSERQKTAKTDGKSRDEGIQINQSLAT
LARVINDISRGAKYVNYRDSLLTMVLKDNLGGNSKTFMIATIAPVSFCYQESCATLQYAK
DVRKIRNRPTVNRTFQTRSNLLELNARLKEENEQLKRHVEFLTNKCNADMYDAESNAEDV
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QGGCVGVTSLTKEIVQFHIAEMLGRAQKSDAQPREGDHELSNKVDYGIIEFELVLQRSCE
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KFGLLVPAVQLRPEAQFHSFMHELRQVVAEIAGKPQRIGGKWSVEESDVLSRLVDHRRRR
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RTTACSAVSPRKGEMEAMFFARNTTALTPLMYTKERHSQQKLSSGKGTAKTESKFGRRAT
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TGVPQLSSRISGGRSATGMSTRTNTGGSLDSPNPSMPGSVRMKPFYDPQVLKHLKQRSNS
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NAAPSVISLRRSTPRALEGTPLREQPQQDQPVVPPLCFDGIAR*
>TCRU_7657 hypothetical protein, conserved
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NLKSTQTTGDDDPAADGAATREEKQNENKVANPKETPVTATAIKNTTVTTGDGDGSTAAS
HTTSPLLLLLVVACAAAAAVVAA*
>TCRU_7658 hypothetical protein, conserved
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SDGSTAVSHTTSPLLLLLLVACAAAVVAA*
>TCRU_7659 hypothetical protein, conserved
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LLMQFKTIGLHGSAVSAISATAVQIGFHGCILLKHSFTDPDIAAQQFSYDVVTALSSGAA
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PRDERQESGAVANDSDEFVDFVDVGALE*
>TCRU_7660 hypothetical protein
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>TCRU_7661 hypothetical protein, conserved
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EKKTREASYEAELRIRVAETEGLTATLQELREQVSLLRKHRSLHGSSQRYELADESPGNS
EDHDGERGEETPKSS*
>TCRU_7662 DNA repair protein, putative
MTLMHAEKPFAASLQRLLPGLAESPTESVLTDTLLRCCHEWGVTAETELLLLLTSGYPFV
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GTTHRKLIVLSGPSNPPLCGGYVIGEDGIRGDL*
>TCRU_7663 kinetoplastid-specific phospho-protein phosphatase,
putative
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>TCRU_7664 hypothetical protein, conserved
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DAALMKKNLSTGRRLRRKVESSRTHRNAGSMSGAAPASASR*
>TCRU_7665 Zinc finger CCCH domain-containing protein 8
MGRGKGRAKGIDVTKHFFQPTGPADRVLVQISPSHTLYVNEEDLSPTQGSEAALALKREG
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MTASSAPQSSPSASTAWGRNNAVGNGNQHGSYQPHQQQHHHQPHHHRQHYPQQQQHEVMK
QKLGASQSRGSRLAGHRIHDDIHWTPLNGIINEVLLESATQQQKGKSEGGHQDLPSIANH
QNSNTTNRVDGPNFPFSGSLNDAVGDDTWVASTLAQTPLNTAIWYDGYAGLWEPTLSSGA
TTTARTEPTTLTAGENPVFLSHELNKMASAASHGEVWGSLSGSNGESTVSTNKHIEMSST
SEALKSQLLRELVGAGGDVNDPSPAETQLRSSTHRNPSISSASFAEAKNSSGLLNLLGGG
GCDTVLNDRVGTPTVFPATPSRNAHTIQHLMSLLTTE*
>TCRU_7666 hypothetical protein
MLDFIISCGINGAESGCSDFPTMGFLLRLMKEEDRENTAVDSRGAIHEQRAALSESNEPE
PPIPTLLKEKAVVPAEPLFTAATELQLPQSPAATMLGFITSSCGDGSDGFPVLQFLNRLL
GDEVVPFSQEGDTRGMSRGVPAAKSVKFATPHRLPPERPRPLVGGAAATVICWPTTQVSI
KSRSKFTPQATESEQPQGSDGVPAVWASSLESMMGPRHLFVKSDLKDDIGPPILERTATF
SPNGNISSREAQDFNSRTISSSVIPCASSELAQPDPCDTAATIKKGFTPPPRPTRSASSN
DVVGSGDRASYARRYLQRLYFRDPVVVRPANGPPQHAPGMRRKEKESVFGRCFYDFTKHI
FTPPHTSGLAAVSHLKNERRLNALSNLGMTGARQGSSRTSSCSALSQPVGHQASPRATSS
FRPRSHTRRAWDPRRPVKHQAQGPEEHKAHQDEVGGGLVVEGRALVISSRQHPPALVRQL
RRRKEPPCGQVNKKQLQ*
>TCRU_7667 DNA-directed RNA polymerases II subunit, putative
MSGENYVEGDLGPVFSQAEPLTLPVVVQLLRGRQNTDEDSGLESPAMALIERIREQVEMM
QETCADEQSVQHLMKMKLRLRGESETGFANAHLANFILDSNGNVTGMREAAEDGEIHGTL
KTARMKPFEVVSLGTLCPKSVEEALVLVPSLARYEPSDLNLALNTLDSL*
>TCRU_7668 spliceosome-associated protein 49, putative
MATFKREDLRRVFFSDLSEQCDEDIIHELCTQFGPIANITWPSIGNLTGSAQHKTFCFVD
FINAEDAKYCYEALYRSRARLFGKELRVSHASTDISIKESGSQVHNRHAVHELHEIGAKV
VVRGVDLNVTEYDLTSFFGQFGKFAVPPRKVRDVEGNFRGVVILSYEDFAFSDKVIDEMD
QKVYRDRPISVAYAMMEDGSGRQHGTPEERENAKLFLEEARKHAERIAKEQAEHEREKAR
RRRENVSWASGIDPFARGQQM*
>TCRU_7669 hypothetical protein, conserved
MLRTSDAHLADAREDRLQRALQENRQLKHELQELREKLKVVQVKFYKLTKDLKRVSPEML
QQLDDITATTLPTVRPASSGDIRAHSLRLPGAKKSTRQVFATSLPRVDAIKTGPTHAEME
SKELQRCREALRQAQLEIASLRAGAPQTTAVAENTTGTVTPVLPSALPPAVCLVLDQLRQ
DIARVTAERDQVSAERDALREQFARTRAEFESAHLLQRQQRSFEKHSFDVLNERAATAES
ARHHSELEYQKIIDALTREKDALALKLRLSEQENSERLKELSSVDPTVLIQLQNEAHDKS
KQITVLTSRMQWAQQQAETLKSECSRLVEELKRFQSIHSETKKQLFEAEHDKSLLQVRCA
RLEELEVTLRRKSEELIHMEQELLRTTGTLQSCNQETEEAVRRELSSRIADLQEMRDNAE
LRRREKESQLLNAQHQLAELRRQLELARGDAAMYREQLQKAEMEISELTTRAALAGRAVE
DLGDEHVQRALTVAAMRRTSSRRLGEAGEAEEALDMWDALKWDENWEADQLREALASAAL
DMELANTRCSQMSTQIEQSRSLLQQISQERDALLDENIEMRRRLSNVQTVFAKQQLEAYR
ATKARGVDSAHARSGLISFHIQDVECDEVLLRSLGIGEAAGAAVSFFFTLDGLRSYDTML
SPTFYSLYEPLDIRFRYDHLDRDEVTVDAIRNTTFVFQLHQVKGTTNTIVAMAEVPGVAL
LSCRELTVSERIQMLNGDGEPAGAITVEMCASHLMLPVLLDRPLGSTLFTADALRAALLS
LRSVVALRVQVFRANGLLGTPVPQPYVFYTTSAPVGLSCVRDTVVRPSSKPFTTDPVFDA
DPVDHRLVVDRELVEFIAGGAVVFILFDEQAKDVQANLGVAEVPLRALLESPQAVVRTTE
ALHPQGTISVGLSWACRA*

>TCRU_7670 hypothetical protein, conserved
MLFFTRQLLAEVTTINSSTASASGRLIRIRKKSKWIDRRSKRIPHNGKDVWLFGEQPSCA
LCHVRFRYKQDYEAHKESELHRNRVRWVETMNWWKEFGEPRYLQHAAAEWDWFEQHVLPK
KAAAMGISLEEAARHFRRATMQETPDWHGRLQPPSARSEIKEPRDQRWPSSPKW*
>TCRU_7671 paraflagellar rod protein
MRHSLPEIHKKSRSVFDSAEEDFRERDRWRTVHRVCGSAIGHDGYLKMLQGVRKKFLQRA
AYNPVDQLPRIMHPRLPIGATTLADGVNASRFSEGLRFTTENGHLTARAARVEVLQTPLC
VLEAEERQYLMDTELWERRVLHQMMVVSYVTFVLREELDELQYRECEERSNIRYEEEKER
YWLQNESETSKGVERCKAALRAKKEKQRRLEEADVLYPLSKSAHTSLVYQEPQKEPDARL
ILQRYVQLKHGLDSALTRTPSPEQQTRPCQQGEKRRGVLPPLAPQTVPASRMLVRSALRN
ALGIADYVAILEKDVEARSIIEECERKEFESILSLFEEQILLLRTWKYKRMHLKRLLYWK
GQGEERRQKIQTALEKHAMKRMPQFSSERDACVGHEKEERERIRIEESTCRELMRKTCEE
ESMRANVGALLAEHEESRTYIEEDEAVARQLWVQDLELALRISFTKECEETMSMIVPAQI
SLLQFLYRQQGAHGSQIVKIQRTFRRWKEGRFGWRITHREVGRIIQAGRDARKIQRGMES
LRSFKASLLADCRAIEDEIFAIHGVERADVLEKEFMHRVVINSQEEWEIAALLRENRQHI
VDKIILPNKSQCIQEEMDQRREVDVGEEFERNRFCSFFYRSLCLIKGKAMIQEREEAERV
FVALDEAESFRKIFDLELDEREILRIAALEREEEREEKRQLLAISLLESKYKSQRGHVEM
IFRLMCLCKEGAIEIEATDPSIRNGLFEAYLAGCLPLLEEASLHCHREYAAALQRDYRHT
IYNSSVDLLLGSEEVARHRVLQTEREVVLGIVNEVRRETGEQLRRLQEKTGAANAIKSFY
RRYKNGDVGRTGMRRFLREALAEKREKLELARIHKSQRRDIQRYRDILEEEIRLAYLEKQ
RAIEFKMQVLEYKTEPWERAELEKMERMMFDIFLSNCSYIESTSWADPTTVLRQMESHER
VSIVRAWQTAFEKVFEPKKSDFRLEIMACKLQRFWCRYSARKRQLFFVNECMQQLLREEA
RRRAELELLEMEGRVCDVLKPMEGCALLRGYLINDVPFFLEHMCFDISLEVGIFEDEWRD
RMLLLWRMRHSAFENAAAREEAAEREEMESFYFYAGVEQLQLVEDESALRDALWNERVYF
LLRILVKAERELRILIQVEFCKEVVEATECKARRDIYKAEYSTLMEILFVQLASPIAASI
TEEEARERERIMGLLEENKCPSAATPDEKNGEHISNTETSHTVDTTTDAMACTEGVAPAA
EQPMDQYRELGELDAAAFVSVETGPDAQTVETESAELDDLRDEKVDGVGDVEM*
>TCRU_7672 UBX domain-containing protein
MSDGDVVATLMAMTSCSEEEAVGYLASANFDLATAHSLYVAEHEHPPARPPAPPPPARQG
ASSPSGTSAAGSPGYTTPPYLISRLDGGVGARQEPYSTASLGRQGPLRPSNMRFPPPFDA
DADPDSALPFFVAPPFVHQGGTSFSHFCERALECDRWVLLSLIGDGFSSVCVNRDVWRYE
GASGTLEMFSIYQINASSERGEQLAHGYRIDVLRDLPTLLIINPLTTMKESRVPLNMKGI
AIDVSEVNEALLSFLGERGSPSQWEERKLATRGTGAVPFKCFGSPIVVEDDADDTPEIVS
SKPANAATEPPIEVIDISQYQVDEGEKHAFSLRCRLPKGQMTLRLKPETPAYLLLEYLAY
RAYQDQPEAYPQGVPKCSLKTGYPPREVNVKSRGVQLGTWEDVHSGDTVFLHIQ*
>TCRU_7673 centaurin beta 5
MPEEKDHGRREKKERHHRKRHRKDHKEKVPPSLGDAAEEEEDWDANRERLERICQIPPNN
ICNDCNNNGTRWASVNHGVFLCIRCSGIHRSLGVHVSKIKSTNMDKWRATEVGLMEAIGN
QRGKSLYEARLPRGMKPLTGAESELTLKTFITQKYQEKAFALENVNEVLRQYYKQTRYGK
QPRKHDTKAYRMVREQENAAKEGSASQQEDTMKALYGVNAEAISKKSKKTRPVHGIFGLV
NVPPDEYDERRRELLSHFRTVEPSSTTAAI*
>TCRU_7674 Hsc70-interacting protein (Hip), putative
MRVLSGVELEAVNRVVEHLRCHPEDLHRNEFRELREYMASLGASIPPPPDTPDVSGVRKE
ANSDDEEEYVSEPDSQRCALEPVSDDDITAYDGTDPTPEDEERAMGLKAQAAELAADGDF
DKAIELMGQALRIVPGKAMYWAQRASYFLKCTQPGAALQDANRALDLNPENVRALRVRGT
VNRRLGKWEEALKDLSEAQAVDYDEGIDEILRFVQKRTNDRRQFQQRKKEAQRLRQEALR
RQREHELREEEMKREQQQQRDQQQSGAGDFPGGAGGFPGGFPGGFPGGAGGGGMQSFMES
LFQDQELAEAMKDPEVAAKLATLRSNPMAALQMMGDPKVGPLIQKMMSKAMGGSSPGSSP
FGAGASAGATSHADAHHSDELD*
>TCRU_7675 FHA domain containing protein, putative
MEKPFYGRTGALEDARQGLPVAGSRFASARPGKWFPSLLTVPQRVLHGILEGDGVDCSIF
RFLGVACVYEELRKRHADGTRHGALLRDVLNWHQASFDEVRDCRCAAADVADGVFRPYLP
AYNICVLKEGQLLLSHAAVTRRAVTLVGRDREVNDILTDHTSCSAQHAALEVRFVYAHAE
TLDQQITACMEGREIDWGSAQDVSELCVHVREAMEKLGDGEDAWLMELQVLDLGSTNGTR

LNGERLRPFVPTTLIEGDILTFGFSTRSYVVVRP*
>TCRU_7676 hypothetical protein, conserved
MPLWTHFVNTKPEVDDNDLPLPKHRIYDDDGNLKPGETTPPRNSVSVTIAKSKASAKKST
PMTPKTRAKLLRSVGASPTAPPRSKKVSAAAVNSPPPTKPRSRTPSRSPSNSSTTPQRTG
TEEKSATPQKSASKDTAPKRSATPRKSTPKRAAASLTNGKSPARSKKRGSSKKSASPAKS
RPSRSPATRKPGSPSKSSSKKASASPRKRRSKRSRSASAQPGQKPSPRWTVAALRSYAKE
NKIDIVQEKTKAEILNKIESHKAD*
>TCRU_7677 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein, putative
MTAYPFPIIDVSPLYQNTGAVMEVAKKIDEACRTWGFFYVVGHPIPRERFQELSRMARKF
FSLPLEEKLQIDIKKSRHHRGYGEVNAEQLDPSAPNDHKETFDMGCHLPEDHPDVVAGKP
LRGPNRHPTQLEGWRELMETHYREMQHFALVLLRALAVAIGIEEDFFVPRFVEPLSVFRM
IHYPALPKTKEGRLVCGEHTDYGIITLLFQDTNGGLQVRDLSGEWIDAPPLEGSFVVNIG
DMMNMWSNNRYRSTPHRVVNPGVDRISMPFFCEPNPNVVIKCLENCHSAENPAKYPPVKA
SDWLQKRFAQTYAYRKSML*
>TCRU_7678 hypothetical protein, conserved
MVNGARAKHHDSPVGTCLFRWMRSAEGACPHSRHRVRRRAIAAVRAALLVALALAAAAAW
MSAVHAVVLRLRGGTVDRAITVGHAVDTVLLDGVSITNGVAVVFDVAAMLPGALRIELRN
CVCDGGAQIYVRGYSGEPASDRSLEVSVSGLSGDYCSLVFVHNLPAHTNVTVRDSTIVTP
GPMRYSQLSGLTDAVASPLVLYATSLLQTQLRVSNTVLGSLHAGGSAVHVGGGVDLLSSA
VVLDGVLLEASGGPTASAMHVASSSRLSLRSHSVFSVTNVSVVSSGGGILLGERLEVVDS
VLRFVGVEGSVASSLVRCDGGTIGGGGWLELHDVWAVGEASSVASLSGVTLSGGTVSIVR
CAAVGATLVSGPAITSGAVTVQCNRAGGRVLRSSGDYRLAGLPSVSVVPCDGCAAALACF
DALTASFSDCACSCLAGGLGEACLPFDVPPARAGGGGGGAEGCVSGVTLTESVTVGGGRA
TACFDSVVFSGPITVAVDLRLMDAFADALNVTLRHCVLAGGAQLRIGGLSESTARLVPYA
LVNMTNVTSLEGTIVLHGAMPPNSSVLLANSTLRATVGGSQYVPTTPGHAGSRHGPVLVL
DGVRLLSTRFVMTRSMLVCGGESCAAILVERGFVVNLSSVFYMDNCAVKSRAHVMYALAS
DLRVSGGSVFSIQNSSWSAPSTEYYKGACVFGDVAVAGGSVLQIVSSTFRLGFAMLIAET
LTVTDGSWLVHRDNEFRTAYVVHVDGENGVAFRDRSVWSILYNNFNYGLYSSTIAHMTSN
WSPPSDSRPTIYGVCNEARGSPVTDYREGLNIGVPVTVLDCGACTVDAVCFAARTSSIRG
CECVCAAGGHGDTCLPAAFPDGLGPLPLSGAKDTEVRCVHGGSISSVDDPDPGVRGLCFV
NLTFTAAIALDLLHFDAPQQTLNITLLQCVLVGLLIKGSGARVHVNVTSSMLDSGALEFE
GDFGASSLILVAGSSLVTTSSYAVAFLDFVFGSNTTLLLLDNLIEANRYAVYFSIGVVDG
GGVIIKGNTLIATEEEDGVESSICIYAVMKNGGHFDVEDNTMSAFNGVYVFEDTVVSSAG
LLRVANCDFVGSAEFSDSALVYFGGYLTVEGGAQWRVEGNKVSAALVLIIAHAQHKIQLS
GSGTTVVLAHNRQVDDSCPFAEMSLSNTLVDSPAKFVVGCNLQGDEEVSYDDVLPEGVVA
FKCGTCNDDAACYMPGTESVDRGSCSCSCKVGWHGASCLPFEVPDAVVPSLPERAVDGDT
SCVVNQTLTKITLNMWKTHHCYAGVTFSGVGAVLTFFLNSMPLHLPINITLTGCTFREGA
ALQFVGGVGVTESAGVLIRVSQTVMQSSVAYFSLALPLHCDIAVTEVDAVQASEVKLADT
ISNKFGVVLLLNVVPRCWSATSRRMHRSVMRLFFTRPGSCRWWVAARCTRGTAASMGTRI
CST*
>TCRU_7679 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MEEETPSSGVLAPALSSTPSVVSRQEVLESKIPVSGGRPEGGREHLPSNAAALMMGQAGK
ASEGSSHNGYTDGWPQHSISRDFFFESVHKEPSTANTLAGDKQHDDPEGETHACTAVGTN
SGPDSFSSTDMTPADVATAAPEPGTEPATAHHNGNVLDGAGAAPAHSSTTPGKTKVPSEF
NAAPALGSDPFDLESVTALVSVGLRCGNTVHGCVSRVLLLLLMGLWGAAALC*
>TCRU_7680 BNR repeat-like domain containing protein, putative
MIGSFRIIRLPRTASSLRSLNGGQRSPHDDVVCGRQPQGLEGGRKGESVDGGIRPSFTRV
GQLTDASGARRAGWLCQRDDRWTERRPFQPAGIFLEGGEEAGRVDLRLTDMQRIYDVGPV
SAENEKFAASTLLYATDEVRSSLVEKEWIKLYCSHEVAAADDECNIAFVDLTEKLKGVKR
VLVAWKEKDA*
>TCRU_7681 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative

MQHSIDREEDTDVLTAEGTNSSTDPATVHRNDNVSGGASAAPTHLSTAHGEAKIPSEFNA
TIPSGHELLPEHGQFRDLSAMALIGDSTVHGCASRVLLLLLGLWGTAALC*
>TCRU_7682 PACRGB
MAFSRAERKQLLRDRELLPPLAESPFGPFPPGHGSRSEAKVFKGSVVVPTASKKASATGE
KRAGGVGVRGDEATEVENVPTKVIRVGRTGTGGMTFSTFNGTGKASSSQSDGRFGDPKGP
GKAGAFKKQKIPPTDFRTHYERGDLPLSIQQAATRSLLWRVNVATLDYHFFLPIFFDGLR
ELEEPFRFVALQGCYDLLEKGGQKILPTIPQLIVPIKTALNTRHPTVIVNVLKVLQKLVL
SADNVGAALVPYYRQILPIFNLFKDRNKNLGDHIEFSQNKKQNISDLINETLNLLECYGG
EDAYINIKYMIPTYESGVV*
>TCRU_7683 hypothetical protein, conserved
MSEALTPPDSWSHGHPDVNAELKMLRGAVAQALVEARQSSDFCRGIKHDISEYFQSEQWR
RVQSGDSIESEQFIPNVMASVDGHLAEFESFIIGRVREELENKVDKDLSEKFDSYRMQLE
HIRQQEEEREARLRFILEDAVQMNCELRNEMKWCASELWDRVSAIEEKLKFMATRPHTNP
GGKDVMDLDLPNALREVIGILTLLSEGLEVERELHNEERQRWMSLMSRAVEKIRLLGERD
EALEANLQELRQVAAAIQHRFGEFSGVLVDFWHRLEMMGSPSVAVEGAACEGSLGMYSKA
GICAKKQMDDFMKKLHEVGVALRALQVEHVGFKDILDSNTVNITEIRRNVEALAVGASLI
AEERERIDREESSLDLQYLIRSTPRDGNGCEGSTGTPRRGDLSLRKQWQFAHLPKLKLLH
RKICNIPVSHAFRLWAAWASGRRQLRRDKTMVHELQEDLDTNSLGSRKYKRGKEEGEEKE
LAVGCRRLGIEVGCAKARIQ*
>TCRU_7684 Small nuclear RNA gene activation protein (SNAP) 50
MPSRGALDPFAVLVDAKREVSLAAIAARAKLSISDLRQLNPGLNSYTHLEPLPVGTLVHL
PPLLDQQGNPYGNYFTIGRMEEALRSLNARLDGLVAEEMKSLPVLRPRKILSKTERIARM
VREESVRQLAHIKEEYTECGERPSLLQFLVDVEPVRQLQSALEEEFDGRQLHLKALENVN
HGIFSKPRRHQQNAITEGSRWSVRDTSEDFCLEEHSHRWEFTFFSPESSLEVQDSWAVLS
CQTLGALLDAFECRNCLPVNMSKNAFIFIGGTFYVDNRHAGIEGENYDDLTAPIRYFQPL
KDVDPGNTQNLAFGRCPVKYMSETTFADLDVRLGEFGVIRHIGWCTHYFYLSSVQSLRGM
KRYHYEKGAYPQRVMKAPTRFVRCRMCRQFAATIACYNDELSPNSPCPYCVPCFELLHAT
DEGVVEEEKFIAIKLPDGKYFTM*
>TCRU_7685 hypothetical protein, conserved
MGRLEQRRLPKEPRRPRRANNRGKQANTPQKLRKKLKRQEDIRRVRELSKRLRDDLKKEE
ERVRESRRANMERKKENEKKNMVVQKIKNDKVIRKLSPKHRKKARIFMLHEL*
>TCRU_7686 retrotransposon hot spot protein, RHS3, putative
MIVVSSPNLDNYDKWATQLKASRIIMNCPDEMDVKAMCAWMKRGLEPDKQAGYWKMVKER
MEKVGPILRYIFDEKIYIDRLGAVNNALLAIKPTDAEKYFSLGGEEKWYSEDPSHKLVKI
VRVKTVEGVEIFLNAPICADIGF*
>TCRU_7687 retrotransposon hot spot protein, RHS3, putative
MGAKDLLLLVLGSHGALASRALEKLGLRVFMRGEFVSALLKGLNELRSSKSNEAQDSVLK
VNHQGHPTRTVGLRELEGGVTRIPMEYGVLCIPAVEDFPLVDGFFFVDSPRRTLVGLQMT
TASAHHTITSTVWLFTERLSAYFEGWDELSRDLSWEMIYIQHADSKKISKWHECDCVNPN
NKTDAEKEIVAFWDGKVHQYQFVVTPDFLSKIGEMRIQ*
>TCRU_7688 hypothetical protein, conserved
MAMVTGRVLLVCALCVLWCGAGCGFADKVVEAAAGVVASNRTDEENLILNWYVLTQGECA
NESTTGGKLNVTAERICMHKVMKEVCDAFYNKTSGVTHDRDVEFICTYYATIPEEPVEPP
TPQGPPPDSAVSNTTIDEGTPKNAPESDVAGRGEGKEDDKEHGNTKQKAVETAAVESITR
STDSDVSTEVSHTTSHLLLLLVVVACAAVVAA*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MWRRCSSTLLGVLFVGGVALSSRGALYVDGLSVQTALGLCVSVEGGVAASGGSVVAFVDS
DFLLCKHAVSVRGAVSVSGSAVALVRSEFVSTEDYAVAFYSTVSLADGSMLLAKDNVHDG
VSREMLHAAGAVTAAGSTLSFVRNQALLPRMLSVSLSLAAGAHLRVACNDAGGRVLSTAE
EYAAAGFGDAGRIDVAGCDDCDRDTHCYAPGTASASMTNGVCVCLCGSGGYGEACVPVGA
LALPPAVGTASSVFVRESVMVRSVFVVPAGVSEVTLRHVVLDGVSPVLYVPWMARDGVRI
VVQNVSLLNGAVLYVMGGGALRGAMAAGSDESGPVELSVCDVEALNGALVLTGTFPAGSV
LTMTDSLLVAARPTPLVYLPGSQSSPYAPVLVLSGLRFVRSVLVVSGVALVTVMTGGRTV

VVDGAVLELVGGGVALDAAVFGGDVALYASARVVASGGAVLRVSGSQVYAAHGLVFESGV
EANTSAVVVNDNAGVLTDGALLVLRGSASFVSGSWLSARGNSISGRLLSLPSYPRSADLV
QSTLTLHGNAGSGPVVMDGTVALGGAGRNFVVGCLTLNGQALQPMDYRSAGIIGEFRPVA
CGVCDADVRCFAAATRAMSGSCGCRCAEGGYGRDCLPVYLPHVDGCNRTPGMQLLSHTAT
LTPTWTATPTPSLSTTQYSPTHYGPTETLQVTETVALSPTRTPTASVSSTLWWSDVACPT
LTVTTTAAGGSLTQNDIRGGGSAVPTRLMVALPPPFRWARDPQLGTHLSFVPVSTAQPRG
FGGPWGAMLSNASWVRNATNPSTVLELAVPVHRGYFIAADETIVIRCDAAAVFGGCKGVL
LGSFTIASNTPPAVASALSAITGVVAGAAAVAVVVTGGLGSILEMQALGVFARMSCASAQ
ERASTVALPYFLSVFAGLDPLWMVVGNALLAAVFGCVHCGVTAAFQRWRGVDAASAWAAM
RFPSLTYVVAHAMHLGIFFGSVLALAMSDARVLHRVIGVVGVLYGVAFFAGVCYFIARHV
GASFTRYWQFLRKPLPERLLYPVGYWHPAAQRRMYGGMLTNMRGSHVYWCVFQLSVLCVV
GLIAAVQSPVGGCHVQYFCMAAVLLAGAGVIAFTNMMRSAFLTVMHTAGFLLLATLCLVS
AANHLAPSDGGARAYAAIVLLLTTVVLAVTVYSVAVWYAEDRHWQELREPRRGGLEALLR
NDEESDEETQKPHEMTSSSYASGTTGASSYRPPAPPLQPMAGDTHSNAQSPLDRSSSASR
MVDYAAM*
>TCRU_7690 hypothetical protein, conserved
MKSVRVGSQSPAAVERLATALSRRVQIVPSANATMPVLHVSVSCARSDAVLAYVSQASFL
DTPQRPKKNCVRVHAPRRCGPDRKVLPQCESPGDPKPSTCACVLPRFDEKAHRRTPPWKK
SR*
>TCRU_7691 hypothetical protein, conserved
MLADVIAGVRAGVSATRSAAVGKTSFTLAVGAGIDEANVRAHHSTFCTVLPRRQDLITSH
IEPSPCGHNVVSKGSRGRRARHLHSSVELSRGEKCGPFRRLASRCLLTPYSVSPWVLSGA
PAFYWMIGAAEMWRTFAAPSFGIFVARRVRDGFLLLHCMGCCKAMLYAMRWKYLTSLRCP
QRVGVAIPQRG*
>TCRU_7692 Mucin-like glycoprotein, putative
MMTCHLLCALLVLALCCRPSVCAKENSGEQDEVSGSTPAQPQETVIPGPDGTVPLTQAST
GQTQGENSTSQASGPGPGVPGSSGTRGPETIPIKEQATSGSSGQSGLPIPIGVDHAKGET
DSLNKPDTTMTNTTNAPATTTTTTTTKAPTTTTTTTTEAPSTTTTRAPSLLRESDGSLSS
SAWVCAPLLLAVPALAYTTLG*
>TCRU_7693 hypothetical protein, conserved
MNEESCAALLMAILDVAPSTRLQYARMLRSMLEMNRTPLEMVILGLQKIAAQSETRRARP
LTEEEMNQVIRSRTDWGECVVLRLAWITASRWFEIAAFTPNNFTLERDGTLILYWPVAPK
TAKADPRRALWFVMIRGRRTC*
>TCRU_7694 retrotransposon hot spot protein, RHS3, putative
MEVSDDTEMGMKVKEGKPPQPWTYKKVGDTLEKDDAVQQSGAAPPVLMVLTSEKGWPYTL
NVLHGAGNDFFINCEVDRAWQIVKGDLSEWSSPHGVTDFTPKQRVLIGAPGIGKSVAAGS
YLLYQLPHCDVTKIQVVFHCFGGDAYVFDKTTRAVTRCSDEDMSISELRRLRERGRNVYI
IYDVAKEGTPPPRHFAPTSGWGMVAVSFPKVTNYDEWAKQIQAARIIVNCPDEMDVKAMC
AWITRDETKEKQAECWKEVKNTCIFWDRFHVTSLMRRRLMDAVER*
>TCRU_7695 predicted zinc finger protein
MIGNNGDAELEEYVLLLQVVRDHMLRREHSGQPLVLQLQREGADGGDQVTLLLGQVMPDQ
PGIARVVPRQGDSPAVPDASLPFLADMGPLLLQALALQVLFGEQRRRMAAPLEKEAVGRL
QRMKLNCGIVARLVSEEQGVCSICQESFSTGCEVYRLPCGHMFDVRCLNQWLELTRTCPN
CRFVLQDVDQQYKDVVAPVWWRSAGENEEEEEDKKFQSINTVAGGESLARSFPPTREVVG
DVNGEAHSDHSRNPQEVFMTQQQEPQQEQPQHHLGIPPPLVQSFRTSSLVPRGSATDRET
LLEGSGGNGFFPVENVLESGLAEFEPVPPPDVPQRTGEGFHEHLIAEEIRTASSVNASRL
GEIRTVGLVNRDPQRPNCLSTNEERRSLAGACEPSLPAPTTREGAAAASSAFGRDPVNAS
FPLFQRVSADGGEHGITTFMPSSISRPPEETQRPRDETMIRNSSSNQQPPQLTAVAGSAR
NLVRVLRRQRAEEVRRVRLGNPNSNNSSSNSNGSIGDALDGNIARRQARYRPVVSRRYFS
HSLPYQSPPLPPPLLAPPQLPLQGNSEENQRRVGVFGSDRFVQHELRRLVGSRSQPGRGN
RRNLERYEAIIRGRQGGRF*
>TCRU_7696 hypothetical protein, conserved
MSMFGAREVPDDTFSSDITNISANYLNENNCQRFWQRLMTCVRESQELDVLYDCRSRMID
LRECVTRHKQSTWVFRETMATLRNEEKFRRWLKEYDESFGHPPILEAVEKVRRKLEKEGG

VDVLNPTVFHDPDVFIPREKAW*
>TCRU_family, tetramerisation domain containing protein, putative
Sk.1
MAEQKGAGVPFNSEAHSQKSYTDMCAAMQGLQPLSRLRVQTRSIEPLSYVCMISGDGMEF
IIPEAAARQSKMISSLLDAIFCLPNRGGFGDSLRNKPNPGVLAVNSINMMPRIPLEPLSS
RTLELVCRYLLQRSTGDPNSTEEFSLLGELDPLSDEDQDVVSDLLLAADFIDC*
>TCRU_7698 hypothetical protein, conserved
MGAAASSGRRVPRATSASPYDHSQAMLLVNGSVRRAARRNLNHPIKNGNVGVDLGAIRKI
DQRSQKTKAADREEIKFDNNDADPATLHILNAVREADSLPDKKASLKLNLLRGCYPLLEQ
VPPHRFEHLAVLVYQKEGDVYFAQGDKESAKTTYSRAIQIAETRVARGEKEIYMVLKRYV
LSMVGMARLWYEQERETTGFTLADKGIPVTFPEERNTPSVSSCDSSFLSDASTFSLNQEI
IKSMTPKPPRRRAGPSVNVVRLPRPTKIKCAFTAEDDFVLRSKMIRELKASPCELLLLRC
IEVVEIGHRRQSELLIPALIELAQIYEDLHLYNRSLLLVRRCLGILSVVYDYDHPWIIQL
RRRGDYLMECMEEKTMDDMATKIQATWKMYKAMCVLEEALGRPVTRHVWIPAVYHSQTND
TDFLKDFVNDLPEGTVLYGTGDFNEIFGSGDVVVENGAADGTRNTNDAHQPLDVIGGVGR
DLLPSTNLERVPSSFRRKTRAMNEVTRRSASIEETSFAAEYPPVQKEIQESVGNTFVPNG
RVVGTTQDTQTDTHVQQTAYGGVLTIRTTTITRTTTEQEVDSDEEDSIDEEEAYNTERE*
>TCRU_7699 hypothetical protein
MSNRRQSPQREQEIGNDDINGKEERELTALSPHDSLPKWGNVQYKPCRAYSVREGNNSST
AIRREISAPTGVVPAAGERGDRMKTPYAPTVYTRTVINGLFEKGAEAAAPDKAVHLPRVR
SPHRDRELPLLVYRQSVPSTSVRKFVAPSMFPHLPDDNIRDASVKKSSENEGGVGFASSM
RQRNCPNDADVLPQRALKNSQTRQEVRMPHSSGINESRVSQTYPHTSNGATEFSNGPSSA
NRNSQDNANKEKLASSKHINGKDAEEMCNTDKGNSIQSAALMPFNRAGERKNDGTLGTSS
RKGRIVSSATVSRGFTYTPSAQALSSYDEANGEAPFMPPNAIRISTTTATKTVRRVKYLP
VDEEYIDSDEEAEPTIDAVPPEFPSTDENNRNSVPSHVPSFPQSRRGFSQEGRLPLTSGK
ENGKLSRNLSKSNSLRTISGISPMSILGSYKWVCRRPVTRESFSFPEAYPAPAPVLVSPG
ESGGAGEPRFLLQRHQQRLVIGAQVDDLKCRQGNWSGFNGGKSCPSSVRGIDEARGKKDV
APTKPNTSMAGGHARPFRSLSLSDSLDDGVRSSERLTSMRSSDACSTVTQAISMDGEMGS
ALDVVVVKKSENSGEQGVATGMNEWEEECEEDVPYNMFPASPTLTIPALKASNRKLNLQL
GQQEHRSLSTSNDSRRWPA*
>TCRU_7700 Enriched in surface-labeled proteome protein 1
MVSVLLTEQLQRVKDVLATWKEVDGRVSQLCTSLSAEKDRTSTGDVCNAVKITAGLVGFL
SGNLSGDTWRDEYLGVNATVNNKEGAEASTVASTKNGVKFTGRGAGAEWPVGKQGENQLY
HFANYNFTLVATVSIDKMPEEGDTPIPLVGARAGSNGENKLMELSYDSGKKWQVLCGEKT
TTELSSTWETETQYQVAIVLKNGTQGSVYVDGQRVGGNGECALGNGASNEISHFYIGGDG
ENAAKEGVSVTVTNVLLYNRPLSEDEIAALIPNKAPTPSVVNGPSQGTAIRLSPGGGRPE
EPGESMGSSGVNGVSASTVPSAKTSSGEEESATQLVSEESSDGSKNVGGGSSAGSDAPVE
TGDRSKVQGDGSSQTPVGTPSTADAYDPNAEAMGHDGTAVNPGASASSGADGETAEGTDG
QEKEGIHAQNGDVNATALSSSLGNVSQGNNTDAGTVRENGLLPLLLLLLGLWGFAAL*
>TCRU_7701 hypothetical protein, conserved
MEAGVPVEPRVVARISLIGGVTTAPSNLLDADIMLRLMGHVITVAEQPSDSLDDIMARRM
GLSLPSCPTWPALVRCCCGDDNTVTEGIAVVYLR*
>TCRU_7702 Enriched in surface-labeled proteome protein 1
MVSVLLTEQLQRVKEVLATWKEVDGRVSQLCTSLIAEKDRASTDDVCSAVKITAGLVGFL
SGNLSENTWRDEYLGVNATVNNKAGEAASAVTITDKGVTFQGAWAEWPVGKQGQNQLYHF
ANYNFTLVATVSIDNVLEEGTIPLMGAKMNGDGNNVLLGLLYDSGKKWQVLCGEKTTTEL
SSGWETGTPQQHVVVLLKNGTQGSVYVDGQRVGNEECALGNGESKEISHFYIGGDGENAA
NNKDVSVTVTNVLLYNRPWDEVEITALNPNKDPTPPVTPNAQEAGTSSALDGKHLTERGQ
SMGSSSAGSGGASPSAVPTVSTPSAGKDSLQQVASGKSSDGTQTVDGGSFSDGEPTVETG
EGGTVQEEEIHAQNGDVNATALSSSLGNVSQGNNTDAGTVRENGLLPSLLLLLGLWGFAA
L*
>TCRU_component, putative 2-oxoglutarate dehydrogenase .1
MMRRSLFQGVYTLCLRGTARSYTDARTIRKPCQFDQIVDAQNEKYIEGMLKQYERDPTLV
APSWVPVLENLGKAPLEMPLVSNFHRPTSVETLTERERLQNMSLSWMILAYEKNGHYIAN

TNPLKYVDGVESQVFHPSTLDPTSFGFTEEDLERVFYVNFGCDFEAIFVSGDTGRKLKEI
VAQLRRMYCGSIGFEFMSSGYFDLRNWFRHQILNTLNPLERQDRLAIFDDVVRSCGFEQF
LNMKYGNQQRFGLDGGEALIPAMRAIIQTANDNEATSCILGMAHRGRLNVLSNILQKSVV
NIFCEFEGKAPKDQMMRIGDVKYHLGHRKHVQLRNGNFMDLELLPNPSHLEAVNSLVLGK
ARARQLYKNDTDCAEVLPILIHGDSAIMGQGSCYEVMGFCGLENYRVGGTIHIILNNQIG
FTTEPSQSRSSIYCSDLSKVNNAPVLHVNGDDVEACVRAGRIAALFRQEFHRDIIIDLIC
YRRNGHNEADLPDFTQPHLYHAIRSHPTLVDIYSNVLVQDGLITEEAVKAKKKEYEGQMR
QALDAAQSSQDFVKVTLTFQPASENQAEMLLPTEEDEDIPKAVETGVETSTLRKVGMHIT
TIPIGVKRAHPVLQRTYTARRKAIESGEGIEWCLAELLAFGTLSLEGVAIRLSGEDVERG
TFTQRHAVITDQETNAKYMPVATLSNKQPLVTICNSSLSEFGVCGFDLGYNIEDPSNLCM
WEAQFGDFANGAQVVIDQFLSSGEEKWQLKSSLILSLPHGYSGAGPEHSSARIERYLQLC
SDTDVVPGNFRQESAARMLEARIQKYNWQVCYPSTPANYFHMLRRQVVRQDAKPLVFFFS
KARLRPPNVSSLAEMAKGTSFLPVIDTAENEDVVARKVLFCSGQIESIVNDHRQKLRASN
HGAHDDVVLVKLEQLSPFPWEQVADVLEKYHSRNSEVEFTWLQEEPKNMGPWAYVRPRFQ
KLMRHLGIEKPGTFLKYIGRPTAASPSTGYGSVHVEEENELVAQALS*
>TCRU_7704 Repeat of unknown function (DUF1126)/EF-hand domain pair, putative
MAYTKSGVMKKEFALPMVPGMTCGEEMLRRNYHRMQAHRPKPYSVNSIKSVPIDLTRSNM
EKTSSLTKTVDDTLADDKDSRRLDASYQQTVNDDLSGRVLRFYGYTKEQVPESSIERERL
RKVVFNVFLEDNTMSVAEQSPDNSGFAFPLALKRHIVPMHDGTPITFADFRVGEPITFYG
RTYMLYDADKFTRDFFKEGGVELEPAQELPTDAFTLLRSRPIAKAHDVRSIAADSPLNIA
LLPEQVRAAQQFLEHDGEVLRCDCVWDDTEALHGVKHFFTLYYFLADGSIAVVEKDFPNS
GRDPFPRYFRRQRVAKPKGDGKFDPQTLGSLTFKEDANTVYYTDDDIRIGNVLNLYGRLV
LICDYDEFTRSHLRNKFGITAYEPIPGGKMPPAVPIGSQRREKTSQELEEMQERKLRESR
MREFADGVVKFLMRLDNAKYEDEIRRFVLAVYPADNTISIFEPVQRNSGIVGGKFLQRQR
CKRPDGELYTAQDFFVGARLNINGFSFVVLTSDERSLNYMEANRKEFSRSDINCIVRKLR
AMLTSKQTGLVDAFREADESNKCGLKMEVFLDIMGRLQLDISEQEILSILRYFDKNNESY
VSYEEFVARVMPEGATVASDDRPWEVIDRESAEKESAAFVKDPRIDEIKRQKEEETTLAS
RGAAKLLELYDQRRQLVLKEFRAVADYSTESVVGPNEFKLCVRKKLQMRGITDAELNALC
AKLFYKDAPRLSLEELTRIFNGTSSLPRNLLEIKQGISR*
>TCRU_7705 WD domain, G-beta repeat, putative
MAEELLGTFNMRLVSTPFGINGLERYTGPLNLKKTKLIQPLNLDKPVIAAGTRGVQNLAG
KGRQYASDNEKPLVMISLHHKGKLLVWDADTVQPLAICSHHDCSVVQCVVTATYLYARVE
KEGDNTDVETMVYVWDAKTFELFRRLSSHDGRVTSIAVSDEDDAKVATASVDQFVHVWDL
KKTLTGPIQKLATNGMAVVSLYFHGMILGSSSHTSLILWRAETGESLLKHKVGGTITVLR
RLYGSKCNSDKNAHQSHRPLSLLIGHDDGFIKEWTLDTSANSMMTLKWESKVHKAYVTDV
TGDGDIVLSCSTLDGAFLLLPSRGRVAPLVSYGARIVVLDSNSKIAIVGVDNGSIRIFSY
VDFLEGEGKPVVLSSFCPHTSGVTGLLLQLREDSTWDSIMCAGADGSLVFMDFTGARGGQ
WIKGLSGHSLDVLPSGNFILAPVESGGGICLFSSADLLPLPQEPELKTSHTVTAIRCVEP
MRLLVGCENGSLMIFQCVVEGSQNISFQKLEEREVPPYIARSFTPSQPDGELAVINLQKG
ILAQEGAFLVIDTKRAEMMFPIRPLTHIYPLRSSIVTFAGSEKYDYTVILQLRDGTMVQY
VGNLAQKTMPVFVRTLVGSLLADVLQGESAGLLMYPSNYILDLAPTASGKVNLTLIYAEG
AALKQLFFSTDPDISVEPRMFCDKDVLNASISSHPIGDEVLTLEPIGHADLGVAVLRDSP
IVDIFSNDGNYLYRILYTGSVSEYQAALRQRRSRSFPCDASSLNNSISFAPSSSSAACTA
SFCAEGYYLAIGYRDGLIQLFDTTRRVVFARLAVHNSMISSLWSFPGVVVSSSTNGALHA
SVVFPRVMFDDYGSSSISSAEGSIMRRTSVSISVVPPN*
>TCRU_7706 class I transcription factor A, subunit 3
MSYWATSEGRALSAGHTSRLSWCMRSGAMAISRSAMTQTELLRDRIVDVGEGVVANFFEQ
LLARLEQHGIRRCLHDDKETYEDGTNNGDKNLHHSISPSDECSMASSLRPSVKQRMEDAR
EPYYYVCVPCELQLTETSTSAATLAMLQDVHYHCSSAEHRRIASWMGEPDIDRTLQNSAK
IDPTGYAWIHVNGIPMLIPRRPGGGDMFFPLPHEAHDQERIAPSGMDGLLFATQQHTEVW
NRPLRSIYTGTKQFLYTVDNNRRICKKKWRTLKRRRNRFVLQHIPLDVYTTGTFVGDATV
PALFEITQQRLPKRAQYGAETTGYRMKYVVSDKPCMVWNDAMETGLSSFVVRNNGIYRVS
LLCAGDAAKWASQGPPPAGSTQDAHTGGEGHSQMLTVEALSQLRAASTVGRNFHVLSTSE

LDASDSLTHSEVTSYVSS*
>TCRU_7707 hypothetical protein, conserved
MLRRCWIFYCPIQYTTLSSTAGKLNEILDLRVQKTPVHSEVLKQFIRTEVMPLLAGTSVD
RRHDSSELRRFMGQLLRDSAFAAVVLRARPGGAYVNTIVDCIKHDHERMQFINKMTSNQA
SRIIEHLCRVGVNDSAVYAPLAARLDFCVLKEVGRAMFSLAEERMHQEVVSFIVPLYCGE
TWELTFDGGVGYTNQWNKNCNVFDAVRVLRVLSKSVRGVVEQQRFDAAKGTIYPLPVESI
HQLRTNLTVFIIQNSEILRGGHWINFTRAMVHFPTEFKTMKYLERHPSVLQAVDSQNLPR
RASRLGLSETVDTDDMAALGLHYVFAPVEQQEKVKKKKLQQPTADGSEKENEGRFDVPSI
DLTKLLPIIEDVPLPKAVQQRRLQLVMRAIMNDMDTLHFTDLVRFIQALRRMEGSSEFSS
SLNAAISAVSRILDNGSKNTTVYIPYDRLVNLANLLTAFRLKSCKGFVNYLFCFLPTVDS
MTVDEATSLMNALAAVAELDGVERCVRVGEQILDKVGHNFDGVTLPLVLSHPLQCAKLLR
ATVLLGAAPSSDAIKRIFGDTNEGLKVSSNLREAGASVLFDVARSLYHFSRLKTTETSWA
ETVWSKGIVGALIPLLTQLTSEFHQEVLSSRENGRSSTSYIPLAWRSSMEAVFPWVDVNL
DTVSLTTMQQRIEEVYPFLRQIAMMAVCIAEAQRKSLAKKNPVAEPLVFSSNAVVHMLFF
LLMFEHILYHGTWQAEIDSGAASANGVKEKMQKMKEDYIAILSTTVCKDEEGNGVTALSL
IDHLFSPESGRDQSHSVLDRSSILEITTNLPFSVSLVVSQGPINELFCERAVAAVISVND
*
>TCRU_7708 hypothetical protein, conserved
MQGVEDVDEKNEEQEPKEEGEEEDEIEEGEGEEQKEETRKEEAVASTTKELPTGSEEQRS
LSSGAEGASNITNPNSTPTTGDDNSKADGAGKREEKQNENKEANPKGTPATATAMKTTTA
TTGDSDGSTAVSHTTSPLLLLLFVACAAAAAVVAAWE*
>TCRU_7709 Enriched in surface-labeled proteome protein 1
MLVTLPVYSKDVSIKENEEMAKGKLHLWLTDNTHIVDIGPVSGKDDDAAASSLLYKSAGS
GDNKEELIALYEKKKVDADKTSHSLWSVLLTAQLQRVKEVLATWKKVDETVSKLCLSSAE
EDGSPENACSPTVKITDGLVGFLSGNFSNETWRDEYLGVNATCLQALLLKY*
>TCRU_7710 Leishmanolysin, putative
MDDTGKYCISERYYTMNLLTENCHCEDDVLLSAHGDVLEDEVVPAAVKLHADRLLVQPLE
GPLIVPSLTTGSVCSRFTVPAEHRSTGVANSDMAQCVAAALLVVVHSANAAMAAREHHDC
DDIDGMELQDDDGDGRTLESHWWRCHARDEWMVPIGCAGCRRGSAPH*
>TCRU_7711 Mucin-like glycoprotein, putative
MMMTCRLLCALLVLALCCCPSVCAADVVEGDNHSKGSDAPENISGENGEQNGTDRSPELK
SKDSEDESASGTQLKEATSTDVTPNSDGASDEPGKASAVDQSGKTPKLEDPVEKTTTTTT
QAPTTTTTTTTAPKAPTTSTETPTTTTTRAPSRLREMDGSLSSSAWVCASLLLAASALAY
TTLG*
>TCRU_7712 hypothetical protein
MQASSVTPLHGACRPLSSFSSSFAVSLGTAIGGERAPEAADGVRREVAAPQLSCHLTTER
GQRPAGLTHASHGSRVLELEEELRGLRSENEKLKLVEEQFWALLVENEELRRAATHTRNS
VEVCCGGGKRCTGSFPHGITGEKKAEKSWCASSCPRALGERMGLLLASELKDALPMDCAG
AVKRQLEREDFVGKYLLWLRTKQREGDFADKPNDFFFSNHGGALATGEGGGVDATFNTHP
VREENCLVSAYPQQDSYEREVALLQRTVACTQCELKEARDMLELANESRAAALQDCARMS
EQVKTLTEHLQEVLKSHKASSELRLENEALNVLVEKQAHEIKVRDQIVAEMRSLLQRLQD
MRSLEESSLSEENERARQQLLERRVISVSVLSEE*
>TCRU_7713 hypothetical protein, conserved
MLSELSDCSARSDNQEILNEEVKKEGRDDASEKYGESFESLSSKASTLTSTTSKSGSEKS
SGRRKGGSLRGDSTNREEGNAKGEAAPVSQDRKTSDEHVVNSRGSRVNNKKKVTGSNGNA
RKTSKRKKSRGKEVLKSISTLSTIYGDDTTPRSTTGGMESMIHRLKKRNYAPQGGESQVT
PGNSHASPQKTQKETNGGDSGDEPITVNTTEELSNLLAKNDELRMRLFENGRAGKYSNGH
QRNKKVENKRSTHEYRRIQKSTISVETSMRREQNRQELRGEREKLISLRNELRRKLAANK
QLNVYYSLIEDCKADIAKLLQEKRALSLVIRQNEKVLINSEAQHASDLACRRLREEIKAE
SVLTQRSLERARRDAFEAVKMYGDAAFRAKKLEEQLERANNKEKTQEVSNDPDVRKLVEE
NQRKAQHIQQLRGQLRRMRSKSPTNATHGSSEASKREAKNERAGLLKRISRLQKRVEELT
AKINEQKAHGEAEVSADSALNAVGHADDSQKPSMQKHHFASANESLTVQEKEARGESTLI
EEPSRTSEGTGLLSTNTSCEHTQSSVDKALEELKRRVGETRLSVETPATEQRSSVTSTPG
AAGPAPDHTSVSEDLHALSDKLTQPSLADVKNDTASTVKDEGELESGTSGEKEVEKSEKK

DEKSTVPSWFDNDDASNGDEPHTGTGNSANEVGLPVSGHNDVKDAGVHKNSLAEAPASTG
KTASLQAEEEEEEDDVYAEIDETKLTGKSESDAKVESDVVPPSSKNEPSWLDFD*
>TCRU_7714 heat shock protein-like protein, putative
MSNLYDVLGIHHEAEDDAIAKAYRRQSMAFNPQCNPNHPDPKALEKQFKHVSQAYVVLSN
PKARGIYDMYGEEGVRHGGTGNQGVPGGIDLDAIDPYEVFRCFFGVDNPFQVIGEISGLR
NNQHNFFSTSAVIPKTLVKVPPIEVSLSVSLEDVFYGAMRRATWQSHHVRQGQEIITEES
FDLRVPKGAHAGDRFVVDGKGNWKEGFARGDVVVVLELLPHDRFRREEDDLVVVMPITLC
EALCGVTLTVKTMEGVDITVLIDEIVHPKYRRRVAGQGLPRNEDLSNPRGDLIVECDTKF
PGFLTLEQKSELRRILDVK*
>TCRU_7715 hypothetical protein, conserved
MVNEEVNGVATVARRLWPATVQKDEDDAAPNVRWEKDLAFPTFRPLRQEEIVKNSFSLDL
REGAGMEYLVEKLIAQNEKLQEVRGLLDDLCKELSEARDISSKAYLTARPGSCRITLPAQ
KAITSHHGVCAVSHVQEEFPASLVSEHAPHWSSAEMQAWKVASLPQLFSLRKKLFSSLYG
VSDAITRKTLDGINVPGVLMDAQREADSAIQAAMHRLLGEAFYVNSLEDVKDFCTLAESL
TGSGVETFDRALLEIQQLTENGDVLNSCEKFQTFLCRAPSLLTPRWRDRYLCAMRNLLVA
FSVNSREAELLNARREELERITQQEMIHAAFLRAAQGRDVISQVPLCCFCSGGLSTERSP
EPETRRHLPDRKRLRTPKAKCLVFDADASRRMVSPRLENGRRCAACSLKVPLNGAKSARD
RESLCLTFSSGKRSCVNVAGNPLPRWWAAKRSQFCSRLTSPNSLYQTPEALRPMPSASRN
LRKKTPGFLSFGPIRAFSADDIQKTGKHAPLTVFSRGVQAFAPSSRPVAWQHTVRNSERT
ILPTRFERREDGFRSPDTVVARRCATHGRE*
>TCRU_7716 hypothetical protein
MEDALDESSGGGTITDTERHFTTVHPLNDVVTLQGLTAKYQKRQIQLFQDADIPENTEKV
ATSMFSEKYISNKITRRQVLQSDAVLKEVLATYSIDLPIHSLIISDEDGEDGAAFSDELK
ADMRADKLECTQPHPAYCFYQTHEKEGGEANSLIDAKKYGPQLQLFFFVEKFHQKLKSAW
SSGEKVESLRIAIRVAKFLSKVEMPSCYPSVYVLVAQVLDTFGNLVTQRIQNTAAEKSYV
VSVLLQKGIDAADDLIPSESVEACYNWFLKISSICELIPRVCIELSLLNCFRFMAKKARV
VSEEVIRRLAMQIRGIADPLVAAHLRWYLCTRAMVALVRPGWATKSGLDQAVIDTLEALE
HLDPALLEKLQNRHNMGRMDYLDLFIPALQWQMDTILRYGDANWPNYQPLLRNVVSIIVE
NLNSPACLLLCVWRAFPAAVLLSCYSVEELLSITFRSFPSRLVSRLKLMEALCLSLADLS
EVPLARAQRLAFLKAAWDYVEEERCRRSSVGTEGVALPAPKQGLVGELIGVCGAMMQFCA
NHVGFKQVNVFLGLVRDIICDVKMLENEKSLEAVKASLFGMLSALVSVVNPLLLLESEHV
VTLLQQLASGDRRRLMFVFLRQFVSGALGAGSSFSPFAMKTVFRLCKIFHDDLINVVSFD
ELQEGTKVVEKVFLLLLKRVGSLEDALQLMCDARHHLSRFDSIKIISVNRALGLAGRFAA
GCAEGKKHDETRALLMFSIVTIPAVTDLIQRFHLLALSSGMALRSGMIVIGEAALEFALE
GLETYRSSCSGKDETRKRSQEESDIADVAVHLLELGVAAPAKGEHLYAVRRLLNWSAGFD
WMPCSIPCVHISLSALRLMTRALQGRFLSFPFCQTEHYGKDPAFVESCVALSLEATHQLQ
RWIEASCHVVSTKSELATDLSTTAIEIFETLAIFDNKDPPLGPALTTLVCAAWRAANAWA
ILSGSLEVSRHILRTARFVQEVVGTSVFEEILLH*
>TCRU_7717 hypothetical protein, conserved
MDCEEELDSERVGRRYAGDFTPVGSSVDSERHTMQEIACGSFPCASVGEVNNGGFVENPP
EEADDVAEGGNSFLKAHRSMALESEARKKGNAENAERVQGRTLLAEETHSPPLTALFGLS
GTPKVSSRDSSMRRNRRGSVQFINFSSTASDNTMVDHGASMDHVIVRTPVQNPNTCKGFL
QAYFSQSAKGCYLRASWRDARVRKPCLNGTHKRHSSYNIYNCVVGDALKISVGGGRSTSC
PVRFPRAETSGTSCAGLEQSPFQLPLEHQNFSAPSTGCSTKCSMNALRRQVPDELLQYRL
AVQNAKNGRYGLSIRELLANPDFVEDDEEEQGEDSVAICENY*
>TCRU_7718 Enriched in surface-labeled proteome protein 1
MDDSEKNVLLGLSYNKEKKWILLCGGRENKEHSSHLETENSEHVVILLRNGNQSSAYVDG
KLVGSAEFECENTKNKEISHFYIGGDGGSAEGQEGVSVTVSNVLLYNRPWTEEEVGALNP
NKAPISPPEEITAAVVMDTPAKPRQMKQETLKENIGGGSGGVSSAASTATTPSSDVDPTV
VTGGGDTMLGNGSPQTPEVSASSGGHVETAGVTDVREGIRPQAGELNDTALNSSHVNLSQ
LNNSDGGTMRGSGLLPLLLLLLGLWGFALL*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MVVFGCGTCNDDAACYMPGTESVDRSSCSCSCKDGWHGASCLPFEVPDTVVPPLPERAVD

GDTNCVANQTLTKIALNMWKTHHCYAGVTFSGMGAVLTFSFDSMPLHLPINITFTGCTFR
EGAALQFVGGDGAAESAGVLIRVGQTVMRSSVVVFAAALPQHCDIAVTEVDAVQSSEVQL
LDTRRNKFGVFLLVNIVLSASSFLVSNVKARATMYGGYGLYSTGTLTLLDGSSLYVQYCS
FAGYMHKFYVYSLSVSDHSVFALLNNTMSSGTSLLYLRHGFSVSEHSVLRVVGNGGSVSN
AIYSLSFFTVRHSSWLDWRYNDVGVGAMFHYSIITTVNIDGSSVVTLTGCKMGSTGLSVP
LLSQADAGYRFVAGCLTVAGRKVTTAAELELNGITNVTTVTACGECTKDGDCFAPLTTAV
IDCKCQCAAGGHGDVCVPAPVPAGPPPPLTPPPPPLSPPPPPPPPLPPPPPPPPPLPPPP
PPPPPPPPVGECISDMVYPEFAQAVGGGLSWLCYRNVTFSGGDMCLTVLIGAMTGDVVNV
TFDGCTWRDGAVLLLLGNAHAAVGALSIFVTGNTFSDALLSPEGVFPPHTNITISGNRFT
VTRLIPRPGLDIRRPSCVATNGLAISNDSAVVLSGNVFQSVTASSSAIYVVKYALSVSWY
SVFAVVGNTFHMAGGDGTLIYLEGPRYSSSLSVLNNSAVVIRGNAVTRPVKCFVLLIWAL
RVESHSAVVFQDNEMQRSSVVFFGGLSWLCYRNVTFSGGDMCLTVLIGAMTGDVVNVTFD
GCTWRDGAVLLLLGNAHAAVGALSIVVTGNNNAYATVGALNIVVTGNTFIDALLSPEGVF
PPHTNITISGNRFTVTRLISRPGLDIRRPSCVVMNELAISNDSAVVLSGNVFQSVTASSS
AIYVVKYALRVSWYSVFAVVGNTFHMAGGDGTLIYLEGPRYSSSLSVLNNSAVVIRGNAV
TRPVKCFVLLIWALRVESHSAVVFQDNDMQGSSVVFFSSYSSNIYYNSWLQLSGNLCRES
PSDAFAFLYPKVNLRDSTVSVSGNQFMSSTVLPTMLLIPTVSSDITNGAIVAACNTVNGE
EEANYVIPSVYNATILTCSDPCTLAASCFPAYTSTASSDGCACTCAEGGYGDACLPVAVP
EPQSTDGADLCVREVRVDVKVNAGFGTSVACYVGVTFAADVVVDVASMSGSVRNVTLANC
TFVGGASLYVVGWLSDPPAGERADVLISGLESRSGGGVVVANRFPPGSRVTVLDSVLIAE
RRVAYRNAYDLGDGFACLVLHSVNLTGSVLTIARTHVAAVFRDAVGVLVVGGVALSSRGA
LYVDGLLVQTALGLCVSVEGGVAASGGSVVAFVDSDFLLCKHAVSVRGAVSVSGSAVALV
RSDFLLTEDYAVAFYSTVSLADGSMLLAKGNVHDGVSREMLYAAGAVTAAGSTLSFVRNR
ALLPRMLSVSLSLAAGAHLRVACNYAGGRVLSTAEYAAAGFGDAGSIDVVGCDVCDRDTH
CYAPGTTSASMRNGVCVCVCGSGGYGEACVPVGAPALPPAVDTASSVFVREGVTVRSVFF
VPAGASEVTLRHVVLDGVSPVLYVPWMARDGVRIVVQNVSLLNGAVLYVMGGGALRGAVA
AGSDEGGPVELSVCDVEALNGALVLTGTFPAGSVLTVTDSLLVAARPAPLVYPPGSQSSP
YAPVLVLSGLRLVRSVLVVSGVALVTVMTGGRTVVADGAVLELVGGGVALDAAVLGGDVA
LYASARVVASGGAVLRVSGSQVYAAHGLVFDSGVVANASAVVVNDNAGALTDGALLELRG
SASFVSGSWLSVRGNSIRGRLLSLPSYPRSADLAQSTLTLHGNAGSGSVVMDGTVALGGA
GRKFVVGCLALNGQALQPMDYRSAGIMGKFRPVACGVCDADVHCFAAATRAMSASCACRC
ADGGYGRECLPVYLPHVDGCNRTLLRPPLSHTATLMATRSLTPTWKPTPSATHYSPTQYG
PTETLQVTETVALSPTRTPTASVSSTLWWSDVACPTLAVTTTAAGGNLTQNDIRGGGSAV
PTLLMVALPPPFRWARDPQLGTHLSFVPVSTAQPSGFGGPWGAMLSNATWVRNATNPSTV
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VAGATAVVVVVTGGLGSILEMQAVGVLARMPCASAQERASIVALPYLLSVFAALDPLWMV
VGNALLAAMFGCVHCGVTVAFQRWRGVGAASAWAAMRFPSLTYVVAHAMHLGIFFGSVLA
LAMPDARVQHRVIGVVGVLYGVAFPAGVCYFIARHTGASFTKYWQFSGKPLHERLLYPVG
YWHPAAQQRMYGGMLTNMRGSHVYWCVFQLSVLCVVCLIAAVHPPVGGCHVQYFCMAAVL
LAGAGVVAFTNMMRSAFLTVMHTASFVLLAALCVVSAANHLAPSDGGARAYVVMVLLLTT
VLLAVTVYSMVVWYAEDRYWQELREPRRGGLEALLRDGEESDEETQELHEVTTFSYASGT
TVASSYRPPAPP*
>TCRU_7720 hypothetical protein
MHECIWDACQVTDTASSSGAHTHAELLRLPSTSRRRDGARVVVVVGASVVVFLGASGAVV
VVVVFAVVSEVSSPFLFSSVDGFLLLCDPVVPLSPSLRRLSVLSSDCANIPVKLFPSSST
IPGPSPDPEPDDPEWSATGDFPTGAGANRLVALASA*
>TCRU_7721 hypothetical protein, conserved
MRSAEGAFPRSRHRVRCRAIAAVRAALLVVFALVAAAAWMPAVHAVVLRLRGGTVDRAIT
VGRAVETVLMDGVYITNGVAVVFDVAAMLPGALRIDLRNCVCDGGAQIYVRGYSGEPASD
RSLEVSVSGLSGSYCSLVFVHNLPAHTNVTVRDSTIVTPGPMRYSQLSGLTDAVASPLVL
HATSLLESQLRVSNTVLRSLQAGGSAVHVGGGVDLLSSAVVLDGVSLEASGGPTASAMRV
ASPSRLSLRSHSVFSVTSVSVVSSGGGIVLGERLAVSDSVLRFVGVEGSVASSLVRCDGG
TIGGGGWLELHDVWAVGEASSVASLSGVTLSGCAVSIARCAATGATLVSGLTITSGVVSV
QCNRAGGRVLRSSGDYRMAGLPSVSVVPCDGCAAALACFDALTASFSDCVCSCRAGGVGE

ACLPFDVPVARAGGGAQGCVSGVTLTESVTVGGGRATACFDSVVFSGPITVVVDLRSMDA
FADALNVTLRHCVLADGAQLRIGGLSESTSRLMPHALVNMTNVTSVEGTIVLHGAMPPNS
SVLLANSTLRATVGGSQYVPTARGLAGFRCGPALVLDGVRLLSTRFVMTRSTLVCGGGSC
AAILVERGLDVKLSSVFYMDNCAVKSRAHVIYSIASDLRVVGDSVFSIQNSSWSAPSSKF
YESACMFRDVVVTGGSVLQIVSSTFRLGFAMLIANTLTVTDGSWLVHRNNEFRTAYVVYV
LKENGLAFRDRSVWSILDNNFTYDSYSSTIARMTSNWSPSSDTRPIIYGVCNEAMGSPVT
DYQEELNIGAPVTVLDCGACTVDAVCFAARTSSVSGCECVCAAGGHGDTCLPAAVPDGLG
PLPLPDARDTEARCVHGGNISSVDDPDPGVRGLCFVNVIFTAAIVLDLLHFDAPQQTLNI
TLLQCVLVGLSIKGSGARVHVKVTSSMLDSGELEFKGDFGASSQILVAGSTLVTTLVHAI
AISGFTLGANSTLLLLDNRIEGSSYAVYFSIGVVDGGGIIVKGNTLRATEEDNGVESSVC
VFAVVRNGGHIDVENNTMRAVNGVYLFEDTVVSTAGLLRVADCNLVGSAEFSDSALVFLD
GTVTLQGGAQWRVEGNNVSAASVLSMPRSQQKIKLSGSGTTVVLAHNRQVEGSAAFAKLL
PPNTIVASPARFVVGCNLHEEGREVLYDGVFPEGVVVFRCGTCNDDAACYMPGTESVDRN
SCSCSCRDGWHGASCLPLEVPDTVVPPLPERAVDGDTSCVVDQTLTDLTLNMWKTHHCYV
GVTFSGVGAALKFFFNSMPLHLPINITLTGCTFRGGATLQFFGGAEAAESSGVLVRVSQT
VMRSSVVVFALALPQHCDIAVTEVDAVQSSAVQLFDIRINILSVLFLRNVVLAASSLLVS
NVNAHSLRYGGFGLHSVGTLTLERGSSLYARYCSFAGYKHLFYVNILIVRNHSVFALLNN
TMSSGAGLLLQQHGFSVSDHSVLRVVGNRGSVSYAIYANNLWTVERSSWLDWRDNDVGLG
AIFYDSGSPFVDMDSSSGVTLTGCTMGSTGLSVSLLKRVDAGYRFVAGCLTVAGRLLTTA
AELELSGITNVTTVAGCGECTKEGDCFAPLTTEVIDCKCQCAAGGHGDACVPAPVPAGPP
PPPTPPVPPTPPPPPVGECISDMVYPEVVQAVGGGLSWLCYRNVTFSGGGMSLTVLVGAM
AGDVANVTFDGCTWRDGAVLVLLGNADAAVRSLNILVTGSKFCDALLSPEGVFPPHTNIT
ISGNRFTVTRLIPRLGLGLRDPSCVAMNRLVISNDSAVVLSGNVFQSVRASSSAIRVVES
SLRVSWHSVFAVVGNTFHMDGGDSNLIYFEGSRHSSSLSVLNNSAVVIRGNLVSRPVRYF
MYFILSLRVESWSAVVFQGNDMQGSLAVFYSSDSSNIYYNSWLQLSGNLCRVFPSNEFAF
FSSKVNLRGSTVSVSGNQFLSSTVLPTVLRIPTVSSDLTNGAILAACNTVNGGEEANYVI
PSVYDATFLTCSDPCILATSCFPAYTTKASSDGCACACAEGGHGDACLPVAVPEPPSTDG
TDLCVRDVRVGVEVNVSFGTSVVCYVGVTFAADVVVDVESMSGGVRNVTLANCTFVSGAS
LYVVGWRSDPPAGERADVLFSGLESRSGGGVVVASRFPPGSRVTVVDSVLIAEARVAYRD
AYGLGDASACLVLHNVSLTGSVLTIARTQVAAVFGDAVGVLVVGGVALSSRGALYVDRLL
VQTALGLCVSVEGGVAASGGSCSTPLAP*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MLSVSLSLVAGAHVRVACNDAGGRVLSTAEEYAAAGFGDAGSIDVAGCDACDRDMHCYAP
GTASASMRNGVCACACGSGGYGEACVPVGAPVLPPAVGTASSAFVREGVTVRSVFVVPAG
ASEVTLRHVVLDGVSPLLYVPWMARDGVRIVVKNVSLLNGAVLYVMGGGALRGAGAAGSD
EGGPVELSVCDVEALNGALVLTGTFPAGSVLTVTDSLLVAARSTPLVYLPGSQSSPYAPV
LVLSGLRLVRSVLVVSGVALVTVMTGGRTVAVDGAVLELVGGGVALDATVLGGEYSLYAS
ARVVASGGAVLRVSGSQVYAAHGLVFDSGVEANTSAVVVNDNAGALTDGALLELRGSASF
VSGSWLSVRGNSIGGRLLSVPSYPRSADLVQSTLTLHGNAGRGPVVMDGIVAPGGAGRRF
VVGCLTLNGQALQPMDYRSAGIIGEFRPVACGVCDADVHCFAAATRAMSGSCGCRCAEGG
YGRDCLPVYLPHVDGCNRTPAMPPLSHTATLTATMWTPTWTPGMSLSTERYSPTQHGPTE
TLQVTETLALSPTRTPTASVSSTLWWSEVACPTLAVTTTAAGGSLTQNDIRGGGSAVPTL
LMVALPPPFRWARDPQLGTHLSFVPVSMAQPSGFGGPWGAMLRNATWVRNATNPSTVLEL
AVPVHRGYFIVADETIVIRCDAVAVSGGCKGVLLGSFTIRSNTLPAAASALSAITGVVAG
AAAVAVLVTGGLGSVLEMQALGMFARMSCASAQERASTVALPYFLSVFAALDPLWMVVGN
ALLAAVFGCVHCGVTAAFQRWRGVDAASAWAAMRFPSLTYVVAHAMHLGVFFGSVLALAM
PGARVQHRVVGVVGVLYGVAFFAGVCYLIARHTGASFTKYWQFLRKPLHERLLYPVGYWH
PAAQQRMYGGMLTNMRDSHVYWCVFQLSVLCVVCLIAAVHPPVGGCHVQYFCMAAVLLAG
AGVVAFTNMMRSAFLTVMQTASFLLLAALCVISAANHLAPSDGGARAYAAIVLLLTTVLL
AATVYSVVVWYAEDRHWQELREPRRGGLEALLRDDEESDEDTQKLHDLNSSSYASGTTVA
SSYRPPAVPLHPMAGDTRSDALSLLECASSASCSVNYAPLDR*
>TCRU_7723 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative

MSVTCGGREHVAADNTDEVSERNATGHKSLVLENGVAGSGFVAEGDADGLTQRNASGRDN
KPQLREFTAQYSGSGICPDDCFALHNDAKLRLRELTVDGTVRVCVYWALLLLLGLCGVVT
VL*
>TCRU_7724 translationally controlled tumor protein (TCTP), putative
MRIFKDILTNAEVVCDNDRPMDVEDEIVYVVKGSYIEVGGEDYGIAANVDEDAGEGAKGE
VDDSRQRVVDVVHNNRYTETSYDKNSYMAHIRGYMKQLLERIEDEEEKKKFQANAAAFVK
RVIKEIDEYQFFIPEGNEEDPDNGMIVLCKWDGEVPYFYYWKDGVKGERV*
>TCRU_7725 hypothetical protein, conserved
MKCEVVVLCGCGTQWSSAAVLDLRSGGQKYLSLMRVGRAKGRSSDTVQGVIGVLWLEDAQ
SAAAHSVADENPVVSMRDADVVREISMWLQKRRSSLKTASPGSGMVVAAFPSIDEGAVSK
HKTPRTSSIYQ*
>TCRU_7726 metallo-peptidase, Clan MA(E) Family M1
MKEQRHHQRGKKAAGDGGGDGEASFRLPRNFVPRRYDLFFAPRPAKGIFFGAAIVTVEVE
APLASPTRCLTMHALELSIEPPHVSVMPSPGRRGRRDLSGEVEKQAEAEEAEQLRCVAVH
TSCVDETITLEFSSCLPNDVGDVFVVGFSHFTGFIHDSGASCGLFYSNSYDTNFLSTHLE
PTNARLLFPCFDEPSYRAVFQLTVEFDSRYTIVSGTRVVREELVEVDEEMFAASFRDPPL
FCSWDALRFLARDTSNNINRDSTGVGHVVVRVDDGVIAHEYANVSTNDINFGPAPHTPEM
RGGVVVEGEEEGEENVSKAAGQQEGRCNPPKNSRKNDPLVSSSNDSPTCFIRRVTFDETP
KLSTYIVGFNTGKFYIIERETTKSKLLCRVIFPAEVQTNHGWYALDLLTKAVAFFDEYFD
FLLPLQKLDLVCLRCFSFLGMGNWGMVNMHLDYMLVNESTPLERRQRIARLIGHKVAHQW
VGDWATVSWWNFLWMREGICRCLEFMFVDSVFPDWLIWDEFLTQVLDDALVLDTQPEKTH
PVQYCNANPRLIEDCFDSISFGKGASIMRMLFSLLGGDCLRAATRRLLQRCSNTCFDSQM
FLDCLLHGEHEAERREMAAAVVRGAEKSGHPLLYVEQNPDGVCCVTQYQMPDLRQGILQA
YVKLQQGKETTNAMDLMAPRRMRVFNWNAEHVLQRSNYSVHAKIVELEETGCFFGRTFCM
RSSQEIIKCFPDRLIYLNYHGTGVLRCDYDTATWRRIFEVAPFLSSQDCIVITMTLFRFR
NIHIGQDATDRMDRCELLLEWLIFITQSSVMTASQWSYITHQIEYIFYMVRDYPCWELFS
KFVCSLYTPLIRRGSLSFTAQEQAVTFESRRDISRTTVLHILQVLAICNCPVILDESREQ
VERALVSIMPQFANDFARGTFTTHNSVAFNVFNDSDAVAVSIAMQCLIEHGDMKTWWTLA
CVVAAIFNISLQKTAEELHLDVVEGIYVAHLDEMHKSRWLNMIAPALFAFDTSSTLPFLL
LVLHNFKSLNTPIAKAILRNKRLVTSLFECPSLVHSMPHITVIRHLLIMHGAMLCSDSNL
ILLMMASVAGEATPERSGGSNGRGKQEPMRAGGMARSLPVANAILAMKTNCLWMDYCCDH
YDSFLSKRFREKQLTTTPLGTPRASVMDMDAMEEDGVST*
>TCRU_7727 Zinc finger, C3HC4 type (RING finger), putative
MSAPSGSPAFAPYVPGRVPSQSKQHHTAASSNANRNSCSSSLPSLVPSTSHAREALDGGN
YVNPGPSQRATTTDLLQVIEQQRKDLLARTDSVNAIQRNFERLSEMYRGDRAELEKLREE
VQRLRERDAAGESELKVYAAVRAELEFLLESHKELQETRRQEQQKFKSNANEAREQMEKQ
QRLITQLQGECEQLCRVSTEGEEKLRRVTSELKELTGEVVQFAREVRGRVNSMPVETLTH
NHSQEMSSNERNMSDAGCTVRAALTDAWDSVDAVCVALRKAHVSMDQMAKRRIERHNVSL
LNLMQQIETMVREAVSQEEAACRETIYARRQCSLQEIHEQNECLLRQRVQEELALTRGEV
QERGKAHDSIVSNLERQVTDIKKCLQDAQAEYENLQQRHQTGVTTLSEIFQQQTLQLRGE
MQELKTQHERELATQRRLHESKLQALREQHMLALQKLKESFVAEYETKESVWQGRLRKLN
EKLTQCTEWMHATRSEMKKVHAREKTTCDFLDASLVAANRAHGESFLRHEATAREGLMEF
EEAQRLSLVRQASDACKAFSAAAEWKAETRRVASFNAVEKDEATRRFLILLDAWATAPVV
ECGRSLFEPRLQEERRLAVKAMCSSQHASLEAMRLQLRELRRGTLSVSQSLHDMRQEHSR
LSSSTLELTRRLELSCAASTSFFSQQQRQQQEERGKTILTIRALMQKLMTVEEAAESAYS
CGICLQVCRNPLTCVPCGHTFCEFCLLNHPRNRISTGNTAQYCPECGLATCNMVVRVRAL
ETLSGNFSFRKKGTKELQRVLEALATQ*
>TCRU_7728 hypothetical protein
MLIKLICDDSCGFVKRLGASERCVAWIVEEDLPLSDAAQIFSLNTAIAEGHRDPGNNNNN
NNNNNNNNNNTTVEVADLSDYVIFTPSSGEPIDVRRTPNELGLRNGTTLRLARAAEQPQSR
MRAPSDMSRSGTQQQQRGRLTPPPQSNTEDDTDEENDEFYASRQIGWFPFLLRPREGEPL
ALISDPLRPVRETDAEPNTRPLCETCGALISHGDALRVAVDRHYKPMLMHQDHLEMSMEK
LGGGHLRRWQSRFIQMSEKSIDWFAEKPRPGTKSRIHGHRYLVRNGHCHVEAIIHNPDPE
TYTYCRDKNYYHFAVIFREPRKMYFFRVPSEQQRAQAIGFLETCIKRLLDRAPVRNPVTW

KQRVDQFLANAAQLGELHTTNRMAIEALQMKTQSLEDELAEALEVKPKLLAALSTETSYV
QTLREELAGYENDVKRAQERVKAEESRLAEEQRLLQDLEAELGDETYKVTVLKQYALQQR
EEAKKRVAELRERAAALQEEERAVFCRWRRLEEQHRAQQETSRQNGLYSFSEDGVGIPSG
SPRLSMELAASAARLTLSSESVCSLSPPLCSPQRPLLFSTSRERES*
>TCRU_7729 Concanavalin A-like lectin/glucanases superfamily, putative
MEAARVKSGYDFTGPGSRAIWPFDSREHGKNHGFVDHNFALVATVTVRLVPYVSTPLLAV
CLGDSKSTKIIGLSYGMNKRWEKVFNGTKTSQNGTWEPEREYQVALMLQDGKKGTVYVNG
QLVGSPENTPTPEMRGG*
>TCRU_7730 zinc finger CCCH domain containing protein 17
MSRRKPNLTLSTPETTLQVLDMGLDFRSYLSRVDDSGIPVLGNVISYEASKIPDVFEPTV
GLLVTILHMYTQSTSTASAFVWLKTYESIQKVYLDHVDQENNETARYATEARLAILSHLS
GGMVTDGSGLYEKLLLLLDQQSGIRGAQAPSQRKVPREPKGAFCNLHLADQKCYQDFACN
QLHLHEAGPVRHRINFFMRLIEVLKAEKRSKMQILHRIKDSIFFARYGNKVTVQCHGKWI
PFFKTVYTDGRLEQAFRMQQFSCNNNGCSDEHCKGIHAQERRVVSSSRQVDLHNPQALAI
QVEDEGQHLLSLAGVYKNQVSEPPPSLSLSSPMVTIASPTSELWRSTVREYVRQTGIPQL
QADESLLRTLQDANVVGTPAASTESLTPLLDELELHAFNSNTSPRNES*
>TCRU_7731 Scavenger mRNA decapping enzyme C-term binding, putative
MAGAGENWFFGRPKSGVFKNTPIRVVNKSPLIRGSVSDFFTRKGGKCAREVLFSNVRRCR
ICKKPCAVSLSACNRCNASLDAVPVTETPNLFSAFMLGIENSGEFPLQISIRYETESCLV
FDDPLALSPVHFCAIPTTNFIPDWRYLLCSPKEGLDIVQGLVDASHKTFREQFLADPEWK
SSILRVSELVEAEHTLLGFNFPPSQNQLHLQYIVPPLLPHQYFMFARGQHFTPKRFFPLS
YVEKCLGDLTERAKPLATYHSLLTIPIDELIDTLDKECGLSYESEHEKFISRVREVQNRF
GNWTEDKFHGVYRLTENDESKRGKLLFKSFSEAISYIDENIAFAEEKEKLQNYGRPYDEN
GKPNGGFYAFPKSLEDIKVWS*
>TCRU_7732 dynein heavy chain, putative
MLTKRKNSADFLQSLQKIVNENDHKPKSHLDAKIELELSRAASPTLLYSFQKPEKSIYEL
RHTALPASKRIKRKGEQMMRSPPREFVSSVESCKMGSVMTALSLWDSQLEEKDSDILRMI
QKAIRPPVKKSIDRVAPNDENALRNLKTDEDCIAFFAAYGSRSQVKYVYLERAPQVLEFR
PYDLSVCSAKRGVEEREHYIMSATGVVHVRPGQPSEVVSLAEWMRESSLFDVLRRIHFFK
TYLVYKALLRWHKNYRAKQFLRTRKSLSREFLLSKATFSNPIVDILKSSYELTMHSPILY
EAQGKHDYAIEEFRVQQSKQRQKTITILGACIDHIESDVTKLIEAMKRKADVPDLNTREA
LEQYLLANAMVSGTKSIRSQRKMKSMHDAREEQFQRMRELKRSIVEYSQLDEFIRLVDCI
ISETVFRTTLSSVQILFNTLRNQGTQELRSIGFQVLLQSTETQLLFNPGEKSIRGVCVET
ISGCTEVASSIVRLCNQKHLNAYFSKIPSVWNMGQVLEADARMLFLQESILQLVGHDYAQ
ANTKMQTYSITLPHIHFLEREWSDILAEWEEETGENPLSSSTLGKLYIKLQEAHDALRVL
MASFVGYTLWINAAKLKTEIEPRMRVIRDCIDATLRSITRDAISALQVYFKQKSQILSER
PVQIQDFAEYVANYKAIVNEAPEIETKLAQADALCDLMDRQFVEFLEDEDKQLKERTLGS
NGSTSMSLRIVFDEARLQAEAFIEENLFVHTRTLEESVASVDEECLGIRQIISGDEFAIL
TDNIEPIIQYLEDVKIKIAELEETEKQFTRYAKLFDAPAIDWSSFNEMANFVSLRYETWT
LLDNFIRNREQWFTCSLNELDTHAMEDQVNAMVRQAVAINRQVQEKGCEEEVTPHLLLEL
QAIRNSMQVIHDCGNKHMTPAHWNIVLKAATGSDNRFHEGLNLQTLQEYNIMDHKEILAE
QSGYATGEWKIVNDLEKIKQTWHDLSFETIPYKNREGVFILTQLEDVIQQLDDHQIELQT
IMASRFVAPVRERVEEWIRNLRLVDDVIDEWITLQKNWMYLEFIFSSDDIKAQLPEESAQ
FTAIDELFRTLTMRANAAKNVYQICTGNNVLGEIKDSNAAIDHIQKKLEDYLETKRVAFP
RFYFLSNDELLSILSDVRNPKAVQPHLSKCFDSIAALVFNGEGCSEIVGMLSGEREEVEF
EKTVYPVGNVEQWLCQIESMMKASLLMHMRKTVEAYPQRVREEWFFEHPAQCIQAVDMVV
WTGEVEQAINSGSLEQYHESYQRQILRTVELVKQSLTKLQRTLVCTLIVLNVHSRDIVQT
LNEGNVTSLGDFAWAQQLRYYWEATGAVNSNMSVAIRHCGAHLWYGYEYLGNQPRLVITP
LTDRAFLTCTSALSMNLGAAPQGPAGTGKTESVKDLGKALARQVVVFNCSDGINYKTMSR
MFAGLAQAGAWACFDEFNRIELEVLSVVAQQMLDITTALAQNLERMDFDGHPIKLSRNFG
VFITMNPGYAGRTELPDNLKALFRPICMMIPDYALIAEIMFYSEGFADARTLARKMVQLY
KLSSEQLSKQDHYDFGMRAVKSILVLAGGLKRQYPNESENMLLIRAMRDANVPKFLREDT
VLFMALIKDLFPTIAIEESQNDLLLRYVKEQMEKEGLQVVDGLVTKAVQLYDTLVVRHGV

MLVGQTYSGKTTVLRIVQGALTQLKLDGHDPEGATPLFNRVHIHLLNPKSVTMGELYGQV
NEITREWTDGIISNIARGVTRDAQHSADRQWIVFDGPVDAIWIENMNTVLDDNKLLCLFN
GERIKLPPTATFMFEVQDLAVASPATVSRCGMVFLEPYYMDGGRGWIPIAKTLIAQKAAL
FPRFRAERMTELLNQFLPMSLDFIRKECREWIVSVDAQLAVSCIELLTSFIRTLDDESLL
PNVLRSKDAQMKPDEDDDLLPKQVEKKVSHAAPPVGEPDEFRPPTITDETVPTNEDALFD
MYFLMSFVWSVGGNLSEESREVFNRFVKKRFVELLPDKMSMDDHLSVYDYVVHKPSMRFV
TWRHLVPSFFFRFDVPYFELIVPTVETVSVTTLLGVLVASSRHVLINGVTGTGKSLSMMN
FVTSVLHGDDPSSHWDYFATVLSAQSRARDIEDRLEGKLHKTRGNALGPSPGKRVVFMID
DLNMPALEKYGASPPLELLRQLITQGGFYDKRKAPASFKEIHDIVYLAACGVPGGGRNEM
TKRLVSRFHLLCQPVFSEYSIRRIFGCILHGFFSAWEEPDVKNLSGDLVNAINQCYNRIS
REKLPTPKRSHYTFNLRDFSKVVQGIMQVSPHSAPTREIVLRAFVHEVSRVFHDRLIDEN
DRQWWWGALGEVTSNVLQMPWDPEFENVLFGDYMRRDRAMYEEIVIGDSLQETLGEYQKN
YAIDCNKTIELVFFKDAIHHITRMCRIFRQPRGHALLVGMGGTGRQSLCKLAAFICDLPV
HEVSITRTFSMTEFRDCMKTILLTSGCKKQPVLFFLSDAQIIWEEMLEDLNNLLNTGEIP
GLMQEEDVDQIVEAVRPLATAAGKKETRNVIFSYFVSLCRDNVHVVLTMSPVGEPFRRRL
RMFPSLVNCCTIDWFDQWPVDALNSVASLIFTHLTLEEEIKERLIELCVSIHVDVQERSE
EFFEELRRHNYTTPSSYLELLTCYRRLLSEQSEQISGQVKRYQGGLDKLQSTQVLVDEMK
EQLVQMQPKLLQAAKDTEEIMEKVQHEQGTAQMVRAECAKEEEVAMGIRHEADGIRAECQ
VELDKALPILRAAENALAELRPDDIREVKSFQKPAARVVLVLEAVLILLGERDLSWDRAK
LVMGRMDFIKDLQNYKRDELTERVVRSIQKYINNPDFQPEEVAKSSKACKSLSMWVLAIN
NYYEVVKVVAPKRERLAEAEAKLKVANNALFEAQERLKGIENKINELKRTMQENIEKKER
LEEDIQLTMVRLDRAEQLMSGLSREQSRWSTAIEFLLDETKGLPGKIALAAGFVAYLGPF
TAPYRSRMVQKWWEKCKELGVPISSTTFDLTSIVTPLQLQQWTNKGLPQDPVSIQNGVIV
HKSKRWCLCIDPQGQANNWIRAMERNSSLRVIKLTDPSYMRVLENAIRMGLPVLVENVEE
TVDATLDPVLLCQTYRSQGRLLLKLGDTELDYDPSFRLYMTSKLPNPHYLPELQIKVTVI
NFTVTQGGLENQLLADVVRYEYAELETRATKTVMDIANGRNQLKEIEDRILHLLTSSTGN
ILDNEPLVNTLKEAKETSEAVTTSLEVSERTQKDIELARNRYRPVATRGAIIYTVISQLS
GLDHMYQISLDFFKKLFVQSLQRTEKSDDVDKRIALLLPAMTLNFYSTVCRGLFEKDKLL
FVVMMFVQIFRPEGVVREVEWEFLLKGSEGRSLVDPETDIWPAWMNEAAWNELTALAEAV
PDVFAEIKDNVYDNEADWSNWFSSDKAYEWFPDSIQFLTPFQKLLVLKACREDLTSHGLS
FICAHYLGKAFTESPAFDLEACFADSSPTAPIIFVLTPGSDPTVLFTEFAERKGFGDKKL
TLSLGQDQGSKAEAMIQQGSSEGMWVYLQNCHVYESWMPSLERCLEELQISSKVHNNFRL
WLTTMPTSSFPVLLLQSGVKLVKEPPKGLKANIRDSFSIEVTPELWDSHPENSIPWRRLL
CSLTYFHAVIQERRKFGALGWNIPYQWNQSDFSAALHSISEYIPEDAAVQLPWNALRYMV
GIINYGGRVTDFLDTRSLVNILEAYFNEDVVQPGQFNITADGVYCIPAELESLDVMKEYL
ANLPPFESPELFGLHANADIMYNRATVRSQLAAILSVQPRSKEAMGRTPEEKVLDMVDEF
ENHLPPLIDKSQASSETYQITEDGTMISLGTVVSQEIDVFNAIVKKLRRTLLELKRGIKG
EVVMSLQLEDMFDACLLGQVPQVWHEGGYLSRKPLASWFQDTLKRVEFFRDWNDHGIPMS
FWLSGFFFPQGFLTGVLQAHSREHKIPIDDIRFRTNVTRYELVEDIVTTPTSGVLVHGLF
LEGACFSLDSLVLQESQPRELYTSMPVIHLDPVRLKEYVSTGETYECPVYKTCARAGALS
TTGLSTNFVVLLNLNAGAATPEHWVRRGVALLCMLDD*
>TCRU_7733 hypothetical protein
MAFVAVRVINGVISGKREQEAGERLLDRLLKALPNAEVIPPTVTDLLPLVDRHVSAGNGL
LWVDCGYSSSDEGSLLTAPVDRRTPKYIGNDALGWYGGGFLPALIQLLLLREEVGISKNF
LHESAFKASGKIHLRWFAVRSFDTPVVDLVAPFVPIHKERDASQELDAGATVSPLAPLEH
LIIYDVRGFVEHLERVVVTPSFSRAREHLSHVFWLTLRGISYVVCIVHDTHTEFFTKALT
CSDHLCGSQGHPLSFLHSIQSVKLGLSFNETLCQTPSTPRGSTSPNWGWCVRVGSHQWED
PLDFVSLLQRLLDVPTCREATVALPRDCSLAASKPTRGAEHEEVKPTQRRRTTVRRITPA
EPQIASLSSEAATKEDVLPDGSNGTSLCASRCTSRTSSEKALPRNSLYSPRLGVVHLREQ
IILEKERLMHAELEAQRAMERHALLEREEHTLQKEAATINGNIEFLRHAIEAEEKRMQHV
SGGNLSEETRLQRHHEEDKERREKSPQFTPQQISEHYENVRKQLRRSIQSQMAALAHQQE
EEESKMEHFCEEQAEQRRLETARSHEELRQIQEDINASTKELQCLEEEETREAFNSQSHR
VGNEASIERTHVTQKDMDEARALMLQKKRHELLLLEEKARRLQEVVEMARESVRRISSVK
EKKERCITRPTTRTFHSYDAPLHVALRLSVRRTLKEEEKLCRARIEREYMECLMSFWKQW

QGEVYCVTLNSPLTKALRAARANYTSLQEEWEKTQREQMGSQQDVERELEAVKAYSAALR
RDLGDMQKRHNACLSEQRRIVEELQHVLQSEADTVLRHITAVVETLLCEAGGESRSAVDD
IRDGRKSNVRRALQTVLTTGCHQVSRHYRQRRQKKTQGTVQDKTHMPISEASLLLIQETC
QEYKKLCEGILERHRLEVESCCLADSCHAKEEILSVERNGRRNGQQTVNATGCDGCEA*
>TCRU_7734 hypothetical protein, conserved
MSPLSFRSRQPFLLVLCTLLLLQFSFFFSGTIVQPVTAARHVLKTVVHHAISYDRRLSNS
ENSVVSFGSQVSLLRGSIALFNPANIASHRKQTVFIPTEQHMTTGQWEMLQDLPVRGIVV
ALSPVDAHNENFFQYYLARGIMRFPVYFLPQDGVAARRLTETLKNLNASEYAVISVGESE
KAVAPVTSNAVMSISLYASLNFRPKGVKKSSEVPRVLITASFDTLGVAPSASTTGGASGV
AAALELWRRFNAGASLMADSKGDETSEPPSLPFGFSVLLGNTARFNYVGTSKWIASREEG
EIDQYQLVICLDELLLSDTDGDDPESENGNNNDATNLFMHAEESFAKSPQFAVVKETAEA
TAARHGIALTVLSAKTNYHHYDVQFEHEVLGHLQIPAVTFSSVRTYRIDQAFRGGRAPIP
LSSINHTAGTISSKMPNILVALNRRVEFVYAFARAILGHSPANGTRTWVGSAAYMMGQLR
HASELQRGPVFSEGAGSLKYAETLEAHMKSSAATFASRHAVSTSVSVSTFRLKLPGVVLL
GPYDQVMSLFVSRTLIVELALLVVALVSVGIFALFEFGAEKTGRLLFDEFAPSLPGKEA*
>TCRU_7735 electron transfer protein, putative
MLTSHTSRSLAWRLHAVPAACRVICGGGSKIQSGSARRGIIYSSGQEFVPFLTTTLFYAI
RLHSDFTGDREKQLTIHVQLPDGTTRDVKAYEGQTLLDVAMEEGLPIEGACGGSCACSTC
HVYLENDAAMELFDDPTDEENDMLDMAFFPQSTSRLGCQLKLVKEKHDGLKIQLPRATRN
MYVDGHTVTPHH*
>TCRU_7736 RNA-binding protein, putative
MSGSARNLTFTPLGEGRAVTRSDRDLVSTSIIIDNTCRVYITQIPLERIERDGANALRAE
FEAFGPVESYKMFTEKSGRFIGSVLCTYRNPADATAAVQNMNGQQIESSVLKVSLSRDHG
VVLLHRAGPKGRRGNGIDGDEEEGRWQHDQYQALLNGDLEDDTVGSYGYRRSGRRRRGGR
GGIRSVDDAFERYIASRDREAMEKYQKTTPSDGDKVSKKEEKDIGEVSGVPSNENVDDGK
VASTSLPASFGGEVENQ*
>TCRU_7737 hypothetical protein, conserved
MRPGRPFKKKKRFPAQWQQKPSARSPSNARKIDDASRFDFALPPIKMPSSKPNMTGCGLA
TQELRRTIMQLTGGDTGTDEALKGLSHSGLGSLPDTCVDNITLGTDGETWTVAHLKRNAS
PVMSFEHDTVHLEETARRQGELVVNDTPWYFPPLKISLLRQRCCYPDDNVLFPRPTLKQF
STLSNCSDATISLNSSSTSNDGEEMVERDGVSDDAEDVKWKPSSRVMHRNKKRKPLTRSR
PFNGASLGVNKKIITRDDAETSRFRRLRERRFMNSIHQWCDKVMLVSEGERISNDPVAQH
EMCMVTVRKEEEALQFVMQLERHQAIQDRERRRQAREREARQKRCGLFSTLKDATRQNNW
RRLLSSWSEQEEEKKDGLEDENKAILRGTEERLLVAVPPRLMIQGTDTSLTRGTNVVYPL
LGTTPSVAIPMHRNRDKRASCSPVGEMQRLLEVISRHSAGTLTRVKSSATFSQNSTLYTP
IPSREGALFPPQSSVYMHTNWVEQIIHADDLPGLKHLTQWLCERAGFVEKTAYSAFLKSG
QQNVTGSEPFLNVTDLSCASFLLPLRLVFNVHGALERDILADAVSLISTRSSVLQHGSNN
SAKSHRKPSPHGRNCLSDAGGIEEDEAEAFDLRERLLKAGDFVGEPPRPYEALVGYAMDV
RAILRQSEWRSLAMKRLAKEEGVEVKRRILAKVVVTLSIHAVMSGQNALGYTKKPELIQS
IRVKDDGMYGSTSGNTDTVDVNRFVCPVKSLLLSSPKKMPNHEVLLVAPMQRAYYAVDTR
QMYFIAASALKETNETLLPILQSLRLQYRDLSQKLMESVSSSGGFLSTRPFAFSFSESEK
VTSQTSDVIKLFQLEAKYSEILATIHRNECAITHYNLHVQSYCEFLRKNKETWGTLYLRT
LRLAYAFCVLVLELGGLPIPPKYHPFLGPVLQLVGCHGGQKELRFRIEDYLLELEERAKR
VLMPLLLRKVSAEQMAELDAAAAAVESGRCVATQIMTSLAVPEDVLAVEPKPVTMPLVLF
SDVPSIVG*
>TCRU_7738 hypothetical protein, conserved
MRASGVCRTLPTSSASLHGDLERFIYPLTRHLRNGGGLPRIVEETRERQFAADLNAPNER
TPGVRMPVTYLSAHTNALLNRPLESADDGDVTVPLYRCPICCCAGAVTEGGKGGVFQLPW
MTPQEMTRHMSWLHASSGSTQSSFTAFNAQEMKRLLKALPSFSKDSGDIEGGLFSPRVVV
LLDVANIELATEEVLLELLTNGESLQFFRRVACLFVCVHEVFIPHTSRPGHIFFQLSRMH
PHSDMYIVYAATRNESGDLVSASVMGELLLQNVRGCGPAVVLLTKDQVQKSCVAEMFNGI
AGKGGRVYLPRFTAASILQSLREANNAGMG*
>TCRU_7739 hypothetical protein, conserved
MLRRSSVGLFRRTPIRRSGGELFVRPTLDQIPPAEECKGFFGHLNGSLKFLRFVDIKWMM

NRAVAMRREYLIAAPTLYAFLWMFSWKGEMMYFWGERSPPRQMDWNTEQTGYLPPDFKPT
VVKRSI*
>TCRU_7740 telomerase-associated protein, putative
MGSESKCEHPAAFFDMHDVENRQKATGGYATDGDDDDEDNHSTMSFVGGLAAELREEKDE
LIGRVSASLMQEVNFTARYRRKDMYKSDEYKNAKRIAFLVHAISLEDGEFVLKLALYVRR
ELYIRYTAALLVALCAYEPKCQPFLKCYMRHIICLPSDWLNIANIAMQRPHLSLALEANT
NDDDSRSTSTTSTVKEQRGGKGRSLPNALRRALVETFSMFDDHSLSKYNTERSVKKFCRR
ERFFEKEVGNCGGTRSARPLTMKDYIRRLHISQPAYVVCCILGKRYPNTEEEFRERGLDE
GGKRTFDPAFCGRRMRLPIAQVWEVQISLRGNKGKVWDDMVAKNQLPFMATLRNLRSIIY
QGCSEATHVAIIRRLMSEEQVIASRQFPYQFLRAYEALENSPDDICKFSKNLNGRRRNNR
HDFFYDTEVVKMLKKRYMDALERSTEISMRRNITPIRGMSIVIIDTDTDLLKSLNGGRSK
MEEAAMLAVGLKYACEHCVLLVALRDVYRVIDWDFRNTGNMLQHVKMIKKICYKAWSLDM
SLSVIESKGNSEVFPYAYLDDLIERRMNIQSIVVMGSRHSCYAGKNAAPSLGDLPEYLRR
IRRTCNEDLLFLSLRAFTETDEKAELRYCHKNDVLLTGFSDAVLRFVAERNSGGARRYIE
RVDEVYDVNRMTVCPGQMFEGELRALKRMALLEKERCAHKDSCAAESLLGGGGFTDTQIS
SASGIAMMTSAPQRQLPTPPMLPPLPTLQSTTRKTPDALPLTPAGPVTPIRFLTPEKGFL
STYRECRFFISSTFIDMNSERNALVLEVFPRLRRWAAEERLFVNIVEVDLRWGITEDASS
SDLSLSVCLNEVSRCSPFFIGVLGSRYGYCPPTLYHRVDEDVDAEDFAWLQQFPHENSAR
MSVTEMEMRHAMFTAARRTGRQAPRTMAFFVRDHSALMGSLPAEDREAYAPDTPTTMQSI
SKLSGHLEAQGVPMIPYNATGMRPRSDGFFSASMNLTKKSALHVPLDMTDFSRKAFVALK
SIVLQYCARPDDASESVKGLKDFGDQEQQQKIYRDGNVNGTEVRGTLYEEECMDQVSFTT
TLLKKFVPPQGLMEKLSFFALTGRLPTDAPSPAFVDATSTGTFYSTTDNKAANFNGSYDT
SNHEKSSNVLLLQGSEGNGLSSVSAAVASNLVHMENSGILVVYFACQASDGSLRRLVYYL
VFSLVYRLRLQEDFCVHESDSVTTLLQLLSRVYSAARKKSNICIILDGMEKSSYAAEILS
NLGWIVLSSNMLGIRFIVTTALSSPFATALKLRVPPALSITLPDLNMPERAELVRRHLAS
YGKRLQESFRVNELKILLRKQNANQASYLTYAITYLRLFSSFDTLRADIAKLPSTLLQLH
TETYKKLEERFGVETCRTVLVSLYLSQNLSGLKEYNLYRLVSNVANASRLVALLTGTCLR
VARKRVLISNASFEASIAARYIPSSSNVVDAYANMLAAELYFRPLLTEVSRYEIRDSIRI
AMDSIKRGSLETCVFRPERYRPSQLLALLHFALRSKEYDAFATIASYVTFIEYLLVNATY
LQRFMNVLLQASTANSLLSRQLQSIIDFMQSEYHVLMDRPKLLRQCIRNLPGCKKIFHGL
DCNSGGNPNTDDMSDNTIGGGGKPCTWINWLNSSQHGEEGRTLAFPTTEPLLCVALSDDG
KFMAVGGEDSMVRVVPIGALDQISASLKHMASVTAIAFFPSRSHILLTGCRRGILRVWSL
EDNSLLQQGMIENTRCISSLACHPTKSIVCSGSHDGICAVWHVVSNAVESAVRPALRPIQ
LLNHHRAPVSCVTYHNLGEILATGSWEGLVYFINMERPMDAGESEKDNPLKYAHQVFDTH
SPVRALAFLPSMVVTCAVALYNGEICLYDYASALCSARLTLHAGIPITSIAFSPDAKLMA
SANERGNVRITYAGVAGTVICTLNGHRQPVTSVAFHKQKPSTLFTSSADKSLKEWSFGQS
DRQERMEMRGTHVMIVTACAAASDGSFFVTGGMEGTAFVFAGREVVGAGAFYNTDGKEDF
FAPHFVLAHEHHRVSCIRIVMQNSRILCGTAAGEVFIWASSPGLNHREGRLLQRIRVVNK
DAYPVVFIECNEVNVTGVDGDGRQVDNLSAANSHRSSCNWAMALTTNGMVAAWEIYDDDT
ATRSLKNKWVNETLSGKISAASDDDAETNTLQSTDANSEEVSHANSETSGVRSSSETTGS
SRGSCETSALSNSQDVHGNHARMKPSLKKSSSVHDAEDTSGQVTIQRASLRWVGQTDESP
VWNELRQQTSTFSTEALNSYIMSPNDAEEIIAAVSLVRNSQTNRLKANSQNEAIEAHVAP
PDAHHHARLLCGRYIAVGRLRCHLLLPSLQRAIVLPMQNPLQLDYFVSDGAPNGSIGNHM
LKKGEFFLSASNSARVKNSWFENEDDNISTAVLFALGTSLGTVLLLEAVYDAQENGPASV
EVEDPLDNLMLKEQQRTRLILRHVTHILENHGDRIPVDSITLTTIKENSREPILQRDALT
TLQVVVGCRDGSTRLFTVFPFREMADGYADSVDTSNGDANLNAEKGKEGEEEEEDKEKKV
ADARRRDLWNEEGIFFASSGITAVTVMRMPEKVSPTRSRVDKTLEDYNKLLPSAAPKFTA
SMSSPFCHIMYIAGDWLGNVYQLRLERDEGNKKTGGNMKPFTTLRWAPERNWMDGLHRPT
AMGAEQHGWGWGAETLFSSHHENTDEAALALNVQRVADWRREERRITSMFVSPQGNLTAA
LADNVSRADSKNSKLVPPHPILTSSAVAAATNSEENKAGVPPYELILEKMPVGLDPSQRR
EWLQRRQRLLVEALQAQRNAVKARAVLAEYSKDALLSLGVSLTM*
>TCRU_7741 dynein arm light chain, axonemal, putative
MSHAGNVTNVYDEKGTVLYRAVPYNSPAANGKGDDPDNVEDREVDFAGTAIVNASVVSGG
ASFVARAKASRMGRSVGVSFSTLADGSSAVAKKEAPKLIQNSLTPEQALATLFPPEPLQV

EEEEKKEKKEKNEEGFGYRTRNTFCSTREFGESKWMKVAAIDHTSRLDCVHLQDHLNRRC
KEENARPSGVLCTIREGIYTDGLRELIRQTTVLCPERGLLLAELATEMQQTTNKYDILFD
SASQYAVRKAIERDMRSYLFDDKKSMESEVRRLENRVNELRAKRDGMIKRFEEQKQSEQN
RHEEEVKYLKKANQQIISEIKRITALEKANAAAAAAAAAQAPHSM*
>TCRU_subunit mitochondrial RNA binding complex.1
MQHCLAVRHFTGRIFQALCHRRFSFARHLQQQQQSLYYSGCRSAGGAALCSTRRWVASVG
SSTTAPSSMPMTAQQMSLETPMAAVATPEGSLPVTYTPGSGPNGALTAPTTAITGHCDVL
SECLAKADELALQLKAQNALGASAEILTQEGMEEFVDELKASATSEMTALVEQMQKTPLL
QHAGMHELRRTLYYATSLKERDWLEDPKYIAAMRMLTVELLRRDNDGVLSADDVLYVSTH
IVSSNFYNRHLWNRMEKAMLKFSNYENIDMASIKAFSTKLFKTRRGCAKETLDIRRKILL
AMSRRVGVLANDFDLPSLLGILQCYTVHDLTPFHLEPLAIRATNHVNDFTPHECATLSHV
LRKWRTMRLEVCERLVERICTADQLTHHMANAAMVSIRACYAKVSDGGRNAMNAEPTRQK
LRAMGEQVGSRLDEVEYPALPVILSILDVIVTLKIYVPKKSLQTIFLQANDMLAVVMEQK
DDLVDPKTGKRVRFITAEEGRQLQALLSHYGNDLAPELAQRLKEAFREGMLPDEASL*
>TCRU_7743 hypothetical protein, conserved
MWRRTCLFLLSPGFRRQSQNVVRHTCLFRAQYGISVRLSEGTPLRLLNTSTSVPVWQCLV
ESIQELAEKADDVESWWRFCRLWRMHFPQAAADALPLLLENELLVHDEQNETGKQEKESN
IMERVPRDLQCLPVFLQALCTAVRLGETRLQLSFPTAKDDASTEGSAMLVSVLAELRVVV
FYLAQERLTHTLYAVHDRLTETTHAKNENSRKDIVLNAVSSSSRDGERVGQMGVRLTPEE
LQQALLLADASAAVLSIGPPVTLLPSLYRLLLPALGACEQLENHRLGALAIAVARSADFD
DPNGDKDNFSSTTATAVDCPSSGDLRPIMTCYTVLSHLHAVARALEVRMRESMQRFESKG
MKPAGTSIRQAQLRLLSLKERKDLEKQRELESGSVGSDATGTKLLETVGIVCSALAARRY
TDDRFWKAVTDYTVAFLQASVNSFPTSTSYPHLLEDVRDILFALDHVHHKAYFDCLMSLM
VKLHLLQEPIPPPSAVRNAMKAVKGQTAATLSR*
>TCRU_7744 RNA pseudouridylate synthase, putative
MEVAWLLQLESEAWASDTKRQLYGTPLIPGFPWYTVRTDPSQCVRRHVVPYYYTFRVFVK
GRWVGKNLLDIYSEEHAHHSRQYYEACMRQGRLRRQPRKHRNVRRNCMKRLYGVDQPDER
EVNEDISGPVILESGDVVLHTVHRHEIPLCMGTTGIDPIVLAAVRITMYGLLVIHKPAGV
PTHAGGRYFMNSCTTMLEYVLAPKRLRAWLLQRDPMLQSIVSTRYLTEAECQELLAYYMV
KDEGSMAEYVSIERLPRPCYRLDKVTSGVLLLGVSQAATRRVGEALTRKTKQMEEVFLWK
LRLIASDDKKTTRVGGVQSIEERTLREFDVGVRKRYLARVHGYFPNDASHALHSCRVRKE
NGGDDDHRTTEKGFFITIPTNPTIRRCDAVNEEALGVVGPPVLLASRLMQFKFRDGDTTE
EPPARDQEGKQQREPFYQDAATFCQPLRYFTSGSGQASEGESLVHCVPFSGRMHQIRMHL
SDWGHPIIGDLKCNVMEQQKSGFHEPALSKCKNSGAQSAKENEEEMGIRIYFHVEELPKV
CREMFYTHDALCWECSGRLPVACFKCPNGSAIALHAWRYEMDHSLLLTRDPGSIANGTDQ
GVGDTDDKKADLEKREQESVVDDESEEALNVCCSLEDLKRYPDEFVRRQGKSVVFLAPPP
SWSYE*
>TCRU_7745 Ring finger domain containing protein, putative
MFLFDAMRHAECSICLQALLPGTGSSASPSNAISPEKKLPSPPRVSPAPQLGEVSSGEEE
FRITFAPGVSRQDTTDNFMTFINALDMYHRAAKKNGSRHRTSREVGCGVTPCGADHGIVV
LPCGHLLHFLCAIQLHEYSNRPTCPICREAIKSPEDCVLFLPLSRPTVFQRGMAVDGEVN
ACDISRTDEDGGDNVQFTGEGSVAPADVYRRHIQHELDELKRRRRNLRSREHFLTNSRDQ
LEEQCISLEQSASDARRRYDVLTRQGTVGLDRLKELRDVALKTHTSMDQLTLELARLLRQ
QRDLDQQLEKYSQRLKRGRLSGQGIHSGSEGGGITRDDDNDDDLPFSLQKRRLKAPMAGV
PFSYYVSRDKK*
>TCRU_7746 hypothetical protein, conserved
MARPKDDKLLREEEEEEEEEEEEEEEEEEEEEEEELEEWTELNDIDELQDGPSTFYVGGFST
IKKLQDALNVVKYRDDIVLVYPGLYAEKEVCMDESRLDGLSVMSVPLAMGPKGGYRKKIR
IPKDERRLGPWYAPFGSDAPKTDAVTPTTTDATQFPVFEGKLILRSTAPFTPQGERKTVY
PIKQYDPREDDEEDEEQEKEAEEEEEENETQKETVKRSRLELQGFSFLEGAVFEPLSRAT
VRHCVFGRSEVEEKANKTQDSDVPLPSPLLETTVTAHPLTEVQVEFCVIYGNQKHGIYAF
PRCALRFHSSMIIGPQFGIVHETQDFWSRAARHAQKNTSSQSVSRSRRPLQQAKIPEKTL
CAVGVYLDDADVSIQDVFVAQSHVGILLVNGCRGTSVIASRVESISSVGILFSGEDGAAK
VKCSAVRWCGRECLLVKGPVPPLPPDPSLLMDIIHDASQDAEAKEEEEQEEEEEEEEEDT

EARALSRVPIPTQHPILRGNAFDGSVRLEGDVSSAAMCDNVIYVAKEGVSPDVPTFTGPA
AEKRFALKGFHVHVRGTTPRKNDSD*
>TCRU_7747 hypothetical protein, conserved
MFAKDPSLLLLGTETGFTAPSRVSRRSSGSVNANLEVGEDEMCAESTKPFIFSTEAAAAV
VKHRPNPADAVGKALLKPGGKSRGSKNFLLRKTTIQHAIGTTHSAFAAQNLLMKGRPVPH
PPRKSLMTNKDRPAMGSHGSAPHNARPLRGPQAVKKPVAPGVPTPKKQQQQRSVSHGTMN
MTTTTSSIAGGESLFASRSREVSFKAGDVAHGRRRRSFIESITLCEDDSWQPTTSVTKTK
RKKMSGNVAPALTPLPRQIVRQLYAEDMAPLPARGADSSSKLFSPQLSLTALNSTWDRTG
EGNAYRDAQYSCSLSQSRTGGDLGALPKTVRIKGFSFLSLHAWNAPPSNVVLPNGTMPLE
RKSQEKDGAKCEYWHVTHPFVEDENRKGEWMRPLQEVGRSERKFISDTDNTEKKKLHVSN
DDDYHNLFHSLQKIHELHHHRHHHMDALQESTAQPELSDIGGFTNSLAACSALLKEPQQL
LDSEFLVSHKAPSSPLQRKSTLQASLSLLDNSWVSLMQATEKNPQFVELSHPGKVLFASL
LYLRALGGFPTLLRINPLRKNSFVVGKEHCVELVFCLPSGRQRDTNAASPPSQTKLSRST
RITNFILEGRHAHEKDGQGKHVGWEERSVIVRSILAEKSIVDRFGKVEVVHVLPPIQNEN
AFMKREADDSHRSQLIESKSKMVSRLLHDPTPEPHADAQSRVPHGLSFPGGFPYGRKTHH
MDCGDLAVAFLMSGKLSQISGVPPEPMDLEALRYKMYALRQHELEDATRKEEFNTAATQR
TGVGFEFPIREARTPSQAATMRTEATTPAGLFLENAANVASMHQRFPAYTPVTIAESTIV
AMADGTAGVFKGGQKAGEYQGTQFSQLRLPRFYIDLVDAVQHALEVQDRLKNENAARARF
LQMT*
>TCRU_7748 chaperone protein DNAj, putative
MSSGLSARRLILQQLTAVAQYSPFRPVLAAMLANHTAASTMTASLNDHGGSKSKSSWLRI
SLISPESSRGTFTLMTEEEMEYLRRRREEDGDEARVVLSTRPAKSIMKGLAGCALNLFLS
FLLSPLLALSVSLEAVRLSGARPVTLVVAPIVGLTWGTVFVVIAWYAALQQLVMCAFYQV
QGPLLFLFRIGYCWNELACRYEHPSGVFGCAHPLLAMYASEEKLRERAMKRESRRRRNEK
RGVTYDRSKSGRGMNENDYYAVLGVERDATPREIKEAYNRLVLEVHPDKNPSKSAASHFD
AVTKAYRVLGNAERRRKYDIGGTSVVEDLGEKKRDAVRALFGGDALHAIVGDVKTGNFSQ
RVVDGLDWTQEELAVCRQRMLERCRDELLTSYIEPLQKSRENSGSSNNNGAGLTEVKKRL
QRLLNTGLAKEVLSAVGQEYMRVVRYSEAMNSLQRLELFLKVIAPHRARRKLDKWRSLGR
IRQHTFKDSAAMVDLAWYTSVEELESTAWWVATATLLDPQLPVEERERRRDALRVIAETF
IVYGQAYKGANRQTMDTLMNSLRDYNQQQQQRKRDGQ*
>TCRU_7749 Leucine Rich repeat/Leucine rich repeat/Leucine Rich
Repeat, putative
MDHISASTTITTEAIKKICVQLGYYRNPICNEKLYLHHKGFDSIEEDAFDPYTDVKVLWL
EGNALTHISCGRDSMPRRKIKPQSEVSVEELAPMLTANAGFSKSAQLESFKAKHVDCCGD
WASPPPQVSVLADEEQVNVTAHANKPFSAAAHDEATADAAANDGGDDRHTIASPIIAADG
AGGNPVTPVPPTATNIEESKDVFQSLYPTLRQLFLHNNALREMPDLSGFQRLDTVNLSNN
CIHSVRANCATFCARVAHFETALQEKAQALMANSKSMQNEVCARDARWKRTMQRNHRPSC
AAEENNNTNDNKINESNAGPDSTLPASPLEETSTTTIVQGVDNVEGRAVVVEREGDAPHF
DLEMWRQRLSAYADFCPHEPLEIAENGKLSDDVPSMCRNPCSSIRSLNLSANYLADAADI
VQLLCFKNLTVLDLSNNQLSNGEAVLLIMERLPRLRSLKLSGNPLVRSLPRYRKMVLARC
PGLLHLDDRPVFADERRLVMAWARGGDEAENKERLLMKEETDKQHIRRLEEFRALVNRSR
YPDDSNNNNNNNTHATNDTNAASRTTSTITVGTSTRREERRNQGGTYSPANLSDVDDDDD
DVTSTETEEEEPHEDVHINNRIFHHTGETTISQDAIIPESQRAHIERAPWNEFDRTRVLS
SNIQPQSRSQQRPPQYVAEEDEEDGDVYIPRTAS*
>TCRU_7750 conserved protein
MALAGRYVCFSGFCDDEENEDDNDDNSARTTKEGKEGGAKAWSLQAMRMLCESLGAVVQA
DITRRTSVLVARQGLTRKRLVAEQHGIPVVSPRWLESHGRLSFADAKVPSLFGYTFCSTQ
MTAEEEKALSTIIEHNGGVFDRTLTACTSMLFVPPGWMKRWRQQQQQRMRGRPSTGPHGD
GPPPVLPEKIRFAWATEIPVVEYPRFLAMAALSSSNGVNMKCDSVAARADFDTIARLCAL
PISVAGGLVLHTQRNDGSTEGGAAKAVEEAEEDLVKGQSDFSHLEKRPREIGEMNAPYDG
DDGPRSKRVRIIQGNDESTIQVPDALQNDGHHGERKTIENEEKSIQTKHEEKVLGPSCVR
KDEPLGLISGDAAVPVPPSCPRRCTVRSSSVEASRSDDAFFSNTIFTSGHPFVQVTLLGC
TTRESVDCVHMILHCRFMRTPVVTPWTDVVVVGSAFIQEYLGDVSAVDEKKGPPRPLLQH
LHHERGQLLARLRDHLALNYGIPIERVVGVEWLHSCYQRMMFQHTPGAMENSHIPFFPAS

LPLREMPPTEKYHLRIPSTVSNFEAPPPPPDGQQGNEPVAPPSSRLRKRKALHALQEQSR
SAYNPTSNAKDVPEAVNTVQQQYEAEIRLADHRVKNLLALLDNAAETIDGGLTPLFSSLF
CFVEKEFSRIDLAVVRALIKHGKGAWLKKSKDDWVRLLTQIGTNAASDENQLVETELIGF
VRRYSVLRKRLYLMQTEDGEAEEAPLRVSTAMDGNHGRKQSSSDVTTHHPTFALYVVPHG
DQRPAECLLKSEIRRGTMPQRHPLRYLPAVTQDYILCCLAAGHMLHPGSCFLFSSPLPTE
AERLARRRRRSESGKPLSVSPWLGPRRHEKAPLTGISIFFLCAMKDEVSAAATALRRVMV
SCLTAAVCELGGHSTVVLLPETVTHVVVIDIASVLESELLPEATVYGYSPWFKTEETEER
EREELLLRGSEWPHALQDQLPEDLVEHVVKGRISLVGVEWLHASLAWGVFLDEASFTLTV
AQQQQQQQQMSQQQRYEGRSVVAGSAATPPLSPSRRAASADITLLPFESSTRTNTITGMA
LSPQAGAGYQFDFSTPTATPIRLRPQKDLLNESNASVPRQSCPRSTLRTPRRQRVSVPRT
ISPAVVLVGESMHTEERDPSEEADTEERCVAATPPQKLEFPTVEKHACTPIRGTAILGTE
DDVTSNGSNDDVVAVAGSRMRPGYLHGEGKNVPLAVAMPQQWDPEASSNSCAGPHHSTTP
PPVLAPNDLGDSLSSRFSHASAALRVHIVHDMPDRERLIASCVRLSEAAVNGSTFFNSEG
SNSSPNGVCDVPGNFRQQHLPRQKNTAAVFTHLQLVGPSVRDADVLVTHQLTQRESVLAA
IAAGLWVVTPKALQDCESRQCFLPLRDLSVYEWCPELLAPGSPRSSLQLAQQCKSRRQQR
QATGTRLFDGNWFVLVFPNTAVGLARARSMRTVLEAGGGVVTWATCFLADQEAEPAGIVG
DKLSSQEDAKMPLTRRSVTPMAEPTSVSSPAALLEFVLSRIRGQEEEFSNGEFDKHDDMT
KPHPKPAKELILLLDGFLQKNTARSWLREIVEVFSHAQASFTEAKKKAFARRQRKQGENR
TQCPAWESTRAGNEVKGSDVRGNGLTMWPVTRSLPRPALFPVLGPPLRVDTRDSENNVEC
GMPFVEVVRVFSSDWVTLVIQKRRKAPLCVVEVPS*
>TCRU_7751 TPR repeat/Tetratricopeptide repeat, putative
MVTMSNERLEFMRHLGITEEDVMDPLLVKGANGNKKGFNESRLDGGRTRETSLDVNFVNT
SSTAFPIVDSSESNVKPLKKDKTPQCKGNNGISTAGLSPEQLKVDGNRAFGEGRYREALN
YYTDAIELLLEEGNYQLREKGHLNAKSNGIIASGFGACDPRTVLLAALFSNRSACYLQAA
KQIGAAEALESAIRDADRAVELRPTWFKGYSRQGDAFFKMKKYSQAVEAYEMALQFDPGN
NNLLQSVEEARQRSATKARESVQSIKKQATVSRGERNAASVKFVPVAVPASANVSCNNTS
MGRRDNVQFKTTARQLWNEFKPEVEASVHQPTGDDYRKEQLRLFREQKERERNGVAIPPS
GDNRSNEESPLKGNATEQKCSGVNVSGTNTTSRRGRLDFIPQEFSSDAAAAYQQRLLEEY
RRRKAQRM*
>TCRU_7752 ARP2/3 complex subunit, putative
MATAYLPYYDCIKCTLHAALCIGNYPSCTVERHNKPEVEVADHLENNGERKVQDFLLNPI
RIVRSEQESCLIEPSINSTRISVSFLKSDAIAEIIARKYVGFLAQRAKQFHILRKKPIPG
YDISFLISHEEVETMHRNKIIQFIITFLMDIDADIAAMKLNVNQRARRAAMEFFLALNFT
*
>TCRU_7753 hypothetical protein, conserved
MLSVRRVSEVSAPSTCNCLVPVYSTTYGAQLDFIVGCYEFMDLSLESTTAGYRGYVTGYV
CEVNDQHIASLREMKLVSENVPRVELPGIFDLNAFSDGSRLMASCTDGTVRLLGHQEGSF
KEVIFPVHSTTLTSCIPFYSSSEIGMCQARWLCTAHQGAVVVYDPNTKNIISSLENHDYD
AWCSATIGPETALSGGDDGFLKWRDVRCGVNAVGRMQFGAGVVSIAPVAQGGIASTYSLV
GSYDENLFLVDSRSQKRPITSIGLGGGVWRCSRQLSIKGLRPESESAMHHYRWVQPSGTL
VIPVMQRGVAFVQHNIYVSEENVFRFLGYLHDETNTTEAVGLPPNALFYDCAILPRRSPP
NKYLSDDAASVVTCDFYNKRIALWEVSGIQHNA*
>TCRU_7754 hypothetical protein, conserved
MPVATAPSLPNLAAPPVGNIEINAPAAMVTEKEPTPDAGANNTPNSVANTAVGVSSAGGG
NGGVTVSREERERQIKLGLLLVRLGGAKETDVFGVRGLVVPPRDLLVIHRPEDDAEARRP
FRWYDPISWFLSGPRPSPMRWSSTTAVSKPSQAVPQKVTTKSTISVASGIDASSVAATVA
AATTTAAASPKVKKKRPLPVVNMQPLKDDETLEPVVKEEREKLLKEEAAVHGVLDSIEEA
RYKYLVPSRILGCEAEVMSVLQCYIKSNAAARNIADAEESLPTALPAAADVLQCGPVVAL
LKRCAEGMVASYSEADGGQP*
>TCRU_7755 Nop14-like family, putative
MRRTASHAKIVQRHERRKASREAKASAARFSSKQSRFQLRQEEINVQEALQPVTSSLLPA
SSTNTNDIATRMTNIPSSVTLSRFERPPAAGNNSAGGESGRRLATTATATFGLASSRRIG
MHAADSRSTRRAEKFRLDDNGRSSVSQSLGAGLLGVTRRTRDDDDGGDLNKDGRNDSGEP
QRKKTREERFREVLANSKEHRAQAQRDREERAQRTTALDAEFNGVMHLLERRDKAQEERE

AFARIGTPQVRALLQSFRENHVAKTVSLRSDGSFTIAPLVGNNNKTRVKTGAPSLDEASM
ALLKKIREEADEQDVITNSALSSHTLQKKEPKVKGDSLVRKSSGVEDGEEDKDDFDRIML
SMQRETRRAVAGERTRTEEEEQAQLDQQALLERDRGAVPLLAQEETQLTRAEWLSRGGDR
AYQMQDEDDNDDYGGEVEDSLDISSVCDSDEVALLDGAMGVNDDADDVTAADADGRAADV
ATGTRTRLEELLSAIEAFGREADGTRASRAERTRKYYALLRSLYQYARDHVLHTAQTFRL
LLIEAQRSFLQHGSLDRATLLLLHSASRIFPMTDYRHEVSTPFLLFLCSALLQMRLKTFA
QVREYTVLAGLLCESVLAGGKFCAESIIAPLNLIALQVPRSVLEPVRLQGVCVPFPVVER
GGAEDVLLHTNTDTPSDAEEAPLQATFALLETEVNSTHVVRYAYRLLSLMADSLRGVPAL
SYCLKEPFLALHEKLIATDVWQPSASVRGDHDALLAKLTQLANDARDRRTPLAMRSFRPR
PIRQFEPLLQEGTTTALKNEVRAMKREMREDHKRVVRHLQAEANVERRQRERAAEAEESQ
RTQKYRELMGSLQAQQHVMKTVDGLLDKARSKKRKSLTGRAGGDAADGNAEN*
>TCRU_7756 SH3-binding, glutamic acid-rich protein, putative
MQEVTVYATAMQAVRRTADNCRRMLALLDAFGVAVSVVLVDSLEMRTFVQELLAKQEAIG
WRKQHGGGMTPKFQLPLCFVGPVLVGTYEEVAELNETGTLPKSLRAAGYGGVFRAAVHDD
IPVGNAAALAAAAASHPVIGEGGYGGERSGNGGTKAADADVDDGNNKNSNNNDDEDGSED
EIPPPPPSPPPPDEDELNDGADSPLDSSGVDKGNKFGIVDFEEDDDEEPPPPPPPDDDEE
EEEEYDENEFPPPSPPLED*
>TCRU_7757 mitochondrial carrier protein
MNARASVVPQDHLPPQKQTSPSFFMKLFKGHAGAATMAGAFEIALFHPFDTVSKRLMSNR
TRIQGVSFADTLRNLNTTIFSSRADASVAQKILYLYPGSSYAVFYKILQRVFKFAGQPLV
RDHLQTHNQQSFTDTFGRRDKLMMESVAGSIIGVGEVILLPLDRLKVLSQTNEAALRHGL
LQLLRQEGISGMYAGTVVTMTRNAPGSFCLFGGMAVTKEFVFGLQEYRKATFFQNVCAST
VGACLSITVTNPMDVIKTRVQNKDPGARMGAVTILSQLLREEGCSALFKGLVPKVVAFAP
KLIFSYTMTEFFIQLMNSSNAERKLLKTC*
>TCRU_7758 hypothetical protein, conserved
MHTDNRDEVDSHDTLPLRAPPSTDARSAEATAVNGDKVSYSSEAVVREKLPLDTANPERR
ILHPGNHTIRIPPTGGTAYNGTVGESWTAPRAVDGTYLRLAPLYESTTHYQLRTGPYYTE
DEAPAHGMTLPPKSSLPTREW*
>TCRU_7759 Enriched in surface-labeled proteome protein 1
MSVTVTNVLLYNRPLNDSEITALNRKLSIPKARGTKTVDGSTPPVVSKKATPEAGTPSIL
GGQQQTEQDPLKKSKDAGSGVLSTSAVSSATTSPPAKESENQSASGTSPEGHSNVDVDSS
SEGGQPVDTEAGDTVQGDGTQQPSLGTPSTGYTNAPTAETIAHDGTTVAPEVGGRSGENG
EMVGGTDGQKREDIHARDGEVKTAALSSSLGNVSQGNNSDAGTMCGSGLLPLLLVLLGLW
GVAAS*
>TCRU_7760 Endonuclease/Exonuclease/phosphatase family/Endonuclease-
reverse transcriptase/Reverse transcriptase (RNA-dependent DNA
polymerase), putative
MEPFTWLPAERYFYPLLNSIGAYQRYTYRLRAVCDAQRQKLLLSGDIEQNPGPIAVLQMN
VSCLTPSKLATLMAQGADIIAIQETWKSSEQIASMHTGDYVLYAQSRIGKGGGVAVLVRK
PLRSKRIPLTIPQHDTSLEVVVVQVALDQNRDLIVASAYMRPPPQVTQSFRRLVNCLPAS
SPLLLCGDFNMHHPQWEPFLETSPSEVAAEFLELCTDAGLTLVNTPGEITYARGTRERSC
IDLTWSKHLTVSDWSASVSPLSDHYMLTFTLHQAFKDTIPSAPHSAPKFFYSWGKCKWDL
FIRDFDAQLPAYDYKKQSTGIKAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERIAT
DSKARYLQLPTPDREAEMQRTRSQFFLLLRERLRNTYLRRISKLNPGEPLAWKYISGRKK
ASLPSPTSMLLGDGQHTYKTARRAANALNRIFLPFHPSHKAVRFSKGINRQSASLNINAS
FLFGQQNNSESAATSSLVSSTSLISCISEPQNNNESAATFTSGSSLSSSSEPQDKNEAAT
TSGLVAHLHSPLDAPFNRTELLAALRNTPYGKAPGPDEVYSEALRHISSKGLRFLLRCIN
HSWTTGTIPVEWRRATIVPLLKPGKSPELLESYRPISLTSIVSKVAEKMVLKRLLWVWTP
HPHQYAYRSMRTTTMQLAHMIHEVEHNRNHYFQVSLPKKSGIGNQLHYRPHRTLLVLVDF
SKAFDSIDHRVLSRLLANIPGVNCRRWLRNFLCGRYAKTRVGHRHSDRRPMLRGVPQGSV
LGPYLFSLYVHPLLNLLNSFAGVTADMYADDLSIIVKGQSREDAIPTANMVLQKLHAWSQ
ENGLAINPSKCEAAWFTLSTHTESDYDREGRWPLVVAGCQIPVMTMGASRTTKLLGMDLD
PRLTLNVAATKQCAATSQRISQLRCIAHKEAGPSPHDLRTFVIGYGASKLRYGSELIWAV
ATDSAKNEMQKTYATLARIVSGVPSTVDPESALLEANMPPLHVLCLRARLSIFENTRACQ

MDWMRRPPPEPPPRAGFRISPLSRDELYAFVDAYTKDYGITESSPREERFFRSSIPPWFA
ASAHRVTIAVELPIDHSITDEEELIRKSAGSAKRL*
>TCRU_7761 pyridoxal phosphate containing glycine decarboxylase, putative
MALQTREQHIKKERATSNICTSQALLANVAAFYAIYHGSEGLKEIASEMHNKAKILSVGL
ESVGHTVVNGAFFDTVTVNLKGITPEDYVTCCVEKGINIFVDYNHGTVSISVDEASTEGH
VVSLLEAAGPKLPVIGVLSKLTEQKRAMPLQMLRKSVFLGHSIFQKYKSESELMRYIHRL
HGKDYGLTHGCVPLGSCTVKLNPAAATLSLSWSEFTNLHPLAPKKQTRGHSALCLDLEQK
IRDITALDAVSLQPNSGAQGEYAGLRVIRSYHNSKKESHRNVCLIPESAHGTNFASALLA
GMVIVKIKWRMEGLT*
>TCRU_7762 hypothetical protein, conserved
MSGSTPGMEFCHTDRRLSRCVCAFLFLLRFLSVRPPDCSEEAHMPGIDAVLREGSCNDDI
SVRCHVAWDSAASWKNVESTVRPRSASESSTVQISSVMPSCAASSPRRSASTAERESVAA
GTRVGDWDAAARRGTVCGQAQ*
>TCRU_7763 hypothetical protein, conserved
MLRLLSWREEYLSAVPGDGSSSWCLDTLPNTTDARDPEETHLSAAMHASLKCLGMQVQLE
VTEGGNVRWSHARPRRRLRGPLRPTMRGNAICRDHAQVCTISATSGSLLPVDPWDGDGRG
RVEQDGFTGIY*
>TCRU_7764 hypothetical protein, conserved
MSAASGIYFQFLVSVSSAGLLRVADCTFTGSTEAFNSALVQLSDSVALQGGAQWRVEGNN
VSAASVFIMPYSWYSIELSGSGTTVSLAHNRQADSSKAFARITSSGLILTSPARFVVGCN
MQGEKEVSYDGVFPEKVVVFGCGTCNDDAACYMPGTESVDRVSCSCSCKDGWHGASCLPF
EVPDTVVPSLPERAVDGGAW*
>TCRU_7765 hypothetical protein
MGGGQAGTEEQVGALLPLTLSPVEALCDGRAQALMGDFAGVDFVFLVVCFAQRQGAAEAV
GAVLAVLLCDTLLGVTRLEGVIHLPLYFGLSGIEVIQQAHNRGSSRFQLLIRWREDEDRW
CSHSSFDLHRGPLAERHRITMIMLAVISCKIIRLQAADGESEFCS*
>TCRU_7766 conserved protein
MHVAVVACWRTQRPPLARLTPIAAARGISSSSTRHASEAGDVPSAAQPADRAATIHEMGK
DSPIAATMQAGGEPVDFRQTAIPKRPSGLKATDVLTPHLLSTAAESPVQLRKRPQFSFLG
DPKDRSASSVFSVHTVPNNMPKPLLPIWASSLTSPQLGKQRLRVENWISTDSMGTLPEEH
VVEFLTWLRGRCISSLYAFFLQQMEENIEFYLRSQYTRGLIARKGFKAGDVILAVPLTDA
STDYDDVDGESVNSATHALAPWGLVLNSETLQRHSLAAQRRGVPSYATIESIVGLRKTAF
DPVPHPLFVDQVHCAMFLACERAEGPCSPLYPYLRLISPFDDDFIRELHHGVLDPATHLE
YSDHCGRFSHWLRQIHQKWLKEHEIAQMIEATCPSFPDSTASGSNEYREDLKAFSHDGNG
QYREPPPSMEDLTWAFRFVLSRQRFFPIRKNLEPFERICTERKRMQVEEDAWTRLVSSVR
WTLLDRVFGVIDHKRAAVNEFDPHTIASVVPVLDMLQHPPGGVANTEVTVEFPPAAEHEG
TAGRGTRCAVIRAVEDIEEGDELTALLPKCYSLSYTLYRFGFLPLRRRVDDAAAISGEFL
DAHASTPAERPRIALPKGRNAGNVYRRGAIWRPWRNEPPARVKGGPFDFTPKT*
>TCRU_7767 RNA-binding protein, putative
MGRRPRQAVHMVNKNFPTPTGHTPSDEHNTAPPPFALARDTEVEPTLRYPFTYHGPSNYE
NFSKRQHRDFKALSKEERQRLVEEEAADTDLLARTVHLRFLPSGMLQGELAALCSECGEF
LRVRLCGNFTVTQNWIYGFVEFADCRGAERMLQRSGMEMPNGSGKPPLRLKCDTAKQAIV
DRVFHDADPATNMKCIFGSGNFAYRTLKEAVDSYYNLKRKESEMLAAQRNSQFPSSIGNK
NSYTPRGYEVRDINGIWHTPAPRHYPKAQEGPAALMCPPALAGGYRSQSLSNSDEEPAGI
TPPLHVSATHGNGIVSGECVRTPPPYPHPTQQMRLPNRLGIGSNYDERSDGAMSHDGKNS
PQFMPPFTAVPLGFEPNFPLPSIPQDPTVARGKALVLSSIRDAQTFFATGDKFYDAVGSL
RALLSVLDGHIFRVARLEVPKGTVNTLVKNGGTEEEDDDEETMQRLTQLRLLAHFFLSFL
YLQKGKNEECLSSIHSVVMCCSSIPVKKAQRTCPSTAPAGPASLARTHAVCESSGIQANG
EKNEKEEQKEEEVLPIGSDLSANEETSCTFNPISQAFDFFGEINFGGEDENEAAVVNAAL
GVLPLEEHDTSLERLGVHKEQSHERGMNLHAYVLNILLAIGLSMELVQPVVTRCVYVLAS
TRSKEVFGATLPELEQTLLDGGLHRLRPVLFPQVEDRNFVKVFFESLNLSETMSDDVFWS
SLLPNHMVRFFPRPRGDAPWQFC*
>TCRU_7768 hypothetical protein, conserved

MALLRVTATAELFLEDEGGIVREQLQAAEFFVCNAKRTMSWPPPALSKYEALLLHGGEWL
EKEEGDEVTLGGVTEVERELGPFLRFYAPLGGLLSKEFRSLLRHGLIRLLTRRALQRLHD
AQWQTHGDDKDFTRVSATSHDGEDVVEASIAPFISIKKGPFNTAVASVHWSSQLLQRLLH
QAAHSVTRISALIPGAVTLIPFSRDLRATFIPRHGLANIDAHGAKKVYRLVFTMGRIEVV
PQSVHDELTADRLASILYYSHLRLAEQMREAGGESLQEPLLNLRDAMDCYHRALALAQKG
ILYPYNHALRPPPSLEDRMENAEEDDIEDEIYSIFATTVLQGGKDITPANRYLNLLLNLR
RNNTACSEVNALYYDSMLAHGRDLFPDAHVLLHVWYALHRQVLVAAANAAHTLLRMQPTS
SSSSDASSTSRRNANVLRQRQMQVARWCARALDVLQRVLAWLNVEKLQGTEEASVLRSEW
LWLHTIKFKLLIRQAKLLRFTGSFEESHKVQEVMEEQLRILSPQMQPLCRGEMEGLLHDV
SNQLAQERALLREEMNQKGGLILRL*
>TCRU_7769 target SNARE, putative
MNRLAQFQAACGLTLIGDVPAPGSDKLGPARVTVTEPPSEQSVQAAKKLEEFYDLVAAAG
GAVERVTGLTREIAAKHSEIMSTFDLMKSSSMRQEVEALTQQLNASAQASAEILETMKRE
TDKLKATPEMESHFIGVIRIEENQRRYLLYRLSKAMEAYERQQNSVESQYRAQTERQIKI
KYTNPDGSAIDDETAKELAQAVLENNTTSSIFQQSKDVLAQIIETRNDIYHIERSMRTLN
QLFNDLAFLVHEQGEIMDVVLRNIETTTKYVEAGRKEMKKARKYQRRSRRKLCCLVLVVA
AIIALFVLAAVLGKTL*
>TCRU_7770 hypothetical protein, conserved
MMRRIIHSTASSQATLHFPVPSRLGVIPAPYRSSAFYTARRTFFGMLRPKARQVKVEDVL
FDKQATHYTGTIFGFSADAVIFYAKTGATVCAIIVIVAVFLKGYAMLSRFSLATVARLGF
MSGFLCSAVLYTVIIAVIRRFRINPNAVYNQSIALVMRNEKVVQHLGSHPRTGDFKAYCQ
SGGFRLPLIRRIRSGSYELSDLLGLKQRKLQMMFILRNPANGREGFVTCDVRRETTGFMS
STNTFKSLAVTLTDSTRTSAPQTIVVIGRPEDVVYRGLMKL*
>TCRU_7771 hypothetical protein, conserved
MFTSSDKRREKWGSLNPLQLYLKCAALRCPYDLPTEGKRHCQEGLSWLSSLFISARNKPL
QGRDLNVLRISQDATSIEKQEHTSRHSSLVSLACQESRELLAHSATVSLDAGAMKFTSGS
KMCEAESSHKEVPQHHDDGQEDEIHPKRDGQKSPLQEFEKNYGTSDANKSRVIVVPNEEK
SVASVVCSRNGTPPQHELQSKTLNSCSVAVGPDEAYSNNGLGTMALGHGDRTEFPVFSEE
NKMENLLATAVERLYAKFQGTALKVAPLDELKQSLVEAFHQARKGRAAEEERVELAVHLH
TLRHQVEFLTDMWNKYKDARMALERQPARKKEAATKVIRVQIIRDYEEPPVSYKKGPFVP
LAPAMQRLQLPNETTYTSVSEPRGKNSGSSVLSPTRRAESSYDSFITSEVEYLDDFEDA*
>TCRU_7772 Leishmanolysin, putative
MDVPNVRGMPKVSVISTPNTKAMARQYHNCSTLEGIELEDEGGSETVLSHWKKRNMRDEM
MTSDVGVGLYSALTLAAFEDMGVYVANYSAAEMLWWGNNSGCGLLEKKCLTDGIIEYPDL
FCNQFDDDEKFFCTYDRLSLGYSKLKRHEEALPEEYQYFSDPRVGGDGLYMSRCPYVKTY
SNAGCTNGNPSDYGPSQQPGLSATHFPVLEEFDDKYIGDVCVDTRCGDGTVSVRFLDDDA
WQECQADETVTPPSGPWRGSIVCPQYADVCTAFPNISSYPIPVVDPPLADDPTSAEGAEG
DEGGVPRKRPRRL*
>TCRU_7773 hypothetical protein
MPQLVGCHTHVSICHQYLLRVKVHGSSKWTTIIQQEAQSRPRGWTRSRKNIGVENHVGAS
HTHHVVLVWDGEVLAHPQSGMRNNDGARHGPHGETLRVQLNGGGENLPQNNVPPLLRQHV
VRLACYCTAIVVNAQIPRRSAVPQRIVHVLRGHLDADRSPAIVPILAGGGVRLHGALSPA
RHLTHHRSRQPAVFLHHRVKPTAVLHGTIGGNASTGATHHHHEPRQQQWQCGAAWLAHGL
GTTCLFLRCGRQQWYYS*
>TCRU_7774 hypothetical protein, conserved
MAKGFLRVNWRACGGWLILQWRRPLPGTTERVAVSGLANGTAPLVAGLGSKACQRVRVPY
GRDSMFRVLSGCHGLRRMLSRRLISMHSTMSVTKLPVHGPAGTHQCQETLPDPVLVEGRQ
ERLALCRHKRGFYACAGYEG*
>TCRU_7775 hypothetical protein, conserved
MCSQYGPLRSSSQRGGPIAVSVANSCLRVAATPKFSKPPSAVHPRNIGRQATEDSMSNEL
KGLAGVYQHQRSPMGSAVELASNTALLGKVHLEVVGSVMLHFVYQVCQLHRRGTRTTARM
LVQTRRPQPKQSPQCHFLSSLTHDGGKADGSI*
>TCRU_7776 hypothetical protein, conserved
MAQQRIQYTAGARGQDKRRVAKGQFKRTQREGPNHIPVTRGHASTKCADSSGDRSKWDSD

DATDERVSLLPDFVGAYQRYTCRLRAVSDAQRQKLLRGGDIERSPSPIAALQMTVPSLTP
AKLATLMAKGADMIAIRETWKSSEQIASMHTGECVLHAQSRIRKECAAAVLVRKNLRSER
MPLITP*
>TCRU_7777 hypothetical protein, conserved
MSGTSLADGSLRSSWETGDTTRIRRHGKNACRTESCRPLPLLSVLLGVSEGLVHRRLSAL
LARHRRQPRLTPRRTVSDVVTPVRDETARGLSERIAVECGRRRGGVPRCTLAVAALSQSR
PASRMRSTPLTMGECWLWSAGSRACAVEPNTGCAATWEAAALG*
>TCRU_7778 hypothetical protein, conserved
MVCVRCRCWAAAICDCAVAVRGVAAVSLLLLPLCVDGELVCAEGCRQVTGVMAMMAGRVL
LVCALCVLWCGAGGADASNLENNAVGGCMASWVLNANKSYTPSGCDKTALTLPLRSVLSI
TAVPASTDPLVTGTAENKSDLAPGSGADFGDAGSPPGRGGGGGGRDDGAGGPGGVGGAS
GSQARGSKASGGGGGGSNGGSKARVDGSLKSPASDVRSPSPVLGDGGSSPGAPTGSVGSD
GSKGFIWAPFLLVVAVNLMLAVQVVMHL*
>TCRU_7779 Enriched in surface-labeled proteome protein 1
MLITLPVYSSKDGNGKGVLHLWLTDNTHIVDIGPVSGKDDDVTTSFLLYESGNGDNKKDE
LIALYERKKVNRELSHNMVTVRLTVQLEKVKEVLKTWKEVDERVSQLCATLLAEKVTSSE
TACSADIKITDGLVGFLSGNFSENTWRDEYLGVNATVKGNDGATEASDGVKFQGAWAEWP
VGSQGENQLYHFANYNFTLVATVSIGGVPKEGNIPLLGAKMAGDGKKNKLMELSYDSGKK
WILLCGDGTPKEHSSTWEKEKTQHVVVLIRNGSDVSAYIDGQRVGGNEQCELKTKASKEI
SHFYIGGDGDKTRKQEGVSVTVTNVLLYNRPLDSTEIDAYNPNKASIPFLVNTTIEGTVS
SSTAGRQQQAGKEPLLESSIANGERAGGMDGQEEEVNTQDRDVNAAALNSGLGNVSQGNN
SAAGALRESRLLPSLLLLLGLWGFAAL*
>TCRU_7780 Aminotransferase class I and II, putative
MELLQNSSSAQKKLQENTRLFRTEMKKAGLTLSGHEECPIVPVMLYDARIAGEFASRMMS
QGIYVIAFSYPVVPNGQARIRVQLSAAHSTEDVMRAVEAFKTIKKELNV*
>TCRU_7781 Pentatricopeptide repeat domain containing protein,
putative
MHPRASGQGVFPRYGGGWMHQFGHVYALQQELLNPQASNWFRAVELWHTARHEGVALNSA
HYTSILRQCVQPKAWEASLRVLRQMQREGIRPDVVGVGCVLATCADADRISEVEEVFDEF
SGKMALDSVCYLALIKAKMAGGRWKEAIAVGKRQEADGLHFLPYTYTHLLEAAKEADDGE
FGLELVRRMKREQWELSERGRVAFKKLCVLHNWEAEFDRLAGFSEEGVSRPQLPERSL*
>TCRU_7782 hypothetical protein, conserved
MPSKKSRRKTSLARQERECSDSPKSSFERHSSNEPAKTAVCAVVAKKEVKVKPAPERRGT
RKTLKEEAESRYKWPCRILGVLCALLLASAHLYFRTGADRDFPCECIASGSGPLVSALAS
KRLGLTGVHLHTADRAAVEKELTTLLTCVVLHRLTGVFKDVTELSTRLRKDAASAKCIIW
FIQDVAVVRGVANSLKELLEENTLRGDEILPEGSRGLFVLVSDKSRQELTDVLPHRVVHM
FHTMTV*
>TCRU_7783 2-amino-3-ketobutyrate coenzyme A ligase, putative
MFCTALRFANPALRQIAAAQIAAVKEAGTYKGERVITSKQSALIDVQSSTQPLLNFCANN
YLGLAGNPEVIQAAKDALETHGYGLASVRFICGTTDIHKKLEDTMTKFLGTEDTILYPSC
FDANGGVFEALLNEQDAVISDALNHASIIDGVRLCKAERHRYAHMDMAELETALQKTQGK
RIRLIVTDGVFSMDGDVAPLDKIVTLAEKYNANIMVDDSHATGFMGEGGRGTPTLFGVVD
KVDILNTTLGKALGGASGGLSSGSKEIVEVQRQKGRPYLFSNTIAPAAVGGSLKVMELLQ
NSSSAQKKLQENTRLFRTEMKKAGLTLSGHEECPIVPVMLYDARIAGEFASRMMSQGIYV
IAFSYPVVPNGQARIRVQLSAAHSTEDVMRAVEAFKTIKKELNV*
>TCRU_7784 hypothetical protein
MGAHHSFPVPSAKAPVPSPVVSRLTYNEGNEYLDGISLNGDNPPYKLILEWLECLPDVRE
FTHVPEAEIISNGEAEALQWDLSVGGYGELSNAPGENVHYISAVTLRTPREPSAGYAEKV
TRAKGCCFARLA*
>TCRU_7785 Ubiquitin-conjugating enzyme, putative
MEPLNDAVSTDQRDALHRTLYLRREYALVANCGEFDDILLVPPQNDSGKQNDCWRGLVAV
RNSPSPWYGGFFAFLVQLPPKYPFESPSVRMEKGFKSHPLLLEDSEGKRCILPFDEIYLG
LDPMRVSVMARLLHHVRSMFYPSEWPTAVLVNKALARCDVERRSVTQEVVLGKPYVEYLS
REAVAFFSNPDCFRDGELQMEASGFQEKWEKAFSLWLGRSWLPAVRLLQ*

>TCRU_7786 ubiquitin-conjugating enzyme E2, putative
MASVQSNCSASSRLQKEFMELMMGGAEGISAFPQNDNLFHWIGTVQGVPNTVYEGLEYQL
SLEFPANYPFEAPVVRFLTPCFHPNVDAYGGICLDILKENWSAVYTVSKILLSIQNLLDN
PNNQSPLNNRAAALWGKKEEYRCEVLLAYREATSKA*
>TCRU_7787 3-hydroxy-3-methylglutaryl-CoA synthase, putative
MRRTVRALAGISGMAVYTPPCRVALKDWCDWTGNDWKKVSNVVGESFRIPGHNENAYTMA
ATATLRLILNYDVDPARIGFLGLGTESSTDNSAGSIIVRGMVDKALKELGLPRISRHCEV
PEFKHACLGGVYALKSATRYSEVDGGNDKVAIVVASDIAEYALGSTGEQTQGAGSVAMLV
EKVPQLVELDTKCSGSASDYRGPDFRKPFRRHFIKEYGSNTEHGKIPDFPVFSGPYSTMV
YLEEVTMAVENMLGKLKQNPGDYYNSVSALFFHRPYNMMPIQAMSFLYVRGLARATSAEH
KKYFEELCSKAKVEPAAVQTELDIIPDYFGMIESGQEPKDVFGATNKVAKAVRADKDFSS
LLSRKMSLGSSAMANFGNLYTASLPCWIAAGLEEAYNKKQDITNHPMVMVGYGSGDASEA
IPIVPVKGWEEAASKINVAAALEKPVNLTREQYEGMHNGSLKSDLAAENRQKEFVVAHIG
SRNDMAFQDIGIEYYQFVH*
>TCRU_7788 hypothetical protein, conserved
MVWWSPWQVMTDDDEVRLQDSEKALNAIFNPSRARVKEPRDTEYSFWGIPALRWSFRGGG
DFNSSISFPLLPARMDCKTTSVASTDSVVTPAVRKDDGAGASPSTREAVQEVLDWGLLRS
CPILGYKLREEGLVDVLVQPPRTLSVGDLRSLILELSSVEQRAKYAVETQLPQQVHNRGR
RGLELFVTPCLFISGLYLMLWKAPRLYFGVSPRSSVLFTRILFLLRWQMTEVEKERVARN
HRWLFQATNARVSLSFLAGLTLAAIAVATRPTIDVVDVGPDVELGKQSVGFYKHSEAALR
WLWIVYYHHPAYKSLAKGTLPPALQNGGARC*
>TCRU_7789 hypothetical protein, conserved
MVSYAPPEFSEELFGVMLESCTPSRSRVEALTQVALRHLTQATDTWSALRKALVRQQDLE
SDENKGLWYLLDSLMKHAPHVFVPLISPRLHDYVVQQMPWHLVGVVSTLGSGALWCDAMI
LTWESILPPHLMRNVKSFVVQLRSGKELTNAMNLSGDTDEVQSVDAPASREQIQQLREAW
EVFFSFVAEGVRASNNTPAASTTSGALPLAQVKCETTPFAGLKREEGTQPAGADDDDSDV
EYVPEFVRGAQHRPLPSLTGDNTTTQKTRRAARRRPREED*
>TCRU_7790 Galactose oxidase, central domain/Kelch motif containing protein, putative
MSLCHTASRWRSVQCTGDIPPGRIGHTLCANGTETKIFLYGGVNDRNESISNYLDDLYVF
DVNKKHWSKIEMTGQVQCSRAFHSAVYYEGKIYIFGGCNGRGRFNKLFSTSEEGLCAQIE
ASGQPPSTRYCHSAVLFERCMYIFAGKCGGRNSNRRLSDLYLFDFQTNTWMECPQHGDPP
TPRSAHAAFTCGRNMIMFGGRSAQGECCEDMYMYNYDTCMWRPIESPNSGPLFGRARNSV
VVHHGRVVVFGGWNGKKKLNDLFTYHVDSNTFEVMHEPDENCPSRRECHVAVVCKNTMVV
FGGRFRGEFMSDTAELDLGPKTLKQNCRDWILRSSFKELHSNRGERLPLRLQQFIESWRQ
LICRVEKIEPRTPLQDSAPNEALSSDSNSQHG*
>TCRU_7791 40S ribosomal protein S8, putative
MGIVRSRLHKRKITGGKTKIHRKRMKAELGRLPAHTKLGARRVSPVRARGGNFKLRGLRL
DTGNFAWSTEAIAQRARILDVVYNATSNELVRTKTLVKNCIVVVDAAPFKLWYAKHYGID
LDAAKSKKTLQSTTEKKKSKKTSHAMTEKYDVKKASDELKRKWMLRRENHKIEKAVADQL
KEGRLLARITSRPGQTARADGALLEGAELQFYLKKLEKKKR*
>TCRU_7792 Enriched in surface-labeled proteome protein 1
MNESKKYTQVLEEGTSPHSKKVDVSRPRTVVNGSDIYMLAGKYSRTAATNPQERGAGDWV
LLLVEGEVSSEESGSIKKIRWNKNQRLAGTFPEAERDSLMQLVAGGGSGVQTDDGTLVLP
VEGTTKGESEKGGKTVSLFIYSLDDSCWTLSKGMSDGGCGDPSVVEWKDKKLIMMTACDD
GRRRVYESGDKGESWTEALGTLSRVWGNKKGEQTKRVASGCTTATFENGDANKKVVLVTL
PVYSKEKCSEKKEKSELHLWLTDNTRIVDIGPVSEKDEDEVAASSLPYKSAGGEDNNNED
RLIALYEKKKKKGLDETPHSLLSVRLTEQLQRVKEVPATWKKVDEHVSQPCPTSGAAKSA
LTDNACSAVKIADGLVGILSGSFSDKTWIDEYLGVNATVMKGTKGVATGYAEGATFQGAR
AEWPVGEQGENQLYHFANYNFTLVATVTIDGVPTKEGPISLMGVKMNDNGKTVLLGLSYN
NKEKKWMLLCGEEKSNEHSSPWEPGKTHQLAIVLQNGNQSTAYVDSERVGDETHSLKNTE
SKDISRFYIGVGGGDAESREEVSVTVTNVLLYNRPLSAAEVGTLNPNKVPIPPPVGGSAQ
GTLLQSPSDGQPPLGRESLNEDGGVGSGGVSTSAVSTATPSAGEGSVKQLALRTSSGGSE
NVDVVSSLDGDPTMGAEAGDTVPGDRPPQTSAGTPVTADANTPTAETVGQFDPAVKTGVH

VSSGESGKTVGGGDGREDVHSRVREVNATALSSSLGNLSHGNNSDAGAVRGSGMLPPLLL
LGIWVVSAL*
>TCRU_of Trypanosoma cruzi C-terminus, putative Dispersed gene
family protein.1
MEAVVLAVTTYCMVLWYVEDCDWQELREPRRGGLEALLRDGEDGAEETQKSYDMTSSSYA
SGKHCFVVVPNTCTAVAPYGW*
>TCRU_7794 Domain of unknown function (DUF4206), putative
MFPTLVSLEHAVRDIKVFAHEQQQRSSLSLSTISLTLAVAPALVARLLNGIEEAFTPEPL
LGAEAFFEGVAVPLLHHLPRKHKTHFPMEETLRVRRPEAADAFRCWVVHSLNTADSLYET
AALLLVGPIVKDATGTVGQEQIMAVGEGKEKTGDFSQFGAERVRRLKESLGPHTTFLNGG
YVMQLLSLLLRVWHPSPNGAGSMEGKSVAVQYEFSLAEALPLFREVPREVHVERLRLHRR
KRKKRRVSTAAAECASEGDASQEKINVSSTTCVPVPGDGTEEEEASDAVMPLWSRLKDIM
LSQRSTVCTAGMLGHTCDRTTCANRHCYWDGDEYCYVADASTQTLKNDVCGDPHEEIVGR
EEEVVEKGVMNGSNGTRLMTQAKPVSLKCGVASDGKLSSQSVSTNTEHPSSFMTFVELLD
AQEQLERAREEVRQKEESVQLRECGLAELEEDYKEKLEMLVHVLHGTRKIYNELVMASVT
ECGGATCEEEAPSAAAVQSRLLNLIEVIYGKADGEEEEEEEEEEDGKRRRRMIATKPIPD
TPASRAAAKLKIAQYEKLRQKQLLQERQHAIYGAVTSAGATGATGPIVLTPLEFPRSLQL
RRQAYLCPGCGIALGGTVRSGLFRINKPHRCHYCTQIYCRECHVKQVAVLPFLVLNSWCF
TPRGVCKRDYEWLQQNWSKPWYTVESGEGRMKQRCFHSVASRDSVQLAKVLRHWFLLCAQ
MVRGCTEPLSDKLAMLLQTYYAETDVNYSLSDLSGLKYSEDVGTALRELRGGNVLGPLDG
VTSRIGSMLIEPSFVAATVGNVMSAVSFGRLLTSWNLDRTVAVAELEEKHTKHRHESSPV
VARGEAGASLASVESDSSLAHSISTTVSTNASKENERQDFLGYLATQIRVMEQHLHRDCP
TCVARATTVCELCEGRDEGARLPLVDAEVVGVRLLERGAVVPGEEEDAPLLRLARVAMQL
VRGDSERRRDVVACGECGTRYHKACLAGARCPHCR*
>TCRU_subclass, putative zinc finger domain, LS.1
MMFLGELVCAGCRKIISYPLGAISCRCRNCNTVNAAQNMHLECGCCGQSILVPVNTLTFL
CPCCATVTDIPQPLLPRVENPFIMGLNGELSSKTIYVTYPHGSSKKGGLMQEAEGPERHK
SREEEEHEMVTVNKNTAANDEEESPRQKQQRRRQREQQSMVMVVGTRIL*
>TCRU_7796 fatty acid elongase, putative
MFPYVEDYDGYAVKRMMLENVDVLGYLSLGYLALVWKGPAVVRRLNGETNRVSNSGRLRY
AIIVWNLLLSAFSFFGMIVVVPAFLTRISQRGMLRALCDKNDEMFYRSSTGFWIGMFALS
KVPELVDTVFLLLQGKTPPFLHWYHHVTVLIFSWHTYCDHTSTMALFAAMNLTVHFIMYF
YFAMCACGFKKTMRKFAPFITMLQILQMVVGSLVTTYSAYKVYTTPEGAAPGCHVSRANA
RMGVIMYMSYLYLFSEMFMNSYARPKKPVANPTAAGKNV*
>TCRU_7797 hypothetical protein, conserved
MALHLTPLKRSQLLDLGKLVESVLHSSCSSSLVSSGGMLSGGNGVVHLVDASVAEHPFAC
GAFCDVFEDPLTRNAWRLYDKMLYLVWWSHRPPCCTECGMQDAWVPSADSEMKCWQCGTG
AGTTFVKDIVEDLPALENEDGEEDGDSDGGDLAGEGGGGAHTAGGGGGVGGGPVASYTFF
YEWLSHVQLMERGKDVVLPAGESLAAVLRAAYDLALLFVMPGLPTTAVAVLQGGALYLSL
VLHRFPAPFPLFRLAGRVDVSQQPHSAHATAASSTRLAVGREEQREELQWVDVELLAALI
GVSLSDFFESSQVAVQYLQNVMTVAATFAVPSVLWHPQRVEGRAEYMMTLRQRRRCSSSL
YSTAVSSGLSPEHTAMIVALELARAFDSQPCDSVEHTERIGAWLDRHGLYPQRQFYHKSS
NIKNNDNNDNDNHGNDGNNNYFHHSCQGVQQSLGNGHESDNLATTSSPLAAIDDTAWWTS
PITTETSPFAGTMQAVLLSPCANALLYVFASAFSMPALELAEMAVSSGLYSGPTRFFDTL
RQAAQSGNYTLMPLSRRLSPIMSVWTSAYFALHSEDRLPLLAALQHIRAANTREKELAVA
RVVQRILRKHQASRQYQFNYSIRVADDSEKQQFKGVYFLSFVTERFAVYTGIRSARKTVT
FDAETGKIALCIIGAKEQQVESLDVQFNGPIVAQIETESAKCVIDCVCQSLGAEVWQVTV
RHLDRCGRVRRRMRVPMLASRLDALASVREATAMASHPIAGHTTLLGWGETEVLFTSLPD
AHDAAYAVRLRRELQQNLFSLPKPSLVFGISENRIIAMYASLVALLERIEQQLSQPSSGA
VSSFLVSAQRSGGSAATWVDVLLGEEDGGESDAVHAGGTRRLKDTPLSQMNGGSGLPESP
MLLPASTAALKLEQQQQQHGASRQTPLRSREVRSVPTYQEVMLGLAGHPGGGRSRLVPGG
RVRAAPHRDRQPRRAAQQQSPRRPGGDAGDGVGHAPSAAPAGLDCVSFNLFCAEECRKRL
YRLLEFVAVYTARRRKRDRSSTAGHTEATVVAGNGEAGAAGHAAEALMTGVRKELPSPRL
NHNPQQQPSTPREKPTLRHNTPPTRHGANPLLMPQSSPRHGPSSATKPTSSPSIAPMHKP

HHHCHSRRQRRSRPAPGESSDDGDQGGQSPISSVVLHGGSSGGVERSPYLRKRSRVQHDE
GRHGGVHEEQTRTVSPQSPSSSSSLSSSSSLSRSSSVGSSSMDTESSANRRSQRGGRRRR
RRNA*
>TCRU_7798 ADP-ribosylation factor family/50S ribosome-binding
GTPase/Miro-like protein/Ras family, putative
MIISEAQDGVDTVKCVAANDRKCDSNSGNGTKSGDVGGEFKPASPEASNATVTSSQHCAI
PKYKVIIVGDSGVGKSSLLSRFANSSFNLEKKATVFLESASVELEVPAARVGEKERVIAQ
LCDTAGQERCAAIRSTFFRGAVGALLVYDVTQEETLLRLSMWYAHVRRYACEDCVCIVLG
NKTDLHSSQFLSKGAANDIVNRLGMRHITASALKGSGVREAFMQLVSSINAVQRAKRLAA
QKQEEKATTAAAPHRSLADPAAASLPCGGNQSSTLFLNSPSSSAVFSSASAPIPMSGGGR
DRGGFVAVTFAVVGGRGGGGGKTQSEEKAVSPNKRCCILW*
>TCRU_7799 ribosomal protein L21, putative
MSHVQCANPVLAKAIESLLNGPKFAVVYCGNLQYKVSVGDVIAVQRLRAEIGSCIALKKV
LMVGGPRFTAIGRPLLTGVRVTADVEEQKRMRNIVSLFATPGRRRVRWVDAPHAATILRI
REIQYAPQVAGELDKYNGMLLNDFAPEKHTNPVYTADDGFDVFRKRDKEAVENASAFLDL
MR*
>TCRU_7800 hypothetical protein, conserved
MAGTTIPFCIFEDGDLCVESSAHPEQGAPSLLISLEPLLSSVVRAKSSWSAGANATENTL
VCHLSAWNKREKLCLIASLRSCIEDASPSNMNVPSTSDPLGVTEVGGGCEVKCVSPGQQT
REDSFPLNNAFVETVVRGSFWRTFGRRGGRDTNQKGVMSDGEVLDMERVHTRVRELRRFL
QQRHESEFRTKKPIAKSSGLRGVQGQRKETDEEETVDMKRLLTIMTGSTRGHSTQSVAFG
GNEPFLVGLVCRELTAGSTPRVLSVRPFVTAGLTTTSCESGEDSVRGNLGNEENEEEKTE
LSLSVMLLELGIDKLDFEKSQMSPIWQTLVSVTDFVYAVGCSTTINHVASMIDDVYHAVI
TAPGPMHARVGCGARPAECPFFFYTVLGEAPCSMKQIPARSHCVGDLQAVFSHLLRMKEM
QESTCSRNPFHWSMLLGHMWFLTKGAHGKTLSSPIEGRMNDAIVAAVELFVATAEGVLLA
MYAMEPLPPLSVWGDDIGTMTAVPRHFTLEDVLHVANQLALLAFDTDVAPCLFSGQLTPR
HDVLLDEYCGCRYHITKEELQRACHLASESLKERISAFTTYSAVQLLKQSSLGITSVWGP
TGGEKRPENVSLACVIEDCTHWIEQFLTVLLLPHYGVEEGAENNNASGRRNGPPCRMMES
PIISTWVPTAKAVVFSEHVKNSLLPALQAIARERESLFRAKEIGESEAREALRLMEDNCI
QLQRRCKRAEAQLAHQRCAAQEAKRRSDILRTQLHESCKCLQTLVKTCVGYEETHRSFTR
ELRFRLKHGFATGEITPMPDSPPQYPWTHDREMEMDALVTTPSKNVVCENSAETEREMTR
PLSDTKKEVSAEETRGPSPVPCEQVALLKRMLCEAHQQLEVSYNTLLCLYEDARGALRNL
STASAECSSVSLNDSRQSFLSVSQQATRTMTPVRSIGRSLNTSVGNAACGEISAVSLEST
PKKSAAGREISCHDVCRSDESQTLLIKDFSKSPSRELTQIACASQCTDAMPSTDHMQLHK
RQQHGAEGKSRQQRRPFSTWTAAVPPPPLPDLGVNSAVDAIADLQRQRQEAVEALTQLSG
RYEAVKRELDERNAAIADANCKQKTEEERWRAEREALLQRLCAATNEKHLAENEYRRCQK
EVESWAQSWLEMMANSAEEAENIFTGDEGIYTFAVNGGENGENGGKEEDGKRVNGKHETT
SICLKTPEEALRSGKMRLRSLMMQVQVAARERVKNVAERHIVALQREIEDAREQVYKEEL
QKRADATATLLKSEERAQMVEEVNRLQEALAVMLEREGALRLDRNELALQKEDLWCRLHR
MESAYMALFNVWEDTMLKRCAFILWQWSSLVMGLCEENAVLSARLKQSQAEVRYLEETLQ
GQADGTQQAAEEIKQTAMQMERNLVAQSTAEKRVSELLRRLDQLVTLYGLSLDTWEQAMA
QRCELIVEHWNDKSPHHLYRQPKTERELTSREERSPQRIETHEPCGLLHELQQKKRRIAE
LEEALRQNKVRCATLEEAVAQLNALLKAQRELGMAGAPSPPLISQEFGVLNTLPARTANV
APSVVNSFYASPNRACETNMREYSLLGGVAAGSSPIAGSKRPAVFSEAYHGVGSARGLDG
EEDALEPRSLSWYLQSFSAIESTLSH*
>TCRU_7801 Domain of unknown function (DUF4201), putative
MSTARSPVAENGSEVNPFEFLACDSNEQQLWEEVYLRQFPDAQEFGALTLEEQREIVAEL
QEEVDLLEEETTVFLRHAESLRMPRVPNALLGSPTNRRKSISTLLLSEPLPQAPEDSTLS
ENLVAMSGELGGEAIALSSSSVRRGQAYSRKSVDANEMYVTLEDRVAMLTKERDRLRQQR
EKDEKEGEHLHELLTATVKEAVGRSKELRLELLQFKREVLNEGSSTASSDDLLRFMAKRY
SMQAKYLDKLNVQCAAAERNITQTQQQLRQRHAAGEAFRAIDFEQLRIENQQFNERIERK
NLELVELKGTSTRTVQTLNTLMDALNGLTAEQNRLRKDLKNRCEYLARLQREMVSVTSEA
DAAERKNATIKSQHEAVRVPKIEHYLAQKAEEYELQKAERHWNRKVEIAGGQMRLVQQQI
RALARATQPTRRWCKRTGHQMRTPSKSHAKSSPGTGESVTLFADTEGNFEVETQKNVSPV

VGGSKALLNMKRKK*
>TCRU_7802 hypothetical protein, conserved
MHVVNLCNLPSAIAHVAHFASTIRRPGSAAPIAGDLNLHHELRDGCSPSTAAGEDLAATP
SGMEIELSDDPAQAARISGRRVLFPT*
>TCRU_7803 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGVFGIAADGEVDVTREKDESLEGPLRGSRENEDGPQKSLGS
VMQRSNTANQALSLENGVMVSQPEDPAKKQVPDEVETQKESEETEEEDYDVVVDEDVEEE
EREEETVETAETEIPNDQTKEEASSPPESKHKKGPTPTAAKGIPTTQSPATPVLPTTQGQ
PPTAAPSPEDSPVPAALAATVTPAVTPSEQGNIPAAARKKDEKQSEDIDPAQESEQPGPQ
DFVLVQHSQGVHESKESNNNPRNPASASATANQRDATFNGRGEPAQTTSSNKSVFEIKDA
NSGTEEGISSDDPTADGAGTNDTKNSQNKHGNTKETPVEVTAMKGATATTGDSDGSTAVS
HTTSPLLLLLLVVVACAAAVVAA*
>TCRU_7804 RNase H, putative
MIPCIRHRRKTLLVVTDSRSLLAALNKGPLSQTDWTEDQIWQRLLTLTRAGWSVHLQFCY
GHCGVHANELADQYATQTMATGQYTEQGIAPLWHTDLLTCFTTQLTNKWRSTIRQDTHRY
LLCGTRPSDLSGKDLITQEVLHRQELVRLARARCGESELWGRLYWAVRDCTNQCRFCNIS
PEQSAYMRSNNDPTAPATDTVPPSAREEDVSPVSRRTLTRRRKEKCPHCDSTSTGFSGLV
SHCRSFHPEHPPPLPELKCDFCDMVFPTRRSTAQHRSRCAHNPDATRHLNRSARRRSLLP
QDQPASTSTPIGPQETLHHLLLECPGTLAVRQRLGIEQDLRLGKFSQ*
>TCRU_7805 Enriched in surface-labeled proteome protein 1
MPRRVFTSAVLLLVVMMCCGSGVAQGDGPSLPQESSLDKRFVWRDTTGDETVSSLRGPSL
VEVNGKVFAVAEAQCTKGENSFTGIASKLLTLTDEPSKEELDANNLKTQVLEECPANKEG
TCSAGKEEKCGCRVADQESGSPNERKVHVSRPTTIVNGNDIYMLVGNYSRTAATGHEEGG
TDHWGLLLVKGQVSGAVEEEKRICWNDTHAIPLTLGDQHKSLTALIGGGGSSVKTKNATL
VFPVEGTKKKENDGAEKNGKSVSLVLCLQGTEIWKLSKEVPADGCGDPSVVEWKDKLMMM
TACDDGRRRVYESDDKGESWTEALGTLSRVWGSKENGNVKGVRSGFITATIDGVGGAKRN
VMLVTLPVYPEKEKNENENGKGELHLWLTDNTHIVDIGSVSSDDDVAASSLLYKSGNNNN
EEELITLYEKKKKAEGDTPSPGMVSVRLTAQLQRVKEVLATWKEVDGRVSELCPFENAKN
DAPTDNACSAVKITDGLVGFLSGNFSGNTWRDEYLGVNATVNKEEGKVTSTENGMNFQGA
WAEWSVGRQGDNQLYHFANYKFTLLATVSIHGVPEEGDTPIPLMGAKMNDDSENTVLLGL
SYKREGNWAVLCSGQTTKKHSNTWEPQTQYQVAIVLNNGTQGSAYVDGKSVGDESCVLKS
KDPKGISHFYIGGDGGSAEGQEGFSVTVSNVLLYNRPLDGTEITALAKNKITIPKPEGPN
TLMVDTHSTVVSGPVAQKTVSVSTPGGFTVNHESSASSGEVAETVGGTDAQGEEGIHSQD
GEVNAAALNSSPGNLSQGNNSDGGTMRGSGLLPLLLLLLGLWGFAAL*
>TCRU_7806 Mucin-like glycoprotein, putative
MMMTCRLLCALLLLALCCCPSVHAGNTQEATEDQDDTEDPNSSLLLPKSKAAASNGGAAG
LAAAAPGGIPGNSHPGSSSLGSTEQPEKGAVEEGPTVTVPQGNAESVKVQRDDKDSKTGT
TRSTSTPTEKIVKEAEDTAKTTTTTTTTKSPTTTTTTAPEAPSTTTTEAPTTTTTRAPSR
LREMDGSLSSSAWVCAPLVLAASALAYTALG*
>TCRU_7807 hypothetical protein, conserved
MRASGPESLDGGHAAGTTSPRSDASQQAACGVHAGGGRTSQGSRASEQTVTGQSQVPGTA
KEAPQGDEGGEPGAQHEADQTTKMTVVTACAETAVEEESRQRDRKMHHVSIVAGMLIIII
IFLLPTCLATRCHQGAEGMVEQRHEFPAMRQLPLGEAFGAKVLLDAQPLAQSQSVCTFRK
QMAQCFLRANCCACGGWLILR*
>TCRU_7808 hypothetical protein, conserved
MKSPWSPSCSQQRPAAEFLYATKAQHRDKAQHHRWGPWILATDGGVDIPTSAGIGILLSS
PRSSEIIQKVSTNGGTRPCSRTTESRALLPAMERLSVHRIQHRRKTLLVVTDSHSLLDAV
TKGPLSHTEWTEDRIWQRLLSLTRAGWSVQLHFATDIAEYTLTSLQISMRRRPRQPGNTR
SME*
>TCRU_7809 hypothetical protein, conserved
MDRPFLPYVLDVAIRDSLPGSAPGPDDMLNEFLHRLVPVARGTLRKMIHNSFANGSLPGS
WKMGDAIPIPKPGKDPCRPESYRPITLLSVLPKLTEGMIHRRLSALLPHHPRQFRICTSA
FYVGRGGTCYRHITLGLNEFGIVEYERPGDDAPTRRPRRHRLWSRLIFRLRSTPLTMGSY
SACLTDFRALATNQTLAAQLPAGPLC*

>TCRU_7810 Mucin-like glycoprotein, putative
MVTCRLLCALLVLALCCCPSVWAADTDTESVDVTEDVDEDGRGGAEQLATAVELPNEETV
PSGLPVTVPGADQGTNTREGQRSTDKLPESDEAADTVQQKSKNGTTGRETDENASTRNTD
KKHEDPFTMTSTTTTQAPTITTTTTTTTAPEAPSTTTTEAPTTTTTRAPSRLREIDGSLS
SSAWVCAPLVLAASALAYTTLG*
>TCRU_7811 5'-AMP-activated protein kinase catalytic subunit alpha, putative
MHSRRDVDSVPREPSSDVQYIGNYAMGETIGKGSFGKVRKGRHLPTGETVAIKILNRNKL
NNAKMGKRVYREMKILKLFSHPNICRLYEVIKTPTDMYLIMEYVEGGELYDYIVKRRMLK
EDVGRYILQQIVCALEYCHHFLVVHRDLKPENILLGPGLQVKLIDFGLANIMKDNEFLAS
SCGSPNYAAPEILSGKLYFGPEVDVWSCGVILYALLCGCLPFDEESIPLLFSKIKKGQYQ
IPPHVSHGARELIEQILVVDPLMRLTIPQIRDNAWFNTNLPMRLSYNETIFLTGQKRISP
KVASRAAKILGMRDRDLRGEIEEGHGSGYVAYKILLDAERAKQIIAEAESFAVEDDLWGG
SKRLATHVSKATERELNLGLLLTQSPAMETLLEVGDATSNKRAYNCGNFVPASVQETKAF
AMSVHTPVSNGTFSISRRPESLTDATNPFGSGFVGSGSSVQRPSALSTSARQGSNTNLGA
SVGDRQHVGSVAKSHMVYTKEEEEFIVRNNVGWRLGLMSDFNAAVSQNVLYSTLTSFEME
WKVLSPFRLLVRTTPGTWAKIGLAPTRSPLTPLSMDPPELLNEHSPNPAITSYTASPPNV
ILALYLLRIHEKHDRGYLLDFSVVKGSLLALDVVLRLSTTLVHRMG*
>TCRU_7812 hypothetical protein, conserved
MFLFCGLRLRNRKCDGVPNVGKLLYGKRKNAIHTTSKAKPSVVGLLMQVPESELRQAAWR
AANVKELNKSTLSEVLKKYRAVNRLDRSEVVVAVADEFSLGLTSSNYCTLMAHANDNKDY
QTALRYWNRACSEKKANEKVHGALLATYRGASRWKDAVQHYNAMLEDKITLDPYALHTVM
NACRRANACDVAITTFSKAVRSGASPNSAVYLELLRCMQQLRKPNQWKMSLEVLCSIEGK
VDLTAGHFNATMATMGGALWTKGVELFQTMKTKNVQPSKETLSTLTLLNPNNLPHAVQCV
AEAHTLGMPITDAMYRAVLTNLFRLKLDHEAVRFAEREFGKCNEDPGNPVNASLSLSLAI
IDGLLAHNRPQEALLFFSTFETRLGNVVGSATRGLGTIGLRSQRWIVQGRVAVVDHNVLL
DPRCESLFSHYDSILVPFSSIRLLVRRVRELFGTLKGRYTKQRLKRLQELTADQSTPMRV
LPMAHQLIAHTYIVDGPITSESVECLRETAREKKDEDEQLREEQRRLTESFFIRKRDALF
SKDGFVARVCGSSIKEGADVAVVVKPGETPVVSGSGPVVLNSPDRMSAPERMLAVAVMLK
SLNPDSNVHVVSPNPVQLQVVEKWNQMHPAIPLTMVRYPEEVTLKAPAEEQQQQPSFDRS
NEEVPVTKKASCDRVPWHERRPLFFPS*
>TCRU_7813 NOL1/NOP2/sun family, putative
MEVPCDTAALGYPETFTEEFIRYCLVHHLPPLLFHDLSEVLERIPRYIRVRPQYMLKNIV
MPPEDNNVAGEVAARQERCQIKAQIAASFGVSSASVEEVEWLPNPYYYAVPRGAAMSRAA
IYQIGMVSAMDAASVAAVVALRPCQGDLVWDVCCSPGMKLSLIADAIGETGVAVGTDINL
NRLFTARSVLRKHQAGNVCLFAADGTSFTLHEAAAALDEMISSGKPGGNGLTPWEERKLR
RFRKRRHEMSVETATASIGMKEERELAVAFSTVHARERICCIEKWKNEHQGFDRVLVDAE
CSHDGSLAHIFFNDATRKPFSAAKATPMTVSSGIDNAHRMQRLHLALQSDEKEAKVQEEL
SPLLQIQLNLLRNGYSQLKPGGTLVYCTCSFTYEQNEFIVRETVSRVNSSKDIKRQYNGE
AVIRHPFLYTHETVSLEVISPIVRLTDAQAASLQERLKMDPDPYGILCAEVRNEEEATFT
GVRLWPRNFATSFQFIAKIWKRPLCSSTTE*
>TCRU_7814 hypothetical protein, conserved
MRRRTSRKHDNATLTVSLNGICKQADFLLLTCVFHKLKNYVQLRQQDTHLKRCAVLLKHQ
AIKKIVTDHFVRWLGNTQRQISIRSGQREPTKIVVLPRAQDFINLGLRYLARWRLWLRYL
RQRQHRNVTLLHDKVTEVRHHKFFFKWYCFLSQEQKKSFLLRIHELESEKMLRAEYIAEL
ETKLQKQEKSINNLTKDAENLQEQKIRQQTETKCIKEAMEMAITKLEKKSTEVPGTKTLH
AAEEMARYGDDVPLRLLTSCMDAANALEKLRKALPDGFVSSDGKEGIADVICQQTKALQG
YTSRMENELAALRSSDKELRQLVEDLRAHDERWELNHKRTARAAKTHQKRQLEGSDWGTV
LRSRPVELQRALITDAADACHVEPECITNVVMAADGLLSFDVQHDPSVSAEELSGRVNEY
PFRTARRVYQRRTAPKDGLDLLEEQLAEKEQKVVELRGFMEMAVTTLGNPDAAPRVSGVR
SAAEEMARYGDDVPLRLLTSCMDAANALEKLRKALPDGFVSSGEFDSIVDVACNRAAELN
DKVVQLLKELQDSKSFAVFLREVLQEGASRILLLANYTPFSHPPSLFKTFDEKVASLSWC
GSEINLDAFECSPDARDSLDVVKDHLLQDRSLTANGPSTAGVLRSFNGALGQMYEMLTRC
KEFFLEQEKLAGQEGEKRVLLVKAVKDAVAALQGWSVASGGVATEGMDELQLVTDMRQES

EVASNTLARLRQLLSGEAVGKKVGSGSLNELRGGESLIVQLPVIETHEDLLNAVSKVYDR
LQEVGKAYNDIYSAFIQFAQEPSPIINDMSGNVSSVAPPTSLSYDPVKRAEFAIRGVHSY
IEGKGREVKELRGVMRRGIVALGGAEESDTDDDLMDQRRSAAKSTAVGEKLAVLCRETGD
AIEDTRKALGIPNEGKLRLPAVISNLEGKMQELDLVTMESALLVREVRSTPTDTQESSSN
LSRNLRPKRKPAALVVDDLKSGWTNGVRPLHPSLSSAEAGTPNLKPDELLRQMRIELQDK
NAEIREIFGACRTVVSLLDGSYKANAQPPQCGGALVPLLTTQAEELERALRLAEEVLSSF
EVQGNSGVGNYLTLLASQLASLRIEKEKLQEEMNKHKTENTQLVTEFNEEISCLKKQNEI
LLKRLKSLQEKLGALKKLRQLRAKKMMEILRLRTVKEHLGRSVILWLGKVVATCTAEARG
AANEQKRLSIAIVQKQHQQNQIAKLLAIALHSLPGEKPTNADVLDTENALMQCALEDEGA
ALEAFARKRLDAAKVWMKSFLRALSSVVSLRADTVALRQSIANCWRGRLEEAYGQVLNAA
FKEIADFDKQKKMECEFLRNRARDREEIARENRSLSCEIAGMKEQLGLAQDYMALQDEKI
IKLQRENRDLRISCVLRREEKESNTSTDVTPSKSLRGGSGAERIMIARAKKLALEAINAM
AGKNVAACIGEVAELTLEMYRRTSAALEDICNAQNAPLGPLSAVVEARLQELQNMRGVQN
NILARLPELFRVPYVN*
>TCRU_7815 fumarate hydratase, class I
MSLCENCNLANECRGIQDIEDSKASASEFHYEPIFQPSDPHHDETEYYMLEGDYIKTVEI
LGKTILQVKPEALTALAQQAFADVHHFFRKDHLSGWRRILEDPEASNNDRFVAHTLLQNA
CVAAGRVLPACQDTGTAIVLGKRGELCWTGGEDEKHLSKGIWDCYMNRYLRYSQTAALDM
FKEVNTGNNLPAQFDLLATAGNEYHFLFIAKGGGSANKAFLYQETKALLNPKSLREFIEQ
KLKTLGTAACPPYHIALVIGGTSAEMTMKTVKLASCRYYDSLPTTGNKNGRAFRDLEWEA
IVMDIACKSGIGAQFGGKYFAHQARVIRLPRHGASCPVGLGVSCSADRQILAKITPKGVF
VERLVRDPAQYLPELPPSSLSTNVVNVNLNQPMSEIRKLLSQYPVTTRLSLTGTLIVARD
IAHAKIMERLNNNEELPQYMKDHPVYYAGPAKTPKGMASGSFGPTTAGRMDSYLCPFMAA
GGSFVTLAKGNRSKAVTEACKKYGGFYLGSIGGSAAILAQNNIKNVEVVEFPELGMEAVW
RIDVVDFPAFIVVDDKGNDFFSKLL*
>TCRU_7816 protein farnesyltransferase alpha subunit, putative
MQPSMLAHDGKNAPRNSLSSSSSFKTVSSSASLGDDVGRMGMLLKNEALQTLFQDVKPTN
EPVAPRQPGVLQIQYSRAFDYVMGLYRTMSAKFSGIGSPSSARWFLLTAFVLCQCNGHYT
GWKDRRDVVLESARLLSSTREDLLVKWGTKEENSSGNDERLEKLMPLVENWLPAEAELKG
PTGSFSEWRAVRWELNAVKCFNLNNHKNFQVWHHRKELLLEALARTDSPSRTSDLASMGL
FDKYLIEHHGVHFRDIDERSLCNEVLNMDHKNYHVWLHRSWFVHAFYFLVQPPSWTALLN
SYAASAGQREKSTAPLRQFVVQEKWEEYCLESNIPPCGLKDELGYTAVLIRDDNLNNSAW
CHRFYLFDHDLIGVLLQTSSQHQPNDVEKVLRELCLDEMHYALQWCVYEPCNESSFVHAR
GVANAYQSAALRFYLSRDATGAYHNCLADKGPISSMEPLPSHYMCLKKKVPWDVFLATFS
LMQQQLCVLRENVAPRAEEHRSRASASDNATVRMLHNCRSQFLIDNVYQVYAALYHGLFV
LLEHLWCCYFTEAERRWVNEVLPPEKYAEGAEAAAGIIKTQQLEYCVRFFLEHEVQAMEL
ARRLVVEDSIRSKYWKNEIKIVMHRDYI*
>TCRU_7817 hypothetical protein, conserved
MLQRKLLAAFRAKLPPRSEKSGPLSSNPGKINTNPAAPPTPAQWNASAGPMTTPYGAQID
HYIRDLEAHFKNSSEAMLDARKAIEGILTEQAKARQEHCREYVLTFVPLVFTLILFLREQ
INRSCAEQTHLFLKEHADKCSSLKRVVL*
>TCRU_7818 hypothetical protein, conserved
MLAPTVTREACQPIINAFRCAAEKGPTQTDVDAESWGREVARINAEAQKAWSEQRKPFIP
AMYLRRRDPAAEEALRLLRVTSKAFELNLRFREIEKLDEMHAKLWALLSADKTRLTITII
EYMEILKKFKAWQEERFEGTPKASPQREASVQSSQECLDDTTPLGSVVYLASVMQPRPSL
QLYLSCPRSPAGGVEVVHIYQRFAKQVSLVKCEAELIMWDTNNDGCLTEDEMESYVRDLV
PRIEALRDITEDILPFYCCTVSRRIFWVLDPGSRGAIRIDMLLQNPVMDEWVSLQLMRED
QPRNWFSAAITSHLYDKFLLLDTRNRGTLNADDMKRYKKGLPTVMDDGLPPGVGPLSSLF
IDRFFETNVMMANSELDFRKFVDFVVAVEFLPSCQRPLFFWNILDIEGCGYLKPVHVNYF
FRETHTKLVAAGLEVPSRETVVQEAFDLISTAEPLCISREEFINAPQAGLFVALLVDCLS
FWTYENREQR*
>TCRU_7819 hypothetical protein, conserved
MDFVEVAPEAICSTSHSRFQNLPYDVLMLCAEYTPVREVLILGTLNHFFHEFTAPDNVAL
WTIFTERVYLLRPPGLRRMLFNESLLKTYTAVHSISRSNMKSWGGMTINDVEDDDLNSNS

EKEDEDVDDEIVTNRHQHSAPSLEGSRRIISQPELIQWVIDHSEEVLLDLRMFCDIIKGR
EPRFALTGLLMALQFVKRRMWYTEVTDLESVRDLLRSTIVEEEHDPGWSVLRTIAGRGRT
MPKRFRVSVSVCMQTDDMAELSARRQMSKLRWKRCAAVAREYLKLREVLRVILAVSEVSD
HPNAQQRYDSVWSALRGTTAMLNAEKVPQHNQLADLDELGAAIPMSASGEELLQQIRDLG
KATVGGIVSYFFAYVIGKVERKAFLSALFSMQHLAGAEGYNGVPFW*
>TCRU_7820 hypothetical protein
MREPYVPFRAVSTAWQVLPKHVEFLRVPRLVENRCELEARVMPLFGTTMHCEATHVLPHS
IQTSEKRSAGDWTKEAASTISVETTAGIMIDVPVFSTSTPKSAHFTDINGSHVEKLFADI
SSVCSHDNTFLRDLDTGELLLPQPEMPAFVGSKTGVRHALRRRRRRLVVLGDRRGRYQLV
AVAIRRAADQRSVVGEGKDGR*
>TCRU_7821 hypothetical protein, conserved
MDAAWKQNPLFRLLAFLDIVGLQPFSARSNLTRDGEFLDVKRCFHTGSVIQDILSSGVRA
LRANIMRLFLDEEERVQMLRLVEDSAAFIKSVIAPSSLTAFVEAVESDLPAWALLRIKET
FGLTDSATTVSEQFLIDALDHWMSQRTPRENDALVLACGVQPALLESARARGDELPHAVE
DFIIDVVFPPPSSDEGEKKGKDRVLDWLIASYEKCYEAIDVDEEEEEAGEDTSSGESPEK
KMRLAEDGRELLTAENLDWFMRERPSAVPRAVLRERRRPLDNPAITVFELQNHYTANELS
VFVKKELGRRQRLKKADCVRAILKYHKPKTETLRREEAKELLPKNNSKKC*
>TCRU_7822 hypothetical protein, conserved
MFKRFNFTRFRCPTRVFLSPKNDAASNTPSLESLEIAIRHFTQSGSYQDTGKLKSLLDEL
VQCDDPRKVRLCKEACRLAHTAGHHARCAELFFSCRTLAPLPLSETVINAAAFTTRPEYL
QKCLSALDNVDLSQGASARGMPPFLLLLLRIYWQSTRCFVRIERSRPLARSINNEEVVLI
LDAIGTNRAENLALLAQYRAICEEAFLLLHLPGEVSFDSWWSKSKRLVLYHAEDEGEADV
YAQLFSWWERHLGAKSSEWFTPICLVCMMRSCVKAERWDFAIRYAALAEAYFLSENNSPD
DPLLQQTLIFFGASMQSTRGATLIRRIRHLFPEYTPSIPVLHNAVRVAGDVADEELAVWC
LQALLSEIQPIPPSSQDIFPCLIALAKCRATNFKKLLHALEESGIIQLTGEERLHLDLLF
IRHSVFCKEELDERMENYLAPVTGSSSSAEFSVRNVNLLLYILQECEHPGFMNYYTVLGR
EFHGRETLLVKAQWVAIALKWAMSQPALEHSDYKLIVKEAHALLDAAVDGSSPVSLSHNL
KSKLRTRLGVVEQLWGKGKRSEEETAGPNNMGDISLARFLRHRHRLPRVRPPEVGNDAFQ
RIKLWRVSDVLASLSQRDWREVIQQCR*
>TCRU_7823 pre-RNA processing PIH1/Nop17, putative
MDTGGGFCFQDISGLAELLEKNDGFKRPEGQKVGYSLQEANAAGDASCGATAGTSMKVNP
SSIPLPSTVVDRQLRLPIPSETREAKELEIKKRQKSKPKGYAIWTAEEIFAAFRARHDAT
VKPKEGAEQPEHSIVHQEIVTAEDVYLGIDATRVTGGPSGLLVKIVMPKLERIADLAIAV
DPYELRVSSSKYYLRAALPQKVIAGKADAKWDSINKTLNVSLSVDDSERLV*
>TCRU_7824 hypothetical protein, conserved
MDYTDIYLRQRRNENTAPQTQLSSAGVKAATEQRVERVLKGAFSVQQLVDRIEGLSTRVD
AFDEKIVNLTRLVKLAQGLQEDKEGDLRRQQHELRSRIKRQEQITVQLQEELAILKEKVP
SAIRETVKEAQQENRNEMMKVRKESEEQLYQLKIDLEEVVKTVQKDVEQNVITVQREITT
SASSQKETQNGISEQLSLLEEAVRRLEASRVTTESTRLASVEATVRQMSDMLDSLQPKAA
ATSKALEVLGEERQRTHDAIMNEIESTREWTIRNLQRVKQHVETISTDVVRLRHEQADVA
ARLNRVSCQADVEYKKLRTLLQLKSREADALGSLVGKELGRVEDMNQRHQGLRTEPGALK
GMAF*
>TCRU_7825 60S ribosomal protein L27, putative
MKFLKPGKVVIVTSGRYAGKKAVIVQNTDSKSKERPYGHSLIAGMKKYPKKVVRGMSKRT
IQRRSRVGVFLRVVNHKHFLPTRYNMDLSRELRGRINVSDASKKAKSKQLVRKLFQARYN
AGSNRWFFQRLRF*
>TCRU_7826 60S ribosomal protein L27, putative
MKFLKPGKVVIVTSGRYAGKKAVIVQNTDSKSKERPYGHSLIAGMKKYPKKVVRGMSKRT
IQRRSRVGVFLRVVNHKHFLPTRYNMDLSRELRGRINVSDASKKAKSKQLVRKLFQARYN
AGSNRWFFQRLRF*
>TCRU_7827 hypothetical protein, conserved
MAETIKCISGMEPQAILAKQQYPNGISQSMFSVFDKCKDKKRMIAPTLLKGVTIAKLWES
IFSNSSDFLKRYHERRKETEVEVGKWVYLNEMGSGYRTVSLLTVVDIPKVGSVTQLNEVH
RFSYTISSSGAVLLLYHISSQTPNVPAGQSFRTEAFLEITAESLNGDCTICVWGGCKKMS

MAFAAIQYMAVPRAIREMTNGYRLMLQMISEDLLGDAVKVATEDEDANGDGQKDGKDAEY
GGADGGGDGGYQAPGMVFQGLMLMLAIVVTISILCSISTLRSTAQISTMISSQLVDGGMQ
GGASRSSLSGNLNLHHSTGVGTARGPITQDQALRYAARDAQIQSLRYRWIEQRVTVQKLE
STVARLWWMNVLQLVFMVLLLMKTFFF*
>TCRU_7828 hypothetical protein
MCSTNSLEGIHEEERPGDAALLWPEGMQRQARGECGPSLLPVGAAPDGTNYAPYVVQSTS
TCAVPFSEMLESALHSSVEALATRAAEDESALINACAPPSSW*
>TCRU_subunit kinteoplast poly(A) polymerase complex.1
MRVAVRLLRRDERIPSPGSSLLNPRSQRAKLRQMMMTHAAQEKQFEEQALFAGLGGASSL
PPVRSKKERTSKATRRVGRDVAERAKCMTDSEWESVPMDEKHAFTKYMSQMLREHPTETT
EQQRRRYFETTMVDARDLDPQKTVRDEYERIKLGLPVQLKNPQHPLGVSQAVYEAADASL
FDPTNVHKLENAMTHIKQVFADYVNKKREGVSTEAERRQLANMTAELNLETQKHLANTFK
YAETRLRQISLEEKHRQLKEIERLRRVAQQKSGGHRRGKKEKRAARTEKLKRMISQAVGL
DMNVAETVLTEMRAQEEFLQFCEVFARLTQGSGFRHTSNDESLSAYVENLRKLYSMNADT
LSTLDVVQYYASKEGSTPVDWAKRWYEKALLLPLQNTPEYKQLLEIQQREQAAFKAKAEL
SEPSDALAIQAESQVARVKVRKVVNIVEKMFMDPRDKRLESWHEKRLRYLAHMQMERQIK
RVRENSKLFEGVECTPEAEQCRELYRNIMERRAALRASSAEITATTDGTQGVVEAESRVD
ENEQKLFNVYDDAEATALFEKIRDITKQVIQQRRIESAAAAKARSLQRIIRSLRGGEQSL
AEELRALHRQRRERITQRLLGVVENDVKTEMEWLENMEEAERPPLLPIPEGMSYVSAADV
RAWRDIRMECERKAGNPFERRKRVFQPELFGQTWRVPDRPLLFWGTGVTAVQQALRHAAE
DAERKRRGIPLAPPYPCPENPWGWRLAKDILDEE*
>TCRU_7830 Enriched in surface-labeled proteome protein 1
MGVKMNGDDENPVLLGLSYNNKEKKWEVLCGGKPTEVQNHIEGQEKTHQVAILLQNKKQG
SAYVDGRRVGATCQLENKEDRKISHFYIGGDGSNTEGQGGVSVTVRNVQLYNRPLDDSEI
TALNAIKVPITPPKETNAQEIVLPSPDGTPQAGQEALNGGEGAAGGSASPSAVSASTTSS
GSGQSVNQLAPGKPPDGNADVDGAFSSSGNPTVGEGSADTTQGDGPHTPSVGNTAAAADT
NVLTAKGEGHDGPALTPDLSVSPGADGETAGGTDGQEEGIHPQDREVKSAALSSSLGNLS
QGNNSDAGTVRERRVPSLPSLLLLGLWGFAAL*
>TCRU_7831 glutamine aminotransferase (GlnAT)
MAITAICDAGDYALVPQPGFPHYETVCKAYGIGMHFYNCRPENDWEADLDEIRRLKDDKT
KLLIVTNPSNPCGSNFSRKHVEDIVRLAEELRLPLFSDEIYAGMVFKGKDPNATFTSVAD
FETTVPRVILGGTAKNLVVPGWRLGWLLYVDPHGNGPSFLDGLKRVGMLVCGPCTVVQAA
LGEALLNTPQEHLDQIVAKIEESAMYLYNHIGECIGLAPTMPRGAMYLMSRIDLEKYRDI
KTDVEFFEKLLEEENVQVLPGTIFHAPGFTRLTTTRPVEVYREAVERIKAFCQRHAAV*
>TCRU_7832 glutamine aminotransferase (GlnAT)
MAITAICDAGDYALVPQPGFPHYETVCKAYGIGMHFYNCRPENDWEADLDEIRRLKDDKT
KLLIVTNPSNPCGSNFSRKHVEDIVRLAEELRLPLFSDEIYAGMVFKGKDPNATFTSVAD
FETTVPRVILGGTAKNLVVPGWRLGWLLYVDPHGNGPSFLDGLKRVGMLVCGPCTVVQAA
LGEALLNTPQEHLDQIVAKIEESAMYLYNHIGECIGLAPTMPRGAMYLMSRIDLEKYRDI
KTDVEFFEKLLEEENVQVLPGTIFHAPGFTRLTTTRPVEVYREAVERIKAFCQRHAAV*
>TCRU_7833 glyceraldehyde 3-phosphate dehydrogenase, cytosolic
MTEGKKVTIKIGINGFGRIGRMVFRAAQHRNDIEIVGINDLLDADYMAYMLKYDSTHGRY
GGMVEVREGALVVNGKKIRVTSERDPANLKWNEVGAVVVVESTGLFLTDETARKHIQAGA
KKVVMTGPPKDDTPMFVMGVNNTMYKGQEIVSNASCTTNCLAPLAKIIHEKFGIVEGLMT
TVHATTATQKTVDGPSQKDWRGGRGAAQNIIPSATGAAKAVGKVIPALNGRLAGMAFRVP
TPNVSVVDLTARLEKPAKYEQTRAAIKAASEGELKGILGYTEDEVVSTDMNGVTLTSVFD
VKAGISLNNHFVKLISWYDNETGYSHKVLDLVAYISAH*
>TCRU_7834 glutamine aminotransferase (GlnAT)
MESWKVLEPSTMSKRGVNTLECITLRKSKAPANKSQLKFSVGDPTHDGNLVAPPSAVDAL
VRCVEGNKCNGYPQMTGRPDAREAVAQYWGKNFAPQQSAHCKGENVVFGCGVSDVFIISL
TSLCDEGDNILIPKPCFSFYDFACELYSVEARHYLCNHEKDWEIDFDHLRSLVDGRTKAI
LMNNPSNPCGSNFSRQHIADLIRVCEELHLPLIADEIYAGLVFSGEKFTSVADFDTPVPR
FILGGLSKVFMVPGWRLGWALLMDTHGHAGDVMRGMQNLSTVALGPCAVLQGALPEILSQ
TPESYFKRNAEELRENAVVLAKAIQQCHGLSCTVPQGSMFIMVGVDTKVFKDITNDTEFY

EMLEDEENVQVVPGEDLHMPGYFRIVVSRPKKIVDEVAARIHDFCERHKKAV*
>TCRU_7835 endonuclease V, putative
MDESKLVPADLARKREMWEDVQRQLAGLVRVPHILESLEQCTEEDTKEMIFFTPTFALPQ
GLLDEFYASAVLGPQLRREAESRKLALPSSLLPLRHVGGVDVSFLKGTNLAVACLVVMEY
PNMRRCRTVYHQCEVTEPYIPGFLAFREVVPLVELMNKFRDGNCAEDMSVYPQLLLVDGC
GVQHPLRCGLASHLGVVLDIPTVGCAKNFMAVDGMTRKSMQCLFEANDEDGGGSKRRTMA
PFVKSMIGQSGTLWGYAATPNAGVKKPIFISPGHLVGYAEAAALVLSMCKHRIPEPIRAA
DFSSREYIRRMARK*
>TCRU_gamma, conserved domain containing protein, putative
Elongation factor.1
MEWRCMRVAVVSAHLLLPHTWHHSAVSCSTQAVDWEDVKVRFNYKDDKMRRMTANLVRVW
SQCMEHVRQYLLDVALMIVEERRHDIVALCVLRGRGMPAIVRDVEDTELLD*
>TCRU_7837 hypothetical protein, conserved
MASGVLGMNASYVPNGCNKYMPTPPLRSALPIPAIQAEDGQVRDTPSGPGSGGGVGGKGD
SGSTPSSGPPPALGIVQGAGDGSAGHPGVSGSEADSLASSSGYLSSQTADTVMKSSDLST
THSGPQEEVLQQEATGTHDPSPSKGLTQVVLPDVQQPKTSTSENIQTGCGEASNCESEQL
VGKTSLGKQDSEASKAQEPPPAQHKESKDNENSTEASSKESQNTEPQQEIKTPVDESDTT
STDASTAVAAQSTSAGSQEEATASSSNGSHSPLQGKVFTGTDTPENAPSPAAAETEKRQG
ENVTKDGDSDSSPAVSHSTSPLLLVVVACAAAAAVVAA*
>TCRU_7838 hypothetical protein
MKRRKEETVGVRRGSHPLWECCTACGGIALKCRTITHEDVARSVRSLFVSAAVGVGAAAS
DLSARWPQRVAVALFSREICYDAFTCVLFRGQFADGCAIAEWRERCGGKCVIAAVRSRAG
RLAAEGIARPSQHRSCLAPSLSHCSILADAGGTQRGRGSRHRHECDRKETRLLLRSEGKH
RVAQRRAQNPLAESAHDTGQWPRSVCVVEDTAVESLLPSGWTVG*
>TCRU_7839 hypothetical protein, conserved
MSDPSLFCRDPPLGTAAHPAKPRGLPHNTPPMSRICAETALKHWNIQRMFVAARREKEKA
KSMQAHLDALLTEKSSREKELQAAIASLPAPHEIEALKTRLHAAREHKRSSAKKINDSDT
YFTDVSARTHGEYRGEARQNREYMELKRSTKVLKDEVSLLKLQLQELTGNVNKNDVCKDA
TDPPGGGKNVVESPNVFKEILELKREKEMWNERIRNATAAWHMATKREARLTRLLETLKR
KMACTPQPSRNPAKSMKKKVKENPALEEVAADSFTPLNSVNFLAVSVSHQPEENSASEPP
NQTREMELSLRISLKGSHDQTHRVSFLGMDDGRDCSHLNEDKLTPQTGKLEKEHAQMKLR
IANM*
>TCRU_7840 Oligomerisation domain containing protein, putative
MQQRLRTLIISSNVSDSITVVSARCSYGCRRVVLPWGGSTTFLSLSQRCDPTQARGVRWA
SSESDSATVAAASSSSYLGFLHDGAGDFIDLGFDENKKGHAFSVVTWEQQPALGVTREPE
VPDGQEYSRLNIPLAHPRAGRTEPRHNSRSIATTSDTICVHEKSDKNEDGDHDAVHLKGA
HTKFNDEGDGGEGSLPYDDELFAEMLLKMEVEGAIDETWQDAHKAHIEDVTELLEVLRSL
KVRDICAIDVSAKTSNFDYMLVGTCEGPRHIHLAAWAVQEADSLKRISKIKRKQTDHTWE
VVPVGRIIVNLMQEPLREEMALERKWAVTKCMDPLTAANAPVSEGRQVKAHGLWTLTLNL
QDLEDFEVDYCKDVLMRQL*
>TCRU_7841 protein kinase, putative
MENYTVIGKIGGGAEGIVFRVRHEPTKKEFAMKVIRCPDHSRVNSALKEIKVLLHLRHRH
VVSYVDFFLLFHNDTIRHEFVADYKNEAQLSESTRSLGFCSTGCLGSNGSPVVRNEVLSD
VFCFHPSEVCVCLVMALCTSGDMQDTIEDARRRLMEVGSHPIPEAQILSWMEQCASALAF
IHEQGFLHRDLKPTNVFFDDDKEIKIGDFGLAATVGLGRQSIVGTPFYLAPERMLHQVYD
EKVDVWGLGVVMLELVTLQDQPINSRVLENPLVVESVVEQVTSMGFSSKLGGLLRDMLQR
FPEGRPSPAAILCRLSGMTATASPHCSISIPIPSAGMSCPKFSTTSCEFYEVESATLACS
HCGTALLEGCGCARDKHHSRQGHERFSLIFSRNNQTTRAHALNDVEVNTLPPEKCKTNCS
TIYAFSRPNLPVFNSIGGSICGTSTEDSSNILIRSMKSTIIRVPQDYPTIATALHSAQSM
PHVRKIVVAGNTIHSTPLTLDDKLPDNLKLIGENPSPVVEVNAATFAVHCTSGRGTLENF
IIRHAGGRISPTDSYTDEQDPKKTLRPMAISIAGGEWKITRCRISCSAGSGISVAAGVEA
IVSHCIILEVKLAGIVVLEGGQGLFEKNKFTNCGFAAFLLKKNSSARLFGNHVTDGAETG
IFCQDASGLVEDNFIANNGGCGVVAKGSDAKIILRGNRVVANGQAGFFCCDGASPIITDN
EIRQNKRAGVLVKTRASPRIAKNVISCGREAGIYVFEGGAGFIEENEVRDNSNAGVLVTT

GGRPHVVRNTIRGSLYEGVWVCKNGGGTFFENDLRCNEKGPKDIEKGCSVVWIGNRES*
>TCRU_7842 hypothetical protein, conserved
MVDDSGQFEVVFLPGEGAILSPRSVMVTVRCSHNRVEEPSVDRDAIDNTWEFLVRGSCGG
QEMRKGEMYNGLKFRLYDVEQEGDKCHIKLGITDYKTNIGTTRNIGVYTELANLRNTTVE
NYLANALGVECFTITSDGKGVLFRRSEVVGEYPNYFCFPGGHPEPGELLNVQQLQSACNN
SLNEGSLVENVTKWFECVNPHVLTRLLFEAAVSEVSDELGVDPAVCVNQGLIGFMKNTHS
RKADACFWIELKQSASEIKACFDLRRGSDAFESVPGSMLFVDLDRIRDREAALRFVSEEL
EGKLAPPSLACLLWAVDRLRNRSSFGVEK*
>TCRU_7843 Domain of unknown function (DUF3336)/Patatin-like phospholipase, putative
MDGTPTRAPTTGTAPPVRTQRSKIADRVRTTPARSLPRRRKGTRSSRVRNDSSGPKCGVR
QASLRIIFRFLYLFFVECLLLRPLHVIQKWIKDYTSRAQKARTERRFINIMNSTESLDTW
LTTASYLDNHRGMQEWKNMIPNKAECDAEGLKHDAYCAKTLAMTENERAIGEFLRSQLHR
TAHGMTSPSNFRYYTGTISSVEEYNEAIVSLIEAFGRSRICQEVTSTLPPCNKRKGEFLL
EEGASLNSKFPTDIVPNKLSKSEHVVDSVNNEQSSTGKRVVASAFDYLEYKVSSVYLSSL
LNWAARPQLPAEKFLTDVQKLKVLQDTLRSYGRSALMLSGGSTLGVSHMGVVRALFEAGL
LPDIISGSSAGSIIASIVCSMKDDQLRELLSDSIMSVQKLQLSPFDHGEFFAKINQLLRT
GAFMNVQKLMECLRNNVGDLTFEEAYRHSGRILNVSVTSEQYSGSHLDRHMLLNYVTSPN
VVLWSAVSASCALPGLFTAVQLIEKLPDGSFRRFLPGQLWCDGSLAQDLPRESLASLFNV
NYFIVSQVNPHIIPFQRKPVSPLVYKERRPRKILSSLWYGCFREIRRWILKLFGIGVLST
TGRWELPYLFLTQRYDGDILILPIGNVLHAAPDYFNIVANPSSEYIAFVTSRAQLRTWPH
LNRIRHSTMIERALFREIGLLKKRVKDEAVVLE*
>TCRU_7844 hypothetical protein, conserved
MVLHVALLGKSTSTPLTRLDLLEALRRNSLRGYHATRSYLWTEDNLFTTLSPVPLFDANS
VGCCYYAFRAELSCGGNNEDFRVAVMLLLDLTAAVDNLVAIATEKEDVESHEEEESNFLL
VELADVLEQSETTRSDYLKRWGAEEHNYHLTMARRVLLAAGHVYSLPLSLESSPCTPSSY
PELQFHFLAMEAEMQNRCREDALTEALHKWANEVERVMREESFHLAVAAVPISVAELLDA
HPQLVQTALLHHTVRQPLSWLAVGTQLSSSSTPLEGVVNGVIQEYRVLVQNKLYVRVPLR
ISRYSFAHLFFAGLPRVLAEKPLSRTETPLALLSHVGEGDEEVEADERELLLGLQLTIAL
HRLRFEVKGEHTFVIERFLQELQCRNEKGDVADITPENASLRRELDRLRRKLMPVATMRG
DSIDWMRSYAQEAAMDYNVTEKEIARLEASMLDNSESGTLSADDADDAFSNKDDEAASGV
SQQLEEMDSFLGARMCEAVLSGSDVEEAALTNVADNFLFLETVQMLAQDDIPAK*
>TCRU_7845 hypothetical protein, conserved
MYSYGNGDLDSQVQRLFANVDYQLEQWNKKYGSKNFCVAPDEVHSVERNTHASDATPQLN
VDSKCLGCMQRAAAPSSTHNYNGENQNYKTPTSYSNEEAGVDVSALAARVSLLEERLRVA
DNERVDLRTRLDAAQRQISDLLEAYKALQNEQFASRMQTLSQPQYDDAQETKRGDRSRLT
DDTVTPTRNFSSVMHSGPANLTSTEFVSPHAVSRALESHVSGEALGAEMWTRTPSQKSSA
QERKMLLEQLARRLSAPSNS*
>TCRU_7846 hypothetical protein
MEAALNEHLLRPIQQLWHEICGAFASAVSPHGVNCAVREGLWDELAHQCVQLPFFRSIYE
YAVATLSGLTLAAESQTVKNYHCIEWLLKERENIWASAEWQITSEWLKGFVKHLLLAAAN
REESEGVHLGHLEKSVALAKETFQEFSAQGKQKYSRRVDALTSDGKSDEDAFEVERMRRE
YLEFFRESCIGLAGDLLFLVRQKDVSQSSSPGNCHVEVEKNTSEGEGRMGAAVVSDSDGD
AGILSSFPLIADEDRWVFFRARPSDSPTLTVDEVACQVSAFYEIHNTANFPMAAVLAEGY
GDDYAELFDALECRCFIPKKSIASVQPEVVIEVSENLPDERRVHFHGEPVVKTVFGSDTR
DSGCFVM*
>TCRU_7847 RNA-binding protein, putative
MHFQNLFVAKLPRSLNDSDLEQIFAEYRPVSAKVMLDASTGRSKGFGFVLFRTEEEGKRA
YEGMNNRDVMIYGHHFELYVYPSQHSGRAAVSPSNALYIRNIPITVPQAQVERFLSTFGT
LAFCAMREDHYGNPVWVVYAEYDCLSCSKNALQRLHGSSEHFYGPPVMVKYADTDEAKQE
RRRRREQGQLAPAPVPRGACPFLPLSYWRPGR*
>TCRU_7848 hypothetical protein, conserved
MSGSTPGIEFRHAEKRLSCGVRAFLFLLEFLPVRPPDCGEEAHVPGIDAALREESSHDGI
SVRCHVAWDSAVSWGNVEPIVCDLDPPVNGASCKSSR*

>TCRU_7849 hypothetical protein, conserved
MSGSTPGIEFRHAEKRLSCGVRAFLFLLEFLPVRPPDCGEEAHVPGIDAALREESSHDGI
SVRCHVAWDSAVSWGNVEPIVCDLDPPVNGASCKSSR*
>TCRU_7850 hypothetical protein
MQSFARLRSDGALSIDLDEMADASPIFETTEREQQRQLQHYGKIATGPAAAAAAATADCD
FSSELRGICRRQGDFPFSGAADSVSPCPRRPFSVVKAEDFDAQGHVMQEEGRRLPQESAS
QEVIDASPRHVTFVSSAGNLKEGSPQPQRSNGDDGDHQRVQHDTLDQPCRTNGGENRMQE
EQEMMISPRERRNAGKPTRLSQDERKELFERIAMPVRKSEEKKDETYLARDEMKKREKDK
EGEGLQRCVFQWPVPSIPTLTLVDLERHNKLANYVRS*
>TCRU_7851 RNA-binding protein, putative
MHQRGIKRYKNGKSGAYTEEYHKLLGKSVWIVVRRLEHADAKSAVSLSEGDVATVFSQFG
NVVDVRFLRHRRTGRFLGTAFVKFEDYRSAILAADEMNSNHESGKEVRLTAAGGADARGI
EVERCDEAEVVAAPDDGESYMAWVASLGIGEKTLTH*
>TCRU_7852 regulator of chromosome condensation, putative
MQLYVQRLLGGDATVLPLILYTIGEYSSSFSALAPWEKSLYQHLVKLLLVAGKHLKNDTN
NITQSVAIEHGALAQRILCTAFLRGGDTATEVCRSLLQVGIRGCREMRLDRYIDVSPGIL
EHVLQFVLFLTKLFHVRPSDILTGRESNQRAEHAGRAHTLSPSLPAQWGFSENSRLETSG
NGIVPRRSNHRRWRDLPGKPSYVPSRQNPLYSDREGEGYWIPPQFPTPVLAFARKFGIGC
EPHLPNLSVSFLPTTLLGSGASEDPHFTVRSPSIVASRRLMEARNFEQQGDSLFSRYLSN
GLLLIWGSGVAFNGLENFATKFESETGSTFSDAFFFSPIVLTPPIPVVSMTCGAKSCHVV
TVENKVYSCGSNEHGQLGCGQSKDTPLFFPRIYGDGHQCFYHVPLCSEDRIVKVEAGSEF
VVAVIRERNQMYFWGGNGCGQCLLPESKTISGPVMVDVPKEYGQIKEVACGSVFAAVLFS
DDKIGMWGKDSMLGVTLSSEKLCDTETGTGTRCAKHTIFSKPIEGEIVALRAGPFHCIAI
TSAGHAYSWGVDRSGSLGHGTEHSGNKIQRIESLANHVVIDASCGSFHSAVLTRDGIVLV
FGENTCGQLGLRGEAPRTTPEPLPLPKPAIAVSCGREHTCVLLEDGDIMSCGTVRSCGMG
LGYGARFNIPQRIFWSYLLLSIASKSIHGMAVGLPRSLSLHPVGASNGIVSTDELRRLKQ
TIMRQGVRTVAAGNGFLFVVTVAGEVQAIGQSQRGQLGIGDTTIPCTDTFKKVVFPERVV
LCAVDCGADYAIGLSSHCGVYSWGWNSHGQLGHGDSVPLHESLFTPREIKALRWKEVTQV
ACGGTFAVALTQEGEVYTWGESLYCGHPRVVTPCLTTPMLLEGLKDVVAVAAGVSHAVAL
SYDHKIYAWGRGPLGNGGSCNTIECTPVVLKFAHCVRQLGCGPFNTFAITDLGELFVWGL
NDHGQCGVHHCEGPPPSWDEGLNSHTDRKQERRQRHATSSSEVLFPTHVAHGVRDAAFGA
SCGFLIWEDGSSAVSGEIHQDGKKVLFHRFTPQRLTMTSRHQNKEGNSSHVLGKESSPVF
FSRCFGGFDMLFVLLEWERPRATEVAGAICNMKACLHSPRTASGGVEKKEKRNV*
>TCRU_7853 Protein of unknown function (DUF525), putative
MSVERLAYRQILKQVGRASLKYKEPGHVCFAVFGVMLRMDDFAAAGYGNTLQRVARSVFS
RPSIAGLASDNSAARLSAAFDVLRRLNDATTSNVKVRERVEGQTENTSHFRSPKGAVKAE
KAPEIQGKVTPVESDKSLQGDDDNNNNNNNSNTGVGEEDDVITIANGTIFIEGSVSRKVR
KISRHVVFCMVLDRLPLYRFLIPPEPLYTRNMRTSFRFPLIVDALLVMAASSNIPGNVPV
VIQNDVRTAEEYRAMCDSISTRTVTVTDHVEVELRAEYVCSRIPDEDVSDVSDDADVHES
ASRGSSHNGSSKSKEYVFRYVVFIRNYGSSRNPKGWHVQLLSRHWVVFDEDVGQVTEVIG
PGVAGNFPLLAPGESHTYESGVSLCGTSGVLRGTFQMNAYNEDGESSCIDVCIGPTRLNA
KV*
>TCRU_7854 hypothetical protein, conserved
MDVLGMEMPQETADLRHILLELEVKIKQTAGVMRQLSTLFPEEDVGTTTNNNNNNNNVNG
GSAKVNPTAKESVAEAVVTPLEELQKYVDACDTLIHDRLAHLRRQVDVAVEVSKSYQKTF
PEHNERVCAAAAANAPGGSPGAESYTPIGGNICYADVRQYLSRFIRWDPLELDRVSNAAS
VVADEAHRRVTSSNAGDGDGNERQSLLFLNSQLPSARIEGTVLSSAQESAPRRGLNAVVN
DLLLRQLQYDGIPLTTAMEMELGCYDGMTAGSNLNSSVEFAPCDVMISQEIRRGLLQPRA
ESDDAGDLIQMVQNAYPHTVHWISRIVSLCNIPATGHHGTLGVGDAITTRLEAFDGSASI
RQQPGDSRRSEGLADSTFLTELGLVSAPHREEARVVENEEELLAEQNIQRSHNRGEIWLT
AQIPSSFAATWGSRAEVGVEGAAASLTGGAMRDQPHEEEGEPSEEANSPDAEVSWSYTEG
EEEEEEGEEEELEYVEEHDEGQEEEEEEEEEAEEIEIDMIMYPGPSTAAHRRHRHHRHLQ
QQQQQQQQQQQQEGGNKNGRDNAASPKGEGSVKLVVSATQQAKILLSDLVIVCALQRLS
QMLSRGKDASMNSKLQQAVDFVLTLRRHPLVEWRMMFEQEFQHANVGDGKKNGKSQEDHF

GAPPLLLTFHHVFVALGYMPLSLGENQQSNKPHNISQRNNNDEEPKDGYNAQKRFAQEQL
LSCVAPFLRLWCGCKDNDFDGLVSSDVSQDAGNEEGSQMHAPVLPICTVPYVWRECVLFE
LLDQAHKLRQLEALLVKHSAASSHSSSSSAAAAVADGRSHPENLLYRLVYPLSTFMLSRL
DDYCEKGLVGGFEEEQQQNHVQQPNTSLPMPTNPPPLPPPQQQSHTTPSETARRHGLNAL
RTLFPAFTNSRSRDRVSTDEASGGGNGAGVVGNNNSNNNHNSNNNNNSNNNNNNNNVLST
QRHPPPLPQSRRQHAIILELPHATAVLSEQDELRRRATPSLLFPQKNACFHSANPTLFMD
SFLHWQPLFQKTMCYCPVTRRRCLDTLLFGVSPERPQEVLSTSGNRPAFNLALLLMCGHV
ISNRAVVSLLERPQRQSRAQATSARCPYCTAETPLDQLMMLHCIY*
>TCRU_7855 hypothetical protein, conserved
MGLPGNTFMIGWCYTLSRDVAEALVSYEPLRRLAYLPYSKERQEEFLSIGMGQEDMMVGF
VLVNEVQYKPLIYVKVLPCHFYNIRDDSGESHVVPTSICVHHLREEEYTALMARFGNDTS
PVARVERVSEDVIYPCCD*
>TCRU_7856 hypothetical protein, conserved
MQDTSRKRKAHESYDCPRRTSSGSLGCHGAFHRTRCVAARCSNRGDIQFGPTRDLAVGEA
RRPVRPSPEHGSIFGEVHHNADPGVVTGRIDVKGETAEGHEPWLRAEERFFHDFNHNHAA
TITRRAKRTRPATPQDEHAIPLQQVNVPVLNLEWIKSRLNPATLERLMQVWGLVGRSPFL
RLLPPVKRAKAHGDFQPLMRVCYEKQE*
>TCRU_7857 hypothetical protein, conserved
MPSYLRNTVVLQLYRDDGEVEFADYMDANSLTFVALGDAERPALCGIDAAAQLHYEGAQR
TLVSGAGIVSGIRRRRLCIPFGMSELSQLLRRAYNTEKGNHNNSLTGSTETVLLAHAFSD
AVWAEESFHCLSTTRRVGNILVSTGIGSATRDLAVDKWRPDQDIMELRDELMIARTVYDH
RHCGYESNRPFQT*
>TCRU_7858 retrotransposon hot spot protein, RHS3, putative
MVAYIIKESVYLFDKTKKSVSELRNEDAFVGLLQYLTRRGVKGHIIYDVAKQGREPHSGL
PSAEWGMILVTPPDKNNFQGWMDQNKAMGIAMNCPDESDVRALCVWMKHNEPREQNGYWK
QVKERMDEVGPILRVIFDTQSFNNRKKDIGEVINAVDSSNAEHYVGVMSDKLWESVNASQ
LVQIVRVRKDSRTERYLNSPASRVIANKIYIHLSTKMRFMEIFKLLMHPDVFLSSIFLEM
SGTVTFMCRGAVNIIIEKLKELKPPEGRALQPAALQRNPEGHPTEFVGLPTTQGDPLEKN
FARYGVVYKPGFQTFPLVDAFFFMESPRKTLVGLQMTTADAHHTTTSTVKQFTEYLSWFF
TNWEEFAQGLSWDIIYVQHADSKPMEDCQRCDFVNPNNETDAEKEIVAFWDGKVHQYQFV
LTPDFVSKIREMRTQ*
>TCRU_7859 SLACS reverse transcriptase, putative
MLGKVCKATSRALHALGIETNKVKTEVLNRDTSGGTAQCSLLLGTEGLVGFYEKGQLVHS
WKSMRGVRQGMVLRPVLFSIGTIATLRQLESSFPNASFTAYLDDATVAAPPGMLGKVCKA
TSRALHALGIETNKVKTEVLNRESQWTCPRNTFGRLPACSVRE*
>TCRU_7860 hypothetical protein, conserved
MAMMMAGRVLLVCALCVLWCGAGGGYAWDFNNESVNEYYYGAHGVYCNASLNATFCNEKR
NASKGEETVSQVGDGVERDNGGGQLNAGGSSGGQGHGSEGSDLRRVGGDAGAQKLKNSGE
GETTPKAPTPPTQPSTLSENLPKPAAPGGPEAPGTTTELQPPPQSQLPAGGTPTTATPTA
DGPFGGAGQQFGEK*
>TCRU_7861 hypothetical protein
MQAQPSLDAVVVYAGKHDVARAHGSLQIKMLALYTDGMPYFTPSSPFTVLHAATITPFVR
SRDLLGISSVFGVTVLDMNRLPDTDTVESRRFTMGLRTANASNGDSRQRLPLSCSQEL*
>TCRU_7862 hypothetical protein, conserved
MSRNDVDGSLNDVNPDLLELSKDPVAWREQRRRALQEKVFGHGREGGSSVSSVAPAPANG
PPSGATASSAPSVSGEFGRKMEEHETHVLQQIMSHKRRRDDAAKSEATPAVSASPVGLSM
KEKLLQRLKNPH*
>TCRU_7863 hypothetical protein, conserved
MASRSVSSSYSDDSSYSSSTRSDNSSSGSGSGSSTTSSEEGVETQTGARRAPTRPAAGDS
ATSAATAVTSTPCSGLRSLQLNPELVFEQPDASWIDIPHGSGSVFRRVVTNYDDFPERRY
RVIDYFRTAVEMFVTQVRQEYTHQYQQAKKNDRANIRFIWRNKGELAICFAACCDMLKLL
YDRFRPGLERPNWDGIVGQFVLFLMAESRIPAAVLTEQTYKTKFLDWRKGGTRYQGEQLT
SNVRFPSAEERRTKIETYLRSGEGYSIESTGVDLPSVVRPVPTHVKMTDAPVGQEETRNN
GAFDVSNLASPLVGFSRARPPVKMRSKSHMKPPQAVIAGKQSVEEYRHLHWLAKLTQITG

CSPTLEFPAERSYMILAFVRLCETSEMPEQFATIMNILVRSSLTIQSAFERGGGMVVLRR
FVGTLVRLKDACGLINLLEQILRLKLSSWSHSSQRSWLRDLLGNSGNDLRWLRALDIVPP
DKQATWSSLITALEQRYVLSNSREEEVRRGAKRARLDNDEALRMSMADNVGVSKLAPYIS
TAFCVSLPGEFCAPPLSSEMEQDTISLLNKKLQYCEEAQVTWRDAILKALGGSCPGIPIP
LWYDPYQLLGVDPYPAN*
>TCRU_7864 hypothetical protein, conserved
MKALDFGVVMQDQRMAPLTQFMARMALDGEMSPFHCDALMISSLYRAALAPFCCVEDERD
SASVCTAVLRDVFAGAEAALDDTVKCRELTPAFITRSSDGSGLLAERRLILRLRSQKLMV
RSVSLRTESH*
>TCRU_7865 hypothetical protein
MALAKSEKCWSLGSREAGLCPWDVRRLDHVLRQATAPKATFEKKLWCVKVILRCIETTVS
EEQVELRRNRQLLSTLRYFLFQPISTPLGARLRQHTLSVYLRLLGGDLAFDELLVMDAGT
VRVLVAALGDDEHADLNHVAILLARRISELPHVSSVLVFEDSLFEVLQDLLEFRHASTQL
TKHILHLFVNLSGHPKLHFKLARSRRLVFFAIETILLVLNTDIVEQASRKMHRVMKSVPS
PLGEPHVISTKRKALPFAPALSKYVGCALRHVSTAVPCAMIIANLLSFPENRASIFSLYP
DLVRALELCDSQKVSIRLWEVARCAIDYLHEDEAMLETQLLMHFESPTVDDATVKTGNSA
*
>TCRU_7866 hypothetical protein, conserved
MTAALNRKFDLLQKSGTCPSYLLDVLTLLVAHANETELFKQELRSAPFENAAPPLRADRG
MVAAAAPQPEMGTQTVTQPEAPGTEKEVLLAAERTLRAYASDLRKINDIAMATSSKKLRE
VKMSNFTEMAAFRDRVVSDAVDRAREELELLRMGWLESMNTEVERAKMEVHKVGLSSQKA
LHKMLEGYRDYVSDGFRLLKTEPLEVMHRAMAECAFCVERLKIMEQQVVPRIEIDALCGR
LKSVERVIAQMLKKRHSSGVVDDDISVVPTAGPSETGASTAAAGDDRPLGLRLRDGGNDV
EGLIVTEVAPNSLASKARISPGQIISHVGDALVTRRDDFTTAMQKTGSAAKLTVYDPETA
VVRILTLKP*
>TCRU_7867 hypothetical protein, conserved
MYGDGDRKTISELRRDAAAVQRRILDQTVQLQRVQNATARASRLIDQLLRLFATEVKEND
RDALFAVLASISEDLDFSNVPLIPIAIALANDHFSNVKRIRAVRNRFLDDNSVIFLAHVL
RFSPSLSQVELLDISGTRVTEKGLFFLLEMMEERETPFALIAKDRVPSEIPVAVEFMQKY
QLALRKVGRKSNCALTL*
>TCRU_7868 transcription factor IIa, putative
MYRESLFGVALAATLAELDSVCCLSEGQKEELWDIFDIAMERALAESPVTSQVRVFSPSP
SIQERNNRMDGDGGGVAAAPAALSTKPTRMVFPANSLPQCSPTASLACCGVLDEGVTYPV
YRVHDGMWTILLKDPTVEVKDGAGRSETIHLDYLKVHLRDVSFKEGVKTKATRKKRRR*
>TCRU_7869 hypothetical protein, conserved
MSAAFPTGVPNLFTTPLAAFPARNLFHSTERPVESGNAFTQEDRLMLQLLYQQQQAIQIQ
LQSMALSMQQLHLTLAGLSKVPAAMGAYGSTVNDTAPSSNPPNFVPMAAQSSFNDTADKT
KASSREAVKGPRVSGEAAEIQSIHASRAKEASRSCTPPQEDLDVSRPSAVNRSTESAAPW
DPSAGSRHSSALRMTRAENPLLSSLRGKLPTPNHSAAGSVSVGTGYSASANVSASLEESK
PSVRPTIHPTSSSSLHADPDNRNVSASRRTLLAKRQQQQRVVLDNRKVEPPRRSHSGAET
TTTGNKRKETFHDTKGSNSASDKKNRRVKEEYGDTSASAAGYDSQSEGYGSYETRQYLKS
VGII*
>TCRU_7870 tRNA-dihydrouridine synthase 2, putative
MSLYQRKTILAPMVRVGNVGFRVFCAAQGADVVFTEEIVAAKLARCHREVRVHNDAAGPM
IEFVAYELFKNQYKRSVVFTTPARDMANQSGEGAPVVLQLGVSDAAVGVAAALLCCEDVD
GIDVNMGCPKKFSVDNGMGAALMRDTSKAASILFALDDALNAPDKLAARGRRVPLSFKIR
LLETAEATADMLISIMEKVGANRVHAITLHARTVNQVAEDSPHYDRAAEAVRRLRSHPLF
KEMCFVLNGSVRSRDDGAVKMAQFGFDAIMIARHAMWDMSVFSRHVSSAGGRSSLTSEDA
EAPLASTSWMDLYRSLLRTHAKYCTPFTYVKYHLTRSIPCIPALRHLMTAVQQEATCYED
LAKIFSLPLEEQESMRGVAAVEMVACVPNREVTLGVVSSNAIKHNDAARSGRVRSEKSAA
TPAAKKPRGE*
>TCRU_7871 hypothetical protein, conserved
MLRRSTVFFLGASRMLFSGGGSGPTPYQDKAYPVQPHSLNELQQPPDTWRKSPFMSKLMD
QSLPVYDDVVTGSGRLYWQEPAKVWHFFEADDTLILEEHDREEWNERPYVAVNHLYEPPV

GSEERPIRIEAVGNPGDQQIVLCFGNCAPHVPQSNYYMMMKGYTKNKCPMCQQWFYIHNR
PWLVMHPDWTDEPAADEGPAYTFAEIEAEFDRDFHEFAVYLNAE*
>TCRU_7872 retrotransposon hot spot protein, RHS3, putative
MTEFPLCRETKILLEVAYTLKEEGVFLLEHWRDFEGKDTVIPIAKGALDTALLYVRREET
RRGAEDTAGRDEEERARREAEERARREQQIKFTFSTKIEDVLLRGRVHANNMKLNDFLTA
ELGGRGVVEANRNVLLEEFFGDPERYIGDEGLLNETKKLYNYVRMEIAARKEMSFCEDLR
SLYNKGVHNLMKWSELAAEVKAGVHGITRDTLDAALVDVRNRTTTSAPMKLEGFYESVHN
ARWHHVVEVSGGEGMGMGVHEGKPQQSWTYMAVGQTVEKDDGVQQSGAPRPRLIVLTSDK
GWPYSWEEDKPIVDCYVNCAVDRVWQIVKGDVTEWFSPGPGTYFTPHPRVMIGTPGIGKS
MAAGSCLLYQLLHCDAEQLQVVFHCLGDVRV*
>TCRU_7873 hypothetical protein, conserved
MAKGFLRVNWRACGGWLILQWRRPLPGTTERVAVSVLANGTTPLVAGLGSKACQRVRVPY
GCDSMFRVLSGCHGLRRMLSRRLISMHSTMSVTKLPVHGPAGTHQCQETLPGPVLVEGR*
>TCRU_7874 hypothetical protein, conserved
MAKGFLRVNWRACGGWLVLQWRRPLPGTTERVAVSVLANGTTPLVAWLGSKACQRVRVPY
GCDSMFRVLSGCHGLRRMLSRRLISMHSTMSVTKLPVHGPAGTHQCQETLPDPVLVEGR*
>TCRU_7875 hypothetical protein, conserved
MCSQYGPLRSSLQRGRPIAVSVANSCLRAAATQKFSKPPLAVHPRNIGRQATEDSIASEL
KGLAGVYQHQRSPMGSAVELASSTALLGKVRLEIIGSVMLHFVYQVCQLHRRGTHTTARM
LVRTRRPQTKQSPQCHFLSSLTHDGRKADGSI*
>TCRU_7876 hypothetical protein, conserved
MAQQRIQYTAGARDQDKRRVAKGQFKRTQREGPNHIPATRGHASTKCADSSEDRSKWDSD
DATDERVSLLPDFVGAYQRYTCRLRAVCDAQRQKLLRGGDVERSPSPMAALQMTVPSPTP
AKLATLMAQGADMIAIQETWKSAEQIASMHTGECVLHAQSRIRKECVAAVPVRKNLRSKR
MPLITPQRDSSLEVVVQFALGQNRDLIVASTYMRPPPQPTQPLGGC*
>TCRU_7877 hypothetical protein, conserved
MSSTSLADGSLRSSWETGDTTRIRRHGKNACRTESCRTLPLLSVLLGVSGGLVHRRLSAL
LARHRRQPRLTPRRTVSDVVMPFRDETARGPSERIAVECGRCRDGVPRCTVAVAALSQSR
PASRLRSTPLTLGECWPNSATSRACAVEPNTGCAATWEAAALG*
>TCRU_7878 Mucin-like glycoprotein, putative
MDDASSAATNTITQTPTANKSGGADESVKSHSSTSLESGLQEKDQSVSSVLGPVADSGTK
AGADPGAATLEKQSNGPSNVLRTEVKRSTTESPSGTSVSLENEDNEAEDAPTTTTTTTKV
PITSTTAPEAPSTTTTTQAPTTTTIRAASRLREIDGSLSSSAWVCATLLLAASALAYTTL
G*
>TCRU_7879 Leishmanolysin, putative
MLTWCVWQSAVGELSECRDGCEEPRDSDDIDGMELQDGDGDGRTLESHWSQRHAKDEWMA
PMGAPSTARS*
>TCRU_7880 hypothetical protein, conserved
MTVIGQLMSSGEVSGLVPGKGGGKRADATDALQKKDRIDMTAPETSDTSPADGLLGNQDR
EGLEPSTKEQTVLGTGEGGTTVSQSRTRQPAEETIESVGGLAKTTKTTAIKSPEGASQGD
LPAKATHLTPSPPVEGPLPNADKAPVPQPEEDSVSMKPNKDLAEEDIATTVDTDQNETSS
GRAESTTTTTLVASDNANNEADRSTGEDIPNNTPDSDVSGTEERRDENKYTNTKKTPVQV
ADIKSVTVASGNSDSSTAVSHTTSPLLLLLVVAAAVVAA*
>TCRU_7881 hypothetical protein, conserved
MEGCPGGKGGRAHRVTGACRCGEDSVPGVDPDIGSRVAALRTGAMRLLPTLRQACTRPAD
HKEPSVSVAPSLPHCGDRPASASAGTSSRRERRNPLSTSERRIDVLLPNLRQSALVRPQY
EGTCRTCSAWRYNSLRGPPMRMPQWRHRLLNRRLARRSPPKSPSMPAGKTRRKHKRGHSR
WTRLFRHRLITDATGC*
>TCRU_7882 hypothetical protein, conserved
MMLRLVAVLGLWLRIGTPQQGVAASTTETKVTSFPERVPRHARCGEVRRSACRLSDRTAR
PFRSGHSVDVTRGGDVHKNPATEEDGFINIWRLNIAGLSSVKNIAFAARLEQRPPDIVLL
QEISNRGDVATKLCGHNDCLRASLGAVVALPFWCATLHRASACRSLALTSWRPLLSVYFR
RAVAAFAWRVSTTLPQQLVNNPHLSISFVACARRDYRG*
>TCRU_7883 hypothetical protein, conserved

MAAEGGPVAGGSGRRGNVNSEGNSNQEDEEGGGSIEGEDPNPTSGGALTAPTRQDQSRSD
PLRSGTCNPSGTGSVSAARMRASGPESLGGGQSAGTTSPRSDASQQAAGGVHAGGGRTSQ
GSRASEQTVTGQSQVPGTAKEAPQGDEGGEPGAQHEADQTTKMTVVTSCAKTAVEEESRQ
RDRKMHRVSIVAGMLIIIIFPCSYRHV*
>TCRU_7884 Enriched in surface-labeled proteome protein 1
MSRHLFTFAVPLLLLVICCTGEAAAADGSKTRSIIDPFTGTTSISFANWKDFEINTESAL
LRVPSLVEVQGHLFAVSEAQCGEKKGAGCCAGIVSKHLDISGYSMDISTSDESLFCMQLV
DTAANNFGITEVLRPTTVVIGDSVYMLLGRCRYSSS*
>TCRU_7885 hypothetical protein, conserved
MCSIFGSRTKTARFVGPVAMDNNLELFHALLYSDGALHILQDGIIKASKTISLALLTEGL
QMINYVLKSWAQLDSSFSELFTPTAGLVGFLSNALYGGGTCIDDYLCVNAILTKKLMRAK
DGFEFTEPWVRGNMAREQPGA*
>TCRU_7886 hypothetical protein, conserved
MIQNFPRLSTPLPGAVLDAPVSTNFIGLSHNADSRWETVFYGIKTASGSTWEPGKKYQVA
LMLPNGHRGPAYMNADLVGSPEMLRTPETRGLKSHASKLGATREAAAAVRR*
>TCRU_7887 hypothetical protein
MMRMSLLYNLHVSGESPSPAIDNMFRLAYRSRHGLVKIYKVMNVSAESKAWVADPKNRKC
DAPGSWLCTGQYPPAKEIQEMLARRIDYGQLEDFNRGKRDDAYYRAYMRRIRNEGRG*
>TCRU_7888 Endonuclease/Exonuclease/phosphatase family/Endonuclease-
reverse transcriptase, putative
MQPFTWLPAERYFYPLLNSIGAYQRYTYRLRAVCDAQRQKLLLSGDIEQNPGPIAVLQMN
VSCPTPSKLATLMAQGADIIAIQETWKSSEQIASMHTGDYVLYAQSRIGKGGGVAVLVRK
TLRSKRIPLTIPQHDTSLEVVVVQAALDQNRDLIVASAYMRPPPQVTQSFRRLVNCLPAS
SPLLLCGDFNMHHPQWEPFLETSPSEVAAEFLELCTDAGLTLVNTPG*
>TCRU_7889 hypothetical protein, conserved
MRPSRKRQARRQHPWQQRSVVHKAQRAPSSGHCTSGVEHLPRGAVVHVALRQQHRPSGQP
HRRIKRHRVVLRRRKFVPHKRRSRARHAHSPTHRHRVLAQQEVAVSKRHNGAAAGSNTAL
HRHAQPQRRLHQQPVHVQRTARRQRHAANHQHANSVAEHRRHMRARNGQHAPSQIHFLQH
EARGGIAKAVGAAIRNTPLCDQHRVHHGDARARRVSARHHHAAAGARLKPANQHIGALAS
RRVGPPPNNVQARSVQKRAVRQRHVAHAP*
>TCRU_7890 Mucin-like glycoprotein, putative
MTTCRLLCTLLVLALCCCPSVCVAGEEDKDGKDRSAVGSDSKNSTPEKPGQETELHSTNS
PSPEAKKEKKGTESVENTALLTSQTTVTIKDTAEPQSDPNKTKEEDDGRSTEERTENTNA
DKANEQNEKPNAMNTTTTTTTTQVPTTTTTTTTTQAPIGKATTTETPTTTTTRAPSRLRE
IDGSLSSSAWVCAPLVLAASALAYTTVG*
>TCRU_7891 hypothetical protein, conserved
MTAPSLNGSECDNTNDGKESDEDYGDDLHRGADSLRVLAHESREGLNAVPTIPGLAEPLA
FALSPAVIGAHALRLIHLPWSSRSSSRVVVLLVPRWPFRMYLSVAWRVI*
>TCRU_7892 hypothetical protein, conserved
MHVGNLCNPPSAIAHAAHFASTIRRPGSAAPIADVLNLQHELQDGCSPSTAAGEDLAATP
SGMDSELSDDPAQAARIGGRRVFFPDVTAQRVLRVSHWTSTCLHGLGPPSAIPHCEDGGR
HPATGRHAATTETCCLCAACS*
>TCRU_7893 hypothetical protein, conserved
MRLATSGLKLQESTEREENAGEVAAALIEANSELMTLFFRHIAVCPPHGPFKYYSAITFT
ERVRRWIAANGSERNVVTLQGLTPTAVLHLMEKYYNTNHLRSWPLLYVPAEIRLKDVLAL
LGEEK*
>TCRU_7894 tyrosyl/methionyl-tRNA synthetase, putative
MFSSNFEGPLLRRSIPFVERWIAELVAAREASLGGTKKNATPEEAPQAVGVKGSKKYGKA
ATVAAAAAAEEEASGSSMSKCHFVIGKVLDVRPHPESTKLYIEEIELGERAGGRRTILSG
LQEYVKQDEFINRLVLVIANLEPRKIGGIVSEGMVLCASRTEGNTRDVKLLEVPAGTPVG
ERVVFDGHDGPFVPVLKKKLAKHFEKVAVDLKTNEKGEVVWGDMPFRTSHGIITAPIPNG
VVS*
>TCRU_7895 hypothetical protein
MRRRRAHHGLVGVLRPVLSALFVLALLTFPFIVWALQTDPEPALPSQPTVSKVIAPAAAQ

GNIHEDSLTVVVVSYPMTRRRNCLLHVLKATLYDWPKDESLVHEVLLVWNGVKETVPDEL
LALKSRCGNHPIPWRIAGLSPLSSAPKLCSKSTMIGACRMMRYGACFQFGCDPPPRLWRG
TCGPLLTAAKQWSSVITAFRLFMWHESGFEG*
>TCRU_7896 hypothetical protein, conserved
MPVRVFVTLPPADGPAVTEEVLAQQVMQEFMAMRHAGSSVELLCSVSSARLQQTIAERYP
LAYNRLLLEGRWRGKWHFFAEEIVGLRCFLYTLRDYAETRDLEVHVAFSELRCCVRDEDA
RAVRQADGSVGALLREHLLQKDALHRWCDEAVRAAQADGGAGGADRALWRAPPPAPSLMR
LARQLRSYGCEGGNFGWLRRRAAREVAAIMTASDTPARHMSALRLRRHVAHCLQSWVPAN
SGRRSAKDLFMAAMG*
>TCRU_7897 hypothetical protein, conserved
MPVRVFVTLPPADGPAVTEEVLAQQVMQEFMAMRHAGSSVELLCSVSSARLQQTIAERYP
LAYNRLLLEGRWRGKWHFFAEEIVGLRCFLYTLRDYAETRDLEVHVAFSELRCCVRDEDA
RAVRQADGSVGALLREHLLQKDALHRWCDEAVKAAQADGGAGGADRALWRAPPPAPSLMR
LARQLRSYGCEGGNFGWLRRRAAREVAAIMTASDTPARHMSALRLRRHVAHCLQSWVPAN
SGRRSAKDLFMAAMG*
>TCRU_7898 hypothetical protein, conserved
MMMVTVRRCVACDLLVLALLCCCCLSVCRATASGVRSTVASTIILVEVEVLSAETDGKLR
WRLPDEEDWRKCAKKPGRTPESGDDCTRLCDEAWGIYDDPDINEMCIFGSDPNNAAFQMK
FETHGDLKNCSLGEAPNTDRVTAGGAQHLAGAAPPVASTAPAVSADGVRQAESGAEGSPG
DSAEAPRNKLPDPTAKRRPDPTTSETVTASPLTSTEGAIQSRQRDDESVVTKGVHGGGET
PGNLQDATPPTGDANQHVASAPEASSHSPSSPSSDDAAQETSHNDNAPQPITDGGTNGTA
TAMQGPGGADSSDTTTVWVRTPLLPLLLVTALVCAAVR*
>TCRU_7899 hypothetical protein, conserved
MALSSQWAQSVVVRSDDGKIFHPKQVSSAAYTYAAVGRPIIVRPRDPRVFTATPSSDWRE
SVGLEGEEKGGGNVHAAAGGGGRASFLSSLVAANDVAGTFWIPDPKRNEVGLLEAIHRRT
AANRTHVLLHSRPLPELQFNFSTCQGDNIDLSHDVFRLSKTSMALLQMERNLADREEIIV
RSDADAGGNGKFGRMDSDGRRHAHASISSSTSISGKTFKDQLRHGLRAIHEEEYYLVRYR
DYSAWGVRYYGDIAKRDHFWGKKYVEQCFAVHVGKEPGELIPITEAQFLFGVELLQRKLL
EQVGIGVTMDINYLALSKDQFRSLGVLLGDGMRDVGVEGEELRRRQEAEKEEEEKRRRTN
LHSDAYEPPSMLDWSPSAIKKRLDHQLRRQYQALGRFVVRGAVLGVGMYVVWSYVKRALP
SDAGGVNSRGQRRNRLGGRDSYRGDDVTFAPKGFLRSVVLGPKEVFDYLLAPTPGN*
>TCRU_7900 ubiquitin fold modifier protein, putative
MSQEEQTAPAASGGKVTFRVILTSERTQPFRVISIAEEAPLTAVLRFAAEEFGIASVDSM
AATTKDGTGINPAQTAGSVFMKYGQEIRLIPRDRVGAA*
>TCRU_7901 Protein of unknown function (DUF3184), putative
MRDLRHPNRRDWRMLKHRLRMRCGGHQKAITVFVLLLIELLGFFTYYGYVQNLRYGKTGP
LVDGDGEQIVFLGETEPRDAAALGGLTTSVQKYTVDELMAKYGSMDFIYTFVNGSEINHA
FRRLMCIRCRDEIKDAEAAFYDRRETPNKPCVGMDILPSAKTVRELLLAFGSEASRRQSA
RDRERDELHYSIRSVEQHMRWHRGRLLIVSPGHNPYWVDEAKNFMASALTSNRGEGMRGR
HARITTVHQDVLMPYGLRLTVDSHTIEMQLFRVLNITPIHLFLNDDYFINRDVDISDLLN
ENGGTYVRTERGLLQKGIRAESGGAWTAGVRHTNLFNTVELDIHEEDYLPENLIKHWESA
GYDIRHKIPVASGDNFIYTARTSQPEKLPPRATPRRPRFFATHAPFVYCTRMFEFLNTRY
ELELAANTMNNRGRSATDLFTPFVYNAFIMARPWQSSPRFLPYLAALHLSRKDKDSAEPT
PPPPPLHVVLENDDACAPATLLRRPASETIYGKFVDNFEGNKRLIQRLQQSNPLFFNIND
GFGGENSSMQLKEFLSGLFPKPVYVERSATGPAIQEPYNKAFEGLMKLPLVIFASYKEAF
CPLLRSLRVAMPQFTGPVILVRNDDKAKGKENDLAKVRHRLNHRVMNAMPVVMCTFGKNV
IEVTVLPGSEIAEEVEEALQAALISFILPVRLPADYIGGKDAQVTALVIDARTRHPLDSI
VALIHALEVPGQSLALEDFEIKTFTETKSSFLLLSREDAKRKAVHWVHGASEKDLLLTFP
LPYALYEDLDAPVKWSFEE*
>TCRU_7902 cell division control protein 2 homolog 4
MSTVNRLRCLEKLGEGTYGVVFKAEDLTTGQIVAFKRMMVGGEDEGVPATAIREVCLLKE
LKHSNIVSLHDVLFEPPKMTLIFEYCEYDLKKYMERNGNKTKAALRSEAQQVMRQVLLAL
RYMHHRHVVHRDLKPENIFINVNRGAKGTGNGVVGAAVAHGPENEGSRSQGAISNGGEKR
GLGDGGVNGTDSSNSDGNDAVQLVAKLGDYGLARVENIPVKKYSHDVVSLWYRSPDVMMG

SALYGFAVDMWSVGCIFAEIVTRKPLLKGRTDVEQLLKIFQLLGTPTPETWPSMLSYPKC
KKLIDAATKIVREQIGSLSQDAKRKVQTQQQQQQQQQQQQQHSNQAQELPRHKEHPCDI
ATRGDEVGLAGYPVRPLNDGSTTNGNGTSEAHRNGYNLPSELLFHSTFDDYVEASRFREI
VGEEGVDLLRRLLCYEPSYRLTAQEALSHPFLSKVKPSV*
>TCRU_7903 hypothetical protein, conserved
MSVNTSAIAADSSCLHASSFTESSYALLGGDDTMRSRTLPPPPLMPLPFSSTNTSNGGIM
AEEKGDLYMGSRPPTQPFSGVDRSCGSHHHDPSFAVHHQAQSRTMPNSVDLAGYHANAGT
TDTTPVRHAELRELLITTERELAEVREECARRSAEVDALRVALGREQEVNHNAQTRHEES
MRELREEHADQTQRLMDQITLLKRLSEGLMEEKSRLAEDASQRKQQLLALLDREREEKSQ
IMADYRQQTEALIADQGKEITSLRNTQQSLREEQERIISERQEIEETKRTLEEKILQLGE
KITNEQMECEKKIQETNQRHARKMDELVAKNEELSRRLEDDSSKLLERRQELEDHVRSLA
EQLRCQEETHTLEQQNLKETYKREVSELREELQAMMNQREQLEEEHEKDRQKLLKNEEKL
IQSLRQAVEEVRQEKEALAEEAARQQEEMQEKHWAKVNQLQNTAESLRRQLAEETAVRKE
AESERELVAVRADGLQSTVSRLTNELETLQVEHRARERAAAQERQNSLEQLRLQLRERAA
EVEALQQEVARHEMEENRLRDELAAKVQALQSTRAEGKRLLEEMQQAAEDREREMLEREG
RLEKTIMLSRAQKTQVEAECQRLQRAITELEGRQQTCERQLEDERRALEEATATVQQSRD
EAEEQKSLFRRVQTRQNELEEELRRKSNDLAKAASRVEELEASLEAANSEAAQQSKEALR
AAKVHEVELQSLIQRQQAEVTAMRLAADQIRGDFAKAREVAAAKEEELHRLREEVNQLHR
DAETRAGSWQGELAESRELHEEDMRRMDEVLYTMRADLSRAQAAKAQCQKDMAQFQREAE
RQRLQLEDMLSQMEAAKEKLQEDARYREQLNIELQGTVKLLTSRLTAQEDDIRRMQEELA
DVNTKLHNAHTFLGRKDAAIGQLTARLRAYEARIGVSFK*
>TCRU_7904 hypothetical protein
MRASGIQWDVSDDGVPPRQGLLSRSSNEKYPSLSERVFLLYNGATGDAEFDIVLLHGLGS
GEFKCWTNKEGLLWPAAFLPQEFPRCRILSAGYTHALWRWQSFEKMKEKEVEEMGQQEDG
WAASSIRRWVAEAIQGKYPSFAPETGGTNHRKDSEDPQGSLFDEIVSSTTASSSSEDEQQ
TLEQCAADLAERLLSDAVGVGRRPLVFIAYSFGGLVIKQMIILAAKVVNLHHAEKGTKVD
EEGKSYHGSGLSEELFLRSIRGIVFYATPHFGSPIASAVTGLKRYYQTTGGPCPSELVTT
LGDHNREQLQSLNEQFFHVIERCSDIGYVRVLSFGETRRLNGFFRIVEPESANPAPDDPR
FPFYLVDADHTGVHRPMSKEQPSYTILFGFIKRMYRTGLLFPNGIKNAVTISREEQMLHD
GKTLEKEAAIVEEPFPKGISISNHESKEALEMRMLLGLLNHSVRRIRTHSTTLFGYMMPT
QLNRLLALAKDIVDYATTSLNEKENDACLLTPVRLVLYWAERAVSALETFFICQAERSVV
DHFSVLESRTLHDIECGVAELRREWEWFYLQLCQTYAVPDSYPVVIFFSQSITLAVADAM
MDEFGCLLVLAIQCVPEACGWERDLVTSWGLQENPAWLPPSFSMVASLLTGWMYLGITRK
YRCAITAFQRLIHDIEVLQRDEGNLLHKTSSRMRSITQEAAFRWWWSDDESGDKAKKMSM
ERKGRVLQVFALLAHAGLCWSQFLSAQNTRPVKPSNLPSADTYGGMFLHSLMEGRRRYEL
LERNLHVDSIMDRPFASMKRVAVSPSHAEGKPYQTEGKEGQKRSVVRKTVPLKGAVSKRG
LTFNWDEVREGESREEVANLFTASVFVSWWIIERTKTLQRSIDPGNGTDIKEDHDKDALH
ERSPWVWENAHPRVKSQWLTLWSITGKTEKKTEELHVRQIQLLMEALGLHNANALALCLT
GRHHLWRRNLTEAAEAYLCVLESTRRVDNPLYRFAAVGLGWVHLYQYHCGMLEGSGVDFL
ALQGAPSGLRDCHWLGQWKRRTMQEPKECSSTVTAADRDDAVKKETGVAPHLGRASALFE
AVLSFDPRDKGALCGMGRVKMLGVEAACTVDFADARRYFATVLGGTEILPGNGWDQKGNW
DNGILAFENGQWESRAAYWMGEIHRCSLDTEIVSNETKAIYKDVKAWWEYAVKRCPQNDW
ALTSLGLLYMEHHHPRHHKDVDMSRQYGPGVDILQRSLAINAQNTWTLWGLAHLAPDVKQ
RQMCHTLLKKLLRW*
>TCRU_7905 hypothetical protein, conserved
MAIIYPTLEDQEKLVQFATRFVRCSIEDIKLLGTTCASLIADVVVINEFILSSSTSFFID
ASGPQTRSDVAFPPIHYCRGYTPPVLVSSSNVTSTMCDLFYRTEGLFRPHEASLRALQLR
LQQGKAAMTKLNEKYNYAFTVVTFGKGGQGMIVKGETSAAGTDISVQTVSATEQAPEVSS
NKTISINGGSEECGKDGRRVYVTFMNFLQTFDLFISWVSSLVGILDGEGAAPSSGTYVVH
DQPENETTMEEDGSKKNDDEHIHTRDKLRTISPAQACDASPTKEPLQEEAKGLAMSSSSS
VGNASSTRPRRSRIIRVTRYELHDVNSIFRLFQTQASLFYLLEYTFYDPRLRRRLLLPEY
YRALSETIRDIGLEIERLQQHKDSLSKERSIGRIIIFSPTICEFRYIRDTLRLYWSLCIV
EDDITALHYHRMQYNKCVLEVGDVIKMLKQLHRPPASVATDISSSNFDNYNGNNSAPPSS
SKDWVLTPEERGAIEAGFEDFWCIRERVLKLCESLTKDIQEKDRTHRYRMPAIPPPPPTA

ATRDAEKGGNFKQWMLSTVNAWKQIVTCGVEISEVSSTLERDDGRFLLSTHSPQYESKVE
LLHLVQRLVTAVEAQGTILERDFPGTFYRDTKTKWSQRATGIVRYLESVSVVFSPPG*
>TCRU_7906 methyltransferase domain containing protein, putative
MFGRIVFFTSCATIFSGTAYVVGIALSPPPSYTVDNRQRLERYDALSHENAYEKKTRGQE
FYLGISRWRRRILRDEGLVHGRVLEVGAGCGGNVNYYESLLHSPSAEPSKDVNEVRKSVE
FSHTPLLEIVMSDRSPGMVESTARRIQQRYGYCPYRYPDYDVVGILDAVKKNYAVINRSD
CGSSLAQKDDGQQSIPGEGVIKRKILHGDGTVKEVLTTPLNDSGYTLADGSVAPILQGSL
PGNMLPLLNRDGQAELGRRESEKRTKGHLTEVKEKNEPIFAVANYAAEQLPFSDNSFDAV
VDMFGLCSFDDPVRALREMSRVCKPGGNLLLLEHGKGRWSRINDHLDKWAPRHAKKWGCW
WNRDIRRYLRLAGLTVVKMEERHFGTSLYIVARPFKTLNEWEAYHAKTMKV*
>TCRU_7907 Snf7, putative
MGIRPSKTQGQRKSSVEAPKVVITSSDRAQLELKLQRDRLMAAIKRYEVVAQEERSKASD
FLRSGNRRKALYCLKREKIQRSQVNSVNDMLDNVQRLLDTVEFNQIEVEVFDALKGGKDE
LSKLNSMLNVDDVAQLMDDVEETVEEARRINDILAQPLDGYVGDDDALLAELLPQVSTEI
PGAETAVEEVTVPTHTLPNPIEPEGRITDGGLGKVGLSA*
>TCRU_7908 hypothetical protein, conserved
MPLPSCTSHLNAHSGQEEEQLSFCAFDVTTRPSRIWDEGISGVVVDLRGAYNYWQQTEDQ
VQLSIDRFVAWMCALEAVQDPTDRFMDLDGILLRAFRMRLMMASDPGIPVFNIRTRLCTA
VYEADTFARATQLLAKRRGTQRPLRCQLFHVYGHVTSKSNVRDAAGGSYSQYGRPLKNGR
GAACCFS*
>TCRU_7909 hypothetical protein, conserved
MNQLIRSRTDWKERVVLRLAWITASRWFEIAVLTPNNFTLEPDGSIILDWPVAPKTARAD
PHRASQFVRIRGQDAFHTINLCRTLQENEKLTNLTNAKVERALAPWEATAHSIKRGALRH
AAQIVETHNLDPHVISQLAKHVGPFDLPQNTVRYLGRYTTMLTQVSSLVALM*
>TCRU_7910 hypothetical protein, conserved
MGLLIKGSGARVHVNVTSSMLDAGALEFEGYFGVSSQILVAGSTLVTESDHAIAFSEFSL
GACSALLLLDNYIEGDIYAVYFTIAVVVDGGGIIVKGNTLSTVENNGVESSVCVYAVDVK
NGGYIDVENNTMRAANGIYLFGDTTVSSAGLLRVADCTFVGRTEFFDFTLLYLDGSVTLE
GGAQWRVEGNNVSAASVIGMPNSKHKMKLSGSSTTVVLSNNRQVDSRSRSPMRRTRRSAA
CTVSASAPWTILIPVCVVCALST*
>TCRU_7911 hypothetical protein, conserved
MSPGDVFTAKAPFVLVEQFCEGRPYDTMTFPDAFEIAPNSWQYRPAVAAVPEVIMSPSPD
AAHSAHKKNKRYLLPLGEASRPTVHGGMHEEQRMQLQRRAQERRDLQLMAGQATYEACFQ
RPCAKDVVAKEQTAENRRRSEVRDAVHTLWLEKNCAFITFCATQRRLRMLSLETRRQKRM
ELEHRAGSLREKPQCLRGGLFWTHREGRISPVAADES*
>TCRU_7912 conserved protein, unknown function
MIPVRLKYFEEGPSWTERRPSSAAEATGTSTGGTAPASLAKAFSVSTIDLSGGISSVGEM
ESFNNALAASSPSFVFVHNATLVARQQMMQSSYVRKMYGITELVRYEPREGAEKGSLALV
RVGVVCESADSAVKLLDSSLGGGGCVRFFMMLQVRSFAGASMTVSAVYIDPAAMLWQRVA
VLTHLFPQLVNADLVLLVSNLFLSQTGALSLETSAELHAVCTAKGFSDAAEESVEKNSGG
HGGVGQQEWSVWVKSSKFAATHLTHEALLPAAAGAKASAGITTVTLSCRCAAAITIPQPR
SAKSANSRGSPASTATPAIMTDPAILSAEAAGKGVTTAAKGGGSVIIERLLQQQQQQQQ
QQQQQAVPRWRTSHSYTLKNNEKLNSHELAFDVSAHFASVPEVVEALNNRSIYWPAEYCV
AHNVILASDNVGPGDKRVMLRRYAREYKNSAALLSQMFLHAGSIHCSPNTGANVHSASQE
VATEKSPWLKRVVAMSNHTKNESNGEDTPSLPSVSRAVKREEELRSRIWDASWCTVIYQV
TPREMKFNITSVVGIGKDNLNEAIQWLNLRSQPKAKAPHGKENPLQNYAYDYALLFSTEH
QGYYLIAATHVPCDIVACRAAA*
>TCRU_7913 hypothetical protein
MYTTDAYRLRIEALERAERILERQEAELTARENLLERAVAIGMQPSQEGWQQHVEDALSS
LRNRSAVQDGGNIYSGGGVQKATAMLGEWEDLVAKLEKHASQWRRKDAEIATRERDLARR
EAALEQERQSLLQESEHLANLRERLSAMRVTVEERTRELNLREAELLARNGKAVEGEDGC
KTALIALQEREAKLKADRERCDCLLEALFELYSRLLLHV*
>TCRU_7914 conserved protein, unknown function
MEGVDWPPRLLLVLRRHLEQVEHPEFPRTPPFSTNSSRRSVLTFLLDAHECARRLSKLSD

SFVDCCRNLVLDIIEQCCASSFLSAKERRVINLLAVQREKRLEGRHGQKRRHNDSDGSPT
GTASHKCAAVLPVEYLLRFFMALPSILAHYDKLGGSTMPSAYKQPLWDYVNAIISIMKDL
DFFDPAAYIPLK*
>TCRU_7915 BRCA2
MGLEPDNVCAHCTFINAPGRVRCSMCFRNIRKRIREGAAEIGSELHLPHLSVSNQSEKQQ
EGCVATLFSTASGQPVVVSEKSLQAARERLDAEDAQIPLTHGNGDAAVATLFSTASGQPV
VVSEKSLQAARERVDADNCATPCDKECGARGMSDSSSAASPSFVGPRRGCFVVPFARSPQ
PRQVVPPNRFQDPPARREMRSLSFDIFAFFSLPMSSLPSSLEVVQSTFAFKCVGCSPELL
LLLGLSAEDDSVPPRSFHTALVRLGACTSSCSENWCQQMLKSTLLKLRGLSLCCSPSLPV
FSVSHALLYLCFKYNREFVDGVRPALRVLTEGDVPASSLLVVSVVCLSLEERLAPHTSVG
VISDGCYEIKVALDVPLTNLVREGILRCGHKLLVCGAKMLLKNFCSPVDCRDDVVLSINY
NCTRPVDPTAALGFYQTNPPVVSSAAVHPLGGLVPSIRGVVERILPPIFVEQVVGNGDAV
STGAKVVRNLLAQLKRLESVLREAAVPSESTNTRRLVRLTSLVLTCEQKEDVMVQLWEDC
AEGCGAESLEEDCGSEFPSEGSSVLIFALTPSRSRPSHPFQHAKVLYTRARLDYRVISSP
SGFVRPLRCSISDADLSMPAGAATDFAGLFLASAKNEAVNSFVIVMLKNEETETPSFCIM
DVPCATPVKEIAITMPVASFTPVIVQNSSFIRFAVDDLGPDCLHVLANEFTKVLQRPASS
YLRTAISSLELVREKAMGRKSLMARAEEILRLRQLSVEARTDVRRYLGELNGRDVPLAVA
SGSTSRLPYYMRAERKGPISKGVVIPTLHARSEMTEEQKSVFPPSPAIHHGERSHIFGNI
IEMRLIRVFDSGRRESVLLPIGLAASDVLTAGPAVPQETLLYDSICFDLVIQVGAVAEQQ
VKATMKSPAVLSGMLEQRLAMRSVCAVAVDEGQVDYFMQRTKILETWQRAPEESWWWFLS
LSHVVAGDSHPPETEGTALLWLESEWRTLIDMLCEGLRDSLFKFSVDAAGEVTRAVFLKE
NCSLRELMKE*
>TCRU_like protein, putative anti-silencing protein ASF.1
MGTQPIVQLLEIELLGDNPASYTQGLHWRMRLEALQALQDPISVAFVWVGSASSADYDQV
LDSFDIGPLERGTTELTMECDPPQVELVPPQEVLGVTILVISFQYRGQEFLRVGYYTQVA
YFDVYLNQCPPEFPHGDLLGRFIAMPRPTVTVTPIAWDEAPMK*
>TCRU_7917 hypothetical protein, conserved
MLSERFVDDMLRDGHAWRRALKQCDTQECLAPSSRAAKSNMGPVFRRGCTDNVCSLRFVS
TLRAPTDTLNIQEKERTLRQRMRGRWNPSTKPINSQRDILLELLQRQLELHGFATAYKES
RDTLLKEQRGVESFYRQQREKRKILERAARHVAQQQEVFMEESQMRQKLLDVERRKRASI
AASMFHGAFIIATNVEFAERKAIFEEFNEQYAIIVNEAHHALQSITGLPYSLYKSLVSLQ
RREGKARGQIVLSHIKHCDSLKMYMNIAIDNCLKAEIAQVIAREKPFLEVLQMKNKKQKH
KFIQ*
>TCRU_7918 phosphate-repressible phosphate permease, putative
MTNPYLWIAVVGGILAFLTGCGVGMNDLANAFGTTYGSRVLTLKQIVLVASICEFAGAVS
LGGEVTSTIAGGIADSSHFASEPYVLMYGMLCALGAAFAWLLLATALTLPVSSTHSIAGG
IIGFSLVYGGANSVSWAKKKSEFPFVTGVVPIITSWFISPLLTGLAAAAVYGLIRTLVLR
PANSVQRALYSVPVIFGVAFFLESFFVLFKGAKSRLHWPVEKALWVAAIIGVGAGIASIA
LIPLLKRRVRLMVEKAERQAEELGCGAAELGQGAEADPSAEKVECAPAADGTACGNITSS
STAQSEEKVDKKFIEPITGAFVGDAEKSSESEHRGTAALPTVTAQLFDKRVEYVFRYLQV
FTAICASFAHGASDVSNAVGPFAAIYSIYQTRVVESKNETPIWILCIGGGGLVLGLATLG
VRIMRLLGERITKITPSRGFSAELSTAMVVSFASGYGVPISSTHCITGAVIAISIVDVGF
WNVRWIIVAKLYAGWMLTLVVCGLISALFFAQGIYAPIRAT*
>TCRU_7919 phosphate-repressible phosphate permease, putative
MTNPYLWIAVVGGILAFLTGCGVGMNDLANAFGTTYGSRVLTLKQIVLVASICEFAGAVS
LGGEVTSTIAGGIADSSHFASEPYVLMYGMLCALGAAFAWLLLATALTLPVSSTHSIAGG
IIGFSLVYGGANSVSWAKKKSEFPFVTGVVPIITSWFISPLLTGLAAAAVYGLIRTLVLR
PANSVQRALYSVPVIFGVAFFLESFFVLFKGAKSRLHWPVEKALWVAAIIGVGAGIASIA
LIPLLKRRVRLMVEKAERQAEELGCGAAELGQGAEADPSAEKVECAPAADGTACGNITSS
STAQSEEKVDKKFIEPITGAFVGDAEKSSESEHRGTAALPTVTAQLFDKRVEYVFRYLQV
FTAICASFAHGASDVSNAVGPFAAIYSIYQTRVVESKNETPIWILCIGGGGLVLGLATLG
VRIMRLLGERITKITPSRGFSAELSTAMVVSFASGYGVPISSTHCITGAVIAISIVDVGF
WNVRWIIVAKLYAGWMLTLVVCGLISALFFAQGIYAPIRAT*
>TCRU_7920 Mucin-like glycoprotein, putative

MGQANTSTTSSSTGTEVTLSVTENPDSKGQPSDTRNNTGRGKESAPAGNSGPTSPASGTE
QGQDGSGRSGSSVTAADAVQKNGDNDRTDSTSGNNSSTEQTNTNVDDPAEKSTATTTTTT
TSTTTTTTQAPITTTTEAPTTTTTTRAPSLLRESDGSLSSSAWVCAPLLLAVSALAYTAV
G*
>TCRU_7921 hypothetical protein, conserved
MSRRASTSAVLLLLVVMMCGSEATYGKEGNSRNGIILKGGDLLNDAENKSMIHTLDSFRA
FSLAYVKGAVVAIVEAHYTSTTDSKSCVVGAADSIDSDKRTWTKGSALVFGHYGISFDPL
LRPTAIVDDGGIKGPLLGVMASQGLH*
>TCRU_7922 hypothetical protein
MTTESSVPISELRPPTYATATIVAMPIVSYLWTRRIHVQRTQHDQRKLLAAQTAFKNGRG
AARRLWERKTAAPAIPPPPTICTAPPTLHPIFQIARRNRREGQRCLSANDAQPRYDETPA
VPLWASYMRGANEVAREMWAPSTWEPRMSLTGQFTTFCRTHEQPINEESCAVFLMASKSR
HRPDCSTPGCCGLRWK*
>TCRU_7923 40S ribosomal protein S23, putative
MTKANGQHAARKLVRLRRKNRWADKGWKKSHTFVAQKANPFGGSSHAKGIVLEKIGVGAK
QPNSAIRKCVRVQLIKNDKKIIAFVPNDGCLHFIEENDEVLVSGFGRSGHAVGDIPGVRF
KIVKVSNVGLYALYRQKKEKPRN*
>TCRU_7924 40S ribosomal protein S23, putative
MTKANGQHAARKLVRLRRKNRWADKGWKKSHTFVAQKANPFGGSSHAKGIVLEKIGVGAK
QPNSAIRKCVRVQLIKNDKKIIAFVPNDGCLHFIEENDEVLVSGFGRSGHAVGDIPGVRF
KIVKVSNVGLYALYRQKKEKPRN*
>TCRU_7925 cdc2-related kinase 1, putative
MSTRYERQEKIGEGTYGVVYRARDTATGATVALKRIRLDTEEEGVPCTAIREISLLKELR
HANIVKLLDVCHSESRLTLVFEYMELDLKKYMDQEEGNLDAATIQDFMRDLLNGVRFCHD
RNVLHRDLKPPNLLISREKSLKLADFGLGRAFGIPVKKFTHEVVTLWYRSPDVLLGSTQY
GTPVDIWSVGCIFAEMVIGAPLFAGKNDADQLLRIFRFLGTPNNQVWPSMNQYPNSTNML
SKPEFLQNLAAECETQFRTVPAYAKLGPEGIDLLRRLLKYEPSERLTAAQALEHPYFSVE
F*
>TCRU_7926 T-complex protein 1, delta subunit, putative
MQAMKKGNENKKDTNTQTDVRLSNITSAKAVADCVRTSLGPRGMDKMIVEPRGEVLISND
GATILSKLQVTHPCAKMLVELSKAQDVEAGDGTTSVVVLCGALLRTVEELLMKGIHPTQI
SECFNDCAKMAEKILEDMSINIEIEDRETLIKAAITSLNSKVISQNSDLLAPMAVDAVRR
IMRDNGDVDLRDVRVVTSLGGTIDDSVLLTNGMVFKQKASHVAGGPVRITNATIALIQFQ
LSPPKTDMESTVTINEYSQMDRALKEERKYLLHLCKKIKDAGVNVLLVQKSVLRDAVTVQ
SLDFLAKMKIMVVKDIERNDIDFITKTLGCLPVANIENLKPEKFGHADLVMEENTPSGKI
IRVTGVQTPTNTIGRQLFGKTVTFFLRGSNSMILEEGERALHDSLCVIRSIVKRRAIIPG
GAAGETEVCLQLGKYARERAQGTQTFCMRAFADAFEVIPYTLAENAGLQPISIVTELRNA
HARGNKNAGVNVRKGCVTDMVEENVVQPLLVSTSSVRLAAECVMMILKIDDIIMTRA*
>TCRU_7927 serine peptidase, Clan SC, Family S10
MARPLIYPILSLVAAATLVTTAVEALYVVPQGRLRETGSGWHPCDPDVPQWSGYFDIPGR
EGDKHYFYWAFGPRNGNPEAPVLLWMTGGPGCSSMFALLAENGPCLVNETTGDIYKNNYS
WNNEAYVIYVDQPAGVGFSYAEVEDYDSNEEEVSEDMYHFLQAFFGAHQKLRKNKLFVVG
ESYGGHYAPATAYYINKANREHVGLPIRLAGLAVGNGLTDPHTQYAAYPSLAWGWCREKL
GEPCVSEEGYQQMSSMVTPCQKAIEICNSDNNFIAKAACVTARVLCNPIIGVYSATGLNN
YDIRKPCIGTLCYNFDALNAFMNREDVQSSLGAKRQVWQSCNMEVNLMFLMDWFKNFNYT
VPTLLEDGVSVMIYAGEMDFICNWIGNKQWTTALNWPGKAVFNAAPDEPFRAPDGTVAGL
VRTAAAASTSNLTFVQVYNAGHMVPMDQPASAFVMISNFLQGRPFN*
>TCRU_7928 serine peptidase, Clan SC, Family S10
MARPLIYPILSLVAAATLVTTAVEALYVVPQGRLRETGSGWHPCDPDVPQWSGYFDIPGR
EGDKHYFYWAFGPRNGNPEAPVLLWMTGGPGCSSMFALLAENGPCLVNETTGDIYKNNYS
WNNEAYVIYVDQPAGVGFSYAEVEDYDSNEEEVSEDMYHFLQAFFGAHQKLRKNKLFVVG
ESYGGHYAPATAHYINKANREHVGLPIRLAGLAVGNGLTDPHTQYAAYPSLAWEWCREKL
GEPCVSEEGYQQMSSMVTPCQKAIEICNSDNNFIAKAACVTARVLCNPIIGVYSATGLNN
YDIRKPCIGTLCYNFDALNAFMNREDVQSSLGAKRQVWQSCNMEVNLMFLMDWFKNFNYT

VPTLLEDGVSVMIYAGEMDFICNWIGNKQWTTALNWPGKAVFNAAPDEPFRAPDGTVAGL
VRTAAAASTSNLTFVQVYNAGHMVPMDQPASAFVMISNFLQGRPFN*
>TCRU_7929 NADH-cytochrome b5 reductase, putative
MVRFVSAFAPGLFTGGLVSAASSAAAWAKQSSPRDAAACASRSSTFTPDEFRPFKLLSSR
YESHDTRRLYFALESGEAVFSVPVSSCIVAKLTDAEGKDLLKPFTPITANNKKGHFELIV
KKHSKDKMSALLFQLQPGEELLVKGPFEKFTYKPNMWKHVGMLAGGTGIAPMYQLLQAIL
MNAKDRTHVSLVYANNQRRDILLANELTTLNKTYNNFNLYLTLLEVPHRWLGGIGYINEA
MIRTFMPKPGERHTKILVAGPPSMLAEVAGDKVFAAGKAPEQGPLLGLLKRMGYTEEQVF
KY*
>TCRU_7930 Enriched in surface-labeled proteome protein 1
MVSVRLTAQLQRVKEVLKTWREVDERVSKLCPTESVGRDTSTGTACSADFKITDGLVGFL
SGNFSENTWRDEYLGVNATVKGNDNGKNKDFRWCDVHVA*
>TCRU_7931 helicase-like protein
MPQAVHTPSDVAYDMPFEPYPVQRGMMHTITNCLQSSSPILPVAAVEVPTGCGKTLALLS
SVLRYQATLEKLTPQELEQHMRYRRWRPAATSLPKSLLAEETLAGSGRSKSNSKGKRIPD
DAVDGEEKWRVPTEFFKQFRANNSKRLRVEMDGTPWSLRRQHEPPSCSVFYVTRTHSQVR
QAVGELRKLHGLHRLKMNILGSRERYCINSTVLKARANNTLPVEGNNLGEICDKLVSLGQ
CEAVCNYGVLGSRAISHPLHQGRLEKVWDMEDLVAEGVATQSCPYYATRELVFFAHVNFA
TYQYLLDPLIRHECKMEAALKNHSIIIFDEAHNVPSVCQDALSLETTLDNLRLVVSEIEP
LITFSTSMATLSYPREFKLTHWTLAELFSLLYDVFTAIVKFVERQEWIDTDTHQTPRRRL
NDDDDEAEGKRGPTLSGEALANVIQLCILDHLPFTFGTVGMEHGSAARCLSNASMDSVVM
FRQVYGIVMSLGVTFNPFQFSIFGLSIMKRWLLVIRFMLQKPSAFAVNICDTTLNCVAQK
GLVEPPPSLRRTVGIRCLDGSLAFHHLLAVTHRVVLASGTLAPFHQLGQDLGISLSDMAT
YEGLHIAGVHQYRISVLTHMMDGARLHCNYGNFRDASFIDRLVSVIFEFVKQVRLGGVLV
FLPNYVVMRMVGSRLSSRICDETGRELRIFIEPKDAMAFSSILDTFRVVTRRSTAVFLSV
CRAKVGEGIDFADNMARLVICVGIPLRPLNSWVVEAQRRYSGEEWYVIDAIRAVNQALGR
CLRNRRDYGAMLLLDDRFERGAFQKRLSKWCAASLKVHHTPASVLKELSTFYRLMTASSA
AEKEQPQQEQSEEEERGGLRERTKAFQCLAPLDRVARMLSASEANRQHSNAKAPLPFSQT
AMNKRPRITTCTHEWSCTAVKLLYEAHNAVEDVAAAELRDALHFLEEEYLELPAKK*
>TCRU_7932 Galactose oxidase, central domain containing protein,
putative
MEWIPCKERVGTLGAREGHCATCLLDPATGEEWVMCVGGYCEGERDGSVMISKVFPQPVL
CWITVAEHLPCFECDGASLTRVGNPTEAYMFGGLDANLNRCNRLFRVGLDFTDRLPTLDV
KDLQTTGSIPPPRTQHSAGGTATYLFVFGGEQDSADQSNDMYMLDTVTLLWKCIKTEAPV
PPPRLLAGPLLFISSHVCVLYGGAHFVNGDIKSLNDVWFCDLSSACIWTQLEVNAADEDV
VFPRSNGHAGGLFREEGKVTAVFVGGKDAVEGCDKVKQVCWCESGEGLLQLRLVEPTLRC
REGPHWRYTPAVVETHQGILLLGGQCRHPQDVVAFYLKCVGGMGSL*
>TCRU_7933 phosphonopyruvate decarboxylase-like protein, putative
MGKLAPELFYNVLRRRGVTRFFGVPDSLLKDFCAFVTDNTHPREHIITANEGNALAMAAG
HHLATGEFPLVYMQNSGLGNIINPLLSLAHAEVYRIPLLMLVGWRGAPGVKDEPQHVAQG
RLSEDLLRVLEVPYSVLSADCDDVEASMQKSLDVAFEHMQSAGTPYTLLVRPGLFSKHKT
LKSWNDLKGIPMSREEAIEQVLRQMDTKDVVVSTTGMPSREVFEIRERSGMGHAQDFLTV
GCMGHCSSIAAGIALAKPEKQVFCLDGDGAAIMHMGSFAVHGGAAAVQSVNGDDASRLLH
NYKHVVLNNGAHDSVGGQPTAAYDISITQVAKACGFTTVREEPVMELGDLVKAMSELKEA
MGPAFLEILVKKGNRPDLGRPTTTPQENKKIFMKFLNDR*
>TCRU_7934 prenyltransferase, putative
MLRRACLFRKITRSWTKGSITSSMAHFPDAVRADPAALRGADCSAKEKRQWTIDDVSRSN
GRKVPKHIEWLTNRMRLWVRLVRADRPVGTVLLMLPCYWGSSLAVTKAIVWEGADPVALF
APFIPVHLAVLFTAGAFLMRNAGCVVNDMLDRKFDELVSRTKTRPLANRAIGMTEASGVL
FLNLAFAFVIVMNLSPMALLAAFSIVPLVAVYPLMKRVTYVPQFFLGLCFNWGIFVGYAA
VLNRVDLAVTLPIFCSGVVWTILYDTIYAYQDRDDDMKCGVKSSAILIGDRKYILTLMIF
PVGLGILISGLMVSQSLPFYIATLLCIWHLQGIVDDVNIYDASSCGKGFLRNARFGIYVF
LSMCLGNVLWTLASEHQRAKDADNIAVPEKSTLMQFLLFRKTAEPPAFNTQDIRWIDRMA
HPVYVAAQEARQDSTQKPLVIPAWMRREYLGENLGNLMLLLGVENEVVVSWQEWWYAQLD

HYNMFSKLAI*
>TCRU_7935 hypothetical protein, conserved
MYEVQDLSDHAVGGLSRKFSDDIWPAFTNSVGNLCDAPNETTKEKERHSLRYVYTHSCQQ
HRVRPKADVLRQLPSFVGEDWVKKVKVLDFSLAYMGSDGCAALVPVIGLCTSMTHLLMPS
IGLTEEAAWPLLAILQTHPSLTWMDLSGNQLNDNVGRWILNMVLENPTIQFVLLRDAGIS
LPLVSKISRQLHREKHERAGGLISFKQSLDLDRLSFSFETTLSASVSTYDASRGRRIPAF
VASGLAELRHRLHHNRHCIQKIYECFMLPKGEADGIEDDCGEPVLDIVNMNGEWDTVSIS
AMYTGKCSWRAFFRGLRLLGIHAVSRSLTESVTFATICGICNLETIYFGKLLSFLRPHVA
LKMVAPWKTDSSSTTHWIVGADEYSLTSELQESAVGPTQRLFSSSTPCPFSALRVLSRSE
AGNSACSLLAAENVAARPHSPESVPLILKPRDSAGLRRKSAPGKLTLGCSNTFNSKALLS
LTNSGTPVGALEDQFRLDRFFVSREMQYVVDRLYDARDTLRESFQPGDGDDAAAPFMVPV
DGLLEQAVSFLGENYREKVVAVLKSSGAEKDVCPMLHLEKWLNSMYIPETRASNVPPFSL
SKERGMWRGVSVERLQSVLQLY*
>TCRU_7936 hypothetical protein
MVLRQSSSVGSCRGSLQRFTTYMLGLADGHTRKHHQTQYALRSHVGKQDAAAADPRCLCQ
VVGQPNLHAAWGGGEVISCRRGWLATVPQLVVWVQVANNRCRAKATNGAAPVEQRGQLPW
KFAEVHHLHAGAGRWAHAEGGG*
>TCRU_7937 Ankyrin repeats (3 copies), putative
MEILLKRSDDPSSKVNELDRNNCAALHKSASDGDVRVTQWLVEHGAFVDQRDITDTTPLL
MAVKMGRKEVVEYLIRQGAACDNADIQGNRPVHFCAIRCDYKILKLLVLAKANVNVQNGE
LNTPLHLAAIYQRPNSKEWEDLISFLLDSGCDPSLENASRKKPSDFVGRNLKKLFSREGA
EMRRKIKAQKEAEEEEDFRKLLELRGTWKTTVMTNLERTKRILKDEADRLHREAEERLRA
EDDARLLLDEAMERRRYQEEQKKKRLESEEKNKNSSRK*
>TCRU_7938 kinetoplastid-specific phospho-protein phosphatase,
putative
MLRALWLWVLLFFFFVTNHGLGRRIVAVGDLHGDLNQTLSILHLAGLVNKRQHWIGKDTY
FVQLGDILDVGPDDLMIVRLLMRLEKEAQAEGGDVIQILGNHEIRNLLGDFSAVDPVSLA
QSGGKAGRRELLSNRTPLGIYLRTRRAIFHHKEFLFMHGGLSTATGNMITGIKAVEEFNK
ALRDTLINNTLSPMGKVGVSLKENEAKKVANPILVRSILNVRCSELEKVLSKKFHGIKSV
VVGHVPHDTDDFSDWRLCGGRLIAIDFGLSRWKKGDPGHVAALEWDDVSGHVQLMESTGK
FPNYEPDVHSSTEHNVKRLLPFIRLAGAVVFLVLLVGLLGRWICSRAINNPLSEKQQGGY
GSVAPCVTP*
>TCRU_7939 hypothetical protein
MWAKYSSSAVEEASKQVKSLATYPSSTPDMSGDEKEAFHETNSRDAFTVALLKHAARNLG
VQYMDDRVETSDSIVMDKLGRIKADIRSRERLLGVENMGLIPLFIEAGDSSLTCEDSIMY
YKKALDIVEANKYIKRDSNVMNDVGVSSFADLGSRFFRYGQYQVAERLFTMAAAISRDKV
TGVAEEISFSTAQCGSQKSLQRLKGHLWDWKKAAEAAHEDLSTLLSDATRNTHSFREMRD
ACSQTDLAGHRVAMPASQFMGTKREMKGLKGTRNGEELKRLVEYVFDPMSVEDGFTRQLL
PKGSKNTTRLLSEHFTGSNPCLALRESIDCITSRIGAKADSINSSGGALRRELQTR*
>TCRU_7940 hypothetical protein, conserved
MPKVHAVADALVINDENDRILELWFRARASVEFCEKHSPSDFLFVANIAGQEDRKTLAGA
LNYAERAPEQIDVCFLCRKVTLSLPLLELLCNTSHTVQLYARPPQEEALDGAAPTTAKQR
KAGGKKDRAKREEDLFVIENADQLFSLNFDLIDLLTLSSTRRFVPVPPDAMLQDCFFEVR
CGTPFLPPAKLDRYRPLKIEVRSVHDLPRTEISQDPLFLTVRFGDTEIRSPELYLEANGK
VGFCRVIFLGTRTPLDVYQDVFFRRLEVSVFKGARTCLGKGTILLRAAVTDRQREFSELV
YLLPSRTTVFREDNCLSKGTMVSLRVDFFTPLPCPTHVLSNGLPAHGHFLTRGIIRMPYA
AKWVPIVLEAFIATLLQLKRAYKGSNVYQYEMPAPVPGAVPVKEKKKESGKSPRTQSISP
PRPPSPTAFDAPFKIVTPPGISGFEVMDENLRIICVEGLAVEVHQIIERLSAVAGRNSQL
ELLMNAELFVPARAYNFFPPFVTLPKTMNADALKLGIGKGTDSAGGATSTAVHGGFDSEG
EFMGDATDVSYVPSFVSSKGPNESTGEPFDSAGAEAGGTGGRIHRIRIGETIESLASKQH
YLLRRMLSDACLSCYTKLHALCECSSLRTIFERDLFPTAEELIALERTFGLTLELSDVFG
KQEFVSVAVEKDPAGSLKYAAADESGDSHYSTIKLNALRWNDVGKMVSFEARKIIFSKRR
VPACVQQRYPGACWMLTSDTNTTVLCAFPTAAQPKETIRYLVEAQVVRCGEMLCLYALAC
DSLAKSCTNSHNAAYEAYLRTSRKQKISLHSKKGEEKLADSTTNRIRNGSLCSEFGGSAG

NDSSVDFLSFEMPTVPQSAVTVRRDLVDRSRRTVQLRTKKASGPTAADYELCWELYRQRA
PTVRPKPPRGPPMRF*
>TCRU_7941 UV excision repair RAD23 protein, putative
MKIVLRSIVGSEQVREVTPDTNIETVKKFLEDEYNTDSLRLCYNGAIPENSKTMTELGVQ
ENAVFIIAGNKRNKNKPQAKPATSVPPPQTKTNSSFEPTSVGHGQGEGAITEPATSGAGG
ASGGITEPQQGAEPPPSEAAPSQGLALHGVDPTLVDNIIAMGFEDREQVALALRAAYMNP
DRAVEFLCTGIPSDVLQRMNEPAINPSASSERMSSLTDRLTSHMRQDDSDSALYNALMQI
PQFGEIRSIVQANPESLPTVVQQLRIHHPEVIGLIQQDLEGFLRIMGNPGQTEFTTSTGG
GGDVPPDSVSIPLREEERVAIQRLVELGGGAWTEEDAIEAYRACEESEEAAAHLLFSNFF
E*
>TCRU_7942 cationic amino acid transporter, putative
MDVTSKTESRLGTFFFRNLLRRRCIYATVASLESSPFRRTLGLRSLVSLGVGAVVGAGIF
VITGQAAALYAGPALAISFLLCVFPCLFTALCYGELAAMIPAAGSAYTHTAVALGEFTSW
IVAVGLTLECLVSGSAVSVSWSSSVQSFLREFSIVFPPEFGGSPIGVSGNGFFLTGNLFN
FPAVMLTLFCSVVLCLGVSETATVNNVFVIVKFMVLGSFFAYGVYFAVTHWADFKFNLTP
FVPPNNGELGKYGVSGILRGAGVVFFANVGFDTIFASAQECRNPQRDLPRGVIYTLLICS
ALYFLVTLALTGMVKYTSLNVDAPVIMALREVGAPPFLRILVDIGTISGLSSVCFACHFA
MPRLVMALAKDGLLPPVLSCVHPRLKTPVNATICCGVAGALIGGLFPLEMLGEIISLGTL
VAFTIVCVSMWKIRIDFPDFPRPFVAPFFPFVPLLGVTFNSLQMFFLPLVAWRNYIVVVV
ISLSWYLFYGIRHSKLHTLDPSSWRGFVYTESGTAPHSSKEEGRMEEACSLELPMEMAGR
RRTSFVSV*
>TCRU_7943 MORN repeat-containing protein 1
MIYSGEIENGQMHGRGCLQYPNNETYDGEWVFGKRHGHGVYTYVDGSRYDGEWVEDRVHG
RGTCYYASGNKYTGDWAFGRINGRGVLEYHDGDRYEGDWKDGRMHGKGAYCYSNGDRYDG
EWKDDKRHGKGVVVYAAADGSVSEKYDGEWMDGRMQGWGKYFYADGGVYEGEWNDGRMHG
RGTYVFPNGNRYEGEWVEDRKHGYGILVYVNGERYEGYWQFDRAHGKGTLMYLQGDRYVG
EWSNGKKHGRGVLTYSNGDIYDGEWRDDNASGYGVLEYANGCRYEGEWEEDHRHGQGVLH
LPDGSSYEGGFFHGKKEGNGRIILKDGSIYIGTWKDGNIVGQGEFRLSESCDLSNPDY*
>TCRU_7944 hypothetical protein, conserved
MEAIKGLARRTTQSIREKVKNREATGHDELLEVTSKKVLQYQKSGEVICSKLIRAAGLIE
ELGRLLKDVGEEYQSISDLPQESSQLATDVLDMGTKLVATAQEHQKGLKEEGFDVLNAFI
KNTSKLRDAEEARRKNRLEYDFFRQKVLDLRSCPPKDTSRIPRNEQKMENWRVEFWRATE
NHKAVCSQLYVEGQRAIDLSVLTLTKVLGSFMNIAGDGFKQQFVNARLPVYPTAPILTPA
PLPPNPMPAFQPLYNAGGHTTVTYGQLQQQLPWPQDQPPQSQERQGWQEGYPSGWSQQWQ
QQQQQPSSVEPHISQHQHSWGQVPPQLQPVFEKWQTPEQQQQHQQQGRNLSQQNTSPVVS
LHASSNNYRSSDFAYTKPSEGNGNGIYLLNSPKTSASSLAEGK*
>TCRU_7945 hypothetical protein
MPLERSFIDPGHASMGCEAGLIPRLRRDSIVRGVLEENEDMLREIDLLRDTVTKQAQELF
TATKRIHVLESRLARLGAAEDASQERTDDSDNVEEVTSVDKAGILRSIFRAISSCQFGDR
HTRIRAYKQGLVRKSAEKARDFGEKSEKKSELLGKEQQDFLGHAFHESNKRLDEVSSLLQ
SYRETPSFLVSAYDELVIDCMVEIIRLSKKMNLMTVGDFGAPPD*
>TCRU_7946 60S ribosomal protein L9, putative
MKIRAQDRITYPEDVEVSVKDRIVTVKGKRGTLTKDLRHLQLDFRVNKKFRTFTAVRWFG
TKIDNSTINTALSHVRNMITGVTRGFRFKIRFAYAHFPISVSVENQLVEIRNFLGEKRVR
RQVVADGVKVYRTDPTVVKDELVLEGNDLEEVSREAAVMHQLCLVKKKDIRKFLDGIYVQ
TKTNVVAEE*
>TCRU_7947 hypothetical protein
MCPTKSGTAKDNMWIQRTEALSQRSQSFTSREQHRKEVRLRAQRILEDNCRSMEERQREK
EELANRVRLAAMQRRLTDIQRLNRATEKRVQHAKMLQEGQMQARGEKLQAALQKLDEASY
RREKTLTFYRLRTAQQVLSTSERAKVNRSLIEREVRARQRLHEEREEARERAAEEEKINR
EIELQQRGLLRDQRVLNSIEYQRQRDHLIREKGLQRERHEERLQQHKLQKGRWGFGKAW
CDANGVEVPSSAWQSRGKNASAGGNDDKKTCAYRRAVTSLGIILC*
>TCRU_7948 calmodulin, putative
MPSVVSGPHAESILCSLSPEEVDMLRDAFIYMDRDNDGHVSRDELLTMVHRCVGDERFSP

LKEYLVPLFDVADKDKDDKLSLTEFLLSFADGPGVVPAEVISSCVSSIRVRLTDEEIETL
QETFRRIDTKADGFIDKEELIVALKENLKHRFPDLHDNNFNDIVAVIMASADTDRDGRLC
LSEFIRSFQEDQGVLPAAFLDAGARKLVQKLTPAEIEILKEAFAVLDKNHDGYLEYSDIY
DALWETIFDSSGDKTQIRELCDLIMVTADHEKRGMLTLAEFVRGFIRNIALTQLPVAAAQ
EKMQSACERLQEMLQSGELERLSVVPDDSFQDTTCVTPGNLVSVLSDIFRDVFPFLEEET
LSTIIGAVVVASDNENDKKISLENFIQCFAEGPRILSIDSSSSPLSKSLSGDELLTVSHV
LHELGKDANSNGCVQEPEVLEAIRNAFRSDLKQTDRVLQYVRDKINRHNSSSSLIVETSV
RDGPCYKDGVLNSESRVMPESKGNNAVKEGSVTVLKGDVTHESPPTGIGVPALLATRKKP
KSQQRRHFAMNSTASDAIVKHHACSYLGFAYDTADRAIFDNELQAEFKKYAGEGQDYIDR
DRFIKAYISMEHYGLIPTENEANRVLSRYCTGDKVHYNEFCIIMLQRARM*
>TCRU_7949 phosphoglycerate kinase
MLQHSKIDMIFKSLRDVVVVGDNDMVILDMNRSACDFFGWSVEEVRGKSITFLIPKYPLD
VSDGTVTLVARLKNSVDIPVVIQSTRDPHASMVGWTILPIILPRVFDFGVHMNLRAALTP
KLSVDDLDFQSRRVFVRVDFNVPFDKATQNIRDDSRIRASIPTIMKIVRDGGRVIVASHL
GRPKKPDDRHSLKRILPRFEELLGKKVVFCPSLEEAPRIVNAMKNGEIMLLENLRFFPGE
DATHTVERNRMALKLASFIDIYVCDAFGTVHRMTASMTGLPRILGAGVTGYLIDREIRAI
SMAMHNPTLPLLCIVGGAKVSDKITVLSSIMNFAQTIIIGGAMAYTFLEAQGHSCGNSRV
ERTAREKGRDLDLHAIARELIDRARAKKVRIILPVDHNCAKSFSNEVPFTTSGADIPDGY
MALDFGPKTNAICSKAVAECRTLLWNGPVGVFEFSNFATGTVSLAEAIQRNDRLVSIVGG
GETAAATKRYKSSITHTSTGGGAFLELLQGKALPGLICLTAQAEPRL*
>TCRU_7950 importin-alpha re-exporter protein, putative
MSLLDPNDPALAQRLNQLAQDANSMNRADREKAEREIREFQNHVDEQSGFVLLLLNMAVT
PGPADSFCSIVFKNTVKMCWNAATAEHCITETDKTIVRDTITRAMFRAAPNVQRNLAEAI
TMIAEIDFPKAWPNALDCIVQVLMVEKDQAMHCAALSTAHGILGRYRSQTDLSEDFVNDL
RIIYTAFTSPLLLSMELLLGEMDKGGVGCKTASQGLTSAVECLRDLTTLDLGDEFIWCME
KFVSVLLRCLQFTNPGVDGVSLIELKTVVMECVTHFLLQFSEDFEKYAGEFLRVVWDTIA
SPLSCESTMDDIVIQGMNLLSAACRGSMRDIFNNTEHLENLVAHVILPNLALQPDDIELY
ETEPFSYIQRDVEGSDFHTRRREAGELVRSLMVTFPDISAPIFSAQLQRLMSAAAAGEWK
AKDLSIYLFSALSLGGQYASFQRGATQKLSNLVSFEPFLKQSILSELSKDVSEQSPFIIK
AGCIRFVATFRAHIEPQLIPEIVALLTTWIRCQDEVVRTYAAHAVERILTFQLSGQQESI
LTDANMGKTVVPLLQHLCIWVQEDKRPNAYAMQCLLRVCQNFSPSVAPFVGDIITFLVPV
VRENAKNPSNPLFSHFMFEVISKCIQIRPEDGTAIEGALWEPMIFILHHDVLEYVPYTLQ
VMAQLLDARGSVSFEPPAHYQALLEPLLIPDMYQQKGNIPAVVRLLVSFIEHYPRYVHSK
GLTEKVLIIFRSLLQYKNYDHEGLNVLTAIIIAYPKEIISPFMGSVYQTLFQRLQTSRTP
KYVRILIIFLSILVTIHGADDVVAQVNLIQNGLFWMLLQRVWLPNVQKITGSLERKVCVV
ALASLLGECAELQSNADTWASCVVSCLKVLHGAVESDDMTSFTPKTQSVGDLKHYTGDSG
FTNVFCPLQGAVRAPIDVCESVKQPDLYFRERIYQALQGPSGVHLKSLLQASPELLAMVQ
*
>TCRU_7951 hypothetical protein, conserved
MSICVTATPRQFLEDVLFGANNEVISIKNKDSSPLARVMRGMILSSINGAPVGRADDEQR
NRRNMGGELLLLFVPGASEEPDEFDLNSGDDEDSNFHQQKVSIGVANHEDVSTFPRSTDV
LLDAAEKAGPGKCIIIMSEGVNPGYAIGVSAERASCTVLYINAVARLKTRQSLAQTAEIF
TKSLQKGLWIYIEQATKSISLLRKLAECITEAQLEGTIHSKARVFLMCEPHPHFPEALLK
GSVTLRSTLRCDDGEVYLDNDLLESRVGNSVVRGAAQPAVDAMPDIKGGRRRVKISHEVS
IVPLEKNTFLELSQSANPALERETATGEGITRFAKYIFSANEKFISLCKVKEGRYAVGTT
GGYVLILDVDGLPLIQFRPHKACVWDVAFASPYDFATACEDWTSSIFNYSLAGQEVSATS
VLSLHGDVFAVTYANPEDPQSAVLSGGLPASVYVLHSDRQTSSLIPVGVSTQAMRSTQRG
YALIGGGNGACSLIDPVSCSVLETTTRHQRKVPAVASFGSMAVTGGFDKMLRVWDVRSSL
RMVNERAMAEVITAVSISDKYVAACSGSDLIVWDLRRLGTPLATKQRAWKDLTRGLIIDE
DVVITASADGVARFWSVGAMGNV*
>TCRU_7952 hypothetical protein, conserved
MARVVAITVEHEEKPPGHFKGAVAKRRIIPADPRRWTDAHLFANLEHVTRRAGSVRRYST
ASAQSGRSTSASASNAATDGDPFLKQACMMMETADRNRTLRVGLSLALVQRDHVTGPNGA
SGGHNSRA*

>TCRU_7953 hypothetical protein, conserved
MHGRNGELGAVCHVANAVHTCSNCAASCARKDEGATVAFKMNVTTHKYAGPYELWWRLFS
PDGTIHPPARNSDADRTGICQLPPPREGKDDTNSGETTAPQVNAETSRQNEDWRQSAAAD
GPNTVDRSPASNTEGNTSETRREFANNPIEMMVPNASTKRPSFANGPRILVVLNAFGIMS
VTCGGREHVAADNTYEVSERSATGHKTPFLRKWRCGQWICC*
>TCRU_7954 hypothetical protein, conserved
MAAEGGPVAGGSGRRGNVNSEGNSNQEDEEGGGNTAGEDPNPTSAGALTAPTRQGQSSSD
PLQSGTCNPSGAGSASAARMRASGPESLGGGQSAGTTSPRSDASQQAASGVHAGGGRTSQ
GSPASEQTVTGQSQVPGTAKEAPQGDEGGEPGAQHEADQTTKMTVVTSCAKTAVEEESRQ
RDRKMHHVSIVAGMLIIIIFPCSYRHV*
>TCRU_7955 RNase H, putative
MQPHDGVPCTAPGHGKAEYPSYPAHAKTLLVVTDSHSLLAAITKGPLSHTDWTGDQIWQR
LLTLTRAGWSVQLQFCYEHCGVHANEPADQHATQNTATGQHTEHGIAPMWHTDLLSCINT
QLTNKWRSTMHQDTHHYLLRSARPSDPGGKHLITQEALDQQEQKHTAREGCGESELWGRL
YWTVRDCTNQRRFCNISPEHTAFMRSNDDPTAPGRRLFPRRQGRPTHRLWRDGPPHSVGR
GNARTVTPHWWDTRTTSVTVGAFIRNALHRFPTSTAIAATRSSPHKKRHRTAQKSPRTQP
RRHTASKQQCQEAISAATGSASLHKQNNQPAENTAPTASGMYRRSGCAPTAGHREGPWHR
KLLPMAAAS*
>TCRU_7956 hypothetical protein, conserved
MARETAQNDGKADLPVAETGRKRGQDQCGAQPIPEDEGAAPPRREDIATSGWVRLQVFSR
GLPEAQRSNGVRLDFALPFSGTFGSK*
>TCRU_7957 hypothetical protein, conserved
MEGCPGGNGRRAHRVTGACRCGEDSIPGVDPDIGPRVAAPRKGTTRLLPTLRQARTRPAD
HKGPSVSVAPSLPHCGGRPASASAGTSSRRENRKSFPTSERRIDVLLPNLRQSVLFRPQY
EGTCRTCSAWRYNIPRRPPMRMPQWRHRLLSRRLARSSPPKLPSMPAGGTRRKHKRGNSR
WTRLFRHRLITDATGC*
>TCRU_7958 retrotransposon hot spot protein, RHS3, putative
MDMQLNDFLVMELGGMGVMPANQNVLLKEFIKDSTRYICGTFLLRDMKASDRYKRMERAV
RDEMDMEEDVRKLYEKGVDNLLKWSLAAEEVKANVHNLTKRFLDAAFIELMSSMAMSAPI
RLEGCYESVYNARWHHVVEVPGGEGMGMEVREGEAPQSWTYREFDDTLEKDDGVEEPGAP
RLRLMVLASDKGWPYSWEENKSTRDCYVNCEVDRVWQIVRNDLTEWFSSYRRTEFKPKQH
LLIGMPGIGKSMNAGSYLL*
>TCRU_7959 elongation factor 2
MVNFTVDEVRALMDYPEQIRNMSVIAHVDHGKSTLSDSLVGAAGIIKMEDAGDKRIMDTR
ADEIARGITIKSTAISMHYHVPPEIIADLPDDKRDFLINLIDSPGHVDFSSEVTAALRVT
DGALVVVDCVEGVCVQTETVLRQALTERIRPVVFINKVDRAILELQLDPEEAYQGFVKTL
QNVNVVISTYNDPVMGDVQVYPEKGTVAIGSGLQAWAFSVTRFAKMYAAKFGVDEAKMCE
RLWGDNFFDAKNKKWIKSETNAAGERVRRAFCQFCLDPIYQIFDAVMTEKQEKVDKMLKS
LNISLTADEREQVPKKLLKSIMMKFLPAAETLLQMIVAHLPSPKKAQSYRAEMLYSGESG
PDDKYYVGIKNCDPEAPLMLYISKMVPTADRGRFFAFGRIFAGKVRSGQKVRIMGNNYVF
GKKQDLYEDKPVQRTVLMMGRYQEAVEDMPCGNVVGLVGVDKYIVKSATITDDGESPHPL
RDMKYSVSPVVRVAVEAKNPSDLPKLVEGLKRLSKSDPLVVCTIEESGEHIVAGAGELHL
EICLKDLQEDFMNGAPLKVSEPVVSFRETVTDVSSIQCLSKSANKHNRLFCRGAPLTEEL
CVEMEEGLNAGSEADPKVRARFLADKFDWDVAEARKIWCYGPDNRGPNVVVDVTKGVQNM
SEMKDSFVAAWQWATREGVLCDENMRGVRINVEDVTMHADAIHRGGGQIIPTARRVFYAC
CLTAAPRLMEPMFQVDIQTVEHAVGGIYNVLTRRRGVIIGEENRPGTPIYNVRAYLPVAE
SFGFTADLRAGTGGQAFPQCVFDHWQQYPGDPLEPKSQANTLTLSVRQRKGLKPDIPPLD
TFLDKL*
>TCRU_7960 hypothetical protein, conserved
MNRSTVSEDIALAGIKKEVLRSLPFWKSFVELREAYHRRPRVFSCDVSIKSRKACSHFVG
FDVLWVQSEVVLVSWRRPSKRNRANDLPPEFVEVHLTFGSMHFVHQNVHLVGDHCSYSLQ
SVVLLQRPEQLQCVAGNMVHFAFLVYGMLHISQRDGFLTEPRAILPPPNSAVMLLGMGGN
SMERGIPYILGEDAHIYIAEIEPAVVSTCRFTGLLKENANTHVCLDSAERTIQKCPEKCT
FIFMDLFEPLSGKMVNTMPLIRQAFDILAPNGILLINEHSIPTVEHLLPLLHLFGDHNVQ

FVNVRGWNESIIAATKPGGNADGLGRKCSKRLATDVLNDFDHTFPGWMPDKNYFLRSQIL
YAKPLTLKLRARQWAS*
>TCRU_7961 SET domain containing protein, putative
MTRGDVVAVFCDALHEQEMAARLTQLANFPFRIFPVRNGPSMYRAVRTFCASRNCYRCAL
NLCTGTTEDEDRASQAVLASLFEQLEVVYCGCRYMTLKQPLDVLFMMCVYAGLPMPLFSV
VKSEEDIEQLSLRFPVKLRTLSPLQCVFGSVVTDMPTLRRVLNEVLQSHEKVLVWEVNGT
KSRELVTLVSASGCVAIAQEGSKDAVWLQQCTPSIEKYSSFFATAVMNNSGFSKLCFNKS
PYSDQLFLEDVELGCSLVDLNAELLLAFSDKKLLEECVRCGEQSFKRPVAEVRYGGNERG
YFVCANKDVKRGEVVFEDEGRSFAIVTRPFVDKHWGEEEKVTFAEYAWPLDADGHVYAIW
ESNPSEWRPINHSCDPNCIFGEEHSLNVIAARDIKKEEELTMDYSTFCDYTMRPFSCSCR
SECCRGIILPDEAALRKYGTHTWHRRPPIPPAKSV*
>TCRU_7962 dolicholphosphate-mannose synthase, putative
MPISYTIVVPAYKECGNLEALTKRVFDAICDAGFAKNDVEMLIVDDNSQDGSVEVVKKLQ
KEGYGVRIDVRTKERGLSSAVIHGISNSKGKYILVMDADLQHPPEAVPRLIRALERPGVD
FVCGTRYGAGVAIDGDWPIHRRVISWGARVLARPLTPLSDPMSGFFGLRKEVFQRGVRDL
SPIGYKIALEIFVKCHVQKYEEVGFNFATRIVGESKLTGRVIIHYLKHLRALYLYAFGKW
ILLVPLLMIFIFFWAVKQVV*
>TCRU_7963 peptidyl-prolyl cis-trans isomerase, putative
MGVTRQVLSAGNGVQPKAGDKITVHCTGYLANGRKKFWSTLDKNEPFDFRVGLGQVIRGW
DEGMLMMSTGEKAELKMSGDYAYGKKGFPAWGIPPDADLIFEIELLKIN*
>TCRU_7964 hypothetical protein, conserved
MFLDEEQCVPEACLAENPVSQKTCLQRPEGEPDRIEQSLLGGHGAKEIHPSWRRDYSSVN
AKSREENKPRSSPSDLATSAMPNHWEDERTGNLLYELRRIVPHLSPEFDCGERDATLILS
AIRSGSAAEGTDSWEHRLSSLEAEKRMIQSRLDRRSHECEELKGTVAELRQKLRATQENT
NASVNVLSKRREELRKQLLLEESRSQKLKIRNGQLEMELERLKEMLRSRLSK*
>TCRU_7965 eukaryotic translation initiation factor 3 subunit L,
putative
MTTNPDIESDIPHEVYSFFRALNKAVDSWDTSLLHELYENQFPGLTQNFYMAGPGQFRPW
PSLRIKAVADCFKNRTAEQLYSFLRLKHLFTDRAVSPNDARSSWDTFNNLFNALPSGSCD
VPNWLLWDIFDEFLFQMTVVYQKRFTGRVGWSVNEGMQLMERVVAESGIEEAIQSENLDE
ITKPGARHAQWMCGFFGIVTIAKVNVLLGDYMGALSALKPLDVYGRGRQILLVVAPAYVS
LLYHMGFSYLMLRRYADASRVFRLSLTTKVSSRKFSEKMQFDCAYMHVISCILGGMQPDN
LSWLVEPRKLSGFEDEKELLSAGDEERFREVFDRCSPKFLAIPPITTIMYKGTDGKELQA
RLFRRAVKQQEDIIKLRGFFGVYQTTTTELVKTVLDVDDGHVPLFAMRLRSRQLVHDGSS
ADLLSGSYAVRSAIDYTVKGENIDVVQKSSYRTTESKYFMRINNLRRRQRHFENQRQERR
QAQPISVAK*
>TCRU_7966 hypothetical protein, conserved
MNTGEVDGVGDGNESCREELASAASRQTVPPRRPTDEGGTDVIAQEARELIERMRVELSQ
LRGSVDLRENTERLMSLRAARHLMAYKRRSDAENQQPENVAEFQRIAQNEFFFVPMATAP
MTRLTVCSHQEKGARQKRFKQRRIDAGPSQDSPPWNSSTSLQNSDKTTAKKVPGSTVSVR
DCPLAPTKGIASTAHTLAEFNRASNCLERTSEEEVDDLTDRKGVASRVDEIWVRDYLRRL
NIVTRGPTESEGRIDDPVLNGVALHHLVSIALNRDLKEGRATHPAIVLKPQNLDDVRLNY
VVALNLLRAAENDATLQIPRECRLIRPESVILRGDSVALFTLMRTVVDAYLPIACEELWA
APSLTWQPHPDGGGYTPSAMRSLELEVCAFLQSQNVLADPVVHQLPPDDAPVPDALSAPF
LAPRRKLWCMRTEGFPSLYIPSVFPFFTNGTALCDLVGRVTGNRLSVYRNPRVKSNCMEN
IQAAFTVLQRYCPTKMSPFFIESPECVFYGDRRYILLLLEDIMRMAHGVPPRRHAPRLTD
TPHFGRQRSSQVPHTLTVGVTQSSSSASMPEVQKQQRLGELASKLFEKNPGKEEGLRDPD
RATPRCVIASPLSEGRRAGRPTPARQVPFSSAPLVETNITLGALDTPVAVLNGVEYMDDE
VAMMQKWLIEVLGPGFHYTAADHSFSVSSRDLQLGGTSLIFSDGVVLAHMIRLLERRRCV
ELESIEMHAKATAAKRRNIKKCVSFLQTEKRALLNVPLLDEILLAGDRLGVLYVVQCLRN
TYRFAVRV*
>TCRU_7967 Transcription factor S-II (TFIIS), central domain
containing protein, putative
MTVPEAARAKALLQLTALLRGLEEFRLQPEKADLYAETVVTRMTSEYSDKESFRDQLMGL

LANIRNLDGELEKVGPSLLATMKPEEMLSSKQRRDRDRFLRKRVREQILYDVTSMLCATC
KLVRPDRLNLNQLALDSEENGTHFDYNFDNLCQCDHRSDEDERSTSTLSSLASENNGSAA
DECSPHA*
>TCRU_7968 Mutt-Nudix-related hydrolase 5, putative
MTAAVRLLPRTTSEWIALVQRALPLRLDELRMPSHFLLKDIHTGRCRSHLQHSMPPHSKR
ESAVLILLSPPVGFAGKGFQEMCMTLTKRTAKLRHHRSQMSFPGGRVDHGETIITAAQRE
TMEEIGIPASSYCVIGTLHPIYSSDGGSKVFPVVAVAESAVEPVCKSPDEVASIHYMHLS
RLLLESERTHCRLIKRHSLTGGMPSYFPCFFASESQAVVCGDVCPTKNTPSIPEDGGLFP
MLRENFPGELVWGITAFITCELLVRLSAVLELSQLREGDAMGLLRCSSVVARDPECIYKE
NSS*
>TCRU_7969 dynein light chain, putative
MTTSNAKEAEGPCNFNYVRQYVSTLNYPLEKMSDMTEEMRAECKEIVVNAIEKHEDSYEH
AAKHIKEQMDKKYGTSWHCVIGEGFGFEITYEMKHLMYMFHRGYMAIVVFKGL*
>TCRU_7970 dolicholphosphate-mannose synthase, putative
MSIEPDHWSFFQLPPFFALQPGPTALARQTSLWGSAIIDHAAYHAPRTRPGVCPFLRLYK
STSDVFRNPSLNRRLPPEAAARMLESLVAQHPNHCAVVLPGNEKGENDDADFAVLLACNE
SGLKGLEQALLSWILDRGAGTTTAHLAQKGVVMTFDELAENNCLAYRRDREPFLKRLSAA
PVPVGDVGALSNEQAIRTLLHSLKSRPLSALSPIHITLFNMDGSDRRPYEGVKFGGAVAC
*
>TCRU_7971 20S proteasome subunit
MSETTIAFRCNSFVLVAAAGLNAFYYIKIMDTEDKVTQLDSHKVVACAGENGPRVNFVEY
IKCNMALKRMREHGRVIRTSAAASFMRNALAGALRSRDGAYLVNCLLAGYDVAASSDDDI
ATGPHLYYMDYLGTMQEVPYGCHGYGASFVIAMLDRLWRPDLTAQEAVDLMQKCCDEVKK
RVVISNDKFICKAVTENGVELVNTVS*
>TCRU_7972 hypothetical protein
MVVLRIIGDEWSWEDRIALAVPPQKMFTMCIPLLISKLGVEKWNGLVLYKTEGKPRKYCR
ATTPIDMSSNPQKERLRDGAVLWVRVGPSLTQQERDRVFQKSLEEWREKNGLKGVSVDGS
DVRRFVEELNSRLNRTDAALLTSQEQEARTAIEGEEHRLFFYMTMIHREKDTLLREETEQ
RQSLEETYIRVAERHYHENRLLLLRTRLVELGVCEEGSRLVVQKEQWREFEMLQGAFQKG
HRALQDARARQLADSKPMLEGQNEGRGKTSKNEETVGTNADAAMLLSVVRAELQRLLEPL
EKVYHEKVEILEKQWEATVRDNENFLASLRQYIISLFRVIRSELRQSDVSLPLVPSDSMG
IKEINEALRQQQGLLKELVQEYRDLDRQVSGALGETALKTTLDTVNVTQLNLYQYLESLR
ELLSATKLLCCGVEEAKTQESAYLTQDALEKQQQEEPERRASSLEGVAVTALHTERMDDH
RNGEKDLTFRIHTDVYNILLLFVSRYVEFSSWGSFQGAEGSRGFLDDLLLNCGSLQVAVD
ELSRTCKVLPHPMREDILHVVEAHAPHLFGVIDLMLHLYAGREAELVLWIRPELNDEGGF
VEHKTDDGLTYYYHTAAGMSQWVRPVIASLTE*
>TCRU_7973 ribonuclease HII, putative
MSEFGACFRPSPPLFAGALRRSTTRWHRLNKVLYDRQPQWNPLQRLQLPLRKTVGDVPTL
DGTLDIFGYQLFRDGLLSPLSPPRTYQQPGQQQDFTGFLPDARKAQKERTRLEARMRKHG
VVLRRSIKETYLTIGCDEAGRGPLAGPVVGAAVCRIPLSSFNNELCAVYDTREEFQIFDS
KSLSEGQRNVVFQNITGYEKLFHLVADKAFVVHHASGDAAPDNVLTKRFPSHMKLQKLPF
KKLLSMQTPYLISYHGQNVCGNYLYLWGIGIANHAYIDMTNIYVSSMRTMHRSCFSIWRM
LNDARFSLERAPRPKHCSIAQYLFSRYCIAAPNDDKKRYVVPSHVELVSGASEFFDTEPV
QPPLILVDGHAAPEETISFFTEIQTGGCVQPIIEGDKRSLTIAAASCLAKVARDEIMNYV
STLYPKYQFAENKGYPVEYHMRAVQRYGVSSIHRKSYKPCATAITKQLKRKAKESQTCS*
>TCRU_7974 Peptidase family M41, putative
MKDVELTASLGVIEVSITPRGPAAGFTQQVGKETFDMPTDVSLFTDICVMLAGRLAEATR
HAELTTGTQEDYQRATKTAIHAFLAFGMSHHVGFLACEPQRLDEGRIYQKHSEKIQAVAE
EEAARLVGTAQQYTKTLIAENKELLHRLADAIFTRKELLKEDLEAILGPRGAARLSLEAE
KVLTAFVQKSEKHGTTVRSTSG*
>TCRU_7975 hypothetical protein, conserved
MRSVWSGCRSIVSPPLWPLRLRHSVQVGAHGGHAFGMCSRSESVVSTFAMRVSLRWHGTT
TPPSASPEGSSGAVHSVLSAAGHNDEEEASSSRSFRGTVRTVRLHNMPRTWLHEEVMQFL
HQVAEHAGIDPPPEATQDNGTEGNANSKEYEEEEEEDMTSAVPNVTSPFVARMHIPFGRR

TGIVCGPPIIQLTSDALAGYLLNDLNFEPDDYRSRIYFTEVVNDKYHEATKMVNKDEAAL
LKMEQQEALESLELDRYLMAPDLLYDIAKMRQRRLVTRRSKLLLHTFADDGRPDEGEDGK
DQSEVKDDDPTNENKRMRLRRHKKSKKTLRCVGEYKELGRGSVHSVPLALPYVQGRRGV*
>TCRU_7976 SpoU rRNA Methylase family, putative
MGRQWGMKTAWAKSFFVPEFIATAAVHDVVDAVQFEEEGGKGRSSSASRALRVNNKGSVS
KGAVAASWRCTRCGSVLRVPTNAHTGRPSFFILAEHLEGVSSSGTAPITGVEPCRVGLIR
YAPNNDPHSSVSGEEGRKALDALQQLLFGESTEDSGKANNGGSGEFPVRVFVAVENPKTP
ANLGGILRAIGCFGYSGLIFSGTRLLAALKHRPVTDTQAAGFSSPYVAIPDITNLFEVLE
GATSFEAVVVAVDMIDGATPLPLYRHPCLHALDGGARKWSRCTLPNLVVYLFGPEDGSIR
QEVLARCHSAVFLPTQGSLNLAAAVNVVLYDRCAAQWRLTASDDDVTAKAAVAASRDAAA
RCLRSRNANNRTSWCDPHSAAVAVSSSQSEKK*
>TCRU_7977 hypothetical protein
MTSRPLEPLQDDERLMSISPLSDVSRYGHRPPRSTSPVRTAAEVPPPRFCLEKATAGIRV
LGLLSTATRWSFGMILDTDGAEKTKSEKEQEINSRHPDAPSSSCPSLHATTLSWNTVALL
AKHVYLIDVVWSPASYASFYHSLAPPSALSLETFFPMPPSLASLSAITAWERLLCAVFFS
TSVEQMVLLRHALSWEEKCRFEDVLAVVRHCTRLLVDGFFRWVPPSTGVRLLLSCHGNSS
SYIHWGGSVGEIKVGLLDVENVVLVQRHLASLRRCWLSTDGEEEMGAGVAVGAHVDNPRE
DLHRTVRAFQRQGSHLRRWAKDNPGGAYDESNNNSNGSPWNLSNTQRLLNAMAVVAHIES
YLESAMPSCDRSTLCRHDDYVNGGGCGIGGASRLPFTPAQRDHLIEMLALLMYPCKENFS
SEGRRIATHWLRVNLAAETNTALFNGPSGLLFHDFLASLAHWLVLQVVPALMTFVSAASC
SGYVDTSSPPDRALRLGFHCAEESVADMADVLRAPTVTSKSSSSAAAADLAARRNVLLGI
TVSDWLRWLRQYHARNGNGNIDGGRDTTCRLQFFSSLSSTGARLLDVFDSLELFSPNSTR
SPTGSGIWPVLSNGVFERHGAWVVAHWAVGSSYAEVSSINSECTSRKSQTAVAAREPLEI
FTLGEFIARYRFSVDATRVATRLTYHLNRRQTVSEGDMWRPLPPLFHISIENFNRFMPII
QAKLICSAAIVDYTSYVSAKEEKEEAAGVWQKNTIRRVGVDLVRDNPVSTREAPSVIIRE
DSGLIKLYDSGALEQLEEARLRGWAQLHECGTLILQAFLRACWSVRWNLVPLRRRAHRQA
IVPVQAALRVRGAALRAGRQARRLLEQRQRWLEERRRHNVMREQLVSRMELQAEGRGNGT
GDGEDGMNPLRATPGTSTSWPAKSLNELIDERANCVPDPALGFGNRLDRCVKDVQGCPSQ
GETNAESDGDNSFDAASAVFAMERKGRGVVQHAEARIRRQLFISLEEKLRERYLLQEYRD
RRVVVQQQIKEHQEAIVREQRRNWKKKNKKRQMMAQQRQQHSVRRAAKEAPHRAVFSFSP
PSVAAGNKCGDIPFLADARTNDEGDTSDVVIVIDMQGDDGDEEEKVELPRQASHVVENCL
PQEVKKATKSRNSHVCASLLSLRCGASGISKASCLTPRTALWRQEHEDRTFIEISQSYRW
HLLRQNCALAEIVLAEMSYRRLIFLAGALERQELLVRWRTIILPYCLITEALRADILAAL
VILQDAPRRHGSPATRMAPGIRVRRVNTTPAVGIRPQQQPCRRTDGLSSSWQKKKKEAVL
EVDGENDISRKRFTEKKENAEAQREFLCKPKFHLLASHFSNPCLSGRVNVATDRRAPAHF
KKEKGPSERRRVVTWVDPPLSSPPPSGSLK*
>TCRU_7978 hypothetical protein, conserved
MLRATCRTLGGQRRWWKEGRPDFMRANERRMRLERRRIDASRYYAPVEPTPQQACTLYRQ
LLKAGHAQLRVTDKAYYVRKLRREFEVTARQTSARVRGIMYERGQWMLLNKLGGIV*
>TCRU_7979 WD domain, G-beta repeat/Dip2/Utp12 Family, putative
MVGKTYLRYVVGPQGGAVASNASLTLCSVVAPSSYVDLATHHSSNSGGRIGLRHRSRQHT
AVASAVVFVASLEAVRVYSVRSGALQHALIPAEAKMPLEVTAICVLSLESSTTGQSSLEL
DGWMLLVGYHNGHVAVFSCGPTNNYGLPLCRFYALGHKVDTTVLALAAGSQRAYMCSGGQ
DTDLTVWDLVTQEASFRLRGHRGGIVGIEFVPQKEDRFVVTGAADGLVKVWDIFLRQCVQ
TLVASDAQVSSLRMDIAGRRLYCGLRESQLKVFNTEALLKADDMHGDDAGTTMTMIAVVV
EHGGIQRKLQKPVTSMSFSHDGAFLLATTSKTVEIFRILTREEVRKKVSRKRKRCAAKKD
GGEETHGNYDNEEEEVEAGVKNSRREPNKVLEEITNGIGPNPGSASGAPAAASATEEVVL
LRTFFLEQKVRSACFIPPTSGSFRDADRLHVAIAFNNNNVCTYTTALTTTELSGGATWTL
EDLKPRQTMEQRGHQSDIRQLTFVEDDTTLLSMSAEKLMMWNVSIKVQQGETEVGEPHDF
YDAKEANVQHADETGVLTCTGHVAVDGAVTMAAISSSLCCVGIQDGSILMVDLPASSVVF
TEPDVHVGGVRHVARRPDSSGFVSVGFDRRLIVWTLALLKQSSDNSQKKSNNDNINNKNN
HVNSNAAPQLLQSMEIELTEAPLFLALSPDNRFVAVGLQNTNIQLFFADTMKPYLSLFGH
KLPPTAVAFSSDGTLVASVGMDKSLRFWGTDFGDCHRAIHAHDDYVTQVEFLRDTHQLLT
VSLDGSVKHWDGDNWTMIQLFRQHQRGVWTVAATANGTCIATAGMDKCIRCFLRTQDIVF

PAEEEERMAQEAMDEEAAKRVAMQTLEQQNPEVAVAGQLTTTAAAAAEKIMEALDLVSVE
LQRRENAEDLTPPHPLLVNKTVWEYLWSVIESVRPSEIRHALSSLTSTHVDALLNYLEEM
LRERAVLNYEIAAKIVLALVAAPPGVAAVGNRARAAIAGEISEAHGVRRLHALRRMIAEG
LDHAVGRMDYNIAGLQFVRHVIEEKEKTRFFDLSKIQGHRKKYHSRVITSGNGKKKE*
>TCRU_7980 hypothetical protein
MADVEESLLELRRLIARARREGGGGTHGKENDNETPKGCQISVKELERRFAGLEEKLFRE
KGLLREQAQELHQRAKRRKRQQQKKKKCLVGQEQWEDGSVPVGTSQNASYDRMDVGAVET
AATDTMSCELSSHFSSSLNGSPPLQQEVPTRDTRRHHDGSHVEEAKETPRDVYGASCVTD
PDAHLLVDITDGSTRIEGIGVGPCTGNNEEVFCSSSCSCFAPYYSFAHAYADDDRQRLLF
IVDQLSNILREERRQKEILLSHVVAPMVRHIEVLERDLVLQQREMTALKREFELLANPRH
VFRSKSVRDEEKMGFDDIGEKSNEEDPVLILLQSCEEQLLRLTEYRRRRM*
>TCRU_7981 Ion channel, putative
MDSASGSSRSSPRRRENRGFLRLLRRKTRAFTLGPRLLGTRVKHLLRDELYFDVSLHSAP
SVVTNEIASLELLAAYHRWLRGVQALLAVLVFILSLLPSAAVVEWTILAVSEAAVLIILR
VYSIKAEYTGLTNVLYRDHRNIFTSPFLLQMLLEIIVWNIQTPPLIFFWRPFFELLDYFI
FVRLYAVAFYIHNAAYVYRFFCRAMTAMTAMPLTTSFTVRTALVYRKAKIVSLATLLSWV
TLSFMYAKAEHVPLHDGFWYAFQAISTVGYGDITPATTAGKLVAFIAWVISFVLIAYLVV
IFHGSLTKNENEHNMYMLMRCQRLSHLLREDSARVIQTMWRFHRLKSPFSDGKMQCAKAL
FYSWALTRNISRLRRERQEWRDATQRFRASRVSPSIGFLDQGHEEHLCHLLRAAQHAQQQ
ADVDAFFRKCVECRERMPTREEVERTVMNNFWRGSFHSTDTVGVCGATTAHVDVTNLLEK
VETLENTCSRLAALMESLAATAPTNPPSLAHSCS*
>TCRU_7982 Ion channel, putative
MELRERAEQMIKPQTPIVIPPVTRSIRQLTRMERLAANRRWLRGAMCFLAVICYALSLFE
EGRVVTHSIILLFSLAGEVAIVCIHRVKAKFHGITNRASGKRREVSVFHSPSLINMLLEM
LVWILQCPPLPDDMNPEWLVGLDGFLILRFYVFLLYGTHVAHTSVFSHAIASLARIRLNY
RFFIRTAFLLEHLAVTLCAVAAGIFIFACSYAKAEGATLGESFYFCVSTASLAGYSETSP
VTFPGRVIAVCVTLLGVIVLCWTVGVMNEALSLTEAERNLYTLFRNNELCGKIPPQAARL
IQRTWKLYRAKRDRHNFISRQIAAFLLSQQAITYRGMRRALIQYETAFLRSTRTLEECLA
SNSTFGSNGTTPLASSNTSPLGSPRTRRPFPLYQEMRLKRNSRASTPRGDGFLQEFGNEF
SIHRSERNRFVSTPHLPTTQQQLTAAVPGMVELELRLSRLEKSLEALATTAESLRGHLGV
ISSVSV*
>TCRU_7983 hypothetical protein, conserved
MTRQSDVQESMKNISSRVEKAVEVRKYDEKAVQERMRKLHADILQKKLAEKKRMDELAQI
PVEEADVALLMQELGCDRMAAEQRLREKKGDLVAVLRDVAGLPKARAATASV*
>TCRU_7984 Enriched in surface-labeled proteome protein 12
MKGRNVLLFAFVLLLNLHIVPFASAQSSPSTSEHIIVFGGPNWEFVVQNKLTELKAALIK
DIGPQLLRKYAFLTIINVSSVEFNKNLRVHVTVLQALLSKGPSSRLLHLWPPDEANSMIT
QGAFSNTLALYPGPERATVISVQLAEKETGSIISDEFLLSLFKLGYAILSLMAVLLFIVL
VWMCCQGCGSKPVEEGAEPYPVN*
>TCRU_7985 Enriched in surface-labeled proteome protein 12
MKGRNVLLFAFVLLLNLHIVPFASAQSSPSTSEHIIVFGGPNWEFVVQNKLTELKAALIK
DIGPQLLRKYAFLTIINVSSVEFNKNLRVHVTVLQALLSKGPSSRLLHLWPPDEANSMIT
QGEFSNTLALYPGPERATVISVQIPTFSKNIKVYEDVLRSLYFLGGCTFVAMAFGLFVLF
VWMCCHCCCRSDEDEDDEDEDELYHFNQNKSKYRK*
>TCRU_7986 Enriched in surface-labeled proteome protein 12
MVKGKLVLLFAALLFLTVAIPVSAQQSTSEHLIVFNGSNWGPVVSGKKTVLEAALVDSIT
LQLLRKYAFNTTVNVTSLSADGELKAQVEVLQVVLSTAPTPDLQDVWGPEEVNSMITRSN
FQTVLALYPGPGKAVLVSVYVPENGKSDRGPSIIFWSMIFMGSVVGALMLITFAVVACCS
CCVYAKR*
>TCRU_7987 hypothetical protein, conserved
MDLSLKHGRILLSLDILRTYGRLRSLILRQKRSCPLWGAFRELGHQQGLITAERERLNFD
YANAVADVQNRNAQLNSQFQEAQINLLVRESNIAGAGNQVLELRQQLEADRAQLRERFN
LGRLTAQLQEREARLNALQTARDAETAGRDEAPAT*
>TCRU_7988 Enriched in surface-labeled proteome protein 1

MGAKVNDGDKNTVLLGLSYNREKRWELLHGGEKTSEHSRTWEPGTTYHVAIVLQNGNQGS
VYVDGQRVCESVQSNWENTESKGISHFFIGGDGGSAENTGGNEGVSVTVRNVLLYNRPLS
SEEIAGPAKNNIPKSVAAHTSSPAVSRPKRSSESLAGGATGEGTARHFGANGDGSTVRGS
GLLPSLLLLLGLWGFAAL*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MVDWARATQRDSPADTCLGRWMRSAVGACPRSRQRVRRRAIAAVRVALLVALVLAAAAAW
MPAAHAVVLRLRGGTVDRAITVGRAVDTVLMDGVYITNGVAVMFDVAAMLPGTLRIELRN
CVCDGGAQIYVRGYSGEPASDRSLEVSVSGLSGSYCSLVFVHNLPAHTNVTVRDSTIVAA
GPMRYSQLSGLTDAVASPLVLHATSLLQSQLRVSNTVLRSLQAGGSAVYVGGGVDLLSSA
VVLDGVSLEALGGPTASAMHVASSSRLSLRSHSVFSVTNVSVVSSGGGIVLGERLAVFDS
ALRFVGVEGAVASSLVRCDGGTIDAGGWLDLHDVWAVGEASSVASLSDVMLSGGTVSIVR
CAATGATLVSGPAITSGAVSVQCNRAGGRVLQSSGDYRMAGLPSVSVVPCDGCAAALACF
DALTASFSDCVCSCRAGGVGEACLPFDVPSARTSGGGDGAEDCVSGVTLTESVTVGGGRA
TACFDSVLFSGPITVAVDLRLLDVFADALNVTLRHCVLVGGSQLRIGGLSESTARLMPHA
FVNMTNVTSLEGTIVLHGAMPPHSSVLLANSTLRATVGGSQYVPTTRGHESFRYVPALVL
DGVRLLSTRFVMTRSTLVCGGGSCAAILVERGLGVNLSSVFYMDNCVIRSRTHVMYAIAS
DLRVVSGSVFSIQNSSWILPSTEYGKAACVFKDVVVAGGSVLQIVSSTFRLGFAMLMAAT
LTVTDGSWLVHRNNEFRTAYVVYVAAHYGMVFRDRSVWSILDNNLTYGSYSTIANMTNNW
LPPSDTRPTIYGMCNEARGSPVTNYQDDLNIGAPVTVLDCGACTVDAVCFAARTSSISGC
ECVCAAGGYGDTCLPAAVPDGLGPLPLPDAKDTEVRCVHGGSISSVDYPDPGVRGLCLVN
VTFTAAIVLDLSHFDAPQQTLNITLLQCVLMGLLIRGSGARVHVSVTSSILDFGALDFRG
DFGVSSQILVVGSTLVSTSGHAISFVKFILSANMTLLLLDNYIEANRYAVYFFNGVVVGG
GIIVKGNTLSATKDDDSVESSVCVNAVGVKNGGYFDVENNTMSSVNGVIFLGDTTVSSAG
LLRVADCTFGGSEVFDSALLHLSGSVTLEGGAQWRVEGNSVGEASVLTIPYPQYKIQLSG
SGTTVALAHNRQVDNSYPFADLSPLDTIVELPARFVVGCNLQGDEEVSYAGVFPEDVVVF
RCGTCNDDAACYMPGTESVDRGSCSCSCKDGWHGASCLPFEVPDTVVLPAAERAVDGDTS
CVVDQTLTDLALNMWKTHHCYVGVTFSGVGAVLTFSLNSMPLHLPINITLTGCTFRSGAA
LQFVGGVAAVESSGVLIRVSRAVMRSSTVAFIRALPQHCDIAVTEVDAAQSSESELPDTR
MNTLSVVMLKDVVLSASSLLVSNVRAHATKRDAFVVYSTGTLTLVGGSSLYARYCSFEGY
THMFYLYGLSVSDHSVIALLNNTMVSGVSLLYQQQGFNVSDHSVVRVVGNSGSVRYAIYN
DDMWTVQRSSWLDWRDNDVEVGAMFYGTVSAFVSIDGSSVVTLTGCKMGSTGLSVSLLSR
ADAGYRFVAGCLTVAGREVTTAAELALNGITSVTTVAVCGECTKDGDCFAPLTTAVIDCR
CQCAAGGHGDVCVPAPVPAGPPPPPPTSSPPPPPPPPPVGECISDMVYPEVAQAVGGGLS
WLCYRNVTFSGGGMSLTVLVGAMTGDVANVTFDGCTWRDGAVLLLLGNVHAAVGALNIVV
TGNRFSDALLSPEGVFPPHTNITISGNSFAVTRLFHWSGLELDYPSCVAMNGLAIGNDSA
VVLSGNVFQSVTTSSSVVKFVGSALRVSWHSVLAVLGNTFHMGGGDSTLINIEGSGQFSS
LKVLNNSAVVIRGNVVTRPVKYFLLVILALRVESRSAVVFQGNDMQRSSAVFFSSYSSYI
YYNSWLQLSGNLCRESPSDAFLFLNPTVNLRDSTVSVSGNRFMSSTGTPTVLRIPKRSRD
LTNGAIVAACNTVNDEEEAKYSISSVYNATILTCSGPCALAASCFPAYTTTASSDGCACK
CGEGGHGDACLPVAVPEPPSTDGADLCVRDVRVGVEVNVGFGTSVACYVGVTFAADVVVD
MESMSGSVRNVTLANCLFVDGASLYVVGWRSDPPAGERADVLISGLESRSGGGVLVANRF
PPGSRVTVVDSVLIAEARVAYRGAYDLGDASACLVVHSVNLTGSVLTIARTHMAAVFRDA
VGVLFVGGVALSSRGALYVDGLSVQTALGLCVLVEGGVAASGGSVVAFVDSDFLLCKHAV
SVRGAVSVSGSAVALVRSEFLSTGDYAVAFYSTVRLAGGSMLLAKGNVQDGVSREMLYAA
GTVTAAGSTLSFVHNRALLPRMLSVSLSLAAGAHLRVACNDAGGRVLSTAEEYAAAGFGD
AGSIDVAGCDDCDRNTHCYAPGTASASMRNGVCACLCGSSGYGEACVPVGAPALPPAVGT
ASSVFVCEGVTVRSVFVVPVGASEVTLRHVVLDGVSPVLYVPWMARDGVRIVVQNVSLLN
GAVLYVMGGGALRGAVAAGSDEGGPVELSVCDVEALNGALVLTGTFPAGSVLTVTDSLLV
AARPTPLVYLPGSRSSPYAPVLVLSGLRLVRSVLVVSGVALVTVVTGGRTVVVDGAVLEL
VGGGVALDAAVLGGEYALYASARVVASGGAVLRVSGSQVYAAHGLVFDSGVEANASAVVV
NDNAGALTDGALLVLRGSASFVSGSWLSVRGNSIRGRLLSVPSYPRSAELVQSTLTLHGN
AGSGPVVMDGTVAIGGTGRKFVVGCLTLNGQALQPMDYRSAGIIGEFRPVACGVCDADVS
CFTAATRAMSGSCRCRCAEGGYGRDCLPVYLPRVDGCNRTSGMPPLSHTATLTETRSLTS

TWTPSQSTERYSPTQYGPTETLQVTETVALSPTRTPTASVSGTLWWSEVACPTLAVTTTA
AGGSLTQNDIRGGGSAVPTRLMVALPSPFRWARDPRLGTHLSFVPVSTVQPRGFGGPWGA
MLSNATWVRNATNPSTVLELAVPVHRGYFIAADETIVIRCDAAAVSGGCKGVLLGSFTIR
SATLPAASSALSAITGVVAGAAAVAVVVTGGLGSVLEMQALGVFARMSCASAQERASTAA
LPYFLSVFAALDPLWMVVGNALLAAVFGCVHCGVTAAFQRWRGVDAASAWAAMRFPSLTY
VVAHAMHLGIFFGSVLALAMPGARVQHRVVGVVGVLYGVVFPAGVCYLIARHVGASFTRY
WQFSRKPLHERLLYPVGYWHPAAQRRMYGGMLTNMRGSHVYWCVFQLSVLCVVCLIAAVH
PPVGGCHVQYFCMAAVLLACAGVVAFTNMMRSSFLTVMHAASFVLLAALCVVSAANHLAP
SEGGARAYAAIVLLLTTVLLAVTVYSTVVWYAEDRHWQELRDPRRGGLEALLRDDEESDE
ETQKPHEMTSSSYASGTTVASSYRPPAPP*
>TCRU_7990 Enriched in surface-labeled proteome protein 1
MNEAKKYTQVLEEGTSPHSKKVDVSRPRTVVNGSDIYMLVGKYSRTAVTNPQERGAGDWV
LLLVEGEVSSEESGSNKKIQWNKNQRLAGTFPEAERDSLMQLDAGGGSGVQTDDGTLVLP
VEGTTKKGESEKGGKTVSLFI*
>TCRU_7991 Enriched in surface-labeled proteome protein 1
MLVTLPVHSKEKGGEKKEKSGLHLWLTDNTRIVDIGPVSEKDEDEVAASSLPYKSAGGED
NNNEDRLIALREKKGLDETPHSLLSVRLTEQLERVKEVPATWKKVDEHVSQPCPTSGAAK
SALTDNACSAVKIADGLVGILSGSFSNDTWRDEYLGVNATVMKGTKGVATGYAEGATFQG
ARAEWPVGRQGEKQPYHFANHKFTLVATVSTDKAPKEEDNSIPLLGVRLGTEGGSKLMEL
SYNSEKKWKLFCAAETNREHSSTWEPEAAHQVAIVLQNGNQGSVYVDGQRVGGE*
>TCRU_7992 hypothetical protein, conserved
MRAVNVSCAPSDGSLSYRVCVGVWAWKKRSAASAETQRENYTFSGFDLRMHGRNGELGAV
YRVASAVHTCSNCAASCAVKEEGATVAFTMNVTTNKYAGLYELWWRQFSPDGTIHPPARS
GDADRTGIRHTPPPREGKNDTKSCGTTAPQVNAEPSRQYEDWRQSAAADGTNTVDQSPAS
NTATNTSETRPEFAFV*
>TCRU_7993 hypothetical protein, conserved
MFKGKTTTRNSTWEPRKEHQVTLMLQGNKASVHTDGRSLGEEEVPLAGERPPEVLRFFFG
ACGGHESRLTVTNVFLCSRPLNSTAMRALRERVPAPTREAAPTPPEKIRVVDSVREHVAG
NITEEK*
>TCRU_7994 hypothetical protein, conserved
MSVHVSCSRTDGKLIWRLPNETGWRKCANKPAEGGGGEDECALVCIAAGYVYEDAGNPSL
CAPDGGPSGARTGIGIFLSENVKNCSSAAAPTAAVVGQAQSGVGSPSREAAEALQESPDH
TDEGGSYPSLSEHVASAPEASSQTPSSPSGVTATGMRDPGGADSSDAATVWVRTSLLLVT
ALICAAVR*
>TCRU_7995 Leishmanolysin, putative
MLTWCCAWQSAVGGGALDDCRDGCEEPRDSDDIDGMELQDGDGDGRTLESHWSQRHAKDE
WMAPIVCAGCRTELTLAAPADLGCMRVRWEMAEPMRW*
>TCRU_protease family, C-terminal catalytic domain containing
protein, putative Ul.1
MNRIEINEEDVKSLCEGNPLMEGVINYVFVKAAAIAQRPDVVYFLDPAVAHTMYAFEDAS
LGPVDEICRVLIVVIPIAEYKALDFNGVHWSVLLLQRMSVNVPFDAFRLDSLSDKNEDRC
LSFLHLLYSCSTCTDHMPRSSTIMKFPSQRNDVDCGCFVCMAALHVAEAVKNWNDGATGL
FDGPLEFPHELDASLFRRSLLEEVLREGR*
>TCRU_homolog, putative Protein translation factor SU.1
MLNNELANLVDQQKRSVQDALEAQKVHIRVQQRKGKKFVTSVQGLNQALNFRRISREFQR
RWGCNGTVIVTPDAGTVIQLQGNWSEEIKKFLLDENMATEQNLEIHSLN*
>TCRU_nuclear protein, putative Y.1
MSTGTADDGKWDVEDGRWPRRANRGTLLQELLEKGLNSEEENLLNDLSDATTDSTFSSSG
EEAIDEIDSDFSDEEVEGVLDGTEVTTEAMLRREEREERQKERQRARRRMGGNVLQRKGA
AAADAPKTAALRLRPPSTIPLEERLQMAHKRAREVRAAAAAASVAKGEQDSVGTMLISSA
GGASAYNVGHSVAKRRRLHGGRARPTATPAGFEEGEEVPQRLLYTSSRSVLEQFGVPVVI
SFSTCLPRMFQT*
>TCRU_7999 Inhibitor of apoptosis-promoting Bax1, putative
MMLRRLNNGVTSRSLTMATGVGLSIAGRCFQQSRRSGLPAVKETTTMVAPTFCMSRRGFS

LQPLRHMRGVKWVKPVTSPMNYGGDNTGGGSTADSLTPYVRQHLSRVYGLLAAGTAVAGI
GSFLMFSTPLGKAMPFWLPMVGGFVPLLWLSFAPPQDPNLKLALFFSFTVLEGMALAPLV
AITMAKGVLGTAIVLTGAVFFGFSAAALLAPRASLLALQGPLFGMLMGMVAISILNLFYP
TAFALSLILYGGLALFSLFVSVDTQAMIERARCGAGDHVQDALQMFLNVVNIFVRIAQIL
GSMDR*
>TCRU_8000 Surfeit locus protein 6, putative
MGFRGHPESANRRTKSAAAAAAGGAGTGADEIPLNLSFGNFEFEEMKRLGRRGGGVRELA
TLLRHAKRQTEAHASMLGSEEGVERRQADLLDTAMRRAVGVKVKDDPKRLARALAKRRNK
KRSSAKKWAERLENLQRSVNTVVEDRTMARQAARMRRKGKERGKQNPRETKRAPGAAAKK
KAKKGADRKGPAAAARNKKPRQGRK*
>TCRU_8001 hypothetical protein, conserved
MTQKSVSVSSSPAAAAAVDYGCLLLVECRKCDGSEAFRLGAELLRWPEEVAAKVYSGGDA
TLPSIPVSNKYFSTKVRIVITDGNALAAENSTTEASDAEDVSLLSSFLRPQSVNKTGWVL
LVDGSVHPDQIPWHRVPNSCLFRVVVNFNGVGMKVQEKMWYDACVTNGFEYVPHLEGYEV
VPAGVERSGLLGGDYRGSARLFQILHNTMWPENCRVPNGVKSDADDKKAERSCADSTNLL
AVIDDNGNDVLHWLCTMGRDRRFFTAQWPLEAGETTLRREKNISWNSVVGEERKALGIAN
KYYTARVEVQCLHSALLCPAMADLFLAQYVDCRPKLALVSWPPKSTQQVVDGATFPQLPV
LIDQLRRWGVEDCVILTRRAKESISSFDVHYSEEQGFEVVYMDDDGLERVDEEARGFGTT
GADRLAEIIHTIEWPQRTSTPTLKPPPSSTSALTSGKKLNRVLLWACGPSTVEEERLLSR
TLHMCFSVSCDHNGAAIASMTSSSMDTPVGSTIVHNRYFDATVSICSFGGARSAIMREPE
PSVEQLLTFGVVALLTKADMSDESTRNSIGAALDKCYAAQIACCGICDSDWLLLDEENPD
RDVMRRLCEAAEETPAYLWYVLDGDESNEALVARVGEMLLHVTSRTSGTMPAGAAGKMHD
VSEHGSGGSSENSDAISDGKDGDFAAASIEVLYGLTDVDGATRLGEVVQQHVWPIRTMKT
IELQQEVRQEKKTEHDTERVPAKERSVKEEAVAAEEGPALLTGCELPPDYLVDPLTQRSV
HVEALAVVADGKLGERGQSPQPQKELEQDLMVWMDKMKRHGHTLPRTVRQRQAEILAIKL
GEHLGKLDNA*
>TCRU_8002 hypothetical protein
MYGKRVAPIDYTLYLEYPPAAPQCNVRSLPEPGNAWPSTAGSPPYFFFFSDKECNAHTDA
KRARGKNTAEPELDDFTRHHRFVLKRRKEVEDARVCYEEHAGTGRMRSPWMKFGTPKTPA
AATALTENCGEGQDSSGSSQLLKSAGAHGFSETMSSLTLTQRLISTATVGSRRPDSSPLT
RIESQKARQTTTEMSLSQRPLRVQVHQTCLIVRDQPTNPVLEPLFKTSTWRILPHKPKWK
LDEANQITRHYDERLLRFLREGVAC*
>TCRU_8003 hypothetical protein
MDTVQEEITVAAIQSELKAATHLFDQKIRCAVEKVDKYLKKGTKKDDINVETKLAEFKEC
ALLFNSACKEMLLAAKKVAKKLAQCDPLRFTEAAAQPKSRKTEESLQEAKQSADAKDKTI
ADLQKRIGTIREDAERVQGELQQKLSDALAEVTAKSDECLRVKAEGEECREELRVARSQM
ALLTDRLGALERRRSHEFAFLERMSNDHERDIAVWQKKCSQALQEVEYLRTEKESLRGRL
VDEKLRVQLRELQQECNRLREENATLRHGGIADETSVNDAGMAKRGVFGMGLTTTCPEGK
NVGTAESPVVVSLEMEKKRLLEQLSVSFEEKLALESELLMLRQQLATVGGNTEQTRRSGE
FKDAPPSSLVDSAMDEDAQMQHDFPCDTRSAGKTASNSGEGSTCGCAATSNSHLDVKNEK
LPKNCAHSDNGEKSRVRELEEYVRHLELQMRDVVTTATMAVDDERKAAEQRLQKEITLHS
EIYESQLETLKQYGERQAREAKEAALRCQQLQGELDLLRTTTKKEKIAQRDLVSEAERRL
SMAEKKIFAVRLDNEQLRVKERVLRRELENMKALLGSQHVSTPTPASTLSRQELKFNSIA
DGGVPSNKEQKLHPCLPPNDCSAGITATTATSDAKSDKGSTNGGSQELASTPRGLSAAGR
LAEVIRQLHERLTALDAEAARVTETHEEEHGASTQRLQQLRAALLYWNRDDDTDDSLNGV
NTMEMRRRIEAEIGSLVESQRAAQGIITAYYAQAGKKRGELVEALEKAKNMRMALKRE*
>TCRU_8004 Fibronectin type III domain containing protein, putative
MADLGDDVSTSGIMDCLYTLYAGSNEGGIIIDPTVSDSPALVVATFGKPPASPAVVLEHT
YDEAFFVSDLMKTYPFSKFMLVTYTDEATPASGPTYVGAPSEGWLEQLPPQFCCLNLFRF
QRHVMFAPLVCEVNDYWIRELRELSYNLHNPQQLVVHLFLRTGFRIKLEALCHLVAECHW
IGNENLVALLLQRMAAWTDKDSQTSFTDPSSAVSGTLQVRCKAHLERVCHFFPKYGMLEL
GFRINGVTLPQDDYGADVRRDLLPKQQLQKKSPLWLLVLHACGSGRTRRSMDEVQWLLEQ
LTLDDVVFVSLAGVVVVQPSHAKEAICQWEANKESTREHNKKHRLPLRVAMLEMWAQARA
VLRHWRHERHCRLVRGGPAVDIRIVILFFAPSNCGSVDELSISSIRHRSAFYRVPVFSVV

TPERVKNSCALLELCLLTQGRIFCSAGDVADFQSNMPTEEACKNLIRTTLQTIRDISHMN
SALFLVANHSSGRPAELLRTSKIFGETITALLRSDTPIRTRSGRYLLLGPIQKETELPVY
ISHHLYEDLDTANTGLRMMVFAYAIDKGEYEVVPIRSLGSLKETAPPERVWWARLRFAMA
LLDDMQARRMASDIRPRHLFECDTESRYVTYSIGDIHLARKGERCGLLLASWILSQCTTR
SAGGLEDAMPSSIASPSPDLSHALLRREDEGWWAMPPAVPFFLHCIPRPFVNLLWTNFPV
HGAYASSVAAILSRTFPFKPIELEASSLSSSATLALESLRCNNAVVRLASVKHVPVLVEA
QARYIVLFRVDLSTERMKMRQLIPAHLSGDLVKSIAHEFRDLGFSEVYCVVHLALRRAPS
FWVSQDDVVVADGIVFSTPFATVRSVKIISVTHNSVEVEWSGSASSVKLICWPLPWNGLR
NVNTLPLVSSNVHEPVIVEHDFSSRCVITELRPCTVYVLEVRPVERGDDRSIVKGFLWSE
GVEMYFATCVEHTKGSLKLDSVTPSATGFSLAFSYPIFTRLAVLSSSKMLELRITPTIST
TASPYGEQSVRTQKKDDGVECVLASFSIHGSGPIFVDVLFDVEIRPIRPQEGADRKRGWS
AYSVSPQREEVGPFEVVSELWCASRSPRVAEMEWQGASISFNVYVKSCSSLGEDVCVFKR
VVSGLGPLCLTLDNLEPCTKYMATVKTASGTETVSTEFFTPPEPPLRDAVIATSNMASLL
LRVQIPESDVDQKFTSVTILPLKVFLSNSDGASASTVASYSNVPVGQPIVLGLVANWRPG
STDSIRSVPNYLFAVTDVSCSTNPDESVMLAWTCAAMHHHSPLKIKLNGELFVPGARNEI
RVVMLPLTPVRISFHGPAIIPEVSSIFLLPRPPSLNPSNCSVSAVIGGAVGVHISRTLCA
SLLRLLRDVKEVVRVFLCVSISETMEKEEIELHVDESGMNGVVARVLVSNCPRKRRMTLC
VRLQENDNYCYDNFLLSHKTEEAALLSRPISLIPQALSEPFTVSIAPPACIQGLHVTALR
PTSVTLAWTLPGRRDLDTAEHDDIYFTVRCAAEEHHGRAFGQNLRLPAHSVNFGGLSPAT
PYIVTFSEYEDDIDKGIRLVTPHELTNDTLSEMLLSVNASLAWGDREGTMTVESGSGHAV
TEAVALRLTLPPAKCVFWTIFSHLAWFGEETVDCDPASPCFCVCAFMQVAAVAESGRSLH
LWSHTDESQAQTASHVFPIGQGEMAAPLPHLDVKWRTNVRHVPRLQEDFSSSPAEAATNT
IMSTAINTTSMNTPSEQRIIVDVVGCPKLQSMDKDHCTVEWNGSCASYTVHWRVDPTGAI
HTETVVREPGRRPQLTVDIRSLRFTVVLFCVQGAVDVSNCALFTVLVPFILTGPRLCSQD
EEEKEEEEENARKQTHRDLSSDLVKVEWHRDVGPNMPHERKESVCSLSVIDRSNNVWVKG
FTEMLGDRFSGKSPDPLSITWLNPVVHLRSH*
>TCRU_8005 hypothetical protein, conserved
MSFSLLSFSWRGASVPPRGLLLLRMGWLLPRSTNRGCSCYCSYSSCHCSRRYFWNPFATQ
CGVNEAAAPPSNNTFQHQRIVEKAHRDASLHNERLLDACLDLLALCGNGSDASRAKMMDS
RDGCTSIDADAIDVIAAVVESTLHDFRKTPSEQFDLVYSALCLPIATTNRQINRCLMVIL
EAFLPELLFRMFEGEDLIVVDPDDASRREALFRFVHALLGRAEVPDGVESEEVVLVYLDD
VRAVFPSLRNNPAFLELEANATSIAMKARLFALLSQLCVEFDKAGTGKVDLAELQATATR
VLGEKKARMLLDGAQPDKDGKIRYTQLTSLLTRPPPRQ*
>TCRU_8006 hypothetical protein
MHPDPVQQSDDAERVFTPFGTLAGRKKDETGSLRRRPPEELSSDSDFMRRQSSMEGKTPI
ADTALALDSIKREVESSVEFSSSSQNQRWEEAWLGNLSLSSFLRRWGNAVVHEGAGYQLS
NCGSVLRRWVRRHFVMAGALLYIFDGDGSTEKCYEAILLHRADVQKKFVSGHNSIVITPV
TSQTSSELGVVEFPSLTMFVDAKQMLDVWFVALQRTSAAPSFPGSATPQRAKASCGYLNA
IKCTQTEQQQQQQVGCAASMPDVVSHAEDAVPSSPSSLFPVSALAGVASIESKARKEGKE
RGVEENPRQEQQSRRTSTVINDGPTGNEDREAIIEAYLQQIQHTTVSASNLKARLQRLAE
KKDKQQLGELLLQFILNRVIDAADLWALLDEVETLSDKMPQTPATSTAKYPSYCWVKEPL
VLSGTPPGRVTCEMAAITSAACSMTSDPIEQRVSSTKKCEAENKEERVDKMTMKNTQADA
LLPHAASAAWRQRRRRLHDRRGVIDSILSELSNIS*
>TCRU_8007 hypothetical protein, conserved
MTKQVVLPAHGDGAPVPGPSGAAVTVVDVEAEEEKEEDAQTARGEEGPNTAAETVRRRDP
NRIDPPLGQQQDPLPRGERLAKRMLTLQRWELPALVSSPTRRSKHERRIPGGNSRSPVGV
AHNARQNELLLSPPRPYLEKPEQQLELYHSLQKRKFVTLHEELHHLRMSHVHAQKTLRLR
GEEVKRLRRELGEKTREIERLKSLIAVLRKAHHQANESGAETDAVEGAGPATVSPSLALF
AATAADGVGGGRGAEARLLLQLRQNIASRDTIISDLRMELSALRQAKKEAEDKINKLTAE
VAEMHARCEKLSAELGVKDKTIEELEKRCAGAQMSEVKSGIGKSGNDNSDDTSSSDVLAL
RDKLEEYRLHHRAADDVIEGIQQQLQRIEVMGLCVPHCSSTGKRPSQQEEGLRGELMHLR
QCLDREEETRAESERLWRRSHEADLRMLETELCSTKAEAEAYKREVARMQKQIATAGFME
AQLQAARNENDALQQRVCELREENIAQSSREKELLHEMRFTKEAYDRREEEMSSLQRRLR
DSKENEDRLREEVEMLEGRLRAVERGLSDAPPPYEFISYAALMKLNADLQERLKTLETEP

QKAKKTPSLVNATDDVTLLEAGGDLAMEPVARATVEEEGLNARMEQGGACLHGVPVQSAT
SIAPSEPLQVKLKDVHDTYRTPSHRLDEVSLELVSPEQCGAVSAESTKRVNKEAGKAHCK
SAIRSRLQDVQWHAIMTADGSDATDKLRAEVSRLCNCLKKCEEELEQTRMELAATKLELD
NARRQQAAYNGPTQGVGERKVSSLRAARMELEHWRRLAVEHESALVELKKRYEGLKIDIA
SLQESTQVSPNTSAPVSAFVLPDWVACNDEHIIEEALRDETARIDEDMNKLRRELHTMRK
ERDHWMAVATGLSKPA*
>TCRU_8008 formin-like protein
MDFLGSFFRLSHGDSLRQLFDYPVFIWQIPCGNSSMDKKGCLVLSNSTAKNIRANCNRLE
KIYKGHYTIFNFSPLMMDLEDNCPHGELMDYSKQPVEDFGLLIELCLTIQKWTQANIEQD
HVVVLAFLEESSGITYPNYAAMIATCYHIFAGCPSDGGSYTLGFVEEMLGIRRSRYHAAS
QEIYVNYFQLLLDVPILPSAHLRRMRLTFVSLQEMLPLNGMKIGLRIENEGNVFLFSDPT
AWEEKRDNATLQLSLNPKPCLFGDFAISLLHYEPPSPTTSGHLESPWKVCVLARWAFSTI
FVSEEIHHVRARDMDFAMQSQLPRDSYMRLHFVGEESEAADTTYVEQLTRRIDQAPRRQM
TLMRPGPVSPPDRRHDASSCRGDNEVAGGVYYRADGMNRYGSRGRGECTERSFLRALLPL
SLLEEGERCRQDDDELALSLSVPQPAHHYDPSSIPTNQPVSPSSSPPPRTPPPPPPPPPG
KKAPPPPPPPPPPPPHGKKAPPPPPPPPKIIGSGASLVSLPGEVNIASSKPVYIGPKLKT
FFWKKMPRLSGIWCFSNDFSAETIIDEPFLLAMFEIRKKASPLSTSSGESKEPKRKGLCK
SSAFSFQRKQNIAIALKQLKLPVDEMCRALIECDEVALPFEKLELLLGVLPTVEEMERLR
MEKVSGNVSWTDVEEYVYKVCVTVTDARERISLLLASEQTEELVSFTEERIDMIEKAVNL
LTSKSSKLAAVLHAVLALGNFMNRGGAHADAVGFRLESLNQMNFVKAVDGKTTMLEVFVV
SLKDRRPDLLQFIEELDCLDSLAGTTVQEVGRSVSQLSFTLQKMRSAVEESKRPEMKEKR
AATFPAGLVDLFPNRMALHIQKHLAVVSELALRHQRLKEDVSAMLEGYGEDSMLDESVLW
NYILQFGMDVANFCKRAEMEGIDKQTLLRAVGVDPNALGETRLNGGMAEEGGAARGGDDG
RSVSGTLQ*
>TCRU_8009 pre-mRNA-splicing factor ATP-dependent RNA helicase,
putative
MDVRRRPRDASLLASASKAAAGEDGVGIDTAMAAAGSPNDMTETQGTGSDEVELAYGSAF
YLQEEYLQRLRQRSHRQEASGEESDNEDGDSKGVTSKGTKGAPSHEADLMVNTRHQPLFF
RLGKDFPPMAPSTTPDDGEETGAADGLLTALSVQEDNSSIILPVVSSMCRLAQSATKGSA
SLAFLRRQQEVERATREAMDTSKSDLARLLRKGEAGQQAAEEHLGTGSYFSNVELKKTGN
EDGLEEDETEMLRQKVRKETARLERMVETPAHNAVASAATEKEDVEKEERSRQQEIMLRR
RQEKLERVQEARDRLAKESSHVEDYAAKRLALMALQRQLPIYRCKEELLRCIGENPVSII
IGETGSGKTTQLVQYLYQRGYTRGGGIIGCTQPRRLAAIGVARRVSQEMGCALGTRVGYA
IHLDDNTTNETEVKFMTDGVLLREVVRDPDVSKYSVIVLDEAHERSVNTDVLLGVLQSAV
RRRSDLKLVVTSATMDILKFSKFFGNAPFYEIPGQTYDVDVQYAAAPVEDYVAEAVFRIC
QLHIQMPLEGKHDILVFMTGRDDVLGTCELVRRRLREMDPKWLETLLVLPCLSEAVSAGA
SGVLDTAPPGMRKCVVATNVAETSLTIDGVRYVIDCGFMKTNVFRPKLGMNTLQRYPVSQ
AQANQRKGRAGRTTEGLCFRLYTEAQFLNEMLPSSVPEIQRSSIDSVVLLLKSIGVARLV
DFDFMDPPPAANICRSMWQLWVLGLLDDSGAITADGRQALEFPLAPSLAKVLVESAGLGC
GVEAVRIVSMISADPKQLFELPKDREEMARQHHGRFYVNESDHLTLLNVMTHFLENGKSR
QWAKDHFLHVPTLLRACEVQQQLLERMRLLGLPTLSCGPKGMDRVRQCVTSGFCLQSAQR
SSSNWSEYRPLLNSGVVCYVHPSSAVYVRSEMPLYVVYHDLLLTTREYLVLVTAVERDWL
IEASRGVFCTKSLTRDTKKASNAPPTSCGPHATLPAGVGNTASVGRSTQLGKPRQLPSVT
AQPKGTMLPSKRRHNI*
>TCRU_8010 hypothetical protein, conserved
MARHRKLENIWEATVSEWQVSWQDMREAKFTSGFLFAIICVLVVIIGNVILLIALNFWLS
IFPAGEAASNASQIAVQVIVCCFLVICFVLVGALFIAIYGVKPLWHALVDTNRVRGPLFR
FMLLFASGATNALTGVLAVHAMSYTPEFVQAVLLSVIPFCAQLWTYIFIPEERKRRYLSV
TLIASFVFFVAGVLLSSMSSFLDLSETGRKAPWNWTLIYLASAVVFGMWCVVQRLYLDAV
MFVREADASQASPGSAAPVCRADSVDLSATQIGPVEKKATVEDGGQCEVNTQPSPNAAHT
RYQNDIHEKEEDTLSEPLLLAQREWGKQNENDFAAKAVLLLVGIVFQALVSFACVPMDAI
PWFGVSPTAADAWTGFRASCDYIFKNWNNVRYGMLHTLGFFMSFVGCAYLNERSPTLASV
VLQLSGPVTSLMLIIVPEWDVYGAHGILGHKIGGVILLLIAGLMYHVWDQASLKELLKRQ
QA*

>TCRU_8011 chaperone protein DNAj, putative
MIRICLVLRLTVHSPRGLQFQVGADEAVAHIRRKYGSRWLGASQEFLNLGSPSAEFLPFY
YCQGTVHGIFRGTVSYSDSTTDSKGNMHSGSRHTTTAPQPLNTIFGPNQTQIYAGYKYNI
RHVHTALRNEENPLYLRKMSMVDATQATINLFEQSTATLKLFVEEEVKRQATETARAIIR
SFHPGASTIGVEFLELNIRLEEVTPVFVPCYVVKAQYDRQEYTLYVSGTNGTVSGPFLIN
ALYAARLSALSVAGMFMLLWPNKVTGLALGSLISVPVYYIAFYAAKMFPSRRRDYFRWQR
KKLRMQHEEKDRDGFRPHVSSKRVEEEYRRSSYWDTHAFQNRQHSSGPVRDSRGYYRALG
LTGTESVNEIRSAYRKRVLTEHPDAGGSSERMAKLNEAYRILRDPERRAAYDMGN*
>TCRU_8012 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily-related, putative
MDEPELFVISTSESEDGDGTDGENVADVSALAEDARSNLSSRHCGVENMFIDEVLFGDRD
RRSVFLPDTGARATDADSLSSFSSSDSDRSLFAQQLVGEEKKRLSQGPGVLEDRGTLEPH
EPLTSTAVLRSMTCADVRAVLEPFFQRKEAAKARFDAVQKWLAEEMAAKTTRMKKSMLER
WRRIVNVSNWGDGSSSRDDVLFPEALVPPAATLLGVLGPSVAKNVLPELQHLRPHQIDGI
RFLWSILAEGPIGRVPAVGCILAHTMGLGKTCQVVIFLHLLLNEKRGCLGRSQRVLIVVP
KSTRPGWQKEFSTWSQYFPLAHRILPIMIDERDGMKRRLDLYRSWWSEGGVLLVGYEMLL
GLTKLSKEGSREDKKGCEFTDLLICDEAHRLKSTRLQISAALRGLHPLRRLLLTGTPLQN
HLQEYWAMVDFAVHKYFEKRRFQEFFINPIEASVAQEASSRVVATARMKTFALIRELRHF
VQRVDSTPLRDELPPLHEYVLVIPLSALQVRLYNRFLHLARLEQSKFNFLQAVTYANKIS
AHPQLLFDSDPASPLKEILSEVESSPDDDDDNNNNNNNAGDNMGKGNRGHGDRRRTAFSG
PVNEGYAELFQPPADYTAAPEDGVKLYIAIRIIKAAMLRGERALFFSLSTKMLSLFEGII
AEMNRRWQQDGSLPRPIRFCRLDGNSSGAERENTLRSFNSLRGADVLLLSMKAGGVGINI
TSATRVILADSGFNPADDRQAIGRAYRYGQTRPVFVYRLVCYQTLEHRMFQQKVAKEWLF
HTIVEEASLKRDALTGLRLQSMIQLLGRSLEVSSEVPALTDEQRDSTARLFKEDAVLAEL
ADSIIYAESHEVYLQHDELVQYGKEEREFYEEYQKKGVFNIDSYVDGVNVGNETEQRKRQ
REKHQEDIGRQTKTLTALVDDVIRGRAEQDPRLRHLLRMMGITVDASGVVSVSSMQETQR
RTREPIAVDGEDGSNSSDDRLIRRLQGEKVARTETTSPLRPIVLNQSDDDDDDDDDEDSI
LFEEKKKKNVGLVIDPSIYEPYKPGRNAYNAIFIDEDEV*
>TCRU_8013 hypothetical protein
MEVSIHLTDVDFSSRCALQDCYVIPAPCHKTASIDKAAVEVGGGEVDNHVDTGTLPEGIL
VSPYLLHPNKSNCSPRPLALLWRCGACGREQCVAREAMSLFTQRSSKKGASRGISSRRSE
PAVCPDCYACPRCNASALSISISREVLYLACCSYCHWRHGVACKDFDGLLASLSAATASK
MMLSYNRAVGDWRRSCDEKLKRREEMLLSLSRVANAEYKKGTMGDGGGAPQHSAVVLEEL
RSAIYGRTLKNRDNLPEWIPFSAPGEMAAATPCETPTASPEEGDKKGVVLFPDNADALTR
TTQMEQHGFFFPSNHPFWGKQSESAATAPFLLMQNIRLPLTAMVIPPAQDGVKTNATAYQ
RDSSFLFVVNGVRRDPSFEQIVQVLQARGGSESRRCQLVTVKLAAAFCLPVLQQQSRHPA
SDESRRWFTWRNFGDDVLCIRRFTMEKQVGGVFDASLVISAGADASEWVSLPPRSGNRAS
VGETFCITLQRTAGTSAMVGFVVEVQTMLPAWPGEGAEETRGAGAPSLVGETEGTTKRCP
HVVRYGLTVTW*
>TCRU_8014 dynein light chain, putative
MASATSVKEAIARFEEAEYRRRTSEMSEEEKANAPRVVAAEEPRVLLIGMLPPIVKMDKD
IATLVNCEHLGLSTNGIEKIGPGLRELKKLKILSLGRNVIRKIEQLDIPQLEQLWLSYNK
IDKLTGLDKLKNLKVLYMSNNLISSWTEIDRLANQCPELVDVLFLNNPICNNAPSMQEYR
HMVLQRLPKLTKLDGVPVDPEEKEEAERRR*
>TCRU_8015 hypothetical protein, conserved
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YRRRVVWETVEKPRAAFVIQTAWRKHRQRRRLLLESVSRLIISLMRLKIKRICAAKEKAV
LLLQRVFRSQKERHFVHFMYQKMRYNRALSTMRNCINRRVARRHMAFLAIQRDERRVCEE
RCAIDSLHIIHSERGDLLRIFQVMQTTAPVAFTSLVTRAIFLEEAIRCTGHCPYSPLFLH
MTREQQFGVLSFSEPPSGRASSLKEKQLGTPFTDGVNFKHSLEKHNSGDRQFPAHGIGTH
SCTSALHTEEGARQFLQELFGPNLPPCPLARRGLKPSRFGEYGDIAATKSPMFQMCDPAG
NDIIQSWLSIDAAPGREVLSKSEVNADSYQAVSLARPPFGELRASVNNLMDAFIELLVRT
EATERKALESELQSRHKEQMREIQRFAVTLQATHVAPLLYVPLLSSMRETWAVRRAEQLF

REEYDERMKIVEEYQATPLRFLNRPILNLAAEERRRRLQERLRTMKEKKEEKGKGDFAGS
PLAAAAPAPTTVPVDGQGNNIHTLVARPVSIRPGSRTPTVGASMPQFQLGSSSFLSPVPR
PPSPPPRKVHDNPTMSCIPLQTSDERTQRRPQKQFGPVVISETPAFSSISSANLASFIGH
LNDGVSSDDTFVGSSSGGSRDTTISHASPATLGNSACPPGLLPSLANSLTQSTGSNEVKG
GSTTREFYFHSSIRSLQRPTSSGDEENVALSLQKATVFTNMENDSGCGDPKKKKKGLEAL
NYCTNNAIPRGVPIPLLRSSRTERSNLGTVPLHPVASEKNLVTRRECGGDYVRGRYRGSS
SFVPVSGFTGADDSLRPVQPNPGGEQLNFRFQAEQGLNTRKTRRNLLEMSGTS*
>TCRU_8016 hypothetical protein, conserved
MGKRRIGGNSRVLRKKKLKISKRVPTSQNGSASAATTGIVKRNTKLRLKKFGSRLSSGKQ
RLLALDALRKERSQLLKQQAAERMVLKEHTRELEARRLRIRKGENAKMERRELGKYIRQL
KEEQKAKHQSELLSIEEALKKNGGKKEYDMKYDADEWEDVEEDVDEFDEDELQSMFAHLT
T*
>TCRU_8017 UTP-glucose-1-phosphate uridylyltransferase
MSSVTAGISEAASACRAKMQAAGVNEACIRTFLKQHAFISKGETGNIPESSISPVESLDS
LEDLTVPADPSLLEHLVVLKLNGGLGTGMGLQTAKTLLSVKDGKTFIDFTVLQLEHLRKT
YSDHLRFMLMDSFATSSETKAHIKKYSWLFDTFDKEVELIQNRVPKICQDTLLPVTYEAD
ASCEWAPPGHGDLYTALYGSGKLDDLLRGGYKYMFVSNGDNLGATLDARLLAYMKSNQLE
FLMEVCRRTESDKKGGHIAYQTACFDDDTAPERRFILRESAQCRKEDEASFQDVEKHRFF
NTNNLWVDLAALKKTMDSHSGTLPLPVIRNAKTVNPVDGTSTKVYQLETAMGAAIGLFRR
SAAVVVPRERFAPVKTCSDLLALRSDAYVVTEDQRLVLCEERAGKPPTIELDNQHYKIIT
GLDALVKDGVPSLRQCTKLIIQGPVEFQSGTVVKGEVVIRNSKKEPFIIERDRVLNNEVM
EV*
>TCRU_8018 mitochondrial carrier protein
MMTTCENVRGVLQNCGDAAPLPSESLSTNAVNRSLSDLHTPTWFVLLGLSSGLRTLLLHP
LNLAISRKRMMAESRPPPVMQILSQAYRGEAKTGPLNPTKGVRAIYRGFGVALIGNLLGE
VTYLHTLELVREELESKPSALQRASSSQGLDFNASSHAAAAGGLAGGLISLLITTPISVV
CNRQLTAGYGMASGYTYCSAWATGREVSGLYRKTNESFLRRGKYALRGFYAGLLPGIAAL
PENAVWWALYSKTKVVLYTLFEPTLSRWERERDANDSLRPFWRQNWLLSPTDNPALNAAA
GMLASLMTTVVFNPLDVLHTRLQVLPLERHGKAKGVPLARVYNLVDSLIRKEGWRGFFKG
ASATVSVSVLDGVFFSLFFELTKLGSDREFLRQF*
>TCRU_8019 Dynein light chain roadblock-type protein, putative
MAATGGGDIEELVKQITDHPGVQGLIIVNTEGIPIRHTFQEQSRPLAVQYCALFQSLAMK
ARTAVVELDNNNDLLFLRVRSKKHEVLVAPDTKYLLIVIQRVGNDDNLPVNIKKTP*
>TCRU_8020 hypothetical protein, conserved
MPLPFHTFPLEDGFGAEDQVLHFLALDVNTWAPRVWNDVVSGVLVDLRCAYGYYWHRGDA
HAQIAIDGFVSCRRALEIDREPTDQFMDFGRALPQDFPDADCDNNRPQHIPSSTLRARLH
MAVHEADTFARVAGPFVD*
>TCRU_8021 hypothetical protein, conserved
MDSEFSEDPAQATRISGRGVLFPEVTAQRVLRVFHWKSTRLHGLGPPSGIADCGDGGRVP
TGLPQHVRGDLLQPSPATPHVAHFACTILRLCLAAPIACDPNLHHELRDGRSPPTTAGED
LAVTSSGMDSEFSEDPAQATRISGRGVLFPEVTAQRVLRVFHWKSTRLHGLGPPSGIADC
GDGGRQPATGRHAATTKTCRCCPA*
>TCRU_8022 hypothetical protein, conserved
MKTEEEFLLIMHAEACAVSLALSAFSAILPSTMDIWVDNTSLQGAANKGRSKSHAMTWEL
QRIYEFVDSRGIQASFAYVRSAENPADGISRGRVFTLQDLAKGKRRCLLAGGPQSLPLRK
*
>TCRU_8023 Enriched in surface-labeled proteome protein 1
MSRRVFTSAVLLLLLVMMIFCDRGAAAVEQAGAAVDPFTGTTSISFANWKEVNGNGREIT
SLRVPGLVKVGDDVFAVAEAQCGERNGVGSCAGIVSKHLNIKDDPMDILTSDISLFCMQL
GDTAANNFRTTELLRPTTVVIEDSVYMLLGNQSRTKPPVEDTNERGLLLVRGTVSDEGGK
KKIRWNEIHLVNPQAIGYSGSLTELIGGGGSGAVMRDGAIVFPMQAKGNDGQSVLLSITF
TPSKNKWEFSSEATGKAAGIHPLWSGEKTDPS*
>TCRU_8024 Enriched in surface-labeled proteome protein 1
MSTPHGVSWYNLGEPITRVWGNSRDPAGDGVQSGSTTAIIEGKEVMLITAPVYPKEDNGE

GHLHLWVTDNARVHDVGPVSREGDDAAASSLLVKSEDELILLYEKRNGEGPRSLFAMRLT
EQLERIKSAVKTLKELDDALRVPTEGLVGFLSSKLDGTAWRDEYLGVTSTESGVALKGRG
AGAEWPVGDMGQTVPYYFANNKFTLSATVAIHEVPEAGSSPIPLMGARLNDTASTVLFQL
SHTSERNWNFTLHKKDFLVKPSGDVGNWETNTAIRVTVQKDNDDEWFVDANGRRIYETDD
EELEEEEMAKHRNADQFGSHRISHFFFGAGNKEDEGNTPVTVADVLLYNHILYRDDLRNL
NARTVSIRHPAAEELDTAVKVTATEEEKQKATQLTNFLADVEDPRIAQPTDSQSVRVLAG
SESSAENAADGLSPRTAAKNDTSVPETNHSASEGSMSPEDRLALITDAKLILHDLRGDST
ARVRVSCVLLLLLVLCALVAVL*
>TCRU_8025 hypothetical protein, conserved
MGCKAGPEILRIIISAIAGVTTVVHRLRAAPPLVCVDVWIDNIRIAGPISDATLWEAQVL
RNADSCHASLGEERESGATHYTFPGVQFDHTHRAVSLSEKFVWSVCAVPALNSLTIAEME
GMASRFLYLAAILCTRLCDHYFFIRAVRRRLSALHRGIVLKTSPANLRPAAVGLGERLRH
TIENNRKRIINATEKASAASITRTHRSMDGEPFSFQTPATLKLTEGNGRSLFSSCRPMHE
RYA*
>TCRU_8026 hypothetical protein, conserved
MVLTWHNEFNRTCNEKSTKEGILDESAFKSCMRVSMKEVCGSDDDGMSSTSHEPEAEEIC
NKYTGYPEEDVDSSTPQDKPSHDAEKPVAAPNSETPKDGAAEMESTPGVTAGDSPANPTE
EPQSTSATTDVANSEAEKSTTGVMPKNAPESNATRKGEEKQNKNKHGNNTKETTVDADVT
KNNTTTHGDGDGSTAVSHTTSPLLLLLVVACVAAAVVAA*
>TCRU_8027 hypothetical protein, conserved
MHGRNGELGAVCRVANAVHTCSNCAASCAVKEEGATVAFTMDVTTNKCAGPYELWWRQFS
PDGTIHPPARSSDADRTGICQLPPPREGKDDTKSCGTTAPQVNAEPSRQYEDWRQSAAAD
GPNTVDQSPASSTATNTSEKRPEFAFG*
>TCRU_8028 Polypeptide deformylase 1
MLSRLSRTVPLLGPRRSAAREKRLKDRVAAQLELEAQVKSRVACYPHRSLTRPALRLDKT
QVNTPLFQSQLLSLKKMASDLRCISFSAPKGHWDATVVLIKGHPDEEVFEVWVSPSVPDY
DARTSIAPMYGMWENCISCGATVAWVIRPQCVTCSGWDEYGNEKTELLDGMRARCLMHEL
DHLHGKTILHQALGPEFIVSGIAMGQRDLWPPNFPSAEAYVTAPHQFFDYVKNIPIVPPG
MEWWYAQNMQQHFQDARLNQ*
>TCRU_8029 hypothetical protein, conserved
MAQDDTPTAGKTPKEKRQYSCNWVRIVLGVSAVAMVAFAWRSVYKANQRELHLRRTMEQN
RQLLSALAEVPGKRFFVTDVNPEVLRKKALFG*
>TCRU_8030 RNA polymerase subunit, putative
MFYKMELQKIIRVEPHLLGRTLHRHLAKYLRNAVEGHPFQMPLLKGSNGEVVRVDQSSSA
IIVAVLDILNTELLEGRVLDDGGVSFLLHYEALVFKLHRGEVVDLMVVAVEREGWWGDVL
GVGKMYISRGQMGSEWVYESDGVEGIWITKDGSRSVKNGEIVRVRVVAETPQSEGVVAIG
SMIGKYLGTF*
>TCRU_8031 CRAL/TRIO, N-terminal domain/CRAL/TRIO domain containing protein, putative
MDSNLQSGGAKARRKTETNGDTDVLVAEVLHRIGLQASDGVGSASSMHEKRCEGENDVSV
VTGSTGEVAELSFSRFPQFEHCCSAEFRRLLTYRYLKANNFDVEDTVAMIVDTNKFRKQH
RLDSIMIFPSLIPLRGFSESEICDTLHLPMAMENPMGSGSHDNTSLRDIQMEYLNNHHIL
RPIVKLITRHYANSIHYWDKDGHPVSYGRLQHIKIHELYRELRRISPLRQRPEDLILLFH
LYGNELLWRVVQYCSVRNRVSGTEQEIGWKETMTTVTVVVDCKGARLLDYIWGPFPRILR
EIINLDQKYYPEILHKLVLANCPKSVAFAHWFSKQLGAGKQSLRRKILCVSEENTPSLLK
LLIDEDKLPAFLGGTCRCEEACVPLNGSTSNGTMCYFFDSNNLARMVHPSGSVLSMEDLP
FEQHEGEAGSLSFLVQKETENFVVRARRKLTLTYEVGVPEEITWEFAVKHGEIGFTAVFV
ACSADGHTEILMPPSTVKEAADHFVFGTRGELILTWDNTRSLLTVRKIQLRVHRRVQRLA
PQREANVATVTEGE*
>TCRU_8032 CRAL/TRIO, N-terminal domain/CRAL/TRIO domain containing protein, putative
MSSVENIPVSIPEMETLCEKKEAAVTTLLQKVLSQYGNVYPPQFMKCTNEEDRRILAYKY
LKARNWKVSDSMEMIKENMTFRAQHNADYMNLFPCVFPLRGFDEEDLCRTIQDPYTEKQR
WTELCYLATAPYYSAGYHYWDKEGHPVLYDFCGRSDLKGLFKSIEAITPVGDQAKDTILR

YHLYMNLVQERLVKYADAKSVEKGGRRILGVTAVLNAEGLSWGMINSQFLDVLRETIRMD
QKYFPEALHRLIVINCPSFVAHAYSLIRGSLDKNTQQKIIFCDKAYSMELLKKIVDEDKI
PVFLGGSCSCSGGCLPGIDSECRSLADAPFPVPRTEYVSIAAGKRHTIEFLLQPDEEAQW
EFRCTKSWGGQATEIGFRAVFASQDDVDTVDSPWSNPAVGSQRTSGSLYGSLEVSSSFRE
LKSEKMEMDCDRFVAKVCGTLKLEWDNHSSWLQTKYLQLRVIKS*
>TCRU_8033 ubiquitin carboxyl-terminal hydrolase, putative
MSGASTGPPGSIVVAAKGKRKKNDGRGWAQRGGATSTKPRNLPVESLNLEEVYHSIVAPS
SVGRQKLAFATAFNPPPFARGILNNSNYCFMNATAQALVFLPPFAQLAISAVVEAELCPT
LATLGKWMLSYWARAPNQLVPPLSLPKAVRGQAASSAAPSNWGKMDGSSQEDATEFMHHL
LEVIQTELCALEGSYSESSTGRIRDPNTSLEGNSEKKGWTFVKGRERLSVREHCDKSRSV
LLDAIFGGAVENHLKGKSKLKDHASVLVEGFFLLQVDVGFSAECSLEMALERSLQRERVY
DSARAKDLLKTMKLRRLPTVLLLQLQRWAVTAEGELVKLDNLVRFSKTLVLPKSTCSDNT
VSNAARTYELVAFIAHRGKATERGHYVAYLANASLPTLTTSQGDAALTFCNDAKVHTVTM
REAIEGEAVYLLVYQRKK*
>TCRU_N-terminus/PTH.1 PTH.1
MGSLFKLRDHWYSSYRGEEFSHFSALTLGNADNNPDAEDKIIFGSFSGTLRVLRPTKKGA
AQPDDTLIEKDFGAPILQVACRPLEPVSGGQPKNLIVILFPKRLVLARLLRERDKEKETE
NTDDFLSALYRFTIHYEVCLASASYNFTCGNFGRASHEMVCVQSMDGQITVVNHNTVVLQ
CFLPRSQFLLPGCFLYCSQRDYFLTNNSAMNLMCYSFATFVSNRIKPEVYMETNENGVSK
TCGETISPSWTFLLGEDAVGIEVCRHTRGLGAEDADIVVLCHYSLFVLRLSGELRFSKRL
DVESLCLTSYLVPNANACNLLIGTVNGSVNVYSDASLDWSAKMATDAPLCLAVGGFFKTR
GMIVSLSTEGTVSVNYLGTDPEEKPIQPLESKETDYVEMERELRQTLHAIKQAGGSEKSS
AKENATVEGILRVEWGIPPTEVEDREAAVNVSLILSNTSPTDPVREVKIAVNVAQPIRVD
ILQHELKKISPNQVEHVSFRFDAQNNKDMIIPSSLEARAVVMYVCKGSLTCTVSATVRLP
LTLVARPTPPVKSMNFVIQLNTNKDVAPSLFDLFPDMAYSVDITANMLSIQYVNGEDATV
LASKNACRFRFQASTMEALWILAEELHRRLSAYYDFKIQFSLQDPIPLESYYNVIDTHLA
VRNEMIEAKEALSRAAQMFCAVQKRLLLLFRERNPTPVGMVDVLLEESYAEIQRCADCVS
VAKPRQKQAAAMLSCCSRLILMQLFIKCQETFKNPDMISLLESIFTCAIDEDADVSWEEL
TDATLGHILQLSKVEGDLTAAHGPVPLKVISGRLKKRISTLFDRMVDGSQIGLF*
>TCRU_8035 ADP-ribosylation factor GTPase activating protein 1,
putative
MSHTEADKTVFAEITARDSECKICFECGAPNPQWCDVHHAVFICLECSGLHRSLGVHLSF
VRSPTMDGWTNWRPEKLRQMQLGGNRRAREYFERNNVPRAPIQARYESLGALRYAAMLEA
EALGNSFDEKSWKPPEWYERLTQGRQREKDAMAPQAPQQHRPFTGMGSDGKQWSEKNSAG
SGDWYNSLAGGWATLSKKATEIAGSAGTQARTLMQEADLGDVKTKLSSGWSTVSGYANQL
STKITNIAKGEDDGDGLTGMTRKAKLAGQESANDPLVTREAYEHIEHRAEGLSPRSSVPF
SKFRGRQ*
>TCRU_8036 hypothetical protein, conserved
MLRRSGPSFRRRTVTEKAVQTEVSFPFECVDTNKHYEELASEQFQDLCRLRDLIREAMKE
VACSVYDVVAFKDILFKIEDELPSKLPVTDILLLSSKLFRRTSGLGHLLACLFAVMFAEE
HADENFHFTEIRVLRRELLDVKQQFARAEKERARLQHMLDDVGRIAMNHSRAVELLETRN
TALQMQTSGLEDQMALLFSQVNRDLHRQCKDAYEKVTNEIDSQDRMGLTRVTFRQTMDSL
SDQLRHSRSLINDVRELVMSCAQGSSGGGRNVDAQISKEPSIRFKLKQVENNFQQLVGRF
SSVKGVVAETAQELVNALQERKNILYLSLQHIRLYDIQNSRMRQSKAIVVTMRKKMEELL
KRISLTFPPGAVTFVDRIGRISTQQWQVGQTLATLRHQKNADQPTEETASDVGKAKNFSS
GIHSSNEACTLQEDQRGSEPLDAELYGTSDVTKIPFQTVYNLVDVIKQAENSMESLNNVL
NFESEINAFLKTLTLSLSTTPRHVDEPLGEMENEDEIIERAVHPTGNFSIQRPSMAEHSP
RKLERESEAAASQYALMSSYHGDRRGSHEVDKLKSEAAEQAERLKKLQEQLDSIQPEFAA
KINFLRQVYEARICDLETKEANYGRRLNSISPQREGRERRESKIQIRSDRSVPSSQLQET
AEPEKGRKKGDKDQLLHARSEWQQTKPVLQANKKTRDATLGELNKMMRGGGDANVKAGKR
SAPRSRSPSTKTT*
>TCRU_8037 PPR repeat family, putative
MRPATKAAAQVIIKRPDGTETRFVRPNKRAESPRVDADLLKRDEDREAVAACPPYTASFN
ALLKDYHEKNSVVLVNAVLERMHAEAIPLNVTTYNLLMERVVCLPDDLIFRLYDEMKEEA

RKENRSVQPNLTTYQMLFRACERKGQYQRAFLLYKQLRELMHIVPDSPTYDTLLGFCAAL
RDVAQASYFIEEMKQNGVTPNVNTYNCLMSVLVESAPYSETLRVFMQMIEKGIKPTIRTY
NTLSKAARIHGDYDRAFQLFEEMKKHGMLPDVITYNTLLCLAEHRLDYVMGCGAHKNVRR
TFEQRKQGQKAIAELSLTLFSEMESMNVKPNTFSFNQLMSVLLKCGDDRIFGVYRTMHER
YKVQKEEIEVQIKREAKKKRAIRMRSSEEPEILQEGVMDSCSTSPTEAPLTLEEMMGMED
VKKPARIAARQIRPNLDTYRIILCACLQMDLASRYNVFYDKMRAEGLVPDHDMAILMESI
CEANGDKVLALQILEEAKRNGVVIDVALFNGYLNVLASLGDAELVGIVEVMQLGIISFNV
RPDVETYNTMLRGYLCMNKYEEVEKLFSSMYLSYSQVTCNAETFCWVLRAYREKRDTEAA
TQLLDSMRRRNVSITIQHYHELMRVYLEADDPRVEDVFWSLRNSKDKSLPGADAECFFLL
LKHYLRQKKYVELERLFTELRADLDVEADAGCYSVMLEMFFLQKRVTEARALFTDIRMKC
VPPSTRIYNALLRIFVSEGDAAMYEVLDDMKANHMAPAANTLGILLEYAEGRRLVSTAVE
QKIFWNPAELLVGL*
>TCRU_8038 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGAGGGFANEAEGSANGAAGKTTPADKIILNWYVLTHEECET
DNTKNGTVNVPAMKRCINFAMKGICDTFYNKTLSEIHGPEVKGMCTYYAAIPEEPVEPPT
PQGPPSDSAVSNTTSDEGTPKNAPEFDGAGRGEGREDQKEHDNTKEKAVEAAAVKSITTT
TDSDGSTALSHTTSPLLLLLVACAAAAAVVAA*
>TCRU_8039 UEV domain/Zinc finger, C3HC4 type (RING finger), putative
MNEIITRFFSCSSHCKPEVLGRILHDVENLCNTFHFYCRDATWGVTQQEKLCIYGGLPIT
IKKSNSDHTSLTPDSREQAPPHRYVLPLQIWLTHLYPIEPPLVFLLSAEQGCRIASNHKY
VDATGRCHTPELAAWHPVSSSLCDVVKKLCQLLSAEGLIPLCFVEEGVSSPSKGHATAVS
QRLRHGLENGDDDKQTDEHERCVVCFSPKEKVLVPCGHYCLCDACATNVTHCPLCRGSVK
FRQRVFS*
>TCRU_8040 damage-specific DNA binding protein, putative
MTTIKELSESPFDKLKVTLSLVYVSERNTFVQVTSVGVNFVKGGKGVYIICKNEFGIQHA
SADANLRLLVFSSSRFVSVVDLNTHHTRASLELDNEVSCLVISSSRGFVIGEWNSGAVCL
YEVQDGEILLTGRIFCSSTSCSMCILSHLHTPRLVVGLLNGYIADISLEAMLMGSAARET
LIRLQPVQLFNLESHNAVLCLGEVPPIIILCDTGFQLTGIDFNDVAACAIIEGSHISSKY
IFLSQSENSLAFGNIVDLKKLNSCFLGLKATVTRVKYIAWWNVFVMSVRRNEKDQILLLM
GHELANSWVPQNELFSIELFSIELLENERCVFLGLFFLEGLTNPPTVMRRIKTRRYFWVP
PLRFRMNSCHNQVDSYGILSNKEN*
>TCRU_8041 hypothetical protein, conserved
MLDEYVAKKNGKLHDAEATECHLSSVVDQVLNYLRNGVRVTKIPSKGNARRRLYFLSEDC
KRIHSCELDHQGFPLNRKRPPVTMWIRDIEKVLIGLSTTSFVNYSGEAQLAKTRQEAVFD
NGTHRHDPTQNITPSNPGTNNHRAFALLLRGGKSLEVFVRLTAIARLGLLLSSVHCI*
>TCRU_8042 hypothetical protein
MQQPEQELSLRQSAIETKEQQLEMVKLDGARGREAVMRERHSIEAVRKTVREERCRQRRQ
WIHQVKEMNAKSPEQVRPLAEERKKNCEQATAKEDAAERALAAEVKMIEEYLPKLISLED
VPVNPG*
>TCRU_8043 hypothetical protein, conserved
MPSYLPDTVVLQLYRDDGEAEFADYMDANSLTFVALGDAERPALCGIDAAAQLHYEGAQR
ALVSAAGIVSSICRRRLRIPFGMSELSELLRRAYNTEKGNRNNSLNGSTETALLAHAFSD
AVWAEESFHCLSMTRRVGNILVSTGIRYVTRDLAVDKWRPDQDIMELRDELMIARAVYNY
RHCGYESNSPFQA*
>TCRU_8044 retrotransposon hot spot protein, RHS3, putative
MKFAISTTIEDVLFKGRVRVNDIKLNEFLTRELDGRGVVDTNRNVLLKEFFKNPKKYIRD
KGVLNEIQARGAYARMERTVREEMDLEEDVRKIYKNGVDNLLGWSEAAANVKKSVHKLTK
QSLDSALQEARNRMTTIEAMKMEGLYESVYNARWHHVVEIPDGDKRKKKGTGMEVKEGKP
KQSWTYKKAGNTIEKDDAVQQSGEAPPRLMVLTSEKGWPYTLNLLRGAGNDFFINCEVDR
VWQIVERDLTEWFSNFDLTLNPSPLLRVLVGTPGIGKSMAAGSYLLYQLLHYDVEELQVV
VHCFGETMYVFDKTIKAVTKYVGRGASKSVLYGLRQRGMKGYIIYDVARKGTPPDTGFAP
STGWGMIAVSSPKVTNYDEWEKQTKASRIIMNCPDEMDVKAMCAWMKRGLEPDKQAGYWK
MVEKHMEKVGPILRYIFDAKSCIVRLGAVNGALLAIKDTDVGKYFTLGGEEEWYSEDPSH

KLVKIVRVKTVEGAEVFLNASICDDIGFRTADRLAKEMATKDFLLLIFRSRGALVSHALE
QLGLRVFMRGEFVSALVKELKELRSSKRNKAQDSVLKVNHQGHPTRTVGLGKLENGVERI
PMEYRVLYIPKVENFPLVDGLFFVDSPRKTLVGLQMTTAGEHHTTASTVNLFKNNMATYF
KGWEKLSQDMSWEMIYIQHESSTMITNWQRCGPVDTKNLSDDEKDIVAFWKGKVHQYQFV
LTPDFVNKIRAK*
>TCRU_8045 hypothetical protein, conserved
MYQLDAVPGRTFAALRLDREMPDLDDGSDFESSEDVSMYSARAGTAQAIVSMLTVAYGTF
AARQRLKALMPLCERWNVRLPRRPSFLQDEEYCRLVIDRLAVKMSSVMERKAQLGIDQNM
SFTLSATAPGAHDTASGTWGRRSGGQSHARRFREAASQSNSVEVHAFTADEPRFSMDDSI
ITVRARRFR*
>TCRU_8046 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGGGYAEDVDVVFGHPGTRGERGGGAVGQSPPAGGSNGG
SGGSKADSPHGSESEPLDSTSDEESSSLDIDQELDPNLPEEHVLQKEVDPIGKQDHSESG
PQDALPPDANGTVTLDSDAQLQLSDTKKKQTEVLTNVGGGEIADGEKDSTGRSNGLSPNK
SDPPALLEPRIKEVSQPTEPSPPPANLSPAPQELPTAVSPAERPPAIAVSAGETNPTAST
GSRNATETTTTTSPSHSKTAPEAAETPSGNGEPNQKRQDTDTPDSMKDGPTSLPVETAVS
SVSKSGIGGAHNKEDKVDDGAQRPNGKEPQDGIEDGNTNDAPTFTEAAQKTDTVNNYQTN
DTTTKGDSDGGTAVSHTTSPLLLLLLVVVACAAAVVAA*
>TCRU_8047 Leishmanolysin, putative
MRADSTNWIRVVVRDAPFLSGECAAAIHCHWEGWMPIRINVSTRDLDDTGKHWILERYYA
LNSLNDNCECEGDVVSSAHGIILEDEVVPAAFKLHADRLLVQPLEGPLIVPPFATGSVCI
RFTHPHMASRSTVRHVTGAWQGAVGGGVLDDCRDVCKGAPRLRRH*
>TCRU_8048 hypothetical protein, conserved
MMMTGRVLLVCALCVLWCGAGGGGCSEATSPGSPGTPSGNNTPNDNVTVGVTEGGVKNGK
PEAPKAAAPTGSGSPEASPPPAQQPKGGASGTPNAGMDNKGRNTEGKKKEDEEKQKEEED
EEEEEKHVEEEEETDEQEDDKKQEEERKKGEAVTGTTEVISAGGEEQRSLSSAAEVASNT
TNPNSTPTTGDDDPAADAAGTAEGKQNENKDANPKETPVTAAVMKTTTATTGDSDGSTAV
SHTTSPLLLLVVACAAAVVAV*
>TCRU_8049 hypothetical protein, conserved
MVCLHSAPFEALCSFIQCDVTIIMAASSFTDSECDNTNDGKNNDEDYDDDLHRGADYLRL
LAHESREGLNAVLTIPGLAEPLAFAPSPAVISAPCVEADSFTVEFTQQLSSGCAAHPALA
LSHVFQRCLACDLLCVVRAAFFSFLLVPNKKHFALRWIFICVAVDARDDAQRVCLLFGGH
EGDFGVCRHHRESLR*
>TCRU_8050 hypothetical protein
MQELQGHRNCVQHKLISAVDPIFLRCRRRDPVIVYLLQFCGVGPVQPLDVRLAFGLVALG
LRENNFKLFHVRDSGDTAVSNSAEYYGLVEEERGDGEGIGGSSRRVSFSREMETRGAETT
SLLPTTIRRFVRAMEGATDMPVACALRVTDGSRLLDDRFSTKMPEERCTLGGSETTGLRP
VDDVVRDAVLPWRFYFYFCLIKAFLFCAFLQLCSCRGGVDGMCCGCGVGGVIHALF*
>TCRU_8051 hypothetical protein, conserved
MRWQQLVPCRIKIQTYQCGESADAEFVTEGTQYGGGLPAEHRVVARISLIGGMTAEPSNQ
LDSDILLHLMGHGIAMAEKPSDSLVDIMAWRLGVSLPLYPTEPALARCCCVDDDAVTEGI
AVVYSR*
>TCRU_8052 hypothetical protein, conserved
MQDTSRKRKAHEYYDCPSRTSFGSLGCHGAFHKTRCVAARGSNRGDVLFESTRDLAVGEA
RRPVRPSPGHSSIFGEVHHNADPGVVAGHIDVKGETAEGQEPWLRTEERFSHDFNHNHSA
AITRRARRTRLATPQDEHAIPLQQVNVPVLNPEWIKTRLNPATLESLMQVWGLVGRSPLP
PSSSGKASEGSRRIPTADARLLQKAGIIEDASSTITGGWIIPFSVVEEKTTGLRRRWIAW
PRDKNRDDP*
>TCRU_8053 hypothetical protein, conserved
MELIRERRSTVVRRIADVSALGRLREEGERGGSINVRAVILVAEKAPSGAIRNFMPHART
ADEREELRGLFDGNIRCGAIDPTAVRQDATVHVGNESNPAGYGGFEVTKNRGAIGDEAGA
PLDNGRDESSNPQPDRLEGTCCFKTCVDNGESLVRDFGSKTKTISQ*
>TCRU_8054 hypothetical protein, conserved
MVEERGGNQGRFVREKRQMDSVFSVGVRREAAASRRRRAAWPRDENRNDRRQAHAPLSRV

PRRFPPMMAEAAPGLDLKASFLRPLFRGRPGAPFDDAWGRRGSQRDTRPAPKSPRPSPRR
RRRRRL*
>TCRU_8055 hypothetical protein, conserved
MSRRKRKARTSHDRRLSVWQNSIPGVDPDIVPRVAALRKGAMRLLPTPRQACAPCGSQVT
PCVVIVPPFLHQGDRLASASAGTSSRREHRNSLPTSERRIDAFLPNLRQSALARPQYEGT
CSTCSAWRYNSLRRPRTRMPQWCQRLLNRRLAHRSPQKVPSTPAGKTRRRHNRGYSRWTR
LFRHRRITDATGC*
>TCRU_8056 Enriched in surface-labeled proteome protein 1
MAAFSSNKASTPPPVDEPSQGTAIETAPGGQGREEQRESLGSSGVNGVSASTVPSAKTSS
GGEGSATQLASGKSSDGSKTVGGSSFSDGEPTVETSEGGTNGREEEEIHAQNGDVKAAAL
SSSLGNVSQGNNTDACSVCGSGLLPSLLLLLGLWGFAAL*
>TCRU_8057 hypothetical protein, conserved
MMMTGRVLLVCALCVLWCGVVVPAVCGLVSDRSVVEEDMVLTWYPEAEKDCEEKNTKEGK
LDLLGLKMCMHESMKEICGNGDDETSSKSRGPKAEEICKKYAGDPNKAVDSSTELPEASP
DAEKQVAAATPETPKGGAAEMGSTPELQRVIHQQIQRKGRNQPQPPPILQIARLKKAVQW
RCRGMHRNPMPQGKMKEKKVK*
>TCRU_8058 hypothetical protein, conserved
MTVIPHAATELGEIGAQHGDIQVQPTRSYGQGPSDAVLTVDATMEGLLLISGTNAKHWGD
ITVAGHLGNLWASQVPNFGNRMLLPIVWGRLVSWGSNKGLIMAERKRLGTDHATAVVDLL
HWSA*
>TCRU_8059 hypothetical protein, conserved
MFSRTFPRRIGSETYGGWPWPVKLPFRADWYHKLSSRQSIADENREYTVIGDILILSIVA
FATYRVNELYFRSNAYQTHLCHLTQAPPAIIANEFDFKKAENNRKVSRAVLDEYREAVVA
CKAQRQPIESVIFNF*
>TCRU_8060 proteasome regulatory non-ATPase subunit 11
MNNIANLLRAQTGGGNARAVPTEDLRDTAETVQISSLALLKMLLHGRAGVPLEVMGLMIG
EQVDNYTIRVTDVFSMPQTATGQSVEAVDPEYQVHMLDKLSVVGRSEKVVGWYHSHPGFG
CWLSGEDVMTAGNYEQLTPRSVSVVIDPIQSVRGKVVIDAFRTTKDALMGGRNMYEEPRQ
TTSNLGWLTRPSPVALTRGLDRDYYSLAITFRKKNHELALLLNVYKKGWQEGFRLENMEK
FDRQTIREKIRTLASLAGQSERFIAQGLDEDDIGNIGRTNPILHLQMEAEGLINANLNQS
IGAMINGVAF*
>TCRU_8061 hypothetical protein, conserved
MAEGTTTKATAALSSSSSSTSGAERRKPLEDVILSPELTHCPLTPKLYLVGGGEHAEARQ
TRLRRQGATPQHKRTDQKLKKRLLKARGIKRKDEDDMTRHRVTEKVAISSSATSSEKQAE
SSVVSERDSLLERLREKERQFDEKITALDETLSCAERGRLQRDSIIDGLRAEVTRLRAQL
ELAAGAKNQADELREKILKERTVALEEAHAKIEALHDTVREKNQRIKHLERELKLRQAAI
AAQPQQKLAVTTTAERVKVPQLQKQEEQKQGMLRTLSPNVVSLEERERERRKREQYSASL
RALQEEVQALEQRYNITRNEKNALDEENYALRSKLEGIQEDFETRVAGAVKAMQSHVDQK
RELEAEVLATRLGMARLLRLLSEVPEMRRYLRATAIDDDMLFTGYTLVAATSDRKAISEN
AGHSHYQRRRNGGLSTLAAGTGVDDGVYGGSLMPWSSNIYLNGKWYRKLQEIIDDENNFL
RSRKICIGDLEDAARCGRGGGDGPPRLPPASDVLKGRQNDKDFWIPYAVFVEAQKFKNRY
FPALSYESFYPFLIAVNHVWNEKTRRRVAIETRRRLYLQQQKQEQEKRHRAAKEQTDDAL
YSNDCLRQMSSSALSFQQQLQQLRHEVRRRVKGKNSLELFHAYDYLIKCALKHLREVQEE
HAALLKRHQYSLRSVCVPKEGHIDEEDKERMINEEGGVGIVDFGNEAFVLLRRALSALAE
EVQEISERSASRIEASCRDMQEFLGALRDQKLRAISFQEQQQQRLGEGESAVLLRTQTLD
SVPVSTLLRVIEGILDFVDEVQREVLAARNAISRCATQADEKSELLFTPAAVDDGSGAEY
DEEEDELEMAMDG*
>TCRU_8062 bilobe protein, conserved
MYRRAKEKRSPLVKRAGAGLPPPSPVVPSSAALDRDAKALQAMLQEMDEVFCVNDGDNER
QRRLNQIGEQQMALQRLCEAALQQEERLNSAAVRHKAAIEFAEDRPVDAGIVLTPRSLES
FSTYGDPGATGMGRSASRNDTGSQIMSAPPLPLCELTKEASATRNTAASFCSYRGRMPPT
HIEAPAVATVSAGITLRRASLPPLSSPALDEDVALEEDRRLIEEFLGVMEVESTHPYAAV
GNGRKYLVKEVAPKLKLQRFSWNRGTTHTTPMNSSPLARDASHEENFDVREEEQLLKRIM
QKKPRPPEDPLQGAHAGSVSRSSDVPKDVKRPTPKKEKMLHGEERSFSTLSGTTAAPSHK

SGKLCLTAAPLNGEHIATGPEKENYEDVKFTHAGEIQELLRKNGELQKEIEAQDVALRDL
TQKTESLARHLVNSMRERNKLHSSVERLEESLARANSELGRFQRAVEEQNKVSCGVDVWR
ATAHAKERELRICEEELSLLRGIVEQRVMRSGNVVMQQAGSTALAQVKSDLEDLIIELAS
AHVLRREAEIHAERVSEELEAAQSHIQLIDNRLAEAEKTVAFQRLQEMRERLLSGNDMSL
PLPSLPTLPSFSMLLEGNVAAWPIDARREIARLANYAESLVAQHAESDRYAELRLSEIRR
ENEELRERCRAYESGVKKLEDETETIRRERMMWKLSEQRWQQMLLDVQEDAALVTDLLQN
RVKGAEKVLDFLTVPHVEQEVKTEMEAFLKNAMRDWDTAIRFTTALQRMEIGSSELQKQE
WTEKFPLSTATRTRREFVLQAIETAMAQKASSSCVSPQPKPPKEGQRLLAPDPASLPPSL
FLSRTTNTQKVTTVVDDEKWKEKVESVSWPLHAPEVKPRALSPPRPSFTEGESVVTRDEE
YQTERHRREGVPMKRVEPLQPPAVSPRESLTQPLKDREIPLFPHHYDPGKIREVSPTREI
RHPQSREGKKRFPFTPKREELSFKNLPEDEGTQRDSAIVVTPAEPSHGNKGIEVFVSGAI
FKEEGIADSTTNEEAVVPPVHSLSTCATETWTNCSQEVEHVAEPPGREGNAGLRSVTPTT
PVVPAVTSTNTFVIAAVETVEGCVLSGEELRLQAALGQRLQRDDAREKSGQAPNSADIRG
NKDFPTILVSDSMLESKKNKKKLSKLSREDWNDDADDANNEPRLHLAAPIRRSDQTEKVF
QDENSSSYSPTEKSKEVPLMNEPNRADDKEKEMSPILFLNSKTKPMAMPDVRESIRGIAG
HVPALSCSLLDTQQSRLAASLQEPRQVTCKTPVAQKLSEEAETVVQNSVTEESVAVLQET
EKETAPVVGESSDPGGRRRPSAVMEFPSLRHSALGPGGRRQLDVQKI*
>TCRU_8063 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSLCVTTTGEDPNAGSGSTSPQQPGKGVMGQANTSTTSSSTG
TEVTLSVTENPDSKGQPSDTRNNTGRGKESAPAGNSGPTSPASGTEQGQDGSGRSGSSVT
AADAVQKNGDNDRTDSTSGNNSSTEQTNTNVDDPAEKSTATTTTTTTSTTTTTTQAPITT
TTEAPTTTTTTRAPSLLRESDGSLSSSAWVCAPLLLAASALAYTTLG*
>TCRU_8064 hypothetical protein, conserved
MFHEKPPLVEPPECLLPDVWPDQVHQSHPQLQPVKGHQLHPQRQQEENQNPVWKRRHENP
CLLESPEVLLQEVLPEQLQR*
>TCRU_8065 nitrilase, putative
MSSLRVSLCQMAVEKSKEANLSKAVGMIAAAATRGANLAVLPECFMCPYDTKYFDEYAEE
ITPGCPTYDSISKVAKENNIWVVAGSIPERADGKLYNSSMVFDSAGNLQHVHRKVHLFRI
HSETVQMDEREVLSPGSTAFPVSINEKIKFGVGICFDMRYPQLAWKYAQAGTSFLVYPGA
FNMFTGPIHWELSARARAMDNQQYVLLCSPARDSNAEYVAWGHSMVADPLGRVIATAEEG
ESYVDAELDFDLIKEARKKIPIMDGMRNDIYSLQWQ*
>TCRU_8066 hypothetical protein, conserved
MFRRLCSMVTIGHILPIGLRQCHVNTVEGVGTLNDKSRVKFGVCEAEIVSETRISQEKGP
DSIGEIKSQDVNSVLENEHFFLEMNRLQYSFSQEGPYIGSRKKDTIETSVDNRSRRRIVR
VPQPDSEYRPNETSFRRLPKNARIPNEYELRALYPQSTGLVLIEGKADCVDHSAFDPDED
PAPMAYSMVTPSDWSKEKEYPYMVVLPDHRGIPRDFEDVCANFFERPMHRQLMLEQNWVI
ISPTINLRHNFQVPVEAVVARFCDWVTENFNVEHRRVHLFGKGNGAYVALRTVMEQKEVA
ISVTAILGRSGTPFRPLDRPQDKVRNFNGVHSLVFVPGLLRKQDWYYKFKFMMDMARIRP
ALRNIHFADVRDHQVYYAINPYEFWNHMKYFRQHSIKMVTEGGYCVH*
>TCRU_8067 hypothetical protein, conserved
MTFSERDAILNDDEEWVNIPTVLRSFLRQMNNELQNNRLTCDAFLDDQKEHDRLLKGILS
KQLERELEMKKSELTMQQECQEVQASFSEVLGTIREQMRHLNEEQQQIRDRIRQIENRVH
DTIAMHDEVRAESSALSKKMNQRSMELEREINNKFRELLGTVEELKTNVRLVSERQDAGV
SETKKDLEVSNVAWRQLGDAVSAEMDNLRIHFQQHEDALGELKSFKTETEREIKKRIKEY
THLHEKICNSLGMVKQLEISSEDRFETVFSALEKSQALTEKLSQLYRKRDEDNNSLMAVL
RKTQGTYNALTGDLKNAIDLRLTQHGTDLEQLNKRIRDLYPSKNEVTALVNEKSERVLPY
IEEMRQRIEVIESAMIHKPNPIMDIENAVNELMKNDRHNYERKYAELHQFISNERGTLQN
EIKEIKKTVGNLDGRCEQAMHAVRRVENIEGDVQRLGKQVHDYNESLKCVRNEMDAFTTA
LNTIQETSGMIFNNNNKNDPHSMICRERVEVKKCVTEVEFLELRASVEREEEHLSRYVAQL
NEIQQRTSRFENLVKEVPRTYQRYMEALDKKLSPALLELDVLRSRIAALELRHATDEPHE
VKRHSSPTRHEESELESLRLNIQQNQALQFAQRKIQEVDVRLDGFQVLCNRLERRVEALS
REVADVSEKTSSIQEEQHPKNVFEDEMKRVFGQLSELKKEMRSCEKGVKSTERSRLVLTS
DMQAIKTSFERFSDLMVTMEKTVGSCITVTSDEWKKVYEAVSTFSGCKLEDVLRRLQKES
EVFVSVERIRLVEEALAEIRSEQMEFKRYLEQFQESALEKVHMNILPQSGDDLNQPRFTL

EERVILLEESARKNLAQMTSNTNDVVLSFDSRVKSLEAAVGEIRAKEPLPLTPSPQIPSS
LSLLTMNDVPLQMAAMGERVTKLESWITTMHKTEKDAVVGAEGFLHGDRLASLESLMVTC
KREVEENSRIVAVCQRRIDEWAERLTGDDSARKTTTAAVIKSGDFLAGVMERLQRVESKT
EQIEQSVIAEQKKDTEMQTKRYVEARFKTLWESILRSIAPKVDRKEVNENLTELQRWVKD
YVDVQLNASTRELKSAIEECVSITEVRELVLGARGSAA*
>TCRU_8068 hypothetical protein, conserved
MFGRRVFGSSTIPRAMYATLHINSSLQARRMLPSLVPLTSSVAGSSRSVIPMVQCTSPSM
PVLETAELDPVLLGDFLRSIFPAKDGFLRLFELWGIGRMVMLAWMRGQMA*
>TCRU_8069 hypothetical protein, conserved
MPNPYIGNGDAARYVEYYASPRMQRDAVYRLYNKGIQRRQESQRRAEEAVYPSQPRIYRT
QKEIDDYVNAMVYSEVFRRQKKLAELEWELYHPTPTRYLTDQDMAMHVQHMYDQQLRKRE
RREREKQRLFGMTPIQKKEVQVREKFHELEENWRPPSFHLKYNDGKMLLVSELAAINSAS
PPSETQAGEARGCRHADPQRLQQLAQPLRVTPKLHKETGKDALMPPFRLFGDVIRKIEKR
R*
>TCRU_8070 WD domain, G-beta repeat, putative
MAGRTITSMCTVEDESPAPLFVGREDGSIELYGSADAACFGKPSLILYGHTKAVTAMFAP
STDEVFSCSMDGTLRHWSTERELEEMKHCLNVSRVGTPLRCLMMHEGALYTGGNDGCLYA
IEGSRRSSWPGHKDVLSCITVVAEDSQYVITGSYDNQIRVWDTRLAKTIRLLVGHQNHVK
CLRVIGAGELLLSFGRDLTIKIWRLPEFGDEDEEDVAPSSPDNIRQATVSFREPTDTTPM
PDHPAATATDGGEESGEVPAKASSSPEVNPGSADESVNKHYRAAVQGATTVKSAIKTRPQ
PPMRQLRCVGTIEIPEAPHVVAATSNEASYCHIGTSDGYVVGVNVRALSRSVLQFLSRNA
AEVRADTRGTRLTLRLSIRSIKKRCRNAIQKKQLELQRAAKHARAKKKAEERKERAAARA
AEREARAAKRAEEEDDDEEEEEDEDEEQDMEEEEEEENDGDEEQEEEEDPLALLDDAQRE
ELAAFRKQQEKERDEEIESLRKAAEERNKVVGKIGSATYDTTRDRFFFLSFTSYKKIGSD
AVLGLVALPGGTCCAAQSDRIKSADTTPGITYL*
>TCRU_8071 hypothetical protein, conserved
MRGVHLAPRHAQHSAPRRNHARTSVQRKVATEHSRVQRDTATDELQHRAVHHHRPPTSHH
GHEGNAGHNQHGPHEPQARQHQHRCVRRGLRAGKTHKWRRPRGNQQGVRHRQHGPRRESA
GQHKRTVQRLHIAHGQLHRPALVAPRRSRTAQRSTAHHVQHGTIQQRHVLHNDPHAVPRH
PRYVEHRTHAVQHNVAQRHLARAGRHNEHRLHRHALADKHTRRGARSGRQRGSFHRHARL
AVPSAAAIAHANTVHHARRRRPGRVAVRVPVAGVAPNNVDAPSVAKTSRCVLLRRRQDTP
TSVVARHSQMRPSRKRQARRQHPWQQRSVAHKAQRAPSSGHGVSRVEHLPRDAVVHVALR
QQHRPTGQPHVE*
>TCRU_8072 Enriched in surface-labeled proteome protein 1
MSRRVFTSAVLLLVVMMCCGNGGAAQAEVEPAPRQGSVPKSHFVWRDKKDGETVSSLRVP
SLVEVNDGVFAVAEAQLKDESGFTRIASELLKLNEKQKEELDKTKLKTQVLVECPAENKS
CASQTEDQDASKAGRKYV*
>TCRU_8073 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSVCVTATGEGQDKNSSSLPPALPQGESVPGSVNPRARTPEN
TEINVAQPDGTSGLGLAADAANSNGQKSSTAASAPDSAEPTEKAQEPATISEAGGSGSPG
GSANSNKSSSSVTASVSSQSQKENAPTTTTTTTTTKAPTTTTTTTTEAPTTTTTTRAPSL
LRESDGSLSSSAWVCAPLLLAVSALAYTTVG*
>TCRU_8074 Enriched in surface-labeled proteome protein 1
MSRHLFNSAVLLLLLMVCSGSGAASAEASNSRNGIIFKGGDSFNDPETENLVQAFHSFRA
PSLVYVSGVVVATVEAHYKNTTDKKSCVSLVAKSMKSNGGEWTKGTAIVFDHYDVKIDRL
LSPTTFVDEEDGYEINALVGGYGTSTTPLTEVTGDGYWAPRMAGGLIPHDDDDEEKKEFR
WQNQSTSKVPYDIWGDYSTKPKRFKQILGGGGAGIRMEDESRYVLPIQALKDDGKVVSLV
ILAKGFTYGWEFSNGTSDEGCIQPAVLEWEGKDLVMMTSCEDGSRRVYRADEEGRRWTEE
YDTLSRVWGNSLNRIGHGVQGGFVSATIDEQKVILVSRPVYSGEEGKQETGRLHLWLTDM
QRIYDVGPISAENENVAASTLLYATVELPSLEEGESKEEKKLYCSYEVAAEDGKYNIAFV
DLTEKLEDMRKVLAAWKTKDAQIAKEYGCGNEKDANKRRDCDDLTKGLVGLLSNTSTDSA
WADEYLCVNATVHGKVESTPDGGLTFKGPGAWAEWPVGDMGQTVPYHFANSKFTLVATVS
IDKAPKEGSSPIPLMGVRMNDAQGTVLLGLSYTHDKKWMVTFNGSHLTLPAHDDDVEWEA
NKKYHVVLQMDYNNGLFVYVDGKRICDTEDYEVEDYEGYKSFYDRSQELLSSNSISHFYI

