

ATG9A

Homo sapiens:

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>NP_001070666.1 autophagy-related protein 9A [Homo sapiens]
MAQFDTEYQRLEASYSDSPPGGEEDLLVHVAEGSKSPWHHIENLDLFFSRVYNLHQKNGFTCMLIGEIFEL
MQFLFVVAFTTFLVSCVDYDILFANKMVNHS LHPTPEVKVTLPD AFLPAQVCSARIQENGSLITILVIAG
VFWIHRLIKFIYNICCYWEIHSFYLHALRIPMSALPYCTWQEVQARIVQTQKEHQICIHKRELTELDIYH
RILRFQNYMVALVNKSLPLRFLPLGLGEAVFFTRGLKYNFELILFWGPGSLFLNEWSLKA EYKRGGQRL
ELAQRLSNRILWIGIANFLLCPLILIWQILYAFFSYAEVLKREPGALGARCWSLYGRCYLRHFNELEHEL
QSR LNRGYKPASKYMNCFSLPLLTLLAKNGAFFAGSILAVLIALT IYDEDVLAVEHVLT TTVTL LGVTVTV
CRSFIPDQHMVFCPEQLLRVILAHIHYPMDHWQGNNAHRSQTRDEFAQLFQYKAVFILEE LLSPIVTP LIL
IFCLRPRALEIIDFFRNFTVEVVGVDTC SFAQMDVRQHGHPQWLSAGQTEASVYQQAEDGKTELSMHF
AITNPGWQPPRESTAFLGLKEQVQRDGAASLAQGGLLPENALFTSIQSLQSESEPLSLIANV VAGSSC
RGPPLPRDLQGSRHRAEVASALRSFSPLQPGQAPTGRAHSTM TSGGVDARTASSGSSVWEGQLQSLVLSE
YASTEMSLHALYMHQLHKQQAQAE PERHVWHRRESDES GESAPDEGGEGARAPQSI PRSASYPCAAPRPG
APETTALHGGFQRRYGGITDPGTVPRVP SHFSRRLPLGGWAEDGQSASRHPEPVPEEGSEDELPPQVHKV
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Pongo abelii:

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>NP_001127287.1 autophagy-related protein 9A [Pongo abelii]
MAQFDTEYQRLEASYSDSPPGGEEDLLVHVAEGSKSPWHHIENLDLFFSRVYNLHQKNGFTCMLIGEIFEL
MQFLFVVAFTTFLVSCVDYDILFANKMVNHS LHPTPEVKVTLPD AFLPAQVCSARIQENGSLITILVIAG
VFWIHRLIKFIYNICCYWEIHSFYLHALRIPMSALPYCTWQEVQARIVQTQKEHQICIHKRELTELDIYH
RILRFQNYMVALVNKSLPLRFLPLGLGEAVFFTRGLKYNFELILFWGPGSLFLNEWSLKA EYKRGGQRL
ELAQRLSNRILWIGIANFLLCPLILIWQILYAFFSYAEVLKREPGALGARCWSLYGRCYLRHFNELEHEL
QSR LNRGYKPASKYMNCFSLPLLTLLAKNGAFFAGSILAVLIALT IYDEDVLAVEHVLT TTVTL LGVTVTV
CRSFIPDQHMVFCPEQLLRVILAHIHYPMDHWQGNNAHRSQTRDEFAQLFQYKAVFILEE LLSPIVTP LIL
IFCLRPRALEIIDFFRNFTVEVVGVDTC SFAQMDVRQHGHPQWLSAGQTEASVYQQAEDGKTELSMHF
AITNPGWQPPRESTAFLGLKEQVQRDGAASLAQGGLLPENALFTSIQSLQSESEPLSLIANV VAGSSC
RGPPLPRDLQGSRHRAEVASALRSFSPLQPGQAPTGRAHSTM TSGGVDARTASSGSSVWEGQLQSLVLSE
YASTEMSLHALYMHQLHKQQAQAE PERHLWHRRESDES GESAPDEGGEGARAPQSI PRSASYPCAAPRPG
APETTALHGGFQRRYGGITDPGTVPRAP SHFSRRLPLGGWAEDGQSASRHPEPVPEEGSEDELPPQVHKV
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Mus musculus:

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>NP_001003917.2 autophagy-related protein 9A isoform a [Mus musculus]
MAQFDTEYQRLEASYSDSPPGGEEDLLVHVAEGSKSPWHHIENLDLFFSRVYNLHQKNGFTCMLIGEMFEL
MQFLFVVAFTTFLVSCVDYDILFANKMVNHS LHPTPEVKVTLPD AFLPAQVCSARIQENGSLITILVIAG
VFWIHRLIKFIYNICCYWEIHSFYLHALRIPMSALPYCTWQEVQARIVQTQKEHQICIHKRELTELDIYH
RILRFQNYMVALVNKSLPLRFLPLGLGEVAVFFTRGLKYNFELILFWGPGSLFLNEWSLKA EYKRGGQRL
ELAQRLSNRILWIGIANFLLCPLILIWQILYAFFSYAEVLKREPGALGARCWSLYGRCYLRHFNELEHEL
QSR LNRGYKPASKYMNCFSLPLLTLLAKNGAFFAGSILAVLIALT IYDEDVLAVEHVLT TTVTL LGVTVTV
CRSFIPDQHMVFCPEQLLRVILAHIHYPMDHWQGNNAHRSQTRDEFAQLFQYKAVFILEE LLSPIVTP LIL
IFCLRPRALEIIDFFRNFTVEVVGVDTC SFAQMDVRQHGHPQWLSGGQTEASVYQQAEDGKTELSMHF
AITNPGWQPPRESTAFLGLKEQVQRDGAAGLAQGGLLPENALFTSIQSLQSESEPLSLIANV VAGSSC
RGPSLSRDLQGSRHRADVASALRSFSPLQPGAAPQGRVPSTM TSGGVDARTASSGSSVWEGQLQSLVLSE
YASTEMSLHALYMHQLHKQQTQAE PERHVWHRRESDES GESAPEEGGEGARAPQPI PRSASYPCATPRPG
APETTALHGGFQRRYGGITDPGTVPRGPS HFSRRLPLGGWAEDGQPASRHPEPVPEEGSEDELPPQVHKV
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Gallus gallus:

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>NP_001029993.2 autophagy-related protein 9A [Gallus gallus]
MAHLETQYQRLESSSTESP PGGGDLLVHVPEGA KSPWHHIENLDLFFSRVYNLHQKNGFTCMLIGEIFEL
MQFI FVVAFTTFLVSCVDYDILFANKAVNHS QHPSEPIKVTLPD AFLPPNVCSARIQANSFLICILVIAG
VFWIHRLVKFIYNICCYWEIHSFYNALRIPMSNL PYYTWQEVQARIVQIQKEHQICIHKKELTELDIYH
RILRFKNYMVAMVNKSLPLIRFLPLPLGDTVFYTRGLKYNFELIFFWGPGSLFENEWSLKA EYKRAGNRL
ELAEKLSTRILWIGIANFLLCPLILIWQILYAFFSYTEILKREPGSLGARCWSLYGRCYLRHFNELDHEL
QSR LSKGYKPASKYMNCFSLPLLTIVAKNVAFFAGSILAVLIALT IYDEDVLAVEHVLT TTVTL LGVGITV
CRSFIPDQHLVFCPEQLLRVILAHIHYPMDHWQGNNAHYETRDEFAQLFQYKAVFILEE LLSPIITPLIL
IICLRPKSLDIVDFRNFTVEVVGVDTC SFAQMDVRQHGHPAWMSAGKTEASIYQQAEDGKTELSMHF
AITNPKWQPPRESTAFIGFLKERVHRDSSVALQQA VLPENALFSSIQSLQSESEPHSLIANVIAGSSVL
GFHMGRDQGASRHLSEVASALRSFSPLQSAQQPSGGGFQTAGRDGEGTQPRGSAMTASGADARTMSSGSS
AWEGQLQSMILSEYASTEMSLHALYMHQLHKQHAQLEPERHTWHRRESDES GESTHEELDAQRGAPVPLP
RSASYPFSSRQPAEETATLQTGFQRRYGGITDPGTVHRA PSHFSRRLPLGGWAEDGQSARHPEPVPEESSE
DELPQPIHKV
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Xenopus laevis:

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>XP_018094208.1 autophagy-related protein 9A [Xenopus laevis]
MAMYDTPYQRLEASTD SPLGEDDLLVHVPEGSKSPWHHIENLDLFFSHVYNLHQKNGFTCMLIGEIFEL
LQFIFIVSFTTLLVSCVDYDILFANKMVNHS QSDHVKVTLPDAFLPPGVC RDRMQENGFLVCLLA IAGVF
WTHRLIKFIYNICCYWEIHNFYMQALRIPMSDL PYYTWEEVQSRIVQIQKEHQICIHKKELSEL DVSHRI
LRFKNYMVAMVNKNLLPLQHRFLPLLGNTVFYTRGLKYNFQLIFFWGPGCLFQNEWSLKP EYKRSGARLEL
SEKLAQRILWIGLANLVLCPLVLVWQILYAFFSYTEVLRREPGSLGARCWSLYGRCYLRHFNELDHQLQA
RLSRAYKPASKYMNCFSLPLLAVVAKHFGFLAGSILAVLIALT VYDEDVLAVEHVLSAVTLLGIVVTCR
SFIPDQHLVFCPEQLLRVILAHIHYPMDHWQRS AHRAE TRGEFSQLFQYKAVFILEE LLSPLLTPLVLFF
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CLRPKSLEIIDFFRNFTVEVVGVDTCSCFAQMDVRQHGNPAWMSAGKTEASIYQQAEDGKTELSLMHFAI
TNPRWQPPRECSAFLSQLRERVQRDSTMGNQKHPTGLMQPLQCSGLSIQSDPEPHSLMANMFSGVSTAGF
PANTEALGSPHVSAYSEVASALHSLSPQQSCHFPVQSQSGISADFRNGSFGSNVWEGPMNSGTLSEYASTE
MSLHALYMHELHQHQTMAPGRHIWHRQESDESSESSQGEGLINTTNSNPSSLSLCPSPAAAWEERLPLPL
STHRLSASTDLGSSVQRTSLARQPMGGWSESDVQPSRLPEFPVPEEGSEDELPQVQKV

Salmo salar:

>XP_014005943.1 autophagy-related protein 9A [Salmo salar]
MAAHFDTEYQRLEASYSDSPGGEENLLVHIPDGNKSPWHHIENLDLFFQRVYNLHQKNGFTCMLLGEVFE
LVQLLFVVGFVTLFANCDVDYDILFANKFVNHTDSSKVTLPDAFLPVDVCSASIRDNAVVMFVLMISGVFW
LHRLIKFIYNVCCYWEIRSFYTNALKMSMAELPYFTWQEVQARIVEIQKEHQICIHKKELTELDIYHRIL
RFKNYVMAMINKSLLPVRF**RPPLLGES**VFYTRGLKYNFELIFFWGPGLFESEWSLKPQYKRGGNRLELA
DKLASRILWIGIANLVLCPVVLVWQILYAFFSYTEVIKREPGLGARCWSLYGRCYLRHFNELDHLMMSR
LSKGYKASSRYMNCFLSPLLTVVAKNVAFFAGSLLAVLIAALTIYDEDLAVEHVLSSITLLGVCITVCRS
FIPDKHLVYCPQQLRLVILAHIHYPMDHWQGNNAHRYETRDQFSQLFYKAVFILEELISPLVTPFILIFS
LRRKLEIIDFFRNFSEVVGVDTCSCFAQMDIRQHGHPAWMSEGKTEASIYQQAEDGKTELSLMHFAIT
NPQWQPPTTETTHFISQLKERVQREATGDRHTLTSLSGSEPRSLIANFLAGPPSLASLHLGRDGSLTNHGP
VGVSDGASALRSLSSMRGSCSSAHRAGHASSASRAMPGSSDARTASSGSSVWEGQLTSLVLSEYAS
TEMSVHALYIHELHKQQSGGELSRLTWHRRQDSDSDSDSVTEEGSGGGNPNPRNP1PRSHTFPISTPITT
PGPIPPSSNSGPNDRGTTTPGQDVTPLQSNSQRRYGGNTDSVGPPEGRVVR SARVPMGGWAEEGRGGRHPDT
VPEEGSEDDMPNIHKVT

Petromyzon marinus:

>XP_032801920.1 autophagy-related protein 9A-like isoform X1 [Petromyzon marinus]
MAEÄETGYRRLDSYDEESPNHERVLVHVPEGSKARWNHIENLDFFTRIYHFHQKHGFACMMLAEFFE
LVQFLFVVFTTFTFLINCDYDILFANKQVHPQPSRKVTLYDALLSSEKTERIRGNSWIIIFLIVMAGTFW
LYRLIKVIYNFSSYLEIRAFYINAKIIPMAELQNFSWQEVQERVLAQKEQQMCIHKRELTEDMHHRIL
RFKNYLVAMVNKSLLPVVR**RVFPAGES**ALLTQGLKYNLEMLLFWGPGAPFQSAWSLRPEYKRAGCRLELA
ERLGRITILLVGLANLVLCPLVVVWQVLHAFFRYAIEVLKREPGLGARRWSLYGQLYLRHLNELDHLELRAR
LGRGYRHAARYMDSFTAPMMAVLAKNVTFFAGSLLAVLLALTVDVDEDLVSEHVLTATITAGVLLTVCRA
FIPDEHLVWNPPEHLLQAVLAHIHYMPEHWKGAHKTETRDEFSQLFYKAAFIMEELLSPITPFILIFG
VRPKALEIVDFFRNFTVEVVGVDVCSFAQMDIRRHGNPTWMSAGQTEASYQQAEDGKTELSLVHFAIS
NPRWRFPGRSNVYLLQLREQVQRDSTANPQPLLFSLSQTIESQSGPYGLLGSMLGGPSSLTAYRSTRDAT
CSLPPEMSAATAAATALMSLMPASLTPGPREELAEMPDPSTPGNTTVTARPGSSSTGAVGMSMSTGGRGK
VSFGGTDFRSSSVGSSFFREGPSQSSILSEFASAEMSLHAIYMHEARRNYATSDAQARYHWQQPENNGDDD
TMDEVNALSGFRESSLQLHNTGSNSGSHSSVLGSGQRETYVSPASIGHSGDYMPNIGSLQDTHGDSL
GLMVTRENTELGAFPRHYGGTSASENMLQPEQGSPRFGLMPMGWQEDMAGLGTIDPHGGVPSCMSPNP
QQINEVAYTFHSLFLNT

Branchiostoma belcheri:

