

NKD2

Homo sapiens:

>NP_149111.1 protein naked cuticle homolog 2 isoform 1 [Homo sapiens]
MGKIQSKHAAARKR**RESPEGDS**FVASAYASGRKGAEAEARRARDKQELPNGDPKEGPFREDQCPLQVAL
PAEKAEGREHPGQLLSADDGERAANREGPRGPGGQRLNIDALQCDVSVEEDDRQEWTFITLYDFDNCCKVT
REDMSSLMHTIYEVVDASVNHSSGSSKTLRVKLTVSPEPSSKRKEGPPAGQDREPTRCRMEGELAEPEPRV
ADRRLSAHVRRPSTDPQPCSERGPYCDVENTERRNHLYDLAGIENYTSRFGPGSSPVQAKQEPQGRASHL
QARSRSQEPDTHAVHRRSQVLVEHVVPASEPAARALDTPRPKGPEKQFLKSPKSGSGKPPGVPASSKSG
KAFSYLPAVLPPQAPQDGHHLPPPPPPYPYGHKRYRQKGREGHSPLKAPHAQPATVEHEVVRDLPTPTAG
EGYAVPVIQRHEHHHHHEHHHHHHHHFHPHS

Pongo abelii:

>XP_002815428.2 protein naked cuticle homolog 2 isoform X1 [Pongo abelii]
MGKIQSKHAAATKR**RESPEGDS**FVASGYACGRKSSEEAERRARDKQELPNGDPKEGPFREDQCPLQVAL
PPEKAEGREHPGQLLSADDGERAANREGPRGPGGQRLNIDALQCDVSVEEDNRQEWTFITLYDFDNCCKVT
REDMSSLMHTIYEVVDASVNHSLGSSKTLRVKLTVSPEPSSKRKEGPPAGQDREPTRCRMEGELAEPEPRV
ADRRLSAHVRRPSTDPQPCSERGPYCDVENTERRNHLYDLAGIENYTSRFGPGSSPVQAKQEPQGRASHL
QARSRSQEPDAHTVHRRSQVLVEHVVPASEPAARALDTPRPKGPEKQFLKSPKSGSGKPPGVPASSKSG
KAFSYLPAVLPHQAPQDGHHLPPPPPPYPYGHKRYRQKGREGHSPLKAPHAQPATVEHEMVRELPP
TPAGEGAVPVIQRHEHHHHHEHHHHHHHHFHPHS

Mus musculus:

>BAB25908.1 unnamed protein product [Mus musculus]
MGKIQSKHAAACKR**RESPEGDS**FVVPAYGSGRRGAEETDRRAGSGVHEHRSRDKQELPNGDPKEGPFWD
KGSLEVVLPPPEKSEGEHGGQQLFSTDDEKAASREGPLRLSKKHLNIDALQCDVSVEEDNRQEWTFITLYD
FDNSGKVTREDMSSLMHTIYEVVDASVNHSSGSSKTLRVKLTVSPEPSSKKECPLTQDREPTRGRTEIE
LTDEPRVADRRLSAYSRRKNADPQPCSVRVYPYCDVENTERRNHLYDLAGIENYTSKFGPGSPPEQARQEH
HGRATHIPSRSRSQESDAHAHHRSSQVLAEHVIPASEPATRALAAQPRIKGQEKQFLRSPKGPCKPLGT
PGSGKPGKALSYCIQAVPLPQSAQDGHHLPPPPPPYPYGHKRYRQKAREGHSPLKGHGQPTMVEHEV
VRDLPLMLGPEGYVMPVQRHEHHHHHEHHHHHHHHFHPHS

Gallus gallus:

