

Axin1

Homo sapiens:

>NP_003493.1 axin-1 isoform a [Homo sapiens]
MNITQEQGFPDLDGASFTEDAP**RPFPVPGEE**GELVSTDPRPASYSFCSGKGVGIKETSTATPRRSDLLDGYEPEGSASPTPPYLKWAESLHSLDDQDGISLFRTFLKQEGCADLLDFWFACTGFRKLEPCDSNEEKRLKLARAIYRKYILDNNGI
VSRQIKPATKSF1KGCIMQKLLIDPAMFDQAQTEIQATMEENTYPSFLKSDIYLEYTRTGESPKVCSDDSSGSGTGKGISGLYPLTNEDEEWKCDQDMEDDGRDAAPGRLPKQLLLETAAPRVSSRRYSEGREFRYGSWREPVNPYYVNAGY
ALAPATSANDESQQSLSSDADTSLTSDSVGDIPPYIRKQHRREMQUESVQVNGRVPLPHIPRTYRVPKVEVRVEPQKFAEELIHRLEAVQRTREAEKELEERLKRVRMEEEGEDGDPSSGPPGCHKLPPAPAWHHFFPRCVDMGACGLRDAHEE
NPESILDEHVQRVRLTTPGRQSPGPGGHRSPDSGHVAKMPVALGGAASGHGKHVPKSGAKLDAAGLHHHRHHVHHVHHSTARPKEQVEAEATRAAQSSFAWGLEPHSHGARSRGYSESVGAAPNASDGLAHSKGVGVACKRNAKKAESGKSASTEVP
GASEDAEKNQKIQMWIIEGEKEISRHRRTGHGSSGTRKPKPHENSRLPSLEHPWAGPQLRTSVQPSHLFIQDPTMPHPAPNPLTLQLEEARRRLEEEKRAAPSKQRYVQEVMRGRACVRPACAPVLHVPAVSDMELSETETRSQRKVGGS
SAQPCDSIVVAYYFCGEPPIPYRTLVRGRAVTLGQFKELLTKKGSYRYFFKKVSDDEFDCGVVFEEVREDAVLVFEEKIIGKVEKVD

Pongo abelii:

>Xp_024089076.1 axin-1 isoform X1 [Pongo abelii]
MNITQEQGFPDLDGASFTEDAP**RPFPVPGEE**GELVSTDPRPASYSFCSGKGVGIKETSTATPRRSDLLDGYEPEGSASPTPPYLKWAESLHSLDDQDGISLFRTFLKQEGCADLLDFWFACTGFRKLEPCDSNEEKRLKLARAIYRKYILDNNGI
VSRQIKPATKSF1KGCIMQKLLIDPAMFDQAQTEIQATMEENTYPSFLKSDIYLEYTRTGESPKVCSDDSSGSGTGKGISGLYPLTNEDEEWKCDQDMEDDGRDAAPGRLPKQLLLETAAPRVSSRRYSEGREFRYGSWREPVNPYYVNAGY
ALAPATSANDESQQSLSSDADTSLTSDSVGDIPPYIRKQHRREMQUESVQVNGRVPLPHIPRTYRVPKVEVRVEPQKFAEELIHRLEAVQRTREAEKELEERLKRVRMEEEGEDGDPSSGPPGCHKLPPAPAWHHFFPRCVDMGACGLRDAHEE
NPESILDEHVQRVRLTTPGRQSPGPGGHRSPDSGHVAKMPVALGGAASGHGKHVPKSGVKLDAAGLHHHRHHVHHVHHSTGRPKQVEAEATRAAQSSFAWGPPEPHSHGAKSRGYSESVGAAPNASDGLAHSKGAGVACKRNAKKAESGKSASTEVP
GASEDVEKNQKIQMWIIEGEKEISRHRRTGHGSSGTRKPKPHENSRLPSLERPGAHVHPWAGPQLRTSVQPSHLFIQDPTMPHPAPNPLTLQLEEARRRLEEEKRAAPSKQRYVQEVMRGRACVRPACAPVLHVPAVSDMELSETETRSQR
KVGSGSAQPCDSIVVAYYFCGEPPIPYRTLVRGRAVTLGQFKELLTKKGSYRYFFKKVSDDEFDCGVVFEEVREDAVLVFEEKIIGKVEKVD

Mus musculus:

>EDL22489.1 axin 1, isoform CRA a [Mus musculus]
MQSPKMNVDQGGFPDLDGASFTEDAP**RPFPVPGEE**GELVSTDPRPASYSFCSGKGTISKSETSTATPRRSDLLDGYEPEGSASPTPPYLKWAESLHSLDDQDGISLFRTFLKQEGCADLLDFWFACTGFRKLEPCDSNEEKRLKLARAIYRKYILDNNGI
DSNGIVSRQIKPATKSF1KDCVMKQIIDPAMFDQAQTEIQSTMEENTYPSFLKSDIYLEYTRTGESPKVCSDDSSGSGTGKGISGLYPLTNEDEEWKCDQDADEDDGRDPLPPSRLTQKLLLETAAPRAPSSRRYSEGRELRYGSWREPVNPYY
VNSGYALAPATSANDESQQSLSSDADTSLTSDSVGDIPPYIRKQHRREMQUESIQVNGRVPLPHIPRTYRMKPKEIRVEPQKFAEELIHRLEAVQRTREAEKELEERLKRVRMVCYSCSDSTAVSPQEEEGEDGEMPSGPMAHKLPSVPAWHH
FFPRPVYDMGSGSLRDAHEENPESILDEHVQRVRLTTPGQSPGPGGHRSPDSGHVAKTAVLGGTASGHGKHVPKLGKLDAGLHHHRHHVHHVHHNSARPKEQMEAEVARRVQSSFSWGPTEHTGHAKPRSYSENAGTTLTLAGDLAFGKGTSAPSKR
NTKKAESGKNANAEVPSTTEDAEKNQKIQMWIIEGEKEISRHRKAGHGSSGLRQQAHESSRPLSIERPGAHVHPWVAQLRNVVQPSHLFIQDPTMPNPNPAPNPLTLQLEEARRRLEEEKRAANKLPKQRYVQAVMQRGRTCVRPACAPVLSVVP
AVSDLELSETETRSQRKAGGGSAPPCCDSIVVAYYFCGEPPIPYRTLVRGRAVTLGQFKELLTKKGSYRYFFKKVSDDEFDCGVVFEEVREDAVLVFEEKIIGKVEKVD

Gallus gallus:

>NP_990275.1 axin-1 [Gallus gallus]
MNITQEQGFPDLDGASFTEDAP**RPFPVPGEE**GELVSTDPRPVSHGFYSKSDAVRNETSTATPRRSDLLDGYEPEGSASPTPPYLKWAESLHSLDDQDGINLFRNFLQQENCVDLLDFWFACTGFRKLEPCVSNEEKRLKLAKAIYKKYILDNNGI
VSRQIKPATKSF1KDCVMKQIIDPAMFDQAQTEIQCIEMDNTYPLFKSDIYLEYTRTGESPKVYSDPSSGSGTGKGLGYPLTNEDEEWKCDQDTEPAASRDSAPSSRLTQKLLLETAAPRATSTRYSEGREFRHSGWREPVNPYYNTGY
AMAPATSANDESQQSMSSDADTMSLTSDSVGDIPPYIRLKRQHRREMQUESAKANGRVPLPHIPRTYRMPKDIHVDPEKFAEELINRLEAGVLRDREAQRLEERLKRVRRAEEEGDDADISTSTSPSHRLPPGGHQPQHNPNRPYSDI
EENPESILDEHVQRVRLTTPGQSPGPGGHRSPKPRSPSESHGLKLSGTLGTIPPGHKHTTKSGMKLDAANLYHHKHVYHHIHHHSMMPKEQIEAEATQRVQNSFAMNVDSHNYATKSNNYSENLQMAVPMDSLGYSKGKALSCKRNKIKTKTDSG
KSDGANVYEMPFGSPEDVERNQKIQMWIIEGEKEISRHKKTNHGSSGVKKQLSHDMVRPLSIERPVAVHHVWVAQLRNVVQPSHFFIQDPTMPNPNPAPNPLTLQLEEARRRLEEEKRAKGLPLKQLRKLQKPKRPGSGASQPCENIVVAYYFCGEPPIY
RTLVRGRVTLGQFKELLTKKGNRYRYFFKKVSDDEFDCGVVFEEVREDDTLPIFEEKIIGKVEKID

