Supplementary information:

Table 1: Proteobacterial and Archaebacterial genomes used for preparation of Fig. 19, the order here (top to bottom) corresponds to their column appearance in Fig. 19 from left to right. The proteomes were randomly picked (small genomes and endosymbionts excluded) from RefSeq version March 2011.

Proteobacteria

1. *Acidithiobacillus ferrooxidans* ATCC 23270 (uid57649)
2. *Acidovorax citrulli* AAC00 1 (uid58429)
3. *Aeromonas hydrophila* ATCC 7966 (uid58617)
4. *Allochromatium vinosum* DSM 180 (uid46083)
5. *Alteromonas macleodii* Deep ecotype (uid58251)
6. *Aromatoleum aromaticum* EbN1 (uid58231)
7. *Bdellovibrio bacteriovorus* HD100 (uid61595)
8. *Beijerinckia indica* ATCC 9039 (uid59057)
9. *Brucella abortus* bv 1 9 941 (uid58019)
10. *Burkholderia* 383 (uid58073)
11. *Campylobacter concisus* 13826 (uid58667)
12. *Caulobacter crescentus* CB15 (uid57891)
13. *Cupriavidus metallidurans* CH34 (uid57815)
14. *Desulfarculus baarsii* DSM 2075 (uid51371)
15. *Desulfobacterium autotrophicum* HRM2 (uid59061)
16. *Desulfovibrio aespoeensis* Aspo 2 (uid42613)
17. *Enterobacter* 638 (uid58727)
18. *Escherichia coli* 536 (uid58531)
19. *Gallionella capsiferriformans* ES 2 (uid51505)
20. *Geobacter bemidjiensis* Bem (uid58749)
21. *Ketogulonicigenium vulgare* Y25 (uid59581)
22. *Legionella longbeachae* NSW150 (uid46099)
23. *Marinomonas* MWYL1 (uid58715)
24. *Methylobacillus flagellatus* KT (uid58049)
25. *Methylobacterium* 4 46 (uid58843)
26. *Methylococcus capsulatus* Bath (uid57607)
27. *Myxococcus xanthus* DK 1622 (uid58003)
28. *Neisseria gonorrhoeae* FA 1090 (uid57611)
29. *Nitrosomonas europaea* ATCC 19718 (uid57647)
30. *Ochrobactrum anthropi* ATCC 49188 (uid58921)
31. *Parvularcula bermudensis* HTCC2503 (uid51641)
32. *Pasteurella multocida* Pm70 (uid57627)
33. *Proteus mirabilis* HI4320 (uid61599)
34. *Pseudomonas aeruginosa* LESB58 (uid59275)
35. *Ralstonia eutropha* H16 (uid62925)
36. *Rhizobium etli* CFN 42 (uid58377)
37. *Rhodobacter capsulatus* SB 1003 (uid47509)
38. *Rhodoferax ferrireducens* T118 (uid58353)
39. *Rhodospirillum centenum* SW (uid58805)
40. *Ruegeria pomeroyi* DSS 3 (uid57863)
41. *Saccharophagus degradans* 2 40 (uid57921)
42. *Salmonella enterica* arizonae serovar 62 z4 z23 RSK2980 (uid58191)
43. *Sphingomonas wittichii* RW1 (uid58691)
44. *Syntrophobacter fumaroxidans* MPOB (uid58177)
45. *Teredinibacter turnerae* T7901 (uid59267)
46. *Thiobacillus denitrificans* ATCC 25259 (uid58189)
47. *Thiomicrospira crunogena* XCL 2 (uid58183)
48. *Vibrio cholerae* M66 2 (uid59355)
49. *Xanthomonas albilineans* GPE PC73 (uid43163)
50. *Yersinia enterocolitica* 8081 (uid57741)

Archaea

1. *Acidilobus saccharovorans* 345 15 (uid51395)
2. *Aciduliprofundum boonei* T469 (uid43333)
3. *Aeropyrum pernix* K1 (uid57757)
4. *Archaeoglobus fulgidus* DSM 4304 (uid57717)
5. *Caldivirga maquilingensis* IC 167 (uid58711)
6. *Candidatus Korarchaeum* cryptofilum OPF8 (uid58601)
7. *Cenarchaeum symbiosum* A (uid61411)
8. *Desulfurococcus kamchatkensis* 1221n (uid59133)
9. *Ferroglobus placidus* DSM 10642 (uid40863)
10. *Halalkalicoccus jeotgali* B3 (uid50305)
11. *Haloarcula marismortui* ATCC 43049 (uid57719)
12. *Halobacterium* NRC 1 (uid57769)
13. *Haloferax volcanii* DS2 (uid46845)
14. *Halogeometricum borinquense* DSM 11551 (uid54919)
15. *Halomicrobium mukohataei* DSM 12286 (uid59107)
16. *Haloquadratum walsbyi* DSM 16790 (uid58673)
17. *Halorhabdus utahensis* DSM 12940 (uid59189)
18. *Halorubrum lacusprofundi* ATCC 49239 (uid58807)
19. *Haloterrigena turkmenica* DSM 5511 (uid43501)
20. *Hyperthermus butylicus* DSM 5456 (uid57755)
21. *Ignicoccus hospitalis* KIN4 I (uid58365)
22. *Ignisphaera aggregans* DSM 17230 (uid51875)
23. *Metallosphaera sedula* DSM 5348 (uid58717)
24. *Methanobacterium* AL 21 (uid63623)
25. *Methanobrevibacter ruminantium* M1 (uid45857)
26. *Methanocaldococcus fervens* AG86 (uid59347)
27. *Methanocella paludicola* SANAE (uid42887)
28. *Methanococcoides burtonii* DSM 6242 (uid58023)
29. *Methanocorpusculum labreanum* Z (uid58785)
30. *Methanoculleus marisnigri* JR1 (uid58561)
31. *Methanohalobium evestigatum* Z 7303 (uid49857)
32. *Methanohalophilus mahii* DSM 5219 (uid47313)
33. *Methanoplanus petrolearius* DSM 11571 (uid52695)
34. *Methanopyrus kandleri* AV19 (uid57883)
35. *Methanosaeta thermophila* PT (uid58469)
36. *Methanosarcina acetivorans* C2A (uid57879)
37. *Methanosphaerula palustris* E1 9c (uid59193)
38. *Methanospirillum hungatei* JF 1 (uid58181)
39. *Methanothermobacter marburgensis* Marburg (uid51637)
40. *Natrialba magadii* ATCC 43099 (uid46245)
41. *Natronomonas pharaonis* DSM 2160 (uid58435)
42. *Nitrosopumilus maritimus* SCM1 (uid58903)
43. *Pyrobaculum aerophilum* IM2 (uid57727)
44. *Pyrococcus abyssi* GE5 (uid62903)
45. *Staphylothermus hellenicus* DSM 12710 (uid45893)
46. *Sulfolobus acidocaldarius* DSM 639 (uid58379)
47. *Thermococcus barophilus* MP (uid54733)
48. *Thermofilum pendens* Hrk 5 (uid58563)
49. *Thermoproteus neutrophilus* V24Sta (uid58421)
50. *Vulcanisaeta distributa* DSM 14429 (uid52827)

Table 2: Source of eukaryote genome sequence data.

Time of Download	Organism	Data	Database
July 2011	*Ascaris suum*	Genome	RefSeq
July 2011	*Caenorhabditis elegans*	Genome	RefSeq
July 2011	*Piromyces* sp. E2	Proteins, ESTs	GenBank
July 2011	*Fusarium oxysporum*	Genome	*
July 2011	*Encephalitozoon cuniculi*	Genome	RefSeq
July 2011	*Enterocytozoon bieneusi*	Genome	RefSeq
July 2011	*Entamoeba histolytica*	Genome	RefSeq
July 2011	*Giardia intestinalis*	Genome	RefSeq
July 2011	*Trichomonas vaginalis*	Genome	RefSeq
July 2011	*Euglena gracilis*	Proteins, ESTs	GenBank
July 2011	*Trypanosoma brucei*	Genome	RefSeq
July 2011	*Nyctotherus ovalis*	Proteins, ESTs	GenBank
September 2011	*Perkinsus marinus*	Genome	RefSeq
September 2011	*Phytophtora infestans*	Genome	RefSeq
July 2011	*Blastocystis hominis*	Genome	GenBank
July 2011	*Chlamydomonas reinhardtii*	Genome	RefSeq
February 2012	*Cyanophora paradoxa*	Genome	+
July 2011	*Naegleria gruberi*	Genome	RefSeq

**Fusarium* Comparative Sequencing Project, Broad Institute of Harvard and MIT (http://www.broadinstitute.org/).
+*Cyanophora* Genome Project (http://cyanophora.rutgers.edu/cyanophora/).

Eukaryotic sequences searched for Fig. 19. Complete proteomes were downloaded, if available. In other cases the available proteins and ESTs were downloaded.

**Fusarium* Comparative Sequencing Project, Broad Institute of Harvard and MIT (http://www.broadinstitute.org/).

Supplementary Table 3:
Eukaryotic sequences searched for Fig. 19. Complete proteomes were downloaded, if available. In other cases the available proteins and ESTs were downloaded.

Table 3: Fasta format search sequences used to prepare figue 19.

ASCTIA

>gi|71754875|ref|XP_828352.1| succinyl-coA:3-ketoacid-coenzyme A transferase mitochondrial precursor [Trypanosoma brucei TREU927]
MLRRTNFFRIGLDKVMSLSSAVQDIKNGATLAVGGFGTGGMPHAIMQEIKKMGVRDLIIYSDGAGVDGYG
IGVLFENKQINKMIVSYVGNNKIFARQYLEGDVELEFCPQGSLAERMRAGGAGIPAFYTPTAVGTVLQTG
GQITKYDKNGGVLKESTPRETRFFGGRLYCLENAIKTDFSIVKAWKGDRCGNLVFRGTARNFNVPVGQCG
QTVIAEVENLVENGDIDPDEVHLPGVYVDRVVVPERYQTLIEHRTVTRHDGAGNKPTKASTRGEEVRQRI
ARRAALEFANGMYVNLGIGIPTESSNYIPAGVNVVLQSENGLIGMGPFPTEDKVDADWINAGKQTISHLA
GSALFDSATSFAMIRGGHMDLTMLGALEVAANGDLANFMIPGKLVKGPGGAMDLVSCGTRVVVTTTHCSK
NGDPKIVERCRLPVTGKHCVCRIITEYAVFDVVDGRLVLKEIAEDTTVDQVKKLTGVGFDADNVITMPLA
PLT

ASCTIB

>gi|192807489|gb|ACF06126.1| mitochondrial acetate:succinate CoA-transferase [Fasciola hepatica]
MYQLAFLRCRYASPIVREARRAFHASRKCQYYIDGPQEPFSPMPGRFPKWASNGDETFGFLKDGANVFIH
GGAATPSLLIKELYEYVMSKNLKDIKLFHIHTEGPYPFNDAEGHFRSTSLFTGGNCRKAIQEGRADYTPI
FLSEIPLLFRRKHVQLDLALINVTPPDKHGFCSLGPSVDVTRAAIQNATHIVAQVNDQLPLTRGDASIHF
SNLTVMRAGSQPCHEMSPRPASEVEDKIGQIIAENLVEDGATLQTGIGAIPDAVLSKLTNHKNLGVHTEM
FSDGVVQLVQLGAITNAYKKLRPGKVVSSFVVGTRKVFDFLDNNPMVDMCDVAWVNSPVVIAQNPKPVAI
NSCIEIDITGQVSSDSIGTTIYSGFGGQVDFLRGAAVSLDGQGKPIIAVPSVTKRNETKIVPHLKLGGGV
VTTRAHVHYVVTEYGIAYLFGKNLRQRAHALIQIAHPDHRESLEKAAFDRLKVMPSPL

ASCTIC

>gi|123975034|ref|XP_001330176.1| hypothetical protein [Trichomonas vaginalis G3]
MLSSSSRAIASLKSRCAYEPYLAKVCKAEDTIPIFKNGMSIGWSGFTPVGDPKVVPIALAEYVEKNNLQG
KLRFNMFIGASSGAKNEDRWAKNGMIARRYPYQNGANLKKNINSGKTMFADKHLSMFPQDLTWGFYTKQR
GGGIDLAIVEATEILADGSIVLGGAVGSAVEFLNAADKIIIELNTAIPSFKGCHDIVAPWKPPGKPYNIT
SVDSRIGSLSVKIDPSKVVAVVESHAIFPGRPVKGADATAKAIAGHIVDFFQNEVKQGRLPENLYPLQSG
VGNIANAVVDGLNDSPFGHLTVYTEVLQEAMLPMFDSGKLKFGSSTSLTLSQWDKLYDNFDFYRNKFVLR
PQAISNSPEVIRRLGVIAMNTPIEVDIFGHANSTLINGTKLVNGLGGSGDFLRNGYLSIMHCPSARKTKK
DKTGISCVVPMCTHVDHTEHDLDVIVTEQGLADLRGLAPVERARLMIEKTVHPDYKDQMREYLNLAIQAT
QPKGAGHEPQILSKVFKMQENLKKKGTMHLDSW

acetyl-CoAsynthetase(ADP-forming)

>gi|9502268|gb|AAF88064.1|AF286346_1 acetyl-CoA synthetase [Entamoeba histolytica]
MQFEPLFNPKSVPVIGASDRKESVGYAVMNNMIKGGYKGNLYPVGRKPELFGKKCYAKIGKIEEKVDLAV
IAIPAKFVPGVCIECGEAGVKGLIIITAGFAEAGEEGKKMCIEIQATCQKYNMRMIGPNCLGIINPRDGV
NASFASVMPEAGGVAFISQSGALCTAILDWAANQHVGFSYFVSIGSSIDTDYADLFEFFAKDPKVTSILM
YIESIKDAKKFVLRAREFAADKPIILLKAGKSSEGAAAAMSHTGSLAGNDAVYDAVFDRCGCIRVDSICD
LWDCAHVLATQNIPQNNRLCIITNAGGPGVISTDRLVSVHGHLAKLSESTMNELNAFLSPFWSHSNPVDV
LGDATAGVYQKTLDIVIKDPQIDGVVVVLTPQAMTDPVAVAKSLVEHGPYQNQSLPHGWVNQKSEAGVKI
LEEGKIPNFETPERAVTAFGYIMRHPDIAAKLKEIPKYLDVQVDYEGAKKLIADVVADGRTTFTEYEGKM
MFSKYGIPIKGMAKASTEDEAVAEAMKIGTPVVMKILSPDIMHKTDVGGVKVKLTTEEEIRKAYRDIMTS
VKEKKPEARIHGVLLEKMVGFKYECIIGCKKDPLFGPVIVFGMGGVTVELYKDTNIALPPIGLQEADRLI
DGTKISKLLRGYRGMPACDVEGLKKILVQFSKMIMDFPEISEVDINPLAVSYEEFLVLDAKIVLDKNMIG
KEVPKYSHLVIQP

acetyl-CoAsynthetase(AMP-forming)

>gi|169853833|ref|XP_001833594.1| acetyl-CoA synthetase [Coprinopsis cinerea okayama7#130]
MSQTVADYLVTDDLTILLGLIAATVFLVNNLYKPQPLVHPILLGRQSDVGRARNPGESAVYRNYGTGLMG
RFPIRPGKDVHILLDLVRAETEGPRTLWGTKLTNRTLQDRAAALGTGLIRLAGLKPNQSTVLLLLNDGFE
FLLTDLALASHGIVSYTLSSAKLLSSVLDSHRPSAIVTHAAMLPGILELIYDSDERQNEYTIVVVDELPR
EVRAGVASNIKLLPFEDVEREGVRVEKILSPVPKPSDVFTISLYEGKNGMIQGAQLTHENFTAGVAAIHA
LLPASHTFSTLDTIASAHSLSTAFGRAVAYTALYEGTGFATLPSSIIYEGEDDHPSGSADYRDLTRVMGY

PIPFPTVLFLKPEHLRSTTDEILQHARKASLLYRFGWRHKLAGITDGFLTRDSLWDRMLFDSARNRVLGK
ISATTRAVIVSGGPVDADLMTPARIAFSVPVINTLSHPLVAAPVLASHAFDLQDFSLTGTSSQKPLPAHT
GPPGVNVEVKLVGVDDEKVESGGDPVGVMYVRGPPVAKLVNVEGYVEVPSGDDDGWTGLGVRAKVQTNGS
FVEMID

succinyl-CoA ligase alpha chain

>gi|159469923|ref|XP_001693109.1| succinyl-CoA ligase [Chlamydomonas reinhardtii]
MWRLFLTAAGSAKSESSALAGFVRGFASQAAHNPAVFVDKNTKVICQGLTGKNGTFHTEQAIAYGTQMVG
GVTPKKGGTSHLGLPVFNTVAEAKAATGCHATVIYVPPPFAAKAILEAVEAELELVVCITEGIPQHDMVR
VKKAMQGQTKTRLIGPNCPGIIKPGECKIGIMPGYIHTPGKIGIVSRSGTLTYEAVFQTTNQGLGQSTVV
GIGGDPFNGTNFVDCLERFVKDPQTEGIIMIGEIGGTAEEEAAEFIRKSGTKKPVVSFIAGLTAPPGRRM
GHAGAIISGGKGTATDKIKALEEAGVTVTRSPAQMGVTMMRVMKERGLA

succinyl-CoA ligase beta chain

>gi|159466790|ref|XP_001691581.1| succinate-coa ligase beta chain [Chlamydomonas reinhardtii]
MLPALTGKLLKQATGSLAALSQCQQLRFFNVHEYQGAQIMSKFGVNVPPGIPATTLDEVKKAVDQMADEK
GEVVIKSQILAGGRGLGKFTNGLQGGVHIVPKAKALELAKQMLGATLVTKQTGPAGKPVNTLLISKKMKL
KREMYFAILLDRKTAGPMMIGCSEGGTSIEDLAEKFPEKIIKIPIDIRVGITDAQAMQMVEGLRVTGDKA
AAAKQIKALYTLFDKSDCTMVEVNPLAEGLDGSLIAADAKLGFDDNAAYRQKPIFDMKDESQIDPREVAA
SKYDLNYIGLDGSIGCMVNGAGLAMATMDIIKMHGGAPANFLDVGGSANEQQVVEAFKILTGDKQVKAIL
VNIFGGIMKCDVIASGIVNAAKQVGVQVPLVVRLEGTNVARGKEILATSGMTIITADDLDDAAKKAVASI
A

isocitrate dehydrogenase(TCA cycle)