>XP_019613418.1 PREDICTED: autophagy-related protein 9A-like isoform X1 [Branchiostoma belcheri]
MAQLETSYRRLDSFYDEEMDSPNERELLVHAVDSNKAHRWNHIENLDFFTRVYQYHQRHGFLCMMLA
VLELLQFIFVLLFTTFLQCCHYEVLFGDKNPHDPDRKVTLPALVPLDQCASSLDSRIVCVLVLASFFWF
LRFIKVYNYFFRYWEIRTFYTAQIKISHNDLPNMTWHEVQRCLRQVQVEQQMCIHKQELTELDIYHRILR
FKNYTVAMVNKSLLPLKFQLPGMGELVFLTNGLKYNLEMLFWGPPWSPFANNWHLKEDYKKS SKRLELAN
KLRSRHLVWGVANLLCPFILMWQILYSFTTYAEVLKRQPGSLGARKWSLYGRLYLRHFNELDHENLARL
TRAYKPAEKYMSSFISHVMTLIARHVAFLAGAIFAVLVVLTIIYDEDLVLTIEHVLTITITLMGVLVAGCRAL
IPDENMVFCEPQLMVCILAQIHYMPDRWKQGAHTYVRDEFSQLFYKAVFLLEELLSPITPLILIFSL
RSKALDIVDFFRNFTVDVVGVDVCSFAQMDIKRHGNPQWTGEKQQTQDVSQYHQAEDGKTELSLMHFTLT
NPTWQPPRHCNKFINHLKEQAHKDVNMLNSAVMVDNPPFQSLQSLSSAGYPSMMTSLMVGRLGPDATLVP
PRDPGTGTPEPSQPGVALPGTATAPGRYGLVRGDISSVEGPIQAPNTGLLGSSTMAPRGTASISHTLPPTPE
PVSLQETMAPTELMAAEMSFSALYMHQLHQTQTHDHQDQEAQRARWRQLPAPAFYGTTPMANQQRPSPGS
VEDSRTSEPGQWHVSGSTTMPGIDEAPSEETDTLSYSPPNV

Drosophila melanogaster:

>NP_611114.1 Autophagy-related 9, isoform A [Drosophila melanogaster]
MSSPHINYRSLAEAAAPFLEHHPSTGQGPSKTQDAKANAAAHLDPGLEHGLEQLDEHDTHEGEDTP
RNSGVMIHMVPETGARARNHIEDLDSFFSRMYQQYQKHGFTVIIVDEMLQVLEFGFVVWLLAFVMHCVR
DVLFGDTPPGGLNPNKTTLSDMVYPTGECANFTWVTVLVVFIAAIYLGIRLLKMVYHITQYADIKRFYN
SALHIEDSDLDNFTWHEVQQRIRRVQAEQHMCI DKESLTELD IYHRVLRFKNYLVALMNKQLLPVRFHIP
LYGEVVSLSRGMLFNIDFILFRGPGSPFQNNWQLRDEFVAVRSNQTELAQRLSKLILGVALNLVLAPVIF
VWQLIYFSFSYANILRKEPGALGLRTWSNYGRLYLRHFNELDHELDARLNRAVDYADRYLNSFSPLAAV
IAKNLLFISGGLLLILALGIYEEHVQVEHLLAILAGLGAIGVVCRTLIPDENLVWCPEQLMTAILAHV
HYLPSEWRQQAHTTKVRQEFSNFFQFKAGYLLSEIFSPFVTPFVLIFVFRPKAIELVRFRTFTVSVRGV
GNVCSFAQMDVRKHGNPDQLTSELEEMTRATAQQPQQEPQQQSLAGGKTEMSLLRFTLNNPEWQMPKEA
KQFLRGVREHAVGELVQAKTSMVQENPLTNSLISFGTMGADYCSIANSVLTAQVTPQQLEISQSLRPGLG
PVSGGFPVAASDFRQMLQNNLSASVGPLDSMRRLRLSRAEGRLEGPTDTLLYGLCGVDPRVGSTPLNVGV
ADMCLSALYLHELNQKQARQSRIDEAEEDERPGTSHWPPRPPAAPASADTGFGRSHTVITSKAAESTPL
GSIRS

Hydra vulgaris:

>XP_012564588.1 PREDICTED: autophagy-related protein 9A-like [Hydra vulgaris]
MMTSFNsipYVRVAPEEDSEFSELPPTVVTTKGVDKNGCWTHIENLDEFFTEVYTYHQLGQFVCLLLRDV
FELTQYIFIVLFGTFLLVCDYKKLFSDPNPVFVEVIHWNNFQMPSSVILCLVVALFWLVRLCRVIFR
VYRRWHIRKFFYQVHLITDADLRNMQWNEVQHKLILMQQVHQLCIHVKELTELDINHNRILRQKNYMSFQ
NKGIIPICIYHFFPIGKRTFLTEGLKFNLLNLI LFNFGPAPFKNSWKLKEEYKDYSCRMVLAASLSHRIFML
GVLNLLCFPIMYQVLYSFFMYAELIKRSPDVFGARRWSPFGRLYLRHFNELDHFEQSRNLKAYMPATR

YMNVFTSPIITIFAKNIAFFSGAILAVLLGLSFYDKDVLTAEHVLSFMATLGIIIKICSGFIPDEHMFVC
PETLMKQILSNTHYIPEEWKGRAHTMEVREEFKMFQYKFICLLEELMSPLLTFFILCFGLRYKALQIVD
FYRNFTVEVAGLDVCSFAQMDIRKHGAKNWSDEGCSKEDQMLSAESQAENAKTELSLLNFSIKNPDWKP
SSHGKQFIDTIKEQAFQESLSHSLSSNQTPFNAGTSFDFTNFIGLQSIAYPALDPAIMVSRNDDVLRNSI
MYLHEVQNRRPISVTSLSKSSYGDNAFENSDDLRRTWFSATSGQTSFGVNKENLLPRYSAMKNPADDRL

Nematostella vectensis:

>XP_032240258.1 autophagy-related protein 9A [Nematostella vectensis]
MSEFKTQYQRLNSVDDSEEDLPPQGfHVgTRGLEEIEKGRWNHIENLDEFFIRVYEHRRHdGFACILLTQ
CFELVQFAFVVLFTSfLLLCVDYDKLFKNPDPTfSEVVHFHKIEHMEPAIVVCLVIALLFWFfIRLARVFI
YFFKLEIRMfYKNALKIPeSIVNLQWQDVQKRlEIQKIHQMCVHKEELTEldIHHRILRWKNYfVAM
QNKGVIPCTY**YFFFLGQR**TfLTeGMKYNLKMILfWGPGSPfQDNWKLrDDfKNLSKRSALADRLSRRIFW
IGVANfLLCPfILLWVVLySFFSYAELVKRAPDALGARRWSPYGRlFFRHfNELDHEfQARLNKAYEPAQ
KYLNIffSSPFLAIiAKNVAFLAGAVfAVLTtFTLVDRDVLMAEHMLAVIAGlGILIRGCYVFIPNENLVW
NPEQLMRQILSYTHYIPETWKGKAHTTEVRDQFAQIFQYKLVNVEELVSPVVTPfLLCFSLRYKALDIV
DFYRNFTVDVVGVGDVCSFAQLDVKKHGnPEWLSEGLSEATQYEQaENGKTELSLLHfSIRNPawkPSDR
GAHFISTIKENAIHEGLNIAGSVTLSEPCSLQDFRSFDCLPGLPYEPAMATSDPTAGLQGGVKAADTRRS
REQHTeALMNTSMLYMHELHSRQADHSMHEVSYPsGPSTQSPRRPETSGLFEETGLTYQAREQTfEQEMT
YMARSHGPEVAFHPGLSGQLGRVEEGSQALHSTSPtAGNssSQtNEQRDRDQETMVNF