Xenopus laevis:

>NP_001089251.1 axin 1 S homeolog [Xenopus laevis]
MSVKAKGFPDLDGGSFTEDAP**RPFPVPGEE**GELITTDQRPFSHTYYSLKNDGIKNETSTATPRRPDLLDGYEPEGSASPTPPYLKWAESLHSLDDQDGINLFRNFLQQENCVDLLDFWFACTGFRKLEPNDSKVEKRLKLAKAIYKKYVLDNNGI
VSRQIKPATKSF1KDCVLQIQIDAMFDQAQTEIQMMEDNTYPVFLKSDIYLEYTTIGESPKNYSDQSSGSGTGKGSGLYPLTNEDEEWKCDQGEQERESVSPSSLFSQKLLDSSSHCAGSNRRLSDGREFRPGTWREPVNPYYNTGYSG
APVTSANDESQQSMSSDADTMSLTSDSVGDIPPYLRKRYHRREMQUESANANGRGPLPHIPRTYTMPKDIHVDPEKFAEELINRLEAGVLRDREAQRLEERLKRVRRAEEEGDDGDVSSGSPVISHKLPSGPMHHNYSRYSDSGCVMQIRDAHEE
NPESILDEHVQRVRLTTPGQSPGTGRHSPKPRSPDGHLKSKTLPGLSGLTMTQTHGKHSSKSGKVDSNLHHHKHVYHHLHHHGKVPKEQIEAEVTQRVQNTYPNWNAESHNYATKSRYNAESMGMAPNPMDSLAYSGKVSMLSKRNAKKADVGS
ESASVEYVPAPEDAERHQKIQMWIMEGEKEISRHKSNHSSSSAKKQPPPELSRPLSIERPGAHVHPWVAQLRNVVQPSHFFIQDPTMPNPNPAPNPLTLQLEEARRRLEEEKRAAKMPKQRYVQEVIGRQRCVSRPAYIPLLNVPVAVSDMDLS
EAELEKPKQKTVSSPQPCENIVVAYYFCGEPPIPYRTVMKGRVTLGQFKELLTKKGNRYRYFFKKVSDDEFDCGVVFEEVREDDMLPIFEEKIIGKVEKID

Salmo salar:

>Xp_014059686.1 PREDICTED: axin-1-like isoform X1 [Salmo salar]
MDAIVNSGVKGVKQCYLVLDGGSFTEDAP**RPFPVPGEE**GELVSSDPRPYGHOFYSFKSEILKNEASTATPRRPDLLDGYEPEGSASPTPPYLKWAESLHSLDDQDGILHFLRTFLKQEECADVLDWFPACTGFRKLEANEQGQEEKKLKLAKAIYK
YILDNNGIYSDQIKPATKSF1KDCVMKRLIDPAMFDQAQTEIQTMEEINTYPLFKSDIYLEYTRTGESPKVYSDQCSVSGGKVLGYPLTNEDEEWKCDHLEEEQGESDPTPSNRKLQKLLQETASQRTVSTKRFQDSHEYKRVRLWQEPIN
PYYVNTGYAMAPATSANDESQQSMSSASDVTLSLTSDSVGDIPPYKQRKQHRREMHESAKANANGRVPLPHIPRTNRIPKDHIVEPEKFAADLISRLGEVQREAREQKELEERLKRVRLEEEGEDADISTSTSPSHRLPPGGHQPQHNPNRPYSDI
GYSGLARLPDAHEENPESILDDHVQRVRLTTPGQSPGTGRHSPKPRSPDGFGPGKVPKGMPPTTGPGKHPARLKGGEAEASHQYHHKHVHHIHHHPAGGPKPEQVEADAAMRVNNGNFWHGTQHNHYGSKSRNYADGTCGSPMDPMGYSKSGKSTLS
KRSFKKAEVARTFEVVPVTEDEVNQKIQMWIMEGEAVNRKKSYPGSGTTGSKTTPSSHEVSRSPSVERPGAHVHPWVAQLRNVVQPSHFFIQDPTMPNPNPAPNPLTLQLEEARRRLEEEKKKTGTTLQTKQRYVMVEVIGRGAARAPALFPPLSVVP
AVSDTELSEEHVKTKKPACENITVAYYFCGEPPIPYRTSVKGRVMVLGQFKELLTKKGSYRYFFKKVSDNDFDCGVVFEEVREDDAILPIFEEKIIGKVEKID

Petromyzon marinus:

>XP_032816874.1 axin-1-like [Petromyzon marinus]
MSVSEKLRQLRDLDSHIIENAITR**RPFPVPGRE**GKVNVMVPEHCNDPGLARANGVKGGSGDGFVGRMMQPRRM
DGDLDGYEPEGSASPTPPYVRWAESELPALLEDDQDGTSLFRAFLQEDEDVCDLLDFWFACTGFRKTDGDKRAK
LAKAIYKKFIKDNAGIVRLQIGISITRTGVKECIASKRIDSTMFDRAQEEVQTEAMENAYPAFLRSDVYLA
YARSGGSESPRCFADPLPAGFPMAMKGLDSPGLQTVKEDEVLSYDSQQTHKRWPEVHCGRMPTGGSSCFSV
ASPRAVGRMPSEKGGKGYRNPFLWPGNVPNPYHMNSGYGRAFPASSANDSEQSLSSDAMTDMDTMSMTDSSVD
GIPPYRLRSCASARDTRQSAKDSGRTEVVHIIPTRSRLPKDMVVEPAKFASELSIRLERLQREDAQEAL EE
RLRRVRAEEEGEGFPVATATCQASTTQVAAGCGGGGQMAAVPVFSFLSEPEDDDPESILDEHVSVMKPT
GCQSPFHGHGGGAGRPSPSPSRPHFGVVRQAAALAIKGEAGTAAAGASSASQSHHRTVYHHHHHHI
HHHAASKAREQLEVEBAQRVYGGGGGGGGVGTAESEFFYAAKSRNGAENLPGITNTLPLTSNKPQTGL
KKSSEGESGKAEEAPLEECPITRVLEEVPDRFRIQWMNVQGEKEAGRHAKTTTTSSGSSKSGSSEATPRA
AHAWSGVATAPQRAPAVGTQPSQPFVQDQMPPLPAPNPLTLQLEEARRRLEEEKRSARVPFRSPQTQET
LQRNRSFORQAGSQNPNSSPSILDLADRELKAGKSAQVEASDSVVVYVFCGETIPIYRTSVRGHVLT
GHFKELLTKKGYRYFFKKAASEDFDCGVVVEQDDAILPIYEERINGKVERIE

Branchiostoma belcheri:

>XP_019639671.1 PREDICTED: axin-1-like isoform X1 [Branchiostoma belcheri]
MS1GQVEYLQDTGGSKFTEDLPTSAR**RPFPVPGEE**TESNHGSQHSSSNTKSEYSTKSDYSKSDYSHSSAGTPRRNTCNDLGEFEPEGSASPTPPYLRWADNLQALLSDKDGSQFLGLYLENEDSKHLLDFYFAVNGYKKLDPLDDKTQRLAKVYAKY
IKEGKGLSHRVKPGTGQYLAKNIDCKPLDISITFDQAQLEIEKFMEENAYRLFLESIDYLCYCRNGGEVSNQVVTELANTSNGVNLTTGAILAPLPTLHENVELSTEDTMETRLPLTAEHLLATSQIRLRSRDRERLRTGNGPNYHQTYAP
APATSANDESILQSLSGSTDDTMSLTSDSIDLGDVSNHRRRRRQLKGMQRQDAQRNGNVMYCPPFPQPTQRLPKEMKMMEPKKFAELLIAKLEKVKQDRENKERLDEQLRRMEGDCGASQASGESQASGADPTQPRLFLPMDTTSIDDDPES
ILDEHVSRLVLTGPCRSPPGRHSVPVRPNKSHISGVPHVFSFGALAGASAMAHNRSRPKDVSKRDSGLDGSTEAETVTHYKHYYHHHHHHHPKSRDGLGEQTEMETQKRVQRDSEMYTTQSRVHQDSMGGTAEISLRHDAREVVVKGKRGGRKEEG
EPFLALPVEITDRFGKWDWMEEGEGERYRGGVNREPKFKSSKTASATSHRSSGKASSAKKPLAYNTRSTPSMERPAVTAERVMPQPMQDQMPVLPNPNPLCLEEARRRLEVEKSTKSGSRHVVDGARKDKGKLPQSKRVPAVSDLEP
EEETRKPQVKKPSAMSMVSGDNTVAYYFCGEPPIPYRTLPGKIDTLAIFKNSITKRGNYRYFFKCTSEFSGNAVQVEDEDEDLPLWEGKIIGKVERIE

Drosophila melanogaster:

>AAD24886.1 D-Axin [Drosophila melanogaster]
MSGHSPSGIRKHDWNECSG**RPFPVPGEE**SRVKMTEGVADTSKNSSPSYLNWARTLNHLLDREDGVLEFKKYVEEEAPAYNDHNLNFYFACEGLKQOTDPEKIQIGAIYRFLRKSQLSISDDLRAQIKAITNPFIPLSPHIFDPMQRHVVEVTIR
DNITYPTFLCSEMYLTITQMSAQBERCTISSGATSGSASGSSGSSLAGACALPPTTASGKQQLPOLVLPQAFINLPSVSVSGPPAGTCSASGVYGPPTSASSSGSISATDTLFRSSTLPTLHEDVLSLDCDFEKVQMQEGSSGLSGSVGA
GARAPDYPIRLTRDLLIATQKKRLEIRPGAAGVYVNPSTNTNYSVYNSRVDSEKRAVSSGSDTSDTMSISCSMDGRPIYQRRHSSTESKAIQASAMANKETNTFQVIPRTQRLHSHNEHRPLKEELVSLLLPKLEEVRKKQDLLEERARERP
GAALLNTERSASDRAPAEALIREKFPALDEMDQDQLDQHVSRWKDQTPHRSPTGMSPCCP1PSRRATDMSIDHSGVSDGMAE5LGHSMKHKSMPDHSSCSRKLNTKWPMSMTDSIGSMFSADTITYKYDASSRSGSSASKLEEAKRRLDEPR
RSRRYAQPMQHLQQPLASFSSSGGSISLPHQFPPLPAKPPETIVVFSFCEEPVYRIKIPGTQTLRQFKDYLPRRGHFRFFFKTHCEDPDSVPIQEEIVNDSILPLFGDKAMGLVKPSD

Hydra vulgaris:

>XP_002155943.3 PREDICTED: uncharacterized protein LOC100206389 [Hydra vulgaris]
MSSTALRPTFMGKAVTINFEESLSKSNINNKSIVANMHIKENGSYCENFNNTSYPNFEKWKDNFQVLEDEEGMRTFYEFGLTDQISVIFDCWYSCKTYRKRLPNKAAAEVYSRFVRIKDSRVPISDQARNNLALRLRANDITETLLLEIEQ
EIFANLRDVCYPKFLKSDFFTFYCETNGQVAHIPSEFHRLNQGVISKMQHNLPTLTEDYADIYHTQASESGEDFHHCNDYVPMPFTFQSRTQRMDSMKQLAPEQFAKLLTEKLERLLLDREAENFTDPQLLNQNVLSSHGLPIQRSYKPAISDV
DSQSWVMPASVRYSVAGASSTSGSCVNIIEQYPKYRNLAQDFLNAVHHGIRNHLGECQCISCQDCSRNSHHYIQESYFDSQELIKNEIFSKSNFDQSQLFNKLEYNTHNAFIQPAEPPPLVDTSKIYAMMEKNERQEKQNNYVAPSPIVRHKKLQ
NVPEAPIAQDHNMLLPQPDGTGTVLTEVKRVLEEPKSTRRLSRSHQQRPSNVHGDHMSAISDPSYDQRHRHVGNWSSFSDTNSVVSYNPSQISSVPSCASRLWNQYGYEYEPKNELLYRGRHLSQDGMKRNENSVNHRDRHSDRDLKSTRRS
HSDVSHPLSETRSERTHGSGNSKRTSKNSTTITYYFDTEPIPYRITIPSSSEVTLGQFKAETKRGNFRIFFKTIISAEDGEIVNEELRSDDEYLPKYNKNIIGKIEKVE

Nematostella vectensis:

>XP_001636924.1 axin-1 [Nematostella vectensis]
MSEELCSTMLEFATISVSSSESDFASVSEAGIVKDDDLKSSVAQLTPRRFTSRDLQENRDRLCITDEDKLAPLGFEPEGRAVSSPTCYCERWANSFTDLLNDSGNSLFYKYLRRREGASILLDFSRECEAYRRMVPTSTQMRTTAKTLFQKFVYPRQ
FCELLGVKDTTRTQIAHHVNDQPADPALFDGAYAEVVSVMKKCHYVGFVNSNLYKDFQAHRTDTETLTGERTPQYPGRYHSGYLPPLPEEKVLGFGEIEEEEQFELDQSCKDAIRYPYIRSAHDEQDARKLLHAPMKDIISQYYPSPVPLASRT
ESENQSLSSDALTDDTLSTLSMTTTEGGMTDTS DGLSIPNRSRRRRGAAHKSRNGGPLPHFFVPRSHRMPKEAKNPLQPEEFAKILISKLEKVKLERELMEREASNLGICESEYGGQSKKILQEALENKQROGKIPLCTMAMSALPPMQDDAS
SLSASNHGSSSSKSTNAQVITAGSTVRDSSSSGSTHRRSRHSHHSTKTPKQEQECADKDSDLASAQGKDPSPRSNTKPANTARPDCCIPLFTLNHQRIQLQWMEMGEEELRQOKTQKVRHQSPSSSSSRGSSKSRQSSSTKGSEHYSNHPSPQPIAQD
PLMPPLPQPEATTVLGEVARRLVATKEMDKSRHHHHKHSKTSVDDISDSVSSCQEKIGSSSTCSCSATDCSSCAQMSLSYDINHAPSYIASSTLSSIPSSASNYPSDTKSKSDSGISGTTRKKEKHNAITIIYWLWGEPIAYRTSLPGKHITL
GQFKTLIMRKGEFRYFFKTKTEDRECEVVVEEVKEDKMMLPTFEGKIVGKVEKVD

Amphimedon queenslandica:

>NP_001266244.1 axin [Amphimedon queenslandica]
MAAIVSGNDHELALAEALQRIGGEPGTDEEDDEELSVVEYDEEQRPAPTASVVS GPAPETTTNGDNGAGGGGRYEVPEPIYIGTPSNSVPLKEVLGEYRSFMLFRRLKDKQCITRNLQFWLACEYYHTQMPLEGIAKAAKIYCRFLKSSAPLHV
SILEATKRKICTIVQLGSPPGYTLFLEAQEVYNQMEVNELQQFLCSDSFSECSQFPTRGPTQNMYGVSVDIGFQPSPRYRNGGSLHSSDDSTSVTSFASQEDVGSHTHTQVLCPLPHHTKSVYTPRNAHSDTEHSSSHPRRQYAGPTTHISRNVL
TQNQFYIEICEKLSAVQRDRATAMKQARNAIARIAGKSYEDIMSIDWFDTPFAIKYVCFDDEGTVAGADDGLHSPPLSLPPPHKQSVGKRTTVESSDTPPSSSTSGAPSHHLISFGLKEIQEALRDLDIASQVRQKRSTLTMSSSASSYISDSGVGE
SNLPSSSGGGPGSSGHNRLSNRVHAYLQNRQRTVSQQSREAAQQLVATMLMNNVSPSDELNPHYHNGRRSYANYPGAYSSDDSSSCFTATSHSSNSEFFVPRRPHPLYGDSNDESRQQSHHHSRYPPGMRRLAPSNRPPSSRYLPQQTTPN
QPPQQQLSTSNRAISPVSHPSSKSSSDTLVAYSWEGKTYANKLQVSLTLGFEKRMFKRKQYRFFFKSFCEELNDVILEEISDNSVTPLPLHEGKIYVQVEGITD

Alignment

NP_001266244.1 [A.queenslandica]	-----MAAIVSGNDHELALALEALQ RIGGEGPTDEEDDEELS VVEYDEEEQRPPAPTASVV	55
XP_002155943.3 [H.vulgaris]	-----MSSTL PTTWG SAV	16
AAD24886.1 [D.melanogaster]	-----MS-----GHPSG-----I--RKHD-----DNECSG RPFPVPGEE SR	29
XP_001636924.1 [N.vectensis]	-----MSIGVQ--EYLQD-----TGGSKFT-----ELCSTML TPATPTG SS	20
XP_019639671.1 [B.belcheri]	-----MSV--SEKLQRLD-----LSHIIEN-----AL---TRFPVPG RG SK	35
XP_032816874.1 [P.marinus]	MDAVNMSVGDYGVGLVD-----LGGSFT-----ED---AP RPVPGEE GE	32
XP_014059686.1 [S.salar]	MQSPYMN--VQEQGFPLD-----LGASFT-----ED---AP RPVPGEE GE	36
EDL22489.1 [M.musculus]	-----MN--IQEQGFPLD-----LGASFT-----ED---AP RPVPGEE GE	31
NP_003493.1 [H.sapiens]	-----MN--IQEQGFPLD-----LGASFT-----ED---AP RPVPGEE GE	31
XP_024089076.1 [P.abelii]	-----MN--IQEQGFPLD-----LGASFT-----ED---AP RPVPGEE GE	31
NP_990275.1 [G.gallus]	-----MN--IQEQGFPLD-----LGASFT-----ED---AP RPVPGEE GE	31
NP_001089251.1 [X.laevis]	-----MS--VKAKGFPLD-----LGGSFT-----ED---AP RPVPGEE GE	31