>gi|6323203|ref|NP_013275.1| Idp2p [Saccharomyces cerevisiae S288c]
MTKIKVANPIVEMDGDEQTRIIWHLIRDKLVLPYLDVDLKYYDLSVEYRDQTNDQVTVDSATATLKYGVA
VKCATITPDEARVEEFHLKKMWKSPNGTIRNILGGTVFREPIIIPRIPRLVPQWEKPIIIGRHAFGDQYK
ATDVIVPEEGELRLVYKSKSGTHDVDLKVFDYPEHGGVAMMMYNTTDSIEGFAKASFELAIERKLPLYST
TKNTILKKYDGKFKDVFEAMYARSYKEKFESLGIWYEHRLIDDMVAQMLKSKGGYIIAMKNYDGDVESDI
VAQGFGSLGLMTSVLITPDGKTFESEAAHGTVTRHFRQHQQGKETSTNSIASIFAWTRGIIQRGKLDNTP
DVVKFGQILESATVNTVQEDGIMTKDLALILGKSERSAYVTTEEFIDAVESRLKKEFEAAAL

alcoholdehydrogenase (NADH-dependent)

>gi|2492738|sp|Q24857.1|ADH3_ENTHI RecName: Full=Alcohol dehydrogenase 3; Short=ADH
MTMLNFTYYNPVRLIYGKGSLDEIEKQHLIPEDARIMMTYGGGSIKKNGVYEEVLKHIKPIVEFGGIEPN
PSHETCIKAIKIAKENKINFLVAVGGGSIIDATKYIALGMEHTYSDDPYDICLKGGKFKVNPAQAKIGVV
LTIPATGSETNCWGVISRHADKLKLPFNNESVFPTWSIVDPCFTMSLPDNQIRNGLVDSFVHCIEQYIGN
YHLNPVVEAETEGVMRTIIGVSHKTLENHQDYQARITFCYAATVALNMSLLCGVTLCGGAHAVGVTLCGG
AHAVGHELTSYYGLAHGETLAITTPGVMRFNKEKNAKKLIQMGEQVFGIKNSTPEAAIEATEKWFKSIGM
KTRLSEWGKGKEEFETIARKFEGNPAGAHKDIDYKGCLQILNDIY

alcoholdehydrogenase (NADPH-dependent)

>gi|27733393|gb|AAO21494.1|AF241248_1 alcohol dehydrogenase [Trichomonas vaginalis]
MGRFTLPRVLYHGKGALENLKTLKGKRAFVVTGSHAMRKFGFLDKVVNYLKEAKFEVHVFDGVEQDPSVE
TVFKGAKAMEEFKPDWIVALGGGSPIDAAKAMWAVYEYPEMTFEKLIVPFSFPELRQKAHFCAITSTSGT
ATEVTAFSVITDYQKGIKYPLADFNITPDVAIVDPDLAETMPKKLVAFTGMDALTHAFEAYVSTLHCDYT
DGLALHSIKLIFETLEASFNGCMKARATMHNAQCLAGMAFSNALLGIVHSMAHKTGAAYTSGHIVHGCAN
AMYLPKVIKYNSKNEEALHRYGDIARFLGMQGKDDVELVDAICQRIRDLCVKIEVPLCIKDYENGMINEQ
EYLAKLKDVATNAIGDACTGSNPRQPTQEEMEKLLLAVFFDKPIDF

alcoholdehydrogenase E

>gi|2052472|gb|AAC47539.1| alcohol dehydrogenase E [Giardia intestinalis]
MSLSDFDYGQELVETPEELNALFEKVEEAAHAFRQLDQAQVDKIFYAAAFAASNQRIPLAKMAYEETNMG
VVEDKVIKNMFGSEYVYNKYKNMKTAGIIEEDKAGNTITVADPLGILAGIVPTTNPTSTAIFKCLIALKT
RNCIIFSPHHRAVKSTIHGPRIVRDAAVKAGAPPNCIAWITKPSVPLAKALMGHPKTSCVLATGGPGMVT
SAYSSGNPSIGVGPGNVPALIDETCDYKTAVNQVINSKSFDNGVVCASEQAIVCVTKEIYDKCIEELKFR
GAYVMTEGREAACQQADPALNEATGKHQLNCDIVGRPARDIAANGSVVVPADCKCRCIVGTFTEVRHDEA
MSCEKLSPVLGICWAETFEKAVDICGQMIDMAGAGHTAAIHTAPHRRDRIEYFTHHIRAGRIVVNSPSTF
GGIGDLYNFAIDPTMTIGCGSYGKNSVSENVGPKHLLNYKKVAIVRRNPLWFKVPQVMHVGEGALAKAAA
DLISRGLSRAYIITGKVMHDLGFTDKIISPLTAGNVTVKVFTDVLPDPDLGTCYRSLAEVRDFQPDMIIA
LGGGSAMDLAKMVRLLYEHPKVDFAGLAQRFMDIRKRIYEYPECLDLRTAKTFSVAIPTTSGTGSEVTPF

SVITDEKEHVKYPLADYQLMTHMAVIDPELVLTVPASLASWTGVDALTHAIESYVSVMATEYTMPLSLQA
IKTVFENLEKSVVSRCPTARGNVHQAATIAGIAFANAFLGICHSCAHKLGQKYHIPHGLANAIMLPHVIR
YNAVDDPVKIATFPQYLYPVALERYAEIADYCGFTNKNDGKSVKEKTEILIKKIYDLYEKVGIDAKISAC
KEAPVEADFFAEENLDYLAYHAFDDQCTGANPRYPLIEDFKELFRAAW

lactate dehydrogenase

>gi|987693|dbj|BAA04088.1| lactate dehydrogenase [Oryza sativa Japonica Group]
MKKASSLSELGFDAEGASSGFFRPVADGGSTPTSHRRRLTKISVIGAGNVGMAIAQTILTREHGGRDRAG
GRGAGQAARGDAGPAARGGVPPPRPPRLRHRPGRHARLRPGHRHGRRAPDPRGEPPEPAAAERGAVPEDR
AGAGGALAGGAAADRLQPRRRADVRGVEDVGVPGEPRHRLRHQPRLLLVPLPPRRAPPGQRPGCPVQAYM
VGEHGDSSVAIWSSMSVAGMPVLKSLRESHQSFDEEALEGIRRAVVDSAYEVISLKGYTSWAIGYSVASL
AASLLRDQHRIHPVSVLASGFHGIPQDHEVFLSLPARLGRAGVLGVAEMELTEEEARRLRRSAKTLWENC
QLLDL

malate dehydrogenase

>gi|71746906|ref|XP_822508.1| malate dehydrogenase [Trypanosoma brucei TREU927]
MVIFFGRAQTRRVTGKVVVFGATTNVGKHLSLLLTLSPQVKELCCFDPLNDVTLRMTETRVRGIVKDLSH
IDTGVVLRAVDDPQQWEPAMRNAQLVLICTGSIPNPSRLQRDLALAECAPEYLVAMELVARAAPHAIVGI
ASGPVNSLVPLAREVLLRHSAFDPRKLFGITSRDVMRTRVLFAKELHMNPYDVNVHVVGGKGDATVCPLI
TQTGFQLPHQRMVQLCEEVQRPENFTAGDHNSTGCRVDSQNVQGQEKFTCPTLSTANAAYEWVTSIMKAQ
RGDRGITECSFVESSIKRETPFFSSRVELGEEGAAQLLPLGALTPYEEELVAAAVPLIVEDVEAGLRLSK
TGVDAVS

malicenzyme

>gi|154415099|ref|XP_001580575.1| malic enzyme [Trichomonas vaginalis G3]
MSVKKDYASLSVAAHKEWRGKIETVVRCKVEDREDLSLAYTPGVAQPCIEIQKNPDLSYEFTRRWNTVAV
VTDGTAVLGLGDIGPEAGTPVMEGKALLFKRFGDVDAIPLCVRSKSVDDIVKVVSLLAGSFGGVNLEDIS
APRCFEIEKKLQEICDIPIFHDDQHGTAIVTLAALLNALKIVGKKIEEIKVVTSGAGAAGIAIIKLLIAV
GVNPKNVILTDRQGAIYKGRSGLNDIKVEMAEITNSELKQGTLAEVIKGADVFIGVSAPKTLTEDMVKSM
ADKAIVFPMANPTPEIMPDLAKAAGAAVVGTGRSDFPNQINNVLAFPALFRGALDVRASRITNEMNIAAA
RAIASLVSDEELNPDYILPNPFDKRIKETVSKAVAQAAIKCGVARINQ

methylmalonyl-CoA mutase

>gi|218775149|dbj|BAH03574.1| methylmalonyl-CoA mutase [Euglena gracilis]
MLRKFRPLCIDLPPKWVEMANKELKGKGTVDKLLWNTPEGITVKPIYTAEDIKEHRSLPGVFPYTRGPHA
SMYTIRPWTIRQYAGFSTVEESNAFYKKAIAAGQQGLSVAFDLPTHRGYDSDHPRVEGDVGMAGVAVDSV
EDMKLLFDGIPLEKMSVSMTMNGAALPILAMYIVAGEEQGADKAKMSGTIQNDILKEFMVRNTYIYPAEI
SITIIAHIMGYLAKNMPKYNSISISGYHLQEAGAHAALELGFTIADGLEYINAALKAGLTVDEIAPRLSF
FFGIGMNFYMEVAKLRAARQLWATKVKELFQPKSAKSLLLRTHCQTSGWSLTEQDPYNNIIRTTVEAMAA
VMGGTQSLHTNSFDEAIALPTPFSSRIARNTQLIIQEETGITKVVDPWAGSYAMEKLTDDLIVEATKVID
EVQLLGGMTKAINSGMPKLRIEESAARKQARIDSGADVIVGVNKYTIPQDGESVEVLSIDNTIVRKKQVE
RLSKIRATRDSAAVEKALDAITECARNGEGNLLDLAVIAARARATVGEISLAIEKVHGRYVAGTNVVSGV
YLSEYENNIKDKGGIESIRKKVEAFEAKHGRRPRILVCKMGQDGHDRGAKVVSTGFADMGFDVDVGPLFQ
TPAEVARHAVEADVHIVGVSTQAAGHKTRVPQLINELKSQNASDILVIVGGVIPQKDYDALYEAGVSLVF
GPGTRLPEAAEKVLNKL

methylmalonyl-CoA epimerase

>gi|300121330|emb|CBK21710.2| Methylmalonyl-CoA epimerase [Blastocystis hominis]
MLANFARRAFATAKPYRILGIQQIAIGGTSKTALQNLWIDIFGLEKIHSFESTKENVKEDILRCGKGPMA
VEVDIMEPYDPAKSPKVNVPPLNHIGLWVDDLPACVKYLQEKGVRFTPGGIRKGAAGYDVTFIHPKGKEP
NPLSGEGVLIELVQAPQNVIDYYEKL

propionyl-CoA carboxylase

>gi|300122043|emb|CBK22617.2| Propionyl-CoA carboxylase subunit ? [Blastocystis hominis]
MFGRSFSGIRGVSKLARSFATEGELPFKKILVANRGEIACRVFKTAKRMGIKTVAVYSDADRNAKHVKMA
DEAVYIGPSPSAQSYLVADKIVEACRKTGADAVHPGYGFLSENWRFAETLEKEGIIWCGPGKYAIEAMGD
KIGSKILAVKAKVNTIPGFNGEINSDEEVLRIANDIGYPVMIKASAGGGGKGMRIAWNDKEALSGFHLSK
QEAKSAFGDDRMFIEKYIEEPRHIEIQVLGDKFGNYCAFPERECSIQRRNQKVIEESPSVLLDEETRTAM
GKQACMMAKAVNYCSAGTVEFLCDKHKNFYFLEMNTRLQVEHPITEMVTREDIVEQMFWIAAGRKLPDRL
INWPLKRYAHAIEARVYAEDPRRNFLPSLGLLTKYIEPRGEFVRCDSGILDGSQISMYYDPMICKLVTWG
DDRATAIKRMDEALNTYIIRGLNHNSAFLQDVIRSKRFGSGKITTNFIKEEYPDGWTGSHLTETEAEQLI

AATIAVHQERLAKEATNDQQMESYEPVCEKDLVATVGEKEYKVHMEFEGEAMTLEIDGKKVQYFEPTTEG
YSMQYCGGNFDVVLRSARAQELSKFMIPKVQPDTSKFLASPMAGSLVKVHVKEGDRVEAGQPLAVVEAMK
MQNELYAQKACVVKKVYFKPGQNLALDDVIMDFDVSA

trans-2-enoyl-CoAreductase

>gi|62287512|sp|Q5EU90.1|TER_EUGGR RecName: Full=Trans-2-enoyl-CoA reductase, mitochondrial; Flags: Precursor
MSCPASPSAAVVSAGALCLCVATVLLATGSNPTALSTASTRSPTSLVRGVDRGLMRPTTAAALTTMREVP
QMAEGFSGEATSAWAAAGPQWAAPLVAAASSALALWWWAARRSVRRPLAALAELPTAVTHLAPPMAMFTT
TAKVIQPKIRGFICTTTHPIGCEKRVQEEIAYARAHPPTSPGPKRVLVIGCSTGYGLSTRITAAFGYQAA
TLGVFLAGPPTKGRPAAAGWYNTVAFEKAALEAGLYARSLNGDAFDSTTKARTVEAIKRDLGTVDLVVYS
IAAPKRTDPATGVLHKACLKPIGATYTNRTVNTDKAEVTDVSIEPASPEEIADTVKVMGGEDWELWIQAL
SEAGVLAEGAKTVAYSYIGPEMTWPVYWSGTIGEAKKDVEKAAKRITQQYGCPAYPVVAKALVTQASSAI
PVVPLYICLLYRVMKEKGTHEGCIEQMVRLLTTKLYPENGAPIVDEAGRVRVDDWEMAEDVQQAVKDLWS
QVSTANLKDISDFAGYQTEFLRLFGFGIDGVDYDQPVDVEADLPSAAQQ

phosphate acetyltransferase

>gi|159472743|ref|XP_001694504.1| phosphate acetyltransferase [Chlamydomonas reinhardtii]
MSLNSSTMSRRQAVAGAPAVAPFRHAGLFPRVRLCANRRVARVAPKAAGNGNIAQGEQGFDTLFLSDISL
VGQRTPLLLGFFNYFERHLPHVGFFEPIAAEALASSELRIDRHVELVYKVFNLKGDVRAMTGVQDAEAAR
MIANGQHSELLDKIYSQYASYKEGQDLVLVEGPGPLMGGTELDAQIAAALNAPVLMTMTGQPNATVADYY
NRAMVKRQVFLDHHVEVLGLVMNGLPRQSHAILSGQLRDKFAAAGLPFAGAIPTDIMLRNVRLDEVQTAM
GAQRLYGDSLLTDVEFDDVVVASQRLEELLEILAERPMGRPLVVTSADRLDIVLGLLAAQLSVSGPGVAG
ILLTQAGSARSGRNYARDTIDRIFAGLSSSGLYKGSLLPVLVTDMPLRDAIRKLDNLDAAILPSSTRKIS
QCKRLFEQYVDANAVVARLQNMVRPNRMTPKMFMHTLKSMCNATPQHIVLPESEDKRVLAAAADVVQRGL
AKITLLGDPTTILAEAAKLGLDLSGCNIHNPNTSDRFDKYVDMLVEARKKKGMTREVAADTLHGDVNFFA
TMMIVAGDADGMVSGAVHTTASTVRPALQVLKSPDTPLVSSVFIMCLPDRVVVYGDCAVNVNPSAADLAQ
IAITSNDTAAAFGIEPRVAMLSYSTLGSGSGPDVQKVSEAVAIVKQRRPDIKVEGPIQYDAAIDPKVAAV
KVQGLSEVAGKATVFIFPDLNTGNNTYKAVQQSTGAIAMGPVMQGLLRPVNDLSRGCTVPDIINTICVTS
IQASRMSSAARAAAAKAAVAAV

