

IRAP

Homo sapiens:

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>sp|Q9UIQ6|LCAP_HUMAN
MEPFTNDRLQLPRNMIENSMFEEEPDVVDLAKEPCLHPLEPDEVEYEPGRSRLLVRLGLGE
HEMEDEEEDYESSAKLLGMSFMNRSSGLRNSATGYRQVQDGFCSVPSARTMVVCAFVIVV
AVSVIMVIYLLPRCTFTTKEGCHKKNQSIGLIQPFATNGKLFPAWQIRLPTAVVPLRYELS
LHPNLTSMTFRGSVTISVQALQVTWNIILHSTGHNISRVTFMSAVSSQEQAEILEYAYH
GQIAIVAPEALLAGHNYTLKIEYSANISSSYGYFGFSYTTDESNEKKYFAATQFEPLAAR
SAFFPCFDEPAFKATFIIRIIRDEQYITALSNMPKKSSVVLDDGLVQDEFSESVKMSTYLVA
FIVGEMKNLSQDVNGTLVSIYAVPEKIGQVHYALETTVKLLLEFFQNYFEIQYPLKKLDLV
AIPDPEAGAMENWGCLLTFRETTLLYDSNTSSMADRKLVTKIIAHELAHQWFGNLVTMKMW
NDLWLNREGFATFMEYFSLEKIFKELSSYEDFLDARFKTMKSDLSNSHPISSSVQSSEQI
EEMFDSLSYFKGASLLMLKTYLSEDEVFQHAVILYLHNHSYASIQSDDLWDSFNEVTNQTL
LDVKRMKMTWTLQKGFPPLVTVQKKGKELFIQOERFFLNMKPEIQSPDTSYLWHIPLSYVT
EGRNYSKYQSVSLDDKKSQGVINLTEEVLWVKVINNMNGYYIVHYADDWEALIHQLKINP
VYLSDKDRANLINNIFELAGLGKVPKRAFDLINYLGNENHTAPITEALFQTDLIYNLLE
KLGYMDLASRLVTRVFKLLQNQIQOQTWTDGTPSMRELRSALLEFACIHNLCNSTTAM
KLFFDDWASNGTQSLPTDVMTTVFKVGAKTDKGSFLLGKYSIGSEAEKNKILEALASS
EDVRKLYWLMKSSLNGDNFRTQKLSFIIRTVGRHFFGHLAWDFVKENWNKLVQKFPLGS
YTIQNIVAGSYTLFSTKTHLSEVQAFENQSEATFRLRCVQEALEVIQLNIQWMEKNLKS
LTWWL
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Pongo abelii:

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>XP_024102718.1 leucyl-cystinyl aminopeptidase [Pongo abelii]
MEPFTNDRLQLPRNMIENSMFEEEPDVVDLAKEPCLHPLEPDEVEYEPGRSRLLVRLGLGEHEMEDEEEDY
ESSAKLLGMSFMNRSSGLRNSATGYRQVQDGFCSVPSARTMVVCAFVIVVAVSVIMVIYLLPRCTFTTKEG
CHKKNQSIGLIQPFATNGKLFPAWQIRLPTAIVPLHYELNLHPNLTSMTFRGSVTISVQALQVTWNIILH
STGHNISRVTFMSAVSSQEQVEILEYAYHGQIAIVAPEALLAGHNYTLKIEYSANMSRSYGYFGFSYTT
DESNEKKYFAATQFEPLAARSAPFCFDEPAFKATFIIRIIRDEQYTTLSNMPKKSSVILEDGLVQDEFYE
SVKMSSTYLVAIFVGEMKNLSQDVNGTLVSIYAVPEKIGQVHYALETTVKLLLEFFQNYFEIQYPLKKLDLV
AIPDPEAGAMENWGCLLTFRETTLLYDNNTSSVADRKLVTKIIAHELAHQWFGNLVTMKWMDLWLNREGFA
TFMEYFSLEKIFKELSSYEDFLDARFKTMKSDLSNSHPISSSVQSSEQIEMFDSLSYFKGASLLMLK
TYLSEDEVFQHAVILYLHNHSYASIQSDDLWDSFNEVTNQTLDVKKRMKMTWTLQKGFPPLVTVQKKGKELFI
QOERFFLNMKPEIQSPDTSYLWHIPLSYVTEGRNYSKYQSVSLDDKKSQGVINLTEEVLWVKVINNMNGYY
IVHYADDWEALIHQLKINPYYLSDKDRANLINNIFELAGLGKVPKRAFDLINYLGNENHTAPITEALF
QTDLIYNLLEKLGYMDLASRLVTRVFKLLQNQIQOQTWTDGTPSMRELRSALLEFACIHNLCNSTTAM
KLFFDDWASNGTQSLPTDVMTTVFKVGAKTDKGSFLLGKYSIGSEAEKNKILEALASSEDVRKLYWLM
KSSLNGDNFRTQKLSFIIRTVSRHFFGHLAWDFVKENWNKLVQKFHLGSYTIQNIVAGSYTLFSTKTHL
SEVQAFENQSEATFRLRCVQEALEVIQLNIQWMEKNLRSLTWWL
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Mus musculus:

