Additional file 6. Alignment of KCTD1, KCTD15 and related protein sequences in fasta format.

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>KCTD1a_Human
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------------------------------------------------------------------------------------------------------------------------
----------------------------------------------------------------MSRP----LITRS---PASPLNNQGIPTPAQLTKSNAPVHIDVGGHMYTSSLATLTKY
PESRIGRLFDGTEPIVLDSLKQHYFIDRDGQMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYFQLQPMLLEMERWKQDRETGRF
SR-------P---------------CECLVVRVAPDLGERITLSGDKSLIEEVF-PEIGDVMCNS--VNAGWNH-DSTHVIRFPLNGYCHLNSVQVLER
LQQRGFEIVGSCGGGVD-SSQFSEYVLRRELRR----TPRV--PSVIRIKQEPL-D
>KCTD1b_Human
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GGGGL--EEDEEEEEEEEMGLDWDEPLEPEDSAGEELEPEPVHMINMDQSAALEPEAPPRLLAPRARGGPPGDGSELDPDVL-----
---------------QRPERARLSENTRLATRYAVRIFREYLSEKAQSPDFETMDKGALCRVLRSFYAEARSKSGQLYSKSSLISIRSSLNRYLN
EPPYCRTLDLTKDPELRSANLTLAAVIRKLEEQGAGPVVQKQAITRADLRKLYTSSVFSTNTPFGLLNKVWFETCMYFCTRGREN
QRELEEDSFGLAMDEDGRKFVYFKSLG-----PYHKSRSSSWSKKRA------ESS---DEENLPRMYETGTEFCPYASFVKYLSKRNPLC
KAFFQRPRDHCSEGDVTWYENKAIGKN--LLGTRMQMLSKAAKLSKTYTNHCIGAVSIATLNSIAG-IGTK------LGS--PAPQGCYA-
EALNGA-----ARHHS-HHPPTHPSHHH--------RPQPP-------------SLGNTYILPKDSQVGPDVKSEAA----PKRALYESVF-----GSGEICG
PT-SPKRLCIRP-SEPVD----AVVVVSVKHDPLP-LLPEANGHRS-TNSPTIVSPAIVSPT----QD------------------------------------------
----------------------SRPN----MSRP----LITRS---PASPLNNQGIPTPAQLTKSNAPVHIDVGGHMYTSSLATLTKYPESRIGRLFDGTEPIV
LDSLKQHYFIDRDGQMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYFQLQPMLLEMERWKQDRETGRFSR-------P---------------CE
CLVVRVAPDLGERITLSGDKSLIEEVF-PEIGDVMCNS--VNAGWNH-DSTHVIRFPLNGYCHLNSVQVLERLQQRGFEIVGSCGGG
VD-SSQFSEYVLRRELRR----TPRV--PSVIRIKQEPL-D
>KCTD1b_Mouse
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GGL--EEDEEEEEEEEMGMDWEEPLEPEDSAGEELEPEPVHMIHMDQSAALEPEAPPRLLAPRARAGPPGDSAELDPDVL---------
------------QRPERARLSENTRLATRYAVRIFREYLSEKAQSPDFETMDKGALCRVLRSFYAEARSKSGQLYSKSSLISIRSSLNRYLNEP
PYCRTLDLTKDPELRSANLTLAAVIRKLEEQGAGPVVQKQAITRADLRKLYTSSVFSTNTPFGLLNKVWFETCMYFCTRGRENQR
ELEEDSFGLAMDEDGRKFVYFKSLG-----PYHKSRSSSWSKKRA------ESS---DEENLPRMYETGTEFCPYASFVKYLSKRNPLCKAF
FQRPRDHCSEGDVTWYENKAIGKN--LLGTRMQMLSKAAKLSKTYTNHCIGAVSIATLNSIAG-IGTK------LGS--PAPQGCYT-DSLN
GS-----ARHHS-HHAPTHPSHHH--------RPQPP-------------SLGNTYILPKDSQVGPDVKSEAA----PKRTLYESVF-----GSGEICGPS-SP
KRLCIRPSSEPVD----AVVVVSVKHDPLP-LLPEVNGHRS-TNSPTIVSPAIVSPA----QD------------------------------------------
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VRVAPDLGERITLSGDKSLIEEVF-PEIGDVMCNS--VNAGWNH-DSTHVIRFPLNGYCHLNSVQVLERLQQRGFEIVGSCGGGVD-
SSQFSEYVLRRELRR----TPRV--PSVIRIKQEPL-D
>KCTD1b_Dog
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LLNKVWFETCMYFCTRGRENQRELEEDSFGLAMDEDGRKFVYFKSLG-----PYHKSRSSSWSKKRA------ESS---DEENLPRMYET
GTEFCPYASFVKYLSKRNPLCKAFFQRPRDHCSEGDVTWYENKAIGKN--LLGTRMQMLSKAAKLSKTYTNHCIGAVSIATLNSIA