GSENEEGSESSYVTVSNVLLYNRLLHEDELSPLMKTKAAAAPEAEVSAPEGAPQNRHLGQ
ASEKDTTPSPQNQGLSPEKSKNEKYSAGSGQTTSADFTGLYTSAAEGEVEEVASSSVGSA
SSLAPTAGEDSPQKVREADVPATEDHFEREQEHSSLSVVQPMTEQAEEAAVATPQRKTTE
DRPQHSTLSDASEDMEESSSHSATLTSDEQTVDPEERKDTNPHTAVGASSGPDSSHSTEV
ASVDGATAAHEPSTDPKTAQGHDEVLDGDDAAPGNKSTLPGETKIPSGSNATSLLEHEVL
LEHGHLSEVAAMALTGDSTVHGCVSRVLLLLLLGLWGTAALC*
>TCRU_8075 hypothetical protein, conserved
MLDLARQHGDVRVQLAFVDEHGPLDAVVAAAATMTGLRLGSGDIAMHWEEPTVAGHFANR
RAPQVSNFEVRVLLPIVCVLPGSWGSSKG*
>TCRU_8076 hypothetical protein
MRRVHKYDTTDIATIVVFVGLRAAPEEAGLPSRRCQPRERPCEGGHEVWRAGYAGVGCYR
DQRPEGLRQGPAETHELIAGFPIHLQCASARHQTVDGHLNLRAHLVQIITVCASEVDEDS
GDDVIPYTRGPSVNVQCKEMQ*
>TCRU_8077 mitochondrial DNA primase
MFRFSFSVRQASKRLIAELASINARKEAADAKAKSSVTSATKHASSSSKTKATSASAADA
EAAAVSVRAAAEGAMPKKTHTEPVVATKLAKIAKRMRKQKAAKAEVTAGDHFHTEVMATK
DSGETPLREAEMPAETVRKASPDADPPKAEGQQMKKKKKKLLKAASPPKSLSQVREEEKE
ASPPVDAPDAEMHKQPKTVHRKEEKVVAKAAAPAEASPSKPEKSDASQQKTPMIKAFRIE
DVLSACTPDDGVFARRLPQGGCQFFAWPGTPLAVASNAVSTMPDTIRTVHAIFGRKKTPI
DLVLDIDCPVPQEHWSMSKIRPFQKKVLDDIMTVVMGEIEAIGEKIASQVVLQSPNLKKA
SFHVHTKLKDVAFEDYESLHGFLYRFHKKVPQVDLQIYRQNGMLRMHRCMKENHTSAITV
FEDKKWNIGFPNGVVPDPVAALHSACVRESGTYSRLLHFEAPRMILVPEEGADKDATGAA
NGASKIPPILLPLTEREAVENVSMWLRTGTREVDVGDWRSWIKLGINTFRIAYHFRDAQT
LRRPAMEELLDAWVEASKKCPMKYRPGVCEAKWSSFDIDKLCKLQDNDWWSSYQRIGRVA
ALNKAADAGGATSATSSKKAEQK*
>TCRU_8078 Oxidoreductase family, NAD-binding Rossmann fold, putative
MMSNQPVSSHNNTLRVGILGVSNAARRALRVINRAGLLLVAVGADDVVEAEKFVNAFLED
TIERQTELTAAQQQKLGGLPVSEASQEDEKVKACTYEELVVCHEVDVVYVAVPLEERDSW
VRRCIRQRKHILTSIPAAPSGDVLQKWVELAAVQRLFLTDDAVLMQGTRMGRLWEMFSRT
GDNIVGPLRAIRVCCSCGCNDHCAMAQCNTCDDEDSQFGVLGNWGWMAVAAVLHGMRYAM
PSSVLGRALRRDESKGNCVTEFSGELLFTDAGPQEVTAYIYVADAASSSGGVGAVEQSLT
AYGTTGSVTLHDFIIPVPDEDGSVHLTVASHDAVQGKQLYRIVRHEKELRVNEPVTFAEL
PWRRLRDALSPNPHAGASRLASRFLADTEEATECMRRSWSIQVVVDAMLEATTISTKITK
KDEERGRGEDGNTTKKA*
>TCRU_8079 spliceosomal U5 snRNP-specific protein, putative
MAEVKLLHSAWDVDRHIVLEGEKLVLIRFSHYDSPPQPLSAGGDPSGGGPMVHFTATRQM
DEVLSALAPKVRKYCVMYAVSTAEVPEFNVMYELGHDREPFAVMFFFRNTHIRVDVGTGN
NNKINFFIEAEDLLPIIDAAYRAGRSGKTITSSEKKFTTAAVRR*
>TCRU_8080 hypothetical protein, conserved
MQLLAVVLFAFIALETTTVVSAEKVLRHPVASSSGRCANGVKAYLLQTVKQRAEVTASET
RARAELNEARTIVEEEKGGQREPKEDTQERVRAAWSKFESASAAAQKFDAAVLNSHGKLP
LECILEVDSLRGTDPNAESWFGQTIHALEKVALHLRLYGETLRGVVLFNLAEYESAVSSF
YDFVEVFSAKSQQAYNEIQQRRNKVTFGVENGGLRELAELALMYTRFITLALVPWMTVFS
VCVLLIIFAPFFLSAVLLPQLVWRVWVQLFFLHHTYGLTVDGLFNSLQQYFGLLTEKDWA
GLQERFLTAVLTLATAEGSLGTFYNGIIAATLIISTVAILLTFIYYWVKLPYSLMAREGG
GGGKGHARNQPRKGAPQTSSSGGSTTATTTAGNAGPKDKSPANVSEAARHSTRMSNRPTG
DGGGNTGNSSEKNTKKKA*
>TCRU_8081 WD domain, G-beta repeat/BING4CT (NUC141) domain containing protein, putative
MVAGAAVSKETREIVRQRRAELNAEKLDEEKRQLRGRWVTDNNALQNAEARKREQLQRHA
PRRVARVNLFTKLEKTDTGLVLEDREVADRVTQDDIVSAVDLQTQEKKYELLLDKLGPYK
VDFSLNGTHLLLAGMRGHVANIRWKDFALNGEVQLKDRVDDAKFLVDHTMTALAQKKYVY
MYTKEGSEMHILSQMANMDRLAYLPRHLLLCAASTRFSVMQYMDISTGQELGAKVPAVVR

DPTSCMDVNPSNGVIASCDLRGVVKFWSPVVLDPLVQLKGHKGVIDDIRFHPNGRFFVTL
GGDHKFKVWDCRTLRALEEYAVTYTFNTIDISSSGLVAMGGGTNVQLWKGIFSSAKPTAP
YMKFGLGYGNIARQVRFCPFEDVLGIGHSRGFQSMLVPGAGDANPDFFYANPHETERHRK
ERVVSTLLDKLPPDTISLDIQVPGVNEARLAEYNENIRLNRKARAIREKKQRRADKSLAD
AAPTGLQVGNDDELDEDIGYWERPATRELKSRKEKLKERKMQKWDKKDSSDKVRSKQTMR
TSKIAQQRRAKVRRAGRRDKSEEESEEEKGERKRTQSQLKKRRREEAEFADDVRLLRGQR
QLSDKEGHEGTVVLSSSELMHNAALRRLM*
>TCRU_8082 MYCBP-associated protein family, putative
MSHFATVPAGDSQRNTVTSDLYDQRDLQEKALETWEKQKRIWAAVQEKIRRRVGKNGQIR
GACMNMSQGAYRARVREEEAAVVNNATPSHVFSGYYTWESTLRTTEDNGAIRYVKAGQTN
FPYALYGKLTDKRRLDVEHPTNTRVVFPDEQILNEARSRELQRPSTGAFPVSFRDSSYYK
ERFKQYYPLIERNMPHLLLPRAYLEVCGQPPPWTSKPEDKVAAARKSVPAVAHVPPLSPK
GKQQQLLQKDQNGQGKSCSHSVEETGSKGESKDVNFTVSTEETVAGAPSLEISTSRVLFF
ARPGEIAHGTVKIHNNGTTTVYYSWAPFQPATALDEKIGNEKVDSEVEKKEEEEEKKGRD
DTIYEEKAGFFPLETSEEKEEVPVSARSGENDIYTKGTPQPSVWSNKKGERKPNQLNVSL
RSLAKKSAQSKSFFFLSAQLDGVILPDEEKTFSFSVRAAFPGCFLRYYELLMVPAASFRV
ILELRAFIQDGGPTVETIARPVAAALEAKAVADTQRELINALAAHPHVYEAAEIAKATQD
CLDAAKAAKEAQDALIAKWRKLWHDSTYTAMRIPFNIAVYGRLTALHQNLARTMSALESP
LHHEEWDGSVQTIQSDLCMLHDAVSRNTLREGFNILLRAAIVSEQEDEPLDLLLQRVAGM
VAFSALARQTGELDDSILLILGLRDPRVPQNGLRFPTGVLGSGNGGITGAAAAAGGGRKV
AAGGGGGNAAAIGGGGGGKSQGKAPNKGKRSASIESNIGRFGSTEKSPALNEMNMTADSV
TEASVKEEYSARLFSGMRRLVGDAVDQFCSNLDCFRCTIEATCALPLLETTAFLRAEDTR
TIQNAVDMEVDFTVDIAPPKKKR*
>TCRU_8083 kinesin, putative
MTVTEPKLISGPTRKASTTPVKKTIPTRTTTPRRPQQRDSRSVPNANPSGRNTIMDDAHE
SSDAFRSRVTEITRFKVFSRVRPFIAEELAEMEGQERRSVVEMTDNKTVILDPKDGWAPK
AQFEFDASLWSIPPEHRIVHTFHDTKRSDYATQKDVYELIGKDLVPHVFDGFNSCILTYG
QTGSGKTYTMMGIYDPNASCGGDGEEGIIPRVSNDLFLILTTKQAEEAKKTELHDRVRFR
VEVSFVEIYMERVRDLLDPALKNSKGNEKLQDARIRQDPYSGPFVEGVTKYQVENWAQCC
LLLERGSMHRTTCATAVHNQSSRSHAIFQLTVIQEQTIPAKDRYSRPTVRCRAGRINLVD
LAGSERGGFQDYVKESAAINTSLLALRRVIDNLTERQNILMEQAKAEITGAYYQERTLPQ
VPFRDSVLTWLLSDSIGGNARTTMVATLSPLVKNYGDTLATLQWSSKARNLVTLVKVNDP
LTTVTGGMANKAGELHNAVRIQRQNMDSLRESLRQKQEFAEQLERESRSMTRQTAKNKEV
LNSVMRQFNAATVQRALHRAVWKKNMNVLKAHHDKLTSQLCERNKEVENVYMKQSAVKEE
MAALQQKLGEERQREEELRVMIAERESKDDAAESVFTALEAEYNAALKQLRTDVITQGDA
ADAHSELPSARRRVDAARQNVDETNQKADMMEAKIKESKQRSWREKIAQDERDAMELRSE
RNELQRKLDDLRSQQEELRTALKKRNKGRK*
>TCRU_8084 ubiquitin-activating enzyme E1, putative
MKHEEEKRQLYNRQEYVVGVETQAKYGSTDVLVVGACGLGAEIVKNLALTGVRSIKIMDS
GTAILQDLGTNFFLTPQDVGQPRADVVARRAQELNRFVHITAVTSPLHEVIPDVHVVVFV
NQRTTALVGENALARKHDVKFVACESRGIVGCVFVDAGPSFSVLDPDGEETVSCIVTSVS
RDGVVSLHEDKKHECEVGSHIFFTGVVSPAAVNADIDPSTIHGRCQSAASPLLKLFEVAE
VISPFILRLKDFEAAVGNSPIEVGTGAYLHTTKRHVLMGFKDLEQSVADPTFVTIFDSEE
KVNAPATLHALFRALHDHGTLPTTPTEVNSLLNVAEAYHSSCNSGHLDVEFSKKALSVIH
GNLNPMACLIAGIASQEVLKVCSGKFTPIQQWLYYDARELLVARGEVAEADLRPSSPTGS
RYDKQIAVLGAAFQSYLSKQRAFIIGAGALGCELIKNAACMGFGGISITDMDSIEISNLS
RQFLFRNSHIGQHKSRVAGEAAMAINHDLHVTSFVEKVSVETEGIFNEAFWDSHAVVLNA
LDNVQSRKYVDSRCLFYKKPLFESGTLGTKCNVQCIIPYCTESYSSSHDPPEKAIPLCTL
KNFPNAIEHTIQWARDNFHVLFTNTPEEVNSYLQDPTTFAVNLERDPATKTMSLKAVRDA
LLRWPMDAADCVRIARRLYHEYFSDAFRQLLYNIPIDKRNENGELFWSGAKKPPTPQEFS
PDSELSMSFVYHCAYLLACVYGLPPFTLSRADVARVAGETSVPEFVPRQAVFATSEAEKE
ESVANLAAEIGLQDLPPVSEFHGRRMVPEFFEKDDPTNHHVEYITACSNMRAVAYNIPPA
DVHHTKRIAGKIIPAMVTTTALVTGLVGLEVLKRLLMTQRQERSGMPANAVPTYEEIQKQ
LSIYRNAFVNIALPFIAFSDPIIASGATYPLPDGTSVRWGIWDRIDVNEGRDLTVQELVT

VLESRYQVELFIIALASGKIIYSQFGNTKDRVKPVSTVVLEKGEQLQDGEDCCCLVATGS
ISDVDVDIPVIRYRFRNF*
>TCRU_8085 metallo-beta-lactamase-like protein, putative
MRFTVGSRCGYSPNLTSLTNQFNRSERLRKWGSVGSSPGVPRIPRLEAKSIAILHESPKV
LLAGRNHCNNFDSNQYMLINKATKQCMLIDAADDWPDDWAAFIASSSLRLTNIFLTHCHI
DNIINLNAFLSICGRKQQEEKMDGEGRGDVDWENGESDGSEKIGLIWCAAEECWVQNFGR
ACERYRRFEEMHLTLPMMRRNLYTPRHVKDTATFGLSDPGNGRNGYFRRKDMLLSTATNR
ASSFIDFGDGVLLYYIFSPGHSPGHMMLHAPTEKLLFTGDLLFYSKVGRVDLPWATGARL
AESLRLFEAMPDNTVVLPGHGRMTTLGRERRENRALQQCYQRQEIGQQEVSVGFNEGYL*
>TCRU_8086 hypothetical protein, conserved
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RRTQDQVTRAQYENVCRDADELVRSLDAEMKRQIYPQRPATRAKTYTERKEEELLGVGGS
DGKGFKDSEQVLQAAVNVQNDALLSLGRAERLQHMTEESGRETHQTLHRQTTEIYQIDEE
LQNLQGGLDRVSREVKWFYRQLAGDRCFVSLFGICVVALAVLVFVMLYKKRHK*
>TCRU_8087 60S ribosomal protein L7a, putative
MPGKEVKKAAKPAPKTAAKPAAKPAAKTAAKPVAKTAAKPVAKTAAKPAKKPTVKPAVKP
AAKAAAPYKKPAATSSFVARPKNFGIGHDVPYARDLSRFMRWPTFVTMQRKKRVLQRRLK
VPPALHQFTKVLDRSSRNELLKLVKKYPSETRRARRQRLFDVATEKKKNPEAASKKAPLS
VVTGLQEVTRTIEKKTARLVMIANNVDPIELVLWMPTLCRANKVPYAIVKDKARLGDAVG
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RNAGKDAAAVM*
>TCRU_8088 hypothetical protein, conserved
MASLRSTLHKIKTDLYEAETAGEAAQAVLQALPRWLPWVGAGACITAYIVTLRVRLFIAR
WRRAARRRVERKYMAIGFLHDYAQPQGEFFTLVGDDNDDDDGEEGDNTALTLSDIEEFRC
SLGIRSPRDDDLLLLVEEMLLVDPIPECWVLYRTSAGLVRFMNVNTQELFFFHPGKREEE
RHIRAELKRRNNVFMEAKFNLLGSDDKSGRFPGSNTSFALRRQRQKKATTAGNNCSDSVG
SGGATLSFSDDEEEVDGKDEQSTFRRLFRYFVEREERKIERDVEKQLAVSPAAGSGPIGS
SRAESRSLRVFPANVVHSGSHTKRVSVS*
>TCRU_8089 Dynein heavy chain, N-terminal region 2, putative
MDLQHENSVSLRFERVIAQFLDGIPRPFLKIVSDVEHGVTFEFCSVGFPPDYTGLTESVQ
FPEFRESQSFAPICLWYCGPSTPSSRMGAHYSPYVGTFRFNGKGVYLQKKVSDLKRYVVR
VPTETCERKGTMSSKFDRDLRTSLFIDFYERIAENQLVHERESLRRIVVLSTQGVSEEYS
GLVEEIVCEIKRLYIRACGHFMYQYMNRNLLFRRIVSPLCLSEPDNDCFTSNGKGKTDDF
CFELALRFKSSISYLGESLPWSRRTHQFFLDLQELWVNRFGRLAIFDINTNHWRTNADAF
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LVNRIRTLIFEALKDLFHFFTAVGEGIISPSKARKIPLLEINLTVGDSGLPCSPSFALLR
FGLADLLDELVDSFNNLPIPEVIIMRTLDFERRTLNSFDAEELPLKGALINCLDVTGSKI
NELIREYSLFSTLPPTNGAYFTRAKEAVIEDRVRLLRESILKITNTSPDFVFSGCIAINC
TEVKKWYVEHWTRYLENYLTTIQSDILSYITATIERCRFYNACLNKEPKTVGELEEISCE
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ICTKSKPSIIEKLGEFRTSTRLQVTTISDGVQELLGLFNLEVCDIAAQTCEELRAIVDKV
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ATQMIDHVQRCRRLLHFSTRNLRAYPGLVRLGRQQEQILNDFECLEGILMCVTAPGLRKN
HWKEISRILGKDPNTNLQIDSNVTLQKLLESRIQDHFYELKQVVDPAIVDFETEASLERM
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VPVDRWMKSFERTLRSSLLHEFRACVESHYYVDSRTWLRGYCVQIIDVALRVIHNRDLHE
ALSLAGSMGINAYARRLRDLTEEYIRIAGAHMESGERRIVSSVIVFLLCFRREIQMALKA
GIQTKEDLDKTAMLRTFMENDRIFIQTLGLRLPYGMEFLGNYTLPVLTPEYIEGGLYTIF
LSFAASSFPIIIGNPERASTLQYCAEYLGRFWWCLQCHPALTLEGIIRDLRGALAIGAVF
CLKDIDMLEKPLILPFSNLFRSIETACQSGKQLCDGGFDKIGFEIKDTTQYVQRDPCFQI
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VSPLIFTVKNLLTVIRETIEFNKVPVAENLCTSFLNQFWQAVRTNERLQNLLEWNMLHTL
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VVISFRLISCAEIYGDACHPGLLSSLAKQWDPLVNHVVVIENANFLQTSIIFETPAFVRI
RPHSGAAFIKGESVRLIAVASELNAANPRVMVDFAIFALPEPTRWKKFLKELLSTAPSYY
TGVAYPVMVTLIDHILDTRHVPNRTSASYGNLFAVASRCSQLYKRWYVYAKSRCESREEW
ISDQAYALQCAVFATTWSLGLHLHERERHVLRVALEKSQLKLNRIAKEIGFTEDVLPSTE
DDILRYIATPVGWKKMEKAKTATSEAGFASMWSRKWDGVDINQRTWSQFFPFPSRETTLT
ALEYLIDAGQSVLITGENGQGKSTILRQMRSNDGWVHQLVCNSTACRAVEISEALMRNMT
LRQSKIYGPSIGRKLVLSVDDVNLPGEGRFSQVMHLFSFIDRFSAILSPSLGYVSIADVV
CAGASTPGPSYEVEVENAVVRVRLPELEDSEIIGSLQKLFDVVCVKRRGLNVSKDIVTFL
VAAHSLALRLMPTKLRGERTSEDTTATLLGNNGNESVPQEYECCSISGFHMTHGVCISFM
HHFLKVSDKALRFLSNSWDDAGAATVIFNFVYAFYANMIEYEEEKKQFKEELESSANMCL
RNCFTPGPVRFDTVQDDIEMEENDGTDLPPCTSGKVQVWMRAYETALLSNVIEEPLNIDS
RSSIIFSPIPPSQHRPPAGLPAGTMAPRLSQINYVSRWLSILISALHQYLRQPQTHVALI
GRYDNGIRRALRVWGFSLRIHVAFLRENYVGPDANEQIKNDLIHIIQQTCRNDGRLVVFV
PNSVLGLAWPMGTLDAILRGGDVTQLFTCEDLLFLLYGRRGMRRNFSGLTMAEYGELKQR
ICNRLSMVTHVLSYKELNHLRSTIRLISYVIPLSLREPEMLSELVNGIIEAEEKNRQPMY
EAVLRGSKHVPSALPMSPGSLNLAGHRLTHLLCDVFNVMKTELNLELEQLLEFCFETKRL
CQFLERLRCDSAQSRHITQLPAAIGAKMKVYKEDIDNKADSAKIAIQQQMKTLLARSQRR
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DSLSELHTSLREVRYSELSPFASAMAEYVGTLMEAARLGEIVRGKNERLSKIRLEHSYYL
SKVDAFDSRASELLKKLEKDRAEVKQLLKRSEEMDAVKNDSGRRQSALALLSDIVDRFIP
FHSSEDTATREALEKKGEGAVIMVAAHRAFFAMLPKEQQVLRFRQLQSHLNGWGIAAPEE
LDDPIVSSLFPSVNNVTNSALLSTCSTYELLCLGALLQRVYFHWPFFGGASPAFEGMLKH
FLSIMCGGCTVASALSKGFKESLLDAARTGDGLLICDASVAFVLHELRPLLLLQPTLREA
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QTTLLQSPITREDVGKKYFGDLSVEDGNPIETFNEALHEANALLCEDLDTLTGPDNSKLA
RLDVLIKDLSNCHGRVLRLKSNQENVMRQLKDTWKYLKQGIYSVESAIRVIEESILGRHW
EPRKLEPFIIGAKELLRPYQSRISPHTFDALPEAHKEFYATINFVERVIQVLGCGWPCEF
RGIFAWYILSSAIIGCDLLLQLRGEVYSPLTVVFNNEQYKALDRLVNRGNNVIVEEYVRE
VYAASSDSILKNVLHQFPVSSNSTLDFNRWGEEGIVSGREDAIRCFFHYWLRLDYATCDT
LASHLYNAFLLSIKEPNNEGLSEMNPLYDYMERSPSDVYCLEEWLRLSLSACIPLCVVSM
NANQTVKHYERYFKSKLLSYHFCHVSATEEVDQLMKTVSVCFSDRPEQQGRGHCILAMLT
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ENKKGVSRRSGNRTPPTFKIANTIELHTGLVSGQVMLRDLWAKERSGVAFPSLWQATVDR
DDLTIILRLLTLWLRKEKNTETESRKGRSLRLSGRPDSRAPLSDTVSSDTSKAQQALLEN
VFAKFAFGIYAARMTTRRFRLAVSEVLSQRASLNTSEGGIREDARNFSVSIAIEEASKAG
LSETGFLAELRNSHEDFLGLCDDESSAVAYRDLLDASLQKIIYGTCESPTWTRLKHSVGL
DPRKSDPTAYAVDLNQAPSRDLIQLIFLWEKDHMEGLLSVLQEKGHNAVVDRVRAAMGQL
TRWVPGETLTVWLPALQYPRLLLYAFAARAVSRKLDELNRVEMVLVMSRRYSLLHDDIIL
FGAAPSDTLEQEVLHRTDWDAAHLAWKKDVDEKDHEEDIVLAVRFQKVSNTNTGGQSGDV
LWEVSPGEKRVDVSSPRGARASVVFLTETSAGSSLKTLEIRSTCPLPVLCASAAVTGDRR
EVEWPLLLDMPLHVIWRGTDNLWKSRKSTSIRRYSTLGEEDSLMRSTRRSMVDAPYSALS
NSLSFFVTIS*
>TCRU_8090 hypothetical protein, conserved
MPLDQKEEFSRYVYEIARVQRQLVSDRIEVLARHHRHAWHYFIGCVTFSASSVMLMFKFW
GPRHIFKNSMYYARPLPPAISMGVALYGVIFTCRGMLMRNRICNMMEDYEYELKRINAHH
CEVGIAQLAWLQFVTDQLRQGAEYRFDFKKLRQI*
>TCRU_8091 hypothetical protein, conserved
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TNDPATAMHAYRRLTLHAIQEIVLQRASMPGIGKNYLEFGSTADRDGSLNRLEHTLETGP
RFISENDFRKDCGVRGFSFGLPFLQIEHKEIAEANPGNGAIDLSFKKRAGSTMKVMESLQ

LQMMLLKEHISKSTRVLDALRQQLPTRDAVLLHEECFRKWKRLKIFEELVVNSLYSSTEG
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KFSLFEETEGKKLIRYFSALQNTVNDIIRQKNDESKNISWDCLLQRLEEKWDVYNIDAVR
ESNGN*
>TCRU_8092 hypothetical protein, conserved
MVDGASATHRDSPADTCLGRWMRSAVGGCPRSRHRVRRRAIAAALLALLVALVLAAAAAW
MPAVHAVVLRLRDGTVDRAITVGRAVDTVLMDGVSITNGVAVVFDVAAMLPGALRIELRN
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GPMRYSQLSGLTDAVAAPLVLHATSLLQTQLRVSNTVLRSLQAGGSAVYVGGGVDLLSSA
VVLDGVLLEASGGPTASALHVASSSNLSLRSHSVFSVTNVSVVSSGGGLVLGERLAVVDS
VLRFVGVEGSAASSLVRCDGGTIGVGGWLELHDVWAVGEASSVASLSGVTLSGGAVSIAR
CAATGATLVSGPTITSGVVSVQCNRAGGRVLQSSNDYRMAGLSSVSVVPCDGCAAALACF
AALTASFSDCVCSCRAGGVGKACLPFDVPAARAGGGGGDTAEGCVGGVMLTESVTVGGGW
ATACFDSVVFSGPITVTVDLRLMDAFADALNVTLCHCVLAGGAQLRIGGLSESTAHLMPH
ALVNMTNVTSVEGTIMLHGAMPSNSSVVLANSTLRATVGGSQYVPTTREHERFRYGPALV
LDGVRLLSTRFVMTRSSLVCGGGSCAAILVGRGFVVNLSSVFYMDNCAVSSQTHVMYALA
SDLRVSGGSVFSIQNSSWSAPSTEYYNGACVFRDVAVDGGSVLQIVSSTFRLGFAMLIAN
TLTVTDGSWLVHRNNEFRTAYVVYVVEENGVAFCDRSVWSILYNKLTYRSYSSTIPRMTS
KWSPPSDSRPIIYGVCNEARGSPVTNYRDDLNIWTPVRVLDCGACTVDAVCFAVRTSSIS
GCECVCAAGGYGDTCLPAAIPDGLGPLPLTDAKDTEVRCVHGGSISSLDVPDPGVRGLCF
VNVTFTAAIVLDLSYFDAPEQTLNVTLLQCVLVGLSIKGSGAHVHVNVTSSVLDFGALEF
KGDFGVSSQILVAGCTLVATSSYAIAFLDFTVGANSTLWLLDNRIAGNMYALYFPNAAVV
DGGGIIVKGNTLGTMEIKGMESSLYFYAVDVKNDGYFGVDNNTMRAISGVYFLGFTTVSS
AGLLRVADCTFAGSAGGFVSALVYLDGSVTLQGGAQWRVEGNSVGAASVLTIPYSKHKIQ
LSDSGTTVVLAHNRQVNSRASFVNIFPSSIVVTSSARFVVGCNLQGGEEVSYDDVFPEDV
VVFRCGTCNDDAACYMPGTESVDRSSCSCSCRDGWHGASCLPFEVPDAVVPPVAERAVDG
DTSCVVNQTLTSLALNMWKTHHCFLGVTFSGVDAALTFFFNSMPLHLPINITLTGCTFRE
GAALEFVGGAEAAESSGVLIRVSQTVMRPSVVIFALALPQHCDIAVTEVDAAQSSAVHSP
DTVNNKLSVVMLREVVLSASSLLVSNVRAHATKRDAFGLYSTGTLKLVGGSSLYTRYCSF
DGYTHLFHVNILSVREHSVFALLNNTMSSGKSLIQCPPGKAFCISTPDSACRITACCAWW
GTASFHLMPFTSTNCGLLSGQAGWTGATTTWEWVRCSTNPNPLL*
>TCRU_8093 hypothetical protein, conserved
MKHIATEHHRGAIADPQPIHRNTRRAVKVQTRPRDQPRDREAVPADRDVRVRWKITLRAK
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ERHVAVAQPRQPAAHSLRNLGVHHVADALTNRRRWCGRRWRWRWRRGQWRRASRHRRRDA
RIAVPSSSALALAANDRRRQRCKAVALLRALPARGNRRHVGDAVELQLCRRRQQTSRDRQ
APSNEPVTGVNPR*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MEGGDGTLIHLEGSGQSLSLSVLNNSAVAIRGNFVSRPVRHFIFSFWALGVESQSSVVFQ
DNDMQGSSVVFYSDFASYIYYNSWLQLSGNLCRVSPLHAFALLNPTVNLRDSTVSVSGNR
FMSSTGTPTALRIFTGSSDLTNGAILFACNTMNGEERVRYIIPSVYNITILTCSDPCTLA
TSCFPAYTTTASSDGCTCTCAEGGHGDACLPVAVPEPPSTDGADLCVRDVRVGVEVNVSF
GTSVVCYVGVTFAADVVVDVESMSGSVRNVTLADCTFVGGASLYVVGWRSDPPAGERADV
LISGLESRSGGGVVVANRFPPGSRVTLVDSVLIAEARVAYRGVYGLGDVSACLVVHNVNL
TGSVLTIARTHVAAVFRDAVGVLVVGGVALSSRGALYVDGLSVQTALGLCVSVEGGVAAS
DGSVVAFVDSDFLLCKHAVSVRGAVSVSGSAVALVRSDFSSTEDYAVAFYSTVSLAGGSM
LLAKGNVHDGVSREMLYAAGTVTAAGGTLSFVRNRALLPRMLSLSLSLAAGAHVRVACNY
AGGRVLSTAEEYAAAGFGDAGRIDVAGCDACDRDTHCYAPGTASASMRNGVCVCECGSNG
HGEACVPVGAPALPPAVGTASSVFIREGVTVRSVFVVPAGASEVTLRHFVLDGVSPVLYV
PWMARGGVRIVVQNVSLLNGAVLYVMGGGALRGAVAAGSDESGPVELSVCDVEALNGALV
LTGTFPAGSVLTVTDSLLVAARPTPLVYLPGLQSSPYAPVLVLSGLRLVRSVLVVSGVAL
VTVVTGGRTVAVDGAVLELVGGGVALDAAVLGGDVALYASARVVASGGAVLRVSGSQVYA
AHGLVFGSGVEANASAVVVNDNAGVLTDGALLELRGSASFVSGSWLSVRGNSISGRLLSV

PSYPRRADLVHSILTLHGNAGSGPVVMDGTVALGGAGRNFVVGCLTLNGQALRPMDYRSA
GIIGEFRSVACGVCDADVHCFAAATRAMSGSCGCRCADGGYGRDCLPVYLPHVDGCNRTL
FRPPLSHTATLTETRSLNSTWTATPTWTPSVSTTHYSPTQYGPTETLRVTETVALPPTRS
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>TCRU_8095 hypothetical protein, conserved
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VPAVLTGGGGPVLRSPLAGQRAAGLADNSLCAACVLPVSADGSGVPISQQLRRMPSAREV
LIIVLCEQRAAGKRWRRNALNTPSGPGAMPGKQSRMAESGAHDVKGQSIFQSPGGTQAQT
VQAAVGIAARETRTV*
>TCRU_8096 Enriched in surface-labeled proteome protein 1
MDTQSSATSGSPVQGAVSLPNSARQLPSEQETLKENIGGAGGVSGAASITTPSADANTPA
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SDGGTVRGSGLLPSLLLLLGLWGFAAL*
>TCRU_8097 DIS3-like exonuclease, putative
MDESGNTGTPFTPRVQAVLVRVVEKNRSFTLFAREVAQEVHISLRDKDQLFKQDKQVDGT
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>TCRU_8098 hypothetical protein
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VVNMWWLQTSHVQLFFPADGLLDARRLPHRVVVFPVRDTNELQLRLASIGFIRAAKGSPD
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EQRRLESECSAARHSREQLEEDMRQQVDMRNEMEGRRVAHLRRQLEWELRMERGRVESYC
AHLARIREEENKRTVMHREALDREIGAAREQKERLLGIISRKRRDTSLRSVFGTSRSTST
RETSLMRAHTSDVEVSGRPYKDSELCRVNEQCQRLSRLCAALRVERDELATFEQSWALGV
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>TCRU_8099 hypothetical protein, conserved
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FSDHWHHTPLTALGFSVDGNSLFSGARESVMLVWSMSSYAYRKIGCSLGPIRCIVPSYSN
GSQLLLACAESTLATLDLLQMRVEVFIEGVQWSTGEACSGLVVGRWMGQPAVILTGLPNV
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LVATSDGGITELCGAVQRMGEELGRHKSTVTPHRIHFMRCLPGAGKERVAVVDEVSGFRV
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SVGAAIRAAAAKKWLGEVLADSAYTAPPMSSVLSLYLKKRSGIPTL*
>TCRU_8100 retrotransposon hot spot protein, RHS3, putative
MELDGRAAMDANWDVLLEEFFKNPKKYICDAEALGEMQASDRYKRMERTVRDEMDMEEDL
HKLYENGVNNLLRWLVATAEVKASVHGATKRFLDAAAEEARNPKKSSAPRYLGGCYESVH
NARWSHAVELPGGEGREWMCMKEGKTVMVLQGSWRNS*
>TCRU_8101 hypothetical protein, conserved
MTQAAGRMARCLSLSVRLDPLRIEDVRGAICSETMPSSILGKAATSIPLPGDAVLKESRR
FCSHMEISPDQIRAPHAEQRIVTWETVGRNELSVFQPQHAKDALDGVRRSPFKRTLPPWN
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>TCRU_8102 hypothetical protein, conserved
MDSDHHLVLHTAGTEDGIPRLAGMLPRRKHAALALREADCDACTSACGTPLAAVIKQLEM
HRGTARAAAVTFPQESARTEWSRPSVLQRQPAPC*
>TCRU_8103 retrotransposon hot spot protein, RHS3, putative
MSSSLEEILLKGSNNNTDMKLNDFLRNYVGGRAAVGEDHNVTMEVFVQEPDAYVQDQRLL
RIIFNLTEYQALEAINRLHHEGVVSLEQWRDYEGKDTVTPIARGKINAALSRAQTSTPVV
FSKVLKGFYNSVYNASWSHVVKVVGSEGMGMEVKEGKPEQSWTYKEVGYTLEKNDDVLQS
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>TCRU_8104 hypothetical protein, conserved
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GCRAGYGAQLLARYLCEDPTMWTRWQGGFHTTRWKQANPLYAGQWWLSSVKAACLLVVEC
HRPSLPSKIFSGGPSPCKGRMSSGRCVGRNTQPRQGTRHYDV*
>TCRU_8105 zinc finger protein, putative
MDDGQHTGGLAFLAAPQDSLRYSEGSDVIHVLIYVSATRYQVILVAVIDGETVLMPAKRL
VDVHFRLGRGSLKSIRTAAREILLQKLRFSSESIVVENEANASDVASHCKHLVLSTLSAS
ELQHAHDGDPMEGFFL*
>TCRU_8106 Glycine cleavage system P-protein, putative
MSQGTTPVILRKVIENTAWYTPYTPFQAEISQGRLESLLNIQSMIIDLTAVNLANASLLD
QATACAEAM*
>TCRU_8107 pyridoxal phosphate containing glycine decarboxylase,
putative
MVETKAEPLKVKVVVGDPNLIDWSDSSLCGILVQTPDAMGMLHDFTTLFEKAKRHGVVSC
CGRDLMASVLLKPPGEMGADVVLGSAHRFGAPLGFGGPHAVFFAVKEEFKRMIPSRVIGI
SKDSTGCPAIRMALQTREQRIKRERATSNICTSQALLANVAAFYAIYHGSEGLKEIASEM
HSKAKILSVGLESVGHTVVNGAFFDTVTVNLKGITPEDYVTCCVEKGINIFVDYSHGTVS
ISVDEATTEGHVVSLLEAAGLQLPVIGVLSKLTEQKRAMPLQMLRKSVFLGHSILQKYKI
ESELMRYIHRLHRKDYGLTHGCVPLGSCTMKLSPAAAMLFLSWPEFTNLHPLAPKKQTRG
HSALCLDLEQKIRDITALDAVSLQPNSGAQGEYCRSSCDPLVS*
>TCRU_8108 hypothetical protein, conserved
MCEYPSKLQYRTYSELPPTSVSVPVEYKPNPPRFDACTLTLLTNSEDALSTTLLSVTTLS
VFLTVPGKLTAEDCTASTSVTAMSQCCGRASANTTTEDRITAWLTRIRTPADSAASAPPK
NRSAAPSRNVHPVSVMLMGRCSGILLRENVNTAPTPLNVTPT*
>TCRU_8109 hypothetical protein, conserved
MQHDRALQRRHIRHVDEGVGHQARLDLAEAANPQLRAARKHAVAQRHVQRVSERVHQAQV
HRHNDRPAEHHRVEARRRTPATNRHRLRQRHATHAALRTATGPRRRHVERQARLAHAAGT
AAAHAFGERRRQRIKARQRSRTAVARHHAHGGQAGHAVVAAALQHTAAGTVALHRHDAAR
DRRPGDKRSASGSAARNRHGTAAQRHTRQRRHRRRLAHRPHVVQVQPPAGTDRPTVAAHQ
RGRDKPLDAHEAQHRIKHREALAKHNAAAAAHNRHTRHGEHRVALQTETRRRRHMHRGRG
RTARRLQQHAVKHHRARQQVHVAANVHRRPARLQRPQHSVAHTQLRLQQRRRVQHKRRRH
RVRQPAQLRVAHRPRRHNRRVTDRHVRVCRQVVHKHKRAVAPGQPAHAHLQAPVTRRLAA
VAPHVDLRTAVAHTIPQLDAKRAGKHRRHVKHNSHAVRDVNAVHQHRVHGAANRDGSVHR
AAPQSQHHRMRRRHPRSSSSQRQHKKKRHTHSRNDPAPHTVPAARTRTHRRPHPPTQTRI
NRTAVAYRTRTVDRNSCLTNPFLQMENPKAQIR*
>TCRU_8110 hypothetical protein, conserved
MRGVHLAPRHVQHSAPRRHHARTRVQRIFATEHSRVQRNTATDKLQHRAVHHHRPPTSHH
GHESNAGHNQHGPHEPQARQHQHRCVRRGLRARKIHKRRRPRGNQQGVRHRQHGPRRERA
GQHKRTVQRLHIAHRQLHRPALVAPRRHRTAQRSTAHHVQHGAVQQRHVLHNDPHAVSRH
PRHVEHRTHAVQHNVAQRHIARASRHNERRPHRHALADEHTRPSAHGRRQRGSSHRHARL
AVPAAAAQARAHTVLHARRRRPGRVAVCVPVAVVAPSNVDAPSVAKSSHCVLLRRRQDTA
TSAVARHPQMRPSRERQAQRQHPWQQRSVAHKAQRAPSSGHGASRVEHLPRDAVVHVALR
QQHRPAGQTHRRIKRHRVVPRRRKFAPHKRHS*
>TCRU_of Trypanosoma cruzi region 5/Dispersed gene family protein.1
Dispersed gene family protein.1

MVALPPPFRWARDPQLSTHLSFVPVSTAQPSGFGGPWGAMLSNTTWVRNATNPSTVLELA
VPVHRGYFIGADETIVIRCDAAAVSGGCRGVLLGSFTIRSNTLPAAASALSAITGVVAGA
AAVAVVVTGGLGSVLEMQALGVFARMPCASAQERASTVALPYFLSVFAALDPLWMVVGNA
LLAAVFGCVHCGVTAAFQRWRGVDAATAWAAMRFPSLTYVVAHAMHLGIFFGSVLALAIP
DARVLHRVTGVAGVLYGVAFPAGLCYLIARHVGASFTRYWQFLRKPLHERLLYPVGYWHP
AAQQRMYGGMLTNMRGSYVYWCVFQLSVLCVVCLIAAVHPPVGGCHVQYFCMAAVLLAGA
GVVAFTNMMRSSFLTVMHTAGFVLLAALCVVSAANHLAPSDGGARAYAAIVLLLATVLLA
ATAYSVVVWYAEDRHWQELREPRRGGLEALLRDDEESDEETQKLHDRTSSSYASGTTVAS
SYRPPAPP*
>TCRU_8112 Protein of unknown function (DUF3682), putative
MPDGCNKTAITVPLRSVLLITAVEALAGDGGSPGATGASGGPGPGDAGGSGGTQKNSNSS
ENLESGASAGGPAGAGRDGGVSGGSGTSTGDQGTGDVSSSAAPPSGPPPAGPPAAPVVDT
SAGSGGGTAGFPGTNPSNTTGDSQTGNQSTAAAEAHNSSLPERPEGTTSGTGHTRQEKKE
EGEEEEEEDHEQQQQSDETQVQQHQQHEHPAESGEESAKDKNALRTNATANTGDSDGSTA
VSHATSTLLPLLLVVACAAAAAVVAA*
>TCRU_8113 hypothetical protein, conserved
MMTTVMTTTALRREVCALLSLALLCCCAPIFVTAATATGAAVQSTDLYSGASAVNVSVEI
SCADSNKMLQWRFPGQTNWTKCVSSLGAYDYTAVASSGDDDTVGQEITEYTTVIGNTEYS
LGTSSDMIEFVLLDSTSGASSRVEEESLCLSADRMYLTAKCNASCKSAGEGTTAFTMEFQ
TTNESGVYKKWLENKTKTNTPAAGTLGVCPLRNSVGRTPESVKSGTPEAAAAASAVQVTG
VEAPAAGQDTGSSSSAASGASSSAQTIEQGISSAGPQPGNTSQPPTGEGVGRTDASGTTQ
TPSATPASGNGGSSGAATAGAASQSGNPTYTRETNNSATTGAQDPGTSDSSAIATAWVHT
PLLLLLTALASAAGQRCGAATHE*
>TCRU_8114 Enriched in surface-labeled proteome protein 1
MDNANAEDANAPTNMGVGQDGTTVTPEVGASSAEDEETVGRKNVQGEEGIHPQAGNLIGT
ALSSSLGNASQGNNSDAGTVRESGLLPLLLLLGLWGFAAL*
>TCRU_8115 Nucleoporin
MGNKYEEEYGKVQLPPRRSEDGGLREGMLIIRADEDYVGAAGDRENGFTPHPARAFAEIY
LQPVVRSVLTAEQFMRWSKRELRLEEANLWSLVLELLLDAEQGSKYNPDAIGIADVQPHR
RWYVSHLSHIQELLQRHTLLRRMNIVVRWLEQTYREGNTLLKLSASRSHEEAVLLRQIIL
SHLRGGELYRAIDLAVTAGDCTYSCLLNAAQMQTVYEPWFHLTPLVPLFGEYGNGEVDQV
WAGNTHRLDNLSQLYEDSVALSNSDEGRSAIGGLDAIVAAVLCGNLEVMEPAFLAAGNWK
DALWCHLRAALVLCFTKTLMNAHHTVQPLYAGFIEKFTGSHDSWQEETARDVVQRLSERL
QKNYLPFASLEEQLQMRVILQFLSPGGVDWMCITDDLYTKRIDGARIISHLLLCLDTAYN
ETLHSYSVQVYSNTLAIALAQYGQQLAQMPLYSTQDAMQAVIAMNLHLRDTRQRAAVYAA
FLVACRRRELESSSRQDVEVNEAKLVQQFCKADPVSALHDEVMRLLNQKTEPTSLLTHNT
VAEAVMWRAMHADSHEDFVVALREALEACVSFWLAEPHAELDAISDVSGILRRNILPYLQ
EKNETLGDMELIEAHFWIKFAEVRSTADEHARSTAQLDVALGGGDRTLVFQLAQDESALL
RELHALTQEALSHGGALVRRSRSCVTAVTWIVQVFAEEVALSVRLASPGASVMMEQLRKV
FALVEQLDGLGYIDPNLIPRQSARELFDAVRAARVACGQKSHDLLVSEAKKTAAARQLPL
*
>TCRU_8116 hypothetical protein, conserved
MSGQTGVDGACDVPQFGWYRPCYLPSRDPPKSTFPPLSKVVVSERLDGNVSDEEALKRRA
ELGFAWELMRPITEVWHGPTIDDKVPPAKDYERLLLDTSSGSLR*
>TCRU_8117 hypothetical protein, conserved
MPQNPQPKPSGTKTTLALRSSPAPPVDSGKAEIAVVGSRVVRLLRDARASVRTHQRPDTP
LANAAPPRPKRGSRLSAIVVSASSTPSQLVTSAQNFDRAMFESSLDAAKGIPQLQLEKLA
ELKLWLANPHHHLWDTAVARLLNMVTSTNTEAQVVMTAASMLLRQNEVHQFSGLPFVIRR
IHGLCEGGSVGKMLEEILMRESLMQPLLQLMNTRELADTHTNVLWDVLEILRSCSANSGV
ILTQLVTLGVITGANALVKYIFSSTCDSPSKATSPSSSSNVLCTLLPSLCLLYRNLSTQY
SHLLRKLGSLDLLVDILDRFREDGVVVQAAARAMAKTVFEDCSLEHYQKGNRACRALVAA
LEANLLLGGLTVSRLCGTLARLVEGSRELRDWLMRHHHWVLVRLVQAYITPQQVATAVHA
ESPHDLEEAQQEDLLQNITWLVGVAAISAECSTSFVIEITPLLVEFLKDLDVKKWHLTFI
YTLMCLSNLSFFFDAVERMEGGNVALVEIYMTAGLILAGILFDGDTEATVEATRILGNMS

LTNAGRDWMESHRCDEVCIVFLGHEDPRIVYNCFGILLNLTAADTCRVASDPDLMQMLLR
HTGRYTREESIEAERIRENSRGITASSGDEDQGLSYTDQIADVVEKLLLNLSGLI*
>TCRU_8118 hypothetical protein, conserved
MDMFTILSASGDPVVIPRDPAIICQSAWLQAALDIGEEEGVVPIASTQTLQCLVSYMKHH
AAHSEDDEQDIELPVSCTCTSSPAGLGYDVHVILPPSDIAFLDDCVGRKNSWPLEAQELF
LELLVAADFVGHSRLMRVCAAYFACRLMSATESDILRWFAMQAPHDGRENGVGLPDEKKD
GLLLLLSDEDRLYFLREMRKVLNIEE*
>TCRU_8119 BNR repeat-like domain containing protein, putative
MAIPPTSLSKGNELFLLVGSSYFVFYPTTQHWIEGGGDIHLVKGEVAPSTEDEPSKRVRW
GRTASLLGLITELTKQLGLHHVSGAGGSGIVLERGWLVFPLTALKGEEKTVFTIYSVNGG
SSWDVGTATTLGYCMDPLIAEWEEKLLMIIECADGRKVFQAGEMWDAWTKAPRVLPRPWT
SEPNPRGLNFALGDLLTLKFGIRSVMLYTQKGFPQGEGKVNVLYLWVTENSRARPVGPIS
MDDDRERTVANRLLH*
>TCRU_8120 hypothetical protein, conserved
MYVDIQLVLRYQLNPYRPPHLPPPLGFEDCIYRNQRPRLREVFMELVPLRPGVDVNDALS
LGAAHGACGVQLYTEATGVFEEFPRNEENGLALIYSTVPWAREELQTTFDAGAEAPSLIV
DDVFISWATLGLLSLNELSDAGALHTEEDQWAGLFDCYLTA*
>TCRU_8121 nitrate reductase, putative
MGGIPSKKSVRNHAIDGVVKSSSKKAQGKKMEASEAATAATRKQTAKTSSKAIGEAQVQN
MITQEGRDIVIIHGKVYDVTSFTASHPGGEAAIKSNVGKEAGETFESMHGSKAHEKLEEF
LLGPLEVAPSVLTEFEVQRRISEDKRVLLIIHGYVYDVTGFVASHPGGEAAIMSKLGEEV
GEVFERIHGKTTKELAKDFIVGRLSSTKVDVKDAAPKSPAVSKAVIETKVLESVDVAVDI
KNITFSCPEKLRIMPGGHISVLVPDGSSNGFIKVSHYTPFVCEATSFTITVKKYPNGMTS
SYLHSLKPGDTMKYEGPLPPNWVVEEDGALRKEQEDKRHVLFIAGGVGITPIYTMVEHLL
KNQIASATLVASYQVPEVMLLRKEFASFIEKYGKGAGKDTTEGGEVNVSPRKKFELHYVF
TRTKEAPIVPETGNVHLGRFGAEVMKQLSPTVSCVICGPPSFADGVAKELVKNNICNYQQ
VHVL*
>TCRU_8122 ribosome biogenesis regulatory protein (RRS1), putative
MSEHQLDIGLLCITNVSLISGPQRPEEDLHESATHAMRLLLNECQELPTTKKRGKFDAST
TLVQLPQPVMLLPREKAPPRPKPLTAWEKFALKKGIALKRKKSNRVFDEEKKVWKDKWGK
RAREEREKHDWLREVGPNYVPNEEGGDPFLDDRRAKKVRLEKQKKKEEHNKRRSEHIARA
QEEVKHLSAVSKHLTTASNGKYDKILSRKKGKK*
>TCRU_8123 histidyl-tRNA synthetase
MSQSVENNALLAEIAQLKLLLAEKEALVANDDTGSVVKKPKKKSQKNMVETEPVQGCRDF
PPEAMRCRRHLFDVFHATAKTFGFEEYDAPVLESEELYIRKAGEEITEQMFNFITKGGHR
VALRPEMTPSLARLLLGKGRSLLLPAKWYSIPQCWRYEAITRGRRREHYQWNMDIVGVKS
VSAEVELVCAACWAMRSLGLSSKDVGIKVNSRKVLQTVVEQAGVTSDKFAPVCVIVDKME
KIPREEVEAQLAVLDLEPTVVDAITTTLSLKSIDEIAQRVGEEHEAVKELRQFFEQVEAY
GYGDWVLFDASVVRGLAYYTGIVFEGFDREGKFRALCGGGRYDNLLTTYGSPTPIPCAGF
GFGDCVIVELLQEKRLLPDIPHVVDDVVIPFDESMRPHALAVLRRLRDAGRSADIILDKK
KVVQAFNYADRVGAVRAVLVAPEEWERGEVQVKMLREGTGKEEGGAERGFAVPLDRLV*
>TCRU_8124 hypothetical protein, conserved
MLRGSSFLLSNALHNPGPFLDGALQIIKLHLAHKNAAADGNARACRAIESEFMREVEMFR
PFFTMSSSLTVAKLYTKKLHSALSYFRLHDDPLMRQLDLIIGKQSMRHGTSGHNGIFKNS
VATNSSALSFLEEREETVLPTELPHPPKPDPLTPPREGALKLPLRHRGHWVLREPEIAIT
RAERRSDPW*
>TCRU_8125 hypothetical protein, conserved
MLRRTSWRAVGYTPVNPDTSPMLAYSQYHWHYNLPQGMERPHGVNRTMTAPYQSAHSLVN
KYRGVWIELEMHPAFRVALEPQLRKLPQGRTIPKTSVDEVISDYINKAHLIQDEMTRDLW
LAKVLQHCAFQRSNEGMALWEKYCHSRFIADGATATPPLPLVKAILFYCSKIDHQGWSFI
FQKCLKNDWNYTPLFDTAQWNFLLKSVGRMGDEKGVRLILEEMLDVQADLDRVEARSIVI
ALNAVTDNDIYEYIKKYLFNFGERKVKFLRIIYSDLRGHGAGKLRIPLKENDKMFYHVCW
HSSIRAPRQFSPRQLYFDYTPSTLGASVHNPNAKIDDIVKDKIEKWKTEGLLPEDYVHED
RVYDRGTAFKNVARQEKWKKMPRIVKSKKMGYTGDP*

>TCRU_8126 pdz domain containing protein, putative
MGVCQAKGTHTKEEHNPSRGCGEKAHFLRKNIENGSPVTSPRNRELQTKATHYLRLFLEG
AESVFGGGYPFNSPDEQYHVALTFLNSCVEVTRMKFRLKTVVIVDLIEKIATEKKLKTIL
SILPDVKENCVDEGFARLLHMWFENNSGFSNTLDRVDDGPVMVGKNMNKNAKNLTGFSSI
LASYLRSAISIQAMNIFPKFVHDGDIMTVEQFGKFLRETQRTDVTDSQVREKYNYRFGGA
IHRYNFNTYLGGLSTNCALDPLRTKDVWQDMTQPLTRYSVNTARIENEADLTRALEDSSR
AFLLNLKKNEEGVLCSGTCPLQTILESIQKNGFVTNSYPIVLCLSPAKTISLELMDELAC
IITKDFSSLLAKGLMFEGSIISDPKFSPAALRKKVLLLGYQSRLKPFVGCFVADMNRDGL
GVRVTDVVEGTPAAKGGLSKDDWLTHINGEAIQNKQHLRERLAKFHLGEEFTLRKENLED
IKIVVGGIVDTDDKGASASLSNILFLKYTDGNSEKPWETQVLGGKTIQNSNLKRKDLDDH
FALFYSEGISANLDHIGIATEMGVQFIDTGILQEAQMWAHGRFVDNGGSGYLIKSDSGME
GTVTATVEIIAGPQEIKGVALTKGRARVYGAGSARVDGSKFTFKGCNDATVTVIDCEFAQ
NGGSFSFSAAFPLALLRSGCRVLPLRQTGGPKDLGVPTPSAYCYIRRDV*
>TCRU_8127 40S ribosomal protein S30, putative
MGKVHGSLARAGKVKNQTPKVAKQEKKKQPRGRAFKRLKYTQRYLAKTLKPGEKLHMNKQ
PPGKAG*
>TCRU_8128 Enriched in surface-labeled proteome protein 1
MVSVLLTAQLKRVKDVLATWKEVDERVSKLCPSESALEDTQTDNACSTTVKITDGLVGFL
SGNLSGNTWMDEYLGVNATVNKKEGSTSTDNGVTFTGRGAWAEWPVGKQGDNQLYHFANH
NFTLVATVSVHGEPTKEGSIPLMGAKMAGDDNKVLLGLSYDSEKKRAVLCSGGKTTDLRS
NWEPETSHQVAIVLRNGNQGSAYVDGQHVGDAQLDLKDIKGSKGISHFYIGGDGDKTREQ
EDVPVTVRNVLLYNRPLTSEEIDALNPNKASISPPEDLTAAVVVDTPSTAVGGPVAQKTV
SVSTPGGSTVKH*
>TCRU_8129 'Cold-shock' DNA-binding domain containing protein,
putative
MFFHPSALSGTYDFGGSQFVALGMSYPQPAPPPVGHTDHPPAEMRLAAPSYHTYPPTPPS
FTQGSSTTSYPGGVPAPHVISHARQDKSNNRKGSRQECESNLTSRDTSPGILSGSGWGLT
MRSSMSSTVSPMSTPPIYVVLQPSPSQNPRMAAAPGNFVSLPPQATLVASNPLSKENGTR
YELGEWYEGVVKRYNPMRGFGFLTATHHLKVISPSIPLRPQPQQQQRQKSTTTATKTTVP
PTTTAGGVATQLKTLDAKDDIDTGVKAHVVRTPVSVGDIFVHQSYIQMQGFRALSVGDKV
VFRIGVLPGKKAHQAVSVQRTQESGKNVAATASASKGDTEKQRSTEEKPAIQQPAAPLFH
TRQSLEELLQNLAKNNTSHDGEPASELPLSMHSLNAEMRVEDGMEGCSLPTPMFNRNFAS
FGATNALDEPETLSYTNTEMDLPDDDEVCDFLATFGGN*
>TCRU_8130 hypothetical protein, conserved
MLGALDHTTTDALHSFHDALQRAQQALQQEELRLAQLTQTVRQQQESNQARRDAIRSQQQ
PRLEALRREIMRIRSLLERQKEEAEAQQQHVEAVRRPRRDAEAESHAHKNSLQQLQRQYL
ANSAAVHAELLQWWQPKNSLLSLEAQVARKREEAAALQMDVQTLQEKLREYTGEHKLGTE
NSMAETAEDERDGGMYIAHAGEKKELTNDKENSDERMNSPALLEQKLLQQREERETFVRH
STETLTLRREDVEQLKTRLKLLCVDVEAADAAQQVAQQEFHSALNQQSDTRALCGVCGKE
ILCSFVS*
>TCRU_8131 BNR repeat-like domain containing protein, putative
MIVDCENGQSLFDSHDMGAMRTEAIGTLPGVWTKSKLGVFREGNLPMEAPITANIEGVKV
MLYTWKRCFSGEKKENVFHLWVMDHNRTFSVGPLAMDNNLELFHALLYSDGALHILQDGI
IKASNTISLVLLTEGLQMINYVLKSWAQLDSSFSELYTPTAGLVGFLSNALSGGDTWIDD
YLCVNAIVTKNAMKAKDGFEFTGPWVRGNMAREQPGA*
>TCRU_8132 hypothetical protein, conserved
MIQNFSKLSPSLPGAGLDAPVSTSFIGLSHDADGRWETVFYGIKTASGSTWEPGKKYQVA
LMLQDGHRGFVYVSAELVGSYATIRTPEMRGLESHASKLGATRETAAAVRRWRASFCTTA
HWVTMN*
>TCRU_8133 retrotransposon hot spot protein, RHS3, putative
MSGNQASAVPQGDDQRRARPESEDVTDQPAATRRRVEEARQPQWTMSSSVKDILLEGSTL
RTDIKLNDFLRSNLGGRGVVDTNENVAMEMFVLRPTMFINDSEILGLITASPSYQELERD
LEERKILLEAINKLQHEGVHFLEQWRYYQGKATLTPLVCEKLNGVFAQVQREKREANERA
MLEAAKVLEAEMLEGCYESVYNARWHHVVEVPDDTGMGMEVKEGEPPQSWTYKKVGETFE

KNDAVQQFSPPRPRLMVLTSEKAWPYSWVGNRRIRDCYVNCEVDRVWQIVKGELTKWFSF
RGWIDFEPNRHLLIGTPGIGKSMGAGSYLLYQLLHCDVEKLQVVVYVIADEAFLFDKTAH
TVTQYHTDEMSRSVIPSLRKRGMKGYVIYDVAKDGRKPSVFLVPSEWGMIVLTSPNENNF
KQWKKDKRVVPIVIDCPHRIDLKAMCFWMKHIQPTEEQTREQLEEQTGEQTREQLEEQAE
EQAMNPAQYWEKVEKRVDEVGPIPRCIFNVLEYNTHVPAIEKAIENINASNATDYMGVGS
DKIWIAEDVSHKIVKVLRMRAVSEIEVGYNAPVSRSAMIKITHHLTNMTPPVDILNLLLR
SFGYLVWAKLEQSGTATFMNPHAVDIIQRNLTELHPGGRSRSRFSVLRRNPRGHPTRSEI
LQELRGNPARMDLKYGVLYEPIVRNFPLVDALFFTESPRRTLVGLQITTANAHHTQTSTV
RLFKERMAEYFNGWEEFARDMSWEIIYAQHTDSTPIRGWQRCDDSANLTEAENREIAAFW
KKKVHQYQVTVTAEILGQNRPPEVSNN*
>TCRU_8134 hypothetical protein, conserved
MTLVPYTPSEWCDIGARLWDMVCQCGETQVQLTFINGNQMSDETLTVAPSATGLCLFHGP
VSKAWQDSTLIGHIANLRAPQIPNFETHVLLPAMGAARELGHQQGLITAEGERLNFDYAN
AVADVQNRNAQLNSQFQEAQINLSVRESNIAGAGNQVLELRQQLEADRAQLREREFNLGV
LNAQLPEREARLNALQTARDAETAERDESPATRHVANDGVTTISHQTGILMAGGVPSSAA
RHSSAAYRLSHGNVGRPHFHPSTPLPSRTSPLGTRLTMEEDRSFCAFDVTR*
>TCRU_8135 hypothetical protein, conserved
MRGRPSFSSIGEKTNALCDANVVISLDTRHLHAMCVREGITHNTGALQKTAEGLPHAAHE
CWRRRPHPTRHLPPILTDSAPRRRCSTRSFKLPDAIVEKGNGALCQRRSTVVRRITDIPA
LGQLYEESKRGGSRNVGAVNVGAENVPSGAIHDFLPHARTADERGELCGLFDGNRSRAID
PTAVRQDAAVHVGNGSNPAGHDDSGVTKNCGAIGDEASAPLNRGRDESSNPQPDRLEATC
CLTTRVDNGEALVGDCGLDSQKFHTGGGRDLNFGLVRRAEDGESGSPPRLAVREDTRAGR
LRHYKVMQDTSREGKAHESDDCPSRTSSGSLGCHGAFQRTGSVEARCSNRGDIQFGSTRD
LAVGEARRPVRPSPEYCSIFVEVHHNADPGVVAGRIDVKGETAEGQEPWLRAEERFFHDF
NHNQAATITRRATRTRLATPQDERTIPLQQVNVPVLNLEWIKSRLNPATLERLMQVWGLV
GRSPFPSVFLRQSARRLTEDSNR*
>TCRU_8136 hypothetical protein, conserved
MAEAASCLDLKASFFQVSLPRETRHLFRCRVEDGTLVELTRLPMGYKASPEILQIITSAI
AGMTTVVHPLWAAPPSVRVDVWIDNIRIAGSKSDVTLWEAQVLRNADSCHASLGEERESG
AAQYTFLGVQFDHTHRAVSLSDKFVRSVRAMPALNSLTIAEMEVMASRFLYAAAILGTRL
CDYYFSSRQCDDDYRHLTGELCWRHPRRTYRRQRLVWARGCDTPSRTIASESSSPPREHR
LPSSRMHRSMDGEPFLFQTPATLKLPEGNGRRSPFLSCRPRHERYA*
>TCRU_8137 hypothetical protein, conserved
MTAPASAVTLRGIPRRHGENVEPTVRTRSTSESSIMQISSVTSSRTASEPKRRSSIAERE
SAAAGTRVGDWDAAARRGTENCLRGVRALLFLLNIPPIPSLDGGEEVHVPGIDAVLREGS
RNDGTSVRRHVAWDTAASR*
>TCRU_8138 SLACS retrotransposable element (part), putative
MEEIQNDLDVIRGALARSRCHAAAAPPAAALHDEREEGHHGGIADNPRNSSHHPAGVPHS
PITGAAVDHDRLELKRLREQVSTLSACESEKTRLEVEMASKEAALRQCVQTSRTALQREK
ELQEQLHHAATSLQEKQVELTMWRERHQRLQREADLLRQEIDALAGQCDRLEVMLGELRE
AVQQAAGENDRLRKALQESQEERDALRRRQVEHDAVVEREAALREELQAVLATNSESITY
LTAARAEIEARQQYWAAVQEEHVALQEALGAAQAAVRVWEARFVLEQAAPPLPLGNDKTK
PEVLVLVDAEVEAEAASPRSVHNETSRNNNSGPSDGSRRDVCEEEEGGEEESHELLLAAL
EAKVVDLALHLQEQRAVAEAANESYATIAAAVTLESRELLGARRLLASQRPEWTHLSETN
QKLQAAALARESHVEALQELVVSLLEELTEQSLYCYELETQLAVRVVKGGMASHTPGSSS
AGETRRSNALHFLQKQRNLKFCASGRRN*
>TCRU_8139 hypothetical protein
MKLRIYFGPKSVILLDANDVETLTRQMARLVQLALPDLFSKFVFPHDDITAPLVTAHGSA
RNEVLARLIPERPVSQSENEANSNQSGSRRELQFQLILEAQTKAFGPQLIINRKQWEWTR
EFLRRELQSFDVGVHDASSDVVAGDGGNSKNSGGGEGNEAAIPLEVILLYRCSETGLLCV
CRHDMFAEAPSMQSVPQGVKDISVMDARGKKMGEIRIDFKHPPTLRSLKHSLQTLLCWPC
LMEISCRIAEKEGLLSIENDADITSFVHSVQHFGHQNICLVVSLPSHSCLPPLLTGTAAL
PIDDPQQGASHNNAPPTGLYDNFESVRQKREETQKMVALYVQLMRGLRINAYGVGTQQMK
ALTKHFSGNAVTLPETSGMKTLTAAEAGRKGTAAPSTVCDVSLPGDHEGETAVGRQGREL

LVIHYELDPVEVHITGHITEMELQSIADAILAVCARQNTSSEGTVENRFQRVSDSMFTLQ
LDKISFLGDAQVEELEACLVDVVKSFGCLQVCEATM*
>TCRU_8140 Ubiquitin family, putative
MVPCHNKDAVGAAEIRVAVTHAGQKMVLVFPAATATVGNLKNELARRSGVPREKQRLMFG
GPVLKRHRREGRNEVRLMDLIAAEPPGTAGGGEAGASLPAVTIPVMLIGSATAVPHINEE
AMAQLHRLVSTTVEVDSRWYRCSYSKGYARQVAFVCRTCVRSGRANPAHAICYACADVCH
ASHDVEEWGVRYYMRCDCCTAACWHNVEKNNKETENKNGEETPQGVQGEGEEQEQQQCCF
IVDSATGLPPATSVVPMNSKNRYPRTLSSWCYCECEENSPADDADGGGVVCMLCASCYWS
SHMTRLCSDAFRRVPCYGDVFEGVLVAFLCRTCDTLVCTPCRLRCHKDHDVDPEYIFPSR
KDGTGNGAPEGVEFSCGCRGCCSIAEFVPEEVVDDAALYMPMPSDVAIEIMNNDPFMGFI
CARCMQEYPWILENDPRQCYGGELPERVPVEQHKRIVSCGTDADAPCPSDVYPFHGMLFP
VDAFTEEMTCKCTPCREAYERFAPRATTATINEMMLPLHDNCDHCGHTIRDEQAFMCQTC
ELQHDRTFFVCRRCNRLRLAKELPPLGGAGGSAGGGDNQNGRTSSTHEAIDINPSVFNDY
DDDDNNNNNMAPNDDHDVAPWDHPISHVFMEDTYENLFSLCGMQIMHNLDAASQAYVLEN
IDATGASFEGAVQRTFGHTPLVFDPDEVAKHHQQLLQQNEESNDQNCGANASAVSRQKRS
RGNENGGSNKSRNIDAEGHSKEELSEKDGEE*
>TCRU_8141 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MGILYTADKKWETMFKGKTKKSGTWEPKKGYQVALMLQGKKASVYIDGASLGEEEVPLTG
EAPLELVRFCFGACGMKNSPVTVMNVFLYNRPLSSTEINALKDKAHTLNGPGRALAGWAA
LEGAAAREHAAVVGLTSAGSGLLPLLLLLGLWGFAAA*
>TCRU_8142 hypothetical protein, conserved
MRRVAGRRVSVCSIGSFTSRFFGDTVDTPEGIRDAIAAYERRQREAELAVDSRSVVFACA
ASADHRARIAAAEAFDVAAAALPRPPNFCFMSLSLDYEAMIDAPEVVWFNLCKANDVTTS
SVKPQQLHMIGGATRYQRPGGGYIQVLLGCIPDLQSEVFTFDAIPEEDDLQDAKRPPPAI
CFAFLDNKLALQYERVLSGRLQLLGSRFGGSPVVGGIFPPYQKGSNSKQTKASKKNKDVD
EGDDCEKKIDSPLSEMGDSIFFLNDRVYTGSAACMILRSAMIKGHHVEVVPSISTERAKV
TSVSSSDGVFSIMTLNERRATDVIRDVYCSRELQGKTSKVFLGIQHEGVCIPFSFVGYPD
NGTLQFSLPEGVEVHSGDTIELLVDDVELDSEASAALLIGMQKKISITHVLKDITVAREA
RKNIVASSVAGFHFSHGGMNVAARPEVKMTLGNSTTIFAPSVLQRCMGKYCPTSGFFSPG
QVFTLGKFTGVYTRSSSYSFLEGLK*
>TCRU_8143 hypothetical protein
MTCVAVEFNSCSVVYGGWTPEELYRFAPHTDVLAPVQGFLEIDESVVVRPRPSMMFATFE
TLRRFWDPHPPAMPSGAEVLRAGSTCCMQVSWKSGVSSRAVSDDLVPAKGVWLRFVSSFS
HRKYTLERTPRQLGILLRALRVSFPHLLVPACSEPNVQTARGLLDFVETHAEAVFAYLPL
LFFLYELSKKSVGNFFDTLEELVRRRQLNESNLLNALRPREASWFGWSAPKLTLKEDSLS
EDVVFMDTHAARLPDSFKVKYMFSQSRREALERARVAATVLRDALLENVEAFDAAVEFCV
NSSGKLLMYGCASWATDASEEQQQLLSESSTEDEKIKGAIAEFMNVASVLQGQIFGPILK
TLVDAIRTSELNMETQFWYLRSMLECAKTVVLNEPLITGAKGAPKSSQAAQNPVLFRQVA
ERYGKLRQTFRTFKLCLEEELLLSENAIRRSLVTCCVHCLHAFTTFYDAFEARHHTRLIP
SDEQRDASIHPLLQLFDTVKGQGKQE*
>TCRU_8144 proteasome beta 3 subunit, putative
MSILTYSGGSCLAMAGDGCFVIVSDNRLGEQLKTISMEVPKLHVINESIVLGLTGLRTDQ
QTFSEKVRFRNELYKLREEREIGGKAFAALISSMLYEARFGPWFVEPVIASIDKKTGEVY
LCAMDLIGAPCEPEDYVCAGTCAESLHGMCEALWRPGLGSEELFEVAAQAMLSACDRDSL
SGYGAVAAIVTRDKMTTRLINGRKD*
>TCRU_8145 DNA-directed RNA polymerase II, subunit 9, putative
MQVSLTHLDDAPMLFCERCNNLLYPENDPLDRQMRWRCNYCRTTEVHDENKLVYILNLKL
KTGTTEELELLAEFANDPTAQRDPTKRCRRCGENDVTCFVNPLGQPHEDMTLYFACANPK
CRHVWKSGESQEQ*
>TCRU_8146 pantothenate kinase subunit, putative
MSFHASQGGDKTDSILGAQVNPVYLKDTPNMEAGSTQVRALSYNFNILPRGCGGFQNERI
DNFLKCVNEYDVLLFQEVYAASVLPYFVQKHICFQKRLVDELKERGFTHYVISKQPSYPT
IFRHNVHSDNGLIIASRFPIEQCGSYTFGCNKRGSQSVRRGCLFAEVMVPLREGGSVPIL

FFNVHLRQDESAVATFSQVMETRRFIDSVISNLYAENNEASKIPLVVAGDFNINGIDPHN
GGKPTKIFMELMQELQPLGGGLSEVILDTHGYHPSTRPSKLFFPSQSKLNRDSLTPQRQD
FFFVTPAVDVRMACIKKFIASSRSPYVYLSDHFGVSATLCVSASDQRIPHKNSTRPLLKT
SMSRGIVHEHSNPLLSMKMQFIPLLLTAWAAMYFNSLTLCVLGAVWFLLWCFVSRIHALS
NERQFATVRSAVVEGKEAVTLNHPREYKTLQGVKSLAELWQKTVQHHSMLRCLGQNKESG
ESEWLTYADVDAKVRELGSGLCALGVVPGDVIGVDCQANREAVILEIACVMYGFTTLTLV
GRGNAFRTLIDEHNVKVVFAGRNNVASILTCRSRHLETVVNVHSFYDAEDDAVARDFGIT
LLLYDGICYNGRLRLVPPPLHVASETVFSLVVDTTTTNLGSSLSVVRMTHADVLRDICTL
VATSVLPTSRKKHLVVHFTPFSMVFNRIFVLGLFAHGSSVATSEGASRRAFTVFRPTIML
AVPSLFATSETQLKRKNERYGCVYSWLFEKAFQLRSVLINVHRRDSPVLRLIFFRSTQRL
LGGCVEKVVLCVSEESTSYRLEEHIAVCYAPCLREVFFIPSEGVFCVDGIPAPGVRVELE
PFDEPSTKNTFGQLTLVRHSAKHTLPIAAKWNDQRTLRLMGPPGGILLPLKGEYVVAAEL
ERIFAQSRYVNDIFLYARPSRPIIAIVSPNRDTVEFEWQQQHSMGVNNNGEAEGGAGSAS
LSWTELSRYASGLLLADFSCIAKLNGLQASNVPEYVHPHPHSFKDHGNFFTPYGKLRRDC
VTRYFTSVIERFYSDTESTFSPTPCYTSSGNSSDIDCAGTLSHDRQFSLQVPAAIDIGGS
FAKFLYVQPPGFFEIPDYMVHESSSLSERLGLRTFHFFADAPVLEEQSQGLRSSNVGTVR
FAKVPSKRIPDFVAYLEKNKPHNFYAEKFRKSIRATGGGAFKYASIAKKRLHVSFEVMRE
MDSVVQGLTLLIRSAPWSIFTVDPTTGIHYPHKLQSPPGDTLSPFPCLLVNIGSGISIIK
CLGPDGSHVRVGGSPIGGATFWGLVRTMTDVTSWEEVLEIMRLDGPGDNKNVDLLVGDIY
GYNAHDLPAMLSVDTVASSFGKLGADRFYEAMAGGSLRRSSGDDNGDVISPLPSPTVSSP
TSLWKGKTKPSAIDIVRSLLNMISANITQLAYLHSRVQNVENIFFAGGFVRDNPIIWSHI
SSTLQYWSKGESHAHFLKHDGYLGVLGSATMPTDSETASK*
>TCRU_8147 major facilitator superfamily, putative
MMDVRVSDNGDIIEERGCCGVLKEELLELRWRVLAVACFLTFGSYYIFDFPGSIGTGSGA
TIEQNFKVRGKVYTQEMNQLLYSVYSWPNTVLAIFGGVLIDKYLGIRTAMLLFTFLVLFG
AFLFWLGVYYTTYPLMLTARVLFGLGGESLSVAQSAYVARWFKHGRGMALAFGITISFAR
VGSSFNFLFSPKIAKAWSVEMAALVGIFSCLISFASCFILVLADIYAVRIGYIRPAPQEE
NKNVMKISDALRLPFAFWILSTICVFCYAAIFPFIGVGKNFFEVKYGYNSDKASGYISAY
QFASAAGSPLIGLLVDNVGRNTIWLITASGCFLLLHVLLIVTMIPGLVMTIAMGIAYSVL
VSGLWPSIPWVVGENVMGFSYGIMTSLQNTGLAVFPIIVGSLLDEYIPNAQNDNSSSSSS
SSPRDGQKDGGLPTLKGYQMTELLFIAAALVSLIASIILLISDKRHEGILTASSRRRMEI
ESEKRDALLESLPEEERNMLFLQRE*
>TCRU_8148 RNA binding protein, putative
MPSRAVLRKKARRESKHRRLEAEDAAVDAALLACYGAQSHLPLGAGETENGVETAARKRP
RNVAVVEAAAETVESMAGMSRKERKRFEAKQRFERQLARLNAAVGKEENTTATKTETAMQ
AAEAGTDALSPTRGETLRHDPKFKNGTFWRIRKERRGRTVFLGNMPARFTVQEVKDFVSS
VFDAYCARKNEDVNKADEEREEISVGVAVVDLVDFLPAPPRVKHRHMFVTLQSKEVAEQV
VKLLDAYKLDGVTLRCNFASDKAQRGEAIRRRLAAPRVRS*
>TCRU_8149 phosphatase, putative
MDKFDFLLSMRSPEFTRVDCDSDVSSFRSSSSSPSPAPSLKTRKILPPAYDEAECDLAEE
LQNCVHSGECNLSQLQLLQVPTNLPLDSLVTLVLSDNKLTELPEEMFLGEKCRHLVRFDA
NSNQLKTVPKSLFELPNLEVLLLDHNDIVTLPFDAVAQEGRTFLPALNYVGLEFNDLQKF
PTEFFTHCPLLNKVLLGQNEGMLEEPVPSDRLFQSVIAQRHKKNKKGGGDSRVILKVDNR
PRFVRQMEEEDWRTALPWLEVELHKIYPDKVLGFMYLGSLRTAQTRTVYRDLNIDYILTI
ARDLDVRVDPGMKHLVLPVEDIPGENILLLFEKAFVFIDKARKEKKGILLHCFAGLSRSV
TVAAAYIMRRYNVTRDEALDIIREARPAAQPNPGFMNMLLEYEKSLRGGKEMH*
>TCRU_8150 hypothetical protein, conserved
MTTGFLREAVISVAVWSAGDFFAQFYHAHREAAQRRLERGEKRRGERPSAGQMAEMLDKP
RVGLSAAFGLAISPFVVQYRRLCIRSLGHTERRMLAAFMTLSVQQFFMTPLTLLAYHNAI
TACRGGFTSPSFLRAHETSAQTGGRYDAMSVERRILSDLLPLTLVASWFVYLPLYLLAYA
SARHARGVCAAACLIPWTAYVSHIQSTLML*
>TCRU_8151 hypothetical protein
MARHGWISPHSFTSGRGSAATRGREGGGGGGGSSPVLGDYYCAPEGGDDESSIFDDEILM
MTDAEKEAFAELQSRLEEECLSQFYYHHHSSPSEGSGAVEGVKGGGGGRFHYDALHRNAS

GASIRIDGSQPVSSARLRHCRSRSSSAGNRSPLAYPSARRSREREAWYRNQLEEELTFRP
QINSTEVAARYMEASSRRSRELNAVDDAAETSQFRPVTNRLRTSSLSDHLSRYLRTPVHL
RLGRTASASSQRRGRQQLEKKPRECGGVQRSRKDRQLTEAFLRRLEETNQRRERNLQRIA
VMHNTELTFRPKLAPGTCRRKTPSVVAPRTREEASGGKTQLRHTSVGSGDPETEVSFPTA
SVRPSPHINSRSRIMKRSLNDLRLFELRRQQRLEQLRAEHEAMERQAVSGKPAVSIGSRR
LTETIFGGGVTHEIIQQYLQRNAWKRAAAIRAEYEARQREEESQLTFHPEVHPAPPHVHE
IAQELALNKSLTVKKSTPKPIFRFS*
>TCRU_8152 histone H2B variant, putative
MPPTKGGKRPLPMGGKGKGKRPASATRKASGGKKKGGARRGKKQRRWDLYIHRTLRQVYK
RGTLSKAAVRVLSSFIEDMYSKIQSEAVHVACINNVKTLTAREIQTSARLLLPPELAKHA
MSEGTKAVAKYNASREEAYAKAV*
>TCRU_8153 haloacid dehalogenase hydrolase, putative
MPTTSMQAECDKMRSSGDECRRKFSGGNLLVVATDMDGTILDPKHRLTERTKDTLYELST
RGVHIIFATGRHHSCVHATRRDLLEHYKRRSTARGVPDSPTTGYDGFYIISSNGARVHNP
NGDLIFLRDLDSDVVRVLYERFGIRDHGDDPRKVISVSAYQTEKWWINRTIMSDEESLAM
FGVVPELHPDLKEFPTTGVGKVCFRCYDRDILHQYEAEIKEIFHGRATAVMSSEICLDVM
AAEVSKAAALREIGRILNFDPEREAIAFGDSMNDGDMLCSVAKGCIMGNGQSRLKESLPH
LEVVGSSSEDGVARKLQEVFQIFHE*
>TCRU_8154 hypothetical protein
MPCLLQRIPGIHNVDTAPPTHTHLPLHQRLLLHVRHNEAEGVRHLVHSHADVLRRVLDVA
RVVVDDANNRTPSRAQRRARHRPRKGRLERRNSSRVQHHVRIGHPIRVVLLRHWKLPANT
ALTEPRHDQRAIQWPHQQTLAVHLRRLGKNHVLENVHLLLRQNVLLLADHLLAKKHVYML
PGPGAESPQPLQVIRKHLDSEGRPVTAHGHSDRTGRLLPARHFANVPWQAIKHAMVRHRN
DEAATGAQQQEQRAAKLAEHCE*
>TCRU_8155 Leishmanolysin, putative
MYLPGGGRGYGPRGGGAAGPRGRPGAGGAGRQPARPGAGAGSAQTLKLRAAQHISASTQA
AADGTLSTGTTLTVVEKQWRPPSWLGLMSHWGRRNAKDELMASFVVSGYYTAITMALFTD
LGYYKANFEMAEPMSWGSGAGCALLTDKCVTDGATLYPDMFCTDSSDATLRCTSDRQSLG
TCAIYQDDNIPPEFQYFATKQGSRRGAMMEYCPFIAPMNGTGCMDGDEAIMPGSVVGPSS
RCLTGENLRMGSTVVGDVCVQLRCGEGTLSVRYRGSEEWHPCAPGQTLTPPAPFTAGSIR
CPLFSDVCLTMLKHSDASSTDVESHPKHLAMVRNNDGSALAVTSAPLLLLLIVIGTVIVA
P*
>TCRU_8156 hypothetical protein, conserved
MGTSMCVPRRRRDDSPLSYFGISVSTLTVYEQRLVQQSTSYIPGVPILLQDIAFYWDSQV
GGAVAGGTTAAVSPDSIWIASVEKTINEFAKKYKLFSLKKNARVGKGSSDAKKRSSGKNA
SRVFDKPFNAFLGKTPLHAPHFVALLTLFLRKLPEPLLTSLYVRQAEDILSNKNLSEEEK
AQALQKSSRQTFMSTHPTEHAVYQYLKQLVQRHRAELIAAEVELLVRSMVREPNENVTEF
ILQQLRPVVGPVLTKSKRELPTDNKPQLNFPHELTSGVLGDGASNTDEEVYSPPGSHHSE
AAEEERVSMGSTPTESSQPNSARRTFSGETENTSGKKKNASGVKPPAEGESGLGSAMSCA
DATGSLQSSVAAGENSAGEAQSGGLPVASKTVKIDPTEEVDSSGSSSSSSSSVRRVLLPK
ERLQATCSEEEEKEEGRSRMPRNIEKPPHREASIADSVQAMSTSSVVLTHAKRERHSTPE
RREKNVPMDAESVSIAGGGGVTEKKAVVDVFSDPRGDANLDVQISKRREGPSLCTSSETS
HPPHDLSEGAVSPVNEEGIDGKYERQEKQQQAPLHKVLPSSLQKKPSQTQLLGSSVAVET
PGRLEDSNPTIFSGKGPFNEAPRCFVEKHPRFAALLGAKQLFLGKEKLPPKQIELGQRPT
GFIMESVDAETKGGDAEPLSMRQLLACTAEGLNEVDRRKLVHYECNDFFSEEVTDRFLCV
HVERVLQKVIYPVIVQIEQLTAKSESIERLLRTNGIVSPPCQAPKIVKQLEDEMTVLKDV
VRQVVETHSGAMEDILNLQQQIEEQRNRLECDAVGKQKWQSDALSAKEMALEAQRRCANL
EKAQLQSHQSCQYMSLKLRDLASEIERGEKESLGLKIEVSTLQRQAVLLREGLLSIH*
>TCRU_8157 sodium/hydrogen exchanger, putative
MKRGLRKFKGDGEKNAGHRLPQRRLNDSSQVLHVPPQNLPGFCGADEAGPNGQSLSCELF
VKFLNNANSGGAERYHSNSPKSQVLLEESFTGKFADGGEKQVMVELFSSAETSVKELGRN
VHKDEGLKPYSPLFLPSFGHSFSSLPANKKKPHCRQGALVWVSELSSSFNSREETRTPLR
ESKMGCIPDKESGNNEGEEFLLRAASQQRSWEKQTSGVPVFHLTPLVEDAEREKKFFDAF
SELSGDGERLALLHFLWNKYFQPLERRRSYTADNWDELRKIGKTASSYGFEVDRERLCVY

ITILWRKYRCFPCSFLLRAVYIILFWGAMYFCSPSAFSHGGLYFDTITTILFAGILGGII
SRLIFVPSLVCIIAAGILYGNIPRRAYLTSGISMGMSSFVNVFGMAVGVIRAGLSMNAQT
LKKQLFPYLLFGMLPLLSEALVHGFLCKMVLNYPNFNWAMLQGFIVSSAAPGVMAPALME
LQNKGYGTKDGPGMLLLTSIVIEASLCMLVIQLIVALEFSTVNTRFAILAFPLQIIIGVT
GGVFFGIFVFYAVFYVLFMEGERIPLENGIFKCMTMRHAAHVHHRCVVLLLLINLAIISA
CRYVSCVGGGIFMSLVLNVTFNTMCMQRGIRDHMEVRSEVLQSFAKLWDYVAMPAMFALA
GAGINVHDIFDRRYIFQSIAIIIAGMGARFIFATLTPFLTRMGFSWKELLFCGIGFLGKG
SVQGTMGTVALIYANEKFGEAKSPEEIAVAQKELEYASLVRNAAVLSTMIACPICSIFLY
RFGEKLLKRDAEDLDIVTTNRN*
>TCRU_8158 protein kinase, putative
MRENETDTDFLTSNVEVGSVLSQCAESRVHECNFYGYRAVCKHRFPKAYRHPALDQRLRE
QRTVREGRALARCLKNGVLAPTVFAVDRERCAIVMERIDGLTVREIFNHEQGNVAQGKTD
VSFLVSFLLRGMGEVVGLLHNADIIHGDLTTSNFMCKREFLEGRPSTENLASRTSSRDSI
VVLDFGLVMEKNSAEERAVDLYVLERALKSSHPFLEHVATRLVLEGYHRTVDPQKGSVTM
ARLEAVRARGRKRSMIG*
>TCRU_8159 leucine-rich repeat protein (LRRP), putative
MRGGTPAGRADAPMPRRPRPLPFLHPASATSTTRRREISPMQRSQMQPGSPIDGKASHPK
TIVFQRIHAPMVEKTALPEENLRALRQTRNLFLCCRGLLSFSQIRYLEHMTQLSSLNVHM
NAISRIECLGHLHHLTELDVSANELRAVDEDAFKGLYHLKRLNLSSNFLTVVNGFQHLPA
LEWLSLSFNELEDVRGLRRLPCPQQLVHLDVCGNKLSSLVELENALENCRDLQDLRVEIP
KTALVLPTAPPQLHLRENPFCVTELTYAERLLQRFQRLVVLNGVSCGYDPTAETRLRGQS
TANIEDCHGEPCWHPLDVTSPALVSSHITSPQQRPEATPCDAVLTDVSLGNASCRVENVT
SGSTSTTGPSSSERSGNSNIKKNMSESHSSHSTSLAWRAKRVSRSVITKVSIPLHKELHV
SSVEDGVFQEELQAKDELIEHLELKFKRSQEQLSLRVALEEDLRRNFEDVRRSHVALVDS
TTCEKKRLCRQVAALKDELSRRSEEAVILQRKNRVELEEQTKTLRECLLRQKKDSAAAMN
RLEEELARTRRGANNEIRELKTRLEEVAQRNEWLEQQNEKTQIQMKKWRNESNNNKMALV
ACETQLHFIDSRGCLQLEESLVRRQLESAAWNGLVTATATQLHLLRSENEFLVLCRENHQ
KAWEEYATSLQQHYREALLQSQARRKLPSTRVDVGCDPIGEYVQQQAVDEEEMRRVQTAL
SLTRQSEHLLFVENERLLKCVADKERELADASQQLQESEAMAGKMRDELERERDNLIRTL
HNLRESIQKKDAEFDEMETEAKLKIDEKRSTIARLESRLEDAEEEVANHRREAAKLRDVQ
DELKRVSAELYAVKQERMESAAAAERVPHPQLTEIVAALEETKEKLASSVMREHQQSLKL
TRAAEALTLLRGQLVRVDEDNSHLRKVLDEKMALLSAAEAEKERLQAHWRESQEAVRVRQ
RATLQAISQIMVGDGDGGV*
>TCRU_8160 WW domain containing protein, putative
MDGDAQASVSRGNDCEMTSGTGPNSAGDVACWSTCAVLTERLRLLQLRGKVLDTRLVELK
RECDTVGRGEPENTWDSKGLSTSTQDDDVKTWDVAHLGERPFSSYPPYSFVRVKTDTSFS
SVNGSNPQQVTRFQEANCCLFNATPAGHSKARDMGHSPSPPLIIVEVMDTGDAAPRPAPR
GIVASVTEETEPLTQTLLDETIATHQLKSDGNMHTERQEQISFLMDQIQQINVPARLASP
AANLFKRIHEGLCNQGNSETESVVLNANGTQTVESKGVGVISAAMDGGQDQPPSLPNAVS
SVENGDVAVIPAEVRRTCNTANNSQKNNFSSILSSVSMPQVLPDLFSLESKPVVSISAEK
SHHEASLSAVDYEDEARVMLQRGEWKEARDKKGRVYYYHPKEKKSCWNLAKELQLLAKAN
GETGKDALER*
>TCRU_8161 cyclophilin type peptidyl-prolyl cis-trans isomerase
MSYKPHHATVPTNPKVFFDVSIGGQSAGRVVFELFADAVPKTAENFRALCTGEKNFGYAG
SGFHRIIPQFMCQGGDFTNHNGTGGRSIYGEKFADESFAGKAGKHFGLGTLSMANAGPNT
NGSQFFICTAPTQWLDGKHVVFGQVLEGIEVVKAMEAVGSQTGKTSKPVKIEASGQL*
>TCRU_8162 hypothetical protein, conserved
MEPIGTSQLRPVEFCCCKENDGLGVSEDGLNKLLNACIDTPSTASFEHLIASTTEIYTKY
PSRHWFLHSRALANYGVQCLVDQKASQAIGLIRQAASIITSFEGETAVLHLRVVLANALA
CEGKCFEALCEYEEALGVMRNYPLESSLTQVVSGKESCVLLSRSYVLEDFDRFLANEEMV
QNALNQGKQELESCSNKAEKVRITWILARLNRRIGEKDASLLLYTSSLRTLLDTPDVEME
IRVMHDIGLLLCFETFDVAQGLPYLQAAAEMSFDTALGKLEELRQQNSTTGRKNYSQNEM
LPVRRAIFTLLDAAVCLAENEDLGKALGLFEESIALMNECGMHKHSAWARIKYADALTQA
SLIDKAIRVYLETMEIIQSMEHEDENLQVACMGMIVPVTVAEVEGRLAHCFQMHVGEYRR

ACIHFCLAIRRCGVHVRSPFTAFEEKHAFSLEEVDSETLCWMLENYASCCERVGRKDIAE
EVLERRVSVEKALGGSCASALLRLAQLHGAENAAKAVELYIQLLTLPEDGIEPDVLLQSA
YGFASVCYGSKDEELELALAKVTAMSCGGKKINSVGDVSCDGPVSQNPNGIVISSFKRSA
KVIMASHAVEGTRSNGSSEDELKALMTLSRGGFFCQRRGDEAGAEELYSLAVEYTLMANV
HNEEYARELAIMLANYATVMAHKDMQKAQELYNRAVEICPTEENVSAAAASFFVLTANYA
AGRACIQRMIDAVTDRVVISRLYGKIAWLGVVCWDELALSVRQECLQHLLFALGLEPNNF
FLTLTDCHVTPIGGFVSVEFKQDLLSGISSSPDPDTVSLACYVAQTKLPHDARFINTCYK
TAVMRFSYSTTLLVNYAKFCADYGAGTLARKYYAAAFCYCHKDPRSNECYADYLAFLNRG
EQQHVPLQQEQIVAGESLARYQVERSTCDMSRHVRGQTLTLYGKYLATFMPSPSVPALLF
EEALRRNAADSRATALYGSFLWNVCVRALDANCTSDVKEKIAVKVETLYREGLRHQPQNV
LLLTSLGAFYVSMGNRFDDAVCVLDQARKLSPHNVVVNRLLCAAFHEEWMEEEKRMTAKS
NARLQSLLETTRQLYEVAVQLDPSDRLTLTRYCQFALHGLQNAALAAELMQRLRGLPKA*
>TCRU_8163 isocitrate dehydrogenase, putative
MMQKIKVAGTVVELDGDEMTRVIWKMIKEELIFPFLDVPIEYYDLGMENRDKTDDQVTVD
AAHAIKKHGVGVKCATITPDEARVKEFNLKQMWKSPNGTIRNILGGTVFREPIMCKNVPR
LVTTWKHPIVIGRHAFGDQYRATDLVVNGPGTFEIHFVPECGGAAQVQKVFDFKSGGVLM
GMYNTDESIKDFAKSCFEYALSKKWPLYLSTKNTILKRYDGRFKDIFAEMYKASYEAEYK
KAGIWYEHRLIDDMVAYVMKSEGGYVWACKNYDGDVQSDSVAQGFGSLGLMTSVLMSPDG
RTVEAEAAHGTVTRHYRQHQKGEETSTNPVASIFAWTRGLMHRGKLDQNEKLVQFSMLLE
KVVVSTIEAGFMTKDLAICIKGMNHVTRGDYLNTQEFIHKLADELRKAYERSKI*
>TCRU_8164 hypothetical protein, conserved
MFRLSCFLRFVGKEIAVPASVDLALLRKILCPTIQPSELVSFAPEAAVLVRRMSVPQAVT
ILELFSRYGVRHEDLMLAGLWNVFKAERPLLSGNEEAGLMQDFAACTATCFRLVFQEGLV
HDPQLLAIAFGRCVECAPHLPFRGIVDAYEGIQLFGRRYFTLAEVALYSGGADGDPQALD
SIKEPSSSTALSSQPNLVDVLCGELESRLRLVVDERCEQDTSYVVRLLQALSAVGIMDAN
VFLSIRKVIEFTKITTKTFLDILISVHGIHTRVIDVLDHEGDDEWLRSERSTLVRVLTDK
LLARNLFIDRRRCDPQFVLRLRQLFEVYPALADDAPRLWDAVRVVRVAHKHATRPNEKKH
RLGGALFKSEYAVKVKPIIPDRSEAERFVPPQFKNWSSPAVKNFRHRGPATPQKMGFGTR
RISKNYIKEKRRKFAPAVW*
>TCRU_8165 hypothetical protein, conserved
MGSNRRTRGKPKVGGDAEDDGDSDGGESGGATQGSKSLPLSLIPRSSASKAVQPRKLPPL
AMGPPSQLLAWPAKQKRIAGVSRAPLALQLEAFIRREHQLYLHEHRQCTHADTLHIVREA
FSVLTEHFMEYRGVLSFIREEYEATVDEATNELRRLRTLNLEAESDRSFYVMELMRQREG
FTTVISNQQAQLQANQGLILSLRDQVATLEKSNSELVTELRVKGKELEEMTTTSKLLANS
MIEEAARNSQILQVHRSDERELGRLNAQVNLLKEKLDESDKRFNALLRQVMFENPVLTRR
DECNGENFNEAQLPLNSEAKKDTKETDQSVVALQRRIDDLLLAYEQLKQQTTGSKVSSTT
EYGEVLRSGESSCPPQDSGVIVMDHVNSSSKLIRSWLREENLTEREVDAMDYLLPPGKCE
EDPLSFLKICHPVRNLRMKKRIVISMLREFWSSRQTNLHFSLKSYFMEWLRKKVGPGKVA
EEVGLNIFSVCQRNFDDPECRAALLTFRSFLPEDVVLTWQKDIKGLENACRASPRVVNDT
IQTALVENAIRVIMPEKSYVHMLELRLYLWRVSKGLEKVPVDMLFNESSHFTYILRKQFL
YEVEEFTLQVVEAIRSLSEDSTTVSLQDITGAISNLDRGIPRGTLHRLVAEATQLTAMDV
ATADANFRVRLQTVLHRFRSSVLLRRATPPLGDDPTFGRRKSNGDDDGMRFIPPRADSVN
*
>TCRU_8166 hypothetical protein
MAGAFSLFIVILLSANAAMGILGQVTVSKKTDTKTVGGTGSPTVSENIHSISVSASVSIS
VPGSVSRSITLTPSHPNDDSSSASSESASSSSSSSSQSDEGSLVVYFHVMNKSLTPAELK
ELLRRSLWQNESVEMGPGNVFSENWIQLSFGLLSKAKEAYLAANNGGLPGVKGASYVAPE
TPSEKKSKVVVISVVVVVLIGLAILILLGVLLYCRYFREKEWILGRYDEDYAMNSVTTPV
NLNELLLTNLAVDGRNSQDTKSQARRGKI*
>TCRU_8167 KREPB5
MKRGVLAFCAAAPAAARCALTGRRVEDWEAHNRTFEMRVFELLKNRLASPTEPLPANQVY
VTIANPCRLIDEFNFAKTTRRMDRLRISLGFLRRHNVLLHGLLFYVKETKTWNTTAGFGR
LALFGESLLRHEVRARTLRLFPSIDSVTYASLTASMLNEDALCTIFDRLMMKSLVGAKPE
GKDRDWSLTKEQRSSMLCAIVGEMSWFSSRTKATDRTHNNALFPPSDALILHVLCCHVLE

SLPAELIYTVVEPRVHRLKEVWVNEPMSIPSQMHLKPRTINALSLSLVKKPISEEERLRK
VAAQAATVCFPSLSSERVVGSFISKMKPRWNYKRFDERRYQILGDDKRCFLPVFSSPTPR
DSGACAVVTLTDERRRELVSPAFKPRGE*
>TCRU_8168 RNA-binding protein, putative
MFDADASPERPVSPVSSASTAEVTAGHDVSTINRTLDGSFIHDDGHLMEYGSKHWIRVTQ
LDPNTTSKSLKYMFYPYGGDEAFVLWDNGVVGYVGFENKYMADLGVEKMDAFIPCRQTQA
LCVTRVTLEDFLIAKSTAYSQKGLVPLLYSDCPVHFITQFIELHRQPCCCAAELVEEIRR
APRPVLSRVLSALTELRSNWIYLEEFREALVKQLLRHIVKDDSTELGANCGTFLGELFVM
GLLTGDPFYLASRILQRGVHCTSQIDSICRIAHVCASMPFPISKASFWALVGQMTMNVSD
PLRAALRGHMRQFQQSMELFPSVQSVIPKNSWSFAKENNGSRLSSDSKSRTLYISHLPPL
LPQQTLMELLSMCGVVNKVRVCRGSGYTTLFAFVEMSTAREARATLRLNRMNLLGCSIRV
QIARNSIQDTQSEDAIVNTDGTVKRGCLFSQHGRSLAVAAAAGEKCISI*
>TCRU_8169 ATPase, putative
MLRVPTRWICSSSPAALVQVNDGPVALCCIIAAQHEAASWEFEFTITISPQHAVRITAQD
FSSVEKHNICFLNDASSRKRRFVESPPAIAGNWDVLQIQTPMNTYFAKTIILEGPRVSLR
GFLDRLFASMIGHYVIVGCEIETENGRYRVNSVELQSGYCGLALVCGTTRVKLNHKPAVS
RHLFSRLIGLDEQVREVGAVIRTMERRPGSWIGVRLYAPEGCGALALVRQCSAESHAALV
HWSPTGIWSQKGDLWGANLVILCIHCMDAMFPLSEDALAKLTARALLHDIGKLTSKRNGA
RAAVVLLGITSNSASEAVDSLFTVKITLDLPDVYTRAALLAHVRGGEDKEYMDEAQTLVG
FSSAAVLEVAQNPPRGYRPPIKALHWSEIGGLKDVKERLRCALILPRLRPELFARFGVVP
PRGILLYGPPGCAKTSLVKAMCSEGYFSFIYLDSATLISAFVGESERQLREVFRKAARQT
PCIVFFDEVEVLGGKRGAGSHDNDQSRLLSTLLTEMDGFSSSSGVCFVGATNKPHLIDIA
LLRPGRFDYLLYVPLPSRDDRQEILSRSLAGTSADVDALADATEGFSGADLTSLSSEVLL
ELLEGPGENKKEGNYTSDGGPEPSCLHDAKAITDLFLARVKTFYKTAYDVAEIEKFHGDF
ASLCGAV*
>TCRU_8170 Enriched in surface-labeled proteome protein 1
MVYVLLTAQLQRVKDVLATWKKVDERVSKLCPSKSAEKDASPGIACSTTVKITDGLVGFL
SGNFSENTWRDEYLGVNATVENNGAEDAGAEPAENGVKFTGAWAEWPVGEQGENQLYHFA
NYNFTLVATVSIDGEPEGDTPIPLMGVRLDGGEKKLMELSYESEKKWRVLCGDGKIKRLK
STWETRTQYQVAIVLQNGTQGSVYVDGQRVCGSVRSELKNAELKEISHFYIGGDGYNTER
KDVSVTVTNVMLYNRPFSFSGENADVEEDGDSPSEDPESAEANSPSVEGEHIVALPAAKP
SEAPEEKTALQRSRKESEARQITTGGKPAATQQVPTAPGLHAVGGATGDAGNVYRSGLLP
LLLLLGLWGLAAL*
>TCRU_8171 retrotransposon hot spot protein, RHS3, putative
MSRAVKGEVIFDEDIRKLCDKGVHNLPGWSLAAAEVKAAVHNSNKHLLDAAAEEARNPTT
TSAPKKLEGCYESVHNARWSHAVELPEGVERKKTGTGMGVHEGKPEQSWSYKKADDAIEE
NDAVQQFGAAPPVLMVLALEKGWPYS*
>TCRU_8172 retrotransposon hot spot protein, RHS3, putative
MAAGSYLLYQLLHCDVEKIKVVFHCFGGGDAYVFDKTTRAVKRYSDEDMCILELRSLRGH
GRNVYITYDVAKEGTPPPRHFAPTSGWGMIAVSFPKVANYDEWAKQLQAARVIVNCPDEV
DVRAMCTWMRRDETPDKQAEYWKKVKKHMYLSGPIPRHVFDEEAFTERCGAVKFALQSIN
EVTAERVPFTGR*
>TCRU_8173 retrotransposon hot spot protein, RHS3, putative
MTLVGLRMATAGGRHTTASTVRPFTECLAAYCNGWEEFFRDMSWEIIYVQHADSTAMNDW
RRCDVVNSDNVSDIESREIRCSVRKRCASTKCQYRTETFEEKKLSEVCKDNNNGKLD*
>TCRU_8174 BNR repeat-like domain containing protein, putative
MRRPQTTLETDPFCFSQGDRTAFIASGGSGVVVEDGTLVFPLMAKNEADDVCSMVICSTD
SGSAWALAVGMSSAECLNPASPSGRDHFS*
>TCRU_8175 Mucin-like glycoprotein, putative
MMMTCRLLCALLVLALCCCPSVCAAESTENTEAEDREAEPEGNGTSLLHSLSKARPEDEA
IGKAAILPSAVPEVPRKEIGNSGSPSNGSGAEQGRNAGAGPASTAAGRESVDVSNTLQNH
DTDGTPVPEIGTRQSAEEASQEAEDPAETTTTTITTYAPTTITTTTTKAPTTNTEAPTTT
TTRAPSRLREIDGSLSSSAWVCAPLLLAVSAMVYTTVG*
>TCRU_8176 hypothetical protein, conserved

MVRQASRRVVKGIEGSGVFCVFFCVGGGVLLAVQNTTTEGSIEQYEDMQKRSRKKKRRSQ
QGMLLSLLKTFPVPTSPANSLHSTDEMLRGRGSAKEVSVGGGFRCRLLDEPFNGVQWVPV
MRREMDFNGNPHLSVSHTDDQRIRLSNPVQSFGRAGLLNRAPSPVHLAISFRSPTLLNIF
DIHSGTPPMDATTIRAHTVTAGAQLSGGVERNIRCGSKIVCGYTDDAKMVCAVRVLLVDS
VMLKKLKELVAPSSFRSSPRMSEHGFEGTRNSVASKTTGMLSVELSVSNPSLFQAVEEDS
KNDGNGGGNSNESPLNYFFLRLQQGLEEAFLRPLERGIVDVPSEDAADDKSMWICSPSFA
RSRHLSKNTEDTVSAEDSAPDSLGKTEGEDEACVTLSPPTHSVVVSGSAGVGSVTGSSLK
TIALEDVAGQHTTSDGIHPNDTVNFVDMKRIDGGNAVEWHFPIVGVKVVSLNPEGLALRE
EGRSTSFTFPKRRRTNTAATSVVAANSNLSQRRRKPGLCLGESPTRRTQRVSRHSSKLSR
VPSGLESLSRSSCTGKVIATSLSELTRVKKGKHARVDRTKAGTLPSDAPQVDMKTSKEHG
RTAGLMEQFEAKSPLFAIALSMPIVRQGNIHEVLQEWIRTQSPSQLLRETAIRNIIHAVL
QHLVVLHRRGRAHGSIKATNVFVTSHVMEALNAMKSYSPNATDPLPVSTGMGNASRLWSG
VTLDTSEVGGGNVDAVSRGSSNSSSGGSIGGGEGGGICVGGGGCSRSTEVFDPLEWTKHV
VLADGYYAQVEKIMKTSLRESFNTTALNSVVRSNSAPLQLTKLLDSTLFLENMSPEYAGE
EMDALQLFVLQEEEYIPPPECITTEEGLTGVPSSEAKNTSLQPESKNASGMGSAFPFRKT
NNTRNPICPFSFSHDIWMLAMLAIHLADGGCPWWMKRHHRPLPRLRCGQWSVRFAAFVQR
CACADPARRPSAEELLNDKWFHTALSEEKNEVIPSLPPPAPSQQVLLGGSNTFALLSRSC
RRAFYDIMLEYNEYAEEWCTRFSQAATVAAKREKKDTFPLSTSNQSGSFAANTGVDEAPE
LSMTNRMEQGCSGLFFPPNGNSNKNSSCNISRSSHSSNSTRTDSLASRSGNSDNMSGTSP
RGRLQSPSGFAGGTDNPAVDGHLMPSHQTAPFFLGAVGVALEMCGDEASPDAGDAETETC
RVSSSRQGGGGGGAGKSVGGSNSSPPRQGYPPHTSSFLNATLDSCEEHQRLIGEFLQAFW
NLHRECRLAADLWCVSLLKHMRLDGRTAELVFPLITEETMPFFAVSDGEVYSMAHGRSNT
AHIKGPTAAATSPQEVVALSAAGKAPPSPSQQQRRTTASISPVAAVATVSPTAFHNYMFC
KWCVTTSWALQQDGRGGGDEGKR*
>TCRU_8177 hypothetical protein, conserved
MSRAKRDGSKGAVAVAPPPTKRPRSPHCDVDDDDNKGGGGREIKKHCHEGADADVCHGSF
IVADLPSNMAAIYTRTLRHLLPEHKKHISDAGIMEEAGGATLTFEVPSKAVAAAMFKRLQ
NAKIYGRRWKVQYYPLSAVQCAKKACLVDVRLVPAAPRALALFALGGVQGFLALVDSNEK
NDTGANFSRLSTGKAATTKITNSSTTSLNKDTTAGISEQRDVRRRSKKKTTKKKTNNEIK
SGDDEDHDIRASEMPFAAATPMEGSDLVEFVVASFVDEGSALHARAVLSGRLIGTSGVRM
FLERHR*
>TCRU_8178 hypothetical protein, conserved
MSRNTKEFNELADKFTKVYDQQRRDLELCLQSRVNDDINFVCQKQKGAYLEGIAQVFCKK
EYDAGVKCQKAAGERWSTECFKENVAFGQCTDTVLKKLYIYNIERNKKNPAAN*
>TCRU_8179 FtsJ-like methyltransferase, putative
MDMNMGRAATGADGFAANAGMEFGACRRWREYLQNTSAMYSELERERAAGWQSEALDWWY
QQRHKKEDEEAVKRQGGMTAPSSTSFFNSDIVKLCERYCEHAERVLMRAAPSYFTPFSEA
TRGPPAGRATEKEKEEKEEKEEQSSPPTFLDLGSAPGGVSKFLVTRLRWRGVGVSLPVSR
GGIASDSSWLHSSTTSAQYEFIEGSITENDWHESIQGRNFYFVNGGAVQDHGQRNAEKLS
NDTEDGGGNHAVVVSDDDAQPVLPWFKFLVPQLRLAVEHVEEGGVIMLVFGVPECASLSI
LLALVQPLVHGGIHILETMHLTKSPVYILITGVCVKCEEEARAAWDKVLALMTQESRDFW
LGETEEGLRLAKTGFAQHRKGLEAVWEKTTSFLRRRRLQAERARAASMNWKRIMKRQRD*
>TCRU_8180 Enriched in surface-labeled proteome protein 1
MSRRVFTSAVLLLLVVMMCCDTGRAAQAADSTSGKGSSPSPSFVWRDKNDKETVDSLYVP
SLVVMDGDVFAFAEVELKKNYDGNTHFFTGIASELLALSGQNPKELAAANVKAKILENCS
SQEEGKCPSQSTKQDISKAK*
>TCRU_8181 Putative intraflagellar transport protein B2
MTSRPVTGMRFQTIHGMGGGPLASTMSSSMRPITTSGGGTTLGRIQAQVQDGNFTSTVYG
YIRDHQYDEAIEILLQQLEEFPRSRAAISLIAYCYYHVGDFDESARMYQQLVKICPNVEE
YRVYLCQALYKAGAYAEASKLCSMIISEQYEMRLMKLQASIAYEQGEIPQTKSFLEKCPA
EDPDVIILQGCVLCNEGNYEEALEKFQEAQAGLGFKPDLAYNIALTYYRMQQYGPSLKHI
AEIIERGIHEHPELNIGSNTEGNEARSVGNTQLLKETALVEAFNLKTAIEFMMKNVQAAK
EALTDMPPRLQEELDPVTLHNTALVNMPEDPTSGFSKLNFLLQNPPFPPETFQNLLLFYC
KYQYFDLAADVLAENPHLSWKYLSQKNQSLYDFLDGLITAQTSPAEAYRKFDILAQHHID

LLRKLTKKLQDAKQSHDKESLRTALRNYDDALEEYIPVLMAQANIYWEIENYPMVERLFR
QSAEFCSEHEIWKLNVAHVFFMQETKFRESIRYYEPVVEASQENLLNCSAIVLANLCVAY
IMTALNDKAEEIMRRIEREEEKLTYADPDKQPLHLCIVNLVIGTLYCSKGNFEFGISRVI
KSLEPYHRKIMTDTWFYAKRCFLALAMHLAKHMVVLKDSTFEEILTFFDQADQYGEKIPA
FVHPDPTKQDTSTRNTVRWEARQLKHLYLQLAE*
>TCRU_8182 RNA polymerase subunit, putative
MKVKILDCKKHEHSAGETLEFQLAEVDNSFANGLRRVMLAEVPVLGIESVTIIQNTSVLP
DEMIAHRIGLVPLYSMKARRMQYARDCLCGGSGCGECQINGELKVSCPSNKHSLQVFMDS
LKIDDEEVYPVSSEERGVWLLTLGRSQELNLRVVIRKNIAKTHAKFMPVATVAMRYASDI
VLNPDGFAKLDTEHRRQWVERCPRQVFRYDDRTGQVLLADPDACIFCRECLLKEPPFNKL
AEPLVFVRHKKDKRGYYEFTFTVESTGALPVLQILYDAVEVLRRKLERVRDGLTEDPNAD
EMVQTRPIGGAPTAPVVVNEDILERDGAEDNLTFVMN*
>TCRU_8183 hypothetical protein, conserved
MRPSPPQPAGARHPNARLPRIAPVNRPAITQEGIARMLETGKLSADVDLEKLLINDKSFT
TRKMKVHPYDARLVPAVMTNLSPYNKMNGFVLDVADIKKVPGKLNLKDLKEWESGERDHS
DVPYTPDFSLRSRSSQTQLASPKREDTRTYAELLDVYSMHEFIIRKGATLRSTPEFASFK
RRYAASWGNVELVIRRLEEFLKSYGIELAYVDGRKVVALATFQIDDLLSREEMLQCFANR
EELEPLTSSVTQQFASGVDGRQLAARKIQATWRMYSQRIAYRHLLVGTQAAIAIQRRWAL
YRSHSLTRKTIKTQKEARLLSWKRTMEEFTKSWPKIKEGRRTIVHLPSLSYPRFHAKHVP
FYFALQMGQLTRVADLRDPLVDVVMVAPFRPEPEVLEYYFTLLEDSGVVNPRGRLTLLVP
EDAKRLPSVLSLTRLLLLSSRLMKCLSSLCKNRPAYLVPGVIGAEELSLAIELNLPMLSA
DPTIAQAISSKTGTQRLIELAELPKPVGIYGLRDRRELLSALASLMTEHKEVNRWLVKLE
TESCSRGHAYFDVNRIRVLKSSDESSKTYDGVLAELMEYAGKRARLVHPNSYPDWEAYAA
MFDVVGGCVEAVPNRIRTSLTANLFIEPTGVVSLHSVVEPMLAPAFTVMGCRFPFQNFVP
YAAVRDAALCVGKAAFRRRVMGYISVDFVLQEAGDGVAAELYVVDVDLCLTNNAAAHLFA
CLVTGSVYDVETGSCANSNKNESLAYAYSGIIHSPFLSAVRHRTFFSLCRSRGLSFDRYR
RIGLVFHMVDVLLCGCLGVLSVGTTRSHVTRAMKEFQNLLNLELPKQSEHSAESNFVYFS
SAIHQLIRSVSISKEM*
>TCRU_8184 26S proteasome regulatory non-ATPase subunit
MAEDKDAVSICALSEDPKEKKGNEKKPREAEPQKLSEEDEYIKIQVELLVTRAGDSNPVL
AATAIQQLIELLRTNKGGSVASVPKPLKYVRSMYAQLERALKDTTDASVAVRLHDVLSFV
AMTIEFPDGRRASLEHKLQGTQDDLAEWGHEYLRFLAGSISAEWKERIGKAEGVNHLTGF
IRQIVSYMVSHQDEPTAVDLLMEVEDMNAILPLTDSHNHRRIASYLAAVSKYLTRPMDTA
ALRVVYDIYVKMESYNEALFVALQLGDRGLVKGLFEKCYSAPARLQMALTCARYRLYLEM
DNEEEELLNEAMGNVRLSQLYRQVAEDLDSLAPKTPGDIFKTGIDGHELTNSSDSSFKLV
CAFASGLVNCGFGKDTYLTEKGALWPYQQTENRLIATTAMLGLIHLWDHAEGLQEIYKYF
YSDATNIRAGACLAAGVAMCGVTSPFDPAFGLLSDCVSSPQKEVSIGAILGLGYAYVGTQ
RDDIMELLMPILVDSDQALEVQCMTAFALAMVFVGSADEGLTETMVSCLMEVVEEQLKEP
ALCYLILAVGCLFLGKQEAADTLLDATQTLSPLIRRYTEIVVRSCAYAATGNVVVIQNFF
HAIAENDEPDEPVENAENNTENKSKPTTKPTALNYKAAAVLGIGLVALGEDIGVEMAKRS
VIHALLVDTVSKGGSNLSGRHAIPLAYALLSASNPSMPVVETLNRLSHDSDAPTAINAIL
ALGIVSAGSNNARVASKLRNLASYYHKERFALQHFSVRLAQGLTMMGKGHLTLSPLLNDR
TLVSPTALTGLLGFLHSALYCDKTILGKYHYMLLTLTPSISPRMVLAVDAQMNVLKDAVQ
VRVGLPVDTVAVAGKPKAITGFQTHSTPVLLSATDKVEIASGKHQAVAAVIEGIIVVEEK
PNVE*
>TCRU_8185 dynein intermediate chain WDRD34, putative
MSAPCNFSDQITGEVVVPSSWRKEAICIDATCQTGPLSLREEAVQTTISALQVVNRLDKQ
VGHEKKTIQATLDGLQYVYAGVEFDEEKLAMFLEESKVDVLSMLYRNAKSGAFSNYEPNW
SAKGTEVVPVATLSSAYAVEGELHVLSLSWNSAGTLLAVAYGRMDTAGWCYSSGVVGIWN
LARPDMDVNAPHHTLEMNLFATCVAFHPTQASVLAVGLYSGEVIVYSEVGSAIPTEMSTS
GSPLSHREPVSSLQWIQSLQEMRESHRFILCSSAQDGRIFFWTPTNKLSQPIAAFSVENK
KGVTVGVQSVKFARPGGGIGAGVPSGDSPLIIGLENGDVGRARPGVVSVLVPRSSENLAS
LDVDWLNGHRGPVQNVDTSPFFHNLCLTCSSDGSVHFYNALERSPLATLEPSAETKHFLY
AAQFSPFRPSVLAVVSRSSFLHIYDLQKSQLKPIASIEAGVDGAPVLCSAFNHVSPEWLA

TGDARGCVRLWRLPSTLIQTTDLERAAVRGSHGRESGENVVRSLWGFAP*
>TCRU_8186 small GTP-binding protein, putative
MAFLRLQIAVVGAPAVGKSAFVQMIHSNGMTFPRNYLMTAGCDFVVKEVQVDDENTVEML
IFDIAGQKEYETMIATHVEHAAAFILMYDVSNKVTFEACTRWMNALKHANSGMIGFLIAN
KMDLVDKAEVTERQGTSLASANQMKFYKCSALRGVGVREPIEDIARLYVDAYHKRIDQLS
QMK*
>TCRU_8187 hypothetical protein, conserved
MIDDEEICELLLAEIRERFPLYESVIETIGSSRVVTCNVTGGAKGFLPYPVVEHDEFTSK
SLRDVVDVVDALRRRGCAEVFLVFVDSGGSLTFYRTSTVRA*
>TCRU_8188 syntaxin, putative
MEDPSWRRNCDLLTDALQSLERSTLQIRRSANKLTTLRDIARERERVKQVTGRTNAKEVH
AIQDALGLMEKYMRLNPAQLRGQGVKLTTEAKVALEKYQKSCDAFYRKCISVEELLRSGR
GTTRVKMLSGTPASSDAEDVDENSDLLQRGAAGTLTQREMFERDLHDEIMAERRRETSEI
AENVKDINEIFNHIHLMVEEQGDTLDIIEGNVGVAQQATRNAADSLRQAQRYQENPRRNK
FLLLLVLFLAVIIFITVLFH*
>TCRU_8189 tryptophanyl-tRNA synthetase
MTNAVVTPWTVEGDVDYDKLIKEFGSHPIDTALLERLERVIGKKPHHFLRRGIFFSHRDM
NLLLDVYESGQPFYLYTGRGPSSESMHMGHLIPFIFTKWLQDAFKVPLVIQMTDDEKFFF
RNIDMEQIEKMTTENIKDIIAMGFDPELTFIFRDFDYMGQMYRTVAEIERTFTASQVRGC
FGFKMEDNCGRWMFPAIQAAPSFSVAFPHIFPPSKGNVFCLIPQAIDQDPYFRLTRDIAP
RLGFLKPAVIHSKFFPGLSGSKGKMSSSTGAAVLLTDTEKMVKDKINKHAFSGGGATKEE
QLLLGANADVDVPIQWMSFFMEDDESLARIRKDYMLGRIMTGEVKKVLIEIVSNIVKQHQ
EARKKVTDDDVKFFTSIRPMGPGKPNNVG*
>TCRU_8190 hypothetical protein, conserved
MSVWRRWHMDAVTEWRSAACPCLVRFAHGWPREAAHAGGSPAKLFSSYWANVASLSDRER
DFFVQCVEYIRYGVDMSPTPSVARTVNRLADVMVAGCVGSGKAAEGVTNTICDVVLMPDG
RPCMGWFLDGFELCHYSAVVAALEERWRVSAGSLWALKERGITAQLNSMTAWNRQENLFG
ASEGWTAERMRACVSRHVRFADKYTFCTERSVDRTHRLSLSFLSSSTNTTPELFLLALKD
CMTSVEELNSNNSNATYPTLCRSFGCLLTLNMPQFVEFRSRVQALGVALCAPKCEDAISQ
AYQSLVRDALDVVSGRMPAPPASSVCSALTSAVRNLLCDLTDVEKALAWFPRVVALCLVA
VTPCGRDEGIRSAVLALPSIEKYLDACEAALLQQHLSFEKPRDVDGEDSSRGDLGLVDST
ALDRVLCGEASALILGDDEVAGTGPFCPDISGAWMPGVGFDSSFYVSNLLAACDALAGML
GVTESIQSAQSESQRTVHRFRHKLRVHVLRRFGFVNASKLWGTPFSGRALPFLNALYVSL
RPSENIAVFRFRNDAQMPHPFDAVGEPSLLLQSFVTKHLAVPGSSPCFFAECGTVQELRA
LAAETETEKKKTLRCCFAPSASGRIFSLEFVPRDQLFSDLAAAATIRLEKAPESRFVDVA
AHVEEGRIVVRLINEPHCL*
>TCRU_8191 hypothetical protein, conserved
MRALRLCGSRSFTFVVVAAQLTVVRASFRRFSRHEIVEAGERADDTAGDDAMLSTALPAS
AEDTFAGEFDELEAASQEIHDLCFAMISHLRKVDPDETEALFEKRCARRFRETIHENKRR
LLHGHGSRGLRRMNCYRTRREYEEATQLFFQFGEKLLLLLTKPVMDRIVESAGRSCRVHR
SDGVHKYRMPLERASWRGFPYRWFKHAPFEVQQLRADMPEVAVKNTRTMRDISTLRSLFT
LMEPQHPFRSTLESRLFEITREYDAVQKPLKRGDFPSLPAQSS*
>TCRU_8192 ribosomal protein L3 mitochondrial, putative
MRSVMQVWRCSVHNVLTAALCMQSRMRTGGGPGDRRIRTDWYRCYPSLMEERERDMYHCY
YPYLFDHGDKMSLYPKIPDNPRMWQPEQLQTTYDAIREDKYDAFIRLREKFPELYQDTRA
WDNPPPFGEFNMFYSVRFGMVGVKAFTCKDYDELGNQFDCTAFWFPDNQIVRHSTRNGDV
GTDRVYVGAMNVPVEFHKPHVAAFYKAAGVPVKHVCAGFPITPDAYAPVGTKLDVRHFKP
GQEVTITFQNTDYGFRGVMFRHGFDGGYVWLGDSKWQRRPGCMGTEGQKRIYPGHRMAGQ
TGASAETYQGVPVWRIDYKNALIYLPTLIDADVGTYVKFSDTINTKGYTLWNEHRGLPAF
PTFIPSEEEDLSKLSTDECQLMSPPLYMYFRDEFAASQLVSQADVEDAKSARPTTAAPKK
KVYDMKKYFEARKKYRQNLQKARKVKLMSLRTRAHEKQEEARRAKILKYKRVK*
>TCRU_8193 Metallopeptidase family M24/FACT complex subunit (SPT16/
CDC68)/Histone chaperone Rttp106-like, putative
MSALTLSKTRVADILSAWKRAQPTAEKFDMFGCIFGALTPTTLENQRSQAILQYLFTSPE

TVCDVALFFSLEKLCLVHNGVSIELPPATDSYKYTAIPYDDSCADALSSFLADKTVGLCQ
KELAIQEGDFASKLIPLLRNLVSAERTVEVAPLLGEFLFIKDEAALSCVEKAAGLCSAVF
RRFIRGLIEEETQRTHPRALSAIQEEISQRLQMPNTVKGLERLEISQFSIASGLTPCVMH
RGTYESQIQVTKLSTQPLRGDIIVVRYGVKNCGYTAFFARTLIVEANAPSNAKDAYHFLY
SVSEKVMELLRVGTRLNEVYTGAINHARTTNETLAKHLPTSLGFSTGLMVLEARGTISEK
GTATIADGMTFVVRVTLEGVPDGGGESFDLELSDTVTIKNGAAQLNTKTTRKLEEILYEG
GMQEEAFDVSSRELNKITRQGQSSVPLLSREAAREEKLKSLLRELHAELIAAGGKKATTT
ATEELRVYEMGRLAYGDIIPYPKEGTLPLQARNDIYVHVEKEVAFFPVCGEIAAFHVSTI
NKVDVKPEGEYVTCTVTFHSLQEANIAYRLHRTKIFVKELSYRASSDVFSEVKIAIQGIH
QRIKNRDTERRRISTTAGGTKLNVTPNSLRLPQVKIRPTATTGRQNKDCIGNLELHQNGL
RFSFIGGVPIDILFDNVKHIIFQPAVNSIRVIYHITLKKGVEIARKSVDEVQFVADVMES
SEAVTGGRKSYDEEIAAEEREQARISETNKQFMRFAQAVEKMSSIKTQIPVSNFSFEGVH
AKGLTTFKANREVLWAISDRPPFTQRVADIEVVSLERVIPGGSTFDMSLIFKDYNKPAVT
LTTIPRSSLEVIKDWCLASRLYYMETTVNPNWKVVLKTILDDAEWDPWRPGAGWAVLNND
FDGDEEEEEEDSDTDDSTYNEDEDEESDETGSSFLEDEESEPDNSDDEDEESVLSWDEME
RRAEAQDRKRGYTSDGDDDRPQKRARVGNTSRAAPLPTRGKAARMPNPGSAVPPPRRF*
>TCRU_8194 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor, putative
MRVGRHVRRLLSAVARRDFGTGGTQCSQTTRLVEVTESPIKDVKIIAMKNPAANILSASL
MSDLLDAISELCNPEKDACRGIVLTSALVGAFSAGLDLKMLHAKLEYESFMHYWGLLQKV
YVTLNTLPVPLVSAINGDALGAGCIIALASDYRVMAAKAGDEGRPFKIGLSATKCGLTVP
PSFAALTSHVVGHRVCEELLQLGELVDASTAEKIGLVDETVEDADQVLIPALDTAERLSS
VVPWCYWMVKDVSRKKLVAPFCTPALRHAECLNFYEMLNNPDVRRDLGAYMAGA*
>TCRU_8195 serine/threonine protein kinase, putative
MLSDEDSVPKERPEPDLSAFCSLTAFSTITVSFYCFISAICLVGSATFVNVYHKLFSDDA
VHAAVGCGVNATSWTVNRARNVLIGASITFILIYTIFALAAVWYIRRTLMDLERSMCQLY
CTFDHLSKLRLESVPLYVNKYSDVDVITEKHTFLLERYSNVLELQQTEDSINNVSLILRQ
FRKLLPDAVFHKKIAGELRESRAGEMAILRTVGNRPSDRLGTMMVAKISSLLRRQNIASP
VAPDGKQGLACPTEFPKTYSSVLQEDINNHGKGKCSCGTLNIAELQNGIDFCLKKRMVTV
VVASLSGLAVCMDEDLQYFQYFSQEFLSVLTDLIDRNNGTVLNAAPDRVTAVWNAFSATP
DHERAGMQCVCESIFTLESLFAKVFIPMGLELTPVVVATSGCVLAGTVGSEDERAMVVHG
RCVSLGEALPSLLMAQGVKYACTGTLFENCSEFFTCVPIEYVTDVDERRHVIYEIVNKPV
PSLQRITEAFKRFQAGEYDLAERMYLKLSRENCEDRWGLRMGQLCSYLARSGGTYQRRVP
QWQMFPVEETDDSTVTQRNKLFYHWRKPEVTPVEDQLRNAILRNSGTCTELAVPPCGVIQ
PRPNFFVSGDHVLSFPPLSEAPKPPAVFDVCDRQGMTFRMSDRILGTGVSGIVSMGLSQT
GALVAIKAIQLPRITHTAFNQMSGVNRRRLRRKGINVDVNVDEALDTVINEVSLLSRLRH
ANIVGYISCAILRDKLLVVMEFASGGSLYNMLHKFTKFKVDQAKRYLRDVLKGLVYLHRE
DIVHRDIKPQNVLLLETGLCKLSDFGTSKCLLKVCNSGQPEGTPPYIAPEAARGRAEKAS
DIWSFGIMMAQMLSGRLPWSNMEEMTPQTFCYNVGHNENFVPQLDEQISAQEKEIIMRCC
NRVPSKRPTAEELLQDPYFSQSKTFTNAHALGSLTSRVDECFQLSSLNASQLRPSSERPY
TPSSS*
>TCRU_8196 hypothetical protein, conserved
MVGRAHHAQRRKQHKARRLHHRQEGRAHHVREGNHARARKQHSSHAEVLDVAVSHGRVHS
RNQAHHTQHRQLEHAPVHVAAPHVRQHAAVHPLLRRRVPIPDGVQQALVQRLPRKLPVPR
EARARVAGNQVAHASRKRRTVQHANDTNHAVLHAGAGHRQCKHGAKEDAEVHRVRHNVRQ
ARESHRRPRTRRVHGAPPLEGRRHTAVHAPKHSGKQRVAHHHPQRVKGSEHRQEVRQRNG
ARTLLRRGAWHPRKHAERLHLQDGAQTAGRHHGNSRRTRNNAVDRRESAGCGQSVRPDRE
GPKQHTLAAAGHRRSVAANDYRLVGSNEVTAVHGHSQLQDGGRIRRVAQHRSPRTTKPAR
LRRRHRNEAQVRAELRVACPSKRRWQRHHKPRRDGAPTAADVVLRQAPTSRRRRHGECRA
RHVTPPKLCAHRRCIP*
>TCRU_8197 retrotransposon hot spot protein, RHS3, putative
MPGKRKRVQGDDNTECQGYTVPQGDCQTRARLSSDDETDQPAATHIRVEETQQPQWTMRS
TVKDILLEGKERITKMWLSDFLQNYFDGRGLGELYINVTMKEFLISPNKFIQDEVLLDTI
KASSSYQELKKEREEYYVLLGASNKLKKEHIVTLSRWSNFKRKSTVIPLARAKITTAYSQ

VLREERWEAEEEARRERQQLGINVSTWIKDVVLEGRVRVNKMKLNDFLTMELDGRGALGA
NRDVLLEEFFKDPNKYIRNAGVLGEIQASDRYKRMEMAVRDEMDMEEDADKLYENGVDKL
LKWLVATAEVKASVHGTTKRFLDAAAEEARKPKKSSAPRYLEGCYESVHNARWHHVVEVP
GGEWTGMDVREGEPLQSWTYKAVGDSLEKDDGVEQSGAPRPMLMVLTSDKAWPYSWKWKE
NKSTHDCHVNCEVDRVWQIVKGDLTEWSSSHGRTDFKPKRRVLIGTPGIGKSMAAGSYLL
YQLLHYDVEKLPAVAYSFGGNTTYVFDKTIKTVTKYLGRGAFEDFLYDLRHLKMKGYVIY
DLTEKGRPASCFAFFDEWGMIVVSSPKVSNYDNWEKHVRAERIIMNCPEEMDVKAMCAWM
KREETKEKQAEYWKMVKERMDKVGPIPRHIFDANKFIAHSAAIEDALDGIKSRDGEKHFT
HGGVRLWYSEDPSQKLVRVARTRGEVGAEVFLNAPISVCLERRIPHYFGKRDE*
>TCRU_of Trypanosoma cruzi C-terminus, putative Dispersed gene
family protein.1
MEDRHWQELREPRRGGLEALLRDDEGSDEDTQKPHDMTSLSCASGTTVASSYRPPAMPLQ
PMAGDTRSDAQSLFDRSSIASCSINYATLDRCR*
>TCRU_8199 hypothetical protein, conserved
MALVPYTPFEWCDIGARLWEMLCQCGEIQVQMTFINGNQMSDETLTVAPSPTGLCLFHGP
ISKAWQDSTLIGHIANLRAPQIPNFETQVLLPAMGAARELGHRQGLITAERERLNIDYAN
AVADVQNRNARLNSRAEEAHINLLVRESNIAGTGNLVLELRQQLEAGRAVNALALKLNPQ
E*
>TCRU_8200 hypothetical protein, conserved
MHLTSTAHEGPQDASELRTPLSQNLSQQKTGTVSSKFAIHTPTDNEEGKIPSPPTKSGSD
TSNSPEQLFVAKPERGNQREGADDSPTDSKEDKNPPATTRKTDAKNTHSSVSSSATDTTP
KPDAVTEDNPPATDSSQKSSGDAEQLTAIPNPNEASDSTEDAASQSAGTATKTNDTAKPA
ESDSDSSTAVSHTTSPLSLLLLVACAAAAAVVAA*
>TCRU_8201 hypothetical protein, conserved
MMTTVMTTTALRREVCALFSLALLCCCASIFVTAATATVAAVQSTDLYSGASAVNVSVEI
SCADSENKLQWRFPGQTNWTRCVSSLGAYDYTVVASSGGYEDTAVVSSGGYDTVVQESTG
YSVGASSDMIEVVLLDSTSGASSRDDESLCLSADRMYLTKKCNASCKSAGEGKTAFTMEF
QTTNESGVYKKSLENKTENNAPAGSTSGICPLKNSVEKAPESVKSETPEAAAAASAAQVT
GVEAPAAGQDAGSSSSAASGASSSAQTIEQGISSAGPQPGNTSQPPTGEGVGRTDASGTT
QTPSATAGAASQSGNPTYTRETNNSAATGAQGPGTSDGSAIATAWVHTPLLLLLTALASA
AGQRCGAATHE*
>TCRU_8202 NADH-cytochrome b5 reductase, putative
MLTYVVAAVIILLTVCLFFKKGVFFSSSMGVALDASKFQNFKLVDKITVSHNSFIFRFAL
HSPTQRLGLPIGQHLHIRCMTTNPEGKPEMVQHAYTPVSSDDDLGHVDFLIKVYFKNVHP
NFPNGGRLSQHLYDLPLGTMVEIRGPVGNFEYLGKGNYTVKDGKGKLKKMHTDAFTMVAG
GTGITPMMQLIRAIMKNKEDRTNIFLVYANQTEDDILLRKELDDCAKDPRMKLWYMLDRE
TSPQWKYGTGYVDEATLRAHVPVLQPRNSDYNRVVALMCGPPPMLQKAVKPNLEKLGYTA
EEMFSF*
>TCRU_8203 proteasome regulatory ATPase subunit 2
MGQQLPTDTKRQQQKWQPPVASDIGKKKKRHGPDTAAKLPKIYPVKACLLKQLRLERCKD
YLLLEEELLKTIGAQREAQENLEEGAMSHYEAELSRVDALRGMPLEVGTLEEVIDDTHAI
VSTAGSEYYVPMLSFVDKEKLELGCSVLLHDRQHSVVGVLQNSIDPHVSIMKVEKAPQET
YADIGGLEEQIQEIKEAVEFPLSHPELYDEVGIKPPKGVILYGVPGTGKTLLAKAVANQT
SATFLRVVGSELIQKYSGDGPKLVRELFRVAEENSPSIVFIDEIDAIGTKRYDTDSSGAK
EVQRTMLELLTQLDGFDSSNDVKVIMATNRIETLDPALIRPGRIDRKIEFPFPDEKTKKM
IFEIHTSRMSLAEDVDISEFIHAKEEMSGADIKAICTEAGLLALRDRRMKVCQADFVKGK
ENVQYRKDKSSFSKFYL*
>TCRU_8204 hypothetical protein, conserved
MVVNEAPWLTRRLEIVFMIAMFLICLLSDGLKCKNGNAFFCIGGSSAMCERDANAFWCDD
MVLPPTPGDDTARCECTAHNNSLLLVHMVEVGPSLTSVPAIKSIRRNNRYLYRIPIAPLV
VSALRNRTGTFITSNTTDGIFGARLFAPLRRSVGLDSPVLGKCTKNTSSLNISYSFDNLL
LSPSSSSLLRGTESMIPFKNDRFALQKHLPNLQRVFGQLLLRRSTELESDRGSCLNAHLV
IVIAVVPGTQTAWINKNAEAVPTTLLDVNTYVKKTISLYLRKKPRYIRLLKSVWFVGIPI
GFPVHRDFNFSTDSTVSQSTSDNGSEEKKENSPTTVGDFPFNVCHPGVEKLELCREMCQH

YGKQVSQYQAANSGLQKATETIGGRVGQRSFFLLYRDHFNTESYFERSYWKDCFQLSING
SSAMARSVASSLF*
>TCRU_8205 hypothetical protein, conserved
MRRCALITVAVTSTSFNTASAAAISQWGARRVSYLHDQHDHCKSYRSATAFKLQPHEVNE
SNVPSAREVMAMIPSTKELQEQLPSALELEAKYVRPAAVNAGPVRRQEEPPLWPNSDTVE
EIMEEMRYGSVEEGDVVPSPSPEHILLAWRALIWGTLYAVIGVSFVVYVAMYTCGMRGVG
DVLGYTRGRAERERSRLAKDGEEVAYYVVDLTNPSTLIEQVREIWNALQEFAEDGDKDEH
ASSSREGGPRVS*
>TCRU_8206 nucleotide binding protein, putative
MIPSLANVKHILLVLSGKGGVGKSTVACQLALALTHVHGKHVGLLDVDICGPSVPTICGV
VGRDVYRDEKGWHPVSLVEDDSTPGAGNLKIMSIAFLLPSDKDAVVWRGPKKDAMIRQFV
TDVQWGTLDYLIIDTPPGTSDEHLTLCEILQPFNPTGAVIVTTPQDVATDDVKKELSFCH
KMGIRCLGVVENMSGFVCPHCAHCTDIFSRGGGRKLAELYEVEFLGAIPIDPMLSLAEDK
GQCFLTAENDEGNETVTAVKNVIGAILKQVERASFQE*
>TCRU_8207 pseudouridylate synthase I, putative
MPRRKCFEGRRICLRKAPKDHTLLGLCVMYCGTGYRGLQLQTHAPTHHTVEGVLIQAMKD
VGLIEAIERGRVKGDVHHFSRSCRTDRGVHAVRNLVCLFVFTERIEALGGCEKIKEMLNT
TLPLTIRVARVTPLMGNFIPRFSCNRRVYHYLIPAYAFVAPCDYWKSFYEKFPQAAELLR
RCYAEARSFLDLSPAESDPLLAALLAAVTRANDLLLRYVVGTHRFHSFSVDVPQRGVSGW
NRKVIMPSSNEAVRSVYRCEIAPRVFLLPRNTTGLTRAEFQAALQIVGKDSSLASSSVLL
SSLLEAAVTAERSSVDDFPSDAPLPFLVFQIEGNSFLFNMIRKIVGTLIAVLRGARETLF
AEAVSPDRRVVCPLAPGPYLYLFLSTYRRYDTVVRGSRSVRFRPIAHEWRGEVTEAAATF
ARSSVAADVIDLDLNRTPAIGTLLAARDAARRVTRPCWEEEEDCHLLSLKDYHPVAVEPH
PPFSEMTMFLRSLRVHNWSIEIVKSPACASVVSSKGGGHLTSNKNDDKLNKTHKRQRQGL
AEDSAAEGGRPLKIKRSCEDTSGGGSGESSVLMKTLDNRDAGNKESPKMDADADGDDDDD
DDDGWIYVAPTEEAARSKRRAHHQKQRERSRAWVHGGTEKEGAAADWEGDGGGSE*
>TCRU_8208 2OG-Fe(II) oxygenase superfamily, putative
MTADVGLLSHKEIGRARSRCRAWMIRLAKHLSPLDAYTVRPDGSQPLDLIALNAGVQAGV
SPFALRQALLAYTQLPEDILNIYFSSLLPFALVHSTMPEMSLMPLVTKAFGMEMMVENTL
GVVCMIRVPNLWATGSSPRGGLSLLYLLCCRAGAVLDAIRRFFQPPTLGVDERVFHGSPP
EDEDDAGVRVLFCEPIEEVPGLYIVKEFITQMEHDAVWSELKGPKAAALELETLAHRNVA
HFNRRFYYGVNRIGVEGDSVNAKPAFYDWMQRRLKNEDPRRKLQDYPSVAQTFSCDQLTV
NFYNYKDGDTAASGIAHHVDSHASFMDCIYIVSLGSHTVLEYNRHGVPPDVAETFGVFVA
PRSLLLMTGESRYSWTHGIAGKRVDILSDRIPPVWRGDRVSLTWRCGRDAPHRRIHCICK
ELCDGE*
>TCRU_8209 hypothetical protein, conserved
MMLRLVAVLGLWLHIGTPQQGVAASTTETKTTPPLEKVPRHARCGELKRSACRLSDKTAR
PFRCGHSVDITRCGDVHKNPGTEEDGCINIWQLDIAGLSSVKKIAFAVRLEQHQTDIVLF
PGNK*
>TCRU_8210 hypothetical protein
MVARICVLLAGEVRAAMDTIVKNYEKYFFPVLCEKQPMPELEAMPSYLPDTVVFQLYHDD
GEAEFADYMDANSLTFVALGDAERLVLCGIDATAQLHHEGAQRALVSAAGIVSGIRRRRL
CIPFGMSELSQLLRRAYNTEKATATIASLVLPRRFYWLTPFWMPCGRRNRSIVSTGIGSA
TRDLAVDKWRLDQDIMKLLDELMIARAVYDYRHFGYESNRPISGMEEEAMKRVNAIESNR
EEARERQLSVFCERTKHEAEKMIKELERRGGATLDELERTLEAKKRESSALQADRESRIW
EYEQTLEKIRKKKQDEESASERLRQAMQQPEQELGLRQSAIETKEQQLEMVQLDRARGRE
AVMRERHSIEAV*
>TCRU_8211 ATP synthase alpha chain, mitochondrial precursor
MKGVAGKLKGILAEYRKLAADSVGGQQVQTIPMIRGARFVALFNQKQPSYFMSAIVSLYA
CLNGYLDDVKVQYVKFYEYLLVHKDLSIMYGSAKNKFFYMYMHELNYLIRFFTLNSPVLH
DELEEMLKQHTQLFLQHYQSKMNAIKSEKEVKALKNLLYSCKRAV*
>TCRU_8212 hypothetical protein, conserved
MPDANSVQSFWRENLIPRWHELLKNECEAEYSKETNLSLKDLAVNCCLHHAMHELCKDLY
PKLFKKTEFSNVEGVCKEYAAEPDEVKCPKRQTQPPPATDNSVKVSVPEALGKEGDLGET

PEEAPLADLPAKPTKGPPSSPMGGQPTNADDVPAPKSEERPVSTRPTNDSREGDTDTITD
TDQEETSTSEAESAAPTPPVASDNDDDNETDKGTGEKVPNNAPESDGAGTNEKKDENKDN
NPKETPVQVAGIKTDTTPGDSDSSTAVSHTTSPLLLLLPVVACAAAAAVVAA*
>TCRU_8213 triosephosphate isomerase
MASKPQPIAAANWKCNGSESLLVPLIETLNAATFDHDVQCVVAPTFLHIPMTKARLTNPK
FQIAAQNAITRSGAFTGEVSLQILKDYGIRWVVLGHSERRLYYGETNEIVAEKVAQACAA
GFHVIVCVGETNEEREAGRTAAVVLTQLAAVAQKLSKEAWSHVVIAYEPVWAIGTGKVAT
PQQAQEVHELLRRWVRSKLGADIAAQLRILYGGSVTAKNARTLYQMRDINGFLVGGASLK
PEFVEIIEATK*
>TCRU_8214 dynein light chain p28, axonemal, putative
MSNTSRATLVKYETPVLLSEVKRRRAMKEKRKETLGPQTIPQPEDVLYSIIPPREYEEGG
ERWVQFVSSTPATRLDVINLQERLDALLQERQARETGICPVREELYRQVFEELIRQVTVN
CAERGLLLLRVRDELRMTLDAYRSLYESSAAYGMRKALQAEQSKIEMEAKIRALEREKEE
MRQQVDELEARCDAIREQEAERRLEEEKRHGEEVAFFRRTYQTLTANLQTVCNPTRT*
>TCRU_8215 Mitochondrial SSU ribosomal protein, putative
MFLRTHVERHRSGKARAFVFRDPTLKMMRAGSGYQQLRRMGMPIQVSKGWRKVDHFHANN
QYQHAWPLLSHDDLGNSDQSNNTRNIMYSMYLPKRNKGTAPWFRGADTYSVKYCEQGRYE
YQRYLMINRFPSEYRKHFMNFLSNIRSSSGPATIPQEALHWLLRMIVDNFNPQHVHYIAA
MKTLQNAGELDMARDVWKIMERQQTWPCTSTICAYLDVCVEAGEKTWAMEAWNRYCTELK
FLQPGEVDPKPVSRVPFSLTREELLYLPKWKKHFDHDPNLDVVDLNRFNRTREVYLRMAQ
VMLAGGERDSFQHFYTKLEEAMLSTPTPVPEPPNPHLVRRPQWSPYEHCKSVHHSPWRVG
NNGRAMALGPSLTTEDEMQSRFFSNDQFLVHMLKEILRIVLQEHRRRHPEACSRGEGEAF
FDQVVDARETLNFCNELIERLFAVLGQKMHGLNTSSLLSVILELYRVMGKETGMALLRRA
NQFLERKAALEDGAKESLTAPNYLQVLMGFADESAYVYDSKRKGLCRYRSGFDPRTTMQQ
LAATVQEIAGNPHVTWAADMHLQVVCTMVGCGTMKANDYFVRNVLRQFCWDSRFLEALYM
EYRRHDDVDMWAELTKRALVWTARYNVNASERLKRLIEDDYDTIQVHTRTFRELAVFQFR
DVEEKRHSRDVVNELPNPWTDYVSHALPFPDRDAGYPDEYGDIGQWRAPGGPGSPVKGPG
YYAPPMEGEHQRGYTAEWRDLKNPMRPPEFPTPWERKYKQYARGQHPSYDMVYAGPMPEI
FPNRYDFRKPTRWDFHDIEKQGKYKTSGPY*
>TCRU_8216 Polyphosphoinositide phosphatase, putative
MESRDGSKTDSCSENGGGWRACDASLHPVRSLVLDRICIYDQPSHCCVIGTDAAKKEYRV
LHFKKSNSEVLNYRDDAAYTPALAQALIERETREANTQVLRAKALLGCIRFTRGYYLLVA
TRRQCVARLGCHRIFEVTDVELVSLCIADPKSMVLLSGAGSSPFLQPRTLEDYYRSQFLS
NSLKQNFYYSHTYDLTNTLQMNMTRARVGYRVRSKFVWNEFLLKPFFSSSASCHASFVSA
KEEETLLVPAAVEQWIVYLTHGSIVQCPVVCGLKPLLITLIGRVSKNFAGVRYLRRGANN
DGHAANHVEVEQIVVDESSLHTQFTRGRFTSYLQVRGSVPLHWFHSATQLPKPPIKLGVR
DIYYTSTRKHFQELLEDYGAPLIIMNLLRQREKRPRESILSWEYRRAVMTLKGFIDADAE
VEKKEEVLLYHEFDIRESAQGAWNNVTAFAEGALEQTGFFVCNRGGTRVRRQEGVLRSNC
VDCVDRTNLAQFFFGLHALGYQLHALGLLYSPVDLALSPGVQDLLLHMYLLMGDAIAVQY
GGSPQVGAGVLNRGTGWDQIMGIKRLYNNMVGDREKQSALNLFLGRSHLYPNAHSGTRDS
MTRVSGAEVEEEALVVGMRNSKGSGSGSVFRNETSDRDSGHAAGRMGLRHFFESRKSRVG
DLLEMDLECSLQMKSALPPAKTDDVRGWWRDPLQRHQWLISASTASSPSKHSSVGDVDYE
TKNETEALIARMCIYERAAAMKQEDENATDEASNGAALQEGEVVALVLTTALNTLVRRTV
MPPFRLFSMQKLDFMRSLMVQREADSEKIYCESSESFVELLHNHHDFPDEVRASIFYQDI
DSVRRMSEECEPPDDMHRMHLAVLSMYGDPLEWNVETVLEALLEVEPKVSAETVNYLRRM
KVDGYALLQHPNTADAIGQRELLRRFIRLVKELPRASLESARRCCAELESETMEWTQTGE
EESYRNGNTSGGSDMIAFPDSTCRLLQPFFKEAVYPATMGTVVRRLLQNMSDVKSGVPRS
DRLRYREKFYHRVPPAVVATQCFSANELHAWLLRNSSRLGLTLHKHVEQHDASEACWKFM
LWLAHANLVTHIIIEPSHGVIVYPVKKLTDFASRTQLFTLRPLQEMHVLNRDGAFKGDVE
LSVGSMAFPPPPPTGCSAVVCAESLVSVALRALSSVQEMTLTNVGDFSENSNFRVLLNAL
FALSTQLVEVDITVLRPREQWCFWVNVFNALYIHAWLAAFVVRAQEYSTFHNTNGYEIGG
YFFSLSDIKNGLLRGNKPASYALLPPFETGDPRVLFTPTELEETADNCGIDMIKKAADPP
MHILRGRILLALIDTFLVPDKLEDAQVYNPRTLFDEEEPTALQNSFSRTEMPPVNTTEIN
DSDDDMSPLHGGGDEEFALQELNPTARDVLRRAGNIPSGAATWLTSWFGNRLASKSPAFT

HPCVPLIPATLQGQIYAIEGHVLRSLTHSSPQATMIRDGTVCPRALLPLLFYPEEFGTNA
DEIPRLIYQLHMNAGGRKMHCSVSLNSPTASISLPGDPMRHREFCEQVGNETQRIP*
>TCRU_8217 hypothetical protein, conserved
MQLATREGWWEEGGEKEEGVFEGAIEEKTVMSFFFDEDSGDEPATKRHCTEQQQRAQGRP
HGGFFNGNGEKDEDEDERPVLARAGSDRVGLRLLQGMQKPTSSSPSVLLSGKEKMRVVEA
YVPLSVGGFMESSAETAVDNLSQIKPGNVMCLRSPASSASQASTGMNFVRETDLSEEERR
YGKRLSSNMTQELFEVGRVDRDTGMLEAIFLDGTRRNLKAYAVRPAGFVEKELFRQWKRE
PNSRPVRTVYAAPQDANASPSLSSTTQTTRTTAVDSAKRKNNTAAVELMPWWVSPQLIVR
VVEKSAGDLFGKKFVVKSLSRKEGKIRLAPWQRSAGNGESAENSPVDIVGCEALETIVPK
VGEQGIIVLGNMRGELVKVMERHRDVNGELASLKVCSTLTGNEFTVGPHEVCQLACPRP*
>TCRU_8218 hypothetical protein, conserved
MAIASDATSDEDDDCQFEYVAPSANREKGAAGAGAQRVRKTVYEEERDARVSAIVSQQGL
KLPLQPEAAPATLRATEKEGKVTERQDAEEGEKKSTKSAPNPTEEAQRLKNQRYSIYRRN
RYLNQNALREVDPGTKRHMQIVYTPSNAGGKQYHTLRRGGYTGTFSGGRRFTPRFPSGYK
RPRE*
>TCRU_8219 malic enzyme
MLARTLLRFEKTGRTARGVDFLRNRFTNKASAFTRKEREHLGVVGLLPPAVESIDDQVER
VWVQFNLLSSPINRYQLLRGIMDINVTLFYKFVQKHIKETLPVIYTPTVGEACERYGAIF
MRDHGLYVSMQERGNIRQCLKNLRKPNIDIMVVTDGSRILGLGDLGANGMGISIGKCSLY
VAGAGIRPSRVLPVMLDVGTNNEKLRNDPLYLGQRTSRAQDREFYELLDEFMEAASAEWP
NAVIQFEDFSNNHCFDIMERYQKKYRCFNDDIQGTGAVIAAGFLNAMHVSGVPVNEQRVV
FLGAGSAATGVAEIIAELAALELETSVEKVRNSVYLVDSKGLVTTTRGDELAPHKVPWAR
TDIAPEQNESLRTLTDVVRHVRPTALIGLAAAGGAFTEEMIKYMATYCKRPILFPLSNPS
SKSEVNPDDAYKWTNGTAIVASGSPFPSSVVDGKVLSPAQGNNLYIFPGVGLGCVIAQSP
YIPQEVFVTAALALSRLVDTEVVLAEGKLYPSIDGVRNVSMHVAVDVIEELQRMGLAKSD
LPRNKSDLTNLVKEFMWEPQYLEPEYYLSKRFD*
>TCRU_8220 malic enzyme
MTSLQLNASNCQGRAILTDRYINRGTAFTMEERQKLHILGRLPPVVETLEEQVARVYGQV
KKYEKPINRYQHLVSVHSTNTTLYYATILAHLEEMLPIIYTPTVGEACMEYSHLFFRERG
VYFNRLYKGQFRNIMRDAGYQKVEVVVITDGSRILGLGDLGSNGIGISIGKCSLYVAGAG
IDPRLIVPVILDVGTNNERYLQDKDYLGMREKRLGDEEFYELLDEFMEAASAEWPNAVIQ
FEDFSNNHCFDIMERYQKKYRCFNDDIQGTGAVIAAGFLNAIKLSGVSPLQQRIVVFGAG
SAAVGVANNIAALAARMYKFPVQDLVKTFYLVDTKGLVTTTRGDQLAAHKKLLARTDVSA
EDSAKLRTLEEIVRFVKPTTLLGLGGVGPAFTEEIVKMVMQNTERPIIFPLSNPTSKAEV
TPENAYKWTNGAAIVASGSPFPPTTIGGKTFKPSQGNNLYVFPGVGLGCALAQPTHIPEE
LLLTASESLNLLTTEGDLREGRLYPPLEDIHNISANVATDVILEAQRMKIDNNKKLPRTR
DELLAFVKKAMWKPVYSGEVGEQVL*
>TCRU_8221 DNA repair and recombination protein RAD54, putative
MPLFRHSGGSGGFPTGFRAPATAGIDSADTAAATLSLLPLRRRERTVIYPDSKGVTQAEI
TVARLAKRAHIEYHQPVREKKAAQEGSAECGNEAEAAVDTGSAQENTHPGGGDPVIEQKK
QQLPQGQDAGCGTAQEGGEEEEEKSEVVSRYPVSPYGKLYFQVETDAATRHESTGIIIIE
TEQLGVMMYDRAGRQFGNRPDPGYPIKEEDVNNAKAGMTLKVASKTVMLITALKEESFRS
GEFFLRYEHQLRKKEEKQKEKAAAAAGLHVIKPKMSFGQSLSGCIFAQPVFRKRPRDGQT
GFTVPVAGRPKTGPSGIRAELKPLHDPDREGAVVLFRADYKRDANGRLQVSVVVDPIIGD
KLRPHQRAGVQFLFDCITGERMPGYHGAILADEMGLGKTIQTVATIYTCLRQGKHGVPTA
RKCLVVTPSSLVKNWCNEFDKWLGEGAVKYFSISESTPKGDRIISRFDGEGDVLVISYDQ
LRKYITRISTLRSVELVVCDEGHRLKNAEVKTTKAVDMLPTRNRIILSGTPIQNDLSEFH
AMVGFVNPGILGSRDVFARVFEEPVMQGRDPDCPEHLRSLGSDRAHYLSNLTQRFILRRT
QSINESYLPPKVDVTVFVRLGELQSVAYEKLSDLVEGSSCPPLVLISALRKLCNHMDLFY
EAVLNSSKEEVREGHGIPKSVLPKGYKSGTLSEAAGGKMHFVSLMLDELRNNGDRDKLVI
VSNFTQTLDVIANMCRQKRISFFQLDGSMPVKRRQEVVDRFNVPESQEIVFLLSSKAGGV
GLNLIGANRLILFDPDWNPANDAQAMGRVWRDGQKKRVFIYRLLSAGSIEEKIYQRQVSK
QGLSANVVDMKSDSKQHFTLEELRSLFCYRKDTRSDTHDLLHCTNCEAVVELLASSSSGA
GKAKELSAPMKFRRVGEKKSGPRMDELRGWRHFARCEEFPLDKVVRAISSKAPGLCSFIF

ADERDNTASAATDGKSREGTGKAATVRVERPFVQDEEQIICPSQQEHLSEESELEIELHD
DDDDEEEEEEEEEEEEEFEEVEDDDDEE*
>TCRU_8222 hypothetical protein, conserved
MRMHGRNGELGAVCHVANAVHTCSNCAASCATKEEGATVAFTMNVTTHKYAGPYELWRQF
SPGGTIHPPARSGGADQKGLRQLPPPREGKDDTKSGGTTAPQLNAEPSRQHEDWRQSAAA
DAPNTVDRSPASNTSETKPSFANGPRILVVLNASGIMSVTCGGREHVEPSIRLHGAAVLT
RRASVSCHHPVKRRTRQNLVKQLHRK*
>TCRU_8223 LysM domain containing protein, putative
MDGVRYQIEQLQHVLGQLDPHRKLAPEDASQLQLSLAKSTAIARRVVERQHRRTFPMRLV
DAGGRHGRPTVSSPTFSSSGELRQKEGCDASRSDPTSAGKNKWVDATEAVSLHGERTRGE
ECRRETIRSIATQHGISVDEIRLYNPQLSFYNDEDVLPYNTYIKMKPQLNRRPHYENGTD
KALSGHYAKETQHHADDTVCAALPIPLAPLPALQEANLHSMNKKSTVTRREESPLPCEPF
MECADSMKGLLMQLPSISPEGSFLERKENCVSYTTASDIHDRSHKKDVNSANCIKTPANV
SASAVSSTAFSVTEPSKGMLSVKNSAEMNTMPSEAVPSSHPCVSRIRKFPLTQCKTIVSS
SSNDALLKYRNRPGVDDFDFSLTTESSSFHSTPTPTPNLSPQPNRTNIQMTYDDARGGAL
ENALCQRSVPWSTHGRQTLNSALEDSVENGLLESNELSPIPKASYQPVENWGDFDTINSI
ALQYNVSIKEVLKWNPYLLAYGADDPLPANFPILLPLPQQE*
>TCRU_8224 hypothetical protein, conserved
MSTSLRPHHPTNAAPSHAMAMKDIAVPLDGSQNCHNTVAETHDMLAYPQIGGDVNACGVQ
DVGEGNDGGVQFGDFFFQNIPPEGSVDAAQSSVFEGFCFDDICDDGAWAAGVTAMGNAPE
EDTENQIHLSAPQPFEFLLPEDATSTSGTAAVAEGTVTESAFDFGLGVAHPTRGIADVPS
VSVPVSTEVLRRSAPLEANEMSGEAATRSSNSTKDTIATTSKMHFGIGNNSSSHGNGGSN
FPVEGGGATKEVLNNVPAVSVGSLRQSLKLTDSSVCSTVGSTTTAVGAAPRVPRESVDDL
LRRADQILSEGKLSDAAEDAATGGHEGNSNQSDTLFSAQVSHWLRRCVEVQESSLASVAD
LQLRMTQTMRMFSTHTGISSALGQQYGKTPVVLTLPLVLTMMESLLEEG*
>TCRU_8225 hypothetical protein, conserved
MRSKSHSTLPRAKYTATTAATTVTSGLPPKKVAELVRQLAESRYEAQQLRQQIQSLHQEN
DSFRASTLHRYIDGSIADVSLPQKKLSQQREPRNQQQQQHEGERPCALNGNVTTARNGGT
VEHSGFMDQKITSPQKAQTSFPPESIGMLLTPPSSFLKAADEPSVKGVENLENRHSSLGD
SYWRKKYAKLKRTHEKTLRERDLQLAEVQHLVYQIHEEHDELRHRHERDSLQRQLEIESR
SRMSLEEKTKSLEEEVLVWRQRFLRLVGEPTHMPNHVVASEVAPTLGDTCDGGNFSSPPD
GLNQTDRSFVCPESALASMIDADAFPQGANALNSTRYGNALERKKNDVEHSYLQHWRKKK
REDVNTFDSHGIQNTFLRPFARMSRHSVAVQVGPSTAAAASQTEKCSQKSVGTLVDFGIQ
NNNANPGLLHFTGETKLTPDARKKVLATFDRNIEDLPKSHFQEKSTGSVSFFTPGPFNQK
SLQDHVYYMVNQVHGRGSHHRTSSVPSCRQPEELHPPSASFGFPMASPSASMAGRGISID
GDQAKRDRLEEDIRKHDQLLEAVAKLQRRAQRFAKTPSI*
>TCRU_8226 SET domain containing protein, putative
MQTATILQRLLTEEGAFFHPVMRLVSIPSMGGGYGVVAAESLKPGTLLARIPRHSMITAS
KARHYLASFEYKQRQALSCSNRPSNEGASVTELEAVEQELSQGLSPSNTIICYILLNAAQ
CGRFSTPNTENSMDMSADSSSKRDKISFQSDHAWMKTWVLSLPSRYNNLLELRPEKADEE
CYSSYEDTGKIISSSDAYLRPYLQFERHRHKVLREQANAEAEFQLCKSTLSFFQTMPHSD
CEERSMPITLEQFLWAYNTLMTRGFAYYSEVWSLMPWVDYFNYALNSNATMKYDERRGAY
VFEVLFPIESGEQIFLQYGAYTDMELLLWYGFTLTPVLLPEVASARTIKERSQKLRMLLR
EGLEIMDDGDISFAHRDEVWLKAVNRALGYCFSPWTDADGSYPSNLSESWLELLLSSYMK
LHNKSSGDGEIYQFPPAAEAANALARLIIGTKTQHKLPPRLTARDCRLGALGPSPSMLRL
LKHISRISSTPNEGTKLTLVNLLRAICWAELFCNYGAGMKLFFLKSETIASPDGTVKSMA
LQASLDAASLLHLLAVEATEEELRVYLSRMCD*
>TCRU_8227 COP9 signalosome complex subunit 5, putative
MMMMRPDAGRRGDRHEVTRSQWEMHNSVITDDAFLSPKMELMEELHKTQPWKKSPRYFQR
VKVSVLAALQMMIHAKRGSPNVTCSNGSGVADSSAASMRNEPSRENWFEVMGLMLGHFNE
DEMIVTSAFALPVDASEVECSMNDASQLYMLDFLQYHQRGGTQEGCIGWYHSHPGYTCFL
SGTDVNTQQLGQTAQDPWLAIVVDPVRTISTGKLDMKAFRTFPEKYVAEQQGTSQHTQGK
HWEGSTTSTWVPSERIREYGVHAHRYYELPITLVRSKDDEAQLECLWSRYWALTFCSNLF
TANRKLMTKQIHQLAEVLESGVASRHQTMMKGDGYLPGHKLGSQHQRKGGGAVDDETPDG

VEAFKQRSLHVRYLTSSLTSEAASGGNTAGGQKFRLSSMIFLLVLARVFLSF*
>TCRU_8228 retrotransposon hot spot protein, RHS3, putative
MAAGSYLLYQLLHCDVEKLQVVVYFIADRTFLFDKTSRTVSTYMSDSSNASFVRSLSDRG
VKGYIIHDLAEPDDAPSGDLPPRGWGMVLLSPPLERNYKEWVKRRDATTILMNCPGESDV
KAMCVWMRRHQPVREQAEHWQVVKGQMDEVGPIPRYIFDERKYDNWVQRCHKTVDEAISS
VILQCIGLGLGGSWDRMKVLYWLARVIRTRGEKFGFEFFSNLPVSAHLGNKTLFKSAKLM
QQHYFNFLISGLTDYLISENFGRCTVFAFLNGSFVSAIERGLRELSPSPQRQSHRCALAV
YSQEGSTRHHVLPPLEHFSERIDVECGVLYVTEVENFPLVDGFFFVESNPMTLVGLRMAA
AGGHHTTTSTVRQFTECLAAYFKGWEVLSRDLSWEMIYVQHADSTPMNDWQGCDVVDSNN
VSGADNNEIAAFWNEKVRQYQVSISSRDAPRRS*
>TCRU_8229 hypothetical protein, conserved
MLQGNKASVHIDGRSAGEEEVPLTGGRPPEVLRFCFDACGGHESHVTVNDVFLYNRPLNS
TAMRALKDRVPVPTREAATTPPEKIRVVDSVREHAAGDITEEK*
>TCRU_8230 hypothetical protein, conserved
MQRQARLPHGVNDASDVSRMDPWKDDRCRDFIALNTIQRLRSYHADTLLPVEPINIPRAK
NLLLLPKAGPDARTCDTEEGCAIDTARILFFGPKSFTSLKSPGCMTAFPHGGGNSGSRSS
FSHSEEVRKSSSAKRFSQTPSMPLNCSPSVDSWQQQGELNTTTGEGGGTLDNGGIKSQGT
HQEAFYAGATPLRRPMSDAVTTPAPRPPEPITGVVTTCEEGNEHINEGRNACQTVSGVVK
FSCAIVDAIVAYYQSLLSRGVVLDRFNSKDLAFSWWVVGRNMDVAALHHYTGPMRRDSLV
ILVRHFYYELLVEQRPKKSLLSGPVFVQSQGQKEERNEAATASPKPEEETVWTDSHDQSE
DAQLPQTTGNDATITAAGEKGDGAKKRPRSRLDPTRTSPLPVSNRLCRRRRLEEGTNGEK
PSEAEKSTGAPKAIGASTVTSNRTASASKQAQHSKGQSIVQTPVAKKVTVPTAQIEPTTP
QPPTAASSSSVATALESTAQEKSHVAATHAGEDTPPVERPHRSSRSANIEDVWRPIRLTR
RRLPPSENSTDFTEATSTIAERGSASVSFLNLIVERINKRMANDSNYADLLTAFPTRNSE
VGCHNVLSNTGNDNAKILHGMHPALMQLFRYYHTSAPDLFVPRTGLDMGEEAGTTEEEKT
NMAERAAKNKIASIFEENGENGEEQQISVTKREPSTAQSHDMITASETLVKVEHINEDAI
SSEPNGLRDESHVDAEAKAPLMQLPFSFSQLTYAQRCLLTWEASLLLNPRPTLPVKRGSQ
ATSGATKCQVKPSIAKQRHYYDYWGNP*
>TCRU_8231 ADP-ribosylation factor family, putative
MFTFAWGLYNSLFSDRTYKVLIIGLESSGKTTLQEQMKCIYATNSNNASQTGSGGGNSIP
TPAPMSVMKNKRIRPTVGLNMDRITHRTIPPRIYVSCSRGSFSLEKDGDAYHSGSIHSAS
SSMSHGSFTPVTTRLTLWDVGGSMQTLWANYFAPCHGVIFVVDSTIGASEDAMSFTATGN
ASTSAVAGVAFSDQAATPSVQSHMSSLDVERLSSTFSPCRMVTSIVDAPFIESEKNDVVT
LRLMEEKRRSSQRKAYARNAAVLRAVFSHPHLTDAPLLILSNKADVMGHCPLAEMQEALG
LVDLALMHESYKNGATDVESHCELNAGGAGEVFGPTSISDHSSNGVDAVGTSGIGKKIMR
LAEVSALDGSGVREAMDWLVFQMRDSARVAVEDDGG*
>TCRU_8232 hypothetical protein, conserved
MLGTWELSASVLRYAPQVLLRQLPSFLVGVVAGYCTVLLFFGPLPLLSGVLQLILTVAIS
KGLAATARVGITKGISLFEGRTSSGAGNRGPVNRHKRHTTERGGVGNERGTCDAVGAVEA
GGTAELD*
>TCRU_8233 membrane protein YIP1, putative
MQPDGFFYQPYSNGVDVGGGGGGGGGVYVDPAGMPPRVQTGYNTHITSSQFFNGEESSQR
TLESQQGSHSHVMSIGVVTPTTSRRDSCTSPKAFGRMSATSSTNNSPSFGHYATRKESPL
PSVASKPFLQQPNSFSVTMMASPAPAFHESALHAPQPFNQSQPHQQQQQQQKPYQQPSSA
GVPPSQSPRTGFVASLLNVILPHDAFASSARQESVPLYQQRFGYPEDDLPLLEELGIFPH
QIRCKALAVLNPFRAMALEAVEDMDLAGPIVFAITLAFLLSLQGKLEFSTIYGHSVLGIV
FVKFLLSLMTDHGVALQFVISALGYCLIPNVILAIFQSFAYWLFGYIGKTMLPPALLIVL
WSAWCATAMFVNGLSMEKQRYLVLYPMFLFYAVFAALTIF*
>TCRU_8234 60S ribosomal protein L38, putative
MPREIKNLKEFLAICSRKDARCVKVKHNPAQTKFKVRCSRYLYTLVVADKKKADKIERSI
HPSVKKITVTARSHAKTNAGSK*
>TCRU_8235 Mucin-like glycoprotein, putative
MMMMCRLLCALLVLALCCCPSVCAAGTKPAAEIGNVILVNPPSLPPGAPPGIGQPGLPGP
GSTVPEALVTVPGQSGLTSKGSVLEPVNDDGKTPASTVLGPKPGVATDDLPLEGNNGMTR

TKSDKNASAEEANLEAEDRAKTTTTTTTTKAPTTATEAPTTTTTAPEAPSTTKTEAPTKT
TTRAPSRLRKSDGSLSSSAWVCAPLLLAVSALACTAVG*
>TCRU_8236 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGGRCDEEKRAGLGSGPEALPESQGLEASLQVKQDLRRG
AGGVKEKVPSTFPEDKVEDDEDDEDEEEVIEENDEGAEAEGGEKTRSEGQGDQEVTIALH
QNSGEKNLSGSEQRTHQSIVSAGEIPPPGSRESKAILTQTEVEEKKETDKSAPAV*
>TCRU_8237 hypothetical protein, conserved
MHACTCLLRDVWFSSPLFPPTASVRRVCVKCWVVGGGNAEYGVRGKFTISVGGRGNGGAP
PTRGGFGAGTSLVEWRRSNSSRPSKVIRSEVVLTPATLLRRLELIFPAVPCAADLSKGAT
CRVGHSDAHEGQMPALSGGLSGVPDDVRACCHQVPWERVVLRRSGHVPASEMGRNSSSGV
VHTTAAVYDVMVPSPFCFLPGETSVISSLARMDEGGDNDNEAELPLDFMHVAGKTCHRLH
HDRTVLLIRCPDSKTRSVWCQRVGVLHHIPGLPDPSVSSLTLREYVDFIKSFSQPLGQST
MHYVTRCGRNNRDAANHSIWERLEDAKGGNRNTEDGMTAECRVLRGAVGVWIIDPWRESV
FFALRYHLGVEHYEWVCCPQHTLFQESCSPSTNPATSMTLEAKRILFPDRREGHRAPSFF
WARASLQRAMLEPSPPHDHSRELSQQSNRRRKTRREGRNAKEDVLSTILYYCVAGTALGA
DEKSKFLTRLLGSDDDLVRLARVWAPLPRSSRPLRGRQILTKADALAEAMKYGLLRLLP*
>TCRU_8238 Ribosome biogenesis protein SLX9, putative
MVNRSTRLQRGPLKRKTTAVAARTSSHAEQPCADDPAKTSSPQTNSIKNVEMTVGVHASP
AVAVGDTPQGKLRLRRRAKKDRPLVAAKTDMKSTVRNRKRGRARGSQPGRGSTATTIVHD
EQRVTRRPAGGNRQRNQHRQLAEKLVAREEHQSRKKAAEKRMETAKAELALFDQVMQIPS
FEENPFAAIEGHLNGTMAFLQPQTPDVGRRKLEE*
>TCRU_8239 hypothetical protein, conserved
MSGHLQCEHDRKGLSATQANMFFSFQTSEDDSSTCIQNNSIHSSNTNAGDNAGGNHQDSL
VTIQRALYAADCLASLSAASTWSGEYPKRETTSSTSNSGGDDGCTAAAYLQVIFSAILSV
AESQQIDLECAVRCCIRSLALEEELFRGDASLTHQSFSASAGTDSVDSNRAHHVDDDKHS
HQRHVKEGKQQQQEEQQLLPGFQIDCKGHKDEFPAEKGAMGQTKDAAAIDVSSDRMHAGV
RMNVSLDGADGEERDHVKDPNVKVIPICDSDPLSPLVYGTTTFGDMASAPRSTSPPLTIA
TIPMGEESYSLLAPPSCVAGMSSKEISRSGSPGNAAGRHAKEPHPRQMQEVMVAGVKSPN
EVPTLHASNAFATHLFQRKKTETSVHEEKEEELSFRNRLEAIMPKEPPQEPAGYRTSHVT
GVSSKETIGVDAADASEKEGNVTSCSAASVAAGPNAYVAATEAAEGNSVMGEKWLAAESS
LEKGFFTPEGIEGRSVVFPPTTEYVPSLLVMDDSLGAGDTTNRGQEEIPHVSSDVSLSTT
APKISGSPPFPKMTPSSFLFSNTELPTNESLLLTTDNTAVSLRMDVKNDMGILSTSGNVV
SSDTTDPLHQGAETGSPSCAKPHPSRAEEASFLSWALPLGVTSICSEEHVREKEGDTVGV
SCKEGKISIDIPATVTDPVPVNSITSPLLQQNRVYYQPPQQQQQQSDFSVGSAATVTVS
PFLPCEESSPSFRWLDDIVVAPMTMTTTTTTTLRSVLPLSEVAAQSTTQQMDENEKRDVG
ILSSSGQVEFVGRTPTEETSLPLKNDYLLLNLCHADEEGDGTAKTSTPSATTAVAASTLP
QGDSHAMSNHATVPSECNRSAGIDRSMLEKNLKNMRQPIAARVQRDEPSQIPSLHEDSCQ
DNESNEMMVPYGLLLLQQLLYE*
>TCRU_8240 hypothetical protein
MPCEDGVGLHIPMERAEVLCAVGTGLVRPWERRIVCYALKHVSAAAEAALPSTESHESAD
GSGSDENTEGRNASMEEISAAGPNKQEEQKRQRREETGGGEGVGNHLWSMFFGASKNTSA
DATNEEDCNADFSHYSGPQFYLLMEMVRDAMIVAKETSQSPASVKTSTCNFSRRMSWNFD
LLTVLLNLLIFHGNVPAVGRFLSVILSSYVMALLFHRCCHDRDGGGIVRVQLSEKKTGKE
EEDDNGLSDMRLVQSDAFISLISRLAQIYFPLWHKLRGEGADLARRTEKKLPAPLLHTRC
VPIPSSRQNSLTMWRKMNSNGVCGNLPDTSLQGLQSRIIELVFNQMNTCNVGVGLLPCNN
EKQGDQMNETTKKKNVEKEAKKKEESKTGKEEKHVDGEEKEKDVTLKWEHVQEIVVCIAL
AELGRLVLLSDDFYAPGNGRHGNHSHHGGQGMKREEEDALRNNTPGLKYLECVRRCGSSG
TVEQMRDMATILRAVEDEWRQQLPTDVSDSTGEELMRKRGSHPLITSNHRWLVNAMCIVL
KFVSQTSGSLCLTPLCQSDQQRECQRPVPYQEKDFYYMNLLLTCCCVAGEQIPKKISHFA
LCLTEFTLSNVLMGRRGGEDAPLLQRDTNDRFADERGNAGGQGDGMDSGAERKGLAGDRE
SNEEAKRQYIAASALCTTTLSFLRCCYKYGSVTLKNEHIRWLSALLRQQVMLWERWLRRA
VLLKSLVRKSAKSSLRHAPHTVQSDTGRVLDQQGPHEESCSFVWWHTRILLDYLCVFRDM
FSLGVACQFVNDTAPFCTSMQELGRVLQMTCWIELDGLKATPSGTYAVAFGVVPFPVLAA
TERRFFIGAMLVYAMSATADTLLAFQMCMENNQAYFGDIGDCGDNTEKDDTKTVSLTGTT

ESSGGNVACVTEDSLIARRLWVNDFFLSVLLPSFGRVMQGIAFCVPDESMLPAILRLGRS
VEFQYVSHIEGAKDHEAWERRSGKTHVLSTDAATTPQTTGQEKKFFFQRMTLSSSSSPSS
IWTSTPFSETLRVAMGVMALASNSQQALLSHISRVFAPMITREDVMARWMLDKFGNLPHP
QQGDAFSRCQILLHVVENFVLHVPWAGWASQSLEVICNVEDASLSLAGGEGTHVESEVSS
LSISSKKERIAHSGYNALRVGKDVQASSKTSSACIGAPRSSHLFSSPVPPPLFEATYVTV
ISCVLLRLASIDFDGPRGLELRNEVEPNRVRAVLFGLIENFFRGIDDAVFRRSSMREELR
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IDAYVDSHHSLICSNVVYIATALYAIERESSPRLPSAVVAGVQSTPYNCLQRLAQHSLES
LLSDADVPATWHFLPLSTFCTNDVSLRPATAGMLDRIVDVPVNSLLPLRWLVSSMPTDVP
RDSGKSRWEGPPVEGLLLQQACALVRVMTIIAALTQNTTNERGAEASINTTSKEFSTAAA
PIFVLHPAALSFLQWRKLCFALHAMRHAEEHNIAPMPNVKGCPFQHLQGCTEDAQEVTPC
VHHPQPQGQELSEEKKHLCFACCTSVECERRYLKPYIEAGLSFMNRSRMDVLICRATTAE
ERRGLFMVLLMLRRAFKGFFVSSDFSMDEDESKWRGVSKGHCSEPYEERYEHKRFPILLR
KQSRREAERVLLLIIAAFAFGIRPLRCAEELLY*
>TCRU_8241 hypothetical protein
MALNRNTAAWDILYALALDGVPGDAPSDRRVADGTAAEEMAEQLEGHRVKPPQPVRIRSK
AVDLDSMRPAMDASGLLLEAEKLLLHEWPQTSVTDRTSSFGDGLGRVMGPDAATWDLNEA
QGLPQPTESSFPGATVAAAVSDVPRSSFYPLKAGRPSEMLTAMNEGSPVQGSSKMKSVTL
PGTSGTTCWRFCEQHVGGVEQTQGQEGNTHAEKLCMEPGSHDGTSAAISYSDSWNHNRRG
ESVHVEDEHNTSKASFNKLLTATPTVHCNPQTQVGHEHSTAFFSLHPLSKNVMQEWNDGR
DDEKDEAIREKFFRVKEIRRLRRAQRMPHGETCHGSTVPNAMMGLFHQHLDVLRSVHHES
TAALEEAVQLLLQERKWITMRCTILYDRLQQLNRHRNKMIKRLQTVHGDSTTAFFADMSV
EV*
>TCRU_8242 voltage-dependent anion-selective channel 1
MPPMLAAAKSLTLYKDFNKDVKDMLTKSYSDAQKWKLESKFKGPEDKLFVNPMATSDGKF
SVDVEYAPRCGAALKATLEPSTCNVNLTASYLCQGHKVEAVGKKNGEYELSHEFVMPSRM
SSHAKLVNKTVEVGVATAVAPHCQVGCGALCTLDGKKNYDLTLGCRYAYAGYALAVRTNK
LRSYTTSFVTPIPKCPHHVLVGAEVVCGRGQGWTGTLGFETACVLFKGNTLKARVNKNKE
WAVVYIAKLVDNWTAAVTLDKNLKPGVLLTHS*
>TCRU_8243 hypothetical protein, conserved
MEADGALILDWSVARKTARSHPHRAPRFVRIRGQDALDTIKLCMTLRHNKKLTNLTTAHV
ERALVPWKATAHSTKRGALRHAAQIVGTHDLDPTRDLAVGEARRPVRISPEYCSIFGEVH
HTADPGVVAGRIDVKGEAAERQELWLRAEERFFHDF*
>TCRU_8244 hypothetical protein
MFSLLGAPFGVPGINYVTVLSMMHCTPDATRRALGYYRSISVATIEDSFYGVMIGNLIIT
CGVLLVHFLVILSLKWKGKGSWTRTAERCFFPGIPLLFLVNLFVGTSFASMQGLSSKVGS
TLVLSIVMLLLFVGGLIVVLCVSMAKARLTFYPILSLEGTTLLSKNSCMSMLAAGWLLRV
DGFWLPATVANGFFLLLMNLRRSRVVWVTLWLWAPLVVAVFAALPAQTAAGCIAIHVVLI
LCHLIFFGAVAVFRPLISPLDNGYYLLVVLVSVWLLAADIELLLHPDNEPALFAACTAAI
VAIVAFFVYIVLKTLQVIAFARRKWAGADVR*
>TCRU_8245 hypothetical protein, conserved
MLKVVPSELQFGALAVNDVPVYCRFSVVNTDPMVSLSVQFTATTVPAVIRFQLWDDMLLL
DDDEIDSGGAQKDRQKRGTLSLFYSALFEGISVIDRLLLGPLESREVVAIFHADPVQFST
VMVQAPPVMVSGVIQLTAASLPSAVTSSPSDTDANRKHHHQHKNSNSHGSGSSSFAMFNS
SLHLVDEKKECNPQANKISPHSTSGGASKTEMSSHGDAAVNESRTKSDAGGRHDPQTSSL
SLLFSRSPTVAAVRSETVTLPFSASVFLSLLTVSRSELRTTMAPGKTHLMDFTVTNASSL
PLPFVIRSQTIPQKNMEFSLYEEDKFEEPKIGRTLWLDRHASMNFTLMVRTSATALAGCT
RGMQEYRAVLQCDNLRDARNSELVYVHINVVAAESQTDLVSVTDPVLDFGEVYRGTRVIR
ELNVCNTSRENVTVRLLDSRPDHCEGVLSLVRSCSTNGNGNEKNNASRTNTNSNNSSNDK
NKNEGNNSNGNEKNDNVVTVDEVLIVPQRGSVPVGVMYVPSTDQENKATSSLNFEFELVI
TGVGGSAAANAGSDISGRHQQRLLIRSVATLFTSTIVASQKNINFGDCQVGQSRRCTFAI
ENPSPLPTTIYVQLRSKIVSIEGVQPRVSAAGGCETLEEFSVAPRSSLPITLRINPKRVN
STYRKQLTIVNVSNPAEDRIIVNIEANNMAPSETKLHDELYTCESKAHCDDGNVDGGGRG
EDGTCASGLRSLTNVPLIVAYSLQSKVEYPLVLQLKSSSTEIETFFLEGMSENEFEAIAA

ELRAYCCYGCEEVVEQFSVERAEEVRNSVVSALQHHTVATSSITLEPRGGRTFYVRIDRT
TGDVDAVTKEDGISIAVEGIEVPRFVRLSYRLCRTRFQLNGQKTKNFGEVNIGERRTTKL
PIVNQCNSLLLLQLSKSRSVTAGHIRMENSDKKCIYCRIRPYATKELELSFYPGIKGSFE
ERIRLTNVLDPSNEVIMTMKATVTKAETFDVSPNSWSFGVVPVPLPVHTLKQVQGTIVGG
GGSGTAVSREDGMPPSVRIGARFSVVNTSNTRRELCLKLDTPAVAQTAGGGGVGSSNPGS
GNANNNVVDAGMSLADRFFKFDGVDVRMQLEMEHGGASSGSIRKLEEKIEKLEQKLKIYR
RKNKMEKVVVAMRQIELLRCALMGKEVDPNTTSTLGEAAGAAGGGIVGPNELSESEDEKM
PVKPKARQLQHPELLSLLLCDGVALPEMNACESTIIVLTLTCTRTTECIPPAQSGTITFL
LCETKDKEANRVIPVDITLVPMEGEDDGEATAASTRPTAGSKLFSTPSTLTIDGLAAGNS
PPQSVNDTSFLAPGAELANALSPLKMPVKLATPVPTPSFFIEPGEGVVATSFMRCPMAIF
THAIAYEACKFTILLRATDETAFVVLDPLRCCGNIINSNLTNNGTSTVSGGNAGNSNINT
SSTHVNNAPAAAGGGGGIVSSTAVVPIKTLDAHFKFVPRNGVVRASESFSITVECTPMSV
VPQRYFIPVKKLQHPSDITYFALEMNPMVDEDLLQVSPREILLRDIVMPCDESRLEVQSF
VVCSRFTMPHALLIRSNRPLLVSLFEDAKCTIPLVSPVHRVFLHEKLRIYVRFRPSERSW
RHKSRLVTAGILVEAIASEMGRETQGCYSVLAQTTLRLSAHVGSGEVLLRENFIDLGAVP
PHCRLAHTSFTLSNPSDRFEVRLRVMASLTLTQVETPELKLSPGAEVQVPVSLQLATPGL
LQESLTVFNLSCRQKPLPIGLSILRLDEAISATVAEKGDELQKQQQQKAEEQCAARRLRE
VPMQPHLESTDEAVVVVLPTAAVVLGEDAVLRLHGPVTTATMHMTNHSTRDIILVAKGTA
PLVLGLPRSSSPVEEVASPSTLTSHVYSRGRVRLDARQTQAVTWTLTSLPNLTVQQIQCI
LRHEVLTIEQTAQVYVAQIIDEVVGFNYNAMLFPMKRSLPAVGQCVLLPRFCLTFAMSEG
RVETPLIDLGVVSIGRSNSTSDTDTTAPKEGDTDHHHHHSGHGTPKRARNSATAAAAATT
TATVNSNPARWKSSDHRGSGTQVVIHLTNLSPILPLCLSIECEPTVRFASNHIVVPPLQT
HSVEAFLVVKLIRTQGPFRFAVYFVNELNPENDMVAYVTGQYYWKAFDLSCDGVMNIAQE
SLSMEALRVTETSTTTDILSESKIVMTPVEPNVEVVLGVTENPKLEGLIQLQVLQYDAAA
PLQKIVFGQTKHASANKAGSLPPLVLNNINKMNSTNINNNSFGGPGVVTTTDAAVISSTS
FSAAAIAAAASAVNSNTGGGSGMGGNTNNGLNNASIGGASSVNTMNTSLVTAVTNSSPSP
AAAAAGTAASAVASVPALTKADELVMGVPSRQKEQHPFRLRCLLMREDFAALSAAFYGQR
KIKNADIIRERQALTFEKLADLERRRVTGSPSMWLGTLQFSNSLTGVDEEVQVFSTLGAF
QTFTVPLRITLTPQTASTVSAAAPTRIGGEGGAETNRMHYGAETVYTGELVVSNPCSQHT
VVLSITPLRDKAYQDTVAFSCIQLHEMPTPQSEGLKLPSTPRGNISMTGEKKHTVTNAAD
PTAVFFFPPPPRTTTATTAAATVLTSEVPNTDETTTTLLSILPQSVQRVRILMRVDASRH
QPSVEQAVALVLFDESVPCSVATVRIVLAPLDEMAQQQHKQEQLFLQSSGSRVEARVAAA
GSADGGGCEGLLEGTVGVDRSTMTTTTAMRSASPTRAATTSGMGNINAAGGIAALGHAYW
ASSSPSSSYLCVLSLHGDCQAVAGCQGTYTCRFTYAKDSPPPTGITIRNNLSDTVVDYSV
TILSQGPQPWLLLPSATAVLEPGKAQPLRLNILSTGAGSFSGYVGISTSAAPGEMLLLQL
TAEVFLPTAGEGLFEIVAPNGQRMSTNAERSVFIGRLFGAGTHRAYVAFEIVNRANIPLE
FPVSVVKPFRMEFNNTPDEGDDLSSATTTSTNTIAANANAKTNAGGILNSGIGRTSSQDV
EGAEDDDGKQQIGVDARPECDVRLLVCHLHNVPEMRGQRRFVVDPKSRVNVSFLLVCDRL
SLPSGVTVSGEAEVVLKCKQARDARFVLKARFQVCGSSMVSPRQLFFAAAEDYTVTIPVK
NLRSREIRVTFRTASPILDVLPGQGREKDGKDEEEMEVDGQPQPQPQPQPGENHTNLLVI
PGGGSATVRVRLDVARVAAMLSWGASGDMAAVLPVLYDHGLLLNAQNPSERVRVELCYVP
PNAFLPATPFSIAVAAAAQPIAKSLKVGRRQISEQRLFNFVRSFWRVLLEAADAFLPEFQ
YYTAQRGIEATDATREATSHIISATAGANSNSTSIVNTSSSNHHNHSNNRVSHTTAGAIA
DYRPALCSLLVDLTWLVEELVHYSVLLSNSRSIEAYGVFLTAAVTNHPLMRAWRRHKANL
PNTRTFAIFGQYWETIDALPCLTPSSD*
>TCRU_8246 hypothetical protein, conserved
MGFELAFFQAIDESSLVSASLICVISELLGATFVSVCLGILLRFVFPWWEAQVRVPLRKW
PLHEGVSHMSGAPKKKLCAAVVNDVSPPCPVQSPRRISLYATEIVAPLNEPTCSAKGGVK
AKAPSNEGISLDDFIEQFFSEAELLDDALLSAALSDAKTATGGRSDRR*
>TCRU_8247 Protein of unknown function (DUF563), putative
MRRCRPVSGRSLRHVMFFIAAVFFIWVLVVDLIAVRFRYDDRAVGRQRTAARPRADMEEL
DTYSSMYCVGHQFNDPRRANVASSFHPDGPRSSDGGEMDAGRVDIVLNGMFLPDKTHNAS
LKEDDMMGSADIYYYPIYNRTCLYKFVYFDKKRNKFFFYVRNISSYRRLLAKGKLRLPPV
SLGSRPLELPRTGLNSFRRKSYWAFVYSPVVVLGPRPRDEAKGGKLRRHEEASAPYHNTL

VAYFLPTASPWNFAHTLLCDLFGFFLGSMEIQRAFAHIFPSEVNFLSEALPDVQLIVTSF
RYFSKDRLPNSNKAFAFFSRRPAIYDVALPSGVYRGLLAGTGTKSWSWVTPSYSASGSPS
LWYSFRDYIIRHTGAEQRPYRRNYSSPNSLRPPRVSICHKEDNRGILNEKELLRSLRERF
GGVEFFLETPVGRGAKEQVEMMLATDIFVCNEGTLATVFFLMNPGSVFVAIPLVYHSPHL
HQRNMSHPDTWWSRPDLIRVDPRFNTGGNIDWFPPAIPWVRVTWYNEIPLSEASIQKPLH
GLRNYMPDYNVRIHLGRFASLMERAIAFLRGRGTLWNVNSSLTLFKQSLRFSKLVHDGNT
TSFGSFEERHQYRFVSLVPKNFTNVINNISLRRIFYLHETPVEIHRFRGRTHRPPNYSIT
ADQCRRLIHLRPELSTSFNTAICRYGMSCLCEFFANGRYPQRSLHDKWRLSGGRCGGEES
WPVYWRRRPEALHTAVRTRTTDGSEASFDLNEVTDYFFDVREERNLSHYLYFSKAHLLES
YRLAEFGLHLKAEKDIVKRLFG*
>TCRU_8248 Polycystin cation channel, putative
MHGDFSQHLRHARFPFGNTPVTREMTENGGVVLQNADVASSGPCHGPPREPPPPPPPPSQ
ANGGKTQAFLALFSRHHDFNTRGCKSEHHRLINEDFFTDPIRKLLRDGNFPFKLVVNCLM
LLFLILIAVMFHAPENIANEEQRKAVLHSFVGNDYIGKDKGNIKFRPTVYLHKREDVLKD
IKEFVKVYYALANISVSELHYYYYVVSEDGAAALRRLMESETPEGSDCFEAIVHGNVHDL
DDAGDLVNLMCVLPVSMEVDAYLYSQREYRGPSPLRHFSVQLTEKDPLGPFSDDREESST
DNRDHRAAHSDRDKYVESVCAPRYDEITGLYYRPCREAPDTSENGTSHGTDGENEGFVFP
LMDNVYRIRLKASIRHLTDTFFNRQEATSGFETVIYHWVIEKVFSFHAGGLVEVEFMISV
KTRRICPFAHPRFFFSVALLLLAVFDIVLRYRALRRIATSRKRVAVPQPTLREEDSLVPL
PQEISSEFSTHAVAYSTGSNASLGAQGDSTTSHASPILYRRSPRSRKPVTRKVKHVPRAG
SLVPETVYTDFYDAWREHLQTSRGESWHYIAIVADTLGLAYVFTTSVRLWGISTPEFCDT
LESIFLGLTGLLLSVNLLSYIRYFPQMYFAVRAMRRVIPRLLGFAMSVAPIFFGFALFFC
IVFGPHSNGEFSDMGFSLVALYFVMFGDAILPAIEDAEGSVYLIVTVLANFMTMLFILFF
MMTMLNLAMSITQHEWGLLRRRFGSCLSANNLLFEVRTRDEVKTEAMEVVIANMELILHI
KSEERLTADAAHERHGEENGSSGCASDTVEGLSRSPRDLQRGDVADMYRRRLDELTEGIL
NEDE*
>TCRU_8249 hypothetical protein
MRCEACDLRSAVCLGSGGAHASVKPVRFCYVCGALLSPIVCEEKASLPTAEGNLVHETTV
PTARESVSFKEIQALLRKRLLARGDSFLISCAPLTSTHQERYSPNMTLKPPPPLSCQGPP
ELVAWRTHSFCDEDVSGASDSPLLFARLTRVEEALSEVVLEFNTRLALLQTNSLRDVNSW
RQQTSELKAELCQRKVEVMTLKKRVEALESKLCKRDTTHDEEAMEEERNREAERCWRSKL
EEKGQESLTAAYHLLCDTLAITHEGSRIDETGRNVWSCGE*
>TCRU_8250 WD domain, G-beta repeat, putative
MAAERGRYIEYVKSSWRCGLSDRLELYDAELAYRMQPLKPHTNVMAYMNEMQPPQAPRRL
SIFESLDLMKAGSHLDTCIQLKPKSEAIQRLPDVFPLTCSESRTCSLAVGVEVFGHEAGI
NSLVLDETEGLLLSASDDCTLSLYNTTEWKLLQSCRTMHRAAIMYAAFLAGDTRRVISCG
LDGRTLLTDLETGHPYHKCRMFSKATSLVTSPWWPDVAYVAYTHGVIARVDTRERYSMNE
FPFTVSPREGEVIHVNTLVSHERWPFLIASGTNTANIYLHDIRMNLHRAYALLTIPNLSN
KTRSIGGLAFSDRGDWMAVNYYREDVYTFSWLDALYSSSIPGEGNDDHVELDNFSMLFHI
GRRHVPSIPIQNAIRLHGRENVRSHFKNVTFMEDDSIVCTGGDDGSVYFWRRDDGTQLHF
TPGDSQEVRVVRYCHSAGKLVSAGADASVKVLEPSRSVSAGVQRARALCIPPSFQESSSN
RVSPATMRTGIGAETSLLPTPDINTSSYELEADIHFSSTSSLLSSSLDHASLLHEEESEL
SLDEDSMNKSFIRYARRTIPGRSTLTQFNTVLNLQENAPLADLILATKKIKDASELVENA
LSQLFCEDEESLYLLSRPFLFELDSLEDLNIGGESETPLFHEEDGSDRVKRNKENTTRGE
DDVDIQFTQNTVMNQAIYSELCKKMFVAVEKLLAYVRCAFSQWTVPKVGAAQIPHWSACT
WGIAALVPTPLDDDWLMNTLNKPIGSPFGVRERDNQMNWQDANHVFSTVGSVDVAASMGR
LRVRCLLYMMDIVLQKNRFLLHKIEDVQSYWQFCAGLELNYVYYYMALGDRESALDRVAG
LERHAEYRCVTELGAVGSACMEKQRSCCELPMIIRMLRVLDADAFPPLLIPLALRIRILV
LSSNTGCAVIAPIVDHIAGDDAVTTSSSAGDLGEEQEEDDEWQNEGRGDAEVLDENTRRI
SVLTREMRNRLCGHSNVVLREQVRRMLRQIRVCV*
>TCRU_8251 mitochondrial RNA binding protein 2
MLRRLSIRPVFAQRYVVAGYFTLSPVRFQGADSSGSEAPADSNAKHDTNTSGSASRWRRL
SASQLRARRPQLPPAFDVVHWNDDDMSSGHLLRVLHRDSFVVLDYHRQVKKIGEEGNKAE
RVVSVMLPAVYTARFLGVLEGRLDKVEVQSRFTNAVFAPDPAAPHTFILNCTSTRPPQQQ

QQNGGNGEEEKFDWTVKFDVAESLMLHRFLTQALHYNTGFARTLV*
>TCRU_8252 mitochondrial import inner membrane translocase subunit tim17
MSTILDPQPPIDPAQKALMMAKDSTLATAGMNVVGGYIMGFGFSLFGAMISAETSTQRMG
TADFFRHSLRSANKLGGNFAYFGFLFGGIEVALEKRRGRKDAWNPTASGAILGGAYGWRY
YKAPGLLGGVVGGAAFSLVFERIIDALGFAQH*
>TCRU_8253 hypothetical protein, conserved
MSPVTLDPIYISFHNDDESMTPLCLVDGRSDTFMVTTGGFPQDIIFSVGTSASSNISHLQ
LALHEAKHIVVEKCTTALPNSFEKLAERILTRSSDNTRQVEELHLDMRSAGKGIRYLRLR
LLSGYSQFVGVFGVTAEGEESQQRIAVLESRPEVVM*
>TCRU_8254 hypothetical protein, conserved
MPPLNSRATRELVKRRRVIPGPRSLHRGIHFHENEKFVAAYKKNSGAKRQDHRDLLVHHQ
KINEELQDVYTRTAALHAENATMEERIEESWRQFERIGGKRPASAVSALSRGSNKSDGAT
LRTYDHLRNNKTGVGFADRLRQVSQEKKELRDRSQLERETRGEAVDYSKGSALHAAKDKR
IALFQRRQLKREHLLRRMGDPTPLKQSGRYDINSGTLRVFNKTIRRVQRDVRHDERTQQV
KERRKGAHSMWDVRGGDENPNRPSQGILRYTREFELGPRQRGKKGRRGK*
>TCRU_8255 hypothetical protein, conserved
MSVVRIQLMGWEEGYALIDLQLPVVTCVLAVIVFLCRRSLGALFLRAVAGECSLADDGHG
STTGQAASYRPAALLMIFRHLPELPEVIATFDAHFPGVLNENDFCAFAKRRVFVHLLTPD
GVREDQNLHQDATHEVDGSRNDEDNSLENANLTKGEVVAPPIVKKRNWGRLRRLLLGDRR
KNKQVKKKKKMMEEDVKGRKGEEVEEEEEEETEFCCAENGGTQNGSNSGRTQKTPLETLI
LQCEEYQWERLVRLRAVQLLNTSISSDENDIWHVHYMKILQSVVKDEDFDDDSCRVTCGG
VLVCAAPRSPVPLLQMALQSGLLCRKMTLHGSEGPAAEPPIIESPVMLSVLSLFFSYLLE
NFIYCLDLVFSNLVHMLHVLLAYITCLWSLHWHFGCSQLERDGSATRTQFMPTEELPGSL
WILPSRSTSLFQRIAEHVNKFALSSENRLVGVCVHDVASAVNLGTLGRVMQQDLQDVYAE
KKSSSSSISGVAAYISRLLFYFTSVSVWLQRRCRMCQALSLGETRFNSVFFAEAAVAASP
ANTRMASSESPTTTTTKEEEVAAWTGDEAMVNRLLGCVERRVRTAEGLPPHPKSTTLSLD
APACGCHNHYYRLGREVPVYYFGGYRLHAMYCTAMPPISAQRSPHTPTYTVTECGGATCS
MLWLPHHSAWKTLTTTTTTTGAVATKSLENEDFFLDELSRHFMEELLAMANLFLGLTGME
ALEASSPI*
>TCRU_8256 hypothetical protein, conserved
MYVCLPRRCGVRDPYFTLFGAAEVDGEVVQSRAARAWWKRLHEPVEDPSKSKCTMRFGST
GKEETVGGLGELQCTRLQKMTCVAEFTLTATLGAFSRGRESFLIYLEVLDDASCGRHFHF
IRGWRTGDKEEKERRLAQRAAAGTLTRLGIVFTASCISSAGCS*
>TCRU_8257 hypothetical protein, conserved
MRQLIHVAPRSAVLLVVMRFVMCCACGCFAASLTCSCSSDKAMRADRAKSIPAVVRDVPL
GSEGASQTCTVIGRNGWAPTRIDVSTRDVDGTRKYCSSERYCAMNSLVAIASVKVTFFYA
EEREVFVSLYLAATVR*
>TCRU_8258 retrotransposon hot spot protein, RHS3, putative
MVLTSEKGWPYSWRWKENKSTRDCHVNCEVDRVWQIVKGDLTEWFSSHGGNDFEPKQRLL
IGMPGIGKSMAAGSYLLYQLLHYDAEQLPMVAYVIGSQSFLFDKTTKTVSTYRGDPRIDD
VVNIFSLRGVKGYCIYDATLACRQPPAGLPCRGWGMIVMTPPDKNDYERWAKKWTLLQS*
>TCRU_8259 retrotransposon hot spot protein, RHS3, putative
MDHWVLYEPKVQNFPLVDGLFFVDSNPKTLVGLRLATAGGHHTRASTARQFTEYLAAYFN
GWEELSRDMSWEIIYVQHADSTPMNDWQRCDVVNPNNVSDDGSREIAAFWKEEVRQYQVS
VSYRGFRGDEALRSEEEPSK*
>TCRU_8260 hypothetical protein, conserved
MTNRVDRSRTPSRTSAGPHRYPAWPGVVGTYCDPPTVARSVEFSSTTLEFDGIAPCSIIV
PSTDVTFVMLTRAWGIRRAVLSLRPPIRSCAPPASTQWHSVTFSASANTSIERRSTVTVI
GPLNTTESKHAVARPPPTATDSVSVTPLTQSCAPPPALATGTSNGRHASPTPPARQLHTQ
SENDAVSASKHASAAAQPSHGTTLTDDRPAMR*
>TCRU_8261 hypothetical protein, conserved
MRPSQERQAQRDHPRQQCSVAHKAQRAPSSGHGASSVEHPPRDAVVHVALHQQHRPAIQA
HRRIKRHRVVLRRQKLVPHNRHNGARHAHSPTHRHRVLAQQEVAVSKRHHGAATGSNTAL

HRHAQPQRRLHRQPVQVQRTARRQRHAANKQHANSAAEHRRHMRARNGQHAPRQIHVVQH
EARGRVAKAVVAAVRNTRLCNQHRVHHSDARAWRKSVRHQHAAARGRLKPADQHINALAS
RRVGQPPNNVQARSAQKRAVRQRHVAHAP*
>TCRU_8262 hypothetical protein
MRGEVDGDCGAHGESDQALNDGQGRANESQMVLTMRLGDFCFNFLDKQEDLFDEAREEQC
ASKSRIVYNPSLCSTPVLMVQPTPDSKKGSIRREEIRSLCLSREGTGASSELWVSFSSAS
PPNWSSLSLFDPDSGNSEEPEPDEYIMLGEGGFLDKICGGNLEPAASDGPMRKSTGDHSA
WAHQKKEPSVVAAKSSASSFRSQVGEEMTGKKTAVLGEGKRNARGNSLGSLDIVNRSLPE
MPRSLLEQCNIAAAPLQPDGSDSEFGLPPYYFTSLMDFMSADPPSDEELPPILQAHEGKK
LSKTDFSKERLSRYHIEGKRQNVNFQRVKAVAFISSLGGDESCSDVPPSIISQTGTGAVS
VIEHEELRNGRILQLKSSYDMDEVICSTEVGRSQTLTSLLNCVHCGQRSFLLSTYAPGFL
STSVRLTRDFLKKLIQRYREGEVVDRTECKIWISLAAITTPHSAVDMLYPEDEEGNVVPI
RNGFIALCGPLLMDLTWREVPSKECLADIASRMRRRLRRHPENMVVGTILVRERALHMDS
EINIPKLVLTNFTFALTRDPRFFCSIGQARASPLRVFFSDALGGAALTTHVTCVGQSTSN
GLTSDYFDYALMLQRVMNSRPFVCDLGLCYLKAEKLLQRIGDLGKSNTSISNDDIETLEE
VLSDTEWLLHNADLAPTKCIRVRTEHPSTSIIFSSEADFLEKDGAKQRRRRGTLNGVAKK
TARPNPFSSPHEASDENTLLPSL*
>TCRU_8263 hypothetical protein, conserved
MQEAYGTHWFSPAGGTPQPYMQMPQQSYGGQYTQGPNCYGGNIGVDPYYKDQSTKLFSGR
NRDVQNSHGGFRSGGTYDISTCGLSGKNSGNEQQDNLAENEVFGSYGMNSMGGFDGAIGG
GSMYFVDEPPPVVYKIFASRRDRTDLMSQGNFNRYPSQFSIRLGSYGSVGNGGANFAREK
RQFFPVDSSGISKEPEVIKSREPNIVPKEFNEDIQPRRPLSPVGYGGYPNDTDFGDQSST
KPFASKDEEHGQEEKAKDTWGHSSISTGLNIRRAPQKHSVKDSRMNDDVRGDTSGEQEEK
EKEKEKEEKKKEKEKEQLEKDVPQSIPLSRSIGATSHNPPCVGSTFGGTETSNQLDSSAL
PGPDRSLGGDKLGSHDEQRVKPRSRSIRGSMRRRPSMSAARSASAVNVSIAVFPEADELQ
DGLALDIVPHRRMSGSQPQLNAFRRSQFTAIEEPKQGEHREQRERSRVAEEPVRPQLMPK
KAKETRQEEQKRLDEEERKKNEEERLRRKSDERKRFEEEKRREEQREEERIRQLVGNTES
AESPEPKTKLVGRASGRSRPTSRRGSLLRAIPEQPPELVVGTMKDTMADTLPLSREHSVQ
RLSTRAAGQDRRGSDGRPGREHGGNEKGQDEEPPRSTSHESEKRKQKGEVQQEGQQNDSK
EQRKANPIKTLVLLERGSQGPNCISAEGNTFIYHWKRHEATEVVIRDLNSMSYRSNLFND
VRDAVCDSHNAAILSVEAPNTGTVFNSPVWSGLIRIVSGVLRNNRIMREGTAELTAAFGF
VYKDKVRDLFDGNGSSFEPLVVHPSPIYGPRIPHLHYGKITSDSAFEEVMSSALRRANAD
PILTTRDGVAIAFLLSRQCRIVKNEAGERTCDVSLSSLVVASAGSDSVPFESALARLKNE
HSMLFHLVLGGPCHTCFMLNLSMVEERDGANRERVERLIELQGKMHASSNYPLRSGSVTR
FVRYVESANKEALERLKVEENPERRNRLERYVQEQEQLLADANKMLAEVREELLQKFSKF
S*
>TCRU_8264 hypothetical protein, conserved
MNQAIRSRTDWKESVVFRLACITASRLFEIAALTPNNFTLKAEGTLILGWPVAPKTARAD
PHRTSRFVRIRGQDAFHTIKLCRTLQENEKLTNITNAKVEQTLAPWDATAHPIKQGALRH
AAPIVGTHNLDPHVISQLAKHFDPFELPKNTVRYLGRYTTMLTQVASLVALM*
>TCRU_8265 Enriched in surface-labeled proteome protein 1
MGAKLNDSDNTVLLGLSYNKEGKRVVLCSGQTTTEHSRNWEPQTTHQVAIVLQNAKQGSA
YVDGQRVGNAQLALQDIKGSKVISHFYIGGDGSSAENTEGREGVPVTVTNVLLYKRPLSS
AEIAGLAKKKITILKPEDPNTLVVDAQSSATSGSPVQGAVSLSNSAEQLPLEEETLKANI
DAGAGGVSSAASVTTTPSSDFAQTVTTGSGDTMRGDGSPQTPESSASSGEDEGTVGGTDA
QKEEVHPQAGEVNATALNSSLGNLSQGNNSDGGTMRGSGLLPLLLLLGLWGLAAL*
>TCRU_8266 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGVCAVVVSAADSGIADASDGHLLHNGSGGGVGGSSPSEAGR
PGGTEDAMGKISNVNGSDSAGSVVSGNNLLFSGGGEGGVSDVSKLKLPPVEEGPNDIKNQ
PQALSGVALPPGVDSTGTSKPDAEKPSSINKSSKGDRTDDVVDISLKKKEELTDVNKEEK
TVLPPNDSESPAPTELGAEEGLKGKPASGVASLPAKGEEGLPETGQGEGSPRSEAASSAG
KQQDSPTVSQQQTHFSLSPSQNEIVPTPGLGKGRAAEDISKNIPPSGNAVQKEGAQHETV
AGGEKPTTPAANTRNTIGKTLPGDSDGSLTTTFSAGPVASRRSTQVSGDAINPDGLNFDA
SSDNVAHNNMTAKVENATGSKETVATNSGKSTTVPETFTDKAIGTVTTGDRDGSTAVSHT

ASPLLLLLLVVACAAAAAVVAA*
>TCRU_8267 hypothetical protein
MSRERGLRQRFLCSGGGGRQGAEGGDEAEPAGRAATEPLVAGSVGVRVQPHGHPHGCCAV
LLPALRRRRLHDVVLPLQAQLGRQAAAHDGQPDPRVVAAHGARAPVLVGRCAHDCGGEAA
RRCGAVCVARPWHAGDCEGRGGHGAV*
>TCRU_8268 Enriched in surface-labeled proteome protein 1
MTTHSVGSQSAEQLASGGSHDVNKNVNVDSSSNGNPAVGTVGGDTKQGNGSPQIPVGISD
TADANTPTTEGEGQYGPTVNPEAGVSSGENGETVKGTNGQEEEEIHPQDGELNAAALSSS
LGNVSQGNNSDAGTVRGSGLLPSLLLLLGLWGLRLCEE*
>TCRU_8269 BSD domain containing protein, putative
MTSVELVSNPTNELSTHRWTVNGLKHLNRKNKLSSLPFWAPNPVMKKHQFRCVLIRGMLA
RVRADDDHIGLLLELIPPPTGDDTTYPGGCSITVRVVNRLHESGIHNIEQTETVVFAPGQ
LQACFPELIPPTILNNHEFVEGDGISLLLELTLETGVNVAVEWANKTVSRVWDAVCDSVN
KVVRKVTKAYAETREEYGTSVVKEEPQSAPWDIVPENWVGREKEWRHLISEQIVEDEGTF
RYGPNRGFSKDEQALLLQCGINQRLITNAHAQFDYDRDVHAGLLVPPGIRQQRYKLVPGK
IKEEVFWANYFWKVAALGLCKNDEQVRMLLTVLNAPPAVKARDISSIGSVDEKTVLEHVK
IAQETADMLVEYLTDEAPYGEMLVEAAATSCQGQVKQLDGYFKRTDLSEETLKMTGFVLR
RLRERLALYAEWKEKHPVPLILPKESECNDDHEGQDTASAEPLDSSHASVSRKSEAKQEF
TADAREPHATSTNPPKEAGDPARDKVEFPLMPWEEEEAEEQKRKKEEKKEK*
>TCRU_8270 hypothetical protein, conserved
MRRITAFCLKSLAATCARSIATGGRVTNEDRRWWLIHLECAPDVTPGTFVAWLDCCGTHT
TKKLIERNIWTIEQVAQLDSDQVDELKYREGCLKMDVVWEHARTILIPLQQREASGGVES
ELQSRILELRKKRELERKREELLKERANINEQREATLRKLREAIAAKKAAILQKKQEIAE
DADNKKDNSTASSSSP*
>TCRU_8271 Kinesin-13 1
MSSWELQLLEVLERYSIGHLIGRFMDAGMSCDDLLSLHIDQYRNYGVTDDEKIHLYQAIQ
HLRREANGRTKPSSPEDSLMMMPTFSVRPTMSADIDELSDEKESRERQYTERGTTVLTKS
ADSREIKRRKSRIVVAVRKRPLNLAESQRGFADVISTNSLDELVLAEPRQKVDLTKYTHT
HRFFFDEVFAETATNADVYRRTAATLIDTVFEGGFATCFAYGQTGSGKTHTMLGSGTEPG
IYALAAEEMFARIDSGKDLYVSFYEIYSGKLYDLLNGRQSLRCLEDGKQNVNICGLTEHL
QADVRSIMRLIEEGNRIRSSGTTGANDTSSRSHAILEIKTRGREDKKLFGKFTFIDLAGS
ERGADTLDCDRQTRIEGAQINKSLLALKECIRSLDLNRRHVPFRGSKLTEVLRDSFVGNC
RTVMIGAVSPASNSCEHTLNTLRYADRVKELKKSIGERRPIEENEQSELLFERKPPMPAA
RPSINGRLSTPPVSVVNLPNNKNGNKSNSKGGGKCKSNGANLAAWKSEGSRRSGVMRPSG
LLPAKALETNHGEIGYKRGREFDDQQQQAEMLARKSVDLDIGVRYDRVVDEIVKLEHVCV
QTHRRYLDEDMKIIKEEFAQIMSVEMPNSDIDAYVTNVLNLLNNKLQAIHQFQGEMLRLR
SMLDEEEALSRQLEQSGQ*
>TCRU_8272 Endonuclease/Exonuclease/phosphatase family, putative
MFRRSTFHFDNGSAVTGGPVQGLHSGLRSMIQPCIAENVLRETAEIRRRMAAVVEMDTID
GKPVYEPSLPRQWVKAPLSRLSTSASRRDWFRLMQFNMMTDAWSPGGNANATTTPVHGVQ
ARVPGFTRTGADPDAYYPYDPSVDKELPPFLQPDFRRAYLVNEIRYYDPDIVCLQEVNRV
FFNDVLWKYIRYCGYGTLYQSSRGYKVRALRRGGNPLLPRHKGKIEEAEDIGNVVLFHKG
RFVPILMPGKDLVQNLHFAHVVAMRDKITNMTLNVVCVQYTAGESEEAAKIRLHEARQTL
QVLDALNRNDTDRAHMSNVICGDFNNVHDEEACVQLMRERFFSMHDVVGGPRWTTWFHED
AQTSAKYQKYYARNRDCFEETDASKRAEREVAKYTRRPIGGQNGGGKMVSAINSEAEKAP
CGAKPAVGQEDDCETQKKEGNEATAMMVEEERQDALALRKQTLKASGIIYRTQDFVFYEP
QTLALHQVLDVPEETHINEQQLLPCGKHPSHHIHLVADVSFTDVFPDVALKSLKD*
>TCRU_8273 BNR repeat-like domain/BNR/Asp-box repeat, putative
MEGMHTNQFLGGAGVAIVASNGNLVYPVQVTNKRKQVFSKIFYSEDEGKTWKFGKGRSDF
GCSEPVALEWEGKLIINTRVDRARRLVYESGDMGNTWVEAVGTLSRVWGPSPKSDQPGSQ
SSFTAVTVEGMRVMLFTHPLNFKGRWLRDRLNLWLTDNQRLEQPRIAGAWL*
>TCRU_8274 Enriched in surface-labeled proteome protein 1
MAKHRNTDQFGPHRISHFFFGAGNKEDEGSSPVTVADVLLYNDALFGDDLKNLNARTVPI
RHPAAEELHTAVKVTATGEEKQKVRQLDVAQPAAALQTATQLTTSLVDVEEAPIAHPTDS

RSVRVLAGSESSAENAADGLSPRTAATNDTSVPETNHSASDGRMGPEDRLALITDAKLIL
HDLRGDSTARVCVSCVLLLLLGLCALVAVL*
>TCRU_8275 Mucin-like glycoprotein, putative
MMTTCRLLCALFVLALCFCPSVCVSDKPAASSQVTTISSSTPTSGQKGEESGAGHADTAV
NVSGSIDKEHQSSDAHNEVQEESTEDTTGTESGTSTSTKRGTKGEEGPAKTTTTTTTTIS
PTTSTTTTTQPPSTTTTEAPATTTTTRAPSRLREIDGSLSSSAWVCAPLLLAASALAYTA
VG*
>TCRU_8276 retrotransposon hot spot protein, RHS3, putative
MKEKGTITPLARGTPNGVLTQVVTEARREAEERLRETQEMKFTISTDIEDVLFKGRVRVN
EMKLNDFVTRELDGRGVADTNRDVLPEEFFRDPTRYNRDEGALNEIQASGHYLGNEASCK
G*
>TCRU_8277 hypothetical protein, conserved
MTNRVDRSRTPSRTSTGPYRDPSWPMVVGTYCDPPTVARSVEFASSTLEFGGIAPCSTIV
PSIDVTFVMLTRACGTRCAVLSLRPPIRSCAPPTSTQWRSVTFSASANASIERRSTATVI
GPLNTTESKHAVACPPPTVTDSVSVTPLTQSCPPPPPPPALAGGTSNGRHASPTPPARQL
HTQSENDAVSPSKHASAAAQPSHGTTLTEGRPAMR*
>TCRU_8278 hypothetical protein, conserved
MVRRRRKRTASHQYLGARAKITPELQLTKIQHRRSHVHVHPRTTPLDRQAHEDALQQRDV
ECLFWRVKIRQIQNNRGGEGHADKAQTTHTGIRIVHGADAATVHAADLRVLRIGE*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MVYPEVAQSVGGGLSWLCYRNVTFSGGGMSLTVLVGAMTGDVANVTFDGCTWRDGAVLLL
LGNAYAAVGSLNIVVTDNNFIDALLIPEGGFPPHTNITISGNRFTVTRLIPRSGLNLRRP
SCVAMNGLAISNDSAVVLSGNVFQTVRALSSAIRVVRSALSVSWHSVFAVVGNTFHMAGT
NSTLIHLEGSSQTSSLDVLNNSAVVIRGNIVTRPVRDFISLLWVLRLESQSAVVFQGNDM
QGSSVVFYSSFASHIYYNSWLQLSGNLCRVSPVVAFAVFNSRVNLRDSTVSVSGNQFISS
TVTPTLIKILKRPRDLTNGAIVAACNTVNGGEEANYAIPSVYNATILTCSDQCALAASCF
PAYTTTASSDGCACTCAEGGHGDACLPVAVPEPPSTDGAELCVRDVRVDVEVSAGLGTSV
VCYVGVTFAADVLVDVGLMSGSVRNVTLANCAFVDGASLYVVGWRSDPPAGHRADVLISG
LESRSGGGVLVANRFPPGSRVTVMDSVLIAERRVAYRGAYGLGDASACLVLHSVNLAGSV
LTIARSQVAAVFRDAVGVLVVGGVALSSRGALYVDGLLVQTALGLCVSVEGGVAASGGSV
VAFVDSDFLLCKHAVSVRGAVSVSGSAVVLVRSDFVLTEDYAVAFYSTVSLADGSMLLAK
DNVHDGVSREMLYVAGAVTAVGSTLSFVRNQALLPRMLSLSLSLSAGAHVRVACNDAGGR
VLSTAEEYAAAGFGDAGSIDVVGCDDCDRDTHCYAPGTASASMRNGVCVCACGSDGYGEA
CVPVGAPVLPPAVGTAPSVFVREGVAVQSVFVVPAGASEVTLRHVVLDGVSPVLYVPWMA
RDGVRIVVQNVSLLNGAVLYVMGGRSLRGSMAAGSDESGPVELSVCDVEALNGALVLTGT
YPAGSVLTVTDSLLVAARSTPLLYLLGSQSSPYAPVLVLSGLRLVRSVLVVSGVALVTVV
TGGRTVVVDGAVLELVGGGVALDAAVFGGDYALYASARVVALGGAVLRVSGSQVYAAHGL
VFGGGVVANASAVVVNDNVGALTDGALLELRGSAWFAFGSWLSVRGNSISGRLLSVPSYP
RRAELVQSTLTLHGNAGSGPVVMDGTVALGDAGRRFVVGCLTLNGRALQPMDYRSAGIIG
EFRPVACGVCDADVRCFAAATRAMSGSCWCRCAEGGYGRDCLPVYLPHVDGCNRTLAPPP
LSYTATLTETRSPTPTWTPSLSATHYSPTWYGPTETLRVTETAALSPTRTPTASVSGTLW
WSEVACPTLAVTTTAAGGSLTQKDIRGGGSAVPTRLMVTLPPPFRWARDPQLGTHLSFVP
VSTAQPRGFGGPWGAMLRNATWVRNATNLSTVLELAVPVHRGYFIVADETIVIRCDAAAV
FGGCKGVLLGSFTIRSDTLPAAVSALSAVTGVAGGAAAVAVVVTGGLGSVLEMQALGVFA
MMPCALAQERASTAALPYFLSLFAALDPLWMVVGNALLAAVFGCVHCGVTAAFQRWRGVD
AATAWAAMRFPSLTYVVAHAMHLGIFFGSVLALAMPGARVQHRVVGVVGVLYGVAFPAGV
CYLIARHVGASFTRYWQFSRKPLHERLLYPVGYWHPAAQQRMYGGMLTNMRGGRVYWCVF
QLSVLCVVCLIAAVHPPVGGCHVLYFCMAAVLLAGASVVAFTNMMRSSFLTVMHTASFVL
LAALCVVSAANHLAPSDGGARAYVAIVLLLTTVLLAVTVYSVVVWHAEDHHWQELREPRR
GGLEALLRDDEESDEETQKLHDMASSSYASGTTVASSYRPPALP*
>TCRU_8280 hypothetical protein, conserved
MATSKESTVEFLTQACCGTIMALFRMGIVDPDSYKDQLVVLMSRYLNNCWNALLRGDDPV
VISTYAAINHDRPNCVFKNFFDLGTHAFPERCPEELLKYSPDDPQHLEDARIEVSELLKA

LFSENIPDDFWNHECDGLSLEEERSIWAQNGCATEEFFVLSGTRSLLS*
>TCRU_8281 hypothetical protein, conserved
MCMHESIKEICGNGDDETPSKCRGPKAEEICKKYTGDPNKAVDSSTELPEASPDAEKQVA
AATPETPKGGEAEMGSTQGASAGDSPANPTEGPESTSAATDTSNNEAQKGGAVAVPRNAP
ESDATRKDEGEEGEVKHSNTKETPAKAETMKNVTTTGDPWLSRPPQRGARV*
>TCRU_8282 60S ribosomal protein L9, putative
MKIRAQDRITYPEDVEVSVKDRIVTVKGKRGTLTKDLRHLQLDFRVNKKFRTFTAVRWFG
TKIDNSTINTALSHVRNMITGVTRGFRFKIRFAYAHFPISVSVENQLVEIRNFLGEKRVR
RQVVADGVKVYRTDPTVVKDELVLEGNDLEEVSREAAVMHQLCLVKKKDIRKFLDGIYVQ
TKTNVVAEE*
>TCRU_8283 Zinc finger, C2H2 type, putative
MVRRTAGTSRDTAQQRQGGRRGSGGRETRTPSSERPTLRCPECLNVFLTWSRLTVHLNAS
AHFSARCVSCDEQLRCYGPTHPHRHEAATGHSGFFGIFYIRGDYRLDHPPVLSHPQYRCV
CRVTFMSSLQIALHLRADHGVTEIPDEAVCLTCNIRGTLADLAKHRLERLMIKEDDVFEV
PGFSPAPYLVRWPRLPPWPLQVRPYAVLYQCPICIKVFSSWAAMENHITSNGICQCMLNP
VGVHPGNRPRGAEGQSFLPEEFEVLLDTSEPEMLSLIQGYSPESGGPAQEDGLLLAFQCP
EETCSRLFLTHGELLEHMEQETHFPIEQEEQAEGAALNRQSWKWNISAYEVMCSARRLVE
DFGFSSCPVCRRVLARGTEVYHQQLFHPTAQPSLPPPSATTDPTNTMTTTTTTYGATETN
P*
>TCRU_8284 class I transcription factor A, subunit 4
MESSTLANAIPFPGGKNILVALEESNLYIYCDLSQDLGRTSSGKNILIATTGGNKPLGAT
NAFLGLNVFCNITEGPKLTDETTSKLSEVEIMGYYCMWQVKGHTLCMMIDFENAWEKLAT
TGNSVVLASSGGNKAVGKTGILCGLNCHVPLGKKFLVEKLSTIVNNDFVSVGDTVELNEG
FVVHVESETQVTLHCEYEYTMETRRLAMPPVVIEGETSLILTLRFVDKKLRSEEKVEQMK
TEFAVLSPKWKNLLLRYGPNHNGNNGRGTVDFYLRFDPTQFIGRSFSGKSLTVSSSGGWC
SIGNEIFIMFNAHKPAPHLSPAEIRSAVQNVLDSRRVEEITSLSLKKVEILVVTALNLKG
SSLADVRGQVKEAVKAYMGSLKLSVPFKTAKKAVNKAFATRKREEFATLSLKTLLAEVSS
ELGAAHWEEETLKAHVKEAVMQCLWGDVRRIRGKGGGLRECGTRLSEGTTER*
>TCRU_8285 hypothetical protein, conserved
MSTKKKYVRGLQSSGAVTEEAGAALTAALNSNPRHRCKEFAARPAQSRVVNLNCLRPHGA
LQEGDFPTLTRSPETPESLLEDIVVMVNASQKLLRRSPDFQLITPLTDAVDVLRATAFRQ
KWIDTVAATCRSAMAYPFTEFRFLSPLPRGYSTGVSVAAEGEVVQRCIQTAETIQRILRV
FVNASNSGQWRFQQLLYHGLRNEKKSAEGLVSVNYNSRHITVCCGLFYYRVEVLDEDGFV
LDTVMIAERLWAVQQHADRNNREICEHKLLPDAREDLFAFYQLLGSLTEIDGVECAAVWE
RLKNTEPANAASLADIDTGIFTVILRTLDNKSASARWYRSALVLEEREEKGVLAVRGHSI
LIHADDLLEFLMRVLCWDDAAGGMSDKNNNNNSNKEGEFLGTGSVFNSDGKLPPGVEHLD
LWLPWKDRKPMRPYAVVTPPPHVFPLSISREDNIPFAYLCMAAVLAVQRVLTPFTEFPTV
LVAFPNRRGDLSAALMYSYEVEEFIRSFCGGSALVERRAKRYLFHKAVQSLAGMIDACFH
EPYPYYSMATLLLKEGKAIGTGTFADNAILGTVDLYVTVGMLGPNKKVLDFETSFLLPSR
FALICSASGNISHKSSSKCPSDAHLIYASLRGSEGNEEMSMGAQLAECITDKIQELRSLV
LNGNSM*
>TCRU_8286 iron superoxide dismutase
MVFSIPPLPWGYDGLAAKGLSKQQVTLHYDKHHQGYVTKLNAAAQTNSALATKSIEEIIR
TEKGPIFNLAAQIFNHTFYWESMCPNGGGEPTGKVADEINASFGGFAKFKEEFTNVAVGH
FGSGWAWLVKDTNSGKLKVYQTHDAGCPLTEPNLKPLLTCDVWEHAYYVDYKNDRAAYVQ
TFWNVVNWKNVEQRLSETGYVHLRSYL*
>TCRU_8287 serine/threonine-protein kinase, putative
MGNGAVKLRTDMHGDVPMGSLNEDDINDDAVTSVITLPKCARDQKMDGSDDMRPIPIGEG
EEKVKGSYRSEPVSLDEVLGPADSVKARYRKNKAIGKGAFGEAYIVERNPLYPIPSPKKA
AGGKGDPEIKKRAGDDATRLFVAKVMDLTSMSPNDRRYAQTEIMCLACNHHFAIIQYYEH
FFIDDEDETIIIITEFADGGDLYRTLHKESSEFCLSETEAGIYFVQLLLGLDHVHRRRMI
HRDVKTANIFLTTRGFLKLGDFGFSQQYDSTVSNPIACTFLGTSYYLAPEMWREQRYGKK
ADIWAAGIVLCELLGKRRPFEADSIPKMKELVLSGAMWLPPVLPENAGVSEEDRQAQKKM
GYISREMREFLEFILQQDPEKRPSASQLLKTPLMQHYLCLLKKRVDRMIALDDEMESNYK

ANPAGFAGSLPEYNISLEVRALVMSGIAEGEAVINFETEREMATSTTPRIESIVYKETAG
SQWKERYLILADGFLTMTLAKGKMAAGSGERSKKVPLQAIRAVAPVVLDVPVLAESSGES
GPFHVKFAFAISTQNAHSIVFATRTEQERDQWLSTMIVALKMD*
>TCRU_8288 survival of motor neuron (SMN)-like protein
MDRSAAKRAGNSQGSTAVYQRGKDDESLWDDAELIRLWNMQLEKKKEDDAAPQLDELRPL
SSDDDSMIASLSGEDMTETSSSSTPLPNTAKKVVPPVADTGAFGLDSSPLQQDGMRGLPA
EIQRVASAYYRAGYEAGYFVGRREKVANKTNLKKRRGKK*
>TCRU_8289 hypothetical protein, conserved
MRGNRLARRGDPMKTRSQRRKERRERISRTNRAQREKKRVARFTARKCMREEDQHMTAIM
ESYARRRKAERDAERAARQKEETEEWEAVSHPGGKAVGQISTATTKSPLRHHPVRAAPST
QKRVVVRGQPKVLTRSLY*
>TCRU_8290 hypothetical protein, conserved
MAVNGSGDYYHGLRIYPLRDVLSRVPLPSLCPLSGVSQKWRCVIVPKIQEAKSQDAAEEE
ILRFLDKNIPCLLGRWRSAPVHSAVGRDGMKFVRDPRWNTFPKPKIAFKAGWAGPGTRME
SPEYHQLVSSFGEIFDHRDETSPQRRKEPEVHVDDSELEEVLDDVAAQNILNLQLFHRQD
TSICPPIPVLGEKLIWPLFLEDGATCDNATRLSQRGAVTWWHLDDSGEFVEQTALSLCVS
EHTVTPPPLANLPQSQLAYFESIDRELFSVDELPGCVPVKLFLYGPKESYDWFMHDDESS
TSGKVAALNIFATPDEALPNDATLLPIIHVAVLESGGRPLISPPNIPHIVITLNDCVMVE
QRRIAYLFLDEVSYFLQKCAFWSGNPIIYDHIEKELQDESFVAGQLIPSMMRLFQEHDAL
NPYDEIIRRRVVTSLLTIAKHEKHYNLSPDSRRSLETLLCGGSAEMSAILQQLTLYGMRV
VSLEERLKGYWDVQQYWPKPGCVLKAPLVTPPHLLSRDLMAKGHGVDWFLPVVYVSSSPV
FGSEKTAMEDVAAEYFSMAGLARRRGDLLAFLRTHGKERDELLDELF*
>TCRU_8291 hypothetical protein
MEEPSKFSLVNRCHCADAGNALSLDRSFDFATSEEIVPIPVHEVELRQATYRRHGNVPHD
VSLHEFVAMLGINWEDTLNPNTKSSCLEHDASIREYYGDSDDEAYRIFQEKMEHFIMRDA
WLKGNHFIEKNILEDYVRLKRFENDALELLYSNDEDSIMALEARMYSEVQSEAHMESLRK
YRDGHSSRRLTKRLTFELCRMNSDESWGVNADCDREGVLANSPPHRQWRGKSYKEHYMKM
YKEAEPLQEPQ*
>TCRU_8292 phosphatidylethanolamine-binding protein, putative
MRRIVGGGAVYLRRGEALTATLCFCRGYHMPGWKTKVSTRDARTREQREADRKARQIEKL
PRPQALHDFQYPYEKTVLSDTMFQYPVYENELDTPHLFNIVPPPDFFIYWNASDFERTSY
PPLPDEDHRLLVPRADLLAWKNHRQRSLKYLRKHEVLPRYLPHVHQDVNLSVVFPGTYAT
RARKCEETGESLPPPPPVSELTPRNFWMTAHCGNYIELTELQHPPSIFFFEEEEGERKES
ASGAEFYTLIIASPDFPYRVPPESDGRKEKGFFLNYMVANLPGGGNGPHAPVAKGVVVDT
RGADKKGDVVMPYVPPLPTEDAGTTRHLCMLFKQSDYASSLTTVMDETEESFIARSDFRI
HAPHREGFSVTANTTLREVDAVLPPDPCAVTFFQTKWDIQVQEFYESRGLPEPAAPPDEE
IEAILAFHAKKPSELRVRARHRPDGSTNIGDDPNFWGQSEPTMMANGSMQSLWSRRTALG
RNGVPVTYRR*
>TCRU_8293 hypothetical protein, conserved
MLRLPSWDQPALINWEPLEPPSPYLPVVQKRVYPSVVSGLVGTVSMSRSMEKSELMNQPE
AAAAEPSHEMRFVEERAAQLRLFKEETEERETIIFSEQLESTRLWVGFLRGVSILLQVDI
QSAEEDVRGIYEREEGRQRMCYMIEKDTVARLIRQRMEDDMRKRISNLMPSYEEVRKSIV
GEEAKELEEILDWFKKKRPFGMRLPMFLGGERGRINPKKPAGRNTKARDGRRQANRFSKN
QPNVHSELDSWPDAFPEASYLEEGRRAWSYIKMIKYSQEKGISSTEDIEEPETAARVEIF
AQEAGEWLSIMARFVNEYYKAKKLAQERDREELIMMEEQLKEMQRREAILARLENEAAID
CEQIMLEELKDRESQWMEQGNEEDNNFAENETEVRQRHDPAFGAGICQPQDLGPCTDAVA
RDEENGLWDIDSEGPPLYPMLGVVFLSALERDSYAGLRTPFLSALAEAQCMLAACEGRSA
GIAAEIFASANCVPFCPVYLLQGLWWSYTSGHKAKCPGVANDAEENVAQLHRLVSLETEA
RLGLLMDQMAAAWKLYQKAAEEASIISNTSRGEVYYVGVRMPIDF*
>TCRU_8294 retrotransposon hot spot protein, RHS3, putative
MIVLSSPKVSNYDDWEKQKGAARIIVNCPDGMDVKAMCAWMKRDETAEKQAECWRMVKER
MDKVGPVPRNIFDANEFIAHSAAIEDALEGMNSRDGEKHFTHGGARLWGSENPSQKLVRV
VRTRAESGSEVFLNAPISFCLGRRIPHYFGKRDE*
>TCRU_8295 hypothetical protein, conserved

MVWCLSDQGGLYPLRRGKACGGSNDTAAGGNNGTVAIPLMVVPLMLDLMDFRRMMCNISV
PIRLLVLVQNGREAMLSLCLQELERVYGWSGRLVVSRHPENIGYSAAVNIGSRLALSLPR
EEVPFVF*
>TCRU_8296 hypothetical protein, conserved
MFLPDLLPSLLRDVHGMTRHDAARMDELAAEAANGPSESSPVLRRGLRVLRSTVNDSRLS
TSALLPDRIRYASAKEREKAFSKHYGHFCAYYKSSCFVSVMLTRLAISTVGYFDENFYPA
CVEDVDYSLRLRLLGFQERNVLYGKFVHRGSSNIRFCNEMELPDAL*
>TCRU_8297 Enriched in surface-labeled proteome protein 1
MSRRVFTSAAFFLVAMVCCVTGWAAVAEGKTRNTIDPFKGTTPISFANCKEFNEAGGKIT
SLRVPGLVKVGDDVFAVAEAQCGEKDGAGSCPGIVSKHLNISDGSMDISTSDISLFCMQI
GDTAANNFWTTELLRPTTVVIEDSVYMLLGNQSRTKPQDEVKNERGLLLVKGTVSDEGGK
KKIRWNETHVVRPEPKGESVSLTELVGGGGSGAVMGDGSLVFPMQAKGKDGKSVLLSMHF
SKSENKWELSSTTTGNGCRDPTLAKWKYEDEDDERLFMMAHCAGGYYDVYMSTENGVSWY
TLGEPINRVWGNSHNRTGYGVQSGFTNATIEGKEVMLITAPVYPKEDNGEGRLHLWVSDN
IRVHDVGPISREGDDAAASSLLVKSEDELILLYEKRNADGQYSLVAMRLTEQLERIKSAV
KTWKELDDALGVPTEGLVGFLSSTLDGTAWKDEYLGVNATVGGGVTSTESGVTLKGSEAK
WPVGDMGQTVPYYFTNNEFTLSATVTIHEVPKAGSIPIPLIGARLNDTASTVLFQLSYTS
ERNWNLTLHKMEFLVKPSGDVGNWETNTAIRVTVRKDNDDEWFVDANGRRIYETDEKEMA
KHRNTDQFGPHRISHFFFGAGNKEDEGNTPVTVADVLLYNRILYRDDLRNLNARTVPIRH
PAAEELDTAVKFTATGEEKQKATQLTTSLADVEDPRIAQPTNSQSVRVLAGSESSAENVT
DGLSPRTAAKNDTSVPETSHSASGGSMSSEDRLALITDAKLILHDLRGDSTARVCVSRVL
LLLLGLCALVAVL*
>TCRU_8298 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSVCVTATGEEQKEANSSSPAQSLGTSAQGPSGGSASQSTSS
KGEEETSETRTDTGRGTDGVTDTPETPDKATPEPVPKEVPGGSDASGSSGGSVSPAAASS
SVTASVPAQGQKENAPTTTTTTTTKAPSTTTTTTTEAPTTTTTTRAPSLLREGDGSLSSS
AWVCAPLLLAVSALAYTTLG*
>TCRU_8299 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSVCAAGSGDETEEVTVLKVDEEEEQGDVADSRHKTPQPQTR
EEKKGRNEVQGPNTAIDTSQEAAVVTGTPQSQNISKNTQEKDDGDSNGRTEHTNTVTANE
QKKAAAPTTTTTTQTPITTTTTQALSTTTTTDAPTTTTTRAPSRLREIDGSLSSSAWVCA
PLLLASSALAYTTLG*
>TCRU_8300 UDP-GlcNAc:PI a1-6 GlcNAc-transferase, putative
MAVSTTPHVCTLLWPFLGEQEGSEQEDSWLLGWNPRGLVIVVVAIVQSNAFEDALRVLDR
IREHKVKENVEGRGSWRKDVSSLAPLSVLGRLRGLRAHSIVLGDEERVRSENWVRSERQR
SDIWIELNKGPVLDQVWCCGYGVQPCHLHVIRTDPCGKYAKLPTVFSATARFGRDGIAEL
LQGRQPLCIPGVHSSLEGVLLPSHMVPLAGPCVSRRLEPESSFLSRSFLRRATEDYSESN
IPVDDILHNGSSSSRRDREKLDQQGFLLEPVDIEPVLTSPVNGLPPRLDFPTTADSAEMS
RLLRSNNRGRALRKYLECCGGKVKSGGGNDDREKNNSDHCGSKEMETNGTKTLEKQSFWE
HYLYVSIGVLLSVLVIFIPVLTFLGKLFCTAALLEFRLRELIHWLALLQGRTHVCGLHPV
LPHMIHEDPTFQRFCAVNFLIRLLVDGLLGTLGSLLLAVGGTALITKSGSFCRYFLYDVH
MGYMEWFEGWPAGLKMNEDLNMTLCFFAKWVLQTSWDFVVDFNWVELVYKLLVYIAPFGA
SCAFALISDVSILVSLHVLLLFHAISVPYRVMRSVTGSLFLQLRGKKYNPLRRRTDTYDF
EVDQMLMGTLLFTVTVFLFPTLAVYYFYFALARGFIWLVQEGLVSATHITLYLPVYPVIY
WALNRWKWPGGFAITTPKVTRVRYHANGTGSSPCTSITVEVTVVSKPLGLHIFLSDFLLV
LKILSDRRPFRMLEVICQAQVWRNTNPLERLIPHLQKDCINAGICMQPASTMKTTTTATT
KAAAAANTDTISASFTNASFVAETATSTTNAPSPSVTSSRH*
>TCRU_8301 hypothetical protein
MSSANAAAAELLEAFRALDTQRVGWVPTLTLKNLLEKFGDFSTSEKEEFIAEADQGGRIY
YERFVKEVLFDDIR*
>TCRU_8302 hypothetical protein, conserved
MFSSVFDDNPFAEEFEGESPMRDGRLSAAGVEKRERDTEGLVEGEPPLKMSCQEVDPDDG
READAEVAAPYIGYLLEDAEEGNEENEGTDDNYIAFLCRVAEMEAALRQSARVHQFRMTL
ATQEKDALHRSIVTLRRSLLESQESRQKASQGAAKAGGAEKAAESQEEKESPVDLAALLK

FCDTVTRAKRLSTHLHLLQGLEKCRDHVTGEHRTASVASGSWMPTPSLTEVDTSFRQPCH
AEMQKFEDLRGAMEKAQGRFDAPVARVMIALQNEIQRLCAKSDALSEVKASLESQAKALM
VRWNEHVLWGTERSLLVAEEKMRSHLLASHPPFSEQQLFLQQKQLQKRLHRTELALATLL
AAVTGTHLKSMTPAALQATLSRQQELESLRDRLSREVFYLRKLLRDKLVTSSRLVCDPSL
AAHTTATAEEGKTVLLQHFCASLAGRLAELTEGIVSELLEGSTACATSAEQEERLFFYET
KAGTLHASIVAFLTENVRLQQEIKDAALIKLMATPDSNAVMLLAERFQTLLHCKRNLGHG
EEEEEEGLGNVRKCENEENEEDLDEQKLLVDIFMESTAGLLKVLNAHLQRVTELFRCEKH
GFREAAFLLRMIVAADRLLLGKVGVPPAAGFTYDIVEEMEEAHVCFKPPKNILQQLPSLD
TLQAIFESHSRRHAAKLLTQYRDAERTRKELQDDVEWCRQQPPQNVGADLRGAQKELQNL
KTALLAAVTREKEVASLEIELVKSREKLAEVRLEKLALEQELAAAEEQLRMAQETEDSGK
NKVMDAPAPFELPPPDPAEGDESIHDDDDANG*
>TCRU_8303 hypothetical protein, conserved
MGSAVARHRENTGPGGTAASSFAGCHTGTTTNRRSHWMPAANKAAEKTESSRNLTAVKSS
SPNASSSSPGSIEARRKVDVKKPEPPPPPPAVSCLVPSKHLPSLRKPLEWELSPLSNAQR
AAMNRGQASPKLLPTETTGTDEKPNETGRGLSPTPMSLSGPPTQESIRKKDIVVRKPPFR
TRIECDEGLPTSVEPGSDGTLPSKSTKKNTPHSGAFNSLASNNLDSRSSDFFGDFVARGF
MPFRDTNLQWFNVDFDRKLLKRREHCDVVWCPIEEIALPEVDETSKEAAKETPESPIAEE
KVISVRNPKKPQQQQQQQQRQPKRDNSNRPRIRPILSSDVPHRMQLAKKAIEDNVIFIYS
RAPKLY*
>TCRU_8304 hypothetical protein, conserved
MDILRLLSVAYGGSKEERTEATAQLESAVQSPDGPRHLVTLLRAGTDLALPAEQSLSALI
YAKNYIMGTFDEHIAAAPGVLEEVKSLLYHGAFHAPSTHQKIIHTCVAGIVSSFEWNYLP
QLLPEITRERTGIPVEHALASLRLLYVFVKRFKTPGLEPMPMKLMVCNCLLSALSPFLSY
GDLQVDHMVLKAMNCVVETALQTNQLEDVPPEALNAWLYEMAHYPERHFVAVSEAAASGL
QNMYETYVHCLKQIAMISFSILNDATRKKNPSPLAKQFLASHASVFLGVWQRWLEYAATC
RARGVHHKTDMYAIRYIKLCTLDRTLYQQYLLPQLMHVVESLLFPYLCFSEEDEPAFADE
GDLSEFAQYMMEEGFEQSEVSQRQAASNAIVAIVRGEKDFHEDLLQKVIEFLIAGLSRED
NDKTFPQAFGFLHLLSILRRHFRRVPEIWETQMARVLVTFVTPRVLPTVPYIPLRCKALV
VCQRYSKAPIPSEEDFAAFTQLVSSLVQDADSRIRLGAIDALCTFLEMKRALPYVRPILV
PLVEECIGFLNRVQTSFVPTALLYLVEHFAPELTSVLEKIGKTLIQHFLATAFDLAQQED
VMDDEHVSQYWRTDMSACALLNAIDTIVEASRHHMEVFCSLRPEVLFLAKKVLEHPDDFE
FIEKTLAILLNVINFSKPIPPECWNVLPLLFQSVDSGIGVDFFVAIEEVLDSFVSNGTLE
FLRNAELMEATYQACEKMLFKCACGVDDQIAVPQLIEAMLHQAKHCEVAPGLFDAHLPRF
VALLLRALADDSIRQGEVRLQIWIIAALMDALYYNAAATMQIITSHNAYPQFFDAFFHFF
RGAIDPAHAAKGGKKRKKDTAAEVVENLSILTRKVIVLGLTALLEEFSANCHGNGGGGSI
GLASFDVYVSPTLALIQHCVFVNDVFLASRCRITEKNLEKIRQGVEVEDVSDVDLNDDDV
LGIDAGDEVATLDDDVEEDEWEDDGEVGHCQDEGDNYESPIDDVCEVTLFLQWVAKAECL
GGGVQRHMKTALSKSLQEFRDAEATALRYRRLVQALDHAKDENYGARSAAAANL*
>TCRU_8305 Right handed beta helix region, putative
MAEYAANAFTRHVSKFSGREVRLLRVGKSVASPFRQISEAIRHSRPYDRIEVESGKYFEA
LAIIHPVELCSAEDGEPPMIISRGPCLKINTDGPVLVQNFSILAKGATASACQGILIEYG
SPIIRDCAISSVYVINDATPQILHCHICDSESGHGLSITGSSGGVYVNNDISYHDEQCVY
INTKGKPELRQNIISQKKGQKNVAVLISARLYGGCEPIFCENIIRGGGEMTNQEEVDPAS
VQFPQMLYEDNSGGWASLVGVMNGAKPFITGNMLCNGVTGFYFKDCNLPRDHFCKNRIIS
CSAWGLVVGKNTSLVSLHNDVQTCGGGIFVSSTASCNVPAKESHSVVLKKCDLFGNFHYG
ILVDRMAVSISECNVFEGSVGIALLGNCTGSNITKNNLTGNRVAAFSVLRRGVAVIEENN
IRGCDNGMYGVFVQDGSDVALRSNSIEGTSNSVFVREGSCILAEKNALRQSSVHHVVLTE
CSQATLKGNVIEGSSYAAVVVTSRSECKAVGNVMYAGMREGVLVEEKGRAIFERNSMSSF
RETMYVKTGGSLQATGNDVTLGHHGVVVDGEESNAVVSNNHFRGMHATAVYALERATVTV
NDNSMTEFSAVSIQVGSGAIAVIEKNSFTNGSDGAIHVDGFGTQCKVLHCEMEKVGYGVK
FTRSSTGIIQENHIRLCQLFGVECNSNQPVTVQGNTITVANVGIDIFSAGDIHDNFIGDS
EVGILAHTLANAQVRNHRVSNCTVGIRLINDTCVNFTDIKIKKPKEFGVVVNGPSASVTM
SNVTIEDSGVAGVFVQKGGVCRFEQCVIKRSKEDGIRMEQAGAVVFEQCSILEQHQGVKT
TGTLGTARADDEPKLINCTIDGSFCEKGVLSTKKSIVRLELCKISARSPEKGCGVVVQDG

GTVLLSQCDVFGCPRVGVIASAMSQLMVENSTIDDCGIGVCFGLEQDSSSSRHTQIKLNN
SAALNMGDNVNKVSMSDDTRWKPPTLSQLTIRGCTEAGIWFESCGLGTVNCTTVVECTKG
IVLQHGSTVMVDATVVRGSMDCGILLLGRPSSHSVLTHLSISDSGGCGVKMEEGAVDVEE
EGEGMEEKTPLTIQNSEILRNAKGGVVLETCAYFERCTFAHNAEAGVLCKGNFCPVFSAC
HLTRNAEKNLEAQFGSRPELRDCVVEHAPVGVRVRSIVKMTRCIAQHLGIAVDLCVGEKS
SDFSRLSECVFANNETGVSCAGAASQENWGQIAIEGCTFHDNRGTSISVHEGPKMLLKTC
NFESSRECVKLTEGAEVTIEECEFKRNSRGITSSHAASVEVKKSIFTTQTQHAISIMGSS
GEAQIVGNSFCGNTTHGIFLSAIGKVVLVNGNSFETDVCSISLQETPQAFVYNNCFHACQ
TGIVFHGAGLCGNVFGNAFEKNRCGCRCEENATTYLWRNTFEENSEYGIFVTGGAIPMVV
DNSFLRHTAPSSVALCVCGGGIGHFAFNRYTGNACGAQLEGTGNKTFINNSTFEENDIAI
RLKEGAVVHVVACTFVSSGSMDIFASGAIERDECVVAYNSFFSNRSAAVTVEENAGVTVY
RCIFCGTEGTGVVHGCRGKGLVLECLFYELACGVRIAEGGGGNIRKSSFIRCATAVEVRQ
LGSGHFDSCKFLARPTSAPVLVSVHQSSTPTFQQCGFVGWSEMLHPLLQSSGGGLVEGSS
FVAGDISVLLESGSQTTLRRNTFLRGVIGVRFNPYSQGQVVQNTFHRHLLAAVNLMDNAT
GELQENVFAQPPEGGGMLVGLHNVLIEANNVLESAPTRAEKEMSDRASLEPNLIAIFAEY
LSEAPHWARHAMGETPHASALPLPILTAMSMPGTKNENEEGNEAENAVNEAAVGDATQKG
KIRPQAKSVEGSKPVRKGGKKILSKSFTLSLSDTIVSAPQGVQETLAKWVEMHGVTLNVE
EEIRPAVPEPMRQIRDHDMLRDFSEHFSAVAEVQHAKERGHFANNESKQTRGAVMHKQGL
DDSKNASSTHSQNATREDSRRSSGVKALFSVKRLLSTEFAPCSRIAARTEAPSGPQVKKQ
AKRRRRRTLPPPLNSCSQKAQPSRQPIRGPIATLTGCLHKCAVESTRRPKKEEIFEKISI
DANSATGLAIFREEETQYSSFSLGNSKGRDSGTLSFPLTGAENVSRSGHDDDAFIRSGVE
SLSRVSVPLSQRSAVPDTQALSQLSGHEGFFTKFEDAVPGSNTMWRETASISSRSCSQGP
LELRGASPLENFSKIGVSAESKTDIERIKMISPRRDLVARDAHGQGTKRHFGGRNRFGGS
SSLHTSSLDEERARLKNGTKEVLYATQINDGDGDDGIPAKRSGPLKETPYGRRRRKDRKG
EDADEVEASDIMKKKKLAEQGLSRTKKNGRKRKKSVGSRNKVANPTSTKVSRTGKSHGSL
QLSSETHYPMPLSSPAVPSSGPGSFRGSMDPARAAETLGKSATKAASSSTFSPRAKGKVG
EVGGSQSGFHLQDKAIVAEGILGNFSASPPVKNGANEENLDSEQLGKTARYPHNRSHTAV
PRSGNESWEAMGLEDTLQPKDASRHTNTASEFKNAGSLLDLSHGDVEGRERNREFVSPTM
LNPPEQRPITVTMSLLELHGEGHASEQESERKEKRSESEDHDEVHLPKIEAPLLQNSHKI
CNNSTANKSNDIHSNNIIDIYDHEVEDRKMGNVLGISPVPSLSGKGRALLGVLGDTVLQD
DAVLQEHVRGACAGPSQSDPLASGGPGASIPLLEDRYIQKGTKMMESAAVATKKEWDEEK
DSDDDDEVEDIIALLRWLVQLREHRLLTADRLSKAVDCIRVNTNVPFFLCEGSRAGEAPT
LMLRLPRTADEAVIIPLFGSTMEMRKRTQRFEEGENNSPQSQRRGLRLIRGATDTSKEFK
EQNLSWMYKMARDEVREADATRIIQVPAQAFHKVRPPPLFASARPPHDHHQESEEIVMTL
GSENESRLCSRSSPQALGVLRVSQESFQTGVADSIVKPLHRSKGQKAFFARAFLHKTRHD
AMTSFNPAIPKETSPYNKSTRVAAFIALGTMNFMA*
>TCRU_8306 hypothetical protein
MHILAEIIGYVNFLLHGILVSLVDFYIMFIHVGLVWKRRRDRHPSMERRDLVMQLAPQSP
QHSRLSSSDMILSLNESFLDRALWKGLNASWDQPTAIVTGVSYGSIGFYVALNLILCGFN
VHGVCRTFKSVSHAERMMQFAVERQCRLHKEWVGKTGRLISHVCDMSDTVAVSNLCAVLL
RDMNIRLVVCAAGYMATPPRLSPQRLEEQFATQHVGHSLLMLRLLQHRIQHMKFYTSVRP
NWRFVVVSCAFPGGTDPTQGNMFDTYDKGDADFRSTYNRYDGWSRAEMCKLLFAFALSRY
VEHDIRLAPFCTVNVLHPGPTRSRAIANSRLPLAGILDNDILALLRLSPVISALYVTDTC
LSKRLDNTNGHFFRMGDDQTVFSATRRKDAGTIASLWINSPFFTGTPLPAVSMSTCKQDA
VWRFTLSYLTSHALLEAKIFC*
>TCRU_8307 AAA domain containing protein, putative
MLNSAAPPTALDDAWTDAKSASIDWTDPEDVLCNSWTFLRIMGFHPALSRYAESHLDEKE
RWQVIFMDPSRKEEQKDALQWWLQNNLLLLREERWCRHCGSQGHTRRGCDQLCVASVKNG
DTSETVFGHVKIEPSRIMSRFIAHQAEVERCKLLQEKQSKGFYSGISGRRNGAEETQQRR
GDSNHLGHPRAKKELLLFAEERRRGVVGRFDANYGVGFIRVPEVGEVKFFLDRVDYGVKE
ISVGDAVTLKIDHSREYPFAVDIRPETPNITLEDVQKFLQRCRSTTQPINVIKTIMTHTH
EWPVVLGLLRGMSAPAYIDAVHTLVELTTFVGNREPIHTPLLELFLSLMLRTPKRADVVP
FFPTMLLDALVKSGELKLGDEMPMMVERWIEVVNLIVLLRHHTNVTTDLTGEVESALKSL
LMASWNKATTAITTTTTATSVLAHTKTPGVSVGALAAAAKRKKIDGALQRLQCQQWEKVA

TLLIPTANDFSIPPPDPNSAFAPQNLPVNGATAYNSTETFITDQCRLLRADTFESVSRLL
PAVNYELPHYKPTAETEAEIPYARIFDKVRFMGRVLTRDKDYASPDSYILHVQPKSPKAE
VASQLLPGTTVCITTSLDRSVISPEEIFWGIITSCNVQFLVGGLIVLAPCESNAHFDILM
ERLKRNERLGKTDHSCMLVTSVFMIGYKSIMKALSAFLGPLAMPLPLVSSLLIAEAAANA
TISAKENLRNPSDLVSYVPLHCESAFLEIIDSVNDRFALDEGQKEVMRRLPSSEVLLVQG
PPGTGKSFIGCRVVEVYIRYKQLVASGDILRSIDVDLLRSTSAEDMLPNVGPIVIITYKN
HALDEFLMDLLHSGLWDDERPRIAQKLIGGAFGGKSELFPLGKRIVRIGGRSREPMLDAY
NLGSLMRTKADKARLNSLKERLFLMNQRLERLLKEIHFLESGRVPKSLFERWLTEEQRKS
LRYEDREEWLQGKRYIGTSTRTAERTLYLDLLRTQLSACLDGVRKRPTVALEAPESVETD
EDGGAPLSVFQEMKREEESPDFNDALPTTYLSAEAMDLAKNPPKCPEGIPEELLSLWSLD
PVLRHEYYAFLFRDCISVKARDCQLIMDAIMNVVTIRNHAMDEVKLELLQGADVIGLTTT
GCAKNQNLLRSLRPSVLVVEEAAEVLESQLLACMTDSLQQIVLIGDHYQLQPKVETFLYE
KVNKLNMSLFERLAKRIRPICLTEQRRMHPFISRLVRPFYDTQTLLDSADLLTRTFTSAA
GVKYLDAVPGLARRVFFWRHTHPEEEASGSRSKVNIKEVEMVLKIVAHLTSEGVHQKSIT
VITPYLGQRRLLRTSLRLRAFSDVAVSTVDLFQGDENDIVILSLVRTKRLTEFLRMRNRM
IVSCSRARFAMVMTGSETLLEQSSHWKEVLYMLRKENCVGDRLPITYRSSPEEIVWMDA*
>TCRU_8308 UDP-glucose:glycoprotein glucosyltransferase, putative
MELGPRDRSKSMNQPHHRPRNIAHCTDWGRGRGRFAATLTLLLLWSVNLILLEAPTVEGK
GVHVTLLAPWTETPLLQEGCEMVAARGAHFVGFYQCMQDVWKRVQAMNSSGGAAKLAQKS
QYDILLDMMEQANWPPTQVKLAKMKLAARLYSPAVEAHWQLARKAKQLIGGCSTEGGPFV
LTAGKVICSEDLLEETLSAPAPVNETQESHEDEAFSLFAELDQMHPNAKGSRVVILYGVV
GEEQTMQLLQVVERHLHAVRLAFRHLPISGRMWEHPLHVQGYAVTVDLKNVEYKVIDEKD
KSDAGTDANDANTVEEIESIDSVGGFNLTLLTQRYPQLKPQLNAFASHLVDMIDRDEVKV
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EELMEFANVVRSGTSPVFLNGRNLAAEKLNLFSFLQKLDEEEQLLEGVQRVFTSYRLPSV
DGDGFFSAKTDALHQAMESVRRSVHRYIASNGLEDGESVPRIWLPQRSVLWLNNIQRDVN
YIYMPAALEAILHLNINGVPVIPRKNLIHAVCVVDPTTFAGLQNIFTILKLEESKQPVRL
GIVFADNKWSPELSVFTRGNDFITDMSLSGVTVIIAATVWELLKGEEHPQDVLEFLSEVV
QARSTRGNLEEDEIKMISSNILTLAGKTTLDNILTDASFVEYYQDTQMKLREMKLDASPF
TLLNGKMFRGNMLHALRQNFMEELHYVRGLVQSDALTERDDDDFYESILRLSGARERYNE
AFYSEKFYADWTSKPVLDFLLHRPFLLPTIRSKKTPLVSSVLTIQSPMGEAALDALVKTI
RNLLQCEDETQKCVNVRFTYVVCDVAKESKRRTMAGDLERLIVRRKGGDDGKQHVQWVYD
FLQKIVAQNNTRQLMDPDLYEGLVAEVNFSSEVKKLLDASDEGLGAQLQVQRGIVNGFCA
QLEADSLSTSSLSANGAAAGREKGNKEGAVYYYVNGRRFVYDDSFLEEDFRTAEEMEMLL
AGAVSEALSKVEFTTMSSELEPSDLESHFYASKVAALSEVLRRDAARGSPMQEENHLPST
SGLTSFVVKPANGDTVPRHTLTVVIDPVAQQSQFLISLCDYVTRSPLGVSCTVHMGATEH
ASKLMRNFYQFVSEMELRFDAVGRVVPPAAVFHRLPSKHLLTLGIEEPESWTVFSLDAKY
DLDNILLDKLPSSSQYLHAVYRINSILLTGSARDAEQPNPSRGLPLLIRSTKTNPEAGVT
RDTLVMAIMGYFQLQSSPGVWYLTVQPGDIAKIFYISQVDDIPVNDGANKNHHGRFNYTA
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IFSVASGHLYERFLRMMIHSVMRTSFDVHGANTTRIKFWLIENFLSPQFKTLVPLLAKHY
GFDVGFVTYRWPWWLHKQTEKQRTIWAYKVLFLDVLFPLDVDRVIFVDADQTVLADLHEL
YNMDIGNAPTAYTPFCRKHPNPATKNFRFWDHGYWLEHLHGKPYHISAIYLVDLRRLRAI
AGGDKYRLVYSRLSSDPNSLANLDQDLPNFIQDQVPIYSLPEEWLWCETWCGAESKARAK
TIDLCNNPLTKMPKLDNARLIIPGWEETDTELEALSEKLLQQQKQQMS*
>TCRU_8309 VIT family, putative
MHEYKHLNEARRAFGNAQRSREIHERGLEKFNIEIRKNSALRNRSLVLSSFGGLLSAAGV
LGATSGLQQVGGRGFVRATLIGQLLLQAVTGGGAAAYTVCLGLVFERLVYDIELKRELWE
IENHLVGEIQEMVAIYKAQGLSEDDALMVTRVFAKHRKRFANLMMVEELGYSRLEPPCRR
EAFVDAAVPAAIGYTMGCLLPLVPLLARRLCASRTHEIGLCTLALGSVFVSVAQSEVFYG
GYASKLKTVKVIACNLSAVGVIFGIARVASYIFRGGS*
>TCRU_8310 hypothetical protein
MEVECKVAPPSRREALCQGSLSRFLSASGRFTRFNAFLHSEADGACGAGSNGGTLYLLDD
RDRPFSCIIIGPNDVIRESANAANAFSISRRGGEKTVLKAPSEAEKKKWMQIIATIIKSG

DDSFAASTDDDSSHKTLPSSNSVGVEVNVSHTAPSLSLSPKMSDVVAESASVMKGVLLKK
DGRIGRYAQRWFELRKGEGLFYAAHKHSPPKSFRCVPLQGLLVVFVENKRKIIIPQSASR
KWKMTLKCLDADEFARWRGAIQLEILCLLQTKNDNESVLTTAETLTNTPLGIPGKMSTAL
SKCLGGDTAFPFSLTSPWENSAALMGIAPGEGTLGQVADAATTLSATELLELEDLQSDTP
CDCTKSTEVYLESIGEKYKPVKNTAGMEADLQKYYAECLPYGFKATLQRLWERLFLPIRE
PYESVNEHLVLLDLDVERVRECLKNTLLLYGEEMALRGAVEELDYILRVYKFVREQLSIR
LEIAAFREHPNQSGLPLGVNGTIDRINKLLDFNTSSASHYDEVLETWKTVFQALQTFRLE
FDVFDESEETILMLEDALNKIYLWLQQNPVELVCVEKELR*
>TCRU_8311 hypothetical protein
MVVSTTVYLLVTAVLCCLLSGTEGALQFEWLKPPIKSKPQTPPKNWRNVLDALLRSIEDA
ELQKSIKNIKESISAGPSREMFSHCDLSILRCLNNNPIQLTLHGMENGMVHFDYLPDTLR
FLTVESSTLNQELYIKALPESLLQLVFHNVTFLSGNATVALNATLQSFTCRNCGLHSISF
TGESGLKMLDLSENTFDAVPFIIPGNLTSLIMRNCLNNFSLVKIMRALPPDVPLLDLSYS
QFSEFMKGITMLPPSLRLLYVSGCPINTDVSYFLNTLKSANRNVERMVARNCGLVGKLGN
ATDLKLLLTLDLAHNRISEVVWRELPPIINHLDLSANAIDGKLPVSLLPRFLKSLNLSQN
GFSGNFNVSELPPQLISLDVGNNNFSGTIDFARLPESIHYVYVQHNRFQGTPDLVEIPAG
IRKILIHDNNWDLLRPSP*
>TCRU_8312 C-8 sterol isomerase, putative
MKLLIAVVVAVAAVATSFVIDSPANWVFDPKTLKAVSHRGIEAARVQHGVNATPEQVIEK
VINELTKTYPRYAVYSGRWLWNNAGGAMGSMTVLHCSFTEYVIIFGTAVGTEGHTGRFHW
AEDFFTILYGEQWASLPKAANPEIYKPGDQHYLPRGSAKQYRMPNACWALEYARGNIPSM
LFFGLADSITSTVDLLTLFQTVYESAWSMIQNLVQGKI*
>TCRU_8313 WD domain, G-beta repeat, putative
MLAHELVLHNTLPGAPSTTRAIPTPFSAFGNVVAYGSGNNVVVRELERPGNVIVSCRHTS
PVTAVRISPSGKLVASGDQKGNLLVWVRQPDARELLNTKQLQGSVRDIGWTNDEERLVVV
GDGKSHFAAAISITGNTIGDISGHTQNIFSCDMRGDHPYRIVTGGADAIVGVYEGIPFTF
KCNVRGHSGMVTCVRYSPNMEMIATASRSSNILLLDGKTAEQRNSIETGHSGTIYSVAWS
PDGRKIATASADKSVKVFDAATGVVISSCSFGTDVMDMQQGIVYTPQGILSLSFGGKLTL
IDENGNIKNVMLGHQGRILLLHPHLNGTMVSVSVERALIWKDTSDPSGTAREVPIASNLI
TAAAGNGDYLYLVSGNDLLRFALTSTELTVLSREVANVTALAITADENAVLLSKHGFILI
DASGRKVAEEKLKNFDGISAAAHDNMVVLGGDGSVEGYRVTTGASPEACVRFSGYHTGMV
ACVAFSRDGQRVASGDANRNIFVWSPFDGSVLYRDLVFHTLRVTSLAFSPQNTSWLLSGS
MDASLIVWDLDKKTRKMEDAAHRGGVSAVAWTEDGKLFSGGSDFCVRQWILPS*
>TCRU_8314 cdc2-related kinase 10, putative
MAAVEGSPSSKEAARRENPKKRVLCYEFDPETDVIGRGAYGEVYKATLVSPSGNGTGTVA
EAQDKFVALKRTLCADKEEGIPASTIREIMVLREISKAMKNGAGKEGSPESFGCENVVKL
YDVFMDKSTVYMASEFCEAGDLSCYLKTLPLRRLSDGQQYRQWMWDLLSGLCFLHRKGFS
HRDLKPQNLVLKAIPSDPPSPEASREGGSRKEPKLTPQYKLKITDFGLSRVEGIPVKKYQ
HEAVTLWYRSPDILLGNTNYNYTADMWSAGCIIAEVASGNAFFRGKNNREQLKSIFSRLG
LPTENNFPSIKQYALYETFFTGADSIQKGQEEKEGNVATSYAAWFENVKEKLNHYFTRYG
SVDIVGEDGVDLVARLLAYEPGRRLTTEEAIQHPFFHTVSHGILSTVGPNAPPTAATSST
THDANEILSTSQEDTQGAASHCSLAAFGVQSQPPLPTQPPEEKLEGVRGMVPTEVGGGNN
GHAPLAGGQKEAHAVDEKDKPSKETDKSLEEGNNPGVTERSKPVESLNFKDRKKRGISTK
LTSRPSMGVVCAERTKNSFSVKGSRVEEAPAYTRGCGQVPKSKAKVAITRASKQL*
>TCRU_8315 RAB GDP dissociation inhibitor alpha, putative
MEESYDAVVCGTGLTECVLSGLLSVNGYKVLHVDRNPYYGGESASLNLEQLYQKFNKGAP
PASLGRSHLYNVDLIPKVLMCAGELVKILRCTVIDRYNMEFMLIDNSFVIKDGKIAKVPA
TEAEALMSPLMGFFEKRKAAKLFQFMGNYDPKNPKTHKNYNLHAMTMAQLYKEFGIGNDT
IDFVGHAVALHTNDDYMQRPAIETVMRCKLYEESFNMYATSPYVYPLYGSGELPQAFSRL
CAVYGGTYMLQTPVTKVNFNEQGAFESIESNGKKAYAKLIVGDPSYFPDRVKNCGKVVRC
IAIMNHPIPNLKVDCNSCQIIIPQKELKRNNDMYILQLGANNKVCPEGYYIAIIGTVVEN
AENPEMDILPGLRVIGDTLETFISVSDLYEPMEDGKVSRCFISNSYDAATHFESAAANIL
DLFQRIHGKPCDFESMKQLGGAANA*
>TCRU_8316 hypothetical protein

MNNSPQAQEGSWFFILDAPVAVRCLQPVFRPGRDDVSSMPVVLLSDQKTGRLRAFDSKLQ
FPCSEPMPTPAEITSPPFSSAALEQEPAINRVLSLCVVEANAVWAGWSSGHIAVYRMHLE
DASKASTNAFTPTTREMRTCDRQWEVVSLLHEHRAAVHLLATGPSPWVFSASHDMRLIQW
HAKTLEPIRDLTRVCRVQEQYRPSPIKMICMAMGCSCTTSLSRPQGHFVLFFSTDQKTLY
GVSLGGPQRANKIISDRDLSIQRITSARPAVTSAAVLVGDGEDDAAAVICLGDDEGNISF
TPLTVVYNTRSEKMSRSASSAPLPSLTSNSSILSDAEYMRAVCDATLTAGTLHINRGRVT
ALSVLSAQADRATGNIRYCLTAASSKNTITLFAVDVSPVFLGGHVTKCTLLSAIPTESPV
TSVVPLFPPVRQSAVAVAFSVFSDGSVAALFQFQNTVTKHGTDNHTVATAAFDQKFIRSA
STKAQPQPQSESLGGALQEQLRVVLDVVSETGVVVEEANRTLEEQRHELRHIRAAKDTLS
DQVTKLLEALNQKSAEVVTLKQQLLHMQERGMTAVASASDLLQDSGCCHQNREDQREAHW
RQKEEKEKEGKHDQQLGIETERDLIQSVLHDTEARFESKLDTLRRENRFLSESLEQLKQE
LHKTREKEDAHSVHNTSDVLQDNKAVHVGENESSLRRLLEQALGALDA*
>TCRU_8317 DTW domain containing protein, putative
MSIRENPYKESMRRLVIYAGLPDYGSTRTVTPPPLTGKGALYFQASESPEWKAHLLSIPR
EERHRASVRRRLCTRLWLAAQNDLCLWCWFTKSMCMCSRIEHFRAQILSDQLNSAVKVTM
VMHAAEVMRATNSGHIAAFILGAPIRVWGVEEDDVYLQGLPAVDEEVGGLCTASLYPESN
AILVENFVQNLQQGQKVHLLLSDGTWGQATSLNRHIPRHIPRVALDVDGSYKSLFEALRK
RTRETGVSTLEATAMAMEQCLRGLNGNSTEGVSSVLPVLTTVMKEFVDLRCLLKFRDVCF
AEGMDEVSGIIKKRDAYRRDASLERLRVLHTKADEDPEVRKQLLPPVLNYCYACDVAVGW
HRMVEHVLGRVHQEGFKKGVPRTPGEKSRSCVCAWYANSLRGYEDSN*
>TCRU_8318 hypothetical protein, conserved
MSFSYDNVVAQGESFMADGRRQAFEVPSCAQTAVLKSGQLQQKHAKNTESQTEEWHLFGQ
SSPRSRRTPQKQRAVHTPPTPRGRRWGSPNSMNRSESTQRYMSLPSMRCKYCFRPLAPGE
TAEHDRYCSLKPLACTKIDSKTGTVCGYICRGRNMLLDHEAHCHAKKSRPHTHCKESPEH
HLKAVVNDSHIKSGTSERLMCSSCGTLVNYPAALARHRMICPEVEVLCPLMCGKTFRRGE
VAQHVKQQALEHAPMPVPNLANCAGDDPKVVLALVMNMLLERAGIFGEGGLNTQRSNETP
SLGYYVSGSHSSILETGRISDSGRPSFVPPKSAQTKLAMTSSPLIDQNHCFDNSPQSAFS
LPEKMPIPRLIVPEPTGRGENCGSSVNKLAGMPVYVKDFSSANESSTRSPPRLASTNGYI
RCLAEAFSGTGE*
>TCRU_8319 hypothetical protein, conserved
MRMPLCLLMCLAVIIIGVAAVDFCPEDGILYPIAVGDTVYGHVSSPTGESCAHASLRILV
PPPPSNLLLLTGGWQYLFGAVVEGALPAKVTFSIIALCDGIEVCRANIRYEVDPNASTNV
PPTPTESSKTTTTTKLPLYPPCAASQDEYQLVILPGKPNIATLPTSAVQLFCPGGLQASI
TQPAIGSAAVLGPNSLQFVYASPDDEVEANITLPYEVKCDRNVICAGVMRIWLHENILRC
PKDHLLYDVKPGARLNATLDTGASCGGALRARLRTRNAADIKFHDGVSFTFNASGKEEDV
IFNARLYCDDMTLCDVTFALIVTNEPRPSPTEAPHTDSTPAPTAAPIAICNEQFNFTVPV
GTELRGKLHVEVDGCGLVTYHQSLYSSRKNLQLNIIGDFVYSAPAEEAVDKLPVDVSCVT
KFWCLTYITITSYIDLTPTDSSTTPAPTTVPVPACANVYYYQTAPGVALSDSLNGMPGQD
PCAYGRYFSLIFPPSVGKLDLTPIGDFLYRPERNEGSCHFSFSMYCLNKLYCQGNAYILV
SSERTLPPSGGKNGSSTPAPSPPSEVKNKQIKCRGTCNEKAWKTYPNPAIWDNSPGAGYA
RRDGHAVDEIQVAWMNNSIVITVYTIIGNLGVRFPTFEPLNRTVGKYFEPKDFEGVVQPS
SLGFELSCLANQGSIGMGEDVWRWKTLGNGTGSGSVGALYNKGTSWYQKFGGKHIGCDTF
VNSCIYAPLLTPALPNTTVAGRWEIDIDDCDATWTGTFPYASLEQLKNSDGNPVWYFVGD
KQIKSTIISEAVRANSWIEPARSFDTQYEAHDVIFDLKQFIVVKKLATAPFSIDSEYFEY
TENGDFAFGVNLLLHPYVTEDMKTSYAADRHVEGFKWITQEWVAPNAQHCTTCKGIKSHC
SAEGKFATSTYIGEFPSGDCPPGTSIVELRKGPAMDGSICSLNRMHVYNRSGFSVPKGCA
TWYQNLTIRGVSIGSGALPDALKRAFSYEGRVMLQLLMTDGTKHDVAMDLSMYVTRFSQD
SYAASGRLGVCRGSDYWPVLDPLGVSLPDRPFELSTATPGPLCIDMLSSTFGPSGWATVF
LQLSGVLSSQLNVHTIVLKYKSTSVFLHYQDPATGAVAMPPKTLGHWWQHTHPFLSFRPL
INRVKNDTLTIGPELNPSEVTDVPFAFAFIPGAINIDTNVEIILTATITTDVVSKSSFCR
TIHVDPMMTQRSRYGPPRGADTELPNNIRKSALEVGVFAGLSIALTITGVVYMTMDNNRP
LPRWVPRGKLIKDTVLAAVPAGLRPAKKQKRIVHKDMYDAMKSGRY*
>TCRU_8320 hypothetical protein, conserved
MVALPFHSILAHYGTNPPLWWNWSRLFTGSSFGGCARTSFGCRVGFVDLVELTRPHTGHE

CCPEVPRTTARVLAEDPEMVRPQSVAPRVVRRLLFGFAVSEPAGGGGAWFSGTNLRPRSG
ANRRTGGPCQEVRIYWLIVQPRDEERRLEARCEYED*
>TCRU_8321 ATP-dependent DEAD/H RNA helicase, putative
MRRCFYLMWRQEKRLPRRFREVPKDFTEIRSSDCRPLVFTAKRPEPLRGVTSLSDIVIDE
EALQTSSLQELSQKPVAKLDLERMGLPPHLVQYLHRRFSHEKSPSGASMKRDDDAGGFQG
LTMVQARALQHFYAQQDVALCAPTGTGKTFALCLALIARLMRDGPMKLFSALFLAQNDHL
CRQIAQWMREMWWYESDERLVFSATSDLPSNVVYQRLTRELIRDAAGKIVGSADRRPYVC
VATPEVFWEFFQRRKQSILSREATLGRKKHSFALTPVLPSIDLVVVDEVDEVLPSTRPDA
AGNLLMKELYRFVKYQAPVQLVFTSATLAGSTVNHVRRFLKKSVLESKTSRIFESEIESF
SQKAKATGNLSKAIVPDGIQHLFYTADTLEEQRECLAAAIKESGHGMEGNAEPTGKMKIL
VILPDSGNVDLFVQRVLRPAQPDERFKVEQIGTQQGSCKQREGKEGGTHANSLTTHNSHL
SPAESIYIRQFILCASSCVRGIDIGDLTHVMILATPQSALDYAHWCGRVGRFGGRGVSIV
IMSRFAVRKISLFCDTLEIPFKVKRRHNAIDVDGERRAFGF*
>TCRU_8322 CMP-sialic acid transporter, putative
MRIYLFGFCKRVVSCWSKQLFFFWFLTFQNAIAVLLISYTQERQLAAGAERFAVMHAVLI
QEAIKFIASFAWCVIDVWRYVREHATERNEKELILDGLDEMQPLPVKVNTGSDVISSSHL
NNSEEINFKDNLLDASFQLSASKTPGQWRLFKNGIVSELFHPSAFRMLLPALLYGFQNCC
VYLALANIEPTLFQVTYQSRIIITAVFMSVFLGRCFLFRQWVALVVLALGVSVAQLGDRT
ASGAERSPEGSFKGDYTVGIVATIFSAATSSAASVIMESFLKSRSSSMSLFTSTKNLHLA
LHSVLCFAVFQALNGSVGGFTESRNASFIDAVRTYFLGFDGLVWVMLVVQAIGGLLVAVV
IKYSDNIVRTFAAVISIALSGLCSSYLYAFCPSATFLVGNAVSLGAIVVYNS*
>TCRU_type-like Zinc finger protein, C3.1
MEASVSLFEGDADMYAEKLASSNSSTSNRNNATIAAVLQEGKKEGVRRPESRNTSGLPGD
HFNVLSADKAETLSIPPELIEPTAGSRRYLAKNQGKGAPTFAFYLCKMYTSNSTCAHGSF
CDFIHSRHVLTNAPHRGGPVKAIQVHWSTPIHSMAEAPYERHEPGSVFHINQSNLSGTSS
QFTGDAPARLRLASDYVYKTRGSEEALLHGSTRLLRLCKHYEREKCGRGRICHFIHRVYL
KPSAQSSMPPSLSSTETTATAMTAPFTYNQTADLNVINLRPSHTGTQPRFLPSANCSTNS
MHGYTRQATGFPFDARGVQHATGGVIMSPPSMLSSQAPSPAQPPHLHLQQAQKQQQQQQQ
QQQQHPQIMTQQAGYPFSSVYTSQQTPYMSSTTVQISATQFQSSNSFYEQLHHRGTQQQN
STSGSQQQSALPVNSVTDYLLPQVLFTLM*
>TCRU_8324 Roadblock/LC7 domain containing protein, putative
MTAERVESVLELLTYTKGVTGVVVCNRDGQPIRDSFQDLDRTRAMEYADMAAELAREAAP
LLYADDTLDSLRVRSRTSEVIIKCHDEFLLVVIQEFSE*
>TCRU_8325 Rab-GTPase-TBC domain containing protein, putative
MLPLGVLTAAEEINAASGRMVSEDLPAKEMSEAERHMSLIQQFTMTRRQFYVKEAQAIRR
QRQLRAAAAAYWESALRDFAKADRVKLCLIILQSGVPASLRPQTWVMALGDALKISRAEF
EAAQQKAPSLMAGEKEGSPYDFHAFSSATISLRAAAVTSNDSSRANTVRISLAEWRSRLI
EDLQKGLPHCMPTEVMQRASQPSTKEEEPNTSNANSFRARDTALADQATPLQEYHVGCCS
DSAVDTKPPLPISEHRNNALLEMFNMKRLENGLDGTTEAVTSDASCNNSTKDGKDEDEDH
DAARSPTPLVSDARTWLHKSAQKSMGVSVDSSFSLLYPNMVFPMHAVNGDGNNLFLSSLL
NENAVRRVDSLLQTYMELRPEVVYVKDMPCLAMMLSLVIEDPWELCVCFTSLLEYGHLAP
FIRSRKEGITVHFNIFDAVLRKAHSALYGLFQRYEVPLDVYLLDWWTTVFLRTLPVAVAL
HVWDLFLLDEHYLYRTTLAILVYRFGLYNRHALSSLPRSYCSQEDVLQTLDPSSLDFYMY
PSLFCRILANDKLCGISMRSIRSIARRVASNRPSH*
>TCRU_8326 hypothetical protein, conserved
MFRFARLARRGKRRTVPHTIASLPAPSLRGSWGKIGRMSSEERREVLEGTWRQARPVQLL
PDASDRDAGGFVEGVSFRTDEEVEAFLAEEMREDRAEHEIPALELSRSFFEELAQSADSE
VDMENALGSTPASDVEREEEERDVHRQFFADFYVQQGIIRAEEKYEFVDAMLRPPTVMVM
MNAGLPFVRLMIRCQLEQHLRALQAGRSGVVFLPHHVHPLLYMVDAVPTQRVGDPLRLPY
TQERSLLAQREMQETLALNSTDDRNASPACSSAETQTEMRSPEVDLMEAILNDRISTHEL
QTIRTGKDETKEVECGSGERFTLEQIGEETALDLQSEIPRAPLSTGHLYWLQRQIASDTL
IDMDMLGLMLPLACGLCRNAGNGAIILDMSSRSLNAQHYSYGKDIAGHFVISRADVAEGV
GEKSLEAVVISLVLPKPSQRKSGRHHYALQRPRATLNEVPEDEATLGVGQLYSPGYHVGI
ENRITGRGPSRHLWEALRGKCDAVLCFPDTTADGRRPRTVLGASGEDEEKEAVANRFVSV

CSKVNKFFPYLRQELAQALEYVGMQGGVVVYATHSMNPLENEAVICSVLTEFKRKYPGRE
YRPFSLLERTTGEEAELLRSFMARGHQGLKKWVPLQDGPPEQDPSFCDEEIVSMVARCSW
RAAPLRTDGDVCFFCVIQLYASFSGLPLPPLPPLVRQTDIPAISAFPWLDTVRLHDHWGL
LIHRSEEKRAFVAVTPATLYMANALNSPHRKNGYSVIDYGVCVSFDSERRSEQREGVVVS
SLSGTLLALALCDSTNEDYRSSHVLELPVAALLELLHARQISLRRVSEVLGSFPSGLGAS
ALAAEGVSTVFLKAAVPKIVKPEGDDMEIHEAVTSELCRLVVVAQAKVQRCPHTQMNTTV
LTLECATVRECSELEERVVAIGDALRYLLRRLDYPTTAWGPMNTVGDEGPQMRDDEYEVE
APVSSAATNDFDSLLGSRARSHHRRKMQRLGNKLRYLGGGQDGPVNDWERDLRHTRRRNR
LAVTPSFLH*
>TCRU_8327 hypothetical protein, conserved
MPSNFSESHSYDDSSNASGNSKELHALLTNTQFALLVVFSGVCHYVALIVSALTVGESTG
TLTLPFVVVKKLLMGFVSAITSFLKRRRERVFVGVGYEDDGASVDRFDAMNQPSEVGHV*
>TCRU_8328 hypothetical protein
MFAGSTTSESLALMSQKVLSRVVVQERENVLLQGDVRLREEEAQRAAEEERAAFAELEAS
VQEVVRLCLSCATSVQDEAVMDAVVQQLTQQIGEEEAAAQSFALEVQHERVALLARRAAV
ADEKTAEEDDAFRQEHCERVVDEEEGRRERLEIMRVEQDRLDLERRTELSTLRYARELFH
VNTE*
>TCRU_8329 hypothetical protein, conserved
MAPPKAPLPARLIAGDFLGFNWNKVTWMAPYNNFYPITVCGGLGGRLWSSFIQYGHFHNR
TGYNVVRNGFLAIPSALAAFFMIFNADWYQALASACFVLRQDVPTWAQEKYAKEMVYLSW
NKPGAMAKHHYAGTVSIPGTEKLIKD*
>TCRU_8330 hypothetical protein
MTVCGCDHAEALSRIRTEIHLVEVQLRRSREARRKYGIGYESNTTGCANETLRASSVDMG
PKREVLLLSLPSTPCDEKLTSCTEAAHSPLARAPAAARKEGTILHLEKGSFGREKFVLRF
LLVDEHEGVMWYKSEQHCRSNASRPLGHVPFWKETRDSRGSRFKRAAVCWPRILPEDCPK
AVDPQKKYFAIEYRSEKDACSKLIFAAESDEERNDWVHFITQFIDVFLAPRAGSENLQHT
PRAPTPPRNCSRFDDGEAPDGNVS*
>TCRU_8331 hypothetical protein, conserved
MSLPIIRLRTVNSNHATAADDPVTASCTLYGFLRSVPSRFECDMAMSDFKRGVQAAQGQT
CLTKNNDNMLNLVFSSVQDRLLRELPKIIPQLARNSSTWRRLLSGAESTSSMNSTPTATR
LQDNARSLRIEESAQPSIPSTPLPSAGTGENGNKGNHKNGDHHSRAEEILVEETVSTTST
RFKSPYEQIPPPIHLTASEHKESRATGGMQGETGEGKDASTIVEHRGKGNNFTGKSYLPH
PLLLAILERVRSSCSAEENESDREEREFTTIMESREKALRTKLSSAYSMIPPEEKNCMGF
LRDMEARVAVAQKLFEVQKFEETTIRMTECALKIEVATMRALLHQIVDAVAEAEERHERE
GPRSPYYAEECHVMAAIQQALDDLAS*
>TCRU_8332 hypothetical protein, conserved
MASLAGPEIMEAPKNVLFRRFAVAPDCLTGCKREILATWSKPSVPSIAMDAEKVDTSPSI
SLDRSAPWVKLPYPAIDVAWCPFKEGNTYAAFLTACSSCPLQMWDADDASLRASYCCDNA
LGKPASPHALLWSRCHTFLAGGYGGTCDRIHVRLYDVLREGDTVHSSYCSPCSKGIVSAL
SDGPPPYGEEMLLAGFIRSGNVDVIDTRHFGAAAVLRGLRSGVAQIQVHPTLEYLVFAAG
RLGDNRIVCWDIRKSNQIFATFDRKMSTQQTAFFGLILPRGTGGRRTCLVSATHDGGVLV
FDDVFVAREPRRIQKSLGPTAGLSVLEDGTVIATVGERQYPVRDTYEANGGESKTNMRLA
KRKRAPFDDSETETEDGFCNGEFAAGAAVFRL*
>TCRU_8333 enoyl-CoA hydratase/isomerase family protein, putative
MRRTIRVFTGKLLWEDFTNTRLITINREKALNSMDLEMVKAMQRAYVHEPHAKGDSALFV
VKGAGNKSFCAGGDIVSLKDRYDVAAEFFYTEYQLNYHILTMPNPQVSLWDGYVMGGGVG
VSVHGRYRVASERAVFAMPETAIGLFPDVGASWFLPRLKMKGLGLYLGLTGARLKGADVA
HTGLATHYVPSARFCELEERLCHIDDPAKVEACLEEFAVKDLPPFTLEPHRETIEKSFAL
EEKTTVEGIYESLSADGGEFAKGAINTLNRMAPTSLRVSLEMQKRGVKMTDPADVFRMDY
IGSLRTHVNSDFHEGVRALLVDKTKDPKWKPAKLSDVTADYVEAYFKPLGNQARQWHPTV
PY*
>TCRU_8334 hypothetical protein, conserved
MSEGVGVGEGTSRVRPRANKENEEGASGPDDSAGRGKEMVPFSAQGEDWASQMLQSLKED
NFRPPFTLSSTVRPYHRSLDTSTATTPGVGAGASPVLEAADLDVTIGSISSFASDFGRRR

RRRREQLALENPAEGERQRKDLERALQNLEEMQRENRERMRIVASYAPSTRVRSPNEKSS
CGSERRLLHYFRTQSAGSLPFCKESRGRALKRLMTSSAMPEPNMTTPMPLPRRQEGINSS
LCDTPSPPQHRRVDHPSTKISEAQKQTTCENINLLRKEHRSGASMSRVIKFEREPSEILG
KSPSPPRANLSPPLRTPVGNEGVGSGGRDGPVNGRDGFGHAQSALDAGGNRCASAVPFEG
KVRRGEPNGGKQVDKGKTPTPGRGGRSTSPPIIILTVDSRRSMGEEDARRLLSAEPIKSP
EPLLRRTPPGPTGRSAGNNPPKKQFAEAMLRSSTMKELPSAATEGVIKENSQPECKKARA
AIPKSSLPGAGAAAPVVAIDKSRVEERHEGHRQPGALNKRPLVGKSRNSVEAPSFTEVAA
KKSTSVINRNLVVASTSKQRKAKSGNGTSKITVVVSGETKTKTQPKPEPRSAGAVRSPAV
VAGRTATASTRYRVTGISTRAAPLRRDDPATLDERGVCRGKKSTSPPYSLETASSVSKQN
SLRQIPRGRRSPSSLTLITPLERESYRPLGNDRPIDTPLKAVRRGPVGEPYSPRRLVPFC
TECGKKHLSEKVKFCAFCGHKREAVAM*
>TCRU_8335 hypothetical protein, conserved
MRRARLLWLSKRLRGTVISWHPFERHGVIRCATDGKEYKIPNARAFETILPTRLRQLEGA
AVEFEAICGTLDVDRVITRSRLEPITAKSYERKSPVDFLAGFCLESSNLTTPEATSEPSA
TCASSLSSPSALFPQPLAGNITVDLSTVMSKRSNEGSAPANREGAENTEIEGEEEESVRA
PRGVKDLRNLVVLDEDTKELLRLRRQLGSDAKAREVLQQRRKEAEAAKTKQRKVLSTHQT
GVVLAWSSLHRSGVVLENATEVPRNASENNMEGMCIIRNVDSFDTALPTELNLVGRTVTF
SKVAYGCHPLKVFAENIRVSGSVNFDEARTAATEAKAKEAAATEHSKRVKQLGTLFEEEM
DHADEPLPTGPLYGVVTRWSGGQGIVETGNRRLYYIHSAADFIQLIDQTSNTIRGAVVRF
TVDKENRRNAREVNILSLATREINSVMPMLERQKGPTKTTTIFGDGISSVNAASFVAGAD
GENSNAIAADGGTGEILADANWVQGILITWSSLEDQGVIQGDDGNRYLLRDGEEHVRDYK
TCKSLLKKGRRVKFVPFGGTGLLACHVVPLETEADEATLAEAELQPKEQRVSEGHAEEAI
ASPMSTAYWINRMDRAGYDTTEVKKMQNRAITFDDDDDDDDKLLDSEDLFKKDHWFNDPR
KNMRLPNSDMTAGNLALIGPASMMNIAMKAHNPQKLEKVKNKYYNRLTEPMKEFAWKQAK
ELAPKYEKRIKEAREKGNEPRFSFY*
>TCRU_8336 hypothetical protein, conserved
MVSKTRRQRQRRKAVLEANDGVLPPVLPAVPKSVHLKKTRPKMKSKMKIRLGHESRVDIY
EGFEDHKGVLWNCPNCQRECRVVGFCVDCATGTRSKTHTGVLMARHKNGKKSTMALAVKK
PKKLKLSKKTK*
>TCRU_8337 18 kDa ER-associated protein
MSSWVSVENFLHGKKAAYVRRGLVLFGLYGVASDYYLMHYYKAFDPSEGQLYVIDWSPIG
RPRCQVHVLPSNHYPNYTPWTPRNGDVVLARTVPNEPNWLQLINGRFVENQTCGVPLAIP
LVEVQEKENQRKRKKEKSQKIL*
>TCRU_8338 Methyltransferase TYW3, putative
MEVRRKETSVCSLLWAEINATVFELASDGRSGKTSAMSLRRCNSLFCSFSSAAASGMALS
KQKQQRRVSSALFMERREKIIADLRENRNDKSLAGRIDPQVAPLVHFINEKFHCYVTSSS
CAGRASLFHKGQVSAAVAAPLAQRKRGAFGQGTLFQTHDPFSDVEGAVEHELIPALESFS
AWRKQQHEGDPLVYETELLQFKFEPMIVHVLCETMDDAARLLQCASESGQMNSGVISCSR
WTSEHRKITCCITSLLCVDVALFAQGRWLLGHASFSSPEWKALLTNTVVHMNTLFHANEV
RRSRFTCELQRRLLF*
>TCRU_8339 enolase, putative
MELLSWKRYDDKYKLSQILTEAARSCVDAHTARPEEYLAAYFTEKCSGDEIRGIVTRAVY
LPSGTVVLRLTLQLLNGMETESAAFVQPSHGEYDAGADETTDPTTYTTEALQKSYFPRLL
QFGARDQKGFDTTLRQISSSAEAVDVGVSVMYGLSTVVASAAARCSSIPLFMYLRQLFPS
LGGDEAFTMPQLCISFFGPGNPSTARLALKDVLLIPAMPEGSIPNEIIQKIFAAFHHFCR
AHNTMMRSDGSLAYDDFENVTDALGLAEEAVRAVGLTPVKDICIGLRFAAAVTSPSLAAT
AVPSAAAWKESKDTTEVMYALFPGDADVSGAQVSEYLREQLQNCTDFVVYVEDTHCDRDT
FGLQRLQAHLGDLLHVSGRDIYARSQYKKVEHGIRGLWTSNFVLDPGAIGTLSDVHEIVR
RVKEFEGRCVSFVAPELVGNAATMAHLSVAMEARFLCMGGLLSTPQCEVLSHLISIQSEL
LHSRALSREAPKIARMELPKPPTDVVPEIKRRMDKKKRKK*
>TCRU_8340 hypothetical protein, conserved
MALLYHRCYDTDLTVVTEGSSSLRETRMSWSYTDPRVDETIVVLLLAASATFKEPADGDA
MQYALKVILFTATAAENQTERVVYMESARREVHSAIFEFHAPLDVSVVKGTSGLVFASTR
QFFFHAVAGGKSLDRFVFLPVERTWERQCHALRPLDEVEPISRLLAEVNGDSQPQLLLMA

KTGFSPASESLAEEDSIDLLLVASREEGTRGSSQKRQRMARLIKRNTTTSHLQTEGLYTF
VLAVVRCTIPTERVATAKWELLHLCVDREVPFQKQENTGSMDGWNTEDPTSSESVIQPGQ
CTWCYIQFSNVETEGRRQGADTKGIQESGARGIVVAIVPQPSHVVTVVCGGFDAESHSYL
LGFVSNQATGSGNVLHHPVEEMENPEETLWSLSEDTHTVQMMVLGKPTVSLHGPSEADAG
RVSPRVYQAQRALRSHSPYKYCDKSTGGWMRQVGLSMVLRFVVDFLDDGIGHVRTELDVI
KSGRQGLYLVAGVPWAKSRHGRFPIPRTVCWIGTAPLPIGKALSSMVLYPDNTAENGYAN
MTVMNATMSDEDATSWYHTLPTSIASSLPAASKNGALRCFVSVNTLLKKTRLTYVLEITP
EKQNSDNGKKIQASEWLYTRPQGGKTALHDDLGTTEILAACLARSVVMRNKSLSKADGLS
KSMLHESLLDGTVPEAVMYEAWQSVALGRSAVVTMSILEKLSQCMEVNVTQEVRELANAL
RHFLLTFLVELDWIAHADNNVLRDVTFLMLGAVNTQKILPGRRDSAIRDEDSFVSLLAPN
ERRSMYWLLRQSDMWLPLVAALFAWVNHIPLSSEDEGEGEGEILLEDVVQKWEKMAACES
GGGRAFDDLLRHLRRSQNASKYQHALVVLMRGNLSLREIASFAVWKDDDMRNPFIVFLQL
LLEVAVACEDAAEASSAPNVDISQIVFFAVQKRLQSDGTLETLLEFLHEWNFSFLEDWPL
TAMSGGLPVVYLILHLATADRSGKTQESHRFVSRAAQVLRWLCGDRVERAAEVLKALCAA
KVPLLALCFTERQRRDYFRSPEAPQSGDSYAGGGGSKISRAMHHILGSSRASLLRGALTD
LGVCSPTDDTTSEKFILLLWTLVLENDESAAFNPNLLQLLHEALFASSEATLQKSVPRAV
LLLEFLRPVFLSTFPRVFAAVGDQQGTVGCALAATAVSPTLPSAAVLGPPLDETERIERV
WIKTLHEIRRLINLHVADCLEVQCLSLLFNAFEASCTTLSEGPRSGSEAATEDIPFTFSP
AEMYFLALQVISNEPPRFVVAVEVMRRRIRSYVLHKMRLAIQREDETLLSSRTSEVDAAK
TLPGKLKRDTLWWDSKVYLNDVAENLALVISAFEKTAPLYSHAVLFLFLDESLALMEDSE
LGRGEKEERPVSEDVRGEMLQCARRAAHSRWAKLHRQEKKFLFRLLSHRLSLPNQEKAEE
DLYHRNELHQQVLRDMARMKEALQQRNVNAALLRAVRKDACHSSFRGGSTVHVDSHEDMG
SGISMFSTELELLFKEEAYVRQGLQRHLRQEYDNLIGSSAFCAALGTLYLALREEQRRRV
FFAFVIEQEDILLTFGFNFFALMKEAFRSGVRVLWKNAMECFQRQLRYLLLQERESRSAV
EAVCFVEHKILVDLSNQQCAVFDAESGLRLSLVEEEEAHRDTFYELFAREEMMAQQRYEA
RLEEVVWREEEAQWEMELQRRQEEAGDEKGADTMRRSSRQHTCLEWKQRQLAATEEKGSV
FLWQPTPRKEIQAPSPLPTSSSSLAPPPAATRAAVKVIATQPVEALPPANALAPLLQMDS
TTATSVEAGGFNALLDASESLFGAFSRLQRQIITTVAPPPTASAKNDTSNVFTAIAPLKQ
EREENKGENEGERMEHFPRISPPVITSALKTPPSIAEKEEGWDDVLEDMSPPSTQTGRDD
DLAKKDQGALEKSPTSHEESSKRLRLRASTKKSKIRAPRQKRLGEVLCLEKAPEGKKETD
ITHHEEKPHENEPQTRSEATVSKGDVALRALEEKEVSPSVDDEKKKVATIGSHDTDQTLM
TRASSGSAEGDQFPTVELKTDVPEVLMDEAKKKEEEEEKEEEVPALRSETSTPLKRDEET
ARFALFREERLARAFLFRCFILLA*
>TCRU_8341 general transcription factor IIB
MATTADFLGKNCPHCGAIDSLETDDVLGEVACTECAIVVAMGLEESVSTRYDKDATYDDV
DRHRKREDMSVSTPHALSLSSSASKTPGGDTTGKIILHPAMLNCIRGLQKKSALPEQVIG
RAVELARRFVGGRRARGQRIEKQQDVAAACFMIAAEQMNHPVPLAELRHLDAALGDVEYR
RAEIVKETHMEEEERRLKAMYVDNLLTIYLRKLSLQLSLYMPRCKRLLGVLHHVDSLREV
GVVDKIIMSLLLALTSRSFQWEKEKTVVNTTGNSVIGSTNSPEAICANFAAKANLDIGKV
NKVMKTANENLQAILAAFAATDSTHGNENTKKEEKEEDNDNSSNMTPVTKRMKVENP*
>TCRU_8342 nucleosome assembly protein-like protein
MQKKQLPPKFFDPVSFGGGKGAKHDDEEEVEDDFDLVAVMKEMTVHERRKVYALKGILDE
YKKARTKFREELAILQMDHLRAAQRLHDVRAAIVRGLRDVTEEEIAAVTTTVASGVQEIP
SDDEDGEEGKSKPQPRGATAGTDEKAAKSVRVVTPQEEKSRLEVAAAAADGGIPDFWLTA
MCNAEVVESMITERDRHALSFLQDIVMEYVEDDPQKGVRLNFHFAPNEYFTNTVLSKTYR
MSFNEDSGEFEIDSMKSTPVEWKSPEKNLTVILKKKKQRHKKSKSIRVVTQEEKCPSFFT
LFTDPCRDDDDEDDDHDDDNGKDGKHSGDAGKKGDKGDDEDDDDDDDEEEAEAELHIEVG
QLLMEEIVPKAAFFYTGKSVDQTAQALHNQIQIQFGGDDDDDDEDEDDNEEDDDAPNTQP
RLIQHGKKGRGGAGGSGGRGGKGKQECKQQ*
>TCRU_8343 tryparedoxin peroxidase
MSCGDAKLNHPAPDFNETALMPNGTFKKVALSSYKGKWLVLFFYPMDFTFVCPTEICQFS
DRVKEFSDIGCEVLACSMDSEYSHLAWTSIERKRGGLGQMNIPILADKTKCIMKSYGVLK
EEDGVAYRGLFIIDPKQNLRQITVNDLPVGRDVDEALRLVKAFQFVEEHGEVCPANWKPG
DKTMKPDPEKSKEYFGAVA*

>TCRU_8344 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily, putative
MLYTQRGHASGKKRATALYLWVTDNNRSFSVGPVAVEDDVEHYNALLYSDGVLHLLQDGA
IGRGATMSLARLTEEPSTIGSVLSNWAQLDASFPKSSTPTTGLVGFLSNAASSVDTWMDD
YRCVNASVTKAARVKNGFKFTGPGSMATWPVNSREDNRQYSFVNRRFTLVATVTIHQVAK
GSTSLLGAGLGAPVSTRFIGLSYGMNKTWEAVFAGKKTTSGSTWELGREYQLALMLQDGN
KGSVYVNGKIVGSPENITTPETLGHEITHFYFGGGEGDINSNVTVTNVFLYNRPLSVGEL
KMVKKSLSSLRPLRAGRSCCTLREGTPRGRKGPLRSTFGSRTTTARFLLGRLPWRMTWSI
TTPCCTRMVCCTFYRMGLSEEVRLCRLPA*
>TCRU_8345 protein kinase, putative
MFQTANSSTPKLSFEKRVIGTSLRLHRDAHTGTNEDCIRSSCNNVFLVSHSFNSPQLSST
IRSTHSGGLEVLTADPPLLLDFSVSSASVRRRKQSRPFFGSNNDFGVEDDNVVVEARESN
SSLNGSRTSDACPGSTVSAPLEVEPLPTSSVTKFYTSSPEKRRKSLSKKERGREVNGSGK
KSVLRRRTGSVPCVTHNSVTRSQDSEGKGPMHVSLAHKALIGKGSFGVVFQAMDRDTNHI
IAVKEISFSEGSESKALKAVRKELALLKLLDHPHIVKCLGEECEESCLRIYMEYVSGGSI
SSVLRTFGPFHEKQASIYTRQMLEGLEYLHSKNIMHRDLKGDNLLVDPNGTLKISDFGTA
KDLLDPTASTALAGTAYFMAPEVILSQGVGLPSDVWSVGCCVIEMLTGSPPFSGVKNQYS
MMMRVAETEGELFPEMIPKGHRLSSGAKSFLRRCLQRDPLKRATAKELLDDPWIVHTPEV
KGSTHCSSRSSNGAFPCGRCGEEGTEEGGSLSHLRQDQTLEKDNLVGAANSGSTLSRSQK
HASTNVQ*
>TCRU_8346 hypothetical protein, conserved
MSTLENCTDALLQQKVVQASNYERLESRLMEMERAKRSLFFGLKEIITDVERRRKDLGEL
QEESTRLQHQLQQGSVKFSALAAFMGEEQKKSMRLQEALESYATAWTGCPARAAFLLRAL
QERSAFCRQLADVVTALNRVRALVEVVQRVDVAKSLIQERLDRLESEAGRLEAALRESHK
KQENLQEDLRGRNNVAQTDAMRAWRDSQEKGRQLLTLEVALQGAHLRSSAEEGLNAVYRM
ALQAALSIADACCDRRDQMAVVSKFKELLCTLGRDKITAVETRTRILTDVLKKRLADLNA
QRECVVLQRERALHETILLRDRQETMRGTAITVEHRMEFLQLMHLALQVFFRRQRARLFQ
MHRERAEREAALVSARAAHEAFVLARRFRSLQQEAREGFVAEESLVRGTVEGNEMDERRG
IHEQATQSFLMTCTNEKARKEEMEMKAAVAAASLPKSPPKILQRRTAVTKDTDDMCLHSL
SQITPKKTTNTRRSRAANAVPHTDKKRPRSHAVLSAATVARRTYPASTQQQEDEANDAAS
DSSLNSLGEFLTLGTRVPLSALKSTARRAPLQPLPTNVLAGGGSGRKKDGSKKCLTDAAA
RRVHYNSPLPRPPGSGNALCALSSALSSAFARTGDAAGTNTPKSKNRLEAGKPRPSILVS
KDAWGEGKADDVFADVFSF*
>TCRU_8347 TrkA-N domain containing protein, putative
MQEKTQHLLDGVVGLTCVDPSLDLSVCAAPFVVSIIAQQCLYLCHAASSCQALLNEGGSS
FWHIMRLVTEARARYAALRAPSSPRPLFRRRAASRSRGHTPSFVAFRSNSPSASSRRGCI
SSGRCGSNTKTDNTSSNHRTNNYDTPCSSAGLGTFFHEQLMLSPLEFRVVVVGGGRVGRA
VVERLLQASYLIHPSRITIITRQTETVAQFAGRGVQCTERRDGRQALLECHVLIVACQQT
QFNDFATTYCPRHTQNTAGSTAKAGNNSEKQEDISCEKKRLCRSKKRTLRDIVDKWRTIE
DDDYANGAPGAAMTRLLKPGTFVFSCCAALETHKIAKELGHLDPLVVNADIDMDTIQSAA
RQFQSGKDNFRSAFVQRVAVEGNSFLNALNVLQQTYLDGETPPADLINRNIFHDSYFSRL
RMRKRRPLSPPPPPSVGTALRAEGVSGSTSFLLRVWRALRCFVVVQMSLLKASEHRPFTY
LQQVGPLLGPILVALPFFSQNRIVNFLGDLLNKKKGDDDEEEGALEGRPLFKLNHRVVAA
CDSDSDSDECHDVPPAEKELARLIKNFPLIFENEEVVLQQLREQYIAVTER*
>TCRU_8348 ubiquitin/ribosomal protein S27a, putative
MQIFVKSAAGKTTAIQTSAQETVAILKSKAGVCDGTLFYGGQCLCDEATLADYGLQREST
IQVMLPVEGGKGKKKKKKVFTKPKKPIHRHKLEKMRALKYFKVTENDDGSFKVERTRDEC
PNPVCGAGVFMAQHKDRKYCGKCHLTYAAK*
>TCRU_8349 retrotransposon hot spot protein, RHS3, putative
MNCPEGMDVKAMCAWMKRDGTPQEQEKYWRMVCQQMDFLGPIPRYIFDAKEFSKRYNELD
RVLRSIKSRADANYITFEAMRAWCTENPFYKLMRVNRERGIFGSEAFNTDSLSYHLTNRA
FPFLEKVIPIVEFLNFR*
>TCRU_8350 retrotransposon hot spot protein, RHS3, putative
MWCSISRADGARLEEGIAVLVEYKAAVHNSTKHLLDAAAEEARNPTTTSTPEKLEGLYES

LHNARWSHAVELPDGVERKKTGTGMGCVRGGQNSHGLTRKLTTLSKRMTLCSNVVQHLPC
*
>TCRU_8351 Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MGVLYTADKEWVTIFNGKKTTKSGTWESGKEYQVALMLQGNKASVYVDDKSLGEEEVLLK
SESPLELVTFCFGAWEMHNFPVTVKNVFLYNRPLNPTEMTAIKDRIPVPTRAPEPQVKIA
PKPAAPAVPGPRELPAAPWRTTVGRTANTQHAPAGRLNSAGNEGTARENGDGGSAYGRVL
LPLLLLLGLWGLATA*
>TCRU_8352 hypothetical protein, conserved
MAAQCGEAPAPWDELRFLNECLVDALAVHLLVSRSFVRGTDGEGGETCYCSLLEEEVQVY
LRQLLQKYTSSAAMRKKLKSARSLYHLQCLTDVKAREEFVLIAAHPSFAETI*
>TCRU_8353 chaperone protein DNAj, putative
MFVDYYAVLSLHPSCSSRDVRDAFKRLALLYHPDRPEEGSTECFREIKEAYDVLSNPTRR
YLYDLGYAEIQWVRQRQQEESQLQQQQQRRREMERMDELMRNQVLQPQPTRNGAYVSPSL
PSESTRRVSSGSSSRVLLTPASTSHRTLAPTCVRREAVEKSREAAAQAVPRQGSGFVAVR
RGRLAVVERSDAGIGAQNTAHGQYRQTVDEFSSSDVRSLPVTGSQSSQGSGENSLSGKQP
SEQEQHLQRWGRHSVKDKSNDGKSTLVPKITTLQWGEKKLMPRRSNAVPSPDFFKRSVVK
TWRVFFHVPATGQRDK*
>TCRU_8354 ATP-dependent DEAD/H RNA helicase, putative
MSGVSQNEWGNMKEVQLRPATLSYLSECAGFRYMAPVQAQTVPLLLRNYDVVVEAITGSG
KTLAYLLPCLEMLQRDRVIEVCREHKNAVVSIVVLPSRELAQQVHLLAKKMLHFVSHVHA
DGTAGLPNYSCQCYIGGRDITVDVNMFKKAGGHVLVGTPGRLYELLVSSKYTSLFNFSGF
ELLVLDEADKLLEFGFRAKLDAILKRLPKQRRTGLFSATQTKELAELARAGMRNPVSVTV
RVGSLNSANMDGDKPQIPELLCNYYTFTRASEKIDRLIDFLRERREQKIIIYVMTCASVD
WLHAALVDVLLKEDAEHIFALHGQMKLEKRQRVHRAVTKGKRCVLVCTDVAARGLDIPEV
GVVLQYDPPVDPSTFIHRIGRTARMGRQGESLVFLMPQELEYVAFMKLQNVLLQPYDEER
DSIEAAREFVSRMNAKRTLMSSQKERRKRIQQVHKDQKLNRKERRERLRKEREEARSGDS
RMARKEVVGDLCESPSILALRHAVWDDTDNKLLGLATRAFVSFIRAYKEHECRYIFQLQL
IDLTDLAHSFALFRVPNCGEIKHMQILRIPLQDELQEVLKVVDERTRERQERRAQLSGVR
RPHCEREDEDDVQLEEERARVEERALKRQRTERNEKLEALKLTTMTRGERSRAWKQAEID
ELLKDSYYVKKERQGKLSSRTVDVIMGVDALENALLSSRERQEAKKVRRRTR*
>TCRU_8355 Bem46-like serine peptidase
MSVVETLVACGFWFCIFVVLFSLLLIVVSYQLREKQNRLLYHPEIPAESTLICENPMDRG
FANAENVHIRTADGVTLRGFIMWPWPGQHAAQQGATTGAFRSQGSGMNVGIPLSSSSTTP
RDSLFPSPLYAVIYFHGNSGNVGHRIPIAELLTSKNPCAVLMVDYRGFGLSDAVPPTEEG
LKLDAQACLEYLWNHPRIPQGRIFVMGTSLGGAVAIDLASRRMNMKRIAGVIIENTFTSI
SDMASVLVRAMLRQFLTSYTEIFFSVFDYYMKPLCLRIGWRNIDLVKRIRVPLLFLSGKS
DELVPPSQMQRLYAATSKSNVMRKFVEFAEGAHNTLPLMGGYSEVIDVFVQEVLRLEAEL
V*
>TCRU_8356 small GTPase, putative
MSSKRQLLKIIILGDSGVGKTSLMHQYVNKKFDSRYKATIGADFLTKDLELNGQLVTLQI
WDTAGQERFQSLGSAFYRGADACILVFDVTQQESFSHISSWLEEFNIQAGKRDSVLIGNK
TDLADRRQVASKTAQAWCAAQSGEAAAASGGSSITASGSGGCCMRYFETSAKENTGVEEA
FIAIATAALAQRATVDEDVVLPQSVNLSQPAPREKKQDCLC*
>TCRU_8357 Protein kinase domain containing protein, putative
MGVLLYEFIAGYPPFYDDTPFRTYEKILSGRFKFPSWFDARARDLVKGLLQTDHTKRLGT
LKGGVADVKNHPYFHGANWEKLYARYYPAPIPVKAKSPGDTSNFERYPESREDRVVPLTA
TQQAEFIGF*
>TCRU_8358 hypothetical protein, conserved
MVDGASATRHNSSIGTCLGRWMWGAVGACPHSRHRVRHSAIAAVRAALLVALALVAAAVW
MPAVHAVVLRLRGGTVDRAITVGRAVDAVLMDGVSITNGVAVVFDVPAMLPGALRIELRN
CVCDGGAQLYVRGYSGEPASDRSLEVSMSGLSGGYCSLVFVDNLPAHTNVTVRDSTIVTA
GPMRYSQLSGLTDAVAAPLVLYATSLLQTQLRVSNTVLRSSQAGGSAVHVGGDVDLLSSA
VVLDGVSLEASGGPTASAMHVASSSRLSLRSHSVFSVTNVSVVSSGGGLVLGERLAVVDS

VLRFVRVEGSAASSLVRCDGGTIGVGGWVELRDVWAVGEASSVASLSGVTLSGGAVSIVH
CAATGTTLVSGPTITSGAVSVQCNRAGGRVLRSSGDYRLAGLPSVSVVPCDGCAAALACF
DALTASFSDCVCSCRAGGVGEACLPFDVPVARSGGGGGGVEDCVSGVTLTESVTVGGGRA
TACFDSVVFSGPITAAVDLRLMDAFADALNVTLRHCMLAGGAQLRIGGLSESTARLVPYA
LVNMTNVTSLEGTIVLHGAMPLHSSVLLANSTLRATVGGSQYVPTTRGHEKSRYGPRLSW
TASVCCRRGLS*
>TCRU_8359 Concanavalin A-like lectin/glucanases superfamily, putative
MNDDLWFKRSGSGGKWSVGKPGQKQFYHFANYNFILLATVTVHRVPKESTSLLGAGLGDG
QGAKIIGLSYGMNKKWVTVFDGKKTASSTTWELGKEHQVALMLPDGNKGSVYVDGEIVGS
SATLPTPETLGHEIAHFYFLGCEGDINNNVTVTNVFLYNRPLSVGELKMVKKSDDKKKVT
VTAPCVGGVSRMLLCGIVALY*
>TCRU_8360 protein kinase, putative
MTTTRMSPDDFEFEKTLGTGAFSKVLVARYIPNGMRYAVKLISKRKILTAPSDEERNRMA
EVARRETRMLLMCKHPNIVRFLASMQTPDDLMYVTELCDGGELLHAITSRQKLPLDAARY
VLAELFSSVWYLHYAPKQSLPIVPNAPLKPITILHRDIKPENIMLTSSKHIKLIDFGTAV
VCQSADERPEGEQSSKGRAQTFCGTTHYMSPELLQDNYTCTASDYWACGCVLYHMLVGRR
PFDEPTEYLLIKSILEKEPHYPEDLDSDAKDLISKLLIKNPVQRPGMEEVKRHPFFENVD
FENLTTKDLSSFWIRKVDWVDDSTVSSCKGCDRLFGFWRRRHHCRNCGNVFCNSCSSNTC
VIPESSYTDPERVCDACFNEVENA*
>TCRU_8361 divalent cation transporter, putative
MESHADTGKIRLLVRRDGVSGPMQTYKISDLAEAMSAVQSLPFVPKSHKELIIPSMAELY
DEETDNMDIVDTNLQPVDFAWLELECDDDATIEKVISYFPIHSSTKEDVKSGRNDNDVAE
IFPLCGYVCIHVAARHATQALLGDEGEESVRVCMIAFERFLLTIFRRPVAGGDEVRAQME
FILPSLNPHTEPVSILVCSLITAFVKEYQKEPSSLLVEVDNVNELVLQIQPSQCDQMDLL
RRIEDLRHRLTRVQTTFLAKERLIQQLLLPVMRRIFITADSGALSRYQRLLSGLLLSIEH
LRKGRDVLNLSSMSLVSGVSMRLLQHCYWMDFVSTVLTEVMMVAMPISIIPGLFTMNVKV
PFQESKGLMTFSMIALVTALVFFVGMIKPLFLYIRHKPPGALVPPSLS*
>TCRU_8362 presenilin-like aspartic peptidase, putative
MQQKIPIDGVAFLLGRRIAALLVPVFACMLLVSWSVLNLSSLIADQQFSPIFSFMDEEAH
DTIRSKIGSSIVNALILVAMLTIMTFLMVLLYACHCEKVLFAVLFFSAGFTLFFMTWMWM
DLFCTRFQIPYDFITSSFLLWNAGIVGLVSIFYYAHPVLAQVYLVVVSVIVGWSMTFFSE
WSTWSMLVFVALYDMVAVLSPRGPLKMLIQIAEKRNEPLPGFVYNSNANPSMQKAERVGV
PPGEDMHTRDGPRENNSSNDADSKTSSQMTSVPRLYYALDRSPFKLGLGDFIFYSVLSAR
AALYAFMPWAASTVAVCFGLVATLTMLLMYKSRFPALPALPISICFGVAVFFLYRFVVTP
LDYFAALSVLAL*
>TCRU_8363 hypothetical protein, conserved
MEDVVDPSAELINELRALVVSGGTMVPFNERKVKAVVDGVSDSFRHLEGISRNPYADASQ
PFYASSMKYYRAKYLRDKRCLLAYMMWRKSQMTRAWWEAKDNALSGVLTPFESTFLQEYN
DVMVEYMTSFAVPLDLRAFTWRPPSTQQLEVRGLVDHVFVSPISGAVISLYKGKQILLGF
EEAETLIQQGVVELVE*
>TCRU_8364 hypothetical protein, conserved
MLLSQPGVSRAALQEENARRKDFFTLLYLAQRRLYSPTNVEWRLMEHCLDDINNKYADFS
FLVAFAASLALRNRKGRFFISRYRVPLYLGLVGYDNALRSTNPCPTMTFWNSVTLLESPL
GETARALHAPSCFYEVKEYPMSSKDVGESYLFWLWDNSKLIVESLFLNSFLRSILDQSCW
KQASGDTTVTSLVINTRFSRWYVFSYQKEAYSGQVRHRMKISLPTLSGQLGLRWSYRSRE
MILERASFGGQLWYGVHFALMWLLGLHDGARVK*
>TCRU_8365 Protein of unknown function (DUF3682), putative
MPDGCNKTAITVPLRSVLPITAVEASTGESASPGATKNNSNSSGASDVGANGSVSAGGPA
AGGAGAAGASGSGSPGAGGGGGGGSGGSSAAVSGPAPAAAPTPLPAAVSSASVAPPSAPG
PSGGPSAPTDAPGVDPSASGSGGTAGSSGSNPSNTKGDSQTGDQTPAAAANDTSPPEGTE
GTTSVIGHKGQEKKEEEEEENEQQQQSDETQVQQHQQHEHPAENGEDSAKDENALRANAT
ANTGDSDGSTAVSHATSPLLLLVVACAAAAAVVAA*
>TCRU_8366 hypothetical protein, conserved

MPPKQNRVQGGNAKSRASAVPQGGQRRAIEEFEGKRDQPSATHIRAESQQPQWTTYSYIK
DILLERNTNRIDMMLNDFLRSYLGGKGVERRNENVIMEAFVLGPTVFIQNQQLLEEIFNL
TAYQAQNWLSPTLCWVDDIHSPSLWWPSCIEHSAVTPRVWHSCFGCQ*
>TCRU_8367 hypothetical protein
MSSQGPVPTMRHAKRLDSTTNGRKIAVTDTSQTNTSRASVPVMQRRLRMKSGSTDAIPFD
GEVNSPSPIAPSCSSRFRDPVMDDQRVLEGSPGLSRSPHPCLLETTKKKKTTYDPLEGCT
FAPTINKRVKVVSSTPLTAKKEGSENDGGEPFPQIKRKPSVVVYKSKEERELEECTFAPN
TARFHKDRDSLAWWTREPFVGAGTESTAASASGSLLTAEDPPVKGGSEEDTEEKQGKCRR
SSSDGRLHQQAVIRNPSPLPIAMGFDKAVQRMLEARKKTRPKFEEMLRASTEESHKPLQP
TVVEPFSLQAEARHLHREQQKPVLYVDVDLPSGKTGRIGVHRGDEAADLAKRFGDAYGLN
EELRQRLELLLSEKLRELLRENGRTLWL*
>TCRU_8368 hypothetical protein, conserved
MSSLKRTREGNDLHDIRASFQRVREKTVLRRSGPYFLERIIFPRLLQPNYRLGGGFPDPT
RLCCEKGTGSPQRHGTLTLPQRIEASAWLRRFRLLRLHDFHRVVPQDQVTGTLSSITDIV
FDMQEQFAVACQARCLSVYSTERWLESCEMCEEPNDASPLVRVKGREWHGFRSGFSAVQF
LSSSLQLVAGYHRAPFVDIFDLEEVDEETCEPQQRFSLTEDHVDVHGTRGGGNSSSRASI
GTNTESIYANDVVAVTEHVSLAALSSGRTVWLDRRSGTAITCTGAFSRVYNIGQRGSLFA
LHDPLTAVAFLCRDHPINILCGSMSGSVQLWDVRCVRECVAMHQAPSTICRLQPSYASSL
RSVVWLNNQAGDVQGINVGHSDMCLIAEARCADFMQTTAAFDSPSLRISVLDPPGLIAFP
YASSNLLVLFDVSALMKPSLSPTARHMPDIHDDMDDADDDDGQHAPFSLLSHGIEERHMI
SPSSSLHGGVVYQIPCNNLIKFGQSPTISACGIWTKCGRIVSGDAMGSVWLA*
>TCRU_8369 ubiquinone biosynthesis methyltransferase, putative
MLRRSMGPGASYVNTVFDTVAKRYDLMNDLLSLGIHRRWKQHFVNDYVRPCPGGKFLDVA
GGTGDIAFRIIDGVRLKEEVFGLVPTLRYLTEVVVLDANENMIREGEARAAREGYLDVKW
VIGKGEELPFDDMSFDSYTVSFGIRNFSDRPKALREAYRVLKVGGVLNVLEFSKVTCPFL
SLPYDVWSYGFIPMAGQILVDRESYQYLVDSIRAFPDQEEFAKMISDAGFGYVRYENLTG
GIACIHTAVKTEAVRVKPEKSPLESVATKAKEEKNSVDDEQLNPA*
>TCRU_8370 kinetoplastid kinetochore protein 2
MSLLEKKQDNSGGSSNSNSSSSGGDFKARKDNDGKAEEGGEEKDGRLRTPRSYAMLSIPR
ELSHTPAIAGLSPTVRTPFIQRCHLHHGDYTSTDNKDEHYRQPLEHMTIIFEEDSLKLTT
TSLLGKGGFGRVYAARSNGGELYALKVSAKKLTEGDWARLLKEVELMNHFSRHPNVVKFI
AAGRDEETAYVVMECCASRSLHDVIANHGLDVPEILWVGWALVDTIAFMHSKGCIHRDLK
PQNLLFDFDGNLKITDFGLSSRIAEAQPRKTVAGTAMYMAPEIAEAVYKRMSHSTHQPPL
QYGQEVDTWSIGVVIYVMLTRMNPYMEAMEKRGTREMDKTQKTLSLFNAVADAAWEWPTG
WSGDPELCDLVNRALHRDTKKRATLQEVLQHPVWNRRPLSCPLSLLYKLNLLERPSSSSV
SRHGSTRRSLTRLADNLPIPTGKRTADDVLAEGMRRVVLTEQRARANLVLEHHETLRVML
ELLKLSRAEADVRRSICEDEQRYRTVIQNQRVTQRSRRRRSEALVSSFSAATVATEAGPV
TRSSRSHRQSSVVLVAPAASTKEESGRIVRASPDKYAVVYPGRDTATRWSLRPVISLPRE
LNSEIEEFRCLNHHIMTKLTAMPHGYNGFDCNVCDREILKISPETPAFRCYKCDYDLCMR
CAYQGRLKDVNFVCVSCAKKFTSSAKLQAHSLQCRGPSWSPSPRRSSRMNTMLWEEAEPR
RGSLLEVRLPDDPKPRASGRPSGRSSTGRASSGGRISIGDSHVASPEDVGTMVVQHRDAS
FPEMPFTRRAGSGGGRRSTPARVHGCKDVNSSFSFELPPEIRLSRLKKGERIQPRTSAEM
QEVMDVDSPPLKKERKEARGGGQEKATPPYKVNESGNIVGIAAQHRAAREASLQQQQKQQ
GQGVIVIRADAAAKPPEMSRQPQVPRSVSSSRSAGAVSSAATNVAPKPIEPHLAKVTRTA
VPTSTPTNTTAPAAPMPNMPKKGRQPSAGGMVTLHGGPPLPRRGPGMPQNTPYLVPQAVP
PPNFPVPRQPSHPLVQSGVEARQVVGGHRVSGGNNAFLALPREEQNRQRFVDDFLSGGWV
RFYSFTNEETVVMYYCAQPGRYGAMFPTEAGVGTAVVDVHSRLVLYVPCMNNESTNRSQP
HPHVQTFYDEDVRLLSVSEAQRHLGGVLESIMGFVNEVARLRAEGLTPAAVHAAYIHQRD
KSSVPKDTKFVYVRKVFPDPSGSFTLFRLSNLRSQVVCNTLMDIRWQSDRRHNVGQKYYV
LADGTAEPFVVDHTGILTQVETVLSNNFRR*
>TCRU_8371 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MGVRESTSLQEEVPPHPGTEVIPKADVERPIHEEEATSPEGATERQTQETTAPLVENEDS
EDVGTASGNASTLPGETKIPSGSNATAPSGTGILLENGHFEELAGMALFAESTMHGCVSR

VLLLMLLGLWGTAALC*
>TCRU_8372 hypothetical protein, conserved
MPGDEPSSWFLETLFTNTTDARNPEERHLSAAAHAALRCLGMQVHLEVTEEGNVRRSHAR
TERRLRGPLDPALGETLFAVTTRRCARYPPPAVAYFQWIRGTVRRGRVEQDGFTSIY*
>TCRU_8373 syntaxin binding protein 1, putative
MAKVPHRDAHIFALWCTPHRRLQLVRARIAPRAMRSKDIMLDFSAPEVLVFHPSMQNGFP
QLLSPLSPPTRESVLNVAESLIVAAFHAMNNGVPVIRHQNRGSICHGFVGTFFEGFSGSA
TTSRISLSGADSCGNPVRIIVDWGCVTVTPLMHQRTCQFLLDDLMPLENNLYEQTCRNRL
GEGSKRQ*
>TCRU_8374 hypothetical protein, conserved
MPRPVRLCLLLLLVTASNTDELTEANKQQLIRDGGLTLDAHLFANLEHVTRRAGSVQPES
TASAQGGRSTSNSTSNAATDGDPFQKHACMIMETGRNRTLRVGLSLTSMERDHAMGPNGA
SGGQNSGA*
>TCRU_8375 Enriched in surface-labeled proteome protein 1
MSRHLLYSAVLLLVVMVCCGSGAAQVVVEEPSSGPQFEWRGINEGGGETVDSLGAPSLLK
VGSDVFAVAEAQCKKKAGGVSFTGVASQLLTTQTAETQEELSSDALKKTQVLEEGASKDQ
KKKVDVSRPTTVLNPLL*
>TCRU_8376 SpoU rRNA Methylase family, putative
MMFSSRLLHLRRTVRGFRQASAPPRGFLRDDPLTRWSERLLNGWPNRCLHSHLFVGLEGC
TSAFNAMNSIRTCMHFGTTFPPFFLSLKRAEDIRSLHPRCTAGKTNSEDLTRPGATLSQV
ARFGEDLFLDDPSFGQIPLVALENYTNRSESILSCRLSSSARIVVGHENNGVSRKYIDKM
DVSGGKGCRAERVVYVPQYGTISSLNVVTSMGIALFYATLDARYPSARSLLRDTEDGREN
GSGHELDELHAYQRFFRQQIPRTAAECNSSRVDQRPIHPLYYKKDATGILEMHRHLRQLM
LRVCSHRRFSSSPGRFGLFVVYENERDQRSFAGIVRNANAFLVDQVLYFGRKKINVVGTV
GTQHYTPPVYLGPFDVEDGSDAETWATKLLQRVELENGGNISWWFLDCGHAFLYMDSTSV
NETAKEPEKMETRDSVEALTWYNTHRADPDFTLSLCDTEERIRETAQGGVVLLVPQEGIL
PPFCLLQRCQKILTLLPYAENTEGSAGLPVSVAAGVALQRLSAVMHPRVSIF*
>TCRU_8377 hypothetical protein, conserved
MSHAEHLGTAFANIVYAFLITIDTEDYDAFICRMFERESREKRTLIAFLMKKRAVYFSLL
NNVLEREEGTEGEGSRLADSWNQDSERRSFRFPQEMPDAPVVGSLERNMAINDVVSQLTI
VRNAFLENILKIPGTVPSGRPPAIHRSLQQIPNVSLNTLVEGVTKTIMDVVLSLCNKIEQ
KYSSSLFSRPIVLADRSLRSDCTGQGDCTLIQMLSSAVEIIWAYSLYFILASKDVVHLPS
GGFVQCSRFLLCDLSMNSVGETTSSRPSLCDLPPVFFLSFDLAMKLEEHFHGILTSGNVL
STPSGMHLLLLSCSCYELLTQVDETLTEDVWRGMINTCASVMKLTRRSSQDWEDVDWSNL
IHEADPSHSTADHGCLVQDLIFIWRRQHGWWGTSMDDKSHVADNLRANSLPIFLREYPSS
FFSSRFKETIAIVLDVCGLSKTSNGGKNERTIGDIFSGLYRCMMHLCYIFNHRVATHALL
NDLLDLLRKMLLLSKKERRLKELVTIVLSLCLLPQSFPHGSAYSDTQQQQCVCTKKVVES
LLDEIDNWRKAKNAICYALSMAALLSRCSLKELERRLPLFFATMESWFASANNMERIAIL
HSTLHAGGLLCDVCANNDSASPYKWNDSISSFFHSVEKMLLNGIGSKPWKNAPFSSSCIE
IASDLLVFTLQQEPFQSSALHWLARLMETKAKSRTLSKSGISAVVTRGRLIAIRTIWALF
ELYYCGSHALVRHGGLAAKEIFLACSHTSENRKRLCALYNTPLDQKGSIKETIIGFIALH
GTCYRPVVATVEALAIFWRGGHLKNVINFVRTSEETRQGITELREAAFHYAGQIHKNGYS
EENMEYAHQLVPIFLIARFWDPPQVLLEYNLALPMLLVGPKTPLYDAVSNIVFPFYFLKR
NEKGMWSCALALHRLVECIIVLLGNDEDDRVAHLAEYVALNLMNLRDRMESLVNEELCAV
KPEENGVAGFSFSKNSYDKESYHKKLASCRSKWAWLLNVLDMSPLSPKESLSSTDSQNWC
AVPAVRNAALVDLLEGLAVVLLGHTKLQVRRNALFLLELVSSLLRLQRIHCGATSQVTDS
SLLDDNHYNAHDPMLSTLKASRPSVGAEEPRYPRVAVADIFEELGEQFDEMYASNKERYV
PLVHVFEGRLPSLASSINDKLTEDAKHKVSRDAWPKPSFYHKVLDCLHPSTIGRESTLTA
TSFGVHCLSDDGTTPHFVFVSTTALALLMYGYCPGSVLVRVVCAIAGEIVERGVKRYIER
SSPVWRSCYALNFLLLCVDNVKSSPDANRLTRGGERNRPGHQQGGNSTFVGGTDDLKDVD
WQIVNRYAAYQNLMNVVTVPLLLNEINTENIPPCFLDMMQYLLLGPMECVATGNTSLVTY
CGVMDSDHPIVTAMHDVLAVGRSKARGGKQVIFHTCYVVLLPMILVISRRYFVKPPFVPG
WKQNTVATQRARMETVLQGVIDSLLLGDSNGKEYAGEHDNEHGLSAESLSRMLYEGNGVS
VRSCLSLQSLPSVIAQSEGKPTSNGDTLNEVKLTVFLRGVLCDVIALVYSKDAKFLEPQM

KSKFLTKVLYSLKYQVLWFLQGNASYPGKGFGQKLPKNMNAGMEKSILALQTVVSSLVQP
TLQRNQLEHAFAIINTFGINFFQWLQESLPTDCKNLETYAPSVFGLAVTLLVADSPLRDS
VFCLLCKLPLGSPVHRNFFSVIVTACSSMWDGRKGPLLSQKYCGKATSSFARSFASYDAP
LSSLSNTWRNDCATLELKNMGSVIYYALAYLYRDGTFGYFFDSTVRSKAYDLLVLLCATL
ELKNMGSVIYYALAYLYRDGTFGYFFDSTVRSKAYDLLVLLCGEAPAEPMADPLDDWLCL
LLKACRQGGGEVESDNRLVQSLFVMASEDILSVGRKSSSAIERQRIALSLLSFFLRRVRP
TESNLRTVLRVTQACRNTSSELALATLWGGWIAYEGRERERFTSLLVLSSMDLADKRVVT
QYIDIYINHEMAMRGKGQDGKLDGRSRGAYYGFLLFSLYQMRLLRHIVSHNDDKGKANLE
PLGEATLNNMQQSDWGWQSLIAWSSFSPGSLDSQANRKMELNVKLKSKFLWIINENIWRI
SLKLTNENLKKNFGVHSFGETPTELGMGRESGKFVEDSAMLQELGFVKPLLSVLFFASWA
IRRLQQRDWRLWKELHRDLSSITGLTMRDSATDLKPIVTPNMFLSSSEDQTTSESETDDS
AEHLGSVAERNTHSDYQTSSTWEDHKVDNTMADRDEDGDEEEQEREGNAEVEAGHHSEES
SVGTVVVNADVPKVSVTEVIASNMKQAAKLKREEKLKRASRINDPLRLLQRDFVALFLHF
TCLLLVHMGFGEMRCREESDELSSRFHVLETAFEVLGILLKETASEGICRSSSSLKSWLK
VTFARLKRCEAMKRDFKNFNDNGSSLTFEPSLFFGGNAFDVGCSDSPSSSVELVLKELFF
NITGQGRNVRGRHFLLRCLHEFSTWLQHNSYEESEAKVRLHTLHSYISLLSLKVARVISF
CLSCTTGVLVVGRDCQHKWMEKTAMQLAGESAFRRFLNALLHQTNALQNDSSSSLKEPFV
RAQGHAFCTSVLRSLACLLSDIIIHEIYYCTGTLTKEVEERKQDALLLSAPFGDNSSFPA
HNLLTSFWTGFAFLLDSNTWQAACDLLAVFHRYGCAEFLGTISSPPFSSLYSLGLNIAPD
LAAVQLVFLHQGKELTTSRNVWRHAAFSEEEDHSLDHAVDVVLNYLNEYAGEKEEPAVFL
AFTELLLLCDWKSLDYEKYAPKFTAFTKTEASGDPQRQQYRVLSTQRDTCPPRSSVFRPF
SSYVCYFAESWKRGLLLLSPGSERTSEGLSSRIMFVLGEFFQIALKVFGVSSVDVLLRRV
IGGNAWKRGSVGMTSSCSKSHHTDLCSLHSCVDLARESHKLTEEHVSLFQHKFETIVVAP
LIFLFQSPETPLPLWSKILALVAALLRYHEQNHGFVTDQLLKFLPDIERGLGVGTAYNSF
TDETPLKDRLVVLVLADEVSSKVKSLRLAAWTKIPCPSPFDSGNGVSLLASLLDNHSVLK
TLVDKLANDPFSAQSIANVGKIAPTEFVGDRTTSTVSSHTEEWELRHVQNVSKWSHEGSD
SEDVKAFHPMATPRPAANHPDEGDLSSLIIQRVQSHTTVSTSHRFGGYVYETLTGANDVV
QLIGQLPLEYYSVAPKGTPSTSPVAAAERAVDHEQPSTTAEKTLSKKDFVPPGVTMMLAS
SASTTAVTSLSNSAENSSASSDDDSAASFT*

>TCRU_8378 hypothetical protein, conserved
METEYQGGPSIKPSSDVVAEYIDAAWNWSTLVEKVNNGTWKAHTVLGAAEGTNRVGVVHH
PTSITKGNKVFLLVGSFDVFYGNEEWGHVDLELTLVVGDVTNSTPGDPGERIEWGDPRPL
FDS*

>TCRU_8379 hypothetical protein, conserved
MDRCTITDPALDVRDIEGVIWRGECLSAMPGDKPSSWNLDTPPNNTTDARNPEETHLSVA
MHAALRCLGMRVHLEVTEKGNARCAPCTAEATIAWATRPYAERNAICRDHAEVCTISFTS
GRLLPVDPWDGEERVCGAGRSHRHLLNRDCQGASVPVAESIETGRGKPSRDLDTAAPQKH
PSPEEKEVASGATMATV*

>TCRU_8380 hypothetical protein, conserved
MAMTTGRVLLVCALCVLWCGAGGRCDGEDTVLVVVSPGGRSNDGQSGPGPAPPSPPGIGT
SGPGSIVPESEGSQEIIAGTYSEGSGEKNYKDEDGEEESVAEDGENSRNHERLSEQPTQQ
EVSHEESPEGKGLKERLKEKDVYPPGEEVIKGAQQSQSQQPPPQQLQVQITAPAGREGTT
AATGPARPPAPAEPSSMDGSRTIEPTDSRSPSQESHDKSPLLTKTESSAPVPPLKDAFPE
QHGQETTTPDSVMSAPAGRQARNTAPSTSTNDSGEAQSEADGNDAQRPNPNESHDESDSG
KTKVPTTLSEAAPQATETVAATQTNHTKTIGDSDDSTAASHTASPLLLLLVACAAAAAVV
AA*

>TCRU_8381 Endonuclease/Exonuclease/phosphatase family/Endonuclease-reverse transcriptase, putative
MAQPATSTWRQGLVLFAREEAKCLLPIRCTRRGRRRRTNGSEGHQMEPFTWLPAERYFYP
LLNSIGAYQRYTYCLRAVCDAQRQKLLLSGDIEQNPGPIAVLQMNVSCLTPSKLATLMAQ
GADIIAIQETWKSSEQIASMHTGDYVLHAQSRIGKGGGVAVLVRKTLRSKRIPLAIPQHD
TSHEVVVVQVALDQNRDLIVASAYMRPPPQVTQSFRRLVNCLPASTPLLLCGDFNMHHPQ
WEPFLETSPSEVAAEFLELCTDAGLTLVNTPGEITYARGTRERSCIDLTWSKHLTVSDWS
ASVSPLSDHYMLTFTLHQAFKDTIPSAPPSAPKFFYSWGKCKWDLFVKDFDAQLPAYDYK

KQSTGIKAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERMATDSKARYLQLPTPDRE
AEMQRTRSQFFLLLRERLRNTYPRRISKLNPGEPLAWKYISGRKKASLPSPTSILLGDGQ
HTYKTARRAANAPNRIFLPFHPSHKAVRFSKGINRQSASLNINASLFFLGSRTTTSLPLH
LLQVLHSHLVLSHRIKTKLPPHLVYLLIFTPLLMQLLIVRNCLLRYVIRRMARPPDRMKS
TVRHCDIFRQRASDSFFVALTTVGRPVRSRLSGDALPSFHS*
>TCRU_8382 hypothetical protein, conserved
MQQVQHDRSGEGHVDKAQTTHTGIRNVHGADAATVNAADLRVVRFEERERSKAVRNRCWQ
TRFAVAASSAHTLTAADAARPRSEAHGVHGARTTVQHHHGCSNIELFSVIRHR*
>TCRU_8383 hypothetical protein, conserved
MHIAADLDASFVVHAGSYVWRLLSSSVAMRRREVERVCSPRLLSCGCDALRVTALSWAPN
PIEGGMAENFVAASWMDEGLLAVVAVVVGARSVCVTAAGIPGDVSGAADAVVVPVDVSCA
QSDGSLSYRVRVGVEEVFRCRC*
>TCRU_8384 Tetraspanin family, putative
MHSVPAYNAYYWVESHDSGCLRFFRALLMGMNILLTAGAVAGLAVGLLERSTMEKTLKNL
CQSCHAIFIAYISVFSGLLLFSLLGFFALCTRNTLLRVLYFIYLFVVFLGAFSSSIAYVL
VSTDRVNLQTGWDKAAVSNAEGMCSLELQFHCSGWKELCNTSNVEFMNPLIRKGNQLSLR
EGALGDVNTAEMLPHTSNNNSDSKIICPTCSEEDQKEINGYNVTCESVVMGKIKEHLKEV
LPIGLSITSIALLGMIVTCLIQHETNYEAYYGGRYHRV*
>TCRU_8385 hypothetical protein, conserved
MTSTRARDVEEMSPKRHVVMIGVSGCSGSGKTVLANRLVELLNSPLRPIAVDDFFDEATC
EALGTWEDPRCIRSRDYARFLCEIRKRLQSDGLSAAECLQDLAGASAFLRSQPAGSLAKV
SSRGSPLDASSREHLGEFAASFQYTTEAVASSERCENKETIYVICEGFLLFLDQTVCDAL
DYFLLIDIDEETASLRRFLRLPRRHLRHQGYAERIEHMFRSRKSLLRLAAFNTSHAVLPP
SFAYLLSNLQYVPPLPSVTGDYERFWLQREYLQHSPPMPPIGDNCGHAASPYAWMEVKDP
LYVTRTLQQSRLAKSDGNGLKHTTLSFDFDQITVDDVTANGDLNIDRISILQKQYFEFRY
WFFYEVLYYHRQLSPLAQENITGTCQRRSCGEAAFCPIVHLTSGVDVPDAKLDEALLSFV
HYVMQPP*
>TCRU_8386 meiotic recombination protein SPO11, putative
MEAAVSSPSSSNTSAAAVVAKRLTRQKKQRPVLASSEDEFIGPDIVAVNTPAAITAEAVR
RMEIFVLQTIHEIVTTTRRSTIRESRLRVIRLQLLVLRLLYQNIHCGIISTQRDVYYRLA
RLIPDQGCINRAIQQLVQTIGIPRQWLGVVPGTRGCVGGSISFHGVDLRCYGSEGLPLPT
TQEELRVVQGDVDRTAASNKDNVPFIGFEIHGKTRYIVVVEKHAVFFRLMEERIFERLPC
VLLTSHGFPTVAARTLLSNLHRAAQSVPLVALVDYNPSGLSILQQYKYGAGGMRESQYVA
VHALHWLGLRTHHIAEGREPNFVGSDNRVASEPFPLRLLPRLPFQRFSQRDVVMMANLLS
RWHGIREGCEWKDNDADKAWYEEALKMQHLRVKVELEVLYQHGTDELKQPASSSLELSDG
NGFAAWVCRAILRHDYI*
>TCRU_8387 RNA-binding protein, putative
MQEEDSKGSRPLVTSAVLIETSVGAFVVDLYGLDCPAATAEIVNMCRCKYFNGCIATEVV
PDNIIIFSHPVEALKGSTFYSCVERAGGNNQGSVSGRAANVDRLMLVEWERMKRYTAQLQ
RRSGKVSVEFLPKPEAGEVGLINRRGLLLLEVPPKADLTADGVSARKSALVFTLGNRHLE
YFEHRFMVVGEVREGIGVIEKLRAAPYQRLSSASAVGTRPTRLIRIKHATVLPTAGTEMF
SDVWYNGIGDSRAFSQQKTLGLTLTAAGCFLHWAGKETVRAANRVIIKIMKDIATAGGEA
KGSRGTDFFLIDENRSQEEYHLSGDTDEVQSVEYNPHYHGEYLSSDDEAPRAESRKERES
RHQAIMRMRQDKLNETRTLMLNLLDGIADVSGELKPPENVLFVCKLNPLTTGEGLRMCFS
QYGRVVSTDVVRDRKTGNSLCYGFVEFEEVEACYRAFKKMDQALVDDHRIHVDFSQSVSK
LWAQRQRDMRKRAREES*
>TCRU_8388 RING-H2 zinc finger, putative
MERTVLHGNASEDVSKTCEGDACSITAKQWDMVAVWSWNVQVGTCAICKSTIADLCIECC
GMGGGISSGNTTSLADEGNNRNERDSLQRNRSSVVAEFKHEHEEHHPPPLGSAMATASLA
WDGVLTGDCLIVWGVCNHVFHKHCISRWVRQRPQCPICGREWKVAKTTRNDI*
>TCRU_8389 hypothetical protein, conserved
MATLPDDVESLHKRIQLSEEWNMRLQSQIQELLRLSHNEVKTMRDRMQNPDIAIPLLQCY
DATILEKQEENEKLQREVDKLKLMLQAANDELEETREAVRMAEAQLKELRMQAQEEHNSL
ENAKHEVEREAALVRQQLARSLDAEAALKREVDQLKRELNMAQGDVAHFQRDTVTLGEEA

KQTQSRLKTIENEKEETQQLGELQRIQLQLLSRENEDKLQELERIRHRMVQALRQSSDNH
VAHLRVVEEKHREVVEGIRTQLNAQEMEVQKLRAQLARMDAGSKGSRYATSLRTTTELLE
AQTRKAQEMELKRLYSELSNLQLQRDDALLRYEQLSSSLRREEADRLSEAQRETQGLRQK
LRDQEQNYEQLDTEKNRMKEELRVLREKCKSHASELQRARQERDQTLKKMEELRRALATA
EETCERLRSEAKNDTAKERQRVHELEQHFDEVLRDMQASKDRANASMIAMERQRDELRKE
LADSQERLTAVQARLSARDREAEVLAAKAEHLQEAVRMNQKQALSCNERVQQLLAQDEEK
SRQLREMTLKVERLQWERARVSRAHDRLLEDVNSRFY*
>TCRU_8390 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCCPSVCVTDQSAASSQVTTTPASTNPGAHGSAPSQSISATGGA
PQETGQRESSSNGVAAENGNTARGAENSPNPHQHSSDASNKVQGKSTEDKLGTKSGPSAS
TEQANRNFDDSTEEAAATSSQTTTKTTTQAPTTTTTTTTTQAPSTTTTEAPAVSTTSAPS
RLREIDGSLSGSAWVCAPLVLAASALAYTTVG*
>TCRU_8391 hypothetical protein
MGTTRRQVIAVALLGSSEYDGDEEEGEEAWNMRGSSVYRNGSDSTLANQISLYRIAVAAS
PPASAWRGTRTRPSALIQPASTAQEENCFACSEDVSAESSEGVERLLQNRLFNKVRSRSW
AFVTLSGSVHGMFCVQEGSLHGSVKPLNDLADQTDSGASLFLLFEQH*
>TCRU_8392 Concanavalin A-like lectin/glucanases superfamily,
putative
MNKKWETVFDGKKTTSSSTWEPGREYQVALMLQDGNKGSVYVDGVIVGSPENIATVWALG
HEITHFYFGGDEGDINSSVTVTNVFLYNHPLSVGELKMVKKSDGKKGNGDGSMRGGISRM
LGFCTFLALY*
>TCRU_8393 hypothetical protein, conserved
MVDGASATHRDSPADTCLGRWMRSAAGACPRSRHRVRRRAIAAALLALLVALVLAAAAAW
MPAVHAVVLRLRGGTVDRAITVGRAVDTVLMDGVSITNGVAVVFDVAAMLPGALRIELRN
CVCDGGAQIYVRGYSGEPASDRSLEVSVSGLSGSYCSLVFVHSLPAHTNVTVRDSTVVTA
GPMRYSQLSGLTDAVAAPLVLHATSLLQTQLRVSNTVLRSSQAGGSAVYVGGGVDLLSSA
VVLDGVSLEASGGPTASAMHVASSSILSLRSHSVFSVTNVSVVSSGGGLVLGERLAVVDS
VLRFVGVEGSVASSLVRCDGGTIGVGGWLELHDVWAVGEASSVASLSGVTLSGGAVSIAR
CAATGATLVSGPTITSGVVSVQCNLAGGRMLQSSGDYRMAGLSSVSVVPCDGCAAALACF
AALTASFSDCVCGCRAGGLGEACLPFDVPPARSGGGGGGAQDCVSGVTLTESVTVGGGRA
TACFDSVVFSGPITVTVDLRSMDVFADALNVTLRHCVLAGGAQLRIGGLSESTARLMPHA
LVNMTNVTSVEGTIVLHGAMPPNSSVVLANSTLRATVGGSQYVPTTREHERFRYGPALVL
DGVRLLSTRFVMTRSSLVCGGGSCAAILVGRGFVVNLSSVFYMDNCAVSSQTHVMYALAS
DLRVSGGSVFSIQNSSWSAPSTEYYNGACVFRDVAVDGGSVLQIVSSTFRLGFAMLIANT
LTVTGGSWLVHRNNEFRTAYVVYVAKENGVAFCDRSVWSILGNKLTYRSYSSTIPRMTSK
WSPPSDSRPIIYGVCNEARGSPVTNYRDDLNIWTPVRVLACGACTVDAVCFAARTSSISG
CECVCAAGGYGDTCLPAAIPDGLGPLPLPDAKDTEVRCVHGGSISSLDVPDPGVRGLCFV
NVTFTAAIVLDLSYFDAPEQTLNVTLLQCVLVGVLIKGSGARVHVNVTSSVLDFGALEFK
GDFGTGSQILVAGCTLVATSGYAIAFPEFSLSTNSTLLLLDNLIEGSSCAVYLSDAVVVD
GGGIIIKGNTLRGAEEGVPLESAVLFESVVVGNCGYIEIENNTMSSANGIYFYGDTTVSS
AGLLRVADCDFVGSAEFSDSVLVHFDGSVILEGGAQWRVEGNGVGAASLLSILYSQHNFE
LLGSGTTVVLAHNRQVNSRASFFNIFPSSIVATLPARFVVGCNLQGGVQRRRGVLHARDG
VGGPQLVLVQLQGRMAWRVVSSLRGARHGCAARGGESRRRRHELRGEPDADGNHAEHVED
APLLLGCDIQRRGCCADVLL*
>TCRU_8394 hypothetical protein, conserved
MKHIATQHHRGVVADPQPIHRNTRRAVKVQTRPRDQPRDREAVPADRDVRVRWKITLRAE
QRVTKCVTGDDDVQRPHSGVRIAQQQQHGAVPPRASIERDVRHVARHRTNQHRQAHAAPA
ERHVAVAQPRQPAAHSLRNLGVHHVADALTNRRWRWCGRRWRWRWRRGQWRRASRHRRRD
ARIAVPSSSALALAANDRRRQRCKAVALLRALPARSNRRHVGDAVELQLCRRRQQTSRDR
QAPSNEPVTGVNPR*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MLLAKGNVHDGVSREMLYAAGTVTAAGSTLSFVRNRALLPRMLSLSLSLAAGAHVRVACN
DAGGRVLSTAEEYAAAGFVDAGRIDVAGCDACDRDTHCYAPGTASASMRNGVCVCECGSG

GYGEACVPVGAPALPPAVGTASSVFVREGVTVRSVFVVPAGASEVTLRHVVLDGVSPVLY
VPWMARDGVRIVVQNVSLRNGTVLYVMGGGALRGAVAAGSDESGPVELSVCDVEALNGAL
VLTGTFPAGSVLTVTDSLLVAARPTPLVYLPGLQSSPYAPVLVLSGLRLVRSVLVVSGVA
LVTVVTGGRTVTVDGAVLELVGGGVALDAAVLGGDVALYASARVVASGGAVLRVSGSQVY
AAHGLVFGSGVEANASAVVVNDNAGVLTDGALLELRGSASFVSGSWLSVRGNSISGRLLS
VPSYPRRADLVHSILTLHGNAGSGPVVMDGTVALGGAGRNFVVGCLTLNGQALRPMDYRS
AGIIGEFRSVACGVCDADVHCFAAATRAMSGSCGCRCADGGYGRDCLPVYLPHVDGCNRT
LFRPPLSHTATLTETRSLNSTWTATPTPSLSTTHYSPTQYGPTETLRVTETVALPPTRSP
TASVSSTLWWSDVACPTLTVTTTAAGGGLTQNDIRGGESVVPTLLMVALPPPFRWARDPQ
LGTHLSFVPVSTAQPRGFGGPWGAMLSNATWVRNATNPSTVLELALPVHRGYFIAADETL
VIRCDAAAVSGGCKGVLLGSFTIRSDTLPAAASALSAITGVVAGAAAVAAVLTGGLGSIL
EMQALGVFARMSCASAQERASTVALPYFLSVFAALDPVWMVVGNALLAAVFGCVHCGVTA
AFQRWRGVDAASAWAAMRFPSLTYVVAHAMHLGIFFGSVFALAMSDARVVVAH*
>TCRU_8396 hypothetical protein, conserved
MSPSRWSYDAVQRLHGSGLGLDCAVCGGGAIGVPSLALVLDKLVGGYSGSLGKLTFHSAR
ERATPRELNPCITTLTRQLQCLPHTGRYAGALVRGGVGSTGRLRSFRAKFFACLRWGIRD
AATACARDGELQWPQQPSVFVRNPAAKAGQYGLFPLVRWSPCAWLPSRLSRWCGEVRACV
AGHE*
>TCRU_8397 Protein of unknown function (DUF3676)/Trans-sialidase of
Trypanosoma hydrophobic C-terminal, putative
MDTATETLYGEHQVQQSTELSTENEGLRSTGTVTTGAKESLSLEAGGRNSERKMGSDSSL
TPSKSDAEPTSAEDTDNISRTERAEVSSENGEEAPQTVDTASGNTSTAPGETEIPSESNA
TTPSDTDILPEHAHYGDLAAMALIAESTVHVCVFRVLLLLLGLWGIAALC*
>TCRU_8398 hypothetical protein, conserved
MARLLPQDCANAWHVGCLTAVKRRNWKEVQEEKEGAHRMTGACRCGEDPVPGVDPDIGTR
VAAPRTGTMHRGDLYRAAFTGGSRSRSWLHIFPVTLRNPTQRDSGR*
>TCRU_8399 protein kinase, putative
MARPHCCCSHAGLSMLVVLLFINFLCASGAVVRFRGSVYRGLAEETLRRGGSTLVVRAVF
PVFKGYEKAPLRSLLTEMLSVSYVVDEEGIKREMQGNSNSWLRQLPQLMEQSCIEVEDNG
CTVRLTFHPLPDCVVEELLLVVPCLPPSIAQELNLSSEGDGGKNCQPGDAFAITPKTLLR
VDADRIARMAPTQYIIGNIIEIPLVRGNIGGFGRRIKVMEGYTCTNAVSALISRSGWDDE
NRVFRFIAHRGGLVTLCYMPFPETLPHVMLEMGESITIAGPEGVSTEPLQIRPGAEFTGR
VYGTNLSEHDVLMITEQSCNEFAVDQIMLPEFSLSSSTRAFFFGTLKEEGLYHVCYRSEG
SAQYINLATLLVKGGDDAVTEKISENILFDEVTGLPHAPSVGRLQIERTGRLVLRQESLN
VSSFLWSGGSIEGQGDINCTETAIITSQCGKLCTLSFILRNYGEMVIDVPQLFLEGEGAL
HNYGNLTITLARTGTEGVGSIRSRSHSNAIINRGGTIRVITVDQGNAVLCQTRIINTRGT
LVLSGNLKITDMINEEKAQLVLESGARVSASDARLGGRIALLENSELKLIEDGAFVSATI
KGNRSRIIITGESLLLDSINVTGDVATDIVGGLADPSGMLIAIYGVNYFGEGTHLNLCRT
RFVANAGLVQLVIEGVLTAEVHSVVFSGNVWIQDNNIVIIYGKGSRYIVSKREEYSLVSL
AVRENATLVALDVVSSHDVHIKCATLLSFFDYFKIDGRFLLRGCVTVPLGGIIGGSVRHL
KLPEDAAVLLPCLAAANIRLPLDAIPPQGASLILGGETLLRNGAELALEEIIMKNAVLNG
EGAVYVGAASILSIDRGSRISLRREWILNASLTYVEGLLEADMSLGPMISGSLDVAGYGQ
VKLYSVQTSPCFTAPYANGGVRWASNPRVECYPFPLLSLPDSSTKALEREEMDRNRLLFA
LPPNIECSEEFLREEAQGRMMLQYFFDMAPFDPPPGVPTVRDMIVSWILFVLLGFTMLYA
FMKFNGLSWKQWSAEIEKEPPLRLTLSRSEFSLHTMNYVVLSLLVFNTLQTSMASIHPDL
FVPVGFMSSLRLRSMHLLMPHHRANSHVTMRLAMMVIFLWGFIEIFLAVMNRKDLRRALC
GTRTKAILRLISSLNYALKFFFFVFSLPIRSLIIDSLACNTFLSELPSCAEARGNLVMSL
FSFLVLCFMVPLGGFLFMTPLKCDIHCRGSVLVAMNALSLAKIAMWKVFYQDPVLLIINN
LLFQSVRVLYFLHSTPTAYGNINRLVFHLSILPFFSHLCTLLHVIRVYLGFVRTCRDGET
YFAVVVFLWIAMLVGMLWYDIIGAKDESVTTNNAAIDAIQRSIQQIQSRIQELQYEFLAC
ASIEEKENVLKAVARLRIELLENQKRYRYEKYCHLAVFYVTGSIEESISLKLPLAEASKN
HCDGLNVEAILASRLSPLSPVTIGDANDSENVPLTQEEMENFSCGPALGSGSYGTVHLGI
LKSGRLVAVKYLSIQNSVKDALSQVQKEVGVLKKLSHPNIIRYFGCCTDHDYILLFMEFA
VAGSLTSIVRNFTVLNESVIQFYTYQMLLGLRYLHQKGVVHRDIKGENILVDGFGAVKLA

DFGSSKILPGISDRSRAGCETLIGSPFWMAPEVIRNEPYGTKADIWSVGCTVVEMLNGGT
PPWREEFENVYSLMYYVGTTDSIPKIPEDTSESCRDFLRMCFQRDTTKRPSSDELLQHPW
LRDAGNHSGLLQKKLPIR*
>TCRU_8400 eukaryotic translation initiation factor 3 subunit 7-like protein
MGFELPEIFVNAPFTWGPPPSEIEMDGMKVRLYQKTDAIAPSDWLEAMLDQANETKQFTT
VKDENRLKALRNLHAKERRHGPERRFVKHYQNARSHFTNKAKRNLTLLPDTVKVPTDVLI
FAEFTQAELAKMQNLQDAPTVTDISLHNRPLVYNNAMEKASCKTPIRLDENNKGEEFFAR
STTVEDGTLRDILKKEAAGTHPIVVTTDEVLALMMTCSRGLHPWHLEIFRYNRMVFISKT
EKSNVEVQWVGETADTLRRPVENDPNESERITNLAKESTKAFNAFVAQACLKTRYQMKCE
KNPFPDTQPRLYRYRRFVMHADTDDHYDIIVRCEIDAVQNDKYVRIFGLLEQCADGVESE
WRKTLDSQGAKWISDEYRRNAQKMSRWVCLCHLSGALMKIGFLSRSYRSNGTLDPNKHEV
LATHTKDPGPLAAQLGIKVGNMWAIADAIIMAFLKQQDLSEALLVKKSGGQSILLIEKME
DEEEEDDDDDDDDDGGSSDGDV*
>TCRU_8401 Domain of unknown function DUF21, putative
MNREALTKNEKITYSLGFVGLLIFTGITAGLQVALFSMDRLFLRILTTTGSLRERRQAKR
LLGILRLGHWTLVALLLSNASAMTGLPILLEDIFDQLTALLVSLTAVLFISDIIPLSIFV
RWSFPICSFFVPLVWVLLVVTAPVSYPVGKLLDRLLGEKEDLLRSDELVALFLAQQNERA
FLRESEVNMLTGALRLSSHRVQDFIVTTCDKAFMLSSRTRLDKKTVEMILLAGYSRIPVY
LNDNRRHILGTLIVQSLVNLCFTNPNKPPRAGEYPLLETLRLPASTTLYNSYLAFQKNSS
NMAVVYDNCGVMVGLWTLTDLLCTLYNTSPAHEGSNTRRQELMVTLLESMKAMNAASRKA
QGNVNAAIESDEFFVGGRKK*
>TCRU_8402 U6 snRNA-associated Sm-like protein LSm5p
MPTISERRNLLNFLGYRLSVELDDGSTLIGRLVSLGPTSNLILTDVERVRPLKRRRGSSK
TECYNSVLFVRGSSVVSVHHTNNITTDRSVVDTLTDRQMETSKAIQLASQSLNVPLR*
>TCRU_8403 hypothetical protein
MSTVRSRATSRSRLQRPVMPARKASAAPSSLVRWHIGENGRISNFDMKVLRRDIFWRLEN
GPLYTLEECRTFLLELSRVAAAWQEEEFPQLMYLVDMHERLMPGVSLSFQWPTGNAELLP
LADISGVEGSLPMLTKVVEEMNRAVARMIDRLWDSRRERLIFAARLLQDIEPLLQELSGG
ALSA*
>TCRU_8404 Tetratricopeptide repeat/TPR repeat, putative
MILHGGEGVPPSGVHSLCYPRYRPPLSTEERLEEANRHIEKNPTDVQALLRRAKLFVRLE
DHQAAQLDLSVIIDLPRGKSRSSELVCAFFLRGVCHVKLSWIDKAIADFTAALEIDPSHS
RSTYERAACHNRKGNYTAAILDYERALQHDSMHVSYFSACNRNARSRFAKTRPHQRHSLR
SFGAIDPPQRDASSLLNVDGVHRNGENGKRPPPAPPHKMYVKTSGLMAEASRLSHSSGTP
IGSPERHQIVPAITSSSALRGNEEAELHQQRGLAYRKKGDYLRAIDEYSAALRLDPKNFK
ALFNRGFCSDKVEDYNAAIRDYEAAMKLEPGYAYTYYNLGISYDRWGGHYKEAIAMFDKA
IALDSNNADFCHNRGFSQRKLGKYREAVEDYTMALSLDPQHFKAYYNRAFCYDKLGEGAN
AIADYTKAITIQDDNPNAYHNRGAAMEKAGRLDDAIADYTRAIQLDDGNPFTYNARGIAY
DRRGKSDAALQDLTQAIALSPNNPIFYQNRAFVFQNMERFPEAVRDYNISLALLDEEKRF
ANGATSKGKATQELNLLILKQYFNRGFCYAREGHYEAAICDFSMVMATNPDNLVALYNRG
ICHDKVGNHKLAVEDFSHLIELDAENAEAHFSRGTALESLGEYAMALDDYAVAFKLDVDR
SDLVDEGDLAKFKSEHHAMVASQRVLRLLKEKKKASGAARRAY*
>TCRU_8405 hypothetical protein, conserved
MSEENGNVLEAFKKEHCALLALLAHAARQAVDTRTGESVFEDLCSAEPSLKDIYPEVNLL
YTIHQVRRALRDRQERSSESVKPLCDAVSAALRNLYGVLPDPLFLVVAEAEEILRKRHSS
SRVLEPYILDLVESIQLVLLQETNSLQRRGASITLRLRDVPPFVL*
>TCRU_8406 Protein of unknown function (DUF2817), putative
MLDCSVVMTAFFTIAMGMLLIDLSSLQENMVCSANYGNASTCPEVFFSQSYHAARMKFKD
AAKEAKAEWKQHTVLQEEGFEYSIDTAFVRGKKAKNLLIHMSGTRGVDGFTGSAVQVKLL
REWNSSRGDGPSVLFVHAVNPYGMAHFRPYNENNVDLSRNYLSPEEWSHVLERDNANNSG
YNEIVAPLLMSRAPRFIDRYAFFYQLLKRIVTKGLGAFKQTLSGGQYHHPDAVGFGGHEE
QRAITVLREVFKAHVGTGIEKSIVLDVCTGPGSEGSETIVSDSREERVVAEKIFKGSKMQ
SRNDETEQIGDIRPSDTFVKNSLIIKQNFGTVNWLFVVRALFLENAAYKHAKGSHVHAVM

QEWLKDAFYPQTMAYKRAVLKKGVAAFDSAWKHLS*
>TCRU_8407 RhoGEF domain containing protein, putative
MPRDGVLEEMQVYDEFALSEMLYVACLETLLSAYIVPLSNTLCLTTSDGNLSSSHCEDHS
DLLRTFGDDVLQLLSCHRAIINGLRIFTEGCGESDSNGNFEGHERSYLANRATRVLRRGV
PAMRAAYQKYVMNFNENARRALLAKSSVPKDVWRSSYGALAQDILTNSLLHLGVEKRNRI
RFSEGCNLSLEALSLLPMQHIARYPLYMDGCIQIQRHVASVNSSNINDDDAARIAKAEET
LAALIDICSTVNATRASVIEFQRMVELQKSLELTEISSKLLSEGDVVVSFELQEEKTKLR
GRCSHGRLILLSDTLFVQLHEKKRARCEKHLERIPLKSIMSVRFSNQASEGVVYITYNPD
TERRKWRVKKQRKKCVVLFLPNETEALIWASDITRAVSDLTPEE*
>TCRU_8408 glyceraldehyde 3-phosphate dehydrogenase, glycosomal
MPIKVGINGFGRIGRMVFQALCEDGLLGTEIDVVAVVDMNTDAEYFAYQMRYDTVHGKFK
YNVTTTKSSPSVAKDDTLVVNGHRILCVKAQRNPADLPWGKLGVEYVIESTGLFTAKAAA
EGHLRGGARKVVISAPASGGAKTLVMGVNHHEYNPSEHHVVSNASCTTNCLAPIVHVLVK
EGFGVQTGLMTTIHSYTATQKTVDGVSVKDWRGGRAAAVNIIPSTTGAAKAVGMVIPSTQ
GKLTGMSFRVPTPDVSVVDLTFTAARDTSIQEIDAALKRASKTYMKGILGYTDEELVSAD
FINDNRSSIYDSKATLQNNLPKERRFFKIVSWYDNEWGYSHRVVDLVRHMASKDRSAKL*
>TCRU_8409 glyceraldehyde 3-phosphate dehydrogenase, glycosomal
MPIKVGINGFGRIGRMVFQALCEDGLLGTEIDVVAVVDMNTDAEYFAYQMRYDTVHGKFK
YNVTTTKSSPSVAKDDTLVVNGHRILCVKAQRNPADLPWGKLGVEYVIESTGLFTAKAAA
EGHLRGGARKVVISAPASGGAKTLVMGVNHHEYNPSEHHVVSNASCTTNCLAPIVHVLVK
EGFGVQTGLMTTIHSYTATQKTVDGVSVKDWRGGRAAAVNIIPSTTGAAKAVGMVIPSTQ
GKLTGMSFRVPTPDVSVVDLTFTAARDTSIQEIDAALKRASKTYMKGILGYTDEELVSAD
FINDNRSSIYDSKATLQNNLPKERRFFKIVSWYDNEWGYSHRVVDLVRHMASKDRSAKL*
>TCRU_8410 hypothetical protein, conserved
MFFRVLVAAVFVWLTGTAGVVDAAVDCGTAVACYPWANGNPRVGNQKPCVSGGRMNLRFI
LDVAAETSAAKGAASTAVYGFCPVVDKLEAFKLHSAHSLATLYSAGNVYNFSKNVGRKYL
SVYGFGMSNSTLFPEKGLSAGAVVIAENGDFLCGSDRSVALVHALILDIGLHRGRFNYIG
ARGASSPGNIVGNGTTTPIEVSTEDPVQEGEVSVQPAMVGFRPTCTPDDVCVFDSASVCI
GDQIGNKNCAKCYTSPKEVAKQNIVVWASYDGTDAKGRPLLSGGMNPLIYNQFAGNMLKN
DFDSLIRRMKS*
>TCRU_8411 hypothetical protein, conserved
MSHFIRTSVAAVGLCGAGAILYRCCWTRRPSPEHKKELLRLSAVALSSEVVDTVLFRDGE
TLKLLRRFVKDVGLHPDTVGTLKSYVKEEFTTNKETVGALRKFVVEDIICDTWVRDELIS
MSKETGKEIIQDRAIYPGLSMHLLASAAQEGLQTPAFKDALRCALRFAFWVALVGFSPEF
IFKEMKNRNHQ*
>TCRU_8412 hypothetical protein, conserved
MSRFDVILCFVPPGSGSKGNSLPEEHFRLTLGDLVDSVDDVLSRATPRCILNAIAKCVHS
APAFSHQMNIIVGKEGSREILFGLLYDLTHHQNGDDAVPLQCMFFASDGASVVCEIVDEE
EMGSVTEVMSAMRHIVLVALKFRCRTMTLVVVEQLSTSLIASMLGYAWCNVWLLLGGGID
VDRSVAVVREALSVRDAVRNFCYFPEEMISGIKDEEVMLRARAFLDGEAQRIAAPWQQYT
ERDETETGNGRLAVENATPRNERAELQALLREREEYFAEQIELKEHELTQLRRALQHAEA
NEEKLTEAEVRITELESCLAEKEEELYMWKGNIDKNPLEASEETQQVKMYFHTGQEELCD
RIESPKNEDIINALQRELSETQAKLREMQQQWEASREENLQNVMEFQEREREWQMELRRR
EKERETVVEECRRLRSVVTSQGSGLDVVKEAIEATRLLQEQELDELLKKIRAISSASAPA
SHRRISPRSGRHSDTQNCPRMLSPAPL*
>TCRU_8413 mitogen-activated protein kinase 5
MAVAADGSSNSVVQLVCTQRGWKTYRVRGQMFEVEDRYTLTSIAGYGAYGVVCAAFDSVD
FRDVAIKRVNHLFEDLVDGRRIWREICIQRILRENCCRNILNLTRIAPPREGVKDFRDLY
IVTDLYDTDLHTVIYRVKNRSVEALQRIMVRVLRCLADMHTLGIIHRDLKPSNILLGDEP
DSDNAVVCDFGLARAGLSHLKEPLDLTDYVVTRWYRPPELLLMCRYSFPIDMWAFGCIIA
EYVIGRPLFGGRDYVHQMQLVLSSIPVTGTEFIENSSGSAMNFLNEIAKKYKDTRPLVGL
LEGLSSDGVELVTKLLAFEPNKRLTAQQALQHPFFARVGGRGKSECTRPTKADFSFDLHA
EISEAQLRRAIWEEMTQYQKKELRGEKEKRQSKEE*
>TCRU_8414 aldehyde dehydrogenase, putative

MLYGIILLALLEWKLGCLRFLLKVITHTVERYSAPTITVPLPRTKFDVAPSTVPLTPRSG
PPGTIQCYDKGTNTPIGLVNVTSPDELRAVVSRARVAQKAWSKTSFSTRRKLLFSLLDYI
LEHEDFICETACVECGKTMMDGFLGEMLTTLEKLRWTAARGEEILAEEVRDVGLVAIHKR
PVVNYVPFGVIGAIVSWNYPFHNIYGPMISALFAGNAFVGKVSEYSSYYASYYQSIVREG
LKQLGQSPDIVAFVTGFAETGEALVNLVDKLTFIGSPAVGKLVMRNAAATLTPVLLELGG
KDPAVICDDADLEQVVPIIMRGTFQNCGQNCVGLERVIVHESIHDLVVKRLETAVKALTQ
GPASQGLYDLGAMTMGESSIQKIQRLVDETVAAGAILVCGGKPSSRFFPPTIITNVTPTM
PIAKEEVFGPVLVVMKFSTDEEAVEIVNACEYGLGSCVFSKDVSRAKRIAAKLRTGMTNV
NDFCINYLCQSLPFGGVGISGFDRFAGMEGLRGNCIVRASTTDRIPGVKTTIPPILQYPI
TDAAFSFMGSLSQVIFGRMLYSMKGIIKLLTIKSEKSKKN*
>TCRU_8415 hypothetical protein, conserved
MSICPGLCGELAVTPFRVFLGTLPTLALEERFLRQLQPVYAWYSTRKRVKEQANEFIEID
LASCDLELLLRYSHVYYVRRQLFEEAIDKQLTLLDTGKAPKMTDPALLQCLHACNTDIGE
RLQYEVGQLQVAKKAACVPCRRELDPNAPLEVYDYTCMMRLVEEDVCGVEDAEMKGRAYL
PRNLVESKVKYLTEKLLGSDAKGALEKREIKLFNRMIPPDYNKVGSVEKLRPCDVTAFFR
FYGERINKAGTENHFKRSLWGHVYRKFATHPSFLRGISMYWARHSGLDTSSNATIMPEEI
AAAVCKQQTLFSAIKFRSQYMYASPDLARQLWRRDVVIPLMRLFPLLGAPAAEDLAASVL
VDAFWARLSVGEEENLLNDSIIRSVRQFVDEMSNMYEAGTEATLKRVEEGCKLAVPQLTA
EEVQLMSPKNEDKAIEESTA*
>TCRU_8416 PPR repeat, putative
MGRGGLARLLATEVIGGDVNACCGLLRRIFSETVEEYVIHALERSGQGLVSDVLTLGKVS
LADDASLVRPGSVAILCHASQRLGDWQSALYFAEFLPSPPSSLFISSLLSPGNYPAILRR
CEEKGWSLDVPHATQVLAEKHGSWTSALAVAEAMERQLHMGEWYSLGVLIPHLSKSGAWE
KAVALFVAGIAQGSLVDPGFVGNLVYRTAQLKQWRMCLYMLSAIEKTKEAAQIFSSDVNF
FKDVMSISPSWESSLLVFNAAVAAGVKPDKFMVGLLLGQCEESNAWSVATQVYDIAQTEE
FVSNIAGDSYQTLVRSFHAVKLWEKALTALSWMAKADEASAATGMEELLELCEQSGQWEA
AVRIGGMLLEKNSYLPVRTRLSLLFASAKGAMWDVAVRILQDSFADANQPPHPLCVCAAL
QACVASNRWKEAVMLLQRAREEEPRVVLPPLAHRLTIKVCVGSGRWSEAMALLADMNASG
LPRDNHSQRLGVWAAALLGDWKLSLEHLRHLPLICRTAQDRLVVRGATRDISAVAKAIVL
KYLQQQIS*
>TCRU_8417 hypothetical protein, conserved
MFDALSALVETASAKAKLLTEEGYELVKQTGMLELEEGYDDTTRGITEVKCKTAPAAECA
TSKESEGPCPAVTRVTKDLFFLPPSQWESPAEEWTLLAESALMEENSCIIPPERILGEES
LVSKLCGLLNVDSIEKLPEIPKFSECKPSQELVDWLTSETECIEFRSLLVPRHVSDEQYW
VNTCWRFFIYRMCRNGSQLLDVMEVVSIEPKPVDTTGVLRKKRIGVPNNATHWKKLRETL
NCRREMAAWIEGQISTVQHEIELALSNLQLLTNITMKRETTELGDSVSESCKYHKAKLDR
LMGELKFQREKLGDSVLCPDHGSLFAQLANVNDQLRVKLEVYASLSSGNPSECRENVSHG
GREEATLKTSPSGGDHDDTTVFEAVLPWEKE*
>TCRU_8418 hypothetical protein, conserved
MSAAFPLLRALGKPARLTEVRVAAAELARQAIFGSSETKLLSQRVACETAGFRCVYHVGE
GLAIPMTFLGSCKEHGDQVVLVHVPGLPGAFPVSMAELGRHKHLFGFEPEGPSSTTDDRE
QLALLCATEAVGSGIGAMKVLDYLLSVSRRRLASLRGTEVLLKVGSRVNGEALQLSFPYH
CGSTHAIKRYYDITPEACSLFGRHMRHGTKMLCRYGVAVMVGVAHDESLGCPAPFWNPVG
GPAACLAPMFNGCHVIPVGEVKLEYNGPSTSSALLTPEDPARYLNPTVDGTYDVTSWLNE
GLFGVKVGQRVEEDCAVYGVCYNAERCEFELHVQELLTGEIRPSVLCFLTST*
>TCRU_8419 hypothetical protein, conserved
MDVTSSTGVRWTFGIDSDVPPPEHRISVGFSQIKRAFFTDLMGSMEGNEDWSQGIAVSQS
PSAERSSKKFSIPSDDSDVDGTIQSSELDSDTEIVNAEVSPLLEVTAVPLLPASRRRIVR
QYSVVALSALGGALLVGLLKRGIGSVIRILVSGLAMTQLLHLMGYADVRWKRLLSDLWSV
SEYKPTSSPFRAAIAVIAGSIERKIAFFCGMAAGVFLS*
>TCRU_8420 Myosin head (motor domain), putative
MPVVFYRSVSDGWRVGVAASLDGANIIVRDGPMEETVSSLDIFNPQASDTGSDAQLLLHM
SDQPSVFLHTKNAALMSPTPLVGLPPVIELIRYRAANDEFLTSVGDNFFVLLGESSFTGS
NPSGREIALKAALAWKGSQKHQVVVSCGHALPSLCGYFLDTCCALFEVTPARRSMIAAGM

NVISAFTSTIGRKHLCYLQAQLCIKGASHHQLQDVRFECNHLLVSGIGDTNESNFKIFSY
ILYGLSDEERERLYINQKQRSFVCQTSILDTTLVARLQEEYVSFTRATETLGLSSSTLQA
IFRQVAAVVHLTEMEFYADGTLSNLSALKGLARLLQLDVEECITIFSSRAICVAAARLIY
RGVVVKLVKKVNAALQFSGGSKPLPPSITLVAVPPPPPAESDDLENIFLATMYEEMTQAF
LCSSDHEVMLWQRAGVRVPEKLQAIFNPLDNYGLLKVLYGLGGVLSVARTLQGEEKMRLA
LTNCAKSAHVKLNATTLMLTIEHSFGARQYQFPRTTDQLTKLKSVYHAEFTDVRTFLLEN
ADVETQETLHLLAQTENGTAEHVVGEEMLHVKPLLDVMRDDKNMFWWIGGVQLGAGFNGD
SVEKQLRETPLRCALELRRQMPHLYITCQVGFIASTFKMLLPSANTHATENCKVAEAILC
AAGATYHVTPEGFLVAAGSLVEMHMKVKEHIHRHVTLIQAFARTLFCGNKLKKRAGAWGD
ILQKIDLQRKKVIGDEKYRFQNRRLHHVQLLDLMEEENTVRSRISEECWGKYISLQHSFQ
EQMEILLVQVVASSIHKEERHLHLAMRHNHKEKLRMIEDYIKERVTIHRAHLDSVIEEQL
GGKCHQKYTEKLNRAHECLLREREKSELRRKQMESALERKRSKSEASRMAREQEVQEKNK
KLLLRQHQSRAVRDKIQQARDDFNETIQAQMLLQDMESKITRQVREEVMSFRRQETDRLT
QRLCEERKRREAAAIQAAKKNERRSVQRELCVQRTKELQESRRRHVMQKQLDMQQRQQRA
AERLERAREQQRRKVMWEILGAETSLRKLPLYEHRSGKTYLRRNKSDGQLSEPLVLSSGK
KAYKRILSESSLRGLLEYHTTKPRANSPYPYATPKR*
>TCRU_8421 paraflagellar rod component, putative
MPNLCVSATFNPPVITMLGSALREETVKLLEQRIPTDVSTSSSPSKDPVKFLFYTNPDHW
RMELSQHFCDDLHKSAVFLTIIEGLEGEGWNLRASNSVRDSESGKDTTKLFFARRD*
>TCRU_8422 hypothetical protein, conserved
MVKAATVKRPFWSYFVPSTYTSRIHRWAYYAPTLMFGVATAAILMRQSYYRSSLADEDEN
TCDRVDRRAYVALPDGRMALVYPIVDTQVTPTRVILSFLDSINPMP*
>TCRU_8423 GTPase activating protein, putative
MAQFPPPSLIGELSAVSDPLPQCISHEATDAYFAAIAGPIVSLPVVSGLCRGGATENVRA
FFWKLLLGFLPTETSRWAPLLERKALEYREIVSIVCRLDEKGDVVVGERSYRAVDLDIPR
TMPSMHFFKSGEPAPPDNGVYATFSPTQQSLRRIIHTLAGVNKGLGYVQGMNELVGHLLY
AFASGRSEVVNEQVESEVFFCFQTMLAYLGDDFCRSLDYDQDTGVSCTIRNFERLLQFLE
PELWEHLGKKQIKSEFYAFRWLTLLFTQEFNVPDVFRVWDFLFSFGEELRSVVLVVAVAM
LNCLRDELLRLTSLSEILPLLQSYPPCDVNDFLKVAMGWIDRYGFRLVKELKVATSEDVL
RLQRRFCIPVPGDASWSSSFRGLMSSVKEFAKHIR*
>TCRU_8424 hypothetical protein, conserved
MSSLKGAPSLNPPPKKGFSYNVFDEEFDDYVSPVGSEDENQKKKKKETVKKKEKERKKAK
SKRAERRALESGGGGEKGTSVRRGEGDPQSVTNSAVDYDVADYDAGAQYSDDFDDDDIVP
APAPPSFDNTRELQRTIKEEEARLERIAEEKMREMHEEQVRRWQQEQELTAKTIQNQQEE
LRAQIEELKRLQEQKTKEAEQESKSVGAPRDPNDDRDDGANAVMVERRQLTENQRRRIRE
RERAVQLRRLEQEEAAKSLFQRLAQDVREVFHELNLSVVASEKERLIKDERYRKEREAKD
RREELERQERMQKEAKEREEREAKFWSAMEDRDARFREFVEKKSLKDEEEREARWKRDLE
DREARLKGDKELRSELESIERERRDREDKNVRERDRTLIQTLLDDLKRQYETQLEETRRQ
FELDRAHAEEMHRMELAAIEKRHAESAGQSDRIHMRQIEMLESHTGNAAKLEKIIEQMHF
DMETTKKMNVTLNDERLAVLRQKEQLISEQKALVDNVLEELKYVKQEMEKERTRVASLYA
KFDISLANFTKEAGDERRRCQETQSHYETLRQQLERDRKLMLHEVSQERKAFEQQYEEFM
AKKLQAMSELQEERLAIARERTEAAVLRERQNTDEMEVLKSLRAREEAYAEKVEAIEEDR
LAVKEMRCEQKRLLDEISAEREALRKEREAFEADKKELLRRFEDLQLRAAEVGATQEQLR
RELELNKNAKAKASMNAAARCVSTHGDTASVLGAASRLQIDLSRQRAVLNRISHS*
>TCRU_8425 chaperonin HSP60, mitochondrial precursor, putative
MLRLSRRVAGNRGKSILFGGDARERMLNGIERIATAVGVTLGPKGRNVIIRQTTGEPKIT
KDGVTVARSIEFNDQFEDVGARLIRQVAGKTNDVAGDGTTTATILAWSIFAEGYKSVATG
ANPMDLKRGIDLAVGVILESLQKQRRPVKDLAMLENVATISANGERPLGQLIASVVQAVG
VNGYISVLDGNTSATEWKRYDGWSTEHGFLSSALVTNSANLESQLESPFVFITAQKLEAV
GDILRLLETAKTNGKSLVIVARGFSETVLQTIYHNHVHKVVLCGVVCAPELSEEELHDLA
ACCNCVVEKVDSIGLVDDVKCLLGAAKRMEQNMDSTTITGWVDPAPRLRLLQGRLDRAMS
EEAKDKLRERISKLNQTFAVIRVGGRSSVEISESKDRVIDALNASRNALAEGIVAGGGAA
LLHASKELDKILQADEEMEQDRRTGVIIVRNAARLPMKRISENAGEEGAVTVENVAEYKD
SCMGYDAQNDRYVDMFEAGIIDPVKVVTSCVVDAASVAGLMITTEASVCDYQTE*

>TCRU_8426 hypothetical protein, conserved
MLRLTRLFREMAPELQLEYVPLLFTRTILGPNGGFAGEERLVKLEMARKYIEDGHAVMPT
EELRQGLWCFNPDTNQYDRFIERNEEFLDFAARKRQWLDVYWRVNTGYLLFGRKSWGQGF
LINCPLRKRDVAQKLWEQYKVRVDPRLIEFREKDRRTGIQDLGHNWCWLYLPGAEELGID
REVYDNKRVKVRMHIRKMTSFYSLY*
>TCRU_8427 conserved protein
MSSETRPTPAEDTAAVVTVQGVEGEALPTTTSTNTNATMNTTHTTTTAAAAAADMTIIPA
VSTGTTTTTKTTTEATIPPPSTTGTGPTTEQEVATATVVGAAHSTGDNVGEPVSALSTAQ
IALALEQVPKKSDACAEDISGAHELASKANSNESFMDGATPKVPSAEQKPDAKSKSSSLP
GKNRKKKSPPGVHKSNYRQPNTPAMAEMRGSSTRTPLHQPLQPPPMYQAPIMVSSLMPSA
LPPPPPPPPQGAFYLAPHGMPPPPPPPPIISSFFSGLGALQSTTPPPLPPPSFMPAQCGR
IPFGTPVGIPMQAMLMTKGPDPALLSTLFTNGTIPPPPPPPPSPPPPPPPPPPPPPPPPS
SFAASLVASLQQQKQQYQPQQQNQSGRPLPMPKNTRVSVGNATLAALVSKEPPKFSCVLL
SGVPAVGKTTMGRELVNELRRDGLGWIFFSGADFLAGTTAKRPVWETTKEIFDALQKRLD
ELLEQQRKERNVKGLVIDKNVKGIEDVYYLASLLKAKQIPFVGIVGMEVNDDGVLLKRMN
GGEEMREKIKYHRVIHARVRALAKAAGMYRGIDAAKSKEEVLNALCTMVLGCCAQPPQRG
IRTDLYANSAAATMVDDHVEYCDVVTRLLELVKPPKGVVHYPGTTDYTPFSTREMSDKNR
VSAIKAYYGVRRLNDGTRHMLMYHDAKLYLIPTHLKAVLRIPERAWLGTKLDSIGCFVLE
GDLVRLPKERNCEKFLVFDVFFWSNAGKPEENKVGPMNWADRQAFLATHMCAESKAFFST
GSDCVVVHQATLNLEKIFDLLNSSENKSEGILFQPINPAHGYDKLYVWRPPSNITVDFRI
GALRSSKTDTDLLEGDAKEAATATKAAPVEEAAATSDVDNSSFSHTAQQSNLQPLPADLN
QAASTLSASQCTSSTVGAGRGAHSEGHITRTFELEVYDKYEKEYTQFEDCTVEVKHSDVV
EGCICTCVLSDEKECTWKFQRIRYDVLRPAYKRDVTFLLEHCIIPKAKLLQWLTHEKIVP
PTTNETSAMRSLAPPLPSPGSTPSKSPTLHSASLPTYATALMMQQSNAQSHAPMRMSAPL
ADSVSYQELLVPGSLTRGSQLHGVSSQPHSKVLSNVHSSLHALAESKMEKPKHGNTAPDS
SALSPLQLLTTMVSSVHIVRTEDLEEKHKNVSTANPRRNHNQQDQRHPPKRDRDRREPNT
ANERDGNDKRGNNRASRQEKTHGGKKLVPVPDTCTQCLKKKQAEDLRLDREDNNYYCYGC
WAKLGWEFCRECGEFNKGYRERTRRRTGEFYCSNCRSNFKKGKEEEEEAKNKDDQATTSR
NEQKKQKQQKQKQPGRDSAATEDTVEKTTKKGATERKGTKNPQRDGVKLNTASAEGEEDN
MSANSLNNVAHLDAENVSQVKKKKKKKSKKKSAGTGTLCEVSERENECASQCTQEPASSK
KVDVAAE*
>TCRU_8428 nicotinamidase, putative
MGKDFCAGESSGPAKSPSLIAVSPLHDALVVVDMQNDFVSPCGALSVPGAMEVIPVINHV
CQAHKFRTIAVAKDWHPPDHSSFCKPAGPGGQWPPHCVQETDGAKLHSSLRLGRMDCVIH
KGADRDAECYSCFSDVNGKKTGLATFLREMDVRRVFICGVAFDFCVYYTALDAVKEMFDV
VVLEDATRAVFPDNISKQRGDLLRNGVKLADSKDLTTSPSASL*
>TCRU_8429 hypothetical protein, conserved
MVAGRSKRQRRVAATATALASATNAATPALRHSSRQIEEFTQQLMDAMTHASMPAVCVLQ
PSTSSSEEREEEGNRPSHSNSPVAAPAFDEHNFVKITATSPPRFLQGGTKSSLTAERSLR
GREARLTPRKSVSHPGHGTPLRASSIQTVCAHNNSNNPIGPGDVSRTEAEVLQQHGPLSQ
LNSLYAVREGDDTGSSTSSHNSTVDDVNDPGGKEVGEGERKRRVYCRRRELLEIPPGSLS
LYTRLAECGVNALDRPFAACVVRRAQGVMEAWASGFL*
>TCRU_8430 ribosomal protein S7, putative
MSVKPHLRKLRKLKRPNPSEDEDSVAKALFELEATHKTLRTQLPRFHINTVRTLSSPRFR
RTATVVFYPLRFLMLVRKIQRTLTAELEKRFPGSIVVLVAQRKITKRPKDVYKLQKVQRS
RTSVAVFENILNDLIYPCDVMGRRWRCRTDGTKVMKVFLDSRDRKRVESRLPIIAHVYKQ
LTHRTVSFGFMWNPKLQQVSSR*
>TCRU_8431 Ribosomal protein S7e, putative
MLVRKIQRTLTAELEKRFPGSIVVLVAQRKITKRPKDVYKLQKVQRSRTSVAVFENILND
LIYPCDVMGRRWRCRTDGTKVMKVFLDSRDRKRVESRLPIIAHVYKQLTHRTVSFGFMWN
PKLQQVSSR*
>TCRU_8432 DNA polymerase beta thumb, putative
MPPRLRPCALHLSNHLVVQELLLHAALSRQHFTPGDRQEYLKLARHIAQLPDACAPFGAQ
RPSRRGFAQTPWRNVAARHVVYERMDQQRGRDLCFRGRRKVPVYYDDAVDHQRSLEHLLG

PHGFRVALIGKMRCGCPVSTRAMFLLTITARNSCHDATANDEEQRERILFERALKGLANS
GYIRCVAKKNMWVCGAVLARCVCLARTPRDCGPEPSSRRGETEQELMLLWSSPQSFQVRR
LFFTGPKSFLTHLMLLAHARQYELTHDGLYQRSSGKLMRVELRSEKDIFTVLQLPYVDPL
YRYAYCLLHNLL*
>TCRU_8433 hypothetical protein, conserved
MKKRAPPNPTSASTFFFWQLLPTTAASCSAAAQTDGGDGVDTGESMREAVAAVLKESFTP
SETTGLWQRCIEEEQANSETIESLLDVSWKRVEDVIARNKRRRCVIEEELPQSLAEVDTY
RFWTPDMAAARFHFPRPEEFGLRTTETVGAGGETGADVLPADTTEQASHDMSSSNALPGD
SSSLVLQPTPPTTPTPSAAATDPTMPGKHRANAWRRTDKELLDPTKSPNPLRRLFAPILR
RRHELPKALTLLLNAVQRVQSEGLPEIEALIEKGYLHMPLHRSFWHISSFITRYLSENSR
GEGREREFAENYKPSAFRFEEAREKLREMGSKRATAPSKCEKAVEIVYSTLLTELRERKV
LQNDCDSALQSITDNTNLQLDGMEKGLQDCDIESRQVLGDLERDVCAYLEKLKEAIESTK
AARKEIYNEYQRDHDRLHSSLHGKLYQLKKSEDMQEKLARRIREATKEWHMEQLKYERLM
QEVVAETLALRQLDCSHNQLEALLDERLPTADSEIKLRWVTDSLQQSEELRSELIAQCRQ
HIERLKKEEHYRRCRMVGYAKENALCWSRCLQDLSALYEGHYDTVTVKCNASMQLRYLLA
YEKDLVIKDLHQLQREFSLLEKSWAKLTSLLEELDLPVPPLAECEKDVSCGEFRRTISEL
VSGRLICGDFARLLPIRGEGRSSPTAGKGDSATAGAGG*
>TCRU_8434 Dyggve-Melchior-Clausen syndrome protein, putative
MGGAQAKEAVQYFTDVACAEADPEEKEFVERLTRYKKDICFGAEYFGASLPVLRELVPLC
VRTQRVRWLFSFCLQQLEHASCNYNQGHSDAFIATLHITEFVVRYAHQVSRGDAAQLLDI
IMGKAPHGTDGATTMQWTSTEANKVCCALMDYCVSVPVTYATAEAHNGVVSLLLSMNSSA
LYHSTTFDGKHMDVFTEIMMSYEGLVAFIATLLKRLVEWGSGRLSPSPLLYRDGHQPSLR
NMYNVFGNGKGNNSISCRESLGRHCAQLLAVLLAHLKGNGQNLAMEYIKKIENEDPVPFA
ALLTAFVNRLKVCPSLCIVLYVLVYDHPTFLHTTMTLHAKELLDVIQEVLHLSYIAATET
GEGNMACNNSISSTHPTTTTLESCQVFIYREVLTPECVAQLLKDMVQFSYPFIGFMTSTL
VLLFSQDQVLNRNMSDTIIEPRFKAGRFSGKMSIISLCVVVLAHGILRAMNERNEPLASV
FVPSLSNLAPFIYDIDAYTSQQLIRLLVLIIRKLRRSSGLIQMDEKEVSLTTESTIREGA
AEMKEDTESQMFLRQLKLLVEAVEAMLQGEDRQNDSLVYELLYNRSKLQEGISADSPCSH
LAAAHAALVPLFRIADYYETELASVTSAESYQDILGVIRRAAREQTGSIPTVKNHSPTSV
PAKSAGSAPWRPREILYVYEESLQSYDFFGPFVWSTLLCDAIYPGGLLWATDTTALEMFS
Q*
>TCRU_8435 hypothetical protein, conserved
MEEGYSGNEVAAGMCAVGSSLPTRSLPLDPPHSSCAPSPVGRSATVIGGAVIRSPMAMTS
PAAHTTSIAAAAASSAAGRAMESASPVSTTTAAEYVEIEQKQAELRSVVEHRIMTLERSL
KRREEEIETLKMQLRKTEEDYQFNYELIKDRDAALEEAATQLQVLYDELKRRKSEELTLS
KRLEGFEKETHHLRQRLRETEVEREQTVQRVQQMHQQKERQLKEAFGQKETALEAEKQRL
HEEYLKRFKAMDDIREETADKSEALAKELEAKWGQQVRGLEEKLVASTKVMDAVQSEKAA
IESRYSEASQALSLLKHENESLQQQHQVFVAEAAEKQRELEAKLNEYNAVMGQGIATAED
SIRQQTRRANMLEVECGQLQSQVTELQERLQASRIQRDDDTKRLMEESNKMRENYRQAET
QMEERRRNWADRERQLTLQLQRLQEELEDARKKGDTAVSRMGELQARYEVSQEERARCEQ
EIERFRRDLQRCREEEQRTAAHAQEVQRTAEEKIRNAGREVEVAQEEVERLKKRLFEAQE
RSQSEAARLTRELHASEAARQALEEHFHLAEDANGQRALIENLRREKEALERRVLELEQT
NAAIRDQVASFTMELQNDPVVKSAKETQRRVQELQEQLLQAREDIQRLRDTLRAKEEELS
RYQLEILRARSAETAVLHQRDQEDQRLREEYQSAKEAYESMRKALRDQKHQKQQQRSRVS
PGKPATLNQKSGSDDDDRRDRHRSGEKKVSCGAERDPVSMREAELWRRKYLQLEQNLRDL
LRERDGLARELQLTRQDVDALTSEKQSLVDLNSLLKAQLREAYRTALEYPQLTLRPPTPE
QHQHQGGQKQQPAIVPMQTDTNLESGKKAVQDSSQPVPSLAVDAFFRGVSAPQSSVDAER
LSALEVELAAMKASMLSHRQSFTRASRSGGGGAVAASKDRDTRRQLQQQQQQQKPQKNTP
QTASMSRSLSRSGAPLVHRGSSVVRHYGYM*
>TCRU_8436 predicted zinc finger protein
MGANSSRERRSQRRSQSNAVTPPANMPPHLANQYSNRRQMPNNGNNVPTAPNYDASRPAP
TLPPPPPPAAAQQQQQQPSSPGNTDNNNSANNNQRGVQEGQIVKMLATIDASSVDYDPTM
QRLKFRVTSVCPFLSYEIHTGVKEYIRGGEVFYMPNKPKMEPPRLTLEGPQENKEINVHI
DVSKLEEKERVYNKHYPKQQPCVIVLRYRIKELRKQENSSANASPVEEIVEHTEHTAVDL

AENPKRRVISQIITAGGSAYVVEDLFGVDGDSPGAANGNPEVMLGTTIVPHEGEEDEDGL
CVICLTVPKDTAVMPCRHMCLCKGCAEELMRHTPKCPVCRGFVSTLLHMPSINGNSPA*
>TCRU_8437 hypothetical protein
MANDSCPNCCAVLSLMGIVLLLLFGGMFRARAVSFHITSVENGWDIDEKARACFNGAIFY
GITLFISVVARIYTRRSQAAKQALLEAERLRESIELRVK*
>TCRU_8438 hypothetical protein, conserved
MDQFKQPLEGIFRDGIPAPVLRAFAPLYQALPSLQDAVTSSRDCYYWRANPLKCVEEDVQ
TVTSFMQASEASFRLCPQQSATLLKCHMTEPARALFFCRDEEWEWRTCLMDQTGIRFWPY
ANAPVGAPWSNGGQTEDFHLEDRFFYENFSWWRRKAAMLAVRRRELEVQAQRKNWLDEQK
QEEKGNLTQSLLPPKPTLAPVGIRMNTS*
>TCRU_8439 hypothetical protein, conserved
MGLNSRSLGSGAIWPVSSREHNGPHTFISCDFTIVARVMIQNFSKLSTPLPGAVLDAPVS
TNFVGLSHNADSRWETVFYGIKTASGSTWEPGKKYQVALMLQDGHRGPAYMNGDLVGIPE
MLRTPETRGLKSHASKLGATREAAAAVRR*
>TCRU_8440 hypothetical protein, conserved
MQHDRALQRRHIRHVDESVRHQARRDLAEAANPQLRAARKHAVAQRHVQRVSERIHQAQF
HRHNDRPAEHHRVEARRRTPAANRHRLRQRHATHAARRTATTATGPRRRHVEREARLAHT
AGAAAARAVGERRRQRIEARQRGRTAVARHHAHGGQAGHAVVPAAPQHPAAGTVALHRHD
AARDRRPGDKRRAGGSAARNRHGAAAQHHTRQRRHRRRLAHRPHVVQLQPPAGIDRPTVA
AHQRRRDRPLDAHEAQHRIKNREALSKHNAAAAAHNRHTRHGEHRVAPQTEARRGRHMQR
GRGQTARRLQRHAVKHHRARQQVHAAANVHRRPARLQRPQQSVAHTQLRLQQRRRVQHKR
RRHRVRQSAQLRVAHRPRRHNRRVTDRHVRVCRQVVHKHKRAVAAGQTAHAHLQAPVTRR
LAAVAPHVDLHTAVAHAVPQFDAQRAGKHRRHVEHNSHAVRHGHAVHQHRVHGVANRDGS
VHRAAPQSQHHRMHRGHPCRRRNQRQHNEHSHTHSRNGTVPHTVPAARTRTHSRLHPPTQ
TRISKAVVACRSRPVDRSTFLINPFLWMENPKAQIR*
>TCRU_8441 hypothetical protein, conserved
MQRRRGVLHARDGVGGPRLVLVQLQGRMAWRVVSSLRGARHGCAARGGENRRRQHELRGE
PDADEPHAEHVEDAPLLRGCDIQWRGCSADVFLRQYAAASPHQHHAH*
>TCRU_of Trypanosoma cruzi region 5/Dispersed gene family protein.1
Dispersed gene family protein.1
MVALPPPFRWARDPRLGTHLSFVPVSTAQPRGFGGPWGAMLSNATWVRNATNPSTVLELA
VPVHRGYFIAADETIVIRCDAAAVSGGCKGVLLGSFTIRSDTLPAAASALSAITGVVAGA
TAVAVVVTGGLGSVLEMQALGVFARMSCASAHERASTVALPYFLSVFAALDPLWMVVGNA
LLAAVFGCVHCGVTAAFQRWRGVDAASAWAAMRFPSLTYVVAHAMHLGIFFGSVLALAMP
GARVLHRVVGVVGVLYGVAFPAGVCYLIARHAGASFTRYWQFSRKPLHERLLYPVGYWHP
AAQQRMYGGMLTNVRGSRVYWCVFQLSVLCVVCLIAAVQSPVGGCHVQYFCMAAVLPAGA
GVVAFTNMMRSSFLTVMHAASFVLLAALCVVSAANHLAPSDGGARAYAAIVLLLATVVLA
VTVYSMVVWYAEDRHWQELREPRRGGLEALLRDGEESDEETQKPQEMASSSYTSGTTVLS
SYRPPAPP*
>TCRU_8443 Enriched in surface-labeled proteome protein 1
MVSVRLNAQLQRVREVLASWKKVDDRVSKLCPLSSTAKNPSTDNACSTTDKITEGLVGFL
SGNFSDGTWKDEYLGVNATVKKKDGAAKADNGVTFKGRGAWAEWPVGRQGGISCTILRTT
TSLLWRRCPSTESRREIPPFH*
>TCRU_8444 SLACS retrotransposable element (part), putative
MTATQSRKFDDAVALEFGHWDKQAMGVEEVPFVILLPHHNGTVEYGLVGLVATNTPNHVV
AYIPSALQKDTEWVMIDGMVQKAQRQPINTHKAILCLCRRLMPEMGPE*
>TCRU_8445 Glycine cleavage system P-protein, putative
MSQGTPPVILLKVIENPAWYTPYTPFQAEISQGRLESLLNIQSMIIDLTAVNVANASLLD
QATACAEAM*
>TCRU_8446 hypothetical protein
MPGSRGLKTCTGYAILNANYLKKRPDGHCPVLFLGENDFCAHEFIIDLRPSKKKTAQIEA
EDVAKRLMDYGLHSPTLAFPVAGTLMTETTESESKRELDRLADALISIRTEIASIEKGEE
STTNNVLKNAPHTAKCVTSDDWDRPYTRKTAAFPSSHSYTEKFWPSVGRIDGTYGDRNLM
CSCALTNFCE*

>TCRU_8447 Enriched in surface-labeled proteome protein 1
MLVTLPVYSEKAGNPKGVLHLWLTDNTHIVDIGPVSGDDDAAASSLLYKSGNNNEEKLIA
LYEKKGAGEKPSPGMVSVRLTAQLKRVKEVLTTWKEVDKRVSKLCPSEGALKDTSTATAC
SNAIPTDGLVGFLSGNFSDNTWRDEYLGVDATVKKGEGSASTDNGVKFTGNGAWAEWPVG
SQGDNQLYHFANHNFTLVATVFIDGVPKGDTPIPLMGVRLDGGKKLMELSYDSQSKWRLL
CSDGTTKRLKSTWATETQYQVAIVLQNGKQGSAYVDGQRVCGSAQRGLEATEPQEISHFY
IGGDGGSAEDQEDVSVTVANVLLYNRPLTFSGPDAEVEKDVASPAGAVSRTKTGDEIKKE
GKPATTQQVPTSSSSHAVGEAAGNAGTVHGSGLPSLLLLLGLWGFAAL*
>TCRU_8448 Leishmanolysin, putative
MRQPRRATPLFPLTVLLLMCCAIRCVAAVPATQYRFGFDVPKRNGPLSTAVVREVPRKGQ
GAMQTYTVATQDDDSGWEPIRIAVSTEDLERGTNKRKKYCEEGEDECYNALGQKVSCKAE
HFLTEAKTQLYTGEILFGAVKLHAERLLVKPTGGTITVPRAVNGPCSHFTVPTRHKSDGV
PNAAFIIYAAARPSGTNSRAVWAATCNTLSDLRPYIGAMNFDPKCMTHTAWSVRVAAHEI
AHALGFSQESMEEKSLVKKPERSVRGTHRRMVAGNHVQEKTKAHFRCDPLEGMELEDEGG
SWEKEIPHWKGHHARDELMAPTVGAGYYTALTMAVFADMGYYRVNWSMAEPMSWGHRSGC
DFLVNKCNTTHNLAAKYPHMFCDAKDTETLRCTSDRRHVGTCTASIVEDKGSLVDKDVCP
VVSLEFHEISSGTTYGTCSDENVDYLRGSLTGGGSWCLDAELLETKGGDGHKSVKGVCTQ
VSCGEGTVRVKHLGGSVFQPCPEDTDIPVAFKDFQKDGKIKSPTYGEVCTIAANGSNPVI
PSALVGGQGDEQEEEAEESAVASGSTPEELVHSCLVWRLVPPLKRSLPVLRLRVSLVVAF
MPVRGVIRGCGPKVRTTLSGEGGDLSVGAREPTEPPAPTLFFCAIARRGRCTSGGRPAGG
LPSGGSQCLRACHSDSVRQQRRFPGDTRCVGTAGRQ*
>TCRU_8449 Enriched in surface-labeled proteome protein 1
MLYNRPLTSSGPDAEVEKDVASPAEAVSRTKTGDEIKTEGKPATTQQVPTAPGSHAVGEA
AGNAGTVRGSGLLPLLLLLGLWGLAAL*
>TCRU_8450 hypothetical protein, conserved
MQGCQQLCGEAPQGAPLSGESSGSAADTEAFSARDNVPSVQRPATLSDRMLQAASRADRL
TPSRASLACRGRKTPTPLQLTVSRAKTRCSTRGARMWSGEIPMWRRTRRSSLRTASPGSG
MVVAAFPGIDEGVVSEHTAPRKPSI*
>TCRU_8451 Enriched in surface-labeled proteome protein 1
MLVTLPVYPKKDDTDDNENEKGVLHLWLTDNTHIADIGPVSGDDDVAASSLLYKSAASKT
ENDNEEELIALYEKKKTNAETPSPGMVSVLLTEQLQRVKDVLATWKEVDDRVSKLCGSES
ALEDTQTGNGCSTTFKITNGLVGFLSGNFSDNTWKDEYLGVNATVKNGTKEGAAAGVAET
AEPSDASLLSTTTVRVITAAGCTSPMTRGSRGRRRSGHSRACGAKNTREMRSALGAGSSQ
RQLTVLKITET*
>TCRU_8452 hypothetical protein, conserved
MALRVVGGGEEEMLSARVLVNNQNTVRATVTLPNSPPRALQKRATGDSAYAQLKREICPV
TGRARKDFTGFTETSSLLKNTKHIPGILREDVHPHLDDVYQRVMRRLQRKANYQEIGAPP
LAVQFGIIDDTDEEKSREKNESDSEDPLNLGQSLISSGTTTKSGSSRHKQLGRGIPPSAA
LAQDGHEAEDDAFFLSQQPCPKTLRLVVEHVTATVTEKLRLAETGSLKNCLCLVFESRAL
LERLLKEIPSYSQFQGEGERLPTAAQLQEMYQEFRRKPVVLPTARFEKEPKNGHVVASLF
DSRTHPLNPMPSHSGEQPLQQQEEQTELGVSQETTTATKTGISISFDTPSCLTSEESRKV
ALLGEVAIVIPPTYAQSSRKRQTSFRLRKAAGAGSRGNLRFSGNGSSFTKTAPNSFARDN
PLDTKRVQGPAFSGRVADDSATNTSSNTTSTTASITAASTAPGGSNVAATGLDADTPTVA
ARTSLADTERKQRATRIFSVGTLTDMNSTSIVHREEYEQLQAYTRTLLVEVEERKREIRE
LQEQLNEELDYTTQKRKVIQYLRETLYKECNVLRSQLSAAQQKQIHYQSLLKEQQQALAH
AATVMNAEVRSATSASTCEGTRLPNLSTTRFSPNEVPSMAVSIGAGMQSFRRTNPNVSVI
GVGRGSTHTEENEDGNGSVVAMGAAATVGGQQISIDITAIQSLLDLVLLAVENDQLIPSV
ATRGAHANLGNIANVMAEDPHRREKNLKKEFAEMQRQAKQNYSIGRKQLTVLLALKEQQI
KDMKNFSDVHFLKGFWNDRCSTLRDELRRVRRAVQEDLESLRQFVVVSMESIARRTHVVD
ASLTENNTLFNTQSALRDVILSAQSLLLPMLTTEYERGYHPWPLKLRNTADPFARMIKAR
YGEKQLLLLREEMNALSSIYLELHHYVMKNFVSPVIKRPLPGKTLWNLCALLAMNNCTSA
EVWTRVREKYTRDMTLRKNIAALNMSILTLMYRQRIVTERSTEAMQQAGMDPRLSGLPVQ
RTVNIIAERLHRVIAERATLRKQRQENARDVYRIWKKSQIDVYEGYTPPSQPQRLVLAEM
HTDAQRPLLAVLSTSHRGENNSLGNAFFSANKSANFWDHMLSTEKEGERSTEEGDSPISA

Q*
>TCRU_8453 hypothetical protein
MEKANFEKTPANIRHNQLILLRLLSGLLLKWREIVKAAKQHPEIAHCLFDTPTRDGDPSQ
ITKWTCKTVSKEEHPPNSVQHSTGKGEKRRAVTAEPCTQGGEHKGEEGGMPSTHLHSHAS
AASSLHEEFIHDLLPDIDWIHALQGQYLLIPQENDSPMAKQRYKMHCPEEILDDHMLENV
IKSVRTAFNGMRALQLTMERRNKGVVSTSVDDTAMAFQRHGKGMTIASGLVSHTLVAQFV
QICATYHRELRETLLKLHGSLLRRMMHILNEVIYELQGMKRGLRDSVELCSMQKKHIRRL
STELHGEEQMRPPSHDTRRASSCHPPNLFAAKSGDCTALQMGASRTTQPSLGASYSLPET
RSLLEYRMFIHEGKRKYGRHEKNGGGGSVTQRECLENPVEHDWNISLGIQDTLRTGGGDC
NYETAVGRTSKASGSRRSSPLPFGLSLPLESVQHSTNLGIKTEEIQFGLDSEDAERHIAF
AHSSSSPPIFQERLPNSPREPHAYNIPRFGFAVEAREGSPGSSLHLEVVDVGHASPAYWA
RLAVGDILIGINGDEIPSTIDMWEGFLARLSLKPGSGLSLKVIFGGGRGITAHLILQDVY
STRNPVDNCSFRKNDCDACSERFERVNSHNNISTHQLPEVSALESTASSSPTHQSGRVVR
VSGKVIRWSK*
>TCRU_8454 hypothetical protein, conserved
MQVNDVSTIHGVSRGRVGHLGHALKRHAPGVGKREIRGTQEAVNVSVTSTPAADGGSNTL
HGENASSRPPRVEEGNTSSMRVDQNSLDGIRGCSIQLSREASPRTESMTHSSFDTKRKGS
PALFMQAASTNSFRRREKYLTNRELYLQLCYEQQMRRRDPRNGLDRKGEDYFYYNHRSKG
CYIPRDPPKDTLFLTYNHIFEYTDGSRFKRVGDAESPRPNPGMVETRTGSLNSLKRVSQK
ELAMAAFTKEGYSIPDHSLFPSSPGRPRSQNSRTVSVDLARSLHVSDLRIQPFRKHVIIE
DVISKNSQRVSKVMDGVSSVVAKGKVNWNDVPANLRRALSDEQVRHAATLESETASALTT
GYRMDGTGFKRYMTDVYSSPLSLVVRDERIEPSSTLQQTSKRQQVVFTDHADRVLLGFSE
NIRLPVMNSDGRPPCQLMSAPEENDKPESGEGGIAGPDSLFNTPQLPGDDSPVQALCSSP
QGEERSVLLPPVVIAAMRDAAWFDSVGLRKLQFDETPVPWSSRLPEKPLPFETSRLQYCR
NYDVGDANPPQAMMHWSQARKLL*
>TCRU_8455 hypothetical protein, conserved
MAAQRREDISVAFGNSSYPTPYGDNTIPGDHPGCRHKRLGRQYAPLPINKSSLTTDLHVP
GCGLGRHGPVLPADINNHIQHTLLIRDTHNSNYVLDSERGGKRHFAEQRGSEQPWSPSLR
RLVPIMSGDAPLLPQRRAIGVYNPTMPGPELKKSLEQREREAARQQVGKAHVNRPPDHHP
LDLVFFYVPTDIARLPSQDDTPAAAASPPMDASPAPALQDLEGERCHAEASAPDESLFFS
RLAFASPSIDDSRMRGAYLGTRRPSIKIADKGKGSTIGEMRRQAEAAQARLEDIRLVQLL
PKL*
>TCRU_8456 Mucin-like glycoprotein, putative
MCATKGSGEQDEDSSSSSPSQPPEAGGAGPANDSTTPSLTAPAVTLPGTQSQDGQEAASP
GSPGTEAPVPISKAKPDGSDGTGSSGGSVNPNASSSSVTASVSAQSQKENAPTTTTTTKA
PTTTTTATTTTTTTTEAPTTTTTTTRAPSRLREVDGSLSSSAWVCVPLVLAASALAYITT
G*
>TCRU_8457 hypothetical protein, conserved
MFRCSLRGLQKAFESHTTTLEDKSFKGKAKSELKKLLKIQLVLIPIVVAWVMFAFPHPSV
EEEKRLRAEYEKNAGWKT*
>TCRU_8458 hypothetical protein, conserved
MGTTTASSLEKVPRSVGCGAARRFACSPTDRTAQSFYCGHSVGITRCGGVRKSRSPDEDG
LLVAWQLRTSGLRPSGLPLLLDWRSNIPAWFFCRSADTRVPQRRGSLTAVTSTRPAVGVP
VVWPSWCATPCHASACSSWHQQPADYKQPFVSVVPPSHTEEAGPPRTPPEPPPGVSTAPP
RRTTSSGSTSPCPSCSSVFSSVHNMKVHARRTNPGTPIVAEGLTCGSCDSSTVSQQVPHA
QVTTENVKRINEQKRTTHLCKLQ*
>TCRU_8459 hypothetical protein, conserved
MLANIGLESESRVRENRIRGRRHVPRDETFGQQPTYMTAPFAVQQEPLRNPRSTAMPLPQ
DILMPEENEKGSFASNCDVPQPQLGEERLSKSGLNIFSWNTEAPKALPSRVRRERDAEEL
LRLKPLDAEVQRDIEVREKFEGNTHSRFLCFSQDGEAGKQLGSRGRDRNRLPQTTLASAP
VLDGISCNRNPTGDAVPHGRRRFPPTACPNEGIAGFAGMGMGGFGRPHKPVGNGANGF*
>TCRU_8460 hypothetical protein
MSVFIIPHSGKYRGYFEFAVVMSGKKQSKLKVTVYDELKKRVVYETKDTWPSGRKMALPP
GDYCVHAELVLPRLDGSTLLLDAVKAQYSIVQRSGSTLSTPTPLSGQMLREELASCASHV

QRLSPYSTEGAIALAARADLVDGGELATRLGSFPPSRRSMSEFNGRSSVNAESVAGDDAA
SVWRSPSRGTPNPALPRIRDPTPAQALRAFSELPSKRATPSLARVSLNAYETAEPKSPFS
LPQRNISLTAHPYAPSEAGNNENTAPAAFNPEPQNATSWLWKLSPTPVKEERMMKSSPGS
VYAMAIDEPNSRQMNYEEIPLVSTPPQQQQQSDYPADSARGSVHTPPQYETIALPCCNEG
VGVRPVNAVNSPDRLHANDQAVPFSYSLPVENVEENKNPLSFRETTPLFVRAEPVRNNEE
EKISSLPKQPNAEKEQQTLHFAIPTSTNGSSAEMVKYTPPVTIKDNQEKSPNRGSAQPTS
PHLPSRKEGPTFVVPPPDVIDVHEPFCLALAFGSPNAATTTNPVFIHVLVEEEVEPGVKP
VEPVISVVPATLAAVPTQARGINYRWVCSPSIRANGRTGLMELLGGVAGKPHTAIAISTV
CVGPSCDGQTLSGIQFVLDNVERISSCQFFVSFREIEEMSNEEEEVTKEEASVNEDDNNG
DTAKAQEKSRQTPTLDDRALGAEVIYNSLPYIRCVVDENGEMTLEVQRKNFVVACEPVQK
GSRVAMYFGTIATNSKAAGGNVGGQQPYLSVLVDYRTVFRYVVPFGKVPEALRVILMSSV
KSSTDAPDSGACMRLREVELLSQQRRLVAFADEVCLDDAKASQISDSIRRKQQEEGPSQH
GAGRPGSVSAWVAGQNPGIRAWRRVTLL*
>TCRU_8461 NAD dependent epimerase/dehydratase family/Saccharopine dehydrogenase, putative
MQMSREFSLIVLGATGYTGKLVCEYLARLGSSKVGPWAIAGRNKEKLDQLKQELGVNLSV
LVTDITSPSSLDKLCASTSVLISCAGPFTYFGMPVVEACVRCQTHYVDSTGEYNFVRQVI
EKFHEEAKKQGAALVSCCGFGSVPGDLGNYFVRQGLGSEVAEVKAFYQMARDGMSGGTAR
SVMAAHESCGLEDKDPYSLLPKDAPRPPTAPARRGVWYDFSERRLTGPSSMSATNERIVR
RTNALLGYGGTYVEAIEGTLGAVVGATITKYMMTAVLAVPFLRRYVAENWLPPAGTGPTQ
SQREGLWYKCIFVATDKSGKVLRRVFLSDTRDVYTASGIYVAECALSALQMAKEGTLGFG
VLTPMAAFGDVLLQRVRSAGVVVEVVEEATTGTATPAQ*
>TCRU_8462 ubiquitin activating enzyme, putative
MNTEERIRYDRQVRLWGKATQQQLQQTAVRICGMTPAVAEVVKNLVLAGVCSVTVEDEAV
LDDNDLKNNFLIQGHAVGERRGRASVGRLQSLNPYVAVHLSSPMGDEGIVRNGALFSVLI
VGVQSLGDAVRSICLQRNAGTDLVVLVSSLGHLTMSIFLSRKLEISYEEQVLTLLTKNVS
SRPVNFQRTLLLMRMSDCPEELPFFDRLAFAMEIVVRYNLLQLAREDVEFAASFSPRRHF
GTAIEATVAGGTIAQHIIREISCVKEGPGDESYTWILCDNRNGTDIQVGHTYGL*
>TCRU_8463 cystathionine beta-synthase, putative
MAQNPSAVNNKKEVPDRRKCILDTVLDAIGSTPCIRLNHVPKKHGVCCDVVAKCEFLNPG
GSVKDRIARQMILDAEASGRLRPNQTIIEATSGNTGIGLSLVAAVKKYPMIITMPKKMSH
EKEVTLQALGAEVIRTETALPWDHPDSLIGMARRLEKEKGYVLLDQYRNPSNPKAHYEGT
AQEIYDQCGGKVDMAVFTTGTGGTMAGVARRLKELLPNIVIVGVDPYGSILADPSVPLDP
KPYLVEGIGYDFVPDVCERKYVDRWVKSADKESFALASEVHREEALLVGGSSGAAMWGVL
QAAKDLRPDQRCVVVFPDGIRNYMTKFPDKNWLVENGLEEGEVTRPTYGSLEAQLEEAKK
KLSEYEAKCGGSVEEGKRCCEKAK*
>TCRU_8464 retrotransposon hot spot protein, RHS3, putative
MKGRQPSTGLPCKGWGMIVVTSPNIKNFEWWAMQMGAEQIIINCPDESDVRAMCIWKERN
GQVEEEEEEEAEEESEEEAEKESEEEAEEEAEEEAEEEADFWKRVKKRMDKVGPILRFIF
NGKKCKSRVRACKFAVNNITASMLQYYAGIGTGKSCNGHHVSHLVKVVRVRRNNIEWPLN
LLISPHFERETLSKI*
>TCRU_8465 Enriched in surface-labeled proteome protein 1
MNENKGVGGGSASTSAPSTVTTSSGKEQSANQLSSGIFSGGKKNVDGGSSSNDDQTVGAE
AGDTVRGDGSPQTPEVSVSSAEDEETVGGTDAQGEEGIHSQDGEVNATALSNSLGNVSQG
NNSDGGTMRGSGLPLPLLLLGLWGFAAL*
>TCRU_8466 hypothetical protein
MTVPSPDPIPDDESRADPTKIILIVCSIFIVLFIVIIVVVIVRRLRRNKRQAGNRRYGGS
VGSSHGGVLGGSNPLSGPQERSAYQSVEEPYFFSDIPVQPMWCSGGKRTEVPSGGQRYSY
PETPTAPVRVNQGRTPQIALGRQPYFYPYMPAPPVRLSEGRRLHLSEGNREAFRSIRMHQ
INHMNEDEATRFHLLRHAETAFVEFGPFVDSDSD*
>TCRU_8467 hypothetical protein, conserved
MSWAVIRRPVKVCATVAAATAFSWLYSCRPVVVTQEAPTIALDSNVGSAVEPLWDYMSFL
DAHTGEWKVESSNFLKRGEVSRHTDEPKVQVLRLGSSYSPDAGNGHPIPFMRVVGFFPDA
LPEEIFNFMTDLYLRRQWDRNYHMFRKWDCSTGPSAPETLNSVKRPIEMVAKKRPVCQND