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>NP_766415.1 leucyl-cystinyl aminopeptidase [Mus musculus]
MEPFTNDRLQLPRNMIENSMFEEEPDVVDLAKEPCLHPLEPDEVEYEPGRSRLLVRLGLGEHEMDEEEDY
ESSAKLLGMSFMNRSSGLRNSAAGYRQVQDGFCSLPSARTLVICVFVIVVAVSVIMVIYLLPRCTFTTKEG
CHKNTQSAELIQPVATNGKVFPAWQIRLPTAIIPLCYELSLHPNLTSMTFRGSVTISLQALQDTRDIIILH
STGHNISRVTFMSAVSSQEQVEILEYFYHEQIAVVAPEPLLTGHNYTLKIEYSANISNSYGYGITYTT
DKSNEKKYFAATQFEPLAARSAPFCFDEPAFKATFIIRITRNEHHTALSNMPKKSSVPAEEGLIQDEFSE
SVKMSSTYLVAIFVGEMKNLSQDVNGTLVSIYAVPEKIGQVHYALETTVKLLLEFFQNYFEIQYPLKKLDLV
AIPDPEAGAMENWGCLLTFRETTLLYDNNTSSVADRKLVTKIIAHELAHQWFGNLVTMKWMDLWLNREGFA
TFMEYFSLEKIFKELSSYEDFLDARFKTMKSDLSNSHPISSSVQSSEQIEMFDSLSYFKGASLLMLK
SYLSEDEVFQHAVILYLHNHSYAAIQSDDLWDSFNEVTQTKLDVKKRMKMTWTLQKGFPPLVTVQKKGTRELL
QOERFFLRMQPESQPSDTSHLWHIPLSYVTDGRNYSYRSVSLDDKKSQDVINLTEQVQWVKVNSNMNGYY
IVHYADDWTALINQLKRNPPVLSDKDRANLINNIFELAGLGKVPPLRMADFLLIDYLNKNEHTAPITEALF
QTNLIYNLLEKLGHMDLSRLVARVHKLLQNQIQOQTWTDGTPSMRELRSALLEFACAHSENCTTMTAT
NLFDDSWASNGTQSLPTDVMTTVFKVGARTKGWFLFSMYSSMGSEAEKNKILEALASSEDVHKLYWLM
KSSLGDGIIRITQKLSLIIRTVGRHFFGHLAWDFVKENWNKLVHKFHLGSYTIQSIIVAGSTHLFSTKTHL
SEVQAFENQSEATKLRCVQEALEVIQLNIQWVMVNLKLTLSQWL
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Gallus gallus:

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>XP_424862.3 leucyl-cystinyl aminopeptidase isoform X1 [Gallus gallus]
MEPFFPSDQQLPRNMIENSMFEEEPDVVDLAKEPCLHPLEPDEVEYEPTRSRLLVRLGLGEHEMDDDEEDYE
ESSAKLLGMSFINRSSGLRNNMSVYRQVQDGFCVPSTRTMLICTGVLIIVAVSVIMVIYLLPKCTFTTKEG
CHKKNRMELIYPLATNGKLFPAWAKIRLPSDVPLHYDLDLQPNLTLTKFTGSKVIVNVNTQVTKKIVLH
SSGLNITKATITSTGGSQEKAVELLEYPPLHDQIAVMAPESLLAGQNTVTNLEYSSNLSDTYYGYFRVSYK
DENSKRWFAATQFEPLAARSAPFCFDEPAFKATFSIRIKRDEKISLTLSNMPKAKTSPVTKGLVQDEFSTV
SLKMSSTYLVAIFVQADLNISMETNGSLSVYHAIQHIINQVEYALNTAVKLLLEFYEKYFLINYLEKLDLV
AIPDPOSGAMENWGCLLTFRETTLLFDNNASSARDKKLITAVIAHELAHQWFGNLVTMEWMDLWLNREGFA
TFMEYFAMEEIFFELHSDDEFLNLIFFKMMKSDLSNSHPVSSAVQSSEQIEMFDALSYIKGASLLMLK
HYLTKDVFQAGIEIYLNHHKYGSAQSDDLWDSMNEITNGTLDVKKLMKTWILHKGFPPLVTVNRKGIISL
HQEKFLYSVEPDNWTSDTSYLWDIPLTYTTNRCNFTHCINAYLLDQKSVAVIEPVEVEMIKFNVMNGYY
IVNYDEDWETLIDLLKKNHTALSADKDRANLINNIFLASLGKEPLKAFELIDYLKEESSTAPLSQALFQ
LGLIFGLLEKRGEQQLAARVMYRIECLLGNKIQDQNWTDGTTISERELRSMLLTFACIHDIRNCRATAASK
MFEDEWMSKNGTMSLPSDLMKAFITGAKTNDGWFLFKMYSSPVPEAEKSKMIEALASTEDVRKMMWLMQ
NLSLEGEVIRTQELSHIATISHSLPGHLLAWDFVKENWEKLTFRKFHLGSYTIQNIISSSTSQFATKVHLL
EVTTFEKSRESSSKRCVKEADITIQLNIQWMETNLAKLQEWL
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Xenopus laevis:

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>NP_001088429.1 leucyl/cystinyl aminopeptidase L homeolog [Xenopus laevis]
METSDNWAQLPRNMIENSMFEEEPDVVDLAKEPTMNPLESEETEYEPRSSRLLVRLGLGEQELDEEEDYE
SSAKLLGMSFMNRSSGLRNSAANYRQVQDGFCVPVSARTVIVCVVVVIVAVSVVTVVYLLPKCTFTTKDGC
HEKKHPLVLVYPIATNKKVPFWAKSKRLPDSIKPVHYTLTMHPNMNTLSFTGTQVIKLNIITTSKNIVLHS
SGLHIIKASVLVNGGTTMADEVLEYYPFEEIAIISPESSLKGECCLLTIQYAAANFSSTYYGYKIDYMK
SNKRSJAATQFEPLAARAKAFPCFDEPAFKATFSQINIIRNDEMSISLTNSMPKAKTSPVTKGLVQDEFSTV
SLKMSSTYLVAIFVQADLNISMETNGSLSVYHAIQHIINQVEYALNTAVKLLLEFYEKYFLINYLEKLDLV
AIPDPOSGAMENWGCLLTFRETTLLYKENSSTIEDQKSLITTVIAHELAHQWFGNLVTMEWMDLWLNREGFA
TFMEYFSVSVFPELNSDNSFLKMRPMALQKSDLSNSHPISDVRSPEQIEMFDDL SYIKGASILLMLKSL
LLEDVFHLICIRGYLKSHEYGSTTSDSLWDSLVNVTGGPNPNVKNMKMTWTQKAGYPLVTALRKGEIITVRQ
ERFLRSDSHATNDSTVWHIPLTYVTGKDAVEPDCEKIHLLKEATGTINVSELPPVVKFNVMNTGYIYVD
YGADGDWALIEQLHRDYTVLHSSDRANLIHDI FMLJAGVGKVPKLSAKFELLGYLVNETDSAPITQALHOFY
HIGLILKRGDLLDSDKLMEHGLELLNNTLIKQTMWDEGTLAERQLRSLLDFACSNFFPSCLEKATELF
NSWRNVNKTPIPTDMVKVVFVGARTTEGWTLLRSTYDSSIYAEKRKIILEALASTDNAKNLQWLQWQESLD
GGSIRSQELPAVIGFICKRSPGYLLAWNFIKQNDLITQKFMPSGFFIQINIVSKTHHQFSTDVHLNEVIA
FFNSTQEKSRREMVCVEAVETIKLINIEWMKNNFDSLKTWLLPSQ
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Salmo salar:

>XP_014016586.1 PREDICTED: leucyl-cystinyl aminopeptidase isoform X1 [Salmo salar]
MEDPFDSEERASLPNRMNIENSMFEEDPDVVDLAKDSAAFPALPEDEVVVEPRSSRLLVRLGENDLDDDEEE
DYESSARLLGMSFMNRSSSTHNPSSSPYNRQAPPRSCSCPSARMLVVGVFILVLVASMAMVLYFLPGCTFT
KAGCGKANSSPTMPEPSYPNSTNGELFPWNELRLPASVRFVNYDLSLTPNLTSMTFTGRTVINMTILHNHTK
HVVLHSSSELIITKATTFQVGEKGSVEVKVLEYKPMWQQIAVSFFEDLKVGQVCVLTLDYAAASLSHTYDGFYN
SSYNOKTGAKRVLAATQFEPQAARKAPCFDEPAFKATFLVRITREPGYITLSNMPQAKTTTLPSGLLED
EFEGQATVMSTYLVAFIVANFTSITRNVSNLTLYSVSVPEKKHEHTHALDTSKLLHFNYPNPFKINYPFLA
KLDLVAIPDFLAGAMENWGLITFRETSLLVGNQSSPLDKQLLIANVVAHELAHQWFGNLTVMRWNDLWLN
EGFATYWQYMSLMTFEPQLDLGNVFLGVRFKAMAKDSLNSSHPVSVSSQVTTPEQVSEMFDSVTEKGRAS
LLMLINSTTLPDGQFKEGLMKMYLDTYRGSNTVTEDLWNSLTQAQVLPQQENVSDDMRWTWTLQKGFPLVTVS
RKGGHVTLTQEHPLLSADNTHTSLSLWHPIVTVYNDSGCCSAPSCRQIFMLRNKTATLNVSDSVKWLKLNY
MNTGPFYIVHYGDEGWTTLDALKTDINTLTAHDRASLIHNIFFSLRSLGRVSFRQVLNLLDYATNETETAP
LTALSLQSLSSVYRLDDRQEQTLVARMKAYTWGHFGQLMDSQDWGEEESVSRQELRSALLEMACSLGRQN
CTDQATALYDQWNTSNQTKQIPGDLQRVVSVAQSNLGLWSLMEAYSYTTYDSEKRRKILQALASTQDQP
SIVWILSTGLEGGIIQTQELPLVISTMSDGFAGHLFVWDFVKENWDKIEKFFVGSYPIQSIIKSTTSQF
STQTHLEEVGGFFSSLKERGSQMRSVQEALETIRLNQLWMDRNLPTLRIWL