>XP_040536747.1 protein naked cuticle homolog 1 isoform X1 [Gallus gallus]
MGKLSKHAAVCKR**RESPEGDS**FAVNASLARKGLEDWMVKQKYSGGSGSSSGSSGLQGCQHRAACGLS
SGRDLSEGEYRDSIGDEHFHLEVALPPEKTGVCVSGDEKKAEKESDTRTGSKKQLKFEELQCDVSVEEDN
RQEWTFITLYDFDNNGRVTRREDITISLLHTIYEVVDASVNHSPSSKTLRVKLTVAAPDCSQKKKSILNHTD
LQ SARHRAESKANEELASSEKKQRASLRVHQSENNPEQSECYRHCVDENIERRNHLYDLAGIENYTSKFG
PGSPPAAQKQDPPSRVVSQTRSRSEHPTFAHHRKSQVVDPSHINLAESSYAKIAEIQRLNRQDSNKH
FVRSPKAGKGNVAVPHSGRAVRNKPQGGAMPASPSARVGQNLPLYLPQSQVHHKHKQRAKENHQMCK
TFQSPGTVVVEKEHVRDLPTVILYEGQVQGMIQRHEHHHHHEHHHHHHHHFYQT

Xenopus laevis:

>XP_041417043.1 protein naked cuticle homolog 1 isoform X6 [Xenopus laevis]
MGKLYSKHAAVCKR**RESPEGDS**FAVNASLARKGIEDWLVKQKPPNSSLKTGYRITQRDSNGDICKYNIAN
EHFHLVALPEEKSEGLFTSDDRKVDKNDGRVKKQHKFEELQCDVSVEEDNRQEWTFITLYDFDNSGRVT
REDITLRLHTIYEVVDASVNHSLSSKTLRVKLSLAPDATLKKRTVLVNHAEQLQNGRHRSECKVTENLRG
SEKKQQSGRLENVTEQTECLRQCDENIERRNHLYDLAGIENYTSRFGPGSPMCEKHDSQAKASNQMR
SRSEHPTTISFHRRSQALDTGNSNMTELSHVKVAEVQQRQGENNKHVRSPRASNKNGLSTSQPGR
TRNKPQSGVSMFVNPPSAFMGQSYLYHPVPQSVHRKSQKTKDGHQMRKAFQSPVNVVEKEHVRDLPSM
VLYDDQVGHMIQRHEHHHHHEHHHHHHHHFYQK

Salmo salar:

>XP_014031575.1 protein naked cuticle homolog 1 isoform X2 [Salmo salar]
MGKLSKHAAIKCR**RESPEGDS**FVNNACLARKGIDDWLVKQKYCTGSRLEQQDCHHTNKGSLSTRDLD
KACAEGISDEHYRLVALPPEKTVDSCCEEKMQGRGSQAPTGTQKQLQFEELECAVSVEEDNRQEWTFIT
LYDFDNNKGVTREDITISLLHTIYEVVDTSVNHSPSSKTLRVKLSVAPDSSQRWQSCQTGTADMPHPTK
TDKCIEDLKSAEKKSALLRRHSDHHTIQHQVLTQQCGQSGRCQRHCVDENLERRNHLYDLAGIENYTS
SRFGAAPTTEFVKAEQPTRPSNQTRSRSEHPEFNGHTYSHHRRSQVAMESSAAPGPDTLCPPRPSKDSGKH
ALRSPKTHSRTHPTQTITGRVMRSGAPPPALPSQAPPHQSSAPYRRHKQRAKEGQQQYRALGAPVGSV
VEKQVRVLPVSVLYEGGLAQMVQRHEHHHHHEHHHHHHHHFYQS

Petromyzon marinus:

>XP_032830383.1 protein naked cuticle homolog 2 [Petromyzon marinus]
MGKIQSKQACARR**RESPEGDS**FVNNAYANRRGLEDPASVLPAPAYRDLVLYCGGVAKELFPPEVSSSLTLQT
PLSGDEDAEDDGGGGDATDKKPADKAALNALNFQQLQCDVLVDNNRQEWTFITLYDFDSSGEVTREDI
SSLMHTIYEVVGTGVNHTSGNSKTLRVKLTVTDPFGQRRRGAPHGIVDQPPSHGQGEATPEEARPQ
KQQPQQQQQQPQQQPPQEQPEHPALRYAAKHGHAIVSISGRSRENKNTLTIKRTRTPQERAGWETSPSPRQ
PAGGNPGCRRRCNGGSEMLTPSPGIQEVVGSILTLTPADGYFCVLINLAFHEGDSGVCGGPVVAASHGLA
EGPPPGCPLLPVVRHRCPRVITCPLVLFPPPFASFVTRVQCMNMMSDLFARRHHNSGQPGQSATARHCYC
VDENVERRNHLYDLAGMESYGTACPSFTQAGSPRMSRRRNAQHDPDTPAGQHGRRETVLHQNRNTPQDPS
TAAAAAATAATTTTAARYVSRSRTKPAVTQAASSRPRGQRGRSVAYVQPLRPVGVGQQQQQQQQQQQ
QPQQQHKHQRGREGCLSPGRPPYYQTRAPAGVDPVWRLEQPQHQQHHQHLQQQQQQQLLHVQQQQPGA
MQTSMVLPVVMQRHEHHHHHEHHHHHHHHYHET