NP_001266244.1 [A.queenslandica]	SG-----PAP-----ETTNGD	67
XP_002155943.3 [H.vulgaris]	TINFEKSLKSNINNK-----SKVANM-----HYIKE	43
AAD24886.1 [D.melanogaster]	VKKMTEG-----ESDFASVSEAGIVKDDDLKSSVAQLTPRRFTRSDLQENRDLCTDEDKLAP	36
XP_001636924.1 [N.vectensis]	SNHGSQHSSSNTKSEYSTKSDYSKSDYSHSSAGTTPR-----RTNCD	71
XP_019639671.1 [B.belcheri]	VNVWPEHCNDPLGARA-NGVKGGSGLDGFVRMMPR-----RMDGD	73
XP_032816874.1 [P.marinus]	LVSSDGRPYGHGFY----SFKGTSILKNEASTATPR-----RPDL	74
XP_014059686.1 [S.salar]	EDL22489.1 [M.musculus]	72
NP_003493.1 [H.sapiens]	LVSTDPSPASYSFC-----SGKGVGIGKETSTATPR-----RSDLD	67
XP_024089076.1 [P.abelii]	LVSTDPSPASYSFC-----SGKGVGIGKETSTATPR-----RSDLD	67
NP_990275.1 [G.gallus]	LVSTDPSPASYSFC-----SGKGVGIGKETSTATPR-----RSDLD	67
NP_001089251.1 [X.laevis]	LITTDQRFPSTYY-----SLKNDGIKNETSTATPR-----RPDL	67
NP_001266244.1 [A.queenslandica]	NGAGGGGRYEVPEPYIGTPSPNSVPLKEVLGEYRSFMLFRFLKQDC--ITRNLFQWLACE	125
XP_002155943.3 [H.vulgaris]	NGSYCENFNNTSYPNFEKW--KDNFQVLLDEDEGMRTFYEFGLTDQ--ISVIFDCWYSCK	99
AAD24886.1 [D.melanogaster]	---VADTSKNSSPSYL-NW--ARTLNHLLEDRDGVLFYKYVEEAPAYNDHNFYFACE	90
XP_001636924.1 [N.vectensis]	LGFEPEGRAVSPTPYCERW--ANSFTDLNDSNGSNLKYKLRREG--ASILLDFRECE	127
XP_019639671.1 [B.belcheri]	LGFEPEGSASPTPPYL-RW--ADNLQALLSDKDGSQLGLYLENED--SKHLLDFYFAVN	132
XP_032816874.1 [P.marinus]	LGFEPEGSASPTPPYL-RW--AESLPALLEDQDQGSILFRAFLQED--CVDLLDFWFACS	128
XP_014059686.1 [S.salar]	LGFEPEGSASPTPPYL-KW--AESLSHLLDDQDGIHLFRTFLKQEE--CADVLDWFFACT	129
EDL22489.1 [M.musculus]	LGFEPEGSASPTPPYL-KW--AESLSHLLDDQDGIHLFRTFLKQEE--CADVLDWFFACT	127
NP_003493.1 [H.sapiens]	LGFEPEGSASPTPPYL-KW--AESLSHLLDDQDGIHLFRTFLKQEE--CADVLDWFFACT	122
XP_024089076.1 [P.abelii]	LGFEPEGSASPTPPYL-KW--AESLSHLLDDQDGIHLFRTFLKQEE--CADVLDWFFACT	122
NP_990275.1 [G.gallus]	LGFEPEGSASPTPPYL-KW--AESLSHLLDDQDGIHLFRTFLKQEE--CADVLDWFFACT	122
NP_001089251.1 [X.laevis]	LGFEPEGSASPTPPYL-KW--AESLSHLLDDQDGIHLFRTFLKQEE--CADVLDWFFACT	122
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NP_001266244.1 [A.queenslandica]	YHHTQMPLEG-----IKAAKAIYCRFLKSSAP--LHVSILEATKRKICTIVQLGSPPGY	177
XP_002155943.3 [H.vulgaris]	TYRKRLPNKA-----AAKEVYSRFRVRIKDSRVPISDQA---RNNLALRLANDITE	147
AAD24886.1 [D.melanogaster]	GLKQQTDD----PEKIKQIGAIYRFLRK-SQ--LSISDDLAQIK--AIKTNPEIPLSP	140
XP_001636924.1 [N.vectensis]	AYRRMVPSTQ-----MRTTAKTLFQKFVYPRQ--FCELLGVKDTTRTQIAHVNDQPADP	181
XP_019639671.1 [B.belcheri]	GYKKLDPLD-----DKTORLAKVYVAKYIKEGK--GILSHRVKPGTKYLAKNIDCKPLDI	186
XP_032816874.1 [P.marinus]	GFRKTD-----GDKRAKLAKAIYKKYIKDNA--GIVLRQIGSITRTGVKECIASKRIDS	180
XP_014059686.1 [S.salar]	GFRKLEANEGQGEKKLKLAKAIYKKYILDDN--GIVSRQIKPATKSFIKDCVMKRLHIDP	187
EDL22489.1 [M.musculus]	GFRKLEPCDS-NEEKRLKLARAIYKKYILDDN--GIVSRQIKPATKSFIKDCVMKRLHIDP	184
NP_003493.1 [H.sapiens]	GFRKLEPCDS-NEEKRLKLARAIYKKYILDDN--GIVSRQIKPATKSFIKDCVMKRLHIDP	179
XP_024089076.1 [P.abelii]	GFRKLEPCDS-NEEKRLKLARAIYKKYILDDN--GIVSRQIKPATKSFIKDCVMKRLHIDP	179
NP_990275.1 [G.gallus]	GFRKLEPCDS-NEEKRLKLAKAIYKKYILDDN--GIVSRQIKPATKSFIKDCVMKRLHIDP	179
NP_001089251.1 [X.laevis]	GFRKLEPCDS-NEEKRLKLAKAIYKKYILDDN--GIVSRQIKPATKSFIKDCVMKRLHIDP	179
	: : :	
NP_001266244.1 [A.queenslandica]	TLFLEAQEQEVYNQMEVNELQQFLCSDSFSECSQFPTRGPTQNNY-G--SVSGDIG----	229
XP_002155943.3 [H.vulgaris]	TLILLEIEQEIFANLRDVCYPKFLKSDFFTFYCETNGQVAHISEFHRIN-----	196
AAD24886.1 [D.melanogaster]	HIFDPMQRHVEVTIRNDYPTFLCSEMYILYIQQMSAQERCTSSGA-TGSGSAGSSSGG	199
XP_001636924.1 [N.vectensis]	ALFDGAIYAEVVSVMKCHYGVFNSNLNKKDPTQAHRDTEITL-----GERTP-----	229
XP_019639671.1 [B.belcheri]	SIFDQAQLEIEKFMENAYRFLFESDIYLYQYCRNGGEVSPNQVYTELANTSNGVC-	241
XP_032816874.1 [P.marinus]	TMFDRAQEEVQTAMEENAYPAPLRSDDVYLAVARSGGESPRCA--DPLPAGFMAM----	233
XP_014059686.1 [S.salar]	AMFDQAQTEIQMTMEENTYPLFLKSDIYLEYTRTGSESPKLYS--DQCSVSG-GG----	239
EDL22489.1 [M.musculus]	AMFDQAQTEIQMTMEENTYPSFLKSDIYLEYTRTGSESPKLYS--DQSSSGSG-TG----	236
NP_003493.1 [H.sapiens]	AMFDQAQTEIQMTMEENTYPSFLKSDIYLEYTRTGSESPKLYS--DQSSSGSG-TG----	231
XP_024089076.1 [P.abelii]	AMFDQAQTEIQMTMEENTYPSFLKSDIYLEYTRTGSESPKLYS--DQSSSGSG-TG----	231
NP_990275.1 [G.gallus]	DMFDQAQTEIQCMIEDNTYPLFLKSDIYLEYTRTGSESPKIYS--DPSSSGSG-TG----	231
NP_001089251.1 [X.laevis]	AMFDQAQMEIQSMMEDNTYPVFLKSDIYLEYTRTIGGESPKNYS--DQSSSGSG-TG----	231
	: : . * : :	
NP_001266244.1 [A.queenslandica]	-----	229
XP_002155943.3 [H.vulgaris]	-----	196
AAD24886.1 [D.melanogaster]	GSSLAGACALPPTTASGRQQLPQLVPPGAFINLPSVSSVSGPPAGTCSASGSVYGPSTAS	259
XP_001636924.1 [N.vectensis]	-----	229
XP_019639671.1 [B.belcheri]	-----	241
XP_032816874.1 [P.marinus]	-----	233
XP_014059686.1 [S.salar]	-----	239
EDL22489.1 [M.musculus]	-----	236
NP_003493.1 [H.sapiens]	-----	231
XP_024089076.1 [P.abelii]	-----	231
NP_990275.1 [G.gallus]	-----	231
NP_001089251.1 [X.laevis]	-----	231
NP_001266244.1 [A.queenslandica]	-----FQPSRYRNGGS--LHS-----SDDSTSVSF-----A-----	254
XP_002155943.3 [H.vulgaris]	-----QGVISKMQHNLPTLTEDYADIYHTQAS-----	223
AAD24886.1 [D.melanogaster]	SSGSISATDTLPRSSTPLTLHEDSVLSLCCDFEKVQMQEGGSLGSGVAGARAPDYPI	319
XP_001636924.1 [N.vectensis]	-----QYPGRYHSGYLPTLPEEKVLGFGEETEEQFELD-----	263
XP_019639671.1 [B.belcheri]	-----NLTTGAILAPLPTLHENVELSTEDTMTET-----L-----	272
XP_032816874.1 [P.marinus]	-----KGL--DSPGLQTVKEDEVLSYDSQQTTHRWPEVHCGMR-----	270
XP_014059686.1 [S.salar]	-----KVL-----PGYLP TLNDEEWRCDHELEQQESDPTPSNR-----	274
EDL22489.1 [M.musculus]	-----KGM-----SGYLP TLNDEEWRCKDQADEDDGRDPLPPSR-----	271
NP_003493.1 [H.sapiens]	-----KGI-----SGYLP TLNDEEWRCKDQMEDDDGRDAAPPGR-----	266
XP_024089076.1 [P.abelii]	-----KGI-----SGYLP TLNDEEWRCKDQMEDDDGRDAAPPGR-----	266
NP_990275.1 [G.gallus]	-----KGL-----PGYLP TLNDEEWRCKDQTEPEASRDSAPSSR-----	266
NP_001089251.1 [X.laevis]	-----KGP-----SGYLP TLNDEEWRCKDQGEQ--ERESVPSFL-----	264
	: :	
NP_001266244.1 [A.queenslandica]	-----SEDVGS---THTQVLCLPHHTKSIVYTPRNAHS--DTEH	287
XP_002155943.3 [H.vulgaris]	-----ESGEDFHH---H---CND-----Y-----	236
AAD24886.1 [D.melanogaster]	RLTRDLLLATQKRR-----LEIRPPGAHGYYVNPSTNTSYVP--NSRVDSE	365
XP_001636924.1 [N.vectensis]	---QSKCD--AIRYPYIRSA-HDEQDARKLLH--APMKDII SQYYPSVPLASRTESEN	314
XP_019639671.1 [B.belcheri]	PLTAEHLLATSQIRL-----RSDSRDRERLTRG--GNPYH--QTYAPAPATSANDEL	321
XP_032816874.1 [P.marinus]	PTGGSSCSFVASPRVGMPSSEKGGKYRNLWPNGPVNPNHMSGYGRAPASSANDEQ	330
XP_014059686.1 [S.salar]	LTQKLLQETASQRTVSTKRF-QDSHEYRVLWQ-EPVNPYYVNTGYAMAPATSANDEQ	331
EDL22489.1 [M.musculus]	LTQKLLLETAAPRAPSSRRY-NEGRELRYGWSR-EPVNPYYVNTGYALAPATSANDEQ	328
NP_003493.1 [H.sapiens]	LPQKLLLETAAPRVSSRRY-SEGREFRYGWSR-EPVNPYYVNTGYALAPATSANDEQ	323
XP_024089076.1 [P.abelii]	LPQKLLLETAAPRVSSRRY-SEGREFRYGWSR-EPVNPYYVNTGYALAPATSANDEQ	323
NP_990275.1 [G.gallus]	LTQKLLLETAQRATSTRY-SEGREFRYGWSR-EPVNPYYVNTGYAMAPATSANDEQ	323
NP_001089251.1 [X.laevis]	FSQKLILDSSSHCAGSNRRL-SDGREFRPGTWR-EPVNPYYVNTGYGAPVTSANDEQ	321