Petromyzon marinus:

>XP_032824577.1 endoplasmic reticulum aminopeptidase 1-like isoform X3 [Petromyzon marinus]
MAGDLHGERAPLPKHMNIENSMFEDDDEEEDEEADAGMPNVDPGADPSLGNVALSSPRTLAASSVPLYT
QHPLISSGGGSADRPAPEDDSRPHTLSRLPIYAGDPDEFDEDFDDNEESSRRLGAAPFNRPDPPEFRS
GRGGGPG**AAAPSTGPG**-SDGPGVHLCCQQMSPRTLMFCAAGAIGTVVIGIALSYVPCALGIGNGCASSNS
SAAGDDHHRGGTTFPSGAGNATFPFTADGEVFPWADDRLPRSVRPLHYHLCLHPNLTTLAVEGYVSVWLL
VDESTHVVYLHANLITITESILVPAADGAPAGGADGSLVAKLLRYEPRDQLMVCVTRKPLTQCGMILLNIT
FTGRLSNTEFLSARVFCDESDRFLSARSEFPFCDESDFKASFDISIVRDAHHTLSNMP
LNETVTRKDGILLDTFFKGSVMSTYLVAFIVSDFKSISNKTKHGTNVSITYTSPGKEQQGSFALENAIKFL
DYEELFNISYPLPKQDLVAIPDFAAGAMENWGLVITYRETALLGPKASGVDRDLWAQVIAHELAHQWF
GNLVMTMNWNDLWLNEGFATFMEFVATGSLPKDWLMDMDFLTEVVMALTQDSLSPSSHAISAAAVGTMQI
GEMFDSYVYKGSVLNMLRTFLTPAVFVDGIRDYLLVHSYGNHAHTDLDWESLTQSAQQHGLHGSVNVTVE
MGTWVRQPGFPLLTTLTAVDKELKITYPKQEPFFIEPAETSIITPSLWQIPLTFITSDNSTSQSKLITDKQGD
IATVTSKTEWIKANTMNTGFVVDYKGDGWATFANKLTTSKSFLSPADRANLLNDVFYLLNVGRVDVEDAM
PLLSLFLPNETSVTPMKVALMHLDRLVLLILSPYAHVDQLLQKHIVKLGEBLLPRLPWNKSSEEVTPVQRSL
DALLSVLCAYRSEKCLNRANVAYLQWSASELSADLMSVTLRVAVRDGRPTWDSVQEHYHRAKSSTEQ
AKYLEALASTSDEDDQQWSLLENAMAGVEVRSQELPRIVGVMMARTSWTGRLLTWDFLRRKRWLLVEKFSQS
SFALSNMVSVTSGFSSYTHLDQVEEFVASLRDSSGELRVFKEARDTIRANHWLATNRVALHKWLTEQS

Branchiostoma belcheri:

>XP_019622707.1 PREDICTED: endoplasmic reticulum aminopeptidase 1-like [Branchiostoma belcheri]
MEEQEEETDILTGPEEVAEDAEPASDEDSLPLQAVVQDGEGRKKQ**RPSSRSQPL**SWLSPRKSSAASRLP
RGQAQRPLRKRKLWQYAPKCSRDRCCFLPAICLTIIFIVLVTSAIYMNSKHKSSCCPYSFLLDTSEKKSAKKDP
IATNGERFRPDDVDRLPSTIVPNSYLLHLHPNLTTFNFTGHVSNISVVKKTDLVVFHVKELNITQSSVKRT
MNVNVSPIVKELEYTGNEGICLRLQGLSAGQNYTIVVHFSGELNDGLIGPFRCTYLLNKGKGDEESRVL
ATTFQFAANARAFRCFDEBPALKAFQALNVRGGRHSTFLPMKQKHIEDLLQGLKMDVFKGSVAMSTYLV
CFIVSDFRSMQLSTDTSDITVAVHAPEDRISQASFALDVAKTVLEIYETTFPGVKYPLPKMDLVAIPDFSS
GAMENWGLVITYRETALLYDADNSSAGDKQWVAIVIAHEFAHQWFGNLVMTKMNWDLWLNEGFASVFEFIG
ADKVSPEWKMLDQFVVSDIQTALSADSLNSHPISVTVHRPEEVEEIFDISISYDKGASILRMLESFLGRE
FTFQGLTSLYREHQFNAAATDDLWKALDQAAHGAGKSNINIKQVMDRWTNQMGYPVVMVTRQNSHLVLTD
DRFLMQPSPACGGVVEFTSPYRYEWIILPTYITSTSPKEQQTVMFMDTTQTTLSLDNNSPEWVKFNVNQT
GFYRVNVDNQNDAFIHQLONNHEALNSADRAGLIDDAFHLNRAGLFGLEKSLELVKYLKNERDVPVPMAT
ALSGSLGYITKLTLETEDQDLNNMMLFVLELLEDITIGEVGWEDQGDQLTKFLRSTVLGAACYDGEHQSTQQ
AHTLFPANMKGTQNVAAANLKTVVTYSVGVQHGESEWNFCWQYTSATVAAEKRRKLLYALANTRDNKLVTK
LLRYTLDSTKIRSQDTRVTITYVSRVATGVQLAWNFKSNWQTFLDRYGSGSFNMAELAKIPAHRFSTRR
QLEEVKSFTQSHDISAAARAARQTIETIQSNIFWLEKNKDKVKTWIKNYFMPPEGGKARSSEI