Branchiostoma belcheri:

>XP_019629286.1 PREDICTED: protein naked cuticle homolog 2-like isoform X2 [Branchiostoma belcheri]
MGKIQSKHACKR**RESPEGDS**FVNNAHFNTGRYRGIEDFIARQKNATGLQLATYKGGRPPEPPAQEMEKA

GGCKPVPVGMADDCFPLEVQLPPETPDGRRTPFYVVGPNDDGSKSSVEEGEKPLGHVEEFECGVSVEGS
DKQEWTFTLYDFDGKGKVTQEDFATLLHSIYEMVGNVHLPSKSSSKGNKNKTLKLRITVSPKNGKAPE
KRVEITEMEQEVAKDEGDGSGNEGMSGECETPTRKKSCSANDQMRKLNLFHFVQKSEKQQQQQHRIAQL
RRHSDSHNNHHHSADEVRRHRHSHHRFPSPRQRQQQLQRAREPRPPQLPGPGRRGPEPQQRSHHGVDYI
LKFFPRKQPFSSIKVKRPRGPPQVKVT

Drosophila melanogaster:

>NP_001262029.1 naked cuticle, isoform B [Drosophila melanogaster]
MAGNIVKWWKHILGGYKQFSVQECTTDSEELMYHQVRASSSCSAPPDLLLLVSRDNNIQLRSPVNIIT
TPPGNASGAGSKQQSHHQTNHSSSGRSHPGHTAHPQDVSSGGSHSKHLRISSTNGKHGKYSNMQQQLPQ
DEDVVDAAATMQQQHTGHASRHLHHHKEERIRLEETCDVSVVEGGKSSQPLQFSFTFYDLGDGHHGKIT
KDDIVGIVYTIYESIGKSVVVPFCGSKTINVRLTVSPEGKSKSQPVVPVPAAGFSSSHASKLKKLPTGL
AAMSKPLAGGGVSGGASALTTSAGNRRQHRYPKRLIKSDDEDDDSNSEKDDAAHAPAADQPSGSGTK
ATGKSHHHQSQSARYHQKNNSRAEQCCTEQNTPDNGHNTYENMLNLKCKPEVDQVDCPSHRQHHQSHPN
HQMRRQDDIYMKQATQVRVKMLRRARKQKTPSQCESHTATGSTTTTTTTTATPTLQYGLENTHVNYQPQSGR
PAVAAQLQSTHGGAHPQHSSSSAGHRGQRSAAPPSSSSSQPPQPFRASPTAHTYLPSSAVGH

Hydra vulgaris:

No homolog found.

Nematostella vectensis:

>XP_032232724.1 protein naked cuticle homolog 2 isoform X4 [Nematostella vectensis]
MGKKYSKQAWIS**EGPEGGDC**VIENDTTTHSCAVSTSAEELSRA PSSHTADFTYKGYPVNLEWPLDYEEK
ELPSKKDFFYDDFPLEVVELPDLPDGKNVEISFEREGLVEASTQTKPLKQETPECGMSVKSSASSDHQEWS
YTLYDFEGGQGVTRDLRLNLVKSIEVLGKSVNNSRNQPKDPLKKLRVRLSVSKERGKGTEGDVPSRHEY
TISAMATENKAPKKSTRTYHMERCDSM TVNPPSLENIPDKRKMVSLIMEQPGPTNGINCQSHRQKISCKR
SSANRPAKPAVTAANTGNMDTPVVNDRGMYSCPKRMQTGFGECPNPPSPKEANDLSRVKQWVDQLCAAHEL
ETVTRSKHRKSYRHTCRQGEPRHDLHRC PQYLDLATDHITYPYHVESQACLFGAASPKPHRRPKRGHHHS
CKYNKDEVMCQRTIVHRHEHHSHHHYHHYKQEPSNK

Amphimedon queenslandica:

No homolog found.