Amphimedon queenslandica:

>XP_003384679.1 PREDICTED: autophagy-related protein 9A-like [Amphimedon queenslandica]
MSKKTRYMRLETDPESSQSSDDdAPPTHiPLHSSQYVKESKWNHIENLDEFFDWVYQYLINHGlfAIVLN
DILELGQFAFLCIfSAFLITCINfKNLFADDVYTNETGVKDVAfGDVIEIDRLEHINPLLVlILFFAfIF
WFHRlCKTIWRFFKfLGIrrFYIEALDIPPSDLrNYNWRDVLERLKSaQNTHKMNIRKQELTEIDVYHRI
LRfKNYmVAMINKDVLsYKiWIPfYGEKVfFTMGlKYNyELLfWGPgAPfKNnyHLHEEYkTAAKkYEL
IQKLRFrITVLALVNLVfSPfIFLYQILySFFTYAELLKRQPGVfGRRRWSlFGKIFLRHfNELDHeliV
RLNRAyLPAGKYMDLFVLpVATILARNVAFVAGSLlAVLFTLTlVIQEDLLTAHNlTlTlGLGVIVTLcR
IfIPNEHQTRDPKELMTEIEEIHYPMDLWKEKpHTVQVSSQfSqvFQLTIAYLiDELLSPlVTPfILyF
SLRNKSQDIIDfLRNFTIDVSGVGdVCSfAEMNLrKHGHSEWQQNSQlARSTDYERSElGkTEISLLNfT
QKNPNWEAGEDADTfLTQLKESVEELHSSQqqqqQSLtLSREdSPpLSLSSHQfGVSRlQGSMdTSIW
ASfTSANDEASSLTPLKLHQVHDVMKtSHGQGSSSSAApPPPIGSIVPSYHPPPPQpQEVALTVYDHCL
PSDSSLSSADIRLESTIGHTPSTAGGLTEPFLPRDSEPPPQT

Alignment:

NP_611114.1[D.melanogaster]	MSSPHINYRSLAEEAASPFLHEHPSTGGQPSKTQDAKANAAAAHLDPLEHGLEQPLDEH	60
XP_003384679.1[A.queenslandica]	-----MSKTRYMRLETDP-ES	16
XP_012564588.1[H.vulgaris]	-----MMTSFNISIPYVRVAPEE-D-	18
XP_032240258.1[N.vectensis]	-----MSEFK-TQYQRLNSV--D-	15
XP_019613418.1[B.belcheri]	-----MAQLE-TSYRRLDSF--Y-	15
XP_032801920.1[P.marinus]	-----MAEAE-TGYRRLDSY--D-	15
XP_014005943.1[S.salar]	-----MAAHFD-TEYQRLAS--Y-	16
XP_018094208.1[X.laevs]	-----MAMYD-TPYQRLAS--Y-	15
NP_001029993.2[G.gallus]	-----MAHLE-TQYQRLSS--S-	15
NP_001003917.2[M.musculus]	-----MAQFD-TEYQRLAS--Y-	15
NP_001070666.1[H.sapiens]	-----MAQFD-TEYQRLAS--Y-	15
NP_001127287.1[P.abelii]	-----MAQFD-TEYQRLAS--Y-	15
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NP_611114.1[D.melanogaster]	DTEHEGEDTPRNSGVMIHMPETGRARWNHIEDLDSFFSRMYQYQKHGFTVIVVDEMLQ	120
XP_003384679.1[A.queenslandica]	SQSSDDAPPTH--IPLHSSQYVKESKWNHLENLDEFFDWVYQYLINHGLFAIVNDILE	74
XP_012564588.1[H.vulgaris]	--DEFSELPTTV--VTTKGV--DKNGCWTHIENLDEFFTEVYTYHQLQGFCVLLRDVFE	72
XP_032240258.1[N.vectensis]	--DSEEDLPPQGFGHVGTRGLEEIEKGRWNHLENLDEFFIRVYEHHRDGFACILLTQCFE	73
XP_019613418.1[B.belcheri]	--DEEMDSPPNERELLVHAVDSNKAHRWNHLENLDDFFTRVYQYHQRHGLCMLAEVLE	73
XP_032801920.1[P.marinus]	--DE--ESPNHEREVLVHVPEGSK-ARWNHLENLDYFFTRIYHFHQKHGFACMLAEFFE	70
XP_014005943.1[S.salar]	---S--DSPPGEENLVHVPDGNK-SPWHHLENLDLFFQVRVYNLHQKNGFTCMLLGEVFE	70
XP_018094208.1[X.laevs]	---T--DSPLGEDDLLVHVPEGSK-SPWHHLENLDLFFSHVYNLHQKNGFTCMLLGEIFE	69
NP_001029993.2[G.gallus]	---T--ESPPGGDDLHVHVPEGAK-SPWHHLENLDLFFSRVYNLHQKNGFTCMLLGEIFE	69
NP_001003917.2[M.musculus]	---S--DSPPGEEDLLVHVAEGSK-SPWHHLENLDLFFSRVYNLHQKNGFTCMLLGEIFE	69
NP_001070666.1[H.sapiens]	---S--DSPPGEEDLLVHVAEGSK-SPWHHLENLDLFFSRVYNLHQKNGFTCMLLGEIFE	69
NP_001127287.1[P.abelii]	---S--DSPPGEEDLLVHVAEGSK-SPWHHLENLDLFFSRVYNLHQKNGFTCMLLGEIFE	69
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NP_611114.1[D.melanogaster]	VLEFGFVWLLAFVVMHCVRFVDVFGDTPPGG---LNPNTTSLSDVMYPTGECLANFTWV	176
XP_003384679.1[A.queenslandica]	LQGFALCIFSALITCINFKNLFADDVYTNET---GVKDV---AFGDVIEIDRLEHIN	127
XP_012564588.1[H.vulgaris]	LTQYIFIVLFGTFLLVCDYKKFLSDPNPVFE-----VIHWNFNKQMP	116
XP_032240258.1[N.vectensis]	LVQFAFVVLFTSFLLLCVDYDKLFKNPDPTFSE-----VVHFHKEIEME	117
XP_019613418.1[B.belcheri]	LLQFIFVLFTFLLQCVHYEVLFQDK-----NPHPRKVTLPALVPLDQCASSLDS	126
XP_032801920.1[P.marinus]	LVQFLFVVTFTTFLNCDYDILFANKQV---HPQPSRKVTLYDALLSSEKCTERIRGN	126
XP_014005943.1[S.salar]	LVQLLFVVGFTVFLANCVDYDILFANKFVNHT---DSSKVTLPDAFLPVDVCSASIRDN	126
XP_018094208.1[X.laevs]	LLQFIFIVSFTLLVSCVDYDILFANKMVNHSQ---SDHVKVTLPDAFLPPGVCRRMQEN	127
NP_001029993.2[G.gallus]	LMQFIFVVAFTTFLISCVDYDILFANKAVNHSQHPSEPIKVTLPDAFLPPNVCSARIQAN	129
NP_001003917.2[M.musculus]	LMQFLFVVAFTTFLVSCVDYDILFANKMVNHSQHPTEPVKVTLPDAFLPAQVCSARIQEN	129
NP_001070666.1[H.sapiens]	LMQFLFVVAFTTFLVSCVDYDILFANKMVNHSQHPTEPVKVTLPDAFLPAQVCSARIQEN	129
NP_001127287.1[P.abelii]	LMQFLFVVAFTTFLVSCVDYDILFANKMVNHSQHPTEPVKVTLPDAFLPAQVCSARIQEN	129
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NP_611114.1[D.melanogaster]	T--YLVVFFIAIYLGIRLLKMVYHITQYADIKRFYNSALHIEDSLDNFTWHEVQQRIRR	234
XP_003384679.1[A.queenslandica]	PLLVLILFFAFIFWFHRLCKTIWRFFKFLGIRRFYIEALDIPPSDLRNNWRDVLRLKS	187
XP_012564588.1[H.vulgaris]	SSVLICLVVALLFWLVRCLRVIFRVYRRWHIRKFFYQVLHITDADLRNMQWNEVQHKLLI	176
XP_032240258.1[N.vectensis]	PAIVVCLVIALFWFIRLARVFIYFFKLEIRMFYKNALKIPSEIVNLQWQDVQKRLIE	177
XP_019613418.1[B.belcheri]	-RIVVCLVLASFVFLRFIKVYVNFYRWEIRTFYQALKISHNDLPNMTWHEVQRCLRQ	185
XP_032801920.1[P.marinus]	SWIIFLIVMAGTFWLYRLIKVIYNFSSYLEIRAFYINALKIPMAELQNFSEQVEQERVA	186
XP_014005943.1[S.salar]	VAVMEVLMISGVFWLHRLIKFIYNVCCYWEIRSFTYTNALKMSMAELPYFTWQEVQARIVE	186
XP_018094208.1[X.laevs]	GFLVCLLAIAGVFWLHRLIKFIYNICCYWEIHNFMQALRIPMSDLPYTTWEEVQSRIVQ	187
NP_001029993.2[G.gallus]	SFLICILVIAGVFWLHRLVVKFIYNICCYWEIHSFYINALRIPMSNLPYTTWQEVQARIVQ	189
NP_001003917.2[M.musculus]	GSLITILVIAGVFWLHRLIKFIYNICCYWEIHSFYLHALRIPMSALPYCTWQEVQARIVQ	189
NP_001070666.1[H.sapiens]	GSLITILVIAGVFWLHRLIKFIYNICCYWEIHSFYLHALRIPMSALPYCTWQEVQARIVQ	189
NP_001127287.1[P.abelii]	GSLITILVIAGVFWLHRLIKFIYNICCYWEIHSFYLHALRIPMSALPYCTWQEVQARIVQ	189
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NP_611114.1[D.melanogaster]	VQAEQHMCDIKESLTELDIIYHRLVRFKKNYLVALMNKQLLPVRFHIPLYGEVVSLSRGLMF	294
XP_003384679.1[A.queenslandica]	AQNTHKMNIRKQELTEIDVYHRLRFKNYVMAMINKDLSYKIWIPIFYGEKVFFTMGLKY	247
XP_012564588.1[H.vulgaris]	MQQVHQLCIHVKELTELDIHNRLRQKNYMISFQNKGIIPCIYHFFFIGKRTFLTEGLKF	236
XP_032240258.1[N.vectensis]	IQKIHQMCVHKEELTELDIHHRLRWKNYFVAMQNKGVIPCTY RFFFLGQR FTLEGMKY	237
XP_019613418.1[B.belcheri]	VQVEQQMCIHKQELTELDIIYHRLRFKNYTVAMVNKSLPLKFQLPGMGELVFLTNGLKY	245
XP_032801920.1[P.marinus]	VQKEQQMCIHKRELTELDMMHRLRFKNYLAMVNKSLLPVRV RVPFAGES ALLTQGLKY	246
XP_014005943.1[S.salar]	IQKEHQICIHKKELTELDIIYHRLRFKNYVMAMINKSLLPVRF RPPLLGES VFYTRGLKY	246
XP_018094208.1[X.laevs]	IQKEHQICIHKKELSELVSHRLRFKNYVMAMVNKNLLPLQH RLPLLGNT VFYTRGLKY	247
NP_001029993.2[G.gallus]	IQKEHQICIHKKELTELDIIYHRLRFKNYVMAMVNKSLPIRF RLPLLGD VFYTRGLKY	249
NP_001003917.2[M.musculus]	TQKEHQICIHKKELTELDIIYHRLRFQNYMVALVNKSLPLRF RLPGLGEV VFFTRGLKY	249
NP_001070666.1[H.sapiens]	TQKEHQICIHKKELTELDIIYHRLRFQNYMVALVNKSLPLRF RLPGLGEV VFFTRGLKY	249
NP_001127287.1[P.abelii]	TQKEHQICIHKKELTELDIIYHRLRFQNYMVALVNKSLPLRF RLPGLGEV VFFTRGLKY	249
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NP_611114.1[D.melanogaster]	NIDFILFRGPGSPFQNNWQLRDEFAYRSNQTELAQRLSKLILGVALNLVLAPVIFVWQL	354
XP_003384679.1[A.queenslandica]	NYELLFWGPGAPFFNNYHLHEEYKTAACKYELIQKLRFRITVLALVNLVFSPPFIIFYQI	307
XP_012564588.1[H.vulgaris]	NLNLLIFNGPGAPFFNSWKLKEEYKDYSCRMVLAASLSHRIFMLGVNLFLCPFTIMIYQV	296
XP_032240258.1[N.vectensis]	NLKMILFWGPGSPFDQNWKLRDDFKNLSKRSALADRLSRRIFWIGVANFLCPFILLWVW	297
XP_019613418.1[B.belcheri]	NLEMILFWGPGSPFFANNWHLKEDYKSSKRLELANKLNRHLVWGVANLLCPFILLMQI	305
XP_032801920.1[P.marinus]	NLEMILFWGPGAPFQSAWSLRPEYKRAGCRLELAERLGRITLLVGLANLVLCPLVVVVQV	306
XP_014005943.1[S.salar]	NFELIFFWGPGSLFSEWSLKPQYKRGGRNLELADKLASRLWIGIANLVLCPLVVLWQI	306
XP_018094208.1[X.laevs]	NFOLIFFWGPGCLFQNEWSLKPQYKRSARGARLESEKLAQRILWIGIANLVLCPLVVLWQI	307
NP_001029993.2[G.gallus]	NFELIFFWGPGSLFENWSLKAERYKRNRLLEAEKLSRILWIGIANFLCPLILLWQI	309