Drosophila melanogaster:

>NP_731786.1 uncharacterized protein Dmel_CG32473, isoform A [Drosophila melanogaster]
MVAWLTVKSVAILFGLASTAFCVATIVLAVQNADLENDLQDALDKIDALTIVDTTSTSSTSTSTSTTTTA
NPNGETDDTEPGSTTTTPGVGGDTTPSAGTSPGGETSPSSSTGSTTNPIYPTLPTGLPDPEKIEWRLPTEL
TPIKYKYVYHPDLTTGACCGTVSIIQFQLNAITNLVLHAKELNVHSISILNMMARIRVAIDSNLDESRE
LLILITLREVLSMNAKAYTLASGPDCLDSSLVGSIISNTYNAQGVDRSIIISTKFEPTIARQAQPCFDEPALK
AQFTITVAPRSQAGTQEDBPALKAFQALNVRGGRHSTFLPMKQKHIEDLLQGLKMDVFKGSVAMSTYLV
VYAPPAQVEKQTQYALDTAGVMAYYINYNFNVSYALPKLIDLVAIPDFVS GAMENWGLVITFRETALLYDEST
SSSVNKRQVAIVVAHELAHQWFGNLTVMNWNLDLWLNEGFASFLEYKGVKQHPEDWMDNQFVIEELHPV
LTDATLASHPIVKSIESPAEITEYFDTITYSKGAALVRMLENLVGEEKLRNATRYLVRHIYSTATTED
YLTAVEEEEGLEFDVKQIMQWTWEQMLPVVEVEKSGSTYKLTQKRFLANEDDYAAEAESSFNRYRSIP
ITYTSSINSEVQSILFNHNDNEATITLPEEASWIKINTNQGVYRVYNGSEQWAEILSALKNSRETFSTA
DRAHLLDANTLAAAGQLNYSVALDLISYLESEQDYVPWSVGTSALATLRNRVYTYDLYTNVYTYARKLL
TPVIEKVTFTVAADHLENRLRIKVLSSACSLGHESSILQQAVTLFNGWLASPETRPNPDIRDVVYVYGLQQ
VNTEAAMDQVVKLYLDESDAQEKLKMLNCLTAVQVPWLLQRYINNAWDESNVRQDYFTLLGYISTNPGV
QSLVWDVRENWEKLVDRFGINERTLGRLIPTITARFSTETKLEEMQQFFAKYPEAGAGTAARQQALEAV
KANIKWLAANKAQGEWLANYVQQSSVTNRIQ

Hydra vulgaris:

>XP_012561211.1 PREDICTED: aminopeptidase N-like [Hydra vulgaris]
MSEASTGLLINESKNKSNKYEGSAWSQHWKLILTVGVVFLIALGVIFGVIINTDRENKLNKSKREELFFPY
SNIRLPLNVIIPERYKIYLHPNITDNKFGFTGTVRILINITEETDSVLLHIKDLNISEVKKYHGSSAMSKH
KGPDESQQVPVKDHLISVEHEFLMRMKQHELEVGRQYTLFIRFNGRLSNGLEGFYKSSYTTSGKEKRY
LATTVYFEATQARAAPCFDEPALKALFELIMVREPQHTALSNMFIKTIINRTDGLKEDHFQQSLMSTYLV
VAFPVCDYGYKSAKSTSGRIEYKVMAPKQEQIQAENFATYAAKPVLDYETFTFQVNVFPLKQDLAIIPDPA
GAMENWGLITYRLTSILYDEKSSSANKQWAVVIAHELAHQWFGNLTVMKWNWDLWLNEGFAAPVFEFIG
ANITEPSWQMMDQFIVDDQONSLLDSSNSHPISVTVNDPAQINEIFDTISYDKGASIIIRMMKNFLGSD
VFHTGLDITLNYKYKFNVAISDDLWACLTKAANNITDVKSVMDTWTLQMGYPLITITKNHEQSEKGLVTQE
HFLLIDVRKTAASFPNYKWDVPITFYFEHKKKEQLVWFRNSADSINIPMNASGWIKANIDQLNFRVYNY
DENDNWLLSKQLQDNHKAFSTSDRSNLIDDAFELAKAGKLDQIKALEMTAYLKNEDYVFPWITALGSLGY
IGGLLQGRSCYSSYQKYIIQQVKPVDVKLGWSDGETHLNRLYRGAALRSSVMHNDTDSVKRALEIFDRFM
NNHESVAPNLRSTVYLAGIKYGGKEQWEFMLNKYLSNFPFSEQRKIMFALADSSDESILKYLSWSMNTS
IIRTQDTCGVIEHISTNIKGTMAEDFVIKNWEKLFERYGRGSFDMSSLIKTVFARMKTKEDLKVKSEIC