Alignment

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NP_001262029.1[D.melanogaster]      MAGNIVKWWKKHILGGYKQFS-VQECTTSEELMYHQVRSSSCSAPPDLLLVSERDNNI    59
XP_032232724.1[N.vectensis]         -----MGKKYSKQ---AWISK-----EGPEGDSVIENDTTTHS                30
XP_019629286.1[B.belcheri]          -----MGKLQSKH---ACKR-----ESPEGDSFVNAHFNTG                  30
XP_032830383.1[P.marinus]            -----MGKFQSKQ---ACRR-----ESPEGDSFVNVAYAN--                  28
BAB25908.1[M.musculus]               -----MGKFQSKHAAAACKR-----ESPEGDSFVVPAYGSG-                  32
NP_149111.1[H.sapiens]               -----MGKLQSKHAAAARKR-----ESPEGDSFVASAYASG-                  32
XP_002815428.2[P.abelii]             -----MGKLQSKHAATARKR-----ESPEGDSFVASGYACG-                  32
XP_014031575.1[S.salar]              -----MGKLHSHKAA-ICKPR-----ESPEGDSFVNVNACLA--                 30
XP_040536747.1[G.gallus]             -----MGKLHSHKAA-VCKPR-----ESPEGDSFAVNASLA--                 30
XP_041417043.1[X.laervis]            -----MGKLYSKHAA-VCKPR-----ESPEGDSFAVNASLA--                 30
                                     : * .                               . * .

NP_001262029.1[D.melanogaster]      QLRSPVUNIIT---TPPGN---ASGAGSKQQSHHQTNH-HSSGRSHPGHTAHPQDVSSGG    112
XP_032232724.1[N.vectensis]         C-AVSTSAEELSRAPSSHTADFTYKGYPVNLEWPL-----D---YEEKELPSKKD    77
XP_019629286.1[B.belcheri]          R-YRGIEDFIARQ-KNATGLQLATYKGRQPPPEPAQEM-----E---KAGGCKFPVVG    79
XP_032830383.1[P.marinus]            --RRGLEDVPAV-PPAYR-----DVLVYCGG                             52
BAB25908.1[M.musculus]               --RRGAETD-----RR-AGSGVEHRS---RDQK---ELLNGDPKEGP           66
NP_149111.1[H.sapiens]               --RKGAEEAE-----R-----RA---RDQK---ELPNGDPKEGP           58
XP_002815428.2[P.abelii]             --RKSSEAE-----R-----RA---RDQK---ELPNGDPKEGP           58
XP_014031575.1[S.salar]              --RKGIDDWLVKQ-KYYCT-----GSRL-EQQCDCHTNKCGLST---RDLLDKACAEG    76
XP_040536747.1[G.gallus]             --RKGLEDWMVKQ-KYSGSGG-SSSGGSSS-GLQGCQHRAACGLSSG---RDLSGGEYRDS    83
XP_041417043.1[X.laervis]            --RKGIEDIWMVKQ-KPPNSSL-KT-----GY-----RITQ---RDSNGDICKYN    67