NP_001003917.2[M.musculus]	NFELILFWGPGSLFLNEWSLKAEYKRGGRLELAQRLSNRILWIGIANFLLCPLILIWQI	309
NP_001070666.1[H.sapiens]	NFELILFWGPGSLFLNEWSLKAEYKRGGRLELAQRLSNRILWIGIANFLLCPLILIWQI	309
NP_001127287.1[P.abelii]	NFELILFWGPGSLFLNEWSLKAEYKRGGRLELAQRLSNRILWIGIANFLLCPLILIWQI * . : : * * * . * . : : * : : . : * * * * : : * : : * . : : : :	309
NP_611114.1[D.melanogaster]	IYFSFSYANILRKEPGALGLRTWSNRYGRLYLRHFNELDHEDARLNRAYDYADRYLNSFS	414
XP_003384679.1[A.queenslandica]	LYSFFTYAELLKRQPGVFGRRRWSLFGKIFLRHFNELDHEDLIVRLNRAYLPAGKYMDLFV	367
XP_012564588.1[H.vulgaris]	LYSFFMYAELIKRSPDVFGARRWSPFGRLYLRHFNELDHEFQSRINKAYMPATRYMNVFT	356
XP_032240258.1[N.vectensis]	LYSFFSYAELVKRAPDALGARRWSPYGRLLFFRHFNELDHEFQARLNKAYEPAQKYLNIFS	357
XP_019613418.1[B.belcheri]	LYSFFTYAEVLKRQPGSLGARKWSLYGRLYLRHFNELDHEDARLNRAYKPAEKYMSFFI	365
XP_032801920.1[P.marinus]	LHAFFRYAEVLKREPGLSGARRWSLYGRLYLRHFNELDHEDARLNRAYGRYRHAARYMDSFT	366
XP_014005943.1[S.salar]	LYAFFSYTEVIKREPGLSGARCWSLYGRCYLRHFNELDHEDARLNRAYGRYRHAARYMDSFT	366
XP_018094208.1[X.laevis]	LYAFFSYTEVLRRREPGLSGARCWSLYGRCYLRHFNELDHEDARLNRAYGRYRHAARYMDSFT	367
NP_001029993.2[G.gallus]	LYAFFSYTEILKREPGLSGARCWSLYGRCYLRHFNELDHEDARLNRAYGRYRHAARYMDSFT	369
NP_001003917.2[M.musculus]	LYAFFSYAEVLKREPGLSGARCWSLYGRCYLRHFNELDHEDARLNRAYGRYRHAARYMDSFT	369
NP_001070666.1[H.sapiens]	LYAFFSYAEVLKREPGLSGARCWSLYGRCYLRHFNELDHEDARLNRAYGRYRHAARYMDSFT	369
NP_001127287.1[P.abelii]	LYAFFSYAEVLKREPGLSGARCWSLYGRCYLRHFNELDHEDARLNRAYGRYRHAARYMDSFT : : * * : : : : * . : * * * * : * : : * : : * : : * : : * : : * : : *	369
NP_611114.1[D.melanogaster]	SPLAAVIANKLLFISGGLLLLILALGIYEEHVQVEHLLAILAGLGAIGVVCTRLIPDEN	474
XP_003384679.1[A.queenslandica]	LPVATILARNVAVFAGSLAVLFTLTIVIQEDLLTAHNILTAITGLGVIVTLCRIFIPNEH	427
XP_012564588.1[H.vulgaris]	SPITITIAKNIATFFSGAILAVLLGLSFYDKDLTAHVLFSFMATLGIIKICSGFIPDEH	416
XP_032240258.1[N.vectensis]	SPFLAIIAKNVAFLAGAVFVLTITFTLVDRDVLMAEHMLAVIAGLILIRGCVYIPNEN	417
XP_019613418.1[B.belcheri]	SHVMTLIARHVAFLAGAFVAVLVLTITIEDVLTIEHVLTITITLGMVLVAGCRALIPDEN	425
XP_032801920.1[P.marinus]	APMMAVLAKNVTFVAGSLAVLALITVYDEVDVLSVEHVLTAITAGLVLTIVCRAPIPDEH	426
XP_014005943.1[S.salar]	SPLLTVVAKNVAFVAGSLAVLALITVYDEVDVLAHEHVLSSITLGVCTIVCRSFIPDKH	426
XP_018094208.1[X.laevis]	SPLLAVVAKHFGFLAGSILAVLIALTVYDEVDVLAHEHVLSAVTLGIVVTICRSFIPDQH	427
NP_001029993.2[G.gallus]	SPLLTIVAKNVAFVAGSILAVLIALTVYDEVDVLAHEHVLTTVTLLGVGTIVCRSFIPDQH	429
NP_001003917.2[M.musculus]	SPLLTLLAKNGAFFAGSILAVLIALTVYDEVDVLAHEHVLTTVTLLGVGTIVCRSFIPDQH	429
NP_001070666.1[H.sapiens]	SPLLTLLAKNGAFFAGSILAVLIALTVYDEVDVLAHEHVLTTVTLLGVGTIVCRSFIPDQH	429
NP_001127287.1[P.abelii]	SPLLTLLAKNGAFFAGSILAVLIALTVYDEVDVLAHEHVLTTVTLLGVGTIVCRSFIPDQH . : : * : : * . : * : : : : . : . : : : : : : : : * * : : * : : * : : :	429
NP_611114.1[D.melanogaster]	LVMWCEQLMTAILAHVHYLPSEWRQAHTTKVRQEFSNFFQFKAGYLLSEIFSPFVTPFV	534
XP_003384679.1[A.queenslandica]	QTRDPKELMTEILEEIHYPMDLWKEKPHTVQVSSQFSQVQFQLTIAYLIDELLSPLVTPFI	487
XP_012564588.1[H.vulgaris]	MVFCPETLMKQILSNTHYIPEEWKGRAHTEMEVREEFSKMFQYKFCILLEELMSPLLTPFI	476
XP_032240258.1[N.vectensis]	LVMWCEQLMRQLLSYTHYIPEEWKGRAHTEMEVREEFSKMFQYKFCILLEELMSPLLTPFI	477
XP_019613418.1[B.belcheri]	MVFCPEQLMVCILAIHYMPDRWKQAHTYRVRDEFSQFLQYKAVFILLEELSPITPLI	485
XP_032801920.1[P.marinus]	LVMWCEQLLQAVLAHIHYMPEHWKGAHKTETRDEFSQFLQYKAAFIEMEELSPITTPFI	486
XP_014005943.1[S.salar]	LVYCEQLLRVILAHYHMPDHWQGNNAHRYETRDQFSQFLQYKAVFILEELISPLVTPFI	486