Nematostella vectensis:

>XP_032239104.1 aminopeptidase N isoform X1 [Nematostella vectensis]
MDEAYDNGSPNQESSDSSPEDDIDSIALLPERKTRPRRLRRRRRIIPEDNGGHLRTNMRCSRRITVYST
ITAVLLICVVIISVFNPSSTDEFEKTEKRSSEFQDEPEKKDDSSFYEDHGGRKFAWQKIRLFPSSVTP
EYTVILRKLDPDPTFGSGNVSVRVKCNEDTDYIFIIHAKQMRLLTKFEVLNQGKEPLKIMETANCEKLEMFV
IKVKGGLKGESYVLQIDFNAVLAELKITGFYKSSSYKDKDGNTRYLATTHFEPTDARAAPCFDEPALKAV
FNWYIRKAEHVLSNMPKETFKKDESGQVIVIFEPYSVMSYTLVAFVVCDFPKSKEATTKRGTLVVRWA
FEDNIDEGDVALSKALFVYKLVLPKQDLIAIPDFAAGAMENWGLITYRLTSILYDEPVSQ
SNKQWAVVVAHELAHQWFGNLTVMKWNWDLWLNEGFASFVENIGVNHHTPEWRMMEQLDKDTQLSMNL
DQLSNSHPISSVVKDPAEINSLFDTISYDKGAAILRMLKSLFLGDVFOKGLQKYLNKHKFGNAETNQLWD
AFTESVSASSSTKNFRDVKSVMDTWTLQMGFPVVTIKQRGDSAVASQKHFRIPHKVPKSLRSQFDYKWI
IPFTYTYTQNDKTKKMAIEKDNREGEGILQFDYNPATSGWIKANYEQHGFRVYVDAENWERLKQQLDT

DHEKLSAADRAGLLDDAFNLARAGELPLTTALDLTKYLTKEEYVWPAAALSNMGFLSRLCENEHHMTL
YKRYALQQLIPIVRKLGWDDKGSHLQKYLRSYVLKLCARYGDVECATAVKSRFADWMRGESLPNLRSVI
YDTGVHLGGEKEFKYMYEQYNKSTVAAEKRRLLFAMSATQNPALMKGLLDMSMSTQIRSQDTSVITSVA
SNCKGRNLAWDFVKKHWKTLFKRYGHGSFDFARLVSRTTTHFSTPQKLKEIQEFFKKHELGSGLASKQA
EEGISSNI DWMKNNIEVALKWEHTQAESKPADGDLGVANVERLENILAPEGFQEEYQDRENQEKPYQN
KRYYSNQHYGRGDDQDRRF SNEYNDDYEPERRGYEQ

Amphimedon queenslandica:

>XP_003386159.1 PREDICTED: glutamyl aminopeptidase-like isoform X1 [Amphimedon queenslandica]
MSRHRNGFEQLDGESSDTDMNLEDNESSALTGKKKKRYLVNDEEGPLCSPGSLKLSKRELICILIGGIIII
VAAIVFVIIAVVLSRSSGNGSPGSSDDKPWNVRLPKLTLPALYRVSLDLDNTFRVNGFVSVDISVNQS
TDLVIFHAKDMLNTVSLTKGVRGDLGISRQFFYSNDFFVYIQLADSLDTNDNLQLNISFNITL RDDLV
GFYKSSYSLADNEVHYLATTTQFEPTDARRAFPCFDEPAMKANFSIELTHANRYNAVSNMFPVARRVSKAND
KATTSFNNTSYKMSYTLVAFVISDFNCSDSQTVNGHIQVRVCARPDVFSDTSYALSVGKSVIGYEEFFGV
QYPLPKQDLFAIPDFAVGAMENWGLITYRETALLYNSTQNPAVNKQRVAVVVAHELAHQWFGNLV TMSWM
DGLWLNIEGFASYVEYIGTDHVQPDWMMLEQFFIDTVQTAJDADGLNWSHP I IQQVNNPDEINGLFD S ISY
DKGASLIQMLRGYIGNESFTNGLTLYLKNKFGNTETELWDALNEVSSSDVSQMMDTWTQMGPVV
TVSASDNNRATVSQKRFFQIPLPEGEQPAASPYNVVWIIIPFDYITENGNSVTKKLVSNQDDTITWDSND
GFIKANANQTGFYRVNYDVGNWQSITAHLMTPPNNRPQILSAVDRAGLLEDAPSLSTSGLLNTITVALNLS
RYLVNEEDYAPWMTALRWFSIFSCKLSTNGQYGNFKRYVSSLMGNITRKLSFNKTGLSHLQILLRTYVLL
SGYKYGDISIADTSLTMFRNWMTDGISVPPDLRLVVYRVIAAGGETEWNYLWSWYKNTNPNYKQICLS
ALAQSKKEYWILSRYLEYSMSQVRSQDTLYVIRSVARNVNGRYLAWNFRDNYDTIFKKYGGGSF SFSRLI
RSITGSFATSWELQEVESFFGKVDVGSASLALQQSKEIVRGNI AWLNNESVIGEWMMNEYLSGAMSA