NP_001262029.1[D.melanogaster]      SHSKHLRISSTSNKGKGYSNMQQLPQDEDDVDAATMQ-QQOHTGHA-HS---RHLHH    167
XP_032232724.1[N.vectensis]         FFYDDFPLEV-----VELPDL-----PDGKNVE---ISFEREGLVEASTQT----- 115
XP_019629286.1[B.belcheri]          MADDCCFPLEV-----QLPPETPDGGRTPFVYVVGPDNGDSKSS---VEE        120
XP_032830383.1[P.marinus]            VAKELFPEEV-----SSLSTLQTLPLSPGEDEA-----EDDGGGDATDKKPADK     96
BAB25908.1[M.musculus]               FWDDKGSLEV-----VLPEKSEGH-EGQGQLFTDDGEKAASREG---PLR        109
NP_149111.1[H.sapiens]              FREDQCPLQV-----ALPAEKAEGR-EHPGQLLSADDGERAANREG---PRG        101
XP_002815428.2[P.abelii]            FREDQCPLV-----ALPPEKAEGR-EHPGQLLSADDGERAANREG---PRG        101
XP_014031575.1[S.salar]              ISDEHYRLEV-----ALPPEKTVDS-CC-----VEEKMQGRGSA---PT        112
XP_040536747.1[G.gallus]            IGDEHFHLEV-----ALPPEKTDGV-CS-----GDEKKAESDST---RT        119
XP_041417043.1[X.laervis]            IANEHFHLEV-----ALPEEKSEGL-FT-----SDDRKVDKDNDG---R        102

NP_001262029.1[D.melanogaster]      HKEERI-RLEEFTCDVSVVEGKSSQPLQFSFTFYDLDGHHGKITKDDIVGIVYTIYESIG    226
XP_032232724.1[N.vectensis]         ---KPL-KQETPECGMSVKAS-SDHQEWSYTYLDFEG-QQVTRREDLRNLVKSIEYVLG    169
XP_019629286.1[B.belcheri]          GEKPG-LHVEEFECGVSV--G-SDKQEWTFITYLDFDG-KGKVTQEDFATLLHSIYEMVG    175
XP_032830383.1[P.marinus]            AALNALNFQQLQCDVLVQ--D-DNRQEWTFITYLDFDG-SGEVTREDISSLMHTIYEVVG    152
BAB25908.1[M.musculus]              LSKKHLN-IDALQCDVSV--E-DNRQEWTFITYLDFDN-SGKVTREDMSSLMHTIYEVVD    164
NP_149111.1[H.sapiens]              PGQQLN-IDALQCDVSV--E-DDRQEWTFITYLDFDN-CGKVTREDMSSLMHTIYEVVD    156
XP_002815428.2[P.abelii]            PGQQLN-IDALQCDVSV--E-DDRQEWTFITYLDFDN-CGKVTREDMSSLMHTIYEVVD    156
XP_014031575.1[S.salar]              GTQKQLQ-FEELECAVSV--E-DNRQEWTFITYLDFDN-NGKVTREDITSLHTIYEVVD    167
XP_040536747.1[G.gallus]            GSKKQLK-FEELQCDVSV--E-DNRQEWTFITYLDFDN-NGRVTREDITSLHTIYEVVD    174
XP_041417043.1[X.laervis]            -VRKQHK-FEELQCDVSV--E-DNRQEWTFITYLDFDN-SGRVTREDITRLHTIYEVVD    156
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NP_001262029.1[D.melanogaster]      KSVVPHC-----GSKTINVRLTVSPEGKSKSQPVVPVPAAGFSSSHASKLKLPTGL      280
XP_032232724.1[N.vectensis]         KSVNNSRNQP--KDLPLKLRVRLSVSKERGKGTGEDVPSRH-EY-----          210
XP_019629286.1[B.belcheri]          NSVHLPSKSSSKGNKNKTLKRLTVSPKNGKAPEKRVETEMEQUEV-----          221
XP_032830383.1[P.marinus]            TVSNHSTG-----NSKTLRVKLTVTPDPGQRRRGAPHGIVDQ-----          190
BAB25908.1[M.musculus]              ASVNHSSG-----SSKTLRVKLTVSPPESSK-KECPLTGQDRE-----          201
NP_149111.1[H.sapiens]              ASVNHSSG-----SSKTLRVKLTVSPPESSKRKEGPPAGQDRE-----          194
XP_002815428.2[P.abelii]            ASVNHSLG-----SSKTLRVKLTVSPPESSKRKEGPPAGQDRE-----          194
XP_014031575.1[S.salar]              TVSNHSPS-----SSKTLRVKLSVAPDSSQRWQCTGQTADMP-----          205
XP_040536747.1[G.gallus]            ASVNHSPS-----SSKTLRVKLTVAPDGSQKKSKILLNHTDLQ-----          212
XP_041417043.1[X.laervis]            ASVNHSLS-----SSKTLRVKLSLAPDATLKRTVNLVNAELQ-----          194
                                     **                               * : : : : : : : : : : : : : :