alanine aminotransferase

>gi|76664072|emb|CAI59804.2| putative alanine aminotransferase precursor [Nyctotherus ovalis]
KKASDAGTNVKGDSDNSTRGIPTGQVMTKQNMEDIVKFCHKNSLVILADEVYQKNIYREKPFISFKKVVY
GMPAPYNEVELISFHSTSKGVVGECGLRGGYMELDNIDSFVSEQILKLRSISLCSNTVGQVMTELMVNPP
KAGVNSPEVVAKHQKEYDIVFGGLKKRSVLLADKLNSIPGLKTNNIEGALYAYPSIFLPERAIKAAKEKG
LAPDAMYCVEALEECGLVLVPGSGCGQKEGTYHFRITNLILDTEEFDQALEAFKRFNAKFFAKYSQ

aspartate aminotransferase

>gi|71755339|ref|XP_828584.1| aspartate aminotransferase mitochondrial [Trypanosoma brucei TREU927]
MGKPDPILGLGQDFRMDPAKRKVNLSIGVYRDDADQPFVLECVKQATLGTNMDYAPVTGIASFVEEAQKL
CFGPTCAALRDGRIASCQTLGGTGALRIGGDLLNRFVANCNRIYGPDVGYPNHESIFAKAGMELTPYSYY
DPATKGFNLAGMLECLDKAPEGSVILVHACAHNPTGVDPTHDDWRQVCDVIKRRNHIPFVDMAYQGFATG
QLDYDAFVPRHLVDMVPNLIVAQSFSKNFGLYGHRCGALHISTASAEEAKRLVSQLALLIRPMYSNPPLY
GAWVVSSILKDPQLTALWKKELKQMSSRIAEVRKRLVSELKACGSVHDWSHIERQVGMMAYTGLTREQVE
LLRSEYHIYMTLNGRAAVSGLNSTNVEYVSQAIHNVTK

glutamate dehydrogenase

>gi|4106519|gb|AAD02872.1| glutamate dehydrogenase [Trypanosoma brucei]
MMRRASYCAGHAFTSLTVVGSRRFFQGERCEAEIVKLTKERGMFSDASVEASVHQLMSRLSDSPYVRHYT
DAEVSAHAHGFLCAKARSALGEPFEHFHESDDSAFYICRKDQASQLRAVRQLTKFVSRERETKQSVSVRC
YTAGDSDIAVFTAKIRPFVNPNPEKGETDIGQLASSAFLEERSPEMQERYQDLINRFHESVVPVHTVREV
DGEVCFSMIMAADRSYYIATLQTVIQEIPGAVVTRCFSETFSNDTHVYTYFVRGATSQQLSDRASLVPFL
PTRPRSLITRLHEDMVFDTEQTVYTDAAVIRLLLTPQPTSEDYRHLRSLVSKEPNGLSRLNNLRTTLSLE
MMSERYILTLISTYPEFMKEIYEDFQVGTTHERRCAIREKITTRFREDQRSEHDLGIFNAFLQFNEVVLK
HNFFKQHKVALCFRLDPSFLRSLGYPRVPHGVFLLAGAQWRGFHVRFTDIARGAVRMIFSKDTMYRRNKR
SVFQENYNLALTQLLKNKDIPEGGSKGTILVSSRYLNTFNQPLCERIFLQYADALLDVVIPGEEGIVDRL
KTPEIIFLGPDEHTAGTFPSVGSLFSKKRGYSAWKSFTTGKDASLGGIPTTILIAMTTRSVRTMVRGVYE
KLGLDEASQTKFLTGGPDGDLGSNEILLSKEKTLAVLDISASLFDPEGLNKEELKRLATARKQLRDFDKS
KLSSKGFLVLTGDKNVTLPDGTHVSDGVSFRDEFHLTKYSAADVFVPCGGRPRSVTLANVGRFLNLSAAD
NDSLLAGGSIQLKTPKYKIIVEGANLFISQDARLAIERCGIVLIKDASANKGGVTSSSLEVYAGVALSDE
EHAQHMCVKDPNNVPEFYKKYVLDIIERIESNARREFEAIWREQQVQEGMPKTLIADSLSEKNVRVRASI

LSSDMCENKELVRYVLSNYTPKTLLEVVPLETLMERVPLEYQKAICAMWLASEYVYTTGISGNEFDFFTF
MTKHMEQAKHIS

pyruvate carboxylase

>gi|300122746|emb|CBK23311.2| Pyruvate Carboxylase (subunit ?) [Blastocystis hominis]
MFKLGTSSSILSKCGWRLLSKRSFEKVMAANRGEIAVRVMRAARELSLKTVAIYSYEDRYNMHRSKADEC
YMLSKEKSAIGAYLDIPTIVDIAKKNGVSAIHPGYGFLSENAEFAKAVEDAGIVFIGPTVENLRMMADKT
SARKVAIDHGIPVVPGTPDPVATYEQALSFCNEVGYPVIIKAAFGGGGKGMRVVRSEQELKQNFELASRE
ALSAFGNGTIFLERYLEEPRHIEVQVIGDGTGRVVHLYERDCSVQRRHQKVIENAPAVNLDPAIRDGILQ
SACRLCSLIKYRSAGTVEFLVDKQGRYYFMEVNPRIQVEHTVSEEITGINIVQKQIQLAQGYSFEELGLQ
QDKITTRGYSIQARITTENPSKNFQPDTGVLSTFEMAAGQGFRLDGIGYQGYEVTPHYDSLLVKMTTRGL
TWEEAMDRAYSGLNEFKVDGVKTNIPFLLNVLRNPIYRSGKATTFFIEQNPELLKARDEHENPEKVVNYL
ANLIVNGHPSELGATGPAPAPTDPTVPPTPPGAIPAGLRDVFLKEGPKGFAKAVRAHKGLLLTDTTWRDG
HQSLLATRMRTRDILAIAPATARMLPNLFSLECWGGATFDVAMRFLHECPWDRLAKMRELVPNIPFQMLL
RGANAVGYSAYADNVNYKFCEMAVKMGMDVFRVFDSLNYIENMRLGIDCVGAAGGIIEATACYTGDCASP
NETKYTVDYYLDYVRKLVDLGIHVLNIKDMAGLLTPQAAKLLVGSIRREFPDLPIHIHTHDTAGTGVYSM
IECAKAGADAVDVAIDSMSGMTSQPSMGAVVAALKNTELDTGISLETVQTLNDYWNDVRGVYAPFESGQK
SGSSDVYLHEMPGGQYTNLMYQSQQLGLSGQWPLVKRAYEEANELCGDIIKVTPSSKVVGDLANFMVQNK
LTKKDVLERAEQLNFPTSVIEYFQGYLGIPEPWGFPEPFRSRVLKGRKLPNGKDRLEGRPGASLPPYDLE
GTKKMLAEKYGESRAQDHDVLSYALYPRVFQDWKDFEDRNGDISTLPTRYFLQPMKSDEEITVDVSPSKR
MYIRYKGMSEVNKQGQREVNFQIDGRPHTVVVNDIKASASVKRREQAQEGNKAQVGSPMTGAVVEVKVEA
GKKVKAGEPICILSAAKMETVVAAPFSGILKRVIVEKGEKLKAGDLLVEIESEKK

pyruvate decarboxylase

>gi|6323163|ref|NP_013235.1| Pdc5p [Saccharomyces cerevisiae S288c]
MSEITLGKYLFERLSQVNCNTVFGLPGDFNLSLLDKLYEVKGMRWAGNANELNAAYAADGYARIKGMSCI
ITTFGVGELSALNGIAGSYAEHVGVLHVVGVPSISSQAKQLLLHHTLGNGDFTVFHRMSANISETTAMIT
DIANAPAEIDRCIRTTYTTQRPVYLGLPANLVDLNVPAKLLETPIDLSLKPNDAEAEAEVVRTVVELIKD
AKNPVILADACASRHDVKAETKKLMDLTQFPVYVTPMGKGAIDEQHPRYGGVYVGTLSRPEVKKAVESAD
LILSIGALLSDFNTGSFSYSYKTKNIVEFHSDHIKIRNATFPGVQMKFALQKLLDAIPEVVKDYKPVAVP
ARVPITKSTPANTPMKQEWMWNHLGNFLREGDIVIAETGTSAFGINQTTFPTDVYAIVQVLWGSIGFTVG
ALLGATMAAEELDPKKRVILFIGDGSLQLTVQEISTMIRWGLKPYIFVLNNNGYTIEKLIHGPHAEYNEI
QGWDHLALLPTFGARNYETHRVATTGEWEKLTQDKDFQDNSKIRMIEVMLPVFDAPQNLVKQAQLTAATN
AKQ

pyruvate dehydrogenase E1 alpha subunit

>gi|151944896|gb|EDN63155.1| pyruvate dehydrogenase alpha subunit (E1 alpha) [Saccharomyces cerevisiae YJM789]
MLAASFKRQPSQLVRGLGAVLRTPTRIGHVRTMATLKTTDKKAPEDIEGSDTVQIELPESSFESYMLEPP
DLSYETSKATLLQMYKDMVIIRRMEMACDALYKAKKIRGFCHLSVGQEAIAVGIENAITKLDSIITSYRC
HGFTFMRGASVKAVLAELMGRRAGVSYGKGGSMHLYAPGFYGGNGIVGAQVPLGAGLAFAHQYKNEDACS
FTLYGDGASNQGQVFESFNMAKLWNLPVVFCCENNKYGMGTAASRSSAMTEYFKRGQYIPGLKVNGMDIL
AVYQASKFAKDWCLSGKGPLVLEYETYRYGGHSMSDPGTTYRTRDEIQHMRSKNDPIAGLKMHLIDLGIA
TEAEVKAYDKSARKYVDEQVELADAAPPPEAKLSILFEDVYVKGTETPTLRGRIPEDTWDFKKQGFASRD

pyruvate dehydrogenase E1 beta subunit

>gi|151946607|gb|EDN64829.1| pyruvate dehydrogenase beta subunit (E1 beta) [Saccharomyces cerevisiae YJM789]
MFSRLPTSLARNVARRAPTSFVRPSAAAAALRFSSTKTMTVREALNSAMAEELDRDDDVFLIGEEVAQYN
GAYKVSKGLLDRFGERRVVDTPITEYGFTGLAVGAALKGLKPIVEFMSFNFSMQAIDHVVNSAAKTHYMS
GGTQKCQMVFRGPNGAAVGVGAQHSQDFSPWYGSIPGLKVLVPYSAEDARGLLKAAIRDPNPVVFLENEL
LYGESFEISEEALSPDFTLPYKAKIEREGTDISIVTYTRNVQFSLEAAEILQKKYGVSAEVINLRSIRPL
DTEAIIKTVKKTNHLITVESTFPSFGVGAEIVAQVMESEAFDYLDAPIQRVTGADVPTPYAKELEDFAFP
DTPTIVKAVKEVLSIE

pyruvate dehydrogenase E2

>gi|151944463|gb|EDN62741.1| pyruvate dehydrogenase complex dihydrolipoamide acetyltransferase component (E2) [Saccharomyces cerevisiae YJM789]
MSAFVRVVPRISRSSVLTRSLRLQLRCYASYPEHTIIGMPALSPTMTQGNLAAWTKKEGDQLSPGEVIAE
IETDKAQMDFEFQEDGYLAKILVPEGTKDIPVNKPIAVYVEDKADVPAFKDFKLEDSGSDAKTSTKAQPA
EPQAEKKQEAPAEETKTSAPEAKKSDVAAPQGRIFASPLAKTIALEKGISLKDVHGTGPRGRITKADIES
YLEKSSKQSSQTSGAAAATPAAATSSTTAGSAPSPSSTASYEDVPISTMRSIIGERLLQSTQGIPSYIVS
SKISVSKLLKLRQSLNATANDKYKLSINDLLVKAITVAAKRVPDANAYWLPNENVIRKFKNVDVSVAVAT

PTGLLTPIVKNCEAKGLSQISNEIKELVKRARINKLAPEEFQGGTICISNMGMNNAVNMFTSIINPPQST
ILAIATVERVAVEDAAAENGFSFDNQVTITGTFDHRTIDGAKGAEFMKELKTVIENPLEMLL

pyruvate dehydrogenase E3

>gi|118678|sp|P09624.1|DLDH_YEAST RecName: Full=Dihydrolipoyl dehydrogenase, mitochondrial; AltName: Full=Dihydrolipoamide dehydrogenase; AltName: Full=Glycine decarboxylase complex subunit L; AltName: Full=Lipoamide dehydrogenase component of pyruvate dehydrogenase complex; AltName: Full=Pyruvate dehydrogenase complex E3 component; Flags: Precursor
MLRIRSLLNNKRAFSSTVRTLTINKSHDVVIIGGGPAGYVAAIKAAQLGFNTACVEKRGKLGGTCLNVGC
IPSKALLNNSHLFHQMHTEAQKRGIDVNGDIKINVANFQKAKDDAVKQLTGGIELLFKKNKVTYYKGNGS
FEDETKIRVTPVDGLEGTVKEDHILDVKNIIVATGSEVTPFPGIEIDEEKIVSSTGALSLKEIPKRLTII
GGGIIGLEMGSVYSRLGSKVTVVEFQPQIGASMDGEVAKATQKFLKKQGLDFKLSTKVISAKRNDDKNVV
EIVVEDTKTNKQENLEAEVLLVAVGRRPYIAGLGAEKIGLEVDKRGRLVIDDQFNSKFPHIKVVGDVTFG
PMLAHKAEEEGIAAVEMLKTGHGHVNYNNIPSVMYSHPEVAWVGKTEEQLKEAGIDYKIGKFPFAANSRA
KTNQDTEGFVKILIDSKTERILGAHIIGPNAGEMIAEAGLALEYGASAEDVARVCHAHPTLSEAFKEANM
AAYDKAIHC

pyruvate-formate lyase

>gi|159462978|ref|XP_001689719.1| pyruvate-formate lyase [Chlamydomonas reinhardtii]
MLTPLSYPIINTVSSSLPALHAMSQMLLEKTMRRGLATVSAAASSAVGRPIPMAVRSPMRSMAAASAAAE
ALPVAPSHSCAADPDKHPHLPDPRPKPAVDAGINVQKYVQDNYTAYAGNSSFLAGPTDNTKKLWSELEKM
IATEIEKGVMDVDPSKPSTITAFPPGYIDKDLETVVGLQTDAPLKRAIKPLGGVNMVKAALESYGYTPDP
EVARLYSTVRKTHNSGVFDAYTDEMRAARKSGILSGLPDGYGRGRIIGDYRRVALYGVDALIKAKKTDLK
HNLLGVMDEEKIRLREEVNEQIRALSELKEMGAAYGFDLSRPAANSREAVQWLYFGYLGAVKEQDGAAMS
LGRIDAFLDTYFERDLKAGTITEAEVQELIDHFVMKLRIVRQLRTPEYNALFAGDPTWVTCVLGGTDASG
KAMVTKTSFRLLNTLYNLGPAPEPNLTVLWNDNLPAPFKEFCAKVSLDTSSIQYESDNLMSKLFGSDYSI
ACCVSAMRVGKDMQYFGARANLPKLLLYTLNGGRDEVSGDQVGPKFAPVRSPTAPLDYEEVKAKIEDGME
WLASMYANTMNIIHYMHDKYDYERLQMALHDTHVRRLLAFGISGLSVVTDSLSAIKYAQVTPVIDERGLM
TDFKVEGSFPKYGNDDDRVDEIAEWVVSTFSSKLAKQHTYRNSVPTLSVLTITSNVVYGKKTGSTPDGRK
KGEPFAPGANPLHGRDAHGALASLNSVAKLPYTMCLDGISNTFSLIPQVLGRGGEHERATNLASILDGYF
ANGGHHINVNVLNRSMLMDAVEHPEKYPNLTIRVSGYAVHFARLTREQQLEVIARTFHDTM

pyruvate formate-lyase activating enzyme(PFL_AE)

>gi|92084844|emb|CAF04130.1| pyruvate formate-lyase activating enzyme [Chlamydomonas reinhardtii]
MNAASMSCAATGLQRSGPLAMNAATTSRTGPASGLPKHSWGASARRAFVAPATISERLQRKLSTNYSVVL
PQYEPTDPSGIPEVFGNVHSTESMSAVDGPGVRFLVFVQGCAMRCLFCSNPGTWTLKGGNKTSSKEIAAD
IKRVRNYLKPRGGITISGGEAMLQPHFVSTVFQEVHALGLNTTVDTTGQGTKAGNWDVVLPHTDLVLFCI
KHIDPIKYEALTGMKQRGASGFADQLAERKIPFYLRYVYIPGYTDGVKDIDKLIEWCKQQPTFQGIELLP
YHVLGRNKWEVMGLPYPLDGTNTPPHEQVRAVIKVFNDNDVPVICAE