NP_001266244.1[A.queenslandica]	SSSH-----P-----RR-----QQ	296
XP_002155943.3[H.vulgaris]	-----VPE-----	239
AAD24886.1[D.melanogaster]	ASVSSGGRTSDTMSI-----SSCSMDGRPIYQIR-RHSSTESKAIRQSAMANKET	414
XP_001636924.1[N.vectensis]	QSLSSDA-LTDDTLSTLSMTTTEGMDTDS-DGLSIPRNSRRR-----RGAHKSRRNGGPL	368
XP_019639671.1[B.belcheri]	QSLSSE--QTDDTMSL-----TDSSIDLGVSNHRRRRRLQGMQRQDAQRNGV	369
XP_032816874.1[P.marinus]	SLSSDA--MTDDTMSM-----TDSSVDGIPPYRLRSCAS--RUTRQSAKDSGR	375
XP_014059686.1[S.salar]	QSMSSA--SDVDTLSL-----TDSSVDGIPPYRIRKQHR--REMHESAKANGRV	376
EDL22489.1[M.musculus]	QSLSS--DADTSL-----TDSSVDGIPPYRIRKQHR--REMHESTQVNGRV	371
NP_003493.1[H.sapiens]	QSLSS--DADTSL-----TDSSVDGIPPYRIRKQHR--REMQUESVQVNGRV	366
XP_024089076.1[P.abelii]	QSLSS--DADTSL-----PDSSVDGIPPYRIRKQHR--REMQUESVQVNGRV	366
NP_990275.1[G.gallus]	QSMSS--DADTMSL-----TDSSIDGIPPYRLRKQHR--REMQUESAKANGRV	366
NP_001089251.1[X.laervis]	QSMSS--DADTMSL-----TDSSVDGIPPYRLRKQHR--REMQUESANANGRV	364
NP_001266244.1[A.queenslandica]	YAGPTTHISR-----K--VLTQNQFYIEVCEKLSAVQDRDTAMQQRARNIARIAGKSY	348
XP_002155943.3[H.vulgaris]	--MPTFQSRQRMDSMKQ--LAPEQFAKLLTEKLERLLLDREAENFTDPQLLNQNVLS-	293
AAD24886.1[D.melanogaster]	--NTFQVIPRTQRLHSNEHRPLKEEELVSLLPKLEEVKRRQDLEERARNRFGAALLTN	472
XP_001636924.1[N.vectensis]	--PHFPFVPRSHRMPKEAKNPLQPEEFKAILISKLEKVKLERELMEREASNLSGI---CE	423
XP_019639671.1[B.belcheri]	MCYPPFPQPRQRLPKEMK-MMEPKFAELLIAKLEKVKQDRENKERLDEQLRMEGDCG	428
XP_032816874.1[P.marinus]	---EVVHIPRTSRLPKDMV--VEPAKFAELISRLEQLQREDAQEAELEERLRVRAE--	428
XP_014059686.1[S.salar]	---PLPHIPRTNRIPKDIH--VEPEKFAADLISRLQVQREDAQEAELEERLRVRLE--	429
EDL22489.1[M.musculus]	---PLPHIPRTYRMPKEIR--VEPQKFAELIHRLEAVQRTREAEKLEERLRVRMVCP	426
NP_003493.1[H.sapiens]	---PLPHIPRTYRVPKEVR--VEPQKFAELIHRLEAVQRTREAEKLEERLRVRME--	419
XP_024089076.1[P.abelii]	---PLPHIPRTYRVPKEVR--VEPQKFAELIHRLEAVQRTREAEKLEERLRVRME--	419
NP_990275.1[G.gallus]	---PLPHIPRTYRMPKDIH--VEPEKFAELINRLEQVQREDAQEAEKLEERLRVRAE--	419
NP_001089251.1[X.laervis]	---PLPHIPRTYRMPKDIH--VDPEKFAELINRLEQVLDREAQRLERLRVRAE--	417
NP_001266244.1[A.queenslandica]	EDIMSIDMFDTPAIIKYVCFDDEGTVAGADGL---HSP-----	384
XP_002155943.3[H.vulgaris]	-----SHGLPIQ---RSYKP-----	305
AAD24886.1[D.melanogaster]	ERS-----SA---SDRA-----	481
XP_001636924.1[N.vectensis]	SEY-----GQSK-----	430
XP_019639671.1[B.belcheri]	ASQAS-----GESQASGADPT-----	445
XP_032816874.1[P.marinus]	-----EEGEGGPVATATCQA-----STTQVAAGCG	454
XP_014059686.1[S.salar]	-----EEGEDADISTSTSFSSHRLPGGHPQHYNPRYSIDIGS	468
EDL22489.1[M.musculus]	YSCSDSTA-----VSPQEEEGEDGEMSPG-MASHKLPSPVPA-WHHFPPRYVDMGCS	476
NP_003493.1[H.sapiens]	-----EEGEDGDPSSGPPGCHKLPPAPA-WHHFPPRCVDMGCA	457
XP_024089076.1[P.abelii]	-----EEGEDGDPSSGPPGCHKLPPAPA-WHHFPPRCVDMGCA	457
NP_990275.1[G.gallus]	-----EEGEDADISSGSPVISHKMPSAQF-FHHFAPRYSEMCA	457
NP_001089251.1[X.laervis]	-----EEGDDGVSSGPSIISHKLPSPGP-MHHYNSRYSDSGCV	455
NP_001266244.1[A.queenslandica]	-----PLSLPPPH---KQSVGKR-----TT-----	401
XP_002155943.3[H.vulgaris]	-----ALSVDV-----SQSWVM-----P---PASVRY-----	324
AAD24886.1[D.melanogaster]	-----FAEAIREKFPALDEDNDQDILDQH---VSRVMKQDTPHRSPTGMSPCPPIPS-	529
XP_001636924.1[N.vectensis]	-----KSILQEALENKQKQKI-----PLCTMAMSALPP----	459
XP_019639671.1[B.belcheri]	---QPRLPFLMDDTTISDDDPESILDEH---VSRVLQT-----PGCRSPGRHSPV----	489
XP_032816874.1[P.marinus]	GGGQMAAVPVSFLSPEDDDDPESILDEH---VSRVMKT-----PGCQSPGHHGGGGAG	505
XP_014059686.1[S.salar]	G-----LALRPDAHEENPESILDDH---VQVRMKT-----PGCQSPGTGRHS---P	508
EDL22489.1[M.musculus]	G-----L--R-DAHEENPESILDEH---VQVRMKT-----PGCQSPGPHR-----	511
NP_003493.1[H.sapiens]	G-----L--R-DAHEENPESILDEH---VQVRMKT-----PGCQSPGPHR-----	492
XP_024089076.1[P.abelii]	G-----L--R-DAHEENPESILDEH---VQVRMKT-----PGCQSPGPHR-----	492
NP_990275.1[G.gallus]	G-----MQMR-DAHEENPESILDEH---VQVRMKT-----PGCQSPGPHRHS---P	496
NP_001089251.1[X.laervis]	G-----MQMR-DAHEENPESILDEH---VQVRMKT-----PGCQSPGTGRHS---P	494
NP_001266244.1[A.queenslandica]	-----VESSDTPPSSTSG-----	418
XP_002155943.3[H.vulgaris]	-----SVAGASSTSGSCVNIQYPKYRNLAQDFL-NAV-----	356