G-IGTK------LGS--PAPQGCYA-EALNGA-----ARHHSHHHPPTHPSHHH--------RPQPP-------------SLGNTYILPKDSQVGPDVKSEAA
----PKRALYESVF-----GSGDICGPS-SPKRLCIRP-SEPVD----AVVVVSVKHDPLP-LLPEANGHRS-TNSPTVVSPAIVSPT----QD---------
------------------------------------------------------------SRPN----MSRP----LITRS---PASPLNNQGIPTPAQLTKSNAPVHIDVGGHMYTSS
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RETGRFSR-------P---------------CECLVVRVAPDLGERITLSGDKSLIEEVF-PEIGDVMCNS--VNAGWNH-DSTHVIRFPLNGYCHLNS
VQVLERLQQRGFEIVGSCGGGVD-SSQFSEYVLRRELRR----TPRV--PSVIRIKQEPL-D
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EEDGGGGLEEEEEEEEEEEEEMGLDWDEPLEPEYSAGEELEPEPVHMIHMDQSTELDPESEPLLLAPRS---GPAEDPELDPDLL-
-------------------QRPERARLSENTRLATRYAVRIFREYLSEKSQSPDFETMDKGALCRVLRSFYAEARSKSGQLYSKSSLISIRSSLNRY
LNEPPYCRTLDLTKDPELRSANLTLAAVIRKLEEQGAGPVVQKQAITRADLRKLYTSSVFSTNTPFGLLNKVWFETCMYFCTRGR
ENQRELEEDSFGLAMDEDGRKFVYFKSLG-----PYHKSRSSSWSKKRA------ESS---DEENLPRMYETGTEFCPYASFVKYLSKRNP
LCKAFFQRPRDHCNEGDVTWYENKAIGKN--LLGTRMQMLSKAAKLSKTYTNHCIGAVSIATLNSIAG-IGTK------LGP--PAPQGCY
A-EALNGG-----ARHHHHHHHPSTPHHHH--------RPQPP-------------SLGNTYILPKESQVVADVKAEAA----PKRALYEAVF-----GPGE
VCGPS-SPKRLCIRP-SEPVDAA--AVVVVSVKHDPLP-LLPEVNGHRS-TNSPTVVSPAIVSPT----QD------------------------------------
--------------------------------SRPN----MSRP----LITRS---PASPLNNQGIPTPAQLTKSNAPVHIDVGGHMYTSSLATLTKYPESRIGRLFD
GTEPIVLDSLKQHYFIDRDGQMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYFQLQPMLLEMERWKQDRENGRFSR-------P--------
---------CECLVVRVAPDLGERITLSGDKSLIEEVF-PEIGDVMCNS--VNAGWNH-DSTHVIRFPLNGYCHLNSVQVLERLQQRGFEIV
GSCGGGVD-SSQFSEYVLRRELRR----TSRA--PSVIRIKQEPL-D
>KCTD1b_Platypus partial
------------------------------------------------------------------------------------------------------------------------
----------------ENTRLATRYAVRIFREYLSEKAHSPDFEAMDKGALCRVLRSFYAEARSKSGQLYSKSSLISIRSSLNRYLNEPPYCRTL
DLTKDPELRSANLALAAVLRRLEEQGAGPVVQKQAITRADLRRLYTSAVLGAATPFGLLNKVWFETCMYFCTRGRENQRELEEDS
FGLAVDEDGRRFVYFKALG-----PYHKSRSPGWARKRA------EAAGGGDDDSLPRMYETGTELCPYASFVKYLAKRNPLCRAFFQRP
RDHCAHGDGTWYENKAIGKN--LLGTRMQMLSKAAKLSKTYTNHCIGAVSVATLNSIAG-IGAR------LGPQAP-------------------------
------------------------------------------------------------------------------APQ-------------------------------------APAPQAPAPQAPAPL---PHD------
------------------------------------------------------------------SRPN----MSRP----LITRS---PASPLNNQGIPTPAQLTKSNAPVHIDVGGHMYT
SSLATLTKYPESRIGRLFDGTEPIVLDSLKQHYFIDRDGQMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYFQLQPMLMEMERWL
QERESGRFSR-------P---------------CECLVVRVAPDLGERITLSGDKSL-EEVF-PEIGDVMCNS--VNAGWNH-DSTHVIRFPLNGYCHL
NSVQVLERLQQRGFAIVGSCGGGVD-SSQFSEYVLRRELRR----TSRG--PSVIRIKQEPL-D
>KCTD1b_Chicken partial
------------------------------------------------------------------------------------------------------------------------
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```