Pyruvate:NADP oxidoreductase

>gi|9909124|dbj|BAB12024.1| pyruvate: NADP+ oxidoreductase [Euglena gracilis]
MKQSVRPIISNVLRKEVALYSTIIGQDKGKEPTGRTYTSGPKPASHIEVPHHVTVPATDRTPNPDAQFFQ
SVDGSQATSHVAYALSDTAFIYPITPSSVMGELADVWMAQGRKNAFGQVVDVREMQSEAGAAGALHGALA
AGAIATTFTASQGLLLMIPNMYKIAGELMPSVIHVAARELAGHALSIFGGHADVMAVRQTGWAMLCSHTV
QQSHDMALISHVATLKSSIPFVHFFDGFRTSHEVNKIKMLPYAELKKLVPPGTMEQHWARSLNPMHPTIR
GTNQSADIYFQNMESANQYYTDLAEVVQETMDEVAPYIGRHYKIFEYVGAPDAEEVTVLMGSGATTVNEA
VDLLVKRGKKVGAVLVHLYRPWSTKAFEKVLPKTVKRIAALDRCKEVTALGEPLYLDVSATLNLFPERQN
VKVIGGRYGLGSKDFIPEHALAIYANLASENPIQRFTVGITDDVTGTSVPFVNERVDTLPEGTRQCVFWG
IGSDGTVGANRSAVRIIGDNSDLMVQAYFQFDAFKSGGVTSSHLRFGPKPITAQYLVTNADYIACHFQEY
VKRFDMLDAIREGGTFVLNSRWTTEDMEKEIPADFRRKLAQKKVRFYNVDARKICDSFGLGKRINMLMQA
CFFKLSGVLPLAEAQRLLNESIVHEYGKKGGKVVEMNQAVVNAVFAGDLPQEVQVPAAWANAVDTSTRTP
TGIEFVDKIMRPLMDFKGDQLPVSVMTPGGTFPVGTTQYAKRAIAAFIPQWIPANCTQCNYCSYVCPHAT
IRPFVLTDQEVQLAPESFVTRKAKGDYQGMNFRIQVAPEDCTGCQVCVETCPDDALEMTDAFTATPVQRT
NWEFAIKVPNRGTMTDRYSLKGSQFQQPLLEFSGACEGCGETPYVKLLTQLFGERTVIANATGCSSIWGG
TAGLAPYTTNAKGQGPAWGNSLFEDNAEFGFGIAVANAQKRSRVRDCILQAVEKKVADEGLTTLLAQWLQ
DWNTGDKTLKYQDQIIAGLAQQRSKDPLLEQIYGMKDMLPNISQWIIGGDGWANDIGFGGLDHVLASGQN
LNVLVLDTEMYSNTGGQASKSTHMASVAKFALGGKRTNKKNLTEMAMSYGNVYVATVSHGNMAQCVKAFV
EAESYDGPSLIVGYAPCIEHGLRAGMARMVQESEAAIATGYWPLYRFDPRLATEGKNPFQLDSKRIKGNL
QEYLDRQNRYVNLKKNNPKGADLLKSQMADNITARFNRYRRMLEGPNTKAAAPSGNHVTILYGSETGNSE
GLAKELATDFERREYSVAVQALDDIDVADLENMGFVVIAVSTCGQGQFPRNSQLFWRELQRDKPEGWLKN
LKYTVFGLGDSTYYFYCHTAKQIDARLAALGAQRVVPIGFGDDGDEDMFHTGFNNWIPSVWNELKTKTPE
EALFTPSIAVQLTPNATPQDFHFAKSTPVLSITGAERITPADHTRNFVTIRWKTDLSYQVGDSLGVFPEN

TRSVVEEFLQYYGLNPKDVITIENKGSRELPHCMAVGDLFTKVLDILGKPNNRFYKTLSYFAVDKAEKER
LLKIAEMGPEYSNILSETYHYADIFHMFPSARPTLQYLIEMIPNIKPRYYSISSAPIHTPGEVHSLVLID
TWITLSGKHRTGLTCTMLEHLQAGQVVDGCIHPTAMEFPDHEKPVVMCAMGSGLAPFVAFLRDGSTLRKQ
GKKTGNMALYFGNRYEKTEFLMKEELKGHINDGLLTLRCAFSRDDPKKKVYVQDLIKMDEKMMYDYLVVQ
KGSMYCCGSRSFIKPVQESLKHCFMKAGGLTAEQAENEVIDMFTTGRYNIEAW

pyruvate:ferredoxin oxidoreductase

>gi|300122846|emb|CBK23853.2| Pyruvate:Ferredoxin (flavodoxin) Oxidoreductase (PFO) [Blastocystis hominis]
MFSTCAKRAVCGISRFNTAFSSTAPKAFIAQFGTKKRVAIDGNEAAAHAIYQVSDAAMLFPITPSSGMGE
HCDAWANKGLKNVFGQKVVITEMQSEAGAAGALHGTLTGGLLGTTFSSSQGLMLMVPSMHKISGELLPGV
IHVSSRSVSKMTTCLYCDYGDVFQTRATGFAYLSSHSVQEAHDLALVSHLSAINSSIPFLHFFDGFRTSH
EMSSIELISPEDIKSIFPFEKALEHKNRGVNPVHPYSIGVAYGDDVWMQTLQTHQPYYDAVPDKVQAAMD
QVASITGRQYHLFDYVGAPDAENVMVLMGASAQTAEETVEYLNQHGEKVGVMKVHLWRPFSLKHFAAALP
KTVKQICVLDKVREENAYGEPLYLDVNCAVRDLDRDIKVICGEFGVAGKEFTPNLVKAVFDNMKAEKPKT
HFTLGVVDDVCHTSLPIPPPLNTLPDSVTQCILYGLGSDGTVGATQEAVKLIVENTPLYAQANFGFDAHK
SGGLTVTDVRFGPEPIKAEYTVQSADYVGCHTTAYVHKYDMLKHIKEGGTFVLNAPWKTVEELDANLPPA
IKHQIAEKKVKLYVIDATSVAQKVGLRQRINMVMQAVFFKLSKVLPEDQATKLIADNIRTRYAKKGEEVV
NMNITAMEQAGKELVEIDYPSSWIDYKMEPLRTFGPEVPDYFKNLFYPTTLLDGDRFPVSAFTPGGIHPT
DTSKYEKRGFAVSVPVWNKDTCTQCNQCSVMCPHAVIRPFLMDAEETKKAPASFVSLPAVGDELKGLNFR
IQASPLDCTGCEVCVNVCPTQSLNMEPLGSVKDVEGKNWDFAMTLTNKGDLVDKTTVKGSQFQPPLIQFN
GACAGCGETQYVKMLTQLFGSKMILADAMGCSMVWSGTSGLIPFTVDKNGYGPVWCSSLFEDHAEYGFGV
NKANQIKRARLESNIQAALADGGVSAELKGCMEKWLSNKNDKAVCDELFEQMKPLLAAEQSKPAVKAVAD
YQDMLPVITTWLYGGDGWAYDIGFVGLDHVLASGENVKIMILDTEMYANTGGQQSKSTQMSAVAKFAAGG
KRLMKKDMGKVAMNYKNVYVASIAIGADARQAIKALTEANSYNGPALIIAYSPCQQHGMPSQLGMSHQAD
EQRKAVECGYWPLYRYDPRRAEKGENPFQLDFKKLKGKVDDFLEGENRFSILTRQNPEAAKELHKQLQEE
VEKRHAERVRMAMSDKQLWKELNKVYGKKK

alpha-ketoglutarate decarboxylase

>gi|161352467|ref|NP_215764.2| alpha-ketoglutarate decarboxylase [Mycobacterium tuberculosis H37Rv]
MANISSPFGQNEWLVEEMYRKFRDDPSSVDPSWHEFLVDYSPEPTSQPAAEPTRVTSPLVAERAAAAAPQ
APPKPADTAAAGNGVVAALAAKTAVPPPAEGDEVAVLRGAAAAVVKNMSASLEVPTATSVRAVPAKLLID
NRIVINNQLKRTRGGKISFTHLLGYALVQAVKKFPNMNRHYTEVDGKPTAVTPAHTNLGLAIDLQGKDGK
RSLVVAGIKRCETMRFAQFVTAYEDIVRRARDGKLTTEDFAGVTISLTNPGTIGTVHSVPRLMPGQGAII
GVGAMEYPAEFQGASEERIAELGIGKLITLTSTYDHRIIQGAESGDFLRTIHELLLSDGFWDEVFRELSI
PYLPVRWSTDNPDSIVDKNARVMNLIAAYRNRGHLMADTDPLRLDKARFRSHPDLEVLTHGLTLWDLDRV
FKVDGFAGAQYKKLRDVLGLLRDAYCRHIGVEYAHILDPEQKEWLEQRVETKHVKPTVAQQKYILSKLNA
AEAFETFLQTKYVGQKRFSLEGAESVIPMMDAAIDQCAEHGLDEVVIGMPHRGRLNVLANIVGKPYSQIF
TEFEGNLNPSQAHGSGDVKYHLGATGLYLQMFGDNDIQVSLTANPSHLEAVDPVLEGLVRAKQDLLDHGS
IDSDGQRAFSVVPLMLHGDAAFAGQGVVAETLNLANLPGYRVGGTIHIIVNNQIGFTTAPEYSRSSEYCT
DVAKMIGAPIFHVNGDDPEACVWVARLAVDFRQRFKKDVVIDMLCYRRRGHNEGDDPSMTNPYVYDVVDT
KRGARKSYTEALIGRGDISMKEAEDALRDYQGQLERVFNEVRELEKHGVQPSESVESDQMIPAGLATAVD
KSLLARIGDAFLALPNGFTAHPRVQPVLEKRREMAYEGKIDWAFGELLALGSLVAEGKLVRLSGQDSRRG
TFSQRHSVLIDRHTGEEFTPLQLLATNSDGSPTGGKFLVYDSPLSEYAAVGFEYGYTVGNPDAVVLWEAQ
FGDFVNGAQSIIDEFISSGEAKWGQLSNVVLLLPHGHEGQGPDHTSARIERFLQLWAEGSMTIAMPSTPS
NYFHLLRRHALDGIQRPLIVFTPKSMLRHKAAVSEIKDFTEIKFRSVLEEPTYEDGIGDRNKVSRILLTS
GKLYYELAARKAKDNRNDLAIVRLEQLAPLPRRRLRETLDRYENVKEFFWVQEEPANQGAWPRFGLELPE
LLPDKLAGIKRISRRAMSAPSSGSSKVHAVEQQEILDEAFG

alpha-ketoglutarate dehydrogenase (TCA cycle)

>gi|171785|gb|AAA34721.1| alpha-ketoglutarate dehydrogenase [Saccharomyces cerevisiae]
MLRFVSSQTCRYSSRGLLKTSLLKNASTVKIVGRGLATTGTDNFLSTSNATYIDEMYQAWQKDPSSVHVS
WDAYFKNMSNPKIPATKAFQAPPSISNFPQGTEAAPLGTAMTGSVDENVSIHLKVQLLCRAYQVRGHLKA
HIDPLGISFGSNKNNPVPPELTLDYYGFSKHDLDKEINLGPGILPRFARDGKSKMSLKEIVDHLEKLYCS
SYGVQYTHIPSKQKCDWLRERIEIPEPYQYTVDQKRQILDRLTWATSFESFLSTKFPNDKRFGLEGLESV
VPGIKTLVDRSVELGVEDIVLGMAHRGRLNVLSNVVRKPNESIFLNLKGSSARDDIEGSGDVKYHLGMNY
QRPTTSGKYVNLSLVANPSHLESQDPVVLGRTRALLHAKNDLKEKTKALGVLLHGDAAFAGQGVVYETMG
FLTLPEYSTGGTIHVITNNQIGFTTDPRFARSTPYPSDLAKAIDAPIFHVNANDVEAVTFIFNLAAEWRH
KFHTDAIIDVVGWRKHGHNETDRPSFTQPLMYKKIAKQKSVIDVYTEKLISEGTFSKKDIDEHKKWVWNL
FEDAFEKTKDYVPSQREWLTAAWEGFKSPKELATEILPHEPTNVPESTLKELGKVLSSWPEGFEVHKNLK
RILKNRGKSIETGEGIDWATGEALAFGTLVLDGQNVRVSGEDVERGTFSQRHAVLHDQQSEAIYTPLSTL
NNEKADFTIANSSLSEYGVMGFEYGYSLTSPDYLVMWEAQFGDFANTAQVIIDQFIAGGEQKWKQRSGLV
LSLPHGYDGQGPEHSSGRLERFLQLANEDPRYFPSEEKLQRQHQDCNFQVVYPTTPANLFHILRRQQHRQ
FRKPLALFFSKQLLRHPLARSSLSEFTEGGFQWIIEDIEHGKSIGTKEETKRLVLLSGQVYTALHKRRES
LGDKTTAFLKIEQLHPFPFAQLRDSLNSYPNLEEIVWCQEEPLNMGSWAYTEPRLHTTLKETDKYKDFKV

RYCGRNPSGAVAAGSKSLHLAEEDAFLKDVFQQS

fumarase

>gi|6324993|ref|NP_015061.1| Fum1p [Saccharomyces cerevisiae S288c]
MLRFTNCSCKTFVKSSYKLNIRRMNSSFRTETDAFGEIHVPADKYWGAQTQRSFQNFKIGGARERMPLPL
VHAFGVLKKSAAIVNESLGGLDPKISKAIQQAADEVASGKLDDHFPLVVFQTGSGTQSNMNANEVISNRA
IEILGGKIGSKQVHPNNHCNQSQSSNDTFPTVMHIAASLQIQNELIPELTNLKNALEAKSKEFDHIVKIG
RTHLQDATPLTLGQEFSGYVQQVENGIQRVAHSLKTLSFLAQGGTAVGTGLNTKPGFDVKIAEQISKETG
LKFQTAPNKFEALAAHDAIVECSGALNTLACSLFKIAQDIRYLGSGPRCGYHELMLPENEPGSSIMPGKV
NPTQNEALTQVCVQVMGNNAAITFAGSQGQFELNVFKPVMIANLLNSIRLITDAAYSFRVHCVEGIKANE
PRIHELLTKSLMLVTALNPKIGYDAASKVAKNAHKKGITLKESALELGVLTEKEFDEWVVPEHMLGPK

fumarate reductase

>gi|72388944|ref|XP_844767.1| NADH-dependent fumarate reductase [Trypanosoma brucei TREU927]
MVDGRSSASIVAVDPERAARERDAAARALLQDSPLHTTMQYATSGLELTVPYALKVVASADTFDRAKEVA
DEVLRCAWQLADTVLNSFNPNSEVSLVGRLPVGQKHQMSAPLKRVMACCQRVYNSSAGCFDPSTAPVAKA
LREIALGKERNNACLEALTQACTLPNSFVIDFEAGTISRKHEHASLDLGGVSKGYIVDYVIDNINAAGFQ
NVFFDWGGDCRASGMNARNTPWVVGITRPPSLDMLRNPPKEASYISVISLDNEALATSGDYENLIYTADD
KPLTCTYDWKAKELMKPSQSNIAQVSVKCYSAMYADALATACFIKRDPAKVRQLLDGWRYVRDTVRDYRV
YVRENERVAKMFEIATEDAEMRKRRISNTLPARVIVVGGGLAGLSAAIEAAGCGAQVVLMEKEAKLGGNS
AKATSGINGWGTRAQAKASIVDGGKYFERDTYKSGIGGNTDPALVKTLSMKSADAIGWLTSLGVPLTVLS
QLGGHSRKRTHRAPDKKDGTPLPIGFTIMKTLEDHVRGNLSGRITIMENCSVTSLLSETKERPDGTKQIR
VTGVEFTQAGSGKTTILADAVILATGGFSNDKTADSLLREHAPHLVNFPTTNGPWATGDGVKLAQRLGAQ
LVDMDKVQLHPTGLINPKDPANPTKFLGPEALRGSGGVLLNKQGKRFVNELDLRSVVSKAIMEQGAEYPG
SGGSMFAYCVLNAAAQKLFGVSSHEFYWKKMGLFVKADTMRDLAALIGCPVESVQQTLEEYERLSTSQRS
CPITRKSVYPCVLGTKGPYYVAFVTPSIHYTMGGCLISPSAEIQMKNTSSRAPLSHSNPILGLFGAGEVT
GGVHGGNRLGGNSLLECVVFGRIAGDRASTILQRKSSALSFKVWTTVVLREVREGGVYGAGSRVLRFNLP
GALQRSGLSLGQFIAIRGDWDGQQLIGYYSPITLPDDLGMIDILARSDKGTLREWISALEPGDAVEMKAC
GGLVIERRLSDKHFVFMGHIINKLCLIAGGTGVAPMLQIIKAAFMKPFIDTLESVHLIYAAEDVTELTYR
EVLEERRRESRGKFKKTFVLNRPPPLWTDGVGFIDRGILTNHVQPPSDNLLVAICGPPVMQRIVKATLKT
LGYNMNLVRTVDETEPSGSSKI