VCLLIPDIKEEVVDHGWFAHRVGHSLLDRFGIADRLFAYQRRSVCYTNLGSGVSPLKVYD
ILYSGSGETVKKATEQSKPFADWLHLCESEKEATRVSVNYQHILIIPISDAASQLWADPL
RLAFGGSMVDGKTTKIVYDEFMDSVRLYAETKKLDGTLMIMTSANDVQMPSSVPMWAQRM
LATFFSNYAHREMLKAIRSHRKKN*
>TCRU_8468 hypothetical protein
MLAFSIISDELRDESSIPTPADLGTSTPPSVASIHERWLCSARASSLTLRFSLISSSSSV
IERSIGSSTPMVTRCAEAANQGGMELRKNRPSRGELSVMP*
>TCRU_8469 RNase H, putative
MIPRIRHRRKTLLVVTDSQSLLAALNKGPLSHTDWTEDQIWQRLLTLTRAGWSVHLQFCY
GHCGVHANEPADQYATQTMATGQYTEQGIAPLWHTDLLTCFTTQLTNKWRSTIRQDTHRY
LLCGTRPSDLSGKDLITQEVLHRQELVHLARARCGESELWGRLYWAVRDCTNQCRFCNIS
PEQSAYMRSNNDPTAPGTDTVPPSAREKDVSPVRRRTLTRRRKEKCPHCDSTLTGFSGLV
SHCRSFHPEHPPPLPELKCDFCDMVFPTRRSTAPHRSRCAHNPDATRHRNSSARRRSLLP
QDQPASTSTPIGPQETLHHLLLECPGTLAVRQRLGIEQDLRLGKFSQWQLLHSRKLLSLL
DHLFGTQMALYS*
>TCRU_8470 Cyclic nucleotide-binding domain containing protein,
putative
MSTISVASEESLNDAPVSIASTTGAEGVTFDSNEQTNLDDMIGVAEPLKHTSTLTSIVDQ
KVALIQKGGAPSVHSFLYTVPHLFTLTEEQITGLNVMLREYSEMDIIVDEGTLLTHVFVL
ASGTVEVINTKVGRASIVGHRRVGSITAPNIFGIDSVILEKPTEFSYHASSLTTLLLIPK
RQFCELFTRSPMFSSSVSVQIVQTLSAFAVFEDFCRALFGLSSSSVCGRRSFGEGGYKLS
IPTAVSIYESSGTVVHKLMHSTAIDTDALHYCVKRLPENITETFLITLSRSIPNYLSDGV
AFSTTISLESARRRRGAWKIAEKGQIIVMARDGFTDIIDFVTNLCMLIVETKKIRLRLQR
LASPLAIDFLRNLLSMDEAVSKTAVRAVLAQLPFSETEIDGLMQVWEGSAIINVLYNILL
HREEFVVHVDVNLSKKFSQDPYQKWGLCINRHIRAELGIGGEEALPSDLTIDIIFSSNIT
IKSLLCSAPEEFRLLLEKYIESQASTTTLKNPDDYYLYVLAQVLEEEDSMREAYRQHLEE
AGFIMMEDSFMSGLVVDLINIGKLPISGINASLRYAAKNRQRMQGNSFIINVDRTFGAQV
ETILRTLVLIFGDYIRSVNLTGGVAGVVGSRGDVVLPTRLLFSKQSFGEDSTDETRVCNT
DGIHEKDVIPFLGEGNVALHRGVCVTIPGVFLYSDSVLRLYKVVHGCTCVDMRSSYVARQ
VEESHRAGVLKRGVKRRFLFYVDTVPLNNDGDSESYTQKGDVLFSIYATARSLLNLILFS
*
>TCRU_8471 hypothetical protein, conserved
MALFSFCTTSEWSDIVAPLPDLVRQNGAVQVQLTFIDENGPSDATLTAATPMTGLRLTLG
SIAKPWEDSGLTGHIANIRAFQLTNFGNQLILPVMGTARELGRVARTDHC*
>TCRU_of Trypanosoma cruzi C-terminus, putative Dispersed gene
family protein.1
MASAEGDRCSFSGGGDEETQKPQEMTLSSYASGTTGTTKCLPPAQQELMTGDTRSDALSL
FDRASSASRMIDYAAM*
>TCRU_8473 eukaryotic translation initiation factor, putative
MTEMLRCLLPHLDKHLALGLLYFYDEQGLDVADALRAVQATTALTAEGEVSVEQERKIKE
TAQRARPALDEFFEKSETENSTYQFKLTGSEIDALRSNRELSRDVLEAKGITSNVMKAVM
ELAYLYYDAARYTDASELLSLCQCVVGYEIDQRTLLWGKLVSDMCTCNWPSAIAAAEKIR
RQQNADVFEEDIFRVANTTTTRERAWLLHWVLFPFFKGGNQYSTHLLNFVFDIKTNFVYQ
SVVETVCPHYLRYICAAAILNKQRRSALRSAAAMVLNVYEYSDPITQLVNAIVNRQSFED
ALALLPEVKSTALGDYFLSLHANEILENARRLIFARYMMTHGVVSIPYVAEKLGTRTADA
EVWLANLISETKQRAKIDSVSEQMVVSSQARSVHQTVLDKLEVVDRR*
>TCRU_8474 hypothetical protein, conserved
MPNCGAPRRPSAAGERRTAGRLSARERWLQSFNPYCQPLLLRRKPSSLLSSAAVPGRRAR
SAASPRHKAVEIRPEVGLPVTNGDALLQLTQEEWSICNLMVTVLEHKSTEEAQRIISEVA
QLALSRRLLARYSGVYADGHVNGEEDTRGDEEENGRAQLIRHLQEHQRREAERRKQLCDS
KRQSQQGDIRARCRKLFNRSGVNGDGNALKATKKRCSPRRCKSSAEGNTMQQQGGHVNLE
EMVMTKTTVPVPSVPLNVPRRAKASKGVLSFDECCADRYGGGAYSNDSMASVLPLRCAAV
SPTDDSVRRSNSFPSAGVNYDDHDAIKGIFSHDDSNDIHTNGAPSAFISTMRPATTSETF
NDLSSLSGSALPPSQLLDGHNGAGLPPLKPTTPTAGSRTSAQLRAKVSSSSVSSSLISPS

SSSLISDVKHEWETGLQ*
>TCRU_8475 Cactus-binding C-terminus of cactin protein, putative
MSKRGREEDEAVEVYAALLRQSGSRAVERIRQRRSGILPIDALVIRYAMWYLDTRAFPPF
SYVTQAQRVISEAIERVSQPQHYAFVPLPALVESLVTENTADVMQQTIAHIEEFIDARDA
LGRWIDENTGGVADYNENEEEEDVDTAVELAATLWRSTLFWVAVLEYIEALSLSSAKVNA
FALRPKYEHALMELLNSIAAPRVVGYWRPTECTATMPSATGTDGSAPGASADVWPKGEPI
KREVMEEDTAAASGPDNPQDSEPARAFLVSKLLADLTALINIPSDSPAAAGINTTFYTMV
HARLNVLAACDRLDRFSTSAAVKPPPLTPSLQALQAQRDASTQARLHREAERMNRGDIGV
PLDFVPKDAYFRAALEKNNEILGEDEEIFEDEIMDYYKHHPQSAAKSRNNVAPIEKDKKA
EEPMTLVKPHRFCKVKTGYTWTQYNRTHYDARTNPPPRSVLWYEFTLFYPALANTKRDMS
RIYRIENTLKGPNDDYCILVFSVGPPYADVAYQIVRKQWDPRPGGVRASFDDTGTYRLFF
RFTNSNYRR*
>TCRU_8476 hypothetical protein, conserved
MTILHNPGLPRVLNRITPQRLELTLMLIKERKKKLRYLGSYLQHYNDRTFLYNAMGGLKG
TKFILERHHHRAQFCHPTLHSERYDVRTVKLKGSQFDQLGNFTRNTWDCSIATTNLFQDA
TFRRHLTSVHKDEAIALLEGWGVKYVLLDEIRKPTVQDSIYVRHHLYAHKFPYIPDPVTN
AYYGDADWKWKGDQKIDYKEHGAETKDDRNTFRSLWSFAPKAISSASGVETKRLASPERA
TTPKDLKKEK*
>TCRU_8477 hypothetical protein, conserved
MRHTSVLLAASPGVGIAPETTPVKYVPSMLNIQNMLWWNGKRSQYRATYREKTWYEVSRV
GAHVKGRRSIMRQKYSPEALRMALSMVPEWFEVADVPRPPQRIRAQSEGIVGRWYSNFWT
LHAVKYQCRLANVEWPFGERQRPRTNYEEPFFFVDFEESKAARDYRSRWINVNRSLVGMS
KRMKEAEEETRYMQFRKQQDTFWSNRKVLVNRVKSMYNQGTMTSTKELPIKTINIKAFLA
E*
>TCRU_8478 hypothetical protein, conserved
MSCGTVAHHPRRQERTSPPPPSGMEIELFDVPAQGTRISGRSVSFPNLLRNAYCVSPTVL
PPVYIDSDQHLQSHTAGMEDGLPRQAGMLPQRKHVAFVLRDADCDASTSACGTPLASVTT
WLEMRKGTVPRGSRDTPQESRRTEWSRPSVLQRQPASS*
>TCRU_8479 hypothetical protein, conserved
MDGVRAVVDGRSRWRRQHSAVVAAVDSDDKIGEGSDGTLKGLSSSDQMPQAGQVGEEGQE
HTGSLEVTNKLAGNEDSQITGEQNVSSDADRPKQTGSQVPAGGQPEDEEGTKSPQPPPPP
PPAESLPQLPRQPPPGTNTLRSEETHPAITAEKHPKPQDGGHSHETKMPQTKGSTKHEEG
ASSLQSPESVSHLSRESTTPLSTSTDSSGVAGSTVENSGANNPTPPAASVTQHDSEGDTG
PAAPPASNTELQSEEIPNAGIIATTYDDDNDSSRAAPTAERTTAGTRSTQTSGDASDLER
ANNDDANDDVAHNGRTAEFEAA*
>TCRU_8480 Enriched in surface-labeled proteome protein 1
MSRHLFYSAVLLLVVMVCCGSGAAGVAGESSVSTFKWRGINESETVDSLGVPSLLKVGND
VFAVAEAQCKKKKDGDVSFTGVASQLLTKKTAETQEEVLEKPEDGTQVLEEGASEGQKKK
VDVSRPTTAVKGSDIYMLVGQYSSKDCQNSGAGGCELLLVKGSVSGGGTSNKKIDWKVTE
SSPQRLFDTQPDSWTRLIGSGGSGVEMKDETLVFPVEGTKKAAGTEEGVKTVSLIIQSKD
TTNWTLSKGMSDGGCSDPSVVEWEEGKLMMMTACGDGPRRVYEIGDMGESWTEALGTLSR
VWGNNKKGVSGVRSGFITATVGNDGDKRNVMLVTLPVYAEEGKEKGKLHLWLTDNTHIVD
IGPVSGEDDAAASSLLYNSGENTDEREGKLIALYEKKKGSEQASPGMVSVLLTEQLKRVK
DVLATWKEVDGRVSQLCTSLIAEKDRASTGDACSAVKITAGLVGFLSGNFSDGIWRDEYL
GVNATVTKEGAEQVENGVTFTGRGAGAEWPVGKQGENQLYHFANYNFTLVATASIDKMPK
EGNTPIPLMGVKMNGDENNVLLGLSYDSERKWHVLCGDGKTEELSSTWETQTQYQVAIVL
QNGTQGSVYVDGQRVGNEECALRNGESNEISHFYIGGDGENADKEGVSVTVTNVLLYNRP
LSEDEIAAFNANKAPTPSLVDGSVEGDAIQSSGGGRPEEPTESLKSSGVNGVSAPTVSSA
KTSSGGEGSATQLGSGKSSDGTQTVGGGSFSDGEPTVETREGGTDGREKKEIHAQNGDVK
AAALSNSLGNVSQGNNSDAGTMCGSGLLPLAASTVGTVGVRGSVRRDWQPRGTLATSPAR
N*
>TCRU_8481 hypothetical protein, conserved
MEAGVPAEPRVVARISLIGGVTTAPSNLLDADIMLRLMGHVITVAEQPSDSLDDIMAWRM
GLSLPSCPTWPALVRCCCGDDNTVTEGIAVVYLR*

>TCRU_8482 hypothetical protein, conserved
MPELEAMPSYLPDTVVLQFYRDDGEAEFADYMDANSLAFVALGDAERPALCGIDAAAQLQ
YEGTQRALVSGAGIVSSIRRRRLRVPFGMSELSELLRRAYNTEKGNRNNSLTGSTETALL
AHAFSDAVCAEESFHCFSMTRRVGNILGLTGIGSATRDLAVDKWRPDQDIMELRDELMIA
RTVYDYRLFSYESNRPFQTWRRKG*
>TCRU_8483 hypothetical protein, conserved
MIKELERRGGATLDEVERALEAKKRESSALQTDREGRIWEYEHTVEKIRTRKQDEESASE
RLRQAMQQLEQGLSLRQSATETKEQQLEMVQLDRARGREAVMRGRHSIEAVRRSVREERC
RQRRQWIHQIKEMNAEFPEQVRPLAEERKKKYEQAKANEDAAERALAVEVKMIEEYLPKL
ISLEDIPVNPG*
>TCRU_8484 hypothetical protein, conserved
MLDDYVAKKNEKLHDAEATEHRLSSVVDRVLNYLRNGLRVTKIPSKGNGRRRLCFLLEDC
KRIHSWDLDRQGFPLNRKRPPVTMWIRDIEKVIGSPTASFVNYSGEAQLAKTHQEAVFDN
GTYRHDATQNITSSRLGTNNHRAFALFLRGGKSLEVVCEAGSDCEAWLVALKRPPHLRTP
AERILEERRGT*
>TCRU_8485 hypothetical protein
MCVPLVHAGARRALHRAYKPCFKFVYAHIGHVAHGFLLGKRPGDVWAQLQSFIGEDAKTA
RESSSLDTQEGGRGCEGFRGWMRLQLEARHDDWPRSVIVRKQRSVTRSTGGRGIGRRLAR
SEERSDTPTKQEANVAVMLVKCFPWGELRCFSHGA*
>TCRU_8486 hypothetical protein, conserved
MPLRCSQEPRPEEDGNINIWQLNIAGLSSVKNIAFAARLEQRPPDIVLLQELNNRGDLAM
KLSGHNDYLQASLGAVVALPFWCATLYRASACRSLALTSWRPLLSVYFHRAVVAFAW*
>TCRU_8487 protein kinase, putative
MDRFIVGSPIGEGRFGVVRAAVVKESGVPAAIKCITTPRLDEGIPHPTAREPLVALRLVH
PFVIRTYEVVPCGCSLALVMERCKTDLATVLSGRTASNPLPALEAKSLFKMLLLALAYIH
SEGVLHRDVKPSNCFLTAEGELRLGDFGLSRVWDTEASMTHEVVSRWYRAPELLLGQRHY
GPEIDVWSSGCVFAELLRGHSGAFFAGDGDIWQLPRILDVLGTPTPTSWPSAVLLPDWGK
AHFEPKRPLPLREFFPDASECALDLLRRLLCLDPQKRLTAAGALRHAHFSEYPT*
>TCRU_8488 Glycine cleavage system P-protein, putative
MSQGTPPVILRNVIENPAWYTPYTPYQAEISQGRLESLLNIQSMIIDLTAMNLANASLLD
QATACAEAMYLAFHHG*
>TCRU_8489 Glycine cleavage system P-protein, putative
MVETKAEPLKVKVVVGDPNLIDWSDSSLCGILVQTPDAMGMLHDFTTLFDKAKRHGVVSC
CGTDLMASVLLKPPGEMGADVVLGSAHRFGAPLGFGGLTPHFLLSRRNLSD*
>TCRU_8490 hypothetical protein
MTEPTESESKRELDRLADAIISTRTEIASIEEGEESTTNNFLKNAPHTAKCVASDDWDRP
YARKTAAFPSSHSSTEKFGLQLAASMEAMGTET*
>TCRU_8491 retrotransposon hot spot protein, RHS3, putative
MLDGDTLSTSLKLNIFFGIVLAPGRPLMKDYNATGEMFIRRLDAYVKGRQLLEGILNLTD
YQVYKLLHEGVFFLHQWRDYERKDTINFRAMQKLDSALEMPDGYSEQRRKFTVVTKTEDV
LFKRKVCVMDRKLNEPLNRRFDGRGFVDANRKFLQEGFLRIPRSIFAMREYWAKCRHPIV
M*
>TCRU_8492 lipase, putative
MRRRRTMTVVVVLLILLCGEDVRADYSVQLATTALYYAKAAYCEAEAIFGWTCASCARNP
GLQRVRVFTNATHSTQAFVGVNESMIVVSFRGTVDVTNWINNLDYIRVPYRNNDCVGCLV
HAGFNCELESLWTEMWGYLQELVAGKGIEGILITGHSLGGAMATLAAANFMSQNSLFPSA
LKVLLYTFGQPRVGNEAFVNWLLASFCRGGHESYRVTHKRDVVPHVPPMFVGYLHVPNEV
WYDNDEDTVHKNCNDVFGTPCSALTADEDPNCSGSIVPTSIEDHLKYLGVCTRCSCDPGE
AMSDEELRLPPELEWIVAMDYVYQQSRNMRRFPFSSRFTRSLEARRRK*
>TCRU_8493 hypothetical protein
MLFSCVEKQGKYRDLWTLRRIAFDTETGMLYCTARETDFRVMWKHQVRVVRIIARPSVVD
IDYKAAKFDVRELFSFKVEGSFRHIDASLLSRLEQPSDKHAVVRPLPKRADPAGKSVGDV
GKGNMLAWYMRTDNETDFMKIYTTIRDVLIRDGMRPPQFWGLPKMDPRIEVPLAEPPLYL
WCRFRTVKRTVFYACVHGHMAIRDADLSLPGRSVTLCDEPLYLTLFDNSVMVFNEERRLV

TGIPAIHIKSLHYSTMEVDASKKDPKNERCRCFLSFRSNSEEYPDILFVPTLERFADANE
ENVPAAQVNRVQTALSKLVLMRQQTPRMADESETPPTELTDVSKLMAGLEDGVESSENGL
LDVYAREENARNLLRLPVRFKLENKDLGDRLLGKLPVPHRLSVLASQLGIKLKKTLTDYP
LSYEYLSPGATVADPTCQKKDHHPLHDLYYISGRY*
>TCRU_8494 Unconventional myosin
MAEVSVTSHDGYCVGDAVYFNHPTECWIRGTLNIIKRVTKRDGFTHILYGCSAVTSDRYL
PSLSETPSLVHVYPLKKQDIHHIIESCVEPTEHTTLNDLLELSYLHDATLLEQVRVRYYE
NLIYTHIGPIALALNPYDYTLPNYTDDNMPKYVMEGSKVIEAPSKNLPHAWTVAHYSYWR
MCTDGLNQSITVSGESGAGKTETAKIVLKYIGVVSTAQCGSQEKSGAEEITKKVNLTSPI
LEAFGNAKTRRNDNSSRFGKFMKVFFRQSPTGGVMTGASIKVYLLERSRVVTHGKGERGY
HSFYQLLASNGEAAKNHRLSHLQLTRAEDYRCTAVGNATIIEGVNDADDFEEVMRAMEFV
GMSEAECNAVWNTVGAVLHLLSLQFKALNDDECCIDINAQNVEMHLRMVKELLGLPDDVL
FKELVTTTQLTRGETIVRKLRLTQAVDLCEGIAKVLYEALFLWLVARINELIIPSSQDEE
KGMQWIGLLDIFGFENFSSGNSFEQLCINLANETLQNHYNSIIFTRDIEECHKEGINTEG
VLFYDNQPCLDLICGVDFSGCGPGGSSKTTNKMSILHLLDEESSLAKGSDLTFREKVCDL
YGGRLLDGKGGHPNFLRLKTDRSSFVIRHYAGDVTYNVEGFRVKNCDATKEVLKCAIRSS
TISFVASLLSSKTSDSGLAVKSTVGSFFKNQLVQLMTEINGTHPHWIRCIKPHSTKKPRM
FNGNEVMTQMRSAGVLETIKIRQNSFSVRLPFAEFLRAHKVLMTKLHPMASKYCQNLNMK
LTEFQVPFHPHDTEEEKIREILRRAGVNSNAQAQVGRTKVFLKLEISQYLASIVRAAQNG
CMLMIQAAARCIFSCRTLHVHYLRRQHQIITAAVFSHRSQLQMRLLELREKEQYLLNAFR
VILLVQKDEMEARIALEENERAEHRSLFGNAKEEKDGIIQILLKRREEQYVVEQHTFAEV
ESQTRCDIEEAELISRQYLYEGTRLLTLEENARDDVELEESMERRSSFEHGYMQIKRHLA
AWLMQVANKQQLDFLAAEDTHRRITTQEESTTFNMFCTLYDLILSELLARVSLAKEEKDA
FSDWCKSWDNEWLHVEKLWLARKSITDRRMILFLQKKERDARINLERSYNYSTMELLESL
SQNEQDALRREKERLALEEEERMLLEEEALFLAREEEKRRFNAVREAAQQLWQNVLEDKR
LVREIRRHEERTKGIFAAKAQLTREYTLMCRRKEIAKGKAITGLNGVGDRKKLEEYLHKQ
KILSQALANHQRLLLEMETNLVEFRSKTSLNSPLRRSPSLLGPAGFIKAREDFSLHSLKN
VSVSTEGSMNLIHRMSMMKELACSRARGPSMTPGAIAAANRLEVYRQNRERRKRETSETI
TKQNAILPFRAEREESSMSTCLKSERGVHSMDYFLRRNPLKDDWVPGPPDSKGLYWVFTP
NGERVPLPSIEKCNSSGVYINDEHNCACGNSPEPYFTSFSR*
>TCRU_8495 hypothetical protein, conserved
MLSPTPLLQRYRLFHPCRENIPLHMNPAKSMFPLINSNNLLAKPRNNWQDFSGRKEFDED
HPLPVVASRLNERTTQHKWSHWDQYLNPQITQSVRDLTPTPEYVGMRSGHNMIKMGWMKI
GGSWKYSRGYNDRRRVFARGQWQERKMTPRFMLAPRVSPGGPRNRYEGKLVFSRLKLSKL
LWAIDTGRLNPNEVITVYHLHEAGVVAEGEIVWPGFVLISSGVSRVPYPIHIELQNASAE
SIRLIEEAGGSFTGVYMTHDGLYQELHPEEYPVFPEQEFPERKGLEGLATNPAKRGWLVR
WYEDEGKYAHPEAGRRYSHYVRPPTERDFPATVGEYEMVKHHQKWHLNQPGTGTLLPWHS
YNTADLLKRSAGRV*
>TCRU_8496 adenylate kinase, putative
MSTGELSAGSAAYFEEKHINTLLEELFHDVMVHLPDDPLQFLLHALDRKTTLRLMVLGPS
GAGKRTQSRRIAQKYGAVVVNADDVFREEMSKETKEGEKVANCMREGIPVPHDVASELII
RRLKMEDANSNGWVLNGFPRTRSEALRLQTAGISPLFFILLDLPYEVAVQRCNGRRYDPI
TQNVYHMEFCPPPEGMAVERMFEDDDSLAAVVSRWKYFDARKDELIECYEPVFVRIDGNR
PVDVVSQEIFEQVDARYVAV*
>TCRU_8497 2OG-Fe(II) oxygenase superfamily, putative
MYSYNNIVDKGEPLKKDVIDRVPLEIAPTEVVLQSRVDERVEVLVVENFLSAAECDRIIA
ACEEVGYTFWRQKDANAACDARQRSGETEARAFRVVDTIEACFPQLTRALSERIQRVVHL
EPKLFGPSVTDSEDMFARDLAGTWVPLSLSSNLLLGKYGPGGHFSPHIDGSTVVDLNTRS
LYTLLIYLNHCACGGETAIFMGEQADVLELDPQTGKYVGKKEKRVGAVYPKKGSAAFFFC
DVLHEGTPVGEGCCKYILRGDFLYRRDPPILTTENDKKAFDLYEQARVAESNGNAMLACE
LFQRVRKLSSGVAELYQL*
>TCRU_8498 helicase, putative
MSSSEIAVKRLRRQWEPEEKTWNDEVLEVPWEELTPPLHKSTVFALKNVFFFFHATSVQA
RAISFLRTSGNSAVLEAPTGSGKTLAVLIPLIERTVRACDAYVAEHGRPLLRRDIVGVIL

SPSRVLAEQTFVVGRNLVSRLPQNIRFVLCDGAVQPAHAVLDGLKKAARGAGNFLVTTPH
DLSEFLAAWEQERAASAVSDDMQELLATQDEETRRRYYEKRGGMQSVSGDTGNAVQLRGC
HSERFAFVVDEADLVFHSPEMRGVVTRFLDTYAGMEEPPQKRHKFAPSKSSSSGQIVTDV
AFVGATVSTSKELRAYAAHIQATLGTQMHTIVLNSSQDFVTQLQNRYMMCEAHEFLPLLV
QLMNLHASKKHFIFFNSPKTLKFVEKLFGSLMKSESPLLYIKHTFVMYEGMNERARLEQY
NAFLNHGTSAQESATKKTQPPPHAATEKKNQVYSGGWKRNGRPPDGKGAILLCTDMAAFG
LDVRDVDYVYHFEPPATVQSYVHRIGRVGRMGMRGSSILLLPCFSNESSLASARERKTTS
TRLNTIANTKFSTSELQSVHMTLDDLSKEQRCYIEDLGKRSELQPYSLPPFAPITSTIRN
IISQQKNLLKLAEIAAMSMCTVPENAEKAKAWFYPKLALCALLLD*
>TCRU_8499 hypothetical protein, conserved
MAMMMAGRVLLVCALCVLWCGAAVANGEKDAEKKKDENSGGPGPDADVVSAGLQAMQVSV
KEGPRNGDHALGAQTGNSTNQQNIVVTSPPESPIRAEEQAEEEEEEEEEETVQKEELEGT
TEEETPKLTSPQEGERTPAPATTRKEEKPAETSNATPGKGQSSADDVLTRPEIHKTPSKE
QPSSTALQEPASAAMAQIKNENTTSADVVSGQQIKEESQHDMQSGSASGKEEAVPTTVTK
KDGPTESNAESTPTPPSASKDAITNDDDKGNEEEIPKHDQEHDGETMSEASQVGNNEGNT
KKTPTVEAAAITNNTATIGNSDSSTAVSHTTSPLLPLLLVACAAAAAVVAAWE*
>TCRU_8500 retrotransposon hot spot protein, RHS3, putative
MDGQAVGRTLEKDDGVEQFRPPHPRLTLLTSDKEWPCSGVVGRYIRDCHVNCEVERVWQT
VKGDVTEWFSGRPEEQFTPHPRVLIATLGIGRSVVAGSYLLYQLLHCDAEQLPMVAHFMV
SGTYLLEKTARTVSEYMGESSFVKVLKGLPRRGVKGFIVYDVAEPDNRLSTCLSSLEWGM
LVVTTPEAKIHGHWASERRAARICDGLS*
>TCRU_8501 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSVCVTATAGDPNKGGPGLSPAQSEGAGVSGQANTSRASSLT
PPTVALPGAENQDGTGEAPVTRIVTGRGTDGVTGTPGFTGNSAKQPHGTPSSQGAGDSAN
RNGQEQIRESSTSGSAESTKKVQEQAPSGATGGKGPSSQPSHGQTQSGNPTSQGSSAGTD
VPGSSNTEGPETIPKQGPGESDGSGSSGGSANPAAASSSVTGTVSAQSQKENAPTTTTTT
TTTAPEAPSTTTTTRAPSLLRESDGSLSSSAWVCAPLLLAVSALAYTTLG*
>TCRU_8502 hypothetical protein, conserved
MAKGFLRVNWRACGGWLILQWRRPLPGTTERVAVSVLANGTTPLVAGLGSKACQRVRVPY
GRDSMFRVLSGCHGLRRMLSRRLVNMHSTMSVTKLPVHGPAGTHQCQETLPDPVLVEGR*
>TCRU_8503 hypothetical protein, conserved
MAQQRIQYTAGARGQDKRRVAKGQFKRIQREGPNHIPVTRGHASTKCADGSGDRSKWDSD
DATDERVSLLPDFVGAYQRYTCRLRAVCDAQRQKLLRGGDVERSPSPIAALQMTVPSLTP
AKLATLMAQGADMIAIRETWKSSEQIASMHTGEYVPHAQSRIRKEFVAAVLVRKNLRSKR
MPLITPQRDSSLEVVVQFALGQNRDLIVASTYMRPPPQPTQPLGGC*
>TCRU_8504 hypothetical protein, conserved
MSGTSLADGSLRSSRETGDTTRIRRHGKNACRTESCRPLPLLSVLLGVSEGLVHRRLSAL
LARHRRQPRLTPRRTVSDVVTPVRDKTARGPNERIAVECGRRRGGVPRCTLTVAALSQSR
PASRLRSAPLTMGECWLCPAGSRACAFEPNTGCAAALG*
>TCRU_8505 mitochondrial carrier protein
MDLFSAAVAGMLARLVCHPLDTTKTVAFTGFCGEGSTTGAHLGNAKKHAFLSSTRSIYRR
EGIAGFYRGVGVAILGSAPGVALYLTTYSWANEFFMKYQKAAFGAVPSWSVHLFCGFLAE
AVSCVFWVPIDVTKERLQSQPPSQPGRYSGSWDALCTIARYEGLSGLYKAYGTTLASFGP
YSAAYFAFYEFFHAVFLEHFSIDSFASALCAGGMGNIAASLVTNPLEFIKTRLQVQRAVL
SVGGRPTSVRGFSYYYAGLVDGLRTVIREEGSRALWRGVGSRVAFAAPNAALTMAIYDYL
RSS*
>TCRU_8506 4E-interacting protein, putative
MGVNIRYTRAELLALAQKQHEYNLTAGALQKFKVIEAESIAPETSPPESHRNDAGGRKGE
GKNGAGSRRAPNTERFAPPARISRGNKDQEAFEEGYKYELERNAMKKQALQETMAKEKER
SDAVAGSKGETKQEVVATVEKEEPKLNEDDEVERWMTSIAMSEEVTKKVTKSRFFSGNDS
DNKGAVSSSLSGGQAFKETSTFSMTTTSKDPWALQGVIPTTTGNAVWGNLETQRNSGIAL
APVTNNAAAPSVVVGQVQLPGHSGVSAPLPAQMAASGALPTSAAPAPAPAPAPAPAPAAA
AAALLATGPSSSSQKTTTTTAAAPLPNNPSANPSTQVWNAQDLEQMLLSGQKLNKQQKPE
AARPKIIDAAALESQLLLQVQKNMARSQPQTQANVQQQQQQQPQLPPPASQLASMTGTPP

TIPPSGQRRAPQLFLPQSPPQLSSQQPVPIHWGATMQKAPPQQMHQKLMQPQTQSQPQPQ
HRHPSMPQPVPFIISGAQGSPYFPQQAVHGHYVTGFMPGQGQQPMMVYRTPDGTTQYAVG
STGYPPSAQLLFSQPQQQQQQQPQQQQQQQQPQRR*
>TCRU_8507 predicted zinc finger protein
MNGPPRRHSRCPDDTDTLFLRRRACVETPSFMDGVNSVERRGGLSEAEWRQLYERVMPNA
CTMSDFQRLVLEGKSHDHFFAKDLHKLVMEVRVILATHGKLRMAANLAVKGRKTVLAHGV
ATALKLLESERSHLFSEDICGKDVNGCGGSSCNISSRAPERTAVEPVNSATVLHPSTSST
DLLRTHQPSRCNTRTLDQPPLRAGVGEVCAEPSVSEHGTDEEVVLMNNSSSPFTRVLSVV
KRFQLRFGSIPLRFEVPIEFLDAVVSRRLRVQLTPFRHPAVPARWPTAKDIVVYVNDQCV
MTPWKRSWPERRMEVAKTFLVLDITQFLNRGSAFQRLQINVFSREYFSQVALMVVQPVTP
EEVMNALVRPLCSPQEETRDAAIFDLYRKVVEDEDEDAILGEVEVDDPVITSKCPILQTR
INIPVRGSRCQHLQCFDCLSFLLSCNKGCYWNCPLCDAELRPCDVVVDTILWRYLQEMGD
GCPLHLRLKSKRSMENERIQKGDDAVEGVMAAPFRWVPHRMASDGHGVILDDHENDDCDS
SDGGAMVPKRQVSGCFRTGVNGGRAFEKGGEMYGGKGLEETNADLDKHLGTAEFPIEL*
>TCRU_8508 BNR repeat-like domain containing protein, putative
MSRHVSTFAVLLLVVMMCCGSGGAATAQVGSNADASTPGSALTGAIAGEGSASGGVEGLQ
RVDLFVPQTTQVLAKGGTSQETERDSFVSPSLVSAGGVIAAFAEGRVYREYQVGRQKEKN
SSDIVVGYIDSSWGWSTLVGKVNESTWRAHTVLGTTDGVDNRVDDVFNPTTTTKGNKVFL
LAGSFYEHKQTVGNRTYSGFKTQLELVVGDVREPTSSKQSERIKWGEIKSPLNGSTIAAH
KGNLTRFLAAGGAGVVMEDGTLVFPVMAKSGNDGYCSMIIYSKDNGSTWSLSEGISPAEC
LNPASPSGRDHFP*
>TCRU_8509 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MPKGKAKPTTESRPWEPKKEHQVALMLQGNKVSVYVDGNSLGEEEVPLKGESTLGLVHFC
FGACDQKEGHEQEPHVTVKNVFLYNRPLNSTEMRAIKDRIPVPTRGPETQLEDGTERRHI
PRIEGVRANAPAGSGLLPLLLLLGLWVFAAA*
>TCRU_8510 hypothetical protein, conserved
MVVPLMLDLMDFRRMMCNISVPIRLLVLVQNGREAMLSLCLQELERVYGWSGRLVVSRHP
ENIGYSAAVNIGSRLALSLPREEVPFVFVTNSDVMFSPGLLPNLLRDVHEMTRHDAARMD
ELAAEVANGPSEYSPVLRRGLRVLRSTVNDSRLSTSALLPDRIRYASVKEREKAFSKHYG
HFCAYYKSSCFTSVMLTRLAISTVGYFDENFYPAYVEDVDYRLRLRLLGFQERNVLYGKF
VHCGSSNIRFSSEMELPDALWYRRVRSLNANKPYAMMKWNRPLACSGGYKEPYDGMVPAD
VWVKDEARIQRIRVYGHDEEQGVPKVDYDRRLLYPVRNKGR*
>TCRU_8511 hypothetical protein, conserved
MPSSQLPATVRVDGSRVQLYRPQPLRDAGFAVAGALFDVVEALDVPDASTLFRKLCATAA
SNFTQDRKNMVALSYGVRSSPKRQLMYGSAAGEGYAA*
>TCRU_8512 hypothetical protein, conserved
MDANSLTFVTLGDAERPALCGIDATAQPQHEGAQRALVSAAGIVSGICRRRLRVPFGMSE
FSELLRRAYNTEKGNRNNSLTGSTETALLAHAFSDAVWAEESFHCLSTTRRVGNILVSTG
IGSATRDLAVDKWRLDQDIMELRDELMIARAVYDHRHCGYESNRPFQA*
>TCRU_8513 hypothetical protein, conserved
MIKELEQRSGTTLDELGRALEAKKRESSALQADRESRNWGCEHKLEKIRTRKQDEESASE
RLRQAMQQPEQGLSLRQSAICTREQQLEMVQLDGVRGREAVMRERHSIEAVRRTVREERC
RQRRQWIHQIRK*
>TCRU_8514 hypothetical protein, conserved
MLDEYVAKKNEKLHDAEATERHLSSVVDQVLNYLRNRVRVTKIPSKGNARRRLYFLLEDC
KRIHSCDLDHQGFPLNRKRPPVTMWICDIEKVLIGLSTTSFVNYGGEAQLAKTRQEAVFD
NGTHRHDPTQDITPSRLGTKNHRAFALLLRGGKSLEVVCETDSDCEAWLVALKRLLHLKT
PVERLLEERRGT*
>TCRU_8515 hypothetical protein, conserved
MLRRTATTLRYRTAWRELLHPLPVRARRAEWMKRDTVEQNEALLRRPYYTLKSYVLPPVV
GKQTTTDTRRPGVYSSSSDSVQDVLCQPRRATSPERLQELREQLQFPGTVGPMPEIMSAT
GRPAESYTEAYGARLRPRYPESWETVPPHQPSRGIL*
>TCRU_8516 zinc-finger of a C2HC-type, putative

MPTATDFVQDYAAKRAAQMERARRIREERQQFQQQQQPMQQQFQQQQQQQQQPSMALSYS
TNSNNNNSNKTHNNSNSSGSGLLGTTTNLTPAARSRRIANVVEEDFKRATKAGIITPDQA
RQLWAMLSDQIVQVENPGTSTLTSSSYNVQIGTPITQELSTRTKRFGNSISLDSLRASIA
QFKEKQKEKQQREQEQQQSQLQDVAGRVGGNGGRARASNNTNEAYELATRVFAPPPASAV
AGTAGAAISRPARRELRAGSIEHGTRQVERAEDPAGGEDMNNWGLRRYESPRKGWRSKQQ
QEQQHAKKPEWNFDVDVEKNDKDDFPETAPLRRLSSRQQRSKVGGIAAGTPSRVNPPMQF
DDMPVGDVTSTMGGEASLRPRQQQQQQQQQQLQSVISKVGINKNKMSNIPARPSARSNIS
LDDVVVGGGERGKTDMFVAPPPTNEPLMPCGLCGRSFRASILARHESACSNLQKKRGVFD
TKEQRLEGIEGIREVTAPSNSVSQKGGKKHPVAVANTNPDKPPKWKIQHEQFQAAMRAMR
QVNVNAPSGGGGSGGKQPMPEAYDDRVPCPHCGRKFAELTAQRHIPKCMTTIARPKGIRP
TRR*
>TCRU_8517 methylthioadenosine phosphorylase, putative
MSHCSNPHGSPVLVGVFGGSGVYQLHNLNEVKYYAIDTPFGRPSGDICVAKVGGVDCAFL
PRHGVGHVLNPSEVNYRANVYAMKVLGVRYLIAINAVGSLDSNYQPGDLVLVDQIIDRTT
GRKSTFFENGIVAHCDFAFPTSAAFRKLARDAVHRTFPGLAAGKEGWRLHEQGTSVTMEG
PQFSTKAESLMNKQLGGHLIGMTTATEAKLAREAEMAYLVIAMVTDMDAWSDAPHVTEAN
VRKTLEQNVDKSRTCTLEVISALGKDFFTDPAHSLLKHAITTSPSAISKEVRERLAVLLA
SCPHLAP*
>TCRU_8518 Got1/Sft2-like family, putative
MDKLTSVVSIASNSGAASAVTGGEGVFEASDSESLCPSLTWKQRLIGCGLCVSLGMLFSI
LSFIAILQMDLVFFSVLFSLGNIVSIIGLLFLAGPTAQLQRMFAGKRWIATTVYLVSVTL
TILCAILLHNALLVLLLCLVQCGALIWYMLSYIPFARNAVKACFGSVMRL*
>TCRU_8519 MYND finger, putative
MSVQKKNNALPPPPRPDPVTLDQIYNYLTSPDVIMEERSYHLVALSSVAFHPSVKLFLFE
HTPLHPTVSIGDDTSAEGHSAEVGEVLEANRRRREAVIKSIAFFLAQRNSTVAHECRWDT
VALLGELCRLENLTPLRAGGNKKNVFGTMSVLSPMREVVQKINHYARANLEFLARLPWFV
PAVQELIGEEETEGAAAAVSSSSASPLTAGTAHLTIRRAERQRNASSTDDEELFGIREPD
EDVRIALKDILLALPEVTHGDGAEAAVVWSPERMNQAQDLMFLDASTTILHLIPLVSRCS
HLQCAHCEKRVSAAGGSDGNKDNDNNNNNALLRCGSCRAVYYCDAACQRAHWSLAHRVPC
KSYKQLSEDIMSQYEAMNKRHHGGSRRKMQRQQKEAVAVLEVPLEPSLFYETRRYLYDHR
DPSFAEMSFMDYFMKYDVRGS*
>TCRU_8520 Enriched in surface-labeled proteome protein 1
MKIRVWAAAVHPHQQRPLLRLPQEKSNPQTSCRQEYFSVEKKNVDGGSSSNDDQTVGAEA
GVTVQGDGSPQTPEVSVSSGEDEETAKGKDEQEGIQPQDGEVNATALNSSLGKLSQGNNS
DGGTVRGSGLLPSLLLLLGLWGFAAL*
>TCRU_8521 BNR repeat-like domain containing protein, putative
MIKWGDPKLLLKKETLQTEDTVNYFFSGAGSGVLMGNGMLVFPLMAKSEAEDIYSMIIYS
TDSGSTWTLCEDISPAKCGAPRITEWEGSLPMIVDCENGQRVYESRDMGTTWTESVGTLS
GVWTKSQPEVILGRQPACGSSHHRDH*
>TCRU_8522 PTP1-interacting protein, 39 kDa
MPHVLFSSLPRVAADALRYEEQEKDEEGTELIAHNNEMDFFMDDYVSLDVAKANATAASK
SAEDEEAMIPPRSIAQPRQSCEKNEGVFALDCDVCLQLSGAADEGSGGRFIIRVPAALPV
SNPSISVTPCPINETTARQMKPMCGKDTMVGVEEVTVLDAGAAWTARGEGYMNGEVSEEE
DGAAFRSSCYSINSYAQHGSIIPKTILMPSNNCEHLINAGNVTITVSAEEQKQARGGECV
VVHAMKLPLNFVLGLRLSFELERALVKCYQENRTSSAPPPVWLSAFLYTTALRCETFTSP
ISTLSPSMCQEWLGESTAVATLEGFCIVALNIIAQMGHLHRQKLQETDDIDETTMAQRGL
LHGNQLFSASQKERVRRWLQRYIPMEAYDGSEESEKTLRRSPGCFLWPSAVTVVFHIALD
LAKFLFPSLLLNLESTILAALQPLLEARTVGSMSTPSLYVSSPVLSPSTPSLRWPQSRRQ
AFLLLTQFPSAWWSWWRRNKNDEKSNNDCGISAICASRGYAALRVLQCFTCSCLQSTPDE
SCHLVEDDDEEECEVAQFLLSAEALFAELLLDREAANVIDRTIKGITWLYHTSLERLKSR
DAVTLPLQTTRASMRYLLVLVCWLTFRPKGYCTTLAQHHFGSLLRLAAMHHERCQSEHLF
NVKLEEEGETMDREQLLLTVCSREYLLLLSNLLRHLRDRCGTRRHRGDYATAPRENPWQQ
LRQGKMSSRLFANDEDGTTNTSHSHPSVASFSTTNAATESLLAPQPPTAQRTAILHNDAL
SSRSLYTIRRVIRAMCHVIRRLERDVLEAYDTSASTSLGTKRMRNLEENTFSNLRVSVSE

LNFGVTPYFARHLCSQPNGRFWEWHLETSESSDEDATDTSASGSG*
>TCRU_8523 60S acidic ribosomal protein P2, putative
MADKVEANDTLACTYAALMLSDAGLPITAEGIEAACVAAGLKVRNTLPVIFARFLEKKPL
ETLFAAAAATAPAEGAAAAPAAGSAAPAAAAAGAAPAKDTKEEEEDDDMGFGLFD*
>TCRU_8524 60S acidic ribosomal protein P2, putative
MADKVEANDTLACTYAALMLSDAGLPITAEGIEAACVAAGLKVRNTLPVIFARFLEKKPL
ETLFAAAAATAPAEGAAAAPAAGSAAPAAAAAGAAPAKDTKEEEEDDDMGFGLFD*
>TCRU_8525 predicted TLD domain protein
MQHVRHLEECIKRCQDGMDEIDAVVDEFGKCIVDDEKVLHLWQSIERSEVELLHALAVCD
TSVHSSYFRVMYLLSHGDEVLAQMQLAKERLLRCFRFIAAKRDRGVMAATAPTDGMDATG
SAAVDYLVREAATILSELRDRGQHLVDNAVLIQKKLVYSLRGEGDVMMELHQQDEDQSGG
MKLEYPLHIFPSFPEDAEKEKNGIAVLSKLKEDHGIESWTPWEESNAIWTDLQLMKMSLR
NAFSAAACKHYFVAAYDFALVMKLLATKCCTVEELLMTVLSLEYRREGDSSLSHFIKTSE
LTERATSPWAASILSKMHPNVLSKEFFLARGNPMPPYFISLTFVSLVWNTAFCLWQKGCV
KEAHQWLCEIDLERLFILAGATEKGTEKEGVNGVCGLMTRHRFTEYGERISLETHVGRSD
PFESAHVDEGGKLKGPRGEYQESARLYPLLCRIVCLRNLCAVLLLCTTPQDVLFLLLHFH
SALQWQAQCVLPQSDCVNWEEREFKRGQPHTDATAEVLTVAMLVVEYYLTQRVIVTVESS
VSSGSPSPMEVEMAVHQVCDELICFLSSAKLSGVEELEQHGFPPAWHVRYDDESNVRNDD
SDSSLGPSWLTVQVIGMTQAFASGFRSSNFYRRAFAAGETNAIHRGAVGDGMKPVEKRST
RSSSFANRMQNTARFIMKSVGGSWEGGEDTEAARKSSFLSSELRAILLLPQCFEVKEYLR
AEKGPGDLCFPSLHGVGLPLLPEEELVDGSCKSSEDLAWRLLVIACRYSKSQSLVSLVPH
SSTDDSDGLLDIVIPELNNSARMLMSELKVHAGDEWLPVWKHERSLSAGRVRTSKLLAAL
ERGTFMSVVRDNPRRDGADIGHHGERAAHPEKEFLHDTIFTRNSIPPAADVMKNNENVAE
EHKGEAEGSAARLWDSPVPTYTPPIHFDFSAFTSGSAEALQATRQIVDDLLRGQEAAENA
AANGEEMTAESNTHCMSVLTPNSRQLLHEELPSIWQFMPWRLIYSSRHHGFSFNAMLSCS
QREADASREHGRISPMLLVIELMTTNRRASTSDEDGPTKLVIGACLSEPLHTGTRRFYGN
SGTFVFQLLLSSAASQSASPQLRIYRATGRNQQFINTMSHSLAIGGGGGCSIFFNDTITH
GSTAACATFDAPPLTHWSTSSSFLSWSSDVAAEGATKDDSTLSYAFDVCSLELLVIGD*
>TCRU_family, putative non-canonical purine NTP pyrophosphatase,
RdgB/HA.1
MAEGSAVLRGSGNHKVTLVTGNDGKRREVQACLEGHVLVENVKLDLPEIQSDSVFEISRN
KALTAYDTIKSPVLVEDTALCFDALGGLPGPYVKWFFERIGPTGLIKLLEGFDTRRAYAT
CVFTYCASPDVVLQFEGRCDGRIVEVPRGEGGFGWDSVFEPDEGCGQTYAEMQDEEKNRI
SPRAKALVALKAHFCL*
>TCRU_8527 Enriched in surface-labeled proteome protein 1
MLVTLPVYSEKDSKKEKGELHLWLTDNTHIVDIGPVSNDDAAASSLLYRSAESETNNDEL
IALYEKKKDGGDKPSNSLWSVLLTEQLQRVKDVLATWKKVDDRVSKLCPSKSAVESASSE
DACSPTVTITDGLVGFLSGNFSDGTWRDEYLGVNATVKGNDDGGNKATLHEDGVKFQGAW
AEWPVGSQGENQLYHFAATKRAKK*
>TCRU_8528 hypothetical protein, conserved
MDNCAVMSRTHVMYALASDLRVADGSVFSIQNSSWSAPSIGVYEGACVFGDVAVDGGSVL
QVVSSTFRLGFAVLVAATLTVTGGSWLLHRDNEFRTAYVVYVVHENGVAFCDRSVWSILY
NNITYGSYSSTIVSMTSSWSLPSDSRPTIYGVCNEARGSPVTDYGVYLNIGAPVTVLDCG
ACTMDAVCFATRTSSISGCECVCAAGGYGGTCLPAAVPDGLGPLPLPDARDTGVRCVHGG
SISSVDDPDPGVRGLCFVSVTFTAAIVLDLWRFDAPEQTLNITLLQCVLMGLSIKGSGAR
VHVSVTSSVLDWGALEFEGNFGASSQILVVGSTLVSKWSHAIAFLDFALGANSTLLLLDN
RIEGNRYAVYFANAAVVDGGGIIVRGNTLRTMDVAYNWDSALHFHSVDLKNGGYFDVENN
TMSAANGVYFFGDTTVSSAGLLRVADCTFVGDAGMFDPTLVYLDGSVTLQGGAQWRVTGN
NVSAASILSISGPWHKIQLSDSGTTVVLANNRQVEGSAFFSDLASSDTVVSSPVHFVVGC
NLKGGEEVSYDGVFPEGVMVFGCGTCNDDTACYMPGTESVDRSSCSCSCKDGWHGASCLP
FEVPDTVVPPVAERAVDGDTSCVVNQTLTNLTLNMWKTHHCYAGVTFSGVGAVLTFFLNS
MPLHLPINIAFTGCTFLDGAMLQFFGGAESAESAGVLIRVSQTVMRSSVVAFLLALPQHC
DIAVTGIDAVQAFEIYLPDTVGSMLSVVILDDLVLTASSLLVSNVRARATKHGALGLYST
GTLKLVRGSSLYTRYCSFDKYTHMFYAAFLSVSDRSVFALLNNTMSSGTSLLCQYYGFSV

SDHSVLRMVGNRGSVCYVIRNEELWNVQESSWLDWRDNDVEVGAMFQDTESAFVTIDSSS
VVTLTGCKMGSTGLSGPLLSQADAGYRFVAGCLTVAGRVVTTAAELALHGITNVTTAAAC
GECTKDGVCFAPLTTAVIDCKCQCAAGGHGDVCVPAPVPAGPPPSLPPPTPSLPPPTPPV
GECISDMVYPEVAQAVGGGLSWLCYRNVTFSGGGMSLTVLIGAMTGGVVNVRFDGCTWRD
GAVLLLLGNAHAAVRSLNIIVTGNTFSDALLSPEGGFPPHTNITISGNRFTVTRLISRSG
LDIWSPSCVAMNELVITNDSAVVLSGNVFLTVSASSSAIHVVEYALRVSWYSVFAVVGNA
FHMAGGNSTLIHLEGSSHSLSLSVLMGITCGVSVSGRFSGQRHAGKLGCFSLKIQFTYLL
QLLAAVERQPLPRVPIGSFCRFEIKGESP*
>TCRU_8529 hypothetical protein, conserved
MTNRVDRSRTPSRTSAGPYRNPSWPRVVGTYCDPPTVARSVEFASSTLECSGIAPCSTIV
PSSDVTFVMFTRARGIGRAVLSLRPPIRSCDPPASTQWRSVTFSASANASIERRSTATVI
GPLNTTESKHAVARTPPTVTDSVSVTPLTQPCAPPPPPPALAGGTSNGRHASPTPPARQL
HTQSENDAVSASKHASAAAQPSHGTTLTEGRPAMR*
>TCRU_8530 Plasma-membrane choline transporter, putative
MSQITPISECKSVEDEVLVVMTVCNEKEEPSMGEACKPGKNDADGCPQQLPQNGWKDTWA
LFAFLLTVGMTVGWGMTLPIEDEISQSLQGISNLLDCHGLGGVKAAELYFGVGVGIPCAG
ISAMLSLLLLQALPSAAIVLSTFLFSAVLLMSSAVAFYKSITPTGVTLAVLGLLYPCWLY
FVRSRIAFSANLLATASFLTQQIPLLFLIPAMLTLPFLGYMMWSLLVLHASVKRGQYNDC
FWTNYIFGLTSIFSIFWAANVVLGLSHVTTAGVVAKWYFAGSENMPARPTWASFQRAITT
SFGSVCFGSLLCTLVGAFGWVCGLGIHSGNEFIDCSIACIQDLFVDFFNYCNSYAYVEVA
MHGRGYMTSARRVWRLCQNCGCSAVFNDALVLTTLRVMTVSIPILAGVGVALFSFSATIG
SIVCVLTVIPLTCVLSVVSAVVRSIFVCFAEIPEGLEASFPELHAALMATDYGFASIHNQ
EKDDTPV*
>TCRU_8531 hypothetical protein, conserved
MESASKFATNVDRHLDGIEYHLRRMRRRSSARTPHACSAGSFNMRQERSTNRCSESQYKT
GQFVRRHPGGSSAARNGPRVLWNRPAKNFNTSASSPPPSRHPLQVKKRGNEGGKGKVVVP
SAKKTRFSNPLGDLKPAPLSRKTSSLLSASLSTVPSSFSPSSTSSTSPSSRRRRAMALSS
VSSNLTSDTLVSFSSLEMSPAGEIATRWLQWRRAAYYLLASHYEKCCAVLTRMRKLGPQK
GASRKNKFEMFSEEDNEETKSLTSPSESSDSIDDLSDGEQTSDTIQNAPMSNLIAKSQHD
VCIALERTARQLAALSEEEAAGRRGIEDEALRAADDLERARNRSMRGATVRERQRRLAAQ
AELEAAKRVHIQRKCRIIEGDEAARRGAIERVEEEELMDLLEAMEQDAWAASEKEAERTA
RASESLKAHLLSKSELVVAAVSQRKEKAIQTTQKLGTVKISQTEGEVCIEREGMVQNQPT
TPKDKSDLAVGRWRKLDFLGQSTHTDGLRAADSSESVPVETLREGGNGVSGDVVGDYIPP
CCSKYTQTSPPIYVSVQTSADIPYVTLRGPEGEPHPPAEAAAPNLEVQLASESSRDLSSR
KAESGPSRSSKCAKATASLETSPGSGVDMEEEERATGSVEQRPVLEVDSPVSHATKPQCS
PRVSHASWRETVVRDEAKSLSETGSPQPVDSVREAVRNLRGKSARRRHGGRVLFPPVDTH
LSRQDSWTNDDDRQVFSPRWGLKTFDFEWSDEFNLCSSAARDLVRVEMRHRRHVERRELL
ERNEVRWEELNHYRAWAARQRELLILVAEAADEANTCKKEVEKEKKEVAYEHEHFLAADA
VAPVVHAPEWIHVADEINDEKEDILPRTEAPQPAVAVNLWPSTAWSVNMTGKAPGIPPHL
RNRPWAAMLTRKKTCGGDKLTSAVGRVSSPMSRGYRRTRTVFSGDSEALVMRVPTDDTCN
APVKRVPESVSTKRSAILPGYAQQYERRLVWQQHRQDAFGMPLPEPFYCRTTMSFLESAE
WCYQKKYVDRYLYASPSARRHDGSARKCADAICEEVGRVHVTWGLRER*
>TCRU_8532 Bromodomain, putative
MAGGSVQAGLGPSTLWGHFVAVDITRTFCSLYAEKLSAVWDRREFSTRLAALMRQWRAEH
WDEIFIGAATRRGVNSDGARRSRRRTDDNTADAAGNAGELQRCQRGVAMYYESIRVQRLM
DEVLFIRDLEEACDELESDKIKRRVLRRRRGLIRAVDEVWRAGKDAADFLLPVTEREAPL
YYRRVRQPVCIASIYCSVWDAEVEDYAGLKALFTLMRSNCELYNGAGSPLVAACQGLVRV
GFRAAREAQTDEEQEEVQNGGLVIPNSLLLETASGSAIGGGVGGNGKKLFPPLTKEELAW
MFPPRYEASQSPVDGGRFTTAEAAGGRNENNAGEPRRVLRLIRRSDKHEPDGSGEGTAAR
TTLVRRLTLRRTMDAAPVVDAAVPSSNKEEVEKKDDKKPTSTGGRKKKKLQEEEEAVGGD
DEQEVTYWIRCDLCDKWRIVPDKIEPLPEYWECSFVGRKCGPLKRRREGEQPPKKGQKTQ
PGRKKKRDGEKAPKEIRRKRGGKKKPQGEELALNDNGKKAGASTLPRAQASSRKEKKASR
PAAPRKRRASLSPSLSSSSSFSSSDSTGSGSDSDSDSDSNDSETPPRRGRGRKPRQTPQR
IRSARRPRATRNLARDDDSDSDNSASRPCPAANATTPALTLEKLVELEEAMDEVDAMPLE

DENPKEILARLRSIEKFLL*
>TCRU_8533 hypothetical protein
MNTKFLEQLRLLAEERKKKREQAKAKEDAAERALAADTKTIEEYLPKLISLEEIPVNPEE
TGIIRRQFDEVFAQ*
>TCRU_8534 hypothetical protein, conserved
MAKELERRGGATLNEIKRALEAKKRESIALQADRESRNWEYEHKLEKIRTRKQDEESASE
KLRQAMQQLEQGLSLRQSTIWTREQQLEMFQLDRAKGREAIMRERHSIEAVRKTVREERC
RQRRQ*
>TCRU_8535 TFIIF-stimulated CTD phosphatase, putative
MTRVAVGARNSDKTCRKRRQEEVTSSKKKDVATAVVKEAPDGEGPFLPHNTPEEGGRESL
PSVSRAVVNLLDVVAEEDSLTPTGARDAAGGGCKGSKGGKKGKTTAMKSDDAGKKRVLSG
TSPKKGKAKQRSKASKTKPGKAESGGESSVENVGKGQGELDSKKENGDHAFSLHQQIPEM
NNISVKVHLVEHDISELQIDRTSCRNGTSSSRLTPSRDLSGFNDCFEGMNSCEVISNNNS
NKNGLSNNSNEGFLSLKEQDTAEKPLSLRYSVMPPLTIPREGRKEHTQQKDGATKNASVH
ASRAPSAPSVSLVSGNSSGADTNGEKFARRSAHSSLEEALDGLLPKNILYPTRQLLTRSL
ASAAEKERTATIVFDLDETLCNNRQHGPAILRPGAVEMLKQLRALYPHPVMHKGETPMEP
TGKNSSTQVLEGGKDNGIQNSSPEATETPTDDGVMLRLEIIIWTASVEVVARPVIARLDP
DGTILDDVIYRDVRWYRDGGYTKDLRRIGRHLERNVIVENAPSCVCMNRRNAILVNDFVS
NPADRQLVIVRAILQEWLYNVNALLVHWHFQKLKQKRHNMIEDGGESPEPDKPMIDPLAR
GGSAHSSVSRSKGELSLVPSSHGGGNLLQELEQKASAIHFLTHHPFLSPGTRYVKPSVWK
KAAKYLHGCAGSTTAAAKPLMAMPAAMAGEIGGGRGPQELPATAPARPVASAKPRGHRSF
VDMARGPREVR*
>TCRU_8536 hypothetical protein, conserved
MRQRQRQLRLELLAPAAAKPRTALSSSSLLWARRCAGLSLSGKKQSPVTPFFAALFPAHF
AGDDVALRRVSFVRRALLAKGEKAVGGARTPGSKWSSAATAAPSSSVVSLRPWHVIANLK
HAVLFAMNDEENSKEKKAGEAEKGCSTLHQEDEHEATCARRGVKKDEGEKCGDGKRHVAP
SEIVRLVRHSIRIVEQKNTRVRADLMMADANAVGGTSRLQEMDDNLREEKDVLRNVLRKV
PKEALMSYVLGGDDGMGGAANSTLEPLRFALKQTMRSSSYAFHLTFEALLRQGQDHMAVE
LFRSWWRHNPHLFPIELGPDLGQDVSSMLSVIRAGGDTTTALQRDMIFRRLAQIPYKKYT
VTSALFTRVMKVALCLGIPALEEEFVLQELIYKGVYMACCASRTGNENGNGQKTEASASH
TDLHFHAFQENYEDWLVLIGAIAAAAVLERHAEDFWREKPGGTLYDRLVFSVREEYTTFI
TKACFPQLIHSSPVDFGSATKRGGDPPRPLVVPGWTRLLFTTVLRCYEEAGVFHASPVRR
PGNSAALWREIHTRLIQQFPHVFHAANTVTTLLSFAALEEAAVSSLGTCRMSFSGKEEAL
CRWRLECLSEREEGNGGGGTFHEFTQSQALSDAPRTSRRLRARVLTAHSTLSKKTMKEES
VDKDSITNDAEICTQQLHWKHRELFGHALSVSTSQLSIPVFLKSQEVINYAEDAMDELEA
ARHNVVEIFREHASLPMLRPASPTDVSNPQERRSCGDILAEASQPSMFLFLRLVSLLSLM
GEPPVVTTEAGENEGGIRSFSLVECIEEDILPYCHPSVAAFLRRCCATYLSRSGVRGIRA
LVGEHQTLLEQLTEEAAVGRLLVGVLWGGETDKKNSCSSKRYSFGSGSLAWQVISQHRQV
IFCKDGRLLLEMILSHLGTLSLAIPDDYRQLVFLSPYVHRVIADPTDTASNALSALRSEL
DWNPAPARHLYISLLELLSWVVEAKRKESEEGKPKGIKKEQSIDEAEDVSTLNDDSGANL
PTLSDTARHWHVVQSFFRRRSLNFKLFSPFLLERVCLIVVHSCPDVELIVTCLLALCQQQ
RGGSGADVSAHMDGESSSFFTPRLLTSLCCLLVMNGLTGNSVRQWRHKNGAPSSAVSPTC
GDAVGKSRLREWHLSCFERILPSMGHILKENREGAEGFSAAFCGDGDGLAVGKNETAHLL
GSIVLDVLLTDAHWLSLKKDNYYVFLFVSAAELVATKGADEAAVHCKKSSFPLGVVLPSR
QLSSSYPSGVRQRVTKLRDALREMGAERRIQIRRSVSPVIRREKGVLEAYSLGNDDGGDE
DDVVNFFLHSVAGGDGVATQCSSTRSDTKAEGE*
>TCRU_8537 hypothetical protein, conserved
MRPSRLWLLQWGHAAVAGTVIPPKRKRQFVMKEGQNSHHGSDVNRHSQKHVSSASFRPPI
NLTHELSQREQYRLHQEQEGAEMCRRSVPGEWLSPIPKRYRLYDGIDEHGYEAARVSKED
RRKMLQAALERNAASVVEYTEGGEENIDLGGMSAGEYHGQTDSMTIPRDSALYNAVLARE
ELDSRKRNNTWTMARKRQQGGGIDIMGKGEDKLMSGGDGTQVIDDKRRRRRQDEGSYTSV
FDENLLEPNYESIGQPRSTYGMRKMLVAGLTSYQAVITREEEAIISDELLQLLQDTRAAY
IAEETRYCVNLYEKELGIPGKDTLAFAMSRAPTLQRVLGRFFHLGLIPSLPNICQVSEMV
GNFSGYPIHKKPATIGPYVGILNLVSTTLMYLQHLDNPWFPRLHMSPRSLSVIEQPCLGD

YKMGYKWTHQPFHTFEYGTRISKDYRIEVMFATVEVAQMRYLDDAVRLTEYAVKKQQEEG
AADKRRLLPPLPSPDTLSEGANEFRGSTVKWLDRLNRQMHASERGARSGEAGTAIDGNAL
REQLLASGCIGAKSRTLETSVQAAVSTDDANEKGKEKFSPTQRRMAALKARYEFAKRLKE
SKPQVGLGGGVHVIEGHSPRKRDSS*
>TCRU_8538 hypothetical protein
MRVSRVYAMCGASSICRRPSWTQPGQEIPPSVANALTQSERDTVGVELHLPSFASVAFAG
RDEMRHHVRRTVEAVDSVIHACADAALPLDYITLRCCAPFSVGESWTEEDWHLALSFLRE
VAMHLLPLFPVSLLFPITASNTLPAPCISKMFDMLHRVGWKNFLVGLPASTSGAMVGATA
EGDQPPMHPAVRGWISLLHGTGEHPHFSRSQPIPWTGLFPWILQEGFFDRFSVGLSVDLY
TSLQSLSLLREAGDESGGENRVSSSPKQARREAGSSSTQEQLLKLRQTTRKEKDLLWNQQ
EKEQQQQQLRTQSFQGSKGPELITLSAPPREFSDMFLSQHQSFLDAENSDVGQEILMMAQ
FLQQVSEEHAPKQEDRLQKKSTASVEYEVGVVNEKKGTSDAAAGRQLGNCTLYWQLLEEI
AQRTRAQYLCTTPCVNPASLLAWKQACVEKFGCKNNGMNNQGDNSFLTFLPVVHTLWPLL
HPVQVERVRRQTIFSAAIMDDKFLTDALEFIPKETQQALQQALRDIPPLYLQRALNGAVE
PRRETQIHHEAGGVRLSCGNGGRSNVSEIFGAGTATHQALFSDMPAGVLHHICDVEKTFR
QGPMKKIIENSIETIRSGGVHASKCHFLISVPCDMELPVLSESLRLLCP*
>TCRU_8539 hypothetical protein, conserved
MFSVVGTAKSGGDGANIKNNNDNPFERLQPPLRSEEDEIRKGIFGQALRLLHTATDEDKL
RWRLAIEEAIAARQSISRMNKKTAVSEGVADVTPLVGFAAVKRPRDDGKGEEEEKETGTE
ENGGGGDGDQRPVVAAAKDSFGFRTGAEDTPMKDTEFIAAYLRTLLDKVVGLSLLELHVD
ALRVLCIILSIPLPKSRSKMTLYSTLASFHYTHCEKLGKRVSSSHNVQAQLKRDEQMIQK
LFPAGSTSQTNSGMGRNRAAGATTTTTASRPSGITKTVNSTTLSKHSNSSCTDKSASNGS
ANHKKGTRSMLTAVDSNVSPLDDTPRSRRRKLVSDTGAKPQTKSPLERDAKDTPAGVEGE
SELEVRHTGKVFADAPVFRQAMAVSRNNEEEEEEEEWTMAQLEKKVASVVQLYDPVTSAV
VVKKLAQMGYRKACAMEKVEAILRSFHQRELVFYDNGIAYLL*
>TCRU_8540 hypothetical protein
MFSTLPNLDDGVLALLIAVCTLVSYLVSLYWWQLVPRLFYPEERKLEEKIALLRAEAERC
NTTDQLHLHGKLTRQVQLLIKELAQTRNQRFSLCCPQNRNKTGNDKRRWLFFGTFLARLK
YFLPTFIDLLISFGFIIPFLCLFGNRPAVVAFPHCFRHCLPSLMNWIEAVVMSVLLGPLL
WSSKSHGCVNGSTWEGNRRNLLPARGCNSDVSGFAFSDTAGTDVPLKTADGRDDGEIKSL
GLLSWFLVCYFAVRFSRRVLLRR*
>TCRU_8541 hypothetical protein, conserved
MQPPTPPMTPFEQDVTRAFQLLGSVRVQSAMLHRSTTFCVDRCLDTEELYTLLRTTQAPI
RYRLNADLAEKKCVTSCSAKWDELYRMTNMRVNEDETRRVQLNAMSSMMEAMRQ*
>TCRU_8542 hypothetical protein
MSPPGSCNALPYSTETRLNCIICTAAAVSSLLAGVVFSVNYFGFFYSSALRSVFNDVFAV
VVIVQMLQALQLFIFAFITVLRGEGILELGNCSQSGMTYAMCNINASLFQYLDAMGQLLQ
TIFFFVLANSRRLTSLEQLDNSDDERIVRTGEIANDRNAHTSWEHGYSSSAGSSTSALTQ
HSHNVSDDRQKRRRRSSNQRGEGSCGIFFLFCSCWGYILPCCDDRLSNNDRTTATTSGAV
AANGNGPPRSFSRFQSPLLPRDDVENEETITRAERHTLLRVTWKAYLAAFLFASISLLLC
WILLVYVPDIVLLPRDNDGSFEKSRTIENTVFFSEEFAWCWIPGSGDLSPSSSSLQRKIL
LLVQLAVGYAWLLLFIFSAFYSYTVLRRSSPSLLRDNPIVICRIVIFCAYPTLVYIISAL
ERFVVTSSSSHAASVARVYLSATVSFMYPFSAAVNVLLFLYTEELMGWMAAAFCKRCCRC
IYGAQHLGGQRPRIDFGSSSDFRDQIFPERVEGNSVITTGFCAVVKAIACSTVTGLPPGG
APYTSTSSNDVFTQGNRTSIRVPTAGSESLPEHRVTHAVHRNAGASMYFPPSNEPAGGSV
*
>TCRU_8543 hypothetical protein, conserved
MFLAVFQEFAHPEVLAQVEEGKICRVDRATEPCTLAKSEEELAVVSRNAKLFIDDETTSE
EAVEATLEALCKLGFTVTHRHPVTSAGCPMRDRVILSYTA*
>TCRU_8544 40S ribosomal protein S3, putative
MGPLSKKRMIIRDGVFYAELFEFLKRELADDGFAGVEHRVTSTRTEIVIRATKTREVLGE
KGRRIRELTACLQQRFHYKEGKLQLFAERVEVRGLSAMAQAESLRFKLLSNLQVRRAAMG
IIRHVMESGAKGCEVTVGGKIKGQRAKSMTFRDGYMIKSGTAHKNFVDVATRHCHLRAGT
LGVKVKIMLPKSMQNEEEILPDVITVLEPKEITA*

>TCRU_8545 hypothetical protein, conserved
MKKIPRHPQPQPIRLPAAEESLKSTHPFLVGSKDESKFLGCTTRVTFPALTRHQMAHSKS
SISPLPEIVCERLPIVSHGDVLNASAGVQNDSSSVDRASDRSLTDIYLGTSLRTTENDEN
EGQDAKEMQEFLLNAFPESLKHIATDEASAECLASESVEGVTDSGYHRQFTEFALRDVYE
LLSRAAAAHEVRLRYLIRQNMMDMEGTNSKLPEAAMIDESTRSLSEWNDVWYQAPNPASG
VLVAVTVRPPRFAAGMVWNGNDSFLLGGTAFLQEGRILQIWLPFGNKSPESSKTMPVNSG
NQMSYNNSVTGGAWGSCQRFQVRLLLREFLSVSKVGMGSMMQTFSLIPENVSVKVTRNQA
LQYGLIQSVLDQCAPGAVSRAFSLQLLLPTKLRNGIILSCVDDAAGSSHGLNQTTPGSQV
DDEEEQRNKPDGSHSSSVIWSLSSTLTKKGPVEAKTFRRQPLGDEAYLVYTNPKLYALVM
KHSPATLTANANVIREYLQYSQRLFLYQLMKRLLAATRTIQRFFRHCIAKRERAVNRMLR
LWGKLELDSRDELKKYTNACATTDRLGFIVASVLWQHVITTKEYKMAMLEEQFSLRRVAY
RKWCAQRLEEDRAKLEITRKGSLSVGLMTDVKKNKKSKRAIHVEVEKMPAVRGGKVVDVA
LLKANNQWILKWGDVIHARFGWYIDPEELLQEYHRRLLISLRNSILRMAEVQEELKKNSK
TMALSPL*
>TCRU_8546 hypothetical protein, conserved
MQEKGVDCNEESGSLLSPSTLTALRHTRLLPRSIPPSFALQSQLIGAEFCASLSAAMLEL
LQNTPSGLSPLDSNASKMLTDVNSPVTALLYDLSAHYGSHTLRRAASHPLGPCYTSRRRR
LSNGQHDGRRQLWSLRAAHRMWCRRCGVYLLAGETKALLSTSRTSSFQIPGDVDDVNSSD
MKELNEKHTATRGTYVCRRCMNNEWLSRGKKVCVSTPPTKSSPSCGQLSEITDEKSPSKT
PLHASDTTFGVSVEARLATIVGRTRRRKRNKRGSVVRTPAMAMRNTSTIPKAALRAVPKG
SLARGKRSRSAASKEPAPRKKDRLAMNIRSAEQDVSAVAPVRREARTEGSPSTSKVVSCA
GRPEFSTDENEVNAQFPTLPRGPPPKGRRHTFKKSGNSSRGNPSSNSFADTLSRLGL*
>TCRU_8547 hypothetical protein, conserved
MSLRLSIHAHSVSPVSINFDALEAYVAGLSVEEALQYILNADVTWPTGDDEKESQKQPGN
IFLDSPVPVGVECWRNLQMEAPQPLSLPDTGRFSLPQMEMTADTASAKHGDEEGEKNANE
TGAGNHGNELAVDSRSLSAFLDPLSSTFHREFQQALSDMVRGERSILRQELVEQFVLFDM
FRENYLATPYAFLSRYSIPMTLKDRRRMVEVFYGVDEKVLKMFFGDRMHKLELEQESESW
FLFGARAIRSQNIQKLIEAGISEGSLKRQWENLKRVCNFLVSAYRGRDGMLIPYTTPVLT
ALQQCFALHGTLGVQYGTFVFGFEHRLRGRFWTPLSYEECTTACQALSLWCDGSQLNIRE
DFSGGCARIARFLDEYRVVAEMHQLIFGEAMRSRWQVQFDEVQRAITINTGGGTSGNPHA
TTAAGTTMLSPTTNVSHALLPRNTSTGKLDGDAQSGFSAASSVTPRTLRPQLSSISSRPS
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RFSANGAFTRAFLQEFPSIMRCLFRMATTISKSGEIEEALELFYGRVYMQLSNLGYRLQN
TQGVEISTLSQELPSPEVEGFSEVAESKYACNSQRGSRGERRATTNTTNTTTAEFAGDEV
GSTGNPAKANPSECEEKLEVVANVLKNTVVNTSLVGHAIALSSRRPCTHVSQHQSQPATH
IFSSHSSVAVDSLICLRELCLLLSMMPNAFNSLTTLTEEDHAACDNEFANFVLALKVLVQ
IHMASDDL*
>TCRU_8548 hypothetical protein, conserved
MPHVLVNMTNVTSLEGTIVLHGAMPPNSSVLLANSTLRATVGGSQYVPTTRGHAGSRHGP
ALVLDGVRLLSTQFVMTRSTLVCGGGLCAAILVERGIGVNLSSVFYMDNCVVGSQMHVMY
ALASDLRVGGGSVFSIQNSSWSALSINMYEGAWMFLDVAVDGGSVLQIVSSTFRLGFAML
MANTLTVTGGSWLVHRGNEFRTAYVVHVVKENGVAFHDRSVWSILHNNFTYGSYSSNIAC
MTSNWSPPSDSRPIIYGVCNEARGSPVMDYGEVLNIGAPVTVLDCGVCTVEAVCFAARTS
SISGCACVCAAGGYGGTCLPAAVPDGLGPLPLPDANDTEVRCVHGGSISSVDYPDPGVRG
LCFVNVTFTAAIVLDLWSFDAPQQTLNITLLQCVLMGLSIRGSGARVHVNVTSSMLDSGE
LEFAGDFGASSQILVVGSTLVTTSGHAIAFKDFYFSANLTLMLLDNYIEGNRYAVYFINA
VVVDGGGIIVKGNTLSTKEDDGVESSVCFNAIDAKNGGYIDVENNTMSAVSGIYLFGDTS
VSSAGLLRVADCAFIGST*
>TCRU_8549 hypothetical protein
MLNRHGTRLDIGTPEDVAELDAVEMALRQEDGISFGGSGLLTERVLNFDHHHQQQQRQQQ
QQQQQQQQQQQQQQQQQQHHYGRRSQQQQQPRRGNGASSQFSPSY*
>TCRU_8550 protein kinase, putative
MAQARITGRKSNKDKSFSSKGKIEKYNQDGTETIIVMGRPFRVLQNIGASENHISSHKER
DHKFAKHLRSFVFLVENTENLSEFPRHFALKRSFFNVNEVLLAHREPEVLARVSDKNIVR

VFHTEVTRSDGKLGVTVAMEYCSNNLYRQLRPDTRVPEGEIVQVLLGITSAVGYLHSRQP
PIAHRDICPENILIHSGSTGAASYRLCNFSSATTEAYHCANREEVAMAVEDIERNTSPGY
RAPEMADPGSGKRIDERVDLWSIGVLLYYMMYLRLPFGETNMGLTGRLKLRFPAGTEMWY
TGSLRVVLAHLLEPDPDKRWDIFALTNFLRFDDEIGKHIGTFFFAQTEWPDGWEQQDVKV
FNRQVPPKAPPIRVNTPKHADNTKNATDAGTTNRMQASSEMERGSSMGGGMGELDAAALA
ALGLDGDSKDPEMRKYYKMLIQEQEDAWRMAKSASQASAKNKSGDTTNVNNRQAQETREE
KQREEKPPKQRQDNPPNDNTPNLFDDLFAPSPAAQASSGSLQAPSQPAVSRNPVTGGQNW
PDSLFSGVQPSQPLPQQQPPLHVQNSYDMMMDSGWGTGAPTMAPGGGTYDVGAMYAGTQM
ATAPTFSMPPHPPQQNFSPSWGISAPPEPQVTPIQQQQQQQSFNHQSTMDFAQGSLPTAV
PAEPKPEAKKDPFADLFL*
>TCRU_8551 hypothetical protein, conserved
MMAMMMTGRVLLVCALCVLWCGAGSVYARDLDNRALGGCMASGVLGMNASYEPNGCNEYM
PTPPLRSALPIPAIQAEVQQLTDVSRDDITLSSDTAPGPGSGGGDGGKASPGPAPAAGGG
DPAVPVGGHAAPAAGDGSPGPVAGPTAGPPVGVPDPAGFPGPGGNAGSENSNTGCREESS
DCEDEQSVGKTTLEKQDSEESKTQKLPATQNTKSKDNEENPAKASSTESQNTEPQQEIKT
PVDESDSTSTDASTAVAARSTSAGSQEEATASSSNDSHSPLQGEVFTGTDTPENAPSPAA
AETEKRQGENVTNDGDSDGSPAASHTTSPLLLVVVACAAAAAAVVAA*
>TCRU_8552 hypothetical protein
MKGALDTVEGPSDQATLVEAPMVTQQDGSVVHAERRRDQDSAGIDLGSCGDKREHVVARQ
RIVEESALFCQSVAAWQTAVAPSHLEDTPVVDDSSHMCLEAEPSALARGVDT*
>TCRU_8553 hypothetical protein, conserved
MACSARSSDSSGSRSRQDASFYTSPSPHTPSSFFPVFTSSPSRSQVYGAQGWQGVEIASP
PLREKTEKPNAVENHPVEPKVAATSEPACILYSKGVKRYGVPSTPTAFSSASTVGLTCSS
SCKMRERDPNTYKRDVECRVAVDPAAQRDWARSLQRCLLETETKAQEFRATAERREQEAR
VAAEEVIRLRELTSLQAKRIEELEQRLAHAQFATAGAKEADAVEQTRVSADSDASLEGFS
IADVKQIVHCAAEALRRIEVEFEAEKHRRCVVEKENNALRRQICLLRRGKVVFHEDCTTC
CKEARHNCAMAFVQGPLRRFLAESADLQEKLTTSSARRTSVHS*
>TCRU_8554 hypothetical protein, conserved
MTVIVMCDGAPASIKAIGWAAVPGHLMRQHDGEQLILLHGWSREDVPRVASSRESPDRLA
SVDISPAQNRLPVSDVMRNTLEAITESKVTRDSLNYKIETVVLSDLFTPMSTTPAATRPQ
SSKKSPLSKKELAAQQQQQQAAAVFTEAELEAAARVAEKEAAQSRAKAIALYARERALHH
KAEAILLGTGNSMDGKNIILGLVAKTVFTEMRQTHVLWFIKNNGCTMRLNTALVRYVVVL
VPVSNDAGALERDCRVVQYALGRRREKSMDTVSAVIVVESATPPKEVERYSQALRDLLQR
EAPATNSRIIEEAADDATPAFAVTDAPIALEKSGTVTAEGTPQEAALDDGEVLPSAEEAD
IAAKEQQWPEVSLCQLRATKQVPEPTAGNAAGQVVKFLQRYKTDVVVSPSTLAEELQMAL
LAVSKPHALFVPAAEPAPCAAATMPPPVVEHECTE*
>TCRU_8555 Domain of unknown function(DUF2779), putative
MFRRKAPEVVRRSVMGAVGKAAEADETLTQIIQVFRDAAEPFSDLDETIEGTVAKEQGMR
MARVTSPTVLTFRGFSASLTCPKKFYLMQNRRDLIPSISIGEAVRLDDGAAFNELARRWD
RLQFGSRAVVVHERDFDLAVQRTEEALVNYFQTVHAQLGEQAPALTIHRPAFAAPFGGNT
ISSTAASPLVLQARPAVLRFRPKDNQWVILETAAVIDPFGNATRLAQCLQRLHFTTLAFR
YWVTQTHIPIQIRKRFLNIDLDTVTEESLKGHRLESTAQVAVPLDLKRSGFLHIRQFFPG
PVTIMDCDPSRLVKYVQRLSLEDMLEADTNSNHRTSGAFDLSNVSLRAEPLVTDLQKEVE
KLQKRGLDHRHLGSSTSSRVAKKKETELKELFTAQQKLLEALIHTHTLRLIERGRDASNV
TKWTSFAHLDGEIVKATFDEGGVSDENSTGGNGGRKKSSCQKNKKNGEQRGASSCSNGNE
LPCVPTYSEFIGAHCSRGDVCPFYAEGLCLPNRIEDPLKQCDNHLFSLPSTSISRKAMWW
TQGLRTARDVLYQYKKGTVKLTAPQLRHVKAVAAGKLFLNPKEIENFFSRIRYPVFFIDF
EATQFALPPFEKMVAYQPTPFQFSIDVFQEDILNETPTHYDYLHFGKGYSPNVDPRRGCV
KELMRIVHLEREKKRLSMAKSGELGRIEKQKLLQEQKEREAAKGTKRRGRPTTKPKPICI
TKNKPLLEPVHPYDGCFIAHFASFEKSCLEKLGQLMDEYKEDIKQFYFLDTLDLFKRAIV
HPNAHGSNSLKKVLPALCPDFQYGVFGEEVSGDDIDAADMDGGNGGRQDEQKGENAMGVY
RLWYHHEGGGSLKDLHQVSMRDSQRRSAKGKSEHAGSTELVLPPARQDFREKAWALLRIQ
LLEYCSLDTKALYEIMRQVWREKESVKGIKPDKGGWVMATPLSREFEL*
>TCRU_8556 hypothetical protein, conserved

MSVEEGGKASLSDKSNGLSAQEELRQLQEKTNAWKQSVAIQLGEAAKKNKQLRDELKEAG
KNHEKEMSALRVQLDKEFRERTNLKDEEISNLQREMTQLREEKRRMAEEHKRDLEETAIR
VRENSQRENVSNTRTDLEQREAELRQLRDIIEQKERALAQAEHEATVTKTSLDRLGEQYR
ELLSIMTHDEGQSVRDKDASDGRSASQHMVNWSDAAHRQQLETARSELRSLEERCAEKLR
EAQGVHETELQRLMEDVYQREEQLMTLQALLRQAQHEAETANQRIAASRAEKERSEQRLA
EKVAALSKELANRMEQSQQLSVEVERLQREVSSQEALVHSLEEEARIREEAFTSLTLSED
NRHLVQGLQEALQKSREEAELWRSRYEEVMQETTNKSVFVPFGEGGGGDSSRDRFVLSEI
AQREEALATEAARLESKARLLKSTEARLEELKRSIASQANFILQHRESGDDVRRRDTEGI
EKERRGGSFLAPQRRYLQMIREQQGDTFFFLLRRLASYFVFVRLRVALPLLLFIVCTFLI
FFSSRR*
>TCRU_8557 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSLCVTATGGEQNKDSANSSPAQSEEAGGAGPKNSSTEPNST
GPTVKLPGPQKQESEGQASDKTTDTGKGTDGVAVTSGITGDSAEKPRIVNHTQQGTSSEK
DTVKKKGEEQKSATTGDTGQETGKESAPPETPDKATPESIPKEGAGASDGSGSSSGSVNP
NISSSSVTGTVSAQSQKENAPTTTTTTTTEAPTTTTTTTTETPTTTTTTRAPSLLRESDG
SLSSSAWVCAPLLLAVSALAYTAVG*
>TCRU_8558 hypothetical protein, conserved
MCSQYGPLRSSSQRGRPIAVSVANLCLRVAATQKFSKPPSAVHPRNIGRQATEDSMNSEL
KGLAGVYQHQRSPMGSAVELASNTALLGKVRLEVVGSVMLHFMYQACQLHRRGTRTTARM
LVRTRRPQPKQSPQCHFLSNLTHDGRKADGSI*
>TCRU_8559 hypothetical protein, conserved
MAQQRIQYTAGARGQDKRRVAKGQFKRIQREGPNHIPATRGHASTKCADGSGDRSKWDSD
GATDERVSLLPDFVGAYQRHTCRLRAVSDAQRQKLLRGGDVERSPSPIAALQMTVPSLTP
AKLATLMAQEADMIAIQETWKSSEQIASMHTGECVLHAQSLIRKECVAAVLVRKNLRSER
MPLITPQRDSSLDVVVVQFALGQNRDLIAASTYMRPPPQPTQPLGGC*
>TCRU_8560 hypothetical protein, conserved
MAKGFLRVNWRACGGWLILQWQRPLPGTTERVAVSVLANGTTPLVAGLGSKACQRVRVPY
GRHSMFRVLSDCHGLRRMLSRRLISMHSTMSVTKLPVHGPAGTHQCQETLPDPVLVEGR*
>TCRU_8561 pyruvate kinase 1
MSQLAHNVNLSIFEPISHHRANRIVCTIGPSTQSVEALKGLIRSGMSVARMNFSHGSHEY
HQTTINNLRAAATELGAHIGLALDTKGPEIRTGLFKDGGIALAPGDTVLVTSDPAFEKIG
TKEKFYIEYPRLSITVRPGGFIYIDDGVLSLKVLSKEDEYTLKCYVNNAHFLTDRKGCNL
PGCEVDLPAVSEKDREDLKFGVEQGIDMVFASFIRTAEQVQEVREALGEKGKDILIISKI
ENHQGVQNIDGIIEASDGIMVARGDLGVEIPAEKVVVAQMILISKCNVAGKPVICATQML
ESMTTNPRPTRAEVSDVANAVFNGADCVMLSGETAKGKYPNEVVQYMARICLEAQSATNQ
AVMFNSIKKMQKIPMSPEEAVCSSAVNSVYEVRAKALLVLSNSGRSARLASKYRPDCPII
CATTRMRTCRQLTITRSVDAVFYDAERYGEDENKEKRVQLGVDCAKKKGYVVPGDLMVVV
HADHKVKGYPNQTRIIYVS*
>TCRU_8562 SRP19 protein, putative
MEVPSTLQNKLAYQTIFPQYLDANLTPAEGRRLTKTQSVENPQLEEIAIVLGQLGYKDFF
IERTLSLPRSQASKKYAIVPKGCVRVAIKRPQSEHYIRMSEFDTQTRGVTVQGIGSKQDL
LRRVAAAIKASGVPRPQPVSVADATGASSKKK*
>TCRU_8563 sjogren s syndrome nuclear autoantigen 1, putative
MASLGSDVQATSNELVSAIEELKERRTEIERSIRCDEEERNRVLAELKALNARLTTIEES
LKQKIGAKSVLDKVIHETSEGFRGIVEASKKLLSNVREGSSGIPRHDGL*
>TCRU_8564 hypothetical protein, conserved
MHLERGGRSQIVIFTGTPPTCRGTALIAEVVMKTESVFLFARRQAENAGNGFGLGCAAHG
GGAIDVPSLALVPAKVAGGGSNGVPGFFGLPEEVGFPQRLGARDATGVSHLRQDTSAAAA
TPSAHRKACRAPDRGGAGSSGGSFRARFFACLLWASGPQQRHLPGMAGCGGRGGRPCLCR
TPARGRASAASSPRARAVRQVSGLSRRVQIIRFTVARTPAIHVSVGRVSSDAFRASASQA
SFLERCSGPKKSRTYALLGAADGAGGPL*
>TCRU_8565 Leishmanolysin, putative
MASRSTVRNVVGVRGRALSVSVVVHSTTAAMAAREHHDCDDIAGMELQEPQRQVVCGHCF
APRWRMAFPSLPPCTLPVSFISRMHRHPHHRASVGLCCRVQLPAHGQSQHGEECCRCAWQ

GVVGERGGALDDCRDGC*
>TCRU_8566 Mucin-like glycoprotein, putative
MVTCRLLCALLVLALCYCPSVCATTEEDNPSTNYDPQEGEGRTNGRQKGTSGSPDLTTKE
SEVESEGGTQDIQGRTTDVISNSEGASGASGEPGKTSDVDQSATNPKLRVPLEKTTTTTA
TTTTTKAPNNMNTEAPTTTTTTTTTEAPSRLREIDGSLSSSAWVCAPLVLAVSVLAYTAL
G*
>TCRU_8567 Mucin-like glycoprotein, putative
MVTCRLLCALLVLALCYCPSVCATTEEDNPSTNYDPQEGEGRTNGRQKGTSGSPDLTTKE
SEVESEGGTQDIQGRTTDVISNSEGASGASGEPGKTSDVDQSATNPKLRVPLEKTTTTTA
TTTTTKAPNNMNTEAPTTTTTTTTTEAPSRLREIDGSLSSSAWVCAPLVLAVSVLAYTAL
G*
>TCRU_8568 Protein of unknown function (DUF2826), putative
MQALRVCVQVPCNNVTTNMLRLGDPHIVVVLTNSAGTAHIDALSGRSEASLRRCREQDVL
AQPRRSWSVTMAQSAVAGGIFTSRMQQRERELLLLLASLLPFVASHADYCLSADHGWHAS
TSDVVCRHFTAPVKHTSRRMLRLWMWCRECSRHYFARLLFTALRQMDVSPPESFTAAPCA
VLLAQYSPVVCRLADSQTPLRWDMQGCGLPLTVLGTAVWMRRPHERMYCGTIKCVKYAES
QQLQ*
>TCRU_8569 hypothetical protein, conserved
MPHDCFYVSLQVHSAVCVFVCVLLGRMSRSKTRKTPRGLPEVHHETIAALNEMEENLRRL
GLRNEKNSATDGPFHEGGVQDYVAPIWKAREEAAKLRHEKEYRQFAAEEQKRENEKMLLY
AKREEALQDVIKKAKELLEKETNAAHDAVSRRAQKMTDRSIRAEELQRQKDLRDRVHRAM
RGSEAEQSFHQQTLPVVDEEMRIMKKQAKATAVYEYCHVIASGLVELAMRVAENVYTIGA
VDDAPVLRFPRDLPALQWRAWVEELIFSKAVSRPMSELLATTPLRELCDPNYKNLSTQKE
EGVSSSQGGSENNGREAFESARDATAYGDGNAVATSAAAEHILKLLVEMQHNYETNLVNH
SVHDAIRLIKKHEKKRLRMELDEIRRQNEAQCPEEVVPGWTHRMPPAGCFVHGDELSGLK
KFAEVACAEVLQEVVQVVPPHKRRISLAAMPDTAKAMAEAESAKSEAEPYRLLTPTMLFR
TQQSFPGQGGGGGGVFGGGGGSNFLTSSPRTLRGLATSVSSAARTKEGRQTEEVTESSQY
IDALSDLLARELAAVHQHNLQLVMRSGATTTEPKVGSRGTPCTLFLVGFPETEAFLRTLN
QKLHNALEFVEHEIIRALRAEEASEGSPPAPLPSRGKNLQKGPTASHDDAAGSRKKGGKQ
MPSTAGKRGAGRAPIPWSEENVPAHPRVFPPLCILGIFLQYDVPSRRRRMQQMSLNPTPP
SAEPKGQKTTANEEEDGESYADWTIEKLHHELIQQDKKMRNVCKTWCTNVSKASVAVESM
MTRVPSAEKQKKRSRSSVTTKPVEALTVNTTTTPNTPSVTVPKVLFFCRKEDITSLPDSF
TSTESITATVSILLNSVLQFITTSGRLVRGQLVPPLRLSDYRFLPAAITQLVELHQRFHC
RWKETIHQYLSSPMSISALHSPKLKATLSTRTDSLTTTPFLHPSPLASAEMGPFFLACPI
CIKEKNVAVKNVVLLETEMHRVFCTFFSDLLQFITQNAFPSSLWVFSRDPSNIVDPNNSS
GVETLSRTLHFLSIDKNYDTSREALYTLLVSGMDQLSAICALLLHCVMDLALTSMGEALA
RLCFWARRHVSVTATLCPETEKPPVLPSATTTPNNANSHVTAKEEVEGAMMKEDGENGED
GKSTATKCGMPYDAVKDSFLASVPRLGFDKVHSMVELLDGRATSFAEFQQELWSYASCLH
QKMLECFWSFINNASAEFNDENTESLTAMASQVTEVLVASLFAFSPLEKGPLNFPDTLAH
STSTSELCSSTITVSIGRAMASVRALRRCCAVASLCAARWIDAMYATALKIPPHGCFPAE
CRPTDIASIFCSPTIVTDEGCAPPPSLAFQLLANRTPALHLSPDEERDCWWETEMEVILQ
IFSIYQKPTLNEAEFTHCAMQVQFNTLWRFLPPRAAAIAERLGIFLPLTPRVAQEEKWGE
EQQQANMEFALFRFANLQCYGELKDSFLREEDASRIFIAAVQAQQQNFPTSLNSLDPTSS
RHASVSNEAERKRWMKKPLLHVREYFISVLLQRLRLDDASGAITCQSPVSGLQEPSTMQL
RQMIKSLPRAVREQGPDSMPVSGPISMEEWKRIRWWPFYEDASVAKAEAFVQRYLLRLLT
VCFGFVNGELCSRPAPFLPDILHIAAGTRGCQATLERYFHALSALDVVRKKKLRHSQESG
LASGSSELRKDGDDAAVLDGPLTAFDFALSVDEAMFFFQRAGETSLRGPCARGLSYGSPK
HLCELRDLMQVGDWSDAEEEAVGNYEDEDDDLLPLATELTLLLEEEGCPALTLTLLGSSH
WGIYITPRLTAIPFNVEMSTVEKGNLDEMMGQMDFPLHCNHGSSKESLVSFL*
>TCRU_8570 WD domain, G-beta repeat, putative
MRTAAAYGLEFQARCIAPFYHPSNGNVESHRFLVGTSCFSGDNKIYLLEHHDETKLLECM
TVWFHEEEVCGLWSSPSLTDPSLFAMSSPTATSVFQVPETLAGELRDVTAFDVVASQVLW
DLDGLQNEVRLTSQDTLRIYALDEGRLGKEVSCFRIDGNTRINCAAVDAHHTSVCMVACE
KLGLYVIDTRKKSPVSIANTAALHGMGLTRSIDFSSCQMNLFVTSGDDGFILWHDMRMGG

TTCAVEKKQHMRAHDHAVPRAILNPFHDELLISCSSDHTLKLWDSSTGGDDNEPAVCLKK
IADFGDSVVDACWSSGAPWVFAGVSYNGKVVVDDVPKEKKMAILLKDG*
>TCRU_8571 protein phosphatase 2C, putative
MPSSSKKNRGKNAVHSNNNNNHSVNHRGGPVKSKKQEESDEFEKVLADLSRATEVAGTKR
AKMLERDAKMRVERVERYKNVIAGRAKEAEMEFDMMLRRKQQKQQFQDLLQQLLAAQRVL
LDAPNTDFQGETVTENPHFDVAVGEMQGWRVNMEDEHLVDVKFPDDEPDSKEGLFCVFDG
HSGKGCAKKCRELISKTARKYWTRVTGESASSTVDFEKVYLEVDGILEKELTDGSGCTAV
TVHVTSDVITCASVGDSRAVLCRNGAAFDLSYDHKPENALERERIESAGGSVSENRVNGQ
LAMSRAMGDFIYKNQKDRDPREQHVIAVPDVISTPREAGDTFVVLACDGIFDVLGNDELV
ACVLSKKQQGKSNLVICEDICRECLAPPAEGGGRSSRAEGTDNMTIMIVDLK*
>TCRU_8572 ATP synthase alpha chain, mitochondrial precursor
MKGVAGKLKGILAEYRKLAADSVGGQQVQTIPMIRGARFVALFNQKQPSYFMSAIVSLYA
CLNGYLDDVKVQYVKFYEYLLVHKDLSIMYGSAKNKFFYMYMHELNYLIRFFTLNSPVLH
DELEEMLKQHTQLFLQHYQSKMNAIKSEKEVKALKNLLYSCKRAV*
>TCRU_8573 Enriched in surface-labeled proteome protein 1
MAPDGTAVTPEVGGRSGEDGERVGETDGQKREKIHAQDKEVNAAALSSSLGNVSQGNNSD
AGTMCGSGLLPSLFLLLGLWVFAAL*
>TCRU_8574 ribosome biogenesis protein TSR3, putative
MGKTKGHPRRDEGQKGWKGAQRGGFCSREPCTNPCSVPLAMWDFEQCDPDACSGRRLYRQ
NALRLLKLREPFHGVVLTPTATEFMSPADVDIIAQFGAAVVDCSWKQLHAVPWRQMKMGA
PRLLPLLIAANPVNYGRPSKLNCAEALAGALAIAGRMEDARCVLSYFSWGDSFFDVNAEL
LEGYSKCANPAEVVAFQGKYVETEAVESAARREIDLNNMDLMDAVPLNVKRGKMRSRNKW
KNEDGRDELEEEEEEEEEEETKKQLAEMETSDDAE*
>TCRU_8575 hypothetical protein, conserved
MAKKHRVKRQKYVEHLLRLEKERDEYLAKRMRSKRSRAERNAEDIFGEAKENLTMGEMKR
ERKESAAKEQAVLSPNEQKEKEAVNASVNMERAENNGDNAALPAARKGLKRINRRY*
>TCRU_8576 Domain of unknown function (DUF4200), putative
MQRGTAPSSNNPFREKSDDLPVPGNEPGNTQTIAEAIKSDDAMMVNELKALSRRAETRNT
ETEKISIRGGVLKSPLVRRIGRGPRTVEIKETHSRETFIAKKREVGLMRLDLANKEAEIR
HLEEEMDRAEKRVRQQQEQLASTEEKFNNFLKHSNLEQDAAVRRAEIESKAKLERLIDIK
KLSAQISHMEQDMRKTEIQLELCKEYKEFMDSITVPQWFYDVLCSLRVNDASEVILREAE
AEYTRRAEELMVAMQKAEARRESHQPVVFAERQKRGGLREERHNDEKNDGSLEEEEGEQV
PIEAQLEKLHQELEAEAQKRQVEATESIKKEVEALSVEEVRAVLDKEYPQERIPMYFTEP
DQILDIFINVEEGNLFLIQNSQELEEELERVAMEYFHEQEEMTTMMRQRHAQMESLATRI
KEAQERLKQLEERLADLENTEDGADAGLEAARGKKDIVSSRRNKAEPVMRQEVLKKLIER
AVTDIFRCITQHSVSPRRPEDGEGLEDKMRSAVRQKPLSARSRSSQAALSPKAKGKKKDR
NISETAPGGGGVEGQSDGEASANMWPVEMLTIIETKIDEYIHYINNPENGIEQSLIMSVI
KMRDKERRHRARVIQLERQSTEREERNKRALQRSQAPVVRRRGKPVMWRSHPPVETVRGK
EVKQGPETEKESDQDDEFFL*
>TCRU_8577 cytosolic coat protein, putative
MRGIPHPALPTLRRHGLCFLLLLLSCVMTPTRADDGAVSIMVPANKEECFVEDIHGVGVK
VFLHYMVTFGGVLDIDAVIYGPDNSHIWDALRETEGRVLFKTRTPGRHRFCFSNKMSTIT
QKVVAFSITVGDSGMERNNGKPNTGPDPLERSLMRIQQGLREVQEVQRYLRGRERVHRAT
TEVANTRVVVWSAIEILIIAFMGAGNVWYLKRIFNKRRVV*
>TCRU_8578 hypothetical protein, conserved
MNCGGVNFPDGTIHPPARSSDADQTGIRQLPPPREGKDDTKSGGTTAPQVNAEPSRQHED
WRRSAAADGPNTVDPSPASNTATNTSETRPEFAFG*
>TCRU_8579 hypothetical protein, conserved
MNCGGVNFPDGTIHPPARSSDADQTGIRQLPPPREGKDDTKSGGTTAPQVNAEPSRQHED
WRRSAAADGPNTVDPSPASNTATNTSETRPEFASNPNEVMVPNASKKRSSFANGPRILVA
SNASGIMSVTYGGREHVAADNTDEVSERNVLLPVPRLSMRIILSAALMCACMAETVSWVL
CAM*
>TCRU_8580 hypothetical protein
MPRCIACATTYVRLGKRIAAHALAASTPRHRWKAAVTPQCTHPNTAASSALPTTIHSGSR

AANTDRKYGSATVLARSCAEAHDILANTPSACISRMEPSPPVTTTATAAAPATTPVIAER
ALAAAGSVADLIVKDPSSTPLQPPDTAAASQRMTIVSSAAMK*
>TCRU_8581 hypothetical protein, conserved
MKRQCALHELRTARVRRHRQKPATDAVAAHRQPRPGRKRRRPPQLQQRTIGQRTGVVVHH
DGGRVGLHTAAKHQPMRGVHLAPRHAQHSALRRNHARTRVQRIVATEHSRVQCDTATDKL
QHGAVHHHRPPTSHHRHEGHAEQNKHGPHEPQARQHKHRCVRRGLRAGKIHKRRRPRGNQ
QGVRHRQHRPRGKRAAQHKRTVQRLHLAHGQLHRPALVAPRRHRTAQRSTAHHVQHGTVQ
QRHVLHDDPHAVPRHPRHVEHRTHAVQHNVAQRHLARAGRHNEHRPQRHALAEEHTRRGA
HSGRQRGSSHRHARLAVPAAAAQAHAHTVPHAGRRRPGRVAVRVPVAGVAPSNVDAPSVA
KTSRCVLLRRRQDTSTSVVARHPQMRPRRKRQAQRHHPRQQRSVAHKAQRAPSSGHSASG
VEHLPRGAVVHVALRQQHRPTIQTHRRIERHRVVLRRQKFAPHKRHSRARHAHSPTHRHR
VLAQQEVAVNKRHHGAAAGRDTTLHRHAQPQRRLHRQPVHVQRSARRQRHAANKQHANSV
AKHSRHMRARNGQHAPSQIHVVQHEARGRVAKAVGAAVRNTRLCNQHRVHHSDARARRKP
ARHHHAAAGARLKPADQHISTLASRRVGPPPNNVQARSAHKQAVHQRHVAHAP*
>TCRU_8582 hypothetical protein, conserved
MQRRRGVLHARDGVGGPRLVLVQLQGRMAWRVVSSLRGARHGCAALAGESRGRRHELRGG
PDADEPHAEHVEDAPLLRGCDVQRRGCCVDVLSQSYAAASPHQHHAHWMHIP*
>TCRU_8583 hypothetical protein, conserved
MYGEHRAAAHTQIRRKGVHHVRPRQDSAVVHVEDAGQAHAKAALHEDRSARFPATHQRRP
RHDKTRRQKPDTVQNKRGAVPGSREARGRRHVLRPVNRRAQR*
>TCRU_8584 hypothetical protein, conserved
MQHNRALHRRHIRHVDKSVRHQARRDLAEAANPQLRAARKYAVAQRHVQRVSERVHQAQV
HRHNDRPAEHHRVEARRRTPAANSHRLRQRHAAHAARRSIATATGPRRRHVERQARLAHA
AGTAAAHAVGERRRQRIKARQRSRTAVARHHAHRGQAGHAVVAAALQHPAAGTVALHRHD
AARDRQPGDKRRASGSAAHNRHGAAAQHHTRQRRHRRRLAHRPHVVQLQPPAGTDRPTVA
VHH*
>TCRU_8585 hypothetical protein, conserved
MVVPLMLDLMDFRRMMCNISVPIRLLVLVQNGREAMLSLCLQELERVYGWSGRLVVSRHP
ENIGYSAAANIGSRLALSLPREEVPFVFVTNSDVMFSPDLLPNLLRDVHEMTRHDAARMD
ELAAEVANEPSEYSPVLRRGLRVLRSTVNDSRLSTSALLPDRIRYASVKEREKAFSKHYG
HFCAYYKSSCFTSVILTRLASGTVGYFDENFYPAYVEDVDYSLRLRLLGFQERNVLCGKL
LHRGSSSIRSSNEMELPDALWYRRVNSLMTNQPYAKMKWNGLKACCDGYKEPYDGMVPRR
RLGEG*
>TCRU_8586 Leishmanolysin/Trans-sialidase of Trypanosoma hydrophobic
C-terminal, putative
MASRSMVRNVTGVRGRALSVVVNSTNAAMAAREHYDCDDIYGMELQDQKGDGSTLESHWS
QRHAKDELMAPIGGAGYYTELTLAAFADLGYFKVSWDMAEPMGWGKKSGCELLQKRCSEL
NLSKYSHMFCNINDGVKRCASDRYSSGWCHSSIVELSKKYPMDSCPITDPALDVRDLEAV
FEKGEYLSARPGDKPSSWCLDTLPTNTTDARYPKETYLSAAMHTELKCFGMQVYLKDPKN
RYVDWFPCTDGTPITWDTPPYDKENVICPEYAEVCTISATGGSVVPVVSWDDEERVWGRT
VRPEFLRQSSPEAPVPVAESIGSGRGTESQDADSAALQSKPLPQGDAEAAVAQHDHQAGS
NTSTPTGSEGEAAPAASGENNNSPTAAVAGAGEFGTTHSEDFFTTEVESSMGEEEQSAPE
EGANPTTLQSRETNGDGDAQPVQESVAPLAGSEGLLPKQSEAPVPENNHSESGSGATQED
RLALLNDANLMLHNWNVDSTARVCVSRVSMLLLLGLCGAVAAL*
>TCRU_8587 Leishmanolysin, putative
MAEANVDKGTEMKEDEIFDSSELVAGIVSAEQHVTQDSVKEGPENGNQSLGAQTGNGISQ
DNGVIMASPASTVRGKEETEGIEEPKSSIEGEETSQLTLPQEGVPPPSEPLTTTLNGNPA
GTLNATPAKGQSSSDDGSAQEEGLKLPTPKAPAAAAEAAAEATTQTKDENPSFADDPSVQ
HVEASQHDMGSRSASGKEEAVPTTVTKTDGPTEVSAESISTSPSASKGASTNDADKGNEE
GIPKRDQAPDGEAKKEAQQGENKEENTNKTANAEAAAITNDAATTGDSDGSTAAFHATSS
PLPLLVVVRLLLRWWPRESQCERGHVAGVCVSRKSVCVCPLAWTLALTSPHEAHTIMCPL
YICMHTHAARWCSLLHDTHRCRPAWLHGRSTVTVSVLFFIALSGRPLSLSLCVCVLLYGS
NESVCALVVPRLGFPSRVCFESLLVLWLNGRIFINHHLFSCVVTFASHFSFQPISLCCLS
KPRNTFPTVTPMVQWLFASPCPAALPLLLMMLTLMCCSSGCFAASLTYHCSFDKAMRVDR

TKSMPVVMKNVPSGTGSASQTYTVIGENGWAPIRINVSTRDLDDASKYCSSDYSYVKNPL
TGHYDCRDDALSSNKRKILIDNVVPAAVKLHADRLLVQPLEGPLVVPSLATGSVCSRFTV
PAEHCSAGAANSDMVLYVAAAPGGVWALRSAALEDGRPVVGVMNIARPFYFADALPPASP
RT*
>TCRU_8588 CYC2-like cyclin, putative
MKTDSVVRFLSLDTLDSDKPLIREYFRHAHHVAIQKLLKHRALSRTLFEIPSLSSQSGIS
ESNFKAERDELSADNNAAFPASDVPARLKLFVLSPSVSEPQRYCQKGVLSETESLQAKHA
VEYEFLIPAISCAVESVIDAHKMWKQRLDKQKEDHQKNSEAEGETTAPSIESAAAVAPNG
HTNGLGEVLDAEVTRDSFNVFDTSTEPSISFSGYVNRIVEYTYVSPSVLLIACLYIDRLL
SRKPSLFLTKLNIFKLFASATRVASKVMDTRTLSNKNFASICGVRNSEMNCLEAHFIRFL
ELDLYVQAEEFYRYVDDLVTTPRSRRPSTKSEVLSAGEFDEEDALMLPVLRRLSMASGNS
SGGSRMSRGEEEKKGDLFPPFLPSRASIASANSQAFTPTKGLTSAAVKSNDYANEVGKKT
KKGDSVAVAGNGVVPVIRVENEEKCFSGPFFSRSTTAANMSMPALPRRASRLPVCSNKSI
SNISIGSNNMSVSRSFETSATRQHRERA*
>TCRU_8589 WD domain, G-beta repeat/PFU (PLAA family ubiquitin
binding), putative
MTDTGEVHFVLRAEGCIHSSDVRHVSCSSGVLLTASRDNTAMILPEQPPNDTITSGLVLV
GHTAFVNFVTFHPFMTLLDGESCIVTGSNDKHVALWNPVTTALEAVLDGHAHGVCCGVVM
LPNSGDIVTGDWGGMCIVFDSTTGGVKQNYTGHKTAVRAVAQLPGTSSVVSASGDKTIHQ
WDVETGATLSVFVGHEDVVQCICAMSATRFATGGNDATIMIWDTETGTTPLRLLKAHDSL
IYALCYCPTRQLLFSVSEDRSLKVWKGGVLDLASSNTQTESVVIQSINHPCVVWSVCFTN
TGDVVTGGSDGVVRMWTADDEMMASVEKLQTLEAAVAAQTIDVKVLTVAGIDTASMLSVA
DLRFRKGTHQGERLIARAEAGTIEVYAWNCGRWDKVGTVVEGPQGQAFTGAAQPREKKYL
NGVPHDYIFDVDVNGKMLKLSYDKGQSIFEAAQNFINENRTLVSQSHREEIQNFILNNVD
PRDIQPGTGTANAVTGAGNHASASAAVGGGGGEPVFSEYAREAAALQQAGVSTTPTWGEA
LRNMETVGASRSDVAFSGYAREGLLLEQEAARRAGAPPATAEEANRSIVRWNSHKRFTSY
NAAGAKKKIDELTGNTRLSALVERVVTAAEGEPNSALLDDIAALYHELPEASRFPALDLL
SHLLAVTVHPFGWLQLLLSDDGNGGDTPNAREFFEECIQNLPHVPDVEALVTTRLFAHVI
AALDKPPPGAKLTADQLALILAMLTKAPQSLLQTKNSNVKTAICALLQNAAVLLAGDPVV
LGKDGASDATRGVMRLLAQLLLFESISSSHTRDLVATVMTLMLSDGSGKDIQTSVVAVEV
GRNTLAHTLRALKAGPEPHCREAAIKLLHCLDDAELQ*
>TCRU_8590 hypothetical protein, conserved
MQYSDVLTEVAERLQAALKVAAQQLHSGRPVECSLALLSSVALEEMSLRWGTIDVLDDHE
GHFELVVGLDDKMLTASFVGLLRRMQEPHEPHTDGGNSAPPIIGPLVKRLSQEGVVPVLL
LLVPAHTGLWSERRRWLKTTVVAHDVMEGKGEHFLPLLLLQELLLTSLLVSCHHKVQEVW
VHRWWVEQQMLKLGGMDLEAFHIHDRSVLFNAADKHPMNYNAWNHRRQLFAFHFQQEEAE
ESVKRSFLLQELDAVVHFFEKHNGDTSAAAYLTFLLEQATAKRGADFDKHNSVALHVWGR
LLVVTTQELRRHYDKGHEAVWMLRLALMRWALRERPPCGWTLQDELDFVSTYASVVTMSG
EDEGNMELDVTWVDVSGAYWWTSYHAVRYGLQLLGMLRM*
>TCRU_8591 hypothetical protein, conserved
MAAPLTAFLLLAGAYYVSRLAPRVTQRVAMAQGGMGATQALHAHQLYRRHEKSFEANMSE
REALLLLGFSEDVADGTGARPSDKEVKEHYYTLMKQLHSDVNGSPYIATKLNEARTVLSR
R*
>TCRU_8592 hypothetical protein, conserved
MKTNGKEMNEVPQSSREDKSWRHAASGSAFPPALPPRHPATAAVRGADELTAPPSLIRDN
AEAKILQHPLITAADYCDRKHLLSHISFLSGQLQRAELLLQNASRAKVSDEELARFDPLL
AQGHIDRLESSLAQVALLREVELERSRALEEEVNRLRLERISLIERVDALDGRMATLEAE
NKQLTNALSSAQLEVERLRLEETSLHRRLTVIDQLQEDGHRYQGLNVIVAPPRGANGRQE
CTNSMKELQMQETLQRLSLLVDMLMEPICIAFDAGVVWITETQLHRASLQLQNVTVPGYS
NDAFGLQTSVEGNSPLGDVDDDTLTPAAMGVESFSEAKLRNELKAARERCRVAEQQRERM
KCLLQEEQKRTEDMAKEQYQQLQQVHEQMVHERQHIMESLVGEVEEKMRNAFRDGRLYEK
RLREEKLQKRRVSAGQFNGAAGFAQQRREGKLPHGASMGLEVEKQFTAGSRSSSGSTGGR
SSGR*
>TCRU_8593 hypothetical protein, conserved

MSTAPRERQFVIAFCSSERKKPFFEKLQRYVEEKESLEREGDDDAHVTFSFVWMQYDPER
NNFSTGTENDADLVLHKVSTLPPKAVGALCRWCAAASRRRRRKRMPPVIIIDPVELTRLV
LQRSLLYKMLDGRLKRPLCPVPHSWLWIRDSASLTPLGLSSFVLSDEEDTEVMGASQSSR
ETWWIVKSDISTGPSFTHQMVIWKGCRPEKSLPEEVLSLLSSCVNSFVLQEFFLHAISVV
IKVYCIGTDVFVKAVPTAPLLRCVLSKMGGPVFVDSQEKFPIDAGWVKEEARWRNYLAVG
GRAYTQCSQIAEQLVRELGLTLFGFDLLLVPKKVSGQCDTPLGASLRDAPLFDEVTGAPS
ALLCSATPVIVDVNYFPGFSGVENVAEHVLDFIKSKALGTPVFKRSSTEGKLFNGNFCC*
>TCRU_8594 Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD, putative
MHGKPLTQKVPLGVPHRGISLTHPSNPVVFLDIKCPKPAAGGEKDGAPHRIMFELFADLA
PTLASNMYGLCVGSSTRLVEQRIQPAGYKGTVMHDALVGQYVIGGDVMGGGGSGFFSAIG
ERQGPLQIPANELEALETTAPSRCQHAEGLYMQYWNHTPGTASAMALKVASTFRIDALER
GADAKMPSDAILIGRMVHRDAEAHERTKRQLLEITRAVFHAKRETVPLLLPTIVLCGEM*
>TCRU_8595 hypothetical protein, conserved
MRGLSTLYCLACEREGCLVNSHFLEVCRVLDTSEECPTEFDFRGNYLGDAGAAAIVRTVA
IMRWVRFIDLRDSGAGAKTVEALVAVADEHPSLRCVDLRGGGNEVFAMSGRRLLAALGRC
TRLVVHVNYDDLPATMARKLQAVKQRNEQLQREEEAAMEAEKRAVMPVLDSLQGKGHEED
LFYLATHDSDGNSLYSEDPNLLHLVDSLNTYMEDYLESYQYVGRVAALLAVDLGAAILPC
IRATAVAVPPSVATSTGRVYPLDVVATIRAVDALLGGLRANPFLLEELIETRGPIFEMYL
NKLRETRGEHESLVTSRLGLCPSYQEKMLLVEMRTLYNRIVAGIVQKSMVDLPSMCHVEE
HLRRVRVEVINRLLEGRERVLPVLMAQVQYFGYNHAKQTTRWAEAYATKKEEPPQKSERM
EGSDEEDEEEPDAVADSSPVTPKRGANMCVEAIFELRELLQDNYTSLRYAVTRPLFEALP
MEIRMFLSDLALRRAASLYTPNIFVLERKEKAQPPGQCAEGWPLTTKVDDPFDIVRIFER
VRSRQDLSEVLCAFEEWYRLRQVECYDVTYVSRQELLSRTRRM*
>TCRU_8596 hypothetical protein, conserved
MSEAGLTAGNAPNGKSQLALAGEIEGSEEHQRVMRATDLLEENMRLKARQTKLQDQLEGL
KHQLLAERSARQGLGAELSDMTERLRRTKDQVDKQKKEYGEVSLRLCAVTAERDDLESKV
SEVWRNMAAMEETLRVKELENKKLREALDNERKEREAQEVLMKAMVSQITALERQVGVSE
GAEELHRRLGEDALCRVGKEVQRVARRLERVADMYSASSLNWDLDQKPLLLLADDDDIDR
GVNIHKGDDDDDDDDDDNDVAVAVAGDGLNKSDVEKMTPNDSLSKRKKRLLGPIYQALRH
LERQLQMQHEEKRTTQNERRVLESHIAALKDELHHLGNDGDDVRERLLRSEAQRAQVTET
LQKTRQAWEHEAAQVTETRCKAASLLHCMDDWCVIEQRIYDMTEELRQLRSAVEEGHRTH
KAYVIQKEGEIDAMMDLHQREANIQKNQLEQARHECERFKRAVASAVMDSSPVSADGAPA
GMQREHDAFRVKYRELLRYMEEELEPLIAEQAKALQEERKRADELQRANGALRLEMKLMN
TAPGDGGGRLSLFEALVLTLRVLSGAMADMREMSQQRRALTRYILAYEHMFGALNLCRES
TWPRSVLRFRRAVVAVLAAQRLIAFRKAPWCSGGVIPSVERGTARIRLPPETSCLVIGGL
IRLPPVGSDDTAEEFLREEAGTKREEKNAVTFVAERDLRLPAINNMASTNSLGEVTVQGQ
ALRGFMDSLLAFVTVPSAIWPLRNVKEPLWRRLATGLRSLRRVSRQDGGQYALEKPRLLL
HLPPRVPLRSEWGEAPPILSQAASNTQWSTIYNREGSHALVQPTARELSDALRSAQETDG
ENASTAYPAPQPTAYHTEEALSLEEAIRQSLLRDANVSSDTQEIQSGSGFASEVLNVIRA
LDQRVVGALERQAKLAERRPHR*
>TCRU_8597 hypothetical protein, conserved
MRSNGAGHLGNDTFMAVIRDDTDNMFLVTKKLVEEPVTLYPLPRRVRFNPRSDIASMDAE
MSSEAPPFTRMKERDAATPHSQLDSPQEEVRCSFHTSADGKLVALISTGRLNHYLIDVLS
ARVCEFKTTAVVTGVAWHPTSPRRLMLLLATGTLLLLFAGTTVLGVVFQDQQKVHLSEVV
LDYKYYIFNGDNVAPTDQLEDLRGRKRESQMSKTTPKAVEHKAAALIKNREASPPAATRS
NSSSSSSESAAQGSKISFEDNNGEEQKGEQWKEEDNIRGKDVITDNETVTETPADAALAM
EGDKDRNSLIGMCVVPPSLSLPVMLLVLNRGGDVFSIKIDERGVPTALVKEFDGCVETLV
GGDEEHQQHRETASSPCVHYLLRGGISGVGYAEDPLAIGTTLLDEDVGRHVVFVIYSSGV
LRGGWFSEPDLLCRDLMRRQMDFAIRLDAAFSPSLSLPCFPSVAHFVGVHSCRNATLIRY
NESAYLCVWPTWSRKAAGWVYREEDQEGCLRVPVASQSAVMPEPVVLRLPYNVNGKSVAV
GANDILIFPETTAAVPLEGNACPRLKAVIAKIANLLLAAIYARSEKYNLTFDTVTTATHE
KKNKKKQSPERECLERLLELTAESYRRWLCGYPHEAKDSINVELAKGVQAAHGDFLARQN
ALEKREEELTTRVQRLLQKQKELSKGIVHSQGIIRDAVLHRFGVDALYGANDALGKTHKL

LNELESLAAVRGKEKRKAETSLLV*
>TCRU_8598 STOP axonemal protein
MTQLHSIASLDYGDGRTCVCRICECGKHRCTDVKIPFFGETTYRDEYVPKSTERDGLRRE
RAAVFPGKAVPGHFKTTKQEAWEPLEGKIVRPAESFKPRPAIGDPLPFIGTTTHRNDFPG
HMPDHERVRYKQEPLPKMKGFYETTNGAMQGPIRKCLDSGDMPKPPKSFRGDESLGQALP
FDAIATYTADYPPKQPFFAPKDRQALERATLPDNRDFETTHSVSYKVPPHSLRHICPAAL
VPPRAPSVDGHLKLSVYEIPSGDIVE*
>TCRU_8599 hypothetical protein, conserved
MVRYGGPRFEFFFTHQFLNNEEAIRKEDAQRVAFILRRREQQKAAQAECEAKKRREEEEQ
QRAAVEAEEARREAERRLESKRRRRSEKQRRLKELSTPVVHGGPLYSRGTYGRVIYPSAR
GVPLPHGRAGAAYMPGVDRHRIVPPPPAADAHPPWISSGTAWMLKRAEEKEEKRYFLAPS
KRDPENLRETKQTIDAIERHHTSQFNKDGTGAQEESAAADALQLPAVGVDVPRKSKRPPS
VFSHASSNEPIRALGTQHMETISTKEDVQNHLSRYGGILSPPRPAARPPTPFENMKASEL
TVRLVRMQQRLGR*
>TCRU_WW domain containing protein, putative Phosphorylated CTD
interacting factor.1
MKRQCVDGALDAAHPGLCFHREVLTYLRWSAIRRDFLEALQASPHLRFIEPKKLWRHSQE
ALGKWVLSQLARDTRGDRDAASSVSFFPTRAMLSSGTYDEQLIRDVSLKCESSGTPTVVA
KIKQLIASFNLSKRCEDAAAEVLQELESASPSIYCTPSLRIIDAAEVGNRTGSQRRVHGA
IAEISVRQPKHARHGCPPVSIPLAAYKKLEMCYKHFAEKTDGERYPRLDYGNRFLLRAAT
IALRYEGCLATGSLQLCADISLKQHLHAAGYHVMDLCASPINAYMGSPKTGSYNNNEDSS
LEGEKVPNHFCSAFPDTDCYFGSLGSALKFDVEAAYNSPVVNPEKKPLLLTLDVPYDEDL
CERLFSKLVNDMQQAASKMMIANEKQLPPPFVVDYVLVLPLWWDLPMERKKLLFTTSGGP
PLSSDEEEASMDAIFKERSAVLNNGYTVPYEWPQRLAKTAGKSWVCFDGIFVGDSYNYFC
TITNKWIPGVTATEVIGLAQPRATADGGQLLETLFASFYGTQQA*
>TCRU_8601 phosphatidylinositol 3-kinase, putative
MATNEGNVVQALQEQKHYDTFHWVLPSSEFIAANDITDYFMIYLRAIGGWCMRRDAYNYE
DEEKGGRGRETLEEENGKINMDMDPIGETQKQNGCGGVETLFVTLQMLHMEQPVTPMLQS
SHTRGDACIFDEWVIFPISVRDMPLDAVVRCCVYSRHGLVGCTTFHPFTASGRLKAGSRR
YKIHAEGSAGPQKKETPRWELLARDLHDGLLQPVPWMDKIVERRLAEMREVQEYEGSTRI
AAGNASPTLSLLFPQVRSRVPVFLLSVPLNMVPTTLPTTPLAATPTRPYLDICIGDENLC
EAKAHALSKSLFLISDADADVHPGLLERRQLQEIMRKPLIHLEGLKVDDEMLLWRFRFFL
ARDPAYFLLFMRCVNWKNEAEQQEALKVMQQWKPISFSQALVCLSFYFREVVHVRRYAIS
LMDRKSDEHILRFLLQLVQGVRYDVREELEQFLLRRALGCWELCSTLFWYVYVETLLEKS
AETESRRGDERERYTVFLQRLVGKLEEVKPNFLQRIRRQEKLTGVLRNLYRTILRDPRDR
LKRMEFATSLIDSKKCGIHELFSSPSEPRGNKAADSATPVTLPTHPCFVVENITSNGFHM
FKSAKMPMKVPFLVQPECSNNSSMCRTASHAAPENAVASGPCFVPLALPSPDVGVIFKSG
DDVRQDQLVVQLVQLIDGMLRKDGLDLCLTPYRVMATGTTEGLVEIVPDVVTFQSVQRDI
AGYIRSHNPTNKAYDAAICRFTKSCAGYCVLTFILGIGDRHLENILLTHDGRLLHIDFGY
ILGNDPKPFPPPMKINKEMVETLGGPQSERYAEFKSYCCSSYNIIRKHAPLILSMLLLMV
DASIPQISGDGKLDPRVNLLKVQEKLRLDLSNSQAAQYIQNVIADSVGSIFTNLWDVIHV
AAQATRH*
>TCRU_8602 tubulin folding cofactor D, putative
MKQEHEEMDPVATAAMLPEADDVDGTSPAEGAEGENDDDWGPAFFEEEDECVSLLVRLQE
ALQLQDDRDATLPTVAEDPNGVAAALYRLDRIIARYQESPHLLHGYLEVLLGPLVATLQD
LLPAATDIWRMEDGIERPEGDNAVSAQEEPDYTLGANYDEYDVDAAKTAIHHVSRAIYVI
VKTAGEKCCTSYFSNDVKLYEDVFYALRLWQRSAKYRREWEVRYCLLLWLSNLVLVPFSL
SIIDSTDRGGSLSDAVLETAMAFLSDTSKCREGAALLVARLLTRPDGEAHRRRFFAYARE
AITDISKSSFPLHGVLLALAKTLKCGQRRELAPYAPGLIPIVAGVLESRSSDALVCKAAV
KVEQRLALVLLRGRSAPWKYQRHVTSLDKNLAVSTPLDVAADVTSSIGAHRTVDNGNHNN
NNNSNNNGETDVENENDECAVENGEGLEEAIGLMLVNLSHKDTVVRWSAAKGIGRICERL
PRVMAEDVIVAVLDVFTNEHSDSSWHGGLLAVAELCRRSILHPQHLPTMLPRITQGLAFD
LIKGTYSVGSHVRDAACYACWSIARAYDASDIEGHVHKLSTSLVVTSLFDREVHVRRAAA
AAFQECVGRLGNFPDGIRLVTTMDFFSLASLQNAYLHVAPLVAENESYRERMLEELVANK

IMHWDRRVRCCAARALGLLATSEVNTAVCEIVPELLRRVTENSVATRHGAILGLAEMIEA
LDASVWPKNVLSQFASLTPRVDAARLFRSRGGEYVRQACCRLLAALAHRRLNLPETIEVQ
KVGGAVARAKTLGKLQEFFEDTWKQILEWLQFDAVDAYESFAATYYTEFIAPFHQKVLER
MLDGSGEERNPMERRGNLLAMGALPWSVICAVPSSTTTEEEEREEGRRAYFLMLLHAAMK
GTRPEKRKELQDAESRRNAVRSLRKILLRIPPGSLQLTSELYECVVQCILNALDDYAADR
RGDVGSFVRLEAIDALPVVVQYGMQCGLCSPLLTLRAAQGLLKQSMEKLDRLRGRAVLSL
SRLAPFLADIADEEKASAISVLCNVLSENKTAEWSLPQVTFMTLACPLLQTDLFAPCVVE
GLAVSAGSLSLHIMQPAVNAFLHGFRVSLENRVFLSHALIEVAAKYAHNERVVVPLCVTI
NRLMTLGVFEESCHMDVVEILRNELKHYATSIHVLLPLVGVLGDLCRSTVPEAREAAWGL
SLVMIASRYPKVRAKMATDMYTALLVFTSAEASDGCAKAMQHLSATQWDANEVAKVRGAR
DVLYCMLNISPPSKLDEGDEVQQQKKKKDRMVAGSYLYLVQEAGY*
>TCRU_8603 BolA-like protein, putative
MLRASRLWKTIRAADIEAKIRASDILQPLQDVKVVDASGGCGSFFNITVVSHAFRGKPLV
QQHRLVNEALKGEIPLIHGFSLTTKVE*
>TCRU_8604 Mucin-like glycoprotein, putative
MMMTCRLLCALLVLALCCCPSVCAKDTELVPNSGSNGNISSLPSHAPATNSASVAPGISN
KNATPGDPADVGPSPSQREAVSQVTAPSGPPSNGLGAEPGKVGGKGSESKDTIDVQQGED
SDDKAGTEIDTNTSADQKDKNARVAAKTTTTTTTTKAPTTTTTTAPETTQAPTTTTTTTT
TTTTTTEAPTTTTTRAPSRLREMDGSLSSSAWVFAPLLLAASALAYTTVG*
>TCRU_8605 hypothetical protein, conserved
MAMMMNGRVLLVCALCVLWCGASGADASNLDNDAVGGCMASWVLNTNKSYTPSGCDKTAL
TLPLRSVLSITAVEASTDPLVTGTAENKSDLAPNSCADFGCAGFPPGRGDEGGGDRDDGA
GGPVGVGGASGSQARGSNASGGGGGGSNGGSKARVDGSLKSPASDVKSPSPVLGDGGSSP
GAPAGSVGSDGSKVFIFGSFSSGGRSQPDVDSPGGDASLSASVAGGNSPPSITDESDALE
KTGAAASTKGRKPQEAGEQSEANRARNELPKLSAPAESTPEAQEDSPNKQEKPKNEAAGR
AATGKEKRRIDAEAQGPSTVMSTASASNGRRTTNSSGSSGRRKPNSTNRLAKFDRRKDKN
AAVTKQKGA*
>TCRU_8606 hypothetical protein, conserved
MWSQWPEVFHTPWWKHSSRHHAGQRRHVSVVAACLPIAGCRPPSLQCGIADGGPSLCKQV
EVQWEKRSARCAVTSGNETLRPLIRVACAGTSESTQSMPLEVVARPSPDVVDGEQPSRSS
WCEFSSSAIGAAGPRRRMSLAKCET*
>TCRU_8607 hypothetical protein
MAKPKLPTLRQKLKRVTVLLIPFIVATTVLTLRFDTAADDGAPEPNNLRHSRAPAADDAA
LAYIPRSVVDTWSRREYLVVLGIPSTDVEERRTRRNLQRTTCWRFPGVATRANDFTGAML
VLHVLGRHPSHGYDYSTALLEEVAQWDDAVALPMNGGRVATNKTVGQYGCLGDEVNVGIG
RKTYMWFDLAPRLFPTARCITKGDSPGSAGRLNVVPGSSTLCKRGS*
>TCRU_8608 hypothetical protein, conserved
MARGCRRRVTWEQRGRRLSGHSQPCGSTHDQNSRRRKACVWMPSSPRPLRKEGRSCCTFR
GHTSGKKRATALCLWVTDSNRTFSFGPVAVDNAADWMLASTLLHSDGNLHLLQGRGNGEG
RAISLARLTEELSAIESVPSAWVQKDAFFSSLSTPTACLVAVLSDAANNDTWNDEYLCLN
AMVEERSEGLR*
>TCRU_8609 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MGLSYTADKTWETAFEGKTTTRSSTWEPKEEYQVALMLQGKKASVYIDGTFLRQEEVPLT
GEAPLELVRFCFGACGEDAGRKTKVTVKNVFLYNRPLNSTEINALKDKAHTSNGPGEALA
GWAALEGAAAREHAAVVGLTSAGSGLLPLLLLLGLWGFAAA*
>TCRU_8610 hypothetical protein, conserved
MASYDGRCALGTHPHTLPCLSVGVIAAGAWSTAAAAGVLERDEVPKEQKKPHPLGEITMA
DESFFYGLLSAFFRSAACRCLTGCLHSTPFEALFCFIQCDVTIIMAAPSLNGFECENTND
GRESDEDYGDDLHREVDYLRVLVHESQEGLNAVLTIPGLAEPLAFALSPAVISAPCVEAD
PFAVEFTQQLSSGCAAIPALALSHVFQRCLACDLMSVLSRPPPPVFCWCPIRNTLLCGGY
LLAWPSMHVTMLNGCVFCLAGTRETSVCADASAKVFVDGSGRK*
>TCRU_8611 hypothetical protein, conserved
MAMMMTGRELLVCALCVLWCGAAMVVVAEVVNSSSEPAVEKSIIAPDPQKGNDLREITDV

EGPKPLEDDGIRDSATLPERETCKNDLTKSPMCNKGSEVVIDSPSVLVGPNEHHEAQDRG
SPAPSEVDKTREKKEVQERPQDVETLPPDPATVKEPKITMPAEHSSSPSPPNATVTASSA
EIPGGGGGTVQRDNMPNTSNDNDGSKSRTAQPDSASGNTPVSADEDTSSNGGAPQVNTAA
DTDSAGSTTALSTTNTKKENNGDSGGSSLAASPAVWNNTDTTTTTTTHDASKYKKDGVKL
PTEDLEQNASKTNPDADSGTTETAAANSEVPTAANNATNITSNTETTADSDSSTAVSHTT
SPLLLLLLVACAAAAVVAA*
>TCRU_8612 hypothetical protein, conserved
MQDTSREGKAHESYDCPSRTSFGSLGCHGAFHKTGCVETRCSNRGDIRFGPTRDLAVGEA
RRPVRPSPEYCLIFGEVHHSADPGVVTGRIDVKGEAAEWQEPWLRTEERFFHDFNHNHAA
TIKRRATRTRLATPQDEHAIPLQQVNVPVLNLEWIKSRLNPATLERVVQVWGLVGRPFPL
YPCPVSARTLTEDSSS*
>TCRU_8613 hypothetical protein, conserved
MGYKASPEILQIITSAIAGVTTVVHPLWAAPPLVRVDVWIDNIRIAGSKSGATLWEAKCF
VMRMAVTPRWGGSRIGRYALHLPGVQFDHTHRAVSLSDKFVRSVRAMPALNSLTIAEMEV
MASRFLYAAAILGTRLCEYYFFITAVRRRLSALNRGIVLETSRRKFRRQRLVWARDCDTP
SRTIASESSSPPRKHRPPSSRTHRSMDGEPFLFQTPATLKLPEGNGRGNLFLSCRPRHAR
YAWPYRPFPPSCHPLWTFGWTTLRCKERRIKADQNDTP*
>TCRU_8614 hypothetical protein, conserved
MPELEAMPSYLPDTVVLQLHRDDGEAEFVDYMDANSLTFVALGDAERPALCGIDATAQLH
HEGAQRAVVSAAGIVSSICRRRLCIPFGNSELSQFLRRAYNMEKGNRNNSLTGSTETALL
AHAFSDAVWAEESFHCLSMTRRVGNILGSTGIGSTTRDLAIGKWRPDQGIMELRDELMIA
RTVYDCRHCGYESNRPFQAWRRKR*
>TCRU_8615 hypothetical protein, conserved
MTKELERRGRATLDEIERTLEAKKRESSALQADRESRIWEYEQTLEKIRTRKQTEESASE
RLRQAMQQPEQELSLRQSAIETREQQLEMVQLDGARGREAVMRERHSIEAVRRTVLEERR
RQRRQWIHQIKEMNAKFPEEVRPLAEERKKKRERATAKEDVAERALAADVKMIEEYLPKL
ISLEDIPVSPEETDIIRRQFDEVFTQEEQTYLAGAEEEKAREERLGRGLEVYIDSVRLMP
TWQRKMENCMMPMQRNTTSVLLWIRC*
>TCRU_8616 Protein of unknown function (DUF3682), putative
MPDGCNKTAITVPLRSVLPITAVEASDGKGGSADGTKNDSHSSGTSDAGANGSAGASPAD
GVPAAAVPGASGTGSPGAGGGGGSGTAAGGQGAGSVSSGPSAAPGGGGGVPSGGGGTSTG
GTQNNTNSSENLESGAFPGGGDSGGGSGGSSGSGGSSGTPTGDQGTGDVSSSGGGGGGGG
ASPTGGQGTGGTSAAVPGATVVDSSAGSSGGEAGPSGTNSSNTTGESSTGDQTSAAASHN
SSLPEGPARTTSGTGHTGKRRGRNAAAK*
>TCRU_8617 hypothetical protein, conserved
MAMMMAGRVLLVCALCVLWCVAGGGFGEEDTQDEFCNNTYLGALTLIANETDKELAEKYC
KNTDYETNCVNTLKKNIAVALENEKKMKDNAAEREPSVAHGAGSSVGSPTTTSSTAAGAD
NVGVSSPLPLSLKVEGGVDTNVHSQAGGASRQPHSDDGRSEAERSHRLEAEGSNQHSVGL
QGKTIHNKDEETPQTGVKSTEAREDTDGAPAPSQDPPNTTESHEDKSRRVAAPDTTPALN
TSSGSNQEQKSQSSSPSGSETTGSSDNEGTEKNSQNAQISDAQLKDEEQHHESTAGNEEG
TTVESAAVQSNTTKPADSDGSTAVSHTASPLLLLLLLLVRLRWWPRESECERAVHRPHTH
SSFSLSVCVPLHGLSPSPHPTRHTHNVPIVYMHAHPCRPVGALFCTTRTAAVLPGCMGGA
P*
>TCRU_8618 hypothetical protein, conserved
MPRGMEAPRLCPLGSAVPQYCWDRVCALSWQQENSLVRHTVRVARAAIPSAVRTLCACVS
PGGCDVDGSFTPYALEFTIRHCLPCLAPGPGGALNVFLCHLAPAARSSHRTMINTSLADG
SLRGSCETGTPLPSANKGRTHAARRELLANPAALCPARGERRTGPPPPVSEEAARGLSES
VSTPRRAVAVWGCVGGKVMVSLTLLRLRGFLSVAVL*
>TCRU_8619 hypothetical protein, conserved
MQRRRGVLHARDGVGGPRLVLVQLQGRMAWRVVSSLRGARHCCAARSGESRRRRHELRDG
PGADGPRAEHVEDAPLLRGCDIQRRGCRVDILPQQHAAASPHQHHAHWVHIS*
>TCRU_8620 hypothetical protein, conserved
MEQPRDRKTVPADRDVCVRWKHTLRAEQRVNKSVAGDDDVQRPHSGVHVAQQQQHGAVPP
RAAIERDFHHVARHPPNQHRQAHAAPAERHVAVAQPRQPAAHCLRNLGVHHVADALTNRR

WRWRWRWRWRRRWWRASRHRRWDAHIAVPSSSAPALAAADRRRQRSKAVAVLRALTARSS
RRHVGDAVQRQFGRRRHLPSRDRQAPSNEPVAGVSPR*
>TCRU_8621 Protein of unknown function (DUF3676)/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
METATETVDSEHQVQQSTELSAENDDVRSTGTETTGAEESLSLEAGERNSERTMGSDSSL
TPSRSDAEPTSAENTDDVFRTEGDEVSSENGEEFPQTVDTKPANTSTAAGGEGIPSTKGT
ARHSDNDTFSGEIAELLSMGLDRDSTVHGCVFRVWLLLLLGLWGAAALC*
>TCRU_8622 hypothetical protein, conserved
MKRGSNLVALSSITFGHPTSSQLVRWKSSSPAEELQRRVGQLVGKGHVDEVAQEVCVGLE
NSVFSMKAFASALFLCEKRHKESIGIELVRKVQASQMVESWTDESVLAVILRLQCAVGDV
PAATQMFSFMVSKKLLRLRSVSVFLAFWCGRGDRRMAFAVYEEALRQGIELRAAEYVELG
RLCVAVGEPVSTLHFMLREMQEHVLTVPEAMVTDVICPWTQAAGIRMAEVQFPHDDATRE
PGTCSFCGCVLRGHRFTAAQKERLLSDVMNVVMMAPRGNPTRVKVAFEAWRRFISTHGQR
IDVLIDGANLGYYGLSSWYEEAKRALLLARGKRAEEIKPKDLKWTKHGPVDVTVNFHLID
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RTLLHWVMPGSYAQCIQELKPLTWHIPVTPQEDTKSCAEEGEREKAIGQEAQEEEGNEDK
DADDGVVVPPRPANRWVCVG*
>TCRU_8623 hypothetical protein, conserved
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PSDCFGHLVAAALSSRSKENPVTGDELKKARLNPYLVRMIIDSRCLDLEDKTVHSEIQRC
VDTVISSEAGRVSLSFYEYLPSLLKLNFVRLSPERYAVMKDSGFEFLKLLCEYPHVLPPG
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VYGIGYAAHLIGMIFLMRGKARNAVYGKMICAFPSPHLLVVPVVPLYNLVSIFTYVRYRK
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ASAILTFLVSILRMLRALAMYDSINCFGFACFGYQRERIIEKYSAFVRMIHVLCLFLFEL
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R*
>TCRU_8624 phosphoribosylpyrophosphate synthetase, putative
MKLSPGNCAVPRGQRVEAGESFFYCERSKPKVETSYRIRLISGTSNAALSESVAKSLNIS
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RINNCEALSELVVSDSIAQNINSQKCSKLTVLTIAPLLGRAIDNLHQEASLSSLFSKSGA
SK*
>TCRU_8625 hypothetical protein, conserved
MPGRTRSQQCCGRCVCGCGCCRLLCAAHDAREEEKRRRDVQRAQNKWHPLDVPKMGQAAR
RFMNEEQRNTRDAAITLRMRFMY*
>TCRU_8626 hypothetical protein
MRRLLEDALSSGDVVQLEKAIVSAQNTALASLKQRRESNYLNDLMLRCRKALVQHLEECG
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GSLRRDEDGGATGTICQRMIEHEEESGRCVLIEQEHAQRVLCLKSVMDAMALLLSHTDRQ
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SRADQRPTAVGTSAAAGTANNISDFILARGTVSSVSQEFHVVVSPGVWAKLSAMMEEEEI
CRHDVEGSENFERNVFLLPMAARSVLLSRVFPRRKL*
>TCRU_8627 Phosphate transport (Pho88), putative
MNPLLPVILLLVNWSIDSTDPEVRQTVSQLFILVHVALFAVVIYLFVRIWLRNDTRALQV
KTAHSNELQQMTVAGYDFYEWRSLFFTKLLLVVAVGHFVASRWGTPFPLLLQCTTNPFTV
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S*
>TCRU_8628 ribosome assembly protein RRB1, putative
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DDEQEEEDGSVDEGLDGMMEEEIIDEGEDEDEDYAEFQREADAVTKGLRRITFDDSALQQ
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HPKEAHWHAQIPGMVITTDYSGLHLFRPMNWRSLMK*
>TCRU_8629 vesicular protein trafficking mediator, putative
MSSDKIFDIIFNMKFTMKQMNKSANAAERASEKEKLLVKKALEKGNPEAARIYAQNAIRK
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>TCRU_8630 hypothetical protein
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>TCRU_8632 retrotransposon hot spot protein, RHS3, putative
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YCLYSWWANSGQTVCPLCRSPWVSS*
>TCRU_8634 ubiquitin-protein ligase, putative
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>TCRU_8636 40S ribosomal protein S2, putative
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GARVGKEVSLAIRASMIAAKLNVVPIRRGYWGNKIGEPHTIPMKVTGKCGSVSVRLIPAP
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EVSRDPTDEHSDFLTMGSKMIAA*
>TCRU_8637 NADH-dependent fumarate reductase
RVIVVGGGLAGLSAAIEATACGAQVILLEKEPKVGGNSAKATSGINGWGTRAQALDDIQD
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RQHLNELKNISSFEIAWSEVRADSDRVEKFLHDFSSSAPDGAPGGGPEEQYTHLLKTVFR
HTVRNMTSKEGFLWIEKRMCALPYPMVLDGKVVERVEREVREIKERMNKLDLAWRAANIT
ENLEDINSTMMQIRESLSESEEIINASREAHKIVLELVLPLIPNTRQSVANQLREINAKI
VGNDESTALLRQQLKEWTRRKSILKTSNEKIMNVELELRRAVYSNSLLSERDFIFSLALI
ARVRLGQNTGIEIVDVVTGLGTCVSLTAAQEAELKETLSYPLGITLLTVGSVGWVMLEAR
AFWLKRVRKSLVSLQRPPDVGGHPRRQVSFVRLCLRVNLLLEAMVPLVVPSFLLYSAVNK
KKGEVSLYSILLFSRPAQRLAMFGVAVAFCILSIIVSSLVGALYRYA
>TCRU_8640 hypothetical protein, conserved
MAMRSPIGGMKRRPFRGAPAPRRSALFSSSSLLQLEALLVFGEPHAIVAAFLQSAQRENC
VALQQVFSCSVSTDVLLCACVAMVTPSGLWPPFVAQRLKMPREGRDADLTSTSWRAFAFA
LVRCIYSVQSHNGGISALGLLCATCLAPSLKLGERLVGLLSDPAVNLSRIRANTLSKSNF
TAADVATAFATCCSMNNVSPEKSDAAWMRLWSEMQARPDDELSPAWVRCHELHLLRLLGA
GRRQEIEAVIRKIIETPLVRCISDATLSELFLLESLSPMMQGKIVAALLEVSRVKSEAAS
AFFHVLSPFERGRRLPSVTQSSSLFAKVLHFLVLQAREEPCFKNHTRVLHDIQGLCRVAN

SYALAASLVPNDSPLASLMTASLDKQRARLMATFVEAVTEVTELACGLTHRIDGNRHDDC
VEATLRGCVDVLTGLLSLCSNRREKLPQRRAEPEWRKRLHRDAAVRSHKYELLCCELPHG
FLSRCLSTLLWNGFVCTGCDLGSCLVSADFVDLHFYTLALLGSLYHATLVAPQQSDISPM
IHSLYRRRREVFGEDVSALKQYVSAANSSGPGLVQCETAVVQYGLAEAEATLALLHARST
VAAGGSIVVDGSFGVWLRKASSTV
>TCRU_8641 Protein of unknown function DUF72, putative
GWGMPFHTPLLAYVPGCPAIHIGISSLSGVPGRDRRMKTLFAQYAKKFNSLEHCYTFHNM
GEETMWKNWRDMCASQLVASSSHSPASLGCVQTSDNGNQKSPPFIFSIKANQYLTHTRML
AIDDKSEEHIMHFFVNRCSILGRHLGPVLLQLPPQFQKNHVNMERIEAVAARIPKAFSVA
VEFRHRSWYDEGVYALLRRLGWALVVAHHHDDPTASVHVDTGVDFMYVRLHGPIGLHIGD
YGPVILSQWAERVVDYICGGVVSAAAADQSQPMAVNAHGREVYFFFNNSDSHVGGTTSST
VDATFLAQRVGELLA
>TCRU_8642 hypothetical protein, conserved
HDTHARILTEHQELLESSISEQLGPLAGFLVHALNRRGPLTLKEVADAVKREPFNNPLHT
GDATKHVGCPLAVPVTAGDMATDAAIKEIMARLVLHRVVCYDTENHVYSVALGYGLFLRT
LFPLVMQFFQRRYGETGVTLLMVFYQLATVPRDAAVRLAMERRPALSEALRHCAHEMERL
GFIEYFSAGGSAEAAATTTTHSTGLSPDPCRLHVGNILAEMLHDAIQQQLLAERFADGGV
AAAVMEAFTTATRTRRLVERSHGFPPVHPRTSASLPLRVLLREVPMAEGVVVEAVSRMCR
PDGDSLLSNDGTATVAIEGPYRFRYDAAIEAMQRDCCERLVFARHGVLGVRLMKLLLQHH
NMEDRMLAEEAIATLSRTREVLHAMLRDGYVRQQEVPKSGVMADRQPKNSVFLWGCSMEK
DLLPAVSMQVAKALRIALARLSVERQTATSKVASFTTTTGSNNNNNHHNNCCAASSTAAT
SVAAGLSLTAGIRGDTGEVIAETLRCQRAVAALESSVSALMGSMLVLDFY*
>TCRU_8643 hypothetical protein, conserved
PQLRLQCRRYHAFQFAGFHGWKIPYNGKLRVTKEELEGTRYFTQRPKEKWDYHRVDENIN
SSSEFRQTHDRPAFEQGMREDNSTTEHGDMHTPKKYRLYEYFDEYTKPGVNKKVAACYAV
KEQWDAEEFYYPGEAWQKNRPGFRSVPKELLNRQTWYHWSDTITKWDEIQPTMRTRSWNP
DWPPPGYTVPKLQCKKEFVFGVEEPGLVSEVERYNWFRSWSDNNMRTGWKDVWLFGILFG
TMYYLARNALDIVAMRAMMSNMYYPGRQFVRPFGVPKDWEKGVFWWQRPLEEFPNQGEVW
YMNEARFKYINYIKKRDAQERLLAEAE
>TCRU_8644 predicted HORMA domain protein
MTSTATEVTQVQSLAAIRNFIRVAVSCVTYLRGLCNDESYQPRQFLGLQLKQLVRSSPEA
DVISQWMEDGAFDALNKGYLKALSLCIYTPNFTELLESYSFSVSYSPDGQRASLRFAGNS
QGDGTMCPLTAATTAMARSRRKRHTRQEVQQALAGIITKLVEVVEGLPPLLCERVLAMQL
TYYEDVTPPTYEPPCFSPASAHLVGLHQQEKKQSANIASLDTGHHMMSITIRHRFFDRLL
SHSSMVAGNSTMTTSTVDTTFSGTEGEAALKQVQDVNAARKQTYSVKDSSRDCPEDQTTN
SLSSSKDLAFLVFTCFVLTKSPAVYRGRVSMGEIADYLRVSYPLEITLEMAQQMM
>TCRU_8645 hypothetical protein, conserved
VVSVFLTRLYNSELVNKGAGRMAPPQLLVYHNQTNTRSGAEVRYFNRIVSLDNVALRRAT
QETPVDEILLLVFNDWDHNVDKFISELHRLSTLLNPLEESVEDDIPDAMINSLKEEPVDP
TTLVSPRPDAFGSALYLDEIRGTKKDEDFAGEWSSSFLFLWPKSTSSSEPLQVIAAIRRA
DFDGSDFLGVKTFGLVLHSPGLFFCSKGMSHVVRYNGPASMNEMSNFITVNTLSHLQLKS
AYELRSVLSRFDVLTLIVCKGEGVKEKVSTSPLREILFNNELPTRFGLRAVLPTFFLQVE
EFEGFDGFNWEELNVVSLQRMEPRSLQFMKSLYMNEFPGDFIKKLELLPTSNNTRLIVLK
RDELTSEGKRGASLADFSARIICFPGPSKKTDHVMWAKTVGARLIDFVENNAMKRFVPVR
VNGKNLQEIYEQHFHVSLMDRAARTRNQPLSKEGDFKTTAPSNSNSKEYKSQLLVLVLLP
PTKMNGGITCEQAVFHAAHLSSQKDGIQFATVSADDSPDLVEELRFSVWRHSNLAAAAFC
EVYVFHPDSKVDAMDLNPDELHSPKEGWLNLFLREKQEKEKEKKKNHDVDDETAVVSHPS
PDEFLTALAEFRKHLQEASNPSIHSEFRTSLYGNRDGFAPWFLWLPPLETVPLLVHVQKQ
HQLEEKQEPTKENGAMAGKSNVTLLLLHDTSCGMTVNHLKAFRLLATCLESQSEPVLLDL
VEYDLSDGFLIPDRDGQRLRSSITKKYHTRYSEVYSQLKPFMEDFKRLQPPQLVVLNKTS
VLTTFGSPFYHNTTNVLMQQNVHKSYIQTLVRLAGHAEPKLKSKTLLKCMQKTLLLESQR
RSRYR
>TCRU_8646 DnaJ domain containing protein, putative
QQRRMSSEMPTEQELRNAYAALGVATSTPFHDVKKRYVELAKQHHPDVNGGNEHNASSRM

VNINNAYATLSRFHKAGGVLPNISQSSSRDNGQSYYTAQDEPYQPWHEDLNPLIYEMMWD
EMRRQANSEAFARAAAASPAATGGGGGGQENRRRQNHQQQHQQQHRRQGSETPRDVPPKA
HGDNSRRKPNNGNYRKTTTWPDADLQAMVNMYQDGKSFEFIANALGKQTVEVVSEFNRWS
EDKKRSMRPAQRRQRGYYYAESPDIEFADFDDFNDPFAYGIGDECDYVDTEDVFFDGGAM
PFSGGHYMSGHRPRRGGGGGSGRRGSNHRPR
>TCRU_8647 hypothetical protein, conserved
VTGNSPPPRPPPTSPAATPGGVQYGERRQEEMDAGERRRRMEQRATDAQRRGEEPVGAAA
ASEMERWWPKENQNWSGRMFSSPFDKNKRKLDGMFVPEVKEVPSPTRPLEVSYAEDNFFV
NPDFHMADEVFDEARRFVPPPSFDPAIDEIDDEGFVDGQVMFDIQKALEEDKKRLEAFGN
PILVEDQVDYLLEPQREGMENMQQRQEFNGFVHWGLLHGAHMILEENHDYKKAHEFVNRY
MRDIDMFQKWLEHPKVRAHIEKKFGIDMHAKFDKLMALVMAMYARSKIQVYEDDPAGALK
SLTACMGFISEGADLKKERHRKAIGAVLAARGMVYCKLKSYERADDDITRALSFVNQKRC
ATLFQLRAEAREALGRIEDARLDEERAAEIWENAEVISPGMDGKPYKFVL*
>TCRU_8648 hypothetical protein, conserved
MLRLRCTLGASFLTLQPEALVRRHGRCAMRPVGYALLVPNRMLYQAAPFISALATQRRWV
RVRANHASGQSEADGSKNDGAEHPKAKGEKSEGGNKTSKKTTGFRAHLEGLKDDYVRFPD
IYNSANALNFILFTVFCLCSTGSNVEEKWWLDNWGIDARLMPLAWGLHSLLMNNFLSMAF
AMMLLHTMCHSVLPTVGSRGLMIYCIITAVASGFLMWTFNYMTNNTAEKQFGPWDIVAAL
FVMQYLHQGFSPICILNSFNGWVRYACWVGAVCILYFDWQPTAAGTLVGFALCK
>TCRU_8649 Uncharacterized protein
PLKMFWFQSLLFALFAGILFSFTSSVVVAMPLRYMVETVSGITGSIGHANGGPGTSLLTR
PSAICQGRDEDELLFGTQGYFRNFSRSTKMTGILIGDGTAQILDGTWSQARIDGPRGCVR
GIFSQKMIVYFVEGQSSLRYFTSDYVHTVMISINLSFTDVKLYEGKLYMTEQTKDEVWGC
DIDADGAPVSCALKTGFKCDYGKYHGITVTKLGVFVVGESAAGICHFDMHGNKLSVLGGN
YIDVFSLPSDELYIMSYTELLHLRVIGSAMVAEKFAGRADATCPPLIDGYDFTLCKNLRL
FVIEQSEMYLATTLNTVRSVTLPPAIVWMELPPPPLPIGYPDDNEVMKRIIQLMNEELNE
HLRTNGTYVSQENMHVDADTWATKFAVMVQQHDFENATTPGEVLTTHFAQTTQFVKDYYD
RVDEVLYMDTSIMPFCNDTMLNAVMHRLVSVVREVLGFPLIYANPPEARKELNFENITTM
KLLMPASFNNDTTRDALMDADMDAALLQILRELYGPENVVTLVFPMPQYDFSKLTDEQLV
EVRWFILDLVRARLEECDVLSASSVDASVSSHSGVCEAVITNRTETVVSHPPFNVQSEYE
VFVPLRYKFNASLCLDGIDWAVLEEIIKNYTEENKPRRKSACDRSCIIGLAVLAALVLTA
LIAVVVVLTSKRRRLAAVVAPVHPKFKSTLDEDEEE
>TCRU_8650 endonuclease G, putative
MNANVVPQDMTMNALDWLRLENLMKKLLLRYEGGIWVVTGPVFSPRYVYGDPRSWGWTES
RSTSAVTPATTVSGVNGDMKKARKVVCYELVGKHDVAVPTHLFKVVLGERGDGSHEVAAF
LIPNEPIVSERPLVAYQVPVTELEKRTGLQFFQKVVPANDTASTSWRGRKAQRQGLDALP
NICRRMSCEARTVALFQTQRSIAQLRAAQSLPELQQVFTRLLEERRQQRPGEKRNHLDTA
VMREYEERRKEL
>TCRU_8651 ATPase family associated with various cellular activities
(AAA), putative
VRDLVKRIQETPLFFWIYITVLVYAVRRLTYHHGYGKKKITVGGQTVYVDRAEETISESV
IDTTKICEGFSDVGGLEEVKSLLIEHVKWPFTRPDLFSGKTLRSHPKGVLLYGPPGTGKT
LLARALAKELGCSFINVKTESLFSKWVGDTEKNASAVFSLAEKISPCIIFIDEIDALLGS
RNIIDSAPHNHAKTIFMTRWDGITQSTAKIIVVGATNRPKYIDEAIRRRLPLQIEVPTPD
ETGRRKILGILLENDLENNLRKKEIIEFVAKNTRDYTGSDLTELCKAAALMPVKEMGDNG
ILPPLELRHFTMALTRVRPSL
>TCRU_8652 hypothetical protein, conserved
NEPPTKVARKENGNKMRDEHFKENSNRVTLFIRCAQIHGRGELMNGFLVEHREALGIQPW
YIARDNGSETESAMVLCPDAPVECVFVKTSRKPYFLLECTESEETTKAFVEKLIDLNNTT
YKDNPVIVEVAKEGLTVSGERKKLELRDAVKRKLSASGKTPAITFTSRPPTASSFIPRVL
RPK*
>TCRU_8653 mitochondrial carrier protein
SVALASTAATVLAKFILHPLDTLKCRLQSSNSRSLRFIWGEYAGKWGPRYLYGGLPIKLA
FYVPYQAIYMPTYNSVRDALMPVDVRKDTRFAFITRTVAAASAAELASCIARVPMETVKM

RIQATAVPNTKAALRLIFQQGFFASVRQVKAQTLVHDIPYSITQWIAYESFRPWTQSLQQ
RHELHKELERGSRLSRYVYNFLCTFLAGGFSGLIASTVTVPLDTIRTRVVVATASNASTT
VLDVVKDTYRLGGAFFFFRGGCTRVLWVTLNMAVYFPLYETF
>TCRU_8654 hypothetical protein, conserved
SPKKPHKLRSFFKMADMYRPGKYTSKDMPKGPTPSNQPWDPVFAHYAFQKATGPLQRKQN
TTPDDHLTVDELEKWMDATAAAKVLGIKESDLPTLTSSQLEERWAKVYNERTNAMQQETV
IAAEVLLEYIDSSVHRKKSRQYYRNYVDNARHALDHEADLRRRGYQQKFYYLFGAVMVIG
CSAVMFVAFFRNVITRRDVENIGASAVAYLNMAFLQPSNPEPAPDYSTRYRDTPTAMEID
QREGRYGNTDPTQAQLVLEVEEFRRHEEAEMLRLLNDENERAQKEAKMQAARGSRVRVYR
SEDFDESGELKEPAALNKDVDPAAAFSQMTFRQFAAMMASQFGGGSRFQRITQNSVRRME
EMENMRKRIDE
>TCRU_8655 hypothetical protein, conserved
MFRRCERRCMNRGHLMPTPSKYSDRPGMWGPGAGPPKDTLARRSMFFRMLVMNKIGRLTK
PFRTNRVRWIWRKTQLQLWKTFVMSMVFMCLLLFGNIWLSFVYHAYTVGPTTPVLERKVR
EHRVSKQILQMVREREKEMVKEEELDSAKKLIEAQK
>TCRU_8656 retrotransposon hot spot protein, RHS3, putative
RARREGQVGFTLTTTIEGVLFKGRARVIDIKLNDFLTMELDGRGILYANRNVLLRDFFKK
PASHIGDAEVLNEIQIKYYALKLESTVREELELEEDVRSLHENGVNSLAAWSLAAAKVKA
SVRDDTKHFLNAAAEEARNPTTKRAPIYLEGLYESVYNARWHHVVEVSDGDKRKKKGTGM
EVKEGKPKQSWKYNEVGRTLEKDDAVEQSDEAPPVLMVLTSDKGWPYTMNGPHRTGIDLC
VNCEVELVWQIVLNDLTKWFSNFDLSLNSSPLSRVLIGTPGIGKSMNAGSYLLYQLLHYD
IKKLQVVVYCFGIKMYVFDKTAKTVTEYVGETISISVILSLWKSGVNGYIIYDVAKEGTP
PDPGFAPSTGWGMIVVSSPEVSNYDGWEEQLKVSRIIMNCPDETDVKAMCAWMKRDETPE
KKAGYWRMVKRHMSLLVPIPRHIFDADECGKRTQDVMRALEWINIGDRGKYFTQGEEKWQ
SEDPSHKLLKIVRVREHGPFEDFANAPICTYLGVLTLSRLARVMSPHDIFFLVLGMKNVL
QSEALEKYSLSVFLIENFVTSIVRDLKELPPPSPSKPRSSVLTLNPHGYPTEAAAITELK
LIDRLQELKYRVLCMPTSPTFPLVDGFFFLNSPRRTLAGLQMTRAHAH
>TCRU_8657 UEV domain/Zinc finger, C3HC4 type (RING finger), putative
TRFFSCSSHCKPEVLGRILHDVENLCNTFHFYCRDATWVTQQEKLCIYGGLPITIKKSNS
DHTSLTPDSREQAPPNLYVLPLQIWLTHLYPIEPPLVFLLSAEQGCRIASNHKYVDATGR
CHTPELAAWHPVSSSLCDVVKKLCQLLSAEGSIPLCFGEEGVSSPSKGHATAVSQRLRHG
LENGDDDKQTDEHERCVVCFPKETVLVPCGHYCLCDACATDVTHCPLCRGSVKFRQRVFS
*
>TCRU_8658 paraflagellar rod protein, putative
TMTAAAATLFQRNKRIYVQEEDKLEGVVSDESFQQKFHQWLDATIAQLDLQFESCEQLLS
ELQQSVAVESGSYWCSKTIIQHCNLHMSEKRLIVAGKNMEQHPTLPELVSLISSLQQLKV
QAFISPKQRRFIEECESELKNVVFESRELLFINNALKTKLRDDGNTRGVFGDLTEFQNAI
EDLSPDIDQCEQLLEASIANGEMGLAEDISRRQLEIYERILTLITDQYPIITNYYTDSRD
SDRRRRWAIFRMADKDISAVIEGKYRQIEACEEDLMKIKEQIENYNNDDSHQRKRYEADR
NLSDEFLQKNKEKQQSVWNRIFELYEELRRCQTELTTLARQRRREIDRRLQMEEHEAGRR
SGHESFIKAAAEHAQRLQGMINNSLAAKELATALNNFVLDGCDSITSKYDKQQNALSEML
RLVQQHHFKRFSDYYIAASRYLYRKERRLEQIEKEIESNEMKKEMLSDRLDTNAKRYAEL
NNNLLLKRREVSQEVLFIRHKLEKAEKAIEPTLRSLQFAAVEYVHPRDIVEKINLNRCST
ILDYREFMTPSISYDEKVRMEELMKLAELRSTIDSENKERLAKQQLRLPSIAKKDYTALQ
RRVNSLLQKRSDEVERIPPIAATTSHDAAVSAYTGAQSTTRTSATGFTTSEIARGSSLAA
AWDTTGGTLTINASLRQPRLEGTVMRALYAYKARAPDELTFGEGDLIVCVNRAQEEGWFK
GVCNQRTGLFPINYVVPHEE
>TCRU_8659 hypothetical protein, conserved
SSVVSFTFPSMKTLSCCLRYLCIQSSTIKIIFSNRTGSSEMRLSGTNIPEYSFSEIVIEV
FDNDGMPGAATDNITGVKKDFSWAVDGPLLLRTLRLFEGCDSLTLELGHDLTSVFIYENE
CERWARIGALHDLGPILNIEHEITLLHRIHDIQSFCHIVRFIATSQEANCTIALRFDSLQ
SYIELKTSNTTGSALVDGEMLQHQVEGRAGTAELFGFAELAMRVSSSATLFVGFGVDSLA
MFRLDWQSVSSERSSAFLYF

>TCRU_8660 cyclophilin-type peptidyl-prolyl cis-trans isomerase, putative
YPINPKNPLVFFEISIGAQPAGRVEMELFKDVVPKTAENFRALCTGEKGVGRSGKALCYK
GSKFHRVIPQFMCQGGDFTNGNGTGGESIYGMKFPDESFAGRAGKHFGPGTLSMANAGPN
TNGSQFFICTAATEWLDGKHVVFGQITKGYEVIEKVEANGSRSGATRQPILITDCGEVK
>TCRU_8661 signal peptidase type I, putative
DATALHRLHDHRLMELQFSQMGRIGKIANQIKSVIRMVTDLGGFLPILLTLSAFFLGWRA
VGIMANCDNPLVVVLSGSMEPAYHRGDLLLLHKISKVNIGDVIVFSLPGRTVPIVHRVHG
VHEDGGTLLFLTKGDNNELDDRTLYPEGYHWVRDEDATGKVFAIIPNAGFLTILSEDRPW
IKFLALSVAILW
>TCRU_8662 Triglyceride lipase, putative
TCALCRRKKELCKCRVCFNCQKTMGIRRHHCRKCWQAVCPDCRERMRYVHMLSEPMKVCN
SCALPYGIATLSRCKEHKHLLWGLYVLQRATEMPNVCIVPSCSTLTYHSVCFNCGLPTTT
TRLHEERLVRLDAKELAKVADSVKYLEANEFSVRCAAVDKYAAEEVENLFRVLFPRFQEV
RAFPTLNSLVEAQDLLLSVISSTVAYEYGNFPSLTMSLSDVPYSRLLKLIRTSPRYSVFE
APGKVKFVSFPGTHDYRTFNVNMRCGRIKQQVWSRLVDGLAGSSDTSAEFRQLCGGVRLI
WEARVHQGFAHEAEESTQQIEQLVNDVRQNGYRLVLSGHSLGGAVAQLVAIRMLRAYPGI
LKDKLKCISIGAPLVGNHQLAQCVERCGWRSNFHHLVYRSDIIPRLLCVDQMARDLADQF
IQSILGLPSSLQRWFKSSSNANEGPMKAMDAMDTQIKEGEDSVEGEKTPPPTTEHRVHRM
YACFGRYHFLNHGGVNYFSTDDSEVAFHRLKEGCGSDNNLLDHSISSYNRAVFLQL
>TCRU_8663 hypothetical protein, conserved
MGRGFGRGSRVAIVTHAQLKTAGKKTPRGLRGSRQKKRRRFQQKHDEQRKLEESLGMKPT
NTSKSEKPLSQQVASIQFPHVVNKRQKGFRQLRRQIVDKVKDLRRRHAEKKKKQAMKSTN
SSTH
>TCRU_8664 hypothetical protein, conserved
ARRHRLTNASILSNMKSMADETNDLTSKIVYAARRQQDAVAWAIKEKELLSEKAKRQLEE
ETRRQQEEEKIEAYLKEVAETSGSAAAEAARRKISRAKSPYIRSVDAFGEKSVKLQHSFS
GLADNRIITWWEKLYWNYMRYIFTHERLIAKDRFGNKFTVTWQFQKGREEQRRMYRKDSN
KKHLPYGSLATDDRLWERWMRGHRGDPPSVAEEEHSREYKKQYFGAMVLEEEEVEDALMR
IMAHMNRSQQTFQELDDDQVYGDAHRATKPLRQAEHHPEKEHATKAQSGATWTLGFVRGD
LFYNEEEVEVMRTELGHVFRNMAWQELEYKRQVRMNKRQHPVRKPAEGTTDPNAPDGEPF
IHYWERTDLGIPYHDAVPDLTTPELERLRVEVDQLEDERLAIRKELGLTDLGDIREGRGP
IDKPGAREPFQPPPLSSRWRPKCWEEAWGTGAGNKW*
>TCRU_8665 mitochondrial DNA polymerase I protein A, putative
MSSRGQPRYRYVPVELTHIEHAGDNSGASLSFSDNLQKWQAFGLNTSAICGSSSAALPLQ
SAARCVHHHLVEDAEGEENEGIVGAAVEKDGGTQKEQKNMDGGSVSAIHRQLLELSSRVG
QVATESKCLPPAQREKRGKSSNGSKKKNSASGSGGAASASEGKHSREYGDELEEKRALKR
SAASGHNGVFTEVETSGVHLREEKGGEKKKKKNEKPNARRSRASDVQKNASKLPQRQALF
TMPPAPEPNSRPAELVAFKEVDDSTSLFEDLQKTLGDPDLIQAPTLFVAFIVHEGETNFS
ISAKTHGKVHFVRKTNPEMSHLSVQFFVLRWKDDVFVLHASTALSFLVRVLEELSGVEIV
TFNAPSLLLLLLSYKQGNLFTLCVSDIRLMSWMLQPSAGADAFTDYDVLLQSCQQQIGLA
AGFRNMENCTVKEIVCHRVYYMAPLYRLLYGQLGTQGLLPAFLKQEKRISLLCAAMKLNG
FPVKLSEVEGFKTRCIARMEELRIAAQKLVPSMPEFNMQNLEECRMAIYEVLQLGTHLTH
ARNDGTDSCSLTVTKSGKLSTSEETLKLLAPHHELPRLLIAYRKTAKLLQTYTVGMMETA
FPFKGNDSEFTDNRIGESSDKKDDTPVKWVTLHPNFVQEGTDTGRLSCVEPNLQNLPRSK
VIADNDNSEPYEAEMATFRRCFAVPIGLTLLSVDYEQIELRVVAHLSADTALVDAMTNAT
DVHRNIAENIFRKSPVSVEERTLAKRVVFGMLYGAGPRTLATQMGVPMERALHVMSLFKA
SYPQIERYQRRVIDQCRTDGFVRTMTGRIRSLPDINDRVMAKRMYAERQAFNSVIQGSAA
DVMKLGMLAVERDVLQLYNGDVRLLAQIHDEIVLSVPTHKLREVVPLVSRSMMHAVSLLV
PLRVTVRIGQSLGELEDWTVDHELGIR*P
>TCRU_8666 carboxypeptidase, putative
MEAYKKLETIFTKIYRFRHLISMAFWDIQVLMPRGGAEARGAALAELQLHVHELLTDPKM
RDLLLEAEKNKEQLGTLQQANLREIRLEWERENLLPEEIIKKKSELTTRAQQIWRKSREE
NDFSQWLPMLKELVALFYETGVALAGNTGKHPYEALLQLYEPGMSLERIDEIFNEIKSWL

PALIREVMEKRKTAGEEVLTPVGPFPLEAQKELSRYCMNVWKFDFDGGRQDCSLHPFCGG
VKEDVRITTRYDESRFETGLMAVIHETGHAKYEQNGGPKEMITQLIARYRSLGVHEGQSL
FAERMVARSKPFIEFLLPKLKELFGDQPAFTPENMVRIIQRVNPSFIRITSDELCYTMHI
ILRYEIERGLIEGKLRVEDVPAVWNEKMKSYLGIETLGNDREGCLQDIHWSIGDFGYFPT
YSLGALVAAQLMASIRRDLGNDVVDDCIRKGELGAILEKQREKIWQHGSTYTTEELLTKA
TGEPLNPRFFREHLERRYRDN
>TCRU_founding proteins of phosphatase, putative TLP18.3, Psb32 and MOLO.1
GPSIFHSSLLMARRGAGVDLLSPLAKLGHSRDLAEDIKASRKRSNKEIIASFEKIRTFDE
IHYRKTDRPWELVPKYSKKRVSDLCGLLTTEDRMEIEQTIDKMQSLCEVDMYVVLVPTVG
YTTPKAFANSIMFDWGIGEPAGNGLLLLIAQHEATVHLVASPAIEEYFDTHFLEPAVREI
FQPLVQEGKPSYATVQLVYAIARQAQEMRPLWQRGLLAMSTRNKVRFAVKTLSYGVFIVP
YLVWGSLIFLLCSVVLVNQMLDTLCPKCNSLMSRVRDDKTMREVMTRGQYLEHVNGCAFY
RVWKCPHCEDGNRVVLASRDLHQSNRCLQCMDCHYYTCSLTKEVQKLPTKEEDGIKQLLY
TCENCRVGREVLLPLLRPLDMKPEEKWYDFLIDRSQTHKKTDIKL*
>TCRU_8668 MSP-B, putative
EDLNDPSRYCTAEGQIRPDFTGGTVECQREDILTEEKKSIILKSLIPRAIKMHTDRLLVE
PLTGYLIVPEYSSGVCAQFTIPSSHHTDGVTGADMYLYVSAVPMNGSSLAWAAACSQLAD
GRPVVGAVNYGPSFVTDSEYSVRTLVHEIAHALGFIVWLMEERNMLKEVLNVRGKAKVFQ
VSSPKTVEKTREHFNCMSATGMELEDEGGRGTAASHWKRRNAKDELMAGKEGIGYYTSLT
MAAFEDTGFYKANWGMEEPMSWGNNSGCALLTEKCVMNGVTKYPEMFCTAESRLLLCTSD
RLELGYCTMELYDAPLPPQFQYFSNPKLGGAPDPLMDFCPYIEKYANAGCSDGNATLMRG
SRVGPRSKCLKGDGLADFMGFIGDVCAEVSCDKGEVSVRYLGDDAWHKCPEGSSITPTGL
FMKGRILCPKYDDVC
>TCRU_8669 hypothetical protein, conserved
MKSFVLPPLHSSVKGDMWCSRVPLPPPSDLVSTEPGPLLPSIDKSRRRQELRRMETKAAA
LELAVEKERLERLESKLRSVICGREHEKRHQLLWHYQKEKAKAERETAAIEARSLALQRS
KYMRIVREYQERGHLLHLETTTRAGMVSEEEDARRHVASLRELVLLEERRRQVEREAATA
EFIAKDLWGIRDWESRIAAMSFYPTEAFSPAACLFSRRNVGTGGYRGRADLLMDYDVCEE
EWKVRLALISKERVDRHLLEWRHGVLRLQFVEETQARKAIEELFVYGSCQARLSAILRVQ
RWWRMLQRTGWNERKRRELKKYVAQRRRQMKSRDYRAILGRMRRQMEAAASPISLEEVHK
SMAAIERAVEMSYQYIFDYFVYTLMNRASNLQETEAQNLREYPLEKDDGTAIIPPVLKLL
HVPYRLYVRQQPLQPYPLWRAVRWIEGSYSFIQQVRLFEEAEAQSRDSICAQEEKELETL
QIYHAVMKNGAWAWRSFYTTILCIEEEETVGRDLLQTWEKNVRGAIVDEAEASMSRCIVS
EEKLRVLDDEARARIEIVAEELGVFARLTEEEWRWDNLLRLRRELWRPGFGKSRWGMEWS
HGMGRKFDSLEAAVRIIQRFFCRASNRQHRSEKARQAMSLSQEMQLKKISADMVKTLETQ
HREENKEEELRAASSVHVEESDGIVESQLEMAVDSFRDWFDLSAQRPMEENYKEIVSRFL
QENRRLYMYMHILFAVVRNGRQRIEEEEAREYSAMQCTHAFVAIAIDALYREETARRQNL
ESDAREESFQWHERAGFLAALAKYTATTKKRIKKNAHPPCMNHMERLLSREDVVRTRRLV
EERCDRSDILLSLHAIVYSATLREEQQERSVLYEHIDECWSAHSPFTLLAKAEEVARRKV
EVEAYSSYGPLLDCECANYGQMTLFRQFLRGHLSFESEARYFDRQLTELLLQRVSLLRSK
IDELVAAETCARARVEYFEEIHR
>TCRU_8670 amidase, putative
AAAVACLACYFYGILFTMVLLILYAYLANKIFEVYMMAGPKTSRQVPPSPIAYCQQLSAV
QLSKAYRSGELSCEHVVRTYIEHIKRVNPYINAMVFECFDEAIEAAVEADAVWAAWRADR
SRPAPSWLLGVPCTIKECMSVRGCPNTSGHPKRRHIIAKNDSPVVKNFRDSGAIILGVTN
TSELCMWYESSNYVYGISCNPYDTRCLVGGSSGGEGAAAGAVFSTFSLGSDIGGSIRMPA
LFNGVFGHKASPHYISNRGQHPAPKTAANHYMTTGPICRFAEDIAPLCHVAARGGFLEDP
RLYPPRPPLRDIPKIGGGKPLRVFALEDFGINGVHTSSSQLAAVELAAQCLEREYGAKVV
YVNLRDRSRCSGGAVPAAFKPFSDTFAMWINVLMSDPTEVKFTALMGEGSPSFNVFWELL
RWLVRRSQHTLPALLLCIMEAMDQNFPKNMGMPSPKFDISSFKRSLEDLLGDDGVILAPT
FPRPAPHHHTPLLTPLEFQYTAAFNVLQMPATAVPIWTADLRDAATTVTPAEVRERRLPL
DYHLPKGVQIVSREINDELSIGVAIALEKSLGGYRYPGWAVLE
>TCRU_8671 RNA-binding protein, putative

DMMDDQSSTSGGPQEGRDADHRQNHGNVLFVGNLPFQTPWQHVKDHFRKAGKVRYTDLIA
DRMGRPKGSALVTMVTAEGAQRAIRMYNETDFEGRRLIVRLFDDGPRPPIVQRGMMPQYD
RQTQQQQPQQQSQRFRGYTGASSGGSNYNNTTNFGRRADYMGRGGYTMEEDLNATSLNDM
GDSVPKPRSQQVNEFGRKLFVSNLPFDCTSSALRETFQQVGNVERAEVILGRNGKSRGMG
IVVMRTEKETRLAIEEFDGIEMANRAMSVRLDNKTTA*
>TCRU_8672 short-chain dehydrogenase, putative
MIHLFSSEALAALICLLFIAIATAAHFFQWSWWCSMTTADTLLAVVSCIFACRGVASGRQ
CKWPSDVDFTSRVALVTGASSGVGYGVSQELAQHGWTVIMGGRNLLRLLEAKRSLMAKKP
SGRLVVLAEVDLSDFDSVRGFSATVLEQKEKFPVSLLVNAAGVLRRHLHRCEDTGLEEMI
ATNVVGPMLLTNLLLPLLEETAERSGVSSRIVNVASSCHTFLGVRQRCSPGEMLAALHPS
PKEGDDKEAKVEAPTVEEFTLGNFVGYYGLSKLCVIWWTSVLARRVSLRFFCNGDGRQLK
VFVACCHPGVITTHLYRDLFPLPVLDHVLYYPSLLIGKTWKEGAQAVLSLCVEADKMVHG
GYYMCTGEYGPNSGINCLSKEARNLEGANNFCIWAEKVIEAQRIIPKKTKTGQSVAAPKK
IMRVKFV
>TCRU_8673 RNA-binding protein, putative
TRDLHHHHLARLLHLVPHLHSAYLENSFLLPLFFSCVSPAAKQHARMLLLSLQRRFGSLC
PPEVRVHILSFLSFPEFAASPPHPICRERSILSPGARKRPREVVGENVSPGCATSPTTDA
AVEREEEEDVVVSMDEKRKSLPKSKTAKSDEKPSATDFLFHVRPPLAATTTTSAKKTTHL
FVRMVSESAQNEETMNRYFGRYGQVSCTLLQQKQQQAMTDSGHTETKAAVVQDFIVSVDS
TDNSLKAVRNAYYPELAFIAFHDPACDTYTLADLDRVLQDVPVEVVRVPAHLDTVTKAED
EKDDANALPLHTFVPDVVVDGLPYWLTVDQLRVSFSEYGRVEDVRIAIDDRSGSFTGTAL
LRMASVEEAIAASEGLNGAVLKDHTLVSGVLDDRLNIVSLQQGTLICQADELLPEDFDVS
ENHRRWV*
>TCRU_8674 zinc-finger of a C2HC-type, putative
SSSLRALTPRTARGANTRASPEAATPRGGSGPVPDLIVARGLYKVLEEVMHDRPPSTRQK
NSQGSGQNSRPNFLFCYLCGMQFGSASLRIHQPQCHLKKLIEWERMDPARRGPRPVDPET
HEKEMKERVALGGTAGGRGGSGKLKGSEIDRFNEVQIQDFNANMLVKCENCGRTFLPDRL
EVHLRSCKPGAASASRPVARSLAGKTAGDKGLVRAQSVSAGAFPSKKSRQPIPLEKEPST
PPASSAARTKGAREVVFSTQIKRAAWGNAEDSEPLEKDSPEAIPQCANPTISTQGVTCDR
DDGDGVVVAEAAYDGAASAASSASVATRSVSRSLGERTAKKLVVHEEAAPRTAVDVGEEK
NDTQKEVNDTKKHCAASSESKDERKSESLPVEEDASAIDDDGRDDAPAVPAATAAHIASA
PAASPPFDDFQALDDTTPPERHAVKIPLNNVSRFKNVASRVHAGVHKKEELPRCRFCNRT
FNANRLAKHEEVCLERNKSNHRNSASAGHHPETAPAAHEEKRRNERDRPWEAHRALASKN
KSSEEIPPAAPPTPGDVAEKSVPSHPQRKKETEAGNGSTEGTKMRFCFECGAKLIAGKQR
FCAECGTKL
>TCRU_8675 Dopey, N-terminal, putative
QLSKRATRYSAEMVKLLLIMDRTHSSNWASLSTMLTQLLKCIESNIEAATEVLPDPVLLC
RVIWKCFDPKGVMGVHRKALDVLQRLCLCVGTSALIRQMPLLLVGVLELLPQCSIQVKCE
LLHFVEVHMLRTLPPGVVAVELPGILSAILGGLEEKDTTEVYRSTLKIMEALHTILRNAE
TMISANSNPIEEVDDNHHEKEIPLGNSSEGGGEVILYSALWLTLKNCPSLRACVLLYLKM
RLCVGVSQAHSVGHGSVLAESEGLEKEKKNICLLAAPTPFSIILGSDPRIVHSAIFATLQ
EQSERKHRLMLDILISAFPLDVETTFTFEERSWLVAAVIQLLGFSDVNISIRRRIAGWLT
GSNPGRASMYVQEVSSFLVAHAFYGVVRWWESRFVPSTATDNRGNTSKMNTLEESYYQVL
FASACKRCLPLADSSASSKMSINLTEAYLTPNVWLRAFMSFFQQFFVLNDADDADDDDDK
NSNNTNNDNDSDDYARYSGAGDGFSPRTIGNPFIEHVVPLVMPFVCDLLVSMELWKRENP
RQSSAIDSTLTAVFSVVTWDYFTCYEHDLISILEGCLDGLREIAAFYLPATGVGEILEGS
QEGCNVNETPNKPIPFCESHGKLISDFQVCFRRLIGLVSAVEPHVMGLMDLDVERTTAFL
QGIFKTSQSLCSIVWGACEILLAHDNTGSESAHFSIAQCLINGCLDSFNFIFFGMFSALQ
DRVELAGSCNTIREKEGALLDSMMRSSTAMAEIVLRGCSACAETLARINDTVFSLFQRSL
QLGGKSPLSSSDNSFGVCEDILVSWVESVFSLTDSTCLTVQKDALQLYADLLSSTTLPLA
LQSAKFIEELTVKFLPRLWELLGTCNAGMQPHVVQLLVRLYATHEGRAILDNITSVATTE
NGERLLLLFCLLDEENVSENVFLPGLFMMLRALDCKDAPLRRLAHSMVRQSLPCFHRVLN
PLFDSLVRYLTSRGAADEEKTVAAEHVDCVSAHFNNQIFLEHEMNGLSPMEFLCLVKSIL
AIPSFLLPLLTRLHQLQPPEGFRALMTTIFPRPLAAAGDQKGESDMPLNSAFAVLGCLLL

GIVRRCLLPQSDGFGEDNPRLYVELCIEACETLNLMLEGTLSLSNPPETVVHTWYYATFQ
TMDFLHEVVKRPELSVTQLLMLKHFVDAVRFLNAVTPTPTSFPLDAYFCMLANKAHKIEA
SETVVDGADRSTARNCIVALKIPKFYTTVALGLEQATATALTSAWAAYDLLSVWCNTLLE
LLPFFHEELDGASAHLLKIFLRVIDQLLVQTTSVTECANLRVIEKCLNAVYGLLEYQLAT
EKQRRQSYASGRGQSVGWFAAHVPIFGSGGGSSSSAQKATGVDAAASIGAVRHSIRPVVS
ILCKLHCAMHKAQAQRVVEGERPRYGVRGRVVCSNLESAIHRVLRLYAQEMGAEFYKVFI
DVWAAGHAQPFTEMFTSLAPRGIHLFNDAVRNRMELLPLIGSDNEMALSFPMFLGDQELI
VQLLNAGTGITVLSLIRVLEELLKQNCSNNTTNCSSSSRRHMLGAELPFDASVFYYLYTF
IYTCRVPSGETQEVLNALIDIAITHLSQGSPSVVCLGLIVQVFSHFVLGQSVPRSSPSSP
CETVEGSCVEWGKDKRCSNIICKVLDALGSVALHTSSMQGELMFSFKMLSVALPRLACGA
LSDQDRIATAVLSFYKRSLLPTIMFGADSQTDADVFARTPLVKAALSVLQAIIRLGDTVT
RRLRQELLDVLCTCDFFNFPQSVIHEWGVIFEWLSQDWTFHGEAVQFLAPSSSHSSRIVA
LIHSADEEERQRVRQIKRLAFYVTCMLPSTLMLDREFCLLIRGRIADSLRSFHSIASGNS
SNGSGSGYRSVRYALFLFRVLVTKLDPALLHPFWPVVLPTAFRALSIPSPSVDAAAGKRN
NTDGELLALQMECLKLLDFVGVIMPDTFSPFHWVFFDDLDATNVIVPNNAKEVFIPIVHR
LELSLRLRTVSLQDVWAPAVSSSSAFTNWTGYQRPLLRFPPICYGSLRGIGPCAAALSLF
YRSGGFLTASQAPEQLLSAASTRLMDGWDEAYVRALVEADLSCVLD
>TCRU_8676 MYND finger containing protein, putative
MSSSGMHSGLFTLHFTPICTAGEERATASGSMSPSTQNSAEFGDWHILLRFAVENEVLSV
RPRGKIFVMGSECGTSGGSEEPVAIPGLGRVPRPVKDRHATVLMRCHCHWQYSEAFRFDV
CFDQLDGAIVGVKGRTLNDVIISCEGSQAYGWYIGEATVTVEGKPFTLPHRLRFVLDPYV
GAQCTMCLDPVYAQGYTCTECGAVEYCSKNCQMAHMSGQHGLLCSILRRTYTQRSGKVLT
ETEKGTELVAWWRCLEDACYSILVDFHNSLGQPIEFFLCTLKSAQEEGLRYRFIVKEGTS
PREVTHEELADFACTVFRAVSENSISEGCTSLAAACLNYIFVFSRHIESIVESHVLYYYS
YLCEDFEGTICSVEEYVTYARPMHELGVALIEFALKSPTALLFWQRIKLAKNVFINLYNV
NTSCHCSKIKELVKAIPGQQRETLNLLSRVFLIMASRAPKKEGLRLLEQAEKCLRDCLPT
EQDTDDEAMDAAESQHNHRSGGFDELDENLEEMEPSSLAMLYFRLATLLLLYGDTNKTRE
AEALKAQGDALIAKAKAAS
>TCRU_8677 hypothetical protein, conserved
PSFFTMIPARRLRLLLGRALEGVPVAAAPSPEAGKDLDDYLLKSYMRENTANEKLTELLL
SISSLGIASREDWLRLKKVCFAHLPELSCRTVNIIFALLVEKSVCGSVECVRIQDQLAQL
NFSKKLRDHECLQTLRCITNVGSRLSPSFIPHALESIQTLVRQCQTELLPTLSYTIGRLL
TSKENRGIPIEVQHSLLESLVVRVDSIDCMLLSQSELIYLLWALSAFCSPILSLRTAYLK
TSYMLLMRGIKMEEIKDGGPMDLLLLLFGLCPLLECSGLGNSILSSQETGLIMDVTTDHG
EMKERSQGSLKRLLDMLNLVLVSLIQHVAREELQSRPVSCVILEMLTWSNATKVLKNAQI
LYNLLICRLLYGEKGMWFCEREKNVLSEGEKQPPLVNYFLFEQSTGLLDILKTRLSLSVF
SSLPLSGFEKASVREIIVVLEAMVYGNISESLKKNYIKGCIMKLPGAIRIVSRNEFSRIV
NLIIKLHLCDQPITRAIHDRCQELGIKKKLLHKKKLNEDANCHMNTKNTSMDDWSSDVIT
LYICETSLKLAGEDKDCKTDVPKLLENLSTRKGMSSATETHCVSIIKSLAKHQLSFKNEK
FYQLSLNSIFSRVKTGLPVGSMLSLILNGVKAGVSCEALVDSLLWVGCRLLEGGMAMADA
KDVAIYFIAAHELDSLNIAFHPVLLGIFQQEKAIDVLSPHLVTRLFLALCALGIDDRSLL
ERILDRVESWCLKVVKKAEWSEEDWKASLVFVHALWTLSSEVVWKPLMQMAQKLVSSMIE
RENEHKTMGYSLFVASAAASFSIHNNAETPFAKGVEKTFISEELSGFLKIVTSLFSENAI
SFSLSRTDALLRAGAMASVIPQYSNIICFLIIAHAVQRFAQGEGNSSKKLTPLGVSLWRY
CLKHVEKIPATDNNLMTAVGFSIRFGASSQAFDRFMSALIEKEADVNMLSVCFIADGLVR
TGKRRSVATQFVAHFSQRNCLDDLPAAALLSLLNFFVRDAERVSLGLARADMLTALVWSS
LSLKLARLPETKGLWTLVDSVPTETRSSLLVFLSEGGLIDKSSVTELVYPVSTVLSWKLN
SINGASIINFLQKVKISLDIRRTNEIAPDLVAEELLKKI
>TCRU_8678 malonyl-CoA decarboxylase, mitochondrial precursor,
putative
RLHGTQPTPWQSEDRVANWCCRLWGLREGCWGDSPSLPSPASMPSWTSPHSGLGRELLSE
VECQIKLAEELKAVMIGEKGRLPESLVESVWDIYESIIPPDVATDLARYVTPTQEIKFFE
FIGLLAELDINLADVKAATEKLTRCVGVIETLHADVKRGEERGGEQDNSASSSELASDAA
MLSAKLVTAKNELLRQCVAVSQAGSPVHYLWLRQSASLERGMKRLMDLRRCVTYFKSRCR

ERLAALQADRKQVGQQLSAPVTVAARRENMDLWIARQRHVSSIDGALEFLFSDFFAKEWL
VMEELTWHSTPPLLLEKVIAAEAVHPFFSGLADMKQRLQPTKNRHLFAFFHPAVVEEPLI
AVQVALTRGIAGSVDRILGRPSPLDNPQRELGDACTHDTRGCNDGSCSDGVDTAIFYSIN
SANSALRGFNLGNLLIKRVVREIEARLNAERRAEGLSLITTFSTLSPIPGYIPWLTTQVA
KLQQDVLECRDGSSAGGLKFLNHRIFGDSKDDEACLFSQLREAVLQFVSRHPDIHADLAA
HLLPQCSNCATGVANLFTMRFLLRLFQMPEVDTNSHHHHHYHPAWWEDSDLTRAIELPLL
RSVAHYLYKEKRRGRILDQVGNFHISNGATMWRLNYLGNCSVAGSRESATVMVNYLYNPA
RVSEQVNAYEVQRTVSVGEKVLQHL
>TCRU_8679 centrin, putative
SPMSHTAKQSTPPGTASQPRGTGKNNAMSELTEDQRQEIKEAFDLFDTDGSGTIDAKELK
VAMRALGFEPRKDEVRRLLLSIAEERRVPGVEAAGPGTEPLAIGFAEFTELMARKMTERD
SREEMLRAFHLFDDDKTGKISFKNLKRVAQELGENMTDAELQEMIDEADRDGDGEVSEDE
FLRVMKKTSLY*
>TCRU_8680 hypothetical protein, conserved
EKRVSFAHELVTEMWTAGISGSGSADPRDDCRTPLDVFLFKNGCLVHQIVDSLRLELELP
LVLRYRVVDYVWQQCYRTVLPDGAELPRRPPNVVCTPEEEARVARVDANISSTSLRLMDG
VSLHSLRTIAETALVLHPYSRRLDPVTRPILAFLRRNCTLQLSRRQNSLVGLLPKLMEII
ILLCQCLESGAQGFLRREGRSDFLHNSHSDGSRSSSLSLLSGSFRDDARLAKAIGFSHRC
AWWLSRLHHRATSRPQRLFMDLKELLLRPGPLCDVKGMYLQYIAHRFFPGLPFLQRP
>TCRU_8681 phospholipase A1, putative
DYVISPHLILLFAFIPLSMILRIFGLGAVVFLPILPLGIIGTAVMFILLPIPILEPVGGH
YHVGIVHVHSRHSQTMPPLAVYYPTNETPRRKGIQYIPFNDVRFMSGLSSRAGVPLYLMR
DFLFVRLRATEGAKPIPLINSSGIPLPVIIFSHGLYGYHRLYSALQADLASRGAVVVSVG
HCDGSASFMRDSERGGKEFFLRQVDWDSPVCEEALAQRVMETRRTLKRLSEKEFWKELGF
ADLDVEQYLRQSPRVHLSGHSFGGATALVAAMQEEQESKPNENPVQSVMVFDPWHKPLQN
ELFLKPIEEGRNRYTTPTLMVHSDAWVQDRSIWNFFQRITTLLFSQPSISSLSEREKRMR
FVTEKTGSTNHYSVSDVVLLSPVIHGCKNSILPPRVQIMEWSNTCLRFIKE
>TCRU_8682 PPR repeat/Pentatricopeptide repeat domain containing
protein, putative
RFMSSTPCQLQGSRVGHYRPFSSEDEMQLAAVLTTKPRHVARYVRQSMLHSRRRITQFRN
SVTFLMIALQSKLQKGEIAPDDALALAESLMRECVDLRQGDMAHLLFRASIRFRRYGMKI
GFQLVKHLFDSYRTDNAKDLMKNMADELRGEESLKMLAVVAYQFAGEYDEARELLQEIPQ
ERLVTSDYTALIEAYGMTSRYDEIMKLVRQLFSTHKTNQGSLDLDAILSTGLVAIRGDNN
GMEQLKEMALDHRVKLSEKAIGAIMRSRLTSAKSAAEVYNLEEALRHELAVQTLGMAAET
AVIARCSELLSRSQKSGDDVMLRKVQHLESVVEECVVNDTVDDIEPSYLLSLIKGYGVLG
RFEDMNRCFTSLKEAGVVRDHRLYDEMLRWYAHAYNLKEVIALKEEMQERQIFHTAQTYQ
HVFRVLDKYYPRMVEKYMNEMRNKGIQIESFMYPTLLRVFGELQDFHMVEQLYREIKSKV
AMGNTNVFSAAVVVQLLKSYQNDMERCNSIIHEAENYGLLANELVQAEIVQFYSVHNRYD
YLHALVSRLPYKSPDMYRVLLRDAAKRKDRRTFNALLREMQENQVVINERIFGVVVLALG
YFNDLDGVKRYFHEALMNNAVRTPLFFALAASAFARLGDTQAVDECWRDLVESKVTITMP
VYNKFLDLYMANNNVEKVQQILNTMMKLVPPNPVTATTVVDMLGKMGRLEEMESVLEEMS
RSTNAVPTQVTYHQAMNAYAKTGDVAKMEAMRAKMKEEGFQENHVTFNILFEGYGRAKRY
EHIKELVEERRSKQIPMEEFGYMGLLNIYSRARMVEETSKLVEEMVASGVPFTSRMLSAV
ASSFSHIGDIPKMEHYISLLLSHPECRHRDVESIYLIYSKMRDTVKLQELLDTENLPKTQ
FIYNICVAAFARSGEHTKVATLLTQMEEKGFFLTRNTSITLSSLLLKAGKLELAQTVLKW
KGCAPHRDEEEGDELAADESQLLRADN
>TCRU_8683 Leucine carboxyl methyltransferase/Cupin-like domain
containing protein, putative
VSFDAAVQRTNDDSVVSKRSAVFHGYFEDPYLRHFVRKFSRRSPLINRGYYLRMLVITDL
IEKCICHLQCADPSIAAPVQVISLGAGYDTLAMRLKEEPQYANVHFYEVDFPSVMQSKSE
LVRAAPKGAFKEDLVAEPAQELVKLHGNNYRAIGVDLRGTEHDLINSLMKASQYFSPNHP
TVLFAECVMQYMLPSSAADLIKLIACSFSRAIFVAYDQVNPADSFGNVMQISLRAKGSPL
LGLAETPGKTAMLRRALECRMQEARFANFHELSRHYLMGDERQRVEALEPFDEAEEWCEM
CEHYGITMATTSHEVGMPAHPAFKETPSETTTEGSEEVAQFLVRVEKWPRGRFGFEGWGN

GQAFSEKLSSGDLIIVSFGGFSATRSHQRTNTVYVHSLREGDCKVITAASSVEPPTLVFH
SFSRVARGVYVVLGGRTNPKDVTMDAYLLQLELPEETEELQKTHLVALWTKLVPVAEANK
LPEARYRHAATTVENGTKEELQRPIFVFGGRNGAGHFLNDAWMATVCGEKIHWKHLQLTG
DIPPPCCSSAVIDLPSTTAVLLSGGLMAGDVCEGAVWRVNWTKGNCRRMPYTVFPRFSHT
MCHVEVGGVACVLALGGSTCRPREGHPSAVLLNPETGEAACVLALPPECPTWTRHCCISL
GNGVVAVFGGGFTCFSFGTFAAKPLFLLLGERSDWHVTKQPKKAVHLSQSSPSPLLSRKR
PAVEAQPFSKEAFLALVRQPNRPVVFRKVNMGRCVDLWANPTYLKEAEKNTIVSVHVARE
TYLLDFVKKNFTFRHVSFGSLVDHCVKAEENPHAAGSEAWYLRAVAPNMKTERANVWKDF
PKLGGDFVLPPAVAEHVESRMHQACLRLNAPPLQLWTHYDTLDNVLCQVVGKKRVVLFPP
SEYNNLYMSGSSSAVLNIDAPDLGRFPRFADACRHATEVVLEPGDMLFLPSLWFHHITTM
EGSYSISVNVFFERFPHEDYDKKDLYGNKDLPAAARLRKRIVEQVQQLVSEPFIEKTSDG
KPLPPDFVEFALRQAIQDLEEISDNMAVAHR
>TCRU_8684 dolichol kinase, putative
VMIYPRLRVEVSYSSTVIMMWVVLLAVMSWNANHSMQSLTILFLSTVALTSPHGESRMLL
PMLFLSEHLLDNLFLSGRSPLEFYASTLLSYLTLVVCRAARKRKCNENIFIGSVICAAEV
IVVLYFISEDCVMSFGAAAFVLLGLAFFLALLPVIGENEAVLISSLVGFYICDMVTNNSL
TEGESSPHAPGLFTKKTHIAARGAVICAISMNAVLFLGSKCCMVPRVNISKSSERVISVE
RITILFWSSLVCVVAVIYYLVGFHLREDALMWMINYFTSARHRPWILLLWGGAVPLSVIC
VERFTGGLRKTARRKLFHFIAVVLFTPVALVDPPFLSLSLSIASSIAILVELSRFYGVYG
SSTLNAFMLEHIDGRDSIRGAVRTHIYLIYGLGLSMMLRFRYERPEPVLEFSSWMELAIH
IIPGLVSLGIVDACAGIVGSTFLLSYRRALGRYLNNSFFTERANSSITHKTTTGTFGGLL
CGVLFWLFILLVAGNIREADAGHSFILILVCSLTECFMDGIDNLQLPLVVDGAVHTLLAF
>TCRU_8685 Major Facilitator Superfamily/Sugar (and other)
transporter, putative
LSMVLVSESISSTLILPFVGLFVARLRNVTPDEAGFLSGILVSVFQLGQIITGKTWGRMS
DRFGRKPMIQLGLFFNAVIAIFFGVSPSIEFCILMRFLHGCANGNVLVAKTVIADITDRT
TESLGFSAITLFWGVGSIVGPTLGGLLYDPVKNPKLSHFLLTEDPALNFFVVHPAVLSML
VTAAFSLLALMSTCLFLPETSKNTVDPLLSLCFSRRNTSAVVVEESIEEKSTQEMEISAY
PGISEETDGPSGREDVQQGNRGCGEALFVEEGSSYRAIPVEGASKVTRMRQRKLGLTLEG
KSNCENKSQSSFGYREALKSSNTQKVLIMYMCIASTEFALLEVIPLWSIASVEKGGLGLC
SADVGWLMGATSVVCVLANINFTSLLRCVQNHRVIWDTSVILWALVSVATPCAIFFPRQW
VFTCVAVLNAIREVALSWNFALVYIFIARSSPEEHLGSMNGIAQSLGSLSRLLTMLVLPP
LFAWSLQGAQSFPFNHHFVFWLTTL
>TCRU_8686 transporter, putative
TPLPLKQMFALAVVLLNESFSSTMLLPYVGLLIAHLRNRPAEESGYLSGLMIGVFMFGQV
VSGKYWGYLSDKYGRRTPLLVGLLSSGFMMLGFGLGKTVWMCILFRFLHGLFNGNVLVAK
TVLADILDETNQAKGFTLVSLTYGFGTLIGPAVGGVLYDPANSNMMQWAGFSKEGIFSRF
PGLLPAVVLCLYINLGVFVCIVFLKESNPKAQPLPRWLAVLIPCFREAKEPELTSSDTTD
VVFEKMADLNDFQEDNKSTKKTEEPMVMKRSFHGDMRLGLERTELGERGYKLSIMDDMEE
LEMDFEEDGGKMQEEEDHDAVRDPEGVEPFGYKEAFLLPITRNVLVLYMLLSAADMAYGE
TFPLWAIANNSVGGLEYSSGIVGLFLLSNSLPCVGANLLFHIACRVAEDKMVLWQISMYA
MAFGVGLVPFAAYIPPVGQFIMIFICGFLRQWFAAWAYGLITLFTARVAPPACLGTMYGI
SQSCGAAMRCVIPIVATPIFAWSISGGHSPPFNHMFVFLIAATVFVVAAVISFGFNM
>TCRU_8687 Alpha/beta hydrolase family, putative
EREKKGEKKMRTGQHSFGGSIVSSGAVIAVSAALHLFATRTLPAAVACYAPAISWGFTCL
CLRKGMSYTYVLIFTLHLVLASICYWKFGSSNAILNRSLLYPLAGSTMALLCTSQLPRVP
NSGMIGVALVQGWSTLGGVLMFLIFPATVLSSIEPQDLRESRLTKFMHQTDGKYVESLTV
PSKHGVNLDVLLVKREEDVDRWIIYFGGNAEMMEDSAEDMSSLTQIVVANWVFYNPRGVG
RSSGYVAEVRDLIDDAVTVVQHISARYLIPHKKLLLWGHSIGGGIAAAVARRECMECPLV
LDRTFSRLSDAAVKFSPLCPALTRLLIRNTIGDLDVVADFKAAAKNKKLVIYHRMDEVIA
YDVASLGRKDALSEMHVNESMVVELRSTRVQSPHNSLLSAFEERMKLCRCVNALFS*
>TCRU_8688 50S ribosome-binding GTPase, putative
MWWTLRLLQRETGTASALSLTEACVTRQLTTKNIRRPKKLQRQMWMDRMKKRRRERVRMI
AAHEESQKASMNNPTLSGRDVIMAQLANEIFSRGHKHVCCATNISFVPDGNAAMPEVALA

GRGNVGKTSLLRSLFRASREVGRSNVKLRRDAMNFFNVGGGVFNVVDLPGFGGTSVPWST
VLQHAVLLRNFVQYRPSLKMLYYCMDVHYKHGVYIQDIDILRFLSKEVPNFTIVLTKGDQ
LDTTKSKDAFRLEDIRRELLFHDITHPLLVTSAYHMGGIDALRFDMVMNCMHAVPTERLT
LTEAKRLSERLLSQRELGTVRQLDLPPTQLQEDLIAWEAELRQERAAGGVTEREDAVEST
ERTIASEGKVEEHNISVASSIKNGYNNNNNSGERSEKESTSMVEMHSSGCSNAVLDPDRE
VAFASLCKKLTNNALMSYVKQTSPWRNPLVWPTNVIPTKHPKSNIMRCPEDPQNPYLTQA
HFVCPRADMLFRRPNVGVRRASNKGRYEADRPLAFLMKPYTVPYFPDIVDVNMHPLPWTF
LGSREAYYEKNGGRRLGVRLSQYASAGEVRALADNPAPAEPDLTKEVRALERARYGSPIA
MLRPPEK
>TCRU_8689 ATP-dependent RNA helicase, putative
VMPAATRYLPHSERTKTHYERFLRDLRRWLPPGLDDEIGEIAEETLSIVCRAGNGTAAGG
SAQLQQVRKQLEVLFDTSISPEALHEVLQYGRLIDDFIVVAEEEEVGNTCGVAHRGGDNA
AGLGDGLGDLFFMQQQEEEAGDSSDDDESRTARDNRRDLMRFAVDVEGLTANDDDEDDGG
AEEGNNNHNNNINGGGRAQRVTFEEVACNPKYVRDSLRRLFPTQTVEECDLQADRLLRYA
GQRQVDQLTLETQLTAFLGGYDDEAVMEWIGVVAASRWAIVYGMQFAEGHNQQEKEAVMD
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>TCRU_8690 signal peptide peptidase, putative
QLYLALGSLLSGAVLVVYLGSRRLLQQTLEKREKQHRFEEVLNTDDTLALPLMGSVVLFV
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VFPRTIFGDHQAVSLLGLGDLIIPGFFVAQTLLFSVEYVKRSTFYFEIALVAYTLSLVNT
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TLSERE
>TCRU_8691 hypothetical protein, conserved
VPSPVRLSGKLCMAARDPGGKTKQGPQHPVPVELTSLVPVRVVSVHGDFFDTELHQDAPM
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>TCRU_8692 CHAT domain containing protein, putative
LNPGARPWYPSCDGALGVHVPPVRRQNDPYQFTAVHRPPTPLCGDMDLNTIQLDALGSAV
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>TCRU_8693 protein kinase, putative
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>TCRU_8694 Possible lysine decarboxylase, putative
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REKIKG
>TCRU_8696 ubiquitin activating enzyme, putative
MLNAAIYERTQILIGDEGVRKLQGVNVFLAGVGGVGGHCAEALVRGGVGRITICXHDVVS
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>TCRU_8697 TLR4 regulator and MIR-interacting MSAP, putative
EWDEPMETPIDEDDPVIKAMPNPEVPELYLPLKCSACGAIVEHAIHLLRPVIEDHLERKK
QAAKDGKKTIQDFHPKEFETVDAFEQLCHEVSLLYGLEMKDAKVSSVFFTKSKTIGRVLG
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GLPIDPRLEDSSD
>TCRU_8698 leucine-rich repeat protein (LRRP), putative
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VNNTPRLQLPSYKNLRPMPQMRDGIQKGVVPRM*GGQ
>TCRU_8699 chaperone protein DNAj, putative
LLLLLVALLVLFFLSTPAEARLFAYSNNDDLYARLGVGRGATKDEIKKAFRKITREHHPD
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QQSPILSKTHQLESLSVLQRILNFRGNRLFLLQVYDDSCKSCRWFASTWEGLTQSSLVEG
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SLLDFVMSFFYDKYIEINSLKVENNNTQYILEWLQEERGSADAVRVLLPPLTVESIALTL
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MSDDPNGTRWSKSDNNIGKSMLRRSGWTEGSGLGKSQEGVTSHIKTRRKDGVMGVGYEGG
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PKALTKEDTNEIETVRITKPQPRPPKCTDTPFL
>TCRU_8701 deoxyribose-phosphate aldolase, putative
MTDLRMTERPGFTGKLNEKILERVRFLAGELQIPDLESKFPHLKVTDGSWRPPLPGDDVN
LAAYIDHTQLKQEAPMADIVKLCEEARQYKFYAVCVNSSRVKLCVEKLRGTGIKTGASCG
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>TCRU_8702 hypothetical protein, conserved
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SVGRGFANTTNSFSLSILNPIKLDLDYGVKNTTPSTNCNSIRLSQRSPTIHKLGALSNFV
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WFFSVSLSCVFVSFLLTEEVRGCLERTSETAVCRTPGMDSVSPPRLYLPRSISIIELVDN
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VVLISLRNVCDAVLVMLLALRLGSGNKQMPRW
>TCRU_8703 neurobeachin/beige protein, putative
SCVRLRFTPLNFELERRTVHLLRQMLMSSFNQTRAWDALRRTQLLNLVVEALGSRSRLHS
LASESTILEDYMRVVELAAEANAFECMRQITLDGSTDAGLFAFFTLLVRIPLLDGGLNLH
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>TCRU_8704 SNF2 DNA repair protein, putative
MERFLQDGQKYCMNCNTWRRFRLSRFGCVFACSCTGVFMEFQKVFRDFVNAVALGERIVE
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ACHAEKTMCESKIRHKDAFKGSYRTTVDLYRHRLTVKGPRRVTA
>TCRU_8705 FG-GAP repeat protein, putative
VFVLMMAVAVGADPVKWAEPLFKKPLLRKLLPEEVMAPETVSSGPLSNESNTCRSGVYLE
WTARVGSSVFATPRIVDLNHDGNKEILVPTYTQYFEALDGVNGEDEIGFPFVHPNFKSYC
SPIPVDMDGDGKTEWLVAMYTGELMVFGDDGKARGAIQVPALPIKKNWMKRNLTGEEAVN
LKLQPVRPSAEYFDRILRARQMVDMTPRFPKMRQKTGDGNHGDAAAALGESRPPTAMPRR
HLADVDLEEEEEENNEQGDERHDVGTMPRAEEEEREMDLFFDEDEEDVNDEGALLESMEK
QHGIGAEGWLSAEAKASMEMLYHPELYKSSVNYEGEKDAFNFRNIRNPTTVVVAEDEVAV
DPHIMSTPVIVDADGDGDLDIVLHLSYFFDMKAYEGEKAELLPSDIDINDYVADVLMVLN
LVTGEMKWMKVLHLSKKNDTIPAYALSSPVIANPDEDYQQDIYVTTTAGAIFGFNGHGKQ
LSGWPVWMSSSITSSPSMEDVNADGLIDVCAGDTEGNVACFTANGKQLWSKTFSGAVTKQ
ITYGDVDGDGSIDLAFGTTSGLLYAVRGRDGALLPHFPIATEGPILAPPLLVNLNNTQPL
SQQETEGLHIIVPSHDGVLYIVSGTTGCVDGIDINEKSSTMVLADDMTGNGKLDLVVSTL
SGSVMVFETQAAFHPLKAWISRVKSTNGLTASEGYVGVFIHPSSRVPRDIRGEQFVLLVT

IYDQRRGDAIKRRYGLTITIGPRILVHHMVYGAPGTYAITLRTPLERMYASLFVVMLLPN
GQRYEDSVALSFNMHFLESIKIIFLVPFLLACLAISFVRKQHEV
>TCRU_8706 cytidine deaminase, putative
IPVELQRLARCAINAHHNAYCPYSKFAVGAALLHKDLKITAGCNYENCTLKGCCAEVCAI
VKGNSEGRRTATAVAVYGCSKVPDVMNLPPPDTVTPPCGFCRQSLVEVADLSNNYEDFLV
VLVTLDKERVKLVKLCDIIPLKFGPSNIGMDLSELA
>TCRU_8707 UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase, putative
YIPRRVVDTWSRQEYLIVLGILSVDEEERRTRRNLQRTTCWQFPGVATRANDFTGAMLVL
YVLGRHPSHGYDYSAALLEEASQWNDVVALPMNEGRVTTNKTVGQYGDWGTEVTVGLNRK
VYMWFDLALRLFPNARYIAKGDDDIFLRVPLFVDHLRLLPHRGIYMGVHGGSSLWENDRS
IDVFFMIGWCYTLSRDVAEALLSYEPLQRLAHAINATAVAEEFKMFYTNEDVMVGRVLVN
ELNYKPLVYVKVLPCHFHDARNGTGHSQVVPTSMCVHHVLEDDYAALMARF
>TCRU_8708 translation elongation factor 1-beta, putative
VKDAMTTLKELNGRLSSQPYVSGYCPSQEDAKIFAEMFGSCTAVAEWAARMASYYQAERE
QILKGTTSSSKKAAAAEDEDIDLFGEATEEETAALEAKKKKDADAKKAKKEVIAKSSILF
DVKPWDDTVDLQALADKLHAVKRDGLLWGDHKLVPVAFGVKKLQQLIVIEDDKVSSDDLE
ELIMSFEEEVQSMDIVAWNKI*
>TCRU_8709 predicted RanGDP binding protein
EEDLVDEELLARLLVQEASPVATPTAPGPLPRPKCMTPSTSTVPSTAPAVPVTEEGSGTR
NGEVTLATDMFLEEGGETTLQRSALPIKSSRRGNQHVSKYSYIRRSMHTKLIKEGAEPVR
ESALEWMCSGCRTYNFVGRKLCRRCRQRDVDSFKHTSPPARHIPLFPATWACHSCGFINR
SEAHSVLSRNKFFCEGCGIRFSGVREWYCPSCHCINSRGSTKCATCYHERPHLWTCSYCK
YDKNSIFFTECHNCLASRSRQVSDSTVLCPTCHQRNDVQWEMCFFCMTPLGMMVSVKRLQ
ERLVGGVDKVAKKLPSETEEGKRKGGGDDAFSELATAESSPIVDKGTGENEDMRSNTSRP
PEPGEDDSQKCLNNEGQQESNPSPERISSTREVQIQEIAANEDGSWWCDECQVLQRRNAG
FCDICLKPKVVANSGNVSAQREETVQTGWTCLSCAHQNEDASRQTCEKCHNAKPQGAGVV
QRDEQQGIRVASAATSDAMETVSVFSFVGDTGQWRCPYCRKMVDVTEISCCGVPREIPFG
YWLCDSCCSTNRDERANCMGCGAAPPAKPWRCFLCRFGNNSKDLFCVRCGSAHPHHWECA
KCGTKCQQASHSRCFSCGAEKTTQEVINCEACCAPNHASRRSCYRCRGRLSSDKWRCGAC
GSTENERQARRCEACGSPREYNMEEIIWICDVCDAAVASGGDLPERTQCPLCSSERTERS
LCLPSRWRCQGCGVLNSYSVPSCLECGGKRVMEGLHTHTTCSSCFRITVLTKQEQCSNCG
ADLSSIINEAGNPISLNGIKSLLVENNPLPTSSADGPMRKCNVAENTSVARRGTASPCST
RENTVTLRQPSNEQRRDADHIVEKKTCTDETLGGRMVTPYFSSSISPSSLAAAAAETVLT
LIPNKTNGNNFLREEVDEPEGVMMDVISEEEEDEEKEVDLEGVEWSSSIPSWMCVNCETK
NLEEAETCVCCGLRRGD
>TCRU_8710 hypothetical protein, conserved
RRSRSTDAAAIAQLTRLGTVTPCVPPVALFPWRTEADFLGLIERSVICITATSKITGRVA
GFVCLDDIPHVTSILAENWENTLKHNEDNNDSDDADVEIAPYNTLWLKSLLAPPSSAFLS
HIIDPRDLDAIRTERKLLLFGYEEEDMISELLSTALINMPGVMQLLVPFPLDCKYPPIEC
LGKKSISLSDCFFEGSLLRIFASKLVPRLQLRLGIMEDYDDFVPEMLRGYGLITALPEEF
YLDELLKDQDAFHKVIIAEDAVSHRVVGIMCLEATIEDQQRVSRQYMTEIFDKFRPMNNR
KDTGNFSTLDIPNVVKISFFQIDPQYAMCADQFLPFVFQEFPYVEYAMIILPHEKDEPPF
LQQFEHVPLRRYQPRNARGEVIPIPQGLWIYCRYAADPIWIQPVLKNDDVESISAFLNEP
FVEFSQKNIATLLEDMRVSSEENTSRENLPQNSMSFMLQSRLGGEGETFIVGVASTRRVK
VGEMYALRANYTVDAFVNYHVGGPRDYSVTDIHLNAEEGRRKFFRGEMQAVMVRFFYIKP
VYRCHISFFLREILRHTNCEVTLVLEDGQASPFPPLLRQLLRAPPRRVQEKTPMAVAEMG
SQGGDKIDGKEPVALGCLFVGTRRIIGDRKKMINTRIIVVGAGSTGLACIHRFLSVPYVH
FRNIVLVSTDGMPAHPNQQSLLWFADHMELLEREQMGLFVGNPVRVVHGLVMDVDTTQKY
VSIDDGTYEPYDYVILTTGRQYVVPNSICCLQQLIQQPLSNNQRGFVPQGTLALSGESSV
EKLRQHLHDLDRNPHNISNVIVYGSGLDAFATATSIVSLGFSPQRIVVVSPETSNPFLDK
DAFDCAVKLCNSLGINTLRGYYVTRLEYDDDGSALTTVVVSPVLVSEEGGDRDNTTGISN
SVELGCSLIVCCEDKDIDSHVLSTLNRRSIVFDGRVIVEANYRTTDKCVYAAGPVAMFTR
RYGTTPGFEDFNTRDVGTSLAEILLGVFGLDEFADKNLREVGDKEEEITAAQNQLYKRVL

QENGSNGADFLMSGGALSTEEGKKNIAELQKKLPTYNSPVASRIRLPVNYVFFCSRSIDF
KPERCLRLFYSNIEENKPVVTVMEELEASPSMNIEDLPTRIPEQNLFVIYIDEQTHLIDA
VVYFGNGAPEMHNYVCLIGMPQSLLNLIYRYEEARIANRDESSHQSSKHEGCSHNDTGNG
SGLNLLEYLRLPKLQIFFYDRFTVFYRELREKMRDHKDLIDAKARAFEFLTEESTLSDGC
RKKNLNELTAESSSFARQVQYELIKFLHESKDYLPQIYFLPDIRSHVK
>TCRU_8711 Polynucleotide kinase 3 phosphatase, putative
MADAYRILKSSGSDTLAGLCSEQKVDLNDVWIPLQSFCSARGRMDTPVFISPATAIVLLD
HSSGKLVTRRGDILARIPLLFLDERNLAIPPSAIPDGCTLFVRAAKSISKKRMVKGLSIL
HRPITREQAFVEGSSLALDGETQVVQKQPRKSTGSGADAVTVAGGIEAALEGRKKTAKID
GLFEEYLQKTLEGSRDGRLANGGVIMKETMANLLRVRDAAPLHFVMHGKSKKYIHVNGIP
WFIPDWRVIYRVFRRGETVETAKTTYTDAARLVAVFMIDNVLIRREPIHACLQEGHPMWS
LIDPNLPSAAHKLAEKGYRIVLLDHYPSLHHGNEIALEAKLNPIAELCQKYFTCDVTVVL
STMSYISAAYRSDGKPFLLPYSGLWQFFITQLNGGLRADAESLLVGESVEGVDHRREDVL
SQGRRDAKFAMNCSLRYVDSDSLKKEIL
>TCRU_8712 Domain of unknown function DUF21, putative
KPSEKSTGKPVVSRQQMNKNIYRVAHHALYVLVYLSLSAVFAGLTIGIMCMDTLTIDIIA
TSGPEPDRTYASQILPLRRQGHQTLCTLILSNMLLNVLVVQETAVLMDYVHELEAFGSIG
WAVKENNDVTSFVLSTVLIFIFTEIIPTSICKSKHSLRIAAAGCVLVRIAMVLMYPVAIS
LGWLLDRFVAHDAGQIYDRNELRKLMILHCEAHGDRSGLLKSEVKLLMAAMEFQERRVRD
IMTPVDQTTVVRAEEVITAEVIERLWNCGRSRIPVEQTPQKYIGVLLVKDLLTLPMPIGD
RPPITIGELVKAKSRVFATVDANTLLPTLLRLFQQVQTQMFLVSREKGIAGESEETAPPY
ILLRTPNHLEAGKKIVGIVTLEDVTEALIKEEIYDEYDRYEFPSDNHLDCLTHCVHIHNK
EIPMPFPEPAQVPRANFYSYYVHNTENIPLTEAQVWSVAYYLTRAVNAFFLWHPGYVKML
LDECGDQQLIPPQVGFGDEVAVENTGSSSQRYPPLNSPTKSENFDTVPTVPIISTSGEGQ
EFFSPTFLSVVPDECFVLYRDGVQTTVFTLVLGGTVQAFVGSSKFPLRRRSFQWFAEEAL
TLENYVPDFDAFVLSPTRVYLIPKDVYARYLRYNEIYTHTYDKIVMMGKKTTGMT
>TCRU_8713 metallo-peptidase, Clan MA(E) Family M41
SAQPGGKGPTAGDGKNDSEGESDDFAATAEDNGNEDSLVERSVLFVLFMFLLSYVLYRLA
QPSGKPTGWASLMKHADIIESIHLYQNYAQVYMEEAKVYLGLVDDQHTQEKLEMLRAACI
TAKVNKQQSKKEPNDGTNSAGFDVVMKGTPLAEHVLVGLGVFAWVIPFVFFPVFVMILSN
SIGKSLAATVDAGKKSQKVKDMVFRVERTSNTRFHDIAGMKEPKKEITEVVDFLRQPERY
TALGAKIPTGALLLGPPGTGKTLLAKAVAGESGVGFIPVCGSDFVELYVGMGALRVRQLF
ETAKKQRCIVYIDEIDAIGLKRSGAGHGEKQEQEHTLNELLTQLDGFSSGKRGDLMILAS
SNVAQEMLDPALIRPGRFDRIIYVDMPVISERIDIFKVHLSALRLLKETGDPAGTEAMDS
SADAATTTAGREDSAEHPATQVKGCTAIDDTAVGAGDDPNASTTVNDSSSSTASSSTSTA
TAAATPNVKESALTISQLQQELDEERQSLKEEEGLSGHASFDFRSLLAKKSERERALIST
YAERLSSLCPGFVGADIANVCNEGAILAAREACEFVDISHLERSIDRVLAGIEHRSRVLT
PFEREVVAHHEAGHAVAGWFLNRAEPLMKVSIVPRGGSALGYAQYLPNENRMRTATEVRD
SISVTLGGRVAEKIFFNHLSTGASDDLRKVTHMAYQYVSSFAQRPVYPAPGTHGTRFVKP
FGPKVSNELDVEAKKLVDEVYESTYKLLLSKKTEMETLARHLLRKEVLTYDDVVGYFGVR
SSRLSDRKK
>TCRU_8714 Leishmanolysin, putative
PRHATPLLPFLVLLLMCCANACIAAAPALQHRRGYDETMGSSGPLPTAVLHEVPRKGQGA
MQVYTVAAQDDDSGWEPIRIGVFTEDLKSKNRKKMYCENDGDECDNILGEKITCEKEHVL
TEAKKQLYTGKILPGAAKLHAERLLVRPPPEKITVPRTMGSPCDRFTVPTEHIKSGVPNF
DFIIYAAAGPSGTNGRAVWAATCNTWEDLRPSIGAMNFDPKYMTDTAWSVRVAAHELAHA
LGFSNDSIERNSIETTRKSVRGMRRKMVAGNHVQEKAKAHFGCKSLGGMELEDEGGPREK
AIPHWKGRHARDELMAPTVGAGYYTALTMAVFADMEYYRVNWSMAEPMGWGHRSGCDFLE
KKCKEAKDFPTKYPHMFCDANDKKTLRCTSDRRHVGTCTASIVEDKGSPADKDVCPVVSS
EFHEISSGIKYNTCSEKGVNYLPGSLTGDDSWCLDAELLETKDGKNKNVKGVCAQLSCEE
GTVKVKYLGSSGFQPCTEGTDIPVTLNGFKQEGKIKCPSYGEVCTIA
>TCRU_8715 hypothetical protein, conserved
EDSAYWGFTGGIDSLLEGVVLQKHWGPVMRLSHEGSLDEWKVTNISCARLTSLGVKPHDM
KNRYMRHRAVKDFTGCDMLSVPFNPRQDQRCINFLTNASNWKELVPIAQTKDQRTIKFSI

VFNPIWVADGGFIEQPLETIIKVPQRPFPLEAVGEVATFHADRLLLTYRVPPTGWACLPI
SMIEDSVAKYKDVVETNEEFFRMSGVNNYNEWVKKDLFDYVREKRYLERSVNGDECIGVS
IQLKIADVGHFLSSVMRIPYEPHNDSWHAFFDLNNIAGERVIDFIRKRNYAGVLHLATLS
MFDYFVGNMDRSPNKNNFVVGGTHIGSNENDIFMLHPNHPTFVYLDHGMTFYYRRPRRNP
LTKSYGAFKRNKPGTFCLFHGPLLRRIRELVQFTGGPMNETVFAWRMQRRLPSHVYSTIG
PEGLLRSSTRGKEILAMADRCLENEHIRPYVLFP*
>TCRU_8716 hypothetical protein, conserved
LREKYECMKKMRFNETQEALARECDLSRIIIELQKRIEDAEASREFEREVHARESFYLLK
ENECLKEQVRTTEKMLLDVRNNYNLEISKLNTRVSDLEDSLVAEGQRAKTREAEQERAIQ
NLCSNLYTTQGELERYVEKNRELASVNSLLEEMRAESWRDKRECTVWYEVLRRREVFMLL
EREAFTELQCLCMQEMNRFWQIKDDSYQAMFCSEAERFLGHIIREAEICYEMKQLMFDNA
TASIEKETWISLHFSKVQELSRLSEKHEALSILLAQYMREVEEIQQGNLEQVLRRKTVDD
ASIAYMLHQRDNEVSDKLRTWKGALQEAHKLLTALLKRYEPFQRGDEVFVGRVMEWLISA
PHVKEVINVFL
>TCRU_8717 Adenine phosphoribosyltransferase, putative
MSLEEVEPNFFILSPDSPLRETIQRAYRWYSPRFSPCDVPRFADVGSITEEWSVMRGIRD
FLVARYRNLPEPPTHIMGFDARGFLLGPMISVELGVPFVLMRKAGKNPGILIESEPYQKE
YKEKRAEAMTIRCGSIGKGSRVVLVDDVLATGGTALSGLQLVEASGATTIEFVAILGIKS
LKGAQLSHSYGNGRFSKIPFFALVDESVLTEANCGDTAGYNGHRIIGYREA
>TCRU_8718 hypothetical protein, conserved
MSHFLGKGNAATFFAMVLTSGQALFFLYHKDSYADNPVMLRSSKPMVMRDVFLTKCSSFF
PNPLSCVYVHKASDAFLNSLTSWLLVRPIVDVIGWKSGVALYAGSGLFSSFAYLFGCQLR
RTKTNTQFDCNATSNGAFAGFAALSLMMPKCYIPASRRAPVYYVGIPYIVKCAYDEYIGP
IFFEKREPGNIELRNWGFVGGVFFAFIFSSLVLRTRSDFGRMNLFWTNLKKTS
>TCRU_8719 protein kinase, putative
EMDRFIVGSPIGEGRFGVVRAAVVKESGVPAAIKCITTPRLDEGIPHPTARELLVALRLV
HPFVIQTYEVVPCGCSLALVMERCKTDLATVLSGRTASNPLPALEAKSLFKMLLLALAYI
HSEGVLHRDVKPSNCFLTAEGELRLGDFGLSRVWDTEASMTHEVFSRWYRAPELLLGQRH
YGPEIDVWSSGCVFAELLRGTVVPFFAGDGDIWQLSRIFDVLETPTPTSWPSAVLLPDWG
KVHFEPKRPLPLHEFFPDASECALDLLRRLLCLDPQKRLTAAGALRHAYFSE
>TCRU_8720 pyridoxal phosphate containing glycine decarboxylase,
putative
MYRCFHHFSTLPLAFVRRTATNSYVNRHIAPSAAESISMLRIIGKEILSDRMTAVIPENI
LRSPLKEVPAMSEQDALSLLHSLGSRNKVLKSMIGQGYYEPGTPPVILRKVIENPAWHAP
YTPFQAEISQGRLESLLNIQSMIIDLAAVNLAKASLLDQATACAEAMYLAFHHGQKERMT
FYLSRDVLPSCVEMVETRAEPLKIKVVVGDPNLIDWSDSSLCGILVQTPDAMGMLHDFTT
LFGKAKQHGVVSCFGTDLMASVLLKPPGEMGADVVLGPAQRFGAPLGFGGPHAAFFAVKE
EFKRLIPGRVIDISKDSTGCPAIRMALQTREQHIKKERATSNICTSQALLANVAAFYAIY
HGSEGLREIASEMQSRAKILSVGLESVGHTVVNGTFFDTITVNLNGITPEDYVACCMEKG
INIFVDYSHGTVSISVDEASTEGHVVSLLEAAGLKLPVIGVLSKLTEQKRAMPLQMLRKF
VFLGHSILQKYKSESELMRYIHRLHGKDHGLTHGCVPLGSCTVKLSPAAAMFSLSWSEFT
NLHPLAPKEQTRGHSALCLDLEQKIRDITALDAVSLQPNSGTQGEYAGLRVIRSYHNSKK
ESHRNICLIPESAHGTNFASALLAGMVIVKIVANGRIDMKDLENSCQKHTKNLSCIMITY
PSTYGLFDREILAITSMVHYHGGQCYIDGANTNAMVGYTAPGCIGGDVCQINLHRTFSIP
HGGGGPGMGPIAVRQHLASFLPDSVFIQNVGGSQPFGQFSQAAYGSASILPVSYLLLWML
GSRGLKKCTEYAILNANYLKKRPDGHYPVLFLGENDFCAHEFIIDLRPFKKIAQIEAEDV
AKRLMDYGLHSPTLAFPVAGTLMIETTGSESKRELDRLADALISIRTEIASIEEGEESTT
NNVLKNAPHMANCVTSDDWDMPYTRKTAAFPSSHSSTEKFWPSVCRVDGSYGDRNLMCSC
>TCRU_8721 aldehyde dehydrogenase family, putative
GMMPRTRVLRFVWKQSYRDLLPPAAASAYVCGQLRWCDSCDGGGVPAVLESPSDAAGVYS
FFSQSTASAVRALRDVTRSAHSLSITDRRLALDGLAVLLRENADLLASADALVTGMCLRD
ARCSLDAALNFILFCEQRLRPPTAAATTAVIMKDAASVDAEEVLHSFGCGGANICGDSHV
VSTLTGKSSVALCVTAANYPLQWGMETVATALLRGSAAVWLPSLDTPLSALWLMHLLHRS
NKNVVADSRGAVNIILCRADDVVAAFSRQQESGLSIVGLKNGFRDHQLSRSHQSHGIPSA

ISHGSISCITRWYYRVMKPSLAVVGSGHHHTETMAVRLDAPRVAARICQHAFHGNGRMLY
ALHIAFVPKQDVLPVLQSVVQYVRNLRLGHSLDPSVNMGPLPGAAHMAAMKETVEAAVCC
GDVKLQHVCGGFDVAMPAGFFCLPCAFYATVASMTPAGTEMSIRVLCETTARLRFGLDRL
GGGPFVVVCGYDPPQQREALEVVLREKEQYVLHYW*
>TCRU_8722 Leucine-rich repeat-containing protein ODA7
NDQLFLQCRGFLRIENLEDYVNLKVLWLEQNAITELTGLETLQQLVSLFVQNNTITSLRT
LAVLSNLRVLNVSHNYLTSLAGIAQSCGQLETLQVSHNRICSLDACTELWELKNTLTSVD
LSFNKIETDGGNLGPVEFFTHLSNVSVIYLHGNPTICGLKGYRRQMVLSLPQLTYLDERP
VFPEERRCVEAWGAGGEAAEKQERAAIQEEKKKHLESCVRVFSDRMEENRAVRDKLTKQW
DEKRALELERLKNMRREFRTQQEGMILMEERCRLSVVDAEVASRLGIEEGFRAAKIPLDA
SERAHRKAYDHEKAVEAVREEALKEIEEEFQQQQSEHEVAQNSTFGLLMSDEEMLQEMEE
EILRVLEPLGGAHQLSRTTLKMTRAVDAVTTRLCGGKKCSASSQRLRLWEKFALWEE
>TCRU_8723 2OG-Fe(II) oxygenase superfamily, putative
ASTSSSAVKETAKMPGFEFSTPNFSLDGGMDVDAENLVKDLVTSPVTELNFVRDMYGPWL
VLTEELQGELFIDHDRMVYLRPANGLGFGVGRIDVADSSLTGIAFSLQLEAYTYPVTSTM
PPCEPIALDVTGFLKRVESASGDYATFSLVATWRKKDGTSGKFNAAKLSPWDPVTSAKPW
EPNVELQGIFQQVFPQPLVLTSHLARLKAAREASGDTGGAHPHHLSLEPYRVGDIPSIYY
IPNYISEEEEQQMLQLVRDTPKELKTQLKKRVVQEWGCMMCEVCNKSFVSDRNIPPWVDA
FNDVMLHDGIFTPSTFPNSIRLHEYQPSEGIGAHCDGPIYFPLVSILSLNSPCTMFFYSR
REPHAQPMEHYNDTFRFDTGIAVEKPVQCAVLEPRSLLLFRGDAYYYHPHGTSDREVDDL
SPEVAGTVVNRHLLKDPNVTEVKKGYRVSITTRNLLPRCNHQPSRVEYGMKRAWYVYNQL
PVPEPLMTPAPLPPPSTSASSTSSPATSAEEMTTAATTRGMPEDKNTPVAAPMKESSRTS
FSELEKKLDALLTQQTTLMREVSEIRRQMAMETTFRNELSTVLNHLSATVLDIDSRLDSK
ED
>TCRU_8724 Beta-lactamase superfamily domain/DNA repair metallo-
beta-lactamase, putative
SVANTTRRSTTKQNVVAEYMRSREVYRGETVAILVDAFRHTHAYMKSCREDRNDSCVAGD
LIPFRVLFFLSHFHSDHYNGITEGWNHGTIYASHGTANILCWRLGIPESRVKRMDFCVTY
TFSLKNGALLYETTWDEEEWRCSDEFFSVTLIPAGHCPGSVMFLFRSPVFGTVLHTGDFR
FTHEQPNSSLLPHVPRMPHFQKEIDMMTNPVLKSVAGKVDVLFLDNTFCDERFNFPSRAD
SLREVNQAILSMFRDHTSSLQGVTKEMTARGHEAKEHAISVAVLIGTYWGKERIAVSIQE
NFLPLCAEDSTCNVVPTYVSPEKYESLRQLEYYCDHFMALPRREGEVKGGGSTLEVVTKH
AVRLPQDTLSCSSMVARDLFPSLDPVEVSTTEIAHYLTIFLVPLSSVTYPGLAAACGGRP
KRRRSGSATEEGVDGSHQNNSPHGEFFPLWGDEGIDLKQFDGVLCVEPSGWTRKARRQIL
SKRVTLLHVPYSEHSSFTELVDFVGFMNPTRIVPTVSLELFQKYEVLFAEKAPRLRQRYS
NVQPLSRFLVPKSPLAVGGSERKTLDGSSENVSKARKQRNPFA
>TCRU_8725 AAA domain (dynein-related subfamily), putative
MILTPTSESNLNNLKVALDSSKAVLIQGDIGCGKSFLANTLADKYGAKETLLQLNVDDSF
DSKDLLGKFSATDTPGTFEWIPGPLTSAVENGFWILLEDIDLASFDVFSVLLSLLEESTL
FLPEKNRRIHAHPNFKIIATQQLRAVGDTFITRKSNSIPFAELWGTVVIECLPPDEVCEV
ATALYTVPRNIVYALSVLLSPRTNTPLVSLRCLLKWCKRVIRRLPATCSLDGFISSTLRE
LMFREAFDCILAGYPEGDVLTSAMEVLAGAMGISPNVAESLVKENRPEMVLAREYVTVGR
VTLPLFSFAMPERESRVAFAATKHAMSLLERIAVAVEANENVLLTGETGVGKTFIVQYLA
DQLGQKLIVHNLNQQTDTSDFMGGWKPLDVGVAVRNAYHKFVDLFSQTFNASRNVQFLEA
LQAAVRKCLWVAVVKQILKGVNSFKLKNTRQSFSEDFVNEWGLLEVTAGELLDKLEKTKK
TFAFQFVEGSLVKAWREGSWILLDELNLATTEVLERVSSVLGDVNALFLNDKGNCEPIQR
HKNFHVFANMNPPTDFGKKDLPPSLRSKFTEFYVNEPLDRYDINTVVNEYIGHLSPDCKT
EEITSFFLECVGKAKSTLCSLDGESRPPSFSLRTLTRALAYVRKATSQYGFALALFDGLM
LGFATSLQRQFHTVVQQLIIRNVFSGKQPPQPLLPQCPSEGYYVSYEHIWLHVGSEKPLK
DESFILTPSVRGHLLNVARAVFADRPVLLEGPTSSGKSSMVKYLAELTGHKCVRINNHES
TEIQEYLGHYVSDERGKLRFVDGILVDAVRNGYWVVLDELNLAPTDVLEALNRLLDDNRE
LFVADTQETIKPHPCLRIFATQNPAGIYGGRKMLSRAFRNRFLEMTIDDIPTTELCTILC
QRYSLCTSFAEKMVEIMVLLQLRRQASQIFAGRHGFITPRDLFRWAERQPETYQEMAEHG
FLLLAERCRKMEERQIVKDIIESVTKTELNEDIIYSPEHWPYVGECYSLVGNGVLDEFGI

VWTESMRRLFTVVGICLHHKEPVLLVGETGSSKTTVCQIWAALLNRPISIINCHQHSEAA
DFLGSLRPAPPNQRNKAIFEWRNGPLVECMLQGNIFVLDEISLAEDSVLERLNSVLEPAR
VVTLAEKSTADVIFAHDDFRVLATMNPGGDFGKKELSPALRNRFTEIYVRPTTDEGEVTL
ILSRRLMPSLEPWANKMASLLCDAAKTSTATGVPQHISIRDIIGWVSFMNAANTHCDERI
AFIHGLDAVILDGIGIGTGQAEFGSRGLREICLRRANELSGIDEGCLQTPFWELFDTLEE
PRLPPELERQFFFGAPSTRQNLSKLIRASIIRKAILLEGSPGVGKTSIVEALGCAFKKRV
VRINLSEQTDIMDLFGTYLPCHSNDENEEPHFSWSDGVLLQAVKNGWWVILDELNLASQA
VLEGLNALLDHRSAVFIPELGEEFTAADEFRVFACQNPLLEGGGRKGLPRSFLNRFTKVR
IEPFGMEDLLCIAFAVCPSIDKSVLEKMVHFVGELHRDVMVYREYGTRGSPWEFNLRDVL
RWARFMEAYQKLNKPCEFIETLFTQRMRTDVDREKVYQLAGRHFGDALCEIHAAQEFDFL
IANDVVCFGGSFLAHRVQEPVKPDMAVPLLLLPSKASVIRSLLLCAEQNQFCLLVGPSGA
GKTFCIRTAAALLGARLMTFSMNATCDTVDLLGGFDQVEGKQGQFEWRDSLILEAMLHGY
WLVLDNVNYCNASVLDRLNPLVEPNGMLSVNEQGLVNGQVRVVRPHPSFRLFATLDPKYG
EISRAMRNRAVELYIDPICIPSFESIAIAGAVSPCKMSQLLERLGNYHREFVIAGFHADS
VLPMSAQLSDALAAGAPNTFTFLKTANMLPMDATLKDLETSIVHKYIRNRCGHWSANKAA
VVDALDRMLSEYLEQRGKCCPLVVDLLSGMNLSEELDGEDVESALIRIRVHRAGLGLKTF
ASLSNTSLIQHSVRDLLLFFVLEQCGDTVSNDRLKTARCQFLSSNLPTFLADNEISETLF
LLSSHDGKSSRTCLDSLWCRSLQILGPCAAWYKGLGGVHVLISDSPVLNNALQHVLEKIL
EFTSGALIPHVQQHICRYLYPLMCLLSASNAPFRVTADNFVSLVIIVALIRSVVKKQTVI
EAGHLIETIDQFLASLRRYLELPYPLIASKSAVQRSIIRPHITSADERSAFVSWNAGTRA
VPSLSDERPFKSLWRTAIFRAEFALVQRVQQIRGGSFFLSPKVLQREIRQFIEVFCTKLH
VLPELEVALWREVLELRLQEGSDGESLAALVPLLTSHFIARHGLASGCHTLHGSWTNAAY
EALKYAAGVPVISIGAQRSDHAEAVKELLMFCNVLPVLGVNPFEQWELHSLEELLSLLVL
CAPHLFPNGMDLNAVRRTSSTPALEMLEMVREGVQGPCSDPLLSAAQPLLQMLASDRGGS
PEDSLRRVALVGALKCRFLLPSSPIDPMHKWLVKKEVAREELGRLTCLEKAFKWSEEVSM
RSSTQQSRLLHELLTAEEMLLLKATKKSVVRPDLSGAKFAHLVSVLHQMCNTTLSDERLS
VVLFERSQEAYKARMTWSELLYQQLTEVLENYGGYEDVTLTMAEPALLSALAAHVSCRLE
SSSRLGNALFSMAEAARMMLFPQISVVSVTLPSSATHALERRLAYLDSCLTLVQSTPARI
LNREFVEQLFKLYREFYRTVEELDAKERREEEMAVLYAEKAISIEGDDEKHLRVLKKLFP
SYEEEFIRMRDAEDDLNEAEAVDDMPQSSLPLSVERAGRHTRLILSGPQGARHVRHLIET
HHQFFERLLALNDNSVFDGEKALRAFKSRFDILSSELHRFGFSGISDTGMMLPAEEEQLL
LGGFAARAVLVTRELLSTEVSLEEKRATGFNVFTDPAPSEIRGFSASLRDLIQAVEHLRS
TYPDTPSLHRCFRIANGIAALPALTTPLMKIMTGCEVLLRECYEWERNASRGTSILSHMT
KLSSFVLRWRRLELHCWSQVFTAKREEWEMKSGMRWFWLCDLIEGADSMTDEALSERCLL
FFRHCMDFMWGAHYGDFHLRLRLLKAFALQLVASSSSSPSMSLSASPLANVAMHLVDLFS
QFSPLVSEKLRLALLPLEEDMEAFTRIMRWEDSTYYAVRATAEKSHLKIGRALAELDEIL
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TRSGKQIPMETSEPRDGNAVFAHGYLFQGVQFLTDAAEEIIERVQALQANGVPQSQKLRA
LKTLFIVMQEQGVPHTHEEQFSSWEELFASKNALLTCRSIHGHLAVGQRVEEAAVEYYRF
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EDIFGNEEAGEENEADENNEETGNFENREEALREAEKELQGGEHELAADAGGIADTDEDV
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SIGSDIDGDDVDNDKESAVSHKSDSDQPDENVFHGGRQDEHTGEEAT
>TCRU_8726 acyl-CoA dehydrogenase, mitochondrial precursor, putative
RKVSYLGGLFNFKIIPGEMFPYPCRKMDGDEAENLESVLESVRSNKNILGNLYGAQIATE
YGGLGLGHTAHALIYEELGNNCIDKSFSTMRHSGVCTHVLASTGTKDLKGKYLTAMSDGT
IKMGWAIEEDGFGSDLSMNNTRAVMNDNGSYVLTGQKRCVDAASATHFLVLAKTVIQRNS

EEGATVANRSSLFICANDAKGLRIEGDSIVLENTPVSDVVGVMGEGFKDAMIALFTDEYL
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CTLVSAFVQATTAQLLRMLELLKSPNTTIDNYFRYATTFIDLMESRDFLYSTAVCCGVEE
YGLFFQKASTLQMMQARALRFVGVRDRVPIKNIPESSLIDDAVVNFGDAVEATFVKSGSQ
VPYQQLLLNRLGEAASMLYAASAVASRASMCVTKGLPSAKVEGKLATAFIRFSVERARIL
SEECCNVGKTADDVYKRIALEVCDDALQ*
>TCRU_8727 maoC-like dehydratase, putative
MLKVCLGRMGRVIRIGDTAFTRRVISQEDVKAFGPLVGDNNPIHFDENAAKAAGFPSTVV
YGMLAGSLFSGLLGSELPGPQSIYLSQTLRFLAPVLVGDEVEARVTVTQFKKSKFMIAFR
TTVSRIDPETGKETLCIVGTSVGMNKTVTFEGESEWTVPRVE*
>TCRU_C terminal, putative RAVE protein.1
VFFPQRCSHLSCAFNALGELRVAMALADRLLFLKEGTLCACGPLFNDPGGEQVGSEKNTE
AATLRQLRFCQFSDEIRVAVVGTNGVTVVDVSEGDMQLRHRRVLVESHLGTSTVKRCASS
FFSLASVLPQGEATSFSTPSWMSGWDASVRREEVRGAVDAEFTSVSSLAIVLGDRAVVVE
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CDPSILFPPSHAKASFNGKDPKKCDKFALRGVLAKLGVYKVAAVEWHHIAAHTILCVTCQ
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KLLLPLQENYGKIVRVDVLPVWKFRAVELGAFTPQAEQLMRTRRYRLLTHFANGMVAKVM
IDLLTMVIRVEAFLTLGVDSLPLCLSTSRGNDGEVLLLGISHERAFVIEQVTRDRGVAET
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PIARVENRLACFLKSLLLLQNSRADPLSDEPLPLPMQGVVSRLVIVAVRLVLLSVAIQNT
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IWKSHLYILGNAPPVSPCIAVSCVAVSHYDDVLAIGTQDGHALLLRFHTILEAKSSCLEE
ASCESKMATYVTGENVLYKASRLQLAPVLKSHSGVSCMVFAPSVLLAGLNDGKLVA
>TCRU_8729 TPR repeat, putative
LGMTASARELRERLAREQLEKARSLKVDTHEQAVEAMQHLTLAVTYKPFFVNALLFRAQL
AARLSRYDHAVSDFSLVIQLEDHGFDRRRLAAAYGARGNVLRKMNKITESIIDFTRAAEV
EPDNGTWLYELGISYLMQGSRALAQNFFSAALGEKVTGRMTENVRFRTLISLGTCKLTAG

DVNGAESVLTKGLEMQETAALHNLLGIARFKREEYKTAVQNFQRALEFDGLSSDYHINLG
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CRYTLGDYAGVFTDISLILQLGHESAELYYLRGRSHYALHAFQDAVDDLLQAATLQPLLN
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DEVVW
>TCRU_8730 hypothetical protein, conserved
VNVQARYRLQSPTLSNRAGDALLSASPPYTWSSSSSFYGDVNQNWFATGQAPSTPIPVKQ
DNDGGVGMGGRGMPPFSGSYAPSGFSMPPALADSMSTPINDKVLRSPHQKVHIPLQHLGS
PPSMLRGKEFTASPTLLSMTPPYPKDVQSIQISPTAMSGHGGMRGHPVVAERPQGRQSKT
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HGKLFRHAPGQIAQSDALTSVKGTQKALPAEALASVNFSSISPNALNAYRIVVTHGDQSY
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KRKEDDAAPRVPLDEL*
>TCRU_8731 hypothetical protein, conserved
MPTGAVMEQTTHIGPAEVTALLVQRDVPIACSTRPNGVLFGGIFHGLGKTKINAKYHSLH
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TLRQLETAFPLLTSVDVQDRRRVVSGALTRFAGGLLSFYDDRVIALKHVPVHAFSLLSLE
EFRMVTSMEQASVAFLFKCQMRHEEVLEALQTVLDAWGKRGAALASSFMRLAVAVILSHA
IGTCALLPQDLRGSVRPFVLRYLPTLLVLHGEEPILGRLAALLRQPKTHKRSTPISVRRR
MEEITRAEPIVVEPSAACAENVARSEMEGGYFFESVAPLPQLDSEVAWKIAKCTCRHTIV
SFPKKHALRNNAVGGSDPDCLFSAFLFSCARLHLSWPLLKSFGDEELCLSLNLGKASHAT
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>TCRU_8732 CAF 40
MHQGAPYMQYAIYPSQQPTMKPYPTMATVSPETRNMLNLLESLFKLELREKAILELAKHR
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TRKLFLEAHICLFLYPFLRGTGSGTGNVTEGLRLTSLGVIGALVKTDDNDVMQYLLSTEI
FPLCLKIMEYGLELSRTLATFIVQKLLLSDLGLQYVCQTPERFKAVAAVLQNMVGSKECT
ARLLRYIIRCYLRLSENPRACEALSRCLPEVLRNDTYKQALEGNPNIKKWLLQLLVNIGD
EGAKKILE
>TCRU_8733 NADH:ubiquinone oxidoreductase, ESSS subunit, putative
MTGWNQKMARAAFRRSKFRRLAWGDGDPYPYTPRATFRYQWDDWPLWEKIWHLAIGIIGV
EFSVWAYYSKLNSRMDWAREEALRRMRLRREAQELMILEGEKFDSDIQPDRR*
>TCRU_8734 hypothetical protein, conserved
AVTVSVRMLKRKLSPDRTRDEEIQDRQNAFVWSEKHIYRPHQHFTFDPCSWSRPLEEKVK
AKRQLSLVDRLRVLEEREREATCVVEEAKETNEYKEDVNYFYSIGKKEEKATSLQEELER
LNALHVLLTAPRHMDTSLAKAERLRQEYRDVLQCVFERLRVAVVDETMTFDALLYSWFLL
LQGAQPLLEALTERRKFDENTLHCVIVTVRDALDTLMLHAAKEMDATGKEEMLLEGLVEL
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QHLHALLRSMARCPDSVNESHLQRAALLTRKVVEGILATLKGVVAPSIRHSMCLSLLGKA
ARRPVFDKNELMRRRDTSCQLVLDACDPPSGVKKPTIAADEVSHVTCACVSLLRQATRAS
HVTRVKVLEAIDFHLVMLSHAPNYDLGITDTVTFVCELLEGGVLDVGTGAAERYLRVVLL
LSRLQFSLCDNQDVLCRLFFFFCSLAPHESLSESTLREWKRLYGIVMHQLLSSVRAVALG
KNYVCGSDRPGTWEELLAFGRYHGALPLSLWYDACQIYFDKATVPLSSKCARALLSLRTR
CKSHIGGVSTGKNKPSSLCASPLDFDSVRLLARMLHVILGEGVAAEDLMNEAAAWDVAQS
AAGNDEALSALLRGAQKCVQERQASKHVVMTF
>TCRU_8735 MYND finger, putative
MAIEESACNDDSQAVTEATSERTVNSATVFRYPFNTMDLGWLVGYIDAFLVKSERWAAAM
RLTTCFMTFTVLHEDPLMEDATFQLHKTMLDRSIKKSWPRRNRDLSNTFDAAYHVFETIC
IVSKYPNLDPAGKAGILRMSEKLIQGMEKPMDNVVIKIDLKKKSETLHATLARLQALGRA

PESLSAFDALMASLKMVFFCYVASLGINNMMLDANLNKMDSYVCCEGCPCHAKLRTTYTL
FIRDVEKTKVIDCLLIMAVKEDDAFLSKLAEGLFTQFDCRSPFLEKPVRRIQNGALFMVR
IALFDAFRHVKALLVDLRASPASLAPQIDNVVLALYIARREMRGMKGLNEHLPLVNKALA
TADSIYSRLGTENASQELRTLKDYITKIFFLVSAPEFHLAVHSKDPLVGKGAKLCCGNPD
CPGKVKEMLKCSGCRVTFYCSVTCQRDDWKTHRFLCKEMGCRKAAP
>TCRU_8736 EF-hand domain pair, putative
DGMISVGAKRLLVSVQDKNRRQKHGKFFDELLLVTQKAKRSPQVINIPGKNEVPVLAVGY
IARAMGLNLSNVEVSCLVEMVEEKDLASRGFVPADALKEVIVEALMTGIMAPPKAPVKAT
PSRKKTASTLPPATIKPISVVRDGEEAIYEAFCVLDLGRRGYLEAEEMRHFLRIGGEPFT
EEEVEEFITAAADPENGRIYYEEFADVLARE*
>TCRU_8737 protein phosphatase 2A, regulatory subunit B, putative
THVTNDAAVPQKHIVEKPHLMDLFRSSASFAKIIAYLQGCSDSVNGTPRSARMVQKASEL
HPTVRFFVETFFPHLHKIVEEVPLQDMKQQRFGNRAFRVFHERLEADVGGLMQQLVLTLP
ARSGERSEEEQRCLAVELAEYIKDSFGNSTRIDYGTGHELHFFVVIMICLEECGDAGGTL
QAEPTTIVSLNFPQPAPVLVDKRDRVCRLRQGMVFDVFGAYLTFMRRLQKHYHLEPAGSH
GVWGLDDYHHLPFIFGAAQLIGKEVPHKTDDSGNGKGYGAILPKHVCEENAVRLHADEYF
YFAQVAWVRENKTGPFFEHSSMLYNISGVESWQKIYAGMIKMYAAEVLSKFNVVQHLLFG
THLPWP
>TCRU_8738 serine/threonine-protein kinase, putative
LNEYRILEKMATGSFGVVFKVRRAADNEVLVMKRISLTEMDMEQRREAAQEIRVMSCLHH
PFIVAQRDAFLFKDSLCIVMDHYDGGDLAALITRQREKDEYLPMGQVMVWFAGISLAMHY
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AKRRDGELIGDVSTCDSADDIMNGPLIGAVRGTLLYMAPEVLESGVCSPSSDVWSLGCIF
YELLSLRHPFESRDLATLMMRVMAGARQPPPGHYPPEVVQLLDRMLSLDAANRPSCEEIL
RAPIMKAYLQQIILQRASCEPTELEAERTWEAQMQRLCICENASSPRLPYLSEKCPTMSP
SQERALVEQITAATPRTEMPLSPGTSTFGEDASPMRLHPDHAHTARSLSKDGSFTVERRK
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RRFGGDSTPTAHYYYSLARVSHVATTASTNPHSHKKGKSNGPSLSSSPLPLPSHGWKHAN
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MVPNRNWWHVLPLVEEVVVIERLLE
>TCRU_8739 hypothetical protein, conserved
PVVRSKSLAVTVAVGIPVAVLLHDTADRWLPKKWEIPIISWFRRKWRQDPETKVVHLALA
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EGLNEAGVRQQRDTALRRRFVHEIRSEN*
>TCRU_8740 PGAP1-like protein, putative
CPCTFSGTKFLVFVMFFTMTSIFAPAAYDWARMQRRTSLQAILTRMHPHFVEVSVKPATE
EYYKLWRYYDFEADRYRDPKRPGFPAVPAVYVHGNAGCFRDMRSLGRFVGESILKQRYQN
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ESEYLNSLCSHQSYERKGSNRVCYVAKEQIRRFSSTERIRREVERIQKEGIWIWTESVGG
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PQFCFFVDRAKLSEKHFSFVQHDRIDPSSQRTSNDTSRNDDLFSFKGEERVSVEKHGRFA
LVRNICSVSLETEMVVHVNNRAVFPHLLCGSFRSFRIAFRGTGGLAPDEPEAQQQYFFGP
YEEERHTFNYSWRPFSTVPFNLTNVYVVYVISAEEQPKIHLGDFELSASPRWNEHRYWVW
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SPFLLVLLATILLENIGYTAARKALTVCLNEDPPLRSDEELTSMMDMREKMTLIFLYALP
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FKMRLRSSVPTWRLVLFWSIPIFLRIAIPWLHISIITTIACFFSYAALWCFPHHRFTPGN
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LGVVYGTLHFSLRHFATMDAEAAVKKRNGENLIENKLKLKEGADKKISLSYSLGDISRFY
PRFNRGLIICSRIVLFFALWASLVSVRRPLEGTIALYGLCLTVVSLALRLARLW*
>TCRU_8741 DNA polymerase epsilon catalytic subunit, putative
HMPVAPDEWKGMESGSRTGWLFNYHPTTVMVADESSVERQGGSGGRAALVLLLQDHDGEI
FFVNLFYRPYMFVSVVEGHEHEVELGLMSLFGPQLIYHVETVEKEDLDLVNHLSGRRRLY
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SERWVDWVQEMREYDVKYHMRVAIDLGIFVGVWYDVIVHEGETKVTRCDDSAYAPAMPRV
CAFDIETTKAPLKFPQPEVDQIYMISYMLDGRGYLIVNRDIVSMDIHPFEYTPRPEYEGI
FETFNEPNEKALLRRFYDEMRKYKPNVYVTYNGDYFDFPFIHARSLFHQLNMREEIGFTQ
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KLCKSRCVQMESLQLAHKCILNSFYGYVMRKGSRWYSMEMAGIVTYLGARLIQMARALVQ
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PIPLTIFRADPTLRLHFLRKWTGDNSLSLDVDLRQLLDWDYYIARFNACVQKIITIPAAL
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VLNNTRILPRGRLATNLQQIDIPPGSKGERVLNALLSTREDVLAVYENHITRSDTFVEKI
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VFFRRVESTLRLIAEIREKVFQEIQADPTVVLATKSEQILLRQVKAFKAAIENKLHGELI
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IQDFPWLKESVDLALRFS*
>TCRU_8742 Polyamine transporter 1, putative
RYLSPTVRFRIPDGDSESRPKTALTTLTLLGVIYTASISGGYGLEESVSAGGPLLTIIFL
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ISALATYIPPILVGASAEALAETPFDEWDNGFWVKVGEAVGGYAMAVVVTVGGVISTVGL
MTTLLATTSRSLAGMGTLNAFPYLSGWLSQYDPKYGTPINATLVNAVVTCLLSVFFSFQT
LVELDQILYCLRLIAILVVFLELRFKQPFLERPYRAPGGLIAASLWGGVPIAFSVVLIVV
SMFGSVVLFFGTVVLVVGTMVISYVGVRFFRPEGFAGELVEEYEDADMQTY
>TCRU_8743 phosphatidylserine decarboxylase, putative
MTTLTRKLHFYKNDVTRGYTNPMRRWVYHYLFAGLAVGGGVCLWGNYQLAAWEALRHPEN
GNRLCSTATLEFLLLLPLNYASRAFGCLSESGYVSESVHRFFIKAIVWWYNIDITEGKQQ
QFSTLQEFFVREWKSESRQLASAPMTMPSDGVVLSVQENVQEEQLVQVKGMTYSIRQLFH

RSMGPVAEGQKRVAIVVHLRTQDYHHVIAPCAFKCKEVVYIPGALLPNTPAGFHWVPSVL
CLNERVVVLGQIHDGDWCGNIGIAMVGGTLTGRIALHFDSRIQTNFLNPPEYAVHRRYTS
HPLLRKGTLLSTFYWGSSVALVLDVPRETSFAVKTGDVVKAGEALITY
>TCRU_8744 mRNA cap guanine-N7 methyltransferase, putative
MLNINAKAFVPQSALEHLVNPGNAIYRYHLTLPIHSVCETSQGNSISNNIHTLLAKRCLC
SSFQGGLGEEPLQLFLSSFFDAVENVPFLTKRINASSGIILSRTILSLTSAVTLINAINE
ASGFLIHVDMPREYRAEVALRLRAAWDDFFEFVRGDLRITSFGYVGSSCGAESGIRYKGT
FRHYFFLSFSPCNYFSEQLIMDYLRSFPFPFLRIVQLNAIVPFMCNSRIPMGLVISVGEI
AKEKLLSDGKPDKTFSIFFSPYNVSETSKCLGEFEEMFVSFLKEYSFLLDRTYIVHIDIQ
IHGKDFQETRPIPVWDLVHFIGNLCEDTATSVLGICFSDDTIEESIQLNSSNREGNVCYL
NETLKKILEDGHSLDICKTYFGHIPAYIKRPMTCIQYESARKNFEKWLAIDYEPIPFTRM
VFADAADSFAKTKYYVRNRIIGEKILLMTDNEGDIFAAELKTGSIFALPHCFGGVSGPIK
NTVFEAVLTSSFRGYLECIILVEDILSFEGKDVKEMNFTERWHHVEKLLLDDQDSQPHTN
PDRVLIVRTSYAPFDQVEQVLQNPPLEQPTLGLVLVPQLSKIGNKRTFSYIWVPLESITA
RFFVGKVEDVPDTNFEIKRAWLSVRGKDNKIVPYNDEYADYSVVAHRFLESGSVIDCLLR
RSDDGAHWWEIIRDYNENQGKRPHSYDFAENLVHVPGLTYEEMLWLLKAHSFKCGRCQTV
SDVGKTNPRYQTYWCQKCWEETGHGECLYCGRPCSMGRIDSYSQRFYCDNCWDIFSSTNT
NAEIGYMVPPPPNVSFQTQVLTRCVSILIDSINSKAPTNDVLELCCGGAVTRKWIKNKTN
RYVGFDLKSSVVESTMEIISSFQDEISDLSSYDVICADAFSKELWTYHITKIHPRQFHTI
TVFAGFHHAFETEMKIRHLLYSIANTLVPRGVFLGCFFDIGIFYEKGEITNDLFTVEWDD
DFLPRNGHFFFISMQNEPRKKMNVVAIDFLVAVAKEYGLIVIPEVCLTFLDMLENDPHFT
MKFLKGEKEYLRAMRTFAFRKDGHPQ
>TCRU_8745 predicted tetratricopeptide repeat (TPR) protein
TNDRRMPPRSKSKKSRKALERKEKKLLEAKIKASQCKCEEGQAFLEPVGRNALPNYAKAI
AALEAAIEIYDGNADAYLLMGNCYRGQEEFDKAIECYTQCLGRDPTNARALEGRAASYAS
LKKWSLAFENYTAVIHLEPENDHLYNLRGLCTLSTRVPGLRLLSVEFNQCVSDFKTSIRL
NEANYYAWANLGRTYEDQGLLEEALKAYSSALKIKEDYEQACLRRACLAFRIVESSWEGD
DGKTGNEAGRAEENIEANSGKKSIPKSVEEVEEEVKSELEMAARRKREEELLQGAIRDFQ
FLMLDKSKKLKWDPCLPLNLGSCFLLQNEINKADEEFKTVLEIISARPQLVADGEAEPIP
DVESIVKVLNLKKDILKEIRGRLFL
>TCRU_8746 hypothetical protein, conserved
MGQRDALCYMCALRMSIMYQAPPPAPPSRLRLPQTEGVEGTIHDDGAPFVDEAYHPHFSI
VYETPRSALRFFDAETGDKLDVIACQNLPFLCCACLGLYQFMDYIHAPAVAAAIRTSPYI
DSDRLSVNVNVHRSMSFLWLMVSTVFYGVHGREGALPNPFAVIPEEHCNFKDFFMSDLRA
RILQYTTYSHAELKDRKTPVGYEIYLREIGRRSKNAVIGTQPQTIQAFIYSPENEGVIVD
ICSEHHRVKDLAGGDVVPPQYCSNRCDGVMNYGVLYEYVQPYLEKIGWWVNDRAAGGQLK
HFVVEGTATITFNLQHSNIMLIGNYRKMKRDLSQSPWFAYGERVGAFSLQEIIANPILPF
FFPEGVASAPWMAEANESTVQIEKRSRCERVSADQQHLEEQRVNPQQMAAQRVFGFGRYK
FHSAGREDVDVRMLGSGRPFVLEIISPSRQRVTPHDLAVFEEAVNKSEKGSVEISDLRVT
DADITVRLARHSQSKVKKYRCVVWCSRAIVDPEHDDYFQAVNAVKDLDIEQRTPVRVLHR
RSMQVRPRMIHSIRLMPLNAHWFLMDLETQAGTYVKEFVHGDMGRTKPHLGALLNGRTDI
IQLDVLGMEMEGL
>TCRU_8747 Tex-like protein N-terminal domain/Helix-hairpin-helix
motif containing protein, putative
MRRLIKCIAAARLKNLPHFRMAMRASSSVAVGEGGDVGKIVQERLYRIIGARMSISPAIA
RFVVEQTKKGSTVPFLARYRRDETGHLDEKALRQLIDMAEELQEVQRRRAFMLKSLKSRG
LLTDELREAFDKLLHLNQLEDAWEPFKEKKTSLSYRGREAGLEPLAKKLLYTSEPLTDVS
EKLRSVKDGAKLFQAIIVEEVQRCDEVRQLMLAECRQSGVISSSLAAAPRKKNAKEIGTD
AFETLKKKFAAYENRRWSVQRISAHNVLALQRGESKGVLLVKMIPHSRSKYTFFSWARRK
FVGFQRREDPKATRLLNQCLEAAYENIMKATHNIIRRDLKKSAEKEAITVFAHSLRHILM
QCPMRNARILAMDPGVTKGVKCVALDENGGVLTRFKCIIMDKANMRDYISGCVDKLKLNK
IVIGNGTASREVADIVADTIEERGLSVEYAIVSEAGASVYSVSDVAREEFPTLDPMYRGA
VSIGRRVIDPLSELVKIPVRSMGIGMYQHDISEMELLRALNRVVESCVTCVGVNALISNR
YVMEKIPGVTKSIVDQIVLARYAKKLKSREDLRRVPGMTEVTYQQVAGFFRFPNSTNPLD

NTNIHPESYSTVQKLLELYEGKERREVGNILLNLRDAELRDVASRIGCGEATLELVAREL
ASPALDPRSELPHAGIFRRFPPKLADLKPGDMLRGIVQSVTTFGAFVDVGLHDNVLVRGV
NIDTVHTGDLLDDLRFEGVDQLGRVRLRYDGVLHARGDAAAQSHRRGLTLESEEFLSLGR
LITPEAQPTLSDSLAVVREERQQIFASSLSLQGPHESARVAATVTNGSGNVVKPLKRPRT
EGGVHTAAAGQTTMTAATAVAAATKTTKTKTTPSSSLTDKAEVAAKSPRSKKRRAGGKRR
>TCRU_8748 purine nucleoside transporter
FSSYGETWLFLTSIVMGITMVMGVSAVTSAPSYMTKYYKYILKDDGAVPSNKKFWDTVLT
FYVVVTMVTQTLFEPMNLTTFCRRFSLNFRLQASCVLMLVELLVLLLIPFSSNASEKGAM
AALMVMAFVGGVGRAFYENTGYALFGTCPPTTVSAFVIGAAVSGALTSALQIIIKASMSD
EFESVKKQAYIYFSTAIGIIIVTMIMLWSLSKNSFARERILELRSKRSFFANIYRNHTPD
IRSNVVPGDLTNANEEKEEEFENDVTSSSGEDPYETGWLLSVRLWPIIKKIYPVQFSCFF
TYFMTYLLFPGVLLAVDVNDSWYGTIVVAVFSLGDLVGRLMCLIRRLWLSRKWVVICTFL
RIILVPLMVLCAKGYIRNLGAAYAISTVTGLTNGYLATISVSYGPETEGLQSDGEKALAG
QAIGVCLLFGVSTGSLLQLAI
>TCRU_8749 TPR repeat, putative
PAGMDPTYYALSLLRRRRLEECIAVSTQYLAVFNEKMRLTSSGTQKQADGVDEPLWFIQT
RALITQDWFDELDVDNDGVDEVLLDGEQNISSTAHRPGTSLQRKDAPTGTTIPTGMAQRQ
GTARPISSRYGYVRPGTQSRNRPGTMSIRPITSRMMRIGTASLQAVPGGPHIDVRKLNLE
KYGRTKPIVARILCDFLLHVEHRPRMVLELGAIALEQQPKDWWWMSRMGQAYYRLGLLRE
AERMFKAALTIQENVADVMRLARVFTKMDQPLKALDLLSEASKKNPMDHHLLLHMARLYD
QLQDAEKSCQLYRRVLQLDSSNMESIACIAAYMFYEKKQPEIALRLYRRLLQMGVQTTEL
WNNLGLCCFYSSQYDIALSCLQRAVAISTEDETLADVWYNIGHIGIGTGDLGLAHRAFKV
ALGANPRHAEALNNLAVLNLNIGQVDQAMNDLAMAIEVSPEQHEPLYNFALLAFKAGNFE
KSYKLLTQALEACPDHPESALLQATLRKSLA
>TCRU_8750 Adenylate and Guanylate cyclase catalytic domain
containing protein, putative
VLFSEFALLHAEFVAAFRDGAGADRVLFATSLPHWNEKNSTSETARKFAAAVPREEDRTP
LSLMGFAATRLVHTLFSQMRHLTAELLTKLYKNADFDVDDDMLYGPFADGRACPATESGA
GCGRNYGATYISVWPLARALDPAVPLLFPSMTPSMKYADPAAGGLTARQLIGVIAGCAAA
LLLVAVLLYFCRISRDNANAPKERTDPVTLVFTDIESSTALWAACPETMPDAVATHHRLI
RSLIAKYRCYEVKTIGDAFMIACKSAFAAVQLVRELQQVFLQHDWGTSVIDDAYHKFEED
RAEEDAEYVPPTARLDAAVYRQYWNGLRVRVGVHTGLCDIRHDEVTKGYDYYGGTSNTAA
RTESVGNGGQVLLTRAAYFALSTAEREQVEVTALGAVALRGVPKPVEMYQLDAVPARTFA
ALRLDREMCDLDDESDLASGDGSASTERSGPSGYIASMLAVLFGTFAAPQRLKALLPLCQ
RWSVRMPRGAGAGCDQDVCRVVIGRLAAKVCGVIKKSVSGDSIEGGLRTMSLSEGAFIGS
DGALRLRRFSVE
>TCRU_8751 hypothetical protein, conserved
VLRRAVVALLDALNGVSSMTLCTKGMGLSPDSHRRRMPWTAAKECVPGAVHSSKEKMVLD
GAQRVDVDCVDRASQVDPLEALRATVAKC*YNTFGGKNIFNVSQVESNVLRQCFGKEWPE
GTHDEDATRTVIYFRRRETTTQPAPIRPADFPRRHAVLFVATVPPSPSVGADVPVDASSC
RFRTHPLIDAPAPP
>TCRU_8752 synaptobrevin, putative
ERPTFTCNDETINYAMYHLCAYDPILGNLLCVGDNVPVVVLTRGRRRAVLPVRKGLRWLD
VHIFAGTSSFLLLSPECLLLVDFTRRHSPSALFSSGKAGALFACLHVPQGMTWGVVGCRG
GSVMYWKLKEEAGSVSLFWAAMAADPLEFCRPFLPTPMPPSCGHIYSIDSNPTSPNILVA
VLSGVNGVCKWHMDENCLSGFYRMPNLNTSMSLKACRMTPGGVYIVAITCDTSTIFIWSD
GGKKTKNKSVEVFWTLKTGCRLPFSPGNSGREEVNESEIEDAPCGIHIARSAGSSSQAQS
DKKCQMHLLLHSAGELVELVLDVEGRQLLQREDLLAHVTAVKLEPPPALDVKDALAVNCV
VPCSRSKYWRGMWTEGDLDVLLMTTRTYGPLLIRRCRLKRNVESIDKLEEVPRGADPSIG
MLLLYPPLETLNAIWSSVRNDKSGSNHWQDVLHGMELTKHCNVEEWDGTLLVLGVFSDVP
TVGVCLLPLSNECIPIPTAVMEQHTAWLSYVPSRNDRQLVILEQAIPEPPRKTEMILRVV
VDEDTVVVFVTHLSLGIVEPLLKLSRECLMPDKAPGGRGDDDDDDEEGPLARAAVLINCR
IENSGDAASIFRLLCGGYSILLQLRDASLVLVSLSGAKTGEEGFPLMVRYPSALFPAHST
VASFDTVWIDFRGSSSDAKLGETNGTCLALLCALSDQKGVVVWDMSQMRILSYYPSNGCD

EWRCKTVIACPQKDYFSEVLAGVMCEIVVMSTTSSGTVATHGSEGVVYLRDVFGRLLLSL
RIRYAPNGSDTWFVKRGDGEAEWYSIPSVGTVELRFCVRVGNGQAMLTRGVTHSLGETLV
PSAPIAFVEAGPSWLFGALEWHSRENPKGSEEEKAEEKDAMAAPISPYTAQSPCEEATVL
ICGERNVDFFTAARLATSGSGKPPEFLCHCNFDHVIEHVVVCKLMDAVLVLTKDANGWRW
VSVLDLHTARRLAESKVMIPFSQERDLRIHPLPVEGGDLHVYIAGRGGVLGHLVFSAVGD
GVKSLSSRSGFFFAGPPCASTPSSFRAYRQLLPPPPAMKQEQGFLKRLMTLPWEEMAHKV
>TCRU_8753 hypothetical protein, conserved
MGGNSSREMMNPYAVNTPLIGVCFTSLLFNSVQGGTLRSSNVYNNFILIYMLGFSTGCST
VLQQPIWGAKLGLLASFIFTFGPNVRLLYTQRLFPDYVRYGMGGAYMTYHALQWYREATY
FEDAMEDD
>TCRU_8754 phosphatidylinositol 3-kinase catalytic subunit, putative
DFGMLAIDVVLGDGTRCMLDFAESLYLGRLLSMRPPVVFSFGSATAMRELEKIVALLHGA
RHTGSSYATNECDSGVKNATMRSHRMADAAAGMGMSASAAPPAELSVSDRIAVVRAHIRQ
MSENRRLFMDVLELATRLEMEETFPLLCEEFSFIFENEVRGKFTKSLFLLQELGGSGQMA
IKTFRKIVMRAFALDDGVSPVPATREEKRQPRPSACDEVAHHWLKQLREDHYFFPGGQLI
GDLTQSVDPEASVWRDETPFGDEFTPSFQRYPFHSPVWEPGDTAKTCPVCGMIFASWSTL
SLNTVRPSHCRCCGRRICARCTSWQLDKSIAKLNKPGVPEEGQLRRACKECFDKAEKLNK
HAFLCEIFVLAGLTLTEIALLRSINPHWKGASELCLSDYRSSLYQHASWKLVVATQTARI
LASSVNILVGHPESLIFLFISMDWSNEKLIKAAYATLEKTLRDAASQGRLNHASTLIWKP
PVSHWHMLCTRACGLMLPSFFAIKMLECLHRAPEAHPTAELMRMLVTKELLLGKVFHLDS
RVCECVIMLLLDIFELKTCQPHVTSVLLRFSAQDRRLALMICQETFTRSRYDELGYQTLR
GLVIDVDCKERPETHVHFLNTLRFLDVLRSAWTDSFKQNDISRTRELLYKNLRKAGLLVV
SREVHDTALINRHTISPILFPFDTSVVLNEIDFGGIVAMHSKQRPVLIPLIDEGGQTRCI
LYKNESLEKDKVMCIASRFLQWVLYKQLRHVVLPTYHVMPLSSSSGIIEIVKDGHTVQSV
IEPYKEHRLLQYLQQLEQQYAQQKEERQPKKQQEATASLKEAAKSSSVNVRENFLCSAKF
FILMNYIFAIGDRHRDNVMVHPSGAIFHIDFGMLLNSRTLAERVTTSYVRFDLDLEECVL
EFMRDDEKKPRGDFSSLGPPPPPTLSQHQGSLPHVSTHSSDDSLSRFLMEAADWFLEVRP
YASILCQLLSHVVFRQALDGVHSVEQLTALMHTIFMRDAAEETCKTLFCDRVRQSRGQTW
LKDLTHDTRKRTWFMVSQGLKWI
>TCRU_8755 hypothetical protein, conserved
LLCLWDVDDTLVASGALGVRQYPIFAEDELVSFFRGCPARHLLLSQGSVDDVFAPDGVGK
LDFLSPFFLSGGDPPGGRSSKVHTGCSNVFVCSKPPNLRSGNGKYQENTPDVNVVRIATS
RAPREQPEDSRLFLSEQAEPPRCASDVRWLVMRPSLWGISLASLSNFIAPSAHTAFLDGS
VFCKMDIVRSLAASGNWDAVFFIDNDLSEVGVVRPGLHIEDYYRMKRLGRLSRFFQSDML
LLQASAELAEKEYGMDFSKTNGILLAATASLSSLNGKKLGKKANKNGSVNSNSLKYQLST
VIDMGRSASSTLTRGQQPFTRVVDLFVAHFHLDGPRYRRITKARQNAIEYREKDQWHSAF
RTGPACNDDDYAEVMSSFALFDAKVKTYGLTTDSKLTPVPGWEPSVDVVTYPMYDRPPFP
RRLPYQYQNICHQITTNLIDQWDPHLTEQQQYDLKKEADNLFRRLIRRQPVIDPMLIVRT
ANTLFSIFTAERRLPRSLGETLKRDVQGLMNG
>TCRU_8756 Cytidylyltransferase, putative
MKLLRLSTKVGMESNNAALRAHLLSLRGTEPVGDPKNPLHVQLQIHDGHRNTLLSHTKEL
YVTALQHHSETFVNVIPLLPLSDDESSPSNDEGTSNDSITLFSAASMTADRGFTPLFSHV
ALGGTFDRLHAGHKLLLTTALFYASKSLRIGVTLESMLKKKTYGSYIEPFETRCKLVSEF
LYSVRRDIDVTVVGITEPSGGTNRDAEIEALVVSPETAGVLASINDERASYGLKPLECIQ
IPYVSAEGDGRVSSTELRRRLHE
>TCRU_8757 zinc finger protein 3
MQGYFALNQPVLPSGWQMAYTATGQPYYMDHNTKTTHWTLPETVSYSFGGYYNPVMVAGA
GGGGGGRGGRGGRGRGGRGGIDQGKRKTKMCIYWEKNGECNWGDRCAFAHGQGELRATAN
SGTSQPQQ
>TCRU_8758 ZFP family member, putative
MMPKDPGLWGTGLLGGTSTGTSGGGANANSRGATGMGGGNASAPITSTVAAANAAATTSL
PSGNSYAFLSSSAVTATSPSVLVQSGGGGVNGMGSNAVGLMPAIVSHDRSQELCKYFLNG
GCLRGAQCQYLHELPDERHLDVNGYGYILNPNVHNAQKTLPLAMNSNPTGTVQVNGGALS
PSPLMLGLSSSGSRQTHGAKAKPQTSFMVGVPTHLPFQLSSSNAKASPPKYRPPEPFLDY

NLPPTLALPFNTPPKDVALQLTRTMLQ
>TCRU_8759 hypothetical protein, conserved
MLASVLRRGGHEASSSASHHIIAPVAALERAAPYTRFNTLRMHAHREGNFRARPAGWRAW
RDPALQDPYAPFVMQSPTRHVDRQGAGMWFGMGHFAMKNFFGILHWRLAMRLSIWGILGF
VIPGATYALRMHR
>TCRU_8760 acyl-CoA binding protein, putative
MWTHRWHMREPVTFLLCTPDGQPVDAAAYLDGICRMLQTEDCVDAAVERVYRPLLVYVSL
LDDPDADPTNTDDGMEALPDEWSLLHLALVMEHAEAVRALLNFHQKHAFTVLENVLNENN
RMILTKMASDDTTKASFAEEGSSSKDAGHLPCKIMECQVRKELGGTVVLFDQEASDTENC
PQVCSVACVTTALKPLLKCLLYERNHSNGKDTNAEEEGPAFGFATRMVQAHCDALPEFCV
RLPSLIVECDTLYEVCHGDLVTLCDILEICRGLLLPVVHGKRMEIVGSSSRGGGKNATSR
EVSHVVGLPRGFHPQQATLPPFMLSCKPQEHQQLAFLVTWTNYRQKAYLESKPPGSARKD
HEANVLSDFQMTLWNLKKSGQMISSNHLWSGILFVLSRLFSGNCSLERFLDIIEQDDFVS
CSDGMPVTFIAAIVAGAAVAAFLTNSSYVQLLSKKVEVLLVDVPGEFSPLRAYLLSQPAT
HAERFEELWLAETPFSPAKKFESRVEMFYWALVEMVLFSAEKKWGTAGAFVGSDKTKKTQ
HFLQDWLSMCQKFFFSLRDRPITCPQRRAMLRSCAEGEVSAGATPTDIDNATEDDESPAL
QRVCEQMRLRLQRGATSLQAIYTSLYPEEAGEGKTTGVGGGVCEEEMEEDGTGGKMAQNS
IRDDFEAAQVLFSTTAKHVSDTTKLKFYGLYKQATIGDVNVPKPWMMDLVGRAKWEAWNE
LKGMNSDEAMRRYI
>TCRU_8761 hypothetical protein, conserved
LSTLLCLGVAILGNVAEAALVFVPTNVLQLSLYQTAQLRFSSNIFVGDPPIRTGDTFYFI
EKNNNNDPACNPAGSGNPENKFTVTASNEMGLLGFSTIVVKSSVFTVGSSYLICYITQGE
AYLTWLSRGDHTSPIIVWSSVYNHYDMQPPFAFGGLELVNLTVSEQAQAGRPINQGLGGA
NTIFLIPCRGTGANCGGTDNLPELCASQPPDSILLNNLRGVMTMSVTGSFTVPYVPSPNG
YAICVPYCYDASVGCGTSVEMSYTVVTDDKSTPVINFGEANPSSYSVTPAAPQARELSYM
LLTGRDLTDRDVVRVIRSGSTCGSPAAPLLTNLRLIRLVAVSDTLVNVTFIAPELITQQM
RGIVCYRHAGSLLWSSVRKDPALPMDDFVIDILQPTSFTMVPESPSTGESITLFFVGTGL
DASTDEVFLTTSPYCNGLLPEIPQFPCKLSGGNQPQCVAIIDPPLNQGLTLHICYRKGGQ
ASYARINGTVVTQSRNPIYTIRPYPLYAGQKGTLTFHGRGLSLRDSVNFLVSGSTCGEGS
AVNTFFIANGVELEAGKTYQYDVVGSGKQCLQICYRIADSTTWSIARPRTMIPVVPTCEA
KNLYVSTFNLRYTSTTTPITAKETVTLTFLPPPPLNSAVKLVRMDDKCVVSFCKIGGVTT
TACEIGQNADDFTSDLTDNKVNMMAGAATTSYILCVSSYGENYIPVLPSGQGETSVAFAF
ETAAANPTLQSHTPQQWRVALASLQTKFGGHDLNSTTDSVLAVLGDALLSTTPRVCPPAT
AVPSTALLSTLIPGPSTTTTTAAYSGSHRRYTGDVVYFCYLWSSGNRITYTGSLAFAARL
PSEMTATTPLSDGFRAGVPITLNFTSNTSALQPENDELFFYRFKLPFASGSNCYCGAECP
ARALVSYPTVPLTPGASPTEVLWKNPQGLDNYNYDAIYVVCY
>TCRU_8762 cytosolic leucyl aminopeptidase, putative
LPFGFKNAAGNLALDSERRCLFAGLGTKPTVREYRLAVTNAVREAQKLQASALVLKSLPA
NVHSMGDLFQEPSVLPSIDVVEKTASFAVTAAYKYTRLRLNKDGGDETKNPMGIFIDSVA
TDAIARGNIIGGCVNEARSLGNLREDEGSPQLYYEWITKELAPLGVKVRHVLRGEKLRGA
GLNLLYNVGKGSRHKPYLVVFEYTGNRHSDEATALVGKGVTFDCGGLSLKPAGSMEGMHL
DMMGAATVMSTIKAIALLQLPVNVVGAVGLAENTIGPDSYFPSSIITSRKGLTVEVRNTD
AEGRLILADTLTFVQRDAKLAKKLKTVIDIATLTGAILIGLGSRRAGMFSNDLHLSQHLM
ASGRSSGDELWPMPIGEEHKNAMKGGIADLRNVSSDKEAGSCTAAAFLSNFIEDGMKWAH
LDIAGPGMGGDKPKGFQPAGAPGFGVQMLLDYFRLTPVDGAVSDAVDVTSTEGTVATSDE
DSTAPATASGAENPPKRKGIKGAKCKKGPEGESEEAAYKEEEAVTAVQMGRPTITNNKK
>TCRU_8763 hypothetical protein, conserved
KNQYELPEQVRWYQTLWEMRNHEFRTTFLTTKRRHWRMFWKYESHLVYERVIMGFIVASC
MFFMSNLDLTAAVFRLPTEDVNELLKQDVWRKYRSEINERKEHASKMLEESSYIHNKNKP
YST*
>TCRU_8764 conserved repeat domain containing protein, putative
MRWVIVVFALFAFMAVGSLAQLDTLPFLFVSKSVSDDYVVAGNSVEFTVTVYNYGQSPAM
DVTVTDILVDGTKRTKRVEMLSFGESAVLKYTVTPKELGNYVVGVAEVTYALEKGKPATH
RAYSNVIRESNAHFLGEKYDDESFRGVVSVVTRERYDRLHKRYIREIVAYSILCVIPALF

PFFVYRAEQNQVELLIRRSK
>TCRU_8765 hypothetical protein, conserved
TSSRMLKKISSDKVWKAVPLPQPFHTALETGDWVKALHVYQRHSYHAPPVDTFDLLKAVM
HATGVRVDDVKSRFNEKIRLSAILQKKTPDEVEWSVFWEALNKGDSKTISAALMGARLSS
ITQQITTAEACAVLLKSAGEDWEAKLVDNFPFATVTRCNLVHVALAQKRWDVAVELLRNV
RINRSDVMTLWPLIEELDWEKVLLLISACPKNSVPFDLALRHILRGGCSLQYLAEHLENA
RVLGDADVVAPLLAHAVEIGDWDFVGRGMEHLVDIGQITQPAREVFEHMGKIHGMETVCA
RLEEHRIPLHHVTVENLESLRL*
>TCRU_8766 3-hydroxy-3-methylglutaryl-CoA reductase, putative
MFRRAILLGCSAAKTPWSECSNAQLVDAVKSRKISFYGLEQALEPDYRRAIEVRREVVSE
IASQQPEAKKKQSALHTIPFENYDWNRVVGQNCENIIGYVPIPLGVAGPILIDGKEYPIP
MATTEGALVASTHRGARAITRSGGCKTLLLGEGMTRAPVVELPSLEEAGRLHKYCNENFL
SLKEAFESTTQYGKLNSLKCVLAGRKAYLRFRATTGDAMGMNMITKGVDKALSVLQQHFP
SMEILALSGNYCTDKKPSAVNWIDGRGKSVVAEATLLADVVEDTLKCTVDSLVSLNIDKN
LVGSAMAGSVGGFNAQAANAVAAIFIATGQDPAQVVESSMCITTMSKVGNDLLISVTMPS
IEVGVVGGGTGLAAQRGCLELIGCGGPSKESPGTNAQLLSRVVAAGVLSAELSLMSGLAA
GHLLSAHMRLNRKK
>TCRU_8767 hypothetical protein, conserved
KHTCVIRVNLFLFLPDTSEYQEYGSVGCVIVGTLNSPPLYKLGCYNEKNEYICTANITTN
NETGACIALQAGGYISFKDEQGKIWSMQFESENQAIEFCCHVVVAMYGASGHPDQSILAC
DVAIGKCDRTVFANDIVKVRYQSWVVQFEAYGSELPILGSKLDGNLQADKPCTLTIPVNH
MSVTPEMKGFEGMVIGMGEEGSRVIIVPVRAKRGSGPSVHMCFYTHLVKKKDLSHVAQVG
TSVAVPLDKNSSLQVMDESRLVFSNKKDHAIPRPKSPPPGFNREQLLIVDRMRDQVQVLF
QQLQEARRQLDVLLNEVRTFERSAKPQSLASAQLEHSIQKLLADTEEGKELLSQKDLTLR
QMEEKNKELQNKVEKFSKTANLLAEEKKNTINSSNEENLDMDRRIAQNQERLTRLQSERE
DVARHLSTVKRLLQVADQDIKTEKQNLQLALVEFQANESKLSAVEETYTGEQARRKLLES
KVIVLGDQLRSLLEEVRVKEGQMEERRKKIETEKLHYMQLIEDERSKAAEEMRELRQEFI
DELSTRDRRYQEERQRVAHNAFERGHFQGIEDGQNEALLEADAATQHLALTAQRHEAEVN
GIRIRLRSAKEKNEADACRLTSQASALHGAIDNLMGENSQMETEFDSLKSAKESVEDDAF
QELRYAIEQLSVAVGRQDLLAIIHSLRVKRDVSYAFETQREAERQRILKEEQKEVYEWVS
GVVDGKYVSFPSMRAQYLTE
>TCRU_8768 hypothetical protein, conserved
RVHATYDVAPLSHKQLFSIYQNWGQTRDELDLLEEVEERISKWKLNKWEMRIPPLLTTRE
KELMRQQQELLKSIFFDWGKCRDALNKDLELISSITGLPKGTVREKNRAWLQEEAAKLRW
VGEVSKATRLRDAFLRLEVYGSRDHRLLERLCCIYGLGLQGSFESAFSNYIVEDPITKKI
YVDEKNSFRDLLAYIIHTYPQIDIIYDFLGFNFIGGYRSSLRRYLECMVSRSTEGGKIPG
RLVFGRGKPAEILFDFGNSNESLVSGECTQGFPDFVFVKGSDMTLIIIASENSWLRNRQL
PHRKQMEGIARRASFVLGIPFSEVRVRNLLLPPTYLDKGSIVRINEAVLGLSKEEQRNLA
PWLEMYQKELDSKDVDFCSLMKSTNEEEWLTL*
>TCRU_8769 adenylate kinase, putative
MKFVLMGAPGCGKGTQSPFITERYGVCHLSTGDMLRDAVAKQTAYGKKLKAVMNSGALVS
DDLVFSILKEGIARPECKYGYVLDGYPRTLRQAQLMEEAGEKVDKVILFDAPDDVIVART
SGRWMHRASGRTYHEMFRPPKVHGKDDVTGEPLIQRADDRKEVVEKRLEAYRKETEPLIN
YYMGKGLFERIDADRSVEAVRQSVISILDPIAVRLGLK
>TCRU_8770 malate dehydrogenase-related
MVFFLRRVAPKKTSGKVVVFGATTVVGQPLSLLLKLCPHVKEICCCGPLTRVDPGANFIT
ARGVAADLSHIDTNTSVKAFETPCDWESALHGAQLVLFCAGSVFDPSRAYRDVALRESGP
ELMLAMELVAKASPKAIIGVVSSPVNALVPIAREVLVRNGVFDPRKLFGVTTLDIIRTRS
LVADELQMNPYDLNVPVVGGRGGVTACPLVAQTALQIPHERIIHVCSRVQSYGSHSSYEE
SGGFPDLSSEEAVSTEIVPPVGLSLAYAVLEWSVSMLKALRGDQGIIECSFVESAMRKES
PFFSSRVELGEEGVAQLLPMGPLTSYETELVETAVPFIAEDVEVGLRFANKKSEA
>TCRU_8771 mitochondrial malate dehydrogenase
MHNSAVCLSKVAVLGAAGGIGQPLSLLLKNNPLVSALSCYDLRGAPGVAADLSHICSPAK
VTGYTKEEINKALDGAELVLIPAGVPRKPGMTRDDLFNTNASIVRDLVIACAKVCPKAFI

GVVSNPVNSTVPIAAETLKKAGVFDPARLFGVTTLDLVRARTFVAEAGGKSPYDVHVPVV
GGHSGPTIVPLLSQSGVELSDSQVKAITHRVQYGGDEVVQAKDGAGSATLSMAYAGAEWS
NSILKALRGDSGVVEYTFIQTDVWPNLPYFSCAVEIGKNGVVKAHKPQLNKFEESLMEKA
IVDLQKNIARGKSF
>TCRU_8772 endosomal integral membrane protein, putative
LLTLLFAFSVEASAFSVLKTIASSYHQGDVIPVMVSSLTSKAKVMPMPWRLVAQCSLKKK
KRYRRNIGQLLFGDQLEESPYEVAVLKNATCVPLCTVTMTPKDKKYFSKLIEGRYRGNLY
VDDLPGLVNITLKKGGARVNMGYSLGYLNSFSGPGKAVVNNHLIFTISYHPVESPFNLEG
RTYRIVQFQITPTSVHYNNAICDPTDLLNGGPQLLSDDRISYSYSVHWVESPLTWSTRWD
VFMKMTTRESKVHWFSIVNFFIITLLQTLALWYVLVRALRKDFLYYNDLEAEEQDETGWK
VVHGDVFRRPRGVGLLSMCVGTGTQLAMMLGATLCVACMGFFSPQSRGMLVSTLLFLFVL
FSFFNGMVTAMLIKYMKMRSWKLIFTTSLFYPAQMFFGYFVLNFIHLGNYAASSASLYSF
IILLLLWQGVSTPLLLLGAAVGFRLNITTPVKVSSIPRTIPPAPWYFDSVLTIILPGFVP
FSASHVEVTYIFGSVWHGAVYYMFGFLLAVYVLVMVVVAQTAVFSTYIQLNRQNYHWWWR
SFLTSASYGVWIFFYSVFYYFSYSTLKGFLSAVLFFGYMGMVAYTLCLLSGAVGFLASFA
FVRVIYSNVKVE*
>TCRU_8773 hypothetical protein, conserved
MRRTTAVLWQHGVHVPRGVVYHGAKMKHWPEQKVPDNFKFTEEQRFRTKAIPRDFGMIPR
DFVLSVLYRHQPCEVSGLWEHCTSDPGVVLDSKRHLREVLKQAREEGFVSFERDPVSNEW
LCFITRERFEEVRQIAGAKAEASEVYSGLRGSSATETSSYTERFKEMNEMAREEHARRLE
EEVKTTTKHLRSFQRKEVDYLPYTDLNGKVNFMWWYETRDVQQRGGDAIPASS
>TCRU_8774 UEV domain/Zinc finger, C3HC4 type (RING finger), putative
TRFFSSSSHCKPEVLGRILHDVENLCNTFHFYCRDATWGVTQQEKLCIYGGLPITIKKSN
SDHTSLTPDSREQAPPHRYVLPLQIWLTHLYPIEPPLVFLLSAEQGCRIASNHKYVDATG
RCHTPELAAWHPVSSSLCDVVKKLCQLLSAEGSIPLCFVEEGVSSPSKGHATAVSQRLCH
GLENGDDDKQTDEHERCVVCFSPKETVLVPCGHYCLCDACATNVTHCPLCRGSVKFRQRV
FS*
>TCRU_8775 glycosomal transporter (GAT1)
MSLLSLCRDYVAERSRDRLLRRFFSGSIAAFLLLLVLSPGSRIAKTLHGRQKRKLLEVKR
QRGSIFSANAHERPRLSVYRRFLFLLRIAVPSLSSRESGTLMIISSLLLLQTYLSLRVLK
ISGQLGKTVIACDLVAMAKKIVVFLAWCLPVALTNSSVNYCVGILTLQLQSNLSRYFYRR
YLNQKVFYPLASSHFVEEVDQRMTKDIESWSLSLTSMYTCLFKPLLDVALFTYKVASITG
ACGSLAILGYHTGFVVFAHAFFPDLEGIVSEQMARNGALVTAHQRLMLYAEEYVMTQGQH
FHRSLMEKYLASIIEHDQWASYVRGGYSIMEIFFLKYGSLLLSSIICGAAVFNKHTEGMS
AADLMAFFVETSYLVNKLSFSIGSILKNLRKIFVLHALTNRVYELQEGIEKAIEDGAGAV
AGEMVRGNYIEFDRVPIVLPTGEVLCEELSFYVKPGMNLLVVGPNGCGKSSMVRLLGGLW
PLQSGRIMRPRNDQIYYVPQRPYMSNGTLRDQITYPLKSSEVGASEATLLHCLELAVFDD
IFAKPNITWDSSLSWAGDTLSMGEKQKLAMARLFFHRPRFAILDECSSMMDVEVEERLYS
VCHQLGISLITIAHRRSVWKHHNWILRFDGCGGFLFSPITFVAEGVVILTNVVNASEPFM
VGEEVRLDL
>TCRU_domain containing protein, putative RF.1
EKRPSRRRYSAANTTGRSKNIRGIISLLKSLPKTEKAAIFDGLHPRDKLDVLRVLGRRSA
RRAAGLPTYRSRIFERSYLFREEDLCEQSTLGRGPGGQATNRRMQTAIVKHEPSGIVVKF
SKFPSYWLNRKAAREILNLRLEEHLLGPGSRIARIRRREVRRRLQQIQTREKMVEKGNIR
AAKMSQQREFHKVLTNVLPFPPTVLLQFGHGYVDSTLFMSNLFEGECNRWWPLLVVAFKH
LNGDVSQEEGCNREDTSEDGKFKVPELFLYVFPAVLFSSRPPTSVEKYEWSEVQKCANDE
AALQNVIRGLRCFVELFGLHLQDRLSPSGDGQSAFVLVRDGTNWLEFRGRMVASDERMTP
LALTCFSHLVLSLTQLRCKRETNAVLAFFRHEAKTGLRGQWAAHG
>TCRU_8777 60S ribosomal protein L44
RCKAHKSFKVVQYKAGKARLYARGKRRYDRKQSGYGGQTKPIFHKKAKTTKKIVLKLQCS
NCKSIIQNVLKRTKHFELNDKKKTGNKDPTW*
>TCRU_8778 heat shock protein, putative
LCCPHRLCSTTPLEQLIINAAQWDASNYYHRLGFCEEVHDLQRIKEHYRVLAKHYHPDNP

SAPPNAKAAFQSIKEAYEHVASNTKKAPDRNKMDEAGFEFSDHVRRKAQMRFLGEGVGLF
MAMTFVFIYIVSKHNKERLGVRYLWNFLLIFFTIQFFPRLLAAAILYACHTNYLVSLAEF
KEQAATSVVVERRSDGDVSVRLDGLTEEVKDKTVLQITITHVPSSSLSSSEAPTGKAAED
FNTLIAPSTSTTLTFDRGVTSVSVPAHSEGVAQYRVRAVDMRRGFILADRTLHV*
>TCRU_8779 phosphatidylinositol 3-related kinase, putative
RSSAAMKRPRPSTEDSAPLREALKVFGQRATALDAELSTLDKPPVAFQGKLWTLVLELRP
YFLVALSSNELQIPEEMKKLCQAEDPHRLLRYVWLALRIYISVARIAAVVPGVLLHSILT
LFSLLPVFGAPSLLAATDEKMLFKGINQALIVLSHRYPSVFQQLLHTLLREDTMGAFIFS
PTPGRRRSYGRCLIELCDPPVVHGVPLGAGSLFALSIVSSSVYESVCVARGLCEIMTDLF
KSNVPFQPTLGERGVLFRLACSLLTVDFHEGPMPRLVSGFIEPLEGVSGAYPSDEKEPSL
LNLFQTSAGATLCVMMSHGFFIKSIHGPMLFYTLTQHLCVMSFAKEMMDLNVTWELELLR
WLTETSVTSGDASTSPVIGETRETDVSDGVEGISLPHKWLENLFLKPRVLNDVIRALIGC
VHRQTSSESIEAGTILLKLLREMIPQHSCMPRLIEEAFYGMAADMINALLDARILQPMLW
LADASPRLGVLHQLIELFPLDTVRPFIQRHLTLRYGKEPADSHLLATANASVVLRDEKSI
QSTFSEAWKRLANGEGVIAAEAVVILLRSAEEIDMESMARGLLEAMAGGTVTLRHLDSPP
HVALLYSALLERLPISSGSGCEALCFMKKVMRSREENSDLALWRTIGVLRGFRKRIAQQC
RSRILVSASPCWAEVEAISDAAAIMLTTLREISEVLEMIALSISDFSFEESASDEAPMLF
WQQMVALVTDTVSITEWLRSHLSACGNGEAATASEVIVLDDEEEEETAKMPETLNLEDGV
FIVASSKRCREQPHRQHSSKAEKEEGEEGEEKMNSDSTTKSNRGGGVEAVLRGISAPLEA
IGWAGRQFLIARSLLGSDELNDTLLSFVCLCVALSPVRWDAMEEIILSRGLNHSNCIIRR
GYAALALRIFFTRWDNESITHMSSDNLLRFEENEAAKQHFFLETLQAAFTGEFQTVLVRQ
GIYRDVPSFAIASLPLVIAPTRHKERSRKACSSVLEVCIKIWEQNDFTLSTKSAALTAAH
AIMLHLSWSVADLCWRDAEMIYTSFFKAMCDLEESDVREVVLASLEDLLPHCVLSDGGED
KLQRIAALLWETPSPGGIFSRVMAHILLEYARESVSVKLEKVQKLLGFLSRPLEELPEMV
AHSRESLIVSLIYLEAGRRLREAGSRRETMDTGLKKDKRENVGDGVLSNFNLAVEMALAI
VECGPLTEMILQALVTPVTITTEGRALTKDVFYVLDAMAELVGLSNGPLKKSHHVPICIV
RRCLCSLSLLIRFLGSHATSIAPKLPAILEHCSVRSQLVRPVCAVWRDLIANCTKEYLKE
HSPAIVVDILSMGQLAEGHGGSRGYDDCDDEGDPLPLLEEAMRIVYESSSQEAFWESYFK
VMGKTNVLIHRLGVNGGNKVSAAESLNVENTPIVSERNATVVVAGFLSVMHSSSTKCKEV
FVRALYQYLSKTDSAGRMEMTRAAGASPQLIPTLLNCACELRDDHIEYILACVGMIGAAA
HSHAPLLATGRELTPREGTISFSLKSGRSADLRGMQFLPEDVLDWRTLAHKLLSVYCPRA
LANTADPTMHDRAAYAVQQLLRVCTDAERQPLDRLPLQTQEVLHVDELNQYTWWSHLEPT
CRQMLAGYTTTRYDKRVITKTERRSPVYFSKMSFSEWMDSWFCDLVERCEGVFGRMMGSL
RNMAKGDHALITFLLPLIIVHLLRAGNVDHCNAVLLEVMNLLHAASPDASHGKEQSGSIY
SQSIMREVVTPGARATGVEEHVQEVFHILEDIEHLRLNLIRAIHQLNVQRGGNVDQSEMM
RVDDVCKQFLLQVDWTTRAKAAVAIGSNVRALRCIESQRYLPSIQDVMQKNISLQRIFAT
LGDRDSSRSLHRTQEHQLEDAAFSYENNGEWSLALQASELVLQQRPNSINHQFTALRCMQ
QLGQLHLMSRYSQALLLQSSRVSAEHRKQDKLFLEARMAALQNYANEAAWRLGEWKNIQT
RQDLPVSLAPPIVAFNNLLCKRGTLKEVFSACKMQRRKIAPVIRAAFRESYAQVYQHVVV
LHALTDIETAAETVMSLRAPPAGSDGKMISVHDDFLKNAACLREFGSLLQQRARLTESTP
ETQELLMSLHRSIFRAFDMKEEVTNTWMQHAKMLRDEGFLEAALSAAKQASFSDGFLDPS
HCTTVAKLLYEMNMSNQAIEFAEDAVNNKLVPLVIRANLRVLVTRWRQETGYQTSREVIA
GYESALKMSDSEKAHHHLALFYDTLYRSIQSPVQESGMVLSASSDDMEDKKMVRNVESYV
LQAIHHFGLALRRGSKTMIVSLPRMLTLWLNCSAILATLTSKSGSISALADSVLKKMNEM
MELYLLQKDTKLPATQLIMALPQLLSRIGHENTRVVEIITGTVVNLMMEFPQQCLWQVLP
IVFSKQHHRRETVHNAIVLEFVKRIPSEKKLVENMLSFFKSFIELCNCPATSLAGGRSSS
EVSIAGQSFMQRIQRILPSTRIILPTMANLSPNVMHGAENSSVFAGSAAFKSLEDRVTIM
SSLQKPKRITVVSDEGERVLFLCKARDEPRKDMRMMEIASLMNTFFLTDPEPRRKRFALR
RYAVSALSDDCAIIEWVNNLSPFRRVVEDCYAMDGTGVRVSQVKVWKSMVDSGSLSKLDM
LQKHIFPKTRPVLHGWFHRHFHSHQEWFNARNSYTQATALWSIAGHIVGLGDRHGENLML
DLRCGELMHVDFACLFDKGESLEVPERVRFRLTQNVVDGMGILGVDGPFRASCQVALRCQ
MKNKTAVMSVVETLLYEPLVEWTRHSSLRQRNFDPKQLIGRVSRRLDGFLDLYSSTREKD
TFALSCEGQVSRLISHSSAVENLAEMYVWWMPWL*
>TCRU_8780 Microtubule-binding protein MIP-T3, putative

DAEVDFWTPTIEAFKPLQLNGPDLTPKLLKRPPFRFIADIVTSINARFAAYDHVLSPAQL
DVTRIDSKEKKVEYLTTLVKYVGFLLGRKIDVNVKKIVSGSEPEKTNAFLQCLALAVGYA
QQDKARRAKNSSTEVQEPSRPTTATTATAPEASNTVTDSLPQHNMPRRISNYVEKAQKKE
LVMREATQFFNKVSGYGYLKLDQEQSMREVGQSIVEMYNELKNNTTATQPSSLPLEALET
AINRQIEVVRQVSLLQEENDTLLEKLEVLLS
>TCRU_8781 Protein Associated with Differentiation, putative
VDAPRVGRLAMEPRWRIIQPRRLLVWLGMTVSTCAAILVGIHLLAG*TRSRNELDHGGAS
ATCMAGPACGYLVMPHGFIFDHFGPKPIFILSMVLFPLGALLFALSFRGTIEGSVVRLSV
FNGMLTLGCTLYDVVYMMTIMSHFPISRGPVVAVLKSYIGLGSAIVGSIQLAFFDGRPDH
YFYFLMVLFFVTGAAGFFLVPLPSYHLTGYEEKHLGIEEKERRLARKSVYLRQQPPTIRF
AIGIAFVVLLVIYLPLQSALVAYLGWGRTQRIIFASILIAVLVSFPLMALPVSCLERRET
QREEGDCGRTERPSAGDEVANEPAVAGGPPKKVETDVDYIAPQYQTTFLQNLKTLKLWAF
LWSFFTLGGAGFVIIYNASFVYAALADEEVDNAIKTLLTVLNGAGSAAGRLLMSYFEVWS
QKRKAEDRVSIIVSIYLTDVFLILSPVLFLVVPRAALPLPYVLAAIGNGFSAASLVLVSR
TVFAKDPAKHYNFIFLASVCSTIFLNRLLYGEWYTREAEKQGGNVCLGRNCVMMPLIFLI
VLSFTAFLSAAYFDWEYRRFGRLVLEERRRLKE
>TCRU_8782 Protein Associated with Differentiation, putative
VDAPRVGRLAMEPRWRIIQPRRLLVWLGMTVSTCAAILVGIHLLAG*TRSRNELDQGGAS
ATCMAGPACGYLVMPHGFIFDHFGPKPIFILSMVLFPLGALLFALSFRGTIEGSVVRLSV
FNGMLTLGCTLYDVVYMMTIMSHFPNSKGPVVAILKSYIGLGSAIVGSIQLAFFDGRPDH
YFYFLMVLFFVTGAAGFFLVPLPSYHLTGYEEKHLGIEEKERRLARKSVYLRQQPPTIRF
AIGIAFVVLLVIYLPLQSALVAYLGWGRTQRIIFASILIAVLVSLPLMALPVSCLERRET
QREEGDCGGTERPSAGDEVANEPAVAGGPPKKVETDVDYIAPQYQTTFIQNLKTLKLWAF
LWSIFSMGGTTFVIIYNASFIYAALADEEVDNAIKTLLTVLNGVGSAAGRLLMSYFEVWS
QKRKAEDRVSIIVSVYFADVFVILSLVLFLVVPRAALPLPYVLAALGNGFGSASLVLVSR
TVFAKDPAKHNFIFLASVCSTIFLNRLLYGEWYTREARRRGVDVCLDRACVQLPLLVMLG
FNVTAFISNAYVHWEYVKFNCQVLDERRRLFEEQQ
>TCRU_8783 retrotransposon hot spot protein, RHS3, putative
YESVYSARWSHVMEIPDGDERKKTGTGMDVKEGKPEQSWTYKEVGFSIEKDDAVQQSGEA
PPVLMVLTSDKGWPYMLNAPHGCGNDLFVNCEVERVWQIVLDDITKWFSNFDLTLNSSPL
PRVLVGTPGIGKSMAAGSYFLYQLLHYDAKKIQVVVHCFGETAYVFDKTTKIVTEYKGNA
ISESVLDGLWQCGMKGYIIYDVAEKGKQPDTGFASPTGWGMIVVSSPKLTNYDEWEKQTK
ASRIIMNCPDEVGVKAMCAWMKRGLEPDKQAG*WRTVKKQMEKVGPIPRYIFDANEFSAH
SAAVEDALDGVKSRDGEKQFTHGGVRLWDSEDPSHKLVKVVRERIVEGAEVFLNAPICAD
IGF*IADRLAKTIGAKDLLFLILRSHGVLASKYVEQLGLRIFMHEELVSAIVEELNELRS
AERNEAQDSVMKLNHQEYPTRTVGLRNWKTVSRGPMEYRVL*IPAVENFPLVDGFFFVNS
PRRTLVGLQMNTAGAHHTITSSVRLFNERLAEYFNGWEEFAQGLSWEIIYVQHENSTMTT
K*QRCDYVNPKNLSDAEKEIVAFWDGKVHQYQFVLTPDFVNKI
>TCRU_8784 hypothetical protein, conserved
MEAKAVFSHQTTTPSSQLPATMRVDGNTVQLNCPQPLRDAGFAVAEALFDVDVALDVPDA
STLFRKLCATAAPNFTQGRKNMVAFSYGVRSSPKRQLMYGSAAGEGYAA*VITEFIRLGA
KKGIFALSCRVIGSKEHRADLLDADDEPGVIVGYVKEGPRVRMVARIRVSLAAPDNIVKN
YEKYFASVLCEKQPMPELEAMPSYLPDTVVLQLYSDDGEVEFVDYMDANSLTFVALGDAG
RPTLCGIDATARPHHEGAQRALVSAAGIVSGICRRRLCIPFGNSELSQLLRRAYNMEKGN
RNNGLNGSTETALLAHAFLDAVWAEESFHCLSTPRRVGNILGSTGIGSTTRDMELRDELM
TARAVYDYRHSGYESNTSISGIKE*GMKRVNAIESNREEARKWQLSVFCGRSKHEAEKMA
KELERRDGATLDEIKRALEAKKRESSALQAGRESRNWEYEHTLEKIRTRKQDEESASERL
RQAMQQLEQGRSLRQSAIETKEQQLEMVQLDRARGREAVMRERHSIEAVRRTVREERRGQ
RRQWIHQVKEMNAKFPEQVRPLAEERKKEREQAKAKEDAAERALAADIKMIEEYLPRLIS
LEDIPVNPEETDIIRRQFDEVFAQEEQTYLAGAEEERARKEKLGRGLEVYRQRMRDEYVA
KKKGKLHDAEATERHLSSVVDRVLN*LRNGVRVTKIPSKGNACRILFFLSEDRKRIHSCD
LDHQGFPLNRKRPLVTTWIRDIRKVLIGLSTTSFVNYSGEGQLAKTRQEAVSDNGMHRHD
PTQNIAPSSLGTNNHRAFALLLRGGKSLEVVCETDSDCEAWLVALKRPLHLRTPAERLPE
ERRGT*RDARAQPSDSDVEMRWGGPPDIRNMRGFVLLAPDAAALCGEHHIPLALFLLVEQ

EPSEKRDRRTITACGVRACSGLDLFFSGRLYDYLCEKRVVPPPH*
>TCRU_8785 Endonuclease/Exonuclease/phosphatase family, putative
QQELVALRPGGLLHYDYRTDAAKTEKLPETFRVVQWNIERGIQFERIVQTLRVIRADVLL
LQEVDINCRRSNYRNVARDLAEALKMEMYFACEFEELDAVDRAPKNAVGPLSSPATAICD
GGDENNGSTSLYKRGRHFHGNAILSAGATLSDPRVIRHTAGIDWETEGWKRREPRHGFRN
ILRCCIHRSERTNSHIPDLYLYCCHFEVFCGTLSRVRQLLDVFRDATSVLNEGRQHIASH
SHYSKQQHPAFIIAGDLNTLADGIVRLSLQFDLGRLRLLSFGEKEACWLQRKVLSRRMHH
VTRGCCPFSYHYPYYVLPILYESIWNSDFAWRWLYGFSTEEIAALDNRHLCFYDPSDKAL
SITLDDPAYYGFVCGKLDWLLLSNLTVAPPSLTEDALEALKMSGSINSETAASLSLWRQN
MLLPTHGYVTFNEHFEASDHKGLLMHIQQQNSLPQETYP
>TCRU_8786 FHA domain containing protein, putative
VPMWRLKVINGCQRNDDLLLPVEPQSSLLKSFYTHWHDEDEERHIRRNTRSRRAHRTPCD
KNKTKRSRRKKKQPSTARRSVITSRNWLQKIPHVALGRHTCLPRAFRLRHTCVSRLHCRV
VYVGDAATHKQLLSRYPSTRRGHAASPKCDTVTVNDEETTEIGVKDDSTSFKGPYYCLIH
FGSNPLYVNDRPLLSGESHRLCENDVVAFLENPFDEEGGVLQPLRPEDAARHDDATKAKG
NQKT*TLSMGIQIGNDAHRSYSVWQHEHTKNGESGGELSTSSHAFEVCERACVFPVFVEV
NGVRIARYRPQHVPPDVLQRFCKAKTAAASTTISAGAAPRRNPPLVVEHERLGGSLNHEY
GSHNVREDEVKIDFVKGSKSPVQRAELSVGLACLARRNGDSFTPPPKYPWENMEQDQGEE
GVDIVGDVVSPLQQRLVPSPLRGGSTRVSKTPEMKSPLAANSIHASCGDEEEPPPAPRFT
IVPPRLPVYVFARRSPSPVEFT
>TCRU_8787 hypothetical protein, conserved
PVAGRRKGRAPPPPAMASGDEPDWLFAENVAPATGSSAQNPAPPSVPFAHDALSFLDFEN
EASAPTALSHGAATPASGTAAPTPAQVAPSSPSLWNQYEFLQRELQGTQEELIPYEDRIK
LLERGEDALCQEVRRLENDVCGKREEVERAALLRTELEEYLELRRQRLREETGGYRSQDL
INTSNALKMKYETDVARLTTLTKEKEASLRAVKERHDAVEGDVRATEVHERVLVQLQETL
KKAIHEMGKSVCVRVKPFLIGSIREIFVQSAQQRLDILSNDRKRRRDEWEAFQHKMKENF
CSFQEERRLKHQTSFDSALAHAVTKFRAALDNRLTTSAQSFAERQRIITAETCKCTQRAI
EEMVQRFREELKAVEQKQCEELKRAVNQYAAELAHHSRLYAAEREAAVGRQSRYAEEEQA
NLSVPPAYKAVEEKLKILGARVEQFRQSVSCDVQEVTSMTFYPGGNTFSSNEKTLMLEEC
ERNTRELSERLDAQWQRYRAAVAPLEQCVNSMADVLREGRVKVATMHQGTESVYRAWSQD
VRRELFSCLTSSGVSSDCEKVRSGVECMTQVMENLLAQLYPLTAAHAEGRAQQRRFWMSM
EQEIGALDKQRGNFNNALNAVFDAYDRLSRVEAELQARRTTLDVAKDDLVAAKQQFDKER
AEFRARLKETQQVGAELRHQAAKWGKKSVPGVCMEYSPQVLRDMTLESACRE
>TCRU_8788 C2 domain containing protein, putative
MGKLQVCICAARNLHDSQVFGLPDPYCRVRMGDHEYKTKVINNSLNPVWNETFRFQVADE
STAQLCVELWNKNIISDDLMGTYSLSLGHMTRGVVNDEWYLLGHSKTNSELHLRVLACDF
GINPSPSDVWKVTTDINNDPALGAGKKPPLAAAPVTISSNVNNTPINPNIGPAVVPAAV
>TCRU_8789 dynein arm light chain, axonemal, putative
DALKRKYIFVDGPVDPEAALIRYDLPFAPSDPKRSLKLRRRLGLPLDERAVDPNVRIVID
SFITPRAWHDEAGVLWVQHGSPHPVSRTETVETHDKLRRRMQELGVQRTGICPLRSLLLA
ECFLEVIRQVTAECWERGLLLLKIHTERTAAQTAHRELFESRVGHAFRLALKGEKDTSRV
QQDIEALKRRTEELAEEEKVLRKECDELASNGEEQMLILEKLHADEITAIKKEGVQKRNQ
LEQMVALP
>TCRU_8790 Tubulin-tyrosine ligase family, putative
ESRKLVVVNCSQTRYHVVRAAAVALGWYVEDEGRCHVPARFHGVALRRDMQAVIKRLLSR
GLSYDAGSSPQIQWLDKSVISSRVAALFCRHRVNHFPGMHVVARKAVLFKRLMRIRRRVR
ASSLLATSMRAFPWSFSASTELPQLERFFCARQEQQSSDGEPFFILKPNKGCQGKGIILT
PEPLEALERLKDKSRDEWLVQLYVTPPLCIERKKFDLRIYVLLTSVVVGRPPRLRRGIPQ
TLGGETHGGHAGLLDGLQLFVHQDGLVRICAEEYANPNRKNCERASVHLTNYAVNRRAEG
FSMGFLKETDDGGVCEGNKRDFKFLQHYVNALPGEDQRVESTAETAALSRWECLLRRIDI
CIMLTLLSGLEELQREFIGTGASRGSRSDGRNCFELLGFDLMLTEELEPVLMEVNHSPSL
FCDSSFDFETKRRVVMDVFRLLEPHVPSIEVCDDASYAAHQATPHACTSDASVGFRQISP
QRTFADSAGGAGGPWCEEEMRMFEEMLQHA
>TCRU_family, putative RI.1

PTHFMPSSAEDLQELLQYMAPGSTVDDIVGGGDSDEDVSTYDIVQGKHAATSRVVLGAAP
GNNAQRETTSISKMQPAQHTTTHASVLRRIRVDDFYADVSSFAGGSGGASVANQRVLNDL
REMTMSNRLMTMQSSREVDRSERATVENVMDPRTRLILYKLVNSGQLKEINGCVSTGKEA
NVYYAIAGDGSDAAVKVFKTSILVFRDREKYVAGEFRFQRYCKSNPRKMVRTWAEKEARN
LNRLQDGGVLAPAVKLLRQHVLIMEFLGEDGWPAPRLKDVRFPSASALDRCYLDICCTLR
KMYGRCRLIHGDLSEYNLLFYRGHVVVIDVSQSVESDHPHAMDFLRRDIVNMNTFFRARG
HQQLFSPQDLYHFITATPAPRGWQRCDGPDNAEEIRQHLLELRETREREGGVSSVGAEQA
KVDEQVFLNIAVPRTLGDVADHKAVNSEIAPFVAELTASPSLQRPLDRHEGEDEAGSETD
SRGEAS
>TCRU_8792 katanin, putative
VMSTSVLQLPCQVYCSRFSPNRAQQLVGFGGKDGAVYVYPFEDYSRAARLEGDASPLTAL
AFDPQQHRVVGGSDSGGVRLWDVTTEQSVRSFDAGHKSTVTGADYHRYTDFIATCSRDKS
LRIWDTRKKTCLQSYKGASAPLCATQFSPNGRWAASGCAKGVIRLYDLVSGKQLNEFRAH
EGAITSIHFHPEQYYMAVGSSDGSVSLWELEKFTKVFQSNPLDTPVDAVHLYGKKLLLAA
YHVLRVYDFTMMSDNTAIAIESPWNIIGDLTYSSLSDEAWFVEFSSGAATMGRLSLGCGK
DVISHPVTSMGTPSLKFSSVWKVEKTPGSAGNTILKPQQQQNQQVCADTAPTRSPEFLAN
SPVEDLLGSSASMLSVLRRRLTHIRVIRSLWARDSPQALEYLRRLCVDKSDCGVLTDFLM
AMQHMRMKERINISTLPDLLDLLACALNSGHESSLLAAVKVFRSMTNKFRVKMDEARRFA
TSLRTVDAGVPEPMMQRYDELSAKFKSVAILVYNLHERKGPVGEEVREALHELP
>TCRU_8793 phosphatidylinositol (3,5) kinase, putative
KRALWVNDRYAVRCRGCDARFNFVRRRHHCRNCGQVFCSECLISSSTTFIGEIFTDVVSS
IVGLQRDPLLKVCHVCDRILQERGIGRQRSWRRVPPPRKGISDKPTANKTVVKHGREAAV
GPGTATTVEVVSLGTTQRVELPPSVGEGVGVISSFSFDEGCATPLRSGVPSLSVYRPSQS
RLPTHPEDPKEQEISYGLTDTPVYSRNSMTDRMNKFLKEARKLRINESPEKSQSDLSTRT
YTPHPKATFRIADARSWQAQFANVFSKSILKRNLRRLESQSSYHLIKRVSRLFMKEEVLS
SLGVETAGMDRTMWIAGLCDISWRIVSQLPIVLHERIEQHLDVICIADGQFVETEIITGV
AFIQNVAFKRMKTYVKTPRILLLSGEVGKNPKPGTDLLEYVEGYEGHLDTQYHRIQIWRP
SVIVVQGNMHHYLQDKILRQSDATLILNVGETIIRRLSRCCKANIVSDLQYVGAAELYDT
SMLGTCESFELVHHGDKPVCIFKTPQVPLFTAVLLRGAEERQLTTVKRVLLSCAATAHHL
ALEAHCVFDLGMTCAESSPIPVNETKSKSTGSDADDDDNVEEEEDYDPPAWGESSSLSSR
HCEEYMQLITRSPRVEDRLETLSMNTGVEFPSEILSFDEKYDELMMDSIIVNTVFLDCVM
GNLPGEETNVGMSFGAAPNYSVRQVREVFPFYNEGDETLLDFLTERAREGDSTRLIVHGN
KRIWVRTFTDFKNTDFRCPDAEQNELSFRFALPKSSALSHPCGKAEEGTHISPVIGRAVC
KNCFHSMGNSLFGSPAACCSPHTLNISWGAFLELLIYSSSRFTLRCGHSLSQEACISFVV
FSRTGGEVTVSIIVESLTVYDVITPPEKLPSGVDTLELYLKTEKEELLRCVQSIVGAIQA
MTASQAQQQQASAVQTQPSPSNNQRIPKPPLANLLNGRGFGLGDSPEFGEDKGMLLLRRA
ADLLLLIPSLKTGEDLTILRLNDLANLVSDFLEWYKNGVFLAERRNGKPPTLMEITAFED
QHWAYCPRGHCGLRLNEPTSLVALTLQVSGLSPGSQRDSLLGYVRNDVRPLYETASKEIA
PNDHDSIVDDNADNNEPMACAEERAQGFPEESMAIMLGIEPSLLPDIAPSSLFISSVLDA
LDILANRSPASKTTFKHAMDVMLPWDKNGVATVTVEVMFPEQFAALQYIYTGGRVDDMLL
SLSRSRAIKPQGGKTKSEFFITLDERFLMKQIKQAELKHFAEFGPKYFSYMSHMYGKAEN
HGKHDATSYCSSALCKIFGVFSIHVKRAKRFLDTPAEIRYFALMENVFFSRRADVTYDLK
GSQRNRTAVEGSSVLLDQDLVNTLRKGAFFYCTNDVKSILMDSLTADAHLLSTSSIMDYS
LIAALNEDSRQLCLGVIDYLHPYTGVKVIESKVKAGIDTVLGHAGRDPTIIDPVSYRIRF
ARWLEGCFCGVPDKSFAVRRAMAKENR
>TCRU_8794 class I transcription factor A, subunit 1
HRFFFLNGILCRTENSDGSFRPADVFVGRDPPPRGTAMLGEASRIFDDSAVAPSFADVDR
DCSIFNTFGVFSGGVLIDPNTRCFVDFVDDIVVTPTLCKEEANGNVPHYKSLEYAKIRGE
GVMCLCSSIEPLNVAGKRDTPLSWPRSMRLTGSAEARFLALRNVDRILRRCLTEVSANRK
MFRLVEGYRCHIKSKRPPQSFMTQNIPFIFQYGGRPFLLQDDSDEKEENRSFPTPGPLFS
EFHAFTGLPKMVRMKTGEVDTYNHGVEFGLRLEKRLQSMLKPLRKNLFIGRRVLRDKSMT
RMRKYWYTFWRYFKIFRVYPAPSPNADGRSEWHLADDRHVNYEKAVLEFEEARRKYGNSE
WDRTAVVDAWDWLIVHERHSFLRRLAKV
>TCRU_8795 1-acyl-sn-glycerol-3-phosphate acyltransferase, putative

IRSIVTAYVILLLAVHWIIAWILQLILIFFTYPFMGREKRQDCCGFIFRFANFISTDVLN
PFWRSQILKPFPNVKGKKVLIMMNHLSAADPFLMVRVLLPLDAAWIVKSGLFRVPFGGWC
LSNANDLKVCFKNKREGLETVKGTVGVMMEEARRKLCRGRPIAVFPEGLRSKNPEGGLLP
FRLGFFKLAVEEGATIVPIAISGTDKCWPLGSVLMDSSTAYFSCGDPVDASTFRTAEELR
DHVWQVITDLRESHP
>TCRU_8796 hypothetical protein, conserved
WRRQLGLVFSSLHLHARHASHFGNGGNEMNLPTGGIGKKIADGENIVARTSETAGINGIY
GNRAQNAIRGMLGPQGQADARESKAVPILGRATVGGTKYTCDRSTAFENWRHICPAPVGF
HLSKLGSATCKMPNDINEAVESLQLQIIKGCNVFELDGSMSDVHQSVARAFYEALQAFEL
ERDGFVIVFRCGIIKQQPFQEELTQVETSNTAVVRNRIVPIFERYKAASLPSMQLKSGFR
ISDLTEDQLARLNLRRVSKTAAAGLSPEWLEAFFTNVAYNTKLECIDVLLLDGFHTLFDE
RPNAHIDDDILQIFAYLENQVRLGVLQYYGISSPYLAPHIQREYPPLPPDAMVPDHIRNR
RPLPPVINLYRIMELARRAGGDSHHLRFVQYPFNLTFSQALNKPLPYDGNHTLYSLTRAL
GLTALGYSPLEATDLMELPQRYHNFPMEADLKSLRMNFFTVCERCVLKEMEVKDSIEKGP
STLPPLEHLFVASVYLAAQRQFNNLFFFTSWATYYMIPRFRRALMRFKEASSTDLKEWCK
QYEQLVNDMLRLRKRMFEHKFGKYALEKSHAIDRVSPTLAMCPMLNQKALNFATYGCDTV
LAGFHVSRYFHEATELNPAKNGELPVPQEEIMALCDSAEVSFANCSPPDPYMLEPILTEG
KLSKQKSKSLEYMVKIDPHNPKFPDIPEEVEPGD
>TCRU_8797 hypothetical protein, conserved
AASKSLRPDPVETERFFLQRLAGLQCEASPFSSTPTSSQTAIKTDLSTFPPRNIPSSRRD
DVRFHRRLSSRFTSPCDQEKSYGNAEMAFHTIHNDVQMRLCWAREALRIIQETLLQPSHV
SRAVPRRLVVLVLYSHTRHNAAVGLHMGCICDHVKAMLAERHEEVLGVLTAAVGVKWRSL
ATAGTSAMSHINNDNNNSSDLAFHDDVLWYPNGGLYTFNALLQCLCGVGIEADAEDKKRE
SLQLHRKILIISEGWFHVRTAAELHQPPQTLSGKFADTVNVEPLPFVLGSAHSEEELRQF
ARYAACRAV
>TCRU_8798 UAA transporter family, putative
MSETQRQRGSTNRLLVLSICVLLFHVLTSLVQEAVFYIPGFHHTLLLTFSQALCVSFFAF
VQLCRSLSVPSSSSPWRRIVDSRRVPLFTYFAISLMNTTSVYLTNEASRLLSFSTQVVFK
SSKLLIVWLVRYIAIELPARLGMARKALKCAEHGAKTYRRSSHTEALSPEKQCGHVSVKV
LDSMVEGRVSTKEIPLGSADIGGHINNCDIAVNFSAGNNSNETSVNGIVAMENTQIVKEV
LSCIIVVVGLLIFTYATKETHKKKGSLKEEGWWPVISGVTGILLALLCDALIYLGEEKYC
FMKHNASHEEVQFYIFLFSVINGFFSLALSGGFADAVEFVSMHHVFITLLLGCSFFSYSG
TFFLLRIVSEYNSSTAAMVTSVRKMMTVLCSYIVYPKPFGFLHFVGVTFVMGGIWQYEEA
RR
>TCRU_8799 Glycerophosphoryl diester phosphodiesterase family,
putative
MKSLLLASSLAVAAGWAYVRHIQLPAGPSRLDWGACVFGHRGCRGVPGVPENTLDAFKYA
LSRGAAGIEVDVRLTKDNELAIFHDFSCNGHLKGVETTKRIDELTLLELKSLPFQADPTG
QIRLPTLEESLLFCRENKLKMLIEIKEMRRARLCADKVLDLYRRYPDYMYEHTVIIAFNP
AVLYYVRERDRNVAVGQLHSGRVLRSWISSGSVEVPWYARLCPTVLDWLLNYVQESINPW
LSGVSLMCPHYDLFSETYKRRWHTRKIGVLLWGFSSPVQCTREMRTPGVIVESDDQHEEF
ASPKPPANFDIFGDQARERERERREEEQRRRLKL
>TCRU_8800 retrotransposon hot spot protein, RHS3, putative
VLASEKGWPYTWKWKENKSTRDCYVNCEVDRVWQIVSGDLTEWFSPHGGTDFTPRRRVLI
GTPGIGKSMAAGSYLLYQLLHYDVEKLQVAAYIFGGSTAYVFNKTIKTVTRYVGSQTSRN
VLRDLEHLNMKGYVIYDVTEKGMPASCFAPYGWGMIVLSSPNVRNYAKWETQVRAERIIM
NCPDEMDVKAMCAWINRDGIAEKQAEYWKMVEERMDKVGPIPRHIFDANKFIAHSAAIED
ALDGIKSRDGEKHFTHGGVRLWYSENPSQKLVRVVRGRGEVGAEVFLNAPISFCLGRRIP
HYFGERDE*ERYFSFLLLVLGKRNTLSSECVEMFGLRVFMFGGFFGALVEDIKELRPPTR
RGGQRGSGGEPLRAPQRSYGLVSLKNPFEGGNLKYRLLCTPETKNFPLVDFFPFVNLPWK
TLVGLRMTTAGGHHTTASTVRQFTECLAAYFNGWKKLSRDMSWETIYVQHADSTPLNDWQ
RCDVVNSDNVSEEESQKIAAFWEEKVRQYQVSIPSR
>TCRU_8801 fatty acid elongase, putative
LRKMEFVQNWDGYAVRDWMIRNVDVVGYISGIYLAFVFTGPKLFAKITGRDGATSVAPAR

QGGAGGGGSKAVRRAMVLWNLSLSVFSIFGTSTVTPTLVRNIMNKGFYEATCTFNDKEFY
TTDVGFWIGVFALSKIPELMDTIFLVLQGKSTLPFLHWYHHVTVLLFSWHTYCVGSSGYI
WVAAMNYSVHSIMYLYFAIAEMGYKHVVRPWAPYITILQILQMVMGCFVTLYAMQESHDG
RGCGMTWSNMRIQLLMYASYLYLFSEMFVKAHVLP
>TCRU_8802 fatty acid elongase, putative
SYTRWAADFRGEHLRSWMRDHTEVPAVAVVLYLILVLYVPENVMAHRNPIKLRFLNMLWN
LLLTVFSICGAYYCLPRLWEVLTSPRISGLMADPNLGPKAPPPKLPGSFYNSACAWNDKI
FFDGFVGLWVAAFVLSKIPEMIDTVFLVFQKKPVIFLHWYHHATVMLFCWHAYAYTISSG
LWFATMNYCVHSIMYFYYFICACGMRKVIRPIAPLITMMQILQMVAGTFIVLYTYVKKQI
MGEFCAVNNPSLRMGLLMYVSYLFLFSQLYYRSYISP
>TCRU_8803 GNS1/SUR4 family, putative
NFKGEFATVVFDDSADILVYCCVLYILLVFMVPEHIMKNREPFNLRLPFVFWNIGLCLFS
ICGAYSCVKNMIALYWERGFYRTTCFFDSSVAYDGEFAFWVFYFILSKIPEMIDTVFLVF
QKKPVIFLHWYHHLTVAIFCWHAGHALIPSGLWFATMNYCVHSIMYFYYFMCACGMRKFI
RPIAPFITMMQLLQMVAGTLIVLYTAYHSYLGESGCEVDRTSIRLGLVMYGSYFFLFAVL
FGKLYLKKQVKPSGTASAYAMSKK
>TCRU_8804 serine/threonine-protein kinase, putative
RPSVALSQEIMPLYRLINSKYSEERRCRQPGPKYNDGYDDRHGHYLVFTGEVIWGRYTVQ
GILGRGSFGTVLKCFDEKHQEQVAAKVIRSGEYFYNQGLMEVDIVARLNSVPSLENLVVR
LGKVFVWKGHLVLVFEMLSMNLFQLIQRTNYNGVSLDLTRKFAYQLILVLKQLEEHNPPI
IHCDVKPENVVLRDPSRSSIRLIDFGSACYLHQGAKLYKYVQSRFYRSVEVILELGYDTA
IDRWSLGCMLVELHTGVPLFAGKNEAEQVARFIGVLGPLLARFIGVLGPLPDEMIERSPK
KDFFFVDSRQTQQEAFLQHSTGVGEGGPVMTDQTQRREHAASPSPVIAAEVLHSLSATSS
ISVVTAASTAPACSYVGHSDVAARAVATPPHSQQQQQLTAEAIGEATDGRQAYRNSFPTP
GNNVCANNNNNNTVAVPALRRPKTALSTALSAKKDVIGHTTIGAAGGGGGVGSFAPAVTR
RGKHATSGNSSQQKTHLGANATAAIPMTTLPTRSSAAVRASTFTPRPRLTSASHPIAHNE
GSLPSSARGTRAGVQQAAAAAEPPQQSGATAPPKSPFVIRYPPAPEHYQSLEETIGVYSG
GPRGCRQGQAGHGVEDYKVFLDFVQRLLCYDPRKRMSCTEALQHPFLSELEVQKQWK
>TCRU_8805 hypothetical protein, conserved
ENLHMWRFSALALHHQQQFRRLASLVAGGARDDKKTLVACSVVAHQRPVLASPTQVVDVT
FCATGVNHALHRQFNAGKTLKGILRGCAEQNALGVAAASGQRYSAITDVYLYALPPQKPC
PLHASNNLHSHPGHGTKPVDETYCVYPIESLKGAVFPCPECWRNLSAVAEMRHDDGEEGP
LNLFVQAQNETSAMWSVSVARRCLMSSPTPAIVVTIVL
>TCRU_8806 hypothetical protein, conserved
KMTPEDIPSLQLIPHSVYASLSLHVYGNPDAPPIPSPWEVLLTATNVNLDKEGYFGIAYI
NKELRHCIIAQRGTTNALSLRAGVWTYFGERNILFSLARQFSKQVRLYLSVTRGETPEWF
ISYTGHSLGAVLAACRSVEERTYAITFESPGCKTFIEKTMSPLKAGDANIITYLRSPNPI
NSLRPQCGYVVQIPLESEQSNLLQPRAVPSSMLRLPSIPSPQEFIRGQVPRVVGIPDIQQ
YVGKIEPLLREMLEHTQQVHAMVSIFSHFKDDDEPSNEQVVLRWPSTLMQFLEYYNAKRA
LEDPVNRKTNLSAAYESLVRDLYVTAERPKNSLPLRFLDGDSIRLLRLWWQETPTRLAKL
PLTLMDHKVLNTITIEDECMCTSVLTAFQAKQYLSLLVFRPEIHKLLTQLEFDPLLGSRS
KL*
>TCRU_8807 Endonuclease-reverse transcriptase/Reverse transcriptase
(RNA-dependent DNA polymerase), putative
QHHGTARNCRGGGVSILVREGPQAVAEPASIAGIELAQATIHPQAGMKIAFFSVYFLPFF
AKSTTAEDLDGQLCADGPQLMDADVEAHTEAWDRNIPSDFRGDTIARRCIENVLQVVNSG
ERTRYTERQGSTAPETALSKDSVVTHWERLSLGSDHCIILLDVPIGGDDTPTVVLGPNRK
LLAWKKADWNKPSEVFSRLCRIPRELTKMCSTERSVVLGTRRATRATVPEWNHQPSPFWT
PWLEEFCRAVAAASDAEGSQRLELRRRESLREASKSRWHTLRSELEGADGNSRQVVRRVY
APRSLSTPAMNFDGPMLSKHLKVSHLMKL*AAKATRHPKPHPPPPIPTNAMDLTINMADP
GYTLRLLLLGPAPGPDGIHGEALRHLGRVARRAVLWLFDIRLRAGAVPRNWRRGAVLLLP
NPERTASNRDSHRPVTLSSCPSKLMERISATRIRDVIESQLALQPSCFLPGNSTPDQLLH
LRAAMHRSAPQHRTAAYFVGHANAFGTVGPDAVILEMRRLSIPNRIARWSASCPNNPSAV
VCIDKLTPSSRTLTRGAPQGTAPSPIMFVVVLRSRRPCPSNVPIRRGFIADAPTTIAQQG

NRDTINSASKEGLSAVAEWTREYFMAANARKTSYTLLGSGKTAPLRLAYEDAPVTMEHMP
TLLDVKFQHPRGMAHVANRHEELDQRPLQLATILSFAWGTRRDTLRPVHIALPQAEATHG
VRVCCWVAFPTSRCTPDPAK*QASKIVA*NPRVSRMKCAVLEAKLQPLRCEARGNALRFS
ASIVRHPQHPARKPYDFIMALRPALRMEVRCPRLPRRCRADGPDEVQHQTCDRWLAHRI*
RTGLSP
>TCRU_8808 hypothetical protein, conserved
TFASAVRLRLLAQRVSAAGVISPSNCGMSLHALRQLGACNVHDRELLKRIDEVYRQADLR
SRANMFHCLACCVREQCSVYKGLPEALPPLITSMQESILGDVDELSPTECILVMEGVVKV
TPYRCATTQLAAILRNRSTALVAIVSNPVELSGIARIAVEAMQEAQPHSTETDGEQGEEY
RLRLGWSRELREISETIESRLDSFGKQDLLTLVDAITLRVTPKMEKTTGTGEDRLRKLGE
WPSRDVPEECRSLLLRVLSSTRQRLTVLSPSQLSAWLLRVVHLHQQHHPIFMSIVQRLGE
QHVRSSMSASQLSRCIDSLGETILICHEENFLSRTDLQFVSSVVTKLLETLVHILEKDGG
SSEDCSAYLVPAMLSLSEEVVAGNVEILHPLMERFFIILYRHFGKLTPRERADVVTAVFL
WGLLNKKPEHQQERQRDAGALKMSGNDVCSPDAWCKVVLNNMDSYSTLDALQIMNEVTSA
VYAEEAGACAYSPLSVRPMLLRLHERLQGSIGNLDGVPSSHLTRYLTSISKLGLRRKADY
YCVLKILQGRELTDFESLRVLGVVARHHLRAVPLITETVRCIPSRAASLHPKQKCLVLKY
LGQVRAQRFVQVPHHPSLAFGAFLTREEVVKEISVLSAMFAFVGLVELRQFENQTIVCLL
QGPLSRHDEFSGIHSATSLSEFIAALCRVDRRLVPTKMIQAVLNVVTSRLATSRSFFVDM
ADISFWLRLVRERSSLGAYVAAMDRQGESEKEGAEYMTAVSNYVSVAAAIAKTRLMDISG
SNDLKTNTFLFNQMAIGYRLGVSLLPEAEERLSCHLDTKHLPQLLSDPRQVINAVTVARQ
IRHLNPTVAKEVFHFVERNVGSLGAQEALLLGVEMTESLSDAGESKDQVVEMMHKLHALA
KQSLNDARRLKKLSVQEVALGALYGVVKRPVSS
>TCRU_8809 L-Lysine transport protein, putative
IVPYGGIASNSFNLASATLGAGIVLIPSGFRDSGIIVATLLLSLCCACTIYSIRLLVLTK
EKTGFRSYEELARGLFIRGVDYFAALLMFMFCFGTCVGYVISVGDLLSPLLSASSVPEFF
RTDNGSRLLVSGIWLVGMFSLSLPKEINSLRYASVVGVALIIFFVICMILHAANNGLQGG
LSKNLYLYNSGTNAMNGLSLFIFAFICQVNCFEVYEEMRDPSPNRMTRDSTLSMVTVGLL
YFLAGFFGYADFGDAASSSVLRLYDPRNDLLMAVAYVGIAIKLCVGFAICIQPSRDAVYY
VLRWGKTSDVPTWRNLLVSGFLALLALILGLFIPSINVVFGFLGGVCGGFLAFLFPAFFY
IYSGNWSLKEVGWMNYIATHVLIILGVVAVVFGTAMTIYSEA
>TCRU_8810 short-chain dehydrogenase, putative
MIFFLFVCITGWFFWSIYGCFAYRCRSVAGKTVLIVGGASLVGGCLVRRFMQLNANVIVW
DSQKKKLDQLLREFGCTNEKEEQAETRECSPSGDTPKKLKGGEMGAGTQLTANLVDLTNR
VQLQRVAKLLGPVHVVVNVADACVSRHFFERNDESSERILLGNVLSSIVLARALLPGMLR
QKDGHFVTITNAAGVVGVARHPDYAASHWASVGAHESLQMMIREMGGSGKVRTTLFCLCS
DLRVAPAVSYVSTSDDNKVVGDKMDPKSPTGSLLVISPFCKRPVTPEDVAERCIWAVRHG
VERVYMPRIFVLFPLLRVLPVPWLMSMISP
>TCRU_8811 WD domain, G-beta repeat, putative
ALHIGRELVNCMDVSSKYLLWCVEGGRAATLHMWESRREQPSAEPLVELGFTPTLISSFE
EKVVVVGDRVVALFTIEWSPFCPIDLLGDVDEEERGKPMITEEFTCSDIPADVTHISWAP
DGATAALSSPQQLVLLDCRVGYNNANHSAHKIRPCLTVDCCHWYGDPGAAFTAFTASRLF
LLSTRNHLVMTRYGNSDVYDDHNDSIFIQLQIERDGHIITRARRVTCFEVGGSEEGNLVV
GLSDGTVKLLRQDSMEVFFTLDVTKQLYRMSNRPPPGMGESGLEVLSVAVGHQWMVLMRP
DAFICYDKKSMDLLEEKTVILSGERAVLSACSGNGSWCIWSPQNQELLYYRAPVQMFLGK
DSKFDVVHAQGPLPSRLLEPLLLPFQQETIAGFNGKGADRKKNKKKLVAERPVTYGHPIK
SSGYASDVPWSVQQQRAKQVREKNLKGARPLPSVPSPLRYKSLTFPGHSFEPMTAANKIL
LSSPIHRAIITAAVFSAGGSALLTASGDTTANWLKYPVAKNGGEGTLMEIHTGPVNTIDV
SLSLNAPLVATGSSDGAVAMWQPTKREAPYIVQNVGKEVRAVKFFYTDKFICYAAKNTVS
FCRYALDDGGGELHRKRNESKMESVLEFTADSAQHVVALDAINYFTSNIMVWAGSNKSVG
IYDVSVGQNIHFMEEAHLNPIHHVAMVTSGRYASPSANVLHMYLTAGLDTTVRLWDIRQR
RSVRQLALHRNTATPVGVAFSPNGALVAVGSENRRVYIYDVGSGAVVDTIDVGDTPTALS
WHPLESVIAVGSAAGSIKLMGQR*
>TCRU_8812 regulator of chromosome condensation, putative
YMELGDVPSSVTNLLQRFLKDDGVIVGWGSGGKGELGTTYRCNLITPLIIGGRDKAVRIG

CASTTSVWLGARGTVLTMGSGRWGELGVPNPKTCPLVTATENGLPIAIVQIELPTFARED
MLIDVQGGFAYIAALSVKGELFLWGANNYAQCSPIMENKCCPTAQRRSILGEKIIQVACS
NFTVLALTASGSVYGWGHTFLLGDEDEVLEQAPEDSVFTLRFGLVDRTVVSEPVKVKALE
DKSIKLLRMGPWHAVAVSRDGQVYTWGLGRNGSLGHGTESDIRTPTKVTTLDSVVTEAAC
GSFHTCFVSAEGSVFACGDNQGGQCGVFGEMKLTTCYPMYVPSYHKVISATCGRHHTLLL
LETGDVIAYGTGLGLGIGTGYSMRMVRGVHILDNYTTLWMSGGSCHNFSLAIPKTLSLVV
LGIPHGDVSPALRVIDLKDGLLTAGLGQGFSILVTRRGSCYSMGLGGWGQLGVDVRGVKD
FTSDQVPVVRNAMRLSYFFRTTITQVSAGICFAAAINEGQRVFTWGSNTYGQCGLGVNPK
DYRIISEPREITWLSDKLIIQVACGCFFGMALSITGEVYTWGVIECCGNGLQPLPADVPA
NLIMNSLGSESHASVLLPVRVSGLSGIVTVAAGAWHAVALNAIGEVFVWGIGSRGRLGLG
NVEDRYVPGKIAIRAPFTHVGCGPFSTFAITDDGRLYVWGANERNQLSAEGNCVTVPTHV
LDEVKEAVMGRHYTLVLTRDGEFLFSGEMEDENGRYVSPSFYDTDALPPLISKDMEEPGS
RAIRIFGGVDHAMVLFEKNVISSDTITGLYYALREQPKHII
>TCRU_8813 GPI inositol deacylase precursor
WGCVLCTFITGLVSQLRQLHGVSANEALSKFCEFFGSPKGLMCRLASLILFRKALPLIDA
NNTPDVVCRTLSYCKDPKCHIFPVGNATVSVKSLRKIHQLERVKAKDLCSQLPMFCPVRR
GLRPAYDEDGDLFSTYPTKRGSDWRGRDCDDKDPKVYPGRNTTDAFRDENCNGIFGVDNV
TGKTYEELWCLNSSSMGVIALGDSVTAHFGIPADFLEVRSLSTAGLANIMGIIANDFDWP
MLSGITGFANVSDYKPNREGFMKSVYSELLKRNKCNHRDYQNIGVNGALVRDLSGMLDFV
ARNRTAFVKPALIFFSMVGNDVCSPPPRATTPQEYYIGLTKALEKAETIFPAGSHVLVPP
LVDGRILYNTMHNRTHPIGSLNNDVTYSDFYDFLNCLGISPCWGWMNTNETVRNATWKLA
QTLNAQLPRILKESATKFKNIKVHVLDDVYSGVLSSFNGSKWELLEPVDGFHPSQLANAL
LGEYMFKKTVELGIIPPANPFNDLIENRFGDQGGH*
>TCRU_8814 hypothetical protein, conserved
RSMSTQTFVASVEKTQQQLAASERKQELVLHGRHLFESETLDDIKTAWTPSVAGTVCHAA
TQLRISPTKGQPFAAMVERSLSREAVEAMDAPSLARIVHACLVLRSPHLYDILFTYIRAL
IKLAPTLDTVSCAVLLNAYGRAQVQHEELYKVICDRAAIVMKDPRTFVAHTANVAHALAR
VHFFHRDLFLVLRDQAVRQASQGPPLVPVTILDAFAEVGFFDDSLFSVLEERLMKELSDL
PAPLMASLIGCLVKAGRASSPLFTACGERIIAIGNTFDPTSIAKTCDAFYRANVLTEEVF
GALAERACKVAADFRADEINLTLNALGSFDLFDGELFPLLASRFVSIVKQGGYVSPVDAA
GVLASFAAVQERSDELVHICTQLLAAHCDALDGATLVQSLWACTVLNVRNEAQQSLMEYA
KGDASRIPSEEAAARQSRQALERLQYVKKAYGL
>TCRU_8815 vacuolar protein sorting-associated protein 45, putative
AYIDRILDGPDGLKVLLCDDATRNILSVVYSQHQLLQHNVVLVDMLSNREHYPMKHLHCI
IFCRPSPSSLACVYQELAEGNFASYSLCFSYLLESNIVQSLANADLLNLTTAVNEIYLDT
VPLTEYVNIAQLKPTALRSAVAPTVNPITYSQWSTTSFDRMTEAIVGLLLMTNRRPAIRY
RGKNKVTEKLAKLVAGKMTTVHQNFPDLKAKDSVLLILDRMDDPVTALVIPWTYEAMIHE
IIGFQCGNEVTIDDPDAKPEERVHILTAHADPFFAQHRYSDYGQVCIAVSELVKAYKALN
NFDRNSVSLDEIKNFMSRFPEARKQSVQVTRHCGIASQLVTEVNGRNLTHLSVLEQEMLA
SSNVTEHSRQMMDVVQDPKTDIDDALRMVMLYALRYEKVGGNNIAQLKEMLLKRNCPMER
ISLIDRLLEYGGADKRLHELFRTSTGHILKIVAKTVGQFGKDIQNVLTQHVPLMKKVINR
VYNGTLSEQKYPVQEVVGSPISVSAVPTIRAKDIIIVMVGGVTYSEAMLLYQINQG
>TCRU_8816 UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase,
putative
EALRYVPRDVVDAWKKRDFLIVLGIPTVDVEARQRRRHLQRSTCWRFPGVATRANNFTGA
MLVLYVLARHPSHGHNYSATLLEEAAQWHDVVTTSIDEGRVTTNKTVGGSGFWGLEAEIG
MSRKTYFLFDFALRLFPTVPYIAKGDDDMFLRVPQYLADLRTLPRRKTYWGVLYQKGGLF
PVDFILGFAMTLARDVAEKFLSYKPLQRLVRLPYSKEREPEFLSLNMDHEDVMVGRVLHE
IRYKDVVFFSERPCRFHNVHEGLGVRNVTESSVVVHHVWESEYETLMQRFGNDTSPAPKR
FRCSKG
>TCRU_8817 hypothetical protein, conserved
MRTSRGFCMSMWDSPAFEHNPLSRYWKRMMKQNGEKLTAQSIPRHIHGYIEASCPRTEGL
VRWFPYKKEITVDGRYVPTISDAIYSYYFPRELNDDERVKYVAIKTGRSELEVAEEVFLM
RKMKLFVAQLLRNKLRSRPLRMPEGVDYSGIERRYTLGISRVAQAMGMSMYGTQSYDPVI

VYSPYCDIGDCIDCICTKQLRTATQYLLCEVAVHRGIARSRMTDVTSEPKEPLSHVEPCL
FEFIKLRLAILALVAKQEHYVVDHLFDGGHRYGGCLIHLFPSPLDPEIIDHEVNHIELDL
DLAQKWMKHYYDHYVAPRRSG
>TCRU_8818 mitochondrial inner membrane signal peptidase, putative
MHWCLRALRYDVPYIILGVVIGWNSDVCCSVKGRSMLPTLIPGDYVLFLPYGMLRVLQYL
FQRPLVRNGDVIVMNISPELTVCKRVIRSTTDESVMRRWNEDQFTGALPEQIPLLETDGD
SEELRAEREARIYDSLAEYARARDWDDCLDRVDRPSAWLWLEGDNPNESFDSRHAGGMPL
ECLRGLVFLKAWPSIGRLP
>TCRU_8819 endoplasmatic reticulum retrieval protein, putative
MPPRDITGKSSAWDEFKRKAHLTYQRYLDKTVPHRAMRWAMFGFLLMFYIIRVFFHGGFY
VITYGMGIHLLYLLLLLVTPLAEDEFAEDSPLPRTAAGNDGEFRPFVPRVQEFVVWKSMF
RVVSICLFLTLFNFLDIPVFWPILLLYFIVLTVTQMGSRIKHMMKHRYVPWNAGKPKYVA
KA
>TCRU_8820 DNA-directed RNA polymerase, mitochondrial
FTPTLDVEEEYGTPVMAPTSSASNESVLSSIDMICDDLFSCKTDVLKSFARTRSVGGATK
SELVMNLIDLANREAHGESQDLSITKRVLGDVFNEEVRVSGVRSQWTNKSLEASHIEMAC
DGHLKFEVMSYTQKTLMVRRNASESARVLRKLIRPFQQDYPRIAETAVGGVFRNFKAEAD
QLVESLPAVEVVGPFTSFLVSYVRYATSANLLTRTNVIERLEQLGLVQMAVEDSSDATLQ
RLMALLDEVVAEVERRAGCFGDKRTAWGTETPEVLRSSIQAFADSWVQQPRGEVGDRAPA
WVHDFVRMFNNWDAIVRTDVPMLEDVPRYIFDCILSGVVCFYLLQKIYGDIIIPTDVPLT
VRSAVRRAMEAHFKDEEKAAQALAKLFAYVQSPGDSGVVKAEFFPAVLSQMQGAFHDTEQ
SVLHNARVALVLREVCATASRCTRTCGLFHMLVKITEDLRFHFRFNTIFKKLSGRDRTTI
RTKYSINMVKTCEYFEQEYGVTPISTKAVGFLVIQLLHMSMRGASSGNVAGSGRPILERF
VSVTGREEYSVVGMSEMEATQIRDLRVAFPPQLSYNSWLHQSDTKEKSVYNVLPSVAVKG
STNQAMIISQAPMMKALDAISRVPWRISKYMLHVQEAIVREGYGFGKIRPAFYPLHYCAK
SRGDISYDVAGNDDAAAAADAYDDGDDCEVYNLQQRREYDTQQDEDWKSLSEQRSNRIHY
LQALRQARSLVQFSHIYFPNSMDFRGRMYPLPGRLNHTGSDPFRALLEYAEPKPLGETGL
YWLKVHLANKMGMSKLSFDERVHYVNEHIEDVVQSAESPLHGDKWWQEAAEPMQCLMACK
ELADALKCSQGAENYLSRIPVAVDGSYNGLQHYSAIGRDAFGAQLVNLVPSERPADAYTG
ILKEMMRSIMADAEKDNPVAQRCLGTGKGQDCNHVKRKTIKRPIMTQVYGVTGYGMSEQI
LDELVKQNKNHGLWTPTDMREMADYLREKVLESLGITFRETQNCRRWITEVTNMIWEAQP
AELRTALCWTTPLGLVVRQPYKVRKEITLFTPHGCSRIPGDAFSAASRKQLTAIAPNLIH
SLDATHLAMTAIEMQNLGLSMMAVHDSYWTYACDLPVLSKVLRQQFVTLYSKYDPLWELK
EQWEEAYFMDLRRHGTLLPDPPKRGDLDLSVVLDSPYFFS*
>TCRU_8821 hypothetical protein, conserved
SLRDGDSVQECFALAPPMVTCLVRHIDRAMAEVTTPPIIERCVVELQSYFQPHIDASRVV
ENCVPGSKLQLQFGKAMDINAGTSSSLLHVYILAVDQPYSRPRLLSHVVKKWRTLLEGLG
QEGSAFVMLYHQDLVDAASFSTQRASGLPGDVHGAKEPDQRKADAAVAALEPYFEELKAL
HFAPHQMCAYLPNEAPIRIVERLRAVFAERTARLTAAFDSYQQRQLRSSHASCSNSNYSN
GIATGTADVWDLHEWWRRGYELAIHLLHFGAVSEAMKVFAKMFSLYYYHSEDYGFLKSRA
TLARLGKLPNVFDPRAFLTESDGSPSVLLDDTAWKASQRL*SQGLFDRE*WLPSVLLDEA
EILEGLLFIVACEIWCALQLGLRNAAFARYKEFLQVAREKFAEETTSKVTEVWELFFLLR
CALSAMRLNWNIAVLGTGVGDMSASVGSRLADTVQHHQVEGDGEPSSKRHRGSLDCSETL
STSVMNEWGTSVASLNMESILVSSLGNLVEGSEAQREGAEQEGGKGDGKDAMKVNRVAMT
ERLLTLCRILHVSWCKDSRWMCRLLTKLSTDALEFLVDLAAVIGYRETGEMVVPLPSALP
PHLPPPEVSEFGMPEIASVAAFASFYRTLAETSAIGYSLLGDRRLAHELYYKCALSYRVE
NPAVTAELCRQRLIPFCRRQGWLQLQAVVHCLFVDSMDLVMRQREEICQPPLNEEETVVL
KESILYIIGALNERGALREEIYILCGRHSPATWWRRLREIDSRWKSRNEAREEPSYSLSL
LLRDPHVFCLQSDSLREKSKRELDETTSSGTENRGGSGSHAAFPEMQAKLGDTFLLHFHV
NCLVDILGPAKEEEEEGSCITLTAMLASKKDWTDPLEPIHLVDVTKVVHSSYNEERQRVQ
WVWEFHPCRAGEYHLLCITLRVGMTTLVYVHDQTSTLSLEELPPRRLTMSPVVGERCHGL
LSLPEPDIGIRLHVSPPDESHCFGDMPNFFRVRVEMERPLSVPQDSTTHASLLSSAALAG
HDGVGCKNCSFDALSRQAQLPAQLQPQCVHRASGIRVTTL*RSQRRSKIQGHWPLFTSIF
QGGTPCIAHRLLQPPSAPAQRSFRESTLLHDVATIRRTDTDHLANSSLSGLKMSTSGVMV

SISDEKTGALTTVPVNEQRIMAQLPTIFRSCRGEKELCGEDGKGDCVNSMHLEGSVLLTV
PRPQCCFKICLNETKRQHQQEEEKENLGKFLGKTRLECLLPVLPIFMSSADECAQVSLCC
QRDMESCTTSVSVPFGFAQAFNVQYAFKCFQSRVYCLVQVENVLNKTSLWLRGAFLELLD
TECYYKLTRVSFTHERLMLREWKPHETMHLFFELTPCSDSCIREKEVCHRVRLQLIYSSW
SMASEMTPLDAHILRPMHIYSGHSSGDNSPDVVPLAVGITAEKSLVGALESHQDRTGTKS
VNSSGAERPFFTVKHPQFYCNSAQLEKLRATCNTFQAPVGTFTSKHSCLFNAIIFVDPQH
LKDHHWSHPGSADDATRKPTSLVRNLIETISEDSFDDAPAPVGASPVDLPGGCVFPIGEP
IRFSVALEPLAHNWPENSDGEEEFFITFKADPSAWLVTGKQRLRRVLSMMEEETLYFTAV
PVPALFCSFAEREADRRPHGREDDQHGKAVQLGRRKQKLSVVPTPTIEMRWASRNDANGE
ETNAENNMVAIDVVQFRTSMRIRH
>TCRU_8822 mannosyltransferase-II, putative
QTQRRDVLLRLASSSGTTLFFLVCGTRMLVLLAMLVSYAVLPKLLDTELLFDTSGLLQND
TSGQWGFLDFPRSWDGVHYFHIAKYGYSHENNCAFFPLLPSLVRIISWLNNFFLSTPLAV
FPISFQVALLNVALGGASAIFLRRITVLTLLRSTVTGRMAAVGGTWLDELPPPPTLRHYS
QKENDSGKDVKKTLRREVGAVLLMWMMSPTAVFTVVVYTESVFSFLTFVGLYLLLFSPKA
GSRIVTIAAEAGAVLCFTLAGWARSNAFLYAGFLLYPIFLQIFLFNTYRRRYRQYHGDTK
ALSRWPSFLRCAVVLLELMVICVPYLSMTYFCFGRFVPQWDPTSRMTIGGRFFSFYGWIQ
KRYWNVGFLTSYRLKNIPNVFISAPIVFFTVRGFWLFYVIPAFEGATSTASKGSNGCGGV
SRKKNNGLQKNRCFYFSFFCRIIEALVQSSNMVYLVILICIGVTMVHVNVVNRFIMSSPA
LYWIWARQIVWDPWGGSTIVMFRIFLMWNFIGVLFFPNGMPWT*
>TCRU_8823 Protein kinase domain containing protein, putative
GCAIGHGGDRGSLVYSVGRTVDASCSVGYPLALKIYPISVTENEIEFIRALFANDLTAFN
RSGESCGVCRQVPYLVLPLAIVTIGGVDRGILMPQHSYSLKQFLLVTRTVPEIPGEGEGE
AEFKGYNKAFTNSLRSFRSFDPIRDCRVVTAIAFQLVVAISLLNEELPHVKNGMLCRGFT
HNDIHLDNILLNRQSGCAALCDFELVGHISQDGEGLPPPAIHRLPPYCRQSPHGLFCLTA
DTWAIGLVVLSLLTGVDPLFDDDKLMDDFGDGPLLQSHTMSEGTVSVLDWEENIKAHVEA
LLLRDDPTGNRLEDAAPLLDMCSKCLVNRPGVSPSVAVELLSQPLFSSYVNSPQEAEFIL
RVW
>TCRU_8824 exocyst complex component Sec10, putative
NSGVNTSTGRQRHAHPPSPTSPPTQQRPTLDRMVFSSVQFSAPAFVNSITNRVLLPILLS
RRKDASPAATSTTATTGAAAGGAGRSWQQFTESGDSDGLQNSGLDGTRPFHEDAAAVAAE
EDHVAIASHLTTTLESALAEIEMVQDEEERSLQSKEVRCRRVEIREKRQLATIRLGLEAT
TARLHEYENRVCNALAATAGIEQHLSQSNARMMRGRSVSQLLKHFKMFTQMNYSELNALL
KNLSRARAEQRGNVTSQWEVGLVSPADPMYFGGSSGGAGGGVGGGTGGGESGGGGEDGAA
ARSEEGETGGQEDVDDRNNPNRKDGAELHPGTGDAPSGGGRNDGSYSSSSREDADRPRGA
LKQGGPRQLRRRVGTMAQDSVEASAWTATTTTTTKSGGGGGVGSREKMHRIETAAVAAGL
DRIFVVRSCTETQVDWCQRLTHLCRELNSVVRNTSNIQLYVEWVRQELMADIFHLVDCFN
ELYKEHPATAVHQPYGRAILKTLELVSRLYTSITDSHDALLFAFYSRTINQMGITLFSEY
SPKPLPPQPPLSGATTTSAPLSAMQHYRRTTEPDLQRTFDFLISRARRDVIVVETIFGTT
NSARQQLLAQVTEGVVKPFVTQQLKLVEFFERDMVEAETRLSPRSKRRASARVADAMTYS
HTMQARVFSFFQDYVKELRNTFEKGEVDFLNKYVDSIFTGRSAFVEQKAELALLKRYHTM
LEEQYTRDLHSLPDEVFDLREAHMKKTKELVECLTEVVARTRIYAPPKDVTLCVLDLIRE
SLENMGNYMDEEVRKMVESLRADREHWRMKPESEEELLRPTKLESQQCGLRMLLFVQSSL
MILNDAITSSCMPLLQSDPRLESAIEEAKESAYEALDENAETLLNLCANAIIVRSLSILV
HYQNRNDYKPKVAKGAEGEMLAQPCTRACTLFCLYITRQFDEAKEFIRLSNGQVPQRQHV
FGMATGAKLDSSSVASLYTTGSKQRSGSTAGNVSNDVFNAVRARARTMNMQQLLFGDGGP
SSFVRTVGVCLYRGIVTHLKAFTVTDRGALIYKQDVTAYMEAMGPVIRTPGLGGAVVEVL
FRLLKETASLLLMPWGHIKGVRETGLLRLMSNEEKVQFIRMREDLQEGFRKI
>TCRU_8825 mitochondrial carrier protein
VSVENIQLLWLSKTIGRTLIAPLDRVKFILQCQGELRRLGTLDGSFSGAWHCMRHLAAVE
GWRSFWRGNLIQVVSLLPITIAQIFIALPTQTFVFNAFAHHSALTYTFSFYAAHICGALA
ASMVSYPLDFARFRLAVDIKPFRGASYEYRHSLAFFSHPVLSESPHLLYKGLGLYVFGSL
LYQTVHSGILNIVEPFVLPETSDSGYGAIAAQIGTGLTVSALSTLCLHPIDTVRRRMMIA
ATEDDLRYSSSMHCVRHIMRTEGPVGLYRGAFFSLVRMVVTTTLF

>TCRU_8826 protein kinase, putative
DRFIVGSPIGEGRFGVVRAAVVKESGVPAAIKFVTTPRLDEGIPHPTAREPLVAMRLVHP
FVIRTYEVVPCGCSLALVMERCKTDLATVLSGRTASNPLPALEAKSLFKMLLLALAYIHS
EGVLHRDVKPSNCFLTAEGELRLGDLGLSRAWDTEASMTHEVVSRWYRAPELLLGQRHYG
PEIDVWSSGCVFAELLRGYGGAFFAGDGDIWQLSRIFDVLGTPTPTSWPSAVLLPDWGKV
HFEPKRPLPLREFFPDASECALDLLRRLLCLDPQERLTAAGALRHAYFSEY
>TCRU_8827 40S ribosomal protein S15, putative
MTSNITQERYEQLKKERTFHKFTYRGLEIDPLLALSEEEFKTLVHARARRHMNRHANRRA
PVLLKRLREAKKDVKAGEKPRAVKTHLRDVVITPEMVGSVVGIYNGRQFNAVEIKGEMIG
HYLGEFSMTYK
>TCRU_8828 SPRY domain containing protein, putative
SVVRRICAEEEAARRSRICLQQLESWKNLRVNAWRERMTLLRPEERSASLQSFSARTRED
YDSSSDLPSLSDSPPCQCDPFNRTLSPPQTSGARAQRSSLLEKFYEGEVMREARRRVRRE
ELERQTQEAAERRKAEEEKRRREREAETRRWMEEMEALRQQEREAQQRLRDELVQREEAE
ENARRAADRAKGAEERLESVRRAYDGAKASNKDALDGLQLRAQQVEILSTEIQRLKDATE
ALQHQHTLDERRQQRRIEELEHELAAASQREATASNCLRETQRELEELRQSYDEKEKAMR
DVNASLRQMQRRTEDNERRLCAATSAAEEEGRRADELALQYKEAQQTMEDLRMELQRCRE
DATQSLKDQAARFEALIAANESAADAALRQLQTDLAAFRQRYEELRQERVAESAATEAEL
GAQQQEARRLHDNISELQKRIDADAAELAECRRELQEEILRNDEAERLLRKAAADISAMS
AELLELQKERDGGNLRCERLEAVIRDANSQAQRARSAVSKQQPLQNQQPCINDTAALRSL
FLRDGRETGLRDLPELPAHATGGHSSSAPQAGTSWLQPVESQASRRDFLARSVGHVDTSP
DTRLRSLAAKVDYAVEAMLFAREYALRRPRREEEEQQQQQQLLTSTSPLREETSRGRDR
RLAAECVVKLMEAVTLLNDLLQTVEPITSGDATGVVGHEKNCRLVKRLRKQRDMLHLLLE
EMRDVDTSGRRRMASAAVLLCDPLTEPLATAVAERLGTVLERLQSGEPSRTSHSTGHAGG
DAGILKGDKITSFTSPSPRIPRGVKNDDDCEVAANGSATRQLYVNGGIRGPNPRHTFGFT
GGRLQVSNNGTRLQRLLLPGVLDTMTVSALGALDHRTILTAQQSAAPSCFEYTIRVCMHC
DGLLVGFADRYLPLEGFGPAQNSLRYTNCYYLHLGRGTLFCPAQGMVDVPYRAFQRAVPG
ITTKEPLSHCNNNNDGATTTTTTNNSAAAVRIGEEISCSLDTATQTIRFRRDDVDCGVAF
ERVSLNRSLFPAFEVNSRGCTIEF
>TCRU_8829 vacuolar protein sorting-associated protein 35, putative
ISINRPILTPKQEQEKWLGETVQAVTEKAARMKKYIRQREFIEVMRSASQMLLELRIGML
APQYYYELYVKVFDEMQYLEQYIEEEHNRGRSLEEMYEVVQHAGNIVPRLYLLITVGSVY
VKSGEQPAIEILRDLVEMCKGVQHPTRGLFLRHFLLTMMKNKLPGDSNRVIANSLESDGG
TVEDTAELILQNFREMNWLWIRIEARAPPKAVEAQSQVQRKKKDRRELCVLVGMNIVRLS
QLEGVERQVYKSNILPRLLSIIVKYREPLAQQYLLEVIVQVFPDEFHLFTLNELLSILED
VSPGVDVCAILASLMERLGNYAVSLREGVAEVSGRKEEKLLQNMFEVFKTRLDAMLTASH
VRDKSNHAPVSGTSSSGDGPQRPHYQLTPSLYVNSMTSLVSLTLKADPEAAVEHISTVFT
AMAGQLVLPLNHAMVTMIERMIVHVIETLKDPSVVLGIRDMDVLTQNLPFLSRRAVALRL
CTNIVRSASHRIGTLDLCARLFELLAPLVRDEPDAPLHHGAVYVGDAAEEFLEEQHLVSR
VLHLLQCEDVSMQMKMLNGVRKLLGQGGPERIAVTLPTLVSLYIRLALRVAITAKTEGAD
VDAKTDGENNIKAVKRVSCHKPFQIIHSGDGKGILEMLAAEKPTESFYLYLTSANAADTC
GLPDVAYELYTSAFQIYEENAADTREQIEMVSCLISSLYSLRNVPEESYELLATKVCQYS
SKFVRKIDQSRVVSLCANLFWRSAFSEESHRRVLECLQRSLKIADHVQETQRLPLFVELL
NQVLHYYATKAPGVTVNYISALIDLVQETTNSTHSMVTGSNSDDGLEVEEPCDGMEGENK
NNGDYVNSEREVYTAARTFYRNTTHYIRSRQQVDERWKEI
>TCRU_8830 Aminotransferase class-V, putative
ASMQEETVAPEPSSDDEASKWLISNIPPEFRKRLNTLDDPAFMMDISSYEGFGSFHSENV
EDLVARENGKYRPPPLPPFAKRVLGRSDLRQVETARNEKEKMEIRERSVQLCEFGLPFRH
EHFTITPEFVFINHGAFGGSLRGAVAIKHGYEDLMEQQVVKYMDRELLPLIVYSVRRLAE
FINADAKQIVLIQNATFALNCAMQLIEKDDVVVFLDTEYLSVYKMMYFRCNDVGASLHEI
SLLNYLHDASIMGNDESLTEEICRQLPSGCTTAVFDYIASTTALCIPVFTHIIPALRRHG
VKTIIVDGAHAPLQLDLNFKELPPESQPSIFVGNLHKWFSSPKSVGFMWVHNSLLDSFHS
VVISHGAGDGLLSEFIWDGTRDYGAYLCIPAVVDFWRAQGLDRVRNHCANLLQSAANMLT
HHFGTRPVARHAPFMSLVELPEALQGPPLTAKHIQDLLHEVYKLEVPIKRVEGRFYVRIS

AFVYNTPSEYVYLREALLGIARNRLLSLWRQRSTALEAGTPVVDPPRVPFEKRNREQGGC
GVSGLEPPPRKRRGIMF*
>TCRU_8831 palmitoyl acyltransferase 9, putative
ESVEVLVEPEKNRYNDTNLALGKMTRVKCCGFTCLWSPDAVIFCVPTLLTLIIVFGVLFT
LWKELSVFELFILFVFLSTAFVSSFLVTCTDPGVYPRLRHGEADPLDGVRELVLCRVCGL
RRPPRTSHCYQCNVCVQEHDHHCGVIGGCVGRRSLRWFLLYLLTVSSAAAMGLLWIFRSL
LTGTFAAAQIRREAMHSSPNRTVHPLVAQESHEEDTFRSLVLILLFVTLLLVVLIVGGLA
VFYVFLVLTSTTRRESQRTQSKFATLFRTKFMWNNLMHVIYPPPSMLCAP
>TCRU_8832 Ribosomal protein L23, putative
ALMMAARGRFYRPLVNQGINLWRYRMGRIHKGWCTWEYQHTRPDPRPFPDPPVNDYFGRS
RLWNPISGKMGYVNKKAEEWGWPHQRPPPTGLRRSQEYFPFFFARYFPDAEVRLVLDSVL
NTETTHPVFYIPNDMSRAELVNYLKNIYGVENVVRIKVRNARGRRYKNELGEIKTMDDYK
IAIVELDSPVSVEFKQIKGTEDTPDNRPQTQIS
>TCRU_8833 TATA-binding protein interacting (TIP20), putative
FDLEKFFLGMNNVDKDLREMALFDLHQALKDPGFQLTESEVDRVVDHVLRCFTKDELDKE
VRNNAIQVAPQLFLFCSERQQIRFSSFLCTSATFRGMEFGDRGSSEILESSAFALGLCCE
SMAERAQVSIEAWQRLTPVAHSINATLLSKLGDGNEDVAKDGIYGSIIALIVPFARTFSS
ETRDGMAKRALEDFSGTGSVCRRAIVCLSLLSPFLSENAFNDVRETAVRGLQGKDPNLRL
LPHLLLYEALVKISPLRMMTDICTVINILLLEIRRRTNEYTSEEDDVCDTIMRVMNSMVC
QYPNELSTSHGDIFTCCVSLMRFDPNYCGDPEEEEAGIEEGGNDTYEDYYMELEEVDTSW
KLRMWAAKLLSSLIQISPFSDVLIQRLDKANVFSVGDRMEEVQLANLQLLNAIAQHPRCE
EAHSILLNLLDSLLRCVSGSNQKVSVTAIKTLQLFFHLYGGNLMNKGDAICHVLSDLAAK
ETNDTSLLNSEVITLSQYVMDTALKEPRNISIAMKLFDTVFYTICKSRFDKVRDRALRVM
QTMTCVALSIDASYTERCVSLLFSLLERKTTEMEVSRAATEAMGECLSNLFLTLSEDTVH
HYLHRLVCLTETNVNALHVLGSAVSRSTAIRISPDLLEHISAYLAKCNYSHHYVVLGVLR
DALKNGSELSKEALDVVMKFIQVDALRSKEALPIRRVFELLTEVCRNYPPVIEQTLEMIL
SSVWNALEALLASGSSFYGQVVEDAASFLHTLCLQLPRQRFTLIEAVLKHILISTSPDLS
SELLSGVIVDNEEAIEKIRSFFLDNPALTCLCVGTVGRSQALPEEWKKFLLENFAGAISE
SARSLGMAAIGRAASNPKNISLFMQIVERAISETKDRSLYWRLIKEVMHIAASREPSPFS
DHLFCKRLMERLLESALEDDVQTNAAVLGSFVSFDLADLLDITCRYLNSDSEIIKATCIS
TQRYLISHCKGEEIQPQLASVIETSLQTLGSNSSVRIRLATLQLFAVVASSQPHLLFTPT
MRDVVYPNVLAELVEDSSLVLTVNLGGYTHREDKGIEVRRLAFDIISILLRDTERQRRGK
VLEFFLRFEELLQCLVHACGPQEKGEVDVDLNNQAKTLLVQLVNTHLKLPWSDSLIMSLH
GKLKAVLELNCEGKSLSAERERVNIRYALNCVMRLTECVPFAYIPQFQPLLLLAQKSSLL
AESMKL
>TCRU_8834 hypothetical protein, conserved
LNAIFTSFYMDVFMRQHMLSVEQNGARAVSKRNRQIFWQLGLGQLIYAFWRGTRDVFFDW
RGSFCFSAFAYLKFWRLSRVGPTWAVSFVLLWLPMLVTFLSSAVQFTLWMALYEHLLVCC
ESALRTVPKGGLGQNDRGFVAYHILSGVGVGTAYYLSELGGMEQEELYAFRLFTTICGLL
AALLLYACGRQQRKTLKGHEGVEEGSAVNSEEFARFAQQTMNRCSMKATMFLWALQGYSS
IFSTAFFNIFLDMSSSTVSVSVRILFLLFTYAAPHAVVAVAVLFYKLVGKKSVVSGVLAT
RAVVGVLFLAVAAQEAQCFFHFMNANFSSSIFLLLLFLNRVLTDAMGYLQESILSDLVDE
DTVIFSRTNPTTEMTRRLLAMVSKPSGYVALAATSLIFAYMGCSHSSRLEETPGAAVLAG
GTALLTSLLTLCAWQRYYNLEGNHLQFVRMALRRRTD
>TCRU_8835 Tb-292 membrane associated protein
QREAEERAQREAEERAQRESEERAQREAEERAQREAEERAQREAEKRAQREAEKRAQREA
EERAQREAEERAQRESEERAQREAEKRAQREAEKRAQREAEERAQREAEERAWQEAEQCA
QREAEKRAQREAEKRAQREAEKRAQREAEKRAQREAEERAQREAEERAQREAEERAQREA
EERAQRETEERAQREAEERAWQEAEQCAQREAEKRAQREAEKRAQREAEKRAQREAEERA
QREAEERAQREAEERAQREAEERAQRETEERAQREAEERAWQEAEQCAQREAEKRAQREA
EERAQREAEERAQREAEERAQREAEERAQRETEERAXXXXXXXXXXXXXXXXXXXXXXX
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QREAEERAQREAEERAQREAEKRAQREAEKRAQREAEERAQREAEKRAQREAEDRAQREA

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DVLDPRYVPEIFMYRWDISFVGYGVKNSYLIRYYLHNGPSATRHAAMAVKAWGKATNVGA
GSAAMLTSYAVTIMFLYYLLVTQQLRWVDPWSLPHPAHLPRYPDYSPLPECDPTELGRLL
HGFFIFYAHHFDYEKEIVSLSRNRRSQRSDIGWIFPQNKKGTFSYNFCIEDPYEDVGTGG
LNLGRHLHPAKFQLVKQEFLRAAQCMERFSPLTAPEKSVLGVRRAELRHFDRGDKERD
>TCRU_8839 retrotransposon hot spot protein, RHS3, putative
AAEEARNPTTTIVAIKLEGLYESVYNAIWHHVVEIPDGVERTKAGTGMEVREGKPKQSWT
YKKVGNTFEKDDAVQQSGEAPPRLMVLTSDKGWPYTLSVLNGCGNDLCVNSEVERVWQIV
KGDLTKWFSNFDLTLNPSPLPHVLVGTPGIGKSMNAGSYLLYQLLHYDAEKLQVVVHCFG
ITMYVFDKNTKTVTKYMGNITSKSVLGGLWQRGMKGYIIYDVTTKGTPPDAGFAPSTGWG
MIVVSSPNLDNYDEWEKQLKASRIIMNCPDEMDVKAMCAWMKRGLEPDRQAGYWKMVKER
MEKFGPIPRHIFDEKIYINRLGAVDVALLAIKDTDVKEYFSMGGEKKWYSEDPSHKLVKI
VRERTEKGAEIFLNAPICDDIGFRTAERLEKEMATKDLLLLILGSRGALASRALEQLGFC
VFMYGELVCALVEELKELSSAKRNEAQDSVLKVNHQGHPTRTVGLAGLEGGVTRTAMEYG
VLYLPKVENFPLVDGFFFMESPRRTLVGLQMTTASAHHTTT
>TCRU_8840 phosphotransferase, putative
ERQEDELPPSPFFDAYVVLDFEATCERNRRLEEPEIIEFPMVLIDARSHRILTEFQRYVR
PVVNPILSDFCTELTGIKQSVVDAAETFPLVFDAALEFLRGSGYGEAPPLRSYLFVTCGD
WDLKTMLPSQLRTTEKTGTAIVAPSTFRRWCNLKVPMRTIVPTKARGMFDLREMLAAVGL
PLKGRHHSGIDDCRNIASVVQELLRRGHVIAPTTDHSGIRQRESSLSRAEDRPLTGLREG
TRVPKKHAEKRPNAPMMQEAGVPERPHLKIVSEEDPLPALLKNSNLVLEEAKKVTYSKTL
TRILRHAADKMGIPVSSGGFVHVDHILRCKPFCNDPLALSHIALVVHTNDKKRFKMAYDD
HHRLYIRANQGHSLAGIDPELRRIESATEMPAAIHGTYYSAWKEICACGYLSTMTRQHIH
FSRGLISDHCVISGMRSNVEVLLYLDVAKVLADGIELWESENGVLLTPGMGSTKRLPLTY
ISKVVDRKT
>TCRU_8841 Leucine Rich repeat, putative
FLEVFLSMYALRCKEFAVEMNPRALQAAVAMQDAVDIAKRDLSDSDTTTRGVTYKLNGVP
FGVSGSQALFPAFACMPLVKLDLNDCYLGDAGTRTLAEVMSTSSRCGTMIRDIHLSGVGI
VDASSLTCVMTAAHQLELLDVSRNRIGTQPHGLAVLCASMHHHKSLREVNFGDNLISGSC
VVTIRAIAEWVVCAGHDDVLHRIDLRFNTLGILREFGGVVIPSRTNLTHFIYGAHPLVDA
LFLNNTLEYFELYGNALSADVIEVLEAKLAVNRRTKKTIQKSHT
>TCRU_8842 AAA ATPase domain containing protein, putative
IMEKAPLLEREQEYNAVHAFIEERLRMSHCRSLFVFGACGCGKTSTILRAMRCVSHRPMA
CDKVVGRTSAGGRGSCGSGRSKSHSSHDNSPSPAIVKRKPVKRRRGENESEDAVDTLEGA
ANGRISVGARDASPEGDFVSSSSPLPAATLRLLEADRRIQCHYVNCADMTSQQLCDAIAS
CFRLAQPRLDASSRNLLSEIEALPRHVTAYKRRGVAAEAARKLLLRDSAVEHVTEPTALK
KCVLKVPLHVLALDEVEYVRAGARGLLTALAALSVEHASQLALVFISNQRELVHVPYMLL
KELPFEAYSAQTLERICARIVANVDFTEKERMQVQLSPALIAYIAKKAVHEYSGDVRQVA
SMSRRLVHTAQQEARDEAIKRGDVRNDETPQRRSGSGITRAGAVPGNTSPASPAAVMTLA
QSQKVLRGTAVVSDRVFEYVAGMPEQMLYVLSCLVVLALRQQRDKSLAQSNVAGVTSTTR
RVRTDAAAGKTEPGTFAMREVHRMYTALMGQQRFPMMNAAGIASAIDSFADLGIISRPQR
CRNEELFSFNGTWSLESMQSALTTRGELLRQERIEFGLDGSENRFSEVLRELKKIAGL*
>TCRU_8843 hypothetical protein, conserved
MSYDGRELSPMAERPVNTAAAVSGKEARSVSGSALPVYDLDPTTRQLLEENEAMLYRINV
LTHDVQLAQGEIQKLNNTIAEKNEELEALREKLGDANIHAQDASGRVINYKTECERLSAE
NKRLLKEYEDVCAELEQRTEDIRQNTGVMRPDSVRGSPALSVEQFNREMLSLFPTVDRVV
NSLKRCVVVDVTNRERVLDSAQKELSSMQRLADSVRRMGVGEEGRVNNIVSSIRKGEKVQ
SHGDLAIMIRWMIVQAFESGLTATEGNLRAIETLLAKKDEKTNGIEKKDAGEKSALPSAA
GAVRRMF
>TCRU_8844 RNA-binding protein, putative
EVPTVRRVRRLRSQFERLVRPADVRPGEPMPSIEGWVLFLTNLPANTTTDHILDLFLTYK
KEESEGYAPVREVRIPLDKNCECCGYALVELQRKDAFERALKELQGVVLPFAEGEPPNGE
EVWRLQIAPTFLGETDDDEALAGEKRVRE*
>TCRU_8845 Leishmanolysin, putative
WEPIRIEVFTDGLKSTRRKETYCQRVGVECDNLLGEQITCKEEHVLSEAKKQLYTEKILP

GAVKLHSERLLVKPTGRNITVPNTLNEPCNHFTLPVEHRRYGVAADFIIYAFAGPSGTKS
RVVWAATCNKWEDLRPSIGAINFDPKYMTDTAWSVRVAAHEIAHALGFSKESMEEKSILK
KSANIVRGKGRKMVAGNHVQAKAKAHFGCNSLEGMELEDEGGTREKAIPHWKERHARDEL
MAPTVGAGYYTALTMAVFADMGYYSVNWSMAEPMSWGNSSSCDFLEKKCNATENLAGKYP
HMFCNDSDKETLRCSSDRRYVGTCTATIVEERGSLAEKDLCPVVSSYFRDASGIKYNTCS
DKGVTSLPGSLTGGDSWCLDAELQSKNDGGKHKNVKGVCAQVSCAEGTVKVKYLGSTDDW
HECPEGTEIPVTLEDFQQDGKIKCPKYVEVCTIA
>TCRU_8846 hypothetical protein, conserved
GEGAKGEDGRRSRQAEGKG*TGPTRNWQQPMRSVLEKTDEVSDVPDGKNIKYILRGTRIL
RLIVNLASEGDRHGVARARGAHIEDLPVTLDLKVLSFAMTTEERFLETAEALKELTDAGL
NTKWAVDEKLLILVIDLSEGPKMSGEHAPGQSFVLASIRANSQLGKSGFHVSMKLHSIGG
KIWPSLPSPRAASEVTEDVSPAMNVARMLDYSLSVSPPRMMMDIHGMHSELIRLDEFITL
DVSKTPLVSLRLNLEGKDGQLLCFTGDILSGIGISLKVQVYKKTDSPPALRRPGKMENIH
VYKEELPTGEDFLVVEFDSSKGNLDLSGKPRRNISNATRLCVNSRYVVDFTATGPIDMLP
TFMEVYQSVVNYLGMTRNPLLTLNMPAVRDAVGREFPRCKMSRELKNLVWEAVRLYIVRN
YVPHELYEVSKSSVALR
>TCRU_8847 Domain of unknown function (DUF4379), putative
TSVKKTKRGRRKPTTSEVKFAAAATATAAASTRGKRVTSRKATENKRAESAMEGEEEDEL
SRSAVFDAGVDEAMDGGQFIWEEEEQCRMQEFDKREVAEEGLNSFRHRRPRSRQSSARTV
ANDNLLDEEDEAGDEERGASAGTSAVEGSSPTLEEEGRLLEDRFPDLAAEYDTDLNHVPL
AEVVVDSAQVASWKCVECGFKWESGVFVRTCLRTKCPQCEKERNPRLGGRFVQLWDHSLN
DPCIDPKAVAASSNKTAFWHCPSCGNSYQARIKDMVAEKANCPSCSLLSIHADFSKDENG
LLQEWHPLKNGDLQPSQVKPNDHTKLWWLCMACGHEWEATLAARLTRTRRAKGKECPVCH
GRGKE*
>TCRU_8848 Enoyl-CoA hydratase/isomerase family/2-enoyl-CoA
Hydratase C-terminal region containing protein, putative
NFPCARLLTLCRPAMLNALSLEMAQHMLWLHLKRPHPSLPRSAIYILKGAGNKSFCAGGD
VRSIVAHGTLCSFLRTTYQLNYHILTMPNPQVSLWDGYVMGGGVGVSVHGRYRVASERAV
FAMPETAIGLFPDVGASWFLPRLKMKGLGLYLGLTGARLKGADVAHTGLATHYVPSVRFC
ELEERLCHIDDPAKVEACLEEFAVKDLPPFTLEPHRETIEKSFALEEKTTVEGIYESLSA
DGGEFAMEALKLLRKASPTSLKVTLELFRRASQMTSIREAMSLEYGVIQRMSSTNEFAIG
VNALLIEKTGDPQWERRTLEEVTAAEVDYFFDSVGLVPWDPEAP
>TCRU_8849 2,4-dienoyl-coa reductase-like protein
MFSPLSLGFTTLRNRIVMGSMHTGLEDLKKDRIERMCDFYGERAKGGCALIVTGGFSPNF
EGKLNPFAPCISSKSHALEYKPVADAVHREGGKIVMQILHAGRYAYSPLCVAPSGIPSPI
WPFKGYHLRPIALPKVWINKTIKDFARAAALVKEAGFDGVEIMASEGYLLNEFIVKHTNK
RTDEYGGSYENRMRFPLEVLRGVRNAVGKEFIIIFRLSMLDLIPNGSTHEEVCKLAEEVA
NSGADIINTGIGWHEARVPTIATSVPRAGFTWVTAACRKYLRSKGISIPFMTANRVNHPD
VIERVLSKDADLVAMARPFLSDPFFVKKTEEGNVHNINICIACNQACLDHIFKGQISSCL
VNPTACHEKERAVIPTKQKKRIAVIGGGPSGASCALVLAQRGHEVTIYEKEDCLGGQFNL
AKKIPGKAEYESSIRYWTHSLTTLNNVKLHLKTEVDASLLNKTAYDEVIVATGCLPKPIK
NSVIKGVEGLKNVFSYVDVLSGKAHVGDRVAIIGGGGIGFDVAYFLVENHDLLGCTGYQK
ENLEQFAKRWGIDLEIASPGGLRKPNIGQSARAVTMLQRSTGKMGRRLGATTGWIHRLEL
RSHNVKQIIGVTYDSFDGKTLSYSIGDKKHNLDVDSIVFCHG
>TCRU_8850 condensin subunit 1, putative
MTDVLEFFVPIHARDLEDLEKTGINQYHISEPCEFDIHPRQQLDDLTRIFDCLHREKSPT
SLFSKPEIFTALFSYIKAIESPETNQTVTKHARHKICHEVSERLKKLLQICLTYLKKKTD
GGVSDALLICLRSTVKMYVFILCNILLSSVPMPEEDENLSYSSQRSTRRRKRTRSEQDTG
IGEDCSGVDQDGRELALTALIDVCSPDLFTLWGGKIEETMLNLILRMVLHMITQKSNVQN
DAQSVSGALAVLLLRVCDHIMAHGSVEPRDFIMPMIELALKTEFASQFLTRFVSEAESGD
ISNDSTTNIVTVLVEGMAVAALHDVSGDAGAAKNMALFFSEVAKRCVSITVRMADVIVQT
IHSESYEIRKSVITCITEMVIQRYTGPMRSTDDEEETKDKYLSEILFRIMDCNPFVRNHT
IHMWGRLVEARAIPKRFHLAVTNAILGRLEDRNHLVRDSALQVIACILRKNWFGHVLNSC
LVRDKLEESRITAARMFDSDDIFRKGLDKLRSKCRPVEVETNGFFCESEENATASFQLSD

EQSSMINRLIFYEKALEFAELIKKALCHATMLLDSRTERDAIEAIKLIVACNEYHIEGSE
KAFLRVLVMIFEGEIKIQCAVRDAFVEVVFTAFAKTSASSLMRNMASAHKLIGFLRGATE
GDVSAVDRIFDLMKCNPSFSRLISGQFMDAVWSIAEGSMDHDVSPTDRRTAMRLFSLLCK
HDWRELCARKESIVEFLRSDAIKDNVLLAYCLKSLESEYQNPHYQPIPVRVEPREHVILE
QLVIHLCRRTSKISSWLMLADAAVNAIHSLCESPALVYTYVLDYIVRRIETEPNSLTQLF
FLLGRTAIKQLVAVDSAERQQLKRLDAEVMSQKPLNDINSNSNADVMHKELGIGSHEYKR
HAIQELAQRRKNAIMSEGSVWYRYSKYVVAACREKSEHFGEKALERVCAVMALSELMVIS
ETFCEQNLNLLFAIVSEKRESWVVKTNAVIALGDLACVHPNLLAPHLKVPTTGFFRLLND
DDLRVRAVTIQVCSHLVLGEMLRIRDHLYTIVKLVADPDETIANNAIAFVQNLAMKEKEK
TGNLIPPLVAQLSQSIPPDRFQLAMRSLLERVEGDKPTESLIERLCLRFEPYSERSKRKL
QMARNLAFCLHELTYSTERSIKKITSEACYQQYKQWLRDEVVLDYFKNIAGKAKRVGQRV
GNERRDKAAIEEWELRMQADSCSLE
>TCRU_8851 hypothetical protein, conserved
LNRLQWLIQRSKVGFKGNPCPFEPTKTQKSVALAKKRAADQLAGDTEFLPFCRGVPSLSE
DASPTEHLRGVDNSRFERRVDLQELNYHYQRMDKSIGRPEIESALCWDLKGKAADVQAAR
KSCPTHSDVSPHALEKKRVAKGFSNPYLATLSRAERAAIFRADILAHPKFTRQSREYRAG
DAWYSGTQLEGPLHVKASKPSVPSTRNCLRM
>TCRU_8852 radical SAM domain protein, putative
VLSERRRATLGSMYSLVGTHSAVKLCRWQKSMMRGRGGCYKWTMYGVQSHRCMEATPSMA
CANNCVFCWRLNTNPTATKWKWQVDDPQAIVDGMLSSHKSLIQGVRGMPGVTDEKLEEAM
NPRHCALSLVGESVLYPYVNAFLHLLHGKRISTFLVNNGQFPDALKELTPVTQLYLSVDA
PNRETMKILDRPVFPDYWERFQQSVVCMSARRERTVFRLTMINEFNMSEENLLEYKSLFE
TGRPNFVELKRLTPAFSGNSQSILRIKNVPSWEQLKAYGKRLCDVIFDGKEYEVASLHEH
SGCVLLAQKRFKIDGNWHTWIDFEKFNAMVLDPVLSDQITANAYLRPTPFWALPESAGEG
FDPAQERHITAKRRKHM
>TCRU_8853 HMG-box domain containing protein, putative
QARHHINGFSLFAKEIQEKEQVLTAKNLRHGHENMRVVSRRWQQLTRGERHSYNKRAREI
GVLKGHDNEKSFNDFNLLMRLLFRSEEMARAGDEFFTAHMARNTLTQLKSEHKKKLREKL
VPKTLRDKNKKTERALPAAWYFPQMRYFESFVEMLRSVAPTQKALFTAVSRVLAVNRIVS
GDLWENLSKKFDALTEEERAKFRPITDEDAPQFERYCASHCATFDVERFDIVRLFAQYRG
LVTAKTSLPEPEATQYKMLMESDRFRESLYFKALRNLERANAGRSTDQGTYISHIHPDGV
NVPPKTYLIYSRMSDVEIATLLAETRYGKSVYDDVMDRAGCFRLEKANALLTETYLAP
>TCRU_8854 hypothetical protein, conserved
VLRRAVVALRDALNGVSSMTFCTKGMGLSPDPHRRRMPWTAAKECVPGVVHSSKEKMVLD
GARRVDVDCVDRASQVYPLETLRAAVATCEYNIFGGKNIFNVSQVESNVLRQCFGKEWPE
GTHEENATRTVIYFRRRETTTLSAPVRLADFPRRHAVLFVATVPPSPSVGAEVPVDASSY
RLRTHP*IDAPAPP
>TCRU_8855 Protein of unknown function (DUF544), putative
MECEFMCDDGVARMLDITAEATAPFDCVYQKRLRTPKGEAVALGVNADKLYVLLDKNAAA
LVATAFTKKDFDDGLLEMLPDLPVVIDPFDSHRVKKDVFCGRSVCIVTQDQNGPCPVVAA
ANALALTGRLKLCPDDCRRIEAKELRRTILNYIIEGNPEVPQFVCPPTRVMNGEKVATMA
GLVQKSLFEARKKLAEGIEGEKFLHRLYHGMNISPIFSVLDGFDAEDDVLLFALAGIRVV
HGWLISSDDRYADLRDMSFNEVSLLATRNETDVSGIANEFLEKTRSQLTEEGLEVLLREL
SEGEVVVLFWNNHFSTAVKLGGRLLLLLSDETYADRSSILFEAIEDVHGAATFTDGNGVN
TDTLLLAVQSLTGNEFNTEAILAAKTLLKDLEGNEPSPEEIVHYLREKKQNK
>TCRU_8856 ribosomal RNA assembly protein, putative
LAALRMASSSASSKYVVPELTQDDVPGGACCVDETTFATQFPSYLESYIRSVWPAVETVL
GQHQLVGKLDLMEGSMTVATTRRTWDPYIIVKARDFIRLLARNVPLAQAQKIFQTEITCD
IIPISMKGNSTRRFIKRRDRLVGPKAQTLKALEILTGCYVLVQGKTVAVMGPVKGCQQVR
KIVDDCMNNIHPIYGLKQLLIKRELAKREDLRHEDWSRFIPVYKKSVQNKEKAKAVRKVK
KERLRVSLKKQAGKEKSIFPPAPPKRKEDIAMESGRAFLLRPQQRRQQPKRDDYQIE*
>TCRU_8857 Leucine Rich repeat/Leucine Rich Repeat, putative
MTQLSPKDEYTRACTKLGCHVNSHLMRELPDTLEALIAVKKLDFSRSMLGRSDVEPLVQA
ILFHCSGLQVLNLSQNYLTDDSIVQICEALLAHTLLLVSLDLSNNPISNKTGRYLLRFME

SMPALRFVGVQKTLMNDSMMRLFPHSSKALCPPVAEHRASTLSTAVTVATSNISSIMKTS
PSSSLREATKDDNPHPSQKTQWPALETLWRAAAVAAPTHNNYSSLGTLISSMR
>TCRU_8858 hypothetical protein, conserved
MRRSVVVLWTFSNNTGHYSPPVYMPLEYASRVTNQKQLVFTHPKDPKYGWNTHVEELASL
HPGILGPGRRTPQLNWYNRGGIVCEIPPVPVYRRHIWCQGHSHFILQHPKIFIKCPPGVV
VCCKWCRLKFINMSTEDDNDDDWQSEEHKISTTPESVSDLMQPKRDIGGVLRDRTFQDGK
EPDPHVYRSVFDPERHRWKHPHHKYEVHPAYADTNKDGS
>TCRU_8859 hypothetical protein, conserved
MIRALQKRVLFSSLVLMEPRNYMCTTRRTQDKANKSAMDQEDKEELERERHLRERFSQKI
QEAMPQYAQQGPESCSNGTCGAQQTPSSMMFFRFMFFLTSLLLLMALLQISDKNSPFNIM
QNIPWWQLPLSSVSYFTLMRALLPYREQRRIKEEYEVASRLNPTLTLDQFFAQRYPNMFQ
GYQTQQQEVVAAVSACLASANDLNFVRTISRAAGSARDIRASVDNIIGTLKREYPHLFQN
TGAPPFS
>TCRU_8860 AMP-binding enzyme, putative
MGGLISTLMDIRNSMSLVPHPVLTGKREQLTLTLPGTETETTSAIYRHSRTGNEAEHRRI
QEEYRARNCVQTLEEKCKTLGSRPAVAYRPLERLERRSVRSADGTERTLDYYHYRGRQVV
SYEDLWHYITSFGSGLLELGVPQRSMITIYEDTRWEWLVSIYGIWTHNMVATTVYANLGE
DALRYALSETDSAVIICSGRTLKMLLTPLRERGLHPIIVCLDSVPVDVDKGDYQIVAWTD
VVKKGAEAKHAINIPTDNDIEAMIMYTSGTSGDPKGVIHTHGSIAAGINALEERLSDLYN
STAETETYCAFLPLAHILEFGIVNIFLKRGSLVGFCNPRTLTDEFAIPHGDFKEFSPKII
IGVPRIFDTIKKGVERKIPPPNSLRRMIFDKAF
>TCRU_8861 Long-chain-fatty-acid--CoA ligase 5 (EC 6.2.1.3) (Long-
chain acyl-CoA synthetase 5) (LACS 5), putative
MGVCLASLMVRRSRISEVPDRYIEERRRYGPVAVACAPPEDDVSSAVYRAAGITDEEHRR
ICKEWYEGENIVHRLEEICAERSDRRALAYRTVQKVETEKKTDSKGHTRNWEVTYLNDPT
YMTYNEFWSRLIAFGKGLRELGLAEGAAVAIAEDVRWEWLASVLAGWTQGLISVTVYANL
GEAALLHALKEAECPALICNGNAVKKLVPLLHKAKLNNTMVIYLDALPAGVDAEGMMLLS
WTDVLQKGLQSCFSYTIPSDCNRTALIMYTSGTVAEPKGVIHTFGSLKTGAAALEDRLTE
LLGPKEEGETYLAYLPLAHILEFITEMIMLNRGSLLCYGSPRTLSDMSARPRGDLAEFRP
MMFVGVPRIFETIRKNVESQLPPVGSVKRSIFDAAYAARLRAIEDGKDTPFLNEKVFSVP
RAMFGGKLRGIVCGGAPLGSKTQTFMNVVFGVPMAQGYGLTETCCNGSIQRTGELHPAAG
QLLKGVEAKLCDTEEYKHTDTPYPRGALLLRGPALFKGYLKQEEATSEVFTKKGGWFHTG
DVVEMDDSGCLRIIGRVKALAKNLLGEYIAIEFLEALYGQHELVSPNGVCVLVHPQRAYI
CALVLTEQPKAMNFASVHKIPGNWPEILQEPLFHQRAAEALTALAKAEGRRPFELLRHVR
VLKDEWTPENGIMTASMKIRRSAVDKRYADYIEQLFEDE
>TCRU_8862 Ring finger domain/Zn-finger in ubiquitin-hydrolases and
other protein, putative
ADGCIGVVRVGYTPEEEQNYCLLLQFDTARDAKRVKNKLLHANLTGSSPTSSEHVCGMAK
VKSSYIETDAGYDGVGIEGKQHGGLEEENIDLEELCSVMHGGAASASTHLQGGCPGSMAW
RNLEQQGGSHLAHSVLLTPMEDFCSICQEIASSKPFIVTLCKHVFHLSCFSKHLEDVGQS
CPLCRFSMASLKSKCYTCGSCSDLWTCLVCGWVACGRGHRHDALHHFESTGHSCAMQNST
SRIWNYRAKDFLHHQLAIELGDEDDVKALKAAAEDAPTNSRFNKGETGVTASSYRRSRWW
WDKEEEEAALDLNAEHVHEYYLGVMQQLMKEQSEYFEGRGETGVIKEGPGGVAPAVTTAE
ATSEPSTAMLRKLVTAEHRQRRRIFSEYMSGMRRAALREKISFYRLVKLEAVRNENLREE
LFLQFQVIQSLHTHIEQTRRRIDEASRRGMEQLALKRATLESLQEKLDLLLKSMD*
>TCRU_8863 Protein of unknown function (DUF788), putative
MAKDTAKKNMRRNEERMRRFTICTLAVNVLSLVFIIYHRGSLPWFRDVVGVGFWAAQEFV
ALFLLKAFAKPTCSSTGELLECPDASNPSELGVYSYAQDLLWVCWVVELLCYLFHWAFFL
LYLPIPAMALYQFWAFIGPLLLRRQPSADESSEGAAIPRNRAERRRQELLQRKK
>TCRU_8864 protein kinase, putative
EMDRFIVGSPIGEGRFGVVRAAVVKESGVPAAIKFVTTPRLDEGIPHPTARELLVAMRLV
HPFVIRTYEVVPCGCSLALLMERCKTDLATVLSGRTASNPLPALEAKSLFKMLLLALAYI
HSEGVVHRDVKPSNCFLTAEGELRLGDFGLSRAWDTEASMTHEVVSRWYRAPELLLGQRH
YGPEIDVWSSGCVFAELLRGHSGAFFAGDGDIWQLPRILDVLGTPTPTSWPSAVLLPDWG

KVHFEPKRPLPLREFFPDASECALDLLRRLLCLDPQKRLTAAGALRHAYFSE
>TCRU_8865 Eukaryotic protein of unknown function (DUF914), putative
MKGGRLRRFAIHVLFGQLVAFLNSVTGVSTTKLVNNNASYPLLQSLTAYAFIFAVYAPIF
LLLYIRNRHRRFLNFVFLQKPWRYAVLGLIDMEANFFIVKAFQYTDMISVQLLNCFNIPC
VFVLSFFILKMRFAVTHIVGCLVATSGLVVLIVLDADGVTRNKVGPNVAKGDLFCLLAAA
LYATSNVLMEWFIKPQPRGVHLESVESANTNQEEEGVNSEVARDMSSFRERQIAEEQNEF
SSLPNNIPVVDSGRERDQEQSSGQVPESLPEVARYIPLVENLCCMSGCALLFTVIQFFVL
EWSSFASGRKTWTDEDWLFQMMFGLSMLFVYTGLPLLFLVASAVFANVSLLSVSVYSIIW
NVTIFNIYPTPVFFASYVIIILGIFVYDISDFRWSWCPHINYPCDDS
>TCRU_8866 hypothetical protein, conserved
FLLDTREFITDKCILRQLTHFAHVHRLGSPLWLGWELAADLGLTLRYMQSPLNIWSPLMG
ESFFPLNKASTFLDAVIQKYPLRQFLHFSKISSAEHLTAKQNLVLSAAASSDGNPRWYRV
PEAIEHFFELPSESSCLYCHPIQQVNEVGLFVLWISAVLFSRMMIAPETKLLVQTPSSYM
SVVNADQLYPSSFLAEKELECLLL
>TCRU_8867 Leishmanolysin, putative
PCPAALPLLLMMLILMCCSSGCFAASLTYHCTFDKAMRVDRTKSMPVLMKNVPLVTGSTS
QTYTVIGRNGWAPIRINVSTNDLYNNRMYCSSDRSYVKNLLTDYYECEGNAFSDNKRKIL
IQNVVPAAVKLHADRLLVQPLEGPLVVPQFAAGSVCSRFTVPSEHHTKGVANSDMVLYVA
AAPGGVWALPCATLEDGRPVVGVMNIAPAVLFHGRLATRIAAHLMAHALGFAHPHMASRS
MVRNVTGVRGRALSVVVNSTNAAMAAREHYDCDDIYGMELQDQNGDGTTLESHWSQRHAK
DELMAPIGGAGYYTELTLAAFADLGYFKVNWDMAEPMGWGKKSGCELLQKRCSELNLSKY
SHMFCNINDGVKRCASDRYSSGWCHRSIIEFSKQPPMDSCPIIDPAMDVRDLEAVFEKGE
YLSARPGDKPSSWCLDTLPTNTTDARDPEYTYLSAAMHAELKCLGMQVHLKVTEKRGVDW
LPCTEEETITWDTPPYNKENVICPEYAEVCTISAT
>TCRU_8868 retrotransposon hot spot protein, RHS3, putative
AAEEARNLTTTIEAIKLEGLYESVHNARWSHVVEIPDGVERKKTGMGMEVKKGKPKQSWT
YKKVGTIFEKDDGVQQSGEAPPRLMVLTSDKGWPYTLIAPHGCGNDLCVNCEVERAWQFV
KGDLTEWFSNFDLTLNPSPLPRVLIGTPGIGKSMAAGLYLLYQLLHCDVEKLQVVVHCFG
TTMYVFDKNTKTVTRYVGNKTSSSVLGGLWQRGVKGCIIYDVERKGTPPDAGFAPSTGWG
MIVVSSPNLDNYDEWEKQAKASRIIMNCPDEMDVKAMCAWIKRGLEPDKQAEYWKKVKER
MEKVGPIPRYIFDEKIYINRLGAVNGALLAIKDTDVGKNFTLGGEEKWYSKDPSHKLVKI
VRVREKSAFEDFANAPICEYLGVLTLSRLTRVLSPHDIFFLVLGMKNVLQSEALEKYSLS
VFLIENFVTSIAEDLNELPPPSPSEPRPSVLTLNPHGHPTEATAISKLKSVGHQQELKYR
VLYIPAVRNFPLVDGLFFMESPRKTLFGLRMATAGGHHTTASTVSLFNERLATYFKGWKK
LSRDMSWEIIYVQHADSTPTKKWHECDVVNPNNETDAEKEIVAFWDGKVHQYQFVLTRDF
VSKIREMRTQQSWGKGI
>TCRU_8869 retrotransposon hot spot protein, RHS3, putative
NSTKTAEGCSLEGLYESVYNARWHYVMEVSDDTEMGMKVEKGKPKQSWTYKKVGYTLEKD
DAVQQSGEAPPRLMVLTSDKGWPYTLSVLNGCGNDLCVNSEVERAWQIVKGDLTEWFSNF
DLTLNPSPMPHVLVGTAGIGKSMNAGSYLLYQLLHYDAEKLQVVVHCFGITMYVFDKNTK
TVTKYVGEITSIVVLGGLWQRGVKGYIIYDVTEKGTPPDTGLAPSSGWGMIVVSSPNLDN
YDEWETQAKASQIIMNCPDEMDVKAMCAWTKRGLDTDEQAGYWKKVKERMEKFGPIPRHI
FDEKSYKDRLAAINGALLAIKLTDVGEYFALRGSKLWYSEDPSHKLVKVVREITKKGVEL
FLNASISADIGFRIADRLEKKMGAKDLLLLILGSRGALASRALEQLGLRVFMYGELVCAL
VEELKELRPPERNEAQDSVLKVNHQGHPTRTVGLAGLEGGVTRTAMEYGVLYIPKVENFP
LVDGFFFMESPRRTLVGLRMTTTGDHHTIPSTVRQFNECLATYFEGWDELSRDMSWEMIY
IKNAFSKKILKWQRCDV
>TCRU_8870 retrotransposon hot spot protein, RHS3, putative
TISTKIEEVLFKGRVRVNEMKLNDFLTMELDGRGVVATNRDVLLKEFFKNPNKYIRDKGA
LKEIQISDAYARMERAVRDEVDLEEVARKLRDKGVYNLLGWSEAAAEVKATVHNFTKQSL
DSALQEASKPTTTIEALKLEGLYESVYNASWHHVVEVSGGEGTGMKVKEGKPIHSWNYKK
VGETFEKDDGVRKSGEEPPVLMVLTSDKGWPYTLNAPHGAGNDFFINCEVDRVWQIVLDD
LTEWFSPHGETDFKPEKRVLIGTPGIGKSMAAGSYLLYQLLHYDVEELQVVVHCFGETMY
VFDKTTETVTRYEGNKTSKSVLYGLWQRGMKGYIVYDVARKGTPPETGFLPPTGWGMIVV

SSPNLDNYDEWETQLQASRIIMNCPDEMDVKAMCKWMKRGLEPDEQAGYWKMVKERMENV
GPIPRHIFDKKVYIVRLGAVNGALLAIKDTDVGKYFSMGGEEEWYSEDPSHKLVKIVR
>TCRU_8871 myosin heavy chain kinase A, putative
CICGAVKYVFSFRRMEWVATSTNVRVLTPLKAAAKGGMRVCYDVEEVEEDGSRTPCVAKL
FLRNISDVVEKDYFSEGEAQCMCEQFANNFNKATFTGIERPHVSFLQCQVLRIPKQNIPA
EHRDAQHGFFSYKTTDTREVMFVMEPRLHGHFTKYNSNFGETYEGDKHFKTPSQIQQRTR
MFLIAEAFSHFTLAESGGSMLLCDLQGVNDLFTDPQIHTEDGKGLGLGNMGHEGIEKYVL
RHECNEFCRALALKPLDGIRPPNGKESRTNNFYVRLRAQLQQDMVPLSKPIGEMTEEEQI
AHAIRLSQISH*
>TCRU_8872 lipase, putative
ADYSVQLATTALYYAKAAYCEAEAISSWTCASCARNPGLQRVRVFTNAAHSTQAFVGVNE
SMIVVSFRGTVDLNNWLYDLDFVPVAYTHDGCFGCLVHTGFNCELESLWTEMWGYLQELV
AGKGIEGILITGHSLGGAMANIAAANLMSQNSLFPSALKVLLYTFGQPRVGNEAFANWFL
ASFCRDGHESYRVTHKRDVVAHLLPMLFGFYHAPNEVWYDNDGDTVHKNCTDIFGTPCSA
LTADEDPNCSGSIVPTSIEDHLKYLGVCTRCSCDPGEAMSDEELRLPPELERIVAMDYVY
QQSRNMRR
>TCRU_8873 expression site-associated gene 3 (ESAG3)-like protein
PRVALIVVHTGYSPGWCRMQVSSILSRVSVTTIGMGANYTHTSRPSLLLDCITDEGLRDE
DVVVVFDGGDTMFTGPLGIKQAVEDFVATTAPTADDLNATAVHLGEATAPLLFESDPICY
APQMELIVPWGPSDKYEKCGWYYERVWEAAKSSADQRMVRFLASRYRYLAGGGMVGRVWA
FREAYKAYASLLATSDKWWCDQSIWSMLHVWSVTRDTNVTADFRIRYGLLSLDYNNSFFL
TPRYGAFGSPALYHFPGGLNEWDKMPTLLNRTMWVDWLRYSPEVVNETRDFVQNATVKIY
DADRKAKTFPFPEVCLLNDVLNPEWLVLPLRK*
>TCRU_8874 arginine N-methyltransferase, type I
FAEDYNPHESAQEQYYDAYADLGVHRVMLSDAPRMSFYRQAVTCETVVQDRVVVDVGSGT
GIFSIWAARAGAKHVFSIEASSLSFFQARVIDDNHLSDKITLLSETVENIVAGGVVSFIA
THEAVLKGCGVAVIVSEWMGFYLLHEGMLPSVIRARNFFGEVNAKLGVCRRIEMIPERAT
IRVAPMSCAPYCEERYCRFWSGLEGVDFSRYGTLECEMQLETSNPLIDTIPASCLLHEGV
VLAEVELSSIAEDAMTSLCRTVHFSFCNSTAFQRHFGVDCTQEVVVDGFTLWFDVSFREW
TLNTSPFHPPTHWKQTTVLLPATVRAERLVAFTNSDATLDAEVRLVATGTLRRCYTIEFE
LK*
>TCRU_8875 major facilitator superfamily, putative
FHLKRHMSMKELLFLLCMSFSYAICFNTLNNILIPKSVARFCNNKQSLWLGFLMVLGALC
QMSAPLVGVYSDRMGGRALFLVYGSAVTVLGLFIFLLVEMIDGIVLLCFAQVTSTVGLSV
VYNMVMALLTDYVPEEQTGEGSGALALLALTGSGVGYAMLAIDVPITYCLCIYVLVTLFC
LAVTLNFIPIVDTSRQPQEPARFCDTLTAAFTVPSFRVFPDFLLACIGRALFNTGVASQL
YLFFFVRDVLNLSSPVRVTSALWITALAGGFVGAIPSGIFSDRIGRKPVVYASLCLCTTS
VMCLLFVPNIEFLYLVGFIHGVGTASYLSVDHALGISTLPRKSGVPIDAAKDLALFATSA
TIGTIFGQVGYGVILQFFVAYTEAGSVYYSYFGFVVIFSFASLAFIASGATVVRIRVK*
>TCRU_8876 cAMP-dependent protein kinase catalytic subunit 1
KPDASNWKLTDLEMGSTLGAGSFGRVRIAKLKGTNDYYAVKCLKKREILKMKQVQHIRQE
KQILMELSHPFIVNMMCSFQDDRRVYFVLEFVVGGEMFTHLRSAGRFPNDVAKFYHAEIV
LAFEYLHSKDIIYRDLKPENLLLDSKGHVKVTDFGFAKKVPERTFTLCGTPEYLAPEVIQ
SKGHGKAVDWWTMGVLLYEFIAGYPPFYDDTPFRTYEKILSGRFKFPSWFDARARDLVKG
LLQTDHTKRLGTLKGGVADVKNHPYFHGANWEKLYARYYPAPIPVKAKSPGDTSNFERYP
ES
>TCRU_8877 hypothetical protein, conserved
MGSHAKKGRRPKSRAANSSAKNAEDGSTATRHVPPAPPCMAKLNAQHWHVLEEGCADVAA
FALRPSQHAQLLACAVPQRLVEILFTAPSSVGRSQEGDCSNSGHAPRQPHSGGFYLQTAA
AEALRNLVVNSAEDAVVDVLAVSTFPTSDSGQQLQPQQEQGEGRRIGFRDGLVTLLMSAW
DTVQKTRREAPLAPPTVVSKNEDDGAMSNEEERMTEGCGANEDPLHAPFMIACRALEEVL
QLIAVCVEGSEHIAEAFSAPGVLHALLSLLETTTGVVWETLQHPALLYEPPVEGRGVMWL
RQYKRREAELLAAVAVAASEVLHLLSDENEVLASLLQSSEVMAPHQAFLTRTLDATAILA
WLRAESSFISSALPHAAAVAAESETKDTKEEKEDAILLSTGRQNIFYQLCEVSLHVQGTL