AAVIRKLEEQGAGPVVQKQAITRADLRKLYTCSVFSTQSPFGLLNKVWFETCMYFCTRGRENQRELEEDSFGLAVDEDGRKFVYF
KALG-----PYHKSRSSSWSKKRA------ESS---DEENLPRMYETGTEFCPYASFVKYLSKRNPLCKAFFQRPRDHCSEGDVTWYENKA
IGKN--LLGTRMQMLSKAAKLSKTYTNHCIGAVSIATLNSIAG-IGTK-----LGG--PPPPPHHH-PAPHHH-----HHHHHLLHHPAGGA
CYASAALNGGPRPRPP----------A-ANPYVLPKDGDAAP-VKAEAAAVAPAKRALYEAVFPAGAAAGGEACGPSASPKRLCRRP-AE
PPNAA--AV----------PAVVV----------V----MSRP----LITRS---P
ASPLNNQGIPTPAQLTKSNAPVHIDVGGHMYTSSLATLTKYPDSRIGRLFDGTEPIVLDSLKQHYFIDRDGQMFRYILNFLRTSKLL
IPDDFKDYSLLYEEAKYFQLQPMLGEMERWKQDRESGRFSK-------S----------CECLVVRVAPDLGERITLSGDKSLIEEVF-PEI
GDVMCNS--VNAGWNH-DSTHVIRFPLNGYCHLNSVQVLERLQQRGFEIVGSCGGGVD-SSQFSEYVLRRELRR----TSRA--PSVIRI
KQEPL-D
>KCTD1b_Zebrafinch
MAAV----------LI----------PHTPLARGTEETYV----------PSWPQTKPRTPYCRTLDFTKDPELRAANLTLAAVIRKL
EEQGAGPVVQKQAITRADLRKLYTCSVFSTQSPFGLLNKVWFETCMYFCTRGRENQRELEEDSFGLAVDEDGRKFVYFKALG-----
PYHKSRSSSWSKKRA------ESS---DEENLPRMYETGTEFCPYASFVKYLSKRNPLCKAFFQRPRDHCSEGDITWYENKAIGKN--LL
GTRMQMLSKAAKLSKTYTNHCIGAVSIATLNSIAG-IGTK-----LGGLHPAGGGCYTPAALNGG-----P----------RPWPP----------A-ANPYMLPKDGDAAP-VKAEAAAVAPAKRALYEAVFPAGAAAGGDACGPSASPKRLCRRP-AEPLDAAAPAVVVVSVKHDPL
PHLLPEANGHRS-TTSPTVVSPAIVSPT----QD----------SRPN----MSRP----LITRS---
PASPLNNQGIPTPAQLTKSNAPVHIDVGGHMYTSSLATLTKYPDSRIGRLFDGTEPIVLDSLKQHYFIDRDGQMFRYILNFLRTSKL
LIPDDFKDYSLLYEEAKYFQLQPMLGEMERWKQDRESGRFSK-------S----------CECLVVRVAPDLGERITLSGDKSLIEEVF-PEI
GDVMCNS--VNAGWNH-DSTHVIRFPLNGYCHLNSVQVLERLQQRGFEIVGSCGGGVD-SSQFSEYVLRRELRR----TSRA--PSVIRI
KQEPL-D
>KCTD1b_Lizard partial