Flavodiiron protein

>gi|162330011|pdb|2Q9U|A Chain A, Crystal Structure Of The Flavodiiron Protein From Giardia Intestinalis
MSSKPKYVQDQEMIPGVYWVGIVDWMVRIFHGYHTDEGSSYNSYFIDDECPTVIDSVKYPFAEEWLSRIA
ACCPLDKIKYVVMNHAEGDHASSLKDHYHKFTNATFVCTKKCQEHLKILYGMEKATWLIVDDKYTLKIGK
RTLKFIPVPLLHWPDSTFTYCPEDKILFSNDGFGQHYATSRRWADECDVSHVMHLFKEYTANILGLFSAQ
MRKALEVASTVEIKYILSAHGVSWRGDAMGLAIAEYDRWSKGQHCQKKVTVVLDSMYGTTHRMALALLDG
ARSTGCETVLLEMTSSDITKVALHTYDSGAVAFASPTLNNTMMPSVAAALNYVRGLTLIKGKPAFAFGAF
GWSNRAVPDIVAELRDGCKADVYDEKGITFKFNYTEELLEQAYNAGVDLGKRAIAYCEKNAPKQ

sulfide:quinone oxidoreductase

>gi|157092622|gb|ABV22505.1| sulfide:quinone oxidoreductase [Arenicola marina]
MASRKVSLVLTGRVLMCQQLPAQAARAAVAPHVASFSSSAPLETAKKMNYKMVVVGGGTGGCAAAHMFSR
KLGKGNVAVIEPADTHYYQPLWTLVGGGLRKLDQSAQPMNKVLPGACDWIKDSAVQFDPDNNTVFTKHGY
EVKYDFLVCAMGLQLNYHLIKGLPEAFDVDPSLCSNYWDKTVIKTRPAMEAVTEGNVIFTFPNSPIKCAG
APQKIMYLTEEYLRQSGKRDKTNVIYNTSLGVVFGVKKYAEALTKIVQERNIQVNFRHNLIEVRPDKKEA
VFEHLDTKEQKVFDYAMLHVVPPMSTPEALWNSPLVNESGYVTVKRETLQHTKYPNVFGIGDNTDIPTAK
TAAAVASQTGILKKNLAAAMNGHEIAGKQYDGYTSCPLVTSKNTVIMAEFDWDGQPLETFPINQAKERRT
MFHFKADIFPQMYWHMLIKGYWHGPGLFRKAMHLGMSR

copper-containing nitrite reductase (nirK)

>gi|156618572|gb|ABU88100.1| copper-containing nitrite reductase [Fusarium oxysporum]
MSRMVTICWTLAPATSQLLPIASRAAASTAFIRNLSLPTRRAPVIGARSFSSNTRSNSRVSHPRLTPALA
VSTGLALSYYLYQRGPQPVKLGLAPEKPEKPKCAHCVDEKPEVIQEKAVGCCEDEQTTTYQEKPLSCCVD
DEASIAMVPAIGGDHKHKIFETVDDETLLISKLPKEDAILTTAPNVPPSITRDHPALVRVPLVTTTKLAQ
LTSQYKYEQWTFNGTVPGPFIRAKVGDVVELSLTNKDPAGNPHNIDCHAFTGPGGGAAVTTAEEGETKVG
RFKLLYPGLYVYHCAAAPVPVHIANGMYGLMYVQPEGNDLPPVDKEYYVMQSEFYHEPPEVDDDGRRSEI
VEFSYPNGLREEPQVVAFNGSESALTRDHPLKAHVGDDVRIFFGNAGPNLTSSFHIIGTHFKNVYRDGGV
TSNPSKGIQTVSVPCGGSTIVDLKMAVPGTYTLVDHSIFRLDKGAVGFLNVSGPQNPGVYQSSQPPRPCV
GCKLHS

cytochrome P450 nor

>gi|117179|sp|P23295.2|NOR_FUSOX RecName: Full=Cytochrome P450 55A1; AltName: Full=CYPLVA1; AltName: Full=Cytochrome P450 DNIR; AltName: Full=Cytochrome P450nor; AltName: Full=Nitric oxide reductase
MASGAPSFPFSRASGPEPPAEFAKLRATNPVSQVKLFDGSLAWLVTKHKDVCFVATSEKLSKVRTRQGFP
ELSASGKQAAKAKPTFVDMDPPEHMHQRSMVEPTFTPEAVKNLQPYIQRTVDDLLEQMKQKGCANGPVDL
VKEFALPVPSYIIYTLLGVPFNDLEYLTQQNAIRTNGSSTAREASAANQELLDYLAILVEQRLVEPKDDI
ISKLCTEQVKPGNIDKSDAVQIAFLLLVAGNATMVNMIALGVATLAQHPDQLAQLKANPSLAPQFVEELC
RYHTASALAIKRTAKEDVMIGDKLVRANEGIIASNQSANRDEEVFENPDEFNMNRKWPPQDPLGFGFGDH
RCIAEHLAKAELTTVFSTLYQKFPDLKVAVPLGKINYTPLNRDVGIVDLPVIF

nitratereductase (NADH-nar)

>gi|169990912|dbj|BAG12905.1| nitrate reductase [Fusarium oxysporum]
METSTTTTLLQQERIPENSEPISTHIHTHSLPPTPPGTAKPSRIGSFHDLQELSSVESPRLDHIKPYPLP
PKFSPKSVLKEDLKTPDNFVERDPRLIRLTGVHPFNVEAPLSDLYDEGFLTSENFHYVRNHGHVPRCEDD
DILDWEFEISGLVENPIKMNVRDLINDYQQLTYPVTFVCAGNRRKEQNIVRKTKGFSWGAAGLSTALWTG
VAIGDLLAAAKPKRGARYVCFWGADRQPNGYYGTSIKLKWCMDPYRGVMVLQMNGKTLHPDHGKPVRIVI
PGLIGGRSIKWLKKITVTQEPRDNWYHIYDNRVLPTMISPEESANLPEVWKDEKYAIYDLSTNSAICYPA
HEEKVPFTDAPASYKVRGYAYGGGGRRITRVEVTLDKGKSWRLANIRYPEDDYRNAPEGDTLYGGRVDMW
WRETSFCWCFWDLDIPLDELKSADDIMMRAMDESMNVQPRDMYWSVLGMMNNPWFRIVIHKEDHALRFEH
PTHATLKIKGRMDQVKEAGGNLTNGYWGEKAPGEVQEIVVKKPEKQICMTNPQINRKITIEELKAHSGEK
EPWFVVKGEVYDGTPYLSGHPGGAASIFGAAGQDATEEFMAIHSENAKAMLPTYHIGTLNEESRAILSGD
ATKTNDDANREVFLQSKTWSKAILDKRTSISPDTKIFSFKLNHEGQKIGLPTGQHLMMRLRDPATREAII
RSYTPYSDGSDCGRLDILIKIYYDTPQRKGGVMTQALDALPIGHWVDFKGPTGKFVYHGNGLCTINDRQR
RVRRFIMVCGGSGITPIRQVLRAVMHNPKDTTPCLIFNGNRSVDDILCKKELDELEAANPSRCRVVNALS
DPPPEWNGLKGFVNQALVPEQMALPKASGEGDELVLVCGPPPMVKAVEASFLGMGFKSDDFVFF

succinate semialdehyde dehydrogenase

>gi|6319478|ref|NP_009560.1| TPA: Uga2p [Saccharomyces cerevisiae S288c]
MTLSKYSKPTLNDPNLFRESGYIDGKWVKGTDEVFEVVDPASGEIIARVPEQPVSVVEEAIDVAYETFKT
YKNTTPRERAKWLRNMYNLMLENLDDLATIITLENGKALGEAKGEIKYAASYFEWYAEEAPRLYGATIQP
LNPHNRVFTIRQPVGVCGIICPWNFPSAMITRKAAAALAVGCTVVIKPDSQTPLSALAMAYLAEKAGFPK
GSFNVILSHANTPKLGKTLCESPKVKKVTFTGSTNVGKILMKQSSSTLKKLSFELGGNAPFIVFEDADLD
QALEQAMACKFRGLGQTCVCANRLYVHSSIIDKFAKLLAERVKKFVIGHGLDPKTTHGCVINSSAIEKVE
RHKQDAIDKGAKVVLEGGRLTELGPNFYAPVILSHVPSTAIVSKEETFGPLCPIFSFDTMEEVVGYANDT
EFGLAAYVFSKNVNTLYTVSEALETGMVSCNTGVFSDCSIPFGGVKESGFGREGSLYGIEDYTVLKTITI
GNLPNSI

opine/strombine/octopine dehydrogenase

>gi|218081329|emb|CAL90921.1| strombine dehydrogenase [Arenicola marina]
MVVALICGGGNGAHVCAGIAASQPGVEARVLTLFADEAERWTKAMACNDFVVTVNSKGKAPTELKAKPTV
VSKKAADVMSGVDIIVLMVPAFAHTGYLEELKPLMKPGMVLVGCPGQAGFEFAVRGILGDLARHVSLLSF
ESLPWACRMLEFGKKSEVLATKGSLTGALQLGDPAPAVDPTAMLQQVLGEAPKLITKGHLLGITLMGTNG
YLHPSIMFGFWSHWDGKPLEQSPLFYNGVDRFSAGVLSSVSDEVVAIAKAVMQQRPQVDLNNVTHIVDWY
RRCYANDITDPTDLYSCIQTNNAYNGLTHPCEQTSNGRFVPNYRYRYLTEDIPFGLVVMRGIATLAGVAT
PSMDKVITWAQGCLGKEYLVGDQLTGKDIPATRCPQAYNLPCLDTILGLA

nuoF NADH dehydrogenase 51 kDa subunit

>gi|51947517|gb|AAU14243.1| hydrogenosomal NADH dehydrogenase 51 kDa subunit [Nyctotherus ovalis]
MIARTCKRLGTMARLFSAADSAKKAETVSKNYGNISDQDRIFSNLYKDQDPFIDGALKRGDWYRTKDILA
CPHDFVIDEIKKSGLRGRGGAGFPSGLKYSFMPKKSDGRPSFLVVNADESEPATCKDREIMRHDPHKLVE
GALIVGYAMRARAAYVYIRGEFWDEAMQLERAVAEAYEKGFIGKNACGSGYDFDIYVHRGAGAYICGEET
SMLSSIEGVIGKPRMKPPYPAGTGLYGCPTTVTNVETVSTVPTIMRRGGGWFASFGRKNNHGTKLYCLSG
HINNPCTVEDEMSISLRELIERHGGGVRGGWDNLLGVIPGGSSTPIISKELCETALMDFDSLIEAGSAFG
TAGVIVLDKSTDVIDAILRLSKFYLHESCGQCTPCREGTGWLVDILERMKIGKADYGEIDQLYELTKQIE
GHTICALGEAAAWPVQGLIKHYRDVIEDRIDKYHSEHPAAAEEFIISHHPVKGTH

nuoG

>gi|11467055|ref|NP_042531.1| NADH dehydrogenase, subunit 11 [Acanthamoeba castellanii]
MKNISFKVNDFQYTINNKLTLIQACLKNKVDISRFCFHEKLSIAGNCRMCLVEDLKQVKPLASCAINVSN

SMNIYTNTLKVKKARESVLEFLLANHPLDCPICDQGGECDLQDQSVVFGSDRGRFYEFKRSVEDKDCGPL
IKTIMNRCIHCTRCVRFSNEVAGVNILGVTGRGSKMEIGFYIENLMRSELSGNVIDLCPVGALTSKPFAF
TSRPWELKSYNSIDVLDSLHSNIRVDIRGTKIMRILPRVNSELNEDWITDKIRFSYDSFRRQRLYDPMVK
ISGSFLKIGWKKAMLFIKKFFCNFLGFNHSSFIPLRGYIGDYLDLETIYTFKKFLLLNGSNFFLPSSSYN
DLTALYSFNTPLTRLDEGDFCILLDVNLRVELPIVNSRIKQLVSKKMLPVFVLGFYSNFNYFVKHISNSS
KTLLHVLEGSHWLSAKISKKFSSKPIFLIGDSSSLLKGSLIVPLFNFTNVICDNWNGLNIISNDSSYLST
KEFNLSSSHSQNSHLLNFPINFVLNYDKAVLVDSSAFQIYQGHHGDTNAINSNLIFPSTSFIEKNSFYSN
SLAIVQKTKKILFSPGNSRDDWKILNALIDNFGFSYFKVRNSFDLVSFLSESTPFILYKRSFSFKCFGFY
EQLVYHFFNYFSVNNNYYIYDSITRNSKIMSLCFNKFKMKGYNFF

nuoE

>gi|123446843|ref|XP_001312168.1| Respiratory-chain NADH dehydrogenase 24 Kd subunit family protein [Trichomonas vaginalis G3]
MLASVNTSRFFARLNKKSVLIQKDFKFSDQSKVDAILAKYPKENKRAATIPLLHLGQRENGGYLTTGVLQ
AISKIVGVTAGRVHETACFYSMFRFQPPNNHIVEVCKGLSCYLTGSDNVKEAIQKATGGTFKEGKSPDGQ
FTLEEVECLGACANAPVMILDGVYYQNLTAETAKIIIECVKAGKSVKELDAVHTHPPRPLP

iron hydrogenase assembly protein HydEF

>gi|159466536|ref|XP_001691465.1| iron hydrogenase assembly protein [Chlamydomonas reinhardtii]
MAHSLSAHSRQAGDRKLGAGAASSRPSCPSRRIVRVAAHASASKATPDVPVDDLPPAHARAAVAAANRRA
RAMASAEAAAETLGDFLGLGKGGLSPGATANLDREQVLGVLEAVWRRGDLNLERALYSHANAVTNKYCGG
GVYYRGLVEFSNICQNDCSYCGIRNNQKEVWRYTMPVEEVVEVAKWALENGIRNIMLQGGELKTEQRLAY
LEACVRAIREETTQLDLEMRARAASTTTAEAAASAQADAEAKRGEPELGVVVSLSVGELPMEQYERLFRA
GARRYLIRIETSNPDLYAALHPEPMSWHARVECLRNLKKAGYMLGTGVMVGLPGQTLHDLAGDVMFFRDI
KADMIGMGPFITQPGTPATDKWTALYPNANKNSHMKSMFDLTTAMNALVRITMGNVNISATTALQAIIPT
GREIALERGANVVMPILTPTQYRESYQLYEGKPCITDTAVQCRRCLDMRLHSVGKTSAAGVWGDPASFLH
PIVGVPVPHDLSSPALAAAASADFHEVGAGPWNPIRLERLVEVPDRYPDPDNHGRKKAGAGKGGKAHDSH
DDGDHDDHHHHHGAAPAGAAAGKGTGAAAIGGGAGASRQRVAGAAAASARLCAGARRAGRVVASPLRPAA
ACRGVAVKAAAAAAGEDAGAGTSGVGSNIVTSPGIASTTAHGVPRINIGVFGVMNAGKSTLVNALAQQEA
CIVDSTPGTTADVKTVLLELHALGPAKLLDTAGLDEVGGLGDKKRRKALNTLKECDVAVLVVDTDTAAAA
IKSGRLAEALEWESKVMEQAHKYNVSPVLLLNVKSRGLPEAQAASMLEAVAGMLDPSKQIPRMSLDLAST
PLHERSTITSAFVKEGAVRSSRYGAPLPGCLPRWSLGRNARLLMVIPMDAETPGGRLLRPQAQVMEEAIR
HWATVLSVRLDLDAARGKLGPEACEMERQRFDGVIAMMERNDGPTLVVTDSQAIDVVHPWTLDRSSGRPL
VPITTFSIAMAYQQNGGRLDPFVEGLEALETLQDGDRVLISEACNHNRITSACNDIGMVQIPNKLEAALG
GKKLQIEHAFGREFPELESGGMDGLKLAIHCGGCMIDAQKMQQRMKDLHEAGVPVTNYGVFFSWAAWPDA
LRRALEPWGVEPPVGTPATPAAAPATAASGV

hydrogenase assembly factor HydG

>gi|159466244|ref|XP_001691319.1| hydrogenase assembly factor [Chlamydomonas reinhardtii]
MSVPLQCNAGRLLAGQRPCGVRARLNRRVCVPVTAHGKASATREYAGDFLPGTTISHAWSVERETHHRYR
NPAEWINEAAIHKALETSKADAQDAGRVREILAKAKEKAFVTEHAPVNAESKSEFVQGLTLEECATLINV
DSNNVELMNEIFDTALAIKERIYGNRVVLFAPLYIANHCMNTCTYCAFRSANKGMERSILTDDDLREEVA
ALQRQGHRRILALTGEHPKYTFDNFLHAVNVIASVKTEPEGSIRRINVEIPPLSVSDMRRLKNTDSVGTF
VLFQETYHRDTFKVMHPSGPKSDFDFRVLTQDRAMRAGLDDVGIGALFGLYDYRYEVCAMLMHSEHLERE
YNAGPHTISVPRMRPADGSELSIAPPYPVNDADFMKLVAVLRIAVPYTGMILSTRESPEMRSALLKCGMS
QMSAGSRTDVGAYHKDHTLSTEANLSKLAGQFTLQDERPTNEIVKWLMEEGYVPSWCTACYRQGRTGEDF
MNICKAGDIHDFCHPNSLLTLQEYLMDYADPDLRKKGEQVIAREMGPDASEPLSAQSRKRLERKMKQVLE
GEHDVYL

hydrogenase

>gi|19548180|gb|AAL90459.1|AF446076_1 [Fe]-hydrogenase [Piromyces sp. E2]
CLVDVKGSWKPLTACTTEVWEGMEIETDTPAVRETVRSSLAMMREEHPNDCMTCESNGNCEFQDLIYRYQ
IDAQHPVRTLLRNKFKKTNHSITEPCYSPFDDSTFSISRDMNKCVKCGRCVRACHHFQNINILGFINRAG
YERVGTPMDRPMNFTKCVECGQCSQVCPVGAITERNECIEVLRHLDTKRKIVVVSTAPAIRVALAEEFNA
EPDFDFTGKMVAGLKKLGFDYIFDTNFSADLTIMEEGTELITRLNEGGKFPMFTSCCPGWINMVEKSYPE
IRDNLSSCKSPQQMIGAVIKTYFAKKINAKPEDIIHVSVMPCTAKKGEAKRPEFKRDGVPDIDHVITTRE
LITLLKLKRINPSELKNEKFDSPLGIGSSAGNLFGVTGGVMEAAVRTAQIITGVENPIPLGELKAIRGLD
GIKAASVPLKTKDGKDVNVRAAVVSGGANIQKFLEKLKKKELEFDFVEMMMCPGGCINGGGQPKSADPKV
VAKKMERMYTMDDQASLRLSHENPEITQIYKEFLKEPNGHLSHELLHTHYNDRSKAIQDMSLHQK

phosphoenol pyruvate carboxykinase (Chlamydomonas)