AAD24886.1[D.melanogaster]	---RRKTATH-----DSGMVDGAMSLSGHSM-----	553
XP_001636924.1[N.vectensis]	---MQDDASSLSA-----SNHGSSSSKSTNAQV---TAGSVTRDSSSSSGSTHRRS---	503
XP_019639671.1[B.belcheri]	---RPNKSHISGVPHVSPFAGALAGASAMAWNHRRG---PKDVSKRDSGLGDSTEAEVT	543
XP_032816874.1[P.marinus]	KPRSDSRPHPG-----VVRPQALAAIKGAETA---AAGQASS-AS---QSHHRTVY	554
XP_014059686.1[S.salar]	KSRSPDGPFPGGK-----VPGQMPPTT---GPGKHP-----ARLGPKEAA---SHQYHHKH-	553
EDL22489.1[M.musculus]	---SPDSGHVAK-----TA-VLGGTAS---GHGKHV---PKLGLKLDTA---GLHHHRHV-	553
NP_003493.1[H.sapiens]	---SPDSGHVAK-----MPVALGGAAS---GHGKHV---PKSGAKLDAA---GLHHHRHV-	535
XP_024089076.1[P.abelii]	---SPDSGHVAK-----MPVALGGAAS---GHGKHA---PKSGVKLDAA---GLHHHRHV-	535
NP_990275.1[G.gallus]	KPRSPESGHLGK-----LSGTLGTIPP---GHGKHT---TKSGMKLDAA---NLHYHKKHV-	542
NP_001089251.1[X.laervis]	KPRSPDGHLSKT-----LPGLGTMQT---GHGKHS---SKSGKVDSG---NLHHHKKHV-	540
NP_001266244.1[A.queenslandica]	-----HLISFGLKE-IQEALR-DLDIASQVRQKRSTL-----MSSSASSYISDSGVGE	465
XP_002155943.3[H.vulgaris]	-----HHGIRNHLGE-----CQCISCQDCSRN-----SHHYIQES--YF	388
AAD24886.1[D.melanogaster]	-----KHKSMPD-----HSSCSRKLTN--KWP-----	574
XP_001636924.1[N.vectensis]	-----RH--SHHSTKTPKQ---EQECAD-----KDSDLA	520
XP_019639671.1[B.belcheri]	HYHKYYYHHHHHHPKSRDGLKQTEMETQRKVQR-----DSEMYTTQSRVHQ	597
XP_032816874.1[P.marinus]	HHHHHHH1HHHAASKARE-----QLEVEAAQRVYGGGGGGGGVNGTAESFFYAAKSRNGA	601
XP_014059686.1[S.salar]	---VHHIHPAGGKPK-----QVEADAAMRVNNGNFHW-----GTEHNYGSKSRNYA	599
EDL22489.1[M.musculus]	---HHVHHN--SARPK-----QMEAEVARRVQSSFSW-----GPETHGHA-KPRSYS	596
NP_003493.1[H.sapiens]	---HHVHHN--TARPK-----QVEAEATRAQSSFAW-----GLEPHSGHARSRGYS	579
XP_024089076.1[P.abelii]	---HHVHHN--TGRPK-----QVEAEATRAQSSFAW-----GLEPHSGHARSRGYS	579
NP_990275.1[G.gallus]	---YHHLHHHSMKPK-----QIEAEATQRVQNSPAW-----NVDSHNHYATKSRNYA	587
NP_001089251.1[X.laervis]	---YHHLHHHGGVKPK-----QIEAEVTRQVQNTYPW-----NAESHNYATKSRNYA	585
NP_001266244.1[A.queenslandica]	SNLPSSSGSGPGPSS-----GHNSRLSNRVHAYLQNOQ-----R-----VTSQQSERE	508
XP_002155943.3[H.vulgaris]	DSQ-----EL-----IKNEIFSKSNFDQSLFNKLEYTNHAFI--QPAEPFPLV	431
AAD24886.1[D.melanogaster]	-SM-----NTD-----SG-----ISMFSAD--	588
XP_001636924.1[N.vectensis]	SAQ-----GKDPS-----RSNTKPANTA-----RP-----DDCIPFTLT	556
XP_019639671.1[B.belcheri]	DSM-----GGT---AESLRHDARREVVGKRGGRGKE-----EGEP---FLALPVETD	631
XP_032816874.1[P.marinus]	ENL-----P--PGITNTLPTSNKPGTLGKKSXSGSGSK---AEEAPLEEGRIRVLEEVP	659
XP_014059686.1[S.salar]	DGT-----GPSMPDPMGYSSKSTLSKRSFKKAEV-----RTFE--VPVPTEDVE	643
EDL22489.1[M.musculus]	ENA-----GTTLS-AGDLAFGGKTSAPSKRNKKAESGK---N--ANAE--VPSTTEDAE	643
NP_003493.1[H.sapiens]	ESV-----GAAPNASDGLAHSGKVGACKRNKKAESGK---S--ASTE--VPGASEDAE	627
XP_024089076.1[P.abelii]	ESV-----GAAPNASDGLAHSGKAGVACKRNKKAESGK---S--ASTE--VPGASEDVE	627
NP_990275.1[G.gallus]	ENL-----GMAPVPMSDLGYSKGASLLSKRNIKKTDSGK---SDGANYE--MPGSPEDVE	637
NP_001089251.1[X.laervis]	ESM-----GMAPNPMDSLAYSGKVMKSKRNKKAADVKG---SESASYE--VPAPVEDAE	635
NP_001266244.1[A.queenslandica]	AQAQLVATMLMNNVSPSDE-LN---PYHNGR---RSYANYPGAYSSDDSSSCTATSH	560
XP_002155943.3[H.vulgaris]	DTSKIYAMMEKNERQEKQNNYVA-----	454
AAD24886.1[D.melanogaster]	-----TVT---KYKD-----AS-----	597
XP_001636924.1[N.vectensis]	NHQRIQLQWMMEGEELRQOKTQKVR-----HQSPSSSSSRGSSK-----	595
XP_019639671.1[B.belcheri]	RFGKVDWMMEGEERERYRGGVNVREPKFKRSSKTASQATHRSSGKASSSAAKPP-LAYNT	690
XP_032816874.1[P.marinus]	DRFRIMQWMVQGEKEAGRHAKT-----TTTSSGSPSK-----	691
XP_014059686.1[S.salar]	RNQKILQWMMEGEAVRNKKSFY-----GSTTGSKKTP--SSHEV	680
EDL22489.1[M.musculus]	KNQKIMQWIIIEGEKEISRHRKA-----GHGSSGLRKKQ-QAHES	680
NP_003493.1[H.sapiens]	KNQKIMQWIIIEGEKEISRHRRT-----GHGSSGTRKKP-QPHEN	664
XP_024089076.1[P.abelii]	KNQKIMQWIIIEGEKEISRHRRT-----GHGSSGTRKKP-QPHEN	664
NP_990275.1[G.gallus]	RNQKILQWIIIEGEKEISRHKKT-----NHGSSGVKKQ--LSHDM	674
NP_001089251.1[X.laervis]	RHQKILQWIMEGEKEISRHKKS-----NHSSSSAKKQ--PPPEL	672
NP_001266244.1[A.queenslandica]	SSNEEFFVPRRPHL-----YGDSDNESRQQSHHSRYPPGMRR	599