MNSAPNTTNAARVLPLVVVVLDAHLPHDEWRRTVPLLLQGCALKEEHRAVLIRRALWRLR
CDQAAVNVLHAVVNAICSLNEADADDETAFQRNPHSTLLYGTNAMYVVGKLMKDALRLPT
DANGNKNNNNIIKNEDNTHVSSFDPVNGGDDVVVERALRAAAGTSGMGGLITKLQLLVLS
NEVGVWSLANTLLMMVNWSGLGEEPAHIWRAIIHALKLRSQLLTEATTMAAEARERGVEF
NECASEITTLVASTPAATNLVRLQLESLVQMLWTLQRKQAAHAGGSLQVTNHLAATGTDV
DILTRLAWDAHATPLQKQACVGAVCAMCASFKSSEATHVAARFALGMLQVDGALQTATAA
ALSSPPPLAAKGEATDVRRRWMANITATDAEWRVRCEASNHIMDLFLDETHDDAVYIPLH
VHVALKSFLGPFQSYLKRRQQLVRETQRNYRITLPEVDDAAHWREVAENLSAFLEYKTQ
>TCRU_8878 variant surface glycoprotein (VSG), putative
NAMQWITFGAIVDEVRLYFNMGSVQVNHLATTYVIAYVSIVFLSCKLYELTGLKVGIVIA
ATANTIGSSLKLVAVYLWPNMTLLYMAQVLNSITEVLTIATPPLIANRWFPEGQRMIANT
VLSSALNLGCGVGVLVPTFFVTPEKQERKHFANLFWFQFSLCACVLLMAVFFVPSRPRYM
ASYAAARQQRGEEKRLKAVRGIFKGHIGQSDGELEQHEHEQQQDSEQPPPQQRQHQGPEE
EGDTYFTDENDEQEVQPINVFSTIMDSLRMLKKNPSFAFLMIASAAELGLIWAVATVLPQ
CLTPFGVSEVESGWISFLNLVFGTIVAPFFTHFVERKRQYKTVLVFIAMLLTINMSIFVF
MLVFGPSPHENRTYYVVAAFILWGGVAGLCQNFIMPLMFEFVIELTFPMAESTSAPTLMW
AACLSNLILTVVFGEVLGEHPTRGEALNVFMGATLVCFIGGLALLLVYPYGRRREYELLM
KERD
>TCRU_8879 threonine synthase, putative
MFNLCVMGSAPATVKEQVERALLAAFVPARFMLTRLEDVKEGEDHGRVMSQSFRLLLEAH
DAPPTNPQEMPYDCRFFWTPESTTEEVVTEVKSLLDGRRFISTRGVVGISTNFLSVVRDG
LAPNSGLFNLQSIPQMAMSQMRHFFTTSTLSYVEGAQIVLERLVDTTMQPEKLRILLMEA
YAPCRWSGLSDVCPVTPLLLDEPDNNKAMEGHHHGANKETGAAADPCWRDMSLMELYHGP
TAAFKDFALQLFPRYFDIAASNECTDTPPSYVILTATSGDTGVAAISGFVNAGSPTRVMV
LYPLHGVSPVQQIQMLSYDNGVSVRVYGVKSDFDFCQSTVKQLFAKRSLAQRLWSDKKIR
LSSANSINWGRLVPQVAYYFWAYRQFVQKKRLQFGDPLDIVVPCGNFGNILAAFFAKRMG
LPLGKLVVASNCNDVLFEFVETGHYDIRQRHLVQTASPSIDILKASNVERLLFLISNGDA
AFVAAQMHRLETEKHFTLQGGALNAMRDVFWSARCTEAECAATIKEVYEASAGRLLDPHT
AVAVFVARQFRRFQLEKGLSHRPLVIASTAHWAKFPRSVLRALRGEEMAYGITNSVGGQV
NPVRACRELYDVILAHCPGATVHPALNAALAAAEANAFSPREIEADVSRVEEELLQFVSV
NS
>TCRU_8880 conserved protein
MWRRGRCLRAPPKVLCLTMIPGGGAMTPALQQLGYTPYTFQHTFTEGRVNTHPQEWCMVL
DKQKPFNPAILEVNHGETSGDRKGFDALVGPPCTLAFEAILKVCPLSTRIILVEETDKDA
WARDAAAIWDPLLRQTGQAAKRQAGVHLHQMVLRMTKGMTGPNRKLFAATTLEMLEERVK
TVVPKDRLLVYRYGSGWEPLCHFLSKPVPYSSDAGVISFPPYESGTELAADLSYRLQRVE
RVVLWVTCFLFAALFALYTPLYTQLRDSVVAYYDEYREAFEPVLRENEGKTLSLRKALVL
AKNTTMSFEEKWRARGGVIGAAEEALRKI
>TCRU_8881 ABC transporter, putative
SFWTQLFAAVHREATERRRTWKEVLIEICVPLMCVACTSFLWCYFGDEYGPEESYVNYTY
PLPNTGIIPHSSFFCYNDSIINPDGSHNFISGLVPCSQAPFIADCSGEEDQIPVKGLCTD
IKKKPVLAFAGYAMAFLNEIPKLDDIFLLHWAASKQRVSLEYGEAYRDAGIFLVNRLSSL
TVTGSLFIGPAANVPPLLVKYFQSASIYFDLVYAGTFDNITELQENIARGGVFAVININA
MTADKFDVEIRMDEKSIPPPGTIINIEYSGGVNGQAGEIYIVSGFLTLQTMLYDFYLKEV
KRIPFNKSHFTPYVISMGSIAYSSPKLIHLSGMLVAFAIVLSLMYPVTLLARRRVVEKEL
RIREIMEIMGLRKCTMDLSWFLLAVATMLLISVLSVAIMRPYIRRTEYFVYFLIFLLHSL
TMIPFAGFVSTFFNNARFASMMVPLIYFAASSLPLGIQMAGAVTKAVFCVIPQTSFFFSL
IILFQHELAGGLGLSDARAALDKPNLALVLVITMGDFFLYLLLMIYLEAVMPREYGTPKH
PLFFILEPCRRFWCHAHEWDEGGPDGRSPDGTYEEMDESVDYAVEIKGLRREYKRGRRTF
VAVDNLYWNMPNYCVSVLLGPNGAGKSTTINMITGMTRPDAGDCRVFGRSVRKELSVVRQ
NISLCPQHNVLWSQLTCREHLEFFGRIKGLKGLQLKDAVMRMLHEVDLYDKMDCNAHTLS
GGQKRKLSLAAAFVGGSRLVLLDEPTAGMDAVARRHIWGLLRRMSFMHAILLTTHFMDEA
DILGDHVAIMSRGVLKCSGSSLFLKSRLAAAYTLQISLTPDANYTAIKHLIASYIPETYS
IFSGATELRCRIPAGNTTNLVPLLKCLESPSQYVGIRNYALSAMTLEDVFLHVVAEAEAN

SSLEDLPVDVIWNCALVSRSGESIGMQFRALLKKRILCAVRDWWALGFQIICPAACILLA
VVLDSIHYNQPVSVELTPSVYPFDTMSDAVGCSAYFTASTYALPGSTHQVHITDRNMLNS
MNLSWYHVDNYLRHPLAHLSSFSCADPNYAAILGTNPIMIFYNTSAPHEVATALSTLYSL
ILQSVVGAGAILRTSMSYLSSAKLVDVNNAFQTVFKGFVVVIPFTILPSNCVSWVVHERE
CGARHLQYLSGLRFFVYWGVNFLFDMTAYLLTFVLIIIIFLIFGQKSFVGPDAIGPTTLL
LLTYGFTGTSMAYVLYLFFKSHVKAQSTVMVICFAVGFFPLVVVNIFNLIDGTQALSEGL
RWPFRLMPTYAVGEGIINLITLDQHRSRNPTLNVWSMSTVGWACIFMACEFPVFMLITLV
VDNPRFRLKMRKLSYHPEKTRVRYFDKDSDVEDEQIHVHRQLDRRENWQDDVTLFHLRKM
YSNGKLAVKDITFGLVRGEVFAFLGTNGAGKTTALSILCQESVPTSGRAYICGHDVVEDG
EKARACIGYCPQFDACLDLLTVEEHLRLYASIRGILRQHHTQVVEALMRLCGVEEYRETR
AHQLSGGNRRKLSLALALIGGPQVVLLDEPTAGMDPIARRGVWKSIQKIAEKCSVLLTTH
HLDEVEALADCVAIMVDGDLRCIGNKTHLKNKFGTGVEMSLRIRDKSCRQKVERLVETFF
PDAVLNEYNNQRFVYSLPKRIPLYAVFEVLQRNEYQVGITDYGVSQTSIEQVFMRISE
>TCRU_8882 Endonuclease-reverse transcriptase/Reverse transcriptase
(RNA-dependent DNA polymerase), putative
DEKVFCVLSGKRRPRPEATSSSPPGFQHHGAARTCGGGGVFILDREGLQAEAGPALVASV
GLARATIHPEAGMKLTVSPEHFPPSPRCVATEDLDRPLCAGGPQLMSTGGNAHGEVWDRK
IPSDSRGDAVVRPRLGTHCGTSTPDSAHCVMLLDFLIGDEDTPAAVPNPDRASLARKMAD
WNKHGEIASTGSVGKNIVSGTRKATKATVPEWDHQPSPLWTPGLAELDRATAAASHA*RG
QRPELRRRDVARGVQNRRRELRTTPEAAGGRQHAVRTPRPRTPAMKSDGTALSKQQKVGQ
LIKLWAAEATRHPKHRSPPPTLTNARGLVPITMAERDRAPRPLPLGPAPGRDGMHREAWR
RPGRVAERAPRLFGRRLNAGTVSRSWRRGVVIPLNPGKTAYDRDSADPALAGHLSQLM*R
IPAARIRDAIESPSTPQPSGCRPGDFALDRLLHLRAAMHRNTPQHRTAAVFVDRAKALNT
AEYDKIILQMRRMPVRNHTAHWPAAFLNNGSAVFGAGKPTSFPRSPQEAPRGAVLGPVTF
IIVVKSLSGRLSNAPQIFH*FLADACALNTQQSDRGMIGSSWHEGPSVVAEWA*ERFMEA
NTGTTKRGLLLTGGAALLHLKYDGAPATMERTPVLLGANSSYSRGMSAHAGKLREESKQR
LPRLTAIWSFAWGNQRTLLEAFRLALDSANQKASGMVARTPKSGRMEGAVLVA*PRPLLD
TVLVRGFRCVPRCEKRGGALRPSAPTVSHPQRAA*KPHGSIM
>TCRU_8883 MSP-B, putative
PDWAPIRFQFFTEDLNDPSRYCTAEGQIRPDFTGKTVECKSEDILTEEKKSIILNSLLPR
ALKMHTDRLLVEPLTVNVTVPKFHLGLCAQFTIPSSHHTEGVFGADMYLYASAGPIKDST
LAWATTCFELATGRPVVGVVNYSPSSVTDSEYSVRNLAHEIAHALGFSAWLMIERKMVKA
VEGVRDKARVFQVSSPKTVEKTREHFNCMSATGMELEDEGGPAAVLSHWKRRNAKDELMA
GNEGIGYYTALTMAAFEDTGFYKANWGMEEPMSWGNNSGCALLTEKCVINGVTQYPEMFC
TVNSSLLSCTSDRLALGRCTIHLYDFSLPPQFQYFSNPKLGGLPDLLMDFCPYFEKYANT
WCSDGNATVMRGSRVGPTSKCLKGDGLADSEGLVGDVCAEVSCDKGEVSVRHLGDDAWHK
CPEGSSITPTGLFTGGRILCPKYDDVCI
>TCRU_8884 TLR4 regulator and MIR-interacting MSAP, putative
AAILKDPRFLIHGPSYAYLDCSACLAFAGYLGERMNASLEYDGRGGASFLATHRLNKENK
LQRNLYATSELRAVEVLEKICSVALEENYVLHLDIDRRIRVYQSGNTDFPYAQHYSVQDS
DALKVISKTAVRDFCTRLMDEEEEAMMNVVREVRELAELELRLCGGNDVNRSSVKTPLPK
IEALVTAVCIGTEASIAAELGRIQRYEKWQESISRRREEAIKKIGGKSEEPIIAKEVVHG
EKDPQPWFSVSKSTFSSSDSEEGDDD
>TCRU_8885 hypothetical protein, conserved
MPRRVLLGNWFEEEAYMRDRRRLMEGRNGGVVDAARETQLILAKVKHHNTPYHLSPMHDD
GFLHFYTPVMLQNAETLGFISLDLEDRALKPTGWRVVCSTAPASGPTLRNCFLLAPAPTG
PTDMIAPPPEEEDVVHYGQPFFIMTVPELCDNPLSLASEHKGPHSASKVTGKYQDVFFSP
DGNSAETMWVADFSNPEYCEDMRDRPVKGDAVLVIRHNHTNVPLASTKAVFYNDFGPEYE
VCCNKFTRSLKGPLTDENYWIFVHSEERGEEGEEKQEHASTTA*EIPEADNDLS
>TCRU_8886 KREPB4
TAMRGATCLLCDVEYDSWGKHVAGASHIARNAICRTYVAPERHDAMMQQLWKHIRLDFGY
IDEVTHKKEDRRRGRLASTIRHLHEQGILRHSIPKISVDGDGVRSVVVTKDAFVNLMMVG
ESYAKQETVDRVARLMPRLEAVELSSVVQYILSKRRLARLFDELDMRRTLLNDSATGDAA
EGPSENRKNGESDIARECDVAAEETLRLRQEEKTVIIFSCLGELQMYSRQDRSHSVATRA

AAEQLVLNVLGTHVMENIIAELVHTVLQTVVEEGTPVWRAYCDDLTNKMFEGTRATPPSL
ALSPAPATGAANFGEIRSTDLLSLYTLQVGENAASVLPTAGRRSWSDVTRALALELTVPN
PVNKSALFAAAAPRLSSKKK
>TCRU_8887 LisH domain-containing protein FOPNL, putative
AMAMARQESLKEAMREVLETKGVMDHVKAELRAAIFHALQDSSAHEDGASSNRPPVPPEN
LLLNELIKEYMAFNGMEHSLSVFRVESGSAKNTSAPVPRAVLAAQLNMTGAPASVPLLYA
MLHESR
>TCRU_8888 hypothetical protein, conserved
MFVLPGMKLPPEGLQVSRSSLPTAASSDPPMSQLLLSYWGLPFYSELPEEGQARTEIMES
YLLGLAGLLRLRNASLKEAFDRFVASLLHDEAVERGFIEEDANLLAWRSFIDYTFLEALE
RLKNRERRARLHIIDTYFSFALRALGRLETLDRQHVATQFLDSLFLKRCQFSPGWMWRRV
PPLPDEVYAESTRAAEPPWAITLFANESSARKCLVEQFYAEFLFSIEVFATSVKWRVHNR
QALQLASMRDSMLNKQATVIQSVFRGYRERK
>TCRU_8889 D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain/Acetohydroxy acid isomeroreductase, catalytic domain/ NAD binding domain of 6-phosphogluconate dehydrogenase/TrkA-N domain containing protein, putative
MNVFDCTLCVATTISQFLVDEVMKQVSLYGGFRHVVRCHGNPQEDFMDVKQSGEPIVLLI
ANQAGREALKFLCDDYHLPKEQRRVLWIHSISSGLDSYKLNELVKELQDIPLTNARGCYS
SILAEHVMYSMLYFYRQTWRSLASRAEHKWDPFLMVELRGRKVGIIGYGDIGRASAKLLS
AFGMEVTGVKRSASTKEVDEYGVRLVHGDAERERVLRESDFVVNILPGTEETKRFFNKEL
FSMMKPSAVYISIGRGITQNEDDLACALRDGVIRGASVDVFEREPLPAESPLWDISDDKI
LLTYHNAVLSDDFCKKAIDCFMLLARDFGSDGFASNVIQIDKFYCG*
>TCRU_8890 EAP30/Vps36 family, putative
MRRGIGVAHVQKKNETQRQMTDLGAQITAERVGQIADQLEGFEETLRSLARKHKDEINAD
PIVRARFRQMADSLGIDLISSKKNVFAGILGLGDFYYGLASKVVEACMRERKFCGSYVPL
NRIVYIMKRQYESAGKDGKRCDITESDIRMALEKLHVLGDGYNVVKLAGVDYIQTTPDGT
RSADDAPLLDTVLKKRAEQILKYHSTRVGDERPCENVAPIFGPSNRVGASRILFAPARHH
DSVDSEKDVETGTADVPFHVQCVAFTQDELEARLMWRPHRVQAVLERMMHNGSVWIDQPS
ISQGEVEGGKLRKRGKTLKELKPAELVYWFIVFSAPFESSF*
>TCRU_8891 N-terminal region of Chorein, a TM vesicle-mediated sorter, putative
MFDKFVAGLVTTYLGNYFENVNREQVKVSLWSGHVSLRNLRFRRDALRAFDTAVCVKEGY
IDELTVIVPWTRLHSECVVVEVKKVRVLLRQKTAAGYDPAREKQEAYERKLHQLNLFEAL
LQQELAGDTKMETTPVAHNGVPTEGVLEEEEEAFLEAQKDVTFAARLKAVILNNVQLMLK
DVVVQYEGCYASGGGVDAGTDQLVGQDYHSFSILLDNFRTYACDENFAPHFTAAKERVLY
KKVVLEGVRVLLNATTFSMQRSGCSDDNYAAETIQDTEEASLGVIRGLSRKTTPSTLRQS
LPARCHRIISPFSAMAFVQYQPVPYRADLPTFRIELHVDRLRAVLSREEWAILLALWREA
RDGEEYDVLRHFRPVGAEKKRPTDNARAWWAYAIQVTLHRIRRVRERRVFVWEKYKRLKA
AREEYMTLFKRDRRRQLEANWLTELTMEEKTRLQDLEMELPMESIKIARRLAYHRTHLER
EQRETLLERRRQKKHQQQEEAEGKSGEMGEEPNGQPAMDVAHTDGKRRSSWWSWLFFSKT
RNTQEENAGDPVGEETPDIQAEIEEMFQLVNAERWTAAQRFAIAKEFGIPESEVESLSDA
GGSASNGNFEGVRWQVSLRAHALELMLRESDGECATFATLAMEGLTANLVYMFNRCFSFS
LDVNDYMVLSHLKEQSRVVSIIRVAKERYVICGCEHEAATSILLKRHHPGSLAEYDAVSG
VPPYEICLKWSPIDCNVDMPFLQACVEFARPLSSFPFVSLSASSPTPSSRGVPSPCERRQ
ETTDPNKRRTLLMMMVEREFLCSWQLLLHDVRIVASEDERQVSRIKLWRVEVKNDPAKKI
EKRRRIQCPTGVSDTFGDDPDDWVNTVHATIGGVTAECLLNTTRVDASFYDVDEDDSKNL
WDRITSLPSFTIIFKKSVMMRRSPSVPLLSASIVFEKPLQIRCSRQSLSVLCTSFLMMTD
IFQRLSQPAAIDTMHDMSPTSPSKVFLAQVLTVDERYLVEHEPSPRLQEEKFYREKMQAP
SLVDNYRRVEVMMGKIVVYHVKRPTFPSHFFELYRGHLHVAQDASEVSLFVECGGVSHTR
RSGVLKAKEVLFGKYKFPSLWSMPLLEAFIEDWCQEHKRSGKENEEREEVKHAFRTVRTA
SRTRPCHHIRMRFQSIEEAKRFAHALGSHAVGHHALDIPPDPTSVEEEDQQGGEQQLCLL
TMEMSIPKCSFYLRDEAIEKHKEGATPPMHKLFMTSVNISYVQQQKKKLISLATNRLSVM
AHARNATVFEVTRSVAKPPASASTAADDDVGPALTLLFQMKDRLYPHAARKYIKMTSSAD

VKLAFSSELLCVAEMLWDLSGILTNQIFGHVRYRSIPWSDESAATIEEKWQTDPAGGLLQ
NDDVSIDLEHLVLSLYYPSDKFELEDEKDAAVDDGVNAKPVAVINGSQVNIHWSNAEGCN
KSCVTLHRPYILMRRVPTGELGHVVAPTGNQCKEETKGGIFTGKPTLSLSFSIHREPPML
SISDFIANGGSAGYRYTHFLFVSGENLNIVYWQPQLWSLIEVFSRGVISRAAKLVWRQPY
IAGSSLLRWPQPDAPLAPFSWCLLNKRFELSQVHFLLPEKSAHLPAKLWGKADFCRFCDE
LRVDGESNSTSPKRFVQHISTLTLEGIEVRGIRRKRTISDLAAVNILTLLSRTRFLCEFS
YELFRVGGWREMRPRRFRIEMPDDFIFQGSTPQFSLVLDWFFVNYLEMPWKGRFAPKKVA
VDPFILAYGTGEESTEWTIDIRYICLRLRDPPRRYRSVEAEEGDSFKTFERSAIDIAVLV
EHFTMGLQWGSGGAFSSRYYVGEASVWQLEPLAQNRVTFFRHPKEVVDESFRFLWFHHET
VGAAAPPTKEEEKRRSTSTNSRMNAYTALQARYNVSVEREVKKVSSWISVGSLDITPEPY
FLFNLKDSLFSLHIRNAYGRILRWEPRVANVLPRPPSPEDQDYSTNYYFTLFRLNLTVPH
LLRPCQRVRSLFFVSIKSIEFVLSSEVHGVNYMWSISVDSIVNNGVVVENDASEGGFKLR
PVFVPPFWSEEGSETGKVKNLFYLARTAENYVTGAMDSVWIVLPLKREIYALCEVFEKGG
YQQLRWLWTFLEERRMWRKGMSSKGRDSSPFSVYFTLKAPYMVVAEHGCVVAGNPNLGRG
VVLSPGDIVVEKDTNGSGAFGVSLSAVGVVSLQEHLNYVMKPMEVDIVGISQKDVMWNVK
IIIHAVVVEVEQSLYELMLQSLVRHFVVTEAELLDVFHAETEDPAFCLQLPMGDPTECES
GDLSLPAAGGEFGLRVCVEWDSFTLCLLRNNFGIFLKMGEMSAMYERPVVVEGQRGIPGV
ARRMHVKLAFITLGADDRPNLLEMRPVTPSISCRTRDQSKERKREVEGVEQSAENLSVYR
CLSFCLDARGKEEEIHVNFGKAVGFFEKSTMHLLLSSLYEPYRRIVLPEYHVHEVRYIDS
DFTLQERLVLSQRTKVRVVQGRHNHITIDGNGHDIHFIDARSPLLSLGDGLTLCIINARI
HLYGKVLEYYMAVGNGSYVIVDATCNTIINVVPSPCGDCSAATAGLEPIVSDIENGEEKE
TSLTVHRGTKKSGHRNSKNNNSASFKSGFGTNNVSRRVMANVVLFLTLPEGARELHVPLQ
QKTNTAHFSRSLVLQATMSARVEMLLFDGHLINESSTFDMSEFSIYCKYLDANGGLVENR
SLVSELALTVHHTRSYAQLENVLKRYIEVLCPYGIELRLCYGDVYLCWDAILGTQQTLGH
IEKNVLDDVVGSEITSSLETPWYTSQQGNTTTDLETYTSLSFNLRYLSVDLVDDSSDVSI
PLFCVRVESLITPMVEKRGLAFKLHVSFTWSITYYNFSICSWCSLLEPVLLDVVLRSEPN
VSLEDVKRRRGLLRAGLHLRPVRLHLSARVMENLRRIWLLKKHLWDAQHSFEQDVVWKPL
GTSKQQFCMYRVVQHVGHEVEVRFAHDSPNHSPTPSILNANETIQFNFPRVEGHELPPWQ
HRLLVSFRNNTELVNVAKTGKRLVFHSPGPMGSHLLVDVTVSEGQKLVEFRTNIAFKNEL
PFTMHVSGVGLISPDGVLHLPLGSLRHRTSFMPHMEKHRSTPCSLGVCYDMLPFLYGQVF
LGVCTVECNETAEDFNSMQASASLRRAVFFFLCFDEKCCVGDSDVIDCRGTFQAPLFIVN
GTSLPMRICLMYRKKSEKQHRSPLHFSKSNSYEHVTTIDVASGERSCITQMNPLKDIYID
IVANQANGEPMGPAPIHPDSNPSPALVHSVSKKECDRIITLHDQRGASIILHVDCTPRVV
TIWCPYWIINRTPHCLQIADVKNGTLAAGLCSEEGIAPGSFDAVGSGISRGGPAYLFNTK
RMEKLGDKAAIYVSIGRYAFSSGIHWTKWSDPVPIGALLECGIVNCSFYKNVNLSLSYTV
EFVGGRMKATRVVTFNPRWILQNCTDTIITCRQSRIKFDESMSSHLRPIDLSPDHSQIID
FSRESDAANAIQVRLPAAAGLEIQRCYWSQPLNIGKLCERAFNIHYEIRMKVQDRRCVYP
EDTVVQLGDVLYVTRAGSDVLMLSCHRRGSTMFVVVSRPYRPPLVVENRTSYTINLRQQD
VPQLVVVYPRTTRGFAWENSKYRPVMELWVAEGKNARSKPLFINFDPQAALKRSEQQQQA
LLLPGGVTLFVRIRGLSRTSYAISITTENTIDTFCSLPYFQFFFRVKVDSIHALFSDENE
DFILLTVKPVKLFFSQGKEAEGPGDEQIFSASVSVIQIDDERRCAKQRVVAQLVDDKSFT
FRFSRKLLRWTPIVYFKEFVINLSSIEIHLEDSFIFQAMKYLEQMRVVLGNKPVNLPPTH
MNGHLLASGIVGEGKRVRATDVWKQQIVFMDHLLIEQTMVSISLYRSPGAQNDPMWEQLG
YLSLFIRSVQDARFVWRRIEQWGVYDTMWLLGASYSAFYKHQLQQQMSNVIHVAGLDVMR
GFVTDLLQGYFTSAIVTNIDLTKLRLGRRAEAHFADDEKSLTIMGGVASNSRNTHEDMLE
AGDDGGGKFGRGITEPHAESQTSIHFHTKHAPENESKIIEAALRLPWSAFFARVKDTDLC
QYGIFAVQRFVRTLDLANPSRMQWQMQDLVFYGNEASGAVQKKIEPCERCEYIEMMREQR
VQSDSLSVLPHPDFGLISWAEFVHHISWGEFVQMCSPSEIRRYAGLVMLSIVGNPNNVIR
IDSDKELTSDKEIA*

>TCRU_8892 Mucin-like glycoprotein, putative

MMMTCRLLCALLVLALCCFPSVCASQEDAKNGQVAVPKVDEKEVTGKGTDPRPTTSQPPT
KEEVEEKQEPNPSTPMSQETATVTGTAKSQNASKNTQEKDGGDSNGRTENANADKANEQK
KAAAPTTTTTTTTKAPTTTTTAASEAPSTTTTTSTATTTEAPTTTTTRVPSRLREIDGSL
SSSAWVCAPLLLAASALAYTTLG*

>TCRU_8893 hypothetical protein, conserved
MVSVRLTAQLERVKEVLKTWKEVDERVSSLCPSESAAKDTPPGNVCRSTVIPTDGLVGFL
SGNLFHKIWKDEYLGVNATVTGAATKTSDGVAFRGAWAEWPVGKQGENQLYHFANYNFTL
VARALGAGSPQRRLRKGT*
>TCRU_8894 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSVCAAKDQSEAAPVPPPPPPESTTSTTGQSGSSSLGSAEQQ
GNSGGEGQSLTNTDRQSKEVSSTAGKKVTKSKTGSESRASSPAEQPNKNAEDAAKTATTT
TTTQAPTTTTTTTTTTQAPSTTSTGAPATKTTRAPSRLREIDGSLSSSAWVCAPLLLAAS
ALVYTALG*
>TCRU_8895 Kinesin-13 5, putative
MEQQLQDLLEQGGLSHTIQGFIDGGVTSVQQLKQLTMQDYQSVGVIVMTDRRKLFELIQY
MKREQANTSSATVSSPTAEISRKADRNSHATPSTAARTTTPSRRNSTPSAAQLRAENENS
SLYEIKQTPILRRDPIRMGDEMNTSTSKATPSSRTVSRTTHASPISIARRTGEGGASKRK
MSRITVVVRKRPLSSSELNEGLYDVLATDPDNEHVIALLEPKQKVDLTKYIEKHRFTYDL
VLDDKQNNRDVYEKTCKPLIETVFEGGCATCFAYGQTGSGKTFTMLGKDAQEGVYLMAAR
DLYSRLESGMSIMVSFFEIYGGKLFDLLNEREKLACREDSRGVINVCGLTEHRVDDTDHL
MRVIDYGNSIRAAGSTGMNADSSRSHAILHITVLSAKKRFFGRFTFIDLAGSERGADTLD
SDRTTRLEGAEINKSLLALKECIRALDQNHRHIPFRGSKLTAVLRDCFTGNSRTVMIGNV
SPASGSCEHTLNTLRYADRVKELRKDKSTRIAAEEIMIGQMPSEEVETLGLSGTFAQRRA
REKKAGTRSSSQLSRDLGTPNLKPIAGGFTGAYRPKAPQQRPRKLTKDDDYPNFSDSLRP
SKFTSTGPVKGAGYPKATPKHSRVGSEVSIRDASPYEIGLFESADSLDDDEDNVILGHRR
HIDAMMELLKQEMTELNGVEMPGASIEKYCRNVDSILTSQAKNIEGVRSMIRQLMRHVEA
RQRR*
>TCRU_8896 squalene monooxygenase, putative
MFCTFTLLVVVTVLILNHVLSRLRFKPTRTNYDYDAIIVGGSIAGPVMAKALSEQNRKVL
LLERSLFVKPDRIVGELLQPGGISALKQVNMEGCATSVGMPCEGYMLLDAKGVGVKLPYG
AGFQGVSFHFGDFVNNLREHVWYNCSSNVTMVEATVNTVLVENTGLLERAYGVEYSISED
YKVPETPFRRDVSAQSQSTETTTAIVRRVATAPLIIMCDGGSSKFKSRYQHYTPAQDYHS
NFVGLILRNVQLPSEKYGTVFLAKTGPVLSYRLDPNELRMLVDYNKPTLPDLGQQSKWLI
EEVAPGLPAEMRSEFIRAAKDTSRIRSMPVAHYPATFPSIRGYVGLGDHANQRHPLTGGG
MTCAFNDVLRLAKSLAVIPRLRGNDVNDMAEIEDRIQKAILQYSQKRFLHCGSINILSWA
LYAVFQSPPLRDACLDYFMLGGDCVDGPISLLSGMELSSLTLLFHYYRVMIFYLLNTVTC
TGAYSCRDEKKPSFSQKCFNAAIFLVNPFRLAGALRILLSATLVFAPLVYYEFVSLWILM
DPTGVFPNMARKMKILLYRVLFDGKHRKPVGI*
>TCRU_8897 mitochondrial DNA polymerase I protein D, putative
MLRRLFRPKHLELPHFFLWGRTAVSTKRGVVQQAGVPAPYSPIAPVASPLPQGTLPNFAG
LKPGAFNQSSVMVLLARAQYALFTLGWNPTVGDFALYCATTNELVCTKKEMLWKAAMWME
ERIGEDFIAGILFPSDGSIPLKDAAVLLREKSRRRLVLAPDTWGITYLSIKSQQEFVRGL
NIPTSLEHAAFHLTGKVYKPVITDPSVFDFTTGSYISSDCADNISAARDALVNWCVLFHV
HKRFGTKGNRKVMDPIDQIVRRVVKAVNVFVVDIDVRVGKGTIAEGFTMIVTIYDAQKRT
QTVHMIRSLSEETTKRNALNGILYGEGTSSISLFVPTARTKSAQLLAFARSCRPSCPFFA
AEVSSLAQFFAGTKVAAGLDDEKDPRATWARIRSNCFPENKSRKEEEALDRKLQQGFTAL
ANKLFSDRLHRVSPALMSAVSTIPPQEEIQKTWKRVERLEEESRKNPVPHVTTSAFLNNV
NVNDAEIVFRLQRWRSNIYENPDRLEREKNALDSLKRYLVLDLETTTVRRYKRVANPFTK
ENYVVLSGARDHTGKVFMAGRYFSRNIALRYDDFEVTSTCDLVDGSSQHSLFLPPLDDYD
VIVGHNIKFDLLHIWRDAELRRFLSRGGKVWDTMYAEYLLTGHEVKLGRGAGLEDIAKSY
GGQTPKLDAVKEAWAKGKETYEIPYALLSEYLHGDLENTELIFRKHMERALLQRQVIICT
ARMDGLLCTTEMEYNGLKTNVQLAVTQSNELMGKVVELRNHLDDAIPKEIPPDCRKYFNW
SSNQHLIAFFFGGKLKLNTNARESKILPGEAFDRHTLYVPAEEYKADRFPKGVFLRPPVH
VIGPADCLITTGGSLDKGTKLFKTYYETYVKQAGFRKSSSIADSLSREMVAVSRTESTKR
SEPEALANLLPRRHLFFVAAITPTVEDTIGKFFIKNAVTGESLTILADHKEKAARIRAFI
EEQVKLHTEMLLPADEENDSSSSSISAFADAHVTILARDAPFSFTRLMHSDPGIREYLAS
HDGLSSVPEPKDRYVISLADTVSIISYYRHMYGAQTEAAWRSRGSTDESKLVYPLRAFPS
PGPSKNATADAFKTKLLQEAAMKLEDWCNYYIDVFLHIGNAALQSEAMEPVVTAKKTRKS

KKNSASRGTFNLPILLRDRQAFVAYHNSLPNDERRRLALMTMIGRTCASVYDAFAVQCSH
DDVVEVMIRGRLSTYVPSQLDAEQVMRKFRSSTTRQLQVGEDSLNYFKKTHGDKTAETIL
ELRTMEKLIGTYYENTDDGTGMVSLVHSVDSCIHHELIHNKTNTGRLASANPNCQNIPKE
DKSPLREMFVSRYGEKGMCIEADYSQLEVVALAVLADDFQMLEDLRSNVDFHCKRVAMMR
PDLQYTEVLLRAKKNKEPEFVKLRQQAKIFSFQRQYGAGVKMISQSTGLTQDQVRNLIEK
ERETYRGVDAFNSMVALSANNFDASIQDGSRNVRGHQFFKGMFPVITGSRYVFTESDVPE
GIMREKSLSAKSTNFSPTHLKNYPVQGFAGEIVQIMLGMLWRHFLRNNNYNGLAVLTNTV
HDCVWIDCHADIFLQVADEVETIMSNVREVLNRLYPEMNITVDFPCDVVAGENMGALRPI
VREETL*
>TCRU_8898 BNR repeat-like domain containing protein, putative
MEGRESEPPRPNISRRVFTSAVLLLLVVMMCCGTGGAAATGVKESSEPQFEWKDVKDEEG
EGVTVESLGAPGLLKVGNYVFAVADAQCKKKDEKVFTGVASQLLTTETAKTPEELFIDAL
KKTQVLEEGASRDQKKKVDVSRPTTAVKGSDIYMLVGKYDSKVAVPGQDDASDAVQLGLL
LVKGSVSGGEGTNNKKIDWKNTKSLPRGPFGTQLDSWTKLIGSGGSGVKLEDETLVFPVE
GTKKKKNEAAEEDGKTVSLLIYSSDNTNWTLSKGMSDGGCSALSVVEWKDKFEYYY*
>TCRU_8899 hypothetical protein, conserved
MNVTTHKCAGPYELWRRQFYPDGTIHPPARSSDADRTGICQLPPPREGNDGTKSGGTTAP
QVNAEPSRQHEDWRRSAAPDGPNTVDPSPPSNTATNTSGKKLEFASNLTAVLAPNASKKR
PSFANGPKILVVSNASGIMSVTCGGRELVAADNTNEVSERNAAGHKSPLFIKWLCRQWIC
C*
>TCRU_8900 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGACGGGRAEVTSPASSPSKDKESQEVEVTTAVAGKVGQSGQ
PESPQETPPTTLQSQKAPANSSQAPQPEGGPSKKEDEAMDNTGLNTEDEKEEEDDEQHEE
EDEDEEEEEEEEEEEEEKEDGGEKKEENDKKEKKETKKVESVPSTTEGTSAGGGEQPILS
SGAAGASNITNPNITQTTGDGDPAADVAGTAEGKQNENKDANPKGTPVTAAAMKTTTATT
GDSDGSTAVSHTTSPLLLLLVFACAAAAAVVAA*
>TCRU_8901 Leishmanolysin, putative
MLTWCCAWQSAVGGGALDDCRGGCEEPRDCDDIGGMELQDGDGDGRTLESHWSQRHAKDE
WMAPIGCAGCRTELTLAAPADLGCMRVKWEMAEPMRWWRNSCCALLQRKRSALIMSEYPQ
MFCEGGVPARRCTLDRYSSGWCADELSMRGQKTPDGQLPHHWSRTGCEKCCRCYLEGRIF
VCGAWGQALFVVSGHASHQHDRCEGPGRNIHLGSVMHAALRCLGMRVRLRVTEEGNARCV
PCTAEATITWVAPPYDEGKAIFRDHAQLCTISATSGSLLPVVSWGGDVREGVWSRTVSLA
STEQALLRASVPDPESIGTDRVTPPKYVDTAAPQKHPSPEEKEVASVATTATECSCPATP
RVRRRRRRGERSSGHRRCGRRCCDVCCGTIIRR*
>TCRU_8902 BNR repeat-like domain containing protein, putative
MFRHLFYSAVLLVLVVMMFCCGSGAASNENTLTDSELPKRKLFHWKDTTDKVTVILFSFP
SLVELDGDVFAVAEAKGTKKEEGGFTGIASELLTLTGQNPKEELDKTKLKTQVLEECSSG
KEECPTQAVDEAGTKSGARIHVSKPTTVVQGSDIYMLAGNYGLHGAAATRNGIFILTPEN
DRSPLQ*
>TCRU_8903 Protein of unknown function (DUF3682), putative
MPDGCNKTAITVPLLSVLPITAVEASDGGNDALVMQNNSNSSGTSNAGGPASEGGSSGSD
GPGGGAEGSSGASGSGTSDAGGGGEGGSSGAGSAGPEASDGGSGGGSGTTASGHSTGSVS
SVPSVALGPPGVDSSTSRSGGEARSSGTNSSNTTGDSQTGNQTPAAAAANDTSPHEGPAG
TTSGTGHTRQEEEGEEEESEMQQSDETQVQQHQQHEHPAESGEESAKDKNALRTNATANT
GDSDGSTAASHTTSPLLLVVACAAAAAVVAA*
>TCRU_8904 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)/
RNA recognition motif (a.k.a. RRM, RBD, or RNP domain), putative
MSTIFPSDARPWSPRNNSNAVSLQKVPSVFVPQRLVTASPEQNSTVQLSPTAAKLFVGQL
PFETDELRLYNLFSAYGNVEHIHILRDLKNRSKGAAFVTYSNVEEADTAIFTLHNRYKML
ANRMIQVSYAKNSPNISPFGSYAALAVHQMNPTNPLPGVASRPSEIRPFQW*
>TCRU_8905 hypothetical protein, conserved
MRWGSRRAGFALVGGGALGGAVLWYAICRKTAGNTSPKQLSAEEFNALQNKALLTEALGT
SRLPWNQSLRWKRGSNRHDGRDFSLTLYRLLGCPHCAKVEWVLRYYSVPFSMVDVDTLSG
AGIPDPRYRLVPQIRLEPMDDTSTNKMPDSTGAYVVDSQRIISAISIPLGFAEQLQDPRV

LETRRWIADRFQAVSFVATNCTWSNAFASYPYVTPPRYHNIVFRVVGASALCILSRYKIL
PRLAAKGTDSTVKMSVKDPAAWLEGELATFTARLQSQHSSQRFHGGKEPDIADLEMYAVT
RVVEAHPNLRHVLHQGAFGEWNTAMDAEVQKRKQLKT*
>TCRU_8906 enoyl-CoA hydratase/Enoyl-CoA isomerase/3-hydroxyacyl-CoA dehydrogenase, putative
MLRRFVHGNWVTTAALAATASNIFSRQTYDLRLKSSTANPVASAKKVPPMRPSVSAHDFK
GSILKNRIWETYPAGEHVTVYVDSGVYAWIVMDRAGSSANALGEAFVGCMQKALDIVEKL
VVDKKACVAIIASAKSNFCVGADLDQLYPLTEKKMAAEATRMGHELFDRIEKEPFPVVAA
INGLALGGGFELALACHHRLLASDGSVGLPECLLGVLPGAGGTVRLQRLTGLMTAVEWIM
TSATAKAQKAKKAGAVNAVIPAEDRWNGEDRFFNQVRRWVGGLVDKPLKPSRGKNLSLMD
CFLQRTSIGRRIIGKKTIESLNSKTKGKYIAQYKALEAVLYSATHSNAEGFAREREAFSE
LLVTPEAKNQMALYFLDEGMKKSERKTGIPKDKVPPVRTVGVIGAGVMGSGIVHHFANKG
IPVAVKDVKQEAVDKGIEMVRGEFEKAMKRKKITPAIMQERMRIVKGGTSSSIFQGMDVI
VEAAVEVMDIKKNIIRDLEKEGIINGKNLFATNTSSLSLTEMQTVSKYPENIVGMHFFNP
VSKMPLVEVIKGKKTSKEAAAIIFNLALRTGKKPIIVQDAPGFVVNRILGVYMAEAGRLA
VDDKVDLARIDKAILDFGMPMGPFRLLDEVGLDVACHVGPILTDGIKSKRFAVASDVQRM
VKDGYLGKKNGKGFYKYDNKGKEVGMNAETKKHFFPESSRNKDENEIVDRCVLLMVNEAC
YILQEQVAATPEDVDIGMIWGTGFPPFRGGLLQYADHRGLSVIVDRLRQLQDVLRDDRFA
PCPLLESMGKNDKRFFPNRPFVPYKERSGIPAVKFS*
>TCRU_8907 hypothetical protein, conserved
MAAPRSRSLGSAVLRHSWDCVCALPPQQVEPLVRHTVRVSRAAIPTAACTVCARVPPGDW
NIDWPFTPCVPDSAIRDCLPGMAPGPGGVLSAFLRHLVPAARCSHRTMINTSLADGSLRS
CWEMGTPLPSADTGRTHAAPRKLSATPAALCPARGERRTGLLPPVSTAGTPPTSAWIHAT
THGLGVGDACA*
>TCRU_8908 hypothetical protein, conserved
MYVVNLCNLPSAIAHAAHLASTIRRSGSAAPIAGDLNLHHELRDGCSPSTASGENLAATP
SGMDSELSDDPAQAARISGRRVLFPT*
>TCRU_8909 hypothetical protein
MQENKYVVNGMPQRQQANKTTRGIRTTPTPPTQYDTIGTHPMYFEILCLASMSKSVTLVL
MLVKAVMSRPMEGMGSRLPEDQLDVKSMILSAVLLKYCSGPSSVLSMILGADVASSLAPN
ITRTAMAALHSTT*
>TCRU_8910 DNA repair protein, putative
MSTHEEQLEHSQRLRTPFRSPSTSRPSSPRPRDQPRIRRLVGTPQEFVAAPSQEAKREDR
VGGSLAHVASEEKVSRYQWRILVDNRERIHGAHGRVIEAFTTAGVPTASCTLPCGDFMIG
IDMPGDSCGSHASPPTARELDSLGATHSVPAAGECGDAPAQRLFSVVVERKTVKDLCASI
ATSRYYEQRRLLSVSPFRSVVWVVEGTTELLRPDERRRVLSACASLAAVPRFRVIRTRHL
KDTVSWLRSLGVAHVTALANAARSGARPPQLADCATCLNVTARIKRALRARTTFARMLIC
VRGCSSGFATQLACKYGSFLQLWRRLRCCGREACDADMDVRRLSSTQRDVYVRLTEFLLA
EEYC*
>TCRU_8911 hypothetical protein, conserved
MAAAFAESLQREVDTAIREAASHRGGLRRRVAAACDRIRQQQALARAEALTPLFRADLLR
RGRAIQKNRARLMQTLKRFARVLPSGDLCESSGLSNVVVVFRVAQEALRVEEELAYWRQP
LPCEEAWCAVCTAVREGGYRADAPLQLPAATEQQQHRRKERQEAALEHLLFPVCTNVGSG
EEEETAAAAAAAPAIPWIALPCFCTVTHFCRHEQVPVVAAAAKGNSGSQPVNPGASGEED
DAMHDEMAEAERGVSSDGRVTQMVLDATAAHLGRLGVRAGDCSSSGEDEEAAESALEEVR
LRVSLEVAARVTACRHAVESLAAGEDGMLLDGVTTVTAAAPLAVPVMALVLPPTEQLFFC
IAYTIGAAILRDEQNERRAAATTSGTAIVVDDDDDDGGGWKGEWGRWMRQESCIGGADNA
PVGPRLLRYLLEYVFCPAECESQRKGAAALVRPSTVRRWLELALGSVPDKDGAMDAMMTL
YMNRR*
>TCRU_8912 clathrin assembly sigma-adaptin protein 3, putative
MIKAVIIINTAGKIRLLNVYEKDIPLGVQQELVRRIHRLISRRSADLCNFVDNFRDWPTP
DTRVVYRHYATLCFVFIVDSSESQLAILDLIQVLVEALDRTFENVCELDLIFHSDRVQLL
LMEMVMGGMVLETSREEILRANTEMQRIGSSKAGTGAAAVTGYH*
>TCRU_8913 hypothetical protein

MPTAGHDVNVVPHQPSLRASCGKQCLGGTPGGSLIPVVASEARQSGHLHQKGATISSAGD
RCLRRIQTVPEVNCSVRYAGAGVKAGEKPVAQVHSKTHEPTRVVVLRGDDLHHAFLIHKM
RRKKSAKCPNRRLKHRHSDVNVKAHILLHPPRVATKFRVEPSDRQRVERIDQRPPVAAHG
VLPCPVHRA*
>TCRU_8914 hypothetical protein, conserved
MLSHASNDPLTGALDTLAVLHQVMRFVPYNRRTLCTMRCISKPYRRAVQHPNGPWAGREE
IIMSKYGHCIIFNAKDDEEGRSSFRLSSVSPMGRKFTTLGVKMLSRYHKRVADGLTRLAL
HHSHIDLECFEALAPLTNLRELELASCRQITSIAEASHVANLESLEVNLCPLEPDGAVGL
LLPKLKRLKLHACYRLSNLNGIAPETAAALEEVYIENCNIYDGTANEFFMNFTTNLRVLH
LPGAHIDTALTFIPEDVRRKSLTSLNLQETSLRFETLCELAPSMQDRLEFLSLDSCTELE
SFEPLGRLQELRFLDVAESLHGEGLHFLTCCTKLELVRMANSQIENIMFVSSLQSLRVLD
APNSSLGDPSLMFLENLPMLEVVVLTKCLLITNINVLCTCRRIRRIFCANTGVTNEGITL
LTGCTELEELDLKMTAVTDVNFLASCPSLKCINVCNAVISCEGCEALLKKNIEVICDSFD
TRSDYIDA*
>TCRU_8915 Probable methyltransferase BTM2 homolog
MEEDKMGCRDDGPTSPGEWLSRAEAKDHHLELANTIKSFHYRLQQRMSTETSAFLSPKEG
QKEEEKNEEAIWSRLIAEEGENMKAYATAMHAIATRYWDPDQEGSEENVSGFRSHVTSTA
GGVTRTRSRCQHENGGEESGNQHGRSTSGPSRHNDRVAYSLHCVADYYLGSCLPLVNTEQ
QLKHHHHDGTHDVSSFDKSHPGHSSIVECTGIYEQIPRIATNTIKIWRRAFYAAHGRQAT
ATEVENATYDALCLHGCGGEKSQERRGNLPLEPLLYKTLLSTCGQGKLTSSAASLAGTYM
SATRNEVRRRRFTNGGDTPPETFLPLQVLDVGSCYGPFKGKTITNGVLQVRLAVTAIDLC
PFEGSNVLQGDWLAVRFYDLGERQKEEYSEGVGTESLVRTGDDADVVTKTPKSTLWVARR
QFDAVFFCLMLSFLPHPRLRYRACLHAHLALKDGGLLVIVSTRTQCTRRGSWVDDWVTCI
EGIGFKRVHKHIMGQVVGLSFSKEAGPEIEGDTAEWLGSMMARPEAECGLRILGDDCC*
>TCRU_8916 hypothetical protein, conserved
MPVSPQYRLFQHRYYLEQSERDAGISHLWHAHRLAEARLRPGKGIADAPEVDFRHPELMD
REQTKACALMTRLQRRVLDEEKRIVKTNKNLLDRILDVNEDKYRERRGMNNRPSEEELRR
WFRADEQARARQRVRGVQEADKQKQNLIIMRQLIDVKPSVDTARQLDQWYKREHRKQVKQ
LSQFKRVEPFAGANVLRKECGLKLAEKEAGRVEFRTAARKPFLWREHKVPTLIDALYSGP
LLPSLQEASMNYVHGNLTLNNTESFTSTWTLPRRRKEKKPEWKSISALDVTLMNYANDIM
LARGEDVPIVRREEENGVTRLWREGLDQNHRAKERRGKAATRQDNGSVMGDANEGDNRRI
STNSINWDKNRWRSRKSILTLLRSKVSGSAEKTTLIATNNVRSTSFQEGDVREKPPRLGK
STSIRFEEDGVPFLGMANTESDRLSFVSAQAYKGDADSDQVYMKRTDMGQAYKGDADSDQ
AYMKRTDMGQAYKGDADSDQAYMKRTDMGQAYKGDADSDQVYMKRTDMGQAYKGDADSDQ
AYMKRTDMGQAYKGDADSDQAYMKRTDMGQAYKGDADSDQVYMKRTDMGQAYKGDADSDQ
VYMKRTDMGQAYKGDADSDQVYMKRTDMGQAYKGDADSDQAYMKRTDMGQAYKGDADSDQ
AYMKRTDMGQAYKGDADSDQAYMKRTDMGQFLEKRSDGRRTLAEWAAELRRSTKPYVPY*
>TCRU_8917 hypothetical protein, conserved
MGKTPSFESLGVHPTLVSALRRVGIHPTPFQARVLANTTSDFADVMVDGRAAGGVNPSSN
SGGAAGADGIASPRAVTAERHTLITIFVTHCLMCSREPSRSTAVVVASSKDCAAQLQKSM
KAFASHCHVEFQMLTNEGQPTPPVIGLSGESGERGAPGSASVSTSKGGRVFITTLRVLRS
WSREFLRSITTLAVEDASRNNERHLEDILRALAPSPSGNAVTSNHSSNNLTASRQTANIF
LMYLAPLTKVSFGIRYRLNRRNRRYYHLQGPSAPPGSALQTASGTLPPSSTQLVHLLYLD
ERDREEILHRVLQMYHSRRIVILTHHKEIKHLHQTIAKWGMYQTGNEANGRGSDYMSCML
RSDTAERQESTLMGFLRDTRTNSNSGAGNSGDNGKSFSALLIGWDAFTAVDLMDVDVFIQ
YYPPQKSLTERERAEFVQVLHTTADPENSRRGRRTLLITFLAINDFTLALFFMQQYGQNG
PILNIAPNHPEFQRCIMETKTVLRIKQKKEGSRRQKDREEGGQYPNASRSSSAGAANAPV
PLPRSMRHSSPGARKEKEQRTTSGSNKGNATASTAVGSSSGGGGGGDGKSRGGGRWSGEG
RGRRAGDAGTASGESSACVSSQPTATG*
>TCRU_8918 cyclic nucleotide-binding domain containing protein,
putative
MSILNALTPVEKRFLDEALGLAEAKLALEDAEEVRRHRKEIKQHADEEEEEQEEEAPQQS
ILPLEKNHNNKKSTRLGPRDAVDRFSQQLQQEIASWEEVKISLEYPFVYRSDKNKDLCLK
MLRRITRFESLVESDLVVIAAHMEILRVRGKMLLAGSLPIHLCPAFLPSMSTAPAVPTPP

NEVDDLLSLIELPTGDAERKRTCEHAIGETHVNNHVYVLLCGRVVLRMPMLKTSVESFVE
PYEVFALPVTVNALPEGSWYETDGECMLLRLTRSTDLALDRLIGDLEKRVIQERVLFLRR
QLRVKVFTHWTAEDYEEAARLLVPLRASWRQVVVTQGMESDAMYFIKEGQCVVARNIPLL
HQQQQEQGLEPKSVSAFNQPHTSSQWQRIRDLHSGRNTVMPSVPVDPTLSSVRLQSLHTK
LVEIVTLREGEFFGELGLLNHNVDWKPDVERIWSKKNWHDVLLGALQAPVNYDALEDTAS
WCSSRRVLADDHSMRTGISTPKQADTAFPPASRQRQATVYTKSTCVLYMLTHDHCRNIFD
EREYAQLKEFAKGYPSCEDIERQYNRHRKWAHYRKALVNDVLLESTSFARQQTKLPPLRF
H*
>TCRU_8919 DNA primase small subunit, putative
MLDEVQLREFYEFVYPVELVTQWLSYDLSAAEKTTDITGAAPSPPVSNDVVKKEQRNIVA
EGYLARREFCFTLLGDIFSRFRSYSTSAELRRDLIRYFPEKIDVGAVYTIRPNQKQSASS
ILPLERELVFDIDMSDYDSVRSCCSGKSICSYCWTWMACAAHVLRRILEEDFGFRYILPV
FSGRRGIHFWVCDRRACKLHDDERSALVGYLTVVVPKASRQIVVADFVNGKPIHPTIRRV
QRDVIDPAFTRLFLESSESNPNSVLHPKGASVVYSAIVAALKMGSRRDVEQRFTQQVPFE
EGNVLDWAYVIRALGDAAENVTAAAQILLMYPRLDEHVTTRRDHLLKLPFCVHPGTASLC
CPLEWDDVVSFNPLTDAPKLQEMLLNRHMDSKWLQPLKRMLEEMRLDVMEER*
>TCRU_8920 Nucleoporin
MFAFLPPAKVARTQRSPLSSMEAPGNSTQLAAPIVAAANSFVPMGIGRVRPHSVAEAEIL
VGDLTIRPSVFLSGMGTHSCWIMDENTRLLRLWNMNKPFWLRSAPRMAPIPTFTEDEGIP
LFVSEIGPEEESLAFCTDYGAVSSLDHSVEFQFHSDEGPLTVSSFACCRKGQSMLTAVGT
VSGLVLIAIKAEGERIVVGFDRVECSVAVRTTPVSFSFGCWWRSWLSGKSSSKDSSRNRT
NSSCGSDGYGVVDAVGHEFTLLRFHLTQATELWAINAASEVFLLDFGSSRCRWHKENADV
RVKWATNISTVLQRKGRVVAFDETASALCCLVYLLPSDGHGPDLEVVTMDVFSGAVRQTL
SMQSIGSLVRSVAESPSHHTRIYLDEAEQMVTVLSGHYCVRLNNRVGVRHPCSSEDVHVL
QGVERPLGSSLLPDGRIVTLDINGPLESVVDADEAMIEAAAASASVQDHQEDYYSDAWRK
SHFTGKREGLFNMVRHVDGILHALRIDAKMSLDSAVLEASEGISSHQALHEGNWARADLD
VEDDNMVMYVTNNLVRRQQEHRRFLLTVLLNNEIGPCLQAQTIARILSTQEALLAMVAIR
RLQNDSSYPLSVTTATNCSSDVEFDLVTPLYRHAISGVWQSDADSSVEEYFRLARSTAEK
ERCQQLLREAIVRVANRTRNENDSKHSLNARATAAEIVFGEPSRLSTLLQALGEHLQETQ
RSVLVDQRTKFDDAMAMANIFVLVTRAIRESREDMAPLYKVPQAVCMMLWTSSELEDYGI
QLQIASACITLSSTLAEVTASSNNMVASLNHATKNTLPSLWKVSATDQLRLLDLIVLIIH
FSFQTHSQGGPSFYADAIRRTLFREPFLREPLGYPFGAPRPSADATIGAAVLRFCEELAL
EFTVGEILVSICLAKPVEDPQQEHESYKLLGDYCQRNVHMFDIALHTLLAQRREWELQLL
PELVPDYAAGTLARDVFLVRDAPQLAWLVKPTAFEALLAEGVQSPSYLAYGDDLITHRSR
SLSMAKLAWVAAGAPTSSTYYAMRLDEEMVTAQKMCLLPETKNMELGPAELVQRLLKQSS
LDAWVYATKVACLLEEELREDILTQILRRAKLQDGDALIHIIKDGASELDVARALEATSI
GRILITAAAEQCTSVVACIWANVLDNTEQRLLSSWMQMRAAGLVS*
>TCRU_8921 hypothetical protein, conserved
MRSSVGREKTQRGGNITRKVGAKKSLVKAPTTPSITSSSRSLSSFIEHKKQQLSLLFIAW
DKDDVGRIESWQLRPIINALFPSDGKTEVLRRNEIREAFAEAVKQSWSPQYLVTLGEVYA
IMDALWSSQERRTRMVMACLRSVFNVVSDARLVISREALLEFGKSVAGADVSAGVVQLIL
TAASETPFSDTINFEGFCQLLLPRLVHG*
>TCRU_8922 hypothetical protein, conserved
MSRRVFASAVLFLLVVMMCCGRGAAAVVEGKSGDAQLLQWVDIFVPHKTQVLPKGERGSG
TPRDLFASPSLVSAGGVIAAFAEGRMNAKYQSAQLIKPISSDVVAEYIDSAREWSTFAGE
VNKETWRAHTVLGTKCGTNRVGVVLRPTTTMKDNKMFLLPWLSRPPQRGARV*
>TCRU_8923 phosphatidylserine synthase, putative
MNREQCGDANKKVSPSKPNRRSNSPRNANMHEGNSDAGDGIQRKGSERKEKKEREGIEPR
SPRPYVREKDFTDLVYMPRTITALFVFIVFVLLMIRYYYLPQMGVVANVKLGLAASAFSF
IVFGVIHLPDSLLVRPHPFVWRAVLASGVLYVALLSFLLFQNLETVRAIMGLYDPALLEA
LPERQYAEDCRISTSSDPYLFIRTACDVFILAHFIGYFVKTLILRDWRFATCVSITFEII
EITLQHALPNFKECWWDHLLLDVLLCNGGGTLLGMFALRRLRAKKYHWVALRNIKGYKGK
TRRILGQLGPRSFESYEWNVFHDPKRFMQFLTLLLLISLAEANCFTIKHILQMRPNYHLV
ILRLALWGLIAMPAIREIYTYINSNNSKTTRLGTTAWVAISALLLETIWIAKLSIEGGYF

QEPMPVYIAVPWMCALFLFFVWFVLFFCVVSLRQRQERRGVWYALSNLFFYTGCGCVVAV
VMMGMPDLQLGRKRFERFMAPYEHRVLFWRE*
>TCRU_8924 TFIIF-stimulated CTD phosphatase, putative
MRPLLIFGLRGTLVERIHASRVPLGMPDGAITVGMSRVWLRPGALETLQALQEHCTLAVW
SSTTARNTAPVMEAVFHVQSAAPKVRFAFVWSREHTTSDEFRRTNPATRDDKHATVKDVR
EVFRRFPDIATPQNTILVDDTPSKGKHNAANFLWLETCEELKIENAGVMPALRRFVEQKL
LAEKEDVRRLLPVRIPWV*
>TCRU_8925 hypothetical protein, conserved
MSFEVADVTTEVDLSKLISFSMSFQPLQLLFQRILQRTKNVESENERQDDEISELRDALK
NLQQRDAEREAQLQELLQQQEELRKQQEELRKQMDLEKQATEDVGREADVPPVDTSQLWE
EINQIKRHIGEFHHPGRRHTIEELYHARRRKGSFTGVMDVKPRRPLASITQIGGVSEVTG
TPMGDVILGRAREQLKVRDEEQPVMPLPEEGGSTGESVEPPLRGRKEEKYVFQMPEEGMR
SQEREEGRYPYSSKEKRSGGDLEVPSFLGDGEDRSIPFRTDSPFPAESSGLLSPGALKGA
SPTSSSLAHSREPSSRSGNLSSIYDRLKKDSKDIEHLNRVVAEMLNEMKDLHADVDLMRT
VNMGEEGVEKPDVTDPNATKERADLRRRVKALEDDVSRLQGIVSSLDVHAAPVPDAKPAF
EAPRSLSIMDGMKGLKERMDALEKAQERMGNKMDGLMNAAMSSGAETGVTPSQLGVLGSA
VNTIEKQLADLQRLGLRNYDTDLEELRRVVDKLIRDTEALEKTCLLLDEKKEDKGDRRPS
TVAPESEGADAAPMQAPPIVKDTSDSSAAVLDDLQRCLQDMQRRMLHTETNVMDLNEQKA
DRAAFQRLADELKNLRQLLELGAGRRGDEDAAQSASAAQGELMQALKEQMAEHMQNFNMV
RDGTTNELDALREYIEQIDHRKADAMLVANKAERDYVENALERLMREVEQVLNATNAGLI
DTLDKSLNVLRDMLEGKATKHDMDNLRRLVSEDHIAGGAPDALAGFRGFRCLGCNRPVET
MRPRVMGNRLQPFVNRLPQNHPGDPIAARIQQGPSAASDGMHTVSDGG*
>TCRU_8926 RNA-binding protein, putative
MPSGGDPRNLIVNYIPTPVSDESLREMFEKFGTLVSARVIRDKKRDGHPKGYGFVVYADR
ESGLRAMEEMNGFKIHNKHLRVSPAFGPGNAQPKSETGDAVIMQANKTGEHWPSLPSPQL
CAPLPYSVDCTDVDPRNEPGAMPFQSVPPVPLSQAVCTTPVAMQPPTVTILNAVPVQFYA
ASHFVLAPTSNKPQMVATAVHPQGSITSPHSPPATPSPPVIVFPNASVGNNRNHAHINST
VMKKSSSNISLIHNAESGIVGVPSQLAPTIQNESSYQTLIRPVSFPPSIPIFQQSEPMVQ
GCNSSFHSSMGSLDVVSITAGSKPLEGLNGILVESPIMSR*
>TCRU_8927 hypothetical protein, conserved
MGKIRSQQCGLDPRAGMSKSGQESHRACALCRHSGTDVRDNTRNIALATPTSACHAMYAP
FLFLLDILPVPSLHCSEEAHVPSIDAVLRERSRHDGISVRRHVAWDSAVSWGKYGANSVA
SIRQRMQHHAKLFGDAVAHRQREKAERLHRRKGVCGRRNLCGRLGCCCQAGN*
>TCRU_8928 Mucin-like glycoprotein, putative
MMLRRVLCVLVFALCCACVCATAQEEGQYDAAVFEAAGGDPKKNTTTTTTTSTTTSSAPK
NTTTTTSKAPTPEDARSPGGPVWVPVPLLLLVSAAVATAGAAC*
>TCRU_8929 hypothetical protein, conserved
MTILDPECFLAHVSKFETYNIDSSLYPPPYVLHGRLPHSNFVCSASLVNSTPSWSFCHTF
ECTGGGNTAEPPMVLECYGNNGEEFVGMCAVELSQLLEASSSKDSIVALQLRDGYFVRGE
ISFHATLEKLRSFDIHIPRMAIAPHSPPGASVYVELSCGYEGSDGAVSVTSERVATEVFE
WAPLPPLLQCRVTPGILTQDGVFGKLFSDSGERLGHFRIVVPTSVVRGITAPASLSEDGV
SSDQFEFDVPVESTPSGFVLRCAGNMTLSTGACPAVCQASAEASFDAERSTETHEFFRGA
LSEDLQVLSEVLEQQQQMLGTVREQLEWVRDYKATIKQRLEVLRRHSTATDSTDVGIRSR
IERELQGCIMQREQLRDELAALRKRRAAATEEHLLRVEEQRRLQETLEEEQAKAEFLREG
VKKLQLEMQTHAKMEKKREQLRLRQSEEQQQLNSEDAETLVEVMRLLERHK*
>TCRU_8930 Zinc finger, C3HC4 type (RING finger), putative
MCRASRGVEKEQARSCLGCTGEGLPNDEPEELCLVCFAEKRMYAFLPCGHVACCSSCGKL
VDRCPVCREERFGYCVVNTTALLQFKCPHCKAILAPELYDGHREVCAIQSRAAQVGHSGP
ATDAETRSKNAATSGRRAGGGGNHPPAAVPAKRSASSHGITLNFCIECRRENAPLVIIGP
CGHRVLCGDCFAGRITCPVCLREIEHGWKSYI*
>TCRU_8931 hypothetical protein, conserved
MAADNVTEAELEVRLEHELLLCEQDFLLRETEATTCISNRATTARKNAAETDIGLLRAYL
EGMRRKNRAVCFAAEEGMRAKVLAAKRRSEELRRILSELQKETTEIRERCASISM*
>TCRU_8932 aminomethyltransferase, mitochondrial, putative

MSVPLRRTVLHSLHLSRKARMGPFAGYDMPIHYQPGVVQEHLHTRQAAGLFDVSHVGFFE
VWGADRHKFFEWVTPSGVTELQDGQSALTLFMNESGGVKDDCIVSKYSDHLLAVINAGCK
GKIITHLKDRLAEFKGDATLVELDRAMVSLQGPKAASVMAPFVEELDRVKFMWGRRSVRV
KGIDITLTRCSYSGEDGFDIIVPIQDAVQFVELLLQNPDVQLAGLGARDSLRTEAGLCLY
SHELSEEVNPVAARLMWCIPKRRMAEGGFIGHERLQTLVQRAKELVPRLRMGILSVARGP
VARTGMPILVGDVVVGEVTSGVPSPTLSRNIAMGYIDRAKARAGETVELEVRGKRLPGEV
TLPRFVPQRYYKG*
>TCRU_8933 hypothetical protein, conserved
MAPLGKKELLLWAAEASGIRPCNKYADLRDGVVLLALASRLFPATVDPRLLRRGPIDVER
NWGALRRVMERNGLPLHLCDRQAVAAGHARHCFNMLVLFYFLTRLSQDSEFCVDFANPID
AGIAEFLQSPQSLLCVGKLPAACEEGTQLEEEENEKRSGGSAPVPPPPSSSSPSSFPPFA
SANSSSYPLHAALTTSSAKTSSDAEEPVRRGRSGGGVAKTQSLQVSNARLQEELDHVRAT
SQLMLAQQRTLLTSEVARMTEQFEIRMTMLRLERDHEVRQCLLDMREKYDIFLSEIKENE
TAASAPSSSPSFMALRALEGKVQTYERELAEARDTIQQLHNAINLQRARYEGFAEKISSV
CAAAPPGVSGEDDFLKTMNALLGTQPQGVRDAVILRLKTLLSQVRVPPSEDQRNEPRKKE
EEEEEEEDGEQECHGTSGGISGEGQRFRMQLEGSKKAKQFPRQQHQDWYAVPLTDGLEAP
SCMIDAETCDAICARANAVAETHTPAASPVRQELQRLVLAIQILQARVQTAANALMAYKE
KQQGLREQLLCLQQSRELEAHEQERTFGARLEEQRRRLEANEAALTTKLRLVEERCSRRE
SVANMLHEKVREMVGSLLKQTHVHDSGGFDSGDESGLALTGVQAALRRLLTDVADSQRTR
DSMEAALGELSKEVAILRHDLARRELEVKSLQTSLAAVEAARREERMELSKATAEADALR
DAMTVEMDACRLYIKRVGELMTMMGVSPPSLHQGPPFLAVATTNENNDTRARTPAPLSEL
NNVNGIVKDMCGAEQIKETAAAPTGRALVTAAAGAGASTASSLLSPEELERRKMEILSKY
GFSNRI*
>TCRU_8934 MORN repeat, putative
MAEEGPGDQEMQQPSIHTYKSGAVYEGSFNGTKRHGRGHWHHPHGETYEGEYVNNKQEGL
GIYRFDDSCKCYIGHWKEGEMHGEGVYYFTSDHSTFYVGEYAHEKKHGNGLYCYENGFVT
SQEWDQGVLQREEEATPLQRVDAEVQVEELTAAVRSVAPKELGVQPPPSEVRSFQFPSGA
TYTGQYYGTKKHGAGHWVHPEGDSYDGQFEHNKHSGWGVYVIGQSGKKYVGHWRDGKMNG
MGVYFFNKQETEYFIGSYKNDVKHGCGLYHFAERGNNKLQLWENGRLKKEADAEETAVQG
YGAAMHKIVQIVRRFAPHYEPLVAQ*
>TCRU_8935 transcription factor btf3, putative
MPNITQETLRKRAEFVRTGGRGSIRRTVKAAHRNTGDEKKVQSVLKRLGVTPFNEIDEAI
FYRQDGSVYYFDKPKVQASMQSHCFVVSGPYDVKEASEIAQ*
>TCRU_8936 hypothetical protein
MSDYDKTKMWLIVGCTVGAVVLILITAFTILIINFIKRRIALAKEVKQQARMQNAPRMPR
RSLLSRNGNRNGLQTQSNLNDGESPPPADAGKWPGPPHPNVLLPRTFNDASSHVMPSVSG
GIATNRPVSRLPRPEPQEDQVVDLPPESIPADYVDPLLWQTEDLDENNAAASQMNDDERR
PPIKRRASFVSFVGEYKL*
>TCRU_8937 impB/mucB/samB family C-terminal domain containing
protein, putative
MDMFYAAVEMKKNPSLVDVPLGVGTFDMLSTTNYVARRYGVRSGMPGYIGVKLCPSLVIV
PTDFDAYHAEAAVVRGIAAAYDPNFTSVGLDELTMEVTAYLQQHPGMTAGDVASEFRARV
FAETQLTASAGIGPTATLAKIASNYEKPNGQHELRLRTRQDVMEFMKDLPVRTVPGIGRS
TESILHGLGINLLGEIYDRRVELCYILTEKTFCFLLGSSMGVVRWTDADTNDGSERTTEA
ERKSIGMERTFRNLSSRLELQQIAHSALQTAHRRLEENELFCRQIVLKTKRASFQVHQYS
KNLPQHSDDLETLRRGVDELLLRIADQYAFLRLVGVRLADIITKSEYEALQRGGMQRTLL
QYCSRSYSNSRTASCGAKNPIKEEVNCKDENNGVEVLCCSANRDAMYDEEGDDDVVCVSP
PVKLRRSEGNSSGGDDIIVID*
>TCRU_8938 hypothetical protein
MKYVCTHGSAGTSQSGVAVSTRKTKPPTCSSTILTLQRKNAALTNDLEECLGIFRDARAF
ADELEKKVAAVPEFLFSMQQHMQSLMLLQHGVFLGNATVLFQLWHRDREALLDAFERQAN
DAYESYQCKKRMLVEQHEAELEEAHGEWQRALESTQKEMVELKRRLKLAEVDEGLKVKQM
LLKKAAAVIERKCCGGCNKETQTSHSVTTAACQTADVYRRSAAVQTTEEELPWHQEPRRP
KEEAEEKEPVPLVVPPVAFPAEAPLKSPAPREEQRKERQRGAMELDALRLELRNVQMDYA

HEREAAITARSNCTFLEETLKSQLQEITFLRDALDHIEAFVFFPPTKYSSSGGVTALERL
ALMGNEGLNSSPQVLPPVVDTPPYGESVFKNKQVA*
>TCRU_8939 impB/mucB/samB family/IMS family HHH motif containing protein, putative
MQRCWARVSPAVFHRRIRGKKRAVDEVSSKLTLDATKAGLSGVNKARVNKVIESCSKGSA
FYLNEERLEAQRKKRHMELLSKSEVYRHLSTADKQALKDKVEMCEVELEAGRHFRNYVHV
DMDMFYAAVEMKKNPSLVDVPLGVGTFDMLSTTNYVARRYGVRSGMPGYIGVKLCPSLVI
VPTDFDAYHAEAAVVRGIAAAYDPNFTSVGLDELTMEVTAYLQQHPGMTGGDVASEFRAR
VFAETQLTASAGIGPTATLAKIASNYEKPNGQHELRLRTRQDVMEFMKDLPVRTVPGIGP
VQGAVLRVLGIRTCGCMLRKKGLLCFLFPEKTFRFYLSAGLGVVRSNADLMRSDGTQKTM
GHEITFKRRLKSEAELKQIVLKFLWLCITPCCSGVWQRNVSHCS*
>TCRU_8940 60S ribosomal protein L35, putative
MSHHVKIRDLRDKSKDELLKQLMEFKKELSQLRVAQQLNSAGTRLGRIRLIRKSIARILT
VLNRNQRESLRKVYAGRRLRLAMPKALRPKLTRRRRLALKDNEKNRKTRRQLRMARKFPR
RVYAVKL*
>TCRU_8941 BNR repeat-like domain/Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MLVTLPVYSKEKGSEKKEKSELHLWLTDNTRIADIGPVSEKDEDEVAASSLLYESAEGED
NNNEEDKLIALYEKKKGDEKPSHGLWSVRLTEQLKRVKEVLATWKKVDEAVSKLCPTASA
AKSALTENDCSAGEITAGLVGFLSDNFSGSTWRDEYLGVNATVNHNGGAEKAKDGVNFRG
AWAEWPVGRQGENQLYHFANCNFTLVATVSIDKAPEGDNPIPLMGVRAGSKGETKLMELS
YNSGKKWKLFCGGDTTNELSSHWEAGTAHQVAIVLQNGTQGSAYVDGKRVGAAPCELENA
DSEEISHFYIGGVGDSAEVQEVVSVTVKNVFLYNRPLTFSGGDADLEEAPHLPPANPQPT
EAVPQSVEGDQKAMPPAGKPSEAPGEQATLQQPPEERETQENTTVGESASTQQVPANRSQ
GSVGSAAALNSHAVGGATGDGGTVRGSGLLPSLLPLLLGLWGFAAL*
>TCRU_8942 NMD3 family, putative
MDLDGEFQHECDERIIPKVLCCMCGLLIDSNPSNMCPSCLRSHVDITESLQKEYIIVYCP
ECTRYLQPPQYWSRADLESRELLTICLKRIKGMSRNVFKLVDANFIWTEPHSKRLKVKLV
LQKEVLNNIVIQQACVVEYVVLWQQCPTCQKVATGQPQWDACVQVRQKTTHKKTFLFLEQ
LILKHKLHESFIRVESKPDGLDFFFAHKSHAMNFLEFLNRNSPITRRDAVQLVSHDSKNN
TAVQHHTFSVEIAPLCREDLLLLPYQNYYLKLGGLGPLVIVHKVYSSIVLLDPKTLRAGE
FTGQYYWKKPFPTFMSSRELTEFYVLECTPTGVTNGRYQLGVVTLCLSSEVGQGREWIVT
SHLGGLLQPGDLAMGYLLEGKNFNNEEWDSQRYNPEQLQEVFLVRKHFPSQRARRHKRIW
KLKHLDVLDPMSMGRNEKRQEELEEERREFEDDLERDAEFRRDVPIYKMSEFELAQRAAT
NGKDCVEPEEEGDEDDGVPQIALEEMLDELRIEDDALVDAEVVVPEQPQKRRRAD*
>TCRU_8943 Meiotic cell cortex C-terminal pleckstrin homology, putative
MSLHAGRGHRTILAPVLLNPYEEGEEEVKKSAGNNNSRSINTVPSLTPPGQALRHSEAAD
ERLSLNLSQPMPPPLPPPPVVLVSPGSQVSEDTGKSDEVLRPGRKAAAFPPPPQHMPAGA
LRDKRVPSPVRVPRTRGPKPSKAALGDNADGVAMSTAAGPEAALTSSARNAVSRETRRPG
LAPTVQHARHASFSSHDVEIQNVGTTDDIVAGNSRSHDAEVGEKKPSQPPLKDSHFYNPF
VVQSAFTQKNPFRNQTFEAFCYAPDYSAPADCRTYHCDSNEWVGFQRTSDGDFCEQRATE
MNSQGQMGPSTSSLSKYLLIGPALGALQSGDWFYKWTRHGRVHERYVWLDIQRHSLLWGP
SPRSSFVLLSHLRLDAVMDLRPDCMFDEATQRTFYRFFLVREEQTVVLATELRDKFDLWF
DALTKIIFANDLPRQQDQSAGFSDGTAAGTMGDKRASHRNALNAVLPGHGSKMHAAQNMF
TDRRTQVLPSD*
>TCRU_8944 hypothetical protein, conserved
MSQTEKNFAAELLEKYFGTEYLFDQANAFFREKVSPKNTAGLTTPPNIKCVSFLRFVNCT
VDEKNISSLREAAASSTLVESLKGEDGEWYLRRRCFLDPKDDPAIRSVVVWPLHRASKPG
EVKEFFSQYGTVESARVMLQPHGETQLHATFVVCFATVAEATACAKANVSFGEAPSALAQ
HFLPSRLNVMPAEDYRAKTEKDIRAREGTQLKQNVVRAQKALVELKGQEIKRFLRKGVTL
TVEGVAPGTTWQTMKMKLGNLSLTNPLLRRGITLLKVEGPDASAPSRPWRAFVVCRDENI
ASEMLKAFSFADGEFGKQLREVCPSLRPLTDEEEDYARRHFPEWCEPLVVAKMAANSKRQ

RSP*
>TCRU_8945 nucleic acid binding protein, putative
MRSDRCDVASTPPADGNDLVTCSVHGSRRLARFCVRIPVYNADRVMVGYAYNCKEEMQCA
ASASRNSFAKQHDIRGVAEVRDDAPPELLTRSVATTPTTAAGVVAATEKDAAPQQQRTGA
ARGPNRYYDLTKQRDSDAAGKKKVCWNCGMEGHEKPECCNTLCRTCHTTRGHHHLCQEPR
PSPFLNLSPTTLLSEDMSFVQCVSCSSFGHFDCSTSRETRIPSCCFCGERGHNAYDCSWR
KRRVPDRWVNRVKEAENGMAYRENSGASAVLPSVFNSLSTVYASPGYNQASAWREGGAPS
YVANWNAGRRENGSYGGGASSGGHYATKSRPYNDRSPYSGYSGDRHNVSHTREMDQYANY
GLKRSRWGDDEDLSRNKNHQQSRTHDHYRDLDSNQQGNQRVGRNHAGSRGEGEKPHVRQS
YHNNGRYQRKQRRRNRGVSDSDDDYENLF*
>TCRU_8946 cytochrome b5, putative
MSEARLPKYAWEEIRKHNTDKDCWVVLYGRVLDVTKFLSQHPGGIDPINDLGGYDITNSF
ESIGHSSRALVLSKEFIVGDLDKDSKPPVVEPKASREDVPLTAYKAGGEMIPLSYILASV
FALMLLFYYYLMA*
>TCRU_8947 Cullin family, putative
MGEREAFANLFGILEVIRRDGILAFADTRVAEKCRCNETLAILATPPFNTAVGELLVRKV
FEAFASSSLAEYHQNMCDGDELLALRSLHEAYRRTLLLLNNWCKQLHAMEFVVRFTVSLR
CHLLQPDLLTGEHPPGKEVLLQFLRNHGRKLLGDIEGTEGRATLMRGILGHRDEVLQRLH
GLTLSSTPDIKALWKSVLVECTRERIEMLDDDLTVGRIISCMQWKDDVVDTFVRMALSPD
PNNSDVRTEVNRWCEELEQLLLVTYGRKRIAALWDVVVEYPDSTPTLQDLRLCLLRCSDD
TLQNELIQTAKKMLASRLHRAGTRTEDILAILIGTIHSLCVLFSRNDQGSVIFTIVGDTL
EHLKKRRDCVSAVVQAITQPSADSVLHVDLQNFSPNSFTSVAADDDEVNEDDLFSVAGQS
PLSMHERPDVLRVLLSAISVTSLVEEYKRLLASQLLGKKLHDFDTTAEEEVLERLKCAFG
EDVLAPCVVMIRDLQASRRHTLHMKEAYRRAAAEGLPQEKRRDWPLSIDVLSTTSWPKLS
AFLPAGETQPVPERYNPHPLFTSAMEDVMEEYKRMKANQRLEWIPSHGYVSLELTQKEAS
TNTMVAATYDLSLFSASLVLYVGDISTELGSPAPLKTVAERMGVKPHVLQQRLSHLFPSL
LVSTDENRSLSLQRNYVSTANFTFDEADEREGQPVGLSPDQVKMLLSMMTAMLKARGPCG
ANDIFNSMKMFGQFPGNIDDMKKLLHMFVTQGRLVLNEAKLFTLPGN*
>TCRU_8948 hypothetical protein, conserved
MKETLVFATARQQFLQHGYAIFPAAIEASLIERLRPALTASTVARARCFIDVPDIESMLK
SKSKLSDPLYTKVMARLQRRKYMLRRYREEKKRRKQLKEVVANFLNGREKEDLTGEELWK
LSELLAREAVTVPGKECRSTIKNDPQMLRAINEYRCNVWMTNKELENIVRDPFFWQPIGA
IASDVGGVERPVLFADAPMFREPYGGPFGYHCTAPSIGVKTNGNHPLAVSLLVFTHRPDK
QKMPLFVLKGSHRFVQDQYLRYVLPNVLSLPFLPMESHIPEQIKRFNFDSSVVGSPIEGG
DAIGPGTVVVLNPHLMIGVGANASTERVAVYKLNLIAENAPPFLKAPSWITAWRSLPREV
NFASPVVFPPFYDKTMSTTSAR*
>TCRU_8949 hypothetical protein, conserved
MDDGLKELQDRLNEAEERVKRMTHLMLRAVWQYVTQQHSSPMVTKGSSVATAAGGAPCLK
VVVSHHHAFRHRKLGGTAMVQHVKGGSGGVDQARLSRELYRKAFGEARQQTELGIVPAKN
LEEDSGGDAIPSVALLLLQSSRERAIMSVFLLRLRLAAHRRRFLHEECELRYAYYRLRRV
LRAWYDFVRDLKSSRQRLLCDVLAHWVKVLERRRKTQECLHRFLVGLIRRRHAFECVRIM
KLQQYFLRWRQRLDVRRTLGCMEERAAEMRGRHKYVEVGSVAQPAGVFVIKDRVFSHWKK
KTEHRLDNRLAEWMSKRFVMRRVWKEMVARYLFSRQQHTEYSSTSAYGPPTVYVDSQMAE
KFMELKAQCAQQIARGRLRKIAFIQWRAKYRNRLSDRFFVFRRRVRVMEAWVEALRRRRV
NCFVITACWCRWRERLYLRLHYLEAQCWRRQRLQRNALLLWRNNVACRLFYRHQTLHSCC
FKWWQRAKLKWARRRLAAGKKRRVIFGWRDVAMREKEQRTMTCVAETLRELVLLVGCFRR
WKERYEHACRARLSQSILSELRREKQRARLFQRWKRLTFWPNAVCKDPSLSS*
>TCRU_8950 hypothetical protein, conserved
MSEQNGAHSLQAELERMNAAIESYALQLDTINSAIESIDSENQSDDVSRQIFEYQTACER
DPANISAEDALDTVTRLENTLKIVRRRNQLLAKENVTQQKLLNDRSKFLLKETKNYENLV
DRTGWHEQCSLNPEDEAQKASDIQEMSQLEVTVQRELRAAHTILKKKEALLRGLEEQLAK
GTDLDAELNNAYNDIRVRKRECRELELRLEHLRKCSKKNDEALTVFENHGQSVSIEYMET
DKDFLKDAVAQMKLVCRRQDNVIRAQLTRQQQLQTRLDTILRSLREMNLEKEYERNVSKS
ALVPSASREEPEDVSSILPKEETIPIHTYRLIFKNKELMNTNVVRKNMLVLEKEGVIQAL

EASLMKYANALNMTTRQLENMKINKGFEMTELMVELQQQHKNYLQQLEQIMQENNKLKKQ
LYRTPQLRTLIKNR*
>TCRU_8951 hypothetical protein, conserved
MLRSMLEMNRTPLDMMILGLQKIAVRSETRRARPVTEEEMNQVIRSRTDWKERVVLRLAW
ITASRWSEVAALTAKNFTLKPEEP*
>TCRU_8952 hypothetical protein, conserved
MEVDGDHDVIAAAKQKLNLLGCLTKAIEAEWQRKEALLQQLQTQLNEEQREKESVWHRTR
NIGADTVATLNELRALEELDMLDSMLVEKNTQLRLQQQRHDMLLQQLANMEAVLDGVGSN
EDFDLKKWASCCERMHRYIDATDRYCTRHTRHVVIHPVSVIHQSIRKMSRTARERDERLV
IQLECLEKQIQHASSLDSTLQSKEAKYRCKWEELRRGNRDRMRKIKNAGEVETMKLRESL
QEVKKEHSHLLCRLKEEVVAPVEADLLSPPPVLENAHEISASLHEPRGEGPDKSTDVNSE
FIDNTLLRSVPILRRSHLTSRGWLTSASAATATSDRDIDDDDTNDTGNVGVAVGVPDAPV
NVAPFSQSAMGLSLHRAASPAPPGEMNSEVEELRCQVIAAERDVDRLQQRYETLREEAER
TLLECVKKERALEEKLCKSREAVSVLEKEKSGWQALHEQMSLLLS*
>TCRU_8953 hypothetical protein
MLASEHRASELPADFLEAFPTMVRDVSLRGDIRLPPITPQQQGALFALAAKYGSACSLVM
DGEGRFHLRNGSSSPHLQEKLAEELRYLHDEGEKYPEEDPLVLHWAFTDRNVHREVVTML
QLLAYDMGIFLGEQLFDGVYIYRVEVALRYLPQWEAERRKLIDSSLQGEADPFPIPVLAM
KDAGIMDAYRKFIRPFLYEWDFATTRCEVNLYREPTGQIPKEARSLGSLFSLRHEVNSSG
KIFFRRWTRHLLHVFSKYAEELRRQDSKGIKKTLSKYGGDLDPVDTENITPHFGHFNCCL
EERYYKKDLAELEEFACRSGYFVHVSIEGDLAIVLATARMRPALAQRYTLVFPKETEHPR
RPRESEAQLHGRVGLLDTVIRQRLLLGKEENDSLYHKRNDKKVSRMDLINASANTSSNSG
SSSSSKSSSRSSSSSSSNIKRRSTDNGKKRVRGRIVGIEESRWGKEGADSALEDENKPST
PKKALPALNLLVGNEMGAYRRFSLAESNLYDTIVGKMQRKLPPGWSVRRDSAGKRYILDH
LRGRAHHGDSSVISMEFAAGQREIYNVVDLMM*
>TCRU_8954 hypothetical protein
MGSSSGSSAQRVDLRDRHLAGNSVPHRSSNSSVRAAQVKGNGPSPGRKIAAAPTRVKSTR
SLLDPSEVSLESDLPRPEAQMQGVSQKIQRLAGVPEGSSLLVHEVDLNGMMGEDAVASTN
SINSATSIKCCIRQLEDDETFYRRFICNTADACIEMLRRVMCYWEEAVKQLREVTDMVVG
VSRFANISAEEVLQTPEEHLSRAFNPGLKGSLMDVKGALDKLQQMPAILVANYDQLVSKN
PGVCETQDSARIFSSPQLNLQKTPQTPQQQILSPRDANFYVRRPSSLFSRCGSLQAMSSR
SHQPIIGITNSHAGFLVGESLESEEVPFSTTTGANMVHSQRERDADPSWAMEDLREENVY
WQEEALRAVLEAEKYSQMLHTVVGFPPSSSFNGNSELESRRISITAMGSPIQMIVVQRLF
IRLLEEKEEGDRSRIESWEAQEWWGLWFSARNAIEKHH*
>TCRU_8955 PhoD-like phosphatase, putative
MRIVMSDEKGSAKTAAWAASLLCFLFMILSIGIVAAAQEGSHELAQIVFVSCNKHDRDQN
YWDVIAATVEHGKDAGQLNKPLKRATGSCAANSPVDALVWLGDAVYADNFSAFRGCYPNT
DLELVRSRFTKQRNAPEYVAFRQTCVRQRQTLAFREDGEETQFVMGVWDDHDMGKNDGGA
EYADKDATQQFFLDFLGVAKNSPRRKQKGVYVFETVPFRALDSNASVNPAKSAAIKELHS
LYDHAVCFLLLDARYFREPSNATRSGDMLGEVQWKWLEERLRNDVAGQNPVSGRERCALT
IVGSGVQVIMDEKVTESWGAFPLSRNRLFLLLRRYKSERVIFISGDVHLGEIGMDNTQDA
MEALGYPILEATSSGLTHSSAVFWGLPTLMRTLFPSPRRVGVYIERNFGVVRLTADPEAL
IMALKRDGKAQRHQFERYINVSVFIHSIPQKGKAVLQLSLPLDVFTIDGGGGTKGRFNTL
TSAVKRTCEDPSKENTENGDCSTVYYPRSAPLPVFTSLIQFLQRHIWPQHTLLQVVSTVV
STSVLLLLAATAVFCIRLWNTGSKRKKREKIS*
>TCRU_8956 Hydantoinase/oxoprolinase N-terminal region/Hydantoinase/
oxoprolinase/Hydantoinase B/oxoprolinase, putative
MNLKYPRFRISVDRGGTFTDFVGDVTFEDGTTHWKTLKLLSCDPQHYPDAPSEGIRRIMR
CYIPDVVPARGLIENEYLDEVRMGTTVATNALLEHNGERSVMVLTEGFADILDIRDQARP
SIFALHIKKNPVLAECTVEAKERVRIISLKEARSTIPWPKEWIKCGESYIVDVVRPLEKD
DLRQKLQKAYNDGIRSVGVSLLHSYAYSKHEEEIKEIAKEIGFTNISLSSELMALMKYVP
RSTTASVDAYLTPLIFNYIRSFRANFKHNMLGTRLYFMQSDGGLTSADDFFGFRSVLSGP
AGGVMGCARCAVQDLGEHVQVVGIDMGGTSTDVSRCDGESVSHIVESEISGIQLHAPQVR
VHTVAAGGGSLLKWENGIFCVGPGSAGSHPGPACYGKGGPLTVTDANLVLGHLNTEFFPR

VFGLHADEPLHVNAAKALFETLTEKIANDTGKPWTVEEVAHAFVVVANETMCRPIRNITE
ANGYSCPSHTLAVFGGAGGQHACAIARSLGMGRIYFHPLASLLSAVGVSMTDIVQERISS
SQIYINQENAEAAIQEQFRSIATSAKEELQRLGFDDDHIVLEHYLSMRYEGTSTSIMVLL
DGTCEGQTVESGESDGAGNLMHRVKANFTHCYEQQFGFLLMKREIMVDAVRVRGRGVQIG
KEARARIAQQKQNSAVHQPPYSTRVKLAPRPISTMKTYLSNGWETVNVYIVNADNGPVEG
PAVLVGEGTSILLESNSIAYTNDSGSLIIHTSQLIEKISTALHPLHLSIFSHRFMSIAEQ
MGNALQRTSISTNIKERLDFSCAIFDKNGNLVANAPHIPVHLGAMGAAIRWQREYYGDQW
REGEMVLSNHPACGGSHLPDITVMSPFFFRGEVIFYVASRGHHADVGGTTPGSMPPFSKT
LQEEGAAIKTVKLIEDGIFQEERIRELLLKPGTCARMSGCRTLEDSISDLRAQVAANKRG
MQLLKELMETYGYEVVQAYMGYIQDFAEASARDALKRVAKLYGTTLPSVDYMDDGSEIRL
KIEIDPETGSSCFDFTGTSSQVLNSTNCPTAVVYSAIIYCIRCIVDADIPLNQGCMRPIR
VVLERGSILSPDDELPVVAGNVLTSQRVTDVIFTALRAVACSHGCMNNFTMGSSDVAYYE
TICGGSGAGDGFNGTSAVHTHMTNTRMTDPEILETRYPVILRFFRIRRGSGGNGKYKGGD
GVVRSFLFLQDLTAVLLTERRVLEPKGLFGGGNGMKGLNMVYVPNEDTAARWSVSPQEML
HDVKRGEWTREEETRSSDGCAVYRARNAGGKNVLAVRCGDILTIHTGGGGGCYPEEAKQE
NKRGTIHD*
>TCRU_8957 hypothetical protein, conserved
MSGAMQDVAAEGVEENATARTTLLRDNTSRSVVTRIPRRGTLISLAPLQKRLVISGARVG
VTIADGLFLSSTVANPLLTVAFIAYESFRAVNDYRRGELNTLGYRTSLTDVALRVGKEVG
TAAVGIAIGNGVGTLIGLSAIPVGGQIITATVLSVTLGLCVGTLITRYADRVFVRLQLQA
QYGYSPNEQKSRRRFEQLLEAQHDLSSFETCRIVQHYRDYRVACGWESHTDVDDYRASAD
INMMPVSFQHFAIVQLQRKWGFLNEYDECRKVFKALMLSHHPDKGGDGELVAQLNHDYEI
YAFCQGWQGGSSGIYQREGTAEPPNKSVGIRKGKRNVIVNFLRSLFRPASNSALEAEDLR
QCGLLALEAGTPTELHRFDEVDWEAMDKEELGICERPVFGTSASVKQRSVSRVLASIHRC
YQLATEAITFAGLVKLYKEEKEWSELERDIFLFNRLQAFVTVTKDDIQVESGDLGSSKEH
ACCGITWRTRAEAVLRREERREAIVSRCFPPCVSSELLGTLELWKTAQSLAESFFKQSNG
AAGGGGNSYNNKSNATNGTAGDMPISDGTGQTLDTLLNIQRALQDLMEKSTQSWKNTDAT
ADESLNPLFIEEVQALGRTASCALAGAHAKSVEDTLWKTCEEFFKGRQRKLESVTSLLNE
IHDVQSSLKNAPVEEQEILQSRLDDYMKQLFLIHYLFGELDVATVELHDIYTMHFPEKSD
NLKKLPSSCAKSIHEEFHMARYVKYERERTLMNYINIEVEPRNAMDPSCPPADQKVPLDC
ESGVADVEFALLRAQYVDTITGTVTPCWLKRYVFPKAEGLEAQRSAEFLFKSIMERELHI
PEFCATHRVTCITDVFSDDYTRQIYFHIPRGGTQLRFGSTHDVPKRIKRIGVRWLHDALQ
CVIELHSCQLVHGAISLSNFTYDDFGNTTLGFFSDALRHRVRGAASLLDDTIDFGALLHA
EVLPYLLRASPAVSPVRNPSVASGREERLLTDTRCMDVANVYREVADRLIGKVEPRWTLI
DARTFVRRFLEFNYNSDERNYLFTKEVSYPAHWATPKTIVPVSLVVDRRVFLHLPTNATV
FLNRNLHLWDVYWKCRRKMVQKRGGGFFSMPASLKRHAPFHPCSDDCEVNERLLWHTCHD
EEEAWRICLVGLPCKRHRLRLAPPWLESGEDGKYYPRRHAATPDWGVIFRVSLGTVVEHE
RGTVSDLPKKRVDVSQRARPPARGLERSAEERCVLLTGAKDPNDPRKWKIEVPASSARCY
PEFMVCCVGI*
>TCRU_8958 hypothetical protein, conserved
MKHIATQHRGVFGDHQLIHRNTRRPPKDQTQPRDQPRDREAVPADRDVRARWKPTLRAEK
RVNECVAGDDDVQRPHSGMHVAQEQQHGAVPPRASIERDVRHVTRHRPDQHRQAHAAPAE
RHVAVAQPRQPAAHCLRNLGVHHVADAPTNRRRWRWWR*
>TCRU_8959 hypothetical protein
MAWPDVITSVLPTTSSWELKPKWPSNSNAPASSIEDDTFTCTRAPLPLIDRPTRTHCSSV
MLSVCSGASKLHRSSAIAAVKVTLTKHRPRTPGSGSSTELMLPPCTQRTSVSSASGSGSG
PRSSGTSAGRHVSPWPPAAHTHSQPLMLLVIAAKHTASTVHAPQSNTLTGAPTLSSSP*
>TCRU_8960 hypothetical protein, conserved
MTNRVDRSRTPSRTSAGPYRNPSRPGILGTYCDPPTVARSVEFTSSTLEFGGIAPRSTIV
PSTDVTFVMLTRTCGTRRAVLSLRPPIRSCAPPASTQWRSVTFSASANASIKRSSTATVI
GPLNTTESKHAVARPPPTVTDSVSVTPLTQPSAVSPPPPPDLAGGTSNGRHASPTPPARQ
LHTQSVNDAVSASKHASAAAQPSQGTTLTEGRPAKR*
>TCRU_8961 hypothetical protein
MCGLHRVGGKRFLGVMDGILQVSVDVWSSDVSDVLFCKLVFSVLESEEDERLLLLEDESV

GWRKLQKLWLRFKNGVNPSMPSACGRVNSSGLMFCRGGVLERWVVRNR*
>TCRU_8962 ATP binding protein-like protein
MRRSTLRCSILERHLRAIASKHFETRFCYVDVERLPALAERFNVMMLPTLMLIENKKTFH
SIIGFDEFGGTDDFSTDTVVKVLSHYGMVNERGMFSDDQSAE*
>TCRU_8963 tubulin binding cofactor A, putative
MSTDNADGGNRFIGRTKQVEDPLVKSLRIKVNTLKRNLKDFEFAKKEVIRETSRLESIKE
NNPERVKQQEGVLGEAQMMVPHSENRVRTALKDLKEFLNEEDLGSRDGELLRSAHESVEE
GERVLS*
>TCRU_8964 DNA replication licensing factor MCM7, putative
MTEVPSQEQAKKTSLAAAATTKYPNYLADRELCKRFFEEFRDLSGTLKYMEILRRIACRE
LKLFTLQLDDIAHYGQLYLAQRIQMNVMGYSEELCRVIDELIPQTEIVEDMVDYLLVEAK
AAGQSLPSLLTRRYELIIVPLSGYAEPIPLRHLKGSLIGTLVVLRGICIAATAVRPKLSV
LVSVCEVCAETTFQQVVGDRLTPLMVCQSQRCKLNNTIGRLLPQYKASKFTKYQELRLQE
LPQDVPRGAIPRTARVICEGEQTRIASPGQVIKITGTYCPDPSTGQGHEAFRASTMVKTL
FRALHIELEKRTYQEAAEDLKTRLEYVRRYPDKEAIIEKLTRSVAPEIWGMEDVKKALLC
LLVGGSSIANGIRIRSDINICLMGDPGVAKSQLLKWIASVAPRSVFTTGKGSSGVGLTAA
VTRDSHTGEVLLEGGALVLSDKGICCIDEFDKMDDADRTALHEVMEQQLVSIAKAGIITS
LNARTSILAASNPKYGCWRRNLTPSENVNLPPALLSRFDILWLLLDESNRERDAELSMHV
THVHLHGVAPGTVTDDGFYGSLSEYFGKDFLRAYIGEVKRIHPFVDSAAAKAISDIYCEM
RAQSVRHTNVVTARTLLSIIRLSQACARLRFSERVAEVDVREAGRLLDCSKISLQERADP
NGRRALTTSDAVIFSTIKELARSRTSIDLAEVRPALMIKGVDEVHLQRCLHTYMEVGVWE
VNGNIIEFSRE*
>TCRU_8965 nucleoside diphosphate kinase
MTSERTFIAVKPDGVQRCLVGEIIQRFEKKGYKLVALKMLQPSAEQAQQHYIDLASKPFY
KDLVAYFSSGPIVGMVWEGKGVVKGGRVLLGATNPADSLPGTIRGDFAVDVGRNVCHGSD
SVDSAKREIAFWFKPEELVNWTSHSVKQVYESA*
>TCRU_8966 hypothetical protein, conserved
MKGLCWVTRVLLKRKTPSTVSNEVSVLSSVTNTPFSSSCQAILRAVARTRHYVKRYWVTL
PQSRRTCNAVVLPGESPTVIHLNVEKVLPFTTLPKKIQKRIMDEHPPFFGSGVGILSTRM
KWKAVTAERLIRLLNEDEEDRALYIDVAIADQLGVKVNAKDAIDIRKQSSISVYNAEQLD
DPYKGEPQKGVALNAMTGKRLGQPAHDILLAVGIMRGYTSPMWVAEKQLKHLNLEVRESR
KGEGVLAPNMTGLIVSLSQLPKDAQQMLLKELRENHSDAFGFDLYFLYNVNGWEVMRSRV
LVKHMAAVNDSQYPYHFVNLRDFGLQNVKFADFAGECQRKLKPLGPEVLDTETTQDDKAD
ENKNEGRGGLALQIARFSGGRGSKGRGVSTKVFFAEDATLRRYYNAVCLSEPHLAVPAVR
SVAILNGKLIGRRDEAKLRSFALKHKFSSPIWVTPVGARRMGVGIEKKHLNKFVAIGAGA
VEDQGDDVVEEFYNLDDFADPNEILSIFPKKSKSAHFLLDSKWRPVLGKQRQDYLTSLKR
STPLWISVNECLMSGFEPKPESQSFSFPSEKRSTGSSGGIKLYNSQLTTDPVRVIGLATV
YTRPQGHTL*
>TCRU_8967 integrin alpha chain protein, putative
MRLRDILIVCVAIIFCIFGWSQEGGLIVWRNFKIPVTDSEVSKYVMSKPVVLDLMGDGRP
VLLASTKYGSLELFKTHLARVNSEDVFVSIRPSSSLKTLFRIVAIAAGKLSRTSKENAIV
VISDDFRLRRISPHDLTEVWDVPLSASWIETYHASVSVVPERIHEQDEGTVLVAMQVAGP
NGTELMLYAAFNGADGQARWHYTSDAENSIGEVLGEECNDGVECLPPDNDTSLRRNSIFK
SQGVKNQFRAQEKPWTFYREAIITLLPHRYSHPWDEHIHPHVFFHAKNRKKRSFRAGNRV
VVKYKDRLIRMNKEDYGALGERLGVMNMHGNAATTANKSRRRAANAMIFHSKNGIEVIHL
YTGSVITRLGPLKSSGVYYHDINDDFQVDAIGTQIGPRMEMHSRHGVDLIDDCLGVIHTG
IPVAEDQLFNATICDTEGFFGRLDLIHHFIDNDIRGEDAPHALNTLELIGSRSVLSKNTR
SVTPLVVQLHTTKGRDLFQVERHAVFMIDSGLVTCVDPSRRRVIWRSQTAAGFYGLREAA
EADAGMAGMSAKERMHRAVSFPHLAAYSFYRGQDESAMSVSGSERYLRTDPFIIAVGERY
MCILSTRTGRVLRTIALEHPPVAPVIVRDLNGDGINDIIVVTKKGIYGFVVGTQTSSDTV
TALMILMVALLAVLFVVREMSVADESKTEFLPTSVHDAHRAAHKMARRATD*
>TCRU_8968 ubiquitin carboxyl-terminal hydrolase, putative
MGDQAPNTDLGPLIGDALTKVNNDILFTDDSALPGTEKLHAYSSSVASWSSPITAVGNGT
CETSPTVEAFFPLPTHAPISPAEAYVRAIMRGMEELQEDGGILKSISRARNEVSPFKDGM

AVFEVSWFAAMRDLALSSMKAARMHLQSSAAELELPTDGKAEIDVEVARKSFLLHLGEMT
EKMVQRYYYQMFFCRRRFPPELQLLFGQLNERLTQNLLATSTGFPKLLAASSVEELDAVL
IHDFDVWISHYFPYFKHAISSGRPMQLIWGENNSLKKEEVAFQVYTTATRVNLKKNNNRL
KKGALFPVKWMDELLHWLCSSEDAALPPPGPFDTLQLVELSSDRPVKHILREGSPESDVI
PEELFDLFWGLFGGGPKYLVEGVFSMQRNIEERLSPPRVSLAFFFEDMGCQPLVLKRVLH
RAEVSEVMRRALRKFQKRHHNCRDSEGGKLDAELWYAALCAENGVNMYVTHVRGVLLEEP
QLVSNQRTTSVGDVVGQMRQIVPTETNTEAPELQFLLRLQEKIDRLTLEARGVCGLPNIG
NTCYMNSALQCLSNIRSMRRALFFLPLSEYVNPVVTREMVCLLIDMWSGMQQSVDTHGLK
TAIGRAVSRFDSYEQQDAMEFIEALLDCMHEEMNTVSAKRYREVLDSDASIPTQRMSEIF
WKDFLNNNRSFIPHLFFFQTKTRLECLTCGALTTLFENNLSLTATVVTPAKKRTLEIIVL
LPTGKRVRLRLKVTCDKKGDVYTTDIVRELTEKFCSENVVAVSTRVHAFSAPPISFYAGD
DDGNMNGNISSSENSGEKNKKGDEEEVDVGGSVLDGYRLIIHGDDAKPLPATDELLYAAA
VPVATELDSKREDVPEEQETQKRAEKDETRDEEEVRVWYFLKGRRTSVYALHEPCYVEWL
PAKVFSDYSSLARHLHERGRELGRRFLKERFPSMDEMQAPALDPITGEQLTGDDRRQIRV
LYQTHRHDTSHLIILDDSEDEWMKFGGMNAICQHSGESRVLLEYDDFLLAPNESFQCMLH
PSVCTPRRHSIRGFLPHFNEMDNAVTLEECLESTYSPDILAGDNARECSKCKARRDSKIE
RRPFLMPPCLIISLKRFRVHMEEASKNNTRVAFPMELDMTPYMDPESPVQNAKYSLRGVV
THRGGINHGHYTATALNDSCKRWVQYDDWRTSFLEGPSTKDAFILCYEREEVEADRSRQS
TGETSRL*
>TCRU_8969 outer dynein arm docking complex, putative
MATNTAAADADRRRSQVAVGILAAQAEVIRQEEAIKQLVADNERLKKEIAAVSGVPYDYV
KADKFSALKGEVDSLERRYQFEKMKKNELTRQYQLARIDLLQSRRLKGGVNAEKENAEAL
QRQVEILENRLDQALTRFNDAISYNKELRDHIGIIREERRVFQRVYKRMEDDLRSKKKLM
SERIEQSNKDLDERDGYLRQVEQLKKAINEQKQDYDGKVRELDMAMVEIRELREEQQRLQ
LELEARQYELDDFESTANTTPPAVGDTGNKRFQPLDDAADIAQEGLDEEGERESPAEDDP
DLNEVLRQLTEFAQNGDLLSLAKEYESLGDMNFSLYKYVNELTTSREEMERDICTLKSVI
AAEHESEEQQKRLIKDLEERLAQTEELLESLHLSTEQHKEVLANIRCVTEDIFGALGCTL
GDSNKALAANARCTESNHLQFLGKIEERATLIMCAFQRHLRNEARRGELPTPQKVKRLLA
PEGATSTTVNDTAEKEEGALERTAKPRGEEEEAASVEASLKPAGEEAETRAEAEAKSEEK
VEAKTEETVPLEGDEDVLTFIPMMNMAGERSVNAARLVRQLCLPSAHLGGDEDVEGLEEG
EGDRVVSHEEVRRQMERRLVSKREREERAHRRRRELKEQIAGQPNTPRKRQ*
>TCRU_8970 Soluble NSF attachment protein, SNAP, putative
MEGKADQLVEEAEKSLKGFSLSKYFGGDKYEKAHGKFIQAATQYKACSNYAKAAKAYGRA
AEMSMASKNEVDLTAELEDAARCHVKANDKDAATRLYRQVAEYYERNQMHIRAAKTCVSL
SEITEGSAQIKWLEKASTYYRMQGSRVSADELIQKVAEAKARMGDYKGAHELYEQLARET
LNDAVMRGGARRLFFMALLTQLAGITRETFMEDLAALRERFEEYQDLDTQFDHLTREHML
VQGVIEAMEVESVEKMEEAIADYDNICVLDELKEKMLLRAKRALVGRLDDLR*
>TCRU_8971 TFIIH basal transcription factor subunit
MSCCVCILHSSGVYCSPELLSQAAYGVSAMFHSLQTCSADFIPSVAVLRANPIEGVRYAY
TSCVNEVPHDAEAKDEDNGAAEQLKNDALRKTGLTARFSGRSVLCLQQAILRCGDAVDST
KKERSENVDVWRCLTGALLTACCFLRARVVENAPSEAASIGFSTAPSARGYLMVFSDVHD
APALSFASECSFSAAALLLTRLHATVHAFGPATLCSVVGSRLQALTRSTGGLCASHFALS
HVGYMLDGDVAERLPQDENVTDRQAQERLVERYVVRPVNLPQGPSSMFNADESNTSYLAW
LCPSCMTVMVRHPWEDEAVKNCPYCSLADGTDGES*
>TCRU_8972 Cytidylyltransferase family, putative
MTTDKVKIVSTNIHTMSGDTNLFVRSLTIALVGPTAVLLAAHNKYTCALLIWFFFFFGML
EWSGIKRHIKVAILLDSERGGDDSKHEALPKEYAAPVFSHSAVIIVKATFSSLVIVAACI
GVDVFLLFLTLYFLVCTLLTLFGQNDPEKGVSVARQTADNVMAQSASTRQVSLSSEKSRS
EMLLLFLREELRMVAEKGPAELFINFCLEYFGFVWITGVTYPILVYDIEGLGRPWILASL
VGNFTLDIVALLVGRSMKGITHPLCQSISPKKSIEGAVLGVLAGAFIFLWSVNFASGGGV
LERGWGPFFLNFTAGVLLGVMGVVGDLLQSLLKRTARIKDSGYLMPGHGGVLDRIDGLLL
VFPTMYCCMRVMNLFS*
>TCRU_8973 zinc finger protein, putative
MSTSSIDGMDGLIGAATAFLRAMGDDQREGSIEWMERRKQALFEGETRDEEMGVSELLER

VHERLSGVGKGIAVGATMPTGVDAKGGTYWFGKRPLPGLTEEEVDAALQWLSEEERRQLA
DEFDALRNDGFVILRTRHVDPAPVGETVVKRDSETHDEDNGRNSDNADIPMSPNRSDGKS
MFFGGNLLEVSYDEEAWPLSTRREICAMAPEGQEMEKKAAASFDKPNMYSRDAAAPKTVF
SSDSLECATPSYEKEQSDYIRDKVRMMLLANRVAKDVERNIVDTALGVAQEWRKERERRL
ELLLERQTEALRDAVRVMESLKTLHRRAMGEYVENPYLMQTWQRNESAQVCHKCRRPFNL
LVMRHHCRRCGLIFCQRCSSYAGMLPDKNAKRQVASQWLRLCQDCYEICCEYQKCVSTSF
AVPRGRCERESRAPETPSSILLSKYPNDDGVLEDKLPPFYVVLPEEWYTVRTITASGWLN
VIRNVPYMFCENFQDGVSSLSRMARPGLERLLSSTTESVKRITDEK*
>TCRU_8974 CS domain/TPR repeat, putative
MPVRPAYEWEQTEEEVLLRVSIKGFKKEAIDVFLSDVLVKVNAVPTYLLVLDLLRPIDAA
RSTYYMDPEDRTNLRLRLRKQEPGIWPDLCIHADKNDAAAIRERRSAAVKRAEDDYNRRL
QERVGKREEERRRMTEEQWEVEKAQRRLIEGRVREERETAEADLYVWEDEQKKERQKLQG
GQQFPAAAAIPQSPADITLLQAAEANETAAPCVRHPSTVVVPVEFTPKLATMPTRSRGEE
DYYRRSRYKPTRIEDSPMFWKERADKHYRHQEWQAAADAYTESIKRDGAFLTCVSNRAAC
FIHLFEYKRAIEDCTLALTMLSNTPASELTQERYRYLMMKLHARRGAAYCWGHCCEKGVE
DLRIASAYCNPEEDGDVLADYQLVESYMKERGLLETKDPLEEKLREASTLYYNGRYAESA
AVYRDVLEANPYDVKARNNLSAVLLQRGLFREALEEASRVLSFCQEVADALSCAGALSTN
LLDSDDDDDVGSAGGENADEMVRQRKAAARKVGERSGHVYALLKACVRGAAAHCGLKDYR
KALQLLEQAVRITPYDDDLQDDYNRVAEKLRMETLIAASTAGS*
>TCRU_8975 prefoldin subunit, putative
MIDEEETGEEMTLTGAELFHYLTKRNQQQLEETRRKLQEYEKLQEVLQNLTDRCRVPVLA
PVAGGMAYFEATMDYTNNILVLLGDGWFAERSAKQAREIAGRRIDFLCREECALVAEASA
LMQRQSLFLAEVPNAKQAMLEVEASKEDAPHGWRGGGGDLTPTAVASAAPRRAEGSGDGA
TEASWPPELRDGDLAVIDELDQLTEEELLEIERELGERIEDDELVERIMTERIIAKKEKR
VREELRKGRGREAQPSAAVEASQEREEAQPPPHFSKIVTNSSPVFDTPGDIGRAAAVVVK
EASAGDVNTVDAATSSRRRVRFHDVVDVVPPEGAATAVKLSPAGGVLERPSSHSVVGDVV
ERQVTVAPSPTLSAVATLADTAPKRKSLFRSEIEHGAK*
>TCRU_8976 proteasome regulatory non-ATP-ase subunit 7
MPPQTKGTTFRDNEEEEELQIEEPVPMSPLISLLHLRHTYASQYVDESKREEAKAKILKE
AYDHNMAPYLRFICESFAWSLEESKMQEMDAINAKKLEELDARLKDAQENLGDVEVRESL
LAKCEHFARIGDLQECLNFNMECSGKTLAAGPKLDLCFQRILLGIAFSDNEIAANGVRDA
HRLMKDGDWERRNRLKVYEGIYHVFIRDFKRGSELLLDSISTFASSELMDFNEFILITVV
ASLPVLSRSELKQQILDSPEVRSANIKDVFHLITVIYNCRYKEVFSALDTVCQHLRGIVY
LSQHVNYFFREVRVLVFTQFLDSYSSVTLNSMSAAFGIPPPVLDSMLGTLISNERIACKM
DRVSDSITTYRGDTTNFDYHRIVKNGDLLLNRIQKLSRLAEM*
>TCRU_8977 RNA-binding protein, putative
MGTGVVKRKPTPSALRKKKAHQRIRKQLRRRLEKKRPNWKAALARAYVGPGNSGKKREPF
GKNKRKRPRDADVDGDAAAAADGDGDNDNDGEVQSDVDEEKQERMNQRDPLETQLFLKRL
PLDTSEEEMMKFFESRFGKVRRVLLVRNRATKTLAGTGFVHCGSVELADKIFEHAQQNTR
ELAAANREEWQEKTTDLSHCQAKRMRFKLRTDACMFRDPFLNIRETRFTVHRVLSRTDSQ
EASAALQKKKKRTKVAADDPRHLYLLREGLILPDTPAARGLHPQYLTMIQQDYEARKDQL
RNSNFFVSTTRLNVRNLPRTMLEKEVRAIFAAPVRSFLKENKEHMDKDKWGKYGPIKNVK
LVKDSAGTSRGYAFIEFVNHPIALHALRTINNNPTIFGDRRRLMVSFAIEDINAIQKLQR
MREIRRQHQTPRGEKSNEEGCMEGPAVHADGQGRTVGGKQKQQQPPNKMKGRKAATGNRV
IGRAAPEE*
>TCRU_8978 hypothetical protein, conserved
MWSSEAPPGGPPEFPTFPLPPGNNGAAQSRSYLAETGLQGVAAQYPSESPIFLQEAHTRR
EEYANEAVQATAEHWIHEQAQREKMRQTARMETGFMFGEATGKEAEECEGSLEFVTGPPK
FVGRIILLLAVGLFGAIPLMSPFALTVFLTGCIVTYAADFAGYRRGCIIAIIGTNGLFGL
SLFLSNLHASISSVGPLCMLLSLLGLLLMAAMAAFLHFHWMQVSFPELICFMERCVLGVT
PILTLPSLLSTVTALVGSRHAPAWFMVAMCVLHKSFYGPLESSFLTRRRLVRLRQENDNA
PENEMVEEVESVQANGRAEAIAFTSLLVYLPFLLYILFQSSFIDAWLPNTLNAVGMICGP
VAYICWDPKHSLWFLISKKKSLRDRIGYDPLGVHETVSMYRKPFLILSVAVSLHWSIYRL
LHSRYRFFFNGVPPPFNGVCLAFAMYLGLYAGYQIKTLLDADTRGEDTLSSRYMRRRVFS

VGATALSSVFFALSAGVPGAFMVLMVLCVSSFNLFLLDRTNSGPMVSFTVFSSLLLMWWM
YRMFSFIVVDLHVLGESLTVPTPVLAMSVLWCYLLSCVAFTLSFSTNKFPFVIALFVHSL
QVAWVEHVLYSQKEENVYPAVLVLFTTAVGVLLASRLYKNETLGIHEAALIAASYVAKLL
TFVVEVTGSYYLAESSESEKRYYHAIEISVTWWSALFAGFVLVVFELKKGRQLENRYARH
LTALFVLSALALTASTTRNFQRAVFEFFAQTRLADSNSIHVILGTSFVFFGLISHPFFSR
HENLHPFLYSLRAVARGALVVGIIFLITQPTRITEHEVEFEFDLDFVDEDVSRYCSVLGM
MLLVAGRFVPMNSVHFIFRALYWFFTTVFLSVGLAMYVLPVPTLLLFCGMCGFVYFSLLT
LDVAHYRKMSYNEGWIVYGVSVCFMFFSLVITGRVNLKEYAGDNPPLVWEIYTAGRSRQL
SVAGVTSLFIAIILKFRVSGKSLLPCALPLTLELVEQVGLLVNYSTVIAVSALTTHNIWR
NGSEPGLHVATSLFLLLLADDGVLFTGLGRGQFRYFPVLVYVLSVLWLCLIYDAYASGQT
AVGGLWQCIRSIFYAMPVVPSHVSLLLLLWFGRKRGGTPTSGVFVFVVLDMLCLLLSTRK
TLQWMAIIGVCGQCARLFEAQFWKRRLETIL*
>TCRU_8979 nucleoporin Nup109
MTELRRITTTHVDWASFACGNILAISTGRNRRRSIRDSRVLLISASGTVLADVKLTDGIG
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LRVGTQDVAVYSLGTGELFVRVRDGAEHMVHNTLWDFEDARVMRVVRGRHSLEVLALLDD
GSVALVEVREDEDGFLEGCCRHHLQLSSTAVPTQAVFACGLTLWVLCDDLSLFGYWFQPP
VSGEDPEPVRFFSEQLFPPEETENLVRALMAGETRTCGVHILFQTPKAVHFRTLAVHIPN
GPYQLPSPATEWSNGVLLWSGYIHSFLFRQCGYELLVQSELGGSPLSMMSLRQNSSILTF
GELQTRLLSHQVVRAAPLELAGLREKCELGVQELESVVANVSDLYATEKALSQLLHLQHA
LVATLHRERELNNEVQSSQSVSMHLIKRLHIVYIHLSIYRLLCSTGFEDKLDVSLREALR
LEEARHASCVCQADLRARFEQEMDLTSVSTMGTLSMWGSPDTAPVMCIDVILSQLSCSDL
CSLRSVVQQTTTMVPAVALLVLYCNHAKKQQEGEQRQAEEKGSTAVRYEFAQRDSVRGEF
LETFCLPLTMDFWAYLSFVADHCLNPVDVGAAYGAGCPPLMDLVPGLINGLTYSGAYELV
FQLTGIVLTLSSTREMDPSVAVKLLFLAYRRGNSKVLEALYRRSRGTVWGNAATHALGLA
ALQTESVKLLSGLITPQTPEETVVESILRRCPNPSMSNVLLMEFYILMRRYADALKMCEK
TVSCHSIDAQRVQVIASHLRSLMPNGNASYGLFRGLDGGENVLPPGPDAYHSRSSLRREL
PPLIPFYSAAVSGDPLRSEEQELEEDVARTVAHISSWRHDKSPLDAFGGSVRRGVTAMKF
TPTPVASLGIFHDGARSVSLPGRSLTPQQQQLPSEPSMSVRSGAEGHSTMGASSTTLPPR
AVAAVSQEYEPLYCEVILKRSKKPCRRERPCKYHDNVRK*
>TCRU_8980 hypothetical protein, conserved
MTDCQNEAAYYPTVDPAQMGPNSDLIAAIPYLCEFRLSTPHVIYKPPTVLDFRAAGAIPL
EHMSESHNKLPTITLSAEIAPYRSNFREFLATATSRFLCPPEREGAEAISEELQFGGHDT
SDQEYWSEEYWKLLQTEELDSAGSMATDSGFQSLGGANPRSTKLASTTSPSRRRRGIARR
KCDFSNASHRRGERENLHGICPSQRSACEDVCPVPSRVRRHPPSGPSSRAGAGMSRDCEG
SLGPYDDSSLIQPPKKAGVTTNVGPKTKRPRKAAGRVLNSLSAKGRHGKGRNSVGTEDAF
AVHPPGIHDDSLLLNASGTGDLDMSISSLREGTGSGGLNIRTTTTGSFSDAHKARVSFSG
SEVPISFPPVKFAPIVQNVFTAPNISPVAHGARDAQTDTLVSAPSSSNIHHRDDNGGSGG
GGVSNSNKNAKKKISTTSVNETTVSRHNSGAFFPVEAPHVERSQVLSFSQRKDVAPAGPS
VGGDASAEGPVHPNPLLGVGKQTSLKCCTLM*
>TCRU_8981 hypothetical protein
MPLPTPPSPLRGTRTREPSPVITEAAPGLPLRQPKCLMDYGRNKPLEEGKGESGSNTRLE
DSCLAVGDGQSMRRPNPTDKLLTYRRMRSRLQQGSPGVGYTTSVIQDDLAAKRAAALEET
GMPMEPFFLARLPKEMTGYIIDIEEQNRQLRQQVIELQEELQQEQRQQKGRIIMGPYRQP
ADAVGGNNHMVEVDAEKGEGYSYATDGFPLISGGSLSKEERERYMNDVLAQVDVIVHAHR
SQSEAMILKYKQEAEEAKIALKNLRELIALEGVDLSMLPAALATLSGPALTAGSGGDNNN
GNGSGDIRKTSTKFSTPSGVDTAIAGVVAVMNEKCAALLSEAVDVVLRDLLQVEAGDDVP
TVVRQSVQRGFELLARHLASVVIEYIRQCTEELRYTHKERETVCRELREELNLSERQRMR
TARQYEAEIRALRDELHAFHVAAAGGDELRGTIHERALEEYTALLVDSRKEAEALGRQLE
EERSDHATTCLRLKSSLQRRSLEFEEAVVQRAEELVRLRDANIAELQQRLDTLSHLEERR
ACGRSTKAVQVQAAESIVLDESNYMPNVISVASSLKGASPLPSQRLATPTQSGNHVTAAP
FPSQLPLAPFTQPPMTPRIPGRVECAPQQENSFEEEVWAKTMELLAKYAHLSQN*
>TCRU_8982 Guanine nucleotide exchange factor in Golgi transport N-terminal/Sec7 domain containing protein, putative

MSLSLEALNSFLRMIGRTTGGGVTIDVEFRETLKQALVAMEELARVAQEGRANFVAAPVL
SALLSAFYVKKTRVVGAALSVLQQLIHDCRISYDTPIILYQYQRNKQALRCGEALFCAVD
DFLVNTADAALQLKGLEVLHDLVSDDNFAYLTGSCVTRCVRTCYQVTLQSSNEAARIIAR
DVFVLCVLRVTRAFVEATPSERRCGTFASSTRLYDCMQDVEPDAKFTPIQIGGYATPFTD
DVVNSVDKTPPLGPFNSYAAEEASSSAGSLQPREFLQYSCSDSIVASALSVFQGGKLPRA
LEDMLLLIKYVCRLASRTCSGSGSTSEKNPEVRVRQIALEMLESLFLEIPMANCDAEHTC
ATWLTMVVAATKYHLLRCIARNLSTIVPSSFFTTSVRILTLLLRKFHYHLARELHALLAV
MLFPLAVSKFSSFSQKHAVLSMVRELVSIPHLCVSFFINYDCNPAFDPAAKYGGMLELLV
DFIVEMTYMDFFDPEWLSLDQQQLLRGECVSAMHSLVDSMLRWVSEDPREYTQRQLREVV
GQALSKSSVGCQGVRRWHEMYLSNGWGSGGNGKGTGTSELLSADLSSSSSSSFSSASAAS
LKGDGRGKPQNWGKPHRVGYHWKHVHCLLQNKRIAQEAMQYINRGHWRDGMKLLEQRGYI
SHADEATRWSDFARFLKTYPGIERSALCSIFERVLKDSDCDRILREYMQLFPYKGVTIDV
ALRDTTCEFMSWERPTFEAQVWAVIQRRFGEAYAAQNPRSITVKDADAMAGVLLFLHTSL
HNENMRNNRMTVEEFVRNGNECVDFAFLEQDMRDMYYRVAQRKWELDELQRTPRQVELEK
KMPSLSSKIRQQQKCSSFSSVADLANEETSFSTAMNTPGNSKSFRKDNDESEGSRLLDNV
VVPYTECPEGFKLRESYHQRYVDVATQHLRQLECEHRMQRLEACSLQPYILPQYAQHVRP
MLLMLYPQIAATLYMGFRVLEERPIFRLILSTYDMLYDLAAVFVVNLSGLRVAVERQIRR
WLEDENAQRLLPPIRGTFMLPLMNLL*
>TCRU_8983 Rhodanese-like domain containing protein, putative
MTANYMYMEPSELVALLDDEVQRNKVAVIDCRDEDRSDGFILGSIHFPSRLQSEGRFNEL
ADTLEREGRSIAVFHCALSQVRGPKAANRFAVKLYEKGMCALSVYVLRGGWDRFHAMYGE
SRPDLTS*
>TCRU_8984 amino acid transporter, putative
MEDNREPNNSTPGGYYPLEIEFKAMEKRAERSPSNSDGNDYFLCAEEVQQERKPETCLSR
AKAFTGIVVPYGGLVSSVFNLASVCVGAGILGLPAAANSSGLVMAFIYLLVITCFAIYSL
HILGKTMEKTGLRTFESMAKQLVGDRFDYFVALIRWINSFGATIAYVISVGDILEPILMN
ASGTPQFLRRTAGRRLLTAAVWAVLMLPLVLPKKVNSLRYVSTFAVAFVMYFVIMLVIQS
ARNGLGNLYGDGEDPIRLFNTGNAAIHGLGVFMFSFLCQINCYEVYWEMKKRSVKNFTIY
STIAMILCLILYIMTVFFGYVQFGGKVKNSILLMYNPVTEPMVMAGYAGMLVKLCAAYAL
QTMACRNAVYHCISWEVETLPYWKHFIAVIALSTVVLLCGLFIPNINTVFGLVGAICGGF
LSFVFPALFYLYSGNWTLRSVGLFDYIATYALLIAGVIGIVFGTVASIDDTITG*
>TCRU_8985 hypothetical protein, conserved
MSRADKRQHRDHVVGTSRDASVRLYAFATTRPRYQVVFSPERPVIVLKTRKGSAHQHPCS
QWAPLASLLFSQRPSTTHAMYVVDTTALPEAMEKEERATPNVGPVIKRLSNVMAKLNAHE
ATMVAAGVSAPLAFKYVIMGEKTLGHTDRLVRRLIILCPASIRPFQQIARDAGKRASGVE
YPKPQLVVLLSDESQAREWREWLQDSIANTNSGVSFLLESWSLSTNVKPSFFESVARESG
SVADGTTVNLETHFSTPHVFRIDFVLSRESKKTEQRVTPSPLTTTGCDDDAGDDGLEADE
AEGERSLSEGSSLEECDCCAESSSVLGITNLQHCRQPTRVILEGRIMDAGACILGTTQGR
VRMHHLDEAAKSSALGANGLKLKKGLAIRVESSLERDEIGRTTLKALRLTPLTRMQEKRS
MTVCSMAEVPTYNVSTIAHAYGALLVRGRKCVLVRGFSGEFDGMRLPYLLHDDAQESAMD
CAVRALCERCDISPDNFYIPSCISPVCYYDRVGTDGVCVCVTMHIALAVSAPSGAARDAM
EEDESPEEPYDWFGYAKAMRILRTEKEREALQELQRCLRRAYDAGVYVPLKGFGVFGDDV
VDATDSSKLPTSNLLAGLELMVVCAPGDREGSIMQLASEIITECVVRVTEPTSREEIEEA
AIATRRAGAENLVLCLSCDLDVNTFSEEELTYWAGRGARPRMMTVLLPGVSEMILQQRDE
AAAAVFVHSVILSDVLLTVESDMERLSPATWGLLHLANRLNSDLALYCGLTARRPINFPS
PLMTSAASVSNLSEESLHEITIRRMGRPLIAARLAPLLESGGLRGCCRDATILWAKGDVW
LRSRPHARGSLTLDARFCCFALEEGDPWQENEDSTTRENVIVLHVWATNAAVKELECVMG
DMLDGMLCGTSPPGSEAASEDGLPPWD*
>TCRU_8986 Sybindin-like family, putative
MTVHLLWIINQSGQLIAKSSFTAPENIGELGAKPDLQLTMSSILFSTYGMSQELTPNANP
VDSAGMTLVECEEHNIHIYETPTLVKFVLVSDSRTRECNALFRELHSLYVEYVMKNPFHI
VDEGGIGQPIRIAAFTGAVKRAVDRYHAAGVLTATRK*
>TCRU_8987 glutathione peroxidase, putative
MGSSTVFAYSALMGGKSVALSNYTGRVTVVVNTASLCSFANSSLQQLTHVQETYGPRGFT

ILAFPCAQFANQEPKSNEEIAVWAQTCGLNFPLFDKVKVKGPDAHPLFQMLQASLGPIRW
NYTKFICDREGIPLVKLDSSSFLEELRRSIEQACGPQRGA*
>TCRU_8988 iron superoxide dismutase
MVFSIPPLPWGYDGLAAKGLSKQQVTLHYDKHHQGYVTKLNAAAQTNSALATKSIEEIIR
TEKGPIFNLAAQIFNHTFYWESMCPNGGGEPTGKVADEINASFGSFAKFKEEFTNVAVGH
FGSGWAWLVKDTNSGKLKVYQTHDAGCPLTEPNLKPLLTCDVWEHAYYVDYKNDRAAYVQ
TFWNVVNWKNVERQL*
>TCRU_8989 retrotransposon hot spot protein, RHS3, putative
MSGRHGEGNDDNGTSPASTVSQGRRARARAESDGDSGQPAVPRRRVREKQRPYWRLDSEV
KDVLLEGELEVEPIRLNDFLRGHIGPSAVVDEEYNVTMEVFLVEPRNYVQDPQLLGQILN
LTECHALQETYKIRGDTYRLYREGVIFLEQWGNFERKDMCTPFARLKLNAALKVAPKQGR
AYMQNGCYESVCNAGWHHVMELPDGEGTGMEVHEGKPPQSWTYKEVGNTLEKDDSVEQSG
SAHLRLMVLTSDWAWPYSWLLSKPIRDCYVNCEVDRVWQIVKRDLTEWFGNFDLALNSSP
KRLLIGAPGIGKSMAAGSYLLYQLLHYDVKKLQVVAYRIADRTFMFDKATQNVSHYIGKE
AGLKAVEEFSGRGMRGYFIHNVAEPIHEPSVRLLPRGWGMIVVMPPEESADRGCKKHLRG
RRIIMNCPQESDVKAMCVWKKRDQSAEAQVEYWQEVRGYMDGMGSILRDLFSERDANARL
SAAREPWNGLPHQMLMTTLA*
>TCRU_8990 kynureninase, putative
MRNNATEKLLSTARAEGLSITENGFAEFMDRTDPLHEHREAFHFPKRRDGGDYVYVSGNT
LGLQHKDVESNVGGVLKKWRDLGVMGNYQHPNPWEELESLGRKEIAAIVGAQESEVITMN
SFGVNLHLLLMAFYRPKGKRRRIVTGNHASPSSTYAIISQLDSRGMNPAEDLIYVSAAHH
ESWESSPVNIPIEQFLSVIEKRGDEIAVILMSAVHFLTGQFYDLQTITKAAHEKGIFVGV
DCSHAVGNVPLKLHDWEVDFACWCNYRYLNSGPSNLGGAFVHSKHTSVENELKPLRGSWG
HDRRNRASLHHNFEPAEGAASFQISNVSAVGMMAMLPSIRLMAEVGMGPLREKSMLLTSY
MELLLSELVPQGSIEVITPVDPNQRGAQLSLRILPNRLADVHSSKDAYECNSGEDSDADR
MERQLCDKGVIVSHCPPNVIRLAPVPLYNSFMDVLLTVRAIAECF*
>TCRU_8991 hypothetical protein, conserved
MGTVALEESKIDDPTALRRIISAAQPCQSHVGRMMDASRAHAHIFAGIEKKSHSVAKKER
DRQLQLQREYQTAWEVAAVRGLQLPTLRTLAPSFTKTADEGSADMGGTVIGGAGYNTIIG
MVPTADTVRRIADDDELISSFRPYRIDALRAARQAAATEDSAPHPDDARHLEPTLRTLST
KHLVDAAAISDEIAQKYWATASAFLDAGVPEEGDLAACSRAVSLAEAQQPACTNASRRVA
SKGTSSFLTTDRFKTSSGIPGVRQPDIGHYHLRYSQVEPRVVGGYMSPIEYAAPQKRQQE
EVSSGTPEGLVEPQKSSVSVTLVMAESTKTFGVSTVAYKEQRATPIDTTTFSPTRSPAEV
KGSHMFISKTARASPALCSPAKDLQYYPYADVRSTVKRSRCPVKFDVKLTERRHECMATS
ATVGMYNVATDISSHPHRLVCMDRDTGREGHWLNKPPAYQSVPEYIDVTNALNMVRPRRR
VVTMAAQVPEDGHDERPKAPDNTVSIERDLNFPKSIFDQCEARRVRRFSTMVGRSTSAPL
KSCEAPENVEFTQVTARTPCAIIHAKAPGHAPLHRPNPTEIGEVPNLRWVKPRTERTVDF
GVVSTVSLPPLITKDLWYDTSNRKLVESRVKGNPMIETQVSREKRAKIFSTAGCGAHTVY
NIDLPRRGKSVPVFEKQITKETQFCGHRLQSERWQRKYPRAPGPGHYNVSYRLVE*
>TCRU_8992 Leishmanolysin, putative
MNGVVSSAHGNAVAEEVVPAAVKLHADRLLVQPLEGSLVLPSLATGSVCSRFTVPAEHCS
AGAANSDTVLYVAAAPGGVWALPCATLEDGRPVAGAMNIARPLCFTDASPPASPRT*
>TCRU_8993 Leishmanolysin, putative
MAGRGMARNAACVRGGALLVVVHSTTAAMAAREHHDCDDVDGVEQQDGDGDGRTLESHRS
RCHARGEWMAAIGVPATARS*
>TCRU_8994 hypothetical protein, conserved
MPAKRPMDSCPIIDPALDVRDADAVIWRGECFSAVPGDRPSSWCPDTLPTNTTDARDPEE
TYLSAAMHAALGCLVMQVRLRVVEKGGVRWVPCTDGATIAWATRPYDEGSVACRDHAQVC
AISAAAGSLLPVVPCDGEERVWSRTVPPAITGQGLRGGIRPRCGEH*
>TCRU_8995 serine/threonine protein kinase, putative
MLFNVSDHSRGATLPWCDELLGRVAARRWGSAAVLVEPGVARRPAGAAVDCPLLRITRDA
ARAMCAAAGDGRRPSSVCHGILARQNCSPCDDAQTHPFDFLCPIGRGNFGTVLLVQSRVH
PTRFFAAKGVTRLLESSPFAATEQQDGDEAALEALRQVFSGKRSEPVSHFPALGDFLREA
QVAAALPPHPHIARSHGVVLSPCVSRRAEEVAPFPLQCASPQAAVGAYMLMDLGSGGTLG

DFFQRHEMHIAEEHLVCWLGQLLRGLACLHKGGLIHRDIKPSNILVRRRASSAWESDVEL
FFVDFGIAALVADSSCETELTVIGSGVYCPPEIAKYWGYRKRCPYSYASDVWSTAAVFYL
FLTCGAAGVDDGMAAVFSTDASPSADAAVTAQFRVARGEYPTLAVLKQVPLLDEEALRLA
MEKLATRRAGHTAGGGADGEPDGVDYTRYTTVDGEGTQACPGKDTDVWPAWVFSPGIQLM
ARRLRVRELSLEFLSLIDSMMAVNPADRPTAEAVLLDSPVFGMRMPWWEKVVEKAVRRVV
EGKENVLLDVCVGDSDEEEEEDEEEAALVRRTMMPLVLPAENHGYVPHNVIHWWNVDLTR
GEPDHTKWLSPTSLLASLLTTVRDLTGLEATRDAQDPVLREVPLYTATSLQFVERVCVPV
RGTDVSARKIEDGPLFRELEAGGHSTGFFIHVQIRIRAIARAGQVLMANGWAEEEDVADQ
EEMARRAMEELVATTEKWLLSREATTGVAALRVLPWVSWHLNEEEAGTDGSTQHCFIVEY
AAAGPGDGQPQPCANESSVTGEVSSVFRDWRANLTDGLQRLCCDDATAPDETTHDGASNA
PRGVLRLEEKLEAMLDALEAVESELMERQKRNEAHQGLLQGHVVHWLSVRAAPSVERCME
TLQGVCGGGDVSSQQIHEWILTTVFTSEGAMALMPVLRI*
>TCRU_8996 methyltransferase domain containing protein, putative
MIVLNGISEEQKKLAVVGVVAAFFSSAVTAAVVRVLSRQPLKAVEEPPPVVKVATEKNKC
ASEAREEKKEGSGMYKSELCARQYMEFHYTPSRTSYAQRLRTISESFDFPQRIAQKFKDF
FPEAKNEQTRALEIGCATGASVLEMSKYFDSVIGVDYSEIFIHFAQEVLRENSVPHVTRV
SFGAVDQGDIEVTRHVRLSHGLFPKRCQFFWGDAMNLLGGGGAKANLVGRHSSRYDDVSW
YQVPAGELFDGVLVSNILCRVQDPRKLLDTLPRLLRKGGILVLASPYSWSDGITPKSKWI
GGLPDGPRSEDVVKEILMKNFELLNETDEAFLIRDHVRRYQLGFSHCTVWRRS*
>TCRU_8997 hypothetical protein, conserved
MLAGVKRRQEPDGSGARKRRRVERWQQLIPDALDAFLSDVLSPPLSSRSLTRPSLTANER
TLLRLLNKEQQLADRCYQQHVALRDRVLREAQTLIRLAAEGTNDDGNRLLGKETEKNWGD
DGAERLFTGHKEGLMDRERKGERLCAVTTGRSPVKSVRTTDLLESEDATGGILLSPTPEA
LGTEVKSVSAVKNITPMKTVTMNATATKSLPVAAAIELTCAGCGEQGGELFQCRHCNLLR
HEACDGPKAESDTGFCAICSHELGLSFSSGGLRSSTSTEEREGLDEDDSSSLSGFVVHSS
DLSEDSLTTSLSSSSSSSSSSPSEVEREERRVLLARAQERKKQPKKQQQQQRRQKQQRCR
*
>TCRU_8998 retrotransposon hot spot protein, RHS3, putative
MQQHDFNLLISELTDYLISENFGRCTVFAFLNGSFVSAIERRPRELRPSPQRRSHRCALA
VYSRERSTRHHVLPPLEHFSERIDVECGVLYVTEVENFPLVDAFFFMESNPMTLVGLRMA
TVGEHHRNAGTVRQFTGCMAAYFYGWEELSQDMSWEIIYVQQADSTPMNDWRRCDVVNSD
IVSEKEKQKIAWFWEKVRQHQVSISF*
>TCRU_8999 retrotransposon hot spot protein, RHS3, putative
MSTASKHRTTTSTVRRFTECLAAYFEGWEELSRDMSWDIIYVQHEIYRPMEGRQKFEVVN
SDNLGDDENREIAAFCREKVRQYLAALSSADARRGEALRR*
>TCRU_9000 retrotransposon hot spot protein, RHS3, putative
MIVVTPPDKNNYEWWAKQMGAEEFIINCPEENDVKAMCSWMKRNQIPQEQAEYWKEVRGR
MNNVGPILRSIFGKQAYDDRIKACQQAVDGMNALKFEGYLDIGYCCLSNDSDLSRKLVKV
VRIRREYNIESPLNVLISPHVERETLSRLESEMKQSDFILLVLRFWDYVPPYLIKKYAVS
AFLNKNLLRAIRLRIKELRLPGRGESHRCALKEHSDKSFTRKEVLPPPERLSNPVAMDHW
VLYEPKVKNFPLVDGFFFVDTNPKTLVGLRMSTASKHRTTTSTVRRFTECLAAYFEGWEE
LSRDMSWDIIYVQHEIYRPMEGRQKFEVVNSDNLGDDENREIAAFCREKVRQYLAALSSA
DARRGEALRR*
>TCRU_9001 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MLQGKKASVYIDGTFLRQEEVPLTGEAPLELVRFCFGACGEDAGQKTKVTVKNVFLYNRP
LNSTEINALKDKAHTLNGPGGALAGWAALEGAAAREHAAVVGLTSAGSGLLPLLLLLLGL
WGFAAA*
>TCRU_9002 hypothetical protein, conserved
MTASASAVTLRGIPQCHGENVEPTVRPRSASESGIMQISSVTSSCTASEPRRSDSIVERE
SVATGTRVGDRDAAARRGTENCLWPCSVTGHSARQKYARLPAAAR*
>TCRU_9003 Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MGVRVGSNGEKKLIELSYGNGKKWHVLCGDGKPTELDSIGETETPQHVVFLLRNGTQCTA

YVDGRRVGNAECALGNGESKEISHFYIGGDGGSADKKESRGDVSVTVTVTNVLLYNRPWD
DTEIGAFNPNKANIQVEVDRPVEGEAIQPSGGRPEEQRQLLGSSGAGGVSAPTVPSATIS
SGEESVMQVVSGSSSDGIENVGGASLSDGDAAVETGEEGTNVPEEEVNTQVGDVKAAALS
SSLGNLSQGNNSDAGSGCGSGLLPSLLLLLGLWGFAAL*
>TCRU_9004 hypothetical protein, conserved
MSVTGVFSKGRGIGHAAVTSILRYIPRARVPWQPSRFGRENLSASDLAVLWSRGRYRDGP
GNYNSGYHTEKTHVLEDNTVTMIPKHELEKYMPDISIGPKALVTPVSLMSARNGHRVTHD
LLHSYDPHIGRLDKPAVVDHDNITVEDPNRVGLNAATLDCRGRIYRWLRRGPFFQEDHYF
RRSLRLNRDGTVPTAAHEAPLMRKIVRLAQRGHLKAACEEYRRITTVPPVEVYRALTACC
IPGGLIADAVAIFEDGNSKLFYVARDGEVLHNVMRCAIKAKHRVRVMWVYNVMRGRYYEN
VVVRAEIDPIWRYRIALLALEYFLDHNCAEEAGTVYSYLVEEDLLQCDVHLRVGLHMREA
LSKGKSVGLSDELLRATSLVTDVATVAPEVARELYHRHVEALRENEKSNGCDMNTRNDGA
TGRVWSAHGLLTALDFKQNDDALPWMQQNFGDIDVASVMRWARFYHSKDLMAKDRPRYLA
RAVAWIELLSKRSHMMEEAPLTYMRKSKPLSLNTNSNLRVAWQTPVARPDGPPRLLAREE
GYTFHHNEHSRFVTETYRHPGETLQSRFLAMQPIHTEVSAKEDFQEMYAQQQEQRALPSG
VVSPTARILHHSVTSEIHGGGGGQHHRSIPRVELSTGGAVKKEKLNPVSPHVAAEKRGGS
GTGNSGGSAGGGGVTPEF*
>TCRU_9005 peroxisomal membrane protein (Pex16), putative
MSSLFQSYVLWVRDNAENALSVERFTQLIIRIVTDPRNFMTTEFAWTLANLHSLSNRMII
STAGRRVGFTEKVAIVIKTLVEIECLLELGLRRFFGHEAAWTVLLALQSIKCVLNMLVHQ
QLFLVPWIWAAVRQRLQLMLQQFMRLPDYGRRISLAVAEGFSALPTTHVSLAPVRSGTVG
PANVRLVIPRVALRQRHHSTPAGFGEKENVVKTSVSLRCTGIDLLGLLVDLALVLRPLLL
LYFSRRAFPYGRTGIATLPVAPMASSHMRSSEKDATPAMSDADDYDGLFLVRAAMSDGVS
NSLLSSWGVGLSFFGLDTVLALLSRYIRRHRVPVVYINNSETCDLPESDVGAKDGEFSSR
SNDFNSHSLHHLGNSTSGNHASSNGSSAPLPPLLPRPPTGDVAELAPVLSRDSLRVQQIV
RNIAFSFLRDPFFPALLQKFVYEHFVVGRVNRIPVLGPIFGFQVAYFLCKQHYCFMYLLE
*
>TCRU_9006 BNR repeat-like domain containing protein, putative
MSRRAFNSAVLLLLVVMICCGSGGAVQGEEDLPAVPKYQLEDISEGDGKLESFGIPGLLK
VGSDVFAVAEAQCKKKDGEDAFTGIASQLLTIKDDNTPEEVLKNARVIRVLEKSTSTSKK
VDVSGPTTVVTADNIYMLVGKYSRNAGQENDADDWGLLLVKGNVSAEGDDTEKKSFGGKL
TVYSAL*
>TCRU_9007 hypothetical protein, conserved
MNYIQLDEYDLYAVDRTFILSLFHGFCTAVPGSVRQELVTTEADAVQFVMILRPRLTSFT
HRSNISLRHPAVSMAARLYYNELRAFIREESRFTGDSAITRNVPVAGSSVSGRENLGERR
GSSYTSWPGVTTKPITTEQLTQNNWELMGSCHDALLRNSQPRRIAVYAIASNDLVNDIIC
RYWERITVPSGSVGFRPSFASGSNEVSKSFTFTESGSGIHATHMTALQYIYLHLRIAGIL
LPPSSLKTEILDSIILDLRVDAMLSGKTGGLSFGRPPEYFGYRPTDDEFDDDSVGLESAP
KDPLHPVNESPIQMVEPSEASKFPFNVNNFRTSLDDLPDISFGQFWISMLELSDNWTSTS
HPMEHAIFLMELYCEVFAHEWDDEELSLLKALRANTETRRQEDAFSLMDDEERSFHILSE
FNHMVSSIDEFAMSGLLYQPNLMPFPKKTLVAAEAPCDHVSSVATVSFQGSMSNVRPSTA
GSIWSESKQEGQLSRQQLEKLQLIASDSSTLRGRHSEGDEDATEYATGKKREEKEEKKRL
YHEGRHMDVDKETLDEGEDVREGAHRRSSRDRKKQLRISRSLREEEEGKEEEGEGYDDKH
VVDREGRRRRKKEAGEGRSRQGDILDNEGRGRRYRIGRDGKRFSWRDSEESSESMYAYDP
SDPNSQRAGAYKKDHLHRRYPQKAFHDYEGREDEEYTVGADGVRRRRRRGGPRRSGYSKS
DKDAKGGEDDNDSWSTESSSFYSVPDDELTPTSLSRRQKERERKQAEHLLRRRKQQEARQ
RRSKMPTAAEIAEKRKKIVQTLQMRGVLISGDALTDDDIAELGDETISEELLRRVLLDAG
YAIDDIKESDFLHILLGDKEPQPAEVNAEERSHVLAALRAQPSRRPPETEYARRRREAQE
KLLREERRAAAKKLREERRLAIKKHEEESYIREEADELKPPFSSLENVEVLGLPGPGLGP
VPPQRPPPRREGPQPFVMPQPVQLENLLLTRMWRPVMWRGVRRRVRGKMPTRRRVLGEEE
MELKSFSQLVIEKPSKEKPAGLHEHSPTQLEMFYRGIRPDRLVKGRVPLAQPTSILGGTY
HQLPSIHSHGKGGLDLQGGLTKTLPPPRQCAPVKLFSLTTKTTFAGALKESLQRYIDDKE
YLDVIYRSYLR*
>TCRU_9008 disulfide isomerase, putative

MYRVFLLLLVVAFLFIVPARPNIEVLSSETQDDVVELHNDIFDAHVFPSGGQIQPQSWFI
FFYAPWCAHCKSLLPQFANASRLLNQIDMSHARFAVVNAVKQKELASRFEVHEYPTFVYT
TGKEGRWHKFHGGYSLDSFVQFSIYLQRSVEAGSFADVVSDPLRFKEVELQLADGRVPMF
VYVPAKGTSKSVLERQAVTRDAQWNIAVDAAASLGNIRFGVLYGDDVPEDWAKKGITSYV
AVVEAGRRCKGSGPDGEVFIVYTDAYRSPRCYEDSSWFAESSSENVGNIKGAGSFRIHPS
FEAFILHHGFRAVEDMTPGFFSVISGFNHHYFGLIVTDGPVTQSDTTMMPVLRAIVQERN
EARAMNTSIASMEGKKHHCRISLAHADGRSRAVWRTRYHIELEELPAFVVVDPRRDKVYR
LRRHTPHFEDIKSQLPWRMDGEQQQMIAAFLDDVEHGKAPGEKMSLIGDVAEYLLLLPGM
EFVYETLGYEDALFITMVFAFAFFSFLLFLALVVEPIMERYTAVHAKTD*
>TCRU_9009 Iron-sulfur assembly protein 2
MLRRSYLLFCVPHLSAVYGRSFTVSSRVWHRINEKNGEEGFQNDQRFLRLAVDSGGCHGY
KYHFSFEENSALVPEEDVVVAETDVLPVGAEGRSGVEPPPRVVVDRHSLTKLQAAVIDFH
SELKGAAFVVVGNELVDESCACAMSFSIKKRQPQK*
>TCRU_9010 hypothetical protein
MSISSDPFAAPAASAKTPPRTALGLWRCILTPHSRTASSKENVNPPPQDSGEAVSADDVT
AGSSTRGYWSLGLGKTCSPDVLQQKPARGTNLFKRLKNILTPSHESRAQPHESDARHEPY
SDVSVEEVVEGDISGDANHQTGLVDVEAMGTTGAEDRYYYTTEDGEVYYVDPASIEYQGA
YQQQEAEEEKEGAVENDNEDQQKKQHHQLQQQQQRGEEHSEHCQGEEEEGGGQEEHSKGP
LRLRGKVAKALASEETKRRRQLQEDCMIVLTDIGRVYRGLARTAAAFAKEMEALRHAIKQ
LEKEAVKQANAVEAEWKKEHAELSRTFRVEMELAKRRHAKRADPTLSS*
>TCRU_9011 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MVVDTPSTAVGGPVAQKTVSVSTPGGSTVNHESSASSGEDEGTVGETNAQKEEVHPDAGE
VNATALNSSPGNFSQVNNSDGGTMRGSGLLPSLLLLLGLWGYAAL*
>TCRU_9012 hypothetical protein, conserved
MARESAQNDEQADLPVAEAGRIRGQDQCGAQPIPGDEGAAPPRREDIARLGWVRLQVFSR
GLPEAQRSNGVRLDFVSPFSSKFGSKQAVSRRGNVCVVCCFISDLGLHHFVCPYRFGAVT
AAARDMALSCSYDASARIQPCGRGGKKGFTQRCEKAG*
>TCRU_9013 zinc finger protein, putative
MGDGQHTGGLAFLAAPQDNLRYSEGSDVIHVLIYVSAARCQVIFVTVSDGETVLMLAKRL
VDVHFRLGRGSFKSIRTAEREILLRKLRFSSESIVVENEANASDVASHCKHLFLSTLSAS
ELQHAHDGDPMEGFFCSELCNENKDGVIC*
>TCRU_9014 Glycine cleavage system P-protein, putative
MSQGTPPVILRNVVENPAWHTPYTPFQAEISQGRLESLLNIQSMIIDLTAMNLANASLLD
QATACAEAMYLAFHHGRKERMTFFVSRDFFPSCVEMAKTRAEPLKIKVVVGDPNLIDWSD
SSLCGILIQTPDAMGMLHDFTTLFEKAKRHGVVSCCGADLMASVLLKPPGEMGADVVLGS
AHRFGAPLGFGGLHAAFFAVKEEFKRLIPGRVIGISKDSTGCPAIRMALQTREQRIKRER
ATSNICTSQALLANVAAFYAIYHGSEG*
>TCRU_9015 Glycine cleavage system P-protein, putative
MHNKTKILSVGLESVGHTVVNGTFFDTVTVNLKGITPEDYVKCCVEKGINIFVDYSHGTV
SISVDEASTEGHVVSLLEAAGLQLPVIGVLSKLAEQKRAMPLQMLRKSVFLGHSIFQKYK
SESELMRYIHRLHRKDYGLTHGCVPLGSCTVNLNPAAATLSLSWPEFTNLHSLASKEQTR
GYSALCLDLEQKIRDITALDAVSLQPNSGAQGEYCWSLCDPLVS*
>TCRU_9016 glycosyltransferase (GlcNAc), putative
MELEDADGILQTIPVFSSKDLPAANIPVDIATIFVSIAAFRDKECVTTLESLFTRAKNPR
RVYLGISEERFEMDSSCIASPEVLKNIGVTRSRKLHWKDVVPFAYNPTDKQKYPKHTPVL
HAKRDEDVITCLLSEGSSDAMPGPGESVLNGCQVLTRIGHPDDARGPTYGRYLTSLFYNN
QDYYMVIDSHSRFVPEWDIKMIERARLMPTWGVMSYYPNGYTPEDPDAEINKTDVMAMCK
GVILDNDIPKLGARWIDIRDHPVLQGFVAAGYIFGDAQFVKDVPFDPYLPFLFDGEEILY
TVRLWTSGWDSYCPGTAFLFHNYMRTDAPRFWSVLTRDEVKVHREFERQTSIKRALYLMR
RNVLNSTQPVVTEDEAHRLNPAIGREMEHFGLGMLRRISDYWRFVELSDEFVKEKDDENR
WKGGEGLCEKATLG*
>TCRU_9017 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily, putative

MSRRVFTSAVLLLVVMMCCCTCGAAAADGSSGAGDAQLPQEVDLFVPQKTQVVIKSGGAT
EVKDSFGSPSFALVGEVMVAFAEGHKDYNGPQHTSDLYTSEIVAGYINATEPWSSIVADI
SSDDWRAYTVFTRESSKDHFGVALLPTAVSTGSDVFLLVGSYYLIRDATGKRWNDDGWDI
HLLVGKATQSTDAKQGELIEWGAPTSLLASITESTRQRDLMRFVGGGGSGIVTEEGWLVF
PMMATRKNDRGIESMLFYSKDKGVNWDVSRGIPAADCVDPRIAEWENRELLMLAYCVDGQ
KVFRSRDMGTTWTKASDLLPRVWITTQAIPRGEGWRVGALITVEFYGRKVLLYTQKVGYP
PGERNDKALYLWVADSNHTVYFGPLSVETGAKRAFANTLLYSGDALYLLQGMGDGKTDGV
FLFRIIEELRKIKSIVRNWIEVDAFFSGLSTPTNGLVGVLSDSSGADKWNDMYRCVDATV
LGAIRIEGGFKFTGHGAGGIWPVNSRGDNKQYTFVDFTFTLVATVVIEKMPPGGSSVPLL
GAMLEDGMGTKFLGLACAENRMWETVFDEQTGQGDFWVPKKEYQVALMLNGNEGYFYLDA
ELLGTSDTMRRREERAYDVLGFYFGGDESGRDSSASVKNVFLYNRKLTPDELKMVKKTGS
PKHESSSSEASGSDSSAHECVYFVLLVSLGLWALAVFYGV*
>TCRU_9018 hypothetical protein, conserved
MAHHRNGAAPHAFFSITNQRTGEVLLELTSLPLPLPTTTATSVEESQNCCRRFNDAFAFV
TEAQARSYDLFGRSMAKESSTRPAAAVVAPRARKEKDVDMMMAYEAPSSSVMDSAEWEDD
DAWPDDGDHDEGEGRGLLGPPTKKTRR*
>TCRU_9019 Las1-like, putative
MLFDPQDGTGLTESRRKALNRIQLVWKARERKNRQLPAYAEATALLMEAFSLDEGDQLSS
SGAVSFYGAAISRAVHLMTGSFARGAADTYRKRARLIGFPEEAVEVRQRVAHGALPLLSE
LRWVCGLVLQFLFHHYWVEQERHVHLMEEETEGEEDNTTSGHGVQQSAPSTTVEEMRQIL
EDLSDVGEDVTDYSNDRVEFLQDGWQLC*
>TCRU_9020 SMP-30/Gluconolaconase/LRE-like region, putative
MELVAELPGRLLTGLALDANDDVFAVCACSGELLRLNKTNGTMIPIMATETSPHALAIDP
RNGDVYLTDRSENAILKLEAVPNAKGHAEKDEKCDNDRGEVDYTVVRYLNSFENRQFVGP
TALAVAPDGELFFTDAGAEGDSSFADPVGAVFRTLQGHSQVVPLCRRGLIRPTGIAVTSD
KSVYVCEQGTNRVLRFVLRGTYYIGSVFAQLQGGMGPSAIAVRKSDGSIFVTQYDMKGSS
SSSSPNEGAGGIITVIGRDGEVSGIVRTTCPSLCAIALDSREETIYAVEADEASGGSRLL
RFRLSPAAQQVTE*
>TCRU_9021 peroxin 13
MYGGYGVCGGGMPSMYGNYGGGISPMYGNYGGGMSSMYGNYGGGMSSMYGGGMGTMGGLT
GGMSGGMINGGMPGGMNGLSTLPGGQGANGILPLQSDQPQVAVSSRPAIEESSQDRRARR
RKERKEEKDAIEKHRQQRRQFAIHSAIEIAGHVLQTLIQLMRSGLELFGVGLGTYYSVKV
LKSLVKSQEDNVSRKVTQVTVARAKKEVASRGLVPGTHRWKGWLMISAFFLLMETLYGLQ
RRYRDANERRATHRQKRGMHTTSDEEGLENRISQSGELSSDDVSSEFSTDYTASFLDCMG
DKSGKGGRLFVAVFDYESPDREGFIGFKAGDRFLIEEYAENGWCEAIHMDTAERPVQKGL
VPGNFLRPLEGETKL*
>TCRU_9022 chaperone protein DNAj, putative
MQMQQDYYALLGVPRTASKDGIREAYKLRALELHPDKNPEGEAVFKLVLNAYQVLGSPTK
RRKYDQEMALRDGRRPVAHATGRNGPKPTQGNNKSPRVPNPAPAPSSASGTSRKPVDEKL
FEDLYKQYQKGTYGGTAPFGRENRDGFRGAGANQQSFAEWFKRKQEELRQAEEVFKAKLD
YAKKLEFEEKRRAEEWRILQERRERERREEEIERARAQREWEGELLRHEKEMASKIRKAEE
EKQKMAAYSEVQKRQQEDLDAHLRELAMMKKELEDERRRLATERELARQESTDQQRARLE
RQRQREKELALELQRAEEKIEVALANQADYEAYEKEREERRLREEDARRLEEERRRQTNL
HEEETRRQFDAEQEEARRKASEELGGKRRAILEQFVKERQRHQDDVEAMRRETDRIEAEM
QAKLDALREAKRSGQPINLDEWKL*
>TCRU_9023 hypothetical protein, conserved
MIPRAAQIRQQQANERRARLEESAARASREDMFARHNVMRGVRIAGSRFANTNRHTRRDP
NRGIITQTEWNELVEQHEDSGFRFRTFFFGLLIFAVAVLALAKYDMEFNVEPPQIESGRG
FGEITSEKGTGINIEELEKYYETLGVKGRLRPGEAQAGVEKGEEDADKERRRENYRVRKE
IRQAYKEHQQQRGQLVHCGRSCEAKSKQVELAYNRLASQVDRELYGVLLDAKDTKSKRSL
DAADLKQAYEAKKKEVEENEKEEEDREMALEELKDAYDILVNPEARNYYLLYGMKPPEHM
RHMSARSGGWGQEISLGVYKNRVILAWLDFLHDYIGLWGETMVILAALAFVLSRVPTALR
QSQRLLDDMDWEASVAEIERSGRKRDETTE*
>TCRU_9024 fibrillarin, putative

MRGGRGGGGRGGRGGGRGGGRGGGGRGGGGRGGGGRGGGGRGGGRGGSSAVRGNVFQPHA
RMRGCYLLAGKDTLATKSLVPGVSIYGEKRVSGTIAGETESTEFRVWNPYRSKLAAAIYS
GVAQIYMEPGSSVLYLGAASGTTVSHVSDLVGPEGVVYAVEFSHRSGRDLEEMTKRRNNI
VPILEDARYPQKYRMLIPRLVDCIFMDVAQPDQARILALNAQHFLKENGGFVISIKANCI
DSTADPATVFASEVQKLKDSGLRPKEQASLEPFERDHAVVAGYYKCPPK*
>TCRU_9025 clathrin light chain, putative
MDPFEGSQPQPPQSNGENAVLGNEQHSPHQPQHDVNSFFEASSGTTMATTTTTGGAAAAS
APGLAQPAYFPPADLRGVNSDDFGSDGKESGVPSFGPKKNGHAVTEAVQKEIERRTANID
AESKKKEAQLKAAAESYMKGIIAQHEERLKEKKAEQMRLQKANEAKRNEYIKSGAVWSGV
ELMTDLNTANNYSKSTDRMRNILKKLCGAKEGETAQ*
>TCRU_9026 SNARE domain containing protein, putative
MPLDEGEALLRAVHQVRKACSDVSSATAELGTARDAMAREKLRKSRLLVTQCEERAGGIL
AAGIDAELSALRGQYNAVRADFDRVNREAIRREKQTWRPLFQNDAVEGDGRGDVSVSPAA
QNSGRVQEIRAIDMSGLYTEEALQREKLLGVREIESNMMDLRSMYQEFHDLVHHQQSNLD
SMTGNVSVAKSSVEGGARELSQASRRQKCGRKLLCTVAIILFIVIIGVVVVVLVAKR*
>TCRU_9027 Associated kinase of Tb14-3-3
MEVINSQETPDQQKTGITRVEDKYLIDEDAVVGRGAWSVVKRCTPIAPYEPPALRPGMKV
VVKIIEKEYLISLTKGNVERAMAEVKREIDVLRHVPAHENIVTFLEYIETEKEFLLFFEE
VQCGDLCEIILQAPEGKLTEEKAKHYTYQTIKAVLHCHIHDVIHRDIKPENLLVSDDDNI
KLTDFGLAKRSKGVCTSAEPRDLLDPVALCMPYPGAERIIGKRVVCSDVIGTPRYGSPEM
FYAKFTQTYYDGFKADTWSVGVVTYITLSGSFPYSAAAHAPEKEVFRTIMDTALPEPPGI
SSDALDFIQRLLNKDPHKRISLYDALTHPWLEGVARPRGSVTVPRLIEKFPSLEVTEVCN
VFDKEAQALHQCIRLLQRENQRLRDEKEKWEDAVAKREREARGTSTPRRAETPSGGSRVR
GARTTAASSVMRVGSPSRTGVRPGRSSIAQESSNGSTRRMSAHRVSARSPLARSAASTVR
RGTPVRAGGTTPMRSGTPSRTTGRSTSTTRGVSRPTNGVTPSTSLAHRASTPGRTGTRST
TPSRSSVLSHVTSAKELQIGETVTYKGYRAIVRFNGPTAFGAGIWIGLEMMEGNEGTNDG
SSFIDKKQYFTCPKGKGVFVRASQVKKL*
>TCRU_gamma, conserved domain containing protein, putative
Elongation factor.1
MLCVTANLIRGWLRCMEHVRQYALGVALMIAEERRHDIVALCLLRGSGMPAIMRDVEDTE
LFDWEEVADVAAQRERMKDCLCWRGAC*
>TCRU_9029 Amastin surface glycoprotein, putative
MSKISHNRQGGNNFSCRVTVLIFTILAIGCAVCANIFPVFKKESNTKKIKQTLWYSQTTV
PGGVGTKVDVSDSLCGQYKLFFQVSEGAAVAAAGIGLIVLGLAIAQLILEEKSSRFTCCA
ASLISLAFSACGACVALIVYGYMKGYCQSDAVLSSQYGPLKDQGYKFSEAFYLICAACGL
FLLSSFFQCCA*
>TCRU_9030 DNA-directed RNA polymerase subunit, putative
MSDRDGDDDRLSLNFGEEQEESTLRSDDEQSEGDGADVVLSGRAASGSAVRRDGKDRVTA
PVLTKYERARILGTRALQISMNAPVLVALEGETDPLIIAQKELREGVIPLIVRRVLPDNT
YEDWRICELDIDFDRPADERYTNI*
>TCRU_9031 hypothetical protein, conserved
MLRRLGANADKLARPVNKNAVTVSRRHLEPMSTWYLASWTMVWYYAFFFWMPMVWTDLMV
PSFVYNKLPVIHFLQEKRAEQKLRRVLDETCTEWTEELDQAHITEAITRSFNL*
>TCRU_9032 hypothetical protein, conserved
MSTPAAFLSSPASLRSRCEEILCDLVETQQGLGREWKNVQPCVLRASQLLLQQAQQQDDR
LEKLEDKMDQVLSALEVIANDCRLKEQRYHMDRGTTETALQELQHSSQQLHDALEMERRA
NQQFHEGILYPGLADLQQQIDRISSGVHPSVPPSQPPPPPPLPAAVVEGKIDIDPKSGVE
DSALKEMVREVRLLRNQWQQFLQQSRSAMPVSRQLVEKGPRMDVTTRAKNGGALLSMMYP
GVDCSVARWHWRGGHVSSPVLSPDSPIPWSTLHVRKTTTGEWLSVGATSDGTTVHSELSK
GAGLPFLWRPQRPSVIELIKGGIYRVTVCLLSSCNCRTSAKSPGGGRHVVTSALPSVSLR
VNHKTVFSFFSGGSTRYTVQRAVDTSRRTASARPTSNNRTATSCQACAFPRRFCECGESV
ICTTSNFVDFLRLPAGLCVSVHCHDSPDTNATHEALLEVELVAG*
>TCRU_9033 hypothetical protein, conserved
MGQSNSWALASDTIKGEQYRAYHAARQNIVHRAFQKCVAPSSTEVSDFNLTKDEQTCVEE

FALLYAAFAKNGFAQLSQLYEQHQREMYEKARLEMMAQQARRELRH*
>TCRU_9034 wee1-like protein kinase
MGTLVPPFAAPEADGSVVNREDTSTPLPVLQNSTAWGPPTVPRTPAKQRRTVHGNRNEMR
VAKISSSQRDPRSAVKDFCRVVTSRKRPSAELSQFSALQLDDPDNSMPLVSREGSSEVPR
RWGSRPTAPPFFSSAAVLFPSQTLSSQGDWLPRRGLSASVIPATPEGFDYSQADTEYSNF
FNQRILTDYREIRDLGCGSFGKVTLYEETSTGALVAVKMSPPLTNPEQRQRFLREKAILT
LARGFPHVVQLSEAWEEGRIPQMYLQLEYCKGGSVAEMADLRRRRGERWEERELLIFLAH
MALALDALHSANIVHLDFKPDNVLIDGEGNYKLSDFGCSVTLNDEGRPRLCFIPSNQRTN
NASTMGNSNNMMEFTALSMPTQVSTMSVEEGDCRYLCADMLNQKRYLKAGDIFSFGISVY
ELMSGEPLPQHGAPFLELRSELPIEVLERRGYSRPLIDLVAMLMHKDPTTRPTARDVLRF
FQLPPRVPELVKRWSTAVETCENEEPSASLEMRFVHAVLEVSLRLVDLARWAIDGASLNN
HHHHNSGDGGGGANCAFGGGAVRRPRNDVEESCTPKTPVIIRRLDAG*
>TCRU_9035 hypothetical protein, conserved
MMELQALIQLVSDYHPGEENSTSHSSLLSAVQQLKAALTDIEKIGEGIRPLVRALVTASV
HLPEEWDDILKALRGVLTNTGVPWLHRAFLLKTLPRMLLDAPTDRWKQYGDVLCEVLVRS
SMPPPGLEEGDARNTQDEASQHPNPQERRVAVTALLSLQEECAAAIVERLVTQLPQALST
CVAIVSSPSAQDGLKKAFEAWLCRPTSSADASCAMEIEKALKEHFQGYGGPKCEQLCAAL
ISSEPLRSLTEIAALQKDLSALAEVDVSHRNIVSNRLSLAFLLTKATEVLDLVYSSEQKC
LEKGVEDFTLPLSAIQLLVQLTDTASVTPESLSIQEMQRLSACLLAVKNADAALDASLPL
IECTLHLVLRGLPCLSTTDEGVRPLLNDLLGVTSTLLPVVEDAVLKIHSAVPLLCDQQHA
INTKAVADDVEGSVQTAQTTFRALRVAQTVVQLCRIFRKKIQNYEEKQREGEYPRHNLEE
LAAAVRGITPSWRREKKKIQRLPVLTNPQSRRGIAHAAGNKKETHHSYKQPRHVDGGGVH
PPSRRHRRDKPLL*
>TCRU_9036 tuzin, putative
MWRRTRVILQVVSAAVSKGTTQTTEITATTTTVTSSAESKARCREARMSLQGLRVAAYFE
NSETASTDEPIAIGQITAQISESVYAVFFKEIALSPVIEVGSRVYVTYSKDTVLALESAN
PHQISTVTSLNTAEGADKNPAAKTTSTALELDRDTSRMHDATSASKTQTTVASEVIASSV
ATNASVELTPARPASTQGAGAIIGGLVAKVNGNGTFAVLLDNDRFDPAVPREMITLSEGR
SKFISNEKFQEVLEWVKSAGVDRRSDQESTSCILFHRGWRADKLYLLDGADVHCLSHLNK
SVRMSVLEKSEWERDQHRQKREQIEERMKEKEMRYVLTKYSGVFSACVAVLGVASVFGWN
FKNYKKQQRSYQLAIAASALSQPHSKRPIRDYVHREDEEQRLRQTLRQQDLFHPRILVFA
GFYGCGKSILFRSAIRKEKMAAAFVDIRPNEDPLRSIVKSLNVQNIDACGDLLNFIGEAS
DRARKAMHGVTPLFVLKIRDGSSLLRIYNEVVALACDRRLCHVIIEVPIESLTIAMTALP
RLDFHLVPNFSVSEAFRYTHHLIDPLELTHFVEVVGTNSNDLDELLAAVRHAHMSATTYT
NQKLVKAMRQLQAAWAKDPSLREAVIKLARFPFEEGQSEGYDYSSLRNEALREIVMYNAV
ADVWMFQQKVFHTAACCWQ*
>TCRU_9037 Amastin surface glycoprotein, putative
MSKLGAILYGVVGFLAFLFVLVGTPIDQFRAKEKGATGNTPCMTLWGIKEDCHSTKYEFT
VGEDFRECPSVLRLFRMAEAFSIISILLLLAATALGVAAHFCLKSLKIFATLLLVVSIVT
VGLVWIPMAYFYNHDVDNCLGTPLKTYFKYGGGFVIIVIGWCLIFVAVVLLRML*
>TCRU_9038 hypothetical protein, conserved
MVARIRVSLAGDVRAAMDTIVKNYEKYFFPVLCEKQLMPELEAMPSYLPDAVVLQLCRDD
GEAEFAHYMDANSLTLVALGDTGRPALCGIDAAAQLHYEGAQRALVSAAGIVSGIRRRRL
RVPFGMSELSELLRRAYNTEKGNRSNSLTGSTETALLAHAFSDAVWAEESFHCFSMTRRV
GNILVSTGIGSTTRDLAVDKWRLDQDIMELRDELMIARTAYDYRPCIYESNRPISNIKEE
GMKRVNAIQSNREEARERQLSVVRERAKHEAEKMIKELEQRSGATLDEHERTLEAKKRES
SALQTGRENRIWEYEQTLEKIRTRKEDEESASERLRQAMQQPEQGLSLRQSAIWAKERQL
EMVQLDGARGREAIMRERHSIEAMRRTVREERCRQRRQWIHQIKEMNAKVPEQVRLLAEE
RKKKYEQATAKEDAAERALAADVKMIEEYLPKLISLEEIPVNPEGTDIIRRQFDEVFTQE
EQTYLASAEEEWARKEKLGRGLEVY*
>TCRU_9039 hypothetical protein, conserved
MRVDGNTAQFNCPHSLRDAGFAVSGAFFDVDVALDVPDASTLFRKLCATAAPNFAQDRKN
MVALSYGVRSSPKRQLLYGSAAGEVYAA*
>TCRU_9040 retrotransposon hot spot protein, RHS3, putative

MITASPSYQELEAIYKLHHGGVHFLEQWRDYQGKDTVAPLARRKLNAVLTQVLRKEKREA
NERAMLEAAKVPEAVMLEGCYESVYNASWHHVVEVPGGEGTRTGTAMEVKEGKPKQSWKY
NEVGDTPEKDDGVEQSGAERLRLMVLTSEKGWPYSWKRGVSEIIPDCYVNSEVERVWQIV
IGDLTEWFSIHGGNNPSPKRRVLIGTPGIGKSMNAGSYLLYQLLHYDAEKLPMVAYVITD
RKFLFDKITRTVKKCSGASSIVDILDGLSDRGVKGYIIYDVSMKSDKPSTGLPCKGWGMI
VVTSPNTKNYYHWTKIAEPEKIIINCPEENDVKAMCIWMKHNRRLPEEKTEEEADYWKKV
KERMDEVGPILRFIFNEKKCKDRFNECEGAVNSITGSMLQYYTGIGTGKSCDGNHVSHKL
VKVVRVRKDNIESHLNILISPHFERETLAKMKREMTAYDFTYLVLSIWDYVIPQILEDEA
LDAFLNEDFLRAIRSKIEELKLTGRPEPHTCALKVHSNKSFTMKEVLPENPSKRIAIEYW
VLYKPVTHNFPLVDGFFFVDSKPKIMVGLQITTAREHHTIPSTVELFTEQLAAYFNGWEE
LSRDMSWEIIYVQHADSTPMKKWQRCDYVNPNNETDAEKKIVAFWDGKVHQYQFVLSPDF
VNKIR*
>TCRU_9041 hypothetical protein
MVRSLPWSVGDQQPMASVMQRWRKSLFHIEYPRLCFLHVRSAGVPGTFGGDLCARRLLGG
RWRHCGVRMRGVLRPLERQAEHVRHVLSYCGRTSVLCRRLRRRTSIRRSLIGKESRFSRE
VEVPEAEVGRSPR*
>TCRU_9042 hypothetical protein
MSHESSPLQVGSVLGPSVDERFSSRSLETYSFADLIRAREEQQRRIREALEEQNRQLRAR
LGSEEANQGGGDPAITASAARRRSSQSPAKQHSVPIEEFITFVTEMKDLLNCAQQADLVA
LHALQDRVDFQNRDLAQRITELEAQMIAMQRRDEFGYATGDSPFAPVPSSVANMVEDKSP
LQYVLHELEEVRHAAEEAAKRVREYDEVLDRHRTSFCLLEKDINVLETKMVDLESLPSLF
RRESMTMEERYAEFTHRLQEEILLQRERCPRSIEGTNDAIMQLEERLKVVERAVFEMNQR
STVEIESRGSGDVECVLPSLVGKKLQEPKKATESFPQAKLDEPDCIQSASAADDPTSSAG
GMAPLLSKGQDDVTTEFVGDLPKETQCLDAKPHTVTSDLTTDAPSMKDRIEPLTKEVDGD
NVMLEGAIARRAYLGIDPSILGNKQMVERVTKVETQLGILEEKLNYFAGKFEVSNTESET
HTGESAPKTGRCNSPDAVAEAKTNHLDISTKSHHSQERINRYLKEDLELATVGLRTEAAE
QIGTACNTAATASPNGLNFMEGNVLLHSASGQTAVLPVRRRMQVSRKEPENFSFGPFKAP
SVPITSGSLSKAVAEIHERKRQKEGAVKEVIAALREVQKRFSELSDRESATQRCSARRSG
QKHLTSSTCDDPVSLLEFIATQKEAIYSKEKQLLDLRNTLWREIAQLEEDERELLSLQSL
*
>TCRU_9043 hypothetical protein, conserved
MPSIGTESNWKRSDCEQRLKSSTASRGTSSSSSGPGPGILLDTQPIFNTLMDGSHNAFCD
NTKRGRKGGEEVGRRPDAAGIETAGPSSGRSFRVRLTHASGAKMYSEPLNSLRNASSLPS
EAGANWREPAEMIVRQNSPTERPVGQQQHDCQPKTYQQQELQVGMDAADPNGTELLDPTN
TTAATTTTTGIQLLKSKSSLDEVCMQRAQEKRLSNVRETQLREMYEAKIAELEDVIHASQ
RAASDAEALLLQKELEWQTARTSMAQKFNGETVSNVSCLLETTLRAREKELEDTREMLRV
ERARWAGALQREEFLRSRFLVAEETRVLYQLYLQRLLEFLRTRVKERPELPLYTEPLVTH
SAVVKAMSEALRSADAATNEEVNSMLEFSPQGARGKVTVEQQSPTEPSRQLTNATLLTMS
MLESTVTDCMALWRREEKRRHDHFKQTLQAVVNGFTEELEAKLTLILSYVGKTEQRIGEY
EKMAVHVFGKLVRNAHDRGRQMDGLQKEVERASREYAQSQRLLTRAQAEVSGLKDEIRRM
DGDREVALLVHRAAECLEDVRQSVRGAVRSAAQDIEQRTLECNTLKEPFLQSMRVIALKV
EAHAEMARTAIRRRQHEDAGNPIETVLRRAGSVGAEEMHRLILSTPCCDSRSQQRHTTQI
MRGEMAGESKNFLMLEELSRVMKNLCRLLENNARQVDNNAAKLAQAIAAWEESIVKKMAE
IWESMHEMLVAAGIPPRPVPVLTVLGGVQRREGGNSAPLFLGDTNAGNSGRMLMHKTQPI
CPSAGVGSRPSCTGSLATSGSCAPSVSFAQSTISSTDFSRAASTAIIPSWRAPLAPLQEV
EQTPELSARHSLEGLTPQSIAVSRTPTPPPPPLSSQMTNTVPPSQRPPPQQEQNLHQRRQ
LFVESPCNSPRPVENSGAPLRMHYTGELSDFEGCELRLSSGAILSRRVAASSQGFE*
>TCRU_9044 cell division cycle 45 (CDC45), putative
MADQLTPWEHINRFYHTKRKPIQLLVAYHADAAAASITLTTLLKACFVPFNFHPVMEYEE
VKGVIQRTSMAQDAEISDGGAPVDELFVLIGLGAPVSLRSFFDLRRHIVIVLDSYRPFLL
DNLRASDNNRLVLWGQERIHEEVEQFFREQRKRELARARRRRRRTHKNQRRLRAYGELA
NDDDEEEREEESEISSGSSDDGDDDDENHDDMTPSQSQEGIDWMNEEVPENLEQLYYAAE
RGGKSCALEVYDLAILLNRVKEAVLWHAAVGVCDLFTRRLIDYGTYLVEMRRLHNEVTLR
KGIRRGPLDDVTEETVNRHHKIASSNTMQLVNLDEDQLFLLRHYSLWGAMWYHPVVASLL

GLHHVEDGTGTLRQLLARCGVSAKLAQQPWGEIPDDVRVESLRLVHHELKQALKTRGSFV
KWPTRIWCVARTTGYSVEVSTFDVCTLFTALLAKVPPGAMNTEETSEASMKEKLREFRRE
QFWRAHDVIDADPNSKLFVAAVQEAKMLQESVATATSALMQPGMIQSTKGIHYTQPSDPT
NASTALETFGCPFRIAVLAEHMLFALTVERGLGKYTREVRPVLLSCPVSRLIGLDSQPKQ
KEEMIQSEEAFIVLFAHEGPTKEGLSPVLPVARWNECVTNTEDFLVPPLRDFIRRDTVIV
DGRESTAHLGEMLHLRSLTAAL*
>TCRU_9045 UDP-galactose 4-epimerase
MHPSLCIEGDSNRNNSQNITVVLKQNLNFQVVLVASSMRVLVCGGAGYIGTHFVRALLRR
TSHSVVILDSLEATHGRSAHIDTEENLARNQKCSSEQLCAGRHAVLELGDVRDEAFLNDV
FTRHAPIDAVVHMCAFIVVPESVRDPLKYYDNNVIGIIRLLQVMRAHHCDKIIFSSTAAL
FGNPAAHASEGGATVSMEPIHPDAKKHPESPYGETKLVTEWILKDCAYAYGIKSICLRYF
NACGADEDGDIGEDHEPETHLIPLILRVPLATEINKRRKALQQAPVEEFVSIFGTDYPTP
DGTCVRDYIHVYDLSTAHILALDYLAGLDPNEKATFFSAFNLGTSRGYSVREVIEAARRV
TGHPIPVKESARREGDPPVLVASGEEAKKALGWELKYDNIDKIIASAWKFHQSHPLGYFS
*
>TCRU_9046 Repressor of differentiation kinase 1
MTEEVSVCCSPQDDNEASCGRFSGGVFSRRPAELCGSIFNRGRLPMKLPAGEASKNTGRE
ASSDKLAGGAASFPREKMADEQRLDPRQRPTSSEDRSPFWIYGYKSNLDNSLLNIGEWSQ
SESPALPGPAPPKEKDFKVGGEEDFETKPRTKFCSVGLRVLVFTHVLLSVAFIAVICVVP
VERTRKKLDLSIHVLADFSSEMVANEIANRFTFLSETVGSVFHSLQFNQTTPLRPWSGTD
MPMVMRQLCAVLATSALSELLLYLHLSSPFSGFGAYCSRQYDGKTIVGKHVAKNVSEYRY
LVDPGTLEYAKPLKPFYDVSRMTEKENSIDFASRSNPFVKIALPWAERNDTRRWWVYSSY
NETMVTYTYPFLDSSGNVAVITGALQLNKLQPHYPKKYQSSDIASLVIVELGTGLVLSRI
PGNTITTMWDNWNCTAKKSMCERPGVENEYIWNTGSPYMRAVINKMGGREGILMLLLRSN
YSKQIFVYKGVRLKVNVNRVFFGDDQLFVASIIIVPKSLLSESMEKTRDGVILVLASVAF
GVALLETWLACCLMRPIRGILKGLELMLQLREGSGPMKGFIFIKELMLIQSYFQTLNKQL
IYMKTFLPYGVMDQGQFKSPDSDSMGSLKGESGNHLALLSTEGKERPFAFSTCSSPSLKA
AVAEKSNFTSKKIVLKDGVNLFFRRYCSVVCLSLPLFDDYDSIGTVLQEYLEVCFLLLIR
RGGVVEIQRPDFLLVTFGAHSNMARNQLQAVRFVIELMQSLSPEILGLLAAVVDAGEYYV
GTCGAANLNARVTYGAELLFQTELVRIVRCLGCHLLVTWPVAVSLGEQFLTIPVDTAFCG
FSNRSVILYELRGHVASLEPRQFSELKETARLIRHGFASMLRGKYEAAACIFSSVDRKEV
RAYRLLQICRRFVRKGITKPYLRCVGKMRAPPYYLKGNSTKSDRATSPGYNTYSKAFVST
LLGNDNVLSSLRTKCDFLRGNEEVGSHSFSTASAREGSLSKYSTAMENHVDTTSEEKCGE
GLFEMFLDSSEDEDEEQIALQAQNEGDRGGMPLSPRGIAKGELPFVFTDYRGNTWTRSAD
KLGVGAFSVVYRGMSTSGDLVALKCFALRARNIDIEDILEEIKLFSQFRHENIVQYISGY
FSNDFFIEVMELVPGGSLDSILSSFGSLPTMAVRRFLRDALNGLMYLHSMNVVHCDVKPH
NVLVAMDGVCKLSDFGSSLVRLTNSIHKISDVVEMRGTPGYIAPEVARGEVPSGKSDVFS
LGITVLELLTGRLPWRFVQPRKDTEPAVGGRDLAAHCVAERGVFDGNGTVSESNVSEFSA
WLPKPHGCIGAALAEVSTADADWSNDPQNSIDSLLGSPSQLLIGITKGEIAPEIPLWLEG
DVRDFLEACVAFDPENRPTVAELLNHPWML*
>TCRU_9047 MYND finger containing protein, putative
MSVAEGFLSHGEPCTRADALGNWLTERYSRWEFLVVFQRQWSRDRRANRLYAPVFHMLFA
SPFSDAGREMLGAADVAPWQLIFYDLSRTCRDVLWGTKGTDLISDVLRAVPPALQPSFFS
VVCVTVGDTHDRLGLFSEQAFRHYKERVERLQRPQETPEVSVKLHRAMPRGRMTKGWDDG
HLPVFVEDAIKWACRRTSEAADVSAPSQEGNDAILAILPRLNKLLYKNTFHMAEDHNFTD
AVSSMGEGENRSLTDRRLEERRVFLQNLRRRVGNVASFTLASQTSSEEAGQRWHVLIIQK
LFVEKEEVSIENLDPGPLEPQPVGAELHLMQDGGEVLYLQSQLCSENSFETVYGDMMHED
GELFAQLTPLEGIAFDDIDRYLDFILTQPQPFGMETPTEPLCKGSCSGYTFPKVVFRRPT
GSVVKDNLIASPHVEILEESPRSPEEWDAARRVFLFLSDHIAPVSFAPDNGHSDGRGGYT
LTKDVAPVPPPTHNYKCTWCGRRRDKLLRCGGCKVDMYCCRKHQMMDWKGGHKKYCGIWR
KAREEYEKLIVPLLHSCPMERPETRSASAVVTLLQFLMASWCELQRSEVSVVHIVGIDDD
MTGFLSELSQRAKNFSMHWKQLRLLLSSGTFGDEEHNAVYAINEGGELTKTAPTSALGDV
WHTQSGKDEGAPEAVMLVRLYNAKYHIFIGQDTEISGGAPSAVASFGNPSGAGMTYLTAV
AEVLADRFIGVVPVICTEPTLFGAHHTLDAILERVRSSNKMNADRKGRVIERLLHADEFI

RINVQGMGYEPLDSHLGGEGGGVGGTTQTNAAEFATKLAPLRLHPNLYYFIIPAETAEP*
>TCRU_9048 flagellar attachment zone protein
MFGAIRSDSPSASSYKGSENFSRSRENSRGYIDSDATSSVSSKEEDRLVTGLRIEIDFRE
ERIKELEESYNQLSRKSEFDKGQMRSQLQQAENNIANFKKEMTKLREKVKRAEKEKLDAI
NRATKLEEERNQANKAAHKAEEEKAKTFQRLITFESENINLKKKPNDAVSNPDKRKNSET
AKTAEAEKQRAAEATKVAEAEKRKAAEATKVAEAEKRKAAEAVEAEKRKAAEATKVAEAE
KQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQRAAEATKVAEAEKQRA
AEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQRAAEAT
KVAEAEKQRAAEATKVAEAEKQKAAEATKVAEAEKQRAAEATKVAEAEKQKAAEATKVAE
AEKQRAAEATKVAEAEKQRAAEATKVAEAEKQRAAEATKVAEAEKQKAAEATKVAEAEKR
KAAEAVEAEKRKAAEATKAAEAEKQKAAEATKVAEAEKRKAAEATKAAEAEKQKAAEATK
AVEAEKRKAAEATKVAEAEKQKAAEATKVAEAEKRKATEAVETEKRKAAEATKAAEAEKQ
KAAEATKVAEAEKQRAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAE
ATKVAEAEKRKAAEAVEAEKRKAAEATKVAEAEKQKAAEATKAAEAEKQRAAEATKAAEA
EKRKAAEATKVAEAEKQRAAEATKVAEAEKRNAAEATKVAEAEKRKAAEATKVAEAEKRK
AAEATKVAEAEKQKAAEATKAAEAEKQRAAEATKAAEAEKRKAAEATKVAEAEKQRAAEA
TKVAEAEKRNAAEATKVAEAEKQRAAEATKVAEAEKQRAAEATKVAEAEKQKAAEATKVA
EAEKQRAAEATKVAEAEKRKAAEATKVAEAEKRKAAEATKVAEAEKQRAAEATKVAEAEK
QRAAEATKVAEAEKRKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAA
EATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATK
VAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKRKAAEAVEAEKRKAAEATKVAEAEKR
KAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAE
ATKVAEAEKRKAAEATKVAEAEKRKAAEATKVVEAEKRKAAEAAKAVESQKQRFLERFSV
LEEEKKAALRAAEMERKKITNIMKNKGVRSSDSVPLVEGNRSVTESSCRNRFRFSCSVM*
>TCRU_9049 hypothetical protein, conserved
MEVEGVVQYRLLGSHPAASGRYHSFGFSGEAVPLEALLQAVVKQHQINLTKYKFEVRRLV
TAGAERQDAQSASKNAANDILPSDALLRTYDRIVVNVLRRHYMDGVTHNEQMTEENRLQQ
VECLLQNEEAAEESQTLGPRNQKRERSSEDTDDPHAFIRVTTLSNKAFPLLPWLRRQTAN
EKTPIPKPVKGICVLCELNCFAEVVIPCCHFSACRQCLELAKAMLTNENECAVCGTLIAK
PNAYKKGQFATTTPVKQEGTSTKTVNTAVLGEQMEIHGAYREKANRKIGEGSTQGRFHDI
VETFEKELKKNMARVLSLIDVPDPLSSKAKEKRKISKTLSVFDEK*
>TCRU_9050 hypothetical protein, conserved
MNTRFRKLSPLPQKPSVKWHLMHEEYHPIFAPERREQVEYWYNKTATGRQRNTFRRICQE
MYTLDPDKEDPVYTAEYTCQVSFCEVRMMIKHYGAVLSDLGKRLARVWILHVATPREKEN
FREVFTGAQSLFCPVTVMKADYTPPDEDAYKEIDRTNFLCSVDWTNLEAQEKRKQVHQQR
YFSRSLSIASNRPRVTKPKNQFDGVSPLATLGYAGDSEEAISTLRKKLEETRESDRYFTV
DGHTVYIAGGPKKANPVFAGSKKNAVIATVYDD*
>TCRU_9051 hypothetical protein
MRRGGTHVPPSAFVPKLSINRSGDLLPERPDLDALGNERHDPFTTNSTATSGGSRGWNAF
TSAAAAATDSSNNNNNNNSRYTNNNETISAYDQSSPTPHNTSALFFAGTSKVKVSGKSVD
SSRLDEPCHGNIIKGYASARSNNDIGRANKRNEVNSGLATFARHDDTRGPVSRGWQRVAH
HFLHGNLRGASAPAKAGRALRGDMGRITSSTPHSSSFEDSFFSSTSEDSELSFRDSALFD
LDVEPVVPPEVLCPSQSHIFAWARHPRHAIILSLFRSRGFVLPQYADLVEYHMSEVFLHY
IDLCCRGAYFVRYQAKSSPKERFFSIRMLPRDMTTRFSEKIPYLAWTMHRAGVQLAGCVP
LEQLVGITVNTRSASFRPNFLSLHTIRGPRVDNHRLNLPTEGGFSLWFIDRHHGTARSVD
LLTCNSTVLDVWTKAFKGLVSVNSSSLVQVPLTSAGVSSEMEKLTKEAQQQVEKSLL*
>TCRU_9052 retrotransposon hot spot protein, RHS3, putative
MPAGRPESVQGGNVEIRAPTVPQGDCRKRTRSDFHTDTDQPAATCRGVGKRQQPNWTLLS
RVEDVLLEGKDRITSMRLNEFLRIFLGGRGVVDANEDVSMERFLMNPMRFSNGETLLCTI
TEFPLYRETKMLLEAAYKLKGEGVFLLQHWRDFEGKDTVTPIAKGALDAGLLYLWREEAR
REAKKSARREAEERAMWEVEERARREQQIKVTFSTKIEDVLLRGSVRANNTKLNDFLTVE
LGGKGVVEANRNVLLEEFVRDPERYIGDEGVLNEIKKLYNYVRMEIAVRDEMTFCEDLRS
LYNKGVHNLLMWSKAAAEVKAGVHGITKHTLDAALVDVRYRTITSAPMKLEGFYESVYNA
RWSHVVEVTDGNGMGMKVEEGKPEQSWTYKTAGETFEKDDGALQSGAERPRLMVLTSDKG

WPYSWEWEEHKFIRDCYVNCEVERAWRIVFEDLTKCFSTYSGTEFKPKRRVLIGTPGIGK
SMAAGSYLLYQLLHYDVGKLQVVVHRFGDTTYVFDKTIQTVTKYEGNEISKIVLYDLWQR
GMKGYIIYDVTKQGIPPASYFAPFREWGMIVVSSPEVSNYDGWETEVKAARIIMNCPDEK
DVKAMCAWMKRDGDTYEQTKYWKMVEKHMEKVGPLPRHIFHAKDFNARFDAVEDALEAIN
SRYADDRFILPGGGLWYSKDPSQKLVRIVRIRGERGAERFINAPICYFLGSRSANILAKA
MSEEGFLLLVLGTRETVLSEYLEKFCLRELIFGRFVSAMAEELKELKSPAHGIQDTVLKA
NPGAHPTEIREIPGVEDIRAKQNINYQVLYIPMVRDFPLVDCFFFVESPRRTLVGLRMTT
AGEHHTTTSTVRQFTKHQWGFFNGWDEFAQGLSWEIIYVQHADSTPLNGWQRCDVVRPPS
VGDVDRERIVEFWKTTHQYQFTLSERFLRRILFPEDAETL*
>TCRU_9053 hypothetical protein
MWIRDIEKVLIGLSTTSFVNYSGEAQLAKTRQEAVSDNGTHRHDPTQNITPSRLGTNNHR
AFALLLRGGKLLEVVCETDSDCEAWLVALKRPLHLRTPAERLPEERRGT*
>TCRU_9054 hypothetical protein, conserved
MVQLDGARGREAIMRERHSIEAVRRTVQEERCRQRRQWIHQIKEMNAKFPEQVRPLAEER
KKKYEQAKAKEDATERALAADIKTIEEYLPKLISLEDIPVNPEETDIIRRQFDEVFTQEE
QTYLASAEEERARKERLGRGLEVYRHRMLDDHVAKKNGKLHDAEATERHLSSVVDQVLN*
>TCRU_9055 hypothetical protein
MDANSLTFVALGDAERPALCGIDATAQPQHEGAQRAVVSAAGIVSGIRRRRLRVPFGMSE
LSELLRRAYNTEKATATIASLVLPRRLYWLTPFRMPCGRRNRSIVSTGIGSATRDLAVDK
WRLDQDIMELLDELMIARAVYDHRHFSYESNRPISDIKEEGMKRVNAIESNREEARERQL
SVFCERAKHEAEKMAEELEQRGGATLDEIGRTLEAKKRESSALQADRESPQLGVRAYGGE
DPNEERGRGECLGEVAAGDAAAGARTQPTAERH*
>TCRU_9056 hypothetical protein, conserved
MRVDGNTVQLNCPQALRDAGLAVAEAAFDVDVALDVPDASTLFRKLCATAAPNFTQERKN
MVAISYGVRSSPRRQHMYGSAAGEGCAA*
>TCRU_9057 small ubiquitin-related modifier
MEENHANDSNNNNGEAGEKPAVKSETPLVSIKVVNADGAEMFFKIKCGTQLKKLFDAYCK
KQGISRSSVRFLFDGSPIDESKTPQELGMEDDDVIDAMVEQTGGNTF*
>TCRU_9058 small ubiquitin-related modifier
MEENHANDSNNNNGEAGEKPAVKSETPLVSIKVVNADGAEMFFKIKCGTQLKKLFDAYCK
KQGISRSSVRFLFDGSPIDESKTPQELGMEDDDVIDAMVEQTGGNTF*
>TCRU_9059 retrotransposon hot spot protein, RHS3, putative
MVLASEKGRPYSWHTIQDLPKDVFINCEVDRAWQIVKGDVTAWFSSHGGTDFKPGRRVLI
GMPGIGKSMAAGSYLLYQLLHYDFEKLQVVVHRFGGGDAYVSDKTIQTVTKYGDEEQCIL
ELRSLR*
>TCRU_9060 Leucine Rich repeat, putative
MSGRGKGENNKKLRHRETNRLQCGVKRTAERTDSEAPSKVASRTTATDAVGDEVGDFDAA
AVSESRVVTSNEDSSNSARKEGDQHVRVPLSDPIYRIMHVLPRSDVLEIVKCRFGREECE
RAAAYFDDSFMKNPLRHLRLQVGCDRPTGLYLFFPKLHYHRGSLRLLDLSRNDLDEDDVA
TLTQLLDLCSDSPSRSGFSVLEVLDLSYNRRIGNRGALFLLSALRHNDRIRAVILKGISV
DDTGAVAVAPFLRQRPFPRMPDGDDEAVTFQETSLRRPPTFFLNFNENRIGAVGTEVLGK
GLPAHVSLTVSKQRPFCDKRGPLARR*
>TCRU_9061 MBO2
MTDVPSVLGDAMDISQSSAVVILNTLVEEGRLIEERSEYLKQKFKEIHNRVLAVYKRDNF
LLKRARQLRKELESQKEQIIVRGNNAREDDAEIQRLKKLLLEAETELSDAQERESILQVE
ALEFDRKKHTMLLEREDALAAEEARLRPRMEAIQAEMSAMGKEVEEMAAEMTNVVSKRED
ILAQEAECKEELARWSTVMADAAKQLSNVENAPERAIRQTQLVVKSYQAAQIELGALDDK
LQVQSDIISKLELKKSTRNTDYVQALANLQKLKAQLESKRTTLATLNTSLEMELEARQGY
QQRIAQLEQLIQTTNVAREKEIGEVEHVRREKERVGMEYMELEHTVSKIIREQNEVKNNI
VSAKKRLERVQTKRKQNTQRIRETQRELEQRQRTFIKEQNRGKEFVTKAESIREDIEAIK
GEITQRALQEEAKHRETQALVLRRQELNRDCGRENSRIAIGKNELRMKGMYVNDVRKRKE
ELEQRLSAMMDVFQKIKTERGQKAAQIQAITQKMTEMSEKKKIVENELVVLCRESALKET
ELVKKKRQVQELRQVCKNLRMEKNRQRKSLEKAFEDERNVKINVQRTNAQIADLEQEMNG
VKLRYHDLIEKRNYAGVQVLDRNDELCVLYERVNAQEKAINNGVLMNNARDEEIRTLRIK

LADLCREVDVVRQSIPKVKELEEQLAKLTDDIDDERWKVEVLENDLTNPKNSHRWRLIKR
TTAGRAFPAETESTPQDVNGTTQASFAMPRLCGGVDGPSDEFLHLQQRCQELEERVNAVN
ERIREKDLILEEVTELSSRLGEQAKTGREFTLALAKKANSHHSSIRAKTRQMMATVSELS
IFQASAIQLQQEVQRLEGLVEEAERLMEQGEAPFVEAEELYLREVEARQRYASIIRRRKE
AEAGVTAASMNFVTTAEQRPNAYIPDDDLGVPKPYGALVPFKPTPTVQSSRFYGRQLESY
QSREITARPGNTELSVDHACRRRLDAVKKPSYLSATN*
>TCRU_9062 hypothetical protein, conserved
MSLGRPDGLVAVSSCFGRWDAVLLRKCGDGALLVRDGRRSIHLTLVSREIEEPRLLLAAW
DPQDFAVRVNHVLYDTGPVEIRAGDKLQLTNLGAWSDEDGLYFCVENVETPEEAFPLGAQ
DSAPKTIATEAPSETPRVCGDENAWRVFMKDRLERVGQVLSLWTNLKSPSSVPLSAVTAH
AM*
>TCRU_9063 hypothetical protein, conserved
MSGKVYAYIAFSFLNAVTAFLIAWLMHIRINSFAIVAVLNEWDLDEKAMACRNAGLMYLV
LAVGLFLHSSYKQHRTRAVEQQRDEAEATNMQEKVPLLYSTALQVDETMPRHGSVRFTSG
YGSSNSS*
>TCRU_9064 60S ribosomal protein L35a, putative
MAMLKKFRGSLAANRSKKIQQLTKKTSTVKRNRKSPRLYMKAVLAGYTRGLHGQNKNTAI
VRIENVNTKEDAAWYVGKRVCYVYHGYKMKRCVRWSKAPARRSNTRAIWGRVTRPHGGSG
AVRAKFNGSAVPASAIGKRVRVYLYPSRI*
>TCRU_9065 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MVPNASKKRPSFANGPKILVTSNASGIMSVTCGGREHVAADNTYEVSERSATGHNFLVLE
NGVAGSGFVAEGDADGLSQSNASEHDNKPQLREFTAQYSGNGVRPDDCVALLNDAKLTLR
ELTADGTVRVCVYWVLLLLLGLCGVVAVL*
>TCRU_9066 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MVPNASKKRPSFANGPRIVVESNASGIMSVTCGGREHVAADNTYEVSERSATGHNFLVLE
NGVAGSGFVAEGDADGLSQSNASEHDNKPQLREFTAQYSGNGVRPDDCVALLNDAKLTLR
ELTADGTVRVCVYWVLLLLLGLCGVVAVL*
>TCRU_gamma, conserved domain containing protein, putative
Elongation factor.1
MTANLIGLWLQRMEHVRLYTLGVAFMIGEERRHDTVALWVLCGWGMPTIVRDVEDTELFD
WEEVTDFAAQRERMTDCVCWRGAC*
>TCRU_9068 hypothetical protein, conserved
MDQRRHKRTARHQYLGARAKITLKLQLTRIQHRGCHFHVHPRTTPLDRQAHEDALQQCDV
ECMLWRVKMQQVQHDRGSEGHADKAQTTHTGIRIVHGADAATVHAADLRVPRIGERERPK
AVRNRSWQTRVTVAASRAHTFTAADAARPRCKAHGLHGARTTVQHRHGCSNVELFLVIRH
R*
>TCRU_9069 hypothetical protein, conserved
MRGVHLAPRHAQHSAPRRNHARTRAQRIFATEHSRVQRNTATDKLQHGAVHHHRPPTSHH
GHEGHAGQNQHGPHEPQARQHQHRCVRRGLRAGKIHKRRRPRGNQQGVRHRQHGPRGKSA
GQHKRTVQRLHIAHRQLHRPALVAPRRPRTAQASTAHHVQHGAVQQRHVLHNDPHAVPRH
PRHVEHRTHAVQHNVAQRHLARAGRHNEHRPHRHALAEEHTRRSAHSGRQRGSSHRHARL
AVPAAAARAHAHTVPHARRRRPGRVAVCVPVAGVAPSNVDAPSVAKTSRSVLLRRRQDTS
TSVVARHPQMRPSCKRQAHRQHPRQQRSVAHKAQRAPSSGHGASGVEHLPRDTVVHVALR
QQHRPASQAHRRIKRHRVVPRRRKVASHKRHSGARHAHSPTHRHRVLAQQEVAVNKRHHG
AAGARLKPADQHIGALSSRRVGQPPNNVQARSTHKRAVRQRHVAHAP*
>TCRU_9070 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MDEYLGVNATVAKNGAAAATGPSDGAKFTGRGAGAEWPVGRQGENQLYHFANYKFTLVAT
VSIDNVPEGTIPLMGVRAGSKGEKKLIELSYDSEKKWQVLCGDGDPKELGSILGTETPQH
VVIFLRNGTQCTAYVDGQRVGNAQCELGSGESNEISHFYIGGDGGSAENKESRGDVSVTV
TVTNVLLYNRPWDDTEIGAFNPNKANIPVQVDKSVEGEAIQSSGGGPEEQGQLLGSSGAG
VVSAPTVSSATISSVGEESVMQVASEESFDGSKNVGGASSPGSDAAVETGDRSMVQGDGS

SQTLVGTPATADAYAPNAEATGHDGTAVNPGASASSGADGEAAEGTDGREEEVHAQNGDV
KAAALSSSLGNLSQGNNSDAGTTRESGLLPSLLLLLGLWGFAAL*
>TCRU_9071 BNR repeat-like domain containing protein, putative
MSRHLFTSAVLLVLLFVMMCCGSGAAAAGEASSPGCSKRKRFVWRDKKDGETVSSLSVPS
LLKVGTDVFAVAEAQCSKGAECDFTGIASKLLELTGEQASKELDKTELKTQVLEECSSDE
KSACRIANQAVSQGVKNLHVSRPTTVVNGSDIYMLAGNYSFEGASDFRAGGWGLMLVKGN
VSKEGERNKRILWNDTYAIPWSYNGNQNEPLKRLVGSGGSGVQMEDGTLVFPLEGTRNKT
NQGDGAAEEEKTVSLILQSKDTTNWTLSKGMSADGCGDPSVVEWKDTKLMMMTACADGRR
RVYESGDKGESWTEALGTLSRVWGNKHEGNVKAVRSGFTTATIGDRNVMLVTLPVYAEVS
KKDKGVLRLWLTDNTHIVDIGPVSDDDAAASSLLYKSGKSGTDGKKDELIALYEKKKGGD
EGKPSPGLVSVLLTEQLQRVKKVLATWK*
>TCRU_9072 retrotransposon hot spot protein, RHS3, putative
MEVHEGRPEQSWSYKKADDTIEENDAVQQFDAAPPVLMVLASEKGWPYSCHTIQDLPEDV
FVNCEVDRAWQTVKGDVTAWFSPHGGTDCKPERRLLIGTPDIGNSVAAGSYLLYQLLHCD
AKKLQVVFHCFGGGDAYVSDKTTRAVTRYSDEDMCVSELRSLRGHGRNVYIIYGVAKEGT
PPPRHFAPTSGWGMIAVPFPKVTNYDEWAKQLQAARVIVNCPDEVDVKAMCAWITRDETK
EKQAECWKEVKKHIYLL*
>TCRU_9073 hypothetical protein, conserved
MLLRGRLASAASPTGVAVRLHGAPTTEPCECHAQRHWDCGTKQPRVFFGASGTCWPQLGG
ASGMLHRTGVVMAPRRGSCDGSDAAARHVAGSRVWPQWSMSSTNMRLSDFLWNYVGGRAA
VDERLQCDDGDVCSGAG*
>TCRU_9074 trans-sialidase, putative
MNNMFWHAPTSTALPILLFLLCFGSGAARAEESLSESVELFTPGKTSLSDEEKSKSLISG
EAVKSFYGHSLVDLEGLMVAIAKANYKSADWNYGDADTWSRHAMHGDKNNFAKLIAGDES
EWSSAVLVKRGGQERQFTSLCDTKAVVKDGKIFLIVSKNNFGNETSYISLYHSEVDPELI
VGEVKGSGKGKHVSWTEPISLKTKFEAQMTANYWRKLDGAHGARGILIGEKGILAFPLVA
TSSLDYGDRTICTVIYSEDNGISWEFPAEAAVAKDCKGAILLEWEGKVLMFEAYSYWGRW
VYESSDMGKTWKRAVRSSFPLLRYAAALDDFSVSDDLITANIETKSVILYTLIPRRRGES
RGRIHLWLADGSRVHEVGPISVEVSTSSTFSTLLYTKGELFALYAKDGVNTDSNSLVLTH
LTEQMRQIKTLLQTWKSVDERVSTLCSSSAGKSAPEGAVCVGHLPTIGLVGFFSDKGNAT
HWNDEYLGVDARVFGEVKKVQYGFELTGSGANIVWLLCGEYSKLDGVKGFYCYDELTLVA
TVTINKIPQGITPLVGMNIISKRSLTLFYDNKMRWRMGEKEEEGSQTIAWELGKAYRVVI
TVHKGEGSAYVDGQSVGSLEGGPSFTSEEEITAPTHPDEDTPSASRESVLHIFFGNIRAG
QKEERNHVTVTNVLWYDHCFSATEVGAMEEAKKVLQPPSKTASPKEATRPPQDVSVDREM
SSSSGKGTTSHDAPMSEKKKDLYPSAQGLAKPPKGQDTGDVSLTGSLVGVLWLALLGLWG
LSVLL*
>TCRU_9075 SEP domain/UBX domain containing protein, putative
MDVKMGGDDKKVELPLLKFRLPTTQPLSKILKPDALDGELRRKVVRNITGDVAPARDDRR
SPNKWVVPFTRSNQEGNYPATLRDQVFSGDGDLLGAMAKRLKILEAQQNAYRMELKEKTE
KLLCVEAKYKNEKARREEVEAMVVEIYDDKEELEKLVGEMRNFLSDYGLQWVGDKGREKA
KNKGANSRVYGIADNAKRKDSPSPITATSRPFEMYEGDYEDKTPMLSSIPVPITSPTSEK
DMPNDTTEAKMVPCTTTGTSTLPFSMEILKRNAKILSDHVGSRGVFTNGKQGGIKEHELV
RIVVYQDGICVNGGPFRPFGWPLCDAVLNDLAEGFYPYEFKQRFPDGFPIEIIDQTSVCF
SKSTVGDKSVGKVRDLRSLQEGKNCQPVSREEFLKRLPATRITGSGQIVHLREAIAQIVG
GPTGNGTLRHVSEAERKLVGEMEETEFKSGGAAVVPNRIKGLVAVLVRFPSGEKVTLHLA
PENTIADLRRELQLAVPGFKAAYDVRLSFPSVTYTDDTKTLRELGLLTSCTLMIQPRRHA
*
>TCRU_9076 Macrocin-O-methyltransferase (TylF), putative
MFCRSFWHRNVAGVMAAIKAGKHEETLLELNETKRLRKNAKDVDYCRALCFLLGEHDALH
ARQALLEELRYFPENTAARMLLYDINGRVRSSLLPPVEVTKREPLFALICDALLDHTMLT
WTRLYGLYRLAKEVCCRDQKGVLMECGVAGGGSVVLLAVVAAHYGGHSRKVYALDTFDGM
PDPTTSDILKDLRTPAGATSWGSGTCSALQDNVRRLAKNFDVEKQLVVVPGMFQETMPDV
VKEIHAEGIAMMHLDADWYESTKCALELAWPMVTKGGVVQVDDYNYWDGCRKAVDEFIQS
RALGGLHESLQIQPVDGNAVYFTKK*

>TCRU_9077 branch point binding protein, putative
MEAKPRPSRWSKERYTNLLIPNYIPPELLLYDEGQFLRAFLLRVLAIDLNRFIETKRCED
YFLNIPVEPEYNSDGQRTNTPDEIVAEKRRKAMDELTNILRQNAEMGPHPAAPKEIVRKR
YFSQEEMDNGAYGAILGARGLVHQELEQTTKCKIVLAGRGITNTLKDTSTNAARIALEEP
HARITAPNEQALQHAMERIEWILSDDPEAQEFRENNRRRMAQIEGRYDPRTWVSSVEKDN
GGAPRPGEKREREEQLDEDVQAFLDEL*
>TCRU_9078 mitochondrial chaperone BCS1, putative
MWRRLSSGVERRFHVPSCGSVLQNSRRALELPDPQALLTSPTGLFAILSGRQRDTPPGSA
SMPLERNGEKGGRHRRKGRRLSPDGNRVSAGGSTGDGSHSGTVSSGAHHGTFFNREAASL
ALMILILTALWEVINSQKEHLVKKMREMLFLTLEVRSSREEFAMILDWMGRQPQGRRARN
ISLMPISIRDEMSGEEGKRDESVAGSEFVPGFGSHYMKFGNTRLWITRTMDNSKQYKSSS
RLDREDEILELVFFSRDRNVVHEFMKEVRASWEEQSKGTVRLYLPNGWGNRWELLSKRLR
RPLSTLYLPRDTIAVVDETKLFLRSRELYISLGVPWRRGYLFEGVPGTGKTSFILGLASE
LSLPIYLLSLQSKDLDDASLLGLINSVPPKSLLVIEDLENAIKAHSVHSSLRNEFPREIG
EGRDSGVSLSALLNAIDGIASSEGRLLIITANDASRLPSPDALLRPGRVDRRVSFGPLDP
ESMKEMVKSFQSRSAEPLLKGAFTLWENGCLPTAAPTTPAELQNELLASIYRNGLTH*
>TCRU_9079 phosphoribosylpyrophosphate synthetase, putative
MSYCEQYLSNGVTNRNGNLRVVNGNSNPKLAEGVCQALRIPVTSCRVGAFANGEINVKIL
ESIRGDDVFVVQPTCGNAVINVNQAVMELLLIIHTLKLSSARRVFAVIPHYGYARQDRKH
ISRVPISASAVARMITELGVNGVVTMDLHCGQIQGFFHGCPVADLSATSEFAEYAKKKAF
NINNLVIVAPDAGAVNRARRMGDRLGASRIVTILKRRVEANHVDSMQLVGEVEGCDCIIV
DDMIDTGGTLCKAAEVLRENGAKEVHAWATHGILTDPACDRITACEALVEVVVTDSLPQV
ESVKKCSKIKIISIAKLLAEAIYRIHSEQSIENVGEIPVPQHHNEDLISVDALVEEGDWP
QSGNRSIKRRSVAYPGKTSSQENSPGFVAH*
>TCRU_9080 NADH dehydrogenase
MLRPTHAVLRPNVVVVGTGWAGAYFTRNLNCKLANLQVLSVRNHCVFTPLLPQTTTGTLE
FRAVCEPISRIQPALATLPNRFYRCVVYGVNFDEKEVNCVGVGVVDTSFNATVQTFNIKY
DKLILAHGARPNTFNVPGVMDNAFFLREVNEARGIRKRLVQNIMVADLPTTDLEEAKRLL
HVVVVGGGPTGVEFAATVADFFRDDVRKINHKLVEFCKVTVLEAGEVFGMFDLRVRNWGK
RRLDALGVRIVKGAVVAVNNKEVVTKDGIVIRTGLVVWSTGVGPSSLTKGLDVDRTSRGR
ISIDDHLRVLRKGAPIPDVFAIGDCAANEKLPLPTLAAVASRQGAYLAKKVNGELSNKPI
MAPFEYRSLGSMVSLGDNAAIVELNVPSKFDFVGLKALFFWRSAYLSILGSWRNKLYVLV
NWVGSAVFGRDTTFIGDLSEDRVWRTLAAEEVSREYARKKAFAKLKMMETKTTITAETLE
KGAEMGYIARQSNNAEDSSTAEAKDTPNTKPQ*
>TCRU_9081 hypothetical protein, conserved
MILDVAGYSLHSLSHLREVLSNRTMQIQHEAREEFVDLPEEELTVNPALQKYVDVLCEHH
NFLVQVLRGCDIFQIIVKS*
>TCRU_9082 hypothetical protein
MSDAAVLAESIGAAPLPVIQLSESLLKSLHIPTQHTCFLRPVFASHVSRQSSALFITSWL
PRVLLVTESGLLLLIDPSDGRVTHEASLLLSGSPPAAENERLVHIVMQQGQQSRDRPKTT
LWMKIALGTTLFAAILRFKGVFQGTPTELLRVILHFVPQRHVSVQQYVLPGPLNNIISSG
LRSVSVRNYDEEDDTSRGMSSSPRAAKRRYMKWFVVEEWKRHKTLHAELEKQQKEKNENL
APQEEEQEVDFPQETAEEDMVPNNDFAAVEAASSEEEEMNDVDEMNAFDHDKKSQGFSVG
EQNSLHEAMDEAEDYYTTTALLQREDFLSANLDVRQPLLQKEGELEEEEMLGFEYKPAVP
PPFLLNETGTMGYGELPGRASENSSMRWEGKNGNEWTSLWRELRPKNSVDVSLNKNGREG
GSSSEEPWNHVDHAPPRKESAPEEKCEAPSSQTGAVCTAGPADITEKSREENECLINAED
PITALEALELPPPLPATSFFRLEQKMDNDNAPTIVDEQSNMEEFPLICNKVAEVTPLQAN
GAHILSVYPLQRPLGDYKRKGAESSDEEQLWQRVYHENLGRKADSRVCQQSPMEKYGRGS
AHVSNLSVGAKVLGDI*
>TCRU_9083 hypothetical protein
MTGGGDQQQGEETADDGMERKRCSSPAASGLFDMPRDPPVYYSPNGEEMTPTRGADARTH
SCAGNSCSGGEGGGRNAWQPPRLEDFAGPFSGVFPPEAAVKMTDVANDNDCRGSDEGSLL
AREVHEMFTALPDVPAPASSKDVTQQTFESGVVTTSKTGCSPRVERKESYGLQLNTGPSS
ETSRDPNQQFLRLLKGRQRREAGHTSPRSSIPKPTRNHPTWRTTNSKGKRNHREEKEGGM

SLNFRVPTSRSPRTTSFSFVFQKEARRRRLNDEILPDGGTYAKSIEDRPKPSVAALAGDR
QHVSSAPMEQREASSLVSVVAHVMDATPTLKTSAEEEPTARLVPPMQTPFFASRSTFIYA
DGRQEKTLQLPKKKTVQHPGIILDEISTSPSELLDGALNSSSVFNYPIDWEKTSIEESRP
LQTERHPTTGILDATVKDNPRNHTVDDEKEDGQQNDSFAFEGMGFNSILPTTRSRWSNSP
VYEIVAHAPSTQTSTRAPSVMSVLQALPAAPPPEQEEQFSLSSCTVEEKAAVAENATEPV
TSVVSYKARFSGKNRSETRQKERPLTSRSQRPLPASLGSYAEIRTSARRFHAGAEARRDV
KVRHQNRQYQPKFHQKRRPHGKRDEMERPPPWEIAAQVKAIRERVCRLREMGMHREAEVF
WYLWPEERQLWHSLTNKLTLLRGQAAELTKRISEWEMGHPEDTLARVEKRIQLIQFKKQF
LLTEWEKVEDLSWEYLTAQLLQGAKKPLRTLIMLPSRQKF*
>TCRU_9084 SPRY domain containing protein, putative
MFYSGWQFPTPQRIVASDSQQDANYFIQETCSPGICLIHFLSTSMRPGVSASAAASAASR
RENNGRIHLKSDVPIHPYSGVFYFEVEVRSIATAGGNGRNSVMSLSEPELVIGICRESLP
QHALPGEEAWSIGLFTAQRMAYINGKGEGEAVRFPTGARQRNSSTAAGNSDDYRARGMKV
GDTVGCIVNLMDGTVRFTFNGELLDVVGTLSRRMPRHGYYPAVGMFRLLPAVSLRVVFPP
LGRAASILRPPMKEKVPPPPPPPPPPPPAAAAAAAVTTITTATAATTAAVPESGTVAAAA
AAAVAAGGVTTAFSPQQEMRTTAAGYFVFNMDKYCESIAEELVRLHQKKTAADLENEREE
DSTCSCRDANIMAAIRKHLAARGMTKALSAFEKEREELQCATAATRVSSPLQEGMGSQSA
EETHATRGEDNSKKSSRGALPGGSGSSLNKISSKLVEEECQGISYSLHIQQLREDIGRGD
MISGTQRILAAGVISPTTREKIASVTEDVNLLPNDFWGIIFFAQRRDILFLLRAAHLVEV
TLDAMEKGLGALLSRLIGMEEPNRGATGDSTGATSVKTPITTAELMRLALHILLEPFEEV
SAAARHHQRASSVGARTGDAAAFGMLDETLAKGESKWPCDDLAAHLFFTGDKTLWSGPEA
PVTLLVRRSVPNMPPPKPKHQRQIVETLSMLLSHQRAVCAREEEQRYANENRTWVESWLL
LVKDAKIQYRARCWCLLLHAIEDFNGALEYRLLVWQRRHEEEMREAEKGGGLGRHGATTH
HREGAGRRLFPSLRSAWRHVHAAAALEPLFNIVTKAFSDRLYRASTAAQLATMAAQNGRS
STFEKGPKRNLSFRCDFMNSEEDEGRYEHGPHTGELASEFGSTLTARNNNNKNELLKKKS
CYNDDVRLSFLYMKSIYRAVFA*
>TCRU_9085 CYC2-like cyclin, putative
MPIEQVILTIHAIYDLPREMQQLDPRREQLELFVQPVVNYNYRGRRVKLLPLGESVMPFS
SSSILFKRERFILDLGNVTTPYASPKCTLPSISPRTSPWRRWYPTAGGETNEEDDSDNET
SNNDTKRNMIHGNQVLLQYPCTLGLSTTLDVMVGVRQHRIGSFVLRCITVGQSADTHSDG
AGFFSVAIEEVRKKKTVTRVVGLSVGGVILSVSVNPNDDKESVLGRLIGDKNRNLASCGN
NQALEKLDVAAMLLEGFSEVEIYQHMRLIVDPDYYLRRLENLIALYPAQGSEEWRQSGVL
LQKYASREEELMRRANLEIGPECSSVSARHRLLAYRYKYHLSDQSVRECLQSVLGEEIHE
TLVTEPEVVFELLTKKFGTEPRPTSYLFPARKYKPDRRTFFFETLHFLVNGSGENLHDVA
LASRNRRAPFTMSPCERPLHLGTSSLRPSESPSEIEILRDKYAPEFSQIVPSIANALQAV
VERNRKLAQLVKEDVNFIIFQQQGLHPQVSFHDFVHRTAEYTFISPSSLLGAIIYLDRLC
LRHPNLIITEKNILRLFLTSVRVASKTLELRSINNRHFAEVFGLDTKSLNLLEEAFIKRL
VFDFFLSPEEFGDYARLLQPSNSYYCRNLSAHRGYASTGGVTDEKAIPESSATQYYQDTP
SNYSSNAQNPPATNPLGTDGQSNIQKHIIVARETGVNEVANVSQGASCSKGIGPMEHSSR
VEVSSKKQLIGIGGSGACGLNYLSVSENSNSTVPTAGGDRGDASRVVAGGISQAERKDKV
VV*
>TCRU_9086 Endonuclease-reverse transcriptase/Reverse transcriptase
(RNA-dependent DNA polymerase), putative
MGSTEKCAVLGTRRATRATVPACNHQPSPFWTPWLEEFCRAVAAASDAEGGQRLDLRRRE
ALREASESRWHTLRSELEGTDGNRQQVVRPCLRPSFLEHASHEFRWPNAQQTPEGQPPHE
AVGDESNTAPKDPPSATDPDECDGPHQINMADPGRTLRLLLLGPAPGPGGINGEALRHLG
RVARRAVPWLFGIRLRAGAVPRNWQRGAVLLLPNPERTASNRDSPPTCNAEQLPQQAHGT
HPRRTHPGRYRVPVSSAAILLFAGQFHPRPIAAPQGCHASQCSRTPHGGCLLDYANAFGT
VGPDAVILEMRRLSIPNRIARWSASCLNSTSAVVCIDKPTPSSRTLTRGAPQGKVLAPIM
FVVVLRSRCPCPSNVPCFAEGSLLMTALSPHSRATGMRATRP*
>TCRU_9087 RasGEF N-terminal motif/RasGEF domain containing protein,
putative
MGAPPEPATVDGRSPLITPDTLHEIVAEYLQSAGMREVAADMRRHVESTRASTDDATTIR
QPAREDRTGSQPSSVGPSAGALEWCLCSYAATRLVVRQLLSDGASKLTSQFKSMGLPAPD

ETFIRYALDSNDKHMWSVQDDVDALYVVGVGWDGHGMPMFGTLHQIIEALTHVSVLPLST
PSEEKLLAQEEFTHAFLRQHRYFTSSHTVLAKLMERFTVPLSVKLGFENFEAHGICVHAP
GTSLSAFLSVSRITRTHRGEEKVVKGGVNSFSPSASLWLFVCRSIQMRVMSVLTLWLREY
PQHFDDAMHHSIHLFLDDCSSISQPWSDCPSQLHAMMEFVRDSISAAAEKKRTGTLATRQ
HRLTDGPPTLASSSPSRTVAAEENFFTRRQAYPTCIFSLRALTDVGSSTEFRTDSWVDKL
QEVVNLCLALSVEQYASGLMSLHLHLFTSLQVEEVLKVLHRSSVAYLSSSSFHLTPVGAF
LASSTDLSAWTVSVLLHAAALDGHQMRDAGHVSSAAEIFLKIYKHFVELVVALVRLNDLH
GAVAVHRGLQHPIVQRVLTQPRVVALIPASTSQNVTRLHEILGICSEKDVAKGKSLENYM
RGILDVDAHPLIPPLQHYLGKLTRLKDEMPSFLTLRTDELYPSTDPGKKTREIVLLHWRK
YIILDRMVSQLKVWHSGARPTAIDRAFENQFVEQKRKIIWNHWQLAEMANELLSAI*
>TCRU_9088 long-chain-fatty-acid-CoA ligase, putative
MFRSLRCQLDKVPFATLFGYNSILQSVFSAPVKKEAIVVEIPGRKTERYTYGQLQKDVLS
MSNVITQRREALMVAYGEPSLSWVQRPRPSNVRSVFSDVKGEVLSCDFMKDDGRYNIAII
GDTGYTFVVSLLAAWSLNQMAVPISASQNYATELSYILGHSRCRAVMSDTAMMKEKFPRE
YDPCIVRSFSSLRNPVANFPWFSRSTYDVETLFDAQTLLAEIQEKRDVSEASTRVILPEH
LLPEEERNPIKDAKDVMDRIAHEQAASEEHREAWRQKMIREQFKAHCIVSDAEDGTGLFY
DTDHLDSLNVVHRHWVEECSFRPSKRDDCVMIYTSGTTAKPKGAVHTHASLRNMVRVLCS
KWEWSSEDTILHMLPMYHIHGLVNVLLCCLASNARCILTKFDDPIRIAHRMERGDITLVM
GVPTIYTKLVAAVNQKMSPIEKAGFKNAVSQRVRLMVSGSAALPVPILDGFREISGHTLL
ERYGMTEIGMALSQPLRPLHKRIPGTVGSPLPTVRVFVHSKSPPAREEDENAGEGRNTKN
YDEIGQLAINSKSLFDRYWGNPVATKKELVVSQEGRRYFNTDDTVGVRKPRDEKEDAVFT
ILGRSGTDIIKCRGFKLSALEIEAALLSRKDLFFEIAVVGCKDETLGEEVVAVIAAQRAA
LKAWGIPTNFNRFESPELNEELKGVARGVLASYKCPGRFIILPEIPRNPTGKVNKKDLKK
KLSL*
>TCRU_9089 electron-transfer-flavoprotein, alpha polypeptide,
putative
MLRRTLSAMAGKVLVVAEMHNGKVSPATLAAVTAGMKVGPVTALVAGKDATKTAAVVAKV
KGVENVLAAKGDQYEKGLPEEYAPLIASVVKDGYTHVFAGTSAFGKNVIPRAAAKADAMP
ISDVTEVKDDSTFVRLMYAGNVVSTVRSLDPVKYATIRGTSFERAPLDGGSAQTKEVEAT
KVEGKSKWIEDTVASSEKPDLQTAANVIVGGRGLKNAENFKILNELAEPLKAAVGATRAV
VDAGYCPNEMQIGQTGKTVAPNFYLGCGVSGAIQHVAGMKDAKVIAVINNDADAPFFQVA
DYGLVEDLFVAVPKLTSLVKK*
>TCRU_9090 predicted WD40 repeat protein
MSAKEYEKTARLALESVIGFGGRIPNSIIAHPDGENLVYGLGACIVIQKINDRSASSFLY
GHNDKISCITVSSSGRFVASGQVTHAGFQADVCIFDYDERRMVHRMLLHKVKVQALAFSK
DERYLVSIGGVDDKAVVVWDVSTGRPLCGAPAHHTESKAVAFFNSNCEKLITAGVGSLRV
WTIDPDDRKMSPSDVNMGTVRRCITTIVVEETDRYAYCGTTSGDVLCVLLERDANAFKMS
GPQNKLPGGINSMILTRSGDVLVGSGSGEVTLLSKINLTVFKSVTVQGAVSGIAVVQQGF
IVGTEESNVYLVESGNFNAELRLTCHSDTVNDVIFPEGFSALFATCCGPDIRVWNASNSN
ELLRIQISGFLCNCIQFTKDGSLIVSGWDDGKLRAFGPQSGKLVFAVNDAHKREGIKNMG
GSSSGVTAVCVDSTSEHIISGGADGLVRFWEVRGATCELVASMKEHKATVNAICISKNNL
ECVSASDDGSCIVWDLVRHVRRDVIYSQTRFRAVEYFVDESQLLTTGTNKTITWWDTVDC
GAIREIPGSKTGEVNSLSISTDGRFFVTGGNDRIVKVWGYDEGVCVAVGLAHSCNIQKVR
VSPDNKKIVSVGDEGAIMIWSVGDLDIHSL*
>TCRU_9091 AAA domain/Shikimate kinase, putative
MAVPPLPSHPTLSVPVAVVVMGPSGTGKSTIGLRLAQELGWEFAEGDNYHPAGNVEKMAS
GVPLNDEDRLPWLKILRTEAIEGASRAAAGSGVVLACSALRESYRDVLRSDHSGNGGRVK
VFFVELFGDIGFISKRLQGRHHAYMPACLLASQYATLEPLRPEKGELGVRVSAALEPEKI
VERVVEELRRWLHL*
>TCRU_9092 ATP-grasp domain containing protein, putative
MTQSNVDQRAYETLRRLGCSEETASRLLYRWWPDIEGCVEELRRRRMPSLMALEVFSQQR
NYFRNLSKSMLPIGKTQLPCFREEHLDEPSSGYPTLTWGEVAERINSSSEVEIFFLDVES
GIITDFDSYEEYYQNNILAEGFMDIVAFTTTVDGLVPLVDYLHARHFGGMQPPRACTLRG
PCVLSSNGRSINFTSGISLGNDVTRTIRSEQVILQPPRRRTRILLGNDVLTSVKQRQDKD

GMQRALKAHGLTHIRGISGFSAADAKRWRREQKIPFPVIVKPVSGAGSELVTICYSDEEI
DTAFSLTRNVKTTQMTDASHMLLQEYIEGQEYVVNIVSYNGKHVVSDVWKSWKYPISLYS
TRLLPSVEERLRREYKCTGRGRLPVQQNSTALLYDRIEFVHNLAELDPSSEVRRVVAYTL
QCVDALGMRQGCSHCEVRIDNRFGSVSQGMPILIELNPRMLGDTPRATPLVGYDQYMLLM
YLVLSAAAIPEETFSPVHCCSHNSDDGRRKEEDMQGLLPWPPAPLLYKSLANEVSCHVVF
LRAAECSVVCNPCIHDIIALPTFAYFTRGNIFDHLGKLGTLTSVEKTVDLLTSPVACVLI
GPVEEIRRDTEYIRRVENKDLTAWLPLLNAALELRPAFQGQTSTFPCPCSETSSDTKLAK
KERKLRPANNTSSFNAAVDEVVSFFTRIELPLFVPVDYFLKLKTLGLEHLVLGVSGGAKE
NA*
>TCRU_9093 hypothetical protein, conserved
MMRRAFSVFLCLPRCPTALPFLNDQTVRFSARCVASYPSPGTVRSDPRSGRKNYNYLNSK
RLVETEKGPRSRRAIRLRDDVFFHRRIQFREEINKCIENEIRYFPENVKRYVFFKNSSPT
ATGNGFQGMRKAPGWVQRRILQIVEGEILKLKNRDHLVELIESTGTVPPTKEEWARYTDK
KGRININLYHHFFVEKHLRCFCVGKRCTEKHRLIQAFLILNRNNFDVCPPLFTWSLRQGP
VRDEELVERGSQKEVRDIIAELVQFQRSSVMRAFEKLSPREKEALVIQAEGKREELRREY
EQERLFGSKLMCGVASLKEVRSMTSPAISYYNQEYYKYVIRCGGSVEATLRQSKDEVPSW
FALPKETKMKYYCFERSSEMHPISGAHLYFRYCSRDYGLSREDSVGKWSMLSELQKAALN
FCFYSPISAPRRSSSAFRRFYYNECYRHGLMMTGRACSNFAFLRRARKIWMGMSADERAK
YEDTESFSSVFPLQPLLSSRAKGSNASNKQRLLESSTASASASTTAEKMETLRGRQEPVA
VSKKNDAVEEEDDENEMFYFKDEIINEDGPQEENQTHEAKILSHMNSRSGKEEILVFSI*
>TCRU_9094 hypothetical protein, conserved
MGVASAWAVQSAADMRSVCRLSLSSSLKCWAVVPVGFLAAPAHRENQIPAAPERARNAMG
VQHVRHDTSAAAAVPSAHRAVCRASDRGGAGPAGEGGVSVQSSLRACCAASAPHQRHFLG
MAGCSGRSSHQYLCKTPVRRQASAASSPRVRVESVRVGSQSPLTAERRASGLSCRTQITC
SASENDAGAPCACELCEVERRLGLCITCFVLGYAAVAKDELHPCARSSVLRARRKVTSTM
*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MQGSLVVFFPSYSSRIYYNSWLQLSGNLCHASPSEAFAVLSPTVNLRDSTVSVSGNRFMS
STDKPTVLRISTWSRDITNGAIVAACNTVNGEEGASYDIPSVYNATILACSDPCNLAASC
FPAYTVTVSSDGCACACAEGGHGDACLPVAVPQPPSTDGADLCVRDVRVDVEANAGLGTS
VACYVGVTFAADVVVDMESMSGSVRNVTLANCTFVGGASLYIVGWRSDPPAGQRADVLIS
GLESCSGGGVLVENRFPPDSRVTVVDSVLIAEARVAYRGAYDLGDASACLVVHNVKLTGS
VLTIARTQVAAVFRDAVGVLLVGGVALSSRGALYVDRLLVQTALGLCVSVEGGVAASGGS
VVAFVDSGFLLCKHAVSVRGAVSVSGSAVAFMRSEFLSTEDYAVAFYSTVSLAGGSMLLA
KGNVHDGVSREMLHAAGAVTAVGSTLSFVRNRALLPRMLLLSLSLAAGAHVRVACNDAGG
SVLSTAEEYAAAGFGDAGSIDFAGCDVCDRDTHCHAPGTASASMKNGVCVCDCGSGGYGE
ACVPVGAPALPPAVGTASSLFVREGVTVQSVFVVPVGAGEVTLRHVVLDGVSPVLYVPWM
ARDGVRIVVQNVSLLNGAVLYVMGGGALRGAGTAGSDESGPVELSVCDVEALDGALVLTD
TFPAGSVLTVTDSLLVAARPTPLVYLPGSQSSLYAPVLVLSGLRLVRSVLVVSGVALVTV
MTGGRTVVVDGAVLELVGGGVALDVAVLGGDVALYASARVVASGGAVLRVSGSQVYAAHG
LVFGSGVEANASAVVVNDNAGALTDGALLVLRGSALFASGSWLSVRGNSISGKILSVPSY
PRSADLVQSTLTLYVNAGSGPVVMDGTVALGGAGRKFVVGCLTLNGQALRPMDYRSAGII
GEFRPVACGVCDADVHCFAAATRAISRSCGCRCAEGGYGRDCLPVYLPHVDGCNRTPGMP
PLSHTATLTETRSPTPTPTPSLSATQYSPLQYRPTETLQVTETVALPPTRTPTASVSGTL
WWSDVACPTLAVTTTAAGGSLTQNDIRGGGSAVPTRLMVALPPPFRWARDPQLGTQLSFV
LVSKAQPNGFGGPWGAMLSNATWVRNATNPSTVLELALPVHRGYFITADETIIIRCDAVA
VFGGCKGVLLGSFTIRSNTLPAAASALSAITGVVAGATAVAVVVTGGLGSILEMQALGVF
ARMPCASAQERASTVALPYFLSVFAALDPLWMVVGNALLAAVFGCVHCGVTAAFQRWRGV
DAASAWAAMRFPSLTYVVANAMHLGIFFGSVLALAMPGARVQHRVIGVVGVLYGAAFPAG
VCYLIARHTGASFTRYWQFSRKPLHERLLYPVGYWCPAAQQRMYGGMLTNMRGNRVYWCV
FQLSALCVVCLIAAVHSPVGGCHVQYFCMAAVLLVGAGVVAFTNMMRSAFLTVMRTASFV
LLAALCVISAANHLAPSDGGARAYVAIVLLLTTVLLVATVYGVVVWHAEDRHWQELREPR
RDGLEALLRDDEESDEDTRKPHEMKSSSYAERDYVLRRDALS*

>TCRU_9096 sphingosine kinase A, B, putative
MSNGKDGLFLLFSPTNGKNTRQSAEAGPGRVNESASCSSDELSVRVRYRRKEAILTYDRT
RENVSLQRLDGMGRVANVVNIPTWNIVNIETLEERGLRQSRHSTMGTAGGTLTKTKRSRL
FLSLFKDVPRRPEKGSQKPGIMSMSSPTQMSSHYCCAGGFTPTLLRRSSFGHIHSSDCPG
CLYYLHYVMQSGSSLQVSTLEFSPLPDCESQGKMGFLVQSILRSVYPSGTKKLILFVSPK
SGSGKAVSITEEKVFPVLYFTRHEVSVIVTTRVFHCEDYIADVVNDINSEHVIVCVGGDG
MIHEAVNGLFRRKQALLMRESAGMKQKKGTLHGEEEEEVHQKEECYEKKEVDRNENSGFF
VRDKYGSIEGKEMAETAQIADLEGAQHVGSNSSKPFARQFGVEIVSRSHSHSDIQPFSMP
LIATIPAGSGCGMAKTLDISSIKESVLALVHLRTCMKDLMSMQYIRNSEKEKAVASFPHL
IVNSAGDKGRTDDSRGGKKERVMAERIAFMTVTFGLLNTIDRGSEKLRWMGNARFTAYGA
YLFLRGVRSYSVRMRYLPWRGREGQQLAKFEKESFIPGEPELPRCTWTNACSHCQANRSS
TRSFTASLGVDGCAIASRGTAGTEPLSISECGSTDFDDDSLPWVKLDGNHYAIFLSNIRD
ATKDIMMAPLAHMSDGAIDIVFSREKGGKKSRSDFLKFFTTMETGNHVKLPFVSYIKARA
VELEAVEGFIMSDGEMMPFTKVRITPLRRAIEFVRGR*
>TCRU_9097 hypothetical protein
MGAPNGALALRKYGRVPFSPGASCAHSTVARCANSFPPKVSTARRLVEVAHGMPTSAALR
GTHAARPHPDIDDDVPPVPGQKSLLPGPKVLFVCVYRPPFAASLGTPCCVVQSDHVCGIV
LHWAGARHAISLLSEPPGGWAVPFLGI*
>TCRU_9098 hypothetical protein, conserved
MQQHSREILKDVTTALQLEQELQLSQAQHGVAILDVYSSEWGNTRALSEAFRRLYMDAGD
QIHLRFYSVECNSVLESLNFPAEQRNPQRPKNLELCRETLPAFWEGILSGRRGKSKSYFV
FYKEGKQRAFIEGVNTPKIVSYVRDLCRIQKPASECTSKAELLKFWEYNFSAAESEVFFE
SFVRAVQEHSAAKRPLTEKEERILADAIGAVDSKVSVEALDKWIGENETIQGAFTQLFPF
LSENGAPAAATAAADGSNFVEGTPGSFAAEKRAFEDDMELPKVFQESVENLMPELWRRIV
ALPLRCPSNTRLVLLSCEKGEEEAREYLQRANDVPTLNRYLAEMGLAAEDIQIMCCSAAE
KISSQSLSYGKLALVLMLCDKDRCEELLGRPEVLFDQLENGTLMSQHFPLAYTVICLCTS
EANSDESFYYCNDASTVESADTLKEGDEVVLPPFSRLCAKNATEGAFTVKFLGIPQVIGL
AATDPAGEGVVLTPWYAKFHVSGREENAITLTFAGNVEEEQFRQSVHLYTERVVAEEESI
AKVAAIVNVLEHALGYEQQPDPSSFTDPHLVERDASAEIAPDQVDSPAEIAPDDGGEISE
ADVAKAAANDDQNGEAEL*
>TCRU_9099 zinc-ribbon domain containing protein, putative
MSEASQFDVSQLEVRLGELEKIWKGVRELSLPLKSTHRRSSLRPRSASPSTKPRTQCRSS
AVTPNAPPRHPSPSLRVRRQQTVGGRESDAQGKRNGRRESVRAAAVERSGLLLPPSTSRS
RSKSPVTVPVQRDGVAGGNSSDMIPNSSSSGGLPPLETGILRQAPRFCPSCGFARPRVTA
RFCQNCGNQL*
>TCRU_9100 ATP synthase, putative
MSEARQIQSMIDFIEREAQERAEELDAAAQEEYDVEKMRLVEVEKVKVRASTEQKKKQVD
IDRRVARANFSKTQRLRVMEERSRIMDELRENTRRKIAAFVKDTSRYQKLLLELIHQALL
AVRTDAVIQSRKEDEAAVQGMINDAEQWYRKTVGSKITVTPSKEYLNTEEAWGGVIVTSH
DGHIICNLTLSCRMRNCFEDQLPAIRYYLFNSDASV*
>TCRU_9101 hypothetical protein
MSISWKVIDFCRHFGVDVPSDSEHVRPETAHLLFNQLARKGGVSLNDATARLRLQNEVEG
ILQEEGLDDGTIALSFLRGQQTAVNPEKLRECVASFLTDRRQLAGDTTPVGKHKEGSGAQ
AKGRQSLPLLEGAGLDAIWRGLVSIEAALFSTAVDLSRKSDELHQREEALEARARVMESA
EADLLKSKSVQQNEMRTIEAELERQRMALLVEAAKLEERRVQLTRMEEELNARSKETRLA
EEAVAAESTALKAEQAKLMVVRATLEQDRRQCNEVAHSFIDRERRLKETEKLLVQAKDEL
TAYERFLMRIREKKGSGKERGGGRERLA*
>TCRU_9102 TFIIH basal transcription factor subunit
MEVVCDGVPCRVEVRGYVISCTPLGGDGAAPASVFSRSEINQLLRSRRDQASAKVVVGSK
SITMRFVDPHDRERFIDELQSMESAGGDGGQWVASTICQTAVDLGLLDEAALDALIKEEF
PRGVVVAFDAIGSLFDPKTFKLRPITDQLESDIFRQLPVLAKIFERRVTDEETRQRFWEA
VVRKYFCFSRTFLEEEIRELEPEETAAPVPAGGEEMGLSSINVMSGRALPKVRSSVLHEL
GPAEASQAVGPHFHARLFCGQPITSRRVGKSRRCDVHPPHAFKEVSRPPSVSWVMPKEST
NRETLELLRRFWRSNVSQKKALRSKLDNVNNNSGSFLQRQCILRAREFIRELGPEEGC*

>TCRU_9103 BNR repeat-like domain containing protein, putative
MLVTLPVYSENNKEKGKLHLWLTDNTHIVDIGSVSDGDAAASSLLYNSGESGTDDKKEEL
IALYEKKKGSEKPSPSLWSVLLTEQLERVKKVLATWKEVDNRVSLLCTSLIAAKGPSPDT
ACGAVRITDGLVGFLSGNFSDGTWMDEYLGVNATAKNGAAAATGPSNGVKFTCGATTNTT
EKRRQLEAGLSQRRLMKGR*
>TCRU_9104 hypothetical protein
MHKPRRRPTSHSSQTHGAPASSHWPKVLFVPDSSSQRLTAPLQQATGNPRARTPLLLVWK
RPHWFASAAGFRTNADGCYGHCNPLSQANAVGVRRGFRTGVVAHMSNVCGIKCSKALREF
NFFGESERPGMSPEPPPTS*
>TCRU_C-terminal tetratricopeptide repeat, putative Fi.1
MERTSSIIDDLFKKDPNVRHILSPSQQELMGLDDAIRRIRAEYENNFTNSDITFQYACLL
ILHSRASYIEEGVRLMESLLYTAWKKRQAELAGASSVKTNLMPGEEVDSQEDILRGSVIH
AASAPPETQGEWEHFEHDAGEQEKETDTKSKRTTSTDELVINYYYLTIGWIKLRNYDKAL
ICVNQMLQLQSDHRQGIALKQYIDAEVNMTLTATGLAGVGVAAAVAALIAVCFRKS*
>TCRU_domain containing protein, putative RanB.1
MADGSEVRKRRPLEPNERDEVLDNTPKYADADTMAQRRIVRVQRTSVSDVVPSLKGAFKA
VPGLAPTAAPSLSTNFGLSGSNSISSGANFALAKVSFPVVGEAPSSVLPGAKNFTFGVGS
SPSESSKDNSGGMVAVGNDAAAGTSSSRETLNFNGARNVFAEAKERMAKTVADVEEEAPA
EEKLATSDALAQAAHVTPLTEEILACASCKLFLFKLETKSWVECGVGDAKLKRRESTEAT
DGEKGVKNLYRLIVRDGYALNAALSRNFHLTKADDTHVIFSIPKNDGVATYLVKYVGQQA
AEHGPEFTKKLKEALKLAQEDFS*
>TCRU_9107 Galactose oxidase, central domain containing protein,
putative
MASDVVYRKLNKYEWSESTPVKLVAPQSGEIIKEVLGGALACFEKRAYLCGGYDARTGRS
LSQLAEFDFSTKQWSKGPSLPEKIRDAAAVAFGEYCFVFGGWNDENYSKNFWMLAPKSPG
NNMASAKEAIISSWKLVQPAGLGPSARVCHAMVLGNMSDEEGTAQNPVLYLFGGFDGEKR
LNDVWRLRLSALIEQGVAAWELVEVKGGTPPAPRDDAAVAFDLAGERLLVFGGFASSLQS
DLHFLSLRGGKNEWTCQLCVNVPSRRQGCVAAVSNGHLLVCLGEDEKGSLSQVLQLSLTE
FKWCMLPFEKDELVGRRGCVGCVGEKGKRIIIFGGGVLPKLHSSLLEFELEKADAGSTRK
K*
>TCRU_9108 Sucrase/ferredoxin-like, putative
MAFAENSHDVIVSCLSKQTLQEIEGLDPAQCGFGREECCEPLPAKLPGSMALKEHLFLAT
DLPATEWDSKTGNVPGYSALEQVVSSRGGMKLTVFYRPGPDRCILRFKYEESLEYMLITQ
HSCITEGELPWESEGAISSDRSNEVFIFVCSHRSRDGRCGYCGAVLVELLRQSIRAKKGD
DETIHVYPCSHVGGHIYAGNVLVYTNHGGICFGCFTAAHVDAFVDFLMGGAAELPASLQQ
RVRGRIGYTKVNSRCCVM*
>TCRU_9109 hypothetical protein, conserved
MVLHKWAVVSKSAPPPPGLRPVARVIPSHPRLRPADYKIPYVLRTFIKDRYTSDMQHIEN
RGMFAEELAIERSRFPRFHKTLTIQTDGSINEREFEFVVPPVVTLFYDRLSAHRQRQLEL
AKIGKLRKERSWETKTVGEESSNPVCNALVFPYCVPKMMWKRPRLADPLSAKSHVRGSGL
TTADH*
>TCRU_9110 hypothetical protein, conserved
MYRGRQRSTILHARMGHLVYCTVIRFVATSFSDGTHGSGALRGSGREINALLREINDLWV
RRGASEHKISVSASNLRPTMATAMTDRSPVQPHVSPTVPAAREDTPRGPVITKELPVLTD
IACTLQELEEELFKLSADEAAVTEPPNNACIRGLKLENENDENEKGAVLSFNGPSEPRHE
AMNSAAAESPAASCFFESLCHHENLSCWMDAEETKPLHNSITLQVSKSSDRTFVLELREQ
PLCARDVVLAVSQALNEVESLTELSEGLVVVFRSVSGIFFFTPQLSELEVSYLARAELLR
AKERLFCRMREARLCGVSFIAELNHSAFNIGAELFFMCDSKLIPESGVCGRVAKVGFPSV
SAGVWPAPCVVQCISSLLGYGEKVGLVVPIMHTIPWSELSERYPQLLQSGCTSQRLQEKV
YRLFNLQWDRLCELLGWGTDRSAKENRVDFLMRHWDNYCALVDTTQGGTNSVLDFAAASR
GISMYVTLLGTSDFCNAASVTMALRRMRYRVLNPPPRGSIIELRATDMSSVTVGESFCVF
TEASSPETVRFIAEHRSFSGNGVIKSALLMGEIEGVKDAADLLDCAVVATNLRPSKLCTL
GEGGNMVEVQLLCSPHVRKIQQREALSSALAYLQSKGIPYIVSKGDAGNRLVAALSLELC
RLATEAEMRLIDAVAREELRFGSNPFQLLDCHGMMYITKVMGRHPHLADERRVPPITRRV

LSAMDAEGFGGEGVHRGGFYNCYGSLNPEIRTEFLRRRKLSRSDIFLRLLFALVNESCRM
LLEGCVETVNDIDLLSIGALTLNLSTGGLLSYVDSGIGCLALLRNMNYLSRDMGVTDPPS
PLLQVMLEAGETFRTLSPETLYQARQKFVGGI*
>TCRU_9111 flagellum transition zone component
MDVADGCVLGKKSLEAEELEASADVLEPRTVRIPATTVSQEGEVIDAASFVPRTPFLSSR
TFLSSKAKRATDAVDPFQPNTLPTDDCFIPRRRPGLRGMTFKTQCKLSVSPSKKVREVGA
PYRESHSKRFRDRVMDARECLSNDDRVLLLVRERNDCKAELREKCEQIKKLEVSLRAVRA
QLARDAAKPGSSVAEQENSINDLLVARLVNENNDLEKNLREARAQISTWKRDARVSHLQE
LKLELAVYQSEVARLYSVLQGGRERDLRKSCVESRLREALDAVKRKGDIIRELREKLSEN
AAALSRSLEDAMRSQSTAEQLQEENGALCKELQVLRKVSIELTHNREELERTRADLRETG
KELREYKRLMERLGSPAEIFTIIKERDAILNMLKEQNAREEAQRREFTRQLGEARQNMEK
CIQKALQEERALAKDKEAQLRHTCRMWKEQYERLVLNSATGRELQEKQMQTQKERQEERQ
QEQRLISSKVPLQSNEQSQPKEVRMRNRLESQSVKSPVVTLQTPSHAGVTSKASLSISNL
PTFKESHCGSGINNDRAFLAENVQQDEIDRSSIKKEKGHESCLSGRHGHSADENHSNSSG
LARVFQQPSAAAAAADTIEEEEVFTMPAKGSPKRSETENVVAGIGSNRIGDLLEVPHIPL
ANECSVEMTSANSLTRNASPIADVASMPFSKHDKNSEDSLPISLKVPPSPPAAAPALPAG
SSSTSAVHLASSLSDVPGDSAGEYFKPKSRYQEEDLWETVSPVEEDESFTVHHV*
>TCRU_9112 hypothetical protein, conserved
MSFFTKVRAVFQKGNNSSPARSGRNGFTHGGLQRDSTCGGPNIWPVNSDVQRDIQEGPHL
NMKAVVRGMRRTGKSTIVSRLCGCSPPTSYVPSSEITADTLFYRGTAERTGDCGGGGAKV
ELWDVVDEGISTSQSASITTHPTLADARSIDVYRGCHLAAFVIDRTRKETLDYAVREARH
VPPDTCVLFILNFYDAPRDAHVVSDGDVDAACKSIRRATTPMILAASAGRLPPEEYSISA
TWVSISAATGHGVELLRSAFEIPYSLLKVLTFEVRIHAYFQFVEEHRAWLLSERARLHLL
EKEKQHGAQGKGKETPETASRPLPGGDALQGGEVRGPPPLNVVSGIRAYHHVEEDENGIA
KDFFNDIQEEEEEGSDARAKRSSSGSSGGPGKRKAYPCEAVRPKASLTSPPPSDPKTKFA
PPMSHLTPSTTKPLVAANSVPSPLVDGSMPQVHLLADDFRDIPDDVLNVGDDQGLDVNFF
GSGLSGEGSSHHVASVSTDKSDDEGDSILMNSNAVPRAPLGITVEPVNEVSIPPDTLSIH
ADVKTLLQEMQKALGTSINEEDTPHMRHENRKGHFRRKKKDAKRNKGQHHPRGRVEGSPE
VEDSIPDDGTFEVIQE*
>TCRU_9113 small GTPase, putative
MLECVENSIKVIVVGDGNVGKTSMLRRFVKGEFVNQYKKTIGAEFMEKNVFLRQSNTTVK
LMLWDTAGQEVFNSLTQAYYRGAGAAIVAFSTVDKDSFMNVENWKKNVENVCGSILMVLC
QTKFDLAHEAAVTNEEAEQLAIQLQLPFFRVSTKDDFNVTQLFEYTASMCLNEEPARNSS
ASGKTSSNLNSNEIHAANAKRQGTQSVRRVDLREPKKSEKKRRKKLCTLL*
>TCRU_9114 chaperone protein DNAj, putative
MGIDYYKVLGVGRNATPSDIKKAYHQLALKYHPDKCTGNREESERRFKEVSEAYDVLSDE
NKKKIYDVYGEEGLKGGVPGAGEGGSAGGAGFHGAFPGGVRYTFSQGDAFNIFRSFFGSS
DPFAGGEEFGGGGPGLHRVFRGFGGPQGFTSGFGSPEMSPMNEVPPVEYTFACTLEEIYT
GCTKKFNVSRHMPGGTEKKMFEVKVLPGYKKGTKIRFVQEGGIVQGYPPNVLADLVFVLD
EKPHPRFERSGADIRTTVHINLKQALLGTTVNVLGLDGTTTALPLTGVSKNGRQLRVSGK
GLPDRKTGRNGDMYVTIAVDMPASLNDATRSLVEKCQF*
>TCRU_9115 hypothetical protein, conserved
MAMMMAGRVLLVCALCVLWCGVGCGFADKVVEAAAGVVASNRTDEENLILNWYVLTQEEC
ANESTTGGKLNVTAERICMHKVMKGVCDAFYNKTSGVTHDRDVEFICTYYATIPEEPVEP
PTPQGPPSHSAVSNATSDEGTPKNTPESDVAGRGEGKQDDKEHGNTKQKAVETAAVESIT
RTTDSDGSTAASHTTSHLLLLLLVVACAAAAAVVAA*
>TCRU_9116 hypothetical protein, conserved
MNCGGVNFPDGTIHSPARSSDADRTGICQLPPPREGKDDTKSGGTTAPQVNAEPSRQHED
WRQSAAADGPNTVDRSPASNTATNTSGTRPEFAANPIEMMVPNASTKRPSFANGPRISVA
LNALGIMSVTCGGREHVAADNTDEASEHDATGHKSLVLENGVAGSGFAAEGDAYGLSQRN
ACGRDNKPQ*
>TCRU_9117 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative

MLAGIYGLEGAAGAGKRRTDEVGLLLTRGNISVDDDGRNKTIHWTDIDTLPVISNIQQNK
SLSVPSGGGGSGVKMEDGTLVFPMEGKKVRTGESNGTDAAGGRNTVSLFIYSPDNKSWKL
SKEISADDCSDPSVVEWEKDKLMMMTACDDGRRRVYESGDKGTTWTEALGTLSRVWGNNH
KGHEKGVRSGFTTATIGDNRDVMLVTLPVHSNEKDNEIEKDVLHLWLTDNTHIVDIGLVS
GNDDDVAASTLLYKSVESGDQGNKEEELIALYEKKGGGETPSPGMVSVRLTEQLNRVKEV
LATWKEVDERVSKLCATLLAQVTSTDNACSAGKITEGLVGFLSGSFSDNTWRDEYLGVNA
TVKSGIGADNGVTFTGRGAGAEWPVGKQGENQLYHFANYNFTLVATVSIHGLPKDGDTSI
PLMGAKVNDGAKNTVLLGLSYNREKRWELLHSGEKTSEPSRTWEPGTTYQVAIVLQNGNQ
GSVYVDGQRVCESVQIKWENTESKGISHFFIGGDGGNAENTGGDEGVSVTVTNVLLYNRP
LSSEEIAGLAKINIPKSVAARASSPAVSRPKSSSESLAGGAMGVGTARHFGANGDGSTVC
GSGLLPLILLLGLWGFAAL*
>TCRU_9118 hypothetical protein, conserved
MAMMMTGRVLLVCALCTLWCVNGFGDARDNRGIEGEKNLLTHTHNGGNDRARYVLTQEEC
ANESTTGGKLNVTAERICMHKVMKGVCDAFYNKTSGVTHDRDVEFICTYYATIPEEPVEP
PTPQGPPSHSAVSNATSDEGTPKNAPESDVAGRGEGKQDDKEHGNTKQKAVETAAVESIT
RTTVSDVSTAVSHTTSPLLLLLLFVACAAAAAVVAA*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MFSASSLLVSNIKAHSLRYGALGLYSIGTLTLLHGSSLYVQYCSFDGYEHLFYLNILSVS
DHSVLSLLNNTIFFGTSLLCQQQELSVSDHSVLRVVGNSGSVSHAIYSLSFFTVRHSSWL
DWHDNDVGVGAMFHYSIINTVNIDGSSVVTLTGCTMGSTGLSVPLLSQADAGYRFVAGCL
TVAGRLVTTAAELELHGITDVTTVAACGECTKDGDCFAPLTTAVIDCKCQCAAGGHGDVC
VPAPVPAGPPPPPPPPLPPTLTPSPPPVGECISDMVYPEVAQAVGGGLSWLCYRNVTFS
GGGMSLTVLVGAMTGDVVNVTFDECTWRDGAVLLLLGNAYAAVGSLNIFVTGNTFSDALL
SPEGVFPPHTNITISGNRFTLTWLVPRSGLDIRRPSCVVMNGMVISNDSAVVLSGNVFQS
VTTSSSAIYVVGSALRVSWHSVFAVVGNTFHMAGGDGTLIYLEGSSQSLSLSVLNNSAVV
IRGNAVTRPVKCFVLLIWTLDVESHSAVVFQGNEMQRSSVVFYSSESSNIYYNSWLQLSG
NLCRESPSEAFAFLYPKVNLRDSTVSVSGNQFVSSTVSPTVLLIPQSSRDLTNGAIVAAC
NTVNGEEEANYAIPSVYNATIMTCSDPCTLAASCFPAYTTTVSSDGCACACAEGGYGDAC
LPVAVPEPPGTDGADLCVRDVRVGVGVNVSFGTSVACYVGVTFAADVVVDVESMSGSVRN
VTLANCLFVDGASLYVVGWRSDPPAGERVDVLISGLESRSGGGVLVASRFSPGSRVTVVD
SVLIAEARVAYRGDHGLGDASACLVVHNVNLTGSVLTIARAHVAAVFRDAVGVLFVGGVA
LSSRGALYVDGLLVQTALGLCVSVEGGVAASGGSVVAFVDSDFLLCKHAVSVHGAVSVSG
SAVALVRSEFLSTEDYAVAFYSTVRLAGGSMLLAKGNVHDGVSREMLYAAGAVTAAGSTL
SFVRNRALLPRMLSLSLSLAAGAHLRVACNDAGGRVLSTAEEYAAAGFGDAGSIDVAGCD
DCDRDTHCYAPGTASASVKDGVCACLCGSGGHGEACVPVGAPALPSAVGTASSVFFREGV
TLQSVFVVPAGASEVTLRHVVLDGVSPVLYVPWMARDGVRIVVQNVTLLNGAVLYVMGGG
ALRGAVSAGSDEGGPVELSVCDVEALNGALVLSGTFPAGSVLTVTDSLLVAARPTPLVYL
PGSQSSPYAPVLVLSGLRLVRSVLVLFGVALVTVMTGGRTVVVDGAVLELVGGGVALDAA
VLGGEYALYASARMVASWGAVLRVSGSQVYAAHGLVFESGVEANASAVVVNDNVGALTDG
ALLVLRGSASFVFGSWLSVRGNSISGRLLSVPPYPRRAELVQSTLTLHGNAGSGPVVMDG
TVALGGAGRKFVVGCLTLNGQALQPMDYRSAGIIGEFRPVACGVCDADVSCFAAATRTMS
GSCGCRCAEGGYGPDCLPVYLPHVDGCNRTPAPPLLSHTATLTETRSLKTTWTATQTPTP
SHSTEHYSPTPYGPTETLQGTETVALSPTRTPTASVSSTLWWSEVACPTLAVTTTAAGGS
LTQSDIRGGGSTVPTRLMVALPPPFRWARDPQLGTHLSFVPVSTAQPRGFGGPWGAMLSN
ATWVRNATNPSTVLELAVPVHRGYFIAADETIVIRCDAAAVSGGCKGVLLGSFTIRSDTL
PAAASALSAITGVVAGATAVAVVVTGGLGSVLEMQALGVFARMSCASAQERASTVALPYF
LSVFAALDPLWMVVGNALLAAVFGCVHCGVTAAFQRWRGVGAASAWAAMRFPSLTYVVAH
AMHLGIFFGSVLALAMPGARGHHRVVGVVGVLYGVVFPAGVCYLIARHVGASFTRYWQFS
RKPLHERLLYPVGYWHPAAQQRMYGGMLTNMRGSHVYWCVFQLSVLCVVCLIAAVQSPVG
GCHVQYFCMAAVLLAGAGVVAFTNMMRSSFLTVMHTASFVLLAALCVVSAANHLAPSDGG
ARAYAAIVLLLTTVVLAVTVYSMVVWYAEDRHWQELREPRRGGLEALLRDGEESDEETQK
PHEVTTFSYASGTTAASSYRPPAPP*
>TCRU_9120 hypothetical protein, conserved

MRLNDFLTMELDGRGALDANRDVLLKEFFKDPKKYICDAGVLNEMQASDRYKRMERAARD
EMDMAEDADKLYNKGMYDLLRSLAQPATSTWCQGLVLFTREEAKRLLFMLQTR*
>TCRU_9121 hypothetical protein, conserved
MARKTVTTDVDPMLQETYLQDDSKDFLPTSEALDRFDAQLAKGEPVHSEPSLKRRMPQAR
GANSLPCRRSFEAASQQPQQQKQQQLYQQYCGRRSSNDAPFQANKGLPEEAQERLEDIEA
VRRLGNDMAGNDD*
>TCRU_9122 hypothetical protein
MCGVFVAADALLKMRAELLEAAHARKAAMLAFEKQRISLFQEASEAQKLLAGMEKEDLFW
KLWWKKLFLLQARLLSRVAHQRLVLGAERVSHGKGVLAHLVMCSPRVQLGVVEGDEGCVP
QECVHVGMGAIPILRNTGVELQFRLVACGAKDNGGGYWQEFNEYYFKRIQRVPFVLTYIA
GNGGLTESSSILAYAETATDGSAACIITFPYVLLDDAEVNSFHTLLVTHPRTQYGIIPPL
EVTLLLLAPPAIVVKDVSLDDKLTHVESHLKYQRKDELTPAFRRELQVCVEVCTDEIVTQ
MLFECVEKDPQGKTYLVERKQLDAGACKRRFLEEGHWIFRFCMAIAVKNEHNEAGVALTV
VVEVTLESMPHHVFREFIPVVSPLERKSNNAPNRPTATFSRHSASTSSQEVPHAAGTLEA
NATAKDGEDFFELFRNDEKKVLMMATDDEVPALRSPLLDQSNSTFKKMNETEWNMRLKSY
ILDEHGVIGLPLLNGTSPMNVSPHLVCYPYNSMGVPRSGVGVPILGWQETRHGVTVTDDY
EKRPLSLEWALEGCEDAPFFWLLRGPGGECVVLHRSNRSRTNNSMEACCFKRFPPLSPPS
RVVAVDVNCRSANDYVVKSMFSASLQCLVCQWASGRLTCTEPGGESMTLLDDDDDGILAT
CTWNPDEEEDASLIVCLQQGRRFFVYSLDDREVIVHSSLPLTCSPVGVDDADDSQEYIGV
APVLGGDAVAMWTATGVEMLFHAPTWRHQKLYTTASSSTQILGVCPAYSFPRETTDNKSE
DGADEFVFFATDTMGTIVLVLLLSNGTCVGLSLDGKVHDLGFLSPSFSSLPSCTLGTLTI
EDLPHVSSLTMRHVKVNGRPVIFICGLTEHHVLRWAYV*
>TCRU_9123 hypothetical protein, conserved
MDDISQVVQKYYEVIDQKDEDIFELYRDNKRLKKQLDEVLAGENDRETDRRTLKLLVTTL
QTELREKQMLIEAQQEEGSAIRHAVWRAREVLNMSSELDYPIESVIGACINLHAECCELQ
ARQEYLFSVNPRTKSLACNNLFEAERYARSAIADACSGAYATLSLFLRCAKQAVAEKQQL
CEAHRAAESAHNQRVELLEKRAQLECSQHERIVEEWKEQVTCVNGRLLLLQRQMRYERAE
KELLMGAVCSRLDLMMEQGADLERLLALAFRAFIRHDKQLQEVRQESLSLRGKLQKLHAD
LSRARALLRRRKESQQQQSLTLDTSGRVSVRTENGEEKNCSVYDALRTVQVEHEVLKVEW
RQCVERERAVRQQAATTISKLKAERSACEATVEACQERCARLEKALQRTRQEAKRHSNEV
NRMKELHGTLCDEAKVHVERIKNLEEVNRVLSEENMTLTSRMEVLQERAQEKEVAWSSAE
RAARDRIAVLEERMKSEKEGFLSELKEWTLVLEEARKKLAVAESERDRERMLRGILVEQH
RDEERMLKKMMAEEHQSAVMVLQGKIDILERACGRSATVIAELREALHRAKTENSTA*
>TCRU_9124 hypothetical protein
MDSLSGLKTRQMQGKDAPLFVRRTLSKDDMSSSASGAWNSEAGSNLSKNCLLQAKGSGQE
KAEGKDPCREIVTNAAEIRRRVHRANIITSRLRDSSGKMMQRLRQKKGFAALNGHGDDES
LVREKLCCEFRTEFSAALEKMRSLHFFGALTTRERIEIPVTRAAFIASRKNMIGIQKNQQ
SLLYRQLFTAWQQHYRLCRDMLRRQRDIGGSRTNTSSFIWRGDSETSSLWEKTAGGVISS
SLDDNAEEGNLDFRKLQDHMNTLHAILWDMQRIAATQQELLQQLEGDPINRDSGRCRRTA
QIAADKPCCGRNHRCGCCTTM*
>TCRU_9125 hypothetical protein, conserved
MALAECKESDRSVVKQGRRRTESTVQRFAKTAIGEGFDLWDRDYLLGAMRLFLFKGETAP
PFQVGPCMDATGEILVQMEEYEDAGEQFTAAAAKYALIQQPGLAKLMEIKALECSKGPRA
ALDEVTAFLLQQTTAPDFSGMTPTLSRIHAYKAELMLKTAADSGTMEKAVDLAKTACQVG
WDRAHTAYLILGDGLQTLGRLEEACEAYANAVKFNSNCIAALERQMGVLKLFINDTSDES
RLKTLRKELLQLLDCAIALHPRPTLLREKAFLLSETEGDVAALQFLDPLIKNPPPEEADA
AGGVAGQTVATLLKAKAAILADGGKMSEALLVAEAALRESPGDEEAAAIVAELQQAM*
>TCRU_9126 RNase H, putative
MQHHRRGPWILATDGGVDVPKSAGIGILLSSLHSSEIIEKVSTNGGTRPCSYRTESRALL
PAMERLSIHRIRHRRKTLLVVTDSHSLLAALNKGPLSQTDWTEDQIWQRLLTLTRAGWSV
HLQFCYGHCGVHANEPAAQHATRAVLTHSLQADRLTSPHRACRGTFSRGGVVLVSVVLAA
TPCCGIPIRNQSPNTATRCNIIAEDRGYLRPMAVSTFPSQPGLAYCSHPCIPRK*
>TCRU_9127 hypothetical protein, conserved
MFRYGDYGPLLPPETKRRREETDVKVRRSRVCPYATRVYRFISEDIATQIKVCSEVLQVP

SAKSFNLSSLAANVSFDVSCPSLVLTMWKDTTLAEIATLLLDSFRDGADHVFFESQDAAQ
GGAASVTCSRATRCASYVIKLYSGCVSAEGNATLCCLATIELRQVLSEESFVFPVRRFSN
VDADMNLSLLPYKFGDPLFFTCVRVQ*
>TCRU_9128 hypothetical protein
MEFLKELPVSGLDALKNKFLLCEHLGGLTEEEFVEVLLRVCADYSTVNSPTEAEVRRVFA
RTDLLGIGRISWEEFSMYAIDSLRKREHRVMTGEKENERFHPYHVEQLLSKVHAGSVREM
RVLPKIGKVMVVTTSIGGCCTMNLCGISRNLPLFGTIRQNSNVPLAWDALPQAAGGLFSN
SIVCSYHGGLVRLFGVTKPNCFDCYLEEFQLMHLTDTQSAIHWVPFMNRLAMGSCKGLVT
LWEMQNQSVMLRKRLSRRLITKMQSRNQLLYVASLDTNEAVKCLDLEHGRVRYALNDHTV
GGATQLLVDDQLLFSAGFERGIVQRPLALSRSEPVLLYDSLLPHQGCISALERLKDTSLL
VSGDTEGNLKFWDLRMAACLQTIKGKKTSSSNDCHTLPELQEDLKEYCAASVRSICHIDV
LGKLAVATSKELLVLSSDVSLRPALVDDRCSCRFVYFPNPEFFLTVHDSCAKLWSAPTGM
LDRCTGPDITKFDITSGCLLEPLNRQLLLGTMGGELKAFSVALLELSLDLTPAIQPYILG
REITDLYTVTRYGDDDRTYVMVTTESTIIIVPFRPDCGPQAVISFQGIVKRFLHWNQIIK
ATAITELHFIVATSDARVHFVNYRGLFSVTHTFHMPAAVEAIITKPAFMLRGRFAEEGIK
SSQSKEFITFFADVSGRVHIAAMRGCTSNTNGKHSQGGHVTLTEQREGYYSKVSGEMIGS
WLPRKPESWIGTQLEERFRQQEIGRLQSRTGKRSSILNTSRTKHARTSILDHRFLSQDMS
LPDPVISSAVNIVFLDHHNVLVTLDEEGTVQFWNVSGAVAHYLDDSLASSPVLIATWQIP
EQEVIFFGAASHPTLHLPLLLTATSDLQVTLWSADGIALGTLSTGREADEASGGRRFGLR
PYRLLSEDTTAELWAKFITQMDRMVLSDTLKDSPLRLRRRSQVTLTFSQGREGVERRPSQ
LNVRRASQHSWRPRPSVSLTHVDSTEETAIVRSQRGSNNSQSFQSDNDKYSGFDEQCEAD
IRSIVKPVYQSLVKCTDSSFSLKKTGVVSLPPLNAATGSRRRRFQR*
>TCRU_9129 (H+)-ATPase G subunit, putative
MPPKQDNVQRLLAAEQKRNKIIADAKARRQAKVKQAKIDAEQEVAAFRREKEQEYEQYRA
QQLSGADAENLELARGTELQLQELRTLTAKRMNYVEDMMAALILQGGELKE*
>TCRU_9130 Glycosyl transferase family 8, putative
MAAVMRSMTRRRQKAYLLLPLFIALTILWLSLVHLVLSVVEEWAVAAKSTAAEVPEKTDV
IVAEPAPATEAPTGSKLKTLMALGYERETRFDLDQRNAWRWSNGSCPMAAVGITHVARTR
HAPIAYLTFISNEKFVDGALVLGASLRKTSVFLQHEVADLVITITSNCVSAVSRKRLLEE
GGYTHVFEVPSLAGRIHAKSGIFRDTFDKIYMFNLTMYEKIVFLDADMIAIRSMDKLFSK
PKIWGPDYVAAVGGKDYFQTGMMIIIPTQEMFNCIYDRLIRGTPPNGFQFTGSSARDGVL
LRDVFQKRFHAINPKYSRNLNPRHRLDMKLPGKQSIVAVHLRGIIKPWHDRRLPNPHTEL
GKKEFGFTYLHWWTLYEEEIHKKSAYYLKALHFQSKGHAPGSKAIVVDGIAFGMQHTDAG
GSLVSPLTHVWMQRHSKDAYTQLLSSEEKRLRNRTLPSMRKIPSPHFGLSCDAVCAQAGL
RCALEALYFTSLNDCEELRSVFGCSRCEMGVYWRPHPGNDFPAVEDVSQEMEHENKERKR
QLRDNSTNLVCRYNYLHDARGVPNCTASYTTTRRYCPCVPKP*
>TCRU_9131 hypothetical protein, conserved
MMRRGLGQHATGLVAATVAPAAAVNFLSSVLVTPSRGKYVRQPSPQWDPLHEDINAHVKK
RIPGETRVDRVRRFAREWRNVELELGVYKDSRGREIKYRKTFVYRYTYPNAFDEFWWPCK
*
>TCRU_9132 hypothetical protein, conserved
MADRSIAVATSPLLADGNDDDCTFSDQFALIARRMCRALLRHPQLALFYDYPHVMYEALH
NFFAHWSARQQRASSLSLTMEQTMNLLRYGESTIRSVGLSEDALARKQTAAELVAVSPLI
AIESLSHELRSVQVSVGVIPLAEIVELARVLDNAQGLVTPFGALNLVHLVALGATLCLAP
EMKTLVLMVSSCLHHRLLCAAVFYEWSLIDTPNANALRELSKRVENEASDDGIKEVVSSM
LGSTLESFGNQPTDPVITDATIEVTAPPAECIASSSPGTRPQKSEETLPTAQHKDGIDGC
KSLEEDAELNDGSDIGVTDTVDVQFWRRLCS*
>TCRU_9133 hypothetical protein, conserved
MNFGKTTTLEDQGVDSNKTTFYLLLLITVNLIERNGSVFLYTATGRSDIGARMLDLARQH
GDVRVQLAFVDEHGSLDAVVAAAATMTGLRLVSGDIAMHWEEPTVAGHFANRRAPQVPNF
EVRVLLPVVCVLPGSWESSRG*
>TCRU_9134 hypothetical protein, conserved
MLDLARQHGDVRVQLAFVDEHGSLDAVVAAAATMTGLRLVSGDIAMHWEEPTVAGHFANR
RAPQVPNFEVRVLLPIVCVLPGSWGSSRG*

>TCRU_9135 hypothetical protein, conserved
MDECIRSRTDWKERVVLRLAWITASCWSEIAALTPNNFTLEPDGTIISNWPVAPRTARAD
PHRAFRFFRTRGQDALDTIKLCRTQRKAHEYYDCPSRTSSGSLECHGAFHKTGYAEAHCS
NRGGVQFEPTRDLAVGEARRSVRTSPEHSAIFGELHHNADPGAVAGRIDVKGETAEG*
>TCRU_9136 Alcohol dehydrogenase GroES-like domain/Zinc-binding
dehydrogenase, putative
MATNAKGYAAPSAKAPLAPFSFQRRAVGADDVSIKILFCGVCHSDIHQARDEWGGSLFPM
VPGHEIVGHVTSVGANVKKFKVGDTVGVGCMVDSCERCVECKRGLEQFCVEGTTSTYNSR
ARVSGEPTYGGYSDHIVVKESFVLLIPSNLDLAATAPLLCAGITTYSPLRHWGTKAGTRV
GVVGLGGLGHMAVKIAKAMGAEVTVFTTSEGKREAARMLGADHVVISKDPGQMRAVKNTL
NLIIDTVGNTHDLSPYILALTTDGVHILVGLPENPHPPVSPFLLLKGRKSIGASLIGGIP
ETQEMLDFCGRHGIVSDIELISIDYINTAYERVMKSDVRYRFVIDMATLGQ*
>TCRU_9137 Protein of unknown function (DUF2826), putative
MLRLGDPHIVAVLTSSRGTTRIDALSGRSEASFEAQQGTGCVDAATTCMECHDGTVSCGW
WNICFSEATERELLLLLASLLPFVASHADYRLSADHVCHASTGDVVCRHSTAPVKRTSRR
MPWLWIWCCECSRHYFARLLFTALRRIDASPPESFTAAPCVVLPAHDSPVVWRLADSQAP
LCWDMQGCGLPLTVLGTAVWMWRPHERMYCGTIKCVKYAES*
>TCRU_9138 hypothetical protein, conserved
MWRCCGRLHVALLRERWALTASPTGVAVRLHGAPTTEPCECHAQRHWDSGTKQPRLPFGA
SGACWPQLGGASGMPHRTGVVMAPRRGSCDVSDAAARHVVESKVWPQWTMSGTNMRLSDF
LWNYVGGRAAVYERLQCNDGDVCSGAG*
>TCRU_9139 hypothetical protein, conserved
MNEKGTITPLARGTPNGVLTQVPTEARREAEERLRETQEMKFTISTNIEEVLFKGRVHIN
EMGLNDFLTRELDGRGIVDTNRDAMLEEFFKDPTKYIRDKGALNAMQAFGHYLGMKRALK
GEVIFDEDIRELCDRVSTTYRGGHWLLRR*
>TCRU_9140 retrotransposon hot spot protein, RHS3, putative
MYLLGPIPRHVFDEEAFNGRCGAVKFALQSINEVTVKEHFSRGGESPRCSEDPSHKLVKV
VREIYAGGVILFNAPISDCLEERTLERLPSVAE*
>TCRU_9141 retrotransposon hot spot protein, RHS3, putative
MLASRDNILPIFFGWFALKSFTESAFAKAMATELTEFEPPTGRQAKPCVLKLAPELHPKG
DEGLLPSEYEKTIRKMKYRVLHTPWAANFSLVDAFFFFSESNPRTLVGLRMTTAGGRHTT
AGTVRQSTECMVAYFNGWEELSRDISWEIIYVQHADSTPMNDWQRCDAVNFNNVSDDEGR
GIAAFCEEEVRQYQVSILKKVLENVVGVLNL*
>TCRU_9142 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily, putative
MLYTQRGYTSGEKEANALYLWVTENNRTFHVGPLFLEDNVNETLASALLYSDGALHLLKE
RANEKGSAISLARLTEELKTIKSILSTWVQLDSSFSESSTPTTGLVAVLSDDVNETLASA
LLYSDGALHLLKERANEKGSAISLARLTEELKTIKSILSTWVQLDSSFSESSTPTTGLVA
VLSDEANDGTWTDDYRCVNASVTKAAKVKNGFKFTGPGSRAIWPVNSREDNNQYGFVNHD
FTVVATVTIHQTPKKSTPLLAAGLGDGAGANFIGLSYSMDKAWEPVFDGTKKAQKNTWEP
KKEHQVALMLQDGNKGSVYVDGVIVGSPEKIPTLGALGREITHFYFGGRRGRQRQQCSWI
PRSLSRPHPRRVWWQFCPMRPTMARGPTITAA*
>TCRU_9143 Protein of unknown function (DUF789), putative
MASLPLASHVPVGCDFYSRINSVSHQCVAVAGYGRGENSKNAETRHGNKLHGAAPLPREG
GQPQRSTEKQLRWVQPPASSEMYSLPPPPPPPPVNSSKTPPATAMAAAPTASLVPVVSRS
EAAQQGRVNSICCYGSLQTWPSSGVISKDCGRGTQQVQEVRNMKSSTNDTPTQWPNSYSH
DAAGGSMYPYGYSSIPVAPFSYFSCGAFGQTIPQACSSGSMYYGASAHCAAAAAAVSGHQ
YNYQHNQHNYYYHHHHYCNQNSQPYYQNQSQHHYAQHQYMFHHHHQKKQQIQKQQQQQNT
GMDPSLATVCDSANSSTEKNGVPTTEALKPVRHAALATPDKEEEKEEGGGEETSSLPRDH
AAEGPPLIDGSEPCNPKIVHEHQPLVESDSTTSRRCRQDHAGGHIQTSTTRFDDVNGSSS
VKSSWGPGAGRGEAATFTSSENILGFIPSFSPISVTPSQNTADTPRRASLPSYHDAIMTQ
RGQGNHSLFPHKTCCTNGLISEPQEDLFILRTAPHKRENNSKFSVGIPQEPLEYEEEIRA
SESTEGVLDNGWQRNMAEGHPRGEPFEASQIPPVFASTDSMRALHHQYHHCYSQQQQQQH
KHYYHDSFLLQSQTLSTGLLNAYGASTAHQRSRSFNAMTPTSASFQCPSTTQASGVNRIN

ANNRIPLNGASITMDSGGGGGGGGAAAAAGSQQTNMPDLMWQNSLPLNNSVSAPLGSKGE
GYADGESASNAILRGTPINSATVCQNILQAPLYEHCGAQEVLFEERDTELPFDSSSYGNI
VSFIYAVSPVVEMDQELEWVSPSSAVTVPPGREKVGGDAPSQTYREPSISLANIWKALDF
PFACRIPFAEPASLAPMRPPQKHLVYVPFFSGFRLRFLEKSATYAKLKSIYQSTDVTSPT
ASHPVTANRTTHMQSSFCDGEFAANLEVSAEEKNRSNSGSSSVAPTSSKLHGATQENMEE
VSHDAEIGLLTWGATERPDQRSLLLEQVHELAASNERYSVLLSANTTELDNQSWFAVLWQ
PVYDQCHTAKHGCGSFIVYYALRPPRHVAGNRASSVVTMMNGDWLSPVFRCDREGVHWEM
WTSNISTPMSLPLSSLVSPSPCEGNNDNAMRAVCMSLLEKAPFASTGSGGEMQTVMETSS
ASMGSHDTKFSPSGRSCAKASANEVFRNSQHAFFSPSSEKGSTYHGTVRIPVVGIIPSRC
RADVWFLPCPRLNSPESNAGRNPNNSGTSSLRRYRAPLFLLTAALQLMSWNALEGFCRQA
MRKKGLYAVDKNLDVSQDEVEVSLTRLRGDTTTTTTSTVGASSTSIGARLFLTRTQKIPS
GRRLLVEGARGYRHYRESVNADAGMTSTTPVVGQESNDHNGSPISSPTAAGTDVSAIVEG
LPDFYQWVQFDAPLLNYAELYA*
>TCRU_9144 EB1-like C-terminal motif containing protein, putative
MDHGRMPASLQVVSSKESRTELLAWLNELLQRNAAAGGHSLPRLHKVEQCGNCVPYVLLL
PSLLPTSYPPLTTKAKTNAKHEFDAVVNLKLFTDALQKNGIPRPGLLTEESDKIIKGAYQ
ANLQLLQWFRGLYDALSQSRGEGQARNHSSGKSLEHGTTGACGRTGSTHLPKDHESQPIE
VDKTSTAVTVVKENSLRSCRAPSVRVGASSLPPSAHSQESASKPVPLTKKTATSFHDPLS
SSDSRPSVAGRQASQGRAGRVSTGRHDTTVRSLSASKDRHASTARTPLRRAGDGAAITRP
VSSMLRSSNGTKRLEAGRDPVAGPSGRMGGKEKSLARPNGADSLQAVAANSTTTNTTNNT
NTLYASRKSSVTRPLLDCRNTDTNGRFVSPMTGKKRLTAPHRGPKSPSLSASHNAHTALI
QVVETETPAHSRHGSQSMSEWGSDDSATASEMLIRVRNERQFYYDKLRQIESIVGPLVNK
SETSREVKHLAQSVLEVLYALS*
>TCRU_9145 C2H2-type zinc finger/Zinc-finger double domain
containing protein, putative
MGGSDEAASMSASTLPTRQLQASSSRPAKRQGDRVVSLQCPHCPRVITGVPSRSIRTNYN
RHLLTHTKERPYQCEFCLAQFTTSTNRRRHVLRLHPELITTWSTPTTAASSGHETHLEPS
DASAVGSAAAGTEAGASPATVGFACRFCGTELSCKGSRTIHERRCSSRPCPPRVLPKHLS
LKPSASNVATSSAEQTDDPADTIFLCPNCEQELSSRQHVKRHLRCYCPFREDAFASDSGD
DVDGGDEGVVRLGARSVTKRSRRILSKRRAGSAERFKGRPRHEGVGAFFSEEVHSTALRA
AEVLVPPATYGQSQTNITVTCPYDDCMATFASRTRWLAHVARRHPKELVQETKVGACP*
>TCRU_9146 6-O-methylguanine DNA methyltransferase, DNA binding
domain containing protein, putative
MPTPLLRFSNATTSVVGVPPLRVYRYTTPTPIGECVVLVDEEGAVCLCNWTDCEEDAVCR
LRRAYQPREILIEEAAATAKEEEEEEEDGDDSETSDARAYAVLQLRRYFSYSFPPMRGGG
RDTSVSFCQQKLHALLDGVPIRCPPSTSLTQAAWAALREVRLGEITTYGALAMRCQRPSA
SRAVGRAMRENHVCLFLPCHRVVGASRALTGFGPGLWRKVWLLRHEQAAIPARQLQRVES
VQETSLKRERA*
>TCRU_9147 retrotransposon hot spot protein, RHS3, putative
MVLTSDKGWPYSWNLIQGSSNDFFVNCEVDRVWQIVKRDLTKWFSNSDLTLNSSPVRRLL
IGTPGIGKSMAASSYLLYQLLHYDIKKLQVVVHCFGGRDVYVFDKTTKTVARYGDEDQCI
TALRSLRGHGMKGYIIYDVAKEGTPPPRHFAPASGWGMIVVSSPKATNYDEWEKQLKASR
IIMNCPDEMDVKAMCTWMKRDETPGKKAECWRMVEERMEKVGPIPRYIFDENEFIAQRRR
*
>TCRU_9148 hypothetical protein, conserved
MLDDYVAKKNGKLHDAEATERHLSSVVDQVLNYLRNGVCVTKISSKGNARRRLYFLLEDR
KRIHSCDLDRQGFPLNRKRPPVTMWIRDIEKVLIGLSTTSFGNYSGEAQLAKTSQEAVSD
NGTRRHDPTQNITLFSLGTNNQRAFALLLRGGKSLEVFVRLTATARPGLLLSSVHCI*
>TCRU_9149 hypothetical protein, conserved
MPSYLPDTVVFQLYHDDGEAEFVDYMDANSLTFVALGDAERTALCGIDAAAQLHYEGAQR
AVVSAAGIVSSIRRRRLRVPFGMSELSQLLRRAYNTEKGNRNNSLTGSTETALLAHAFLD
AVWAEESFHCLSTTCRVGNILGSTGIGSTTGDLAVDKWRLDQDIMELRDELMIARTAYDY
RPCIYESNRPISNIKEEEMKRINAIESNREKTRERQLSVVRERAKHEEEMAKELEQRGGA
TLDELERALEAKKRESTALQADRESRIWEYEHTVERIRTRKQDEESASERLRQAMQQLEQ

ELSLRQSAIETREQQLEIFQLDGAREREAIMRERHSIEAA*
>TCRU_9150 hypothetical protein, conserved
MRCSFNGGESRFCSHQTTTPSSQLPATVRVDGNTVRLNCPQPLRDAGFTVAGALFDVDGA
LDVPDSSTLFRKLCATAAPNFTYERKNMVALSYGVRLSPRRQLMYGSAAGEGYAA*
>TCRU_9151 retrotransposon hot spot protein, RHS3, putative
MNAGSYLLYQLLHCDVEEPQVVVHCFGETAYVFDKTTKTVTKYVGEITSRSVLYDLREHG
VKGYIIYDVTEKGTPPDTGFAPSTGWGMIVVSSPKLDNYETWEKETKAIRIIMNCPAKMD
VKAMCAWMKRGLEPDKQAGYWKKVKERMDNVGPIPRHIFDPKIYIDRLGAVDGALLAIKD
TDVGEYFTLGGSKLWYSEDPCHKLAKIVRVKTVEGAEVFLNAPICCRIGFRIADRLAKKW
LRRIFCC*
>TCRU_9152 Retrotransposon hot spot protein, putative
MLAAGRPLMKDYNVTMEMFVQESDDYVQDQRLLRIIFNLTEYQVYKLHHEGVFSLEQWRD
YEGKDTVTPLARGKLNAALTQILKVERREAEMKFAISTTIEDVLFKGRVRVNKMRLNDFF
TRELDGRGVVDTNRDVLPEEFFKDPTKYIRDKGVLNEVQASGRYLGVRRAVKGEVIFDED
IRKLCDKGVNNLLGWSLAAAEVTATVHNSTKHFLDAAAEEARNPTTTSAPEKLEGCYESV
HNARRGHAVELPDGVERNKTGTGMEVHEGKPEQSWSYKKVGNAIEENDAVQQFGVEHLPC
*
>TCRU_9153 hypothetical protein, conserved
MMASASAVTLRGIPQRHGENVKSAVRTRSASESGIKQISPVTSSCTASSPRRSASIAERE
SVAAGTRVGDWMLLPCGELKTVCGHAQWQDSPLGRSTQGCQQLRGEAHRERGCPGE*
>TCRU_9154 Protein of unknown function (DUF3720), putative
MAMMMTGRVLLVCVLCVLWCVTVFGDARDNRCVEGEKNFLTHTKNGGNDRVRLTADCELI
STRMGLIKAVEAGEREEESESDNAPLEKTEKSAPGTLLAVTEGNAAPGPKEGKGAAGAAT
PSPSGPGVPGTGDETRQLTAAGQKGSENKNVDPNNKASNKSQDQHTDQLPSSPGSSSTRS
DEKSSLTGTDEINQLPNDTETKGDASRQDTNGSDEAIEKEDGEKEKEKKQEKNTLLPEKH
EGQNNGGGKPPPVPAPPTGEESPIPDQENSQNPKKVTNENKPSGSKTESKSTQPPLGDAT
QGQHSHNTDTEDSTKNVATGSPAETTTTSSTSTSGSGDHVQNKVDEDDAQSSEEQHDDLE
TGNTNVVPTLSEAAPQTAGTATTAAQTNHTTKSGDGDGSTAASHTTSPLLLLLTVVACAA
AAAVVAA*
>TCRU_9155 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MSRHVFNSAALLLLFVMMICCDSGSAQTEVQQSSDPKSCRVSSPEEFFVWRDKKNDEAVS
SLRVPSLVEVNGGLFAVAEAQCTRNNNCGFTGIASELLTLTDEKPKELDTSNLKTQVLGN
CSTQVLGNCSSGEAQCPFQTAVLAGTQRVKKVHVSRPTTVVNGSDIYMLAGNYSWTYEAK
KDSVFQWGLSLVKGNINNNEEGSGNRIQWKDTYDLPWISSSRERKFLTGLIGGGGSGIKI
KGDTFLFPVEGTKEDGKAVSLIMYSSDTAGWTVSREMSDDGCSDPSVSEWKGRLMMMTAC
DDGRRRVYEFALTESWTEALGTLSRVWSSKHTGHEKGVGSGFTTARIEEKDVMLVTLPVY
PENKGKGNEKGELHLWLTDNTHIVDIGPVSGNDDDVAASSLLYKSGGNNNNEKLIALYEK
KKGKSSSGMVSVLLTAQLKRVKEVLATWKKVDGRVSQLCPPLSAEKDRSTGTACDAGKIT
DGLVGFLSGNFSESTWRDEYLGVDATVTSDIGTGNGVTFTGYADGATFRGAWAEWPVGKQ
GENQLYHFANYNFTLVATVSIHGEPKGVTPIPLMGVKKMNGGKSAVLLGLSYNKEGKWEL
LQSGGSRNALSSDWEPDTTYQVAIVLQNSTQGSAYVDGQRVGNATCELENADPKGISHFY
IGGDGGSAENTESREVVPVTVTNVLLYNRPLDDTEINALNANKVLISKLEERSTAAEETL
SKAVSKPFAQGVVSKSSGEPQQTGKESLMGSSGGNGETAGGTYGQEEFQPWVREPNATAP
SSKLENLPQGDNSDAGTMREIRILLLLLLVLGLWGFAAL*
>TCRU_9156 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MEIDGGEWTNGTAIVFDHYDVKIDRLLTPTTIVDEIDGATNALVGGYGTSTTPLTEVTDG
KYWAPRMANGVVSYGTDDEKKKEFRWGIQSTTNLQGVLKDYSTNPKPFKQFLGGGGAGIR
MEDESRYVLPIQALKDDGKVVSLVILAKKTSYGWEFSNDTSDEGCIQPAVLEWKEKKLIM
MTSCDDGSRRVYGSSTMGNLWTEEYDTLSRVWGNSRTRVGHGVQGGFVSAMIDGQKVILV
SRPVYSEKDKKETGRLHLWLTDMQRIYDVGPISAENENVSASTLLYATVEAQPFKEEGKK

EEKKLYCSYEVAAAEDGKYNIAFVELTEKLEDMKKVLAAWKEKDAQIAKEYRCGNEKNNW
SSECDEALTKGLVGLLSNKSTNNTWSDEYLCVNATVHGEVESAPDGGLTFKGPGAWAKWP
VGDMGQTVPYHFANDKFTLVATVSIHEVPETGSSSIPLMGVRMKDAQGTVLFGLSYTHDK
KWRIIFNGSRLTLPAHDENAGWEANKKYHVALQMDCDDGLFVYVNGKRIYDREFDYEDED
YEGYKSFYDRSQKLLSSHSISHFYIGGDGKSSSDNIHVTVSNVLLYNRLLQDDELNPLMK
TKAAAAPEAEVSAPEGAPQNRHLGQASEKDTTPSPQNQGLSPEKSKNEKYSAGSGQTTSA
DFTGLYTSAAEGEVEEVASSSVGSASSLAPTAGEGSPQKAPETDVLATEDHFEREQEHSS
LSVVQPMTEQAEEAVVATPQRKTTEDRPQHSTLSDASEDMEESSSHSATLTSDEQTVDPE
ERKDTNPHTAVGASSGSDSSHSTEVASVDGATDPATAQGHDEVLDGGDAAKDYLRTTPGE
TKIPSESNATSLSDHDILLEHGHLSDLASMALIGDSTVHGCVSRVLLLLLLGLWGTAALC
*
>TCRU_9157 hypothetical protein
MRRTSGSTHAPGEEEKRYDDVRARREPAVETAGHLASQVVRSRREAHQPRLPTAGKQTRE
CVAARLALPTHQSTSGQRGLSSRQRRRREGDPSQGEVVPCRRRHRSPVRPLN*
>TCRU_9158 hypothetical protein, conserved
MRTRCRRRIFHVCVFLARTAVGADAVVRLASNEGTGCCGVSTVAVEVAVALSAPSLFRLR
HCALLRRERRLHDAVSRYLGPGVYLDSRWGSPELSDRVWRAMARNGFATMRCCRCVTGVR
RPNCSGPRNGPAEYFLLGDLVRSRRHVRSTLFGGNKCCRYQRETGA*
>TCRU_9159 hypothetical protein, conserved
MAEAASCLDLKASFLQVPLPRETRHLFRCRVEDGTLVEPTRLPMAHKAGPQILQIIITSA
IAGVTTVVRPLWAAPPLVRVDVWIGNIRIAGSIGDVTRWEAQVLRNADGRRATIGEDRES
GAAQYTFLGVQFDHTHRAVSLSEKFVRSLRAMPALNSLTIAEMEVVASRFSYVAAILGTC
LCVYCFLIKAVRRRLSALYRGIVLETSPANLPPSAIGLCE*
>TCRU_9160 hypothetical protein, conserved
MEESNNYFSARASNTAVVDGLLAQRESVLAGRERHLETAPAQPQAQLQEREALISALEAR
LAALWCRYARTARSSLFQERAPRCTRTRAEVGASTPPHHERLMAGDVPASTVPQRNLTGE
MAGQHP*
>TCRU_9161 hypothetical protein, conserved
MHSLTGGRQAVNELHVFLRAMSGAQRLWAKRIAAQEAKVRRFMILEDNCRKKLRKSVLRS
TNEQLKYLVNTDLLGGMELKLPPRAAFNAFHIPTKQVSGFSVFAMARLHASPTLMSEISR
IGFIADLLGSWEILPPSGKERYEAYAEKIRRETAAGQTINYNHQTFSKLTGKEEEENTDA
TWESTAYLCFLREGQRQLEASVGPLEETDWLAIAPREWNSLTLRQKKRYFQE*
>TCRU_9162 hypothetical protein, conserved
MDAFQAKLDALQKQSKEQIMATITALQSACGEGVQPVRIAVAIGNRLTHGQIPNSFPVIC
LIDAMAATQDEACIATVLEEFWRIAPSLFVNYSTADEALREKVLRAVKRWGGKRLFPSTY
GEKLLSCISGKEMNKMDSEKVHHSVDNNVHTISHSGNATKDKMKEEFSRSEVSGFCAILQ
SCVKMIEGLPPHRASMYLDVVRKEKLLHTPSKSALLFFQGLHAELSRESALYNSNVVKNE
HQANSALSGKLDTKAALGNLLDKLSKEQTSSVDAATAAVAAAGGHKDLAFNVIRYTSPMQ
SDICQRLSVAQRAGFGEWHRRTKNEYHYPKKESNTRREFRAPAGSQAGTRAWFPTEQQWI
SENDMAALKLWLPKETVQERDSSNVYNVVRKRERDA*
>TCRU_9163 hypothetical protein, conserved
MVMRRCIVVRSIAQLAVFLRDVVQHAPSSGISLVDVESEIKERMQAMKAGADVLELSSSW
REALTEVNGTHFISGTTLYPCNWEEKMQNVAASIPYEGVIEKELIGRIIEEESRFLPAVS
LGEPISKWVQRRFSNILWVSRSATNGTPIYRAVGEPLSMEAECIARVLQLLGRRKLPVYT
DVNLIVPLLPVSMSPKKGNWLRFFERQAVQDHFDVDVEAYVRVSPDCSPSTVFVDATSVE
VARVDDMLAAKGILDSLCAIKVFRRPNDPVWSTDDVIVQSFLEPEHAIGAAIALMEKRND
LKVYILCGDGAKERYKTALGDLLGQEETIITICTPNSNEEISVKKR*
>TCRU_9164 ATP-dependent DEAD/H RNA helicase, putative
MNLYNWENESHNRRSKIKKTGTVVFHANESVDASFSNLQKEYQIGREVHPSLDGDEKKEK
RKAPLMTAATAKALVKKMGFTSLLPCQAQCYRGIFNRRDVILHSRTGSGKTLAYALPIIE
RHMILEKHADAAATGPFLLIFVFSNELAVQTKGVLKNIYPKLHICVAGFEDLASQRCDIV
IGTVPSIDGAIRGKQKDDIQKGLKRKRHNEGEVEQTEKDDFNDDCDDDNDVEENENEEDC
GNLTEGILEAGAVDASEVRAIVIDEVDLTLGPRFSNTGRRMRNLLKFIRKANGSLTDGLM
KDFRSHHYVLCGATIPNWVLKAGFLGVKKYYYQLVAVGMAKLPEKLECFMLHCPYTSRVK

TAARLLAVESFGRTVVFGTRRQIEELENELSAKKLELSFCSLSPSKDEIDRIAALEDFNG
GVVSVILCTDLAARGLDFVDVHMVLMLSLPMYNMSVENFVHRAGRTARNSQSGRCLLLQE
EREKDTIEAIQKNAHVVFKVYLPSGTKAKDGDATKSTRGMENYLAVAKPAAVKTKTTTKG
SVTFALTVRNPFKYTNPNAIVPSAIDVLKKNLGELFVNANIIEDHHRETVTFEYPADESH
EVRRKLWKFALKEITPNQET*
>TCRU_9165 hypothetical protein, conserved
MSIVASFVSECVRNGRWIRGLLALHGSLHSDEVDVSKARIQLATTIINKDWCTALALVRT
KDTFYLDELSKFIYECSRSAYFPSEVFVNVVETFLQSVRGRNESQNRIFVSAIKWTTWNQ
ALQFLTMLESPDGKSIKEISEWLRISRVFGSNEKRYIINTVLMQLNSSDLDHLKVATQAN
QRTKRALPVFSATGRQENSGLVKALNSLKTNDFLSMTSVAGVANATMRGENVSWKLALSL
VLKHRVVEDLNEMFARLIGVCCPQNWRVALDHFHLEGKFALWLASCQSWRAGLIVSQSNL
IPVSEAYDILSRCATPNTESRKLITLSGASKRICAPSKRAIASMLASGYLLEELQLSAFS
KVCQRTGDWESALFLFDRVATDEFQRRAIFSLLESCPNTTTEKVLGLVNNLHPASASTTY
MMIKHSKSWTEALHILRYVMARGTRCNPQILSAFMDVDPPFNVLSLVLGKMKNATNKGIL
RRLKSRENGGFSR*
>TCRU_9166 nucleotide binding protein, putative
MQTPNSECVGPESPEAGIASSCQGCPNASICASMPKGPDPDIELIRQRLSGVKRTVMVIS
GKGGVGKSTLTKELAFALGQMGLNVALVDLDICGPSLPRLMGVRGEDAHQSAAGIEPVLV
DETVSMISMHYLLGDKNEAVLFRGPRKNGVIKMFLKDVIWGDVDIMLIDTPPGTSDEHIT
VASILQQCGGVTGAILITTPQLVAEADVKREVNFSHKAKLHLLGIVENMSGFICPNCKES
SVIFPRANSQGAGKRLSDEFGVPFWGEVPLDPVLMKACEEGVSLTDIVDGKSPTIEILQS
VAAKLVASLEME*
>TCRU_9167 hypothetical protein, conserved
MFRLRAYSSCAIGFHVFLNTRRSLSIEESAEREKERTLREKVLARYRGTNFPELVNIRYG
HFAEKEGATRSAASQAYRAVSQDRFFGQNASSGRQGVDWFMLFTGLALFYVSSKMLLQRL
SGTSLDGASVPLWTANPETQAKFLLFSLQFDPNNREQIQQAYHSVRQAYPFTDFFQWLRV
QHPEYGQGIVFSYEAAVNSLVTIISSGDSWALMNLARGFQNALKKRNTNSAQRIDDFLTD
VGALAGAQSPGRYSMLPGYAPPQPPLQPLQLHGDEPMNIQGAIESPPSESHGSVPFQ*
>TCRU_9168 atp-binding cassette sub-family e member 1
MPPKNRQEEERSKLTRIAVVNADRCKPSKCSLECSKCCPVNLQGKLCIEVQKKSVISKIS
EELCIGCGLCVKKCPYGAIQIINLPSNLEKDTVHRYGPNSFKLHRLPLPRPGQVLGLVGA
NGTGKSTALSILKGKVKPNLGRYRNEPNWEEILRYFRGSEHQAYFQHMLEDKLRVLLKPQ
YVDQIPKGTKGVVGELLARSDQRGMVEHFMNVLDLKNVKDRELDKLSGGELQRFTIAALC
VQNAAVYMFDEPSSYLDVRQRLTAAQVIRSLLKEDNYVIVVEHDLSALDYMSDFVCVLYG
VPGIYGVVTMPYGVREGINVFLDGFVPTENLRFREEGLTFRIVDDFDEVTKRTAQNSYPY
MTKKLGSFNLTVEPGNFSDSEIIVLLGENGCGKTTFIRMLAGHQKPDNGAEVPQLSISYK
PQKIAPKFQGTVKDLLQTKIYDAFSHPQFQTDVLKPLTIEELLDQEVQNLSGGQLQRVGL
CIALGTPANIYLIDEPSAYLDSDQRIIAARVIKRFIMHTKRTAFIVEHDFIMATYLADRV
IVYDGTPAVNCKAGTPCGLLEGMNKFLKSLDITFRRDPTNFRPRINKLDSVKDREQKGSG
NYFYMMDTTDVANKKPNASGNEDHEDEDGDEEKEEVAHKRKSKKGKH*
>TCRU_9169 hypothetical protein, conserved
MTLVPYTPSEWCDIGARLWDMVCQCGETQAQMTFINGNQMSDETLTVAPSATGLCLFHGP
VSKAWQDSTLIGHIANLRAPQIPNFETQALLPAMGAARELGHQQGLITAEREQLNFDYAN
AVADVQNRNAQLNSQFQEAHHNLSVRESNIAGAGNRVLELRQQLEAAHAQLRERFNLGV
LNAQLQEREARLNAQQPARDAETAVRDESPATRHVVNDGVTTIPHQTDILMAGGVPSSAA
RRSSAAYRPPHSNVGRPHFHPSTPLPSRISPLDARLPMEEDRGFRAFDVTTWPSRIWNEG
ASGVVIDLRCAHQCRQQEDEQVKLALDILVEWIGVLEGGQDPTDRIMILTGPY*
>TCRU_9170 hypothetical protein, conserved
MAETASCLDVRASLFSSLFTAGDSASLSMPRGGRHAGGAHTAPNGIQGRPRNSPDYYYFS
NCGVTTVAHRLWAAPPSVRVDVWIDDIRIAGSKSDATLWEAQVLRNADSCHASLGEERES
GAAQYTFLAAQFDHTHRAVSLSEKFVRPLRAMPALNSLTIAGMEVVASRLFVCGGHFCSG
VYATTTFSSRQCDDDCPHLTGELCWRHPR*
>TCRU_9171 cullin 1, putative
MGRVPASDDFRRDVVKAYSGPLFATTFDFGVLWNKVDSVCNKILGWTDSPEFRGQTVIQQ

VVRAYTIVYRLVSAPCLDCPKLVRGTNAQQDTIGGGSEGTQALVVYYLLRETIRKRLSSV
VTHRLKMSLTAEPPTLLQVYLTEWRTFIIAVNHLKVVFSYLHSPWQKHELPSEQPLLPTE
VVALVQWSDIIMSPEICEGLAEQIFNLISRDRLHRLDEGSTSLVRDISHSLAMLNDPRHT
AYSSLIEESYLVHLQRFYKENINVLKAGGILSYIERSLIIFEDEMERVNRILNKCTMLPM
LQRLSDVLIDSEIPYIKSYLPTWILNDRGYFLNKMYQLLSKNSTGLLVLKEIFEKCVFEK
GVEDISRICEESIRANENVYKAVLEGIISVHTYFLRVSESFEGNEVLEKAMLSGLEKILT
TLTYVKSYHILGEELARFAHTKLKSNESKEQCEGILREIVTVFQLLPSKSSFLESYPKFL
SVRLLFEPYSEEQERFAIRTISQATECTSDFVYRCEVMLMDVTENSVSLRDMFDTKYGNS
HNKSSEWLFQPSVLTSYSWPDASCDVNLPTPSILLPKMREFQLFYSQVRPKRHISFVSRC
SRGVVRMNLPRDSRVPSIDLCVGQSQLLLAECFNNRTDWSIGNLLQTMEVTNNEIFLRSL
NAFAGCGILEVYDEGGPVDLPLRSVMAGKYVRLGSNPDTRKRKLNLFPCDWEGGFQIATV
SSNDFVSDPVDASHHMVDQLKAPAVQATLVRVFKASGTLSFYELMEKVKDESLQKFMPSV
QQVKVALEFLISRGFVIRDNSNGGTFSYIC*
>TCRU_9172 Dynein light chain type 1, putative
MTQLSSATVKLVEMPKDMENYAIHCAQDGFSKLYTEKDVASYIKNEFDKKYGPTWNCFVG
RNFGSYVTHETNHYIYFYMGQMGVLLFKSS*
>TCRU_9173 A/G-specific adenine glycosylase, putative
MNELYRAVQKATIEWFHINEKRDLPWRQSFSPTDVLGTTIGANDCMRNPYHVWVCEVMSQ
QTQMGTVISYFQRWVSIFPTVAVLAEASEESVKTAWSGLGYYRRALYLKKGAEYVMKHFN
GRLPVTAVELQQIPGIGPYTAAAISSICFGEKVASVDGNVVRVITRLRCEREVDPKAAKT
MKAVKQWAQELMDEGPCENPGAFNEGLMKIGSSVCKPSGRPLCEECPLQRFCKSYAAKAR
GEIEAIEGVIPLRSIAAKKKREIVISVIHEFRYGCVNEGMMERRFVVIQRPEGGLLGGML
EFPSTTYGSSYDTIPIEEKAVLNSLKKLDAENGAVRYLGSVRHIFSHIDMEVLIYCALWK
SPKPYPGTDDVGIKLKETDSYINEEAVCASLVKGLAVSPSRIFVKTEEEIRNSSATRLLL
KILQKLLLAEKSKRELESMSILKNLRKTGDK*
>TCRU_9174 Methyltransferase domain containing protein, putative
MFLLCLRDYSILRFLLYDWMIAPMRSMWYREVLLQCPMDASVLDVCVRTASSLIANRDVV
RSKKLILTGVDYDAGYVRAAQDNIIKYGLEKQVNIVHSSILDDTTSRFDVIYFSDSFLTM
PKRLDVLKNCCRMLRGSTINGSPCLENGDDGGCMLLFTQTLEKPTVNLYVLPLVKRLLRF
LTTIDFGGTTCEEEFLSVLKHSELRVVSLRVMNESWFYRQVMVVAKPLK*
>TCRU_9175 Mitochondrial import receptor subunit ATOM69
MTSDCSVGKARWSQGDEGEEALEIRIPIVLPPSVRPRDLTVEVKDLAVLCVRHRDTSIMR
WRLYEPVATEVEWRVEDEGMLLIVDLIKKNPTVWPCLLDLPMRSTEDDKLFIWGEKLDAL
FREHHPPIPMNLEEKEKRKMKKEEEQGAAIEINDENLDKLLEEAAEEVTRSRSNTNDKEF
INAEMENYKSEEEEIQKKLIEVTNTLEAGAEGEVAKRAQSQRDILEEMLRLHNIIREKRA
QPATLTSFIEITQLDICKARINVGAMEDEEKEEYASESESAMTAHELMATGLKHFEQQEI
QMALHFLRLAAIHHNHEQSILLLHSIYTQLQSPRGPFLLLKRALNDDDFSTAANLKVGEQ
FDTGARHFLPMFPAALYFYQRAAKAGSVHAMLALAQLFLRGCTSSTMLSTEQMEGLKSIE
KYHAWIEQAIDRGCGSAYFVKGCMYLKGEHGFGKSYKMAKEFLEKAASAQPDVARRAPQV
FLMLEKLRQEEEGGSEKKVVASPLTLAKAKEKSVYSEGEDGNEKDTVQVSASLERLKNIN
GKIAATNSGLQRSKKMMGRSTGSKVFWERTVTTGLALYGLYTVAFPIRVILLPTVYTVLE
RLLPLIPWLGANPPPMQF*
>TCRU_9176 hypothetical protein
MQHAAAIHNNILKHTRTFIVFDARRTPRAVLYGEHGATADTQVRSKSVHHVCLRPNNAVV
HVEDAGQVHTEAALHEDSSARAPATSQRRPRHDKPRRQKPDAVEGKRGAVPGSCVARGRR
HVLRPANRRTQR*
>TCRU_9177 hypothetical protein, conserved
MLQGNKASVHIGGHLLGEEEVQLAGERPPDVLRFCFGACGGHESHVTVTDVFLYNRPMNF
TAMRAPKDRVLVPTREAAPTPPEKNRVVDSVREHIAEDITEEK*
>TCRU_9178 BNR repeat-like domain containing protein, putative
MGTTWTEAIGTLSAVCVNARSGVPQKESLHVDALITAIIEERKVMLCTQRGHASGKQRAT
ALCLWVTDSNRTFSVGPVAMDNAADWRLASTLLHSDGNLHLLQRRGNGECSAISLSRPAE
ELSAVRSVLSNWTQKDIFFFSFSIPTAGVVAVLSDAASDDTWNDEYLCLHVTMRNAVKDN
DGLQVTGLESRAI*

>TCRU_9179 BNR repeat-like domain containing protein, putative
MLVTLPVYSKKDDTDVNENEKGVLHLWLTDNKHIADIGPVSGKNVAASSLLYKNAEGETN
EEELIALYEKKGDGEKPSLGMVSVRLTAQLQRVKDVLATWKEVDDRVSKLCLFSRAKEDE
RK*
>TCRU_9180 BNR repeat-like domain containing protein, putative
MDATRVVCWDLLRVTFLFGVSGVVVAVAEAHFKNNKDGKLRAGIAAKSMEVNGGTWANGT
GMMFDYYDIKVDRLLSLTTIMADGETYALVGGYGESGAPWTKVAVDGYWSSRYARSTVLS
EDDDKYKREFEWNQ*
>TCRU_9181 hypothetical protein, conserved
MGQTAPYYFTNNRFTLLATVSIHEVPKAGSIPIPLIGARLNDTASTVLFQLSYTSERNWN
FTLHKVEFLVKPSGGVGNWETNTAIRVAVQKNGAEEWFVYANGRRIYETDEKEMAKHRNT
DQFGTHRISHFFFGAGNKEDEEGSHVTVADVLLHNDALFGDDLSKPQRRDSSYSTSGCRR
TAHCGESHRDGGRKSRRSDSLRSHSWQLQRGRPQRRKTQSRQLHCRRPNS*
>TCRU_9182 hypothetical protein, conserved
MDNCAVMSRTHVMYDLASDLRVSGGSVFSIQNSSWSALGIEYYEGACVFRDVVVDGGSVL
QIVSSTFRLGFAMLMANTLTVTGGSWLVHRDNEFRTAYVVYVANKNGVAFRDRSVWSILD
NNFTYGSYSSTIAHMTNDWSPPSDSRPTIYGMCNEARGSTVTNYGD*
>TCRU_9183 hypothetical protein
MRIFMSNRCVYPSRLQYRTYSELPATSISFPIEYKPYPPYLNACALTLLTNSEDAVNSTS
SSATTLNLLFTVSGQKTIEDCTASTSVTVMSQCFGRASENTTTEDRITVWLTRIRTPDDS
AAAAPPTNCSAAPSRNVHPVIVMLMGRCSGILSRKSVSTASTPLNVTPT*
>TCRU_9184 tyrosyl-DNA Phosphodiesterase (Tdp1), putative
MNKLLCPFWVNRVDGISVDNPSALTLGDLLYCDVNDQEEVWSYVLLANYMIDIEWLVRVA
PSLLQTKQQIFIVSGEKEYEKKIQSSFLFRYIKAEKVRIVEPKLPLPFGVHHSKLVLCVN
ANGIRVAVLTANFIQDDWAYKSQGIYVQDFPRKQNSPKTDQANLTFSAGNEIRGNKFKNE
LLRYLNCYGIISNTENTVAIPSTLFDEIDFSAVCVEIITSIPGYHRYTDIHSFGLGRIPK
VLHSIDTELSDSIRAPLLIWQFSSQGKLTNSFLNALENAMSTEWKSIEEANKKPLRPLVQ
IVYPTESEVRESLEGWRGGLSLPLRLSSCHPYINRRLHRWGQGTRGLCKIEFLRRRALPH
LKTYMRLNEKKDGIKWFILTSANLSRAAWGEWQKKGDQLAIRSYEFGVVYGKGSFISFLE
GEPFSVTPSRKIPLPSLVEGDGLVEVHIDQGGKQNIEEGPSLFLPYDPLHLEPYASTVQM
QDQRGNNCESWINTDDIPWVIDMPHFGKDVFGKEIHRAMELDGRCEHTSLEMGKKNISRP
EIRFIKRQRPD*
>TCRU_9185 hypothetical protein, conserved
MDFGTHHQALGGFEPYRTRRESPGAPNTKFRDPIAPAHRAGAARELGAHRGLIIAERERL
GTDHAYAIAGARNRNTELHSQAEEAHNSLSAREAGIAVAGREQQLEATRAQLQEREARAG
AREAPRAAREAETAAREEAPTSRRGPADGPATRQNTAEDGGIKRQRPTRRLVVGGAPSRT
ARRSPADERQ*
>TCRU_9186 hypothetical protein, conserved
MDFGRALLPAFRTRLMTASDPNAPLSKQRARLHTAVREADAFARAAQPLAERGGAQRPRD
VSGVAFVGARRPHAKPEARPEGINRDADGRQQRRRPHPCRHRSPSRTGGAPNLHSIFQIA
RRHRREGRRGLFANGARLWCDGAPAPPLRAGDARRASEAARGLFATSAWGRRRSQAGAPQ
PPAARANSRTKRRAARPFRWQSTRRHRPDRRTPGCRGPCRK*
>TCRU_9187 hypothetical protein, conserved
MRITRSKSDATSWEAQALRNPDGRHATTGKDRESGATQHTFLGARFDHTHRTVSLSDEFA
RSVRAMPALNSLTIAEMEVMASRFLYVAAILGTRLCDRHFFIKAVRRRLSALNGGLWRRH
PRRTFRRQRLARARDCDTSSKIQS*
>TCRU_9188 hypothetical protein
MTTERPCGERNGHTHSSSAADGTFDQPDTAVLLYGGLPPMPRPLVQRGEGSREREFDQAA
VSPSPVAAVAASSVVGGDTSPGSSPHIGVHEADDSTKNYFDNSNEEEHMDLFISAMSPQN
CVDRPQRRARGALMPPLPSPGEADAGAMMQSEMHTTPMTKTHTPDLRVTMYENEELRREL
ATVRASLRQALQTIETRELECVELHRLVDEMQAQLNGLKPEANLRPTQTDAQGNGEGSTR
PETSAFKLQATKDTTGPQIIGKYESKEEWRMTPSRELFAAEVKHDAHTEASTTTAIAAVK
VNATDAPTTVGETISMEQLCEERDRLAKELAQTKIVLAEQETVLDRLGLRFPYPGALVGA
ARRTIPAFEPLRKSRKQKPGPLVVDRTTQMRGERVERME*

>TCRU_9189 ATP-dependent DEAD/H RNA helicase HEL64, putative
MEERYNPFTGYQTPRHQQQSYRHNGGAMSRGGWGERVDAPADKMKPVDWTRVKLVPGSWK
VLDTKAIHRAAHAKAEVVPAKQLTEEESNEWRETHTISIFGEGCPPPLSNFDQLSAFVPA
YLQKKLTAQGFTSPTAVQAQAWPILLRGRDMVGVAKTGSGKTLAFMVPALAHIAMQEPLR
TGDGPMVVVLAPTRELAQQIEQETKKVLPHDLRCGCVYGGAPKGPQLGILRNGVHILVAT
PGRLIDFLEIKRINFFRVTYLVLDEADRMLDMGFEPQVRAICGQIRPDRQTLMFSATWPK
EIQRLAAEFQKDWIRINVGSTELLANKDVTQHFILTQEHAKMDELKKLLANHRNQRVLIF
CKTKRTADDLEWQLKRWGYDAMAIHGDKEQRQREFILERFRKDPRLCLVATDVAARGLDI
KELETVINYDFPMQIDDYVHRIGRTGRAGAKGEAFTLITKREKQITPAVVTELIAIVDRA
QQQVPDWLREWGEQRPRYQVMKRNRNMMGFGSSRHMPALYNGNRASFDAAGGGHPGNNNG
TAGNKRGGEGGVFGLARHGSNGAAPFSSSRIEYKRFDDSDDDDGAAPPAKKRSK*
>TCRU_9190 Haloacid dehalogenase-like hydrolase, putative
MNQLVVFLDIDNTLYSGEEYHSLAEQIRDGLVEYVGNWLQLTPQESEAYVVHCFEKYGLT
IAGLMHEQKGFDAEAATDFLYSRCDFSHLQENPRLREMLSRLRRNHHLYFFTNASRRHAT
KVLQALGLSSDEFPMSGFTYEDQWAQTAPVPCNKPMRNAYIAVIKVVKKWLQDAEWVTAE
CMVMVDDSACNLIEPLALGLNAVWVSHGNPIPDVLAEKKNTGRLFCITDIIELEDIIKQI
TINREN*
>TCRU_9191 hypothetical protein, conserved
MMEYIVGSGASDWARLELNKPGRSKLYDLHLNRNVHGGICVKNSQPHDPFYCGWRQFNEL
PPQCARNSSTLTSFGENEGAPSDNKRQIGPPSLCGEDKCPLGEKNNLDFLQNPELSSFYG
SVLDLLHDQSSEMPWHAATTDRPGDTATHTPALSQTDTTLPTTLCGLFISDKTWINGCPS
SDEWKTPAPVMKNNAGCNLAPPLVTPVGELPVPWNPEDSPEHWKKVPAQTTSHRLMGTTE
GEVICSSLPKSVIPSCPKGNFIKQLLAQLTTGTNETFAVTSEKKLTLMSKKPEVKPIPID
LIAIERPLTDFCDVPLVNNGMVKRSECSSGTLLSVTSPGGMMPSCCKPPPAVGSSPISSP
REGTLEMGGCVTNGDKNGRLIGVVPWQGNNLVDSPRTTYSGDCHSGHSSHSYWHTPFVFA
LNRKILGDLHRNSPQSIDSRDLIDGLSFSALKSVEEWPPRKRKDVLHLLKRFQARDLLQH
LRVVSFSWKSPEGVCRLLESWRRRGIFPPDVQFGVYYWYTMKWGCERLCLEHNGCGSLAE
QGRGCEYALRGFRRKCRYPHRCLFCGAEDHGWTEEKRCKRYLSLQREMERLGVTDDVALI
LLEAFGCEE*
>TCRU_9192 C-terminal motor kinesin, putative
MSFDAQNRYRVVELLRSLYASPNVEGERETILALANLVQQGNAQLVLDEIKEYLKRGLPV
EQERSMIILDQLLLNCMPQFAGMVSSEKWTERLLKVAKSATVESVTYKIIETVILWQKRY
RTDGFKRCVLRFSQSKVLGETFNRVLHRINAEQRSLTRSRNQSRDSAGQEEVGQTDKHHA
LNRAETILLEAQGDLASLEYALEHPHILHDEDIAKECKQHKLRCMRLLETGQHEEYASEL
MQLIERFSEALELYEAMTGLDMGEGEAARRRALYGDDGGGETLDSDDEEHARRLRERAAP
KENAEQVMLKAQEATQQLVQQERSITAELRNQLEELRRKHEELQNKYKDAKVKNRDAVAA
LEEYADQIEALKAGGANFNNATAVFGASGKGTQAVSSISVEMGRRMRDNVQVMRQSLREI
REQYAADIKKESAYYSSQLTSAIASIVAASQRDRQADHKALLWTQELYKKEMKLRKQYYN
TIQELKGNIRVYCRVRPLTPKEISGGHNSVMEFPSTDELKFVDQNGRPKLFEFDEVYPPA
ATQAKVFEDTCPLIDSVVDGYNVCIFAYGQTGSGKTYTMGGGEGELKGINTRALERLFQV
IEERENTEESTVVISVLEIYCENIRDLLGPKDAGKLSYEVKQGGPCGTYVTNLTEVPVNS
PKEIHDIMARANRCRSEGQTNMNEHSSRSHMVLYIVVRTTNKQTRMQSFGKLSLVDLAGS
ERLEKSGAEGQQMKEAVSINKSLSALGDVISGLAQNNKHVPFRNSVLTFLLQDSMSGQAK
VLMFVCVSPASYNCSESNSSLQFASRARGVAFGQIKKNTVVAT*
>TCRU_9193 hypothetical protein, conserved
MLGTLFSSEEKYGPRLTMSLCHCSSEDGDHPARALRHQVQNSTGWQSDKGCVYPQELGFA
FEGEVELHFIRVLSHERKIASRIEVFIAEATKEEIENGMIKPYHSSNFRRLGYVCFVTTT
DNAFGARELKTINIRQKCVYVKLLISRPYSSDYNLFHQVGIVALTSHGTIRRTYQGAPTR
KICLIGETVEVPLDEMLPPRLGNPQSVQPQDDIGLEIDQVTARRIAEIVLLKERAVAAED
YDLADALKSCLLSLERVGKKLYYLEKEKATAVKEEDYASAKNLKRQIDNLREEAYRIPTS
VPEKAESSKNSNRLYGPSSGKKPPLTSELMTAELRGGEQMPSLHAATPLPALLDESPVGG
RDLYMIKNSDNLMRFGKQENLSANVDGNLISEFAEGKEEWERSINRVIRELSSRQDQASV
LQGEALTEARNSENVFGTYCCACLFGKKGSLREAAIRAIISPVGFTALCTHSHMVMEALL
SYMALPSRGLCDPVAGVVFACCEALQAIIKDNIPDLPPISALISHIQRLLPALVIRLGDN

NSRIREMAESVLMSFSDLALEPVVSSLLVDPGKDKKRPVSPKVHVARMNMLSSLVDRYGI
NGDESISLEVGNVLSSAVLNCLQHSNGEVREAASRLFAKALLIAPTRSACYMEALKPAQQ
NLVEQQMEALKVTAPRVMTQDELVSSATLNSSAVLDENEMRPAGRNCHSNSEGRGAHIAA
RKCQFCGQFDENFSEAALDIHFIRACPMLCPCPLCDQVTEIATLQQHLTTECENRHLVRE
CPICREAVRVEDINKHVALNKCIKAVPTHSVCPLCHARFETGLAGWVAHLASPPGCPNNP
RKYDGSGPQVR*
>TCRU_protein (LYR family), putative Complex.1
MLRRISFLQKLFGLNRLVKTGSDVPSHFSPRIFGSEKNEKVNSGEQKYTGPIPGATGKDN
HPGIYGSKPMPSYFEESYPRTEKTLPSKRVLEPNEPRDRSDNVNAPEYDTSLGKFEQAPY
FTGGPPAMRYHNYVREPANKEAVEYRDVIPLPPFEDHHPNFSYASATGKREGNITLLANT
VANWEIKAAMMSLYRSCLKGLPMVKHYYWLLTPLPEMKYKVRGRFLQNQHTKDPDAIRHL
LHNGWMEYQEVILFRRSRASVAKFFEWESQDELVRGYTSEEGKMQEERAFWNGEEQRREG
PYDGHWSWLGKECEKEFKLIAGRIPVSWTTSKGYFEKGEADGTNYWEKNLDYEGWYIKNV
DPDRKNARHEMQGWVESGYNQPKHYASKNRRGYRRLVKDVETMMETSMEDLYTKNREQLF
QYLIRETHPESNRINAERTLARQDDDFYSTKFEEYERYLKQAMREMPNPRLWKTDAFYFR
LRYLIAPLEYNWAKVPIGTLQEKLFNEWISDNLNYAVMNSSVFCSIKNDKSRNPMANTWG
DFYTNYDPDIPETRKLPWYHPEFDYDRRYKWDERCMRMKRWVQGGDIDSKLPFFDSIVAE
WEQYVNRPERFRAPDSAERRYGAPRMVQLYRSLNRLMDVALANQLRKVLEKDSGKSAEEL
SKQPVVETQALLATLNFSKFCFDVPIIIYPDGAVQPKLGLDGGPVALRA*
>TCRU_9195 leucine-rich repeat protein (LRRP), putative
MADGEEEEVCNDTENPEGQAQDEHTPLDGVVEKAVAEEKGRTALGSSFDPHTSSETGRRR
VGFVDGAGRSQTSISAALKGDSQIPTSARTTHTRNVKGGLVSGRELSNGFDRLVLLTTDN
NSSTKTIWHKITGPPYRLRACWCDPRDVAMPYGSILHYHCKHEPTGGDMGEIGTNGKPLE
HKNPSTRANTRRVLQRILRSSPKEGNEGKKIVYNGCKATSHRCESIGFYGSSKPDRSSVF
FFASPHPMHAIFAEPALGAR*
>TCRU_9196 nitroreductase
MKRNGIKRGLWDSLILYWRWNRENLLRNVSAFAENGRHVIGMDGPVEAGSEKDVGRGNSY
MPPIFSSMPPSPSSSSSLPLDAMKRVVHERRSCKRFDPTKPIDLDVVSDLLAMTVRAPTA
LNLQPWVAVVIHEEEQRETLSRAALGQPQPRDAPVTVVFAGDMEPESNAPAALEMGLESG
YYHSLYGAAYLRHAYYLLHGGPCEAMSHVKAIVSAWYSESTGNAMLSVPRNKQAYAWKQV
MIPATTFLYLATAAGFDTAILEGFDEAQVRRVAGLPPRFTVPVIISVGHGAKNGFHSVRS
PRFPTKHLVRWGKF*
>TCRU_9197 Domain of unknown function (DUF4139), putative
MPRITVGGDDDRTAGRVVIRTDSRPDAVTVYENQMYVRRVAKVDLPATVTATGENPAGDD
AGGTEDGDDVLQLLFAMPRDFERDSVQVRFDERTAALVVLRGVLFEKNSVEDDRDAAAGD
TQRQETQDEQAKGIMMQLQEVEQQIELNKVEQSAARDEAELSARLFARACGLLSDGLGTA
LEVGFWEAQLAGVENATVHANEERRRLEKDAANLKVEKERLQSLLRETSSGDSASSKQTE
SVCIVLKVKEAVPHAVVYVSYMSPGASWRAEYEVVLDSQQQLMTLRYNAVVQATGEGLYD
VALTLSSVAPRRGAAEPQLEPWRLSPTSPKIECPHMLMLMSTTDGSVKGSAPSIEAATVS
ETMGMVNFTVPSRRTLRGDGSKLRVPLTVLQWKADVSYSTVPSVTEAVFATAVCTNADEY
QLLPGDATVMLDGNFVANTCLTRTAPGEKLSIPFGVDSSIEVRRKLQERYTTNMKTNLFN
RASRQRLLLAYATTLTNTKSQETVTVTVQERIPKSNEQKLTVRLLEPKTDAVDWTDERQR
RLEVDGVVEMQVALKPGAVVTVPFAFEVEAPIDAHIYGL*
>TCRU_9198 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MQGDTPPQTPVDTPDKADTNAPIATDVAQVDPADKTEVSASSGEDGETVGGTDVQGELHE
EPGEVKAAALSSSLGNVSQGNNSDAGTVRGSGLLPSLLLLLGLWVFAAL*
>TCRU_9199 hypothetical protein, conserved
MSSGVSLLYQQQVFSVSDHSVLRVVGNSGSVSYAIFAEGSCWQLASSTNLTALLLHPNPR
QKFHTHSAFVSIDSNSVVTLTGCKMGSTGSLVSLFFQAEAGYRFFAGCLIVAGREVTAAA
ELELHGITNVTTVAACGECTKEGHCFAPLTTAVVDCECRCAAGGHGDVCVPAPVPAGPPP
PPPLPSPSTPPPTPVGECISDMVYPEVAQSVGGGLSWLCYRNVTFSGGGMSLTVLVGAMT
GDVANVTFDGCTWRDGAVLLLLAPLSGQAGWIGATTTWDWVRFSRYGIPLL*
>TCRU_9200 Mucin-like glycoprotein, putative

MMTCRLLCALLVLALCCCPSVRGTASGEAQVSTPGHLPPLPQEQTPETNSSVSNAPTVPE
ADTSDNPDQSVVKSPAQETGESKSSREVTVKTKTTTTTTTTTTTSAPTTTTTTKAPSTTT
TETPTTTTTRAPSRLREIDGSLSSSAWVCAPLVLAASALACTTLG*
>TCRU_9201 hypothetical protein
MRGGVGGRCAARVGEPGVRCAWVGVRQRGGGQRVRRRGERQRRCADRWRAAGAAGVGVFC
VRVVAVNARQQHQRQAPVGAVVPAQCGPRAEHTDAPRERRQRARRDGRHRCAWGRRPTIR
RGVPGAQRAGAAADGLQVRRHHRGIPPRGVWRVRRRRALLCCCDEGDVGVVSLPLC*
>TCRU_9202 hypothetical protein, conserved
MAANTDRKYGSATVIARSCAKAHDILANTPSACISRMEPSPPLTTTATAAAPATTPVIAE
RALAAAGSVSDLIVKDPSSTPLQPPDTAAASQRMIIVSSAAMK*
>TCRU_of Trypanosoma cruzi region 5/Dispersed gene family protein.1
Dispersed gene family protein.1
MRFPSLTYVVAHAMHLGIFFGSVLALATPGARVLHRVIGVVGVLYGVAFPAGVCYLIARH
TGASFERYWQFFRKPLHERLLYPVGYWHPAAQQRMYGGMLTNMRGSHVYWCVFQLSVLCV
VGLIAAVHPPLGGCHVQYFCMAAVLLVGAGVVAFTNMMRSAFLTVMRTASFVLLAALCVI
SAANHLAPGDGGARAYAAIVLLLTAVLLAITVYSVVVWYAEDRRWQELREPRRGGLEALL
RDDEESDEDTRKPHDDRTSSSYASGTTVASSYRPPAQQELMAGDARSDALSLFDRSSSAS
RMIDHAAM*
>TCRU_9204 hypothetical protein, conserved
MPSDRHIPGSASYLSGELLLVEMPKMRYGSDLLFVRRRAETAWEWLRPGLCSPRRICDQC
AVSRSRPRSSAGRWFRWDFWRLRLIGKIKFPQRLGARNAMGVNHVRHDTSAAAAVLTAHR
AVCRASDRGGVRSSGRRRRFRAKFLACLLCGIRAAPTAFSRDGGLQWSWQPSVLVRNPGA
EAGQCSLFPTSESGVRARGFPVASYGGAASLWLELSDTNNMFGQ*
>TCRU_9205 Concanavalin A-like lectin/glucanases superfamily,
putative
MNKAWESVFDGTKTAPGSTWEPGREYQVALMLHDGNKGSAYVDGVIVGSSATIPTPEMQG
PEASFFYIGGDEGDSGSSVTVTYVFLYNHPLSVGELKMVKKSDAKKGNSDGSMREGISRL
LGFCTFVPGSGATWPVNGREDNDQYGFANHDFTLVATVIIRQLASGSTSLPGAGLGDGAG
RKIIGLVVRHE*
>TCRU_9206 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MGHDGTAVNPGASASSGADGETAEGTDGQEKEEIHAQNGDVNATALSSSLGNVSQGNNTD
AGTMHESGLLPSLLLLGLWGFAAL*
>TCRU_9207 hypothetical protein, conserved
MKDTWRAHTVLGAAEGEESLGVVLRPTTITKGNGVFPLAGGFDVSYEGGCWSEGGLELKL
VVGDLTNPTGGKQSGRIEWGDPKPLSKLISSASHKVTGRSSLLLVAQVF*
>TCRU_9208 BNR repeat-like domain containing protein, putative
MGTAWTEAIGKLSAVWVNARSGVSQKENLRVDALIAATIGGRNVMLYTQRGNFSREEEAN
ALYLWVTDNNRTLSVGPVGMDNAAD*
>TCRU_9209 hypothetical protein, conserved
MLADTGPNHTMGLSRSHKKKWETVFKGKTTTRSSTWEPKKECQVALMLQGNRASAHIDDH
SLGEEEVPLTGEKPPEVLRFCFGACGGHESHVTVTDVFLHNRPLNFTAMRALKDRVPVPT
REATPTPSEKVRVVDSVSEHIAGNITEEK*
>TCRU_9210 hypothetical protein, conserved
MPAGLPLPNVNALKGPESKAGSLPPNTQEKSKFSDASGGAAGNKAKQSDVETDDPSSSFA
NTGDQTVEKTLLLPQTPAVLLPVPSAELSPEVPPVTPVQANPDGEGSLPTAPRASEASQR
ELQNKASSPNKTGSESPDRPSRDGMQKQKDKVTTQLNTTKKASAGGLAEKTATFISANGN
GDVQNKEDEDDARQPKPNRVQDDAEAGNTNVAPTVSEAAPQTVETVTTRKRETNETGDSD
GSTAVSHTTSPLFLLLVVVACAAAAAVVAA*
>TCRU_9211 retrotransposon hot spot protein, RHS3, putative
MERGDAWPRFRLMVLTSDKAWPYSWGACEFNRDCHVNCEVERMWQFVKGDLTEWSSGHGG
TDFTPHPCVLIGTPGIGKSMAAGSYLLYQLLHYDAERLPAVACFICN*
>TCRU_9212 Leishmanolysin, putative
MRHTMLLLVLLLCCVSGFVAVAEHHCISDEIEKKVGPRTTAVVLELPTRESGMMRALTAS

DPDWAPIRFQFFTEDLNDPSKYCTAEGQIRPDFTGGTVECQREDILTEEKKSIILKSLIP
RALKMHTDRLLVEPLTGYLIVPEFLSGVCAQFTIPSSHHTDGVTGADMYLYVSSVKISSL
*
>TCRU_9213 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCFAGGRCDEGEAAGLGSDAELPPAPKPLATPPVGSQGLQNG
VPVVTEEVSLISSPPQDEEADGDEGEGDEDGDADGETDESKEKPTEGQSNKVETAAPGSD
STEKNLIGSSQGTDQPIVSAGEISPSGSQESNANPSQPEFEGKKNDTGKNTPAVENALTT
GNGENTMPADIAGGNPPPPPEDGVDSREKDGEVTTSGDEKNVPSPATAATPQSHRDEGSE
GTGEDTKATTVTANTTDTKNTQNSDGSTAVSYTTSPLLLLLVVACAAAAAVVAA*
>TCRU_9214 Calpain-like protein CALP1.3
MPFRSDRAEINYAANPCNTDVASDPATEVGVLDNASIFSSSVASETVEKPQNNVVSVNDN
KEGDEAQHSQDRNRSVSQVESTERKEFTSATNLRHKSLKQPIRWERIELAAPLDDPEDEF
DLGTAQKPIFQEGTKGVKNEFLNGEPTVEGEVMSCFEEPGLLYRIVDKKKKTWAFYNDSL
AFEVHVSCAFGKHSKVQPLGNTTMRQEPDGSYTAEVVVYPVETEKFIKGYVNGFSSQLRA
LPLSDEYFETRETLQHENFLEKEFDAVKSLVGEWKGAEHALKSCIENNVPFVDFDFLPVW
KSIQLGSTRAPKKMLWLRPRMYLPEGHVEQVRLFRRPIFPGDVEQGELGDCWLMCAIATL
EEDPGDVMRMFRNPFGAETARRERAVGAYRVTLNTSGLWRSVIVDDYFPGYAGMLRFAHS
SDVCEIWPSVLQKAFAKLNGSYGLVQSGDPVHALTDMTGCPASRFDEVFAVAQENGGKEL
FQQLLHYQDSGFQIILTTAGKAPAFISGTNKIASLFDEEPELERILGGTGILPGHAYTIT
DVRYFPKEGDLQLLQIRNVWGSCEEWSGPWSSESSEWDSHPEVRDACGSSHRDDKVIWMD
WQHVLKYFSGGGVIYRHPSYDYRIPLLFTDCRPSLVIEVTVDSPVWMCFILSNVNPRTVQ
DYTSHLGKSHEYPPLMLSLSTAQAGKYDEHKVINNTSVDAAKPSRDKWTFTQAREISMLC
RLTPDESPYLVIPRMMENDDTVSGSTAWFANLQDQTYPLHFRNGNAAPSDVDSEEAAEIP
VVLGVRCSRPIGAEGNGGVKVNFKRIEGENVVFENFPKFPAETTALNDIYYQVMSPTQGY
AVEKMGDSLS*
>TCRU_9215 adenylosuccinate lyase, putative
MSSSVDYTQDTPLFALSPVDGRYRSTTAPLRAYFSEYAFFKYRVRVEVEYFIALCKEVPA
IVPLRNVTDAQLQQLREIAVNRFSLADAEEIKKKERVTNHDIKAVEYFLKEWMASNGLAH
VSEFVHFGLTSQDVNNTAIPMMLRDAIKATYIPGLDDVLKTLEGKLGEWDMPMIARTHGQ
PASPTNLAKEFMVWIERLQEQRRQLIEIPTCGKFGGATGNFNAHLVAYPSVNWRSFGDLF
LSKYLNLKRQQYTTQIEHYDNLAALCDVCARLHVILIDLCRDVWQYISMGFFQQKTKAGE
VGSSAMPHKVNPIDFENAEGNLLASNALLNFFSAKLPISRLQRDLTDSTVLRNLGVPIAH
ACVAFASIVRGIEKLLVHRETIEKDLSANWAVVAEGIQTVLRRECYPKPYEALKELTRGN
REVTMETVHEFINGLTGISEELRSELLRITPFSYLGYVRTHV*
>TCRU_9216 spermidine synthase
MPGSELISGGWFREENDQWPGQAMSLRVEKVLYDAPTKFQHLTIFESDPKGPWGTVMALD
GCIQVTDYDEFVYHEVLGHTSLCSHPKPERVLIIGGGDGGVLREVLRHGTVEHCDLVDID
GEVMEQSKQHFPQISRSLTDPRATVRVGDGLAFVRQTPDNTYDVVIIDTTDPAGPASKLF
GEAFYKDVLRILKPDGICCNQGESIWLDLELIEKMSHFIRETGFASVQYALMHVPTYPCG
SIGTLVCSKKAGVDVTKPLRPVEDMPFAKDLKYYDSEMHKASFALPRFARHINNSE*
>TCRU_9217 Ribosomal protein S15, putative
MQLRDSMGIAQVKNVTGRKILRILKHKGMAPEIPEDLYCLIKRATEMRKHLERNTKDRDT
KFRLILVESRIHRLARYYKRVKQLPPTWKYESSTASAMVA*
>TCRU_9218 Vesicle-trafficking protein SEC22, putative
MASKGCFIAVLIARTHDHVPLCSYTDENYANSNEIRQQEQRVLERMESPAAATDRTSAKG
SYYQSFDHRDCIYFAFQDAATDLTIITVVNKLLLRNSGDVGAMNRLACGLLDLVFSEFLQ
AYTVSEIAATNVRPFQFIKFDATLQKLIRQVQQDRQGNNVVIGGPGAASQGSGQRRQVNP
HYDALRQELTDVHFVMRKNLEDLMTRGEKLETMNQFSAQLVDQSSRFYKKTVHMNRMRLL
RLYGPPAVVSLILIIFFYFYLF*
>TCRU_9219 hypothetical protein, conserved
MATKEIQLPQAQSREPVVHPCDVIQRGAFHKDNAERLHRIRTTLGWGAAADTALTETTLL
SARRLGAIPSSFALYHHYRGTASELTPMDLYGQPEDDPNVQPSSRAIVEKSVYGYELTMR
NLGM*
>TCRU_9220 DNA-directed RNA polymerase III subunit C11, putative

MFFCPFCGTLLLIEPHHPTNRFACSSCTYVAPIPSTHLLTVNHSLLKFNKTVEDDANVKA
NGIKTKNEEVDGGQLITVRCQNDEKFCDGNRAHYVQIQMRSADEPATTFFKCLKCGFQWK
QD*
>TCRU_9221 CNH domain containing protein, putative
MLAVRCLVRLYEMPPEYGQISAFDTHGSTIFVGTDHGVLLKLAVEGASLSDTAQQMTQNI
TSSKDGPDSNGRAHNLATHDATYMPMFASSEASEKIHTTLVRFTLLSAMKKKIERLQHSR
THTLLFVLYEHRLVVLNSVSFSHLQTIAEHVGTFFVSDSQSNSPQRAGLHVVCASELNGK
GLSVFEFDASRGESARAILAQELVLPEPAQTLVTYGSIACVGMRREYSLLSLSDGSSCGV
LPLGGEKQPLLAAGDGEVFMRHNHSIFSVSMRSMPSGRVMGRTIRLKDEALSFVVRHPFL
FVFTEHYCDVFSLYDDDMSGRLMLPGCLFSSQLGRGDFLYAASKKKIWMASLHSLRHQLA
NLVEYFKVEEAFHLLGSQRAIGTLDLQGIELELHIMAGFAYLHHCRPKEAVLHFNDHIDP
RDLLLSLLECIPPGPEEYSPELRALLARKHVKKDTSATPKAGRSTTLKAGVASKHGESYE
NSDNDDKDGVDNYWAEWEGRCPYNTYAGELHHAWLETFETFPLVPRNSDNVDESTYRQVT
EWGAVTATDFLEHAWELFKDEIVLYFRFRLSQASDVYARAMEYALLVLALEAQDHRAAYR
IVAYGSSIRLEDCYDLLSSLREYRLLACLLFRRGYFQEANLVLTSRVYVSSILPSLEGNP
PDATGVISPAYKILPEAMHVHLDRLLNATLKSPCMNAMRHSTHEKRVSLNMTPTTTVLPA
SLTEAMYLVSKLNLSALRELLHESPEASWTLDEEGCSLLHVLFSLLVLLETSEEDMTPEG
KSALLNLVLSCAILLLDYGAPVAILNAQGLSCLDVVALVADDALLDIILTALLADNDLKE
IADAVEKGNTMPTP*
>TCRU_9222 hypothetical protein, conserved
MPLLTRGQRRLLEYVGHDGGTKGLKRRRMEDVAPVLHKRKQKWTRKFTTETASTDVSLAE
VPLSSEVLEFLREYCPKAPRKLRQSQLRVISDLSGAFGENSEKEEGETFTVKRVELKENA
EVFAVVALAALQRRALWSGSTPQGASLFVLVETDADAAALAAHMGKKYKMTQTLVLDGSR
FPTFPAVEKDDAATATTLAERTALVIASLQAFVTVDARSAIWKFIGAYAIWLKSSKPPAL
LQEMADGTRSELEEKLCRQRWRCLGHASLAVVIAPSRVFLFAPVTDTLTTSVPIDDGEKK
KNAGRDNAVDTGNSNKNTQTEERCTHTAATRRRPVTAHYAVVEGAHRFQTLYTLIMSLRE
GQGLVVHFATKEACQFMYNVLYALGELPKSLLLLTDYEGPSTYASVQDKDEDRERLCAQF
DKIMLDAARKDFSTKREKNRVVVLSAFGLVPQTGTIFVQYDIMVDVVNFAQFVSDVLTPA
AYNIAATEPTKRRRSRTPPPRGDRKESQEGDVAAASKATPPSKAMYQTVLLFLRRNELQP
ALSYLQRPAKRLNITFEQLPQLPSATRFLLSLQKMRSLNKKQFSVQNAAYAAYRATMLLY
SLIGPSDVYNERCVDLSKVAEEFGYTEVPILDLRTRDTPFRPKEDIFRAAAERAVVERRK
MRAYVNEHIVGEAPEEHVADNMAEAEE*
>TCRU_9223 nucleosome assembly protein, putative
MPVGRNVAVEHDDDVDISTPFHKYFNPNYSAEFMSKLPERIQQRAKVLLHYHEEYEKLRK
NFEEKETALRRQYDELYAPLHDHRKEIITGSREPTDEEVAKGFPSEHEGQVEIKVTEAEA
DKSVVGIPGFWLRVLRGHVLSDSLIEEHDEEVLNHLKDIRSGVLDGSYGSFAVVFVFGSN
DFFQEESLVLSVKHNDDGVKITRTPPTWKPGKDVTVETVTKKLGGKRGKGAKTKTFTVPR
NSFFNVFKEMSKDKAKAGGDGDEEDDDEDEDEEEQIEQLLNVLHTSIIPCAVNFYTGEAP
DGSSDLESADFDDDDDEEEEEEDEDEEEEELPKRGPKGRGGRGGNKPANAQQECKQQ*
>TCRU_9224 hypothetical protein, conserved
MPLSGEDQTLSARLLTLPATEHAILLNRFKFLDLVQRVAAADVAEMVQTIGLEALSYKGA
LEKIPPTFAVAADATKPAFAEKPTRRGKLSPPRKGARAANVPTETPPRRHRFQTREEELQ
FINRMSQPQKDRALPEFYLRKPPRDQQEERLMYARMDSSYSPLLGAYNAAAATPPINLKK
NKRRHEQSDNDDDDDNNDDNDNVVISSSGDRLVSGGEPPKVRLVAQTPTRGGRPPPQPSP
HRLVERPPKEPKHSNTYPEVKKRTGTSGAEGVSVAGDREGPFRVNATKNAPTQYEDAPQA
KQKQQPLHSDAWQNPHMEVMTPRTIQNLAMRHRGHFAPKAKPKAAAEVPRVPMEVIRHAS
ALLTGRSVASSPYLSGTQDPQQPAAIPTHSVSWDAQTPQFPSATSQLQPTNSSVHRGNRK
GDSDSQLGQTTPWTTSITLSDDVLAELTSTVDSMLRDHRAVLDSIMKDRKDPLSQFQELS
KDTGKEAHGVSVDNSGDNVSGITQKVKGKRAKLNITPDDEESARILQQAHDVLEDISDDE
DELLLVSRLQRQLGAMDRELEAIEQRDKQQQQYGSSKGEKEDLEDGDDDEQLIHRKESPK
GDRRHVRIDDSKKTVSGGDFNFGRGNCRRRRGEMPRAIVERLRSSQKEHQEYIRYTEKQW
NSSHVTEQVFAQRLTETLVEDAFQEVLQEVGSILDTYVEGLVLHELQ*
>TCRU_9225 Predicted coiled-coil domain-containing protein
(DUF2360), putative

MAEVQREHEFTRTADAVNKFIISTTQFLNRFAAQCDSQLIEICRSLQRLEILTVLLENKL
KSIDDDFSEVNAATPSTSAAAFPQSASVGVGGSTPLAIVDREVPPPMPGLLSASGGHHHP
PPPPPPPHLQRRNGPPPPPGVAIQTRVNGSAVVPIQPPPPVPPMPPSSLGQLPVGSLPPP
PPPMPLLGGFTMCTHPRLQGYFQMLALRVPVEAVKAKMQMDGHQPEWLDTPDAAAPTTIP
VTNNTPYDSD*
>TCRU_9226 nuclear cap binding complex subunit CBP30
MPRGSGFVHPNTPATISYSPGEQISLSELRRACRREECVVLPHTVGIWRAAFRSYVRAEG
LSQFVGDIEAEREGEGPILPPLRAPFSSFTPKRAAAQERVPQQRAIAHDKVEKDNLGVSS
GKGIVIVSRHKISGEQRFVYPDHDGVLSSGVVPQVVISEEEKAELEADKKHYVSPMDLPD
EERAALEELQSLWRSRANSRSEQGARHRAAGGTAMPGLNTPEEADGYDNDRYAKRSRLES
RTHETHATTDSEYNTGDMLDDALRLAGEILNFS*
>TCRU_9227 hypothetical protein, conserved
MSELQAAAGVFGRGTAAGDAIYRCYARPTKESTLDPELLARLQKMRLEREAAEAALFRPK
PVPKSKAMISRPRVGLGRRISEEEIARRRLDALPHKKREESIQRELRAFGRPSLLPPLYK
SPPITVAEKERLRQIFQFGELPPKPLNFTGANRVRYALIDRRFRLKDRFETLKKHVDALR
EELRQLRQQPQKSAPPETMADGKGNENEIISSGVEIIRRFHRRDPAKALERRMLEQELTT
SIGEVLQEMKEIDFDLRQLDENEAKRYIPKP*
>TCRU_9228 hypothetical protein, conserved
MLPNSLNDAHIAEAGSDDSFGIRPPLLLGDPQQMNLPSSSSRVAFTLSNSLVQFLSPLQL
QGFASRLIETFGLRHMDELAARVTCEDDVDALLGSHASLQQRRELWKGVCKWKRTANKRG
REWTKKSDKKKAVVDGNSRDVDVMSEKMHRSTTRYFIDLEKCTPSQFIRQFAFDGYKESE
TCLAKQQPAEIRISNAVGTATEGADNCSAPGTVISSPGAPSRSLSRTSSVSTLEYTHLLP
EKRYRREKLPVSTLSMGPGTGTAGGDEFLREWGLHGDDAEPKRDSVHSSVLSEAEGVVQI
RELIEECCAEHEAMRVAMCGALSSAVVTYNEGLMALQEKLRRVLAVKSKKRRSGPVGSDV
SAPLERAARLVSEPPLRVEMHPAESQWGEIVSFHTHVKKRSLESIEHVNKRRHSPRDDGG
GGGESLEFCAVATSVEPNTDNMRPSSPVNAIIVSSPSGNMIEDAMPSLSDFTSPSRGSYR
HTEALAREEYTRQHGIALQNPPDGMPRPINNDKSQAFPAVLQLEEEIKGSFPANGWDEGV
ADGTTECEEGTGAEEVLIACPSAVAFTRSACGNVNAGVTSQDLVEPCGAFSLDDFGLQAV
SKEVNYSTLGDAEKPVFIGEVLYGASNLNSVAVESQVIDVDAISSLESFTKEGERSSRTQ
QNNDYAISVDDGSEEMSTHSSPMALKGGLSAGEHVWMCSQLPRERQRAVSRISSLSTSQE
SGNDYMDSLSISVSNRARGLNWTTTSSMAADMQNLLAKSHQDEEKKVQLQNDAINADEEH
TAMITATRAPSPHCLLAPQGLPPLPSRNLMNKTPLNGQEPMEETIEELTSERVMKMSYDV
LRQWCLRLGLRIVCDEAHFKDAEEQEFCNVTDMDVTGKEDNRDIVLTQGENSSGWWLMES
SVDINEDDQKTLDGSCSSHSPQRHPMNEGNGTRTPPTFALGVDTDELEWRDLQRAAVTEQ
MQEALRLFITRRKFMLKVVPFFFHRLPRFSGGDPYRPVRAAELVKNQLALTRQELEEQRR
LAKKKEAEEVVCCIITSLAADAAESIERQAFLPVKEKNTFTGEGTKNLPTSTPIYSSQTT
CNAAYAELPVYDQLLLMEPTDVQTAATVVHADFPHVSKHRVETLLEESGIPIKVSRHVCN
SQEVGGGELNATQRSASSCSPPPSSLTCTAQKGQTASTQYSKRRFFAQSGWAQQRRNR*
>TCRU_9229 Arginase family, putative
MAARTDDPRLLSLFSAQREEDADIVIIGFPYDEGCVRNGGRAGAKKGPAAFRFFLQRLGS
VNNLELNVDASHLKLYDAGDITASTLEEAHEKLESKVFTVLVRGAFPFVIGGGNDQSAPN
GRAMLRAFPGDVGVINVDSHLDVRPPLSDGRVHSGTPFRQLLEESSFSGKRFVEFACQGS
QCGALHAQYVRDHQGHLMWLSEVRKKGAVAALEDAFGLTGKNTFFSFDVDSLKSSDMPGV
SCPAAVGLSAQEAFDMCFLAGKTPTVMMMDMSELNPLVEEYRSPRVAVYMFYHFVLGFAT
RSKPKAEN*
>TCRU_9230 paraflagellar rod component, putative
MLSPTTATSGYLVPHSAFNSTFENVMFPVRTLYCPPVPPSMLMGRYKPPPRPGRKYRNDL
SLAGPRDHWAQTQVARIWRGVLTRRRLRNERNHFEVRTRRAIMIQCWWRRLRAIWRRRFL
RGLVDEWIVSRRESMLAERLRGYGVMLSWQRRRFENAVIKLQRVFRWYLSQRTNVFADAT
QPPREKLPFPLRIQKKVYFPWRRREEAKDGSIKAASSNPGQQKKERSTSIQFRKYRREPQ
PTSVEEAKVINDAMREREARNAVILSQPEVQDRMQWKRDGLLLNDFDHNAGMIQRFVRGK
WNVWEKVTRKVTSDYFNDKVCIIQRSFRVFKTLRHITRVQISVENRAVRRNQAYAKEKLA
RMEEEIAWQYNLLNNAARTIQMLWAYYKHKSRQTDPFREAEGTAAAAAQPPPPPYNLILE
HIARERALRIAARSKMETAMEEARKRARRIYKRYVPESIEVVSGEGMLFSTARDKTEQNE

GRIIFGPGVM*
>TCRU_9231 Domain of Unknown Function (DUF1042), putative
MQREIIVWLQSLDLSHQVRHPQQDLSNGFTIAEIVSRYDRRVGMHSYVPGCSTECKRRNW
KVLLRDLKRLGCGSVTAEMAEATIQGKPGVAAMVLDNLYEFFCNRPIPPRATDGSDGNKM
SILNLLDALHDENMNHVAKTLERKPLPLRSMENDEIALGKGIKQPGFARPTAVSLLHVAN
RDARNAVLAAAVPADELRVQQRNEKLLNEHNLLHKAYRYAEPQRFAPVDHRRLAAIGKKD
GKSESVFKMPFQDDAIFADKVSMVEVNMLNKRLLGALQFRESADNAKADSREKSREKATK
KLLEACGHNLSLGLSKLLRTTLETSGFKELLGESSNGIDDKNILTFFVGHREEIPFAAAV
ACWSALLNASSAIASTLLIRPTEYMYILRAVRFICVPEMLQIPLLHVSALPDMHNTGSES
IHTTSTLTHGFRSLLRSKDTSDAILSLTEDLNTPQQAVFSNKRIFHVASVFVFLCSIGKE
VHAVSPQLAYSLLMNYFVPTMSRIFCLSSAAILEAIARVVVAHICGDGSKSKKGESGGNA
TESGEEQQLQQSEKTEWNAALRLTSLLAGSLKTAFVGDESTDSTNSGSKRAQYNLFLLHV
LRIARESLGTDGMEREEPKSSTLAAQQEITITSEVSLSSMSLVSSPTTPVELCARGVMGS
LGSSSMRERSIGVAMVIQFLAWDRWDLALEPFLFVLNDVKQRGASGSFLQRAADAWELRV
FLLELLTITFRKALYVIAEESANVVRGGSMVPSSTEKMMSPTVASVIRQKIDFVVLEEAT
VLCLEVFFEAPLLQRQLALQIVGARLLPDEQRNVAAMWLRGLFAFSVDQLDFLLRPHEAE
PLCMQDPTCSTHHRIHSASSRFPGTLTSEFDGEKGGEVYSMPPQQPGSVDSSKEAFSSVR
VLLGRVEPAYVVSSLNQLWDTFSVVQAALMFEDILTTAQVFSVVLAAVLSPQLREAQRLR
LIQNLHAVGGLLASVTPIITDEDSAHGKVPLVVNDDGGEKALDVTLRGLVVTYGQRGAVK
NESGREAVSTRDNVVAPAGVSTSAHFVVENDERGETYDEAKGDAKKKGKSQEEEEDPVTL
LESHEKAFWTSVLRLLRAQLLESITNEQSFQQQRKKKKPLSISAPPGNSWASVCRVTKTD
TPARMRELAAAVLLTLYCRYGGVSTDLISKETSLCDACQWLTDL*
>TCRU_9232 hypothetical protein, conserved
MRRPIGCGPRLLLAFGCLFVLAFAVTQVSALTVGCEKVWSGPSSTNSVKACLSNRNRIED
NWRYYIYPGFAALFFVLLLIIFPICFCICACNGTCCRTCCFPTSAAQHYNGPSCLYLAAV
IAILWGAGSMVAIIMGAHTMHTGVQDAVYNAKHTTAPYFRNIAKQVEQYTMVDGVILPII
EKETQVVVDIYDTVMRNIDDFDRKYLKYLDDAAIVSYSLGWMPFVLLLFALFFGLCRISR
CLPACFSCVYYFVGLVFALLSVILLVAAYFGSALNGELDRQLARRPGILQWYVVPYFESH
FNAQVKQLDTSIESLISLHVADACTAINEYCDNNPVFSDQKPFFCPSAVKCKTFYELLEQ
VSTVPVKNPNFCTPAPDASPSDASCTIALCATNCFDRAGVPGVSAARTASVDVMKKLQVS
KNATIARNLVNPLMDPDMIADILLLSTGPFTELSEGFWMAGTGYFISILVFALGIYTMLR
GRVVWGEYVERKKAH*
>TCRU_9233 tubulin binding cofactor c, putative
MDFDDPSSSEEGGGGGTNSVSSGNEPPSPAVATQVISLPSYPRPETATLPMAVGKRNCRE
VQSFVFDDDNDDGGDDDEQNGSNDSDKKEIMRRGLERASYDFCEGHLHHQLVESAENVVR
PLARHGCDALRGMGRLGDQLTEVTDTHELVDNEEGAVVGEETEEEEEEEEEEMSKDMVE
SDDKEMLYVEENREWDSVLRTMSLVDVTLLSHFYVGSNLSGEETELSMEGSVFVTETMVK
TISLFYTKPAKKPGDEAAEILQMALDTLHRLALHMRSMQTILTEAGLTIDNQIQEDEEGE
DVESEAIADRSGVDLRKVIFRGVHSLHVDSSCRLIGVIDIDACTVSLSDVVAFSTLPFSQ
QELVAILKSVIQKVAVLHDAGFVHGCLHSGNVLCCTDDGRTVLTGACGIMSNPLLPADAS
FISPRLARALQPFVKLVWSHHEKVNEETFPWTSDPAFHRAVLERYGCTSETEMRPKTSDD
IYAIGILVVTCLLGVPPFHSATLKEVVETLSSHNPEDDDDGSSLLGNVLTSNYALQRFRI
AGYTEAFIASAKDFVHMCLTAASNPGIGAQFVSKSLLKHSFFVEFPIQPNPKSSSEGAPM
REDEVDEAALMDRTVHCLLYPIFLSMDCVKKDCGTTPLLPRLLRNSIFASRWDALHYGQS
YHHARGVACKTDTVGILWPSLERRQVLKDDESQGEETAVKSLLYRSLVHAFKPFSQKMAD
SNTVTLTSTVESKGMRVDVEAHALVFSGKSNNRLVLYRDEVPVGYGSSVDTLILQDLENC
VIEILMGFRFVLVSNVRGCELLLGPCHYLYFEKVFDCVPVIVSSAHLLLRDVSHVDFHCG
GGAAPRAYGSAPLPANVTALPYTMAYAGLTADFAAVSLPQEHMVTMLPRGSVSNASAPVS
RTIKLYNMLRGGFDYPYSHALAALGTRFTHENDGISNLFLFFSEVAGKSVRIAQIHGDQN
ATLGETSSLSPKVSSRFSSWPYRHGRDAESELKDMAADGSGSSYPIIFIMDLVGDCVIED
CSHCTVFIVGSSESVTVRRCTEMCLFLMAKEALFEYCYRMETHLLLTEYLLLDHCYQMNL
IPLALEAPHLEEILASIIDGCSDESLRRLLEHALSQKNEKALNVLLRAEFNGDAVELEEC
VDMHIENNREQMILVDFVPSDVPLSSFFYEASQGLRQLSKWVVVPFLQKTWKKDKDFTHN
IELPPVCLHDLVNAFILRLPGTLNPCAAPDGASSLFDVVLERISFGVVHLVEAVRTLIIR

DCTGPLDIIVCSASRVIMESCENVTFQTACGAFIARNCHVCHVALHVNTPPRYEDCTFMQ
ASTLNITSKDFESHLARAGVEIEVNLFDQPIVQCLHAEGDVPSSDKVPEMDAVDSVERAR
LILQRPVTFVAPLSATCLGIEDASFIGSLEDRVNHEAKVRPCYDNDIIAAFSFLLHRQLM
PSLTTHDPLKSAEIEEPRFVRLESPRITLMESQQVEERHFDPLFERIADDAGIDSFDAEE
ESSLPPALKPGSGLPQLPEHNPVTGTTDLSPRGNGFRVFGNDSESERNRVPHDDYPCGDE
ENIDVVDAAMSAPDDDDDEDPTTDRKWCEMGGDKTSGEHQYPSEAQPVSRDTSLPQGTFT
DTRLSADERESAMEPVTYRSAPRDGSVLDDRKSATEFMAAPLRRSGCESAGEQSPEVVSS
ADGKKGIANVSLATSPSCRELDLEVNNSNEKKSSCSSDKNVKNMSMPEKVFLGNALSFQN
LILGVHPDEEEEVRSVLSRVAASREAMASARQASGSSTMELRRRVVEAVKRLQRVVEAVK
RLQINLK*
>TCRU_9234 protein kinase, putative
MGFADYLQKQRCPRTEREEVIEPPPMPPSDSTVENRKDGHVVVTSPVNLRIVVPEDNGMD
DCKHRSVIHIGESSDSDDDDLNLEEEGKNRQRGTLLLAKDPSPSSDGQNDSNINNNNSSS
SGYCYGFISSSTKTPSVVCVPPVSAVRWNWWTGFGINDDELELNGSTLDEPMTPQSYSSM
RFLGESNQLNRSAVIGSPKTSTTSDSHVQGRLQQDGKVGNRTTTRSESSQCSLSNTFNRQ
FSELQRSGMARTPSASTEFRSRGTGKPPLPITVYCSIESAPHFTRSPSRNPCGFFEASSA
KESSGFKPLTDLELNSLPPEPAELMSVNFGRTRSFSFKKKVVECRSADEQLLGNHQKLLN
GKYVIYTKRYLGVGSYSKVLLCYNLEDKIYYALKVFNRMKLQRKVLGVDCALHKVHSEIA
IMKKLRHNNIVALAEVIDDPRSRKIYLVLELAERGEIMSMRNDGTVIPIDDNKALPESEV
VRVMRSVVSAAMYTHRLGIVHRDIKPQNILLTSDGDVKLSDFGASIVVDNSAMRVRREGS
VAFMPPEMLVSSLVHVAPSCIRKPSISSSSHGSSTRVIPTTSSCLLKTEKVDKGIGTMSS
VSSREDSFGEQCNPRQTEVGPESTLAVSARRSARINVDSSASVPQPTPEVDLFKADVFSI
GVTAFVLLMGRLPWRAHDVRSQLNAILAEPDPFEVEFRKACEHTEKGSKSPMKNICEPDS
LLLLEKDDPLTRVETIYTADDTILDPYKEERMASREGGLQGGDTNDMCPLEAENPRGCDS
FTLLPPNEEISFHSKRDEDLMGCMHINGRENDKKMPANDPSRMNPVLNLSHASSCRWDTQ
QTCNFINSSNANVAATNAGWEHIGKANEFVSQADQFSTQSGGTAINSVALGSTAQCCQSS
GGWLDSTISGSPFSPLILGTPKSFQQTYVSTVENSEFTMRTATSRKVWIDGDRSQPSLPT
KNIKGSISANAIDFICSCLHVDPAKRSSMEKLYHHPWLQGIMTNEEEKMSSLDGASAIPC
PADMQTGKQNAKSGVEEKSLCN*
>TCRU_9235 hypothetical protein, conserved
MYPKNKPLPPEAASRAACLSIKKENEKAKQAASGIGVSGLSATSGRKGQSEENSTAASSP
HHSPRSSGLPKQNSRNSPKLPMPPSYLDSLKGSPLYESNFINDGVFNGGANTVSQGNGVF
NSNKNHMFLPNSILPPPYEISSAGSNGMVDGKSYDYYCGRGAFPPAPMMMPPTSHHIPAP
GMSAEGAYFEGHQMHGFAAPPMHSIPPPPLPQSQPPIPWSMQEKKNPNPNVSLGMSMEPP
CYNVPNGRGMHGQASYYYAPNNQNGTQGKYRRNNLHSSNSSREKGGNMRTTEDSQGERGS
EKSDARQKAIDDLHTRQLSMESNFSTQVQEKHDEGRQQQDLSLVSWRENRCHSCLQHRQC
VSLLVQVIVVLLERITEARSALRGSKAVSGDEVVSNSVSSSDTREVTVSAEVQQEEDLLT
LKEQLNELQDVLSNLQEEGVGMEPNRRRLLDGIMAFPQLLPLSTAWFNNLEESTSSSSDG
KPLTEEKFTISREVASEVKALMKALDFETTRPITLSLVAPSFFSLNASPHATVLKKNTTP
STSD*
>TCRU_9236 hypothetical protein, conserved
MAVVATTALETEGQKNAQERPVAPDVLTPMSPSSQCYLIGVVSFFVFALAALFGVRALME
IDYSDDTLLMVEVAESVDEK*
>TCRU_9237 CYTH domain containing protein, putative
MGEANGIQVGIKLLLEDRDNFRRLAQLPSLRLQGEEIYVDYFFDFPSRILKQNSDVLRLR
VPVAAGETATQKLSSLALKNNNRVERGDQMYFASHVHKLPEAVKDEILSGVDLMEVLRRH
CSHAREDSNAPINCMIQKLESLENMSGAAEPIEMVGSLSSHRRVYHYVSPDSYGNETGTH
EHALREKSLLQGASIRLDETDFPFGKKYEIEVTEITDPVNDVREELEHFLQLHHIKYSRS
LESKSSRFMKYSEGLRAPSLDITGVHLCIMGAEGYNEVLRWLENDCQTAAVIPLPSGMSQ
GSKYLMSQAGAVSEYFSGRGELPISSHNVRDSVSQSLRHWSQFSLREDVNPNGGGSLQQA
EDHEEYQENYYFDDAVEGTLRQNHCVVELRCINQGAAFILSLKKDQNVVNGSQNATTLRG
EISGDIARVLLRDPTTFLKTMKDYNNVASALWSDFGLQELFVVAFYRTKRRVFTRSVTAV
LPSWILQDAGRRQMSDDDDVDVQQCSANTASLSQSIIDQMPFLHIHLDLTLHDFCMPPHH
YAAIAAESPSCTYGTVAAFSSTKNAVSLYEVGVTGLAPHLQELVKHWLTSTMNNLGVEWK

PGNLTKVEQYLVLLLERQRHDQGGVTQHDHN*
>TCRU_9238 histone H3 variant
MGSLKKVASVEKHSAFSSESKLPKPRKNLASRKIHTEGRIVAKKESASAGTRKKHRWRPG
TVVLREVRRYQSSTEFLIAKAPFRRLVREIVSNLKDSFRMSATCVEALQESTELYVTSVL
ADANLCTLHANRVTVYPKDIQLALKLRGERL*
>TCRU_9239 Receptor family ligand binding region containing protein, putative
MPPHSRCSIAVAVVCLLVLAGFVNSQQEPLRSAILLDLRQTKMTNTSLQAAIDKYINSSV
DISKMFPQRPFILDSNGSLLSALGHLEQLFFHEETFIDVLFLVETADISVAVVDALRRNE
KTAGLTILSAHTSNPKLCDVETNPNTVCVVPQDIVNLRGVLETVSSELAWYSVAVVFSSD
AYGTGVESVLDSQISFARSAPTVVTKVFIKVSGTSDDDDDVIRKVLEYRPAGVLCFVKED
EFMRLRAAVVRLGKQDELFLLGSREAVNVLAFLKGSVQPLVKLWGALFVSQYTSVVNLVK
QGYFDLQQLDDYGAYVVSHLFDAMQAVTLAGNISSASIRSVRFDGLTGTVAFNAITGQRE
GIVYSLLSKTYTADHPLVTWSWNSSTSQPVITNLNPTATRAIILPSPLRAVTVCLAAARS
CSEAESLNAMAYVFLRHNQKTSSIHGATSFIPLVINTGVSGVEGLVSLIPVARACSVLLG
PGRGRVALALTPVVNQFALTQLDFNTAEGVFADRLAYPYFSRSTPTDSFNYLVFGDVCAY
FAWERVLILGLNDQFGNARLESMQKSMRQRNIHLERTHMIASIDKEQLVNAMESIYTKDI
SRIVIVLLPLYGEDAKMFFELFTELSYMKKYIFFLGKELCQYAASHPEEREKAQSSLCIF
PYVEPQRLEAINNESAHSGLYNNQVRILSQGGFAAEETYCNLTTIRHGAAFAIDAAYTVI
DSVDRAVNAGVSLNLSANIMPFVRSTSIDGFTGMFTIDKAGNRDLAPFGVDIQMVNRTLY
LGMWSSNQTSPFRYTATEPIVWMTGGRETPADTFRDIQFILGTTVSASPGTIVLSVLGFV
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>TCRU_9240 hypothetical protein, conserved
MSLFLTGDRFSSFLFAPEAPEHHEKHIEELVSRSRQGPFENRKAYTFPLDVPLTTADVER
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PMTKILVHRRKWLPYRQRLPVYQCRGPVLDALRNSQVLALVAPPGSGRTLQMPQIISETE
IFKSKRVIVVCLTSLSACRTVERLREERGEDATSRTVAVCTPTRYDVEEGTLIAVTTPEM
LVRQLLCDPLLINVACVILNDIHLRSPITELCMSLLRSTLRQLREENGIKRRGGSLHVVI
DCFEDAVATTIVEFFGKEFTARLNLSQVLQQDLKTSGTEAQHLNEVWSPSCVMLLEETMQ
WLAKCEEEGSFIPRDPAEDLRNYVENIGVVARIMAAEEAEFTNDEKLRSYWCPIIVQAVK
KYDCAEREDALRGADQQKQEERRQHLPSVVVIVPNAHIASVVEEALRLALGDSTDNEDLE
QSTSFSLHLLLDCLTVQEVDCVLQAGEAATRGGRRLVLLTTPNIAHSALPSTREIGLVVD
CARRSYASYDESTDADVFVTTYSLVQELRYRRTIARLRRGDGNKGEQDVARFPVCMVVQL
ISKPIFYGTKHRHISVDPGHHSIFNLGWDEYVQLYHLLQAREEGLRCRETGASLEDSENN
YLLSSMVAQLVPFIFIGVPTASTSRYEKLRRTFLAVEHHLQRLGHLEIKSADSIPRLSPI
GVAATCFSWPVEVVRLLMYSRLHDCVVPASVIAAAWMVGNMFFVGKMESDTEELMKEARV
FFSQDSGSDVASVFNAYHTWLSSRNVSTEAQDAFFNETLTSKKAFMLIEAQQIELLRVLE
ATDVFRLPSTCKLSCNDGDGGGSTVKNAGATDVTKAVTTSTIDAATVASRILEIPVNNLD
EGEMVFRCVTSAVYPSCAVPHSDGRVSRFGFPDKLINATANGSTTLPLRATMQPAVFSHR
SVMSVEEVYQCHAEKPFLYLFRTRVAEKGLDVLKEAVPLFTDAAVVACGNWHEWPKSPAT
RCRGWTSVLTNTWRQTKRARRLPPPAQLPAVSIKLKPYDTVQARPVFVQADDTFAFGMRS
TTAKWLQQMRDQGRRRIRALLCDKSWPASSEASLGLKEAWEWWSRRGRGAQDWLREERTT
HNTAISNGLKPGDSLYPYYQYSSNPGRPTAVVPPKKHIGSSTTNSFSAISSAAVAAAGGV
DGVAFTAASDAAARQSTAYVGKLPDPVMDKNIQHLAQSIAKARSREQEATFLKMYPDLFA
FLHPEHEFHGYYLHVLRRLDPDLEILGDDLDELEKFLKELEEEVQREVGITEGNVDPSYE
AQTYNAVDAAVDPGSNAQYQFQEVNAEEYMASYGMQVETAAEHARRPKALFKMHDGRASG
PTAVDGTAPEATKLGKMGEEAPTASSFFTQPAVSDNQNKPAVLPDLPLESVTARKPLQVD
PNASIGNFTFDRGSKTEGPVFPANEAAESNRGMSGGGGMTLMERLLAMKGGTSAAADKTA
EPVSSGTPRENVPLQTSSAQTVPLVTVGVWPSTPLPISQSPAANLPTASSGTSLPVEAVS
QQAPTATIAAANAPTAAELLALMGVIPSTPALNPLTIPPPPLPAEVVASRHPSILAYPLP
PREFGNIPLILAKALGETMGVKVGPTRIVGNIARIDVPNHKVEARALALKSFTCLGKKVN
IFKNDRIIDGVRPVFNKGQTTRSTLREDVTRLLHRADYGPEELEDDEDNNNNDDDGSHNA
GLPLHESNNGVGPVFPHYHHYMQQHEQELPPDEPAVPKKSAHPPQIGLLTDSEDDDDDDA
DSSSSAESSELVQS*

>TCRU_9241 U3 snoRNA-associated protein UTP11, putative
MTRGKGRNPGVGNLDKHIKRTIHKERSQPASRKHLGQLEKQKDHVVRSRRRKAKMQKLLQ
LKRAAAQRNPDEFHIGMTKAVLDIASGKMKQRAGSKEGNQKKTQKVLEQNTRNVQYLQYK
AQADLHRAKELLNEDASIAITSAPPKNKHIVFVENDEEFRRFNPVKYFDATPEMLKQHPA
VRGTISILQSTVLPEEVLLTGPRMLSSSQRRRERREMQEKLRKSGVKTAEEREALVKRLR
AKKDMKKYRFSSLVEEAATSAAAIGGGGDEEEPRDDVELILQQRREKEQQEAALAARNLK
EIQQRVERSRSLHALAKTIKRQNEGLRKSLEQKRESRFKPKAARRAR*
>TCRU_9242 kinesin, putative
MQSYSPAGSPLNSARPASTPRRRENDFRRVHSSRSITTTHHRSIVEISQGQGNAMRVYVR
VRPFSERELSLSMPHHSTVRIDVENPCLITLLDPQKDFRPRETFSFTRCFWSVLEQGNND
MCRGRTAGEIRGSIDMFINNNASSARGNRSRCLNTSLSNTSVLSARGRAAAENSVSFEGA
GSNAAIVAGSVVTHPPYSSQQDIYDEVGRPILENTLEGYNGCVFAYGQTGSGKTFSMFGY
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LGTQGNMDRPAVDIVDHTGMDPNELQGIIPRISADLFSGLREKRDTDPSHSYRVEVEYYE
IYNEKVYDLIRPQKDADLRIRHNPVSGPYVEGLTSKVVANEEEVARVIRKGSVERHTAAT
KVNDRSSRSHAIITLNIMQLILDKNDNTCKKQSKLNLVDLAGSERTGAVGAEGKQFLEGT
KINLSLTTLGRVIDCLADLAQSKSLSVPVPYRDSNLTWLLMDSLGGNSKTSMLATISPHS
VNFDEMRQTIRYASRARQIVNKAVINEDPQVRQIRLLTAELDRLKKVIRDAGHNEFSRDY
VLELQRRNNFLEKRCQEQEMLIVELQAELEGRVMTNRTEDSRAISARRARPGHLPETSAR
QRRDAVEEEKNPTLLKARLVEAKSENEVLRRQIAEEERNKRPDASNSAEQVAELNIRVQN
LKREVDKMRKYDAKKEQYMQRYSFFYVDLASDILHRVMLQKEEEFVRQVAHLFISQNGEM
GDGIRRLNKAHREEMEQMRKRHVEEMEELHKLSSARLKESIEKSNELYQQLIDKHVDKLN
YVEERMMNNKEFYEAELKRLGEENEKTRVRYEEQLDRARTQHQKETRKLREQLSSGASDR
QRSGEAAKRLQEEHEKEMNRRQEEMDRYRQDKEQEISRLKKQVDNEKLRYESDMLEKERQ
RRSLEREVNELRRELLKAQTERNRMEQQHHTELQNLSQQQERLVHVSNGLLSDWDNRSSA
MDASFTQLRALLQTQDYLNFRARLRDATLERKDYTAELEAVEERKRRDTQRLREIVQQLR
QNQEDSKASIQRFEEDIMKHLARSNKARHSGNSSNKNSHENGNSDSNSNAVKKNTDGNGA
SGANKSPTSVPPARAEKKEPSVKARGGTSK*
>TCRU_9243 kinesin motor domain containing protein, putative
MTPCGNTPTDGSPRPLDTPSTGNDLTKHGQKSLFSATRVYVRIRPFSERELQECGGHPPT
TVKLAPDGGQITILDPSNNYEPRLTYAFEHCFDSTSAVEGGDQEFVYQRVGLFVLRNVID
GYNGCIFAYGQTGSGKTHTMIGPPLLAACEAQYEGREASVMARTPPAAKNKWSPFKTPSR
PEKSMMISETQGGSDMTCVADNNTLSMEGLIPRLARDIFNSLRLKHKMNSSHSFRVEFEY
YEIYNEKVFDLMTGESNGTKTELHLRHQPTCGAYVEGLVRKHVVEEKELLQWIRRGSAER
HTACTKVNDRSSRSHAIVSLHIAQMTLDEDDNSSRVSSKLNLVDLAGSERTGASGVEGKL
FKEATKINLSLTALGRVIDALADLSSGKQGVFCPYRDSNLTWLLMDSLGGNSKTSMVATI
SPSVTHYQETCQTLRYASRAKQIVTRAIINEDPQVRQIKALTAEVSRLQRLLRERPQVGH
SNEEVEQLQDRVLQLEQDVADRDFTIDELRSQLLEKNVSEMKKLADENSRLQHEAKDLRR
AKLTVLRLQNELQVATEEKERLRAQLAALEKEKQEQVASRLIIHPEKSPTKAVAGSKRSD
LELQLGNDTLQTLKRLGIDSENGNYASLVDAITRCAADATKKYDAMLQKNTILIDSHSWS
LRENLKQLERKEWEVLTAMGNKLLASFERACAKSEKMQEEKIKEPSMPLVMPRGTQDKGQ
TRQNVRELSTAYATVNGMKEQLRIERERAANSERQRDCLQQQLEKLATERDDLWRSCEKQ
KKETQRLQTREKDLNEKLTATLLQTKNNAELLQRNSTGIFEALALLMEERLEAYRCLLTE
EAGERCSLVDSRHASRLHHERRLLDGKMDEMREEHKNALAQAAAHARSLQENMDRLRNGI
SKQERDLVEFAAHMTSALTAQSELRLALFHEKLQLLTDFSERYAATLYKSHSELWDKLAH
VEHDAETRVGDARSLLEEETVHFNEKLQQKEEEVRRVKELHEVEMRAQQAAKRLEMETWN
CQTRQYLETVEQHLHGALKFNEGKIDLLLEKVHHNYEIHVQQLFNQLEETAGTVRDLQAE
INAMRHHHLQEMCMEKEQHQSELKLIQLLLQKKDDEAYETQRQLQLTYNEKEKELQEIIN
TTKNTRDEAHKNLTQSIQLLKAMQKLVETNSSLYNEHIDGKWAIVSNAMESLKAEHSALV
ANMDRRAAETQRSHGEKLSSLQQEHQLTVTKLRREVNIARAVLQQQREDGKKEAAALRTA
HSEQLSFFIRKSCMLFAEHVAERQSIAQQEEAARVEMAVALRQMTMRSLHCEEVQRELVG
THAAFAAHCTAEHAAWVQAACEVLSSVGVATRRRMGEWREKHVFDCLRLEEKLREILVVW
EAGESTMLHAFGDSLLLRAKEIGVITHEVNVAKKALLFEMDSPMERKLPPISNTVMTMMI
FLLRYKQCAYEEFAVHRASVEDVRHTLSVGIATETLRREYEVTTTALEEHFYQEICALQR

ENAELRVQLSNLRENLEFQASLDQLEEEISLRNAKQDTKRHTDGSHAGMYGGNEKANAAT
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RSAVPIDASHSSLTASPATRVNQVPRFSKKPKRVDDFLWTMENSQR*
>TCRU_9244 glycosomal malate dehydrogenase
MVNVAVIGAAGGIGQSLSLLLLRELPFGSTLSLYDVAGAPGVAADLSHIDRAGITVKHAA
GKLPPVSRDPALTELAEGVDVFVIVAGVPRKPGMTRDDLFNVNAGIVMDLVLTCASVSPS
ACFCIITNPVNSMVPIAAQTLRKIGVYNKNKLLGVSLLDGLRATRFINNARHPLVVPYVP
VVGGHSDVTIVPLYSQIPGPLPDESTLKEIRKRVQVAGTEVVKAKAGRGSATLSMAEAGA
RFTMHVVKALMGLDTPMVYAYVDTDGTHECPFLAIPVVLGKNGIERRLPIGPITTVEKEM
LEEAVGVVKKNIEKAETFARSKL*
>TCRU_9245 Ankyrin repeats (3 copies), putative
MTKKNSKNSHAAAAPVSALEVQFWNCLKKGDVEGLGEVLLVRTEDKETGAVKFAVNREVA
RSLVNSPNAKKMLPLSYAVSQRMEEEGLHLLLRAGANVDAVDGSSERSTALHAACWGEDD
IAVALLLRCGANPLVNDAEGRTPLHVLASLNAAALFLYVLEAATNFKEESQEGLLCLENR
SPVLVSAFELLGKKDISHFTVLHTAVSDINGGSDRVLVDLLDFLTQMAKTQPAEVETLVN
MKTDSEGTALHLLLSCPNLNEGVITRATERLLQLGANPAAVDKWGHTPFSTLLMTHSSAA
AANVLRVLLNAMQKRGEKGQLEEVFLHHDVENGFALIHHAIASQNADAVKVMVEFLQCAD
GADGVQKIRQWLGEVLTREGVHVTFMLAESTCDEIAQILLNVHAIDEAAYRRCKEECEKQ
REKQEREREQRAKEEEGESEDEGEDHDAERSTGDYSGFGVTANVGSRVQQARKARAQAMI
QRRKQAKKTVDEGDVEGFALKRNSRSFWLLVAAAFLVFLLLLRVYGVLRDGPKKNSHHK*
>TCRU_9246 hypothetical protein
MHSGRGASPPKRLPLRRATSHGKTRPKVPAHRAYVSDSRSPLSTRFRVPPISPFTPPPQL
QQQEQKLLEAEEPQGKNDWSGSQELLGKSGFSPLPKLPNHAAPAQSRQLGEFLAEPDGEH
GPNCHSYRADDDDKRDLSPAKLVEISISNSVIVAGVVDVAPCRWRLRANPSPYPMRLHIR
EMDANTYPMHRLFRLIQKTVAHGENGGEDKSLRSQQPMEGSLYIYKEDNPHLQFAYGLPN
IIFLSGSMVLADVVRVDQLPLHGVAVKFRWIEAFSRRYHVDDNSSPFVGDLTRDNSAGSA
AQNYVPFLIYSSSRILQGLNGSDYLHCENNGAKRSNSSEKWLFRKNDYRPLLSSEERNAS
SPYSPPVNTVTREGALNLLHVSVVSRAGDASPITYLHTPCTR*
>TCRU_9247 hypothetical protein, conserved
MEDGIEFLESLPLMGFQMDGSHLHNVLKRVIQEQQKQAQFQRQMSIRLSDMEDDLRSMNT
RQKELEKALGNFGPDALRKMRQQIEYLDEGLESVARDVKEARQLADEAARVVEDASREIQ
SVGRGLGTVQDRQDRLQQELDDTAGEIEKQNRQLGEAMRTVEREQAEQIQQVQNLFRDFE
HKNGPGNLEKVREMLEELSERTDKNFRSVEESARAVDAELNRHRSDLNGLQANIGSLDEK
VRQYLSNIARDVDAKCQMILSTLREHERSSLEIEEHMVAAGQALARKKGLKEARRSDSIG
TRRNVW*
>TCRU_9248 EAP30/Vps36 family, putative
MNFWEWQTGEGVMGDEEVVLHSQNGVAIYEGENRTHWNDGKLTVTTHHIIFRTLSGESHV
LRLPLETVYSSGKSAYSKGRLGFSHAKIIVPLPGEDVYVKFSFRSGGMEEFFAAMQRAIH
EKHWIPKIACDAPAESSPLSRRTQSVATAPVSATASTRMNRAASALDKTGPLEMEEGSCS
PPKPLLSVTDKAGIAGLMRASAEKVQLRESLRDIDDVMKKASSLVESIRYLRERQRGGEK
TTNEDETGIESIEATLGLGAMVRASSTGSSNGRFHQELAMELHAWMTHKKNESVFGAMPI
VPLIELFSLYNKARGGSDLVSPSDVLLSCRAMTKQAYSRYTLKQLSSGRMALQHKDPSLV
LGKLARVLGPRFINPKDPASKYQASGDTVPTTATFPTSWTLLKSIDEVQFAASIQVACSV
AEDLLEELEAEGFLCRSGGEMGHIEFHWNIFLF*
>TCRU_9249 hypothetical protein, conserved
MGTNVEATFDQLRGILDAEDFGSWSNDDANILLSLLDQYHKQKCKLQTGRTRNPGGREGE
AERQDEDDETVIGEVDRSLTKVRHFLQERLPYGTIAEPKVPHSSTLSSLVQCGADPVAGK
GEVRPPTFSVDAFMYLEEDIEELVQRGCIAREYCRTCGSIAIGLCDYITHSFSQDQLVYI
SCYLIPSLSDASYVFTTDLCLRRREKQILNASAPFTCQHVVDVGSRLGVVLLSCYFAAHQ
QRLKTTRRVTGVEIDDKMIGLQHDAIARFATRPTLLQLDLVHSSCLEGPGAEVLREADVI
ILHNVFEYFISSTVEHLKCWRRLREILARRGQLLICCPSLEETFASFTEDDVHGMTKGDR
TAGGPVSQQGEVEFNRKRQREGEKKKDGGVVESWCRSWVEEIDVAEVREAFLAYRHGNYS
CRDAHSCDGEMDEELTERIQSVRVYMVK*
>TCRU_9250 hypothetical protein, conserved

MEDDVVRGRCAAIVQHLLYSGENRMAQTEQQRLLSAVAEELRQRAILMYRLCRAKQEKIA
LDQTEDAAYCVLAAVSSRQPSLWAVLTTWSRALRPRSPELRFGTPVLVTVRLKEVEQFIA
RSSHLQLALGAEDASPPAKSSSISMMGASLTHGRKRKHPREEENTPGAKLEPELASRLAF
DYFQLNIAKSKKFYAVVAAHEKKLGGVKLIEKKEESSAKRMKRALCGPRKGKRGIPEGDG
LSNSSHNNYNGGFGLPTEEEGEDDMGDYSLLFPPALSLPSSSSWTFGAAPPATIPQCFFS
SVSLNAVADRVEATCSALFFDRLQRCLRNPLLYSSLASMEEFNADMFHDAHNHSLPASQL
GAVYLIASQGARVGFGGSLRSPRHFLHPLRARPTSLMPVPLQMVTSQQLWRRLLVAGLWL
HVVGTELDDAPAHLKVTRYCVTVVRVSQGEPCCSVCDTLVREKPILRLSALTHEAENRDD
GQPIRSWEEMKSVGLSASSANGSFCDELLRCLSVRLEQKVRDQSGREASSQSHPSTRITL
ANTTKRGVHASLCTHSTCLTTLRELVVDIEGGYPLPACRAALIGGPKNEDALLRLLRDES
RREEEEEKSTHHSDATANMSREVKELLETVPCVPNVREVDGVLECAACLQQFHQGCICPA
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>TCRU_9251 hypothetical protein, conserved
MDKVSILHAFPSESTFLADVPSSILRRPVERARRHGSREIGSHDTHEAFMRALSGSIHAS
QSCIQGGGDEKVLSVMRVVSINGSVDFHERFLAECESYCRLCSRLQHAVDWLLLRKSRCK
DSGTPTGTASHASDVDSLSHVVYPLEPTAFLAAAFALPSLASISSSLPGDEELLAATAAD
GKRGGSPSLQSSRTVPYCFFHWCPMQRLLRIGGDSGGNNRLGSHGSSTSSSGGTVFPGAL
RRTLMERVTAIANIAGVCGCVSPVHNALSVHNRCKIGLTLSAYMDDNLPRSVTTDGGGAS
TKMTAYEADPFSRWRDDILWRLLGSLVSALAVLHASGFHYRGELSADDILCFALPNDDDD
AFTGDTMWQEGERDSNSIGQRLNGWVKGNQRRWLITEATPAHQAFFMFATLPRSLFVEES
KDPSELAAAQRRDTAAVGRIILMAVEEMKRRRGAKGMNSCSELIFVAERMATMEEAGGRM
LAAEAPAHRFAQLQAVQLRTHLWFLRAIVDERDAELEAAAAAATFQNSSSSKATESKDRC
FSSRLLMNNEAFTEKLNERERLLSEREKNLERFLVLYELTAERLDELPAKKDGLDLLKRS
LLHVPGARSPAIPGTTSPPLSATASTWSSGAKQPRPKPVRCPATTAKCETAPSDRTRPLY
GLLRFSKSEAAGSASASGATATLSSRSVTVLADKGKQSPGPRTQQWTSQVTSEKSSRRGV
VLPSSPSLLHLNWKRVSSILAREGANTAVATARSSACRRKSILAGTVGRALTPRTEVSSA
PATTAGGEKVPAVRERSSKRTMSVKRGSFSTAPTQVQSRKMTPSRGQRQASILLSPEISP
LGRVKEENSSLLLASCYKTPPRATSSSTPMPSRGSPTTTNAWNKMSTPHSTNSTTQGATP
RHLQNSVSSIIAKELKMSPDSALSLSPMTGHLLGTTPKEKSPFYNPLLYMAPPEGAMNLS
MSPDKSLSAKQPAKSPTPAKKEPRAPVFGAHSPLLQRDGSTRAVNMHNGRTEPNSLEVSR
ETPNRRQRGDGASAKTGTPNNRLLNGAHRPSSDDGAPSPRFFIRFSEHVDEKEPDIPQSS
KVGRPRSRCRQEQEEKTTPRALRSRIANDGWVNHHLEVLEKLRYDFQQSEMLKSARSTPS
GKALGRGVRGPNAAAVVGASAPPADRGKNRDASTWGDGSSQAAAGAAAPQATSEGAKLMY
*
>TCRU_9252 60S ribosomal protein L23a
MPAKTAVSKAAAPQKAAAPKKAAAPQKAAAPKKAAAQQKAAVAKKAVREAPKKGVKKTAK
KGAPAAMTKVVKVTKRKAYTRPQFRRPHTYRRPSIPKPSNNMSAISNKWDAFRVIRYPLT
TDKAMKKIEENNTLTFIVDSNANKTEIKKAMRKLYQVKAVKVNTLIRPDGLKKAYIRLSA
SYDALETANKMGLL*
>TCRU_9253 deoxyuridine triphosphatase, putative
MNRVQSGFRVPARVLNSLAHLQDGLNIFMDPDWRQIRHVDDWALAITMESAELIDSYPWK
WWKNVKAQTDMHNVRIEIADILHFSLSGEIQKRTQDEKGADDVALKSLKEMGFFCRPPAH
AKSTAASGQRTNGGDGDGDDELLELMFFPLTEVASAVATFRNIIQLASIYRFDLITKGLL
LAAQDLDFNLVGYYVAKYTLNQIRQLKGYKEGVYVKVREGVEDNELLHECVQSVSVEDVL
NEGTYLKAWEKIACSVFDAFGMPEEERRHAYDWLKSAALDGKG*
>TCRU_9254 hypothetical protein, conserved
MRSRNPEVRAARIRRRQNDAREDDQNGNDGYAGRSKRGGAGGVLAADAAQLMARMRHRSE
ERRKAEVRVGEREGWIKSRYADISGGVRFVKDEVLAELIAETKSSFLRLDQELSEDHNIA
TRRLHAAVFAHTTDFLQLFRDVNRASNLMESLKGRVQGTKAAISAISKFSTYAAGAAEED
SRAVSEVFGVSLLFGGGGGVNNSGTGPVIFGGRNNNNRNNVKARARPSLISLRLTWGGNA
SHKTFATHASADSSDADVVRHHDGNRSSNSDAGIYTGGAHLVATTRSLNTPSVRLWRDAT
LAAGGTSASMKRHSHVRLDLDRNLGMPSSQDIALFADVLKDEVIQLLAGRQYLEAAELLR
GVEETAVAKGCLPLILRLEDMLVTAIRTHLLRVPMPLMYSESLHIPLIQLLLRLGRVHKG
TRLFFQLHAAWVDAEMDKMQLRMDPLYGALIASDFLVGAVQEVLLRQQNLWNAVGLKAEG

KNSDYSLEKDEGSGKKGDKVSHGATTTITSTNNNNKGSRSTGYKFDGDEGGIGNKAHVRA
QPGMFIMPPNSAAVLWVRERVDKLARDLLGARALSYGIGAEGGDPSRFRRAVVMAADAIR
TLRRMDDSGYAGCDTHLLRLLTPSLVYLQADFSVCTGSRLESTGRAMVEHLIRDARLMYK
TNEAAYNPKMCEEVARRNNCGCRELYQRLKHFPRISYALLLELLLVPASSSLFTTKGSGI
EASQPLRQPLSPEKYTFLRYANGCTRSHGLFLLSLIRFVAAMTGQDSLPLEQMGQQSTQE
PNGEFRGNQLECVSFLLSNALVIESLDITMQRLFLSFLRTTLRQRQALVTFLKSAEFLKM
HRQLFCAAGESTTAFSSYSTTRWLIGAMQLLLADVLSASVWVAFLSRGGALSYMLCDAEL
VFCSQYMEELRRVLPCVVQGWMAAILSLAHNINTAQELLVGDDALLLSSGYDATAVEVTN
GRETSTVAAAAASYVGGGNGSHEAAAQLLQAAAVDESKLTPFLMELVRGRFSSHTGDEVE
ATWSSAPLQPSSSPLVPLLCGLRHALGNYPHFPMGGGFDHSDELFLFHWCVQISLNTLAF
FQEHFVLPSHVVNEQRGAQHGDTAARSTRPGATGASRYPLRGCVSPQEESVLGALAAGGG
NYVSGLALLQFIVFRLLRDVLCRIETWSAVYGLLPERWRQSESILRQQLFFFALFVRLWT
PLFVGGSKSTPQGRPAMTNMNGTIDGAPALVILQWLTCTTRAKGYQKEHPHPPQRHVFDV
EGLTFSSTVVSSTQAPPVSREMGTWRSQRNNVRSGDHRQEQGAMEGNSTSLPKKNPAGTS
SLKDGNTSSDNTGPSMLLLDVIGSFFDALQEPRALPAITSEVTRVRVERVLASVDLAEFA
RRAELDRSEEEDDGDDDDEYDDDDSVASSSTGTRTTGTSLSTLSARAADRAEESIRARVT
LLHFHDLLVYYLAPLL*
>TCRU_9255 hypothetical protein, conserved
METPSESTLPSNVDKAEIIAPRGGEAWAIDFSLPRVRRRITRKERDALISSRIRQQMQQL
QRPSSGAKKKGEGEMMRVGQAADSEDNRHMRIVAVDGMADLSDLVPQNLTTTREDLEERL
CLRLPRLLSVTKQYPKSCGVSSLASIWNYLYTRLGEADVGVSRAPVAQEEIMTILGFAPP
FDEISWGPFTGNGTLFRWFHAINRHFGVKGRAYMLYKPQGKGRTSCTAEEALRELKRVLR
DPHAAVVYHCHNHYMVPVGYQEIPLAQTDFYAPQVPELNTETTIFIGEVSRGRHEAMYAR
KWSEIVKDLMCRSPQFYNIRRPEMGIQTRVPKKKNNDAKGDDEAAAATAAEQQRQQGQRE
SETPVSALPPPPTSLFEAKIAPVASGSETTTTAGAGTGRKKKTGGGNLHCLICFRSDEVE
EHPERYEDPSTDSNSSSSSSSSSSSSSTESDNNEKEGMDDVEAE*
>TCRU_9256 hypothetical protein, conserved
MTNVSHDGGGGHSTARTGVESTANEATRNFILGLPKEGPAPGSADAASLQAAEAFVGEIQ
EEIMAYDMANARAMETYARSLWAKIPFFGKRWATETSADVLGGTPPLESRGNENVNTATA
TAAASNMRGQYRVERTSAEVAGGNKRPPQQRMNSWLFKQRHPGWVPLIQRWWVPCVCVAG
IVVIWTPDVWKLRTLYWCDYKYALFRQAIHKAYWRATMSAEEYEQLMQELEQGRPLSAKA
TKCPL*
>TCRU_9257 SpoU rRNA Methylase family, putative
MQRGSRQLYAVNKSIGHRWSAIPEPPPPQMDRLCGTHSVLNALRAFYNAVGCRHPHRQKL
HCLFVRDFRLALGDAKAYDTSHSHEEEDGERKEGKEGDSHGDVWVPHQYPKIQRIVRLAR
AMRLDIKAVERRELVRLCGERRNQNVVLEVAGYTPWDVAACPWPSGGRNAPGHGNNGHDN
KGRSGHSGGGGGDNVLFLDHVIDPGNVGAIMRSAFFLGVRCVVLSCDSAGCTAAMARASA
GVMEHMAVYRSVVPTTTFLENTIAQHRARGDPCSLEMYAAITMPMDAIMRSGCQAKGETE
KGGEPMRRRLLLLGNEDRGLPPEVVRLCSHAVHIPSPWMQQYERRWLHHADTTATKGNCA
KGKNGVVLEDDVVLLRPQEVSLNVSAASAIILATLLAGDRVVEIHRIG*
>TCRU_9258 hypothetical protein, conserved
MGATPGDGSKNAESSRRRSNAKTNDNGGVVPAPPSSSSPTPPPSASSSSSSSFPTEPATT
TKTEVSLSSPSRRLALFGSRALAAGSKGRLPSSSSSFNNTASSSSSLRAQQQQGVTAFGS
LRRDLAAHIRPSSDLSSQGKYLVVGDGMMAPFMALCLRVHGLDCDLAHHLSNNDMDRGTI
VLTPSVTQVMGDVLNVSVPSGSVVGRILTFDHVGNDMCDVDLNEFREKGESPTFFCCDRL
KLERALLSLCEVGSHSCHVLPKPHIDKGGLEPLENGGVRVRFASGMQQDYLGVICTSRSQ
ELVPELTFTNEELQQRAENAEKFRESLAKAVRWMELCVPPLPELGRFEKRFTPGSQEIVE
LLTPRDAKMTVRPTMMATKLFYNVTITIPDGTTDPRLKSTSTKQFWDDVVMHWTSGVPGY
IPHTMFRPMMTHMQQHFTKSSVLVYRTPLFLMPHWSEGGGRVIKIAHAAHGSAFDAIDVG
DAQGFTDCFGLARTVAGGDDVQQFLRERRLQVMEELDYHALLLNYGVKERGQLAYMSSRF
AMKILRRYKKSWRSILQNYVTLMPKVAK*
>TCRU_9259 hypothetical protein, conserved
MSFPLPKKYYLLVHDAARKVLGTDAEISAFVSSKRKFQCDMLINASATDPEMTGRAGGGD
HSYQREFAVGLQRYLGSCDVVVRSRRLDVVFMDREVLQLALGAPRRAINNLQRGEEINGE

PDWTRRNRLRISLGYDEDLFTNVCDLKMNIAARLMEKFVFDKYYNSTYHGSVEQFMQRES
PPVTYWQAHGYTLAREYQFDHHVTLAGTISQNFAKYYGEFAFDNPYCPGEDLNTISSVQW
LCKAWKQIPMEDEEGNVRELQLGTKQQPSHPQS*
>TCRU_9260 Condensin complex subunit 2, putative
MQGNESQPPQPLRRGEHNAAAMLPVDPSFIFDEGRGTVPFTQQGTQQPTLSASRQRPRFA
TAQDLDDALLQAIEGKITRKNAWVSKDASNLLEGITHTVESTLDAATTTDEYSSFAKVAT
VVEGCSKVWTSRVDSTYQRSNQMVRRLLRNEEGGDDGSDGERNVADDDGSGEGPASAAAA
ERRKKAAQRRTQSVRTIAMDPSEINLDGRGRMTLVHTGMNAQFRAITEKFDQGNAQGLLL
HNTPLGSAGNLILDVDYARDTGRDYSARRIRLYGGSRKVKEEPEDEETVTFAVAEEEFDA
GLDAPLELPPFQSIFLTTASAGHSPLSGDGSVSGSGAGGGNRLSGNSSMNAEEEEAGRPS
IMLPSLLLLPHTAPIQAEELGGGHMMTAGEPQGQPQENPQELGAVTSLFPTEYQQQQQPP
EYDHGMDDGDWGGGMDYGDVCDDGNTVASVGVADGGDANSEFLRERAVVEARHLVSGATE
LNAMDGCLFGENRLALEAEDPTSWFPLAEPPANALLGSGAHKNSELLRLHKEHRVVQAFA
QTPGASTPANKRVKREKTVVFDLPGELISTSAAGGSGDGGDVVSSLSSSSFLLSGKGIDS
STLKQSTTVGKNITSIGKELLLSKDPNAILAFTQSAVQRSRAQEAGLLLAEPPVPGKSIP
SYLPFPITVPSFFQPFSTSLLQWNLLRKSATGQNFALSSAAPSRRVSGMTAKNDWDTGRN
EDSQSQFGNHDDADGGGSGSGTVGAMPAEFFYGGAEADDEFMGAGGYDDYDEDGGRAYGD
AEDPLRQVEAQILSSFERLELAQAASTTGTVLNDGRRSGANELAGADPMRLAKVLQPPQT
ALPSQVDVAKLRQAMWELLDDAIQRSSAVKEQCHKREVQQKTAGHKRRRAANGDEEEDED
ERDSERPSGNDLPRFSEIVMSILPQVPTISATGTLSPAFFFFSILFLANEHGVVLESVPG
LDDLVVRGVSHPTTPAAAE*
>TCRU_9261 ATP-NAD kinase-like protein
MLRRVLPLFCYSVPQISRVGIFPLHLDPPTVQHREIFRLLVGERGFDHKNVSSSGSHAVY
GGGDGYRHDNNNNANSQLAGSLWCLESLAESLKSSECVPFDHLILVPNTRFPVTLRLSTH
LAALTTLVTRGLSRVHVDFTALEHPDEDMPCVYELTQKYRNSTLVHWLQDAHEMQKWAHF
GDVKLRVPMLLLQTVSFPVSMVGKPRDPRFIGKYFPGGSGALLAADRASTKKQPLGQPRQ
EKKTEDAASVPIINGGNHDEHDKGAIIGNRGGNFVNSPRWVNGGYGEQEVEISRSYISSS
TSSWLASSDNVPLLLQPSEQAELSKISNGENGKKDADYILRKDADLSSSVSGGHSNAGEM
NGESETEMSESGTETQPNHTVDNSSRPSSAKEMKEREGKEEEIDTMNMPYDTMPVRRKVR
HLVEELFSTHQSIEGGHGRSSTNAPPPHVEVHTVHRCTGADVRQALWEREVDPTLLLTEP
VYRYINSHGLYHDYRKDNYPKLTQVQHIGASSNTSSSSSMSSTTAWRRGKVQAIGPAAVL
SFPGLIPRLELHYDRNNILAREYYEKLSVFEANADEEPDLIVPIGGDGYMMHCIRNNWSR
FIPFFGVNAGHVGYLLNDPSTLGELFFAPLKLHTTIMLYCLAEKETETGEKVLLSELAFN
DAWVERSSGQTALIRILVNGEERIHLLRGDGVLVSTAAGSTAYCQALGASPVPVGAPLIQ
IVGSNVVSPAQWRPTHLNQEDHVELEVIDSLKRPCRCFVDSVDMGNVTRMLVRSSRAAGV
VIAFTSSCDLQQKLYQMQFPNNM*
>TCRU_9262 hypothetical protein
MALVQSHYGSDAIHTRLNDDPPSSEEIERRRGAGCLPYSNRLVHRLVVLPVTPPSIYEGE
TTQSPVETQGTHNVRRANERDRQRRARYASLLRSHYVPLVPFSTFTEPQERSFKLPTISK
YPAARRQPQCAQSEEDYMMCGGFYPGPDQYDHRGGPRLGVMQQHTVQLERVHSRHVAPPP
SRLINAPGNEDMLFPI*
>TCRU_9263 Tetratricopeptide repeat, putative
MEKENRKGKTQDVAPPPEFRVDGSVADDSSRRDASVSQGASEEQPAQPSDDELLHEVLAM
NTLAMQRCNTEALEYATTILSDAYMKLHNHVSSGDERLMDTLRSTTLNNLGVVECHRGQH
RQALSHFEAARQLEEKWGSASPSVALNTCAAYNALGMYDKATAAAIETIDMLRTLTIQEE
KGKTSTPPVAEGGSYSLQGTGIEVAKSENKALWGAAWHNLAVAQINTAKLTKHPTEHCNA
AVLFQNAMRATHELLGNDHPMTKSVTETYRAVRDVLRSYGVYKQHHTMLTVPPRPVDPRD
EEDDMERYLQQCAGKSRRRAKDKFHRDLTITFCGEATNGVKLTERLDPTPYPGAVDVIFR
DKSRKKMPRVLRGMTLSGTLLRAGQLYGNPHPLLYSLPPNYDPMDPSNPDDGCNLGSNPY
VGMTSNSRAPAPWKDSPSKQRKKNTTARSALSTQFHSDPNFQRIPPSLTHQQSTSNYHEI
LSVQQQPPSSYNPVQEAYRSMPSSSKSKPDSYNQTPSSYNPTQEAYRSMPSSSKPRPDSH
NQAPGAYTPTPNIQQQSPSTHQQAPSSSQPKSAGGGSGKKARRSTPGRITPPSKARPESR
ELARGQKASPKLPPLGKAPARNGPASGSSVRTRDDGKNVNAQIHGAYKLGTPTAEPTYEQ
VKYILLAEPQENQRQQRGGAGKYLVDDPTGQISLLGDAERHKAGSGCFSEADGKKNHPLF

DAMWVAAQRPMDASETRAVGRPSYYVSSVLDISKDSVRLPEEALQMMLSSNSSSEDETAP
MPVPRIM*
>TCRU_9264 kinesin, putative
MDQQSKAPSPTPASPRRPAVKNILKNVESHVRLMSHLEYTSTSSSYTSLRLKNAQTDKWS
DPFNVTRVHRATPTDIFYHEVIAPCVSNCLAGQSYLFLVSGPCESGRSQTLYGSPHHSEK
GIIELAAEELLRRVTETTDGEETGVFRATVTHSAFITRGSQLLETVSGNPVPIVEFPPPL
GSTPLPQMRLLDSASNAVQIPTKKHMDTSCIVQFHIYRPVDSSGRRSMATITFVDVAAFR
LPHCTEVIHLIETVRRVAGLSNAGDPDFKHTKLTTLLESALVGYVTLMSITTISGRQDLH
ESACDALRFAESLSRIHQVLMLVHINIPKWLLDTAEKLEDLRMQRERILSEQHSRGVYDF
YRAAAKWLSEHVSDVDGTFDKLLEETESIRQEVSHEVKAQIKDLQARIQEEQQECALQLE
RTRAAHAVTSSQLEAVKRLDETIATLDQQLTQRDFYSDHKISEMRIEISTLENETNMHRQ
ELTQLEKEEKLYDSKYKEVVDVLGKYAEDLAWAQVYFAHAIEMNAINQKKEELEAELELA
SRVARRATDTLRFDRERRSKISRLTMMQQKVDALRERVNPNSSANNGSFSRSECHEGSVS
LSPGRRRRRYVSPRYSAM*
>TCRU_9265 hypothetical protein, conserved
MIPKLNINSILEMSGKSREQNAAGGNRMEAMRTPQEMLSSTPLRVRSTVKSVPRIPHDGS
PTHSWRSSATTKFEESGSGFDLPRRAEELSYVLGGNVLQIQDVQTLQLKAVEMAERLLRM
EEWYKEQLHERSSYLEHRLMQLTASTVGGCSQPASPPIDRLVAPAIIRSRQVPSSTTTGL
SRPTLNVGAAASIRQNAVPAAPNTPNTGLANSRTPDSSRHLIHHRNTTPVRDPPFSSQSA
ALRHTPFSRRPNRDGGLNSGGRSKGSGIERRKLRSASLTISRGSRGSSDAGIEELVDDSS
RRRKKRRSLASPLLVAVPVTNNTPKHQRPSSGRLGHTP*
>TCRU_gamma, putative elongation factor.1
MEHVRKYAFGVALIIGEERRHDIVALWVFRGRGMPAIVEDVEDTELFDWEEVADVAAQRE
RITDYLCWEGPTIPRPVLEGRVFK*
>TCRU_9267 O-phosphoseryl-tRNA(Sec) selenium transferase, putative
MNERALSLAEGFVSANYVQAGGEALRANERLVRSVLAQRRCPEKGMSDVAIEWLLHQLAL
MDTNNFPAHVGAGEREGRVAAPLVARRNYGLAHGIGRSGDILSDQPKAAGSSLIHKLTNC
MMLDLLRLAGAPSIESAVVFPMATGMTLSLVLRALALLRRDEKRKEMPDLLKGAVEDEPR
YVIWARIDQKTALKCIEAAGFVPEIVELRHAPLQRKGTCGLGLGSETCLHPFFLQVHLDD
IVAAIQRVGGPKHVLCVLSTTSCFAPRIPDDVLAIAKHCKFMNIPYVVNNAYGVQSRVIM
RRLDAAMRLGRIDAMVQSGDKNFLVPVGGAVLSGKKHVVERAAALYAGRASISPIVDLFI
TALSMGRGGFQRLWEVRYEVLNMVQQGLRRFAMARGEVLLEEEDVNDIAASASAVGFTGA
AATASCTVRGTHRNDISFAVTMHTVGGAANAKAIGARLFRGAVTGPRVIVPDSTIKQLCG
LSFRNYGMHTDEVLPCPLLVMACGIGTTAEEVRGVMERLEVAWPLPRTLSSAPLVAASVM
EPPLEKIKDVAPEVVVNYGVDDSGEEEEAL*
>TCRU_9268 translation-associated element 2, putative
MVKQRMTALDVRASVEEMRSELLGLRLLNVYDINPKMFLFKFGHGENKRTLLLESGIRMH
LTQLVREKPKVPSQFTLKLRKHVRAWRLDSVTQLQHDRTVDFRFGVGEGASYHIIIELFS
KGNVVLTDHEYRILLLLRTHKDDDIKMFVRELYPVTRPFEEQQEKEVMAQSESGKEKEEE
QRRTKALQQEWHTVFARHADYETIRSTLSAVHHFGPALADHILTVTGVKNVKKGEITSDA
ETMFKLLLPGMLQAWEITFSPLPGGGYLISNHRQRKESRKGGQEASSKIEEDKSQAEEEK
SMNVNVADESQQQMQAVQYDDFSPVLLAQYSSDGVVTSFLKSFGSVCDAFFLYTETEKIE
QHNEKKTTSVISKRNKFERDHQRRLNALEMEEQENQRKGECIIQNAVKIDEAIGLINGAL
AAGIQWDALRSLLKRRHAEGHPVAYMVHDLFLERNSISVLVESNEQEDEGEEDCDVTPMV
IEVELSKTAYANATTYFAKMKSNRIKYEKTVAATAKALAGAEKKGERLAAKQKTKKAIVK
ERRRFWWEKFSWFRTSCGDFVLQGKDLQTTEILIRRVMQLGDVFVHCDVDGALPCVLRPI
GSAWTTAFVEDVEGDPQEGCQAKTCRIHMTSLDEAGAWCVSRSSAWEGKFSVAAWWVHAS
QINGGTASGCYLFDGEKHYLRPQPITFACGLLFRVSTRRIDPNDRDELPNFISEGELRPR
HLEEEGEEGEYGAFLPPDSATTLHPLPSFWELRGPRRHPQPQQQRQGRRAAEGKAAQKGM
TASKKTTSTPSTTTTTTTTQKVIAGAERGGKGSGAGGGTRVASAPSPQKSMQQLTKHQRK
KLKKIQEKYKDQDEEDRLYGALLNGNQMSKVQLEVLALQREKEKRHELFPSKAFEEKNFD
EKREEDVEEVTEFIDEDKSGETNSHNESSISLLRNNSVDGKEGHKEEEEEEEVENEKHNA
GQPQSKTRAVATSVEESCIANDEELRREWQYFTSQPKPMDNIEYALAVCAPMSCVISYKY
RAELSFGNAKKGQVTTSLQGHFLAMTKGVENASEVRAVESLDANVVMEQLRGNLRCLTTR

QKK*
>TCRU_9269 Long-chain-fatty-acid--CoA ligase 5 (EC 6.2.1.3) (Long-chain acyl-CoA synthetase 5) (LACS 5), putative
MYVDNALCMPNGVCVLVHPARSYICALVLADETKAMMFAKEHGIEGSYPDILRDPAFQRK
ATESMQATARKADRKPMECVRHVRFLNDEWTPENEILTAAGKLKRREIDKRYADVIEELF
ADP*
>TCRU_9270 hypothetical protein, conserved
MVAIAEGVFEYNVHESKLFGVRFSDIVAGYVKAAETWPSIVAGITKKEWRARTVLGSRNG
DNRLCVLHRPTVVARDSKVFLLVGSDTLGYDSSDDI*
>TCRU_9271 hypothetical protein, conserved
MSCGTVADHPRRQERTSPPHLAVRAPVARGTNCVSPTKRPAVHMDSDHHLPSHTAGTEDG
IPRLAGMLPRRKNVAFVLREADCDASTSACGTPLAAVIKCLEMHRGTVRAAAVTFPQESV
RTEWSRPNVLQRQPAPC*
>TCRU_9272 Leishmanolysin, putative
MNFDPKYMTDTAWSVRVAAHEIAHVLGFSQESMEEKSLVKKRERSVRGKHIQEKAKAHFG
CDSLEGMVLEDEGGPREKEVPHWKGRHARDELMAPTFGAGYYTALTMAAFEDIGYYRVNW
SMAEPMSWAAAVAATSWSTSAIQPIILPPSILTCFAMLKTPRRFAAPPTTVTLGRVPQAS
LRTRGVWWIRTFALLFLWNFTKSRLGQRTGRARTKMWIISLGR*
>TCRU_9273 hypothetical protein, conserved
MTMGASRTTKLLGMDLDPQLTLNVAAASQRISQPRRIAHKEAGPSPHDPRTFIIGYGASK
LRYGSELIWAVATDSAKNEMQETYAGLARIVSGVPSTVDQ*
>TCRU_9274 hypothetical protein, conserved
MCSQYGPLRNSSQRGGPIAVSVANSCLRVAATQKFSKPPSAVHPRNIGRQATEDSIASEL
KGLAGVYQHQRSPMGSAVELASSTALLGKVRLEVIGSVMLHFVYQLCQLHRRGTHTTARM
LVRTRRPQPKQSPQCHFLSDLTHDGRKADGSI*
>TCRU_9275 hypothetical protein, conserved
MPLGELSALPLLSVLLGVSEGLVHRRLSALLARHRRQPRLTPRRTVSDVVTPVRDKTARG
LSERIAVECGRRRGGVPRCTLTVAALSQSRPASRLRSTTLTMGDCWLCPAGSRACAVEPN
TGCAATWEAAALG*
>TCRU_9276 Endonuclease/Exonuclease/phosphatase family/Endonuclease-reverse transcriptase, putative
MEPFTWLPAERYFYPLLNSIGAYQRYTYRLRAVCDAQRQKLLLSGDIEQNPGPIAVLQMN
VSCLTPSKLATLMAQGADIIAIQESWKSSEQIASMHTGDYVLHAQSRIGKGGGVAVLVRK
TLRSKRIPLTIPQHDTSLEVVVVQVALDQNRDLIVASAYMRPPPQVTQSFRRLVNCLPAS
SPLLLCGDFNMHHPQWEPFLETSPSEVAAEFLELCTDAGLTLVNTPGEITYARGTRERSC
IDLTWSKHLNVSDWSASVSPLSDHYMLTFTLHQAFKDTIPSAPMFFYSWGKCKWDLFIKD
FDAQLPAYDYKKQSTGIKAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERMATDSKA
RYLQLPTPDREAEMQRTRSQFFLLLRERLRNTYLRRISKLNPGEPLAWKYISGRKKASLP
SPTSMLLGDGQHTYKTARRAANALNRIFLPFHPSHKAVRFSKGINRQSASLNINASFPFR
QQNNNESAATSSLVSSTSLISCISEPQNNNESAATSTSCSSLSSSSEPQDKNEAVTTSGL
VAHLHSPLDAPFNRTELLAALRNTPYGKAPGPDEVYSEALRHISSKGLRFLLRCINHSWT
TGTIPAEWRRATIVPLLKPGKSPELLESYRPISLTSIVSKVAEKMVLKRLLWVWTPHPHQ
YAYRSMRNTTMQLAHLIHEVEHNRNHYFQVSLPKKSGIGNQLH*
>TCRU_9277 Reverse transcriptase (RNA-dependent DNA polymerase)/RNase H, putative
MLRGVPQGSVLGPYLFPLYAHPLLSLLNSFAGVTADMYADDLSIIVKGQSREEAIPTANM
VLQKLHAWSQENGLAINPSKCEAAWFTLSTHTESDYDREGRWPLVVAACQIPVMTMGASR
TTKLLGMDLDPRLTLNVAATKQRAATSQRISQLRCIAHKEAGASPHDRRTFVIGYGASKL
RYGSELIWAVATDSAKNEMQKTYATLARNVSGVPSTVDPESALLETNMPPLHVLCLRARL
SIFENTRACQMDWMRRPPPEPPPRAGFRISPLSRDELYAFVDAYTKDYGITESSPREERF
FRSSIPPWFAASAHRVTIGVELPIDHSITDEEELIREKRRVSEESLALHSHRSWILATDG
GVDVPKSAGVGILLSSLNSSEIIEKASINRGARPCSYRTESRALLLALEKLMIPRIRHRR
KTLLVVTDSQSLLAALNKGPLSQTDWTEDQIRQRLLKLTCAGWSAHLQFCYGHCGVHANE
PADQYATQTMESGQYTEHGIAPLWHTDLLTCFTTQLTNKWRGTIRQDTHRYLLCGTRPSD