XP_018094208.1[X.laevis]	LVFCEQLLRVILAHYHMPDHWQGNNAHRYETRDQFSQFLQYKAVFILEELISPLVTPFI	487
NP_001029993.2[G.gallus]	LVFCEQLLRVILAHYHMPDHWQGNNAHRYETRDQFSQFLQYKAVFILEELISPLVTPFI	489
NP_001003917.2[M.musculus]	MVFCPEQLLRVILAHYHMPDHWQGNNAHRSQTRDEFAQLFQYKAVFILEELISPIVTPFI	489
NP_001070666.1[H.sapiens]	MVFCPEQLLRVILAHYHMPDHWQGNNAHRSQTRDEFAQLFQYKAVFILEELISPIVTPFI	489
NP_001127287.1[P.abelii]	MVFCPEQLLRVILAHYHMPDHWQGNNAHRSQTRDEFAQLFQYKAVFILEELISPIVTPFI . : * : : * : : * : : * : : * : : * : : * : : * : : * : : * : : * : : *	489
NP_611114.1[D.melanogaster]	LIFVFRPKAIELVRRFRTFTVSVRGVGNVCSFAQMDVRKHGPNPDWQLTSELEEMTRATAQ	594
XP_003384679.1[A.queenslandica]	LYFSLRNRKSQDIIDFLRNFTIDVSGVGDVCSFAEMNLRRKHGSEWQQNSQLARSTDY---	544
XP_012564588.1[H.vulgaris]	LCFGLRYKALQIVDFYRNFTVEVAGLGDVCSFAQMDIRKHGAKNWSDEG-CSKEDQML---	533
XP_032240258.1[N.vectensis]	LCFSLRYKALDIVDFYRNFTVDVVGVDVCSFAQMDVKKHGNPEWLSEG-LSEATQY---	533
XP_019613418.1[B.belcheri]	LIFSLRSKALDIVDFRNFTVDVVGVDVCSFAQMDIKRHGNPQWTGEKQQTIDVSQY---	542
XP_032801920.1[P.marinus]	LIFGVRPKALEIVDFRNFTVEVVGVDVCSFAQMDIRRHGNPTWMSAG-QTEASYY---	542
XP_014005943.1[S.salar]	LIFSLRRKSLEIIDFRNFTVEVVGVDGTCFAQMDIRQHGHPAWMSAG-QTEASYY---	542
XP_018094208.1[X.laevis]	LIFCLRPKSLEIIDFRNFTVEVVGVDGTCFAQMDVRQHGNPAWMSAG-QTEASYY---	543
NP_001029993.2[G.gallus]	LIICLRPKSLDIVDFRNFTVEVVGVDGTCFAQMDVRQHGHPAWMSAG-QTEASYY---	545
NP_001003917.2[M.musculus]	LIFCLRPRALEIIDFRNFTVEVVGVDGTCFAQMDVRQHGHPPQLWSGG-QTEASVY---	545
NP_001070666.1[H.sapiens]	LIFCLRPRALEIIDFRNFTVEVVGVDGTCFAQMDVRQHGHPPQLWSAG-QTEASVY---	545
NP_001127287.1[P.abelii]	LIFCLRPRALEIIDFRNFTVEVVGVDGTCFAQMDVRQHGHPPQLWSAG-QTEASVY--- * : . * : : : * * . : : * * : : * : : * : : * : : * : : *	545
NP_611114.1[D.melanogaster]	QPQQEPQQQSLAGGKTEMSLLRFTLNNPEWQMPKEAKQFLRGVREHAGVELVQAKTSM--	652
XP_003384679.1[A.queenslandica]	-----ERSELGKTEISLLNFTQKNPNWEAGEDADTFLTLQKESVEELHSSQQQQQQQ	596
XP_012564588.1[H.vulgaris]	-----SAESQAENAKTELSLLNFSIKNPDKPSSHGKQFIDTIKEQAFQESLSHSLSSNQ	588
XP_032240258.1[N.vectensis]	-----EQAEDGKTELSLLHFSIRNPAWKPSDRGAHFISTIKENAIHEGLNIAGSVTL	585
XP_019613418.1[B.belcheri]	-----HQAEDGKTELSLMHFTLTNTPTWQPPRHCKNFINHLKEQAQHKDVNML---NSA	591
XP_032801920.1[P.marinus]	-----QQAEDGKTELSLVHFAITSNPRWRPPRGSNVYLNQLREQVQRDSTAN	588
XP_014005943.1[S.salar]	-----QQAEDGKTELSLMHFAITNPQWQPPTETTHFISQLKERVQREATGDRHT---	591
XP_018094208.1[X.laevis]	-----QQAEDGKTELSLMHFAITNPRWQPPRECSAFLSQLRERVQRDSTMGNQKHTP	595
NP_001029993.2[G.gallus]	-----QQAEDGKTELSLMHFAITNPKWQPPRESTAFIGFLKERVHRDSS-VALAQGA	596
NP_001003917.2[M.musculus]	-----QQAEDGKTELSLMHFAITNPGWQPPRESTAFLGFLKEQVQRDGAAGLAQGG	597
NP_001070666.1[H.sapiens]	-----QQAEDGKTELSLMHFAITNPGWQPPRESTAFLGFLKEQVQRDGAAGLAQGG	597
NP_001127287.1[P.abelii]	-----QQAEDGKTELSLMHFAITNPGWQPPRESTAFLGFLKEQVQRDGAAGLAQGG * : : * : : * : : * : : * : : * : : * : : * : : * : : *	597
NP_611114.1[D.melanogaster]	-VQENP----LTNSLISFGTMGADYCSIANSVL----TAQVTPQQLSISQSLRPLGLPV	702
XP_003384679.1[A.queenslandica]	SLT-----LSREDSPPPLSLSSHQF-GVSRLQGSMD---DTSIWA-----S	632
XP_012564588.1[H.vulgaris]	-TPFNAGTSFDTNFIQLQSIAYPAL-----	613
XP_032240258.1[N.vectensis]	-S--EPCSLQDFRSFDCPLGPLYEPFAMA-----	610
XP_019613418.1[B.belcheri]	VMVDNP----FFQSLQSLSSAGYPSMMLTSLMVGR-----GPDATLVP-----PR	632
XP_032801920.1[P.marinus]	--PQPL----LFSSLTQTIETSGSGPYGLLSGMLGSPSLTAYRSTRDATCSL-----PE	635