NP_001262029.1[D.melanogaster]      AAMSKFLAGGVGSGGASALT-----TSAGNRRQHRYRPRKLIKSDDEDDDSNSE---    330
XP_032232724.1[N.vectensis]         -----T-ISAMATENKAPK--KSTRTYHMERC-----                    234
XP_019629286.1[B.belcheri]          ---AKD-EDGDSGNEGMEGCEPTPRKKSCSANDQMRKLNLEHFVQKSIEKQQQQQQHRI    277
XP_032830383.1[P.marinus]            -----PPSHQGEETATPEEARQPQ-K---QQQPQQQQQ--PQQPQQQQQPEH        232
BAB25908.1[M.musculus]               -----PTRG-RTEIELT-DEPRVAD-R---RL-----                    222
NP_149111.1[H.sapiens]              -----PTRC-RMEGELA-EEPRVAD-R---RL-----                    215
XP_002815428.2[P.abelii]            -----PTRC-RMEGELA-EEPRVAD-R---RL-----                    215
XP_014031575.1[S.salar]              -----HPRT-KT-DKCI-EDLKSAB-K---KS-----                    225
XP_040536747.1[G.gallus]            -----SARH-RAESKAN-EELRSSE-K---KQ-----                    233
XP_041417043.1[X.laervis]            -----NGRH-RSECKVT-ENLRGSE-K---KQ-----                    215

NP_001262029.1[D.melanogaster]      -----K-E-----KDAAHAPAADQPSGS---          347
XP_032232724.1[N.vectensis]         -----DSMTVNPPSL-----EN-----                    246
XP_019629286.1[B.belcheri]          AQLRRHSDSHNHHHSADSVRRHRHSH--RPPSRQRRQQQLQRAREPRPQPPL---PG    332
XP_032830383.1[P.marinus]            PALRYAA--KHG---HAVSISGRSRENKNTLTKTRTPQGERAGWETSPSPQAGGNPG    287
BAB25908.1[M.musculus]               -----SA-----YSRK-----                    228
NP_149111.1[H.sapiens]              -----SA-----HVRR-----                    221
XP_002815428.2[P.abelii]            -----SA-----HVRR-----                    221
XP_014031575.1[S.salar]              -----RA-----LLRR-----                    231
XP_040536747.1[G.gallus]            -----RA-----SLRY-----                    239
XP_041417043.1[X.laervis]            -----QG-----SGRL-----                    221