LSGKDLITQEVLHRQELVRLARARCGGSELWGRLCWAVRDCTNQCRFCNISPEQSAYMRS
NNDPTAPGTDTVPPSAREEDVSPVRRRTLTRRRKEKCPHCDSTLTGFSGLVSHCRSFHPE
HPPPLPELKCDFCDMVFPTRRSTAPHRSRCAHNPDATRHRNSSARRRSLLPQDQPASTST
PIGPQETLHHLLLECPGTLAVRQRLGIEQDRQ*
>TCRU_9278 hypothetical protein, conserved
MSGEKTVVVHSSVCPDEEELPSAVQTPSLHPAQTSTVSVGADDDDEFAITYVAQKSAPVN
IASARSAPQKRLRNSAVEQTSASLDTDAMESKPDDTDHPHDRSEYMRWQARDAARPKKLL
LQ*
>TCRU_9279 hypothetical protein, conserved
MSWPTWVLNETNRKIQQRIDHIAYELQNKFSDIELEREAVAVLQRNLAQVKQHVLSRTKA
AVEDQKRLQRDDDALQILQREESHSRADLHALKSRQKEVQELLQGVSRAVQAKAKALEKE
HVISEVLEQTALELSAASASQKNAHEAQRDLERQRHRLERVQASLTGAHNSLRMSQSALQ
RGEEEFAQVQGELRALRLNIVRGKQDKTESWLAVSRVQEAITVCETQTAANTEAYASGEQ
TLAARRALLDQLQKKHQELLAQQQTISKSIDVHRRNQHALLARLHASTSEAQEQENATAA
TQRQLAAQRDVRQQALLSYRNTLALWDGRNAQLQELLLRSRELECLCKETRVGGGVQSTR
AFEDTRASLQRGLQQLDDRIVRIRAATLSCLSDLQQEGRFAEEINYDVTKTREALAAAEN
ELAARRQSRDMCQTHLDALEARLSSMKLKLEQARDLVREKDRHEQTVLEGVVQELQAQLH
RLTHRGLALRREITPLQCALNAHTRSADDTKEKIAALTEVVLQRRAELRAIESDAVRLAK
EKETALLHHSRATLELRSVRRVAESHVEWMRGSATLEDILRGQALVLEETVLADIKNAVV
ELHLEQKAQAEKQAELRRRQEQLQQLKCRYQNVMESMSRRMVAAGGMQEGEPHAPSITSS
PETLQARCILQSSSDRERLRERGNFLDGRIVFLEHETKTLRKMLHALRAGRGGRQSSASG
PMAHPKTEGELLRLREGVRETRRSMEIELQCVVEVLRTLQSRKRDLSRRLKDVARRLTEL
QAIKRNRESVVRRLKTQIKRSQPNLKQRSSLIYTQQ*
>TCRU_9280 Concanavalin A-like lectin/glucanases superfamily,
putative
MATWPVNSREDNRQYSFVNHRFTLVATVAIHQVPKGSTPLLGAGLGDGAGAKIIGLSYGM
NKTWEKMFNGKKTAPGSTWEPGKEHQVALMLQDGNKGSVYVDGVIVGSPETIPTLETQGA
EASFFYFGGDEGDINSSVTVTNVFLYNRPLSVGELKMVKKSDAKKGNGDGSMRGGISRML
GFCTFVALY*
>TCRU_9281 Concanavalin A-like lectin/glucanases superfamily,
putative
MNATVTKASKVKNGFKFTGPGSRATWPVNSREDNRQYSFVNHRFTLVATVAIHQVPKGST
PLLGAGLGDGAGAKIIGLSYGMNKTWEKMFNGKKTAPGSTWEPGKEHQVALMLQDGNKGS
VYVDGVIVGSPETIPTLETQGAEASFFYFGGDEGDINSSVTVTNVFLYNRPLSVGELKMV
KKSDAKKGNGDGSMRGGISRMLGFCTFVALY*
>TCRU_9282 hypothetical protein, conserved
MTLVPYTPSEWCDIGSRLWEMVCQCGETQVQMTFIDGNQMSDETVTVAPSATGLCLFHGP
ISKAWQDSTLVGHIANLRAPQIPNFETQVLLPAMGAVRELGHQQWLITAERESLNIDYAN
AVAEVQNLNAQLNSQFQKAHHNLSVRESTIAGAGNQVLELQQQLEAGRAQLRREFNLGV
LTGQFQEREARLNALQTARDAETAGRDESPATRHVANDGVTTIPHQTDILMAGGVPSSAA
RRGSAAYRRPHGNVGRPHFHPSTLLPYRTSPLDVQLPMEEGRGFCAFDVTTWPSRIWNEG
TFGVVFDLRCAHQCWQQDNEQVKLAFDNLVEWIGALEVLQDPTDRIMNLGRSLLNTFRMQ
LTIASDPGIRLSKLRARLYTAVHQTDAYARAAQLFVDWRETQRTVRCQRCHIFGHEASTC
NVRPRGNYSQYRRPSKNGRGAAARRS*
>TCRU_9283 hypothetical protein, conserved
MGYKAGPEILQITINSAIAGMTTLAHPLWAAPSLVRIDVWIGNIRIAGSIGDVTRWEAQV
LRNADSRHASLREERESGATQYTFLGVQFGHVHQTVSRSDKFVRSVRAMPAPNSSTIAEM
EVMASRFLYAAAILDTRLCEYYFLITAVRRRLSALNRGIVLETSPANLPPAAVGLGEALR
HIIGNNRKRIIKLTEKASAAIITSASLHGWGAVFIPDSGDVKIAGGKWKRKPFLIMQAEA
RAVRLAVSVISAILPPTMDVWAHSTSLQGAANKGSSK*
>TCRU_9284 phosphatidylinositol-4-phosphate 5-kinase, putative
MGGIQSVGGAATSGHGFTGKQVSGALAAAADAQRKSHRERLKAEEDLPRAVRRTVSGVIQ
TLDEIGREKYQEKRVLQFQVPDSEGNMGTVTVHEYAPEVFRFLRQLDGLGEDMFADEWTL
PEDRLALELGEGRSMALFLKSKSMDLMCKTIAEEEVNVLLKLLPQYTEHLSRNTNTLLMR

FSMLLRIEAGAEVGFILCFGDVFAPCRTLNEKWDLKGRIPKPGKYQHFPKLIQRPYEPNP
YLIETPRDTIELPELVGSQEERVVVVEAADKDKLATRKDKDLTRLFWLERHERNKLIRVL
MKDYEFLSNAGMMDYSLLIGVAYNETKVSRSGKLVRSMRMTYPMGSERDADLAEVRPASL
PRRCPTPHDFRAGITSLQDQEIYYIGIIDMLTKYTWKKKTANFFKKFLWKPETLSTIPPV
EYRKRISKYTKIIFPDVNATDNTTKPSC*
>TCRU_9285 Integral membrane protein DUF106, putative
MSQNILLDSNIRDWVLFPLIAIVIFVGMLRHYAGLLMKSHPKPKMEKMCCVNIANYGKLL
LVEGKKLSPEAFSRRAEAMRQGPLQKKVEVDPIEMMNDPSMMGEMMKNNILMMVPNMGMM
MLVSYFFSGFVVAKFPFGLASRFRGMMQSGVDISDLDCNYVTSLSMYFLIMFGSNGLLQL
LLGADAGGSDQAMLMSQMNGGGPQQPVDYGKVFKSLAEELEFAQGGHKWMYENAPEMLLK
GK*
>TCRU_9286 hypothetical protein, conserved
MVILGLQKLAARTETEQTHPSTEEEMDQYIRSRTDWRERVFLRLAWITASCWSEIAALTP
KNFTLEAEGTLILDWPVVPKTARADPHRAPRFVRIRGQDAFDIIKLCRTLQENEKLTNIT
NAKVERALAP*
>TCRU_9287 hypothetical protein, conserved
MLDLARQHGDVRVQLAFVDEHGSLDAVVAAAATMTGLRLVSGDIAMHWEESTVAGHFANR
RAPQVSNFEVRVLLPIVCVLPGSWESSKG*
>TCRU_9288 3-ketoacyl-CoA thiolase, putative
MFRRNAVTLAVKRVFVVGGHITPFLGKGSPLFIDKKHPDFGKKENKTLEELLADAINGAL
EKTGLRKDGRAALVDKLVVGNFLGELFSSQGHLGPAAVGSLKGSTAFLNKPAMRVEGACA
SGGLAVQVAWEALLAGTSQLALVAGVEVQTTVSARVGGDYLARAADYRRQRSIDDFTFPC
LFAKRMKAIQESQHFTMEDTARVVAKAYANGNKNPLAHMHTRKLSLEFCTSASDKNPNFL
GNETYKPFLRNTDCSQVSDGGAALILASEEGLNKMGISPNDSSLVEIKSLAAASGNLYED
PPDATRMVTSRAAAQQALALAGVKPSELQVAEVHDCFSIAELLMYEALGIADYGKAKELI
RNGDTALEGRIPVNTGGGLLAFGHPVGATGVKQIMEIYRQMKGLCGEYQMKNVPALGATL
NMGGDDKTAVSTVIANI*
>TCRU_9289 Cytochrome C oxidase copper chaperone (COX17), putative
MGIETWKTFPKILTEYPKHGVPLPCSDQNPRLRCPETRWARDFCLAQGGSCEYKIEAHFD
CLEQYYPREKVLELRKAFKPNTLDYPTSDTYIRYRHFYVGAAWSGGKHGWEGTM*
>TCRU_9290 Leishmanolysin, putative
MDDTGKYCISELYYTMNLLTENCHREDDVLFSAHGDVLEDEVVPAAVKLHADRLLVQPLE
GALIVPPFDTGSVCLRFTVPAEHPSTGVANSDMAQCVAAALSVVVHSANAAMAAREHHDC
DDIDGMELQDDDGDGRTLESHWWRCHARDEWMAPIGCAGCRRGSAPH*
>TCRU_9291 retrotransposon hot spot protein, RHS3, putative
MKRAVKGEVIFDEDIRKLCDKGVNNLPGWSLAAAGVKAAVHNSTKHFLDAAAEKSRNPTT
TSTPEKLEGCYESVHNARWSHAVELPDGVERTKTGTGMRVHEGRPEQSWSYKKADDAIEK
NDAVQQFGAAPPVLMVLTSEKGWPYSWHTIQELPEDVFVNCAADRAWQTVRNDPTAWFGT
HGGTDFKPRRRVLIGTPGIGKSMNAGSYLLYQLLHCDAEKLQVVVHCFGGGDAYVSDKTT
RAVTRYSDEDMCVSELRSLRGHGRNVYIIYDVAKEGTPPPRDFAPTSGWGMVAVSFPKVT
NYDEWAKQLQAARIIVNCPDEMDVKAMCACITRDKTKEKQAECWKEVKKHMYLLGPIPRH
VFDEEAFNERCGAVKFALQSINEVTVKEYFSRGGELPWCSEDPFHRLVKVVREIYAGGVI
LFSAPISACLEERTLERFPSVAE*
>TCRU_9292 hypothetical protein, conserved
MLAAGRLFMKDYNVAREMFVQEPDDYVQDQRPLEEILNLTAYQALEAITRPLHEGVLSLG
QRRDYERKAYDHPSCKENTKRSTHAGADRSEAGGRGKAKTNARNEIYHFH*
>TCRU_9293 hypothetical protein, conserved
MSAANGVYVFGDTSVSSAGLLSVADCIFVGRTKGSYSALLYLDGSVTLEGGAQWRVEGNV
VGAVSVLTIPYSWQKIKLSGSGTIVALAYNRQLEGTYPFADLVPSNTIVKPPARFVVGCN
LQGEKEVSYDGVFPEDVVVFRCGTCNDDAACYMPGTESVDRGSCSCSCKDGWHGASCLPF
EVPDTVVSPLPERAVDGDTSCVVNQTLTSLTLKMWKTHHCYEGVTFSGAGAVLTFFFDSM
PLHLPINITLTGCTFLDGALLRFVGGAEAAESAGVLIRVSRTVMRSSVVAFSLALPLHCD
IAVTEVDAVQSSAVHLPDNVNNMCSVLLLHDVVLTASSLLVSNVRAHALSYGGFGLYSFG
TLTLVGGSSLYARYCSFEGYKYLFYVYRLSVRDHSVFALLNNTMLFGASLLYQHSRFSVS

DHSVLRVVGNSVFSSYAIYVNKLWTVERSSWLDWRDNDVGLGAMFYDSGSAFVSIDGSSV
VTLTGCKMGSTGLSEPLLSQADAGYRFFAGCLTVLGRVVTTAAELELHGITNATTVAACG
ERTKDGDCFAPLTTTVSDRKCRCAAGGHGDACVPAPVPAGPPPPSSPPPPTPPPPPVGEC
ISDMEYPEVAQTVGSGLSWLCYRNVTFSGGRMSLTVLVGAMTGDVANITFDGCTWRNGAV
LLLLGNVYAAVRSLNIVVTGNTFCDALLSPEGVFPPHTNIMISGNRFTVTRLIPRPGLDL
GSPSCVAMNELVISNDSAVVLSGNVFQSVRAPSSAIHVVRSAVRVSWHSVFAVMGNTFHM
AGANGTLIHLGGSRQSSSLKVLNNSAVVIRGNVVTMPVKYVILFLWELRAESLSALVFHG
NDMQGSSVVFFSGYSFNIYYNSWLQLSDNLCRVSPVVAFALFSPTVNLRDSTVSVSGNQF
ISSTFTPTALWIPTGPRDLTNGAIVAACNTVNGEEAKYGIPSAYNATILNCSDPCALATS
CFPAYTTTASSDGCACTCAEGGHGDACLPVAVPEPPSTDGADLCVRDVRCDVEVNVSFGT
SVVCYVGVTFAADFVVDVGSMSGSVRNVTLANCTFLGGASLYVVGWLSDPPAGERVDVLI
SGLESPSGGGVLVANRFPPGSRITVVNSVLIAEARVAHRGDYDLGDASACLVLHNVNLTG
SVLTIARTHVAAVFRDAVGVLFVGGVALSSRGALYVDGLSVQTALGLCVSVEGSVAASGG
SVVAFADSDFLLCKHAVSVRGAVSVSGSAVALVRNEFLSTEDYAVAFYSTVSLDGGSMLL
VKGNVHDGVSRGMLYAAGAVTAAGSTLSFVRNRALLPRMVSLSLSLLAGAHLRVVCNDAG
GRVLLTAEEYAAAGFGDAGRIDVAGCDACDRDTHCYAPGTASASMKNGVCVCACGSGGYG
EACVPVGAPALPPAVGTASSVFVREGVAVQSVFVVPAGASEVTLRHVVLDGVSPVLYVPW
MAREGVRIVVQDVSLLNGAVLYVMGGGALRGAGAAGSDESGPVELSVCDVEALDGALVLT
GTYPAGSVLTVTDSLLVATRPTPLVYLPGSQSSPYAPVLVLSGLRLVRSVLIVSGVALVT
VMTGGRTVVVDGAVLELVGGGVALDAAVFGGEYALYASARVVASGGAVLRVSGSQVYAAH
GLVFDSGVVANASAVVVNENAGALTDGALLVLRGSASFVSGSWLSVRGNSISGRLLSVPS
YPRSAELVQSTLTLHGNAGSGPVVMDGTVALGGAGRSSSWGA*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MDYRSAGIIGEFRPVACGVCDADVHCFAAATRAMSGSCGCRCAEGGYGRDCLPVYLPHVD
GCNHTPGMPLLSHTATLTETRSPTPTWKPTPSATHYSPTQCGPTETLQVTETVALPPTRT
PTASVSSTLWWSDVACPTLAVTTTAAGGSLTQNDIRGGGSAVPTRLMVALPPPFRWASDP
QLGTHLSFVPVSTAQPRGFGGPWGAMLSNATWVRNATNPSTVVELAVPVHRGYYIAVDET
IFIRCDAAAVFGGCKGVLLGSFTIRSDTLPAAASAFSAITGVVAGAAAVAVVVTSGLGSI
LEMQALGVLARMSCASVQERASTAALPYFLSVFAALDPLWMVVGNALLAAVFGCVHCGVT
AVFQRWRGVDAASAWAAMRFPSLTYVVAHAMHLGIFFGSVLALAMPGARVQHRVIGVVGV
LYGVAFPAGVCYLIARHVGASFTRYWQFSRKPLHERLLYPVGYWHPAAQQRMYGSMLTSM
RGSRVYWCVFQLSVLCVVGLIAAVQSPVGGCHVQYFCMAAVLFAGAGVVAFTNMMRSSFL
TVIHTASFALLAALCVVSAANHLVPSDGGARAHAAIMLLLTAVLLAVTVYSFVVWYVEDR
HWQELREPRRVGLEALLRDGEESNEETQKPHDVTSLSYASGTTAASSYRPPAAPLQPMAG
DIRLDALSPLDRVSSASCSINYALLDR*
>TCRU_of Trypanosoma cruzi region 4, putative Dispersed gene family
protein.1
MQRSSAIFFSSYSSYIYYSSWLQLSGNLCRESPSAAFLFLNPTVNLRDSTVSVSGNRFMS
STVTPTVLRIPKRSRDLTNGAIVAACNTVNDGEEVKYSIPSVYNATILTCSDPCTLAASC
FPAYTATASRDGCACRCAEGGRGDACLPVAVPEPPSTDGADLCVRDVSVGVEVNVSFGTS
VACYVGVTFAADVVVDVESMSGSVRNVTLVNCTFLRGASLYVVGWRSDPTAGERVDVLVS
GLESRSGGVVVANRFPPGSRVTVVDSVLIAEARVVYRGAYDLGDASACLVVHNVNLTGSV
LTIARTHVAAVFRDAVGMLFVGGVALSSRGALYVDGLSVQTALGLCVSVEGGVAASGGSV
VAFVDSDFLLCKHAVSVRGAVSVSGSAVALVRNEFLSTEDYAVAFYLTVSLADGSMLLAK
GNVHDGVSREMLHAAGTVTAAGSTLSFVRNRALLPRMVSLSLSLAAGAHLRVACNDAGDR
VLSTAEEHAAAGFGDAGSIDVAGCDDCDRDTHCYAPGTASASMKNGACVCACGSGGYGEA
CVPVGAPALPPAVGTASSVFFREGVTVRSVFVVPAGASEVTLRHVVLDGVSPVLYVPWMA
RDGVRIVVQNVSLRNGAVLYVMGGGALRGAGAAGSDESGPVELSVCDVEALNGALVLIGT
FPARSVLTVTDSLLVATRPTPFVYLPGSQSSPYAPVLVLSGLRLVRSVLVVSGVALVTVM
TGGRTVVVNGAVLELVGGGVALDAAVFGGDYALCASARVVGSGGAVLRVSGSQVYAAHGL
VFESGVEANASAVVVNDNAGALTDGALLELRGPALFVSGSWLSVRGNSISGRILSVPSYP
RSAELVQSTLTLHGNAGSGPVVMDGTVALGGAGRKFVVGCLTLNGQALQPMDYRSASIIG
EFRPVACGVCDADVRCFAAATRTMSGSCRCRCAEGGYGRDCLPVYLPRVDGCNRTLYRPP

LSHTASLTETRSLTSTWTPSLHHRALQSDAVQFDGDPAGDGDGGVAAHADPDGVGEQHAV
VERRGVPDARCDDDGGWWEPDAERHPWRWERRPDAADGGAAVAVSVGTRPAARHAPELRA
GVDGAAERVWWSVGSDAAQCDVGAQRDESVHRPGAGCARAPRLLHCCRRDDSHSLRRCGG
VWRLQGCAAWVLHDQVEHAARRCQRPLGDHRCRCGGCGGCCRGGDGRARLRPGDAGTRRV
CEDVMRLGTGACEHRCAAVLPVGVRCP*
>TCRU_of Trypanosoma cruzi region 5/Dispersed gene family protein.1
Dispersed gene family protein.1
MRFPSLTYVVAHAMHLGVFFGSVLALAMPSARVQHRVIGVVGVLYGVAFPAGVCYFISRH
TGASFTRYWRFSRKPLHERLLYPVGYWHPAAQQRMYGGMLTNMRGSRVYWCVFQLSVLCV
VCLIAAVHPPVGGCHVQYFCMAAVLLAGAGVVAFTNMMRSAFLTVMHTASFVLLALLCVI
SAANHLAPSDGGARAYAAIVLLLTTVLFAVTVYGVVMWYAEDRHWQELREPRRGGLEALL
RDGEESDEETQKPHDRTSSSYASGTTVASSYRPPAPPLQPMAGDTRSDAQSLLECASSAR
GKIDHALL*
>TCRU_9297 hypothetical protein, conserved
MPSDRHIPGNASYLSGELLLVEVSKIKYGSGLLFVRHRAKTAWEWLRPGPCTLRRRCDRR
AVSRSRPRSSAGRWFRWDFWRLRLTAKAKFLQRLGARSAMGVDHVRHDTSAAAAVLAAHR
AVCRASDRGGVGSSRRRWLFRARFFACLLCGIRAAPTACAWDGGLQWSQQSSVFVRNTGA
GAGRCSLLPASDSGSRARGLPVACCSGAVSSWPELSDTNNTSSQCDDAGAPCVCELCEVG
RLLGLCITSLFPGHAAVAKNKLHPCARSSVLLARKKGTSTM*
>TCRU_9298 hypothetical protein, conserved
MALTGGSTAEYRRVSSFLVHVAWPNNKIFVQLDKEFPVGVDHVLQNMPTTAADRAGGCCV
LYDSDNVLADFTMLRANDVTSVPRRVAEA*
>TCRU_9299 hypothetical protein
MGCSNSKNQKGREDKVDPHERILEREGNSASCGSRSATDVPERNRKPGSPSKKESKGKKK
KKREGVERGKDVTVEPSGTGILSETPGTALRARPLHAVEASGMKAPLASSLARGLQAIEI
RETRVIHPPHPNRAGADGVDNYAVSSSSDMLASVITTSPLELEPHSSRPPAGTQRHVDAS
SEAAGELPLSIQRSLTFDQYAQENGRRKRRMYPHALDDESPLRNSRGMGAAVSTPVTTSS
MTTTTSTTRSSTPTSWVGKGKALHKTEIVEPVGAVVLPPMAPPIRAAREEMPTEAAIASK
ARPTPIVGTNGVLRRGLYDLPDESGSGDGGERRRAVIYGPTAPKGEHPWTFNSAGWEVLE
QIHRLLRERDLRASQVYVSGMETSHYE*
>TCRU_9300 hypothetical protein
MGNCCSSNSKKRRLPKEAHVREQLHGEVKEDGRPKLNVQPSDSAPLDGVQLTSCKAESIG
EPAQKEGAHGGSKKSDNLNGEDDSDDLKFFTLPFAFTPREVGEPSNNGTPDEERESLRDA
EDTATGEFEFVTVQGSPLSFNQSPGQGDNSAGPYAGLYSMDTMTEPIEMSDLFMSCRSFH
RAASSMISGTQPLARLPSERSWRLSLPPRPATRNEDASEAAFMSCRSVPLPTPLLRDPKV
EGWHRSAPFSRGIGADPSHMLPKAQNNVTFERFSSVAASSARAETPEMRDFSRMESRNES
LLWQSCISIPSMLFTRDDKSLQAPMAQPTCGFGQSTLQGQKEACAQSLPLSPENLSPMPR
FPQLQQKKLPPIVAARSSLPDLPLYPSSKGSRGSTHAASYASFRWKKNFLPLQSSGPSSA
AQSSAGRRPAEFAGTALTTRPRKGRLSTGHAAGTMKYVRGASCVEFGYQSPWAKLADMRA
KSTAISLSSQTTDGRASTGSHEGSHRGSVQKQERREDEEKELLDQSGHGEDDDTLKEREE
GLSCQFVDPVIREPRGKDAGTSPNTGGVEDSVAPEAVGKSGSPLQAVNTWETLHADAFAA
SRVSNGTKTSVSLGEGAVDLEQPGLNDASEAEEGSNGGARMPLAEVNDMKARTALPDGVV
EQNPEYFSVLSPPPILSIAFAGCNISSEDVDRETYGDDSSANRIGDSVIGDQFGKDTGVQ
HEFDAAKRSFVA*
>TCRU_like, putative Cytochrome c oxidase biogenesis protein Cm.1
MGARASSEAAAAAHIPDADEDIADELRRQQQVLDEKRRRYARLSSEAVRQKRDKKKNVIE
DVYEEDFETIDHIQALRFPPMVVKELKDAVANEAERRCAEVEKTMARCLQDKMWTTWKCQ
KERDRYTQCVDEKKRDNELLMAYRWKYKLGTLHGEIIGRDNMMRRIWHEHFPDRELPHPW
VKDR*
>TCRU_9302 Ctf8, putative
MIRVVAPTEGVLQEMLLLELQGKVSIPPKLIREASEKQQKQGFFSGVKQPRDAEESLAQA
EVSDGALGQETVVEVPLGHIDDDPRNKKRCSLRIGTLLVEGSRGQFGEPLLVLRQRKSQP
CQQPQHGAQKSPLSSSPSLPSPRCCLLQEWLAEHPEEMTLDAASASVDTNEMPTKTYELV
GIVERYVHLNSKPLRTSL*

>TCRU_9303 hypothetical protein, conserved
MRSSSRFAHASTSSSAAALGKGKPKSLSSAPRQETGHHAAMLFMQRHRFFAPGAYLADAT
TNRAVTSPTARRRRRYEPYSWVLQRYIERGSVDLEALIFHPDAPSPVETLLTVMRHRTPC
QRLTVHALEAVFNQTRLTFSSGTASFTLQTVSHLLRWRCPQLYDNPAVRVLLCQALLFEN
LFSDAIEVLQDMPDAWITPGLWAAVMEAAAEGKIPHSPLLWRLLTLAPKNTPSAGRVVGT
GQRIPTELMREEPVAASKASTKHGGEADKGYNNNRDSRNTMNDGDMVTLSAFEVRLASLK
RLALDAGRLEWCRLSMGEVGYAEQHYVALRDERAWGLGTLHLNSEDNTAEGVVYGLDARL
AARLMLRANVSFYGQASPLIALHILRRYLSTCHVLQKQAGLVNATAADGPTGKSSLSAAN
ASMVLVAGSHPLSASAALVGGKAAEGVKRHEQIHPSPFLLFFKIAREARDVVAGGGDITA
AFGQSHITPSGGLPMIHWGVVWRFFQTLNRESPAWFTVMPEEAGELSKYVIDALCRGANP
WMSLNVARAASSRHVVDGLDMSLWLLHRLDVSHHTEEAREVTKKVFRWLLVDVGVHLLPQ
LHHHLIPASRVLIRLGLHEELKQFYNAVLDNVYAFSEGFRADFMRVMEDLVCPMCSSILP
EQDVYVERSCPLCLTVVPSKDPNALPSFQLSNEHVTRLREKRKALRAKGRRNLHERIYRW
SKNDDDGKGNSLPSHEKGEASSSLPTRQPLDASSVFKREILGETVPLIPGVPVDQNMPLF
QLEEGGHGENIEGAGVSMLPFDVHAAMEESSRRLQLQEAARRYALAQRGVLTSARLLAAP
PSLLLSDTSHTMLQRQQQGWQRGQQNKLLVHVRTDGPWICVWCQEHNSEWGSRVQCTACG
AETGPLAPWRHFAYAESGDVMQEIRARVANAEARPVDAVVAAYMLMVYRRAFMLRATPHD
HERIDQLIRRLCWLHERVLAGYLYVRFVSPRSRSKNDTLWAVAKLFGCTEAEYAEISAQE
LIHNEKKFFQTIFTPTTCKVCFGSHAWKTCPIITRDFSSTTRASINMSPEEKQRAMLQHL
RLVVEAALQRGAENSRLVVDAYTAFVKSPYRELFAEVHSEEVNRLSILLSHYHQYRRAAF
LLCHIPLHLRNDQAYLVMAHYFNVPAEEARGLLRKRSAVGVEDESHPNFVQVALTCCMCL
DERHASFECPRLLQWLNEVDAHGSMVSVRASEAVLYDPLRENQRVKRLRAQVDGWTSAGP
ERLHAFYRFLLQRVDSFQEDLQGEEIEDGDTPDVVSLEATTAVTVRKPKRRIDADDLIVY
AINKTIAKLAAVGQEKGACRLYARAPGAFISRHTTYAMLRMQRFSEDGIRTLLNSGTVSS
SPSSAAASIDDATVLGLSSEAASAAAVPLQRHCLLCFDPGHAYLECPELSAQPTNAAKLE
YVATQVGGIRCTSDGIRAAAAYVYHMYNLGNLTGDMLRAHPSLVRALLRLIRRCFATGQL
AAGVRVLRRIPTEVVPPARVYTDLWRAAGLQEEAVEDRRAQLLAIYEAEGLVPDIDHPPA
RQTYTNRLTTNLSRTLHDELCRHCYQHGHTLATCSVFHAEVSFGRDYVAAYRMSMMSEQL
DRDWQDAYLLKLTDFFQTHRIFMPYHIVGIANALNAIAAMWSFRGEPGIAIRHLLSIPPA
YRRRQAFKHILHALNVPVAEANSVLANVYFSPDELSSSFSSSKRRDDSPTVISHGSSNGS
IPGSQSTSSGAVAQHLLMPKPAIRDVAMSAVLNNFPEALAAIEKSEERMAAIRRRNATQQ
VAAAPRIQTAATAAKGEGVTPYQGKGGTTKSAVGTPFSSSTSFPALRVVQSGDILALRED
FDPVLTELEVAVGMKLGSRHVLFTSAVDILSAAASKPEDSRQEPPPSSPSGMMSSVAAEE
RREVEKAAIDTSREQRFSDEATVVTVFTKDLRHERAERKKDEPRRWEEERGGKRSVSSLP
GQKKETFGNHSPRQQQGRQQQQQHHSRRPRYHERQQQQQQQWRGKRANDGNAPKYSN*
>TCRU_9304 hypothetical protein, conserved
MQPLSQTSSERSNLLRSHDGLFSGLSPGGMENTGRKINRFGRGGSGGICETIAQAPLRGI
YLRPTVFMIDGTARHLMEVLYPLNNDSSSSSSATTTTNSTSTFFLPAKANEENSMWWGSR
YPYSRASWVVFEYSLAPALLPSAAAETISKTPSRYTEEELVRELPFHMTHSAESAQWLLE
AAKQMSRSLRENRHSAPFRVECCGTVGKLFPPRRVSVPLGGDAECLRPGGSVLLGGVEVA
VRAMRPGEEFAFIIINPTSVYDDVQNAYGTHFSHNPAAFPMRCVYIRIKLLNHLPREPLW
LPIAQKYILNGSSSTPPSQLDWMKPTSEDVHGCMLPLLFFSSSLFFTNSSDATFLDAVTY
KCALRALFVSNASAFLNCHVVGHPGASVAFLLDAMAPHSQSGLAGAEQLTRRSPGGTGAT
AQNNSSSKDGRDNEEEEEVEGGRGRGRGENVPTDEEALKFLRLAFFSVPRDGATLSCSVT
RRSPLTGSMLRPRSLAGVELGSMSLPLWLDVLLQTMRGGEEEIVNMRNNCEDDGAFQCSL
ANDLRTSAFLQSRVMEDMHVNNIVQRERPEEQGTPLDMSIQSPNSASSAQTLLSDGLRGE
FGSKNFPPHELHCRISLESFANVHDVASFFFVDPANSLRVVQKLEQEANALRKLGKQRLT
ESQRQSKTDKEKKYHFKRISRRNENGSNIDGEDPAIPACAMVEPMTVHPRPFGHISEPFE
ERGIVKAIQKLELVVLLLTFHVNERRMLARGVSVALMEKRLVALMATFRDLGRLYTKLRH
ESALTLAMEAFSAAILLAPRNPQLWMRRGVLRLKMHTNHSAMCDLSRAKFLAEAGLRRLY
FSRGTETCEGGGEGAMPSVSTATASTSAAVSVGPAAAGDFSAHEESTLRHILVNAETLLT
ELRLLAEERDTTPSASHQTEAECQE*
>TCRU_9305 C2 domain/Ankyrin repeats (3 copies), putative
MSLENGIQQGRITVKVHRADSLVALNPDGSSNPCVTATIGQQSQTTAVVRGTTNPSFDAT

LTFIACPLPTILTLRVYNKATYTEAEELLGSATLTLFSASPMTRRTLQLGHGGNVSLSQK
ARDGCGSLDVSYEVVIMTPSEVAAQTKKSVANDDLPEFLRDDSGIMKFTSAYAAVEQPPP
APPPPPQVTALPAPSEPLGAPQLSQPPQPMQPASTQMPQLPSMLSPPQPTSVQQPHIFSS
TSGLLGAVAVPPPTPQNASEPVTRKNPFVMASSSTPPVVPPQNLPTNPSFTVAQGVESPA
APIFSGSTYPTASSDPAAPTGQSLHAMQPSMHGISALGDAFDVQQVANTGGVMAGEFASR
PMPLPSSQSNIRPNPAAISSSVNSSTTPDTTFASSSSATSSRQRPQQQDSGQNQQQQFVT
PLPPPPPPGKQPLSSPQPSTSVTGAGIAPTAATHTTATTTSPGRDGEKPLKKVTIMASAK
DQTGGAATATTKKSTNAVTKRALVKALPLADRGSRLTAVSPMRENRRSSSANGARSSSRG
RASALSATLSTAHHSPALYQWPDDLLAAAAEGNTAVFQKLREDDPLLSRGFDNVRDYSGR
TILHIAAWHGHTNVLRTLLQASPSVPIIELRALRSNNGNTVLHSAAQGGRADVVQWLRFG
HPATGTLVGLRNLRGLTATDCAREAGFMDIATMLDES*
>TCRU_9306 YEATS family, putative
MEEFTRAFTIHFDGTVYKSTVDCRVVGTLRELLVKTLPAPLSPPASSAVLPALKDTATWV
DGYACSFGGQRLSLAVSTEVAPTTLYVALAARNRVDEKMSASGHADPLKRRRSFSTGNRG
RNDNDNGDRDDDNNNNNSGSSGSSDSESSSSGSSSNGNLNSAIRQRQQSYWHHGTSQNNT
GKNSNDDNNSSKCEESEYGNEEEGEDEDCDEYDDSHGNSVEDWNDGVNDVNAEMFRYDGR
QQRAVLPIIVGGVVRLIDIESRDKSHQWTVYIRGLFNETDYLARCIESVQFVLDPSFTPS
ERIVKTAPFELTEVGWGEFVVKMHVKLRHYPRPVQVALSSSSFASTATHKSEVKVASSLL
SSQPMVPLSGISRGPLLSPVVSVLSRHHYHSGTHDNSSSSTTAVTSVNKRWGVVKTEVKV
EKDDSNDETSGIYGTESMKPSDVQSPGQPAIMTLGMSPGVVTLSHLLRFSHRPRRFHCIP
PLGRPYEPEEHVGYTIVQTPVVTEQYDEIVVPDPPAPILEVTEALPIMFRRRIATVKTAR
AMAQQQQQQGPLFGSGAPLGVAAAFNEGGVSCWEYIMQEEPDDAVLAESYLESLEKALSS
LVGAQQHGADVFSSASYTASQQQEQQQLKQQALHGVDAPIVVKLPRGRRKLTGAEIDLAA
LRTVKKGLVEAIEKMRRELVLRQAAQTYQHYM*
>TCRU_9307 hypothetical protein, conserved
MPLHVPQEFLEDALATWERLRQWTDLNNYLCVLRSSPFYRHSHSERDPYSLRLARRVAEV
MDSLTARADLPVDEDVTPRGALLALANDVRLAFSPLPVAYYYEMGATCASPQESPFSKID
PAALNKNGNSAARTVDAVSSEGSLPLYDWNTAIMNRSVSGTMIMEGLHVLTCPSVQLRIE
LAIARLRQRVKEELVGGVDWDAFPHTPKELQALRVTTMLLDDFEALYRRLLVTFPCARAM
GSSHVPVALLPLAYEQYYQLGDWVLETEITSRTKPGAWVQSFEPKKMQFTLLRPDRHSHW
GLRFNQSGKLVGLSAVVRSATIVGDKLHQFMQASKGGLSPIACNLKKTDFNNLDSTQAAE
KLDALTPTQKRLFIKVQPVSDSIPTVEQLAFYSTQPEASQPQQQQESQNLPVATLVLHRD
NFSVSWDLAITRKLVVMSVPSGILSPEAKAFFARYPTRVRIFGINGVEMVSAAQVEALSS
MVNTIVLDLQIIPPSSSLLTPQDVDQQEERAPPVASQVNSSETEEQCGSGRPGSEDVAIL
ESCGRHPLAAPSEAVVASTSNPLLARVEDRQSRPNPKLRDKKEKTIVGYESPMDPPREIL
SNATVASSAQEQECTTPSRPLGKEAPKRAGTSGVNLQKALEETILRDVDRSTLSEQPLVP
IFSGYLKTEKELHVPDAKEEATDSADTPARGHCTGNHVVKSTPVAAVLCDDFTPSLDADG
PGERVPKAGANEASPSPLSSQSEEREQQKQQPPVELSGAAAVTAGPLKFPNDVTLNLLTL
DEMFLSRQSAEKKWGLSMERVGQDASRAIRVVGLPLVMDPQQLQHPFHKLFTSHKGGWSI
MSVNGTPAARLPEVMDIMKHALHMQIKFHRRW*
>TCRU_9308 MSP-B, putative
MNYGPSSVTDSEDGVRALAHEIAHALGFTLEIMEKRNMLKEFEGVRGKAAVVQVSSPKTV
EKTREHFNCVSATGMELEDEGGNETALSHWKRRNAKDELMAGIPGIGYYTALTMAAFEDT
GFYKANWGMEEPMSWGNNSGCALLTEKCVINGVTNYPEMFCTARSSPLSCTSDRLALGHC
AMKLYDAPLPPQYQYFPNPKLGGVPDLLMDFCPYIRPNIKTRCSNGDKALMRGSRVGPRS
KCLKGDGLADSEGFVGDVCAEVSCDKGEVSVRYLGDDAWHKCPEGSSITPTGLFMKGRIL
CPKYDDVCIFFDTINGGGDVSSLLSAFPPIPLVMLVLIFISMC*
>TCRU_9309 hypothetical protein, conserved
MRRPFWAGACVHTNFSSRQRDGDDWHLTGGVVLETSPANLPPSAVGLGERLRHTIENNRK
RIIKPTEKASAAIITDASLHGWGAVFIPDSGDVKIVGGKWERKPFLIMQAEVRAVRLALS
AFSAILPSTMDVWVNNTSLQGAANKGNSKSHALTWELQRIYEFLDSRRTQASFAYVRSAE
NPADGISRGRVFTLQYLAKGVELAKGSGGVLWLEDPKVCHFASNAYTFILSEQSERATIV
ANG*
>TCRU_9310 hypothetical protein, conserved

MAEAASCLDVKSSFFQVSLPRETRHLFRCRVEDGTLVELTRLPVGCKASPEILQIIITSA
IAGVTTVAHRLWAAPPLVRVDVWTDNMRIAGPKSDVTLWEAKCFLMRPAVTPRWGGSRSG
RYALHLSGGAVWSHSPCGIPE*
>TCRU_9311 hypothetical protein, conserved
MPTLSYLWTRGVYVQCAPERELLTIQAPFKKRPRGCRTPLMNAGDGSPIQSATSHQSSQA
AHRAADAPPYISNCPTKSSRRAMGLIRKRRSTVVRRITDIPALGQLYEESERGGSRDVGA
VNVGAWNAPSGAIHNLLPHARTADERGELCGLFDGNRSGAIDPTAVRQDAAVHVGNGSSP
AGHGDSGVAKSCCAIGNEASVPLDRGRDESSNPQPDRLERKCCLPTCVYNGESFV*
>TCRU_9312 hypothetical protein, conserved
MGAARELGHQQGLTTAEGERLNIDYANAVADVQNRNAQLNSQFQEAHHNLSVRESTIAGA
GNQVLELQQQLEAAHAQLREREFNLGVLTGQFQEREARLNALQPARYAETAGRDESPAT*
>TCRU_9313 hypothetical protein, conserved
MRVERGEVKVYSIQRDAAVGSPSVPQASDAATSKMGRSHRRRVRFTPEALENNTASFGAA
DAATVVYPMAELLAFPTPDITTMVLATVCDSTSGDHELIVRVELRASTVEILPSIMSLAE
EIEEWATVHDRVMMGPPRCHILHHDGLLRM*
>TCRU_9314 hypothetical protein, conserved
MVKHNVLSNRPHHRTNSHHRTARNDRPPRHGQPHAKTRGHPGARSKAPIVVDDGTIPAAF
ISPFQASQPQAGQHSATVVRTSVSGPSQQQMLFYSSVQRRGGVFTKSEYETKAQLARTGV
LPNSIAYRKRARIAMEEKTGKPQTLQGRFAEMQSEKVQEDVRQAKALVVKNTNANRFAVE
ESESDEL*
>TCRU_9315 retrotransposon hot spot protein, RHS3, putative
MEVKAICTWMKQGLDPGKQAEYWKMFEERMKKVEPIPRYIFHEESYIDRLGAVNGALLAM
KPSGVEEYFTLGGEKKWCSEDPSHKLVKTVRARTDEGAEVFLNASICSDIGF*
>TCRU_9316 hypothetical protein, conserved
MVQCVPHCGGPAVSSTPAGSVSSPVDAGDVTRDYIALAVPLLHILQQRQTTQALAVAREI
TRRWGEKAGPVADLLRLLQHYEDLQQQEEEEEEEGEESDDDDDDGTSNSTASSDAVMSSC
STDDDDDAGSVENGAAESGDVTQTLRQILARLPPCDAAGTSISAGLNATPVVNDTAEESE
TEEERRIFNDIAGAVEREMKRLAIIRKHR*
>TCRU_9317 hypothetical protein, conserved
MRRTWIKLVIKTATNGNGGVAVATGATRPATVMLSLQSQRCIREIMVRQVLLSSKPLTSN
ELVELVKRKYHEAKETVQTTSMSSQEGACRKATETPVVASVGDDDVEKEGEAVTDSPVEY
LRGFLMSVSTGPANVLPTQDGISPCPVESTVRLILAIDSQFRVSPAGYVCYPNLPSLILA
STDVEQKETWLHLGRRLVRAEEARHCFSGSDHGAMAATRGNSRVPSRWSYMLSLWFMLDA
FTETEDVVDEKDAATERNGTHEDMTISMRLMTQWVNAFDERELPPLLLRELLTAEGQSIS
RSPSVSAPQELRDSVEGKDILRRWCFEAREGFLSSMLVNAPQLTQSQPMLLQQVNEQLGF
FFLFLSGAPISLGRMSALIQWASLPFASQYRSLLHFLLIYTGNPAVAQMERNGKRRREVL
KRWTDLLRSRLQEDRGRHRHPRQIGGRHSLSGRYASQEHMEETADVDALPASSEGNDARD
ISHGKASWARQISSEQYALWMQSSSGPMVNPKLMDVCRCLFLTPTEMTPLDVTTLTPSEV
LESFTAKKCAENDVVVFSVLPYVLERRICRVIRVWWALEGQYTTEVKPSDAIAVISVQRL
CQLCLWEHEYGAAAASRMMLHYLRSVITGETTVQLVPPSSVSKIMTSTSVKDAGCWLVVL
RSTA*
>TCRU_9318 CMP-sialic acid transporter, putative
MPREVQVEVEKDVEDVSETPQTVPTETPQFGLLPSLVLSGMYVGTSIMLFLTIRHSKVLE
KRGILSYDSTSIVMSIEVAKTIASVILRYALSGEFLLFSVTFGPRRGELWRMSWVYATPA
FLYALYNNLTYLNLRLFDPGTLQLFMQTRILFTGFLFVFLLKRVLSIRQWAALAILTLGL
VIKYISPTVMQAVDVRILAMLLQAFLSSLAGVYNEVALKRETHISIHLQNFFMYLYGILF
NLLLGLMIAPQEYLKDSIFRHPHIIFLLIILSGTLNGLTTAFILKFINVIVKAFASAVEV
ILMVVLAAVLLGEPITQQDFMAGILVMCSVCLYYTNGCGSDAPTKSR*
>TCRU_9319 hypothetical protein
MQPIGVRRIRSSSTDHRRSSSDADVGGGIAGGTSAGPAAGNSTQQRRTYDVDMTSLEKHR
RLFAMERELQRWKEKAEVSTRDAKLREQELFRVKSEHAAVRQRLEHIIRDLLEKQKGFAE
EMQKSRNEMELLRKDAAADNSALVAAQEAQLQLQRELEASQSREAEATGELSVVVEKLAK
ADTYIQTLSDEAVAYQLEIQRLQEELDAAGEELQKKNKEREAEDKLRTSEELARRRKATR
NLWTELVNAALECADNCDSVSRECDEFIDVIKEEQQRVGQRQNIVRDGDSEKFMVTMPAA

KTHPQAHVTFVSCKPTGEELERLLQVSLSSQQPGERVGDNMDDAVVWEGTTRVIARLLRG
MQLALRETRDDVLVAGRAYAELCRAGRSMAEDLAELQAACAKERSTVAALEERLEHTQET
LRIEKERADGLQASLDETADIMAEAAALAEERTSRMEKLLRENNALEEALQTQRKSLRER
DDAIAAVELKLRTLQDTMRREKNEWYSMHEELHRTKLAVKTALEERDTARSQLHELEQNI
QALKEESQQCDVNCRYLRKCVEELQGQLAQVKKDRDLLRETKDSVEVERRRLLTQIDCLK
RSGNTAACVTDAAPASRGSGGGGGGGGEVYSSVWFSPTVQRWKVPHGGKDMEASGENRHD
AGSLLQSSERKEPVDKVRWWEAKLQAITSSMSSTMPLVATPSACRKDEKSGLMDNLQLLE
TNSATLASLAYGNSPPSQKLKDNSVPI*
>TCRU_9320 hypothetical protein, conserved
MDVILTTSPLLVSSSPLKGGASSVFTQVPQPWSLLAHHRNSRYPQPQWKAEMSSTSTCGA
AEGMSERGGFGASVGTVSTAPCSPMDVQEEEARPYSPTVSTVAVAWGKLPELLPSTEPLD
SRGGAGGGDGSGGWESSGAAMAAAAAETMEKGRSESKLLTFLRKHASPSLKVEKREVLGA
FAAVLQEVRELHLSQCPLCAPRRPPNWWTSAREEKRCRDTPNDRNNRNVKKVRQQDEEKD
DNCDEYLELDVLGQSHIFMDAERRGGEGRKQQKKKQLENGKYIDCSQTSLTRMHQRLYVE
AVEFLEHVYSRRDHLHATCPVMYALRPEAHLLRRECAALGGIVLLEALLLGL*
>TCRU_9321 hypothetical protein
MEGSSKTPRQPQENSQKSTGQPPKLQVPPAKSPSQASDLGEADAGPVGIEGTGRNVIGGS
LDKNKDPKGREGHISGPPSGGASLSPISNNVDASQMNGGALPTQDTTSLKNNEQSGPTTS
SGNAPLNRETAERS*
>TCRU_9322 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MHGRNGELGAVCHVANAVHTCSNCAVSCARKEEGATVAFTMNVTTHKYAGPYELWWRQFS
PDGAIHPPARSSDADRTGICQLPAPREGKDDTKSGGTTAPQVNAEPSRQNEVWRRSAAAD
GPNTVDPSPASNTATNTSGTKPEFASNPNEMMVQNASKKRPSFANGPRILVASNASGIMS
VTCGGREDVAADNTDEVSERGANGRKSLVLENGVAGSGFVAEGDAGGMTQRNASGHDNRP
QLREFTAQYSGSGGSPHDCFALRDFAKLTLRELTVDGTVRVCVCWVLLLLLGLCGVVAVL
*
>TCRU_9323 hypothetical protein, conserved
MLQTKDASEHEEGETISSDTQRSASKEIPEATTPLSASKSGSGIAGSTVEKGGVNNPQPP
AASVTQHNSAGDTGPAALPASTSELQAEEIPNAGIIATTNDDDSDSSPAASTAERPTAGT
RSTQASGDASDLEQSNNDDVNDDVAHKDKTVEFETASGNRDTQADNDERYTTVPENATNK
TSNTEITADSDSSTAVSHTTSPLLLLFVACAAAAVVAA*
>TCRU_9324 hypothetical protein, conserved
MFCVGSTKLRQAVALFTIKSFRARQKILLTPQNLDSVFTEKLDPQDRLLRQSSVGPGASR
ILVLDKNQRVRGVYHPLLCLPYPLNGDGVLGIPVESYLQRIQQKKQSNGDSTEGCTFIVV
AHANGLGIAVYAADGNACFPLVNVKLPAQRCTGRGMMNERDMIPFIGTTSLVEDFAEIMA
ENYSEYIHFCSTFFFLANPNTSISFHAMRSAWKLRGYTDTSPLSFTDNRWVPLPDLVAQR
DPSVPLYCRDDGGDKVVSIKGLTAGVKVGMLELDT*
>TCRU_9325 hypothetical protein, conserved
MRRGCQPSFLLSSPVCPLVVSTRGIIACKGIVENRITKHYSNRTVEEAKAEREAQIAKSK
HPNPRNRKEELSHLTHHCSYEYIPEFQRWANDMMAVYNDPQGYGHDMAYHYHRIWKAKSP
TKRGIEDGSGAFEVCKIHPK*
>TCRU_9326 GPI alpha-mannosyltransferase III
MRNLGGGRGKNCYADDVPHLPWYGILLIFLYRLLLSVSIQTAESPDEWWQSTEIAYYIVF
GKGHLPWEWHMGLRSVVFPFILAIPFFLLKSLGLDSTWAIWFAARLMQALVITTIDLFVF
RLGRLLDVELGRTEKNALRGARMPKLFLDTPTKDPAGRVVSDRSVAYFALFLSLSNWYIS
YTGVRTYSNVVEAMLVLITVQETNYIRFLLFSGLACAFRVTSGVVLFPLVFLHVAWAVRE
RGVCRGLMRIILWGIVIFSLLVSGIVVSDSLFYNRWVVTPLAFLKFNVLQNASRFFGEHP
WHFYLFPCLPALLGPHVLFTLAAPLVLWQEKVSKAVALKIFGLFSFILWPIACYSFIDHK
ENRFMTTVLPICFVVTAFVLARRYDRSLFVRRLHKAFFVFNVTVLILAGYVHRRGPLDVM
LEVRNGPKMDRLDIVTRCYATPGYSFLHGKVNHLGLIDCPVYLNTETGLPKPTEDIMFRK
YPKDYVLWKYDGIHTFNISNPDGKRSADELGQIVSPMSSPHPDVMVMYRDTANKIKHLFL
EKHGYKLYRSFFHTPLLIEPGEDNYMEMWVRNVFQAN*
>TCRU_9327 hypothetical protein, conserved

MLGEEEERKAAVAFYLQEQDDAVLCAFGRDYFDGARKGAACGGVFTAWLSRRTYVDLRED
FKEHEASLPRHLRRGKWTISRGFRTRPFLTLGCISLALTTLMKSVKFTLANYRYQEFVAD
DIGFTLLEQMCANLPEGNERFENLLDEALTNSRAASASPSDGVANSRMPKKKTVTSALMQ
ESSSLRERKPPSFWDGVAVGLMGSVMDCYLPSRPVHTYYGMQCGMRM*
>TCRU_9328 hypothetical protein, conserved
MKTNSLADNRALLQVLSLSENTELTPTDILSCAIVGGVVGIFTDEKKRYVDSVLLPSSRD
LTTLATFIAEGFFAPFLRSALGDHLPRYTIIAESGCFEALSLPVILFPDCFLLLPSPSVA
SPNNTTPPVFPFGGGAINVSLDGFSMASVSSVPTEVADVLQLHQHRSHVALLLLKNVNEI
LRDAEVWKLKVLKEKMTAGISEMAAINAVMALFYEVKMLLLCCLVSSKKAYTVEKDFFTG
NHNSAQKYFSELFSPDELCRIFDHKSRSSAEHVEKWYDAMMTTLIDGVSAQDSELQAYIH
ELQRSLAEDERRITGAPMYLLHRPHDAASTTLIHLACVHSELPSLELQPGEMSLLLDPLG
ESLLFDAEPSRLCTLLRRCALVKLTVTQLRDAERILASSPWCELCDTVVESVQYHLNNDA
FLSVVLEKNSSFLVKLVRWLRGMPAAEEDGTMVRLTETRQQEVLGMSMANHIIEYVIHFS
SFGAAIAQFIREVVSCTEISEPQLHTWVDRSIIELENKPSAAVGLFALVVAFSLAQRGWD
LPEATRESAIRLCTQHKQQPNCVTLLNLLRRYSQ*
>TCRU_9329 hypothetical protein, conserved
MMRRCLCYAARCKWGQRTWSPTASSGGAAPTNGVSAQEALQIVYRPMPLPQTVEYEEDFG
HNLMIHREFVSKRHRDQLSFELGALAYSEVELRRGRQHLAGVMNRERRGVAIGAAGAPSD
QLHMQTDVDPDTREVLTARYLFDEKRMQFCDRFQNFLQSRLEGHAAQSSDGGKGGEDKHY
LFSLMEACAVIYGCETHAAREVYFRMFLSLDLESLEAEQEALRHRIAEGKLVRQALEQSE
EKEGEGNAVLPVSRGNSSTTLDDDAAFIASIPELSLFEDTPEVDEGGSVKNETHPPALAD
KEFLPAGVVDDSGSLRNSSHSAIELPEEFEEYAPLYKAYLAHAKGESGIASYDVSTLGST
GITAERRRWRNLMDKIVREEYHTMTETEQMDALILNEQLHTVKFFDLKVGDTVREILQLL
QRETGCGSSAHRDEPLCISPHHPERRI*
>TCRU_9330 carnitine O-acetyltransferase, putative
MPQSKSANASRFWELDSAYEVRCLRTQSPVKALESTLFFNELMSVNGATDTGERPGSAQE
SSYEDHQSSLPRLPVPPLKHTCDLYLKSIQAIATSEEYFQVTKLVEDFLKPGGTGELLQS
LLEAWEQKCDQPSWLEEFWDDSYLCTREPIPVNVNYFFQLQPHPRQSDGSTRVSQVGRAA
SLLHAATEYYLSIFHGTVEKEFERYVPVCMSQYRFVFTTSRIPGLRRDRKVCYSTRPLTS
DEKKSKFSEYVAADPTHCVVIIRNRYFKVEVIKDGTQYSVEELVLALKQIENFATSRKDP
GAPVGLFTTLERTDWFHTRERLKALGNGEVLQAIQSAIICICLDSVEVQSPDESARLFLH
GPGTNRWFDRHNIIVTRDGSAGINWEHSVGDGGTTLHVADFMFRRDCERFFSDTDVESLM
EEPEKVQASLGMVSELQWSLDNGLDELMKAAFADFKMLIESNETNVLHFQQFGGVFLKQN
NVSPDAFVQVALQLTFYRLFGRNCATYEAASTRTFSHGRTECVRSATRAVWDFCHAASEP
IFSKRVASCVPKQRELLRIAIESHADYMRLAKKGLGVDRHLYGLRVMARMHGIPLPELFT
DRCFYRSATWRMSTSHCGSSALDTFGFGPVVGSGYGIGYMIKESSIEFVITSNRTHPFTS
TSVFATMLQSALMHMDAILRSENVEDRAVSCPFPSSHPCGFNDFEYSQQEGFIYQRYDEQ
GIKELAHVLQETKGKTEFAEDSLSSWH*
>TCRU_9331 hypothetical protein, conserved
MTEGPLIVVGSVTLDQAARCYSPLSAPLRVRLEYAVLRPVVNPAWAATFEADIAYGRISV
PLVQPTACSECMTPLNVPSSFLQHTPSDSIATLQPGELYQLDVHLETMELSKVEEKYVLQ
VGMLRLILLSGKTELADVNHVVQVKKNDDGELMRLIMNPLV*
>TCRU_9332 hypothetical protein
MQQEHLVEAIVTITQVLDYRALEELKIRLSKMLANDSYAPHQGRGGMGLGGGPSSFGGGH
RGAHNNPHQQRYQHHHHQHRGGNRGYSGGFQHDRRHFDDYRDGPGYSGNGDGVPHLQHYH
RGGGSGGGRSRGGGGSDVPQPTSHRSNENHQEKRRWTQNAKDTAGATTDGEKEQQRKPGN
GRRGRRRPNQSINEKE*
>TCRU_9333 BNR repeat-like domain containing protein, putative
MSADGCSDPSVVEWKDKLMMMTACDDGRRRVYESGDKGNSWTEALGTLSRVWSNKHNGNV
KRVRSGFITATLDGVDDDKRTVMLVTLRQYSENEEKGVLHLWLTAIRTLLILGRCPGTMM
TLPPAPCCTKVLKMEIKEIKRS*
>TCRU_9334 BNR repeat-like domain containing protein, putative
MDATRVVSCDLLRVTFFFGVSGVVVAVAEAHFKNNKDGKLRVGIAAKSMEVNGGTWANGT
GMMFDYYDIKVEHLLSPTTIMADGETCALVGGYGESGAPWTKVAVGGYWSSRYARSTVLS

EDDDKDKREFEWNQ*
>TCRU_9335 hypothetical protein, conserved
MESKAPAPPSGDATQGQHSHDTDTENSTKNAAAGNPAETTTSSTSTSGGDDHVHNKADKD
DAQSSEEQHDGIETGNNNVVSTLSEAVPQTPETVTAAQTNDTSKAGDSDSSTAVSHTTSP
LLLLFFVAFAAAAAVVAA*
>TCRU_9336 hypothetical protein
MVDAVAFLLVLVLLLVDLLMLLLVEAVLVELLPEVKATVILPLLLFLLLLLLLLLLLTLQ
LAAVVVQRGPRALIHLTQQGTLQQEIRRLQQQRLTTPRYPKDR*
>TCRU_9337 hypothetical protein, conserved
MESGQYTEQGIAPLWHTDLLTCFTTQFTNKWRSTIRQDTHRYLLCGTRPSDLSGKDLITQ
EVLHRQELVHLARARCGESELWGRLYWAVRDCTNQCRFCNISPEQSAYMRSNNDPTAPGT
DTVPPSAREEDVSPVSRRTLTRRRKEKCPHCDSKLTGFSGLVSHCRSFHPEHPPPLPELK
CDFCDMVFPTRRSTAQHRSRCAHNPDATRHRNSSARRRSLLPQDQPASTSTPIGPQETLH
HLLLECPGTLAVRQRLGIEQDLRLGKFSQWQLLHSRKLLSLLDHLFGTQMALYS*
>TCRU_9338 Endonuclease/Exonuclease/phosphatase family/Endonuclease-
reverse transcriptase, putative
MEPFTWLPAERYFYPLLNSIGAYQRYTYRLRAVCDAQRQKLLLSGDIEQNPGPIAVLQMN
VSCLTPSKLATLMAQGADIIAIQETWKSSEQIASMHTGDYVLYAQSRIGKGGGVAVLVRK
TLRSKRIPLTTPQHDTSHEVVVVQVALDQNRDLIVASAYMRPPPQVTQSFRRLVNCLPAS
SSLLLCGDFNMHHPQWEPFLETSPSEVAAEFLELCTDAGLTLVNTPGEITYARGTRERSC
IDLTWSKHLTVSDWSASVSPLSDHYMLTFTLHQAFKDTIPSAPKFFSSWGKCKWDLFVKD
FDAQLPAYDYKKQSTGIKAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERIATDSKA
RYLQSPTPDREAEMQRTRSQFFLLLRERLRNTYLRRISKLNPGEPLAWKYISGRKKASLP
SPTSILLGGGQHTYKTARRAANALNRIFLPFHPSHKAVRFSKGINRQSASLNINASLLLG
SRTTASLPLLLA*
>TCRU_9339 hypothetical protein
MALAIRPALAARLLLGCVQVDRSLWAEGTLQAQHPHAPTRLSRQRVECMLVAGGPPREVG
LRNKPSRDSHRCQGRQRQHRRAMKEENPEYNTRPTKPQK*
>TCRU_9340 chaperone protein ClpB1, putative
MHVVLGAGKSEGAMDAANLLKPSRARCELRTVAATFFEEYHENVETDAVLGRRFMPVYVT
EPSVYECISILRGLKERYETHHGVQIIFLDLGALVAGVR*
>TCRU_9341 retrotransposon hot spot protein, RHS3, putative
MKRAAKGELIFDEDIQKLYENDVHNPPGRSLAAVDVKATVHNSTKHFLDAAAEEARNPTT
SAPEKLEGVYESVHNAGRGHAVELPDGVSERKRGREWGA*
>TCRU_9342 hypothetical protein, conserved
MARETAQNDGQADLPVAEAGRIRGQVQCGAQPIPEDEGAAPPCREDIATSGWVRLHVFSR
GLPEAQRSNGVRLDFVPPFFRVHSAQSRLSPGEAMCVLRVLLRRRTRLVPFRVSMSFLEL
SRLPRGIWCSAARKMPPRGSNHVGAVARRVSHTDVKAGQSALRRAKVASFRQGSVFASRG
VPSSISTK*
>TCRU_9343 hypothetical protein, conserved
MHGTTPLVGELGVNACQQVRALYGCYSMLRVLPGCRGLRRMICRLVNMYSAMFVAKLQLH
GPAGTRQRQETLPEPILRPVGMTVRAPGDGG*
>TCRU_9344 hypothetical protein, conserved
MRPRCVAPRQRGSRTVSAPSHLHSLEVRHGDSCTSSLVPRASAKDTSVHLAASPAPLRRI
VGFRAPTRHERLTRLRYIEDVRGAVCSETTPSSIPGKAATTILLPGDAVLKELRRVRSRM
RISPDHIRAPLVERRVLARDTVSRSGVGVFRPRHAKDALDGVRRSVLEAACTSLGPV*
>TCRU_9345 hypothetical protein, conserved
MDSDHHLPSHTAGTEDGIPRQAGMLPRRKHAAFALRAADWNACTSACETPLAAVTTWLEM
HRGTVRAARRNIPTCIWTDGMEHATRTLPHPEAACPELKLSASGRTAIMPSAVASPCCWR
SVRNSLVPSRFQACDDSRHGGTTSPLSGIGCAAVLLGLRLCSASATLSRSSVALSASHVL
RSPQLSAQFVLACPLVTGIWIGPSRRVRLTRPSATVCLAWPLAPAAY*
>TCRU_9346 synaptobrevin, putative
MEERLQAGRPESFEDLRHRLALPAGGGDPPSLSPTPTTASRQPAPAQEREGMCSRGRYAE
IKSTAARENVSLNEARRIMNENQARLQDRGERISKIANRSRELAEEAANFQDLARKLKEM

QKNRWI*
>TCRU_9347 retrotransposon hot spot protein, RHS3, putative
MFILEGYYESVYNASWHHVKEVPDGDERKKAGTGMGMKVEKGKPEQSWTYKKVGYTLEKD
DGVEQSGKAPPRLMVLTSDKGWPYTMNVLNGCGNDLCVNSEVERAWQIVKGDLTKWFSNF
DLTLNPSPLPHVLVGTAGIGKSMNAGSYLLYQLLHYDAEKLQVVVHCFGETAYVFDKTTK
TVTKYVGNITSIVVLDGFWQRGIKGYIIYDVARKGTPPDTDFAPSSGWGMIVVSSPNLDN
YDEWETQVRASRIIMNCPDEMDVKAMCAWMKRGLKPNEQAGYWKMVEKHMEKVGPIPRHI
FDEKSYIDRLGAVDGALLAIKLTDVGKYFTLGGSNLWYSEDPFHKLVKVVRERTKKGAEL
FLNASISADIGFRIADRLEKKMGAKDLLLLILGSRGALASRALEQLGLRVFMYGEIVCAL
LKGLKELRPPERNEARDSVLKVNHQGHPTRTVGLAGLEGGVTRTAMEYGVLYLPKVENFP
LVDGFFFMESPRRTLVGLQMTTASAHHTTTSTVKQFTEHLAAYFEGWDELSREMSWEMIY
IKNAFSKKILKWQRCDVVNPNNETDAEKKIVAFWNKEVHQYQFMLTRDFLSKITEM*
>TCRU_9348 hypothetical protein, conserved
MPRCIACATTYVRLGKRIAAHALAASTPRHRWKAAVTPQCTHPNTAASSALPTTIHSGSR
AANTDRKYGSATVLARSCAEAHDILANTPSPCISRTEPNPPVTTTATAAAPATTPVIAER
APAAAGSVFDLIVKDPSSTPLQSPNTAAASQRMTIVSSAAMK*
>TCRU_9349 hypothetical protein, conserved
MRDSFAATSLVRAGGVTIAFAEGHAEYKGSHYRLNVRPSDIVAGYINAAETWPLIAAENN
KDKWRVRTLFRTVNEEDLFGVACNPTAIAKDNKVSLLVGSYNM*
>TCRU_9350 Zinc finger CCCH domain-containing protein 35
MNFDEVDIPEFSLRAIDEIWDQWNQSNDLFSGMNLPSSHKQRQNDSKATTEVRAVYDAEF
KYLYEVPSHLLVHVPSARLNITRLVFCRNYRSFEADSCKMGNNCKFVHADVDVSTLEAFP
IHVNYIWRDEKLCTYKRLPPGEFLEVLSSDMCTVETLPSERILLTRGALAHQDIAEPLIR
CKHYDANQTCFTGERCNFVHVMYVDPNCQGSFKRAPKAIVEARGNATNASTKMAHHNTTT
NQNNSRGNNKNNNNGNFSNHMPENLHDAQASNLNWAPHVNFPPFEQSGLNSMVFLQDLNN
GASFGSGSAMPCQDAGISTGVLGMGCLMPSLASNGRQATQPSSLHCDKTEGSLQELLKML
QVSQHPTSYGALSTNAQSLNGTAGPQQISDGNISAANNTGLTQEQLSGVLSPVFSLLAQR
VSSSHTFSVGSSPLLEEPSAVGTLLFLPRGATEAVAIQPVYDTSFLGAITALGSQQQRSA
QAVVQKSPSSMSQPTTTSGGGTSQNFPFPFVSPGNGNMNSGVLVTSGGGRGSNGVIGGGG
GSANNSISIAGPTADYYTRAFEQLQGALNGNSAWMRGV*
>TCRU_9351 hypothetical protein, conserved
MMPEGGSHLVGSPASRVGGGDNVHDVSLSVGRKRDVRRAQGRSPDYRVFDVVVPLSAASA
AASRGTRLSGVSPPRVQVSREDPENNPPAPSTATGQALELTILPKTPEDTELSAALVGTR
DLRNGLLDQKLQHLQRETNALREELKETSRRLAHVTVKLNEQKVEFSGLTHRYGATVEKL
TAAECTVKRLEEHIVQERGQHGVLREERDKLKVSLKDLEWEVEKLRRELREERERPAMDP
RQVQRMLEDRTRYVPAAEFQRYCEEMRDKQHVFVSRFVASLDTLLVQHEEDETSVFVARS
AVLSAATDLEARVASAETTLGVLCDQLAVFNEGTERDMTEMITALIVENKELWQHLSKLK
GDHDVAIAQLKAIRRKGENVPHDQYEYTQKQLALTAEKLSTAQKTVQAQIDLAKEHEGQM
KLLLNTNESLQDQVRRLTEELDQVKEELERKGKLLDENKATANEVLLRAEEFQEKAEDER
RRLNKTIEQLNENITSREQEYEQHIRNLREERNAACHDLERARHELNDTQQRAESLQREL
DTRTCYFENYRQQAEDHQQQLSRSLQEEMTAARELLEQELNVTRRELEDQRAAVRELERE
RDDEQVERRAAQAVAAGLEAELSQQRRENEQQQHRLEDVTTRVQRLETEADQLRQTRDTA
VEETRQLQREVARHQGRTQELEQQMQQERESHTQQSTQLRQEMREAEERRSTMQDDLKKL
RLRLLELERDKQQRFSRERTDAEKESFVRENARLHEQYQEVQQENVALRESLQLLKGKLL
NHEQLSQQLEDVQERLKQLPMLRQAAEDARCDAMRASQETEMLRQERDAMAAKLDFFLEE
SKQAAKKDEEWTRIFRDAAEQTRRLSGQVSVVKKQQQSHRSPSIFVSAHPSGYSEQYSNY
QRVLGNGGSSTQRKQSPPLRSAADASPQPLAPPISRPWH*
>TCRU_9352 heat shock protein 110, putative
MSVFGVDFGNLNSTVAITRHGGVDIVTNEVSRRETTTIVSFLDNERFIGEQGLDRYVRNA
QNTVFLLKRFIGMYMDDPFLEAERRFLTCQIEGDKDGRLMFGVNYCGNMNYFYPEQVLAM
LLQRLRLYVNAAAASDSKHSVDVRDCVLTVPCYYTSEQRRLMLQACEIAGLNCLSLVNDT
TAAGIDYGIFRGSSLAETEAEGQVVGILDIGYGTTIFAVAKFWRGHLKVLGRTFDRHLGT
RDLDYELLKYMAAAVKEKYNVDVTTNKRANLRLLQACERLKYLLSGNQMAPLNVENIMDI
DINIPSFQRSTFEELATPLLERFKEIIRRGFEESGVPPEKFHSIEMIGGGCRIPMFKRAT

EELLGRPPSFTLNASETAARGAAITAAIFSPKFKVREFVVSDFPTYPIKLGYYLENAMST
SAVPFLPDVNKVVTVLGEKDHFPKLLEITIKSPGGSKIYAFYDNEHPLVKMHLPLGKFII
GEWEIGKPPKGSAATEVRVRVRLHASGLLHVDSAFSVETYEVEEPATEESEKKDTAASNK
SAESKITDNEEETSEKKTSEKKMVKKQKQRRVELTVTPRLDVIGLPGDMVLLFQKQEVEM
NERDLLLINTRDKKNELESYILDNRPRIADGGILAEYVTKEQQANFIQLSNEYENWLYED
GADAELSAYEERVKILREIGDAANARRLNFEDITFALEAFKTEVCNARELALQTIGKMEH
ITEEELRAAAKKCEEALEWAEREVKKYQQAPKTAAPTITRKDLQEKQVNVTGSVNVVVKR
PAPPKPKETKPTEAKNAPESGNEEEGANTQPPGTQESWVENEEAAKGDDALD*
>TCRU_alpha subunit, putative pyruvate dehydrogenase .1
MFRSASCILLAAKTIPINPQKPFKLHTAGRDDVPPVPTTATYDTEQMKKCLEMMFRIRRM
ESLCDQSYKLKKIRGFCHLYIGQEAIPVGMENVLTLEDLIVTAYRDHAWYIVRGGTPGEV
FAEMFGKEGGCSKGKGGSMHMYSVKNNFFGGNGIVGAQVPIGAGLGWRFALENRDKPRNV
AVTFYGDGAANQGQVFEAMNIAAIHRIPVIFCCENNQFGMGTSKERAAYQPEMYRRGDYI
PGLQVDGMDVLAVQEGTRWAKEWCLSGKGPIVLEFDSYRYVGHSMSDPDSQYRKKSDIQD
VRKTRDCIHKMKDFMLGEGIMTDEEMKKLEKDVKKEVDQQLLPAEKQNPTPRSELFTDIY
IGEQYEHRTTQGTVYAKP*
>TCRU_9354 hypothetical protein, conserved
MRRRRVFTGPFFVQHTSNSPFSYPFIAEFLARRFQRSPPGRLRLPKEHSANNSYTSGSSG
SSSSLRRRYDVGVFENTSGMPIGEVEEGRRGFLGFGRRAGRTMPVNPLSVLRSREMDSRE
DRSTSLFLQAVQMLSGKRRSRDVRLTLQLTPEQQQDIVNRYARTRWYGFIWYPFRNVTER
QFKWWRRFAHFALLIVALFGLAVALVLYYREVEAVLRLSPEDRYDYQKMVTGMRYSEIYR
LSMEVFQKEDPLEALPAPARYHLLIEAARKKGWHRVDWELESRTRYPRSSLEDMDFIHLF
YWSIMYIGSLVTGGGELFSDRFGDLMEVQETQRRREMEANFVEHGPEPPEIRIGEKGGGK
SA*
>TCRU_9355 60S ribosomal protein L34, putative
MACPRVQYRRRMHYATRGNRMKLVRTPGNRLVMQKRVKRSQGPHTPWVLGHKRLAGTKAL
RHTEARLASRHEKSTSRPYGGVLSHEQVRDRIVRAFLIEEQRIVKRALKAHAKSQKEKKR
RNSKKKRKEEKKAALTKKIAAKVGARSALTKKTTAKKKAASRVPVGAKVKK*
>TCRU_9356 hypothetical protein, conserved
MEMIHQLSRQGFFLEGSLASDERSASEERELVVQRLPASLQAMLLRAKLTLTDAEIQRMS
CATADQRCEALRMIFEGNSADEAILFLLHESSRNSTPVSSAGLANPSTRAETMELTATSH
SVTRRSNGDKALGPSSSLPSTHSSHSPREKEEVTVHFPPPPSLRCTGMTNFYSAGDDKDV
KEISSLPGVPSPHSYPQPAPARVLREINVNTAALSEPMDLAGKMMGQPHVKSKKSPSPDV
VEYSPPVSGGTPAMTVNKAAQESGWSNFSPVPMYPTSACSAWDDHFKTFIVHPNQLKRLE
ELERQMAPPAVVRPLRDGAFRRLMTDEHRQFSRQNTKSVKTPPTSSSSSGNHQKHTAGSG
KGGAPLTSRTQSTYYSPGNEHVSPTPYVPPLQIVRKKKGKEDVFTRLYSVNSLRGTPRVS
TARERTCSLFSHGSITTARGDKLQRSSSVYIGRTPRQRGEVVNAHPTWWTTCRRRTSHDQ
RFQSTPVRVPSSGKHGRVLAESPVTRKRPPAPNSFSPESPVQRLQRTATTIDRYSRLVGS
SKWGASCDAYGTCYSESAMKGKQRDGCNMPASALGNRLKRSSTATTWR*
>TCRU_9357 pumilio/PUF RNA binding protein 2
MSEWENIASSVINDGRKSGEAKNSLEVDWFTNSHDIFSGGRDAFLVDPRDVKRAETAPSV
LTMYSADGTLCVGGSLEEEVPPEEEYRYTEEYHVLYYSKYPRDPRMLVPLRSCGGVKRGG
ETGMPRRRGVTETQKSPQEAENVTDNRETTNDTVQESEENIQDSNDTGTAYAKSLLESLS
MKQKQQQDQANKQNQRQFDDPTQSFSVMEADQAPLGTVMESSLAFKTSAGSSLQNQINKE
ANSNGAVQLQDGSTSQFLRRSATASRRTSQYGNSISQNGGLKNNTRRQVGGNDHGSIRAS
RNEFSSIREYLDEIHSECPYDDVKSHVVALSKDQDGSRFVQRLLEDERNVEAIFMEVLPS
TCDLMIHVFGNYVLQKLLDVIPMDSDMFRQLLEKVSGKLKEYSFHTYGCRVVQKFLEKAS
TEMRENILLELKDCMVDCVFDQNANHVAQKIIEVMPEKTQFMTEAFLPSLKALSRHPYGC
RVLQCVFEKCSSVPEVNVRPLLEAVFEHVHEYVMDQYGNYVVQHAMLNAPEDLRKRFVDL
LIPHVYALSCSKFASNVAEKTIVKANEEEMQQIVEILTCPLGGSEDGSYLVLMMQDPYAN
YVVQRLLQEVNKQQQQHIAEQTRRHLANIRRSVYGQHLVQKMENMGMFTWVEGGMCNNAP
YREQNYMVSGSNRKTRGVVGGRNGARGPSAAQSNYVTPVERPLAANNSYRQPAASVAVAG
RTMLPLAAAGSGYSYGYVDSASEAMLTPSQQLPQHQHHLMPVPNVTIGVQPCYPGMIPPP
PPPPPTQAPNHQHQQRRLFTLHGQRDPYNVVDSAPIPQHQPQMPQANNVSATNPIYTNGN

GHISQTQVDKWAHPYQTLNPPVQQTMSYTVNASNAYPGINAASAF*
>TCRU_9358 chaperone protein DNAj, putative
MTGELEKSRRLYQTLLLPNFSSIEEVRQAYKALALKYHPDKNLNDPSAAEKFRDVRVAYE
ILSSLERKQKYDCTLRLHQPLGANSFSTGIRTPRAGYTSDVGCKSYTMPGNATSNIYEEL
NSYAARKAGERQRRTSSAATPRRDRASQYTKEQKEFFRKREKEHQANIRKRREQEKREQI
ARDLEALRREQERREEILQRSQQLRTGNENRRACASAGIRRASPFPRAAPENTPQGGTNK
EVPKIFLARDIHSAAVLPDTVRPIPSPRPRRPFCGANEDRGERLRQEKERQAEVRRAEQE
KYLERLMRQRMREARLKERELEAVERRERENLRRILFLDEKSEREQLVEPQEKLERRRIW
MEHKLNIRNCVLRSGLRRTVEKEEANREFLLSLQEEQFELLYLQKKESWGRAICRMDEDL
SWKQLKSHHNEMQRVIFIREQKEIMCTYCMEFEALRFTEAMTFALIEVQRQEHVNRLQLI
KEFHDYSRVHYGLLQELLANGVMEGALIVERTLLINEEESARALLLLELHEWRDRHALEK
DELNEVLNLIKQRASERHANHLKEVKQTRIAERRAKEATIAALQVEIRHLQRAMRAASLP
VSPGGERGGFVENLPCGVEFLGEEGIDTVARSSLDLRCGALRDKDATVSNGGSRHCRSWQ
*
>TCRU_9359 EF-hand domain/EF-hand domain pair/EF hand, putative
MGQGFSRAQMEEYKELVKDRFSEEAIEFLFMKFHKAAPEGVMTPVEFKRYIDSTGVYKNY
RRTHLASWFPSYAKYTHSKGGNRAVRKTSEQILDREMYLHLFRAYDRDCDGVISFREFLL
YHLAVMYSTEELFVVVFNAYDDDQDGYLSLDDIRNTITAATRYVGDCDVEDQEVQRVIDE
EAQRLMFFLDVRKDGRIRRDDMRLITQKHPEVLEKMKNLM*
>TCRU_9360 Protein of unknown function (DUF3648), putative
MGKPHLTAGGKINRREGTEPVVESPRVSYGPPPTELSLENFPAKGSTGFADINDEAQCHR
FCRRQQPRRKNPMMMPRKIRKVHPSKDFMLEEAPPLEGSISLQLCSQSLEKDKILGECFE
SQTNGSGRSMAGDGMPLNGSCRLVSPHSFPKEKQSVLLSEEGNLIDEAPCATNNAFPEVR
ECSFCGYMCIDEKIKPSENCFSRNILIKEETERFPPSPTKRNQGNRTAGELMPAPVVIPI
REYCDTEAVSTLLHREKKQPEQQNEYEEENQEKNHILSEEIPSGDHLPASQERIGQLPKS
LQLSGSVFAKSQTSLVTTFAPTNMGRGDGDGGDSFSLWGNQQQHGITSTAIKNGNAMYEL
NGRSTSSLSEPPTCHQHHHRSYSFTPEVSSSLSQLVDEQIVAYLSQTAEKMMWRRQKQLR
CVSEYLTEAIAHEAWRKGVQYGELRYYVFGSVATYTVLPDGDNDMTFDVEGLVNPTKIIE
REEAPVNSHARAIMSRSGSIRAIIIMIIIIMILILIVIVIVVIVIIIIIIIISHYLKQLQ
LQVESFFQVWPSTCVKTTLMSTLKPL*
>TCRU_9361 hypothetical protein, conserved
MGDGAVKKSKRDETEEERRARKDRERAERKLREQNEAEKLAQVVDGDKRERRHKRDETEE
ERHARKERERAERKERERERERRAGAAEGGSRERVHKRDETEEERHARKERERAERKERE
RAKERQEQQENSDNEDVIKKSFVHDDTVVDDELPTWHLESNEAKTSGVIPGWKKDELSAA
MEVENRAIRHAVDEAREAARREERRRAEEERESEAIERREKRRKEREEKKLRRSQMSDIS
GTVVGKSTIGVSDLQRQGYRAQFEKDLQRATALRRLVDMDDVSAALVDVPPQSQYDMYIR
NFGDMGRKQTGVQAPAEEDRIDFEVQAERVRVRHRAVEVPRDLGLCPENSADRPMQLVRD
LGQDNVGEALENNEVMGEPSLSNVSSSRVIDSTLLASFLGRVFPVMQAILDENDEERAGP
EALGSKSETQFSTSYTTFSCVATCNRPVLKVLFNPCAPAYLAVLHGAVGGEGPSMELDRY
LSVIVIWNVYDSFSPEKILVSPSLLTSICMSPRWPYLVYAGAEDGSLYVWDTREPERNHF
TAGCFQRNAFRLPSFATSWQTGNHMAPIVAIAVAGYNTVVGVRKDENEQLVSLDATGETY
FWVVNEKDQSKGAISDTENGLNMFSTVRLFLATSKCESRVNALSMNQESFALDFVPTDPS
HYVVACSEGVRHISRFGSIAAPSLYGPCSLFFARPVAVPSCVRYGTVDSRIFVVGYDDGT
LRLYLHTDAAPQLSIPLSNHSVKEMRFSGCDKWLLWLLDASGTLFLLDLAKKEKEFPVLS
QTLLNPETGSCTCFDIPPEGKADNRAIVLGFEKGLIQLHTLSDFTHPPSSDREEHWL*
>TCRU_9362 hypothetical protein
MVLSASHQSSTERPYLSFLTKPQNQSYVERGDDLHVHWSSSSSQLDDALGSSAFGEEGLT
QSTSSENDESDDANEPALNAYGLSLTQDSYDERSPFEELYESLRTTSSNLHPFFDMNEQR
LMVENERMQRHYELFLSMGQKNAPPLNVLSILSKSLLNEAHRVHVSLVRRYNRKCHEKAL
PLKNEREINRQWQHIKLAVEQDLYMEGFVAVQRRLSCMCIFNPDTDERLYGDNENARQQR
LLRQKCVLDHLAAQAREGGGLFYSPELQRT*
>TCRU_9363 chaperone protein DNAj, putative
MENAISPYDVLGVSSSSSVAEIRAAFKRLALCTHPDKRKNGSTNEEEFGVTLEIYPFHVV
KEASELLLDPLRRAQYDHGREQAYVRSVGAVSDTHDLSEFFLAEEKVVYDATMKDGGVLK

MRVYKLECRCGGVFELFITEREVETQGVNKRCECDCCSLVILVTGGRALFI*
>TCRU_9364 Casein kinase II subunit beta, putative
MSYPTYTGVFSDDMAAYEDEADEEALPWIVWFCELKSHEFFCVVDREFIDDEFNLTGLST
MVSFYHYALDLILDLETQNSARLTAEQQRLVESSAETLYGLIHARFITTQRGLKLMEEKF
AEGEFGRCPRVFCGGQAVLPVGQSDVVRESSVKLYCPKCQDIYYPRSSRHRTLDGAFWGT
TFPHLFLMHLRENGKVISKPKQHYVPRIYGFRLREKGDAKEEHDDQQIAARVETEETEER
AAEVSVGESNTPANTPNNSRLARDCFRDPNGERAEAPQR*
>TCRU_9365 hypothetical protein, conserved
MIAPLRLGKSRVVYILFLFLLEVAVGSSMINLEKLNTGITRLVSVKKYPVTRPQNVPRRT
KGRVFRLGVLHSKEMTEAMLLRNRRGFVNSQVNTVAHAPSIYHWLFHRCGVPFEETQELA
NSGGLTVNGKTVDRSGLESQMEWVELQKLDIRIRVEASTADRTSGFTIDNNSKSTNNDGR
KGDSNGLPAVMWVPALKRALHRQYFFVYLQPGISITSDQTDPRSFVHRLTPLVGSVAGIG
MNILRPIGFMNGMKGFGLATNDVSMVRYWNNEFLGNFGVYDVRFARGVPSEVLRRLAEEV
QQLLNDGIRKQLSKDVIVPCECTLEPTSAYKKKHHKHKGDFVAGLYSKPLHDERLIIRSP
LLPYRVARKIRRAGGFITMVRSGPFSLPPSLPQTKQRPLLPQELALMFTFERKLKTNRVV
LSLREFEADNDLDGIEPEVILPSA*
>TCRU_9366 retrotransposon hot spot protein, RHS3, putative
MVLTSDQGWPYSWKEEDSLRDCHVNCEVERVWQIVKKDLTKLFSSHGKNKPSCHPRVLIG
TSGIGKSMNAGSYLLYQLLHYNAEQLPMVAYFIGNRTFLFDKIAKTVSVYMGEASILNIV
GGFARRGFKGYIIYDVALKGHQPSIGLPCKGWGMIVVTPPDKNNYEWWAKQIGAEEFIIN
CPEENDVKAMCSWMKRNQIPQEQAEYWKEVRGRMNNVGPILRSIFGKQAYDDRIKACQQA
VDGMNALKFEGYLDIGYCCLSNDSDLSRKLVKVVRVRRNNIEWPLNVPISPHFERETLSK
I*
>TCRU_9367 retrotransposon hot spot protein, RHS3, putative
MDHWVLYKPKVKNFPLVDAFFFVDTNPKTLVGLRMSTASKHRTTTSAVRRFTECLAAYFD
GWEELSRDMSWEIIYVQHEIYRPMEGRQKFEVVNSDNLGDDENREIAAFCREKVRQYLAA
LSSADARRGEALRR*
>TCRU_9368 N-acetyltransferase B complex (NatB) non catalytic
subunit, putative
MADRSVVRIFDLIDEGRLASAEGLLDAALSKYPDNHAVLAAEALLLLKTDQLDMAREKAE
ALSEQNVVDGRAINALLHVLQHCCSWEALARTYERIKGIQNERNMMENLLQTYVRMGSYD
MAQKTALQLYRRWGDSRYQVWVVQANLCQVKPGATDDILLKLSSKMLETTILTANGLITS
STSRMYVEVLHQQHLYNEAVVYLCSARGATVGVPEARLELLATTLHRGGDLARANAVAKY
LWSRQPDNWTFVDLYLKTLSECDPTDVVLELDGPNEESRILVQLSERDRTLTDALYFCHT
LQSPSSSSGAMRPCRGPFMAELEILLRQGDADALRQKTIAYAKRFYNTACCFLDLSTYLD
ETSATAIYTWSCSEMSAEEDVLRYHARRILGLRCHVAMWGAAREQQPDSTSMDDLLRACR
NAYEEAKPLSAQLAWSEEGLFDGYITAALNIVLHAYHATRDLGWVEKGLLLFEGVDRKQN
NSAWLIYSVCFAHLLGLADVEACRQLAFKSVQHDTMSHIGYWPLLAGVALDEACQWNDLA
WEHYRALKKDCSLLRSKVFAFVSWPAMKDVQEFERRQTNSIARVVCAVHRIAAALRRCQT
QRNVFDLMRSEEHTMEEAFEALCTTREMELTDNTDWALVRSLVLGNIHGEKVKALTDSLV
GMPTREERITHTRQLLGSLMLLHDVALLEEYRVQLANDSKLKKAKKSVASAPTKPSMPKF
LCEGRFDSMPTLPMISSIAPTLLEFVRAQGTCAVMPHTTAFDDALQSVVGSQQPYDFLFP
EAFILTTLLQVGAVSALPILAWSKDLQNALTQLHDLCPEKRAATAQGYAKKLFEAKASRV
KAFLSDLLRDVVAVSRRR*
>TCRU_9369 glycosyltransferase family 28 protein, putative
MAFFSLVVLLLSLMVWRFVRVVRGKPSSIHRGRNAPLNVCVVLGSGGHTSEMMRAIRALP
LDVWRANRPFYVVSATDSHSAALAAEFEKDQLRRCCRLITIPRAREVGQSYFLSIFTTLQ
ALGSSLLLIVSEKPDVLFVNGPGVCVPVVGAALLVATLSPPWYYRRPGIAYMESYTCVRH
ISLSGRLLMPFCDVFTVQWQSLYDACLGKWWRRNGSLFFVGVSQDVDDMPLPMAQRQTTS
NASGSEQVALVTVGSTQFVSLIKAIDDEAVCQALARRGITRLLVQKGASAYEMRVRNAYS
VTVEVFSYRPKLHEIIKDAALVISHAGAGTILETLECKRPLIIVPNRDLMSDHQLELAEA
LDAARYLFCVQVGSIRQKLQSLDFSTLRVFPGTKLAALREAILPLLAAADFTADDAEE*
>TCRU_9370 nuclear cap binding protein, putative
MAEYLVDVTPRMAYVDRQELLRSLLSEKDFVARRQEQLERSTTVYVGNLSFYTTEGQIWE

HFASCGHVRDVVMGLNEATRTPCGFCFVVFEQQCAAMCAVSDMHGSLLDDRRITVSWDVG
CDASRRWGRGAHGGQVVDVLRQNLDSGRGGLGALRCGELRIGTALAEEQLVHYNWVPPKR
VQKHARGT*
>TCRU_9371 hypothetical protein, conserved
MKDCRSSPPLTVYPPACRMGDGAGSCAIVASPVSQPCEGAVIGDDYVRMLLHTIREHDAE
KPALAQRIEDCVKPERAETQRLRRELAKKDQEIGKLQQELSETCLMLQEERERANRLLHE
NTVLHAQAGDDRARIASLLRLRQQAKAAPAAVSSEEDANADGRQQRQGRDRKQSSTPVAE
QSRFGSPFHRKSNKSSNSFGGGGTMSLRQAVLAPPPAAGEDLLKLEADTAVQEALQPPRS
STVVTALGEEVRMLQEQLDAQRATYEQERKKRLLEERERTRRHADDVERYIRTIDDLHAL
HQKSLADLIHYRHGTRIEQQEMHATIEKLRVSLDEALTIVETDRRRHAADLQLMQRRMGD
NTDTVMRRLRQELEECRALSLVEKEQNAALLAAREAEIEKLRGELKRERRRQRRVEERHR
LEFEGVNSEVSLMRQAVRAMEKRVYYSQYHSLST*
>TCRU_9372 PUF nine target 1
MLKNYENVVGYSQDMLERFLHRWYDPGRSYFVYGGHGMGDYLELEENKVGLQCHELAAIF
GGKKFEAITFDACLMASLDCAYHLRNNTRYIGACEGYLWEPDTSLDHHVFNTYTASAMSR
FRDPKHILLAVQRDYCSKSSLADFAVLDTTHVEALRNYVEEHVMQRVYDRATFYNVQQQQ
KLSCMAEEALQLSRKNSNADIKMPASSSSPSSSPDTVAMRAMATKLQNKRLARRSKLQHA
VQFEHALYPSEPGDKYILDLRSYLIDMAREEEELAIASPSPRTAVVEAHGSLPNEKKHLH
PLFAKGSAHEGLDLFHRVVVNHIPPEEKHIYASHLGGLSIPVYEFSSMSKPLMPWNRVNR
QIFKQRANEFLRRGVMQEVKMNQRTHSGLHETEGRSSSSSPSTGSPGPTIYLPISGYSGN
TNGNRNKPGSGNLSGPQHCEARR*
>TCRU_9373 hypothetical protein, conserved
MSTRTNLAFAGYDVEGGEVLLKDALGMLYHLQPTWKRIELASENIQRRDNNDDDWEGESF
TESYCTDSYVSSASTYTSGENGGSGFIENGFAKVNVREGETACDCKASCENDLESAVAPV
HGTVLTLKEPYTREEELLSICFLGTEITAGDLENYKTVVVLGYNEKGDVFLLPMPTLVLK
EGVCVYHCLPALQLELRKLYRYYDWVKNTEDSSHRDTVTLKLPLGEESMNCPQLDRNSLR
HVYDVFADRVYYLSAWSAQVEFVGVAWGVPWVKVIAVEGETGGTSPVSGEGNNFCSYIKP
LHLCHDKRQLYEAYGLCESGQILEKPGTLTSSALPAAELMDKDENLEGARSQVEHAFEDS
TDPNSNLGSSSQYADFTPRSCSEALEEPSQTDVGATALQSPFFVYGDCVTCTETCGNSMD
CDATPTALERFGVLHGDRLVGVDGTAFEGREATVLGVYTGWLVLLVDGEKGATVLRNVQE
EDELLSLFNKICSPHPDNKTGAEARPAKDKQSIYLSPPDHNDNDNDNDSDDRYDDDNNNN
GEDDDGVIHPLASLEGAADAAATEQCGGEGLDGSEAGSSDRTSAPQSLFFTSFLKAVAYW
RTQLLSEEDQKQQPLAFVNYYGTDTQRRMMDAVDLLQRHKNLFDVDFADFGADSYLRLNA
SSCAAERQPMSVHRIVQLLVENECT*
>TCRU_9374 hypothetical protein, conserved
MSVLKAELQRELPLHPEPNMLDLYMTRYDYDYNRDMGEAGTGEGTSGDDDEGSVSGDVRN
RPIFRFCQSLEGSNNTTYLTDYVRHDRGVKDLTGLLRTACGEHDVASAFVRDYYPPGLRK
HATENGAHPISVYKKDYTHSGRVPKGKPSLYAGSRTAAFDPNFLLIPTTEQDLRAEAVLP
PKITSKESLLPKICPSEDNHSKEGTLFASRRPQLTIADGPPTDYYCTSWVYGDRSLAYPS
QLPRSIEESPNAHLIGTMDDKAALLSLLAGKKKRVGKPYPMEDETNPIPIRKIEQPYCGV
TRRLENEGHVNMSIYRSDHIHQGMLPELPDAVALAGADTVGVSGERRLACAGEMLAGTLT
RYTKKIQSLRNSHGNLLKENPDPKIVDPYTWRQIKSIEKRIAVDKADPHRHKLH*
>TCRU_9375 hypothetical protein, conserved
MTALARRVQQAADFIYRARQEETPDGNPLVAARNYITAMEIIAAVADEVPTKDVNERRFL
LHQLRQRMEMYYERAELLLGVAEESGLVDKPTAEGGLPMAPHFPRGDGHVASFTTVEALA
CDSVMGIPLSAGEGNSNVPHTGPPMQYYFSEPPPVPPPAPPPVEAEDPLEALIKTMSFDD
EKKD*
>TCRU_9376 hypothetical protein
MPKPFAARRRATNEPGSELLSGTSTCSTAPEHEGGVPVNMTIWLHPPRSGARPVDSLPKR
KLEQHPIHTHTHAPEQNRCRHQGPQHSMDALTSTGGGAMPGPARHARHNLSDGESVTTPK
IEPQCTHAARLETQREEGQARTATLPPRETPSSAQEANAGGGRRTVRPKQHTHPFINVAL
LPIPRRQSVGPPRKCTLPGDGATMGSPPLGFCRPACGFWRCGNDGLTRHRTACHGRRPDV
VQTGQRELCEERSPHLLRCPARQAPGQKRGVDTGEVRDLCFTREFAHFLLE*
>TCRU_9377 hypothetical protein, conserved

MDVWVDNASLQGAAKKGNSKSHAMTWELQRIYVFLDSRGIQAFFAYVRSAENPADGISRG
RVFTLQDLAKGGTCEGERRGLVAGGPQSLPLRKL*
>TCRU_9378 hypothetical protein, conserved
MGHKTGPEILQIIITSAIAGLTAVVHPLWAAPPSARDDVRIDNIRIAGSRSDVTLWEAQA
LRNADGRRATKGEERESGATQRAFLGAQFDHTHRAVSLSDKFVCSVRAMSALNSLKISRM
EVVASRFLYAFMCLLLFHQGSATTAIRT*
>TCRU_9379 Endonuclease/Exonuclease/phosphatase family/Endonuclease-reverse transcriptase/Reverse transcriptase (RNA-dependent DNA polymerase), putative
MEPFTRPPAERYLYPLLNSIGAYQRYTSRLRAVCDARRQKLLLSGDIEQNPGPIAVLQMN
VSCLTPSKLATLMAQGADIIAIQEAWKSSEQIASMHTGDYVLYAQSRIGKGGGVAVLVRK
TLRSKRIPLTIPQHDTSLEVVVVQVALDQNRDLIVASAYMRPPPQVTQSFRRLVNCLPAS
SPLLLCGDFNMHHPQWEPFLETSPSEVAAEFLELCTDAGLTLVNTPGEITYARGTRERSC
IDLTWSKHLTVSDWSASVSPLSDHYMLTFTLHQAFKDTIPSAPKFFYSWGKCKWDLFIKD
FDAQLPAYDYKKQSTGIKAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERIAADSKA
RYLQLPTPDREAEMQRTRSQFFLLLRERLRNTYLRRISKLNPGEPLAWKYISGRKKASLP
SPTSMLLGDGQHTYKTARRAANALNRIFLPFHPSHKAVRFSKGINRQSASLNINASFLFG
QQNNNESAASFTSFSSTSSSSEPQNNNESAATSTSGSSLSSSSEPQDKNEAATTSGLVAH
LHSPLDVPFNLTELLAALRNTPYGKAPGPDEVYSEALRHISSKGLRFLLRCINHSWTTGT
IPVEWRRATIVPLLKPGKSPELLESYRPISLTSIVSKVAEKMVLKRLLWVWTPHPHQYAY
RSMRTTTMQLAHLIHEVEHNRNHYFQVSLPKKSGIGNQLRHRPHRTLLVLVDFSKAFDSI
DHRVLSRLLANIPGVNCRRWLRNFLCGRYAKTRVGHRHSDRRPMLRGVPQGSVLGPYLFS
LYVHPLLNLLNSFAGVTADMYADDLSIIVKGQSREDAIPTANMVLQKLHAWSQENGLAIN
PSKCEAAWFTLSTHTESDYDREGRWPLVVAGCQIPVMTMGASRTTKLLGMDLDPRLTLNV
AATKQCAATSQRISQLRCIAHKEAGPSPHDLRTFVIGYGASKLRYGSELIWAAATDSAKN
EMQNAYATLARIVSGVPSTVDPESALLEANMPPLHVLCLRARLSIFENTRACQMDWMRRP
PPEPPPRAGFRISPLSRDELYAFADAYTKEYGITESSPREERFFRSFIPPWFAASAHRVT
IGVGLPIDHSITDEEELIREKRRVSEEALALHSHRSWILATDGGVDVPKSAGVGILLSSL
NSSEIIEKASINCGARPCSYRTESRALLLALEKLMIPRIRHRRKTLLVVTDSRSLLAALN
KARSVRQTGRRIRSGSVS*
>TCRU_9380 hypothetical protein, conserved
MAALRARAGTAITRGRRRVRGKAPRRKGAWVLAGQNSGIVHGRDAVFHSLLAVHSVARSH
NSSVCDIAGRFGYQQHCRRDRAGHELVAGHSQRGVAEIHRGAKNSKGIGWGHAAEVAAQL
QPGVVVDVGGVP*
>TCRU_9381 hypothetical protein, conserved
MDSDHHLPSHTAGTEDGIPRQAGMLPQRKHVAVVLREADRDASTSACGTPLAAVTTWLEM
HRGTARATAATASHESVWAEWSRPSVLQPRCSLCEHHSSFGPAAVICDLNPHHELRDGCS
PSTTAGEDLAATPSGMEIELSDDPAQATRISGRSVSFPDVTALRVLRVSHWTSTSLHGLG
PPSAVPHCRDGGRHPATGRHAATTETCRRCPA*
>TCRU_9382 UEV domain/Zinc finger, C3HC4 type (RING finger), putative
MNEIITRFFSCSSHCKPEVLGRILHDVENLCNTFHFYCRDATWGVTQQEKLCIYGGLPIT
IKKSNSDHTSLTPDGREQAPPHRYVLPLQIWLTRLYPIEPPLVFLLSAEQGCRIASNHKY
VDATGRCHTPELAAWHPVSSSLCDVVKKLCQLLSAEGLIPLCFGEEGVSSPSKGHATAVS
QRLRHGLENGDDDKQTDEHERCVVCFSPKETVLVPCGHYCLCDACATNVTHCPLCRGSVK
FRQRVFS*
>TCRU_9383 hypothetical protein, conserved
MMASASAVTLRGIPRCHGEHLKPTVRTRSTSECGTVQISSVTSSCAASEPRRSDSIAERE
SVAAGIRVDDWDAAARRGTENCLWPSSVAGHSTRQEHAKLPAAAR*
>TCRU_9384 nuclear transport factor 2 protein, putative
MTEYSDCTEVSKKALEFRQQFYQLLDDPNKRMDIVNLYAPGTPLLCEWNGHSLPDAASIT
AYLSGLPRTNHKIDCVDAQPLPGNEHADSFLMTVHGVVTYDNEHRREFFQRLVIRKVDGR
YYIINDYYRWLSEKE*
>TCRU_9385 hypothetical protein, conserved

MLGDHYRLRIQADGIPSDASEEIPTGHHGATKPVEKFDAEVQWTFSPIIRVARRVPSQSR
RPPKKPVAVAKSRSRAKCRKQVSFKSDVEPFIQPPCGGAELESNGKLRIVTTGLRLTSAK
ETKLRRLGIVMNPPRSEFGRAKVLVIDGPLMRSVKLLTALPFVEHIVDRAWLDAVLALPL
KISSETTTSTATRLMDFASFPYSERRTRRSIETVNAFSLQELIQVPACQRQALFAGQLFW
VHPEAEPQDPPDNDLKYVILASGGALTKDVSCATVAVMPQVNVTSSMWGQAYSCPQEPLC
IFIVPNDLFCAVLQQRRLTTSTVRCPVGVSVLPPSPTTAMLREKRCLSSPRESTKKSKSR
RK*
>TCRU_9386 Complex1 LYR-like, putative
MRRIPSFFEAPATLATAISSRSHHCGGSFGGNDGRSSRTDGGANYSPCCSTHGIRGHLNL
APLPHPTQLEALPFRSEQWRRAFCQLYRVIFKLHRSRLLPVQREFGDRFVQVEFQRHMDA
TEKHARIFYQSWYGYVAQLEAGETSREFTEEERSQLTPEQKETLRELRGHVMRVRQTDPD
FAL*
>TCRU_9387 hypothetical protein, conserved
MDLRVGRRRTALTGPQSPNTTNAGGSTNNNSCGVGGAFSSNGGAQQNSNNAGGRTKSRLL
PMSRNNSLSAPPPPAWKSTGLASGTHIRRRPPSVPGRTASPLQTRPGVTRLKKEIIEHRS
DPSPAPSRPPRTFTKHSLAASPPLLSLNPLTGLRGMMDHQRITSAFYHGNDRGKLFTLNR
PAKTNQRNPIIPDSGTATPSSPVSGSRGVGRRNIVLDVKQGSRPVTGRKHVLEALPQAIR
TAAEDTVRSYKELCEALGQAPQDAWIDAVLEGVNKAATLSRTTCIGVGSPAEVRFNAKER
EKLAATAGVYLDHGQTKKVGTKTSLTKRPRAVEGKGGGVTPNLCGHSVATRDPRELPAVD
MDKDSAGKDTMLDRMVVYCQHLRPYQQKMDVLRQRRKDVEDALGRFLALCQNCSDPGETS
SKLVAVNALESHANLLTDGLKDLQRCNVALLLRLREYSREVRRPLGLVGCELETNAVGQQ
QLEKKSPGMKENENMTSLFNVPCTEDVASPRKSINFPSTKDPPYAYLNFLREEESRIVQQ
LNEVCSRVREALTNGLTVTIADEAMLETPLFLSSATTGHPLSFEREHQQQQQPKRVTGQG
FSSCNLVGSGATDNSCRTTPPNSATTEDANTCGPFVGVALVDWVSLVDDDDNNIDDHTGS
NNSNSCSHKHATGNPKLVLGGGRKCLSFHSPPKRRAGGKVAVRRTKSTSAPNAAQKRKNV
GKMAMVTKTPTTTTTTTTTTVKHKKSKTLSKTGSTSSATEVILAVHIKEAEETWRAIKGL
AGVGVARGSFKRQIIRTESKQKGEENKDFTPELTPQHEQPSGANLFISTPPKIELEHNTT
NKFYGFCPEDKLEEEAAQGKTLGVSLASDVSKYNETNKKEPAEVICQFFRRHMQEKKRQI
NELQQLQMSTVASLSLERSAVCKAEFNTDVAMATRIQCCWRQRMARRMLQQRRERVEKEA
RQQQKWHIENVMAFRIQRLFAKIVARRRLREATQMRCAASKALQVGAKMAENNRTDGNNE
KSSRLMKLRERFEQARERRRNLLRSTPDGTNSFSDAIIHPPCSSSSPLDKALPIEKQPPE
LEPQPENGVTAKVPPLELKSSGISTFDIEGYQPETENFNVCILHRLLRAPKPLLYMTRVL
CDAYPTQPVSALAFLKAAEEAKYKGGGRSSSRQRTTQEKEGKKKEGDKEGKEDKVPSKQQ
EEGQEIREKNEKGRGAHHQQKMKDESEMRWELRPYRMIRHGLIARKAAMINREGTKHVCP
FSIRVKSFVEENEMKHEQPVAKGFQRPFERWGTAHAFQRRVFSAAAEYAWKLIFSHTPHD
DYKQRMLKTKEEQEARLERVEQRNRMILACYCVRSEREWLKEASKDLGFVARIWNPKKSL
DPNDPDFERHCRETYEFVEDFLYQCFPTITNLDEAPTFLMGAGIFFLLKSMLAYNREKEE
EDDKTMGDGLAVYVDKIEGRRADPESAAISYLSDLLLAPQQQKAISTCEVLNLLDNLTLW
CRFPEPRRAVTTASGLGKKNDEVNRNTAHGSMGDDVDFSDTCEGMYERTIRSIEATTRLS
DFDTVSFTTSHGESSAKMSEDRRPRLRQVLRTPLLKSSPAKRLDDAAFDARIAHNANNKK
NGVELEIVYPKGYLVGLSERLMRAILGLRVELEVCEDLDATI*
>TCRU_9388 hypothetical protein, conserved
MVTKPSTWWGKLLGSLFPQYYARQALANLGLGQMSNDELVNRMHFALQAGDTDLSALIAK
ELARRRACLYEEEVGRTSIGRDALHSGGRLSTEPRMRTRLSTGFGGRVSGVAPDSNTRPS
TGSSFLVPEVLFQKRPRGSGGVGGENMLRF*
>TCRU_9389 retrotransposon hot spot protein, RHS3, putative
MSRAVKGEVIFDEDIRELCDRGVNNPPGWSLAAAEVKAAVHNSNKHFLDAAAEEARNPTT
TSAPEKLEGLYESLHNARWSHAVDLPDGVERKKTGTGMGVHEGRPEQSWSYKKADDAIEE
NDAAQQFGAAPPVLMVLTSEKGWPYS*
>TCRU_9390 retrotransposon hot spot protein, RHS3, putative
MYLLRPIPRHVFDEEAFRERCGAVRFALQSINEVTVKEHFSRGGELPWFSEDPSHKPVEV
VREIYAGGVILFSAPISACLEERTLERLPSVAEYNSFLRLMLASKDNILPIFFRWFALKS
FTESAFAKAMATKLTEFEPPTGRQAKPCVLKLPPELHPKGDEGLLPSEYEKTIRKIKYGV
LHKPWATNVPLVDAFFFFGVQSNDGVGLRMNTAGGHHTTASTVGHFTECLAAYFNGWEEL

SRDMSWGIIYVQHADSSMPMNDWQRCDFVDSNNVSDESREIRRSGRKRSASTKCQYRTET
FEETKPSEVCKK*
>TCRU_9391 hypothetical protein
MVSNSLLAILLLKYYGLIVGIAKANQGVPSSASVGIWSKYVSFTGEEWTKGIAAESVTDW
RTDIAVERREEAVHMPQLNGRKALTKDGKIFLSLERFPAKNAGAMLETPHRWELVPVLGK
VVGLQRWGKAHHVGCWETFQGCC*
>TCRU_9392 hypothetical protein, conserved
MVGLSVTADNKREVAFDGEAGEVQHGNWGLERTYRVAVGLQNGMGTVCVDGETLGSSATT
VTRGAQLLDVSCFYVGGDGCSGSGCS*
>TCRU_9393 hypothetical protein, conserved
MEGCPGGKGRRAHRVTGACRCGEDSIPGVDPDIGPRVAALRTGAMRLLPTLRQACTRPAD
HKEPSVSVVPSLPHCGDRPASASAGTSSRREHRNSLPASERRIDVLLPNLRQSAIVRPQY
EGTCPTCSAWRYNSLRGPPMRMPQWRHRLLNRCLARRSPPKLPSMPAGKTHRKHKGGYSR
WTRLFRHRLITDATGC*
>TCRU_9394 hypothetical protein, conserved
MARETAKNDRQADLPVAEAGRIRGQVQCGAQPIPEDEGAAPPCREDIASSGWVRLQVLSR
GLPEAQRSNGVRLDFVPPFFRVHSAQSRLSPGEAMCVLRVLLRRRTRLVPFRASISFLEL
SWLPRGIWRSAARKMPPRGSNHVDAVARRVSHNDVKAGQPALRRAKVASFRQGSVFASRG
VPSSISTK*
>TCRU_9395 hypothetical protein, conserved
MRAVCQSRLTWERRHRHRSQVSTVLGDDVASCRGVGALVAYRNSAAGRCCEHDGDQGDFT
PREGSTPCPVWEVRRSACRLWVRTARPFRSGHSVDITRGGEVHKNPGTEEDGYITVWRLN
IAGLSSVKKIAFAARLEQRPPDIVLLQEISNRGDVAMKLSGHNDYLQASLGAVVALPFWC
ATLYRASACRSLALTFWRPLLSVHFRRAVPAFAW*
>TCRU_9396 hypothetical protein, conserved
MNCAGGDWRATLKEKIRSSEEALHRLNERQANHENARKFLSSAFDTPHVSSLDVPPRFIS
SQAELEDKVNCLQSQVKNCLTELETEQAVRSDGIRDVQRHLSIEMGEMRAMFQQLKRENE
YLTETVRLLEKRLLSTSTFAPTGRTQAGVDVHTPTTSTTAAAASTSSDLVKRVEELESAV
TRQKRLLEDRQTRLDGVLREMVGVKIDSGMERMRSVAREAARDSMEDLLRLRLTAVQSMF
NGELQKVMESSGFTAEVAQATERLFHQMEKDVLRRVDQLDSAVDAISHGSRQHERVLNDM
ESRIVQKVTMLERELEASRREMRDGIAKNAQAGEERMAAAQLALESTVAERIAVACKSTA
SKDDVFAAVTASQERLEQQCSAICDRLTATVRAHDAAAEKYRKGVAQLEKRLDGLQDVTE
EMRHQIVHVDQLATSAKGDVEKWGDRLREALTASEEARALAKESAACAQKAEDETREGLA
RIGVELQKLSHEHEKSTVQIRQLNEKLAAAEAHHAATRVTLDELSSRCTSTLPPLSARVD
AVHRTVQDVCVVKLEENSQAVTELRTLHEQLQANASSMAKTDARQISDLRREFFVGMQSV
EERVLQAVRDTQQESSTGITGLRALIDRLNASVKTHDERFASKNALDVISEGLTERVVEL
EGRLDTVARQVAQDAKRLSSPSSPSEPLVSVLTHEKLERELENLRRRVDDVQRNAVNERE
DVEHHMRASMQEEVDRFKQLLHRLREDTSSQMQKLRLMLSEEAENRSQQVEEASQREMQR
LQLQMDRLREVLGPRRLVSAILDENELLSEVAEALQGAFASRKDTDDSIARVKQRVQQAE
QHLHELEARCDTHGNAFTRQMETYESSQRLHAERLASLELQQERVVETSKRWQEESRKDH
KREMEQLTVQFDERLKALQSATVEVELQTHTMLSTLQHLQEDQMVLQREVAKTVAAQQFA
ENHIGTKNDDKNDDPENNMNEHEVWKAQLKERIDLLESKTDATACSTADAFDTLRESIEH
CVTLFVQEAASTSLLQDSDVSANELTGLDSVLLFLLEQLCQAHDALQALQKGALGTLELV
QHHEDQLALLPSMRSLALLSARQVEKLSEVIGLQFDLHVDSSLVGQKERELGEDE*
>TCRU_9397 hypothetical protein, conserved
MSLLKADQVRRELFVKYRRQIAAVLGETEDGDPIESCECEETNNGGDDTNEKGNESYDEE
EAQQQQEEEGGGMEGMGLRLLERFRISYARQHLLRQRAMRMPDDYIKETTEGADDAKCAS
HSSHAADETTPCTEAAAVAISAGATEGNEVEVEGWRLVYNEPYPSIRRIMRRVQDESLQT
LMRESRVPITAYRDAAYTAQRMAVLQQMEEQIGRERAILLARQQKMDGKLHPIE*
>TCRU_9398 SNF1-related protein kinase regulatory subunit beta
MGQQNARDSKLLRREVRVDTAPVVGDANHRNTSGGQKGGSRYATMRENILQQPAQYRDPM
TEVTLTSSGGTTMGHDGTHAVGSTAAATAAAAAEALAKQKKYPVVLRYADKDAKQLLTKK
QNVYVTVETLGWRPVQMAPSEDSFYAILELTPGSHRYRFLVQDKEVVDSTQAIAEPPQEG
SKDPPANILQLNEVLLMTKEDEEIIDDGEGWGQNHEMFVETRNYPPIAPVHLRYTPLNTP

PTAVRCTRDGVISSAGEIMSPENLPLPLNVTINHVYFQRREDHSVMGLTTRYCNKYTTVV
YYSRMGAPNG*
>TCRU_9399 60S ribosomal protein L9, putative
MITGVTRGFRFKIRFAYAHFPISVSVENQLVEIRNFLGEKRVRRQVVADGVKVYRTDPTV
VKDELVLEGNDLEEVSREAAVMHQLCLVKKKDIRKFLDGIYVQTKTNVVAEE*
>TCRU_9400 hypothetical protein, conserved
MEGVEAATTFLSAGSELVVSVPHKTKRCSANLKVLSLTGGVEPRVDVLGAPALVDVSYNL
LPGMVFSIFAWNNASIRIEGPKQLILNCYRSTIPPFLRPVVEYHCIIHDARTMADKNSLF
GPIVLICGKNDTEKHAIARTLCNYAARTGWCPQLVDLDCGIGQMLGAPGTLCAGVIEYPM
TLDEETTTGPVSVCFFTGSTEPQIRSGSGEWNMFAPYMHYTNLLLTCVNGRIAKHLGGIA
ASSGAVVVLPELKGISGILFVENLLRRFNISHVLCVGDDFLFSGLQERIMKMQNPMNSHS
SVSTRIDRLSQSFHYPPMDAGSEYLSSKLEKYFFGGGAIDLQPSEINKSFSSIEILLLKD
NDSHAVVTVVEQDSLEAIVGCVGALLESSTISDKDVLSLAPFALARVQGVDAHGVNLLVS
THSALSEKLILVVGSFRWITH*
>TCRU_9401 vacuolar sorting protein 33 , putative
MGLRSEFLRLSSIREVIKTEISSLLDSLDSGAKSTKVLYISPHLLSTFEAIGVSKELFSK
DHGVIGAFPYEAEIVLASAQHAVFIMNPDLENIRSLVVNVLTYAQKHAKTSISVFFVPRK
PLIIEHILGKEYQLLRSLPGLRLGEFDFDLIPLEDDLLSMQQPLALKHLIADGDITVLQW
IARMLLKLQTSHFGAISLIRGKGTRAAKVVQMLGRMQSEMGSEFLTGLTPEIDSLFILDR
ALDLLTPLLTQLTYEGLIDEFYNIDSGYVSFPFNLGEGAKIEIGHRVFLNHTDKIYGEIR
DKNFTNVGSTLYNKSVWIKKSYERRKEVQQLKELKEFMKGLPEMQEMHRLIGIHTAVATE
IGKRTQSIEFRRRIAMEQSIIQQVNEREVIDYIEELINKTASITDVLRLISMFSIVNGGL
KSKTYDFFRENIMLSYGIPQGLAAFLALERSGLITKHDGKQLNFSAIRKHLKLWYDALQE
QQPNDIAYAYSGYASLTVRLLENMISYPELWNTPTDVTELIPGEKAEIRNEVETPGGTPI
TMVFIIGGITYAEISALRYLQEKLADAGKARRILIASTNIMNGGQMIGSLLPFFTPM*
>TCRU_9402 chaperone protein DNAj, putative
MSDPPKRCYYEVLEIDRKASLDDIRRAYKKQALLHHPDKNYGNVDNTVALFKEIQNAYAI
LSDSEERAWYDAHRESILNGGETDVSTNDINLYGYFSSRCYDGFGDGEGEFFSVYRGVFD
QLIEDESEYETRAKDWPRFGDSLTDWNSVAEFYSYWKNFSSFKNFAWKDEYKINEVPDRA
SRRMAERINQKARAAAKKEYVQTVQSLARFVYRRDPRVEAEMTRQQEEERRIAEEKEQKR
LEQAIRRREANERIWLAAAEKEAEEERARIDRGETMDGQTLELLYEKQRQVEKMRKSKGS
NADGFAMLEGDNEDDNGGPKLNCPACKKQFKKAGQYNEHINSSKHKAKVRQLSGKGVCVE
TLMKDSK*
>TCRU_9403 DNL zinc finger, putative
MRRCLHLPVRPVLPLWKKNRDVLCFFGRFCGEKTGVINASISNLPGTENTETSSSKIEAY
ERLQEQFRGLSEDDQRLIFDALQHPEQQPQSKMGGTGIGTKSGDMVAAFTCGRCDHRMVK
KFSKHAYTKGIVIVQCPSCEVRHLLADNLGWFVDEAKNIEQLLREKGESFVRIGNDYQVE
PPTDNESSNVQK*
>TCRU_9404 PACRGA
MSYEIQPIVKGTKRDPALKRYNKAAGKSPFGAFPPGYAPKKTRADVVKSRDEEEPVSLRG
VKFAYPGTRHGFGGATSSLYKGRPNNTNSDAFSTNGAGDSKPPKAGAFKRRMIPPTEFRR
YYDRGDLPLAVSHGSRPSIDWKVEVERLDYHHYLPIFFDGIRETEEPYMFLARQGCLDLL
KRGGAKILPTIPQLIIPIKTALNTRHPEIICATLRILQQLLVSGDLIGEALVPYYRQILP
MLNLFKSRHKNRLRGDTIDFGQRKRDDVGDLVEETLQLLELHGGDDAYINIKYMVPTYES
CVFS*
>TCRU_9405 COP9 signalosome complex subunit 2, putative
MEEEDYYYYDENYGDEEEETWEAALENAYVTAKSMMDTMPEQCAAGLRGVERDDPVGGKW
TFKAFKMLVRVCRRIESYEEMLSYYNKVSTFSQKCVSKAQLQKAMTKLIDEAQRVPVEYL
RRMLETTIEVTSRDMGSFGKLWFNAKLKHATLLLESNALDAALEEMGVVLEWCKEEDQFA
LKRSSQLFLSYALLLGIYSKKNDYSSMRETFFLATSIINTIPPSRVMGGVMECGGKMYIH
FRDWQSAFRAFSDAFLHYNESGDPRKIGCLKYLVLTRMLGGSTIDPFARQETKVYEETPE
IVPVATLMRSFAANDVRGFLEVMAFYREAFEADSVLQSCLDFVLEQLRLQALAAYLAPYQ
RLYIKRLEEVLCVDAEEVERLCVRAVMEGNLHAALDDEEHVIIMQKEQLAGPQEERLQAL
TRWSNALTQLNEETRWEVERIT*

>TCRU_9406 membrane-bound acid phosphatase 2
MLRMRFLFLVLALLLAPVMDANAAITHVSILHRHGARSEPLFPNMGLRDATQLTPNGEIM
MLNLGKLLRATYGTFITSYDPAMYDTFSEYFDNCIQSAHGVLRAFFNKGSQFLPIVRHVP
AETDWLLGFNHNFPNVYARPQWFFAYWNNDALARGMLSTNDIEMLSNELGSWCAEKPMQC
ALFAADALQSRISEKRLPEQLQTLFQEKLLPIVYGWNKHTYGFNSEDPYAVIGSPAYALA
AKVLHDAEVGEKKVCHYSVHDSTILGLLNALGAIQLGDTNPRWLPRFGSVLAVTTYSNGN
VSFTYAEPQQEAGSSLDYVSGLLPITVRCKTFEGAEYMASTCPLNDVWRYVNRSRPTVAD
PFCYLRPEDGCDVLETVPSEHCQYYRKYCPIGACGPNAGLDASRNYTCFSFFRRKFTKDY
TLASIVAGVCGGAVGLIVGFLISLLLQKTEEKEVRRRRFVQMGAGETNA*
>TCRU_9407 kinetoplastid kinetochore protein 17
MKSRQPTKNRINMHDIIATPLGALPGAVDAILRRPENLDDVEVQSIFKEASFILLRAEEA
LASREADAFCVLFKLFSEGLAHSAASFGKGIATFGENGALLQTLRDIFRVAVEQRAFPLQ
CPAVIELVQVVGSLCDGSCIKDTCGALFMEGLVYMLDDMYRRSIEEAHAGFLAQRAAATA
LINLVKGSKQNKQRITSWDFLADCCALSVDVFFQLQCIELLFRLSRHNKSLLPHICSRLR
PQVLEDIRQLPNDSTLLTKMVELLHNINAGREDILLFPLSRADVAHTTIMEDTFSYFTMN
YFVVLVTSSNADNVTIPYNSIRSVTLGKDGRVLFRLDEFPTKLEALLNRAAGEDTIVLFM
TVDQLALFKESRIRSWIVSALEAKKERKRNGARSGAEAEAVTTSASHNAPIGGGTKRQRS
DSLQLTGGDSHVLAVFQKIMKASDENASMVLEKMKQLINSKHESREEEVAAILKASMDDI
QRMVDEGHVANDGVRDTLRGGVEESIQSIEQRLLDSQTKVAGVVEQLNVALQELKSSNTA
IHEQIACIEIILQQSLEVSREEEASMCNSLKADGEESIERIEALLDRQLIGQSNPMSVIS
EFLRTSTEGSVL*
>TCRU_9408 Peroxisome biogenesis protein 2, putative
MSWVVDSAGAQFPLAMVMKQQGALPTSQTFTALPENHVLRVFQLGALQTQAELVDILRSS
LFDIFDLDALQSYRYAYQDELVFFLDVILYWGSTWRRSQSIGDRLGNIVMRDETKALENG
QSSVVRLVPSLAPTRGRLLVHAILTILVPYLVRKLQRKSMEEDWEGESPGSLRARVAKTI
RLASTAWAAFSLLHTLHFLATAQYRTLVERLLSLRLVYGSQSTQRVTNLMYLNQHVMWQT
WSSFLAVLNIGRYLSRLTRSLQAFTSPSGSLTLGDNVCCACHSHPTIGQRSNCGHLYCYY
CIKSRLLDPRLAGSFRCLRCGTTVHTAFPLQ*
>TCRU_9409 hypothetical protein, conserved
MDPAAGVFSPFHELEGKNGLLENAVKLGTSEHSHDAQATASTPTVGLRETGRKKNKARDE
DAFRRGTPCGGCGMNYTTSTVPTGGMYLCVDCAAQLESRPKGYRFPPNTLKCCPASVAEG
GDSVVRCCACRSWYHCACLNIHDRALKEYLTLSTTKWYCLEPSCCEKVLQEKLKKRR*
>TCRU_9410 hypothetical protein, conserved
MLIQMISFLAVVVLFLPLNCDAVLLLESVGRSLNFTRQASRETQSVVFRTDVSRLLDWHV
VRGAQGLQLRVALLLRFESPTPSENTEPFLAVMDEIFIHCLYAPISLSNADDAVSVIFST
SHATVYILYPCGYDDASASLHMLAAHWRDGNLSVTSDEPVLSLGVAKRWLLSHDSGGADA
QLLYIQGLDGVTSAILLEKGDPFGVYPSSISRLKFPQKSTMRDTELVSSCFLHNVGVSGL
VRHSRLDETFHFELYRIFSSKQSAELLLETSTTIFTDLDSEERRHCSLSSRVAFTGCSLT
FSSAPALQVEITLMAMLESPTASGLREIGGWVRCGTTVLKGRAEIKDGGLHVLVLPLRRV
QFKPAVQMEGVREEGEHTRGRLGHCTFHHSNDTLDCDGGEEPACSCRCGVSRHCLALQLW
WRPSTGVDLFFCDWLGMGLFEGFTFVFVLFTVTFVIHFAARLLLLHRHLFFFFLV*
>TCRU_9411 hypothetical protein, conserved
MENKAPGTTERPGGYATAGGASAHENFFHPRKKMNKSVQRAGLRYSRRVAVWFTAGITLF
LVIPSYFGPLYVEYVSGKDWLERANKSIWTRRNEKDYDLYMTQRQNGWLEYLGLKHYNIS
GEENIGEIQAYRRGKQ*
>TCRU_9412 hypothetical protein, conserved
MKIISDVYRQTFPKKLRFDKACLILHAELLMIARRHKHKKYIPKEEICDVLNQYEPLPGS
PWLQLPVIRHVLLIRPINSVRVLLGWRSWLINRSVDEEFHRVKRWMTVQEGTGAKNFKAH
RISGFVLRERFVAEVLDPFHVAGMYQRMMRWGLFVVIVLLLFIFASLNLDALVYFFLVRW
CGMGRKEVLEWFRGITERHLITEVPPAYKTLLPPPCVLHMPSDGVERYETKILELVSPDE
NIVVMAIPCPQVGSKKFFAAVGKAASLCDAVMMEGVSFEYIDRIVPAAFLPLRDNTFPAL
GLHHRFIDIVRGKREPPFLYPTVSEMTWKVYWTQFFVPFEWRCVYSPTSFSASKGEAKMC
WGRLRELIETVSASQADAGEGGAEPYVICLPWTLHQIVNLEASLIKYGFRVGRVFSMEWM
DRDYMGRHFCDYYGIAEG*

>TCRU_9413 palmitoyl acyltransferase 10, putative
MSGFWSVQRVGNIRVCFGGALCFGPDYAFMIATMLLIVVCSLLFLIYTTLLGARVVCGCG
AVVTLGFMFRCATIDPGICPKDASLLEGAPPREAPVEEVFYVDAHGREQHASVERKWCYC
CNNYRPLRAIHCRFCDVCIARRDHHCPWVGTCVGERNYRFYFIFLWSTLCLTLTVLTGGI
WSLVGRMKVLSREVSYANRSAFLGALAETHYVEPLLVLVAIVTCCLVFPLAAYHTMLVAR
NMTTVEEMRGESGQVHYYDRGYCLENMKASLCAPIPPSNLVQLTRQCTSSTNIVVETAEV
*
>TCRU_9414 peroxisome assembly protein, putative
MQPATAPYILRSLYKDEHIIDNHVTRPLTGLVTALFGAHWTNRYDSHLSNLAKGLYVVLS
LLRGQTLGEEFCDLLPVTRGNPTRMMGITRKLLLSLLLALEPVALFQFAVRMFPAVPPHD
VIANVRKFTLMLLFLFETYATLVHRLLGVRHLSLLPSQKLQNDDGAPYTYFGLGILVLLE
LIVRLWRYMERRRLALQQGSHYDVSRDEESQEHEDSDADDNQNAAAGKCMLCLSNRKQPT
ATSCGHIFCWRCLLDWIKSNSHGAICPFCRRQITVQSSVPLYLYVAKEAPTAGGVHDTSA
*
>TCRU_9415 Leucine rich repeat/EF-hand domain containing protein,
putative
MAVARAESIVNADLGAVEVNLEGVGLESLEPVLPLLSRLPRLKALRLARNKLTGLPNDLT
GICQLEYLDLSANPITGASTIMQGLSGLAILRHLYVDLPCESEEDEVIVAVQSLESFNGT
SLTEVFEEVRGAMEGDKSDDGDTSPAPRIFDATDTSVLDEAPIYGQEQQRQQQQQQYSST
QFQQWKAEETKNIQGLYTLVTNFTGNVFTQKEFNMYVANVVRHLCALTAAEPDPSSREGE
KLKAKKVLYEYCLEELCRVVSGRDAVLGRALTEIAKAQACLLESYDHLWRRITEDMNGRI
AVMKKDMQDAIQEIESLMGQLGQKENDSNGGSGTNAVNGMELQRLQEEVGKLRTENERLQ
TKLRLVEASACSPDAVAPGALRNSSASADHSRISPSSSRAPQSGSKVLTLKQLKQAIEDI
YASKSKYDIKCSESHLPRETMEQHMYTYLNQRYGLKHIILDWATAIIQGIKKYNLEDNDV
AVFGKILRNEIDEEFRFVQRQVRETVHELLRVYIKGKRPSKSDTDINKIVQKKTNGTLLE
DEWVDIVKYMYNTEDAVSIIMRVRDYLRQVSQPRRRSSIQRGHEIASIHDVQLPYAELIR
ILLDFQLEGHERFLARFHSIFCRHDADRNGIVNAQEFNAILKTVDASKTDEEIEALLELI
DPFGNQLITYSECVTFLSAEIVRMMKAVE*
>TCRU_9416 hypothetical protein
MEDVSTLPVSAGAATHVTTPFPVDHMSITTDELSSLFSLARGSNANTRPPPSTPKEIKKA
MEKVQAFKPTHLNGFLHGYLSGRAQVAEEALCSICQLAVRSNCDWLYQCQLLALRLLLAE
LESRSSGVVPKTKPEDLPLLSQLRRSFPEYQGKAPCITFSNCHFLFVGETSPEGEGQNKS
DFSAEVSVRNQGGSRCSVKISEVHAFIDGEVVSGEYLGCARMEERSIRSGEATTFHFILK
PIPRRHVSLFEQLVVLSVDTYVKIFVTFIVVSEKQKPFCTGFPRCLAITVRDSPVGVYTC
PLMLQLIKHQFIRQQGLTSKTIAHLLVGKSGNFITHNREVMREATRVKEILEEEMDFAEV
LATYRSSLPKNNRGTAELPYSSAQPAGYLPGSVLPTAVAAVFSMSCFPNAATRLPAALTN
AQPDVLMGLTLIWLAELDATVFDASLFACDPMNYLGMLPPHLQGVIFWILDLCGGLLIHS
GVNGTSLRHLALTFAAVLMRKKRLTDDAKAESVFKERVFHQGAVDPSADTMLTDVALHQA
AVTAFVHWITVYRASYESYL*
>TCRU_9417 Vacuolar sorting protein 9 (VPS9) domain containing
protein, putative
MRRWTGESESDSDPVGGENPLLPLGEFCGSGSNFFGSTALGMTSTLATEPPAAAAAAATI
SSSSITAVPAEGGRNGSSVPRDGEGAPAAVSSSPESKPEKMCITMEFGDEYNGDVKMDRG
TAIPHGYGTLQSSSGKHCYVGGFVNRSRDGDGKLLTERYVLWSKWKMNRPDTTNQTRIDY
PDGSKYCGFLTWRQDNAAAQYPSRGPKTRHSKFSNWVQMNTPVRERWGELVGPNGDRYFG
QWENNLPSGFGCLVTSGGDRYVGLFEEGKFHDTGTLFSLHYGRQNTCHSLLDGATFAGLC
EAHSRQATEVGEGNDRENEENDHAESTLAMKGLEKERWGGVIFDGVWEKGRFVGEGYVTL
PCGTRIFAEWKSSTYPTNGRVFLGSFYNRPQAGMNARGWFQCFHWEPLLCGACEELKAQE
YAACALYRERLHSATTQEEVQAVLADFCGNQGAVRNALKLFRRCFYFLHGTCGKSSEIGA
GLCLNKLGWCYLRKTYGGCIHRRHGRPIIVGDVDLAMTDIISFVRSVERWVVAMLGDAAV
ADNSSEIFVARRVLDYVLRDTHDVLLNLYLHAFKEEDASLSVALERLREQTTLDDMGVVF
ARQQSEEQLFDPYADAIRVIEQLERNVHTFTGKLRVLAQWSREIDLAARLAQVNLDDKSL
SLLPRRQVHLESGSADDLLPIYQYVLIKARLRHLYVHAKLLVDLSSEDMFMEFTSPENFF
VTTLHACTTILASLHPLLRDNCQILAPSSFFEEQLRSAIRSVKRRATQFLDVFSAHTSEI

CAVYDADELRDIAVGYIRAWLPETLDALPTRNCTQTERNSLILKVSDLLKSTTARKFSHL
HDCQCPRGVAIFCWLTAAHIVSVLKLRLGILAANQTDEPADVLWVETDVAVFLERYYRLD
VQRKKGSRMGTDDSLVLLLQEPLRPSLLHLAASVLLVAL*
>TCRU_9418 hypothetical protein, conserved
MLMAPVTVGRLELAPQRDRALPSSDGSRATGSPENESAQDEKLKVAESSEGGGTEGGAQP
PTQPAIGGRKGSLPTKPAAVPGRTNKTNSGGRNRRKGQKGLTADMKFHGQRMAKVAPKHD
VGLNTTSAQVPGDAPQEESGGEVAVEAAGGDEAERKEVAARQDTVQHAPSPIYERPSQSS
SFSDGSFAALDWKEECTVQEIFKQPPLSVAAEKTETYRRGDKAPAAEADNCTAFLPAAEF
NAAASSTTTNHNASHLNGEDAGPSTEEVEKKNATTKPKAHQPAKLPPQPTARVQEGHRHR
H*
>TCRU_9419 hypothetical protein, conserved
MLAAGQLLMKDYNVTMEMFVQESDAYVQDQRLLRIIFNLTEYQVYKLHHEGVFSLEQWRD
YEGKDTVTLIARGKLNAALTQIVKVERREAEMKFTISTTIVDVLFKGGVRVKEKKLNDFL
TMELGGRGVVATNRDVLLEEFFKDPTRYIRDKGALEEMQMTDAYAGMERAVRVK*
>TCRU_9420 small ubiquitin-related modifier
MEENHANDSNNNNGEAGEKPAVKSETPLVSIKVVNADGAEMFFKIKCGTQLKKLFDAYCK
KQGISRSSVRFLFDGSPIDESKTPQELGMEDDDVIDAMVEQTGGNTF*
>TCRU_9421 hypothetical protein, conserved
MCLRRVGVRPPLFLTLSVLHSAVFTVTPITVAHARRGGGSASNAVTRSVHLPRSRSYAAF
RRLLSNMQENTSHGKACGGAEAAIPFDEPLAANAALLEQLGVMDLAERRKHPFATFTTAT
DTNSMHTSLATAITEACRVGAACHLSSNFIFRKIAAAIKKDDGNAEWVPLMAAAVLLRHA
AEAINFKSGLLQRYKNGSDAVPSRHDAPAWPRSDQGELARLEWVLFQEIRRGYEILTMLP
KRRKEFVEMQYSKLKENGGIQLALNLQREYMDELRGRIELAVALQDGRVAIDAIETLFTV
YEIAQRLGGEEEIERVRADLTRDVCTAISAFCSSHDFTAGCTLYEKLIAMMPWPKHPAST
ATDSSSAQHEVKSDRHETTAMEIAERLRLLTALANCVGMDVVHFTYVQDAVVELFSNTDV
GYLPATRKISQESLCAVLRALSRVTLDPQARMSASQSFFCAIQHNSQADVFLAPEVTEAL
LQVASAARDGNVALLLYNQLTAPRVHREDAPANIIAILLAENDALDDFTRFLSFVGLRRR
VMASSAVHLLAAKLLLQRKPSNVLYTVLEMIEEKHEVEPQRTFFLRLLVFYRDLQRQTTM
DGSSVAIPRLHEHALVILGEWRETLRRTGVRTAALTTIQLLQQIRQHLVGMVALQEDASE
GGMGAVSSILTCIEGMLLDFSLGWLNHCAAASRTPQYHVTSAELRRWGFGKTNETNDTCR
SGVVVKTLSHAVMWPGTIATIPLEERRVLLRKAYDVLYSATKAGGKFVLGFGDFVRLCWL
EDASFLPSDTNTAVSPSCGDAFNLSLDRLNSCVPPVYVTDALGETILHENLSNLLSSSSL
VIQRDVCIEGASADEPLRSRHYGFTEEEWLSRWLDESSVVLHMGRGVFEHQLELLLRTTS
RTQGRQCEEESCGKSPAVQCFVSVA*
>TCRU_9422 hypothetical protein
MPKAFKVRNEASRIAIVEFLVDKRVRFLEYLCSLHQDEVLWMGTVRLTRSDVVRSFRGSG
NSHGEWGGTTEYRLRSTESIDMQTSSASGHEHTEDVVVSVGPVAGVPYTVPASWLSTRMP
CYVCLAMSLADILHIPLSVFDFVDCVYAMLLEMDVRFASGATAKALAQRNLRSHRQQHHF
QQHTAFSTESMSFFGGEHSNSTGNTNSGGVMMGAVGGGFFTMGASDVETSVKYLYLNLEH
RAYMTPTEVRYEEVIIPLCSLLKLTYRRLGDYDVARNEESVKRILSIDRRLQHMFFSAIS
KELGKIARGKLLQQTLLLSTSGLFAGLGGSTHDNTTGLLRGLLGLSAGAVVPAMAAARSG
TTSGSVKRGMPDMFLVDSEEELEEEEEEDDEV*
>TCRU_9423 hypothetical protein, conserved
MAPPLLAVRQFTFRHELPCTEDQVGTGNCETNKNLEATTAIPIARVTVQVLSFNRRCFWV
HLSESRESSDAPPPPFGPCAVAFDGVAADATSSILIDDAPLAVHDEEGESGAGAPNPHAA
LAESLSQRLANRLKKECASPGVAVYVACGFAGEKVELWGTPAGSSFDVTMRFGAALFSFV
LELIREEVLSKSKA*
>TCRU_9424 Cytochrome b5-like Heme/Steroid binding domain containing protein, putative
MPGGVYTSAEVAKHAVKKDGWLIINNDVYNVSKFYDDHPGGRDVLLNLIGADATDAFEAV
QHSDAAKRLLAGLKIGTLAQADAKKYMRLNDVKERQRKATEKTACWLVIANKVYDLTSFT
ELHPGGREVLLCEAGTDATLAHEKIGHSEQAKEMMKSYVVAELHPDDRRSTTSTAKESLE
KNSNSVYTRAKDTSVRDFVLAQIQLMVFLSLGIVAVGFALIYV*
>TCRU_9425 histone deacetylase 3

MPKRSRAKKQVGRDTRVKTEQVNGASEAVATICKVGLETYIRNWMSEADGARPPPPSSLP
SLTSFPTILDVMMGMSSPSTPEEGAMNATGPDAKQKDGRIGRSAEGTGVVYDDVMLQHES
TDPTDYERPGRLKRTLEHLRAIGLLQCCRRISRHVARTKELRLVHSIAHIDSVDQLEVAA
LLRHPETSYSVGQDLYANTSTSRAARMAVGCVIAAALSVVRGEVMNAFALVRPPGHHASV
NEASGFCFFNNVAVAVRVAQQELRQRGISAPRALVFDWDVHHCDGTESIFYEDPSVVVVS
IHQHGTGRGHVLRKAPTVFTDTIDLDALAALMEETTGEEAASNGDNGHNASVGGDDWHQH
QTKEEEEEEEEEAENAEKVQRQNPQLSPEEEGDGRKRAARRKPVDYVKLAADLEEDDEAI
ARMFGISPEDLKKSSSSFSMSKSSDGGGGGSSGSRSSSSHFYSAHLVQKNLPGDTEGLSL
DEEIDNDKDGKFYPGTGHVERVGGDTRAEARGKNINIPWPTLGMGDLEYLQVFLDIVAPV
VREYEPHIVFLSCGFDSAAGDLLGSMCVSPSGYYLLTKAVSALCPHLVVALEGGYNLSNV
ARCSEAVMRALLESSGTAPLPRSRMLWCQTEELVKRVRQRHEGYWRCFSHPE*
>TCRU_9426 Concanavalin A-like lectin/glucanases superfamily,
putative
MFNGETTKQGGTWVPKKEHQVALMLQGNKASVYIDGKLLGEEEALSTDERPIDVADFCFG
ACDFGDDDDNDDEASPEKPSPTFA*
>TCRU_9427 hypothetical protein, conserved
MPGNQASAVSQGDSGRRARPESEGDTDQPAATHTRDEEAQRPQWIMSSSVKDILLEGSTL
RNKMKLNEFIRNYFGGRGVVDTNENVSISVFVLRPTMFINDNEILGLITASSSYRELKIE
LDEREILLEAINRLHHEGVDFLGQWRDYQGKDTVTSAARRKLNEVLTQVLREARREAGER
E*
>TCRU_9428 expression site-associated gene 3 (ESAG3)-like protein
MVRFLASRYRYLAGGGMVGRVWAFREAYKAYASLLATSDKWWCDQSIWSLLHVWSVTRDT
NVTADFRIRYGLLSLDYNNSFFLTPRSGAFGSPALYHFPGPPYFWDKMPTLLNRTTWVDW
LRYSPDVMNETRDFVQNATVKIYDADRKAKTIPFPEVCSLDDVLNPEWLALQLSK*
>TCRU_9429 hypothetical protein, conserved
MLRSALSVTLCQSKYVKRRQPRRATHHAMSSTKLGKGRFDLAEALYRDRQRVENNRTLPW
HARMKQLRSLLWKFFLAFMLFWSWLGTYVVPYVKGMHSRELPALGEGIRIPEELQQRATP
MPAFMHRANGEKLHK*
>TCRU_9430 hypothetical protein, conserved
MHLEGRRPAVAVGQRVRRCGSLNIVVTGNTFSDALLSPEGVFPPHTNITINGNRFTVTRL
IFRSGLAIDRPSCVAMNELAISNDSAVVLSGLVVSNDSAVVLSGNVFQTEMASSSAIHVV
RSALRVSCTLCLRCWATCFI*
>TCRU_9431 hypothetical protein, conserved
MAFWLTGVTCVSADHLQPVSSPKEEADGRDAVVKQGEEEERHEHAFDRNGKSECRGTMHL
APLTRTATGTVAWLREERMLNGSKGSNRTDRVGGVHKPSTSSASRVPVHVVDETVMCNLV
PLLPRTHAQFGFVSQIVPCTLWPLPHDDAPTTARAMSLQHAAALASELHYDSLRRLEAPT
TFLSSPTASPGALVEWHSGGVGYTTDTEGLWEEQRVVRERYYHLPPFFMDDDTSQTSSTA
VENADEGNGDGVDDLRQRVVRLRTPPSTLTGAVREQLHRFCRLQQERLLRNDRSEWVLCF
ARLVTITYELNAVLEQLITQRDISNANPMATATHSLSLAATDTAGCCCDCGCVLPTCDAL
LDEIFLIGIVPNGEPHRLSLVSPSEAHRILVEQQRKTHASVDDGGGNLAETTAGTAEPQQ
AIAESLMDLMTSALRESLCRRICVQYELLRILRVKGLAEAHRDLVLQYSRWYTSVPTPLA
VLHLFAGSTLFAPLVAQRWPNRSSPRLGVMNSEVGVKRKRGEDEEDVDGVDEEDDVEEKG
NRNIEEERDEEEEEKPHSTSLSRNGEDPNLVADVVMTTPTMGVPFEMDLLDDDYPARFAA
WMRRHGSGNAGINNNAGSSGGGSSSNHGGNIGGGCDEGTLTTTVGWLRRHRRTMTLKEIG
AFARKKH*
>TCRU_9432 hypothetical protein, conserved
MESPRWLLSNNLQNSPRAPRRTSPVCIWRNARCQEEKLSILSEKKRGVRTICPSSCAPGS
GGTRQPSAKMFAAVPERVVLSKSSPRALFSRRPDNSLRAAPPTSANGVAGGGSDASHVKR
DELRRAFPKRFIQEKIEFQKGFLKQRRETPKSSTPRRREVSNESMQSKWQRLFSSMSNLQ
NKNNVASSSRSVGSAMQCVSPRMISPPSSVGNCGRQSSRGQQKNDVLCPGQTSPSSSPSD
GFTTRSMQKQLIRKQSIPIPPARHGEKREPETDRQHLLCGSETFRLNSGRHPSQQSSRVL
SSSPSPNDVFHDTPIQTGLHSGRRGYSEIRVLDRSPTLSSGRSSQRPLSHSCPLPDRLLA
HRSTLTHEFDWPLLRSATSSRSSHLIRRNAPIKPMRRTTEREVLTPQQFLAVHLPSCEFD
SLLSCVKVQRSASVANGNDKDADSIREGDYLFGCENKPVLDIDTLVKRVQEALESGSECL

EMDVLRGSVPVVVRERIRV*
>TCRU_9433 chaperone protein DNAj, putative
MDVHFRVLGLPRGCDEAALKKAYHQKALALHPDRNPGGTEQFKRVNEAYEALCVHFRRNG
GRDSANVSTATGVGAGRPGARPTAAFFTFKTHYANAGSGFQYARHQHTTEETTPFFTEEE
LFGSPPGGFTFDKRYSRAKCFTQTGSRKANNNNSSDDYNSNSNNNKNEFNARSYGGGTRF
GTSQMYERADERWRRAHGDRVPVSGYSTQNGAAPPPTFPSAYQQNQQQPQQAPRTRPAPH
SSSFTAEVNGGMDGRQQGESVRSKARESNGDTRSQKQRDGREGSRTYSHFTNDIEEDYAD
IFDHDSDESNAEGDASAFASTTTPVNDILNEFEAKQTLHEMRREWERLKKEMDRKMPGVS
ATGRNPWDRKGGRDANREEDYVVHERTPSMREDEAFQQHIRQQQRLNESHMRSIIGEKLQ
LKKVLFTQRYAPEPADVALMSDSDVFVLCELLSEVGQRMKKVLNGRMLKGLCSRCSAAPK
LQCNTIFTCGHTSVCAECALTCGVCPVCAAVRCS*
>TCRU_9434 hypothetical protein, conserved
MAAPHPHPLESVVLRTELGRVCALPRQQANLLIRHFVRVSRAIPPYTAARCTPLVPGGWE
MDRPFPPYELDVAIRDSLLGSAPSPDDMLDEFLHPLGPVARGTLRTMIHNSFANGSLPED
SMSGSDDGDSSSPSQADISWLPLSSMVKKSDGEDSLGL*
>TCRU_9435 zinc finger protein, putative
MGDGQHTGGLAFLAAPQDSLRYSEGSDVIHVLIYVSAARCQVILVTVSDGETVLMLAKRL
VDVHFRLGRGSLKSIRTAAREILLRKLRFSSESIVVENEANASGVASHCEHLFLSTLSAS
ELQHAHDGDPMEGFFL*
>TCRU_9436 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSVCAADITLTEPQTERKGASLPSTTPETRSETQDAADTSQL
RSPEEGSSLDPENQVDARGKDTSPPSPAEEGAIRSSGESGSRSQDSGAAEENTASSLPPA
PPTEPSKKTETNPGDKDNSMKIVTPEDTSETTTSTTKKAPTTTTTTAPEASSDTAMSTET
PTTTTTHAPSRLREIDGSLSSSACVCAPLLLVVSALVYTALG*
>TCRU_9437 hypothetical protein
MPTGPSVTLQKVHGITPLVTANLIPLPSTTGSPLAGKGARPSPVSCETLSKTPTPSSGAA
ENASNSHLKNGSFTSNRMVALGEIFTEASEMARTGDLTERRDPCTFISKRIVSNKKNYIP
EVCVSWPRFAIDDDPRIMDEATSRKGGPQSIDGTPSNSFSSVIDECVAVRVPCHDDHFKQ
GHDIRGIKSGSLPPTKALELTVTVPTREETNPGLHVPSFNTISSTPHPSRDK*
>TCRU_9438 hypothetical protein, conserved
MLPSSSHRGAEDAAESLATSAPAVALNAIDALSVSELRAGMQQFLRSSGALGSLKTQLRS
VIVSELLKRRGPSQKSSAVRHTRDAEHEEDEVEDDGWTQRLADALVEGHLRHTGRSFSLA
IFSSEADVSFGSSGDDALAGMLHLNTSVALRRRTSLLHSVLEIYLRQMGDKRGQPPGYAV
GTQTDMCEKELSPPPLELRLAAVDAKYALSFSRLRESTREEVDRRMAVYREELRVQMEQG
YQQRLRAFEQQQLNEARRAAEEHYGVLLQHKMEEMRELERVSVQRIEAERARLGQARDDL
EIQRVELERRHRDLHGLLEERDKAIAATEGRLHDAKQQISLLTTQLRKYEELCGVRLAEA
DAARDREWRRVEDLRRLQAEHLAELQLKDEEISRLRFRLKSILANHGVTSWREEAGEEGG
REQANTIREAFTRANAFQERFSAAYHVPSQQKQQASETWHSTWQPTVPPELEKAVAVDVK
SHSTEPQVVPQFKTCVSASHQEQQEEEQQQPQEQKKEEVKETIAPFSPPNTTLVATVAEP
VKTATDSTSPHHQLVGMTVSSQEFGGKEGNGEGERKYSVGEEHSSSGSCKKGGKVVAVMK
GTSSSSSFSCANPKQSRDSAISDDLKIQSASSSSPNSSVHSSSLKSAPVGNQASIITATA
ATAPPIEEGRDALYEEEKRGRTVVEADEDTARRGIVWAFKAQHTVLLQRQTAERKERYDD
GGGRGTSLDTYIAQARQRQQATESIMITRDSDDDVDSDILFGKRESSEESF*
>TCRU_9439 nuclear cap binding complex subunit CBP110
MRVPEINDENVRERGGEVPFSFLFSSSQSGAAAAESAPKTPDQWLWYFYLTAWSRPFFPH
KLPSRPLCTGEGNNKNGKEKGNSRDVGLSFEESLALVGFPAADLVAAYDAQWHQQSQTSE
AAELQAKSLARVGSDCMYPLIPRVVESSFGRVFRALAVHEYLSAAASSSSLLTSSSNSVE
KLVQKALGVARQNHQQDAEENAGKIVTEEKAIESALQEMFSPDAKTSQYPLLFTLEGTTP
KDGSDGGTTKKMEEEKEFIKEANRARLFAALTVEVFSRVKQLCACMLLAFVGAIGGKVAK
ARACGVVVGIVEYAIAYRCYREDGTGRCPLTAAVLLLCSLVEVQDTVTRERVKEVGKEEK
EEEEGVSGGLIATIIVASLQELLFAAVLGGPVAPHRLPPGVAPGAPKSLGKTSAKKKQQQ
QEPFFEWTVRPVVLRALALHEVDALLQVLLPVLLQQVGFEWPWSECLRRARLLEKTPQES
VTILEGVRLSTRAVFDELLAAVGRRTYVSRFQNLLPQSYESLFVAAFPAEVETDGGAQND
GDGKGNENAQRPLFILPKYYKAAGEALIAFLATSGLSGTTVRETERVLVRNTDVQPMIVQ

LQALGRRTDDMDDNDEDNQLTEDRNLLTTVRLSDSEKQKLLLRYRCEVLLASIVVYTQLQ
TLSLVQQLVRQLAPLIEKLLLPLMQERTLRRPFVARRKKHSLIDDGTLDEGNIEFTPEFK
VLMDDIHYEFYPLEWIPEVLNAQLTGGSSELDASKLAFYSVFAAVAYQFGIVLHGGPHGL
RGGDDTDYKGRVKAYRFFHVLLLNSLVDAVASSCELEGAMALAATRRVGGTHRQNHGNDI
LNDENSQSLLAQRGAASFHAVVNPADVIFALAQCLLPPKLILSPKTAMLGLDDENQRPCE
GWLRRVIEWAQSTRTQWMMQRQNVARSTVPLVFLPNSLTFDAVPLAREVIRGLRRRLVEK
IHVKKVVSTTGQCSLSDPLLQQHLLILQSLLETLALLPQHSSENNAKMFSAAELLWYSPL
FSCELRLSGHFST*
>TCRU_9440 MSP-B, putative
MCHTLLFQVLLLCCFSGSVAVAEHHCISDEIEKKVGPRTTAVVLELPTRGGGMLRALTAS
APEWAPIRFKFFTEDLKDPSKYCTAEGQIRPDFTGETFECKREDILTEEKKSIILKSLLP
RAFRMHRDRLLVEPLTHRIIVPKYSSGICAEFTIPSSHHILGVTGADMYLYVSAGPTEAS
ILAWANFCSELANGRPVVGVVNYGPKAVFDSVYSVRVTAHEIAHALGFTVDMMEERNMLK
VVKGVRGKAKVLQVSSPKTVEKTREHFNCMSATGMELEDQIGATTTSSHWKRRNAKDELM
SSLSGIGYYTALTMAAFEDTGFYRANWGKEEPMSWGNNSGCALLTEKCVINGVTKYPEMF
CTAESSLFQCTSDRLALGHCTLKLYDAPLPPQYQYFSNPKIGGASEHLMDFCPYIEKYDD
SRCSNGNATVMRGSRVGPRSKCLKGDGLADFMGRIGDVCAEVSCEKGEVSVRYLGDDTWH
KCPEGSSIIPADLFTRGRILCPKYDDVCTVIDACRGGGGVSSLLSVFPLIPLILLVLIFM
SIC*
>TCRU_9441 RNase H, putative
MIPRIRHRRKTLLVVTDSQSLPAALNKGPPSQTDWTEDQIWQRLLTLTRAGWSVHLQFCY
GHCGVHANEPADQYATQTTATGQYTEHGIAPIRHTDLLSCINTQPTNKWRSTMHHDTHHY
LLGGARPSDPGGNDLITQEALD*
>TCRU_9442 hypothetical protein, conserved
MGPRCLAHQLFVQLDNKFSVDVDHVSRNIATTAAEWAGGCCVLYDSDDVLADFTLLRVSD
VTSVPRRVAEA*
>TCRU_9443 hypothetical protein
MTDALFGLSSESRTILDRYLQWTRLACDGLKRGVHLDASNHQVGNIIQETYTRDELKDII
SAHTEVLLHSLEARMEGFAAASAELLCAVLRDADRQRVTIGVDANAVLSAATATASAAMV
GTTATGLLLDHERKVLGGPRGRLAPLTVADADVEASRQLTEAKEEIRRLQEKVHHLSDAY
AQVMNTRDALNSHEAEATASQMALRQKEQDESSCQTIEELRVALAAAKQDLNARLNQSTQ
YREVKKILAQKNEQIRKLRAHLAQFDPAFLQNDDGGGDTIVEQDD*
>TCRU_9444 hypothetical protein, conserved
MGVRSAGGGGTVVLAGNVGITAILAGLAIVLSAVTYIANRRRTNEPHLPGHVSLRGKRAV
EERRGLHGNSNNKTGGVTGTGGGGGSASRQTGGVGGGGGGATTGPKSYCALRAERHVGQY
NANLLEWRDDVIGVRMLFSPILFAVETEERQAPLLLVALRYLRQPEHRVAVIIESCVTAA
TAEEYRDGSLARIRDCVKLLSCGTTRIGVTSHPSAEYCYMDAGNNLRYALSVFLTHGNLA
VTAQYVADTRVKGVLPTAFNELVRSIQLQSPRPTPSYLLCAEPRLGLGFRLPLDFAMDDQ
LREALVVSDDSLVKSVGFEGSHGNSNFVNAGHHGVSKLLPAELMSSKRSLRHSLGSVEEK
TSAGIECGTPFAAVAGCGSRRMVVVACYEPPARGRVSWQLLFERLLRTTLARFSAVQGGG
VRDDGEEQGKGTAPISVVWCAGEQELSRKNDKFNTFIVRPQQLVVPINGDGAVDDGTSDT
LLLDGSFCVQEITLDSEGASFPVLRELLQLQCEEEGEEEDKKDVGGGPRRDEKKKMMEPA
VFSAYLSVFCLRIRDECVSISFLSSATRHTLGEFITFCHRTLDTVSVGNHFGQSTSIIYC
NTRHEVMPFSILLEPASAGGTTSVLVEEPIIGDPLALIHVSGLERVKVLLRVFPFPSAPL
TSSHSQRRMAKRLEKIVQNYLSQLPDSVCVHHLGTTMLGSRAALEIHYEQMVDDDDSDAG
LLALDEEVGHINPFASYWGTSSYSAVGISAAESATKSTFSSFAPAGAPTLTSSCSVDPLL
LRSSSRDSREEVASMRVAVVLCFEGFGFLFIASSMDYSLNAVRQVVRQLAANVSVGTGVP
T*
>TCRU_9445 hypothetical protein, conserved
MGLLCNASIFALMVLPVFLLSKGHHVEFRRLIALAAIIVSCMISESTLLGSLAGVPPLQN
LVTVVVIPVFDTLLMDFVLNDPKARKVLHIHDAGDDAAAVLTALWTAVDLLLYRWFRWYH
FISGLGFDAENLESAVEAFVDLNARLLSSRRINGWSHNSVKSNSKRRAWIGVAFVRVLTT
AVGVANGSTLIGNVLFTAALVLMQLLLPPLPENGSREE*
>TCRU_9446 hypothetical protein, conserved

MEALVAKAVERLGKKKLWLVVHTLRRVNAADCTVAGVREALRGIRLYVEDDKFAEVAAQF
VGKDGATFNVAAFVRAFLATLPPRRQYAVSLVMRKLDPESSGFVSFDTLREMYDVMRHPL
VLKRADPSELVDEFIADFEEAREEDGITTDELAAYYVGISHTTLHDEDFELRCIRSFSLD
RPRARLDAESSTSHAGKLRSRTLSTYNAAKHPLYETTSMGYGKDCEKVKYDGKFSLKHCF
TKHAPMQRGGGATSMNM*
>TCRU_9447 kinetoplastid kinetochore protein 13
MAECFCAELILKKGPETLQRRISLRIPKDGTPVTVGRAPENDIVLDAKLVFASQRHCQLF
VRPVMVTTSDEDAVKEERKEGEEAIKSRRQKRPRVGRDALQLELCLVDMGSSNGTFVNGV
RVEENAVTPLRRCDMLVFGGMRDIAVGASLPVDVVTCAPEIVTWCVALNEGEVNVDYVAT
PPVVLCADFVEAEEKRMALELLRRMTSPPPASHRFTTAMTPPPTVLKRWKEAQSGQEEEE
EHNKTPQKPSAREVVLRDYADNNNSEKNEAANAQNEIGASTRRSGTIAAEILVHGDTVWN
ATHPFVILRAVRVGMHNFFLSRAKNAARKGGRLRIGDTRKKDNQLSHLYTLTLTETHWKW
VMNNAVGSYTGRGGKVTNAKQQSIVEYQLPWPYVERIMYCESQYGLTALLLPPDVKNLLP
PLAELSVDSAERPIHVTWMVDPAKDRNKGKIETVGSAPVTFQQFLRELRHICARNKAPEP
QPLEESEFLDRYAPDL*
>TCRU_9448 histone H3, putative
MSRSKETARSKRTITSKKSKKAPKAPGAATGVKHAQRRWRPGTVALREIRQFQRSTDLLL
QKAPFQRLVREVSGAQKEGLRFQSSAILAAQEATESYVVSLLADTNRACIHSGRVTIQPK
DIHLALCLRGERA*
>TCRU_9449 histone H3, putative
MSRSKETARSKRTITSKKSKKAPKAPGAATGVKHAQRRWRPGTVALREIRQFQRSTDLLL
QKAPFQRLVREVSGAQKEGLRFQSSAILAAQEATVSYVVSLLADTNRACIHSGRVTIQPK
DIHLALCLRGERA*
>TCRU_9450 histone H3, putative
MSRSKETARSKRTITSKKSKKAPKAPGAATGVKHAQRRWRPGTVALREIRQFQRSTDLLL
QKAPFQRLVREVSGAQKEGLRFQSSAILAAQEATESYVVSLLADTNRACIHSGRVTIQPK
DIHLALCLRGERA*
>TCRU_9451 hypothetical protein, conserved
MALKHPKRQRPLCLFIRRLPHDITEVKLKGIILERVGCGDVGDMIDVSVLRGCPRRGDRP
HVLSTAIIALCPVQEGDKNVANRVVEVVKEIFDGRVVFDGGDDVPDAMASVVEWVPVYFG
ISAPIRHGAAGKKTKNIAPLECRTGNVEDDEDYKRFCAGLEKAACETQSEERMEETQELG
CEPTPEAAPKSLLVQELLAECGHLKKVKMIKTKRKEKKKEKERAGKRKRTTTKEAAKHDK
KELLKKPPRQSKQEGNEAAAPEEFKAEGKKVRRLRIIKADEGGEALAEVGGTQKEIGVDA
ESTKARRRKRQREMKKGLRRRIKQRDKEAQVAAEAESDRGKANARRRVRKKNRQKAEGEK
TGKANTAELSRRNSKEGKKHAGESGQQKKEPTRRKNKMRARNKHRPREEGGWSSHDAPTT
*
>TCRU_9452 NADPH-cytochrome p450 reductase, putative
MLFYLIGTIVIAAVFAWLTGILGLNSHSHAKTPVKTAITEKKVSTERKEVCVLFGSQTGT
AEMFAKTLVREGTRLGVPIRICDTENYEGHDLEYEHLVIIICSTYGEGEPTDSMKAFHDW
LMDDSRTPDEELRNVKYAVFGLGDRQYRYFCEEGIVVDRRMAELGAQRIYGLGCGNAGEN
IEEDFDEWHRDLWPAVSRVLGIELRQHAEEPMEPACRMKVWEPSEEASLPFPKLASVLEP
TQRLPAWAPLTANKELLRNTTERSTRFIELGIEDTIISYQSGDHLGILPHNTDAMVNAYL
QILGVSEEEAMQVFSLQEKKTGKNVFAARVTVRTALKWYIDLAGPPRKSTLRAFAHYAKD
PAEKEALLKLLRVEPESAKEYAKLSAKLRTVHGFLRKYHTISVPLEFFLEMMPRIAPRYF
SISSDLLSHPGRLSITAAILEGGLCTGMLRELQIGEKIPVFVRKSKFHLPLREKERPILM
IGPGTGVAPLIGFLHRRNAWKKRGNKLGKAILFFGCRRKEEDHIYSDFMTECLENGTLSA
LDVCYSREQATKVYVQHRVLARADEVWDILREGGNIYLCGDAKYMAKDVERALLEILQEK
ALMSEEDAQAYLAKLNNIGRYLKDVWSAS*
>TCRU_9453 hypothetical protein, conserved
MSFTVLACTDIRGEKVNVELPFREPPAALAELYSTLEHVFRGEEKDINTKRVEKSTRPSE
PFTVSRVQRYEEDTQGWVELTDVRQLRVHDQLYVFRKHATRDDISSRRDIPAPRSSLYFS
GLRLLDVAKVDAEHGMGLNHTGNRSPSTPIIPYLSQRPGASVGTRNANRRTTNDFSNTAP
VFHANSSGGVTSNGTIVPATEHGRNVYFGLTEGLTSEQVDVVFAVGDSNQQGYLTVRDLQ
GIFHTCQIQFPADVVEDLHRFFAKEKRGEAVMTHQDFYDFAREFVQTVSVAYFRLGIHER

QKVIEQERRENSAALDELQLQRKALEERLEAVQRQITKEQEKKARLRNELGELERTNDPD
CREQEQRLLNKEFSVFQYRQKLHQEEKDYERLAAERRRRAPSMALGKLPT*
>TCRU_(mRPN1) Mitochondrial RNA processing endonuclease.1
MWLLVARAKRHPSGAVGVSPEASSAFFLEETRRWERVLGHSSCFTLAPHMQEFGETETGN
EYVTAKCSPDMAPENLWRHVMGRKASQLREKLHALMELGLLKLTTPNGDKTDPNKFYRDA
GFQRMECIGDHNWGHSVCHRLVVLFPEVNWRTLTNTSVVDALRTVLESNQHLDYVFTALR
LDEILRNCGTQKISTKLKADVIEAIAGELHVALWSLEPYDTDGISTRFSMHGATVAPSLA
IFVRVCLNELMDIILYCHMAKYNVPLVRAVVELCRREAYLMDWLSSPYYALSKSRRWRSS
TTGRPRWILPSPPPLHHEPQPQCCGASTHIAISWAYAPVPVTTPDEIYDTETVLTDGLLQ
ETKRPVTAAVERHNTWLAARELMHTCDAFRLLSRTQT*
>TCRU_9455 hypothetical protein
MPSGSSFRRQDNRIGLIGFPVQNLSPPLKFLVNSSDPEVLVQLTLASGRGFANLSGATGA
RNQPLPSFETGRSIRQEGQEEERRDSTNLKNSCQSKMMSFMFGTKPKKSILQSDEIVSPE
YHNSFFSREGDYTNEKVRDKGVLNTRKRQPLFCNQHRYALMYDMNALEMEQRMEIWKEFI
QELYILVMEQELVRWRLWKATVYSASAIFTAARNTIASFLNYLVEIDLDTSYTEYNLTEA
EGTSLSAKKNWWPGWHRVVRPWRKQQVSKKGTVAVVSTSFLNNSSCAKKNISFRSPTPRS
VIGGELGRVNAALRVHFIEYVILHLRYKLWEEVLLSNRSIIRDNMDALEYIPNISFSLAN
SQSKSIHGRWELFLGGLRSVAFSTVPRAFDLSVSLYFDLMSDVSASSQRSRQYGNATGGQ
YRGKRLGLSSLGHIVHQSAANSLAGPGGASARAYSEDDNTISVGSDIIEADAGPGEDASL
LYRSFCGTGDWVSNTPVSFLSATDPTNATSPAAHAKDHYKVKDSTLFEPTALPITCPSCS
THLGKHLALPISLEHLERHEILTCEALEFKQILRSTEQEWTWSTEILTPNLSLVRGMGQL
QWRRIRNMLLQMVEEKSIMFTRYKDELRLMGLYLDFLGFVSTLERSAMNVFYFFRFGLEK
CSGTTPSLQ*
>TCRU_9456 BNR repeat-like domain containing protein, putative
MIVGKYDSKDCLSSGAAPWGLLLVKGNVSAGDNEKGIIWNDTVSIPCNTIGERDVSWTRL
IGSGGSGVKMKDETLVFPVEGTKKKTEGAEVDVKTVSLIIYSTDNTNWKLSKGMSADGCG
APSVVEWKDTKLMMMTACDDGRRRVYEIGDKEGE*
>TCRU_9457 BNR repeat-like domain containing protein, putative
MLVTLPVYAEKVENEKGKLHLWLTDNTHIVDIGPVSGEGDDAAASSLLYNSGGNTNDEKL
IALYEKKKGNDVKPSPGMVSVLLTEKLKRVKDVLATYSDFWKW*
>TCRU_9458 hypothetical protein, conserved
MWSRTVSPASTEQGLPGASVPVAESIGTGRGTPPKDVDTAAPQKHPSPEEKWLQTGCPDR
PRESSLGGRERSSETDGRQDTPPTPGDDTLLLLVPFRFFCLPLLPPCQHSMELRCGRRCA
ARRLRFLLRDLHSALDAQ*
>TCRU_9459 hypothetical protein, conserved
MLLWKHACDCCRKTVCDDCAPKVNGRRECRACAAKAKEQQSRQRNPSNPASAEEERAARM
RAAEERMRAEQQRGRPQSRGVQRPGPPVTAPPKEFSLQQDRDYGTPSPSPHAGAPTRANA
EENPVLAAALRRRQQEQLGMKANWENSSEKTRLLTAILEVLHQRGEEEPFGLRSMDEAKL
QAYLRYVKNRDKKSGSV*
>TCRU_9460 hypothetical protein
MEKAFEGAKRRPRGVQDLPHASAYSMRKTHGRCVPQSAPENERRGKSAEAGKTSGDRNCC
GNSANDVAGSKTAMTKVGAAETVKSDNIEEILIDSPTCDDDNPDTSSENARAGDCDGGPT
LMELAMWEAEVTRRQAEVARDVGCIRNSLAVLDAYMDDAAVNKHSTGPLEKVPKDMGVGN
KREVVALKMSPKKAIGGQTAVAKDIVLSSDGDDDYLQLTPSRGEKPPARAGGARTVPNKK
VTIDVTDL*
>TCRU_9461 hypothetical protein, conserved
MNDVQIGVLVAMCVVFVVVASVLFFLLRLWGCRRRTDRKRADADPPKGGEYVLHFIDFSG
TPRSFDVRAMAITDARSLQSALAEACGLPDDTSLTLLCPNGMGQHVEMDLNQLVFPDNQL
ESRMRHTEEQPLLLSRELSDPQSTGTVRQLVEPSQQNYYNGIDVSYTRSSSCVKNAGDVS
HGPDTTGDVPPPIILPLCSRIGSATPVSIAAVRYVVQGSDTLLDKDAAAFVEEAMMGSTR
RTVTLPCGARVIVLPSERAAWLLDDYDRNVGVPLIREAAEVVQYNVGNMGSAQWRPYKHP
IFLPPGRWCICAESSTADHRFVETASRVFTVDIVPRKR*
>TCRU_9462 hypothetical protein, conserved
MLSALLSEITAAPTRTRQNAELETALEHHLSELVVQHRLLKAALLNLMELGQQTAVGATP

DADAVIFDKITSEGGTVLTCGITLGMTYLTTALILSGHAIESENAVVVLNVVECHLLSSA
STAYNHLRGHNYALQRFEQLLNGYVNILDLRDPMNYQRKLFYLHQAAVSFSPSPEYLSVA
HALLVREATRCRCPWPALAVMRQPILEVSPADTGAGLACFHSYYCSGGLLLAAMQCWEDA
TVWLRSALCMSKNLQRKSALEAQAEVAVTTTATFSASPTTALGESGEIRDTLLRAAKAFI
LVSIISQGDLHNPADRRRAQRVMQQFRGGNADPYFRLLSAAAKRDGKLWGTLEKHFESLW
KQEGMAELVAEAGLRLRRHVIRDMARVANRVYISDILSALRTHSLLEMGDVDGAKEIPAL
IQTLLNMQEEGELLIRLENVHPGMMWEESMTMEEEGNDMGVKALVARLELPPKRIPAVLG
TRRLGCGLLSLSDVDIGKKQRYEQVQLRCAMEERIRRYESARAALMRATEEAGIENAQLA
EDDSGR*
>TCRU_9463 acid phosphatase, putative
MGGRVFVPIILLLLWTHVGKFLELTVVAAVTPVDSRQPHPHGTAAPIPDVEKTPEIQRRR
DKVGESELVITKLFVLNRHGHRTPNAPYWDYCPRDRKNRRNYDVYAEDLTGLGMKEEYEL
GQYLRQKYADIIGDRFNRSLHFFRAVGEPRILQSAVAVSQGIFPDGFGPGGFLPNRPQFV
PVFSDMDTHEYLLDDVPCFRRAESDVKHWIKSSLAEFVADSNVAEVLKYMRKVCGTPTKE
PNSLFAYIKIVADGMIFNTDYGLSVCGGSITPEMLFRIRNVSMQFLLARLYHTDEQQTYT
AVDLPYRFLRIMKQNSPPSGKKLNDFVDTRQESVFYFVHREALYAFAGFFGFMYNVPGLP
RNELPVASTLIVERLERNHSLRLDKERLTYVKFILKTPYHGTSTIQIPRCKIPQLCRLDE
LQHIYDQRVARTGTWEKLCNYTYSEIDHDTDIR*
>TCRU_9464 hypothetical protein, conserved
MDPSKRICLKNIPPDCTKREIAEFVRSRSGAQPHSIDLGLDREGCIRRYAHFSVEGTKNV
ISVLSGAVWREVAVTALPAKPHYMYRLAEARRKRERQEAEERGCVEAAWKERTARWMEKT
GGELRNEKPPKSFYATRQRYAAVASEIARKQREEHRTKRAASLSSGGCGMRNHRHQKEEE
VAAEEEEAPEKRHPRQRGTTRNKSNLHYKHSRGEGNVPVRREKKPNTEAPVAATQKEKQQ
PTGPSKEERKLSGLQAKLAALRAKMK*
>TCRU_9465 hypothetical protein, conserved
MWSAAVDFVRTISDRITGALLGTQARIIEFFLIWQYGKQVEGQRRMRLRHLRQQQQPAAR
NSQSTDSPRTSHSDDGEVDHRQAVAGLTLLGQRVPNLMGGYYRQKLQSVYGRPFSMLAEV
KRRREQITEDVWLYRLNVRTSPTTRSVEGSTESATASHSGPHTKNAHAQSSESDDIPLLV
WLVMPWECESSVTLRFVFRLAYSLSCDAVLVKVPMDGTSGPSETVKLLFDALKAGKRKTH
ARRILIGGSELAAMFVLLLLERRCPLLQVGAYAAADPEVARRAFCQGVILVDPFVGWETS
VPPRPTTTGRSSSRGNAGYFESRGRPPPNAGDVLSAKDRFKQVVLSSSGGCIQQWFPSPI
TYEAPPIVVLVDEGGFWLREQCDFNARVDRCGAEENGERVFFLPYTIERAAAGTLVSLSC
QMEIERLCRMVEKFLGELLQRKEPSTASTSSGDCQQLRRDDGEVRSRLSEGEATFLAGFV
A*
>TCRU_subunit B, putative chromatin assembly factor.1
MKSTSYQPIRVRTLEILWHGCERDEEAVQLGLQSVAIEGIVSIDYNTQQDRIVTCGGDGY
IRLWQLNPEATDSWLANSQSDMTACVSFVTGMRTSWMPLTARWSPHGSMIASAHCDGKIC
LWWQEKREDGKKEEEWKDYRHLSGHVIDVYDLCFSPDSRYLLSAGGDGSVVIHDLEGSTV
PVVQLTEVHHKFCRGVAWDPWCKYVASFGGGPPLLFFTHTAKTTGASRRVHLTGQRKAPG
DYIGESCATTFRRFGWSPDGSLVAVPYGKASHHSNSQNQHHQHKNNNKDASETRRGDDMI
HCVYVYTRNALDKVAARLTIRGYSEVRGVLWAPCFLQPLDEEDGDGDSDGGNGSGVEKSG
RIEGEREGARGGEETATNRAERRRCALAARGSWGPDSYRMAMAVWTADSVVVYTTDSDVR
HSDYTDLHMRSISDVAWSPNARYLLTASLDGYVSVISTGGSLGIAHKLPLFSTESVTVGL
CRMMSEIHSLGEKLETGGRSAANSATAAKTSSGGGALLHAPVKKKRKLAEEPQKRQQESV
QTSGAIPLSELSELMENI*
>TCRU_9467 nucleoporin interacting component (NUP93), putative
MSMLHDVSGGVLTSKNHLKTAAGVATDPGGDVRGNIARITARARQLLADDTDTRVVRNGL
SAYETSRKVAADISTRARTPGQTGPTQASVELFMASLGFNLNEQQRLLQQLQANQLPLTV
TGDVGTATKTPGAFFQEQIDDELGSTLESFVANRRNETMRRSMEEMHHRVENLVQERSAT
IIRSSWEKCCNEVADAFESFSLKACSGGGDVSRIKMSTSSLIPGGSMRPRAGVRALLNGR
DATSIRILNKIAGFANIVDTQPPLQWIRCFAAHVADDAPSVTDDIALLWTTVEQIVQPIL
QLGSASTTLTFVASSRHMIERKALITVLSRILKVEPERFGELENMHATRVVSILERYTSS
SNPWAHIYTAMRCGRYDVAAMVANNVGLRSVEKKLEEYANAHMTRRSTLPPAVELRPLYE
EEDTRLDPYRQIVLFLLLLGNTGENSEVVLSTVASLSSKVARSLEDTLWIRLFCVRSIEV

RGNNKVQSLTEMQRLLLDDMQDLVELVRGDVVRLASLLIHALLPSSGLRLLIEGDSTYVD
GIHLAMCFHNSQLLPCDDVEVPIDLGRLLPQYCSLVLLDVDKRHARIAYAGAAVFRYFLR
TNLVDVFVEYCGNELVCAKLFGHRGGSRVGDDGILLQETPSTELLEAMERVAEAGAARGQ
TELAVHVFSVLERAAALVRDEARANYALSRALQIICPALSHAFQQQASRESTCLFMHAAE
LQERVACSERVIPHAYAEAFQLLCTMSEFFVSAARGEVEVALRCFWSLPFVPTAPDDIER
CAEIFDSAPESVATAAPPIVLLAMQNMLKLAEVLKTRGQTNDATQIKRRAQTVTMWVRRW
KRHVARSLIDELASLEELFAL*
>TCRU_9468 small nuclear RNA-activating protein
MEKQLDIIASDFAALYHEMVKHLVLTPHGLNMDAFQAVFDRMHVEYLHYAGSSTTQPFYM
DVIENVLQLAAAYLSLPTDVSPNSRAFGLYLVFFLYSTQPCIESSPVSVRIALGTLQSYL
DDIDDTAGAQQTVFSQLGRRVTEDERRILLALHQARAWHVMPFVDVSLHLQALLKAHDSE
GVPLVMSAATKRPQVLSTVKTDGALSKELEAYEALKRRLGLDDVFGMR*
>TCRU_9469 ATP-dependent DEAD/H RNA helicase, putative
MLRNALNCIRLSSRHYAIKSTGASRKGSLELVGVLCGGVGPSTHGMDEVPGEMKEGEIRH
RKKEVSSGDGSGANGSPYMVQISDRYGMPAELPAGASQSFEELETLCPSDTLREQLQLLR
ASRRWETLTVVQRAVIPLILDHRDVLCIAPTATGKTFCYVFPSMLRLVLHAKGLEAAVAD
SSENELSRPNVEKLLKDKIARGEICRYCELGIADVKVCPMTGTPHPPVPELLDKQLRGAM
WLNELTSVAEPLVLILVPTSQLAMQVHQLCTQLHVDFRVKFLVRASSAEEQKRHLNALEG
CDVLITTPETMLPALYKRKLSLRRVKMLVMDEVDDLVSVNHFEKVKIILGALPKGHDRPQ
RLLFGASLPPVAYQMVREQMLLPSHRFVLADVKTDKLGHALVDGCSTASAAITHVVFMVS
QVEKISKLAWLYSTGKLRPDQRTLIFCNSRHNVAYVAEQLQKLVPDLHVTTLTSRSSATG
KMGTLKLFRSGVSTCLVCTDILSRGIDFHNVVYVVHYDTPLEFDTWVHRSGRCGRHGVSG
YCYTFFQPESVKLAKPLVAHLRQTQQLIPPKLQEYANQSLVDTFKSSLFYHPTRPYRSGD
PQRQHPVMGRGMPRFPDYKQERLNKNFRPL*
>TCRU_9470 delta-4 fatty acid desaturase
MPQVSAEKAVGAGMTDVVRIDGVYYDTMKLAAIHPGGPMMIKMANGTDATRIFVSYHRRR
FPHTKYKQMQVAAAEVKCELIPEEDTPNFDLYLELCERVRPILRPTNGFAPWYYFIKAAV
WCLLLLTLDLYAVFAWRPHSLTPLQSLAMAMVGLNVQHDANHGALSRNPVVNRVFGLMQD
LLGGSSMSWIIHHDFIHHIYTNDPHRDLDLEIPLLRLHRFVPKRYYYGLQHFYFLFLEAV
FGPIHVASNFLFLWSGPQKRLLLLRDEWRLSCLLTTIPLLRLAFNFLHAPSIFDALLGSF
FQYILGGMYLAFFFLVSHNFAGVKKQGTSDGECFLRAQVETSSSVGGWWLGHINGGLNYQ
IEHHLFPRVHHSYYHYIAPIVKDFCLKHGVSYIYFNTLWDNVASTVKHLNTYGHGKEEEL
AGKK*
>TCRU_9471 inositol-3-phosphate synthase, putative
MPTVRVQGGRNVQYTEEAITAKYVYRTTRVKKESEEEVIVGPVNVALRFRTLRKRAKCGL
MMVGWGGNNGSTVTAGILANKHGLTWRTKKGVLHPNYFGSITQSSTLNLGMTSDMKEVFV
PLKDVVPMINPNDLAIGGWDCSGMNLVDAMHRAQVLDVALQDALYEYMRDMKPLPAVFDL
DFVAENQQERADNILSVQHKWEAVEKLRSDIRTFKKVHELDKVIVLWTANTERFSDHTKG
VHDTADNLLAAVKRNEKEIAPSALYAMAAILEGCSYINGAPQNTLCPGLVDLARRHGVFV
GGDDFKSGQTKIKSALVEFFVAAGIKPECIASYNHLGNNDGHNLAAPKQFRSKEITKSSV
VDDMVASNKLLYPPGSKGPDHCIVIKYMPYVGDSKRAMDEYTFSIFMGGSQTVVLHNTCQ
DSLLAAPLIIDLVVLTELMERVFVKIEDGECEECDGTSESSYVQMDTVLSILSYLLKAPC
VPEGTPVVNALNRQKQAIDNLLRALVGLPPDNNMLLECSLPSLRGMSQQ*
>TCRU_9472 hypothetical protein, conserved
MPMREDYPRYPRDVREKQIVSRPARERRLAELHLTAFPNVLNESAMAAPDTEHPLKEKKK
GKKNDEMNAAKVVMEERAVAPMTTNQLLARMVEMAWEEKHKNAASGEKQSLTAPDGRFRP
HNVSFDRSSTYRLDYCNKEVPGFHERVRVIPDYTKDWTETDKSNIENAKKLPYLTMPESL
LKKRPTVYRHDYTPSAGRDDYRTLPYNTNLQDLSTSYAYSAYSPEDPARVIKYDKAVASC
RSPRCVLWKTFSPRGSFMVKRHTESTAEELQRLRELRRLQLSKSSDSSTSPRKSPTEVST
LTKRTIVIPGMRGMGYRQAPKEGKDYIYLPRDHFCHQVVYDY*
>TCRU_9473 hypothetical protein, conserved
MGCRAQPEDQRGQERAALFCNSPHRRSDEDTADHRLCDGNTSWRSHSVRLPGNAIDRDLN
FGVHATAAARQIVPRRHQLRLAAEAGASHHTMRSFLVAYVHIALFHDGGAIFPYLAPACR
RIAELRYR*

>TCRU_9474 RNase H, putative
MSNPSHDHGASRTTKLLGMDLDPRLTLNVAASKQCAATSQRISQLRCIAHKEAGPSPHDL
RTFVIGYGASKLRYGSELIWAVATDSAKNEMQKTYATLARIVSGVPSTVDPESALLEANM
PPLHVLCLRARLSIFENTRACQMDWMRRPPPEPPPRAGFRISPLSRDELYAFVDAYTKDY
GITESSPREERFFRSSIPPWFAASAHRATIGVELPIDHSITDEEELIREKRRVSEEALAL
HSHRSWILATDGGVDVPKSAGVGILLSSLNSSEIIEKASINCGARPCSYRTESRALLLAL
EKLMIPRIRHRRKTLLVVTDGQSLLAALNKGPLSQTDWTEDRIWQRLLTLTCAGWSVHLQ
FCYGHCGVHANELADQYATQTMATGQYTEQGIAPLWHTDLLTCLTTQLTNKWRSTIRQDT
HRYLHCGTRPSDLSGKDLITQEVLHRQELVHLARARCGESELWGRLYWAVRDCTNPCRFC
NISPEQSAYMRSNNDPTASGTDTVPPSAREEDVSPVRRRTLTRLRKEKCPHCDSTLTGFS
GLVSHCRSFHPEHPPPLPELKCDFCDMVFPTRRSTAPHRSRCAHNPDATRHRNSSARRRS
LLPQDQPASTSTPIGPQETLHHLLLECPGTLAVRQRLGIEQDLRLGKFSQWQLLHSRKLL
SLLDHLFGTQMALYS*
>TCRU_9475 Endonuclease/Exonuclease/phosphatase family/Endonuclease-reverse transcriptase, putative
MEPFTWLPAERYFYPLLNSIGAYQRYTYRLRAVCDAQRQKLLLSGDIEQNPGPIAVLQMN
VYCLTPSKLATLMAQGADIIAIQETWKSSEQIASMHTGDYVLYAQSRIGKEGGVAVLVRK
TLRSKRIPLTIPQHDTGLEVVVVQVALDQNRDLIVASAYMRPPPQVTQSFRRLVNSLPAS
SPLLLCGDFNMHHPQWEPFLETSPSEVAAESLELCTDVGLTLVNTPGVITYARGTRERSC
IDLTWSKHLTVSDWSASVSPLSDHYMLTFTLHQAFKDTIPSAPKFFYSWGKCEWDLFIKD
FDAQIPAYDYKKQSTGIRALTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERIAIDSKA
RYLQSPTPDREAEMQRTRSQFFLLLRERLRNTYLRRISKLNPGEPLTWKYISGRKKASTD
RVHL*
>TCRU_9476 hypothetical protein, conserved
MQDTSIKRKAHESYDCPSLTHSGSLGCHGAFHRTRCVEARCSNRGDIQFGPTRDLAVGEA
RRPVRPSPERIPIFVEVHHTADPGVVAGRIDVKGETAEGQEPWLRAEERFFHEFNHHAAT
ITRRVARTRLATPQNEHAIPLHQVNVPVLNLEWIKSRLNPATLESLMQVWGLVGRSPFPP
SSSGKAREGSRRIPVMTRDCYEKQE*
>TCRU_9477 hypothetical protein, conserved
MTRHDAARMDELAAEVANEPSEYSPVLRRGLRVLRSTVNDGRLSTSALLPDRIRYASARE
RETMFSKHYGHFCAYYKSSCFTFVMLTRLAIGTVGYFDENFYPAYVEDVDYSLRLRLLGF
*
>TCRU_9478 hypothetical protein, conserved
MDTALNKPIANAMLCSDGALHLVGARDNEEKSSLFPAPLTEELQMITSILRNWADVDASF
SASPVSTVGLVGYLSNAGTANTWIDECRCVIATVTNEKNVTNRL*
>TCRU_9479 retrotransposon hot spot protein, RHS3, putative
MNAGSYLLYQLLHYDVEKLPMVAYVIGSQSFLFDKTTKTVSTYKGDPRIDDVVNIFSLRG
VKGYCIYDATLACRQPSTGLPCRGWGMIVVTPPDKKEYERWTKKMYATAIVTNCPEENDV
RAMCIWMKRNRPLQEQAEYWKEVRGRMNNVGPILRFIFGKQAYDDRIKACQQAVDGSTAS
ELERNLGIGCCYSSNDNDLSRKLVRVVRVRRGNNFESPLNVPISPHLERETLSRLEDEMK
QSDFIFFVLRFWDYVPPYIIERHAVSAFLNEDFLRAIRLKIKELRPPGRREPHSCALKEH
SDKSFTRKEVLPPPERLSNPVAMDHWVLYEPKVQNFPLVDGFFFVDSNPMTLVGLRMATA
CGHHTTTSTVRQFTECLAAYFNGWEELSQELSWEMIYVQHADSTPMTGWRRCDVVNSNNV
SRAENREIAAFWEEEVHQYMAAISSDDARRNEVL*
>TCRU_9480 protein kinase, putative
MDRFIVGSPIGEGRFGVVRAAVVKESGVPAAIKCITTPRLDEGIPHPTARELLVAMRLVH
PFVIRTYEVVPCGCSLALVTERCKTDLATVLSGRTASNPLPALEAKSLFKMLLLALAYIH
SEGVLHRDVKPSNCFLTAEGELRLGDFGLSRVWDTEASMTHEVVSRWYRAPELLLGQRHY
GPEIDVWSSGCVFAELLRGYGGAFFAGDGDIWQLSRILDVLGTPTPTSWPSAVLLPDWGK
LHFEPKRPLPLREFFPDASECALDLLRRLLCLDPQKRLTAAGALCHAYFSEYPT*
>TCRU_9481 Glycine cleavage system P-protein, putative
MSQGTPPVMLRNVIENPAWCTPYTPFQAEISQGRLESLLNFQSMIIDLTAMNLANASLLD
QATACAEAMYLAFHHGRKERMTFFNYRGTSSHLA*
>TCRU_9482 Glycine cleavage system P-protein, putative

MALQTREQRIKRERATSNIRTSQALLANVAAFYAVYHGSEGLKEIASEMHNKTKILSVGL
ESVGHTVVNGTFFDTVTVNLKGITPEDYVTCCVEKGINIFVDYSHGTVSISVVEASTEGH
VLSLLEAAGPKLPVIGVLSKLTEQKRAMPLQMLRKSVFLGRSIFQKYKSESELIRYIHRL
HGKDYGLTHGCVPLVSCTVKLSPAAAMLFLSWPEFTNLHSLAPKEQTRGHSALCLDLEQK
IRDITALDAVSLQPNSGAQGEYCWSSCDPLVS*
>TCRU_9483 hypothetical protein
MITYPSTYGLFDREILAITSMVHYDGGQCYIDGANMNAMVSYTAPGCIGGDVCQINLHKT
FSIPRGGGGPGMGPIAVRQHLASFLPDSVFIQNVGGSQPFGQVSQAAYGSASILPVSYLL
MWMLGSRGLKTCTGYAILNANYLKKRPDGHCPVLFLGENDFCAHEFIIDLRPFKETAQIE
AEDVAKRIMD*
>TCRU_9484 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MVPNASTKRPSFANGPRILVASNASGIMSVTCGGREHVAADNTDEVNEHDATGHKSLVLE
NGVAGSGFVAEGDADGLSQRNASGHDNKPQLREFTAQYSGNGVSPDDCFALRNDAKLTLR
ELTADGTVRVCVCWEWLLLLGLCGFATQHGGHVPRFLRVFFYYLHFIVVFRCSPGIMSVL
YYFMVGCCTPS*
>TCRU_gamma, conserved domain containing protein, putative
Elongation factor.1
MASSGDDSRCAPGTHPHTIPCVSLRELDELKIDYSHTDTRTVAALDFFQHCDAAGCTTLW
YNKYNKMQCMTANLIRVWLQRMEHVGQYALGAALMIVEERRHDIVAPCVLGGRACRRL*
>TCRU_9486 hypothetical protein
MRPPQEPPKVSSIHDTATQGDPPTEDRAEQTLPPAKANDNSNDHSEEGTAEESTVDTPAS
GAVQTEGDESETPGSGLKKTKTPHTTVEGSNTVKPGDSESSPAAPPAGESDTATTTRPNN
HDARSLNNNGNNAFTEEVDQKEAAIKPKSAPDSIDTAAANSEASTTAITISTNTTNKTNT
VDSDGSTAVSHTISPLLLLVVACAAAAVVAA*
>TCRU_9487 hypothetical protein, conserved
MAAPHPRPLESVVLRAELGRVCALHRQQANLLVRHFVRVSRAIPPYAAAAARRAPLLPGD
REMDRPLTPYEIDVTIRDSSLGSAAGPDDMLDEFLHRLGPVACGTLLER*
>TCRU_9488 Mucin-like glycoprotein, putative
MMTMCRLLCALLVLALCCCSSNASDTELAEQDSSQKTMTTTATQATTLTLGQSGPKGEES
GGEKGNTAVLGDGGVTTVPGPQLNVTPNVLATEVKNGMTETTSDTSTAAEKAGQNAEASA
KTTTTTTQTPTKTTTTTTAPEAPSTTTQATTTTTTSAPSRLREVDGSLGSSAWVCAPLLL
AASALAYTTVG*
>TCRU_9489 hypothetical protein, conserved
MKTNEKPVENPKAEPGKEKLSSEDDVPEQTSQGVNDGVEPSNDLTNEENVSVVLIEQNGE
SDGNSESTQPQHLAVGDASNMDAERGTEIGLPKNNPTANNAVTEGAKRGENKHGNRKETP
VEATAITNDTARTGDSDGSTAVPHTTSPLLLLVVVVACAAAAAVVAA*
>TCRU_9490 Leishmanolysin/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MELEDEGGTREKAIPHWKGRHARDELMAPTVGAGYYTALTMAVFADMGYYRVNWSMAEPM
SWGHRSGCDFLEKKCKEAKDFPTKYPHMFCDATDKETLRCTSDRRHVGTCTASIVENEGS
PADKDVCPVVSLYFHDTSGIKYNTCSEKGVNYLPGSLTGGDSWCLDAELLSKNDGGKHKN
VKGVCAQVSCEEGTVKVKYLGSSELWHDCPDGGEIPVTLKDFEKDGKIKCPKYVEVCTIA
GNGSSLVIPSVLEDDKGEEQEEQVEESVAASALPPAQEPHAEASSPVQPLAEMPSPRVQE
ALQQPREEIKAQASTAEEPHAEEPRAAASTAEESHAEASIAGKTSEAPVAQAASRQPQQE
SYAGQNKTVGESATTEQVPANTSQGSVGKAAASNSHAVGEATGDGGTMRGSGLLPSLPLL
LLGLWWFAAL*
>TCRU_9491 Endonuclease/Exonuclease/phosphatase family/Endonuclease-reverse transcriptase, putative
MNVSCLTPSKLATLMAQGADIIAIQETWKSSEQIASMHTGDYVLYAQSRIGKGGGVAVLV
RKTLRSKRIPLTIPQHDTSPEVVVVQVALDQNRDLIVASAYMRPPPQVTQSFRRLVNCLP
ASSPLLLCGDFNMHHPQWEPFLETSPSEVSAEFLELCTDAGLTLVNTPGEITYARGTRER
SCIDLAWSRHLTVSDWSASVSPLSDHYMLTFTLHQAFKDTIPSAPSIFYSWGKCKWDSFV
KDLDAQLPAYDYKKQSTGIKAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERMATDS

KARYLQLPTPDREAEMQRTRSQFFLLPRERLRNTYLRRISKLNPGELLAWKYISGRKKAS
LPSPTSILLGGGQHTYKAARRAAIALNRIFLPFHPSHKAVRFSKGINRQNTSLNIISSFL
FGPRNSNELISTFASGVLSLPY*
>TCRU_9492 hypothetical protein
MLAFSIISDELRDESSIPTPADLGTSTPPSVASIHERWLCGARASSLTLRLSRISSSSSV
IEWSIGSSTPMVTRCAEAANQGGMELRKNRSSRGELSVMP*
>TCRU_9493 hypothetical protein, conserved
MLAAGRPLMKDYNVTMEVFVREPDDYAQDQRLLEEILNLTAYQALEAITKPLHEGVLSLE
QRGDYE*
>TCRU_9494 hypothetical protein, conserved
MRASGPESLGGGHAAGTTSPCSDASQQAAGGVHAGGGRTSQGSRASEQTVTGQSQVPGTA
KEAPQGDEGGEPGAQHEADQTTEMTVVTACAETAVEEESRQRDRKMHHVSIVAGMLIIII
IFLLPTCLATRCHQGAEGMVEQRHEFPAMRQLPLGEAFGAKVLLDAQPLAQSQSVCTFWK
QMAQCFLRANCCACGGWLILR*
>TCRU_9495 Reverse transcriptase (RNA-dependent DNA polymerase)/
RNase H, putative
MSPELLESYRPISLTSIVSKVAEKMVLKRLLWVWTPHPHQYAYRSMRTTTMQLAHLIHEV
EHNRNHYFQVSLPKKSGIGNQLHYRPHRTLLVLVDFSKAFDSIDHRVLSRLLANIPGVNC
RRWLRNFLCGRYAKTRVGHRHSDRRPMLRGVPQGSVLGPYLFSLYVHPLLNLLNGFAGVT
ADMYADDLSIIVKGQSREDAIPTANMVLQKLHAWSQENGLAINPSKCEAAWFTLSTHTES
DYDREGRWPLVVAGCQIPVMTMGASRTTKLLGMDLDPRLTLNVAATKQCAATSQRISQPR
CIAHKEAGPSPHDPRTFVIGYDASKLRYGSELIWAVATDSAKNEMQKTYATLARIVSGVP
STVDPESALLEANMPPLHVLCLRARLSIFENTRACQMDWMRRPPPEPPPRAGFRISPLSR
DELYAFVDAYTKDYGITESSPREERFFRSSIPPWSAASAHRVTIGVELPIDHSITDEEEL
IRENRRVSEEALALHSHRSWILATDGGVDVPKSAGVGILLSSLNSSEIIEKASIDCGARP
CGYRTESRALLLALEKLMIPRIRHRRKTLLVVTDSQSLLAALNKGPLSQTDWTEDQIWQR
LLSLTCAGWSVHLQFCYGHCGVHANEPADHATQTTAIHGAWNSTHTAHGPAVMH*
>TCRU_9496 Endonuclease/Exonuclease/phosphatase family/Endonuclease-
reverse transcriptase, putative
MEPFTWLPAERYFYPLLNSIGAYQRYTYRLRAVRDAQRQKLLLSGDIEQHPGPIAVLQMN
VSCLTPSKLATLMAQGADIIAIQETWKSSEQIASMHTGDYLLYAQSRIGKGGGVAVLVRK
TLRSKRIPLTIPQHDTSLEVVVVQAALDQNRDLIVASAHMRPPPQVTQSFRRLVNCLPAS
SPLLLCGDFNMHHPQWEPFLETSPSEVAAEFLELCTDAGLTLVNTPGEITYARGTRERSC
IDLTWSKHLTVSDWSASVSPLSDHYMLTFTLHQAFKDTIPSAPKFFYSWGKCKWDLFIKD
FDAQLPAYDYKKQSTGIKAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERIATDSKA
RYLQLPTPDREAEMQRTRSQFFLLLRERLRNTYLRRISKLNPGEPLAWKYISGRKRHHFH
LPHQCY*
>TCRU_9497 mRNA processing protein, putative
MNGKLHRLLQRIASPHLALRLTKEELCLSMAAVARLRLRKEELLHLPLDSIITRTQRVSH
LCSPIELGMISDGASALFCNRADMADALVCELYAAIGKGATTRLDHVTAVVRYASTLGSY
SNETIPVILMSAPKILSKKDSGSTLQLFLRVAQAHLSETEFHSLVEELRKRASPEQMKDV
NEKCILPLIERGSQTEAEEENDEDDDDDNNNNNNNNNNKTAWNSPRARNWLSQRVRRDEAW
SPAEVVQAMELYSHFGMRDPVLQKKLDEVAMSVMPTASKIHMDGILKVMATSSHLFPLTF
EFIRQLRTKSPESHNSDASSDADSTSSLTRNFKTSEAYEKLLTGQHIPEDWMLDVIQEQH
AAVPVDVAAQAACIFAEKGEIPEGIILQLSMQLRELSPEGLAAFLRAMRRDPSGSLFQHS
VALSAQFTENVVRDATVEQLLRICTACSFPLPRGIDTKERGAFMEAQGRLGEAVLTRLIS
VMQTPCTILFLCRITKLSSALDENNEILQFVCSSVCARTSLAVDDALEILEMLHFRKYVH
EPLLDKLEPIFREIVELVVSKMQSGEEVPDAEARQIARFIVLQTLFDVPDFEASATLLLH
TAEQFMDRTPSEVLPGAGLLALKQRRMATVHMMLAKVTGKVSTLSDEALGMLARLLAQSS
VGSPGKNLVNEIVSVVVGRLSHKRRLPPDFVGLAVVVHCQHGDAGDGIPENVMEYLLEWM
GALSSEVYTELCGAAHLLKAGDTLTNGLIDEFPLRLNQLTTSEIANVAFGLGEIDGIGHR
LSHQLVAEKCSDYVVDNSQEFWSGTDIARLIYGFSRMLCTKRSLYNVFSTRLALRPVFLP
MNQKAISLVVAAFGRSKYLDKKLFDKFVRRMQEYSDDLEAPELMLAIRGFSRVMLLNDQL
YNELGNKAAEKANDFPLDSKCALLASFGSLGIEHEKLATRVLDGIVEKLPELGDANKAVD

VMTSLWQMHHELETDPRVDQLANWIVEQSEELTGDAIGKLCAILNDRNWRHVPLVKAMAE
QSVRLQLQQSVSAECCRAVLDTLGTFMIHHQGARENLSALGRSVSKERIQLSEEEEQQVQ
LLLRR*
>TCRU_9498 exosome complex exonuclease RRP44p homologue
MFAKKRSTVHEVRGHTARRGGGGVTRNDIGCGIVGCSLCASAVCGERGPCVVPTSLIIIP
DTNVVLHNMNALEDAQIQNIVFLSTVVSEVQNRNKGIYARLQRLLGEERKQCYVFSNDRH
EQTHCMVEREETPNDYNDRCIRVAARWYGRHVSLAFPASPPSVALISHDKLLRQAFVTAT
EEVATPNLSCVTLRELVEKAISTQSDLLEKIQYEQPAGMKESSKVGALFQQHVADGALLM
GINNGTYLRGKLRVSETNCFFGEIRGQWEGHNFSRVLLPGRSNLNRAIHGDIVAVELLPV
SSWRGPKDAKPLDENATEAAAVAGGYMPVGRVVGITSMERRPFCGSIDVEELTRLTASEG
KISGAVSVLFQPKDNRIPRIRISTRDLEYLKDKRLSVVIDDWPEYNSFPVGHYVEVLGTI
GDKDTEAKVILLENDVPHYDFSEAVYDCLPKGQWSVSKDELERRLDLRDLCVVSVDPLGC
RDIDDALHCRVVNENHLEVGVHIADVTHFLHENTAMDEEAAKRSTSVYLVDRRINMLPQL
LTENLCSIVSNEDRYAFSILWEFDEEYNVVRDYFGKTVIRSRAALYYGDAQRMIDDVNDK
SEIAVSLRHLMDISRHFKAMREKDGALFLASQEFKFKVENDHVNPTDMQVYQTFEANSMI
EEWMLFANAAAARKVYESYPRWTLLRRHQRPAENAFDNLNEALERKLGLRLDDTTSLTLN
TSLNACIDPDDAYFNQLIRILVTRCLRQAQYFSSSEVSQDEFYHFGLAMPIYTHFTSPIR
RYADVIVHRQLAAALGIMQVSEKHTDSVKMEAVAANINYRHEQAQRAGRDSQNLFTGFYL
RNFAGQVIPDEDGYVVKLSETHVFVLVPKYGQEGKIPKEQLVRVPGLLDKVRVGIELRQQ
GDVLRTTLAFVLVGMMKEGEDGRGEFCTDGENGEKPATDDAAGEEGPVRKKFRRKQEGDE
GKNNKE*
>TCRU_9499 hypothetical protein, conserved
MAREDSEVRVLQDPLTYMRAIHKDAGARWVLGLKPVEDEMEAREKHSEDTFTGTTLFPEV
ASRWSKGWLRVPILLGLACLVHLVYVIATGNKRNPLDFPSTEEELWNYSRWQKDGMLGFL
KRVRHLWLTSSLTASFTLALSWKFGTAARHFLALCGVGISLLSVMAMIAQFIILWAACGE
SPISKLEECSVPFVLYWTFSVIRLGGPPLAVWGVGPVLDIIWDSRAWWKFLLGLPFFFFT
VSVSLWVLNEPVFFGGDDVYQWCGYVTLVSWGPLLVLCCRQRRFQLVFVKKTHKE*
>TCRU_9500 retrotransposon hot spot protein, RHS3, putative
MIVASSLEVRNYGEWVRQVKATRIIVDCPDENDVRAMCAWMTRDETKETSGVLERGRKHM
YLLVPIPRHVFDEEAFKERCGAVRFALQSINEVTVKEHFSRGGESPWCSEDPSHKPVEVV
REIYAGGVILFNAPISACLEERTLERLPIVAE*
>TCRU_9501 katanin, putative
MSEPITATDDMGKSLRLARRYAMESNYEVAVAFYTGLDKDLEAFAQCSGNAPGRARWVLL
REKVAEECSLVRSLQEELKALVNPADAARLERVQREADSTQLSQKASSSGALSARDVTPV
RVTVAQPACPPATREGVKFLSSLPPTIPQSSLDGPGVRNELLYGDKDRFGPVEGPTVRQQ
RFNGGQRAPMRHNLSNVASRTKSAGSTSNPSSPHRLTARARVATRRTGRPNGCERKPQGQ
QVSIPRFPARAGEEELVSLIESDMNAGPMKVSWDDIAGLEEAKGLLEEAVVYPVLMPEYF
QGIRRPWKGVLLYGPPGTGKTMLAKAVASECSTTFFNISPATLTSKWRGDSEKLVRVLFE
MARHYAPSTIFIDEIESLCGHRGDGGEHEASRRAKGTLLTQMDGVGVDTGKIVMVLGATN
HPWSIDEAMRRRLEKRIYIPLPDFNDRVELFRINTKSLKLSPDVDFEHLSKKLEGRHYSC
ADITNLVRDAAMMTMRRLMEEMDKSELKRRAAEISKTVADQPTTMNDFLSAVKNVPSSIN
VEQIQKFEAWKREFETNP*
>TCRU_9502 hypothetical protein, conserved
MSGFRGAGRLEDDGKENRKRVQRSEPACGGLVGWQIASKSRCLACGRLASMCDCQKSRID
PQLKRQKLESILLSTPYVRSKQVRALEDISREESKNRRRLVERWGDDLESMRHLAFTHHR
ILLLILEETAGREALMAMERKAWSEGMVTVDRHIVLCAISFHEREERLQLYASAQREVQV
VLAWHEVTCHLLGLRSREAAFRNALVNHEAATRAALISHNVELLNRMDANEKDRFVFYEA
FRERRDKLVVEWQGGVEAIQSAIAADQRQVEWMLQGRNQLCKLCERQRAELKAEEEECRQ
RMSEIARKKQHALMERVQVCEQQRCTLAQQEVNSRSAILQDEAAACKALWLFFKDGEREA
REQEQLRYERCGVELRAAIHQLRSIAGEEAAAFAQLKAQEHHEKDLRYKWMLEKEKQRKE
LEQAALHHLRLIEEEEGMARQASMKAMQEAEVGIAVWLQQKTRTLRELVDTALGQKGEMR
LREHEERFALVSRKAEHEDAVRRWIDQKEFARQSLIKEETTHRMNTVEMERAARDEFRWH
FDSALEMCRSFIYERITEQNIFQQKALQVLNDIVEQEAKAMLLMRRLIFDDRERARHEEN
HRQFLEIWNAEAECRTYIVQQEVRHRESISTQMHLQRSFFAKEAQELLKARICEVLATEE

SQRLVLLHHFSETTEQIYFSFRQSREEARRSEKERVLAELRQRETELLEDTRLYREDEWL
TFDHTENRLSEPQESSAFPLVDDGLWNTQRQLVMAELGGEEADVMTLPPAAVGFLASIID
AISRRESSLTATLRQVEVAVNEARQKVANQNQLLSGVKERWEESKEKLKRDAAEHNTRVA
MYRDARQRDEAQLERERARLQTKTEELRRMQNSVSGMRDAIHNQYRKR*
>TCRU_9503 Protein of unknown function (DUF812), putative
MEEEIAVVQLLQYGLPVTRSASFASFNSAALYELLTAALTRFFSTNGEEDQKQTPPSFEG
AENATSRLRLLSMLATRLQRAGCEFISPDHLMYPAEKTTRKILMWLIAELHRVTTTSSVK
DDVKLQQTPVGQAILSLHSVVQQHNPCVKKKDTKESLPRCECVIPAVPAFFFAVSAQERR
KGGVQPPLWQQFCQGYDAMQGFPRSPEEAPYQPQWREVLLNSFQEANAVERTFESEPTSN
RASGPLMLRDASGVENFIKLPRASRKRPHKKTSALASLQPLRAYALDADVFYFNTSEDDI
SVQHTTSKTAAARETALEMAEDHHDTLTRQDVYAPKEKHEILREYSEAKKELRHLKKKLT
ELAAQKMGCDEELEMLQVSYGQICGERERQKAETERIAQALALLDTPEESEVQLERQVAE
FVEARENNRREVQVKLQKVEKKHTELLERLRVAGGDHEEQLLQLWQAVKNVQRQIDEKER
NVQQWQEKVLLSNTTDIDIFNFLSFIYEMTSNVCRQQTQIDSVERDTAAYNTRIEELEGR
LRLSFFEQASKLYQKAMVFDDGNVFQRLHKNLNEMRDGYQALISATAKHGEFILESYRME
ERLQKLRVEVEVCDTEKVKTDLANLRAEKCSSSPDITGSGR*
>TCRU_9504 NAD dependent epimerase/dehydratase family/Saccharopine dehydrogenase, putative
MSREFSLVVFGATGYTGKLVCEYLARLGLGKVGPWAIAGRNKEKLNQLKQELGVNLSVLV
ADITSPSSLDKLCASTSVLVSCAGPFTYFGMPVVEACVRSRTHYVDSTGEYNFVRQVIEK
FHEEAKKQGVALVSCCAFDSVPGDLGNYFVRQGLGSEVAEVKAFYQMARGGMSGGTAHSV
MAVHESCGLEDNDPYSLLPKDAPRPPTAPARRGVWYDFSERRLTGPFFMSAINERVVRRT
NALLGYGGTYVEAIEGTLGAVVGATITKYMMTAVLAVPFLRRYVAENWLPPAGTGPTQSQ
REMSWYKCIFVATDKSGKVLRRVFLSDTRDGYTASGLYISECALSALQMAKEGTLGFGVL
TPMAAFGDVLLRRVQNAGVVVEAVEEATTGAATPTQ*
>TCRU_9505 ATP10 protein, putative
MSLRRLFNVGATGKRCVFCVERTLDTCFLQRCFESKNHGVDNDLSTQKLNESHAERPTPD
DITASSSTVLRGLQREKKIVAKKVSRDEVSFSPTRHAGKTGRMDDAYTSSGGSNGTNHLD
GGARVSTAGNRFLQKLSELENSAVLTPPRSSGFLKLQKRGSEEKVLSERRRMLVFRDVGM
DLDKPILSRDVFLVFKYFRYGIEFAVDNELERMLRYFNEHALNELKIIQSSKLMRGPSVL
SRKKSLSAHGGGPFQLSPAFPFMQAANMCQFCSYTRETEQMVADLMRPSSPCAFFCRAKE
DATANFAPKARYFSEQDLAQMTSFSSSTFRRPAVVIYTQLGQKLGAQADLEWRRLAYKTI
CPSLLKCLPTADAKGEGHVQSTCEQNTGGLRYRYKEDSVTVRRHGMPFDVVSLRSMDVYK
YRWVHRLYVRRFAQSLVPSPPSLEHAATDAQINGLITASTTFVGCKLLQPFYSVLGLRNY
LSPHVMLIDHEGRIRWLTAGCPDDYESEHFPALLKQLEEEYHHAKSR*
>TCRU_9506 regulator of nonsense transcripts UPF1
MSQLVVTEDPSVDSRCIKTNDEINDPNVSENNGPKLAEVGCAYCGEADPHSLVMCISCKK
WFCNGGHGTSGSHIVLHLVKSKHRAVQLHAENPLGDSALECYICRSTNIFSLGFMPSKEE
SVVVLVCREPCLHSKALRDLNWDATTWLPVIEERQVLPWICRVPSAPCKKLTLHDITTLE
LFWNSEGQQVLDNVEKAPAVPLRFENAVEYVTVFSTLIEMDSIAAKERKELLFEDISCKL
QKEFGGKHLFLLKQLPPSDVGLRCGDHASIWVKGSSRLLNGVVVEIGKSQLGEEEVIFEV
KTYEIERARRALNEILAASTVSFRLEYDSTSDQRKCHALNLMMTDWASLSAYLYFTILGR
AEEAAKRFSEVDINLPRGRLSNLNSSQDTAVRTALRNPLTLIQGPPGTGKTSTSVAIVLE
VNRRIRSQILVCAPSNVAVDQLAERISAAGLKTVRLHAHYREVVPSSVKHLGLDSQVEEF
IASSSGNRRLRQLLELKLAGEVLDEQEQKIYNDSVRDIEEALLGGADVICCTCIGAADRR
LGKMRFQYVLIDEATQGTEPETLVPLVRGAKQVFLVGDHCQLRPLVFSLPAERAGLRRSL
FERLLMTGHRAVRLDVQYRMHPALSLFPSDQFYEGTLQNGLTEEQRDASRVFPWPDPTRP
IFFYNTTGSEELSANGSSYLNRAEAALTERIITKLIRDGKVKPDDIGVITPYGGQCRYVM
NYLVRCGPLPRTAYERVEVSSVDAFQGREKEFIILSCVRSNHRQGIGFVVDWRRLNVSIT
RAKRGLIIMGNVQLLSRYPAWHALLAHLMELSLVVDGPIEKLVPSKVVLQKPRNVSEEQ*
>TCRU_9507 hypothetical protein
MVHHTFLLPRSSFPVFLRGEVRTTADTDVNEVNKTLPLGALVQCEKLRCPRNAGGSGIIF
HVMVRNGGLKLTVEVCRQPVPRLDSAKQRHRMRVSQHTVPNVFFKERLVAQQLRLIPVLC
DPRWPVMGEKQINVWKFPSASRG*

>TCRU_9508 glutamine aminotransferase (GlnAT)
MAYSFGDLRCSKRAERCQNKLKSFVSELLSASAAGSSGKGLISLAIGDPALDGNFLPPPI
LTSNFVKCAKSNICNGYCPCFGLNVTCNSIGKYWKTNFAPSMKGEVAADHVIVASGSSDA
LSMCFGALCDDGDNILLPAPFFAHYDTICSYYNIQTRFYHCNHEKDWEIDFDHLRSLVDG
RTKAILMNNPSNPCGSNFSRQHIADLIRVCEELHLPLIADEIYAGLVFSGEKFTSVADFD
TPVPLFVVSGLSKRFNVPGYRFGWVVVVDRDGYGAKLLKGVRKLATRTLMPNSLLQHAVV
SALEETPQSFFEDCANRMEAGAMVLYNGLKDCPGLKLVRPRGSMFMSVVLAFEELDCSVR
SDVEFSRRLAEEENVHVFPGEPFNMPGALRITISRSLPMLHEAVQRIQSFCERHRRA*
>TCRU_9509 Protein of unknown function (DUF938), putative
MTRRSYPSLNKRWVFTEPPGTGRGLQEEGRDYFAVVTQACAPNFTDTTAHDAYERSRRFI
VRLKQKDAGRGIRETEAVVSLPASVDFGLEEDYAMPDENCSLLFRKKKKKKQVR*
>TCRU_9510 hypothetical protein
MPHAAPKTDGRNTVGLRAGKTPVKICLEPTPLQMAPLVPKCMVQHEWELPCRPHAEKDIT
ATVDGESVVPLRFHDVLLERRLGSKLSRRRCATVRFVPVMWDAGSILRLKFEKLTSANSC
FSFV*
>TCRU_9511 hypothetical protein
MWAEDHVLLSNMLRSIQTTRAKEEGKEMKTMATMTVQDDEKDAVVEDSYGRVWDRLWTVC
RNFSVWGSKLAFSLAGEQRVNEEDLSSQAPRYAECILE*
>TCRU_9512 hypothetical protein, conserved
MWNVRMRTLALLEESFSGSPVRLVADGRNDGGVGGIEKLNGHNEAYFCPVFIPSKARYHS
ERGTISLLIQDKVPFTLVVQPEELTLYERLVDRLVNKWWGDVHNNGQGGTEDVTDGDELR
FLFPRHGLQRNSTLLSQELLSTRPCTPPPPPPLSRRRDASDVRHLVKIHALPLSDQGVSY
VRNYILTELVPRALATSLPSSSSAPRAAQWFWVMDDDIQRFYMAWDEKNHVITPRELFTE
VYSRIQELHGNICDMNGIAIFSLEYPRFAYTYGDSDVALNSYNNIASLFRYDLLPPDCKY
RFRIREDYDYTLQLINHGMMTARFRNLSFEVPGMAEMAGGMTDYYKTQKEDIRLQNKLFL
ETWPAVAQECIKGKGALQREDIRVRWDLLHPKRNPDPSATLRCRTPMQKKAHKPLSNGID
ETESMAKNGCENTTTIEMSTRNLKDKRTRSSEAARGANKQRKEKQKQKMTLKTNTSLNGK
EEEARRKRVNCGIKRQPPEWKGYALERWRYLTVHEAERLHLHLIPSEKLRVGQTVAVVPP
MFDQNPSVVEAVLVDKRVMRRRRSERNGEQGATDAKKGSEVDIVVEWCAVARGLPLLYVT
RCYELPMEGVDVAAAAVDAFFEKEWEEEEEEEDGKVE*
>TCRU_9513 hypothetical protein, conserved
MAAPSLNGFECDNTNDGKESDEDYGDDLHRGADYLRVLAHESQEGLNAVPTIPGLEEPLA
FALSPAVISAPCVEADPFTVEFTQQLSSGCAAGPALALSHVSQGCLACDLLCVVRAAASS
FLLLPNKKHFALRWVFICVAVDARDDAQRVCLSFGGHEGDFGVCRRLREILR*
>TCRU_9514 polyubiquitin, putative
MQIFVKTLTGKTIALEVESSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLADYN
IQKESTLHLVLRLRGGMQIFVKTLTGKTIALEVESSDTIENVKAKIQDRRAFRRTSSA*
>TCRU_9515 Domain of unknown function (DUF1935), putative
MGCGSSKSKTKADGFVNGRPSDSFSYDEIRKCTERDNGLLFRLVSGDRKQWAFYNDSKTY
EFHITVYFSSHSRVEPLGDTTVVRDPTDGRLVAKTIVYPCLTEPFVQGDIDGFDAEYQAV
VLTEEYKRKRAEMKSKKHAAQANDDLE*
>TCRU_9516 Domain of unknown function (DUF1935), putative
MFVSRFLSVQPAGQEGYWDKGRQTEAMIGELGGKTAPKLVLRTALEKDRHGFRGSTGRFD
EDWQKTERNAWPVFIQKGVTAPNHSEGSCSMTSGSGEGKEVRISSSCSGDPSSVERDPRA
GYIHQRWPCRPAAITKRGQPPLFLGPGPSTKIRYDKLFCCFNEGNGLLFRLVDEIHHTWA
YYNDTMEYTMHITVSFGRDSTVEAIGKAECIIMDAALGSCSIDLLLPPGGTELFMRGEYN
GFRGHYEIASSRDVATGERRK*
>TCRU_9517 Raptor N-terminal CASPase like domain containing protein, putative
MTSEEEPTQTRVESSSSPRGFRRVTLTASVLNEAENEQGIPLEPCTDAEVEAMERQRWGR
LVQEGLFHQSLHFQRWDEEALLRGSLYRTRAVAARTTVRPTTTAALVLSLNINPVLWLGE
NENEKGDEASPKASRLYVWRAPALLPGDNLNILSQLGQQLESQYRSLSKRPLIVSHCLNA
RPEGFVRALAQCRHQAGPQKKVIVHYGGHGVPRPRGGSLFLFSSNGEPVNYSLDTFSSQV
GFPLVMVAECANAASILHHLLENRQKEEVNNHFTYRQYGTNIGVSTLEESERPDMVPGWD

RYEVASVAGMEGNAMKSTTNAPFLSKLRGLGSAAASSTNSLLHDDLFFLGATEEGALPRH
PKLPSDILTSCLTTPLRMALLWFIVEHAQTADIHPLLIYLIPGELTDKKTPLGALQWAFM
SITECIAWFSFPYALFMHLFREDVLVAPLFRGFLLADRIITALGGKVTVYPPLPRTSDHT
LWDTLDNIIDRTFVSLWRAVRPTPPTVLNAVEFREWLDWNATSWRYEKGSMTLPSLGDRC
VVVPDFLEEELNCLAGAVERITEQGFFRLVSTDRQRTELIGGSAITTRWSRAEDDSPLSF
LRVNTPPNGGNFVGTKPFPHIMRLPMLLQGLLVMSHRDQATELVCRFVDAGPLAVTACAE
VGIFSMALVHYWTRRDLRHLLPTLLFIYAKACHTDPSLGDADPAQRNVIIDTCMEILEHP
VTVPAESSGEAGAWQRDVLGSWAEPRGQQLLAASLLTMICLHSGGGRRRCRERDAFRVCC
NLLQEAAAKAPRVPLRENGLEGEGEEESGREENFWDDYSPGGPDNNPVLMTAYVLGLIAL
FVVIAWEGTLSVAKTDEKEEDDQHHQQQQTGGSGGGDALAVRAYISTAVDALQALLITTS
SAIRGAAIKAITVVLVSLITDDETAVMCVRAIVKCTSVQRAPLEGNTDNRLEFVGALSLA
IKWLIGRLSVSLSLEDIRRAVRCELNKAWRKALGTTTTSRGCEENITNYRDPDLPFVSPS
PLAESPVASFTLNGVDSLLRMLAELTCRLGVASNDPCPLVAAHAQKILRDDLSMLHVRYL
PLFQPAGNVPCGRGGATTTSRNSGIANFFSGVLNTLTSRGGKHAIREGHQSGHVLRSVGD
EDLVEELLDTGVIFGERAAVSDVSVSLRTVSVHDNMTISSFVFTLLSFLGELLLIPMDDH
DPRHPFNLEKDAYILKYLRRLRDELRVTVSSSYGSCGYEGHAVVSPLLPSASSWNHPLSL
LMMPQEDGTRGHAPSLSSPLMPSSSTVGADASVSWTTDRQKSFRLLAEKNISAERNGHIQ
VFTFHPTERHFITGTNQGVIQVWSFAELEGFLLASSTSSPGSSQESGELCRLLSQIQLSE
VVARPGCAMPPSTVLKYMYGTQLTIPQCVSLSGVANERLTGGAPDVPLSRRAGLWGTNDY
GGRVARGVDPLTGLHLVDSAYRTLLCAVGRSGSVQMFSAYTDAATVRRVTSFATMTYEES
LRSHQCLSSYHTPAMLLHVSGADGSIASWDLNCEQKVSAGAGRREILHSPSALASHPYDV
FTFAVGAGSIYLYDLRNSSRSTHVLPDPTSLGQSLQRQLRSLGDYKPLCLHIGFSCRYPH
GLVTGYGGEQGVVMMWDDRKLQQPFFQRVVSETGGAGSSSFNSVGYMDVQHYHYALMTLS
VTADALFVGDALASPSSKATSSSGGGGNSCRAHIRLKQQPGAASFHPILPLCGVAGGTYL
QLYGRKKLSMPERHA*

>TCRU_9518 calpain-like protein, putative
MGSSSSKLTYENGKPTFGEATHVHPMFNGLLFRLSDRKHNRWAFYNDSMEYAIHVSILFD
YDSQVVPLGLATAYRVDDPEVGKEDDIGKYVVEVDVAPLATELFVEGRVTGWTVDTLEAR
TAANEQDFRL*

>TCRU_9519 calpain-like cysteine peptidase, Clan CA, family C2
MGSSTSKHNPRELLATPAMRGAVEEWLFNGLLLRIIDRNTGTWAFFNNSRDYEFHVAYLL
NPDSAVQALSKTIITPQDDGVLCETSVYPLETQRFFVGDVTGFESKIEALPLSAEYLQSH
ADIDERKYYRRLIPPSAATF*

>TCRU_9520 Domain of unknown function (DUF1935)/Calpain family cysteine protease, putative
MGNGVSSTKGKSGNNNIVTTHFNGGDASLTTSASLKGILKNGDETKTNGKNNTNPLQGQQ
RSVLASPFRPASAAELLPATYNGNLFHGTGTSRQTVDLIDHYNLSSTVEKNLPARMYNSQ
WRGCVRFKNGSPLLLRGGDDVIPIPLCTDGGGGVVFCYRIISVDGRLWRFYNDTATYELE
VVCVFSANSKIEALGLTTLRERSDGRAEVRLVVHPGDTQEFIYGDVERYEEDIRLRHVSR
AFIDASARACEPFLKDEKASICALLSRRGKKTGPGNNWNVPSEELLRWCVEEKVPFLDLE
FPPNLFSLVGKEQSTQKKVLCGWCKPKNYIPTEALVDEPRVLRSSPQPMTVGVSLTGGQG
VVGALAILAEDYFAVERLFRHPMGSAAAVEEERVDASRVTLCKGGWWISTVVDHYFPVLN
MKLLTGKCISDPAELWVSVVEKAYAKLHGNYTNLAETDALQALQELTGYPTCRWDSMLRD
ASSHEELFDKLCRFCELGFIVVLDRPNLTSGKRSLQRLGLQEGNACVVLSMKMFRPLPSN
GVSGQLQQQGIHRLVRVRNPFGSSRDWVGDWNLWDPAWKTNPLIAAQCGHDKECAEDGSF
WMEWRDVVCCFHGCGACFTHNLFYEYRVAGQCGKGGVPGCVIKLEVSRRMYILGMLQQEV
RGVEGMLQPILLQLSRRYVPEATQMPSSVDALHNEANTKSQQSLKRSDARKQEVVLNSTA
DCDCPSPDLLTFRASSQVSFICELLPEYSPYYLIPRTTSDEMAYVLGLFTSVPCGRGGVG
DGAPATRSAPGLSTPLPTAGGSFAQAKFMRLSSKTRVFSNSLRFEVKSETPVKCRYQVSS
PTASPLTFPSKFTDNCIR*

>TCRU_9521 Calpain-like protein CALP1.3
MGCGASTTQRPTTVAPEWNAPFEKKEVKKNEKVVDEFEETTVRPLPEKNSFEKKFKIGAP
TFVSEDITPCFDNGLLYRIAKDDVWAFYNDTRNYEMHVEFTFSRTSLIRAIGNTKVNQVE
SSGEYVAETVVYPTETVMYVKGSIAGFKSKIKALPLSEEYLQGKVRSCNLLIEPEMNRVK

EFAADFPTDDTILAECLERNIPFIDMYFPPNQDSITKGSDRPMKTVPWARPNMYLPDGYA
PLVRLFRNKISPMSVDAGELGDSWLVCAIAALAEYPKMVRDMFHHPRKAELTAKERAIGA
YRVTLNKNGWWTNVVVDDYLPVLGGRVKYARSVDDPCEMWISILEKAYAKLHGSYANIIV
GDPLLALQDLTGCPTTRYDESFASDVETGDTELIERLERYHRSGYIISINTPVRDPQDEE
KEKKYKEMGLMMGYMYTVRKVRHFESEKISLLQIRNPWSSDLEWKGDWSANDSKWSQYPD
IAKACDQGEPEPGTFWMSWGDVQKYFNGCGVVFLRSSGMDCRVKGNFVKGVPDVCVQITV
KKKMELGCTLSQRDHRGTRNSHDDYPPIMMTLCSGRGSVDTMQVEYNTNLDADHPTNHFT
FMQSRDVGMLCTLTPECSPYFLLPRIMSDEASVPYVIGLFTNEKFGESIKAEFRTLPPDS
QAFANFPSFSGNGTSVMATFQVNRLGSGFPQSFKNKELVEKSSVPREGKRSEKRPSKGPG
KVNGAPVRA*
>TCRU_9522 Calpain-like protein 1.2
MASYGPKDGTVSGGSMQILNDEFDEGTVVDVNKLSEYRYGLPVYQGTSTACFDGGLLFRI
VEEKNGERWSFYNDTPNLLMQVELDFERGSNIKALGNTTLEQKPNGSIVCNVTVHPLETE
LFVEGEPNGYTSNIRAEGVSDEYLKDLAVQDKNTIDKETYELYKLVGESSSSDEMVKVCV
AKKVKFVDFAFPPEQESLQIGSIMQMKVIPWERPCMYLSDENAKQIRLFRSGVHPTNIDE
GDLGDSWFIGAVATLAEFPDRVRDIFRHPVSIEEGKMEREAGVYRVNLNKNGWWTNVIID
DYLPCMGGCPKFARSKRDPMELWVSLLQKAYAKIHGGYGFIIAGDPLHALQDLSGYPCSS
FNNALTEARVTGGGELFGNLFQYSNLGYQVLFVAPTRETLNRGAMNGVSESTYARVGLRL
GHVYSALKLLFFPEYNLRLVQLRNPWYRDGDAIWNGFWKKGDRKWKQYSDVSAACNYTEE
NDFTFYLEWDEVSRFFMGCGVCFIQHPMYDFRVRGCFMQNVPTTCLEISVGVPVIICLML
SQDDMRGTNKQEYSPIMISVAHGFGSMTPMSVDLNSGFDTDHPSPEYAFFQTRETSMFYE
FLPENSPYLVVPRAMSMYPKLPYVFGLRSPVEVGTPNSQVRVAFRALSPGCGIFDNARNF
DVSTVSCQTEYQSINPEQFFPDIYAGTVIQVE*
>TCRU_9523 Calpain-like protein CALP1.3
MSAENQWEELEDLPQQNKEASAEIDNDLQDGSHSDADKANGEVGEIQETSEYPVEKAEAN
NQPEFCDQEVQEPRPHPPEEEYPAEEPNTYPEEEPHNEEVNKREVPVEEGVVRGENKESN
EDEFPPHTQEVHHLVKPRKTPLKKPTRWDPIEYDLREDSDDEFEMATALRPVYEEEEEFG
VPKFKNGEPDYQGEYLSCFDEPNLLYRILNREEKTWAFYNDTRHYEMHVRFIFGKNSVLE
ALGNTKIHTRSDGEHVAEVFVYPGETEMFIKGRVNGFTSKLRAVPLSEEYHQRRQEVAED
AIQREVAQIKAIVGDERSAEKVLEACLENNLPFVDLEFPPCQASLDTGAKKPFKHLPWAR
PSSYLPDELLDQVRLFRGPIRPSSIDQGELGDAWLMCSIAAISENPQSILKMFRHPVSAE
IGRKERAIGAYRVTFNKNGLWRSVIVDNYLPISGGKPKYAKSTHDLAEIWPSILEKAFAK
LHGSYAHICSGDPLHAIQDLTGYSYCRFDDAFTKASQSGKDDLFQDWLKYNKAHYQMMLS
TPGKDPNDKGSSDPKLVKLYQSVGLISGHAYTVLDTQYFADHELRLVKLRNAWGRTAEWN
GDWCGDDEKWEQYPDVAEACKFQKDDNSAFWMSWEACLYYFNGGGVSFSHPSLNDYRVPS
KFVECTPSCVLEVSVEQPTWICFTISQQDRRGRQDAVEYQPVMLSIAQPLEKGLYKVVQN
SSADAYSPSCDKWIFLQARDVSLIHKFLPEHSPYLVIPRLMSMTGQEGEVPYALGFSCNR
VVGHDGVTVQFKALDKENKVMHNFPKFDPEATPVVVDYQVKSPHKGYPEMKQGQTVY*
>TCRU_9524 Formin Homology 2 Domain, putative
MSVTSISPIGGPTGSGTSVRDAIDILLYEENQGQRKRKLVLELNTLVQGAEFAEQFLEED
GLNILLLQIKTASGNLQAAMLSVLRNLLVYVNAVEQIAETPELVERIYGLLVPSHDGSLV
PLNIAKPTLETLIVICGMVEGGHKMINQAAKKRIGVGVLPYAPLVPLLSGDDLLVTHKTL
LFMNILLKKKKEVSELKAKKLFFRWKECGVLSLLKRLTVIEDADVAKQLASFQRLSNFTI
PRSWEEASKYRLQYEEAKRKCDAAMDALYVFQQQQAKVRMLKQELERTQETVRAMRLLIP
HTSVNYHPARRFHAGGGLHVDQLASGKLEPIDVSAGQNEITAARMALLEKFVTANDIRPV
VSKMFAAGPAGRHAAMNNDDEHFAPSDGDDEEDMMPPPSDESDAPPPDDEEDDKSNNEEA
VSNGAAQQKQQQQQTAPKGEKPLPPPPPPSLPAPSQQHPQQRSALPAKAGPPPPPPPPTS
AGGKKGAPPPPPPPPSGAKKPPNGNLPVPGPAAKTPSAPSKVFFKGPAPKKRMKPLHWDK
IPFPDTVESVWSLINAGTLHDTTFDYAEFEQLFSQKEVEAKPVSQPKPQKVLLLREDLHR
NLSIVLHKLPSIPNVQRALFDLDANVLSREMLTAMLAQAPTDEVRAEFLKNANKKPEEEY
EPQEKYMAMMIAMPEFRRRVSAWLFSMEWEESRQAVLKPMHRLQESMVAVLNSKYLPYYL
GLLLNFGNMMNYGDARRGNAGAVNLSLLDKLELTKDNKGKSSLFTYLVTTVKVRRPEALH
LIDEMKPVLTANVMQISWGDMEMAMQEAEKAVQVFQNHCTLVKKKLVELGTDAEDPFVPF
AVEFTMRVTGELQELRQHYGRLDNTRIKFLQYFGIIDAKKKPEDIFSQLVPFIERVRRSM

QEMVKKERRNMKKGQKLGDGEFAHVVQKLQEQVAL*
>TCRU_9525 Eukaryotic membrane protein family, putative
MREQILRSLFGSTKSERAGRSVHDGDDPSHLPKGTGFNEYLDHFVRMPEMLVEIEFYFAL
TILGMAENLLSMLLLPLKCIVAFPRLERRDIVALVLIAVGMLTYCSLSLYATHLYAYLYH
VVRRTSFIKLVMVFNILEVVDRLLSALSQEVIEVLTISVQNWEKKNPQHPRPEVLFTHSL
WLPVGSAILSVVCVAVHAVTLLLSVVTLNVAMNAEDRLLLALMVGTNLSEVKGAAYKKYN
RESLLQVTAADAVERLKFLLFVLVMALQHMHEQFHVLDIADMLLVFLGEVFVDFTKHLFV
AKFNGISLSVYRTYAQLTILDMAAETVLWRLGDNIHIRCVDEPQLHVDNVKTLLSASEGF
FPKYVKRTGYVPVPYAALLLWSLYPFVSMMLLRAPLLFALSLAILVLLKILLSELIRGVA
TRFVVRSLIVLQHSEPRRGNGGAAGILFGVSPLGTPFVGSLKGGSEDADGGPVATLQLTS
FLCSLLSLEPFDLQAGKAKR*
>TCRU_9526 protein kinase, putative
MFTPGKLSPYTDRLLPRHERNDGGKGGTASISMLSNCLNQLGDDAQKEGPERHMHTALTP
NRCSLRPMGQGYGMKSSSFTMGLTTREKRRPPSLFTTPASFFAPTQQLTPTGWTSKQMPV
LPPSQSPQKGPTLAPTGCTIGCESNHGLSLSLPAQQQVGKLPQSPAAGAIWPNDRRFAWP
EKASLLSLSEDKRVLLAGPFRVSNEGCLTMQNVLLLNAEKRGGSVPLSTGKDAPQQLLLP
ETILAPAEPVVNNSFTLLSASMDTRYSPITYSLDANQAVSHDPFKSEGRMRFQENSFAVP
PPAQAVGDRVHEVEEADSPEFYSLPGSEDVSAMSLLSYSELPLKSKSLTSLPPNVVRYGD
LRIMSQIGVGASACVFMAEHMPTERLLAVKRIDLSPLFFDWNMLRGSNLQRLKSTTRLRQ
LQLIVVRELQVLHLAYRSPFMVKVYNAFYTEDIMALDLVMEYMHYGGLDHLQKLLCGRDE
TDNAVEDDLGRAGRRTKRKTEVPERLVAVVGEQLLRGVQHMHERGYIHRDIKPGNVLVNK
KGIVKLSDFGLSQRCDAVNERVGDKKNKTHHFSGTKREKSSPPMQKTLSSGGSTSSSDSV
HCSGTDKYMSPERQRGEPHGKASDIWAVGMTLAEFAVGEYPVDLTDCEDAFDRASRIAAP
LNLRNYARSCPLSEEFLDFIRISRLPLAAERPTAGELLEHPFFRQWKDEPFSIEDYLHEA
LMES*
>TCRU_9527 Tb5.20
MALVSRTFAEYYHALVTREPLPDELLKRVYREETGERKRIEAELDAAVNDLRHVIGIMIG
ERKKNRDTHSCRQITYDKHTLQVMEQEKAVWLPPIPPRSVMPPRRRFFPGFPFTKYNRLA
EEEQELRHWLSSLEARQRVPIEEACSHSWLLLLCFYQCNEQETNGRARVEREEDEERLRI
RRDVFRLAPPDYFRYLWMERYGTKSEPKEKTFYEVCEESREAIENEEQDDWRCMMRWLFD
MYGVSLFSVIRREVAERYEIEEVENNELWLSIVSLSRKTFGPYGKHTAALAWHAGGRPNL
IRSLTSLAAGHDTREVAEKLRWDVEDERRASAPHGPLEEASCEEMNDAWRELELEQESAD
GKMNKTSPETYSTAHASSKESSREEKFSTTKPEPETASVPEEHRSSRKVSGAVPEGEEYP
TEAERPVAADEDGHAPETASVPEEHRGSRKVSGAVPEGEEYPTEAERPVAADEDGHAPET
ASVPEEHRGSRKVSGAVPEGEEYPTEAERPVAADEDGHAPETASVSEEHRGSRKVSGAVP
EGEEYPTEAERPVAADEDGHAPETASVSEEHRGSRKVSGAVPEDEEYPTGAERPVAADED
GHAPETASVSEEHRSSRKVSGAVPEGEEYPTEAERPVAADEDGHALETASVSEEHRGSRK
VSGAVPEGEEYPTGAERPVAADEDGHAPETASVSEEHRGSRKVSGAVPEGEEYPTEAERP
VAADEDGHAPETASVSEEHRGSRKVSGAVPEGEEYPTEAERPVAADEDGHAPETASVSEE
HRSSRKVSGAVPEGEEYPTEAERPVAADEDGHAPETASVSEEHRSSRKVSGAVPEGEEYP
TEAERPVAADEDGHAPETASVSEEHRGSRKVSGAVPEGEEYPTEAERSVAADEDGHALET
ASVSEEHRGSRKVSGAVPEGEEYPTGAERPVAADEDGHAPETASVPEEHRSSRKVSGAVP
EGEEYPTEAERPVAADEDGHAPETASVPEEHRSSRKVSGAEEM*
>TCRU_9528 hypothetical protein, conserved
MEMAPYTAMEWSLIGSSVAVLVKQRGEIQEQFTHMDEKGQSESMVSDSATISGLRSIPGK
HRQTLGGFEPYGTHYGSPGASLTKFRDSSAPAHRVGRPVSWGSSKG*
>TCRU_9529 hypothetical protein, conserved
MQYLILCTGAIFEGEGAGRQRHRVREMWSPKIALRISGVDPPSPSRESALGKRGCWHAPK
SLMRASRSRSFAWGWAGLSINGVRARQAPILVAQEDRPPPQCWMRAPRSGYSLPPLDVEA
ARSDYQRL*
>TCRU_9530 hypothetical protein, conserved
MAIDGLVSCRRALEMDREPSDQLMDFCRALPQTFRMLIAITTDPSISRPPHFVPAFTWPF
TRPTRSRGWLGLSWIDGEPDHHNSDLCGANCVVFIETRLLHATCAPKGASRTTDERQVTA
KGLLAAYEGGGKQPHPFHHHLSAHKASHRAADTSSDLSNRPNQSTRRAMELIRQRCSTVV

RRTSDIPALGQLYEESERGGSISVCAVNVGAENFPGGAIYNLLLDARTADQRGELRGLLA
ARIFISGRVRFISRMLRSMLEMNRTPLEMMVLGLKEIAARTETRQTHSLTEDEMNRYICD
RTDWRERVVFRLAWITASRWSDIAALTPNNFTLERDGTVILDWSVAPKTARADPHRASRF
VRIRE*
>TCRU_9531 hypothetical protein
MSSGVPSISNMDRSILAYCSRVDVATSIAIKKAAQLSSFIGCSCVRQKVVNCPAREILCS
HVDGAHISQATSFALFILPAQSGMSVIRRTTVERRWQISSIALLDDFVGPFKRSDGVSAV
RCDSCEDWWEVVGLLSFAFMGGKQLFCRFLMAICAASNSIWLRCARCT*
>TCRU_9532 PQ loop repeat, putative
MSPPDLTPITETPSFVNEGEEMNLEVFLRYFVADVLPYAVVLGSVLLKFPQILKILQHRS
ADGISLASVYFEMTAYVITTSWGIAQALNFKDYGENMLIMGEVAFLLLLVGYLQRSMSCA
LLVFIFEAVALVVMSSGFLPRIFHEWLLGLQIFLGMSSRVPQIIMNYRNQSTGHVSFLTY
YLAMVGGIARLLTTFHNVSVEKGKYVMLMQFGVAVGLNATILLQILAYRELTRKKLDQQN
LEKTLEKDKKRE*
>TCRU_9533 hypothetical protein, conserved
MAGRPIPPSGLVKAVAGVTQASRGDTKKAYWTISTTEVLCTRMHSWQSTFDCYEFLRKRH
LPIADEAVMSLLLRLQIALKGHGASASTVLEVLNFSSSFEVESRGRRHGEKGSNFIFKSI
NTDDVSHSPPSPLAFLLHSTQYQPTLRPLYHRLRYIVRNMAHSAGESSVVVGNDHHGSNS
VRYYQALFSDLLPILLAPCVVVNLSLWHNLRRRRWEDALRTIHNLHFYSLLKPYTRELQK
VRLKSDTKSILDAVSHDVCYKACIDPPSLVPLMDELLLRWESYWDALKGKTEAQRVFSGV
LRSSSSFHCAAAFLDNEVTVSFTLEDDKNSMEQTLKEKASGPLAILSELEKSSLDVLRFA
ALISFYRECKEDDEIQEELEIFHRLMEATTRIADFSVCRRVALEWANAYEGGVPPSERCR
VLPSISTEQLVLTRLILRAPSCEIVLQVLDEWPFILCDHSCALEGRKRKILFRKKIPTTM
RCREVIFALATRLSPLTFLEEIVNKRLSASSEVLEKCVREVVRDSLHRGSLHDAAENFWM
CQAHLELATLCGMGDPSHSDDELALLLREYLSQRLSVREKRNFISGLFRRVGEGNYRVFI
NAVCILDEEEVDGFRRAPTKNTCALSLLLQVMVSWVKDDQQLGDAAVLLRHIVCALDEKN
LESFEHELDKPEQRIHSSLHFGWTSEEVMTLFFEAVACLGFLTNDKAAREGTEADTALQW
LRLLSEIPPSLSDEQTLVVWLFWTMRALVQWEESLNSSFTSSTVAEAITESVLAAVLNLS
LSLEKCGEDAVLPPMLLNWLASYTGMPWGDATAWIAKHAGVEASQRRRFLFIRLPFGHAT
FDSSTDAPSRKRLLSSIEWELQKETIHRCGGLGQDTPHGDDKLEMKLQGLFKTIRVTLLR
AWQSRAFSVCSSGEMNPNMTDAFFPVAPRVPVYKRKGFLRNRSRAHDEIALFSFQELVGC
LLEETSLKQDKATNKET*
>TCRU_9534 seryl-tRNA synthetase
MPIAAYHRGKWFTELKEPLKYAGMSSCFRKEAGAHGRDTLGIFRVHQFDKLEQFLVCSPR
EEESWRHLEEMIRTSEEFCESLGLPYRTINICSGALNNAAAKKYDVEAWFPASGAFRELV
SCSNCTDYQARGVNCRFGPNLRNVSANNVKEYCHMLNGTLCAITRTMCCICENYQTEEGV
VIPDVLRPYMMGLEMLKFADNVPSAEETEPK*
>TCRU_9535 cdc2-related kinase 8, putative
MKRDRDDSVVGTPNGKWDVSPHGTLGVEAKEFERNAVRRYVFGLVHLKNEGPKANAVDVS
ESIVRSFNERFRRIVKIGQGSFGEVYIVFDTVTQTHLTMKRMQLLRGAGRRVMGLCNTTS
REMNLLRVLKHVNIVELFDYHVVPDGTLIMLMPVIAYDLVSLIRLWRNGGPRGEPSAGRM
PLPTIKCIFRQLLTGLAYLHKERVIHRDLKPTNVMINEKGVVKIIDFGWARFCPARWRGP
MTGPPCPVAYRPPEVLLGGEHAVKYDASVDLWCCGCILFEMLSGGKMFINARSEAEAVAG
ITDWLGSPSSKSTLYYGHSAASLIRFKQNRPSRLAHRCELLHIDRDSVDMLDKMLQLEPK
WRMPAEELLRHRWFSSAPVACEPHEISLPEHNMYRWLDSKRPS*
>TCRU_9536 hypothetical protein
MNAQETGERGWLEHYLDLSADEDARSDGGKQSCFVTSEELFERLQEEPSLDEQTIGVHVY
TEPEVSWAPFSLFSGNHHFLVIETSSWWWSIELRDGRIVVQRGKDFSSVQNRCRCRYRRR
RFLQNGPCLVFQGTFEWCCLRDLFFFIDCEGFFNGGVLSDKFSSLALVNYIFKECGVRQL
VGTSHV*
>TCRU_interacting factor 3-like NG.1
MASLIRRVMVAMGEIAPLWLADQSWDNVGLLVESPDSNNSGIVLLTVDLTPEVMEECLRH
NVEVIVAYHPPIFTAFKRLTLADPKQKIILQTVRHGASIYSPHTSLDAAKGGINDWLASI
VDSSGACRPIQPCECVNGHGNGGFGGNDNDELSVGIGRLVALHQPKTMATLVNDIKTGLR

IPTVRVSLPHGWSGNTSVHSVAICAGSGSSVFRMIREHVDVLLSGEMGHHEVLAANAKGQ
AVILCEHTNTERGYLEKELLPKLQQKLEKGVRIIVSAEDKDPLVVW*
>TCRU_9538 cell cycle sequence binding phosphoprotein (RBP45), putative
MSAAILNEIEETRRLVDEYYFRHITQLHAARSTFTQHFDQLASLLNAGASSRHEETGPVM
IDALLTTPSRPNYVNDEAMLASPSMASPPVNRATLNYDHLLTEVSGDNSVAWQNCPGAES
EADSRKRPTLDSIPEERRSRSPPKDRSVPCQVLVVFKRKRVLQFESQTYVAPGEYVVVGG
DRGEDIGLVTHSWTLGERDHNGEKKWGEGVGRVLRVASALEVSQLQGVQTELEERAVEVA
QKKVEEHGLPMCIVDAEYQFDRKKLTFYYRSQHRLDFRTLVRDLYKTFRARIWMEADVPS
*
>TCRU_9539 hypothetical protein, conserved
MQRKRRLLSPSQSNLRGVPQCDVSEPFSDIEGSARACSVRSEGLPALPGEPVMDGGEIDR
GGAPTLPVGGVFHKERELNERELALASQKTNLAWNLQESLAPLLVDQDDELRGSNPAVLR
DSSFQREDVNRLDDYVVHNPADVIDGMNRVSAYVGGRAFGGTFLKTSSNGISIQVQCCKV
PRVQRTVSPVLRVQPLYSPWNPENVLSYFMQQQQEQEPQLRQIPELQVANSLDVAVQTEP
ATEDATGGRPLTIERDETVTKCVQTLMDAASSTSSLTLTRASGASSRTGSRSSGSRIQQK
QLSESALNGEKEMNEVAMGSSGNSKKGSEAQRPSNETRSDKSSHGENKNANDPTHEVGVA
PPVEFSPPPKSVTDLHGPPARVQMRTLSTIPEGSAEMMGLLESNERCKTSRELNFDSGFQ
CATPVVRTTAWYLPNSRVLHHTEFKNLLCGDWESPLKSVQVESAPRDWSPVVRDATVQVS
LVEPQEFGLAAEDLIVEFPLPPDLPCPDMPPTGRESKTERSSACCGPCSSGRRFSCCFPF
LKRAKKKPVL*
>TCRU_9540 hypothetical protein, conserved
MKGICDTFYNKTPSEIHGPEVKDMCTYYAAIPDEPVEPPTPQGPPSDLAVSNTTSNEGTP
KNAPEFDVAERREGKEDEKEHGNTDKIILNWYELTQEDCATDNTKNGTVNVPAMKRCINF
AMKGICDTFYNKTPSEIHGPEVKDMCTYYATIADEPVEPPTLQGPPSYSAVSNTTSDEGT
PKNAPEFDVAGRGEGKEDEKEHGNTKEKAVETAAVKSITKTTDSDSYSSTAVSHTTSPLF
LLLFVVAAAAVVAA*
>TCRU_9541 BNR repeat-like domain containing protein, putative
MKDGTFLFPVEGTKKENGKTISLIIYFSANDGWVLSKGMSADGCSVPSVVEWEGKLMMMA
ACDDGRRRVYESGDKGEFVDGGTRDTLARVGQQTGR*
>TCRU_9542 hypothetical protein, conserved
MRQLIHVTSRSAVLLVLLVVMMFVMCCAGGCFAASLTYSYSSDKAMRADRAKSIPAVVRD
VSFGYEGASQTCTVIGRNGWAPTRIDVSTRDLDGTRKYCSSERYCAMNSLVAIASVKVTF
FYDEKREVFVSLYFAATVR*
>TCRU_9543 hypothetical protein, conserved
MAMMAGRVLLVCALCVLWCGAGGRCDEGGTGVTPPGANPASGAGTTGNAAGQTAPGEAEG
FSAQQPQLEKVGDSPSGGSRSQVDLQLQSPTIQLTPSGAEHTAPSTHSKPSGEQMQDLPD
EGPPGKPGILSSQEEGKNKTIVNKQSNGPPSHLSNNDFVSRNSEELTEDNSRRAETLVAA
PSEEGQERENVTPSLEQPRETSTAAPTVTTQTTSMTPPKDGESGSIKMSEASPQSTGTTN
TNDTATPGNSDGSTAVSHTTSPLLLLLLVACAAAVVAA*
>TCRU_9544 Concanavalin A-like lectin/glucanases superfamily, putative
MNKRWETVFNGTKTSQNGTWEPERGYQVALMLQDGNKGSVYVNGQIVGSPENIATPEMRG
YEITHFYFGGDEGDSDSSVTVTNVFLYSRPLSVGELKLVKKSDDKKGNGDGKKGKGDGPM
RCGVDGVAYKYIWEIGCGRCGLMQSIEEALQRACECVCMHA*
>TCRU_9545 hypothetical protein, conserved
MFHYSIITTVNIDGSSVVTLTGCTMGSTGLSVPLLSQADAGYRFVAGCLTVAGRVLTTAA
ELELHGITNVTTVTACGECTKDGDCFAPLTAAVSDCKCQCAAGGHGDACVPAPVPAGPPP
PPPTTPPPATPTPPPPPVGECISDMVYPEVAQAVGSGLSWLCYRNVTFSGGGMSLTVLIG
AMTGDVAH*
>TCRU_9546 hypothetical protein, conserved
MKRTPHPSGVEILFDAKWHQYKLGHTALRSVSKVLDKYFPFDEKRVLALVSKKTGQPVEE
VKAGWNRQALLGKNIHEYIENKLCGLPPPTWTVVLKSQQKKKEEEEQKKRNSGKKKTDVT
SPSTSSKQSIVDSVLHGDEAAYMNAADRVIENILRHYDIIAVEQVIASPSWGIGGTVDFI

ARNKRTHKLLIGDWKTSGSVASAFRFGSFEEPCTGCLMHLPNTKFYRYAMQVIIYGEILK
HERYLSDGFFGRAVKPINVAVKSISVSPHDLHDAFEYGIVQLLKDEGGGVCVELKGVTES
TVLPVDAHDNTFMQLLKNVMRG*
>TCRU_9547 ubiquitin carboxyl-terminal hydrolase, putative
MGVNSSKGGKLKRELSPQNEPIRSLHARGISLTSEAELSVPVPKIRPLPLKIETTSNHNG
SSSSVGEAGGGDARKNGINGTSGKGAADALFTSPECSCNPTDKLRPPLSPKNLFCPTSPI
PTYSNELSVALPSTPMLRSYRLHSFSQQESTLSSPLSPGLSSPPIHTRFLEINGYPAGLE
NYGNTCYCNAVIQLLYHCSPLRLRLLELYQIYAKGAGHTGFEEDTLLALVVDLFAKMHKA
NNQKRYRKDAIAPKALISSIKEQNAAFNNTLQQDAHEFTMFLLSKMIETEKRMMGDEKNR
ALFFGAKKGKGPKWWNVLRRGRKRDGSWQATGVGEVQEEDVELPPALRDGNDVPRPANAP
SGSGDASDARMAATFTAAAAAATRTTTAAEADWSAVSPIQVIFGGQFASLTACFECERTK
TTREVFLDLSLDIEQGSSLLRCVSNFGSPELFYGANKLHCEHCKKHVVAQKLLRVHRLPE
YALLVHLKRFEYNEKTGKLTKRSDHVAVPNEIDVVEYEPWDDSNDASKTGVSECDSHAPC
PPGSPSVAVEARTVAEGEDEASAPRPSVHLMNKLDGVVHRKGRFALSGFVTHLGEGPDVG
HYFTCVRHGGRWCLFNDATVTELTEYEVQKFWGVPIPVSGVVTATAYILLYERVA*
>TCRU_9548 piwi-like protein 1
MMRKTVLGLAPVAIQTIAARSERQRQSRSQQQQQSFNTANSGGRVAWANGGGNPNQKQSK
SLWCSAAEEVALQDVKRKYANDRFLDKKTRSFVRERLREEGVSSNLFPVHVSPDTTLYVY
EVEATSRLLQPQLSDAAQEEEGENRVKSAGRAKGRCKKGAGQTATTATSRDPITKRVDAT
RAWRVVRRFLQRCVPNAPPFVNVRQKVYSLSPLPTNALQLPAEYLDLGWVACKLRFQGKV
SMTQMAPSDIQELTNKIAMWTLGQQENGKKAFTVAREANGKLVCTHDSFIVGGMRIFKGT
IVRAVFIDSNGAIDTKNCAASALPAPPSTAVLTTLRAGHHPTEPLRFLVKEFLREFEFKE
TPVQSYRIEDASGVIMASLWKATKSAKLSPGTVYEATDYRVRVFENRGSMRLVEMTVGET
ALKPVEEKQTQKKSAEVKSTSGGVGPTKRRGKKKGVVPPTGKEEATDAINNKVTPGVTEG
GSSSVMPGALALKIDTKGTVAAELSLWEEVKQHFGSGPYDEATEERIARSVQGTPVIISA
NLRHSMIRFVRFNIDPEKVDLDPVLQRLLPDLEPGQPCAVLKDHSVVPLQALHCCYDPRM
KSWQDISVSTCSFLPTRRLDVLRVFHAVLEKEMRRWGLILASEPFASKELSLLPAPQKLT
SYGVGQGASLNHKQNRSGSLRHPPPPSFPTTLAVVAIASPHAEEEVRARITQTGQAVARS
YRSLITMTVPDEKEAVRFLLQQLTNASDGTLKDPNTAAVIISAERETRASRWILAECLTR
GILGMFIPPATTLKRQNLLCENVRIQLRTKFETDPAHGVNLPREVPALAQRRVLVVGVDA
CHTTTFSTGSVVGILCAPERNHLLPFFWKHEMRGQEADRVTEHFRLVLQRACELYDGLDE
VVVLQDGDVSSEARQMQPHLPAGCGFTFMCLHKRTNVRFVHRVLGGNQFPKATAANVVKG
AVVQALTPISLQDDSVVPSFYLQNHDCNMSTARTVQYTIHSTSPTLEVSDVQQLSHVLSH
VLSTQATKLPMATRCAHRLSSVAERLLDAAPPLTCDMIPAPLNERLWFF*
>TCRU_9549 hypothetical protein, conserved
MLAAGRPLMKEYNVTMEMLVQEPDDYVKHQRLLEEILNLTAYQALEAITRPLHEGVLSLS
GNVGIMKEKDTITPLARRKPNGVLTQVPTEARREAAERLRGSWAVRVGCFTARVL*
>TCRU_9550 hypothetical protein, conserved
MKASLESYSKSGAHAISGTEGTLTPESPLAFLVLWMRALQLHREPKKQFMDLGRIVLQVF
RMQIVIKFDPSIPIQKLRARLRTAFHEDDTFARVAQPFMDRRGTRSQQQRSLLCQLCLIY
GHDASTCKVRPKRVFQNYKRKLKNGRRAAARRSLMLATAVTPNPPTPAIPNRHRTAPPTL
HPIVQTADGIDEEGGRDGSRDVGAVNVGAENVPSGAIYHLLPHARTADQRGELCGLFDDN
RSGAIDLTAVRQDAAVHVGNESNPAGHDDSGVTKNCGAIGDEAGAPLNRGRDESSNPQPD
RLEGTCCLTTRVDNGESLFRDCGLNSQQFHTGA*
>TCRU_9551 hypothetical protein, conserved
MQDTSRKRKAHESYDCPSGTSFRTLECHGAFHKKRGALRRAAQIVETYNLDPHVISRLAK
HFDPFDLSPEHSSIFGEVHHTADPGVVAGRIDVKGETAEGQEPWLRAEERFFHDFNHNHA
ATITRRATRTRLATPQDEHAIPLQQVNVPVLNLEWIKSRLNPATLERLMQVWGLVGRSPF
PPSSSGRAREGSRRIPTADARLMKEAGIIEDALSTITGGWIISFSVVEEKTIGSRRRQIA
WPRDRNRDDPYEANVPLLHISHYLPPVMAEAASCLDLKASFFQFSLSRETRHPF*
>TCRU_9552 hypothetical protein, conserved
MRSKQRGFGGPTASPFTHTSFPSYFIPLGYLRIRPAAQANNPVRFPLTLPPADGPAVAEE
ALAQHVMQGFMAMCHAGSSVELLCSVSSARLQQTIAERYPPAYNRLLLERRWRGKWRCFA
EEIVGLRCFLDTLRDYAGAKDLEIHVAFSELRCCLQGESHCAVRLTDGSVGAPLREHLLR

EGVLHRWCDETVRAARTDGGAGGADRALWRETRLRGTWVHCGSADTSSIAFNRGWRRIVT
GDPRGTSSWRLWGEKRGRERGEPRVGEGGCGLLRPHLVVVTSVCCHDSAVIFCFFFTGGL
YCAFSLVAGRRGCVRAVHLESLVGGP*
>TCRU_9553 Mucin-like glycoprotein, putative
MMMMVTVRRRVVCDLLILALLCCCCCLSVCGTAVPAKSFVFVHFSCPGTDGKLSWHLRGE
EEWKKCPKKPEEVDQDSDERARLCVAGGDFYEYWKSRRRIFCRRPSNRVEFMFEMEFATY
GGLRNSSSAMAINNDREATDGAQQLQSQPQTGTAAPAATAAASTKAVVGQAQSGVGSPSR
EAAEALQKSRLTTQPRTALPQVRAKTSPPAR*
>TCRU_9554 Complex1 LYR-like, putative
MYWFYSRDEVSRRMMHHSLEQRCQRIREMERCNAAGNAAIETPVVTEFKSSVYHVHPDCH
GRIEQMPLTHNRGILRARGQCGSDVGGPQQKFCARRYKALFPQGWELHQPPRASVC*
>TCRU_9555 hypothetical protein, conserved
MRTRCRRRIFHVCVFLARTAVGADAVVRLASNEGTGCCGVSTVAVEVAVSLSAPSLFRLR
HGALLRRERRLHDAVSRYLGPGVYWDSRWRSPELSDRVWRAMARNGFATMRCCRCVTGVR
RPNCSGPRNGTAEYFLLGDLVRSRRHVRSTLFGGNKCCRYQRETGA*
>TCRU_9556 Acyl CoA binding protein, putative
MDYAFPEKYFKVARFFDHEFGDIESTARLDDKQKLLFYALRQQAEHGPCTGAAPSMWWTR
ERIKYDAWKQLGDMSRFEAMVNFVRLLGECLGGDVNWVEKCKALENNIIHAGDSESFTVP
DGGGSTHAPGEEDTWDDDVRDHLEPTVENVRYLASQVMRLRREAHQLRLSTAEKQTRECV
AARLAPPPIKAPAGNAGSPQKAVPVPPGRPVARRSGTLPPSPPFSFPPTKLTEVALGSPR
LPSPSPGRRGMGWAGWLGRSERARGRGGENETPLCGVHGRDWGVAVRVSFVSLSINWRCP
APCAPVWANVSLARTERALNGAHGLFGCALLWCSLSFAPLPRLFSPQPHLRFFLFSRPVV
FVPWPDGGCTVTSRQRQRPQGTTKI*
>TCRU_9557 hypothetical protein, conserved
MLSALRLRGIRSAPAPAMLIGVPFRYSIAAAPNLTPSPTKPPVHPSRRFLLGVAKGLCVR
CGGRASGHKSGAGPCRGHLQRHRRGRGGQRASVRGAGRRAMMKS*
>TCRU_9558 Protein of unknown function (DUF3676)/Trans-sialidase of
Trypanosoma hydrophobic C-terminal, putative
METVAASVNGEHQVQQSIELSAENNDVRSTGTGTTGAEESLSLEAGERNSERTMNSDSTL
TSSKSDAEPTSAENTDDVSRTEGAEVSSEDGKEVPQTVDTASGNTSTAPVETNIPSELNA
TTPSDHDILPENGQLGELAAIYLIGDSTVHGCVSRVLLLLLLGLWGTAALC*
>TCRU_9559 hypothetical protein, conserved
MAARIRVSSAGDVRAAMETIFKNYEKCFFPVLCEKQPTPELEAMPSYLPDNVVPPLYRDD
GEAEFADYMDANSLTFVALGDAGRPALCGIDAAAQLHHEGAQRALVSAAGIVSSICRRRL
CIPFGNSELSQLLRRAYNTEKGNRNNSFNGSTETVLLTQAFSDAVWAEESFHCFSMTRRV
GNILGLTGIGSTTRDLAVDKWRPDQDIMELRDELMIARTAYDHRHCGYESNRPFQA*
>TCRU_9560 hypothetical protein, conserved
MVQLDRARGREAIMRERHSFQAMRKTVLEERRRQRRQWIHQIREMNTKFPETVRPLAEER
KKNCEQATAKEDAAERALAADVKMIEECLPRLISLEDIPVNPEETDIIRRQFDEVFTQEE
QT*
>TCRU_9561 hypothetical protein, conserved
MRLWRFDCVLRVGRSGRRHASTAAKALPVRMIGVVHKVFPDRGYGFVLAVPPPASLLSTA
PHPASSTTMEEIGEDAQITASVSQSLSQGDPLSVWFLLRKGDASTTETRGKLEGAASPPT
PLPGSYVRFSATCHYDKAKQTHLWRAQEVVPCDPEEELQAALRRVRDKRWDCITSEDVRR
EMRQVARRYLLEEQRAVKSASRKDDDAAAEASQRSLREGEMVDDIAMEELQMQLTQERVR
RHFHHLNKASQRFFVREVDLRRPMISAQKDMEMQTNPEGDVVAVGRWGFSDDERRRWERV
LQCLKEQE*
>TCRU_9562 hypothetical protein, conserved
MSSHSSDVYVMEDAEESLRTSPANSPLEDLVRSSSFTSLGSSNEKCGRHPPPPPPPPLPA
ATARTICTVGTNTEQQVEESVSNLLRSGIMGLMHTIAGDEFAHHMLHKSRQDIQRSYIER
ITGLAQNTINVLHKLIACQSYPMHGKESASEIAVLDEKAEPEWLSELQISIAKTDALLQG
LTEKKETLLTATDAAEATCSIPTMPAARSNVRFSASQQTSSLPSPLQDKTGRMQELEHEL
RMLQEQMAEVRVVFAKEGVDSVVPLYSELLSLRAAKRQAALREVENTMAYLATQQCCFDQ
QLEVMERRKRSLELEASRRFYEGGDAVIGLMEDVEKLAQAGRKLNWLRDEYRRRVREVDP

VVCANFSSFPGEKRQRTSNTNFSVLLDWQSEKDQEIMALRGELNAQRQEMEEWKRRYEAA
VGEMSRPQESPVFNSLLQAVEDRVSQEAAQRCTLLCRLFGWELLQLTDDTVALARVGCAE
ERLTLPMPNPSGDETSAMARSIVLAKKVLEGSLVIRGECQKHEDAEEEHNDDAGEQAPTP
KDNGEAEAGETVPTMKETPFPTNDDHDIEMEVDDSAETGEMDTEAPSEENPLVTENTVDS
PGKLEPSFYSSGLWEE*
>TCRU_9563 hypothetical protein
MIGCVPPAGFITASDGRTLAPLVVGRGAPTQWVTSRPVEEGEVLWSECLFVFGVGEGGGR
LLMLTEDMEWNKTALMVWNAMVSKGGEKVTVWSVGFSALARALLVAGSRCPAVASMIVEP
RSISLHSDSVAVSLSTLLVKSYEKMKGASPFTPIEASWLLIAMQEGSLPLHDPVDTGVAS
LSCFLSFSRKVAKVPLRAASNASLFIESVTKAGEVRVCCRARKNIPAEARVRLHVGRSLD
ASVTVEDKLQLEWGNYCCGIEGRLLGVA*
>TCRU_9564 Monooxygenase, putative
MRVVIVGAGLSGLSLAAFLRRLNVDCVVLEQAPFLRANYQMPFTLFANALSCYKAFGMDH
VLSGGDVVSEEYFGILDERLRWLLRVRNRTVHLRALGDGEMLPLSTAPPANSESIVSQRI
QEKMKQDLGSVPLRATFSADYLRRILRYHVEDVHFNSRAVDLLPHDGIKGGVHVVLENGQ
TEWGDVVVGADGAHSTIRRLLYPSEYIGTSSRSLGMTQVDGFVELGHDVCPTGDYPVEVW
GRRRVLSCVPLYCDGKVQLAFSATLYDPPMEVVDIHSETDAMAVRDVYRALLHREFAAFG
DDITVLLQRAEVAVPTELVEVPVMPRWFNKRAVLIGEAAHGSLPSFLAQDASLCVEDAAL
LAASLLDVPLHSDTGFEYVFKQFETLRRDRAERYIRQSRRARRFTSLSYSTVRDAMLRAT
PSVALMWFQRWLSNWRYNSQQLEVDPKIKAETAFRG*
>TCRU_9565 Regulated-SNARE-like domain/Synaptobrevin, putative
MVTIRYALVASAEGVPLADFQAVPSMHAGGAKKILANIKRPLVERKCVTFNGYSYDMLPH
RDGTVYMCVTEESCSRATALKFLEVARKHCNSRSKNPVVLAAELRKEVEMFNDKLNAKIR
DIRSDVEKVRGEMITNVDKLLDRADRLDALLLQSSALEGESSAFRQNTRTLERQYLCHRI
LIYVFIAFVVLVLLFVIVLAACSRDGVNFNRCKRN*
>TCRU_9566 hypothetical protein, conserved
MMLRRLFVFDAARATNMRFLTMTSEVRDNLTKQLSALKEECRGQGLDLADMSDASRVAMR
TVQEGLTRASVEDENFKGKSITLSASMKAYTARLSNLQDEARSIQTEVDALLKMMWGTEA
PTKAASFASPPRSTEEVGVSSSFSAAAAGGKGNETVDDEFIVEPPPLAKALGNDKRPAER
VEAERVQGTAHKPVEEMRVEEIEVETIEVEVEPNESPADNMKITDITKELYERGVNFSDC
LDARTLRQRYKDVLAGKISPGISPGTATSSPATAEANTNQPRMPQHRPYQQQQQQQQQQQ
LNTNESGLAHDPYPNAYRKMVDPMKHVWELKNELAAEKGIDPKSVDLWSGKCKLEDHKLL
YDYPSVQNYPIEVRQKGDIPR*
>TCRU_9567 FYVE zinc finger/Protein kinase domain/Protein tyrosine
kinase, putative
MDTVDPRGTQGESENNGNNIGNGNGNGKEGGGGSQAKATSEKNVETVRRVFTPKCLKCGV
TFPSPRRTIPPKRWECPTKGCGGKLWQPDDASQVCDVCGAMVARFTRHHCRRCGYLTCSK
CLKFKTILTEWSLTEKQRVCRRCAVPAVPVAISGWLLKLGQRATFFGEKLHMRYFELRGT
VLLYGRAKSNGEADEGLTSVSLPKDARRGRGTGSGISTSDGANSSSSNSHMNSKNNNNNN
NCGSSSSSSNAQPPNSILTGQIDISGAKVMDVAIHPHAFCIVGPFLPRGYVLSASSQAAK
TQWVEAIREQVRKAHQQRGDEEFEDDLESTEKVLYAGSGADKNVNVSMRDFELLTVIGLG
SFGRVMRARHKATGKIYALKILDKDQVVQHHLVPHTNAEKLILSEISHPFVVKLYYAFQT
KRHLILVLEFLCGGELFFHLQRCKRFDENRARFYTAEIGMAVEYIHSKSVLYRDLKPENL
VLDREGHVVLTDFGLAKRDVAEDVRTHTFCGTPEYMAPELVKKSGHTTAVDWWSLGAFLY
EMVDGMPPFYSPNVAEMYEMILHKPLVCPARFSPELKSLLGRLLEKDPLKRMTSGEEFRA
HPFFNGLDFDKLLRREIRPKFVPDVRRNDLRYFDKRFLHESTKIAQLDQPCDPSDPVSRA
FEGYEFNVHVPTTQPAMEEKRDDIDSHDDDGGDVKDGGGDATHTA*
>TCRU_9568 protein phosphatase 2C, putative
MRPLSGRSDDSSGGNSPAPLMNVSQVSLPLHSQYLRSETSSEKVSDMSQQHRRGSSSGST
LPVAFPPIMPRFQLPELTSPRSSGINSAGMGLSLKEGVSFPVTPVKTPLHPRSPPPSPAE
KPGNKMMALSFKERQRVSEQLHRFSSKERSAGLAPQSSGAPRVVAGRCGRVPKGTISFLR
GNSGEGISSNAHMIGKGRGKPMKGEEGDDKAGTTDTRDSTPSLPQFSPVISPVTCERQSH
DDNDSIRKDTFAVMLRQPSTVLSFKERQRRTTTLSPCFRRSPTSWMQTTTPNDSGCRLLR
QACSFTTAPFPRELDGAKLERQPRRLLDGGEEDNPAAKLSDDAGPPLVLLSSWGTPRGGD

SSALVRQWTFPASSNKLQYSFAESSESRRSSLERTVTPRHIKAVPLSGKLSGTQNPRDNS
RCAPGPVTPPIVSPRLICSRVLSPSSGSLKARNDTAEILSTSAKVNTVKKRGSKEHVTIC
RVARTTSNVLCSSEVLEDPADLGSPPPKSNATVKQRRNDSAGPDKEGRTPLRSSASQGNF
QTAASVGITSGTDRRERDKILKRPASYFSSQTPPLLGEDATMASKTAEDNLVQTPQNVDE
SSSQLESGSSTGRVEVSASRFPALEGFSVFAATRENGRKSSFSSLYFSMMKHHRSQRLMP
NANQPSQMMPDEETNREVRGDSGFDELMNGDDDSFTGSLRTIGILETEEHVFLSRYELLP
EGQTQMEIMLGSIRTIGGQSFNKSNSGPGSELRRGSFMNPSARHDRFDEEEGDSDDVFTF
GSISPKYATDPVDEDPLVDCKVAARLLFDAEKGVMLISAEEEVGKYISQAACMGANKGVS
GEEQSMCKCSQEFIAKDVRGVDYSRYHAHDLYHHCVYCNRRPAAFLCLHCLRSTCPSHVT
RHYKECEAKCTLFLNLLDIMTSFDRIFWCEKCRCFTWKYTEVYDPLVDQLAVTRGTHLKE
AVRDISCVGYEVQLKKLNHRQHQLSLYASPALEAFSPSVNASPNFSATPAPSAAASPMPF
PMDSRHERLMSGANHNLALEKRSVAIDTTTSAAVAAGGLPIARLPQRDSGKPLPESEVLR
MGEAVQKLVSLGAKVQGWRATQEDAEAAFVVAIPALSPQLLSDTDATSPPPKPIDSPEDA
EPETIAMALFCVFDGHGGDAVAKLAASNFESHLRKAMASARHDDVQARSLLFQLDFESST
ALFSVGEASPVAARENAFNRQLSRPDDEKDNEVSNDDIVPEVGFTSETLRRYVESTNACR
ASPPQAAPVPNFVAATADKPVGTQALFSMVDVGGLGDITTDALSARSNLRLYNAASPVVS
QREMEMLRAYFASIMEDALLSLDDDLRHSPEGMRGDYQCTGCTACIVGITANFILCANLG
DSGAAVYTPCSIRQISVTHRITDSAEESRIKAAGYAITGNRIEGMLAVTRALGDYDFKQC
GGKGPKEQAVIAVPDVTIMPVPFLQDNARWGVVAACDGVWDSATLHQVHHAIINTPNDLD
VAGSVMDAVLQAREMSLALPQKASALLDGVDAAETASLDAQLLTSAAGIFAQCVAPSDND
EGIGMDNCSLFLIERR*
>TCRU_9569 hypothetical protein, conserved
MLDDACTEQKQLALKWMVSHAAPSLSSVVRCSDVRSTPAAAAASSSNLSDCYGGAAHRLT
QSLLRRGTQRGVPLNSKAESPTSATGPSRSFRREVTDVLPATTISLEKELPAKKRVLRRS
ASGGMQISASLSSSRPPPPAAGFSRTFSQRVSGSDTCLFVERSLLRSSGELRRVIGTPSM
GRRVSFSEGTAHAASRRWNESGRKSRAILDSHPSSCDVSTTAAPRTPLKRLESAPILQGK
PSLTKTEEGASISPLRLCVGAAVGSSGQKPFIRQMTRRGSGCLVMPSLALRNTGGKLSLA
TTPSPMYIIKKHAFEFKGARESNASTKTCVPSTSAPQGMARTTAREGTEGDKDSNSQKLF
HQPQRNNKYNQKQSQQQQLLKTTSVFARSNTTYVSPVEKGSSTNATRNGSAGVPFARQVS
QLCLMVLQERDRRLERQKPMREKEASEAKPKGGEDEAKLRQPSRSMDILSSSVVSLPFRS
CFEEVEAEERTGSPGEVLKCVRTVLEKRGVPRMQDSDSSMKLTGNSNENMNACGVSSSIR
SSGASTTVRSGDGATHKFAAKKSGKKVEEVKTGGKMDSNVCYESPTDGEKREKEREAVEE
EEEDDDRWWDAEEDPWWCFNVLWCRSSESLPPLPDFVPSLNLSLLRIPDEFTARTTKYAI
PMPTPVTICGENGVRAGGKFRESLQCVSNNFTDTSDALAGGRGAERELNQSLRKLRIQLL
LLETHERRSRRMVSQDETAAWKAINKKCGLDLLKHRRR*
>TCRU_9570 multidrug resistance protein A
MGREFDAETRASLLAVNGEEGDKQRSFDERAKKAMRNLEKCEQQLNTRRHQWRKRLNDLW
GPEPPYKLQPEDAASWICGQLYYTWIGDLMFRAAREELSEEEMPGPTRMSRAYNSGLMLS
RVLQQQRFQRRVWDAYIGVEVRHRRDRDSAGELRWVGYAQQKRTPRQLYAGVEWRVPPTH
RLKEENRNASRSPFTNGVVEGEYLFNTSSGNATATCERVEDIVIHCPLPEKKRRQGGMPV
TTQKRPKPMSVARALFSALGYHVYVLIPFRLLRDTCQLAVPVVLQYYIEYIETADPSWRD
GLLLVLAFSLLTLVQSAAGSKLTQLGWRSGYTFQNALQGVLFEKCGTILRKALSHPEMSV
GRIVNMVSSDMNSARSFPLMLPFLFGAPLQLIFALALLYRLVGWCAFAGFGVLILFMPLQ
GILMRRYYTVYGRLSRATDARLKATNEFFSGVRIAKFMSWEPSFIRRIEERRREELAALR
ASQLLYVSVSFLTNAIPAFVVAVVFLLYIEMGHELTPDIVFPAIALLGIMQTPFVMIPVA
LSGLVRFVVSMRRITKFIECEDADDGMREMLLQHTANSQAIPEEIKDLMHTPMVASVAAE
FTRATISTFVPQKLPPNGKELRAAQKKKKPDGAEPTSSSQYYELRPKDLLHGITLCIPKG
KLTCVVGDTGSGKSTLIESLLGGHEVTSGFLRSVPNIAYVPQQAWIMNATLKENILFFSD
MDEARFRRALRCTQLESDLKLLLNGVETEIGEQGVNLSGGQKARVSLARAVYATGRELYL
LDDPLSALDAHVGEHVMHECILGELRSTTRMLVTHQLHQLRYADHIILLQEGGTVAFAGS
YEDYGRFIAGREATPIVAVAASSSVEGGEAVGELQAPKSEITGVNNGDDDNSDNDLSHNA
STLLFYEDEDNEEQSQKQQQQNKKKKEDGSTDEKNMDGKLMTDEEKAAGAVSFLTYVKYM
ETCGGATLCGLVFLLFIVTEFLLVSPSLWLSFWSVKRFELEPKTYLLLYVAFVAASALCS
PLRNASAYAVLRIGSWRLHSQLLRSVAVAPMSFFDTTPLGRVMNRFSKDMSTIDSNLQSS

VIFFLQSILSVISSIVVMSISQYFVLIAIIPCLLVYYRLMVFYNSANREMRRIANRSNSP
VFSVLGEMLSGRWTIAAYDRTAAFVAKALRRIDTVYACSYMQTVCDCWLAVRIEILSNVV
LTSVALVGVLLVMLRFGHVDVGLLALSLTMAVSINSQLKYVVNQAASVEADMNCVERVQH
YTSNIEHEDLMEEIDEAIRVLAKNDKKRRKREGDPITPAGITHDDDDTSTATVSVPLLQE
SHASDASPELSFSSAGNNNHNDDDGTRENVAAGSLEFRDVTMRYRAGLPHVLCGLTFTIP
AGQKVGVIGRTGSGKSSLLLTLLRVVDIEDGQIVLSGRPIRSYSLRALRQLFSMIPQDPL
LFNGKVRENLDPLNVCSDAQVREAIRLVGMEDRLAAETDPLQCPVEEGGANFSVGQRQLL
CMARTLLRRGCSFILMDEATANVDPTLDKQIQHVVTHVFAGHTVITIAHRLHTLATYDVI
LMMEEGRVVEMGSPYDLVRSADTRFAQMVRSLGESAMQEFMASTQAPTR*
>TCRU_9571 dynein heavy chain, cytosolic, putative
MRKGKKSGTFYSSPRSAAGDTTSVKAFSTFTPVTAFARTSCKATSSSTLEFLHSDPRHVR
VCVNDLVAFEYIDENHQWQWGLATVAASPAPRHVQLLLWRHDAASLPDPQSAGSDLVSTE
ERERVMARLEQLPQRRARVNEEIEAIHKAIAIKQAAYVVSRRRIENAASAAERALVEACT
RIHEVEARDWRETRCYRNPPEIVVLVMEAVLTVIGEKCVSWAQIQSVIRSPEFVRTVELF
DPAKMSAATKEGIQSKYLSNPRFTYGDAMNGSQALGYLQQWVVAQMDAANATEQLAEYDM
QHLNDRFAIARMEEQIDAFRQTLREYADEEERLHALLEGRSMQVNKEEDGGKDAHKSFGA
EDRGALIGTNFVWTLTEDTIVTLRSAILCNYDRPDSTIVRLTAGQVQELEDALKRRESGW
KDEQRADAARRTLQNALEELRGEHGRKLKRLQELESSSHATQQELGERRRELEKLNQVIT
EGGLSLHTPWPSSTSTPSHATPRRLLPNTLQLPVFGPAADSALLSRDGVEEEFAEKIADL
ENRLKRALHENPTAAQVQLLEDDLRAVQEELRYAKEELDNFRTANAPNYYTSSALRMEKG
STPEAQLAAAQRQIEELEAALEETLEHGRQSQGQSLKAQEKSNGKGGDDEIQGRIQRLNE
ELQRQRRDTEGIAERLNEELHAHKETRQKLADKECELKVLWDRQCEADREKESTRAALQE
TERELEKLRGHLREQKEELHASRPKEYRWELEAKAPRGRRSLQLHEILGRLRDEAGRQSL
EAKATEMVLDEVRALLGKGLTAY*
>TCRU_9572 hypothetical protein, conserved
MYVPHGRDVAKALLSAEDPKAMEKNNNRNINNNNKRRKKKKKDQQEAPLSLDDVEELSRR
REQLQSDLETSLARIAEIQAWIRQKNDESHDQNADAKDSHRQQQLECALQELTAARAAVW
AVPVGLWKDLYSLRHPPPAVAAIVKTAVCLLGERLYMSWERCCGIRDLRRRIVKREPSAV
TAAELATVQRCDLNLKWSLDRVVRVHPTLGPLHRWIAAMLRASKAAAKAGNVKKEVGEDG
ERKSAAAAAETAALMREMEEHAEYVQLAREELAAIDALLRDATHEEDVHDACVETPCSSP
KTRSNMTLSITDASTRPQTESLASGRSSTLSATEKGSVRQQPLRQQESRNADVADAVRSS
TFSFSFSFSAAAAASTSTAAADVPSIVPRLRLESCGVGNVESNTGMAGSVVRSDAPRVIR
ARFEELRASPRIRSPRLGRPVTVHSARLVEGSTCNNSKTFLDSVSPCGTAALLQERADLL
QRVHDLEDRLKEAYHRNPSMAEFQLMRDEMTAAKQELLALRVEHSQLLGQTKRCSLYRLR
VPRENGAQDESCDGDGGAAATKIRELEEQLRAAHEKIQQLEAQAALNTLRGMNASVSSEY
SDRVTQTGGDNPFNAHATLPTGGGEDNAVSCAPTLRQKQQQQMQQQKRLDDALQQLEAQR
DALAVSEERLNQEMHAHHARQQQVRQLQEELTTVWRRLESAEHQLRLTLEERDDHMEGRG
GVATCRSMPGESRDVAASLHYELKQLHQRDVANQQTIERLRVELATLKRRRAEERQRQKE
LRAARAAMLERLEKTFAEALRRQDCSMRAIPQALARARNELGQLNMQRS*
>TCRU_9573 hypothetical protein
MASGEEEGSIPPQEGGDDNTDTVVTRGDGNVERQGEVDTPPAVKCRRLSDLSVTTTSSDS
GSSVITLKSIEQMPSLDPSKMEQSPSRGSAISPNPGRAFEIALLHLPSEGEMAALPEASL
PHHPCCPVLRAESINGMDATASPATCAAVQDNAACATLTSCQEFREDGPSDVNTGAGPAA
GPDRMAAAVDHPPESSNEKMGGNEMESHDERPSEQMPRPGFAGEIAPQYGANESASPPLP
SPLNVTSKPREKILSSHCLDGSGASEVRRSVTLNPTDMPPPSNVVGNASLSNSSSVEMEK
KSSSSLPRFRASSTQKIALHQDALPGEEIKIEPVRSSLTEKQQRAVRHAPLALTRYHTPP
PHHMLLSASSGRGKRRRSKQDALTRMPLDDGEGSTDVHVVSLESGYTSHNEEACTSPQKL
GGREVDHAPPPVEDVKQTEGPVRSAIYEHPEESEPQNEMGNREIQRRLSDFMGAFQDSSQ
RNWASVLSISPQASRGIVRSSSYTASIFKKRQTLDNRRSSDGSAPLVQSIKDLASTETLE
QCPMCVESPNTLAEVATRISQILLDVPNDGPNDASPLPEVTSKPLGRLKSEATSPLIFLA
ETKVHGPTPPPATTEVNFSPSPSPAPPVSVLEDKDSNLQESDVRTGFTPPCRADDAYLGN
LLPGTIAPFAPAPLSWHRRVRSTVAWLGDYDDDKISIYSPADLSLALPPSDFAANATYLS
KQKEKHTEGSTASESTGEEDLLEGFYPGAYKVEREHRFSSGVVFILEREDCFACSDNNTE
GGDVTNVVRRSSRRTSAVPQVLPMNSPIICSPHNKEVFNQHPTLPIPQQDGVWQSVEDAD

DNQGQETKKSLQRHSLSMDQYASLSLSSIYRPTSHKYAPDPNKMFCPITNVFRLRQHFPD
SSTTTSDDDGDGEFGCDGGYKFSDYGWEGE*
>TCRU_9574 Flagellar Member 4
MNSIHALLELGVQRRNVERELRNAKRENGEAKKQRAMGIVSAIETKQQMLLRSLAQRFVY
PASEYPPTTELAELSDVFTNLLRDVVEQGKIFLLYNCSSDACEARRCTCAKEGAGEVGDC
SKGRQRGEENCRLCSTSGRGLLDVLGRISAKVLHESHAGASSCVDNIPLIERWDAELQAA
LHHVGDVVSQAHTEMLVVLDALSDGRFPYLTSGSSTKEGPPLWTEIVRLFEDAFESVLTD
VVRLLLWCIHQHLLGRGGLAARPLFAVKSHWSYSASSVVTCPLPSELHERLMRRWKKELI
WIVVPEFRLSQMTKRSVPMLGRVKRPMLRTMFMEDSANNRLWEALHYATSQRCDELQETV
RGLTNTYSFYFSHEEEYYPQLGAQRLRELVNTVRSYGMNGVKHAGAGAFVVQTEVLQQVA
LSKLEPALKSALVTTVPATMRGDEGITVFRWKALMDVKDDASPAGSLSNRLNALRAGRKV
PNKYDKGLEPLAHTQRFLEEQRAEVKRMRQGRGTALEEGGKTQAETKQSNGNGSTGDNKR
SAAVAASTAVSRRYINRFASSSISPPILNKLGQQPLAANAMAIGKKMGYETTPPVRVLPG
SASTTTQSTHEEKTPTGSTSHVSPLHPQSGSGRKGGWNFPSRHSSEVRLPTLRNYTPSSS
QQFIRTRPASREAIAQNGREEQSAPVMSCVDISKQSGEEQKRPASKEAIAENGHREQPTP
VVTSASSGVERDVADDPVAAEPDPLTATSTLNSPPKTAVVNAAAAESAKRRISSLKKVCP
FLPEVPFSGIFLEDLNLTDPRVEAAMNRMRAVRGNASVTRDYRSIAMAEDSLCAVVESIA
EEMFNATSRMLSRYPFLESRVRGVLLGNIPELETDEDIQSLLMIRRDAERARRSTASIDK
CLRERAEALINDIPYVVEPERYSAHPFLLAAPSASSATSHRSRDEKANNDGDDSRATQRV
GLQVPTPLGSDATSEVDKTPQAETVLNDGEPHRAMDGREEQPRQSNGQEQPMGAVLKPVT
TGGSTSKPLAADPGQKVVENNGALSSERPCESHLPQSSSFARARMGGGAPACSQTVVQAT
EEKQNFSIPRVPVADTPLPAGRTGRASEQIQLLSSKPPVGPVVNASRENPVPPFYRQGGK
PFSLPLEEKQGANEVVQRAPHGIPTSNNIQSLTDFPIENQKMTPCGPTFGTVKRFLESER
QELERLESILGGVRRAGMGLKEGKGLPTVDAAKQMPSEEVGKRNSAEDMQQAAGKSQTGL
PKKTSSSFSTTPNVSADGNGSVGLSTPQPAAARRECAQLGLLFEQLPYMRRSNEGNELLR
KLIEERRRVSEAHYTRERDLAALQSRQLKRSSQSPLPMHPNLLAEVAARSSLGAAVPNGA
DGGQARLLPSLSQGPSHDSCATQQQQQQQQQQHSYGNQRSTWGRYTIERNPPTSVTVQR
RLSSAPGLSQQSNEDRMRFPTISVGISADHISQAPDKTEYEKSSNNHIGMSHRYMLLCRQ
AGIKPNSMLLRALPDTQGVSVSRVDTSGNYIGPKGLMPLLQVLRDNTGLKYLNLSHNNLE
NDEVIELVSFLMNPSGASLQSLDLSDNPISLAGGAAILRLAQARPSLLSVRLRGTLVPQP
VIHSIEEVCDSNRASAS*
>TCRU_9575 Kinesin motor domain containing protein, putative
MLPGRQGGGRSNFLVAVRCRHLDAREEAAASLRFARRGGTRLHCVFLNRPGLSSLTPEAA
AAAYFPRGGEPRASVVLVDPDACTDFTAKGRSSAVLAEGPSQLMQLGAEELQRVLTGHDG
VRCFNFDDVFPPAVTNEEIYATLVQGLVIAAENGYNGTVFAYGQTGTGKSYTVFGERDNG
VPGLCTLVAADLFGQRSRPAWLRDTCVPVSGVGGPSQQGRESKRMVFVSFIELYNERLRD
LLVDPATATQAASAPSQEEGSRGRRLLFSRYDDLDIVEHPVHGVQVPHAKSIRVRCVEEL
ERLLEEGDRRRTKASTASNKLSSRSHAILQFTVRLCMGAAVDQGDACCTRHIVADRSETQ
ALCSFLTAKLLMVDLAGSERISGFESLTTAVATAGSVAHGTCGVPHQRDSRRREGSNINR
SLLALGNCIKALGRACRQQQQQQHMYTASGDSLSCTSHSLMHQKQHAIYTRYKTAAFEVH
VPYRDSKLTRLLKDSLGGNTRTVMLATISPSCTSFEETLSTLKYASRARRITRQVRQNIL
VEAADGDEEEDGNDEGEKEEELPETVHGGSRGASSGGNGKWASERESNHRLRLLELETEV
RCLQTQLHVAQAAARKMGLPRSIEDDVKEVAPVVSTTTASSVVSDGESGKRMELDRCLEI
YEQTRCELQALVRERATASARRENGLGIPRDLGNKGPIRELLRQERKNALLWERQRRIDA
FLL*
>TCRU_9576 hypothetical protein
MGQRSRERHFDPNPLAVGAARVARQSGTCADGMPATEVCARAARPMRRGMGRGEQREEEA
QRDQQSTQDGGRAKQFAYLPVRWKMDAEKIKWNVLRRIPVHVSQSTPCRGTVSYSRHRLA
DAVTAAANFINLSIAAPLEGEGPYRLPGERFAFEKDSYKSLGSSSRKTLSFVRRANNEVT
VCQLPKSISKMRGSVSNTPSVPVNVEAVPNSPSVHNTLPVLEAEECTLTTLKATPPLPQL
LSSEECAPHVIEAAESEQPAAEEVADARVAVESTRAAIVSNDAVPPAALVDGVVFPKSAY
GVVDPVYAVVERSLLKERHYLEKLQEIIKEVLLAERESSPAAEESAVAILPEEKKEVKAP
GPLKPVWYARPKQPQVPSSQRVKGGRPMRYTALGDAVVRSAWSGSL*
>TCRU_9577 hypothetical protein

MGDTRGDSTGETEGLQPQGFMETSDPSDPAPQDTAVSGETHASPGGTITRDAVAAVPGEE
EAAAAAFSYNSGGDVQEQSTAADMAAGEDILVPKNHEQSLSTNVVTFGIVEKVLEDERDC
LLEMQGILEAACDAERKRYAIEGGLSADTIDTDSIRPYNLCEGSAEEEATAYDISDEGLE
KPAAVGDKGTPIITKKCGSAETEDDGGGKASRVLSKIEEDLRRSRLPLPPGKDGRLYMQF
MPITDAVVRSAWGTLQSKWVAELEAEMLPEDCRSTRKLREILTAAAAARPQPRFPPHNGP
ESLPPCGHSPHSMDVEKANCPVACHAVQSPETAFPPGPQRAVGCDGSNPLQEACEWLTPG
GVYTPVRSEEAEAVELPPIISSVYTTRPVFVPQQEGDGVYSSATHNKPLHSSSGNDSASS
AGMAALPVIFGADGLPIGAKENGKPSAKPANYPCAMASTALMAAPLPNTKNHLGAVHPKT
GKQPTSIVAVNHSSDEAAEHLPTVTDNTRNSTGSTEGTIASSAVSTQSVSALGKNAGQGR
IKQTNPRPSRPPSLVVDRVRKLSCSLPIYATAEKGLEEKLSVMERVQDIVEEFYEEYTRS
LENSTEPSL*
>TCRU_9578 hypothetical protein
MPVGGSAHSFTSDMEWLQPRTEKGELAPSDIAAHSLCVLRPLKLSELQRGSRHAVYSAGK
QTAGVLSGADGRGRHQLLRQETTTADVAARQGRIPAMFRGPAKGCATYSSLGDAVVCSAW
GKKSLAAGTWEEAILFTSRLPEKKSSLTTRHLPWGKFTIRRTRHPSPKERAALAQPLAYA
APDTTCAVTVADTVASPDSTVSPASPASPDSSSGLLLSQLGLRGFSKRTKLRSCQAVFER
TSKVLLREKGYRERILEIVEEVCDAVRAAAAVNVADNDEGDGVQMMGDFPAASTVSLPTG
GVFGPPTAVTEEASSKSRSISRLHTMDHSCKQFLSVDSASAMPPLSLQKEPVPTSQEQQK
FPGASGERIPNAATQETVLPRLRESTNRPLGVEAVRDVGSTPDDAAAAKENKETQSNGME
KEVYEFPSRHYHNESAKVEETSSGFHTPVAFRSQYQIPQPVPGAVLAVFNAVDVPSHDCI
RRVVGRPLMEGEGEREERACPKRLQDAL*
>TCRU_9579 Pyrophosphate-energized vacuolar membrane proton pump 2, putative
MGDMKRFIVAVAAVCLLAATVSAAPAGGEGGKLLLKNDIGAHRLSQKEGDANNPLAKGGS
NTKERTPPLMSADVTTVIIVTSAALGFSFAMYWWYVVSDIRITPGKDQGMRNAYLTDEVM
RNVYVISRRVSEGANAFLYAEYRYMGLFMIAFGTLIFFLLGVAYSSPQEGSRPVASPWAN
AALSLLAFFVGSLTSVFAGWIGMRIAVYTNARTAVMATEGSEEGDQSLGFAKAFQTAFRG
GITMGFALTSAGLFSLFVTVKVIGAYFDDVPENVLNVYECVAAFGLGGSAVACFGRVGGG
IYTKAADVGADLVGKVERNIPEDDARNPGVIADCIGDNVGDIAGMGSDLFGSFGEASCAA
LVIAAGSAELSSEFTYMMYPLLITAVGILVCIGSALIVANNSGVQRAEDVEPTLKRQLLF
STVAATVALVFLTDFGLPDTFTVGTTATTKWRALVCVMCGLWSGLIIGYTTEYYTSNAYH
PVQEIAEACETGAATNIIYGLSLGYFSVVPPILAMAVTIFASYRMADLYGFALAALGILS
TMSIALTIDAYGPISDNAGGIAEMAHMGHEIREITDALDAAGNTTAAIGKGFAIASAAFV
ALALYAAYVSRVGIPTINILDARVMSGLLVGAMLPYCFSAFTMKSVGLAAMDMVNEIRRQ
FQNPAIAEGTEEPDYESCVAIATQAALQQMVAPACLVMLTPIVIGVLFGRYTLAGLLPGA
IVSGVQVAISASNTGGAWDNAKKYIEKGGLRDKNKGKGSPQHAAAVIGDTVGDPLKDTSG
PALNILIKLMAIISVVFAPVFESQLGGIIMRYIE*
>TCRU_9580 hypothetical protein, conserved
MAKGFLRVNWRACGGWLILQWQRPLPGTTERVAVSVLANGTAPLVAGLGSKACQRVRVPY
GCDSMFRVLSDCHGLRRMLSRRLVSMHSTMSVTKLPVHGPAGTHRCQETLPDPVLVEGR*
>TCRU_9581 hypothetical protein, conserved
MCSQYGPLRNSSQRGRPIAVSVANSCLRVAATQKFSKPPSAVHPRNIGRQATEDSMSNEL
KGLAGVYQHQRSPMGSAVELASSTALLGKVHLEVIGSVMLHFVYQVCQLHRRGTRTTICM
LVRTRRLQPKQSPQCHFLSNLTHDGGKADGSI*
>TCRU_9582 hypothetical protein, conserved
MPVVTARERRRRGCSAGRRPCDTHTPRRCARSALVPFCHGQASPRRRPCVVALIEVDVGG
VPAALTGGGGPVPRSPLAGQRAAGGPTTLRAACVLPVSADASSVPRFPGTSQAAVSKGGA
THRSERAAGCGYKMAQQRIQYTAGARGQDKRRVAKGQFKRIQREGPNHIPVTRGHASTKC
ADSSGDRSKWDSDDATDERVSLLPDFVGAYQRYTCRLRAVCDAQRQKLLRGGDIERSPSP
IAALQMTVPSLTPAKLATITAQGADIIAIQETWKSSEQIASMHTGEYVLHAQSRIRKECV
AAVLVRKNLRSKRMPLITPQRDSSLEVVVVQFALGQNRDLIVASTYMRPPPQPTQPLGGC
*
>TCRU_9583 hypothetical protein
MDYCLGTPLHHHHCCQLKGQHQEQQNRQEYLKEEQKKRCRCHDRQLKFHCLHCLHHHQEN

HHQELLEQQEEQEHRHQQEKHQRRNSHLNSNCSVFQQDYLFQPRLRRQ*
>TCRU_9584 MSP (Major sperm protein) domain containing protein, putative
MTDIDGSNVPAPTNAALIVSPEKFNIVPYVKEEFVVQITNVSFDTVLFRMLTTNPLRYLV
KPRKGVIKPNASISLTVMLNRSNLNEEEIHEEYDDFRIEYCVIGPNDVIEPHCANVSDIV
KARKVEDKRQVHLKKFRCRLEPSAKAQKRQSGAENVKSSPLPSAATERPASPRQTESSNP
SAVAAKMDPRELEVSTLAEKNRRAMAQKEKEWKTKTAIVLAVLFVLLGMWFMSA*
>TCRU_9585 hypothetical protein, conserved
MESKGTPTTRHPHVLTTARRKKETLWHGTPKRQTNPTTAVASKSEVVATSPHDGGSGRLP
EDSQEATDEVVTLSSASSPLSRALDGSCMPFAPPLGSDMAVTVACGPVNRTSLLSTEEKT
AHASLGQTDAMTDRRRSEEMLYYLEAARALREVTSGVEAREQCLRDEIERQSTLYSAKKL
DLAEKQKVYERLHESTLRLTRNVRRIDSENDRIRDRLTKLQMTIEKMESRKLPRHIQQDV
DRVVRCESVPSWQGANQRVGGCEAIVPMRSVGSVAKNTLMTELEMYTRKLRSAEVRHDKL
IKELQLAVARRKGRAAAYNSFGASLSFSGYSGMGNRDGSFLTDSVGESIAIQQLERMIDD
SLIRCK*
>TCRU_9586 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGGVCTDEVGVPASVVASKRTDEENLILNWYVLMKEECA
NESTTGGKLNVTAERICMHKVMKEVCDAFYDKTSGVTHDRDVEFICTYYATIPEEPVEPP
TPQGPPSDSAVSNTTSDEGTPKNAPESDVAGRGEGKDDDKEHGNTKQKAVETAAVESITK
TTDSDDSTAVSHTTSHLLLLLLVVACAAAAAVVAA*
>TCRU_9587 hypothetical protein, conserved
MAMMTGRVLLVCALCVLWCGVFGIAADDAGGADGSAVEYLFPRWRAQLRRDCAEEVSSRT
GGGANASAVEECVRRRTDGVRAVVDGRSRWRRQQFAVAAADGGSGGNVKEEKTKTLSKEL
HQQPQVSNVVTPGMNESPGRAHEPSSIREGGAESEESQSSLPEVLSEMQNSVLESQKVLG
GVGRKTESTANVPTGHESVADGSGHIESPEIRVTGDPEEESSQKGSPKLTASSQAAGAGE
APQPPTRVGGGTQKDPGIKNPETAETPGEQIKKIAEQGTPQEGQVPKVQQNVSRSANKQS
RVEQEVDPITTPVNAPGVAPQQEKEGEAENEETADEDEAEEEIETQKDIAGRPLSPIREK
SSHSISFVHGSAASFSQEEKPTAHVISEHLPISETVLGEGGRQHGDTATPHNVNSSNAPS
SVTEPGAATTTKTTTTTHSASNLNSDGVKLFTEEKEKRDETPNLNSASEGTKHTPVNSEL
PTTATDHANDITNATPPADSDVSTAVSHTTSPLLLLLPVVACAAAAAVVAA*
>TCRU_9588 hypothetical protein, conserved
MSRRVFASAVLLLLVVMMYDTGRVVKAAEPTSDQRSSPSPSFVWRDKNDNEAVDSLYVPS
LVEVNGGVFAVAVALLKKNEHEKTHFFTGIASEHLELSGGTPKMLGVSNLRTKTLEKCSS
QER*
>TCRU_9589 hypothetical protein, conserved
MCSQYGPLRNSSQRGRPIAVSVANSCLRVAATQKFSKPPSAVHPRNIGRQATEDSMSNEL
KGLAGVYQHQRSPMGSAVELASSTALLGKVHLEVIGSVMLHFVYQVCQLHRRGTRTTICM
LVRTRRLQPKQSPQCHFLSNLTHDGGKADGSI*
>TCRU_9590 hypothetical protein, conserved
MAQQRIQYTAGARGQDKRRVAKGQFKRIQREGPNHIPVTRGHASTKCADSSGDRSKWDSD
DATDERVSLLPDFVGAYQRYTCRLRAVCDAQRQKLLRGGDIERSPSPIAALQMTVPSLTP
AKLATITAQGADIIAIQETWKSSEQIASMHTGEYVLHAQSRIRKECVAAVLVRKNLRSKR
MPLITPQRDSSLEVVVVQFALGQNRDLIVASTYMRPPPQPTQPLGGC*
>TCRU_9591 hypothetical protein, conserved
MSPKKRSRSNPKAGVTATQALDAANMIATAMNAANADTPVTTGGGGHCGAFAPCGPAESG
VTHDEKNVKARGTVEQRPKIPSDLEGLVLHSTVIAPDVIGIRCMAVHPSGMEMIVVREDG
SIVLYGIDIFQNVPHFERIRHTGGRANRTITRVRYLPHGRSLFLASYLSGQLVVYCGETL
SPLYVHQRTGGAIWDFCVVGECIYAAMADGSWQQLRAENNGSVPKLTMQRIIPKVSGADR
ALSVCGSEQWAIAAGTDDAGNVVAWRLPREEERSDNNTTATTNNNRRRVDNMNNNPPGGR
PISLSDHEALWTSRFPKGIGLCCAVSGGVNGGAPVVAVGTSMGDVVLFDARHGHVLKTFT
HHKGPVSTLVSSGGVLYASGWHESLRSYRCAADGEWFPAEVKRRTHYHEASELLVQEQQQ
LIFSAARDGTVMYAPIGSLFTSPAMYLSVTTQQFAFAKSKNVLLQTRRGRIEGFRTDAAL
RHWMPLFAYKVHGKFHIQGLWCDERLHYMLFATDERAALLHVCWRDGAEDALKLGRIEEV
VALPVGRGVLDCCFTQHNDKNSDAAACESCYMLLDDTVVHITLAEGYPVVATSIRSSDAE

WVVDIRPNRLLLDTGKNNSITVCGLRGRLTCCVAPDGTIDPSSFVWSQESTRMAVSVPAL
RHHSPSTFVALTNNTRYMAGLGTRSPSLLPRTLPHDVRFIARIPPLDKSVAGFKHETLRF
IACFSRGLMYVTESSWYMLQRCSVEAAFVLDGDEQLLLLVRNLEGTLEALPMCWKVRRFG
N*
>TCRU_9592 Nuclear cap-binding protein subunit 66
MSQTRTLVFITNIPDFLLEPLSTASTSATIRRRENRDPLYERLRALLAANTSGVMLVMHL
QTRGYALALYASEKEALEACKTNIVPEQPGHKYSPLLLRILRRERPAPSEAVYTPTLTVE
GEVVQKAELADTRGLELVYRGRAVAKWCPHTLAREDCPFGTACYRLHKRAYQKTVLKRPR
LGEAVVHHMTPEERALVHRISCNTRRAEECVIPAEMRIDFSLHVSLTRDEAEALVDDAAG
VVPASVLQRVEAACAGHGGPYFVKFDFPGGAPWDWSLHDDREGLPRLRQRLPFPENGAPT
PLERDIFCQQLLYHLNQMNRFETISSALRALAHSPKVQEALRRVAQNPRVHEGKPEEGEG
DAVALGICIRPWLFLPTVGVEVSVLLEGGGDRVRGIVQRRSALRLMTCFSFLQKHGMNLS
RYAVIGSGQDVYAEESLETEMRRVEKAVKRAVEGLRQHLRQQVSRGGQLPSNAAWCFQLA
VMPSKSPSSVAAGEDAAEMRCVVLSMKPYEEAFEEFTAMHPSLMRDESVTDVIWNTKRHT
YVALFPRELMERLKED*
>TCRU_9593 hypothetical protein, conserved
MDRGDFEFPPDPITEAFDSTLETLNNVPLRVLSNVPIEELPPTVVPSGQKRPIREMMRGG
RRVRRSRLHRTKADVSCEPASGTFSTSPTDAAEGGEPTSSPKNSFAGHKRNRFDWSEEEL
RDFYKFLSQYGTDFNAISVMYIGRSRKDVKRLYHRELRKRSEDVRAALSSREEIDLGAFR
AQLKKREELQQVPVRQLEQEEEEALRLIEAGALQFQSTSNDGETPAGGSGNKDLEFDFAA
VKNMTAEEIQPTNNAKTADSVKCDDREDNLNKNTSLFSKCAESSGVRNTELGTLMDEKLL
DDLMELDKPLEDDFF*
>TCRU_9594 hypothetical protein, conserved
MQLCYGCRHAFPASSLEPCVFSDIISDRFDEIHKIVKEMNTKTPEENHRVAKLQMALREL
HSAVHQEISALKEQKAKLEASRQRDRQEMDLGNQSRLSNLQDTNAMLNTQTMGTNLSRSN
FVKSTPRATFNGMVPTYKLRKMNSALDLVSAIIYSVVESLAIRTRAAVAMLWLPPPGVVS
TELVAPFVVGRDMSKLWNSAPYRVSENSVPCLVSETGIAVNLKPSQRISDSKLSENVPIM
ELIEMKNTAQLIVPVYTRYGAIQRSVLAVLHLIGDPVFPYPFGLRNEEMAVQTAATLSVI
LSSYYETMGGEWANRIYDPLLLVSSAAYHGGLDMRSMEKCIDDFAPPATLIYRCKNDKKD
DDDAREVIKTLRYAMMKRAVSRKAVWSVKDLHRFATNMEQNWISVLNTNSEMELKMIGLE
EKVLRGGLERGQPRPLSRQDIASHTISDTSAAGRPVSSSAISVCALPPMFDKSKALKPEQ
VTEIEANALQRLQKMGVDTAPFVMPKEAEDVDFV*
>TCRU_9595 hypothetical protein, conserved
MKTLQSSLRGRGGRGGRGGRGGRGGRGDARFASRYTDARFRVSRRGRGAWVGNSPRDAAL
RDPRFLKHLKEARGAPADSDEDEEEVEEDYQDLDQGSEHAAADEGNIPLTEVDEKELDDE
VAAWSASDVEFIEPRRRVAIVNCSWDHIRAVDLYAILFYALPLGGQLIDVAVYMSDFGKK
MLEHERVHGPDLWVRKDEKAGTREAGLHDQKDINDREMMSKRMEIDDNCSDDEDDPWEDD
NPAMLYEEGGDGELFSQGKYRRYERDRMKYYYAVATFDSAETAETVYKQLDGMDIEASGV
VLDLRYVDDEEVFENPVNRADRIPANYRPLASFKAAALSQTRFRISWDQDDIFRYRSIRD
SFTGNTAEDDIAAYIAPPDSSDEDDFVDANGREKKDSVREKLRIRKKYAELLEEIGGLTQ
DGQYSEAEEGEAGYEPSDGDGDDNSLNRFSDIDLDEEEEGEANMSGEEGVMGDMEATLDL
DAGTKAARLQREAEIKQMMNSADLGSRAELKYRLRRKEMRKAKKEMLAQERENELAQRQE
EREKKRQILRETLGTDDAGATHMSGREKRKSHAKLVKQRVAAEREAKKKMRASNLLGVSR
EVREAQRREAVTDTIDPRFRNKLLTDTRFHLDVAQKDKRTKSELVDLAAAVATARREKRQ
ESQKDAKAESTVEYFLNRPAKKTRKERGS*
>TCRU_9596 cop9 signalosome complex subunit, putative
MAEEEEEEGSYTEAQVASLVASQNLGKWELFVKSALKEVAPSEASRAAIAYALRNLYEAA
RVNLIFAVQAGKLLLAAGTHRSAVWGAALFDVRGAVADWCVQAGDEEQAQELWRLMLPVD
DDVVSLKLLTNLLNSALRTRNFATAETDCLRGLASYKALSMRTEANDVVNAFLHAFASLL
AVRHRFLESSQRFYELYVRTKSLDHLRGAIVCAIQADASATRSSLLGAFFKDESAMLLGE
LYDVLNRAHHFHFLRPSDLQRFLPYVEPFSDTAAVERAFIQHNLQAISRVYYNIGFEELG
TLLGITPSETEQLVARMASERRLDASLDQTTETVIFSRPENTSVLEAWDARITAVCEELS
HAADLVLSRHAELSEHLLLK*
>TCRU_9597 mitogen-activated protein kinase 1, putative

MASFNLDGQIEQRYKILRHIGSGAYGIVWCALDRETNTLVALKKVFDAFGNQQDAQRTYR
EVMLLTALRHESIVLLRNMIRSVNGTDIYLAFELAETDLSTILRHNVLEPIHRQYLAYQI
VKIVAYLHSRGVIHRDLKPANIFVNSDCRIKLGDFGLARCIQSQGEDAFRDLTGYIATRW
YRAPEILVNSANYTAAMDMWAVGCIMGELLTSSPLFMGSSTLHQLSLIISAVGEPTTGDL
ESLGSSETWPLVDALPPVESCPLYETLRQYDPDAVDLTCKLVVFNPTRRITAREALRHPY
FAPFFTESDVEELNKATMVSLPLPDEKDYPAAEYREALYNVISDRFRQNVAV*
>TCRU_9598 Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MGSSNAGSGSAYTTTVSTITTPAAGEESVMQMASGSSSDGHKNVGGGSFSDGDPTVETRE
GGTNGQEEEVSTQVREVNATALNSSLVNVSQENNNDASSMRGSGLLPSLLLLLGLWGLAA
L*
>TCRU_9599 hypothetical protein, conserved
MRVASSSILSLRSHSVFSVTSVSVVSSGGGIVLGERLAVSDSVLRFVGVEGSVASSLVCC
DGGTIGDSGWLDMHDVWAVGEASSVASLSGVTLSGGAVSIARCAATGATLVSGLTITSGT
VSVQCNRAGGRVLRSGGDYRMAGLPSVSVVPCDGCAAALACFDALTASFSDCVCSCRAGG
VGGACLPFDVPVARAGGGAQGCVSGVTLTESVTVGGGRATACFDSVVFSGPITVVLDLRS
MDAFADALNVTLRHCVLADGAQLRIGGLSESTARLMPHAFVNMTNVTSVEGTIVLHGAMP
PNSSVLLANSTLRAMFGGSQYVPTTPGHAGSRHSPVLVLDGVRLLSTRFVMTRSTLVCGG
GSCAAILVEHGLVVKLSSVFYMDNCVVKSQSHVIYSIASDLRVSGGSVFSIQDSSWSAPS
INMYEGACMFKDVAVDGGSVLQIVSSTFRLGFAMLMTNTLTVTGGSWLVHRDNEFRAAYV
VYVTNHYGVAFCDQSVWSILDNNFTYGSYSSTTAYMTNKWSPPSDTRPIIYGVCNEARGS
PVTDYQGELNIGTPVTVLDCGACTVDAVCFAARTSSVSGCECVCSAGGYGNTCLPAAVPD
GLGPLPLPDARDTEVRCVHGGSISSVYVPDPGVRGLCFVNVTFTAPMLLDLSYFDAPQQT
LNITLLQCVLMGLLIRGSGARVRVHVSVTSSMLDFGSLVFEGDFGVSSQILIVGSTLVTT
SRHAISFLLFICVNSTLLLLDNYIEGNIHAVYFTNAAVDGGGIIVKGNTLRATRDDDGVE
SSVYVNAIALRNGGYFDVENTKMSAVSGFYFHGDTTVSSAGLLRVADCYFVESTEEFESA
LVFLSGSLSLEGGAQWRVEGNSVGAASILSIAHAEVKIQLSGSGTTVALAHNRQVDSRAF
LARFLPSSIVVKLSARFVVGCNLQGDGEVSYDGVFPEDVVVFRCGTCNDDAACYMPGTEL
VDRGSCSCSCRDGWHGASCLPLEVPNAVVPPLPERAVDGDTSCVVDQTLTDLTLNMWKTH
HCYVGVTFSGVGAALKFFFNSMPLHLPINITLTGCTFREGATLQFVGGAEAAESAGVLVR
VSQTVMRSSVVVFALALPQHCDIAVTEVDAVQAFEVQLPHIRTNMLSVVLLQIVVLSASS
LLVSNIKAHSLRYGALGLYSTGTLTLERGSSLYARYCSFAGYMHMFYVNILIFRNHSVFA
LLNNTMSSGAGLLYQYSRFSVSDHSVLRVVGNRGSVSYAIYANNLWTVERSSWLDWRDND
VGLGAIFYDSGSPFVDMDSSSGVTLTGCTMGSTGLSVSLLKRVDAGYRFVAGCLTVAGRL
LTTAAELELSGITNVTTVAGCGECTKEGDCFAPLTTEVIDCKCQCAAGGHGDACVPAPVP
AGPPPPPTPPVPPTPPPPPVGECISDMVYPKIAQTVGGGLSWLCYRNVTFSGGGMSLTVL
VGAMAGDVANVTFDGCTWRDGAVLVLLGNADAAVRSLNILVTGSKFCDALLSPEGVFPPH
TNITISGNRFTVTRLIPRLGLGLRDPSCVAMNELAISNDSAVVLSGNVFQTVRASSSAIR
VVGSALRVSWHSVFAVVGNTFHMAGGDGTLIHLEGPRYSSSLSVLNSSAVVVRGNLVTRP
VKCFMLLIRTLDVESHSAVVFQGNEMQRSSVVFISGDSSNIYYNSWLQLSGNLCRESPSE
AFVYIHYTVNLRDSTVSVSGNQFVSSTVSPTMLRIPTVSSDLTNGAIVAACNTVNGEEGV
Q*
>TCRU_9600 hypothetical protein, conserved
MRGVHLAPRHAQHSAPRRNHARTRVQRIFATEHSRVQRNAATDKLQHGAIYRHRPPTSHH
GHEGNAGHNQHGPHKPQARQHQHRCVRRGLRAGKIHKRRRPRGNQQGVRHRQHGPRGKRA
GQHKRTVQRLHIAHRQLHRPALVAPRRPRTAQRSSAHHVQHGAVQQRHVLHNDPHAVPRH
PRHVEHRTHAVQHNVAQRHLARTGRHNEHRPHRHALADERTRRSAHSRRQHGSSHRHARL
AVPAAAARARAHTVPHARRRRPGRVAVHVPVAGVAPSNVDAPSVAKTSRSVLLRRRQDTS
TSVVARHPHMRPSHKRQSHRQHPWQQRSVAHKAQRAPSSGHGASGVEHLPRDAVVHVALR
QQHRPASQAHRRIKRHRVVPRRRKVASHKRHNGARHAHSPTHRHRVLAQQEVAANKRHHG
AATGCNIALHRHAQPQRRLHQQPVHVQRTARRQRHAANNQHANSVAEHSRHLRARNGQHT
PRQTHVVQHEARGGVAKAVGVAVRNTRLCNQHRVHHSDARTRRKSARHHHAAAGARLKPA
EQHIGALASRRVGTPPNNVQARSTHKRAVRQCHVAHAP*
>TCRU_9601 BNR repeat-like domain containing protein, putative

MLVTLPVYSKKTEGVIANGKGVLHLWLTDNTHIADIGPVSGDDDAAASSLLYKSGDNNEK
LIALYEKKKGNGKTITRYGLCASDCAAAAGEEGAGDLEGSGRTCLQAVPF*
>TCRU_9602 hypothetical protein, conserved
MKEESCAALLVAIDVAPSTRQQHARMLRSVLQMDRTPLDMVILGLQKIAVRSETKQTRPL
TNEEMNQLIRSRTDWRERVVVRLAWITASRWSEIAVLTPNNSTLEADGTIILDWPVAPKT
ARADPHRAFRFVRIRGQDVLDIIKLCRTLQENERLTNLTTAKVERALAPWNATAHSIERG
ALRHAAQILETCNLNPHVISQLAVHVDPFDLPQNTVRYLGRYTTVLTQLLPLVALM*
>TCRU_9603 hypothetical protein, conserved
MFRAFDVTTWAPLIWDEGVSGVFLDLRGAYNYWQQADDQAQLVVDSLFAWMCALEAERDL
TDRFMNFGRILLQAFRVRLMTASDPGIPLFNILARLCTAVHEADTFARATQPLAERRGTQ
ISLRCQMCHIYGHDVPTCNVRDKTGGSYSQHGWPLKTAEGLLAASYESGRRQPHLFHHLP
PLRTGIASHRRCSTRSFKLPDAIVEKGNGAYPPTTLDCGTTEHLHPRLGSVV*
>TCRU_family, putative Se.1
MFHQMLDAVHGSFKVFFCDAHAASLLSCSLRLHDLMVHGVTLLGDPMTPRQPIMSSPAPY
LVAVEDASVSRVVEDWMAKVPHRDVHTFALGCTPHRSPQQLEWARIAPRAMRSKEMMLDF
AVPEVLVFHTNLPNEFPQLLSPLSPPN*
>TCRU_9605 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MGEGQDGPAVNLEASARSGGNGETAEETNGQEEKQIHPHDGEANATALSSSLGNVAQGNN
SDAGAMRESGMVPSLFLLLLGLWGFAAL*
>TCRU_9606 hypothetical protein
MNVSNQKGSHGVMGRVRLRDQTQLMAAWHGPLCSGGSMRNKIKKLIERVAQQAHWAWLNT
QVPANKMEIDHVLVRPCVCEEMWNRAASLLATLIFRLCSAAHVATRDKSGRIAAARAWMS
AHEATSVFSSAYMNAEAE*
>TCRU_9607 hypothetical protein, conserved
MARETAQNDGQADLPVAEAGRIRGQAKCGAQPIPEDEGAAPPRREDIATSGWVRLQVFSR
GLPEAQRSHGVRLDFVPPFFGYIRLKVGCLRVRQCVCFVCCFGGGLGLFHFVCPYLFGAV
MAAARDVALSCS*
>TCRU_9608 hypothetical protein, conserved
MTLHLVAVLGLWLRIGTPQQGVAARTTETKVTSLPEKVPRHARCGEVRRSACRLSDRTAR
PFRSGHSVDVTRCGDVHKSPATEEDGFINIWQLNIAGLSSVKNIAFAARLEQRPPDTVLL
QETSNRGGVATKLCGHNDCLQASLGAVVALPFWCATLYRASACRSLALTSWRPLLSVYFR
RAVAAFAWRISTTLPQQLVNNPHLSISFVACARRDYRG*
>TCRU_9609 hypothetical protein, conserved
MRRFLHVGISHLCLARFLIVGTRGSVPEIGFLPVFESRRRRRMRLGGENAKNDTETGVVP
VVPAMDEYEAKSICFEKYGFIQKPLLVKNWSGFLQELRRIEFRWALAPNAGGVIVFTALE
HGREGEKVLCNLKGSTGCAPIAEFFECCGGLIQGRCDKYFVKFLDPDGGEHVVKIISKRQ
IAASDNVIPVFDEPILPVLAQHNCRGTSVEVSVTDSRTGVLTPVFNDISLQTFNYAFLTS
IPVFLKRNDVGIRNADFVSREQMRHFRFAWCFLRRESLMTAVEMSELDLLLPP*
>TCRU_9610 co-chaperone GrpE, putative
MRAFRLRGASFFGQGALVSYRTPRAWCSNQEVKEKEDTDTKKATEGSQLKEETFAKLERE
LESARENISELKKEVLYRAADAENARRIGRDDVEKARSYGISSFGKDMLEVVDTLEKGLE
VMSKVSTEEIESNKNLSSIHTGVKLSLKLLLNNLAKHGIEKLDVKVGSKFDPNIHEALIK
TPASSEFPSGHISIVLKVGYKIKERILRAPQVGVAGEGE*
>TCRU_9611 kinesin, putative
MGEEENKNEEPNRIMVFLRIRPPKKGEIDPANGTHFLLDIQSDNKTCLLESKTYTYDYIF
NGDVDQGDIYTRVAEPVIGNVFKGYWGTVMVYGQTGTGKSFTMCNFSPNNMGIIPRAMKA
IFDSVESDSERSFTIVFSFIQIYVDKLQDLFNPEAPELKINRDKNGVSFPGIVEHAVKNE
EDFRRLYDDGNQYRVITATKMNPESSRGHAALFIQVKSVPKDDPGGEVRSGKLFLIDLAG
YERFSKTGVQEGQMALEAKTINASLLSLGNVVQALSDRSEHIPWRNAKLTRMLEDAIGGR
AKCSIILTAGPSSEHMHETLGTLYFGSRAMAVKTNAKLAVNIDYKKLAAKLQELLTAAEG
RINTLEVEATRRQLEREEAEAAFQAEWARIKKVQQDQLNELLASGATKEQIEELIRSNEE
ENQLMEEQQYQQRQALEERHEEELRTSLERQQQSLLNETAASATNMSKDIAELQRQVSQE
RQEKERFKLKAKEAEAEARRISMEMNELRVQMEGNDIGALSGSPSNPEFKKEFERRIESV

KSMYEENMQLRISEIQELHNEEVTRYKGLYEDLKRNMDKEIRFQKDALVASYEDEIDKIR
QSSADVQNKLKKNHLVVKQSYQTQKEALEQENKELTAYSEALLKQIRSLGAQPAERPTNT
TKSLSSVIPGDANKRIQDLMNTIKELRAELAYVRTEKDAMTREKETEEARGNDRLNPAQV
RQLKNENEMLKQSKKHLEEEVFSMKAELALSRHQVEEDDDEDDKEADVFGDSEGIPAFIK
SVLKIPYFPGTQAIQNAHKSILASLTTDLDEYRRMLKYRFFFIGAPNGGKSSVVKCLATS
SPPMIRNTPEVLTPTVHPTFTSISVDDAYCSRNDWYKTYVQFRDLDAPQQQQSGGFLNSI
GISKSSKSGVVDPAKVYIDLLDLPSDSVFWRGIPPYFLPSKGVVYCLVYDLTKPVEEVKQ
DLEKHLTLLHAACHRAYSKDIGGDAVKIGFCLIGTRKDSLKDARDSAVLIHINRIAVLLG
DTFFRLRGEDNRGLVCIGNFAVSTKEEHARGSHANSSSNFYFYFCG*
>TCRU_9612 hypothetical protein
MLGDELLESSAEKTSHLLQAQQRLRQGIVTLLTCLLRERKVRWAMQEKELRSLISDHLCL
DSKTSYGVFTENYVVRELFSRGVIIALPNAIIEPKYLPRLGDSKPLPHDGVVVLDPNNLL
VNYSLFMCPNSLTRVPNGTPFLKDREVMFFDYSALSRCQTTWGQGIVTGDVTQIVNAKLL
PQVGNDLKTVQELFCVMGLGLPLGAEVAVISPSHFSVRMSDCLIYYLSYMISCNGDGVAR
QYKLNANPPTLFSSLQTRLVPFSHLPSKDPRHLVMNWVDASFLVFGKSRLKYGAFGSKGV
RDATTKTDIPLRGIMKQEGQYLYICITGRHTNSEEAIAASAAVMDAVHYELTSLCKRNFR
GVRVKYQEVLLTGASLKRESFVTGQATILGRYRAEPKVIAAQKQITQNLSDPKANEIEDA
IINLPLKLREKVE*
>TCRU_9613 hypothetical protein, conserved
MLRRCCPATLHMAPSTAMVAGVFVNNQKRFLKMAKSAFGFYLARRGQRKFPFLRRPHIKN
THAMNLSAPYFWSFMTAKSQTYFLPEENYITGDWTGKFFVSKLQVYTLQHATSGSTVRVK
SFPSLFELSSPSRWNIGKELNTLTKPRMDLIDEQMLTKKQRLDYVKAGLLPK*
>TCRU_9614 hypothetical protein
MVIYSGRKALNSRVTDLEQKVCAETVKRQAAEKELLQYRSQQSPVLLNKSETMQKMLSEI
EQVKEEKRNILEWLERGVLEAERVSKQLSQISEAIHRTELFESDVNQTLQKMNNHHNELQ
QILHGMNMQIGLMQQDIEIKERNDSIQIASNGSNKAECDPFFEEYLIITKKVENLKDKCA
LLEKAEETMECLAACSRLSLHELGKISVAVNSNSVWEDLEKTNNDSDFFDSKSGEAETNR
PQVFFPSAKVAIDRCDSCLCTIWSGLSRFGFDQVHLRRQRDIQFQEACMAVERDSKKTVE
NCAGSLQELRDELEVWKNKQRLFERLVCEAESAYQSDLSANPLQREDNEVHDKGFEDRVE
STGDFSDNAKRKALSLGREHFQLKKTNDKLKRQLDVSMGDYNSVKELKHAYRDLEVRKNE
LASVNEKLRVINRWMKQCAWEVDKDVPMEFQGRAA*
>TCRU_family protein, putative DJ.1
MTKKVLVPAADGTEEIELTCITDILRRAEIQVTVASAMESQNLILSRGLKITTDSLLKDE
SAAAYDGVFLPGGLPGADHLGKNAHLKKILEEMRSQGKWYGAICASPVSALAPMGMLEGV
KTVTCYPAMKEKIPSHVHWSTDPVVRCGKCLTSKGPGTAIAFGLAIVAALLTKDCALRLA
KELLVDETPFVERALSNF*
>TCRU_9616 Metallo-beta-lactamase superfamily, putative
MQRCRVFFFTYIGSPARFRGSGNEISASFVLTRTVDGGPMKIHCIPGYISALYLVEYPEQ
GKLLLLDSGFPSDLERVRFYVEEVMAAGKFKKQRISERLRLVVSTHSHIDHAGASKGYER
CGIPVACPSGMEKCYRGVKGRIAQIYEAHLSQLVAARLGRKVREGSFLFSKGLLGPYWQM
PVGALRLDDGTPLPLGFHDWVAIKCPGHTSHMVCLYHSYSRIFYVSDMFVAIKKGFFPPL
PVDFDWAYTRTLHRLRGLPTRCALLPHGGIIDVGDRCGSWNALIDEIVLHYELEAKRNSR
FERARCLIAAGSHLLQGEHLLPDVFPRGPLPVPPEGHEPPQLHIMDS*
>TCRU_9617 hypothetical protein, conserved
MDNLFIQIISGTPRQKHDPVSASSPEYTILCAQAPTAEDRIALLMKRFPTSTEASSAQTM
CYLLQTCVSASVSPDETEHMVEALVEFANHHPTWIETVCWICALIHYYCTDEVTVSIFSE
CGAPSVAVRALKDNIQNNQLVLAACALLSHFNLYPIGDGISQLARALQAHHSDLLVCKMA
CRALAEFTSYVMECPDSFVSSNKEFLEANGVEVLEKVLREHIGDEETTRYVARIAANVTS
SGIPSSLESDSKVISYLAEAMGRYADSDLLCSHALHVFSNFPNSPYIEWDAVATLFKATE
SEATILEAFHFLCSVAMNVKTQKQLIYSTGCLNRVLELMRKYESSGAIQENACSLISYLS
FDSETITSKITESDGILLVLKAMQNFPDNEDLLVSACAALSGLTFNNLQGQQVIIQENGV
ARILDAMRSGKSARVQENAALAIGTMCWNSDLKADVVRLNGVELIMKALEEHYTSPGLVK
NTCRALAQVAFNCENYRDAMCESGVIPLIIRGMAQHPSYDRVQMHGCVALSYLSWNSEEN
SANIARNKGYGVIIDAMRNHLHNYEVQEHASRAIANIGTAPFEDLDMAPEQVVAAMRRHE

HVSEVQEETCRAIVTLSLVSPAYKDKLFELNAVECVLAAMRNFRGNQVVQQESCNALAHL
AYEHAKLNKAVTEQNGVESLLIAMKIYVNAPKVQLNACGGLSALAFDNAVAQKQIYDLDG
VACVIRAMSTFERLRMLELGCSVLGTLAWNTEIKEKVAVVAIPEILKAMRVHYQSPLLQK
STCRAISQFAFNSENSRKLLAESGAIPLIVSAMRSHITTDKLLVHGIKALTYLCWENNQV
AEAIINEGIEEVLEKIVNLYSSSQRVYGEAVHLSKILFRKMSSSPQAKMCSPPFFSPVPM
SQTPGPRVTRAENTMFPSPPAQTDENVPHFYTVPQELIRQEGRAQRNQWSNQEHHVRGDS
KGDGAGRRRRNRRRGGNSSFERRPTQLETQEGQGADTHHADPYASRAQEIDNCASRPLSA
EDLWDDPDPKTYHGNRRLGNLNWQQAEFVRQQNEGKRSPGAVPGRGGGRGGRRRGNHRKN
GVGRRQVDQEKDH*
>TCRU_9618 hypothetical protein, conserved
MSVPEWAKNEQSIDEAKSYLRQGNSVDFFELISSSVLREHPNNIAVFCLELVQKIADGKE
TSVYDESHKKKVEDNKYVREKNVCEFLNEWILALLRERPTTDGDRIEFHKRYLQSVIAGG
SDRNGGAVSEGEEKLQAEEGEGQKAENP*
>TCRU_9619 RGG protein
MMRHWVSRVASWGCRGPQRAICTTQCVFQRGQWGGQRGGGRRDYGDQGNQGDYGGQRGGG
RRDYGDQGNQGDHGGQRGGGRRDYGDQGNQGDHGGQRGGGRRDYGDQGNRGDYGGQRGGG
RRDYGDQGNQGDHGGQRGGGRRDYGDQGNQGDYGGQRGGGRRDYGDQGNQGDYGGQRGGG
RRDYGDQGNQGDHGGQRGGGRRDYGDQGNQGDYGGQRGGGRRDYGDQGNQGDYGGQRGGG
RRDYGDQGNQGDHGGQRGGGRRDYGGRGGRERHSRGGNSTREGRNRGEGGAEERPLEGPF
DERAAKNLFELKRQYKHAKSGRDRRDIQREARRAIRRARVDPSTQDEKTVTLLLNCAATF
HSYPHSEGIKQAIQWMRQNIAALSPQNLALFANALGTLSAVDSDIILLQEVTPAVQSVFT
QMSPVELVMILQAFQRNKIFSNASLQESMLRQLSSCVSQMPATQLSTLAGVLVSSPLRKS
DETTWQELTNAVLSKAVSGVDNMHSREVITLLKAAPHLFVPEEPSLQLIQRAIDTVGFHT
DEQVGEILESVAGYRNLEKPPGENLSRKLDELVNVLWTRLQKVAPHVDASSATWIMHQSC
RCGVDVPPSIMEAMLEAVTKDMRYHRYTFRRCAALAEALAEQKAPAKALLLLLGDYCIGR
RPPREDREEADLPDEEEVTKETRMDIYSRFLGDLTRARIALENAHSANSENGEPGESVRV
ILPQRLEESVSAASPRELLKCVRVICTSAEDCQVRNRANDEKLMTLAEQRMSSEHEGFLK
DVPKEFLEEFLGTVKDRPRAQKVVLACTG*
>TCRU_9620 hypothetical protein, conserved
MSGLWSFRETAAPLPCLSDAARASLPTAAIDDFIEHAAVGVTDTSMEDPVRVFGLVNDVD
VAVQELQNAWLERIVGHEQASPYHLRLSHQEVSGAVTSQTENRVSTADGYEPLSPEEMAV
VKSVLKMPGKSNERKATSRVRRRGPTVPRAPVLHATALVSQRKERQTFSGANAAEGTGMA
VQKPIDHPIDSYEQKEKSLLHRDCSEKRTSNLTRHVSQMLHCTFLERMQRRAEKRRLARS
ALRTSRLPDSANGELSTAQNVPSDKSRKKQPNLQYDALPLEIQVALLSLEGTRNTDGELN
RYFQYEAIATRWHSAHLNKKAWECWRKRQRIRTDGSEHNVATDAASSAAGACSLLQANWG
SNLGPPPHAELAKLDANKMRILRWYFVLWVAFLETARDGGVNLGISAGGA*
>TCRU_9621 rac serine-threonine kinase, putative
MSVEYSGYLQKTGGKFYKKNQTRYFELRGPMLCYWKRRPSGPHVSPTGTIDLTNARFVEN
PKDPRSWTIEGDHLSKTFTLTADTEEQREAWVREMSKVKPENREQPSTAVQSSGDVHAVT
LYTGGRHKVSLDDFELKATIGAGSFSNVFVAREKSTDKVYAIKEMGKELIQQHNMLSNIA
AEKHILQTISHPFIVSLHYAFETKKCLYLVLDFLPGGELFFHLAKEKVFDEYRAKFYCGE
IALAIGYLHSLDIIFRDLKPENIVLDEDGHACLTDFGLAKMNVSNASNFTFCGTTEYIAP
EFLLGQPHGRAVDWWALGILLYEMIEGIPPFFNENSNEMYEEILKGELKFGDVGGEESGL
PVISENAKALLRRLLDRNPQTRLQDLEEFKKHPFFEDIDWVKLSRREIQPPFRPSSNILC
NFDEDFTSKEPRAGFQEEDGGEHGNIACFSFDGQMGPA*
>TCRU_9622 hypothetical protein, conserved
MSMRGSATITLIAAGLLAFLTATSCVFVVCAQETLSIAGSVSVALNASQYIDVQVVHGST
GAVFRSQPLDATRSFSFTGLPLTVNEVRLFLRLPERRFRLDRAASSLSARIPNVASGDDV
AWLHLTAAVEEVSNAVPEKRPQGGSVLTAVVTVTSMALAAVGRHRLLSLLQLPNFKLSKP
RKVIVTSGG*
>TCRU_9623 hypothetical protein
MENTSGTDTGATAMNIAMASTIVYGLVLLAGSCFFFIRRGKGNFSLRGVGVSVFFLSAFA
VMPTVLALGIAGAWICAAYDSLGGAVAFLVVPGMILFFLLLAWCAAVSRDLEEVGGALDF
DRL*

>TCRU_9624 RGG protein
MSGERKEALKNDLPPIPGCDTDGQTYKSAEEMWAAELRGNLYDAETGWYGRSLQYWSKVP
ATVSGVLGGMEHIHDVDLKESRAFITSIPDRGTSRALDCGAGIGRVTKYLLSTLYTVTDL
LEPVANMLEKAKEELKGYPVGEFFLSSMETVNLKPNTYDLIVIQWTAIYLTDDDFVKFLA
HCKTALTLRGYIFFKENCSCDERFVVDKEDSSLTRSDAHYKRIFAAAGVEVVKETMQKEW
PDDLFKVKMYALR*
>TCRU_9625 hypothetical protein
MIFDKLPLAPHLTADTALQDTVESVLASSHSLLNNARRLSDAGFNGPQSLGEELLVGRED
RAASNSAVSESFGLTVGAFHTKLEECRDLLRRVDSERRFFRERALEMQQALEEEGKERKH
LRAQIAESQRELRKAQRQAREAQKKTRDMELALAAATEEQMRMRRFLRALPVEKENLLLL
VPDRRFEEAFRDKMSAIKYKRRYDRARELHERRSEDVERKLMLMEDKFVETPQDELASSL
ANIQHFNSISLLSTSTLPRLSNSLSVSQLAPTGAVRDFLHFQFQLPFSHVTAKDDYIDAR
IQRSAYKEPLRGLREGLFWLSHRLKRTQDVGLCNMYNVVLESLQGSGNSSAPVMFGPKKA
FEVAMEKLQKSHRELLYQLVEVVNSSVTQLLENESRVTVKPTVSRRDVGCSVYSAPPMDV
RMTSLEMRLDAQRRKSASFDADSSIAASHAWPKKREIHEKVKITLQQLITLHDALHNTLQ
KVRAHCHLDETKPNDAFEELSLAATDVFVEDPRYETKVAEAVEADLQQITQLTDLVLQDT
KPPQLARKKGTSAAKSIGVDITKRRQEKQKIAGPGSPPQANRTAGRQSGDAYLAQLASSF
TSSPKRGKNFPRRSSGTSEPENTDVAPNNSTGAKDNDVPKAVAAFIVDGPANTQSGTGSC
GTPSLPVSKQRHTPSLSRPPGVQRLSSSSLSKVTLPQFMVSEGKKR*
>TCRU_9626 50S ribosome-binding GTPase, putative
MLHCGRLFAKKRVPPLGYSSREFSRKLRSPRASKPWRDRHVVSGGQIEVSPSTENNVHGD
LSTRPPLGIRDVRVNSAGDFTTAALPEANYDTMASNSMLPVEQEGDSGVATVTSTPPVAK
LPFGKALELKVEDVKTYKEGPVPLHLQQFRRSRREAAESILLPRHINQLFHKIMGWTEDV
VEVDSELAPLDPGADGKAKASETQPELKKSAAVLRQKYDTLRDKMKYGVLLDSYEKDKFA
IEHQLEIAGERFERKFMEWEGMHVLDQDSTAAMQGVLENKSSIVMDLPSSFHIPVVNRDC
CKGCGALLQDKDENVFGYVRRGDIERYILDRQAKMKARAEYADRMSELQAHWQKHGRRVG
EEWLDFMTQEEFDAFYKDQNKPFVCHRCHALENLGVEGRRQIWSAPDFTEKLRALREKKC
VVVLVVDIADFPGTMVYDLPGLISMNNDVIIAVNKMDCVRNRSFNYSNKDRAIAARLVTE
RYVRRWVIGIALQFGLPRHQIKDVVPISAKRGWNVDKLIAAVEEASNLNLTRPIKPMPTY
FVGVANVGKSSVINAIAHKLYVPVPPHPESRKVYYTRKAKDGTEAVFWRWYTPPNVNQAE
MIDIPSRHDKKASKLLTVSSLPGTTVEANAVRVSLTKGAPGDAAYLFDTPGLLPHWHHSS
PLTLLQMRRTLIRKYRNPQCFILMPGNTLFLSGLAAIDVVKGTSRGMLFMVYTSQKVCNA
IIATERSDEFWQDQLGKALDPPGSLEQLGDLRLTESKCYLFECYPRHRRRPKADVYVCGI
GWTSFCVNETCDVVLRVRTLPGVIHGVREPLRYKDLLAFRGWPKLRRRFTAAGLPSDEGD
WDDSIATVVRLTADGPGTQTTVTGAEEDGEEASAAKLVRKAILPRRVSASSTAFDVMLAD
LTLNGSVTHTRGADSGE*
>TCRU_9627 GDP-L-fucose synthetase, putative
MPGENFGEVVLITGGSGFIGSHVVDRAMREGYTVVAVDNDYTGREQNIAHHIGKENFHFV
KHDVRHPYPEEVLRHKYNYIFHLASPASPVHYQADPIGTTLTCVNGTYHSLLLAQRDDCP
VLIASTSEVYGDPIQHPQTEGYWGNVNCTGVRSCYDEGKRCAESLCFDFHRKHGVKIRVA
RIFNTYGPRMCFNDGRIISNFLIQSLRGEDITVYGTGTQTRSFQYCDDLVEGFFRLIRHP
TEIGPVNLGNPDEYTVLDMAKKVRDFVPGTKSNICFLSPCEDDPKQRCPDISKARRVLGW
TPVVPLSEGLRRTAEDFAARVSRGE*
>TCRU_9628 adenosine kinase, putative
MSHPAKLYVQCNPLLDVSAGVSDEFMARYKVERGTATLLAEDQAGIFEDLENLPEVKHVP
GGSGLNTCRVAQWMLQAPKGSFVTYVGCIADDRYGGILKNSAEKDGVKMVVEYTTREPTG
SCAVCITGKERSLVANLAAANCLSAQHIYSPDVEKCLMEAKLFYLTGFTLTIDVAYVLHV
AKKAREVGGTFMMNLSAPFLIEFFWEQFSQVLPYVDIIFGNELEARTLSKAKGWDEEDMK
EVAKRALKELPYSGTKGRLVIFTKGPEPTICVTKDEITVVPVDPLDPEKMIDFNGAGDAF
VGGFLSGYALGKDLTRCCILGHYAAGVVIQHDGCTYPEKPILSPWE*
>TCRU_9629 hypothetical protein, conserved
MLHASRLAWGPFVLNTRVIPDWWQSFQREDQHRVARARATQLRTPRDESRQNDVTPITLR
EADELVKTYTRNHNAEDLSWIVQYIRETMGEPLNLLYYHSLFRVFNYTRDKENIEQLLHV
ITESGEADMGTYALVVDALHCLSPVDTLARIMRMIAVTQTSFGTLLSESGCPLLTSLLHH

LANTGKYPSTASLLVVLWIRALGAQLCDWDYVHVLSALLSHPDDFPQIRSALGAFSDFSR
GTVSPEALFRRLEDRGELSPPSSPLNTIVAAMRVSLSQAGVNLEEPVSNCVINTRTAGLP
SMVEHIVNDMTSVATSGKFNGDLLSCYHVLALLYSTLRNDTAAVETLRYVAREIRRRERS
VEYDGGNAALAPIGEYVHHHYLMDIGSVLNRVSMRTLQRARADYAHLAQNASSDVSENDV
VAAESYAILFVRSNEEAEEALRQASQSVDLSSQRTRRSTKLLFRRFVELCARHPKRNCKL
TPVGLEERRKWGRYLDARDTSLALFGSAKQARDSMKHLFYNDNKLPELRSHAMIERDMND
TAALFKWRRAPTIASLRVRSSLPHVRCPADPVPRHLWDPDVYNPYPQVMLQMSPMDDERV
TEDIFQELWHVLMNPSVVGTDQWYLRDTEMYLLLLRCLIHRLDWEVAVHLTLKTMENLTY
TYMMDHEVTLMFKEIGDPAGCLAFKVATKLFDGRIIKDGQSKREKFHQEQFGEV*
>TCRU_9630 N-terminal domain of unknown function (DUF4140)/Domain of unknown function (DUF4139), putative
MATTDPQPQQEPECTEVSPSLTAVTVFRDRAQLTYVASASLPVGAHVISMKGEKGWESVL
RNTLQVHLEGAENQQVVMRGVRFRTHVTKEDVRERVRELEKARDKVRELIDQIADKKAAN
DAVEAALKKMEEKLLIMGECGVGPEVRASMGPMVGFLSKPESWSELVRFITRRKLALGEL
RLKLSRQQDKHEEEENEIIKKLDELTGGRHKERQETSVEVMISVYAPHVNLKLAVSFVAM
GVSWTPLYDIRVDPERSVMDVTYHAQVCQGTAMDWNKVLMKLSTATPHFSAAPPVLKEWN
ISLDPPKFPVGFSRFLSRSLPSNNRRERGNEEAFPRPQAALVEQAVVSSSSTSSTFQIVG
LATVRSDNKPVKVTIATHTFPVKLVYHAVPKLSPWTYLIVKAKNTSPYVFLSGKANVFAN
NTFVSNSQLELVPVGAELTMSIGTDDAVKVTRKQVKRAKSTLHAMLRNRKKVIEYVYEFT
VKSSLTAEATLVVKDQCPVSSHKEITVRLIEPSKNMLTECAKVDDNDCSVDNGGIVEWRL
LLPSGVFTRDFRFAFQVEHNENMDVSGLDVED*
>TCRU_9631 Spc97 / Spc98 family, putative
MEELQCSLLGFSSTLFPLAACATRRSCGGTGGTQTSAVLSQLHLSERALVEDALPLGAMC
RALRSVATDIAVGRTEGLYLSAIGAAITGILEHYEKAVQNATTATAVAGLRPVYFPAFTL
LTEMIDQQKSTDAILFTIRSFVLNREIPQEFRVCLGESVWMGLLYTIAHYIAHGVVLHGR
KDFFISVRSKGGKEDHTLHTDLLPHGISVELGMLILSVGKERRVVLSESESHGREYLEQL
ALGAHDETANTVFKAIYNSSLCAGGFLAADELETRIEAARALWSKTLWLKVGEQAALHEN
LVALRAVFLCHRGDLWHAFVESAFPGLVDSAVQKTILKEAAIGRVVADAFVHALSVSGLG
DAPIYERFSMFIVLPLEIGDSKLRSIEETARTILGYMRGLGLHYVMPRGLHLVLSTKALE
YYQRIFSFHIASRFSLHALHNVRHVFSGAFVTNKQPSAELRRTFLLMQLLLFLHTTLGYH
MQVDVILLQTAELEKAMEKCRSVQDAKKCLDRYVWHVAEGSFITEGSGPLLLACESLFQC
SIALYVLCTRYRLTSWAVDGVPIPLEVSAALAALETRVHQDVVAAFTGHLSGSATRATER
ALWARLDFNRFLSAGVRFNNRKTEFPQPTAAKTRAVSGVRVASAAAQATIRGGVASAHDA
PASRRRMDLLPRAAPSTSNSTRG*
>TCRU_9632 hypothetical protein
MHDFKVGGVTVLWGQVLPVEEMALEVKCMPQATDIIAVQTFTGFVGGYNFFQSHGEGKCG
VTVPGALLFGHRTNGFAVGWDAVKEDYLANAAHVRYSSSWDVLERPTATNDGEEEMVKDR
T*
>TCRU_9633 hypothetical protein, conserved
MESSTGANEGAGEEERNVRRRLSSPTREVGEKKKQKEHSVEPSSTREPLPSSSPFEKKAV
SGLFFIVTEEGAWRKTMFHANSSQFAEAERCWEEHRTTGKMHHEPPWRVCSVAEDNREHP
YYVRWLDTMELPPLEELLNKKSGSDGATEKCGGDGVGK*
>TCRU_9634 p22 protein precursor
MRRVLFSAALSLVPKAPLFRRCVPSVATAASMGPLVAMEQRRLASHAALSSALRHELEEE
QQRSEKPAKPELPAGWTLERKPGQMLFTMRKKHEDEEIIIRCLGEESGDDDVVSLDFDAY
ITCNNKALVCRMSFESEEVIMGQVSFLDDAKLALDDSVEGNRKRQWLYKGPKLDELDERL
VDSLTSYLKDRGVNEDLCRFMEEYFFWAEQAEYEEWLSAINRFVS*
>TCRU_9635 hypothetical protein, conserved
MLHQAEEYVGAVPLIIFLSDTDCTVQEKPAPLTYVLPRSSVLMAVRSEVQNFFSSYTVVK
ADALPLVWLTWRGEPVPWHYPIGAIKDSINALLIAERGNTASRAYHTESSPLSPAELYPT
VFGSPLMLEVRITCVTAERPLAVPFAGQEEALSRRSTDQAMGEFLKQVIKGTFSAMYGSI
KALMDVRSEVINDLLNFATCISVGDPFVQALRAYNERIVGLRRLAGKPKNVAVMINNPFG
KNSMHFALFRVPLGVSGVGDDKFTHDKFEKARSCVESNNSNCSKDHEPSNPSDKLSGDVK
PKEHPLETPFGMVVWRALLEPYLKWRNLNGEDGANSTCAEPFFRAISPFYNGLDTSASVN

AALSSPAADALANDFIAAGDANTELIGIRVTIPATPPQERRLCLIVQGLQPPLCTPVGYL
LDRFASADGRLYVTLAAL*
>TCRU_9636 Mo25-like, putative
MNEAKMEVRSNKGFLQFLQSTEDPMIVDANLLLLLQDLSSPTEDAIFLSSADLFHLLQVL
VERTNDDWLEVRKKIAFVFSDLISKGHGDVLADALIYGRLEKTTSGEARASHIDLRDSCE
ENSDPAAALRQLKYFIGKLAFAHGTVERCVPAADVFRTFMRVPSFLEIILSPAELSSDTT
EERTSPHPQPKQHGFHESCIGILCRSVASYTTVLCTETWRSLTTALYTNKGLSASLLLYY
FNEFVAMLVGCLLGRNFVAKLHALELLASVVEDPVFLRARRKFAESPALLCALLPLTNSS
SAHIRFLTFETLKVFIAKGNKPAPIRHILCINRDMLARYVEDYSTKEIAINKRLEVEKQK
LLQSLTSLEPLTHEEELLLGI*
>TCRU_9637 protein kinase, putative
MSSSPAPACPTFDPQHLNLPDAEPVGSGAVSQVVHSKLNFPPYTPIAVKIVSKVQLLQQN
KTNSAMNEKRALLEMGPHPFIVRLFGTAQSTDELYFVMEHLPNGDLLEHIRTCASRQTIE
ELIAESTSDASSLRGSSLKDTAIRCLNFHDIQLITAQIVMGLTRVFRKGFVLRDLKPENI
VFDHKYRACLVDFDTVDVEGTSFLPKSNGGVALPGGVAADKKCKAKRRLTVSAIREMRKM
SAQFCGTAQYVSPEMIGQCQWSYSSDLWALGTIVYEMVYGVHMFAGCNAYAVMKRVLGGV
HSGNIPFPNVNLGPESDALDRVKDFICRLCRINPTERLGVHPVTGQFDEEAIRGHPFFGD
FSWSLLDEQVQYYRAPVVLTTPSDSGSVRTPAVQGPLHPQLLDDGTASLKSRYHVLPVHS
KEYAEYVFEATADANPFERWMRTKVEDPTGVSDHETTKHNASFVEDMPIATPVNDGDVDE
ENSDEYSDVVDDVGMQFFGVVHPDFLDIA*
>TCRU_9638 ubiquitin fusion degradation protein 2, putative
MLEINGLAHLLSLTREQPIVVVAFYAEWCGPCQRVKPQYAALGERYKSTVTFCRCNIDRN
PDCVERFGVRSVPKFMVWSGGGWHAVGFDGQLGELERHIDRAVETHRTSSASNGDHTLGN
LHRVLARQMQSLARAVASAHDETAMVREACEAVCNTLEQDTERRPFGAAMLPYFASNEFN
AAAVDALFAHFATRPEPRCSDGEYIINGALSNLIEFFLSTTLDNTRELNVLRQALYALVS
CTATLQILVRSHLFYNDSLSSGLQLEYGTVLGALLGVSTQIRSHRLLPPYSMSSERAQLM
SMFSTEVDDHSKQISDLQFQMQASCAGNKRIILALLQAKVSREPTLRYIGTALRLNAGYT
KTVHHNLPLSSRYFMTQLNDVLLEAALPLFEKAYDPTTIPPFYVLEDNADNTVVDFGEDV
ERIVHYDESHPLPPFPALSEPFKPSVHLFFLVARSIMLSAGVMIETHQRVEQDLAHPQLP
PEQRAVYVAEKSLIEGLIGSENLGRKRVQVLNGIAAWLVRLMNVSPGGVLSKEPPEEWKY
LPQQLVDLVILGVKMAPLEYFDLEHIVSLMLVLMGNTTYFPKPHTHALFPSFLTRLLQNE
ETKRALTSHRWFTQHIVRSCVLCYIAVEKSTYEKVSVRYMLSYCTKSFLMFDSLCQPVRE
EFEVDGTILERFSHMVTADVNEAVDQLVETLTQMNRMVKEGADLSVSARASLSNNGENIR
RGNAQRRQEGMATSNSNNNNNQNNNFRSADGNVNEEEAEADGDDGEAPLTYHQLGLGLRE
RILLFEASMNLFIQLAISFSKGVAQNMVAQQISQMLARSLVSFAGAESKNLKIEYPERYN
FRPREILNRLVDCLSQFRRFQNFMRSLCNCGVPLREILQAIETVTERGLVGEHLIWKLRE
IASTLETISQEVQDDEALWDEAPDFAVDALLLTPLIHPVALPADVKDLNDLVYVNEDTIH
HVLLSESKHPFTKEYLDENMVKEFNAREDVTEARRNLQDRIAKWMKAAKEKR*
>TCRU_9639 chaperone protein DNAj, putative
MYSGTFCGTLGRTLSLLPQRWCCVTPHSSLHVAVRLVSSSGIPIANYYKRLGVDCAATAE
EMKAAYRRRALECHPDVVSDDQKARAEMEFRAISEAYDVLMDPQKRSEHDKSLGLDRVAS
QKTTAERQGSAAAEASTSSRVSSTRRRKPFVRGDAERKFREAFHGMSIDQVIFQERLRQR
REGKKQHGEAASPSSREESFRRVLVDAAERFSEKVRRQYGPSMLRHVKLQSVPPSGPQPP
PSDYMPFRPFYGWFAPEGVRTVPEPRMGPTSHVNEENVEFEGPSTPTQRDLPKHFPTVRA
LDGSVMSRADAMRHLERERNAPYNMGKLYSYHRPY*
>TCRU_9640 hypothetical protein, conserved
MRRHALKRVMMSVPAASAIAAPNRGIFTAWGSIPLEAWASQEPWLTRISSMSKYRSFEFF
HVPEVEAPEDVQLSAVEKYLLSCVEDDTNRLLNLSWTYGFDSFWSDRVYSHDVLFQILYQ
HNYPIYKFFFGDCSSNEEGRKYIEKKLNYLKSVLQWAVMTERCYTTIAKARFTLQREVWN
SLERERYLMGCVEALEEFKKEVPREFAEKAIGELETELSSVRHWVWDCPNAKRLYKQLS*
>TCRU_9641 Flavinator of succinate dehydrogenase, putative
MLRRFSRRLAPRAKHHDELVKMWRESPRGVDKASEESGLRFRDTRPTPQNEPDDAKRRRL
IYQSAYRGMVEMDIILGAFSRHSLEGMPREQLDEYDTILRHFDSDLFKWLVMDEKPPASV
ACMSTYKVLQEFVKGGRERLLGQAV*

>TCRU_9642 RNA-binding protein, putative
MSGPLQKPGGFIPRPPGMPPLPPGFKIPPGMTPPSAPPMPPGMASMPPNMRVGAPPQPRI
QVGNDGSAGVAPPVPMPPGGYTMPPGRYPQPPAHLVPRPRGDVEHGFQNHQQLLPPGLVR
NPNEMYAARDDHAPVLLPGADPHGYPASSYPQGPYGGAVGPEAGDHRGGHLYRGRREDEL
REPTNTVWVGNLDLHEHTEEALRREFSEFGGVIRIARVPDKSYCFVHFRYVEEARNAVEA
LSARGSLGRARFNYGKMFEYTQEELEMPRDVTGHRPSRRGREEDRHDNDDRRRRSRREEE
RMEPTNVLWLGDLPPTVSNEELNENFKVFGKIKTISRLDSRNMAFIHFETIEDCTQALDL
MRDQPIGGARVVLNYGRAQRNPTSTETGLTPDGIPVNETPTNVVYLGQLASDVTEGDVED
LFEPFEGFINSKFIQSSGIAFGHFDSIEHARAARIALNNALLRGATLRISFGKSNHTMTM
ADRMRRGKPAPLGNDDANGDFTAMPPPALGLGGVMGALVAGPGAPAADAGAMVSLPTMGV
MVGSQAAPPPPTFFTRERPTPEMTLDARLQSLLGATYNNCGEADKSVSPSVIQAICDLVD
GCVDEQSMKRLDDTIFLYTPLNSSHVFGILAKRIHDYFNDDPHKKLLVLYAATRVLLGAK
TDYLLFTKAALNAYLMMLFVASEGQTPGGMEMLTSIIENVHRNPFIERQRLDAEFIEVFR
EQLDEIHRRAKVEQDLASLLTKKRRR*
>TCRU_9643 hypothetical protein, conserved
MGHGRCTAVVLLYCAVVSVFLASLVLAGDDGLSTASNMPLFEQVIVQPFTVSVISGRYGV
FNATLALRASPIFPEHIHGELIPIGEQRRGSAEQLSLEHFNYPRPMEGEMPTPGMVDAHP
SLLRIDVQLRFSGSTSGTVTAWALPAVVGVLERGLSEVEETDAAPTAQASFLFISESKSM
SPSTLSDVPSMARTATGIVELEGGRSGSFTFRFFSEHEFSLNLQLRTEDNTTDRSWVYGY
VPPDNTLLSRPDRSQKAWWQNRGIWVFAITTFIMRAVMAYFETRRAANLRRKRTAAAAME
KKKIK*
>TCRU_9644 hypothetical protein, conserved
MLNSTGNSSLSLQRTTAVSDTDARFIVLIVRDLATYLCRSGETHPFFEDGPIPAELLGYT
PASSSSLHETVASSKQKAALQLVSRLRDHVLNRNIVVIFPIQASSEYRERLLMFLFEKLG
VRTIIALSDVVADTFAVGLRDSLVFHASLRALSVSRVESGVSVKYAASASGSLLHLLKPH
TTGTGELCGEENFAKKNAGAFDDTKEGDNWKEDGASAEKGDGNDVSSLLSRLSVNGSSFF
AAAVNLLDETYRKALVAFFGGEVYQRVVSLHEHGEVGTKRRRNDGQEDVQSTDKRANGYP
QDEGGGALRRLIAAVAGDTSLPVIVTGEALRVAPLLRKFLEEAVRECSGKTAATGTSSSS
SSFSSESFETSSSSTTNGSNSSESSFEAGVSFQLQPLPLEDSPWMLSLLGGSLVSQLSLA
ELSKLRISRDDALLSKGSIIHWRSLL*
>TCRU_9645 hypothetical protein, conserved
MIRRFGSTVVSRSRTPSVPLVSAPTHSSLRQFHSLYGIAVSLVTCTGCILCFGSWANNIC
NVRKYGRWRFRNTIDDAIMVSDFKTARYIGGFIGFLFYWFVVGPKKYSYPSNLADVPDNK
RFGPF*
>TCRU_9646 Protein of unknown function (DUF1077), putative
MAKPNSTPSEKDMQRARTLRLLNDLRMQPLKSLPMTLFLMWMVGNDVGIFTIMFVGMAVV
NPLQSIFGTNDVFKEFEEEAKGDANIRSALSHSKLMYIASCLLAFAVALVKLSWMGLMPV
NAMDWLDSTPPDYKEYTQGFFAI*
>TCRU_9647 hypothetical protein, conserved
MTSIALWVARRIRTFDLKHSCRTRPYAWYFSLCLLFVSWANYAQYRRLRPMYPNYEEYRL
KEGGRMLEAKRQEMADVMRYNSMVSTMRSELSGRG*
>TCRU_9648 hypothetical protein, conserved
MAAKGRHSITPVSTLGRFFSVIDCELHRINIVYLVKGYNLRYSLTVATLLLLLALTFAFP
TEQPVYVGVVSLLAQSFSVLMIAGGLYCATGGVFTRRRQQEEWLLGNVKDVLHLLMENAS
SSKAGYMFLALEAMARLGNVLQGSACVCALLLLWICWLLLKMNSERP*
>TCRU_9649 Hsp33 protein, putative
MRRTWPARCAANTLAPAREMERRLRSRDMTLRVTTKDATLRLVYASTLGLLRETLRRHRL
AARTHGCCSFLELLGTHLSFTNILAALQEGEERVSSRFTADEATVVTEALALGECRCCVR
GDNNGSIEGPSFPLIVERALYGRRQAFTSATSARFDRIVSEDEEEINDADAMSTLRIGLK
NTPCEKLMEYFRHNISLHGYNFFCQSEGLTSALWCCTHLGDPSIQQALAFCAEDVVMHGA
AGNSLEADTKLDLALERSGLSYGVLLQPLLAGEAVEMDIRRLQRVIVDASINTPDVFREL
THRAVENGLACQDNIALFTGDYEGAYAIATAARQSTQDPALAMLAVEKVRCKLGFNEFRL
SLDSAAIVRNGVDYFCRCSKQNFMRSVVTLPKEELLRLMHETSFRCTFCAKEHPLQPGDW
QKAMQGRAE*

>TCRU_9650 importin alpha subunit, putative
MFGGQGEKPKGAKQTPSVKAGAERRQRQMISVRQKAHGELMKHVRGDHGRVSVEELSRLN
GDPQDVWTYDAQTAPEMVPRELLPEFARLVMEGKSEKEVFHGALLIRKILSVERNPPHDA
VIKSGVVPYLSELMDRFDNPKLQFEAAWALTNIAAGTSENVSVLIQFGAIPRFVSLLGSE
NEDCRDQGAWAIGNIAGDGVRCRDLALQYNALPALLRVLTIPHQPLNALRNAAWAVSNLA
RGKPAPPLDSVSIALPVLSGLLYHSDKEVVIDAAWAISYISDGSWDRVQAVIDAGVVPRM
MEFLSSPVIPLQTSAVRTAGNIASGNNEQTQIIINCGFLSVLGNLLTHCKRDIRKEACWT
VSNIAAGTLPQIEALISSNVFPLVIKCLEGSDLDVKKEAIWSVANVVLCGVVSHLRYLLD
CNVVPALCEALLLHETKILTISLESLMGFLQLGDDDFRAGISEENMVAQAIIACGGVNAI
ERIQSYTDNNLYSLALSILETYFNVEESFPQGGFEASAEFGDGTAKQDTEFDF*
>TCRU_9651 hypothetical protein
MLFHDQDSGNTAMSNFAEYYGLVEEDGGGEGRTGDSSRRVSSPREMETRGAEATLLLPTT
IRRFVRAMEGTTDMPVACILRVTDGSRLVDGRLSTIMPEEWCTPGVFETTGLRPIEDVEG
CAAVAFLLSRSIFISGLLASLFLPWRSWLHVVRVWRRQSRPRIVLEALL*
>TCRU_9652 hypothetical protein, conserved
MLRRCTSPVFHGGELSRCRRNFRRSKPKFASLAADAESVTEGTQYGGGLPAEPRVVARIS
LIGGVTAEPSNQLDSDILLRPMGHFIAMAEQPSDSLVDIMAWRVGVSLPLYPTEPALARC
CCVDDDAVTEGIAVVYSR*
>TCRU_9653 hypothetical protein, conserved
MQKTYATLARIVSGAPSTVDPESALLEANMPPLHVLCLRARLSIFENTRTCQTDWMRRPP
PEPPPRAGFRISPLSRDELYASVDAYTKDYGITESSPREERFLRSSIPPWFAASAHRVTI
GVELPIDLSITDEE*
>TCRU_9654 RNase H, putative
MIPRIRHRRKTLLVVTDSQSLLAALNKGPLSQTDWMEDRIWQRLLTLTCAGWSVHLQFCY
GHCGVHVNELADQYATQTMATGQYTEQGIAPLWHTDLLTCFTTQLTNKWRSTIRQDTHRY
LLCGTRPSDLSGKDLTTQEVLHRQELVHLARARCGESELWGRLYWAVRDCTN*
>TCRU_9655 60S ribosomal protein L22
MVAVRAKVGSRGFVRQKQLAKGKKVFKIDCTIPANDGIFSEEILGNFEQYFQENVKLNGR
KGKLTEKVRVGLRNNVLTIATTMAYRKKYFKYLTKKFLKKKDLRDWIRILARGKDTYQLK
YFNIQDQEEA*
>TCRU_9656 60S ribosomal protein L22
MVAVRAKVGSRGFVRQKQLAKGKKVFKIDCTIPANDGIFSEEILGNFEQYFQENVKLNGR
KGKLTEKVRVGLRNNVLTITTTMAYRKKYFKYLTKKFLKKKDLRDWIRILARGKDTYQLK
YFNIQDQEEA*
>TCRU_9657 60S ribosomal protein L26, putative
MASIKCGSRRKARRAHFQAPSHVRRILMSAPLSKELRAKYNVRAMPVRKDDEVRVKRGAY
KGREGKVTACYRLRWVIHIDKVNREKANGTTVPVGVHPSNVEITKLKLNHNRKAILERKD
RSTKSDKGKGKVTAAEKAMQQMD*
>TCRU_9658 hypothetical protein, conserved
MGAAEPERRMVLAKCETWAIADGRLQRFTAYMLGQGGGLQTVGASSDRRSHGKVWRTKRA
TPPARPLQAWWKSPQPISLVAKSIPA*
>TCRU_9659 hypothetical protein, conserved
MPIGVAARSSPAAVEGEQPSRSSFCRFRTPAMGAAEPERRMVLAKCETWAIADGRLQRFT
AYMLGQGGGLQTVGASSDRRSHGKVWRTKRATPPARPLQAWWKSPQPISLVAKSIPA*
>TCRU_9660 hypothetical protein, conserved
MPELEAMPSYLPDTVVLQLYRDVGEAEFADYMDANSLTFVALGDAERPALCGIDATAQLH
HEGAQQALVSAAGIVSSIRRRRLRVPFGMSEPSQLLRRAYNAEKGNRNNSLTGSTETALL
AHAFSDAVWAEESFHCLSTTRRVGNILVSTGIGSTTRDLAVDKWRPDQDIMELRDELMIV
RAVYDHRHCGHESNRPFQRWRRKG*
>TCRU_9661 hypothetical protein, conserved
MAIDDAVTLWNTLPLSTTAESLLIASPFITTHDGLSRPKPDRGISLVTVKRFPLIVMFVC
GGNTPSGLSSAPLNVLPVTTMFSDPTAAYALPNSNSTAPSLHVHPSNVTFATSPVIAPTS
TVRLMPPPLNVTLR*
>TCRU_9662 hypothetical protein, conserved

MTNRVDRSRTPSRASAGPYRNPSCPRVVGTYCDPPTVARSVEFASNTLECSGIAPCSTIV
PSNDVTFVMLTRAWGIRRAVISLRPPIRSCAPPTSTQWRSVTFSASANASIERRSTATVI
GPLNTTESKHAVAHPPPTVTDSVSVTPLTQSCAPPPPPPDLAGGTSNGRHASPTPPSRQL
HTQSENDAVSASKHANAAAQPSHGTTLTEDRPAMR*
>TCRU_9663 hypothetical protein, conserved
MQRPQHSVAHTQLRLQQRRRVQHKRRRHRVRQPTQLGVAHRPRRHDRRVTDRHVRVCRQV
VHKHKGAVVAGQPAHAHLQAPVTRRLTAVAPHVDLRTAVAHAVPQFDAQRAGKHRRHVEH
HSHAVRHVHAVHQHRVHGAAHRDASVHRAASQSQHHRMHRGHPRRRRNQRQHHKQRRTHS
RDGPVPHTVPAARKRTHSRPHPPTQTRISRAVALCRSRPVDHSSCLSNPFLQMANPVTRF
RQIVIPVLPILILQVIPNTLKR*
>TCRU_9664 Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MWKKVDERVSQLCTTLLAQEVASTGTACTTDVKITDGLVGFLSGNFSDGTWRDEYLGVNA
TVTKKDGAKKAHNGVTFTGRSAGAQWPVGKQGENQLYHFANYNFTLVATVSIDGEPTEGT
IPLLGVKMAGAGTSVFFGLSYDSGGKWQLLCGDETPKELSSTWEKEKTQHVVLLIRNGSH
GSAYVDGQRVGDVQTKLENTEPNEISHFYIGGDGGSAVSTGGREDVSVTVTSVLLYNRPL
SSEESIALNAKLSIPKQTSLKTVKEVTRSPEVRKPPALETVPQNNLGGDQLTAQQSLKTS
EDAGGAGASTTAVSTVTNSPAGKESVNKSTSGTSPNGHQTVVARDGDKVPGDEPQKYPAG
NPDTADANTPTTEGEGQDGPTVNPEAGASSGENGEPTEETDGQEEEIQPQHGDANATALS
SSLGNVSQGNNTDAGTMRGSGLLPSLLLLLRLWGFAAP*
>TCRU_9665 hypothetical protein, conserved
MRASGPESLGGGHAAGTTSPRSDASQQAAGGVHAGGGRTSQGSRASEQTVTGQSQVPGTA
KEAPQGDEGGEPGAQHEADQATKMTVVTSCAKTAVEQESRQRDRKMHHVSTVAGMLIIII
IFLLPTCLATRCHQGDEGMVEQRHEFPAMRQLPLGEAFGAKVLLDAQPLAHSQSVCTFRK
QMVHCFLRANCCACGGWLILR*
>TCRU_9666 hypothetical protein, conserved
MGVHSGSSLWVKDRFIDVLFMVGWCYTMSRDVAEALVSYEPLRRLAYLPYSKEREEEFLS
IHMQHEDVMVGRVLVNELKYQPMVYVKMLPCHFGNARNETGHSQVVPTSMCVHHVREDDY
AALMARFGNDTSPAARVERVSNDVVYPSCD*
>TCRU_9667 hypothetical protein, conserved
MDTITYVCKERHANAVRFEVPLISVKAHAFGDDVPALMSSHRRILCMNVKQSNRLRVLNR
QGKYAETDVRAPVLRQLVSSEGHLDHCAFFAVGGEEVSRLKPVNHANGEIQILLRELNLR
EELYGVAVGSGDIAYALGKAHIFEVDMETATKKAVMDLASKTVVRYPVIAYHHEAKLLLA
PAKQNCLDLISTNTRKSILPKVWEPHGGLVPTTAFFVQFHAFENESAGNIFIVTGACGNT
ELRLWCYNTTKQTFSLMQDLCISVESVAETTSASNEKEEFFLVSYTPTEEYITLCSRRHP
LAVVVELHQNNFKIDRITSWKLQGPVLSSVAMVGKVAESALSGSVGYQLMLAVRTASGFY
EEVLDVEKLVGASNTAAIKQNSVAAWFPDNETEVSVMATGLPTALTAVSSSVLGDKTTNA
VSQAMASRIVRQQASQFCDKLRSIDERVVDLQKRASEVMRLFQEARAREEAQTIGRKFAA
RNKGRLELQQPQAQSPKAESTDTLNASQQNFLDQIHSMLDEVDAAAAESAQETVKVLLTQ
RLKDAVAKGAKEAEQTDLGIVAPTIRSTDSMQVFSNAIDSAMRLLVRAIKDHHAMMQSPL
KASITASTECATKAKEFVASLKNEMQKLLDELNETKKAVSQMNVTAVQVDPDVLVSRAVA
AAEANDWSTAFTIALEASDITVLLGFLEHKVCVDNMSTIVRPQKISLPTFLSLCLQLSFE
LDTQPGSIPLRIQLLHLFYVEWDDALKEIKQKATGNASQEKLMFELTKREIHNVLEQLAL
VEDHSLDRRSRNQLRLLKKLMNSFLAEA*
>TCRU_9668 Sin-like protein conserved region, putative
MKFGVRDRRDADDDDEVIATYNVYASPLQQQLHIFQFPLRRKTQPYETDEVRLFVTEGVT
HVGKEATPPSASSASILSPSSRLTMHCRLDTFGSSSFVEPSHQQQRQLPMQQTEDRFCRG
EQQRRNSYHYALQSHPFQPRCDYAVGFIVDGAIHLTPVSTIQQFTPIVKPTTLIAAHRVG
DEFTSVQSTPIVPGLAISDRINREMLRQRSVMLNTDAATAKELQYFPIGSVESMAMRRRL
CSTTYDVSSLAQTVGNQRSNTQTEDSLFPPELLISGGISGGEDAAVARSLLRRYAHRYSV
LDQVLVLLQRCQVMKLTELRELVVSPDQTLVPPPPTPSTAPQQPQGGVTDKQLLEALREV
AVWMHGVWVSKTASRFKGTVAALREVILLQFFESEDASLTRSEVNKLVNGTALRRTVKEI
LESVATLNSNEPDPTKRVWRLRHVPADAALRRAMLQDAENVHRQEVTFQRMQWEHFRPHI
KAHINAINAGMPVSRLLLATRRHGMGTDATKLTGAAVVAAGASPASFKEDDLAPIVAHIR

RLFLEYGVLNKQRTKELVMKGKQQHYPDATNPMLSAALQRCVQTFTNATWVLKQLGEPKV
DRYRPLILETAVELVNFETRAFHALLEEKRRQQSADEGGGSDGDGVNHEEMQKIVSRVLA
EVAVFKQHERLWHIKSGNVMME*
>TCRU_9669 endosomal integral membrane protein, putative
MIVADYTYQLLVDDLPIWAPFGKVINAVPMIYLHRDFRLGINGPRIVDVRVLTTAAEELL
AGKTYVFTYSTHFFQSAVTFENRFGKYMREELVEPRIRWFAIGNSLLLAVFLVIVVAVIL
FRMLRTDYQRIENELRLREEGNEELVDSTGWKQLYADVHRVPAYPSFLCALIGTGVQLAV
VFVLGTASAAYFSLRRNSSQDVVTVVALLYAFTGVVAGCVSSVQFLWYATLIPVLSKKWM
RCMEFTMFVFPIFLVSCGSITNIVAHLHESARAVHIGGVTFFLALLVIGYCPSVVVGTLV
GRYGYRRRILLPRGHRNLPHVNQIPRLIPLPPNFLLSTKLFIFLCGSMPFGSIAFELSLM
LSSLWLNKLYFFYTFLLLTFLVFVTVTSCISVTATYVLLNIENHRWPWISFGFGASSGIY
VYLYSIYFYIYRTTMSGLFPLVFYFVYSATLSVAVGLIGGSIAFLTASLFVKKIYTFVKS
D*
>TCRU_9670 hypothetical protein, conserved
MSDAAPQNPVDILAGASTLYEAIETVCVINGDKYVDFMVRLPKEGFARQTEALLHAICEL
IPSDPFMEVFGKTRAPVMLIFAPMLLSRAAALLASPHSDIFTPDAEWHAISMFLMAIQSE
LLASPGQRVVRVTELPDPPHISSIRHTRAWSSILNQTLLEDLVPLPPSTHNRRNVFDAAS
FGCVLYFIICGLVHLLQIILAAPTRIVCGTGTLGFCREIVRLLLTPTVIIYGSKESSIQI
ASASLLVAVRGVLGMREAVGEMRQVQLIEQWITAIRSWFDLTTQSGNAACMQFLFPYMLS
SDMLLR*
>TCRU_9671 hypothetical protein, conserved
MWSRRNAFSLTDIGEAACASLADTPLDDRRSSAEVVNESKINFITSLAYALIPEIKKEEA
EGILSWALRNRGDDGVTEKCVAALNQIEYFFAGTDSGHLFMFPLFPPSMRPFMKSSTGGE
TVSVPWNAAGLRRTLHRHRREESVMSISTLGTLVASAGSDAYVHLSVFHPEPQHIASIAH
PAAVHSMLMWGGGLFVERERDPQRRSVVAAAESPILYIFTGDEVGLVRMWRVNVEKRTYF
LATVFVISAHAGGIGFASPLHYLACEDGDRARAPTKQSKTIHCLAIDDDRRLLGGVEGGI
VVWSLAELPWKQREEDHILCWDIERRQMNSIVMSTLEFRTRRLVNMGMWVKGTALLQQSM
CSGEKERDGTNGNRADVKMMEKKSKWKPKYGTHVANGFDVGIVSNFVALPSPRGDDVSST
MLSLLQKTYVSLQFPSLKNTVYFPLFAVEPAFTALHVLSTTGSTCFTLLVLLHGKRIVTG
GSDGKVMVWLWDASAEVYIKGLVSSESQGHHGLSRHICLLRSPDIFLSFGYDDGLIKEWH
VYDEPELLMRCERCLRVLPVNSYAVPSHVSPIIEEENAGGISCAVSFPMFHALFIVGLFE
STIQTFSLSEVQGCTPPEDYFYNGYKTVRLIPSVTADISCATGGGDGRLGRGN*
>TCRU_9672 hypothetical protein
MEPTTITTKVPTTITTMEPTTITTKAPTTTTTTTMAPTTITTKVPTTITTMEPTTITTKA
PTTITTMEPTTITTKAPTTITTMEPTTITTKVPTTITTMEPTTITTKAPTTITTMEPTTI
TTKVPTTITTMEPTTITTKAPTTITTKAPTTITTKVPTTITTKTPTTITTMAPTTTTTKV
PTTTTTTTMAPTTITTKVPTTSTTTTTMAPTTITTKAPTTSTTTTTMAPTTITTKAPTTT
TTTTMAPTTITTKVPTTITTMEPTTITTKAPTTITTMEPTTITTKAPTTITTMEPTTITT
KVPTTITTMEPTTITTKAPTTITTMEPTTITTKVPTTITTMEPTTITTKAPTTITTMEPT
TITTKVPTTITTMEPTTITTKAPTTITTKAPTTITTKVPTTITTMEPTTITTKAPTKITT
KTPTTITTMAPTTITTKAPTTITTKAPTTITTKAPTTSTTTTTMAPTTITTKAPTTITTM
APTTTTTKVPTTITTKAPTTITTMEPTTITTKVPTTITTMEPTTITTKVPTTITTMEPTT
ITTKVPTTITTKAPTTITTMEPTTITTKVPTTITTMEPTTITTKVPTTITTMEPTTITTK
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TTITTKAPTTSTTTTTMAPTTITTKVPTTSTTTTTMAPTTITTKVPTTTTTTTMAPTTIT
TKAPTTSTTTTTMAPTTITTKAPTTTTTTTMAPTTITTKVPTTITTMEPTTITTKVPTTI
TTMEPTTITTKAPTTITTMEPTTITTKVPTTITTMEPTTITTKAPTTTTTTTMTPTTTTT
KAPTTSTTTTTMAPTTTTTKVPTTTTTTTMAPTTTTTKVPTTTTTTTMAPTTITTKAPTT
TTTTTMAPTTITTKVPTTTTTTTMTPTTTTTKVPTTTTTTTMAPTTTTTKVPTTITTKEP
TTITTMEPTTITTKEPTTITTMEPTTITTKAPTTTTTTTMAPTTITTKAPTTSTTTTTMA
PTTTTTKVPTTTTTKVPTTTTTTTMTPTTTTTKAPTTSTTTTMTPSTSTTKAPPYVH*
>TCRU_9673 hypothetical protein
MTRNRLFFSLLLLLSCSVIVGANSLEKKAATPGKAEGAQPQSISPSSSSPGDRTGVPLKL
ELGELRDKTLLTAKDAFGNTTGAALQCMQAKTDVEETKKYAEEAKKLFDKIGRDYVSKSA

ALADAVNASTDAEEALKSCVEAEKAAVDADTAVLAALLEVLQHSKFWRRDTAVSTEKLAN
VSKHSANATNEAQKAEIQASKAAEAAKRAAESKKKAAAALDTVKEVVAMAEMLKKKFFEN
ERLQKEKHKAQLEAERRFIQEKLEKKEAEVKKALNRAAAADKRVAELERARQKQSKEQGN
EGSGHRRVRRSGSDSSSHYAPAYEPRLLLLPLLSFTLFCFVAWC*
>TCRU_subunit mitochondrial RNA binding complex.1
MPYLFPRLAGDWTCACGFSNFASRAVCFQCHRSKLVLPRDVNEPRAAMEAQQSSFRRGDW
MCACGAHNFAWRDRCLSCEAPRKASDKQRQGSGQRLLPGDWICEKCKTHNFRVRNECMQC
GWKPAVVNPAGTTSPRADSSAKQAPWTCLTCHTVNEKKTTSCEVCGSINGAVEAPSRPAA
VSARRDDWHCDQCGFLNFSSRARCKNCGTLSATASGATDPSLWICGCGYKNFRDRESCRD
CGALKSSQP*
>TCRU_9675 60S ribosomal protein L44
MVNYPKKKTMYCPDARCKAHKSFKVVQYKAGKARLYARGKRRYDRKQSGYGGQTKPIFHK
KAKTTKKIVLKLQCSNCKSIIQNVLKRTKHFELNDKKKTGNKDPTW*
>TCRU_9676 hypothetical protein, conserved
MDGVRAVVDGRSRWRRQHSAVVAAVDSDDKIGEGSDGTLKGLSSSDQMPQAGEGGEEGQE
HTGSLEVTNKLAGNEDSQITGEQNVSSDADLPKQTGSQVPAGGQPEDEEGTKSPQPPPPP
PPAESLPQLPRQPPPGTNTLQSEETHPAITAEKHSKPQDGGHSHETKMPQTKGSTKHEEG
ASSLQSPESVSHLSRESTTPLSTSTDSSGVAASTVENSGANNPTPPAASVTRHDSEGDTG
PAALPASNSELQSEEIPNAGIIATTHDDANDSSPAAPTAERTTAGTRSTQTSGDAGDLER
ANNDDVNDDVAHNGRTAEFEAASGDRNTEADNDERYTTVPETATNNTINTEIPADSAGIT
AAFHTTSPLLLLLVACAAAAAAVAA*
>TCRU_9677 BNR repeat-like domain containing protein, putative
MSRHVFYSAVLLLVVMVCCGSGEAAGVAGQPSVSTFKWRGINESETVESLGAPSLLKVGN
DVFAVAEAQCKKKAGDVSFTGVASQPLKTKTAETPVELFSDALKKTQVLEEGLLPKTKRR
NWM*
>TCRU_9678 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MWPVNIPDDKVRHVFLSHNFTLVASVTIEETPSNNTPLLGATLGDTNSPLTMGILYTADK
TWVTMFNDKTTESGRWEPKKEYQVALMLQGKKASVYIDGKLLGEEVTLLTGETPLELAGF
CFGACEMHNSPMTVKNVFLYNRPLGVDELRMIKKSDGSMHGGVSRALLLLMLLGMWGIAA
LY*
>TCRU_9679 TFIIF-stimulated CTD phosphatase, putative
MMSGTPVTFTPTPPLVPPPPKGCVLLRENVYEAGRSHDVDEVRVRRKPTMSRQKNQLVDP
PAGASKKYTLVLDLDETVVYARNGPLYARAYLRDLLRSIKDEFEVIVWTAGEREYAKNIL
EEINQDHIIQHLIYRHKTWFSSEDYTKDLKKLGRNIDYVIIVENTPDCVRANPQNGIIVE
DFEVPSTPPITSQEKEATTQAVEEIPPASPSTSTPPPSPLLTPTPSISPTKPKRQFTDRT
LLLLQEVLLALAESGETVPGFLAKCPLLTQHEVLGSNGQSIPTYYLGKRRKRGAPPTLPP
QKRVVRDNLFLDGDAEMEGTRNRRIRL*
>TCRU_9680 DHHC palmitoyltransferase, putative
MTRDGGIPTTPGAYFQEPAVQENSPRKASGEGFFSPMTGGPQNFPEQQRRNFYSLRPAGT
KRVLGRSHLLSCCVLTRDGANSICIVVILLLVVLVFMLGVLPRGEIYSYVVVSLLATAAL
ICLVMSVTVDPGILLPLPPDPTRQPETVLVNGKEVLRKVCPSCHIVRPPRSSHCRFCDYC
VEEFDHHCGVLGSCVAKRTFRFFGGFFVFTALLILFIGIRSLVTLAKPDPHLNTGQGRWE
MAAAIISLVASGLAGCIVLPLAFYYVYLACMNYTQKESAQLSPGFCEPNHDYHRGYWRNF
FSRYFGPLGTSRITAENADFYV*
>TCRU_9681 hypothetical protein, conserved
MTDCNDKEPPPPLDERTLQNMRIAKKIGAETFEENTAILRRMAWRGARAFIVCGVGMAAF
GYAMRRRRQQQLQQEGLRERERLEDDPTARYLEEMRGLGFDVDTLEEELEAERRTVKAR*
>TCRU_9682 hypothetical protein, conserved
MSLDDIDAFRAELLRQKIIFEAELRRQRETFEERLSRLSQELADREADCRNLQAVVTILG
KKVENLMDRHMATPHRRSSPARPASSSAVSGQQGLPTRISSSSTRQSSPFRRNNNFSAPA
SGAPVSTFHAPSLSSLGSCQNSPARISNGRRPKLGNEGAPDHHLRRVGGTRL*
>TCRU_9683 retrotransposon hot spot protein, RHS3, putative
MEYGVLYIPKVENFPLVDGFFFLNSPRNTLVWLRMTTAGAHHTITSTVKQFTECLAAYFE

GWDELSRDMSWETIYVQHAASKMITKWQRYDVVNTDIVSEKEKEIAWFWKEKVRQYQVSI
LSRDF*
>TCRU_9684 hypothetical protein
MPTGTLTESWLHKNKLPSVKHARDPAATAKATETTAGIAGAAAGQLGVLPPPPGTEEHAK
KRSRGQESGYNKNVNRNKGGWNGNGRYKRARRGGVY*
>TCRU_9685 spliceosome-associated protein, putative
MALAKKKKLAIRQRREQLKERERLVQKSLRSAAAAEAAGDLVEYILPEEDYAMGTAPPSS
TTGTPHDAAATSNPNGGSGNGNFDVEDKDRVHLPSVTVNEPTKTVARGSRRRQKIPWESL
RLFIAERHGPEVSALVTEHDGNAEDPYFTVFLKSVRRTVPVPRHWNQLRAFLVNQADRER
ATDLVPPEIAALGVERIRATRDKKANPDQVAFVTCFISGTPLRRKQFYVNLSRFGDIYYE
GKWIPKNHHEPGHLSQRLRTALGMGPHSPPPWLYGMQAMRRLPPAYPTIKVPGLNAPIPP
GAQWGNGEGQWGQPPRNEKNTFLFPGVMEEVAAEETPPVYWGTVPPLLTSETNLQQGIVA
SPPPTTPTTATAAKKPAATTKLTITPVPFHPQAYTPVTAARYVASAPQEYVRVQDNTAGA
TVALGSILVPKTAALSSSVPPAATSKEPPEKRTMLTRPPTKF*
>TCRU_9686 hypothetical protein
MDNAQFLPSHLNALLSTPRLPTGLQAPEVRDKLLSKVLAFCLLERPRDVDGSIRDAENLL
RKYEGMEGELISILHEKYGQPSEELVEKAKKLSNKYRNTLLGETHEVRSPSTEVANMGLH
ALANAGHSILARMQRERELEDVTWRRVHAAAKGMLVSLEEVQRRVAMQEVEVARLTSEHS
RRLRELEEEDRNQEELKTRLASTVTQLQLTLMRLRGGRHGGDGTVEAIRDIEYKRHILNT
QRREEEDLIQLYRRVLRQHLTSYPLSSLREEIGRVDAELRKFMQESPL*
>TCRU_9687 AMP-binding enzyme, putative
MLRRFTRNICRCSAAPACFNTTASAAAAAAAAGTAKTGAGSRTEYSEAKGPVEVPVLDQL
VGYYVNIQSRKMYYKDFLRIEHQAVRWAFADIRKNSEALAHGLLQTGLRPGQRVLAIQPS
NCETFVLQLACAKVGALLAVVPHQNISADKLRFYLNEFQPNHFVAREWIVVPEVKQGVLV
ERNMHFWDMIYNVIPELGLSYPGQKFQWVHSQEFFFLKKVVITDHNMNLLGVTPMRKMLV
WGPFSYYEQRLRRLSALLHPDDPILALEDFNPAVEDKLHITFSHRNCINAGFLFAQLMQL
KAETRFGVMPNHHTNPVGSIIAPYAALTSGAVLVHIHSDMFTDDHAINGIEKLCVEEVQG
ILGKKADFDLLLCHTGNFDADQYEHLKWVALFEDASDPFVSDEYLQKLAKELSLEDVFVF
RGPLESAYMLTWRSLKRGQRGMVPHAEAKVVGDRGTADATILSANTRGNLKLKGPHISPG
YYNNAGLLTELVDERGFCNTSREAIMDEKGNLTLQRTQIY*
>TCRU_9688 intergrin alpha chain protein, putative
MSAQTNYYAMRPAFELRLNTPLLEGLATIGRFDGRTPSLVCATTTQQLVIHTSKSHETVA
QKGGSAALNSASSLRTLSFGKTPTALTVGRVQDAGNRKGVDALYFGSATSLLAYDVERNS
EYFYKNMEDGVHAMTWGVVNTVKESTGNGNPIPLVIVGGICTINGFDESGTEMLWTVTGD
QVSALALMPWGASDNRGESSIISPAINPSDAPLSLVAASEDFELRVFDGEETIASIVEVE
KVNQLVYSGIPGRFAYLSANGTVGVYDRTERVWRAKGKHRPVSAAFCDVDFDGVPELIVG
WSNGRLEVRGDDAEKRGVLFKDTYAAPVSAVLAYDYRQNGQPLPVICTVDGTVRGLQLAN
VKEGEERQAVMRSQGAFRLDTLLREKQALAAELAILEEQLARQCSGDTDVTLPQLGTVVR
HNLLPNPKTGQLDIVFVVQNGYSDTIIQGCILHSETLFPGKEYAFFTVADPSTTLVCPVN
IERCVEARVTASVMVGATNAENYQLYELSLDIPKFVMYQHWERDQAVPFKEPAGYVTLYL
PKEFYFPHLGAWLEETFSFSSTPAMSGDFRLAFLDMRNGHRLVIQGKAELRELQIYGETM
EICGDVVESLGAAAVDEATAVCHFPAEFQELQAAIHSVEAFNAVRLKLTSSMADAAAGVK
PLLTRAEDSRLMSDITNMRRLYAQLYDLNKELIAENMKRCNNYGELKAALKQLNAYIMKA
GRLRIGQAKTRLISDCRDAVKFGDTRSLFSLIRTGQK*
>TCRU_9689 retrotransposon hot spot protein, RHS3, putative
MITHKTSDFLKKFLTSLRTKRWRPLLGLFKKMCSLSGNVGTMKEKDTITPLARGKPNRVL
TQVLTEARREAAERLRRTQEMKFIISTNIEEVLFKGRVRVNEMKLNDFLTRELGGSGVVD
SNRDVLLEEFFKDPTKYIRDKGALNEIQASGHYLGMKRAVKGEVIFDEDIRKLCDKGVDN
LPGWSIAAAEVKATVHNSTKHFLDAAAEEARYPTTTSAPEKLEGCYESVHNARWSHAVEL
PDGVERMKTGTGMGVHEGKPEQSWSYKKADDTIEENDAVQQFGAAPPVLMVLASEKGWPY
SWNTIQDLSKDVFVICEVERVWQIVKGDLTAWFSPHGGNDCKPERRVLIGTPGIGNSVAA
GSYLLYQLLHCDAKKNQVAVHCFGGGDAYVSDKTTRAVTRYGDEDMCILELRSLRGHGRN
VYIIYDVAKEGTPPPGHFAPTSGWGMIAVSFPKVTNYDEWAKQLQAARIIVNCPDEMDVK
AMCAWMTRDETKEKQAECWKEVKNTCIFWDRFHVTSLMRRRLRTLWSGGVCIAIDQRGNC

ERALFTGR*
>TCRU_9690 hypothetical protein, conserved
MWRCCGRLHVASLRGRWALTVSPTGVAVRLHGAPTVPPCECHAQRHWDCGRKQLRVSFGA
SGTCWPQLGGASGMLHRTGVVMAPRRGSCDGSDAAARHVVGSKVWPRWTMSSTNVRLSDF
LWNYVGGRAAVDEDYNVTMEMFVQEPDDYVQDQRLLEEILNLTAYQALEAITRPLHEGVL
SLGQRRDYERKGYNHSSCKGKTKRSTHAGTGGSEAGGRGKAKTNARNEVYHFH*
>TCRU_9691 hypothetical protein, conserved
MNAKFPEQVRLLAEERKKEREQATAKEDVAERALAADIEMIEEYLPKLISLEDIPVNPEE
TDIIRRQFDEVFTQEEQTYLASAEEEQARKEKLGRGLEVYRQRMLDDYVGKENGKLHDAE
TTERHLSSVVDQALN*
>TCRU_9692 retrotransposon hot spot protein, RHS3, putative
MNCPDEMDVKAMCAWMERGLEPNEQAECWKKVKERMDKVGLIPRHIFDEESYIDRLGAVD
DALLAMKPTDVEEYFTLRGGKLWYSEDSCHKLVNIVREIADEGVEVFLNAPICADIGF*
>TCRU_9693 hypothetical protein, conserved
MRWLPAQLRGCGTGRRDHIAAVVARTFFLQRCHASSTASTFGARDGEGLNNRDTGKPRRS
SRGGTSSHRPKFARRGGGEGQQLGESKKEEEGASATTIQGGNNSSGGFSLGNGMEVQQPA
LSPFVEEDKIGVNDVFCGRNEARAFNEDALVSAIEGMHQTLASTSPPFFRGAPVVGASSC
GMTSNAKLAKALQRWPEVLHRLRAIALPLLLKASDTTPPSVSSVAEACQALTEALIVVDD
VSRTTGMRAERMFPATLVLALWSCLPRFYLQAQHFSRAPHAHGSLAPALAEGLPSFWWEF
KNARRALALRTRELNDLLLPSDLVRVLVCMEQCGALSDDIIGPIGTQLLRRHKTSAAPLN
GPQHVATNHLLSAHFVASVVDKEESPFQGDTALAFARLLGRAYIVNHFQLHRLMHTILLP
QVVVALQASAPDEIILFELTRCYIRYAVSGSAVSQLTALWMPHLSCMTLDKCSELLGILG
NGGVGRVAVVAEEDYFPLVEAVLKRASLLFHHEHQSRSTGVPPAANLVPGALADVSTVVS
ADSVVRFICALVTVNSVHWGEMYVLAATALERSLDGLFVSDVVRVTRALLRRNSHIPYHS
LHSRLANRLLIDEAALTDVKIGGLSLLAAALMSSPSSTPPATSVSSNKQLPCDMQTAVLK
SPGGADLIGLDGARALAVFRRHGKRLGLRSFAAAMCVAPLAQLPRRSQESVIMHFTSISS
ALEVPWLLRGMMSLTSQIPEAVDPVSVQRWFSRFTAVDVARQLDMEHAAMLLRILSDDEY
SRDCALAKEKIVKHTSTLLLQEIVSLDALIPLVVALQRANVFFPHLYSRICRILLANVRQ
TPWRLLLPVFHVVADEFTRRPHGNGSVFRDVWEQLRTRLMEEAASSLEAEDVVLALNGLA
ALDVSDRRVFSVLLHRLWTIYLSVCAPTGAEYGSATAETSPKPVVWVDGLLSGCTPSALA
VLITTLIYTGRGKVIDAFMPWLLLRTRPVVKDLYPIDLLHLMPALLYCFIAASTMDGDAS
CDRTAWLCSPVNHTILHTTYDQCRELFLHMYEDEATAKDPTAIRTQRAEWTPKVRVSVSR
VPRYLFAELLVALCQCGLRDKAVATASASRVTRRLCMQLPVAELVDLTMALCFHFPPPPT
RLEEVTVNDEGGVTRDEKGERYEKKREGTNCISSCKGTEGNDVAAATSSAPAPHQRFLLP
VLTALWDRAEELQSSHVDALLRCLRHYYGEKVDADFLDRLLKHKEATLAGVHASHRRPQD
TAAAEQGPANLDEPTAEDLFVS*
>TCRU_9694 ubiquitin-activating enzyme E1, putative
MSDVVLRTPFTIRERGWQCLVRRSPPPIFAVAGYSPENTTWDEVRLLVVGAGGIGCEVLH
TLALSGFTDITVVDMDTIELSNLNRQFFFSEADIGRSKAEVAAAFVERRCPGVKVHVVFG
RIEDQTDDFYRQFHAVILAVDSVAARRWINQKIAEIALWEIVDVAKEGHEGRKEKRITSS
IPFIDTGTEGYEASCRVILLETGNTPCIECVLDLYPPRKTVPFCTLENVPRSPEHCVLYV
QFRLWKERRPGETLDSDDREHMEWICNEAQRRKEAFGITGPDIDFSFALGVVKNIVPAVG
FTNALVAGQATLELMKLLTGVAPSMQSFSYFNGAAECGGLTSYVTPLSPNPLCPVCAPRP
VLLLTSQMTPRRVLAAVKEQIRLPTAVHGKCELQESSWSDGTLRVRFEGDAEVCLLYKKT
NPLRTRIVGSTIEEIFAASGHADAFSRWCSGSGVTFNVEYSSTDVYFSAEALMSGDARA*
>TCRU_9695 RBP32
MSQTNTHACQLNPHARVWTPKTHDALAAFSNEDAAALPSAPEAMCHLGRIGAANEGRPMA
DDPLFAAAAALGDFSHFCMQYSLMMARQSYRNFCCHWQMQNYGQCVADYEDDGDYMSPPT
VAAFCDAPLSRGLPTDTHTNSEVAIDNLQSNPCNEAALVQKTKNHHFSFSPFLPFSHPPH
FFDSFLAPNMGEIDTMNSWQRGTSPSCYSSCLLCGKDDHYYSACQLFDGKTVCFIDNSDF
AVYAMRHDHWIESATISDVYLFVRLAVGIFPHHALLHVGSKEIILEDYPLETLCCDLRIF
PGVVVSVSVRQPPFETNVAPLRFHNTRIAAKRERGQPENTCDVEETMGDAALDASTIART
SELSVSLPLFEPQADVGDHAVAESITGTSTDFIEGENTSLSKGGDTAVSFPKEPRHDGND
LGNPRTPMAKQEGSTVVSTVSVTSVAKSSSCCFWTSDASETSGNHLNCVDIVRKDNRCNE

QPLAATSAEVTRMKQSSDATATHATIPTSPGKLAPMDEVLDDEELRLRRTVHVRFIPVQM
PFAEIRMLLWSCGEVHKVRLVKPSETTSPRRMFYVCFVEYATDEGAERMKKLQGHRLGEF
FRLAVEGSRHTIHGGYFTDFEAHTGRPCTFGLREAERRAVERRYFGVCDGGSDAACKGGG
GPKSGAPKSTCWRRGKERSAKACLDAPVAPATMNTAETQETGSDKGEGKAKREKCVGETG
PYSLRIVSACELVGRLRRGGRRRRDAVAGVGGGAAAVPAALSDVLGRGVDMSDEKFLQDC
LHDFASRYLQQLTPRSVFEFLVLLEGCKYCSATPTFFLLLARYEVALLLHYAPFRTLEGV
AVTAARAIHWGNDFTQVLKDGTKNGARIAPIWHSLFTSIPPARQPFRVPRYDDQKGNELP
GSRGELRLYPCCGKVLRFVELLLHISLLLDDFQSNTPQRNGGVETDPAVLLAAPSAKWND
VTHVAQKMLSCARCLLTQLLAEIVSEGDDLSSELPVWRSKVSQILKLLPPESGLSTGSLV
SAFLPGRKQIAVAVLASEKELFNF*
>TCRU_9696 hypothetical protein
MRFIFEGPLTRLLSIAFLLLLHIFLYAVDVADRGPGAQYRDARWDFWFTAFNNIASCWNG
SAFFMGMTHAGCVFGCALLGACVYLLVFHVLFGRIIMRLPICGAQSPAEWRLIIKSFGDY
YFSSDVGRQRGFCFAMAIGGVLGIYGGAKLYNALLYRFWPGQVSWALIRPIISGVDTVTA
LRCFWVTSLFIDWYIFMFVFDIMYQQGSLNIYLPHHTFGGFAASINGTCFWKRKKQLGEN
SILALRMGIYWTLLIFGWTVIAAVFLTLEFLCGPAKVLFANPLIPVTSLEIPVGVGCLCI
LLEFIIVAQEWTWPTFQGHPHLFFPGMVVATHHVFFLFLVLIFQCSLDIRIVLAHILLLK
DREGGLSPKGAVRLCIALIPAMLGVILLLLVIVRSSLWWEMCGAVGDAIGLYSEHMYLRP
CPPPSEEVRRLAERENEKFVRLHSRSLYCKAEQENMKEKLRVRKAIKRVGRQIHAGAKER
DGLLRREKRHGDRNTTAAAAWNNPSSDDCFISLS*
>TCRU_9697 hypothetical protein
MEPRAEEKEECSPVLHEKERGVGQSGRIGEVGREEAGSAAVVDSPRQGMSSRELGCSLPA
AHGASRRSSRGMFEQVKTVRQELQEKVSRLLGRNGTVVRESQHSPGMYTVRQFQNNLAWA
IVSKDTVRFDELLNKYLDCCNEGKIVGIAGRTSPREKHENTAADAAISVSVGNERSLVDR
VFHHETGYTMTHLAVVSGIESLLRSCLAFGSAVHRYEDLNGDTALTLALWLQPEMAFAML
DLGKDVDITRIGARGRNLLHSAVTLRQETPPWESRLEFIQRIVEQDNSLASQKDFFGFTP
AEWALENAAYFSSKKECMQIVEFLRGVDAAYREWMQRIGSR*
>TCRU_9698 hypothetical protein, conserved
MFAVNLLDALAEAAVLLMFDLAPTSTCGDEDSDGDFGRARFTGVNSWSSLDSCIPRSHMN
AVTSVNNSTLTPPQSPSIASGSFVQLTTEELQTSLLESPIGGLDHHCRSTEHERGSSLAS
TISGWTVPVRSLRPN*
>TCRU_9699 hypothetical protein, conserved
MKRDEWFAALQKLPLVPCGESTGLPRYRAVEAYHCTFCAYTVCARCYNAVPTMLLFPSRD
ASAAAGRGFLGPRRGDGEVEDTFSMNDGLPRPNTADDVNFSRPRCFLCRKGLLVHENVPV
HEWTCEGPRPARRLQRGAGASYDMDVVQRYYTMKEQREKRALSQAPLIAHFHAAEGPPTH
VAFSSVVGEEKDDVIGNGPLNRRPFCVEGGSFVFSVQNPRMEVSCVWCGVDRRLSEAHPS
FVGDETITPLQKFHCPPSLPGLPPRRFRVRVPYGVYGLHNVHALALYLTNDIFRKATTKL
QLTTADALTVEENEEPPPWRRGQLRTGKVLPRHAVHPLLVVDVLHRIATSDPEWDLLSVE
ACATCVLNAAVGPLKCQKGCQGVTEEKATVEAHAVEETTSNNNNNKNDDKNRGDHDALRK
DGDHNDEPRDGSMNEAAMLNDRRGVGPPLTWPSGLRCDELLLTLDHLLQGRSVAVYGIAS
KYFFLQHVSQCAELLHYGVAVADGYRTSASCLITQFREIRKYLRQLQQGSEQAMLRSFVS
HDTNCESLELEMRSKAPERDHQQVEGQDEEREYYLIDVPTTEESPRSQSYRAPLRSRVGG
EGVSQSRQCCRELSEDKNLLLPKERELGETPLVCQGAECMTPYSPAPCAKPRERSILLVR
GEEAEDEEARTPLAAKPSRSYQPQQQLQQEEKERKVRAQPFSQHDTGLDGKASAWSRRHW
LREHSDWNYDVPLHVAYGMKRPREDGGKEKVMEDEVSLVQPIQGRRSRPPRITVSSPEVM
GSLRLACRAPLRKCIAWTCLPSITAHRLVSATEPTMTLALKGSAPVGIIILHGVDQLDTP
ALLELQAIAREHPYRVVLLCSFDDPNWLLSSAAGLLDSFRLNFIHLRSLLLPRVREMLAI
NSLSLLTELEAPATEAGRFSRYANRKGTFSSGVSLPLHDTIRRILFSLPSSFSELLRCMI
KRQEASGENVFIPMSLHQENFDECGMMISMARLKAIERELTSNRLAVFNSAENKLMIPQH
RKLLKVLEEVLEQRNAVGCASNGAAPVET*
>TCRU_9700 metallo-peptidase, Clan ME, Family M16
MLRNSIRRWIPVINRTARDSLCAATIDHCTPVVYSSLPNGCRVATEYFPSCQFATVGVWI
DAGSRFEDLRNNGVAHFLEHMNFKGTEKYSKRAVEDLFEQSGAHFNAYTSRDRTAYYVKA
FNEDVEHMIDVVSDLLKNGRYDPRDLELERPTILAEMREVEELVDEVLMDNLHQAAYDPI

SSGLPLTILGPVENISKHIDREMIMEFVRVHYTGPRMCFVSSGGIHPDEAHRLAERFFGD
LPAKNNRPPLQALYRGGHTVMWNEQMATANTAVAYPICGASHPDSYALQLVHNVIGQFRE
GQHDQFAYQHLNPKLPWERLPNMVQMRPFYTPYEETSLLGYQLITTPMLPTDSAVSHRDE
SQDKLLDYLLQTINVLAATAVDEAILEGAKSEFKASVMMMRDSTTNSAEDLGRQMIHFGR
RVPIREVFERVDAVTPAIFRDTLAKYTSSTVPTVSYIGSASAAPRFDAVTQMKQRTGNAL
*
>TCRU_9701 hypothetical protein, conserved
MVRRIPRGSIASAGSCGRESREQQSNSTSPNNTIIEISIMPELNLDETLRVRDVFSEFVN
DEYITTMFTLRVVLSQLGMYPSDEELSFLLGVFENKISVNNLCHYLRFYKRKFQIFAQQR
RVENPEGNAQDESEDTLRAFVSLGGAEDGTGSVQLEDLRKVCRDFGLTIDIDAMLVDVVD
IEYQKTLNYAEFCDMWQSRRRRRDQGSVASVQDSQIDILSALRALGMDCSSALLLSNKSP
ECSATVAKDEMGVEGYKFPLNADPGSSFQQQQSNNITVLRSEAQNLQALKRFLLPEVAGG
SMAQDTTALVKRKAVRHHSTLPALHVAALAENDRKRGYYPPREEGTNAATGGGGGKDDGG
LPTLTGGTGGGYRAPSPMILSLRNSAAYKKRLQAFVQRSKMRSRGRVSSVQTRLTSIPPE
DDGRS*
>TCRU_9702 DNA-damage inducible protein DDI1-like protein
MIKVFCTNENGESCTIAIDPQSSVEDVAAIIEVELGVPMLEQVLVTADGTTLQSDKTLES
QGIRDDTSIVVIHTAKDYRAAQTQKEGAEEKGLSVEARPPPDRETHVSRRQGVGEEHNVQ
HRDPFLRQERPRQQQAGIEAARAYMSEGTQRGHVGTSRPRHGVPQSTDHARARIEQLFNQ
GAERFSGQTSLQESDPEVQRRIYESIYWENVNENLESAYEFMPELFVRVPMLFVNCEVNK
VMVKAFIDSGAQRSIMNLRTAEKCGLMRLLDTRAKGIMRGVGVRRTLGVVHMAMVNLGGL
HIPLSLSIIDDDKMEFIIGLDQMKLHRMIIDLRENCLRIADTRIPFLPDSEVPELATGDE
VVDEEFEAKEDAKGQQRGSARPPEASSNTAEEDERGGQWGRQAKKEREARNSVASTTNVS
GAVSAPAQDFGTNRGNANVNKERSIAEVMAYTRMDREGAVALLEAADWNADLAVSIFLGE
*
>TCRU_9703 hypothetical protein, conserved
MSGLPVNGASSGGSSRGETTHFRVKLGNIPNPASSTTLDRASKTEKVHSFPSSSSLNSSE
TTLTAVDFCTWASMANAMSCAYTSSGYPTFLTTNSVRSDIYGAFVELRIPSLHSMTLPPE
ETLVVVPPTPQSCNDRMNASCASASTLPCRVTGTGGPSRPLVLVVWKRGSHLFSTHPATV
AALSPSTKSLSVNSPKTPSYLVRLRSNSSSFSKNTRSSPSAIDNVQTSSRLNELFFGLPP
TVPTKSSSVQKNGVADGFAPNINDVTPPRNEDDEAETQAGKSVKRPPPSSPPPEEPPIEG
VPVQLTLVTAGSFNHLTTYAVRHQEGKVLAAVPVQTIVASSSMRRITAHCPFLLGMDVSE
NYVAPALLTEGERNVLHKEELKQPKKQFMSFKSTKSSERAKAEGLELRFEEIQVEGVIND
GKNAVNVVSQCVAVEPFILIGNRNGDLLLFSIFEGKVLQRLNFSGAVKGGTSGDSTSAIC
NQLVSAPVSCITEVECGIEKRLALVVDCARLCRARGENGFTIPYVTTRGGPPSVFAVGFG
NGHVLIVCVTVEGAWISKHFSSFGHRLVQAISMRVPHFLTRLWPNDAEASFASHETRQRK
GFFPAMTVCVSAESLVVDGESSLAAVSCDGGTIRLVKASEMEVELCHVTALENHSVGDFL
AVQWVPSHADATLYPDLLVVTNEDDSITVCQVAYLSDGRKNGDCAVVRDQNTSLAEDSEL
LFSPPSVSYPAYPQAVREGFVRVTRRLFHRSWVGDLCALPIPSRGHLLVATSYDSRSSFW
PLFFSDASLSVDARNNPLETCSLESFLQECFSGCLIHDKNAASFASQWADNVIPVEPVFA
VALHADPTVRCAACGAGRSYFFVSLCLRGRVKFWEVRPVVD*
>TCRU_9704 hypothetical protein
MRRNAADQRAMRLEIDSRRISKITLSRSAASGARATSKKTAAVRCCGASRRMAALRRSNR
SRVELSGQLGLDGVSDACHELAGAAAQRDGSVGSRSDAVFFGLRKVMVTTTRRQSRRTAS
ARRRLFNSRKTARPAAWPRWRGSFPRIPSEPGAGPKSNSRRVRFGSAMVVGDGVPSIRRG
RWRKAVLWVPCRSRRPRLCLAGVPVCAGHGAVRFRGWRAGGEAHTQGTLLAGCCRPWPRV
WSGRAPSAFGCSAQCFPASETGWPAAPCRDRCVGGFPHS*
>TCRU_9705 UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase,
putative
MAKTKLPTLRQKLKRVTVLLILFIVATTVLTLRFDTAADDGAPEPNNLRHSRAPAADDAA
LAYIPRSVVDTWSRREYLVVLGIPSTDVEERRTRRNLQRTTCWRFPGVATRANDFTGAML
VLYVLARHPSHGYDYSAALLEEASQWHDVVALPMNEGRVATNKTVCGDGSWGDETEVGMS
RKVYMWFDLALRLFKTAMYIAKGDDDMFLRVPLFVAHLRLLPRQRIYMGYHVGVGSFGKR
GLPGSTFMVGWCYTLSRDVAEALVSYKPLRRLAYLPYSEERYDEFALLRFQHEDIMVGWV

LEKEVKYHPLVYVKVLPCHFHDARNETGHSQVVPTSICVHHVREDDYAALMARFGNDTSP
VARVERASDDTIYPLCD*
>TCRU_9706 hypothetical protein, conserved
MPASLSSGPRTHRACAGARVAQPERHLPRGRSLLVGALVIVEASKTKPESGFSFARRRAG
TAGRRLRPGPRGLWRKPDRCAVSRSSPRCGDEWRSQREEEAFPCGFFCVSVVGRPGRTDG
IRPERRVAVAIAVVRVCLKPRCGGGPMRPVPHERGRSPCAWAPVDC*
>TCRU_9707 cysteine peptidase, Clan CA, family C1, Cathepsin L-like
MSGWARALSLAAVLVVMACLVPAATASLHAEETLASQFAEFKQKHGRVYGSAAEEAFRLS
VFRANLFLARLHAAANPHATFGVTPFSDLTREGAQPPWSACRPSWASISGIPWNGRARGG
APRGGKPAPTTNGTDSARRVGN*
>TCRU_9708 leucine-rich repeat protein (LRRP), putative
MFASVGVSEEQVFGDLYLAWLKDTGEKNSNDSRKLFREVVERGFGERQIILRKERLGANV
AASLAALLHRSPLTRLDLHGNTLRDSGCEMVAHLIRDIPNLVYLDLGANDIGPLGIQTLS
YVVAAHKKLQTLILGSSIKDAYANRINAASATSLLEGCLRNRTLRHLDLSGSTIGIPDAI
LNIHGGTGAVEFNVAPPPRSPGSSIFPTARRSQQGQSSLGFGSGKGLAGSATGAAASGKG
VAETDGDIGGSFRRPIDVLSELISTSTTLTTLKLREVRLTTDAALRIIHAAMKSPSLSFV
DLSGNALTGAVGDAFGELVWNRAGALQTSGLHTILLSNNPLIQPKSGMPAPKLFSALSMD
RLVLRLHLDNCGVDDDAIEALCCALKRNGALQSLHLNQNAITSEGAVMLARALCVHIFLK
EVSLEGNKILDEGACAFAGMLETNRTLLSLNLAHTWMGERGLVALGVSLVENKTLLRLNI
AENHFTEDATEAFASLLESNHHLLRCRMQGNSIGHHTVLRIEKITSRNREAHRNMEKDEL
EENVIHLHYQMYKLDEARAELENLQRKKMELGRALETLEAQLKLDMAEAEKKDRDMKDAI
ENCITQEARCLEEKKRLDTELEEAKKQLEVDMETAKERLAAEVAVREKVEEEHRQLKLQL
EDMMNNGPQREAAKRQQLKELNEDCQRWSLQRKEYRNAIAEAQATVNQLQERDGAGTKSK
KGKKRAGKAK*
>TCRU_9709 hypothetical protein, conserved
MVWLVIRRSGFGTTYSRCSYLVMWGEYKQLLEPGTFPANDFLPPHLRLDRRSYLDLPDTE
IALPPIIDVSIAEREQVRNLEHALPSSQRSDFHMQFGPLRSQTIVMTGGANERYVRRRLG
ISPKDRERLESEKNKGEDG*
>TCRU_9710 Protein of unknown function (DUF1448), putative
MSSSNADLHATVTKRFTFWFDREFRYNLPDEGLVVQTARGEVLLSKLSPVEDTKGNNGEE
GVLYVTNLRCMWQSKANPHKNLSVGYYGIQGIEVREANSRLRGTTEVLYITSRFGSSRYE
FVFTQLMRTNCQLFIVPTVWRAYESSRAYRELRMRSSLVRDGDVILLPGEQLFTRLEGVT
NVSEDKGIIGVFFTTNVRIVWFAQHAPHINISVPILQLTALRMRPTKYGAAILLETSSYA
GSCLIGFRVDPLDRLRGLFRECVSLWKAWSARPVLGIAVTLEDAPPREEGDANMKHISDD
GGDGPFSLLSPQHRKLDGENVVTQVETDAFAAYYADVGQKGTDRRPEYDASIGLAVERLR
TGVTLRELWTVVT*
>TCRU_9711 protein kinase, putative
MSDVFYLNIPRGRVPRGASGAASAAPTVSLHDPLSRAVSPASSNARWGVVPMVVGVLSVG
CALSLAVRLWQYRQQCLSSIMSGGGRVLRGEGGKPQLRRRPRRCSSLLNNARRDDTPLSQ
KEPVRLTTDERIPSPTAHLPEANDGCCDDDNRRNGLEWHSLDHQGEAGDEDFDTRTSSLN
SPLVFVTTTGERYKRVSQLGRGGCGLVYKCFNLNTGQVVAVKEVRLEESTDGDRAEEMRS
EFELLSRVSHPNIIRVIGCHVGKKHARLFLEWAAGGSLCDVMKAIDRSFASGLHEDLVQS
YVRQILEALQCLHEHGIIHRDLKPQNLLIDHAGRLRVTDFGLSRLVAEGASAVETVVAGT
PRYLAPEAISAGRFSCGSDLWAVGATMSELFTGRPPWSHLGVQQLPSLLYHIANNPEDHP
VIPTHISKEAREFMAQCFRPEPGDRGTAAILLQHPFLTRERRE*
>TCRU_9712 BNR repeat-like domain containing protein, putative
MIVDCEDEQRVYDSRDMGTTWTKATGTLPGVWVNSQLGDYPDGGLHVDALITATIGKRKV
MLYTQRGNFSGETERTTALYVWVTDNNRSFSVGPVGMDNAVKGELAGALLYSDGKLHLLQ
RRVSAEGSAISLSRLTEELSTINSVLSTWAQLDAFFSKLSIPTAGLVAVLSDAASNDMWY
DEYLCLNATVTNATKVADGLKLTEPDSRVMWPVNIRESDVRHISLSQNFTLEGTSRGKRK
GPLRSTFG*
>TCRU_9713 SLACS retrotransposable element (part), putative
MQREYGTDHTGNGSERAAGTGIGFRATYQKRFEATTHVFNNGGGRHPMRIMRVGLPMEDA
YPSHSEARQEEPAVITLQPEKRAPIHLTQKLLMQQYLSTWILEEHVRTGEQRARHYPKWA

MTATKSHKYGDAVALDFGHWDKQAMGVEEVPFVILLPHHNGTVEYGLVGLVATNTPNHVV
AYIPSARRKDTEWVTIDGMVQKCSGSP*
>TCRU_9714 hypothetical protein, conserved
MHADDLTLVFLDAYILACGAAMQAAVSPVATWTAEHSLMINADRSGAALFCIASHRQSDK
DKADHRLGGGKPRVKPHPVRLLGNATDRLLIFGLHVTAAAEQTVPRCRQPRLDARAGASQ
YTMRSFPVGCVHSALHHGGKAIAPCPAPTHLHSLEVRHRDGCTPSLGPRASSKDTSVHLA
VNPVPLRRIVGFRAPTQHERPTLLWYVEEVRGAICSETMPSSILGKAATTIPLPGDAVLK
ELRSVFRHMGISRTTSAPLMLSSELLPGRCEPQRGGRLPATARQGRPGRCQTIGR*
>TCRU_9715 hypothetical protein, conserved
MVTTTASPLEKVPRSVGCGAARRFACSPTDLTAQSFHCGHSVGITRCGGVRRGRRPDVDG
VVVAWQLRTSGPSLFRIALLLDWRSNSPAWFFCRSAGTRVPQRQSSLAAVSSTRPAVGVP
VAWPSWCATLCRASACSSWHQLRGDHRPPRVPTGQPQHLRGGPLQPSPFRIAHAALFAST
IRRLGPAAVICDLNSRHEMWDGRSPSTTAGENLAVIPSNIDAELSDDPAQPTRISGRSVS
FSDVTVQHVLRVSHWTSTPLHGVGSPSAIPHCGDGGRHPATGRHAAATETCRRCSA*
>TCRU_9716 cytochrome oxidase subunit IX, putative
MFRSALVTTRRTYLNAFNAKAKARPNFGLRGVGFWTSEVYHKPGQNYWMALCVSGPFLII
GAIMYDGFWAKLDDIAGGGPSHLDYGWRKQDRKPWDFAFDIGEGYAAGPPTLRPAPGAVD
LGHH*
>TCRU_9717 eukaryotic translation initiation factor 3 subunit 8,
putative
MSNFFDVSDSDESLDEVIHHDEQVERKVAQIDPKWFEVTDDEDADERQVVLSRNEKSLNE
IQTTCDLFDFNVDHESWSEAEKAFIQLRQKASAHKEKFKVIPWPFLECLRNTPDLSEKMD
EKETFKRPEDFYSLKRLIKALQELTEIHKNDIERLHDEESEEDGGDEGQGEEEKELTEED
ITQKLKQSVIQKGKRAARCQKLAQESKKRGLTALRITALGILAEALLEEDTRLPYVATAT
WTKSFDAVSRIYSLITENPAIAVKEVFSGDLTSKRAVIMDGLCGLLQRLHVHLQRIAQFK
TGATDEYFEIIQLENQLVDLADSVLGYYQQRKRGKAICCQILIDILGSRRQQAHDILYHK
MTRLTRNIVTTSVIETVRELYQEILVIGNEEAKCSALLYLAYQMGLEGKYRDGRDLVLRS
GVEETVEKSVHLAILYNRVIAQLGLASFAAGDVIQAYNLLSSLWSNRNHDVLISQRMPDY
VKENDEEELKFRDLLVPPHAYIQHAQLELATMLSTLVVDTPKEAKKPYEGSRHQSYFFRI
INQMAYQPLLGDPVEFREQLTAAYINLKLGDYAKASEVIKSMGAWSMMPNGDEALKTFLQ
HLKEAAFRIFCYNNRCNFATISVDLMMKKYGLDENEVKCIINDIISESNSSLIAFWDRED
KYLHVDRSNTSRLQYLVEGIAESVVEVAQYSERRVRDSDFRGRGRGRGRGRGRGGF*
>TCRU_9718 hypothetical protein, conserved
MDDTQEEAVRELKKHLQELEDTLSAQEKILRNRSQKMTSILVSVVNTERALDENADELRE
TQLQLENVVADNRIAHTERERIQTASDGCLPRDEYVRELSEADAGLKEKQGQVQDLVAQV
ESLNESAESAEARRRLTLVSLITILDDLHTSLTRSIQRVPHEEDARARGVLRAIRELSRE
RERAIGYCVRKKREVTDVIELKKQRVNELALDLQKNLSVIVEDQEKSALSVVEKIQEERN
ALREEVESIKTANQRLWDVLRDTKYSSDSVQGGDSKREVAISVNDALRITAGVEEEKEQL
REQLKLFEAKRTKLQRLIEELRASINTDMEKHALKLRDLKREIQVQQYESHKLEGENRKL
KSLCDSLAVTLEA*
>TCRU_9719 BNR repeat-like domain containing protein, putative
MQDAKKKTQFLEKEGSEEKKVDVSRPTTVVKENDIYMIAGTYSSNPADGCQDGADVATLK
LLLVKGQFSDKEKKIDWNDADGIPCTFLNQEHKSWTRLNGGGGSGVLTDDGTLVFPVEGT
KKEGEAQKDVKTVSLIIHNSKDAASWKLSKGISDGGCSERGYFETSAGKGAIQ*
>TCRU_9720 hypothetical protein, conserved
MPIVSYLWTRRIHVQRTQHGQKELLAAQTAFKNGRGAARRLWERKTAAPFIPPPPTNSHR
RRTAPPMSRPMFRIARRNRRKGQWSLSANDARLWYDESPTSSLWAGCVRRANEVAREMWT
PSTWEQRMSLAGQITTFLSHARTADQRGEPCGLFDGTVRRGAIDLTAARQEAAVHVANEW
NPAGHGGFEV*
>TCRU_9721 hypothetical protein, conserved
MNQVIRSRTDWRERVVFRLAWITASRWFEIAVFTPNNFKLEPDGTLVFGLGRGAETARAD
PHCFLRFVRARGQDALDTITLCGTLRRNEELTNLTNAHVERALALWGATAHSIKRGALRH
AAPIMETYNLDPHVVSQLTKHFDSFYLSKNTVRYSGK*
>TCRU_9722 hypothetical protein, conserved