>gi|159473685|ref|XP_001694964.1| phosphoenolpyruvate carboxykinase, splice variant [Chlamydomonas reinhardtii]
MALLSSRSSANCTGRSVRRATVAPAPVVKPHSSVAMRFTNNTKQDAAVPAPCDMQFVLDSKFTRESGLQP
RVVFRNLTTPQLYEMALAHEPGTHITSSGALATLSGEKTGRSPKDKRVVRDPETEKDLWWGPYSPNYVMD
DRTFLTNRERAIDYLNTLDRVYVVDAFVNWDPESRLKVRVVTSRAYHALFMSNMLIKPTEEELKTFGEPD
FVIYNAGAFPANKYTQFMTSQTSIDLSLKHKEMVILGTMYAGEMKKGVFTLMHYLMPMQGKLSLHSGCNV
GADDDVTMFFGLSGTGKTTLSADPKRPLIGDDEHVWSDKGVFNIEGGCYAKCIGLKATTEPEIWNAIKFG
TVLENVDYNPVTREVDYESERLTENTRASYPIEFMNNARIPCVGPHPKNVVLLACDAFGALPPVSRLTLE
QAMYHFISGYTAKVAGTEMGVTEPTATFSACFGSAFLMLHPYKYATMLAEKMKAHGTTAWLINTGWTGGK
YGVGKRISLKHTRAIIDAIHSGELDKAEYVTTPIFGLQVPKAISGVPAEILSPENVWPNKDEFAMCLNSL
GHMFIRNFEHFNDGEQFVGKDTAARILTGGPQPIAKEDVEKKGFGAFKTQ

phosphoenol pyruvate carboxykinase (Giardia)

>gi|159119302|ref|XP_001709869.1| Phosphoenolpyruvate carboxykinase [Giardia lamblia ATCC 50803]
MSLHPVVDERSQTIIDQLNCPAFNELLLDAIELMRPSSLYIQTSSKEEIDYARSNALAQGEEHQLAMPGH
TYHFDSPDDQGRDKKNTLILLDDQTGLDADVMTRDRKEGTAHVREIMKGCMEGKQMLIAFYCLGPVNCSF
SKTAVQFTDSWYILHSENVLYRNGFAQMVNRHMKETSANRSFYAFYHSVGRTDSANRPVDIDKRRIYINP
VEHLVYTINNSYAGNALACKKLALRLAIYDSNHHPEKNNLTEHMFLSTFANPCIPNDKLNVCGAFPSACG
KTSTSMAPGSSIIGDDMVYMQIVDDNMGIRRCKAVNIETGMFGIISGVNPSDDPLIYDCLTSERECIFSN
VLVGEDGRPYWDGMYYGKSKNDMVNEPGLLPSSGRNYKGTWTKPELPIMHGNARFTLNLKELRNVSPELD
NPDGVDVDLILYGGRDSNTCPPVYQAHNWAHGVYIGSSIESETTAATLGTQGVVVSNPMANLDFLIVPVP
MYLENHVRFGRLLGSRAPKVFGVNYFLKDPTTGEYLNSKLDKKVWVAWACGRTRGHYRAKCTPIGWIPYY
EDLKSLFRSELDTDYTEEQYNIQFTINVENYIQKMVRIMKLYGGKQAPTEWVIMECRVMRALKKLLAEKG
SAVSPSAFDDYESQSWFDRAFVEE

acetate kinase

>gi|159472745|ref|XP_001694505.1| acetate kinase [Chlamydomonas reinhardtii]
MLAGKVPVGSAVPPRNTAPSGKGSKVLVVNAGSSSIKFKIFTAETLLPGAAGLFDRIGEGDPANCVLKAS
VPDDGGKPKKFEKKIPAKDHLTAMQDIMSFIDENVSSTFASEVCAVGHRIVHGLDMSQPKLLTPDVIRCI
QDASMFAPLHNPPHLQGIYASQKVFGPDVPQVAVFDTAFHQTMPPESYVYGLPYDMYEKHKIRRYGFHGT
SHKYLVDQAAAMLGKKVSETNVITCHLGNGSSVAAVRGGQCVDTSMGMTPLEGLLMGTRCGDIDPAVVLH
IQNQLGLSASETDTLLNKKSGLLGLTGSNDLRTVIEGAGKGEPRSQLGLDMFVRRVRKYIGAYMAMLDGQ
VDAVVFSAGIGENSALVRGLICDRMQALGIAVDKDANAAAVGGKQADISGPGARIRALVIPTDEELSIAQ
QTLQVVRGAALAA

alternative oxidase

>gi|71747778|ref|XP_822944.1| alternative oxidase [Trypanosoma brucei TREU927]
MFRNHASRITAAAAPWVLRTACRQKSDAKTPVWGHTQLNRLSFLETVPVVPLRVSDESSEDRPTWSLPDI
ENVAITHKKPNGLVDTLAYRSVRTCRWLFDTFSLYRFGSITESKVISRCLFLETVAGVPGMVGGMLRHLS
SLRYMTRDKGWINTLLVEAENERMHLMTFIELRQPGLPLRVSIIITQAIMYLFLLVAYVISPRFVHRFVG
YLEEEAVITYTGVMRAIDEGRLRPTKNDVPEVARVYWNLSKNATFRDLINVIRADEAEHRVVNHTFADMH
EKRLQNSVNPFVVLKKNPEEMYSNQPSGKTRTDFGSEGAKTASNVNKHV

propionate:succinate CoA transferase

>gi|16130821|ref|NP_417395.1| propionyl-CoA:succinate-CoA transferase [Escherichia coli str. K-12 substr. MG1655]
METQWTRMTANEAAEIIQHNDMVAFSGFTPAGSPKALPTAIARRANEQHEAKKPYQIRLLTGASISAAAD
DVLSDADAVSWRAPYQTSSGLRKKINQGAVSFVDLHLSEVAQMVNYGFFGDIDVAVIEASALAPDGRVWL
TSGIGNAPTWLLRAKKVIIELNHYHDPRVAELADIVIPGAPPRRNSVSIFHAMDRVGTRYVQIDPKKIVA
VVETNLPDAGNMLDKQNPMCQQIADNVVTFLLQEMAHGRIPPEFLPLQSGVGNINNAVMARLGENPVIPP
FMMYSEVLQESVVHLLETGKISGASASSLTISADSLRKIYDNMDYFASRIVLRPQEISNNPEIIRRLGVI
ALNVGLEFDIYGHANSTHVAGVDLMNGIGGSGDFERNAYLSIFMAPSIAKEGKISTVVPMCSHVDHSEHS
VKVIITEQGIADLRGLSPLQRARTIIDNCAHPMYRDYLHRYLENAPGGHIHHDLSHVFDLHRNLIATGSM
LG

glutamate aminotransferase

>gi|242398987|ref|YP_002994411.1| glutamate aminotransferase [Thermococcus sibiricus MM 739]
MEYPKLVVTPPGPKAKELVEREKRVISQGLGVKLFPVVPERGYGALIEDVDGNVFIDFLAGAAAASTGYA
HPKLVKEVQEQVSKIQHSMIGYTYSKRAIEVAEILAEKSPIENPKILFGLSGSDSIDLLMKVARFATRKP
WIIAFIGAYHGQTYGATSVAAFQSSQKRGFSPLVPNVVWIPYPNPYRNVWNIDGYEEPDELINAFLDYLE
NYVFAHVIPPDEVSILLAEPIQGDAGIVVPPDNFFKELKKVLDEREILLAMDEVQTGIGRTGKWFGSEWF
EVEPDFISFGKGVASGMGLSGVIGKAHLMEMTSGSALLTPAANPVISAAAYATLRIIEEENLLKNALKVG

EFIKKRLLEMKESYDVIGDVRGKGLMIGAEIVKPNTKVPNPDLTGKICWRAFELGLILPSYGMFGNVIRI
TPPLVITKKIAEKGLEIMEQALKDALAGKVKHKTITWH

beta ketosynthase

>gi|82408974|gb|ABB73268.1| beta ketosynthase [Rhodococcus sp. SW09]
VDPQQRLLLESAWEALEQAGIQPDSPDLTGTGVYIGLMGGDYGFHLMSQRNVDAEGYLMTGTSDSVASGR
ISYSLGFTGPAVTVDTACSSSLVAMHLAAQALRDGECPLALAGGATVMSTPGVLVEFSRQRGLAPDGRCK
PFSDRADGTGLSEGSGMVVLERLSDARRNGHRVLATIRGSAVNQDGASNGLTAPNGPSQERVIRQALANA
SLGPTDIDAVEAHGTGT

beta-hydroxyacyl dehydrogenase

>gi|51473740|ref|YP_067497.1| 3-hydroxyacyl-CoA dehydrogenase [Rickettsia typhi str. Wilmington]
MQNEIKKVCVIGAGVMGSGIAALIANSSHRVVLLDILDKDSNDPNKIVKNAVKNLHRQKLPPLSYPDKVN
FITIGNLEHDLDLIKECNLVIEVIVEKLDIKHQLYNKIIPYLKEDTIIASNTSTLPLKKLKENLPNNIKS
RFIITHFFNPPRYMELVELIIDNTIKDEVIEKISVFLTKILGKTIIKCNDTPGFIANRVGCFLLELVAHK
AIAQNLDFVTIDQIFSRCLGLPNTGIFGLYDLIGHDVMKLISSSLLSALPKSDDYHRIYFNTKVFDKMIE
HNLIGRKGEGGFYRLSVSNGKKIKEVINISDLSYHPVQKVDISFNNLDELLASDSIYSKFFSEIITEFYI
YLTSLVPSVTNNIYDIDATMKLGYSWHYGPFELLTIAVKNGWNSIIKNADLMNISLPKYLASKEYQKIDK
QKFNSKKDFLQESTIVLANDSANLIHYCENLIFVITTKMNTLNHNVFYLLQEAVSKAENYGKNLYIFPQG
NNFSAGADLKLILSYIQDGNFDNLENLLKLGQQTMRYLKYSSVHIISCARGVALGGGCELLLNSSYIVAN
QELNAGLIEFGVGLIPGWSGVTEMFARSNGDKTKLIRNIKNIIEQNKTSSADYFKADYDVSNMQVNMNKH
YILDEALKLNVSNKIVSIPHKIALPKINIVSEIDTSKYNDLQNKVLNKFQNIIDKHNEISEAELLTYERE
IFLELAKEPQTIEKLHAIVG

fatty acyl-coenzyme A reductase

>gi|298200319|gb|ADI60057.1| fatty acyl-coenzyme A reductase [Euglena gracilis]
MNDFYAGKGVFLTGVTGFVGKMVVEKILRSLPTVGRLYVLVRPKAGTDPHQRLHSEVWSSAGFDVVREKV
GGPAAFDALIREKVVPVPGDMVKDRFGLDDAAYRSLAANVNVIIHMAATIDFTERLDVAVSLNVLGTVRV
LTLARRARELGALHSVVHVSTCYVNSNQPPGARLREQLYPLPFDPREMCTRILDMSPREIDLFGPQLLKQ
YGFPNTYTFTKCMAEQLGAQIAHDLPFAIFRPAIIGAALSEPFPGWCDSASACGAVFLAVGLGVLQELQG
NASSVCDLIPVDHVVNMLLVTAAYTASAPPADPSPSSLALSPPQLPLATLPPGTVADVPIYHCGTSAGPN
AVNWGRIKVSLVEYWNAHPIAKTKAAIALLPVWRFELSFLLKRRLPATALSLVASLPGASAAVRRQAEQT
ERLVGKMRKLVDTFQSFVFWAWYFQTESSARLLASLCPEDRETFNWDPRRIGWRAWVENYCYGLVRYVLK
QPIGDRPPVAAEELASNRFLRAML

glucokinase

>gi|159113013|ref|XP_001706734.1| Glucokinase [Giardia lamblia ATCC 50803]
MPYSLSGDLGGTKCFLAIHDLDVLKTDPRAAPLLEHELLCKDYQSTGDLINDFLKRWDRETPIVGCLGVA
GPVTNGRVCITNLDWNESEEELQNTTGVGKMKLINDFAAIGYGLLAIRPDDYLDFDARNGSVSTPTVVPD
NSTGIVSYAGAGTGFGVGFVADGVAYAAEGGHTTFSPMEAEDHALAQFIKEKYNTDHVSFERVVSGLGLR
NMHDFFWKNLSGLASPVLREHVLSRDHDIDMGFLAKCAETGDKYALKIFKKFFYYYGFYLGNICVLFRPK
DYFIAGGILAKDLNLVCGPCREDFCRGLYTKGRMSHLPNGVSFHVVTNQKLGIVGAAYFCTKM

hexokinase

>gi|71746804|ref|XP_822457.1| hexokinase [Trypanosoma brucei TREU927]
MSRRLNNILEHISIQGNDGETVRAVKRDVAMAALTNQFTMSVESMRQIMTYLLYEMVEGLEGRESTVRML
PSYVYKADPKRATGVFYALDLGGTNFRVLRVACKEGAVVDSSTSAFKIPKYALEGNATDLFDFIASNVKK
TMETRAPEDLNRTVPLGFTFSFPVEQTKVNRGVLIRWTKGFSTKGVQGNDVIALLQAAFGRVSLKVNVVA
LCNDTVATMISHYFKDPEVQVGVIIGTGSNACYFETASAVTKDPAVAARGSALTPISMESGNFDSKYRFV
LPTTKFDLDIDDASLNKGQQALEKMISGMYLGEIARRVIVHLSSINCLPAALQTALGNRGSFESRFAGMI
SADRMPGLQFTRSTIQKVCGVDVQSIEDLRIIRDVCRLVRGRAAQLSASFCCAPLVKTQTQGRATIAIDG
SVFEKIPSFRRVLQDNINRILGPECDVRAVLAKGGSGVGAALISAIVADGK

glucose-6-phosphateisomerase

>gi|120744|sp|P13377.1|G6PI_TRYBB RecName: Full=Glucose-6-phosphate isomerase, glycosomal; Short=GPI; AltName: Full=Phosphoglucose isomerase; Short=PGI; AltName: Full=Phosphohexose isomerase; Short=PHI
MSSYLDDLRIDLAASPASGGSASIAVGSFNIPYEVTRRLKGVGADADTTLTSCASWTQLQKLYEQYGDEP
IKKHFEADSERGQRYSVKVSLGSKDENFLFLDYSKSHINDEIKCALLRLAEERGIRQFVQSVFRGERVNT
TENRPVLHIALRNRSNRPIYVDGKDVMPAVNKVLDQMRSFSEKVRTGEWKGHTGKAIRHVVNIGIGGSDL
GPVMATEALKPFSQRDLSLHFVSNVDGTHIAEVLKSIDIEATLFIVASKTFTTQETITNALSARRALLDY
LRSRGIDEKGSVAKHFVALSTNNQKVKEFGIDEENMFQFWDWVGGRYSMWSAIGLPIMISIGYENFVELL