----------QD----------
----------SRPN----MSRP----LITRS---PASPLNNQGIPTPAQLTKSNAPVHIDVGGHMYTSSLAT
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TGRFSK-------S----------CECLVVRVAPDLGERITLSGDKSLIEEVF-PEIGDVMCNS--VNAGWNH-DSTHVIRFPLNGYCHLNSV
QVLERLQQRGFEIVGSCGGGVD-SSQFSEYVLRRELRR----TSRS--SSVIRIKQEPL-D
>KCTD1b_Frog
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DEDDLEDDMQLEWDP------EEGALLEPPYPH-------TPCHPAQRPALPA-----GPRSAMVLGEDVLLQLGSAGGGGDGGGGCVGSPS
ERPERARLSENTRLATRYAVRIFREYLSEKSQSPDFESMDKEALCRVLRSFYTEARSKSGQLYSKSSLISIRSSLNRYLNEPPYCRTL
DLTKDPELRSANLTLAAVIRKLEEQGAGPVVQKQAITRADLRKLYTSCVFSSSTPFGLLNKVWFETCMYFCTRGRENQRELEEDS
FGLAMDEDGRRFVYFKALG-----PYHKSRSSSWGKKRSCPGGSTMES---DEENLPRMYETGTEFCPYASFVKYLSKRNPLCKAFFQ
RPRDHGSESDVTWYENKAIGKN--LLGTRMQMLSKAAKLSKTYTNHCIGAVSVATLNSIAG-IGTK-----LGP--P-----YLTDSLNGS----RH----------RPAMP----------GNTFILPKPTGGLSEAKTET-----TKRSIYNSAHSIY--ASGDMGSPP-SPKRLCIRP-ADPSD----CVHVVSVKSDPQP-SCPETNGHMVLAASPAVTSPSVMSPVQVTKQD----------T
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DGQMFRYILNFLRTSKLLISDDFKDYSLLYEEAKYFQLQPMLLELERWKQDKEAGRFSR-------P----------CECLVVRVAPDLGE
RITLSGDKSLIEEVF-PEIGDVMCNS--VNAGWNH-DSTHVIRFPLNGYCHLNSVQVLERLQHRGFEIVGSCGGGVD-SSQFSEYVLR
RELKR----TSRA--SSVIRIKQEPL-D
>KCTD1b_Zebrafish
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GEPDSCAAAVETGEAVLMRNTDQLESV----------AEGDLLFGPEGDMHRSRLSENTRLATRYAVRIFREYLTE
KAQSTDFESMDKHALCKVLRSFYSEARSKSGQLYSKSSLISIRSSLNRYLNEPPFCRTLDLTKDPELRSANLALAAVIRKLEEQGA
GPVVQKQAITRSDLRKLYTSAVFSASSPFGLLNKVWFETCMYFCTRGRENQRELEEDSFGLAVDEDGRKFVYFKALG-----PYHKS
RSASWTKKRS------DT----DDDNLPRMYETATEFCPYASFVKYLSKRNPLCKAFFQRPRDHCSDTDTTWYENKAIGKN--LLGTRMQ
MLSRAAKLSKTYTNHCIGAVSIATLNGIAG-IGSK-----LAPL----------RASPE----------TVNGAHVLHCE
DELELKPQKQVTKR--PRTLVYPV---------SVAGPGASPKRQCARA-DTPT-----VTARVSSRCEP----------GESPH------MLPS----QE----
----------NRSNSVGMSTRP----ILAHS---PVSPLGTAGIPTPAQLTKANAPVHIDVGGH
MYTSSLATLTKYPESRIGRLFDGTEPIVLDSLKQHYFIDRDGHMFRYILNFLRTSKLLIPDDFKDYSLLYEEARYFQLQPLQVELER
WRSEQDSRFTSR-------M----------CECVVVRVAPELGERITLSGDKALIEDIF-PEIGDVMCNS--VNAGWNH-DSTHVIRFPLNGY
CHLNSVQVLERLQQRGFEIAASCGGGVD-STQFSEYVLRREVKR----SHRGVMTSVIRIKQEPL-D
>KCTD1b_Stickleback
MARMPASGDAGRDQMSCPKRHA----------EGDNEGEDEDEIHEVQITGEEEDEESD----------GDGVDLEWK
SRGYVLGSCSSAAQMRAVVMPSMDREEEG----------EADPFSGGGSGGLESHLEGDLQRSERNKLSENTRLATRYAV
RIFREYLGEKSQSPDFETLDKETLCAVLRSFYAEARSKSGQLYSKSSLISIRSSLNRYLNEPPYCRTLDLTKDPELRSANLTLAAVIR
RLEEQGAGPVVQKQAITRSDLRKLYESSVFHADTPFGLLNKVWFETCMYFCTRGRENQRELEEDSFGLAVDEDGRNFVYFKALG
-----PYHKSRSAAWSKKRPDP---------DEDTLPRMYETRSEQCPYASFVRYVSKRNPLCRAFFQRPRDHCSATDVAWYENKAIGKN--
LLGTRMQMLSRAAKLSKTYTNHCIGAVSIATLNSIVGAAGSTTSTTLYVATETVNGHAQSNLPYLSRVADLKPAATTTVNTSSSTTT
TTTNKVIADEDPGAPH----------AKRLCVRP-GTHAESL----------IERDQSEKGPAAA
TESPMHTHPV-----T----------ARTQDSCVSSQQ----QVSVS---IVSHLGTAGIPLPAQ
LTKTNAPVHIDVGGHMYTSSLATLTKYPESRIGRLFEGTEPIVLDSLKQHYFIDRDGPMFRYILNFLRSSKLLIPDDFKEYSLLYEE
ASFFQLNSLQAALERWQTEQKCGKASL-------A----------CECVVVHVAPELGERISVSADRALIKDVF-PEVRGVIFNS--QNTSGN
Q-ESSHVIRFPLNGHCHFNSVQVLERLQQRGFWITGSCGGGVD-SSQFSEYILRRESQE----SRHP--PTLIRIKQEFQ-N
>KCTD1b_Medaka_Hd-rR
MARMDGGRTAAQEEQRSPEG----------GGGPEEVQRVQNSGDEEESD----------YDAEDWLWGSETT
VLDSSGSARQTRAVVMRSTERGPSEGNLEPHRCITP----------PGVDDKFRRGRLSENTRLATRYAVRIFREFLRDT
AQSPDFETLDKHALCARLRSFYVEARSKSGQVYSRSSLISIRSSLNRYLNEPPHSRTLDLTKDPEMRSANLVLAAVIRRLEEQGAG
PVVQKQAITRADLKKLYESSVFDTGTAYGLLNKVWFETCMYFCTRGRENQRELHEDSFGLAVDRNGRKFVFFKALGPNPRSPSH
GTRYVAWTRRHLDP---------QEASLPRMYETGTELCPYASFARFRSKRNPLCAAFFQRPRDQCSVSDVTWYENKAIGKN--LLGMR
MQMLSRAAKLSKTYTNHCIGAVSIATLNSIVGNRGYR-----CAAETVKGHAKSMMQRVRRV-----SASLLLHPLSSSSSASRRRCQVG
QNGASPPAKKLRVHTQPDDVTSAKESHMTHMGEQVILQTCRQQNRKNDMGAEIRGGGDRA----------
VPRGQRASCAGSRSTAPALFLPVLARCSSRLFASIYLSRNNPRPRPISYQRLSRDGGNGYHGLNASESEEAPASGQFCGRVRARVP
QTAADAGSGVQGARADVCGQRRASPRSIPEAERPLGEFLSYRSHAGSVSPLSNQGIPAPAQLTKSNAPVHIDVGGHMYTSSLATLT
KFPESRIGRLFDGTEPIVLDSLKQHYFIDRDGHMFRYILNFLRTSKLLIPEDFKDYSLLYEEARYFQLQPMLAELERWRQDQELGR
VSR-------P----------CECLVVRVAPDLGERITLSGDKALIEDVF-PEIGDVMCNS--VNAGWNH-DSTHVIRFPLNGYCHLNSVQR---
----------SC----------V
>KCTD1b_Medaka_HNI partial