MRLPASRAFTSPRVARHRGAVFGHADRALPPYSALALGMDVVASEPLASSMQFLQQERLP
PFLALTLLTRCWTKWTVTSAVTRAPCGHGSDDGGAAALAILLAASEDTLRSYDKTEAGGD
RNRCEHISRRRLREKERLSKGSMTVAKAKDRSGYHHIVEIMLRCCGNHLTEKTLLSLMQY
AVQVEESEGAVLTELMGFLASITNSDQRRYEGCLRAVLAASLPIHIAPIVLSILRRKEIN
VDVVKLCLHHLAIVVRGRHTGALSVESAMGGFHECAVTALRWLLGEAIEGYGELYIQVMS
CLKHAPVFLLCEVYNTMEEHKLVTPSVQCKFLANCGITVAVSNTVPCECIEVIIRAFRAL
VRSDRETRHIEEGLVHGSAVLVSIHREELVREAYAARPTLRETPHSVLAHVRNGDVSQSH
QALLRLAQSREEGWINIPSPAMLAIHAVCSLVGRLGDPADMNPLYRALVSFRNPGMIISQ
CIEYVLAGICDRVARIDKEVPKDAAPRSVLNLVLPILRTVALYFGDEINTDMILELLETA
VSLRHFAVPLTSSILWNLQRSSSLALKELFSRVDPSTNGIPFLNYYTLCFARDQGKRETV
EHLSTVWRCDADPILKRHALLAPPYKLWKCSSCGRLNSDRFNYCLCSALRNSFLVCSRCG
HAQDERWKCCQSCGERMCEDFIAAAVVRRSWTCDGCGANNPARQTFFCFRCKAPNGPVAK
LLQSLERIEKKHCFCPGNNALDAKKSLGELMQYCRKCGWLRESWAAANSIVWCCEGCGEL
RSSLDRACPDCPQVECLPFAVVRNIRDSPLCSDCRLPSVNPFASQCLRCDGSLQRNASSE
EMVARKATKGDGQLAFRCSNCDVMAVGDAAHVCQECGEDMRESDFIHVAPRHCEGCGKDV
EPLHIEAMCMHCTTFLPPVEREGWSVPVVCETLKGLVQLSERDGINERLVTLLQELMCSF
KTHVELRVMEETHVFVAVELGRLQTRLFKFIAYDAMARRAIALAKQLLEHIDTKCGFLGT
KHFLNGQCLYCLGTHPKELCVHNKEPWICEECGAENKNADVCSYVCQNCLSLRPCVQEKC
PTDAWECLQCQRVNVEFEAYCIFCGVQRAAVESAVEEAAEVCPFVPAKCATCALVHLEAR
CPLCHNDVPESMKNAEGVVCMVTNRYAFIQPSGTEHPNQRVYVGEPWLRKHQWAKGEKVI
FTARVNERGGFRVTSIRF*
>TCRU_9723 NADH-ubiquinone oxidoreductase B18 subunit (NDUFB7), putative
MTEYLKDLERTEPGDPMPPINLGPYDNPLLWNMLDPFGADRGHQRRPMSVSRNFMELHNV
PIMFRDQCVHRWVPLHRCIKNLKPVTWGTANCHEFEEAWVVCRAYETYRSQLLKSKFMEL
TKDYTAEDKKFFPSLLYLGFPTYMNSFYWTMAASQRLSGWDERDPANPMMWREPNRALMR
SEFSPTIWEKGTMTNAIGHKLIPDEIVYDMVPGFPLPEDKRPETIV*
>TCRU_9724 galactokinase-like protein, putative
MPSYSDKRIHATVSELKLKFLRTFNVVAEDDVEWLLFTFAPGRVNFFGEHVDYMGGYVCP
AALKEGCHILVGRVRHLCDGKLRFATEDDECFVLDRLGQAKHDKNWRTFVRGAATLALND
LGMPIDAPELQGFCAISKGTLPMGSGMSASASFDVALLNAITTVATRRYRGKCYVPGTRF
PILPPCSREERIKLTKQAHRIETEFCGVNVGIMDQFSAIHATEGSFMALDCDSLTFESHP
LSYLLGDSACFLLINSMIRHELTGSTAGGYNTLRSDAEGAQAVVKKHKMNNAAFTFRDLA
RNPKNFTKEDPVAFVESCRPHFTPGQYDRGIFNIAEQIRTLQFIELCRPECPLSQEERFR
KAGELLNATHQGQRDLLKISTEELNFIHRAINLEEGVSGGRLMGGGFGGCILLLLKKNAV
ESVVKNVQEKFKSRFGLVCDVYPVVLGDGAFVASLWQGVKGKL*
>TCRU_9725 ribulose-phosphate 3-epimerase, putative
MRSFDHQDKSTFLSGRRKKPLRPIISPSIMVADPTQLLLEALHVLSPEGGAVEWLHVDVI
DGHFAPNMSFCSDTVAGLRRHLPHVFLDVHLMVAEPEKWVRPFADAGASQFTFHIEATQE
PVALASKIREAGMQVGVAISPRTAIDGLIPLIENGHLDMVLVMTVEPGFAGQKFLSEPLA
KVRQLRGRYPHLNIQVDGSINLVTVDEAALAGANCLVPGQAVFKAKNRQENVIHLRRVVH
HHLKSHL*
>TCRU_9726 hypothetical protein, conserved
MNPALPHSYLSIAWRRDRVTAVLQFCSMVVSGVAGSVGQRSIERSAKSLARLLSEYGSVT
RVCNWLVVLLELSPAGVRRTMRASPGFFTGIARIVTTIFLGLFLASEEVELLAAGGVLSK
VWRPHAARMVPIFFFYYNLLKAGTSAALLQAMQRISFEATDTQSVIRKRHYKELFLSFME
GIAFMVYAMTLLPSNAPRLREALNEGLWMDRVYSVFSSLCPQAVQVRPATQGLLGLLATA
PFLLLSS*
>TCRU_9727 RNase H, putative
MQKTYATPARIVSGVPSTVDPESALLEANMPPLHVLCLRARLSIFENTRACQMDWMRRPP
PEPPPRAGFRISPLSRDELYAFVDAYTKDYGITQTSPREERFFRSSIPPWFAASAHRATI
GVELPIDLSITDEEELIREKRRVSEEALALHSHRSWILATDGGVDVPKSAGVGKLLSSLN
SSEIIEKASINCGARPCSYRTESRALLLALEKLMIPRIQHRHKTLLVVTDSQSLLAALNK
GPLSQTDWTEDQIWQRLLTLTCAGWSVHLQFCYGHCGAHANELADQHATQTMATGQYTEH

GIAPYGIRIC*
>TCRU_9728 kinesin, putative
MSNIKVAIRCRPLFENERPAVGLEFYQGRRILLDNKTYDPDHIFPPTATQDEVFAACQPI
LQSVKDGLHGTVMVYGQTGTGKTHTMLGVPGGTDGIAHRMIAAMLEHVQQRTLEESKCAL
TLSIIEIYNEKLTDMLSENGDAEVTLVGGFPKAMVKLTLSRLSDANEAIQRGLSWRHTAM
TLMNERSSRSHVVFILDLEEQNAYTDTVELAHLFMVDLAGSESLKKSQVNGVAANEAGKI
NKSLLALKSVFLALANSNEATRPSHVPYRDSKLTELLRDSIGGSARTLMIACISAVGRDI
EETKSTLMYAVKARSIRNAANTEREKLLVRLRSFELENQRLRNRLQERVVERGGYYVNRE
EHERIQQLEEEHQALKVDLEDLLRERQQNDALQHINISQTAILQAMIEEKEDELCRFKQT
YHEALTQFDAQLCSLQRVVQEAVSGAYEAAQRSAEVVAGRLEEWRVHALREENEDGGLNE
EEKNEEGEGTRMARGQEGVLALSRDYEKEAVRLVDRINDGFRSLSQEVLAVTQSHCATVQ
ALQERRQASLDSLQRTLQEQVREVLSAYVREQTRLDKELEDEHRLFESGISVTANQSSSP
ADVLPFRHMVRNVCRDAVESSKEYFPPCSLDENLAESLRLINESLRVKAASTSLVALVQM
GNMPPSRSSNSSLSTTTTNTATTTTPTAANVMTATAAFVSSGDSQPSVLSTKVVNRAAGN
NGVVKAKRLRSGSAMSDSRRTSARQEK*
>TCRU_9729 hypothetical protein, conserved
MDSLSFRLVRPMNRLTQLALLKHFQCHPEQLTAFNAKLIQRYALLDYVDHRTMLEILTKM
AKQPPTTASLIGLRQTLQAVQRFPLALEADKRAFETELLNSVLATPADTLSSVEYGALWS
FTTQTTAWEDVLRLSNTFPLQSTLPLQSEREFRIVLNQMLMSAIPVALTSPVSSSMDSQP
RGVRLLKELVGEETALKRAFDGIVHSDACWTERESAVFTFVGVVHALGRWPSEHIPEEKA
WKQLALHPTTSHDVDLHQLLRVLVRVYSPLVPEYVRESLDEAMSTDLWRCYSELPNAPVA
VFFGLGEPRLRFPDDQKTEEEHAMDRDEKTQEGLATTSQSRQMQEALRRLHERAVEKQLR
SDGPPLGVSVLINLLISNTFLRVQGDLFHAIIAALKGALASPSSLRSVTPLQAAIIAACL
NQVQQMLTGTHASSLTVGDTGKDIEAIARLLLPLLSYKHMKDHGSARCVSMLLCDCPCWT
REWGLEEGCLNLLREHAQDGFTRAQLQRILKCDSHGLLSLPVEVKGILEKQAAEVPER*
>TCRU_9730 RNA-binding protein, putative
MDEKPRLVEPAVTLWRAANVIIIFGFPWQTSELQIRNYLLHLHPSAAPVTVRLYTNPTNG
SSRGICFVEYNTKHRSTGRKSEQMEEEECVVTVVKKKIEETPFARQYLTAVLYHLTNQNW
DRGGRLPDLPTDPPPTRGGWVEGYGDEGFSVRCGAVLGLANTVTASGVASMQALRKRLRS
EAEAA*
>TCRU_9731 Urocanase, putative
MTSMKKVLTSLAVGIPSPLPPPCKELDESVPHAPKRTPNLSPADRRQAIANALRYFNTAD
HEVLAEEFSRELDEYGHIYMYRLRPTQYEMRAYPITDYPAKSKYAAAMMMMIMNNLDNRV
AMFPHELITYGGNGGVFNNWAQFCLTMKYLCEMTDHQTLALYSGHPLGLFPSHPDAPRAV
ITNGMMVPNYSTREQYDRLYAMGCTQYGQMTAGSFCYIGPQGIVHGTTITFRNAGRKYLG
VEDLAGKVVLTSGLGGMSGAQGKAGVICGAVVVVAEVDPNALYKRKGQGWLMEVETDVEA
LLRRVRAASAAKEAVSIGFLGNVVTVWERLVKEKDEIVHLGSDQTSCHNPFNGGYYPVQL
TFEESKKMMVEDPAKFKELVQESLRRQVAAINEMSARGLRFWDYGNSFLLEASRAGAEVW
TPDDTVRSINRFRYPSYVQDIMGDIFALGFGPFRWVCTSCLPEDLELTDRIATETLEKLM
KDASTNSQKQISDNLLWIKQAGENKLVVGSQARILYADCEGRQTIAKNFNDAVRDGRLKG
PVVLSRDHHDVSGTDSPFRETSDLYDGSSLTADMAVQNVIGDAFRGATWVSLHNGGGTGW
GEATNGGFCLVLDGSADAERRAKLMLLWDVLNGVTRRAWSGNACGHEAMLRAVSRVEGLH
VTVPQHVHPDVLKKY*
>TCRU_9732 Tetratricopeptide repeat, putative
MRRREVDFVENVAGAEELAKQKQMALALCPPQDTKSEGQQRQFFIPPMKPPGRASSSFSH
GGFPRTRESLISKAQRDALTVSAFGFGTTRHGQPDKSAAAVQDGFSTAAGQTDGIVVSQS
EKESVRFHLCVSALSEGCVATFIHLFELSHRDPVCVDELAQTHFTVPDDRLEWVKNQLSA
IEVLRRQSEFHNVYERCQALADYFEAERDHDEAAWHYETALRFAMESLDRPLEQKVRGVY
AAFFERRKQFRKALTLYEAMYKLALALEDEKTALEANCHVMRTCNALGEELKRTSPEEAK
RFFDRAVAIAKNIGSARDEAAGFHALGLICEQLGDLQQALQYQQSFLDVSQRKGLIENER
KAALVVASLQERMQLSSEAMQSLKQALAVSSETGDLEGVCHATMQLGQACKSNGDEEMAL
HYFRANFEAACRQCNQDLLDQARVALGFALGENYFKHAGGGRGYVPIVCYDVKAQLEWMS
KGVL*
>TCRU_9733 Elongator-like Protein 3a

MSCSSSDEDDTFTGPHRPDMAKVRAKLRNLPTLERLLAEKDPHAYTDEQMNTAMTFIEAI
AQAQPSSVQQIEQQLRKLMKKHRVVAKKSLLLAAYRKWLQAGTERRGNDVLERYFVSKAP
RSQSGVLVVTVFTSPYPEGQKFSCKWNCYYCPNEPGQPRSYLLNEPGVRRANRLAFDAYT
QFQDRVKSLVAIGHPADKVELLVLGGTWESYPLSYRESFIRDLFYAANTLHDYSEVNDGT
DSNAATPQPSQSRPPMDLLQEQMLNETALCKIIGVTLETRPDTINEEMLQQLRRFGCTRV
QLGVQHTDDAVLLAVNRQSTREEAVRAIKLLKDSCFKVDIHLMPDLPGSTPEGDKAMFDD
VLYSADLQADQWKIYPCQTTPFTVIEQWFKEGKYQPYGLDNLVDVILHAKRRVQPWVRLN
RVIRDIPHEYILGGVEVSNLRQLLATKLQREGCRCQCIRCREVKADVAAAEKLEEATLVE
RRYVASEGEEVFVSYESVDGLTLFGFLRLRVHIQNWITPFDELRSCALIRELHVYGRLVP
THKEADTAKAQHRGVGSLLLERAESIARAAGYKRIAVISGVGVRNYYRRKGYVMVIRPSC
GFFLVKELQIINNMEEKGKMTEAPNGRDESPRGAGERATEVEQNTTTPHGDEHMSSSRGW
WRYISAFWGRWKRPRGGE*
>TCRU_9734 gamma-tubulin complex subunit, putative
MSDGGGGGGGREFVFPSKLPKVENGVFLPREGSPRVIPFRAATQLRGAGSVQHSLSGVAS
SVAPVPSLEQVVGGVLRRGEEDRSAPGEDVGGTNNSVEDKKCGGFELPGRIFGRRDRSSA
DAAGVRQAAASSKTVAVVTGVMPRYRDTMQPNGDAVECMPHEGDGSPTYAAGHTSGAVEE
SEFISDVLFMWMGVEKTKYFTYDATSHRYVMSAEVGAMRQRQSFLTLQECGWLAHQIDEV
LRSSTTERSFLQQSLRSAMRRQLLQYHCLVASFRERRSPPMTFSDLVVAFKRVQPKLQVL
FTILRETESVKGGELASKLQRLVQQGSTRLYALLSEVYMEAVSPLLYMAVSSITKGEISD
PFNEFFVKSNPRIDNTSDAFWSSKFALLPEMLPTTVSRALAEQVMLVTKNVSFIRNCCRC
KQWHMDPAIVTAAQSASFDTIGAVVRDAMCFTNTAVLKLIREEFHLDNVFRMVNAFLLVG
NGGFYEILIDRLDPVLSRLSHMVQTSIVRDHMQSALLDIVPYTRHLDTDLFSMLQCEMVK
DDKIIGWDAFLVTMTVPSPLNNIFDVTAMKVYRRLFRIMFKVKRAEVALKKSWRQSVVLD
RIIGRLHNTSREVIAWREVAADAHLLGLQLNHFVNNLWSYLVAEVSTVSWDLLMKALRQC
TSLDEIRAAHIAYLQYLTLHSLLHGDCASMRQNIESVLSIVRQYVGAQALLTSLLERGNG
DVFSIKSEYQRLTDDFQREITSLLTTLEEQHLQFDFLNFLLLRLNFNHFYHDTMFGNNTE
F*
>TCRU_9735 ATPase family associated with various cellular activities
(AAA), putative
MIDRGRVRPAPFRIPFNDNLPLDSSTGGASFLLVMIIAMAPFLVGVINVLWPVVMRTWRQ
LWGNSVSEARRTITGRFHRSDPIYRCREGGACDHSGILFHAALLYIARGGGGTELLSEAE
WRNKPSVLFLFDPLKSDSHLLIGPNSFEAAGIFQSKVEGRVFCERERLHRYTVLRLPTSG
TWMAVGDGIQVTYQRQREDKEKVGRVNHMLHLKAAGPSGLHRIENFVSQLLRHYVTALPT
TTNSTRFYFQMQLGGDGLRFTRSPIPSAKTFDTLFFPQKRDVLSLLDRFLRREGRFAVEG
VPQKVGFFLYGPEGTGKTSFAAALAAYTSRHVISLSPSLFSTNQQLLNVFFGCQLECIGE
NEPFEFAYSDVIFLLDDVDPSDPLLRRRSTAASGGRSKEAGKTLKCGAQGPQFGDATSIS
SLLNVLDGVVETPSRIAVMTTRDPSGIDPSFLRPGRFGYKIHMDRMRLPELLELLGLHYG
TEENCATEINADAIKAWDGMKSNGFKKVRQLGQEEINKVRRCMAMVAPDDFSISAAVAES
MCFAAPSLDVFLDLLSRNQHSGQEDAFKR*
>TCRU_9736 receptor for activated C kinase 1
MAVVYEGQLKGHRGWVTALACPQITETYIKAVSTSRDNTLIAWGSNMDRNSEECEYGFPE
RRLEGHSAFVSDVALSNNGDFAVSASWDHSLRLWNLQTGVCQHKFLGHTKDVLSVTFSPD
NRQIVSGGRDNALRVWNVKGECLHTLGRGAHTDWVSCVRFSPSLETPLIVSGGWDNLVKV
WDIASGRLLTDLKGHTNYITSVTVSPDGSLCASSDKDGVARLWDLTKGEALSEMAAGAPI
NQICFSPNRYWMCAATEKGIRIFDLENKDVIVELAPEAQQKSKKTPECMSIAWSADGNTL
YSGYTDNVIRVWSVSEHA*
>TCRU_9737 hypothetical protein, conserved
MLRRGRLFLATAASNKPETTNSPVIAPGVVRSLYRMLLREVVRLDKSAVSKTLFPLTKEL
QSITKSHGPLYVPNGVKYLAVLREVFRDVNSPANINLAFDTLTRIRAHNEKVTARVSLFM
KDHVPLLTTMQASQPKTGAYRAETAACIVQNGPKYAPLGGSVFSVPTKVVLRQTRTVDLA
EGVALVAHPLSSTHVDRRVLLITERNPHVTTAVVLDMLFTYPLSRGNPMFPEVFWGHEVH
DGGFSQIGFTMPPTAQVIILHTTEPPTEPESPQYLAWLKWKERKPKTQAGDTPSEHHSLL
CKPLIRGGVLEDGTVEPTLYLSKVESLPYLAQLVPGKPRSSLRVYWGSMRWPTQQLEAEV
ANGHWIPVKLSPSFFGPFPLVPESGKVVERFPTKEEMEEARTMRERRYGVDVSLPQAFPP

DQILRRRECLWDQIMYCLGGEFSALVGCVNPFSGTARGVLPLEVAGPSVMSGALPAEDAE
TLVHEEDDMEEGEEEVEEDEEHDVGEEIHDIGLSGMAKEETTTLRGREGGDASSSMPEKP
PECGSGDDKKKK*
>TCRU_9738 Ubiquitin-like autophagy protein Apg12, putative
MTEGAAAQKITLRLTAKAGITETLPNMNCDPGETLGQVQARIKKKLKRPVLYLFVMRGSE
GFIPTPDQTLESLLHAYAESDGQRELSIAVSTGIFHG*
>TCRU_9739 2OG-Fe(II) oxygenase superfamily, putative
MMNITRLLREALHNYVSLRYAPSFQQPQPREVIGVPTRGIPPNFLPAFVVPEAIGEEEEQ
ALLAFTEPWFSRLPYNDGHMDSLIHHFKEFYRSYREIAGDAADNGSNSTHEEVDEKTAAL
ARTALRRCRKLASEYLANIPLDDRVHFLRLNSNGFIRAHVDESRNSSGIVAGLSLGSARV
MTLTHPKHPEERAELLLAPRAFYALIGTARYEWEHSVDWSEDGTENLERVRGNLLMEGTP
VTFDGRETQHKRGERTAVIFRGVSPIELLLTKMRMKRAATSLNGLYMSSADTLMRIGAQP
SSPSSLAAVYACTAPCPRRGTSRTTAVGSRPYFFIIASNPQRCFTAGSAATHCGHVVWW*
>TCRU_9740 hypothetical protein
MLEDEEERARKGSAHSVGWDEQSEEQQRRKKVGIVHILCGEPARAGHLLQRFIELLLELD
ATPREKSAGEGAAGNEEAFAWISRADGVIWRMYQLLGVDVLFAVM*
>TCRU_9741 chaperone protein DNAj, putative
MLTSSRCLMSLGISQACRIMGFAAPPVEKRMLKRRYVELVQKHHPDQGGPGASADRMASV
TEAYKTLQRLLDDGRHRRVTLSSTQHNGHNGSSSRNGQDDMNMQAASFVAPGVALSTSGW
TLPWQRGRTKSSRQEQERQLHEHATSLFDFLKRIRAMEREELDRAERLKSELKSSEGSHG
FTVEHFEEMRRMQQQTASWTRRRHSLPILIWRYHRERLARAPKRCWETVRYILFGQ*
>TCRU_9742 Domain of Unknown Function (DUF1042), putative
MDLESSIQREGLPREVLVWLRTLQLPRVVRHPKRDFSNGFLVAAICSRYWSSVSMHSYED
RMSAAQKRSNWELLQKQFALNNCPLSERMINGMIACREEYANSFLRQLYEHLTGRMIVEA
APLTAAEVSQPRTFLPQSVPPAPSRKISVDFVTPSADTPKRTASRVRELRSSNLMALARS
ESISSVPVAKNYVIHAIAGEQMSDDKNADDAEEEKEEKGGSDSDGEKKKQRGEKKVEFFV
SLRPAEVQQTVVRAVPQGSGQNATRDEKKRQQRQQQKQQQQSDEMQSGTCDATALETIES
IVRKQAAGQGWICVRDEPTAFTNYFLFEENNLGALLHCRLWSTLLGSVSDLADRILRHGG
FMADIAALFLQRPLPEETINQQRHQLQMDNGFTTPKLWKKIASPRGNSGSKRFVFLASLL
SSISDVDKFLAVSMYYDDILPHSAEAMRTLDRVTADEYASLLCAALPSDRKTAARLLPDM
LLATDNFITVSNTFEAKRSYYLFLRAVLLRLSRNERCSSLRNKRYSSSAATTTTTTTTTT
AHDPLLLAAFEIIGHNCVSALTHESSTVRLVGVYLAEALAFAGCSTVSLFMDILPFLSAC
MKLASPLFKCVCAAWMRTAMKRLCNPFGDEKRETEVREVYDEEVSAYAGPYLSTIMQHLY
DVLVTPGRLKVRTYIAEQLALCLHDIPDVGNMRRLFNPEKLAVAIFSVFQTTPPELVARF
IKPPSPADGKVSAGGEYNGQMSSGGVSCPLLGPLLVDGSLLDCYPLALAEAILTVFPLEA
GGSKLTPTREMAAPFPMGHRGTNSPDGMAMTSRQIMTRANLMLRERIVPVDVAQRVTWMY
KLIVGSRSGCGFPKRPASLSETAATKRWNAVMRQMYRDIAVLSAAAEMLCTQKGALTDNA
ANAIAQMAGMAQQIVLRWHTELKNDGAPPPRPLVSSPVTSSERMLLAMEWYHNSFGAMTP
KEQQKQQQQQQNRVPAAPSRN*
>TCRU_9743 RNA-binding protein, putative
MGLKSKNSARTAVETVTVRTAGKTPHRRVSFEAADVPKRKSSGESEAVKNTKNSAAATKR
AIVGGIIEARKRPREEEDGEGDEDDDTAAHDFHDDEEEESDVHYVYSDSEKEENLSELAD
NENESETSQEEEWENPFEKSKREGTRLSYEALRLRFLPPDFQEPQLFKFLSQFGSEVLNC
FCVRSRRTHQSKGIAYVQFDSPAVLPTVVEECHGMSLGGRAVQASVVTLHRAMPSKEKIA
QRRQLAYAYKTRGAPLHHHDIRKKNPIAALIKYTRVEKANNEHLKRLGIDYEYHGFEEQL
KKIPSHLIIRKKKRARKAHRNDKNATDKRNNVELTVVSSSLLSSGTAAATATGQRRMKKS
VMGDSTAVASPSSAPTASQAGNKKKRTVATAKKSRRLETSISG*
>TCRU_9744 mitochondrial carrier protein
MYGPGLITQNEVPIENYNVSNTSLHAVTLHTTEIGPHEHTNSVNRSYSDLNSLQFLLYAA
VFCWIRTALQQPLNLALARQQTCPIAGSMTTMQIVRYVYGAEGGMRGLMQGMFALTLGCA
LSEALYLWLFEYSRERLPMKSEATRDAVSGYVSDAVCRLIHLPLSIVALRQMTANKMMFG
GTYKTSGIFRTILLMYRENGMRTVFAGYGTTLLVGCQWTAVWWAMYGYTKGWLYEAADGF
LEVDNQDNLNLSASSFSSWKHWLLAKDDNIVLNSVSSLVTSASTAVLFNPYLVVRANLQV
KPKARLWGVVRDVYRTQGMRGFYVGLALNIGTCLIDGVLASTSYEYAKLWADKSHHRQNH

SE*
>TCRU_9745 ARP2/3 complex subunit, putative
MYLLERVHPSIQAAVDRILTGANKTPDAVVRDFDGCEYHIHVEWKASRINEKEEEIGTHP
ASQREAHFAAVTIALRHSTPFRELNAHRNFDDVLPTLFSTDTRKFVMNDANSRSDGAFVA
EVHIPAGVAATVRNEALQSAAQLRIWSYIPVFARQCELFLSQPEASLKPVVLHYHTEEAM
VLFSSKGNFIVAIALRSASKDEAVFTKHFLQAMMDAKKLQREISAAPAFVFDHGKPPASL
PGNLPVSSLMDASVFWCSFQLFRRHMEPKEHLIETVTQLVNFRSTLAYHIHAGRTYMHAL
MRKRVESSMQVLNRAKTKTTGKAKVTLH*
>TCRU_9746 Uncharacterized conserved protein (DUF2181), putative
MMFGTVNVVNNCVPQSWAHAVNSLAALHAAASLLSSGTEECPVGLEADVRVAPDDEKMEP
LLHHDPIPAGEASTCVTLAAWLEELASIVRLRSGRLGVVKLDFKDPDAAAMAHRLFAQSS
TLYGKLSTNFLFWWNADIVAAGHDDTVKISMNPRSFSEFSEVKLHAMIHAFASRLGFGLS
FGWRLPGSFNSYALEDIVRMREFLQRLAAYNADAGDDESSDNNGVCGGIPSGDLRVRPMC
VTFALRYSAVFERVARENREALWQSLDELVSETQRMFTTAERVPSCFLSFWRARDEQITE
EQIGLAKARFPTCTVDFN*
>TCRU_9747 translation initiation factor eIF-2B subunit beta,
putative
MLKWQMDNRVEEPASLLDAIVRNTETLVSSIRRGKKGNRSRRSLSAAAACGMLKIMRQVV
TEFRDHEAQRDSSSNEMLRANCPADIVATQQVRRLMRLISFVGVTVLRAQFSTLMLMNVT
RRVLSLIRKSAMENAASISELEVLAAKRINELEGSENNDSPYNLQPQTQDSEPHQVSLER
SRTSSGSVLFSPVSVACIDERRQRTSCFHKALTVRFNMNSTEQESILELDATYEAEETKT
ADILGTGIPGEQSLRRAPSRREVGDDERVAEFPVCIDGFFDSLLESMEVFEVEVEGMCDE
LCARASRQLHATDIVITIGCSNTTRHYFLSALEAHVKFKVIILEGAPFPLHLTQKLAVEL
RENGAEVQVLPDSSAFAVMGTCTKVLIGAESVLANGGLLATIGTHPLCIAAKHFAVPVLV
ATTTLKMSPYYPRDVFCTSLVKISRTDAKEIPWKTYGHPYDVLPTPYGENVENIGSLTVN
SPATEYVPPELITLYATNESEYTPSQIHRIVRENYNPED*
>TCRU_9748 hypothetical protein, conserved
MEEEPGNVSTTTNGVMEGNKSPQRGSVTEIPTLRARRFPTSRTGHFWTPTLRHRTTATQE
IGIRSLDSIHDHGLTEAIFAPNTPKTTGDPFLSVIYPAKFGRESEGDNETSEMEISMRQR
NSICRTQVRVEGYFQDESEGFVALIPNDLPRSTFLYVLTASEGRDKLFKCLQYGLQLMIC
LLKRPMLFTTDSQQFAGYWAERFWRNINTIRHGRSLFKLGRWVLNLFFLEDIYGRLVLKY
GSMGREMMNGLESSLGRFLRLSSTWCALSRSKNDGSLGTENSMGAVSKPSVESLLTDDMY
FYAARAEFPWMKTPTSLPMMPMVREASKHTLADNITTTRFYVKEKFYNSIFEMESKRDHP
QQREQLDIRPATSKNGSPDTAGSFLSPPSLHSTLAATSYLGTRRHHGQQATRPFEKLLHP
LCATGDDDDGNYHPDAPSYTPSMNTDNNTIELATESSSPKRWEKFFHKTHSAADGNKTDP
CRGFFASYQVLPYEPRLGDALHSPRGNNNNNNTNNAALPYSGTRGPVCSTKFLSTVEDPD
HNVNSEARQDDGNHSDVSLTSSGILGVKGYKDCVLGGEQGIPAEMGNPAHWRKRLLQFST
PLMLLLGVRTISTIGRRIVRDILLLSSERFLNVSCVEKNRPLLQRRANWLWLAVSSIDLF
LNTIRLMNRGWYKYATARHSALYHCRCKDYDETDFTWRYRDLIARRKVDLYFPEVDFDFG
APLCSSPAYFEAADPEHIAPACLTCGCLFVESQSGAADDLPKQEEKAGRKHDPNGKPLGG
FREKEEILCSRGNETVRLKSFGTPTQPTMAERAEVAILLIPWMVRKLLNYLLLLRVHPNW
TATILLQLRYMTEVYLAFMYCFGGYETGKSDATLEEMLHVPGAIAGLLGAVIGLHRVMKS
APK*
>TCRU_9749 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MLVGEATHSLSSGRGEWIEWAAPISLMSLIPEELKSELKEFMGGGGSGIVTYDDTIVFPL
TARNQNGYPVSLLIYSKDKGNSWVVPKGVSPVDCFGPRIIEWDYGTLLMVTDCLDGRKVF
ESNDMGESWTEAVGALSWLSTDAPPDPYGRRYLLGSIITAIIEGNNLILYTQKGRYPPGE
RGLPNAFYLWATDGNRTFHTGRLSVDDKENKATANTLLYSGDALHLAEARGTATISTIYF
SRLTEELEIIKSLVRTWERMDAFFSMSHTPTDGLVGFLSNTAIGPKWMDEYLCVNATVTN
GVKVQDGFKFPGHGSGAKWPVNSRKDNGPYTFANKRFTLVATVFINELKTGGSSNPLLGA
VLDKAVSQVLIGVSYNTGGKWETVFKGKTTTQSSTWETGKRYQVVLMLSENEGSVYVNGE
LVGSSETIPTSKERMFEVSHFQIGGDERGRGGDVTVTNVFLYNRRLSEDKLKTLRKGGDG

SMRGGVSRVLMLLLLGLCGIAVLY*
>TCRU_9750 trypanin, putative
MNLEPTAIELIASEVDSTLKQKNQMIRDLHFELKKGEKLVNTTLVELERRCQAVNIPPLS
REQFLTARVV*
>TCRU_9751 hypothetical protein, conserved
MSKQPHLGILCVDVSELLRASARRKVTRRDNMLLYKGSYLITDPVPWTPRSTSTRSQSNS
PAHGSSVSSSRTRKSRKYRCSHRSRARRSGSKNRKDKDHLNDDFLEEGVTIKTDAAPAQG
QRGEISVAGSCSRGANVRRRKLPVKRLAGGAHGATSPVSAWVDGRQLSLLSGDPNDSVSG
SSSTMPPSLLLEEQRRRQQDPRERAETPSPRPPSSQHEEDEQHRFPDVSSTLSDFAREKL
NFLMKSPPGRTFDNALAPRKLSLSVEMVSDRNYQDKSGAVEDGSEHVSLAMVGTLGAAAV
APTPDPWGAPPPPRAKSNMRQLKNFTGSGAHSCLIRDARGVERVMILGAVPMLPRPVANL
PFAARGRAPGVALPPVFRQAARVVATPTKRPKRF*
>TCRU_9752 kinetoplastid kinetochore protein 1
MDLFSATNRSARSQQSNSTANGHHSSVSSAASRSAAPAQSRRSGRELLETTSEEDKSLFV
RCVEQVQRQLKPNINSPSTLHTLASYYTREEPYVEGRPFCVSLSYATFLFHMQMARVSES
DVQLYAHLINAILAQISDDARMTHPFVLRVLRDAVFGLPSPTCVGGAHCVALVPPLQYRA
FACLATSLVDLRIVPVDILYQWQDKLEALCDAQSPLVANRALTLIVHTIGTIRMDEQIAA
LQYVLKTRPRKMNVDFLLACYERLKRAVPEPVKGPMYGRAISIHCSELFLRFRSPIRREY
VERFLYPSLSGADMQSLVQIPATRQHLCGELLRQCTPGMSPSNPYYLCLCAVMQWAFEDE
IDGAMEMVELINCQMPHAAYFAATLAVDTRMSVAMFAKIIIALVRGAGLAMTGREVSDDV
ATALRNRTNVYSVLFLLREVVRNCSITASRRATDMHKALSIAVPEKTVEALGKLAMEAFN
DRNEATVDPQLICAELAMVLHQLHIGEAMDAAVAHLRDVTALCIFCGLGRGASTLCEVNG
TMHMTGHASVGRVLTTLAECAGIPSVEGKLIQLLRDPATQMDSAVHFLLFHILSHAGQHR
HTLFQAVEPYIRSTLTTLLSADRASSAGLVPSQQKANVLMLHVKIVILLANSIEPSYVES
ILRVFCEVRLRNNHDALALWYMANLLLRQGKGNVELLPTDPAENNYSVNYPSCAPMSNTT
ADNAQLLLKIIDRSHGFSDEMRKLVGCCVCKLIQDFNVQSPNIIGALLSPFGFVPVGLQP
LSEYALPVGASSTFWTFFVHQMKTSAPARVAFMTALAKSISQRFRISAPADAVCIDGTEA
TGHLFAVMMYEAMKRNPPLTRVVLHMISQWVKQQNHPPGRFACLLYICTQLLTVVVQRGT
GLDAIELAAETRQDMHQFADAVTKTTTIVRGQLPRLARLGPLVRQENIWFYQVLHRLHHK
ARRLVEETTGEKCDEGSSVFDEGFNTTMNKTAELTGGASVGTNVQEAYLLDSLHQPDDDT
VFEDYTEGDDTMSPAQPSLAQREKQAVYDPLLQEEQRKRQKEESTASAPVLRAHNSSLSS
KRDQSTMTSSAGSVGSVRERHPRREVSFVSVDDAEDATKNMNEDPEGALPLPIAHSTQSA
VGNNTAAKDHAYHSLVSRGVQTSYQESRGVSSSVVDNSSGRENESASTMNAGVTQNEMRR
YRRQEPSFIDTKNNNDDANNSWREPDLEAENEGDEEPIDNLALPILQASTPHVDGVAIPS
GLVLEYLATHQGAKSVLHELQQFEKELQATRAQAAEVVSYGANNYDEPHQGRVFTATASP
HTTILPVTMERRPNNYSVPHATRAPAPSKTVMARLTMIQASERQGQHEVQAGIQDENEAS
VVKKRRVEDERRGAELSRNDAKKAMLQTPAAKMGTGAQFFLHQSVSSVMKDLGGMRRQVE
AMNSVMTPNQGGTIGVPLNQVTPYGQMVLPECFVEQNNDTAVREIRQVMGTHNPNDSRLS
TGGRRKIRGTGGSIIGELENSAAWWDEKSSAPMPQFATDPQYSMELF*
>TCRU_9753 major vault protein, putative
MQAQDTLLRLKPYEYAHVLNKNNNVTELIVGPQARVIASDERLPKPVTPFHVVPRGSYCI
VENPHVRGSDGVTPVRDRDGQVKVRLGEREVRLGSTAFPLYPEEKLVVVSPMKFLRQDEG
LVVQALCNYTSSDGVKRMAGERFLFTGPGTYCPRVEEEAREICRAVLIMPGHAIRLSALE
TFTDRDGKLRKKNEQYLRTKPGSYLCSVSEKFLGNVSPIVLHPGEGRHVEVLQRFLDERE
HGKGVERIAGEKYLITYEDSPSFLLHPYERIVKVVNKFHVSKKQYAVVIDENKSYRRFIT
DASFYLQLGESLEGDAIHDSYILHEGQALLLKALGDFQDTDVDPPVRRRAGDVWLLQGPR
EYIPNALTEVCKDKDNKEVRERIILTNGKGIYVRDNATGEVRAVNGPDAYMLAASEELWE
KHLPPDVEKCLEQQKYLSMETSVGSPSCPPSPCKELRGKTHWTVMYKVPPRSVTQVYNYR
TLETRTIFGPERVLLEPDEEFTVITLSGDLWHFDNPGNCLPKESNYIKSLHLFLGPSNMT
DIVHVETRDHAQLALQLCYAWYFDVTPGDELAAGKCFSVGDFVADTCSFIAGRIRAAVAS
LPFQQFHKNSAKILQEAVFGVDPVSGGTKTELRFEANNFVVTSVDTQRMEVLDSRTREGL
QKSVKIAIEISTQAQESNAQQIALAREQHSRGLLERQKMQDQVENEIQRRVLLEAETRSL
AMQSSGRVRSIADATAKAASVEQEATLEAARIRAKKDEITNNILAEVERMKRELQHEYEA
QRVALAHKLEAELADIENKKFSAVMDAIGPETVMEISKAGPELQAKLLENLGLEGYLVMD

GSTPINLFRTAAEMTAQSSA*
>TCRU_9754 Ribosomal protein S5, C-terminal domain containing protein, putative
MFHFTVGSLKNLNSWYAKGTMRGGVPRIYYAWMRPGSFTRRRFEKMRNPFVDLETGTSLY
FRDTRDSAEAVAHAADSKGLKGMDNAIDLYNEYRIVPDLYPEGFQWKHKLNTEYNQWRSN
TWLTPDLIPQEHRGRFLCNFQLNIVAYDMRVVKFSPKDHRQWIYCVLYVGSGKGIAGWGR
AVAPSTQEAKKEAIREAFSNIIAVDLEQEGPMYPVRVNADGVRVLLYPAKRIVANFRVAD
ILCAFGFQHAGCRINLKATNNPKSPTHTVEGVFEAVKALRSVSEIAASRGKVPHSLIYNI
YPYLEEIRRRKGMMAMHPPGKDGLLMPDRVVDNRLPDHLKKGYYDDVYWKDFFAGSREHL
NEPKMGLRGDEMRQRLESAQSRPISSPTGSGRRTLEDVLKRLGKTTKDLGSIPIVNPRLD
IKLPTHIKRNYSLH*
>TCRU_9755 hypothetical protein, conserved
MMTMTGRVLLVCALCVLWCGAGGGGRAEAPSVISDTPSVKGNDSRGDNVTVGGAAGGGQN
GKPAQSQAAGVSVQGANEAAAEAAPAPQPGGVTSEKAEAAKGSNGQKKGKTEEKQDKEEE
EEVEEDEEGKEEEEDDTEEEEENGANEEEETKKGEAVTGTTEGTSAGGREQPILSSGAEG
ASNNTNPNSTRTTGDDDPAADGAETREEKQNENKDANPKETPVTATATKNTTATTGDSDG
STAASHTTSPLLLLLLVVACAAVVVAA*
>TCRU_9756 hypothetical protein, conserved
MWTWLLPEASVARGEGSRLRCHDGNGVLLPSDTAGAPQEAEKERDLPDIDYVAADGVTSV
VGQSLGDEAVSDKAGGGATATGPKGPDAADDAQGAVDPPPREDDAAVVHGGWEADMKDAP
PPIHGSNTAAAACPFPLLLLLAAAAAVPTLSSGCKRERPTSTGMFLSVYTYTLLVCILCT
RDMLYALSLFCVGR*
>TCRU_9757 Leishmanolysin, putative
MPTWCCPWQSAVGGGALDDCRDSSEEYHDCDDIDGMELQDGDGDGRTLESHWSQCHAKDE
WMAPIGCAVCRTELTLAAPADLGCMRVKWEMAEPMRW*
>TCRU_9758 Protein of unknown function (DUF3682), putative
MAMMTGRVLLVCALCVLWCVTGGVYARDVDTNALGGCMASGALGENGSHMPDGCNKTAIT
VPLRSVLLITAVEASTGRDSAGGTKKDSNSSGTSDAGASGAVAPPDGGPDGGAGAGGSAG
ASVPGGGGGGGSGAGVTGSGSAGPGGGIPSDAGPPAPAVVAPPPVPPSAPAASPAVAPAA
PVVDSSAGRSDGTAGSSGTNSSNTTGESQTGNQSSAAAAAHNSSLPETPTGTTSGTGHTR
QEEEEEENEMQQQSDEAQVQQNQQHEHPAENGEESAKDKNALRTNATANTGDSEDSTAVS
HTTSPLLLLLFVVACAAAAAVVAA*
>TCRU_9759 hypothetical protein, conserved
MNCGDVNFPDGTIHPPARSSDADRTGICQLPSPREGKDDTKSGGTTAPQLNAEPSRQHED
WRQSAAADGPNTVDRSPASNTANNTSETRPEFASNPSEVMVPNASGIMSVTYGGREHFAA
DNTYEVSENNATGHKSPLFIKWLCRQWICC*
>TCRU_9760 Mucin-like glycoprotein, putative
MMTCRLLCALLVVALCCCPSVCATKAQLEDTGSLVEEVGEIQPPLPQQTPAQKGEGPGAE
NGNTARGAGKGGGKTTPHPQSSATPNKVQEKGAEETSGTKIVTRTSAEQTNMESEASAHT
TTTTTKTTTQAPTTTTTTTTQAPSTATTEAPAVSTTTTTHPPSTTTEAPAVSTTSAPSSL
RRIDGSLSSSAWVCAPLVLAASALAYTALG*
>TCRU_9761 hypothetical protein, conserved
MQDVPQAESGAGANLPTAGTGRTSEETGQDKEEEDGKQQEEDKNKEDEMEVDMKEEEDDE
ERKKNKDDTGATKKLSAGSEEQPILTSGAEGASNITNPNSTPTTGDDDPAADGAGAAEGK
QNERKDANPKETAVTAAAMKTTTATTGDSDSSTAVSHSTSPLLLLLVVACAAAAAVVAES
RGGR*
>TCRU_9762 hypothetical protein, conserved
MESGQYTEQGIAPLWHTDLPTCFTTQLTNKWRGTIRQDTHRYLLCGTRPSDLSGKDLITQ
EVLHRQELVHLARARCGESELWGRLYWAVRDCTNQCRFCNVSPEQSAYMRSNNDPTAPGT
DTVPPSAREEDVSPVRRRTLTRRRKEKCPHCDSTLTGFSNLVSHCRLFHPEHPPPLPELK
CDFCDMVFPTRRSTAQHRSRCAHNPDATRHRNSSARRRSLLPQDQPASTSTPIGPQETLH
HLLLECPGTLAVRQRLGVEQELRTGKFSQWQLLRSRKFLSLLDHLFGTHMALYS*
>TCRU_9763 Endonuclease/Exonuclease/phosphatase family/Endonuclease-reverse transcriptase, putative

MEPFAWLPAERYFHPLLNSIGAYQRYTYRLRAVCDAQQQKLLLSGDIEQNPGPIAVLQMN
VSCLTPSKLATLMAQGADIIAIQETWKSSEQIASMHTGDYVLYAQSRIGKGGGVAVLVRK
TLRSKRIPLTIPQHDTSLEVVVVQVALDQNRDLIVASAHMRPPPQVTQSFRRLVNCLPAS
MPLLLCGDFNMHHPQWEPFLETSPSEVAAEFLELFTDAGLTLVNTPGEITYARGTRERSC
IDLTWSKHLTVSDWSASVSPLSYHYMLTFTLHQAFKDTTPSAPPSAPRIFHSWGKSKWDL
FVKDFDAQLPAYDYKKQSTGIRAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERIAT
DSKARYLQLPTPDREAEMQRTRSQFFLLLRERLRNTYLRRISKLNPGEPLARKYISGRKK
ASLPSLTSILLGDGQHTYKTARRAANALNRIFFPFHPLTRQ*
>TCRU_9764 hypothetical protein, conserved
MRGVHLAPRHAQHSAPRRNHARTRVQRIFATEHSRVQRNTANNKLQHGAVHHHRPPTSHH
GHKAHARHNQHGPHEPQARQHQHRCVRRGLRAGKIHKRRRPRGNQQGVRHRQHRPRRERA
GQHKRTVQRLHIAHRQLHRPALVAPRRPRTAQHSTAHHVQHCAVQQRHVLHNDPHAVPRH
PRHVEHRTHAVQHNVAQRHLARTGRHNEHRLHRHALADKNSRRGAHSGRQCGSAHRHARL
AVPATAARAHAHTVLHAGRRRPGRVAVRVPVAGVAPSNVDAPSVAKASRCVLLRRQQDTP
TSVVARHPQMRPSRKRQAQRQHPRQQRSVAHKAQRAPSSGHGASGVEHLPRDAVVHVALR
QQHRPASQAHRRIKRHRVVLRQRKVAPQKCHSGARHAHSPTHRHRVLAQQEDAVNKRHHG
AATRRNTALHRHAQPQRRLHQQPVHVQRTARRKRHAANHQHANSVAEHRLHLRARNGQHA
PSQIHVVHHEARGGVAKVVGAAVRNTILCNQHRVHHSDARARRKSVRHHHAAAGARLKPA
DQHFSTQASRRVGPPPQNVQARSAHKRAVRQRHVAHGPCHQVHVHHDVHREGHTNVARHR
RPETGVHLHTHTHVPHAQVGAVGARWLGDSDGQARIAMAALSAPAGAAITRDRRRVSGEA
RRREGAWVDAGQNGGIVHGRDGVVRPLTAVHTVARSHNRSVCGIG*
>TCRU_9765 hypothetical protein, conserved
MWSVVGACPRSRHRVRCSAIAAMRVALLFLLVLAAAAAFMPAVHAVVLRLRGGTVDRAIT
VGRAVDTVLMDGVYITNGVAVVFDVPAMLPGALRIELRNCVCDGGAQIYVRGDSGEPASD
RSLEVSVSGLSGGYCSLVFVHNLPAHTNVTVRDSTIVMPGPMRYSQLSGLADAVASPLVL
HATSLLQTQLRVSNTVLRSLQAGGSAVYVGGGVDLLSSAVVLDGVSLEASGGPTASAMRV
ASSSRLSLRSHSVFSVTNVSVVSSGGGIVLGERLAVFDSVLRFVRVEGSVASSLVRCGGG
TVGSGGWLELHDVWAVGEASSVASLSGVTLGGGAVSIARCVATGATLVSGLTITSGVVSV
QCNRAGGRVLQSSGDYRMAGLPSVSVVPCDGCAAALTCFDALTASFSDCVCGCRAGGVGD
ACLPFDVPPARAGGGGGGAQDCVSGVTLTESVTVGGGRATACFDSVVFSGPITVAVDLRS
MDAFADSLNVTLRHCVLAGGAQLRIGGLSESTARLMPHALVNMTNVTSLEGTIVLHGAMP
LHSSVLLANSTLRATVGGSQYVPTTPGHAGSRYGPALVLDGVRLLSTRFVMTRSTLFCGG
DLCAAILVERGLGVHLSSVFYMDNCAVRSREHVMYALASDLRVSGGSVFSIQNSSWIASS
IEIYEGACVFRDVVLDGGSVLQVVSSNFRLGFAMLIAETLTVTGGSWLVHRDNEFRAAYV
LYVIKENGVAFCDRSVWSILDNKLTYGLYSSFTHMTSNWSPPSDSRPIIYGVCNEARGSP
VTDYGDDLNIWVPVTVLDCGACTVDAVCFAARTSSIRGCECECAADGYGDTCVPAAVPDG
LGPLPLPDANDTEVRCVHGGSISSVDYPDPGVRGLCFVNVTFTAAIVLDLWSFDAPQQTL
NITLLQCVLMGLSIGGSGARVHVNMTSSMLDSGALEFEGDFGASSQILVAGSTLVAKSDH
AILFMEFTFGANMTLLLIDNYIEANRYAIYFFISVVVFDGGGIIVKGNTLSTTEEDDGVE
SSVCVNAVGLKNGGYIDVENNMMRSVNGVNLLGDTTVGSAGLLRVADCTFVGGTEFFDPA
LVYVSGSVTLEGGAQWRVEGNSVSAASVLSIPYSWQNIQLLGSDTTVVLAHNRQVDDIFP
VADLSLPQTIVELSARFLVGCNLQDDEEVSYDDVLPEGMDVLLFGCGTCNDDAACYMPGT
ESVDRGSCSCSCKDGWHGASCFPFEVPDTVVPPVAERAVDGDTSCVVNQTLTSLTLNIWK
THHCYVGVTFSGVGAVLTFSFNSMPLHLPINITLTGCTFLDGAVLQFVGDVEVAESVGVL
IRVSRTVMRSSVVAFALALPQHCDIAVTEVDAVQSSAVELPGTVSRTLSVLFLKNVVLTA
SSLLVSNANARASKRDAFGLYSIGTLTLVGGSSLYARYCSFEEYTHFFYLDILSVSDRSV
FALLNNTMASGTSLLYQHSRFSVSEHSVLRVVGNSGSVSYAIYSLNSWTVQRSSWLDWRY
NDVGVGAMFYDTESAFVSIDASSHHCD*
>TCRU_9766 BNR repeat-like domain containing protein, putative
MSDGGCSDPSVVEWKGKLIMMTACDDGRRRVYESGDKGDSWTEALGTLSRVWGNKKGVRS
GFITARIENREVMLVTLPVYANKADKE*
>TCRU_9767 hypothetical protein, conserved
MEAGVPVEPRVVARISLIGGVTTEPSNLLDSDIMLRLMGHVITVAEQPSDSLDDIMAWRM
GLSLPSYPTWPALVRCCCGDDNTVTEGIAVVYLR*

>TCRU_9768 hypothetical protein
MKKNPPLDPPRRARGGRAGRNPRFLRAAGRAASARDPGRERRRKQEGREALVLPRDRGFC
EGHRVFQKLVERTIVGELADFVDARVS*
>TCRU_9769 hypothetical protein, conserved
MAVFSCVRCGYMYEFLVSNSYYRKLTLRNDHCPRCDQLSLFRFMSVSGMVGRMPFKPVGV
PAPSYATLWWRKKRDGKSAAAPLDAVCKGDRW*
>TCRU_9770 actin A
MSDEEQSAIVCDNGSGMVKAGFSGDDAPRHVFPSIVGRPKNEQAMMGSASKKLFVGDEAQ
AKRGVLSLKYPIEHGIVTNWDDMEKIWHHTFYNELRVNPESHSVLLTEAPMNPKQNREKM
TQIMFETFGVPAMYVGIQAVLSLYSSGRTTGIVLDAGDGVTHTVPIYEGYSLPHAIRRMD
MAGRDLTEYLMKLLMESGMTFTTSAEKEIVRNVKEQLCYVALDFDEEVTNSAKTVNEEPF
ELPDGTIMQVGNQRFRCPEALFKPMLIGLDEAPGFHEMTFQSINKCDIDVRRDLYGNIVL
SGGTTMFKNLPERLGKEISNLAPSSIKPKVVAPPERKYSVWIGGSILSSLTTFQTMWIKK
SEYDEAGPSIVHNKCF*
>TCRU_9771 actin A
MNPKQNREKMTQIMFETFGVPAMYVGIQAVLSLYSSGRTTGIVLDAGDGVTHTVPIYEGY
SLPHAIRRMDMAGRDLTEYLMKLLMESGMTFTTSAEKEIVRNVKEQLCYVALDFDEEVTN
SAKTVNEEPFELPDGTIMQVGNQRFRCPEALFKPMLIGLDEAPGFHEMTFQSINKCDIDV
RRDLYGNIVLSGGTTMFKNLPERLGKEISNLAPSSIKPKVVAPPERKYSVWIGGSILSSL
TTFQTMWIKKSEYDEAGPSIVHNKCF*
>TCRU_9772 hypothetical protein, conserved
MNAQKGCERSTERSFETQSITEENCGQQSQYLNTKESSPLSAFQLLGKLKAVINEVALAL
ENPAKALSVDDCISITEEGLRAFKTIKVGRRIDGRRQLNLNSSRLSGASPTNREVGDGDH
AESDAALSSRRQLLCSPNSKKVSPKRMESEYQRRDGIEAARQASALRSEERQRKAEERRL
EKLQEMKSKLVAAGERSFQAKQRRTQAEERLRNDTLERHENGARRVEEAREQTKERARRG
HSRVEEVRLNYELRNQTKALLLDRKMSEVEHNQEQKREELQRHAQERNEAMLAVAERRRN
LSQERIERQQQREQQRRENLRRHEEQKKLEKDLKEQRAEEWEKKVQQRQRDACAEAEARG
RKVEERIQQSVHLREEKREMLRQKLEKQEQKIKEARQRKEREADTKPTIKELMPFISSQE
EEQLAQKLAKVVAVTARQGKSYMEIYQKESTMSAKDLNRSKLRSIISRLGSNTSSASLVQ
CRQSLHDLLGMTEFADVDHEYVRYFNSYESFARVLMDSRRTSDMVTFRLAHNALIRFLTD
ANEGKKHVLMFIRSGNLAPLLLCIRDEIKGLKRHSHSIPLAASLEILQLCFERIAIDAQT
NVKLITVRDQLLADLDAAGIDRYCVAVTRAFTEEEDLKVVYSATRLIHSQVSILSKKKGD
FPTVWFRQVACAFFTLLENILTPDGCPLSATGTLLSARRITIIFIVFRVLNSLARWRLDI
LQELLHDASIDKGGSNIHVDPKVVPEKTPNVITLTEIFHVLSGFFTYVQTHADLLETIPG
ENTVDEGVRGSFESALKFGVTLAQIPPLPASQPSNSSTAGLTMTPARPPYYLRAALHECL
LLIGYLCVQDKQIQGMFAWGKGKSLLSRILSALPLQYFTSACHILYPTLLAIIVNMEDNL
TFAKREMDIKPLLKLLEEEYQALPKKAKLYALQRHAELNPVTKEDQDKPDQPVRWVDLLG
GDDDEFFIQLRQTAAPAPAPTPVPTTLPLSTPEKEKLYRQLKNPGLTPSGYFKIERRLPL
ALWPAVMEQLTRAVHETNKGE*
>TCRU_9773 p25-alpha, putative
MSIESAFYAFASFGGAPTKEMDNAHFSKMLKETKVIGKQFTSTDADLLFNKVKAKGARKI
TLSDFVDKAVPEIASKLKKSAEELIADISSCSPEARATKADAVKFHDDKNMYTGVYKAGG
PTNVDRNSGSLSGVVDRRVAQTDVRGTTASQK*
>TCRU_9774 hypothetical protein, conserved
MDRESSSQFTADRDAESVPRITSREELAAPLNNTRSNAELLGNLDDDDGSKNYSNEKAEN
GLFRNEESLMSRETLWGSPCRPKSDFSISCGASLRDGTLSKAFQGEQVPMQLNEENLCQM
KREMAEGKVMLQPELIDVDPYHIKRRAAKDKNVSVISVASEAEDATGSSIVNSDVEGAPV
FLKTDMSKRSCPSTSLWSVESVYGNSVVPDILSRSNLDRFSTQLLMGVKELRPEMLLGDT
MQDLLGVSDLTKSGGQESLCVEGESETRDDYIYPFEATKTYEVMQGHGRDGRASEHSGFR
TSVDEATQTRGEAHEGTAPPAPGTRPNNNDASTEFSFSAFPDYRTSGSLMVWPPSPNTCS
EEHHFLSGYKKPTVPSKIERCVDVSNESNARAIHEMRQMIERALQEINELKTRQVKLSAD
MTILQRCLRSHFANEVKQPHSLERQAPELQEVQGSDLGKEETQLVRTEAECTPLTFPELQ
TLWQKLEDVLQGLRAHHEGQMSHFIRQVIDRFGQINQIVSYTLTKLDALQQQQQGDHHDK
MEVALPVDLISDGEKVYLMVDVQCCTTEHCEVLLPISVKATVGMCKRELLRRLHRQGLVE

NNISYADVILLRDTLTLYEEDVLGDVLVPALQNIGASMKLVKLTLRTIFPKSVHSFSPTN
DEKCARTTSPTAQHNGIPSVGAFSADHVATSGRDARAAMTTLERQSPLQQYATTVRHLTP
ADNLRFEDLGVLRGGAADELSQNESLYRRLIWELERSELEELRKDEKLQRVAVAKEGLKR
VRLTLLDRVTYSTVEGHRHVARSALENLDTLLVPGATVEEICMATKMAQKAVKSIGNTHG
EEKRVAEMQEAMRAEQERKQRTIEEIKELCDEVTHRLRIPANLLKRAESVAHEAQRAITL
APNMTLKELEEVHQSLVNFRAAVCI*
>TCRU_9775 BNR repeat-like domain containing protein, putative
MSTENGVSWYTLGESINRVWGNSHGRTGDGVKGGFTTNAIIEGKEVMLITAPVYPKEDNG
EGRLHLWVTDNTRVHDVGPVFREDDDAAASSLLVKSEDELILLY*
>TCRU_9776 TAX-2
MPRYYTPKEVRAHCFEDDAFISANGKVLDITPLIQRYQGTRFASLVQPLIRAAGTDISHW
YDKNTMDLKTCIDPETGFRTYAQPFGRFAHIPTVLPDSNIDLSYEVPWWKDEQYVIGNLT
RKTRKIRIINTLNGAEHTLEVCAEENLFEIVNTRFLKYNAHALSYTWRRHDPDGRDLDMT
KTLDENGIVDESEEFESLGLNADFYIPALHLYYDDDLTEA*
>TCRU_9777 2-oxoisovalerate dehydrogenase alpha subunit, putative
MFRKSSHAIMHSGGLFRTPRPLCRALQEALTKAQSVWNLDFGGTPTVDELTFHQRKYPST
PMFHVLDLDGRVVNPKQEPEVPKETLIKMMEAMLRQQSIDLILMEAQRQGRISFYMTSMG
EEASAVGTAAALDMRDELFLQYREAAALTYRGYTVKDMVAQCMGTIENELKGRQMPIHYG
SRALNVHMISSPVATQIPHAAGTGYVCRLENERETDPNKKRICAAFVGEGSASQGDFHAG
VNMAATMKSNTLFLIRNNGYAISTPSSSQYAGDGIFARGIGYGIPCARVDGNDILAVFQT
VRKARELIRTTNQPVLVEALVYRSSHHSSSDDSTWYRSREEVEVFSNLFLPVARFEKYLE
RKSLWTPEQSRSLTQKVRQETLAELHRQEKLPKWPVSSMHDDVYKEMTPEMHQAQKELEE
HYERNKKEYNM*
>TCRU_9778 Protein of unknown function, DUF393, putative
MSQLYRGRSYQNILRKLPRNLVVFDGHCLMCQARVRHVLERNFSYFSFIRIMQGVDPVKL
EANKMLFCSFDSVEWREVRRNFPHLLNDADGVVLIEKVPSKTASFLSRVRQGQKQRRQQG
RTGGMNSSEEKRGLKNFFQTNNFSFLLASSSVTTPRRLAGSFDVVEEDVDIVVSVKYEAV
CRIGMKLDRWLLRTLFRCLYYMLPRWMGDRWYDYILRRRRLWGTSEEDAVRYPKRVPGLK
ERTWKL*
>TCRU_9779 Protein of unknown function (DUF971), putative
MMRPLLEQQRRFTSIISRFSSAVTSHVSSLADTHFMPLSEQCITEPRRPYPRRVSMQENL
AERLTLQRSLRAHLVPLQVIVSKEKLYIELVWPSAALRAVENQKETMAHTVKGAAADGDD
DGNDAALHHTMESPARTVSSDLRQRRPLEEHRTRFLAEFLRAYSPSTDVIGSDVLIYGRR
GITITDVIPVGNYALRIVFSDGHSGGIYPYEYLFHLGCEKYSRMREYIRRLRAKHKSRDP
PKRAPSQRLSRIRSAQRAEGRHMNSHGQDDQ*
>TCRU_9780 hypothetical protein, conserved
MIAHTIVFTVLLLVTVVPPLYIYNPEEHPGESLGPNPVGGIFPDSPPNHWVRQQLYILFV
LPSCAFLNSLFVYFTYYRHLRHVQFRAELSSVAHANLRTAAMIVAEEQQGVECNVDNAFG
GSRSGGGVTNRSLLALRPFCSKSSINSTALYARRHIRPEGLSLHMYSTSPWFPELRELQK
VVEAQFLRPAEKTREVVFSCLHKDVLVPFEKRMNLQEGSMANAIRFLSDRESKCVTEPGM
RVYLTEVELKRRRSFNNESMLRSEPSEDLF*
>TCRU_9781 hypothetical protein, conserved
MAAPSLTGSECDNTNDGKESDEYYGDDLHREADYLRVLVLESQEGLAAVPTIPGLAEPLA
FALLPAVISAPCVEADPFAVEFTQQLSSVCAADPALALSHVFQRCLACDLMSVLSRPPPP
VFFCAQ*
>TCRU_9782 hypothetical protein, conserved
MTEVASVPALGGRDYFFAPKGRVFPNHGFTSRSIVYKRFAENTTPLALSVGLVLPTMVDI
QMKLDECVAEGVDMPLSKVLGIMKEAGKVKFLIFADAVSRVAVQTGFACLLIHSNTAYGN
SVVFLWDMYPKMHQIHVADLVKFLRLPPFFSRLFGPLPTQSELRVYNMPISPLAAAEDCM
KRSTLQLLSDVVVDAVECCVMRKLVRGSSKGSGGFLKRSAVHVTLGVLKVCGSAVGRAVA
GARGEYWGEIVGIAVAPVAFAQFSVVMHVTRRRHSRGVKPSERTRSSSGGRSKESGAQRG
NGRRTPLEKKA*
>TCRU_9783 hypothetical protein
MMYAYDILQQRNDAKEAERPKNKVARYQSKNVRPSCWINEEIRTAGEVDLPPVLPPPASS

PFCMTTSSSDWLVRDDGNAIRDMVQTAVGGETRLQEPDAALYTSLSTPREVLTSPSIECE
LCTTSSKDVRYVPHGSMESAVAVEEVVVIIDAAAEEREVPLDASEGSSDDDNRQQQSALS
SLVALSENLEGSICPRGGDGIVDAAADSSIVLETEDECDNGIVLPDDESFSITFSSTNIE
IPLPPLSPPQQQDNTSHGVMNSVDAFGVFSGGTALQLPQIVMVPRVENEPLSSIEEFGQS
EMEQRSTPLTSSSSSSPLPLPPYGAELFQEGCPVVAVASVVAASRQSSLAAEETQCPPPP
RCFDYYLRRGKAKRKQREAEAEECQRRLNEEEERRHTPQVSLYAERRGPRSFNEYVEASR
EWETLRASHIKSITAQLESADETRRRAVVKVNVTSERLLKEMVGRRKRVGVVESSTQHAA
ARQSWLKQLQEKYAPSFKPTILRTTGRRKASESETQRKGGPHAIEDSCYDRFMRYREKSE
KKREQLRQREAEKQHQQPKTRRTITQITEYVRSMWERDESRRDKLRRQVEKEREEEKEKM
RAMKPQLSRRSLELAERFRQRQRTAERSAPTTTSVPHVGVSHQDGTCQRLWGAADGKKRS
PEPKPPTPPTNRKLSFSSKSGSCHCKPLRRGLRGIVPPAVSPEFEERNARLLRMRQQRAE
SRRHEVEKELAQACTFRPQVDPVSRRMAESHRRESVRPNTLQQERSSCFGGKRRPCVFSA
TMAYVTKDVEKDLAWASDVRVAMQVDEAVEGNLFIPHDEDTDEENLKSHIEGLEAILEQW
KQLEAEYRI*
>TCRU_9784 hypothetical protein, conserved
MPRTFLSVEEHTLSGGSLPPSLLYNNLTFVEECGALVYASRKDCIVRDIKAKKTHVLPIG
TSEKEMIVHCTATLAPIGLLHPDHSLLILITTESATQLWAKESPLGLVPHNGSNGNGCCG
AIVSSSTGVAHVLVSTNKGVVIFAEFDATPNTPFRVQSAVKGHMEHAVTAARLNPFHDSP
LFAVTGDSVGRLLFWDRDKQPFAFFETSECVTALQIVSGGDFAVAANGAGKLQVFDSRTG
EMRVEICAHSRWINTLAFCTATNTVISGAEDGYFTVWSMPKSTVNGVTLVEPIATQHVPN
VLPTGAAFRADGTQVFIAMYDTNRITEYALV*
>TCRU_9785 hypothetical protein, conserved
MFARRALLGRTTALRSAVVARHTGCGSNEHALRCGRRDFGQLFSNLATHSLQVQGCASLS
TLLYSPLGTVMLVLLAYNVVVIGSKHVIYTMEITGKDYVQDQQLHMIMKYGITACVLLAM
EVLFVEV*
>TCRU_9786 hypothetical protein, conserved
MSRRQEKPFSEEEEEEEEEEAEEEEEEEEAEEDEEGLGDRKASLKHKGRKDDAEGSEDGV
ADDKKAKKKDQADEDDGLPPRKPAVREIQLLLPGHGAEKITVSVRISPEPPLNPTKKSEL
HEEHADESEEDEEQMDEGVEEEEDSRIQRNQQFCPPWLPHLLSDDTLHWERTLRLMYGYT
APPQPLTTDDKKENMQQETSRTVSHDDLEEEEAKEEEEGEEEEEEEEEEEKGEKPDVVKS
NEMEKGAKEEAAAKEHRSVSIIVDTPSRGVPNSRSASTFSAATFSRRETDGLDSTSTPRS
KESGLRNPAPPMQPVLRFTDAHRVFFLVRSADGQRWYLLDTIPQQRRRSGSNVGGGSAKR
SNAASKDEREEEEEEEGEEEDEDEEEEKEVKEGLKMGFNQEEEEEEEEEEEDAVPSARNL
DMDSVICIDALMLAALQSPTALRCCLSQREPVSLTCVEHWLRMDLFAAMPIFTAIHRMML
SVYATGNSRLPYELPGAAMDFNLFFTASYLNHRIPAYPKLHINSTPFDQRTTNDKEEVSF
AGERRCIETMEAMLKVRTLPSRRILLRHLSSVVGIRLLLWLLLEIPKELLLAWGSNSSTG
VDAILNSRFNPANKGGLDAPYNEEDEEEEDEEEEDEERTKKTAPGVAAAIAAFLQRKPHE
DGPRFVPSPFLLAVVVEIRRRMKREAKGNSPSEFTLVECVGHVLPQRVEDGRPRKDPLVS
ASFSLLPESTAGASEGLATQPRMQKLYQSDLVMLLLVVTSTPTRRSLPCPERGSRRGSVL
VRPSTHMLIGLSDGHHELFEYLLRKKAEKVRTSKETMESGYFRLLYLCLLRFKNLASLKI
LLSMTPLFAVLGPHDRSPFGDLVYAWTLDRDLIIRNHLELFLDTFWNELYYRTLEKQYDE
ATIAKGRALLLLDKMMERRKAYSSTLQQMWTSAHSPSRVALIKPQPRNLAVGGVASFLQK
TLETPTWSSPRRAVAGNVSLSEYSDECLQAEEHVRLTFESLALAPRTYLTPETLYIALFS
GPQQNLILLRYLMIRCRVVTVCANPLKEVAVPAMEYALRVGNTGAIKSLLTIGVTLHDYI
DDGNLAEDMFLCEAVSPNEVAPLLGIWKQKEEQRRINPLVSYGIIRTVQSAS*
>TCRU_9787 Axonemal inner arm dynein light chain, putative
MTESLLKLQPQVVVGTASGNGVESPRRALSIPALRLADARKHAASDVLRAGGSNGVLTTN
TAVSALVVRECTATKTSYHSVQPFAAAAPFLNETESTWRTLAVPSCKISPAAEKAFLVEE
FNKKGTVAYPGGAVLPALMKNLSDVERVLYTLLPPRRTVCKETGNTILQCVSTEPSSRVE
VADLHERLTERLRQRRARDSGICPIRREVYAEVFDELIRQITLEEPTRGILLLRIRDELY
QTLAAHSSLAERAMYFASKQREEAGEGMDELKRRIHELEEKRLELIVRKKAVQVREEQIL
RAIEQENNTRSKLRQDELGYYRRANRQLTQRIKSETERTNAQGVVIPTILTGKESNENGD
PQAAT*
>TCRU_9788 hypothetical protein, conserved

MTDPVRRDPTEFLRVLRRMSRTTSWQKTMMFASKGRMVGYRLTREHYNTILFSQSLWGRA
LEIVRVIRAMQEDRVQPNGATYYYIVNGMANADHGWNYDFKINHRLEKIQHWRVAMEALE
ACEANGFDSTDTMHNSAIITMVIPGFNKWEQASRLLEKLLREDRRMHPTMVKFYHDCLIR
NMRPREASCLIRLAAEQGVQGYEDKWEADVYKGRPHDSELKREILSVDNQKQDLAYTFAA
LQLRGDQVAQPKELQKLLEEETVRNIEAERSVPVPYSAGLHSTEINSVFRPRVYRQLWYK
WQHIANRYRPTAALKRRQLAPKDSPTGIPGFNRI*
>TCRU_9789 hypothetical protein, conserved
MKDGRGGLVGKDEAAKETRLSWAEKARRQMAAERRYEEKDEVNQHCIVHLLNMEAQEELR
AENYPRGGLLVPLQALPLDVWDIITLFLTFRDVQLLSSTCRFFWVQLHRRESIWRFQLER
FRREMTILRSDRQLLCMEFLKLSSCTAYERLKLERKLYALDARREWHFRESEKPDRSIGI
FSCPLIFNASDDNSENHNPSSLGDEEEEWVLLRIRVLRPTPRSTSLLGTCTPSSDGNRFD
QIMSRRVDSIYTPSEYLTICDNINHGDFTWSRMVVQDCTADEDGLLLFALLQTLRRAKRR
PIRHSSGNEPQTSYHLILRRFRGTLLAICRYEAEQILKATLHMPRILDDFFIFNDLSWTG
SGDAAGLVPLLQTRYFIAPELCHRGRVGLIVVDPVRVLVVVGKECVTRDDPQWDEVYTTA
LETGRPPQGSGMNPQPSGRV*
>TCRU_9790 Cornifin (SPRR) family, putative
MLTAAVPPPTQPPPVEKFPVPTGTTRVTAGSSYPSQLPASVPIPQKKSSVSLPTAAFVAQ
QTQGPTLATTTAAPVLKSQFTQPLVVPVVATSAPTLEVLPTCIPVVPSVLWYNKQIQHIS
AKPSCGAVSEAVSSLRVRHSDEHRASPSMYPPKNRYLWQPAPLSENIASESWRGTYWKYV
DVHRYIARRYCGNPPPKE*
>TCRU_9791 mitochondrial RNA binding protein
MLRRTSGNKALHAFVRSPHYRSVPSAGPNGIVINRDMLIHQFRDFYKTLQHSSLVDKVHL
MSERPSVEALRVADQMASIGATFLGMPLTGMEHRATEFMESMRYVRGAGGPSTLASYLQD
TESCRCHSGDIVCLPTGIAVGHGPRTNAVAHSTLRQLFEVKEDQFSFDVFTLEQEGDAPP
LGDYFGFAGNNVLLTWKDEHGLLAVDQYQQKQPQAEMNVVYLEPGCHFLSFYGVDFTTDV
LVQKGYERSMDSIAAAGLNPIPVQWSEMDKLGVSMRAAVLPLKFLKANVGGMLSRNKSRG
ARWQTHQIP*
>TCRU_9792 hypothetical protein
MTSNDINAFKQYLWSLFQSYSYIPSGGGNGGPPARRLSESGYRAVISLVATTDVMSRFFL
AEDEITQRECLKRMDSERFREEVWEEMISAEERLRDCAGGVTEDAGNKEVELGELDVAIS
TDYDYHIMRPSLGQKTIGWNIFIAVLLLRLSNSLHLRIEDHILRGCQEALHPLARLLPVQ
GSRVASKVDGFASYLSQVERRPCIDKERPATTVMRLALEEHARDPAPRRSSASGSFFTSA
RIKTSLHDKASGSGVEVAAEVMQPTFVSPFERRRMRNVDALGRLEQFAGSVGGPSSATVG
AGTAAHRLKPRCERMDVKNGIPNDEHPHQSSPPPRPKHSSMMVPAVSRPGCIGSARGRNV
PIEVMKLHQRLTRGNENRLEETGGDALFRGSRGSMKRSSLETTLEVWNSTHMKGNIPSAD
TGSEVYHARHDEEINKSDDERCRPAAQCSFLASSCSPSPNREQIRGAKKILVPLGTNLQD
GPSCSLGEGPSLCKENIPAAVSALDGTLRQRKQIGAAKGTIACGEPTGPREAPQQKPLEL
PSSQRGTRRQPGPPLSPSNRALSRTARGQRPVQPIVPPTRAPPVDGWGSQNRNSD*
>TCRU_9793 hypothetical protein, conserved
MLMASRMRREGVTSRRLTLRLSHNTATTSVFGVSLLQSRGIRTVIAPRPAVTTLVYIDKY
GRPLRNSTETDLSLIRTRDNKFYLQRVLEGGEVIRWRAPGLDHLKNVTNFETYTLNEIDE
YGGVVIPADLTPTASNDPPSFHDAVYYINRVEAKRKFTRKDRRQWHRLLFAHWKESPEKF
LNHSIGAYGMPFLFVLWLTIRGFHSIKNNKPFWDVNVYGKTDEEQVLQDPWLRLKRFSDR
HPEHEGLDMTVTMMSPGQSRLSSSRAEIRETDFTDPHFHSELWWKIRHVRYYGHWPKGLA
E*
>TCRU_9794 thioredoxin, putative
MSHNIIRRIFGDRKLPENLSGNDYERFMQENFPKWIQEFEESGFLEATKLPVIKSEDEFL
QKLREHKDDLMVIKFWKHACIPCLSFAEMYKQASEQCKAEKRRIVWYSVDTKDIDTRSLV
EYQLVTGTPTIQTFSGLKQVGKEIRATNAEELMKELTLREATVMSR*
>TCRU_9795 hypothetical protein
MEPFYPEAIPVELPQQYIHQQCAEGNALIDAQNDILCGQSEFFEVVTTLSNKDDSRDNSG
ELGRNEASIGEAGGGRNGRPNRRNSPQSGKKFSAGENPLSRPQKGGHIICEVSPNGPDGS
DRIYLRRLPSTRVYGRAHYTRSNSAGSTVWREKEEDGPNVSHSVDSTKSVMHDEDKKKKN
EE*

>TCRU_9796 hypothetical protein, conserved
MSLLGGNSVSSWAEDETHGGGPRYGEATWPGNVSAAFNAGQATSAANREGNSDIVAARPQ
RKPLLFGSNEHCQLECLASIAYLVGSPLQRNQPTVMEPVQRSMKLVRELLRRGVDPEKVI
RVIESREGVSGAGERGC*
>TCRU_9797 beta-D-hydroxybutyrate dehydrogenase
MSGQKRVLSGRVAVVTGSRKGIGLGIAMRLAMAGADVVLNGRRQSPEDSAIVEKVAAYGT
RVRCFAANMKDRAQVEALIKFTEKELGAVEILVNNAGIQHVSPVETFPSDKWDEIIALNL
TSAFHATQLCLPGMRQRGWGRIINIASVQGLVGSMNKSAYCAAKHGLIGFTKVVALETAT
TGITCNAICPGYVYTPLVEEQIKAVAEAKYGGDMEAATQAFLCEKQPAKAFVTVEQVGDA
VVFLASPGADMIRGTTITVDGGWVAQ*
>TCRU_9798 hypothetical protein, conserved
MSRLVVHKESLPAQVGIKRRRAPAVAPASPIAVGREEDVGKKTFPATDDADGNTTDNNRR
EPVETDDGEAGRAHPVDSVSEGEEEESSEDEEMVELERERRRIEQLHQEKQRTKDEKTCG
GSAAAAPPVQATRAGSSNNNNNGKSTTVGGVSSYNHDVLFRRREWREQNIVTAADGAKDS
KKARWEAVHNSAQRSAAFRHFMKSHFK*
>TCRU_9799 major facilitator superfamily, putative
MLEPERSGKPVDADEIHDTPHAEDVRNVVEDSASVEPALAPPPPPSAEENPLEASISASC
ARAKVGYFAIYAGLSASPYYGLLLEHRGFTPLAVGVLIAFMPFSVIILLSPLSYLADRYQ
CAMSIHLCASTVSALLLLFVIPSTSHFLIAGLMMLHFAFRVPVGPFMDQRTMSILPPDRK
TEWGKMRSYGAYGWAFGALTISALISRSDWWGLAVIYCLGMATAMYIGFTIVPHDETERF
QRKFVDVLRHVLSHRRLLVFLTALCFMGMGYAIINTFLFIFLYSIDAPTILLGLSVIMTV
VVEIPLFRSSKHVHEYFTDRQLLCMSIFAWAVRVTGYSFLYNPWFVLCLEPLHGLTFGFM
WLSGMHFVRRAFPKSLSHSSIGFLSATAFGVGPLVGNIVGGSLYQYLGARGMFRFMALCM
LCISVVFLLLDRQLEHLGYSVEVEEEGEMKAKDVVVETSLSTATAAAAAEVDGETRE*
>TCRU_9800 hypothetical protein, conserved
MVHEQRCPPGVCSDSRGIAPRFSQDEDEELDEDGFQDLVPTSLAELTANEEVHTAHFVEG
DFFPEESPAPAELQSVDDRNDDSTELLQDASSLLSSSPSENRGPRASSNDAEDEACPSSL
TGTCRTVKRVRWVDEGVAPMPLVQRATTFLLHHFEREKEQQPQQQQQQVVELERVPQALS
PPPVLREEKNGDGTTYLSCKAHRPARRFVLWKRSKGAADASAQELPFKLQPPGNNPSTRA
VTLLAALHPPYRAEHVGQAVLMRSATVAQSAKKGEALCDGGLQMPMVRVSELSNFPVRIP
F*
>TCRU_9801 QA-SNARE protein putative
MSLSPCPFSRDRLQEFSSLRRAAQHQAEWLGESRWKGNEAAPVSPAEATLNGNSEKGMHG
HAMSPWIRALEHFLELENTINLKIERLHEQQRAFLQPKFLSDEEEEAQRQQIEENAHGIQ
KLLRELERMIISGMRPQDPTNEDEVRASENAKKHLSSRLSMIIQSFREGQELYATQLRRC
EEKTQRYKQIGSCEAHKRMEREERIAQYLELGYTQVDIQELLEEDAKQKELSREVQEILK
SVTELHEMFKELGAMVVEQGSILDRIDFNVQQTQIDVKRSVAELKKARQKQGGCWVM*
>TCRU_9802 RNA-binding protein
MRSLTEEETKRLFDKLAQYIGPNTTHLLERKGEEEEHVFRLHKNRIWYMPLRLAKLASCV
AKSNLMGIGVLFAKVTHNGHIRIQVTALDYIAQYSLFKVWVKPNQEQKFLYGGHVTRAGL
GRITESTPKYQKVAVFSMGDVPLGFGVAALGTLECRKCEMNSTVLFHEADVGEYLRNEAG
LT*
>TCRU_9803 recA bacterial DNA recombination protein, putative
MVAAFAARGSVQWTAATRSRTAVGGNSVDSQQQQQPHEEVEESKCGPCDWSVFLLVSDPS
SVSPQHIHELLKKALASATANSVQCDGDADSLPSVMLKKIKFVPFTTPNDLLVFFRFLSR
VEYFESCHHANRRRVLVVVDNVARLWEHPTCGATNHARHWMAAALVREVRNAILIGNGWR
DVGSGDVEKRERHHHAHDASVSGQEVSVDCRGGSVAVVFVNGCKSVYHRKLATERTLPSK
PLGVPVWLAAAADVRLFVEPLCNADLFLQHDRSSGDFCGTQQSEHAARAAMRVRLVKGGR
TVGGEVTAV*
>TCRU_9804 protein kinase, putative
MSHQIRSLSELQEEVNSLDSRYVLEKIIGAGSYGIVIRARDTLNDNELVALKRVNKEIFE
EMILAKRVLREIKLLSFFNDENIIALRNILTPLDSEDFDHFYIVMEIMETDLKQVLRTGQ
ELTEAHVQFFIYQILHALKVIHTAGVIHRDITPANILVNQNCDLKICDFGLAKEENDRGE
NMTDYVTMRWYRAPELVMEDKNYSAQIDVWGVGSILGELLGSRPLFQGKDRVRQLDKIIE

VIGTPSEEDIKSLGSLPAQKYLRKKETRPPLDWRAKYPKASEEALDLLKRMLVFHPDKRI
TVDEALRHPFLAELYDEQYETINIPLFSFDEQEQKTVHDVKKAVYEESVMFHEKYPKTAP
RHRQLQQQQQQQQQQCGSALPSMDVTGEGRSAQRTIERDNVEDVDNGRFDEMLEAS*
>TCRU_9805 hypothetical protein, conserved
MACRWGGHRFALLQKQTAAGYMASAGKVGSEEKWAQAAMEYLHEKRHCNDSRKRQHDVDN
ERRIALAFDRYCAIGEKKFAARMSRLAARMTEALEAMAELGMEQAREEALLLSSEQPPGN
YRRPSLTPPVPGYEPGYGLDVPQLSSQQAEYPPIVRPTDALEFGANADPSFPFVDAYRVE
DLTALCARELEERHGEIREAAPLTGVEGEAWEAYVALQKKALARQQLIFDLCNDPELREK
YDADAEFREQQWAERGMLPLEIKEEELREVERHYAQEPAYHAFRKI*
>TCRU_9806 FHA domain/Protein kinase domain/Protein tyrosine kinase/
Kinase-like, putative
MNLRGVEDNARRDPLSNTQSTLVEVSSENPAMTTERPWGFLLSDKHRVLFLSERRQITCG
RSPRCDVVLDDPRISAVHFTITFSVEVSVPSPGGRGPYRHPSRATRPHMPSGTTITMGQP
LLGSQDNFFSFQEQHDDAHHHSRLPRKRASEVRIYLEDHSSNGTYVNDTKVGKGRRCQLQ
SGDDIGVVAFQQSNLSGGGGEENGVGSATDSFSLVPVDDVTTLSIGFPNTIYVEKFCFQS
YHLLDNAVGLEVGGRKNTQQGPGAGKERESLKQSVKAPPFPLQLQWGCPIARGASSVVYA
GMDVGTGRRLALKVLQDDGFSSPSSPRASVMEGPPGTSWKPPRQIYSSNVYQKNNEALHG
FPALSDEYLREFYFLTYLTHHRIVQCLGVKKIPRGICIVLEYVAGGTLQDLIKNFGAFNE
NVIRLYTLQVLQGMEYLQSRGVVHGDLKTANVLMTEKGNLKISDFGTSRFVQTIYVADSD
SDVLPGRGSGCPTQGAEKKLCGTPIYMSPELISTQESTFASDVWALGCMVYEMAMGVPPW
EELHDLSPHIVVWRIGGAKKGPSLDCLRRCGASPTLLNFLECALHLDCKKRLSVEELLKH
PFILGQAPIVCSQSFPLFSPSSLEWSPRMNSPRMQMQLANGNLGTAVNGEKPLRVSEEDE
PNYGMVLGGEFGDMPQQELLQPLLELGGPAVVAEMRSNQSNHCTSSSSQAAGAESHQAIT
CEPNCRWKFENKSFVQTEKRSSVTNKDASSVRIPRRRLEGAVCLRQGRGSHGSMNSMDAV
RQGDNIRDAAAALTSYEITAEFSRLTGLFGE*
>TCRU_9807 Transmembrane amino acid transporter protein/Tryptophan/
tyrosine permease family, putative
MSQGGVLGSALILAVTTIGAGILTLPSAFSDAGVVLALVVLIFVALLTVVSIDYMVICID
KLGVNSYEQINRELLGRYNEEFVRWMLLVYNTGSAISYLVILGELIEPLQPAISLHFPWL
VTTKHTLFVFWIFVILPLSCVPDISFLRGASFLAIAVTCFISSLVVVRYFVPNGCGGGDD
DNVSQCSSGMGTSDAVSWFSGKHPLLALPIMMFSFDCQSLVFQVYSGLKEMNRRNMMRIS
VISLLLSGTIHAAVGMFGYLGHPTDVRENVMSNFDPTTDTLFAIGYSVYVIPVNLAFVII
LFPTRDAIFLMWYGYSSATEAVDRGYVTDSGLEKYDACQQRIPTRDHLIVSVSLSVTCLT
AAFLVPGVVSVVALLGGVCSSSLCFTYPALYRLRLHKTGILPYTKYWERPLNWVMLIFGL
VGGVLGTIVAAKEFF*
>TCRU_9808 F-box domain containing protein, putative
MQLSRRLPERRGGSNIHLLESQEIVGSMLTDLQNPLSPRTVAVELSNEIKTLPSSVEMKE
INCGLFVHDVVGMRPKGNALSRRTTPPHSYCSLDHQLPTELVSVIMSFLDTRSLFQYRAV
CRSFNNAFLSHGIQSLAPSLTSAAMDPTVGTDTLTGVMRIREAILERRERVWSHWLASYI
ATRLSQNVEEKTLQKMQLEGKALGAQLRYERRSCRRAREEWLGHQADYYRARDNIRRNWF
NVTSLGFIAGSGVAPVILPDGTLCINDPADTILLFVRRDRGMLSCVTRRAKGKVPSRAAE
ALRDLWCLFDEMTFSSRLSLMCYDPYMDALRVGLENSKILFVKVRSAVVAGLKRRLESEV
EREESPPSPKKRVPRLRTRNSREGVEVVALYSTAGEALATFAPVHGDAVGLPDYEWSVAE
MMAATKKHGFNLDFSRVILIRHDQDVTASFISTSATPDVCFTEKDVLEIVALRRTLAKGG
PSADSNERGNAAGVDGSHSVTSAPAEVIVGCGVTGSAGFPSSDEPFGNNDGGTTTPPINP
TEDGRSAVEVNAADTVDMKQVVKKYVFAVFNEQATLSAVVAYTREVAMFTFGAHTSTCLG
VGYTGEAKRVYMIQAPVFRRCETTTREAIEEGEATVACVTAHSILICQQLIFRAVEEVEK
CVYSDPDDEKSGGDEKHKRKNRKGSAAPLRHCTWYFLRGYCYSSPSREMTVLREVSSPSL
MAFLNPRPWLQQHVMAFADWCREKKNMRQQQQQNNPPPHLKYWWCSLRDGHPYFRVPFI
LYITRYMPFILFQRQYIALDRQRIPSEEQNRFQEVRILEDVSQLNLFVSSMALSPSHAFF
LLGMVSGAILLLSPSCADARDDPPKVSFVEPERPFSRLEEASTRTTFARIRRRRGIMGMQ
RITPPHNEENSEEQEQEEEEDEHVALTTPHPPSEPLSHLYRTTPIRTEEEILRQRRRRQP
YLHSLTATQVFGNGFREDTFIQKLQRDTSSVFRSMQDRLSSANSLPLHAVWIIAPRGNSQ
ISNGAGVRSMHLDEWKLTTLSMSFEVALYDLTPESRSWQDGALVVPLLTISPYKRHPLRD

FPAPNEEPWFCAKMRRMLQFATKRRFLEPEITWRNGLLVVSSILGGRRYTIFDFGVAFRD
PDKRIKKGEESAVAYSATQKEYRQCTSGLMLSLPMGGENVVALPRHFPLLLRWEFLSLMV
LVVRCLGIFFAAVSITLMMLRIDEYISIPHWSVLLLYSPFALNVVVSDILLYDPYYVKGC
GVPFYIRILSNLLMFLVFPILFTVRRDAYDRFHPSWVLLTIPLDVSIALASVPSLYIAAR
QSESFWGCVSMRRLGDFFGQFLCIIFIVLLSMYFDGPSVENPSKPKFDLLLAFLPFFLLL
FFAFLRAIIEYYKTRKRAYAFFLIYVLLVISVPVGMFIWQFSHYYLAVSKRSSVVHVSLI
QTCFAIPVFILFFFFCVTLSSFTLLVSC*
>TCRU_9809 Right handed beta helix region, putative
MEAVTHIVNPGGEGAFSSVADALNAAVSGETIALKPGLYEELLKVATEVTITAVPDDSLA
ESEAVITNGVVIVANVTMRGLQISGKIDVRKGHAVIEDCDIHHGSDGVRVGEGAKLTIRR
SRIHHCESGGDGIFFTPGSFGEVVDCDIYECRVNGIHAHNACVTAGNNRIRDVLFGIYFR
GQSTGAMEKNSIEHVRKFGIYVTEGSDPVVQGNQVRECGMHCAFVSQGGKGIWTENNFEG
SMHVLTGCAAKLGSNQINGKLDVDVAPVVA*
>TCRU_9810 Protein tyrosine kinase/Protein kinase domain containing protein, putative
MKDKLRAMGHPAMDAADREDSHAGCFSDSVGMQTYSLNTSLGAMHIMSRLNNEMSFVEDT
ASGSFGVVKKGVLDLDRQCYAVKQTKRVISGEGDLQQRLQEVYTLSACSHPNVLRYFDGW
VEDRAVFVRTEWLSDGSVADFDRPFSEALLRSVIHQIASALHWLLCHHITHRDVKPENIL
ARKMEDGTYTFKLADFGLARPLFRDRPNTGEEFRGTNDDDGDRRYLSPEAFAISEFSQQK
GEADVYALGASCVELMGGDPSLVRNGCYTGNFHIYSAELQNLVQWMTRLDPQERPDAFMV
ALLTVDPALKSTKGFARRMAAIEGLRASVAELEKKVTEANTTEKEEGGA*
>TCRU_9811 START domain containing protein, putative
MSNDELFVESSGQKYKLQTLSDFRAFKQFALSEDNWSSHYSDAVTTVESRPPEDTSVGLN
IVRVRREMRGVPGLDLYDNLHDAKYREVWDENMIEGYNIVKLNAHNDIGYYSAKFPWPLK
NRDFCNIRSWMEFSNGEFIIFNHSVKHADCPEKKGFIRARSILTGYLIQPLGEDGCVLTY
ITQSDPRGSIPHSVINFTATRLVPKVMTKLETSTKKYPAYVSQNHTVSREALPWRTPKMD
WNSSYHFPGDEMAFRNVFVPHINGDTSDGEPHVTPDAATNAPGEKSPSAPFVASAVQTTE
SFSLAPVAPNFSDDTVAVQQYRALMQEAINTVDRTFLQDGKPPEMSQYLTRLSYIIDGIR
QTTPH*
>TCRU_9812 actin-like protein, putative
MDITFVADCGSHTVKHACFSKTDKTLGFDPGVSEVPSTAYLDDALDVVLFGRQLAELLSD
SCPVDSGLTLSLLLDVLLPQWKRELILKCCFEYLDAKRVFLGYAAATALFSVGKTTGIGM
DVGYRGVRFVPVVNGIVQTSLCAEVQSVGARGADCVLNRHLPEAEEPILRALKSSACWVG
EEPVALPSRLTLPDGNTLPFPISFAACREAGEALLFHQPHISAPVAVHYAYQKSLMDFPF
LNEWVLFGGASAVKGVREVFRGALSHAVAPLQVPPHHLQAKVPMHAPLSGCVILSQLSSF
KGMCVHAAEYEEEGPHRCIHLKAVDGR*
>TCRU_9813 hypothetical protein, conserved
MGLCRALKFRLIARYELMRARMAMRGMADHELIGRYCGLALIPFTVYICAGTMQGYAKDR
VKDSLSKRGK*
>TCRU_9814 Putative intraflagellar transport protein C3
MLLTSGRVRRRNAAPIQKTIQTKASVVDQLEEALQARDFSKATTMLEFYKTTNQPVGDLS
INPWLAYSAFHMNDVGKAIDVYKELLSLERCDPMHYIHMGCCHFVNGSYKEAEECVLRGP
ECSLQTRLLFHIAQKLYDEEKLLVYHQKLKDTVEDQLSLAAVHYYRGHFQEAIDVYKRIL
LETREYVALNVYVAMCYYKLDYYDVSLEVLNVYLQTHSNSATAINLKACNHYRLYNGKTA
EGELRVLIDLQRSTYNVENDIVKHNLVVFRNGEDALQALPPLINVVPEARLNLVIYQLRH
DQFEEAYELIKDLEPVSTPEYILKGVVNALIGQKLDSEEHLKITREYFNLIGTAQSECDT
IPGRQCMASYFFLLRDFPNVLLYLRSIKPYFLNDDTFLYLYGIACAGTGNFAEAEESLTA
VRSEKIRAEFSYTSWLMRSHIMNNHAKRAWDIYLKMETSAESFNVLQLMANDCYKVCAFY
YAAKAFDVLERLDNAPEYIEGKKGACIGVFQQVFANQEPVDSLFDVVKMLESSVQQHASE
PQVSQQFESILKVMKEWLKESKLKRK*
>TCRU_9815 hypothetical protein, conserved
MIRHGLFDATATLVPSADVLKAMHALYWRGGFLGTCVAVLPRVLVTAGHHFNAVKDDVGD
FTIRQPDMTEAHVEHALKNGANDILVLWVDRELEHIPLRGFLPPIQARVATVWLSTKWPH
ETIVSPGVVVESGLLNCVARGTVSTSGSSGAPVIDHFGDHVVGMHLTSNTRDGSRVSGFI

PARKIISVLAEMGVSCRAL*
>TCRU_9816 mitochondrial carrier protein
MSSADIPAIYGVREDVGVPFYISSSELVAGSVAGFVEHFAMFPFDTIKTRIQSGSSPNIT
SALRQVFRSEPLTHLYRGVFPILVSAVPSHGAYFGSYESAKRVFGEESNASILISSSCAA
AAHDTIATPFDVVKQRMQMDNGGRFTSSLRCARYVFEENGLRVFFVSLPTTILMNVPHVA
TYWTVYEGFLAFLGGGRRDKENELAVEYVAAALLAGTMASVVSSPLDVAKTHLQLGNESR
FLAVLRNIVLNRGVRGFFAGVSARIIHTASSGALMMITYEMTKKAMERW*
>TCRU_9817 hypothetical protein, conserved
MTGSQALRRILYVDAEDGSVARRGYHFGGAYEPLLYSTMLEQPAGLQPRSGFRVACACLA
GCFFGCLTMKARNMERWWLGLFFMCGMYYNAVKAQKVNNGLVGHQCGFFAAGMGVLGCGC
RLAVHAGSARMNRRLLFLFASLMWYEVGRYHMWAEHVSEFRREITPERSYDLLAEFVPQE
IETEFLPYRSVSSE*
>TCRU_9818 inosine-adenosine-guanosine-nucleosidehydrolase
MPKAVILDQDGNHDDIISLALLLAWPEKVRVIGCICTDADCFVADAFNITGKLMCLLNKR
ANRPLFPIGISSFHGVNPFPMEWRCSAKNMDDLPSLNIPEHTEMWEKLKPEYEKLVGEEL
LADLVMNSPEKVTICVTGPLSNVAWCIEKYGRRFTDKVEECVIMGGAVDVGGNVFLPGTD
GTAEWNIYWDPPAAKTVLECPHIRNVLFSLNSTNTVPVCSSLVKRFGAQNEYLLSQFVGS
TWAMCTHHVLLRPGDGYYAWDSLTAAYVIDNNLADLEPMALEVEINKTKDEGRTFRSTQG
RTCTYVAKNTNAELFYDMVLSSMRIC*
>TCRU_9819 ribonuclease inhibitor- like protein
MSEVTNTTEISQRDVLFTESSGADGVYEVAKYGGEVESYLYRYKTKGRRSFLQDQTTAST
FLPRILPRGFPYVANFISFEELVKRGTIQSCSQEEVDFSVKDLQLLYESKCMDQDLLPSW
EREMRFMELISANCRGKFFCLKESGFGPMCAEAIAHILSNNRKYTILDLSGNRLRDEGAC
SIAKLIRINRTIVHVGLRSNDIGHIGGVALARALLENNTVVSLDLGAHSGINGNHIATEG
AEAIGVMLRANKVLSHLNLSSNGLGVSGVSFIVGGLDGNCSVKHLDISVNNLGYAGIKAL
APVLETTCITHLSLQRNSMGDNGGMVLFKAIAGAIEDGEDKLEYLNLEVNELGEKTAKAM
QRVLSSSTALKTLRLSYNSFGGASKYIMEGLAENKYLRSLFLSFCEIREADGAAIGAALT
ANSTLQHLDLSNNKLKDAGSKCIAEAMKTNEGLISLNLSCNKIADGGGKAIALFLTSNRT
LRELNLRRNCMSNATGELLDDQLRGNMTLEKMNVGFNDFRYKSLIGHRTTLARNAEKNKS
LIVPKLKAEIEGLSFKERDLSQAEDEIEMERRIIKDRSEQLLRRNEEARVASEKARREIA
DLEKNLSAVRVRFESAEEVLLRTEERVSNEMAEISGRKANMEARVQQERDKVDRLQREMD
RVRRQLKQLEEAEASRLKPLFLEFSIAEADRDREAKECQYEADKLAALELQRKELEKKLG
LSLPVAGGVSAPTAKKRK*
>TCRU_9820 hypothetical protein, conserved
MPKALRGKIETCAKKYAKLEEEQSRDGISPFFLPCQLRCSIETRVGRTLFTLWCRMMESY
RLDATAAYPSDTESRMSFIVADKHTPAAKENTTLFDLFSDESEQFQGVFGSSHMSIEAMI
FYLHYVFADVDAAAWVIAFCIIDELQLRHSIEKYMERLCNSSRGIFFWLHLGNCWRILFV
AFSLALKWHVDYKITLKYMLDVLPSSSHDSFSLHGICAQTEWRMFHALDYDVSVRPDQLL
QLLEEFLTLDERECIISSITHETALGRL*
>TCRU_9821 hypothetical protein, conserved
MSSREELVRERLLAELSTLRERHDALRAQVGKLQGQRGLPDDSPVRRGKKNNTPLGQADR
DAIEAFFNSSEDDFTKEFNEGQGRLQRTELLDRLTMPSRGG*
>TCRU_9822 eukaryotic initiation factor 2a, putative
MASHGPVKDIERVDYSTKCCCRTTDEAYYQAPKQYFVRHPTLSRRKLTLTEPFNVPFDAS
TFEKVLIELEKASILSAAAAVTVDTEQSGGDNTQKPQWMKDLDKRQQRFLAACLGVTTWD
GRDVCFYEEKLPKENDVVWVKVIQVNDTSAVVQLLEYGNHEGIIPYTEITRIRIRAIGKV
IKVGRNEAAQVIRIDKEKGYIDLSKKQVTLKEAKECEARFLKGNEVRSIVCHVADECGIP
AAQAMEMIAYPLYRRQPGKHAWDWLHELNRNRDVEGILGPLHLPEKAQKLLLATLEHTVR
NDTATIHADIEMTCFQCDGVNALREVLLLGRRFKADQEPQIPISVTIVGPPRYRLRAKTE
EREEGMRRMRETIETMAIEIAKRGGILRVVHGPYALGEEEQLKDEPNDDQDDDDDETD*
>TCRU_9823 hypothetical protein, conserved
MDGVRAVADGRRRWGRHRYAVAAADGPFENDSTPESSLQGQIGSGAGVTGGQRLEPSLGS
DTGISDKATAEEETLTRPPEAPELVKNRTEEIINDQEKEKEKKKSAEEGNEDEVNDNGED
DNASTESPGDDYDEEEEDLEAGTNKKEGRDGDVVGDNSLDDHAIVQLAAPVDVERQERSL

TLNNGRSGGKGGAGETRVPEGAGLQGAEKESAKLTHETGADLMETEGLKEGADQTDAGKQ
QAIDEAKSNEAAPPATREEMKKEALKEAKKATANEDVIRKETTEKGKNGAERGNGESSDK
AGKEEKENEERKVEEANNEPQDGSETANTDVALTVGEAAPQAPVTATVAQANDTGTPGDS
DGSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>TCRU_9824 Retrotransposon hot spot protein, putative
MSGRPETVHGGNGEGPAPTVPQGNGRRRARPVLEGGTDQLAATRRRMEEARQPQWTLDSR
VEDVLLEATARSTNMKLNDFLWQNLGGRGVVDTNRNVLLREFLKDPTRYIRDEGVLNEIH
ASSHYKRIRNDLRNKVVFDEDVRKLEENGVNTLIDWLEAAAGVKAVVHGITKVSLDPFLE
DVRNSMKMSASNKLEGFYESVYNARWHHVEEVPGGEGTGMEVKEGKPPQSWTYNAVGETL
ERITVWRNPVQRVPG*
>TCRU_9825 hypothetical protein, conserved
MDAAVSKLIANALLYSDGVLHLVGARHNEEKSSLFPVPLTEELQMTTSILRNWADVDASF
SASPVSTVGLVEYLSNAGTANTWIDECRCVIATVTNGKNVTNGPEFTGQCYP*
>TCRU_9826 hypothetical protein, conserved
MESKATEQPSGDATQGQHSHDTTTEDSTKNAATGSPVEPKTSSTSTSDSGHHVQNKADED
DAQSHEEQHDSLDTGNTNVVPPLSETAPQTAETAATARINVTTTPGDSDDSTAVSHTTSP
LLLLVVACAAAAVVVAA*
>TCRU_9827 hypothetical protein, conserved
MCRHIVDKRTLSAADWAGGRQSAARWSERSCGAHVWKRSRRRRRRAGHRSEGGTATPTQR
LLVIRMLRAGLSKSGQESHRAVPPLGHDVRVNTRSRVLATPTSACHAVCAFLFLLHFLLA
PSPDCGEEAHVPGIDAVLREGSRHDGISVRCQVAWDSAVPWGNVESTARPRSASESGIMQ
ISSATSSCTASEPRRSASIAERESVATGTRVGDRDAAARRVTGNCLWPCSVTGHSARQEH
ARLPAAAR*
>TCRU_9828 hypothetical protein, conserved
MAMMMTGRVLLLCALCVLWCAAGGRCDEEERAALGSDGGPPPGSAEPGTPRKETQELKDG
APGVIETASPPSLKPTGEDKDDDDDDDDDDEETEAEGESIEGQSNKGGTVLPDTHSGER
NLSGSGQETGQPIVSAEEIPPSGRQESNANPLQTEVEEKKDSGKNPPAVENPLTTVNGEN
TLPGDIAGVTPPPPPEDGVDSRKQDGKDTTSVGEKNIPPPETTATPQSHRDEGSEGTGED
TKATTVTANTTDTTSTKQ*
>TCRU_9829 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MQGDTPPQTPVDTPDKADTNAPIATDVAQVDPADKTEVSASSGEDGETVGGTDVQGELHE
EPGEVKAAALSNSLGNLSQGNNSDAGTVRGSGLLPSLLLLLELWVFAAL*
>TCRU_9830 hypothetical protein, conserved
MAKELERRGGATLDEIERALEAKKRESSALQADRESRNWDHEHTLEKIRTRKQDEESASE
RLRQAMQQPEQGLSLRQSAICTREQQLEMVQLDGVRGREAIMRERHSIEAVRRTVREEWC
RQRRQWIHQIKEVNAKFPEPVRPLAEERKKNCEQATAKEDAAERALVADIKTIEEYLPKL
ISLEDIPVNPEETDIIRRQFDEVFAQEKQTYLARLEEEKSRKERLERGLEVYRQRMLDDY
VAKKNEKLHDVEATERHLSSVVDQVLN*
>TCRU_9831 hypothetical protein, conserved
MVARIRVSLAGDVRAAMDTIVKNYEKYFFPVLCERQPTPELEAMPSYLPDTVVLQLHRDD
GEAEFAHYMDANSLTFVALGDAERPALCGIDAAAQLHHEGAQRALVSAAGIVSGICRRRL
RVPFGMSELSELLRRAYNTEKGNPNNSLNGSTETALLAHAFLDAVWAEESFHCLSTTRRV
GNILGSTGIGSATRDLAVDKWRLDQDVMELRDELMIARTVYDHRHCGYESNRPFRTWRMK
G*
>TCRU_9832 Protein of unknown function (DUF423), putative
MIVVGVLGFIAVAAGGIGEHVLGPKMTPELQKAWGLAVQFNLLHATALLAVFTALKGVDP
NGSAARRLNRAFHLLLLGTILFAGSIYAMGFGVPGKVIGRLTPVGGVTLMLGWLTVALAG
F*
>TCRU_9833 hypothetical protein, conserved
MATLSVARKDDIADPRQFGISTDDTAIYLEDSVDEPTARCISSAPSVVAILSPQRLPANG
GHAVDITEYDSNSIGKGFSAKSDRGPPLSDLTNSGTTRLSFSKSPTPRRSLSLVPHRYAS
SRTLSSSEQRQSHHHHGHHHHSYHGGTVSVERCVDAAHHEERMVPLAEYERLQRERNRYE
KMYEHQKALYEDMAQKQTETYQELQKKIIDVVALSTRNEENKRFIRQLKRDMADNRTRVI

DIQNRALEETKQEKTAREQYQRQLQEYEEKYALLIERQETKLSSLGSLLKDVTCMRGECD
RIQVSQLDSLLKAAYSKNTALFGDLLRQGRQIDLLFENKASLEKQLEQLRREKREVEAKW
AEERRRMAAETERYSVQLTEQQRSILELRQMLIRTLGSETLAQGDERDVDDTNENDSSSY
SSGCSSRDLEENEEEEESEGEDDDDSDNLKENLDATVALPPALPDTDAKKDSPRPPLPHV
ERPLERRATDLATLSAQIQAKLRSLPGGQV*
>TCRU_9834 Ras family, putative
MEETLHCKVILLGDGKVGKTCLQYSFANGLEYLAGYREYQKTAIENYELLLPINDSNEGV
GGSCIVRLGLWDTAGQEEFDELRRMCYTSTVAPVAQAGDGNASGAAGNPKPPSSPSACDV
SVFILCFAWDDPHSLTNVQMRWYREIRRVEQDLAFLRNGSHYRPFNVLLCGTKFDLRVDA
DQRGITEGMVTREQAYTVQKSIKADALVTCSSKTGFGVRDVFHTAMLLWLQRQPQYAREL
TPNFLEALPIDGDCDNDNGVVDTSNKQSIERQSCQLF*
>TCRU_9835 cytochrome c oxidase assembly factor, putative
MRRALGCLPGHVFRRPLMVASMKCTFRPFRSQAAVAVDAEQEEIEKDKAALRKYSMLAAL
AVLSAGTLWYGSRQAKKRYFGSVGSARVNVETRGRPALGGPFVLVKTDGEPVTQAEFLGS
WTFFYFGFTHCPEICPVELNRMSKVVDAVRARRPKDRILPLFVSCDPRRDSLEAIAEYIS
AFHPDFVGLVGTPKQVNDACKSYRIYYSLPSAEAAETNDYLIDHSIAIFLFDPKGRFVDF
FGNRYDESEITERVLHYMEQLERDPEWTNW*
>TCRU_9836 hypothetical protein, conserved
MNPAEGCGAQAVYPAQVGFGVGALQCEERKATRLGCNLGEEKTVRQLLPGTTVMPGTAKP
VAGHHSPLRPEQSRSPSAKTAEQSGACRPLRTPDPRQAPNMTLNPAPVEARRNDVKSRRE
FRLRIASKKRPEVHGITANDDESLLRTPKEERGSCKNEHDLRRGCSDETDDAGPVPTTSS
FHDHQRSSSSRTVGSDEGIPQYQLPSVEERLRAIREERSQRLEKMQENLAREKAGTVAPR
PKTLKRVNQGRFKAIVGRPASTASGATASLLIRDRSVDHPQMESPKMKQESLIGCDVLSA
PCLTRVSPVVAQRTEEEPITPLEIEKDDHMA*
>TCRU_9837 hypothetical protein, conserved
MALMGRRRFISPFTRVKARWLGIGDAELLARYGERGIFRTIWMEWRGTLVCLACSAVVII
NHLQSNNANEILDNIELNRQRYYKRDFTPEYVRNAPQAVYDGPKGYVYRDEASGLMLNAD
HKWVSDLSREERRGRIEAADVTPEMVEAAKKLLRSSQYE*
>TCRU_9838 fructose-1,6-bisphosphatase
MEPRVNIPATLVQFLMHSQPLSSRGEFTLLMTAIQTAVKVIEKHIRSAGMQGLFGYLSDH
SSNATGDTQARLDVIANNAFKAYLISSSSVSFLGSEEEESLVLVEGERQGHYIVFFDPLD
GSSNIDANISVGSIWGIWRVSDEKKITTMEEATEVLKKLSGKCLVSAGYAMYGTATNLVL
TTGHGVDGFTLDPTIGEFIHTHPHITLPASRAIYSVNEGNFCNWEPWFQKYMNHVKAGPK
LYTARYIGSMVADVHRTLLYGGIFCYPSDLKRPEGKIRLLYEAAPLAMLVEQAGGKASTG
KGRVLDVVPKKPHQRVAVYMGSREEVNLCLSFQKSEQKRSTSKL*
>TCRU_9839 KRI1-like family/KRI1-like family C-terminal, putative
MVKKDLFANSSSSNDDDDQEDEELAQQMVTAAMRERRRDPHAYAPFSGKKKMSFVGTAPQ
KARSDSESTDSSGSGDGDTWKEEQRPMFQADMESMRKIKKTKRNGINNTTADGDDGGIRI
NQQYAAKYEEVKRRKEIQQLTEKYGKRLRLNGGEEDEDEEDEEDDEAVLLTEEKELAFAR
AFLAIRQSAVKQAGKQKHGDDEKNEIDASSTHGDGNRNAEDGTDDPLGPQNVFFPPTEEQ
IRENTEIFTRSIAKKRQQRKKFTLADEYRRGVVTGVETHASGHESNDDDEGRHQPQGNRR
IQPRTAKERALRESFLKSVAESTETFDVQLVDAAMQTGEREAEHTNSSKARRLLQGAFSI
READKSDPANEDPDEAFLREFFVEELWKPENNKKRKQKVLNRGNYENGSHAEAEVEAEEE
EEEEEEEGNNYAALAELAQAEEDERFYAEAELWERAYQDRAYRHQEEEADHVQTFPRAIG
EHAAGIMRKSVKSSRKDARMRRLERIKELREQQVAELRRLKTLKRQEIESQRALIASVAG
IRGNQGSDICNKKEKKKLRGNEDQDEEAAMARLRELWSEKDLEEEFDPQKFDKKMAQIFD
DAYYDENNVDEEEMAFFEEGEEEVGKMKDGDDDDDGRGKDDAGGERSGEEEEEEEEAEPE
WYKAKSLEEAVAMTRKKTLNGKPNKHDGIHVVDDALALLYPSVSLQAAETASFSGRREHI
EHMIRENKKKKGEKGHEADGKKEETLRQLREDLERKEKEYWQLHHDSTLDQGAIKTRFKY
RQVAPEDFTLTVEEILSRDDRQLNMLVPMSCYAAYLQEDANRRDRLKIERRRQRGFREVD
PTRSSRRYGDVSKTALVDVNMTEEEGEKWSKKVRGGLRRLRESVTLEEGADMTGVDGSGR
GKGATTSQKAPPPQQQQQQGRTHHSKKARYEREEGGGQTRQYLHYQQQQQQQHTQEREG
MRRGGGRGRATKGGGALHIARGNGGPVRMRERN*
>TCRU_9840 hypothetical protein, conserved

MHYYDVMHPINVAWLMYDVVCVTVRSFSPETLVRKRVKRAPKEGREKEQQQQQQRGRRLH
RSSQPGSRTGSANTTLNVSAYTSGELPPPVPNRNAMDVSRSHRHRSRSGDHSERGKETDD
KKRSSTWRDIDVTRQTVLLTHVLRATPITVLRFFCQVQTDAETLPLLGFRDLSDSARRLL
QLSAGAVFAPEVVIPFLTARFLLNVAQHYLMERVFFETNLVVRNLRSRRAWRKALGWTLS
LSAHTMTDPIAFSVLTPILLFRVRDLSPVTGPLRYSPAGISKGIAVGFAGVVLEMLVVPA
ASQLCQRAFVRIVDATEYLLLRRYARRAFASSGGAKEEIASNMNSEDERGDLTGSFAGSL
NSSRVSNREPAAKTRKEEGAAARRPHDASGKHSHDDLSKVESGSRKLDEHKSEERRRRRR
EEAEDRKKVDAEHRVILRAIIYRVCSALISQCLVQHPLTVFAHMLYGRAVLNATGLLTLY
DDVPGVTLTWNACLEFLRRSVLFDVGAEQSSGVPAVEILRSIGGFIGYEFGMVRSSIRCF
STRDVAIRDLITRAEANRKNRAVSGGDSGIGESALESVELMLLTIASLSPLFTAVQFTAM
EKLLGFYMDVWVRLRGE*
>TCRU_9841 hypothetical protein, conserved
MSGWKRGPYPVESRGGGGKWASHRNYSRRLSTHEDYEDDDKRRSHHYYHRSTGSGYIGGG
IGGAVKRPGSRHGRRRERSYDLREEDDDVDYEDVDSDESASNDFEENSDYYDHHRRRKRQ
RRESPYRRHRHRRRSSSSSRRRDSHRPHRQQEKCQQGDDELHGTGRRRRRYEEDYSKSSP
ATEVERRQKQLLSALDRQLATYQGRFRGEGDDNKDSNSKKGYQEGQEEGCSGSGRTSLPS
SRVVLYGVDLGVQQCHLNSMLEQLVGRRPLSVFRPAAALRQSLCDTASSGVGSLPEVPPL
GFGSDRSLHLGLHDVDGAGGVVVMELPRDGDTVAAAVAALNGAYVNGRIIGAVVHS*
>TCRU_9842 hypothetical protein
MHDAALEKVGEGLSRNTALHTFVASGNAFTASGIAAFARLIQQNVTLKNLDLSTEALYHD
EAVYADTHRLLSGVGRLDSVQL*
>TCRU_9843 FERM N-terminal domain/FERM central domain containing protein, putative
MTDATCPQWLSQAEYLRCRTDPYRALDAAQRRVNDIRRSILALRSSIKALEVHPVVQLGR
AARHFEKLRAEHFALDDAHSEKLQQRAALVRIADTLREEKRALLGEINVARRGVMVQRVE
CDDISAACRRHEREQKARLALQEVQEVQLAALIEQERDCSERLAAARAEFDALSSVAEQH
NQRIRSLTTFHEHLIGTRAEQERAAAALRNDVTQQEAELAEVLAGLWDYKTEVSTRVVAL
QRLAQERQDELERVRRLSEHEVDTLAAHNKALGDALKKTSESLLRVRTESRAFKDTTRHA
IADGQLEVQKYMGVVELVEEQNLGLRSAIGRAEEVLRQSAHHAAEKNTINNKSLIEQANL
VSKLHMEVQSTLEEVRLAEAQLCSFCREQPSAELPSLQQNKEGAAPRSGVNVDTGLPSPR
GSVAETSDKFAAAHGVVGTRTDELQEVSRLREALNALNLQLLRERGEREAERQLEEDDRL
RSAADAEVTHRAEEERRRLSQQDAEKKGAGEAALTYTVQFVDGTKRRVDAFPSDTVAVMI
SRVALRAGIVQWRMFYLAELVDEGTVLGSVHRYLSRSAALEDEGVTPQTVLLFEFKHYKR
PLHWDDAVAQELFFRQLQQHIVREYYPVSEAVAVQLASYELQAVFGDFTAQKSLLYFDRV
GLEAYLPISVSAHEYDYWQQRLATNHRRRAGLTATQARCGYIDVVSTTPWWGMTFFDVRD
RDNCPFIAGVAEDGFYVFSASKQECLDAIPFPDLVGWERCPAGVVIRRRGTHKMTLYATS
QLQAKELVDLLSEYYMLLPQRVRDGMRIDVGDVETVSAGLVSPTVFEFPVVSRPHPAPYG
SRVECMKAAYMSYCAEVDELGQQHVPAAALLRAMDRAVDDGTALDALDLAMADPPVDDRH
FAVLAEILTFTLREYEPPEKHEGWKENIAVTAVLLAQPSVERQLLTASSVPTIAKVIALF
PALQTLDLSYIPLDTASEQLGGALARGAKQLRRLVLRGCRIGARALHSILVIFGSQKPNA
LEHLDLEDNFLTHAAIHPLCEVLMDGRAALKELDLAFNRLEPSGIDAIAKALRASPQLQS
LDLSGNPGVEPPSMRAPLLVTKGSGIARLSLRSCKLHFALFGAMNAELMSNGDIVELNLS
ANPIGDGVDTRAAMTAFVFLGDPRSACRLEVLCMEDCGLMEGSLGDALGGAMASNRTVQQ
LFLRSNGLARKTGFLPPLLTEAVGTHSVLCVLDLSDNGISHAGCMRLFAALVRSNSMCKL
YLDGNHLGAAEERQATPSLLSFLRTVSH*
>TCRU_9844 Cupin superfamily protein/Cupin-like domain containing protein, putative
MSTRRKRTRVERDAPFGRGLLGERNDTVFQWLLGKTQKEFFRHYFEKKPLHFSHGAATHF
TEAQDGLPAVKWSTELMLQLAAEKSLSYTTDINIVRFDAVQKKRVPFRSEGIVTEKEMKH
SMRKGWSVRFLRPHEYIVENSAVLAMLEEAFACSCGLNSYWTPANSQGFAPHYDDVDVFL
LQLEGEKEWRLYDPPERVDVLSRHSSEDYNPEELPKPTQIFRLVPGDVLYMPRGTVHQGR
TYNHAHSLHVTFSANQMNTWADLMKHAVTHVVEKLAANYIHWRRSLPRSLLKRLGAIYHP
TFRKESGLALLTEKRKKRRRLLQLSFRQMAAEVFHHLSSEKFIDECCDVYARSTLAKQQP
LPRSVVEGTRSRVTLSLSSTVRLAASHCARLVLSEEGEAHVYHCCGNSPVCFGAPEGLLR

FEVDFAPAIATILAAPACGVRVSDLPFPSFDNSDDILLNQLTLAEALCDAGILAVL*
>TCRU_9845 ATP-dependent RNA helicase, putative
MSKKVGAQIKRFLQENATIPENKTSEEKWSSSDGGNVLSWLAQRNPQQPSRGAIDYLSKA
RQPEKPQAGAQSSLPKPRSQQQREQQQPQTHEQLSTGSAEEPAHTLSEKLLGAQVVQQVK
VGDRVIVSGGTFPMEGLHEQQQKRQQQQQQQSTTAAKTYRGRGYRESKEERLKRRFEKMA
KEAQKRHEEALRTDPEYKKNYQTFQELQAAQQEAQASFLERYARQEHLNLNGTVSERIDI
AVILDLIEQHDVIFICTDTGSGKSTLVPKALLELSQNTRVVSTQPRRTATISIASRVAAI
RRENVGEDVGYWIRGEKRGDDQTRLWYMTSYTLLLHLLNNPLNPPFTHIVLDEFHERQPD
IEVTVALLRLCLLKRTANFKLILMSATLNTADWEEYFTGLKVATYKQSEPEHPIHDYFME
DVCALIGTGYDEPLNFLDRSVDFSLLEKHMAIAQTLVAYLNAYADPQHAILVFLPGRAQV
EQFQLWLETNMPRPVDIVPWHSSVDLSVIEDAIGRRLPYSQKIYLATDIAEVSITLPDVV
FVIDLVLVKRPKINKDDPATVLHPPLMMQWISKGSVAQRRGRIGRVQQGFYFCLLPSSIV
ASLPDHANPPIENSRVDELSLHCLQLVCNPVAIFSICHGQPLVETITVSMDTLSHLGCII
NKKDPLAEGERIAEIHSNNQWGPLVLEEAKNVVLAEIDQYEYTFIGRILQLIPVSPQPGM
LVVYGILTGLESLMILAAAVTSSLSPFAPNPQEHSRRRRYAVVQAMEETENVMRDMCCGL
RSDIVAVMKAVLRFRICVSESAGDAVHVRQWCLDHHLSHDKLKSILDLEQHIKYELANFI
SFRDVADAQELEMQLEKVAPIVVVMSNVAFASQSLEVTAEGNTFTNSKETAVGVFTEITA
VPDIHSPSCLRWQEGDIVVPVQLSLLGNRMLASFTTAIASHKQFWLSLLLLTHRIQYAAF
ADDEGAFYVFSVRYHNIQRYVETDAETGYAVLHFRQLLSASCQTLRLQHEHQDMYDDEFA
VLLQRYGLKPLLEAQRDVITSMAAFLNSTEHLTVDEVEHDEDDLDEVSMITLALPRTKED
*
>TCRU_9846 Concanavalin A-like lectin/glucanases superfamily,
putative
MDNAREKEVASTLLYSDGKLHLLQRRASGEGSAISLSRLTEELKEIESVLSTWSQKDVFF
SSLSIPTAGLVAVLSNASASDDTWNDEYLCLNATVTNATKVKDGFQLTEPDSGVMWPVNT
RDDNVRHVSLSHNFTLVASVIIEEAPSENTPLLTAVLVDTWTPYIMRLSYTADNKWETIF
KDDKKPATESRPWEPKKEHQVALMLQGNKASVYVDGESLWKEETLLTDGTPLEPFGFCFG
ACDFGDDDDGDGDEEEEASPEKIGKKTRVTVKNVFLYNRPLNSTEMRAIKDRIPVSTRAP
EPQVKIVPKPVAPAASAVPGHGKYQQHRGGQLWGEPPIPNMRQRNA*
>TCRU_9847 mannosyl-oligosaccharide 1,2-alpha-mannosidase IB,
putative
MTALSGLTGDDRYERAARRASEALFAARSPQTGLMGNHIDIMTGRWHLFDSSVGGWIDSA
IEYFIKSHVMSGDIGDWERFERTVRDVNRYLRKCGMLTTVDMRSGRPFSFAHQSLASFFP
GNLILGGHLAEATESNWPIHSIFKHFGALPEEFSLGSGGPHGGYPQRPEHVESVYMLYRA
THDPAYLVMGKELALAINLRMRTPYGFATLRKVDLPHGDEQHSDTMESFMLAETLKYLYL
LFDECNAVHVQGKLRGSIPSYCAAVESGSSVGSHVGWVFNTEAHLLPNTAEWWGPVSAES
AREEEEVSGDTLRQRRLDVIDSLIDDLHELQGGGNGRGGGNTAPPRFYCANHALSDVERI
SKSIFR*
>TCRU_9848 hypothetical protein, conserved
MNQPRDREAVPADRDVRARWKHTHRAEQRVTESVADDDNVQQPHSGVRVAQQQQHGAVPP
RASIKNDVRHVARHRPNQHRQSHAAPAERNVAVAQPRQPAAHRLRNLGVHHVADALTNWR
RWRCGWHWRR*
>TCRU_9849 mitochondrial DNA polymerase I protein C
MFFLHCPSTEPNDELKYSVAIDDVVPVTDEPEMLTVMQLKEKIAKYRPLRALQSFKKHGK
KSYDLRNLLILTNCTHDKLSSLVDTGIVQTIAETVLGTNGADESPLERVCFCDLQRALPP
PPQGADSFESDFLGLVDVAENAGLSARGNWEALAREFVSVGGFDGALKALVSHCASLLGT
SRDPFRNTHPLPLSLGAELRGLHGQERASTRGLLWIVTPEELHPILHRSLRGRNASSGAD
AIERITVLLSSDKQIDLSFFKALQQLRFTEKKMQLFEEGALFRAVLPECKDRVHGELCHT
VTATGRLSSQSPNLQNIPREEDLRRLIVSRFGRREGRMIEADYSQLEVVVLAALSRDTRM
LQELHDKVDFHCLRVSLMTKEPYENVVRKAKQERDPHYIQLRQQAKTFSFQRQYGAGIAT
IATTTGLTEHEVERLISAEEQHYKDLSRYYRLVMDCVEAGADRLLRLRTLDAATWSPAMR
RMILLTEPLHYFVVPTGSKFDFAKDKKSIPRLKNYPVQGLAGEIVQIMCGKIVRRFYEKR
NYDGRAFLVNTVHDCVWIDAHSSVADEVMHDVSEIMSSTSKVMSSLWPDVKLDVPFNADV
HIGPSLGEFSK*

>TCRU_9850 glutathione synthetase, putative
MELLGDAEQLVAKCMMLGLTIQMAGHEDATTHLAVTLQPTTMRRGEFDVLCRRQLLWNEA
VNNTARNFQFLLDALRETAASDTEFTGKLVNILRDVYLGTSPYQPLMLGIFRTDYMHDGA
AAAAAASTVAETMEEDAAAWKNVEINTISSSFAGLSPLVSDFHRQIAMYQRALGGGSANN
TADDHQNNEAMPNLDNAGVLERSTAGKIVPEALAAAVAAWSSQQNFEAFRDAYGKEQQHC
RLLDPIVLFIIQENERNTADQFALIFELLESHGIPSLRRTLRELQVSMKLHPVPNGPPLA
IVDGRYPVAVAYFRSTYVLADFPTKASWDTRLAVEQSSAIKCPSIPYHLLTFKKLQQLFC
DVGNVLTPIAFCGDAVRALQLQTHFVPQYSLNPAEVGEDAVQRVIDDALQHPARYVLKPQ
LEGGGNLIAGQAMQEVLRKKELTDPLLYNKVRREYILMSRIEFPVRSGAFLVNGKVVQLE
KNICSELGIYGVILSDAGGCLLQNACAGYVVRSKPADVDDGGVMAGVAALDSLALV*
>TCRU_9851 hypothetical protein, conserved
MMLSTEEIATITLKSPFVHEYGDTPYFRRCINEFSLQFFVRYRTSRDDPSQHRWSRLLEV
VDRHTHGTDAASTSTATKVTPLQWKEKLFFIALRVEGEEKCVELPRLSSKLPTVEEVMEY
CARRAESQLQEGGHGDERVDVDSVKGVTARAQLPTVKEIAEMKAFRQNQIVNHHWTPDEV
EAMREQNERMGRVGACSAPIRLTVTSLHNMRLETELGIASSRHMTGHTATAMERRSSTQL
SLHGHANSPATSQSPIRSQSLRGSGASLADLTASPLPATPVEPSSLLSQEVLQRWEESKR
DAESFYAYVSDEHRSAYMKKIAQITLKNYERNKRDRLRGIANEKRLDRKGNLLESGGLWI
VDDQVRAQLARMYQIEQDGETVTAAGGGDAKKNAAEAPSDDTTTPETAPPPLSEEDAMLQ
QFVAQRKAQELSFASVPEEFMSISDENRVDDKTEEVRRPPSSARSPELLLMDTSSRVLVS
QLLHKTASSMLKRPTLSCASRASSQTSMAILGGKPPKKVMRHA*
>TCRU_9852 hypothetical protein, conserved
MENQRLASSILQPLASGPKTTTSTASVTRQKRGRASYLYDRNGKRLRGLKGEAAKLMQDH
RFFSSEEEIHHLEQALAVGQRSLETSMEAGDSGVGGVGTHKLPTLPDMFGVISPTATGGG
TVETMNGENVAHGSLVPPTHRWSLVQQRHVTIGSASQRTDGPDAPSLELRCISTSGYRWA
RADALLVENALMSAMLTEKEEGGEGEGEKDGGDNGGDWTCGQGNLPGAWLTHLLSVPPEV
GLSVLHSSTGPSPFAFLTVSPEEYATLGLGNDVYQPAVLPDEGNDPDTVKWRFDYASTCK
LLELYERFGNFVVVADRWRYSNSREKGAFQSAEGVGATSLETNVPTPPVEVLMERYKLVS
EAVLRYRLRLLQEVLKDEDGRDEATAGPSSSCKSKPPTSGLQVKPAEERALPSAHPLTSL
MEKHPVLVAQRTRQEWLTQRYRELRQSNGTENAPHEEKEKEDELDETDMLSRHRADVLKR
FLDLPLPSQEQLTQAACKRNEVESDVSLFVPSFLPPPASPFWYDGLLEQSRRRRLREILM
REAEMNVPYFRALLAERRVSSQATVLFEKLRVLTRDTTTAVQEDEKTCAAEFDESAEKRG
GNLGRQGLCKKRKKKKQQQLADAVGEDSYQGIQEEVSRIHLQCERLRLCVQAGWFLPPPE
GDVGGKSTGSGAAANRALSNFSEALLLSLPPSVPRLHLGVEHELEKHLWEDHRALCDDDA
EVQQLLCEARVLYTQNLVLRRFSGRCGVLEASLKKLASEAAAMEMY*
>TCRU_9853 hypothetical protein, conserved
MNVDRVTTNCDDRSRTPSRTSAEPYRDSLWPEVVGTYSEPLTVARSVESARSTFELAGSL
CCSTIVPSSDVTFSIFTITPGISRAVSSSTPLIRSCAPPSSRQWRSVTFSASANTSIERR
STVTVIGPLKTTASRHSVACPPPIVTDSVNATPLTQPCAPPAFATGTPGGKHAAPAPPRA
HRQEHSEKDVVSAPKQFCVLSQPSHGTTFTEGRPAERYSTALLSNLPSARLHCTDTTPPF
VITGPATSVFPVTAQRATDTTPPLLTVTDESNAAEDLSFRAHTRYSSSQPPSPIFPPLAV
TTGASIRPTTSTKRSTERETVRRFPNANPPPLLLTDAFVTENTDLSSKLRPDKGGTYIAC
VREPCNASSDTPSSTTMLDFSCTPPATCIAAPPSVDVLKIVLITYSFECNSNVAYSTSGE
AGASLIPRIGVYFTGPVTAIVESQIVTFVCSGSLCANTSEQNSPFRPLTFITRLWPLTGA
LR*
>TCRU_9854 hypothetical protein, conserved
MRVYDAKASPRNNLNGFECNRGTLMKLRHCRLQPASLHDNLARVQDKAIRYSNGLICRNN
GGAMQQNRCIHTKVCLKKYAQGTRCIHNTVHHTYPRPQTKHTVKNNTALVHRGISHTHVY
GVFAVPCYSQARQPALQQCDVDRPRCRPEIAHVDDERRSEMQTHKAQARNTGRGGRHLIH
CATTHAWYLCRGHRKRWSWPKFHRDLRRQARNTVAVSSAFVSTFISSALYRLRSKAFSNP
RALTTTVRRHVHSHGDTTVILQRHSIQIVARNVHRRPHRLWWSRERKVIPHGCATVRARD
RQKVVSKHRPGASGFKLNLIQKKNTLDSKVVVPLHQPAPLVYGQRLHANYGFARTKLVPG
NLQNASPCYCDTVTLPRIAEPFDRPHPPRIVLDDKDGAATHGQFGCNESHHMEVGVHSTV
VHVERTFLVQ*
>TCRU_9855 hypothetical protein, conserved

MALVTLKWFPLMVMFVRGGNAPAGLSTASSKLLRVTTMLSDPTLTFAAPSRTSAAPRSHL
HPSNMTLTASPTIAPTATVNRMKVPLNVTLR*
>TCRU_9856 hypothetical protein
MRVEVLLPSKRPFGLNTTAAASAPPVTGKTLLPDTTRSDLSVLTDPKRPTTLALSYAAFL
LINTQESISSIASSTWKTEITTRPTLRSSNKVDLLFTSRVSRCTNASKTPETKLRSTLNT
ELLCTRTAVKLSSLDTRKAARPPPETWNELSVIAKAEYDCTAMPPFATYTTTESDPPVWK
LLSMRIRAEWPLSTKSLVTTQDG*
>TCRU_9857 Meckel syndrome type 6 protein, putative
MVELNFLPHLKSRRFYKEQLENLERQPCHTEEQKKLKSLLLRLLNLTCELERVYLKEMVS
AWRRIARLRGENPDDCFAPFPPSSVGATPNEESTPFSPSNPTSQRDGVEGIGLRRGFLGL
SEGAVSLLSDGPSELQVQMPTNARLRMYSRYHGEGAVMTPIQEENLLEYTPVIEGVVAPP
HVLVDGGSQVGENGVTSPSPSSPPQVFLPSSTLQNSKSTLFQVLVFFRTNFVVPPHFVGC
TAPRALNSSKLLFLNETFELRTLQEPQEILLHILSVRGGSDGDCVIATVSVFPSLTRAHL
LLPLRAPISFSYRGTTYRKHGGGVLPGLVSLSTTWTTIKGMTVEEIEGLFLRGDADPLDP
QHGPLLATLKAHYMELRGNTTTLPARADVPLPGLSEGATSGMRHRGHRPSTTTRPPHPLE
GANWSKRLELLHRRWLFYMAGVTLQDAVEARLFSQPVPLEEFECYELQSRVEREAQSERR
KLKFRIPSDAQSLGDAEVDLLPKVFILSPLSSKEKLHLWQERLRRLKARRTSSRKLEDHE
LLERHVILPKLRPVKGIHLTPESQLNPRREARPKVDKITRESLVVKQDSRIVVHIMRATT
LPQRSDGTPLEPFVEVGFVCETVVSRSEVGTSPSWFETLNIPFSPPDFDDETLSLIEDDI
VVSVYDKVEIPMASTSLVTGVVSHETHYRTERRLLGKLRLPFFTLYEADQARVEGQFPLS
TPRWVLGYLPDGPDTTAAINPLKLLRGESTHSHPSIQLYIALWPPLRHATSKEMDQSTIS
RLLTQLNVSAQLHYLHGIAMKWRRDALIRIKALSSVNPVAQMREIEPFVFCTTGDLTLVC
RYLIANGGPPPLTTRTVEEAIRFVSLLPFCIDTLTWGDKDVWSTNAEFLRIREGDYEELS
LLLAHFLRFLAPEEATFVVTGRGVVHHHVVMVLHSFGGELRLIDPRAGCVCPVHDPHLTF
FRDVHMVVSHNQLWANVQLSGAPHRMEWNLNDRRFWLPCFDHEDENVRACLPYIAAIQRQ
FLLFSMPDPQKEREIEQQLHKAVRRALVGWRNNRRLAFHHGVVPILQALLRDAEDELCQY
ASVRREAVTMRAREMLNDYFGDELLKDPFQSDQWRGEHRSQAAGGDFRVDVKRPSICIMG
SPVNAAYEPNDTTYQSILQQVFETAVHEVGTNTVSFAIGVYVKGYTSDVYSMWVFLVALY
EVSVSSSY*
>TCRU_9858 Divergent AAA domain containing protein, putative
MRQGCRMHECDVSDVSAAATEEAVANVIAAAANCSDGSDVVLIRLRLLHGPSETHTGWSR
REKDMLLLCLDRSVPRVCPPIDPLQYTQTPPEFLLENGVRVVRLSITPSSRYSSFTTVPH
RVEGSCLRPHSTSADITDNNSASAAGAVEDDEDVANTTRLARRRWRKAAWMTARIFNEGG
WYHAERRYAKVHNETVGSGRNTVNSENILDAAMRLTEKRLLHVDVFGMEFIGVIVALTSR
YAYVAVPFFQDGRSIPHWTLVSRLGIPSLLEEEKKKNSRKRERSDRVVDDSKYFLNEEEL
VSHDARPLLRLPPDHCVRVVLRAHKVYCKHQRSVIDGQALTSVAFEDAAIISCTAVGDKN
NFMESLSTYSDVLQIVQASCARFLRGYGKYTEMPADNAGERLFTALTDTVSVHLKKLRGR
EGQSPVTVSSPQEIPTLVEGTCVEFKAKVERWQDSADDISPGQRRHSTVNLERIRHTVAA
MASTMGGVLLVGVTDDGEVIGHARDALKELRLSGFCPAMVKGTVTVTEMRAVSGDRPTTM
PKDWWKKANPQQQEQQTVEEKTDRVVTVITVKRGPAPFYTTSRCSLPYTRGFASTVPLHV
VVCARRIADLLP*
>TCRU_9859 Snf7, putative
MSFIKDLFHRETPQEAMRKYKRGLDRTIRDIDRERNKLQVQERKIVIDMKKMAKQDQIDS
VRILARDLVRTRKYQQKMYHMRTQIQGVALRIQTMQSTGQMATAMKGVAKAMRGMNNRMN
IPEMQRVMREFEKQNEMMGMKEEMMNDVIDDVMDDDGEEEDETEVEIQKVMDEVGLEFKS
KMGITDSMLPAKQQEDAEDDKELEARLAALKSSMK*
>TCRU_family, putative CBF/Mak.1
MSASTESLLDLHKRWYERPLPLRSCSLKEVANSAVSKDDMDAMFREAQEALDAETAQSQK
DKGRWYNSQFISRGTTADKIASAAVKLSDVDFMFFLDGFNLLFDTARTDTHHYEAALKGL
AVVWPKLLPRRPLKRFVSQFFATLPTDARDRKTVLVYWYIEDYLKRTYAQFLSLAEAMLK
DRLQKRREAWLEVVGKLMCSIAESRHVAMAIIVDKLGDPASSVAHKAYHHLLALLTESST
HQAMLFVELEKIVFMKNCPVNTMKYAANVMNQFVYNKEERKLALKSVQTYLSLFRQLVMN
ASVDLSVTTAILVGLRRAFPYAGTDIAPLEEHLNALFVLANTGSFMQRVATLSLLQLIAQ
GKGATEEFRNRWYRALYNLLLISPKQLSHSTQMAGFFSMLHKALRMDKNEERLAAFAHRL

IQRSLYFKESVVCAILLMVGELFQAHPRLRALVLGTRKKRSTDEAERYDVRHREPQFSQA
TKESLWTLGTLVRHSHPSVVKLAVMLMFQEDVVFDSHPLDELTLPNFLTMFVDAKAQPKK
EEMSTGMSVFSRAVHAPNIPSASDPYFIQASAQQVDVSALFLHRYAVQRQRFVDGLSQVR
STWGDASGEADVALRVKDVDASLFGPSGMLREPKTTASGGANGESTKTERKKLSKKEKRN
KEKPVEFDEEVLSNDSDKNEGHHKDDDDEDGFDFVGSDGDLEWGSNDEAAYDDLDNDDEE
EDYEDDDYDDDNVDDIALGGKKGSDEVDGEDLAEILESNRKGMSKKRQRAEAWLDRATST
SAAPSSQSTPYSRRRHHHT*
>TCRU_9861 proteasome regulatory non-ATP-ase subunit 3
MPLIVPTPPAHPAQSPNQANGELLGRLMKLYRALCVRHDELGQEVILNDILAFLTRTHQH
DMAESVIATCEISLPHRSNNQAARYFYYVGLTRALRLEYVDANQCLQQALRKAPERAFGF
RVAATKLALVVQLLLGEIPPRSDFLQKDMRESLSPYLQLASCVRFGQLSRFMSILQQHKN
IFEHDRTYSLILRVRQHVIKTGLRRICHAYSRISIPDICFKLSMENPADAEYIIAKAIRD
GVIDAVIDHEKGHLISSDTVDVYSTSEPLLALQRRIQFLNVTHNDAKRSMRYTAADPELE
EERRKVDREEMDSALRAALEDEELGGTDFEDGLP*
>TCRU_9862 cyclic nucleotide-binding domain containing protein, putative
MSEVLPNESVQQKNDEEGEKSEQKKESDTPLQPENDEFASEAVLMSFVPPIPVDRLENLE
MSFSRRRSLRNCSISISRNVDTECGISLRSAPTSCRSSKVSSLRTKGSVPEGLERAVAMV
QTYPLMAVEGTAFENQILRHGTGESGVAAFAGRSLTSTSNTEEAESSISDLTEVLGRLRT
GSSAVLFASRLKRACMWNAIIVNVLAHRAWHESFRLQRLRATLELLLLPVLLRKRGEKKS
GKGHFFRPRPRGPCVLCDDEGLKPQGNFIWEHSAFFRKLGNLKFCEEVAEIVVRYRYSAG
DPIVSVGTPAQDAMYILISGNCDAIISSDEPNVPVRRSRLAVGEGFGGLYGGREVFTTLY
RSISQCIVWVIKREEFESTFSQHADEHMKNAYLDALKKHNMEHLLRDYPMPQCMSRVPIY
RRIDGLIEEYAKDFVPIVLTKGDILFEQGDRPGDVYCLVEGHVQREQTGADMRYETGTKQ
IISPNESDNNFSLSTRFVLLGEEPHILPGLLRYRCTVFSRAALFYKIKGERFVDALLDDA
KLFLYVRERLTAQIRQSMRISPDALAKVPLLREMPTLHLNAIANAAEPRVVERCISICDP
AQSVREIYLVVSGDVRDPRNFNRTTTLPMSPPASEDEEAVENTNTKGKKEKNVKIAPPGR
GKGKGTLAVHSPNETLGVQSPHFKDSGTAFGNAETTHFQWHFFHRNSKGEFSSGVIYPDE
QHELTPPLPPNPAKNFICTVGGGWEGLLLEKWPNGWETTNTVELWAIPTLTIRTEFNSLP
KSLQNSILMLARTTQMHALCLPSIVVAKLPPMSSFLPPEKRLTKQGLGIEKSPSQEKSAA
SHPRKYAGSGQSHERSTATGNRHGRAAGDLSGSHASILSGSSAFFSTNDTSGSKRKNLPK
LTSRPPGPDSNAKKSLRRWTRGKDIKKVAETKELAFAGEETPIEAPKPKAGPPPLLFIRK
NASKGVEKPPIITPEMCAIYAGQEPEKGIIQYPQLPENKRMVKVRNFTMPADQKPSWPVV
AGGKKQWFQVVPSFAPLPGTIHNQSYIASVPNLLPNAALMVKRDKGCGEVLASQANYFAF
LAHRKRQHEMGCESPSPPSAAEPKISSSDARSLSPQIMGRPVPGRHVYCV*
>TCRU_9863 hypothetical protein, conserved
MKNWALSENGAKVVEVSHEAAHVASAASNLLVEREDLLWITSDAPQHVTLKLSPHHPTLR
YVGWHVWHDYLTNPKTVEIASGESTEDMMAQLICQAVSGAGTQVWKLPNAIPPKHLFVRV
KILETFGPGPTYMNNVVLFANDPGTRFRAARSTELTLPKNKEGSPARMSVLLKELDEDIR
ALHPIKTVTPNKNMLLYVPQEPTVVFQQEDAEDEETTSPTLRDPTERQGSTAMNRTPSYG
ITQERSETVTPGYAAQAGGSAEVSRGFNDRLCALEQAVASLTQSMNHQREDLTMIKRLLL
QQASERRRELEQRVTASEALSAKQQLQLRSHEKLHRVSRHQVSVDFPEDALRSFVESVLA
PKLQKHAKRTEAQTIAKLDGFLKDVVSEISLAVDDRVRLHLQQASLNNTGYLPYMAPHNF
EDRKMEPMYTPPRLAKRDEDLIHVEYRVPPPAPTTVPPRPVASSAAAPPPVSSVRSRQGR
DIGSAPVSIIRDISMDADLFSSRPVGTPQQ*
>TCRU_9864 hypothetical protein, conserved
MQSRRNSMMSRVCRKYARVPGQHGDGNIPAFYPIAINPGWWGQPFGKVKDSKSQLFFMYG
IFFPFLLYWAFDLSFAQRTRVATVGKRALYSNTFFRQLDLDDPDHAIRYEKLREEVAENK
LEVRWGGSNFLASYLWEPGDPQPDIRRQTPPEHHH*
>TCRU_9865 hypothetical protein, conserved
MPSVNSGYTFEDFLKRLERSPKTHMSPLYHEHRELFLRRPDMFSRAVRSVTWEKGCALID
AAYHSQPIALVTYRALLARMLLHNQYVRRNGSGNPVPWKAALRTYSEAILAHGNAVPTRM
TISALRLLAPQRQWVAAISLLKLSQANGKLTIHMPIDAAGCCATPSLWKTAMALLGHVHT
QSPNLLPECIQSLRPIGTDESTVSTAANALLIDKNGPTPEQKHVLSILNDVVASAPWETA

LSNEMCTSYLTHLVASTTYTTQEKTEALISGTRHFSWEAFIRLVTAQDASILKISGNSTP
QLPKKTEMEKKTRRELEVSPLNSPFFSESLQLLENAPETAVPLIATIIGKLPSAKLAAKF
LSEAASMYRGTIATTALRHSLVAGALLRKCSEESEWRLASSVLLSMSPSPLPCDVATALV
LQMREAKQVSLVVEILQKSFVPAKTMLTREAMEAVLVCVLAHNRAVSMPAFQFTPETLKR
RRIATVHWLSALSWATDLVQDEVEGRILRTESAVSVGSVGHSFPKCIPLQKPLSSRMLSL
LIHICVRAGSPQGALHAMGYARAVDKTELVLSEAIQALLYCMIYNRPYEAEAIVREAEKK
HGKEKAQFLERLLLAIQETNEHELGTTGN*
>TCRU_9866 Domain of unknown function (DUF543), putative
MSTEPVLQPQTSISNEEKWDHCMENFIRKTTLGFACGVLPALLISRSLVARASIVLFCAG
VGSGIAYGEARYLFDHNVLFDRRHLVQIELFTPKK*
>TCRU_9867 DNA-directed RNA polymerase II, putative
MSIPHGMLIYNNDITADSLVDTKGTRKITEEISSKMPNSSLFKLDKEDHTLANLLRMKLH
EDALVHIAGYRVPHPTQHRVELRVQTSSDGSGRPIPSPKDALLKAIDACMQDLQSFEEQL
RWEAQSKGISTE*
>TCRU_9868 diacylglycerol acyltransferase, putative
MATPRASPQNAPRRLRTGRLGTEHTAVLMTNPMSIALMTVWALSCEGALLLNILADVFQS
RAPEFPLVPTITTSVGLNVLCAFLTLLLGRLSFRGFYFYQPFAGGQSFVVMQGFGYGILV
VSSVLLFFYVEQIGTTLAVFRYGTLTVLGCFSALADIILMTSLLFFVPTRYRGGRGTKTS
HVATDDAAVWWHDLSASPNCEIGIVASFCLAILMCSSFAEYYPRIRRMSSVVGAVLLSLG
LFITHVVVGHTYTPGYRLFMPNAGTFRMSLMQAFGWFLAFATLHLEMILYEAGPSAYSSW
HILCGLGSVISLSTLLLFIRLHRFPASTQSEISLVGEYGPMVLTLTSSIHAAVVWGLALV
LSSNVYDQEPQLRQGLVMCQTLSSLLTFALPPCTHLLGRIAFGREYEVWMPFKGPLEFVV
LQSAGWTCFGGAIFFATLQITESLHFRFVIIESSLTALSQGFIHASLHLFDEGRKGGTTR
NNVFTPNRSDESDEVADANSIEYEEAALCEMNRSIVPTVLNGEMLTSILLCSIGLIMRVI
ADVAVGSGSEIDEVMHIPTHSLLKVSTILSILVVPLAHVSMRKRISVWCPFVGCGGYVAM
QSIGWSIYAVNLFIVVANSLHERRQGFLSPIVDEEHLFLEYTMEGLLMTLPLVCIIIGAF
FETQEQTRKKTVQERKKQEVLELFRVLQRAIPDDDELQHAEALLRAIAGPRWMEPPATDG
ARLIREAEETAHARQEAATNIVTILSVASALAFISAAFLAERQPVFTLVFGAAGITVTTI
SCFSVHYVYGTFLHRASGRYSFFMPFSGGPTFVTLQAVGWGFYTISSLLIALSCAEGRGS
AIVFVTTGVCSVSAQYCILNSVPRFDPTPRPMSVLELNAEGIFAVLVLIGSFAFAMVYDV
YAQGRVSGIASSLFPIAVLAVSTCFAVPLGLVSLKRNACDFTTSPFSIFDNPINSGEGDN
EIESMQSGVELSTTSLTAGSTRSSIPDSSPPPHTDTTHLRQPSEVSAESGGGHSPGHLFS
PVGDISSVSSRHPRNSFRDSVYMTCFMAAAASAILASTLIPFALVYIVYCYAYSGMAALS
AASATLRILLFGFGVAVIVPVFAPGRSRGQRKSLFLCFYEASCCYALYSIPTAVVVCSLG
LPFVVKTSGAYAFSVSMVVMSCFSTIPHIHLISMLVNVSLLGYFWHHHFHAFLLRGEGAF
TPWKFVVDTVLTAYWPLYFHRFLGQPRVTGRLNSPRFKRLLRRWMLCAVAEHFSLSVIVD
GKELNRGEKNHAQDDYVNLNNPKNKYFFSFHPHGIFPGTALWVPNTPQWEEIVGKNTENF
LSVHCADVIFAVPMLRDFVLALGCLTVARRGIESSLLQGNSVLVVTGGQAEMLCSKFSDT
EMHFVTHHSGFVRVAMTHRVPLVPILSFSENNLLSNVCFPRMQRYTVSKVGFPFPTVPYG
KFYLPLPNKLPITIVVGRPILPEPGMDCPENPEHVQRYQQRYFKSLEVLFFKYRAKAGYP
NMTLVLHHRNEIHRVSAAAEETKEPTGEQEKERKTKDLE*
>TCRU_9869 hypothetical protein, conserved
MQRPRRTQKNLLAARMPVEKRRRGRPLPMKADDGSPIQPATSHHPHRTADAPPADASSCP
TQSSGRSMELIRQRRSTVVRRNTGSSAAGKAQEGERGDSRNVCPAGVGAGNSSSGAAHNL
LLHARTADERGELCGLFDGNRSGAIDPTAPRQDAAVHVANGLNPAGHGDSGVAKNRGAIG
DEAGAPLDKERDRGTYLQPGRLEAVCCFSTCVDNGESLV*
>TCRU_9870 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MSRHLFYSAVLLLLVVLCGSGAAHTVQTKTAVDPFTGIGWTSSQWEAPTKVNETLFSLRV
PSLVEVNNNVFFVAEALCKEKGESRSRTGIASRHLDLTDDKPKEILTEDTSLVVQFPEGV
ATGTAEAKDTMRPTTVVSGDSVYMLLRNQGVTPLVGKSANARDWGLLLVKGSVSGGNVIT
WNETHAVTFENDEYAAKFLTQLVSGGGSGIKTKDGTLMFPMQATKKENTSLLSMRFDKSE
NKWKLSHQTDVDGCRDPTIVEWGDDRFLMMASCERGYRDVYGSTESGRSWFPYGETLTRV

WGNSHDRKGHGVQNAFIKVTIEDKDVMLVTLPVYPKEDNKQKGRLHLWVTDKSRVYDVGP
ISREDDDAAASSLLMKSGNEKLISLYENKKGDDGSYSLVALSLREQLERIKSVVKTWSAL
DGALKTCRSGSSATVDPRKKGMCAGPVPTKGLVGFLSGNFSDNKWRDEYLCVNATVNNGE
PRVRNGLTFKGPGAGAEWPVGKMGQTAPYYFANNKFTLVATVSIHEAPKEASSPIPLMGV
IMKDNSSTALFGLSYTHEKKWRFTLPNGTYGGVEDDEDDEDYEGAEDDEDDEFAEDYEDY
EYYEHYEYYEGKYNWQPNKTYQVMLQMNTKEWYVYVDRMRVYSGHYNWDLFKDHRVSHIY
FGAENKEGSESSHVTVSNVLLYNRIIYGRGRKMLNASKVSIPNPGEEFLTEKEEETPSSP
EEGKAEQEVGEALPRPQSSVEAPEGSDAAAVSSGIRGSHGKREEETETDGSGELASPPAL
SSVGTSAHSGDDGMGVREGTTLQEEVPPPLGTEDIPKADVERPIYEEEATSPEWATERQT
QETTAPLVENGDGEDVGTASGNASTLPGETKIPSESNATSLSDHGILPEHGHYSELAGMA
LFAESTVHGCVSRVLLLLLLGLWGTAALC*
>TCRU_9871 serine threonine-protein phosphatase PP1, putative
MTSNVVHNLIERLLTVKGSNTQRQILIREEDIRSVLNSVRDVFMSQPMLLEIRAPVRICG
DTHGQYYDLMRIFEKCGFPPYSNYLFLGDYVDRGKHSVETITLLYCYKIVYPENFFLLRG
NHECASINKMYGFFDDVKRRYNIKLFKAFTDVFNTMPVCCVVSEKIICMHGGLSPDMTSL
ATVNEIERPCDVPDKGILCDLLWADPEDEVRGFLESDRGVSYLFGEDIVSDFLDMVDMDL
VVRAHQVMERGYGFFANRQLVTIFSAPNYCGEFDNDAAVMNVDEKLQCSFLIVPANS*
>TCRU_9872 hypothetical protein
MMGVSPEAVLLDFDWTASYVLATDRLSTAAMNRATARTVSMEGGADGADTNPRNSGGGMP
LLQLAMDVARVAPPSEVASISLLVSPVSGGRLRLLATASSEVQGGGEGQPPERMLLPNDR
LTMELDAESLDALIAALRTAVDGMDSLSGC*
>TCRU_9873 Transcription factor Pcc1, putative
MQPAKVRVEEKDQDTLECVLRLPLRAAEPAQIMIQVLRVEPPVPGTSREVQLWADDSTRS
TVYVKIEASQERSLRAAVGALLEQVKLILRTMDAFPVIARHNA*
>TCRU_9874 translation elongation factor 1-beta, putative
MSVKDVNKRSGELEGKLKGKLFLGGTKPSQEDVKLFNELLGAENTSLYRWVKHMASFTEA
ERKAWGAPVKVTATTSASAPAKQAPKKAASAPAKQADEDEDIDLFGEATEEETAALEAKK
KKDADAKKAKKEVIAKSSILFDVKPWDDTVDLQALADKLHAVKRDGLLWGDHKLVPVAFG
VKKLQQLIVIEDDKVSSDDLEELIMSFEDEVQSMDIVAWNKI*
>TCRU_9875 protein phoshatase 1, putative
MSAVVTRKRSRSQSAEKTLERREAAPVPRLETSIEEEEKSAIRQLVTSVLQDWRGAQKLL
NEDIIRTVLRRVRPVLMSQPMMVRLEAPVNVCGDIHGQINDLVEIFRAGGMPPTSRYLFL
GDYVDRGKYGTEVISVLLGLKVLHPDKMYVLRGNHESESICRIYGFFDEVKRRFSVKLFK
EFTDVFNCLPIAALIEEIALCMHGGLSPELRNLNQINQIRRPLVVPDAGLACDILWSDPE
ENSCGWMQSQRGVSYTFGEDVVRRACENLKIDVVLRAHQVVDNGYAFFAERRLVTIFSAS
NYCGEFTNSGAMLMMDENCKCSFQVFKPQY*
>TCRU_9876 60S ribosomal protein L13a, putative
MVLPTRQAVDRRSRKGCKKHRPEIIVVDLKDHVLGRAAAIVAKQLLLGKKITAVRCEQLT
IAGTEIRNKIKYLQFLRKRKLSNPKLGPFHHRSPSDIFLRTVRSMLPRYTKRGQKALRQL
VAYEGIPTNVVRTGGRVVIPKAQRHYCYRSERPYTVLGNMCKHVGWKYSDVVKKLETARV
EKAARHHKKTEKLRAAWKSARKEALSRVSKNKLEVLKKFGYA*
>TCRU_9877 hypothetical protein, conserved
MSRAPRNGIALQRHATLDRGAPYQRQRLPPAPHSSGMSLTASENNSRGPRRLTFNNFATF
NAREKKLPPDANARAAPNTKLWQLQERASFYCHKCRRDNIISDTIAVDAVHQLMLCTRCF
IRIIRPRSYRPSRVVPFPSLLSWLNYKPSKVMEMSEDIASRPAEAVAPSGERVANPTLGG
GDRPTHIQNLPAIAMKTIPSVRGDVAPTDRGPTLARQQDEIHPCCRVWGRCIHGETCLFR
RAPYDLCLGFLMGLCLGDEEKCRFLHQHVFSLPNAADPVPAERRAEDLEDAESAWGKWIA
RRKNSPNSAEWQLWHNGPVQDLLDAYAPVTSEKEEEQKEARSGGKPAIKLNFADISAALQ
GLKQ*
>TCRU_9878 hypothetical protein, conserved
MQRCILARVVNSLPSSLHGITSNNDSKHKVFFPLRQAVAEPSVDTNTEAYRHLAHELSLL
SQEEFGRRLYRFSRTNFDPTQTTVVHALVSELISRRVQEVSIKCVREYAHLAHVAKLHKL
CLDVYFARANLTTIGSVTENNDTKVGDFAVPDFVVDSAYALCSTSDLIRLASYCVKHLQQ
LPSLGWEVMSAFSLVRAFWRCICVASIHGRQQDAEYKQALKDASYIYDEYMELVYPDAYK

ELTTQDAIRTVQRFVQYASSADEGEMLFFRFCLQKGFLRRPRDTTRGEGDDGFGMNAGAT
VEGGKISEEQWFYASLIATCRVGNHVDSALRYFDDIGSYLGIVQVSCNDLLHSCSRKIRQ
DDPKRPEAAIGSRDRKSMEKVSEYLIFQLLNVLQIAKENAKIVFIARAMLRDGVQLGISV
WSIVLIAAGETRAADLALAAFTQAKDALGDGSHALDRRGNEYLLQTAINALSRCQVPRFE
EEYLQPCHDQQLMHCTNEFYFCALLQHAHNSMDPANGAQEVLRRMKEKGTPLTTRIISRL
MKIYLRIESPKLLELYQHATQQLGTFRSSWLDELLLWADRRRYELTHGERKYILDEVQRV
HGIKGTQGDLGGLRTQYALLKYDYEYSPLEVFASTSYPPETEPTILDSRVHFLLKHPHCV
AHNIEKWRNGCTFWINNTVGDEEKAQRFLRLSLLTNEGATTTNGEIKPEEFRLYMGSMLE
ALQKSNNCVV*
>TCRU_9879 hypothetical protein, conserved
MALKLQRSGIQHRGDNAHVHMRTTPLDRQAHENALQQRDVECLLWRVEIRQVQHNRGGEG
HVDEAQTTHTGIRIVHGADAATVHAADLRVVRFGERERSKTVRNSSRQTRVAVATSSAHA
PAAADAARPRCKAHGVHGARTTVQHPHGRHNIEDDSVMRHRRAPCLVAHAVDDRVRVGWW
*
>TCRU_9880 hypothetical protein, conserved
MRGVHLAPRHAQHSAPRRNHARTRVQRNFATEHSRVQRDTATNELQHGAVHHHRPPTSHH
GHEGHAGHNQHGPHKTQARQHQHRCVRRGLRAGKIHKRRRPRGNQHGVRHRQHRPRRKRA
GQHKRTVQRLHVAHGQLHRPALVAPRRHRTAQRSSAHHVQHGAVQQRHVLHNDPHAVPRH
PRHVEHRTHAVQHNVAQRHLARTGRHNEHRPHRHALADKNTRRSAHSGRKRGSFHRHARL
AVPAAAAHAHAHTVPHARRRRPGRVAVNIPVAVVAPSNVDAPSVAKTSRCVLLRRRQDTA
TRVVARHPQMRPSRKRQAQRQHPRQQRSVAHKAQRAPSSGHGASRVEHLPRGAVVHVVLR
QQHRPTGQAHRRIKRHRVVLRRQEFASHKRHSGARHAHSPTHRHRVLAQQKVAVNERQHG
AAAGRNTALHRHAQPQRRLHQQPVHVQRTARRQRHAANNQHANSVAEHSRHMRARNGQHA
PRQIHVVHHEARGGVAKVVGVMVRNTRLCDQHRVHHSDARARRKSVRHQHAAAGARLKPA
DQHIDALSSRRVGPPPNNVQARSAQKRAVRQRHVAHAP*
>TCRU_9881 hypothetical protein, conserved
MDAEPEHGSLQSDAVQADGDPAGDGDGGAAAHADPDGVGERHAVVERGGVPDTRRDDGGW
WEPDAERHSRRWERRPDAADGGAAAAVSVGARPAARHAPELCAGVDGTAARVWRSVGSDA
EQRDVDAQRDESVHRPGAGCAHAPRLLH*
>TCRU_9882 hypothetical protein
MLRWTGGSRARASFWQPSGDYSTGFRGADNDIHDSRSRNIHHCHPTTSHEWRSRHPFYSD
NRNETKGFPRRSYTNRDATVASSSESGGRRSPSSARREGRVGGVDCMALEWSLKAAAAAA
ASSSAKPQRQEALEGWKKPTCNMAVGHSRAEDHSLALGDAAHPECQCNHAESTMAAQMEP
RGLELPCPGFGEPRAEETWTEPACSPPFHVSSWEPDTWTLSDAPTWAPQECFLSHLPESA
EEWELKECNEFPPPLSWGETHHDPMNVFLDQRTFFASSNVPPEDKKVNAFLDESVTAWMD
DDYPCDLLWEEYIEPAAAREGEWGGVWDIPIVPGCLPGAAITRTGESVGCWTPTHSDIYA
ETSDQACFDGSLLLQTPKESSLGKCRSPVVSRAEPNAVLALTSMLRGMNQSQRMPYAHSR
ESFTHLSRGRGGRNFVRYGSDAAMREPYGFQPHSGQILSDQTPAAARGGGMRGRGRGWHR
GYSSHLSGGVPSSRFQAFQRRYRRG*
>TCRU_9883 hypothetical protein
MNAWFHATQAKCEVVFEMKLALYEEACAFLESSCHHDAGDDGDGDINGGGAEAAELLPQL
LLMEKMRLEGPLKPPKRRGFLDTIEEQLNAVYNGLEEGYNLNAEDTRVFGHAVFPPHVVT
GTDVSDSGTGSSVGPQLYGELTSKGVRQLHRAVLQCLERVGIVAQTEEVKVEEQGTQGPH
QPTRHAVVGVDVGSGTGKLLFEWSLLAQRDAMLPTHWTHVGVELAPSRMQIARRAMSGSA
SLVYSPTRQRWRVKLPCGGAGQQREDGDVKVVLCEADAFTPGLLSNETFVPLADGGTEND
AAPGDFNKKVSSHLVVFCCGLGFPEPAVCELCASLERMWQKPHMASSAWQSLTCVFLLRA
FTGLRSFPLFRLCTETTGPHDASVGSISTIKLNTTWMDEAPARLLSFRRVCDR*
>TCRU_9884 engulfment and cell motility domain 2, putative
MTPLLHSLADHVSLFTMAVAMGGIAVFIYHAHRGGKLGKLLPSSCRGRRSPVLNGVVAGQ
QPEMATRKAIHHIMRGEIATLGELVYFFRGVGNEKKIFIDPVLLSYLQRLLAADTPPDAI
PPELHDAHLRKMLCQLCHCSEQATRLKMERATSFDAENPEHMRLLRELWAAAGKLPADFS
HRSDKWVEFGFQGLDPATDFRGGGVLALRQFLHFAQTHNAEFKEMMAFNKRAIAAGEDSW
YLLAVVSIQFTAQLLLQQDHTFYLPQLEVLYDTIRREDEDNEKKLGVTVRHVGDARAEVM
ERSCGNKEKGDTGGGNQSKAVRTPWSEKSDFEAGFYLLHHQLLLHFKTCWHRDLPHVMEY

GKYMPTVFRSFFVQA*
>TCRU_9885 hypothetical protein, conserved
MSLNANAKEWRPAGELASFLLPASTSERECNTVVGNGVAADVSADKNDAAVPSLSQEEEK
QKEQKQSLDAVMASPSYYPSFTRAGLCAAAAVAGGAAVELEGVNWAEEFERVMALTKELI
ERQMNGERDASSKLDGGHTKPGHNVSAEQDSPQKPQGAVKAMDPSRYPALPGTDEVRPLV
SGKWVNAPAALLSKSSASVSGEAHARTAPAAAAAAIASSTHPSPAAGVTELDENGRPLPP
LTSKGNRRWKKPTKAQQKREMAQKNAFEAFANALLHSVSPFMAPLRERCKTSLPHIKVDQ
RFGKSGQPQTAVAQFVVAPLITNYRPRHFHDLTPGDLMEFHYDFAQVLKQLKSANAILFG
YGPVWKRYAVPYCYVNCKEYRQEVLNLCPDEVPNMRVEAIYEDDILKDITNVVLAVEELE
PLHNMSIIQAMSRRVNLAPLFDAFDTIFKPIENYRIVIRDLHRAPSTYLIQTSNHEIQQK
PSPLVLYNDPNLWYELPVVSRIKVEEKTTGDALEHHAVGSATTSASTKNAKGKSNVVPNT
RNGHFISAECGPRSKRSNPGEISSLALVAPVVGSVLCVFMTAFILWRRKSSR*
>TCRU_9886 hypothetical protein
MRRLVLKQGGLQRLRLVVIQTQAVLALSLNNRMRRLVLKQGGLQRLRLVVIQTQAVLALS
LNNRMRRLVLKQGGLQRLRLVVIQTQAVLALSLNNRMRRLVLKQGGFTCCEAVAVTRSKV
TVTLLSHDNRLAFPLTVKGGLQRLRLVVIQTQAVLALSLNNRMRRLVLKQGGLQRLRLVV
LQTQAVLALSLNNRMRRLVLKQGGLQRLRLVVIQTQAVLALSLNNRMRRLVLKQGGLQRL
RLVVLQTQAVLALSLNNRMRRLVLKQGGLQRLRLVVIQTQAVLALSLNNRMRRLVLKQGG
FTCCEAVAVTRSKVTVTLLSHDNRLAFPLTVKGGLQRLRLVVLQTQAVLALSLNNRMRRL
VLKQGGLQRLRLVVIQTQAVLALSLNNRMRRLVLKQGGLQRLRLVVIQTQAVLALSLNNR
MRRLVLKQGGLQRLRLVVIQTQAVLALPLNNRMRCLIFENCGFVWLWLYCFTYAK*
>TCRU_9887 hypothetical protein, conserved
MLFSLDGLLVKGEEETQLSAAEGQQLVALYRLFHRLQHSSQPVRDGGISRGAAVQRVPFP
AFLRPVRSRMGATAGSLAGVRAHMDVNVPDRNEEARGDEREEGPGNGTSNADDNDTEPVA
VLCGNTNRAANGMEEAHVRASLSSGSGANLSSGHGSGGAGAAVLQICTSQRELFCVQRVS
PETNDAIFFCGAAVVQPPAS*
>TCRU_9888 hypothetical protein, conserved
MVIEYLNSADTQRLIEFLGDGKLKFSVLEKSFKEAFPKDTHFNVSRAIQQLVQSMIKSGE
GVGIVSSFFTLDIMCKMECETAKCVFYDALLELERVMRQDVCFTEQIKYASKETKEGKKS
LEAINAEKYRFHCAAKGFAFRLLANKVSLDETSLAVLYDKQEQIDAALNAWEINSLQLKE
SIANIAHCWTQDVEKNSCEALSKNSAIFDSGVRAALLLQAARPQLPSLPLVSGELQFLTP
GGSPGSDLLFFDTEPVTEEWKLSKKLIALSCNSLLNKEEQQQLIHTLSSGDLFHRLGINI
ELLSLMAIHNPDLSAALILKLPPQEGSQCIQQILKSSVPPEHAETVLLHASKILQQVNIR
AYINGKLHLFKEKSTLSTSDKNSIKSFIMTLYQLVTKASKENKEVYIAETLKSEITQLCE
RCDLPEVSARWEELK*
>TCRU_9889 hypothetical protein, conserved
MYGELEYVSFAYITPSGKLPCELVEKQQLSSMKQIIASYKPSDTNTTNNTSSSSSCCICR
TNSSQVQAMPVLKESGTKVYVKFFDTLRKVTRTQCFSVRLRSNMSYIYEMIHAWLPDVGN
LVCYTVHSDSHGVLYPLVKTVLHPQDDVPEIIFSQKFFLPFYKFTHCWGVVNLFVLRHHD
SLVPGYIPLIVYRSSMHSKEALQEQICQLCCTSPLEANYMKSQLFFNCTVSTGFVDLVSF
FDSFTDDSASLSQIVVVYPALAPGDLVHLDMVDRTNRRFGIQGMIKCSRQKDGLVCYDVE
EMTTGYLLEGLTCVQVLPL*
>TCRU_9890 UTP15 C terminal, putative
MDQKLWSLPVKRVPVAQKVDRSVIWNNACLCYEQKLFGQVTCVRYNNTGTAVGCTSTNQL
TILRVPQTEGVITNEQREKKCFSLRFRDDDKMVLLSVNQRVIARSMQTAFERQFSGHLRE
VRDAIFLDRHNFVSASDDTTLRLWDIMNENELLISKTHTDYVRCLENYSPGCFFSGSYDH
NVNLWDTRVGFEHPIQSSGHNIGSPVEAMLHTHTNILICTAGDQLILFDMRKGLSTMLLQ
ESHHTKAVVSLAFSKRNNVLLTGSLDQRVKIFSLEKGGLEPLAGKKFDAPVTAVTVHPNL
SEFAVGTAGGDLRIMRLGGALDQNEKEEEVELVEDELGAKDKNTQDDFLGTKLHDVRQQL
VSYQYNRAIKTALYSRNSDVIVSTLEELIRRGALHVAMSGQNDRTIVRILRFLVNHVDSP
QFCESMMIVMDVIFEIYATCAGKSNFLHREMMIARRRLGSVLATLQRMEHTLSIMELIVN
DV*
>TCRU_9891 peroxidoxin
MFRRMAVTSLQKGLSRRAFCNTLRLLNLDYQAYKTATVREAAPEWAGKAVVNGKIQDISL

NDYKGKYVVLLFYPMDFTFVCPTEITAFSDAQAEFDKINTQVVAVSCDSQYSHLAWINTP
RNKGGLGEMSIPVLSDLTKEIARDYGVLIEEQGISLRGLFIIDDKGILRHITVNDLPVGR
NVEEVLRVVQAFQYVDKNGDVIPCNWRPGKPTMKTEKANEYFEKNA*
>TCRU_9892 agmatinase, putative
MFARFLTGVKAVAPRGSDWANRLGPVAAFGYEAGASKSSMLFDYFIQSPVDCDHYAEISF
HDSGPIECPPETVMFMPVLKCGHMLEHASVNPTPTSDDWYMAALEATTELLEKGYIPASV
GGDGSATLPMVEAYKRLFPSEDVVVIHFSAQPLVGNPRAPLRVLLDKGLLKGIVSVGNRL
VTSEDRKIRKHHKMFYMDMHAIYSKGLFCIRDIRNDYPVFISIDANVMDPAFAPAVTCSV
AGGLSTRELLHVMNGIRGPKVVGLDVHGYFPDFDVYRKDGVGLTQIALAKVLKEAILKAY
SISTQTEEEGMARVQMLQRQGTVSENPYPDH*
>TCRU_9893 hypothetical protein, conserved
MADSNAVTVQEDLCDLQTQLEQRRSQARNLELQVARKEAELRRAKEEQALLKELRMVNEV
TLRKKQQKDDAHDNTRLKISLESLTQVISLEDEIKNENRRTAELQDSANVITRQMEDVEK
GIENVVSRLALVRQVTGRDGRENALLSGPATKSEWIMRKKNLTALHEEQNTMKALSALLS
ERIEAINKEMEEQRQKAEQLAAAKQSLVETNKEYDALLEEMKSMERLIKKKERLLDASTA
KESDDYKKIKQLEGDKKVLYGTLSKFRETNVNNSKSILSLEVRLRQLETKLEAVNLFLQH
VFAQVEEEEEPLENIPEDATEVPLQQFEELCRELELSRETLVQRDDQLNAHDAKVEQLGR
KTFVLQNAIASRATSAQLQVKGKEKEFETLMSHVDYMKAEFDEEYKKLSRENAMLQSKLA
QTS*
>TCRU_9894 Domain of unknown function (DUF1767), putative
MSALSTEVRARYHIAVSTRFVERLSAADGTVTAEYIYHRALNENFKDITDVGTLPHGIAS
QVSSTLTIPVVLQVNSSRDATQPLRPCADSCEEEMIFAAAFQKTTNTRLLRLVLSDGHSE
IPAIELTTLRVFRGIPVPGEKLLVKEGTQIKNGAIIMTEDCVVPLGGEVLQLKKEFLSKR
NRTDVPYQTSLGLEAAPRFQPLRVHSAIAGGAPNRQPVTADQGGGYGSNRGKGGGRGYRG
GRGSGPRERNRH*
>TCRU_9895 GDP-mannose pyrophosphorylase
MSEEKKSGANSKGMRAVILVGGYGTRLRPLTLTMPKPLVPFCNKPIIVHQVEALRDAGVT
EVILAVAYRSDAMRKNMEYWSKELGVSFVFSLEEEPLGTAGPLALARDILLQDDQPFFVL
NADITCRFPLRELLSFHQKSGKEGTIAVTKVTDWQKYGVVVFDEATGVIDQFVEKPKNFV
GDRINAGIYVFNKSVLNRIKLEKTSIETQVFPQMASAKQLCAFILEGFWMDIGVPKDYIE
GVGKYLRSLNGTPKESQEVYGLGQAHKTDDFTVIGSVIIDPSAKIGKGCVIGPFATIGPG
CVIGPTSRIRHSAILDESTIGKGTLVDSSIIGWKSRVGSWCRVVNNAVLGEDVEVKDELF
LNGIKVLPNKSIVQSYHEPEVVM*
>TCRU_9896 hypothetical protein, conserved
MWRCCGWLHIALLRGRWASAVSPTGVAVRLHGAPTTEPCECHAQRHWDSGTKQPRLCFGA
SGTCWPQLGGVSGMPHRTGVVMAPRRGSCDDSDAAARHVAGSKMWPQWTMSSTNMRLSDF
LWNYVGGRAAVDERPQRDDGDVCSGAG*
>TCRU_9897 retrotransposon hot spot protein, RHS3, putative
MLRVCAQCEAEPCGGTSGRRGAKENGDGNGVREGRPEQSWSYRKADDAIEENDAVQQFGA
APPVLMVFASEKGWPYSWNTIQDLPKDVFVNCAVDRAWQIVKGDVTACFSPHGVTDFKPE
QRVLIGTPGIGKSVVAGSYLLY*
>TCRU_9898 retrotransposon hot spot protein, RHS3, putative
MIAVSFPKVTSYDEWAKQLQAARVIVNCLDEVDVKAMCAWITRGETKEKQAECWKEVKKH
MYLLGPIPRHVFDEEAFRERCGAVRFALQSINEVTAKEHFSRGGESPRCSEDPSHKPVKV
VREIYAGGVILFNAPISACLEERTLERLPSVAE*
>TCRU_9899 inositol/phosphatidylinositol phosphatase, putative
MSVDSVGRSLADLGEPIQRLLQQIQRNLTDEELDMFAKIKVRQLAKVYDMLVLEEDPERI
LVWLKKEHLKAKGIDPEEVKEKTRRKVLTEGGRDPIAYFKEIEKKNIELISNLKKSQEER
EKKRAANTAERQRRREEFRLRALKRKQEERDEDDLEVMKPEDLADIEGVFDRFTSKQSTF
DNSNGVQDEEWWKRDEYRWDYEKHGLKGGRWTSVVEGGSIRAPEFEIQMREEWYRIQCWW
KTDTQRRNWLAFRDDEWWKEELYITDWLENGENGLMWNAADELSGYNRRGNRRQAVKIEL
DRRVLWYKANGPKGVVKTWCALVEGSKEHCTVEEKFERDDYYKNGDWWKSEIHVNSLLNN
PDECCALRFAAAAAMDQEWWKQSFFRADFEKGGVLWKTLNEELAVRGIEDFAAEEEVERR
RNWFKNYWWKGEKYIQDYEKNRSAGKLWKAIDAGSTAIADAVLLRSREEWYLACRETEWW

KGEKYIQDWADYGEKGFLWTAAWRNAALQGDGKNKASSLALKKREEYYEKNFWKQNKYVR
DYIAFGEKGVLWKSNQVSAAKDSDWWKSTSFFCQWLLANHAFPGEFWKDPDVISDYWKNK
DTGKKWTASNILAATLEKGNVDKASSDELVIRERFYEKYWWRQREYWNDFCARGTKWSAL
TPEGNGKCSAVELKERENYFQPISLSRVVLGYQRLIESDAIAPVAGLCVSFEELCLRDQY
YQRSWWKSQAGLTDYVFHGGDSLYIRAASYDDARALEGINFSSPIERATRMLFFDNGFLE
YSADYEYTGEFVASADWWQEPAIISDFLEKGEKGTKWKACNSASGKCGFAEKDVSSKEEQ
KYRKDFYVANFWRSLECLQDFRKNGIKGKLWTSSQPLGKGERVDEKHLLFRAQVLSGYPE
DSWIEEMETNWWKASEVRADFYANGESGCMVSAVNAYAAVERLGTKIEYKADEDEIKKRV
EFYRTHPLSLEDGEKCHYIYLIEPFWITPESVEDYWMNGSRGKRWSASNAAAFSCSLGDK
FAATPAELKRREEVLQRNFWRISAYKEDFLTHGKEGKLWNKSEYGGMGDVISHEEQIMRI
SYYLRLSEKYWADCRYAYDNWWKAPEVRNDYYINGSRGSLVGAATAAVASMGLYRNEQYG
VSEEEKEKRMSYFKTHPYRDSRVPQALLSRELKKIAAMGELFWVHHYCLEDFLLHGAQGT
IWSAGDAAAASTGSAWRFRTKPDEIRIREAFFSRYWWKASKYRLDFIQNGFEGALWTKKD
FNGAGEKASEDEILERMCYYACAGLECEKRLEEFALCWWKSPNSIAYYMIDADNSMYIKA
RSPQAALFQPQIVEDMTASSSLVENRQRYMVVVTPTDTSDEITDSQIMAGVKSGNNMWWK
NEAYQREYDTQRPLEHWKDPECISDYLKNGHKGNRWKIAGSFFPKNMNELCGNEEMKERE
SYYRVNFWKSTESRNDYELNGLKGTLWTSSEPNGKGKPVSETELSVRMAYYKPASLWKLE
FDPGTDAKSTWCGFHDDILRCFWYERNWWKCILRDDYFARGQLSPLLRVSSLGALLHGSV
TSSEWHVSEEEAQRRMSYFDGLGENEWWQNPVVLSDFHKCEQGSLWNARNFKEALLSIGL
ESPADLTELERRKRWYRANGWKSAEMIQDYTTGGNKWNSAGSSDPVLCEEWMEVHKLVPA
EEQSRRKRWLDHQLSDEQLQVRRAWLLQRSQDARRIHFSELGDLLAQLNDGVHPSDDEIQ
AIEDAIRADQKYHSIFEGITRQDVMKAMKATRFYIGATKEERMRSEQEALEALQKEEMDR
LEEEAAHLAQEAFEELEAAGEEYVPFDEAADAEEEEYLKALEEEENAKMNPNEDDLEMAW
ELHKEEEEEEITENSEDGHREAMKKRQRTLEEAFAKEEYGGEMGDEDTDAVKGELVDDVK
AALEDLVKDDGWKEDETSRWNAKQEEVEDSMAAANEFVLPLREVANPQYLKGYFTLMKYT
PSVNLINTSQKRIWVVDHFTQCFYNLAKNNRIRKEHAAKKLIQLEKNVLDNTRLRMMFFD
ASHSYDVQFVNANERERFYETASAIRSVIRVFAPDLVGENDVKSRVIIDGTGANALSVIC
PDASSKPVKRQLVGECRINATRHLTEPISVWCGTFNIGGHRPPKRKEDLQRWMPRGKYEI
YAIALQEASFRTHDNEWTDYVQDYLGDDYLPIASMFIWDIILLVMASKRSLLKITNIEGS
TRGTVHKSACGNKGGIIISMQYLETSLCFCTCHLTARNEHFAMRNSMLEEIIGNIRLGIL
DADVTAQFDHVFFFGDFNYRCDVDVSKAETFIKSKNYEELLAHDQLIKQQNSAGILHGFL
EPVIKFAPTYRINVTSSEYVLKSSPSYCDRVLYKSMLDSWIKCTGYSSDPELMLSEHRPV
SATFIVRCVRPVLSCFMKSQRPVPEFVFDDITVKDYTGGAIRKPTLCICARFAPNTEPIL
SRETNTATPIWKKETIPVLTSVTQVQEYLETRHILLVILEGSERREVKQGRGTGVITLKG
RVIGKEDTHTDFETDIVFRGKSVGKISGSFMWRALKHAKEE*
>TCRU_9900 RNA-binding protein, putative
MTRVYVGNIDKRATKEELLEFLKPMEKTIEDSWLARRPPGFAFLTITPSQAMEFVEKFNG
KEFRGRVLVVETSTTTTLPKERSSRRRERRETRRSGSRKRYRSGSRSRHYSERRRDRSYG
RRRDRSRERRRRRRSYSRSNSRSSLSS*
>TCRU_9901 hypothetical protein, conserved
MDSDHHPPYHTAGTEDDIPRQAGMLPRRKHDAIVLREADCDASTSARGTPLAAVTTWLEM
HRGTARAAAVTFPQESGWT*
>TCRU_9902 hypothetical protein, conserved
MSGNKASAVPQGDRQRRARPASEGDTDQPAATHTRDEEAQRPQWTMSSTVEDILLEGSTS
STEMKLNEFLRNYFGGRGVVDTNENVSISVFVLRPTMFINDNEILGLITASSSYRELKIE
LDEREILLEAVNRLHHEGVLFLGQWRDYEEKDTVTPLARGKLNGVLTQVLTEERREAGEK
ARRDQQQVIFNLYAVIGDLLFGGRVRVMEIKLNDFLTLEMEGKGILHANRNVLLRIFLVI
PRGISAMREY*
>TCRU_9903 hypothetical protein, conserved
MLDDYVAKKNGKLHDAEATEHHLNSVVDQVLNYLRNGVRITKIPSKGNACRRLYFLLEDC
KRIHSCDLDHQGFPLNRKRPPVTMWIRDIEKVLIGLSTTSFVNYGGEAQLAKTRQEAVSD
NGTHRHDATQNIIPSSLGANNHRAFALLLRGGESLEVVCETDSDCEAWPVALKRPLHLRT
PAERLLEERRGT*
>TCRU_9904 hypothetical protein, conserved

MPNGPLCVALMPPRSHTTKGLNEHWCRQQELSPAFTAVVCAFPLEIQNSVSCCAERTIRK
KATATIASLVLPRRLYWLTPFRMPCGRRNRSIVSTGIGSVTRDLAIDKRCLDQDIMELRD
ELMVARTVYDHRHCGYESNRPISDMEEEGMKRVNAIESNREEARERQLSVFCERSKHEVE
KMAKELERRDGATLDELERTLEAKKRESSALQADREDRICEYEHTVERIRTRKQTEESAS
VRLRQAMQQLEQGLSLRQSTIETKEQQLEMVQIDRAKGREAVMRERHSIEAVRRTVREER
CRQRRQLIHQIKEMNTKFLEQVRPLAEERKKKREQAKAKEDVAERALAADIKMIEEYLPK
LISVEDIPVNPEETDIIRRQFDEVFAQ*
>TCRU_9905 hypothetical protein, conserved
MLTPYQLELVEQAFHSLAPKGDDALPRIDEIFRVFDVSMHPRVKEGVMSPGAVLEMLAYQ
FGESEKEQKGVTFDVFMRFHERMAMEAANECVSDTEGFLTDTIRGVWRLHELLEPTFIRP
VIPIEGFPSNIYATQLMSLVWPDESKPPRSYVLHVIHGVVQPLFSRGDLPPELRGFFAYP
AELAGMKLIEVPVQISMQRWLDFVWEYAEGKYVAVPGIISARVDLETVPEYLRKLIIEPK
VVKQLPSVQFVSTIKSLNPMYKRTSDGYGYGITEEIKRVHRWKCETHDGTACGLIYHGRV
GKFTKKLYGQAQSLAASGINL*
>TCRU_9906 Cullin family/Cullin protein neddylation domain
containing protein, putative
MSGEVKELVHWLRKWDPINRSLLHFANHTHALYPFEISCKILRAVSSSSVSLVGGHEDSE
ALPQPKETKGGMVVAGNVEEEASAAFTEAADSSNISVLYARVYDMLSTFGKVEFWSNAVI
FQHLLVSSLLAWVARLCASSGDRLHACPAISIEELTPQLLWWKSHELRDVWEEAVRNNSR
PWTELAGLMSTEPETDRKRSRERSLVTVTSCASSLELRPHKDGEGECNSGARPHGEEERK
KKEEEVEDILDLHTLVTFALHYCRMRWILKVVFLRVDVEMNDIAWRIMRSCVHATLEQNS
TMIRRVLCRTVEYCVKGSQSPDGFKAVELTQVEGQECLNDLSSSSVSLDALRRLRDRDIS
LVCRVFSMLDECCVHDISRFATDGVVQFNQQHGYELACRNFGPLLVSNGKDKNEVPALQD
AFVALQNCNNAFMRLRAAMLLYFGGTTHYVDELSGPGRERVAQAERAFSVGFCQGVVLLQ
FVDVWALPLWLCACEEEHERRLFSASRHARWRSVDDMSEGRDSSIVFRSFSEAVSQLGEV
ENIKNKYSLHISSLPLRPGLETLIFFLSPEPKLLSEFETRFAASVRRYLEELLQKSHTTG
TPLRALPRDVYQRCVFLLRLTNQLLEASAAAGCEGAHATLRAVRRGMQTFFVEREPCVIL
TLASALHAQVTGRNSHGGPNGDDDNDVRGYGGAYLEILDTILELASLLHSKDLFVNCYCG
LLATRLMMAQHALTLDIETEAISRMAIRLGDSLAAEPFALLRDVRASMTDPRCIIPDTGG
VQQSELLRHVRVLCRIRWEKYALVTVRLSEVQRCFEEEEWFDAGMLHAMQSFEKRFDTTE
GSASGNKLRLNASLLGSRDARFFGGRGSLGNDDEEESHVISRNDHVLTAAGGGGGAGGDR
SAGFSRSSPPGPVSLPAVGGAVQRRRLSWSLGSGVLTVVCHAARGSTGDAASSVQLVMPP
VGLLLLQALERYGDSSTTASLSGPTRCTLDFLHGKLPVDVPKTLLAAVLGGLVRHRIVRR
TVHASSHSNDGGDGDGGGFSTYGLPASFEGCKKRKVVIDVENAMHHWVPYLQEGPDDSKA
IVMTVDGIIDTERLRKLEAGIVRIMKEKRSLSHFDLFASVAELLMTHFVVTAPVFKRCMA
RLIEREFIARSERDTYVYVA*
>TCRU_9907 dipeptidyl-peptidase 8-like serine peptidase
MSSVPLTTYIEQLKALDGLLQVSGKPQNLRIVGEELYWLQGIEQELYAVSLVDENAIPRR
VIAPPEDAGCESTPTKSQPKSKEEELLRERLRSHVSGISGYQIVPSDGTVFYTSGTSMFM
YRPSNARPPLNIFDYIDEEESRRHFGDRKRPFLCLQHLQYPEKPGSTGGNAGRSPNVISF
VYGSNLYIATVVEQDDTRAAPIHVEVECVTNFGDAMHECGTADYIMQEEFGRYTGHYATE
NYVLFSYTDTSILKNVSLIDGSDKSSVETMPYAWVGDPNARTLLVVYLRETKCFRVVPEK
SIAAVAPWAEYMPRFGFKDDETIYFSLLSRTQERYCVLSCLIDSLPEVDVTALSSYFFTD
PANRDTTTQIMVSLTTECEEHIPWAWVDVPRGPPILFGSTHDVLLRHATETKEANWHIYV
RDLAADSKEEWRPLTKGNWNAKPGSLRLLQDRVVFMANADGRLGNVIYSVPLGFSSVEPA
TAAQLTRLSPSHEHVYSFTVRNGYICYVASTAETPPQLYIASLLSPESRRLVQTKFQDSD
KKGAVDEGKGTPISFLHSDDLIKTELVTTISRRGVPLSGRLFRSPTAVPGTPAPLAMYVY
GGPHVQLVYENDYELICKPLFQVMAKNGISVLVADGQMSNANGLVDLSICKHNMGNFETS
DYVDLAKHVTASPLQPSGFIADPTRIAIFGWSYGGYATLLAMSQASDTFKIGFAGAPVTD
WTLYDTGYTERYMGELYATDAGAVEAQKRNVKSAAYTKSTISQFVTGLPDDLNRLFIAHG
LLDENVHFTHSCALINAMVAAGKPFSILTYPGERHGLRQKKVSRLHHDAMLIKILVEML*
>TCRU_9908 hypothetical protein, conserved
MTAENVVRTATAVASLCDARAVDAQLLHNSCEAAATNLLRRSRRYVTATRVSSLAVAASI
GGAGLIASWHYRRIYRVWRLRYPARVAQQRRVMWFLAASGLALLLFVLSPVGFMAQHEAR

LHDVQRLDAIAVRALMLKRRYESLVRMAPTSSEEAAKRAGVYNRCEEDWAELMRERVAID
ENV*
>TCRU_9909 Glutathione S-transferase, N-terminal domain containing
protein, putative
MVLSLIGPLDDPHVHRVLLVAAYAGTRLKVVPVTIGKENETESYRRNCHPLGRVPVLKSD
EGYLFETNAIIRYLARTERLYGLDGSERHPSPQHLVPYILYGKSVQEAAEVDAWLDFVVT
ELDPHILPLIAMEKEEKTLKRNPRGEDAGAKALPLQPRVDALHEGLNGLEQRLVFKKQLR
KLQATGGGGGNNPVSARTGNMEEVDEGLSEEEYWLGVTPRGSSVLRGYHTYNIKTQLEDP
NQINSAREIASNNEGAAHEGGGVPYLSAHFVLSSPRPSTQASRFSMHTPRRSAPAASDML
FLVGDSLTAADLVVSLAINQALLLKQLCTTLKQRYPQVVRYHCSILRLPVAAQLRKALGI
NIL*
>TCRU_9910 hypothetical protein
MKEGSWRCTDPYGSAQAQLEAKKYWRAAPMPTCSSVRSASDWRRCKSCPHPLMERQLGDH
QRTARRVTRLHQFCRGKLECFPYARDNRKILQIHDVPGGLEVLLGTQGPKRGIRGRRGFV
RRIAVAPFYGALECIMCATPGHSSWMRLGPPLRRRLRQVPACRQL*
>TCRU_9911 protein phosphatase 2C, putative
MWVQSRLLCRVSKDNLLSFYYRCVKFVPHPLKQESGGEDAFLSLVGVQAVLDGVSWWKEN
TAVDAGLYSAALARAMYNYVEEELLGDNPSSSLALLQKAYDACKAEEIEGTSTALVATLQ
PPTEEEVALMGLEDRHKNCILDICSVGDCTALIVRRGRIVFITEEQTHDLDFPYQLGQGS
SDTPCRGLKYRFPVECGDVLFLGSDGVFDNLFPHRVAELMWKLLNNVCLRHFSGVPGKWG
RVELFEDTMHALARGSEDVIREAWNCARDIHSDTPYARKAVAGGAYYEGGKQDDMTLLVS
VIDQERDAGSGDRIVRGAVMNPYPYRDWP*
>TCRU_9912 hypothetical protein, conserved
MSGCGRRHRAKHLTLQFLDADGWKGPAAGESMAVCIESPQNQHVRVLLFGPNSTISGTAG
SDGEVNGNGVASPVECVVFVPGKFRKVIWLAVKDVIVVADGTTVAFKPSPDQLKTFFRDN
PEWKSRLLAAQKMVETCKPAVEQLPQYTKTAHTTTSVLDRVGEEHFSSGSASSAGDEERG
DMNPNRNNIRHRTQLFYDSEEEEEEED*
>TCRU_9913 Retinoic acid induced 16-like protein, putative
MEQTCQGVASDTVESPSSSLVLSVADAWASIRAYFMEVQAAVEDVALAEIADRLPHLTHS
LEVIRKALLQERSQMMQTGFVPQVRKVDTYCAGSVSSKSDVLISLQRPSFKDPNSSSHFG
SKACTDGVWRLPPCYTFLWDEPLLTSHEGENAVDEGEISPIGDIFLFSLCQFAKHDDPPG
ARRIILWFLSRLLSEEDLPCLPYRGDPPRSLLQMFPGNTVVPLMDMLRQVAARLRPKTVG
KEDTMGMSSTSNTRESNTDAMEEEREALLNLLCALTERMEQVPALAMFFIPEAVTDAKEE
VDFETNPESPPTVGSSFSILHELLFYATIRGESVHPNKQQTIYQLALRGLLSLAKCPDPA
IQDYVKKQTAVASATLMGARTTLLTLCTVPYNDDTNAQLTYLSELLRFWSQLILLSPAVS
DAWGVEAMIESSFVHGALVPLFCSAEEKVYAAAALVTARTVRFVGRSPSFYVSAVTRALL
GTHIDRLSGNPMRLTVTPKEMLSSLPSTVTLLEYVLLPHLAIPSDEDWSCTEVTLYLLDT
IALYEPVLFMEFALSLSISTLAEVYVEALQRALQSEPKNAYGKSTTVTSDGDNTSVTNSS
PDKARNAEYLQQLTSELELSAAETSPYLDVTECFSARLRAPRGIMLWTNAETIAEEILSR
LLLVESHVPACILEKRQRIMNRSCRGVDEEFLESVLEGSGHSQTLQETSFASMDNQAAKK
ESNNIWFHIGVHQSPLVERLCEITSKMLIIPSIVCSLLTQLWSTICVLPDFRVLYTLMDS
RYGQLRQALFKLRDTIDEGLQHDEDVAFALASAAAAVAAKTNMKTELVDVGSQNKLLAES
NLSIGSIHTTASHLYTRTYLYFQFIQLGKSLCWVRDIVEQEFPNQELLVALKKHRHFLEA
CACVEAFRMELDAAIGHVTLSHSLMCIKTGKEHAKRNLHDI*
>TCRU_9914 JmjC domain, hydroxylase, putative
MCVEVKQGGGTCVLELDGRTLTFEKFRECCLEPNVPAVIRCAVPECETGSKEGFVSCLER
MTSRLAPMSLIDAYGEGHHVPTVELMTGTNSDSDQFECMECRMRPLGEVMECWRRKDGVL
YLKDWHMQLECESQGRATERNSVEKKAVFDGYHCIVHGDGLYQVPEYLGHDWMDDFCRCL
GGGEANYCHFGDTESDYRFAYIGPPSSWTPLHFDVFGTYSWSLNVCGEKLWFFPSPEGNQ
RLLETSLYGLMLPVDIRTTTGTELWAVLQRPGDLVFVPSGYLHQVHNVSGPRFLLPPKNT
LRPDDAANPKKAKVLDNDDTGSVSLVISINHNWCNEWCVERMVEAFCRDANRLQRLLTEE
DRVLLFGEDCTAWHKHVENLLIGGTNWNFACIRSFLKHRLACLSIQNDGKGAEVGLRRLL
KKCLAEVDAVELRITHTCGS*
>TCRU_9915 drug resistence protein, putative

MASFWELVRDWAESLHIPNFLQSFSGGVRTTFVPLFARQLGSTDSQLGFIIGSAGIVKVV
FDMFFAFATSVYGTRLMMVAGMLLNALGGLVATMAWSPFVLALASMLWGAGVGLFFVARH
VFIAKAVPRNICGRLMSVVGGIARWCSVLGPGVAGVLTDICDIRVTAFSIVPMSLGCAYM
MATNKRIREVDEGIREEKGTHSISKEFHDMMHVLRNYWEIIVRVGFYSLIIICLRQCRGM
LLVIAAMNMGLSSSMVGLVLVSSYSVDATFFFLGGYIMDKCGQSYVTIPTSINLGIAFFI
LSNANSLASLILASVFFGVAESTSSGMLLSLTANHSPSTGRAPFMGLIRTVQDSGQVLGP
MASGVIMDYFGFASVCYVMGAVGMLSAPWAYFLIPEKPPCHLEEEAANFSEGSAAVTSLV
TDEEGKKKEFLVVDAEGERCLSLDEELSLFDDAVSEKESVNMVVPKE*
>TCRU_9916 hypothetical protein, conserved
MSRQAVGWLSSKLGINIDGRTETEEKTDSAFFPSHGFSSAAMKIDMCLHKINDAVFGRDS
DSGAGGESNFIGSSSGVGVTSGGEEVELDENGLPITKNWYYFDKELNRWNVSPEAPAAIK
EEYERRLKEDEDEREGRNFVPPPPLPPPPAPPLQPFVGEHPSIYPRGGLFPTGAPPPPQQ
QQQQNQQHGTHPQGLFGIQSSMGTPHHRPQYAMPKYFDLSTSAPHIPTTNLTTPHISTYV
HPQPQTQEHQHQGQQLHPHQPQPNQESYQQPGVQTQFIRQQQDDPYQQHEQRQTYKQQHP
LHPQVPLSPPASGYDKGEPNQLFHHSFQNSVPGHPRGYPY*
>TCRU_9917 intraflagellar transport protein 88
MEFASNDGAEEDLYAAFEPESENAFAASPRNYVSETHEVGGGGAVNPLMQAPPSRWGATS
IGSAWGVPGSRVGTMGGGVGAARPMTSNRGVGFNAALTQFNSGAIFDPAGQGRTAMAMGP
APPLKKRGENSPEEQCAEVEKLIHKLIEESAMLALQKDYGSALEKAKEASKKERQLCKQR
EQLGLADQINADLTYAVHFNLAVQYQNHQLYTDALNTYSLILRNLQFSQAARLRINMGNI
HVAQGRYLLAIKMYRLTLDETPTASRELRHRLLRSIGNAFVKLGQYRDAVASYEAIMEGN
GDVNAGFNLLLCYYALGEPEKMKRTFQKLLNCKPVGIEDEDDIDEKKDVLVDDALCKKIK
EDRSHFLNCIMTAARLIAPVIEKDWRAGYDYLIERLRHYEMRDSTSHVASELEMCKCLYY
LKHKSYKESIDGLKAFEKKDKLLRARAATNLAYLYFLEGDHENGEKYSDMSLESNRYNAR
ALVNKGNFLFMKGSYEKAKVYYNDALAVEADNIEAIYNLGLTAKRLGLYEEALKMFKRVQ
SLVDSHEVMYQIADINDLVGNPNALEWFNRLIGRVPTDPNILARMGSLYAREGDDSQAFH
YYLEAYRYYQVNMDVISWLGAYFVKNEIYDKAIQFFERASQIQPLEVKWQLMVASCHRRR
GDYIQAKRLYEAVYRKYPENMECLRYLVHLCKDAGLIEEANEWFKKIKKLEQRQQEETDE
GGCRDEDEEAKGGTHAAAGRRAVSALTNRVGDMTREDELDEPRISLSEEKPTHEDDDEID
LPGI*
>TCRU_9918 hypothetical protein, conserved
MQPQQQQQQPLGFQLVREPYRATEDQFRAFVRGMDAVLNQWTALHLVAHHCDPSALQSMY
QELISWFQSEGEVYSDDLEIFFENFFTEVRSVLIEDDSMKEVGDVLHEMYCRCCQNDFIL
VEQYLTSLEVYRRVNPVRLSVDAGSYDDGDSEKGTEATADGALGAGAQGIQPTFNEEGEG
GAPVANASQNPRKKRGKKNAYERDNDGWCVVQR*
>TCRU_9919 mitochondrial RNA binding protein 1
MLRFAFGRGSLAHAAWSRCAASVAGVQSLPKFEIHDVRDDPALGTMTRVAVDGKLLLISQ
YPQLGPRKVDPNDLSPQFDSDRRISVRMRHVDLAGLVCVCQSRISKYEMTNRGYTLVFER
VPEGYRLHGQIHRVASQKMEDWSVNFDKHFAVTLEHFLESALTESFGFRQHYAARAADGG
AQEANTVVGSASGRPQRRGNTDSAQRR*
>TCRU_9920 hypothetical protein, conserved
MWRKCISRRAGVAAPAVSVRSILLRDLRTSVEISKGEIKYPAVLLWRWKSNRQKHLVLSV
QAPDGTEGESSAEPNSKLLPVSAPTPADYFFGRVFLRPYNVAQLLAVLEGKAPHVELIRE
HASLYLGPVAVPSSGGTGHRCAKGGNGALTALPSAYSLAGKLTVKVQTNNQSTSVDDELP
QDDDYENDESRAGATYKLDDRRNFRATVKGEDLIFIMKHLDAVLGDMFGIEHQYHSRVAL
EILQKHRLGGIQSYNRNNGSQLQPVPRYRSESLYTTKVQTLSEDSATTTPMATLSSVAPK
PTKGGDNGVGDLRFAAASGLAGVAFGAAATPLFSKGTSVIEPEDVNEDSVDLREVGEEVD
IPYDSTHSPATPAARFVDHDEKHDDEEEDFNEDKAGELKEFEKEDPEEGAAQENGEHGKD
NEHDDDNESEGDDEDDDDENDDEEDDDEEDDDEDDDDDEDNDEEDDEEDNDHDDDEDNDD
EDNDDHDDDDDDDDDDDDDDDDDDDEESDHDDDDHDDDDDDD*
>TCRU_9921 vesicular-fusion protein SEC18, putative
MPHRVTSCLLFWLCIYFLAILSFFTSVSVRAAKAPVALPFPDWRGGNQTSGALELLAISG
CERPSRPGRSRETYRCFADGDSMSPVTLKIRGRGFPQGTPLRVLLKEHAPIPFRCKEGEN
ECDLIMMECVNVRPSKIFPQQILTCALPNPLEVLHHKPKWMKRLTQNAMWMDLELRLKKA

GMKSGLNVRGKEEVTIGVLSRSVQLCLAQENADVGVKENTFQEMSEDPLELLFQNEDESV
DVHSQWLSLGIGGLGNQLHTLYRRVLLTRLPSLRGVVKTIKLPHVRGVILHGPPGNGKTL
IARTIANLLDDRAKVTIVNSADILSKYVGDSEKNLRALFLSAADVDDNGMGERRDGTKNV
LEGQLHTIIIDEIEALFRRRGESGDEGSAKAVYDGLTNQLLTLMDGLEGAANILVIGLTN
QLHVLDRALLRPGRFEVVIEIPLPDREGRRDMLFIHTRELRENHQLAPDVKLDLLVSRTE
GFSGADIAGLVRAASSHALIRYRDSLGIALAETSHDGDSDEKGKVAEFQISNEDFDLALR
DILKSKWQTTPGEMLGDEINDPYNGAGVPLVDYDGSFSRNKEATRRLLRSIHQSRLVDAA
IVIIYGPPGSGKTVLARELLKLSEFDSKTYLTGGVLHNRPHGSPLDEILTALRSALHSNG
DIGIVIENVENYFRNNGPMDGVTLKLALQEFRTATHSHMPSRMHGAEKGTSSSFKRLLIL
TTSEKEVMYELVDGNEYDLLLSLRLIQRKDLMPLLHHYAVISPEVVTAEEVIRAYPPSLS
YRQFLRITDLALWRAHEDYLSANAAEINKEETFYSRIDARFLQARRGLGGNGNAISLNSK
EHLGNFSEAVRNVVSAMGFVDNFHELVSVDDTVEGDEISW*
>TCRU_9922 cysteine desulfurase
MFRGVCGLLGAAKATPTAAAASVTSTAAATAGVSSSGGSVRSSTCDTRPLYLDFQATTPL
DPRVLDRMLPYLTERYGNPHSRTHRYGWTAEDAVEKARAEVADLIGTSPKGVFFTSGATE
SNNIAIKGVAYYNKSKKNHIITLQTEHKCVLDSCRYLEMDGFEVTYLPVEKNGLVNLQKI
EEAIRPTTALVSCMYVHNEIGVIQPISEIGNLCRKKKVLFHTDAAQALGKVSIDVERDNI
DLMSLSSHKIYGPKGCGALYMRRRPRVRVRSPVSGGGQERGVRSGTVATAQVVGMGAACA
IAKVEMERDSAHISRLSKRLLNGLQSRLPHITVNGDLEKRYPGNLNISFSCVEGESLLMG
MKNVAVSSGSACTSASLEPSYVLRALGIDAENAHTSIRFGIGRFTTEREIDVTIEECVRN
VERLREMSPLWDLLQEGKSLADVEWR*
>TCRU_9923 vesicular transport protein (CDC48 homologue), putative
MSSQMRRLMMKQRQNGRYYHGQQQQQQRQRDYADEVHPSTRRNQRDDVDKRSTTGKNKRS
RGEEGIQATAANGEEVIERLGIIPKVTLDEMGGLAKEIPIIKELIELPIRSPHLFSRLGA
DPPCGVLLHGPPGCGKTKLVHAIAGSLETPLFFVAAPEIVSGISGDSEAKLRNLFMDAIS
AAPSIVFIDEIDTIAGRRDQTQRGMESRIVGQLLSCMDQVAQAWRQENKVVCVMGATNRP
EAIDTALRRAGRFDREIALGIPTMAERESILNIICQKLNVASDVDFFELANMTPGYVGAD
LHLLVKEACILAIRRKYNELEATGELENPNAEALISFTVTFDEMKEATKRVQPSAMREGF
TTIPNVTWNDVGALEDVREELFTSILQPIRAPRLHRRFGLDHPVGVLLYGPPGCGKTLVA
KAIANQSGANFISIKGPELLNKFVGESERSVRMVFARGRASAPCVLFFDELDALAPRRGS
DRANPSSERVVNQLLTEMDGIEGREDVYVIGATNRPDMIDPAMLRPGRLDKLLYVPLPSV
EQRVSILATHARRYPIDASVDLNRIAHDPRLQGFSGADLAALVREASLHALKKLYRSTTA
EELDLLERNLGGESIEKTLLPSVCDEDFEASLQKVRPSVSAEDRESYELLHRHIIQSARS
TV*
>TCRU_9924 hypothetical protein, conserved
MLRCTLCRHALPKIERRKRKGQHARPGLPDLPKSAGGYFFLQMRPYLPIAWQYGWRWRML
QGLWLGTALSFAGYLLYVMYFRDSDEVIAAKAAKYTYVRNERGEVIDIGYKPLIDASRRA
QRRAQRLLADDDDGD*
>TCRU_9925 hypothetical protein, conserved
MLRRLAVGPCVLLRLRFDGAAGEAGRGSVRYKRLPESMQPKSLGENFTPFPLPKYDEDFG
YGPVRLRNIPDIEKAKEREQRRGPALMESSLETSENETNMQLQVEGSALPSSSDVSSDPL
CKKETVGDGDSLGGYAVSRHYPQIDRLECNRSLKSLLLQFVQRPQVEARCAALADMASTI
STRSDAELVRMFEEVSSPFAYDGRGLNFLVTTVKKFGRPYAVTNSLVTAYVNLMNAATVT
LVQEQPWRLSRCPALTIQLIHFMALIKVFEPNKWFTSSNHAPSNRADYKHPRGTNQKTAF
WRTGEELFDFMVELVRCDEHGVVPPLLDLCTDEQLVDLLNGFLAIMPNGAPLGSVFNSIM
GCFLQRARSNLKRSLTSQDFGTMERMYLTSVMADASNDELLKILFTDSSCPRGPNFFAAL
SRRQETLLHEKALVFLQEAIDTANENHDAPTLLALMESGSEMLLSMVNKDLAHEFAVKNQ
FDYQILRSFQHFGVVADRLRMEQSGTSARIPLLMRDVQAQLLASNTAQACLVDETASQSS
AFLSEYVLPYPARRPSRPLMTMLSQLDYLNSMSSVFLLHSSLMATSTDQLVSAVRRLQSG
KDSLIVSMSCLRELSVKFVTSPKQKEREACERALEIIAYEVEKGRIVLLPFSEEIRLHDA
GTYCDEDLILWSIAVFFARELPLVKVRTLMHSDCTARTPYRFLKGRHNLLVSSHSLYDKD
APLLSALHSKELRLVTRNAKLRTAVRDRKCTLHYYNPIRARFVYRRDKAMFEKYHTNARN
LAPGFSRGALHHDWRGLGVYTPDHPQVSYRPLTWRKSELKLRAA*
>TCRU_9926 hypothetical protein, conserved

MWTQQLSLQKPNAQQTPEEKRKQALVTANVFIENNRGLVRKAMDQYQSVAGSNYWTYGYM
GGAMVTTMAACLSIGGRVPFFRNYASWISLAGGYFGGKAMLGMHNSYNLASVVNVINKSI
DETRKMDEQHGFSIPEYAREVDSLKRMKYELIPYSTEAIEARKHDVKNMSLNESADALVE
AYEKRKQASAQRK*
>TCRU_9927 Exocyst complex component Sec6, putative
MQKRGVASSLRNPQTFGGAAEGIDDSQLYTSAELFPYLSVEDRENLNREVVAAINNELVH
HENLEVTVPRLLRSCATEAKELRRAINSMASSQMLEGHRAVQIVKECGERIQDLRELFME
QGDLITGMEVTSGSYKQLRQLHFLRENILSVIKWAEALKEVRYTNLYKLVEQRQFAEVHK
RLRRLQLIRRTVSEKADSKYRNVFEPYFEKLDAVQTMFVSEVYKLLEESSMHVAIQMALE
DLPDAGTVAEVFPEFKQLEECVQLCGEEVGGGEDGTGIGVLCTADGEPLITEEKVYRAVR
KCVARLWEEQVMVDVVDPIAQISTYLEQMKKVAPLLGALELTLIPLSTKFSFFALVVGSI
HDEVMNVLQGYVDPAAEVEATGLLEASQFVQWYKESMTEANYAIYIDLNAIDSLSALMMT
SAVGGLSAHLIRLCRACAISVGTGRSEPTTMKNGLPVTTGPVDMFAVLQQSLGGLSTAIE
VSVMRQIGVACAEAIGAYLEECKIRSDYDFWEEENESMRISVEEWTTRRLLFLYAFCNDC
STIERNMDTIEIKFAPYWDDEEGGEYSSPFQQTQDLISEHALFYLDEIVLHVERVVDAQW
ALLFRSKDWYSVDDNPTQVIIDTMSDFIDEEFTKALEETRMRLAMRSMLTRYVQKYLTTL
MEFLGEIIRHQNNRSVEDWNAFVDCFSRDTVLAMDMWDERVKEGNGKLVNSARRVLEVIM
HLLSVKKPVDFNFIVQKDLLDDYGDCPSFVVRFILQARQNELDKDSRDTMMALWNERVAF
QQRGPDDVPTVGWSQPPSFLGALDRSLAELNKRGGLFRTSPRKRRVKAEQKRREDEKQAR
REERRVRREADATAKKMKGPFKAGMHSLQDDTVEVGKLADLLK*
>TCRU_9928 hypothetical protein, conserved
MKRERQFTVNDEDAQRRRAQTDSGDDETLLKEEILTVEETQTVLVRLPCLDFFRDAHICE
EAAANGRAEATHEGDERHPSRFRADGLTFKSGTLETAHPVVVLRTKEYGEMEFEGSWVAS
HEKSVFDAPSSNRVVVQLCERGDEQTEKGIHGSVHDASGSGSGAFNEPRSVSDKRGASTG
VGVASLLKHPSVGITADEARGRKRARNASWGYGRIDVPCATLVLRRVK*
>TCRU_9929 hypothetical protein
MLRHVDWETQQQSSLSRSHQYHQHKLKGTRTPLPRREAPPPPLLASTTPSPSSPPAVGIM
SMSSPLPHEYHVPSLPQENSPDRFSVLNANKRVLNDIQKDCLHCVDDELTWRQEALRKER
ELTEREEEFNTLVQMQHAAYKERLEEISRKEKYLMEWEQRLRSAEKLMQARSEKK*
>TCRU_9930 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain), putative
MQIGYGIRGGRGGGRGRGGNFDYRGRAQQPFMGTNVATDTLCVRITDIRQPVTEDMMYRV
FGSISTNPQRLQIAPSSNPNETVVMAQFSDMYATQRVMENLNNRNIFNDGNKMVMTYATW
EPAPVLPAPPTAVYGAPAAAYGGVQPQQPNIMYQQVQPQPSVYVQPRPQPAQQMPHVPQP
QLPQPRAGFDQPRGGRGRGRGGPGGQRGGGAAVGFDPMMVGYPPMAYPMVPPMMPMAGNM
MANYMNPKSMQNTPTVFLSVTVVPETEPLQTIFTLLETFGGVVTIRRNHNKKDILTVKMA
SIPEADNVVQHVRKVPFAGGTVSAKRFPTYNERTPCTDDGDPLDSATSQYDFTTARHRSP
GQRSKCNPSNVLKVTGCAGYSEADVMTYFTSENFFPDRIIKDEEGAFTVYMADTATAVTL
LVKCHNSVCGEERSNVLFIEGPKENNENHTEQNLDEGAAKS*
>TCRU_9931 DRBD4
MMSVVLRNIPPQCQEDDLRRALLIYGTAVSTAIAPHMRQATVTMRNSQEVRSLLHQGCIN
LFGQTVTVEPAPYGSNGGAPAMLPPHLGTTRINVIVEKCTYPVTKEILTQVFGMVAPPLN
VVCGPSGPTTTGWVDYADATTARRVIQQLNKNSIYPECCFMSLTLDRSGVGAPAMGGYAN
SPMPYPQQQAAQQPPLQQQQPMPFGHANYGAMPGSVIPRGGMGGRGRGRGGLMGRYGPTY
AANGPMAHPPYAASSTPYAQPPNDAVVIVSNMPETVPLHDLWVLLEVYGNVNSLKRQFSS
KSNVVAHFQNVYDARLAVQYLQGCPFHGATLLLKHFAGYVERGGRTEWNSGPATDPATHA
VLFSSGYHHRTKPTAAFNPTGRVRPGKNLFISNLTEAITDEDIKEEFTKAGFELDGYYRK
NPSVAIVSLRDIETAVQALILVHSQQLKERFLRVTFSHFPPGPRSNGEEENETPAAEAKE
TLAEKPTEEE*
>TCRU_9932 hypothetical protein, conserved
MAKGFLRVNWRVCGGWLILQWRRPLPGTTERVAVSVLANGTTPLVAWLGSKACQRVRVPY
GCDSMFRVLSGCHGLRRMLSRRLISMHSTMSVTKLPVHGPAGTHQCQETLPDPVLFEGR*
>TCRU_9933 hypothetical protein, conserved
MHADDLSIVINGHSREDTIPAANTVPKKLHARGQESGLAIIPSKCKAAWFTLSTHTESNY

DRKGKRPLEVAGCKIPVMTMGASRTAKLLGMDLDPQLTLNVAAASQRISQPRRIAHKEAG
PSPHDPRTFIIGYGASKLRYGSELIWAVATDSAKNEMQETYAGLARIVSGVPSTVDQ*
>TCRU_9934 hypothetical protein, conserved
MPVGTARERRRRRCSAGRRPCNAHTPRRCARSALVPFRHGQASPRRRPCVVALIEADGGG
VPAALTGGGGPVPRSPLAAQRAAGGATTLRAACVLPVSADASSVPRFPGTSQAAVSKGGA
THRSERAAGCGYKMAQQRIQYTAGARGQDKRRVAKGQFKRIQREGPNHIPVTRGHASTKC
ADSSGDRSKWDSDDATDERVSLLPDFVGAYQRYTCRLRAVSDAQRQKLLRGGDVERSPSP
IAALQMTVPSLTPAKLATLMAQGADMIAIRETWKSAEQIASMHTGECVLHAQSRIRKECV
AAVPLRKNLRSKRMPLITPQRDSSLEVVVQFALGQNRDLIVASTYMRPPPQPTQPLGGC*
>TCRU_9935 conserved protein
MRSALVLPALLVSGGCAAWKQRCCQPKLLTTAATRCVGSLVFSPTRIGQKDQRRGDRGES
RRLTFDERAERRMGKSREQKIVRENLLQEAEKVIQEDVPDELEQIFMQHFERANVSAMKV
LNMAKCLELLEADVGGGRKVLLTKVAQVVKTNNSTIEIVPQNASFASPILQRVTRFDGTL
QVTKEQQKIKVVMPPVTTARRDKAVQEIHQVISLFKQKTKHVRTNASKALQDASIEENAL
RELNAQLDTTVNAFTEEKVAELEQLAADVTSMGVDESDFGA*
>TCRU_9936 eukaryotic translation initiation factor 4E, putative
MSSVLKADVKEYIPSWANKRSSGVNPAATSTTKNGFATSVPTSNVMTTHSGCTGINAQNF
TSSPRAAAGLPLCSPTTALRLPTRMSPMHAPFPSVSISMNPNATDFVPHLTGANSLAPLP
TSTADLAEEKERQQKQESHLSSSMKWTTTSTRKNITQPALPLAVKANFTPTFAPIYVEKT
EEEILEISKRSSLKVGAAAFVPRRTLNRVMIAKPSPFSLTPATGEMTLGDLWCLFYLPAG
LGECIRENTYDPTLVFRVDSVATFWKVFNNIPQPTEMKIGTLYFFRDGINPKWEDPGNRD
GGILKMKLDSHCINDAWVYLLCRTIGESWSKSVRDTVNGVALKARERAYLLEVWVTEQSA
ELMMDISELLRPLLGDVFSVFYAPHSVTQERAAAAALAEKKRSRNNRRRW*
>TCRU_9937 aspartyl-tRNA synthetase, putative
MSDPGKSNTAASQEDVSGNVASKSAEKKQTKQNEKEARKAARLAEENARAAEKAAQLAKY
ADLFGAAPLLQSTTYCSKKFSEIYALTKEHVGKTVTVRARVDTTRKKGKLAFMVLRDGTD
SIQAMAAVAEDVPKEMVDFIGQIPCESIVDVEAIVCGVEQPITSTSQQEIELKVNKIHIL
SEALRVLPFTLEDASRRETDEGIKINFDTRLGCRWLDLRTPASNAIFKVQSRVGQYFRQF
LMDHDFVEIHSPKIIAAASEGGANVFKVGYFNRDAYLAQSPQLYKQMALQGDLKRVFEVG
PVFRAENSNTHRHLTEFVGLDVEMRINEHYYEVLDTAEELFCYMFAQLAKHTGELEAICR
QYPFEPLLWQLTPEKIKELGVGVIEDSVEPTDIYKARVRNMGTRMLRIHYPHCIALLNTV
LEEKLSLTDDINTTNEKLLGKLVKERYGVDFFISDLFPTAARPFYTMPFPDDERFTNSYD
MFIRGEEISSGAQRIHDSSLLLKRAQSLGVDLSPIKDYVDSFRLGAWPHGGFGVGLERVV
MLYLGLSNVRLVSLFPRDPQRVTP*
>TCRU_9938 hypothetical protein, conserved
MWRRISAGSLLVHVSATHRCVAKRIPPPLPPGARGTPPRAASFGKLPPPPPLPGAVAAST
GAALPWKSPQEVLSAFVEFIPTFYVPIHCVAAILSEDCRKHFIGRGRFLSFLKRYRFFFD
LRIIDGVRCDVKLRDDLSHPRRGAADEKFVMTDVGDVINYVAKPEFIVSIESIEQANTSV
ALKPACAPPAVHVRLEEKVPVLERLKALVPEEFALLDHVEEGIPEDVLFHPYFDCQGGLI
SIASKFPEFFQVADGMIRRRPPHLAPLSVNDYTLEDSPIPSVAGLVKREVCDSDIPHWVN
ITSLYEQLTREQKQQIKREYKSFAGFLRSHGRSLSLSQDMLQVAKWIPHQRRAPTSAASP
GASDTTGSPEGTTTTDGKSDVAQAHGVTVQYEYTHTQVINELFDKFPPHRTLNLEELLEL
VAPAMRPSLPKKVLAWIASYPSYFIVDDPTEKDPSKARIRRASDRQPLDVALELYRWIPE
EGISEAALLTKLSEVHRDYVKRIGLRHIVDSLSEWLSFTEAPGGGGGGAEGEEKVFLLRR
LQTEVELERAIHTEESKLASGDENSLPAQIEDAEMERRWPKLKYEGTMSQQQASVARAQQ
RRGRGDI*
>TCRU_9939 essential nuclear protein 1, putative
MPGREKGRRVKRQKNPLGDDLHADRFASARRHAVAVEDDGDADEKGVLLPGRTTSRILKT
ARQQLEAIADEEQLGSAYNAEEDDEGDHTVTDPGLAELECEEACRGGVYEDYDEDEEVVI
EYDDTESMATEIPSEMDVGVDMYGMDDEEVRLLQKFQPPSRVQSRNLADMIMEKIREREG
ARDAAGDTHDGASVGEWEDERVDPRVARVYTAIGNILKSYKSGKVPKAFKVLPNIKNWEQ
LLMLTKPHEWSPHATYQATRIFAANLNERMAQRFYAAVLLPMTHQHMATEKKLHPALYMA
IRKALFKPVAFFKGFILPLAADEECTLKEALVVASILQRTHLPPVPTAVTIVKLAQQPFS
GPRSVFLRVLIDKKMAMPYQAVDALVEYFHRFVHTQSREDKLPVLWHQTLLSFTQRYKGD

LKAEQVNLLQQVCTKHFHYLLTPEVRRELNAAPNAARAGYRG*
>TCRU_9940 hypothetical protein, conserved
MKEEPMSSNKRIQLLRERLELYNATIAEAMGVVTGVAGTETTAAPGTNTNNNDAKNSGHA
SEWQRTEREGGRSAAAPCLERNLSAEFNAARATGRAAAASGADNINRSEGGGGARRIDRR
TVPPPPTPPNESRRGDLRSCSTSSASHDDSTSTYSFESGEEAFLNPFLNETISVEEISAS
VRKVRRTEMDSTARAATSVLVGGRQKSTSPHESNRDMSTVDEGDNNERSSLPLPPSPPEE
AKEEARNRKDTTTAEAASWFAGLEMANNKLAVTEQAIFKLQRTVDIEHFKRSLPQRQQAL
QLAESRDDLVKKEQALRRREPTGNSLAMIYEADALDLDQQLQQLLAECNAAKALFTRVHE
RKAAVAEKERLLKRKLGELEDLQREVREKRQALTTLERRNEQREAMLAVRGEAYRKDLEA
HKAREQSLQERISGVEELSQKVASWMKILDERDTKIEAKEQRLRRVQSDLVRRSEELLCY
RNGRAKPPSRMASRQTNSP*
>TCRU_9941 hypothetical protein, conserved
MPYKSSTESSRRRARTPVAALAAADHPCGSQTPADAETTRRAKSDVPSRLRIRSRVERGL
HQEAKKARMEPRTVQSQHEEELRLSRELTLHCDAVVQRVHALADKTQIQEERLSQTLKES
IERSPIRQSSVSPKREAVGSLSPQPTSTRKTPRESLSRWSGMFGTPQVPKAPPPTPAHPD
PAAGASSSVGWLAKVLGRSPEAQPIPNSKGATPSLKCSNSPPPADVICGNPKNGAASSSP
SHAAPAEHSSLLMRAVQRLSGRFSSPPQEAGTPNCARKSVVFKEPAELEAKTPQRPTKRA
EGPQESDGLAPRGSLLYPPAPPPSLQKDAARRSPNRSPSSSDGEQQSAVGPDGSEVVAVM
QNFSHSRAFHKLTKADLVAYAKLHHVALAMSSTKRELFEVVRRLVQAKTDETQ*
>TCRU_9942 SAM domain (Sterile alpha motif), putative
MGRGGLTLLLLAVSLCAVLCESSPQDKNTQVEPITISPSPIANKPVQEWSVPDVEYWMNH
TVGYAEFGKYVRKYLVDGPTLLEMEPADFEEHFPVDNAIQVVKLTAHMKLLKGFCLCGAA
ERAIMDFWSYFAKENFRVWVVGGTAVFFPRLAMLYTFFFDDELYKLLVGVPVPQASALST
AALDVVLATTRTVPVSHTLLYLFCLAAAPDLFMAYEVACLAFTNYFVMPFFFVHYILQAF
NSYFFLFLLWKGNAFPPNTSVLEAIWMMHSYTLFVPPAALLLYPIIPYFLQSLLVYVLMG
HTVVVVVAYTSLFFESPKTPGETA*
>TCRU_9943 leucine-rich repeat protein (LRRP), putative
MTVPLPWESYTPRAFLQGSSGTFHDFFWDVVHTYVGHSCESLRLLREGGMALSTSLRTGS
SCTHDSVRPVVPPQLLTTGVIPPMVPMEELPAVDCCEKDTAIAKLRERCFRYGESVLRLL
KIAEDYSASWGRLKDYEQKQLDIALSNERASRIRKDEIYAYFTDLIFSGKGLRQVTEDIT
LFSNLTTLVLSNNPQLTSIPYLPPACLVLVACDCSIREVCASTTLTFLGLSYNAMEQMEF
LGGLPNLRVLDLTRNAVFSIEATVEALRAHPLLEDVTFTGCPIALLDDYIERIDAACPRL
RLLDHVSTGGLPKSPSEAMKHTPAVVLSVELTRLEGLSALAHIPVLREETPLAAFSEAKA
TKVRKKARTALQGPLYECSTSITLQGSWGGNGDGDNDGGAVLVKCEKLRLGPEVPAATQQ
RLSKRKLRVSATQMENVRVIDHLVTANVMPTAGLSQSLARPFVLTVKIHDDIRFPSGNCV
ALTCDIGSFYADASSLLLSTAPMPRCITMQEPLVVSKMALEEKRFQAKEFRESAAAAMES
LKLFTQSSEAFSGVLNLSGTLPRRRNKSLMVTAQGAAAERFLAETKRREAEMGELTLLAF
IVERRIRELQQLELTATMGFSLGSAPKVVEADSPTTGRAKATLRGKGERMRR*
>TCRU_9944 Tryptophanyl-tRNA synthetase 2
MRRISRFAAPLVCGGRSCATTRGHDASRTERKEDVVTPWGVAATGPRGVDYDRVLARFRS
EPVDEPLLQRLEETCNGRGEHRTRGGGTNGIAPFFPPRHRLLPQGFWSRP*
>TCRU_9945 hypothetical protein, conserved
MFFHTLRRLAVSKAAIESYIDYLRNADRELPALSEILPRHQANTKELLQFHSLLCEVMQE
NGFNFMGIKVIPPSSAALQCLRWTDAVCVPLFSNAFQQTDFSVKQQRIHFVEPLFVLRLG
RDAPSQLTANAAVAVCDTFRPGIELNGSRFPFYPPHATGFAADLGGCIGVCLGEETDLGN
TSLDTLGNHYFVMTRKDEPLQVGSGKNCLGGPSAVVALAVSYAASMGKPLRTGHYVFCSG
VGSRSPAVPGEYKVNYGVYGSVICSLS*
>TCRU_9946 hypothetical protein
MPSSAEYASMMELDEVLIQRFLAGFQGETEEQLNSLLELKSLVEPLDPKVAQGVVFRNSG
NCSATIECLRKLGEKHSVKTEINGHGESPRDKNIERSFFSWLFKRKPKREVTKSTPEGAS
TKADDDGTPSSSKVKENVSIFISPHEIREKPLPQERENNVSQEKEQNFDHVSLTRPVIRR
SHEEEELSKEYNFYGKPSTNFVSVSDPGEEFQKIYSKFLESMS*
>TCRU_9947 cell division cycle protein 16 homolog, putative
MKLVALLESNARRFLENDQPLSAISLTAILREVKPNSPSYSILHAKALFAAREYDLAMRL

ARSVINDDAENSEAVLIAMKSAYELGDTKECSFFADRLKQIPFMNVIALCYLGKCAEISG
DTKKAAYHYQLALEIDPFCGEAMTALVERKLLNITDLRALIDSLRFPSDAEVLRASYKAR
LPSELVSQEHQKYIPRTILKLQAATAEYERNDLQQALVLTTELLEMTPFNREGVCLHLSI
LVNMKATSKLFDQAHFLGNNKAHTELAVYAMGCFHFSLSNYERAGRFFSRATELDASFAE
AWIAYGHCYAKLEEGEQALGVYRRAMNYFPGLPCCSTFVGMQYSRIHQWGLASYFLEQAR
QIIPNDPLVLNEIGVLHAKTHRLQEAVRFLRMAYQSLPNPENPSEHRDCIIFNLATVCRK
IQHYDEALSFYTLYVKCRPNASHGHCGLAFTYHLMGNMKVAIAHYHIALSIKADSFYRDM
LDRALATEFEEKAVGTAWRPGGGLGSPSPDDVSFSTVSRTLRSESVAGESMGPSPGPSLG
RSLPF*
>TCRU_9948 hypothetical protein, conserved
MQAEARAVCLALSVFPAVLPSTMDIWVDGNSLRGAANEGSSRSHAMTWELRRICEFLDSR
GIRASFTHVQPAGDSADGISRGRVFALQDLAKGSGGVLWLEDPKVCHFVITN*
>TCRU_9949 hypothetical protein, conserved
MQDTSTKRKAHEYYDRTGDTSSGSLECHGAFHRTGRVEARCSNRGDAQFGPARDLAVGEA
RRPVRPSPEYCLIFGEVHHNADPGVAAGRIDVKRGTAEGQEPWLRAEGRFFHDFKHRAAT
ITGRATRTRLAAPQDERTIPPQQVNVPVLNLEWIQSRLNPATLGSLMQVWGLVGRAPLPP
SSSGKAREGPRRIQTADARVLRKAGIIEDASSTITGGWIIPFSVVEEKPAGLRRRWIVWP
RGKNRDDPYEADVPLSHISHYLPPVMAETASCLDVKSSFIVSLPRETRHLFRCRVEDGTL
VELTRLPMAYKAGPEILQIIIISAIAVVTTVVRRLWAAPPSERVNVWIDNIRSAGSKSDT
TLWETQALRNADSCHTTGGAANWAPRSKPSCGCGLVTLAGRHP*
>TCRU_9950 hypothetical protein, conserved
MRGQPSLSSIGEKPNAPCDANVVISLETMRLHAMCAPEGITHNTGVHQKWQRECRTLLMN
AGDGSPIRSATSHQSAQASRRAVDAPSDLSNCPKKSSRRATELIRRRRSTAVQRNTDIPA
LGQLYEESERGDSRDVRAVNVGAENAPSGAIRGFLLHARTADQRGELCGLFGGNRSGAID
PTAAHQDAAVHVGNGSNPARHGDSGVTKNRGDEADEAGATLDEGRDESSNPQPDRLEGTC
FLTTCVGKCELLVRDCGLNSQQFHTGAGRDLHFG*
>TCRU_9951 hypothetical protein
MTVATRQSTMREIDIKLVCVGAANTGKTTFLRYWETGNPPMHLSTTIQMEFHRREMSIAV
PSPAYFEKKNRSVEEFKRTTSNNFVGDNALDGNDQRLHREDAFGCSSSISGDNSNSNKSN
RDNAYNIAQPCSLPLSPNTNGERLLSSSVGKENGNNGNSNSSHGFPHNPFGSEYVLLPPR
IPPPHLKVFPNSSSTGRRICSIFYENDVKNETEGKWPLVHVPAIVKVWDIQGQESTKKMT
RIFYTGAIAVLIFCEMSNNMDSIISALSWKGDVEQKIHIPKEKSLLVSSTPPAIGGKFDT
RGGSSSKGQIEEIESENPPCWLVVNKYDLLSGFASPPEWASHAALDELCARHGFAGWSYA
VGRRGVNVEAVVQAVIFAAMERFPRKFTWVWENETIHVSSNGKGSGVDPVVLRTRKRLKE
HQRGRCCSN*
>TCRU_9952 hypothetical protein, conserved
MQVSLHNRVKTYNLTAGKSLPEWISERKKNKRLAGGEHRIELIHDLEFPHFARTIFRTAN
GTHLFVSGDYPPRLKCFDVNQLSMKYSFNADMPILSGVSLSPDFRKFALRGEGRQITVHH
SAAIIDRVRVPHTMRSLAYHPYTAELLSGGTSHEIFRLSLETGAFVESYKTQSASGINHV
EVFKNHGLIMCAGADGVVEAWDSRAGSCASRLTVTGPGALSGIDENCELRHIATDDESGL
LFSCGTESGHVLLYDLRLQKPLIVKDHMNALPIVKTYFFQGRSTSTGEASHILSADTRSL
KVWNKKDGSNFTSIEAPADITDFCVLRSQHNMAEPYECSDSGVVCICCDAPRVQVHFIPQ
LGVAPQWASFLEVLTEELEEKEMTTVYDDYTFVPKSEMDALGMTAEDLAGGKVRPAMHGA
FIENRLYRELKAVIDPGEFNRYVQENAKRKLQQRWENRISKFKRVSNGDDDGVAHAVHSD
NDDDNAMNGVGAKCQALAAARADPRFQKAFVGNSASSFALDASNPEYAKLLQIINERRAQ
ASRRRQRYESELFTIVPDAESDGGNDEEGNRRNGNSDDVNDSGDDDDDARRHLKGVQSSG
KQQRRRQRPRTQNDTKEADGILHDSNGKENKRQVTLYEVKKGSRVSFTSHDKAIHASRKR
QRMEKLPLEERLRRMSAKQ*
>TCRU_9953 heat shock 70 kDa protein, putative
MCRDQFERCLEPVKKVLQDAETKPQDVHDVVLVGGSTRIPRIQQLVQNYFGGKELNRSIN
PDEAVAYGAAVQAHILSGGRSEKTEGLLLLDVTPLSLGVETAGGVMSVLIPRNSTVPIQK
SQTFSTNADNQRNVEIKVYEGERPLVTQCQCLGTFTLTDIPPAPRGKPRITVTFDVNTDG
ILVVSAVEEMGGKTHAITITNDKGRLSKDQIEKMVHEAEQFANEDRLNAERIEARNAVEN
YTFSLRATLSEPDVEAGITLEDRQKIQAVVNAAAAWLDENPEATKEEYDAKNKEIEHVAH

PILSAFYIKRTMERPHDPSTTGGAAPEGNGGADAPPQPTDVD*
>TCRU_9954 hypothetical protein, conserved
MRGVHLAPRHAQHSAPQRNHARTRVQCIVATEHSRVQRYTATDKLQHDAIHRHRPSTSHH
GHEGNAGHNQHGPHEPQARQHQHRCVRRGLRAGKIHKRRRPRGNQQGVRHRQHGPRGKRA
GQHKRTVQRLHVAHRQLHRPALVAPRRHRTAQRSTAHHVQHGAVTQRHVLHNDPHAVPRH
PRHVEHRTHAVQHNVAQRHLARASRHNEHRPHRHALAEKHTRRGAHSGRQCRSTHRHARL
AVPAAAAHAHAHTVLHPCRRRPGRVAVRVPVAGVAPNNVDAPSVAKTSRCVLLRRRQDTS
TRVVARHPHMRPNRKRQAQQQHPRQQRSVAHKAQRAPSSGHGASGVEHLPRDAVVHVVLH
Q*
>TCRU_9955 hypothetical protein, conserved
MAIDDAVTLWNTLPLSTTAESLLIASPFITTHDGLSRPKPDRGISLVTVKRFPLIVMFVC
GGNTPSGLSSASLNVLPVTAMFSDPTAAYALPNSNSTAPSLHVHPSNVTFATSPAIAPTS
TVRLMPPPLNVTLR*
>TCRU_9956 hypothetical protein
MQRGRGVLHARDGVGGPQLVLVQLQGRMAWRVVSSPRGAQRGCAARSGESRRRRHELRGE
PDTDEPHAELVEDAPLLRGRDIQRRGCCVDVLPQQHAAASPHQHHDHRVHIP*
>TCRU_9957 hypothetical protein, conserved
MTNRVDRSRTPSRASAGPYRNPSCPRVVGTYCDPPTVARSVEFASNTLECSGIAPCSTIV
PSNDVTFVMLTRAWGIRRAVISLRPPIRSCAPPTSTQWRSVTFSASANASIERRSTATVI
GPLNTTESKHAVAHPPPTVTDSVSVTPLTQSCAPPPPPPDLAGGTSNGRHASPTPPSRQL
HTQSENDAVSASKHANAAAQPSHGTTLTEDRPAMR*
>TCRU_9958 retrotransposon hot spot protein, RHS3, putative
MSANDILFLVLGMKNAIQSADLEKYSLSVFLRVEFFTSIVRDLKELPPPSPSKPRSSVLK
LNPHGYPTEAAAITELRFIDSPEKLEYRVLHIPTFPTFPLVDGFFFLNSPRRTLVGLQMT
TASAHHTTTSTVRQFTECLSGFFEGWEEFAQGLSWEMIYVQHADSTPMSDWQRCDVVNSN
NVSEEEDQRIAAFWKGRVRQYQL*
>TCRU_9959 hypothetical protein, conserved
MALVPYTVSEWCDIGARLWDPVRQRGEAQVQITFINGTEMSDETLTVAPSSTGLCLILGN
VTRPWEDSSLTGHIANLRAFQVPNFENQLILPIMGAARELGRVARAHHCRKEALEHEKRP
CRRGRAESKRSASFAGGRGA*
>TCRU_9960 hypothetical protein, conserved
MPASCLSEIAALTPNNVTLGPDGAIVLDWPAAPKTARADLRRASRFVRIRGQDAPDTTKL
CGALRHSEKLMNPGTAQVERAEAPWNATAHSIERGVLRRAARLVGTYNLDPHVISQLAGH
GGSFGLPQDTVRYFGRRTTTLTQVSSLAAQVRRETPRKDRNPG*
>TCRU_9961 retrotransposon hot spot protein, RHS3, putative
MCSTVRDILLDGETDISWMKLDDFLREHFGSRAAVEEQNVGMWFFLESPDAYIKDQQPLE
EVSNLKDYQLLTDMRKLREGNVHNLEDWIEFKEKATVTPLTRKKITDALTQIQKEVARLE
AEEDVRRDTEEKTTKLEGFYESVYDAKWGHVLGFYDNKIRENRMEIHEGKPPQSWTYEKE
GLTFEKDDSVEQFSPPRPRLMVLTSDKGWPYSWRENKPIVDCYVNCKVDRVWRIVEDDLK
DSSSPEQRVLIGTSGIGNSMNAGSYLLYQLLHYDAEKIQVVVHCFGGDVAYVFDKTTKTV
TKYVGIEASVSVVSGFSQRGMKGYIIYDAPTNEAQLPISFAPSTGWGTIVLASPKVRDIN
*
>TCRU_9962 hypothetical protein, conserved
MAMMVPGRVLLVCALCVLWCGLTGVSADGASGGHVTLGENVLEIVGGQSTSSLAIPGAKG
ASTGGVLVGGEHPTSDSGTPVDVSFLPGSDDGSVSDSSEEDSALTKDSPRELKGKAQSVS
LVVSPPKVKEIVSPESNKQGIVLPAPAESENHNAGGVGAISNREIRDNGGHANASSNDSD
PVLPSLSPKVQLPAISQAPGIPPPLSLGQQTSTVTILQEVETPAARSRETSVSSKEISRH
AEDPAEGKKGIPPAPTHSQNSTDEKHKTSLLQIGTESAAPKPLSPDGVLEQNSEGTATKD
AMKTDVDTGSPAATSESSISTSEIVAVQNKTDEKDGNEQQPEPKGLHNDPDAGNTNFAPT
AGGTAAETVKTITAQNNATSNSVDSDGSTAASHTTFPLLLLLVACAAAAAVVAA*
>TCRU_9963 hypothetical protein, conserved
MKFTISTTIEDVLFRGEFRYKEMKLNDFLLLIFGGRGVVATNRSVLLEEFLKEPARYVPG
ARVLNEIKITVRYLRIEGTVMEEMDLEEVVRMLHHESVFPLSNGRNMKEMTQSLPLQGEN
*

>TCRU_9964 retrotransposon hot spot protein, RHS3, putative
MMLTSDKGRPYSWNRKENNSTRDCYVNCEVDRVWQIVKGDLNKWFSPHGRTDFTPKRRVL
IGTPGIGKSMNAGSCLLYQLLHCDVEKLPVAAYSVGGNTT*
>TCRU_9965 Protein of unknown function (DUF3720), putative
MAMMAGRVLLVCALCVLWCGAVFGHAMEDYWGEGGGNGLRHTSNGGDDGVSLKADCGLLS
TRMALIKAVEAAEGEQEMNVTAPLENLEDNKLGNNTKGSGVAGLEGNDGVAVQPPTKKPL
NLGRSGAGEQEGMSRPVDANDGKRTSHTHNQSVRDPEELKAVESSSSSGSPGTEGIKVHN
LENTSERNESYKKTPTEENNLFSKYDCTELALKEEPEKTADKKNASHEAPTETRGIPAKD
TEIQTATPPSPPATMNGHSSTVNLRPIQLLQHVQDDNAEFRTPSLMANGGAANNEADKST
DERIPNSDPAADDAGTAEGKQNENKDANPKERPVEATAMKTTTATTGDSDGSTAVSHTTS
SLLLHLLVVACAAAAAVVAA*
>TCRU_9966 RNase H, putative
MERLSIHRIQHRRKTLLVVTDSQSLLAALNKGPLSHTHWTEDRLWQRLLTLTRAGWSVHL
QFCYGHCGVHVSEPADQHATQTKESGQYTEQGIAPLWHTDLLTCLTTQLTNKWRSTIRQD
THRYLLCGTRPSDLSGKDLITQEVLHRQELVHLASARCGESELWGRLYWAVRDCTNQCRF
CNISPEQSAYMRSNNDPTAPGTDTVPPSAREEDVFPVRGRTLTRRRKEKCPHCDSTLTGF
SGLVSHCRSFHPEHPPPLPELKCDFCNMVFPTRRSTAQHRIRCAHNPDATRHRNSSARRR
SLLPQDQPASTIATISPQETLHHLLLECPGTLAVRQRLGIEQDLRLGKFSQRQLLHSGKL
LSLLDHLFGTQMALYS*
>TCRU_9967 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAAMVVVAEGSDGINEITGKLSRGSQSASQVGHAEDPKIL
KPNDGVSNTSEKPLDAQELSNVSPQKGCVEQSSIFHGGMEVKEEKLEEKEPENAEPRRNG
KEQSQDAPEGTRGRKGLMEAQGDPSPKTPAEEMPTIEEATGPAKEQAPGQGGETGQAAKP
PQSLPATSPPASDRGQPGGSSGADRSVGGSKRGEGSNLKISASDGVNQSAVGSLGSGGGS
SGGDGGSSRGDSLGSFLSAAGTSLSSALDTPSTQDTQSSEGVRHSEKMPLGTAVPNKQPE
ERSEPKAKQGTSTSEEAAESQDDSGDAVEKEKEKRDVGLKSTISPTPNTSNPPVTQTTPR
ASSAEPSPTTTELQVGGETSKDNVTITKRNDTATPGDSDGSTAVSHATSPLLPLLIACAA
AAAVVAA*
>TCRU_9968 BNR repeat-like domain containing protein, putative
MSRRVFTSAVLLLLVVLVFCGTGGAAQAGVDDQSSNPNFVWKDISDGETVESLSVPGLIE
VGSGVFAVAEAHCKKNEKVFTGIASQLLSMEKGNEPKELLEDAKKGTQVLEEGTSGKEKR
VDVGRPTTVVEGSNIYMLVGKYCREDAANCQADAENIKSGILLVKGEVSEGDKKIDWKTT
DGVPCTLGEKENSLKRLIGGGGSGIKTNDGTLAFPVEGTKKCKAQKRMERLFR*
>TCRU_9969 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MLGDGSPQTPEVGVSSGEDEETAKRTDGQGEEGIHSQDGEANATALNSSLGKLSQGNNSD
AGTVSESELLPSLLLLLLGLWGFAAL*
>TCRU_9970 trypanothione/tryparedoxin dependent peroxidase 1,
cytosolic
MTTVYDFQVNAADGKPYDLSQHKGHPLLIYNVASRCGYTKGGYETATTLYNKYKGQGFTV
LAFPCNQFAGQEPGTALEVKEFACTRFKADFPIMAKIDVNGSKAHPLYEFMKSLKPGILG
TKAIKWNFTSFLIDRHGVPVERFSPGASVEDIEKKLLPLLGGARI*
>TCRU_9971 hypothetical protein
MRPFFTAAGEEGQEKKGEEVTVIHELPSDTPAACMAVDIMKLGHMNTIKPRLLLIHEDGL
LFLSTSPPPCEHDEGVSKVDGRSSFLDYRVRRFIPLCAIDALTLYARGTVLRIQVMREHD
VVIWRSEKNTICRELKNAGLGILTVANRIIELYASVSLSSLVLHSVEDLTLPTSLQLSKN
DIGRMFLLAESYAPLRTRFVRRRRTARIMKIVACEHRKQCDGTECIDLRQCAEMWGGGGG
DEEDGLGVEVGVVVKLFSWNAEKVTRSFCTITCRGQSPHSDALLSFVQDYPVVVMMEKVR
MVSMATSIVSQWPPTDDVVKMRRSKHDMEDQKDILDARHDVVYDTTPIAGARSLLLTKHD
VVLFNDEAGDAQRSGALVYSLYSLARMGVELPCHGEDAGGGKLTMIFEGRAGGQDMPTRA
TTLPVGEKEEEEEEEEEGERIQQTTIVMEFPTPPSRVDRCEGDYREQLCTAGMIANAILV
LLGCDGIDVPVLVRSPSSSSSFETLFSLAETEEDEGDEDTVRVLEKKHRRLFPDFVREPR
DYRRPVGVIPRRFASDKTLLARQVLRLTARRVWKTCLLVVTPNMLFLCDTTTLVRRRVLF
STLMGMKLLLHHSEGPVLLMCIYGEHDLVLKQHSTTPSWLPLNTVADVIVGEHPMIFLDE

VSLAGARGKLKNLLRLRLLRPPRRCASVPKHKKWFHAYLSNASMEVFYDALRQERKRMHP
KEGAQQIDTSLPLISSCERISEGSISDPRVLHLIEKLMKESLVGLWRGTIFVNVKLKEEQ
EGVHPTQHQRRMELDEEADYQNGVMSFTRELQPRLLTPVCMDMTENSVLHVCDGVVCEGQ
AQMISTTTSGEGELRGVQATLRMQEKQPYNTVAVEQDGIHALFGYLPNNNLGGFARTELL
NAGLFPSGVDFLATEQRDILVSGRGTAMNKKCQSFSLLPFHLRSRFLSLEDLTPMTTAPG
KFISSSPSTPLLVPYRIADDVALWAHEVPNPLFLMNIGPTWTMVRFQCNDDAMICVGNAA
FVRHVHCTMRSVTFYHTEDERNTVTCFFYPVNQNGNASWSEDKNNPAPCWGKTTHVRRLL
QDVLLVPFSSFLLQDASHGISQYGAIRLLNDTVFCRVGRYRWFEIPLPLLIKDWGGGSGV
EKMTRFCQCSC*
>TCRU_9972 asparagine synthetase a, putative
MTSGDPAAFIQLQEQIVTVKQVFSSALAKELNLVEVQAPLLACCGDGTQDNLSGTEKAVQ
VHVKGIPDSKFEVVHSLAKWKRQTLGDHKFPVGQGIYVHMKALRVEEELDTTHSVFVDQW
DWELVMPPQERNLTFLKNTVQRLYAAIRQTEEAICSKYNLDRVLPANIQFLHAEHLLKMY
PEMNIKERERAIVKKYGAVFLIGIGGNLTSGEPHDLRAPDYDDWSSPVSAADITFPCGDP
TMNSLASLPGLNGDILVYNPVLDDVLELSSMGIRVDAETLRRQLTLLSNEDRLGYVWHKR
LLAGEFPQTIGGGIGQSRLLMLLLKKKHIGEVQCSVWPKEMRQNYPLL*
>TCRU_9973 hypothetical protein, conserved
MESVTVQQPEREQQERPASVAGAGSAPAVIPRRRGRGTFNQPMRADQPLVNNTKASAVSD
GASVLTAVTTTVLPAVSHPPAPRVPEEDLAAEYGGQKRDIPLNIRENFGVCETEHETDTV
RQLLFRGEKRRRYCIIVGELQNPSRPITLKLFGHKGLKPFKLQNKLIRLVNISVGRPRPQ
RPAVDDDATDANCDNNNNKAEEEKHDHSEELQTEGFPGQEDANGDPETISEECDEQHGKV
DSEQEKQTEETKSMEQEQAPQRENETVSLENREIKEGDTFQRGEDVDFYADEETVLPLTV
ELRDSNTSNMGQPSSVANSPVLTATRFDTLRRYFFDEFKHLLSMEDVRMQHVSINLNLGA
AYCCLAREGSYSTPLKYATFSEFVQRMNEESMQLYFLKDAPTCVSRAVDRECGALQSEAV
FSLVKICFFSNERQSRSVARAMWDAHENRFVLLDMESSGVTFTWTVFSVDETGVAVAAPK
SANEENGNVGAVGSGTAPIGKVVMRKKTVAFPFELEFHAYHRWKQHTEHPAAPIAEAILD
KLSLAEHNLIHHGSTIGYESMDLSHVCEVDAESEDFNVESIIVEHTSRVKPRGTDLTVDS
TSSLWIENFAAARALKSRIAQGMVPITTVSHHVAREKPRGRGGRRSPTQEVAKQNLVTPA
SRLTFFRSRSSTVHWKLRPGYSTDENLAPLSEALCFAQQVINTANEIERTSVRGGAAPDA
L*
>TCRU_9974 WW domain containing protein, putative
MADISKDEKKRKKKKTPVMDVNGDAGVKDEEVQQLLQSGVWKTMKQEETGRTYYYNTKTK
QTCWDLKKELMKQRRAQEERIVEDTAAEERTTAKVEEREAEPSVSSRGAAEAYVDSAASV
TNQHMDLTVVPATPLTDDAGNNNNNELRNDKGDNSHQTVFSFSEKGRELMQIETYKDPLE
RLMDETNLLEKLMLSSGTSQAMALDFQRSYEALARTNKALTTQMMKMKQEYGAMEMALKE
ANMKLYEKDLALRELQCRTRAVDKKDEAERTLIFLREQNQELVRQVGELTVALSRGFNEL
AYQRALTSGVGEVDPDKMAANPPSLGQKDSLGTTLDRVLTNAVTRSIICSVCMGELEKLR
LSLLSDEEKTVVPTSRVTCPSTATVGVGHHHHAHYVPAVPHAVACNYPDQPTAKMKGGKD
SGDTGGSSGYFQRQPPPSPPSSPYQQQRQGQIGTHGGLGVQQSSCSAPQNDLAHYSYSRN
GVGLQSYPYPRQLPSPEKAYGRTAWNAQADDGENDKYADHFPRVSMNRRSESRNSVVSAA
SVFGGFRIRPSH*
>TCRU_9975 hypothetical protein, conserved
MCRPLLVFCATSCWRRSARLPLPLFFSPLNLQVAPFTSWNLQARYFSTTAGGSREGTNSS
EDDYVFDPTLSVQKDAAIHVAKKSLDAIVRDLLPENAPDAATQKVRAYLQQHPMDTLITQ
PTVHITHVEDPESGRETKMSLSPCDLSEALEQAQEREMNLVQMGTRGDVAYCRIRREIPR
ILGLVGPELEALREEEKQEGSSHRGGSDQAGGKIRELVDHSFRDVVDAHFVGWKSKKIVE
DIKKRHPVKITIKEFQSPEAAIGKIREMCHAMQRYAEEKLIYHHFTSIVANDREVSVSFV
PSLPSEKGNSWKHIKYPGEKEWAHANKRMEEACRKSGRYGTYVKNNMLKPRSLGQTFFRV
DKYGRKID*
>TCRU_9976 KREX1
MALSRTWCRFAVTTYRQSKVSDRFQLLITKKEVECDYVAVDATALVAMGLRLAKNVTTEQ
RRHKEVARHVAQTLQQLLKKVRCKKSLLIAMDGAEALLKAERTRTSSLTRKVEGRLMRLP
GTALMQAVEERLVRMMPERQIVPGEVVFSGTCVHGCVEQKMSAWALDLASRETFNGSVDS
LCFIGASELYLNVMALSPFYNITSVVQNNADLRQMRLQDILEWLELDKKAKEGESVTIAK

MRTDILFLFLLAHGASATELNPISGVGFQELVERYMSSITATPTPDATPSPSGHQATSSA
SAEGSFLFEDVSGNALRLNVPLLCRILQMVARKEAVPRTDAVSEMHLEHTLQTHAMLCLG
GTPEYDYLPIMPSPPQAHSSTPTLVQFAGHLSALCGTSPYRIARCAVPRLNATGSTEKNE
QAPEKRPLTAAEYTILCQSLPATVESLIHQYVGVAPKPDVGKTITTASTAEAHRIVREVL
SYANPMKPNKCLCLSPSYCWLQSEKTQLWRFEYVDVGVRSYQGETRRERNAIKGMTLEIN
MSRDGPSHFAPSSGTWEPIVNFPCGAEGEKGTTTNTIKGTEATATALQEKDLTKKDTESP
PATETATENEVKLEATAQKDASDPVLTTHSARSSKEGGRSSNKNQTTLKLLTWNVMFDRY
SGKPTPLGMPGIDWCSPKRYPVLARVIQQEDADVVGMQEVEPVFWEFLSKQPWMRENYYF
SCGYTSPSISPWGVLMLVHRRRFPVQSITYLNVPAWTNHVSLMPVVCLQLPHGPVHVAAA
HLLAPYTKSHETARTSQDSALRHHMLKTLTGDVVTMGDFNDWPTNEFLMPAESQYVDCWP
LIYPHDAGKTMDETNTFCKLKVEEMFFGRSDKLFLRSRRLAPVEGHLVGTKSVNDENGNK
DAPGYLFPSDHYGVSMTFALKP*
>TCRU_9977 hypothetical protein, conserved
MLRIVSLGSIVDDPRFIYRNKHKAMPYPVGYTIERGVFIGAGGNALGEKAKVLFPGDEGA
DAHVADVYFTASIKKGLDGGSLFEVIRSDRPDVVHSGDNPSTPWRKAFDAAAQDFSERLG
EIVGEKRDANGGMVVRGPRWFGLTLDSVSARLKTLPGASVVFRDGKDASREGKKTREGGA
TTATAATTTEKGKKDSRTRSSAASSQQVLSRTDTSAPSKRRRVTEKEQNDDSDTKAIIDD
DDDVPLNLLVTGRISGLHEPCQVCGLRTSFCPMTGKPHGVAKSQRSSGVSAQGEASGKKS
RTPLKSNVPSDTVETASNRAGRKRLRDTNGVDAANAPTVKRSRGGASKPANRQKTVKVET
PSASAASTQDGQRRRLVQLKLPGQESKTESVDMEEMPLTTLLARKMLTATGSVKTVSSPL
PTLPSPTQSPFWRPPLAEPESQKALRVLQRLIRAEEVIHVPFASLLHLPLVASAKPRTVK
KKKQEGEDTTVAEEPGEDAGNVMDEDNSAAATIAGKKKNLVEGKDRHPLDITDVAFSVAG
KRYVKFMQLYTSERMKLDLLKKADVIQPVQRTRGTEKKHTETTEGVAPAFSSSIHADEEN
NELRQELQQS*
>TCRU_9978 40S ribosomal protein S16, putative
MTAEKSHTHKQVQTFGKKKTAIAVATVTKAAQCNIRVNGVPVSQILPETLRAKIMEAVNV
VGSRHFARLRIDVTVRGAGQVAQAYATRQAIAKGLVAYYQKYKNEVEKAALKDKYLAYDK
YLLIADPRRCEPKKWGRHSARTRFTKSYR*
>TCRU_9979 40S ribosomal protein S16, putative
MTAEKSHTHKQVQTFGKKKTAIAVATVTKAAQCNIRVNGVPVSQILPETLRAKIMEAVNV
VGSRHFARLRIDVTVRGAGQVAQAYATRQAIAKGLVAYYQKYKNEVEKAALKDKYLAYDK
YLLIADPRRCEPKKWGRHSARTRFTKSYR*
>TCRU_9980 Opioid growth factor receptor (OGFr) conserved region
containing protein, putative
MGKVQESQKECPELSLQSTPDLGGDLEAHLARLRESADEVAAAGGNFREHPSVSFYRGSR
PVQVRLPPQKEGETQNVTSCLHVIALHQALLPPCRDGTSFSEEEQSARLSSSDGLELLQL
NWNRLLWLFMPSVQLGTRTEGCTLTEADQISVKKNEEFTKDSLISYCEMSQALTWKDYKQ
LRHPSMMDRVHYSYVVFLRFYGWRLYDEESGILDRHRNWRARYKMLVPRSDVHDGSVSDS
EVTIGFYSALSRILCVLLELCLTRYAVNLIAFLLEEMHKGRLLFLQSKLERSWLPQILHS
KQVAESEKERLRRQLYRLVHSDSD*
>TCRU_9981 DNA repair and recombination helicase protein PIF1,
putative
MPGRWFTAASERRNKAHYAGGALLRRLMSTATRHGPIASGLCRSMGFMSIERSPVPFSPL
LLTAARGFGHLVREVDPHGFKGDIHALRHKNSASTQRYVAEALASEENIIFCGAYHTGKM
TILRAIGEVCERKGKKVVYVSADSRRACRIDGMLLHHFLGLRYFGKNELPSQDQLEGALG
RHVRLCESTYASCVPSLATADVFIFDAVDQIAPTILTSIDRVCRDLRGRPREPFGGLRVF
AAADFWHLPVHPSSDTGGYVYQLDNWDELFPRQRLLEKIHGQARRLTSLVNKAYFGLLTP
GDIEELEARSATRGLTVEKEDESRGVEDADGSDVDDEEEDGASNESSCGSGRRHSKHESN
NNNDKSKESGSLFAGHVASLPPQKLISNVEAIVKFTSRFPKQPAIRVLPPRFRTLKRTEI
GNYVVSMLLQSSLLSSFSLVDSLNLDVGSSVHLLLGAPASFGVPPGTVGEVLQVKEHVLV
VHFPSVHRTVEVPRMRVSVYHSFYPEVRYEIQQFPLFPRQNISPLNILNYQHAYNVDIDC
HRLADTNDLGNILARMRSFDDFSIQRIQDFVRLDGMIHEPTRIYYQRISNRPLSTAAEQW
CRNCKSYVPTNEFYSHWNECIRQVRWCSECNTRIPLERLEPHQEKHQIVLCLDCGRAVEW
RRWEGHRLTCSAMMREVSPENEFLPLRTRQLALELGLDKRDLHTMRAFSRSLLPKSRKHC

SGGSV*
>TCRU_9982 chaperone protein DNAj, putative
MGYGVLAFVLYNGSFITSNDKKKEETGKEKRGFISQTVSLLPLSGFGRIGFEAWYNTSEW
QSIGIGFATDLSLSILPIGYKTRNSRGRATNTISFLYTRKQHRIEIPIAAFISSEFRWVL
LWLMTPWVCYRAARVAWHPFQRSRLATIYRQRRLEHRTEMDLARVRAMHEQKAVEVLSLR
NRLAEEKIGGLVIINAKYGVLNPRYPESLCSPVKNGAANASQRLPWWRRWRTKLTASLAG
SASKSKEIITEEDAVASSVLVLDVTVPLQNFVRDSQLVLPEGSKSKLVGFTDPDPFTEEE
KELKIVYWFQRRRHVVTLTDSEPVELPRREHLMES*
>TCRU_9983 RWD domain-containing protein
MPATEMQSMEMDMVQGMYDSYELISVDPPTYSVLLTATADDPPELRVTIVYDSEGYPETA
APTVRLEHIAKHRRMQTATLAKEIEDLCAEQIGMHSVISVLQKAQEYLTDYAAMEEKAEL
QRRGDALTKAAASASTAAPDPTVRIGTAVTRELFAGWSEKHIAEKLQKRVLSEKKSTKLT
GRQLWDGTLKNADWDLFEALEDEQDIDLYTLANGEGEEVDEVEYDLDDTAEEG*
>TCRU_9984 chaperone protein DNAj, putative
MRQSALAVLLPLLQRHAQSISRRHFNVIQRGNDREVESLFALLGFGKESEVERVHRTRDE
LRQGYLREAMKLKDPQRNAKDAAKLADLRRAYTLLSDDQFRARYASHHCVSPDATLHVHV
DGGQTAANFNPEHQSFEFVDHAISFSSSSLLSSCAQRSFGDFTGPFQSATGVYSSPADAH
PYQPRESSTPQNGNGINFMLRISFDESILGCTKSAVYEKDITCSQCSGDGRQVLNRPRKC
PQCRGRGSTHLPSATYHIERSCGYCGGKGVAPPPKCGRCGGAGVIRGHTVSVPIDVRPGT
TTMTVRRFRGKGHDGVRGGNAGDLIVTVLVQEHRLFHRDGIDLHMVLPIPLSVALLGGVV
SVPTLHGAQALRIPPCVRNGQRLTMDGQGVCLDGESDAAEKNDLEACEGSANPKQQHCQQ
QRRRGHLYVHLLVVIPRGEELTGAQRCALESFAAEGEGGINQENGEKGEQETPASLKQRF
RHWMTSL*
>TCRU_9985 homocysteine S-methyltransferase, putative
MSTRQVTGVLIKDGAMGTLLESWDVDYAKAGSMWSSSVLLSEMDLVKRAHRAYIDAGCDV
LLTCTYQMHEEGCAASKVTMCELVDRAVQAARHTMPQRKQKGLTEESTAKERRTGGIDVF
RYALSSIKDNGQERVVLLAGSLGPYGSSLPGGQEYLGEYSIHEAVINAFHARRLEAFLCN
VGEKHAFKVDFLLLETFPRLDEALGILSFVNQHEILRTAPFCFSFIAVPVKNPLPENADD
DALDNWWNAAASSIRLPDGNTFEGALSELRGNCGTALVGMGCNCSGPLEVSLVATALLHK
KRQDTEGPLVLLLYPNSGEKFTDGQWKKPLQQIQTSAAEGLSMRDLKRILARGGGNLITF
MKFLLQLLQQRPEATDWLFEIIVCGACCRSTPEDIAALNQVAREEPYLHA*
>TCRU_9986 hypothetical protein
MLQLFQHVQKACLQRLGVSADAEQGNADDTTPPLAISIRRLRAIAGGTSVRRSLAGAVAA
AVPEDAAPPKQLKPVLYPTPDGALRPASGQRKSSRPTLCSSELFPASMTPEDSRGSQGEQ
SSPNVRRTLGPIFAEDVSSPPFTAAVESDRETPLRRRSLLAVAVDNGLMETLIRVCTPAK
LATEARDDFFTLEERVEALYTIVYLAFHTDNGKSMRQVDTREERQKNGKGEGENTSLVCK
LDLFQLAATACDVLKRVVEQTLEPGGVHTEGKNEQHEIERDAQTLRALVVVANTFFILLG
CQNPSHWQEEEDGWDMDEATMSYIDVPSKKIFSLYEATTQEGDFCLCSDADSSSYQFMIT
ALTENGLWQYLLRHVAFSFLSRPGVPCASHDHLEEPIARSKQREASEYQRIARNLGVRLT
LKIMTLLLLRSVAAVDRDLSSILCCLTPAEEEELEFGWHRAFPRLKGQEKSHPSLSLMEK
QFVFTLRRLSGFLVFRRLSCLAANAMHILFTRLLLLPAPINVDVHVVLMALFFVEEHPSS
FLMQTPTMRDETTTSPNHLRGIDSYAGSRKTGNTAVVSDFLNHLLHLFSFNLSLQRKKEG
GRVPKKQRYIYAVRTTSTELTLSGALLSVVLLLEQKQQERKGKIEEERRHYHACNGISIE
AMMTRHNLYRKCEESPEFQTAFSAGLGRTHQVMLLFSAISAQDGVAVVPLTTLRLEGTQL
TAFSHLVRPNEPLPSALHRRMVESEAWAETLTVGVRSSASIAASAAGVRRKKSETTFSCA
LTCPVRLGTLNRQRQGYKDARNNEGAVRGDGLSDRVLQVYLKAPYTEEPTGAKTISSGAI
KATCVVPPEDSPPPMFFGYEPASFRDGVHAGGGNGNHNNHNNSGGGKVETMFVNCDPLKY
TQLVHNMSCSSSLQRTTMTYSAAVNLTIVTTPCEEDGQELMWPFDAVILACSTVHGDELQ
LSSQPPQKFIYSPQEEKNKALSEPRGINEREAQSRHDRRRKVALQRGASPPWAGTRGEKV
LCHASRRDRDAIASAESPSLAAVNEESHLSGAEGGSSRMKEEICVPNGNDPEAQAGCSRH
SHENGASQSGQNEEEDDENMFTDLDAYVASIKPLQVIDFGLQRKEQEVALLQKQLEQSKA
REESLQERLQEVVAQREELISSLTDRRVEVELCHTEIIAPLRREVTLLRHSLSLRNQEMS
SVISLCQTLRNENASMAEIIRDVRGQVENLARNAEHQK*
>TCRU_9987 hypothetical protein, conserved

MVKTVPDDYFPTESDGRQTELSKGEPSSSGGSRITAWFLSRPYTQFVDFGVPEGGALRNA
IDTVTSLVQGDKMEAAGRVVEEAALHVEVFAVNGTLLAMGTNVLLSVIFNPMRTFFLEIL
LKNERGKLMVALQHTFFGSDTASATKGVAHGMNSNNVSESPSLINRFWVILLSLDSDWRR
RTEVAMILVCILLCVLILLLRLRFAKYFKSLELQLLQQPSKTARRPGRNTTDPQGMSLPF
IPLTSRGKLVPDKLPPAMYDVSDEAYAHDDDNENSNSGNSPPFLSRTM*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MSGSVRNVTLANCTFVGGASLYVLGWLSDPPAGERADVLISGLESRSGGGVLVANRFPPG
SRVTVVDSVLIAEKHVAYRGAYGLGDASACLVLHNVNLTGSVLTIARTHVAAVFRDAVGV
LFVGGVALSSRGALYLDGLLVQTALGLCVSVEGGVAASGGSVVAFVGSGFLLCKHAVSVR
GAVSVSGSAVALVRSDFLSTGDYAVAFYSTVSLAGGSMLLAKGNVHDGVSKEMLHAAGAV
TAAGSTLSFVRNRALLPRMLSVSLSLAAGVHLRVACNDAGGRVLSTAEEYAAAGFGDAGG
IDVVGCDACDRDTHCYAPGTASASMRNGVCVCACGSGGYGEACVPVGAPALPPAAGTASS
VFVREGVTVQSVFVVPAGASEVTLRHVVLDGVSPVLYVPWMARDGVRIVVQNVSLLKGAV
LYVMGGGGLRGAGAAGSDEGGPVELSVCDVEALNGALVLTGTFPAGSVLTVTDSLLVAAR
PTPLVYLPGSQSSPYAPVLVLSGLRLVRSVLVVSGVALVTVMTGGRTVVVDGAVLEVVGG
GVALDAVLLGGDVAFYASARVVASGGAVLRVSGSQVYAAHGLVFDSGVEANASAVVVNDN
AGALTDGALLVLRGSASFVSGSWLSVRGNSISGRLLSLPSYPRSAEFVQSTLTLHGNAGS
GPVVMDGTVALGGAGRNFVVGCLTLNGQALQPFDYRSAGIIGEFRPVACGVCDADVRCFA
AVTRAMSGSCGCRCAEGGYGHDCLPVYLPHVDGCNRTPGMPLLSRTATLTETRSPTPTWT
AKPTPSLSTPHYSSTQYSLTETPQVTGTVALPPTRTPTASVSSTLWWSDVACPTLAVTTT
AAGGSLTQNDIRGGGSAVPTRLMVALPPPFRWARDPQLGTHLSFVPVSTAQPRGFGGPWG
AMLSNATWVRNATNPSTVLELILPVHRGYFIAADETVFIRCDAAAVSGGCKGVLLGSFTI
RSNTLPAAASALSAITGVVAGAAAVAVLVTGGLGSVLEMQALGVFARMSCASAQERASTA
ALPYFLSVFAALDPLWMVVGNALLAAVFGCVHCGVTVVFQRWRGVDAASAWAAMRFPSLT
YVVAHAMHLGIFFGSVLALAMPDARVQHRVIGVVGLLYGAAFPAGVCYLIARHVGASFTR
YWQFSRKPLHERLLYPVGYWHPAAQQRMYGGMLTNMRGSHVYWCVFRLSVLCVVCLIAAA
HPPVGGCHVQYFCMAAVLLAGAGVVAFTNMMRSSFLTVMQTASFVLLAALCVVSAANHLA
PSDGGARAYAAIVLLLTAVLLAVAVYSVVVWYAEDRHWQELREPRRGGLEALLRDDEESG
DETQKLYDVASSSYASGTTVASYRPPAPPLQPMAGDTRSDALSLFDHVSSASCSINYAFL
DR*
>TCRU_9989 hypothetical protein, conserved
MWRCCGRLHVALLRERWALTASPTGVAVRLHGAPTAPPCECHAQRHWDCGTKQPRLPFGA
SDICWPQLGGASGMLHRTGVVMAPRSGISGDGSDAAARRGVEGTRRPEWTMSSSVKDTLL
EGSTLRTDMKLNDFLRNYVGGTAAVGERPQRDDAGVFSGAGCLRTRPAAS*
>TCRU_9990 hypothetical protein, conserved
MDGVSITNGVAVVFDVAAMLPGALRIELRNCVCDGGAQIYVRGYSGEPASDRSLEVSVSG
LSGSYCSLVFVHNLPARTNVTVRDSTIVTAGPMRYSQLSGLTDAVASPLVLYATSLLQTQ
LRVSNTVLRSLQAGGSAVYVGGGVDLLSSAVVFDGVSLEASGGPAAIRRVTGAWR*
>TCRU_9991 Leishmanolysin, putative
MLTWCCAWQGVVGGGALDDCRGGCQEPRDRDDIDGMEMQDGDGDGRTLESHWSRRHAKDE
WMAPIGCAGCRTELTLAAPADLGCMRVKWEMAEPMRWWRNSCCALLQRKCSAPNMSEYPQ
MFCEAGVHARRCTLDRYSSGWCVDELSMKGQQNARWTVAPSLVPHWM*
>TCRU_9992 hypothetical protein, conserved
MSFGQSDSLSESSLNKNNNTPTRNDVHGATSNGSQTPPTSSHLRPIGGDSPNQQSVDLMH
PMTPSVDTPRFGQNGICRMSDWNLSPASFSIPLNCSTPPPPTRLARATSVLSSSSQRYCH
DPYSLGGSQRLSPQSNPISNAASPPECPIPSLSIEGFDDNATGPLTIVTVMAAVPKERNE
TRGRRKGRNGDHSRNSKALPDLPPPRVMRYLPPPPPGIDNVTNRILSLEELHPIAKRWYD
RTIAAEASYSQRISSSVWLPTFGAMAQQQPLIPAGRAVLCPRVEHYPNSFWQWLADAERW
WEGAVRPHTGTAIPPPPPPPYLFGA*
>TCRU_9993 50S ribosomal protein L16, putative
MSLLQRSVVLRAYHYVHPKTGRPIRQFRRYGDPRFINNEAALIKGQWGLITADFGMVTQS
QLENARLAILRRLPRGAFTLTMHTDYEEFPVVKKSPESRMGAGKANIHHFAFKFTTGIPL
FEIMPVSSRRLNQAEAEGIFLAGRPFIPLQTVVVPQGRVDEYHVFK*

>TCRU_9994 RNA-editing complex protein
MVSKYRRLLQHDTSEENENGERENTRQQQKKQTNIRSCKASVRASDEDEDDEIVLDELHE
EEDATEGEGGKKKVSDAHSAGASADAAAPSVRRFGRGRKEVDSATLSVGDHEDEVDVKSD
QTASREGYARNSVDAKDHKNKNKIVVDGKEEKEDEEEEDVDAGEDQEDDDDDANAKDTAM
TGSCGARLYSCDACPHAVFTTHTALLSHVEERHAELVPDHARLHRIAEKFSKVWSRALKA
RRDAIALWGKKVFAVAVQRDAGEEKMQEAHRARAQLELVVRRWHEKARVFIFGSSVAMGV
WDGMADIDFAVVDVEALDAGNWPPLEKNAVRSITELLRRAGFSFVNLEPISHARVPIIKH
HASSPILTVARKDAEDIVARSVRFVLNAPASREDRVMLEGSVRDAVGPTGVQQVWWNRTG
DVMSMTLENTTTAIRAAICSPAFVTPTLRAKVQPVHDECRPELYNVDFDLSFRAFGIRNS
NLLRQYLMSHPCARPGAIVLKDWSKTSGVNNSVNGYFTSYAVNIMWIYYLIQKKYVPYVD
PLDIPASLMNETNFDPKYIPMVDPTLTQEELDVLYQNAGNMLVGFFYFYSFEFDWEHHVI
SLNRPGITTKKMLGWHVEDVVPPMSSSLSAGVGGGVNSNTGGAGGGGAGATTKRHPTRYE
LCIEDPYEENLNLGRHIGITKSLRVRTELYRGLLSLLKDGEKESCVFASTDLAESADATG
PLSSKLPVRALFRLMALATQAIAESKRFSSMDNASGDIAGDGEVMTSTSTGTAVGLAPSS
QSKTSSTTGMVGRVSEKQLENIFLEKAALEYQLTRKVWNWQQLIHRLGYKIHRGHVLPRR
ELGVRCIAKRDADESLNDMHGSKNPVVRGQDLTESILRDLSRGFMTLTPEWVAWSKPWAS
QHLRGYSRLTTTADHLVSADASVSTSNKGVPSGGEPAMGLMRGTRRNAFPMIGRRNIPIS
VPMPMMTGAGVATTIARLCNGVKRLLPLKFVR*
>TCRU_9995 mitochondrial carrier protein
MAESQPYGYAPSSGEVMVDMAASLVGVFLQRVVMAPSHRITVLTVVEAELVHEGRLPSTG
FGGIIGCVRRVYAKEGLRSFFRGFLIDAVLAVPSAVMEEVSSSLVSELLGVVLPFDRVQQ
MSPLVWVTLSLVSTSISVLIATPVTGIQNTIVTNYVGDIVAPHPAAGDVKEYVKEGDFGE
EEKEESYKYNSAWETAADIRRRYGFRGFYRGFGLDAMAVFMYRGTYYYALQILPPVLHNQ
YPHAVACSLAIVARCITQPFEVISRRMQLTASSERKGYKGMVDCARTIVAEEGYSGLWAG
LRLRLLVTCVWMAAVELRRLY*
>TCRU_9996 Mitochondrial carrier protein, putative
MSSEATVVEHQPAYRPDDPEFYLQDQGQRSPGAELVNVLGRIAIRVARLIALNCLWAPVN
RIFLLQCTEGELIQNGRLSHGGFGGMRGCVHYIMKKEGAVGLFRGCFTEMALSIPAYIAQ
VTVILFTVRLQQQLVVISRPASVMLGVAAPGLRVLLTAPIVGSKKTVMGNFAADIVACKG
DVVTTDDEEEEAYLYCSAWEAAAAVQKRWGWKGLFFKGVDVDIIAIYTQSLTMQFMGMAI
APKVEEIIEEQFQRPGRKAAAMIACTIGVRLICSFLFQPFQVIRARMTLLSTSVRQKQKR
NRRFWHHAKDILRQDGITAFWAGLRMRFLLDVGGILLSTLMVH*
>TCRU_9997 hypothetical protein, conserved
MTEGRFETIHNLRPKNWDGRRHWTNWHHLYDCEKDHLERESCPFHDLRAGGQFQYEYMGG
GGFQAPIPPNRLNDRPNGDRMDFAKGRGTQVGGLGDIPLDVEAGNPIKHNKHPGKTVIHT
KKNPLNRGLFSNYPYMPDPLDGRAAARDPRGGEGGIRAGRVDGFGQAPEWIADPYNDKID
RGRIHHLKAGPLNYGPEGIPPWMPEGEPEKSKKRKYGAFYAGKPSGIINDIEWIPDPRIE
TGVKRHARPFRTWHTRTKWSMPTHAPWSTGKITAEPFRGQNLDVTTAGLPSLDTYRRVNL
TPSIGKEAALSLIKAPEPVRLK*
>TCRU_9998 hypothetical protein, conserved
MLFRKSMSGVRKLSGRKPVVSKLFNCFANSPSSESFSLDAVLTDACKRINISIPSSSKEI
AGYKWWERLCRACADKPSTSYYGRAMLRQRLVRALSERLAVDEVFRLDGHEIEKEDIIEP
LVVMGLPRCNGHQAAHVLSRSGLFLAFKQSDTFAPSLLLDVERCDAFYRRFKWFSFIYPD
FSCVRTVNPNQIDDDLTLQLMCPESYAWGFLHGLDEYLLECLQEDQTPVYQHLRRMCQLF
QWYRRCGHFSECVLRDINPINNPIEEQKYGSKSPLLKAQWLLFCPFAILSIESLHEAFPD
MRLIWVHRALSQCIPSLCSSLAIHNSLYTGKSPSDSQLVTLGDKVLGTFGSGAEYAIDYL
ADFDKNRMVHWSNRDVKRHTTRLATKTLDYFGIDVDRYRRMQMINGQTEYIEVFRPLHDA
KMPYFGLHDGVVSEVFESYIYQFEEFAYENRFGVTIEDYQPLAAPADQQSLGTLRVNGGD
QPSFPSFADSQPIDGHFLQENKGFK*
>TCRU_9999 vacuolar transporter chaperone, putative
MSNFFEKGLSIICCATNSTKPWAEGEADGDEKYMNLQGPGVRNLTGSVNDKRICVPQKID
PKTFFANERTFLKWLSISVMIGLMSLTLLNFGDTSSTAPELAGLVLLPVSIIFMAYSLFI
FRDRANKIYMREPMRYDDTRGPTLLVLVLGAALLTATIFSVQRHYYKAMTPTIHGGAIFS
*

>TCRU_10000 protein kinase, putative
MEVGDQTERHDASTDTIIEELKTLAKYMLEATEAARQRTLSVEGYKSYEALLGALESSAP
GTNCIKESTVPQYHCDPVNEISFSGGDELRKKAHNLPLLLNFAEKSKKGTMCLKQDIYNG
ELDNEESSPSEKYEDDVGYSAEDIPRLNQNKISSNTRLANFDCSGDSEENIYDGVKTQVI
FKAVDPTLYQEISGCTWLPEPLCIRLDTGETIEDDSEEETADIDDGEDDTKCKKKRVFRV
PSFPFGGGVTEGQAQLLSKMFSDAMRRGGLSNSIGPKYITKKEFINYEYEECSTTEKSRD
SFVPKSPFEFVVELEREVVFDAVQAREERRREFRRLAGEGRAPVTMGSFNLRVIMDPLKT
GFEEEKTFPIERGTIIADRYQIIELLGKATFSRAVRCYDLHQPFYEDDDDDENEPETECI
PNDDAEENKLIDGKKRQRVAGYAEVCLKIINNSKDFFDQSLDEIRLLTLINKYKDPDKVH
VIRLIDCFYYKEHTMLVTELLSDNLYEYSKYNREEEETFYFTIPRLRRIARQIVEALTYV
HSLNLIHADLKPENVLFVSHRRCVVKVIDFGSSCFLSDHLSSYIQSRSYRAPEVIFGCDY
DGRIDVWSLGAILAELVTGEVLFTSETVPEMLARIVYVCGQPFPRRMLWEGRHTAKFINK
FGCIYEQGNKDGEDSAEDSSYYYLYTPVFQPRESQSVYEQDIEKKRDDIADLGDTRGSLP
NEGPYSVLRQKLAAHNVTDEYFISFVEACLTLDHKKRPRSKDLLSHPFLTQSD*
>TCRU_10001 Leishmanolysin, putative
MAPTVGAGYYTALTMAAFADMGYYRVNWSMAEPMSWGHRTGCDFLEKKCSEITDFPTKYP
HMFCDDSDNETLRCTSDRRHVGKCTAAIVENKGTPAEKDVCPVVSSYFHEMSSGTTYNAC
SDGTVNSLPGSLTGGDSWCLDAELVETNDNSEHKSVKGVCAQVSCEEGTVKVKYLGSSDY
HSCPEDTQISVTLNGFEQDGKIKCPKYGKTRGLLRKRTFALLSLRTFTKCRLGQRTMRAR
TEL*
>TCRU_10002 Mucin-like glycoprotein, putative
MMTCRLLCALLVLALCCCPSVCATTVDEDQDVAGSETLAPMATVETEQASGTPDNLKGGS
QKYAGQTSNPTSDKEETLESHSAPQTHDGAPVTAVGQITTNPEQPPTGGTESANKAKERP
LSLEVTGKADAQQPTSATAAMKVSDSDATA*
>TCRU_10003 hypothetical protein, conserved
MLDGLPRLGLEPNAGCITTCGAAMLWHALANSTPGNNSSQLEDRKAASCHPNSPSTVDDL
LRRLEDMYSASALMYADDLALVASGAGTHACAAAMRLALSLVSTWAAERNYKINVGKSES
ALFHTSSDTRSDDGMANLHLGNGNLRIQSCSMRFPGKTMDQLLNFGTHASTAAKRTMPRR
YQLRLIAQIGASHHTMQSFLIGYVHSVSLYCGDAIVPCLVPTYLHNMEVRYRKGCKTSLG
ISAPTEDASVYLKANPPRSGRHSGLLRSHNTNAIYASMITRICVLLSIRNPCLRPCIIKQ
QLQYRSREMLLLMDCAAYVTLLGCPTTTIVLLLPNIELFPGTLCVAIKRDFISHLLSKDA
SDDFRRTAFDSIYSSLVL*
>TCRU_10004 hypothetical protein, conserved
MGYRASPEILQIMITSAIAVVTAVVHRLWAALPLVRVDVWIDNIRIAGSKSDAALWEAQV
LRNADSRHARMEEDRESGAMQHTFLGVQFDHTHQTVSLSDKFVRSVRAMPVLNSSTIAEM
EVTASRFLYLAAILCTRLCDCYFFIKAVRRRLSELDLGIVLETSSANLPLAAVGLDERLR
HIIEDTTVGETSSPRRRHRPPSSRMRRSMDGEPFLFQTPATLKLPEGNGRGSLFLSCRPG
HARCA*
>TCRU_10005 hypothetical protein, conserved
MELIRQRRSTVVRRITDIPALGQLYEESERGGSRDVGAVSVEAENVPGRAIHNLLLHART
ADERGELRGLFDGNIRCGAIDPTAVRKVAAVHVGNESNPAGYGGFEVTKKLRCDRRRSRL
AP*
>TCRU_10006 hypothetical protein, conserved
MQNRSAQPHSQVEEAHNDLSAREANIAVAGGLPAERECALAGSEQQLETDNSQIQEREAR
VGAREAQRAAWEAETASREEAPATRRGPTDGPVTRQNMTEYGVTKKPH*
>TCRU_10007 hypothetical protein, conserved
MALVPYTASEWCDIGARPWDLVRQRGEAQVQTTFINGTEMSDETLTVAPSSTGLCLILGS
VTKPWEDSSLTGHIANLRAFQVPNFENQLILPIVGAARELGRVARTDHC*
>TCRU_10008 hypothetical protein, conserved
MVWCWSDQGGLYPLRRGKASGGSNDTAAGGNNNGTDVIPLMVVPLMLDLMDFRRMMCNIS
VPIRLLVLVQNGREAMLSLCLQELERVYGWSGRLAVSRHPENIGYSADVNIGSRLALSLP
REEVPFVFVTNSDVMFSPDLLPSLLRDVHGMTRHDAARMDELSAEAANRPSEYSPVLRRG
LRVLRSTVNDGRLSTSALLPDRIRYASVKEREKAFSKHYGHFCAYYKSSCFASVILTRLA
ISTVEYFDENFYPAYVEDVDYSLRLRLLGFQERNVLCGKFVHRGSSNIRFSNKMELPDAL

WYRRVKSLMTNKPYAMMKWNGLKAC*
>TCRU_10009 hypothetical protein
MMTTAMTATALRREVCALLSLALLCCCASIFVTAATATGAAVQSTDLYSGASAVNVSVEI
SCADSENKLQWRFPGQTNWTKCASSLGAYEYTVVASSGGYNTVGVVSSGDGDTVIGSTGY
SLGTSSDTIEDVEFVTIDTGSGASGRDEESLCLSADRMYLTAKCNASCNSSVSDKTAFTM
EFQTTNESGVYKKWLENKTETSVAALPFS*
>TCRU_10010 small nuclear ribonucleoprotein SmD2
MLDERPTKTLRTESGAKKVSSKEFLKTTVSEGPFSVLDSAMRNGTRVFIQSRFNKSLVAT
VVAFDKHFNLVLRDVVELAMVNKEQKERSIRNMFLRGGSVVFIVKLPHNAA*
>TCRU_10011 hypothetical protein
MIFVCQTCGSAITGAWRHDCETQTFTCHGELCKRRYKLNNGLPQSYQQQKQQQCVMPIVV
MPPQTPRDSSYAGRFLAAQGLRARSRLMGDDKDFYLPPPLSRMFPTMQKQPTHNPNEKAP
GNNEESPAVQKEPLTFIKLPQTRESLPTLNMETSKEGNTGNIRTIHRIQFEGDDWDAVLP
CRKNELYMALQLDICNSLPFPSSFSVQIMRTGGGFFAYITITRSAEVSDDEVCRHLSEYH
FPETRRIYQSAQLQLSAQFLTQNSGEYIQCPNTPSVFAPSESLRHGLWGGKAIRINGEPY
QCSRVPQTSVKNTTATLKVDDSYLLDPSSLQKNELIIDNKSNKRSTEVEKEEVAGIANHS
QKTSCNSEKEEESRQNDLAKLIPAEKNYYSSINNLSTGEKINNTSVLMYPEIEGGRSMES
LPQSVTVVPRGERPMSSKSFGVSLVHENEMEGGRSMESLPQSVTVVPRGERPMSSKSFGV
SLVHETEMEGGRSMESLPQSVTVVPRGERPMSSKSFGVSLVHENEMEGGRSMDSLPQSVT
VVPRGERPMSSKSFGVSLVHENEMEGGRSMESLPQSVTVVPRGERPMSSKSFGVSLVHEN
EMEGGRSMDSLPQSVTVVPRGERPMSSKSFGVSFVHENEMDDWCLPPRGQKWRSLLDKDV
SLRMVEMNGWCLPPRRFFVLEDRDSNHVCLSEEVFVCDNGLSSLSKPSVMPCGDSMAPCA
VSVGKSEVFESSMTMDRVSFEGGGDARSPVFHGMHCEAATSPLFSGACNPEERWLDVLPA
RSIDKNPWKFSQYTARGRSNVSAQKILPVAEAVGLLKGSSNVLLEESEEALMLSVGETDG
HLLSDGDVSSRHLELTETKDVASAQGGNGLLGALKDQHVTVEGNKLEGRTLPTGAENYEV
APLKKNVVPWDTQESSCAFEVYELSASNSSESSCVEIWLEREGPRAFSRLLQHLEEAERV
IRKPVELLRRLRDNEDGGYCYQA*
>TCRU_10012 hypothetical protein, conserved
MWRPTRWLSLRLTPDPSLVVLPAGVRRVEVYRNAVSSREESIIWDELSLVLEREGQKALS
ERSTPQSKIMKHTYLEMHGDQRFTEVKSWQRKELRRLPGLVWSPTLMACMRDVAPALLGS
VPDTARVVEHNMPGYEMHIEHPTVGCCFLYLSLLSDTVLSFDDEPTGRRGQVFLPQRSLM
RCSGEARWGWRFGEQPNDTHTFISDAGVRRVVETDMRLSVQLWRFTPQLLDARVLQDRVE
ASIRRLEEREKNGSDVRHTEEPCESPKSDFSAASVGQNTGGGPLGGDYAANTSPHPGGGT
KITMGTIEKDYDKYKQKFQNVHGVLQEMKALQDAGQPINDMWLKRKILDGQGNAEQDTSD
GFDAEDVEGTWDRVDARARFYKARLKSMDYDGSASLNNTMPDITEDAPLDMKKTIRKIAP
LVKDGEKIVASFPGLQ*
>TCRU_10013 hypothetical protein
MRRRTDRRRFGAVATFVPLLVFVVVALSVCQDALRSVKHSFSEVDFEGEQQLRQETRKEE
RSPLGATFTSKVQSILNGSRLVGDGLDVHMFVLWQHAYPQWRAILQDICKSFVVLELAEF
DWGDTRMGLQRFLSNLWVLYNGKGGWEREGMAKKVQQCGYGRFIAIAVADMNPQYARKHT
AHGVDIVNVMAHKKKVLYRKWSGGGFKVHGTFSTHEANHDIRVLLHTTIEGLLLRAMETQ
AYARDIVSAYLDDPAPFYTTREVYGATNLDNNGSNGKADDNATRYHQQGWHCDAFFFALG
SLMQVAVVDGRTGVLLWSQRSSLPGTPLAVHVVTKTECAAWPDKLELRILLSEMWGAVAL
LRASPVNAVGVTLSSEFTVELEGSTRVLLLTPFK*
>TCRU_10014 hypothetical protein, conserved
MSWCTAGEVVELISVSRLRHDVPEVERKAADLRLIELYTSAVNIGDVLTEVVVASNAVSW
NLRLAAALTLESFVSERTWCEGASFSDKERVLNEILAYLRSASFAASAAEEQLHVLLCSC
LGRIAGLEYPAARWDEFMDECVSAIVSGDAARQQTGRVLVQQTIILRLAEVCDANAKLWG
RVASVVVRRLLEWATGPAGGRESRALCLRVALCLLRRRPRPSETTEAERPTCSFIFSDEF
RCVVGRSLEEGLASFEAGGSHTILLKDCGLLLDVAHHLLSDEAFAHLVFRCSIRLLSTCE
AAYLSDLEENSSVDLCVDSALECLVGVLQMYPEASLLCDSEKFLLTLFSYMTRAVELEHG
DESALLDALQEDCFVPLGCAGGDTAANAGAVLELLMEANPHLLGIAVGSLCVTVTELQQG
PSSAHWRAWTTALRCFCRVCDEKEVSLTDSLPDAAGRLLSPLASLLRQAVDPWAAAELIE
LLSLCVARAEQESVCRAFLSILEAVFDGAGENFTWEQSLLLAVTVYAVHRLFSTCVTSLV

SGILCDTSAWLQRALVVLSRGGPLAVYCCTHAVQTLVRVSPTCQLPSASLVLAAVDSACC
HCNVPNASSLLAGFVWSLFLHAPGQCNMAVEVIQHLLSYCLQNGLRRAELRHSLTDFLLR
FLKSSMEQAACLQCLEPLLNKCLPVVLQFAAEDAPHDDATTRLLSSCLAAAASGGHAGVI
REDISFVLFEVLCSSVQERHCSTTLSKVVAAMSATAIVSPTLLDGDMTATVSLLFSNIDA
AGGKGLNYVGCCLLPALFCVRHPEYLEGIVAAFTGAPLHTHLAWGTMFGFLSSVASFADH
FTTMYFLAAWFSLLRHAIASRLAGREVLAVVAPCCTVYDLPSMHVKSLPKRRVEGCSMAQ
CIATGLALVAQRWQKSAKVKLLDEEVLQPLSLNRRFESLACRSAAEVGIDALFLMSPAKA
AQWLLGAMSAGGYGLQVDAAVRFAGES*
>TCRU_10015 40S ribosomal protein S13, putative
MVRMQGVGHGKSASSLPFCRTPPSWLKIASRDVIDAVCKLAKKGLAPSRIGMQLRDSMGI
AQVKNVTGRKILRILKHKGMAPEIPEDLYCLIKRATEMRKHLERNTKDRDTKFRLILVES
RIHRLARYYKRVKQLPPTWKYESSTASAMVA*
>TCRU_10016 hypothetical protein, conserved
MRRVGIFASCVILRDGRLDERQQPSLGAPLDRDQLQGLEAEAQQRGFMRRDSPDAKVYME
MSFRQPERIGGGVPVANLPPVKREKTEFDAYQRSTRDFTSQVTPYGTTGVGLGAGFGARE
DKRLGFLRPRKLQPFGGESSIVPKYDENGMPIEAGLTKEQLLKKRLAYMKSFEGTTMSHR
EHFLLVDLDFERDAMIFGNTREEFEKNVTKLKEVISKYTRWERTDNFYYYGIIALKALTA
WVLMECVQQHYELKLLAGHYEDFVEAMEETVSGLDENLQRDMRRAREELQSHRPDFRPVV
EAVRREKRRLLDAKATRMAGPDVSTVSNRNGNGKSHLPGEDVPAVGIEEALGAHGAEGKQ
GRQPPLLAQEQLQTQQRPAVVPLTATSGVKDQHPMDTTHEELYLTTLREQEAQHEMRRLQ
EAAASSRASYSVFGTLWRKLGGTGVDSVLVTPLQQEDFARLSYAASPTSIETLRAIRRIL
LPRSEDHIQVVREEMLEYKQQKESKHVHPE*
>TCRU_10017 hypothetical protein, conserved
MRLDVVLNASLLLVSNVKAHAMRYGAFGLYSTGELSLVGGSSLYTRYCSFDGYTHLFYSN
ILGVCDHSVFALLNNTMASGRSLLYQYRGFSVSDHSVLRVVGNSGSVSYAIYSLSFFTVE
QSSWLDWRDNDVELGAMFCYSLITTVNIDGSSVVTAWQLAVHAVLQLRWVHTPVLPVRAQ
CE*
>TCRU_10018 hypothetical protein, conserved
MMLHLVAVLGLCFLIGTPQQGVAASTTETKVTSFPEKVPRHARCGEVRRSACRLSVRTAR
PFRSGHSVDITRGGDVHKNPATEEDGHINIWRLNIAGLSSVKKIAFAARLEQRPPDTVLL
QEISNRGDVATKLSGHNDYLQAALGAVVALPFWCATLYRASACRSLALTSWRPLLSVYFH
RAVAAFAW*
>TCRU_10019 hypothetical protein
MASPIFQEPGRPPSAKKLWIIVLSVPRATGRDGAGIHSTCRRGQGLSQAKSHRWSRQVHT
VGKADPFPSHQEPKERNERQQQYKAVWHVKRHKMTDKQICLLPRQGACAAKFSAEHNRFQ
RMRVRRRHAVEISPPRAG*
>TCRU_10020 hypothetical protein, conserved
MEGCPGGKGSRAHRVTGACRCGEGSIPGVDPDIGPRVAALRTGAMRLLPTLRQACTRPAD
HKGPSVSVVPSPPHCGDQPASGSAGTSSRREHRNSLSTSERWIDVLLPNVRQRALVRPQY
EGTCRTCSAWRYNSLRGPPMRMPQWRHRLLSRRLARRLPPKLPSVSTSQT*
>TCRU_10021 glyceraldehyde 3-phosphate dehydrogenase, cytosolic
MRGRRGKALFSANGEKTLVTSERGRREKTVMTGQPRDDTTMPFVGVNDTIDRDGKSLPTS
RAQGTALRRPRGSLVKDSASLRVSWPQRVPPWRRNKQRTMASLKEWRGGRDATWKIVPSA
TGAAKAVEKGIPAPNGRLAGMAFRVPTPNVSVVDLTARLEKPAAYEQLRAATDAASEGKP
NGLLGRTEGEVVSTDMNGVAPMSVFAVKAGIYLNDRFAKLASWCDDGTGYSHKVLDLVAH
TSAH*
>TCRU_10022 Putative methyltransferase/Methyltransferase small
domain containing protein, putative
MHYEDFEVITAENGASSLSFELACATAMDHYIRCTAPHDKQETDKYMSPCSTGLRVYEGA
RVIAAFVARFGRVLMPYTFEYDTCGYPSSWVVELGCGCGLVGFTAAALFPELSVAFTDAS
VDCLNLIGASAERNGLALIQINGKGFSGVFENNEHRVLVAHPLEWCEDDTVRLISTIRRI
SNSPNHVKTGDIRMVLGSDLLYYRVDIKALLSNGSLHSVYGTT*
>TCRU_10023 hypothetical protein, conserved
MDGVRAVVDGRSRWRRQHSAVVAAVDSDDKSGESSDGTLKGLSSSDQMPQAGQVGEEGQE

HTGSLEVTNKLAGNEDSQITGEQNVSSDADRPKQTGSQVPAGGQPEDEEGTKSPQPPPPP
PPAEPLPSMPRQPPPGTNTLQSEETHPAITAEKHPKPQDGGHSHETKMPQTKGSTKHEEG
ASSLQSPESVSHLIRESTTPLSTSTGSSGVAGSTVENSGANNPTPPAASVTQHDSEGDTG
PAAPPASKSDLQSEEIPNAGIIATTYDDDNDSSRAAPTAERTTAGTRSTQTSGDAGDLER
ANNDDVNDDVARNGKTAEFEAASGDRNTEADNDERYTTVPENATNKTINTEIPADSDGST
AVSHTTSPLLLLLVACAAAAAVVAA*
>TCRU_10024 BNR repeat-like domain containing protein, putative
MSRHLFYSAVLLLVVMVCCGSGAAGVAGQPSVSTFKWRGINESGGETVDSLGAPSLLKVG
NDVFAVAEAQCKKKDGVDFTGVASQLLTKKTADTPEEVLENPKMGHKYWRKVLLKVKRRN
WM*
>TCRU_10025 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MLVGQYGRKDCQNSGADGCELFLVKGSVSGGDASNKIDWKDTENPPQRLFGAQPDSWTRL
IGSGGSGVEMKDETLVFPVEGTKKAEGTEEDVKTVSLIIHSKDTTNWTLSKGMSDGGCSD
PSVVEWEEGKLMMMTACAGGRRRVYESGDKGESWTEALGTLSRVWGNNKKDGQATAVRSG
FITATVGNDDDKRNVMLVTLPVYAEEGNEKGKLHLWLTDNTHIVDIGPVSGEDDAAASSL
LYNSGENTDEKKDELIALYEKKKGSDEGKPSPGMVSVPLTEQLKRVKEVLTTWKEVDGRV
SQLCTSLIAKKDRASTDDACSAVKITAGLVGFLSGNFSGNTWRDEYLGVNATVNNNEEGA
ASALASTKNGVKFTGRGAGAEWPVGKQGENQLYHFANYNFTLVATVSIHNVPKSGSVPLM
GVKMNGDGNNVLLGLSYNSGKKWHVLCCDKTTTKLSSTWETETQYQVVIVLRNGTQGSVY
VDGQRVGSEECALGNGESKEISHFYIGGDGENAENKEVSVTVTNVLLYNRPWDEAEITAL
NPNKDPAPPVTPNAQENGTSSALDGSQLTERGQSLGSSGAGSGGASPSAVPTVSTPSAGK
DSLQQVASGKSSDGTQTVDGGSFSDGDPTVETREGGTDGREKKEIHAQNGDVKAAALNSS
LGNVSQGNNTDACSVCGSGLLPSLLLLLGLWGFAAL*
>TCRU_10026 hypothetical protein, conserved
MWDRVWRRLRGRVGVPGVVYSDEMDAASQLRDQREASTWRGNLRNVRVETAPALLLRTSG
GDQVLPGPEEDPYTFWERIGFVPVHPSRVRPRQYYHPITDFGLYDYDEVSPEEKELTAAW
MAKVLEFNGAVPLGILCAAGCIVLPLHTVYRMPLLVAAGATGVMVEITRSYMSAARERQD
LDDFILAKEIWYIKNVEAYQLGIPFIPKGREAEYHSYMDGTVSSSQVLPDELIDALH*
>TCRU_10027 cytidylyltransferase, putative
MSDDTAASYRFSGLKLTPWSAIDVTVVRRLALVAMCGSFNPIHLVHIAMYDAARDALMHH
TEATDAPSNVVVVGGFFSPVNDHYGKEGLRPFAQRAAICKAALADHPSLAVDEWEGLQPM
YVRTVHVLDHLQKAAQRWYETDAAPNATQLAWVRQHPVSVVFVCGSDLFASFLRPGCWSL
KLLKQLLDNFDVMVVRRACTNVGCEDMLRRHGSFLRENVKDTENGCTRLLTLDLAAYRFM
EVEIFANETSSSAVREALAADHAADISNLVPAGADSLIRAFYANNTQND*
>TCRU_10028 Cytochrome b5-like Heme/Steroid binding domain
containing protein, putative
MVQERRSCSKMMLFTAVVSIVVAFFLLLVLPPYDDNRKIVADTKPGKDAQTFFASLDDFR
CPNVAYFPREEVARHASETDLWLVINGNLLDVSSFVHEHPGGLLIMEGAGGHDVAALFSQ
FHPPSTVKLLEKYCIGRLKE*
>TCRU_10029 NUC130/3NT domain/SDA1, putative
MTEPAFRGTLLLLQNCTRRDPEAYRDEFISQLDHFKALSKTIMTQKATNPQYITVLNYIC
HVCHCYPAESAEVAEVVLRLLQEYKGSAMTPELRLALVKSLALLRSKNIVSAVRSFPLFF
QLLQEREKNLRRLILSHIVSDVRKVNMPGAKNGAQVNKMAQNFLFSVMTEDDPVQARCAE
MVMIDLYRRRVWANERTVEVLTQACFTRHTPILRTALRFFLLQMPKITSLDDDDGDDEAV
DPGREISRMKQKLKIVKKTSKRERILKREMNSIRQKYNKEEKAEELLAKQHVDPIRLLRN
PHQFVERLLARLQKTTERFEVRILYLNVIARVILEHEVVHLPLYGFLERYMEPSQLHVTQ
LLALSVMCVHRLVPPDALEPLVKAIANHFVSDRSSPDAITIGLNTIREICKRQPLAMNAD
LLKDLTEYKSQRGDRGVIMAARALIQLYRDVYPELLPAKLRFGHGGTGMGEKQRPVYGKE
HVYTDVPGLELLYPAMDDEKDEHSFCCGSDDSDEDDSDDSDGTWVTDSSDCDPDGIEGTF
VDASDCSGSDAENEKCPQLVPVGGAVDEPPLKRSKGEADTNSDVLSLGTGGEVSRDRSGS
CRSSTVPQDDGPRKPCGAEGDTASVEEEEMEDSDEDDDFAEEEWDEEVEEKEEIDDDEEE
SMEEEEEEEDEGEGVDDDKDDEEMEWFEDTEMNSRRPAQRASSASKRLASPSSAAAYTVP

ASAQRFLSDADFERIRRLQAQKGSHRSLRGKLRDHEAREKRRQGLIHSVSADLSSHDIEH
FTEKKREEDREEKIARAQEARRARSKFEARKKKKSKLNATHSEHAKRGKLFNMTKRSRRV
GAKLKESASDRSNRGKENKKKDIKFRIRRGWKA*
>TCRU_10030 inositol-1(or 4)-monophosphatase 1, putative
MAISDAELDIAVELALRAAHVAASIIEKAMAERENTLLDINTKVNSVDLVTQYDKQCEEE
ILTILRTGTPQYDILSEETYSDVGLSDKPTWIVDPIDGTTSFVHGLFDCCVSIALVVDKE
PILGVVSAPRMHEVYSAVRGRGAYCNGQRTYVSEKRRLEESVVLLHQAVNRSEPAVKSLI
SIQKELACIPVHAVRNHGSAALDMCFVASGRAELYFEVGIYAWDIAAASIIVREAGGVVH
NIDDAQSLDLMSRGFCCANSLELSKVGIDLSKKYKYKESTLGK*
>TCRU_10031 otubain cysteine peptidase, Clan CA, family C65,
putative
MTSTAHDREMQMAIIQSEIESVPLLSDPVEALSETCSLVKEFANSASILPKVLSLFASDN
DDRYSGIRYARRDGNCFFRCVVFSLLESMLGDSELTARYLEQATELRTKLIEDYGDFVED
FCEAAIAVIRQIESGGCTTSEELYALATSHDSEYVIYFYRYAVSNYIRGHKDDFLPFVMG
LNYENVEDFCRAEVDAVSSESDNVQVVAFARCFQLKIVVEYLDGSVGTRTTRHSFSGDSS
GTGDNTSLVVTLLYRPGHYDLLYK*
>TCRU_10032 hypothetical protein, conserved
MPIRNWSASTPQEGLPSAVSSHNGSRDVGPPSAVPPSVDKNGNKNCTNQRSGAENSAEAS
SSRGLFGGMEIVRTRHRKSAGTTAGSRTPRDESLPSAQHVKEYNPLMESSAGASPFFMRF
ELSPAAVRDEVEAPQVTQMRQRLERFFEEYVPSKLSQVERTIKKFMGREEELFTRLVAIY
GPEPRELKASSLPKGENRIPSGTASEAESAFDFISSAAKNQSHEKRKGAAAEAPSLAGGL
PFMHGETEELPSRQMSREADHTPLDSVSKPKNALGPAASRRVGRPSSSFDFLSTPAFAAA
QMAPLHATEEKEEEVAQSAEYRETEAAERPPVYRNVLELDESKKGNKKGEDTTENTGKVP
CNMKHRRSGEKSSCCAKTEETDDVSESETIWDRQRREIRELQDEVLLARANLSHVLDEIR
TSIEQRRDCMTTISKLENRIEECVAQEAFEEADHLSGDLEQLRIHVKELDKAPVRLLTSL
GQQRDATVGMVRSLAKLLQKHRQELIDSKDEEDRRVRKFIEEVTFSLETRKGRVSTAMER
AERVKKSAMREQKSLLERKTSLREKTLKQNEGLRELQGQLLNEKMGIDAEIATLEAKLAK
LCQASAEKEAELQDVTSNLRRMEAKQESMENDIDSLIKEEEDRMHRAAADLEQLQQESDV
LHAETIEFDTKRELLLSELQDGVTRIDSYEQRRTLLETETLSNLQLYTNSVVELLRLRNA
GRGVLFTSPSLISSEADACAGVAEEEESPVLHINRLEKQLSAINADDETCEALVVSLGVQ
LTEMRNKIPLLELAKKNAAQAMRFKEAQLKADEIRRLTASIAETAAAAEDAQERIRANAL
KRSSLQQQMVDERSKAAERVREFLTRYHDTLEAAVTATSASASPNVLQLPEEDQGHDELA
EAMQLLIATLQQECSDVLVPEGEEEMAMANEPLEDMPEEIKTEKMDEDLDVQEVQDASEG
TREQ*
>TCRU_10033 zinc-finger protein ZPR1, putative
MPNSPGVVKQQEQQQYQPMPVKDEGPDANVAANYIKTEFGEMNTVESMCPRCGENGTTRL
MITNIPHFKEVIVSSFECLHCGERNNDVSFGGVFGPKAIRYELEVKTKKDLDRQVVKSDF
ATVRIPQLELEIPPGSQRGILNTVEGFLEQTEAGLQLQQPMRRIHEPELYEKLEAFCQKL
QEFRTGNASFTFTIDDPSGNSYIEAYYDYYHPTIDPQLTRYEKERTDVDRQLLGLTIEYN
TQRTEQEQREVQEGQFDDMVRMETACPACKQQGFINMQQVDIPYFKETVIMAFRCDFCGY
KSNEVKSGGKVSDTGLKIELRVESEDDLKRDVLKSETATLNIPEVSLEVLPGTLGGFFST
VEGTIMMVRDQLRDLPQAEFGKGDSAETDASSKKLMEFVGELDDLLHVKRPFTFILDDPL
ANIYVQNPREHLPPPEHEDPRLTKTSYVRTFEQDEELGFHQMKVD*
>TCRU_10034 hypothetical protein
MAVEMRHRLQAIARYLEEGEALFHGAVAHAHDEYEEDDAKALLDSRPSTGKTGLASPSTS
SRVPRVFRMTPELRNALRTGLEVHKSAERVLQEASMNPIFTFATMRC*
>TCRU_10035 hypothetical protein, conserved
MTGDQRAVQSAAAIERGYVKLLDCSLLLEKEIEKYYLREEAAIRERVLLLDQIQSTIADE
RRCLEIDHQECRSQISAARKSHLTLQCDQTKFSQLVSRTGSVLEKEERQLEERLSWVNER
LCEETRELELLAERQSRFERDERAMERRELQQFNAEQSLEKAMRELKTLESEIEERKRAL
EKKHETISEWNRSLESREKELARCQEDFREDLKRLEEDEKYFGVYNSSSNVVSVVSQREV
MDDHNMTIEKETQCEEIDVEDEEDHTE*
>TCRU_10036 Rab-GTPase-TBC domain containing protein, putative
MEELRNIHHSAQEGRLEEALLRRVLDFARHRPFHAFHSLRWRLLLGLLPVNVEAGRHFHE

WEECTRAGIRDWNEMNDNLQQRLVATDSAVRPVEKKGLVSKDEFSSFSSSSSCPDDGESR
TVENPLLPGVGSLYALRYCVDTIRATAQKDLDRLHWDFPLFEKSTTRKALMDLIVNYCLR
HDYEYKQGMHEIAAFIFYLNHTDSALLEEISKSPEEADKALIDGFGRICPINGVMAMTFS
LFENVMGGSGLRLYEWYHSSEEYARDGIATASHRTQRELLAEFDPVLHHQMNVVYEIEGT
SYLIRWLRLLYLREFSIPQCADLWDVFLSERFLARHDDYSLNNSIVTMLAASMLFYVKQD
LMVGCIDALKRLMKYPPVEDVGTLVEMTIMQQDPKKNGIGRYFTPPERHELFGSKTPPPM
EETSALATSSALLSPIEVMNQQGTILASIIARLELLWMPSSDAMSNDAGHAAETHARTIE
ELKKVRDVLLFSNGSKTHYA*
>TCRU_10037 hypothetical protein, conserved
MVAIAEGLFEYNAHENKLFVVRFPDIVAGYIKAAETWPSIVAGITKKEWRAHTTLGSRNG
DNRLRVLHRSTAVARDSKVFLLVGIDTVGYGNGDDI*
>TCRU_10038 Concanavalin A-like lectin/glucanases superfamily, putative
MLYTQRGYASGDNATALYLWATDNSRTFYLGPLFVDHAVSLTFSSTILYSDGALRLSRGS
IVGTRRGISLARLTDELKTIKPVLSTWVRLDSFSKSSTPTAGLVGFLSDTSSGGNTWTDG
YRCVNASVTKASKVKNGLKFTGPGSRAMWSMSRWGPNRQYSFVNHRFTLVATVTIHQVAK
GSTPLLGAGLDAPVSTNFIGLSYSMDKTWETVFAGKKTTSNTTWEPGKEHQVALMLQDGH
KGSVYVDGEIVGSPETIPTLETRGLESHASKLGATRETSTAAMWQ*
>TCRU_10039 Nucleolar protein 56, putative
MSKTLYVLYEAPTGYAVYKVLTSEEIGAGDVALQKDLQTFATFSPWVKLISFAPFQSPEN
ALEDAVCISESLVSPFLNNFLSSVLAKKAKKGDVNWELGVCDAKLGSAIHDELKFPVVCN
ENVVEIGRCLRMHAEKLLPEHKEGDIPRAQCGLGHAFSRNKVKFNVHRSDNMIIQSSALA
EHMDKGVNLLGMRVKEWYGWHFPELAKEVPEPLKYAKVALLIGSRSTLEERDAEEVTQQI
ADILEGDEALAARVYEKAVTSMGGDMAEVDWLNIRAFMERVTSLGSYRESLQQYLVEKMM
LVAPNLTELMGQNIGAKLISKAGSLTNLAKAPASTIQILGAEKALFRALKKRKGNTPKYG
LIFHSTFIQRAAKEHRGKISRYLANKAALACRIDCFMETPPAVFGEKLREQVEARLNFFD
TGNRPPTNMVAMAEALEQYQKILRKRSKRQREAQAAAGGNGDDEVKQEVPKKKRARREEV
Q*
>TCRU_10040 hypothetical protein
MSACSPSRFSEEDAVVLDRWIDAVCGEEMQFPAHRRGQFAAYKQRLEGIRAADGHSLFHQ
MSRSGTRETLALQNALSVLKQLCKCDMEETEKVRKEIQAVKRTLHERSMAVEEEKMDGSP
APSPEVTSGFNPVPAAESSHDAYESSRKVAERYVAEIDRQRESNRKNVELCHGRKLKLLD
QRNRLLEEENALREAEQSVTSQFDEASAALASKRDALAREQAAWKELQQSSSFAEAQGAG
NMNAAEDEEEEKKKKEHVYALAEARSLLNEASIKIAQTQAELSYQDGSHSVRFRQARQRL
KDWQDMAEQIRRIHDQLQARTRVINMVVEANAVALEAESGLGHLERLRKLNQLLLEKSAK
ILGLQPEGKEEGGKGIVSSAPGWGEGVLRDLFTSRQSVASSVSMTDAASSLSTPRRRSSV
SQTTPTVTVTEISFSPGVGDAMSPNAHRSPLEKERRHRQAYALLTELQRWEMALVKEAAA
LYGICEKGISSASATNSSESPNATLQELRSMLLEA*
>TCRU_10041 pterin 4 alpha carbinolamine dehydratase, putative
MIVWSRRVSTSVLFCGVFNGPFSATFVTPSRWKGDYGFNVFHNSNPQHGGSYARHERRMR
EDEVADFLRSVKGWVPADETVTASPAVEGSSEAAEEEKGPAPMTVFTGEEAIKREFVFPT
FHDAYLFMGRVWAFCYGSDKYPHVTWDGTHITVYLYSPSFRGISKREARLAAFLNDQYNM
FRKSKRQQEQLLSVAVKQTRMEELMGDVVAEKLKQREEERRRPLAELTESRAIKWESLLD
ENSSGKKETK*
>TCRU_10042 exonuclease, putative
MPTARSKRQRTPSATSSPLLTHALEAPSRRIASTPASVMPHGEEELLLPPPTSKLCAHGS
AHQGTDDSKARDEKNIDVNNTSNAHFGASSANSNGSMITAAVAEQFSAVEIYFQLVGQRN
QGDFLFPRDVGDLLLWSVPAAVPLIEGPRVFFLKNKSRLRDVVMICVNGWTHDEMILAYA
SNPAEDDGIHEKEAKHSPRGQPLRHEAEEMKTQNGNSWTERIGRAMLAPVRAQQCWARKE
CGVQFAPMLLPGARSSLVREIFWRNDAPKAPRDGQRRGCPSLNKTNAEQKCEKSGDRCVA
VVGKLPSATSEAAAAAAAASSGVGNFFKRALVIHGEATTNDETSLSPAAGAASSVPSNVA
EVRRPDDADPSLWGDRATLLRYALSIEKDRAVLGGLGYVLDLPSDCAEAAEWKTFDAPQP
STGEGDGVQPVRVFAMDCEMVLVADNVSALARITLLDVRAGAVVLDTLVKPSTKVVDYIT
RYSGVDEAMLEGVTTTLQDCQRELQRHIDTETFVVGHSLENDFRACKMLPNCYVLDTVHL

FPHPAGLPYKNSLRFLAMHYLQKKIQQGSHDSAEDASTSAELAYLKLKHGPEFGIRKRVS
ILQLIENSAMAGGGTTGELGKRDETPSEHPATPPTDSSSSSLCMELNLFDDACVLRDIIP
SGADAKNGSLLHAVPVRHDRDAMRKAVRCLQQRRCEKQHTEDGVPCSYALTWVQLTQTVE
PRRQDVEEKEEEEEGRSWEQLQLERVDETNRRVMQIIRAAPHNSLIVVLAGGGSTSAEGT
SSGNSRGVCFAFVKDDNSPGPPVAWLDAEPQVSVTATSPAGAAVGRGGTVETPPACQQQ*
>TCRU_10043 hypothetical protein, conserved
MSTPEVVKRRASVQRPDGEERLRELRRDLEYERLLGDDDMAGALMYGANSREDRIMQMDA
LVEMQRKIFRRGSTAHAIVLSANVLTMAVMASQLAMFRWKVTEAQTLTEATASIQHQVMR
AQKCGFTVRRVAATTSTRDSEKEKFRRKDSFVCAHAAEERTDLIPADEKRKAAPATDAAS
RAPAVGAEHMQHVRDSEDNARPVSPPSSVCSAESEAAVRKPPPDDMVAQLVVVDTFTHEP
FSDIVDHLRYFDRENSLGLVIVLMLHDNYENHSPGMVILPKHTTTVSEAYSLGYDLVLRR
CFDHTVVKLFTEVFMSAKGRWCKEMHSKGIVGNYHGMRHILLEQDDVAPRNGVLSVPDVD
ECSNNGSDDMGPLKNFQGSYMSSTLLSSTLASLPPRLSTMGVRGALASAPNQRMHQLHSI
FNVKDILTNVMSPSKSVKHATKRLLRPSNSIRDFLAGGHGGEIENGYKNDENAEKIYEDA
LVDEKEEVESAVVAAYKQEILRLVTELECSERTVALLKNEVAQLGERKSSDTNSGAQSPF
TSNSYNDSGPENFISVSKEQQVITLRQRLASVTDKLMAYEMQNNNRTRKRNNWLQDNRIS
ASPITTPRRGTISPEGDAQDVFSNTATTTHGVRTMESSLLERTGTIGERTLNLTHSQIFS
PDVADDGISNLCSEIASLLQERKRSTREMKLRASEMERLEDKNVRMATRLADAMETILVQ
KELIAELEERLQQKNHGEIKLKSEKGGKKRGEKDLDDDGDGDGGRPHGGASIGRNAKAKR
KKQETPAAVARVSTWVKSVPSCTSTRAPSAFHSADLGEREQMRGARPTYPYGETGKRSPP
QAAQKQQRKTEMQEQSRPSPTRPNHLQKQGHVPLKKTKYNNESMETDVSLTKLKGIFNDI
VATNASGDQDLGEKARAQARVVAREYAVRQMKANGGEKAPQEVEIGIQEKSDDSVERLRH
AHMEAVKTSEDILNRGEDSEAFAQAIISVIAIEQELHRGEQNHISQAVTEATGKAVTLHD
DAKTVEGSAMVDSNGKTSGVGSVVENKFLQKKTGNILQGIESKNHGNHGKERQNQKEPKA
EGSNGAEHGSALQTAAVAGAHDGDVADARSNFLNELYLEHHQALMRFLQLVGNEHATLRQ
VLQDETDELVGKIEAEIRRLGGEVETHYLVSIDTALLSRLAALLDGAERSFFMPSARKMR
LNTLAFNGSSDTTDTRRDTYSLRESVSPEDVANLLSRQDVTVDDIPPWLIELLERADDEF
DPALQEDPAATEWVKKVLAKVDTVRKKRGKELTELLRQRRENLMRARAEASQRSNMSGDV
TGECDSNDSVVGVMGAEETEALFVCHPSLQRVFSPSLYGHSLPPGKPHAVLRRRSLLGKN
VLFAEPNGDVRTEVSKRLLKIQCSSTKDALEGDSKFFSVLPPVGLRGLSRRQQAQFQTMH
GAPNLLQPREPPRDAALAPENVRRTATRGASRIAATELDQSPFSPEELAGRIMAYRPAFP
RHEGTARITARMTAAYPTFAIPVAAASMPPLSSGTAGERGGPLQHPHGALESYVSWVYGV
PSELLFPMLRGAAPEESDAVLFLPACAYTEKDGGNATHCIQTSFVRRMLARMDLFSSPAT
LAARRLNAQLQMSMSDWRMGVVGRAITPAPRGNHTPQQKKI*
>TCRU_10044 hypothetical protein, conserved
MQHDRALQRRHIRHVDESVGHQARRALAETTNPQLRPARKYAVAQRHVQRVSERVHRAQV
HRHSDRSAEHHRVEARRRTPTANRHRLRQRHATHAALHTATTATGPRRRHVERQARLAHT
AGTAAAHAVRERRRQRIKARQRSRTAVARHHAHGGQAGHAVVAAALQHPAAGTVALHRHD
AARDRQPGDKRRAGGNAARNRHGATTQRHPRQRRHRRRLAHRPHVAQLQPPAGTDRPTVA
AHQRRRNRPLDAHEAQHRVGHREALSKHKAAAAAQNRHVCHGEHRVAPQTETRRGRHMHR
GRGRTARRLQQHAAKHHRARQQVHAAANVHRRPTRVQRPQHSVAHTQLRPQQRRRVQHKR
RRHRVRQPAQLRVAHRPRRHNRRVTDRHVRVCRQVVHKRERAVDPRQPAHAHLQAPVTRR
LTAVAPHVDLCTAVAHAVPQFNAQRAGKHRRHVEHHSHAVRDAHAVHQHRVHGAANRDGS
VHRAAPQSQHHRMHRGHKRRSSSQRQQSKQRHTHSRNGPAPHTVTAARTRTHRRPHPPIQ
SSVNRSVVAFRSCTVDRNSCPANPFLQMANPVTQFR*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MQGSSAVFHSKYSLLIYYNSWLQLSGNLCRESPSKAFAYIHCTVNLRDSTVSVSGNRFIS
SARTPTILWIPIIPRELTNGAIVAACNTVNGEEGARYSIPSVYNVTLLTCSDPCTLATSC
FPAYTTTVSSDGCACRCAEGGHGDACLPVAVPEPPSTDGADLCVRDVRVGVKLNAGLGTS
VVCYVGVTFAADVVVDMESMTGTVRNVTLANCTLVGGASLYVLGWRSDPPAGQRADVLIS
GLESRSGGGVVVANRFPPGSRVTVVDSVLIAENRVAYRGAYDLGDLSACLVVHNVNLTGS
VLTIARTQVAAVFRDAVGVLVVGGVALSSRGALYVDGLLVQTALGLCVSVEGGVAASGGS
VVAFVDSGFLLCKHAVSMRGAVSVSGSAVALVRSDFLLTADYAVAFYSTVSLDGGSMLLA

KGNVHDGVSREMLYAAGTVTAVGSTLSFVRNRALLPRMLSVSLSLSAGAHVRVACNDAGG
RVLSTAEEYAAAGFGDAGSIDVAGCDACDKNTHCYAPGTASASMKDGVCECVCGSGGCGE
ACVPVGAPALPPAVGTAPSVFFREGVTVRSVFVVPAGASEVTLRHVVLDGVSPVLYVPWM
ARDGVRIVVQNVSLRNGAVLYVMGGGALRGAVSAGSDESGPVELSVCDVEALNGALVLTG
TFPAGSVLTVADSLLVATRPTPLVYLPGSQSSPYAPVLVLSGLRLVRSVLVVSGVALVTV
VTGGRTVVVDGAVLELVGGGVALDAPVLGGDYALYASARVVASGGAVLRVSGSQVYATHG
LVFDSGVVANASAVVVNDNAGALTDGALLELRGSASFLSGSWLSVRGNSISGRLLSVPSY
PRSADLVQSTLTLYGNAGSGPVVMDGTVALVGAGRKFVVGCLTLNGQALQPMEYRSAGII
GKFRPVACSVCDADVRCFAAATRAMSGSCGCRCAEGGYGRDCLPVYLPHVDGCNRTPAMP
LLSHTETLTETRSPTSTWTPTPSLSRTQYGPTETLQVTETVALSPTWTPESSVSSTLWWS
DVACPTLTVTTTAAGGGLTQNDIRGGGSAVPTLLMVALPPPFRWARDPQLGTHLSFFPVS
TAQPRGFGGPWGAMLRNATWVRNATNPSTVLELAVPVHRGYFIAADETIVIRCDAAAVFG
GCKGVLLGSFTIRSDMLPAAASVLSAITGVVAGAAAVAVVVTGGLGSILEMQALGVFARM
PCASAQERASTVALPYFLSVFAALDPLWMVVGNALLAAVFGCVHCGVTAAFQRWRGVDAA
SAWAAMRFPSLTYVVAHAMHLGIFFGSVLALAMPGARVQHRVIGVVGVLYGVAFPAGVCY
FIARHVGASFTRYWQFSRKPLHERLLYPVGYWHPAAQQRMYGGMLTNMRGSRVYWCVFQL
FVLCVVCLIAAVHPPVGGCHVQYFCMAAVLLAGAGVVAFTNMMRSSFLTVMRTASFVLLA
LLCVVSAANHLAPSDGGARAYAAIVLLLTTVLLAVTVYSVVVWYAEDRHWQELREPRRGG
LEALLRDDEESGEESQKPHEMTSSSYASGTTVASSYRPPAPPRPVAGDIRSDALSLFDRA
SSASCSINYAFLDR*
>TCRU_10046 hypothetical protein, conserved
MYQRTVTASHMKRVAHHRKHGVPRHPQRRSNDVNGARRFRHALKHIAAQHHRGVIAYHQP
IHRNTRRAVNVQTLPRDQPRDREAVPADRDVRARRKHTLRAEQRVNKFVAGDDNVQRLHS
GVRVAQQQQHGTVPPRASIKRDVRHVARHRSNQHRQAHAVPAERHVAVAQPRQPAAHSLR
NLGVHHVADALTNWRWWRCGRHWRRWRWWRPSRHRRRDAHIAVPSSSALAPAVNDRRRQR
GKAVALLRALPAHCNRRHVGDAVELQFSCRRHLPSRNRQAPSNEPVAGPNPR*
>TCRU_10047 hypothetical protein, conserved
MPGTESVDRGSCSCSCKDGWHGASCFPLEVPDTVVLPAPERAVDGDTSCVVNQTLTNLTL
NMWKTHHCYVGVTFRGVGAVLTFFLNSMPLHLPINITLTGCTFRDGAALQFVGSAEAAES
AGVLIRVSRTVMLSSVVAFALALPQHCDIAVMEVDAVQSSAVQLLESVNNLWSVMMLRDV
LLSASSLLVSNVKACAFGYVAFGLYSIGTLTLVGGSSLYTRYCSLDG*
>TCRU_10048 kinesin, putative
MSKAAVSRPRVYVRIRPLNDREKKEGNGDLICRGDPRMPDTLFIKGEDGGAELQTRFDYV
FDRDAAQSDVFDIIGSEVLNTLFSGYNASVFAYGQTGSGKTYTMEGNRSKTEGLGLTPRL
ISALFERFKANKDITDSVCEVSLVQIYQEKIQDLLAGQKHLEIHMDRTGQYIARDATWAR
VKSLEESMKLYTKASEMRATSATEMNLVSSRSHMIMMVKLQWDEPSLPGSHAQLNLIDLA
GSERLTQSGAKGDSMWEAIHINKSLSALGTVVSKLVEQAKHKGRRIHVPYKDSKLTYLLQ
SSLGGSNLIHFILAVSCSALWSGETKSTIEFGKRALQLVLRPVRNAIDYTRLAEMEEMIE
RMRSHIASLEEELRNKRSNEAAEFLKLKQIPQQGDENNDRFAERRHQSRQKKKLKVQTEL
ARIMANLPETFDDLTSHCVLFPESKASFRELGGLQRLVYFVDRSASTFYRSNAAQTIASV
LDDAGREMFQDIGGLDALTRLLQVKEERCKEAACVALEAACRGCLKNKMKLTPVVYTELV
ELIYNYSNQQVQEAACTAVAAIVDLYPDARRSFERLEVVPKLLETIRNAPEEVVNLTKAA
TNCVGRLAHGDSEMQQLIASFGGIDLLIDVLFSPAGTRDHQVPILASYALVNLCCSNKHN
LDIARDNLRYGEVKFRLLEGLARAFGINAAREGYGRATAQETESPFPYYGVTIMDKWSVT
SSGGRPIFSTFMDNPQFYLYVTETTDIAFMIQDVLYESRMLKKKKNNTVYMGLALFEGDP
ELSKAGLKQLDFHGRMVEIGKYTSNCENVLHCTLQPSETPYVVVPFTSQRGRQTEFALSA
FGDKPIQLTAVPEQVGWVRTVLEGFWTELTGRGGSGFDWRCNSQIRLQPKENCRVVFVLS
YLSVDRQRAQSREEEGEEQNMRPRLHGRLFTTFAPEKRYLKALVPLPQKSTFAASNNFAS
NSYITTSANLKAGESYVYIPFTETPYEDQWRLSVYCDTDDVTIAPIEGNKAEWYCTSSAG
TWAGKPISVQVETKGKMVAVASSPGVFLRIRLLNTKGKKLEGIDAYWNSEASVEYKSQGV
VTVQVEGMMRTDKGQEAAREMKFDVFVFTENKCTVQHVDFAAVPSTLPHPTKSTPADLLK
YPVEVVDADVPFDTIDQSDDEEEEHNDVVNAEENEKELQKVIALRNEENARLMNRIVEQQ
REIMQLRQVHNGTPPSNSVSKNTTNGRRQRKSRSVTPLEPLPNMRKQTLKKSDGGAGAKG
DAEETAAGLEAWSNPENSEKVSGGPAKALQEAVEYSLLTLNSIERHTRAPTEAEWADMQE

DFRELQRRLFFALEKIPLT*
>TCRU_10049 cysteine peptidase, Clan CA, family C19, putative
MKYGRKVLEAESKRTENSRGYALQGDDGYLKHNQAFPLAHGSHSTSPMRKNAYTGVCGND
HADGDCADGDIREREGEKPYSMGMSDHQIHRRYRTNHSNKDDALKQTNTQNSPASGRLLY
SPVLKKNRVEAISPVNGGANDKATRAMSSTEARRGLFDMSEKKSTGTGGETAVTPSRYAA
PCYGKPNEGISPYASRAGGDHYAAPTINSRLKEYSSWKHAPLTLGLSLPDTHRKCSEPVT
AGTSLQKRSRWDLAWGDHDNNESTIGKMALTREGEGRAGVNTSTTGNTSTSIPSSLFGCS
SKVAAGETARTSKNFTTPLTAPYIGMPKQISLAPSTSPPAAPPPTSAATATATAKTQLTS
PPLRAAVSPHFSGAYRQYRLASESPQSGSQESPGYREKSPYAAAGSSMFPGEAYYDTKIP
ESRFSLLYGASEKEAYALSSSVAKNSMLHHYSRGFYGPPLLDRGSSFLSGFINPHNDCYA
CSVLTLLLRSPYFCRALYDAHKLELSPKLSETPDSDAFSGDGTGDMGTMYTRWSFIPNKR
HRGPSFNSVHQILLHFARLLEKPEKIMYGIDMAPLRQFFSTSFFTGEQQDAHEFFLSVIN
KLEEESMEELKSRKAKKEKSDDGNNTMTSEYGANPMLNDENTGEGKEVENKIIIDSSLIW
INKLIGGKLLNIIRCRNEGCGHEIVTKDSYINLCINLRIAETMKVDSTLTPPSSAADNRD
FAPDGPVGRSFSTPPEVKLDELLLRKTFERKSTINCCDDVQTLLDHNLRYVSIDKYTCDA
CGSSQNQDQGGSLLGPAPPILAIQLNRYYTVVNSYNDVRVVKDKTPVFINNELTLYALRE
EGQVDCDKKQLTPCVREAERVARLREQHAEKRHQQEREDTGKLTIDPSGAGKNASNGSNV
EQMDKKEKEEEEDAETHVDAIRCLYRLRGLVRHIGFSPFVGHYVAEFATDAAASESPKAE
STTTTSTTGSSDVDTEGGKPSRVWHIADDIRVEVLPLEHLQKRRSCSTDSYLLLYEKVAE
EEVSCPVWRVLPRGKN*
>TCRU_10050 hypothetical protein, conserved
MLCVRCRCWAAAICDCAVAVRGVAAVSLLLLPLCVDVLLVCAEGYTQVTGVMAMMMAGRV
LLVCALCVLWCGAGGGYAWDFNNESVNEYYYGANGTYCRLNSSIFSFCEEKRNASKRQEA
ALPKSTVQSGTGSGQPNAGGSSGGQDNSSEKNGSNDSEKTDAGPQESQPPNGNVTETPTP
ATVTAAQASATRTPDESDGSTAASHTTSPLLLFLVACAAAAAVVAA*
>TCRU_10051 hypothetical protein, conserved
MAEHLLEQLRDVVVLQPSDGAVGNGEMDMSAANSHKYSVVSTFTNSPFVKAVEDTENNED
DEKELIRLLDELSHRIHCSDAADDVERPSGSFAVEKAEALTLRASHMAPPIYGSPAPAGG
SPFNYASCVSQTTKPPPSFAEAVATTPPLSEVPVELSPLAAHYVPPMPAVQQDPILLRNT
HGVFMLRPITKPTPPYTPPSLTSSISQPPRYALPPAALPQSQPHFLGSSLAQVGGLADAQ
LPKKSGFSPYEIPHSMNNVIGGSQILGTGGAGNYTYISTSVKSKSTSHMQPPPPYPS*
>TCRU_10052 hypothetical protein, conserved
MQITPRKSDGTAPVSQLPIFSRSNSSAGLGVGGHSARPSVHLRCSLLRTPPPRHHHVSPL
GTAAVASAGGGDGTTSPSLAPSEAYPFPSSGRRFERLHSGRRGPGNHSEEILPYLDLDSV
ASEAETAANAMSREELESAVRELETENLMLKSAVLRAREELTKQREGLRETYEAAEKEGE
SIANHLTRRVNAVREQKARLETQLHKEEAMKEEQEQKLLKLKLSSFKLSKCVQREEEETL
TALTNRLQQLQTQRQNFENLLLEQSSSLQQLQELVDSFQTQTRCNEGLRVSREGCSEADG
DSNSAAADAIAPAEQHSLRSETAEHADPASDPQEMLQYLKHEVAFVEGLQREAFERGERY
KLRRQELEQRISHAECERRSNRHSLEGIHQELVETTATVSELASAAELAMETQIDRQIHV
RGCTGSFTSGSREFQTPSRFKESPKGPATNSAQLQSNSPSSKK*
>TCRU_10053 paraflagellar rod component, putative
MAEAERRFLDAVEKAYNDKSPTLYFSYDEDLEAIPVAIKALRETLEVLHVDNSYSLKWLP
PAIGDLGRLRWLNVSYCRLNFLPIELGRLSHLERLYLSNNRLQSLPMEFWQLKSLEELRL
DNNKLRVLPGGILFLPRLETLTLENNPLLTPEEVLGAAPATLVPHIMCVDCSNCCVRLRN
YEVLITFHNIAALQSVPFVHCLCSQTCKQHLEVRLAEYDALHSSVKPSSPSS*
>TCRU_10054 hypothetical protein
MELDDILGDNPPAAVDLVDIDDILGDPPAAGTQNTNPAAPASAPNESLTEMPFVLDVPKP
RRPPAKGPPPPRAHTVQLQFFRDPPPHVKTYVTNACYYANQVSMINPDGSREKRGIVLND
SNIYVMSSGAKVEQTIPLTQVEALIMQDIMTPKSLGISKEWQTHILLQLRDFPDLFFSLP
DDKKNDPTTGGTYGEKIPVLEVVLAELLRAYDVDLLVCSLREEESIHHLVKRTVTDAAMR
RECDEILAYRTSLTATLNDLMRQDSRLVMNCNEIEVSGASHTATTLLKEIELIEGKNEVM
TAALNQANVSLNRCLSKEHELRGSLQAKEKAVQEEVDRRVAAQQGEMIARQALEYELMKV
AHQTEMQHLKLLCEFLQARIERCRRSPAVTVADLESHLEELKRLKQSVLSRKAEANKKLA
VAKRHLVDSEAALQKVTNEVAVLQKLPPGTPIPPDFNRELAPTFLPVHLPQKQLGDQSVG

VDVNAPPHMSSSSSSKKISNTQETAVVLPDDDDDDICLEKPPTQQPARNKSSIILDDDL*
>TCRU_10055 MORN repeat, putative
MPAKRKSEKKEEQVFVEEEGRYVHEEQSARYVGGLRRLTESTFRCRHGRGVFMSPTIRYD
GDWHEDEMHGNGELRFLTTGDLYRGQFSHGVFEGTGTYTWASGASYEGAWRANRMHGLGT
YTDVNGKVWNGKFYNGTGPGLTPFAGGICKEKAAVKKEVEEAVALKTAGVL*
>TCRU_10056 Mitogen-activated protein kinase 10, putative
MSSKGEAVMRDLIAELEEMHSHYTVQRFISSGSYGAVCAGVDENDCAVAIKRVFNTLSDG
RTVNILSDPFLCKRVLREIMLLNHFHHPNILGLKNIFIHLQPPNQHKLYLVTELMRTDLA
QVIHDQRIRISPQHIQFFMYHILLGLHVLHEAGVVHRDLHPGNVLVAENNDIAICDFNLA
REDTQDQNKTHYVTHRWYRAPELVMQFKGFTKLVDIWSAGCVMGELFNRKALFRGSTFYN
QLDKIVEVVGTPNDEDLKMFSSAQARDYLHSSLSHCKKRPWQDVVPSADEVALDLLSRML
EFNPTRRITAEQALQHPYFVSLYDPLDLTEARSEPFHFSDVNDITKMHEMFINEVQRFNT
LRERRDLIAQQRAATAALASAENVLGADHMLRTLSLMEVSELVQNP*
>TCRU_10057 hypothetical protein, conserved
MSLLPLLPQQQRTTTRYEPLAAQKTSVTFRPKLPGIAGSDKTLSRDFSLLCGKYAPLHRA
ALMGLTAGSEGRATCQRRSMASLQRALHWLMYQEKQERALIVSTSLAMSPVQYYGDEKVE
GSWPPWRFTRDPPIITTEEELVTTVKKSFTGVFQRIHSENASLKRLEEEESAFRERDIVE
PWSFLWRKVGIFQELLQGKVMIWKEFLQRLEVWRQLTEVIREEKLARLSFLSEYVSCRAP
LPCKHLLWDLEVLEESAVPLEPEVNLLCLFVSIVVGENASLQDSLLVEREEELSVCHRKH
RLCVSAFAGIQQIRRNEAERFETLMEYHAFCVKLAKGKNAYTILQKPHRPQVKTTREKSL
EMRRQYLRRMVDLKGSLIFPYFTYLTIVKNVGVERGTRAEITKHEFVEFCFLMYTYEGLC
RHAVAAEEELLMQKVVMDVEAHERQIICRTETEALEKDIQPDEFLCRSRTLMQAQLADRE
RELQSTRLRVTIQLLVEYERYHRGGIMLFEKKLRTMNRLMFFAIFCRDGEKYVVRRWMLQ
HEVRLLVEEEEQMRLRIVNEEAACIFTPATAHTWLVEYGDTMYGKVQKKKLQDASCRLME
EQQQAREVVVSQCLWERRVLFQDALCVPLCSTKSGTNTPACCGCRERVKGELDIRKVMVS
DLSEFLPGDVILTLFGFSAL*
>TCRU_10058 DnaJ domain containing protein, putative
MDSLPGRVSSSPPPLYSVLGVPVNVSQAELARQFKRLSLKLHPDRVAYRKDTETTNEAQV
QQRYQRITEAYMVLSDPERRAAYDTRHSVNFSSRVTALREALERNEAFVAPVAKRHCSES
ASGAEGRGMSESSSRNKNKSDGDTDNSGEDEDEEYIPE*
>TCRU_10059 hypothetical protein, conserved
MFLTRIKHIGQPFTFLSFTLNEFVGRNKVEPCATLSVSRSSTSKPWELSIHQRKKLIYLD
PLPKEALYGSVVAKQFLTKDALPYVNSVLIASVNGVPADSARNVRRELGRCDTAVFHLVL
RCKKYHPAEKEQQEGTAEALEATETEPPQHGTNVRVAVPPAAVRRVGRPRKNYAEAKIPM
GNQKLNAQQTKTVPSPKRSPEQTKPPTPPESIKMMPKSVHANADATAPHNAASTGVRAER
TSRGAVSKAKGLVKGISIHI*
>TCRU_10060 haloacid dehalogenase-like hydrolase, putative
MSYQQPLDSQLFGGDIKVIKEGFLHFISKYGHPSSMTYLAVVTDLDGTLLNEHHSISEYT
AETLRLLKSKGIAIIFATGRAYFDVFHTVEKCDLHGGYLITSNGARVFDPQRRAIVTHDV
DPDVVSELINIKLDDENQDAEDSLFTTNFYRHEEWLTNRGSERMLAAYAGSGFRYKEMDL
NTCPHDGVHAVFFSGKHEVLLRVERVLESRFQGKVEHSMSHPLVLDTVRWGVNKGNAMCE
VAQLLGISAQEIIAFGDGMNDLKMLQMAGKGCVMGNAQSRLKEALPHLEVIGCNTEDGVA
RKLRAVFDLLN*
>TCRU_10061 zinc finger protein family member, putative
MSRGKSPLSGSSKSMWLVRKPSGGEVWTYAHNPYDDSFQNNDTNSQRLLNPCRHYAEGCC
NRGSACRFHHDARHNIIVTPHSTPKQRAITPLIGMPCFFGTNVAAGPMSPIKSLGTAQGR
HSHASSAMDSFASTVPTETSTRQHSLGSLTESKSRLFGGASQYSCSKMGILPMDANNSDS
PMVSPVYQGDVLLRTDFLPATSQQLSQQQ*
>TCRU_10062 hypothetical protein, conserved
MPQKNGGETLTPEELQLRVKQGLQKRKKCALCLQVFYVNELPGAITHKSILELRRKWGLD
VRRGDRMPPPSQLYKREELCVFCMQFFDSSGAVQAQQQLLASTRGGVPARLALR*
>TCRU_10063 Myosin tail, putative
MPQQEQQPSIVLPRAAWMWKPRSKRVIEHNLGGIAASFLGARNLGAQEWKRRYVFVEGNT
ICYGKSVGRREKVIPLEVIRAANYATRDVLLAAKAPSAKAHFGWFMYINGKELLFCCEDN

SAREEWVTFILAMLRFMSGLANPAPLSARGEGIKTISSLIAMHNEEKRKVAAEGSLATPI
NSSNTVNPLGSDGHTEASSRLLGEKMPNESKTLVGSEDEEDTETTGNLLSSGNMDDIVDT
VMSDEDGNATHVTHSPLRTDVIQGENSVDMHALVLLPIASQRYSHIEYKLESLAEHFKAG
DNVQNVVFSRSVEKIGKRDTVQDRDLFLTPQYLYLFAQNKLTGGVYARCIETSQITGVIE
STAEENLLSIIIPFFHDILIRFHRQNSRVGGTEADVKIQFIAHLYQIHLNHQTGRRFLFR
EVENIKAVIRRSVEEPHLPLMSYPEDRMRVGTNKELFPLLRTHAESVVFWSSMVTRVKED
RRLQLRALAITDGAIYLLSDTLVKVTRRIPLVDVQDVQFDRDSQTILLHCTEIDALFTVQ
SSTEFIRIIALVPEVVMQCCGVKMAATASKHLYSNVRLGEVGKLKDSLGFSSPTANFMRH
MNLPSRVLSSMHPVRFKTYFGKQQQIEGTEAAGVHNTDGVREMLFRKRPGSRAYLARYRF
VEEIIVNFEEELNILSNIPSFSADGLALNGALSTDFDLGPIHYSSMCIQLDVKSISTGII
LNGRVLSKNGSRRVVCVSARGILLLHYNDELGKLRKAFKGLLLGRKGTSGSDAMPTDSFG
TNDPRVVVFLSWPDVVGLVRCYPGHGTVIGIMTGSGHSCDYMLDVENDLNVDTFLRCSAG
SYVQQNRRSLHSYEVLSLFTAPHIENVRNALKTTVFDPRPTIALRRPIKYYVSDELHLAV
VPDIAEACRRFGDNTIYFSGVAWRYRAAALTKKKKKEKMTGLETRDVNSSTWATHKSFII
VITNCAIYWCTDGGFEILRRTELLALKEVYLSPAEPDALLITVPKEYDMYFCIDGRGKEF
LAQLQEAYAAWTDYHRYLPHEPRGCCHNLPYAGLPTKVVSCLASMGRLKKPPHFDEMQVN
RSAEETRARIELLQRRYLAAAISKHEVALETASKRQLSGGRNENPADAGRVSWAKVYKSL
NATRTILEFAHRRAYLFSLRSSTHQEMEQAQMLLYEFNTMKDLVERMKQATSTEDLAMYE
AAAEEAKKYPPLLHFLEEHREVHERLTKRSVVLENITGFINNEMHPSLKEAEETLQTLFV
AAMESGVQSNVLDELRRRVDLRAQQEQFTAQLQMHEMAVSAGGEIKPPERVLLLLTEAAR
QLEIPVSAVETALLGVPPALARGEGRKQAQQVQLQQQQLEQDMRKVILATCDAIDVAVYL
GNVALLQDVLRFAEKYAFDDVKKRVQWGWEQIAMRREHRAKHHMPHRLIQHIVTRRTSHD
WSAEEVRELRDACKEALEHLPMDVPLMQRDCQLMQLQLRLLEEEEHRLILRDSLQKQAKK
DWDRYKEELQKKEEDERNATQERERRQAEVIGRRRMEYLLIWQCRTQKLCASLRESIRLS
NVADVRRCIRQCIFFQEEIHDGLLNYKCCIYEREVQQMREEILADLKTAATRGQAFLIGN
ERENQVHTPNASINSSEAAVTENVEGEEVGEGGMAESAVPPELLVLIEAYKPKELVEYVR
SHASELTAEAIFQIKELWSSSRERHQWVDKLHRAIHTAFALKNHELLQTQLDLAKSAGYM
DEVVEGAIEVVSAMGAQQNTTSRSGSGSRSSSPDVKLNEAHDEASSVFNLSRTYDARSSD
AAERVMGQLHYTTLELLLPIEKVSFVSGARLQEKRQKQMMDIVQLWHEVFHHRLKPLGSV
FRRRERDCFDFLQFVSQYNVSGDYLAPYINRLLSDFERVKKYNVTQGRSSSFLLIAYMFQ
RKLFERIVYEIAQLGPKVRNEVLFEDALLNKSICDLLVLARMGEQMEWPLMVIEAPDGSA
AHNNNLLTLMLGVEEFVADGKQQDMCDVSRAAAMRNCANLLRSATRVLSNYFARGLATLG
VCPSVKDARALFDEGLNKEIGLIAHEHIIPAAMALLHAGFRPTYHLVRTRRVWDAVLEFG
ESLQQGSRKLSGMSVFGVIQLVEALTDVTGRKRTALLRLSEDELANMRLQMFLTECLNRN
VLAAFLQIFFQSEEGTTCWANEDGVWNFYERDRTVCYPPEDEGTKELMEVVTRLSELPFV
LVVDRDLW*

>TCRU_10064 hypothetical protein

MIRERAMSSVFSLLEKEKPASSGVWSGQKQQQEARPLLWSRRGDGVRPAVKTNVSRHETG
ENVGLNESHSVFGGGGSSMASCSLLSHILHRMLPEADGIATDEVLAVARTIEKTYLHKKE
IANTDAGMGVGVHDGGGGLLGQLIQEQLMLIRQKKRAAGAVMVEDTHRRGRDVESLAGHL
LMPSPSLSSNNLPRPNFATYDEMRHLEVQKDSSLPCRTAFTPAALTAVPVLRPVPASRAL
YPVVVMTTPTFSLECQKVSVFVTIEQDIFYGIGVLRCMAPESYRHGGAGFPLARQPFRWF
LARAAELEHIPRNTPLISSRSSAPPFVCESLLEQWMQQDGGDTFVPLDSLIAIGVASSRV
LSSSPPIMIGLEIDLNPDHDLDHMQAVEATLLQRYWTLRRKESSGFSMSHACLEEGVPYV
VGVEVYFGDGIEDDDSAETWVAVLRDFVIPKGSHTGRTERELRNLLVPPQRRF*

>TCRU_10065 hypothetical protein, conserved

MSHYNTGIENIPSLFDLASALTGFIADFAQVVLGTTQTSFKPAVLEDDDLGEYDPTARSW
EGTGRLRYRVPLYPIPSERHTRDKTRNIRVLMDNCRRLCVEDQLPSTKEELQFWTAYRFM
KYQMYLAPTCIIMPPLYIFWRMFHDRIPRPLRGRTIPITLSLALAEQWAEATYPGHQLLS
TALKAKTPMGDAARAEWLRLQPIDIPFYIYTAYQFQHFFGNPPATLQFGGDVASLCS*

>TCRU_10066 FAD dependent oxidoreductase, putative

MGISASRASGVNDLTPSPRHGGDTDEVLKGFDTSTPTAAVIGAGIAGVHVAYELAQLGFR
VTVFEKSRAIGLGETQYAFPFVGVGLLQPYVHTIRMSRELLRGTLATTCPDIISLEDSWN
SFFSTDIHRWLWARRWNAISEEQVMYYTNNLSRLSLDVVEDLARRHRSLSPYILSRNVSV

GTLDQTSSDAGRVATAATAHSRPLLIDPVGWTRELAQISQKQYGVEFALGEKLVDSTTYL
RYSSEVMSTLRFAREVDGQPEYRNRRFDVVVLTAGNYTGPLTWGSSQLPIIGLGGCSVAF
KATSPDKASNPITELFSGASPGMISFSPSSHLVAYKLPSCGDPRNSEEEKIIVQGLMSFD
STNKSESNVVGILKRLEKYLRVKCKMNIPLLEQYQQERQDFNSTAGGVTQPDHMRVTRYI
RAFTPDGVPLIANNGASFNSFVCSGFGDHAPDMAPGSAKILAKLVELKASVMLHHDEEEM
RQRGQQIDVVMTEKRLDQLHRELQMLWNGWLATTGPPPGQEMETFGHNPFSPSRFGGVVK
EKASDVTHRSFINRLLNLETSLVRTCEPWGHYINQHAIKLARQDNMPDWLRTIVYYYFNE
EEDDEELQHSRKQYAEGIQRIREEFEGKTHTSSSSQ*
>TCRU_10067 hypothetical protein, conserved
MALVTGWIDDARRGYSSYGVDLIRTGCLLLRTTPSVTYRAAVLFQRFQAVAEQVRRKRGD
YQDEYSITEGNSSRDVLSGARKTSYTVPIHVGTERPSGVLMFGDPYAPLDYCLFNLREHD
DITYLTAACVLIATKMEDHSMRVRLIVGVFMRLNQRRRGEPVIEQLQPPPERYDDFKSCI
LEAEEVVLQALGFQTFVESPFKYAIFFLGMLIEEEKVGVAADTDTAENSAFYFNGFSSNL
VLKKWLADAVSWLNDIPRCVELYAEEAHVLAVCSLFATRPSNITALPDNWSLAFGLERTK
LNAVLRLHRKHLEEAVNSGNKNVQLLIETRQTKPCYPTATAEGTPSPAPAVTASTAGNPP
DAPPSLPPKKATELSPLVASSSGIKIPSATPPLAVAPVVAPFKQLESLHSALQLNFVPRS
NAGTNNHNHKSPKVTGDTTKNVNDIGNHHPVRADIPDRSMPTGGGVSVIARQSIEEEFHF
EDLKELQRRRRQEEENEEKRTKRRRSSSHRRRHHSGERRKGRSSDRQREESRGGRKRRHS
QGGHKSHRNEQQQQHRFNASSQNSRSDRRDERQRHDNRPRHDDRQRHGGRQRNNGRQQRR
ER*
>TCRU_10068 hypothetical protein, conserved
MYSCSAQSVPALLTDLVLHNYADHLTSQRTPPANYPITETRTDAASLEETLAPLQLIHGK
VFTSAIGIALHGAESIFRYVAYDSSEENEGVPHDEEQERQEEVKDENENFRGRCLYFVGE
HRLFSPYYCPCGAYGYQSIRRQEAWLCKHLLALRIALILEKKGLVRDVIRKRQVTRCQLR
EMMQSLD*
>TCRU_family protein, putative PR.1
MASFPAISKIHPRKQGISSRLSRLSLEESDEVLTERRCADGNNILHVLSALWSVSLEQPQ
RTPKEFFLRPAVPIRDVYTTRLLVNLLWFSRNYHNMALLISLFVIFCAPPCALIVTVSCI
MHITKRYTSRGTPSTVSDATKKTRRESGRSGIMVLLTLLQIGCCIYVWYLCGFFSVVMCI
ATVATPIVAHAFFTPYTDDAFELYCEFLRKRYLPAPRPCSPTRSFSSVDPTFEVLNRLGS
VSMSPTHSNSGRGNRPFISPHSFTLPLCTHKKEKAEMHLRMKYLEPPECQGRYSPSSETL
TENSSFSKEVIDECMDPVELATPVAGAENSTEVCAAASLRHLKLHLNIEGVTLLQQSQES
GVLQPLQDPLDGDNNNGVATCEEENENYPCERRCTTESVEEKEEEGMSLVGSILTENISS
ALSSQATASPRCGRCVKGIRLVMEVPVDADKYECKWEKSETVMNPEQGEE*
>TCRU_10070 hypothetical protein
MLRLALDAHSGSLRTSERVSATMNCNGGAGGRYDDATVVPEAYDDDATSWSFCVSSSLRQ
KHPRYAASARGFLPSRRVTLLWGEVPFHLKNEKLR*
>TCRU_10071 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MSVTYGGREHVAADNTDEVSGRNATGHKSLVLENGVAGSGFVAEGDAYGLTQRNASGHEN
KPQLREFTAQYSGSGVSPLDCFALRNDAKLRLRELTVDGTVRVCVYWVFLLLLGLCGAVA
VF*
>TCRU_10072 hypothetical protein, conserved
MRTKRWRPLLSLFTKVFSLSGNVGTMKEKDTITPLARGKPNGVLTQVPTEARREAAERLR
QTQEMKFTISTNIEDVLFKGRVRVNEMRLNDFLTRELDGRGFVDTNRDVLLEEFFKDPTK
YIRDKGALNEMQASDRYLSMKRAVKGEVIFDEDIRRLCDKGVNNLPGWSLAAAEVKATVH
KFTKHFLDAAAEEARNPTTTSAPEKLEGCYESVHNARWSHAVEIPDGVERKKTGTGMGCV
RGGQNSHGRTGKLTALSKRMTLCSNSVRHLPC*
>TCRU_10073 immunodominant antigen, putative
MTVTVDLFNHAKASNNEGRVWSVDAATFNEVPEAQRVLADSQFYLAYTMKRRHVLRVVKR
SNLLKGTVRAHSKPIHAVKFVNYRSNVAASAGKGEFFVWVVTDETEASNGKPDLAARLTV
KVYFKLQDPVTIPCFSFFINAESQRPDLLVLYETQAAILDSSSLIERFDVESLEATLQRN
CTTLRTLNQPVSENSLCSVGSGGWFTFTTEPTMVAACTLRNRSTPSWACCEGEPVKALHL
LDATVEENVSVLVAASTKGVYQWLLTGVAEPNLLRKFVIDGSIVAMESSRETFAVFDDRK

QLALVNMHSPHNFTCTHYMMPCQVQRNGFCFNRTADGSCVLADMSNRLTIFHLRSSRREE
QQPGQKPSVVATAKPGCVSSGTDAASSSHTNTTSAAAASPASPPVSAPAKAAAPPAAARS
AEPHVGSKIIANLVNQLGINVTQRSVVSTGAPATTRSTAVTSTATAPQRTSPYGHNGRPV
TAGLVAANSGASAASSPTAAAKPTGEEKAPAACDTSSVAINATRPALHNASLPQAPTDGV
LAAAVYQSEGEVHQSLERLESVITNTSQVLKLLPDTIRRDHEQLLNLGLEAQMTELQQSR
PTPQTQPKDTSSANSSVFETYTLVLIADSLSRNITKGVKRGVNEAIMLHLDHEVRHAIGN
RLRQTQKNIIKSRLDEALKESTTQFTAQLTQTVENLVKRELAEVLGSINGSLTSLVKENA
SLQKELNSIMSSGVLDEMRRMREELCTLRESVAKQKATMPDSSLHATSSFQGRRSAPETI
LATALSMVREQQYRQGLEYMLMAQQPSLLLRFLSILTRENESAYSELIENVEAPNDVWCS
VLLQLIEAAATEAEKEVVVGVAIDILSERDQLAQNGALGSKLTTAMRAFERQARSETTSR
SFLQCLKNLEKLLQS*
>TCRU_10074 WD repeat and HMG-box DNA-binding protein, putative
MLPQLQAHPAGATRVCVDGAHVLTGGTDGVVTFYPKKRWPSCKQLWARQCHDGAVTCVAL
HAVLGLAISCGRDGNVVLHENVLSASTSRVICRVTGEVRCVLFDTERRRVFIGGDSLRCL
QMSPQGCSVQTMPMNVPHPLVGLALSPCGNLISMASASGAVGVVSACTSISTQATPFSQE
ELLPEHQAAMERLKGVCFVLPKLLSPTAKRDDAVAYRLCWARGGDGSLLLLVPGVTEAQV
LRFEEATSPPYKHRLRPIAGIDSFGMTDLLGVTCYSLSTNILCVVLAGTTGVVVAKVDAR
KWVVTRLQGQSFADVTDVHVDAMSGDVVVGTRDGVVTYLRREAPKALGSKRTADADAGPV
AGNTDVSKRKKMRRENRMNDGEKAQDGVKKNPQDTRRQPDGDDGENGGIIGDSSSESGSD
VDDGASSSSFTSVAKEDFRQVVDDLKRTNPNYKDDDSEEEERPSRWRSQNPKEVLRIAEE
ACRKQRSVFLDDEAEESSDNDSEGNDVMEGEEYVSREHGHNGQDDSGSVADATDENESLA
SLHPPHDFSLRAKNADTGTAVFDYSFQIGATPVGEEGSCYLAYNSVGYIHSTADGTNIHF
HDMSIQAVRILERGTILMAALSPVGAAFVLTQDAEMDSVDDTPRLTLYYRTFVALGAQSD
WRVRLYPGETVRCLTAGIRFTAVATSRYLRLFSLSGLELAVLSLFPRIVAMVGTNSSKIM
RSFKADFDPLAVCYLESGGEMRLQVLDVGSRSVVLPPVVVPLTTHSDGTLHQLQWMGWSE
DGPLHFADTAGVLRMFTFNWGGSWIPVLDPRCMADRTYNLWIWGVSDEAVFAYRSCKSDP
PYPAAIASGLPTEHVRLFLPLTRCGTERDMVTWDHLLRREVRADEVKRRSTFYTAVIAKH
DALHDKKIIELFKNALKEHQTTRALDLATYLELRDNIEVCAKEANAQGHGKLVQKLLALL
EVRVKAKKKRRCTLPLEGSVVSERERDLLLRKMLAKEKTSGAGAPQPAEGAVEATEKEVS
PPSSAGVCAVTTPERRSRVDDAPTSVASPSRRHVTFTDQEGTSPTKRLAEVTTTTPSRSV
NRESSHSPQQPTQSTTPPTRTKPQNPFSKPAKTTMMTFTSSSAQPPPVSRPSSFLVLGDS
QSSMVLDMAEGLEAQRKQEQKSVSPAASLSKQSTDMKTCSPEPSAAAASEGNSRRNSVLI
NGNKRVLSPVIDAAKEHLRPAANLFCPKALPVARPAALVATADTTADVVVDPFLDQLEGG
TPVTLEALLVDVGHEASQNVAPRSASFGEALRKRYREEEEEHDEDGDGGVMDMAVPRMAF
*
>TCRU_10075 hypothetical protein
MMPQEASQHIAAHFHPYGREMENDFKLLAMNATAFVPGSVERLRSSCWMSDGERFVDVVD
TANITPILHPWWRRQVDGPIPSSVFYSSVRAASSAFPRAAQTSLPYSADGAVGDADRHEY
HHCDNTALQRFWTTQENATGGNVQRAPETQQLATAWYQLNYGIPVSSGVLEQPYNIIEGA
DAPLAAPVVRPLPERATAPAVSMRDVDLVVDSPVPLEDTSGGIREELLALCRRLDAVEAA
CCLHSSSSVRRGAEVTPIPPPLSSVEEAAAPVAPVTVSPSASLSPPRSRESSSGVTLERL
MNAVRRARERAKEQEQHRQLSSMSSALLNADASLSALKKTGDGTPDKGS*
>TCRU_10076 Ion channel/Calcium-activated BK potassium channel alpha subunit, putative
MSISGGNLHAGDDVMNDVVDLTMIGHDRRYAAFSPYVRSWRYRNRTQYRPTRRAFLLQIQ
DHEREKNTRSDCKSSFLASYFSYFCGPRWRGQPPFGFPMMTGPKLFFQAFVRKHPVLAIC
VWLFLFVCETAIVTLYIVQTTRPGKVTWVEYGMHDFDWYATTQTILSIVLLSQLLVAYNV
GPVTITIVLVTSGYRIITYFVALVSGMGWVSRLYVPLFLRCWPMRQYFLFVLDSLATFTP
RNHRLDVIRFAAGPLSFFVALLFTFGCIFHMHQVFRGYNLEIDLAIYWMVVTISTVGYGD
IIPHGLDGHFLAIVIICVFLAMMSSLIMLVISTTQILREFPRYTGRRNHFFVYGHVSRED
AVSILEEVLTLYPMKTVCFCYTAFSPDVLAIGRHPRYRLRSKFLQVKFLDRVMLERLRIS
ESSAIIILPGKDAVSKTVDADSMLWSTVFQRRAPHVPQYLRLRFAFHARLLRGRGMFMID
QNNKFIMSAALLLPGVLPFLVNLVRISSASGTSPPNLWDESEKDNWKNLYEYSRRNIFAT
CPVPWFFVHLTISRAVRLMKLHDVLVVGVEEGSRKVMRLDLEYALEQGDTLLVIHERGRV

SLLEVLKRLEPGGSGAVTSLGGSTVNNDAFVDSQPNWGSFTMSGQDLFGLETDEKSVGMN
DNKLYYPFNRSFDLMDEEAAKAPPGKGRGAPSWLSNGVGGQKGVPSPALQELLIRDSSML
ELRRQLLQEPFVDKHPGGVSLKELPLGDSASMLRELLSCRRAAISETHDTKMDSIERLEQ
QINDILTHVAAEYTNGVGKEDSTENFLFIDQVTSFRKPAVASLYEKYLDEDVSHNELSEM
MHSIHSIYTQSRLTLLTSRKLSKEFLDWWKRTFRYPLRYIRGLSTSESHLEYAIWQSGGI
SKLRGILLYCSQLGAWDFSDIPLITVGNNVCAKLEASAFHPVREPVEEETEPISLPEQNV
VLELKSFVSCISVSPYHTDPEWRRRGEKQFQDSLAFMMGRCFSPNMLQTIFIHAHHDQRI
IYFFAMVLQQQGKMDHYDVAPWLSCGRKFGTAFQLCGNQLLHFQTFGDAFSFLLSRRSWV
AIGVFRLFPASEGLPGLPRYFITNPPLRMPLRPDDVIYALSALSNTFNTADGQKQN*
>TCRU_10077 hypothetical protein, conserved
MSNTTRLTSRNLFDAVFATIPADVVLDTGPDSLRERCALMESRRAAAAAAVESDDENNKN
NNDEGEEKRTAVQRKNVVSEEGFLFGSFDASTNTGVMDVSAMMRHAAAAKEGAAAVASMG
DVSLRPVLDVQLDADDEAVQEATKYAALFVEDDEEHEEAEKADNESKEKEEGVTSGADAS
RSFDSNQRQRQQQQQNKKSMANASAFPSLTAEEQIVIMRPEEGIRHEGRCVLFRNSKGFG
FVAPEVGGPDIYFTRDDVAYFFTRRVLEEYYGGNLLNIMNLRDASWRATGRGGGGAGGGG
MNGGAVSVLGAFPSTAAAPVSHKVTPCDVEEGEKVMPDANEKGGNEEGDTDRKQKEENKP
NEKNDEDAELIREVDKNANSLVQQAAALLTPENAKLLLLFLQVGKPILSVPEPVSFTVRW
NRMGNHSSRRLRADNIRGLPGNGYALMVEQAWFERIFTRAFGRSSGEKGCKSTEGEKDDC
LLRHRGTICMYDADELRGVIRPDENDMQGVSFTGDAFLWDPFMDPARRRPSVGLVVHYSI
AGRDRHGKYIATLITATDDTAISEANTEWASGGGVEDREVREQGGDGIALGGGGVGGCSG
TGGGGGGGHGRDEETAGRKRRRDEELLLLEEDDYGII*
>TCRU_10078 hypothetical protein, conserved
MPIPSPPPPMRFVPNGVGGGGARDLTAVKEPNFEVLETSSPVPARVIHNAPASAVPSGTQ
RPVEAPPSTHATGAQHHPKAVHSPPLACPALAMTSTPASSSSSSSQQVAQLWQLVQDLT
AENAVLQQRVRVLMEGETHDATLPGMLTAPSSPEETEALLLRVRRLEAALKVEAMEREAL
EVRLQAQEQVLTRLLRR*
>TCRU_10079 Putative integral membrane protein conserved region
(DUF2404), putative
MASWLIFVCGVIGGAATTLFLISFLFVKAGVMIETAVEQKEMRLQKRVGNTCGDELCVWK
VEAICMMARYDNDIVGNAIPIRAVLFGKTISVYQIDSSHRSKDGDQTIVDAEHLIGKINT
AIVSSALEKLSKYHRHTDTTKRQAPIRGKCLVLRRKEGLPLFIEDPMKEMSRQQRRQQRK
QEEEEEGEGSGRRQRQRRHRHEDHYSREGFEENNDGNNRENIYGDENGLMCMGELDLEDV
DNEPCFGDWTAVVFKLPTRREMERWFNLLQATPQSEEWRMFIKHLPFTDVFNLVVARLYF
ENTRTSGLHDLLIEKLRRKLHRVSRKLPKHIHGEILLDQLEIGGEIPLIRGLGEPSVSPN
GEIELDFDFLYRGGLKFSLRFAITYRGVRVPDIIFNIKILELSNHMRLSIGPPPSTKIWV
GSPRPPQLRLEFTQEVASHDGILNAVLKLMPDMSLVMSNVVKVKLFEDMLLPSMEDFPLP
CFSYSPPSSEDGSPLLDTATVSSLGQDAGTVQRRISAFASESSTFGETRASSILSSVEVF
PAVRDDGPPLPLSTDGREYSILPLDKGSNLTASSDSSSLSSGALPASSVGESWSRTETPH
FNGLVSRMKRRVKNLF*
>TCRU_10080 Putative integral membrane protein conserved region
(DUF2404), putative
MLEIFTLFLYGWIAGVIAVPICYLYGLESFTQFVHCGNKVLWFLYAYLSGKDVAATHFRQ
TSYNESAISSTSLSALYSADSKTPLPDTTGVSPARHMSVCRLSYLTDDNVFGAAHDCRLV
LHDKYLFVYEVQNSHGVGSHERVITGERLRGRVRTDRIVVQPSFLPGGSRRGGNAGAVHG
HVLHIRPRDGGPLFEGDEEDREGSPSGTYASFRGGTASNSGMTRSAKNNVGDSTVLSVNG
IVKSSSGSSNQEKVYGSLAVAESDAESRPGNKHTIVVKFYYMREQERWQSLLRGQQEAAQ
WRDYLQTITTPDSFNLVLTRLFRQNMRTTALTNFIGAKLQKNFDELSMRKFPREIEGRIL
LDDFLIGEEVPIFSNFSSPRIVAGGEMIFDFDLLYRGGATLCLCLNLTYRGIRIPHVVFS
VKIKYLSARMRVSVGPPPSKKFWLGILSPPDIRLEVHQGMQSGRGFLHRILVSLPDLSPI
ASNLIKLYLMHDMGLPALDDFPLPSLEKTPPSSPNALQKKKWDMRFDRHNAVARSRGQAN
LQQEPPASGTLEEATIDGFGSTTKEESEFFSPARTPALKVIASVDEGTHSMGHGDSSSTV
NVSGSVLATTATLRELSQGVLLSPSNIASLPPNSEDGRRLRLKVKARNVMRLAVKRVRGM
PESLTGGSF*
>TCRU_10081 hypothetical protein

MRREMASDILNNDLSSPGRYLGRRPLFTLGWDMVLAEESAPQLQAATTADINSDVENGRE
KQGSDTASTLSIMAEMQHSGGTAHAARVDAWVEETALVSSSTQATVGEEIKGRHPLAMSH
WSPPDESPPAWTRPSFVESSEHPPSPYAGQVVRLQEVFPAIGGRRHRRIEEERVKAGEGK
EDWLLPERQEKREVEPSASVSERRVSRETKKETTHAFDATHSGSSSTMGGGAGRRDKSPL
MEVKRITRSWQEIIMQKAGRGGSKEKIEERREGKQPCGSPRIQQPHLHPNHSGQREWDAI
DTRQEETAMTAEAVMNMQRAADELAHRVLMAEREVAERRAEYAALREDITRCLEAMELPL
RKQKRVLRELRSENQRLRRLLGL*
>TCRU_10082 protein kinase, putative
MDRFNVGSPIGEGRFGVVRAAVVKESGVPAAIKFVTTPRLDEGIPHPTARELLVAMRLVH
PFVIRTYEVVPCGCSLALVMERCKTDLATVLSGRTASNPLPALEAKSLFKMLLLALAYIH
SEGVLHRDVKPSNCFLTAEGELRLGDFGLSRVWDTEASMTHEVVSRWYRAPELLLGQRHY
GPEIDVWPSGCVFAELLRGHSGAFFAGDGDIWQLSRIFDVLGTPTPTSWPSAVLLPDWGK
VHFEPKRPLPLREFFPDASECALDLLRRLLCLDPQKRLTAAGALRHAYFSEYPT*
>TCRU_10083 zinc finger protein, putative
MGDGQHTGGLAFLAAPQDNLRYSEGSDVIHVLIYVPAARCQVILVAVSGGETVLMLAKRL
VDVHFRLGRGSLKSIRTAEREILLRKMRFSNESIVVENEANASDLASHCKHLFLSTLSAS
ELQHAHDGDPMEGFFL*
>TCRU_10084 nucleosome assembly protein (NAP), putative
MAVVGTEDALAREIQTRIDLLQAELHKHVKDVVVAGNLKRNAHYTARHEIITKAIESGEL
PRTFWADAIVAALETPEVAEGNEGRLLGNYDAALLREYLQEVKVEYTEAGVKVMLTFAPN
PFFQETVLWGEERHYAGDEEEEEGKGKDSDNENKNKNNDKDEDDDGDNDADDVCRFSGIT
WKPGHGPEDDGNDHHSGGGGNAGMDKGRNGTSRKRERSPATTQGWSFLDVFSKMLPHPEE
DEAFDEADDDELADAVENWESEMEDRRDLLLTLVEDVWLDPIAALMRKRAEERDGSSGPR
LKRMKTE*
>TCRU_10085 Domain of unknown function (DUF1935), putative
MGCGPSTQCASTVSGSDVTGWKPHAGEEDENGGGTRARFFRRGHAKSGGKRSNDEGQRTS
PPLVHSYHCGGPSVSGGEVLPALWYSDCTKAAWKKDGASLAQDDTVLLYRIVLPRPPYEV
WAFYNDTKDIQFYVTIQFYPHPEQRRELLMPLGATTVVWLEDGSQNGMDAGSAVAKLVVG
PTETALAVEGHMVAYRIIVNGFPANFMMQ*
>TCRU_10086 calpain-like protein, putative
MGCGASSKPSTVEYKNGKPSFKGDEIVRGFDEGNGLLFRIVNNKKKQWAYYNDTTEYEMH
VKVTFGEDCDIKALGKTHLEKLESGEHLATIVVHPCETEMFIEGRVNGFKVKMDAVPTEK
NKRPKEEEEKK*
>TCRU_10087 calpain-like protein, putative
MGCGASSRPYVDYRNGKPNFKGDEIVRGFDEGNGLLFRIVNNKKRRWAYYNDTTEYEMHV
KVTFSEDCNVRALGRTHLQKLESGEYLATIVVHPCETEMFIEGRVNGFQAKMDAVPTDRY
KHRRRRRKGGCCS*
>TCRU_10088 Thioredoxin-like, putative
MRRTAPLRRTSRRGPGGWTEPTLRQAAALVDGNVTSGAARGPSTSFVGSPSPAVKSAFGV
DDFSMIRRQQMTFTKLIQLTMDATFRPKDSDSKIYGGDGATQRAALREELKTMDRRITPF
AHEELLNDYLKNIVAFSSPSGQVCDRELLRGRLVGLLFFTESERSLAFMRKLKSFHQRHR
QDFVVIAISLAGKEMMDVTRQHGFFHCAHRDGATWVSRDAGVMVRPLTPLPRLIVVDGKN
GEEITRSGLTAVLTHPDTCFAAWRRGAPGHEWWDYLKTFYL*
>TCRU_10089 Domain of unknown function (DUF1935), putative
MGGGASSTSCDDPTTTSRIKYRNGYPKVLGDEVIGCFSTVDETGEVMAPPGLLYRIVDRT
KRQWTFYNDAKEYNMVITGYFGPLNIIKALGKAKMWREMPSGLLIVELVVEPLRTEPYLE
GVVTDGFDLRFRALPT*
>TCRU_10090 kinetoplastid-specific dual specificity phosphatase,
putative
MAVEGLKQYLQRWRQGGRVSGATPTTSLVDTELPRSFRPHRIVPRVYLGALKDVEDTWEL
HQRLLPEEMLLIVSTCACSFMPQLEMRQILPVGKKCREKGVSPRVRRLAVCSWEQLEERI
SNPLGGVTSPAAAEEVMMATAQWLSQSLESGSFVCGGKTMEARVYRERKENDDVGLVYLK
LCLPWRDEPPFPVWEHFHVSTAIMRAVVDGLGKAVVCHCIAGVSRSVTLVCAFLLRCFCD
DSTVSSRPCTAKEAVKTVIGFVREVRLCACPNDGFMQQLAEYTSRLLSASVNFP*

>TCRU_10091 hypothetical protein, conserved
MELSVLTSTESSQGSSEEEKEKDAPECTSETSTVEQFVPALICMRCYMPIAQYDEILPHR
ATDAWASQVYTYELDLFENKPPLWCYSATNPSTHRFDLVRCDAVIALRRHLLSFYGQWSA
EHSFFVGHEWCCVACRACQNFLGWGFRRTLNVPRDTENETLETEEDAEVPVDNNLSFVGI
ILTRCVGNDKFPLSQFEACAAIGALLGPS*
>TCRU_10092 Der1-like family, putative
MAQSFDGWLNSLGPFTRYTLIAVVLLTALASMQVVPLGYILLSSAVFKELQLWRLITAAL
FFGGFSFPWLISVAMFVSYLNYNETYDFNGKGGDFIWMGLFLILGNAMGGILLDMLVTSF
SLLMSLCWVFCKRHPELRMNLYGFDFHANTFPWILLAFHLILGQSIVGDILGIVVGHIFF
FCKDVLPKTHGMDPLRTPVWFQRYVMPNVGFSGVNTLYPAVHPQDARFSRQAQPPNAGQR
HRWGAGHVLGSE*
>TCRU_10093 ATP-dependent DNA helicase, putative
MGLDGGVAVPAAVSGAQRGEECAAECERLVSALDEAQRAAVCEDTSASLLILAGAGSGKT
LTMASRIAYIILTGVAAEKILGLCFSRQAAEALRERVATVLPPSMAAHVQRLKLKTFHAF
GLECLRRHGCIDLATEVYDARRQRELASAVVEAHAVHHKGLEAVLALVEYVNKAKTKKDM
RAGTEIDPSRQAAYLFRFYQAMLHEQHNAVDFGDLEQMFLETLRPVGRQEQPSEEGVEGN
GGSNSNSLMSVVPPPRLPSPVALQLRAQYTHIVVDEFQDLNEVQLECLALLAGDTCRVTC
VGDPNQCIYTWRGATTNSFERWRSRFPQTKIVTLGTNYRSSEEIVSAVNAVSQISQQSFR
GECGRRIILIRCPHAWEQMSLLPRVVEELLRTRDRGLKYSDIAILCRTRRTVRDVVTALE
REQIPVCELRPSRPNSKALVRAMLSYLRLCVHPHSNLDVECVIRDAPNHFSAAAATKFIF
AMQAECLQRRRELSTAKLQCEDSHATYSYYTILRELVHNGFAHVHERLRTTKPQQKFLRN
FIEVTTAAHDALGRMYCDIEEVVRDVAERAGFDGGSATSVQIRRRPCCGIKRRRSSAPLR
RSAAIWDDVMGDAEDEVGVMEEEGDAMSISQVLVEASRTVQQQVLVEKKNVDSSQERYGE
IKNGENDMGDAASAVKAEAKVQNDAYTVLQRVIDEFLALLPTDDFGPLKGGSNVKMESTQ
VPRVTVTTVHQAKGKEWLSVIVPCCYEGEFPIDVKRAEERRVFYVAMSRAMRDLVLMTAE
FGSLAPRDYDDGNGAVGGAEQPLHITPYLRPLMPFMETLSMTSQEQLKGGNVGS*
>TCRU_10094 serine peptidase family S51, peptidase E, putative
MMTHIEPSTIKGFFAGSGLDAFGEPAVVDRVLMLTGLFDMEKKVLTAPVHVAYIGTAVYD
IPTFKERQTKWFVSRGCTVAEVRVADLSVPNTVDKEELEFLGKAHIVVVSGGNTLFAIRR
WEETGLDVCLRAVAVRGAVLAGGSAGAICWFTSGHSDSADPSTYATAMLRAACGDTVAKK
DYDDDDGNAKKTSKTEQQQQQEEDASWSYIRVHGLGLLPGLLCPHYDMRETNGVLREED
FDKMMKRHPTERGIGIDHWAAVVLPGDGTYEVFSVPGKGRGTNKDNTMAPAVYVKDVVDG
QLHSVTMPERGRLNEFLRQPSGPVVRDPFEAYYAMANPTATGDKLLCQCR*
>TCRU_10095 hypothetical protein, conserved
MVAIAEGVFEYNIHENKLFGVRFPDIVAGYIKAAETWPSIVAGITKKEWRARTVLGSGNG
DNRLCVLHRPTAVVRGSEVFLLVGSDTLGYDSSDGI*
>TCRU_10096 hypothetical protein, conserved
MPRMCASRVTWGQRGRRLSEHSRAFGSGHDQDSVGTKACVWMPSSPRPLREGHALHSERI
RLGGNATALYLWATDNSRTFHVGALFVGNAMGETLANAMLYSDGALHLLQKGVNEKGSAI
PLARLTEELKKINSVLSTWAQIDASFAESSTPTAGLVGFLSNAASDHII*
>TCRU_10097 hypothetical protein, conserved
MLSRHVKTRVRDSLRWLTDPTHAVHTCSNCAASCARKEEEATAASTMNVTSHKYAGPYEL
WRRQFPPDGTTHPPARSSDADQTGICQLPPPREGKDDTKSGGTTAPQVNAEPSRQNEGAR
QSAVADGPNTVDPSPASNTATNTSETKPEFAYV*
>TCRU_10098 hypothetical protein, conserved
MLDLARQHGDVRVQLAFVDEHGPLDAVVAAAATMTGLRLGSGDIAMHWEEPTVAGTLRIA
GRLKYLISGFECCCPSCVCCPEVGSPAGADHCWRAETEHRLRQCRRGRCGSECSALLSGG
RSA*
>TCRU_10099 hypothetical protein, conserved
MAPVQRIRYCISLHWTLTLGPRVYGMTSSPESSSTSDAHTVIVCTKWALRFKRPSTVWCR
ADAHWRWIGNPAISSWIFGRALPQTFRTLIAITTDPSISRPPHFVPAFTWPFTRLTSSRG
RPSLLWSGAQPNKNNDCCDFSCVVFMDATHLHATCAAQPGELLAAQFVIKKRRGAAGCLR
GRKNTAPSIPPPPSNPRTRRRTAPKTLHPIFRITRINRREGQWSSSAKKFTVVRRTSEIS
ALDKLHEGSERGGLRTVCAVNVAAESVPSGQFTTFCCTHERPINAESCAAFLVAIFGVAP

LTRRQYARMLRSMLQMD*
>TCRU_10100 hypothetical protein, conserved
MNRYICDRTDWKQRVFLRLAWITASCWSDIAALTPNNSTLEADGTIILDWPVVPKTARAD
PHRAFRFVRIRGQDALDTIKLCRTLQENEKLTNLTTAQVTRALAPWNATAHSIKRGALRH
AAPIVETHDLDPHVISPLAVHVDPFDLPQSTVRYLGSYTTMLTQVLPLVALM*
>TCRU_10101 ATP synthase subunit, putative
MPTIRYKNRDELIVGIIGDEDTVTGFLLAGTGDNRATLNQMSGDKKNVEQPNYIVVNPNT
PLVDIETAFTNMCANDAVGVIVICQHIANDIRHLIEEQKEPIPCILEIPSKGGLYDAERD
FVLEKITRALGIR*
>TCRU_10102 hypothetical protein, conserved
MRRTFLSFNKDGRAEERLNGFLSVAQESKTNFMTRRQGLCMREEELFLVDEDLLLNHLLA
GTSLKYDAEAVTLQGAFDERVEVDNVVRISLELLRDDFGERQKKDPNYVDWDSKLPAFRG
D*
>TCRU_10103 hypothetical protein, conserved
MLQLTTVRCFKGLDSLKGFGSLFGDGTRCDNAGSCSGGRGGVSFLNSGFGFGSFSNGLPT
KISSGFSSGSQGFGSFGGGRGSEGGNWSGPFGGPLGGLFDKALEWCSEAHAHDIARRQGI
DIREIRFEKTPEGGVKVFVDAPQATPKQIEQLGEQVMVECPVARFRKTHLTSPQQTVQWL
RLPDRYDR*
>TCRU_10104 hypothetical protein, conserved
MPASLSSGPRTHRACAGARVAQPERHLPRGRSLLVGALVIVEASKTKPESGFSFARRRAG
TAGRRLRPGPRGLWRKPDRCAVSRSSPRCGDEWRSQREEEAFPCGFFCVSVVGRPGRTDG
IRPERRVAVAIAVVRVCLKPRRGGGPMRPVPHERGRSPCAWAPVDC*
>TCRU_10105 hypothetical protein, conserved
MNPHHELRDGRSTSMTAGEDLAATSTGMDAELSDDPAQATWISGRSVSFPDVTAQRVLRV
SHWTSTRLHGLGPPSAIPHRGDGGRHPATGRHAATTETFHRCPA*
>TCRU_10106 hypothetical protein, conserved
MVGDAPRHCASGSRDIPTGICTDGMEQAECVAAAACHELKCSANGRTAIMPSAVASPCCQ
RSVRNSLVSSRSHACDAPRHGGATSLPSGIGCAAVLLGPLLCPASAGTSSRSEHRHPLPS
NKRLIDVLLPTPQHTGTRPADHRQPSVLVPLLLLSLKRQDRPDLLRNLHLACRRHLLVER
RAADQRRPAQAAAASSRLPTI*
>TCRU_10107 hypothetical protein, conserved
MRQLIHVTPRSAVLLVLLVVMMFVMCCAGGCFAASLTCSCSSDKAMRADRAKSIPAVVRD
VPLGSEGASQTCSVIGRNGWAPTRIDVSTRDLDGTRKYCSSERYCAMNSLAAIASVKVTF
FYAEEREVFVSLYFAATVR*
>TCRU_10108 UEV domain/Zinc finger, C3HC4 type (RING finger),
putative
MNEIITRFFSCSSHCKPEVLGRILHDVENLCNAFHFYCRDATWGVTQQEKLCIYGGLPIT
IKKSNSDHTSLTPDSREQAPPHRYVLPLQIWLTRLYPIEPPLVFLLSAEQGCRIASNHKY
VDATGRCHTPELAAWHPVSSSLCDVVKKLCQLLSAEGLIPLCFGEEGVSSPSKGHATAVS
QRLRHGLENGDDDKQTDEHERCVVCFTPKETVLVPCGHYCLCDACATNVTHCPLCRGSVK
FRQRVFS*
>TCRU_10109 Mitogen-activated kinase kinase kinase, putative
MSGDLLEILGESRNWVLKRHRVLGKGGFGCATLYEEVHTPGSFVVVKDINMQIMKKEEEM
KAVEMEVAILRRSCGHPNIVQFLDYYHDGQFMMYIVMEYCEGGDLARLEEQMQFRVFHQP
ERFVASILIQMLVGLYYLHVDQHTLHRDIKPQNVFLCSDGTIRIGDFGVSTVLNQYGCRA
KAVCGSPFYMAPELCEEKAYDGKADLWSLGVMMYELMVLERPFNAKSIPALTRQIIHGEF
SPIPRELHYSAQLVEMVESFLQTSPTARPTLRRVLRSSYVHSHLDCVPIVCLLSDHYARL
FGEELLQQILQKHKDSTNTTSQVTTVVSRNSASVQEVERCKNHSDHSDGASAQPLAHQEI
SELEQWLEANGDVTDAFIDAQLPRNRADGQELSNSPSDIGRAVKTGRVFSDDIMDDSISS
EQGKGQQAEDDVRDDFYEDDFESESSG*
>TCRU_10110 small GTP-binding protein RAB6, putative
MHQISSLMGRQGGGGVNAAVTVADASSSTAAVVKHKIVLLGDQSVGKTSLVTRFMYDTFD
QQYQATIGIDFFSKTIPVDNRTVRLHVWDTAGQERFRSLIPSYIRNSSGTIVVYDITSRA
SFLGTFKWIDEVRAERGDSVVIFLVGNKLDAQEKRVVSTEEAQKKAEEYNLVFMEVSAKQ

GKNVKALFRKMAEALPLPDDNASGIGKKGNGVGDSSSQPFVLGKQRDPFLLTPSRLPQSD
RDGLQTNNNNRGNDDTNGFANYMQGRCC*
>TCRU_10111 hypothetical protein, conserved
MTHGDTSVFARATQQTRDTFLRGGTASQRFLQRYRKYPYPVRMAGLFLLGFALGGVIETF
ACKTHMYESVMAKKDMRRHEFDEFVADFRENMERWQRQDMMQRRV*
>TCRU_10112 paraflagellar rod component, putative
MSSQERNPSTAAAAAAVVVSNDGAVSAVENDAISSKGESLQAGLALKAQVCVQLTPSAEP
LLLCASEQTLDKMHQVEAYNNGNNNENDGKDDAITKHTSSHVEEAEKLYAKAEASVANGL
SRCIDWLRARDLFHEAGALFATGGHADAAAKAFLHAGVITQAFKSESETILMLSLAADNL
QVVQPAIAVDVLNFLSNAFSKSGLVIQAARCKRDAAELLDYRLEMPVEAVQTYKEAMQLF
GDRNVTKSFTRGCMERISALTVLQLKFVEASELYMEEAKMVQRFLPKTRQFLYSLLCLLA
NGFGSDDRYFDALYYTRKKFDALQEEERHFQQGKEYTLMRQLIDANDHGSLNEFDIAVFT
YKSCATFKPDIVFDILIERCRSNLYEHMEQYM*
>TCRU_10113 ribosomal RNA processing protein 41B
MSRASLRRDGRGHREMRGKELRTSELTQFDGSAWYSQGLTTVVAAVNGPVAARQEDYRKC
GVQVYVNRAVRIPRAGGTDRLCVEEQRVELRRMDAEVEMFLTASIQAVVRLDQFPRCVLE
VHVTILADDGALLSVATNALMCALLDAGVPCRTTVAAVSIVALAPEDGSPVTAPTTTTTT
TAAPEASSLLSSSLPLALLLDPTRVEEGGDGVRTCATATFVLSNSADGSNNSSGGVLVSQ
LQTCPRSSMHGGRMSSKDLVGMVALAERAAVSIFSFFRKCNVPLE*
>TCRU_10114 hypothetical protein, conserved
MQPRYHTPSSFSSRISGEKSDGSASEPRDAADSHLSSFASRMLLHVLSGRAMKTQLDDGL
AEWMEGDNSVEFGGCDDDDDDKYEFGDNSNAISLTAVSLTPSMSVSSIARAEQILQKSVP
LVNGGRHIALTTEDVRRIRDKELLRFLQANSSMFVKYLQRQREHAPTATDAAAPPSTGDA
TKESTDIEQELSTLANRIETFITAFDSDGEEYHICVDSEGNVLVPVAAEEEEDRLSTAAV
TDADEGEDEADVVDDGRDREEEERERENTAEVDEAFVHRTEIAESELEGGAGEGNCVAPT
ASAEQTESHVEKAETSGAAPRRGRFGRRVRVCSSSPAAAKKFLSLQSSSSLQQQQPEHPK
KKKKGLAGAKKHPLPTGRQPSLPVRGIGLSGEQNQRIKEIMRTDFTAELSPYRAVPAERL
AALEERLRWFQEVRGPIGAESSNANSSDNDDEYEDERLAAMAAEEVSLSPRLPSPPQPRQ
RTAREIGDAYMREAREQRIFESRMRLINARLSKLHDLSRMEALLPTAGVERFAGVPPPVW
SRDVPPPLSEDDIASMLEVARRENALAVEKGEAAASHGGDRDVAYLQEKLQHALRRAESM
VTSFPSLPSSPDVS*
>TCRU_10115 Eukaryotic translation initiation factor 4 gamma type 1
MFTVTPGPLSLARSETWKPSVFRPPTRILKAAPLTNGGVTLLPRPCNSGSNVAEEQTPKE
PRLLPPPALGQSPCLKPTPGCANLPPVGSSSSSFLSLGADINTCSQKFTEAATEKRVYPP
EMFLSARRDAAHTPYGVLRWVVRHYLHIPSLKVPAHLQLSLNETDETDDGLTRGALGCSL
RGGRTRAKPVRLTHHKVMSILSRITPAKYDVLLEEMMLLPLRQLEDTELLEICKVVFEKA
VQEPAYSGLYARLAQDVCSMKDGGRETEPRDQSFSRRFRRMLIASCEAQFQRPLQLSADE
LVDRVTGVPLGEEEVEGRRTRLKDRLVGNIRFVAELFKIGFLTERVIEDVIRILVRDYNP
DEPTAKEEAIFEVFQTLLRHTGAVLKEHMPQLLAQSLGIAKTIELSHPKPRVVFLMMDLS
DLNRANGWVSPELVEQHVQRPTKTGRTKKNSVTAGEKSAAIVPPMSLASLVSTVEKETTR
NSLDAGRTAASTPPLNGEQEVNGANNPVSVNHVNVHGKEIVKEDGSINNPIIITCNNNNG
NTSNNKNTSGNLKSSLRSTERCSRGQHQPYGQLVLTHVVSGSTENYFNSSMDSLQLNSPL
TPFGTGSEKMASCQPDVRPNQINMSQPHTASEGIRSPHTFVGSTPLTDTTVNMKDVTEQL
MSLFRNGEEATAVSMLRGMELKNMVVCLTWWLRLATTKTSSFDDRNKVASLLSSLLSNCG
GTYDAKTLFLTILEWIRFDVEKGEYDNCPRMFDNMAQMILQCHLPCNDALPHVDQVRNMV
QCGLFNVLLRELTISGGTDQMVTVVKSCYLVSLQVLKNLHDPDDERQILRIAAQNRFRLL
PYLLSVSSVTSNAMPGTPSMRPRVPSSPSLSLRNSPLGESFTNTGHYDPLAQCLVFPRVT
EDPEFVLFRKMRDAAAEVGVFPPTTAPRWRDEAVQLALSPLGNNSTVCELIAVMRVVGAL
LACSCVTENNGRMLASSADVDYVVSEILSKRPGILYQGAVAMELIMYHTQTLNDTAESSK
TDSMRLRPLKRIFDQWCAQDIMRRAAVLELLDAFECAGDPFSVYTAYHDNIADVPWHLML
RELRGY*
>TCRU_10116 retrotransposon hot spot protein, RHS3, putative
MEVKEGKPKQSWTYKKVGNTFEKDDGVQQSGEAPPRLMVLTSDKGWPYTWEREVSEFIPD
CYVNCEVERVWQIVKDDLTAWFSSHGRTYFKLKRRVLIGKPGIGKSMAAGSYLLYQLLHC

DVEEPQVVVHCFGETAYVFDRTTKAVTKYVGNKSTRGKER*
>TCRU_10117 hypothetical protein
MGSMLQPEGQRDAVRDDEADPRVVAAHGKRAPLRVVRCAHDWGRVAARHCGAVCVVRGGG
MPAIVRDVEDAELLDWEEVADVAARRERMTAACAGRALRSRGLCWRGACWSERGVPVRD*
>TCRU_10118 hypothetical protein
MFPGAGSVADSSAASDGARVVDTAGASVVVVLGASVVVVVVVVVAFVLVFVVVVGTASSV
SLFACSVDVLVPLSCPAVPFVPVFCTVLYSGFTFGLGTVKRGASGKMFPGAGSVADSSAA
SGRLFSGAGSNELVTFLLASASGVALSSSSAACVVMVVVVVSTPPSAFSFA*
>TCRU_10119 hypothetical protein, conserved
MSRFDRVVIFLDIDGVLLPVPRFTFGGGELSEQSVLILQQIVKGCGGREKVSIILSSTWR
NFPDQVRRLNQFIEKTTGTEVPAVAGGTPNGTPKTTVVTYFPDDPSEQRLVRDRVDEVKR
WIHTHMQDYPEAIGGRWFAIDDMQLDVDERMRGHFLKTETETGLTEGDVARALDVIASLP
TADVAAKNAVAAMVDPVLKDEEIDILKSRCRELSATVSQLQDSLRQSQDEVHALQKQRHE
WERERKELTRRLEDVSYRLAVHDFAKKNDVLRAAVAALENKTGKERQELEKRIKVLVELL
RHKKLLEKAARKQRKKLNDVNEGKGSK*
>TCRU_10120 hypothetical protein, conserved
MALAESHKASEENSAGARTLFGNVTNKSCTKTVNTSQDTPRGSHFCRKTNCVTAAAAPSM
AAPPRKNGSVSSLEESSTHVDRQTPRELGGGGAGAEERHVGCADPVTLLEEQEEVSPRKK
MQRPRKFLEKYFFLKNLNALPLTPEREKNGATSAPFRRVSVEEPATGVSGLGAPPPPPPP
PPSENNGDHSTASLVRSRRFDAPRPSVLFYVDILPNKQPQERDGSDNVRMSPAKVTVSRR
SSINMQKHEVVPPTLVVRWLSQEADPPLPEREADDGKVAEELTAPNNPAKDVKSVSRSRS
ALEETSSYTDGIDLSAISAIHEEEVLIDFDGSTTSTRLPFSTLDQVKDILLKESRIQEEG
ACAVLSTPKDVAEGFTQQPTHMPETDGGITEDNINHWILSFAGRPCGNADTLWHAIDEFL
SLYFMDQFKAHEAEVLEAAFVVGYTQMVALPMTRMLESSDRRILCMKRDIYIRRMIEFFM
LTLPVRRGKKLFGRIRSASCQQTRQSLLAPRSVSQSTHQLGCRFSARGVRSLPGVMQRDA
RVSGRGGKAYSGAAEANFKAFSQAPSRPIRLRAYRIVPPVPRKITPKRSPRDDELMDIMK
LDLS*
>TCRU_10121 signal recognition particle 54 kDa
MVLAELGQKIGGAISKMSSKPLLGEDDVKEFLNEVARALLQADVHVTTVKELQQTIRAEV
AITSEAVGLNKRKMLQTAVFSGLRKILDPGVKPFIPAKGKTNIVMFVGLQGSGKTTSCTK
YAAYFQRKGLKTALVCADTFRAGAYDQLRQNATKAKIRFYGSLTEADPVIIAKEGVAELE
KEKYDLIIIDTSGRHKQESALFEEMKQVQEAVKPNDIVFVMSATDGQGIREQARQFKEKV
PVGSVIITKLDGHAKGGGALAAVAMTKSPIVFIGTGEHFEDFELFQPESFVSRMLGMGDM
RALMDTMKDANIDTDSELYRRFQDGQFTMRDMYEHLQNVLKMGSVSKIMNMIPGMSALSG
AAGELGDVTLKAFIHIMDSMTAAELDDARVKKTMTPSRILRVARGSGHSIHEVHNLITSY
TKFEEVVKKMGKMNFKAMSQDPGSMLSGRMGQQQMTQLAKALNPTMLRQMGGLGGLQGMM
KQLQNLK*
>TCRU_10122 Protein of unknown function (DUF523), putative
MCRRRLAPADVDIRRLLDAYRSGHSSRDVHSSVGGMMMGVRPTLLFSACLLGQRVTYRGG
SCAPPVHRRTPVGFIVDCLWREQRLVDCLPICPEMDLLAMPSPRPPLRLVKDSRSGRRRL
VTSPPTVSEYVIPPPEMYREEGNGVKERLLQRHPRLAKELLVRRLAGMDGCVFKSRSPSC
GVLDARMYAAESGGSYEGTDGFFVEEWVRPAAEATTMPLPLTTERQLCFGDVASSSQRIR
LGGNYAVLSFLADVWARFDARIDAATFSSL*
>TCRU_10123 aldo/keto reductase, putative
MVRVIKGKGKGGGALPLLESSGGMRIPHMGVGTYELYGDESRIAVLAALRLGFRLVDTAA
GYHNEEHVGAAIEESGVQREELFVVVKIAPKAMASEELVEKGIRESVRKLRIAYADCVLI
HWPGCGGLKPEEAEGHRAARHRCWKVMQALKKEGIIRHLGVSNFAPRHFPHLVGNAAEEA
HLFDATNPCRPVINQIELHPLCVQQEACDFCRERVIILQQYSPLAQGHAKLVEHPVLCAI
VKDLFPGYTVQDVLLMWGLSQGFCVVVRSRSKEHLAQNWAAAKAFFDEGLLSESQKEQLK
NLRESMRVVEDHHFCWHSEHID*
>TCRU_10124 Galactose oxidase, central domain/Domain of unknown
function (DUF4110), putative
MGTDPVEDVVEGTFSLLAPRVRQGMIIPSSRLHCRRLNFSPHAECHGDRHATGSDRMDVE
SHCPVARYGHSLTEIQQDVLFLFGGVSQAKEYLNDAWILRLYDAEIKFFQLEVVGDVPCG

RFGHSAHRMLDGRGVIIFGGSNNREAFNDLCVTLLSQWTKTHQAVFQRVDMHSPPPNSIR
PVVGSSTWNFATTTTTTTTAAAANTTRETSSLVWPSPRRSHTLVPMAEGKAILFGGHGVV
SFNDVWVLDENALQWKCVETRRTDLQGFLMEIPAPRYCHSAVVYPDPTSSADGRSDATVS
RVTTSTTDAEMGRSLYVFGGVLFSPVGDNTLWELNLSKFVWRRVKVWGSVVPPPRFGHTA
CVLSHYMVVFGGTDKFQSGNTPGDCFMYNFCSCEWSPLSRDFPDNLIGIPVLSVQTSEDE
TLETERTSQLNCTALSHLPVALRGCQSLVAKRTPSFMPPGRRSHAAARSSRRKIIIFGGW
DGNRIDGDCFQLILAPSTLREWSYDFLVGARRRRG*
>TCRU_10125 myo-inositol/proton symporter (MIT)
MRLSIKFFAALGGFLFGYDTSVINGALFQMKDYFGFSEHSWKAGLIVSIAVIGAFVGAFI
PGIASLRFGRRTCIAMADLLFAAGSLLMAVAVNVEMVLVGRAVVGLGIGISSVTVPVYLS
EITSAESRGATVVFNGVSLTGAQFIASVVTALLVQFTSIKVGWRVALGLGALPAIVQLVG
LVFFLPESPRWLLAKGDRENAFKLAERFEVDICRSDESECSENFAINYSGIFKKAIRRRL
LIGCMLHVLQQASGINTIMYYSAVILYDAGFKDPKTPVILSIPLAGINAVSTISGLFTVD
RWGRRVLLQISANACLLITIAMTAVGFFLGNQIPYSIGGWVFLSLLGVYLIFFAPGLGAM
PWVIMGEIFPNHLRSTAASLATMCNWASNALVSQVFPILMGSIGVGGTFSVICGCIAFAA
VFIQLFVVETKGLTLEEIDLLFNRKNEEEITSENGTNEENFSRKENYLNRGNRNATENNS
DPRPFA*
>TCRU_10126 Cell division protein kinase, putative
MTFSPRGTKSGEFAFDVCKLKLGSGGSGTVFLAQHHCTHELVAVKRLFAKGAAECGKSPL
QCARLAGHRCYHHHHHHCSCVAHHGKRPTSARTATLTFEKDDDDENLLRDVDGHVSCSSD
LSNNSQIYDDDMHDDSDGIFEEKEDEEMVEVKGVVAELEKENTSGEGREKKSSPAWGRVP
SVARSPCESTILQYLGPHHHIVKFLGSYTSPSRVTFFAMELMDSDVGRELRAANTAFMKE
DIACPLLYSVASAIAHLHRRGVAHRDIKPSNILLRRVNAAKMIVSAAEQCAPAMPGAGLG
SMHMERRPNNVFFSEEKEEEQQYFKAALGDFSAAHFMHESTKVGSGRGTLYYKSPEQLMG
RAEDYFACDMWALGCTLFELSTGSVAFCGSTDLQVLHQIYAKLGTDFQFYPEKIRETTLF
DSLSAPSTAFLELLKGLLALDPKRRLTASEALKHPFFDPIRHKYGVDSENMEVTFPLRPR
CCRPVDTTRFTFRPVCSTPAKRSQRAIAGVFSRVKCGLNLSDPNLSCSGRRCSVWSSSFS
GSLTPRAASTCMKSHHESINASRRCSGGWGACSAAVPLYFSSFTPRAGGMSAQGKDDNPK
TIGPPISPVALCFSPATSVKCRGSSMSANKAHTATAPAASTLATTVSPHGKTLRWTPSSK
ITLGNARTNFLFERVVLGGDACGGGCPTGPRVLLDDDSHSCRHDVDSPPVRKILFESPHQ
SLIYRLNDSSDNAESSAVAVDEP*
>TCRU_10127 hypothetical protein, conserved
MSWLKAIEKVCARVAVGPAAQTSLVSSIAVAGRLVPAVNRDGWQQKQQEKDEEHTPATRE
AEPSTAALHGVSDTWSSALAVIRFSQSGPQRDIAWQMHHLPLPLAAQCMAILFEAGQFAM
GVEFMHSWQHPEAMTTIRAKSRATNWMRKTIKTLGVIGDVETLRTFVSVLHQSLLEQKHR
LQRQPGPHTNASSSETSVGVTSEDSYPFLSALGMQRTRLLLVKTVHELSMQDEGVVPVYE
KLSWINATAVATRPQGAQSPCLIPFILQEDFVNFIEPSPSYDENLLQQIGPAFLSGFVHP
TQCGPAEILSMPRNEIRCLYKKGIGPSGKLWTEVKDLVLPDSPILQQAFQAATLVDALFG
PVEHILPRHRRGKKRTSELTKNQSRLRSFFISQLRSSRSLSRRRWSCALLRYPRLLQRLN
LSPLMVFCESALTFCSFKVHVPFVRCCMPLLRRLRRMGHDEKAARLVWNHLSVDSPVLAL
LFKENPWALEDAVTVICRTMRTGVGMRREAWMGHRSLAVLRVAAVSGLLTPAHCIPTCAA
ALECGVHFATVQQLVEEVFGHDGDTTQWVLNMVRLTTESHTTRLLVPLESPSHSTRMRSL
LRRYAYESNAICSPPLVELCVPSRSKILALWTLVNDEFTSISLCRLICRLFLDGGSLMDL
NNISEAPHVGLQGLNNFFCEEVLASIAANCTTERSYVIFMDAILSRRRLRDAQRCKQLLL
SEMDDECGHVVLPTLAIEKVSIPSGAC*
>TCRU_10128 PPPDE putative peptidase domain containing protein,
putative
MVLCCCQNEEDAVADKRVEVSQMERKGLRRCAPPKPISQPVQETAVQVNVYSLLEQNKQL
KKVGMGVYHCGVVVYGIEWGYGECVESANASGLFCVYPGQAAGTLYRTLFLGVTTHSPQQ
VDTILHRLENEWRSSEYHILNRNCNHFAQRFCELLSTVQKLQIPTWCNRAARVCNKLVPR
RLATYVHRLIEEEAPKASPPDRSRVREIPESVIPRDWYLHPSISQKPRYVIPFESRNSRP
DLKAPAKQPVGPTAGVATRTDSDASLKDIMTTPPISNGGPLQSESPAVERSVLPEIPLPL
MHDLNEVCFFTTGHGVSFRSHDDTTPSAASQVTFETRREVEHNVQIESLNSQVSIAHVGI
LGSEEEHTEATDKLIPIDDCVQGGIKEGAMQEEEKEPTALFQSIHMDEMDVKSALTRFTE

EDATPITCSLPVVALHNDEDGNNDNDDTAKEELKKEQEKERLVNDKYDASYHTESIEPWQ
TSIKGNKLFCKPTIFSKSLEDNSKINAKKMALKNLVRRSSYSWDMFSRVPQDTAGCTTKM
VKDDLCLFLLQTEKRGTVSTNVGSFSELDRKPPLDDVEMNTVSSSPIYSDPEGDDEKHDA
KLGDLGLCFVTRERISEDVLSKTKSSAGAFNPLLHLYGTPALRRNRSWPP*
>TCRU_10129 hypothetical protein
MMDSLSCSGGPANGMDDAQDARGGGEDVEGRRAPVAHRIDHVGTRCRVRFIQDDFFCPMF
RVEGSPVSYVLLDEGPFSIRLDSDVYMPIVAKMEVNGRLFSSEYRILANGSRIVREVHEH
HIATRRNFMYRSLVVFDNVLQREVTPGEMELETVEEADEFTSLIRVLFLPVRGGTTATRG
GSWRINYKREPLAVEMVRIGHRALLAKLFGVQLNTLVNSMQQASISKASSNSRPPSRAGS
PMCTGTYNSRRVRGSDANIFLPVRSRSSISVSSRPPSRSVSMECGSRFQASSPTCLLKSS
GGVQSLRSHGQHASSGGICPAARSPSPRGGRSKPETETMSTGSLNSPPLPSVLSIKPTPR
VKLPPPLHPHLGGSSRSSSPAVAGREKFSFSLQSHNIPNGKRVVEEIDRNHNSYHICVKC
NAVFDRERLLYNQIVTRLKEKVFSLEQENAKLRMGCSDAFFVIRRTGSDDQSVETSRVED
LDATLSPSRIVIS*
>TCRU_10130 Unconventional myosin
MRNGGRAGSVTYISSSSDDDDTKNRDCRDSVVCGGESQETRQLTSQRGEVGAGEPPKSTN
KPRTSVISGDTKNTSSSLASKESATVQLQTPFMRTELGPGTQVLFLPGPVLPSEAASATA
WELGRVVEFSPTATTGKRAGEKTKEISDGVVIVERVGRGGALDGSRIQVDLKCVRRYSYE
GSPLDLNDFSTLTEPSDAVLLYALQQRYFGGLHYTFTGRVLLALNPYQRTVYPPHAPHPK
DIVESVKEAFCAVKSCSTKGESEGNEFGLESDVDAVEPPCPVALVVTGDSGAGKTETAKF
VLHHLLGQMAFDKESDFSSSHEVTASQRTICGRMLHVLDAANCLLESFGNALTPLNGNSS
RFAKCVTTYLNPRTGEGVGAKVECYLLEVSRLVARVPGESNFHIFSMLFDGRYGLTPEER
NRFDTWDPILFRAMHSGSNELCLSFSPYTLFQFRVALRSVGFSDDKVAMVLQVLCGILYL
LNIEFTARDMFAPASVSPASMSALEKASNLLGFSFTDDHRSLETLLTTVRLGTDLRELHC
GAAEVARDSTAKHLYESLFQYILRRINEALLPSNTAMETVCAEFTILDIFGFEFKDEKCG
NNDLEQLLINYTNETLQRLYEETTFDILLAEAAQEGVNIEWPSEWNQERVPTLELLVQRP
RGVLNIINDDSVLAQRSRQEGGANLAALLTSLQKSFPGLIRPHRSSPSKVSLQHFCATVV
YDTSNMSSKNRISTAAESTCAASSNEFVQEICGAFLASSTAEGYMPLVGNNTKGAAPRSH
ATTIIAQFRSQIELLMTRLKASNIFWIRCIKPNRNKSPHEFDSELVFSQLKYGAILRSVM
LFGQGYCHSLKYKLLVKKYLFLAVRGYCCDAFQHGIFRKHLDFSGSRGEGKPPLRRPYSD
KQTRLKHGTAFNAAVYSARFREACVLATEFVPCCMDGALLLGSSKVFLRSSTLRALLALG
KLAKEEASQWIGRVGRGFMERRSLAVARLQYMNEKRLAGIRERIAAELPQREALERERE A
LLARASEGRAEHLAFLSRQAMRSSKRVERSWKETMNLLTSELTKAIGEMTAFDKARMEKE
KEVREEAAMRESCRRRIKYNMSREKLRREVTHHHLIETQREKTRKDEVTRRSRADIDAER
EKVIREEIVKARQLQLRVEQEVLVEQRRRALLSRERQEARQVRLHLGKQQRRIADRVRLK
EEVRQRRLASQLYLPSQSFPSPEISSLVFGGVEKTATDVTVDDFAALGLVKTPLSGGTRI
KLYASQSLPTQRELNSSTTVDDRDPELEWIVQKDMMTLWESLQDGLNT*
>TCRU_10131 Kringle domain/Chitobiase/beta-hexosaminidase C-terminal domain/Fn3 associated, putative
MLRDFHAVILFSLLVWLAGDVGVVYGSTKCDPVEGYYLPNGEDYRGHLNFTEMGIPCQKW
NEQQPHRHDTHIPDPLTGVGNHNYCRNPSGLERPGCFTMNPSIRYQFCDVGLPCRWTPPE
TVLQFEPSSGTELRADQPVKITCYPRPCEIYYTLDGSTPTTSSGILYLRPIVLSRNSTVN
ALALFASEKALQRQAFYSIPPRPTPSGAYFSPLPSEVSQGPVLLFLKGLRDNDKALIFKN
EDLRGFPYEGPFWLNESTNVTAVINGEDLVRASYVFFTTGVILEMYPASGKYIGGVSCLV
YQSDPQANNTISINGLSWQPLSEFVFILDTVGINVVGVRSISLGGVMNAVWRKYEIAEAI
PPVLLPAPDVVYTEPIRVTCKDPMGRALAVDKKDEELIYSIRLDIPGRFSVNCTYLDDLH
NKRSAHAVYEIEPIPLPMPLLRPECGRSFPMIPLLLVTTIVPPPDAGYERDPWRLGLNAS
STGATLQKISGNGSFLLKPTQTDAINVTVTLCTHSSSPLEADSPILICRYEMLPLGLSVT
PWFVGRIGCENCSGSVDLLLRQLSNCLSFGTTELIFIQTVGSFVMIQLQRLPTSLRMEYY
TRTGDCLSDKYLTDVRNETSGSIQLARWWAVNRTSSSLDFVTGAEITIVVKGWGLDSGEF
HFVREEFPCNDIGVSYSTRNSLDLFSLKLLFVIDTPGSYKLCASLNDALYAVPSNGTLIV
NSSRLPVLLPAPCGGSSEGPVDVVLDMASRGVNPYLFVSIDNGFWYRVAAGTAVHVANLT
PSVTSATLAITAGQRSVASTVCVFYLPQGEMPKRATYNWAVAFTHEGRSNVLLSVNGTFS
GKSRVELRAYGPRRGQANGSVSTMNETALQRAPSDIPFFVSLGTFMGTFTVADSLLTLVG

GADEYPVSIVVSVDGTSMDAEPLNVALSPLAIAMHSCKNCISGWCFRDQCVCIGEKNHTA
YLCVENPLSPKHPDSASSRFKLLMVYLLLLAAVFIFVGFAIYNGTKRGAPQRESEGGLAR
P*
>TCRU_10132 small GTP-binding protein domain containing protein, putative
MFLRNLLQLHSLHSRRRWEQRIASVLSEHEESKVDDAARRFARIYKERRYTSVEEAFPLH
DKARWVGLSEPSGTSPGANRAVAQPSNPHVLKLALLGPQNSGKTSLLNALSLSHIGAVSN
RSGSTKDWIKGVATVHNTQLVLLDTPGVVIINSDKDRRRHAAPSARAWDALMVTELVLLT
IPAGLGFVEPEQKAVAREVVHRASLRKMPVVLVITMMDKVQTPKHRELYFSMRTDFESMC
LPIAAVHETSVKGCGGLLELKDFLCRYATPGEWEFFRNEATDATTVDRLSELLRQCFFEV
LPHEIPHQMRHRIIGWTKKDSGTTEVITEVFFDRPAYMFIFYSKLEAICYRAQRVVEREL
KGRYRFVFQAFIAPGGVSSR*
>TCRU_10133 transcription factor IIIb, putative
MPLCSHPASAQYSDRVRGTVTCTLCGDIVQDQQLELDPVFARGEKANARSLRSLGHFRPT
RGVIGTRMPSARPSTEAARRGMLSIARQLDISDDMVEMAVALYKLAVGLNAVSGARPAIL
SAVLYAVCRRERTSHMIYDFSDVAGESPYEILSYMRNICEATHTELPVIDPSCMVHRFAE
QLNLGPMTGPVVVCALKVLRAMRDDWIACGRRPMGVCVAAILVACYMFNIPRSPDEVCGF
VRLTAGTIMKRLDEFASTTTAGLQSIDEYTKNESSLPPSFSSSQMRSNGMDVDAEMRKLS
ATYYELVSEAKVSAPATPERCEKWRRFLVRHCEMENTVANEENLDLTKLSPQQQLRILGL
PNAKPIDPEKVRESVRREEVKILLKQEHFDPVSASQSNSGVLQLPLQTQLDMPMQPMTAY
YRKLMNHDPNVLGIRRDFDFSEMGDDPSQSPSIPPIAPGSVETMPESLTEVLYDSERRFA
LPWEFIILQDPALEDTTDLDLYLVLDNEERLRRRKVGEALYKEDWDLGRARTKEEIEKLE
DFRTSRKRRREPIKEHATVQDALTRALRGRGAGSVNVSQIDELVPGLVSKFDGGTEDDWL
NE*
>TCRU_10134 hypothetical protein, conserved
MEAYQSLSNRVASMEDLLRRSESTMVMVLQRLKVLEEHASASEARNRGERAARYEELSSR
MNTAMENQNSQIVFLKDAIMRQSSSLQVLEERLQGTSKALEQKTNSDISGCYQRMQTSEN
SFTAALRNLESLLHSQSSAMNSLEQNLRVDMHSMQQHTNGEIMGIRQRLEMVESALNSSL
KELHKSVSSDIRALSENFVAKIQNSVQSMDAALLGVDQKVRADMRSLHESLGNDISVVRQ
SVSAVEVSMRDALRALHGTLANDITNMSSLQQEFETAHRAEYQRLLAELAAKREQMETID
ANWRSSVMDLGDKLQDGWRNILSQVASVDLKLQQKVSHVGTSVEELSAQIRRTAESLAHS
LEVKMKSLENLSEDVTNGKRFMTALQEEQQRLREELKGFSAMVERSGGQLRSFLEAAVQA
SHSDLLERIKPLLSYRSEMHTAVAAALNKLWSEANRVFTSQGEMDALQNQIQVLDDAVRN
EVSLLIEKGRVLERRVEDQRRHDVVTENRVSINPESGALMPLPVLDELNNVWVELRNLQK
QMGMPREEVLSVISDTRKQLFDVALNVAKSNEKEFRDILSQVKKDVCEILSHSNRPNGVG
NSNEAGNNAHKPKRTVVRVLSKNPLNPPPSNELPPVVRIGKGPNSYSLVELQPKGTANDL
QEAPSRPRTRAVEAATHLPSVIHPSPEPTGFVSIATSLSTIPSPTYQ*
>TCRU_10135 hypothetical protein, conserved
MRSCLVGCVHSALHHGGEAVAPCPALTHLHSLGGRHGDSCTASLGPRASSKDASAHLAAS
PAPLRRIIGFRAPTQHERLTRLRYMEDVRGAICLEAMPSSIHWKAATTISLQGDAVLNGL
RRVRRHMRNSPHRIRAPNAEHRIVVWGNGSRSGFGRLPATARQGRPGRCQTIGR*
>TCRU_10136 hypothetical protein
MTGVLPRWVKRSLPWSVGGSAARGVRDEAVAEAPGPSRVPAFVLPACLACWHAWRLRCQP
AREAPVKKTVKQSRHPHGRLSQTIGTPGRARRACALILWMNDRTLPQIGQEDVNPPLVAR
QEVAVLTSGRSSGRDGPFSSV*
>TCRU_10137 Reverse transcriptase (RNA-dependent DNA polymerase), putative
MLRGVPQGSVLGPYLFSLYVHPLLSLLNSFAGVTADMYADDLSIIVRGQSREDAIPTANM
VLEKLHAWSQENGLAINPSKREAAWFTLSTHTESDYDREGRWPLVVAGCQIPVMTMGASR
TTKFLGMDLDPRLTLNVAATKQCAATSQRISQLRCIAHKEAGPSPHDLRTFVIGYGASKL
RYGSELIWAVATDSAKNEMQKTYATLARIVSGVPSTVDPESALLEANMPPLHDPLPARTA
LHI*
>TCRU_10138 retrotransposon hot spot protein, RHS3, putative
MTTTGEHHTTTSTVRQFTERLAAYFSGWEELSQELSWEMIYVQQADSTPMNDWQGCDVVN