NP_001262029.1[D.melanogaster]      -GTKATGKSHHQ-SQSARYHQKNNRAEQCCTEQNTPDNGHNTYENMLN-----LK     397
XP_032232724.1[N.vectensis]         -----IPDKRK-----MVSLIMEQPGPTNGINCQSHRQKISCKRSSANR        285
XP_019629286.1[B.belcheri]          PGRRGEPQ-----QRS-----HHGDVYILKFPKRPQFSIK--VK--RFRGPPQ-    371
XP_032830383.1[P.marinus]            CRRCGNGGSEMLTPSPGIQE-----VVGSIILT-TPADGYFCVLINLA--FHEDGDSV    337
BAB25908.1[M.musculus]               -----PNADPQ-----                    234
NP_149111.1[H.sapiens]              -----PSTDPQ-----                    227
XP_002815428.2[P.abelii]            -----PSADPQ-----                    227
XP_014031575.1[S.salar]              -----HHSDDH-----                    237
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XP_040536747.1[G.gallus]	-----HQSENN-	245
XP_041417043.1[X.laavis]	-----ENV-	224
NP_001262029.1[D.melanogaster]	-----QVDCPSHRQ-----	413
XP_032232724.1[N.vectensis]	PAKPAVTAANTGNMDTPV-----VN-----DRGMYSCPKRMQTGPGECPNPPSPKEANDLS	335
XP_019629286.1[B.belcheri]	-----V-KVT-----	375
XP_032830383.1[P.marinus]	CGGPVV-AASHGLAEGPPPGCLLPVVRRCPRVITCPLVLFFPP-----PFA-----	384
BAB25908.1[M.musculus]	-----	234
NP_149111.1[H.sapiens]	-----	227
XP_002815428.2[P.abelii]	-----	227
XP_014031575.1[S.salar]	-----TI-----	239
XP_040536747.1[G.gallus]	-----	245
XP_041417043.1[X.laavis]	-----	224
NP_001262029.1[D.melanogaster]	-----HHQSHPNHQMRRQDDIYMKQATQVRKM	439
XP_032232724.1[N.vectensis]	RVKQWVDQLCAAHELETVTRSKHRK----SYRHTCRQGEPRHDLHRCPOYLDLATDHI--	389
XP_019629286.1[B.belcheri]	-----	375
XP_032830383.1[P.marinus]	---STVRVQCPMNMSDLFARRRHSNGQPQGSATARHCYCDENVERRNHLYDLGAMESYG	441
BAB25908.1[M.musculus]	-----PCSVRVPCVDENTERRNHYLDLAGIENYT	264
NP_149111.1[H.sapiens]	-----PCSERGPYCDENTERRNHYLDLAGIENYT	257
XP_002815428.2[P.abelii]	-----PCSERGPYCDENTERRNHYLDLAGIENYT	257
XP_014031575.1[S.salar]	-----QHQLVTQQGGQSRGCRHRCVDENTERRNHYLDLAGIENYT	280
XP_040536747.1[G.gallus]	-----PEQSECYRHCVDENIERRNHYLDLAGIENYT	276
XP_041417043.1[X.laavis]	-----TEQTECLRQCVDENIERRNHYLDLAGIENYT	255
NP_001262029.1[D.melanogaster]	LRRAR-KQKKTIPSQCESHTATGTT---TTTTATPTL---QYGL-----ENTHVNYQ-	485
XP_032232724.1[N.vectensis]	-----	389
XP_019629286.1[B.belcheri]	-----	375
XP_032830383.1[P.marinus]	TPACSPTQAGSPRMSR-----RRNAQHDPTPAG-QHGRRETVLHQRNRTPOD	488
BAB25908.1[M.musculus]	SKFG---PGSPPEQARQEHHRATHIPSRSRSQESDAHA--IHHRRSQVLAHVIPASE	318
NP_149111.1[H.sapiens]	SRFG---PGSPPVQAKQEPQGRASHLQARSRSQEPDTHA--VHHRRSQVLEHVVPASE	311
XP_002815428.2[P.abelii]	SRFG---PGSSPVQAKQEPQGRASHLQARSRSQEPDAHT--VHHRRSQVLEHVVPASE	311
XP_014031575.1[S.salar]	SRFG---AAPTTEPVKAEPQTRPSN-QTRSRSHEPENGHTYSHHRSSQVAMESSAA---	332
XP_040536747.1[G.gallus]	SKFG---PGSPPAQKQDPPSRVVS-QTRSRSHEPETFH--AHHRKSQVVDPSHINLAE	329