----------RENQR
ELHEDSFGWAVDRNGRKFVFFKALGPNPRSPNHGTRGAAWTRRHLDP----------QEASLPRMYETGTELCPYASFVRFRSKRNPLC
AAFFQRPRDHCSASDVTWYENKAIGKN--LLGMRMQMLSRAAKLSKTYTNHCIGAVSIATLNSIVGNRGYR------CAAETVKGHAK
SMMQRVRRV-----SASLLLHPLSSSFSASRRRCQAGQNGASPPAKKLRVNTQPDDVTSAKESHMTH----------
----------MGEQ----DSSKI---PS
TSPNSTGIPQVAQLTKSNAPVHIDVGGHMYTSSLATLTRYPDSRIARLFNGTEPVVLDSLKQHYFIDRDGPMFRYILNFLRTSKLLV
PEDFREYCLLYEEAVFFQLAPLLKELERWKAEQESPSGCR-------Q----------CDCALVHVAPGLGEKVGVSACRSVIDEVI-PEV----
TMP--LSAGWTP-DCTHLSRFPLGSRCRLSSVQVSQTSIN-------ACPDLSD--PQVQAFLFQ----------S
>KCTD1b_Pufferfish
MARMAGSGAAKEQVSWPQRT----------CTEELHEDQEDIQEVQISGEEEDEESDTGGV----------EPGRE
ARRASLEPGETRAVVMRSTDRGEEG----------GEEGYPLEEEPQRPERNQLSENTRLATRYAVRIFREFLSETA
QSPHFETLDKDALCALLRSFYAEARSKSGQLYSKSSLISIRSSLNRYLNEPPYCRTLDLSKDPQLRSANLALAAVLRRLEEQGAAPV
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ALGTRRRPDA----------EEEPWPRMYETGTRLCPYASFLRYLAKRNRSCRAFFQRPRERSSAGDLTWYENKAIGKN--LLGTRMQML
SRSAKLSKTYTNHCIGAVSIATLNCLLGAADGR-----AATLEKVKGQKASPLRPERR----------GPEDPSGPPRAKKRCVR
AG----------
----------SAAEGLGRGEERPGAAG----------GGHAQEEPPG----------PCPGQE
FSLLYEEACFFQHTPLQSQLQRWRRQRGCRSSWP----------ECLLVHAAPELGEEVSVSAQRAVIQEVF-PEVGDLLRPA--
MNSCRNP-ESTHVSRFPLSSCCGLSWVQVLERLQRSGFCITCSCGGGVD-SSQFTEYFLQRE----------
>KCTD1b_Shark partial