XP_002155943.3[H.vulgaris]	--PSPIV-----RHKKLQNVPEAPIAQDHNMLLPQPDGTGTVLTVKRV	496
AAD24886.1[D.melanogaster]	SR-----SGSSTASKLEEAKRR	614
XP_001636924.1[N.vectensis]	SRQSS-STKG-----SEHYSNHHKPSQPIAQDPLMPPLQPEATTVLGEVARR	641
XP_019639671.1[B.belcheri]	SRPTSMERPAV-----TAEVRPMQPFMQDTPMPVLPQPNPLICLEEARRR	735
XP_032816874.1[P.marinus]	--KGSEATPRAAHAWSGVATAQRAPAVGTQPSQPFVQDGPMPPLPAPNPLTQLEEARRR	749
XP_014059686.1[S.salar]	SRPSSVERPGAVHPWVSAQL-----RNVVQPSHPFIQDPTMPNPNAPNPLTQLEEARRR	734
EDL22489.1[M.musculus]	SRPLSIERPGAVHPWVSAQL-----RNSVQPSHLFIQDPTMPNPNAPNPLTQLEEARRR	734
NP_003493.1[H.sapiens]	SRPLSLE-----HFWAGFQL-----RTSVQPSHLFIQDPTMPHPAPNPLTQLEEARRR	713
XP_024089076.1[P.abelii]	SRPLSLEPGAVHPWAGFQL-----RTSVQPSHLFIQDPTMPHPAPNPLTQLEEARRR	718
NP_990275.1[G.gallus]	VRPLSIERPVAHVHPWVSAQL-----RNVVQPSHPFIQDPTMPNPNAPNPLTQLEEARRR	728
NP_001089251.1[X.laevis]	SRPLSIERPGAVHPWVSAQL-----RNVVQPSHPFIQDPTMPNPNAPNPLTQLEEARRR	726
	*	
NP_001266244.1[A.queenslandica]	LAPSNRRPPSSRYLPQQTTP-----	619
XP_002155943.3[H.vulgaris]	LEEPKSTRRLSRSHQQ--RPSNHVGDHMSAYSDFSYDQRHRHVGNWSSFSDTNSVVSYN	554
AAD24886.1[D.melanogaster]	LEDEFRRSRRYAQPFMQHLSQQFLASFSSSG-----GS-----	647
XP_001636924.1[N.vectensis]	LVATKEMDKKSRHHHKKHRSKTSVDDISDSV-----SSCQEKIGSSTCSCSA-----	688
XP_019639671.1[B.belcheri]	LVEKSSSTKGSS-----RH--V--VD-S--GARKDKG-----	759
XP_032816874.1[P.marinus]	LLEEEKRSARVPP-----RSRQ--TQETLQRN-----RSFQRA-----	781
XP_014059686.1[S.salar]	LEEEKKKTGTLTQT--KQRY--VMEVIQRG-----RAAARPA-----	766
EDL22489.1[M.musculus]	LEEEKKRANKLPS--KQRY--VQAVMQRG-----RTCVRPA-----	766
NP_003493.1[H.sapiens]	LEEEKKRASRAPS--KQRY--VQEVMRRG-----RACVRPA-----	745
XP_024089076.1[P.abelii]	LEEEKKRASRAPS--KQRY--VQEVMRRG-----RACVRPA-----	750
NP_990275.1[G.gallus]	LEEEKKRAGKLPL--KQR-----	744
NP_001089251.1[X.laevis]	LEEEKKRAAKMPQ--KQRY--VQEVQIRG-----RCSVRPA-----	758
	*	
NP_001266244.1[A.queenslandica]	-----	619
XP_002155943.3[H.vulgaris]	PSQISSVSPSCASRLWNQYGYEFPKNELLYRGRHLSQDGMKRNENSVNHRDRHSRDLKS	614
AAD24886.1[D.melanogaster]	-----	647
XP_001636924.1[N.vectensis]	-----TDCSSCAQSMIL--SYDINHPPAPSYIA-----S	713
XP_019639671.1[B.belcheri]	-----KL-----	761
XP_032816874.1[P.marinus]	-----GS-----	783
XP_014059686.1[S.salar]	-----LF-----	768
EDL22489.1[M.musculus]	-----CA-----	768
NP_003493.1[H.sapiens]	-----CA-----	747
XP_024089076.1[P.abelii]	-----CA-----	752
NP_990275.1[G.gallus]	-----	744
NP_001089251.1[X.laevis]	-----YI-----	760
NP_001266244.1[A.queenslandica]	----NQP-----PQQQLSTSNRAISPSVHPSSKSSSDTLVAYSWEQK--TYANKLQV	666
XP_002155943.3[H.vulgaris]	TRRSDDVHSDVSHPLSE---TRSERTHGSGN--SKRTSKNNTTITYYFDTEPIPYRITIPS	669
AAD24886.1[D.melanogaster]	-----ISLPH-----Q-----FP--PLPAKPPETIIVVFSFCEEPVPIYRIKIPG	683
XP_001636924.1[N.vectensis]	STLSSIPSSASNYPSD--TKSKSDSGISGTT--RKKEKHNTATILYMLWGEPIAYRTSLPG	770
XP_019639671.1[B.belcheri]	PQSKVVPVAVSDLEPEEETRKQPVKK--PAS--MMSVSGDNTVVGYYFCGEPIPYRTTLPG	817
XP_032816874.1[P.marinus]	QNPNSSPSID---LDADRELKA-GK--KSA--CQVEASDSVVVYVYFCGEPIPYRTSVRG	835
XP_014059686.1[S.salar]	PPLSVVPAVSDTELSE-SEHKVTKK-----PACENITVAYYFCGEPIPYRTSVRG	817
EDL22489.1[M.musculus]	PVLGVVPAVSDLELSE-TETKSQRK--AGG--GSAPPDCDSIVVAYYFCGEPIPYRTLVRG	823
NP_003493.1[H.sapiens]	PVLHVVPVAVSDMELSE-TETRSQRK--VGG--GSAQPCDSIVVAYYFCGEPIPYRTLVRG	802
XP_024089076.1[P.abelii]	PVLRVVPAVSDMELSE-TETRSQRK--VSG--GSAQPCDSIVVAYYFCGEPIPYRTLVRG	807
NP_990275.1[G.gallus]	-----LKPQKR--PGS--GASQPCENIVVAYYFCGEPIPYRTLVRG	781
NP_001089251.1[X.laevis]	PLLNVPVAVSDMDLSE-AELKPQK--TVS--SPSQPCENIVVAYYFCGEPIPYRTMVKG	815
	: : : * :	
NP_001266244.1[A.queenslandica]	SCLTLGEFKEKMFRRKQYRFFFKSFCEELN-DVILEEISDNSVTLPLHEGKIVGQVEGI	725
XP_002155943.3[H.vulgaris]	SEVTLGQFKA--ETKRGNFRYFFKTTISAE-DGEIVNEELRSDDEYLPYRNKIIIGKIEKV	726
AAD24886.1[D.melanogaster]	TQPTLRQFKDY-LPRRGHFRYFFKTHCEDPDSPIQEEIVNDSDLPLFGDKAMGLVKPS	742
XP_001636924.1[N.vectensis]	KHITLQGFCTL-IMRKGEFRYFFKTTEDRECEVVYEEVKEDKMMMLPTFEGKIVGKVEKV	829
XP_019639671.1[B.belcheri]	KDITLAIKFNK-ITKRGNYRYFFKCTSTEFGSNAVYQEVTEDEDLLPLMEGWKIVGKVERI	876
XP_032816874.1[P.marinus]	HVLTGLGHFKEL-LTKKGYRYRYFKKASEDFDCGVVYEEVQDDAILPIFEEKIKGKVERI	894
XP_014059686.1[S.salar]	RMVMLGQFKEL-LTKKGSYRYRYFKKVSNDF--GVVFEVREDDAILPIFEEKIKGKVEKI	874
EDL22489.1[M.musculus]	RAVTLGQFKEL-LTKKGSYRYRYFKKVSDEFDCGVVFEVREDEAVLPVFEKIKGKVEKV	882
NP_003493.1[H.sapiens]	RAVTLGQFKEL-LTKKGSYRYRYFKKVSDEFDCGVVFEVREDEAVLPVFEKIKGKVEKV	861
XP_024089076.1[P.abelii]	RAVTLGQFKEL-LTKKGSYRYRYFKKVSDEFDCGVVFEVREDEAILPVFEKIKGKVEKV	866
NP_990275.1[G.gallus]	RVVTLGQFKEL-LTKKGNRYRYRYFKKVSDEFDCGVVFEVREDDTILPIFEEKIKGKVEKI	840
NP_001089251.1[X.laevis]	RVVTLGQFKEL-LTKKGNRYRYRYFKKVSDEFDCGVVFEVREDDMILPIFEEKIKGKVEKI	874
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NP_001266244.1[A.queenslandica]	TD 727	
XP_002155943.3[H.vulgaris]	E- 727	
AAD24886.1[D.melanogaster]	D- 743	
XP_001636924.1[N.vectensis]	DS 831	
XP_019639671.1[B.belcheri]	E- 877	
XP_032816874.1[P.marinus]	E- 895	
XP_014059686.1[S.salar]	D- 875	
EDL22489.1[M.musculus]	D- 883	
NP_003493.1[H.sapiens]	D- 862	
XP_024089076.1[P.abelii]	D- 867	
NP_990275.1[G.gallus]	D- 841	
NP_001089251.1[X.laevis]	D- 875	