XP_041417043.1[X.laavis]	SRFG---PGSPPMCKHDSQAKASN-QMRSRSHEPETIS--FHHRRSQALDTGNSNMTE	308
NP_001262029.1[D.melanogaster]	PQSGRPVAAQLQSTHGAHH-----PQHSSSSAG-HRGQRS--AAPP-----	525
XP_032232724.1[N.vectensis]	-----TYPYHVESQA	399
XP_019629286.1[B.belcheri]	-----	375
XP_032830383.1[P.marinus]	PSTAAAAAATAATTTAARYVSRSSRTKGPVAVTQAASSRPGRGRSVPAYVQPLRPVG	548
BAB25908.1[M.musculus]	---PATRALAAQPRIKGQEKQFLRSPKGPGLGTGSGKPGKALSYCLQAVPLP---QS	372
NP_149111.1[H.sapiens]	---PAARALDTQPRPKGPEKQFLKSPKGSKPPGVPAASSKSGKAFSYLLPAVLPP---QA	365
XP_002815428.2[P.abelii]	---PAARALDPQPRPKGPEKQFLKSPKGSKPPGVPAASSKSGKAFSYLLPAVLPH---QA	365
XP_014031575.1[S.salar]	---PGDPTLCPPRPSKDSGKHALRSPKTHSRHTPTTT-GRVMRSR---GAPP---PP	381
XP_040536747.1[G.gallus]	SSYAKIAEIQQLRLNQDSNKHFRVSRPKAQGNVAPV-HS-GRAVRNKPFGCGAMPMAFPS	387
XP_041417043.1[X.laavis]	LSHVKVAEVQQRQQRQENNKHFVRSRASNKNHGLSTSQ-PGRTRNKPQSGVSMFVNPPS	367
NP_001262029.1[D.melanogaster]	--HSSHSSQPPQPPRASPTAHTY-----LPSAVGH-----	553
XP_032232724.1[N.vectensis]	CLFGAASPK-----PHRR-----	414
XP_019629286.1[B.belcheri]	-----PK	375
XP_032830383.1[P.marinus]	VQQQQAQQQ---QQQQPQQQHKHQRQREGCLSPGRPPYQTRAPAGVPDVRWLEQFQ	605
BAB25908.1[M.musculus]	AQDGHHLQPFPQPFPQPYGHKRYRQKAREGHSPL-----KG-HGQ-PTMVEH-----	418
NP_149111.1[H.sapiens]	PQDGHHLQP-----PPPYGHKRYRQKREGHSPL-----KAPHAQ-PATVEH-----	408
XP_002815428.2[P.abelii]	PQDGHHLQPFPQPFPFPQPYGHKRYRQKREGHSPL-----KAPHAQ-PATVEH-----	412
XP_014031575.1[S.salar]	ALPSQ---APPHQ---SSAPYRRHKQRAKEGQQQY---RALGAPVGSVVEK-----	423
XP_040536747.1[G.gallus]	ARVGQNLPLYLPLQ---SQQVHKHKKQRAKENHQQMC-----KTFQSP-GTVVEK-----	431
XP_041417043.1[X.laavis]	AFMGQSYLYHVPF---PQSVHRKSKQKTKDGHQMR-----KAFQSP-VNVVEK-----	411
NP_001262029.1[D.melanogaster]	-----	553
XP_032232724.1[N.vectensis]	RGHHHSC-----KY-NKDEVMCQRTIVHR---HEHHSHHHHHYHYEK	452
XP_019629286.1[B.belcheri]	-----	375
XP_032830383.1[P.marinus]	HQHHHQHLQQQQQQQLHVQQQPGAMQTSMLVPVMQRHEH---HYEHSHHHHHYHYHYE	662
BAB25908.1[M.musculus]	-----EVVRDLPPMLGPEGYVMPVQVQREHHHHHHHHHHHHHHHHFHPs--	461
NP_149111.1[H.sapiens]	-----EMVRELPPTPAGEGYAVPVIQREHHHHHHHHHHHHHHHHFHPs--	451
XP_002815428.2[P.abelii]	-----EMVRELPPTPAGEGYAVPVIQREHHHHHHHHHHHHHHHHFHPs--	455
XP_014031575.1[S.salar]	-----EQVRVLPSVLLYEGGLAQMVQRH-----EHHHHHHHHHHYHHFYQ	463
XP_040536747.1[G.gallus]	-----EHVRDLPTVILYEGQVGMQIRH-----EHHHHHHHHHHYHHFYQ	471
XP_041417043.1[X.laavis]	-----EHVRDLPSMVLVYDDQVGMQIRH-----EHHHHHHHHYHHFYQ	451
NP_001262029.1[D.melanogaster]	-----	553
XP_032232724.1[N.vectensis]	QEPSNK	458
XP_019629286.1[B.belcheri]	-----	375
XP_032830383.1[P.marinus]	T-----	663
BAB25908.1[M.musculus]	-----	461
NP_149111.1[H.sapiens]	-----	451
XP_002815428.2[P.abelii]	-----	455
XP_014031575.1[S.salar]	S-----	464
XP_040536747.1[G.gallus]	T-----	472
XP_041417043.1[X.laavis]	K-----	452