SNNVSRDESREIAAFWEEEVHQYMAAISSDDARRNEVL*
>TCRU_10139 retrotransposon hot spot protein, RHS3, putative
MRLNDFLARELDGRGVVDANRDVVPEEFFKDPNKYIRDKGALKEIQATDAYARMEGAVRE
EMDLEEVARKLRDKGVDNLLGWSEAAAEVKATVHDITKHSLDAALQEASKPTTTIAPKKM
EGLYESVYSARWYHVVEVSGGEGTGMEVKEGKPKHSWNYKKAGDTFEKDDAVQQSGEVRP
RLMVLTSDKGWPYTLNLLRGAGNDFFINCEVDRVWQIVERDLTEWFSNFDLTLNPSPLLR
VLVGTPGIGKSMAAGS*
>TCRU_10140 hypothetical protein, conserved
MWRCCGRLHVALLRERWALTVSPTGVAVRLHGAPTASPCECHAQRHWDCGTKQPRLPFGA
SDICWPQLGGASGMLHRTGVVMTPRSGIPGDGSDAAARHVAGSKQRPEWTMSSSVKDILL
EGSTLRTDMKLNDFLRSNLGGKGVVKKNENVIMETFVQEPDAYVQDQQFLRIIFNLAEYQ
VYKLHHEGVLSLEHWRDYEGKGYDHSSCKGKTKQSSHSDTDRTA*
>TCRU_10141 hypothetical protein
MITYPSTYGLFDREILAITSMVHYDGGQCYIDGAKMNAMVGYTAPGCIGGDVCQINLHKT
FSIPRGGGGPGMGPIAVRQHLASFLPDSVFIQNVGGSQPFGQFSQAAYGSASILPVSYLL
LWMLGSRGLKTCTVYAILNANYLRKRPDGHCPVLFLGENDFCAHEFIIDLRPFKKTAQIE
AEDVAKRLMDYGLHSPTLAFPVAGTLMTEPTESESKRELDRLADALISIRTEIASIEEGE
ESTTNNVLKNAPHTAKCVASDDGTDHTPGKLLHSLRAIHPPKSLAFSWPHRWKLWGQKLD
VQLCID*
>TCRU_10142 Glycine cleavage system P-protein, putative
MGISKDSTGCPATRMALQTREQRIKRERATSNICTSQALLANVAAFYAIYHGSEGLKEIA
SEMHNKAKILSVGLESLGHTVVNGAFFDTITVNLKGITPEDYVACCV*
>TCRU_10143 Glycine cleavage system P-protein, putative
MVETKAEPLKVKVVVGDPNLIDWSDSSLCGILVQTPDAMGMLHDFTTLFDKAKRHGVVSC
CGTDLMASVLLKPPGEMGADVVLGSAHRFGAPLGFGGLTPHFLLSRRNLSD*
>TCRU_10144 Glycine cleavage system P-protein, putative
MSQGTPPVILLKVIENPAGYTPYTPYQAEISQGRLESLLNIQSMIIDLTAMNLANASLLD
QATACAEAMYLAFHHG*
>TCRU_10145 Leishmanolysin, putative
MLTWCCPWQSAVGGGALDDCRDGCEEHHDCDDIDGMELQDGDGDGRTLESHWSQRHAKDE
WMAPIGCAGYYTELTLAAFADLSCMRAKWEMAEPMRW*
>TCRU_10146 hypothetical protein, conserved
MYTTKRKISHESRPASPYTTTRTTTNSNSNSNSNKDNKIGDELLPLHGNPRPWGAGGAGA
AAATGDADGHLQKAGKKLVNSINTPAVGVKPDPGTRAVNPKKVPNAAFSTLPPFAHCSSP
TGANGQGFPAAAASAGRRGAGESTKKGKNDIFYAPVRYVRPTPKERRERIYAYYAAKKLI
RETEANSTPSPSEFPTSFSSHEATTRVAAPDGTPSASDTGARDCINEHVEPQKDGGNEVS
ESLRKENLLHSDSVNAEERLLEQLRYLVDRYEKLYNRKTFDWSKRVFPVPALSQLLHAED
SGEQQQQQEQQQGKEGRPDSPTEEYAFRSKESSMAPGCDDWGRRFELTLSAPHWQGLSGL
DESFPLYETDPSIIHQSNGEHVDDAPRDALAFEQERRTQGVRRHLMKALLSFDLVSQQSR
RGRDDGRTSTCRTAGFQNYPFEDLTGVCETLLDTPVDAAPHSHVRQLLKWLAEEPTVQKC
AEATGRLATYVLMRSLPVELYEGDPEDYRTLRQRIRKAEAMSCSRTREAFSVGDWRKRDS
PTQLTQTEPQLTELRHVSEVKSDNNKPLTAFNEETKVDNRYFLHQDSMSLTQALQSVALQ
KGIWLSSTVPMMQRPPLHACGLPLRVARGIALWQRPPSGSKDPTLQGSQGLMNGNANTVE
TFKSGKNSRVNSPEEADDWRPKTLAPLLIIAFGGYGVAPFSTCGSPQSTPKGMTEEVDFS
FASEQQHASDGANNTILSAMNNFMHPEPALLPLQSVMRVIYDSVRLNRLISMDEIADFFP
PVILELLMDVVKSFRDIFQSILNMSFEPASSRSFFLHTYRETLLSWATIIVCEAAMGHAA
ERAGLGPLKVPWTSGVMPDKFTEEQLEKIAFSGLVERTLPSMTQWEYDEQLFIHTIDTLR
SVVIETIGRVKGELYFFMTGVDSRKAVLEQHRERLRRFRAREQAIIAEAEERLQASLPGG
NVGVMRPTSAVQSMIQGEGDRPQSPPRIHSPHRAGRSSSRSCSRHEQSHHFPFRRRPDNC
KRSFFSNAGNDSCQHTGELSSMLPSNLMPRQPGSKLHAGKRHMHEDGVFAENTFSSLQST
LMHSPEWGDNIALESQVIDDSASPPLSLRKELVPLKNFSLSSTISALFKKSTASCKASQG
QQQPSPGSFLFRTVSSGMQPIRSMGRQTVSELAEKLTVRNVRRELVSLKIRTRQSTVVAR
ESVEGETLCSQMSQQKKMASTQATGNCGLSDTCKYGLVSAAGGFGMTVTTPSSFFWPSFT
APNPLDGKRSKPTSDETTLASVVGAKQAASVARIRRACENTAQFYLHFNNMINADGSGRC

TGAESQWYATGSMGFYERRAVATIKRSRQVAGFDLHHLSPITALERCVQWPSSRGAPSHT
GRQEEGEEEEQREEKGGGGGQPSPSAQTLRAKACQKKRWWTLKPKELHLGEKMVPWTL*
>TCRU_10147 conserved protein
MPSSSQMRKEEAELRKIAKQSRLSRKESAARERRQEKRMKNATGPTTNTTQTRRRGAIIL
PSEVEEMRQRMLTDTPSATSGRAKRGSVNVGGDKKKGVKRQRPSSASPASSASSKHPRLQ
EPPYGIEVHYKKEQILVDVKLHHVPPVHVDVSETTDEMLVVDTSKHTKKYRLELPIPEGM
RISSNQAEYEFDVKNGVLNCVLPIKGEIPNSLKAEREKILENIRRQKALRFRISEDGELK
VRSRRALLAKSEGAQAALMEEERKKKTQAQQEVVDAEAGEDEDKNKEETAAATDSSKREA
QGTKTHPKRKKNNATEEEEPPKKRSKKEISLTPHAGVERTHDFHKGGSDTSDQPERQTPR
PNTKKAAGSSVFDEEHKKALEIAKSAEKAAQMTLRERIAHAKLLQRKMQERLLVRSSRRK
LRSERTQESLSRILEEQKRQLLARAELNASIAASEKKTAAGRKENGKTVTFAVGTKEAGE
*
>TCRU_10148 hypothetical protein, conserved
MSGIAFTSSTELCLGHGKQPGYARVLACRRYGPVKGKEDEVAAVFLDEKKNKLRVWRERK
GITTLRGAGKYTTRIIDTATDGLFAALFFHHDKGRRLGLAIVQLSSSSAARLAGDPVDCS
EKLDAVLADLLSREKKGKETTAQLQICCSGLKQTDSGLVVSLLVSTRTGEVYIVIGSVWE
NKWRCFGLDAAFGMPASLCIQSDRVVSVLSCAVGPPIDHAIAVTSPTIELALSVFEAINV
VSDDNERKSYVSSRPAGLQYCVMLHEAIFSLDDGDPTIRVCYQSQLFPLPEGEGGVCVTP
LCRIYADNELQRYAVVASLASQSYLVHLRRSPFNMELVSGCTKLGLQSPPSSVVWLRLQH
PLRPEGGLQIVLVLSQDYRLYAAEAFGKAINVEVGDGSNMVRFIPPAKSCFGDEQTVESF
ADSTRLVRVGENELLCSNGLLAVVLRVTALDIDGDMPCEGFFPSTIDDAMPERRIVTLVK
SLSHIEKKSNLSQTELFQLVFRRVLPLLRLAGSCQREVFLAQRVFQALLSAAAPKSASDW
RNLWGLTMLLQRTLSRRDLDHSVVYTDMFFVQLADNYVRFQGTLAEQEQANEALLSVVSE
ELKCTWKKFVQEQDDDTSFVLDSLAERVSLVILAEECVRRMVVISALTNGTHVVSVGNRL
SHVIHTIATALLASCLEVPVYINEDNEGRMFCQMKQVGEKSLFLPPHPFKDRAEFEYAMT
LSTDLLCVTSPDTHATVYPTALLSMLQSRRYHVVSAFLQIFTAPLTECLMPLGPICNNAQ
LLTECSAAVFLTETTLFENILSEPAPSDILCVLCGGSLRNDYFNTDLWRYIEGILSKDTQ
AVIVAAVIHAMTDRLIASQNNYSASVIKVLMKEGLKNPLQEDASVETCRKRLRIMLDRLE
HLWACVAPWLPYKLEDIASNVLTSNAAVQNGRHKGKTISNDSVVFRTCVLCFRLLALIGY
SQHTEEEITELTKQATGDASILARVASLLLQAIDNLNGTALPVESLQWRCVDLAAMSVPM
CAATPGLAGFMQEVLQQSEASLTVITPLKQYYYTVLDRLMEVAEANGNGGAGAPFAELRV
QMWERKRGGSPTTEKSIQYFLWSKGGGADVPEWPGDHKLPNRRYLINTEWPDTMWPIEFV
PHFLEECLARTQERIHGCDTTDCPKEGYSSPQFSHALFHQLCTLSPPVRNHALIAPSETT
GAVTKRSVPTLSQEIHVGRDGRFPSSVDSASVLVAPSTARWKTSPELRPLATNSPHVSGN
DDALTTSSSALSSSPARVARSPPRFSVSGGSLGAAAAAAAANALFPPERVAWWETEDTFD
EAARRQSAIQETLKDINIEITTTATSYTTATSEIEMHSPGEFEKSARSMSFSPNRCKRHN
VHHYRCAKHRLNGIHMKERYRSGSRSCHGHTRLVRESSHFISSAAPKEKALMNFKLLQFK
NVLRPPELPLSMATEERVQLVEPGIPKGKEDLTPPQLLSLRGKPHMPRVNLFAWIGAEKN
ESEGAGNGAGGKNELTARSPGFLAGQPLPLRTLTPPGLPPSSVFISPSSLLTLKVPANAH
ATSQETAPRAMEANRAQEEDPRVVDTDEALGPITSTTLNVLVTPVPSTVQQKVPINVTAP
LLTSISYETMPPSSSDEKHTGLMRSGGAASVPIRREEEVVRESLKPEVPLPPTISQPVAT
PAEGKVRSVTPLKEPVLSPSEKVAFQKYVDELKATGAGAVPVPVPPPKVRESPPASTTPI
KALGVSREAPELRKEYDTLEVVKELLAKHEERQAKHFHDVIETIRTSIQRPTYSEVNSHS
AVQPTQGLSAMEQAALVRHTIQQKDKLLMMNQDLLELHARDERLVASPVSKEAQTYASTR
TVAGGENALPVSQSTVPLAVPWQGANTTSTTKGEVATMSSGVQVGVGLKKTDDATTMATA
PSPSPIPPATEQAAAEAPTAPASQMIHDNRNVMTNIVPDPSSAMSINRSLSSLYQINAEL
LRVNATAADMERAIQESRELLHRHASLGNAHMSAVEGSLMVDAMRRRTAALEQQLTTMNT
TSVKIPYGEDQKREGAEKWHAPSELERIPSQRVLISPTVEGGSTVCVDEGATRKTSPPCH
FVFTNENIETESDSLLGFDPPPPPSVSKQEATRHIFQSHTEEILRGDPIAVNAVTTEAKV
VPSHTSAFLSRATDPVSVNRAQSLSVDRRGNSLQPRGSGSSSRQMMDLAQLYKAAESSSM
KLTPRKSVTPPRTRMRVVSSPEPVPERLSMYMPSTAKTRTRRANSSSKSILHASEPHHRS
LSTEGKVPTTTAVKANKTETAMAPKRNSTKAPSSGRESRRRDTLALHTSRRLAELQRAFL
*
>TCRU_10149 tRNA nucleotidyltransferase, putative

MKNGKKGKNTGEVERMDYLFSGIDTNDDTLKCIVALNRTLTPLFSKTDSPLLLSSPSDKL
VAVLFMLCLPFYHSSPREQLTERLYALCLNGLKLPLASYNVLRRMVECYKTLTRHRLDLC
GITDLGVKDAAKLAVFEGLGELNEKKMIPAALKIVLSSYLLLEHRRELLESAEVNAVASI
ISEMWSVLEREPGLLDSMTRPLPLKGDELSKLIPLDLPQIGPALLALRKYAMFHPQASRE
DMILWLREEKKSL*
>TCRU_10150 hypothetical protein, conserved
MFYDSGSAFVRIDSNSVVTLTGCTIGSTGLSVALLKRIDAGYRFVAGCLTVAGRLVTTAA
ELALHGITNVTTVAACGECTKEGDCFAPLTTAVVDTTTWVWVRCSMTVAPLL*
>TCRU_10151 hypothetical protein, conserved
MTFGNDEQPASVTARRGGVAMTFGNDEQPANVTARRGGVAMTFGNDEQPANVTARRGGVA
MTFGNDEQPANVTARRGELDERDRMYGRKTGVECFGGDFDWRRSASYRSPKAQRPTIFER
GGFALGEPESAVANEDKISTFFSSTARPYMKNISPRPFCRTTGMAPPEDICGGTPVGRWR
ASSPGPTFGESGAGQVLRNGGDWRPNAQRRGAAREDSPVPGFTGLPRSRATTVLDPFGKL
CNRPSPHPTVDAPFQQMAGESHFYPSQNDRWQSHDVNNGVHRTRIAEHRDGSFWRPTSFG
GPPPNGTSDPLASPISSISRSGLLMYEDNNASARGGFGGNFTPDAFHRFSHRPTVSRLNT
GIGCGRYDTTNVNHPSNSAGAFADSGKRVGAGINSSFNSPFARTGFLYDDGVSRLPIIDE
YGSPRNGSRVRPRGVQAMDIAWSGQWASSPAPSRSAHDIPGRRAVPYPVTSRVASIAMPW
RNTTTTGDGVNKRGLLASKPPLAPSSRAPPFCFSAKPAGVRGTVTPSSVRGLTLRERVRL
RQQQLRREANLQAVNENLHENYCMGNDMKRLRKEPNGFISEKACPDINASGEPNVVTGNT
TSVPGATAEAAHNGDTRTAEKQGAAYLGSYGEQVRRLESLTEPFIQADGVNVSFCLRDLA
NVFLCLPGGALKENDLTKVAWLDDGVSYFVSAKPMRFRGGWESYLQHLNLYQQPFYLRER
AFIFVLRVPYHPNLRVCVAVHNLDDFIALLQQRPLKPILLTKEEKWMQERLYGTDSGGIG
SQAQTNSKRVGFFRRLFQRLHITKIDSRKEETRDEAQQCGGWAPMTWRRRLALLRLHAEA
TLRGSAWKTFTTPLLTDPALLHARMSFLSNRTATYAALRHRLNTLQALAATMVTKQREGC
AREQPRMIENRVDSEKSLPLASNQTDPLNERPLFPLEARTPATTTTASGAKNVKTKREPF
RVDRVGDGSATALRRPHPAPPAMQPVETSAAATTRGVIEKRTEMQTKCRSTLAPYASSVS
LSRPQSPTPASQSDPVGVSGQLLPRETKRDALIQVAENMARRNNIPNEISPPPMTTVLKF
VSSLDQTEKQGQIFDGCSKQTSISCVTTPNPVFAGLLPTPTEIHRQGECFNISVSQIQQL
LQWQWEYHQNCYEAFPLPVFCGALVTPPAAYFDLAGGLKKRNEGSGISPLSRSLLLALIK
WGWLVPMDYKASREGTRLCFLSEDPLSSLFGLQSRTGRGTFCLCFLVFGMWRHQAMWLAL
LYIVYNLLQAIMRVIFGGFHRRPAALDSATSIAYLQSEAAVETMLEKRQFFRTQSLATRI
LRTQSFVQNVLSRAVMLMRGHSPFLSLIIGLEVLMTCLLILIYKYSVCHLLPNKHLVPGV
MVEHLLQALGPFAWVRNSAVVRWCAPLILPSGVDGKTLGFLFILYFFCFLLPWSPLRWMC
RRTWELFLHDDALVRRPLLSF*
>TCRU_10152 anaphase promoting complex, subunit 10-like protein
MEPPPREGQEGDNDQNAYSVYSESPSIINDEEILTREKLGALITLHDAVWTVSSAKHGNG
VTCLLDGSHSTFWQSDGVLPHVISIDYARLTPVSVVALYLDFQQDESYTPRRIRVQSGTH
SGDMADVAAVTVDDPRGWVFIRMNLEVETSEPWELEIMRGTEGGGAGTHALGASRARETA
EGISSSPPFFPQDAIVENDDYAEFMGDGVWCKHIRIILEENRQNGRDCHVRGVRVLGPMR
QSVFTTASFSQHLLLR*
>TCRU_10153 hypothetical protein, conserved
MSHQGVYEDDFELDEDEISTDRERGPPLTPKSVDASPAAREVTRGKETLLPEPHCMHGKK
SIPTFKASSGRRPPQLIHPPASRIAKVKPPVVTGNHQLLHLSKLTSVTQMEPDSERLKQS
VSRNEVPARTSEPRTDVLSSSSTSLSGRKCASSPALAKEKDARHCATAVAPREHLRTLPP
MAGRRASSNEEKHVRPPWHQESGSVFTNEEKKNYEGADVWKRNTNISPRKAFAESQFKVF
SGAVGSPQAPPTAQPPQHGGGDEKSTLNAKEVLWQRPKQISGSSCGRISGKDHESSFCGS
SSDTESLPRNACRRKKRKAGVKNKEERASVQDNETYSSDFSSDTESPPRNASREELQKAI
FKTRYEVANVRRVRRALEISLQSTKRSSIRRGYRRAHMDVDRLERENQHLQRLLGLREQW
IGCPDLALRIAEEELKYSLDELQRAKRRQRELWTENRRLSIFLTQVVRDHKPVEEKVASQ
YREGMYNRLTIQTKLDTLREKLAATRESSARLSNQIRNLEDRVRAAGLTCMKPEEYTAMQ
RAVRRNKEQIERLSAIVTVPLGTKEDGSHGDMRSSSESLSSVQYPGRSQMDALVMKLVKQ
VERKEALIKLLRQRLAETEPTVSTGKEGELKLSPRECALTGERRNSLASQLTPNMLVRNA
GSLSPRQMDSEVIARSISFSKKEGPREPQHQQSKKGGDRVNGAIEPRNAEEGRATGAEQP
TSGLAKQDKTLLEHSEWHKNGCSSSPGIISSSNTNQPSRAVYEAVANDAKNPLVLNDGTT

VKMNGLPQYIGLNESQIPIDESQSRLSPTTLTKLSSTKTGDTPFTEESSSVGKEEAGNAA
QGTRETGRTTPLWLREY*
>TCRU_10154 40S ribosomal protein S3, putative
MGPLSKKRMIIRDGVFYAELFEFLKRELADDGFAGVEHRVTSTRTEIVIRATKTREVLGE
KGRRIRELTACLQQRFHYKEGKLQLFAERVEVRGLSAMAQAESLRFKLLSNLQVRRAAMG
IIRHVMESGAKGCEVTVGGKIKGQRAKSMTFRDGYMIKSGTAHKNFVDVATRHCHLRAGT
LGVKVKIMLPKSMQNEEEILPDVITVLEPKEITA*
>TCRU_10155 NLI interacting factor-like phosphatase, putative
MMTATFFRRSRVHFVGKKLQSLVAFGLRDEYSPLWPVPLPPQPPHFAGKPTLVLDIDETL
LHTYGMRLVREDTVGFSLYLRPHAREFLQELKELYEIVFWTAGTASYCSAMVDALEVQVL
QLPRSFYNVEEIKHLVRGSPSTEHVNFFALSRTQTLEENSYMKYLPMLGRPMHRVIMVDD
NVRSFPLNPRNAVKISPFLPDDRVLMEYSQALSLMKENGDEKKEWDASLLEVINRGKAEI
LRLEQDEALLQLLPLLRSVAKAEDLPRELDHWRDDDYVRCDDFHETMNSRSVARQRILGS
VLPSRRDTPIPPLKTHVMNRCFLDEANIAMQTQHMRCIRSRL*
>TCRU_10156 hypothetical protein, conserved
MLNRETCDSSVSLASCRSCVRGGSRPSVATMELLESIGHAEERIMAAWTRIGLAEVDRQN
KWNGFVEGRLRPFLDDYIRLQESEEMAIAAENDQLFREMFFSSLRLKERPRSKELAQLVE
AVLSQGAVNNTVVTAGEEPEEQRHCTDIAADGGEPYVDREAKERDASATLPSFVSVVAAL
LARGDGGVGSRGASLASRAREDGSHAQHDRENRGLSMPMPEGTTTDDAAWVAFWQLARSM
THQELHRNLETEVERMNALADTRLQQLCLLYKQRALLRLSPQEQARIRGKYAEKLLFEEL
HHKHSRKLQQPTSTTPTAGCSRSSSDNCDRGVMTPGPSSSRATTCRSCHSFAKDELDLLS
DTLPERLRADHECPKLCGPDRDEASIAELQEENTGRGTIFDVDLGDVTRFGRRQDLSLAR
IDAEAQEIYEEINAQNVRMAAQAEKELQCVEELWRLFEEGADVVQDGPAFMREQTAESHP
DGERILPSRQEFASRLMQLRLEYDGQEGVAERCGAVAVDETCDRRTGLIYGITAAGNNSS
SNNAANSNVTLPVLRSAYTARAQGCSSYFANISETTHSSTVAVAAGVTGTTNQLPSPLMK
LFTTRSYAPVLSFIVTVREELQRRLLQCHVQFAQNVTSQLTDLYRCYFEKTRDTAYYVAP
DYSQWLQENVEVVAEKRYRPLMHCGNESSGGGGGVWQQFLAEFTPLDGNDKLCERIADVR
HVVNRASAEANLLRRRLRILDEAEPLLRRRSEILEQQQATQEGSRDRLLSKRINMAKQLL
FEENARRQFARELPKIYGQLEELLNRWNETMDADEGHHASSSSSSTVRRLVLHGTDIAD
LVRQFHDDVARTHGGRVGRSPPLSRKEGTGFLTPQRTPRAAGPTTHSHPHSHDMHVEQRR
AALSTSPAPRPVTKTLSAQSTPARAKLHAAKKSVNPASSVSPAPVKRRPVITRRQGIRSV
PSVNEFLQRQPQSAPRRCSSSRNKPTSVSPRVDTSTKK*
>TCRU_10157 calmodulin, putative
MAIPKEWTDTWNLFDERKTGTVSQTDAKHIIRSLGRRYTEAEFNELLQGVPDPVPYQSFV
DLMQKPYTGPSEDDLRTALRAFDATDSGRLKLSELITLLTSLGEKMPEHEVKQLLAEVRT
DEEGRVEIDDLVRFLCTPVPSMTPDIAELQKQLAETS*
>TCRU_10158 protein phosphatase 2A regulatory subunit, putative
MYSCRQSPFFSAELSVSTNDKLLESEGPGSCSPPVRRDDVAAVAVSSASPAVLRETISVG
SSPPPRLFEEIFEDAAGNLSIPVIDTLSVRRRANESTEFSSEAAERSTTTQSSQSPAAIN
PLRSMNPAFSLSPRAANDSGVLHLAPRTPSVTISTDRDKPPVEYNYVLGTVEGRRNFVTD
ALRLAKQMSKGKIVEELIPVLLMAANYDDSVCSIVGVLPGIVKLVQALDEDSFLCFLGLI
MNLCCSADHGVLRAISASLQEIVVYVSEDIVKNLLLPLLTSMTMSFWSSPRAVAASLLGI
FASRPTLVKESGMTVMQWFNCFIELSRDKCQFVQEMAVSSLHQWVAVAEAHQVNIAEMPI
SLVYECMKEEKSDAVRYLHVAELVRLAECIGKEATAKYLQFSFIAASKDTSWRVRHIAAK
HLGSFARLCTHPDDLLDVFVALCADEMKETRAVVVEQLGILFLHVVSQEVLAKMCLAVAP
LAKDKEPVVRESVANIFYVLLSPNNVVDYTPKQQQALFALLTDKNYVVGRSAMRNLELVA
ANLGKYLRPGKNVGNSERRNTLSVPLMNRRGRRSKRAMSLPSSAHAGIGTLIPAPVGSVS
EKQKERAALVLSGIINQLHIVSDSKNWRTREAVVISIRHFSAALTEEEFMPLVYIIRSLL
RDSVSAVRASAVETLSAVAIAYGPEWAALMTFELFQKEFAFKSRTPYMWRVVAIQSLSGI
IPVVSGLSPMDLRRQELLQQWTRLLRAFSEDDVSNVRLAVAKSLVEHWHWYRVCGVHRDI
LRQCAERLQHDSDVDVLQVAERLHLNALAEEGEKPYKYGVMREGDGVTRRV*
>TCRU_10159 hypothetical protein, conserved
MGGKTGTATERCSGSDVVCQVHATATTAAPLAVRPHNMGMAFMSRILFQVPLTAEGKTVR
HCCQPGPVLFTFPIDGTHLLVACGSDKSQRDGGSTVYVVRLCPDDPPTSLPSRLPIAVIS

GCVQNYNVPFSPRSGRAFPAPVAMETSAGSSRSGHLREGNADFAARPSVPMGLATEPVPM
ADDAVHGTSPMKFLPSRPGQLHSFLFADAATHAIWAAEVDTGTLTVRVVPPSLYWGNEGG
IDAATAADAKAQQQHPCSDGALKPGALLGGIEGFVDGPFHMARFASPSALCWRMDDDFAG
EEDSGGPRQPHTGRDTFRGDVLFVSDRGNHAVRYVDFQNRLVRTILGIDGVPGYRDGDYR
VSRLHDAAALVWCTSGLLFLDKPNGAIRLITGLKRKKKNTVTALEREKEGDVPQTVAQLN
MPVASSEEPTTHAKLRVWTVAGGRHGKMGPYVDAKESHRASLGMPSALALLPGGNGVLFT
DSQHGALRILSLRGVETLIGPHNCLTLSSLSRGLLACSHIVACRLVTSNNSSRHAFLVSS
GVQGTVSLLVPCDGTECVGDGKAIDLDSTNVTSLLPEECALVASGVLRKYTCVDEKSSIR
MMGKTGVFPRGGTKTHGSGNDPHRKNNHTTMLSSSLVVRSGASSRVQFLAPSAKCGPLDE
AMRQLFYVYAYYARKSSAPTTSTKLYPLGGAERPDDVNMSYSLSLMSFWRFLSHTEYFGA
CPLWAKSSANPFACMVGTIPGLKSNENGDDAAPGLVDWRRTAEVLYELCVRRHGYRVLSI
MGFSLFCRVILLLHCSMREQGRCETGQKEGLHSNVDRPMLPSIDGLRKEEVVEAYKDTVR
QVRNVNIHLRQGVGEAQNEGRGFIAADDVLCVLVHNEKSLQRLFEAFSRKILLHRRPSCT
TTEGDESHKRRRRLRDVLLPADTRGHTSTEFAYGMSYSMFHKLFHALDVFPILMGESLLR
RAYVDALLTPLFQQQQQQPVLSFAPPIFQEVEKMYACGGAALSFLPFVEAFVRVALTAFS
LCTEHDRRMYPTAAAKVEALMRWVNRSVEQHHKHKRGAAERDGPYRIESPGGKRALLFSS
FIPFDVHARVEGRHPRPTRQDNP*
>TCRU_10160 hypothetical protein
MVRRCLLRRWWTSRQCGDGGSSHGQRHGTPMRTPGSWLLCHFTFHSILAHYGTKPPLYWM
WMRLFTGSSFGGYARASFGCRVGFVDLVELTRPHTGHECCPEVPRTTARVLAEDPEMVRP
QSVAPRVVRRLLLGLAVSEPAGGGGAWFDGTNVRPKSGANRRTGGPCQEVRIYWCIVQPR
DEERRLEARCEYED*
>TCRU_10161 protein associated with differentiation 3, putative
MEYRINELGRFRILLGGLAASLCMSVIYGFNLLSNHIQNEFDLNANDLTTITTVGIVVGL
VTFPGGILLDYAGPKWVLAISTVTCSLGALLFGLTFQGVIAASVLRFSVFCAFLNFGCFW
FDTGSLMAVLGSFPLTRGPVVALMKTYGGIGSSVLAVLNYSFFYEKYAAYMYFLAITVVF
LGGFSIIFVQFPPYHIVDREKKTLPLEIQERRKLIEPYYLQQRPPIQRFVVGCIVVISLI
IYLVTQSLCLAYVSGISKNTRIGITIGAIILLFSLSVIVAPFRFLGGMSKPPNEELPPLP
DELAETVQLSSTEAADRAVKETHVPSDIDPQYQGTFWEDLKTPDLWMMWWNTFVTWSCAL
VISFNSAQIYRALNDNEYDTATNSMYSAIIGIGNALGRLAVGIIEFLILRRSPERRPAIT
CLYPVASCSLFLSVFFLLVLPLRSKAVILGFLLGGIGNGAGWASTALVMRSVYSKDIGKH
YNFMYVGAFFGIIVLNRFAYGEQLTRATKKGPHYPNCGGKACIQNGFIVFLCVLATAIVA
STLVHVRYTRFIKNTRAACGERNPEPTVSNAEKHPEGSSATANN*
>TCRU_10162 hypothetical protein, conserved
MHKESSSSFSAEEVVAPGKSPQYMQLPSPVYFVRWVDERHAIIGAGGGGRRFGMANLLAI
ISVDSTQGPCGTSSSGKQQQRTPKKEPLSPTIPWNFVAAIDMEGNIPWCASTFLICTDTT
QLARGVVGYIAVSHITCFTLVEVYECCKVNTLAMRRLACIEVPADAKNPDKKPIALVQGA
VVVAHDEGGVYVYGLHSLLQRAHSTEEEKTVRRKVEEAEAEAQKVSPSSSASGEAKDAVF
ETPRILQEAEPLAVWPLPARLNDLHANRFFVPKRKPGIERSRKRNHSNHMLIVALVQDKT
LRITTMKLPRRHKTIYKEENGDIKEGKATTCLVDTCIFTGKDCRIPFSLMKSSMRLVQVF
GAEDVAPSKAELIWLKARRLHRETGVRGLMPIASFIVVVYDVLGNQSYMLTARVSSTAST
RNGDFFSKDSEPESNAGKKPSNRLALQVCFAPQPSPLVKEGITSISACHYRRPCNDSYAV
SGEGVGTVVPSYWLAGTVEGTLAFIVHAGDGTFQTVLIRPSKNKREARQFPALHREPISC
VAVSQMNDVLTTDIAQNVVVSTLPFFEEPQFASSLCEKRKSVTSRMPCREGRMNFSVDDD
KAVACAGGDAITAVADPTLFAGDGKEIFVRPKCVALSLFPPKQGSTSSLFPFLALATSFS
VRLLVAVVIVPSIAMLIAYWFS*
>TCRU_10163 protein tyrosine phosphatase, putative
MLKKAYLLAYNGSMLTGWALILFKVVNHVASGKNIWDVYPLIARLLLVFQGGAVMEIIHA
MLGLVRSPVPTTFMQVSSRLIVLFGSLRIGPTESRHSPFFTQMVVAWSLSEIIRYAFYAT
NLLDFKPKILTWLRYTAFMLLYPVGISGEIGCFYKALPYIKANKPWSMELPNRYNWTFSW
YNTVWLILLGLYPYGSYVMYTYMLQQRRKVLGFTTRTAPPASGATTATKSSKKQ*
>TCRU_10164 hypothetical protein, conserved
MERRERLLEEYKGLQANLEEALELKQSNQADYEVDALIEEIKEELRAAVASLNAMEEIEQ
TPGLTKTFGPDDKSVICYAESAPYEVHFDNMAWYSCVITDIVSPETSLDRIRYKVWILGY

NVEEEVFSEQLRLWQPQTAEGEGALRSGVICHAIDPQSGKFRSAKVERLTLDNTVIVAFD
AVADETETETAAATSAASGNVTAPFIKEVPLSHVRVGRFYEELRKRPLLTPEERAKRRAE
NLERKRMRMQAKRQLEADVAAQNANDWQRLVDDMGMGNGPKRRKR*
>TCRU_10165 hypothetical protein, conserved
MRPRDLCTAAFYDDVQRIQQLIRAALSGEEEEEEEEIVDNADEEDVDEEEQLSIRRLERA
QKRRATVASLLGKPGLLRVVETGEEYGFMFRVEETYDSEGGRRLKPKFKLTRKSRYPAMP
LHWAVLGRSHRAVEFLVKNGVDVQLEVPDLPRVTAAFICACNNSFETARRLEKAIQGQWQ
RLQKEEEQKREWVEALEYKKQERERLAALEDEEEREEEEDMDEGRDGDGANDNDDDDDDD
DGFPEEDA*
>TCRU_10166 hypothetical protein, conserved
MPRAYYKPFTVYEEAVGFHGTRRNAYFCCALLFAGLMFKILLLSRYSTASDFSDLSSLKD
NPQYSNLVAERMELAESLASLEGMRRATKNRRAPPA*
>TCRU_10167 iron-containing hydrogenase, putative
MSTSNFSASLMLAGMDYIAPSEACTLPTRLQRGADGSVQRHASGNEVVKITLQDCLACSG
CVTTAETILVTSQSRAEIIKVRASELDRPFLVTISDQSAASIAAHLKVDSRRAFHIISGF
FRTVLKSQYVSDLRWAQHISVEKTAQEYCHRLQHARDKLPMIVSACPGWVCYCEKQGSAI
LPLLCPVMSPQGIAGCYAKRVFPQLCHISVQPCFDRKLEAARDTSIDGNERYTDFVLSTQ
ELMEWMMETDASIPWEAPLNSSFEFLPPPLLKESSSVLAATMEGSGGYHRFAMQYVAENV
HNLSFSRDDILYEMKRNANHHVATSPSNPGEVYCVAYGFQHIQNIVRGLKRKLASVSSYT
FIELMACPDGCLNGGGQVRSGNLTSNLETIAAVKAIFGSYLFSCVGQRASGTESRVDVTG
APDRKEGEPLCFSLTAFREVEKRVGTPLWCCVFHDRQQEFEATLNNGGVRSLKW*
>TCRU_10168 hypothetical protein, conserved
MLRKPLGAAKCQFFVRRFLPARGAHKNTPPNDMALVMQADCDDAELYPVTITTSTALVQQ
SPEALLNNANRPLLVPLLLLLHRRGVLEDRHTRQEIARFLVPSVHLDWLPWLWGDGTVSV
SSSSSSSSSSPPPGDISALRTLPPVAWRGVIEHEKPNDPSDNLHYWHQVFFALSSNPAFT
ETGTFDSAHRELLTMMRDYYIDVARVQQLLPPLDDGLIVTRMPPVLLRKLRRSYVEQYRL
MQYAELLRAVVDGEELVMPVDGTALLHDAELFEYYLTIPGRRESGVERDKRWACTLEYAT
FSFQKLFRQQRWKGASVSTALTRPVTLLMNVCVFAKNDNSEGDRYREAILHVMRLFHAQC
GNEGDVNDDDNVASGTAWGLLRLLRDTGVESMLAKCKRLHFGPMRGLLDVCTVAVVTEML
LSLETHTGSEGIKQKFWHDELEILLSPRKIIGSEMYDVIKSYGHPYFATRYGLLNLGARV
KAALEVVVTIPESVERYTTDLENWGAFIGRPLRLNICDVPSSQFLSSLLPSSRVGGNSFS
TWRCGCQTVNSVQVGHVSCIGCVSRNLVEHEWTCPHCSWCSNSGDYMDKCIDCHRPHSCR
ISAEGADTASGWNNLPVTPFLWYCEGCFSYSPLGGDAATGGGICSDCGLANKGWSTSYFE
WRCGCGEVNSPFRRWCWACSVRRKHAFCKCVSCGTEWKLQPRRLVPATTATAVGDICPSC
NGFHPRDVAAWKRRLLRCPFCHWLTPSDVEGCQNCKRTLGVIRQFLTGLPDCPWLCHACG
RQHHHRDNEGTLHPPWRESIEACGSCGALRIDPVLFEKHEAWVCVNCEGRLVRGFNCPHC
LFLHPAVPAMEVGAWRCVVCLSVNNSWNGVCQRRGCGTRRSADSPALPYSPWRCGRCGGH
SRSAQVPQCEHCGTVRAAAYPALKSAVDEKRLGRLAELEALLAERAAASDDTAPDLNLGN
TPTDDWTRCLVDSMRLSIPLG*
>TCRU_10169 hypothetical protein
MELVDVEEFDLLRYLQLSSLKDENHLTEEERQSLEKQRHRVLDEAQYVGHLAQERKNRMR
EQFLLRGRAPKPRSYVRDASDKYGLFWFGRGKYEGDSDGEEKDVDGNAATCRSQREKRQE
EKLGHDDSESEDISDEERFKVWRPVVGPPLRRDKAGSMPPVPPSSRREVLRKAPVSNPKP
VPAVETRRYVLTPPWAEHYNVNSDVSKGGRANQVKRQHELYKHGVLPRGVDGIDEALRHA
RNAQDLLVERQKLRMRKAKQQNQRELKRALEEQIMEKKRLQLSRREEEVVQIYGPEMRHI
LDGVFGRNPSIQQQLHFVENVDDGDNDNDLFLKLLQTELPQQPFRDRSSTGESRVRESRF
ALLTTCEDQKRRLSTTARGTPTENKLAEDTVTPLTPPLTMNFSRFNQQSSGKIIDNELQH
RESNRHHHHFSYLSDKQGDMNMAGLVNSTSNSY*
>TCRU_10170 CEP19-like protein, putative
MRENISLTDLGPELWILVYHLYDKHKSDPDVAFRELTLRTRCMCSSEDLLIARSPSSLLN
TQWYREMNTRYRDLRRRLKESQRVVLEEAEVVTRSLYPAGCVAKEYADALQTCAAMLTVS
VPSQVLARFTEYRVQELASLDVATVTVEELVDDLIERPVLDALTPSQWWTFDTDGNGSVS
LNIIGLRARPAQIDILYTRSEKKWRCRIHLDGILHETGPTAPIARRLARTHGALLSEERF
RTCLVHLQSLMKHAVEDGDIGHSSNSTMKDCHYGHEYPQKQQQKEQASALASAIELDRRR

DRTQKPLNALNKADVGLLYRDPEAALDNVDLNDADDVTLQEFKAKMEEKFLEKVVRPGDS
GYEYDKRVEVKPTERSEWDDSD*
>TCRU_10171 splicing factor Prp31
MDENEGGWEEFAEEPQQYGEAEDAADIYAEETLATAQKIASDDDALRFDSVKEVTLLLRS
AYMSRMLQKLGDYSEQEVVKKTILPEDPEYQFVIDSSTLVLRIEVEKSKAVVYLRAHYGQ
RFPELAMFFSDSVLYARIVRLIQNNMDLSVVIDQLDELIPSQLTAVVIACASTTAGRELS
EEELHRVVEACQEIDILEAAKQTFLEYIQRSMPLICPNLCAFLGTGITSQLFAIAGGVSA
LSTLDSTELARLGSKRADSSGVLIRTTGFLSNSDLVVNHPPQMRPKALRLVASTTSMLAR
IDANRRASSQHEGYRQREMVRLKMLSWLDPPVLRGAANNTYARRGRKRPRRQTR*
>TCRU_10172 hypothetical protein, conserved
MTGCEGNVQQATGSQGRLSSRSRDVYMRMKRLRSHESGSAEDTAPPRLRICLDNRGDANS
VVRRALGVVASPSSTLLSTEQRPCALHFRLLSKVGLSASTTDDPRDTHDEVVPTPTPLLS
VERLWNLPGCMVVDCTTEERKREPNSLPILEKNGRKIDGNAISTRGTEDWLLYILDKDVA
AEEDEPEEQKEGEGAVDDEFGFDDLIITRPEADGGAVTPNFCSGRYRAHRKRCRDDTTPE
YILSLGPQSAEGGGRTDDCEGEISLYAMLRDHGQDPFLLEEDAGCEPELYIYPDHRRDDE
YDSNAADFSGNEYPDEQSTSSNASVRTDSEDENNMVRRPKGCYGALWYDEDYAEASLSSG
WSSHDDGY*
>TCRU_10173 Tetraspanin family, putative
MHAKLLGISTPEKGRPQEMEMYVPDEEVDWTSDAYNRLYGERPPQNRFNNCTYHRFSTAC
FSAFLILLGVAMSAVIAIGGSKSKELNFCHDCKTLILFLLVPGIFFVVMGIVGGVSAWRE
TKICSALFSLLLVIAAFVVLGTGVTVVIAYTQVVSSDDSLALYWERAVSNTPSRICDLQC
WLHCSGFASTHCCVSNVTAERLPDVSPCYLLAEDGVTTLDPNTLQPVSWPLLTCAPRCNS
SNIYNATCKEPLQEFFMNLFPLTTGGLFALGLVFLGFASLAVYRITVTGGRTSYLRYEY*
>TCRU_10174 hypothetical protein, conserved
MDGDWLRTPSFGAVGPTFGGDGVARDKTAKMDEAANGGFSPSDGPGVFVGIGISSIAAYV
IYAMYRGSRRGPPQLFWTTPSVRKSRPPSNCNGEVSNDADDHVMRPSLTLVNFPKQMWGL
FERSLRPLINAEELELQDARVAFFHDVTEITPNNLEAVVRQEVLLAFEDLRGNPCAVYRS
VLAVDGEPINPFWGAEEAVKASRGRALLERHCVGYTVDGGRVEILSHDTEGMVGAVNDFS
SPMKTDLHLDDVDDALRRCFCATARSFSLGKEKRWDAMGDFSSRDPGKSISGPYARSFGV
LWLSPVPLFAMLGAALRYSCAEFDGWRRLSEPDNDASSPFWMLRRVWHWWRERKESKLVV
KKYEGHPGDKFIVEIESLQDLTCIETTYSDLLKDALKGARQFGVDMETIEIDTFPSAVGT
VLRCSLRPGLTVFQALRETWRLTALVSCLKCDVQKFRLLVAVRLPEVSNSRANVRDAHAS
WPHVRVFPVSREEAESFRPSFFSSAQYFRLLKDDDCVEPAEAFRRIQEGNLHQLCYVVAE
YVTGDFESYLEECAGDGGVNKAI*
>TCRU_10175 metallo-peptidase, Clan MC, Family M14, putative
MSRAVKREPQKKLASGTSGPRSLETTRATQVDRTRSLPSQSKKEKVAFKKSLRGSSNVSR
GAKHTHSFYGPFPPLLRMPPVREMYLAVLAEATRKIAGDFSPRNGRNISGDENVVAAMFL
RQLQAACAAYTGGASSDIGAANPSGDGSHNGSDAAYTHAGLIFYRHLYDLHRWLFLCGAH
ENGRFIVVKHAWQALFSKKLRSWRIFMSILGSDMIVTDENAASGFLTMLYNLLRNTSRTR
RKRVVKMCCQLRFSQLCISILEGYEDAFAEAVRMCDCGNGIRTSSGTTLQRERGLQDPNT
QFLGCNGLNSPPFPIMRVVEAAAMLLGLCGSEDAKVLRVVRRKNALSLLLRITELLFATV
AHQLSHIKANIRTDARENGEVSTETACSRNEAQLHHNSIYGHVLGTCDALLHLIVALHQL
AALPVIADLIGARGVSLCVQAGWTLHSFLSKTMHLSRAPYSLLQNQIETLAVWLIELFSR
LCCGKRASKQSLEAARERGAVGMLIEFSTHPAGRAEIGLFSLNALNVLTTRDSGCREQLY
GDSGGLYTFIRRIVVAAELAGRSPAHWHKLYLSLYALIGVVTIPGEWAATRPNENAFPAV
RVVPTQSFFSASMPNLPPNLSSFREGGTTMPLSMLPVDFQPDAFSPELHKEGDWGFNEDM
FVFSAPEELPWAFSEDGLPPSFETVGPVFPGIDVEPMESRRYSLLHTPEALQPPSSETRV
RVLKHLIERLCTSLQRMDCIIYERPPLVLKPSSQAVTDEMMMAIPSTTKGMYSSTGGRGG
VEGSPTTVEVPSLPGLLKFRSDFECGNLQRAVAIDSKEYDLVLSPDTNTNCHVQWFCFSV
EDYTPGMTYRFNILNMEKPSSTFNEGQQPLMLLVENESSGTKASGLPRWTRCGQDIFYYR
NLYQRPERCTTTASEMVETNGIGTTKNHDCSERTSNSGQRGLKKSKKVYKSKPSGSEKSK
GVAFCYTLSFSVVFPEKKGRVFLANCFPYTYSNLLEDLRQWEQQAAATLGASVVVAVQKL
CCTPGGLPVPILTLTARNPVDEDAGSSEEKSTGDETGVAASTGIEKRPVCIVTSRVHPGE
SNASWMLRGLLTFLLGDDEEAQALRNGFVWKIIPMLNPDKIIPMLNPDGVVLGNHRCSLG

GADLNRDYADPKPWNNPVIYSLKQLTYHIIHREQRHVALFSDLHGHSRAKNFLIYGCTRR
AEVQESKSAAKRSTATVPSSAAAFPPSNCALDSRRQMSTSAASAVSAVSASSSVEKILPC
FLSVLSPAFAMSQCSFTVHKSKRNTGRVVMYREFGIRMSYTLEATMMGGKDGLFFQNAGV
FLKKPTGDVLGLRQEVGGEELGSDEKIKASMEEPWPQEVSYTTLQYEHMGALLVRGLHLL
TVNSEGPSAVKKEAIERAWSLISATLGNVDAPNAPSLTVMGGSYAFSTRKERRLEAKKVR
KEKTTATSTLLSIEQRRELLRTLFVRPKVPYAQPMDIGPVFLGSDSDDEESETSESENED
DVEEKENASRQESDGDDETDGVDDDNDDDDDDDDDDDDDGAYEDEELTSSEVDGAYFQE
*
>TCRU_10176 hypothetical protein, conserved
MRRSQKKVWGAVSCFFHATSQWLRRHQSGGSGVSNIDDFAKILSQAKKNSPDCGCSSDFF
NGRFAGGSATIDPSMLQDMHRTLNQSLSPEVRDSMRAMMEGLKRGDGLPQMGVMAFGLGE
NERGKKVARGAKLAFDPNTGKVSKDFVEKQLEEDDPVLPKETVGDYHTEGAIEVEFEEDA
KRHASAAAETISEAEVVLEETPAASMGNGNNAKNERV*
>TCRU_10177 adenosine deaminase-like protein
MDILCGGVPVARTILEAFAAALLCQPARDGWHRNAMSALNGGGAVIAGIVLQLPSSPIEE
EDTPFFICVSLGSGTRCVGYEPPLCSSEADIFLRDGHAEVMARRGFVAFLLDAALYLAQS
ETGHHPFVERCHFLCKGPEGKKDVGTMWQCFRLRDGVTIHLVSTEYPCGAMSIPRGGGHV
LLSTPSGESLSSATGIDLTSKKDEPFFASCDAAATDARPVILSYGHAIAAHRSHPAEEML
HVGRVKPGKGRQNLCMSCSDKLLRWHCLGVQGRRRARLFPRPMSLTSVWLPQTPDGSADS
TDYGASSYCSLEDAIRALNGRICYFCPMMSLEGGDDSSKGNSQMPHSMPAPFPVSFYGFK
PLFFRSLLTKCACTADTREKDDCDVDKNGKSDSALSRSAWLKMASGVKNDSISMLRSKRQ
REVDTSEMNNDALSWRKGGVAVLNTKAGLPRGITKQDAERTAHELLRLQPVLLGVGGHTN
TADDAALEVIAKRFPLSRLWMAQQQRRVMQRLSRQRKDTSMGTLSLLGKDGSQKDVGGMT
ISSFPLPVILFPLEGAKEQEVVVAGGSAHYWLQRARQSRNAMMNPLRNEGGTSAHIPLLW
VEKGLSV*
>TCRU_10178 Glutathione S-transferase, N-terminal domain/
Glutaredoxin/Glutathione S-transferase, C-terminal domain containing
protein, putative
MKALKLFTNRICPFCQRVLITAKEKRVTLEEVEVPLGDDMPQWYKELNPRETVPMLQVDG
KKCMIESDLISRYIDRISSPENALIGSGPYQRHRVEFFLSEIGDLVKAYFGLVRDPFNEE
KRKSVDHNTAYIEGIIAEHQGDGPYFLDDTFSMAEVMVVPFLACFRPVLSYYCGYDIFHE
APRLKKMYVTSMQRTTVKETISKPEEYIIGFKSKVPKSHVTWSLAPGYVLFVNKYSPFSD
RPRLACALKNIDLPMLEIDLKQLPSWFRWFNQRETVPTLLTPRGTYVHESQLIVHYLDDG
FPEHGPALLPKDADGSYHVRFVESNVDYFMDAMYSLIKDPKNTNAKEEFDWAAGELEKLL
AEHQFGEGPFFGGATMNAADVSLLPMLVHLKACTPDLTEGQDLLANYKLLAAAAEAGLTS
EAGKKVFLSLSEYSSIYKTFLRPSS*
>TCRU_10179 hypothetical protein, conserved
MASSMLIRVKLSLADIPVRRLIVCLGCGDYQKNEARGALGNRVAQQILGTCAPAPSDIHN
PDKNRLHARNAHGRARQNHCYHRGERFFRGMAVNGLFRSRGSIRSPQVWDSEPVVDYMGL
WCDRLLLGEHTNPSRCALLEPRAPFVMVGESLERVLLAHRNFQGADILFVFASSCFPFGA
LHLVSFNDALLKIPRGGPSVYQHNSIGTVLNRLALSSDEASAIVMGVGDTHGLLVSLTAE
ERAMCESRILPLVSFAAALWTVNPAKAREYLQSNPKDNMRLWRTMQSSMLSTRDTAVLRA
YESGRPLDARISRRQTIYLAETLLSRLFPEDTER*
>TCRU_10180 RGG-containing protein 2
MEGVWGQPSAVDEEAWSAAPPSFNPPVRRVDPLTLTAVEVEIDGIKKLVGQRVQVSGVSD
ETTWHTLKDHLRQAGEVTFCKVLSGGRAVVEFVTPEDASRAITELQASELEGATIFLRED
REDTVLVNTRKKIREARDAQLRARKEEAEHRRREQAIAEGDVPSSTSSSATEAATANPQL
*
>TCRU_10181 Mpv17 / PMP22 family, putative
MNPSRLGRSISFWLRESPWRSNVCIGTTIGCSADIVTQVLVRNSCARRDRVLSQDDSPLL
VRCPDFIHRLLTRLRFEKDNTPAPVIDLRRSFIFCSFTVVFNTFFFLSLYRRLDALFPPA
AITRRRSLLKGFLSWIAANATTPLYLSYVATLSHYFIYRTGRRQLCATEDGDFGWTVDVP
IFLEGVEKQLDRQLREDWPDMIQYSLIFWGVNWIPLFYYIPSHFRYVYSSFLQVAWCAIM
SHLMHR*

>TCRU_10182 hydrolase, alpha/beta fold family, putative
MANNTIAALSCDRYSLFGEKCVDVGVCRSTGVRIWLCYQTFGKRDAAGGVVLLIMGLASP
SLLWDMKFCECLASRGYYVIRFDNRDMGRSTFLTDRRVMPATATTNSAEDETDVWNTNAF
SSSSSSPSSSDSWFGAFGDSKLHLMRLAYSGAVSGGRKLLREVYTLEDMARDSVGLLDAL
NVRKAHIVGMCMGGVIAQLVAIYHSTRVESLSLLSTYSGSLQAGRPSLREAFALAQVVTY
IACKGFAVPASLRGKNGKSGPSPKEEEALAHTLVNLIARFAPEAEPSFSIDRKACFKQVQ
RILRRSSDFSGVLRQYVALLNAKDRTAGLKRIHVPTVILHGTKDPIVPYVNGKQLAGMIP
QAKFVTLEGIGHVLHPALREKIIDTLAANMQQSRRGKQGLPTKSRL*
>TCRU_10183 hydrolase, alpha/beta fold family, putative
MPPTPDTIVKVGKCARTGVEISICYNSFGDPKNPCVLLVMGMMSVGMLWRDELCERIAAC
GYYVIRYDNRDVGLSTHFSDFPGPHVARMILPRILSFGEKLPYTLEDMAADGMNLLTTLG
INKAHVVGSSMGGMIVQLMAIHYPARVRSLSIIYSHTGNPNRVRESWRVKLGFLEKPASS
ALEDLVEFKCHLALRMAGDGYPIDRDKQREFMKKIIERAPDDPGSLRRHLSAVQRAESRV
EGLRGLKTPTLVIHGMLDQLVPYENGIEIAKVIGRSAKLVLFPLMGHSIPEELFPAVAQE
IVWNAQRADASE*
>TCRU_10184 Alpha/beta hydrolase family/alpha/beta hydrolase fold,
putative
MRSEEMVTFVRYCTASDMRIELCYQCFGDPLKQMPVVLLIGGINMQIYAWDEAFCEKLVK
CGFFVVRFDNRDIGLSTKVEKRGSVIPARLLLPKALAFGERLPYTIKDMARDALGLLDAL
GIPSAHVMGISMGGMIAQTMALLSPHRVLSLTSIMSTTNAPDLPDPQLWVKMWLLRKPPV
NCTLDELINFRLESIKKLLRGTLPVDEEHLKQGYLKSLQRSSYSAGLVRQAAAIRRCPGR
DEDLRSLSCPTLVIHGQQDVLMPPAHGHRTASVIPRAKLVILESMGHYFHPAFFTPIISH
FVEVANACEENGKYGRPIGLNIPYCISSFPGVSVEEKSSSCTEERHLGRAEASLSVHSPD
KVTKTEMPLNGQTAKCACSNTTGESADVSVVACRCASEISVEDVRQNILEEQLAEASLVN
TPETSINQE*
>TCRU_10185 casein kinase II, putative
MSASSEVNTDGKHRYARVNVDKPREYWDYESARIQWSSPERYEIVEKIGRGKYSDVFLGW
DTKVRRQVVIKVLKPVKKKKILRELKILQNLQGGSNIVELFDVVRDPCSKTPSFIFEYVP
ASDFRTIFPILTDHDVRYYIFELLKALEYAHSMGIMHRDVKPNNITIDHNRRRLVLIDWG
LAEFYHPATTYNARVASRYFKGPELLVELPMYDYRLDMWSLGCMFAGIIFMKEPFFHGKD
NNDQLVRIAKVLGTDELMEYLQKYNLTLSPLLEAAVGRHSKKPWNTFITRENQHLCSPEA
LDFLDHLLQYDHVKRVQALEAMQHPYFDPVRAECTGNVAENKVTV*
>TCRU_10186 cysteine peptidase, Clan CA, family C19, putative
MLNVLDIVRHVFWNDQLFDRDFLPPEADLEKCQTTLADLATMTGAERIAVFQECGIHNSL
HPVFLRALQRLTAIHGSGKIADNYMLHHHLSAHNWSPSLSSAHLLGYSFVNSEAFSTEKV
DGPIPRPKGKMVLNSGGAISKTKYNGLLNQGATCYLNSLLQALFHISEFRWTIYQMPTGE
EAEEKNDTGVKRTKSIPYALQRLFCLLQRGNEAVDTTELTESFGWSSTDSFIQHDVHEMT
CKLLDNLENKLNHVQQSEKGDHSSHTKNNAIGQLFVGVLENFVCVDEVGYHGSREELFYD
LQLVVKNTTDIYTSFERFFQVEVLDGKNKYCLENNGKKSYHRAEKGVRLKLTPPILLLHL
ARFDYDIERGETKVLSRWDYYNNLDLSKYMPHASKEDTDYTLCSVLVHSGSDAGFGHYFC
FLRCSDAWYRFNDEDVSPASLREVFGANFGGFKLNYWGSEVPNTTNAYMLVYIRTSQIGH
LLRSIGPEDVPWHVVRQIEWEQKEYERLLKERAEDHLYGKIYFIQPNDIEEEHEFLSCRR
PRGKQFPTNTTFRVLLSTEALPAFQSFVEKQLGIPISEQLLWYPLERGENGHVFLHKQVI
QGVTVSDILCGEKECCVFIVTPSTVNYIEADDIEEGDSVKYELLHHKLYIPLHLKVVFLG
CTVLAYKKRVTSAEAIQLIEPFIQKRITEIPADANLRPNHHLTGGGSKCPVDPETPAAPS
NERPLGAWTVPPEKIEAEKRERLSVLCEYDHNAYSKCSPYLNSGDILVWQEAISEEDKSG
VFYPDIVSFQQFLRRLVPVEIKLNHPPSYSTLINTQLAENMTYEQLQRYVARLIGDPENY
DRIRFTMHSPETKLPYFMKGRKKDRPTLGKLLSPPVPRYVALSRYLYYEYCKYTVTEIEA
AHSLQFKLFNERVKPISQHWILMPREIPITPVELFSTCVREIQEAKSNSVYSFPTTPVLP
KTEKEKELQERDVLDSDMMFYQDLDPDDAWKELRLVDVWRGRIYNVFDKDHPRTFENSTF
EESAEYRIEKIPRPIEGVPLQNQSLIHVHHFTMVRQRSNSVETHGDPFSIYIDHAEFAPG
LLRRIAYKLGLSEAAVVDWKMALVRENYVVEVQPGVPLGKQLFEFSLESQYQPNQQYPLK
MAFLGLEHAPLLKRPVKRDSRVVILN*
>TCRU_10187 dynein-associated protein, putative

MSEIEETFQRISQRPNVTGIIVVNNEGVPIRSTIEDTVTQNQYAHLITALAAKARHCVRD
LDPTNDLSFLRIRSKKNEIMVAPDKDFTLIVIQRFSDM*
>TCRU_10188 RNase H, putative
MYAEDRPIIVKGQSREDAIPTANMVLQKLHAWSQENGLAINPSKCEAAWFTLSMHTESDY
DREGRWPLVVAGCQTPVMTMGASRTTKLLGMDLDPRLTLNVAATKQCAATSQRISQLRCI
AHKEAGPSPHDLRTFVIGYGASKLRYGSELIWAVATDSAKNEMQKTYATLARIVSGVPST
VDPESALLETNMPPLHVLCLRARLSIFENTRACQTDWMRRPPPEPPPRAGFRISPLSRDE
LYAFVDAYTKDYGITESSPREERFFRSSIPPWFAASAHRATIGVELPIDHSITDEEELIR
EKRRVSEEFLALHSHRSWILATDGGVDVPKSAGVGIPLSSLNSSEIIEKASINCGARPCS
YRTESRALLLALEKLMIPRIRHRRKTLLVVTDSQSLLAALNKGPLSQTDWTEDQIWQRLL
TLTRAGWSVHLQFCYGHCGVHANELADQYATQTMESGQYTEQGIAPLWHTDLLTCFTTQL
TNKWRSTIRQDTHRYLLCGTRPSDLSGKDLITQEVLHRQELVTSQGQGAGNLSSGADYTG
P*
>TCRU_10189 hypothetical protein, conserved
MRGKPGFSSIGEKPNALCDANVAISLDTRRLHAMCAREGITIQAPIKKRPRGCRTPLMNA
DDRSPIQSATSHQSSQAARRAADAPSDLSNRPTQSSRRAMEIIRQRRSTVVRRITDIPAL
DKLHEESERGRSRDVRAVDVGAENVPRGAIYNFLPHARTADERGELCGLFDGNRCGAIDP
TAVRQDAAVHVGNGSNPAGHGGFGVTKIAARSETKQTRPVTEEGMNQVIRSRTDWKERVV
LRLAWITASRWSEIAALTPNNFTLKADGTLILDWPLAPKTARADPHRASRFLRIRGQDAF
DTIKLCRTLQENEKLTNITTTKVERALAPWDASAHSIKRGVLRHAAQIVGTYNLDPHVIS
QLAKHVNPFDLPQNTVCYLGRYTTMLTQVLWLVALM*
>TCRU_10190 Reverse transcriptase (RNA-dependent DNA polymerase),
putative
MHKDGPRLWDDTLMEAERMATDSKARYLQLPTPDREAEMQRTRSQFFLLLRERLRSTYLR
RISKLNPGEPLAWKYISGRKRASLPSPTSMLLGDGQHTYKTARRAANALNRIFLPFHPSH
KAVRFSKGINRQSASLNINASFLFGQQNNNESAATFTSFSSTSSSSEPQDKNEAATKSGL
VAHLHSPLDAPFNRTELLAALRNTPYGKAPGPDEVYSEALRHISSKGLRFLLRCINHSWT
TGTIPVEWRRATIVPLLKPGKSPELLESYRPISLTSIVSKVAEKMVLKGLLWVWTPHPHQ
YAYRSMRTTTMQLAHLIHEVEHNRNHYFQVSLPKKSGIGNQLHYRPHRTLLVLVDFSKAF
DSIDHRVLSRLLANIPGVNCRRWLRNFLCGRYAKTRVGHRHSDRRPMLRGVPQGSVLGPY
LLSLYVHPLLNLLNGFAGVTADMYADDLSIIVKGQSREDAIPTANMVLQKLHAWSQENGL
AINPSKCEAAWFTLSTHTESDYDREGRWPLAVTGCQIPVMTMGASRTTKLLGMDLDPRLT
LNAAATKQCAATSQRISQLRCIAHKEAGPSPHDLRTFVIGYGASKLRYGSELIWAVATDS
AKNEMQKTYATLARIVSGVPSTVDPESALLEANMPPLHVLCLRARLSIFENTRACQMDWM
RRPPPEPPPRAGFRISPLSRDELYAFVDAYTKDYGITESSPREERFFRSSIPPWFAASAH
RVTIGVELPIDHSITDEEELIREKRRVSEEALALHSHRSWIITKKGGVGIPTSAGIGILL
SSPHSSEIIEKVSTNGGTRPCSRTTESRALLPAMERLSVHRIQHRQKPCLWLRTVSLF*
>TCRU_10191 hypothetical protein, conserved
MAAEGGPVAGGSGRKGNVNSEGNSNQEDEEGGGSIEGEDPNPTSGGPLTAPTRQDQSRND
PLRSGTSNPSGTGSASAARMRASGPESLGGGHAAGTASPRSDASQQAACGVHAGGGRTSQ
GSRASEQTVTGQSQVPGTAKEAPQGDEGGEPGAQHEADQTTEMTVVTSCAKTAVEEESRQ
RDRKMHHVSIVAGMLIVIIFPCSYRHV*
>TCRU_10192 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily, putative
MEDETLVFPVEGTKKKADGTEVNVKTISLIIHSKDNTNWTLSKGMSDGGCSDPSVVGWKD
KTLIMMTACADGRRRVYESDDKGDSWTEALGTLSRVWGSNRKPHEKGVRSGFITATIENR
DVMLVALPVYSEKLEKGGAQKGELHLWLTDNTHIVDIGPVSGEGDDAAASSLLYKGGKSG
EANNNEELIALYEKKKGAGGKPSPGVVSVLLTEQLQRVKEVVATWNKVDQSVSQLCPPSA
EKDRPTENDCSGGKITDGLVGFLSGNFSENTWRDEYLGVSATVNNNEGAAKATLHAGGVT
FKGAWVEWPVGSQGENQLYHFPNHNLTLVATVSIDKVPTTEGPIPLMGVKMSDAENPVLL
GLSYNKEKKRKLLQSGGKTEELSGTWEADAKYQVAIVLQNGKQGSIYVNGKLVWGCAM*
>TCRU_10193 hypothetical protein
MLSGSGTDARSKARSSAADETVLLHTPSILAVPRNHCRKATASGEYRAHLRVVTENSFSL
VVGRSNPRNRRPARAWGTTGVTLFSHSQTHPHAEAPQCRMHDSTEMYASSVSLASVVLVG

SVSRHHEEGLSPGTADKHSPLQITAAAFLTSSAGPMMGQLSIGRFADPSWIIRLHTNHSN
TDPTRSVWQERPLFRTSGDIHSCSVRSTSSAAAHSTNSFTSASAPPSPTSPSCSSGQPVR
PASAPCSSRRNQSVTSTHPSRGAATSATPVSSRHHRHPAAPRHQCRRSHGAPLQPSRQSS
SAPPRTALCHAQHHVSIGNTSGTMPSTHREPNANAARGKWGHNQRTLQWLHEQTIRMRVD
SSRDNFILENGPVRRGYNVILTLAIVIQ*
>TCRU_10194 hypothetical protein, conserved
MWTRPHPRRVRRPRRGKSPQDAPTGDGVLLHSDTAGAPQEAERESDLPDIDDVAADGVTS
VVGQSLGDEAASDKAGGGATATGPKGPDAADAAQGVLDPPPREDEAAVVRAGLGGRHGGR
PASDPRQ*
>TCRU_10195 hypothetical protein, conserved
MMMMTGRVLLVCALCVLWCGACGGGCSEATPPGSPTSRGTPLEKSTQNDNATKAVAAGVD
RNGQQKVPEAPAPPGSESQELSPGPSQATQPGGGEASQMTSAKIDTEGQKEEEKTDEKEE
KEEKDEAEEDEEDEEEEEEEEEEGEEGEEEETDDQEDDRREDGEDDKKQEEEKKKEEAVT
GTTEVISAGGGEQPSLSSGAEGASNTTNPNSTPKTGDDDPAADGAGTAAGKQNENKDANP
KETPVTAAATKNTTATTGDSDGSTAVSHTTSPLLLLLIVACAAAAAVVAA*
>TCRU_10196 hypothetical protein, conserved
MQKTYATLARIVSGVPSTVDPESALLEANMPPLHVLCLRARLSIFENTRACQMDWMRRPP
PEPPPRAGFRISPLSRDELYAFADAYTKDYGITESSPREERFFRSSIPPWFAASAHRATI
GVELPIDHSITDEEELVREKRRVSEEALALHSHRSWILATDGGVDVPKSAGVGILLSSLN
SSEIIEKASINCGARPCSRTTESRALLPAMERLSIHRIQHRQKPCLWLRTVSLF*
>TCRU_10197 Endonuclease/Exonuclease/phosphatase family/
Endonuclease-reverse transcriptase/Reverse transcriptase (RNA-
dependent DNA polymerase), putative
MHTGNYLLYAQSRIGKGGGVAVLVRKTLRSKRIPLTIPQHDTSLELVVVQVALDQNRDLI
VATAYMRPPPQATQFFRRLVNCLPASSPLLLCGDFNMHHPQWEPFLGTSPSEVAAEFLEL
CTDAGLTLVNTPGEITYARGTRERSCIDLTWSKHLTVSDWSASVSPLSDHYMLTFTLHQA
FKDTIPSAPPSAPKFFYSWGKCKWDLFIKDFDAQLPAYDYKKQSTGIKAFTRALITSYRR
HCPRGMHKDGPRLWDDTLMEAERMATDSKARYLQLPTPDREAEMQRTRSQFFLLLRERLR
NTYLRRISKLNPGEPLAWKYISGRKKASLPSPTSMLLGDGQHTYKTARRAANALNRIFFP
FHPSHKAVMFSKGINRQSASLNINSSSLFGPQNNNESAATFTSGSSLSSSSEPQDKNEAA
TTSGLVAHLHSPLDAPFNRTELLAALRNTPYGKAPGPDEVYSEALRHISSKGLRFLLRCI
NRSWTTGTIPAEWRRATIFPLLKPGRSPELLESYRPISLTSIVSKVAEKMVLKRLLWVWT
PHPHQYAYRSMRTTTMRLAHLIHEVEHNRNHYFQVSLPKKSGIGNQLHYRPHRTLLVLVD
FSKAFDSIDHRVLSRLLANIPGVNCRRWLRNFLCGRHAKTRVGHRHSDRRPMLRGVPQGS
VLGPYLFSLYVRPLLNLLNSFAGVTADMYADDLSIIVKGQSREDAIPTANMVLKKLHAWS
QENGLAINPSKCEAAWFTLSTHTESDYDREGKWPLVVAGCQIPVMTMGASRTTKLLGMDL
DPRLTLNVAATKQCAATSQRISQLRCIAHKEAGPSPHDPRTFVIGYGAPNYAMAASSYGQ
*
>TCRU_10198 hypothetical protein
MLSTDVAVKREERKESEAVTPALASIGTQMESNEELNGARRMVSQRKTEQQRQQQFSADG
LLTSEALAREDRDSELSRRKEEAVEIELQTLVERHPSPAEEATAANAAETFSATPAGGGG
VLHGQWRELRQREMGENDAGR*
>TCRU_10199 RNase H, putative
MIPRIRHRRKTLLVVTDSQSLLAALNKGPLSQTDWTEDQIWQRLLTLTCAGWSVHLQFCY
GHCGVHANELADQYATQAMATGQYTEQGIAPLWHTDLLTCFTTQLTNKWRSTIRQDTHRY
MLCGTRPSDLSGKDLITQEVLHRQELVHLARARCGESELWGRLYWAVRDCTNQCRFCNIS
PEQSAYMRSNNDPTAPGTDTVSPSAREEDVSPVRRRTLTRRRKEKCPHCDSTLTGFSGLV
SHCRSFHPEHPPPLPELKCDFCDMVFPTRRSTAQHRSRCAHNPDATRHRNSSARRRSLLP
QDQPASTSTPIGPQETLHHLLLECPGTLAVRQRLGIEQDLRLGKFSQWQLLHSRKLLSLL
DHLLGTQMALYS*
>TCRU_10200 Endonuclease/Exonuclease/phosphatase family/
Endonuclease-reverse transcriptase, putative
MRAVEAADGDDAMNDTSSALAQPATSTWCQGLVLFAREEAKRLLPIRCTRRGRRRRTNGS
EGHQMEPFTWLHAERFFYPLLNSIGAYQRYTYRLRAVCDAQRQKLLLSGDIEQNPGPIAV

LQMNVSCLTPSKLATLMAQGADIIAIQETWKSSEQIASMHTGDYVLYAQSRIGKGGGVAV
LVRKTLRSKRIPLTIPQHDTSLEVVVVQAALDQNRDLIVASAYMRPPPQVTQSFRRLANC
LPASSSLLLSGDFNMHHPQWEPFLETSPSEVAAEFLELCTDAGLTLVNTPGEITYARGTR
ERSCIDLTWSKHLTVSDWSASVSPLGDHYMLTFALHQAFKDTIPSAPPSAPKFFYSWGKC
KWDLFIKDFDAQLPAYDYKKQSTGIKASTRALITSYRRHCPAACTRTVPGFGTTLSWRQS
GWLPTARPAIYSYRRPTVRQKCNGQGVNSSSCSESACAARIYAASAS*
>TCRU_10201 Reverse transcriptase (RNA-dependent DNA polymerase), putative
MLLGDGQHTYKTARRAANALNRIFLPFHPSHKAVRFSKGINRQSASLNINASFLFGQQNN
SESAASFTSFSSTSSSSEPQNNNESAATFTSGSSLSSSSEPQDKNEAVTTSGLVAHLHSP
LDAPFNRTELLAALRNTPYGKAPGPDEVYSEALRHISSKGLRFLLRCINHSWTTGTIPVE
WRRATIVPPLKPGKSPELLESCRPISLTSIVSKVAEKMVLKRLLWVWTPHPHQYAYRSMR
TTTMQLAHLIHEVEHNRNHYFQVSLPKKSGIGNQLHYRPHRTLLVLVVFSKAFDSIDHRV
LSRLLANIPGVNCRGWLRNFLCGRYAKTRVGHRHSDRRPMLRGVPQGSVLGPYLFSLYVH
PLLNLLNSFAGVAADMYADDLSIIVKGQSREDAIPTANMVLEKLHAWSRENGLAINPSKC
EAAWFTLSTHTESDYDREGRWPLVVAGCQIPVMTMGASRTTKLLGRDLDPRLTLNVAATK
QCAATSQRISQLRCIAHKEAGPSPHDLRTFVIGYGAP*
>TCRU_10202 hypothetical protein, conserved
MQKTYATLARIVSGVPSTVDPESALLEANMPPLRVLCLRARLSIFENTRACQMDWMRRPP
PEPPPRAGFRISPLSRDELYAFVDAYTKDYGITESSPREERFFRSSIPPWFAASAHRVTI
GVELPIDLSITDEEELIREKRRVSEEALALHSRRSWILATDGGVDVPKSAGIGILLSSPH
SSEIIEKVSTNGGTRPCSRTTESHALLPAMERLSVHRIQHRQKPCLWLQTVIPF*
>TCRU_10203 hypothetical protein, conserved
MEGCPGGKGGRAHRVTGACRCGEDSVPGVDPDIGSRVAAPRTGAMRLLPTLRQACTRPAD
HKEPSVSVVPSLPDCGDRPASASAGTSSRRERRDSLSTSERRIDVLLPNLRQSALVRPQY
EGTCPTCSAWRYNSSRGPPMRMPQWRHRLLNGRLARRSPPKLPSMPAGKTRRKHKRGNSR
WTRLFRHRLITDTTGC*
>TCRU_10204 Endonuclease-reverse transcriptase, putative
MHHPQWEPFLETSPSEVAAEFLELCTDAGLTLVNTPGEITYARGTRERSRIDLTWSKHLT
VSDWSAPVSPLSDHYMLTFTLHQAFKDTIPSAPPSAPKFFYSWGKCKWDLFIKDFDAQLP
AYDYKKQSTGIKAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERMATDSKARYLQLP
TPDREAEMQRTRSQFFLLLRERLRNTYLRRISKLNPGEPLAWKYISGRKKASLPSPTSML
LGDGQHTYKTARRAANALNRIFLPFHPSHKAVRPSKGINRQSASLNINASSLFGQQNNSE
SAATSSFKFFTLI*
>TCRU_10205 retrotransposon hot spot protein, RHS3, putative
MRRAVKGEVIFDEDIHKLCDKGVNNLPGWSLAAAEVKASVHNSNKHFLDAAAEEAWNPTT
TSAPEKLEGCYESVHNARWSHAMELPDGVERTKTEMGMDVREARTVMVVQES*
>TCRU_10206 arginine N-methyltransferase, type II
MESVAATAASMANERKRRGFFESRTAWLMPSEEGVFQSLSLRHFGFTAGKMLQFALQQQA
ACGASMCVFPIDEAAADGSSGRQTNGCSPLAALASNLDGMKSGMDQTWGLLSRVGSWGPS
VCGRVTASSWDLSADERSPFPGLLRLAAFLGLSAVLVPLPNGDVTTPAFTDAVTVLTDHL
RQNRTTNIWVYCDASSQAHRVAFSRLRTALMWGDAPPSLTDAAGCVAREALHRVTPYLYF
SETFGALPSEWLGEPVVAFEVPHIDKLMRALRSGPFHLEPDSNLPKDILPLINSYWATAQ
PPFISLAAFIVELLRRRAAPIFSVKDFIPAYTLLNQLYERHVLDNRRDNFSSFEDILQLP
LQPLGHMLSSGVYEVFECDFVKYQRYHAAMLNYFREWLEHHDERGHGRLCSKYLKNTGGD
KMDVAYVVLLGAGRGPLIAECLAAASSIGIRVHLFAVEKNPEAMEFIRLRLRSDPQWCYN
ISACGHLVETMCADGRAVTATIEGPLPKLWGLCDLVVSELLGSFGDNELSPECIDGFCED
FRRYQNSMGIPPNPHMVSIPQEYTAWIAPLYSGRMEESLADTAVSGLTVLLPWCHDRRAA
IFHSMFVTDLCRGVSLSTPQPCWTFQHFTGRDFQKEREALLTFRMNTAGRCSGFIGYFTA
VLFASKSNCGADNVGDVDISTTLSTTPEERTPEMFSWFPCFFAVEPRDVLEVEADDRLQL
HLRRCVNVEEKRVFYSYDARLLKGREGEVKATTAVINDGGWAASILLNS*
>TCRU_10207 hypothetical protein, conserved
MTTVTMRERREGREPHTFLDSCHLAEHTSPRLNDLRHSNRSGGNPEATTSTVFNRFSSVS
PQHPGISYDSANCTRNGVGGSGYMPPPPPPPPSFFFGGSSGADSRGVGWPPPLPATYWTL

PQDAPWIPPPPIPHNTSGASCGENCREAAAKWPTPQDIPFPSTFPFPPHMLPPFLPISPN
MDWSHIPPPPPWFPLLQGPQHPKEQQWENYREDNKSIIYDDYEEDDDNEGSVTEPGPRRG
RGPAPHRRSSRRQPSISAQEEEHMRLIAREAKRRQLRASASHTSVRDPVKGSMKGGRQAP
KNLSSTRGRNKICATPASARRLSPSSANSRHIVTNSRSSSRSMAHQQRRNYYAEACALKV
PSPRLKDAMEKRPSHQNVRMSNTSRDHSRGHKNHAGVKSRNDNSSRLSNAARHSGIHHTS
YQEAARQDERVAEYLKGIEDLYKRLRSSYEEFQRDPSKFIRNASVFKEAALAKAPPLPSA
AARKSSATRNLLDDADTVGGKEYNTEREVSQGKGIPLLSQESQRIRDELFKLEMQWQRLE
ELKRGSTGERGAAPVEMLQEKGINDPPLRMQNGTGTGKTKINGGEVDDSRNGEKNEGITS
MDGSQYGANVKAIATTGGFRRDKPTASIPSRSSTPRFAGDQLQNGLSDSGQWGRRNLTGN
NATSGHGPFTRDHLLGLVRERKAMLE*
>TCRU_10208 hypothetical protein, conserved
METPKVTCDDVNELVAMCSISLEKAITSLQQCSSSLFVLLYQRLYNCTIKDIESSPYTLQ
QKQWNVTRVLNELRDKRGIDVAGIDAEQIIQFNEEHISRLITLFLNIAYKMRLQGGVGAG
ASIPVGSGKLPSTRNLLPTAVSRPVLAELPHESAEDGTWYAPVRTVEEGERMLHMDEMHF
AQFPQEHAKVAPLDMDEERVGQLPGPLSLPHHTHHGHHRHVPEMEERAGGGTTGDVAFMR
SGEEDEDEEDILMGTPVKDEHEYGGSAGSYGNGDEEEIPTNQLVNAWNAEVIPPKQYNRV
INSSEIADVRERLSLMEEQLINEARQRERRQRTGVPRHLDSSQVGFFDHDGKVARRLRRR
EKPKVVFPRSLVPDTVSKEDFLRQEPKRMIDYTLRNEKIEMLRSVRLIDDLQKEIRRKMF
QRHNDATRQLRENLRQSLEEDRREKLERMRQIKDEDQKYRSAYKAIMAAACNDLRTAEDL
MMERTRQLAEYHSHSLRESRRMCQYMKRESKERMRHDLLRYASTVTGWQSHFVS*
>TCRU_10209 hypothetical protein, conserved
MGLLVKGSGARVHVNMTSSMLDAGALGFEGHFGASSRILVAGSTLVTTLFHAIVFPEFSL
GAKSTLLLLDNYIEGNSGAVCFTNAFVVDGGGVIVKGNTLSTIENNGVESSVYVYAFDVK
NGGYFDSENNTMRAVSGLYVLGETTVSSAGLLRVADCTFIGSTKVSNSALVHFDGSLTLE
RGAQWRLEGNKVRAASLIGVPKSSHKIALSGSGTTVALAHNRQLDSRLPFFNFFPLSIFV
TSPARFVVGCNLQGDEEVSYDGLFPVEVVVFRCGTCNDDAACYMPGTDSVDRVSCSCSCK
DGWYGALCLPFEVPDTVVPPVTERAVDGETSCVVDQTLTSLTLNMWKTHHCYVDVTFSGV
GAVLTFFLNSMPLHLPINMTLTGCTFRDGAALEFVGGAAAAESAGVLIRVSQTVMRSSVV
VFAFALPQHCDIAVTEVDAVQSSILFWPDTVSKRLSVVALDNVELTASSLLVSNVKAHAT
KRDAFGLYSIGTLTLVGDSSLYVRYCSLDGYTHLFHVNILSVRDHSVFALLNNTMSSGTS
LLYQCLDISVSGHSVLRVVGNSGFVSCAIFVDDSWTVEESSWLDWRDNDVGVGAIFHESE
STFLTIDDSSVVTLTGCKMGSTGLSVPLLFRADAGYQFVAGCLTVAGRVLTTAAELELHG
ITDVTTVAVCGECTRESDCFAPLTTAVVDCKYRCAAGGHGDVCVPAPVPAGPPPPPPPLP
APTPTPSPPPVGECISDMEYPEVAQAVGSGLSWLCYRNVTFSGGGMSLAVLTGAMTGDVA
NVTFDGCTWRDGAVLLLLGNAHAAVGSLNVFVTGNAFHDALLSPEGGFPPHTNITISGNR
FTVTRLIPRPGLGLRSPSCVAMNGLAISDGSAVVLSGNVFHSVTASSSAIHVVESALRVM
WRSVFAVIGNTFHMAGGDSTLIYLEGSRHSSSLIVLNNSAVVVRGNLVSRPVNYVIFVCW
ALRVESQSSVVFHGNNMQGSLVVFYSTFSYIYYNSWLQLSGNLCRESPSDTFAVLSPAVN
LRDSTVSVAGNQVMSSKGMTKTLWIFLGTSDLTNGEIVVACNTVNGKEEENYGIPSVYNA
TILTCGDPCTLAASCFPAYTSTASSDGCACRCAEGGHGDACLPVAVPEPPSTDGVDLCVR
DVRVGVKLSAGLGTSVVCYVGVTFAADVVVDVELMSGSVRNVTLANCTFVGGASLYVVGW
LSDPPAGQRADVLISGLESRSGGGGVVVVNRFPPGSRVTVVDSVLIAEARVAYRGAYDLG
DASACLVLHNVNLTGSVLTIARTHVAAVFRDAVGVLVVGGVALSSRGALYVDGLSVQTAL
GLCVSVEGGVAASGGSVVAFVDSDFLLCKHAVSVRGAVSVSGSAVALVRSDFVPTEEWRF
IRR*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MARDGVRIVVQNVSLLNGAVLYVMGGGALRGAGAAGSDEGGPVELSVCDVEALNGALVLT
GKFPAGSVLTVTDSLLVAARPTPLVYLPGSRSSPYAPVLVLSGLRLVRSVLVVSGVSLVT
VMTGGRTVVVDGAVLELVGGGVALDAAVFGGEYALYASARVVASEGAVLRVSGSQVYAAH
GLVFESGVEANASAVVVNDNAGVLTDGALLELRGLASFVSGSWLSVRGNSISGRLLSVPS
YPRSAELAQSTLTLHGNAGSGPVVMDGTVALGGAGRRFVVGCLTLNGQALQPMDYRSAGI
IGKFRPVACGVCDADVSCFAAATRTMSGSCGCRCADGGYGHDCLPVYLPRVDGCNRTPEK
PLLSHTATLTETRSPTATWNSTWTPSPSTPHYSPTQYGPTETLQVTETVALPPTRTPAAS

VSSTLWWSDVACPTLAVTTTAAGGSLTQNDIRGGGSAVPTLLMVALAQPFRWARDPQLGT
HLSFVPVSTAQPSGFGGPWGAMLSNATWVRNATNPSTVLELAVPVHRGYFITADETIFIR
CDAVAVFGGCKGVLLGSFTISSNTLPAAASALSVITGVVAGAAAVAVVVTGGLGSILEMQ
ALGVFARMPCASAQERASTVALPYFLSVFAALDPLWMVVGNALLAAVFGCVHCGVTAAFQ
RWRGVDAASAWAAVRFPSLTYVVAHAMHLGIFFGSVFALAMPVARVQHRVVGVVGVLYGV
AFPAGVCYFIARHVGASFTKYWQFSRKPLHERLLYPVGYWCPAAQQRMYGSMLTNMRGSY
VYWCVFQLSVLCVVCLIAAVHPPVGGCHVQYFCMAAVLLAGASVVAFTNMMRSAFLTVMR
TASFALLAALCLVSAANHLAPSDGGARAYAAIVLLLTAVLLAIAVYNVVVWYVEDRHWQE
LREPRRGGLEALLRDDEESDEETQKPHDMTLLSYASGTTVASSYRPPAPPLQPMAGDTCS
DALSLFDRASSASCTVDLALL*
>TCRU_10211 NPAPL
MKRRRRVVVSQGAVVTSDDTPTCTDGKHNNKLNNNTDDHDKKDNDNTTSLNGTPNVPNSS
SPAPACSLFSRFQQRSSDFSGEWLMMEEADVPLVPPISHELAEKLRQHQDTIQRERCGAA
APSRKDGKEAMHTTPAAGTATLSVGERETSVVEDEEHVPQDVGVKKLLGGGDDGGEGVGI
HGDFLSFLPPSSALSDVAQSDLQATLTLQEGRDGRVVPKSSSAQSLRSQSKDLLLTRQRV
VPLWSVERYTTHGGYASNAAIALHQEVCDFVKYLRPSEAEIFMRRIIAMEVRTIAKRLWP
DCEPIVFGSMSTGLLLPLSDLDMSILKVPVPTEEALTALAREISREGLCHAAYPQLILKT
KVPLVKFQHRLSLLDVDVSINAEDGQRNSAIVADMLRSFPEARPLIVLVKYFLQQRGMHE
PYHGGLGSFATTLLVISFLQNHPIYTERPEERAYTGLGRLLVDFFRYYGMYFNYHQCGIS
LLDGGRYFLRGETSALTPSSPTGQSSSQGLSQVMIEDPGCVQNNAASSLRSFHVITSVFT
HAYMALTALFDAPVGVEQEFLPDAVEIARRPTLLSRILHVDGASVARRQFIDAAYDGLLQ
DPVQKEKLMAMTTASSMEEMLAIRKVQLQGGASWNGITNIQERKRPRSGSGSGGSSNTSS
SSTSSNSSSVRVAFRRDRRR*
>TCRU_10212 protein kinase, putative
MERSQWYTQCRSYVALVCTAVGSFSADHPTVLISLGVTAMAGALAVYVSTGSPRWKGAPI
LFRQRRSGSGRDFYRKNFRPAALTAVCTSTKTPWPTDKEDEEDVLSEAAAEMSEALHADV
DSLSLPSSSNPSFQQPHRGHRCQNCATVCGFCESAAVMRVSSVASFSSGALCTHCFFRSM
SGRISNSSGLDTPKIVFSGEGTPAVTSVVGNGASTAALSDGEVGSHLGGIDWKTLSPLKS
TRASGVKNALAHARDCRVKEAFNSPVARSPKCVVGRASDFPTVSGEECIPGPRGYDWQRQ
FGETDDVSGGNLQQTLSHLIGAADRSCLPHVQSNHTCTLDGVSQGWEIPQPGFISPDGGA
STGLNTSAIRGSHDVEVGGNASDVLSNLSIPHSSSKCAEGCSGEQMSAETWDTRTRHVQL
EARLRSLEKRLEQQLRGSVGHRCDTKALTASQGPEPAAVLHTSESHPQEFLGKSLYEGPD
AVGLSQRDKSLPHHQGPPVSAGATERMVSATPQQHDRRVDDVFVRPRGDGASTYSLSLTY
HDAHGALRTIDTHTLPPLKLSPRNAVVTPNSTATTGSLGSSGQHSLSVTSQEVRRYFRRP
LANIWGYNSRANTGLLLAPLPPLEPTTGPRLQGVAGKRGELRIGAFLGGGCCGKVYECLN
TETGEVLAAKQLQFNSNEPKLRDRLKQLELELEVLSVATRHRMPWIVGFHGAEKRGHSVL
MYLEYCPRGSLLDYMLSRGSTPSVMSSKMMSTASLPSFSGTIEPVDSESSVSKNISQEIK
EPKSVLESSDGCSYLAYSRTPVTFFVASAASRNKTVSPEMPPLPIEEVQRLTRQIVEALH
FLHFYGYAHLDVKTANILVTEERDARLADFGCSMRLRRSEAESESCESPGQTVLSFYDGR
KERMSAASGAASSETHEAAAAPPYPVLAEDDAITELRGTAVYMAPEMIRFERHRIGTAGD
VWSLGCVVMELVTGAAPWRHLARDKLRVLFRIGSSREDLPLPPSVVQAAEEARRSLAYKA
ESQAAIDVTASLTEDVKLQKRRRLEIIKVGDETEIEADAASIPDSDISGSTEHCRRMRLF
AALENFLFLCLRIRPEDRPSCEELLLHPFLTTI*
>TCRU_10213 40S ribosomal protein S9, putative
MRNYNNFNRVWKAPRRPFEKERLDREMKLCGQYGLRCKREIWRVNMTLSKMRRTARLLLT
LPENHPRRQLEGSAIMRRCHDYGFLEEEKDKLDYVLSLTVPDILERRLQTVVFKHGLAKS
VHHARVLILQRHIAVAKQIVTIPSFIVRVSSEHHIAFADASPFGNGRPGRVKRVKRKAAK
KGAAGGDNDE*
>TCRU_10214 hypothetical protein, conserved
MQRGGWEAVSQDDHAGNDTSGAAGSDDRTNVTRSGQLAADTNANLLRALRMSEATNETGY
ATLQQLGRQKETIGRTLASVDGTREDLSGARRAIRDIRIGVYKEWAVKALVLLLLLVMDI
ILFYMKFVRK*
>TCRU_10215 protein phosphatase with EF-Hand domains, putative
MGFFFGDSHESYLARYRLRLLMDKWLDVLARRRPEDPFECLVGLINAYTQNGVGLVTCEN

KWCEMVIPVSEYAAHLSNCSEEGKWVKCARCNLRVEASRMRQHKRNCKLESCTFCGEMVV
PCLRDMCPYKLKVDAERAFSKQLCDPNKRDNVVSAKENVKPPLSSSIEPSSAGAPLYLRQ
PLSFPDNLRDRLICIQDLWRNAAFQERFQELSFKFVWRAVELYREKRATKVQLAVHGDNP
KSTSSHRLMNYVAPMMGCISASRFEALAKTITSGEVVEFEAAKQIISMAVGILAARPLVQ
RVTIPEDGAAVVIGDLHGQMKDLCEAIKLTGGLPNPRRYLVFNGDFVDRGSNGMGVILYI
FALLCAFPTFVFINRGNHEDTRVNAEYGFETEVCGKYGMEDAKRLLELIVDSYEAMPLMT
LLDGMILVVHGGVPRVPVTLERIESLGRMRHIPTAGDITEDEQIVVDILWNDPVERLHSR
KLGLRHQAEHWRTSKRGCGVEYLAPLTEEFLRQNNLRLLVRSHEEVQAGFELIHNGKCCT
VFSASNYCGVAGNRGAIAVFSKGSLHPVFHTWYVQNDELDTDLYTAKEFLHEIMPSVGNS
GDTTEKEEKSMDGRPLEEPDEKRTSAIADKKREFEGLKMTKNGLEKGKDDMEADDTAAYD
TSVERRLNSRLNVLMILAGIIFRKRYAILSGFVAADYSQSGIIYKIEWCGVMRSVLEIDL
PWYYLCRFFAAQQELDGVPCVRYISFLRRFDALFSSQYLLPFQVACVRRVFGDMDLPDDL
LSRLDNTDVFEATTASSPLHGQCQTANSAYSRGGVTPLASLHGTSRSRSLLSSKSPELHA
TQSQGSSCPIEAWRSLKIDFNLLVSILRSESRVAAKLEDDAMYALFQYLDQEECGHVVLG
NLVDLVEATLVDEEAGAVLLETSISLDTEFAFSFGDKWRDEPPKGKGAVTPPIISLVTTS
LVDGSGERQADAGVEMATPSNTADAFVVNGQEKESDGTLYEKTPLLPIVAAGTPESTGTH
ERNSGPGLSHAANRPFMSTVEESIMDALWIYPALLRLHEGFDYGSLSALRRNFRNLNRTG
DGRLTFDQLNVAIQLMGRHMREPLTTEQSKIIFSAIRLGGRRLAMARSLDAFLNTRSDIH
SSMSFPSCMLHGLSKDSITDIDDGGELSHITINEFVTFFSITSTGGNLNSTRSNADSPKT
SRVGENYNPLSMSDRRHAELGNFLEDLRSWPQLEVLGELTVKSFSSRFDGSTTLLRALQE
LLQSSPKPTKLMAGLSVSRKFSPLHFTKCGNGFVCPPASSQQKKSPLTGVLSAEESMPER
TQPNSGTTTVVPQESGETRSPVDTNSLKAVIPARVHPDRTTVAPTAVFTPATGSAVGVGT
ERKQRPDKIQTKPKHISTSPRDLVPMSSNHSDARTVGTVAGQSVPQKFLFALSNPSSEGE
ILKTTPAITQSQLTGLTPSVRKVSLSNRPQSRLPNLRVPLMMTPAPPSASIEPPNASLRR
K*
>TCRU_10216 hypothetical protein, conserved
MLLRVRGTGASPENSQATLMYLRGFRRTNTRPPSGEYLLAGIGRPLLYPHFHVGIQTPGI
EKDIELRRQLPYVVWKELWNVYDIAYDELRLFPDPHATTALLSSSGSEGVEDTTGFTRIT
ARSGANMAVVVTHHIVEDGTPVTGHDMYAGGQIVVLDLSDVPLADAATRVAVELAWTAGY
ASMQGALNHASHVVVRLPYICDMATVGKCSPLVQEGLDFMGEHIALLTRSFTQGEADGAA
PGVDVSFIGAGAVQLQETLDRLCSSKEMPINNDLPDDKQKGSVARKHVFIFAGDQHAQQQ
QPHITQLLQSIESSIGVSLSFESVPLKGLLEGAEEQWDAATTRENQILNFCPCCGHCGGH
*
>TCRU_10217 kinetoplastid kinetochore protein 9
MSEGLLTQWRDRVVEAETEISVVQEDISALLGRRKEIKQDISRYDRLVQREKQEMLKRLE
EVEGQARELEERCQKTVQQKARVEEMYVQTLDNYESMHDTVKEIQAEEQRLQEREDVETV
LQRESLAWAEEEHGLRTKLSVLQSALKGKRKQRHEEVTALDTELAAAERQLLQVRHERQK
DMQAQTPQLQVTKHSRHGTPLESAQFAVAAAADANDKEQQFITANASTSVPTRQLRSCLK
NTSATTDSYSFSDTKTQPGNGSINKNSTGSSSVCHTVPATNFNSAPVSRAVSQALVAGDD
TVLGGVDSTHVTPHRAYSYASGKKAGSRKREIILLGDATNR*
>TCRU_10218 vacuolar-type Ca2+-ATPase, putative
MRRSSNSFSYGSCDEMEEETKMRRSRLMESVRRRTSIRLNFTDGDDVGVSIRTDLENIFA
RANEGMPLYENLGRVEGIAAKLQMDLSNGVRSDTVERRRTVFGRNELPEEEELSFWRIYK
AAWSDQMILLLSGAAFVSLVLGLTVPEPGRDKADTGTGWIEGFAILVSVLIVTTVSSVND
YRKELKFRQLMEENSAQPIAVIRDGREQVIDVTEIVVGDIVSLSTGLVVPVDGFYVRGLS
VVIDESSVTGENDPKKKGVQAPILLTGTVVNTAEDAYMLACAVGESSFGGKLLMESRQEG
GPRMTPLQERLDELAGLIGRFGMGSAVLLFSLLSLLEVFRIIRGTDEFHMKTFLDHFLLC
VTIVVVAVPEGLPLAVTIALAYSQKKMQEDNNQVRRLCACETMGCATQICSDKTGTLTQN
LMSVVQGYIGLQRFNVRDPGDVPTPIVLRNVPAASRDLLVEGLSLNSSSEKVVCRTGRDG
ESVARPYWQWRADKGNKTDNALLDFVDRVLLQDGDPTDMTSRPHQRVRERGRAQGFAIFP
FTSERKFMSVVVAGPGGVLTQHVKGGSDRVLEMCDRYVSASGEEEPLTDAMRTKIVVQIR
SLANDANRTIGVAYGRVNGEALPASEPTVPLVWLALVGIQDPLRPEVPDAVRKCQQAGVT
VRMCTGDNLDTAVAISRQCGIYNRLRGDVAMTGKEFRSLVYDAYGSSANMEKFWPILDRM
VVMARSQPLDKQLLVLMLMMRGEVVAVTGDGTNDAPALRLANVGFVMRSGTDIAVKSSDI

VLLDDNFRSVQRAVVWGRTVNDNIRKFLQLQLTVNVSSVVLTFLGSFLSSSHTSPLSTVQ
LLWVNLIMDTLAALALATEEPSEACLDRGPIPRKAPLVSRRMWCTILAIAGYQTVSTLLV
ERFGGSWFDVSGGEMQTIVFNVFLLSVIFHMFNARKLYEEMNCFEGLWERSRIFVCIVGF
CFAFQVFSVEMLGSFMQVVSLRGEQWVGCLALSFLTLVFGVVARLVPVEELPVPEAEMDD
MEPEARRMAMKLTADVEAHAAREGAGGHLLLGRRLLAQAMWQQVREHHIAVRSVNAFRRA
RIDRDMHTSVAKDIYCRLASTMQ*
>TCRU_10219 hypothetical protein, conserved
MFHGFPDVQIAPRDTVISEEFHLHDKEGRMGTLLQPMAQRMRISFSALTCLGSYAQNATC
HYALFGRLCGVQLNETIEVTNVLPPVINPRPPEDETPEQREKRLLAQQREERQMYERMGK
MFFKEELDSYHVGYFAICSAYTNAPYSVRTVQQLAQLALDGNPSVLVVYDPFRTSLMGKL
YLRAFVPTREYVEFYTRLTDKRNILRENRLMRECNVGKGGVLREVKVEVDVDEYQLLCLS
GFNVAPLSSTCRTLHSEVMTDYMAALIESVRHNADELSRGLHSESYFSQKEESYGPLGQR
IDTLLKLMQLREQTQHLESLCDGVLLNTSLLRDL*
>TCRU_10220 hypothetical protein, conserved
MESSNQSRNTRIVDLGRMSREEVIEIAKKQARSIREKSTRINTLEGLVEQLTGRPASEVG
AAVLNSSLTSVGSLPPVPSEHRSELAPQQNMEEERMAYAKEISRNEEIIRALQAELDGKT
EELTALQEKVNAWKEKVKIASCRDQEMIAELQSRLEQQANAGTTSSFSVATPATIPPDVL
ERAVREKLSLWQERVKTKMREDMDRIRQLEEKLESTQKAQKLAADEELTDRGQNVEMPPS
LVQCPPKPDSVPRSEELTEDVIEQAVQQRVERWKELVKETIHKDKKLIQELQEELQALRS
ASTESHISFEAPTEVVNSIGRAAVTEVKQLQKNMAFQEAKYQKQMATLTREVQRLERELE
VARQEQERAVGATEAMQRDAARERDEAVATLTREVQRLERELEVARQEQERAVGATEAMQ
RDAARERDEAVATLTREVQRLERELEEARQEQERAVGATEAMQRDAARERDEAVATLTRE
VQRLERELEVARQEQERAVGATEAMQRDAARERDEAVATLTREVQRLERELEEARQEQER
AVGATEAMQRDAARERDEAVATLTREVQRLERELEEARQEQERAVGATEAMQRDAARERD
EAVATLTREVQRLERELEEARQEQERAVGATEAMQRDAARERDEAVDTLTREVQRLEREL
EVARRERVVVIGDKNCLACVSKDARMGEWKKSVKLIIERSDEEKKMLALELASSKEGAHR
AQLEFTERVEFLRCSMSSLQAELLRLVEERKVMTESLSRLEEFKAMVVRKIMVK*
>TCRU_10221 hypothetical protein
MMVRHVFAEVFVASVHDALARSQGIGGDKDVVNDLKLSRVTKDIATPSLSSSAVVPLPYP
LGRSTLQVTGMHVSLQETEKGEGQGTDTGDFVVLLRAHVKGMLDIDARVFTVAAMKFCGN
NGTERASLDKRGAIEDRRYAAGKTAVLSAPKTLSGKLHQLPRTGFAQLDLRLQMEGVSFS
VQVLPAGPGYSRSSTSVNSSSSFKNGSNGGGGSLRVRVVGVVSPLLLS*
>TCRU_10222 hypothetical protein, conserved
MSLHCFFGVAMRPDGVPVTPPMPPNSSLVLSHCALTSTTTGPVTLYVQSHDQPHRFAVCT
LSPKHDIYYVPLQLVFTQKVSFILVAAGEKRPDDGSKQKVRKDGKNRNGKNAHDTPTSPE
NVVHLTGYFESDEGHLAMASDNDDEDDEDDLTDSEGCDGDVKRGAEARGASGRKHGKLGG
EGQQAPRNRRNTSKTTSLGGEENNAGNNHAGARKKRKRG*
>TCRU_10223 retrotransposon hot spot protein, RHS3, putative
MPGNQASAVPQGDIRRRARPESEGDTGQPAATRGRVEDVRRLMWALDSRVEGYTPWEDYE
SVYNARWHHVMEVPGGEGTGMEVHEGEPPRSWTYKAVGRTLEKDDGVEPSGAPRLRLMVL
TLGKTWLFLCGMQLTTAM*
>TCRU_10224 retrotransposon hot spot protein, RHS3, putative
MDKLGPILRYIFDEGRYNNWIAKCHNLVDGTTSWGIQRYFVFGTSKLWEDNKVLEYLARI
VRARGERNGESPFNAPITAHLASKTLCKLAQLMTQAEFNLFVSRIRDCLTHANFGKCAMF
AFLNVAFMAAMRRKLKELKPPTRRPSHRCALEVYSQEGPTSHYFLPSAERIGKKTCINHR
LLYIPEVENFPLVDGFFFMDSNPMTLVGLRMATAGGHHTTASTVRQFTECLAAYFNGWEE
FSRDMSWEMIYVQHADSTPLNDWQRCDVVNSDNVSKKESQKIAAFWEEKLRQYQVSIPSR
DF*
>TCRU_10225 BNR repeat-like domain containing protein, putative
MQAKNKDGTSVLLSICLPNLGREWELSLETPGNGCRDPTLVKWKYEDEDERLFMMAHCAG
GYYDVYMSTWNGYNWNPVGEPITRVWGNSHDRKGYGVQSGFTTATIEGREVMLVTTPVYA
KDNKGGKGRLHLWVTDKARVHDFGPVSRGGDDAAATSLLMKSGKDELILLYEKKNGDGSY
NLVAVRLTERLQRIKSAVKTWKELDNALGVPTEGLVGFLSSTLNGTAWKDEYLGVNAAVG
SGVTSTESGMALKGRGAGAEWPVGDMGQTVPYYFANNKFTLSATVTIHEVPKAGSSPIPL

IGARLNEKDSTVLFQLSYTSERNWNLTLHKKDFLVKPSGDVGNWETNTTIRVTVQKDNDD
EWLVYANGRKIYETDEEEMAQDSNADQFGTHRISHFFFGAGNKKDQ*
>TCRU_10226 Zn-finger in Ran binding protein and others/SPRY domain/
HECT-domain (ubiquitin-transferase), putative
MEEREVEVTENDDVQPIKPVWFEPLDGETHELIGGCDAMLRYKRSSEGSAHPRLQAEVRV
ETRLEVDGRWVVELWNTLSGTQLLVAESLLQRVRNGFKSVDGRMREESLVLFRNGLLSQP
RTNALPTFVMELLTLDEDILRRRVTCRQSDARGVRAALSLIGMFLANHEIDQLSWESRIW
QDAVKRVSLASSSLGRNPGATELATFVLEHVALCHLSMPQIVEGTIAFLTSDISVGEVRN
MLSIQRARAELCVLALSLLLRAKENFVPKGMFYLVSLLQDFMVCEGTHYLSRFQGCGESL
EEEIRELVHRLLTSVFGALHRIMSLPEGERERQGPHRFLWDADDFGPFALVTLSLLASPL
DARDIEFVLRKIASQVEGLLPNFTDLSRSASFKVSEREEGSMLEALRALVNDSIADHSNS
GATGHADQPFIGMTMTGASERGIGVWVPTGRDRFCSTVVPLYTPGSQVSTSHIFSASSST
SVPLVNGSPITPSNFCVAEVELLSMPSRDLIVALTTKQPSGLTAYSMKDDPNGFYFFPNE
GTLHHNGSQVSLPPIFQGDTLAFSFSFKPKSSTRVLRILLNGIRILEFLAPRHQLFLVAG
VTDVSTLRSSSFRVCFRPYKGMSLGASTVVCGNNDAVVNGLPTRHSISVFATNVFFYLIS
FCARRVTQFRRQGGAASASLQAACPANSGARTFVPHTEEVWRGFVDDCCNPLRQNVESLI
ESIKRLPPLSQINDATERVKRNAASFVYHRFLMDYITMIRTAIRCSLSPVDMLSTLSRVV
CCEDVGERERCAALTIACSILCDPHRGIALGTYNPLQLWDCCRSLSRHVTELAYNPVFTM
KSAAAELTVFSGGRRLKSVSASHSTSRAMRNTTSFASQGIPLDGSLGEVVAFSVRLQRGF
ACDTLGRFYYIGLACLYPMSSATTLSSYPGDWQSIVYTYAITDYFTDVSSPSARSELPRH
AKNWMSNEENIIFGSGDVITVIVHTKLRCISFERNGLSLGALYTNIPSMVKVLFPFVELF
NKDASALFLYTPREIGIRARFAMRAMLYHWGTELIPRLNEMLKANDVVALQVLGADGDEM
CFWYRNPPRGELKGSRVVRLVRQLGSNAEVVVEGTTKSMMVLAAALEPNYNVVISNDLPA
TMVLDELMRIVSTSISFTTNSEGCDGVHIRPTKMFLCALRLLSEMELMPLFSYDVEALRA
LLIQLIRVLGVPDAISSEGQYILLEAWNELMLLPDDDELWISIPHDAETNDVVMERDHDM
DNNETEGGIYDICLRCPTCDKEWGNCTSETHVTPYSPCFTLHCVLQRLGVPSPFTGFICE
WYLPKMHFCVTIRMGPHGEIEGEGEEPRGIFTFSAKYVSNQIIRGSCAYKCAENFTTRSQ
MDEEWACELCTFINLADSTRCAMCTTARPGATWTCLLCGYAFNSKNNNICTTCGHQRMGA
TETDSRVEKKLAYCEGCGEHREYTTFDDFVCHFYCEHCQRASRWLPEEKYTGLIEATLVG
AGDTMDWVIILGDNITVYSSLKNDTYSLEAMKQAAELASPGASDLSRYVPPLVQVRTTGT
DASNSSSALQQQQQQQQEQEQAQEKEQEQEQGREHSRGVVSAVLFFCSCIVCRWGPDLAP
EQLANMDLLRRLRVLDDSWLTGLEKIPSEAARGIFSFSLRVLLAGTSSEQVIRSLSSISR
VLMNSHPTLQTQRHYLLYALCVNAMRGSGDRAVREACYAALNALIEESSGQRLNANSLRD
VVAITPVVAEQQRLMVHASLRGVDVSSGTNVISTSWLIEAVERMERRERLPAIFDEPSPD
IFPYLVELPDTRMGEGGELIVGQVRGSVGVFASKGGRYYYELVIPANFSNDRSKTIIMGW
GTMQHEVLSSGQHVGSDIHSWGFNCQDRLRVLTGEQAISTPRPIVGSDVIGALLDLDAMM
MCWSVNGEQLMWVAVSTQGKGEAIYPFVSASVEPLGVVVRLGHTQFKPDGYEDFSPFSHE
MARRESHVKPQSYEFYAQLCSLGNDIVNCGFTLDSLLDTSAWFDRAQEVITQYPLLCEEM
AEDTLEGLRPYFQHLRSINSLAISVAKSHDILRNSPYLMRRYQKTRQLLFFSARWAIVER
QIERRLIRSKLRHHREVLIDLNRAKAMAQSSESLDFMTRFEGSITGQLFRQTRDADIYLD
AVMFVISLAGEVADDAGGVTRSVVTMMCDELNYREEDDGRRVDPLLPFFRLTGHTTMAGV
VPNMDFYRENPEHRLLFVEVFTWLGKLIGNATMSGYLMFSFTFPRLLWKFLTFDNLTIED
YHADIDDTVRGALNDDEFILNDEFFYSIPGIEWGGESVTDTMGMVRSTRGYPVVTPTRST
ADVASIFPTDGHEESVTVAQRRKEAERALLHQYDELLLAMLSGITFVVPASSLQLIRWDD
LQQRVCGNSCATAEDVISSLDLSLLSEELCHMLKEVVHGWPQQRRSQFLLFCSGQRRIPL
PEKVQVACGDDPIAIPTAHTCSPISLLLHPYPSVAVLREKLEVCLRHVYEFGFA*
>TCRU_10227 hypothetical protein, conserved
MELLVGVNSDIVSCITRIIQRHAAQVRALREEEIAINARAEQLEHLTELLMGGEISPSLH
EFSLDAPQSEEENKWVDEEVLTDTPSAPQLVTVDGFEQKARMEGSPLPASQASSQDMSSV
EPLREAEGEKRSSTTPSPMRRELDEFFPIAASKRPRQACVTEGSCRRRSRVEMRKNDAGA
EAIITATDILATIPCISSNATPTATTVDAVLHEEKPRSYVRSHRRRQEDYAADAAMYVRG
HEGAQVACTPSVYWEIAFPKGLHAHASACEDQGE*
>TCRU_10228 hypothetical protein, conserved
MPRCIACATTYVRLGKRIAAHALAASTPRHRWKTTVTPQCTHPNTAASSALPTTIHSGSR

AANNDRKYGSAAVLARSCVEAHDILANTPSACISRMEPSPPVTNTATAAAPATTPVIAER
ALAAAGSVFDLIVKDPSSTPLQPPDTAAASQRMTIVSSAAMK*
>TCRU_10229 ribosomal P protein AGP2beta-1, putative
MTLQTRRDKYDTSQLTPSSLVALCADCSSFCLERTARVLDNQSRAPKGWENQFAAVAKQR
RQEDCELCERYCHRVSSVCPDSKDIELFEALGYKEVARRTSLDGLPTVQQMSRCENAVSE
FSRVLFSLAHKPSKVAFEDVDPKSGLKKSEEGGDGEPTELHKKVLSGGSIDDAILQRWST
ARKGRAEMEEMGVIRSAEETASLRQELGRQRSEEYIKTRGTTPKW*
>TCRU_10230 BNR repeat-like domain containing protein, putative
MIVQCKDGQSLFDSHDMGATLTKAIGTLSGVWANSKLGVFREDNLPVEAPITANIEGVKV
MLYTWKGYFSGEKRENVFHLWVTDNNRTFSVGPVAMDNNLERFHALLYSDGALHILQDGI
IKASNTISLVPLTEGLQMFNYVLKTWAQLDSSFSELFTPTAGLVVFLSKASSGGDTWSDD
YLCVSAIMTKNAMKAKDGLKFTGAWVRGSMAREQPGA*
>TCRU_10231 hypothetical protein, conserved
MELDGRGALDANRDVLLEEFLKDPKKHICGAGVLGEMQASDRYKRMERAVREEMDMVEDV
HKLYEKGVDNLLKWLVAAAEVKASVHGATKRFLDAAAEEARNPKKSSAPR*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MARDGVRIVVQNVSLLNGAVLYVMGGRSLRGAGAEGSDEGGPVELSVCDVEALNGALVLT
GTYPAGSVLTVTDSLLVAARPTPLVYLPGSQSSTYAPVLVLSGLRLVRSVLVVSGVALVT
VMTGGRTVVVDGAVLELVGGGVALDAAVLGGEYALYASARVVASGGAVLRVSGSQVYAAH
GLVFDSGVEANASAVVLNDNVGVLTDGALLVLRGLASFVSGSWLSVRGNSISGRLLSLPS
YPRSADLVQSTLTLHGNTGSGPVVMDGTVALVGAGRRFVVGCLTLNGQALQPMDYRSAGI
IGEFRPVACGVCDADVHCFGAATRTMSRSCGCRCAEGGYGRDCLPVYLPHVDGCNRTPAM
PLLSHTATLTETRSPTPTPTPSQSTTHYSPTHYGPTETLQVTETVALPPTRTPTASVSST
LWWSDVACPTPAVTTTAAGGGLTQNDIRGGGSAVPTRLMVALPPPFRWASDPQLGTHLSF
VPVSTAQPSGFGGPWGAMLSNATWVRNATNPSTVLELAVPVHRGYFIGADETIVIRCDAA
AVSGGCKGVLLGSFTIRSDTLPAAASALSAITGVVAGATAVAVVVTGGLGSVLEMQALGV
LARMSCASVQERASTAALPYFLSVFAALDPLWMVVGNALLAAVFGCVHCGATAAFQRWRG
VDAASAWAAMRFPSLTYVVAHAMHLGIFFSSVLALAMPGARVQHRVIGVVGVLYGVAFPA
GVCYLIARHTGASFTRYWQFSRKPLHERLLYPVGYWHPAAQQRMYGGMLTNMRGSRVYWC
VFQLSVLCVVGLIAAVHPPVGGCYVLYFCMAAVLVAGAGVVAFTNMMRSAFLTVMHTAGF
ALLAVLCLVSAANHLALSDGGAKAYADIVLLLTAVLLAVTVYSVVVWYAEDRHWQELREP
RRGGLEALLRDDEDGDEETQKLHDMALSSYAIGTTAASSYRPPAMP*
>TCRU_10233 Male sterility protein, putative
MSLDIHQGFSRKSFFLTGGSGFMGKVLLFKLLKEFPDLDAIYILMRGKNSRRLKRYLGPQ
ERLEKEVLGSPCFDPLREALGAEGFKARSSRLIGVEGNIHDDRLGLNDKDCQRILTSVNY
IVHMAATVNFDDRLTVAVDTNTLGALRVLAIAKECRKLEAMVHVSTCYVNYNLRGSTVEE
RLYPLPFDPEAMCKHILALNENEVDDVSSRLLKKYGFPNTYTFTKSMGEQLVYARRGNCP
VSIVRPSIVGCSYKEPFPGWVDALTAAGGLLLTVGMGVVRDVCGRADAVSDIVPVDFVVN
TIIKVLFKTQYHYKGQGVKVTNTVQPQRRHVGGALLNALAKAELPKKNGAGGVEGVAPLA
VIATQQRQQQQQELQQQQQQQQQTQSQPQREQDGTISVPATCLTPSEAPGASLPFVYHA
ATSSSLNCVTWRRLRDATRFYWNGKKKHPKALSPMTGEIIESNIKYMMRFILFRELPYYV
LRFVANLPNPIGSEEKQKLVERLGRAVFRSKDLNRQFRAFVLHEWVFATAHTELLDDGLN
ERSRSAFYFDTYMINWWFYAQVYAHGILKYIVRDVGGFEFPEQPSIPTEVFKRASSL*
>TCRU_10234 Amastin surface glycoprotein, putative
MRFTPPLVLESLRLFFALTALVLAVSSLFFPVFICDVCENETDTSNVSVKGEITFWKHSL
WPSESVKNESNKLDLVEYFNCHKGKVRIQMVEGIAIIVCVLTGANFSMCIFGFFFGHILF
IGLIVYLFLAIGLSACVIGFLLEWYHLGWCEGQPPLVEEGRMSWKYGIGWILMVGVCAAS
LVGLLLSICFSLFRRKGG*
>TCRU_10235 Succinate dehydrogenase [ubiquinone] flavoprotein
subunit, mitochondrial
MLRRIFARFSPKLSKAYPMIDHTFDCVVVGAGGSGLRAAMGVAASGYDVACISKLYPSRS
HTIAAQGGINAALANCEEDDWRWHVYDTVKGSDWLGDQDAIQYMCQEAPCVVSELESMGL
PFLRTKDGFIYQRAFGGQSIHFGGKQARRTCAASDRTGHAMLHTLYGQSFQYGVNFFNEY

YCLDLIVEDGCCRGVVAMSIDDGTIHRFRSKYTILATGGYGRCWFTTTSAKSCTGDGTAM
VARAGLPAEDMEFVQFHPTGIYGPGVLITEGARGEGGYLVNSEGERFMERYAPKAKDLAS
RDVVSRAITLEVLAGRGCGPKKDHVLLQLHHLPPEQLHEKLPGISESAHIFAGVDVTKES
IPIVPTVHYNMGGIPTLWTGEVVSPRNGDDDAIVPGLLAAGECACASVHGANRLGANSLL
DIVVFGKSCANTVIFNLTKEGRNQPELRPDAGESSIADLDGILHNKGDIPVARIRERMKE
TMALYAAVFRTEESMLKGQGIIEECYRDYSHVFVHDKSPVWNSNLIEALELRNLLTNALL
TITGAAVRRESRGAHARDDYPERDDHNWMKHTLAYLDDKNGKARLAYRRVHNEMLTNELE
SIPPAKRVY*
>TCRU_10236 UBA/TS-N domain containing protein, putative
MVLENAPVTGLLLGISVLSLSFTPRQYITLQHPYVASGWKTTIRRLPLETLPFGLIGVSL
IDVTCTLLILFQMRILERRWGSSLFLAFVMTSAMTGSVLLNMFITESTPPLNLDQLRILS
SGGSIVPLVALVTRYVLEVRSLCRWRVPLLPIVITEWSLVFAPLIRLVMFPATEIRPRTH
KQRAIHVDIGSWTRLMLTLLGIVWGIASKETRLLKWWLSFSSRYICRPFINFIRPVLSCM
AGSTSVVELGIPQQNSGEQTVTSGRYTVDNLAGLQVEGHVRVHRARPPANALFGEQMRRR
NERNSGSHGGSTVMTDAVTEERIAQIMELGLGFDAETIRLALIDANGYVDMAVEKLVSRL
*
>TCRU_10237 hypothetical protein, conserved
MQHDRDLQRRHIRHVDESVRHQARRALAEAANPQLRAARKHAVAQRHVQRVSERVHQAQV
HRHDDRPAEHHRVEARRCTPAANRHRLRQRHATHAILRTATTATGPRRRHVERQTRLAHA
AGTAAAHAVGERRRQRIEARQLSRTAVARHHAHRGQAGHAVVAAAPQHPAAGTVALHRHD
AARDRRPGDKRRAGGSAACNRHGAAAQRHTRQRRHRRRLAHRPHVVQVQPPAGIDRPTVA
AHQRRRDRPLDAHEAQHRIKHREALSKHNAAAAAHNRHTRHGEHRVAPQTEARRGRHMQR
GRGRTARRLQRHAVKHHRARQQVHVAANVHRRPARLQRPQHSVAHTQLRLQQRRRVQHKR
RRHRVRQPAQLRVAHRPRRHNRRVTDRRVRVCRQVVRKHKRAVAAGQPAHAHLQAPVTRR
LAAVAPHVDLRTAVAHAVPQFDAQRAGKHRRNVEHHSHAVRDVHAVHQHRVHGVANRDGS
VHRAAPQSQHHRTHRGHPRRRRNQCQHNEQRRTHRRNGPAPHTVPAVRTRTHRTPHPQTQ
TRISRAVVACRTRTVDRSTFLINPFLWMENPKAQIR*
>TCRU_10238 BNR repeat-like domain containing protein, putative
MGIGWEKLDNWEDVPDAGGKYGSLRGPSLVDLQGHVFAIAEAHCKDGGDCSDVGFTGIAS
KYLDLSGVADPTEILTADASIFGADLLKEGSEVISARNGITRPTTLVLGESVYVLLGNYS
HTGPQVGGTNERAFYF*
>TCRU_10239 BNR repeat-like domain containing protein, putative
MQAKDKDETSVLLSMRLPKSENKWELSSETPGNGCRDPTLVKWKEDEDDERLFMMAHCAG
GYYDVYGSTENGDNWYPDGEPITRVWGNSHNRTGYGVQSGFTTAIIEEKR*
>TCRU_10240 Protein of unknown function (DUF3676)/Trans-sialidase of
Trypanosoma hydrophobic C-terminal, putative
MQRGSDLQPQDPQPAELTEVTDVEMSSGSYDEEMPEEEGEADDRSGGSTSSVGASSDMDT
ATETVDSERQLQQSTELSTENEGLRSTGTGTTGAEQSLGLEAGDRNSERTMGSDSSLIPS
GIDVEPTFAENTDDVSRTEGTEVSFEDGKEVPQTVDTKPENTNTTPGGEGIPSTKGAARH
SDNDTFTGEIAELLSMGLSRDSTVHVCVFRVLLLLLLPGLWGIVAL*
>TCRU_10241 Leishmanolysin, putative
MNGVVSSAHGNAVAEEVVPASVKLHADRLLVQPLEGLLIVPSLATGSVCSRFTVPAEHCS
AGAANSDTVQYVAAAPGGVWALPCATLEDGRPVAGAMNIARPLCFTDASPPASPRT*
>TCRU_10242 hypothetical protein, conserved
MNCGGANFSPDGTIHPPARSSDADRTGIRQLPPPREGRDDTKSGGTTAPQVNAEPSRQNE
DWRQSAAADGPKIVDPSPASNTESNTSETKPELAYV*
>TCRU_10243 GTPase activating protein, putative
MGPIAKWLVIDLLEHSDPQHFLLVKDGVTVKGNRARNGVGHVGRIILIRKEQTECEVVED
EDDTKDSAPSLNLLFAEEMTGNEFPTPSKRQESGEYFLVWAPYSFFEFCTHNALRPRPDV
SPGATASTVESLEWRYIMCVAVKNIAKIRRCSLPDGTRVIELFFLDGTTGHPLIFLNGGV
TKFLDALRGIAPLRQSSVTADEFLLYANDDAELGANDCYRSVSRARSSGGGLNSEKRASF
DGQERGGFYSVPAFLEGLTQPDDMEQMLYERRDLSRIPRLFATLATKIGEVRLRRSRHLI
QNYGKSMSTYPVSSSPTHTEDSRTEEPFEFVEELIPVECQTPQIPEPRNRTMGPPLTAEM
WNSCFIGEERRIDRNRYAKAMAIAHAGGIERDIRLQVWCFALHVYPDVLESTEAQRQSVR

DVYKSMYERLKEQWKGIFPEQECHFSAFREMRTSIEKDVIRTDRSHEAYVDADGVKQRML
YNVLMTHGMLNFDLGYCQGMSDVLSPIAILAETEEEAFMCFSRFLSERCEGNFRKDVKVG
MKQQLEMLQVLVRFFIPRLYNHLVRQCAEEMSFCFRWLLMFFKREFSIDDTMLLWDVILT
CPYTPQFELFVTAALLKALSPQILEQHLTHDELLKFTNGIAGKLDVRHVILLAQDFYDGV
AKCAMAMERKEAAVGNNHRPAISEIFSLLTLAELEDSHAVSRFGF*
>TCRU_10244 peptidyl-prolyl cis-trans isomerase, putative
MSLPCTNSLLSRVTSIEKAAEVAKKAAPKVVELSEEAKTLPPHVRGVTDPTKLNAQTPFF
KCPPWAGLPAVACHLQCSRDGVPLPSFGLERFPFYLFGRSRVCDYVLEHPSISSIHAVLV
FHGDQQCFVLMDLGSTNGTKLNGSRIEKKRPLPVPIGSCIQFGFSTRMYKLSRGPPPSSK
RLREERGEKAVVEEKAGNMHSGNVDVKSRLVGDVASSSTPIAAKTADETQGDEAFVAGTE
NHQREVNVAKRENGVSAVVATPYPPHSSSSLAVTATAMDVTKQPGTVTASDPLPPVTPPP
PVKRHLYQVLIKHKDVRRPVSLAPRNKGDKITRSKLDALTLAEAIRARHGDQTSVWSLDE
FTAVVREYSECGSAKRDGDLGMVESGTYTEKFDAAAFSLGCGMVSAPVETELGVHLIYRA
E*
>TCRU_10245 Kinesin motor domain containing protein, putative
MSGGGQSRRSSIDVLIRVRPLRAELQEMKSAWDISASTLREKGNPDSLFTFDHVYGTDTT
TQTLYERSVRNSIVTNVVKGYNGTVLAYGQTGSGKSYTMLGGSVSGDYSSPDGIVTLAVR
DLFSDIEQEQQRNPSMRVTVYVTMVEIYNEQLRDLLAPPGAATLPLLIRENEHGVYVHNA
IKRQVASARECVQVIHTHAAARVSASTAMNEMSSRSHCVVRILVERIIPLEDVSDFFFMS
SEEEGETGDGMKRKIVAALNLVDLAGSERVAKTGSTGVRMVEGGHINKSLTILTTVISRL
TEMSVSGNGSSGATPTFVPYRDSRLTHLLKTAIGGNSLTAVFCCITPAVQHVDESRSTLQ
FAARAKAIKNKVSVNEVADSKTKLRMMEAEIRRHKRMMLATTIYLWSKNVRIKHLQEKLD
ELCHLGAADPAAAASASGGGPYALRTTPKEQQRVIIEELTRQNGVLQQELAEAREALERQ
LGPENKTLAGTQVTAAVAMGLADDGEKQQLRADVRDLEQMLKETLDEKSAIQASMDELDN
FCKELEEENAAHASANKKLQTTCQELQKLLDAKEGADCAAMEEVNLLKEQLSKTQSNLLE
KGRGDEYLQQLTKLHIEHQELQYAHHQLQERHNREMNEAGVEMGELRRKIDELEDEMAEL
RDANKLQNSYLWRLLSVASVVSRGKAVDGDEITSTVRGAQVDAAVKTLTTFVQTSLEKNP
ASFGSHNDVQLTPPNWKPQDEHQQGIIGNGGNKNDNSKDNTVLLKRIDELQKQLLAKDAQ
RDVIIDSKLKRMQNLALRLHTNNAAFVEELRRSYTLCEELFRFVEKQPKLAPKLAKAGLE
PMSFKAAIDRALQSKIPTKPYGHN*
>TCRU_10246 proteasome regulatory ATPase subunit 1
MAKEKGACQTANTVRVKDKDNEEKEIIPLDQDDIALLKLYGSGPYHAPVKELEEFVKTKG
EEVNKLAGVKDNELGLAPPVQWDLNSDQEVTRSENFLHVARCSRILNKGQADAKYIVNIR
DTAKYVVKLGNRVAPEDIEESMRVGVLLGYSSIHIEIPLPPRIDPSVSMMQVEEKPDVTY
NDVGGVKDVIDRIREVVELPITHPEKYTQLGIDPPKGVLLYGPPGTGKTLLAKAVANRTD
ATFIRVIGSELVQRYIGEGARMIREIFQLARSKKAAIIFFDEVDAVGGARGGGDGDDEIQ
RTMLEMVNQMDGFDSRGNVKVIMATNRPDTLDPALTRPGRMDRRLEVGLPDLEGRTKILR
IHAKSLSCEKTIRFELIARLCPNATGADLRSVCTEAGMFAIRARRKTINEKDFLDAVNKV
IKGHHKFSATAKYMVYN*
>TCRU_10247 endoplasmatic reticulum retrieval protein, putative
MPPRDITGKSSAWDEFKRKAHLTYQRYLDKTVPHRAMRWAMFGFLLMFYIIRVFFHGGFY
VITYGMGIHLLYLLLLLVTPLAEDEFAEDSPLPRTAAGNDGEFRPFVPRVQEFVVWKSMF
RVVSICLFLTLFNFLDIPVFWPILLLYFIVLTVTQMGSRIKHMMKHRYVPWNAGKPKYVA
KATT*
>TCRU_10248 Uncharacterised protein family UPF0066, putative
MVVMEQKGAVGPSLPGSGRIPRRDSSEDDDGDGVGTVKSKKQVERNRPMRLGVRPHYFLP
GDIVWVRPAALPYWPAEVVQAELSTNNITARLFDPPPSLSLQADGNFSRDHVTVSATKVF
FFDRLSTPEEVEVCIEQRLQRKTHNVSAYEADFQRAVLHANRLVRIVLSPEKLQPRFICG
VGVVHSLMRTHISAPRQPHTKNFTPQTAVIKLRVGLENAVRDLRGFEFIWVLFLFSYATD
AEDTGDANGPGVLDSIPGGTQRRRRQGAENSAGFKTMLVPPRDSQLRGVFATRSPHRPNF
IGISCVRLVAVQGLEVHIADHDLLHGTPVLDIKPYLPYCDAHPNAKAGWVEELENSGRVG
ADHKYDMQRMQVDRIFEDE*
>TCRU_10249 N-acetyltransferase, putative
MNNEHVLVGGSRLRLVPYLAHHVPRYHQWMGDSELMHCTASERLTLEEEYENQRDWLCAE

DKLTFVILAPLSIAVNKAVREQRGNTAFGENPVVRDVHDDDEGGGETEEVSEVEGGDYAT
ADDSQGGVKREAPWGCTSSTTAHPRRSYGACILANICPEEEQEEERRIGRTYVMVGDCNL
YCIGINEAVELVGDDDAHPNAHGKCFELGVMIADRAFRRQGVAEEAVRLLMSYAMDKLGA
SCFIAKILSTNTSSIRLFTMRLGFTFLKEVCIFDELHFIKRFADAAEREAWMADVAYTVG
LYDANTEKEMTVLHSMPDATEWNREGVYGRMGPVTQSLVFGVVRKNETEI*
>TCRU_10250 ubiquitin-conjugating enzyme E2, putative
MQDLQRIQRGTNSFFSARPIDGDLFHWRAVVLGPESTVWEGGIFKLQLDFTDEYPCAPPK
VRFLTRDMFHPNVYVDGNICLDTLKTEWSPILDVESLLMMIISLLSDPNPSSAANGEAAL
LYTNAKDKYEERVRHLVEASLEQSFSEDEDE*
>TCRU_10251 proteasome regulatory ATPase subunit 5
MSKDATATGGGRERGGGNATQASMLSNEELANIETLTNAQLRTRANQLQREIQQLKNEER
SRMNELQRLKKEVEDDKKRVKDNNKLPYLVASVSEILDMDDEDDEVEELDVGRRKSKRKQ
KSAIIKTSNRHTVFLPVVGLVDENKLGPQDLVGVNKDTYLVLDTLPPEYDSRVKAMEIEE
KPTEKYTDVGGLDKQINEMIEAVVLPITDKARFERIGIKPPKGVLLYGSPGTGKTMLARA
CAAATDACFLRLAGPQLVQMYIGEGARILRDAFALAKQKAPTIIFIDELDAIGSRRSDEG
GKHGSREVQRTMLELLSQLDGFGSSDDVKVIAATNRIDVLDPALLRSGRLDRKVEFTLPD
EEARARILEIHSRRMAIHGDVNFEEIARMTEDMNGAQLKAVCVEAGMLALRNDRVYVAHE
DFAEGVTAVQSRKKSSLNYYA*
>TCRU_10252 hypothetical protein
MLVELTPEKEASRVEAREAVLAAKTMLAAVSGASLLSREAFINICVEASLAFLREKRRQK
SNGDNGNRLKPNTSLSPHSDVKRSSGKKSYHHHRGGGNSDEKRNHAAKMKRRHDASVIYR
KYEQDERGEEQKKENQQLSQFSEEELGRLRELVEREYGVSRHGDAAGTGVVVPAQFTALP
PAKLEAATIIRQVLEDPYRRGAISRQQYAVIVLAVMEKLFPDLVTVTNDTMVSYHKSHSR
NRSSSGSSVAHDRTVEENDVQNGEEIFMEEEEMFILDPPQELHAALRPDVAELTRQLTER
ALQHYLQPDNNAHERELVGGEGFRVGCVINDVSPLPRNPYGAKKPQDFYQDSASTSMSFS
VQFDDAFEEQVEKLCQLLEKKYALDLSSARAANIHQRVSESRDNASKGANNKTGKTDCMF
TVNAESPSSCDGDCTGEAFTAAAAARERREELLTAALHYQEELYQTQTRLRGIMQELYET
EHSKSDSIV*
>TCRU_10253 guide RNA associated protein, GAP2
MLRVLRHSILVPSSVVAFSRHHQGGMQHAAANMMDKQAPKVENVSHEKVWALWNEGNLFS
LSLVQLQGFLARAGVRTDPSAKKAVIVRQVEEYLHSKDTAAKNGGQASPQQQQQQQQQQG
GFGRWNQSTVMQPETLLDLAQAGFYEGSVNMAPKAFQLLVSNTAADVVVSRVNTTAFPGF
PANTECYTLGASEKDVALRSRYSKVLQWCCLNMSNLQMDGELFLDFGKLLLQPSVMRKNR
SIVSSYTLQQRMQLNHPYTWVSTLPESCVSKIKEELLIPEGFMPLGKGAQLTYSGTVKRA
KDQLHLELDNKGKVLSVNSAWVNVQTAWCTHARGPDVRLLLRSRPPIRRQEVEMFASMPI
IQLSEDDVSDVLPSEHGQLIYLSEDETRLFEKVTDKGVKITVRETKRQPLIVLRDEEEDP
RLEYSLSVAIPANARKATDVRAVGLSAFELAGRLASIVTEDFVKEYGCEAKL*
>TCRU_10254 zinc finger protein family member, putative
MQGALSPVATAATKHTPHENRREHQRSHHAAGRRHNTVAAPQLNPHDHHHCEHFMQQQQH
GHHVVTHIEPSNTSHGVPLLPPHIHSMLYHSIVGYTAESSLSEGCGDNVGNMKNHLSIPT
NCLHTPSQIRYPPQSQTSCEFSAFMHSNVGGPASLSSVAAKIIPPRATMITPSPYSENVS
VGNFSASPSTTRGCQTTDTKRKLSNSSVVYSPGTSPSKGSGIPSTELTVRALERELRAAE
KDELLQVLLELSSCNPEAATFIQSKARLFSFRHTTTTGGKKGENTEDASEMDPSGTNKTT
AASVSAKTSQQPQQGLSFGIIDRCSGLLHVTPSKPLAFEEDTSFSNSCEKAASMSGTSPN
NLSSRNLSSAQMLLQTPPNHGVTRARGERRCATSQTVVVDAFVRAEDRPWCDKVHPCLRW
YGSCRYPTSCPFVSSPQSLCLNWVRGSCVAGSECSGVHRLPDACPSEVLTVFELCHGADR
GAVAHEKLQRQPHQQQDSQHGSHYNQQPCIYTDSNLQGRDGFDTPIGQLISDTAGIPASL
EHYYHELHYSKEINFPNQQQGKEDGFCHCRSCRTPCEEFDLLAGSQEEQSWKSSKYLPPP
VAQPVPRCLNDSFAAAESSEGRNTPGVTEKSIWREPTQSLTCQPSAACGAEYEEEASELY
PPHNSRTRNQSPVSP*
>TCRU_10255 prefoldin, putative
MNGQAAESGGGGSINITQLPLEQLEELRKQLQVDVNNLSVAHESLLSAQSRFLSNCEVLS
EYQKVCEAARASPEKQPEALLCISSALYASGRIVPSDRVLVDVGTDYFLEKSMGSARSYF
AGRSDAVRENIEALEQKIRVKRAQLAQVVDTMRGKQAALQQTSAA*

>TCRU_10256 hypothetical protein, conserved
MPNVRRCRWDHKTLPYVPERPCLLYYIIPGDTVPRVAVPNARGEYPHLIPGMPYLESEEV
GEEEAWGCARDDQVALPIMEFAPPPIQTDAATQVEWNQLPVPPLAHLQRFAAPPRQGGNE
LSSE*
>TCRU_10257 hypothetical protein, conserved
MGMLRESQPAGANNDDHFKSDKKDDSDFLLLLLLLLIFPVVFLAYFLTRYCRNYSYRRLA
RRIKLWGSGKPGDVDALGMGRAIDGGEWLKERKRQEGNPVEDNNLLLDLSKPVEEFDPIS
AEAEKHKKRWQRSRDLGDAESYNTEELNAEKDATADATDDGAAARGSAGSGAYDAATTRV
WLRNLVSGTYANADGTGVVHDVGAVPKTAATDQSGETGAGRQLYKASSGDGQQGQFLRGG
STGRSFEEILASLAPAIHEKGCAKQEGPAVTSEADEEVEEEDEEEEEAESSVFSRR*
>TCRU_10258 hypothetical protein
MHGRGGAVSSAREESFVYTSPILFRQMGFCKGGGSTAVGVLASPQRKWQEGTSGRNGGNE
GVEVEKNSPARPWRSGNFPPTASSPSPSPKESCGFLLTSPQNDHRGLFTSSMSSPATNVN
LATTTAAASSFGAWKDHQYNIPLEGAASFHEQVRDMFRRRVALAVPANGSNLLNVKESPC
NGLSPFQANGVPSRPVKSQAEWPSHDGFMASKWDMTDRIEHTTRNQALRILRTALYGIPS
SAVRQTGFTGNAADDDEIAFVSLSYSFEAELRGWLILEHAEVWLEEDMARQKVYMCEDHA
RRIMRMEVAKEIHVEKNKRRHAARMREAPSHFAELAEEERDTLLASIRDLEAEEAKLLKS
VHCIEQQVKWSQQNLSIQEQETLTGIKMERHEMISQLRQLEVRLEEAIEQRKRAVLDATF
GQSEGFLLTSSVPRCRVSQEGEIEDGCGLHRKNRDLTFSRSSATGGLRGRTPGSDPAGML
YAPTANGSMMSHLDGKTSSMDISSLPTLPVASSSHSISLNRDGRGAFSRVMREAMEAATA
ASTLPHKDYLPQSSH*
>TCRU_10259 hypothetical protein, conserved
MEVYRRITERVRGALWAHHGRLMPERQFHRILAYVYNNKYEHQIRFDRMEVVGRAWEGRV
EVVTTPAGYLKRVRVNPCLEELSSYRQQQLILAAYADACAQGRRLMEKAEINIYKQFLKD
LKPIVMGIRDNPEFYTVPEDSVETVGGTLHMGQGPTPTTYRTIPAAKAHIPVDEIRARQE
WEKKWLNSPQGQSWALTLRGKRYFALHGPQYRPRGAPGAKKVTMPLDLPAPYTSMDERRL
LKKNWMAYLDNKHMAEVMWTRAKIADREKLQRRLQETGQAWHRPINKEAVSRW*
>TCRU_10260 hypothetical protein
MSSCTGRSSWRLEGTLRVLLLAVSSQGVVGGHDTTGHVWSVVDDICQALVRLDGTCLQVY
SSSLSSATRGNVLRAIILTGDAGLHQLLLGRGEEKDTSLLKLSGCRVGAEAEGEKHDVPS
EEQLVEVISTHVMASMNNDGSWESLKLWNSPQWFIYVSGDTALHFTGAAASLPASVLQQR
PGIVLWFHPEEAPVVCDVPSPEATVWFADWWRSLQRSLLLPSVEPAMDLLLFGRREYSGD
ATAPCLTPGCLLVVEDDNGSWQVDWNHTPFEATISSHSMTPLLPHEEIGDFVRQSSFCFP
TEMEDLPIPKKGQRLPDRLSSEDVLEMLASEPVAKSSTEYSVSESGEIAPLLQLEFIQGC
FAQIFLCIFADDTSLKPLSFAEPPPFRSSSSSSSSLVWYLQLVMQYAETGGTLTCALGGS
PQLFLTPSADTASRFFLSSDEASNKESAGWNLHSVDHPGVLMKAVPSKNGWQFFLFSRQA
MSPTPCVRVTVTSANREGAQERIFASEAAASSCSGLVYPETRVVLEDELPKRQREALFWR
VRVVPPENAEELLYLAVNLDSFGLAAVQTTELSNTSFLPVYASLTPLWRAHIMTQMKRHP
HSCGIGPRASCHLPFSLISPTSFQSCVTLGSRFSPMSEKDFFSSCFSLPEKMKRGAAFLQ
EMAGQCHLPLFVAASARFRQEPLHVVFVGSSAVGKTTMVQWLWAWSRGWGDAHMLRALHN
WLQRRGDDIVEGNGEEDEGETSVLTALLQSPLPSPLLGEETTTKIQSHQRVELEICGETH
VFVGHDAQFLLQSFVGVNEAVLTVTDAGIPVSVKVVDIPGSSPRELLRTHCKAADVVICV
VDMQDQFSLSWLEERLDVIAAGSSLEKETEWSGSFVAARIWQQQQQQFVLLKVNDESPRQ
VVFSRDVRRFLRRSGEVMRTPNIPWLLWSLPCVDEGAILRCSGMLYRDFVKLLQERHACR
LVFAVMGWENDIVIRLQKLACRMDDNDGHSNDNTMREQPRMHELFEEMVSKELGRTIPTL
SPSICDVVAKEVLRSGATTPLTKGLPLWWRVLRWLMMGFSISDPLAHCVWLAVQTERENK
SVPGQTSIGNNNNNNIFRENEEGRGNNDVDDEGDDLEILDALSNWWEHPISLRRLRFFLE
EFYRLRWNSQQSSMDSFVFIALLARDVAKLTFVNISLASVGTWLGHAVGSGNRISDGGDA
VELFFALMFCRMGGERLSAVLPEDTNKRTKFFHESLIMSLVVFRLLHDASPLLGALHCML
PQEGVESNSMVSIHGNLVLQRIHNPFMISTEEEKLFYAVVKQAMGSGSEETVCKLHDRPT
PSSKEWEFIEDDAETMSSWNGTLYFENKKGRRAKNAFSVLEVVRSFRKVWPEADFDYPLE
WYNKWTEEEEARFIDAFYRAIQRYEDGEHELRQRVCGDEALERFAPPRRTYIVTQPGYTE
VDMELEALYCGDATTVEEEDLAPLSR*
>TCRU_10261 50S ribosome-binding GTPase, putative

MLFKTPTWRCASSITFDLLGRMPLRSPPRYAQQQSVTRKVADGPSLAALPAAPSRRPRHA
TQQALLEMVPEPTADALCPSADAVDDDIVLDGVHAKQLCEVAASSERERLCEHHPAARGV
GSDVIDLVTDAFKEERERLVAQRRRVLYEMTHPNPSDYTYKEKLVPPPPLSFGKITEEAK
QLGNKVMLGQQYTLVRQAGLLREDEDAGSTAVRGQQRRARRKPTLYDNHNYFFEVNDLYQ
EIVLVGKACAGKSSLLNALLGQTLAKTSSTPNTTRQISFYQSVSPEEMQRYLNVKGNGLV
KLPGGGVQLTFVDVPGFGIEGMSDHWRDKAIALTDAYLGVRRSVNTVLFCVDCERGLTKV
DLRYFTWLENLHGVFFIVLTKCDSVPHSRVCSVMQQIYATITKYRRKYRKVFPFILPTSA
KDGTNVELLRGLIAETSGLIPGDRLRQMLKAKADADMDAALKEEARRVQEAHRVGTQKAK
AFFTALKGEEMQNPPDSSAGTAPSLPIQMNSQKYVLSLGGNDRAAMNAHMSASADEPLLL
FHSEDSNEMMKKKKNKDNMRDASYHLGDVEENEKARRRQRFLAWRHTHPLHRYKSDYGTF
RLNTGLERPDAEWLELPYMEANVKDDSDDVKGGECFAAAPQKGLTHVQEEEKNNLRSINP
TVLTGDTAMNDEEYGKTTPTRADLPSAVIGLGRTSGRSVMRQQTNGVVSCFLGVLEKYAS
RDKQMGRSKRQCAKEAMWRERVNMGSVTRFLVEEEDGRIGEYKAGKKFGPSLVEPCNVEK
RRSQWAARQFAQQAVTVCPTSPWTALDVLRKKRERIKQEAAMRGMTKKDLQAYLRNAGNV
IEDFEKFEGEVTAAKYMNEIRQAKTLRSREQMHLNSTAKISYRSMPVGLWKRYGERNTYW
PTSRVKGR*
>TCRU_10262 hypothetical protein, conserved
MINKNTEERDKAKAKLLESAGVEMAKLVETRSRLKQLDDDQRYHFRRGTHVKQRHVSSLK
EQDIMKGRVYKDESRQFGDVVLLEDECKDLTEWVNGAKRELEDNKRSYAKEQSELEEQLQ
VMEDNGKEARELRAFFERENDQLKGLKQDLQRVMLYARARHHELLA*
>TCRU_10263 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MLVTLPVYANNAEKGQVNEKGVLHLWLTDNTHIVDIGPVSDEDEDVAASSLLYKTDNNEK
LIALYEKKGDGEPSPGMVSVLLTEQLQRVKDVLATWKKVDERVSKLCPTSSAAKNPSTAT
ACSAGKTTDGLVGFLSGSFSDNTWKDEYLGVNATVTNKEGAAEADNGVTFKGRGAWAEWP
VGKQRENQLYHFANHNFTLVATVSVHGEPKSGSVSLMGVRVGTDGGTKLMELSYGSGKKW
QALCCDGTTKRLKSTWEPQRQYQVAIVLRNGTQGSVYVDGQRVCESVQSKFENTESKGIS
HFYIGGNGGNAENTAGDEGVSVTVRNVLLYNRPLTFTGGSADLEEDIASASEAPVEQAAS
QQSRKKRETQQVPAALSSHAVGEKTGDDGIVRGSGLLPLLLLLLGLWGFAAL*
>TCRU_10264 HD domain containing protein, putative
MHRRRLRETTLLDRVHEHVVLPPIVLQAVDTVAFQRLRSLKQLGASSFLYPGAVHTRFEH
SIGVAHMARNLLMSIKRRQPDLGIGDSDIDKAMLAGLFHDIGHGPFSHLFEDVITTRCGV
PFNHEEMSERITRRALRTLLPIDEVEDVVALMRGRCGPSTKYGEIISNKRSGIDVDKLDY
FIRDSLCCFGKPTVDVRVNRLFNSARLVCEDGQWQLAFEEKLALSLCELFTLRAKLHKNV
YQHHVVKAIGHMIGDIFHLAAPHFVVGGHTLLECAADDVLLLKLGDWVLEAIESSSDERL
QPAHNLIARLRARDIYRLVFSRTLDPEAELPPFWLQQLSTDILACASVSRPFTESDFIAD
LVVIHQGRGRSDPLQSVLFFNPKRPSQPLSKISPGERYSPLFTPFAFEERTLMVFERSDT
AGAVRAACERLVADDSHQHFFVETLPFYNQS*
>TCRU_10265 Trm112p-like protein, putative
MRLLTHNFLCCIECQSFPLQLRDVEVEVLPCEFNSAFIRLMLARMDYGFILAAFNAMKDG
QQDLLESASHLPKSLEDVDLSDQSEDLKAIHHVVQEMAVRNGRLVCQQCQREYPIRDFIP
DMVIEGK*
>TCRU_10266 kinesin, putative
MEQVKVALRVRPLLPTERERGEDANISVLPGGTNVRVVTRVNRGTQNQLHTFEMDYCLGP
EVNQQGVFVGLGIADMCDAVFEGKAATVLCFGQTGSGKTYTMSGQAELEDTGQMARDGIQ
FAAARYIAAMRDRLMTVNGDASMTIKLKVSYLELFNERIKDLLNGSEGLRCRWSRDANSF
FVEDLMLVECLNADDFILALQEGLFRRKRAEHFLNTHSSRSHVLFTVYVEVSEGDGPTRH
GKITFVDLAGSERLRDTGSQGDDSKSINRSLFVLGNVIEKLSKCHPLGRKDHIPYRSSVL
TQLLMDTLEGGCRTLLVACVTPSSRFVEESLRTIHFAQRARKIRSRPVERVDAAQQEIYD
LKMEIRQLQNENALLRRALNLSETGAVDQILIQKFKQKKAEVTVTSTPAPAKNAKNTSIS
DHPLLKNATHREEMSHAHSNRESVQRPTPLGILDRLPSTCDLAARPRLLSPEMRHSPSSM
VSSSAAISAEFGFRAVPQKSNLLFWT*
>TCRU_10267 hypothetical protein, conserved

MPSRGKPEGVVANITAPVPSFQDEKFIERLLHYITQGDDTSLVMSTAKALGAEDYMIDLK
NQVVLDLRIDFLRFCADQKYGPSQILHLMRWMDHFQSVVENGCDTEEMRSELMNFVSSEI
EEGWKWRQTPPVDEIATEPPPSSKNLSKKGMRATDKVAIEEVEAAALLPRENIYLTKEGV
GPFCTYLLHGIIQHASLHAYLACHQRETRAPNDIFVFTELPVIAPPLRLYNALEKPSTEP
STKNDMLKRLRGTELALLMNEYEETMIKEELWRKTKQTEDEMQIFIENDGSKRAVEDTYE
RLEADLTQRQRRILQRITALEKKLSLTSSTQTL*
>TCRU_10268 amastin-like protein
MSFLPDRDHGEEEVCDSEHTAPPPQEQRQLPPVAAASSVPLQPRVSHEEPLTATCDAQAA
VSRAGGAGDGGGNVKVRKLRIFDDITTTTSSSEMSGRHVSTIKGHSVLRHALPPPRESDI
AEQNMSSTVPPTQPSSSTQVAPEAVAAPVSLHQVEISVSNRAGDAPVAPAEVRSSRGPEG
RAWRGSPPGSRGDAHGEYSVVSMSKKFSEKIEEFWEFGTQADTHVLVMFVSSVLSFVLTV
VAAPLSQLDMVWGACYTYWGYKENCDSLIYNNRTPFITCDPVRKRLQAGAAFSMMTVAFL
FVAVVCSGLLLRQNLLKLRFFTLLVLTIALVFQMLSWALVASILGARYCEDRSLPRTTTY
GVAFGMSLTSWFFIIIGALACIVPYFY*
>TCRU_10269 PRP8 protein homologue
MQSEDDQFSKQNGTALELVEEWESRHGRIAEWRRLNTERYGYRAAYHEAVTEKDDVPPEY
LRKLVKDNGDLSGKSFGTERKLCVALLKYMPLALYKLLENMPMPWEETRYVNVVYHMGGV
LTLVDDTPTVAEQLYLAQWGSMWTRMRSHKVELQQEGGAFRRMIHKGNENEPPIEYGDYI
MDREPPEAVHDELDEEDSAAIIDWFYDPFPRLVHPNQIRGPRRPNGYYFSINVVECLFRS
ASPILPTLDDRNYYYLWDLKSFYTAKAMHLAIPRAPKFESPPAVCEEDEDWTEFNDLRRI
IHRDDPRRPRFTMLTERQIAFPFLYGSVVEAVTVAPYHYPAEIRVENEDPALPCFSWNPS
INPIKALKRNHAEVTVTNKDVLCSVALQHVQDGEELVKTEEGICRVQLPANFAPFLEDLS
LEDADTKQAMMLAFAPAPYNRFEGEMKRRVDIPVAEHWCRDPPTLVTGDTRDKTLRSYTQ
LLKHHVAKNLRRNRLQARKRHRENTEEVLQPSRRLDELGRLKFFQKTKVDWMEAALQVMR
QGHNMLVQLINVKCLPYVHIDYNFEAKPTRTLTTKEIKKSRLGPAFHLIRELLGFMKQLI
DMHAMYRLGKTDAFQLADATHYLFSHLGRLTGVYRYKLRAMRQIKRTRDLKHVLYSKFNV
GEVLRGPGCGFWAPAWRVWVFFLRGMTPLLQRYLGNLTDRVLRGRESKGKYDGKRITRQR
VETDKDVNIKEAFRRELREMLPEDVRADVIRTMDQHMNEAFRHWRAGLQWSVPGLARPLT
ELVNKYVKLRAEEYIRVTQYQRKRINEGDTVDKQAFMKNLGRLTRLKLMEEQERQRAYLE
GRDALVISPEEAKEIYRMMANWLTDRGFKKIEFPKVSRPAELRLLELSLNRLRDQHNIAN
RLTQAQREEQARIEEAFNSPHETLSKIIDCLARVRRFKNVEVEYMDTFSTLYPIYNVVPS
EKLVDSFLDQYLWYEAMDQQRLFPNWVKPSDMEPVPVLLYKWCQGINDSPGLWDVTRDES
TVLLHANLEDSFYDNVDWNLFRPLLEMVMDKTLVEYIVSRHDVVVEFKDMSYQCRKGLLR
GFMFSSFLSQYWGLVVDVLLLGTQRSQEIAGPARRPNPFMTFMRDPLLATSHPIRGYCRY
KNEVYVLLKYTKIEADDVRRRYLDETKHDSRRRSLNASVYGFKNANQWPRDARMRLFLND
VNLARAVLWEFRGRLPPSIAEMNESNTFVSVYSKDNPNLLFDMGGFSVRILPVCRTEEEV
LENESTWNLQHAKSKDVTARAFLQVAPDHVNHIRNKARRAIMMVGSSTFQSIAAKWNALV
TEIVPYYREAILGTDSLQKVLARAEHRMQSRVMMALNSRSKARFPPAMFYAPTDLGGLGM
LSVGHSLIPARDLIYSRTTSTGVQFFYSGLTNADDIPIPNVLQYYTPWETEVRESVKAWT
EFSVRDREAKAAGTRLSLDDIEPIINKGIPRIRVLFSRHAKLFQFDKGFRCRMEFQRFLS
GKYLKNWWFHPEHDGNICGGVLEKYRVDIIIALGGVEAILEHSLFKGTGFPSWEGIEFNR
SGGFENSKKDSKLAKQQRAGLANVPNRRFALWWCPTINRADVQAGFESKIDTTGVFMCGK
LETIKKSLIKIFSGSLWEKCHGAVVNDIASKMKDAMADLDAASVTLQQQHPQKSYTYTSS
APDVVMVSNSRWPVTAKPTVLSDEAGDEYRSHLTSKFWIDVQLRWGNYDSHNIAEYTRKK
FYEYSSAKMYPFPAGIVVGVDLAYNCHSAFGYWIPQLKPLMVKLMSAIMRHNIALNTLRD
RMKRELQLFSSAPTEAGLSVTNIAELFSEGMRTWIVDDSATYVTSEQPTAEGGRKFRSEN
GAVLLFEPTTGQLKLSIVHKSVFAGQKRRTKLAREKAAEEIASWLRSTPATQRPGKIIVT
RSRFRQTLHNMLVLDYPNIIIGQSDLNLSIPMVLRHSRLVDLRISATESKGWEFCLYDDW
LQQFQPATCFNLLNLILRGYHVNLNRTRETLVPDLHVEVHHSHFWPTYTREEWERVSIRL
QEMIIADSARRMNVSPNQFTEMEKKDILLGKKMTTIEIQEEEKKELEEMRRTKLIQEQTV
NVTVKSGEKIQKKIKAAFDFGNSTTSSNWRTRSLADAAAFDESTTIEIDALGAVASSDQL
IIPMETLKLFIPCCDVQAQCCAYLFGQALPEAPNIKEVLCIMVPPQKGSAVECTTPVHIP
HKHPALVENHLSLLGVLRCGGGEPALHSRDLALHGRLLASNDELQTEGLVTAVMGISQDG
LNMRCYTTTREGISWALENYAKALEQEPTEVAPKHFAPCRATLSEDLQGFLLVPTGGDWN

YAFKGATWRESTEFDVSADIPVFFFAAQHRPDHFLNFARLSEEEETIDMADMDDTMA*
>TCRU_10270 24 kDa calflagin
MGACGSKGSTSDKGLASDKDGKNAKDRKEAWERIRQAIPREKTAEAKQRRIELFKKFDKN
ETGKLCYDEVHSGCLEVLKLDEFTPRVRDITKRAFDKARALGSKLENKGSEDFVEFLEFR
LMLCYIYDFFELTVMFDEIDASGNMLVDEEEFKRAVPKLEAWGAKVEDPAALFKELDKNG
TGSVTFDEFAAWASAVKLDADGDPDNVPESA*
>TCRU_10271 24 kDa calflagin
MGACGSKDSTSDKGLASDKDGKNAKDRKEAWERIRQAIPREKTAEAKQRRIELFKKFDKN
ETGKLCYDEVHSGCLEVLKLDEFTPRVRDITKRAFDKARVLGSKLENKGSEDFVEFLEFR
LMLCYIYDFFELTVMFDEIDASGNMLVDEEEFKRAVPKLEAWGAKVEDPAALFKELDKNG
TGSVTFDEFAAWASAVKLDADGDPDNVPESA*
>TCRU_10272 EF-hand domain pair/EF hand/EF-hand domain containing
protein, putative
MLCYIYDFFELTVMFDEIDASGNMLVDEEEFKRAVPKLEAWGAKVEDPAALFKEIDKNGT
GTVTFDEFAAWASAVKLDADGDPDNVPERA*
>TCRU_10273 GTPase activating protein, conserved
MMFSRVKDELMRRFSLATPERNDESFHRKMPIAGLQSLTALPNGRENTADAVRKKSRALP
EEESLYDEAALRKVLAKDTVELDELCSTCRSGCPATFRREVWGYLTGNLQPFLSSRATVL
ARKRQEYVGYVQSSYSSIDWDAALRAVETGGTACVNLAPAEIKDGDDDTFVGACATSSVR
QRQVVGGAQYGIASESELRMLKQIRKDVPRMSAGVAYLHHKRVMLSIERILYIWALRHPA
CGYVQGINDLLIPFISVVLSSQFCSSKTVAELHSLTARELDELFSTDAVSEEEWMCTIEA
DTYWMASHLLSGMQENYTYNQRGIYSMVRHLEAVTRVVNVKLYKHLIEELQIDFNQFAFR
WMNCLLLRELNATQSLRLWDTYLADVERDWCTTHVYVCAALLIWFSPVLCNERDYGVVMK
FLQNLPTEELSAQDFNALISQGVMMQKLYNNALRHLL*
>TCRU_10274 hypothetical protein, conserved
MKPGVRVENMETMEAPALQQPVKSGRGGYLRCPFDIDSAFAAVAELNAAGGALGHKTHRP
HAVRGSGAGNDGDNDEDDVCRPWNRAGVGAKALSAKERRLQQQDAERIYGSMAACNVDEN
TGDASTVPDKGLAVALSTWEKTALQRVLPRGVFKRKRQRNNENCGEEAVDGEGCNEVGRQ
QRQNNVLGRRREGEELSLSAGVGDSHRKTGGDQHENAHPREFGGSYATKKTEEQSRTEKN
KPINRLQRLDAIRNAALFGKKK*
>TCRU_10275 ABC transporter, putative
MTHTFTDPLVDLASVSFQYPHGGGGSAGGIRDVSVRVNGGDRVLVVGHNGSGKSTLLSVI
AGRRKASSGRATVLGSDAFDDTRLQQHVTLIGRPWPTEAFFATTVDQVTSKAPLPERKRS
VADALHLDLGRAVSNMSSGERRRVQILHGLLQKSFVYLLDECSTDIDIAERMTVLDLVRS
ECVVGDSCCLYATHIFDGVSDWATHLLLMQGGMVVDFKRVSDLNAPLEVFVCHFLTRRHR
DLFDYTSKRMPVKEAYNDDWKGGGTVTALPSEKEAVIVCDRLQYRNIFRNLSFTVYRGDR
VLLCGCNGAGKSTLLKMMGGKQFFNNSNGSLRIFGKSCYDGMTLNGLVAFGGEWWDTAPP
GEMHVHEMLQLQTPRAEWLCKVLGVDLSWDVRHISTGEQKHVQLLLHLLEDKPVILLDEA
TSDLDLDQRQELLSFLYNESANRGVTVVYATHIFGGLENWPTAVMMLDRTTQGLHAMWRG
SDVKWAEITRELIALKGRENVK*
>TCRU_10276 hypothetical protein, conserved
MHSALRLHGTGPAPALAMLIGFPFRYSIAAAPNFDAEFHKAVCPSFAAFSSGCGERPVRQ
MRWASQRSQVWCWTSSGPSAAAPSREARAANFHPKRRAQGHDEVVRFSGGVLRVADNGGT
KTQSITTRLASGRGCSFASNTAHFILLTLGFHATILLACYFAGSGVQRDVGKATQQHTLT
PCVASACGSAMCTGLSVSLLVPHAKDKIVASWSGR*
>TCRU_10277 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MKKDAFAAAAAKVPAQEVAAQTTNVSEPSRHPANVPVITPEAQQDATSSPRIQHSPAQTS
ERESGPADFKQTFPDIIVPSTSAGVGKVEEEAPDSGALASASSQTQNAGSHELIGTEMPF
SGEHFPPNIDLPLMGQVDTADEESPRIGNTDDQAPHSVSPDVSESVGTNSDPDSFSSTNV
SGGADAAPAPPSTAPGETKIPSELNATIPSDHDILLEFRELAAMALIGDSTVHVCVSRVL
LLLLGLWGTAALC*
>TCRU_10278 hypothetical protein, conserved
MLRSMLEMNRTPLGMAILGSQTIASRSETKQARPSTKEGLNQLIRSRTDWKERVVFRLAR

ITASRWSEIAALTPKKCHAGAERDLNFVLARGTEDGESGSPLRLAVRGDARAGRLRHYKA
LYDTLKQRKAHEPDDCPGGTSSGSLECHGAFHKTRCVAARCSNRGDAQFGPTADLAVGEA
RRPVRPSPEHGSIFGEVHHNADPGVVAGRIDVKGEAAEGQEPWLRAEELFSMIFTIILPQ
LRDARQGRVWPLHKMNETSRYSRSTCLY*
>TCRU_10279 hypothetical protein
MYRPRKLPCFSSVRRSSLHLSPRTVSSTGHAEDSVAGEKLRCANNNDRVGLVFCECFKGM
EKFLVRRPGCPPQQPMTSPLFTTASGVVSSSAPPSTSGGGSVRSAKTVRSFFPGTSNLFY
DANAPNLHRENLSSIPGNSGPKHVGKDLHGNNSNGVRQHEVRSPLMLQPTTSFAGQQTTS
DKSTAEKATAYADIQRYSYAYALWQNRNAALLQMGVDMQEMTSKACYLRDLHQEDLKDGM
RQTTRFSFYVVFPFVFLVSAVLFNESTLYSAQLKYLRLVDYDAWLEANGHNSGRRGGIVG
GGGGGGGFSRYEQRR*
>TCRU_10280 60S ribosomal protein L38, putative
MPREIKSLKEFLAICSRKDARCVKVKHNPTQTKFKVRCSRYLYTLVVADKKKADKIERSI
HPSVKKITVTARSHAKTNAGSK*
>TCRU_10281 hypothetical protein, conserved
MLRRSCLWRLGNYRQHSDKERDRIAQERQRRILYDHAGNVKLSGLLFLFWEEFRLPILCV
AGGIVFLIGYNKLIYYLSAKEFAHEKSIDQQSEANARLSGKLKGDRYLVKPRRQLDDPDF
LNIPSYAGKGVYSSKLFDDDSASTDPLFSEKRRN*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MGLSVRGSGARVHVNVTSSMMDSGALKFRGDFGASSQILVAGSTLVTKSRHATAFWEFTL
GTNSTLLLLDNYIEANIYALSFSDSVVDGGGIIMKGNTLRATGNDDGVESAVYIETFDVG
NGGYFDVENNTMSGANGIYLLGGTTVNSAGLLRVADCSFAGSTFPFDSTLIYLDSSVTLE
GGAQWRVEGNEVSAASVLIMPKSAYIIQVSGSGTTVALAHNRQVDNSYPFADLPLSKTVV
ESPARFVVGCNLQGGEEVSCDGVFPEDVVLFICGTCNDDAACYVPGTESVDRSSCSCSCK
EGWHGASCLPFEVPNAVVPPVAERAVDGDTSCVVNQTLKNLTLNMWKTHHCYVGVTFSGV
GAVLTFFLDSMPLHLLINITLTGCTFSGGAALQFVGGAGAAESSGVLIRVSQTVMLSSVV
AFSLSLPQHCDIAVTEVDALQSSEAHLQESANNMWNVVVLHDVVLTASSLLVSNVKAHSK
RYGAFGFCSTGTLTLVRGSSLYTRYCSFEGYTHLFYVYRLSVRDHSVFALLNNTMSSGRT
LLFQHSRFSVSDYSVLRVVGNSGFVSCAISAHIPWALQNSSWLDWRDNDVEVGAMLCCFS
SATVSIDSSSVVTLKGCKMGSTGLSVPLLSQSDAGYQFVAGCLTVAGRLVTTAAELELNG
ITNVTTVVACGQCTKDGDCFAPLTTAVIDCKCQCAAGGHGDVCVPAPMPAGPPPPLTPST
LPTTPPIGVCISDMVYSEVAHAVGGGLSWLCYRNVTFSGGGMSLTVLIEAMTGNVANVTF
DGCTWRDGAVLLLLGNAYAAVGSLNIVVTGNTFDDALLSPEGVFPPHTNITISGNRFTVT
RLIPRSGLDIRRPSCVAMNALAISNGSAVVLSGNVFQSVRASSIAIHVVRSALRVSWHSV
FAVVGNTFHMAGSDGTLIHLEGTSQSFSLSVLNNSAMVIRGNAVSRPVRYVIIFVWVFCV
ESFSAVVFQGNDMQGSLVVFFSGFYSYIYYNSWLQVSGNFCRESPSEAFAVFNPTVNLRD
STMSVSGNQFMFGTGTPTLIKIPKRSSDLTNGTIVAACNTGSGEEEANYVIPSVYNATIL
TCSDPCTLAASCFPAYTTTASSDGCACACAEGGHGDACLPVAVPEAPSTDGADLCVRDVR
VNVEVNAGLGTSVVCYVGVTFAADVVVDVESMSGSVRNVTLANCTFVGGASLYVVGWRSD
PPAGERADALISGLESRSGGGVLVANRFPPGSRVTVVDSVLIAEKRVAYRGAYGLGDASA
CLVVHNVNLTGSVLTIARTHVAAVFRDAVGVLVFGDVALSSRGALYLDGLLVQTALGLCV
SVEGGVAASGGSVVAFVDSDFLLCKHAVSVREAVSVSGAAVALVRSDFSSTEDYAVAFYS
TVSLADGSMLLAKGNVHDGVSREMLYAAGAVTAAGSTLSFVRNRALLPRMLSVSLSLSAG
AHLRVACNDAGGRFLSTAEEYAAAGFGDAGSIDFAGCDACDRDTHCYAPGTASASMRNGV
CVCVCGSGGYGEACVPVGAPALPPAVGTAPSVFVREGVTVRSVFVVPAGASEVTLRHVVL
DGVSPVLYVPWMARDGMRIVVQNVSLLNGAVLYVMGGGGVLRGAGAAGSDESGPVELSVC
DVEALNGALVLSGTFPPGSVLTVTDSLLVAARPTPLVCLPDSQSSPYAPVLVLSGLRLVR
SVLVVSGVALVTVMTGGRTVVVDGAVLELVGGGVALDAAVLGGEYALYASARVVASEGAV
LRVSGSQVYAAHGLVFGSGVVANASTVVVNDNAGVLTDGALLVLRGSASFVSGSWLSVRG
NSISGRLLSVPSYPRSADLVQSTLTFHGNAGSGTVVMDGTVALGGAGRRFVVGCLTLNGL
TLRPIDYRSAGIIGEFRPVACGVCDAEVRCFAAATRAMTVSCRCRCAEGGYGRDCLPVYL
PHVDGCNRTPGMPLLSHTATLTETRSPTPTWTPSPTPSLITKHYSPTRYGPTETLQVTET
VALSPTRTPTASVSSTLWWSDVACPTLTVTTTAAGGSLTQNDIRGGGSAVPTRLMVALPP

PFRWARDPQLGTHLSFVPVSTAQPSGFGGPWGAMLRNATWVRNATNPSTVLELAVPVHRG
YFIVADETIVIRCGAAAVSGGCKGVLLGSFTIRSNTLPAAASALSAITGVVAGAAAVAVV
VTGGLGSVLEMQALGVFARMSCASAQERASTAALPYFLSVFAALDPLWMVVGNALLAAVF
GCVHCGVTAAFQRWRGVDAASAWAAMRFPSLTYVVAHAMHLGIFFGSVLALAMPGARVQH
RVIGAVGVLYGVAFPAGVCYLIARHVGASFTRYWQFSRKPLHERLLYPVGCWHPAAQQRM
YGGMLTNMRGSRVYWCVFQLSVLCVVGLIAAVHPPVGGCHVQYFCMAAVLLAGAGVVAFT
NMMRSAFLTVMHAAGFVLLAALCLVSAANHLAPSDGVARAYAAMVLLLTIVLLAITVYSV
VVWYAEDRHWQDLREPQRCGLEALLRDDEDSDEETQKLHDMTSLSYASETTGASSYRPPA
PP*
>TCRU_10283 retrotransposon hot spot protein, RHS3, putative
MGVHEGKPEQSWSYKKADDTIEENDAVQQFGAAPPVLMVLASEKGWPYSWHTIQDLPKDV
FVICEVDRVWQIVKGDLTAWFSPHGGNDCKPERRVLIGTPGIGKSMAAGSYLLYQLLHDD
AEKNQVAVHCFGGGDAYVSDKTTRVVTRYGDEDMCISELRGLRGHGRNVYIIYDVAKEGT
PPPRHFAPTSGWGMIAVSFPKVTNYDEWKKQLQTARIIVNCPDETDVKAMCAWITRGGTK
EKQAECWKEVKKHMYLLGPIPRHVFDEEAFTERCGAVRFALQSINEVTVKEYFSRGGESP
WYSEDPSHRLVKVVREIYAGGVILFNAPISACLEERTLERLPSVAE*
>TCRU_10284 hypothetical protein, conserved
MGIGVAPSTRLQYARMLRSMFEMNRTPLDMMILGLQKVAARSETKQARPLTEEEMNQVIR
SRTDWRERVVLRLAWITASRWSEIVALTPNNFTLEPDGTLILDWSVAPKMARADPHRPSR
FVRIREAGRFRHYKAMQDTSRKRKAHEYY*
>TCRU_10285 RNA polymerase III transcription factor (TF)IIIC
subunit, putative
MSGVAPHRRFVSVELPFCLPVTTRRSPISDGNGLKEEERRMVEAFVPPSFLRPTLDEIFP
SFGEGTGRETAKTPTGSVAIGKKQFKHRAAIASASEYYTGEVFSGWRPLDFEAEADNMQA
KDSKQILLGLTGEEGKCEREKMLRESFPSFTPQVLLQGFYRNDVLLEVTRTRRVKRLRDP
VSGRVVKEMFLQEDEGSSQSKATVVGVVSREVDLVRPADFCFGPFSKDVLAAAPALCSGN
LFPPAHFVAEKNPFEVECDFGGHFQLEVSKPPGGDVTRDNKEEGPLEWDFEVMPTLSVMA
TDSSIPPPMLPAQKDLLRRLNGGDAEKECVEVRTTKKLLEERPVWIAQELLDAVLQSGIC
PRRHINKKAMSCLTYLIKNGPFSRLRIRIGFDPYASHKTASLQRIVLKINRRSELGTLLR
DISRVPHIADVLGEIEKKHAQATENADAKLLNVLPCPSRGSFIAKLCELIQDGRLYVAIQ
IVDLSDDAFLRDLLLRVPPATDMPLEQRNCRNGWIGEAGYHRVAAYITESLYNLIKNEVT
PALESRERSEGPTRLTERRRSEGSSTPSQCESNTDNDEEEEDEKDADSLNSAASAAL*
>TCRU_10286 Tetratricopeptide repeat, putative
MALSTHRSVRVSPSAAEEWMMSLTAQGAIGTVNPENPSSVVSAIRFLLQMSIELDNHGNY
VESVKCAESALLLRHVNEATVTPLLAPLIAEELIPRGRSRTVDQAEDLVLCCNNHAVAAF
NEKQFLAAEFFLGKALFLTDLRGKDEANYFIGAESRRLRLRAATLNNLGCMEKRRQRLEE
SLGYLRQAVELEVSLDTTSRGSPSTYLNLCTVLNELSQHHEAVNAAENAIAALEEQMSRQ
NKEQLPVSAMMLVVGLYNLGVSLEHRGRDDDDFKARAAYNRVLEVSRRHFVDPNCPTVEL
AMEAVRRMHAETAFHVDRVEAKSQRRKRLPSDPTRPLKPLSQEKEEQNLVQTLPKDLHEA
PEKSWPQLQQQPPKVPISPLVPVTEAVAYAASQSQSIHSRISCPASERSVVSVPFASPVT
SWSRGAPSSLPSVGTPASLRSASVPIQAHTVPGPAAPRAVASSRVSITFHADIPTATGQR
SSLFQSQRLPSGDGKQPLPRPAVLAPIVREADSTPTTTNTASKGEQRLSLSSVLQPRPSQ
KTVGSFDSVTASGVLNPFARRVFGNVASQDQQRRSSVFTSLRSVTGSEAQAMEKHVRRSM
LQQSKAEEAKRRADVPGRRGSAAAKAKEREQKRLAREEARNDAEMAEVLYEKFVNGMRAD
KLNRCHSAAIQIQRIWRGCLARTLLYLMVVAARKIQRVFRVYLVKLIATRRAEEERLAKI
QAEREKQEMGAAIVLQVRVRQFLRRLEIRRAYFARKMRRYYSARRIQRGYRAYLRWREET
IAALMEAQRLEERRKMQLAMNAARRIQWAFKRYLRRKEEIKASELLLRSERAAAKIQALV
RGVLARAWFSYYKLYRRQQELRSAANQKRIILIQACARVLLAVQLRRLKEVDLLHRLHQA
ALRRAATKIQCQWRRRVARIKFERLLAEHEMRMRRATKIQRWYATCVLRRRFLELHERNR
RQDAAAKIKQWYHDRKLHIKEKEVARYHAYLARRQRLALLQAQSIVLLQAWGRCFISTVL
VQSVRSSFLRFTLYTEVFQRIGRGYAGRRLACRIRCRLLYESRMRVEDHRRTVAACVVQR
AWRCAMAKDTVEQLRRRHAASASIAKHYRGYVCRKELVRLREAKRLEKETRAVLVMQRAA
RQFLQRLELVRLDRYHRIRRQKKLAHMRREEAAVTLQAAWRGRATRMALERERKSLEALV
VHVVKIQQAWRTRKFRRNINAEVKRRSYERMSRSRAALTVQCFWRKMMAAEEAARLRELS

RLRQAKAVVIQSWWRRFLAKWELETLRNQRREEMALQLHYMERWENTVTLVNTALRVCLA
QQQLLARKRKQLLTLLTDKERERFLSRNGAAIKIQAVYRGHYERVYARGIRREKEEEERR
KRHREALEKRSAVIIQCAYRSWRAIREANARRAAKRAKALEEEMEHLTTVDPHEVVRQLF
WVYEFTTRRDLAKISLESSNARRRAAKVIQRGIRQWLARRQLAKLRREKAETHAAKTIQA
YWIQYRSREMQKSSERECRAAVIIQAHFRGNLVRREWEQLRKQMAYEQQHKVLDEEIYDR
AATKLQSFWRRIWAQHMAEQLREERRTIKVQQVLDEAASTIQRAYRHHRQRRSIAGSKNV
I*
>TCRU_10287 pre-mRNA processing factor 4 (PRP4) like/WD domain, G-beta repeat, putative
MELIDPVIPSSDHEVQQGLRLLEAPIHVFAETAAERRYRLLKLMIEGGYRSLEEIRNKRL
MAPASLPLSQGGRRGHNASSLPFVSVRTKEEFSLASPALVERRRALLPLTMTRAERRIAN
LKEVFLASSAVVRPTHQTAVNQLRRMRLTKSVRNVKMGYGSGSNGGNASSSLVGTLCMPL
TSCAAVPMLPHTVITGAADGVVTLWNTDACQPLVSVSSCDSGWGQVRHLAVHPAAPLVFS
TTMFDYTIAVWRITGESFVDGDDNKTNNTVVSASSVKHSARVGLERVDRSEEQHSACIQR
LAVDPTGSLLASTSDDSTVCLWDAAAFLPAGKLRHLLKQDGYEAACGTLDVCFHPDGSLL
STTDKAGRVVTWDVRSGMEAFTTAGKYGGHLNACTCVSWSPCGVRFASGGADNVVHLWDA
RYLSRGAAEAPCILVGHEDVVTSVSFCANPVFSVLPSAVISTSLDGSVRLWDTDTAGVCL
HVLHGPFPVRAQCRPAGGTGSAVLTVAHGKYWSMWDIIADGEEVEVIPTETEATSTMAAA
LLRHGVVPEEDEDEEEDEMMALRNEGKMAANDPEVSSLSDNNMDDDDDDEMSFLKKK*
>TCRU_10288 hypothetical protein, conserved
MLRGMTAFLEAVDERAGQLARQQAVGEEATSLEVEMEKSEEKEEGNEGRSTNGMYAAGDD
PAPHALGSQVSLPPFPAQPTETHGSKNNGGMAPSKKSTAAAVSPEDEGGFLQGKWNHVEE
GATAAAAALMIQRDLESSLLRRKDEEIDVLAQQVRRQQATAEAARQELLQRSLQVHQLEE
SLRAVRARFDEHKSKSRRLLEDKQREYEELCRRVEQQERRKHAPGSAEMDNYQNSKDVAA
RQREEELAGTIASLRREQERLEAQIAAGRREVDAAHEQRIAVAQQLEFMQLDLRGAQEAL
ESEVTAHQRSKALLQGRQRELNELRAAVEKNGGSFTAAGALISFRGDDAGSRDNLLLSRQ
LLEKQNALEAAMRDAAEWRRRCERATLRLEEERTTRVNITNSQQLTRDAADFRPISFRRL
TSTGRLTMLVVDLIATVDNIAIRFGRLLRRQPVLRLIAAFYMLFLHVWFLMALMVFGRSA
DISTLNNKTP*
>TCRU_10289 hypothetical protein, conserved
MEGGGLGPKTDVTINVSGTVTLPLHLQALETLEDPVLQAEIMKEAARIAISEKLSGFDKM
HITAAQRCGNPSCEATLEFSDLCCAIANLQHAYEHAMGYFLKIQQLIDKKRTQLQEENLK
KSEEEEEEAGPEDVLAAIHQLIQDALDGPGEAPFASVIRESAHKNTTVEAGSMADGDDGD
GAADYYDEMHNPEAEGYAPLLDHADTGLKEEVEEEEEATIKTEKKEGLRENETAAAER*
>TCRU_10290 hypothetical protein
MASQRPTVWGGNGGSGSSNGDSHRRLINEAGDDVSATPAGPYSNGMGYSRETEQRVARIV
AEYEYKLLEERGRAQERETRLLEELRREKAQVERLTNEHSRQEEGLKESPGGRLVSMEEY
ERLQQQLKETRLLLQEAERRYQQEKRELLNLRTSQLRSETSKRGQEGDIIARAMQVMSEY
EAVVRSSEENSIARLSQHMEMFEKEWIRRSREFEEKKAAFEAAMMEKTRQVLAEHEHDVE
GISRTLLEKTTHALCNHSELRLEMEREVMRHADIFKEEYKEILEKEFYDRCKMYDEKIAE
RERGWVKVLQEERKKIVAAEQLSIKEHEKLHVQALEDAMRDLSQLREQLVREHQEQQTEA
MKDLITRREDLQRDHEEQIARMNEKMQEMKQECAAVVGDMQNKMRDLHIQTAAKEAEMAR
RLQEAKQRADEAALAKGLEVRKEVEKQWLSMLEKERAKYTTDLQRLSKEYQNTIDRMRNE
QAEREGALLASYEQRVVQVEEAAELRWSGRVEEAMQGLERHMEVVQMLRHDNENMSARIE
RLTQESELIAAEKEGAVGRARREQDVLWHEKLEEMRQRYDKLLDEALGTTDDAASGPRVS
RQEYEKMVASVKEWEEKCVALKQQYDRRMAQEQDELNAAWGKRMDEERAQRASWEAEQLK
QLAKTRDVFLQDMEEKEKALAETHRAERDALYQAFLQQQKSERERSDAAIAQAQQEASER
CVAVFNEQEKAFQERIRLLEERISQSMADVRRREEEVQEEFLRKTDEAQQSAMDYIRQER
EALQTAYDKKFAELYDEQQRWEVQRTTLHEEITGKYAERFAKAKAEMQQHLPAVMEMMLS
YQEQCETTWLQARGEELEVLNKAMLAYMKRMESFRAADAARVQTQAEERIRMEQAAMEER
ERALYETIQARQESDEKSVLQHATQMLEEQQSVLAEATWKRSQEQQQQWESFKTEWLQKT
WSMEEAHRSEIQQMRRGHEVMLEEERQRWRKELERQRAELQADQQRLVEQLRQLEDVLTG
KHESAMKAERQYHEDIVVELRKQHERHLAEEKQRTETVLREREAAFELELRRLLERVEKQ
SREQHDWTNERVQAIQDEFDGMVRNVKMDAQRNQEEYMKRVAELQQRHLAQLQEQEMALR

QTYEESLGAMHKAMELRLREHLTLDMDVEQRVEEKRATLREEMEANCVAFMEEQMERIRA
EQQAREEKAQNMERLYMDNLAALRSEMDEMLSTHFAQTEGRARETAEQTRMECENKLQAF
FSVVEEEQKRCATLGDQLREAHAQMDALRITHEEQKLKALRELQLKYENVYKEMHDALRA
EREELVRRALGEEEQRLLKELTTREERRRHYTDTSSPYVTPTPTLGRYAVPQEGTPVASI
QQPQNYQRGGDESFLHSCLRATPRTPYGGSNGNNRADAFFGLHDEKLHQLWCVMELPEAE
QQQTLRRWSQLPPPQRALEIQKETRRLELQLPILEVVTRREFLMHRLKEIEKSSFSNNNS
KSGSLGSDAHAEELRKELLRLTEHLKGEIPRHESMYGCTFRFRGVRYMETLLDQ*
>TCRU_10291 hypothetical protein, conserved
MSSGATAREGSLGVHQRSLGHLPQPQRQAGEQQHQQHQAIQQQRQSNQQQQQNASQRSEV
GDTYRYLLRHHVHSKLEDIFSNVLSERPEDPLHYIVEHLRANGVKSAGKDCLIETADFNS
LNRSRNEKQQPSESAPAQREVTTEERRDNKQLAARDPVAQEVKSEGVVERHTEEGTPIEE
TELPRPPSTFLGLVSANDTPAQVDLEAGTFPSSSPNVLAIPSAEPHTQTPITSLCSTRTN
ICVMRPSSALLAPWTSVRSSRNDTPYGTTGFRLGTGGGPETTYSSTCTTVLDRDDSTRSD
LSAFSLASVDMQDFLQEFRSAKAECVGVETQLVDLEMLSEILQCVNIPIPEIPLIAELFD
DVKRISTMRYGSSVFSTEEETSQDTTTILTTASAVSSRAADADLRDRVYFEAFLARMAFM
IQGRYPAEVIRGTFYSILESVVRKVRPADGVTQQHEQQQQKKKTGDEPRRTSSSSGSATS
RLTRAAAKSQCRTSGNTFVNSAGNNLATTPHQSLPLTQTYPTVTQTKSAHCAAANDGQPA
AELSPLMHGVSLAVCVEEGLWRGLGIPVSKAEVVNALCLLGMPVDDNYEFHVNEFVRLVM
ALTGQSVLHPVGEKASSWLLSSVGRENSLVPLSGSCKEDGV*
>TCRU_10292 Ribosomal protein L1p/L10e family, putative
MPQDKRLIVTKAVVHKIQRLHGADTEAAAAEGIFIEFVVPPVVVSQCPDLLTEHVFQLPN
RTYPRNGRTTCLIVPRVISRDAFKINKRHGYYDAVVTAEAICKRDAAEAVRRAALVSKTF
SHFVVDERIVSKLPPCILAAVTASLPATARERDVVSSSAPGPITQTEKKVGVGKRKGAKL
AEPLTTTTTTHVPALPKTSRKCITPLRNLEDRTSLTFRLSQGVLGGVVRVKNMGLLTFRV
GHAGMTAGDVCENAKCFIFALKREFPTVWKYIHEFTMTSGVTEPIRFMEVHIRK*
>TCRU_10293 DNA repair and recombination helicase protein PIF6
MTSLKPKMTVSAVRGRILVTAEDGERIGQWGGTECFLSRQSGLGPCLVVRSSRHKRHEGT
FFQLVGLRRVLSTYAMEGKLTIMVPHEQRLCTVFIETVADVDALRIMAALLQDRSHWKDI
EKNVACKKGRAGRGSKANEQGLRDPGAFAMPEWDNKDFYIDDAAAPDGNDSGVVISDGGK
VTTPTSKKENMYPKNTVSTHSEVDANSMASTMGRGLSERVAPSKEGVSWTVEQVRAVQLV
RTGRNVFLTGSAGTGKTAWLLHLLRHVLSGTEGVVATATTGIAARIIGGLTIYAFSGIGR
GDGSFEKIYRRVKSRPEVVRAWRQCKTLIIDEIGVLPVNIFLLLDAIARRVRNEPDTPFG
GIQLILLGDFLQLPPVDSSSAVFMSEDRTDEKKPESNWCFDCPLWEKLRLAAVEFRQNHR
HESDPVFAACMEDIRYGRYTRRVEGLISTCLGRRLSDRFGVKPTVIVARRQSATAYNMEH
LQLLDDVNFHRYASEDYASTPGYDLDKEVSLLPLLELRVGAQVVLLASLPDAPQLSNGDL
GVVVAFSEQTHGTALPVVCFSSCGGEEVAVQRVRMDVLAADGRVVAARTQIPLQLAWALT
VHRVQGMTLPMARVEINRSFFECGQAYVALSRVRRREDLVITEFDPSAVRADPKAVAFYE
KMFPRDSKAAAGGTEDGGALVELGGMDKRLRPHAFVAATSTKKRRGNGGDTKDTLWDETP
LFDTPLPVGVSVAAPPVAHDALKMLAVASGAIPQLTQEGEHADFTYSQEQQPALQHTLLM
DDD*
>TCRU_10294 thymidine kinase, putative
MFASHTSTCTLKLRYAEDQRNFRLAFGFCASSIQQLFADISLQMMLENESHGHIELIIGP
MFAGKTTELMRRVRRELFAKRSCYVIKHSRDARYSRESVSSHDKLLLGATAAVAELREVG
DAWRPFDVVAVDEGQFFPDIVGFCNTAADAGKTVIVSALDGDYRRQPFDGICRLIPLAES
VKKLTAVCMECHCRSASFTYRTVSSEKRELIGGADMYIAACRTCFVTKSKKRAEMEAKGS
VQTVDKCSDTPAAEKQKGEQREVEEDPITPPTTIAAAETPLSASAARKRPVDVDENVPTD
AERCKSKARLECH*
>TCRU_10295 hypothetical protein, conserved
MAESGALARGRGLRSVSAGIRSKRAIPTVSVTAQSHSTAACNVSAGEDGDTQDETMALRV
MLQERTEQVERLEALVSEKRLIQRYDDVLERRMQQYEAQLAQLALTVRGNTPTPSNKKPL
GKERKDPAKDVTNKGSPLSVREILDEVHQMRYEKHRLEGELAKKESELKSLRTELEHAQN
LVQVGELPLKTDVAGTNASCNAKPTHTSAVNEEVVTSLRHQLAEVQEKFARTEAKLGMYQ
KEYRALRQTVRREKELLEWQRKHRDAVGIRPKDTPHLEVQEFLLDQWKDTKNMVSSRHR
IFFRGAEWLQILNEKPEAMQTAFLKDASLELCAPCGFISVVEMQAGSELVTIEVEVRRPS

QFPDDKVELFLLHCPFAEMQRLVESRDEPKDGWDRVQEQLTEAQRVIAEKESEVMDLQKR
LQRAEALLAEQHVQRDADDRWVHAALDETEKTVLVIYKELKDQWEKGEGLQARLQSATES
LAARENELAELTVQLQTANAEAQRQEERAAQELEEVRRRAFAELRDVEDKRRQELSEIRR
QQQQQIRQAAENLRLVTHSMRLDCGMHDEAALASLDSRGNEILRALLLNEAALAANAIPR
TVVSLTRSGNELRAEVQLQVNALAVDNALVAESVRKCQAPTAMLFLQEWLGVKELAKCRN
REIQRLTQEVKAMSSKVEEVHERNAHMMSKTEVSLREERDKVCEFEREKAAFVEELDRVG
EALGTQDASLPLPERVSRLVTAIAEAEKMKKGHETRWRAEQARVQSLEKKQREMEKDHRH
LVEMLQESKQDLENATESLETLQSEHQKLLKEYGSIQKLLNSQQEEMIRLQATRRHQHYF
WPKGVDQWTSTRVAESTEDPEEVQHDVMVALRRAYEEYDELYETLESSIQQRRKMEMLER
EKLQGREAECNELNQQIAALQKELRKHQEEAIAVESTHERSEAERDELLSRIQKEMQALS
RRLAKNDALQRETESAKKALEEQVVWLQQQCEAHESERKKLQEASALVENDRSTMEKKLE
ELQREMERRSKRAEEMMRQLVSEEDARRALEMELATLRRSNKTRKKISGVSTGDKEEEEH
PKKLGAATAPEVKRLREFCMHALKLPLTEKQQTLGDIVAFMEQNCVSTVEEQESLGAALI
SMSTASKLLRECVAAAEEHKGGLIHRTPASRSSANGSSVGNLSAFGRSLSYSGGIVSAAH
PVSPPVLASRKSVTPTPLARIASGHQHLRQQTVSKRTQPKDLASTATEVVCLAQVLSGVV
AHWRDNEKQSAARRNEMPKKSFVPSKESGQTQHANSKPQQETGRQPDIENEAAVPKPDGN
YDFLRRSRAHALCVALSVKDHLDDALTALQSVLEVFREGNYAAKDRFEVDPIHDLRMSEG
CVVYALKRISQSADILFSRGERREIEARRGADYFKPPGGLRNVPSPNARNILPSKRLSKE
PRRECDGLLPCELNFSPSPSTSPNGKKGDGNCDEGVTVGFRQHMNAEDKQLIQWALIEAR
RRRQC*
>TCRU_10296 bilobe protein, conserved
MFLRSRSSSPTSRVRSSSLRSVSPTSERWDKTLSTYSITGTARSVEYGGNLRVWTAEMDG
RILIRAAARGEILFEASARESAFCTVLRKVSARQIWAAFSDGFIRCYNSINGNMEHEFVQ
HDGAVRSLASSPVSDYVYSGGDDWKVYQWSKSRCTYIRLFSGHSNGVQCVLVVPGTTNAG
AVYATEDILEENDEEGTIENSLPSGDDGEPKDEFVLSGGDDMTIKVWDPMAPLQIETDEA
CLATLRGHSGSVRAIEIHPRSGYLWSGGDDCTIRVWNWYSEETRRCVATLRGQHSGPITS
IAYIAPRMWSSGKDGFVVVWNTRQLAPLQRLRLAPRCVNCPILSMRRLYRAMHWTVWLGG
PESTIHVLHVSEEEHGAGAVLHRRESRRTLEKRKFPKSREYHLARKPHLIRLRERRKEIE
EQLRNYRARLLEENILLPERGAARVRGGTPSGGSEEDARIAEIEVLRATVAELENQVKAH
EETIMRTSYIAKEKDGVIRSLTRQLSEKDSELRRMEEELNRSMRRHASSQEVGRARSMEK
EHELQEGRAETTESNAVFDPYKEVEQLQSQQKLEVEDMRRQLLDMQKYKELWEEKDNELL
QANEKIEELQASLDTERNFNSLTQELSRYTREHTTHVSCRKQSKFHSLPYTPTTHHYYKR
IFGTCWPDLEKEYQKDLKETLWAEYIDLISNSDAIVREITYTTAKDCLIVDATIESKEKE
GQEIQNRIESHTFSRTLALHGILASSFLVSTPDKGNISDEQYEAVAAAKAKAEAERDDAR
QKLRGAEEGLESFRRQAESRRAQIAGLQSAASSTRPTPSSTRNAAPPLYTVTAEEYEAVA
AAKAKAEAERDDARQKLRGAEEGLESFRRQAESRRAQIAGLQSAASSTRPTPSSTRDAAP
PLYTVTAEEYEEIASSGVGARQSYFLPQSSNWVRYHYNLGNAFVPLVRHYHQLVEDVLLL
EFSRATRLPIDYIRRVEFVSGGSAAEFYACPSKDTVDVDFLLRRHSFSTLASLMQLSNSV
RKQSLCSCPSEATAANVSPVMANERAQPSVRMASLGSQKPISGPWSLQDSNHASILKELE
LFRSRRALASSMRRSETTLNVSFDLPNRINPIASVDPSELQREPVYCVTLDEYHTLLQQL
TNAYRTQTDDDDENGNGTRLWNEHVVARAEEERRFTRQMSRLEPWYADSGVSSKKKHYWK
NDEA*
>TCRU_10297 Leishmanolysin, putative
MPRPLFTTIITLFLLQLLGCSIGCLALSPTAHHCMYDEIMKKASLPKPTMVRELPRKGRG
TWQTYTASTEEDDSGVWAPIRIMVSEKDLNDPSKYCTNIGEPRPTFLGFDKECQLHDILT
SRTRAELLQNIFPAAIKLHSDRLSVRPNSSPLIVPRSIKESHCKHFTVPEEHYTTGVENA
DAVIYLAAGTHFPFAVSCLAAEKDVRPTVGAMSFSISGLHHSWFAVRVIAHELAHVLGFN
YEQMRAQNMLSSISTNSFQQKKGIVTSVLTKQKAVEHYNCESLEGMPMRDEHGDNLRMHS
HWDQRYAKDDLMSSMVTSGAGFYTAVTMAAFADMGFFKVNFSMAETMNWGKGVGCNFVNQ
KQCMPDDYKNYPEMFCHRNTSDTRRYCTSDRVQLGICSSFSDDQCLFIQPMGFGSCRDTT
SILHGSRMGTSSWCLDGESLKVNEEVLETEPQVISVGGVCVEVFCGRKEVSVRYLGDDDW
HECPEGGKIFPANTSVDFAEGYIKCPRYEDVCTITPSGRSGIPFQENGPIHDDSSNRK*
>TCRU_10298 U6 snRNA-associated Sm-like protein LSm7p
MAAELAHIVRKKEGILALEPHLDRRVVIALEGKEIHGILKGFDNNINLVMASAELWVKNA

LLRRIGACVVRGGSLVSVSSGDTTILQHNPFE*
>TCRU_10299 WD domain, G-beta repeat, putative
MSSRRARLSPRSQPQQSSARSSRAGTPSLCPCSPPTSATKLGKKNNRVSSVGPQKFRSRA
LDVTPLFTVEGAVRYIDVINERTAWTVECDGSISVRSIPKGNEMKQILGRKGVFCTCLLF
VGKTGKVWAAFSDGFLQVYDVNTFLLENTFVQHTGAVECIVEMEDRIYTGGRDWKIYQWI
PEMYCYERQFAGHGNTVRCLCPYTGSTGAVLFTGSDDGTVKAWNPYPSVKQSKENNPCVH
TFVGHTRGVLSLEIVAPNNQLWSGGEDTKIRVWDLQTLNCVAVLEDHNSPIACLSVVEHR
VWSGDKHGRILLWDLRTLSPLQELSRQMQVEHRSVFAVRKMLQTVVWKVWTTGSAGHIHC
WNAESMPLIFDSDTPGEMLPHTDEENMRALEVDNEALRKEVARLTTQLEKESAHAMSEKF
NEMQNQQLIMDTNEGLRRQLRETQRLGAVGNGGNTEHGIRSPYTELGYPQAPRLDLSMPF
SDASRNGGETGGNERGEAPFWEPVTMSIYRNDVTPIITKIERFFPGSAWSEILQDHENEL
RQTFIREAAQALGVPEDKLQHASMEPNPQGLFATIKVSHSSDTSAEELKRPLKAHPFVPV
LNLYGAALAKKNEWLKEALIQAHNENQSASQSMQDNPKTKTNGPSAIMDKNEKIAHLSNE
LESVKRQNVRLQNEIKKIYEQLAVKEAPSRINAQEEYDALKSFVDNSLKPLISRLERTNG
EKELDLRANEERIRQLLHEKEQLQKQLAAKEAPSRINAQEEYDALKSFVDNSLKPLISRL
ERTNGEKELDLRANEERIRQLLHEKEQLQKQLAAKEAPSRINAQEEYDALKSFVDNSLKP
LISRLERTNGEKELDLRANEERIRQLLSKCGRSCSLCALNTGAFFIHSEGMESDRHVLLD
ALVEAEESARVRESDLLALVDSLQNVVDRYVVEKEKLVARLETLNGELSEALKERDMAMS
DGKLLEEECAALRDQLRGELLAQIPVGEQKLLAAYLDEVQRRREVEKEMYRGLSKRVKAS
W*
>TCRU_10300 adenylate kinase, putative
MTAFLDNKLEYLQKHNIAQLTEHIVRNIMEDLPENPIKYVHDLLERPIPPQIVIAGPPGS
GKGTQCQAIVERFGVVHISSGDLLRAEVAAGTEVGKMAETFIHNGEMVPNKIVINAVRKR
LEQDDVKERGWLLDGFPRSRDQAEALESSGIVPHVFLLLEVPDTIVVERIENRRTDPATG
MVYHLLYNPPPPEDVALCERLIQRDDDHRETVEARLRIYHEKLHGLKEHYGTLVETINGD
QSIHAVTEGVLAVVERRRLK*
>TCRU_10301 Leucine Rich repeat, putative
MASPKEMYEKECRALGVPPNSGLLRMLPESTVNLSGLSVMHLGHNFLGDRGVVPFVHIIA
HASSLHTLNLRENGIGNEGVRVLCRGLRRLPALKVLELSGNPFTFLAARQLVYLCEDSPV
LSVIGVEGTLMTEKLKTSIIHRIREAVKRREARNQLSQQPSADRDDGQKDMAEGVAEAEG
KVVERAAPIAAEEATTLRSRNVGGPCLRKSVLSLVSQDSMSTAMSSKFKKNEPDDQAGPR
GANEFASPCSPLPPPPPDDAHQSPLWFDASEDEEQKEEKKEISVATAENDEKMMIDTAGS
ISFLVDVEELRANSVERELRAQEEMLPWQVSRADDPLRSLHSTHTRIASHRTTEKRSESG
TAISFPSSFTLELRTAEAEGKLAECTKSTKGDDFLDLLFGSEVD*
>TCRU_10302 pentatricopeptide repeat domain containing protein,
putative
MRKDGDSKVSVVDGCDSAKAGNEGARVAAAMPWDDLCEAIVAAYKAGQDIVVLQRFEELQ
AMPELDILLETQRPGGTTTATPTSTKMNGNIHEEIAAAATAAGHPINADALGRVEFCWGR
ALLAAKRLAGDDDEHIFTIVEAFEQRFERPSEYLRVLAITADSALEVLRLHQLMEGSFST
SAVSAALHKFPSLTASETRELLEFLQANDVSLTKDLSEQLERQFVMRMKTEDAEDVFQEM
CSAGVEPMSTRPYNLIFMKTLPFRHMSPVEYYLDMLDRGITPENSTFRILSKQTQNDGLV
NQHFSSLAWKNSASNRRRDEDERGGTQIFFAMSLEELAKSKPDATLEEALHVFCRMDVEG
TPLTNGSPVISALLTHFCRQGHLEDVERVLHLSQERGCRPTSVTVQKLLRGNHPDRFNQA
EMVLQKVVEAGEVIQVECVDLLRHFVVGNIRNKAVRVFRAFVIQGHQHPNEPIPFAIASM
AMKLGPFDWALGVMAILLATTDKPLGRGLQSRIRYTAHDARGREVLAVLEKCDWRHERLL
SATELQEPEINSKNHSGNGGAAGATWTDPKNNQRVERSVTWLGALHVALTEMGVEPGVME
AYKNALLQAIERAKEHRGSMETS*
>TCRU_10303 hypothetical protein, conserved
MREMHPAIAELKRRSRAVGQRLQPLDGRPTNIVPKPPTYRRSSGPTGQHASTLRPYPSGQ
ISQSCTASGFASTEKLDGGRGSQHTPINFADATSTNTTTTTKKSSSANKVKGRESVSGSV
VQRMPTKPTSVVRNPRPRNDASQGERITLREHASSLVISKDRSRDIEGHAAAEGSMASHG
LPSDGKSHLYGYVYSEWKDKSNASKSEMFASNRDEELYLFEKYRDSREWNKMLPRSVLDV
LEGEKMEDPFTTDIWTRALKEKEKDISGFYACIRCHVPLVASKYQIPFLVRGIAAFSRLN
TEAVEVSVGGFSAVTSSFTKKANPLELHVHCRCCGGFLGILAPCTDIESAASSRAIFAVN

SCCLEFIRGSHTQCCLDGVYGGDEDGASDGGIVTVNSLDGGEINFDDPNIFEM*
>TCRU_10304 hypothetical protein
MFFTAPPPCAQKDADDTVRADANDTKASSPEQRQPLKIAPEPGVVVESWPESQTEKETKK
NTAKKDASRGRGIKPSQSQNTMGDMGVVLADGGEWIVPEGKYRWSGFDPAAEETHVAVEG
AAARSKPVPFSKAASSQALNTKQQHQEGRGQRQGGKDRGDKTEGKESMPTAKPPAENSGA
TISRSVRRAPAVVSSSQHPEKVEGKKQQTEAGTTEYIENSAVKPAAPMQTLGSKSRPRGL
KLPRLPQQFPRGDSAAHDAASSLKIPSSLELDKIRQLASVLKREKR*
>TCRU_10305 Utp14 protein, putative
MVRRSDRAVGDATRKKPAGGLRGRRQQRGKRNSNDDGLLEVQEKGVLNLNNPLIPPELDE
DIDDDIAFNSEDEEKYGHLFRKKPTSDTARLTAGAKQKNGTKKKKVGKHAADVEETGDAD
DALLLQQLRALGEIEDGDDLDFHERDGAGDDDDYIDLVEMLDAGQGEEREAGDKKQKKKT
KKKLDESGVAKKRRRALVTEEAESLYGLAATDDKYGSAIRQLVTATPASSTQTRMQKSLD
NKRNLISVDVDEHTKAKLTRREVRKVVSDELAKYNSFLREQREAKHLQFPMPMPDSNPVP
TTLGAISVAAQERFATQENAAGTAAALATTTTTTDATGDALGTTGNASRVSAFRLAGKVN
ALLSSAGLSRPELAAPSAEDVFIPLVDNDDDNGGANRAAAAQNEKEGSVPTKSYMAKLKA
MLSYENARRRRLNRIKSKTYRRILRKEKDREKERREKAFEILHPEKARARLAEKLMKARV
EERVTQKHKNTSKWVRHAKRFANFDGNTKDAINEQNLLHQRLMQKMEEDADEDAYLNAHV
DGHADSEAASSEEERVVDYLMAEAATKQQQEGGNKTEKSSQKLTSVLWRSITEVEKEGED
DGQTTGSQMTPTEKARMELRAMNFMQQAKEREEKRYAEVLETLQEDIRRDMCGQAVGSDD
EPSDLDEASETEEKPKKLKSRAKSLKTVETHVGRKAFLQRHGEQPDRKVVESIQLKRHRG
IDAQRGNEAEETHRKTSAKEDANSTVRSTRDEGSNDGVADGVATEKDKAAIFHTADLAGS
GKEKSEGFAGSRQPNISSVSNVGSETVFSATPKRASSTRITILPADAKRPRDVNGTNKGE
EEGVLRKAEGKRKKRERLGEKKSEEENDEETTLQQHQEYLIARAFADDEVDAEFLAEKTA
QVETIMKPVDKNATLPGWGEWGGKDERLNRHHQEKLKLMDLQRQIEKTTLMKSRADAELD
HVIINHDGVELVPDRMLLHMIPRPFSNPTEFARSMRHPLGPEWNSAFAFKEANQPRLEVR
QGHSMLPLDLTLRGKKKTAKTKRRKVLSTAAV*
>TCRU_10306 Armadillo/beta-catenin-like repeat, putative
MSTTESRIAGLLSVLSESEDAGHCALSVFARSLRETAWKQQHHHHSLNGAPVGGGGYVDL
SDVLAERSLALLREEEAILRDKEVVRVAYDKLRAEMARVEAQLMSLERRAQEAAQQKAFC
KLAMNLLVTGDVPEFYVPDADRSMDAPRENTDATNGNVAGSTVECTEAAPEVAPMSSTSP
KRPRRNTTSQKRHSESQPQKVLNENGTHGEAREESPSIEESENYDNLAGGGKSQQISTLG
KNIPRVHGGSGSCPTGSALLAMLRLPDVKEMTLLHAIESYDEYHFGKTVVWSTKKQEELL
PVVLGLLKHLPLPRPPIQLAELHILGHFFRSPYVTQSTTDPTLASLRKPTSLPESVVTSM
LHTLLREGQAVTILTRLLHSVNNDVKCEVLECLSPLIISGCGNTNNACNVAESASEKTRT
FPDARKEFITSGGLQPLVGIVASCTSEAVLERSLVLLWNLIARNDDEEKVRGEVQRLGGL
RAVLDLLYTDSIPILENAAMAIGYITREETSKVEIREAGGLEKITATLRHPYESIQTKMA
GAVWNCASNAENRTYLRQIGCIPALLELIGSPYEFVQENAAGALWNLSVDPENKTQILDY
GGIVELAQLIAKSHSLSVVENVSGTLWNCSAAVESRPAIRKAGAIPVLLSVMNRKPVPST
QQRDGAVAKNASAFLPISDKILDNVAGTLRNCAINDQNKPAIREAGGVELLLGKLELGIL
KQPGSIPMLALDKMASTLWILTISPEIKHSVRLSGGIPLLAKILEATSVTAAKKKNAKVL
VQLTMSVKEKLVGLLRNCSTVQENRPVMVSAGVVRALVHVVEDCRLAMSAKASVSPLASQ
QQLPSLQLKETVASALWYLSRDDKVAPREEGGLELLCRLLREPDQPSAVLEQAAGAISSL
TVNNQENRTKLREFGGMDALLRLIEEKTPLAFSQRPKNGVDGKTVSETAGTVAGPSSGTN
KTENTVSNTYAVLNALLAVRNSTSSNEENLRYVAEWRCSLEGEGTSLPTTSFTGCLLYII
QHGSEDCAREAALCVKNLCGHAKALESLLQQDAVELIGGLAERGSSDSVRRAATMTLHSL
ARAQRR*
>TCRU_10307 hypothetical protein, conserved
MPLNNSGAADTDKKSETEYFEGEIAPLYVSLSRSAPLPSEDYVRVVALSGAGDVSSDAPC
VQMNARTDGNWKNGSCIQNLAESEGNEPVRHDFALHLRGARNCRLLDTMLDAYDLHMGAI
DRDAIDGIAENKADRTGKDAVGHLPPVVLPQATYKGCKALFLYLELITTRVPTTISKPLR
APIEELLQPWEMNFLLKDCMDDTTSHAISQQMNDGKEGKTKGRKSVGDARTAYYSVIVNN
APESLNLITELAMLSDFLIVEPLRQLTCAFLASLALGASSEAELLRLCGLSRPLTEEELD
PLYAQFPFLRPDTVSDL*
>TCRU_10308 MEKK-related kinase 1, putative

MSDEDSGEYLDTLANRRLPSTLVSNLCDNDGDADTLNSSTSTAGPPGFRRTGRYQNRPWE
TGSNTSCSSPSSATQQRYGRTGAFKHNGSYRSVYSNKQYSTGKRRSMSNASTVVSLIGSV
PEWSRSFCLFNPWRAAAASRSSFHYANQALFAGKHVVPGPGGSLSSSITPGAAPIGLENH
RRSVSFGVSQNHNVGPGGEGYAGRSTSTLFYAGHLSPSSVSTSPIIGGHRSGRQSMLWGT
STPTMTAFHAVGGAAWQLGKGVIGNISPARKELAMLLPSFCSYLSLVGKPVISGNADHPM
DMRKGPLIGVGGFAKVYAGMDCVSGRLVAIKEINIAEINDQAALNAIGKEFGLLKSLRHP
NIVSYQLFEHSASQKVCRIVMELLTGGSTLALLEKYGPLREPILRKFARHLLEAIAFIHK
EGISHRDIKPANILVSDRGVVKLCDFGCSKRVNELSKSTNCVIGTPLYMSPEFIKGEFDP
KSDIWSMACSLFELGTGLLPWHHAKVRDNLPLMFYITTTSETPLTNLPQDDVQEFSLEFK
DFMEQCFIRDVKQRPDAADLLDHPWIKGARLSPAHNSFSVPFPGGANSPTWPLVTRPAEE
ELFCQYELEEVAAYISVDMCSAWMLKIGTGLPSILFSSQMHQQQQQQSQSQSQQHYLSLQ
TDIRSRSEEISPQQNPIEQRHLESPGAISGSQCHSPAVSSRGGGWVSVSPTVTVDAAQND
QFNYSIPLGASEGRFVLPSYSTSMMLPSAAQYLRINADGSLDFVPVDEETVEVDADVDDA
FACSHEHFFNRSPSSNFAFRSSSPPGVAATVHAHEGHSRHCSPGNLNNNISHSAISAGRS
PANRNARHGPAVYNQSMSLMSNSSFPSRGVSPSRRSQTASTASLTASQHLPTLLMMTGSI
SVFAGASMNHSSDDVSAEAQGGVPSSSTLSRFPDSIRDAGGRLHMSLSVPTGGSDRRVNI
ELSVDPEDVHCKYIERRPSYVVAFSEDIRAQLAAKMNELAPSSVSSPIESQWAWAGSSTS
RCVSRGAQALSSQSFSPR*
>TCRU_10309 AP-4 complex subunit sigma-1, putative
MGIEFFLVVNKQGQTRLAQYSSFMSIAERTALEGEVVRKCLQRRESDCSFVEHLHYKLIY
RRYASIFFIVGIKNKSISSTSANANGGAAAGNSLGGASVAPLGETGSGTDELLEEGELAI
YEFIHLVVETFDKYFENVCELDVMFNVEKAHFILEEMLVNGGIGETNKLLILQPIVLMDK
EPRKL*
>TCRU_10310 hypothetical protein, conserved
MVLRQIEVRTTHDKVLEARENAFMESIARENENPFQQAADALLGAVGRLYTNYLYTSGTL
LLAWAWWGLYPRYARFRHKHFVRFRRKSQSEFRRWFFYTRHIPKWDKKYLQRVELPRRMP
HGTPAARKSPQCTHSSVILTSSSSSLTSSHDTDAGAVTSERHESARSQDPFITVRLTDGA
SFAGGFREQMERNVASGICDLNESLQQQLKEGRILSREAVDPDVLQGEVKQLVKQAGGIV
VLKETHETRRSVPVDREIWWVSPEEARRRREWWFWLQLLVAARILEDLLDMPEMPDFVQ*
>TCRU_10311 N-myristoyltransferase
MAEEGSGLHQFWNTQPVPQSSTDAADTVGPLEAAGTVDDVPTDPVAIASTLEWWSPDMDN
KDDVRAIYELLRDNYVEDVESMFRFNYSEDFLRWALTPPGYHSSWHVAVRRKRDQMLMGF
VSGIPVTMRMGVPKKVLQKNKTTEEKEQGPEEKNNDHKSQAEEHYLEPRKICEINFLCVH
KLLRAKRLAPILIKEVTRRVHLMNIWQAVYTAGRLLPTPFATADYYHRSLNPEKLVAVGF
SVIPQQYQKFQNPLSMIKRFYELPAKPKTRGLRPMEPKDAPQVANLLRKKLATCDVAPVF
TDEEVAHYTLPREGVLMSYVVEREVSGGGGGRVDSSRGKQNDAGTQKQITDFFSFFSLPS
SIIGSSKHSVLNAAYVFYSANTTISLVHLMSDLLIVAHQQGFDVCNVVNIMDNGDYLSEL
KFGRGDGNLHYYFYNWSYPIVQPSDVGLFML*
>TCRU_10312 WD domain, G-beta repeat, putative
MQSGNNGAPLPISVTVVRQQYYPRVPPELLLKEHAGKFHLSGFTTASLLDAISPRVRPQL
PPFVTQKDNIVTANDEFTWSLIRENVKRPPVPWENIRRPISATQRFTKKAAATTETKCQA
NTVSPLSAVPSSSAKMGNEFPKECDEFIFEEATASYLTAVEFVRKSLNCNNDEMTGQKID
AGKEQLQSLQWTLSSDVTMEERESLWGYSTGAVVLVNLRSYAADIRSRLYYQTASTRDQR
LYMENRLDIDGETSFEDSDAFSSVAEEQQKANPSENDGYTREHGIFQFGSEKAPRGVLLL
GYHNVGGVCSLVYDSLNDLAISGGVDGTLFVWDLHQRYRGALRERYMKDEEAKNMRPTGQ
FAAYVYTRRLTQRLSHAHKCAISSLAMHCELLISGGVDGTVKVWSCLEFVDLSSRAALPQ
YVEQQIFTCNGWVRHIWSAPGRNVQGEDVFVTGENGFIVGFKGRTVSQQPVIQTLDREKK
LLNALRKSAMAPLTLAIGLTRISRTDTANSVRFPIITKPGLGSGSTSTRLPKPATTEKEA
TKLLQLGIITRALCLTRKLQTIGEEARLANSPVHRHAVQVESTSAITRIIPLVERNLFIV
LGYSPVVRFLDMTRLSVAAVVIHPSLSAAAGEGKIDDLQATFPDNSQGVGKGNMKNTSSD
ESQSKGRRMLGSKNGSRGNAEPLRFLDVLYIASYDYLVLLDNRNTVYVWDNVENKFLASW
KTPDTKEIGKQKNALRLLPCGTRHYEGDEPIAGKRVSAHVQYRPKRRVACFYDQAGALEE
TLETEEDASGAITIPFFLLCSVGLELCGVVIEAQARLEVKAHHDTIVGIFLRQPPLLYFQ
RNNDKNKTEKKLEEADTFELDGSSVKVMSSVSQMYIPSPFTRSSTIFTESNRSRKTTEKA

DFALPTEWPPNSPKKNEDDACIRVLSCSADGTICFWGGSFELLTVYDQRSVSEKNNEVCT
TVSHKLFEFDGIVSPFDAPPCTTMRKNGVKNKVEHSECIDITSFYFSTRWNLAVTGHDDG
SIRYWPCGKELATCVWHKGLHRNAVSGLVAARVMERVDMVGALARIGSVFKSLEAMEPNE
LLASISFDGHLAVWEYPQQLKAQLRDCTRVSFNELLCIAFDEINELFVIGDSAGTISSWF
AKDLGPRRSIPSRPPSPWRPSTAVALPASFVEQSFGTSSNMSKRQKRRGTRGSSVLSAVL
EKQQEKKRIGHTEAVTALIVDGNFVFSGGEDGRVFLWDLRIGLLLREYFLLHDVDEIAHH
CRKTMPASTDCSSMCSKENNPRSIVHMHSLHSLDVKPYSENVTCMVLLRRRNGNFLVATR
EGWVYHFEQSNSYPRSTYKHNSSVRCMCVFQDGCTDDDAVGDNDLADGGDVCSGISRAFE
VVVGDDEGKMALIRESYFFSTV*
>TCRU_10313 hypothetical protein, conserved
MCEGVTSDEALHRFDLLRQHLFEEDDTWYAMRAEENRLLYGDTVGRKPKATASIPQRRYF
NCFYDSFKQRDDKFNLNILREVLQKEWAEREKLNEYEEEEFYAICRCAGNALGVTAWSRR
YRTSLPLVEAEEFGRRMIVTEFFAMLLEAVFILEGLHRRTISFLREPLARKAIEGDEVHK
WVESRRCQVERERREESMFEAEERQRELAYHNWKRQQAYQVYLFEKSEEEERMDVERLQR
FYVGIISQIFRKEHMEAQYHQLRYQMRKRLLSAELSRHIIGNEATERSNIMVLQHEQFCT
LQAEEVKSFLWTRRNTMLNELVDRERGGEGCVYAYM*
>TCRU_10314 TFIIH basal transcription factor subunit
MAAAPQLTSSLDVLRPQLKGVRAEHGALVSLRDAPAFEMVMRLNQRYKGKLVTAIMTQSS
AHDASKSDDDVQRNLNEANCSTMNFVRASEEKRLVFVPEAYEAFLGNEMQKWLDPFYGRN
EANKSKRSRAERDMLSSDDEEFTGDGMEDDEYSSFSE*
>TCRU_10315 syntaxin 5
MVVQRDRSHELYSLFEGMKGVGGASIQETSSAAFLAAEWNTPRPPHSGLHSSSEVQLFNR
FAQAFSMDLAKVSESIMRLTKLTQRQSVFEDQSSEITGLTQVVKSSLQRLQTDLETLEEL
KQRALVAQKTAASKRNGGTSAESHSLWNSGGGADSVVRTSAKHSDTVVDTLRTRLARTGQ
EFRTTLQQQTRAMKDNAQRRNMFTTSERMQTFESALFQDQERHQLQRQQLMSGTSNAQYY
KQRAEAVRELEATVVEVGELFNDFARLVHEQDEVVLRIDTDVDNALRHVNAGSNELMRYL
ANLSSNRGLILKIFGILFFFLLFFGLVIVR*
>TCRU_10316 hypothetical protein, conserved
MIHPKLLASQELSLRRITVQQQGFTPPFAGNDANNMSAPINSANASVCSASVPRQSSVRS
ELTSPSTFNSTGSTFSSVPLNKTVSSSLDPITAGGTNSTAPASIALPKIRVRPEWESALA
NANPFVFSGQKLHGSQLSTRRRVTVRYVADQYDRQWIAQRETPSNSVATKGKTGSIDSST
TPSISVLSSSSSSSLRHKISLSLLEDLITAFEVGSYGNPEIPVQRQPVSSFNSVLATGAD
ASVVEEVRQYWLGKRQALGGNIPCIPSLHINVQEDNQVSLCHNDILQLCPLPFNHRDWSI
AVLQRRIPNVSEVKLAEADMEVVKTEETGSVGRKRRRCDTDKAMSDELFSAKMMNEETAA
KKERHALVSSALKVARAVLEREEKKLVHTHLSLYELALLRQAAMEGYDSLETGVSTSACT
PWASDEALQEDWMDEDEVGTGIYNGMGSGLVAAAVESVMAIDRGSC*
>TCRU_10317 protein transport protein SEC13, putative
MLRSPQPRFPQHVPGAYPPQQQQQMPPQPQSQPQMPMNAQPPAQAIQQQLEHQDVVHDTQ
FDYYGQLLATASSDRTIGIHVVQNGQLQRIATLTGHEGPVWMVSWAHPRFGMALASAGYD
HKAIIWKEMSQSSKQWAPVHVIDCHHGSVNAVQWAPETPMVATASSDGTVAVTVFEGGVW
RDSLKLSNNSNNIAHAMGATSVSFAPMRPSLGGAVLLASGGCDSQVRLWCLQEGSPMANS
FELLEVLEGHTDWVRDVAFAPLCAATRHAVLASCGQDKSVIIHRKPWDQLGALIQERQRS
SSTNGPQQYLQKESGGIWERSVVLFEEPVWRLSWSPAEEVLVVTTGDSEVYILRENGEFT
QPWLKTPLSEYQSGTR*
>TCRU_10318 nuclear segregation protein, putative
MTTTEAAAVVAAPSKRMPPWLSMPGGPKEPNSAAFRAKMSALAEEKRALLNEVKQLRASL
GPREGREESGKELDGLRQRMGEIDNQRKVEQEMRFKKNEEIQRIQKLHDERVSRLRELSD
DLGGFTTIKEIDDAIAFVTRRMETSGGGLGAEKRAVRQLSKLEEAKRYLVELQPLTEAIT
EAKHREAMLQREWQEINERIRNLRAEYNEQRATKQQKEQEIRSSGVNRAEIYKKCEEING
KITKLSGEMDRLREEHKKAMDAWNTWREEARAKYIAKMEEERKERRRRYLERKNAAKIEA
KRARALRRQNPYEAEIDACKTLLRYMQDQKVMVQREEVELARKRAAATFDPTNFLPEGAV
LLNDGKKFSEPHKAVPGGKSKTKQNQKQKSEKAPPKNRVLQHPEDKIRLFQLINEEPPVA
LSAIDGAVETIRSKQKEYESHIKTGELELSSDDEEEEEEQPQEEEETAAATEEVQKKKDE
VEKEVTADKIGLVTQNEETVEA*

>TCRU_10319 hypothetical protein, conserved
MAEGFLRVNWRACGGWLILQWRRPLPGTTERVAVSGLANGTTPLVAGLGSKACQRVRVPY
GRDSMFRVLSGCHGLRRMLSRRLISMHSTMSVTKLPVHGPAGTHQCQETLPDPVLVEGR*
>TCRU_10320 hypothetical protein, conserved
MCSQYGPLRSSSQRGRPIAVSVANSCLRVATTQKFSKPPLAVHPRNIGRQATEDSMSNEL
KGLAGVYQHQRSPMGSAVELASNTALLGKVRLEVIGSVMLHFVYQVCQLHRRGTHTTICM
LVGTRRLQTKRSPQCHFLSDLTHDGGKADGSI*
>TCRU_10321 hypothetical protein, conserved
MVWPFALYALELSFRDSSLVLAPGPGGVLNALLRHLVPAARCSLRTMSGTSLADGSLRSS
WETGDTTRIRRHGKNACRTENCRPLPLLSVLLGVSKGLVHRRLSALLARHRRQPRLTPRR
TVSDVVTPVRDKTARGLSERIAVECGRCRGGVPRCTLTVAALSQSRPASRLRSTTLALGE
CWLWPAGSRACAVEPNTGCAAALG*
>TCRU_10322 hypothetical protein, conserved
MALVPYTPSEWCDIGARLWEMVCQCGEIQVQLTFIDGNQMSDETLTVAPSATGLCLFHGP
ISKAWQDSTLVGHIANLRAPQIPNFETHVLLPAMGAARELGHQQGLITAERERLNFDYAN
AVADVQNRNAQFNSEFQEAQINLSVRESNIAGAGNQVLELRQQLEADRAQLREREFNLGV
LTGQFQEREARLNALQTARDAETAGRDESPATRHAANDGVTTIPHPTDILMAGGMPSSAA
RRSSAAHRPPHGNAARPHFHPSTPLPSRTSPLDARLPMEEDRSFCAFDVTTWPSRVWNEG
ASGVIIDLRCAYQCWQQDNEQVKLAFDNLVEWISALEGLQIPPIES*
>TCRU_10323 hypothetical protein
MANDSQNITWSSIIIIVIIAVLVLALLLACMWFNVYWRCCLLSRSSVVHIRVENQNIAQG
NFLYPPHRTQPEEGQQQETLHGHALENRVRTRQHRLPRTYHLPDGRTVLHVDDFRRIPEA
APPPATEEGLQRQREEAERVPSPVFYGRSSYLLRSMSSIFSSFCFQTTPETPAATSMGPK
PLSARNKKDTQGANDDNNSPSVRRKANEPIDIPSHGVDDLKRDKSP*
>TCRU_10324 Protein of unknown function (DUF3720), putative
MAMMTGRVLLVCALCVLWCGAVFGHATEGYCSEGGGSGLRHTSNGGDDGVSIKADCGLLS
TRMGLINAVEAADEGGLGGDAGSSQDESKVSLQDKKLSGNTEGDAALGSGGGVVADPPPP
PAAAPLQKPGERNTGEEGKQEELDKKGNEAEDKSRSEPAPQKPKPEQSSSSASGGPGTQS
DVELALEVTSEGNKFSDDALKQEDAGKTEVTKISDGEPEKGKSNTALTETHESQAEQKET
QLPKPPTLPTTQVNEHYSPGDTVTKQQLQKPQSEMDPNTNSQTKSVVTITANQHNEPSAD
HAGSRPPSPAANGDAANNETDKTTEDGIPKNDSAADGAEKREEKRNENKEANPKETPVDV
TAMKTTTAKAGDSDGSTAASHATSPLLPPLIVACAAAAAVVAA*
>TCRU_10325 Trans-sialidase of Trypanosoma hydrophobic C-terminal,
putative
MVPNASKKRPSFANGPRILVASNASGIVSVTCGGREHVAADNTDEVNERSATGHKTLVLE
NTVAGSGFVAEGDAYGLAQCNASGHDNRPLLQKLIAQYSGSGGSPHDCFALRNFAKLTLR
ELTVDGTVRVRVYWVLLLLLGLCGVVAVL*
>TCRU_10326 Protein of unknown function (DUF3592), putative
MSGRVYRFFTGREQPQWLWDLALEIRIPAVFLAYVVYVNTRCYYDALNAYQANSRWAMTS
GKLLELRKLNYRYISVPRYAVRYEYEVDGKKYVSTRATTGTPYRNWMERFYNDTITESQY
LQAIPVLRLGERCTVFYDKKNPGAHSALAHDANSFEISILSFFTVVPLLMGYLMKAHWWM
LKKAYMPNKKMRVRFPPTARPPPPPEPPKNVSQISPLPKS*
>TCRU_10327 Ring finger domain containing protein, putative
MAVAFIFDAGSLYQVSENGGELICLPLVCPIQSGADVACFSVEEFYFVERDSPLLLRRWR
VSLDCKEYALPGPVQNVLVHRQKVYCCGKDSLFVFDPLSEEFETLELQRGASDLEALDHG
FVFLDENQEIYAYQFNQCPRKVELTRRGIRLLGRYSQYVVVLLDSGQIVCVNEKGEVWDE
ILSYTFTKPFISLSSGALLTVNEGGKICLYARDTTTPIVSELQVTEPKLLSVPSAQPEGS
CLICLCDFEEGGGVTLDCGHRFHRDCLAEFSSRADGFRAKGEHVVFTYAVCPGGCGSQIR
HAAAPLSEYMGRLRREINLDAENRLREMKNKTVEDLLYYICCRCEKPFYGGERRCFRSNN
VEPVKKPCELICSECNDDFLCPVHKHNYVLYKCRYCCNPATHLSFGNRYLCNRCDERWET
TEPEPIACPGPGECPLKGAHSTDGSIPLGCMLCASFSAMHINLFAPF*
>TCRU_10328 hypothetical protein, conserved
MLRLGSYLLCAKSIQRMAGAAELSKDYKKIEDEEKYLAEAEAKRKEYENYPLRYRLLECK
PGLPLALTKLKYLLACRRTHPEAGGNAEDFLRVSLAYQDIMKDYGVETVENKIVNLGNFQ

VDDHEARNYLEARAQIKSFIPISTLTDHIRKIEEVKARLGDDLAEKIAANDDEAMLLLED
IEEIMEEDGLRTVRLGLLEDGSVRVENKMLLTDGTEKPLCLEKLSKNQEEQIKKREAADD
GTLKSVSDEPTGQQESNLNLGQDTDGGEKAIWTADVSAEDIEVLTAKDKVQDRSDVAGLA
SRTATEVMKNTEIVKQVRLESSILFVFSLCIFLVVYVYIEGLMRAKMQSKKRPETMEHVT
TDTMLPWWGNDAEYESQVKRIFVEEWRRARASSRRVQTFQDGVARESLDEETKKEMDLKI
FTVTAERLREMRERADKHTGRQ*
>TCRU_10329 hypothetical protein, conserved
MQLVCLGLAVAMLFAVCAECADSMALMFAREISLRDVGNVSVSASFNDAASKYVENAFKP
NTVFAESFASPPDVAIVARHWFVGAQDKVLDSFRELNALFDKWSKTPVAALVSSLNQLSF
TDLGRQPSVVSFNDNCSYGDESIGIGSPDFGFDNLSFLFTMQVNPSNGLKQRLCQILSMH
DCTLITLDSSKEIDGLYVAQVTITSSNRNLLLIKILNNVQHVSTLFLDRILLVRVAGVQV
YLRKKLPPLTYKGNTADCLSHYWYLIFLMLLLPLALIAGQRLKACGAESGRKSIRAMEWD
IRSGVRFKGQFQTHFSGRGQASSAVISGIFPSGTQHGVQNREYAVWQNAPGAKQFPHQGQ
NMYYDPNNAWQPGEGQDSQQIYPITSRV*
>TCRU_10330 DDRGK domain containing protein, putative
MSFPLIGAFLLLLLLLCFVGVFICRRQVVPTRVSSRGSTRTSLAHKGSEADTEDDGDGES
MTARHGPPNPQEVAALLRRRQVQRAQGRGDCAPDDGAATPQPKLTRLQKKKQEKDREREE
RRQAQEAAESNRRTRQEAERQRQEDHQRDEEERLLAEEKALQELRDEKKRQDDEEYAKWI
GAIGLEERGEIGDEERVRQEALLAFLTRRAREVEARQENQTEQLLQSASPTATAKDEESS
RSILVLSSVAREYNVTVELLVKLIEKLLNDGVIGGVFDDRGKFIFVAEAHYREIALFIQQ
RGRVSVKELVRECNRVILS*
>TCRU_10331 hypothetical protein, conserved
MKQGDEKNKDGSNGRASPDTAHYTVVSLDSIEHHYLEVLRELAMEPQLEAFKDEYEKIHR
LLRKSNDGEKRLSAKIKELQMDLEVHGTKVEAALKLSREDEEVIATLRKEIEKAWSLADS
AHAREKEGREHIQQLRKQVAELDALVEKSTRNTVSQAAYLRELILAKKQLEGERAVAHSK
VSQLLDEREAMRSNFERVQHDNEMARQQLEASLSSYQTLLDSLSDVQRVRESLEQQVREC
RATSDRQMVEAEERKAAAEGLSAEESHLKVLAAEERDAVARMAKQLEEQQRRFKTEADRL
AVAEAQNAEFKSEIPKLKATLKERQSEVVRLANALRKVRKSAEEQQVNMRRVVQTREDLV
QKTEKLHNSIEEQLLVLETEEKELHLQELRLKKTIPEKTELIVNNSRTENERVAMEGNKV
EEEGKRHNLALQLDQLLCENELLRKTVFELEQSQAKILDHGQHMALQYHQTVEQTRKYCD
KARLLQQQLTDNEKRHKVQQDLLDRVSADRARTEKQLKESEMEWSMLRQRYATNDEEIQL
LKMQLVAKEGALCRLHMVRRQLQRDISNAEQRASHLKDDVLNAHSRREALETEAHQLTHL
ISECDAEKSKYQSKFAALVNERNVLATQLIRRNEELRLLYSKIRLQESALEKGASEYDRQ
VRNIINTRDRLAELRLRCRLALVRLRYSEKLRNRKQSIEQELFTEQQRCRALVDELQRPV
HVHRWRRLEGDAPEVLDGIYKAQDLERQILKKHDMLADKTQLLAKRTAEYDAIRRKLASL
PGPELAEDLSLYKENLERREEQIEGMNAELQEVEQHADVLKEEVRQLLLELGDAKRRYFG
AKHKNDLLRREQAVFRSTWGESSAIANIALAAASAHQQQQRLAGSGGGGSGKDSSNQQGV
WLERPVGARRPCLWHTRTQMRRERMLQEARLVQALSSGAPAPNYPLQFRPQQRQFVGGGF
ALTR*
>TCRU_10332 hypothetical protein
MNVFFVVGIPKGISVVVFSALIACRVDEVIATNYFVILALPFYFFGVLTLLDSILYRIFI
QKLRGNPAGSCNIFVISIPFITAVGLVLASVSIVSMRLNDLDRARHGAAGDVFSLHAALI
PVYFLLGCFLFSTLMIFCFVCFFLLTEDGEASNSPHGDAATEGNDEQQGSEAHSGGEKGV
GGGHGDDGKPSRKHSFFLESRRNRDVRDMPQGAPDTPTGSNGEMFLPQRPRQGLSDID*
>TCRU_10333 epsin, putative
MSIPTSIHAAREMIRVMASGNEFVVLVHEATNEDPWGPTGAQMDEVCRAFARGSFDIMEE
IKLRLKHREKAWRPCYKSLLLLDHLARNVPESGLPAICTVIPTLRTISQSFYYTGSKGTD
HGLSVRERAKKLCDLLSDGTLLREEREKAALTRFKLSGASGVGGGGYPTSHYQGYLNSPM
PPSLSPHDAYENKTHFGRTREEQERYDMELAARLQHEEEVRSGVSAGDAERMFNRQVQRQ
PASVEQAARNSDLELARRLQEEEEKKRQMNFANESLPSAQSAPTPKPANSPPPASAAPPV
KPEPPKKDFLDDLFAPAPVMTANTSAQQPGWTESAPFHQQKSASVDPFDAFLDTRIRQQQ
QQQQMLSVPFPQQPPQQQQMAYGSYSPSMAPPQQYTGMVAGGGGGWTGATQPSMMMPPGA
GGSGWSSGVPTQASYGGPPTQTPWGVPSSTSNAGASSGAQRAPFFSNGNSDMQGKASFTN
VSEGAKNMSLIEQQMAQFAGQLSGQPQQQPKSLNALMAERRQSE*

>TCRU_10334 hypothetical protein, conserved
MLRRTTVVRGHATSNLFAPPFSGRWFNPPHQWTMTDTFMPFFFIGSAPMAICVYLYHAAY
MPHYSHYQDQNYYASQVYTKEFIHKYKRLERWRWY*
>TCRU_10335 hypothetical protein, conserved
MSGPVVNAETALARCIEAMHDTLQASLADALPQSTELSEVSGAAVELVDTAAQRLEWELG
VERQRIDRLVGGLDQHFSVLEHAVSSLPDVPVASIDRDIEKLNAEASSLAQAIVAAYDEV
ESLAAQLEHEINFQPVPSI*
>TCRU_10336 pentatricopeptide repeat domain containing protein, putative
MRVTAVLRRGKVDIEPWMGVSCYPVSPSFVGGLPAVKPGYDHYKMIRPQRPLRAIGITGS
LPPVLYNRMEQLVQIENAIALQRVERQVEMTLSQLSLGIRNAEEFLEKHLLHAIVRPSIH
TLWFHEEGLRKNQHVLSALGAHHLVPLFSLLAYDFERGKMSLYEAVELYEELMDCSVAQP
KVVQRELTNQMVRCYCLDDEYEKALDVVLEMKAKKIRRTFVTYAPLFRMIRAKEDAERQL
ALLDFMYNVEGGRILKFLYIDVPRMFYMFGVFIRYNWVLINCAFTAFCTIVVLYVANFGL
*
>TCRU_10337 RNA polymerase I second largest subunit
MSKNPSLRSSRSHNSSVGENYTSTRSSVSSRHRRQEQKREVLLPPANMTPFERLQLLRNA
LTRMQYIGERHLHSAMLDTAGGEKVICFFEKLRERLPKLEYNPRKLGCPDGNGPKQLQYI
REQTLSLQDAANVVLKSCETQKGKCDAVYEGLSYHYLQEVLRELEEIQHLLSHAPSEMPS
RFNTDLLADLVSFQINEFDAFAEQRVKAFVSEAKNEGTLFTAVVNELSQRAPSSTGLVSI
FVLDVAIGVRPGRCARIVIEHAQHNLTKLENRLHTAGSVLSAMTPEKDLPTEAQRREIAI
LKDRVRGSLAELIRLKKKWEEEELGTFERAASGQHVLLSLVEMKRLKEAEIIEEAQLIHD
RAMHSCLLFSAPHYYRRYGETYAQPCHVQIGFKFLQGEQAESQPKSMTLYALVPEFFSLM
RQHNIPAQEHERYAALVPSKHHMWVAFSEFPEMVRGARCSLRGVDTRSDHFRAFEEQKEV
GGYFIMRGGERILRSLLMQRCNVPLNIFRERFSSQGPFFSPKAVVIRCKRPSGLTIQNYF
YYATTGEVVFSFARKVVWHIPVLLLLFSLNTRHCSSLEMYKLLTIGFTNCSSSHVARVEA
LLQHHHQKPYGSLVHFLDYMGVLGQMYRRYHETSNTFHFLPQFHSTCQGQHDAWYGLFML
RRHVLPHLNVNEPTRDLSPTATQEECANWLSPKLLQELNAKLDAMIAIVRQLYAFFDGAN
EHQGNDVPAYQEIFTVSQVLMGGFEVCLNKYMKSFVYRLGSHIPSHLFQSILQLGELPGN
ESSGVINQLRQYTDYCERRSINEPLDALHRLLITGNLTLDREEDFYCPQTSGWVVMAEHL
NFYRFFEQLRCLHRGKTIAEMRSSEVRKYPCEAFGFICMVHSPDGADCGVLNHMSVSTFV
SESVPTGSRSEEDLLARITEEFHGLRNGGSLDSLVDRLVGTVPVWVEGKMLGYLAPEEAK
RVCNALLRKKALKTGSSMELSGIVRRHSVNAFSMVEVVYVPPGNKDPQGLYIFYDNGRMM
RPVQQIESTSHGDELPFPLVYIGTWEQTWLDIASVPSDLLDGLTQLNRKYEFMEQNGSNI
LSLTSATIPFFEHNCSPRNLFQCGLSKQSAGTQLQTLAWRKEAKLFRMYCPQRYISRTLP
MDYYGLDDVNLGVNAVIAILAYTGYDLDDAVILNSTASQFGMLTAGITVAKVITASGKGE
KDDVFVFQNLLSNGQPFTPELDAHGLPRKRAVPGTTELLSFDSDHKYPTLRDSSAVYCCA
KRYERIDPLMNKKVYEYTRHHVTKWWQFDKGENAWVHSVVPLTYDGPDPTSALVVFRIPR
PPAIGDKFSSRHGQKGTLPLHIRAYDLPFSTRDGITPDIIINPHAFPSRMTVGMVLEMMG
AKLGAIQGRFCDHSAWSVVDERPRSAEVIGDALQKAGYNRYGREKLIDGISGEEMEADVF
MGISGYQRLRHMVNDKWQARARTDAHTHRAVTKTGQPVKGRKRHGGVRVGEMERDGLLSH
GSAEVVLDRLLHVSDKAKAFICVECGSLLSIYERHATEYSTWKTCKFCGAGSQEATDTIA
FVEIPQVLRLWAAELTGIGIRVVLKTRDEAS*
>TCRU_10338 Raptor N-terminal CASPase like domain containing protein, putative
MFNRRRAAAATAISESALVEERLAAFAPHHLPALLTGLDADEVQDVIPGDFSLTERSTRQ
KVKSTQVILFLCLNIGSDPPDYPRIEPCARLECWIDPHVAQISRFALEGGSDSIAEILER
QYRSQQRDAVFKRAVDAHLEEAKHLMMSSRRKADKGRVLLHYNGHGMPRATEYGEIWFFD
KNRTHYVPINIVEMSQLLDSPTLYVLDCNSAGSILQHWYKERLHQTRPQDMFFCACSAGS
FLPLNPQLPADVLTACLTTPLRMTLEWYVNFSHRKHLLPHVTAEMINNIPGELSERKSPL
GELNWILIAVTDTIAWCMTPPSQFHQLFRQDTMTKALFRNFLLADRLLREVGCVPVAHPP
IAEQAHLHHLWDLWDYTLERVISQLPDLLTPELTVNPNYTYKPSTFFMDQLMAFEVWVES
GDLREQPEELPSVLLALTQISYRVPALILLVRYLDSGVSAGRRAIHCGILPYASKLLVQT
PEVFLIVSVLWMQLIRASINQGTEELFKSRLEKYFIRVLQLDEKKTNVVPVEDGRTGASV

VNGSNFFQTGGSTASFVELGDGVVGSAATPNGDTKHYLMKDLDLHRCKAMACYVLCQLMK
RGGEHQYLACWNNQLLNAAFFLLVSPNAEVRSWSCLVLAQLFLGLRHAKDFAAMECTSRL
DLFTSLLQDKSPIVRSSCVTLLASLVGFRVDELPVERQVRRVQMEKSLLIKLRGFIFDAS
MSVREELIFFDSQLLFHYGSLVPSLQCSTNPDRYMDYIQEVGRNSPGWMVDEPDVQITSQ
LSSSRPTNNSRFDNTVTFTTGFLSRDDLPPSAERFCLDAIEPKVLKLLREMVHDAALMLF
ALYHTCDASKVVAAINVFKNQNLPQSHRFANEALRSMSRVVSTDSSCFLSEADRARSTRN
ADSMRQLVLEMQDRRLEPMYSSNKNKSSKAEDNGTGVWNNGLSTSAFTRHQVLSSLLPGD
QIISAAFRALEPTMVLATKNRHIYHTSYETYSTQTHVHGFSVRLFAPLHDVLVVNDLSEQ
AGLLLVTKDGGFSLLRGCWKEGQGMPTEVATFSACSPRGHIDIKSVYRSYNANLLYGGPI
GSNGGTEVHVLSLDEEQVIQRLRVSGDPTLTSLTAHTTTRAIFAGCSDGAVRYYDDRQKQ
GFLGVIGMLNCKGASSSVNSSFSSSVEAVVGVGPVEVGTGALTFATATRSAVRLYDSRKF
TEPSLEVDIFSFCGGHGGWPSVSRSPSIVAFATGVHTGLLGALLSDGSYLALNARGRILL
EKPLKVSNTQGSLLPGSFVVHPLRPFMSVGGEIFYMQ*
>TCRU_10339 hypothetical protein
MLRPIRLFPVMLCKPSRCAASATWFGGADDSNSIMGVVKGLFICFCGIACINLWSRGNAL
GKVNTENDVYIPVAALRKRARDPRTDGFVDGFSEAEEAQNTEGRRS*
>TCRU_10340 hypothetical protein, conserved
MSAKAPPKTLHQVRNVAYIFAAWAGLQKGFAEKSANDKMWVEHQRRLRQENVKRQHAAHA
LEELKQDEELERSIPTIVPKELHELVKALEK*
>TCRU_10341 Cyclin, putative
MTALSLALGIHDQATTKFGSKDFCDAVEAEAAAANAHQYRMFLLAMESLLQRQWEHYCFH
GGNHITKSQQLEEKRLCRYFSVHCMNMEGRGCRDEKKHRKLFGSGAAGPLIDFIYRLICH
SHCSIECYPITLALTGRFFVEMRKESVATEYEAAVDHLPCVFAVLLLITAKYRDDNFRSN
RYFSQLAELSLMEWNALERLVIRVLRFNVNVPFYEYVAYEKLLLKEMMRQEEKKCGFPSI
DQSPRSEKMESLMHLDSKNDMSMLFVDHVEMAMKDNASFHSCGVTASSPSLRSQCPLMSV
EDSPVSWRQGV*
>TCRU_10342 retrotransposon hot spot protein, RHS3, putative
MSGRPEEGLYDNEEIQAPTVPQGYRRRARSEFEGDTDHFSATRRRVEEARRPQRTMRSTV
KDILLEGSTLRNNMKLNEFLRNHVGGRGVVDTNENVAMEMFVQDPEMFIQNERLLRIITT
SPSYQALEAINKLHHEDVDSLEQWRDYERKDTVTPFAREKLNAALTQVLTEERREAEERA
RREEQVIFNLFAKIEDLLFGGRVRVMDIKLNDFLTLEMEGRGILRSNRNVLLRDFISDPT
RYIREAGVLKEIQASGAYARMEKTVREEMDLEEVVRKLYKNGVSNLLGWSLAAAEVKATV
HNSNKHFLDAAAEEARKPTTTIVAIKLEGLYESVHNARWSHVVEVPDGEGTGVEVRDGEP
PRPWTYKAVGRTFEKNDGVQQSGAERLKLMVLTSDKGWPYRWGLNKLIRDCYVNSEVDRV
WQIVKGGLTGWFSSHDKNKISPDPFVLIGTPGIGKSMNAGSYLLYQLLQYDAKRLQMVAY
IIAEKTFLFDKTAKTVEKYSAASNIVDILDGFSGRGVKGYIIYDVALKGHQTSTALPCKG
WGMIVVTPPDKNNYESWAKLVRAKKIIINCPDESDVRAMCVWKEHNRQLEEEEADYWKKV
KDRMDKVGPLLRYIFDDSEYKSRLVSCEGKVKSMNLFATHYYSILGTNEVCDDSHISHKV
VKVVRVRGGSNLELPLNTLMSPYLGNLVTCKLAELMVPNDFNLLVLAIKHNLLSKPLEKH
SVFTFLSEAFVNAIIPKLRELKPEKNAPPHLCALRVYPHERPLKPCIFQCLEKFKKKINM
KYGVLYKPVAQNFPLVDAFFFVDSNPKTLVGLQITTAGGHRTIASTVRQFNECLAAYFNV
WEELSRDMSWEIIYVQHADSTPMNEWQRCDVVNTNKLSPAEKKIAAFWEKKVHQYQVSVS
SRDFPREESPPTVEEQQQQETD*
>TCRU_10343 hypothetical protein
MNGEVSVERKFSPSQPGYGSEGCRQSMGTTTNNGARRFSATELGRTVGMPYSFDTMRYLK
DVMRRREDIHTMRVMPKTHLLAQLVLLEQSGREMLIHQERFCRQQIAHKRDDERSKREEQ
RLQQKNRDRLEEMKRKQVEELAALKEGVTSFQRQIDAEVKEKLRIVCMLQPRMNVAAAVL
AEVKNEASPFLLLPELMEEEKRVAKALKADSRYSKSSADCGAVPHWMRTCVAGSFNVAAI
LQDAPYRATVDDAVKVTNAFLRKVVVVRDVNDRSVVGWVHVRAGSDPATLATELVRLPAP
EELPDQGNIGVVWPKEDFLELSRRAKANNNVETQQLLQSVLGMSSASLHCVGLTTHEFSK
KEVDTIGSLASV*
>TCRU_10344 hypothetical protein, conserved
MDMDALTQRQADKIEFVLRDLVRDLELVSLLPTSLSPWTRKVCLETVRSQLSSGVEDGVE
EEEDDDVRVAQLIYGVAERHGDPTDVDGNEVLLQMAEFAELEKEILDLATVAGSVEESDL

NRHHMLFRAILDTLQENEYVSMVRELQERRANLLVTKAESSLAHLIDPGVLALKNAMEIL
LSLVMARNKTTVNEDVRNYRILHEAVNREKTASADVKALKREYQETKESHKKEVEALETE
IQRLEEEIDYTRSVVAMELSAFLEVNQQLQGERQMQDVGHLEEVKQLAEKNKETLATLVN
RNQEEANALRTQRAKKEAAVSAAITEYDVQISTLQAATATLNKETEEDTEAIVALDEELD
VLRTEKNEYQLEKFVESMRDRHYEEMQLAMDENTRTIQASFRAYMARVRFQKTQGSSKKR
GRRSKK*
>TCRU_10345 trafficking protein particle complex subunit 3, putative
MSAGALNFSNEGEKAFESGDKVSAEFFAITYGALVQQMVADLVQEEDVEVVNQQLDAMGR
RIGSRLIEEYSVRSGVPACRTFAQAADAVALVGLRMFLNVTATVEPLREVGTDAFSIKFA
ENPLALFVELPEGPLRERLWYSNVICGVVVGALGMVGFLAEATFARDMLRGDAINEILLC
FKGREKETFQIER*
>TCRU_methyltransferase, putative EMG1/NE.1
MEYRQKSARLPKSAEEKSRWRRVIVVLEHCPLAVVRTEYGFELLSEKHRQYHARNKQDPA
EWRPDVVHQALLHLMDSPLNRAGLLQVFLRTKKGVVIAVDPRLRVPRHIRLFEKMMVACL
YKMKVRAAHGHISLLRVVRNPVTDHIPPNCTLFRVERDGDSVPDLYAFCATCGVADGDAT
KKRKVETFAAGEAAPSHFAQHHSEAAEARKFYPFAFIIGGMSKGDVEAPYAPKGQVKSIR
ISDRGMSAAAVCSAITHAFEEEWLRDDNETE*
>TCRU_10347 OTU-like cysteine protease, putative
MGGCSSSQTCLTKGPIPSQLTLISENADCGAADAECGEPIANYVAASPNGLEREKEEEEE
AGRKCLPHLRHPQLTIRTGANDMEWGEDGWAAGPISDGCKYALTPVVPVTPFTTRDVRKR
IVSEFQKHYGGCGDTGEAVTPCTIDEAKKPSNKLSDDAAENTPMDTKQLEAPTPSAISAA
LPNMDRSGVEMTPVASIGEESKGVTEKWEGSSAVSFHPMTFQAINQTPQPASPQSREPSL
TKPQEGDAQQESFFTIETSKKRRSFIGLRKNFKKNVVNRGSGSVGVDKEEKEANRSLSRS
NSNAKPQTDEAPLLSREHFIRIGTQRLEKRLFELKLVEHRVKGDGNCQFRALAQQLLGSE
DLHEIIRVHVLTYMKGVRERFDCYFANKEEADGYYGRMLKSGTWGDELTLRAASDSLHIN
IHVLSSEQQNFYITYHPGADSPLPPAFLVDVATLRQQRHLQGNANMSHLTQTATVVKEGK
GGGSGMGALVVETEAEEGGGGRGRGGCACSGKSGGVQPTAFKSLKTAASTQNTKNHENGE
EEEEVIVDACGLQRSLQRKLTQSTIRAAANPKRGSFASGGYPESTNRNVFFAAVEAPAVA
MTGDAANKSGAGGYLDLSFTVQSGEESFVGGSSQSTHLRTVSQEIARLCSVGTESVENKG
KQHITLLLAHPTPVETLPSTQQQVESTPSLHMPITTTVSNALPKMDSSFLLVSPLHGDIG
GITPSVACDSTLPAAQTSAFSSDMDVNTAVCVANRFPVLMDDESVFVFEGHSEPIDVFLS
YLSPVHYNALIVAEERTTPSAVSLMPQQDKLGPCAESLSLPDVGTFLPFLKRVVSDKMVL
GGTSAL*
>TCRU_10348 ADP-ribosylation factor, putative
MGQSKTKLHIITCGLDNSGKSSIINRLKPTALQSEHISATVGYNVEVFEKGSAKFTVFDM
GGAKKFRGLWETYYENINGIIFVVDSSDELRLCVVKEEIELMLQHPDIARELPKTNGAKI
PFLFYANKMDLPNAKTAAELVDLLDLTTLMADRPFNIFASNALKGTGVNEGFFWLQNTLL
RQSNTISSSSSSRGGARQRNRRN*
>TCRU_10349 hypothetical protein
MELSPDSHRRRMPWTAEKECVPGVVHGSKGKMVLDGARRVDVECVDRASQVYPLEALRTA
AATCEYDIFRGKNIFNWSLRRNQMCSGNEFTARSGRRGRTTKTPLAPSFISVAAKTRRSP
RQYDLRIFLGGMRCSVCRHCSPSPSVGAGFPVDASSCGFRTHPLIDAADTAAHCWYFWDD
RCTAPSSWCSGNGDENTADQVQSDGAGGPVSVSPTPAASTEIDGAGEESNDCQGSNSFLH
HSQSNSRKNSQQHQSLKMTKEERPPPTATAPPRSPTPPPILCVLLSRMRAAAAAVVVAVP
A*
>TCRU_10350 hypothetical protein, conserved
MTRSTLVCGGGLCAAILVERGLVVNLSSVFYMDNCAVMSQMHVMYAIASDLRVSGGSVFS
IQNSSWSAPSTEYYKGACVFGDVAVDGGSVLQVVSSTFRLGFAMLMATTLTVTGGSWLVH
RDNEFRTAYVVYVADEMALRSAIGVCGRYFTTTLVKARTRRSLHT*
>TCRU_10351 Doublecortin, putative
MLSAAARREEIQKKIELLRQEREREKQAFDELALRDDGMTPSQIAEAARRKAMEEVPTSL
QVGGTTISVGDYVETIDDPHALLVAENGIFVPDPVKQVYLGERGKITCILPSFQEKSAVE
IVFADGASKVFLTECLLLGKKSRPKKSSAPKVSHKAVYFDAEDLHVPEFVPPAKPEPLLQ
PSWSNINIPSRKPKAMLENLKPSKPPTIPTDTTTTTATLDVTKATTTLVPSVERKDSNAG

EETFREQPKTNFLFVSNGAPSASYVMRMDSETLGSHAKTDQSIGLVKEVLSERQRRKVSA
REGLGSPIDFDAPAAVPLIGRGERDNLLKTPRVDPITYKPSKKWKGFLANGNSDSAIPTR
CPAGYRARFSTSDKNTKIPRVDGKQCMVAGVLPQQKKLKFNLVAFPKGMSKLEPVLSMLT
DKLNWRPLGQTAKRLFTREGVEIMEFDAIRNGMSFLVTPGHAYTPEPVAKTKLNNTTPTT
ALKATGTLAVGRHSRPTSAPTAADALAVHNINLEPQQAPVKETNSLPLPSQLPKSSYTLS
AHKGRQRASEKGIAKPISVRVFSNGEYGDCHYDPFPFRTVTLRPIHKTIRAVVNTIEREL
EWNSLGKKVETLYDATGSEITSIEELVDGQSIVASSGDRFVIPHPNSVLHQDVMRVLGNS
NVTPIFTSGHPKNF*
>TCRU_10352 hypothetical protein, conserved
MEMSAFEDNPFADEEDDETTSYVEATSRKRGREETATEEPRREGSSQEGEDPRQLTLATG
NIPTMTTVAANDLDVGGDDVQSQKELLAEINVDASGSIVPSVEDLLTGYDERQEEDEFNA
LVVKAAGLESEVKQKEKLRSEELDQISRSNRELRETVEQLRGNFFLINEEIDSFRRAQSA
VVEECNKSHGLMELLGDAQRSKGVLEQKVTDLTERLLAEDSEGIISASLRDLFFSCIVGA
TNEPSDLAAFDAEAEKKRFMLCEEALEKLRTGEMPSVTLPIVEALMTMLRELVVRYETLY
KSTRALQDCVAFKTSSLRELARESLEWYARSASRTLVGSGGTLRTVPAEAQEGALGNQHL
EATLHHLEYVLHQLLRVPNAITVSKQHAPSVAAASAFVYCQELESHTEALGQEVLRLRKL
LATDTPTLQHMSESQATQEPGALETSLPHALMKSEWLMGMTNKLLERISAAGALWRSLKD
PGRKKNAPAVDLQLAFYQKYIVMQEALLRLLCTLNSVLQGKVHIVSVIRQVTLRDGDDTA
FSVLAEKILQESENDIGDLHGELERVCSESLRQFEDESSELLNEDGMRAEQSRIRLKDVR
KFFAHTVETLDRLVNGATPASGPIQVPITETPPLKPEETNEMPIEMSFLPSEVKGEVFVQ
LAIKYHEEELQEEFSSFQRRNSALEERLKWLSTQPSSSAVLQLCSVHKAIDAVKQKLEGF
AGQETKRTALQDELTTIRGEISAVQSVTVEMRDKLNDLRGKLHARCDVARS*
>TCRU_10353 hypothetical protein, conserved
MSRGSFRLIAVSCAAVSVSAAALIFRLVKNRGRREDPSFETVPVSQWTVQQVAQWLRSRG
VSEEAVMSFFRNNIDSSVLFLLDEGENIAKLAPKVRDQILIRRGLRELRDQETYESAGAQ
TLSASETCTREAEEDRVAAFLMKLNAITSMLTSNEYETASPTIQRRQRQECMECSQALLG
EVQHFAPGLRVQLIPLVRRVEGLIIPPPTRVTPATAAEPSDLEAQLITLHEMVDGFLRVL
DSTDTHVISDPQIALLRERVESQISHVMEVASRLPPQYGEPLRKKCELVLQRIQHGSTAA
ASGIAVESAQAAPEPQATLLAPMVKRLREVFTSLKSSALVNMEPAGRLARIAEMLKDVRN
IQQAAASSGDARAVEVVNQVAGNVVMVLEQMEALTREEMASMRANIIEETDEDQSAQVEL
PQIFTSLQAIIKVLHSDKLARAPHEVKQQILSRLQKGLRPLRQQIAGLPLNQATASVAEM
IERSNELVDSLLDRQEGPHEGLEAKQENEEEEEEGTAPEEAEGSRERPLPSRLIPPVVER
QGNVLDEALLELERMFEYINSEEYERMSPKKKSDTARRNLIHLINIENRCAQFDGFDQLR
ELIDPMKEILRTGMRKKEERPTPGPTPLFLNISAHLQQMNTLMNSDGFQRADLNKKKNAA
RSIIPQLQKITSTLSLLPPHERAAVERLLAPVNETLKSIVARNENNSENLTDPQLVVAEV
EEVLSTLQSEDFRTAPVQQQQNIVRQLLQRVERLKEECAQLGRAANPLLTILHRLTTQLQ
SFGQAGRYANAAVAAGLGETADVVSNEVDEDNEGNSNDNTDNAEEVGDEMPATNGGGRRG
EIVEERRKLFKAVTDITSELRKSNNNNIILSAEEAQPLLGLLEMVDSVGCTTAYERRLRD
EFENQIQRASGNGDVTGEAASMNLQKLVRTFSLLKDRLSASPPVLPTEMVSVMTTVEEAL
SAADEQNVPWRRHPQVVNLIGEVLTAIQQRQAEMREQFSTGEEDALNETAPDPCEDPPQS
EEPVGTGANVISQLQGDTGDTPSDALEGLQNSQTAARDSTRFPDANLQAEEEVEGNETRI
ARLLLEMSEQLRDGSVPDELLDRYSMLLDLVGSSYRDPSLLEAVESIREQIRLQRISNRD
TSSEEYDSSEENMENEKVEEGEAYKSEETSSKLREDAGQEKVSGASKESSIREDTLATQS
TELEPTTDDQGGEDISKDNMSKSFLSQLSRNCVPGGARNELLLLPRIEKRIFSDEQHFIE
NTTLSDIQNVSKVILHIEKNNDVKDNPSLRDRVKRVKQAFARQLEAFHGSDQQAIAVHSS
LKLCCRDTVTSDESIREFFICTSAEAEEFGEMSNNRELVRSLTEGTPAQTTVLSEVVKQW
AGRSKAVIFCEGAGSMGGTELSELVLLREVLVNRYGFEVFAVTDSNASKMSGILQEIASL
GTKRLFLFCLTQSDPPSSPLTFSFNDGSVLPLRDALQEALDIERVVLVHCQRMKLTILSA
LNGRGGTFLSVELTEAAGNELRAGRCWLFDNLLTPAVTELLSLDEKPMLCPEDLATYTVT
ALTSLRVEFGSFTEGEALRMGFFVPCDLVE*
>TCRU_10354 hypothetical protein, conserved
MAEAARTVRHYVSDCLQERHPYDAKKAFAGRPERDRGLVYSGMQPLSTDNWIDSLSDPTV
GNAQRVRALRLLIAHSASQEVKITLLRKGIVPAVVAALNNASSAEFERQAFSLMRSLCVL
PQGCRSVMEEGGLEAAIRSMHDRSNSEEREGARTMAVMVLYQISFNTAGVRWLMEADVPP

GFELLDAPIGSSTLVVTKEDVIAALVFVIENDTQTLSDILLYAVTSLAQLTALTEGIFAS
LQGNAAAAASSLFRTYTMETSWLVEEEKIRLVMQLLTVIWNISLEQTGVDHLDELGVPDD
LFRLFAVVYKSPIWLFGSLFRALTGALSAVYKLLSVKMRSLEPLDGEYSRIEVLYKFLRS
INRDVSMAKHAKREPHPDLVAISKNMVLCTHFAAEVKAVRDFTHNYLKEMDKDGSTEGFY
FRRQLFYSTKWEEEFDASV*
>TCRU_10355 Nuclear condensing complex subunits, C-term domain containing protein, putative
MPPKKVAGACCGVEDVGRIFQQIHQSAAHFHKCKTSLLKYADKDRTGITDAVSRVALLVL
KESPRLAPDSLKRHYGFLTEVCKGFRERFNSDGIAIALMKTVEPFHNANDKNVRLGVVSV
FDALLKTVDQTDTTEERQNFYQNVAEMLKLRAHDKFPAVRERAVSAVSCFQSGKKDCDVT
QQLMALLCTDSSADVRRQILRCICARKEFLEGYFQGMIRCVRDVVSRVRVEAWDALGRFH
WKYIAAYATAKNIALPQLILQGLSDTSSSVVIACRAAFTNCWLHRDYRDDGEAMLELVLD
GGGGLEPYEAISTEILLYCRKHKNTKTYLVNTESVSAASLLLWKASAKLLADAEGDDETA
VLLPLPQFSALLQDTVYAYARPDVDPKTVKFKNLDEADIILRILLSVFDIYEENGYLAHA
DNTTRSSLLRIIGFLLKVVPDDDPALFIDVAIRSLKSLTGRTPEEATKTITSSLDSLFRS
LKLPQMYALGYDDVEAFGRKSRERQRELFRLRMKLRGGETSQEEYDRLKEEMDRDEKFLL
RMQFIILSFLSHSQRGDNIPTFCSHIIQLGRQQDNEIVKVASTTSLGLQCLVNPDTVHTF
MPLILSDANEIVGNSDRCVALAALGVAFDLVMEYGLRFFDCPARDAGYSSHHDHTGAAEL
GAATVTKHTTAMAATAITFSNNNDDATTTNTTTTTTAAAASGGGLTAIGVEARLQHERAL
AQEDEHKVGGNNLLNTLRLFLRSHCTERNPMAVVGFCKLLSCNRVPHTQVPEIIADILMH
YVAYRQEEKGNACAAYMVDYLNKFLYSFASSHPNRQLAFAQGGMMAFTALLRYNPSVALR
LMELITRLSDAYVLVHIREIDPVTAKQVARLAEGGNQSTEDSTLTKNSSTRTTATRNSTR
SGHLLRELSRFSLHEYIASELLIEIAQTDSEEVLDACLETLEKRMYFYAKEVPTWLLFVA
NRALDTVCSSAKGRLQKWRDEVCNRFLNSTESDRVANDANMAKWQDTLDARERALERLLD
SDIANVVCQTIRCVPPRDVSDVGLSAVKVENKRARETDTAFGINSILGRQRRTRR*
>TCRU_10356 peptidyl-prolyl cis-trans isomerase NIMA-interacting 4, putative
MGKEKKKATNKDGGNDGGGGGKAAKDTSGGSGYTKVKVRHILCEKHGRAMEALKRINEGS
SFADVAREYSEDKARSGGDLGWRRRGEMVGPFQEAAFALPKGGMTPEPVKTSFGYHIILV
EDKQ*
>TCRU_10357 helicase, putative
MSSIPIGDVGVSFPFNPYPAQVEYMRAVIDALKGRCNALLESPTGTGKTLCLLCSALAWL
EKRNGMTQQRYQIEGAGRTRVIYCSRTHAQLSQVIRELKRTRYGDIFSMSLLGSREHMCV
NSQVLRLPTAQAQQSMCNTLREEKNCRFYRGFQARNDHNTAVKDGKWVHDMEDLVSDGRK
CGYCPYYSEREEAKEADIVFLPYNYVFDLSIRKQLPFNLKGSILIVDEAHNLPSVLGASS
CMNLQPLELTNAIHDCSRAIEMKRILMDTAAADDNSQDGLMDEQEFASLKIILCRLESCI
AEENQDDEEKKKISSHEVNGSLPGVEIVREGSYMIPFLSKALITRDLFFGGNNQNGGGIN
DVITKAIAVLSQSESAALGLSKVQQFLNFVYERCESDDDEAYRFILRGAKGANRGSNQRS
LGYWCLDTSCAVKTLVAGLNSLLLTSGTLSPLEHFAAELGIEFGVSLKGAHVIQQNQVLG
CVLCKGPSGEKLNGAYAYRNSVDYRVGLGMSLVNISRNTPGGVLVFFPSYVALNAAIDLW
RAGSGRPGESLTVWGMLEDLKPVFVEPVEASDLRTIVSRFQREVDSAPSRGAILLAVCRG
KISEGIDFADNHGRCVVVAGIPFANHTDLFVRLKREYLTRVASHRPKVRGKLFTGDDWYM
NEAMRAVNQCVGRVIRHKDDYGVVLLADERFAERLDGLSEWVANRCSIYREFREAYASVA
HFFASFRRRSGDVAPPFFSSFGCVDSACGVEADARLGFPTEERVPASAEMAKRFASEKLR
QARAEKEEQMRSRIADARELPAAPYRVKVASGGAISDGGVGGQEISATAPTAARQLFRKQ
VLPVLPPADTVLVGSTSKEFCQFLRRQLQSASYDKFRDYLRQIASTRNDSTLSSDEMKRA
LSSAVDGLAGLFKEAAGERDAELLNAFGQHIPEEFRPYYMHLVRKRRRTSE*
>TCRU_10358 serine/threonine-protein kinase Nek, putative
MQLLDTCVPDLERYIIGEYLGEGSTGIVFRVSDALTKKDYVLKQISLESVGAEERLRAKK
EILVMNDVDHPNIVKFRESFSGANSVNIIMEHCESTLEELIERRQADGGEPFPEDVIIEW
MAELLCALAYLHSRSILHRDIKTSNIFITGKNHVKLGDFGVCTVLTSASVAARSMIGTPL
YFSPEVCEEEPYDQRSDVWSLGVVFYEMCTLRRPFEAEHLPGLIRQILTKEVAPFNTGLD
TRFEEIVRGMLSKNPSDRPTAQELIDSHLVVPASHPSHPSQKPSRGRLIQHYYGPELAFR
KKETTSSPSDSRLLRKEEEDQEGQWPVPLQPKPLPCKNKSRSSAVTQRESIGVVKGVHKV

VTDRRNVGKVAGKELSHEERVKAMKRIKDAKSKINMVELRQNMLYKRFQLFGELNVSPTD
EVPVVIELQQRLQPARVTEATSDSSLECSPTMRSRSRFMEDIATVIESHSADGKKIALEE
LEDAALLLCQYKVTNYGLC*
>TCRU_10359 hypothetical protein, conserved
MQNDLAQILKSIDWESIRGENETAPSGAPSMSPTVLNDGPLPHAEGSVSGNVEGVREGSS
MTSTGISVQQQQIPTMPMGPTGGTYYINTPSYQAISMPPSAPARGQVQTQPMVFAQSGGQ
MVYMQMPYFQHTAYQHNPSPQQIYSTPQNPYYHPQFVQLPVEGQMMTQMPQIPQQQQYFQ
PSALHTIGVPATAFQQQQQQQQQQEVVDNQGGFVCLLPGSQLAQGTPFYYYGVRPTSHY
VTTQAKDNFFDLPPYNNVLWQRSSHPADRSELAGKREGKGRTPRVPTCPVCGQSNFASES
AFRSHMRRKHEDTGSTLATEKSMETSENVTPAATADEKDNAG*
>TCRU_10360 hypothetical protein, conserved
MQASDRYVMMERAARDEMDMAEDLHNLCEHCMDNLLKWLVAAAGYKQVFMELLKGFWMQP
PRKRGAQRSRVHRGTWRDTTSLCTMRGGAMWWRSVAARGRDRR*
>TCRU_10361 retrotransposon hot spot protein, RHS3, putative
MVLTSDKGWPYSWNRKGAESTRGCYVNCEVERVWQIVSGDLTEWFSPDAGDYFTPKRRLL
IGTPGIGKSMAASSYLLYQLLQYDVEKLPVAAYSVGGSTT*
>TCRU_10362 BNR repeat-like domain containing protein, putative
MGIGWEKLDNWEDFSDAGGKYGSLRGPSLVDLQGHVFAIAEAHCKDGGDCSDVGFTGIAS
KYLDLIGVADPTEILTADASIFGADLLKEGSEVISARNGITRPTTLVLGDSVYVLPGNYS
HTGPQVGGTNERGLLLLKGTLTDEGGRKKIKWNETHVVEPQGRGDSRSLTELVGGGGSGA
VLRDGTLVFPMQAKDKDGTSVLLSMRFPNSGNKWELSSETPGNGCRDPTLVKWKEKKDDE
RLFMMAHCAGDYYDVYMSTPHGVNWYTSGQPITRVWGNSHNRKGTVSRADPPPQSLGKGR
*
>TCRU_10363 Protein of unknown function (DUF3676)/Trans-sialidase of
Trypanosoma hydrophobic C-terminal, putative
MSSGSYAEEMPEEEGEADGRSGGSTSSVGASSDMDTATETVDSERQLQQSTELSTENEGL
RSTGTGTTGAEQSLGLEAGDRNSERTMGSDSSLTPSGIDAEPTSAEDTDDVSRTEGAQFS
FEDGKEVPQTVDTKPENTNTTPGGEGIPSTKGAARHSDNDTFTGEVAELLSMGLSRDSTV
HVCVFRVFLQLLLPGLWGTAAL*
>TCRU_10364 TerD domain containing protein, putative
MAFDLRQKVFRIPNNIAVSAGLRWDFIGADPVDLDLSAVCFTNEGMFLDCVFFNHPFPTG
VNAEELRSSGVLVDPHQLPFMFVSGDSRIGGEEENQLPGLALAAKRRKYQLKNVNNRNNK
RNEMNRMGAMDALFSRLYNCKRQKREVVVCGGEKNIL*
>TCRU_10365 hypothetical protein
MYYFRAEKQGTYFEGWSMRLFAFDSQRRHMYYTEREKCVNRSPNSVTETHWPTGSPTAPP
WKKKFKVTKLVVVSTVHEFHLDDPHLKETDFFTLELHGRTRALASDEPPAEPLLIPAATE
GDGLQGATLEPANRDPFRLCQLYELLRDQFSTLSRNQGLRATASAISVSSQSALSETDQV
RTIQSPRSTSAKERHIVATIRCCNEEDFRQVWYIVQMVLGFDRLTIRPYRGLPPYDPRNG
IPFGHIPMHLWHTFMELENSVFYVFIRGDLVGHDHEGNAEVWLPNAYLCITHDMVLVMRE
NGTIPRWIHLYNVNTFEYNTVAKRPFFAFLTDDPSPDVLFIPKPPVYGPVAISNFSGKKV
VLNVCSILREACFASNGIRRATEFLDADWASSVREYFNTKEKTRRFKFSPLDGFDHSFSC
LIPKVHLARVWREVLREQNARSHDDVAAIPLEGTGGQTILSGADMKSVRHQMEVERSRSH
DEIVGMPLDKLLGHRRERLNASLEAPKIRPDNFSRNPTQGSEEVVYQEPGAQYICPDTSL
KVSNTGREKKFGLEGKVDELVNASFAAMGIAKPSS*
>TCRU_10366 adrenodoxin precursor, putative
MSIGFCAQKSRQRLLWRRLTPSSSMCLLHDSAFFSRCQLRLCANVAGTAATPGKVRVHAT
SAEGKTVSFTAPTGITLMEAIRDFGRLDIEAACDGTCACSTCHVILREEDFEKLSEPSED
EVDMLDLAPSVTKTSRLSCQIQLTDALDGITVKLPPETSNQMS*
>TCRU_10367 MSP-B, putative
MRRFVSTVLLFLLWLAGGPCALAEHRCIFDRVALNLSQLQTAVVQELPRGRAGAWQAYTV
STPDWAPIRIKVFAEDLKDTRKYCTVRGDVRSDFTGGRVLCRRQDVLTKEKMRIMVNRLL
PEAVKLHTERLFVQPVSGVLRLPRFKLGVCGEFTVPIAHHLSGVVGADMLLYAAAAPTIG
GTVAWASTCVTLQDGRPAAGVLNLSPSFIAPKRESIRVVSHEIAHALGFNSILMWRLGMM
SRRSDVRGKAMTFVVDSNETLARAREHYGCSTAPGMELEDEGGEFTAHSHWERRNAKDEL

MSPLVGAGFYTALTMAFFSDMGFYRANFSMAEPMGWGYKAGCSLLQEKCMQNGVTAHPEM
FCSDILKTPACTSDRRALGFCSIAVHDERLSPEYQYFVEENVGGYRNTFVDFCPIIIPSE
IGGCADGNSFLMPGSRVGPQSLCLKGNSLEMEFHGRIGDICAEVSCQAGTVRVRYLGNDA
WHLCPEGASLTPKLPFIGGQILCPRAVDVCSQLSDTSPGESAHEENQDEIDTPDKREEKG
MDDTSAPAEKKHDDRRKREPSLLEKMCRLLGINCPKINWRKVWPFFSSRGMG*
>TCRU_10368 ERAD-associated E3 ubiquitin-protein ligase HRD1, putative
MLSLNAYIFLSFLVPVVFVLDYANAYREYFTTVVELTNSSLFRLLCVNVFIATTFLFWLV
ACRVFFGKLNHTETELLRNSVPLYIAECVVGPFYFGVSVLGPFGVAALFTVVLALLHGVA
RERTTTLHVVESPTERLRMLSGLTLFFLLAMPLDLYVVFDVFVNTARERDEYLTLKYSAA
IMYLQFAISNINFLVRLLFTEVIGESDHGPLAFYAELFFSLLKSSVFIVSFTYVCIVSQA
PFPLLRVLINSAVDVVKKIQSLVTYLSLTRFVHSMKNASEDILARDSCCAICQDEMKAEQ
NCKQLPCGHCYHEHCLRRWFEGMSTCPYCRADLLRHMRKANRSVHFIIFHNRRRNAGNNE
NTNNNTNNNNAATSSAVPPSFTREGNAVTDTLRNSAYEQLNPTEEEEIRRAYARYCDARI
HAASRVTGTSDQTEEQLREPAASIGIVSSLLEARGEHATRETLFFAATGGSNDSRTEGGA
KEGETLKTVTDSDLIMRRKYLQQLDAYREYEEAIRKASETLRRRLLAIETSS*
>TCRU_10369 hypothetical protein, conserved
MLHGSLPSLASLRYRRPYWMLFLKDVDNWKIYTVIQQPDHQRTEMLYQAWLGGLDRPYTR
PKCMANQPLWLSKKRHILRKDRLDGPETPLEKYVLEWHKRFHSFQGTERPTVDNLHTALD
LVERPLDLSYAFQLLNQCRNVNNIRFAKDTFLVFLEACLRVDRKDCALYATENAEALGFW
HIEEDYRRYLRGEQSWYRLSPLDNMYYPLEENVKLNAGRSPPSSAAVAEGDAEGTAEKTC
FEAAAGAAAWSDDEGSMKAGSSREGMIVDDEIARLEAELAALEEEGTDGDDVKGPKGH*
>TCRU_10370 nucleolar RNA binding protein, putative
MVYALLELPAGVALFKVDGERRRLKAMLQFKSTADALATTTQVVNGELSKPVRKFLKKNL
VEKEITEELAVADSKLAKAIKETLAIPCVHGDETLATFRALRANIDALLQEVSAEQLNQT
ALGLAHNLNRYKLKFSPDKVDMMVVQAVALLEDLDKEINKYAMRAREWYGWHFPELAKIV
NDNLLYAKIVLAAKTRFNVRDIDFSDFLEEELEQKVKDAAMVSMGTEIAEEDIENICRLC
SEVVAASKYRETLSAYLSSRMQTIAPNLTTMVGEQIGARLIQKAGSLLSLAKYPSSTVQI
LGAEKALFRALKQRQATPKYGILYNAQVVAKAAAPNKGTMSRVLAAKTSLSARIDSFGEG
DNAPALEYRSKVEERLRQFEEGVTYGHSGNARGGGARLQQKRAHPNGGDNSNHGGGGAPY
KRARLNDGGFQQRK*
>TCRU_10371 Putative papain-like cysteine peptidase (DUF1796), putative
MLRSSSLLRDVSFAGMQMPRKYVSMGGWCGPALILGKLGLRTEAYPFDFSRCTLDGILHF
IREGFAHGFYPPGLPPYRPECVGIWVLYRGQHTAFAHFDLNDPKIQAQFSRKMKRWDKLI
DAPEMPVTFFRTISARDPMEEIRLIPEVEAALVARNPTLDFRIVVVAHDQGLFARSVELT
PLSPRVSLWSLAYTRDASFTLFDRSQQAYADIVLHSLEEENWPLDPARMPTPVGLRDTEA
DYERRVLYRAGGADVSFDSLRADAFPWRSHDNIALIDGVASVGGTCVGIGSTRCTDGRCA
FCGSTDYHKAGRPFRTDRPFTAEEDQLILVHLYRILTGGDKIEAVEELAHKMNRGAFEVI
CRIQFLTNSSVKIMDYAWEHEGE*
>TCRU_10372 actin related protein 3, putative
MSYPVVVIDNGTGYTKMGYAGNEEPTYIIPSLYADNETVRRRSNDVFDDLDFYIGEEAAA
RASSCTLSYPIKHGIVEDWDKMERIWQHCIYKYLRVEPEEHGFILTEPPANPPENREYTA
EVMFETFGVKQLHIAVQGALALRASWTSGKAKELGVAGKDTGLVIDSGAGVTHVIPIVDG
FVLNQAIQHIPLAGRDITNFVLERLRERGEPVPPDDALLLAQRIKEQYCYIARDIAREFD
TYDRNLPDHITKHCDVNSKTGQPYTVDVGYEKFLGPEVFFHPEIFSGEWTMPLPEVVDRA
VWSCPIDCRRPLYRNIVLSGGTTMFPKFDKRLQKDLRVIVDRRAKKNMEASKDPNRQITY
DVNVVSHDRQRYAVWYGGSMLGSSPEFSTLAKTKEQYEEYGPYICRQNNMFHSVFD*
>TCRU_10373 hypothetical protein
MIHVASVFIQAINAATLEDVERAAEWVLCELQHPHNEADGVAGREPKESKPSPDNTAVSA
PTLDGVAALYAEAVRCQCDGKTFREALGPLHLQYQKAIVLSDAFDAALEGLYRLGIMGGM
RQSFLPQLTGVSWSLSHELGDRTGTPITPSAPVFDFVFTGNSCATRPPTKEGNEVLARVA
CTSGQAEDLLETLRDMLAEAERLTRQK*
>TCRU_10374 hypothetical protein, conserved

MEAALNNPIANAMLYSDGALHLVGARHNEEKSSLFPAPLTEELQMTTSILRNWADVDASF
STSPVSTVGLVGYLSNAGTANTWIDECRCVIATVTNGKNVTNGPQFTGQCYP*
>TCRU_10375 retrotransposon hot spot protein, RHS3, putative
MYGELVCALVKGLKELRPPERNEARDSVLKVNHQGHPTRAVGLEELQGGVTRIPMEYGVL
YLPKVENFPLVDGFFFVDSPWRTLVGLQMTTASAHHTTTSTVRQFTECLAAYFEGWDELS
RDMSWEMIYIKNAFSKKILKWQRCDVVNPNNETDAEKKIVAFWNKEVHQYQFMLTSDFLS
KITEM*
>TCRU_10376 hypothetical protein, conserved
MCVVNLCSLPTVIAHVSHSASDIRRLGPAAPIADDLNSHHELRDGRSLSTTAGEDLATTS
SGMEIELSDVPAQATRISGRSVSFPNLNAQRVLRFSLYVHPFTWTRTTICHPTLQERRTA
SRDRQACCHNGNISPFSCVMPTVMLPPRRV*
>TCRU_10377 hypothetical protein, conserved
MDKADINQLAKDTVTRGDADRQDNHESDEVIEEGKEGDGEKYAEKPQEKDNTQTQTREGQ
NNGGVSPLLPPTPSAVEGSPPAEKENSQNSAKVKDKITPSGPKMDSKAPEPPSGDATQGQ
HSHDTETEDLTKNAATGSPAETKISSTSTSGSGDHVHNKADEEDDQSSEGNKDSLESDNT
NVASPLSEAAPQIAETINAARINDAASAGGSDSSTAVSHTASPLLLLLVVASAAAVVAA*
>TCRU_10378 Mucin-like glycoprotein, putative
MTCRLLCALLVLALCCCPFVCAAESTHTEVKAAVAANPQSPPSVIPSQGTSEPGSPSNGS
GAELGITAVAGPASTAAGRESVGVSNTLQNHGTDGNPGPEIGTRQSAEKANQETEDPAET
TTTTTTTTHAPTTITTTTTKAPTTTTEAPTTKTTRAPSRLIGIDGSLSSSAWVCASLLLA
ASALVYTTVN*
>TCRU_10379 3-methylcrotonyl-CoA carboxylase alpha subunit, putative
MLRRTRFCHAEFKKILVANRGEIACRVFRTCREMGLLTVAVCCESELNARHVQEADEAFV
LGPSPASLSYLRGERIIEAAKRLCADAVHPGYGFLSESPEFAAAVAEAGIEFIGPPAAAM
ASMGSKSESKRIMEAAGVPVVPGYYGEDQSFECLCEEAKKIGFPVLIKAVSGGGGKGMKI
VKSVDEFKLMLESAKRESMNFFKDDRVILERYVTQPRHIECQIFFDKFGNGVFFFERDCS
VQRRHQKVIEEAPAPHITPDMRHRIGTVSLRAAKAVGYVGAGTVEFIFDTERNTFFFMEM
NTRLQVEHPVTEEICQVKGKPLDLVRLQLETAQGIPLGFTQEDISIYGACVEARIYAESP
ANGFLPGSGRLKYIREPPQGIHRGTRVRIDSGFRSGDDVLVHYDPMIAKLVVWGENRSKA
LEGMHTALDKYHIVGVQTNVEFLKRCLKNSSFIEGGVTTNFIEKNRTDLLRTKPLMNPVL
ALGAVSFLNYYGSAASAFRLNHTLFQRVPFLVDGRRVTVQVSVSRDGYFLCDVDGSRCGV
KVEHWKPINTGTVEFSVRMDDGCRFDCTSVITGKAIAMVLPEEFYILNLHSLSEDFGNAS
LQEAGSARVVSPMPGKVTKLLVPNGAKVKQGEAIIMLEAMKMEHFVRATCEGELEFFVRD
GDTVGGEHLLANIIPPSTS*
>TCRU_10380 hypothetical protein, conserved
MYAVNPWGKVLLIGSSVGTYAMGIGMRWRESNVQVIEKRVDPRYELALRRRCVCTGQTAR
LLTDLGCTKARIESVFQRAKGWRFLRPSLEIIKESTVFPGCADGEAVYHCEEGSLLRMLR
TEFLRFGGGVSWGTEAFDAFESGDGSGAWCLRKTYGLETEAEAIITMAKVSSFASVLMVD
NPDRMAVLFYEEHGVFCPNKELIEKVFGRNDVAIVMGLGMVIHLWYTNNVIAWRAIRREQ
KGSSGFCINELHPVIRNVLENSVEKHSCVRLLPATMPAIKDSVLHVKLSVLGDGLLPVDP
FEWRGDRARCLVEEASALCRAFYGKKYHRGSVAYLLRGIEQDSLSKRASMLRRDLADAER
FLAVHPVIEEEPHAVSMQQVGS*
>TCRU_10381 dynein light chain 2B, cytoplasmic, putative
MEIHAAQAAREREQRIKCVEEILLRIASHEGVLGYLVLNPIDGSIFKHSGFGGDAKKMQK
YAEKVNGLTKLAYSTVRTIDWKDDLTFLRLSVGLTDILVAPDVEKRYVLVVVQEIKQ*
>TCRU_10382 hypothetical protein, conserved
MSLNGFIIGFNSSSAVCPVGNTLLVGAGSCVVTKRGGESNQWVPGDGRYRIDHLAYSSLP
RLICVTETRLNVVLHVFSYPEFNRVQKVEEVAKVEVQDMQFSPNGEILALLTCIPCSSVT
VFTLQRGRTLERRISVELADKFWKYLAFPPQRKDCVAVWDAGEVALISQLLLLSSPSNVV
SLDSHGKEFYSCCWSAYGILCGLQQGAIILFDELKMEMQDYLTCPGSGAVTYIVCANPFL
LVGTEDGAIFGYNMDEKELELLLRVEYSVERLFLSENGSDAVIVTQAEVTKLDLNNKQSA
VMCVRETGNTVKVLTVGDYVIAVSEDGSLMRYDKEKNTICQFTTEFGDQAIDACAVRSAV
IVVYHSGCVRSFIVNGGFTFSSQITLGEMPLTLCESDGVSSLAASDGTTVYFFALQDNLL
YPRGSLNSLTSQVKKIRWNIGGHLSVFAACTNGEINMVQCIGTDGSSFDTVAVEAVWRLD

YPVNDFLPLYLDDDVVNILVHSVDKDTKLYVLERRRERDIKPLRPLFLMRDHEGSGGSVL
QYFGKTAVLSGGADGKVVVRDVSHYLLKLTPIPPSKEKRRPQGEFPIRHMGKEGITSLCA
WNGDCGFVCGGHDTVIHFITSGEPISDSWKEPVWKKEKLLGVSDAMQTPMEGSSTLGEFT
RSSVLSDLTEIRAEVNKLLKERSSAVHVEDFLLPSQRESFSAECELAIQKAKEDDYYRLL
HNEFTQYIIRNECWDTMEVPRAKVVSLNDLTVQVYNFHCRKADPGEEKLLKKLKFLRMLQ
IKVGNYFTFSSLVKRRESHSNPLQQESDIADETSELLYDAMDVYTNSRAVIQIHLLRGRI
LRLKMAFNLRFDNLCERKKRELQRIEERNGRCRRILRQLGETSIPADLCFTPVFDVEEDP
KTVFEVFDSEIDPELLKLSKKNESDAFIISPTDEAALKTWMDGLEKDADVLAVKVTLPAF
ADESLEQYVEPEDRTEEQQRAYEQYEKQLAEQTIYVNERKEALREEIAELKRVNSDAARA
IDEEISSLRRKRMEVAQLVDELESHQMNALRRIFLPTTILNELLNVIKEKKELQSRLKQL
QSLEMHRQNLLKTEESRLQQLIEKEKDAVAHMRDSPPFDDGTWGEKLYRRFTRWRAKYEE
GQALAPLADQNENFPLPLWKLYCECCSIIVESKRVATHSTATVQKLTESLTEVEAELTLV
GKKLDEKEAEEEFCKQDATRKVLNVQNLYRLRQGQVQDEEAMLNADFIDFSFRWTKDVLD
YNTLIFASFDEVSRIMGNTSHQRQAMKMASWETERLQYCVGTLEMELRQLHTLRVTRQMQ
ESIYTGALVSREGEVEKLNRRIDSIRQMMSRRVEDRNRVIKRLNIQINDRHLENTLLGDQ
VQRVKSVVDDKKAVWGMLGEHDNESTRLQERMRELYENSELEELARCQQEELVRLKREVD
RLRERTFPSFAVVSKKTVT*
>TCRU_10383 serine/threonine-protein kinase NrkA
MTTFTSFLGVDAAENECKYIKKKLIGTGSYGEAWLVERLEDHSIFVAKLMDLGKMSSRDK
QYAYSEIKCLANCNHPNIIRFIEDHEENDQLLIIMEFADSGDLDRQIKARSHDNFRHFRE
HEALFLFLQLCLALDHIHSHKMLHRDIKSANILLTSTGLIKLGDFGFSHQYDDTVSGVVA
NTFCGTPYYLAPEIWNNQRYSKKADVWSLGVLLYEIITLKRPFTATNMKGLMAKVLGGDY
APISENFSTQLRDLVRAILVVDANQRPSIREVFQLPYVKEGLKVFRQIVKKNTRIVETVK
EAMISHVSEILSSAPDSEPRSGLVGQINLDVSFKGYVKKLGSGSVHSWKERFLQISRGVL
ILSESEADREGKALSLEQVQSACPVPICTAKREFVFALNTIGGKSMWFQAESHEKMEMWI
HAIQQGLGVS*
>TCRU_10384 retrotransposon hot spot protein, RHS3, putative
MKLNEFPTRELDGRGIVDTNRVVLLEEFFKDPTRYIRDKGALNEIQASGRYLSMRRAVKG
EVVFDEDIRKLCDKGVSNLPGRSLAAAEVKAAVHNITKHFLDAAAEETRNPTTTSAPEKL
EGLYESVHNARWSHAVELPDGVERNKTGTGMRVHEGRPEKSWSYREADDAIEKNDAVQQC
GAAPPVLVVLASEKGWPYSWHTIQGLPKDVFVNCEVDRAWQIVKGDITAWSSPHGGTDFK
PRRRVLIGMPGIGKSMAAGSHLLYQLLHCDAEKLQVVVHCFGGRGACVSDKTSRTVTRCS
DEDMCISELRGLRRHGRNVYIIYDVAKEGTPPPRHFAPTSGWGMIAVPSQR*
>TCRU_10385 ubiquitin-conjugating enzyme, putative
MSIGASAMRLIMRQIQDIEANPTDGVHIHRSDNLSELLFDLTGPEGTPFSGGIFHVVLYF
EEGYPEIPPRGVFRTKIFHPNVAEKGDICVNVLKQDWKPSLGLRHVLTIIRCLLIEPNAE
SALNEEAARLLLEDYDAYRRKAEMMTKIHAMKGTRPPHDVPPPFLSDDGRENGQLLSRGI
ANVGSASLPASEGFVSSQLRNASESALNKRSAVSGTSTNVVASKKAVEKKRAALKRI*
>TCRU_10386 hypothetical protein, conserved
MRQGQGRQVITPSLPVSQEVQLTEEDEQDRRWIVDSESRSSLLFLSVSSTTASHSRRNLS
FLTSHVGKFDELPISHTRKISVTLPLPQIVSGHLSELRTASLDPEVAMPALVDKMSITAK
HELPIYNIRTVVRKENHPLWSPSTLTQLEYLFGLQKLGHSTLSKGVQMASSGELGLPGTM
ERPLLLSEGESHGSCSKITSIGVGDHQQDSGLLRTPSNEYLAIKGRTDPLGREQLWALCH
SSFESQTGLQGLGPREVASLIPMLLRDECVCRQVIVEKERHEALLTLPMPPHATLNWIHP
ALVAGIEEITIMEEICRKYILEEESNQIAPIWDFYVFEHRCLVVGTKKLTCFLRRWILTY
RGRKMRQLEQLNSLWRREEKSRLEIIQTWLEARKGLFTRLLIATETLFRVVIEELQIHAQ
YAHGLISISLKAQTDLFFHLYGAVMPRAIACGRISGCTRFKLLDLNDQHGRGCLSSWEEK
GRLAISCMMQREALEKFLEGPKRQQIVEEEFFARGRLTCILFAMLERCHRREIEIVEACE
CQLDVLPHFNAPLALGEQQNEEKQAVLYLTAVQGCPS*
>TCRU_10387 hypothetical protein
MQEDRTWALEDKAWNQIKHHAVETTERAEKRLADLRELHAAVKDHLLLLNVREEDTISRL
HGESKKLVRQIQQREEELIKMLRDDCALQRTQIEKLQESIETQKKLLETQKSQLEEHKRD
VIERAEAQRQVTELLRQSAFFEVPELHCYNVTSATIVTDRHLTLVRDVASFFFPSALTIP
IADNSIYLPLGRGKEKCESVVQENASMILHDGILHYIATTGGKKPFSNPVESDAVRIYCD

APVVLGELSSLCNAVDATRTTAAVLQQTQCFRTASQEGARIEIDFGDRRWVECSAYALRH
GHATEHAALRSWRLLGSRDRVRWVVLDEQRRNNMLGRSPFNVASFTIDEEQVYSQVKTTR
HSASALGCAFRYIALELAGPDAVGKYHLELGGMELYGYLVNTLSL*
>TCRU_10388 translation initiation factor IF-2, putative
MPPKGPKAAPKAAARKGPPAAMLAKLKQHMERQKEEEERRLREAEEEERRLREEERLAEE
QRKFELAERAKEKQRRKEEERQLRKDAKKDLRNGALERMAAAGFILPDVDKIREEQQHVR
DKPRHKQEPKPREKTQVAHPKQVEMAAAPPEEEEGEEEESEDDGELTVATDSEDEVDEDD
WEALMERDDRRAARHLENERIRAARVERVEQRRKENEERARLRAEAEAAERAKQHVLESV
ASLRSPICCVLGHVDTGKTSLLDRIRSTNVQGGEAGGITQQIGATFFPREALVGATADIN
KKYRYNLNVPGLLVIDTPGHESFTNLRSRGSSLCDIAILVVDIMHGLEPQTRESIRLLRQ
KKCPFIIALNKVDRLYAWTANENMDIEQTLSKQKDNVRSEFDSRVNQIKQELMAEGFNSE
LYYKNKDMRKVVSIVPTSAKTGEGISDLLLLEIQLVQQFMEGKVTYKDDLQCTILEVKPI
TGYGVTVDAILINGELHEGDTICLCGQNGPIFTQIRALLTPQPLKELRVRGDYIHHKQMK
AAMGIKIAANDLEFVIPGTPLLVVHNGDDKEKIAHEVMREANSISDQLSPDGVGVTVQSS
TLGSLEALLAYLKDMKIPVASASIGPLHKRHMIQLLSMKRKAPRYAVVLAFDVQVSEDAR
DIAKKNDIDIFEAKIIYHLFDMFTRYVAEYENREKERARAIAVFPVQLAIIDEAIHKSDP
IILPVKIERGQLHPGTPLAIMRGDTPLLLGRVMSIERDNKNIPVARMGNECAVKINSGET
GVVYDRQFTKSDSVFSLITRPSVDAIKKFKDELSEDDINLLATLIKVLKVPPR*
>TCRU_10389 hypothetical protein, conserved
MEEEDMKRVNAIESSREEARERQLSVFCERAKHEAEKMTKELERRGGTTLDELERTLEAK
KRENSALQADRESRNWECEHTLEKIRTRKQDEKSASERLWQAMQQPEQELSLRQSAIETR
EQQLEMVQLDGARGREAVMRERHSIEAVRRTVREERRRQRRQWTHQVKEMNAKFPEEVRP
LAEERKKKREQATAKEDVAERALAADIKMIEEYLPKLISVEDIPVNPEETGIIRRQFDEV
FTQEEQKYLPSAEEERARKERLGRGLEVYIDSVCLMTTWQIKMKNCMTPRKRNTTSVLLW
IRC*
>TCRU_10390 hypothetical protein, conserved
MTKIPSKGNACRILFFLSEDCKRIHSCDLDHQGFPLNRKRPPVTMWIREIEKVLIGLSTT
SFVNYSGEAQLAKTRQEAVFGNGTHRHDPTQNITPSSLGANNHRAFTLLLCGGKSLEVFV
GLTATARPGLLLKRLLHLRTPAERLLEERRGT*
>TCRU_10391 MMPL family, putative
MLKEKKLAMAMMLLYCILLPFMAYFSWKFLNNTGLTFSAPKKTIVYDAMQTAELYFPYQL
PLDPLYMLLTSRNKSKSILEDPHFEPFCEYLVDQVKNKSSPFFGVVEGVDGFCTIPNYSS
LRYHFIGGDHNESSLITIILSSSVDSRNVLPTIVSVVDTWCDLNDVQFTREYTDKRLISR
DATGGIVGDLFRVDVISIPMAFMVLVYCVGSVRLLLIPLFTLPCTVSIAFGIMYPISLWM
EVSSFAPEMTLGVVAALSIDYSLFILTRFREQVTIQELLLGRNPKAELEVVKNTATMSAD
IICVSGLAVSLAVGILSFLPVLFLSTIGLTMSITVLCTVFVSLTVQPALLLIFYDFFGHP
PTWTEVWHKLLACCGCGSSLPSDSLRTDIDEDVSTAMPQDPLLADSEMSRSELELLEYGR
QMSSYWFKIGRTSFRHPWIAAATVLIIGAPFFYFALQLRMDFNVFTQIPRDSPHGDVLRR
IQNDIGKGSSIPFYILFSVRGTYDVSFWKTNEMTNTIKSVIEDIVATTGQPYSSIISPNM
IMKNEDDAVYWLNSWESFLLYYTNNEYEYLFKRTVSFPGNKAAFIFVTPPVNPFGASANR
YLNQIYDVLKKHASANVYFDYGILGASSDSWAIMNKSLDFFPFQILFALGGIFIIIMVMF
RSLFLPVRLIATVIYTIGVSYGVGVVVFQYNWLHPVWKALDGVREFCFLIPLFAFLFLSA
LSLDYDVFLTTRIIEFKKMGYSDEAAVAKAVWKTGPIISFAGIIMFLTIGSMVFSSVMML
SQFAVVCATAVLLDTFVVRPLFVPALMGFGFGRSLWWPRQFPELKRDVHDMRIDTTDTPE
GISIEEEVDREAAFRVDNVRDEKVFKPEKPNQRPSALAPGNDLKKH*
>TCRU_10392 Myosin-like coiled-coil protein, putative
MTSVSERLVLQLVKLHQREEEIERERALLREREDLKASLGKRLAQVQGQLQKVESVRATL
EELNRAEEEKYHEARKEDEVERERLSESLRDAIDTVNAYSEEVMKMEAKANHENKSLKEQ
LEIYAKHLSSGEDKYDEIMKAREAEYAKIESKRDTEAARKPQLEKELEDETREFEAARKE
HAELQEKVNGCLTYLSDFQERLLKARETFESAKNEKERQMRKIRSLESDRQLMISRAEKS
KGERDKEHAKVMLLEEKINTLKKQTEKIWAVVAMLDGGEADKEARNEKN*
>TCRU_10393 hypothetical protein
MRQSGISYKVQHLLDSLVHDKKCADSIPSASDSLAASQTEYVVKRLKEGISKEKLTLYLL
GIEGAVVPLPLVPQNYQCQAGKIRNFVEWCFPESARLCEVIKRTAENLPALREALDAPTI

DRDRVCTLFTDHICEIEATKGVRPFYYTELMDFIMEKGFELGIWHSYIFQDAAMAIKEWG
AQGQTRTRVAIWSICPVAVTKALLRHSDYGDLTHYVLDYFDPSVAGSALELSTYMSIRRQ
LERRFAPFASDINILFVTSSSNGAVAANASNAIDATFLSMRPFNNPLTLDTLHGIDIATV
SSFYQLRGGSVSYPLLCAEAREYMDGRAQVKAIKEEEQLSS*
>TCRU_10394 choline/ethanolamine phosphotransferase (CEPT)
MGGGIGSSGGGGSAGSGSGVVGGPPHPRRISLNPIVHEHIPPDYLSNLKKYKYSGSDSSI
IARYVMQPYWNFIVSLVPMTVAPNAITLTGFLIGLSSSILVMFFFFFYDAVYPAWVWYYA
AAALFIYQTLDAVDGKQARRTQTCGPLGELFDHGCDAFLTPLVQVILCCALDLPSWMTFA
YSTMSSIVLFCAIWEQFSTGTLDLGYINGPTEGIFMACILFIITGLYSTSIWDTPVISPY
ELKISFFYGEVSFVIFTLRSLIFLYITVAACLTVGANIVHVVGRPGVHVKGTPFFVMLPM
LFLLFFHVCLFLTYTSIHDKYPFAFELSFGFLTSYTVTRMTVARLCAMPYSLFNAFYLIT
FCVTFGALVVHAHFRQIEIKYLEPSLGSAMVALAALGVWQYLHMILSLFTQISYYLGVPL
LSITSREEKDARAME*
>TCRU_10395 nucleoporin, putative
MSGSSLLSCVVSRVAPSLLAPRRDDPDAFLRHLQLLSKDFITRFSSPEAILTPYFSSKEK
IQPAATSASENSVLNVPSSAHGAVDELCPLQIALKFLLGEKESCNRMHVFELSIFLALLR
HPCQGYRNILLWSSLIEKLEELGFYYVMQRRISQLWESVKQQEGELDAYNELRLIRLSCD
VVLFFGEHAPQIPSQDVLRELALLAQEMWAESASMVVRRCALVISVFLTKYSLISIEALC
SYKTSVDSPYCLVVLASVPALRERTDVNPELLRAALEVVFTTTVYSTPIATYFSDEGVHS
VSLSLVQRQFAKVLYDLFSGVSGEFWGYFTGAALLSAIEAVARYACLWDFLPSGVPLLRP
YIRNFLAEGSSVYTVSLFNFYASALAYHVGFDVLVDEEAAILNRSTPCYITYGSLLEGEA
EEKGAALTHNTEGLTMVMTDTPMKKTFRLLAMGWRSFRGGEKVVVRSAFSLLHALMSNYS
SHQKVLEEVIGCKLYSLFPHVATVVLTDSVDDDDVELVETFYDTISSFHPLLGNVAYAAS
NLLRPDLMKGVGVRYESTEIALLHLKIYDTLFKSYENAVPFVGIVEAVTHIPHGLIPCSF
LAMEFFVQWLSVVRAVPLEVPRSLFQLLSKEESMARLIYRLCEGIFVLLRELQSGNVFLC
SLPATPLLEGAICLLSAAVCDGGHHNTLATCVIATYGENTLSACFMLYCVIFSPNASVSL
VESTAGLLAYVLERSQEKLFGTMRFHTSTELRRILLSSIHHELQLSTATNKSVNVFRLAS
LRYLLCLDPASFFFLMLPEERDSGGGSSELPLTCILRDKLGCVEITPLEKVEAFDLLRAL
DDLDFPITSAVNLLSDIIGGSAYVQAAFAAAVIKYICGSIIGKMHFEGSRSAKYGERGGS
QQRSPSRSTIQNEKGNLSSEDVAAIRVMLETGSRALEHCSAFYQVIERQTGTVNNWVDSR
LSGDAPKRNSQELVLSRVTQDVVSNLSTFTSIGLSVNSLQAGSGKIKLKPMLLGDGFLLW
NDGEEDVISLNHMASALEAMTRLTASLEAVAWLTCGEKEAHFASSKLLELSLQGMQMVGH
TAIPLRGLMWSCFEGWLSLARGAASVHMQSLREFALISSPLKLNVLFQDFVKLMISNHEH
IDVVCQGIKVLLAFQPVGSLDEGTAIQIFEFILKFLETHLNRAPLSSLTTLILGCGVIYG
RMGKFSPVRCALSTLENLWTFATNLSYKIPATGPASKLSDIFDHVLGAASTVLLQNDELT
TYFSHKRVIALANALGQFNDAAIYDPIANLYGPQAWHRAWLSVLLLLHAVLVNMGGNRSD
CSEWLNAVSTLAATSPRFQDAVSGFVSFGDVKETKTFAWELREMQLCTSIIALLASFGFS
NASLTPHVRRCFCHIRRYQIPTVAAVDERVVKGLLVTTIRDQLSYLIQQSPPPTFSEEDL
FIVTIERYRTSSTNSSYVLHEDSPQQRMVGDGSELREELLSFDVLRSFILRELNIIRRLH
QDSAPGAEAHYPPEHTPLSHSSFTTATSVDSVLEVEFHEGGNQNSAPHIENVKLALGLFV
RYARLYLSTRSLALLDRQELSVSLEKLLHALNRLIHDVRRLGNSVLTGIVENVREDLKSL
AGILQNS*
>TCRU_10396 flagellum targeting protein kharon1, putative
MATAAVERPTTAEERVLALNNPPPRPQKAPDISHRQRAAINTRGAGVARSLMSGPVAADI
PDSPPPAAASKKIVHASPSDFLAGPKEPGHVKRGVRRYEDRNESTVGKALTEEWILGRKE
DDPVPQHVVRQRGPKDNLEGLCCSVRTEEAKPRLQRAPGLAPPHTTAAPYSETELPPRPA
EAVPVKGKRRFHEQTSVNLFGRAAISTRQAEADRKAERLLHSRRNKANESLDVLNLGQYT
REDLNEVERKIVLGPRQFIPASLPPRQRPIIARLKSHANETHDIFGTGKGVEDVEPVHRK
NPGASAPKNSCAANIFGGPPLEQKPPRPFRPSQLLTYEEAPNLSKKRKDLVEAPARPASA
NAAASRSGKKLEAGQLFNSKSPDIEPRGGRSRGVYAPKTGTNNIF*
>TCRU_10397 hypothetical protein, conserved
MLANTESNHTVGLSHSHNTKWETAFKGKTTTRTSTREPKKEYQVALMLQGNKASVQIDGK
SLGEEEVLLTGQRPPEVLRVRFGACGGHESHVTVENVFLHNRPLNSTAMRALKDRVPAPT
GEAAPTPPEKI*

>TCRU_10398 retrotransposon hot spot protein, RHS3, putative
MVLTSDRGWPYSWERGESGILPDCYLNSEVERVWQIVKKDLTKLFSSHGKNKPSCHPRVL
IGTPGIGKSMNVGSYLLYQLLHYDVEQLPMVVYFIANLTFLFDKTAKMVSLYTNEASILR
ILDGLPDRGFKGHIIYDVAMKGHQPSIGLPCKGWGMIVVTPPDKNNHEWWAKQMGAEEFI
INCPEENDVRAMCIWMKRNRPLQEQAEYWKEVNGRMNKVGPILCFIFGKQAYDDRIKACQ
QALDGMNASKFEGYLDIGYCCVSNDSDLSRKLVKVVRVRRGYNFASPLNVLISPHLERET
LSRLEDGMKQSDFIFFVLRFWDYVPPYLIEKYAVSAFLNDDFLRAIRLKIKELWPPGRRE
SHRCALKEHSDTSFARKEVLPPPERLSNPVAMDHWVLYEPKVQNFPLVDAFFFVDSNPKT
LVGLQMATAGGHRTTTRTVRRFTE*
>TCRU_10399 BNR repeat-like domain containing protein, putative
MIGSINVELLQGVDLFVPQTTLVQPKDGAVPVTTRDSFGLPSFVSAGGVIGAFAEGHMDG
EYQGGQLTKPFLLLLLRGTSTLRGIGPLLLVRSIKDTWRAHTVVGAAEGEESLGVVLRRT
TITKGHGVFPPAGGSDVSYEGRCWREDGLEPKLVVGDVTNPTGGKRSGRIEWGDPKPLPK
LISSSSHEGDWTEFIASGGAGVMVEDDTLVFPLMAKDEAEDVCSMIICSTDNDSAWAFSE
GISPAECLNPASPSRRNHFSWLLTARVARGFTSRVTWGQRGRRHSGHSQPCGSTHDQESL
RRKACVCMPSSPRPLREGGSHCALREGMPRRRKGPLRSAFGSRTATARFLLDRLPWTMLQ
SGGQN*
>TCRU_10400 Protein of unknown function (DUF3720), putative
MAMMMTGRELLVCALCVLWCLSGFGAARDNRCSEGGGNFFTHTRKDGGNDRVLLEADCGL
LSTRMGLIKAVEAAEAGPQPSRPDPPQVTEESLPDNKLDNNANGTGAPDSEGVSVAVEPP
AGIPPTPGGSDTEEKGKKSEVVNTSGEKVAGGQEQKDVIEADPQHQSVDQLSSSSSSDRP
DTESVKQPSSRENSKSTEISDDPLQEEDNPRSESDSHEEEEELVKKEDKKNASNEAPKET
PGDPTKHTEIQTATTELNGQSSPQALEDVEQPEEVQGEKDSNDNSQTKSVASIAAKQQNE
PSADHGESGPPSPTANGDAANNEADNSTEDGISNSDPAADGAGTREKKQNENKDANPKET
PVEATAMKTTTATTGDSDGSTAVSHTTSPLLLLLLFVACAAAVVAA*
>TCRU_10401 amino acid transporter 10, putative
MSRTNPVVPATSGSLPDDGDSPSHHSSHEMNGSERKRTGEDAVPEKLMPVSNEPPASDTI
LAKLKRCVIVVIPPGGILASAFNLASSSIGAGILGLPLAANSSGLVMALVYLAVITSLTI
YSMYALGLAAQRSQIRTFEGVALALLGRGFALFAAGVRIFHGFSGCVAYVISVGDIFRNI
ISSSDSAPQFLRESTGNRLLTALVWLCAMMPLVIPKHVDSLRYFSTFAVSFMIYFVLVIV
VHSCTHGLPDNIHKISVSKDDDAPVVLFNSGNKAIEGLGVFMFAYVCQINSYEVYWDMTD
RTLTRFTLASGLGMTLCFLLYAMVSFFGYMDFGRKVDGSILLMYDPLQEPEVMVAYVGVL
SKLCASYSLLFMACRNAIYHIIGWDADELPYWKHCIAVTILSTIVLFCGLFIPKIQTVLG
FAGSITGGSLGFLLPALFAMYSGDWTWRKVGCVHYVCTYILLLSGVIGVVFGTGATIWAT
ARG*
>TCRU_10402 SPFH domain / Band 7 family, putative
MGQLLCYTCVEQSDVALLETCGKYVGTAGPGCHCILPWTSKAGTLSMRLYEHNIHIRSKT
KDNVFVNIRLTVHVQVIPGRENSAFYSVEAPLKVIQSYVENCVETKIPLYNLDALFIERG
TISQQLKSETDAVIEGYGWDIVSALITEIDPGAAMTEAINSIQKNQRLRVAVVDEAETKK
MRRIRAAEAACESRRLAGRGLAEQRKAIVAGLRKSVTEMRHDVPGLSNEEVLNLLMINQY
YDTMKNVTENSSGSLLFMEGATGLQSYSRDLRNGVAQVMR*
>TCRU_10403 tRNA-dihydrouridine synthase 1, putative
MAYNETLLEKYRGLVRRGEPFRSSTCPYCNGPRSAGIKHIDPKRKPQSPWDFWDNIVCAP
TAARSNDGSDAHDHVGNEGVALGAEQTHRAPPRRRPMYVVGPMVDQSELPFRMLCRRYGA
TLAYSPMLHARSFAQSAQYRARYFSTTPHRAELAMTATASGEGEAAEDAGRTSDGEETDH
PLFVQFCGNDADTLLAAARHVEDDCEAVDVNLGCPQGIARRGHYGSFLMEDWDRVHNILH
CLAVELRVPVTAKMRVFDDDALTLKYAEMLRDTGIAVLCVHGRTRHNKRGLADMEKIRRV
REHLRGSIPVIGNGNVLTFEDVRRNMSATMTDGYMCAEPLLWDPRLFAAPLHPVRNGRCF
AECREARLDAIRTAQEYLQLVQRYPVDLAFVKAHLFKMLFHSYEMHPVMHGWLTNFSCNG
RGGNNNNNAGSDVNGEVEDGDIDDGRSPDGASKSGSGNANKAESNVKQVAGNLDFFAFAM
DALGEHLRQLYAAEVSCGVEGPQPKRAHEREKDVNEDTSSSAERKVETSHDAFAEDDVFG
IDFDLNKK*
>TCRU_10404 hypothetical protein
MIDAISLLTVIFVCLGVSALLLWGGIFFCHRYKLFTSVFGEEGEEVRGIPLRSQAPPIPE

EERRRNLQRAQRRQRRLARRQQPQAAEEEADGNVDSDDGGSDGSAMSLHTRGSNSRWFRT
RHTADSLSCTTVASSGAVYGHGNYLSRQNTTAPPSPLSQITVNESCGSATCRSRRQRRNR
NHRHRLRKRDSSKNDGGNPNNNGRSSPFGGWADDSLCSCSSCVSSNEAQDDDKRHVEVEI
VSPRAERQRFTRRHIIEQNAAMSGFFTAPAIGWSHEPYAGPHT*
>TCRU_10405 Translation initiation factor eIF3 subunit, putative
MNDDYDNFDEYNDAADDWEAEAAEEEAREKEILEQKANIEEQKLKKRIKAPAKVKKEEEE
EETIAADIAAALITMKEKASSAGEAMHLLGDGDEGARRLIADMPVKTEQDATELGEAIAK
RLLTFSRLPHFNTMLAVVFQDFAQEFRTLYAANMEATRVHVSSEEAKRRIKKAKKAKGSN
HHDDAATIETTVNKEPDIEKKDRDALDFDAVNDAGGAAGVSIEEEDFM*
>TCRU_10406 BRO1-like domain containing protein, putative
MTFRFITVPLKKPISRKEKPDAKFKRTPSVEKKIEKKRALCILRLESICKAFEKGSKYKD
ISWQTEEGREKLVKDAIDAVNLYENEVATTLFGYPVFATEYYYSWGSSLLDNGDVFLDDF
RYDLQCMYFNVAAILMNMAEYLLCWQMTPYNASKLEKESYRFLLQAAGYFSLLQEMAHDV
KSYCVGTTELKRSEDLQEEILEFLRLVALAQAQEIGATKAVENEVSGGKSMVAKLLNQVV
QFYKKAIGIAQESITSSKNEFLHILTFSQLKVDVFEALTFSYAASSIFDNNPSEGLWFLS
QSDIYAKVVVNHRDQARKRKKSIPFRGEDLIQNCCDVVQKNCERCTRINSLVHRVKPAEG
PLTLPPAYELAHMKEVKLPAKFPHQVTQQAPTFSPEGTQNQN*
>TCRU_10407 hypothetical protein, conserved
MEIWKTTENVLAIADDVIALIANGCPLNEVKCDQHLNMFIQSPVSTNRVDKAIQTEYYTV
ARAVQHCNLTKSIAVQNISLSADLGTQTDSSVISSEVQTEPDMSHTFIQEAFKKANNIII
SRFVNIEEMWMNLLNRLHRFNLEFRRLSTSLDSVRRSRDFFEGKLRQSQWVLNVYALVEE
EIEARRDISEEEQGSRYNIALMASCVMIGFHRECEKDLLVTRNELIEKLNDIDALRRQLS
DIHEGNTICTTTDKSEVCNCVSEKKLTEHADDLESTKEMKRLLTECWVVLGQDI*
>TCRU_10408 Ubiquitin family, putative
MFRISPSLAWRRTAAFYLRASKLGQYEQEAFEARRRLEESKNYPGPIRSATPGDTRFYAG
SLESILQDNDRHYWRAVIDDPQVQYVIPLRIRFKLFTWVTTGWEQRLHIVQTMAPRDITI
ARLIELVTIENQSPYLCSSTFTLAVNGKELDPDKSLSDYGITEHSRIDAIEKLDHLPHKD
SERPLDWTVDEMTTECLKCSPYKEMGMQPQPNLAPRYEARPKGYFGRNNYSGMKQQS*
>TCRU_10409 40S ribosomal protein S17, putative
MGKIRTKTVKRASKQLVEKYFSKLNKDFYQNKRVVMDVTIARSKKLKNKIAGYTTHIMKR
LARGPVRGISLKLQEEERERRMDYVPEVSHVDQAIQDGVHVDKQTFSMLKRMETGVPRHV
ALTTVVAPVTKKGGRRAPARK*
>TCRU_10410 hypothetical protein, conserved
MRESDLVELRVLPRVFPQHPYARHTAGLGARGRATLPHVLSKSGVLNVKVIGIYCSRRAA
GDCATQREEGVEGIKKKFKKENGEEAVLPNEILGNRGGECEGTNCKRHIYVRVQFNKVLV
DTVPLEVMREKYPQVLIDYLLSTAVWT*
>TCRU_10411 splicing factor 3B subunit 1, putative
MTDEERSGEPVLKSHRWETAAGAPASLPTSSRWGAGTPRQLGGDTPKVIVNAELSAWRGH
STPTPSAYMVDSVKTPTMRGQGGQTPTFGAGGTTPMLGGTTPMFGGTTPMFGGTTPMFGG
TTPAAGMAFGVTPNHQFEGTTPVQSRFAGGDSQSAITANIEAQARKLEVQWRMKNKRLTE
EYLDTILPPEFKLVEAPADYNPPPPEEPNFYELASKSLDVFVVNQSNDAAAAVTYDIPES
LGEGMPQMKPQDAPVFEMLLKYHNVNPIPDEVLPSYLLMKNLFRIKNGDTNQRRIAMRFL
LDKARIFGSEPLFQFTFHVWRSGILDLQEQHHFVDFVKGVIARLQKEVRSSTKEIVHMME
VLLSAQEAAVREDGKDVLALLTRVVGYEAVFEAIKEDFAHVENGVRRHTAKVVAIVGYAV
GPATALQIIHGMSLSPVALARQTSARAITELASILMHAITAELVELVPIFEKLLRDEPRV
KREAANALAHVADATCPYGIEELTPLVHIVREECKRGIGTTAGPFVRAFGSLVPLMAPYD
AQKYTSDMMPTLVNQFNTPEDEHRRVLLQVVRQCVSADGVTANFIRDVILKPFFDGFWSV
RRVAAERKTAGALVETTVAISRKLGSTEILQYLVQDMKDENEHFQRMVIDTVRRVVRAVG
TVGVPDTLVALLLDGAIAAVKQDESGLNRVVLEGLASICSSLGTRLKRYLRQVFDLIKSR
RDMPGMIRMQAAELAARIAHTVKEAEGVLFLQDLGRSLFDRLEDDEVAVMSANIKATRAI
LVELTAAKYQPSVRELLKKLTYIIRNRNSNVQLNTILLIEEIATNCDEDVDAIQLQDLAT
KGLFELLDADRRETRRACTRTFGIIAQKIRPFAIILELVDNFKQDKRKIRICTAVALGAI
ARECGPFTVIPYILNEYKISEGEQVATIVQHAVLKAIRYIFEAIGAVGKEYVYPLIPLLV
RALTETEIQHRRMAVEACRAMTLAVAGNDGFEEVIVHFLNFIHPNIVELLSRNETKISEE

RLKMVTAVVSFYEAARLVIGPARLLQYLLQGLFHPAKKVRDIYRRTYNMIYIVSPEALVP
CYPRLEDDEEHTYARHELEVIL*
>TCRU_of Trypanosoma cruzi region 5, putative Dispersed gene family protein.1
MRFPSLTYLVAYVMHPGICVFSAFLLTMSDAQVQHYVIGVVGMLYGVAFPAGVCYFVSCR
CDAEFKEYEGFSNKPFPLRWLYPVGYWYPAAQQRMYGSIFSHVRDGKAYMCVFQLSVLCV
VGLIAAVHPPVGGCHVQYFCMAAVLLAGAGVVAFTNMMRSAFLTVMHTAGFVLLAALCIV
NAANHLAPGDDGVRGHAAILLLLLCVVLAITVYSIVLWYVESRNWRALREQRKSPDYCLP
DGKDEEQVKEKRIESHPVSPEETTV*
>TCRU_10413 apurinic/apyrimidinic endonuclease, putative
MCVSIVRLCGAVSVMPSGPKEQKPVAAGGGKRTRSRSPSATPPKKPATRSTRIRTPTPPS
RSLNSAGAEATSPTRPLTAVLPAPPPSGDDTRKTEKDIWSQVEPFQRRTAAKDFDSKHML
KFITWNVAGLRGLLRKDGQAIQRLLEEERPDALCLQETKLNPDDPQNGKLGEVPGYCFVD
HVCRAKKGYSGTRTYIKNTAAAEWKTVTVKGFGTLKSPQDVGHSDGDEEGRVLTTYFGTQ
GKGSETFALALVNTYIPNSGMSLERLPYRCQKFDLRIRQHLCALGRSYNHGKEGGDAPSL
AGFIWAGDLNVAERDYDRYFAGSYKAMQKCSGFTPEERASFRETLRVANAVDTFRALYPK
AAPVYTFWSARINGRARGLGWRLDYFVVSAALARHVVDCFTMPHVMGSDHCPLQMWLRR*
>TCRU_10414 Domain of unknown function (DUF1738), putative
MFTPTRTLLSAVFATSTLWAASRSTRVEKKNKKAPELTSARDGGATAVAKPHVDVFTTMK
DSLDNILGGAAVPRDAGPVADCRAHEEETAPPTEAETFPKNEETNIEEEKVAAKHEMPSY
YKPMNTHEQIYDAEVAQRLCVAAASRHFRSPVWSTRTAFARFGYTVKDGEEGVDVSTMMQ
TVTLYNLEQTSAPDASVSDSLKCSGKTLPEWRNMPLSAAGRPHSRHVQRTLQEHPSYAQC
TSPYWITEEEAVILGTAVRPSQRGCGILIKRPSAAARLPVSGEKESRPVSQESTSRSDED
FFMLYNAAQLEAPELVTRETCPPLLFLSVDGHRYNVVLSLYMRKYCQKYNLNMQPMVVFI
TTSRLRILGGDLRPMENDVPPFTCVINDEIVSFHHSEHTTISEKLLQKATALRRERFDRA
PASNV*
>TCRU_10415 COP9 signalosome complex subunit 5, putative
MMMMRPDAGRRGDRHEVTRSQWEMHNSVITDDAFLSPNMELMEELHKTQPWKRSPRYFQR
VKVSVLAALQMMIHAKRGSPNVTCSNGSGVADSSAASMRNEPSRENWFEVMGLMLGHFNE
DEMIVTSAFALPVDASEVECSMNDASQLYMLDFLQYHQRGGTQEGCIGWYHSHPGYTCFL
SGTDVNTQQLGQTAQDPWLAIVVDPVRTISTGKLDMKAFRTFPENYVAEQQGTSQHTQGK
HWEGSTTSTWVPSERIREYGVHAHRYYELPITLVRSKDDEAQLECLWSRYWALTFCSNPL
TANRKLMTKQIHQLAEVLESGVASRHQTMVKGDGYLPGHKLGSQHQRKGGGAEDDETPDG
VEAFKQRSLHVRYLTSSLASEAASGGTLLVVKNSVFRA*
>TCRU_10416 Iron-sulfur assembly protein 1
MQHSCHTSSYTSATTTTTTTVSTDSNAGRSHDAKGSVQSPMPYKSTHKGSGKAASPLRNW
GCDNHAANDTAAPSSSLLHAGVSAAGAHAEANGSEASARQENLAASRSSCTEDAGVVSSR
PLSPLQRRQLLFRHKAAFTLTPQALRRVKYLLKRCHEDPEHHHHPKMPDGIRIGVSRRGC
SGYSYTVKYHYPEDEKMPPKETDKQDTRRSHGNNGDTSSATGMHTGDVVVLQDGVKVVVD
SNALFYVIGTEMDYVTRSVEEKFTFRNPNQKYSCGCEESFMPFDLDEQEAK*
>TCRU_10417 EF-hand domain pair, putative
MVFFIRVAANVRGGNRNIRLRFSSHPTLCELACATESYFMTAVPQGQSSFQLDAMMLFDE
FALRWVELYSAAQLSTDCQVYAFAKRGMGRPVQDRPPRPEMSRRSVCADREVIPPPGKTV
ACIASLKDGTSLFSFSLDATEDGVLTDIGESAADEEDACRCRRCAPITGSLDALGRHNAR
HGDRIRTVFDALDAQQKGYLLFTDLKRAVDAQRRVFINYSAKTLMALADQDEDGRVSYKE
WASFAVSHPAVVDAFFDAFAQLSRRRAPGGSRAHAPQASWSSLTTCPLSMEAYERSRAVL
THEEARLAADAVRLKALRDAWEKSGVGRRKRRGTTTESTRQSWRVHSVLLY*
>TCRU_10418 Concanavalin A-like lectin/glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MGVKTNGQGNPVLLGLSYDSGGKWKLLCGGGTSKEHSSTWEKETQYQVAIVLENGSQGSA
YVDGKQLDGNEACALGNRGSNEISHFYIGGDGSGAGSQDDVSVTVSNALLHNRPLTFSGG
NADLEKDVAAPAEAASHTVAGGQMTTAGESATAQQLLPSPSQGSVGRTASSSHAVGGATG
DGGTVRGSGLLPSLLLLLGLWGFTAL*
>TCRU_10419 BNR repeat-like domain containing protein, putative

MSAGGCSDPCVVEWDDDKLIMMAACDDGRRRVYEINAKEDSWTEALGTLSRVWGSPKGAN
VKGVGSGFTTATVGNGDDNNRKLMLVTLPVYSKG*
>TCRU_10420 BNR repeat-like domain containing protein, putative
MSRRAFTSAVLLLLVVMMCCGSGGATADEAASGEGSSPETYFDWRDVKKEETVGLLRVPS
LVEVNGDVFAVSEAQCTKGDSVCDFNAR*
>TCRU_10421 retrotransposon hot spot protein, RHS3, putative
MEYRVLYIPAAQKFPLVDGFFFVDSPRKTLVGLQMTTAGAHHITASTVRQFTECLAAYFN
GWEELSRDMSWEMIYVQHADSTPMNGWQRRGVVNSDSVSDDESREIAGLWRKRCTSTKCQ
YHLGLWRRRSSPK*
>TCRU_10422 retrotransposon hot spot protein, RHS3, putative
MAAGSYLLYQLLHCDVEKLQFDVYSVGGSTTYVCDKAIKTVTRHVGGGASTDVLWDCVMK
GHIFYDVTEKGTPPAEYFVSSTGWGMSVVSPPNVGNCDEWETQVKAERIIVNCPDEMDVK
AMCAWMERDGTTDGQAECWKMVEERMDKVGPIPRHIFDASKFVAHSAAIEDALDGINSRD
GERHFTHRGVRLWYSGDPPQKVVSVVRARGEVGAEGFLNAAISVCLGRRIAHYFGRRDE*
>TCRU_10423 NADH-dependent fumarate reductase
MGGCLISPSAEMQLEENTTSPFGHRRPIFGLFGAGEVTGGVHGGNRLGGNSLLECVVFGR
IAGDRAATILQKKPVPLSFKTWTTVILREVREGGMYGTGSRVLRFNLPGALQRSGLQLGQ
FIAIRGEWDGQQLIGYYSPITLPDDLGVIGILARSDKGTLKEWISALEPGDAVEMKGCGG
LVIERRFSERYLYFSGHALKKLCLIAGGTGVAPMLQIIRAALKKPFLENIESICLIYAAE
DVSELTYRELLEQLQRDSKGKFRSIFVLNRPPPVWTDGVGFIDKKLLSSSVQPPAKDLLV
AICGPPIMQRVVKTCLKSLGYDMQLVRTVDEVETQNSSKM*
>TCRU_10424 hypothetical protein, conserved
MSSGTLAHHPRRQERASPPSQAAWRLSFLTSWHRQRGSAAAASRFPNLLRNAYCVSPTGR
PPVYMDSDHHLPSHTAGTEDGIPRQAGMLPRRKHVALVLRDADCDASI*
>TCRU_10425 hypothetical protein, conserved
MQQGTIPRGSRDRPEESRRTEWSRPSLLRRQHATSVLSYREAACPELKLSANGRSAIIPF
AVFSPCCQWSVRNGLVPSGAQACDAPKHCGTTSLPSGIGWAAALLGPRLCSAAAAGTPLV
RHSVRVALAAIPTVVRTPCACVPSGD*
>TCRU_10426 hypothetical protein, conserved
MAMMVTGRVLLVCALCVLWCVAGGVYARDVDTNALRGCMASGVLGGNGSHMPDGCNKTAI
TVPLRSVLPITAVEASAGESVSDSTDIYPDSLLVPPSPPPVTGLPEALKAPKAPQDPPES
DVGQTGVGNRLSLVPNDDSSGAGGFEENGNSNKSGVSASEFSTVVGASRSPIPPEVGGSE
NKSGAPPNLKLEPPETNEPRERILVETNKDTQKVSKLEENPESSRKKEKANIRGTSEEAG
KNEAGRSGVEAHGPSSVLSADGQLQHQGTTVTMTQPPPPSPEQQTSAVSPSPGVDTPAAR
SREAGDPEEGKGIPPARTASHNSTDEKHKAPPLRSEKESAAPKPPSADGVLEQNSEDTTT
KEAIKMDAHTDGPAATSEQSTSASESGVVKRNESEDGDNAQRPEPKGQHNDPDAVNTKAA
PTASEAASYTAKTVPAQKNDTVTYGDIDGGTAVSHTTSPLFSLVVVACAAATAVVTA*
>TCRU_10427 BNR repeat-like domain containing protein, putative
MIVDCENGQRVYESRDMGTTWTEAIGNLLGVWVNAGSGASQKESLRVDALITATIEGRKV
MLCTQRGYASVENRANPLYVWVMANNGSFYVGPVGMDSAVNWELASTLLHSDGDLHLLRR
RGNGEGRAISLSRLTEEVSAIKSVLSAGVQKDAFFSSVSIPTAGLVAVLSDAASDGTWND
EYRCLHATVTNAVKDNDGFRFTGLESRAIWPVNTRDDEVRHVFLSHHFTLVASVTIEEAP
SGNTPPLTAVLADTASNRTMGLSCSHKKTWETAFEGTTTTRRSTWEPKKIEWHLCCKATR
PLCTLVVSCWRNRKRCR*
>TCRU_of Trypanosoma cruzi region 4, putative Dispersed gene family
protein.1
MPGTESVDRGSCSCSCKDGWHGASCLPFEVPDTVVPPVVERAVDGDTSCVVDQTLTDLAL
KMWKTHHCYVGVIFSGVGAVLTFSLNSMPLHLPINITLTGCTFRSGAALQFVGGAAAVES
SGVLIRVSRTVMRSSTVAFMRALPQHCDIAVTEVDAAQFSSSELPDTRMNTLSVLLLKDA
VLSASSLLVSNVRAHATKRDAFVVYSTGTLTLVGGSSLYAQYCSFDGYTHMFYLYSLSVR
NHSVFALFNNTMVSGASLLYQQQGFNLSDHSVVRVVGNSGSVRYAIFNDDLWTVQRSSWL
DWRDNDVEVGAMFYGTVSAFVSIDGSSVVTLTGCKMGSTGLSVSLLSRADAGYRFVAGCL
TVAGREVTTAAELALNGITNVTTVAVCGECTKEGDCFAPLTTAVIDCKCQCAAGGHGDVC
VPAPVPAGPPPPPPPLRPPPLTPSPPPVGECISDMVYPEVAQAVGGGLSWLCYRNVTFSG

GGMSLKVLVGAMTGDVANVTFDGCTWRDGAVLLLLGNAYAAVGSLNIVVTGNIFIDALLS
PEGVFPPHTNITISGNSFAVTRLFHWLGLELDCPSCVVMNGLAISNDSAVVLSGNVFQSV
TTSSSAVYVVGSPLRVLWKSLFAVLGNTFHMGGGDSTLINIEGSGQFSSLKVLNNSAVVI
RGNVVTRPVKYFLLVILALRVESRSAVVFQGNDMQRSSAVFFSSYSSYIYYNSWLQLSGN
LCRESPSAAFLFLNPTVNLRDSAVSVSGNRFMSSTGTPTVLRISTVPRDLTNGAIVAACN
TVNDEEEAKYSIPSVCNATILTCSDPCALVASCFPAYTTTASSDGCACRCAEGGHGDACL
PVTVPEPPSTDGADLCVRDVRVGLEVNVSFGTPVACYVGVTFAADFLVDVASMSGSVRNV
TLANCTFVDGASLYVVGWRSDPPAGERVDVLISGLESRSGGGVLVANRFPPGSRVTVVDS
VLIAEARVAYRGAYDLGDASACLVVHSVNLTGSVLTIARTHVAAVFRDAVGVLFVGGVAL
SSRGALYVDGLSVQTALGLCVSVEGGVAVSGGSVVAFVDSDFLLCKHAVSVRGAVSVSGA
AVVLVRNEFLSTEDYAVAFYSRVRLAGGSMLLAKGNVHDGVSREMLYAAGAVTAAGSTLS
FVRNRALLPRMLSLSLSLAAGAHVRVACNDAGDRVLSTAEEYAAAGFGDAGSIDVAGCDA
CDRDTHCYAPGTASASMRNGVCVCACGSGGYGEACVPVGAPALPPAVGTAPSVFVREGVT
VRSVFVVPAGASEVTLRHVVLDGVSPVLYVPWMARDGVRIVVQNVSLLNGAVLYVMGGGA
LRGAVAAGSDEGGPVELSVCDVEALNGALVLSGTFPAGSVLTVTDSLLVAARPTPLVYLP
GSRSSPYAPVLVLSGLRLVRSVLVVSGVALVTVVTGGRTVVVDGAVLELVGGGVALDAAV
FGGEYALYASARVVASGGAVLRVSGSQVYAAHGLVFGSGVEANTSAVVVNENAGVLTDGA
LLVLRGSASFVSGSWLSVRGNSICGRLLSVPSYPRSAELVQSTLTLHGNAGSGPVVMDGT
VALGGAGRKFVVGCLTLNGQALRPMDYRSAGIIGEFRPVACGVCDADVRCFAAATRTMSR
SCRCRCADGGYGRDCLPVYLPHVDGCNRTLYRPLLSHTASLTETRSLTLTTKLQSDAVRA
DGDPAGDGDGGVAAHADPDGVGEQHAVVERRGVPDACRDDDGGWWEPDAERHPRRWERRP
DAADGGAAAAVSVGTRPAAQHAPELRAGVDGAAERLRWSVGSDAAQSDVGAQRDESVHRP
GAGCARAPRLLHCCRRDASHSLRRCGGVRRLQGCAAWVLHDQV*
>TCRU_10429 hypothetical protein, conserved
MVDGASATQRDSPADTCLGRWMRSSVDACPRSRQRVRRRAILAVRAALLVALVLAAAAAW
MPAVHAVVLRLRGGTVDRAITVGRAVDTVLMDGVCITNGVAVVFDVPAMLPGALRIELRN
CVCDGGAQIYVRGYSGEPASDRSLEVSVSGLSGSYCSLVFVHNLPAHTNVTVRDSTIVTA
GPMRYSQLSGLTDAVASPFVLHATSLLQSQLRVSSTVLRSLQAGGSAVYVGGGVDLLSSA
VVLDGVSLEALGGPTASAMHVASSSILSLRSHSVFSVTNVSVVSSGGGFVLGERLAVFDS
VLRFVGVEGSVASSLVRCDGGTIGDGGWLDLHDVWAVGEASSVASLSDVMLSGGTVSIVR
CAATGATLVSGPAITSGAVSVQCNRAGGRVLQSSGDYLMAGLPSVSVVPCDGCAAALACF
DALTASFSDCVCSCRAGGVGEACLPFDVPSARAGGGGGGAQGCVSGVTLTESVTVGGGRA
TACFDSVLFSGPITVAVDLRSMDAFADALNVTLRHCVLVGGAQLRIGGLSESTARLMPHA
LLNMTNVTSVEGTIVLHGAMPLHSSVLLANSTLRATVGGSQYVPTTRGHERFRYVPALVL
DGVRLLSTCFVMTRSTLVCGGGSCAAILVERGLVVNLSSVFYMDNCVIRSRTHVIYAIAS
DLRVVSGSVFSIQNSSWILPSTEYGEGACVFKDVVVDGGSVLQIVSSTFRLGFAMLMAAT
LTVTGGSWLVHRNNEFRTAYVVYVAAHHGMVFRDRSVWSILDNNLTYGSYSTIANMTNNW
SPPSDTRPTIYGMCNEARGSPVTNYQDDLNIWTPVTVLDCGACTVDAVCFAARTSSISGC
ECVCAAGGYGDTCLPAAIPDGLGPLPLPDAKDTEVRCVHGGSIRSVDYPDPGVRGLCLVN
VTFTAAIVLDLSYFEAPQQTLNITLLQCVLMGLLIRGSGVRVHVSVTSSTLDFGALDFRG
DFGVSSEILVVGSTLVTTSGHAISFVKFILSANMTLLLLDNYIEANRYAVYFFNGVVVNG
GGIIVKGNTLSTTKDDDGVESSVCVNGVDVKNGGHFDVENNTMSSVNGVIFWGYYRELRG
AAASGGLHLWRE*
>TCRU_10430 hypothetical protein
MWSQWPEALRTPRWKHSSRLHAEQRRHVSVAAACLPGAGGRPPSPQCGMADGSPSPCKGV
DVQWETRSTRCAVTSGNETLRPLIRAGCAGSSDSSHSMPLEVAARFSPAVVDRERPFRSS
WCEFR*
>TCRU_10431 TPR repeat, putative
MTRVGRRGWLLLSGIAALVPVVALCRCFGRGWSMHASKREPKEDDDDEENLYDDTVAVGL
DKEERERYHATLLLLKEKANAHFRAAEFDAALEMYQGCVDMCAALGADDAEAVQIDQVVR
ANVALVFLKLQRPEEARMLATFLLQDDTHPVEGDLKVKVLYRRGLASQALGDRESALCDF
RAAVLFSPGEKNPAAEAAIAALSRGVGT*
>TCRU_protein, putative SH.1
MLTPIFVCEQNESFVIVSITLSALCKVTTAVFSILDHQFTFHCAPYYLRLKFDQRIAEGR

GERATYTVDTNVLTVYIPKEHRDEVFTHLDNPGYLIATDKERQQLVQCVGGGELQGEDSM
APDEDETEFRQQLPSACGVEDGCADYGFAGSFSGMFASLDSDITAEVLDLPRNPDETTGV
ERRQLRLQSENSDFDEDALLLSFEDADGEVQRLLRYVPRHRLDYFAALDAEGVRYVVPSA
PMEETTNNYTTATEEDDNGKGVLEEEEEVLPMSTGVVDLWAGNIAEFKRPLVEEISQPTE
NEVDMPIGVSSTNVSALPTGSLAVPQQRPRALFSSEEHGVLMKIRPPRLLFPPSSLVVDA
LTVDILFSEAYDDIVTEGTGCSESLWNICKLSPALSWLDPAENVYDACIFFARRALIYPL
HRNFALIQRVFSSVGVRLLLGKSYVIKAFLRVRAILAHAEHRHVLVTLFLNPLIGYWLGV
EDAEERLLRLALELHAHVTRVEAEMERPLPTSSLLVQKKRQLLPLHLLNLGLPIS*
>TCRU_10433 Cornichon protein, putative
MRFIVQQQDVWRVLRNASKHTASERKRAYFFLFAYCLSVAALFASFLHFIGAWVAAGLIQ
LVMLIFAMLYALNIADCRDKCLNVLECERIVNPVMEVYVGLRALQLLHAIFFIQSIVLSL
CYTMALLFLVWRISRGAFFVDATSLWREVGRLEQGSYFHISIDVLLFVVYLVCMVFAIVA
RYAK*
>TCRU_10434 Importin-beta N-terminal domain/HEAT-like repeat, putative
MAGTPTDTSLGLEQLHGMLHTILHSTDNNERRSVESTVVRALNASSNLMLLVRLVQDVQS
VSAGVRQLAAVLLRKKVFSLWRAIPVGSRAELKQVLLAQLGIEPVRVVRFALAHVISRLA
RAEFLEPVEGWPELQVAIRTAMEDPRGDMRELAMVLAYSIAEVVGECGDLNTLVTEAVLQ
GMTDAEVSVQRAALKAMGALLLFVDVQEEDRIVVEKKKHERGKLLQHLIPRCLELLAVYG
PLEERTNICVDVLDLLEQLVEDLSVKKHEGILRTLGIEMISVLCNTVNRPRVRQNSSEVL
VTLVNLKPKFVTTTLLEPMVSACVQVMGEDGTISLPEEVTRLEDSEMDIKNDTNDEDAEM
LHVSPPCMYAGRLLSTLATKVPAKAFTNVLLPFVLRVSENMQGGPLERKAAILSLACLAE
GNPGYLRRKVQYVLKLTHDFLCDSNPIPREAAAFSLTYFCTHLQPEVLTHHRELFHMLVP
LLRDENDGVRRRVAGAIDTLCENVLEDVEPYVSLVLPAVLEAIGRSSLETQRALCGVISS
LASTRCPSFQVHAAQCLELLKTPLTMTSPETVLLRAKATEAVGIIANAIGKEKFMPFFSF
FFDRVADNFHTRQAELREESFGFLSNICEVLRVDFIPYLNDSIGTALQTINEDRTHYENK
HLLAEGCMRNVNVKNSNAKNDDEDNEESEGESDAEEIYARVRTADVEEKSSAVYFIGVCA
EVLLADFGMSWIDVCWPALSDLDAHFHSGIRCSALMALAKLTKAAQGSEPVVKSTAQDTL
TSHARRLLDSLVNDTLLPCIHGEKDKEVVASACDAFALLFDYFGPQTMIAGVDVFLESVK
TLLKQGTACQQSNEDNDDEEEEECPPTGDEAVDLGEDHDGVLMDAVCDMIESFAKAYVTS
FKAYFDAIFPFLLPYAADDRPSEDVVMATGCIATIMEAMGSASEPYIEVAVALALHLIET
TDESSAKANCAYLLRVLVECFPCRFDNVSAINPLLQALWGIAGSQDEIPAAVDNAVSATC
TMVRFLSPTTIPLSSVVPALLERIPMRVDRTENANAIRTIIHLLTSQREFTKSHVWIAMV
RCVATVLAALTVDEEQKQLLVVQGAIPFIDSCRPEWRETCAQLPVELQAALERYGCC*
>TCRU_10435 hypothetical protein, conserved
MIGTATEVEGGATFEGPGVWAEWPVGNRWRNQLFHIVKKEFTLVVTATIGAAPAGSGSAL
MVAVGGAGSVRMVGLSVTAGNKREVAFDGEVGEVQHGNCGLERT*
>TCRU_10436 retrotransposon hot spot protein, RHS3, putative
MHGEFVIELAKELNELPPPSPSKPRSSVLNVNHQGYPTRAVGLKELQGGVTRIPMEYGVL
YIPAVQNFPLVDGFFFVDSPRKTLVGLQITTAGEHHTIPSTVRLFKNNMATYFNGWEELS
RDMSWEMIYIQHENSTMITNWQRCGPVNTENLSDDEKEIVAFWDGRVHQYQFMLTRDFVN
KIREK*
>TCRU_10437 hypothetical protein, conserved
MPELEAMPSYLPDTVVLQLHRDDGEAESEYYMDANSLTFVALGDAGRPALCGIDAAAQLH
HEGVQRALVSATGIVSSIRRRRLRIPFENSELSELLRRAYNTEKGNRSNSLTGSTETALL
AHAFLDAVWVEESFHCFSTTRRVGNILVSTGIGSATRDLAVDKWRPDQDIMELRDELMIA
RTVYDYRHCGYESNTSISGIKG*
>TCRU_10438 hypothetical protein
MAKELERRGMSTLDEIERTLETKKRENSALQADRESRIWEYEHTVEKIRTRKQTEESASE
RLRQAMQQLEQELSLRQSAIETREQQLEMVQLDRARGERPSCGSGILLRRCEGPSGRSGA
ASGGSGSIRLRK*
>TCRU_10439 hypothetical protein, conserved
MLDDYVAKKNEKLHDAEATECHLSSVVDRVLNYLRNGVCVTKIPSKGNARRRLYFLLEDC
KRIHSCDLDRQGFPLNRKRPPVTMWIRDIEKVLIGLSTTSFVNYSDEAQLAKTRQEAVSD

NGTHRHDPTRNITSSSLGTNNHRALALLLRGGKLLEVFCETDSDCEAWLVALKRPLHLGT
PAERLLEERRGT*
>TCRU_10440 ribonucleoside-diphosphate reductase small chain
MSGEKHPREFQSQEQEEPLLRENPDRYVIFPIKYHDIWKKYKEAESSIWTVEEIDLSSDL
ADWEKMNEGEKFFIKHVLAFFAASDGIVLENLAQRFMTEVQVPEVRCFYGFQIAIENVHS
ETYSVLLDTYITDTEEKDRMLHAISTIPCIQKKANWAIRWIRSSSSFAERLVAFAAVEGI
FFSGSFCALFWLKKRGLMPGLTFSNELISRDEGLHTDFACLLYENYIVNKLPTERIREII
CSAVDIEREFICDSIPVRLLGMNADLMSTYIEFVADRLLVALGNERHYNSKNPFDFMEMI
SLQGKTNFFEKKVGEYQKAGVMSSEGTTKVFSLDAEF*
>TCRU_10441 ubiquitin ligase, putative
MVFGRVLQPMEPASWDTRQVMAYAALHQLAGITEVRGEVNRPLREKWELLVRTDLNEFYA
TNDFSQHPVGRDDLLDTSSSELLVRRTHSDCAAVFRENPEKLQAVVEAGLARLNKDTLHE
CYLAGKLPALEWWLVMTLDDEARRGLENQGAPRVCGRALTKHEAIAHCLECAVDSMCVFC
ADCFQNSPCRNHKHTVRYGGGGGICDCGDPMAWNSASFCSKHRGFQKNDDPTASLPPVQK
RWLEVLARGLSLYQVTIMQFFTLHVKDSIESKDRDLTMRWFDRTLRRTVALSLYLANAGE
GSRRLMCLSLMGETLLKRPIVFNVDGEEKEVYVRYSCAEEIFLQNMTLVDLKGFIIWENS
LLYLLDGCISDPLLRVPVAELLLKYGERLSVMQHRHVKDLSVQVLSVKEVVDDLLQKTPN
PQWECVIGRETILHRLLSTLLYVCCYVHKDRELLPELTQVAFCACHWFENVLSASENVKV
MVVSRQLFRAWCKALCLIGTSSKICRETRTSSLENDNVDKDYAMMMEAELRHSFNLVAHM
VFIVGTALLSGSEPILASQQKLLQSLPPVWDKVPDVSIGYSYHRQVLDTLNLQHASSLFF
SENNTDMEGGPCRVYMREMLMECLEFINAALAEKRNAFKPVNYVLSGQDAEHMLPRYDLL
DEKSPNPTSFVIPHMRFFAMLVKVWTRLLRQQNLIKKDSPVEDDACTNSGDHSRGVESFY
SLVSEVFASTQAKTDYWIDECLMPSVLLGQIERGLWRRDECDVTLRSLYYLNNTTPEMDY
DIYLLYVLMLITPSEAFATQLLQRHAVTKANEPRGSWYPLFLRLILTLCLTEWAAVIHDE
HDLRRVLQREAVHGMVVSNDFSFHIMEIIAGRFKYLIPGLDPSTLLPSILGEVAVTEQRH
RTQVFALKDAATWRSNVNLYHPLVRDQALQDLQDLYERLVRREQMARERETTGATTKATT
TTSSSSASRVVFPLPKLPWLEEQPGTTQGNNTMGSENMVHHKVCLLLQTSAVLSVAIAAV
HMYLSFVMEKKEKSSNVSMSERSLLHAISVLYIAMQACHVISSSASSFSSSFTQGPMRGV
DWDMVKTFQQQFMPPSGYTWEDLKQLLLVEGIMDATTLKEKLEIPLVPNTKRDFLLRKTS
KGVTTISALHQIYAQYRESEKDMYGIAAMTGYILHGVEALSSLPHANEEEAEQKTRSEIN
EQRRLRLKERQAMLLRRVKANDAKSAATIVASLDDNVKMDGDSVRDARGIAVSSKSVMAT
LLLRLAEVECCMCRDPSNEPLMLFASTFTSDTLYRLRFDESEREAPMAYKVNGQIHLCGH
AAHRKCVAKMIGRIGLILERVFRASIPSIFGPKDFNCPICVMVCTTLCPLPTLAFSSGER
LSSVSSSSSASLFEDVRSDTLKAAEDVSELHQEIARATVGAPSARLSGEDALVKPSELQL
NDPEVWVLAETIRTIRNQMCVTLEWVKAGGEVRYNELLTLLSVLVSIDVSLLASHAAKLK
KEFYRKGDELCLLLVNLLHFPERAAASFALYTRLLILSSDHGIIIQSASEKEEEGGNMDA
YNKLLVAIWRELGCLTLLKVLILDTSPSEVVRCEDDRVTLLPLNSEALITLAGRQRAVLT
MLCYLLEVPFQVEPGRDVGTALSSLVQSVTAVNGREEPTAWLSGIPPAELMQCKPLLVPY
DGPMSWRKFIVCRVFHLSNTFGDLLLKMSSSEPCSVCGDNEAQRVWCALCGHSLCLRPSL
TPPELYDHARTCGNGLGIYLHPATNVFLVLLTVQGRHLQYRGLYADEYGQTIVRDFRGRD
VPLDDEAIKTWLSLWIQSQWGVQSTVVKKLALGNLRNL*
>TCRU_10442 hypothetical protein, conserved
MFGQCDHAGAPSVGELCEVGCLLGFRTTSPVPGHAAVTNDKLRPCARSSARRAEQECPES
TMYRDRCRERTRFWSAAGREREPVKVDTLRGALPVHRMLLNGFLVPRCGAMHSALRLRGI
RSAPAPAMLIGVPFRYSIAAAPSLTPSSTKPPVHPSRRFLLGVAKGLCVRCGGRASGHKP
GAGPCRGHLQRHHRGRRGNGLELWSAGGHCEGRAASFCPKRRAQRHDEVVRFSGGVLRVA
DDGGTKVQSIATRLASGRGCSFASNTASSTLLPLEVHATILLACYFAGSGVQRDVGEASN
TMR*
>TCRU_10443 hypothetical protein, conserved
MGCCSSFRLGNESTGRAPERGGCSQIVIFTGTPPSCSGAVLHVEVPESNSEPGSLVARRR
SANGLGLGSALCGGGAIGVPSLALVLAQVAGGGSGGIPGGSGSPGEIDFPQRLGARNATD
VGHVRHDAGAATAVLAAHRAVCRASDRGGVRSAGGGGVSVRGSLRACCAASELHQQHVLG
MADRSGRSSHP*
>TCRU_10444 hypothetical protein, conserved

MFGQCDHAGDPSVCELCEVGCLLGFRTTSPVPGHAAVANDKLRPCARSSARRAEQECPES
TMYRDRCRERTRFWSAVRREREPVKVDTLRGALPVHRMLLNGFLVPRCGAMHSALRLRGI
RSAPAPAMLIGVPFRYSIAAAPSLTPSSTKPPVHPSRRFLLGVATGLCVRCGGRVSGHKP
GAGPRRGHLQRHHRGKRENGLELRSAGVVTVRGGQRASVRSAGRSAMMKS*
>TCRU_10445 Endonuclease-reverse transcriptase/Reverse transcriptase (RNA-dependent DNA polymerase), putative
MCSTERRVVLGTRRATRATVPAWNHQPSPFWTPWLAELDRAVAAAPHAEGGQRRELRRRE
ALREASKSRWHTLRSELEGTDGNRQQVVRPCLSPSFLEHASHEFRWPNAQQTPEGQPPHE
AVGGESNTAPKAPPSATDPDECDGPHPISMAEPGYTLRLLLLGPAPGPDGIHGEALRHLG
RMARRAVPWLFDIRLRAGAVPRNWRRGAVLLLPNPERTASNRDSHRPVTLSSCPSKLMER
TPTARIRDVIDSQLALRSSGFLPGNSTPDQLLHLRAAVHRNAPQHRTAAYFVDHANAFGT
VGPDAVILEMRRLSIPNRIVRWSAACLNSTSAVVCIDKLTPSSRTLTRGAPQGTVLAPIM
FVVVMQSRCSCPSNVPYFAEGSLLMTALSSHSRATGMRSTRP*
>TCRU_10446 hypothetical protein
MMASSACLPPSSAKSTTAEDLGGQLCADGPQPMDADVEAHTEAWDRNIPSDSRGDTIARR
CIENALQADNSGERTRYTERQGSP*
>TCRU_10447 UDP-Gal or UDP-GlcNAc-dependent glycosyltransferase, putative
MLVLYVLGRHPSHGYEYSAALLEEASQWNDVVALPMNEGRVTRNKTIGSYGPLGDEADVG
VTRKTHMWFDLAVRLFPNARYIAKGDEDIFLRVPLFVAHLRLLPRRGVYMGVHIGTSNFG
DKGLPGSRFMIGWCYVLSRDVAEALVSYEPLRRLAYLPYSKERDHEFALLRFHYEDTMVG
WVLEKEVKYQPMIYVKVLSCHFHDARNNTGHSQVVPTSMCIHHVQEDDYAALMARFGNDT
SPVARVERVSDDTIYPSCN*
>TCRU_10448 kinetoplastid kinetochore protein 18
MASVEALLRLPTDEVQLCPPVVTDGDLSVVFREMETIMRKCLYAVRHALVAPFSVFLHLL
LQPAILECQDVSRALLAPIEEGRCIDLLAGICDTLLRPEQHEFRGKLNIEGFFELIQQLC
AFSTLKDPLGVVLMPCFLTFLHVAVEKEDDYRQGRGCASVLITLIRGSKANKNRMSVQCG
LIGEVLTRSNDIFFQMQCVEMLFRLYTHNRTVLSTSTLPDFLKKCVPELPNDENLLTSIQ
TLLDAYNMEYASFKRLQFTALLIEAGNEEVCGHTSMYFFPLILVIMIPGCSGDNITIPYE
HIRSVKLSKERKLGLRLHVIPVRLSHLMSHDGDKDTLMISLTQSTFSAIRSSGVHEWIAD
RKRRVPISLIRQQIEASSLVTTAAAAARSFNSRNATINDTGFIPDENGHSISVPTASHAS
EKVFPNRGVKMQRQQTHSEPSSPNGKQPATEKKEVEVAKEVEEYALRQLHEAASYKVARM
RQDCQGELQCAVDFMQEEVEKMRRLNARERDEFEASVREDLTAVRQAEAQLKARAAECVQ
SLNQELTEIQALSELLKGEVGRLREKLLVALQRSESVEEESLVRLKSMVDEDMRSMEENL
LQLISSTNPLSFLAKYLSRKLDSDEAYRA*
>TCRU_10449 hypothetical protein
MDGTQQLRARRRYRALLRQAESLQKLGQIDETLSAELQKLEQEYPDLKKALGSVEGGIRL
NTDCAINKDKTEKKFFSEKTATITASTCPTEEKKQDLDSHLASPAGHFTDELKHTDFSND
RMKRKPTARFSGGVAFFSCAVNIWTESHLPSLFSIFSYITITLLTILVAFLHRYFVDPCS
LVGKSISPLLLSYLVHFQGLALIHLKRPERISRAMLLVYLVFDVLPSMLFVFFVYMLTTI
TLELFEQGFSY*
>TCRU_10450 hypothetical protein, conserved
MNDVTIDLANKQIKKKYVYGYDLYSDSVRKYYPVNDIRTAKNAILNNIHDYLDHLGEFET
NYNYKKERITLHLSIVVTVLINSVLLIGKDFLKPYPRTTYILMGIAGLFCLIACLLESSQ
ASDRVVFTAAGSSFRGNGMRRRDYLRALRGRKICVRVNEVPNSTRVIIEAQLVGPSRPFA
ASSVYYSVFKEVSYGRYFSKDGFFYPPPMVEDVDMLLRSLNSSLPKKRQ*
>TCRU_10451 hypothetical protein, conserved
MKKIVVGTPVAKVPVSKGAPQNNTASEIFLQSAKEAVVMSEKRQDATSSPPQSQHSPAQP
LGNKNGPAASMQTSSADAIGPSTSGGTGEVKEEEPSSGGMVPALSPALSAGSRPLPTRSP
ATNRTLALNGTRMLTLPWARTAAPIHSAPPTRRPRMAPQKSLSPAQTQQLFNATIVCWTA
LAPHRLIRAQRLRSPRSHRSSTHRRPWTMNFLVWRISPGWCPWV*
>TCRU_10452 hypothetical protein, conserved
MQHDRALQRRQIRHVDEDVRHQARRALAEATNPQLRAARKHAVAQRHVQRVSEHVQQAQV
HRHSDRPAEHHRVEARRRTPAANRHRLRQRHATHAVLCTATTARPRRRHVKRHARVAHAA

GTAAAHAVGERRRQRIEARQRGRTAIARHHAHGGQAGHAVVAAALQHPAAGTVALHRHDA
ARDCQPRDKRRASGSAARNRHGAAAQRHTRQRSHRRRLAHRPHVVNVQPPAATDRPTAAA
HQRRRDRPLDAHEAQHRIKHREALAKHNAAAAAHYRHVRHGEHRVVTQTEARRVRHMQRG
RGRTARRLQQHAVKHHSARQQVHAAANVHR*
>TCRU_10453 hypothetical protein, conserved
MQHDRALQRRHIRHVDEGVGHQARRDLAETANPQLCAARKHAVAQRHVQRVSERIHRAQV
HRHNDRPAEHHRVEARRRTPAANRHRLRQRHATHAVLRTTTGPRNRHVERQARVAHAAGT
AAAHAVRERRRQRIEARQRGRTAVARNHAHGGQTGQAVVAAAPQHPAAGTVALHRHGAAR
DRQPGNKRRASGNAARNRHGATVQRHTRQRRHRRRLAHRPHVAQLQPPAATDRPTVAPHQ
RRRNRPLDAHEAQHRVGHRKVLAKQKAAAAAHSRHVRHGEHRVAPQTERRRRRHMHRGRG
RTAQRLQQHAVKHHRARQQFHAAANVHRRPARLQRPQHSVAHTQLRLQQRCRVQHKRRRH
RVHQPAQLGVAHWPRRHNRRVADRHVRVCRQVVHKHERAVAAGQPAHAHLQAPVTRRLAA
VAPHVDLRTAVAHTIPQLDAQRAGKHRRHVKHNSHAVRDVHAVHQHRVHGAANRDGSVHR
AAPQSQHHRMRRRHPRSSSSQRQHKKKRHTHSRNDHAPHTVPTARTRAHRRPHPPTQPGI
NRTVVACRTRPVDRNSCLTNPLSSDGKSRDTIPINRYPTTTNPNTASNS*
>TCRU_10454 hypothetical protein
MYQVSTPGICQEGIVSCLSPGPQYEYGFSPSDISVQLPGEMCVDDVCPPEPTIYSKGSLS
SPITEEDKSMHMQSCNMRQDSNRSAPPTGGRLSCVSGAYSMGSSQNSPLREARSRDISLT
SLLADLEGCGVLKEHYGEVAERDDGPESNGAKASGPHRNVENSYIAASRGGAERGANTYG
GLASHLEPAIWSGGRWGNMGIYMQVPDPSVIPGPGPGLPFSVNRQNVFVMGQFDLPVYAD
GDVFMGSRAEDKKESNSERMKEQGCQP*
>TCRU_10455 hypothetical protein, conserved
MRHPRRHNMSPCLFLFLEQLLVLLFFCQLGNAEQLPECRDLGLFRPTAHDANSPTTTPLE
VVGGDANVTCLLRPGAEVATLLGSPEGRLLSPLRDRVRLAGSHVEPVAKNLKKNRVASFL
LRAKLFLYRFSAYPWGDPAAVERFFFQRRLRITFDVENPPGGMESRSQLLSRAVFDHLLA
TSFAPTAELFEGKGNASNKDVRLTCNLGEMLAAYRKASNDVSFISRMMGNIGLGALLSLF
FGYGGYSATVRSVAGGGDVSPVFLETAEGGSVYVFEELGPNGRSSLWLPSWVAAWLGTRP
MASTETLFLGKDGRHRFVYEAQLPAANPVCLRLAVAHAKELVIHVEYFLLFDVFWLKIIL
VLCLIRFLQPWIEDVPAFQVLLAGMGGTIVLVGFVLLFLFRKLQNMTLGKIGLFALLTVG
GFSALAESLLSAYAAFLYAYFNYYEESDLIFCLKCVLLLVGVACGFFAKFFWASYLFSLT
RWTLRWAQLGTVACAMMQNREATIVFLATAYVFYPSRLLRFILWCSRSQELENRENEPKE
KFPGSARREVAYVQPLCVEGFIGGSRALSSEEKLRLYDALGNEYTQRALAHLADSVKEDP
RRYASRLKNPSDVVKWARQYN*
>TCRU_10456 Ankyrin repeats (3 copies), putative
MVNLDNANTQLGLDVYFPGCDTYYQQSRPAYLPYMDGSLYKPWQPRHPWMQSAERQRRDN
PSTIEEACVYGSLAHVITFWAQGHEVKDRRALFEGNDATLLMWSALRGHLGVAKFLVDQG
VKVNAANGLGHTALHWAVTGVQYEMTRFLLDHGADPRQKDHQGYSAYFTAVQANNLPLLL
MLCEQHPIDPQERDFEGHSLLHWAAYTNSLVIFQYLVENCHFDLDVPDLNGRTPLLWAAR
EGYAVILEYLVLRGARTDLADKDNYTALQYARFRNHREAVYVLTKAPIFQRNGSTFSVKS
DFSPMEISGSGYINVRQMRRRGTVKMMVQEPIFMVMSLLGIFYVAFSYLLLKFIPPLISH
IVLGIFFFRNSLWMLILGYPVQGGKPELSFIQKMGIGNSFGESARGIWLFRNRDGSCLFA
IMSFWLLQQYAWAKMGLVPIITSYPTDEIALKDHPLESVYQPTGSIFWGFFFNNKAELEG
FLLLFLFSLMMLSCIMCKLLSMRSTYEPSESSLKTSPVWAIMRQRAYGWLHPRIISIEKH
MLIPLRTFYCYERDVFFRRFDGYSIALECPIAESNHGWFFLFVTSAACFQWLIFFWAWEQ
TSERLQCPRYSSFSSRVVGSLWNLIIHALPCRDGTRLGVADYGPWVSWLQYVLPTEANYL
GVWLLQYGLVASIMATFVAVRQWVAAANGATCLELANPTATGSEGGLVSIFPPTISFSAP
WLPPEGITEGVTLPVDDGTVLHSKARKKNSRCIYADYGNALLNIFLFCLGRSGRRWRGAV
AVSPANAPLFTLSALGDSFSV*
>TCRU_10457 hypothetical protein, conserved
MPRTEGQEEVGTTKRKKTPGDPIHTEDPRQPLRISNASSTSAAHPSQTLNRSRESDAAAA
TSSPSESGSGDGSDGVESEGEDFESEMSDIDRYCQHAALFSNSRGVDYFLNGMPSTEPLR
RRADDHQFSGGEYSLPSQESEALRTNMMMSSMGNTSLEIRDISGDDATKAIVACGSPMER
EVQAFYTHHRMAPSFDETTTNTTVGTDECRSTCHTRCLCCQSLIAVTLDSNGSVDDGNQK
GKEDDNLESSSQRVTGVQTEQTRECNYLTIRRSGHDMVDSHATLRRQGCSALYDRRHQHH

RRQQQEQFHTCTGSNAHFNAKIQDGAAKSMGNMRQDWRHQQNQGQQQEQREKPRQRKESQ
EGSFSSNTVTSLFPSLPTFSPTSFVRAYVGEGNYPWEATLDNRPALTVSCCVAAMNWVVV
QFLQYHVLDTRDHLGLFVIGTYIIFSSYYMTYYFLERYSLSFARISHDKKFYTIANLIKA
GILVSLVPFATSHLGNIIMFDVWDTNTLRNLGCIYTIPDFVSMIVVKRMSWSTWIHHLCV
LLFNFFSTTNDYSQENICRCVVVYAAFSTFAYCVNVLLASRFLGVSPNVARVLSVVAVVV
YIFCCATNWTWQVYYLRKLIRDGHGHWTVYAYMPLMSLVMYDDITLSKWLLHNAKSTAFA
AANYREHQHRQQQQQQQQQMAAARVSHRV*
>TCRU_10458 kinetoplastid-specific dual specificity phosphatase, putative
MTEVYTTPEVAAGEGRSGLFSAATPGRMRSGVHDSSALPETKTIGASVSSFQEPHGAACG
DTDTSHERPLWIEEEDIAFFFAAMTWNVELLEVLLSRAENPLLSDVAYGGSYDCQQQQQA
TRVPEEENVTTLARAAFPTLEEALLTASAAMRTPPRGKSRLPGGNHSRRSKRRRIGRGHT
TQLTIYSTFLYEARVEVDYEDEVEDEKEEVAWESKKYKKSGRGKFHFTTQAPYKCGAIKM
KKEKYAAYSTEEEFYQSDVPQRCLEAHDNFHAAAISETTANKVTVPAGPVLQGTILQKED
EKGKEKTQQSPPCPPVTIRDFFRLFFQSFLIVVVAKLRYQEEPASSNRRSNPLSPLESRA
LCFVRRYRVVFKEILRRHVMGSEKEVERRATQSLLVDAFQCDEARDGNWGAGWKPSYSQV
YISGREPVYQPLLLDFLNITRVVQCYANPPQSDVNDFRGIGGSKDMALNKLYCWRRLLLE
GSDMSQGNLQNVKRAGSLFLCSEEQEVAYELLRKCLSPLAWEPYRTFGPYMIYTAELPCS
SRLIAKLVIPAEDQESYDLSQHFQEGVFCFLHGIPFFPFDAARSGPQNVPSLLPRCCSLV
HCSAGMHRSSGLAIAYLLWLVALSCGELPVVRDSVDLLVEKNEEGQGRQYQTIASYLSVF
LGNRGKRPNTTETMAADVTATPTSLPLPAAAGDVWTDAEGSHVEKHGNEIDSVANNNTSI
LELCVEHVRRQRSMAVPISAVRELLRRYACCLHLQ*
>TCRU_10459 RNA-binding protein, putative
MGRDSRGDRYARRVDAETDRHGAVDGSSSASKKSTRYGRYAGKRRSRSPRSGRRGGSEDR
ESDRYRSRRHSESDEQRRRRHGTGRGRSGSKEGAKKGGGRRRSRSRGSSSSSSTSRRVDG
GRQKFEAVDVRELLQPEVQTPAGCMTSSLPGEMILALIQQQQQQQQRIPVIFQQQDEKET
MRDAVFPSPDTPVATVASPPPAKNDGVNESQKLQEQQEQEQEQRGAEEANEENASKAAGP
SRVLPSVADFVPVIPKSLLSLLSAPGGSNNDGSGGSGGLTGTSASGETEEGQQGALTTTT
GALAVLQAPKLSPEAERRAREARRAHISSFPQRTTRQELLDYFTTIIPMVRRVKVQREMD
EFTEKLREEGGPGADIERREIPPNAIVDVDRVVDIAVNSAKSKPFAFLEVNLADLVTELV
EESQRDPERFTFISADGRSYPITIRRPRDYQVLAGVDRRKVVMLGFPLTLSAAKLRLVFE
QYGPLLAFDVKAGMAYGEFEKESDAVDFVSELHGETLGNNVVVLMPLYDWLKVVCTHAEI
DVALDPDDPVSGASLLAKDGQIAGSLVPVLADDVAKAEEPVNHMKELVEFAVRLPDVVLH
FAKTFPHLSTLYGSTVPIYPTRVLVLLNLFDEEELVLDETYERLVDEITCEVEKYGRVKT
LIIPRRAPPPMPPKPPKNYFASRINTNKKSGDNLKNSGGHNRQHHVNQSMGGVSSPDGEN
EDCYKMENDDVDEEAKYERAKAEYLRAREEYTERLMHPIHGGFGRVFVEYESVDEAAEAQ
RAIAGRLFGGRTVVTSFMFEDVLNPPTAEEVEAEAEKKVQLYLESVGACGDEEKEELQAE
*
>TCRU_10460 tRNA pseudouridine synthase D (TruD), putative
MLFAPGHIWRVRRFVAPFHLLHANPGVRFAAAMEIRRQQSTSAVGDDDDDHDGKSLPSHG
GTKSRRGRSKRRDARGKQEGEATKLGFHQQKENDKGSSASVVLPTILTNGKVFSSSVPAA
HSEDSLAVARSLEVHRRLLSEAQLHLHMQAGETVASGAAHVAHEKIERRRKKWALTEVEF
DVGITERLFPEIRRLSSLHELHYGDALMREVDAASYFASKDSGKIPEQLAANGKTVEMSL
TDADFLSFEEQEPLQQPVPATSSSFSTVPSSLGESGGIPPDKEERKQQSQESVSCQLQSE
EKVVVHGVRTPWFVPEGGVVRLEPLSSSDAVCLLCFVLHLRRQTLQHLPLAVQKRMKEAQ
ALQGAASNDKKSLGRHLSLEDVMLYLDTAPPPVIGFTENLPPSKSPAFLFVLYTENVSLQ
NAIGHMAALFNIPQRAFHTCTAVSKMSCGAVLCAVGPNHLQREHLLLLNTMRHPGFVLRV
GSVRAVEDEKSCADLFGDLSLWQPLNEVELLLRRVSCGSRHELEHRLRAVQEVGAVFFCA
NREASLARAATDVLHGFFKSALLNALHRRNAPMAMRHFLSRPNPITAARAKRVSTDATVR
QVLKNYILVGGDWSQTVARTPYVWRRRWLSALRCSVWNMMASRRLRHGGRRVLPGDVVLR
PEYRADAHRRMLTTVKAEHVMLVNNESEAAECSLEDVFIPFLRGVYPSELFAPENTQHPI
MTRSNMLTLLREAHAPQLLLGMSDSCRLLLDIRSESSPLLFRRFIIRPIDITFTILEDKP
PMKSIHFDAARVLENDRLRLQRLPLAGKSIEKESSQTSGDTVAKFSLASSLVSQSLVLGC
TTIGARLSNGLLAEEFFTPPVREEYVALGHVERQLNGNLVLAAPRTGDDALKTIDRLFTI

HVHAVVRNGLAALGHMLREYFILVGVEREDDSALQHKIHRVRRELDTETRWLTSPTFCRA
CYCRDHDALESCAEYQFKRGKHESFKRREEVIQELAKADTSAMLPPNATTGMTDMGSSLA
TVENPKDDNMVLELELRLRRRSEEQKWGVHLTSTLYLSAIDDVTVVSECRLRWGANVPYS
PAIQKVFRNEMLGQNEHQKGNATKKSDGANPQFVALSQFILKAMGGTESLLRAGDDDSFL
PLINTSEGLPLSQFHDVFPPPTSILTDGVATAESRLGAEDVNSRKFLRQCKWVLTSINDT
AVTERRQVAAVFVKLGKRREVCLQFRATLQVFGGCGAPCLIAGEKLPETIELVLNRRGPF
TGGWGLKFGSNSLALLNLSQLIHADSSSGLKIVFDPPSLPGVASTETVDGKYVLSRVNGE
VVVSQRDVLERLQRKKFHGEEEFLRLQLVLCSQRGEENIGVTEGEDATVVNRLSALGTAG
KEGGEYGQIASQEGATVETDGGKSGEKEVLPACSPQCTPVTPAQRKRSVATIVINRKPEA
PSGRWGIRVQRGTLRLQRIQSNHDFSFQVYAAKRQQALRIADTLRFNNLQKRDRDQYGLN
AGLMEEAEAATSDVAFYSHFVYLIVGVNHRRVESIEELRASLAAAARSTKESVVLQVQQY
RLAQLSVQIVRGGGDGSVALEPVGFRVSRDMVVESVEAGSPMARAILAATNDGCSLRHLI
NGGSSPTATAGEHGDCSVSNLSGSKSHLSTSKRWDFHLDEDMEALSELPAPVKGATTASD
AGASGIITPPVYWNMVDGVKLMSMCGGNGRTRFVWRVSYGVRAGPLRTPQDVARAFAADV
KEETLFLQQCLIDD*
>TCRU_10461 protease regulatory ATPase subunit 4
MQKQLGYHANPEREELRQDVINKTAVRNAAQERLRGLMQEVKAQQEELEHVQDQISALLS
IGQYVGEILRQVDEERYIVQSISGARHLVGYKKSIKREKLKFGARVALEIITLTIVKVLP
RAVDPQVYNMQITGDEKNVSFQEIGGLQEQMRQMREVVELPLTNPELFLRVGITPPKGVL
LYGPPGTGKTLLAKAIASNVDAAFLKVVASSIVDKYIGESARVVREMFAYAREHEPCIIF
IDEVDAIGGKRIDGTSSDREIQRTLMELLYQLDGFDKLGKVKVIMATNRPDTLDSALMRP
GRLDRKIEIGLPNEAGRLDVLKIHASKLTKQGDIDYDSLVKLSEGFNGADLRNVCTEAGM
FAVRAGRDYVTNEDFNKATRKVAEAKKLEGAPHQYADQ*
>TCRU_10462 oxidoreductase, putative
MQVEVPSYGPADVLRVASSCGCDPETILLGDDEVLVHNSYAGVNFVDTYFRSGLYKKPNL
PFVPGEEGVGTVVKKGANVVSPNIGQRVAYFGNVTGSYATYCVVKMANANVVPDGVEDKA
AAALLCQGLTAHYLTHDSYPCGPESRVLVHAAAGGTGLLVCQMAKLRGAFVVGVCGGEKK
AELARTVGHADHVVDYLASPDWTLEVRRLVPGGFDAVYDGVGKSTFEGSLSVLRPRGFMI
SFGNASGAVDAVSPLRLKDAGSVYLQRPFLADYIRDPEEKARRFADIWNWFTSQKLQVTY
GREFSLADAAEAHRYLENRMSTGKVLLYCNSKAN*
>TCRU_10463 hypothetical protein
MSQRKLKGARSASASPVTADTADGWVIVGDSEKLFPTPAASGDFSSARDTKIRCAEGKRI
HLQSTEQAVNTPITRTDNSAHVSSFRNLNVQWNEAHSNSSLFSDEHSVNCDFLLRDRTRS
STTAAEEILSQQFEDNVYLSIPSPVPTPATPSKGGTLSPTADARNGSNDNSTSVGSFLTF
FSNGGRCNLVNICSPMWKTYWGVFCSTIPLSNAAVYYCVFAAAAVFVVQFGSSVTQRASE
ENGRCCLFGLASRASPLVCVIMVAVGPLLCIGVKLFEVLFPDAEAAVPQSSEERSEAKGK
ENEEVFLVPLKFALSSFLTFILLTEKNGGGSNVKGGVFDDHDGSSTVDDQKEIAADGKAD
TKPGSVEQHIRMSSLLLLGVGGGALSQYVIVSCS*
>TCRU_10464 Leishmanolysin, putative
MLPVRGRALLAVVHSASAAMPAGEHHDCDDIDGMELQDDDGDGRTLESHWSQRHARDERM
APIGGAGDCRGSAPH*
>TCRU_family, putative Se.1
MAKVPHRDVHIFALGCTPHRRLQQLVRARIAPRAMRLKDIMLDFSAPEVLVFHPSMQNEF
LQLLSPLSPPTRESVLNVAESLIVAAFHAMNNGVPVIRHQNRGSISMGLPGPFLRAFQAL
LRRAGFRLVAPTAAATRCGSSLIGAVSR*
>TCRU_10466 RNase H, putative
MDLDPRLTLNVAATKQCAATSQRISQLRCIAHKEAGPSPHDLRTFVIGYGASKLRYGSEL
IWAVATDSAKNEMQKTYATLARIVSGVPSTVDPESALLEANMPPLHVLCLRARLSIFENT
RACQMDWMRRPPPEPPPRAGFRISPLSRDELYAFVDAYTKDYGITESSPREERFFRSSIP
PWFAASAHRVTIGVGLPIDHSITDEEELIREKRRVSEEALALHSYRSWILATDGGVDVPK
SAGVGILLSSLNSSEIIEKASINCGARPCSYRTESRALLLALEKLMIPRIRHRRKTLLVV
TDSQSLLAALNKGPLSQTDWTEDQIWQRLLTLTRAGWSVHLQFCYGHCGVHANELADQYA
TQTMESGQYTEQGIAPLWHTDLLTCFTTQLTNKWRSTIRQDTHRYLLCGTRPSDLSGKDL
ITQEVLHRQELVHLARARCGESELWGRLYWAVRDCTNQCRFCNISPEQSAYMRSNNDPTA

PGTDTVPPSAREEDVSPVRRRTLTRRRKEKCPHCDSTLTGFSGLVSHCRSFHPEHPPPLP
ELKCDFCDMVFPTRRSTAQHRNRCAHNPDATRHRNSSARRRSLLPQDQPPSTSTPIGPQE
TLHHLLLECPGTLAVRQRLGIEQDLRLGKFSQWQLLHSRKLLSLLDHLFGTQMALYS*
>TCRU_10467 predicted C2 domain protein
MGKLSITVHGCRLLHSPGLAAINPRIRIVVDGVYKFHTRSKKNTHTPDFDETFTVGNTHR
LAIVEVQTYHCPTTGSSVEDECLLGSCRISIERLVEGQKKLFQYFLAAKDGTGLAGTVTI
TLKTDIQGGIMPFIDDTDEKEYVKRLVRLLLRCNKELLGDIDLLMASVKGLPMPQRVRTS
MSNSSLEGISLEQSISGDRFVTFEDLVESLCAKYNCREEPGYTLSLVVEGCTCLERPTMY
LPSNVVVVIRGPMQDFVTPHRPFTSNPVWGTPTGATSLDIVDPFNFVLDIILYQVSAMSR
WEELARAQVSLSTLTPNYLSARQIFLLGEKSFFQPYIRGMVHLTLRPHGFGAVSLQRAEH
LDRFHERLNRFFYRYDQQRIPQVDLLLRSRSNNLEELMSELEIEYGREPGTMELWLSVLE
VSSLQSDAKSDLDDSNVVVVITMSDQVVRTSQKRVVVNSRTEIDETFVFDVARETDMIKL
EVVRAGQESIVYGRIDFSFRMMQRGVRNDRTLHLVGAAGTNEAYLSGLIKISIFSEQLGH
AYSMDVEAASMYAGRLRRYLHLRAPEKLHLVDIVIDTVFDIEGFLRDLAKEYGQEDGTYG
VYISLLGCRQLPSRLGFSMNAYVVVRMGITRYETRVVKNSTEPDFFENFEFYVDRPHEMQ
ITIFVMDRYDLGDDREVGRVVIPLNTVQLAEQCHQWLPLEKPNKGGVAGLVGVKYTVNDL
HLRDPEHREGEKKRLVEDHSRDRPRPQNPLASLTDRNRRHGNIFSRIGGWRNKLVRMAAH
NLPHERTMNGGSMTGSDLSSGPSSDHEFFPQPPLNIIDESIHSIDEFCSVSRPGSSHTLF
LTSPKEVKSSAAIPSYLQLQPLLRYEKRLHVRVLYCDYLDDKRWIPPSPYVMLSTLEKTQ
CTKVAFLTRSPKYNETLVFPINDPNNDYLSITVITDTPYGKKCLGHCVLSLKNIQKGTPR
TRRVSLVVLPHRSVAMERGNICLTLFGENFGLDYMPSVDAENRFSGFLRKILAGQIPQQL
HRLEWYIGEYSLRENELLEKIFALRETGGEEELAADLKLRVKSVAQLYLNGQLVASGLCF
VKVRVGRRTLHRTKSVPGANGCFNIDEECSLTIPHPTKQTLRITVHADTKGTFNCGECEL
SLLDLHQDVVQERTHFIVKNTGLPLATPVGYITISLLSNNFGSLVSPMDRSDESQYVRLR
NYYYYYLREQLHLVDVKYGGIFNVEAHIQRLTEKYGPEAGNYHLHLEVVRCQSFVSRAVG
LYCIIQSGLTQFRTNVVQGGGEYVFLEAFDVPIGLPEKEEVQLIVIVLDEGSAVGTEMGR
TVIPLQYIFRGKETRLKLPLVYKAQTSVASLHGAIEVLLFTRDFGVSVDQQRSSEGSNAY
ERVEGSILPYRSEGVHRLSSLFVMEQAQNEGSREETPINTPFRAYSPSFSDIRVRLLGLS
GFPEEEAYIKVRLNGGKTLLRTGNLQGERLKCINEEFTIDSSLNIQDVIITLKLAVVKLR
RSYVLCYCDFTIPQCSLGGMSRRCLRLFDSKGKFFGNLRIEVVMPASVVRRSVAREVLDL
NRFESVVDDVSSLLLKYSPKDLRKLDVMLGRCDDMRTVHRQLRQQLAPRVQATVHCMVHR
TELLSPTKGRLMVETVVNEDVVCVMEHKIAAHGAVDAASDTCREFSYPPLRIDITSCEAL
LFRVIGEGGAEEGELCRAVLSLRALLTPELYDMGEAITVSLVNVKRQRNTVHASLAGTLT
FSLKVPAFERYPRTVLLFCHSPPRVNRDFVRYYLDRICSLLKHYDANSLMDIHHTVYEKY
VARRAWTVDLPNLLFTLIERWGPEVSSFPPPPPPTLQDAQ*
>TCRU_10468 SET domain containing protein, putative
MSICFGADHSPEAVGKWAKKCGIFLHPDVAFLVPTKTMGFGVFARKPLKAGSVIVSCPFA
RCISPYAEKNSVESPCVKALAEMHITDNVLFVVLRLMAEAVRPLSPWMPWLSACPRMPNH
FFDVAAVGPVFGLAPSADTGKAPMAGVPLTWTGISQQLHDLNLEGRWSAAQEAIRRHPEH
WPEEKATFELFCECLAQVLSRNFYREEIEGREGPYLIPCLDIINHSFTANGKFEVRGGGR
KHPMEFCVVAAREICRGEQVFCSYGRIGASRFVVEFQFVTDSIVKEDMLRFSVDVIAEMT
LALISLESESLSSAVDLANIQRRIEWLQRLGILFDEGFYVSRLPSAAAGGGDLPASTAKE
IQTLFNVFYLLTVGASTFENLTRSINREWQVERKGEVVALVLRLLAMRAEGARAQLAAAE
VHFAEAQHHARRKMLQMSLNSELEMIQLLQKHLGEPC*
>TCRU_10469 trypanothione synthetase, putative
MVENGEVEASVPLPYGEQQGSFMGVVAFSNRDDGFFSGEANYLYQNIYTGYRYQCVEYAR
RFLILTTGCVFGSCGGANEIFEMKTLKHVSTDAKLDFIAHPNGKSKRRPTPGDIIVYPRD
SQLLPWGHVGVISYVHNQKVGIAEQNYFFSLFTSPDPGYLGGERCVSRYLDLELTADGNW
QLRERQRNHPDCLGWMSYPRAPRRSSIHEPLQVPPEQRRVRATPLDQEDHPCLWRFALPE
DKFPFRSLYVFRHGTGEALIGAVTAFSRIVRVTLEFLFNRCQLSAGFAALFSSLLGAGFQ
DIPKKLKDVIEAAANEDDNDALMEHAIAAYFSLPEDVVAAMRREFRLAMTHMSAHITYRF
NLAADVQKQLESGVEMHCLKAVELHDEAWVVENVNFGNPWILSELSVALASKGSCQEFLW
EATRPEAICLIPCEFRTDFLRYVKHVEKIRGSRTGFTIIKSSSFRGDDADTVTASILSFC
ESFQYPTFVFDESRVWYDSEQSKLYGRSTTGANLHVDFCFCMTEWPDILSAAADSFEGKL

EGRSALLQAAIDPRADVVFAKPLWSLLCSGSVNRIKDGANDTSVKFFDISRCLYEFSLPK
QPPETLESDVHEYRDSCRRCHLISAPAPELISKSVRGETVMVDFAASCVTGREADGKAAG
LMYLFL*
>TCRU_10470 hypothetical protein, conserved
MKRRRREKEDMGPAAAALRRRSVFRDARASTTQLTAAQLIADAQEMQRGAGPVNDSTKVV
INSPEELALYRQKTRAELEERVKRGYSFLGNWVKYARWEAQQKDFERMRSVLERAVIFHG
TSPVLWREYAELEEEYGFLNHARAVWDRGVTALPSATDLWLKYLVLEQAAGQEGRVRDVF
NRWLSGPAPPNCAWELFALFEAQCQRADACRNVARRYVETHGEVETWLFYGSTELNVLGN
VERAVKVYETAMNSLPESHINGEKDCRIPLAWADALTTAKKYEDARHVYHRMLRECTSID
ALDNIFAAYSHFERLYGDNENCEAVAVAVASAMYQQRIARNPYDFDAYVSQYLILRDAVQ
HNKDDESSKENSYEEALKCLKSAVRTRVDGTKDPIAMQRRAVIVMEYARFIEERDITAAR
AALASCIREFPFKTAWCPRLWVEAAALERRHGAYSEARRLLGAALNLSACPEVFNAALQL
EEEACATGELSREDRVQRSRTIFQTAIKQFPQDFTLWEGYAKMEEKEEQFHRSDALRAAC
IHSLSAAARAASSMADRYALLEKVDQAWARRLALKRRIVRAVQKKLHSLGTRNAEETKTE
TTTLQKLYRELLDSVWEDYKYEAIEWKRKITTTGGILSSPPERMPDLMAPAVARWGEAVG
AVTKFALVPTQRTGEYESSSVDWMRAVFREMLERERPDLLRQLGGVDDNASYEAVQQAKI
WGEFLVSPIVTEWRRFEATYATPEELEAVKEFMKPTKRRTRLFAGRKF*
>TCRU_10471 hypothetical protein, conserved
MLSTLFFDEADASSALHVKATRQQHAEGEEESFEVSGGPLVTRNAMHCFNSGSIPIPSLR
ATLLWWLDRDAPRVHLLFTSSSPGDVSYCCRKMSVEVPATRQTIIACGLTHIREETVFAV
TWVTSIPEVGLLRLQLQRSNDHHSQLLLVPDGRAVLTSRLFRVAEAFENEAETFSYANGG
YNKDVGEEVGIGTSFSACILASLPREKALDGLLSMIILSNGISLWWVEMGEDGAFAEKEI
HIPNSCNGNISGSSQGSGVASWLPSWPWDGKRVKGQWCLTVSAVQQTQYILVLHCSGLLE
LYDSSVESMGPIFSCALPKDAIANSRAAYQWATLLNDDIHVVTCFGGSEACRCVWLRLPG
SMADGNFQGAECMSIIPPTDTSTLIGCVALSAENFALLWDFGLEGDACLCPSISIGSLLH
STQQGISGILHLITARPEGNALENGEGGRIENCQGNNTVALLPLKGSEVYFCHSHPLDAL
TFVGNELVLIEKMDGKVRAHVLSDKMSLLEALIESSFAVGRPVTAFTRNSLSLSAMHLIP
AVVRDENNPHCMDTEAFEEGVELAASCVDGADNLAALLINTVQNVPVALTIGGFQLLRSA
AHLQGYVPSGLVDDAAMRIALENAATHVEVSFRRTSFCSFSRRFVQHTVSRDLLSRIAYL
VCSYIGWMCSDLAYTASLELPRVRIVLEFLSAAYHAMSVAGPNVASVVPCVGENVISDVL
QLLLQFKPGWGEAGEDALYAVQVAKRLWASDGELGMRACVTWCNLLGRRYPCLQHFRILR
DIGAGRTTRSSHFMTMCVTVSFHLSSLPAHIAVPLLLDNELGICGGGFLHMAFADVTVED
WRALVTTNTTLVAKLYRVALLRRVIYPRDAHHASVSGLLIRNLFLTELVELEQYVHLAGG
GFLRVHRALVELRLETHMFLARVALDEAKIDDVFRSLEELLQCAAAQKTTAVYLEQVLSI
LGEVAELASASQEITDALVSLAHSNAELDGYLATKWYLYAARLSAKTASLPQAEVVRLRA
ARGLFCFLCKRHAYGQAGRMMTDLVNVVRCSAPRSSAVEGVLEMSALAVTAVELIAPDVY
LHTQQDEREPLTLAAYGPATYPNVLDQTPSKAPLNRNHLPWLRRRHFQAFCEKKLMEVNQ
YVDCTDLWTENPPVEVQEAAVRRFVTVLMESRFWLEARRFAAMMGHDVGTVLQGHVLDLM
TSTDHKTDEEALVEWFEMIEGCEEFSSAENQFDPLRRTVVAALSCNFEKAHPALLESLEQ
ADRYEALQALMEAFEILHYRRSMVVTANNVANEEENEENLHSAFSDSGSNETISATQPWL
PLLEALRIGTSVFTDSLYNDEDASKMSEAPMTAGLFDRMACRARELLGSSLLLERLSSKQ
AGSTAEKFLKSFEMIKESKLANGVVH*
>TCRU_10472 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MQRWRNAVKVKDGFQLTESNSRVIWPVNIPDDKVRNVSLSHNFTVVASVTIEEAPNNNTP
LLYAALGDAGPEYFMRLSYTADNKWETMFEGTNTTTTEGSTWVPRKEHQVALMLQGNKAS
VYIDGESLGEEEVPLTGETPLGLFGFCFGACEIGDGVEEEEASPKEIGKKPSVTVTNVFL
YNRPLNSTEMTAIKDSKPVPKRAPEPQVKIAPKPAAPAASAVPGPREVPAAPGRTTVGRT
ANTQHAPAGRLTTAGNEGTARETGDGGANGDAGSAYGMVLLPLLLLLGLWGFATA*
>TCRU_10473 Nucleoside 2-deoxyribosyltransferase, putative
MSGVYIADPAVFDAETGAACQDRVRTALWVHVAVPLIPAGNVAPGAGGMRVKKMEVVRRR
DAVIADLCLFCLDGPDCGTAFEVGHAAALGKTVPTFTFDWRSMREKYGGACDASVMTVED
LGLSFSLVLCDGAEAFYSFDAALHRFLRHRSEWRGCDCGDVREVRVNALGPGGILCTTWR
ASPTQWPADIPCCVSQQQRSRLTPCGTVESGVCAADCCLFSAFSAAFVCGPEMLSCCLRG

GYPFFFLLFWL*
>TCRU_10474 protein kinase C substrate protein, heavy chain, putative
MFPYIFFFSLVITGCSALEPSYGVQDGFLEYFAAVHPERPFNCLCGNVSIMGHQVNDDYC
DCPDGSDEPGTSACTNDRLEVNLPKKWKFRCKNIGFKPQEIPHNQINDGLCDCCDGSDEY
SDIIACPNVCAETQEIEEKKRLENERIREAGMREKEKMMEQVRKNREDDKVQLENEIMEL
EELRKSIEEKSVKLVPFEEKERAEKRRLLDEYNAAREVWEEKRKKNQTSNLNARGNLTTN
CIRWSPTKICDPEEESPLVDKGCDDIIYPFEAGFCECINKETDSKVAYDQECDHEPLQCS
NVCENPEKDNKEMDDDRFDMDDGASFELPEARDLRFELKESRERVEKLSSSVEEIQNRLN
RSINTGDVIRTFSNECFSLNTSAHTYEICPLKDVHQYDKDTTHGPCIGRWGRFGDNTYSL
WSSTSDYTHMIFENGDRCWNGLTRMTDVYVICGPENKLVQVEEPSMCRYTMVFETPAVCE
*
>TCRU_10475 protein kinase, putative
MSAGGEAYCSPIRRPIGCISADTSLRSPLGSWYSWARDQSRTGMSPVGSPQGRSFAVHSR
PDDFTPRRASPVAPNYASRTSGIGPMSPRYAIVARRRYQVMTADYPAYPQGTPTRILASH
GGTYSSAFLNAGGVGSSARYSVKNASALATTSQSAQQSSLLDVVGVSRPSSVHPSHPQQT
KQQPQKPKEPQKQRQIATPGQKLRVSRKEDDSIVTSSNDLSNTDDGITVPVKVSIPSPYP
SSGAPRTATNQLSMSNPTEAFPDYKSIAVEPIPQQIVQKVSNPALHCVQRASVQGTLQVS
STMENSFLDSSRCSDLNITPNRELPIHESLCITPHPKPTPAVYAARMYPTQQSTTVHRCL
NAIPAPKAPPQPITAPGSTTPGTTPVPSDECSRSSTETLNLISRCARQPSPVYNVISSFV
SSRPLIEKFVLRWRNHYEENKNAYCEGGYMSVTPGKKLNSRYVVVQKLGWGEFSTVWLAY
DTMHKTCGKPHQAFVALKIAKCDNTVSVSTQYEINLLRYIGMQASPFAPLTNLVDHFEVP
GQYGSHVCMVMPLHGSNLLSIIDQMKAKKGLRSAQEIRLIKEIVASVLVGLQELDKLDVI
HTDIKPENILCSLPDPKVLDVIETFCRRNKDRSAMVPYETVRDAISQGDPNHLVCLADFG
LSVALKPPNGWDNSNESSESKLLLKSLIGKKREFPVEKPGTVTNLRGTMVQTREYRAPEI
IIGLDFNTRTDLWSVGCMVFEIITGDFLMDPKRRTKNERMMDVEHLAMMMQLLGPIPDEI
IRLRTRRDPKRPPPRYIHRYFNESGRFIYSEKYRLYPRRHLDRELETFLPTAEAQGAADF
IMHCLSSYDPSRRPAVHDMLAHRWLSDVMGQRKC*
>TCRU_10476 hypothetical protein, conserved
MKSHLVAVLGLWLRIGTPLLCIAASTTETKTTPPLEKVPRHARCGEVKRSACRLSGKTAR
PFRCGHSVDVTRGGEVHKNHGTEEDGYITNWQLNIAGLSSVKKIASAARLEQHPPDIVLL
QETNTRIATAAKLTGHNSFLQAALGAVVALLFRCATLCRASA*
>TCRU_10477 hypothetical protein, conserved
MEQAEPAAEAAHKAHTSPRQETACFEPNSSKKWRTKIKHYAVASLCFWKPARKKLGPHPA
RAGDISAAWRRRTLIPWNRWCSEMILGPRLCSASATGKSACSSFCAVSRATLHYTAAAAA
RCTPLFPGDWEMDRPLTPYVPDVAIRDSSLGSAPDHDNMSNEFMHHLGPVARGTLRTMIH
NSFANGSLPGSWNTVDTIPIPQPGKDPCRPESYRPITLLSVLLNRKNDSPPSISVIAAPP
TSIWLYTFAFNIGRDDTCYW*
>TCRU_10478 hypothetical protein, conserved
MRQLIHIAPRSAVLLVLLVVMMFVMRCAGGCFAASLTCSCPSDKAMRADGAKSIPAVVRD
VPLGSEGASQTCTVIGRNGWAPTRIDVSTRDVYGTRKYCSSERYCAMNSLVAIASVKVTF
FYAEKREVFVSLYFAATVR*
>TCRU_10479 hypothetical protein, conserved
MDNNMEADAERDAIQSDAARADGDPAGDGDGGAVAHADPDGVGEQHAVVERCGVPDACCD
DDGGWRRPDAERHPWRWERRPDAADGGAAAAVLLGTRSAARHAPELRAGFDGAAEWLWWS
VGSDAEQRDVGAQRDESVHRPGAGCARAPRLLHCCRRDDSHSLRRSGGVRRLQGSAAWVL
HDQV*
>TCRU_10480 retrotransposon hot spot protein, RHS3, putative
MIVVSPPNVGNCDEWETQVKAGRIIMNCPDEMDVKAMCAWMKRDGTTDGQAEYWKMVKER
MEKVGPIPCYIFDANEFIAHSAATEDALDGINFRDGERHFTHGGVRL*
>TCRU_10481 retrotransposon hot spot protein, RHS3, putative
MAASLTDGAHLDKEWPYSWKWKENKSACDCHVNCEVDRAWQIVKGDITEWFSTHGGTDFK
PKQRVLIGTPGIGKSMAASSYLLYQLLHCDAEKLQVVVHCFGGSTTYVCDKAIKTVTRYV
GRGASKEILWDWGIV*

>TCRU_10482 hypothetical protein, conserved
MSGNKASAVPQGDRQRRARPASEGDTDQPAATHTRDEEAQRPQWTMSSTVEDILLEGSTS
STEMKLNEFIRNYFGGRGVVDTNENISISVFVLRPTMFINDNEILGLITASSSYRELKIE
LDEREILLEAVNRLHHEGVLFLGQWRDYEEKDTVTFLARGKLNGVLTQVLTEERREAGEK
ARRDQQQVIFNLYAVIGDLLFGGRVRVNEIKLNDFLTLEMEGKGILHANRNVLLRIFLVI
PRGISAMREY*
>TCRU_10483 hypothetical protein
MTAFFCLPQTFGNVLEPRLARTYKKVLWDLTKVPAFWKRCTSILLIKPGKAPDAAKNDRP
VRITSSLSSVCGRAVLEGALLATHGPMCDAQYGFLCCRTTVEARTTRILVPVRLGRETPE
RRREIGCKNHPSRSSKGCRESIPALLGFTDAFCKASHRHIMDGTLSLGVST*
>TCRU_10484 retrotransposon hot spot protein, RHS3, putative
METTVRDEMDMEEDVHKLYKSGVDNLLKWLVAAAEVKANVHDVAKGFLDAALQEARNPTT
TIAAMKMEGFYDSVHNARRSHAVEVPDGVERKKTGTGMEVHEGRPEQSWSYRKADDAIEE
NDAVQQFGAASPVLMVLASEKGWPYS*
>TCRU_10485 retrotransposon hot spot protein, RHS3, putative
MYLLGPIPRHVFDEEAFTERCGAVKFALQSINEVTMKEYFSRGGESPWYSEDPSHRPVEV
VREIYAGGVILFNAPISACLEERTLERLPSVAE*
>TCRU_10486 retrotransposon hot spot protein, RHS3, putative
MTVVGLRMATAGGRHTTASTVGQFTECLAAYFNGWEELSRDMSWEIIYVQQTDSTPRNGW
QRCDVVNSNNVSDESREIRRSVRKRSASTKCQYPTETFEETKLSEVCKK*
>TCRU_10487 Leishmanolysin, putative
MAVPSLAPCTLTVSFISRTPRHPHRCAPVGPCYRVQLPAHGRPQHGEERCRCAWQGAVGG
GRLDDCRDFCEEPRDSDDINGMELQDGDGDGRTLESHWSQRHARDEWMAPIGCAGCCTEL
TLAAPADLGCMRVRWEMAEPMRW*
>TCRU_10488 hypothetical protein, conserved
MMMTGRVLLVCALCVLWCGAGGGEPSETPSPAPPDTPHEKNPQKEEEAFVGTGQGVKNDE
PEIPQAPAPKASESPVVSAESLQAQQSGGGASVTASATTDNKDQNAKEDKKEEEAKDDDE
DEEEEEEEEEQEDRDSIPDGREEETEVIISEQETEQDKKNAGNQAPTETPGGPTNNEEIK
TATTQVNGQPSPEDLGDVKQSEEVQGEKDSNHNPQTKSVASIAAKQQNEPSADHEESRPP
SPTANGDAANKDFDKSTKDGIPSNHPAADVAGTAEGKQNENKDANPKETPVTATAMKTAR
ETTGESDGSTAASHTTSPLLLLLVVAAAAAVVAA*
>TCRU_10489 hypothetical protein, conserved
MAMMAGRVLLVCALCVLWCVAADGDVVGPVTSGDSGGGGQSPLADGSHGGSECSKADISH
ESKSEPLVAASGEESPAIHLDPNGVSSLSEEHLRPEKREPPKENGKSHNHRLKMHRRLK*
>TCRU_10490 hypothetical protein
MPTASVLAHHVHAAALRRRHSSPLQDESDVILSLASNERSSCYVVQAFLPDDEFANGYEG
CVAAEFERRWFFLTDGVKELQALADVIAGVNAGVSATRSVAVGKTSFTFAAEAGINEANV
RAHHPTFCTVLSRRQDLITSHIEPSPCGRNVASKRSRGRRARHLHSSVEVSRGRKCEPFG
ICHLAAF*
>TCRU_10491 hypothetical protein
MESIHPVEYRRVVVSGSKDPVEYFVRAKGDGRAVVPAQTETRTGWLMCPATLRSIASLDA
CRAGGSPVSVGFTANPLAPSEGHSGAFVL*
>TCRU_10492 hypothetical protein
MHGVPVGDAEGGVSEAWDNMYSGTGVWRWPEEVLCQRHHRLMAIDFGALIFGALRTGTTL
ADQVPLAI*
>TCRU_10493 hypothetical protein
MTVKGTIRFEDLGEPVQRLLRSLKGGYTEEDMALLEYVSVKDMARIYGEMSSERHAEEIW
EELRAALKARQEKAARRELELRNRQRQIEADREADERARREQEALEEAERRAAEARRERH
ETLRKIGDDSV*
>TCRU_10494 hypothetical protein, conserved
MSWSTRCFYGPLHEVADPLVLRRVMMRFWSPFCRGFVGPDLHTYDFKKVFDSIRTSDSDF
TCQVNGRVGNARLIEDFFLFVLCGFDFVDVKLEKSSTADVASDPCNFRGTYTLAHTRPFL
GWIPPRAAHSLGTAATDNKPDVCKDKNVDASGSAEQTSEEKLMISSTRLSVERQTRLLKV
SFSARMEGSENGISHIILRSPVVDVIMGSHDCPATLQSCLKNEEALKAVVTLRRANVRPE

LITDKTLLEITAKKESWASALGIL*
>TCRU_10495 synaptojanin (N-terminal domain), putative
MSAHRCSGDIVIIGSRVFFCPQNEELPYLEWEAEKQRFVLVQRDDCDAAPLFVSEQTASG
ELEYGAVRVPCCALYGVIPLRTTSILLYVNHQEHVATLPFSASHEVFAVKRFAWMRLPSP
KTRSPVYDGLKEDDGGQNGSYQDLSEDILGKYCALIDRFCTESQQHSGGSYFFYSPTINL
ALDPCALAEGPTKKRFAASFSGNNVDSHKNTRPRLDNVGEHSLLAFQWNTPLLQAFTPLE
VYSGGIFLYVPVFIRGLVSMSSAPSDGVQLLLINRLSYRWAGTRYNRRGLDLEGSGICAN
FSTSTLWVFSAEAEEQEKDASVASLNGEKRMASYQIIRGSIPLHWSQRANLAFTPEVSIS
SPARAVTELISHLKLLNKLLRGISTLHFIDTTSLSKVERPLSEAFGAAVTKFCESDLRHD
IPYDVHYTKYDFKDRMRRNLSYDEISNGLNELASGCVNGEVKRLDFTQWCRKPMSKEDGC
LDVGEDDTCHFFWNKIHQQKHYVRVNCLDCLDRTNLVQSMIVVNVLPRMICYVRGEKSMA
NNCHNENDAATEDSDTEEEKYEESIGLCKELWAQQGIALSELYAGSEPHFLRFLLKGSLG
PFGRQQEAILASRRWLQQNFYDGDKQDIISIVTRQHDPALAQSEFERRFLRPFSFLNKMV
VLGLFVAMFALGVNLIVTLFVPRDRISTGPVLYSIAWVIYIGVLIFLIMRDGVSYTNSPL
FR*
>TCRU_10496 hypothetical protein
MSGTRGDANGFVEDLEVLLEDDALPHREPVVRRVRPPSKRKPKRWEMMPEFGTVTTAVVD
GLEGTLSTSIDNGGIFAMRPRFRKDVEMDKQKHLFANAGLVAQTLTTDSLPPVSSVTPVK
KEMERSSFYISGEENGIGLQTSGFCMQKAEKEVSFSTLTEPTPWKQPAFEELGNDYGVVD
AGCFFHSKYCFNDATRPTRSPESLRLQRHLHSPTLYDETADIFEDVDDFIPGSPFKRDLC
LPAPQYARHPPKSSKRQVRLCAFSSTLIPSSSLPGTTVDDTVDSSLVTYGSPVALQRYDN
SLLPNHSTAAFHDEGATKEPKKLPSGSTPSKHLGPLGLYPFFSSSGTHSFFWDAHGYYGG
FFEA*
>TCRU_10497 NADH:flavin oxidoreductase / NADH oxidase family,
putative
MATFPELLRPLKLGRYTLRNRIIMAPLTRCQATEDGHVPRTESMLKYYEDRASAGLIIAE
ATMVQPNYTGFLTEPGIYSDAQIEEWRKIVDAVHKKGGLIFLQLIHAGRAGIPGKILQQP
KSDQDPLAGRLLAASAIPIKDHRIPVYFAASGEKETYGVPEELTDDEVRNGIIPLFVEGA
KNAIFKAGFDGVEIHGANGYLLDAFFRESSNKRQSGPYAGTTIDTRCQLIYDVTKSVCDA
VGSDRVGLRISPLNGVHGMIDSNPEALTKHLCKKIEPLSLAYLHYLRGDMVNEQIGDVVA
WVRGSYSGVKISNLRYDFEEADQQIREGKVDAVAFGAKFIANPDLVERAQHNWPLNEPRP
ETYYTRTAVGYNDYPTYNN*
>TCRU_10498 hypothetical protein, conserved
MSEREEKPKAVESLAAHSGVRTLRELEEQEKEQLRRALYTDPLAEESTALEEKLAAEDTA
NQAREARKEFNQATMRPMSEKMKGFRGFMCLLGSVQSKNVVDVFIFTTAAMFTIPIVVLL
FGMHVVAPYFGADSGVCGGFMALGSTIAIMAMYVIYAFWEPFMGQSTAGMIAQEKKHQ*
>TCRU_protein homolog (BBS1-like protein 1), putative Bardet-Biedl
syndrome.1
MSLKGESQKKEKFWLYAFRDHLAGIQAFTSCIGVADVHGDGDYKLLVADGKRRLKIFGGT
SLVKEMQLLSVPSALTSFYADGGDAVFRPVVAVACGPNVLMYRNMVPLYRFTITPVEIDS
VDEAVWEGLRNNTISVAEAADMLKDRQADGVELSTRSIDLLVYDNAKERERFVEMVKDTP
LSQPSVVTCMSSLYLDRTEEGSRGCLVIGTENRYLYVLKSFSTDVCLRIRVPSVPESIVT
AGALRTEYRIILACRDGRVYSVKNGKLSNSTIYPDGQIVQIARYDNLLAVATTQNTLSYF
TLKGKRQSSVFLPFPVTNIATITENVSGKARGIIVALNNGEIRVYVGNLLLHESQAYGTV
TAMHFGRYGREDSALILILQNGSLVVELLHRHASFECENAREVGPAPEQDVPIPVPQLTS
LFVAQAERERKYSLDIHRSFQRDICQIRLQSAKLYLSMLSGNGEGGAAGVNIQRREESIR
MITAVQGLGPVYKLRITLQNLSQKPMHNLTIFFSYPSTSCKLSKHIIEVPFLTPSSLSTY
GVLLERLDGDIVDGGISVYLTSSSSSVPLAAAMLDLPDPIIVEEGF*
>TCRU_10500 RNA polymerase III RPC4, putative
MPPKLPNLKYKPRRVVRPKDELDESHSTEGMEDMSLVQLERLRLQQEAALQQQQQEQQQT
FGVGTATLHSLRGDSAASVLPVDSASTRRAPRLQSAQIAASRAAAFLAPEAERFPVDTMS
KILEVRADTPGMTVYHPTPLDCTLPARLKPSDEDCFVEGDDQRVDATTQDDGVAFLKEYE
EELRRSRLANMRFEREVLRASADKIDAEISMGCSDKGEFVWFQLPRFQADPPFLLTQLPS
GKIGEVKVYKSGRMLMEICGVYYELAVEGYTAAGDVACNVVAAVTPSQQPDEKTSCYQLG

LLEKKIVCTPSITLDK*
>TCRU_10501 hypothetical protein
MVFVLLRCLFTFIVFHTGVGYAVLLALRLPLAVLEEKEHAKKQNDNLNIPLDSLKIWIMI
TFLSSLSYMGAEKLPFFLEARAIFTWLLLLLPSSSHSKVYDGAFEPFFERARKSITGIVS
TRMLARSVGLLFLRVCIGTGLFIANKIIFHRLLEEDEILKVVRGLLYAAQALEGTEVTRP
KTSRSLLPPPPNSMGTELL*
>TCRU_10502 hypothetical protein
MGSVPSREFHESPDALFFTRCGTTLKLARLPLTPHFFPSENCLAFQQLDNCCRSQSMKYG
FTLCDGPSHKRHGCVGERRRRCGCYARENDDWDDICEEELELDPSVPCQQDMMELVPPTD
EMANTFVLHAKKNDIKNASMTKESCSSGANHMATEELYRLLVTQGTVPAIVETNAEMKEL
YEKEIAWRHARRMICRYHQRLRNGAEARSETNEETAVRLAEMVSPPRCFLRALPTAVVAV
VDSEDAMRRAPPKSVIPPDGALHLMENDGMLFLASRKNERYIVPPTPVRVVGCNSLLPAM
CRGTPWLRGYATTPVEEEEDAYIESLPPSQRPPVLCACQFFEAAISEKAFGRALIEGLGY
YALHSRMAGMDDLVARPVWHLGLASRVPLLHFIAEIRQLVSMAAYPTGMALSIRGNCLLF
RLQEAALRAMCQLLCPCTDSFAPQSSCQHVWRQNVPRSALYEYGGRIGVSRTNGTLCASK
HVYDAVQKHARGEGENTVGISRLLVFTVVNPWQTSTPLSDFGKRYDVIEKEDTSSNVFND
GDLLVYDNVRRQWTRLLQSDVTLETLLLCWVKRLLVAATFRHDDTGWLRDTEGLIVQVGR
FHIWSEVHDGLPYFFGAIPKFAKERRRRMLRKTREKFLQEEEGAKRLHEGKRNEKDSAMP
AQDPAGRHFACTLSTHFKRHGDAANYFCNGSFTWNPYGRRR*
>TCRU_10503 hypothetical protein
MSPTVLVTSLTALLLYVAFVYPIMTDAARFPWQTLPPGHPGSGSPVIYPPGTIHYVRQEK
KITPRPVFQRAWYVGFFLMVVAVIIIYALLYIMVLLRFRAAEQASMRNCLAEENRGPIRN
PLYADFSEY*
>TCRU_10504 hypothetical protein, conserved
MLQRSFLRCIWLGGTASIPALGHDARPSTGKYINVIPPTNIAKSIAAGSLPPEANVAAVQ
PVPGKHYSKWNRVLRSEIYDELLKLPLRYKLHDFSKLCPPSSSSSTLQEPQLQNVGVVGK
GSVVNYNPPLGPADPLDTIPFFVHRNSNGFLPGRVYSMDARNLMPAFFLRIQQVEGDVFR
FEEELLKIFPTKKIFVRSHSIYVYNVGMDGRMILHHWLLGLGF*
>TCRU_10505 eukaryotic translation initiation factor 2 beta subunit, putative
MAEGAKVARIVRRRRAEGDDDDDENEHVPQVEVEQQKKKTSRPKAPKAMEAAPDATLATH
LDPVTMGAGATSSIPPPSASTATVAPTAMTMGDRLDAPQVAGSVEDVFEIAYDNYTSNDL
YALLKRITRQEVERRMIEHEQLRQKQQRVPQVERFLDATSKTGSSGSSGGGGNKASEEGC
GYNYSVMLRRLFFALNRNKESSAMTERNRLPEPKLEKIGKKKVIITNFGRICQAFNRPIQ
DVKDYIEKELSVGGNLDSNDALILKYEIQKSTAFDNILYKYLDEFVKCNSCHKIDTTLTK
EGRRMELRCNWCTATRTVQAVGSATYSAQVGKRSKARLQAMTL*
>TCRU_10506 hypothetical protein, conserved
MSIDASLFFSREEPAPWPQLSGHGCFIRGARHSGKTSFAFQAAVNTAQDGGRVVVLCREH
VLYAKMPQPFTPLGSLDEDALLRIEFMYVDSFPDAFREVGAWSTPDDVPALLLLDDDSFT
DAGDTRRTAQVLSALENVHAWITRCGRCFNYAFVSNSFPEIWQGAELPFAAFPLVCFLFG
STGSVSVQTTVGDMSEPKPLRLSWHNGLCMEK*
>TCRU_10507 hypothetical protein, conserved
MKEEDAATIQPLQEPHSAWKRALDLKALNTGRQRLPGAPNGTTLVGWTTDTLLPGGEKDA
AASGGRGGNVPRGTLGGTHATDVQQSALEFIQEMYGMKPLDAPVITKGIHASERQKRWGG
PVLFQPSRLTNNQSPTKRESAVLRRVKSHHGTGAIRDPLLRRLSSRRTLSQDHLGTIVDH
IFQGYMQTNSRAKKPLLAPVTKAETDDSVSLFVSNALDSFLVREASFSLRDAQSMNSFLT
LGGDCNFSKLLSFQGQSQFLDDDDPSELLTKPAFEGRMALFAPVESQAEVSVSGPLPEGS
LAFVAGVEAPCPSPVSLHSTLETETPPVATRGAKRITGQPCLNFSREMSLDSDEIQVKPL
DILRNNKTGDVPTNIPKNEGYNGTNPENCVLPTSSGACPLPCYSNAIKFGRLVAPRSKGI
EQLISDEDLKRSVLVAVEQRFRKYLCALEMDEATEISNANKRGNNNVNTANPNTQPVVIA
VAAPQPMVQNLLDFFGK*
>TCRU_10508 chaperone protein DNAj, putative
MGLNYTSKAHQAEQEASKTPDREEVSAGFPLGNVFALQEPKHALAGLSGAAQNLVVGVGV
GLGSLLALPVVNGHRDGARGVAKGVAMGVAALVGMTTYGVATGVRQFAKGVYNTKEAVVE

AARGERYWDSQQGRWVDVHLESAFAELPAGDEDLFTQAREAFGKMFTGMSSNATHASEGA
AAAPLKDYYAIMGVQRTATAAEIRSAFHRKALEMHPDKNPNNAEATLRFQEVLEANNILS
DEGRRAHYDKYGSADSILDQNSSYMQFEEALGANFMEMFVGRLSYALYFIPNTFLTDGLK
KEFQRRRTLRLAQRLIRIVDDEGRLEAVLPAIRDAVSTRMGPKLMSIVAQQYVAAARQHL
SGSLFLRQLDIFATSKWSRLVQMADVTAVGVPAALKAARSTLKEDDQVDILVTLCEGDVQ
RTVLRASRLILYDTSATSEKRRKRAENLSILGKMVEGVCRMARSSE*
>TCRU_10509 hypothetical protein, conserved
MTLARDVAEKFVSHKPLQRLVRLPYSKEREPEFLGLNMDHEDAMVGRVLHEMRYKNVVFF
SERPCRFHNVHEGLGVRNVTESSVVVHHVWESDYETLMQRFGNDTSPAPKLFRCSKGRYI
FDC*
>TCRU_10510 hypothetical protein, conserved
MSRKTYFLFDFALRLFPTVPYIAKGDDDMFLRVPQYLADLRTLPRRKTYWGVLYQKGGLF
PVDFILGFAMTLARDVAEKFVSYKPLQRLVRLPYSKEREPEFLSLNMDHEDVMVGRVLHE
MRYKNVVFFSERPCRFHNVHEGLGVKNVTESSVVVHHVWESDYETLMQRFGNDTSPAPKL
FRCSKGRYIFDC*
>TCRU_10511 hypothetical protein, conserved
MQHDRALQRRHIRYVDEGVGHQVRRALAEATNPQLRPARKHAVAQRHVQRVSKRVHRAQV
HRHSDRSTEHHRVEARRRPPAANRHRLRQRHATHAALRTVATTTGPRRRHVERQARLAHT
AGKAAACTVGERSRQRIEARQRGRTAVARHHAHGRQAGHAVVAAALQHAAAGTVALHRHD
AARDRRSGDKRRASGSAARNRHGTAAQRHTRQRCHRRRLAHRPHVVQLQPPAATDRPTVA
AHQRRRNRPLDAHEAQHRIKHREALAKHKAAAAAHNRHVCHGEHRVAPQTETRRERHTHR
GRGRTVRRLQQHAVKQHRARQQVHTAANVHRRPARLRRPQHSVAHTQLRLQQRRRVQHKR
RRHRIRQPAQLRVAHRPRRHNLRVTDRHVRVCRQVVHKHERAVAPGQPAHAHLQAPVTRR
LAAVAPHVDLRTAVAHAFPQFDVQRTGKHRRHVEHHSHAVRDGHAVHHHRVHGAANRDGS
VHRAAPQSQHHRMHRGHPRRRSNQRQHHKQRHTHSRNGPVPHTVPAVRTRTHRRPHPPTQ
TGTNRALVVCHTRTVDRTSCLENPFLQMANPDKQVRQIVIPLLLILILQAIPNTLKR*
>TCRU_10512 splicing factor TSR1
MSESRSGDSVEEPPRTISHEKNNNNNNTASTATMNPTSVFIGLGPAASSISDDALRQRLE
EVAPVLGVRIRGRCAFADVPDPETAERLVAELDGKLIGDARMAVQISRNKDKQRPPGNQN
HNNNLNNSGRTSLFVGLGPAGGAISDRELRSKLEEIAPVTGFRRRGQCAFIDVADMAHAS
RMIHELNNQYIGDCRLSVQYSRDNKSSRFGGRMEKRSRSPVRRRRRQRSRRSDSLDRRRY
RRRRSYSYSSRSSSSRRSSVDSDDSREYRRRDRRDKRRRERSRSYSSRSRSSSPSYRRRR
D*
>TCRU_10513 hypothetical protein, conserved
MLRTVLILGRVAGARRRKLHVGLRGVRATKQHERLYKRLREDEAERAFMQKIREDRNRRE
KIIAKALRQALAKKEREESKLLRQYEANKVKAVEELRKLKEKQEAPPAVAAPQVQKPVRV
PCAKKAELTREEIQQRREKEREAEKAFFEMIEKLRKRRESEMLAEQEFEKQIRARMASVE
KEESGLGGSESPAVPSATDVTADTVTAQDVNFASNQTTELKEVAEQTEDITLKEMEEHSE
LNVALEEPSRVASAKVSQEKQRPSIGKEKKKTLQTKQEQPKPREKRRKRIKVTDHVPATP
QMTAENPADYVPSVPDRVYPPVFQQPTHAVSLTGFNEPPVMSSMAQTPDFGQRHVQSLPS
LESPVIPLRPRALDTFLPVERMARSMPVSFPHIIPAVRQARERPTSGAGLHRL*
>TCRU_10514 syntaxin binding protein 1, putative
MDEEDVYWCSCRHCFLAQCVEELSAALKELDAYHSGLAQGGEPKANLAELTSAVRASPEF
RERQARPSLHINICTRLVARCQEKRLAEVCEVEQDIAVGHKPFRKNLDGVRRLTRDAAMP
RPVRLRLLLLLMTASSTDELKEANKQQLIQEGGLTPDAHLFANLEHVTRRAGSVQ*
>TCRU_10515 hypothetical protein, conserved
MLRRAVVALRRDALNGGSSMTLGSKGMKLSPDPHRRRMPWTAAKEYVPGVVLNAKEKMVL
DGVQLVDVECVDRASQVDPLEALRATVATYEYNTSTGKNIFQLASQVEFDGRGQRFYRKE
WQEGTYDKYVTLSAIDFNRDGNKGTAYGYVTFHGETTTRPVQIDFADVPGWHMEFRVERA
VPFNAIVPPPPSIGTDVPVDPRSYRLRAYPFYDAPNPPEFVERLLKDRGVIPDSPVETTE
LPNESEGSDDTTRRNN*
>TCRU_10516 hypothetical protein, conserved
MERRRCGTMPARSSRRWWIGWGCFHPPSRLSEATHRSLTADRAASHSFWKHLGRCVYTRR
VHKDDTTDIAAIDVFSWMGGHEVWRAGYAGVGRHHDLHPEGLRQGPAKIHELIAGFPIHL