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LDLTKDPELRSANLTLAAVIRRLEEQGAGPVIQKQAITR----------
----------CKAFFQRPRDHCNESDVTWYENKAIGKN--LLGTRMQMLSKAAKLSKTYTNHCIGAVSIATLSSIAGIQNHQ--
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----------GEIIGVKVETAMTPTLYEPVYSDDTCRP--------PSQKRLCVR--
------PSDCQVLERLQQKGFEIVGSCGGGVD-SSQFSEYVLRRQIRR----LCRV--PPVIRIKQEPL-D
>KCTD1_Lamprey partial

----------IGRLFDGTEPIVLDSLKQHYFIDRD
GQMFRYILNFLRTSKLLIPDDFK----------

>KCTD15_Human
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-S----------TGTAEGGNMSRL----SLTRS---PVSPLAAQGIPLPAQLTKSNAPVHIDV
GGHMYTSSLATLTKYPDSRISRLFNGTEPIVLDSLKQHYFIDRDGEIFRYVLSFLRTSKLLLPDDFKDFSLLYEEARYYQLQPMVRE
LERWQQEQEQRRRSR-------A----------CDCLVVRVTPDLGERIALSGEKALIEEVF-PETGDVMCNS--VNAGWNQ-DPTHVIRFPL
NGYCRLNSVQVLERLFQRGFSVAASCGGGVD-SSQFSEYVLCREERR----PQPT--PTAVRIKQEPL-D
>KCTD15_Mouse
MPHRKERPSGSSLNAHG----------