XP_014005943.1[S.salar]	-----LTSLSGSEPRSLIANFLAGPPSLASLHLGRDGLTN-----HG	629
XP_018094208.1[X.laevis]	GL-MQP---LQCSGLSIQSDPEPHSLMANMFSGVST-AGFPANTEALGSP-----HV	642
NP_001029993.2[G.gallus]	VLPENA----LFSSQSLQSESEPHSLIANVAGSSV-LGFHMGRDGGQASR-----HL	644
NP_001003917.2[M.musculus]	LLPENNA----LFTSIQSLQSESEPLSLIANVVAGSSC-RGPPLSRDLQGSR-----HR	645
NP_001070666.1[H.sapiens]	LLPENNA----LFTSIQSLQSESEPLSLIANVVAGSSC-RGPPLPRDLQGSR-----HR	645
NP_001127287.1[P.abelii]	LLPENNA----LFTSIQSLQSESEPLSLIANVVAGSSC-RGPPLPRDLQGSR-----HR	645
NP_611114.1[D.melanogaster]	SGGFVPAASDFRQMLQONLSASVGPLDSMRRLRLSRA-----EGRLEGPTD	748
XP_003384679.1[A.queenslandica]	FTSANDEASSLTPLKLHVHD-----VMKT-----SHGQSSSSAAPPPI	674
XP_012564588.1[H.vulgaris]	-----DPAI	617
XP_032240258.1[N.vectensis]	-----TSDPTA	616
XP_019613418.1[B.belcheri]	DPGTGT-----EPSQFG-----VALPGTTAPGRYGLVRGDISSVEGPIQAPNT	675
XP_032801920.1[P.marinus]	MSAATAAATAMLSLMPSPASLTGPREELAEMPDS-TPGNITVT-----ARPGFS	685
XP_014005943.1[S.salar]	PVGVS DGASALRSLSISSMRGSC-----SS-----AHRS---	658
XP_018094208.1[X.laevis]	-SAVSEVASALHSLSPQQSCHPV-----	664
NP_001029993.2[G.gallus]	-SE---VASALRSFSPLQSAQP-----SGGFQTA-----GRDG---	674
NP_001003917.2[M.musculus]	-AD---VASALRSFSPLQPGAAP-----QG-----	666
NP_001070666.1[H.sapiens]	-AE---VASALRSFSPLQPGQAP-----TG-----	666
NP_001127287.1[P.abelii]	-AE---VASALRSFSPLQPGQAP-----TG-----	666
NP_611114.1[D.melanogaster]	TLLYG-----LCGVDP-----VGSTPLNVGVADMCLSLALYLHEL	783
XP_003384679.1[A.queenslandica]	GSIVPSYHPP-----PPQPQEVAL-----TVYDHCL	700
XP_012564588.1[H.vulgaris]	-----M-----VSRNDVLRNSIMYLHEV	636
XP_032240258.1[N.vectensis]	GLQGGVKAADTRRSR-----EQHTEALMNTSMLYMHLE	649
XP_019613418.1[B.belcheri]	GLLGSSMAPRGTAISHTLPP---TPE---PVS LQETMAPTELMAAEMSFSALYMHQL	728
XP_032801920.1[P.marinus]	GAVGMSMSTGGRGKVSFGGTDFRSSSVGSSFRGEPQSQSSILSEFASAEMLHAIYMHEA	745
XP_014005943.1[S.salar]	-----AGHASSASRAMPGSSSTDARTASSGSSVWEGQLTSLVLSEYASTEMSVHALYIHEL	713
XP_018094208.1[X.laevis]	-----QSQSGISADFRNGSFGSNVWEGPMNSGTLSEYASTEMSLHALYMHLE	711
NP_001029993.2[G.gallus]	-----EGTQPRGSSAMTASGADARTMSSGSSAWEGQLQSMILSEYASTEMSLHALYMHLE	729
NP_001003917.2[M.musculus]	-----RVPSTMTGSGVDARTASSGSSVWEGQLQSLVLSEYASTEMSLHALYMHQL	716
NP_001070666.1[H.sapiens]	-----RAHSTMTGSGVDARTASSGSSVWEGQLQSLVLSEYASTEMSLHALYMHQL	716
NP_001127287.1[P.abelii]	-----RAHSTMTGSGVDARTASSGSSVWEGQLQSLVLSEYASTEMSLHALYMHQL	716
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NP_611114.1[D.melanogaster]	NQKKRQARQS----RIDEAEDERPGTSHWPPRPPAAPSADT----GFG-----SRHTV	828
XP_003384679.1[A.queenslandica]	PSDSSLSSAD-----IRLE-----STIGHTP	721
XP_012564588.1[H.vulgaris]	QNRRIISVTSLSKSSYGDNFENS DLRTWPSATSGQTSFGVNKENLLP----RYSAMKNP	692
XP_032240258.1[N.vectensis]	HSRQADHSMH-----EVSYPSPGSPSTQSPRRPETSGLFEETGLTYQAREQT	694
XP_019613418.1[B.belcheri]	HQTQTHHDHSD-----QEAQRAWRQPLPPAFYGTTPMA-----NQQRPS	768
XP_032801920.1[P.marinus]	RRNYATSDAQ-----ARYHWQPPENNGDDDTMDEVNALS GFRESSQLHNT	791
XP_014005943.1[S.salar]	HKQQS GGE-L-----SRHTWHRQDSDDSDSVTEEGSGGG---NNPNRP	755
XP_018094208.1[X.laevis]	HQQHTRMA-P-----GRHIWHRQESDESGESSQGEGLINTT---SNV---P	750
NP_001029993.2[G.gallus]	HKQHAQLE-P-----ERHTWHRRESDESGESTHEELDAQRG---APV---P	768
NP_001003917.2[M.musculus]	HKQQQAQAE-P-----ERHVWHRRESDESGESAPDEEGEGAR---APQ---P	755
NP_001070666.1[H.sapiens]	HKQQQAQAE-P-----ERHVWHRRESDESGESAPDEEGEGAR---APQ---S	755
NP_001127287.1[P.abelii]	HKQQQAQAE-P-----ERHLWHRRESDESGESAPDEEGEGAR---APQ---S	755
NP_611114.1[D.melanogaster]	ITSKAAESTPLLSIRS-----	845
XP_003384679.1[A.queenslandica]	SSTAG-----GLTEPFLPRDSEP-----	739
XP_012564588.1[H.vulgaris]	A-----DRL-----	697
XP_032240258.1[N.vectensis]	F-----EQEMTYMARSH---GPEVAFHPGLSGQLG-----	721
XP_019613418.1[B.belcheri]	GSVEDSR-----TSEPGQWHSVGS-----TTMPGIDEAPSEETDTL	804
XP_032801920.1[P.marinus]	GSNSGSHSSSVLGSGQRETYVSPSASIGHSGDYMPNIGSLQDTHGDSLGLMTRENTL	851
XP_014005943.1[S.salar]	I-----PRSHTFPISTP-ITPGPIPSNSGP-----NPDRTTPGQDVTP	796
XP_018094208.1[X.laevis]	S-----SL--SCPSP-AAA-----VWE-ERL	767
NP_001029993.2[G.gallus]	L-----PRASYPFSSR-QPA-----EETATL	789
NP_001003917.2[M.musculus]	I-----PRASYPCATP-RPG-----APETTAL	777
NP_001070666.1[H.sapiens]	I-----PRASYPCAAP-RPG-----APETTAL	777
NP_001127287.1[P.abelii]	I-----PRASYPCAAP-RPG-----APETTAL	777
NP_611114.1[D.melanogaster]	-----	845
XP_003384679.1[A.queenslandica]	-----P	740
XP_012564588.1[H.vulgaris]	-----	697
XP_032240258.1[N.vectensis]	-----RVEEGSQ-----A---LHSTSPTAGNSSSQTN	745
XP_019613418.1[B.belcheri]	SYS-----P	808
XP_032801920.1[P.marinus]	GAFPFRRHYGGTSASENMLQPEGSPFRFLMPGGWQEDMAGLTID---PHGGVPSM-S	907
XP_014005943.1[S.salar]	QSNSQRRYGGNTD---SVGPEGRVVR SARVPMGGWAE EGRG-GRHPDTPVEEGSEDDM-P	851
XP_018094208.1[X.laevis]	PPLSTHRLSASTD---LGSVQR--TSLARQPMGGWSEDEVQP-SRLPEVPVEEGSEDEL-P	820
NP_001029993.2[G.gallus]	QTGFQRRYGGITD---PGTVHRAPSHFSRLPLGGWAEDGQS-ARHPEVPVEEGSEDEL-P	844
NP_001003917.2[M.musculus]	HGGFQRRYGGITD---PGTVPRGSPSHFSRLPLGGWAEDGQPASRHPEVPVEEGSEDEL-P	833
NP_001070666.1[H.sapiens]	HGGFQRRYGGITD---PGTVPRVPSHFSRLPLGGWAEDGQSASRHPEVPVEEGSEDEL-P	833
NP_001127287.1[P.abelii]	HGGFQRRYGGITD---PGTVPRAPSHFSRLPLGGWAEDGQSASRHPEVPVEEGSEDEL-P	833
NP_611114.1[D.melanogaster]	-----	845
XP_003384679.1[A.queenslandica]	PQT-----	743
XP_012564588.1[H.vulgaris]	-----	697

XP_032240258.1[N.vectensis]	EQRRDRDQETMVNF-----	758
XP_019613418.1[B.belcheri]	PNV-----	811
XP_032801920.1[P.marinus]	PNPQQINEVAYTFHSLFLNT	927
XP_014005943.1[S.salar]	PN---IHKVT-----	858
XP_018094208.1[X.laevis]	PQ---VQKV-----	826
NP_001029993.2[G.gallus]	PQ---IHKV-----	850
NP_001003917.2[M.musculus]	PQ---VHKV-----	839
NP_001070666.1[H.sapiens]	PQ---VHKV-----	839
NP_001127287.1[P.abelii]	PQ---VHKV-----	839