QCASARHQTVDGHLNLRVHLVQTITVCASEVDEDSGDDVIPYTRGPSVNVQCKEMQYLIL
CTGAIFEGEGAGRQRHRVREMWSPKIALRISGVDPPSLPRESTFGKRGCWHAPSIN*
>TCRU_10517 hypothetical protein, conserved
MGYKASPEILQIITSAIAVVTTVVHRLWAAPPLVRIDVWIDNIRITGLKSGATLWEAQVL
RNADSCHASMGEERESGATQYAFLGVQFDHTHRAVSLSEKFVRSVCAMPAFNSLTIAEME
VMASRFLYAAAILGTRLCDYYFFIKAVRRRLSALNRGIVQETSPTNLPPSAVGLGERLRH
IIENNRKRIINPTEKASAAIITDASLHGWGAVFIPDSGDVGIAGGKWERNLFLSCRPRHA
RYA*
>TCRU_10518 BNR repeat-like domain/Concanavalin A-like lectin/
glucanases superfamily/Trans-sialidase of Trypanosoma hydrophobic C-
terminal, putative
MKLDDKNPKALEATEVRTEVLEECPTDGRNCASKTEDKDDSQGGTRVHVSRPTTVVRGND
IYMLAGVCMSKGLSDCQVGVAGVAQWGLLLVKGNVSGVDESIKRICWNDTISILCNAIGD
NDDTLTGHIGGGGSGAKMEDGTLVFATEAVKENKVNGTAEDGGNNNVSLLISSSDAASWT
LSKGMSDGGCGDPSVVGWKDKTLIMMTACADGRRRVYEIGDKGRPWAEALGTLSRVWGNN
RKPHEKGVGSGFITATVENRDVMLVTLPVYSEKLEKGGAQKGELHLWLTDNTHIVDIGPV
SGEGDDAAASSLLYRSDGSSEANNNEELIALYEKKKGAEGKPSPGVVSVLLTAQLQRVKE
VVTWNKVDQSVSQLCPPSAEKDRPTENDCSGVKTTDGLVGLLSGNFSGNTWMDEYLGVNA
TVSNNEGAAKATLHACGVAFKGAWVEWPVGRQGENQLYHFANHNFTLVATVSIDKVPTRE
GPIPLMGVKMNDAENPVLLGLSYNKETKWKLLCGSGSPEDQSRNWEKDTTHQVAIVLQNG
KQGSIYVNGKLVCGDAQCELKNTDINVVSHFCVGGDGDKTGSNEGVSVTVTNVLLCNRPL
DGNGINVLNANKVSIPKSVAARTSSAVVSRPKCSADHLAAGATGGVAARGSGAHGGGGTV
FGNEVLPSLVLLLGLWGFAAL*
>TCRU_10519 Leishmanolysin, putative
MLTWCCAWQSAVGGGALDDCRGGSEEPRDCDDIDGMELQDGDGDGRTLESHWSQRHARDE
WMAPIGNAGCRTELTLAAPADLGCMRVKWEMAEPMRW*
>TCRU_10520 hypothetical protein, conserved
MMMTGRVLLVCALCVLWCGVCGGGRAETIPDSTDTTPEKKPQNEEEPVGGDGKDVKNGEK
QVTQVPTSPAPISPAAPKEASPTVSESQKSPANTPQAPPPGGEALGTASKTNSNNNENTE
QKKKEKEKGAEEEEEEEEEVEETGKEEAVASTTEGTSAGGQEQRSLSSGAEGASNITNPN
STPRTGDDDPAADGAEKRKEEKQNENKDANPKETPVTATAMKTTTATTGDSDGSTAVSHT
TSPLLLLLLVVACAAGAAAVAA*
>TCRU_10521 BNR repeat-like domain containing protein, putative
MSRHLFCSAVLLLVFAMLRCSTGAEQVGMKEPADPQFKWEGITGDEKLDSLGAPSLLKVG
SDVFAVAEAKWKKDDASFTGIASQLLTTKTTDTPEEVLKNANDGTQLLEEGTPKDPNKRV
DVSRPTTAVKGSDIYMLAGVCMSKGLSNCQVGVADANQLGLLLVKGSVNEVANSKKIVWK
DTESSPQRLFDAQLDSWTKLIGSGGSGVKMEDETLVFPVEGTKKEADGTEVNVKTISLII
HSKDNKNWTLSKGMSDGGCSDPSVVGWKDKKLIMMTACADGRRRVYEIGDKGRPWTEALG
TLSRVWGSNRKPHEKGVGSGFITATIENRDVMLVALPVYSEKLEKGGAQKGELHLWLTDN
THIVDIGPVSGEGTMLPPVPCCTKVVKVVKLIIMKS*
>TCRU_10522 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MDEYLGVNATIAENDAAAATGSSDGVKFTGRGAGAQWPVGEQGENQLYHFANHKFTLVAT
VSIDNVPEEGDTPIPLMGVKMNDSDKTVLLGLSYNNKKKWLLLCDGGENKELSITWQPGK
KHQLAIVLQNGKQGSAYVDGKRVGGDEQCKLENTESKVISHFYIGGDGGSAEIQEGVFVT
VTNVLLYNRPLSSTEIGALNPNKASTPPAVPDNAQGTPSQSTPAGTPLTEKGQSMGTSGA
DSGGASASAVSTVSIPSAENDSVKKVASGTSSDGTQTVGGGSTADGEPKMEKREGGTDAQ
EKEVQPQVREVNTTAPNSSLGNVSQVNNSDAGTMRGGRLLPSLLLLPLGLWGFAAL*
>TCRU_10523 hypothetical protein, conserved
MLEEAVLDGKAVQLWELPARLHANESLLREFFARHFDRTPAAHIKKVVFNKNSGGNAEGR
SGTSPRVGGEATVEFFESGAVHLVLSRIIQHELVERDESHHMELRRGFIYLGQDRMLVEG
VVHLVQSPPVGSKSAHGSNAPAVPLNDAMPPSAKGAAAVAAAAATAATTTHTAAGTNGDE
KGNSNIMRGGNRGMICGQEEEEEEEEEDEDEESEMDDDDIDPDGSERAEGERRLMSRGSE
ANQQTRLAGRTDAVVLCMTFVCLFDRHQHEGGAGCRQHSGDANGFGITPHVVFQLLRGIC

LARKIVMFNRRDPRESGGGMKQRMARALVEVGGEEDAKKVVDALHGVALELAYSGPNEDE
VEYRCRIYARYNEDGRTYRQLTVPLNTKTALSVTPQNIAMMGPLLQRQRYDREMPGNSDT
AREAPLSEPGAMQNRQQNQQPNYNREQDGIAVRNKENNGGGQGRRRRRRERSGGEGMQQR
SNDTENVTKRCRLSTERQDFHPHGNNGEERKGERQCAANTLEDATRPAGTTEKSNFDYNK
QQWQHWQQQKQLNLEINKETQRYDNPQKPPYANVGVAATQQPDVKKPLPPGWRTIYSTEY
ERYYYVHRDPVTGVEVSSWELTRIP*
>TCRU_10524 SKP1-like protein
MPDQLLVLIGSDGKQATVSRSVATQASLVLRDLLDGREPTTRLEALVSGTGDRGDKTSES
QMAGTQSSTASASIPSAGAACGNNGGGGGSGATPAIELPFPYFTGDLLRRICAHMTYRYN
YQPPNRSDEGASAGNGKGGNGGGGGSAWSHGRNVMREIPRPMVLPLCEYLDPYDRRFIED
WDEATTVLMVKAATLLNYEELLCLASAKLAVYLSEKSVEGIRAFLGVESDFTQEEEAELK
KELERVLGER*
>TCRU_10525 calcium-transporting ATPase, putative
MQGRSAVVHVHSGDTGKGATSGIINALSGIIGHKRLEQFASEVSGHQGLLNLLDVRCEDP
TAWSGTRGIRGGVLAASVHERRERFGANRLMRHQKKTFMTFVRESVEDDRTLQLLIGSAV
LSVVLGMTTSDYREGTIDRSTGLVEGAAIFLSVFIVVTLSALNNYKKQEQFSHVIEREDQ
SRQLVLVWRYESASGGGLMLRPMEVHVEDVVVGDVVQVSAGMELTFDAILFDNRYVVCDE
CSVTGESEEIIKDLQRDPFLISGSSILDGSSEAVAVVCAVGEHSFAGEIAMAIHGTEKKN
TPLQDQLEALAGRIGKYGLLAAILTFAALFLKEAYRILVHASPFSPMKFFGNLTTAIAIV
VVAVPEGLPLSVAISLAYSMRRMLQDGNLVRHLAACETMGGATVLCTDKTGTITSPDMKL
VRVFFEGRSYLRKGNAPNGTVSRNEAFVKLPSTHSALRLMECVVASALDPELGRARSRTG
EALMQLGSNLCVVADDGRVTPFYYDFEPLLAIMRDNSSFVRFPFSSLQKKCTTVLRLPNG
VSRVYVSGAPEVLLEECRKVVVENGRLEPLDKTRRVYYEGILREYAQAGLRTVCCAYGDV
DSFEGAGKAYGMPPAPPNVPLNFLVLLALEEAIRPEVPGSLEMCFRAGLRVILITGDATL
TAVNIASRCGLLSLVRPHYRNACSGSFSSLQDLDALIVEGYVMDGAEFRALKDEELIEKC
IQKLCVLARATPLDKKRVLRLLKCHDPLAVVAVTGDGTNDAPALKTSDVGFAMNTGSDVA
KRASDIVLLDNNFAGMVKATMWGRNVKDNIRKFLQFQLTVNCVACLVAFTGVLINEKNMS
PLKPVQLLWLNLIMDTLAALALATELPCESALLSRPPEPRHASVILPSMWFQMATQGSFQ
FLSQIYMLSYGYRHFKTQNASEMVRNDSSTMEYFGPKHLSIVFNVFVLMQVMNFFNARLL
NRDESFFGRWGDSSALLLIVTLIVVLQVFIVQYGGRLMSTVPLTASDWLFCVVYASGSLL
VSAIARWWWWNVLHSDGGLAAHWTRRCFGFLHSPISEKRM*
>TCRU_10526 Nup53/35/40-type RNA recognition motif containing
protein, putative
MWKQDIGQWVERKGRRGWAKQPQEPQQQQQQPQQPSVPLSPAMRAGFIPEGFEDRHEKVT
FVPESAENGRHLDDKNNEAFSHAGERWVAVYGVLPGSIMDVREFLDVMFGRTVEHYYPLA
YATSGSDLTPILAGGQNWFYVKFEDPVSAARAVYQSPLAISLGDGHRATTIATDAAASVT
TTATALKKSRGGVGSATKEEVVGVAWCTDARFLRKECEAERRRGETKTFRGVSGDNNHQG
PQRKTDNVQNALGVTPRGAERLQRTQPPLSHSEGGGVRLPSRGLGSLLYDVLCSPWNGRW
TATPSREHASSRMCGGSMSSVSPSSSSPPRPEVFEGEHGGVDGRSSSKRRSAPNEGDIKS
EDEWRAPAPTRDISPPLFLYSRGGRHHYYDPDRQIHSALPVRPLCGNESVLSVFRADTAE
RHILRRVVVFLGRLPYRISRLFDFPSLRLENSEEVSAAADDSQWLSLFGVFGVDWRYQQR
RQQLLRNRHYNAAARFLSANIGYGETPVIASWTPYRWYESTTVFSLFCCLFLFLAVFFSG
LWNDGVSIIDVESTGRWGNDTTSPSATGVQVTSYDSRKHEAPRLTAGQLQGIMFADGIYG
SDRYTARTL*
>TCRU_10527 hypothetical protein, conserved
MFVEKVGRGVKNCHLIVLCSDSPIFDLRTLRTIISHAVALASPLPPPLHSDGASVTLLPS
TAAEDYDAESCLSNAVFSAIQGSTRRHSFSSTCNGTITPLNTATGGKGGKTTKGSKKSAA
VAASTSRVATPTEGKSIGTNVTGRPRAEWYSVVESRQWGVPVVFIHQLPELDRSEGEGGA
LTLAGQGAGTSDFCTLLHRALQIIAEDMNAAVSLHEDAPAGLLSLDDTNLSEMQHEALSG
EQPHVHAKEIPVVMALQDPRVLPGLLNCRTALTHPIDTRLIVNFVDGRLNELLGTSNHGS
SSTRSRTSAAGRRQNPRDISSSTLQKNSKDADGTCAPSDSNNTLDAWIERQQREGMITVT
TSPTGAPNACGAICLREIFEEGGEDKRVWVQHCVQKVLPAMHHVIRDITRYGEWVSSKTV
YSIPITLTTPRPLMQPQTKEEGFPTMSESAVESSAMLRLRKSQTTAPPSSFSPTTSTRTG
GVDEDTFQFPPLSGDFSLSFSATKRLLDGEEEKWSYYVRERKVRGQWTCISAARALATQV

TVSLARQQRPRVVCPARDEENCPLLDVMNERNETCAADKMKENAVASLLLQLRQYASRRT
VLSTLDTDISIDMAAGKGREPSVVAETPGGSQLLENSTAGEKSQSQFNAMATLPMDHTMD
RPTHPPSPEEIRWVTRQFVKKGIGAFLFPPEESLRDDPPSMLSPDQLKSAIKMQELLEET
LNGHTLNDGEDAMDSQLLRLIEEDFKRAEKEVSCEWSHVWDNIAFPVGLMNFDEKLRRSL
ERSLTTRERTHILQQVYLLQLAMQSCMTGTVAPTNSVVLPNHGNCNLLTHSSIPKDEAVG
FKLRSVEECMTMAVAIRRLYEFQSRFGFHICRLIRCFIPDTLETLGGNVTAMYSRHAENV
HPTNRVRAMMLGGVPIPRKRQLRQVWCYYVSGIPSVDVLNELHESQRVTTSSYPETSSAA
PVGITTRNTTSTSFGGVIGDLLRQKLLQNLQESTQLLSLPAENKVKVKGVCCSEGELHTA
LEGRHILYPCENSIVEVVTTDRSRICRYVKSSELTCTLQYCIPPSPQLNTNTGGADPATA
FPSSLPSTLRKRPRDASAHFTTTFDDGVVFTCTPQWTTRAEHEGPGGAGEGENIANASSA
SLKSGVSRRSKAMSKAGRRSVNVSVVLAGGGQPSGRRGPLLGRQRRRSREDGEAFAAASE
RSARTDHLPRIFPVAQDGSVCLWTAGPENIPGNEAANGSVSATPKAEFGTIPNLAITVAA
NGVTVHCEEQEGILWFTQHESSNSLVPELLRCMHVYDANATWHETMEVEVRRAVLEELGA
VCRYFHSGVTQMIYPDGAVVTRYPMPTSNLGGAQDFCETLVTATGACYVRQFRGGFFDPF
LSAKRNNLKMHVAYDRGNHCRVVSRADGVIIAFYYFHRNSHESRKSQGGGGRNMNRENGT
KEHHSEEEVDAYDNYDSDACVWGNFKHPAFDTNVIARVTLHADSTCITTFSSRATQETWE
NPPRPLKTLLEHVSLVGRACSGTVQYCVEAPSLPRVFVCVPMYSDNWSFSEEQQGVSIPG
TFDADSSLGAPNNSFLSKCSSARAADVHPSSLLASPVPLPASGVKERFSPVSPRCKPYDS
FYIVFGDGSVLRRRVLYRGVRGTVTSFLETLFARSTSTSIRVIHESGLAIVEPFEALRHN
MEAVASLAIGEGLAMFDIALGGLRLVDHQHHLTEVHGLYSPGPVSAGIKSTTLEFLLRQL
VLPTYTPHTVTKARQEEMRQDEKVADAESRANRAKGICPPLATRLRELAEGFVIEHNLLR
TDILNTATRQWEGGNLETINKKSMQDVTSGASWGKLTTQVGKCGSAALKALESPAVPATI
TRTVGVLPILFSEFENDVVVQYIHQHDVENYMHAKESEPIPVFLSHSTAAGEPGVQQLTF
FRAEANSGTADAPIAREPTSRFFLMSRSFSGQLCSSSGLPIGQGGAVGTGSLLSEAVQRQ
EKLSFFLGRRLVFPTTQWLPPAMQPPRRFLKPLFDPEVNDKRAGITVLAGESVGNNGGID
GSPSSYEKLRILFKFSDVAPKTQRAVLASEILRHEQLSSMVTHQKAINALAPKIPYEANN
EQRRLREKYLAAAT*

>TCRU_10528 ribosomal protein L18, putative

MVKPHLRHYCVVGRETPSEKNPAPTVYKFEVFAPNFVVAKSRFWRMMREKNKVKSTHGDV
LSCKVVKDRKLVARNYSVDIAYYSQRCGYTHMVKEFRDVSKAGAVSQAYHDLASRHRARY
HNIEVLGVKSIPNHQVKRLSISEYHASNLSFPLLHRRVKAPRKDRVVFVKKNTKRAVVA*

>TCRU_10529 SNF-7-like protein, putative

MNRLFGKKNKTPKPTLEDASVRLNTRSEAVDARVNKIDAELMKLKDAILKTSGTTQMRYK
QRAMQLLQQKRLYQNQQDMMMQQQFNMDQLQFTTESVKDTKVQLDALKEATKGLKREFKR
VDLSKIDNMQEELRDLYEDTQEVQEILGRAYDVPEDIDEDEMMGELDALAFDMEKEPDPS
YLADALATPGTKLPEIPGKEKPQNENEETVDPYSLETQLGL*

>TCRU_10530 WD domain, G-beta repeat, putative

MRQRHERARDLRSFGFPAATMGWSEEDVNALSLSSSGIFRGPVSSVYDRLQAREALEQQK
QAARASSAESTEQNWEDTGVWTKAVSERLSNPSVSLIILERMQLVFISYEWCRKRKRRSA
SCLSDANLREMDMMNDLDAMIDSRERELSMRGVLKGSGEYLPASDNAASMSTLMTAGIPF
SVFERFIVEPYFDALFPPIRTGRRTADSFMDTLGTCGCSSTETRKISFNFTGRSQRKKKT
SYQRKRVSHVEAAENLFSLMDTNGDGLLSWDEFSGYILQCGQRDLMAGGYDSGDGVNEGK
PGGGKDATKTVRNTTNILNRYMNFTPTPLNVNPWQQQCPLVRHLYHSEPISRLLFANRGR
RYITAAWDGLVKVWRPNPRLADAYGKPSIVHERTIFTAGAPIVDMVLAPASLGDAEILAV
VGMDGTVTLLSVVTGEVLKTFIGRCSLPPTAGLGWQITPSKRRELEVAHVKNVVDPSLLE
EDIREDVEGSAVVLRPVFKVRAYRREAIEIFFTEVSRYFIGLDVVAPTYEHLEKRRAVKT
DVLLQFGDGPEKPVEEAQKQRFPAMPFVENEVEWAKEATNSTGWGTIDEDAQFLKEDNLD
DKNLVEDKEALMNEYPAPQKKKPNRKPIRDIRTPATNFSSSFFHEYSTKHIRACNKCWFA
RSVAFARYERTNSASVLPPGVFLLLGFETGFLQFYQLRPQLFTISNLSLTRLEVPTTHKP
VLILKLHRKAITSILTSEAHDLLVTASDDGTVVVRHMSRLQVPYVTLGDGVPAPDRPPPV
HPNGHTKRITCICWHKTRNLIVTGGADRIIIFWTPSSSRQLYRIDLRIFSTSSGSSGTPI
DASFFEPLPHSPLLLVLDTRRVLYFIDTVSYQCLHILRDDGLSSLKAGDMLRARYDLADH
RLILGGRHVRSWDIRQRDEYPEGYCGHRRPVIGLAYQQAWSLWVSADDSVVIIWDTKVVD
LRLGQRSSMEQVREEGGESNSASHSTLQLARKGYRWSAQIDLVRSWSVDGGICCFAVDQS

ESSHVFVALLHERHILEYNSFNGSVLRSFDFPAEMGDISSLACGVTTGGRAFLRPVSFLC
GTFEREQSPNGTTALYALASGSDVLSAVESTSGVHRSILTTGVGVSCAIIVAALGLVVVG
HRGGISVTPVAEATTCPIACLRLTDTPMRRKPDRKKGENVAASDQPRAPTQHLRTTTKTT
VTPSTSTTTNIHRGQRRPPTYPNMQSEEKGHCRPSPPLDLVALLTGPLLQDPVTLTREFM
QQRERYLFYNDRPKTSFTGTSLGSRTESNATSTENEEEERNSRDAGLPPLLLFSDEFIAA
SSVFTGNFGVLLREQLTALGYVGQIVPIRETGYAVSGGDDGVVQFWNLRTLSEVMRYRVT
YTLEAVTAMEVSDDGFHLAVGDASGYILLIDMHLIAWDSAVPLEMVSGIERDVCVLRRWR
GHRQSATSVRFVRQTEGMIHLSTVHSHTAKKNAPLRRPPRQGLESDVAAADDNNKIEIKT
DSNQSSKHEAIFLCTSGEDSYIYTWCWEARPSMGGSVHCIGCFGGAVEAPLKPPVDKLTD
AAWQVLELVRKVYIEERLLSPGGALSGTKMQVEIHTAVLELMEDMRVVKSGALLPRLGAV
PRERQSQSFPSHLRTRNYSRVPHSDSVQFAAERCPPTYVLAFEEGLYYDRGIVELLERMV
TEIRAVQKRQQSVTNVASCRVSLVEPRRSRKSLQTPPNMFLDKNTASDETRSALTFLSLP
DKTTGVNATVTATSVGNAANYSMRRSTDTRGLSLTGPLLFVSQTSPQESYPRSDFGKNGS
VGGGGGGSNTDGSRAARSGMGGFSFPFSVTSTVAQFSMSPTITSPEPLVVRSVPSLGTPQ
QNSPLFQMNEGDWSPLPPVTVGFKKPSPLPRPRFTGTKGAENGGGRSTTLNSLPLTADIV
GITKTKGDDAKRRYRGVKVLLREKARRRSHNLLFVDNVKKRLSLQEADDVTSGNTEDRRA
ARRERKRRSTIWEAARIMNTLMAWKAPRESNRSSIMSGVGPEGDLAECAPFTDPVKAPNF
KFPMFIPLTLGTSHAMTSRSSLQLDSSMSVSALLKTEMLAMNATLQAALHEKQVLMAQER
AAAAGNTTPPQTHFGTR*
>TCRU_10531 hypothetical protein, conserved
MSTSTDSKCQNPTVPLVASLAQVVCDKTSGQSHWCNKESTSEGVEQAKAHQKPMRAPRVA
LPREACHPFFYNYEVSDSLLQWLKIFIVGLLLLPTRVLYALLLLALASLFAVLTSILGEG
SSGGEELQLKQEEEQRGCVQAPRRSRRRLSRAVMRWLTLSLGYWRIHRQKVFNYGRHADG
SYAEAPVIVANHCTLQDGFLLLGEHNVSLVAGPSEAGWMRVVAWGEHCIETHEVNSRLMF
WKQQKHGAARNDCHWPLLVFPEACCTNSRALIQFQTDVFAAGLPVQPLLVQHMYTHFDPS
WCCAMPPLTGMLLRTMCQVYNTVELTYLPVYDPSPEEQEDATLYAENVRRVMAHAMKVPA
TEHNTTDVRLILLAHRLKLPVEAINVEVGHPHFMRMSYERMEHMLCRFAAALRSRKVNSI
GPKIYLQWRYRFCVPEGFMTSSELGNFLMPFGDYPLLLDRLLNHLSRHAAVRGIFIAFRD
FLSAMYTEPFPLRKESPGTLQTGREVYMDEVEEEVAVTFVLRRTFVLLLLAADTLFTQKK
EMSMDTNRNCEPSPSSLVLSSSSPTCVDGVEKGRTSTFIYGHEVRHPTRRPKNDGLYSIL
TATAEDTMDSVLCDRHLDRDMFDVLCDILFIPHRTTMWRGAPAKSAAQLAEEDALFAYIR
GGANPGVVKTTDMSFTGDDNTKSYITLHAFLRFGRMHRATAEYFHACCEHFLLGDDLA*
>TCRU_10532 phosphatidylinositol-4-phosphate 5-kinase, putative
MDTMDSAALQEVVGAFKEEVKRNRLQEKRLQRENRTLLRCLVRLQQQKQVGREPCNTQDV
PPLLVHDGMLHINGEEEECSQEGDDISGSSPSWPSSTTSLGEDRHHPQQQSQSQSPYQRC
GADLSVSTSSPRQETALHTQPNGGAEAGVLGDISPTLRDDGNFCELSKEALQVRVRSLEK
QLLRERLRRKAQAAEFTAELEILRFALDDAEKRAARPQPWPMDNAAEFGPDPPLLLRPHD
GTSDSNLEYHETPSVELATHSRTSTAVSMENAEQATGTEGLEVPRNVALCDMGGCVEDAA
GKPRNGLLLSGVPACRLSRTDSKNTSVDMYRDCMNSPNDDGAMAAMSKLEPLRDFSTESD
RPDTQASEEFLSRAVLRMEGRRQRLRNAVMLRNVLEGNDDGNGKKRDPALDPPKGQMDAH
TTAETSPNRVTMPTSSSLRKILLMRELRHLSHRRPTDLSASSFDDAGAGVSRPKSSTPAV
ANTISNVNPNQLGVGVDPKGPHNRTWYAHQVLRVAFAKVILGSYPPYSSSSSAAAVTAAP
VISTRNSFGRISDGCEADTLQERQEHEPQGSLSEAHYLSSDTSSYSVTEEERGFNMEERS
FPKADDTLHSQQSPLTSKGLYRNISSAAVRRAIDEMISLRFRCCQNQPLLETVATPFPSV
LPLFHEENTDSNLVSTFAMDPSSPSKYREDEICITLHSPVLFSQIRSFLGMEMNEFREAL
GENAMWRQSISPGKSGTSFIFFGNFVLKSLKESEFKFLKNRFLRSYVSFCELNPDTMLPR
FYALLSFSWLRLRSCKRYVLMQNVFFTRYYIHRIYDVKGSTVGRSTKTETAPRTSYGALL
LKDNDLPAQLIICGPLQRAHVLAQFRSDVNFLQSLNIVDYSCLIGVRSRVFSRKEGPSKT
IVLKERRGSSWQQTVTSEAIGVGTEQLHKMDNSCIHGCDGGLLSLPIYSAGDDTTAREDV
YYLGIIDVLQEYTPAKRFENFAKGLWNDRRHISVVPPKEFAERLYKVLENITV*
>TCRU_10533 protein kinase, putative
MLLTNHFTGSSLLEDEAVVLKDYVVGQRLGEGSYGSVYLATYIPSGVRFALKILQNDCFI
GRESKIIQEATVMQSLEHPHVVKMYKFLQSTSSFYFVLELAEKGELFDLVISENYFLEVN
ARRYFQQLISAIDYCHSKGVAHGDLKAENLLLGENNNLLVCDFGFSSRPQLVGFDDDDKS

DNSEILQPIGTLHYTSPEMALRQKTPATRDPFMQDLWSAGIILFFMLTGRLPFDGRDDEE
TLHLIQTGEFSFEEEEQKRLSESAKSILVRMLALEPTDRPTLQQIIEDEWFGENLDAALF
PHRHSLKQSSVFLDFSTQHHVTPEEEAVLEVAFRKIDIDGYGRITRDEVRDMLATLRGER
VGAEDVSELIQLFTGNADSAFITYKQFRDTWVKKDLAHRPFRRRNDFQLSKIIGTQMDMV
EREVVRQLRLAFDSVDDLHTGAISVDQWKRLFKRCEIKVTEEEIYSLMRFFDERDPSSGS
EITFDKFLMGVVKREMLVRHPMGPKLAAATNLAALLQSRKVSECVNHGFFVVGLQNAVVE
KLKNCRERLMFMYNDDIASDTENVYSFRYLGSAALLAGTTMESAGPMLASSSGPPSAALG
LCTSGDFALSSSLGRGFGQSSVSESLLNNHGISLNNGTLRGNELLKHTMSSSTQAAVSQT
HRALAFGGTGAVNQVNGVCDVDVILAPASLGYTLVRFRRIYGKTRDFHEAVAFISSLLEV
ERQQAMEDTLPRGESELL*
>TCRU_10534 MIF4G domain containing protein, putative
MDHQTMSNVPPRIGSAPLSHSQQSFPRVESRTAGAFRVCPLRPGGERPPPLQPSASPSTN
FFDRAAPQPTETPAASHPANCIYDIAEFVKCQHTKESPPKGILDFVTELWKEMPENKDSR
PEHILSREELFRGESMPSKVMKERKLHNEVLGILGRVGEGNLPKMKEELTNLPIRQSTDK
EIQDVIQVIFNKSIQPEDSIFVPYYVKLVVSLINDIGEGEPAGRFIRNAIIRQCQRTFEN
AEEAQAQLEREIANLPEEEAEQRRLIFAGKQKANINFLGLLFTHGLVREKVVLHVLEWLL
YGTERKRRFPADYELIHFMNLLLTCGKSFSKEGQEFVPKFRAVLEELMHMHPQRRMQFLL
LNTVETIDNNWEPPFGAKATSSSQEHETERRPVSQLPPRNKLVLAPPMNPIPSRDGFWEA
MDKFFVTSNAEEVITLLADIPDETRIVYCTSVIHRYMTTTRCVQQRARLGELFEELANKR
VLPVEDVRKALFIHLRDAVKEDLFTDVPRYFCNWAIVVKGGRDVFPPSLHTEFLNILVDN
GASRETLVNMVRDVHKIQSESPGSVETDARSRFRVLPALLRYTPPLLSGYSMDDTEDVFR
QLRECDSDVDYFYHLCEQEDSKGVFMCINSLGKAPHLAFSMISAIFTFVRFDVEALCREY
KESVKKLVNTKQLHLLLEEVYVTWQALDRTPENSFLLFVKALRSLNAARDQLDKFKTLLT
KNYGTAGKKDAAMLDKLK*
>TCRU_10535 hypothetical protein
MDEASALIAWGRQVLVNRRLQKQRERMQREMSHDIDAVQHLNHIGARHSAMSEASSACDR
DGVVSPHRHEKSMAKGNRVQQPLERHVGHDGVASKRIESHPRASIFRQDAVEASQLQRRV
EVAKQTLQELSELDVQNDKVFWQHMQELQSMLEQVELQKEPFRHATTLSFGKNAVGESTC
GSATTASTPRQKNGHEQKLSRKEQLEELWSLQKALLKSLQDEKFGGVAVASLATCASDVP
NWDDRLWCVLRQAIHDWKLRLVPSLHHFLNLVQELPMLQQEEDKKIGLRRPLPQSSEHAV
AMEASIIPLTSQVMLPAEKNYPALECLDKLPLQEAIGVVIDVLARAGMETEASLASIIKL
SDEKDVQLFNLLEEAEGQLKQQEDMLEQAQELIGTLQREKMSLEEDGAALHDAVEVLQEK
VVSLRAQHEKGQREETEVAAELQKHKVRLYELKQCLEREASLRNDAVKRTEEAKRSAEDA
ARQTTLLQDELQREKERQKSVEEEVLQLQRLLRVAKEEEEDATTRRQWQSDEVRVAQSAL
QKSKEAFLRQKEKHEAEQKTFVSFRCSEQEVLGQITTEEEACKECAKELETQRGIEAVMR
EELATLHAELLEAQKEKAAVQRSLQIMNEKLEAAKTALLRDEEMPGTIKGTFPPPAAATT
TLVSPSASLSSPQRNLVEVLHPKSSNSKNGKSPAPLHVQLNKSPDSKVASLRHKKMSQLS
KQENQHGTKMTPAQPHSNAAEVTITPKGLQRQQEEVRLEQSHLLVGNPQRKQEEKQQQQK
DNDGDHDEVVPSATARSRNPSLLSPGVGSGQFVPLVVSLPSRQSGPSRPANTSGQ*
>TCRU_family, putative Se.1
MAKVPHRDAHIFALGCTPHRRLQLVRARIAPRAMRSKDSMLDFAATEVLVFHPSMQNEFF
QLLSPLSPPTRESVLNVAESLIVAAFHAMNNGVPVIRHQNRGSICHGFARTFFEGFSGSA
TTSRISLRGADSCGNPVRIIVDWGCVTVTPLMHQRTCQCLLDDLMPLENKLYEQTRRNRL
GLGSKRQ*
>TCRU_10537 hypothetical protein, conserved
MWSRTVSPASTEQGLPGASVTVAGSIDPDHGTPPKDVDTAVPERNLLTEEKWIRPGYPDR
PREASLGGRDRSSETDGEQARPRLPVVTHCCCLSLSAASSACLCCRRGNTLSICGVVGVS
LQGDCASFCLACNQHWKPNRKTSISMVPFLHMHVLCVLRLTLCLKLVLLPMSTAPLVLIA
DVGATVWSYGIACVLVGFSETHIHTERCESNVRTQDTHTHIQAHCLCDFYLTWYAGRVGA
VKADGSWQPREPSNGVCGCVRDHMFHQMLDAVHGLSKVFYCDAHAAAVLNCSMRLHDLME
HGVTLLGDLMTPRQPIISSPAPYFLPWRIRL*
>TCRU_10538 hypothetical protein, conserved
MAMMMTGRVLLVCALCVLWCGAGGGYAEDVDVVFGHPGTRGERGGGAVGQSPPAGGSNGG
SGGSKADSPHGSESEPLDSTSDEESSSLDIDQELDPNPPEEHVLQKEVDPIGKQDHSESG

PQDALPPDANGTVTLDSDAQLQLSDTKKKQTEVLTNVGGGEIADGGKDSTGRSNGLSPNK
SDPPALLEPRIKEVSQPTEPSPPPANLSPAPQELPTAVSPAERPPAIAVSAGETNPTAST
GSRNATETTTTTSPSHSKTAPEAAETPSGNGEPNQKRQDTDTPDSMKDGPTSLPAETVVS
SVSKSGIGGAHNKEDKVDDGAQRPNTKEPQDGPEDGNTNDAPTSTEAAPQKALTATITQT
NVTATKGDSDGGTAVSHTTSPLLLLLVVACAAAVVAA*
>TCRU_10539 hypothetical protein, conserved
MLQEAVRPIEHVRIGKHVFPLCSHPILRKKLEDDAILEREIERRLQDPQLQLAMSDVVER
LLKEGVKGSISEEMTENYLDEALGRIDEHFGDIRTVGTSSASLPAKLTTSDYRRNFLPPV
RPLPPTVSRVLSLKSRIGTAPAGHGLSIQQRALHAAREHKHHVTPQRDVNKEVDDETGSF
ALVGLSRKHLFSSCFSGIEEEEEVDFSPTNSVPRKFSPKSTHRRGDDSERRKSKTGSSLH
SRRGTSPEWRNALRLLFYSMLSLRLEESGGVRLEEMDLRGRSQGLLRLQGSVLSMLNQEA
FGALDVTLDGNSSAIHRRQPAVTSILQWSHAQRAERPIEVGKTALRQKVLNTLARPHQIS
SMSKKVVRATGTSLNSAWEKMEPSVTLGIATRGTQLELPSETGRSRIMASIMERIKVGHT
EMKSNDNVQT*
>TCRU_10540 replication factor C, subunit 1, putative
MVAVTNAANVGEPWAEKYKPKTIAQMCYPSSANKLKAWIETFDSGSSRMRAALLSGPPGV
GKTTSVYVVARELGRIVVEYNASHFRSGKSLREHVTVSINNNTFNMNASSYAKSILLMDE
VDGCDIGGVKEIIEMTKTTKIPIVCTCNDRWNQKLRPLLNYVEDFRVSRPPCNIVANYLC
DKVLAREGISLSKQLLQDIIQRSGSDIRSMLNNLQMWCLNRTSLEQKALAACAVQSAKDE
DVGLFDAAEMFLLQGTSRGKPRSIEELQTAFYNSDLVDLFVQENYIHFNPEDRDWMEAVA
DAADSISLADALQRIMYYEQNWSVSRAHVQLSSIAPCAITRGHYESFLSGQQVFFDRQRP
VKFPTWLGQNSSANKNKRIIRCLTLQALSPSTGGISGNQEDVLLDYIPLGWEAALTQPLV
ERGKAAVDDVIRFMDQYHIMRDDWEFIQTVPHFKTMRTSNDNVATGSIPAAVKSAFTREF
NKTHRTESFVKGALQHMGGVETQSEWAEEDTEKENGGNELLKTNAGAKKTAAAKKTAKKE
PASKPKAKKPSLKTKKTAKKRGRKATPSDSEEEFTGDSSDDD*
>TCRU_10541 hypothetical protein, conserved
MQRVRGIPSPANPTCPSEEEEDEELVRQLVEAADVDEVIERMEMKHYRRISPILQGLRPF
RRASASSLKRRPSSCETRLGAPLRSPAEDAAGPRGSHEEPMKNMSSLPHPVASTSPTPSD
QSTREQRRQLLALGIKAPARSPHASDGDASSAPHENDHTEKPSVNRRHRARSHRKKILRP
PIESPSVVNSPLTPLSPLSPSQGRRLSNASQRRRRHTDIHRASSFGGSPQHFGDRQWDLQ
RSYRELSGLRPPSVDKPSRRSQIARHEYYDPSHDPSFGVNAYRGAPTQPNTDTSFIWRRS
SSPPVILPPFASPVEDDAGTQYTGRASHYNRGDYWGHMRNGFDGTPTATTEEAHTPDDVE
YDEEEDVEFVSGPPRIIEREQHLRSRVTEPPLNKFDGRVVPKGSRRKSVGKVSPARENSN
NNNNRNIDYDHGNDGFRDPSYNTHTVEPRLPHYVNAKGAGSSNKFISPSDREVTQEGHSL
SSLAAPSRDYAMMDLKEEVDFSHSRRQSWSHSTGMVERGLSTQLLGTSENTLRPDHKLVR
QNGQRMSPALSPTRQDTPPPVSQNPRDEKTRSERNVGSNRKVDEGAQKHRRGQKHADEDH
SPHSVNRTERKEKNMVSPFLSSGSDSYSYTYSSQSSSSSAASVVNSTPGPPVEAASKNMP
KSSTVAVKPRLEVKVFPPHNPRVHPRPKSLGWKRRNPPLLLPHSVLQRQPAMAPPPPYGM
TMASTATVRPLLRNSFVEMRSDGTMGRGFISSTRTSNARFPSKQQRPQTTYSTSIPRFDR
NAQSVPGSTTPRASCVSSPSYPQQGSTGASVPMPKPLPTQMVPRGSCRSASEPAATARFP
IGAQPIVWRTSDGDSVAGKNRRVPPAVKTGLTLYGVLPQQRSMSVGDNPPPPCKIPLRAR
NSIGERRSLSANRVVDVPQRRPSQNALLAANRTRRSSVAISFISPSDGEVCPAQTVFIQL
PYKAK*
>TCRU_10542 hypothetical protein, conserved
MAERFCLHLAPLDVSLMTDENDGAVIPLVYVVVHMQERGEVMYEEAEMRAEGRDAKSNAL
LTRLYHGAASIVSEIEEGRVLLGNSPMASSSRQSSAHVHLQNGGRLFFRHPVEGGDYMLT
VTIPAGVWRWLGPITLQILLATAVRGYEIALSVAAVASVPTYYPLRDRLTESSDAVEDAV
RSRIRRVMEFVVFLNECEHRETASSAALLHGGQEVVVVTRRLCHDRPSLIRKNSRLSRTL
QQLLWSATSYSDYVSLSGAVSSGGMRDGYKRLVVTAAAVWYHGEPLFSSGSSDDYEAYLL
PAAIVAYADRCLASREATGVQQPITVKCISMHVDNPRIGSRTAGYVKQHGNAEENTAAIT
AAFVSLGGWIVTLRMEAALNAFTGAPMPHIVSGVTNLITRKLEIPQFEAFVRLPTVEKLM
GVSQTTASTTMTASNTSFACILRAVRHLGLFAHPCGDANHLTTAFRDVCLYRHRKTVTSA
VESNEWSLWPQHAQRAVQSLVELTALTFRRRRRKTCGGIDRSAPFSLLRGRDSVLVLLAA
PVYSPVPKVVFFLAEMEPQGIPAAEGLRAFATWVLSKAL*

>TCRU_10543 hypothetical protein, conserved
MSATVSPRSYWAALREQRTASRTPVTPSSPAEAAATPRPIPLSPTCRELGQHSHGESVVI
ENSSILGMFNDPSDAAAGELVHVSKASNGRGRSRSLVMDFIDECVLKGMPESLIVEHVMF
MVHAMQEQINLTEALHARFHHDRLRQYEVSELTNMLERQQVYYGQQQEYSNNNKKRQEIE
EAKWNLVQGKGRKGHATPHRFAPSFVGPLSTDANVRTKAVPAVSRAAVGSRAVGGRHRES
ASRLGTERHLRVAFTQTPTERSEQQVHGRMVSRATVAPAFQRFMRPTDASNRKERRKYST
ILGESLTHPLQLRSDQQQGFSWTARQEGKSHGLTIKKEVFARRGRQRLVGEVGNTGGSQL
TWSDGDDDDKKNALSLSRCRGAGGSPGPRIEAQQQEGEATPSDVLISPMSPPHSETLGDG
DEATASRVYDVNRWNEKKRKEVLTDSGRRGIEDSLLTVPPPSAATAAPPLSVHTPSFFPN
PQLLVYIEQSRRKVREAERVLANSPGHDSRRGVQ*
>TCRU_10544 Rab-GTPase-TBC domain containing protein, putative
MAVSSARESVTDLLSGREDVGTVSSSTMAQGSTTIKTGELGEDGGGDGVVSDRSNALARV
FEELLDAEVSMNPSKLREASRAGIPSLYRSTVYRYLLGITFVDHSREMSLERMQEKDFEQ
LLTAFGRIVASDGTGQRPSVKGRIMQPLASPRLYDSETIPLITRDESQFANGYRCSDRSF
SVGYAAWIKFRANLRYLPRFVGNPERRQRMECAWQALHVTSSGATPDEVESLFELALVFE
SVHGTARDIYFSTSSLYYLLTHHGNVLQNAQCLQRMCGTFLMLFRATNFDLYRHFVAESV
TAVEWLPGMLKTLLAGRLHEEDLLRLWDVYLADALEYLGFPLHPYVCLAILEEMTEVLLE
CEKSGIIERLRHLPRIEAGSIIQKAISLKESVFSKDLL*
>TCRU_10545 Protein of unknown function (DUF3682), putative
MAMMAGRVLLVCALCVLWCGGVFGRAMDDYCSEGGCMASEVLGACFSQMSGGCNKTAITV
PLRSTLPITAVEALAEGETPVAGLNDSGSSEDSVAVVPVSVGAAGAAASPSGPSGGSDGK
NEPSGPLSLDVDSSAGSSNGEAGSRGSTSSNAVGDPPRENPSPDVAAAAHNSPLPGGVAG
TTPGNKGEKEEEKEKKKELDEENKRNHGQENQSRPANQSEGEIGREGERLHKKTKDPKGE
KEQIQVVEHSIENQGTLHEPGKQPREIKRENDQSKHQNEELKAGQEKENPLQAIKQNSDA
EEEKEKKKRQDQRPQEVTAPLASSSGSEAKRKSQPPVPPEALHTKELTDDLREQLEEETP
LVPAQSKSHGTTDPQSSPASAIAGGAAVTHDADEENATGRNDDEPTETVFTEDHQQHEHP
EDIQKQSAKDKNAVSTNDTATTSYSDGSTAFSHTASPLLLLLVVVVACGAAAVVAA*
>TCRU_10546 Concanavalin A-like lectin/glucanases superfamily/Trans-
sialidase of Trypanosoma hydrophobic C-terminal, putative
MQRIYDVGPISAENENVAASTLLYAADEVPSLEEGESKEVEGRLYCSYEVAAAEDGKYNI
AFLDLTEKLEDVKKVLAAWKEKDAYIVKEYGCTVESNGKKRRECGVVGDLTKGLVGFLSS
TSTDSTWRDEYLGVNATTTKVTGGKVTSTEKGVKFRGAWAYWPVGKKGQNVPYHFANHKF
TLVATVSIDGEPKGDTPIPLLGVKLSETDSPLFFGLSYTHDKKWMVAFNGSFKAPSHDDD
VEWKPNTKYHAALHMDSDDGLMVYVDGETIYDSEDEVYGHEDDEDYESFPQKLKTLLRPH
GISHFYIGGDGKSESGNIDVTVSNVLLYNRALKDDELKALTKADAVGTPEANVPSLKGAP
QSTHASETLIQSDSETSVIKEVKQDATSSQQRQDAPDRPPEEKNKKAAASVTYSDSHAVA
DTKRREEQMEKAATDVDDLPPPLSPAPEAASGHKSPDAEDALGVEHPEQEEESLLPIVAG
STVDETSETDEAILQSRTSDDPAQQTTLPLVSEGVDDEPSSLSTSTSNQRGDREETEAHS
HAAVGTNSGPDSSNTTEVTTADVTTATIEPNSDPTTVQREDDVPDYVGAAPNHPSTEPGE
RDIQSESNAAPLLGNDLFDVENITDLFSVGVKGDSTVQGCVSRVLLLLLLLGLWGTVALC
*
>TCRU_10547 BNR repeat-like domain containing protein, putative
MPQPRVTEWEESLLMSVDFEDDQRVYESREMGTAWTEAIGKFSCVWVNARSGVSQKENLR
VDALITATIEEREVMLCTQGGHASRKKRSTALCLWVTDNNRTLSVGPVGMENAAD*
>TCRU_10548 hypothetical protein, conserved
MPAGLPLPNVNALKGPESKAGSLPPNTQEKSKFSDASGGAAGNKAKQSDVETDDPSSSFA
NTGDQTVEKTLLLPQTPAVLLPVPSAELSPEVPPVTPVQANPDGEGSLPTAPRASEASKR
EMQNKASSPNKTGSESPDRPSKDGMQKQKDKVTTQLNTTKKASAGGLAERTATSISANGN
GDVQNKEDEDYARQPIPNRVQDDAEAGNTNVAPTVSEAAPQTVETVTTRQRETNETGDSD
GITAVSHTTSPLFLLLVVACAAAAAVVAA*
>TCRU_10549 hypothetical protein, conserved
MAKGFLRVNWRACGGWLILQWRRPLPGTTERVAVSVLANGTTPLAAGLGSKACQRVRVPY
GRDSMFRVLSGCHGLRRMLSRRLVNMHSTMSVTKLPVHGPAGTHQCQETLPDPVLVEGR*
>TCRU_10550 hypothetical protein, conserved

MMLTESEKRHAIIDFCNTGRRAMAFRLYRGILAIERRVMLIGYLTERAALLMRVTEAQEM
IGRRLTENDWKTGLLDKMRQHRVGRRRSVAVSVESSGSNNNNGSSSSTEPVEASPAVFSE
EEKALMPGAVAAASTTTVGRSLSAPSSFWRRSLQQNRLRLSLSPSLPPRPYQRHSGNCPA
HVTVAEVIKPFQPEQKEVPHRQQRFGACHVTNRNASGTEKFMNCKSNTFSAAGVGAGGSH
*
>TCRU_10551 hypothetical protein
MPPLLAINICIVSSYFDAAAIPLSWSLCPTEGYGSMQWEKERSYRLIGLEEKALRRGYGH
PHCTVAQLSIRPSDLDALRNVVREIWLSMKELTERQDATISLAALDDGPFFATSKDGEEI
RLPSIRILRSETLCALHEKISCAVLPYHVLPTTLDVGKAAFHPSFPADNAATVEWMKNYL
SENCIDAYSPHITLGATTVKPMTSSFLFKPTTVPWRECRLVVSRMGNYCSCFEIYD*
>TCRU_10552 hypothetical protein, conserved
MDMSITVQLVFAPTGCQFPVEVKHSRTSPVFTSSSLASSSQWGVAHSSKIFVSDIVSCVH
SCRLTPLRNADTEGNVKIFVELFDYDTLRPLLTNEPVVEGQKLLLFVPTIVADSLAEHLL
HQWRLTAADNQIVHTEEEERWKNLRQAVLALNVPLKLHQDLMEKELKTSIQLLEITYSQL
NDAKENVPRVLESMKEVKLFYDPEVPLTSLAERSHLDAAVQMGESKLREAAKILDSAQAM
APAVMEAIKAEAQASNDVEKTSAWKMFFPSIKDGREESSVTALMYEVDRKVQVVRSIVEE
VAKITKRLKRCQHYASAVLGHVVEPHKKLCLLPEGMEAAREVVHRRIILRRAIRRVLVPL
EVEYHATERIIHKFAEKWSQWLPDSLYRGVSTPLPPLYPPDDFIAKDMDHLFLDIEDDET
EKLLAAIDAMSSSVPQESQVTEKRLQQMEAKLQRCKAVLESAQKEKAELEEALKRMGTSS
LSTTHPQS*
>TCRU_10553 YjgF/chorismate mutase-like, putative endoribonuclease/
Endoribonuclease L-PSP, putative
MSVVASGRVAANLQRLGIKLPAAAAPATNYVPYVCSGMQLHVSGQLPKNDVGGCMTGQLG
ASLTVTEGQAAARACALQVVSQMQAALGDLDRVKRVVKLNVFVNSSPSFTEQSYVANGAS
DLILSVFGEEAGRHARCAVGVAQLPFGAAVEVDALVELNN*
>TCRU_10554 hypothetical protein, conserved
MASCSVTPEQELQIIQTILALRSLGDTTSSERLRQKVRRCLQESTDDEAAVATADQLLRR
YKKIVKKLDGSYEMERELKKRRSEMEMRRASRFVDDEAESGDDDEDEDEDEDEDNEGEKP
*
>TCRU_10555 hypothetical protein, conserved
MACAEVVLLRDSCSAVRVFFEVQRYRKNRALRSSLADYVLRALTAEATFPMMHGTSDFPS
LSLFYVGEATCSGAPCYVALPTFGRFFIDYCLTWGHHAHYGQARRYAACCKMAILQTVGG
GWASLRRADKALRYAIMLYETAALIHDTATLRKCRLFVGWAHLWNGDLRQAVEIFEQQLV
EAQVEGDAVQERRCISAIHHARHNPSVVVACGARGQGSFFLSECWAELFE*
>TCRU_10556 cyclic nucleotide-binding domain containing protein,
putative
MFVPDQNQLHALYIFRCGELRVGKPNEEMLALLAEDDWAYLSRLKDEAHERGVPIDDLQM
IEEDTAEVRQKREAMVPLAMRRVLRLTPVIGSIDALVHVGARGALAIVDVARELPFLEVL
DFSNLTSLFLADPYQCEGVTGNDVIEAICRMAATHPSLRVIDLAGQPIGTIAAHHFLELL
RRNRRIQEVQFDRDAVDCRLVAYIEREMRHNAALPRVPPVLPRAPSDSIKRLPVHDRKTV
QEQQLLRRLLETETGLGDIMSLEGISEAVLYARTMSTTEVVTRSSGLRGDGVHLFLLKSG
ALRAKAGPRGFELRRGDYFGETYGDVLFSPGLLEEAVRGVVYCIPLSHCRFLCDAWAGRV
EAYYPLLRQSALLQALDVWMRLRMCCCATQRVFSRGDVVISPGDSFKGIFLVTAGMFGVL
GPTAKSPRAQEFTVGDVFGEEAFLARRQCSSVTIVTENFAETNSCLVVEGCAARVLRSHL
LPVLTTLASAYSQHEDLMPVRK*
>TCRU_10557 Leucine Rich repeat, putative
MWRELYTSACADSAVTPRGELLALEGGTVRLCGNTFGRFHQRVTDDEVVALSETCARLPL
VAELHLEYNEVSSRGATALADALQNGFRSLQYLDVSHNAIDAEGANALAAAATNHEALST
LLLRSNPIGGACGPFMERLLQSDDGGNSSLLATLDLENTEQDTKSLVHIARGLARNSTLT
TLNLGRPLMNNPDDVACVVRHLALALKENTTLQTLGMSHFNITDDDLRLLCSSLRSSAVV
CLSLKGNKLSQDSGETLSTLLTQRTDFISLDVTANRLRDVGAVSLASAVALHPGLRALHI
GSNTVGGRGISAIAKAVETNTSLTSLRLWGNDFSDESVAELYALRGKIDSLPEKDISFYV
VDGRPMLARE*
>TCRU_10558 Alpha/beta hydrolase family, putative

MPCTPTNTKLAPAASAWKSDAPVMQGGVESQSARWFRWRPTDAACLERSEALMLEGVRYH
QEFVAGLNTISNVEFRRGTVAGDGGRDVMLLIHGFAGGLACWAQNWEFFSAEYELYAIDL
PGFGRSERPCVKVSSLEGSMQFICGYMERWFCEMNFGRPVILLGHSFGGFVAAHYAMRHG
PSRVKLLALADPWGVNAADPRRIELAPVHHRLALKIFYAVNPLSLLRAAGPVGPKLFKSL
RPDFANRWRSFLASPQVFYEYTYHCNAQLPPLGEMLFKACCHADVAAKTPLVGVLPGGLS
KAIPLVVLYGSHTWMNAECGFTMVEKMAEDGYKAKADTVMNAGHQVFTDNVDAFNEKMSQ
MIRSMVREGTSHP*
>TCRU_10559 vacuolar ATP synthase 16 kDa proteolipid subunit, putative
MSETLSCAPEAFLFGMLGAAGSLAFANVGAAFGTAKAGVAVAHLGIVQPGRVMRGIVPVV
MAGILGIYGLIVSVIISNNMKTTGYMLFSGYMHLGAGLAAGIASLAAGYAIGIVGDICCY
AYAKTEKIFVPMILMLIFAEALGLYGLIIALLMNNRAAAVTTTCV*
>TCRU_10560 cyclophilin type peptidyl-prolyl cis-trans isomerase, putative
MISCGNEGDAWVVELHTNEGVISLEIYAREAPSVANSFLRLVESGQLCGAKFVRMVPGFL
VECAVDVTRKYGEFVEEVTGTRLHHTGAGVVSCPRLEEGGIAGTRFFVMLGPQPVLDNKC
IVFGRVCSGMQIIEKISRLHFASDNFRLYSPVEVRRGVVRRLPKDPRPSSSTAASVAGAL
HVRQRCELGTSLLEGLES*
>TCRU_10561 ABC transporter, putative
MYNADYFGSFHDLEGSWMDPGEFEMDCGYQDDALQENFCDQTPLPEEWRSFAPTEDPWEF
QQQRAEFMQEEEAGPSSEFRACEVPELSFLDQFLAVVERVFRQCLRTKLGLLLEVGIPIL
FFCITVFLWSLWGTEKFTETNFVNYSHMQSFIDADFYMFYVCSRTPGGVHGLPPCNPGVP
LDCKGDESTLPVKGLCVYASVGASLLLHAFLNSFNGRIAELPTLDAIVVFQWLARKSFKM
DSSPFGIYPKTRFSAITSSGMLYFVGDPTFLRGLTAEFEKSSKFFNYVNGGIYNTMKEAE
RQFENNPFNWGIVHVRRADRHALDAIIYLNATAVPDFDEIVSDAYPGGFQFDRAEMYVLS
GYLTLQKLISEYYINQLSPTLRLDTTAYIASQAFVEYRQATFLMNARDILPLIFVLAFLY
SVSTRTKAIVLEKEMRIREAMLIMGMKDVVIYAVWLVRSVSIDFFVCIFISILLKCTYMT
QSDPFIIFCVFFLFTLTTIPLSGLLSAFFSKARLASLLSPIIYFILTLPTMATSETNSAL
TIIFALLSPSAFVTILKHILADEFARGFSAKNLADSLYEPKTVVVLCVMLVDFFIYFILM
LYLDAVIPKDWGTNKHPFFFIIDPIRWYFSKGDVYEGGGPDGRAPDGVFEHDGEEEEGIV
VRICGLRKVYRRGGKRFTAVQNLYWNLREGEISVLLGRNGAGKSTTLNMMTGMVRPDGGD
CYVYGLSVRHQLSRVRREIGFCPQHNILWPELTCREHLEFFAKIKGLKGAELEKAVQRML
HETDMLEKIDFPAMRLSGGQKRKLSLGLAFVGQSRLVFLDEPTAGMDVGARRHIWELLRR
MSSFHTILLTTHYMDEADLLGHRIGIMKNGSLQCSGSSLFLKSRLGLGYSLTIAMVPDGD
FDSIHQIVEENIPNVLFLGYSGFHLSYCLPMSEASNFSELLYSIEGHANYGVCGYSISAA
TLEDVFLRVSQGLDEIRMHDEDYSFLWNCALTRSPALRQFCVLMMKRFQNAFRDRRMQCF
QLVCPFFCVLLAMLLGLVSFKKNQELNLSFDLYKEKVLLDTAQCEDFWGQKPLLSNVLVN
ETHFGNAVELGSYTSDTWFSHEMPRYASISCIDRDLYWKMGKINPIIMLHNTSAIHQTGV
TMAAFYQLLYKNISSGRGNISWSIGALRGGVDSLSSIEVILMGTILMIPFTFFPSNPVAW
VVKERECGALQLQKIAGLRLMIYWLSNFLFDMAAYLVSVIFVVIIFAVFRRDEYVGPDTV
GALFTLFFVYGLTSTIAGYLVSFFFSEHSTAQMVVMAAGFVLGFLLLMVVFIFSLLEKTK
DLSDHLRWPFRILPTYSIGECMINLSNFRQMKMRGLVNSAFDGNITGYPIVFLAVEFPIF
LLLLLFIEHPKRRRYWSRHFYSVQRSTNQEIPDQDTDVEEERNAVYMAKQMGIVNSVVTV
CGLHKKYSNGKVAVRNLTFGVLPGEIFGFLGTNGAGKTTTIAMLCQQLLPTSGSAAICGH
DILEESSEALKCIGYCPQFDACLELLTVEEQLQLYAGVRGIVRRQCDNIVSGLLQLCELV
EYRDTLAHELSGGNRRKLSVAIALVGGPRVLFLDEPSAGMDPIARRGLWNAIEAVSDNCS
VVLTTHHLEEVEVLAHRVAIMVDGTLRCIGGQTHLKNKFGSGYEMSIRIESAELYEPIVN
FVTEMFPNATLNEFKGQRFVYTLPRDASISDTFRILRDNKELLGITDYSVSQTSIEQVFL
RVIGEIEPDF*
>TCRU_10562 hypothetical protein, conserved
MTAMDTEGDVTQMELSALLVHIERCERLLRHPTLLSRLPDEGETIRSRHALYVSERSRRE
VGGDASSSRKENDAVEGSVRQVERQISQMTLSTEEASEKTATLPMECHTSLNTDGWTVRE
GGKAVESYEGVARAVGEKHRHSRIPVEMIVRQTFGGSLCEAEIQRMLRDVPPNFFLTHDE
TISMQRKLLSEERLEALTRLRNQRHAEL*

>TCRU_10563 Thioesterase-like superfamily/Acyl-CoA thioesterase, putative
MLLQDVIGEFLSLPPRALQLERVSEDIFCSVYLWTPTHSKATYGGQLVAHCVEAAYRAVD
DPHTDIISLQLKFLSAGRSDCGSPVVYSVKSLHNGRSFFSRLVLAMQQERHILSAIITFS
RQERGGLEHQLCLPGCPAQSELTGGSSSSLFYYMRSLTSSNEAREASRGESAVARVGYVN
FMNPHFIQSTVPWELCLRVEPEGWTLLRDATGISEKRLNIIVACWLSDFVVALSTLFPHG
FPNNDICQFASLDHTIYFHHPDRIRVGEWFLYEVFSPWAAQGRGIGQGRVYGQDGTLWMS
TVQQTLMRTGKGYKSRL*
>TCRU_10564 hypothetical protein
MHTALHANKILRQHMLYVSAPLVVEGIGGNAAATALQGGARGTAVNSEQHKFSRPILVDA
KNYSVQHASRHLEAVEKSGSVKDLEILREALIVCCSSTQRFPLPQVTLAELLRIFHEHMQ
YHLDLEGLLAGDYILNSFSLFFACDRQEAFQRYTMPLVELGILRPIDANYRNLGKFEAAR
FSYRPPCLSDLHLLPFRESLSRFICIFCHKSCIEGGNELIYVSHSRWLFGPQPSAPDAKD
SLSSPFSPFPEALRRGFLGPLMQFVTSFCIDDCKVHDAWGSDCCIVRLDGVKVALVLLSL
NNTSLTVLNPEENNLDRCDCPTTVLFGFPEGVPDAKIRLALQCMFDVVEMREGPRVDFGV
VFGQSPDEFRRWCRSIGNNFFYMTSDLFFNPQVSSCMSSLRPDWELISLPGTEKSRYERN
ERGFTSYEPHILNPLLRAAPLSSRAFALALDLRCCFERAISAKRTLGGCFAMVLLVGVRV
ILSDCHPYLTSLLRAEARLDNFALDPDLQLPSSPLADETFGGRDDTVNFSSLWSRLVCSN
FRGSTLRLAWRYLPAHVVRLTQNETEGMDTNGLFYRLASVSTGDVTLVMLIGSGRRFSVL
EGTEVDEVWGELEDVCLRELSEREHEMMILSSAVAECEPPQRFLDGDSREWDALCVSHDL
TTGALRLLGQRGGVLALDNIALEPLFSNGMLHAQSLLGHPFCPPQRYDDDAMATYFAFAE
LPVTRVVLGRTAFGGGRDRRSAGALYSCQRGGQEFFFTENKLSTFRSVEDNFFFFLASQM
CDGEVTI*
>TCRU_10565 hypothetical protein, conserved
MWSVIRALQGESPACEDNFAESRYERNQRCILMHEMKRYPRSLDPEIFTRPFGELEYEKV
RAWMLDDRVGRRRQAVDHLLELYVLQRENVIRSLRYGFLDVLLSTLHNDESEEMRCKSAE
ALAFLLRETKGLDMLLAMDDEGGTVGKLLKALDDPSKEVVILVLRVTIACRAAYNAYEAT
VRLVKYGFIERCIALLRHEEVRVSATACSALATIFSVKEAFIRFIRSGGMAEVTEALKRN
GVFVASEAAEVVTQAAVYRLGKKAAVNHCTLVALRPYMTHDNLRVRTAVTGAVAQLTIYE
PGKQQAVDENIAPILLELLMHEEERDVLVNVLKTFVNVAEHPAGRRQLLGAKGRLQFIAR
EADDYQPLNLSVAEALSQLERKC*
>TCRU_10566 Flagellar-associated PapD-like, putative
MANEKKSPAPIDVDLADLQAEALNRFNPLVFTFSVQTGNTVCLPKVVEAMTRDPAFAKGF
YVLEKRRSTSISQATRGKQGDRRSKQADNTKSTATQFYEDYVRIAVDREIKRREEERARG
EEYAALLALYLEEGLTEAEAAEAARKEMEEAAIEGTSSEEGDVRERLYVFLSTYPTNMEE
VTELHNCGLSLHAVVSLSSRVALSGSVAAEKPPQASDSSKVKGKGREKRETRRSELKDRS
GQNDDKNRLTLATELQQYLEGTKNPLHYLKNICIHSYDVPTDAIPNASINTTTAANATPN
ILGDTAPLAVYRLRGTEGNVFSAIVDAVVMLEERYIGFCEWKERRVRVDIPSYVPLRYPQ
AVAPSSATVEEKGKKRHVASRKKSAVSTVVVPFSNAETIPVFDAQPKNMKGVVAHRSVYD
TILSLRKQAYFDRQTFCTACVLQVAATLSMPNPELLDPFLPLSKREEQQMLNDKKESSLF
VNYVFDIAMLGVDNAHQQLLLCNKEKGSTEPFSPEEESLKKTVPSSILSSQPRKLNDVLS
SRDDGNVDNVTLDIRDASVSLLFQSFGIEVEETKKAIEEVTSIGFIYSGRHGAIAHALRK
NKLDSWRSVHMNADGCGLEVLYRGDGASRTESSVYTFCGSATFADYVNWQNYCVNEGLYY
NPPLPDSDEEESSEADEEEEEEEEEEEMYDVGEDGDEGKTVKVKSSRRKKVQESPPVDVL
QVADAALRRRRTYEDVLRRLFQKEDVVQEAILSGTGAHCIAEERQWMFTDDGSTIEVRRV
VGNTPQVHCVVTDPVDLSFGFLTMAELPTEEIPLVITSSVRCFLTIDDVVQFFFEVVADN
TRAVEQVAYMKALESAKLEAKAQYEAFEQTKTSRSSKEKVPLPSLAALEEALISQIAVPK
EREQRKPMTNARALFHDGTAAAFSAAEKCLHFSTVQNLHHSSLIDIFVDVCVGDKVRSVR
ISHIHAITVYADGCVMLNAQEIEGYLVSIDLFGNYLTINKEGAMLYVTAAGKRSIIRADG
QKLSLEPLMVVTTGERRTDTNVLLRQDGVQVLLGSGGQLEKVIYGTGCFSASSDGGGYTW
HFMGFPEIRVHRGDGRLGFTVDRMETIMDVREQTLQLIHHRSGGEAILDLKTHRLHVRPI
TNGNCFTMDCAFGGLVASSEVADYCVSPFGRCGDVRENVFKEAEVVSREFLERYEETGGN
FEETALQRNFNTFDFPLRVRNSTCRQKFELPTSTLSSYMRYAERSIDRVLSSGVQQSKDL
IRVLVRLNNCDDDDGVLIFMNSWLSSVLLQRLKSEIDPTFSRFLSGVSFSGGDVQEQILF

LQPPYESAGEEQKSVVPMASSVEQFLLMSHWPNAIQAPRDNKVTAVHVLSTRKGTALMTD
NLAELLCSSRLSLSEAEVWSKAMHTLPLVERAEVAGRNPVDGTKRCQTIRDYTVSGPRVT
RAGFLPHKKTRLARDGKFNYWRSTGILVAAELEEATLNEKNGNTAADISLFEGNHECSAV
VASHASADTPEIIKRKGNFVPFMHLMVERGMPPQEHRFVPTLSVMPSVLSFGRVIRCNRY
ALPVVFTNTSTVPCRYRVTLPTECKDILRVHYPRHFLAPGLTVMAQVEISGRQPLGAMSF
SLNVTHEGGLIPVKVEIETVEEEEALLSFSYNSTAVVLGPALINSFVPGTTRRLPPHLLQ
RAAAKEGAAEVLETM*
>TCRU_10567 hypothetical protein, conserved
MGVASAWAVHSAAEVRSVCRLSLSSSLKCWSVLPVGFLAVPAHRENQIPAAPERARNALG
VNHVRHDTIVAAAVFAAHRTVCRASGRGGVWSSGRRRRFRAKFFACLL*
>TCRU_of Trypanosoma cruzi C-terminus, putative Dispersed gene
family protein.1
MRGGRVYWCVFQLSVLCVVGLIAAVHPPAGGCHFQYFCMAAVLVAGAGVVAFTNMMRSAF
LTVMHTAGFVLLATLCLVSTANHLASSDGGARAYAVIVLLLTTVVLAATVYGVVVWYAED
RHWQELREPRRGGLEALLRDDEESDEGTQKPHNVTSSSYAPGTTAASSYRPPAPP*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MSPARFVVGCNLQGDEEVSYDDVFSEGVEVFRCGTCNDDAACYMPGTESVDRGSCSCSCR
DGWHGASCLPFEVPDTVVPPLPERAVDGDTSCVVNQTLTNLTLNMWKTHHCYVGVTFSGR
GAVLTFSLNSMPLHLPINITLAGCTFRDGVVLQFVGGAESAESSGVLIRVSRTVMRSSVV
AFARALPQHCDIAVTEVDAVQISEVQLLDLMSNMLSVLLLRNVELSASSLLVSNVKAYAL
RYGGFGLYSIGTLTLVGGSSLYARYCSFDGYAHLFHVNILSVSDHSVFALLNNTMTSGTS
FLYQHHEFSVSDHSVLRVVGNSGSVSYAIYACNFWSVQQLSWLDWRDNDVEVGAMLHESE
SAFLIIDGSSVVTLKGCKMGSTGLSVPLRSLVGAGYRFVAGCLTVAGRVLTTAAELALHG
INNVTAVAVCGECTKDGDCFAPLTTAVSDCKCQCAAGGHGDVCVPAPVPAGPPPPPPPSP
PPPPPPTPVGGCISDMVYPEVAQAVGGGLSWLCYRNVTFSGDGMSLTVLVGAMTGGVANV
TFDGCTWRDGAVLLLLGNVHAAVGALNIVVTGNTFSDALLSPEGGFPPQTNITMSGNRFT
VTRLIPRLGLVLRRPSCVAMNGLVISNDSAVVLSGNVFQTVRALSSAIRVFRSSLRVSWH
SLFAVMGNTFHMAGGDSTLILLGGNRHSLSLSVLKNSAVVIRGNLVTRPVKYFISFLWAL
RVESLSAVVFQNNDMRGSSAVFYSTFASYIYYNSWLQLSDNLCRESPVVAFAVFNPTVNL
RDSTLSVSGNQFMSSTVSPKVLRIFTGSRDLTNGEIVAACNSLNGGDGASYDIPSVYNVT
ILTCSDPCILATSCFPAYTTTASSDGCACTCAEGGHGDVCLPVAVPEPPSTDGADLCVRD
VRVDVEVSAGFGTSVACYVGVTFAADVVVDVESMSGSVRNVTLVNCTFVRGASLYVVGWR
SDPPAGERADVLIIGLESRSGGGVLVANRFPPGSRVTVVDSVLIAEARVAYRNAYGLGDV
SACLVVHKVNLTGSVLTIARTHVAAVFREAVGVLVVGGVALSSRGALYVDGLSVQTALGL
CVSVEGGVAAIGGSVVAFVDSDFLLCKHAVSVRGAVSVSGSAVALVRSDFLLTEDYAVAF
YSTVRLADGSMLLAKGNVHDGVSREMLYAAGAVTAAGSTLSFVRNRALLPRMLSLSLSLS
AGAHLRVACNDAGGRVLSTAEEYAAAGFGDAGSIDVVGCDDCDRDTHCYASGTASASMKD
GVCVCACGSGGYGEACVPVGAPALPPAAGTASRVFVREGVTMQSVFVVPAGASEVTLRHV
VLDGVSPLLYVPWMARDGVRIVVQNVSLLNGAVLYVMGGGALRGAVAAGSDESGPVELSV
CDVEALNGALVLTGTFPAGSVLTVTDSLLVAARPTPLVYLPGSQSSLYAPVLVLSGLRLV
RSVLVVSGVALVTVMTGGRTVVVDGAVLEVVGGGVALDAAVLGGEYALYASARVAASGGA
VLRVSGSQVYAAHGLVFGSGVVANASAVVVNDNAGALTDGALLELRGSASFVSGSWLSVR
GNSISGRLLSLPSYTRSAELVQSTLTLHGNAGSGPVVMDGAVVLGGAGRRFVVGCLTLNG
QALQPMDYRSAGIIGEFRPVACSVCDADVRCFAAATRAMSGSCGCRCAEGGYGRDCLPVY
LPHVDGCNRTPGIPQLSHTATLTETRSPTPTWTPRPSHTATLTETRSPTPTWTSRPSATQ
YSPTQYGPTKTLQVTETVALPPTRTPTASVSSTLWWSDVACPTLAVTTTAAGGSLTQSDI
CGGGSVVPTRLMVALPPPFRWARDPQLGKHLSFVLVSTAQPRGFGGPWGAMLEQRDVDAQ
RDESVHRPGAGCARAPRLLHCCRRDDSHSLRRCGSVRRLQGRAAWVLHDHVEHVARRCQR
PLCGHRRCCGCDGCCRAGDRRAGPRSGDAGTRRVCEDVMRFSTRACEHRCAAVLPVGVCC
P*
>TCRU_10570 hypothetical protein, conserved
MTNRVDRSRTPSRTSAGPYRNPAWPRVVGTYRDPPTVARSVEFTSSTLECSGIAPRSTIV
PSTDVTFVMLTRTCGTRRAVLSLRPPIRSCAPPASTQWRSVTFRASANASIERSSTATVI

GPLNTTESKHAIARPPPTVTDSVSVTPLTQPSAVSPPPPPDLATGTSNGRHASPTPPARQ
LHTQSVNDAVSASKHASAAAQPSQGTTLTEGRPAER*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MPGTESVDRGSCSCSCKDGWHGASCLPFEVPDTVVPPLPERAVDGDTSCVMNQTLRSLTL
NMWKTHHCYVGVTFSGVGAVLTFSLNSMPLHLLINITLTGCTFREGAALQFVGGAESAES
AGVLIRVSRTVMRSSAVAFIRALPQHCDIAVTEVDAVQTFEFDLPGTVSKTLSVLLLRNV
VLSASTLLVGNVKAYALRYGGFGLYSIGTLTLVGGSSLYTRYCSFDGYEDLFYVYSLSVR
NYSVFALLNNTMTSGTSLLHQSGAFSVSEHSVLRVVGNSGSVRYAIYPINLWDIQRSSWL
DWRDNDVGLGAIFKVWDFAFMSIDGSSGVTLTGCKMGSTGLSVPLLSQADAGYRFVAGCL
TVAGRVQTTAEELELHGITNVTAVAACGECTKDGDCFATLTTAVIDCKCQCAAGGHGDAC
VPAPVPAGPPPPPSPPLRPIPPPPPVGECISDMVYPEVAQAVGSGLSWLCYRNVTFSGGG
MRLTVLIGAMKGDVANVTFDGCTWRDGAVLLLLGNAYAFLGSLNIVVTGNTFIDALLSPE
GGFPPHTNITISGNRFTVTRLIPRLGLGVMRPSCVAMNGLVIAKDSAVVLSGNVFQTVTA
FSSAIYVVGSSLRVSWHSLFAVIGNTFHMDGGDGAPIHLEGSRQSSSLKVQNNSAVVIRG
NVVSRPVRYFLLIILALRVESSSAVVFQGNDMQRSWFVFFSGHSSYIYYNSWLQLSGNLC
RESPSEAFASLYPKVNLRDSTVSVSGNRFMSSTDTPKTLLISSGSRDLTNGAIVAACNTV
NGMEEAKYVIPSVYNATILNCSDPCILATSCFPAYTTTASSDGCACTCAEGGHGDACLPV
AVPEPPSTDGADLCVRDASVDVEVDAGLGTSVVCYVGVTFAADVVVDVESMSGSVRNVTL
ANCAFVDGASLYVVGWRSDPPAGHRADVLISGLESRSGGGVLVANRFPPGSRVTVVDSVL
VAEKRVAYRNAYGLGDASACLVVHRVNLTGSVLTIARTHMLAVFREAVGVLVVGGVALSS
RGALYVDGLSVQTALGPCVSVEGGVAAIGGSVVAFVDSDFLLCKHAVSVRGAVSVSGSAV
ALVRSDFLSTEDYAVAFYSTVRLADGSMLLAKGNVHDGVLREMLHAAGAVTAAGSTLSFV
RNRALLPRMLSLSLSLSAGAHLRVACNDAGGSVLSTAEEYAAAGFGDAGSIDVVGCDDCD
RDTHCYASGTASARMKDGVCVCACGSGGYGEACVPVGALALPPAVDTASSAFFREGVTVR
SVFVVPAGASEVTLRHVVLDGVSPVLYVPWMARDGVRIVVQNVSLLNGAVLYVMGGGALR
GAVAAGSDESGPVELSVCDVEALNGALVLTGTFPAGSVLTVTDSLLVAARPTPLVYLPGS
QSSLYAPVLVLSGLRLVRSVLVVSGVALVTVMTGGRTVVVDGAVLELVGGGVALDAAVLG
GEYALYASARVAASGGAVLRVSGSQVYAARGLVFGSGVEANASAVVVNDNAGALTDGALL
VLRGSASFVSGSWLSVRGNSIRGRLLSVPSYPRRADLVQSTLTLHGNAGSGPVVMDGTVA
LVGAGRRFVVGCLTLNGQALQPMDYRSAGIIGEFRPVACGVCDADVRCFAAATRAMSGSC
GCRCAEGGYGRDCLPVYLPHVDGCNRTPGIPQLSHTATLTETRSPTPTWTSRPSATQYSP
TQYGPTKTLQVTETVALPPTRTSTASVSRTLWWSDVACPTLAVTTTAAGGSLTQNDIRGG
GSVVPTRLMVALPPPFRWARDPQLGKHLSFVPVSTAQPRGFGGPWGAMLSNATWVRNATN
PSTVLELAVPVHRGYFIAAEETIVIRCDAAAVSGGCKGVLLGSFTIRSDTLPAAAGALSA
ATGVVAGAAAVAVVVTGGLGSVLEIQALGVFARMSCASAQERASTVALPYFLSVFAALDP
LWMVVGNALLGGQRAARRSVRVRALRSDGRLPAVARRGRGECVGCDALPEPDVRCGARDS
PRHILRLRACTGDARRPRAAPRDRCRWRAVRCGVPCWRVLLDCPPHGRELHEVLAVFEEA
AARAPAVPRRVLAPRGAAADVRRHADEHEGRPRVLVRVPAVGAVCGGPDCCCAPARGRLP
RPVLLHGGCAGCGCRRGCLHEHDALGLPDGDAHCELCAPCTAVSGQRGEPPCAERRRSEG
VRGDCAAADDCAACGHCVRRRCVVRGGPPLAGAARAAAWWTGGTAAR*
>TCRU_10572 hypothetical protein, conserved
MLTRTCGIRRAVLSLRPPIRSCAPPTSTQWRSVTFSASASASIERRSTATVIGPPNTTES
KHAVARQPPTVTDSVSVTPLTQPSAVSPPPPPALAGGTSNGRHASPTPPARQLHAQSEND
AVSASKHASAAAQPSHGTTLTEDRPAMR*
>TCRU_10573 Mucin-like glycoprotein, putative
MMKTCRLLCALLVLALCCRPSVCVAESEDTAGKSGKGSVPTISMPVYPKQVSDPSSKTPS
PPKINDEVGGTEQSRTTGTVIETPQSQNTSNNAQDQDGGKPTTEDADIDKANMSNEQNKK
KYASTATTTTTTTTTRAPTTTTTTTTTAAPQALSTTTTTEAPTTTTTRVPSLLREIDGSL
SSSAWVCAPLLLAVSALAYTALG*
>TCRU_10574 Protein of unknown function (DUF3720), putative
MAMMTGRVLLVCALCVLWCGAVGDARDNRCVEDDGNVLTHTHNGGNEGLRLKADFGLIST
RMGLIKAVAAVDGGDGAGNDSLENKDKSPQGGVLAGTKDNEAPGAGGVQGAAGDENGQLP
AAGREGNENKDVDPGINAATDSQDKTNDQLSSSSGSTPSRSGEKPSSTGTSEMTQLPKDT

VTKLDADLQDKRESSEGIKAEETEEEERQKIKAHTGSSESKNNGGETTPPPLTSSDEESP
ISDQENSQNSKKVKNEATPSRSKTASEAPAPPSEDATQGQHSHDTDTEDPTKNAATGSPV
EPTTPSTSASGSGDHVRNKVDEDDAQRHEGQHDSLETVNTNVVPTLSERASQTPETATDA
RTNDTTTKVGDSDGSTAASRTTSPLLLLLVVACAAAAAVVAA*
>TCRU_10575 BNR repeat-like domain containing protein, putative
MSRRVFTSAVLLLLVVLMCGTGGAVKAAEPASGQGSLPKSPFDWRDTKDEETVSSLRVPS
LVEVNGGVFAVAEAQCTKDGVSFTGIASQLLTNTADNKPKEVLEDAKEKPQVLEEDISTE
KKKVDVSRPTVVVSGNNIYMLVGKHSHEDAANCQAGTENIKSGMLLVKGELGEADKKLIG
KLLTVYRAL*
>TCRU_10576 hypothetical protein, conserved
MATIDAASSTTKRRYAAKVEKGENAWRREWSSFMSGINMKELRKGGGVILPKSADLEVAE
PNSRGDACNFSYLFASPAEKKAARLARQREGDERRKKGALQRAGQSSNPLAQLSKHERTL
LEARQRGLKIDGMKRKEVRQFLHLTISKEQQEAERHQEEFRPHELMDKKLQWYQQGPHPI
DIIAEKLVVRKAAKKAKQLGLRYNYLMPHASWLAKREQRRRERLLVGLGRRYVFDEEGRM
MDMFGNYVDTMFSTAVTQGVHAGETGREEHNAESQHPPMGEQKKRDSSVVPAPNMCSDAL
IEPWKASSSYVRAVVRDRRVAEAIKNANITTSYISSSFVMGPSIGVDDDEENPLLAQKPV
KRTEPRRVKAREMRSKAASFEP*
>TCRU_10577 hypothetical protein, conserved
MAPTDPKEWAKKVRSKTPVLLEVGKPAPKAVLSFGGCGFLVTYALGVALFLQQERAEFLA
HSFLLGAGTGVIPAVALACGPRAVNIEKVRDAIVDNRFLVTDEEKRVEVFTEYINKLLPR
NAVELVNGRLALTIGFSNKDPGYMRQTKENVHFGHHIAQWDDVNDLAQCIMAATAPNTEK
PMVFRDADNVVRGTMMSLSSELDQYCRHIYIHGYAGYRYNRQQTRHNIFFGRHGFVANTH
FPFWRQVWLAFAPNIGGTARKDDLLEAYDAGYNDARRYERWEEDPYHYAKADRSPSDDFN
FRQLRANLFGGKKAAERFEL*
>TCRU_10578 btb/poz domain containing protein, putative
MSSKLYETPELVGDEGLPLVSESPLPKEPQTHTFVAEQQNRINEENEESANGGNDGGDAG
DDEVVMETLLNQFEHLQNSAKAYIRVSQSAFSRLQLKRQRMEQHERSLRHRAEMVATSSF
SPKFKLNIGGMRFHVQRATLLQFSMTIFHLLEDERFNAQKDEFGHIFFDRDPWLFRELLF
LLRERQQRIIEAGQFGSGPLPGGTEYNRLAQLPLTEWRRLMDEAKYYGLNEFVNEVVTTR
FQWQQCEIAPADFGEYARGALSHESNSFVPLEGRCFSTCLLANDDVFLFGGCAENEAVLD
SLYRLWLESDGVDEECSEGIVGDGENARPVRMQRLRYDLVQPFCAGDDGRGCPAPRSGHA
MIVLHNRYVLLFYGNDLHSHLNDVWLYHITRNTWIRVKVRGTPVEPRSGHTVTVVGNRFY
LIGGKKLFGVSRRIFSEVFEGVFDINRVELTWSSAAWPQQSESLRRQQEEEMPSLPYEGA
AVSAAATAVSREDEEEEEWLCSVPPIAYHTAVEYKGRYIMVYGGMCASAGTNVEGDGAGE
GRWSSIAAASSLRRDVSPKLYQFDTVEYKWRSLQTSAGTQNLMLSDIPQSGHIALRHQDE
MYVMGSYKEQRQFAIFQLSLRTLMWRQVQTTVAPMHSIPRGRAMPSGVLLPASQNNPNAM
ILLYGGYNVTTRQYLDDAYLLAL*
>TCRU_10579 hypothetical protein, conserved
MAVSSSIFLYITGGRTLWVPGHTPAPGETKPVQILNFASPRELSRSFYLFDMPIQIVNDP
STAAMIPGGKTPEDVITAVNEFRRVCMEDQDFLLKRCYDANKPPPPSQNIPQQQQPQQQP
QPAQQQQPQQFMTGISRMAEALGMRQNPTFNAAGTNLNQALLLQLLQQQQQQQQQQRSPM
PPHASPLQQPPPMTFNRGAMMGSGNLPAGGNMMMNSAGMMPSVPSAGFNNNYFNPMMSMG
GRSAGLMPPPNTYPLPHAMGTVSPPIMGHRGAGVGRGILSHSPFQAPVRDQPEALPNLPP
IPPDILEMYMNPQQKLMCATMPGPRCTVWLREHEIPPATKNPRYVFCKGGIVLMLKTKGS
EVANSKPVELFEQQVCAHFLIHNYCSRSNCLHRHHTETQLRQLIAGKHVELKSMTKKERH
RLSELVLEKEREGLARAAEDREKRSRDKMEAVRRRGGTGGSTPDAEGLASTQNSQPPVAR
VDVGSSDDEDNDNNKKKNESEVVDKSNSKEGSNDIHAGEIKGEGNKSSELPQERHENETV
EKTRVEKPVVPRRVAPFSSRRVLNPADIGVTDDDDDDEASSSSSSSSVSSSASSSKSST
RHADTVKKTTETASENCDHEKREGSVKVSVEATAPDPLPPVESATEEGVAQETHDARDEP
AEAVKMTEQPQTATTAGKENVEADEAETKSQKEGVDVADKPTVVVAAEEEEEERATVEKN
EEENTETPAKGEQPHPASDDAPQVAEGDGGKKNPKGKTGGTKRARSPVAKKSTAKGKKSK
K*
>TCRU_10580 mitochondrial processing peptidase alpha subunit,
putative

MYRRVHVHAVALQVRAISEYKFGQAPLTKPWGNVVRFSPPAPSKALEAQKVKVSQLHNGA
RVITQQREGAMVSVGAYILAGPAYDPVGCPGVHGLMHVALTTSNYNNSLFQLDRGIRSTG
AAFSHFEKDKHFIGIRLDARADMWKSQNTGKKNDKNSFTLNLVQDTIFTAIAAPRFHEAD
IERFRDTVDNSLKEMKWQQPEEYVMQKVETVAFHREPLGNPRHVPENNNGNITSKILMEH
YSQYVTPERVIIAGVNVNHDELIAEYENTPYPHSKSAPHHAAFEKQNRVAAFDINAEKNQ
YTGGEAHEHENRAKEMGTKPDMDNETIVAVGYLSFGRGMASIKRYAAALVYQQLYNVLIQ
DTVRGAFGGSSNGIHSFYLPYQSAGLIGFTARSEPQDIVKMVTAGMRDIQSVKTDNAAAV
EAAKHRAAVDFMSRNLETVRDLCDYLGTSLPLTSMAQNSTQYMKPEEVIDAIRSVTPEEL
KQVKECAMGSKPSLFGHGEMLAFPSLRQMGF*
>TCRU_10581 hypothetical protein, conserved
MVGDAPRHRTSGSRDSPTCICTDGMEQAECVAAAACHELKCSANVRTAIMPSAVASPCCQ
RSVRNSLVPSRSQACDAPRHGGATFLPSGIGCAAVLLGPRLCSASAATSSRREHRHSLPS
SKRLIDVLLPTPRHTGTRPADHEQPIMSVVPLLTPKRQDRPDLLRNLHLACPRHFLVERR
AADQSRPAQAAAASSRPSTI*
>TCRU_homologue, putative S. cerevisiae PS.1
MFSPLSDITNVQTALSGKYVKNNSTIISKKVAIKRHNPYGWKCLEDSLVTSCTAFLSEGA
SLIKIPAKQELFAEKDEAPPTPTMPPVCNVLVQFKCHQKEFSSPFLAAKGQYVVVQGDRG
IDIGVVIRLNTEGCKTYVERSGPTGSILRHATQREVDYWATDLKEDEAIAVSFCQQRVQR
HGFDMEILHAEYQFDKKKLTFYYSAKSRIDFVQLLKELYREFGCRIWMEKVRIQD*
>TCRU_10583 GPI-GlcNAc transferase complex, PIG-H component, putative
MSETKTDSVSSRHVSPKVLLEGHITSTNVMVDVFQTDYNDCFRSYRVCQRNPFGPNTSFL
LRIFSVNDVMLLLVLIALALPSLPTFLGPLQGANWMYFSLNGTEKKIDGVVPLLMDKWTP
NSFLPRLFLMIFCCILSVWRMVAGFQRAHIEEVMVIRGLGMQITNYNVFGWICSQRFIEL
KLIRSLVIHDAFFRYQAIFFLSATIENDATRLVLFEETLPRLAVLCPVLCGLRHILYEEP
ENGATLAELEGVESERLDDTMEGEYKATDDDSDITDRENGDSFAFTNALEREGNYYDPPL
MEFLHTK*
>TCRU_10584 hypothetical protein, conserved
MSRSRFYRVLQERGVGFAMYLYIFGESMTLAVLYALHNDGFSTGDVFDWLKLLSADSLID
LERWSQVGPVVGGLRLSPRLLCNYLVANALTYPLYAMQFAFCAATLPLLSRVTSPVSYFL
HACRARGKKGRIVPKAPSVGVKTEGRLTR*
>TCRU_10585 hypothetical protein
MMQRAESSFLVSDSIDKFCPNVHCPHRAAVERERYTSMQLTAVNRVLEEGQQYLRLKNGR
LEAEIKSKNEQLQQLDTLARRETTRREELEEQLVEIRRTIHARYSAAYSHAASQEAEVAR
VQQERKLLVEQVLQLQSALNEMVRLNEALQYALLSNGIDASTAISASVKPPTSTPRLPSN
SHSSSPPSLSSSSPSSSSLSFSAPSPKHTSVFPPLHTELPGELNENSHDLEKSHESFNKE
RKEAVTILPPVREKQRDDFNSDLMTMQNVVSELRSLKAFLNSIGGAESLK*
>TCRU_10586 Bacterial transferase hexapeptide (six repeats), putative
MPANIVPGFVPYFGFMLKDVGARLAIMAHYLQTNRHMYPVIRHQNVRAYRGMLPWTQDSA
FIAPSAFLSGNVVLGHDTCIFYHVVIRNYHVREETVLGDHTVVMDRASFLGQVNVGNGVY
IGVGSTLDCCTIGDGVYIGPGVSVALGAVVENGAIVAAGSNVPKDTRIHAWELWAGNPAQ
KIAEVTQEQANEVAHIVHEQVGVAKAHVQAIHDHIHHTEELDGEWLHLAITEMEKQQQQV
TLKVPVDIPLEAKRFLQPRVHMRRPEMHMRMSYPVNRVAPWMPKVADQTANA*
>TCRU_10587 hypothetical protein, conserved
MPKRSRSVLHAYILPHTKLLRNEKRKKRHESLDVTAKSLVPPEVDAADNEVVPHDGDCGM
SEAAFVGIETHDHVQSKSSEGREGNAEKNFSSLDDEPFFPEADWLVGLPPSCRDVQREPN
WLERALMLARCSNRCINLFQLCDDNRDSAFPMPPYPTCTHLESTAQKEKCRATAVANITA
AFYAAPSPVDPSVTFGASVVSRAH*
>TCRU_10588 HCaRG protein, putative
MSSASPSSETKTTSAAAVNSPLQRERILDVDWTVDVLVSSGQISRVGIPTVALTITLSSG
SVLRYRLTMEEFHQWRFTMAKVVRDQLYLEKKRAYIDH*
>TCRU_10589 ubiquitin-activating enzyme E1, putative
MMRVYIGHLLFPPKRSFFSQASCSRGDDDVGIFSSGDAKRFKGEGWATGVMEMTDVSSFQ

VSAASITEAVLKAFEPWVGQHEKINGRPHIDVHVHPAGKGASFCLVPGILALSLTTSACT
ALECPEKVRMADMEAAARYPRITAVSLESFNGEVWDDLPVYWEERQVMVTNTLTETAMTQ
VAANCCVSPAKDETLHGEETLMEKRILVVGAGGIGCELLKVLVLYGFRNLDVFDLDTIDA
TNLNRQFLFQKEDVGASKADTARKAILNWFTSTSSERMLPVIRAHHADIKNEAYDDAFFS
QFALVLNALDNVSARQHVNRMCMRTDVPLIESGTMGYNGQVQPIIRGLYECYDCHPKAAN
QKTVAVCTIHARPTTMVHCVHYAKELYERLFGEGKREEKDEFAFVDAIITQQEEELQSEA
DACDGDLIICSMAAALAGSLFYEKIQELLSMKTVWATQPPVPLSKDLIQRMAEEMSVDAT
RVKSLHILRDTSLCLEDTVSLFLDAFTRCVRRGNRHAFCKEDDDAVDFVAAVANLRAFVF
HIFPLQSVEEIRSIAGAIVPAIATTNAIVAAAVVQQALCVLGMKETTCRFGKPQMVYVRR
VPQVRRRPFPDPCGCNIHVTHGSDRKGDSSSDEKTGKKNDAIQKRWATDLFLVHSAPPSL
PSSNCLVCREHYPTVRVFLDATHTTLGHFLCTVLRERLSMTAASVFCGANVLYEEDEYEA
LATTPLADLMTAADRPLELLVDDLNHEVEWRLVVNHSPAMEGSDAVKLEGIDAALQLEQK
LVADSKKNAAATAAAENDNGNGDRVVPTKTGGVENDDEDDVVDSPSLNVKDAAAGNRATV
TVVLSDSDGDDVDVVEIE*
>TCRU_10590 Reverse transcriptase (RNA-dependent DNA polymerase), putative
MVLKRLLWVWTPHPHQYAYRSVRTTTMRLAHLIHEVEHNRNHYFQLSLPKKSGIGNQLHY
RPHRTLLVLVDFSKAFDSIDHRVLSRLLANIPGVNCRRWLRNFLCGRYAETRVGHRHSDR
RPMLRGVPQGSVLGPYLFSLYAHPLLSLLNSFAGATADMYADDLSIIVRGQSREDAIPTA
NMVLKRLHAWSQENGLAINPSKREAAWFTLSTHTESDYDREGRWPLVVAGCQIPVMTMGA
SRTTKLLGMDLDPRLTLNAAATKQCAATSQRISQPRCIAHKEAGPSPHDLRTFVIGYGSS
KLRYGSELVWAATTDSAKNEMQKTYATLARIVSGVPSTVDPESALLEANMPLSTSFACAH
GSQYLRTHAHVRRTGCGDPRLSHRLAPVSASRHYLGTSYMPS*
>TCRU_10591 Endonuclease/Exonuclease/phosphatase family/ Endonuclease-reverse transcriptase, putative
MEPFKWLPTERYFHPLLNSIGAYQRYTYRLRAVCDAQLQKLLLSGDIEQHPGPIAVLQMN
VSCLTPSKLATLMAQGADIIAIQETWKSSEQIAGMHTGDYVLYAQSRIGKGGGVAVLVRK
TLRSKRIPLTIPQHDTSLEVVVVQVALDQNRDLIVASAYMRPPAQVTQSLRRLLNCLPAS
SPLLLCGDFNMHHPQWEPFLETSPSEVAAEFLELCTDAGLTLVNTPGEITYARGARERSC
IDLTWSKHLTVSDWSASVSPLSDHYMLTFTLHQAFKDTIPSAPRIFHSWGKCKWDLFVKD
LDAQLPAYDYKKLSTGIKAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERMATDSKA
RYLHLPTPDREAEMQRTRSPFFLLLRERLRNTYPRRISKLNPGEPLAWKYISGRKKASIP
SPTSILLGGGQHTYKTARRAANALNRIFFPFHPSHKAVRPSKGNNRRNTSLGIVSSSSFW
AAEQQQVYLYIYIRGFVTPLLMHLLILRNCLLRYVIRRMARPRTG*
>TCRU_10592 Protein of unknown function (DUF3676)/Trans-sialidase of Trypanosoma hydrophobic C-terminal, putative
MSSDSSLTPSKSDAETTSAENTDDVSRTEGDEFPVENGEEVPQTVDIAPGNASTLPGETK
IPSESNATAPSNTGILLENGHYSELAGMALFAESTVHGCVSRVLLLMLLGLWGTAALC*
>TCRU_of Trypanosoma cruzi region 5/Dispersed gene family protein.1 Dispersed gene family protein.1
MVSLPPPFRWARDPQLGTHLSFVPVSTAQPSGFDGPWGAMLSNATWVRNATNPSTVLELA
VPVHRGYFITADETIVIRCDAAAVSGGCKGVLLGSFTIRSDTLPAAASALSTITGVVAGA
TAVAVVVTGGLGSILEMQALGVFARMPCASAQERASTVALPYFLSVFAARDPLWMVVGNA
VLAAVFGCVHCGVTAAFQRWRGVDAASAWAAMRFPSLTYVVAHAMHLGIFFGSVLALAMP
GARVQHRVIGVVGVLYGVAFPAGVCYLIARHTGASFTRYWQFLRKPLHERLLYPVGYWHP
AAQQRMYGGMLTNMRGSHVYWCVFQLSVLCVVGLIAAVHPPVGGCDVQYFCMAAVLLAGA
GVVVFTNTMRSAFLTVMHTASFLLLAALCVVSAANHLAPSDGGARAYAAIVLLLTTVVLA
VTVYGVVVWYAEDRHWQELREPRRGGLEALLRDDEESDDETQKPHEMTSSSYASGTTVAS
SYRPPAPPLQPMADDTRSDAFSLFDRVSSASCSINYAFLDR*
>TCRU_10594 hypothetical protein, conserved
MRGVHLAPRHAQHSASRPNHARTRVQRIVATEHSRVQRDTATDKLQHRAVHHHRPSTSHH
GHEGNAGRNQHGPHKPQARQHQHRCVRRGLRAGKTHKRRRPRGNQQGVRHRQHGPRGESA
GQHKRTVQRLHVAHGQLHRPALVAPRRPRTAQPSTAHHVQHSTVQQRDVLHNDPHAVSRH
PRHVEHRTHAVQHDVAQRHFARAGRHKEHRPHRHALAEEHTRRGAHSRRQHGSSHRHARL

AVPAAAARAHAHTVPHARRRRPGRVAVRVPVAGVAPSNVDAPSVAKTSRCVLLRRRQDTP
TSVVARHPQMRPSRERQTQRQHPRQQRSVAHKAQRAPSSGHGASGVEHLPRDAVVHVALR
QQHRPVIQAHRRIKRHRVVLRRQKVAPHKRHSGARHAHSPTHRHRVLAQQEAAVNKRHHG
AATGRNTALHRHAQPQRRLHRQPVHVQRTARRQRHAANNQHTNSVVEHSCHMRARDGQHA
PSQIHAVQHEARGRVAKVVGAAIRNMLLCDQHRVHHSDARTRRKSVRHQHAAARARLKPA
DQHIGTLASRRVGQPPDNVQARSAQKRAARQRHVAHAP*
>TCRU_10595 retrotransposon hot spot protein, RHS3, putative
MWFFLESPDAYIKDQQPLEEVSNLKDYQLLTDMRKIADGHLNFLEDWMDFKGKDTVTPLG
RKKLNDALTQIQKEVARWEAEEDVRRDTEEKTTKLEGFYESVYGAKWGHVLGFYDDKIWE
DRMEIHEGNHRSHGRTRRKV*
>TCRU_10596 retrotransposon hot spot protein, RHS3, putative
MVLTSDKGWPYSWRENKPIVDCYVNCEVDRAWRIVEDDLKDSSSPLSRVLIGTPGIGKSM
NAGSYLLYQLLHYDAEKIQVVVHCFGGDVAYVFDKTAKTVTK*
>TCRU_10597 retrotransposon hot spot protein, RHS3, putative
MKGYIIYDAPTNEAQLPISFAPSTGWGTIVLASPKVRNINEFARQRVSHLIIMNCPEDMD
VKAMCAWMKRDGTPQGQEKYWRMVCHQLNFLGPIPRYIFDAKDFSKRYDELVRVLKSIKS
RDDAKHVTRGGTKEWFSENPFYKLMCVDRERGDFGTEDFNTELLSIHLMNRAFPFLEKVI
PLNEICSLQ*
>TCRU_10598 Concanavalin A-like lectin/glucanases superfamily,
putative
MWPVNTWANNVRHVFLSHDFTLVASVTIEEAPNNNTPLLYAALGDAGPEYFMRLSYTADN
KWETMFEGTNTTTTEGSTWEPKKEHQVALMLQRNKASVYIDGKSMEEEEVPLTGETPLGL
FGFCFGATL*
>TCRU_10599 retrotransposon hot spot protein, RHS3, putative
MNAGSYLLYQLLHCYAERLQMVAYYIGDESFLFDKKTKTVSRYKEGTRITHNVKGLSRRG
VEGYIIYDIAKEGRNPSTNFPCKGWGIIVVTSPNEGNFKEWEKQSISVRIVMNCPEKDDV
KAMCVCMKRNGSTVQAVYMKMVEGRMDKLGPLLRYVFDKRAYKDRMDTCRSIVDKMVLSD
TQSYSVLGTDKMCEGKHVSHKLVKVVRVRGKEDKSELPYNALISSHFAELTLCKLATLMV
PNDFNLLVLAIKDDLISKALEDHSLFAFLSAAFVNAIIPKLTELKMKKNKDDPPHLCALR
VHPHERSLKPCLLPLLKDSDGKMGVESRVLYKPEAQNFPLVDGFFFLESKPKIMVGLQMT
TASEHHTIPSTVRQFTECLAAYFNGWEELSRDMSWEMI*
>TCRU_10600 hypothetical protein, conserved
MWWCCRLHVLLLWRRWALTVSPTGVAVRLHGAPTVPPCECHAQRRWDCGTRQPRVSFGAS
GTCWPQLGGVSGMLCRTGVVIAPCSGSCDGSDAAARHVAGSKERPQWTLDSWLDKVLLEG
KERITKMRLNDFPRNYFDGRGVEEFNENVTMKEFLISPNEFIKDEVLLSTTKALPSYQEL
KKGREEFYMLLEASNKLGDECAFNISQWRDFERKDTVAPLARAQINTACSQVLRDERRKA
EERERRERKQLGIDVSTNIKYAVFKGRVRVDKMRLNGFLTMELDGRGATDANRDVLLEAF
FEDSEKYICDAGVLGEIQASDRYLRMEGAVRDEIDMEEDVNRLHEKDVDNLLKWLVASAE
VRANVHDVAKGFWMQPPRKRGNQRSRAHRYTWRDCTTLCTMRGGIMSWRFLTARGR*
>TCRU_of Trypanosoma cruzi region 5/Dispersed gene family protein.1
Dispersed gene family protein.1
MVALPPPFRWASDPQLGTHLSFVPVSTAQPRGFGGPRGATLSNATWVRNATNPSTVLELA
VPVHRGYFIAVDETIVIRCDAAAVSGGCKGVLLGSFTIASNTPPAVASALSAITGVVAGA
AAVAVVVTGGLGSILEMQALGVFARMSCASAQERASTVALPYFLSVFAGLDPLWMVVGNA
LLAAVFGCVHCGVTAAFQRWRGVDAASAWAAMRFPSLTYVVAHAMHLGIFFGSVLALAMS
DARVLHRVIGVVGVLYGVAFPAGVCYLIARHTGASFTRYWQFSRKPLHERLLYPVGYWHP
TAQQRMYGGMLTNMKGSHVYWCVFQLSVLCVVGAVNHLVPSDGGARAYAAIVLLLTTVLL
AVAVYSVAVWCAGDHYWQELREPRRGGLEALLRDDEESDETQKLHDMTSLSYALGTTVAS
SYQPPAPPQPMAGDTRPDALSPLDRVSSASCSINYAPLDR*
>TCRU_of Trypanosoma cruzi region 4, putative Dispersed gene family
protein.1
MRLMRSVLVVSGVALVTVMTGGRTVVVDGAVLELVGGGVALDAAVFGGDVALYASARVVA
SGGAVLRVSGSQVYAAHGLVFDSGVVANTSAVVVNDNAGVLTDGALLVLRGSASLASGSW
LSARGNSISGRLLSLPSYPRSAELVKSTLTLHGNAGSGPVVMDGTVALGGAGRNFVVGCL

TLNGRALQPMDYRSAGIIGEFRPVACGVCDADVRCFAAATRAMSGSCRCRCAEGGYGRDC
LPVYLPHVDGCNRTPGMQLLSHTATLTPTWTATPTPSLSTTQYSPTH*
>TCRU_10603 RNase H, putative
MQKTYATLARIVSGVPSTVDPESALLEANMPPLHVLCLRARLSIFENTRACQMDWMRRPP
PEPPPRAGFRISPLSRDEPYAFVDAYTKDYGITESSPREERFFRTSIPPWFAASAHRVNI
GVELPIDHSITDEEELIREKRRVSEEALALHSHRSWILATDGGVDVPKSAGVGILLSSLN
SSEIIEKASINCGARPCSYRTESRALLLALEKLMIPRIRHRRKTLLVVTDSQSLLAALNK
GPLSQTDWTEDQIWQRLLTLTCAGWSVHLQFCCGHCGVHANELADQHATQTMESGQYTEQ
GIAPLWHTDLLTCFATQLTNKWRSTICQDTHRYLLCGTRPSDLSGKDLITQEVLHCQELV
HLARARCGESELWGRLYWAVRDCTNQCRFCNISPEQSAYMRSNKDPTAPGTDTVPPSARE
EDVSPVRRRTLTRRRKEKCPHCDSTLTGFSGLVSHCRSFHPEHPPPLPELKCDFCDMVFP
TRRSTAPHRSRFAHNPDATRHQNSSARRRSLLPQDQPATTSTPIGPQETLHHLLLGCPGT
LAVRRRLGIERDLRLGKFSQWQLLHSRKLLSLLDHLFGTQMALYS*
>TCRU_10604 Reverse transcriptase (RNA-dependent DNA polymerase),
putative
MVLKRLLWVWTPHPHQYAYRSVRTTTMRLAHLIHEVVHNRNHYFQVSLPKKSGIGNQLRH
RPHRTLLVLVDFSKAFDSIDHRVLSRLLANIPGVNCRRWLRNFLCGRYAKTRVGHRHSDR
RPMLREVPQWSVLGPYLFSLYVHPLLSLLNSFAGVTADMYADDLSIIVKGQSREDAIPTA
NMVLQKPHAWSQENGLAINPSKCEAAWSTLSTHTESDDDREGKWPLVVAGCQIPVMTMGA
SRTTKLIGMDLDHD*
>TCRU_10605 Endonuclease/Exonuclease/phosphatase family/
Endonuclease-reverse transcriptase, putative
MEPFTWLPAERYLHPLLNSIGAYQRYTYRLRAVCDVQRQKLLLSGDIEQNPGPIAVLQMN
VSCLTPSKLATLMAQGADIIAIQETWKSSEQIASMHTGDYVLYAQSRIGKGGGVAVLVRK
TLRSKRVPLTIPQHDTSLEVVVVQVALDQNRDLIVASAYMRPPPQVTQSFRRLVNCLPAS
SPLLLCGDFNTHHPQWEPFLETSPSEVATEFLELCTDAGLTLVNTPGEITYARGTRERSR
IDLTLSKHFTVSDWSASVSPLSDHYMLTFTLHQAFKDTIPSAPRIFYSLGKYKWDLFIKD
FDAQLPAYDYKKQSTGIKAFTRALITSYRRHCPRGMHKDGPRLWDDTLMEAERIATDSKA
RYLQLPTPDREAETQRTRSQFFLLLRERLRNTYLRRISKLNPGEPLAWKYISGRKKASLP
SPTSMLLGDGQHTYKTARRAANALNRIFLPFHPSHKAVGFPKASTDRVHL*
>TCRU_10606 vesicle-associated membrane protein
MAIISSFVAFQRVAVAEDHVTPPMRPVIDKMLERLPRHDTKVSYQYEANVYHFLVENEVV
YCCVSGNQYQNRTVFGFLVQVRDSFKSQFAGSVSRYPRSSEITPAVCGKFCATLSTLTRT
FNENPQTDKIGKINEQLDNTKQIMLENLDRLIDRGERIENLCDKTGQLRDEAQGFHSNAR
ALKRKMLLRNIKLAIALICVLGLVGLIVAFMICGVDFKKCKK*
>TCRU_10607 hypothetical protein, conserved
MNVLTSEPTKWADTVEFSIDCLFSSQSARNVEDVLSKASTRKHQKNLLKAVEPCITKMIE
NPNGISILTSLVKYGTIVTVSNVTRIVLHSCEKVLTCEKAPVEVCEAPLGVLLERILYRE
DCTEDCRMNLIKILKSLDHSLLLGSSVFLLATARLMIFDRAFAVSVCSNIKAKKAFFQLF
LIKTKKNVVIRFCELVLSMEERREDLTDLCSVFVFNALHTLYTANSSLRPWKEVTMLLAS
CGCIAVVREMVKLLSEWPDISVYLRNDHYAKVIASLLARNPEMNDGIVLLKVLFQKKEDF
DEIIASRKSSQLRLLATIAEKPAYVAALSETLGESPGKRLLAAAVRYRNINKPKALATKE
VLLQRIDKIRSASGAIGSLDKTLKRRRE*
>TCRU_10608 TPR-repeat protein, putative
MDYASAIRQQAEDLQDELKELNLWQEEVLRQEEANKKRRIHPANTDAIPPVRGTVPSLKE
AVLNSNKRISEEDPVKNAKEKGNTFFQAGKIKEAIEAYSTGIDLDAEGTVAHVLYGNRAL
CYLKLERWVDAEIDASACLRLNHSYSKGYFRRAMARKQLGNLRGARTDLEAVLALIPNDA
SAISEMKAITQMLQFERENAGPVIKKKKVIITEVDEEEEGENEQKGETDNKKSGSTSNGN
EPFELERREHFQKGMQELESAREKRRQLQESKVKEEEAKLNQRRRTSARVEVIEEESVEV
KNESSIPQATMEEERIKSMVLNSVDSKTHPLKSTENGRDLQNIAPRSLRTFCRPSKETLK
TPKSFTEFERVFTDIRGDEDLCCYYISLIPPANLRALFGNNMTPDILVWLLSTVKLLPGN
VAIAFLQGLCTIKRLEDIALFFDSSEKKVVQEVLDVIRSCGASQKDMTLFREKLRVA*
>TCRU_10609 chaperone protein DNAj, putative
MVKETKFYDSLGVSPDASVDEIKRAYRRLALKYHPDKNKEPGSQEKFKEVSVAYECLSDP

EKRSRYDQFGEKGVEMESGGIDPTDIFASFFGGSRARGEPKPKDIVHELPVSLEAFYTGK
TIKLAITRDRLCPACNGSGSKVPNASVTCKECDGRGVKLITRSIGPGFIQQMQVACPKCR
GKGTDMREEDKCDSCRGQQIKKDKKIFEIFVEKGMHRGDNATFRGEGDQIPGVRLSGDII
IIFEQKPHPVFTRKGDHLVMERTISLAEALTGFTLNIKHLDDRDVSITSTGVVDPSKLWC
VSREGMPIPNTGGVERGDLVVKFHVVYPSAQSLQSNEISDLRKILHYPPQQSPPPSAMLC
HLSETNIDLEKEAKRRRQTGGDDDDDAPQGHTGATCTQQ*
>TCRU_10610 aldo-keto reductase, putative
MPGANVLSFKPLGGPVLGVSHRLPLRNGNSIPQCGFGTYRMNPTVAGAAVEYAIHCGFRH
IDCAKAYDNQNAIGDALQRVISTGKLKREELFLTSKLWPTDQHPIHVEKACRETLAELRV
DYLDLYLIHWPVVWNHSPHLKTDDEKYPKDANGLPAVDDSVKLIDTWRAMCELVDKNLVR
SIGVSNCSENHINEVMSDGSLYAPVVNQIELHPALVQRDLLNFHGANQIVTAAYSPLGMP
SRFTHPNYKGLLYDASLQSISEYSGFSVARLLLNWNLDMHNVVIVRSTNKEHIRSNAKAS
LYALSDPVRMILDRFQERVGTIRTINPTDFTRGGGSFFD*
>TCRU_10611 Tat binding protein 1(TBP-1)-interacting protein
(TBPIP), putative
MALKKAVKNSDGKDAETAILQWFECEGEPATVQSLTDALGSKFGKALVQSVLEQCVSAKK
LQAKDIKKARLYFLNLAEAAERHGGVCPVDPARIELMQQIQQQAKLISDLSKELNTLLQK
PSSLQRASNIALLSTECAALKQRVENVKREINQGHDVKKDEDFSLLIRRYNRARELWRER
KHMAEHVIDAILGDSCDSKDLADHFGLISDQEANVSLNETAITFPRVEGLADV*
>TCRU_10612 hypothetical protein, conserved
MDVQISEEADLSDIFVALKDAVHGQWDADAEELLIKGLMAFQANFSARFSSVREELENLG
KDVCTASIQVSNAMNLFVLLAQKQFVQNRVSLDDDDADDDGCDAKSRVASGETDPGDEKQ
TSVDDKILEDTEARAKCVYQEAIDLGVRVLEERTIPLFSDGTGSDEGATANNDAPKEEDD
TFAAHYFSDQYCHIHFMALIGSERFLNDPYGGYFDDGGVDSRRSSPLDHSLESEANQLAV
TTEQGPKFNAASVAQSKTAPPPPPPPPPPPPPPPPPPASANAVKAQIAVPQRNKRDISK
VFASSDSSDEPDSRPAPISRPKPSGKSASAFFEGNNSADSTSGDSADMPAPKAPTKSTWG
RKPVMFADASSSDSDSEASPPAIKARTVPSRMPLKHGSSSSSLLSSEGETRKAVPPKVVV
DKARASMPPKTALPMVAPRKAGAKFLESDSGVSDHITPAPINVVQPTGNCTSKTISGNFM
LEHEKEALVSPDEKNGQTITVGLSSSVPVPASFPPSSETEQKKPSVVERASIKAIASLPR
RVCKNLSTSSSEIEGPSTGKRPPSRPTNSGVRKVPPPPPSKKTEVEGATRLYSSDSDVGG
AAYAPPRVLRKLTAKWASNRRRVYSSDSDI*
>TCRU_10613 3-oxoacyl-ACP reductase, putative
MPWCLEGRVGVVTGASSAIGRQVAARLYNEHHMRLACVSRRDLTALVPPECTCLKADLLS
SSDAEAVMKSVQRALGPVSLLVNCAGVTLNKIHLRCTDDDYDAIMNVNLRGALSITRAAL
RHGGMLREGDGCVLHVGSVVGSLGNEGQVIYSASKAALSGAVKSWAREYGLKNLRFNVIA
PGLIDGEGMGLALSEEQREWWRTRCPMGRLATVEDVTDAIIGVSLCRFISGQTIHVDGGL
C*
>TCRU_10614 protein kinase, putative
MDRYRLERYPCARTPTSSLYLGTDLTTGERVAVKVVDGSTPSGRRRIQRTLHGIQLVLRV
GRHTGIVGIRGAYEVDQKAYVVMDCMAGGSLLDYVTRRGPLGEAAAAAVMRRLLVAVAHL
HSFSVMHRDLKTENVLIQLPRDYREPPENVCICDFGFATSNIPNNECVGSPQYSAPEVAM
VGIRQCKLTKCDYSYDEKCDVWSLGVVAYAILSGALPFDGSTPTEVFTNVLRHNIPFPRS
AWQNVSEAAKDFVLFLMTPEPSKRPSALQSLEHPWLV*
>TCRU_10615 PRP19-like protein, putative
MFCCISNRVPHEPVVSRLSGCLYERSLVEQYIAEHGRCPVTGEALQKDDLIAVRPTVLKS
VAGGVGGALSPSSETVPGILAKLHSQWDAIMLEQFSLRQQLAQTQQELAQALHQYESACR
VIATFIKDRDAAGTQADEQAAGEKAQSLRDNNNNKNKSGGSGGGLSVPEAVLRDLDEYDK
LQRVKRKTRVTPPSLASEQNVRDFVEEASIDVAKSVWAAAFFTDNAVFVGLDDATVAHYE
VKNGRVCATGLGHERAVHHIILHNTGSALRVVSASDDATLRIWSCEAEALLCQGVVRQHD
GGIVGLGGVVAGHLLLSASAARIGLADIDQMESIASITAAAEELSAFTCLGVHPYGSLAA
LGVDGGGICIWNTRQMCVDTIVPFNVESNVCSVAFSADCFTLATGLVGGKTLLWDLRKMS
GPIHTLSSPSVTSARVSPVACSEVPVVAFDSSGKYLAVAGKEVCLFDWGKSTLQSLATLS
SHLQPVTGVCWGVDARSLVSCSVDKTVKLYGTA*
>TCRU_10616 tubulin-tyrosine ligase, putative

MDAQSFATADVDPTVPRPKEEAERQQRRHQDTEQSEKQEDESSLFFLGESAFSVYEEMAA
QLRQLGWREARSKGLIVQCDLVLGDRFTIPYSLLRCERLPATSRYGGYRWINYFRGSHRL
TLKASMARILSGSDATYDEWMPSSFVLGGDQKRRPDDREAFLRWVEQHPEGTWIIKPSSG
SKGKDILLTRGLSGIEKFIQELDPSSRSIFVAQRYVDRPLLYRGRKFDVRVWAFLKTPYD
IYAFSQGSCRTSSVLYDADNFGNTLAHLTNHCLQEESPQFGQYESGNELWFPQLSAYLRE
VYKEDVFGKKILPQIGNIILRTLLTMKGELEVLPDMPYKCFQLFGYDLIIDEQLNVFLLE
INGSPGVATKYLHPVVKETLAIVSGDDALRVWDVDTVRFVKLWGVGDALPDGAARM*
>TCRU_10617 hypothetical protein, conserved
MPRDTSKNEAAGPTEKSDDEPKKEPIMSRAARRRAKKPQVTVTLEMRQAARERLRELRRH
LRLLKSNGARRKVAKAEAKKREREKTEAEEVCARLDVGARPLKKSRRE*
>TCRU_10618 dynein heavy chain, putative
MKKGHRGPSTPTPAPPFQHAVVVPEELLRDKTARERRAITRGYLAQWRLEEREKPVIEQL
VQQKMTESAAQASWRTRVSQLPPVRLPKMSDATAAPLPVRMPKILANSLPSLRAASPPTT
LESCRRVTPSPPSPQPFSNTATSSATVQTKTTAMPGPAYTRTYFQLEDFDNTDFETRTPQ
EWVLLGEKDGGTPARSRYFDKRSNEVQWLPCRVVAYDDERSCYQVVWESNGCSKWTKRLN
IIFDAEDEAVWHERVRQAEAYRAETEAALRGRMYLQSLDGSRIAPMDQDQMDRIIGLVAK
RFPLTALRLVEQCTRELEELYYFSLKRAQHWREMASPEEQRRVELLGLPPPPPSLLPSTT
LSAGSGELPPSTLRGTIETPSPNFRVARNFIAENLFQTHALLHDTVYAIHNQWNEYRGEL
LCITQWDPRETPIGLRNFEELQAHRGFSISEKLHNEWSVNVRCTIQNNLDMHFKFYEDNL
ERYKVSRMSRFVNFVNVMMNSQLRGLLLNSLEEFAAFIHRYRVMPSVDDTPMDELQEDLE
EAEHWRRRQEEWNERQRAAMAEAEAEQARNAGGGGRGRQRKSVAPPPEEEKEKEVPFVWR
LGTFCNRLQYTKRVVEMTMNPKGLRPLFVLNLVEDSGRVVFSPSLEDVSRKVKAVFEGCF
ELVDKIQGMGDQLFPLLPLQPLALQPLDVFDPAVCEARSMVEKALAENVEAPLQLQQMYQ
TFEYVLQLDTRELVEEVNARQLSLPDFDWTFERLSRDRERIVRRTPNHVKYEMFFIDCKG
IKASLVAKATDIQSALMEALAERMRKTCSNMISEYNNMSERMALESRSPEELQEFRDFLD
GIPARQEQLNATFETLTEGFDLLFKYNYEFSADACNDYRTAYEWPRHLQQELEDGNFRSK
EYRSILMQKLRDNCETLTSEIVQLGNVVDDFAHFGDDARADAYHEQAKALEQRIRDHQEQ
VQLYNSHETLFGLQQSKWPQLKEIRAQLEPYSLLWEVVSLFHNESERWLNTRLSALEPLE
VDRQLMDWLKKIAAVSKKVKEAEPMGVLKRIRAEIAAFKPYVPLLYALRSNLQGSHWKAI
YQACGVPKEKQSQGTGGVDSNEWRPFNEFIKLGMLDFLPQIESIATVAQKSFELESELMA
MEVEWKKLLFDMEPYQDTHKLKANDIMQLTLDEHILKTQSMLGKPIVRQAPALQARVSRW
EALLDKIQCTVDEWFKCQGTWAYLEPIFSSADISRSLPKEKQLFLAVDESWHKIMELTRM
TPQILTRCQDETLLRVLTENNNNLDIILKKLQQFLETKRMAFPRFYFISNEELLQILSDS
KDPYLVQPYLSKCFEGIKRIQFADAHDILAMESSEGEVVQLIRKVNPGDYQNLVEQWLQA
LEKVMRDTILDQLRQATGDYATRKKRTEFIRAWPGQVVIAVCSLYWTMEATEAMSSEGTV
GLTTYHEKCVGQLDDLIVLVRDRNLAAVERCTLEALVVVEVHGKDIIGQLSEKGVDSPKS
FDWLAQLRYYWEEDHLYVHQINASLRYGYEYLGNTGRLVITPLTDRCYRTLIGALHLNYG
GAPEGPAGTGKTETTKDLAKALGKYCVVYNCSDQITAKDMAKLFKGLSQSGSWGCFDEFN
RIEIQVLSVIAQQVAVIQEAIIQRRDEFLFDGVQIRLDPGCAIFVTMNPGYAGRAELPDN
LKALFRPVAMMVPNYAMIGEIQLYSYGFLHGKELAEKIVATYRLCSEQLSSQDHYDYGMR
AVKAVLTAAGRLKRAYPDEDEMVLMLRSIQDVNLPKFLTQDVELFKGIISDLFPGVQLPE
ADYVHMHNGLVKVCETRNLQLTEYFELKIRQTYEMIVVRHGMMLVGFSFGGKTKILQCLS
EALGLMEAFGKERRTRLMTMNPKSVTMPQLYGKVEPSGEWTDGILPYNFRRAAQDTSTDR
KWLVLDGPVDAVWIENMNTVLDDNKKLCLQNGDIIPMSKEMNLIFEVQDLAYASPATVSR
CGMVYVEPDSLGWRCLLDSYFNTLPETLRLDPDIMTALRSLVDLFLPPMLEVARKQVKSV
IPQGALVAISCFIKFFSALVSELDADENVPVADAHTEARTLLMKVEGWFLFSLVWSVGGC
LFTKDRTTFNAALHAELAAAASSGSYKFTLPLIENKRSFFDVRLETEGGARLAQWTEYVP
EFTIEEGLEYQDIIVPTSAQTRYAFLTRLMIGAMYPVLLVGETGTGKTIMTKALLKGLPE
DSYSTNMIQFSAKTTAGLLQRLIDGSLEKRRKGFYGPPINKKMMIFVDDTNLPQLEEYGA
QPPIELLRQFFDHGGWYNHTKDSIEFHRLVDILLLCAMGPAGGGRNHVTQRFTRHFNSIA
IPAFDEATLRKIFGTLSEWILSKGFPALLRGMSGALVSATIDLYETLVDKLKPSPEKSHY
TFNLRDVSKVFQGIDMANPSKIVDDRKLSTLWVHEVSRAFADRFIDEKDTSWFLGEVGKL
SMKHFKLAPENLHDVENPTLFSTFMNDEGYYEELPNLVDARKTLESKLDSYNMGTNSAPL
DLVVFNYVLVHVSRICRVLRQPGGNLLLVGVGGSGRRSCAKVAAYLQECDYMTITQTKDY

DHNSFLDDIRLLLLRTGMNCYATMFVLSDTQIASESFLEEICCLLNTGEVPGIWDTKQDK
ETYENAVASLREKGRELGRPDTAEALQALFVERCKKFMHIVLCFSPLGSVLRERLRKFPS
LVNCTTIDWFREWPEDGLRSVAARFLLRVELTDHERQAAEEMFVAYQQQVRDLGKTYLAE
VRQHTYVAPTSYLDLLSTFARMLEEKRTELTAMMHRYANGLTQLKKTEDQVEVMQQELAR
MRPQLAKKQEETEELIKEVEMESKLAEEQRAVVAVDEAAANEQAAAAKEIKDASQKKVDE
AQPLVEQAQRAVLDLDPKALQEIKALKTPPQGVKYVIEVLCTLLGGSYKPKPVRDPLTGN
VSVPYWEHAKLTLLTGEFKNTLLTAYPVIVDTAPNEQIEDVKKKMTNDMFKNENIRKTSV
ALLGVATYIRAVVEYYKQNKIIKPLLAQAAAAQQEYDTAMESLNKKKEELRIINEKLAKL
TSHLDRVRKDKQDLEEKVNDTDVKLTRAKKLIEGLGGEKVRFAKESQRFENELKYVVGNV
LISAGVVAYMGPFLHKYRAKTTQTWLDMCKKHKIQVSEDYALAKFVGSPIDIQTWRLQQL
PSDGFSIDNAVIVKTSDRWPLFVDPQKQANNWIRNMERANGLIITRLSDPDCIRTIRGAI
TEGRPVLLENLEETVDPVLENVLLKRLTREGNVTVVHLGEPVEWNENFRLYMTTNLPRPH
YLPEVSTKVTLVNFMITQEGLQDQLLQRVMMSERREVEEKKQALTLEAAENQANLKRTED
KILAILSSEGNILESETAIEELDSSKVQSDQIAKRQEEIEAMERISDRTRSLFIPVASLG
AILFFCVTELANIDPMYQNSLNAYVAIFQEALQQSEKSEDVDTRIENIRTTFQKSLYRRI
CRSLFARDQLLFSFTMCLKIYDADTAQLRWLLMGGFEADDELTPNSFASWLPEQNWKLLW
RASTQIPLLSDFIKIVQGNEEFFRDFYEASDPLAVEPPNIVGEKFGGLLQLILVRCFRAD
KIVPAVTDYVRNLLGKYFVEPPLYALEDVVDELSHDPSIPLVLVLSPGADPNLELDRLAE
RRGMSSRLFKLSLGQGQGVFARQLIEEGVRGGHWVFLQNCHLYQDFMPELARIVENYSDS
GAKAKLNDQYRLWLTSLPSETFPISILQNGVKLVQEPPKGLKNNLMQSYLSNPVADPKFF
NSSKKPSIWRKMLFGLCFFHAVVQERRQFGPLGWNRMYEFNDTDRRISVRQLNMFLEENE
EVPYDALLYLTGQCNYGGRVTDDWDRRCIVATLSLYLTPLILEDDYVFSSDAPNYYAPPF
GEYESYVEYIRGLPSQQPPAVFGLHENADITKDERETRVLLEATLLTQPRESSDADSKLD
PKATVKDLAHHVLLRLPKLFDIEEIQRKHPIDYSQSMNTVLLQETIRYRRLLLIVRQTLT
DIQDAISGKVVMSADLEEVFNAMYDGKVPDVWKRQSYPSLKPFGSYVSDLIERLGFLQKW
CDEGPPPMFWISGFFFTQSFLTGVMQNYARKWKVEIDKLVWKFSVLAEETCTTAPEDGCC
IYGLFLEGAGWDPVNAAICESRPKELFMKFPLLRLLPCRSQELPDTPVYRCPCYKTTDRR
GVLSTTGHSTNFILTIDLPRHPADSENHWVLRGVALFTQLPF*
>TCRU_10619 RNase H, putative
MQKTYSTLARIVSGVPSTVDPESALLEANMPPLHVLCLRARLSIFENTRACQMDWMRRLP
PEPPPRAGFRISPLSRDELYAFVDAYTKDYGITESSPREERFFRSSIPPWFAASAHRVTI
GVELPIDHSITDEEELIREKRRVSEEALALHSHRSWMLATDGGVDVPKSAGVGILLSSLN
SSEIIEKASINCGARPCSYRTESRALLLALEKLIIPRIRHRHKTLLVVTDSQSLLAALNK
GPLSQTDWTEDQIWQRLLTLTCAGWSVRLQFFYGHCGVHANELADQYATQAMATGQYTEQ
GIAPLWHTDLLTCFTTQLTNKWRSTIRQDTHRYLLCGTRPSDLSGKDLITQEVLHRQELV
HLARARCGGSELWGRLYWAVRDCTNQCRFCNVSPEQSAYMRSNNDPTAPGTDTVPPSARE
EDVSPVSRRTLTRRRKEKCPHCDSTLTGFSGLVSHCRSFHPEHPPPLPELKCDFCDMVFP
TRRSTAPHRIRCAQNPETTRHRNSSARRRSLLPQDQQASTSTPIGPQETLHHLLLECPGT
LAVRQRLGIEQDLRLGKFSQWQLLHSRKLILLFDHLLGTQMALYS*
>TCRU_10620 Reverse transcriptase (RNA-dependent DNA polymerase), putative
MLLGGGQHTYKTARRAANALNRIFLPFHPSHKAVRFSKGINRQSASLNINASFLFGQQNN
NESAASFTSFSSTSSSSEPQNNNESAATFTSRSSLSSSSEPQDKNEAATTSGLVAHLHSP
LDAPFNRTELLAALRNTPYGKAPGPDEVYSEALRHISSKGLRFLLRCINHSWTTGTIPAE
WRRATIVPLLKPGKSPELLESYRPISLTSIVSKVAEKTVLKRLLWVWTPHPHQYAYRSMR
TTTMQLAHLIHEVEHNRNHYFQVSLPKKSGIGNQLHYRPHRTLLVLVDFSKAFDSIDHRV
LSRLLANIPGVNCRRWLRNFLCGRYAKTRVGHRHSDRRPMLRGVPQGSVLGPYLFSLYVH
PLLDLLNSFAGVTADMYADDLSIIVKGQSREDAIPTANMVLQKLHAWSQENGLAINPSKC
EAAWFTLSTHTESDYDREGKWPLVVAGCQIPVMTMGASRTTKLLGMDLDPRLTLNVAATK
QCAATSQRISQLRCIAHKEAGPSPHDLRTFAIGYGASNYAMAASSYGQ*
>TCRU_10621 hypothetical protein, conserved
MPHPIFQIARRDLREGQWSLSVNNVRPWYDELPTSPLWTSYMRKANEVAREVRAVNVGAE
NVPSGAIHDFLPHARTADERGELCGLFDGNRSGAIDPTAARQDAAVHVGNVSDPAGHYDS
GVTKNCGAIGDAAGTPRDKGRDGSIYPQPDRLEGTC*

>TCRU_10622 hypothetical protein, conserved
MAGGVPSSAARHSSAAYRLPHGHFGRPHFHPSTPLPSRTSPLDARLPMEEDRSFCAFDVT
TWPSRIWNEGASGVIIDLRCAYQCWQQDNEQVKLAFDNLVVWIGALEVLQDPTDRFMNLG
RSLLNTFRMQLTIASDPGIRLFKLRARLHTAVPQTDAYARTTQTLVDRRETQRTVRCPRC
HIFGHEASTCNVRPRGNYLQHRRPSKNGRGAAARRS*
>TCRU_10623 hypothetical protein, conserved
MLAHGPISKAWQDSTLIGHIANLRAPQIPNFETQALQPAMGTARELGHQQGLITAERERL
NFDYANAVADVRNWNAQLNSQVQEAHINLSVRESNIAGAGNQVLELRQQLEAVARVLRER
EFNLGVLTGQFQEREARHNALQTARDAETAGGTSPPLLDKLSMMA*
>TCRU_10624 Thymidylate kinase, putative
MINSVYHSKKACVEALRAVERLQPSWWTPPCSEFLHRVEQTPTVTAQPNQKTLIVLEGID
GVGKSLVAQSLIEKLGDSAVLIRTPHPDLSGIRETFRAQTEETARAFYSAANYLAAWDAF
HATKERKFVVFDRWWCSTCAMALANSCRLAALPAAGDAVYQWPQDLPPFQLGALLYVEEH
IRQARIRQRAPEDAEERRLRAQQEMREVAMEAYRRFGLLNEVHVATYGVAVNRILALMTE
KGLPHSATPFSAEELAALRQI*
>TCRU_10625 Glycosyl transferase family 11, putative
MNSRAYLTTNLVGGLGNQLFLVANLLATSRRNGVPAVLKRLPWSSSNEKPRDVYWQSIFK
DLDAYNVGRDIPVNLPEVIVPEQRPVAPVQLDATAKCLYNMVGFFQSEAFFADHPVVRDV
LPSDLRNAAAKHLYDNYGDPSTLQHVGLHIRRGDYLRMRDVFEILEVDYYDAAVRQLLGH
SLQLQSMGRGGEGRGGAHLLVFCEEERYGLSVVGYFRSKYPGLEASLVRAAGERVPFECG
SHAPREVLELLMLSSCDDVVMSNSTWSWWAAYFNFRPLRRVVAPSKWFVQHPYPQSNHLY
CENWILL*
>TCRU_10626 Mucin-like glycoprotein, putative
MMMTCRLLCALLVLALCCCPSVCVAKDTPVQASSQMTTNSATQASTDNKKVIVQPDGKGS
SSFSSATVGLQGKDQSEESLALVPVGDKGTKADAGPGAPTPEKQSKNQNNVVNAEGKKST
TESQSGTSSSPENEDNKAEDAPTKTTTTTQAPNKTTTTTTTEAPTTTTTTAPEAPSTTTT
ETPTTTTTTRAPSRLRETDGSLSSSAWVCAPLLLAVSALAYTALG*
>TCRU_10627 hypothetical protein, conserved
MAMTMTGRVLLVCALCVLWCGACGVYARELDNKNAVGDCMASGVLGANRLRVPSVCDKVA
ISLPSRMVSFITAAEASTNDDASDVVEGNPDSPSGAAAAGSVSGGVGGAGGSGGGGVTSG
GSGNSAGGSDGNRNTSEDPKGGGGGFLQSPPSVDPHSPRIPNGVGESQNTEVSLSTEETI
SPEAAAEPGSTASPGDTPPKVETQDKSEPKEEDKDPSFTQAAAPTSVNGKASTGERNQQN
DVGKVDHSSNQTPPPAPPSAVTSPVLSKEPAPPGKEPSPSNVSLPAPNVPQTTKGQEQKP
SILTTKKESKTPEIPSEDNVLQQQGQNTTTEGLMENSSPGSQARNTEPSTSTSGTGEAQI
TADADNAQRPNPSESQDDLEGTDINNSPTADEAAPQSAITLTTAQKNETATVGDSDGSTA
VSHTTSPLLLLLLLVACAAAVVAA*
>TCRU_10628 hypothetical protein
MIPCRSNQQQHQNISNTRGSDYNFTEFCDGRNSSAPVRSVVAGDTGKEQCSQQQNGDAVV
MTDIMERTGASTSAERETNCSERSLLKDNKIPVLSMSEFTTVCPQFVVTPTIAAPNTPNF
SYFNAATPCLERSPLLSSSFYASPSGCEDEKSLGYSAAVFESDGEKDDDCVSLKSADKTK
LKAPYLINTSPGSIAAIELALLTNSKEDEHTQSDGACSIGKDLESALEEQGGYGTWHLVT
SRLKAVHLRHMAHKYALEVVRQRYGDRIIDDSSK*
>TCRU_10629 hypothetical protein, conserved
MSTLSSLTAPLLLRQRCRENANAVTDDRERDDTSASIVLYSFPEDFISCMCGNAPQSCGF
DRISRIGDSVLDTQASDIASSPLRLPHEWTFASSPFPDTAMGWHAVRTNRLDYVLQMWSQ
MTAHLLSPSMNKGMGVSFFPARLPNCIVPCLNDHSCNSTYHEVRAHIPIHLVHSPFLDDG
SVGNNVEDLDTLMKFSTSRLMYSRRLRSLIHDGVMSFMSVSVRCVPTLTRDELLQAESTG
TFVGDGSKDEDTLDCTCSCRTMNFKPIHHLLLPPCTALEPPTPIVLTLRIENYDKPLEAD
KEDESKTSTGEGVREEDVKLSIHAVVRVTRTRAGDALRWKPEMLAFESLTSLFPMRFAVL
GASAIEVGEIGVDGRVPAWVQRTGLEVFRAWQQLRDTWDRLPPSPKPLPPRILTATPSGS
VKTQHDPYGVLTQSPTSHESHTMGSRNPESMEEGEENRSVSGDLECNGSNLFLHKMDRVL
DPLTESPETTGVEVAGTSVVGEEEEGEEELVMDETKHAILSLAQDLSECRRRGTETLQAV
QCQLFSLLSPLASEKQITSCRRKNRGTKYGNEKETGALNFFCLFFGTIAEAENGDEILQQ
AITTLSNRCHGPNNTYATFDECVKDAAEMIQELESRLRAEPFVIMSVRQHHSKNSINGGA

AAKNGRKRKDGVSLFAAAAKCLATGNNRPSGAACKRSFGKSNGESDDAVTVLRFSSSAIV
GARQAIGDTLEKLRMAVAWGRQRVMDINFIFKVCQEVIVPCVEAHTALAKAEQKERAQLQ
TDHLLCLAIAREAISAVHNATGREGEKVVIVGEEKTEEGEEKKKTLEDAAGARALNGAIR
TCNEDTPGVVTAGFEKQDEEVKTGRNECTDGLKQTSATDAARPASFADPSVAIAATTKKR
RKNGATSNPNPRPQLTGLRVPAPVVNTPLKKRKNDGNSGVKKSFFSPKEAAIQMGVLNLA
FSVFLFLCVLGAMAFFFP*
>TCRU_10630 hypothetical protein, conserved
MSWRQRTPHGRSAEVEDSIQYLQRYFDDAEPDKRRPQLFSPTKEGGVVAAGVLPASAARR
ERWAGYTRGAASPGKINDQSLRSTRKSERGISSSRMSLSYNRPSPLRGEGPLRNERSPPI
RGERTRATNLSFYEPLSLRYGYTTNTPVGRPPLHHQQNVIRGGTVAQKGASSGGLGGFSP
RRDDLNVRYWQHDGKNARQRHPESAVSHGRWMHDDPDSTLDIENAEKSRYMYSPRRRHSY
QKEGLLDESKNYDDNEESEEEEEEKQKRRKKLPPSNRVYTRGEGNGGERHRTTGDDHAPE
GGVNAPTAEVTSHSMRHATWNELPRPLEKRPEEAARPQDVFPYPKHEDNLRSMLFYLKNY
YALEPEESLRGIETMTPEDVLGLVQCFYVDAYRVVRHARDVAGVGRAGFTDKDPPMECVM
GLASDGELTMRTKDETEDGVAVAEMAPPRQPSPPPEIVNHSLASRRPPSQEYRRQGAAMI
SGSSGGGGGGGGCVARTPLGRPYTPQSHARLEHPTLDGANTSFLTDGTLLSVVPPQEPSS
GIIKRPLKELMPILRSGSTLCKHVENGRPHTRFFRVEDYLGEHRGEEALMPHLVWYPTAT
DRKPSEALKLLSLLGVHLLTSDAGGAFRKLFRRSRGVVLDHSRRPVSDGMCVVFRFEKRD
VAVSFLTEADRQLWVGGMMGVVEKNMQMASRLHQ*
>TCRU_10631 protein farnesyltransferase beta subunit
MAAYVGSVPPATLTTLAQREVELSLLQFLRQYHPKVDELWRTHPDAEPMGTAEEMCMDAS
DDCKSDHLPRLHRELHDRYVQGRFLFLGESTQGLYSSQPWLAFWALQAADMLDITEKLYE
HVSPDALGNFILGCLQEVKKSGTSNDDDMRNNPMDMDEQQESVLLRNPVSIFDDDNDDGK
RLVGFAGGQLAQIPHLAASYAALCSLCILPRTTYLRALPRAAIKRWLLSLRCKDGSFCMH
TGGEADIRASYCVAVMTVLLQLNDVPAYTDGRDDTVLTEQTAAFVASCQTHEGGFACGLN
ASEAHGAYTQCGLAALILMRYPHLCKYAALRRWLSARQLKFEGGFNGRTNKLVDSCYSYW
VGASHMLLRVGESYMRLLGQTETPRCLTAREALLLDHAQLIDTTSMCPMDDDAWRHAEEI
HRQRTAHVEAYLHAPSHSTWKQQTVTQSFLDEDVGDFYFNQRRLLLYVLSCCQDKEMGGL
MDKPGCLNDAYHTCYSLSGMSTAQNLQYLPRSCTNETLMYATALRRGYIPNERDDYEIVL
AVHNSNRGVGCGCYRSQERLSPLNPIFNICQSRVLAALRTWGVKSFIC*
>TCRU_10632 Golgi complex component 7 (COG7), putative
MHTSMEAANAAEVAELRLDQLASEHVDIKRWINTTLQGLLCAEGKTAESEADVEACVTKL
FNRLQSHLQEVSGSVEDTIAQALVRLPRTGLEVGRMATEAQQLQSQMQSIQEVAQSAVEA
AAKPYFSQLNAFKKTQEKLTRCSDTLRKASQVESSMKQLDDLMQQLRISPSEVDMDAVAG
AIGEVRRNLAELRKLEVTFGEKQLEAVERYEPIVQHAVEVECMDVLRRREVDRAVQLLKI
LETIGRAEAVLQQYSVESMANEKERVERMLIGSTSGATISPARAAELLKSQLMPSIGYAI
SDQLDYLLRMVQLEGGANADTLPMEKNAAKPHDAEALTVKLMRFMVDEVTGSIAYALGPI
LERVERNEELIACYDAVRQLKLEEDIGTHVLGVGPMGGGHNNAVGSSDPLREKLARQVTT
YAFSEMVGRFGKASLLEAFAQREASLVANIIVGAPKHTLRREQFQAVMNVVIDAVKRIVR
FFPEKTLPMCIGKWREALLEMISRLRPTPKTPQGILLGNLSSARSVVWQLLQNAAKATSE
YLNSPELQRLYPSLADAVNDQLRTQLWAPLTEALDDCTAECQRAAKRTIIEPVVAKANGY
DSQPSWGSKQNEEDAASGMSPPASYTPAQIAPSELVRALGEAIVEIPLALEALRGDGDGR
PNGIEDLLEEVAGNWLEDIVRTAVADFIENKVGNITICFPSGVPDAAKKEAAAVEQLTTD
LNYLKSILSAVSGDPFEELERTLAKLKAVALPSGKPITIRHLLSGGG*
>TCRU_10633 Zinc knuckle, putative
MSKDCASDIDVKNAPCFFCQQAGHRANNCPLAPPEARQPCYRCGEEGHISRDCTNPRLPR
SEQSCFHCHKTGHYARECPEVIENLKCNSCGVTGHIARRCPERIRAARAFYPCFRCGMQG
HVARNCPNTRLPYEGQLCYVCGEKGHLARDCKSEAPLVA*
>TCRU_10634 universal minicircle sequence binding protein 1
MGDRACYNCGQPGHLSRECPTRPPGAMGGRACYNCGQPGHLSRECPTRPPGVMGDRACYN
CGRMGHLSRECPNRPAGGFRGVARGACYHCQQEGHLARDCPNAPPGGERACYNCGQTGHI
SRACPVK*
>TCRU_10635 Glycosyl transferase family 2, putative
MLMVFFFGVEFLLGDDPAYGFGVDPTRADYIHCVGERLLVDPTTRWMGGNNGTDVIPLMV

VPLMLDLMDFRRMMCNINVPIRLLVLVQNGREAMLSLYLQELERVYGWSGRLVVSRHPEN
IGYSAAVNIGLRLALSLPREEVPFVFVTNSDVEFSPDLLPSLLRDVHEMTRHDAARMDEL
SAEVANEPSEYSPVLRRGLRVLRSTVKDDRLSTSALLPDRVRYASVKEREKAFSKHYGHF
CAYYKSSCFTSVILTRLAISTVGYFDENFYPAYVEDVDYGLRLRLLGFQERNVLYGKFAH
RSSYNIGLSNKVELPDALWYRRVRSLSANDAYAMMKWNRPRACCGGYKEPYDGMVPLDVW
VKDEARIQRIRAYGHDEEQGVPKVEYDRTLLHPVRTKGR*
>TCRU_10636 BNR repeat-like domain containing protein, putative
MLLAIVGAQFNRTVGSGSASMQLMAWISVDGGRTWQSYAGPEDRDAFSAHPYRLPFPSSF
GPFGPLFAFVEGYDLRKGAIIRFPDERRSGVESVIHFLETGPGRSGGLSMNSFSVSIRPP
YPYKSDELIGFLNDASTPITRMKDGTLVFPVQFLTFGGDTASTVMYWNSV*
>TCRU_10637 BNR repeat-like domain containing protein, putative
MITSCKYGRRRVYESTDKGDTWKEALGTLSRVWSNSLAGLGLHIQSGFITATIDGKKVIL
LTQLEYPRHDSKGEIHLWLTDTNRIYHVGLLATGNSATSSSLLYANDKLYCLYEAGVGSN
SGAFFLDLTSELQRI*
>TCRU_10638 retrotransposon hot spot protein, RHS3, putative
MMLASDKGWPYSWNRKGAESARDCYVNCEVDRVWQIVKGDLTEFFCTHGRTDFTPKRRVL
IGTPGIGKSLAAGSYLLYRLLHYDVEQLQVVVYFIADRKFLFDKTSRTVSTYMGDSSNAS
FVGSLSDRGMKGYIIYDVAEPDDAPSDDLPPRGWGMVLVSPPFERNYKEWVKRRGATTIV
MDCPGESDVKAMCVWMRRHQPVREQAEYWQVVKSHMDEVGPIPRYIFDERKYDNWVQRCH
KTVDEATSSVIAQYSGLGRDVSWDRTKVLYWLARVVRVRGKTGGSEFIFNLPVSAHLGNK
TLFKSAKFMQQLDFNLLISWLRDYLISENFGRSTVFAFLNGSFVSAIERGLRELSPSPQR
QSHRRALAVYSQERSTRHHVLPPLEHFSERIDLECGVLYVTEVENFPLVDGFFFVKSNPM
TLVGLQMTTASGHHTTTSTVRQFTEYLAAYFNGWEELSRQLSWEMIYVQHADSTPMNDWQ
RCDVVDSNNVSGADNNEIAAFWNEKVRQYQVSISSRDAPRRS*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MVYPEFAQAVGGGLSWLCYRNVTFSGGDMCLTVLIGAMTGDVVNVTFDGCTWRDGAVLLL
LGNAHAAVGALSIFVTGNTFSDALLSPEGVFPPHTNITISGNRFTVTRLIPRPGLDIRRP
SCVVMNELAISNDSAVVLSGNVFQSVTASSSAIYVVKYALRVSWYSVFAVVGNTFHMAGG
DGTLIYLEGPRYSSSLSVLNNSAVVIRGNAVTRPVKCFVLLIWALRVESHSAVVFQDNEM
QRSSVVFFSSYSSNIYYNSWLQLSGNLCRESPSDAFAFLYPKVNLRDSTVSVSGNQFMSS
TVLPTMLLIPTVSSDITNGAIVAACNTVNGEEEANYVIPSVYNATILTCSDPCALAASCF
PAYTTTASSDGCACRCAEGGYGDACLPVAVPEPQSTDGADLCVREVRVDVKVNAGFGTSV
ACYVGVTFAADVVVDVASMSGSVRNVTLANCTFVGGASLYVVGWLSDPPAGERADVLISG
LESRSGGGVVVANRFPPGSRVTVLDSVLIAERRVAYRNAYDLGDGFACLVLHSVNLTGSV
LTIARTHVAAVFRDAVGVLVVGGVALSSRGALYVDGLLVQTALGLCVSVEGGVAASGGSV
VAFVDSDFLLCKHAVSVRGAVSVSGSAVALVRSDFLLTEDYAVAFYSTVSLADGSMLLAK
GNVHDGVSREMLYAAGAVTAAGSTLSFVRNRALLPRMLSVSLSLAAGAHLRVACNYAGGR
VLSTAEYAAAGFGDAGSIDVVGCDVCDRDTHCYAPGTTSASMRNGVCVCVCGSGGYGEAC
VPVGAPALPPAVDTASSVFVREGVTVRSVFFVPAGASEVTLRHVVLDGVSPVLYVPWMAR
DGVRIVVQNVSLLNGAVLYVMGGGALRGAVAAGSDEGGPVELSVCDVEALNGALVLTGTF
PAGSVLTVTDSLLVAARPAPLVYPPGSQSSPYAPVLVLSGLRLVRSVLVVSGVALVTVMT
GGRTVVADGAVLELVGGGVALDAAVLGGDVALYASARVVASGGAVLRVSGSQVYAAHGLV
FDSGVVANASAVVVNDNAGALTDGALLELRGSASFVSGSWLSVRGNSIRGRLLSLPSYPR
SADLAQSTLTLHGNAGSGSVVMDGTVALGGAGRKFVVGCLALNGQALQPMDYRSAGIMGK
FRPVACGVCDADVHCFAAATRAMSASCACRCADGGYGRECLPVYLPHVDGCNRTLLRPPL
SHTATLMATRSLTPTWKPTPSATHYSPTQYGPTETLQVTETVALSPTRTPTASVSSTLWW
SDVACPTLAVTTTAAGGNLTQNDIRGGGSAVPTLLMVALPPPFRWARDPQLGTHLSFVPV
STAQPSGFGGPWGAMLSNATWVRNATNPSTVLELAVPLHRGYFIAADETIVIRCDAVAVS
GGCKGVLLGSFTIRSNTLPAAASALSAITGVVAGATAVVVVVTGGLGSILEMQAVGVLAR
MPCASAQERASIVALPYLLSVFAALDPLWMVVGNALLAAMFGCVHCGVTVAFQRWRGVGA
ASAWAAMRFPSLTYVVAHAMHLGIFFGSVLALAMPDARVQHRVIGVVGVLYGVAFPAGVC
YFIARHTGASFTKYWQFSGKPLHERLLYPVGYWHPAAQQRMYGGMLTNMRGSHVYWCVFQ
LSVLCVVCLIAAVHPPVGGCHVQYFCMAAVLLAGAGVVAFTNMMRSAFLTVMHTASLVLL

AALCVVSAANHLAPSDGGARAYVVMVLLLTTVLLAVTVYSMVVWYAEDRYWQELREPRRG
GLEALLRDGEESDEETQELHEVTTFSYASGTTVASSYRPPAPP*
>TCRU_10640 retrotransposon hot spot protein, RHS3, putative
MSERHGEGNDDNETSPASTVSQGRRARARAESGGDSGQPAVPRRRVEETRRPQWGLFSWV
EDVLLGGEARGNYMKLNDFLRRHIGPSAVVDERYNVTMEVFLVEPKTYVQDQKLLEEIFN
LTDYQVLQEMRGLRRDTYNVSQMGVRSLKQWRDFERKDMVSPLARRELDAALRGVLKEEK
IQMSEGFYDSLYNARWHHVVEFTDGEGMGMEVREGKPPQSWTYKAVGRTLERDDSVEQSG
APRLRLMVLTSDKAWPYSWPLGPSIRDCYVNCEVDRVWQTVKGDLTEWFSTRGENNFTPG
RRVLIGMPGIGKSMGAGSYLLYQLLHYDAEKLPVVAYSVAEQTFLFDKITKTALHYVGES
TFLKAVEEFSGRGMRGYFIHNVAEPIHEPSVRLLPRGWCMIVVTPPEESARRGCKKQLRG
RRIIMSCPQESDVKAMCVWKKRDQSAEAQVEYWQEVRGYMDGMGSILRDLFSERDTNARL
SAAREPWNGLPHQMLMNALA*
>TCRU_10641 SpoU rRNA Methylase family, putative
MRLGRILQGYRKVHPKNIREAPLALAEVHRGNEGKGIGPIVLENLDAAVQMTPNFSVTGR
QLWNSTKLLRESRHMRRSFGACVFGGASAIQHVWRDYRIQPHVVYVPNTEPTVPAWCLED
ELPTCVVCCSPVDINKSLLSAERGDGYAAEFPTPKTHSLETFLGAHKPSRLGSVLVLVGL
RIPSNVGVLIRAAVDMGFESVLLDDCVDIFHEKVLRASGGRVFSPNIKIFETHGASIPLL
SSIALENQLLPLLALPSREAEPAFQVARRLHESNAARRRNRDPDAGSTDDHLGPMLVLGS
ESKGLRGLEGEWTVPYRAVSIPLPNSFIDSINVSVAGSVLLHAFRPAAEKYIAKTTEALL
NACSAAGIQPLLAKEGWETGEEK*
>TCRU_10642 hypothetical protein, conserved
MFRRRLFLASPSLSSSSPAALVPSTWKTAPPGWYLVPHSTVEAQKELSVAKLFSFLNHGA
QYAFLGQTMALAEEIHCIPRLEWFYTELYFLLPPTPAAEILACYMNDQECLRCGLRNQTC
GTSASGIQWSEELHRRVENRATEDFCWVLTADQRKTEKFLQETYIQWHHRADYLVTRKSR
EKKEFRQDLTLQQVIQEGQERKRRMQQRRLRTEQRQENIASGKATKWDNFTHDVLPRDIR
EALDREGDGMEDVRLARAGSATGGWSRSYRTHPNFR*
>TCRU_10643 TFIIH basal transcription factor subunit
MLKTVLLLDGSEAMNSSADYLPTRLLALRPQLGRFVHAYLDANPLASLGVVTMRDGVAHR
LNSCTTNASDIIRTLEVKYFLFGGSGAMSLENGLRFALSELVDMKRIAKRVRRTEPRAGG
KEAREEPTARLRILLVSSSVTVIDPHDVFGVIKMMAKLRVRVDVISFCGAVHVFGEAAVS
TGGTLYTPMNYDHLTEVLGRLASPDKRHVCQEERPAMIRIGFPVYINCKEPEGGEGGSTN
YVACPQCALVQTSIPSTCPLCKLLLCSAPLIHNTFIAHNELCPVSENVVDAFEGTDKPTE
DYLNERCSLCQYGMMGEDGRPLVWRCNSCHCLRCVSCEKYVRERIGLCPTCIASPL*
>TCRU_10644 SET domain containing protein, putative
MKTRQIPAGAVALKRHCHNVIDALGSRTPPEAFLFRGNAYFALGQPFFAIADYNTAAQVL
QLSGRHQKQCYEALDCFPEYQVGTYPADNSHLHLYVQPYMNERCEVTQVDGVVGRGVVAK
ENLLRGCVVVRGAAPWIRYPMDDGLCAFCARPLPERFFTCINPNCHEEYCSRDCRTMALS
LYHSRSCCNEGLQALELDMYTQMKASGTSTERNAAAAQLLMLRVLAVSVQQQVIPSALSE
LRILSGRLLFSPRVLAHSFLEIYERFTRFCHTATSISYEEMIGVLARVTANCFHRDTCVE
LNLSRSMLNHSCVANAAEELHSGEIKTTRDVARGEELTINYYPQLKNLSFEERSKELERR
GFECHCSQCRREKGVERRNLNE*
>TCRU_10645 hypothetical protein, conserved
MGDEMRASPSDDASITSLSFGSYRPKSQGTPYTSAGGGEAYFNPADLWKYVVRYIRDEGS
RQEASSVIMVGPDYHFRPPQWMEDKNVSIDGTPLTEEERRAPNFWQTKYRQELDVGEAIQ
QVKRVKRMESKHDIIGSFAWVGRRLGWMEPLDEQFARRKAEARYQKLEKDFSENDLENTG
DRSAVHKVGLSTPWKVFMESVETGQPIAKVANEYRSCVDFYGLDPFLDSSLPLIWFSTKC
GMAMGIAQGMVKAIQAMNVDVQFLKASGVGILAILNMSVFASVVKWGGNCALFSAAFCMG
DRLATVIKYRLLPPHDAQKRSTFNYVMGLAMSGGTVGIMPWWILGDLSFSLRLSVLGGFV
GGLLGLTVGTVIGRLVVLNTARLEATNRDLRRYEALLRRQRRWADGEREKLRRQTLVWW*
>TCRU_10646 ubiquitin-conjugating enzyme E2, putative
MLSRIKKQRAETRDAAGQSHSSGGGPSTASSEPVAILRLKKDLDNLDGIRSTIDIPDPQN
MLRMKVTVRPPYPSIWQGGIFEFLLEFREDYPYEGPRVRYLGPYRIWHPNIEGDEYTEGE
GGLRGDVKNTWGVCLSFQTEWKPTMSLRDIIIMIELLFQDPNPDDPLHGTAKQAAQMMKD
NPAKFRDKARRWMRGVYIE*

>TCRU_10647 cell division cycle protein 20, putative
MDFSFSSPPPSSPWGYPDPSSPVLRTPLSTPDRFISDRHSQDNDMSHFFLTTKENTVPLR
ASPDRRGGSVSLTASTHRATSLGFDADGALGAAEGAGSIGKARKYAMDSAPSDTPVLATE
PYANKLARTLFPDSQSTVLGIHSQVLLQHQTPESEKERYRNSLGVVFEENRARNFRSKTF
RVVARAPERILDAADMIDDFYLQLIDWSAKDILAVGLQGAVYLWDAKTCNITHLPCQRPP
NGIFCGVTWSEDGNLLALGTDDGSLEIWDVEMQRITRRLYQHTDRVGALSWNGSAIASGS
KDASIRVNDLRDPVESWTLRCHQQSVCGLRWSPDGVRMASGGNDNQLLLWDSRTFSVRSQ
PVLRLNKHTAAVKAIAWNPVQHNLLLSGGGSEDKMLRFWNTSTGECINCHNAESQVCGVL
WNLSGTELVSSHGFSHNRLTIWKYPTMRRVADLTGHTSRVLHLCMSTDGEVVASAAGDET
IRFWRCFPPCEKNGRGSSRIGVSRGANSHQMSSQSSSPHVEAFIRDELALR*
>TCRU_10648 hypothetical protein
MEHPPSRLHLSEAERQGAVTVPLPSTGGGGDESRGVLTVMCVVEAARRQLRLDDTALQLS
LHGVVLSPQQDLAEVLETLPCETRKRLVFLLSPTPANALDRQERERSKKSKQVMFVESSS
PASTRAELAAMTDGEVAQSLPMHFSPNLERGTQLTTSQCVFLESWLKPNRCARCQCVRAQ
HSVFTPTRQERLQSAMVLARKTISRTRRCQSTEREGGLRESGLPYYYADPHQWEPQRGER
YHGRGESCHEFCALWGSPMLCRNCQRVKETHEIEVKHAVTQVSTTTARRPRSLVSSLVHS
GGNSPPAYARKTCQHLAPSSSSEYCTVCYTQRVKQISRVGPRSPLVDLTPRRQRVSPARP
KANNVADWLAVPAAGKEVSAIQKKDACSSDDKIRRRAKQRNGAESTKEMALTHANNAHSF
SSSFLSTAVAKKKKSILTVPPRRINCGALRKGIPWDLVLPYMTFDDLLVCRTVSSAMCSV
AISIIYENCYYIMDILDIPIRKRELLVKHANRYASIILDALQEKRPCSEPTDAATHPRRL
FHFCILRFLGALQALSPERENGLTERGTQEGRNWAFTDCLEYFPPVLPRDDALALVTRGN
MVGEVCAAQKLLYGEEARVALRSLIEKLAWCDSNSLPPMATQGITDAFEAISVAAAASLV
YICDDTKLNGMKSNTKNTRFMSLGGFFEEHTLMPLVDFLLSVEVVTKMKWRTRKFLDALR
KHHHQLYRSIV*
>TCRU_10649 protein kinase, putative
MGCGASSRVKVPPVCRRSSSDAVSFMPARQTEEFKRGLNANNGGVFGEKTAGADIGFAGV
GWGDDERHGNGHRFDGSGLNSPAGNNLSHGGGPEWNANYIGIRKNLHEGSDDEFDVKSVN
DAEESRGNSSGALTSGDNEAPNLAVFFSKPQECFYCHTAAVTYECQYCEAFYVCDDCMCN
ENCVHDPTHPMSAIYELPSCCSRTCSSSVGTIDDGASSLFYDPCDVCGRVINDVELVYHC
TECNAVICNGCFQANGGAVHEHEIKPFRRSIRSSTTGSALVNKSRNSEGNKVINDYVVVR
LLGRGSYAKVNLVQHHRTLALYALKILRRNRTNKAKRALLGRASSGDDWLREIAVMKFVS
HPNIVKLKEVIDDVEANKVYLIMEYCAKGPVYTAGEPPLPLEKVRKYSRDIMAGLLHFHG
EYLFHRDIKPANCLVDDNDVVKIADFGASSSQMKNLSTEGTLAYSCPEQLSGERVTGNVV
DSWAFALTVYQMAFGFLPIATESLSELRVNLLNDQPIKIPTDADPELRDVLSMMLEKQLS
RRMLLQEAAYHPFFRMEGNMVPSPPSRAPGDDANTGLKDLYARAMDMVTRGRGVEDCFHG
VRAIRKLRRKAHTWDVNSMDNEDSNSVDSGNPSPSPIVDTMDACHPYTSEADAFQVVSML
LETLKKGNIKLIGRPLTEFPSFLTDASSTTTEIRLSNNGFSSVGRVSFSQFMLLREVSIT
NNSLTSFPVEILSAPRLRKLDLSNNRITEVPAEISKATILERLSLHNNRIRYVGMDESGR
SVFSGRCMRHVRLSGNPLTHLPEALQTCPRLELVLDDLPVLVAEWSQLLPEVSVVVVWND
ICPLRVCPEIPVLTSVKGMHLFSLAILETLSIRHVVLPHFGDWLPIGEVTAEDMEHVSQR
VKGDEGELPDKFRRPLQKSLVNGTDDRGSTMPRMRFRPPILRRAACRYLHSYFIIGGTHY
DENGGYLALLNYLQKCIKRGELVLLCFDEKKVTRAMRERIIGVLCELIQENSPNQLDMNE
CIQMVINATKGLYG*
>TCRU_10650 kinase binding protein CGI-121, putative
MERIGDFVVLSYHDVRDAASLHEQFKKRSISAAVIDSAYIMSRLHLVVALHRISSAPLII
GHDDCQPKMTRKSTARTARDVFAALSHTRNLYRVLEHLTCSETTRAVVIVLSAPTEEDVA
AVLDIVQGVRHGLLSLETYRDEAAVREFYGVGESEAAALEVTIVNRLATSDI*
>TCRU_10651 inhibitor of cysteine peptidase
MSHKVTKAHNGATLTVAVGELVEIQLPSNPTTGFAWYFEGGTKESPNESMFTVENKYFPP
DSKLLGAGGTEHFHVTVKVAGTHPINLIYMRPWTGASHDSERFTVYLKAN*
>TCRU_10652 hypothetical protein
MRDGTVGAAHEIWTSTVDMLVSERSSLQLIVDTLHATLDYHQVGRGPANYNNNDSHSLLR
NGDGNVFASEEEVVELLGMLPQVLRSAADPAILQLKERQRQSMTIAGVARPPPLSRHTTL
YRLMFAQAESSLSSSIGSGECGVLDCIARVLISGVGTSGMSSSRMLSGKPRQVFVTANRE

KSWFTGNVTIAALRSLGEIVELCLHDTGEETRVGGSISSAYSGRRMTLLGGEDTVEKYKL
LLDALGKSLCQTGLFDHLWHALLFRPVMNTQRIAIVRVLCDVSRVDLLRLPVVIKRTRHM
MTPAVWGERVSECILSDPTAMVKESIAVMLYEGLQSVLGADRRGDDYDDHVYWRRWLTNR
SLRFLLGVLATGASLAVLQPVLGSLFLVLEQDLWEGATLQRRSGRSVTERIDVTSIVEVC
ATVLVHLFTGPAAVNGRRFDDDGDKQLKRYRFLVRGAVRLLRLALKRVDQLLGSPNIVQQ
PKGGGDAEKEACALLSACVEKQVLAAVMKCLEMSPDGSSMCSFVTRSMRAEMVRFVRDLL
ERASPPLFFLTCKLVPYLPTMLQIILDAREEGVLDDRDCCNADGGSDALPSSQLYVEALC
SDGVEMISLLGMMLWFSPSVRDRFLDVLASLQFTPEQQGVFFDSMESIARSLPSHAVRNL
LIVDATGTVLNEVGRLPWQGEQLQTESLERLLLLQLHRQREVVNREKVADRFTPEGRWMS
VQQQRWKLGPQHGYASRVLVCFVLHHLRNGSGKREVGDDNDDEDEEGEAGGVSVSPIQPS
TCKGTVGQRVGGIIGEPQTIPRCGDETILLRPRCTLPLGRQASRRGEEAEEEDVEEGSGC
HESASDKLWLQRELGSHSPDASRPKLQQTMAAPTRISASVASRNAMDPLERVRQRQLESI
ATEEKAYRVALGLFASLASRYYRHLLTPQAALEYLHRQEHGAPQRRHVNPVSPTAPSART
GVNNSSTTLRLWTARDVCREDLFYFSLPLSAICEAAIADLVERCKRHRQALQRKLRTLPH
SSRGRRWFLQDAATNIMGRLIALFQILLHHIQREGEKAVREAIAQMPILPEVEDEDFVND
LAERYNCRHLTLRELHGGTLVEVTKFIVRCFSRPADPGGEDATDSSFRPRMD*
>TCRU_10653 glycerol kinase, glycosomal
MKYVGALDQGTISTRFIIFDEKQCLVAQHQIPHRQLTPQAGWLEHDPMELYRASVACIVA
AVEDLRRRVPSFEKLEAIGIANQRETTVAWDRVTKEPLYNAIVWNDLRSYEVTANVKKEL
GGGDDLFFAKMNGLRISTYFSAFKMRWMLENVPKVEEARKRGTLCFGTIDAWLLWKLSGG
KVFITDVTNASRTFLMDIRTCKWSPELCDKLGIPMACLPEIRSNSELLTYVLSDEGGLST
ALRHPTPIMGSIADQQGALLGNMCFKEGESKNTYGTGCFLLMTVGERIRFSGHGLLSTVA
YQLGSKSPFIYALEGSIAGAGATIEWLKNNMKLIDDVSDCEKFAQTVSDTQGVVFVPAFS
GFLAPSWDPSARGSIFGMTLKTTRAHVLRAALLAIALQVVDVLEAMEKDAEIKVQFLRVD
GGLTKNHLLMKMQSDLLGINLHRPTMAETTALGAALCAGLAAGVWKSLEEVKTISQQANV
WRVIRPAASKDSQQMLRAQWKRAKQQAKWAKL*
>TCRU_10654 hypothetical protein
MTGERKAKQRRLEKSAADGLREQMRSSWPRVLTVEDDGTGENHVKLCVEHDAPHDHCALE
CWNLQGLIGENERFGLFVSFFRHAVTGEEELSDGEGSVTYAAEVSWVIVDHEKKKYYRFS
ELDHRAPIMAAYLAADGGITGDEYFLQALSEQFSQNRLPLPDRVMKGTTSLHTDMLDLQY
GDNRLTVIPKKTGKKNTSFSWYKLSLSGTTFETGDADPQREVRVVVELTLKPTQPAVLHG
NKGVVGLKDDWGHDMFHYLIPHCMVVEGTFRMMRASDDLEIARCPDLKGAKLWMSHSFGC
AVPRNIGESNYLRKQCQQCGYLPHFWNCCVIHLDNETADAIGVVYALDPAHWKPVDIYVT
LQSGTTGKIEHQHEGVELVAKSTSQHRSDATGILFTTQWTLITPFRDDAKLEVLLDATFP
DQEFTTLFAQPSVWLGAVQVSGKIVASDGTSTGVTGKGFLQCCGKDGLNNVKKMHDMLRE
VSTARMEDLEVGVKDSLNEMVNSFAASATSNVKTLMSLQGQTLSDAHLVLFTSFLGVYGY
IFHHPTGKKEALEAIQWCHGKWLGYFGNAYIDVKTLMLRSFMLRELSYVLKSRCASWIPT
HMQVIDLVVAPPSNINAVMGKDNCSEEEVVPSLPHFGTSPSKLDLSQLRANFSGKWTLDS
TRGTDNISTFLSAQGVHVLWRNLIANTSLNLFVTVDEEKQTMRFNHRRSFWGREFVIQLD
GSYGEQRCASRGTIRSRACVFPGGTGVCIEKKISNQMIERDWYTFEDGGETMVEVMRLYS
DKAAENKKDSPSVLPISVCVRYFTLCLERSVS*
>TCRU_10655 ubiquitin-activating enzyme E1, putative
MRKHTRNHESDHYALYSKNKKFYRTDTSQGFNCNKNKVDTAFVNAETEAAEMSVVEAIAA
PAASAIDSRFLDKQSRTIGTYGLETMVKLISFKVLIVGCGGVGIEAAKNLSMAGVHTIIL
CDPAKAQPKDMGVNFAVTEAAVRSGLTRAEASQRLVSELNPNVRVRVVDALSEAVVSQVN
ALVFTSAAPDYSLGTLKRWNKFCHDHSSPISFIFAFQGGALGSVFADHGAHFTVKDPDGR
PMLQKSIVEVITKQDKTGTAYTRIRYETPEGQTPGALRDYTRFKFTEVRGLCKANGESVN
ENIFNGVMCPNDPRDTVRIYPSLESQGHSAYETGGFLHELKEVFQLEFRTLEEAVVSPGR
FVPVSPMMDGSEESQSHLALHALLNFLDRHGRPPKLHDVSEAEEALSIAKEINIENKRRS
KANTETYQMFLEPENEEFPARLAPPPPPVPLTVDEVDESFIRTQSLVADAELQPLCAFFG
AVVAQEIVKITGKYTPICQWFHFRCDAILASSALYTSSGDYKPTNSRYDHLIALLGKNFQ
KKLESLRVFMVGCGALGCENIKNFALCGVACGPNGSFLVTDNDRIEVSNLSRQFLFREEN
VGQPKSVAAAARMRIMNKDVAIDPRQDYVGATTEHLYHDIFWDGLDVVVNALDNMETRLY
VDQQCVKFQKILVEAGTMGTGGNVDIIVPGKTTSYADGGAADASGGIPMCTLRNFPYIFD

HCIEWSRAQFDDLFVFPMQTVEQLVEDPTAFKARIEREINAAQSSGERLSLVEKHLGILH
PLQKVLSILSSGVNMEKCFQCAWELMFYLFRDRIMDLQRSFPRDAKKKNGEDFWSGHRKY
PTALNVDPKTIASNKDAVEFLIAASNLFACMYGVHPPKHEPRFNDANNRWMQQYRSLEWI
NKIIGKREVPVYHPGAVEGLDDDILDAIQTHDGAKKEETKEEQLGQLLCNIMTLAGSCRG
TKATPLDFEKDDDDNFHIDFVTAASNLRASNYDIPTQDRMKVKLVAGKIIPAIATTTSAV
TGLALIEYFKALQGNDISCLRNGMIDVGTNNYVLFERDAPIKNRTKIVSTYLPEQDYTYK
KKLIRVPDGFTKYDSIDVPITIHTTVQQFATMLENQLNALLPAGTEGSCEIVGIGVGHGM
LWNGSKKHANTNLSLMQLIEQQKMTEAGGKLSQPFWQNRTQFCELSVTVSLDDGDTSVDE
ADVETAMIRLRITQ*
>TCRU_of Trypanosoma cruzi region 4/Dispersed gene family protein.1
Dispersed gene family protein.1
MTAAHYSPTQYGPTETLQVTETVALSPTRTPTASVSSALWWSDVACPTLAVTTTAAGGGL
TQNDIRGGGSAVPTLLMVALPPPFRWARDPQLGTHLSFVPVLTAQPSGFGGPWGAMLRNA
TWVRNATNPSTVLELAVPVHRGYFITDDETIVIRCDAVAVFGGCKGVLLGSFTIRSDTLP
AAASALSAITGVVAGAAAVAVVVTGGLGSILEMQALGVFARMSCASAQERASTVALPYFL
SVFAALDPLWMLVGNALLVAVFGCVHYGVTAAFQRWRGVDAASAWAAMRFPSLTYVVAHA
MHLGIFFGSVLALAMPGARVQHRVIGVVGVLYGAAFPAGVCYLIARQVGASFTRYWQFLR
KPLHERLLYPVGYWHPAAQQRMYGGMLTNMRGSHVYWCVFQLSVLCVVGLIAAVHPPVGG
CRVQYFCMAAVLLAGAGVVAFTNMMRSAFLTVMRTASFVLLAALCLVRAANHLAPSDGGA
RTYVVIVLLLITVVLAVTVYSVVVWYAEDRHWQELREPRRGGLEALLRDDEESDEDTQKP
HEMTPSSYASGTTAASSYRPPAPLQPMAGDTRSDTLSLFDRASSTSCKIDHALL*
>TCRU_10657 hypothetical protein, conserved
MNGSRRCRQGLKHIATEHHRGVIADRQSIHRNTRRPHKAQTRPRDQPRDREAIPADRDVR
ARWKPTLRTEQRVTKCVAGDEDVQRPQSGVRVAQQQQHGTVPPRASIERYVRNVARHRPN
QHRQAHFAPAERHVAVAQPRQPAAHCLRHLGVHHVADALTNRRHWRWRRG*
>TCRU_10658 RNase H, putative
MTMGASRTTKLLGMDLDPRLTLNVAATKQCAATSQRISQLRCIAHKEAGPSPHDLRTFVI
GYGASKLRYGSELIWAVATDSAKNEMQKTYATLARIVSGVPSTVDPESALLEANMPPLHV
LCLRARLSIFENTRACQMDWMRRPPPEPPPRAGFRISPLSRDELYAFVDAYTKDYGITES
SPREERFFRSSIPPWLAASAHRVTIGVELPIDHSITDEEELIREKRRVSEEALALHRHRS
WILATDGGVDVPKSAGVGILLSSLNSSEIIEKASINCGARPCSYRTESRALLLALEKLMI
PRIRHRRKTLLVVTDSQSLLAALNKGPLSQTDWTEDQIWQRLLTLTRAGWSVHLQFCYGH
CGVHANELADQYATQTMESGQYTEQGIAPLWHTDLLTCFTTQLTNKWRSTLRQDTHRYLL
CGTRPSDLSGKDLITQEVLHRQELVHLARARCGESELWGRLYWAVRDCTNQCRFCNISPE
QSAYMRSNNDPTAPGTDTVPPSAREEDVSPVRRRTLTRRRKEKCPYCDSTLTGFSNLVSH
CRSFHPEHPPPLPELKCDFCDMVFPTRRSTAQHRSRCAHNPDATRHRNSSARRRSLLPQD
QPASTSTPIGPQETLHHLLLECPGTLAVRQRLGIEQDLRLGKFSQWQLLHSRKLLSLLDH
LFGTQMALYS*
>TCRU_10659 hypothetical protein, conserved
MTNRVDRSRTPSRTSAGPYRNFSWPRVVGTYCDPPTVARSVEFASSTLEFGGIAPCSTIV
PSIDVTFVMLTRAYGIRRAVLSLRPPIRSRAPPTSTQWRSVTFSASANASIERRSTATVI
GPLNTTESKHAVARPPPTVTDSVSVTPLTQPCASPPPPPDLAGGTSNGRHASPKPPARQL
HTQSENDAVSASKHATAAAQPSHGTTLTEGRPAMR*
>TCRU_10660 hypothetical protein, conserved
MERQRALHEVRTARVRRQRQEPAADAVAAHRKPRPGHERRRPPQHQQRTIRQHTGVVIHH
DGGRVGLHPAAEHQPMRGVHLAPRHAQHSAPRGNHARTRVQRIFATEHSRVQRDTATDKL
QHRAVHHHRPPTSHHGHEGNARHNQHGPHEPQARQHKHRCVRRGLRAGKVHKRRRPRGNQ
QGVRHRQHGPRRKRAGQHKRTVQRLHVAHGQLHRPALVAPRRDRTAQRSTAHHVQHGAVQ
QRHVLHNDPHAVPRHPRHVEHKTHAVQHNMAQRHLACTGRHNEHRPHRHALAEEHTRRSA
HSGRQCESSHRHAHLAVPAAAAHAHAHTVPHARRRSPWRVAVRVPVAGVAPSNVDAPSVA
KTSRSILLRRRQDTATSAVARHPQMRPSRKRQAHRQHPWQQRSVAHKAQRAPSSGHGASG
VEHLPRGAVVHVVLRQQHRPTGQAHRRIKRHRVVLRRRKFVSHKRHSGARHAHSPTHRHR
VLAQQKVTVNKRHHGAAAGRNTALHRHAQPQRRLHRQPVHVQCTARRQRHAANQQHANSV
AEHRRHMRARNGQHAPSQIHAVYHEARGGVPKVVGAAIHNALLRNQHRVHHSDARARRKS

VRHHHAAARARLKPAHQNIGALSSRRVGPPPNNVQARSAQKRAVRQRHVAHAP*
>TCRU_10661 hypothetical protein
MHGHSQLQDGERIRRVEHPRRVAQHRSPRTTEPTRLCRRHRHEAQVRAELRVACPPKRRR
QRHHQPRRDDAPTAANVVLREASSNRRRRHSERRARHLAPPQRAAHRRCGGPRGRQLHRL
RHLQRLRRPVRRRTVVRRAQTRRPC*
>TCRU_10662 RNA pseudouridylate synthase protein, putative
MAHGRSLPAVGSQATVPRKYMRAVRRGMWNLWRHHPGTYAPHGQHHMLDEALRYAAAFQE
RSARRWAEAALGPAQSYRIREPCVGEKGDAGSGPFPTLQHLASLDEEKEEEQIFPTFFER
QQARLHVALQQWVFYSGFRCSQAEFMVRQSKVSKTLLLSPMRVIPSSRSNTEGARCLEAS
VRRRGARAYVDLLVKHKLFMQKEEEWTTLCELCGHIGKRQQIKMEEGGSFQLMALPFLRS
SNPHASWERSLAVLSWAMQFRNHKQQSTHHQQYCQHISSMDISDVLQQYAQHFGERTQVP
LLTHDDDSQGTLVLGNAAEQDVVARLQQWWVAAREAEKQNPRLAGICGLDRTLRDRIHVE
GRKVTLTSSNETSAGVDTVFPELLFQGRWEDVLHHIERIAADYLRRCGPAAEQQQDGEEE
CEEKGSIGQDVAGVFDEMHEERRVAIGDVAPSPSIATENVFAMFFNRPRPILIKGKLWVH
TTASRLGRIPRALLTADETPAEKELLYRPPTAGLRPRRLTIDERNRKEQTRCTEKSPSPA
LLELRRKMWIHFQLPKHVAHSLVRFEGVGASMLPYLYRSPAKELAPWLLVATIAAIAQRQ
EFEGIHEALHRVRMQTLYTLFLPVPYYAAFQEYCAELIIQLGNLLAPPKVLRVAVRSIFC
PPSFRHFYDILKGRRIPMETACRKFWWGSLEDALDAESKKVTCSSFFQSAVSKWERARGD
LDTMKEFFMCKAASLRNYHVSTWIESCSKVETLAGLLDILVQEINFYGPPLLSPEAATAL
LTAVLILHSTEGGENKVSASTDTLRSLGVVYFVVPADRVFSAAPYFKGIYHERYISSTSL
DWTVGWDGAEALLVGRSIRRITKYPTTTKEAFFRVEHRQQGSHDENYFPKVTFRVPEIRL
RLMAVHLLDAARYFEDQGQQLQKDEKRTTTVSSQVKGMMPESKPEIVARHLPFGAIAVNK
PAGMSTTLHVAYPHLIQYLARCVPWKGDDIPVLFQHGLVNRIDVGTSGLVLVTDTGNSLV
ATRRASVVDRRVEKIYRALVLHCPPPESRAGSEEFWYLNPKGVINWNVFANGADYSLQLA
AHDPERKRGLPPAFMDRRPATTIYRVLNYYPSSGVYYLEVQLRSGRRHQIRQHFAQICHP
LVGDGRYHERARSMGEQMGLYRPALHASRITLLPSSLDSATDAIDDASYTRKEDSEKTVV
ECPLPDDIRRALRWLQEKEERGKGTDHV*
>TCRU_10663 Mitochondrial 39-S ribosomal protein L47 (MRP-L47),
putative
MRRCLFVRNAAAFYEFVDNNFLNNKRPPVPGGAWPLESLRVKSLSDLQQIWFLLLKERNM
LHSTREQYLRHQEELGAMPAPSRLKMVQESMRNIKRVVKERDAEATAQATAIFQERLERG
VYRFPPGPPPPPGAHDPTVVVKVILSRRVEADRLREIFGRYDVFEPHKGIVRVELKLPDE
VLRKKEEAEQLWTQYVAEKSDVKEYHRWSASPSVYDYASVELAPGVFANDAVAEMSTRNA
EDDDGNNSNNNSAVVGADIENDKTSGAGDGAIVAARLPVPASKQRPPPPKNPLERIKAER
RSYLARTVIQLGYFPNITMQVPRYATVEEVPRPTHPDEIEGPWEAYITYDRRNGLEYAQS
LGVTTIDGAEVIRIVEHKREPQPYAKVDPVFLEALRREKAREETLMKWPHVPEWKYEYSE
YTRKHLAEIVRHNYSNVVDYVDREVLLTGRSVWECPIDIDYSCGGAKSVPPHAKKPIRYM
DIKISDVGVTDI*
>TCRU_10664 adenosine monophosphate deaminase, putative
MERRQVSAESEFDASVLEDEQPRRDSLHTPVLDGGNTVVAQVLRYEANSKGMRGGIRQLS
STQRDYGGTGQLQMVSPLGGGAGTIISGVHRRRSLRNRGSFINQVRHGGSKQNTYVVQLD
SDTGGIEMQEASQYLLNAVKMREKYKAVDKGQQEGTERLVPPVALSFESGYIQFSGQCTQ
IVPWEQFYDDVTALYITLQHPVCRRACSQRLQVLEEKYNLYKLCNNEIENLDRYRRGGGV
FANSTKVDNGVYLSSIMNPQWLVEYIQEVLELEGGEVVYLAGDTKEPQTLESLCEQLDLT
DPSQMSVDGLGLSPPSEKRLYRYDVLDPELNRAGRNTAELLRLFLTPDTLNKGRYFAEAV
RPIMAINSSRQRSIQATESIIEICGLSPDDWEKMANWIHENGLDEQQNNQWLIALPRRQM
RKETTREPLEHYQQHLENLFLPLFMATLAPEDPKNTQVASFLSRIGGFVIVSDEEERESE
FQRKARRPAEVSWSENVCDLYFAYHIWVNLCSLNAFRRRKGLGTLQLRAIAGGRSSQMDV
LVYSYLLCDSVANGVILDHQPVLQYLYGIQRIGMVMSPLSNNGLGLPYMQNPFHIFFCRG
LNVSLATDRPLLFHLSKEPLIEEYGTASRLYQLSGIDICEIALNSVMISSFPYGTKAAWL
GEALLTEGPKGNIFEYSKVPTARLELRQDMWQTELNIITEAAKQNSRVDDTTTVALQMPV
TAVINAANCSTSTGEYSATSSVTTTAIVQSNHVLLNQVPFVVLDPKIEYPRVVFVGPPER
DPSHTVATQLLHRALELRAQYVGLNRLGEVLDGKDMLNPHEIENAFRRDEAFDENEWMFK
TVEGVLVPHEVHQIPRLPKDMFHYDNFRVHVQELRLILENIHVRNFTTRRLDLLEHKFML

HLAVNRSLEAGTTAKKASQNRDFYQATKVDNNIHVETCMTARHLLNFIVSKANNNGDDIV
SHQEGKEPQTLRQLLQELQISPNTLTVDDLNVQVDTTLGVAGAQYTPEGRDELLTLLLKT
DNQMKGRYFAELTKLTFENFKHDRFTFTENRLPIYGANDKEWELLSDWFDTHGMASFHNQ
WMVQVPRIYSYLRKRGKVNSFAEYIENIFKPLWAVSLHPSKDPRLFHFINHISGFDCVED
ERRPDTPLHIATKAPHEWTSEEEPPFNYYMYHMWANIYSLNEFRRRRKFSTFTFRPSCGE
TGPVDHLIGGFLLANAINYGVTLADDAPLQYLFYLARIGVTVSPLSNNTKVLGYLDNPFP
HFFRRGLMVSLSTDSPLMFHHTQEPLLEEYSIASKVWKLGPNDMCEIARNSVLLSGFDTA
FKRERLGDLFFLSSSRSNDASRTHLSDIRVAYRFETYHSEIGLLEHICGLEFPKALLTLS
EESAREAEFLEAVKKKKEVPLGGIINPQPQEADIDKLQQQRLLMQRQLEELTKTLTELQR
QNKQLTEKLAEEMARDQQAQQMRRRSFEGRWDQIMESEGRKRSSVVAKRIDETSLGRLFG
STIISVLCSPGGAAGGGEEATWDGAGDDADDSNSQQQQQQQQQEQVQQNEGQSNGRTASM
QFNTMGSLGAMAGGNNASNAMSATLGSDAKGIAAVTTALVNFQENMWSRKTGDNDSQFPQ
KKLGSQKGCITSVLPPISTDLALTSFNGASPKKGHSLAKQPPTPPQRSSREVDVQRSAAV
LPHLFQ*
>TCRU_10665 oxidoreductase, putative
MRRSASLFGLPTVRTVAAAGWRYHRHGKPEKVLQYERFRVPFNRSGSQVVVKMLAAPVHR
HDRNMISGNHGPVKALGFPQVAGVEGVGVVEEVGASATLNLQEGDLVWVNNPAVGTWATH
IVTEADNLDVVPNRADVDIEYLASLSLFHTAYHLTNSFVSLQPNDVVLQTGASSSVAQIC
QGYIRARGAKLFQTLQLGRTEHAHLVSFFKVRGAFAVVPYNYVRTNYMRRLLSDVPPPKL
LLNHTCGNYASSVVNLLGDNGVCVTYGSTSGKPMQIANMDAIARGIQFKGFFLPSWIRRH
TREARMRVHQNVVESMTISQGHGIFRAQRFKMDGDSPFAFSNAWDAPLGSRKPILRMVGE
YGEWRRPRSDQAAWNIGRAVWDDLLQQMWESAGTTENPQSMKYYTPFKDIYSHFHDAKQT
KEMGHRDVFFRRPNAPRHNAAERA*
>TCRU_10666 histone H2A, putative
MATPKQAAKKASKKHSGGRSAKAGLIFPVGRVGSLLRRGQYARRIGASGAVYMAAVLEYL
TAELLELSVKAASQQAKKPKRLTPRTVTLAVRHDDDLGMLLKDVTLSRGGVMPSLNKALA
KKHKSSKKARATPSA*
>TCRU_10667 histone H2A, putative
MATPKQAAKKASKKHSGGRSAKAGLIFPVGRVGSLLRRGQYARRIGASGAVYMAAVLEYL
TAELLELSVKAASQQAKKPKRLTPRTVTLAVRHDDDLGMLLKDVTLSRGGVMPSLNKALA
KKHKSSKKARATPSA*
>TCRU_10668 EF-hand domain/EF-hand domain pair/EF hand, putative
MAATRRISAAVIATAGFLFGGGGVFVAYNWWRNPVSAKDCLGQCFAFKALNPKDPRARFH
FYATRNADGSEELDPAGLIACLCLLDEESRQSLESGGGNHLPPHVRQRLEHVFQLMDINH
DSSFSYEEFCILLTLLSARREHLEMAFGVFDRDEDGRLSGHDFLYMLNALMVDPAVQFFN
VQPSLTRQQRMTYSTPGASPTPITDGSGNSKKKHMSASAAVRDALLASPLAEHFFGTHGE
KFISFDEFWSMLREIRREVWTLEFGLHDPRNTGFITLQDLQQIIFRRNSNEIPMGVMEKH
FSHVEGNSDERTMKCVKKEFVSFEFYLKVFDFLSECDAVAHGMNLLLRAKLPEVLTTPLE
QQQRQPPESKTRMLDTSLLNRDEYEVDSAEFYRVLEACKGLSHLTREDADCLVRIFDLDR
SGKLSPIEFAHACELRAKFFTSREPRFNEPQQNVVQRFMTCMQQLK*
>TCRU_10669 Protein kinase domain/Protein tyrosine kinase/Kinase-
like, putative
MAQTRPTARAMRHPTANDGRSCTDRRSTLLAESFPALIGPSLPSKYREPRPLGRGASSTV
WTLIDNVTNEIVVGKLCNLALMSEKNKSFARSEAVNILSCEHPNIIRLLGTYERNEQLLH
ILEYADAGDLQTQVEVRAKHYSRVKNGSGSASRKDAAEAVPCYYKENEVLVILAQLCLAV
KYIHGKNIMHRDLKTSNIFLRKNGLIKLGDFGFSRQYGQSLSSDVGKTFCGTPYYLSPEL
WRRENYNHKADIWSMGVLLYEVMALRKPFISPNMEKLMQCVLTEGSYELLPRERYSQGLC
DLCYAMLRVNPHERPNITEILATPIMLNEGLQHLKKNLLRLRGIEEAVKNRLVWEVDSVQ
RAFHVAPTLLRPGSIQAEQKEAHSSLNDEGGAAMDPSVV*
>TCRU_10670 hypothetical protein, conserved
MFSLEFASGRPLGSAPYYSLVVREPYIVGRDRSSDIVLDHGDIVTRHASLTVMHESQALE
QQQKRVLLHGANGNDDGVKELEEDSGEVAGSFLNDTREETSDVVSLGLPEMNGLRDGRGE
HGSEGIDEEGEKKREKGTELSPGQLQGNDPLVLRLVNLREGGHVLANETEVVDHPVYLAD
GAQLQFGAHIRLRIRFRPLLVSIARNAFSSDHVRELEFMYYRLGATLTGQGGPTPHLDMP

QPISKLHCVEAINDDPLCLMALASGYSIVQPTYVFEWFAALAQSASSPLTVLPPPVRFEV
PVQYRGATAAHAAFYLRPESDVCPFPLYPIPTTATRKRSRDTLFKGKSFCFLTNAVEHRY
KEPVLTCGGEVLHLEDILVIKKETAAATAKKTTATTTAEGSDAVNEDHGVHFAEDDNPTT
KEKEEEESTTAMQYVVVDAETEAAMRRQEHRSLDGLRRLLDDTHRTGIAVPIIGERSLFH
ALLTNRFTAFEVSLPAATDAIQPGDQHPLNGENVAAGIEYAGGESEVPTSATGLEARAIN
FLTDPTKGVLQPRQRGELHIRTLSPSLNRRREHLTDDLTKSQRRGRGRQSAPRALPAVDL
FEALRHRVRAFVLKEGSKLQENLAGSWRNLFVDPEVLEHAHACQSHSVRYLEKMEYLLPE
IGEHPRIASDMRRCQRNCHEMLRTAQEIVELAKCASQRCQHPSRPRRMSANGAIFYPSAG
LMGGWMPLRSSPSDAEKLDTEPREPSPLLRGGRQWMFQQGANSLPVTPRSSRGKGAKKYR
ALLATDTRAAPANDRASNQTDLSAPALDAATPCGTEGTPRPAPVFYLSRRLSNMVSPSTI
RAQNAAWRSPRPTSRPSQREPRQPTETREEFHGVSRDTATAQASLSKRTLVTHPTPRGVK
SSKKTDVQMSPSARVPLSQEYSLPVRRGSHGSSPLRWQHLQRTPRPRHPRSARCGSPVLV
TKSTGRRQHVRMENS*
>TCRU_10671 Probable N6-adenine methyltransferase, putative
MKTRHDIQFCLDEEKIEFNQYWYSPKTINVLLDEVRHHATACAFLSTPSLYFTLVGGRDE
AMTNKDDVDTDGTAAALAARGAAASLITSSRLFEFDRQWEKDPGFVHYDFHKPDHVPVQH
FAAFDYVLADPPFITEDVWAAYVQTAKLLLRPGGKLLLTTVMENHTMLESLLDAPLFIAP
FRPAIPHLTYQYVCFTNYKFTRLSRVNSELPPEDPKILAATQMANDLRESEREFTAQMRQ
RDRQGEQPLPAAQRHDVPSAMMADIPACDMKWGYVPAGLTVYANGSETPPEETGDQDYGS
AYREIESLRGMLDKFKRLIDLSQKHLDALSRLQQKCTKQDGKGVSATDFAMVAANEEFTT
TIEEMRGVIKSVEASEARLTAEGGETALNHIAAMKECVEAYAALPLERQKLNELAADATR
KYKSPVFNRMKELLQLLKEIKKQNQNQKQQEGTSAMAAEENSSS*
>TCRU_10672 retrotransposon hot spot protein, RHS3, putative
MAASSYLLYQLLHYDVEKLQVVVHCFGEDAYVFDKTTKTVTKYMDEIISESVLDGLWQCG
MKGYIIYDVARKGTPPDTGFAPSTGWGMIVVSSPNLDNYDKWATQLKASRIIMNCPDEMD
VKAMCAWMKRGLEPDKQAGYWGMVKKHMENVGPIPRYIFDANEFIAHSAAIEDAVDGIKS
RDGEKHFTHGGVRLWDSEDPSHKLVKVVRGRIVEGAEVFLNAPICADIGF*
>TCRU_10673 hypothetical protein, conserved
MAARIRVSLAGDVRAAMETIFKNYEKCFFPVLCEKQPTPELEAMPSYLPDNVVPPLHRDD
GEAEFADYMDANSLTFVALGDAGRPALCGIDAAAQLHHEGAQRALVSAAGIVSSICRRRL
CIPFGNSELSQLLRRAYNTEKGNRNNSFNGSTETVLLTQAFSDAVWAEESFHYFSMTRRV
GNILGSTGIGSATRDLAVDKWRPDQDIMELRDELMIARTAYDHRHCGYESNRPFQT*
>TCRU_10674 hypothetical protein, conserved
MVQPDRARGREAIMRERHSFQAMRKTVLEERRRQRRQWIHQIREMNAKFPETVRPLAEER
KKNCEQATAKEDAAERALAADVKMIEECLSRLISLEDIPVNPEETDIIRRQFDEVFTQEE
QTYLASAEEERARKERLGRGLEVYRQRMLDDYVAKKNGKLHDAEATEHHLSSVVDQVLN*
>TCRU_10675 retrotransposon hot spot protein, RHS3, putative
MKFIISTHIDDVLFKGRARVDKMRLNDFLTRELDGRGVVDTNRDAMLEEFFRDPTKYIRD
KGALNEIQASYRYLSMKRVAKGEVIFDEDIRRLCDKGVNNLPGWSLAAAEVKAAVHNSTK
HLLDAAAEEAMNPTTTSAPEKLEGCYESVHNARRSHAVELPDGVERKKTETGMGVHEGKP
EQSWSYREADDAIEENDGVQQFGAAPPVLMVLASEKGWPYSWNRIQDLPKDVFVNCGVER
VWQIVKGDVTAWSTRHRGIDFKPKRRVLIGTPGIGKSVNAGSYLLYQLLHCDAKKLQVVF
HCFGGRDAYVSDKTSRTVTRCGDEDMCVSELRRLRGHGRNVYIIYGVAKEGTPPPRHFAP
TSGWGMIAVSFPKVTNYEWAKQLKAARIIVNCPDEVDVKAMCAWMTRDETKEKQAEYWNE
VKKHMYLLGPIPRHVFDEEAFNGRCGAVKFALQSINEVTVEEHFSRGGESPWYSEDPFHK
PVEVVREIYAGGVILFNAPISDCLEERTLERLPSVTE*
>TCRU_10676 hypothetical protein, conserved
MAEAASCLDVKSSFIVSLPRETRHLFRCRVEDGTLEELTQLPMGYKAGPEILQMITLAIA
RVTTVVHSLWAAPPLVRVDVWIGNIRSAGSRSDATLWEAQVLRNADRRHATMGEDRESGA
TQYTFLAVLFDHTHRAVSLSDKFVWSVRAMPSLKYLTIAEMEVTASRFLPAAAILRTRLC
EYHFFIKAVRRRLSALNRGLC*
>TCRU_10677 Leishmanolysin, putative
MRQPRHTTPLLPLLLPWLMMVVCCTGVCVAADRAVKHRCGFDAMMKKYGRLPTAVVREVP
RRGQGAVQAYTAASEDGDDGWAPIRIKVSAEDMYNPLRHCTAAGDLRIDHEGRAITCEAD

DVLTEERRSIILRQTLPAAIQLHSERLSVRPVTRPVVIPQTGLGLCDKFTIPRRHRTAGV
AGADMILYANIFPTYGPAAWAVQCSLLDDGRPFASAVNFDPKKLAVTNEYVRLVAHELGH
ALGFGRDVFLLLNMISEVPNVRGRPKVSVVSTPNAKAMARQYHSCPTLEGIELEDEGGPE
SVLSHWKKRNMRDELMTSDVGVGLYSALTLAAFEDMGFYLANYSAAEMLWWGNNSGCGLL
EKKCLTDGITEYPDLFCNCFWSAGYDFCTYDRLSLGRCGIKWYDEALPEEYQYFADPRLG
GDDLFMSRCPIVEAYSDTGCTNGVPLMPGSIVGPNSRCVKGQDLQFDDEYIGDVCVDTRC
GDGTVSVRFLRDDAWHECQAGETVTPPSGPWRGSIVCPQYADVCTAFPNISGYPIPVVEP
PLADDPTSAEGAEGDEGEVPRKRPPPSSRRPRHSGNGHVVIRKTLASRVLSPAWGPLFR*
>TCRU_10678 hypothetical protein, conserved
MKLSSEISLMKNGPDDLTEASSVTHTGANRGKGGFTAASVGAKQMMPTTKRRRRMNAPVQ
VSARFLPYDDVCGATVDGATAVDDVTAERGLGRRVSCFEVNEDMAGRYLQQASVENEFLP
LTQWDVEISSSFLKELHSTLSYTFAGDYVASSARNHQEMETAENKRWFDMFRAWPLELAS
SGYAEWWLRHPRCCADATSYFAHIIEGIMREERHRKLCESDFFREELNSEFLQGALSMLQ
AVYADPPRSLKAMFLTPLHHQRLFFLSCRLGAHKYPFCNGKKKNTRVLALCLSLASAISQ
RIAGTQLTMRHDLIRFLGNVQSAWQSLLESRPDEATLRLEFDRVKSLLAFALD*
>TCRU_10679 sedoheptulose-1,7-bisphosphatase
MSDSTTFLEELEGEGVPSSVADVVAAIAEACREISIDLRTDTVRAVGANNSFGDEVLSVD
DMAEKHISSCLTGCRHVLAFVSEERPTLTSTPHLGRGMYTVSYDPLDGSSIIATNFSVGS
IFALWPGATPIGLRVRDMVASVVAVYGPRTVLFVSLRPVGVVEFYYHGDRWTRVQNGVPR
TLKSRATLFAPGNLRAVMYLPWYKELVTSYMNSGATLRYTGGMVADVCQIIVKGDGIYMT
PESPHHKVKLRLLFEAAPMAFLVECAGGRSTTGTKNMMDVRVVEMEQKTPIALGCLWDVE
RYESMCSVYKKGTLTSGSKL*
>TCRU_10680 Flagellar Member 8
MLPVLSAAEGCSFVRKSPVGIQDVAVPLRIMEDVRSAGLQSADVVDSLFRKKDGLVDRDE
ENRHFSHSVEPSKLFAVYRIGFVGKGWRSVVDKHLSRLKDCFLYDLSDISKFVPRSVEGV
SCSSSGDVVVTVLLEHLSSLSQNEVLRMLDDAPFLSMWRLHDECIAEGSVGRTTTFHRVG
FVGADWSSKINGELVGAAFVKDVVEVLHVRPEDVRIAGYYVSENLVIDFYVEHSDSITEG
QIDELLNATMFENVWEVYRRERNPVMQELQPLRVTPRQAKIRANLSKIPKSVAARQHHGL
YVNNSVGYPRPGLRYRQPRTDLKQCPSVPEEPLYVPHEKHLPTWDRGVELPNVALSPRAL
PWPLRTDYTKAQQQRRVNLNEVSEVLGLQRQQGSQLQPESADIPNACLGSSYQESGSTRR
GESRDRLHQYRERIRRLLPK*
>TCRU_10681 ATP-dependent DEAD/H DNA helicase recQ, putative
PALPSSFSPFTSPTLSEVKTQMLDVTERLRQAQRRRDDLILQEDEEHDVTPAILETDRVV
AELEAQFLRLRQIQAALLQRPPPSDCSSPVSNMGGRVSCASASSAAAAFSTTNTPKMFTT
TPGAASACFSYVNASLPILDRSGGAFDMTSVAPDAVAMRAQRLVQLACAAGEERERNTNV
MLHPELREGKIHESRLPTESARHRFSWETYEQESSHLQQRSSPTRASAELPVNSVNRYSG
ENFSWSADLRRTMIDVFGLHQYRFLQLEIMNACMDGRDAFVLLPTGGGKSLCYQLPALMP
NPAQVTIVISPLISLIQDQVYALIANDIPAIALTGQTSDAPRRALFAEWASGRIVHTLVY
VTPEYFGRSDHFVQCLVHLASRGLLSRFVVDEAHCVSQWGHDFRPDYRKLAILKQHFPAI
PISALTATATDMVQQDIISTLRLQDALVFKGSFNRQNLSYSVRKVGRSVGQVVVDLIKHR
FPPRSCGIVYCLSRKDCENMAAELVGAGIRASYYHAEASGKNEKQERWTKDELQVICATI
AFGMGINKPDVRFVIHAAMPKSIEGYYQESGRAGRDGLLSECILLCSPSDKQRHEQMIYG
SNDWKTSMSSLYRMLAYTMNDVHCRRMQQLGYFGEDMDEHYCLKQPEGSVATCDNCASKR
SDRWETGELDVSAIVIDLFNIIVHLGSLTSKQLIGVYRGTADVGKAVETRMRQAGAPPEY
KLGARHTKFILERVVLEALLLGIFKERLERVTDFVTCAYLEAGEGVGIKVYHDVQSGRRR
IVLAVRGESAAAAPREALQAAMKATSGRECGTCETAAPGSKCKRKRGVTAATSAKTTHLA
VERNQRQTVKGKGRRREIKGGVILTECEHSSSSSVSSSSISPSNDSLVGFVTEGSSVTSL
SSRSPPCRKLCRRHHSHRSLSSYAAGESEVHLTTSSATALSLSAETPRKAVVPVSAARLR
QLEADLLTQMEALVQSLAERSEGGRRYNVMPKKTMQMLVATLAEPGWGSVSQLGDLEGLG
KNKVRKFGADILRLYRQFRHEHIGDVSELTLVEEEMLRQTTTVIANRHRLSRGDTHAGQI
IEDKDTPVKTHGSGFPAPPQGIRLLLDSDGTPRKSTHPTTTPTTTTAAAADATMLAVSAP
LTTPATGHALPKKTLFKVPNGTPIGSVLPEAPSPRRQQMQQQQAQIFTVPGSPMPPCSAC
TTHDPTVLHPPTVLTFLRPVLQQTADSLVLFPAPQQQQRVVHPAIDQEVLGATPMPSQVE
PVLLAQHPAVDLMGVDYLLRMCEESNARTPLRPSVGANSNAAVHDHVNRAGGAEIITVDS

>TCRU_10682 hypothetical protein, conserved
LMHGTSAAVQPSGRGELLLWINSVCTAQYPSVESLRDGVAYCTIVDAVTSRVAENCTALG
LPEAKIAQSRAKRASLLLSRVEWGVTTVTCINQDPSSDTLQERGHCEKNMQTLQFMLRGC
VPQEFSLEVDVTRLAAGKLQEHIMLLKWMYQFLKKMLNTYSRSALERRANTSEGAGHVEG
VRPTRAMKLQQKMVREKYMELDFAGPVPNNETKNNEVETSMREDPTFVKDIKNKNKSQAI
RMGSFPTIVSGAVDFSEDEGEVLPKFHVEHLDETSKENRHVCNRNSQLNIDSNGSHFFLN
LDIESLFLLPQECLAVMEDMRREVESYEAITLAAYRHHQHCLTGSKDEQESYFTGGCSIN
EELLLKKAPIISLEQLGLLLEERDKLWQTLEVLQNVLLRNLTGLIDGIGSTNSASPLIKK
ILLALS
>TCRU_10683 Hypothetical protein (DUF2410), putative
MELHVFDFDGTIFYSPKPSARLKKTHGGNVYAKLMRPLQDNGLGWFQSLSTLSPPAVPKS
PPIQDWYVTPVLRRLKELKQRQSDALATGASECVKIFVLTGRDEKFRSRIEELLTHAGLR
DMMSAVFMKPHETYGTVKFKLETFYTLIARNRPDHVYYYEDRAEQGQQILDGIRMLSHAV
HPNTPESFYVYSVILEETGTVCPFSQEEKNERGPCAPALRWWEETKRRASPDPLSSIAPF
TFTVLLVDPILAARSECSLTANAEDTLLSQLRYEREAYEFASPSEEK
>TCRU_10684 Bis(5'-adenosyl)-triphosphatase, putative
MRGAQLPAHLALCSSPCRHWIVSAGNGSDSFEFFCRSRGQMTEGHGSFPSRTPVSSHAVA
RFRLDHLLPGDWSRLLQHCRRLTSPGGSYNYSSPGDMAAVMRGTNAAASEKASQAVVNSA
FMHIVERTVGDFFPNNMIYHELQRRYVVPPSGAIATNEDAVDFFSWLLHLQEEEEKEGGT
TVSCIGCEADDVGKDPFIQNALAMEKTIQNERVFLAGFPHIVGDDGKHEDTYEPIFNFFP
HRVVISDCIPYRSRYFVVMVNHKPIVPGHLMVVPIRCVGTIHGLTLDEVEDWGRVMHLTI
RVLKQVAAARQKNSGNTHSDSSHCNDDMEGGFSIAIQQGTLAGQTVPHLHTHVIPFDPCG
KLAGEPEDEEVQQRQPCRTGKQMSEESEMLRSHF
>TCRU_10685 5-formyltetrahydrofolate cyclo-ligase family, putative
LSDVKACLRKKHLHQLRALAKSDPAFMQSESAKLCSILYERVQALRKLRPAKSLLLLCAF
LPLYYEVDLQPLFRRLWREMQSVDVPNIKIFVPLVLLPWEGSNVATTTSIPLWQRPWETA
AARFLSAMLLVEVFDEEDLRNSFEKRGRYQLTEPKSEVIDELFCTDVGARSEKDYYPRHF
IACDDYDVLFPECEKPANLIEQKRLLVGSENPGWMLVLAPGVLFDSIGGRLGKGGGYYDR
FLQYSREAAADAVVSWGVGMEMQLMPEGTNLPVCTHDASGGGTRDSPLDAVVTPAGFVRC
A
>TCRU_10686 hypothetical protein, conserved
MWRLQCALQGLPSKKRLSAEDGTKMCVSTHPYCDHASLILDAEQSNEMSGDICLLSASPE
LDGKLLALHIDEARVELREARQLISSSYSFYMYEQEALLRFSLVGGVHSNDFMDTGPREK
NSVIDLHERYWHHVNSTMLLPDESSEILLRLRRHSEFEPTVSVLSGESVYRLNLDSLEKE
NAFNFGRTAANATCMDCWGPQSLVVCFSSGEVSLMDWRDPSGVLLVNTYAPQRASAPDCP
RKVSAAPPRAGILSCCALEDSFRVVCGLGDSCGTVVVTDLRKALTTSLRSKKRGRSTPAE
DAWQAVIAGSFSIPTSYPISDMRHCRCDFGTIGMVDTGGSSILTSINSLEDGSMNARKKQ
SDTLRGVISSFPASSSGSSDGVGIIPHARSLRCDVSSDGCFLVSTRVTPGYTALLTRQGK
RADIQLNRVAHEKLRQEPFVSVAVLGSTVCAQTSSGNALCATLQ
>TCRU_10687 hypothetical protein, conserved
MRAMYSVFSLLRDRLLVAPISPLKAAEVLCSEHPCADSGVATHLVNCVDGNGVLLQLPLL
LSLVRCGYRHVPNYDQHKALITQWGPMEETLFSALWIRLRRLTAAGSTAWDETLALHFDV
GEGKGRGGCRLEPMDSLLQTLQLFVDVGRFVHHSTLSLKAHRLRLLADVFLPVMRRVDVA
WREINEPNSPVVIAPEQLQELGRLAGQCLCLYGKYLLLFHQGLCNMLFAGLSALSTMLQS
DKQGGALIKACTVRDALSEVRVVLVGLLTRKACERQHWVVSMERWMELVLQLAEVFTLEE
AACLEYLDEDNKIETSNGLYTLHVDVLSALSTVLAVYHRSVLMELNSAVNEPIAKACDNI
LKRGLGLLRQLLLLVTGARKDNAPSSCNAIHNLGIGGNYLTVRAWCACCEAAQVLHAALP
RARNWTRIKSLTMPKFGRLFLVMRCVVLRGRMSVGGGDNDALVSLTFYLTLVRALRRWRT
APSSKECFSLDALWNTARMRLPGSLNASPPPIRLLILLLEELAAS*LLISQGCPNPLCVM
RNETIAMRETVHAMWSNCLKHIQGRFEVGKTALVDEDVAAIARGMLHIGAAANCVQKDAV
VGLFEDHRLLLSRLCALLLPVESGMRRCFAAVRNRQEGVYSGWDGEDDEEDENDYRTLIS
GGAYWFVCETCLGGMLWHKPDEVMVEFTGVTCYCLLRHRGTADIIATYVEFFAPVLMQGK
KKTCETDPVEEPFAALQSINWMCMTPSAVACRGAKQCSQDAGDMAPFFTPAALFFIECHQ
QLLLLPTSNVLPSHARRILRVLFAMSPGFFACVPELPRFLLRRLLKYTTSFSPAVTAVTE

NTTSRKEGGREGACDSIESADPSELWEVLLWACTAKIARLKGCLPDEINDFKFEKDGAIF
LKVASSIRLEEDAEATLRMLYAVDDESEDMFFTTRQRVVQRALEILQ
>TCRU_10688 3-methylcrotonoyl-CoA carboxylase beta subunit, putative
KKEERLRDFSELYAAHSSQYESAPAAIRPNVLRYPCDPTSAEFQENLRRMEGLTAELRRR
VQVVIEGASENDRKARERHVSRGKLLPRERIEKLIDPMTPFLELSQLAGLDLYPGESCHS
GGIIAGIGVVHGIRVMILANDATVKGGTYYPITVKKHLRAQKIAWENHLPCIYLVDSGGA
NLARQDEVFPDEQHFGRIFFNQANMSAAGIPQIAVVMGSCTAGGAYVPAMSDESVIVKGN
GTIFLGGPPLVFAATGEKVTPEELGGAAVHCRTSGVTDYFATDDLHALYLTRRIVRNLSR
EEGSKDAESKTFTPPLYDPKEIGGFIPDMAAEVVKSFDIRAVIARLVDGSEFDEFKAQYG
NTLVCGFARFEGMHVGIVANNGILYSESALKGAHFIELCSQRHIPLLFLQNITGFMVGKA
YERGGIAKDGAKLVTAVATTKVPKITVIIGGSYGAGNYGMCGRAFGPRFLFMWPNARISV
MGGNQAATVLALTNSKLKPDAIESLKSEVKAKYEKEGSCYYSTSRLWDDGVIAPEDTRAV
VVQTLRTVRLAPRQETEFGLFRM*
>TCRU_10689 exonuclease, putative
SLPPSWRDALVEGERRRQKKSLDSSEERPSAPEVCLLCHGFRHVRPAESPRIEPALLRRT
ILHPSPPAFMSAICVDLETTGFSVQRDDVVSIGAVELRWDGTTLQQWVLGARSFFRTVRP
SKPSSHQAEAVHGLSFEMLRDAPPLEDVISDFAAFLIQLDGNLPQSGQTEENYRAKPGDL
SAKKRCTAATTTGCVLTLPPVIAHNANFDASFLQRAVSRAGWRVVWDEYAPLTCTQSMFR
ALYSHQAADLSRACQFCGVDTSGRDERHDALHDAQLCGRLFLRLAEKWPS
>TCRU_10690 hypothetical protein, conserved
MRRSLLCLFTLAESRSMFLDAMGMPLPCPTATLPETLQVLAEHNHADTALVHAALARLLS
LDSTDADSEVIASFKPQGTKPVTVTHATSESGATNDVVGLPSSPSSHLMLQLMFLHANDT
VVRERCCRCIANMCQLSSPSLTRCVVEPSGVNSDMDQVKRDHSVADGLVEGGAVELVLGT
LSMASRLSTKGIVWSSLALLNLVCLSSEGVQRAARAKGESLLADVIASMAHEAIAAGSLS
GENCVAMDAMLGALARILTTEADSNMTGVHYRFEQAAYGTVEAVGWALFCLSESAIRDIR
GFEETEVMNGGGSGVRRGATLFFPAATPSQQSAVLAFLPPLHKAWMILKSLSGCSRNMPI
VYEALHMPGDGGGLRTMIDAVLLFGVELEGLSAVGAIEEATLQQSMLLHAMEAFVDLSAT
RKDLGHRALAEAASLSDAVEGSHSRGGKEMPGDGGEMEGISAVIPTEAALHVTDTLAAGV
VSNIAVSTLVRLHTAQKEEEAAIEYTQGGGKKAKINVYNGAVFDLLAKCTLTLANLAGHD
IAVASLNTMAVLQVMLQEVTDFLSAIRAEHRASPGELFTSASQQELMALVQQCALTGQMY
AALWGILRTPDGARAVRELQLHRTVREIQTVLEAMYTEAFPDVENSAGGASKRVGTQEGC
TATQRSAALTATKKTTPTSAAVVETMRQLIPLGQKVLQCLRLAFV
>TCRU_10691 hypothetical protein, conserved
ATQAVESALQRYRSHVRGKILGEALVESSTLAAAALEEMTQSHARTVEELNAQIAGLQEQ
MFEAAAVIEALGGKIAGDTNTSSSPSVARRSFALDVCTTSREKGDESTRMPTETEELRLT
EEKKQRLSSLGESTSDAFHTAQSGSRGTGRTAPPEIDATHSALYAELLQCRGTLKLQQQQ
QASMETQLKELTALLSRVVKENATYRQEIQLLRATTIPVEEHRQILHERDTLEQECRYKE
LELQHLKEELETALNGLISQPQEGTSLLDLGVIHEGAPVQPSQPSSSFMSAAPRGDVTHG
TGEKDTIVCSSHISTAEGLASDPSWNEEGLQHAGLWKTAIRELEQQAVLAASQLSAAERL
REAESRIEELEAIQAELRTSLETLEAEDKCVREDCEQLVFRNAVLSQQVASLLVRVERQR
RALERQEKMNLLVEEGDAVSDSEILLAGEEPLRPDSRRAQRGRVASAVQSLLERRRAVSA
FAPSSPSAGGAAEVTRGGGNGRGSFLDLTLQPAEPLEVEGGLRTGLGVFARNSHRPRRSL
ALRNLGSPSVEVDFTRVPQLPATDQLTGVALGRPSHYATLDPARLTTADNSSGSSSRHTN
HNDFHSVGSSGSATKTLFVSDNTEENRQFLELLREDENLDRYSINSMAELLQRNQELLQQ
LYVATKRAESAERRHQERDSEENVVEEGESRAASDVEAAQPHRRVRRKRSREEVSSTELH
SQQRQKVVEEEGESGGRSTPQRHTLRHGYYNEEGGDERRQSFKASDDRYVQLEEHLDGQI
DAVLRNHESQLILTDNGLAASLLRIMELGRKPGDGYGSSSISSLRCHGSNTEEASAVEAT
TNIMKDAVVTSLVRLCTELGVQTANQAVTLASVQQSEHAEMMQKCWAEAQRVLLRSAADL
QAAVASLPHPAQYTEAKQIEEVAIEGAGGRNENDEVQLLQSITSLLRTASLKEHSIQRVL
QLAARRQRATKRVCGEQRQEADNDDDDDDLDNDQHVLRQLKVQLEGVQTQYEKLLAAHHE
ERKQHTALLDRMWRMEEEKVDAVRSRDEALERMTWMMTREEYEATVDALDAAKTTIEDLE
AQLRYAQETNNQQLAEVDRWRQVSLDHERQREEDAAIVATQLAEKDRLIAQFVQQHQQIE
SHNSELLASICRMEANATQQRDKIASQDDREGALREQLRRAELALLEQQCTQDLLFAIFP
GDRALEENRNLIQVMRAEKERLAETVASLQLELEKVHRDLASARLQIHAAEQARQEAELQ

LHEVSFSRANVVPAATLSSLPTAEGMPTTTTTASATGTVELELLQRTNASLLAEKRGWTE
REALLREQLAALGRDPVSENARRYGLKATRSFEEQLMEMDERCLGLQTQVAEAEKLRDTV
DHLTKNVESLTTQLDAARNALAMQQESNETLQEEMKTMAAAIQQKEESHDAVKLTLAEKE
ELISSISGAISTLEKEVEKMDERLRASDEERQRLYQDNVKLIENVAALMEDVKKKEAERK
AAQAALAQGLASASSSSYRWRGRSAGSGTPGPKSITGSLGKAPN*
>TCRU_10692 protein kinase, putative
MDRFIVGSPIGEGRFGVVRAAVIKESGVPAAIKFVTTPRLDEGIPHPTARELLVAMRLVH
PFVIRTYEVVPCGCSLALVTERCKTDLATVLSGRTASNPLPALEAKSLFKMLLLALAYIH
SEGVLHRDVKPSNCFLTAEGELRLGDFGLSRVWDTEASMTHEVVSRWYRAPELLLGQRHY
GPEIDVWSSGCVFAELLRGYGGAFFAGDGDIWQLPRIFDVLGTPTPTSWPSAVLLPDWGK
VYFEPKRPLPLREFFPDASECALDLLRRLLCLDPQKRLTAAGALRHAYFSEY
>TCRU_10693 selenoprotein, putative
RKNRSTFRPVLLEVAGSLDDTVCQEITRRLRQYRNRYAPILRLTATLMAPAVQEVELFGH
CERADVTDGRATNGKKGIAEGEETNGESGSGSMVAKRLRGDSLIAAPCAAIMAERRIEVV
SRLHENNDGMSAVEKLEAFMAYQFLPLALTHNCHPKLSLSEKSFILRHYVHEATRTSSFL
IADIQEKTAAIIDPQLDISMYEADISALRLRLCGVVLSHCFVDVVMGHAALLTKHPEAVL
LSSTPWTQEVDVPTEGWPTLSLSPRLQLHCVPVPSFSPECMLVELHYNSTLLALFTGTVI
GTDSLPRHEFFADFPGLSPKSNVSSCEATRTATTVAQRFLKERLWDRYFAQTGEGKNGQT
PEHVVVFPSHGGYNNVTHQLDLYWALHVGDLKRMKHSRNMLGKLLDHESYAAYVQERPPL
PKAPLFSHVREYNLLLAPSAFGGSGARLVSRHSLPSCPLPRFNSVASAASSAMTPIVLDI
RDTIDHQLAHLKGSVNFPMNFPATAYGVKKAELWLQCVLQPLQPIVVICRNEEEFPLVRK
RLELLSPGAPIETYTAKELESFSSPLSAAGAEVRVQGFIITKPIPESIVSSFLPRQLVWV
SDSAASAFLRIDNYQQLQYLEPSEDTLVLDCRTSYEFKNGSHKHSVHIPLSELCQLTALD
TMLSSSSLNRTNKQETPVVDFYTPSPRLGQKILEKLHESFMAENARRRFSFQGIKNIIVY
CASLSLHHCRLAAASGI*SGHSSDSGA*RPSPRLGQKILEKLHESFMAENARRRFSFQGI
KNIIVYCASGYRSIIAGSLLRRAFEAATVPIQVRDVVGGALQIMKQRPDLWTVKDRSIIC
VS*PR*
>TCRU_10694 succinyl-coA:3-ketoacid-coenzyme A transferase,
mitochondrial precursor, putative
MLRRSLLRMSGLDKVVALSKAVGDIKSGASLAVGGFGTGGMPHALLGEIKKTGVRDLCIY
SDAAGTDGYGVGLLFEDKQVKKMVVSYVGNNKIFAKQYLEGDLELEFCPQGSLAERMRAG
GAGIPAFYTATGFGTVAQTGGQITKYNGDGSVACESNPKETRLIDGRWYVMERAICTDFS
LVKAWKADRSGNLIFRGTSRNFNVPVGQCGRTVIAEVENLVENGELDPCHVHLPGVYVDR
VVVPERYTTPIEKRTVSHPRSEEKNKAMKPGEEARQRIARRAALEFSDGMYVNLGIGIPT
ESANYILPGVTVVLQSENGLLGMGPFPEEDKVSPDWINAGKQTVSYLPGAATFDSATSFA
MIRGGHMDITMLGALEVSANGDLANFMIPGKFVKGPGGAMDLVASGTRVVVTTMHCDKKG
LPKIVERCKLPLTGKNCVNRIITEYAVFDVEMGQLVLKEVAEGVTVEQVKKITGAQFLAC
DVKTMPLAPI
>TCRU_10695 hypothetical protein, conserved
RAMKHRSLAPDDPFGERSTFSDPSDGLFAAWSGVDFNVFADAASSDEVRTAHFGPEWSRF
ATVGRLSVKIMREQGTPGVASAVSSKGGNKVLPRPPTAEELHSRELQARRKALEGNYATY
EQYVMKELGIEDGGNEDEHMEEEMDDATEVANASEESMPLPHFMVERGEGQAHANDTNKQ
ESTNGKPLLRTREGLQVPEPLMQMILDALGEPHGDRHLPRSDPLHWNTEVVILWVRKMEA
ARFALVSAAGTGEASLLEAPLMEDPSMHEAFRMARTNGKFLLHHTVPNTMFQVMRRWYLR
RQEIALTFMKERQEMKNTTSISKDDVNDATFKSALEAGRAKLDELAAKVTPILIQETISQ
CYPYCH*
>TCRU_10696 hypothetical protein, conserved
LFLACVFIMFQLFFPFYFAAATRLNSFTVVVLEDQAAEALRKAPDGAFLQTPSYLVQLSS
HWTVVERNVFGGDSPDEEEKGGQMLHCRLPRPQTQEMVASLEKSYMKFHQGRVRAAIWKW
LLDLTHRDGCVFGDGEGTLTGVSEWYLFCPHGLIRKVNRTAVAALYDVSPSELPRVVKKL
VQRYRGSGEKMGCGNALDKWTSVIGKYKKHITQPYWDANRRAWGLTYPNDRVCVTGRVNA
SAEGETKRREDTRVEAGREMWETVVRLYCRRGRGSSPLQEWTVTEVRQSCLYEIVLLSPV
VCEWEQRMEHLGVNPIPCIVV*
>TCRU_10697 selenophosphate synthetase, putative

KKMSHENEAKVPRFNPTDVGLPPEFVLTDYTRLKGCSCKLPQPKLLALLRAVSTTPGQKD
VGMDCSVVQLLQKDEHGAPLFMVSTTDFFFPSVEDPYLQGQIAATNVLSDLYSMGIDRCD
TVLMMLAASTEMDEMEREVSTREIMKGFVDQVRLAGSDVTGGQTVMNPWPLIGGVATSVV
TEPEMVRPTGLCIGDVLVLTKPLGNQIAVNLKQWVRRPSPIYLETIQGKMTTEEVEELYN
AATDSMKRLNRNAARLMRRHGAHGATDVTGFGILGHAHNLAVAQEKEVCLLLEALPIYKG
ALKASTLMSDKYQLLKGYSAETSGGLLVAFGDLCTAERYIKELCEVDREPAWVVGSVIAH
CGDGSPHAKLQDGYKIIEV
>TCRU_10698 hypothetical protein, conserved
PPPKEMVESVLYAVDQMRHQQNAWNEVMHRFFATEARQQEESDRLTRQVQDAEATSLGDA
SFADWVARRAEMDLGEDMIKRWYHINGLLAKTPFVAIVPCPRCLSTSGRVELASAFDALE
LERSFIQTVPLHLPLSKIAPTFIPSSFHLPRTRNVSKSSLGNLQYVGVPCTYGKDVLNLL
SESSLLAAAIDRTPCLLLNDYIPRAALCIHSVTVGGICVAAEVACDVRFATKIGLDLPIH
EREKNGKDIDVLSRALKKFLEDEIASFLANRSFRAFLLVESVSGRERDLWSDQHPLLETE
LRFRLLNIDTLDGCEFECFTQQNILDIVQRMTQCHDENGRFYPVLRFLEPP
>TCRU_10699 hypothetical protein, conserved
NRVERSMEGWSVIANITDFTHAVCRVSDGRGSAILVALPFLDSTARCDVIQDGRQSPQVR
RDGTGVLLTTSFVFPSREEAQGATVTFLEQPVAGTNAREGRRVEPFQAPVNVEKLFFCST
PGASVLPRSRWGVGGAFMPVPNSTPFSGNCTATGGSLHGSKFSFIGEENEENEEELGYTL
TFCDMNPTEECSAPIGIVVPPLVPPGHSFISSSEVSASVSCVSLPQQLLQHRPAASYLER
QEPQNATFFSSSCGTGSLAGRHATQRWDSYPIKPLPLPLLLSRIAEVRAGDRHLMITHIN
GRERHYVVQTVKRVGNDSCEYEFFDPASEFSSGGPIFDMRGDFVGLQHQSGDHSYGILIS
SIVRHLFQSSLLGVCRLPIVDVSVNEKNFDLDTVVPDEVFNQPFHINQRYCVLNVGAGDQ
LIEYEDFQRLRMRSDILGSTQPPSLVAPASDHVWKEFYRDFRSLILILFAFSHAPKVTKL
ALEEITSHDHRQNLPNVASLGGIGIVLEIIDGYPQNEEIVLAALTVLGRASLYKSNREAI
YRCDGVLTVLEIMNEYSHHASIQHWGNYCLYNVMASDSPVRTESIELFAYSQGVAVAVEA
LRVHSAERYVLRHASFALSCVVKEDVQYIFGMIRGGLTNVIVDRMKENSEDPFVFLGLAT
LLRELLFGLGKKNLLAPLTIPAVAIALDSGVWCDGIHLFGLDALNNRSSGEEVGNVLLDI
LVKEGVFTVLGKVMACESLNRYSSDSMTLLEACAGSVLVLL
>TCRU_10700 Octanoyltransferase, putative
GMRAYFLGRRGYCDVLELQEVIFRKKVERQMQRLRGGTNEDAIPDTVLLVEHSSPVYTVG
RRDTSEGIPKGCTVNVVKTRRGGGVTFHGPGQVTIYPIANIQLLWKHCTSLEKARSPIEW
YSCVLEQAMIDTARDYNIPTHRGRVGVWSDRWCDVPPRKMGSIGLQLGNWVSMHGAGFNV
CNDLRYFNDIIMCEMPDASATSLVEEMRLRSLNKTEPTPKTIAPLLLYHFLMNLRQQENI
VSTRLFDLSDETEWQRCVLHGIE*
>TCRU_10701 hypothetical protein, conserved
MDAVYRLMYTLAWVYGVASWCMCFYVFFSSGEGCRWFTTLQNYLLLLGATGAAAAVPFFE
VPSATIFITFSGWSFYAMLVSAHYWRFKLWRRHVIPVNAPLMFLFLWEVER
>TCRU_10702 hypothetical protein, conserved
PMRYSPGVLIGNWYEEMRVREDKVTFYRSSNQTDKTHWDATLNLSEETYLDGLKDFVVLG
QSLQLVNVATEAALALDMAPKFSPKPNHYLVTAVDTPQPQVRSTWVLHRAKDENNIAYTK
QLKEENVLHYGQHVRIANEEASLDGFCYLNSGVLDIGHPGKQPLTAVLGANKDNVFVIVK
PGEKRDDIRDGGPVRLGDAVALFHASTNRPICCTKSLKNTSFGYEFEVSCAFSGNKHSRS
LAAVALHPENLFIIGGSTHKARTNISASVNTSLKSSSGLSNKMFSMSSGIGLELIMARIR
EGSLRFGGRLGFRTLSKALGTACNEQRTTQLNREQIHHSIRLMGVAIQPMELDAIFKRFD
RDGNGLIVAQQLLRELRGELPPHRLDAVICAFQLLTIEGGGSVEYKDMLNLFKFNVSLQP
DVEEGVISCEEAIFDFVNCWPGKNDTSTVTLEDFVAYYTDVSPAIENDERFVTTVQRSWT
IPETDAYRSGRPRRHVTVIHTDDTAETIEIPDSLVLNLHDVVAVRDVLLKHGVKDIKEIQ
TNM*
>TCRU_10703 cyclophilin type peptidyl-prolyl cis-trans isomerase,
putative
RVFMDVAIGSCSPKRIEYELFTRKCPVAVENFVKLCTGENVLPRVPSTAGMGDPSFGDQF
LPQVTYKNSTFHRVHRGYLIQGGDVVSGQGTEQLSIYGETFDAPDEVSSSVFDQRGLVGT
AVSAPHLNGSQFFILTAKEAPHLNGTCICFGRVVKGFDAVEEIERVPLTPSGFPSRRVTI
VDCGRL

>TCRU_10704 Vps54-like protein, putative
DPAAVLCAFLMARRGWSRSRTALTLGIPPLVLEECIRNGVSSAAIRSQLALWVAENKDES
LPPTLLKAVVETAPSLTVGASEYLQDGDPLATLDPVTESYFVELGSSVGQSFISILNDPQ
DAAEINSNWGLWLGSVVSGALDHKGQTKRAETTVSLGPSLLTSSSSSGTLLARYGLQEDY
SSYLHLVTAPYNRNREESRQASTIADGNERLGIANTPSSVENLPWPTGVPKEFFDSFYDV
SCEVCFLERKLRELGGDSVVEGNNTSITAQTFGEDFEVMETRMKELRLWESAVEGCLLQH
VQSRSEQFFYASHEFGNRAAEAREALESLRQTRTDIGTFGKGLVQELLTTARCYRSRNNL
GSLCNLAGTVMSVSSQMVAIENWVALPERDMMELPVIVEIFCTLQDAILAEHCTGTFSKN
AGTLGVGWITKVSAMKDIPRRVLHLKEKLCVMIMEELEVILLPATRGGGDDGHITRTFRS
AMKMGIWPSAARHCNDLLVDALWTAVREAFIAFLMSHCEISDSTANNVLSTAVTADSSRE
EKLTLFEHSNACRFPLYIELLGLTLDHVLDFVTQAAQRWGLLLVDISPDPSVSDTEGVNA
EDTRKYFSSLCTVAESFVALLLEVRSQRGKTPTNLRDLETVVSMSCAFLPNMVSNLQGVL
AICGNIGDTWGFVSGRRIKSAVTRLVKEHLRSHHAEGVEKLRVSIENENWQPEKIDPAFQ
STVDVLCRSDDAAIEELRTHAVFTEVMGENGFCHLAAPVTTATAMARQMVVSAPFNPSSR
PLNTCEADTKKLLLIPPVDGHTEGRVVSSSILMLITLLHECDEYLSRFPFLAFDVMGKIY
DLLRLYDSQCAALLLGAMAVENGVLDTITTQHMAVASQNLAFLYDGIPLMQRRWLRATTV
DKLSSPIVEDIKRVRKDCATHRCEFLGKISGLVREKVGGLGTVSAEQWQASGNEWVMTML
RETARLMRAMRPILPAEDCRGVVVPLLGTFARMIRSVTMCPAVDADLRAVMLSDVLLFKA
NVERFGFDVLRCAMLFNSEAEAMTKSVEPSASEADVVAWFF
>TCRU_10705 THT2A - glucose transporter, putative
GDRQPDETPTFCSLENLKVAQVQVVGGTLNGFSIGFVAVYAYFYLMSTDCSMYKKEVACN
RVLNAECSWNGTRGECGWNGFTCFWGHGKDKTPCLDDSRCKWVYSDEECKNPTGYSSSYN
GIFAGAMIVGAMIGSIYAGQFAARFGHKVSFLIVGIVGVVSSVMYHVSSATNEFWVLCVG
RLLIGVVLGLVNVACPMYVDQNAHPKFLHVDGVLFQVFATFGIMFAAAMGLAIGQSVNFD
KDTKMDARMQGYCAFSTLLSVLMVALGIFLGESKTKFTSGKHEYDGTALDPNEYSYLQML
GPLAMGLVTSGTLQLTGITALMNYAPKIMGNLGMVPLVGNFVVMAWNFVTTLVSIPLARA
LTMRQLFLGASLVASVSCLLLCGVPVYPGVADKNVKNGVAITGIAIFIAAFEIGLGPCFF
VLAQELFPRSFRPRGSSFVLLTNFIFNVIINVCYPIATEGISGGPSGNQDKGQAVAFIFF
GCIGLICFVLQVFFLYPWEESTPQNHGDTNEESALPEQQLPIEVATPGN
>TCRU_10706 Adenylate and Guanylate cyclase catalytic domain containing protein, putative
GFVAALWSRKYVVGENVRVTLINKSTTIAESGNSVEKAFQDNPGIFILANVIGDKNLQYY
LPVIRDRKIISFAPFTGSTVIRGWDPYLYFVRADPLAELFTLIRYALTFLRVRRLGFMYL
EGVSFGDEEYEATKNVMTRFGYNLSGVFAVKSSLXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXRMLTDNRTAGAYLLAPSAVQDITVETWRSAVAGGIKFVSGQVITTG
TNPVARDIQYAAIRRFQDVMRRFMEKFLPESSSIRKKFPDDDIEGEMMVAGWIAGEILSQ
TLSSREWANNRDAYLASLYNQRRYMVDNLVIGDYGGSCQGVAESEGAMCYCNQGGRTVYM
KKFVDGXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTVDPLVDGTISFWT
WQCSPSEAVIVPPLNGFAIAMRDNPLAIFALRAFGVGARAAVVNNSLIKRFAFTVQVVNS
TVDGAAAALVSELKVKLVDVVTGVVTKGMLEVEDVAFINPMYLQPRIGRFRKNVIRLLPT
LEQQFFVIAEYLGNVSDGSVHAVIRGDDGATMAEVLXLSLETFGGSLLSTKLLAGGDKMA
DHLPEEGDVFVVGISADDVGAIAQHVVSHDGVRVFVIFLEFSMLYPEFVAAFRDGAGADR
VVFATNLPHWNDDKTTSVTAQKFNAAVPEVNKRTPLAMMGFTTGLLVVTVRSRMEKVNVE
LFENFFFSNVAVRVDDMLYGPFIDGNACPVTQSGAGCGRNYGATQISAWSLARALDPAVP
ALSPAVTPSMEYRMPVASGLTARQLIGVIVGSVAAALLLIALILLLLHFCRDSRDNENAP
KERTDPVTLVFTDIESSTALWAACPEAMPDAVATHHRLIRSLIAKYHCYEVKTIGDSFMI
ACKSVFAAVQLVRELQQMFLQQDWGTSVIDDAYHKFEEDRAEDDEEYVPPTARLDDAVYR
QYWNGLRVRVGVHTGLCDIRRDEVTKGYDYYGGTSNMAARTESVGNGGQVLLTRAAYMSL
STAEREQVEVTALGGVALRGVPVPVEMYQLDAVPGRTFAALRLDREMPDLDDGSDFESSE
DVSMYSARTGTAQAVVSVLTVTYGTLAPRQRLKALMPLCERWNVRLPRRPSFLQDEEYC
>TCRU_10707 ATP-dependent RNA helicase FAL1, putative
AVMGDVEQIVEKEETDIQANVLAIPTFEAMGLKEELLRGMYGYGYKKPTAIQKRFIVPFT

QSRDLVAQASSGSGKTSAFCICLLQVCQSALRETQGLVLSPTRELALQTQDLCNNIGHHM
GLAAYASIGGKSVEDDIRRLESGVQIVSGTPGRVFDMIKRRHLRVNHLKTLVLDEADEML
GKGFKAQIHDIYRMIPPLQVVLVSATLPVDVLEMTEKFMTEPVRILVRRDEITVDSIMQY
FVAVDEEKNKFETLCDLYDTLTIAHAVIFCNTRKKVEQLAKKMRKEKFSVSCMHGDMPQA
ERDEIMRNFREGKSRVLISTDLWSRGIDVEQVSLVLNYDLPFSREQYIHRIGRTGRMGRK
GLAISFVKHDELRLLRDVEQFYATQIEELPANIA
>TCRU_10708 hypothetical protein, conserved
MDGIKGKPAMLMTRGIMEMRQNPPGLVCTLRRFKHPTTQKEVALYPIVNFAAPHYFRRVL
DGDILERNFDKVLCEDGRLPFEAGSRLARQQQMLKRIFPFFGLRPVTINGSKFDGIVQRD
PVESRMAYQMIVDGADPPVDPRARRAMERIETYPDGTRVVCPWGVYHLVYMNHKLRQLGY
IVESEEAVEVVGYREAALVFGILAVLTFWMSYAIFRMIFG
>TCRU_10709 hypothetical protein, conserved
MSAADNHRKKPAALLESLFMWEMVASFSTPLTVCELERICRDVHAVLTFSSTGTRLMQRY
WYAQYHKLIWEENRMDPSRRTLDFTLTRSEGKRNWKKMYREEYPLYLARTIQGKGANNNA
INMAKVRFKKEWRNEILSGEELAKLQITPQEALARRVARDLVSLEGEEVNGTLSFHHHHH
NNNNNNVVVATGASSIGGDGGGVPQQSQRREEGEATTTTMAPRHQTDKRGRRKGGHDGQS
HAMKDPALGLSRDDYNNDRRLGKHKSKHKKGGTHRWSTFASGELD
>TCRU_10710 hypothetical protein
RRDALNGGSSMTLCTKGMERSPDPHCRRMWWTAAKECVPGVVHSSKEKMALDGARRVDVD
CVDRASQVYPLEALRATVASYEYNTSTGTIFNASQVESNVLGQWGYREEWQEETYDEDVT
RTAIHFRRHETTTQPAPIHPADFPGWHALFCLSPRFPIPSVGALPVNASSCRLRAHPLID
AADTP
>TCRU_10711 DNA polymerase eta, putative
MRCIVHLDMDCFYAQVEAVRLGIDCRTEPYILSQWGNLIAVNYPARKCGIARFDTVEKAR
EKCPHVKVSHVATYAVGDTEYKYHENARKGTHKVSLEPYREASRKIFNILRSFEGVEVEK
GSVDEAYLDVTLAAQRELASIRLPSAQCSSHLEDVMHPETNVIPDRRAEIDAWLFEKGKE
FNEIFDTALHPQATVEHQLLLGAASRVVWKLREKIYQELCYDCSAGIAHNKILAKSISSR
HKPNQQTLLLPDRVASAVWDAPYQSIHGFGGKFGESVCRACGNAELFRDAWLVPLEKLQS
VLGVDDGTYAFYRLRCHGKEKIKEQSVTKTLMASKSFSPPTSSSEGLRKWITVLSSELCA
RYKEFCETNNAKGQRLNVKLGNQGLRQLGGVSNNTLALPELVTTETLIAAAMQIVLATFV
RHPGIMINAVTLTIGFFKKLSEVEGKNRGRQTMLTNFFSCKAAEKRGRGDLDESNVITLS
SSSSPSEGSTEEKTSSTEVV
>TCRU_10712 histone deacetylase 1
RPVALIDTSCYSADCSLSALVPQHAMKPYRLLVTMELIKSLGLDRHCRTVVPPLIGIEQL
QTYHAEDYISNLGLHSSQSWLWNTEISKVTFSGDCPPVEGIMEHSLSTVSGSLMAAILLN
SGKADTVIHWGGGMHHAKCGECSGFCYVNDIVIAIIELLKCYKRVLYVDLDMHHGDGVDE
AFCQSNRVFTLSLHKFGESFFPGTGHPRDVGFGNGRHCTMNLALWDGIDDFFYTTIFEHA
LSSIVKRYIPDVVVLQCGADSLAGDRLGHFNLSSWGHGKCVEEVKKIGLPMLVLGGGGYT
LRNVAKLWAYETSILCGKKLPLNTVVPVQRMPLSGWLFEGSTQLLVAQDEENKPLPGVNV
QRAFRMVIEQIDKQCPNI
>TCRU_10713 transmembrane emp24 domain-containing protein
SLFMLLLLLGAATPASASVHFVLKDTHPVCFVEEVDESTRVVSGEYTRAPGAAANVPARI
VVRDPNGEEVSSNGLMVGAHAFTAPVGEDTSGQYMLCVHVTERGWEAQSEAQGILVEFRT
DQKSSIIPETEMPMLKRQKVDGLEVFTFRDFGGEQKDILRPAEYIRRVEGALSTLITLVS
DTHGEIEHLVGRFKRMRRTSESTYTRIWAFGIITVLVMVVVTWLQFTFLKSTLRQKKLV*
>TCRU_10714 hypothetical protein, conserved
MPKVRNGSSKRMTSRQRHKIERKKREHKRDLRRAANSLKKSGLGPKRTKKRRELAKMALK
VSNAHPDKEAILQRVLQAREYACFKHAKQPEKPFEENADHRHLESACVGTCSVSSLIEAK
KTLTYIPFQESNNFSYQFNKILEELVFPPPGSLMKLPSVAYLITLDSRCAVQCIPWGLID
AIVQESNIYHKNGGMRKILLLFAITKVDLVSVAAVVTQISLLAHALFERYMKVNKDEEFL
KFNDVVSIAFCPFSKIFDKTTRHVIRILRQFFLSEHCSNSNQHCNLEGKLCSFVIGLPNT
GRRTLSRTLLQHGTDSCVSLVPVSAAQLQMVANKNGHNEDVGFKLAFPNAKEITLLRFPE
DAILSRELSSLSGGDVVFKPFSFVERMSNPEVIGCMLFAGAIDKVALAQGFCQPGEGFIG
SSSEKQNIKAAQRFFRSLGHTVRMEKGFYVSPLFVSNAGTMGKISSSSLTASVDFASRQK

STQTTLLDTSFSNATPNKLVRISSVVAPSRGKKRSNTSVRRMDSHNVLKLGARTFVREIC
QGKNVPWAVMRPPTKKCLTKTEVDAASVLFDISLCLGKRLGTLEVHQNPADHFSVLLDHV
ASLLKEYLVFLPGNVVEFDPDCIVAPIHDLYNTEKATEEELANKIRGDGCEEKYDDSDED
ENGQQEEDSD
>TCRU_10715 hypothetical protein, conserved
NAVRKCSSQTVEGASGSKVGEKASVKSTAAFTPTGPKRKDWRTHKEVVYVKGIPMKGSIF
KLPIKEQILICIIFSITGAAAVMFVRPVIRSLVKDGFLGLPEDSGWVKGPWLYRFLYVAI
MYPAYSLLLFIIGSIFGRRVWFSFMIHKMWSRFLTKSAARRLEYFLDLQHY*
>TCRU_10716 methionine aminopeptidase, type I, putative
MPCEGCGLSEAAMQCPTCKKLDMPPSYFCSQACFKEHWADHKLKHTQSALPTIPTMTEAA
MNAFNFTGSLRPGRITPRRAVPPHIPRPDYANRADGLSPAEEKDRGAKVRVYNLQSLHDD
SKETADIQRVKKVCRLSREVLDIATAAVRPGVTTDEIDRIVHEATIERDMYPSPLNYYNF
PKSVCTSVNEVICHGIPDSRELEEGDIVNIDVSSYLNGFHGDLNETVFVGKPDADSVRLV
HAAYESLFAGIKVVKPEALYKHVGDAIEACAVQYGCSVVRAYTGHGVGHLFHTAPTVCHY
ANNKSLGMMRPGHVFTIEPMINLGTWQDVTWPDNWTSTTRDGRRSAQFEHTMVVTNDGAE
LFTDWTDGIPTYQKQLEGWNIPLP
>TCRU_10717 DNA-directed RNA polymerases I and III subunit RPAC1,
putative
NEEEAEGNSDVPTSESSPTTSTTRRVETMTFDVERISPPIANMFRRLMMTEVPVLAFDRM
LIEENDSVVPDELLAHRIGLVPIAGPVLKMQFVTESNQVGFDALDPQRVLVFELAAEGRR
DAKSTSVYSGDLKWKPLPGQEAWATGADEDRVFLVHPDIILTKLGPGQRLKLRAIALKGI
GGVHAKWTPVSVCFYELKTSIYLREPIRGDCATKLQRICPVGVFVVNEEGESEVAEVENC
TLCRECLRRDMYPEIADKIVVEKDKTRMRFTIESIGQLHASQIFRYALALFAERVRDLAG
RIRGTEAIVTGAAA
>TCRU_10718 methyltransferase domain containing protein, putative
MPSPVVLTRSAPARALNIKMFDRQLKGLQRCLVDAPACDLHKLCAEQMLDRRAFVKRDTP
VVLEVGAHTGWFFRQMLEKKQLFGLKQYIQTDVCEERLNRNYEEVKHMIPPDVEFVQICC
DEEEPDPFGVPERTVDMVVSCLSMHWVNDLETAMVNIRRVLKKDAFMLHSMFGGNTLYEL
RGCFSMAQTEVLGGVSPHISPMIDGAGLSTLVLQAGFNLPSIDVDRHLLLYQTPFNLMEH
LSTMGESACHYMRRPLNRDVLLAACAAYDVMYRKNELIPATFEVFHTIAWSPSPTQAKPL
ERGSGMVPLSSWNSQNKRRLQNVLDEFAQNPDDGALQARAEELFQQLREESAALLERKGL
DVRGLDGNRDEDAREMEKSKPAPPFQQ
>TCRU_10719 Putative Phosphatase/Protein of unknown function DUF89,
putative
VRMSVSAGCSGRQSFLVVFDLDHTVVDCNTDEVVPEYLGRGEFQRSLMGAEKPMQSTNLV
DTVLAPFSREQLGDAVEKSVIMDDGMPDVFRFLLFLQQKQQKSASVEAVANAVHVEIAIA
SDANLLFIEKVIEHHIPFARHAISQIHSNSFHDVIDGGELRRCRIGWYESAGHNCPCCNL
SKRPNMCKSRIIARLLHASRLVDPTVIFIGDGANDFCPVLNLLRPRDYLFARRGFPIHRL
LSDEQSAVGGCCRIDLWLNASELLQSFKRTMSPAERLPTLVRLRDAGPREFRTVTLRQRI
PEIIERTLKDNEEHTTAEGRRLLRALVEATRNNAAVAPLPGQQFVPPWLQGYAFLPEFDT
DVHMLNEQRQRQQQEVNDAVIAPRWGQIPWLQGEIYFYHLFAQYMMLAEGGGCKNGETAA
DEWVPNLVTPYAICSPIGTHDCPLATHAVMAAGGATPFQSFDPSFLAKDGSTFASDGVVV
QEGRISYRDIAAGDCIAPLHGYFQPYRDFFMREKRDVLHNFLKLKICPMLACVPWEADGS
FVPVLLRWMLWGNGIDLSMFTLDQLRESHSKGEAGPGDKTGRGDEGAMEGTEWPAQIDVN
ALRVAEARAAMGQDDRIVGNQLEKLARLVCLIVQTELKETVTIPQTIDIVMDNFGVECVA
DIIFSLWVLQHHPSLRVSLHVKSMPYYVSDVTPPDIALLIQEMEDCARQEPALATRLMPF
VRLLHEALSNGRLRIDADAVWTQPSEYRELPPHVCNRFFYTRRVLSEAELRKRQEERQSS
SVSYSDCSRYTAHSALVIFKGDLNFRRLVGDRHWDRRGFLSTLSPDEREASAVSKLLLAD
TPRVESGRHLQEGEEETDEVISFQRILSSYWPVHAVPVCAIRTIKSELSIGVKTARQNEL
DRTDPTWRVSGRYGVILLA
>TCRU_10720 hypothetical protein, conserved
LPHPVVAVRTVNLPCGCVVLAAGGGIVSVALLSTMMRSLPLEGGAAVEEMCALGPLVEVG
NLVLTSGLVTCMTVALLPGGGAALAIVGTSCGSLCLFVVESRAGGNQPALFKVCETSLCE
YSDGLISVEDLVTDVCVGFDPAGRPEFIVAASSTCVVVVDTQRFDEFLRAKATEAVVRVF

TKNHPPHVGQPMSDTFCVSFATAEVVRVLVPERYHAAFTMDVALVVVLDNGEVRYITRSV
VGGSVQLLIEHHMQRQARQSEVGLSILLDDDPIRGSPRALPHVLYAYSLSDVVHNVCTSA
VGPLAAKKIILNDATLCYNAAARQMRLIVAGAEGQSAERTGQNCIASGWWAIAYNVVCPN
DTLKHAQSLTVSSFSALNSSLLPRDRRGLAAVLAVSDNQLLFACGNELHLCTVAGDSMSG
GYGSLRHVHTTRSVVNSVATAGSLGGGKSFVIVACGSSLTLL
>TCRU_10721 protein kinase, putative
RREMTASTSLSVLLSGTIVVPGWFFLATAGLFTAVFLFMPWSTNAGQFIFMSASFLVGIL
SATLYWWSSRKNSLLVALRDEATVDQAILQDGGSVFLENHRNTGSPYQQQGRGHPRHVQL
VSRGAISSCSAASSCWVWWHEALPAMELCILGLLVILSPHVMATNVGIAQNIVSRNDGSF
KVVNIYPVVNVWKVNLLHFWFVFAFNIPLAAGITVGLVHFAVLMAHFKSLDLGIIVASLL
WLLISLICIPVVAVKRFRERCRRRWSTGLLSMSGDSPSSIPHASRDGVCDASNRVVALPS
STCGGTRGGRRRCLIRPGSAGSSSEERPHLFLSIPTSRTQVPWGTPSIGNGAQFNEPPRL
DVMQHGTDSMAPAGDLRATYLLLSSGGGVILGASESFAAHVGLTVRYLVGQKFMSVLKEL
EVGNVAALKETIQKVAFLHDDSFILGKDEEEWDDRYSCSRIGDGRSSHTELGTNADAFID
SDGAEYSTAGGEQTSMRMGEDATVRRILIRGRRPRHPSSTMAPSLSERKERPAKNGMGGD
QNDLLPVEHIPGEAEYFSLSLDVWKGSRDDFKNCFLVLCQPRLHCVLDWMPWPCLLVHPV
TGCVLHWSREAERQTGRLAYDVVGLPAHASPIPNFSGLVSSCCDIKEAGVGEVEHEGRRG
TRLEPPIPAILHIPSSPSLSLSVTFKPLTGDFVEDEGAALEGSVTGLARPLQRSPWKGER
RNASDSCRALSSSLDSRGFCRGSRKGEVAANTASFLSQCIPESLLKNCGDPAKERVGCCS
SALASMQESVSAWVLAGVPLLFVIHDEVCMPFDSATVGPCVKPENDFIHAPGGVLSERRA
ALDEPPRPDPREMLPASSAVQKGTNGTDGTIAPLHGADREMDRQPHETPSFPEGREKINA
VEKAETEGEQQNVCNSTMNIIGNNGNSPGAEAAVSDGFLKQPQFSTRAAVGLTPTPLSLQ
TSIYNSQRHSPFHVNMGKVNVTETDFPGTHRASNGEHHDTRGNSSKRRGQNDRGSRGHPP
HTPLNSRDTKNLKAVMVTPLVSPPPQECPSSRSMNGVDAHGEIALSKDQAELNHQQHPEQ
LSYQQQQQQQQQSLHPQPPLTNFPPVSSAPESTVQSDFIASMVSNVNAAGEETPIWAML
RSSDETTIPSCFIRVPPGEGFLFGRSSKCHATTSDGFVSSIQFKIVRQLHSEVLSMQPTN
QQDIKKQSLCLNHLRNSTPTSPHSCHAPMENWVVTLYDQSVNGTYVNVKKVSKGKHSILR
DHDLITFRLSSSRFFLGFQFLLTDERGVPLSETAAAAVPMAVSSVSSSGMPRRGTLHRRH
PTSSESGSLIAVSSSQLGGVSHSNNGGGSGWRLATSTRSRSGRPGGTTTPHRETIEWKIG
EEMLGKGGNAEVFLGINLTNGKLIAVKRVLLPTVAHDDPDHKDVLQQYRSLQEEIKVLSR
AVHPNIVQYLGSSQNQKYFNILLEFVPGGSLRHLLDNFGALSPGVICSYLRQTLEGLRYL
HQRNIVHSDVKGANILITDKGRVKLSDFGTAKLLNRQHSQSLDRAGRAEAANGNDATTYR
LAGTLRWMAPELLRGDVGPTKASDMWSVGCALIEMLSTEAPWSEYEFESEEQIMNLLRYT
TETPEVPECAELPELTAIAKRCLTIDPASRPTCEELLQLVVEAEER
>TCRU_10722 lanosterol synthase
SGDSPSMSSSGAFSFESVVPKPPTTWSEQMRSVLLAAGRMLSLFLFFFFTWPILLLFHGL
LTLLDRHNRRVVLKHQQRWPFESVPHVRPVRVAASREFPIENWHLRCEDGRQRWCYGELL
NEEEGNTLGKAQAAGLTILPSEDVPMVGEHYEWAAGNVVTPTKEPDMRAIKAKQRRFLEQ
YQLGLHNTTEIRRRASPEDAMRDGVEFLLRLQDPYSGHWPNDYSGPLFLTPGFIFTKFIV
AGGDIRKMFPPHRDHQHKNDEPCRCGEAERVEMIRYLRNYMNKDGGFGQHTEGHSTMLGT
ALNYVALRFMGVPADDADATRARAWIRSHGGAVSVPTWGKVWLCIVGLYSWDGINPIPPE
LSLLPAWFPLSQGRLWCHSRVISVPFSYLYGIRWAPEPHPLLEALRQELYTEPYDQIQWD
QHQSNICNLDCYTPLSSTYKLVAVLLKLYEKWHIKSLRRHALEVAWSHVAYDDEDTKFIC
LGPVNKALDMLLTWIREGEKSGRYQNHVSRVADFIYMGPEGMRVCGYNGSQLWDTSFAVQ
AVCACNMELLYPQQMSLAHHYVDVAQVQKDPKSAAHFYRHRTKGAWNFSTASQSWQVSDC
TAEGLRVVLLLRHNPFSVSRIRDAVDEILSLRNAKGGWASYEPTRAPLYVELFNSSDVFR
DVMTDYGYAECSSSCIHTLALFREHYPGYRRAEINAAIREGLKFVLSLQRPDGSFYGSWG
VCFTYAAWIVASALCISREIPDMANHPSCVRLIDFLLSHQNADGGWGEDVTASVRSLWVD
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ISGVFNGNNPIHYPGYKNTMPVWALGMYNTWKKTY
>TCRU_10723 Rab geranylgeranyl transferase component A, putative
DVQGLGNLFAAGDQETEAVCPIEEMLVDRLQLSREGTTTAGFTPLLEQFDKGTATQERGA
EERAEGNLTPLRVYFRNKRHSLWGHRLWNAAKYMVKRMDSRMIDVRGKTVLELGAGLGVP
SLAAFRNGARCVVATDYPDGDLLEILEMNVKANCRADLIDADAAAFLLQEAERLKLAQGY

EKSGETVFSEAERQRALSTRCVVEPLLWGKQEHIQKVMSYTGGGGFDIVLLSDILFNHVC
NDDLADTIVRVLQRSQHAAAYCVFSHHRAHKQVEDLEFFDKCVARGLRCEQVDEENYPMM
FPDDSGPAEIRQPVKTYKIVHYFDDAGMAFQPGNDVFDVVIQGTGMVESIVSAALARSGI
RVLHCDGEDDYGGAFKTMTVERMREYITGPLPASLDGAADNRDGRGDHEENHPRCNDGVI
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GGMQLRSIPLSRAQVFATNHMSPLQKRRLMKFVKDVEAPLAEQLHALTADVGDDSLSEAA
LERSRIASEEAKLMFAQEIHEHPNETLSTMIERKYGVSGAALDIVTLLRQLDTQPVDVLH
SVELVRQVLTSVGAFGSMTPFIQPAYGTSEMPQNMCRVAAVWDATFVLRRSLFLPCCHRE
KSAVDRSTPSIEMSNRQRVKTKVVLVPRTLASHFLASSSSSSSFSPAPAEALTVTEHNNN
NIINNEVRFSRVIMVATTPLVSWTALRSAGCTDDEVAGKDDTIQSFPPLFLALCEVRPGV
VVHIQQVSAASEQAPNDGSSVVVHFTANAREMGAEELRQFVSQTFVRHASSPDVNNCHWI
DSTALLFLASFTVREEVEALRGFVRPVAVDGSDVSETRKAHPYAVEEYRKRLRKQRQICG
GDSDDVDYSPIILPVQTLFPNLIDDSAYLRAARQVYDEVVKKLQPQEGSGKTYTFLERLP
PIS
>TCRU_10724 protein phosphatase 2C, putative
MFQAFPLQHKRMTRLSLPFISVGVCEVMNCATRDHMSSFTVHNARNRGAHLAATGSSSSH
FEAVAPPLTLSVPFMSEVVAGGLCDSFTGNYCSRYIGKYLARALSIHSVLPEGIAQLRRE
LKDDPIINLLMAAHSRERLLHSRKSHADKKTPQGVSRVFSEWEMQQYAMFADNAFMNACR
ANEMVGGLNDKLVLRNSEAANSGCRAVWFTATVAPVALQERRQERRREVDQGGTAPPPIR
WEAKTKGCEDSVEECKGTAPISPFCLDVLVSNVGDSRAFGIARNTLTSEARSILDATREH
VVPLSSDHKPLRTLELRRILSAGGVVRSDVGDIIDGNPFYNVSRSFGHWSMKCDSQRPPS
EQKMIALPACCSWEMIPGDVLVLSNHAIFETRCQEESSMDEIAKVVVREIDRGASPEEAA
AALCNYSIRFGAEHSLQVMVAVATSADSAQAPCEAKKQEWIVPGPIYAEPCRRSPEYRNA
LQADCERCALSLAELLGLRWRQVRNLIPSRHVLPLMTYYGKECSVLQQIMDEEALLFSHE
SLPPCGCSDDVLMEYDEAHMMRAFERIAKSLM
>TCRU_10725 Diacylglycerol acyltransferase, putative
LMVVWTLGFVVAMTTGAIADAFQGNAPIFPFIPTACLAVGLNGLCALFSILLGCSLWDSF
SIYQPFAGGERYVLLQVCGWTLVVSCSSFIVLYLIQLEPPMYRYGALTILEGFASIGNIL
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IGALFQIISSPAMVVFTIFHLLSGILVHLLIEWRQMEGFKMLRGPVETFFYLLSLLVYFV
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MGQICIQFSIKAFASGFCTEAKQGLGLGKRSESKSEKESIISGELILSLLLQLASIILRL
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DSSRFCLSVKPKRKCTAIKEVAEEIIDGTQEEDDILPLFSTEAENRHGAATLLVVMMCFS
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GSVFVALQIAGWVSYACTFVLTVIYTLEDKGGCVQLLTGAFFSVFSQIFILFSIPKFDSR
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FFIMALGIMTAVPFILITLSRSARRLETVAYSPRRDIDTEEDVPLGRRKSLFLNITLRLS
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GMLEQLVSFRECVVTCGLYSLPIISFWIALGPAFFLPFHSVGAYHGIYVLLLGCGCSFSS
VPHVAKVWCVCMLGYASYLEYLRVLDSGTVVAALSTLRYYAVDAVVLLVWLWYLPSYDGE
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TALCGVFSDAWKQSIGYNSKTHVTIHEASVLFNIPIIRDFNLRLGALSVTRSSIASTLAR
GNSPLIVIGGQAELILTRRSDKVMSLITYHHGFVKLALKHKVPLVPLISFAEQNVLSIVR
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EVYFASLRTLFYKHRAAAGYPEMELDFYTRNRKKVLS
>TCRU_10726 hypothetical protein, conserved
GEATRILSYRPRWQYAFPFRSKRITDFIMVRENSVASIAYTYQHPSNQVIVTLIPLQHFA
HPQFFHQVDGLCSQHDSVLMEGRTPLAGAPFSTIVPPRERVASVRPLGHEDDEGWEPREV
ERFWQPFSWGVKDSPHMTIVHAADKYDYEKLPWWCSVRFNVPLIGSFAREKHCLDMIYPL

LSNGYKSFAIPWGAAHMPIFNEMLIDNGFEQIGMCSLVVLNRIDGDISAGEYERFRRVEK
RYHRVIQSAWGLAAAGALMLMRGMVIVEYRK
>TCRU_10727 NADH-ubiquinone oxidoreductase complex I subunit,
putative
ARRFFKSDGTPYNSDMTDTLHGSEYVHRGGVEAIVEGVAAGQYAEHKPRAIMFVNKRPVE
IIPQEENLLEVLEREGIRVPKFCYHPILSVAGNCRMCLVQVDGTQNLVVSCATVALPGMS
IITDSRLVRDAREGNVELILINHPNDCPICEQATNCDLQNISMNYGTDIPRYKEDKRAVQ
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PVSQLCPVGKLYLGDADENNAVADELD
>TCRU_10728 hypothetical protein, conserved
DEVTLEDYEELLLHSAPSETLEKENHDGGVIETEATHNVNQPPLSSTMRLVNNILELLPS
DGTGTRLTTITPLLDVEAVSELFGSVLAFVQLFPHRFRSYQVEEEDGSLRWYVSRVQAAR
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KPISTTGLLQTFPMELQDSIRELGGGLLRLLKNTLAQDYLDLSEDTSFVSVKGILSSQGI
TTYHCLSKEATHKSVVSVMPVADYADDAWNVELNLDDDDDFLTADDDASDDVEPKDGFIQ
SVSVATAALPSTIQHQQQTKNKSSMSSASSKVTERIEKHRTPPPLPSKKKDLSSSKARMS
SEELLKAHTTMALLRGRRSPSEMLDLFVECVPTTHVPVQQIKVTDALARVLGPRNTLHKV
IKIYSYYFDRNKQSDTVRLKPTLQHERLGAANILYDAVTNGASSTGPTQRKLKETSVTRA
FPVLNTPIRTKMDLSATRKKGGLPLGSKTHTTSTVVCSNSECFSLLKALRHDRYVGISEW
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EAAAIEQHLKPIWLSIDRLLQKLPLSAQNSVQDVSREYGGVEPWLRQFGRMCWVDKEGKN
VRKYCAAAELDDIQHVVVQYLHSTLPTTFVNLKYDIIPNKLSSDKLTEEIIAHQSDGILQ
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FFGRNT
>TCRU_10729 hypothetical protein, conserved
AKKHSNFVELRRTLVDAAAVAAFIQEHHDTKLREVKQVNSFFQALSKCTEDLFTLLCQQH
RHQVHLALERMFELYATGRVKILPAAHEFMIRCEQNGVRRMEWAAGLESEVHTTDSAAVS
TNVSTPTGTEAVQKQQQQVPLPLLLSPRELLKKLAVIDPHGRLERMIEMSSTLGDIHTCA
RRLCKAIESEKGLEYATKCQLISKIASKARRISATVLLPEPPHLSSDDLATLSGTIDILL
SLTQRALATRPSFTSQQPISKLTHFAKWCDGYGLLGKSQVESVAALEAQATRDLGSQATQ
LETVMMLKALPSGDEAALRTALDNIWNEKEGHFEPYSADVLSSIAVLAGAHGISDAFRAQ
VAGRLMKTQQERLSQSGADLPRRALRFVNAEQSKEKQESIKRMLAAEEDKRR
>TCRU_10730 LMBR1-like membrane protein, putative
MSAGSVFSTVFFFFLSLVATLLIFRYYTKISAKDMPVLCRVFIIIALFSSILPFPLLVVD
INAAIDAKADPSMPKETWLIGVWYAIVSATYIMGWAVLPVSQSYTEVGDFAPTRKIKHAI
RNNLKLYAISLIIIVVLFGYVVFLKGAYNSIADILKLAISLANAWGLILLVLFMSAGLVG
VPKMLWRSSDAVRMLRRAYFRAVDIQEDLDMASMDLAEVKAELMTIHPLVAEEHKVYWTH
MMEKITKADREILQHHSAGALVRPVTGENHTDVSLKHLEELHARVKYSIKIVRRMNHLWD
STIRDCLAYDEFILGVKSTNNPFKRFWFPVRGMVYRGAALCTSILTLLVLWSELLLPFQP
LTTRQLSVIALAMGSEFQLVGSMVFMFYMAYCSYWAILQLKVFDIYVILPGISDNASMCF
GATFLARLIMPLGFNFLLIADLVMNDTDVMYGHVYRRNMDVSLVLGSWLNQFIPMFIPFV
SIMVLLKLVDRLLIIIGVEVHNPDDVMNDTVRQRIEDGHRLVTHTLGQPLTALDLGNLGI
SSGETASVKKANDASTGQTRTLERGERYKEYLARKRA
>TCRU_10731 Nuclear Dbf2-related kinase
SMKKEAQKVLKGAAYTEASPISEVSHQKASASKAFLENHYRGMLRETRSGGSARPVGPRQ
REPCAEDFVLLKLIGRGAFGEVYVCHRKDDEEKQLYALKRMRKTDMVRKKQTVHVRSEKD
VMAEAAAKNEWVVRLHLSFQDETYLYMVMEYMPGGDMISWLCLKQKFDLESTRFYIAELS
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LSEMAGKPDTASPAERHGVVHFRDRRMFESIVGSPGYIAPEILLRQRYGIACDWWSVGVI
MYEMLYGIPPFFSPNPNSTCYKITHWREYLLYPDNCDVPEDAVDFMQRLMCDPKDRLDFS
GIKKHAFFYGIDWERLRETKAAFVPALTNLLDTKYFPEIDDGDKVQRGEERNIVKEYDPH
GVMFADYKF
>TCRU_10732 hypothetical protein, conserved
MSLRGPSLSVPNAEGVPRLTDVALYLCGKAMVSLWPLLVASDPEAAEKFAMWYFHRVAFM

HERMAGHGNEAETVAVASDMRNGGETNFSLAFNALCRGPVENESHNWQQQQRQQRERSSL
PTVFGFAEESSSATGLLLQTESLALAEGNARGGGDSNAAFTCFEELLDLCRDVAGRDIRE
DFLRCVISLITGDVSYPTRAPLTLWGDRSVKERAAVILSTLSAMLTLKNEFTAEHVARSL
TRSFAVWMDVSWSCASFGWQMHVARVVGQWLVDFESLLTSVVLPGTMPFLSQPTRLPQKP
NLSTHGPSSRAPHPELEGKQKLNIASMYMALRRICEGTLPNDRNLMEMLIQSGCGVRFAD
QNVLEYMMSDSAAGGGASDTQLSHQFILLRITSGVLLYAQFYLSVHSLEAALHCAQTAVL
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PRFHAGCLGYMGAAILMLICPGTVDTYLRSVIIAGIVAGRPAFSEATSDGQAVLGGGHEN
NNNTNTNSHADTEAVRGGHSVVVQSVAQTVRFALWLSEMETFLDPSSTVVTEMITGVGRE
TMTIIAGHYGVRSSLRAINTASLGQLLTQIDEEASTTSSIFSYQPSSLLLRELVRQIAHR
ALATQVGAADALPGSGPFNILHDFLMAVELHYGEDGVEVLRGDFFFISTYRFLFAIWLRN
HGYMKSAYQELTRIADSMLFHSRCCMDGSMMDGEAAFASNAAEAMEEDISASAVKTAAMG
TKIMTNGTEKVKKSDLQYWPPDHLLLWQHMHFERAQLARYLGYSSTLPDIAEKLRRVSAG
SHFVMGVLYADLIAAMMCFQRGNYCSALHALDKVLGSAKHIGLTLVQAHAYLMRVFVLLT
CGRWNDVLETLGSIRSIPSLLEPGFLLARLRAQCEAMMECTTATEADLAAVVEQHVQRME
ACGCFLEESEEEDSIGITLAEKLCVYACIARFMVTPSADQRHSWDNNLTTLTKKLRQRQF
QEGKWQVLSNMPMRRVCRDILSGALLQQL
>TCRU_10733 conserved protein
VKFSLEALPPNLQQEFSCEENARNLRHMIQLSSGAAASSTEAVIKVLPSWVHVVSWQCGA
CGCQWSARPVDRMDPQVSSFYACPKCVFGVKSEENARPRLLPPRVRRLAEVHPLLAAQWD
DRRNAVIHNRVFFESVTDVPLPCSTVVWWVCPHCQKSWKESVDSRVHRYEQQQQQHHKEN
EDLRHGKATLPLCPLCEGCGVCSSPHSDSSTSSSSLSLPQQSGEKSSIGVKRFLQDDAVL
LAEALLQPHEDPAALSLQSNRLLQWRCRWCTHEFTASIADRFLRYHRCPQCSGAVATPLN
LLAIQRPDVLREVARTVSSAKLLKMTIHDDTVVTFVCRICMSPYRLSVRLRCLLKRGVTA
CPKCLWNRSQFAKEVALANEQRGASKAIPRISMKKLRLKRRGRDTFDTVRNQLYQRDTEL
MN*
>TCRU_10734 AGC family serine/threonine kinase, putative
GTGKWKKKKQQQKMFLKLFKREKKEKDEERSGEKSSEKKAGNNNHTDKKAPPQEKVTKDD
FESLDVLGKGSFAYVVLVRRIGTNEYYAMKVVNKQGLLDHNRYRDVFVERNVLSRINHPY
LLKLYWTFQSEHKLFFVMEYMPGGDLDKYMNNLPSKQFDLFTAKLYAAEILLALLFLHEH
SVIYRDLKPENILLTGDGHCVLADFGLSKDFYNPKEGGDASTKDMRANSFVGSPFYVAPD
VLKQSEYTNAVDFWSFGILLYRMLCGRTPFNGKSMREVFDNILYSDLRFPSSVQLPSEAK
DLISRLLIKDANRRIKGPEIKAHLFWTGINFDEVMERKVKPPKWVPIPSPEQVMAERAKT
EGASTSAKNPGQLVNTPAQSSQLNSRQQQLFTGFSCTADNHL
>TCRU_10735 hypothetical protein, conserved
MMRVCRPQLLRVSPLLRVWAAEEDDANAPPTTFKNVKPGRLLRLWRQIRHRSWIVYTWDE
EWTSPGSEGYLHQQRLEQVCFAPLSAYGMVPGSYCDPLLYNTKHTSPFRWHVANTSSDIV
GHWYMEADEIFRIKDWQPKNPDDPTEMFPRPPQQILKWDETVDEHGNRTFRYKYRYDFMG
PTGMWEAYPRYPFSHIYLNGQDHHGRAEGYGFKQGHLLRCSEEEEEVLRRIMEEEDKEWE
MVKRTEVVQEPWSXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXNRPKGEPLPYQVTFNDGITFEDNEGRPPVHPESHYEQTPKEAP
YKKYEEQDTKEEEEEQKRRKSAWDQSFKESIAKYEERYGVEAKKGDSDKKSSSDTGKS
>TCRU_10736 protein kinase, putative
EMDRFIVGSPIGEGRFGVVRAAVVNESGVPAAIKFVTTPRLDEGIPHPTARELLVALRLV
HPFVIRKYEVVPCGCSLALVMERCKTDLATVLSGRTASNPLPALEAKSLFKMLLLALAYM
HSEGVVHRDVKPSNCFLTAEGELRLGDLGLSRAWDTEASMTHEVVSGWYRAPELLLGQRH
YGPEIDVWSSGCVFAELLRGHSGAFFAGDGDIWQLSRILDVLGTPTPTSWPSAVLLPDWG
KVHFEPKRPLPLREFFPDASECALDLLRRLLCLDPQKRLAAAGALCHAYFSE
>TCRU_10737 Enriched in surface-labeled proteome protein 1
VHTFRVPALFDVDGVMVAIADARYDTSNDNSLIDTVAKYSVDDGETWETQIAIKNSRVSS
VSRVVDPTVIVKGNKLYVLVGSYNSSRSYWTWQPDGSDWDILLAVGEVTKSTAGGKTTAS
IKWGSPVSLKKFFPAEMEGMHTNQFLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXKTWKFGKGRSDFGCSEPVALEWEGKLIINTRVDRARRLVYESSDMGNTWVEAVG

TLSRVWGPSPKSDQPGSQSSFTAVTIEGMRVMLFTHPLNFKGKWLRDRLNLWLTDNQRIY
NVGQVSIGDENAAYSSVLYKDDKLYCLHEINTNEVYSLVFARLVGELMIIKSVVRSWKNW
DNYLSSICTPADPAASSSKRGCGPPFPTAGLAGFLSHSTSQNVWEDAYRCVNASINRGTN
LTRGFTFEGRNAGALWPVGKQGQNQRYRFANHRFTLVALVSIHKVPRSTRPLVGASLDGS
GYRKLLGLSYDKEQRWVPKFGQAASFPTGSWELNKTYHVVLAFEGGVGYIYVDGEPLRGS
GQRLTGVQLKSVDISHFSIGSYGTSDRGTDFQITAKHVLLYNRRIEPNEVQTLFLGISKI
VATSE
>TCRU_10738 hypothetical protein, conserved
FLTSGMKGGEQCLFRYYEILPLDFEPEYKLGYTCDMCSKDFSKTPFFHCAQTGRDLCMAC
GENLALNQFSALIGRMMAPNILWKDSQKDIIVVFCYQIQFEYFGCHFSDGSNLLIACEDE
LPSFYIEVGISLEKATTLRKAELLMRFPWSNEALEMSERDCICFYRMTKCLDRPRPCFLT
SFRQDGLFIEFCFSDGFSEILHCGEGVVLVVKGPFVISCLVMNLPLRWGKSLPKAAASLL
EWFLSG
>TCRU_10739 caltractin, putative
MASFDMLREDILDVFNVFDEEGTGSISMQELIRAIYTITGTRISRSDLRSLVQAVQEEMK
EEAHARKTPLGVDLPPRANSLETSISPNADGENDAVDSSLFVAVVLKTLNRHTYEQELLF
TFHLLEDKNYPGFITKDSLKKAAAEMEEHLTDQEVNEMFDKLVTGISSSAVDFTTFASVL
EAAKR
>TCRU_10740 hypothetical protein, conserved
QRMLTNEFRDNPDERLKLYSSLANIACKRTEHPSDSWTAVMLKAAQDSWSRIRQLGRENI
LREVSTEVGVPNKDYSKRVLSVLLSKWPCLEYWYEREGFLLLLLGLLSTKTEVVSDVRVL
SQILLRVVLPALLDPQVSLREVAGKLMVQIAGLSRELAVFIRDYMLKKLEMPLEEKKEFV
TCEVEGLLSGTAMLMAQFPSIFHSEWWKRMQPLFQQLAIHSAASVRQRVAGLWASRSVES
FEVLCMAMVRKSESPSDGDEWWRMVEVLLMALQEQLTHLLTLSNKAVAVGAKANGIFIAD
SLHASLLFAEMPQFEVARMGKQLVPLLTQFWVRFSSSLAFVEDCCGPRARRFRKCVHFPS
LFLPELIWFLALWRYVHSRDGVEKVRKAVTRHLMPLLSGKWDVSLNSHETEKGFSQSEYS
LAVLMLCTYFPDCFTDSLGRDLIEFALSEEAWKRALSGDIDSARYGVDFALSVRSVGGTV
AHLVPVWLQWLPGAYAHQQCLILEAVKIAIGSPKHWVSRRPFYFVYRSSFDAPTIQDGGE
DVSRGFYWLKLYCPTVASLPEVACSALGTDLSAGEFPVEVHEVVYESVYVSKGTEHSVLN
IVRSLMQMECEATHKAESIAVVSAAVIARLENVSPSWRDALSFSLGGSGGASDTVVCNTG
DGSDGRGGDFDDWDDSDSGFDAEGIALEVEIREARSLLMAILENCFGADEANFLRAMRPT
ERKAVKLLM
>TCRU_10741 nucleoside 2-deoxyribosyltransferase
MSRVYIAGPAVFNEDMGATYYDRVRTVLGMHGVVPLIPVDNVATGAAEIRAKNLEMIRHC
DAVIADLSPFRSHEPDCGTAFEVGYAAALGKTVLTFTSDRRSMREKYGGAFDASGRTVED
FGLPFNLMLCDGTEVFDSFDAAFHHFL
>TCRU_10742 hypothetical protein, conserved
MAMHLLPRVCATLPLRLLDCSSCALLHALGQKPTSVTFSAAARFAVDAITGAVFVGGATE
TLVPFTLLQTLHESVLATSSEAQRRAAWKAVSGGNQLVVLVEPCDVPRLIKQFPQYKKVC
MCVPSGPLASRMLFGQKHLEEFYAEDLTPAVAALSSVEGYSWTAWLRSSLTCRFEGLYVP
SIRVAESVAHLLSSDGGCERVVLEEGIRGLTPRWLETVMKTTSSCGVPLERVTLALCRNE
KNDGDLFSRAMGMGIGSLAASTVPAPLFAHTEELVGIDDVVTFATGWNDVCGRISAEELA
SLDDCIEYCGAMREEW
>TCRU_10743 PLAC8 family, putative
EIESTLPLGLCGLDQLEWSGQAGAVWECWKLAPCCGHPDLLGVIYCLLHWTCLSPFSMCK
LYASSLDDPCSVWPHCFCILCCPVGRWFTRYNLRKKNGTRGNIIGDCCCVFLCLAPCACC
QELRSVNASAWRLFPDFTVCGGCVPGCRFLR*
>TCRU_10744 hypothetical protein, conserved
GHIPWIEWRQLIRIVTAARCTLLSSLAAPSASGSTDLPGTGGDKKMYSLAAAHSESSNEI
CLRPIMLLFHQHECLACHALLKNVGISAEFELLSEYMTMVVAESLEDITEKYPYPLPHFH
NDSLFVNRGRRKGKLRREEVEALREAFAGQGEYFPRVFFVFPQNGSVMPIFNEEGDSDPA
HPHFYHEATSLVRSMMVALWTMNKAVSFSEL*
>TCRU_10745 hypothetical protein, conserved
NEKIQEILRDMDDSPHILYYTKEPLHIHRHGRRKKVLIVSTPYHVYLIKAKGISLYTRWP

NKLLAVSSTQNIISIGTLDLSQGQQLQTFTQTAVSEEISRDVEFKTVQLECASVLQATNT
ERWLQKLAADARWRTEQLKNYESHPAQNGAQEANEKEDEWSGAESEGSDDSTGPLWGQKQ
QQQLLPQRPREGETSSLFQKAPSRYLAVASLVDGEFTDYTALKNAYIRNEEDILQGDLAA
FIKENEGQVEKLCESHYPAFLHAARQCFFISEKDAELVGQELGGATTLARSSVMEMKRAA
ADLNLSRCVKQNVAHVGSLLRSTLELAEILETVEQRVRKQQLLGAVVSLKQLMRGAAPFA
EYTLGEYVIHHRVPQLSQDIFTAAVHDFNAWLKLLRESSLPIGTAALKWEGIVQSGSVEK
KLRVSEEGEWWVEMSYVRACIRRAPFTESSSIANILHGTSIQEVFEELHHGTYYRNYYAE
SRMQQLKLDLFEAPLSSEGLDGEATVGELEKYCATALGFVLIEDIVHNVTEPHVQSTTEI
ICMWERLSQAMADRARHVSKLLLSDPDYTARMMDVFRLLRSFVGIAVESVKSVRLSPLIL
SLVVESMSDSIISSWLQEACVEVTQVVLTDTLLPLNATSSEEYHAYVTRFYVDRCKSIEL
PLPVCGFTSGCVTLPYASMVPAIGDTALRFLSQCHSIMVMDDGAVVRQSELNNVDEMLLK
YLSVLFRTVAELLQTHMVSVDARAVLQLAVYVTSCATMSVIVSCVEQQFVLAWHGDCGEA
RRETLGVPRLLADSATLFAKAVQKGIERLLAAFVAETEDRLQPVAEIDYWKRLVEIRRGT
AAPTATRAENNAGTGKGLVEAMEYIIAMIPKLTAVLQVSVVRSVL
>TCRU_10746 LEM3 (ligand-effect modulator 3) family / CDC50 family, putative
YGRTIYGGNPVVQQTLPAFYLYFTPVYVVLAFFFVAALFIPLGVISILASDRFYEVRQAY
NEIHRYQYIPTNPAVNINQGIRSFTVGNKTYKQGTRTRVMLEVRETLKAPVYLYYTLGNF
FQNFRDYHNGASRNLLRGTERRSGRYKECEPFQKPGFLNDALGKEVHVNVDGKIHVMHYG
DFIYNPCGMAPWSMFNDTFVLYRVVNPKTGNSPSAADLVMICNSSDFGPRGEPLGQSASP
NRCHKKGITWKADEEIRYKPLQPQLKWWSLRYPYPNDNVYLTNGWYVDEPGHSLTDPSDY
DLQVWLRGAALPNFRKLLRIIDVDLEKGQYVMEIEEFFDVTTFRGSKGFLLRTTSWVGKD
GHALGIAFLVVGALSFVLGASFAIEFFLQRNRDDRPLPEPKARWYIFDPNGVEMRVYYEQ
LTKR
>TCRU_10747 hypothetical protein, conserved
EIRRRLRYQKGLSATRKESLLRECHYFAAGAGERKRSFLQSLTPCFQPNRDTAHTRRNSS
HGGRKKNSLFHVLRRMAEFIASTGEYGDPLVPLQGGYEQLTPANGLRRSELVLRYTEAAL
SISNDRMASIMTLAFGRCSHDEENITSLGTDALPLDSGSENMPMNGEEEKEETSFSLTRD
DDDDAAAPFTSLEAVALLRWCAWHMRTALNGLQDNGPQLMECIQLAVTLMSRFLRFIVDI
GLQGGAVDSAVDELELSDMGYAVADQVLLLLYSCAPLRARGCFPSFSFFPSLAVGSFHED
NDEAAPTVCVSGKQLGRVVTMRPAVDMMAIIIVIIMVQVRPLMTDRSLRISEDAQQAFLC
SQRERWERALKFLLRTQRWNEWVDASLDTPPPAEKNEEENETLAAEELRTLLALPMSVLQ
TLKYVLAQHGQWGICRALWKETVRKRFQETPSLSTSTDSSLSPFAALHHPFNVDNIITAL
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GCGPVEGILSPSFVWRRTAAHPHRVRATLCILCFQLVVKCGLTHTLEVEDLYVVTSILRQ
FLQGQFRRGVTRAPAAASVSEEGGDEGEEEEEDGRYRIGENLAEKDGERALGLLPVAFAA
ATRRTKMIAAEAHIVAITEVFLARRREILPFRDEEAEEGAKRTGTNMDPQLDSLHTAATT
VVVAAAAAAAAGNNSKEKRTNKRKSQSAVILSLLSREIMALMAMAPYGNAVGRTWQVALC
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PVGSLLTWEQSLRLLPCTPWASNIQRRLLRRVVQERDASELPSVQGLIQAITLPPRLLHA
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ALRSVLWVAVRAIGGERVAEEVLHASLRRGMWATGLAFHQLLQTEQPEMLRKHHRIEAYG
ALLCKGLLSQSALTRTIAEVLKWARGAKWAEASDAFIRYAEEGNLSSGQTMRESREMAVV
GAPPSNWAALFPASVPSQLSHIAHTVRYSMLCTPGRWKHALAWFPPHTLPLPLHHRLHLH
LLTGAVADFSENESVENANEGSVIHGVHGKAETASRLLPSPISMSLVQIALQEKLHRTRK
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CFVHLTGRMRPDAATAALALKACVKGHQWVLALRIFRQSVLTSATPPPRVVTYAVRAALV
SGAWQAALRVVRRYQGTTSPLLANTVMQAYVHSECWNDAVEYFYECVKRGICPLDESLAM
AITASQAVSAEYRDAARVVGAIASALEDFCHVHGVVLEHVLVVYREMSPGP
>TCRU_10748 hypothetical protein, conserved
PREWYYYCGKLLSILALSCVVKFSRLVEVMLRSRKIIQPAMWVSYLCYVVFFALWIYTSC
FVQPRHPNWSETHKYLIYSAACAATAGGVLWTIAVWPIFHIWTIPLGMVVLVLFLEVVAI
IPWNSRKMKH*
>TCRU_10749 ubiquitin fusion degradation protein, putative

MFPVLESLDVFRKQLAAYPGEFSERGELVDGGGRVLLPSSCLAEISTMNVAYPLQFCIRS
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FIHLSDPRQVLEMHLSHYPVLTRGTSIMLHYLDRDFIIDVIDITDELDRSVDAISTVRAD
AQATELKVEFERPLDMPLTPSENELPVQEGTNVIGTAEGVEFAPFVLKHPTIVKEKEEKS
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AFG
>TCRU_10750 hypothetical protein, conserved
VAQRFNSDSLLHDIFSELDACDITQRNNQLKMETSTSSKKMNGGGTTATPVETATAEEAD
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SPQHFTPAGDSSRRLSALPQLNSPGTVAVVTLVGKVLSVAQMHGGEGSIEENSVTAVDEN
GPHARFLVQYNVPFLPSSRPVTVQVRCYGATLASFAKRYIKLGDLVHVLGHVLPLDSSSA
DGPSFCVCALPVGGNISVVLSAE
>TCRU_10751 prefoldin subunit, putative
MAALVEAERMEREKALVEAQQRVNMLRETVRVMANRQVALMSNKRRLDISTNELTRLSAD
HCVYESVGRVFLRTPVNALIEKQTAQAESCEAEGTRLSNEKQRVTEQLKKEEAQLREAAE
TYVAEMNARQRQRQ*EQ
>TCRU_10752 ubiquitin-protein ligase, putative
EMNGNFVFNGRSRPTHLSLSRDHQPSKDAILAETRKKRERREINRVQQQAALRIQRKARL
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AILGRSNSINNLKSFDRELYRQIMSLRSMSEEEIENLSLTFTYTVDILDEVREVELLRGG
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>TCRU_10753 hypothetical protein, conserved
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KTYFATLSSSVLCRDATHDALRGAAASLFKDLMRGAKLRPPSFEVLGRRHETRRIPLLGA
SFSTSAVLPTRTGAAITSSTLLLRMRQGELPRNASHDWEKRGLVCCSVSPSMPVAVTSSS
GVVQRGVQQLLRDLRQSCPHALNLCIRLEEFLPAGDEEAEGHAAKTTPANSPRKLLREEM
DPDEVGVWKRPAATVDALMRWQYFNWDPRAHSKDELPHHRRCQSVHIFVDASRIKGKNAS
STTDLAGTRRHSAARSLMPPRFSEKLEEMNFKRVSHRGLAETFAALRRWSVDSHWHAIEG
RRR
>TCRU_10754 DREV methyltransferase, putative
MAPNIMDDLSVYGNGRRKKPPFSYTPNLVCLPNHIVSKHVSMCMDEETTEWLRLAGDVSV
MKTLLSGILRAFFSQTTSNGILNRGGMFVMSTAQAAQLLLGNGNDQRSSTSPPFGTLLDI
GAGDGGVTSRLQPLFQHVTVTEYSIPMRWRLWQRGYEVLPYQDPFRHKDGSRRYYDVIAC
LNVLDRADKPLELLQSMRDSLSPNGILLLAVVLPWCPFVENGIRQRRPTETLPMEGGECC
RGASYEDSLQRLVDNVLIPCGFKLDRWCKLPYFCEGNLRVEYAVLHDAVFVLTRSDGDAS
SAEKE
>TCRU_10755 hypothetical protein, conserved
VMFWRGWSGSILRRRHLKRGGSVRALRELRKIAILEATADKPLHEREGKSSSLLASSSSS

FSSLARGSVLRSLDSAVEAAYDRMNFSKGFHSDAAVSGLSTSPKAASLSHFLTECRRLRV
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EDALHALEFLAIVKVDDAGEKARALVEAKRPRWCQSCHTYLVLSLFRHVTHKSKELKFTS
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HESPAYREWHMQRDTVDGVLWGLCATLQRKDARFVNSFHFVQIMETISRLPPHFLSRPPH
PRRRAIQNFGVFATTATSNSSSSTDGEGATLLSRARDEETPQTTEEVWGYLIAKACIFIP
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>TCRU_10756 beta prime COP protein
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ILHGPSGQFIAVIGENDYTVLSSLSMRPKTYGTCLSFVWGPENGSYAVLETSMTLKIYKN
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DGTIPAVPMYAFAAKRLLLYRMRVELELVARVLPPSLQDPTTRVTHRLLCPPSSSSPLSN
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DVFSELLRVFESDANDAIVVFTKGCTVDVAASLVTADAAEDDTIPALVLFHEGEGNNQDD
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DGVLTVDELSRYSDGSFTRLVIERAFECHVPHSGKRHIMDYKTYLDFVIATEHAATLPAM
KYIWSILDLEENRKFVTVETLRCFCKAIANELIANGLMTDISAQSILSEVIDMINPKWHE
WVELDDIVRSGHQATVLPILLSYRNFYAYDCREQTAAAANDEYA*
>TCRU_10758 heat shock protein, putative
ILAVDLGVDWAKAATLGGGSGASLIPTIVLNDQANRKSPQCIAFRFLPYDTDDILQRVER
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YDMGGRRTEVAVYEFAPSRQRLGTITLRTAIVNNTLGGRAFDRCIARYIEREHFPKARPK
AIEPVLGVSKPAARKAAVSLMRAVQNARERLSVNQEAPVVVQGVQEGDSGDFTTIITRAV
FEQECAHLFDEAVRLRDEAIAQTKGIVSSVRELTRFEVIGGATRMPKLLERLSDGYGRAV
DRTLNSDEAAVVGASYMGAARANIPIRGFAVVEPLMNDVWFSLTPLLQDPRDAAAPPRNS
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VEEEGEEERKENYNVSDQSSENESNTSEATAPRAEDKSAEKEIVERVVRSFPLSLVLVPL
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ANWREVVKEVEQWLDDTSDNVEISELQRQQQRMNKLQIG
>TCRU_10759 hypothetical protein, conserved
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DGSPLSWLRENLQLLEDGRKSLNERRASMPEGSPQWPRYMFPSHCCEYIYDPSNDSKLAF
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MVSPRPHPFLSFSEAVDTDDVSLMDMSSCYVFEREAVVRRAELAAILRVLCTAKDADSCD
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CWGRKNLEIMFDLLGVASLQRIAGAPVEAVTKNEKAAVLRQIIYELATVLSEGDAEFAET
SCAKINGTSSVDAEVQTRLLAEMALQRLAHELIHLHTMLLMDQAYETYVKLGYPSEGMLE
KSGFC*
>TCRU_10760 GTPase activating protein, putative
DGVSVFLFSTHHIPHALKPYLSTTSVSTRLVEQCLWSYRDTIFLAREYGHKTDAERTQLR
VHLLQLQREKTNGRKDTTDRSESAPFFVEGQLWDLMLREPGKHPILLSESLRYQQILQDM
KHLARGLLAPIEILRHRNYWLLLQEDVQLNLSDRLLHYRVVLRQSPPVTMVTRLWCDLWA
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GSCSGSRVTDDTQTAFEEEGDNLAFGPLLPHRVGITTLRHYAIRVPLLSLLRSLRVWKEE
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CCGHPDCSAPPTSSCFDDVMKLLVKFHGVPLEAAQNFLYAALHELSLLLRKECELPRMAS
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VTAEGHERMRRVIKAWLLMNPDLTYWQGIDSVCAVLLTVSFTNEALVAAQMQKLTQHYIP
HGPVESSISGAKSMEDHLHQLVMMLRYCDPRLAVHLLDEVECHPEIFAISWFLTLFAHSL
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VLRDAALILRSVPSCGVAVAPLQRLGGGGSACGVSHVNVQTILQAFNDSLWRAAEGAVGG
GWMQSGLFLVDLRTHRGADVLPQRATRVEERVVGALLFPLAALHAHEDDDDTGAMKYSQR
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>TCRU_10761 KREL1
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IGRVVLNGELFGAKYKHPLVPPSEKWCTMPNGKRFPIAGVQIQREAFPQYSPELHFFAFD
IKYSVSGAEEDFVLLGYDEFVEFCSKIPNLLYSKALVRGTLDACLAFDVENFHTPLPALL
GLGNYPLEGNLAEGVVIRHVHRGDPATEKHNVATILKLRCSSFMELKHPGKQKELKETFI
DTVRTGALRRVRGDVTVIADSMLPQVEAAANNLLLNNVSDGRLSNVLSKIGREPLLSGQV
SQNDVSLMLAKDALKDFLKEVDALVLNTSLAFRKMLISNVYFESKRLVAQKWKELMKEEE
TAQQEA
>TCRU_10762 Ydr279p protein family (RNase H2 complex component), putative
SHPSSCCSSDGGSPRRRLELDDEGSQSVSCGPMDVGAWTAGNVRYDASDHTVALPSNGLS
RHMMVLPRVLLHDATTVITTANNNNNNNNNNDSNGCNNINRTTRHTACKYIEDGDIERSPS
NTVDNAYLTHNTSPRPAVHSSPAVCDAPPSACEVSLFSGCDFVRLPHPRHGGPALFLCPP
TIERKPGDVKDDSARVVLYEVQAQLPLGGFGQTWFVNDIVEPNEELLVVTPFDVTFLALR
QVATHARKEMFVSPEDIIMGATKTRGGGSSEWPGWRVAMAQCPALTPVVEEMQSHTVLSR
LCDVKSVGGDQYYRFSEERMGQWLREKVQRVANSPALRAILQIGPSPPTNTATTSIRGVH
GGNDKTTALPTNTAIADVPLPVAFGVVAEYVVEEMSQTAARLCGSA
>TCRU_10763 cytochrome oxidase subunit IV, putative
ANKEMLSRRSLTAAFAAMTKQPLMQQRRHDHDRWYGHALELDSHNYKFTGEPPSWMRQRE
RTEEETAFAKSVLPHVDFASSYECLLFDADRLNGHLNRKEFGNEVTFRLEKQSNTVARAQ
QMLKEKKSSSDERLENTMIARIFDEEHVQAEMKYVKCIRANELAEDNRLDILPGGSPNSL
REKTRWNVNTELHPADRAEIGARLTAWLPEKYHIVYFDDFQTVAANDPSARREMLNIVQN
VEREYADEAKSSGYEKDLKEVVNELLDDVDPSRHITSEAIKACTDLNQLEEWSRVVHEYN
GDDRILDIYARAAELTKNADHQALVKNMKEWRKLANKI*

>TCRU_10764 acetyltransferase, putative
MKRKRLDVFTIKTLFREYMVEYLHCGFVGKEDFTDVFMCEACLSWLSSARELREHMEVCP
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VLFEVDDYGYHFVGYFSKEWRKSVACNNSLSCVMVLPPYRNKGYGAFLIKISYEMGRIEG
IPGSPERPLSAAGKKVFSRIWREEILQAIFSLNEEGLPLTMNLLSWESGMAVEDVAVALH
RLNAVFFVNKHGPLLHLPSGTKAFAKRRGMLNIKSLIWTSL
>TCRU_10765 U1A small nuclear ribonucleoprotein
MELLRVRGLVFYFGVEFCRLTILRCFSEYGMLYDILLDVPRGEALVSYTESASAQDAYLK
MNGFLLFGEAIEVSITTAPASDIPGCRVTYRRSQSLILRGASSLWVELNLKHVKGVNQIV
FVDPNTTIVFFANQRISTMIKKLFDGRIDYKGNPVSILYLKQ
>TCRU_10766 hypothetical protein, conserved
RWMSALEEHAFLELLRQIEKERYAPNLGERAILCRTLNSAFNPIGMYFASVGALCGLIGA
NHTQRLFWRMFGMLMGSMYSFEASWAFQERQPCFSFFNDIRSVDGQLREKASEYHLVVHL
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FALSYYK
>TCRU_10767 hypothetical protein, conserved
YKPVLIPREKYAKIAHGRNIFLATCLGGAALVWGVSLIPQWLIYRSLRRMYQTYCRGRVL
DLTPKIADASNVRLYEMSKAIRVEFIVDQKVIDDGRYKIDGSLPEAVQAERRKAMTLDFM
VKNDHNWVGSTVVFDIIEKGETKMPDFQKYDTVVIRNELLNRSEDDARQFLNAALTYVAK
DGYVLLMDFGSPSWPKLQSCVRWFNSLTRSSMHLTHNYNKWIRDDARYLLIEEHRCLMGF
HYALALRPK
>TCRU_10768 hypothetical protein, conserved
SRETGMPPYSRVINLYERFTVLSAAAIRREVHGLLGTTTCSTPLLELREVCELLLKIGER
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SNEKLLRLGFALQRPQSQRRRASLHFTDSNNDDGEEEEEERAEYNAAMQRQLFLELRRRR
RYKDLMQCVMNWKSKGLLPTRRRTGERDSDGIRKVSDEESSSQPMGVSGTETTLTEFAAP
FNAEEALRGLIFNTSSSSTLYGSSGGQWEEALRECPEFFIITLQEPTAALQFLRKTSVEM
VTRFALCLLQVDSTVQLTHAPYTVHNRPEQRVAWETIASLCFALRPHLLHAKKVVKVDLL
QAMLRALREEAATIGDNFIARRSANPSIANDARLLAMRSAVESLCASLSHQQKEAQARFI
GLPLFIEVAVALRDCGVQVPSALAQCVFLCLGDSQLHQWNEMSSSGSQAPVGRELLVTLL
SSPPTDRWVSALRLLRLCDERREFVVTAAHLRCILSGLQSISISHTWQTALCVANSIMNQ
YDIFPDESSVEKLMLNLHAASWQRAFEVLHLYDKNHIAPPPQLLRDLHVVAMKHSSWDVV
LRVMQCIEEVGSEQASFMNHVYCLRAFGCAGKWKEAVELLKHLKGISGLEMSGRSVFNEV
TVAVPVMGMVENEHWESVVRFAVTLFRQCGAKLTREGREVALAAELLALLHIGDVARLAF
FLNRHSREPMDAHDVAAEKYADDDPQLEGFGVPSFVEELRAIVQRAMELHSLCGMEHLNA
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>TCRU_10769 uridine phosphorylase
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>TCRU_10770 hypothetical protein, conserved
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ESSVAVLEHDIETRRREYAKLVLMYKNANTDHQIAKEALQKFKDKFEEGRRMKDKALGDR
RLRVERALKETHYLEVQEVKLQNDIETEHQRIEEAETLHKERIRRRQHSVSAMERISMVQ
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LQLQDQVREEKAKLEQLSAVVRRLREETRHAKLCGVGRPPVTSGLRDEVVKCIEEATVKR
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RQLEKRRR*
>TCRU_10771 hypothetical protein, conserved
MTFFDLVDMTVAYVQYMYILVSISSNSFPDFYLEPFRTLRYLSLEFLDRFSEENRYNNPL
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GCEQRWGTSLAEKAVMRSEVNRRALAALMAYENGNKHYLRRCHLAVIFPQAVVAVVGFIA
GIVFIGLPPISDIRFFQVSRVGRMAGSILIFAALLTFMWVTLGIFRSGRKLQLKMYDLLS
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SCFPCDFSIHTQNCPADLQMRLCGRLDVHRLLAYDQSVPCNEVNVFYKATMVVILLSYTV
AYPIFLVVVAHRGTTILEKEYPLEKRLLDEFTERELYYEKVRKSANVSAPVYQAYRRSYR
KARLTFLLQRVLLVAISCLMSQGIKESLSWLGLMLILLVSMLYFLYTTLLHPYARPVENL
YGAAQQFVIVCVASIGLVGNRIGRDNIPFAVSVFFAVIVFVAPLAALIIGLVRTFRKDRE
RAERLQRRLQNGFAVENKSSRGVPTTPTAQNVRNANPSLNVVGDSVAHWMDGDIKVFNGS
NTATEKRERQDGMDTLSRNKSPKGRKRSSERILSKTLSREVREMGNDTSADQKQQKEHEQ
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GTKRDRDGTVAEQQQNSTTSDVKNCTYAKTPRNGAFFRWWKRWQKVLNISDFSLKYKDVL
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ARLKERKNLKYPPLVVKRKESVSLASIPSIMEAMSFRFGKAETDSPSSTEKEGMRLSSTK
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AKKQIERLERLCKRSLQNPGTGQRRPTVFAPVFPKVHLEGVEVSDWDEFMQQLLAEVSCP
AADSRGALLNFSFPPKSESQSNSMPVKRDRAATTVTHEDDKKKKIKEGKETPELSSLKEI
EEVGHTVSMDSRLSNNVQLLLRHFVLRRRLCDVFKKQKNRLRALQQAVDFRIAVTIKKYM
QWFFLALSVCTTVALVLCLSGMLYGMKEDFVDGVWRDNSVEREMMGYSSWENFTVHCCCL
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VTSENRVELLGCSEELSEMEKKRW*
>TCRU_10772 hypothetical protein, conserved
MIYDVLELIMNYTQYLHLMVLIAPSMFPTLYSSLFWVVDIVMNAVFSNGGDHNMSNQTKP
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LCASFFWMIAGILLLLLLLGKLRDTDALWQNGQTILAITHALSLHEAVVMTAISASAVVL
LLVIGVVLRLVLGARERARVLERLRQLECAPCTEEERVARRLLQFDSTGLENEEEMEKEA
RVRRARAEMAYQRLFWSRYKETHSLSLPWTFIKLIMCILCVASAFVFALAPKMDFLRAIQ
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ILRNAISLFPCQTVACTVFDGSSYSDEDTSSIGSYAACMQRKTTHVSCLSSDPNVPCNGI
DGFLMASAVLATSAYAVFFLLLYGLVARQALRALQRYPLADSVTASSTPFACKEEQRTGI
GRRFDGDVTDTPPTMPMDSLFATNASALTASRVKKASKKIDVLYRERVSSSRNEAQFLYA
PYTYAFRYFKLVVLAQKTLMVIISTLMRQGSGVASPWMGFAACVLIHAGFAVVLIVCRPY
AEPLEIVVSLALQVMLSVVAAMGLTSALASTAVPVPLWSFVTSCLFLVPFVAVIAGEILT
FRQHSQRKAWREKDAKQSSCRSNRHFWRRWGNWLVGYFRKARPVPSYERCGGDRLGNEVF
IPALYFVRDKKETMKSVGGGPSLTRGRVADACTRTPVDDTVVQSAAHSDLVDISRVPTNS
GCRFLQEPRGNVTSDGKTGAKRHWALLRDAVYSGHFLTVFDSHRKNSFEVPTASRRGVKN
TARMPSFSPMRFPEEQTFHSIAMTTLLASVANESRWEKSPYFSPSNKFGELQKQQARRGL
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VAQTMRLLLLFLGVVAAMAAALCICGMIHV
>TCRU_10773 retrotransposon hot spot protein, RHS3, putative
TNIEDVLFNGSPRFTEIKLNDFLAFELYGRGILRANRNVLLKEFFREPSKYICDAGVLVE
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VIESMSPMTMSAPMKLEGCYGSVYNARWNHVVEVSDGEGTEMEVREGEPPQSWKYKAAGY
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FSTHRGTYSAPEPRVLIGTSGIGKSMNAGSYLLYQLLHYNAEKLPMVAYFIGNRTFLFDK
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NNYEWWTKQMGAEEFIINCPEENDVKAMCAWMKRNQIPQEQAEYWKEVSGRMNKVGPILR

FIFGKQTYDDRIKACQQAVDGSTASELERNLGIGCCYSSNDSELSRKLVKVVRIRREYNI
ESPLNVLISPHVERETLSRLENEMKQSDFILLVLRFWDYVPPYIIGKYAVSAFLNKNLLR
AIRLRIKELRLPGRGESHRCALKVHSGKSFTRKEVLPPPERLSNPVAMEHWVLYEPKVKN
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IYVQHADSTPMTGWRRCD
>TCRU_family, putative CBF/Mak.1
MQRYLMNTSYLQDQLKELHALHNKTVTEYGELVENLFKECSILCDVIPNYKISATLEDED
GAQGGRKQKEVYLVQKLEHEVLAQYEHFLQLLRKLQRKTHPEQQALGSRLCAQLVNRAAD
FNHADRLLSLAIHFANAKSTRVAQPALKALAELLDGQMVSDATESIVSSMLDIVRKQSYA
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VNDETTSMTTKLHALVAVATLAQRDATATAGEWRVDLSYFHEVLFRCLPEALDIPRSDTE
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RAVDLLVLSQKHLPIPRVAAFVRRIMQAIPLCPPHIGLSLLTLVHRLILRYPAVGGIIIG
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TQGQPPVVTKQLDALGPYEVLESYDPSTGELRPPPPPPESVRRR
>TCRU_10775 kinesin, putative
QHGIIPRAIQLVFDRAREMQLEDGNLRFQFCCSFYQIYNERVMDLLNPSTTHSPNTGLKV
GWCRGDVFAVENLFICNCDEPEKMRRCFFSGTKEKFMGSHAMNQQSSRSHCVFTIYVARC
DADSPETPIRAELSIVDLAGSERVAMLSRSPSSSMLKDSPDINASLLTLGRVITALTANG
TRAKKGKPADRSHIPYRESKLTMLLKHALGGNSLTTMIACISPSDRYVDETLSTLLYAGR
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TDDGRVNELAEKLVQACEALKNIIALNGQLRDAFDTVKNAKSELERRELELNAENLALRE
RIELLESIVLKEDFMGESTRDFDFAGVEENEWPCHTLLDGPSLFGVGIGSSLTGVHNRPL
SADLASPPHSSEKHVKRRGYSTVIEDGDGRGPLFAPSSARTPSGSQRRVFSVTRNKRSAN
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AVAIKEMEGTLKQLPRGIAATVPQSLKFSSEFGSLSFGGSREGLTELEQRRQQREAKRKA
LLAEQQALRDNVTRTLVNATEQLECLRYAGTGAVTSHPYSGDIAGRTKVSRTGAPSISSA
PANCGMNRLRAYLD
>TCRU_10776 palmitoyl acyltransferase 3, putative
FIYIGLQLGGIVTLFFGISLIVGCTVTISRIALPLLATPGTPYFFLLWITCSVLSFTTLF
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CNRCVAKMDHHCPWINNCVDAENHRYFFLLIVYLFFSTGIAFFLLLMAYVRLWWHGEANG
SIYGPCGYRLRSFPLYLTFALCGTIFACMIFFIVWSGLHILKNETQIERVIVGNKERLLR
NSMVPFRNPYDLGRWRNLLTLLETNDDPVLNQTKKGSTMMKVALLLWLALPTLRSSTCDG
VHYPTFDDEV
>TCRU_10777 hypothetical protein, conserved
DECRWGFRGAGYHMHLAVEFPLQYDEVCVFLELPRAFFFDAAEVKQLYSITALGEDVTRE
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YEEVDTATPFSLQAFFGRESFVRRCIPALSVQDWKTAARCHTLPAPVGQESRSPSDNKTV
GSLTPSNCLDIPVALLSSAPLVYIALVALQCVGVVIVVLSLL
>TCRU_10778 hypothetical protein, conserved
SSDNEESEIERLLQRSSRPWHYFYPRARAHSSLLACYHAMGGLGPVLPQHLFGVFSRALS
LWNATNKDKMQNYKHKDIPLNVRLTRHIYPCSQVPLVSDSTVGMMEAALRYLRPSEGTPV
LLPGMLLYPHYQLLELFDAWKLRVIGYDVEYVTMRVEEEEFRRKMRNICHRDHWNKGAIK
KGNNCSRECPGIVLLIGIGARFVTNAEKIVQIARNEFRGVTIELHPVTAMSLRPENHKTG
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DGMSFQLALLVMHLWALVAQNSRTKKKHHTAGGMQADGAVRLSGTVARANRIFEFLMSSG
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AIKSMQRCVEADCVSLWEFLSHLRNNVEVVSAGEPTTPRLCVASHSDSLLLRVQSPDVAA
QALRTAGFDAVPAVNCVWDSRDKKSREQKGVAPTLREIIVLPDCPQSTALSRHALFLPLY
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KDVNAFFADPQPLLLWALLGPVPGYFLSKL*
>TCRU_10779 WD domain, G-beta repeat, putative

PSTVVAMTVTPDTVWLAMADGGVEVRDGLTAGLLHRFASAPRPTSVTRIWSLIAVTTQSK
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GKVIRVLHGHTNYVRCLYAEGNAVVSGSDDCTVRVWDAGSGEAQLTGHFHGRAGVSALCR
VGVTMWSGDNDGRVIAWKLNTCEALRVLHAHGGRVASLRKIGSRVYSGGADGIIAVFDAE
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RWYYATVRSHHETNERLLKQQRELMELVFLSQGGENAVRHVLTMNEEMKSSALLNCWMMQ
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>TCRU_10780 WD domain, G-beta repeat, putative
QELGEIDKRFVTASPARVMVTCAHHVWMALENGVEVHNARTTELVKKWNVEPSGGKKGSS
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FHGRAGVSALCRVGVTMWSGDNDGRVIAWKLNTCEALRVLHAHGGRVASLRKIGSRVYSG
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SLRAPDLEKRRRRGKRLPKIRLVPLSEK
>TCRU_protein, putative AB.1
SRAGKWGRRFLFGAGVMAASYVCADHWTANSFTRSLRTIKTTVQISYLYKTTTPKTSEEY
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RIIKEETGKKVEELFSYFDPVPVASASIAQVHRAKLRPATPQDEPMEVAVKVQKPKIRYQ
VFWDLETYRFVTWMIGVLFNMPVGWAKKSIIDGIRRETDFSAEANNVEQMRCHLAGNPNV
YVPKLHKELVTPRLLVLEWIDAVKLIDVETVRQQFDAVTVLRTVFDVFGDMLFKYSFVHC
DPHAANVLVRRPPLSEQRDGSQRQVKKCKNPQVVLLDFGLCCPETERFRVEYALIFKSIV
LRDTETIMKIITTWGITDADVFASIQMQKPYESLRRGNHGEVTKMELFQMQVKARERAQT
LLANQELIPPELPLVGRSIDILRGLNRLYGAPINRINMFVRRAVAGLGPINSYESAQYYL
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>TCRU_10782 hypothetical protein, conserved
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RMRELAEFAGRTMRDGKANDVAREYKVFLCALDWYFHHTEDPKEKRFVASTFLPLTPKKL
CSYVFSTESVNLDSVGKILPPAMLFHAGMQYAAKGEKENLLSLFTDCKQLELSQNGFRLF
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NPPRTRADDLFLGDACLQTLYALRDAKRWKEALAFYTSLAPVMPEAAHGVLCSVVCGMPV
STPWEEALATAQSFGNVPEKFLKTLLCARDPDCVSALQHQSFHSWRYMLQGYAEGGRWRH
ALRLIKGCKEVELDAWVLLLRSAQRAPVGDLSCEFFKYLPQVVWSHKALLRLNILIAEGH
GYLKELRDAFQSQKENTLVAEYDALVCFLMEGSFPSKKLTFTDEYVIHRLLMSPAPSVGS
IWVTVGWNNNTLEVFKRRYMGNMKSFVQGHYKIHASCIAKKYCSNREGTFTLRVIPPHAT

LNTSDTLISVMGDVIVAYKPPGVEPHSYARLVAQRIQAGVMHYSAYHLSPSSCGLILLLA
STIPTKAVHLEMKVLARVFPVSTMSLPLLSTEFYKAYTMDVISGPFSDGGVVVKAKCCSD
LDGLLAGSFYRLTESLAGEGWGISLQESGTCSGAKKDEFVCLTELVLSIHHVGLEKERMY
FSARIPPSCMAQLAPE
>TCRU_10783 RNA-binding protein RBP6, putative
QIQQQQQQQQQQQQQQQHHHHHHHHHHHHHHHHHPNHHHLQQHQVHQQRNVMSLRVPQS
TPFMQISVAPMNQNLVSGYNAAPGGYHQMGHSSTQRHQTTPVPSNDERYRKQLIVNYLAP
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RIKVGYSTNPLNIVSGANNQHTH
>TCRU_10784 hypothetical protein, conserved
RLTIFNEPIAPWADAMVHSALLKRASAAVRPMAHVLTSSQVHQLGLSVRPEYLLDAILPE
EALWSTMHAGFARAVLVHSERWRKINRRRGDVPVVVDITAPALSARGVALTTSEETLSTL
GRIAKEHGYETPFWLTREEIMYFVFSHGRVRTFLNFDASRFPGPLRAGESIPSVEVENDR
GEICRVMNVSEFLKRVAPSASGVNRYGLFHCFRQFVPINVLTKRRFSHDVEDALRKCSIS
FGCWCSVWGTIHDYKKLGFEVLDGPLGVWVFDELDSPMYLTSAFSCTNPKAVFSHVYPND
LI
>TCRU_10785 retrotransposon hot spot protein, RHS3, putative
EGLYESVYNASWHHVKEVPDGDKRKKKGTVMKVKEGKPKQSWTYKKVGDTFEEDDAVQKS
GETSRLMVLTSDKGWPYTLSVLNGCGNDLCVNSEVERAWQIVKGDLTEWFSNFDLTLNPS
PLPHVLVGTAGIGKSMNAGSYLLYQLLHYDMEKLQVVVHCFGSTAYVFDKTTKIVTKYMG
NITSIVVLGGLWQRGVKGYIIYDVARKGTPPDTDFAPSSGWGMIVVSSPKVTNYDEWEKQ
TKASRIIMNCPDEMDVKAMCAWMKRGLKPNEQAGYWKKVKKHTQLLGSIPRHIFDEKSYI
DRLGAVDGALLAIKLTDVGEYFTLRGSKLWYSEDPSHKLVKIVRVKTVEGAELFLNASIC
DDIGFRIADRLAKEMGAKDLLLLILGSRGALVSHALEQLGLRVFMYGEIVSALLKGLKEL
RPPERNEARDSVLKVNHQGHPTRTVGLAGLEGGVTRTAMEYGVLYLPKVENFPLVDGFFF
VDSPRKTLVGLQMTTASEHHKITSTVNLFNEHLAAYFKGWKKLSRDMSWEMIYVQHENST
PMNDWQRCDVVNPNNETDAEKKIVAFWDGKVHKYQ
>TCRU_10786 hypothetical protein, conserved
VVMNLDVIDATAEALPLELLNATNKELTAQLSRHEQLCDEKLRDVEDLRRRLQFMKEHLS
NVRGEIVSTQSLVECKRREVDSETHMYRLLDRECGRLKQEQNHMQAQQAEVQERLQAVQN
LIFQENLRMAELKGAMTFNQEELEQWDIARKQKEADEEAVARYTKDDEVRVRQLNTAVER
LEAKLRDRKRQLEEEVMVTRNVQLELDRSAVEYRKLHHDRGSLLDEWEAVVRTIHERDAA
IRSAAMRYAEGAEWLGQRRAVLMALSAELDTARDEEAMTRVGIKEREQRAEKHRDVLVSL
EGHVVAMEEEVETLREQLARAVRERNNSRIRAEESRAAVAQRAAAYDRVVEKRAQTKKQL
HGEFDTAMDLEQQRATIARLLQEARATDRRLEKEVEELKRENFGAGERLQAAGRLQDELI
AEISGGQAQGRNLKAKISQLDRESFTQQEILYNVEFNVQQMERKVNRTKGERTEDERNRL
NEKIAAMQSTLDDLCTQQRALDTQVKRVREEARQANLEVARMREQEKSTCDKALQLRLEC
DSCAVELRKLRKVREDELVRVDTQELQLQGLKRTLHQRSGELSDLEGQKRQLSVDVSQRA
SEIAVHHEILKMEAKLAEEERRRLVAELQERQRSLGALRNRYDVRVGRMDPDQAHLTQVQ
LVVEAAKEREALQHKGDALDARVARLERDLLKLERTLQVIRASNSNYRHMFDRVQDNDAE
EKTRRALEAKRRELKTFISRRALEASEYQEVLHGRASELQQVLERKERTLNAVEELRQAC
EHAHGTILEGRETIIRYNQAINKARGAVTSEVAADVELQERRQRHEATVGRMLQLLRRHS
EAAGETAHALLMERL
>TCRU_10787 protein phosphatase 2C, putative
MFMSVRKPPLSSSKGTAKNPALRKGDMGTGHETSQGSIPTVPKTVPLRNNTRCSSGNPFL
YGSQRGGALPYQTTNSLFLGSVAQGKTGESSPRNNSNGNGNSNNIFGHEEPTISTGGEAL
HSGSGGRSIVGRRMQSKIDLKRNSSDNVAAVLGGSSLANVDRTANGATRKAFSGPPSTRV
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KNVLEHTPFSSRQGKKGSHGSVDPFATTHILNGVGTRLPPQLDEGGTRWGKDVSTPFALA
SVKLQQLSLPERSTSPRLASEPPAASARCSGAVANSTKLSGSAPEDSSTKSNILQYDFRV
VASTGKTFNSPIKLTVGVGSLQGHRPTMEDEHFVRLNAATAAGQSVSLLGILDGHCGRRV
AELASRHVPDNFVAHSALGENNALAFVESIIQADRAIFHALGKGTGGGASVSCNSSGGST
LIAAAVHGRMLYVACLGDARAVLYDGNTTIPMSEDHKPTTKREHTRILQCGGFVQFGRVC
GILAVSRALGDYEFKFNGNRFIANRELMVSNVADVRQINLTDSSNFLLMACDGLWDVVEN

EEATQFVRDFLSYTPDVGSSPEATKRALNNCCQKLAEFAVDRGSTDNVSVMLLFFHDVAD
VVAGFDKPVGAVASPPASQVLSPRLTGPSRGIPFGSSMLDGGLHTSSGTSGTRRPSFGSV
SSLHGRGRS
>TCRU_10788 hypothetical protein, conserved
FLFSSHLVVLRAAIRAVSSRSTCSSMAAPCTSDDLNREMSSHLTPLEILFTLVSPGIATA
PCVTTVSTLYSNMPFKLDEVIDTKKLKSQDTCQNTHRWLRTQFGTLANGLRQLHATNGVS
HWGVYVSHDGVYAVKACSAEESEEAFSTACASRLNLSSSETESLLEVFMPVFPSFAPPPS
PSEPHLSGSKKKRKGCVPVGMFTPQMLVPYVPTFFIPMEKLLAELPEGYTVAHIEQIFAA
TGTLEIVTLEGEKFVRLHGGRRLVDFRRDAAGEVAHERWREYQPDPFLCESFRRLFPPSS
RWISLRQLITGAPDSLVRALLPWENYKTLLYFSQMQHVFGFTPEGEGELCWVAPVTCLSY
HDSPTPAVVSELVGVLDGQRVCIADLLAQSAHRISDHAKAQIIMYYGTLLEFFRAHGDVF
CIVDDTIVGVASPRGTAEKTAHTLEEKLEEALVHRNRRTAQKLRRRIAMEKDPDNPYADR
DVLLDAILRYVPQKRSISLNFLLKSLPPSLSDFLPSKPLSIFQQAPDKIRVFEYRYRHRL
HLIRPGVPLPPGVLRQHYTEPELLYLCAAELQQQPRTAVDLYGRLPHGAKEVIRQQYKDI
LELLRPYPQYFTVVFKDALRLDTRSTMITLIQMPPTVELSEADYGAAAPDDPVLRQQVEE
EDMEA
>TCRU_10789 hypothetical protein, conserved
MMSKAAYMMQDQLRRNYTLITDIHSPNIFIVRGFLPFPQGLAALTVLFRGKLAADVYSHP
YFIEKQSDPSQPSPQLHLTEECQSVMKIIKGLHFMRDDSSKLDNTMVFVTDYNVETKGRM
PTFSSEAEDAAEMAEREQRIGEDVGKWEERTLRHRWRRAAAARRHCSSGNGGNFPFSPNS
ALSLHTRQSHVVEDEQQSALEKTRRLVEREGAHTVLYNPIATDPKTFSATIRKLNEEERV
VKTIVVPTRQGWGSVNVWAEAFPDADILCSGDGLHHGALRQPSAKEERRVGGCMNMGNGV
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VIPLGEVAQHRITPNIDLLRVAGDDQTNEYVLYDCESGALACTDLFHGEYGDFDPVNTWM
CRVWFKFMKGGNYKRIDFVPQLKWLQVKRHGNLELLRGTVDMLTRTRPINYLLYAHGTPP
RIEDPADSLRLQWGMPPL
>TCRU_10790 choline kinase
IPDDASLRRAAIVDVVLLYCSDVLFPSGFCVAAGGDSASAEIRDGAETRCSHLPEENAAA
GDLCVERLSGGITNELFRAHHPSDHTRSVVVRVFGRETERVISRESEFFYQSLFIPTYVR
GANFLIYQFFNQYEVLPFTEMSLEASKMACEVAAFQVRATLESKCDHQNPQLSGEERAYW
DAVGVTLGSNSSAEFGTCRFDREENYTLHALTKWAEQMLSEGVLKKVSAKKRAEYEEAAR
HLEGEASWMRKLLLRHASSLGESVCHNDLLSANIMRHRLNGMLKIIDFDYVKRNYFLFDI
ANHFNEYAGLECDYDRYFPSDEEMSRFIGIYRKAMRAELNKCREDARCRELGEIIPGQSH
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RLKRYLETKYTFSA
>TCRU_10791 hypothetical protein, conserved
CTYWVMALLVLLLRVLVPHLRNMARYGGRHAVEAATVDGNKNNVGDGVQKCVSAGHKAMG
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>TCRU_10792 hypothetical protein, conserved
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CDDADRIVSSVGITFSSSQDWVN
>TCRU_10793 cyclophilin, putative
NPKVFFDISIDNKPSGRIKMELYADTVPKTAENFRALCTGEKGRGKSGKPLHYKGCVFHR
VIPGFMIQGGDITRGNGTGGESIYGMNFRDESFSGKAGKHTGVGCLSMANAGPNTNGSQF
FICTANTPWLDGKHVVFGRVTEGIDVVRRVERLGSESGKTRGRIIIADCGEV
>TCRU_10794 pumillio RNA binding protein 4, putative
LQSVLERYPYRSQEVQCVVNELLPCLPQVMASPYGNFLVQKLLEIAPDEDRLRMLSQHLS
GSLCEVAVSPHGNYAVQKLIDSLRSRREVEVVCAALQRGVLMLMNDLNGGHVVQKLLQCL

PQDVAFVYDAIVEKTIDFCNDKQGCCVVQKCIDSAPPERLPQLQEAVLKHFLPLSMSPYG
NYVVTHLIRNCDAMNQRHVVDRAAVCVGPALKMLCTNKFASNVVEIILSLCSEEAKVQLC
R
>TCRU_10795 ccr4-not transcription complex subunit 2
NNNQAARYGAGILPGVHMTYPASAAAAAGAPNPYQSMRGAYPVATTAFVTQQQQMIAQQQ
QQHQRIHQQQQQQVHHPQPQAQSTQQQQQQQQQQQQHHHHQQQIQRGRVAVEGPYGLLAL
PGLIQHSVNAENPESAAFLYLTRGFDLNSLGINVAQQRPLHPTLASLALERPEVPVVPEY
RIPDCYRQAKPRQPTLKLLQKYTDETLLYIFYSMPRDLLQLAAARVLLERGWWFHKVRQQ
WMRRRTAGGYEFFNQNKWKMESEENYQPNLAEVEKDLSDPAHAGPSAVIAGSSS
>TCRU_10796 Emopamil binding protein, putative
TMAALGIPLFAKLWFILTAPLLLIDATFVFTRSSSTGVPHPLADTPPFNLWVLYSTYDRR
YAPNDDAFVVLQSCMNILEAALGLFAFLLAERGKAIASLKLALVVGVMTLYKTLMYFSLE
AIEGGKYTKHNSTFDALMMIALPSSLWIIVPAAIILQCSCRLPIAAS
>TCRU_10797 tatD related deoxyribonuclease, putative
SGVPYLVDVALNLTDCVFRGVDWKGRRVHADNFDDVLRRAGEQNVKKMIVTGTNLAQCVK
AIRLCRRYPSQLLCTVGIHPAHCAEMMLPMDWARIEEAADDDVSIQVPQPPSSVVDTTAN
CQYTEDRLKKLVELIEENRDVVVAVGEIGLDYAELSYCPREIQQKYFIRQLRAFRSLRLP
FLFHSRDCGTDFVQIIEEERREWPSDFPFVGVVHSFRGPPEEQQRLLAMSGIYFSINGSA
FREKSTAEQICSLPLDRVMLETDAPWCDIRKQHYGAQFVRTFFETNCKGGPFVSTLCNER
RNEPCHLRQVLEAYTGALRRFGEKMADEALRGITEEEVVRQLFNNCVTVFGI
>TCRU_10798 nuclear movement protein, putative
MSLVESQKGMTDLIPCNEQCGGDYGNYSFGQGDLDVTVTVPLPENTTKKMLLVQITASKL
IVGLRGKPPIISGYFYRPVKASECTWCIEDKRLLVINMVKTNSQHEEWWPCVVVGERQID
MKTLKPPSKHVSELDESAQATIAKMMFDQRQKMQNLPTSEEMRLQEMMR
>TCRU_10799 syntaxin binding protein 1, putative
SNGIRGCVRDYIFRHMLDAVPGSFKVLICDAHAAAVLNCSLRVHDLMEHGVTLLEDLMTP
RQPIISSPALYFFAVEDASVSRVIEDWMAKDPYRDAHIFALGCTPDCHLQQLARARIAPR
VMSFKDMMLDFSAPEALVFHLNMQNEFPQLLSPLSLPTRESVLDVAASRLVAVFHAMNNG
VPVIRYQSRSSICHGFARNFFERLAKLCYDEPDFKRGADSRGNPVLIIVDRGFDTVTPLM
HQRTYQCLLDDLMPLENEVYEQTFQNRLGVDSKRQYSIDEEDVYWCAYRHRFFAQCLEEL
PAALKKLHADHPGLARGVEQKANLAELGSSVRALPEFQEKQARLSLHIDICTRLVAQYRE
KRLAEVCEVEQDIAAGRKPFRKNLDGVWRLTKDAAIPRPVRLRLLLLLVAASSADELTEA
KKQQLIQDGELTADAHLFANLEHVTRGAGKVQRDGAASAQSERSTSHSASNAATDGDPFL
NQAYMIMEAAARNGLNASEYPMMNSPYESRASAAGGGAPMEAVGRKKTLRVGLSLASMQR
DHVMGPNGASGSQNSGAAGNNAGPFQGGRDKGENRLDLGGGAGTIALTSPQRIVLFVLGG
VTCSERRSAYEVSKKYGREVIIGGTSLLRPEVFVQGLS
>TCRU_10800 hypothetical protein
LRRAAVALRAARIGGSSITLGTKGMKRFLDPHRRRMPWTASKECVPDVVPCNKENMVLGS
VQRVDLDCVDRASQVDLLEA*RKAVATCEYNTSTGKNIFHVASWMESNGLGQWFYRKEWQ
EGTYDRYVTLSTIDFNRDENKGTAYGYLTFHGETTTRPVQIDFAEVLWHAVLFGVFVPPL
PSIGADVPVDGRCSCLRAHPFNDA
>TCRU_10801 heat shock 70 kDa protein, putative
MRFCGVFRFQRTRVFLQQLPMPMPPRRPGSTVNMQHSMEMEAKRRMELDEATRNRFVVVK
EETRERDGRVIGIDLGTTNSCISYIDKETNKPKIIPSPTGSWVFPTAITFDKNHKVRLYG
EEARACVRTSASATLCSGKRLIGRGVGELGRVQSQIHKTNMLTINEKGEVAVEIMGRTYT
VVHIIAMFLRYLKHESEKYLKEPVDAVVVSVPAFFTPQQKVATEDAALAAGFDVLEVIDE
PSAACLTHTVLRRDKDGDAEGTQLFKQCIVRSLVFDLGGGTLDCAIMEHDQRRGTFTLVA
THGDPLLGGDDWDAVLSQHFLEQFERKWRVPLEDAEGNVGQGVATYRQLILEAEKAKIHF
THSTEPYYGYNRAFHFSEKLRDIVPLEATLTHEEYVEITRPLRVRCVECLNKLFEHTGIH
VKDIDHVLLVGAMTRDPPVRRMLSEYFGCPVSAEDTCPADYAVAIGAAIRGAMLQDKFHD
LSANTRFLSGTAQAMRHGGTFRRIWNRMNAWITRSVNPNAIGQRWRGRAKGLSDEDIANY
AKELVEFESACHRRLLLERAENDANFVMRRVTADSNKRQGMQEKRVRQLSEQLKFWQYMV
HNFHDHEEELHRTVRELEQTLDELEGNAEDNVSALTTEGTVNFAKAIPVNYCGEEDNAKS
TPGSYPAEAIAKTEKPKATSTLETDKAKNDHGGQKAKPKGPKIIRRPVPLPKTSSEAQEL

VEAGHPALRGADVVMTESTRSSFFEAQMEDRAWREPPTPPGEEGSWQEVKRAVEAGEAVG
SPISPQEMQRPMTHEEMLEVILAMAPIDEPISEDHARRRDLALDLQTMTVVKGMVDMEEL
ETQLNENAKAQEQCQRTQKRAEMSTPADASASLF
>TCRU_10802 hypothetical protein, conserved
SSERWRPFLSPHLKEYMDRYWAVMFTVGSRPIETGHLRHYVSWYCTRMKVVQLDHHIYAE
SLHRQLLEVAQTSELPLLFVNKKLVGTLRDVQELESAKKLKDVLHFGFEWRVGGGGVGER
PLQGFLPSPYGDTEMFRGRYRGAPVARPVVALPKLHPLDRRSEE*
>TCRU_10803 cytidine triphosphate synthase, putative
ATGSSYYLPSPSTRFLDSNDRIKFVVVTGGVCSSLGKGVTTSATGALLRAQGYRVCSIKI
DPYINMDAGLMSPFEHGEVYVLEDGGEVDLDLGNYERWMSVSLGRDHNITTGKVFQKLIE
KERAGGFLGKTVQLVPHFTNEVVDEIFRICQKAVCESNKGPEICMIELGGTVGDMESQPF
VEALRRLRYSIPPQDFCLMHTTYLPVFGGAQKTKPTQHSSRTLLSLGLQPDFLICRSEER
LSREVKEKLSNQCGVKMSDIIGAPNVDCLYEIPVEFTNDGLVERLLHKLQLRPKVPVMDV
PSYGTYVEYTRILRDMSNPLVRIAFVGKYVTGGGDAYFSVLQCLEHCQIALHVRLDILYV
ESEMLEGPNAEEAKKAILECDGIFVPGGFGKRGVDGKCAAVALARHHNIPYFGVCLGMQV
ALIQVCREELGWKDANSEEFDPSSTHQIVRIMDCDRHSMGANMHLGARNVHLVEKNSIMS
TIYSGADFVVERHRHRYEVNTTYLGQLRGAGVLISGVSDPTFGPHTRVEAIEIPSLRFFL
AVQFHPEFVSSPMDPSPPYLAFMAAASKKEYKWPESCAARRVKK
>TCRU_10804 transmembrane protein, conserved
MSFLLAIVRITGFVLFFMALLHVKKTRLRHLPSRRTRVSRHHGETCVWMERLANAVIEMF
YVSLQEKETKTMMNDEKENQRRQQTATFDAAGSRLRSQGNNTRSEDSTGVKGAPRRLLDF
IEERLEAMLEDRGIAANATFKVHSIGRRPPSVRAIRVTNLTGTEFTSNLSATPQAGVGSV
AAGNSSMATTIPCTPGVPVATNTAGAVSAGVSNPASQKVKGRTAQLGPHAPDDMGEMRSA
DSLYDETLGGNTASLPATAVELEAEVEYSGGADFSLQADICLARGRLLPVSVRVNEVKYI
KAHVRACAKLQYERATMDSRRKPYLQCTFWLESEPTFSLKMSTLFTRYYINDFFAVPLIA
KFFLLRFVRRRMMLPNGAGVTVKVPLPENIVDGGTQMWCASISDVATAVSSVN
>TCRU_10805 hypothetical protein, conserved
YDLPIQVHEILRLNHWQEAIRFISSLSSSSQKEGAEERPLTSSCESLIAALLYHGHGESA
FTLWRIASTNFDFAPSPMTMMKLAVYTLLVDRKAQEALDLVAMATIPLESKTVAEGPVLE
LIALWTTVLAALSLDEERNLQEKHVKLEQKVEKALVDLLRLSLQTARKGDTQLNAEMLQL
ALHALLSLTLLRDGSEVLHRLISSSFLESDDPSVGTLSRVAEVLSMKPFDYNTTAFFSDD
VSFLITRIFLLPVVWSSENSTPLLLGLEVYRSFFIAKPEPLSSEVGNAYFPFTDNASTSN
TTTNNNASATHTTVGNVFLRRLIQNNLEKSFLHSVVLHYMNASRTSLMTHLLETPIKRDL
CDLLSYRFGKAFISVVNESSLSGAQRTPFLGYVSRALSPFFSRDARQSETGPHIGVGTCK
SIVCRNKNFYLELLSNLITEVPAAELKAWRRFVVLLTGAIIRDTDGSAPATISQELRLQL
HLRWWLPELLAMVDTTRECSLWVTPQRAVFPGVITEWEQSVCMILRTLHEKEHRNRSENP
LGWASLDNAIIKDLHSTDEASQISHGVSRLLVQRVVRWEWLLKGLWNFARETSRNGSQST
WRNLLEVCVETLNHCRVFHRHDIARDLIETLFLPAAPFLPSLAESPREGTYCDKTLIALL
INGSNDTLRTSTTLMELRWRLVDEVSRWMPAFQGWAFMRGLQALLPCFPHDAKKSFISLE
NLINDLLNGNGKDEVPGTRERERVGKVFEWYEEACRDDLSLRTPQLLCPLSRAMRRASLI
NSFSELMKNTFWDIQRGFHAPRPSSASRLLVDTLIFYYAHHAVATTRARLAGDADILLEL
SNTAYDNARNMVAAFAENYILALWKEDCFPALEAMLLKPAAPNEGSNASSTSSVLAFPKA
MSHKDYFFSAEIAYLLPEAEREALRLFLLLTFAQRFDGFLYTTVLGRLPRSKTDPARVAA
FVDRLVAEEPCLFFSLGTVAQQAAREKWRLREFCASIAASHEKGETKEQEKRTRIGDRNH
VRTIRELNRCIDNCDWAKALRAIPHVISDPLHVARKALLACEKAPKGATWQGTMSIFVNS
RHSWEQVSPKKNRERNKLGDSSRLRATIGIQECGRIMTLLADARRWCEALQVFELLGPYG
MDGYTFSQACFALRTGGHPELAIDLWAMWRAYVGDAVEPTAQMCGHFLRCGVVGNTTVAD
AACVMLKLAVHASARQKVTVTPESFSPPNDDCTPGTTLPLSIEKEEKTITALLRDRWHES
WQEALRVALVSERPRIIHAVARESPSNYHLYEAVMQHVTRAHRNLSMEERSAIAGHLDLK
TALNPQGNSVDSGEDRAARVLRELLGDEE
>TCRU_10806 hypothetical protein, conserved
AVRKELLEKASELVPNYGFANASLFHTALGALQEKNEYKNNKSMADVDFAQLFPRGFPIA
LVEHIVENTNKAAHVRLEESFNKNTILDNFAKNSGSYQVGQYKLPGVKNVVEEAISTKIE
ALQPYVEYWPEAVALELKPANVPFAVKNLSEFVDNICYYAERMENLGAVIASGNLLLQSR

LYYPTIHRDLDKKGHERHQQETDEERFWRGFSSSIPLSSGPHVGGGLLNYGWYIKRTKVL
TVFSLAMFSFVGEGKGYSGDTRAMIRCII
>TCRU_10807 hypothetical protein, conserved
SCFPVMSFLHVPGKMSQPLWLMMGTACLLQTAHDTAALGRLFLLSAKHTFAPWHFIADPA
RLKIPETYRKTRFVVVHLYLPDSEGRAIATSFVELRLVALHPSADVALLALKPPAASPSG
KIEPNAHVEEFRRLAETAGGGLTLSAVDPAVGDSCLVSGYRGVGSLGLLDTADPDLLQRL
SAAQREELLAKLKCVEGQQTATTAKVEVLHTSGMCRATEGRCYHGMSGAPVLVNEHKCGG
ILYGKHTEQTEYLGYTPARSFDEWV
>TCRU_10808 hypothetical protein, conserved
ELPPIPSMLVQAFPLEAYLRNLNNKLSDNLNAVQRSLVELQEGVKSCETLFTNVRQFLRE
QVLLELQESIAGGGGEMPEGFSTELLLPEFLRDPQTVAAEGSCASVGSLSGYDGGKVDSE
LRKMYSFKKKLDMERLERIRGREEREKKARQQSEEARKRLEQMCEGLELSQKQYMEELER
LTLWLRPSPVEDDEDEAVSSGVGSAGRSEAGRDNRELQEVMRGAPLLVEFRRLILRDVMD
RLGELKDEQSMTMGNIMASLKEEMRKELCRNLNGAADGRVGPEGGSRGEAVRRLKGFDQN
YVQRGEVVATLQEKADRATVAQKADEVYVHDLEKRLLERMEDLEERMTIYEAERTEFRRI
LRSLVDVHRRGEDVHNSDSHRDRDAANNDRDDGATRRARALPNFVVLDEAIEPQRARECE
SLAAEEPRAPRRARQRTDLTTSRASARVQEKNQSPCGVVERKVEMGGKAVGLTANQEAYA
NYVTNELNRRVVESLPPLPYER
>TCRU_10809 L-galactonolactone oxidase
WTNMACIGECHPREQHHPGSIEEVVALMRRMKQAGERCRVAGAGKSPNACTFTDEHLIHM
DRLNRILSVDCERQQIVAEGGVLLLDLFEKLGENGLMLRCVPSYVLTTIAGAIGTATHGS
GTNTRSLSDYVVEIVLVDGSGELRKFDASTPNELSLAACHLGMLGVVVQVTIQAEKLQIW
RLRSSPVPLLKLIEGDILERRVSDSVFYRFFWMPNTEFCYESIGVCLEGAAVKGGVGFFS
HTNTSSSSTSRKIPQSLNVVRPSSDAALEYQTWLEEQKRPYTRLCKALKGNWLRHGVVQA
ALAAATFYPQMQPYINRAYRKIFYSASEVQYGTPIECFTFDCLFKQWACEWAVDASKAIE
AFALLREMIASENFSVHFPVEFRFTDADKTALSPAHGRKTCWIGIVMYRPYLLYARDTLR
YYQAFSDAMTAMGGRPHWAKYYTWGPAQLKEAYGQNWEEFLQLRKKLDPDDLFANDWWKS
LDGQGPLLNSTNSHL*
>TCRU_10810 hypothetical protein, conserved
MPTWSFVELSCSFLSPKMVGESPFFAPLEERLSTKPPSLSSALWDYMHCTKRAINTRIIG
FCEPTLKQCVDDLVLYTKASKWGGCNAASLEEVLRRRRGDVDIESLPWEPRESYKKWLKE
QGRMR
>TCRU_10811 IQ calmodulin-binding motif containing protein, putative
RYLTNATAKKHSIFERFLQQMKKYHTFQPSFVEDGVYSTLMASRRDSASNAWDTVGKILD
ASSSFAIRHNADGHFLTTVENIPSVIRHISSKSYEAPANRPFSGDSLKLLSPLSIKDKDD
AAFYLWRREHSNASPDEVREELQFRDKERAGEWRKFFASKKLQWKADLDVLSGNSRDDMS
LQSTPAYPREKEQPELPTELLDKQIEQGLLWGVFSNGEIQAKHGKSAAVERAPTLATEII
SDYRKSNELQEWMERKWRHHTHRHENAALRIQCAYRCHRARRVAARRRYARRLAFMEARR
VEEESMRAWSTALRVMTDELNNTGDNFNSTWRSLNFVFSKLQAKAIARRARKKAEMDSDC
EVKEYAATTIQRVYRGYCGRQLARIIRFPEVFEQLRRNRLQAAAIMLQATWRGCATRARI
RRQTEAVLLIQRLVRSSAARSRLRHLRATRREEREQLTSQFAAKLVCHFLKGIIVCRRER
ILRFREQAELLQRVTSGLFARQTMHRLNQSLLRLVLWTQRRFRSARGRELARQQRELTDA
LFQHLRRVDAATVIKRAWRRSVMAAAKAPRVDMAEKRNFKSTAITEHSMEEAVVMIQNWF
RCMRILRLERAERDAAREQLLLRESAERILCFYRRFKSLRSSP
>TCRU_10812 Alpha/beta hydrolase family, putative
FWVLHVIVHVIYIDIPRLRRAFKLMTEEKRTEKIEERIDFLSAGTNTRCFFSFESFADFT
YTSPPYNGHISTLLCAFRPPKPIKYTRQVVDSVDGNPICLDWFLAEEKNSPANGIMIIFP
GLASWSQTNYVQHYVWHAHDRGFHCCVFNARGMGDTPLTRPRLMSASWTGDLRWVTRTEL
SRTALSLRFGATAQNVWGVGFSLGGVVLAKYLHEEGQNMTKEFPFDAALIINSPLDTLAV
SANIMQPENALYQKNLFGGLIRYAIRHKDMLKQLPGVNDDGIRKDPLRFLKRLRTINEFD
AHITAPHNGFSNPEEYYAAVNTLTSLRQCTIPTLCVIARDDPVTGEPPRKEMRELVTANS
LVAFLELPYGGHLGYIGSPVEEWRGDPSFMELLTCNI
>TCRU_10813 pre-mRNA splicing factor ATP-dependent RNA helicase,
putative

RTVVHLPVEEARGAIVRMIRRHNAVVIVGETGSGKTTQIPQYVWDDLVSREPPEQQGIVG
CTQPRRVAAVSIARHVAKQRGGSVGAEVAYAVRFDDTCSRQTKIKYMTDGILLREIQTDP
DLSHYRCLLLDEAHERTLHGDVLFGLLKDIVRRRKKTLTIVVMSATLNAEHFSKFWWNAP
IGVVHGRLYPVTIFHTVEPQADYVEAAVSTLLQIHEKEEPGDVLCFLTGQEEIEDAKRIL
ERRMKVMPSTLQEFMILTLYSAMPYEQQLRVFEPPLPGKRRIILSTNIAETSITVEGIRY
VVDSGVVKAKFFSSKSGMEVLSEVDVSKAQATQRAGRAGRMTAGKCFRLYTAQAFESLAE
NTVPEIQRSSLISVVLEMKSLRIDRIMDFEFMDAPNPKAVVRAEETLMLLGALDRQGHIT
RLGQRLIDFPIEPMAAIVLLAGKALGVERDVTIAISMTMTENLFFTSREAKDGADRCKAA
FAKSAGDHATLLGIYYAYKRVPKDQRKMWCESNAVNPSQMLKAEDVMTQLGAILNEHSDE
ELLSTMVRRSPNLAGNGAALHRKRRRDSEKDASGDDETSELLKGQTSGMVKLRDFELIRR
ALCYGFSLNAAFYNAKIGNYQTVVGQQVVHLHPSSVLFYQRKKPALVVFNSVVRTTRRYM
KDVSVVQEEWLRDAASFLR
>TCRU_10814 hypothetical protein, conserved
AKKEKPPHAPFPKDVVDAISCGVCNFMVGKAYGDVQLLFNASVQTRVRVNEDDVLTAIED
LCNPFSDVGQWIRQITITHESDTAPFLLGVSRLPAYAKCKRVCSTVVEACEAVMDHENMD
QLSPRLLRLNEYAGAEAFANALCLPSSICTERQGLSAARYEEVRNMIDEDTVEEIDPKEM
EIERMMDHMERKENRRQTIFSRDEITSMQKAFLRGDKEAVAQVDPSIMDLSDEEFSALQS
MIRGRAMGQEQPEEN
>TCRU_10815 ABC transporter, putative
VGIVLVADGVYYTVSWFQARCGRLQSSAAQLTSAGDKPFNEERDAPSVRQYWVELSDAIL
KAPRTPLKDGERRIALPVAAEDIADGVLPDAVRIIWEDQVRYLLDRREVFLLLRSAVRGP
SMTNKDDIISAASLALLWRLQLIRSVYKAVVIDGDVSQCSDDLTDLDEYSTVFYRELVCP
LELFFSASSSAGIAACWFSLSEELRHLRRRRRLLQLQNTWSLVKYMYVGGWKKLVSCAMM
GLLTAVAAHSAITGLAVRDHIEQLLSVTPRLFLQYSRGGCIDTSSHANMRAVLGLLAFEW
ARLVATVAVMRVTEDYIHTSASCHRDSVKRRLYEALAQTPLAFFDLRDPDAVEGLIYYVN
DLEGVDVQLNDFFARLVRAAAALAAAAATLDRRSSVVVVATVAVSNLLTGVLSILRRKCA
VDLEEGNVDAEEEENGNMATDGMMLRGMEIIEHIHELRPYGADMTLMGWWTEQMSQGHKG
PGTVRRIVRVVLSLRRLWTIDALASLMKWLLPAIVTAQAAARSQAQGLLMEAMRAVQELL
DEVLDARRVIEVVVNNAYKANALERILDPRNWEKEEVLEDGVGAATRDMNGGDNRESLCD
EEARKGFLLRGGVEVEVLRIRADGLQFQYPTLPTVNAFFSPASFTLQLQDELTGVGRLIC
VTGPSGCGKTTLLRLLLALYKTNANSLSLQLRRRRRRTMKLHSTCNGDGMPDGNHVCGDD
GEVFWLPVASIPHRFLRSTLFSYMPQIATLFPGATIAQNITLRSSISVTNLSLLSRVREC
AEAAACMDFIERLPQGLLTPLSSITGWATPGTLRLSCGQGQRLMLARALYHGGGVLLMDE
PTTGLDEASRRAVMTQLRGLLQSGRLCGALCVTHDVELLQQADQIVRL*
>TCRU_10816 pyridoxal phosphate containing glycine decarboxylase,
putative
MYRCFHHFSTLPLAFVRRTATNSYVNCHIGPSAAEPISMLRIIGKESLSDLMTAVIPENI
LRSPLKEVPAMSEQDALSLLHSPGSRNKVLRSMIGQGYYEPGTPPVILRKVIENPAWCTP
YTPFQAEISQGRLESLLNFQSMIIDLTAVNVANASLLDQATACAEAMYLAFHHG*KERMT
FIISRDVLPSCVEMVETRAEPVKIKVVVGDPNLIDWSDSSLCGILVQTPDAMGMLHDFTT
LFEKAKQHGVVSCCGTYLMASVLLKPPGEMGADVVLGSAQRFGAPLGFGGPRAAFFAVKE
EFKRLIPGRVIGVSKDSTGCPAIRMALQTREQHIKRERATSNICTSQALLANVAAFYAIY
HGSEGLKEIASEMLSKAKILSVGLESVGHTVVNGAFFDTITVNLKGITPEEYVTCCVEKG
INIFVDYSHGTVSISVDEATTEGHVVSLLEAAGQKLPVIGVLSKLAEQKRATPLQMLRKH
VFLGRSILQKYKSESELMRYIHRLHGKDYGLTHVCVPLGSCTVKLNPAAAMLSLSWPEFT
NLHSIAPKEQTRGYSALCLDLEEKIRDITALDAVSLQPNSGAQGEYAGLCVIRSYHNSKK
ESHRNVCLVPESAHGTNLALALLAGMVIVKIKCLADGRIDMKDLENSCQKHTRNLSCIMI
TYPSTYGLFDREILAITSMVHYDGGQCYIGGANTNAMXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXCTAPGCIGGDVCQINLHKTFSIPHGGGGPGMGPIAVRQHLASF
LPDSVFIQNVGGSQPFGQVSQAAYGPASILPVSYLLMWMLGSRGLKTCTGYAILNANYLK
KRPDGHYPVLFLGENDFCAHVFIIDLRLFKKTAQIEAEDVAKRLMDYGLHSPTLAFPVAG
TLMTEPTESESKRELD
>TCRU_10817 glucose-6-phosphate isomerase, glycosomal

YLKDLTVHLNESNAAPANTSMAVASFNMPHEITRRMRPLGVDTDTSLSSCPSWRRLQELY
EIHGSESILKNFDECKDRFQRYSLEVDLRSSDKNFVFLDYSKTHINDEIKDVLFKLVEER
GIRAFMRALFAGEKVNTAENRSVLHIALRNRSNRPIFVDGHDVMPMVNKVIEQMKKISEK
VRRGEWKGQSGKPIRHVVNIGIGGSDLGPMMACEALKPFSDRRISMHFVSNIDGTHLSEV
LKLVDLESTLFIIASKTFTTQETITNALSARSEFLKFLSSRGIPEAGAVAKHFVALSTNA
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VSTHTGPIIFGEAGTNGQHAFYQLIHQGTKLIPCDFIGAIQTQNYIGEHHRILMSNFFAQ
TEALMIGKTPEEVKRELESAGGKSEDEIQLLIPQKTFTGGRPSNSLLVKALTPRALGAII
AMYEHKVLVQGAIWGINSYDQWGVELGKLLAKSILPQLQPGQKVTNHDSSTNGLIKLFNE
RSHL*
>TCRU_10818 hypothetical protein, conserved
QAYKKNWCEVILGSTSGLLFLMVLAVLYAVYTLCLPYGDSISFGILLSVVLHPKSTVEYF
GSRYEMRCCAERMRKLQQAWASRSRLSGVIGSLLSLGYFFSCASMQGVMFLGLDKLSVSA
RWGRRGGDRTGKARNEAGEKREFLTSTPTGRVILRLLVVTIFTVVAHSTIGIFFFFELHA
VLMAVFAVTVVIVPEERFTSVMWRLWCFALALFFVVALSYNMAVDVLSISDAVKRTTSAV
VNARKEWSHQKTYFSNLNNISVHDADANATSFIFSSSGIEEMIMTKLQETVLKEIDDTLR
HTNATELAVAVRQVIGPMLTTFPSEISIGSLKNKSKELYASLFRRGDPLLTVDWLSVLQN
LLRRWRPFFAFLTQLLFGLGSNMMGLFDSVYATMLFVCVLRYFLQLEHTILYYGVAKMLR
VIHPQGGEKHARMIEREITVSFRTLLQSFWHLSWFHFCITFCLFNAWSFPTPFFCGMISS
LTAVFPLTPKWFSPVAFALGSVFFNAVASDGFLGAAVDQRVWSCFLAFLASYADEWLLCV
SRGLRGNPLKDFTGVKREQLPTFVVGTALVLGYVTYGVRGILLGPMTVIVAKVLFDNWD
>TCRU_10819 predicted WD40 repeat protein
MEGKNCFRTKWSQSPVYSGGNIASLWLPAPRGTSSSSLISSSSGKEALVMACGDTVNVIW
ASTGDLIASYKLPLEDVILRVDAVSILHPEELEVESTNFAAKNNKRRMIGKKKEGAERKA
NKEEVNETSLDLSLHASAPPGSYIAVGTRTLQVYVLQLDCIHEKEDVKMSSSLVDPSVDN
SGGFSCVLTPLRSWTAAQQAIAVVQFTFSGRHLVSGSTDGGVKIWDVFNHHLTHNLRIPS
ASLVHSVYVDPAEKYICVGSFEGHVAVFDFVDKTLISHGHFHVSAVESLCLTPNNEHLFS
IGRDRKLAICTVDSSTLREVRSFVVKEHVSSALFESPFRIHVGAMDGTLSTYSVSVTEPL
RLSRRMRGPSVAADGPPDDEWAIRSLLVVQNPKGVHEAGPLYGLLDDGNSSSLYAADAAF
NISHLLPDMEGSGYYASSTLVGFLDQVLDLKPFPPGFPFQRMVVTNSKDVRCYSTSGCIS
SQILRGHKDIVLTCAFSADAGIIATAGKDCEIRFWSTANWKTIAIGQGGHEADITSIVFN
AKQSESYIVLFSVGVDENLRLWDVGMHVLPALPHDEKRVKMSIIASPIIFSHRSGINAAH
EGPIHAMAVAPNDQYLATAGKDKNVNLWKINGKKVFRDASLKGHRRAVSCLSFSPCDRVL
ASASNDGSVRLWSLISLTCVKTLQMDRTPVLQVAFFNKGTQLVTGNAEGVLRVWAIAESE
VVWSGETHEDRIWALSLVEQENENVLLLSGSADGVLVATEDYTSEEAERVRSERHEVILK
EQELANAMRRGRYTEAFLLALKLNHPRNLRQVIMKWSVKDAEDCETSLCRSILPSLGEEQ
LLRLLQFTREWVSNARHCSVASLVMHCVLASHHFTELASMPAVRTILEALLAYMQRHSQR
LHEVLRRTYYVDYVTRSLGPLTLTSEPPFIRDVATVDDGLALKRQRAE
>TCRU_10820 kinetoplastid-specific dual specificity phosphatase, putative
MSRCRKKMATNMLPAFNLDIVRQYTDVIMDVENEEVCNAAACHPITDINNRVFIGTWRDA
ADEQLLRRHRITHVLNVARELIPEEELCRMKSIQFVKSKCIPLSDSQNEDLERYFDEAFE
FIRSAVHQGRILVHCRRGISRSAAIVIAYIMASEGQSFRTAFENVRMKRPCISLNLAFIQ
RLEEFEAHLHLMR
>TCRU_protein, putative Generative cell specific.1
LFSLLLFALMVATTPFAAEGLLLASSSIEQCDRVGTDNSLPCEKKLVVTLSVDSDQAEDV
EEFVILRDAVDKTKGTGEEHVEFQPIRLTTSKSRVQYSYPLFYERNFNAKPYEEEITTEL
VGCDDTFSPKATCGLAMDTAGRPIPYSQGFCCRCGPCQLLGLCPVGSRGLQVCDIFRGAA
LASCLRFGELWYSGYSMGSATIWYRLSVKLTTDSQNNSKTKEAVFELGPDVLSGSSAEFG
AWVSLIGDFVPAELPLVLSNKMLFIPSSPRIHERVLAGQKEWLILDKHHVSMQGRDCNKV
GVSYEAFSGQGSRCQLIRGSCLADQLEDYRSSDLAVEARGGRGKYLARFFGDFVVNNVNN
SRTRLSYWMRGSLATMLTVVISADRLQYLVSVSPGEIVSAVMSKSTVEESSRDGSVSVIV
RNIGHVTAQYTLGVGNCSGNVFPIMAQTLSLRPRGTVIRSFDLNIQDVAEERIVQCDVTL

RDAKGAITDKKILKFRVTSKVLTNDTQGGNAPTGGGASVDGQAPPACSRCEWYKISCFLI
HGCWWQPLVYVLIAIAILLGIYYFFGLSSRSSEPKLH
>TCRU_10822 palmitoyl acyltransferase 2, putative
CCGRSNADVAILITLYLVTSYSVHSYYTFLFPQTLSALGLAFLQPFRRVARPNSSFPLHL
HNLFNVATKEWILFGVSLFLFFLAIWAYLAAAVTDAGRVPSEFGQHAPRSASLALRVSGA
LNICPVCGMYKPQRTHHCSRCRRCVLKYDHHCPWLGRCVGFFNYKLYLLVVFYTFLLTLW
VGTLLLSDMVVYIVRHYRVVGWKIVHRDVGPFPIGPDGTCWTDRSWLVVPLTIRCILGSH
MVLCSILGDSFGACPPFLGVYICLLEAMIFFVLTASLLRKHCWLARHSLTTLDLVIYQHQ
LDEGLSSGRQINIFDIGVKGCLHQVFGDGDERGEHLHPNFIVRWFFRLLPFPAYPKQAEL
HYSSPLGIDDTENLLGETPFSAVSHTTVSVPSYGTLNEAAPPYNMINKNDKNVSTDVGRR
SEYRHHPSQYPGQTRHLLGLSFPTVLSL
>TCRU_family transport protein, putative se.1
QKKHFLRQRQKEVIRAMIASAVPLTQAGAPSVVSRASGGEVTELTVWRLLIYDDIGRDVI
APLLRVGDLRELGITLHMHINSKRDPVPGAPAIYFCSPTEENIRTIASDAVNELYEWVYV
NFSSQITRRGLEMLAENLNRGKLQSIQHIHVFDRTLNYVALEDDLFVLMQEDSLVTLNSR
HVRDDEVEGHLNAIVLGVSHVLLSQQVLPVIAHSKTGAAEEVARRLSVCLNDHINERTLV
PAASTVLSRPLLLIVDRSSDLATVLHHPFSYRGLLVELGDMHLNKVCVREEDGKESAFEI
DPDRDEFYEANAIQDFSAVGGNIEAALRQYREEYAALSETACAGEDDTDANAMSRLLASA
PKLGEKKRMLDAHTKMAYSFLHHIRKSHLDRFHGVELGIIKREGLDKEEFEKLLLTGLGT
VEDRQRLYLIAYLLDTEGEYESLLQRCASAFEETPFPALAYIKHLRNWSLNAVSSTTEES
SAAQGFAWGLAQTLAKNIANTLGANAKSELPLTKLVDALLQDPTASPKGGTTTRTMGGGS
TLRAKLLETVVGYDPRTKKPLDLADTHFSQVIVFTIGGGCVAEYDDLKTWEAAHPRNVVS
YGCTALLTGNKALRQLSLLGEGTT*
>TCRU_10824 60S ribosomal protein L35, putative
RDKSKDELLKQLMEFKKELSQLRVAQQLNSAGTRLGRIRLIRKSIARILTVLNRNQRESL
RKVYAGRRLRLAMPKALRPKLTRRRRLALKDNEKNRKTRRQLRMARKFPRRVYAVKL*
>TCRU_10825 Glutathione S-transferase, C-terminal domain containing
protein, putative
EKATAVFQRMWKEHPRPIMATVTVMGGYLVFKGAALLISRHMRNKLLATLKNLEKDTVHL
FVHHRWSHGPNFFPHCVKVETFLRLEKIAYTVHFTSDASLSPTGRLPFIVYNGTIVGDSG
PCMEYLKETLHLRLDDGLTPEDRAIGHVTRRMVETSLNYGLQRSTLVDRPGLMQQMFIKE
YLVEPKMARRLVRSMRFKLVKALNTLGYNTLSEDQYPQEFLHEVQSLETLLSTKPFLLGN
TPTSYDCTVYAWLHVAWEIGPHGPAIKYLRKSDVLSEYITRMKNLAFPDINELGMSSESQ
KFIPY
>TCRU_10826 hypothetical protein, conserved
LQKAARHGSYATQFWTRPDHPPYRTRRAMLTAHSRKAIKRRLVLPLDAHDWGRALEVLDA
GYARLGRTAEDYQRVIRGVANETAPQRRGDALHTLNALRDKAYMGEIGSSGFWVTLVWAY
ARLRYPREGYECLLQGERRFCFSPLTKQHMGETLLPLLAEHGMLDEVNYVVENFMGTGGS
RQDRARVASILAEAAARSGSWEHAIAALHPEATTAMTTLNPRTLACLFVSEELSEGQEEA
PETPRRARQISTEALRCMMCSMADDGQWEMALQSLRELERRQGNNDERDNTHDAAGSIER
GQKQRKQQQELSLSENELQRLLNSLGSRQRWEEATALFVSQYFPDKSVRGNEEVRPLQLT
TLNLLFASFPRNMREFRLAAPDDRLESHGSHTDPRQQENETVTVEIDALHHPQQAVSLFD
QIFSQRDDVSVTDLMMATVGPSLVQLGQWDRALHLLRQTPALSAAKTPVCTLEVHREVRR
RLVALLYYLHGAISLESRYYTLYYFPFAFPKETFRDLLPPSEFLAHLRKQREEEEKTSIT
PSCVPKVSTRRRFTSRRLSAIVQNTEKHDDELRRRLLPLYANRANAFRGGDAEKDPRPIP
KGLHDTANGWNFYGRGGEMVFMNHRRTAHPFSMHPKLMRSITDPYRGWSPMQNSCWAHRE
RVRKWNGSSAV*
>TCRU_10827 hypothetical protein, conserved
MSRLLEATMAISSVPSSLTAAYGQSGEETWRVVDVFCLGSQCAWFIVKNGSHLSSINVTS
RIDKHILFPEKGMSQDGTKEDFFLLLRELQRVAGVVSVDGNDTARRRGDCLRCPGESEGI
AAVSTLYVQGLHVVLFFVMKCHCMAIASFVIDPPVEANDGGSSKGKAQLLAVRWCSGEMK
ENESSHYMFSRQLSVPMSAIVEEYKSDSFPLNSTSFLSSSSSLPGLQQGQRYPKRVSASL
LRNTFPWFILRIVFARVMGWVEYVDFVWQEDLERNVPSPWRTLQGFRQFTWGSLQLEKLS
GVPGEVRALRWMPFLRDYEERYPLLAVLYQKAPVSGDPFLDCLAVSMLSVLRRRQQQQQQ

TPMCVENDSWVGLRETLHGSLMEGPWCLEALTLAHPSFLLHAVLPGGGNMGGGHDALGVF
LRPAYVMYPMSTFLRDENVYASWEPLVATAARDNKKSEEMYFAVFTEDGEVTRCQVGGFI
ESAVACPATSSGPRRVSSAAGGTERVVAVVLAMRSGGDVLLLEVWNKTNVAAAAAGGGGG
VGVGRSIREQKNASGDAKMAVVNCRNIPSWDAGVPRSLRHLHRLIGLKWEDARGTVFLLA
AHEDDNTQQVDCSLLMAELVPQGGDTPRFIWFGASNGFIVDGGSNSHGFPLNVGLPALVQ
PLSRVDGEYNLGSLQHAPLHPLCRCAVRQNEAVDAYEREVVIFRSGDICLVRRNTPFSTH
WRNYDPNVFCKRLSRVQWPHSGKTAEVDALFLLFASGSSDISMESFWTTTGGKLPTPVEI
DGGAISLHELQLLLVCRATVILMTAEGQVVCVSDVHPPLAVMNDGDSRGLVGTETMGSMD
GERFSLLSCMIRFFASFQGNHFFICATSASSLPSRENGCRECFFLFLQVTCSGDQQDDSA
LPLATVCVVDIIHVKTDGHPLFDFLPTGRLDDCAKMTALGEATRMGETCVFARDMMYCAG
AKLYTVPCVLRCRASTRGVWMEGKFETPSSNSHHVVLDLKDLLHEESKATIWRLEPSLLQ
CVPLPSKRERGRMCVVILLSFVSGPTLASAFHCSSVSRRRWESQLLVEGKGTTEEMAVPF
VRLVTQPA
>TCRU_10828 UEV domain/Zinc finger, C3HC4 type (RING finger),
putative
TRFFICSSHCKPEVLDRILHDVENLCNTFHFYCRDATWGVTQQEKCIYGGLPITIKKSNS
DHTPLTPDSREQAPPHRYVLPLQIWLTHLYPIEPPLAFLLSAEQGCRIASNHKYVDATGR
CHTPELAAWHPVSSSLCDVVKKLCQLLSAEGLIPLCFEEGVSSPSKGHATAVSQRLCHGL
ENGDDDKQTDEHERCVVCFSPKETVLVPCGHYCLCDACATNVTHCPLCRGSVKFRQRVFS
*
>TCRU_10829 hypothetical protein, conserved
VMRKTALLLVRLPKSRRPRERPWEVFNTRDFGFSEGSQNYSMWLLTASTCAALLLFEGYQ
QALRILGRGDTCPACEAAREHYRQRVSDKEREIQE
>TCRU_10830 UEV domain/Zinc finger, C3HC4 type (RING finger),
putative
TRFFSFSSHCKPEVLGRILHDVENLCNTFHFYCRDATGVTQQEKLCIYGGLPITIKKSNS
DHTSLTPDSREQAPPNLYVLPLQIWLTRLYPIEPPLVFLLSAEQGCRIASNHKYVDATGR
CHTPELAAWHPVSSSLCDVVKKLCQLLSAEGSIPLCFVEEGVSSPSKGHATAVSQRLRHG
LENGDDDKQTDEHERCVVCFYPNETVLVPCGHYCLCDACATDVTHCPLCRGSVKFRQRVF
S*
>TCRU_10831 ABC transporter family-like protein
LLYSVIFSLSLAVAVRCFTNRWSSKMRLRSRVIVLASVKKIVEEWEEPCLLEVDKLMTAS
TTVDVHHKRFLNLHEENEKVKSDVAPFHGAVCSMAYAPAVNVGQWLRLWYVGRYLCASAV
EDMLWMQRLGYIIKFVAFRRLTLMAEARYYAALWRSALYGGSGDHAAMDVPAPRMPLWLV
GRRPFWIVPLSGKDSGHYLCLPLSYFPVEAILTSTAEETWIKKLVDILPLLSEEFSLRYI
SDTLRTRRTIRLVRLLFQWKFPSSWQLLWNEIDRLFLTYATPLAKGQLQRGEAVCRRFYE
EKLFEGVELVTGEGIDMEDGEDGVFYPTRNKRKRCVECDVLLRDVRVSRRLQMLLHLRSL
SHAVRVGIGLMAPQYNFFAEWMLLKFLSPTTTDGDRHKILMGFSGHVLRDTLGAIMRAVI
WSLDDSVKANICAVLRNELHHELNVKLATADEAFLRRCIEEGIAGRDNPVEKSSSYAGHV
ASQILGRFDYERRGVMARIIVVLLSIWRREIGVALFAAIVALFDYHETAHVLSCWLGITV
HKELYHELAQMEEEGLPPAEPRYGLRLMMDVLAGEGGRNEETRPRTCQRNKKSHPFLALI
VCGGNFLLDWPLSANTFPESNGDTTTRHHLKALERLLDDVVNSGDYSLVATESSTCRQKL
CGGSLIESLRLNAAFVREFVLKVALQTSEAPVTAGIGTRDFGKGHALHKKAESILHSEEI
ALLQNPQGMSHIPRTLSFHDVFDKPPRFILRQLGLETVFAYRAAMVANQNEFRSLTESLV
DFVSSPFHNVFTRTFVHLMEFTERVIFYAIFSPYVKSPWKSWPIIRHLVSPALCGSGVHR
TGEDTFGVLGGVSLLGRMSGYRATLKVYGDDSFGPPFLLCVQLSRHLPTTLHDASPTHYA
PPLMERRRAWRRVIQLHGEVEFDNIGRIVGGFSLLKGIDFCGVYFAYPQLHHHVEDGSLQ
PTLSNITVRFPVGQMTAITGPTGSGKSTMISLLKRMYDPLPKLRINEEYNAWCNSQALID
VLRHCLCASTPPTTDGTVNNIILIDNIPIGCFSTSYLRSAVGMLEQAPCIFERLTYYENF
SLFAPDVFMEDVVRAAKLCRCEGFVESRALAYDDFAGPLSSGEKQRLALARAILIGCRGL
KVLLCDEPTARLDGYNESLVEEALRGLLGPPRCMTIVVVSHRLSTIRNATHVVVLNEGHV
EFQG
>TCRU_10832 vesicle-associated membrane protein, putative
MQGETKIYGGVLVRLSDRLMLCKAPGCPTNDFSIPGTVWAEVVSKCSAPNFRTTSFISLD

SEGLSGVEEGAEGPLQLSYHIMTDSELAFAILANKAVTRRQGHAALDEAAKTFRKMFVES
VAKLNTKMVDVFVKPYRDVLLRMSDSGEPEEKVRKVKMAVAEVKDLALDNVERVIQRGQR
IDDIVQSTEDLQFQAQGFQRSSRDLRQQLWWNSVKGKLMVGGVAAFFIMIVLFVFFSGNG
NSK
>TCRU_10833 mitochondrial carrier protein
MDSLVAGGVAGLVVDLTLYPIDTIKTRLQSRSGFYQAGGFRGVYKGLSAVAIGSVPGGAA
FFVGYDLTKRGLLDDGGEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXN
LTTVRRLTSQAVAAMAGETLACLTRVPTEMVKQQLQAGHHHDIYRALSHITHNIPPDAAP
VMAPRKIRWLGLPLLFTGMPIMLLREWPFSVVQMCCYEGLKACFHTEERPKYLPLCGALS
GGTAAFLTTPLDVLKTRIMLGQVGAAKRTTPRGTAAVRAAFHDLLCEMPRATDKWGGAQR
FFRGAVPRVIWISIGGSVFFTTYETVWR
>TCRU_10834 acetylornithine deacetylase, putative
TLIHNAERNKANLWATLPGDGGVTKGGIILSGHTDVVPVDGQKWDSDPFTLTERDGKLYG
RGTSDMKGFVAVCMSLAPELLKMRRAKPIHFAWSYDEEVSCLGGMELAEFARDHDVRAEG
CIIGEPTGMTVVIAHKGTSHFWVRVRGKAAHSSLALTGESCNAIDYATKLITKLREIAEE
YRRNGTRHDFQVPFSTLSTNLISGGNASNTVPAECEFLFEFRALPNETVSKMMQQVRSYV
ETQLLPAMKAEFEDAEIVITPRNETPSFEGSEEAPLTKLACAINNDYKVWKKNFCTEAGH
YSGIAGAPTVVCGPHGGAIHCANEYVTPAQLDKCREFVLKVAE
>TCRU_10835 hypothetical protein, conserved
ASQTTADRLLVSHHHHRLIDSRYWDCATPSKALSVLGLLVRSGTMIDKLDKAASEALSAM
GPSMTMSEQALLGKWSSFLRLKISADGSSSTPQNVGSDICSTDINESVVALYSLFIRDSQ
TSVLAGERSIVLSTDSVLRLDPISSLMLLEMMLSKSFRQGAAWRNENIAGALLTRLRYHV
IYSNVIGFKALWWILHILSDKESVLQRRSVESGRLFRACLRRLHDMLPGLTPGDCLLLFP
LLKNSLYDKPFIICADIMRRVVTCELEELGVVPTSVIMHTLECGDLVPPFRRRLYQLLCE
DYRMGDIGKGECLFLLSIIATSPDMDEVEKNNYEDDTGCTLCESLFAQLYVTAKSMNAVE
CVQVLEYMEFLATSHFSVTIPQDLLERLKKRVFSWTRQALKRPNLTVLELQCEVEAIHRL
EGVLRRSVLLPFLAGDAAVIGEISRKVNYRL
>TCRU_10836 hypothetical protein, conserved
FGVFQNAHINSFPVRAAIDIGTGGMISMAVGRVDAARNAVRDFMYQTTLPLHLMSANAES
SSGPFVLSSRTFETPPSSFILSEKTRTDIRNKMRMLHGALRRDQYDGLSERAAVVSWPLC
EAADALSLAEELTREFKVDVRVLGKTFHVSTLCHTSKPLFGTEGAATLLRKKGVKDRAFQ
KDHRNTDDDSLQLLMQQIVRRREKRRARHCSTENQDCHHVNIDEHCAVLPRQQLEQLAFL
AHAAVSKCIAPQRMLVITEDRHKGLCILAADTTKEDVTDKEGKKAVVLRNTPISGGLLLH
VLPFDILAAQRLLLTAVQRRADLSENTEDRRSSNPVLREEFRELRCLLEKMIAPTLPAWV
HEKSGAGGLICGSSFNGGVLNIAARVAQRTNVSLDHLETNAEMHYCGLTDVLLAVNYPDP
TTVLPSAAFASALMRALETNRFEYLPEVGIAAALLVQPSLWIYDRREKVRTTLQKKKFFS
GSSAQRTFRRPHARENPSASPEASWQLNQSWNPLSYANSTKGT*
>TCRU_10837 Protein of unknown function (DUF2475), putative
LEMDYVALTPTELTLWKEKAAPTIRKVTNLLLRGGAIGFLEMERNLYIGSEEDGNISRDR
RRVNPVLFKSIMNKSGVLLTPDEYRNLRTAYSDEGGFLVDDFIALVCPLKSLGDREAGIL
RDMCGDVISAVIPTIALADLMHTLEEALLPGDVAACEATPFFASTMTELKMIFTPLRYPK
AFVPPQDVMNAFAAILLNSPEAGEPLLKCLATVRLPPAPPSPPPSEMPFFFTGTRTAPWQ
KRGYEYYTDRDNRDEWIRGREEAPPRPMYQRHLPGYQGHLPTYKSKFGRSFHPIEESVPE
LSRPKEEQGPVAADRYGPAVELKGSWLTRHNFKLA*
>TCRU_10838 syntaxin binding protein 1, putative
KPREPSNGVCGCARDHMFHQMLDAFHG*FKVFCDAHAAAVLSCSLRLHDLMEHGVTLLED
LMTPRQPVISSPARYFFAVEDASVSRVAEDWIATVPYRDANIFALGCTPHRHP*QLAWAR
IAPRAMCSKDVMLEFAAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPA
FATKTVAASAMGLPGSATTSRISLRGADSRGNPVRIIFD*SCAMVTPLMHQRTCQCLLDD
LMPLEKKVYEQTCRNRLGVGSKRQIDGEEVYRR*YRHCFLAQCVEELSVALKTLHAYHPG
LAHGVEQKANLAELGSSVRAPPEFQEKQARLSLHIDICARLVAQYREKQLAEVCEVKQDI
AVGRKPFRKNLDGVRRLARDAAMPRPVRLRLLLLVTASSTDELK*AKKQQLIRDGGLTPD

AHLSANLEHVMRRAGNVQQYSTASAQGGRSTSASASNAATDGDPLLKQACMMMETDRNRT
LRVELSLASVQRDRAMGSNGASVGQNSGAKKPPGHFKGVVANGRIIDLGGGGGTIALTAP
QRIVLLVLGGLACSERRSVHEISKRYGRGVFIGQISLLRP
>TCRU_10839 3', 5'-cyclic nucleotide phosphodiesterase, putative
PRSQWVERGVSCATCGKRFSLFTAKSNCPCCGKLCCSDCVQAECAIVGGSAPSKVCIDCF
SMLQSRRRVEPDEGSSFREFNAASAFPLQTRLLADGRVESGETSRVSPPNDGRVQHVSRA
NGYSNSLPVLDEYVDDLLRKSELLRMENDVLLNRLREQEAEIHALRLERDRAVARIVPDG
GSMAGRSGLPQVSDEIVKELRGELAVAHLRIESVKRELKNALDRAKSSETMVRNLKQVLC
NYKEEVVRPLQSREEVEMLPGVSGHRDMISTRRLPPSIVQDTILAVVPPKSCAAIGTDVD
LRDWGFDTFEVASRVPSVLQSVAMHVALAWNFFASQEEAQKWAFLVAAVENNYRPNPYHN
AIHAADVLQGTFSLVSAAKPLMEHLTPLECKAAAFAALTHDVCHPGRTNAFLAAVQDPVS
FKFSGKGTLEQLHTVTAFELLNVTEFDFTSSMDNASFLEFKNIVSHLIGHTDMSLHSETI
AKHGAKLSAGGFDCTCKEDRLEALSLLLHAADIGASSRGVAIARKWLVILQEFADQAEDE
RRRGLPVTPGFDTPSSVEKSQIPFLDFFVIPTFDLLHQLFPSIEEPLHNLRKLRELYAAK
AGVTTPFPPPVDYRSREERIRSLEAELAYFRRREEEFHRQLQELRTASENENKSSAAPMT
REGALNKQSQLVCRGGKYECRLGGCRRWVSEWEGCEGLARCVHGPPVSSKTVESDTGDSG
PRGRRGSKAETTKAYERKLGEREAALMATARLLENREKRLAVFSEKLAEIAEGLHEERKR
LQPMEEFKTPCFSRETELISEESASMDVTHRFSTQWEAEERLARKYRELDELLLIVRAMR
MGYAARRNTNLGWKALSATLAEREAAISEAVELSRQRRRHLEEG
>TCRU_10840 2OG-Fe(II) oxygenase superfamily, putative
KTELSVTLHRLRDADEARRRVPPPLLHVCRGLETAAMEFAHRTLLHASIPEVARNEFLND
IGRRSVFRIWRYSPGTGCRPHYDPGLCTALLQASAPGLELNLQEELPSKPERQGDYRYDE
TEVEDRINALPGWEAPSPPSEEDDTLVLRSNMARVLSNYALPPVLHRVRSDWAQRGERVR
YSLVVELRPSQPRRWYNM
>TCRU_10841 Leishmanolysin, putative
LPLHATPPLPLLVLLLMYCTIGCIAAAPAL*HHRGFDEMMGRSGPLRTAVVREVPRKGQG
AMQAYTVAAQEDDSGWEPIRIEVFTEDLKKSTNRKKTYFENDGDECENILGEKMTCKKEN
VLTDAKKQLYTEKILPGAVKLHAERLLVRPASEKVTVPRTIGGLCERFTVPIEHKKNGGV
PNFDFIIYAAARPSSTESMAVWAATCNTWEDFRPSIGAINFDPRYMTDTAWSVRVAAHEI
AHALGFSKESIEGKSIETFEKSVRGKHRKMVAGKHVQVKAQAHFGCESLDGMELEDEGGT
REKAIPHWKGRHARDELMAPTVGAGYYTALTMAVFADMRYYRVNWSMAEPMSWGRSTGCE
FLEKKCSEAKDFSTNYPHMFCDDSDKKTLRCTSDRRHVGTCTANIVEDKGSPADKDVCPV
VSSYFHNFSGTTYRTCSDENVKHLRGSLTGSGSWCLDAELLETKDGDDHKSVNGVCAQVS
CEEGTVRVKHLGSTDVWHDCPDGGEIQVTLDGFKQDGKIKCPKYGEVCTIA
>TCRU_10842 Domain of unknown function (DUF4520), putative
YNEVAIADRVVRACAWTDNSADFVFGDGTVLSFCDEMQTYVAFPRVSHAPLNSQAALGSS
GHSKSFNEGDIYGAESKSQGEYFFTPLTLSKYENKVREALHIYNFYSPRPRIVTGLTATP
CEVWRQNSPIDSLVIAADRRLFERRGSRATLWCALRRISLTLHGGRATFSVRWPAPAVER
NMARSIFVRPVDEHGVFTGMLESVRSFHFVWVEQTFPVMDPPEAWAEMLETALQLDADAP
VGSVGEGKEDGASCRGESDVEECCLVYRTTPCTAQDRQPCRFSKMVREHVDSLIATLQMQ
SAACNRLIRDPCERVVWRYDADPTGRVPHAVYWGLFAEFQHGHSTTSCRRQMWDGRNTRG
RLVPHPAIGTVLAMVREDESLVVAEPQSQSYVIHHWRRDGTYHQYHQSPDGELGLPPVIP
LHCKRGTGNEVGEEPIEMVWGQDGQNKNNSHDKSSLSMMASEQADGLITSKIATPPLYFS
GNLEEAPLSALHRGRYLPDVGASCIQLSQLNLASLRAHKQEMLGDIASANAGAYATGTTG
FTTGEPTFAAKGGVAEAAQSELQRIQMRFVSNDPALAEAAANGNVVFLTSSIEAVGTFVA
LTNGTIRCHFDDRTILFLVPGADDREENLVATCLFRDATQCSMRLVKCAQHHRMYRYVAH
ALQFRRFSRLSPEARTAVMNETAALKLQYLDETEWQRERKMEWELQQLLSRTEALLSGND
ELSRLNHSLLREEKENASSYFS*
>TCRU_10843 retrotransposon hot spot protein, RHS3, putative
LMVLTSEKGWPYTLNAPHGCGNELCVNCEVERVWQIVLDDLTEWFSNFDLTLNSSPLPRV
LIGTPGIGKSMAASSYLLYQLLHCDVEELQVVVHCFGSKMYVFDKTTKAVTKYVGNKTSK
SVLGGLWQRGVKGYIIYDVARKGTPPDTGFAPSTGWGMIAVSSPKVTNYDEWENQLQAAR
IIMNCPDEMDVKAMCAWIKRGLDPDKQAGYWEMVETHMEKVGPIPRHIFDEKIYIDRMGA
VNGALLAIKYIDVEEYFSMGGEEKWYSEDPSHKLVKIVRERTDEGAEVFLNASINADIGF

*IADRLEKEMATKDFLLLILRSVMLLFPTLWKNWVCVYSCVGSLSALVEELKELRSPKRK
EAQDSVLKVNHQGYSTRAVGLRETEGGVTRIPMEYRVLYIPKVENFPLVDGFFFVDSPRK
TLVGLQMTTASEHHKITSTVNLFNVRLAAYFNGWEELSRDMSWEMIYVQHADSTPMKKWQ
GCDVVNPNNETDAEKKIVAFWDGKVHQYQ
>TCRU_10844 A distinct subfamily of CDD/CDA-like deaminases, putative
MWDAIHFYKAYLPPAESNRTLQYVVLALDDESSSGFAAPRNCSVCVESTEKRVYPLLRES
VHVRPSDGPPMIKRDCDIYSASSSESNEKTNMQKRLRFFLCKKEDVVPPQLKQLLGKVNY
CFLLCGKSFHGEACSCNKAHFLNKSVWRLELSTFGFKEFYVSSGFYVHCIKTEQIRPTAG
FLFACGLLHEGVIEAAQPILCRYSERCRYGSRCLFVHADIRTEERTAMQASLPLKSLLKA
ESRLPMFLSQLDELGLHTVGDVQQLSNNAFDAIVARSEPCWLVQWLNIALVRDIQTKHML
KNVLATFPDIATPVSLPPCLTNVLSLIQLSVKEFYSLVLPVKVQAACEQIRTRFEPDRHH
NIVDLRKEPEGSFLSKLCPIIMSFRQKNAHVSWRKKDPNRPVVTSLITYIDPEECDCQVD
CSGRGRPPALIKPNGREREEKHPRSTWCNCTRSFVLAVNYELSTPSGSRCSEQNALGKLA
SMGLPTSAIREIFVHGEMLGSKKDPNPLFPCGVCENMLRKVTRDVHDAYGGDVVLYMFDS
TVNPKKLVYLPINEISYRGGSGFKKFLADLRD
>TCRU_10845 hypothetical protein, conserved
VLVRLLVFFVSMETDAWPTFQYPLPRWRLMNCDRRAQDLIDCDPESYRNTVFVFAIPGIV
VAGGVAMTVLLYLICKYVFDCCGGRKQSPNFCCPLRGHSAKYSREDLLRPVLLAVMVFGL
CATTCIWGCVSQHHLVSTVGEIHNISSFAIKNVEKMNLDFLERMTITLYDASKDVTYPMS
LLRSKENENLYKETAARTGDVSSMLNQTVIRLFDNIVQFSWEPYVLFGVSFGVSFLGMIF
ALCNRRRESIFVFLIMALLTVMTWGFNGLYSASSFLVSQSCFEMTEFTERRTNVVKAVTK
CDDTRFGGQTAAFEENFRQLSRSICEEIKPYCYDKTITPDMNVAQKKVFACPTHMVCRYV
TDDEVMSWVRTALHTAPQVTQSATASAEAQKKGYTCPPTPEGVCDLRACSATCRKDGVLS
DVGKTAKKALYAIFGLAEARSAFDTVDSQLKGCDAVFTGIIPLIEPFCQAAANNIYNLLQ
CTGLLGVTLIVALYTYGMGSKRFIPFEEALLPQKD*
>TCRU_10846 ras-like small GTPase, putative
MSSELLSLPKVLLMGLRRSGKSSIQKVVFEGMQPHDSVNLPTTVQPDKSQVHSNDFVNFE
VWDFPGQSDPFDPNNAGPYDVEQLLDNCGAIVFVMDCRELIEDSRARLIDTVCAAYRYNP
ELSVEVFIHKVDALSEDHQADLLASLQRHVDLEAKQRLESAAPLRLNFNLTSIYDHSVFQ
AFSLVVQKLIKPQSPYITELLQMLNSNSNVDLSYLFLSRSKIFLALDERSRAKLRTYGLC
SDAIEVMMKMSQIYTPSTKERRENCHGISATNITNNGVGNGHRVESVEAAVAAGANAIIK
ISSEDYIYVKELPNSLTVVLMAKKECFQSRTLIDYNILVFYKAACDIF
>TCRU_10847 paraflagellar rod component, putative
SVCPFSTFMWDAPHAELVPPGFTPGSVADAMLHISDLTLRFDLFAKAVEYSFHPVRYAME
NHPIHTKTLHKRQFDVIRYGMVLDEVERLVIVPMPRLCADSGAKVSQEYAAIFNGDFNDA
PCASHPILPEYCFVVYQLPKSGNEGGGSIPTPLFRMVFRNEAFNEQMKMHLVKDFPLFRL
RSVYVSHAEFYALQRQLEIYTKASATSETLPDSALEETLGISKLRWMFDAWLMVLEGIAP
SWLVDKGVGPDIVTLFLASHRPIGKYDVKETIEAYTQLPMDNRVRCSYYTAGERMRQRVH
VMQRFPDMINKWRQGAYDLRFFGEEITGAEPTVHVAHCIRMLLCRRKPGRNYIEDDEIAA
FVPADDECKPLQVYNTLAAERLRLWVLKGLLTAELHGVHCLMLEFDTAMVLSMCVGLLWG
SGEEERQREFVFHVCKIIVETVEDYVQHSGIIWRVIIVTSDENSLKSSMLCREILEVTQM
AKTRVEVEERQRMAAGKRVSSTPSDTGITAQEEVEGEEEHGENKEKEAKEGAEKTLTGPA
AATRTLTSAVVAMAKSASYKHGPFEDVARFSESIRDRAARFGVRISDAELYPIFLALSGG
EDTVPISEIVQLILEKELELNDGRRSKLCRETRLIWPHDHPICALDSCGVPCDKTTVWNF
VKSFQRRPYRANVGDYMATIGFTPGNAPEPPESLNYVEFSVLMLALARQ*
>TCRU_10848 RING-variant domain containing protein, putative
GSRHLLEFTGEADNMINIVAQLLDSRYDENIQPSNCLGLYINVEIRVKDENDEGGKSSDV
WSSASGSKSSRRKPVSPWSSFWNAIATILDSSAFCDILPTVMMRVAPTPVPTVYQFIISA
RHGYAAPASNYKCQMRVFIEQDPAEEMARMQNVFALGLPLAFLLLTAPFILWRIDLLPGY
LVDIDVVNWLWYMPYLLRDTFVNVAVGCGTTIWGLYKERRSREHQRRLEEQHRRLMEEAQ
SLPSVHEEPTPFPSFQPQPQPGTFAAADVGFTPAGRNNNNNNNNRQQQW**PXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXFEKERRDSTVVHILPPPPSHPGTTSTS

PAAAAETVEALAEARGEEVDVITRKKQNKEERQKLLNNREEFEVKPQSSVSSSPTRVLIA
ASNLHYRHGNKDKDASAASGPRELLETSAPCVVHVHMSAVEMQEGVIDELAEGGNTRYRK
NPSSESRAFLYKEEEQEEEENVCRICRDGEEEEKLVSACECTGSVRWVHRTCLDRWRMES
AKRNMRNVNRCEICKKPFNISIRRRTLLWQSSRHLVLGVTLALSSVVFFFAITVFLRKTL
GTISCRAPWRSVSYTTMFNLDGIMLTMFGYFMLVLLATFAFALVYSRWHTREEIEAHVQE
FQALPEFWTFRNTTKVVAVYVIGIGQALCLGYLMKLWIYRTSNVVWNWEASPSIGAVLYM
TFLTLGMSAVRAGREFFHNQSLSNASDIVVVDQQQEQQQQ
>TCRU_10849 succinyl-CoA synthetase alpha subunit, putative
MFFRTALRSWINNNTKVICQGITGKHGTYHTQQAIEYGTKMVGGVNPKKAGMNYLGLPVF
GTVTEAVKATGADATVIYVPAPHCAAAVEEALDAEIPLVVVITEGIPQWDMLRVKSMLLS
QNKTRLIGPNCPGIIRPEECKIGIMPGHIHQKGCIGVVSRSGTLTYEAVAQTTAKSLGQS
LCVGIGGDPFNGTNMIDCVKFYLEDPATEGIILIGEIGGTAEEEAAEFIKNHPIKKPVVS
FIGGMTAPPGRRMGHAGAVVSGGQGTAKGKMEALKAAGVIVSESPAQLGELMAEAISKK
>TCRU_10850 syntaxin binding protein 1, putative
MEEEQPREPSNGVCGCVRDYIFHQMLDAVHGSFKVFYCDTHAASVLSCSLLLHGLMEHGV
TLLGDPMTPRQPIMSSPAPYFVVEDASVSRVVEDWMATVPHGDAHNFALGCTPHRSPQQL
VWARIAPRAMRSKDSMLDFAAPEVLVFHLSTQNGFPQLLLPLSPPN*WSVVVVAASRPVA
AIHAMNNGVPVIRQQNSGNICHGLVATFFEDLPGNTTTSRISLSGADSRGNPVRIIVDWG
CVTVMPLMHQRTCRCLLDDLMPLEKKVYEHTRRNRGADSKRQLLVDEKDVYRRSYRH*FL
AQCVEELPVALKKLHAYHPGLVQGVESKANLAELGSAVRASPEFRERQARLLLHIDICAR
LVAQYREKRLVEVREVEQDIAVGHKLLRKNLDGVRHLTRDAAMPRPVRLRLLLLLVTASN
TDELTEAKKRQLIRDGGMTPDAHLFANLEHVTRRAGSVQRYSTASAQGGRSTSASAGNAA
TDEDPFLKHACMMMETADRNRTLRVGLSLTSVQRDHGIGPNGASGGQNSGAAGKTAGIFQ
GCGGKWGIPDLGGGGGTIALTTPQRIVLLVLCGVACSERRSVHEISKGYGREVVIGKSLL
RP
>TCRU_10851 leucine-rich repeat protein (LRRP), putative
LRDTQTHR*RDMLLDVSRAPGEHTSLDGIQELQDAGEGKKIGTLKAQYNNLTTLNISTTL
ATALQHVTSLTVSYNCLSTLQGLEAFPLVEFLDLSHNSLRVLDAHSTSILRRLRFLCRCD
FSYNEIRLIDFDTPLHGGSSKENGALGSGDWFDNATLDELTVLNLAHNQLIDVPDLRCMP
LLEELNLEYNRIEQLTDLESRLPLLALTSLSIAHNGLRSLQDFLPLTVLAETLKVLFFRG
NPCTNNATVTKGCAVRPWLLWILPQLEVIDDVPLTQEECQTAAQMFRQHGELSYEAMDVM
NSHHGLQLEAYLQKFSSPPQAQSARLVGDMMPGRKMEQSTASLMGAGSSVSPSLGGMAAR
LPNMAGAPKMGAGASDRFLRPQPAETVLPMMQKKLKQLSGVVEVLWKESMSRRVFATVVI
QKYVRGFLTLLHLPASIQGRCARIRNNLRRSFSRYSLLPPSPPPQQQQQQTTRTMAPNAN
VSEAQRSHNNGRDPNEYAVLVKQLRALESQVRHMSGLMGEFRQFLNQRRNAAAITIQKHY
RGYVDRRHWSRLKKLYDEFVASLRPEVVMIQRVCRGYLSRVRLMRCCKKTREIRLLQAEV
TQLRCTVEEMQAFIEQSRRRQR
>TCRU_10852 NADH-dependent fumarate reductase
KQPVVIVVGGGLAGLSAAIEATACGAQVILLEKEPRVGGNSAKATSGINGWGTRAQAEQD
VYDSGKYFERDTHKSGLGGSTDPGLVRTLSVKSGDAISWLSSLGVPLTVLSQLGGHSRKR
THRAPDKADGTPVPIGFTIMQTLEQHIRTKLADRVTIMENTTVTSLLSKSRVRHDGAKQV
RVYGVEVLQDEGVASRILADAVILATGGFSNDKTPNSLLQEFAPQLSGFPTTNGPWATGD
GVKLARELGVKLVDMDKVQLHPTGLIDPKDPANPTKYLGPEALRGSGGVLLNKKGERFVN
ELDLRSVVSNAIIEQGDEYPDSGGSKFAFCVLNDAAVRLFGVNSHGFYWNRRGLFVKADT
VEELAALIGCPVENVRNTLGDYEQLSKENRQCPKTRKVVYPCVVGPQGPFYVAFVTPSIH
YTMGGCLISPSAEMQLEENTTSPFGHRRPIFGLFGAGEVTGGVHGGNRLGGNSLLECVVF
GRIAGDRAATILQNNDTYLWGEKWSQLKLRNVMEEENGFMWLHFTFPSSFQVSGLEVLQG
VVLRSVSGDKSVEVYTPYTLPDDEGVVGIALNPLLTGNGVHWLRTLQPGDTVEMKAAERV
DRGYMNMLNAPHKVVIATSRGIAPMMQILRAAMEGPEKDTTIHLIYIADRASSIPHREKL
KALAEASPERFRCTFVLQHPQPGWSGAVNYVDEVAASVFPDPALVIFLCGASEETRSIKN
SLLDMGHDVATIATV
>TCRU_10853 hypothetical protein, conserved
SPIEVASHFFTGVNDPRVGTMDFSLDGQYFISSHADDALRLIDVLTMRHNETIQLEAFGV
HCARFTQSSDVVCVAPRYSSDGHLYLLSLTSAQLFAAMAFVSDDVPELRAVSNTPVYSTI

SQCPQSDVIASVFSTQGRLLLFHPLISGAIAASGERTVMGNRATVSFSPDGTKLVVGDDC
RVRVFDYRKMFSSPLASLDNKAIFTESGAASRCKGAEVAADGSHLLLTSFGGEAVVYALQ
LGLVSCSYFHNVARRHFIGAGDAVGAKFMFPNITGSIVVQLSTYMNAGRHLLVYDGYDGQ
FSGSCRRGALKYELQCKDSDVPVALSVNSKYALLATAARGVTWWSF
>TCRU_10854 poly(A) export protein, putative
VSTVRFSPSGCPYLLLGAASWDKTCRVWQVIHQPNGMNIRSQPMTFAVSDAPILDMSFSA
DGRVFWGGCSKTATMWNLTTNQKIIVGSHDLPVSCIAHVSSNTGTEILVTGSWDGRLRFW
DLRQPMPIKEEILGEPVFGLDAQRSFPMAACVTGRKVHIFNLQTMMKTNELKPPPLLKFN
LRCVACSPQKDGVVVGSSEGRLSFIPLQAEVGCTFKAHVLVEDNVLYMHQTNFCVISPRV
PHMISGGGDGRIGCWDYKKRCIVGYGESETRLENRNKSISAGDISADGSLLAFARSYDWA
MGKTGCIPNEPHSIHIRSA
>TCRU_10855 ADP-ribosylation factor family, putative
MDPQTQKEDNVMGVVRCVQEKGYGRTSFLTYKKRFWVVDQTQGRIEVYKNDQEPFPLAKY
NASEVRGVIFSGCKQNKFYRLVLQLRHARNVRFRLNSMAERDRWYAAITRLIERYPAYNR
DQNVLRVAQRRTMTAERSLGVSITLAIAGLSDIPDDLLQYLVEAVDMAIETISSVVQKYG
SENDIPRRYTVTVATASGSQPNIGPQYDPTTRSLVMNVTITRDIMGNVRFSVANSSDIMK
ITQSHVWRDPRIEGWITTSKSCVAVCRDIGELLGIKKPFPFTFQWRKNLRDTVRVEQYLR
RHVHEEFLRNVQQQIVQVAEEFGRDEGVTDDSVYIKYIGDYVSGIAITLDEKTVDADKPP
ELFVTTTVEYQQRCRHAVVMISRYFEAYRKPRVVAQSLRDQLVNVVLLADLSKRMSEVRT
SIAQVLGGNGRVKIIWDNLLRSCAKVSVPLLLRSLSHLVLSCSNIYVERLEGIRQLLSGI
TPSNEGYCPLFGTIFKNINSIVVDFVPFVTGKTLTLPDPQFQQGILTDYFLCSTEGDQGA
MMDLVRKWRVVPQANQAYAVVCQLVIFPSMPVATFREWCEEHLRDIPEVDEYVDTDDSCS
CSSIPSDDFGDAVAFERSAETQVLDMHRVVSLIYDSQGVSVSLKIGADAICDAINALEAA
FDGRRIRKHDLVRVLISNLRRLRVMYSHTIGGETTSFLDLHSAVNLLYELCEYEESVSGL
EELLHKYALQRRQELSTLGNGSITEPNDEMPINLSGCVYDFQCVSRVALNHLLPIEAKIA
RRGWRVGFMAGLENVGKTLILNSLMGLVQSTIPTVGLSKQVAAFEEWIFSLNELGGRESF
RENWRYYVKRMEAVDFLLFVVDSMNKRGFKDAAAYLRAITDHFTTVPLVVIFNNYRVGSR
GTPPLKELEASIKLDVVRHRQTARSVFVGTCDITVVSSSHRTLPATLLSALNELSTYFRQ
VSPPERMAVQPKEGGNSE
>TCRU_10856 Polycystin cation channel, putative
KMLLQYVVNCIILALLITFAFIYQTPRNKEINDSRFELAGFLFGAEGMSNAGFEKEFQTI
GEFLSTFKGIIGAYYGLPFSGTGSFMHYVVDKDNSTTVPPLLELTYFQECYESTKCLKTF
HKSFTILKEDPLGPFAHPEVLINGTESCEPREDLDGLYYVPCRTSPMGQLVDHLMDVKLT
FSLYSLVRQTDGSPRSRVWFVAFTFGMTGHSSVMTMKASLDCVDRHIPERLPIMISCTLL
PLVFLGFLLRIRTFPRFSASILEIFAFQKSCLDEVRTLPSCFHCQEGGWRCLGFLSDAFV
LMFGITALASQFYPERVSGLEQAVTIFLGFSILISCTRLVSILILFPRCYVIIDSIVTAG
SQLSMYSVAVFPIMFGYAFCGHVVFGAFGGYFGTLSRSIVTLFCTTFGDNIIDTFLVMDQ
STCILQMLFGRLFIGTYLLLFICNILNVAHSIIQDSYTYSVRMYSASRREDSRIQYDASG
VSTEELADFLEKLR
>TCRU_10857 hypothetical protein, conserved
MDTVVLTVSSLVHQAETFTFPVVRSKSLAVTVAVGIPVAVLLHDTADRWLPKKWEIPIIS
WFRRKWRQDPETKVVHLALARNAVLFFFVAMALSESPYYQTPVDYVSDRVSSSSARRALD
EEIKTSRRVAFGAANDVVGE
>TCRU_10858 predicted zinc finger protein
MALLEYVSVKDMARIYGEMSSERHAEEIWEELRAALKARQEKAARRELELRNRQRQIEAD
READERARREQEALEEAERRAAEARRERXXXXXXXXXXETLRKIREEQAEEEAAAAAAEE
AALLAAEEEKLRRKAEKRRKRQEARERELQEQQEALEAERKKHAAGTSASQKKAWEEYVA
SHPLEFGIGNQNIEQQHVEHKLRAPPSATTDLLNRTYTPKCPNCATKFMSPPKEWDCPLC
LRRTRQHIKVWQPDDSSSECMICHAAIGRFSRHHCRSCGRLVCDTCSMAKAIIPALGFNA
ATKICDDCAQMGQ
>TCRU_10859 3-demethylubiquinone-9 3-methyltransferase, putative
SAGTMRGVSAAEIGKFRELQNHWWNPDGPLRTLHFFNPLRVKYINDTCRNFSKRSSLLAS
SGITPGMRILDVGCGGGILSESLVRLGGNVLGIDMCEESIAVAQQRREQVLQDVASCTLQ
NGAASLEYRYASLNTIAVEEKQQFDLVVASEVIEHVDDAPRFLQDLCDATKPGGLLIIST

MDKSIRAAISHIAVAEYLTALVRPGTHDWSKFVPPKDLSRCALQHQVRQVDLQYIVACPN
ILMSLSTRQMQLAFSLSKRFDTGHYFWSGLKVTAPA
>TCRU_10860 Protein of unknown function (DUF2009), putative
TVAEYELMPEPIQNADYIPLRLNPRERKIQRLMRAVIMASHYTDKVDNEAVLKTNKRDAI
IVKEITNSLSGLITGLDVEKGAKLLREKDFSPFAREIQLAVEASRRYKMMNPDFLRTDYV
KFLYMVQDAVQNENVREMLGFVVAEQIVTVGFYCRALGFESILQDNRMPLCITPVPFIKN
RNKLNKALRHKDVTVNGLLKEYSRASGRTLDEVEIAVRSLNDANHFANDNVDSTNQMLHL
LKEFFSPDAPTDLTNLSIEEGENGSRLSHNHRRQYFFVLQSLSLWKNICRRMFSLWTIAE
GDMLNPNEPYEFRYTGQGYQRVQKAPNLYRAISEVVQQTKDELGEWVGSDRIHLGDDQVP
NAFHFIDKYAQVSRIIIPILRTIAHIDTLAESYEHNAYMKEVWDGSMNAKRAILRDFFRH
GFDGSGGDNMDDAGSCVDGRLTSAWNWCNNIRWKPFYPLFLLAGFSSFDGELGL*
>TCRU_10861 elongation factor 1-alpha, putative
RIFQRMNRHKKFYSTLGDKLHDDYYDDDDDYYDEGEEDDYGEEELQYVVRTGDIPAKPVK
TSSTAGFTAPQEELLNNEELPLGEEQGWCSEDVDYPLITMLLAEFRKKWESCVTAQELKV
EPKLCDIVEAIRDHNYDVDEAVTFTLRRVTVKSLDAGTQKSTNMPSPLQCSANACAPAPT
PTLATAVEPKPGGRTLKLGKGGKNTEILPANKSNMVKETITKSASGARNTRNISELKKNA
VQEIMPDPNKRDCTFVIAGHVDAGKSTTLGHLLLLLGKVSQSEIEKNEKNARQLNSGSFK
YAWVLDQSEEERRRGVTIDAGSCCFETEHRRINILDAPGHKDYVLNMISSATQADAALLV
VTAATSEFEVGLANGTKEHLFILKTLSVGRLIVAVNKMDTVDYSKERYDYVVRELKFLLK
QIRYKEEAVVGFCPVSGMQGTNILHVNREATPWYEGPSLVQLFDQCPLESRLLDAPLRLS
LQDMQGSRLFCKVESGRLLKASKFVFLPSDVQVHVKTILKPTLDEFVSAAFAGDLVVIDT
DSSLVGLSPGCVGCSLIDPIQCSTDFEARVQTFATLQSSILPGTTFTMVVHALTVPVKVV
ALVSKMNRQGTWSTGMVKCIPKVTQAIIVFRSAYKIALEPAEVCRALGRFVLQQDGNTVA
GGLVEKMMF*
>TCRU_10862 ABC transporter, putative
PFLVSVSAACAVVLARVFVRRRSRNAVLLVLEARAYEMIDVFFKAASGSTDDMPEREEEG
ACVEVKLNWKNAKLLRVPALLFDGGHLDIMDLFEVYSGLLRNKSSDKLLICDSWNCLVAI
VRHHLRRHVKEDNALLLDEMQAEGLLAVCILLRRRYDITKSSLLLNSSPLVESFPEGLFQ
VFLSAYRKKKSIRLGLLSFLKLVWGSCSTRQLIGLICVLLLSPDVILMALVGWHTDMHWM
PLCVTEIEKALTPESVSCEHSFFQFMKENFFGATGALVAIAVNSIGPIELIYCLRNFVTG
YILMDLVTAFHVSAYLALATADYNPDDNWSLSQSVLNALWQVSSLVMGELQSQLPFLTQL
FCSAWVVMRFPAVALTIWLGAQWNDLVEFLNESLYLESQYAKRHLLSLDCFPYQEEGESR
NEKKDCEEGRMLLGGQLNFPSPISLIMKAGDFFVGNNNAAGGTRKSFFQLQTVAPAGMRQ
HHGLAVLLLVFLELKLISKPSWNCILQNASWPVAPTALVRHIFYTLEKALVFETKTTNSQ
RIQGVKAVMQIMLCMREGIFEARSGSRYVTEYHQGFMFFRQNGMELGVVKAFVEAPYGSR
NDKREYFIRDFLRGVFRTTSAMPLLLTSIATLCSSKAYLEQDALEQSGVISHLEFIQRAF
PLFPTFADLFYEEHGLSAAQVDLARVQRQLTLGGSSLGCYQVLEELQFVQHKIDRPIMGP
PPLMEGPWSIEFHDVSYRYSEDKPYILWHVSFRVEKGSFLGITGYSGAGKTTILRLLNGT
YAPTMGEIRINGIDIRRYPARMLRRRIANVWQEESQLQLFDHLSIADNVAFGNLWSCSVT
DIYGALSAARALNFVQNRSSNIFAPLRAQEFSGGEVERLCIARALMRKSSEVCVYVFDEA
TSAVDTETERSVFCFLGLTREAKRTRQTTCVIVSHRLATLKSADTVLVLNDGRVEQLGCW
DELCKGEADSCFLRMMRSQQLPLF
>TCRU_10863 hypothetical protein, conserved
MPPKKRGQNTRGRDKIFRNAVQHVHVGVGHSVLGDIILRPVAGLVSRTGVKDDDNNAYEE
CAFLVELNELMLSHSTTDFKRFRWEVLELCESKALFRLNHRRIAEKLLLCLMRRDKFAEG
FEAFVRLTVAFARDMQEKFLAYFECFHQAINGGILNSKGQLMADTRRLQLIFAAQVAWCR
EMRPFWLLKGQRKLVERTIRLYVRQMHDKKEYIRRLSAEVLASVCRMVRDLVPLVVEEAC
LDVVQDFEAYCANSTLVERRAASEANNDNGAKDEEGVVEDDDEDYFDGKSEKELKPRPTV
ISSSLLQAYEQSGLVVLPVVDGLCFLAAEMFRGIRGSLSTNFENHYVLLAHVFGILRRTQ
FAGTYCSGGGMNEQEMFGFTEEETKNFIHASRWTEMFMDARDEKDMKGESQQGEEEVVVV
KELVQMIGGVVIGSALRMIVEETVTSSSAAGNVAGDEERENEEERQGVRASSLQMLRAVT
ALLEFSPPHAHLLGSLLHAADYKLLRDPSATSTLRKTSETLLEKARQQIQTVSKEMTDTK
AMKYDDWCRVMRACGGILEVFTPLCVGPTALTSHAKTLQGIFLPLAQEILMTCLSISACH
HYHYQHKNNNNKNHAACDASVGDWDVLRRSTKRMLFAFMQDVLQKNYTFFLRDERRLIEG

EKDPS
>TCRU_10864 hypothetical protein, conserved
RYHMHIVDGGDPTSTVTAATLFAHLTLRCGHLRNHLLLSASTTDAKRQRDALPSSLNATR
MVQLAAAEPSSGRSTDDKILLAAEALLRGDENFRASLAVDTEWSGPVAEVKDRIIPYPCF
SCGFVQSEVFLARSGARYFDFIATADVASFNYLLNYYQAVRMLEDEEERARKGSAHSVGW
DEQSEEQQRRKKVGIVHILCGEPARAGHLLQRFIELLLELDATPREKSAGEGAAGNEEAF
AWISRADGVIWRMYQLLGVDVLFAVM*
>TCRU_10865 hypothetical protein, conserved
SRGCCHTPKNGRVNSSAESCPTVELPDALDMDEAMTLNVYRPYGEKEAPLQEATKQFLYT
LITTPDEQEWKDMLAAAIRLDKWREHHLRAVLRSVHQTQYDIAVSQGGREGKIKGGCTPA
TRLQRALGVMQTSVDEGYHPTPESVHALLVVLLRAILRGHGNDVTGMDLKELKRQSPLTT
HEVVWQFLAWMERHNYHVMSAAVLEELERLIEGFTREGKNEKRTCEVRQNRLEYLRNERD
LLLEGSQLLSKRG
>TCRU_10866 tatD related deoxyribonuclease, putative
LPMIDVGINLTDNMFHGVYNGRKRHPADLDAVLARAVSVGVRCLLITAGCLKESFEAVEL
CKRYNSKSLQCYCTVGCHPTRCGEFAEDPEGYYGKLRALVAEHTVGKEGGCVAAIGELGL
DYDRLFFCDKSVQMHYFVKQLELAEEFQLPLFLHDRNTGGDFFHVLAQHRHRFKGGVVHS
FTGSKEEMKRLLDLGLFIGLNGCSLKTDDNIAVARSVPLDRLMIETDGPWCEIRNTHASH
KFLLDAAKCNGVSDALLKPYPMCRKEKFLEGAIVKSRCEPCHLVRVLEVLYSLHREEVTS
LEDFAVMIYNNTRKLFPFRP
>TCRU_10867 major facilitator superfamily, putative
MVGAMEKQTPSPGRRKRSVRTDTPEDFPGKEVIRQNYMSLGLEIAKCIDILVTASPLPII
TLYTAAVPLSLWSLALAQALYFFPQLWSTVICDRFARRFNGITTYTATLIATAISSFITA
NALRTHSLFLYLLARFVNGLFRHALSFSALAARELSDASKGYDTQKISIFSLMAAMLFGG
VLGEYATDVAAAIEMLATMEFATAVTLMLLSFTCTRGTRTAPGATSVEEYKNWLLRQPYS
CISFFVPTALCVSCASMSQCMYPFIDRQVFQLHYVFIGLHMAVVIAIEAIIAPVLIKRCG
EMNQWMIHTCAAFLLFGSWLSPWVSDNGLLLYLGATMLFTDLPAAMLGVVFSSVAENGFK
TSDRVFSSNLHRHVKQFCKQWSPILLIFVHSMLIDRQDATRVVLMPFSVGLVTIILTNQI
KGALAAIFVSGWAIGTFSSLGDE
>TCRU_10868 Nodulin-like, putative
TAERRWFLQFFVSILICLNNGACFCFGIFSPYMKQKPFMYSQSDINLVSTVGVILSYFSL
PTGFLYDHKGPKVILFIGTLLGFLGWLGMFLMFVNVGSPLLGTNVLVMCLFYGVLQFSSS
FYETGSVLTNLDAFSCYQGRVIVIQKTFMGLGSSVIVQIYIAFFETHFAGIGPFLLFLLI
YSLTVGVLGTLIVRLPSEKTQCLGLNVPDEEMIQSGGGESRLFRLPFNVGTGILFTSIAF
ILLVTLMENFISFSDADREAIGIVTIVLCVSFSFMILVTPSYSVNRGGYDTQSTAITAKT
TTKAEAAAATTNTDVNAVTGDTATPTFPPSPPPLRFPLSSFPTEVIGKPANATNEIYATP
CKKGGRENGLSLLSRGPRGYSHFREGLSPQDVDLDVPDAPDLTNGKEIELPLERERHVSR
GWNSRSGENFAAESEAARQEVKLNSKSLWYNLRRRELWLMWYVCLASWSSATLVSTNSSQ
IYESMDFYGYSPTVNVVLVSIYGVASAIGRVFIGLAHPILVRKKIPVSSFFCIAPVLNVI
GLPLFLAMKRGSLAIPFFVVGLATGVSWGSTILIIKGLFAPNNCGKHYSALYTAGIISPL
IFNVGLFGPIYDFYSKRQGLWETRQCEGRVCIWIPLVICAIVNAIALPLSVYFVSRIVKR
GGLL
>TCRU_10869 hypothetical protein, conserved
MFKHRENMAHAPFSIDPQGSGTTMKAVSFGQEQRQQHGDRVNVPTAAAKKRPRDIRGIER
FRQVIYGEKGLPRLHAMVARNPILMYPPEGIEAARKRMQKKCEEASAVSREGRPERKSNL
NDSHPPEGDEDVWTMFEERQAAETSAAPDGPPLQQSSGNETNAPSFFAAAPSGASVGGTT
NDQELANYHRRQLDALMGIYYEFNHLTFMKLPMKDTLQLLQRCGRGAVAQVMEFEMQLRM
QRETRLKELDAVAEEERELKRRQMEVHEKRLEIQMQVAEKIQ
>TCRU_10870 essential neutral sphingomyelinase
MPTEITVLSFNLWGIFNSKYRAARMARFAAKVAHYDIILLQEQFSKEDFELIISNLPSEV
REKRYFKRFPSAFYGSGIAVISRFPIKSALFFTFPLQGYPERVLHGDYYANKGASLLRIH
VPCTTRRGVSPDPPYEEVLLYNTHLVAAYQKTARLLNWRDELYLSVRLSQAISLAEFISS
TSHPTDRVIIGGDFNATQRSLELQAMLILLRKRGYKLVSVLPPSIMYRPEMSEREKRINT
VTLTYSDANMFNSPKDGWLVEGGDVPCQIDHIFFTSNTLRLSAFNDCPDAAADYPFKMPI

NGEEGPAGVVVFTGNNEVQIPPEEGIGVKALKWFSRLSCAFWCGQLFAYSERQTNENSAN
TLEPRFCPISDHYGVTARFQLGEEEEEEVDGSTEAGKKLAPKKGYMEVALTKAEVEVLTE
AAVFLDDSVNKLYRESRICMWLAAAMTAVVLGNIIYMEYQAQLREEHTGRVLKELFNFAK
LRGTAMGQEELSLGFDSTSWGQWLRRVFSMNSDNSQATTAIKSKTVASADVALDYAGIAS
KLHSRGLWGLVSPAITICGSIFSAASVTVALLQRVANAKVMTEQVNML
>TCRU_family, putative AB.1
RRLFGRCVGYFVGGTAVATVVVMTPPLELVPAPVLPARVLLEGVGRVCRCVYVAGNILMD
YQLNLHEGDSQDAWNAVHLRSASRLVELAETNGGLYVKAGQIFANLSHILPPQYCTTMAA
LQDAVISRPFSEVLATIERDLQRPIDDIFSEIDPHPIAAASLAQVHRGRLKKEQVEVAVK
VQYLDIAHRFRGDMRTIQLMLGIAGFFFRGYDLSEIVCKLNNTVANEMDFTLEADNCERA
GRDLKAGGFGNRVVTVDVLRDYTTRRVLTTRLVANAAKISDRRAIEALGLKTRTVAAWLY
DAIAYQLFITGFVHGDPHAGNILVHRLSNGQPQVVLLDFGLCTELSDEMRAELACIWTAA
VTHDTPTLKQVAKRFGCEDYALFASCFLQHPYEAFSAETNLTTKATMEMMREQVRNRMHE
VNNIVSGLPKEYALVLRNIMAVKAINRELQRPVNRPLRMLRYSAVVARRTSSRWQLGFML
LRAWWSEIISSL
>TCRU_10872 hypothetical protein, conserved
CSRRYNLLEHKTKGSMFMKHLDLYARRDPQLAPYLLREVDIEYKRKCRKVSFCIWMCVFT
VVTAFQMRMQGEQLHYLRLYADCVRAEQDAKDEDEIRRRKAFVAVVNVVRDAFDRDQKWS
RSDHEKALKVL*
>TCRU_10873 hypothetical protein, conserved
DMGLPPAVIERQTKVLNYSSSTAAALAGQLENCVRLLRGHCATLHYCNEEIEGALLTLGV
DVTHSLLSSISGVIEGLETVAGTCKAMCESHFEEVRQREDLFASLCNMYVTLKERNEFTE
RELRSIVAERDRQNAAFDRAVAYVETLIAERAVWHEKNGYNCVGLPLVEKLFSESCHEAL
DVFDRIAQETRTPDGMSLNCIPSNTDTPGKLVKRWETIEDLRHANGMPSARLQYIPPRDE
VLLLREVLEMGTGSRVLLRDVREERNNLEECKKKLCELGVTTLATLKLARAELNGFREWL
TGLEQRGHP
>TCRU_10874 hypothetical protein, conserved
LLLPLAAVTVGALSFARICRRCIVRVYPSCVTIVYETRRKTILTTSMDKERGANDDMTHF
CHFRPLMCMIRYFLYSSKSLVVLPPTSFFGAFTLPRAVIEECGEGRAVDCTVEAIQVTDG
YVRMVLTIRYCIPFQQLERYLAAVGPMPPNERIAMAAAAAVKARAAELSVGLIINKSRRE
DSFLVSFREHLASKLISEACVKLIDATVESAEICEK
>TCRU_10875 folate-binding protein YgfZ, putative
MGFKCLLSSRSLIRVSGAAAHDFLQGLFTNDLRLLHPGGSIWGCFLYHTGRLMCDAYLYQ
PSRVHGGDVCILVDVHRDVVDTLHDHLLDMRMRRRLQIDNAGKEFVVVAASSYGNGGIYE
AEEEEEKTPPPSSECETFMDPRSFAFPAPLHKSIFPLSKAPSVTDSVARYETFLYTAGIG
EGPDVFKPAKSFPFECNTDFLRGVSFHKGCYLGQELTHRTHVMLVTRKRTVPLRLPSFQE
ETGGGRRSVEKGEALLIDGRKVGELLTVCGDVGLGLLRLRYVDAATRTAPGLKLEDDVPV
VITIPGWWEEKEVKRMLSQ
>TCRU_10876 SET domain containing protein, putative
MAKLVEVREMGEDYGVGTFTLQSFCTGDVLLEEAPVVFAQSFVSQRGPAGVRCCKGCGMI
VATLSEECERLACLARTMMQRESPVEGGTVSRRVSGDGDDGGVGASQEECEETQMPVIIC
SPHALHETLKEFAASNLFCHKVSMNDGDDHRNNGEEALLPGTGSMSGVRFCSDGCKERYL
HELGGRFLPVLPTAGAEATLKSAATAIRTTSTTHNLQKPSANTIMCFAVTLDAATMEQTW
PSKAHVLATLEYLVENFNERLLLILSLLARCLHDTLHGAFISSEQLQGRFAEKVHEFVLR
FAEGAARPLTEQQRAFLRFSWKCVCRWLDLCCQEETGATAGPEPFLWLTLQLYLRCFWLL
DANAHMFVVVSPLYSLLCLHVPTPQAVYQRGGENGELSRTPLGRQMDVLRELFHVVEPDA
AHATGVALYDAATKINHSCVPSVRFVPTHGRVGAVVVALRDIEKGEEIRSSYIDLVAYNS
RVERRGYLLSHYGFECDCSLC
>TCRU_10877 ATPase family associated with various cellular
activities (AAA), putative
SMAMSREVLLVFLLLVCTALRVLVPELSRVAKEKFFFFSRVYLVRRVTAHLCMASVGILS
DRNALLQNAIFYFLYHNFWRTSLPSSVWKNKKSLLLLMDPLRHSWEERYDSPFRVDFFGD
ADDGFREDVNWRSQREFARYLLVRVPVEGSWVPVSEDGVELTYDRQREKIDGNEGVQRTI
LLRAVGDSDADERIKRFLQAALDFYVGMLPSVLNYGRVFLQMHAPPSERESEGRVFFKRY

PLVQHKTFDTLFFPEKRKILKMVDDFLAKRGRFATEGFPGKLGFLLYGPPGTGKTSFVKA
LAAYTGRHIVSVNLAFLRSNQELYDIFLSREFYCVGDTNPTYFGVGDVIFLLDDVDTSSS
MVRSRVRKRTVRMHRAATLESCWNSTAIPFGGDADKRDDTEIVAADDSDEEDGDKSTDEE
NEDSEGGGVASQQQITLVNQILRSVLESQRPGESHASLGDNSADNEKTVDFSFLKLLQST
ESANLSGLLNVLDGAVDTPGRIVVMITNHPERLDPALVRPGRFSLKLRMDYIQLPALLDM
LGLHFGSVRPADGGDTNEKKSEKLSANEASGAKALPLPKLSDAEAERVRQAIAAIQEKKK
QAGGDFLGLTISPAEIESMCTVCNSLDEFIGLLDSRF
>TCRU_10878 XPA-interacting protein, putative
ATRPRPLVVLVVGMAGTGKTTLVHRMQHYTMEQNKRAYFINLDPAVADVPYNANIDIRDT
VNYKEVMKQYRLGPNGAIMTALNLFATKFHQAISILEKKENLEWIVVDTPGQIEVFTWSA
SGQIIAEAFAATWPTVLLFVADTTRCASPQTFMSTMLYSSSIMLKQQIPLLLAFNKTDVV
SSDAVVLWMKDPDALADAVNSNSDDGSYAGSLVQSLSLFTHGFYESLPVASVSAASGRGM
EALEQALEAAKLQYLSDRLPEFKKQEKRRNEERAATSEKMLFAYQRDRVDD*