Alignment

XP_032824577.1[P.marinus]	MAGDLHGERAPLPKHMIIENSMFDEDEDEEADAGMPNVDPGADPSLGNSVALSSPRT	60
XP_014016586.1[S.salar]	MEDPFDSEASLPRNMIENSMFEEEPDVVDLAKDSAAPFAL-----	41
NP_001088429.1[X.laevis]	--METSNDWAQLPRNMIENSMFEEEPDVVDLAKEPTM-NPL-----	38
XP_424862.3[G.gallus]	-MEFPFSDIQLPRNMIENSMFEEEPDVVDLAKEPCL-HPL-----	39
NP_766415.1[M.musculus]	-MESFTNDRILQPRNMIENSMFEEEPDVVDLAKEPCL-HPL-----	39
Q9UIQ6[H.sapiens]	-MEPFTNDRILQPRNMIENSMFEEEPDVVDLAKEPCL-HPL-----	39
XP_024102718.1[P.abelii]	-MEPFTNDRILQPRNMIENSMFEEEPDVVDLAKEPCL-HPL-----	39
NP_731786.1[D.melanogaster]	-----MVA-----W	4
XP_003386159.1[A.queenslandica]	-----	0
XP_019622707.1[B.belcheri]	-----	0
XP_012561211.1[H.vulgaris]	-----	0
XP_032239104.1[N.vectensis]	-----	0
XP_032824577.1[P.marinus]	LAASSVFLYTQHFLISSGGGSADRPATPEDDSRPHTLSR---LPIYAGDPDEFDEDFDDD	117
XP_014016586.1[S.salar]	-----EPDEVVVEPRSSR---LLVRGL--GENDLDEEEE	70
NP_001088429.1[X.laevis]	-----ESEETVEPRSSR---LLVRGL--GEQELDEEEE	67
XP_424862.3[G.gallus]	-----EPDEVVEPRTSR---LLVRGL--GEHEMDDEEE	68
NP_766415.1[M.musculus]	-----EPDEVVEPRGSR---LLVRGL--GEHEMDEEEE	68
Q9UIQ6[H.sapiens]	-----EPDEVVEPRGSR---LLVRGL--GEHEMDEEEE	68
XP_024102718.1[P.abelii]	-----EPDEVVEPRGSR---LLVRGL--GEHEMDEEEE	68
NP_731786.1[D.melanogaster]	LTVKSVAILFLGLAS--TAFCVATIVLAV---QNADELNDLQDALDKIDALTVDTTSTSS	58
XP_003386159.1[A.queenslandica]	-----MSRHR-NGFEQLDGESSDTMNLN	23
XP_019622707.1[B.belcheri]	-----MEEQEETIDLGTGFEVVAEDAFA	24
XP_012561211.1[H.vulgaris]	-----	0
XP_032239104.1[N.vectensis]	-----MDEAYDNGSPNQESSDSSFE	20
XP_032824577.1[P.marinus]	NEESSRRLLGAFFNRDPDEPRSGRPGGGR-A- APSTGPGGSDGPGVHL -----C	165
XP_014016586.1[S.salar]	DYESSARLLGMSFMNRSSSTHNPSSSPYNR-Q-A-----PPR-----S	105
NP_001088429.1[X.laevis]	DYESSAKLLGMSFMNRSSSGLRNSAANY-R-Q-V-----QDG-----F	101
XP_424862.3[G.gallus]	DYESSAKLLGMSFINRSSGLRNNMSVY-R-Q-S-----PDG-----	102
NP_766415.1[M.musculus]	DYESSAKLLGMSFMNRSSSGLRNSAAGY-R-Q-S-----PDG-----	102
Q9UIQ6[H.sapiens]	DYESSAKLLGMSFMNRSSSGLRNSATGY-R-Q-S-----PDG-----	102
XP_024102718.1[P.abelii]	DYESSAKLLGMSFMNRSSSGLRNSATGY-R-Q-S-----PDG-----	102
NP_731786.1[D.melanogaster]	TST-S-----TSTTTTANPNGTDDTEPGSTTTPG-----	88
XP_003386159.1[A.queenslandica]	DNES-----ALTGKKKRYLVNDEEGPLCS-PGS-----L-----KLS	55
XP_019622707.1[B.belcheri]	SDEDS--LLQAAVVDGEGRRRK RPSRSQGL SWLSPRKSAAASRLPGAQRPLRRKLW	82
XP_012561211.1[H.vulgaris]	MSEASTGLNESKNKSNK-----YE--GS-----AW	24