-S----------SGTAEGGNMSRL----SLTRS---PVSPLAAQGIPLPAQLTKANAPVHIDV
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LERWQQDQEQRRRSR-------A----------CDCLVVRVTPDLGERIALSGEKALIEEVF-PETGDVMCNS--VNAGWNQ-DPTHVIRFP
LNGYCRLNSVQVLERLFQRGFSVAASCGGGVD-SSQFSEYVLCREERR----PQPT--PTAVRIKQEPL-D
>KCTD15_Dog
MPHRKERPSGSSLHAHG----------

-S----------AGTAEGGSMSRL----SLTRS---PVSPLAAQGIPLPAQLTKSNAPVHIDV
GGHMYTSSLATLTKYPDSRISRLFNGTEPIVLDSLKQHYFIDRDGEIFRYVLSFLRTSKLLLPDDFKDFSLLYEEARYYQLQPMVRE
LERWQQEQEQRRRSR-------A----------CDCLVVRVTPDLGERIALSGEKALIEEVF-PETGDVMCNS--VNAGWNQ-DPTHVIRFPL
NGYCRLNSVQVLERLFQRGFSVAASCGGGVD-SSQISEYVLCREERR----PQPT--PTAVRIKQEPL-D
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NAGWNQ-DPTHVIRFPLNGYCRLNSVQV----------
>KCTD15_Chicken

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PDSRISRLFNGTEPIVLDSLKQHYFIDRDGEIFRYILSFLRTSKLLLPEDFKDFNLLYEEAKYYQLQPMIKELERWKQEKEQRKHF
Q-------P----------CDCLVVRVTPDLGERIALSGEKALIEEIF-PETGDVMCNS--VNAGWNQ-DPTHVIRFPLNGYCRLNSVQVLER
LFQKGFNMAASCGGGVD-SSQFSEYVLCREDRR----PQPT--PT-IRIKQEPL-D
>KCTD15_Frog

----------MSRL----SLTRS---PVSPLAAQGIPLPAQLTKSNAPVHIDVGGHMYTSSLATLTKY
PDSRISRLFNGTEPIVLDSLKQHYFIDRDGEIFRYILSFLRTSKLLLPEDFKEFNLLYEEAKYYQLHPMVKELERWKQDKEHRKHF
Q-------P----------CDCLVVRVTPDLGERIALSGEKALIEEIF-PETGDVMCNS--VNAGWNQ-DPTHVIRFPLNGYCRLNSVQVLER
MFQKGFHVAASCGGGVD-SSQFSEYVLCREDRR----MQPN---T-MRIKQEPL-D
>KCTD15_Zebrafish

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PDSRISRLFNGTEPIVLDSLKQHYFIDRDGEIFRYILSFLRTCKLLLPDDFKDFNLLYEEARYYQLSPMIKELERWKQEREQRRLAN
-------P----------CDCLVVRVTPDLGERIALSGEKVLIEEIF-PETGDVMCNS--VNAGWNQ-DPTHVIRFPLNGYCRLNSVQVLERLF
QKGFNVAASCGGGVD-SSQFSEYVLCREDRR----SHNT--NTPIRIKQEPL-D
>KCTD15_Shark partial

----------D
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>SeaSquirt XP_002123395
MKR----------
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SNLALPDDFHELDQLLQEARFFELKLMVGQLEQFKESRRVSKTHK----------DCVVIRTVPDLGERICLGGNKSIIASIF-P
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>SeaUrchin XP_785600
MS----------
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----------VTTPRANS----------
----------VTPPPTSTGIT----------
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Q-DSNYVIRFPLNGFCKMNTVQVLQRLLQNNFGVIASSGGGIE-GSQFSEYVLSRKYGQ----------LT
>FruitFly CG10440
M----------

----------DRERERDVKALEPRDLSSTGRIYARSDIKISSSPTVSPTISNS---
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MERDRDRDR----------
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PTISNS----------SSPTPTPPIP----------AVSPAVTGVG----------
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F-PETNQAILDAR-TGAAWNQFDGRQVIRFPLNGYCKLNSIQVLTRLLNAGFSVEASTGGGVE-TQQFSEYLLIRKSAM----------
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