TGAHVIDEHFANAPPEQNVPLLLALVGVWYINFFGAVTHAILPYDQYLWRLPAYLQQLDMESNGKYVTRS
GKTVSTLTGPIIFGEAGTNGQHAFYQLIHQGTNLIPCDFIGAIQSQNKIGDHHKIFMSNFFAQTEALMIG
KSPSEVRRELEAAGERSAEKINALLPHKTFIGGRPSNTLLIKSLTPRALGAIIAMYEHKVLVQGAIWGID
SYDQWGVELGKVLAKSILPQLRPGMRVNNHDSSTNGLINMFNELSHL

phosphofructokinase PPi

>gi|67482265|ref|XP_656482.1| phosphofructokinase [Entamoeba histolytica HM-1:IMSS]
MTERRHVHQRNDLLIAKKPEEPLPSLEITSLGECKYENTYASPEPFVNGMKMSMSAIKIDGIPVNECEVD
LAGPMEKIFFIPERTKVGIVTCGGLCPGLNNVIRGLVMNLQNRYGVKQIYGLKYGYEGLVPELSEQMKLD
TLTVSDIHQRGGTILGTSRGAQDPKIMAQFLIDNNFNILFTLGGDGTLRGANAINKELRRRGSPIAVVGI
PKTIDNDICYTDSTFGFDTAVELAQEAINSVHYEAKSAKNGVGIVKLMGRDAGFIALYASVASGDVNLVL
IPEVDTPIEEILRMTERRLMSKGHIVIVIAEGACQNLKPKGLDLGSDKSGNIVHWDAVTYIRQEIDKYLE
NKKIEHTIKFVDPSYMIRSAPCSAADAHFCLCLANAAVHVAMAGKTGLVICHHHNNFVSIPIERACYYLK
RVNPEGPMLSMMKSIEMVE

phosphofructokinase ATP

>gi|72386991|ref|XP_843920.1| ATP-dependent phosphofructokinase [Trypanosoma brucei]
MAVESRSRVTSKLVKAHRAMLNSVTQEDLKVDRLPGADYPNPSKKYSSRTEFRDKTDYIMYNPRPRDEPS
SENPVSVSPLLCELAAARSRIHFNPTETTIGIVTCGGICPGLNDVIRSITLTGINVYNVKRVIGFRFGYW
GLSKKGSQTAIELHRGRVTNIHHYGGTILGSSRGPQDPKEMVDTLERLGVNILFTVGGDGTQRGALVISQ
EAKRRGVDISVFGVPKTIDNDLSFSHRTFGFQTAVEKAVQAIRAAYAEAVSANYGVGVVKLMGRDSGFIA
AQAAVASAQANICLVPENPISEQEVMSLLERRFCHSRSCVIIVAEGFGQDWGRGSGGYDASGNKKLIDIG
VILTEKVKAFLKANKSRYPDSTVKYIDPSYMIRACPPSANDALFCATLATLAVHEAMAGATGCIIAMRHN
NYILVPIKVATSVRRVLDLRGQLWRQVREITVDLGSDVRLARKLEIRRELEAINRNRDRLHEELAKL

fructose-bisphosphate aldolase class 1

>gi|161968|gb|AAA30153.1| fructose-bisphosphate aldolase (ald) (EC 4.1.2.13) [Trypanosoma brucei]
MSKRVEVLLTQLPAYNRLKTPYEAELIETAKKMTAPGKGLLAADESTGSCSKRFAGIGLSNTAEHRRQYR
ALMLECEGFEQYISGVILHDETVYQKAKTGETFPQYLRRRGVVPGIKTDCGLEPLVEGAKGEQMTAGLDG
YIKRAKKYYAMGCRFCKWRNVYKIQNGTVSEAVVRFNAETLARYAILSQLCGLVPIVEPEVMIDGTHDIE
TCQRVSQHVWSEVVSALHRHGVVWEGCLLKPNMVVPGAESGLKATAEQVAEYTVKTLARVIPPALPGVTF
LSGGLSEVMASEYLNAMNNCPLPRPWKLTFSYARALQSSAIKRWGGKESGVEAGRRAFMHRAKMNSLAQL
GKYNRADDDKDSQSLYVAGNTY

fructose-bisphosphate aldolase class 2

>gi|159119664|ref|XP_001710050.1| Fructose-bisphosphate aldolase [Giardia lamblia ATCC 50803]
MPLCTLRQMLGEARKHKYGVGAFNVNNMEQIQGIMKAVVQLKSPVILQCSRGALKYSDMIYLKKLCEAAL
EKHPDIPICIHLDHGDTLESVKMAIDLGFSSVMIDASHHPFDENVRITKEVVAYAHARGVSVEAELGTLG
GIEEDVQNTVQLTEPQDAKKFVELTGVDALAVAIGTSHGAYKFKSESDIRLAIDRVKTISDLTGIPLVMH
GSSSVPKDVKDMINKYGGKMPDAVGVPIESIVHAIGEGVCKINVDSDSRMAMTGAIRKVFVEHPEKFDPR
DYLGPGRDAITEMLIPKIKAFGSAGHAGDYKVVSLEEAKAWYK

triosephosphate isomerase

>gi|71755425|ref|XP_828627.1| triosephosphate isomerase [Trypanosoma brucei TREU927]
MSKPQPIAAANWKCNGSQQSLSELIDLFNSTSINHDVQCVVASTFVHLAMTKERLSHPKFVIAAQNAIAK
SGAFTGEVSLPILKDFGVNWIVLGHSERRAYYGETNEIVADKVAAAVAAGFMVIACIGETLQERESGRTA
VVVLTQIAAIAKKLKKADWAKVVIAYEPVWAIGTGKVATPQQAQEAHALIRSWVSSKIGADVAGELRILY
GGSVNGKNARTLYQQRDVNGFLVGGASLKPEFVDIIKATQ

glyceraldehyde 3-phosphate dehydrogenase

>gi|72390505|ref|XP_845547.1| glyceraldehyde 3-phosphate dehydrogenase, glycosomal [Trypanosoma brucei TREU927]
MSVALFFSSFLAVPYFPCICLSFCGAEFIRANQTSKRLTTNLNMTIKVGINGFGRIGRMVFQALCDDGLL
GNEIDVVAVVDMNTDARYFAYQMKYDSVHGKFKHSVSTTKSKPSVAKDDTLVVNGHRILCVKAQRNPADL
PWGKLGVEYVIESTGLFTVKSAAEGHLRGGARKVVISAPASGGAKTFVMGVNHNDYNPREHHVVSNASCT
TNCLAPLVHVLVKEGFGISTGLMTTVHSYTATQKTVDGVSVKDWRGGRAAALNIIPSTTGAAKAVGMVIP
STQGKLTGMAFRVPTADVSVVDLTFIATRDTSIKEIDAALKRASKTYMKNILGYTDEELVSADFISDSRS
SIYDSKATLQNNLPNERRFFKIVSWYDNEWGYSHRVVDLVRHMAARDRAAKL

phosphoglycerate kinase

>gi|115503965|ref|XP_001218775.1| phosphoglycerate kinase [Trypanosoma brucei]
MSTAPNAKNNISLKKSVGDVWPLTAKRVLMRVDFNVPMQNGHITNDYRIRAAIPTIRRVIDQGGICILLS
HLGRPRGVSMVAGVRDIRRRYHEAQFHDNKGKTAFFSVLPGEEKVKILAKSSAREEATHISPEVKSGKTM
LFARLPEDEKKSLLMQYLNENKDSALPQMSVSAGYEEQYSLRPVAVRLAELLGQHVYFAHDCLDARVEVS
RLKRGNVMLLENVRFYSEENGENAEEREAMAKILASYGDVYISDAFGAAHRDSATMTGIPKILGHGAAGY
LMEKEISYFAKVLGNPPRPLVAIVGGAKVSEKIQLLDNMLQRIDYLLIGGAMAYTFLKAQGYSIGKSKCE
ESKLEFARSLLKKAEDRKVQIILPIDHVCHTEFKAVDSPLITEDQNIPEGHMALDIGPKTIEKYVQTIGK
CKSAIWNGPMGVFEMVPYSKGTFAIAKAMGRGTQKRGLMSIIGGGESAGAAELCGEAARISHVSTGGGAS
LELLEGKTLPGVAVLDDKE

phosphoglycerate mutase type I

>gi|71747944|ref|XP_823027.1| 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Trypanosoma brucei TREU927]
MALTLAAHKTLPRRKLVLVVLDGVGIGPRDEYDAVHVAKTPLMDALFNDPKHFRSICAHGTAVGLPTDAD
MGNSEVGHNALGAGRVVLQGASLVDDALESGEIFTSEGYRYLHGAFSQPGRTLHLIGLLSDGGVHSRDNQ
VYQILKHAGANGAKRIRVHALYDGRDVPDKTSFKFTDELEEVLAKLREGGCDARIASGGGRMFVTMDRYE
ADWSIVERGWRAQVLGEGRAFKSAREALTKFREEDANISDQYYPPFVIAGDDGRPIGTIEDGDAVLCFNF
RGDRVIEMSRAFEEEEFDKFNRVRLPKVRYAGMMRYDGDLGIPNNFLVPPPKLTRTSEEYLIGSGCNIFA
LSETQKFGHVTYFWNGNRSGKLSEERETFCEIPSDRVQFNQKPLMKSKEITDAAVDAIKSGKYDMIRINY
PNGDMVGHTGDLKATITSLEAVDQSLQRLKEAVDSVNGVFLITADHGNSDDMVQRDKKGKPVRDAEGNLM
PLTSHTLAPVPVFIGGAGLDPRVQMRTDLPRAGLANVTATFINLMGFEAPSDYEPSLIEVA

phosphoglycerate mutase type D

>gi|6322697|ref|NP_012770.1|phosphoglyceratemutasetypeD[SaccharomycescerevisiaeS288c]
MPKLVLVRHGQSEWNEKNLFTGWVDVKLSAKGQQEAARAGELLKEKKVYPDVLYTSKLSRAIQTANIALE
KADRLWIPVNRSWRLNERHYGDLQGKDKAETLKKFGEEKFNTYRRSFDVPPPPIDASSPFSQKGDERYKY
VDPNVLPETESLALVIDRLLPYWQDVIAKDLLSGKTVMIAAHGNSLRGLVKHLEGISDADIAKLNIPTGI
PLVFELDENLKPSKPSYYLDPEAAAAGAAAVANQGKK

enolase

>gi|71746974|ref|XP_822542.1| enolase [Trypanosoma brucei TREU927]
MTIQKVHGREVLDSRGNPTVEVEVTTERGVFRSAVPSGASTGVYEACELRDGDKKRYVGKGCLQAVKNVN
EVIGPALIGRDELKQEELDTLMLRLDGTPNKGKLGANAILGCSMAISKAAAAAKGVPLYRYLASLAGTKE
LRLPVPCFNVINGGKHAGNALPFQEFMIAPVKATSFSEALRMGSEVYHSLRGIIKKKYGQDAVNVGDEGG
FAPPIKDINEPLPILMEAIEEAGHRGKFAICMDCAASETYDEKKQQYNLTFKSPEPTWVTAEQLRETYCK
WAHDYPIVSIEDPYDQDDFAGFAGITEALKGKTQIVGDDLTVTNTERIKMAIEKKACNSLLLKINQIGTI
SEAIASSKLCMENGWSVMVSHRSGETEDTYIADLVVALGSGQIKTGAPCRGERTAKLNQLLRIEEELGAH
AKFGFPGWS

pyruvatekinase

>gi|159469714|ref|XP_001693008.1| pyruvate kinase [Chlamydomonas reinhardtii]
MVSLGLETVLAGTPSNICKTKVVCTLGPKSRSVEVLEELLRAGMSVARFNFSHGSHDYHQETLDNLRQAM
ANTKVMCAAMLDTKGPEIRTGTLKDGKPVQLTAGQEVTITTDYALPGDEKTIAMSYKKLAQDVKPGSQIL
CADGSIVLEVVSTDPAAGTVRARCMNSAMLGERKNVNLPGVVVDLPTLTDKDVDDLINWALPNDIDFIAA
SFVRKGSDIDTIRQVLGERGRSIKIISKVENQEGIQNFDDILAKTDSVMVARGDLGMEIPTEKIFLAQKM
MIQKCNYAGKPVITATQMLESMIKNPRPTRAEATDVANAVLDGTDCVMLSGETAAGNFPVEAVKVMTKIC
REAEASLDYYAMFKNILKQAPMPMSPLESLASSAVRTAHKVHASLIVVLTREGSTARLVAKYRPLVPVLT
VAVPVLTTDSLTWTCSGEAPARQCLVTRGLIPVLAEGSARATDSDTTDEILAAAIEHAKRARYCAKGDSI
VALHRIGNASVIKIVDIK

pyruvate,orthophosphatedikinase

>gi|397141|emb|CAA52673.1| pyruvate,orthophosphate dikinase [Entamoeba histolytica]
MQRVYAFEDGDGTNKKLLGGKGAGLCTMTKIGLPVPQGFVITTEMCKQFIANGNKMPEGLMEEVKKEYQL
VEKKSGKVFGGEENPLLVSVRSGAAMSMPGMMDTILNLGLNDKTVVALAKLTNNERFAYDSYRRFVSLFG
KIALNACDEVYDKTLENKKVEKGVKLDTELDANDMKELAQVFIKKTEEFTKQPFPVDPYAQLEFAICAVF
RSWMGKRAVDYRREFKITPEQADGTAVSVVSMVYGNMGNDSATGVCFTRDPGTGENMFFGEYLKNAQGED
VVAGIRTPQIISKMAEDRDLPGCYEQLLDIRKKLEGYFHEVQDFEFTIERKKLYMLQTRNGKMNATATVR
TGVDMVEEGLITKEQAIMRIAPQSVDQLLHKNMPANYAEAPLVKGLPASPGAATGAVVFDADDAVEQAKG
KKVLLLREETKPEDIHGFFVAEGILTCRGGKTSHAAVVARGMGKPCVSGAEGIKVDVAKKIAKIGSLEVH
EGDILTIDGSTGCVYKGEVPLEEPQVGSGYFGTILKWANEIKKIGVFAAGDLPSAAKKALEFGAEGIGLC
RTERMFNAVERLPIVVKMILSNTLEERKKYLNELMPLQKQDFIGLLKTMNGLPVTVRLLDPPLHEFLPTL
EELMREIFEMKLSGKTEGLAEKEVVLKKVKELMEVNPMIGHRGIRLGTTNPEIYEMQIRAFLEATREVIK

EGINDHREIMIPNVTEVNELINLRKNVLEPVHEEVEKKYGIKVPFSYGTMVECVRAALTADKIATEASFF
SFGTNDLTQGTFSYSREDSENKFIPKYVELKILPANPFEILDRPGVGEVMRIAVTKGRQTRPELLVGICG
EHGGEPSSIEWCHMIGLNYVSCSSYRIPVARIAAAQAQIRHPREN

40S ribosomal protein S14-A

>gi|10383793|ref|NP_009960.2| Rps14ap [Saccharomyces cerevisiae S288c]
MSNVVQARDNSQVFGVARIYASFNDTFVHVTDLSGKETIARVTGGMKVKADRDESSPYAAMLAAQDVAAK
CKEVGITAVHVKIRATGGTRTKTPGPGGQAALRALARSGLRIGRIEDVTPVPSDSTRKKGGRRGRRL

40S ribosomal protein S23

>gi|6321556|ref|NP_011633.1| Rps23ap [Saccharomyces cerevisiae S288c]
MGKGKPRGLNSARKLRVHRRNNRWAENNYKKRLLGTAFKSSPFGGSSHAKGIVLEKLGIESKQPNSAIRK
CVRVQLIKNGKKVTAFVPNDGCLNFVDENDEVLLAGFGRKGKAKGDIPGVRFKVVKVSGVSLLALWKEKK
EKPRS

40S ribosomal protein S2

>gi|6321315|ref|NP_011392.1| Rps2p [Saccharomyces cerevisiae S288c]
MSAPEAQQQKRGGFGGRNRGRPNRRGPRNTEEKGWVPVTKLGRLVKAGKITTIEEIFLHSLPVKEFQIID
TLLPGLQDEVMNIKPVQKQTRAGQRTRFKAVVVVGDSNGHVGLGIKTAKEVAGAIRAGIIIAKLSVIPIR
RGYWGTNLGQPHSLATKTTGKCGSVTVRLIPAPRGSGIVASPAVKKLLQLAGVEDVYTQSNGKTRTLENT
LKAAFVAIGNTYGFLTPNLWAEQPLPVSPLDIYSDEASAQKKRF

eukaryotic translation initiation factor 2 alpha subunit

>gi|6322466|ref|NP_012540.1| Sui2p [Saccharomyces cerevisiae S288c]
MSTSHCRFYENKYPEIDDIVMVNVQQIAEMGAYVKLLEYDNIEGMILLSELSRRRIRSIQKLIRVGKNDV
AVVLRVDKEKGYIDLSKRRVSSEDIIKCEEKYQKSKTVHSILRYCAEKFQIPLEELYKTIAWPLSRKFGH
AYEAFKLSIIDETVWEGIEPPSKDVLDELKNYISKRLTPQAVKIRADVEVSCFSYEGIDAIKDALKSAED
MSTEQMQVKVKLVAAPLYVLTTQALDKQKGIEQLESAIEKITEVITKYGGVCNITMPPKAVTATEDAELQ
ALLESKELDNRSDSEDDEDESDDE

60S ribosomal protein L2a

>gi|14318555|ref|NP_116688.1| Rpl2ap [Saccharomyces cerevisiae S288c]
MGRVIRNQRKGAGSIFTSHTRLRQGAAKLRTLDYAERHGYIRGIVKQIVHDSGRGAPLAKVVFRDPYKYR
LREEIFIANEGVHTGQFIYAGKKASLNVGNVLPLGSVPEGTIVSNVEEKPGDRGALARASGNYVIIIGHN
PDENKTRVRLPSGAKKVISSDARGVIGVIAGGGRVDKPLLKAGRAFHKYRLKRNSWPKTRGVAMNPVDHP
HGGGNHQHIGKASTISRGAVSGQKAGLIAARRTGLLRGSQKTQD

60S ribosomal protein L11-A

>gi|6325359|ref|NP_015427.1| Rpl11ap [Saccharomyces cerevisiae S288c]
MSAKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIRRNEKIAVHVT
VRGPKAEEILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSIGIFGMDFYVVMNRPGARVTR
RKRCKGTVGNSHKTTKEDTVSWFKQKYDADVLDK

60S ribosomal protein L15-A

>gi|6323057|ref|NP_013129.1| Rpl15ap [Saccharomyces cerevisiae S288c]
MGAYKYLEELQRKKQSDVLRFLQRVRVWEYRQKNVIHRAARPTRPDKARRLGYKAKQGFVIYRVRVRRGN
RKRPVPKGATYGKPTNQGVNELKYQRSLRATAEERVGRRAANLRVLNSYWVNQDSTYKYFEVILVDPQHK
AIRRDARYNWICDPVHKHREARGLTATGKKSRGINKGHKFNNTKAGRRKTWKRQNTLSLWRYRK

40S ribosomal protein S5

>gi|6322583|ref|NP_012657.1| Rps5p [Saccharomyces cerevisiae S288c]
MSDTEAPVEVQEDFEVVEEFTPVVLATPIPEEVQQAQTEIKLFNKWSFEEVEVKDASLVDYVQVRQPIFV
AHTAGRYANKRFRKAQCPIIERLTNSLMMNGRNNGKKLKAVRIIKHTLDIINVLTDQNPIQVVVDAITNT
GPREDTTRVGGGGAARRQAVDVSPLRRVNQAIALLTIGAREAAFRNIKTIAETLAEELINAAKGSSTSYA
IKKKDELERVAKSNR

Proteasome component PRE6

>gi|6324535|ref|NP_014604.1| Pre6p [Saccharomyces cerevisiae S288c]

MSGYDRALSIFSPDGHIFQVEYALEAVKRGTCAVGVKGKNCVVLGCERRSTLKLQDTRITPSKVSKIDSH
VVLSFSGLNADSRILIEKARVEAQSHRLTLEDPVTVEYLTRYVAGVQQRYTQSGGVRPFGVSTLIAGFDP
RDDEPKLYQTEPSGIYSSWSAQTIGRNSKTVREFLEKNYDRKEPPATVEECVKLTVRSLLEVVQTGAKNI
EITVVKPDSDIVALSSEEINQYVTQIEQEKQEQQEQDKKKKSNH

Meiotic recombination protein DMC1

>gi|6321027|ref|NP_011106.1| Dmc1p [Saccharomyces cerevisiae S288c]
MSVTGTEIDSDTAKNILSVDELQNYGINASDLQKLKSGGIYTVNTVLSTTRRHLCKIKGLSEVKVEKIKE
AAGKIIQVGFIPATVQLDIRQRVYSLSTGSKQLDSILGGGIMTMSITEVFGEFRCGKTQMSHTLCVTTQL
PREMGGGEGKVAYIDTEGTFRPERIKQIAEGYELDPESCLANVSYARALNSEHQMELVEQLGEELSSGDY
RLIVVDSIMANFRVDYCGRGELSERQQKLNQHLFKLNRLAEEFNVAVFLTNQVQSDPGASALFASADGRK
PIGGHVLAHASATRILLRKGRGDERVAKLQDSPDMPEKECVYVIGEKGITDSSD

Proteasomecomponent PUP2

>gi|6321692|ref|NP_011769.1| Pup2p [Saccharomyces cerevisiae S288c]
MFLTRSEYDRGVSTFSPEGRLFQVEYSLEAIKLGSTAIGIATKEGVVLGVEKRATSPLLESDSIEKIVEI
DRHIGCAMSGLTADARSMIEHARTAAVTHNLYYDEDINVESLTQSVCDLALRFGEGASGEERLMSRPFGV
ALLIAGHDADDGYQLFHAEPSGTFYRYNAKAIGSGSEGAQAELLNEWHSSLTLKEAELLVLKILKQVMEE
KLDENNAQLSCITKQDGFKIYDNEKTAELIKELKEKEAAESPEEADVEMS

Proteasome component Y13

>gi|6321574|ref|NP_011651.1| Pre9p [Saccharomyces cerevisiae S288c]
MGSRRYDSRTTIFSPEGRLYQVEYALESISHAGTAIGIMASDGIVLAAERKVTSTLLEQDTSTEKLYKLN
DKIAVAVAGLTADAEILINTARIHAQNYLKTYNEDIPVEILVRRLSDIKQGYTQHGGLRPFGVSFIYAGY
DDRYGYQLYTSNPSGNYTGWKAISVGANTSAAQTLLQMDYKDDMKVDDAIELALKTLSKTTDSSALTYDR
LEFATIRKGANDGEVYQKIFKPQEIKDILVKTGITKKDEDEEADEDMK

DNA-directed RNA polymerase II largest subunit

>gi|6320061|ref|NP_010141.1| Rpo21p [Saccharomyces cerevisiae S288c]
MVGQQYSSAPLRTVKEVQFGLFSPEEVRAISVAKIRFPETMDETQTRAKIGGLNDPRLGSIDRNLKCQTC
QEGMNECPGHFGHIDLAKPVFHVGFIAKIKKVCECVCMHCGKLLLDEHNELMRQALAIKDSKKRFAAIWT
LCKTKMVCETDVPSEDDPTQLVSRGGCGNTQPTIRKDGLKLVGSWKKDRATGDADEPELRVLSTEEILNI
FKHISVKDFTSLGFNEVFSRPEWMILTCLPVPPPPVRPSISFNESQRGEDDLTFKLADILKANISLETLE
HNGAPHHAIEEAESLLQFHVATYMDNDIAGQPQALQKSGRPVKSIRARLKGKEGRIRGNLMGKRVDFSAR
TVISGDPNLELDQVGVPKSIAKTLTYPEVVTPYNIDRLTQLVRNGPNEHPGAKYVIRDSGDRIDLRYSKR
AGDIQLQYGWKVERHIMDNDPVLFNRQPSLHKMSMMAHRVKVIPYSTFRLNLSVTSPYNADFDGDEMNLH
VPQSEETRAELSQLCAVPLQIVSPQSNKPCMGIVQDTLCGIRKLTLRDTFIELDQVLNMLYWVPDWDGVI
PTPAIIKPKPLWSGKQILSVAIPNGIHLQRFDEGTTLLSPKDNGMLIIDGQIIFGVVEKKTVGSSNGGLI
HVVTREKGPQVCAKLFGNIQKVVNFWLLHNGFSTGIGDTIADGPTMREITETIAEAKKKVLDVTKEAQAN
LLTAKHGMTLRESFEDNVVRFLNEARDKAGRLAEVNLKDLNNVKQMVMAGSKGSFINIAQMSACVGQQSV
EGKRIAFGFVDRTLPHFSKDDYSPESKGFVENSYLRGLTPQEFFFHAMGGREGLIDTAVKTAETGYIQRR
LVKALEDIMVHYDNTTRNSLGNVIQFIYGEDGMDAAHIEKQSLDTIGGSDAAFEKRYRVDLLNTDHTLDP
SLLESGSEILGDLKLQVLLDEEYKQLVKDRKFLREVFVDGEANWPLPVNIRRIIQNAQQTFHIDHTKPSD
LTIKDIVLGVKDLQENLLVLRGKNEIIQNAQRDAVTLFCCLLRSRLATRRVLQEYRLTKQAFDWVLSNIE
AQFLRSVVHPGEMVGVLAAQSIGEPATQMTLNTFHFAGVASKKVTSGVPRLKEILNVAKNMKTPSLTVYL
EPGHAADQEQAKLIRSAIEHTTLKSVTIASEIYYDPDPRSTVIPEDEEIIQLHFSLLDEEAEQSFDQQSP
WLLRLELDRAAMNDKDLTMGQVGERIKQTFKNDLFVIWSEDNDEKLIIRCRVVRPKSLDAETEAEEDHML
KKIENTMLENITLRGVENIERVVMMKYDRKVPSPTGEYVKEPEWVLETDGVNLSEVMTVPGIDPTRIYTN
SFIDIMEVLGIEAGRAALYKEVYNVIASDGSYVNYRHMALLVDVMTTQGGLTSVTRHGFNRSNTGALMRC
SFEETVEILFEAGASAELDDCRGVSENVILGQMAPIGTGAFDVMIDEESLVKYMPEQKITEIEDGQDGGV
TPYSNESGLVNADLDVKDELMFSPLVDSGSNDAMAGGFTAYGGADYGEATSPFGAYGEAPTSPGFGVSSP
GFSPTSPTYSPTSPAYSPTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSP
SYSPTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPAYSPTSPSYSPTSPSYSPTSP
SYSPTSPSYSPTSPNYSPTSPSYSPTSPGYSPGSPAYSPKQDEQKHNENENSR

T-complex protein 1 subunit gamma

>gi|6322446|ref|NP_012520.1| Cct3p [Saccharomyces cerevisiae S288c]
MQAPVVFMNASQERTTGRQAQISNITAAKAVADVIRTCLGPKAMLKMLLDPMGGLVLTNDGHAILREIDV
AHPAAKSMLELSRTQDEEVGDGTTTVIILAGEILAQCAPYLIEKNIHPVIIIQALKKALTDALEVIKQVS
KPVDVENDAAMKKLIQASIGTKYVIHWSEKMCELALDAVKTVRKDLGQTVEGEPNFEIDIKRYVRVEKIP
GGDVLDSRVLKGVLLNKDVVHPKMSRHIENPRVVLLDCPLEYKKGESQTNIEIEKEEDWNRILQIEEEQV
QLMCEQILAVRPTLVITEKGVSDLAQHYLLKGGCSVLRRVKKSDNNRIARVTGATIVNRVEDLKESDVGT

NCGLFKVEMIGDEYFSFLDNCKEPKACTIMLRGGSKDILNEIDRNLQDAMAVARNVMLSPSLSPGGGATE
MAVSVKLAEKAKQLEGIQQWPYQAVADAMECIPRTLIQNAGGDPIRLLSQLRAKHAQGNFTTGIDGDKGK
IVDMVSYGIWEPEVIKQQSVKTAIESACLLLRVDDIVSGVRKQE

centromere/microtubule binding factor 5

>gi|6323204|ref|NP_013276.1| Cbf5p [Saccharomyces cerevisiae S288c]
MSKEDFVIKPEAAGASTDTSEWPLLLKNFDKLLVRSGHYTPIPAGSSPLKRDLKSYISSGVINLDKPSNP
SSHEVVAWIKRILRCEKTGHSGTLDPKVTGCLIVCIDRATRLVKSQQGAGKEYVCIVRLHDALKDEKDLG
RSLENLTGALFQRPPLISAVKRQLRVRTIYESNLIEFDNKRNLGVFWASCEAGTYMRTLCVHLGMLLGVG
GHMQELRRVRSGALSENDNMVTLHDVMDAQWVYDNTRDESYLRSIIQPLETLLVGYKRIVVKDSAVNAVC
YGAKLMIPGLLRYEEGIELYDEIVLITTKGEAIAVAIAQMSTVDLASCDHGVVASVKRCIMERDLYPRRW
GLGPVAQKKKQMKADGKLDKYGRVNENTPEQWKKEYVPLDNAEQSTSSSQETKETEEEPKKAKEDSLIKE
VETEKEEVKEDDSKKEKKEKKDKKEKKEKKEKKDKKEKKEKKEKKRKSEDGDSEEKKSKKSKK

Proteasome component Y7

>gi|6323547|ref|NP_013618.1| Pre8p [Saccharomyces cerevisiae S288c]
MTDRYSFSLTTFSPSGKLGQIDYALTAVKQGVTSLGIKATNGVVIATEKKSSSPLAMSETLSKVSLLTPD
IGAVYSGMGPDYRVLVDKSRKVAHTSYKRIYGEYPPTKLLVSEVAKIMQEATQSGGVRPFGVSLLIAGHD
EFNGFSLYQVDPSGSYFPWKATAIGKGSVAAKTFLEKRWNDELELEDAIHIALLTLKESVEGEFNGDTIE
LAIIGDENPDLLGYTGIPTDKGPRFRKLTSQEINDRLEAL

T-complex protein 1 subunit epsilon

>gi|6322524|ref|NP_012598.1| Cct5p [Saccharomyces cerevisiae S288c]
MAARPQQPPMEMPDLSNAIVAQDEMGRPFIIVKDQGNKKRQHGLEAKKSHILAARSVASIIKTSLGPRGL
DKILISPDGEITITNDGATILSQMELDNEIAKLLVQLSKSQDDEIGDGTTGVVVLASALLDQALELIQKG
IHPIKIANGFDEAAKLAISKLEETCDDISASNDELFRDFLLRAAKTSLGSKIVSKDHDRFAEMAVEAVIN
VMDKDRKDVDFDLIKMQGRVGGSISDSKLINGVILDKDFSHPQMPKCVLPKEGSDGVKLAILTCPFEPPK
PKTKHKLDISSVEEYQKLQTYEQDKFKEMIDDVKKAGADVVICQWGFDDEANHLLLQNDLPAVRWVGGQE
LEHIAISTNGRIVPRFQDLSKDKLGTCSRIYEQEFGTTKDRMLIIEQSKETKTVTCFVRGSNKMIVDEAE
RALHDSLCVVRNLVKDSRVVYGGGAAEVTMSLAVSEEADKQRGIDQYAFRGFAQALDTIPMTLAENSGLD
PIGTLSTLKSKQLKEKISNIGVDCLGYGSNDMKELFVVDPFIGKKQQILLATQLCRMILKIDNVIISGKD
EY

T-complex protein 1 subunit delta

>gi|6320058|ref|NP_010138.1| Cct4p [Saccharomyces cerevisiae S288c]
MSAKVPSNATFKNKEKPQEVRKANIIAARSVADAIRTSLGPKGMDKMIKTSRGEIIISNDGHTILKQMAI
LHPVARMLVEVSAAQDSEAGDGTTSVVILTGALLGAAERLLNKGIHPTIIADSFQSAAKRSVDILLEMCH
KVSLSDREQLVRAASTSLSSKIVSQYSSFLAPLAVDSVLKISDENSKNVDLNDIRLVKKVGGTIDDTEMI
DGVVLTQTAIKSAGGPTRKEKAKIGLIQFQISPPKPDTENNIIVNDYRQMDKILKEERAYLLNICKKIKK
AKCNVLLIQKSILRDAVNDLALHFLSKLNIMVVKDIEREEIEFLSKGLGCKPIADIELFTEDRLGSADLV
EEIDSDGSKIVRVTGIRNNNARPTVSVVIRGANNMIIDETERSLHDALCVIRCLVKERGLIAGGGAPEIE
ISRRLSKEARSMEGVQAFIWQEFASALEVIPTTLAENAGLNSIKVVTELRSKHENGELNDGISVRRSGTT
NTYEEHILQPVLVSTSAITLASECVKSILRIDDIAFSR

60S ribosomal protein L4-A

>gi|6320215|ref|NP_010295.1| Rpl4bp [Saccharomyces cerevisiae S288c]
MSRPQVTVHSLTGEATANALPLPAVFSAPIRPDIVHTVFTSVNKNKRQAYAVSEKAGHQTSAESWGTGRA
VARIPRVGGGGTGRSGQGAFGNMCRGGRMFAPTKTWRKWNVKVNHNEKRYATASAIAATAVASLVLARGH
RVEKIPEIPLVVSTDLESIQKTKEAVAALKAVGAHSDLLKVLKSKKLRAGKGKYRNRRWTQRRGPLVVYA
EDNGIVKALRNVPGVETANVASLNLLQLAPGAHLGRFVIWTEAAFTKLDQVWGSETVASSKVGYTLPSHI
ISTSDVTRIINSSEIQSAIRPAGQATQKRTHVLKKNPLKNKQVLLRLNPYAKVFAAEKLGSKKAEKTGTK
PAAVFAETLKHD

T-complex protein 1 subunit eta

>gi|6322350|ref|NP_012424.1| Cct7p [Saccharomyces cerevisiae S288c]
MNFGSQTPTIVVLKEGTDASQGKGQIISNINACVAVQEALKPTLGPLGSDILIVTSNQKTTISNDGATIL
KLLDVVHPAAKTLVDISRAQDAEVGDGTTSVTILAGELMKEAKPFLEEGISSHLIMKGYRKAVSLAVEKI
NELAVDITSEKSSGRELLERCARTAMSSKLIHNNADFFVKMCVDAVLSLDRNDLDDKLIGIKKIPGGAME
ESLFINGVAFKKTFSYAGFEQQPKKFNNPKILSLNVELELKAEKDNAEVRVEHVEDYQAIVDAEWQLIFE
KLRQVEETGANIVLSKLPIGDLATQFFADRNIFCAGRVSADDMNRVIQAVGGSIQSTTSDIKPEHLGTCA
LFEEMQIGSERYNLFQGCPQAKTCTLLLRGGAEQVIAEVERSLHDAIMIVKRALQNKLIVAGGGATEMEV

SKCLRDYSKTIAGKQQMIINAFAKALEVIPRQLCENAGFDAIEILNKLRLAHSKGEKWYGVVFETENIGD
NFAKFVWEPALVKINALNSATEATNLILSVDETITNKGSESANAGMMPPQGAGRGRGMPM

Supplementary Table ##:
Template protein sequences to search for homologs in Fig. 19. Sequences were downloaded from NCBI July to October 2011.