XP_032239104.1[N.vectensis]	DDIDSTALLPERKTRPRRLRRR RIFEDNGG -----H-LRT-----TNRM	60
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XP_032824577.1[P.marinus]	CQOMSPTIMFCAAGAIGVIV--IGIALSYVPCALGIGNOCASSNSSAAGDDHHRGGT	223
XP_014016586.1[S.salar]	CSCPSARMLVVGPFILVLVASM--AMV-LYFLPGCTFTKAGCGKANSS-----	150
NP_001088429.1[X.laevis]	P VPSARTVIVCVVVVLIIVSV--VTV-VYLLPKCTFTKDGCKEKKH-----	145
XP_424862.3[G.gallus]	S VPSRTTMLICTGVLVIAVSV--IMV-IYLLPKCTFTKEGCHKKNR-----	146
NP_766415.1[M.musculus]	S LPSARTLIVICVFVIVVAVSV--IMV-IYLLPRCTFTKEGCHKTNQ-----	146
Q9UIQ6[H.sapiens]	S VPSARTMVVCAFVIVVAVSV--IMV-IYLLPRCTFTKEGCHKKNQ-----	146
XP_024102718.1[P.abelii]	S VPSARTMVVCAFVIVVAVSV--IMV-IYLLPRCTFTKEGCHKKNQ-----	146
NP_731786.1[D.melanogaster]	-----VG-GDTTPSAG-----TSPG-----GETSPSSST-----GS	113
XP_003386159.1[A.queenslandica]	KRELICIL--IG-GIIIVAAIVFVIIIAVLSRS-----	86
XP_019622707.1[B.belcheri]	QYAPKCSRDRCC-FLFAICLT--IFIV-LVTSALYMSKHKSSCPYSFL-----LD	129
XP_012561211.1[H.vulgaris]	SQHMKLILTGVG-VVFLIALG--VIFGVILNTDRE-----	56
XP_032239104.1[N.vectensis]	CSRRITVYSTIT-AVLLICV---VVISVFNVPSTSEFEETKRSSEF-----QD	107
XP_032824577.1[P.marinus]	TPSGAGNATFPFTADGEVFPWADDRLPFRSVRPLHYHLCILHFNLT--TLAVEGYVSVMLLV	281
XP_014016586.1[S.salar]	---TPMEPSYPNSTNGELFPWNELRLPASVRPNVYDLSLTFNLT--SMTFTGRTVINMTI	205
NP_001088429.1[X.laevis]	---PLELVYPVIANKKVFPWAKSRLPDSIKPVHYTLTMHPNMT--TLSFTGTQVQIKLNI	199
XP_424862.3[G.gallus]	---TMELIVPLATNGKLFPAKIRLPDSVFLPYLDLLOPLT--TLKFTSGVKIVVNV	200
NP_766415.1[M.musculus]	---SABLQPVAATNGKVFPAQIRLPTAIIPCYELSLHNLNLT--SMTFRGSVTISLQA	200
Q9UIQ6[H.sapiens]	---SIGLIQPFATNGKLFPAQIRLPTAIVPLRYELSLHNLNLT--SMTFRGSVTISVOA	200
XP_024102718.1[P.abelii]	---SIGLIQPFATNGKLFPAQIRLPTAIVPLHYELNLHFNLT--SMTFRGSVTISVOA	200
NP_731786.1[D.melanogaster]	T---TNPVYPTLPTGLDPEKIEWRLPTELTPIKYVYVHPDLT--TGACEGTVSIQPOL	168
XP_003386159.1[A.queenslandica]	T-----SGNGSPGSDDKPWTNVRLPKTLTPALYRVSLDLDLN--TERVNGFVSVDISV	137
XP_019622707.1[B.belcheri]	TSEKSKAKKDPIATNGERFPWDDVRLPTIVPNSYLLHLHFNLT--TFNFTGHVSNINISV	187
XP_012561211.1[H.vulgaris]	-----NKLNSKREELFPYINIRLPLNIVPERYKIYHFNLTDNKGFPTGTVRILINI	109
XP_032239104.1[N.vectensis]	EPEKKDDSSFYEDGHGRKFAWQIRLPSSSVTPEEYTVILRPKL-DPDFTFSGNVSVRVKC	166
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XP_032824577.1[P.marinus]	DESTDHVVLHANNLTITESILVPADGA-----PAGGDAGSLVAKLLRYEPRDQLMVCT	335
XP_014016586.1[S.salar]	LHNTKHVVLHSSSELIITKATFQVGE-----K-SVEVKVLEYKPPQOIAVSF	251
NP_001088429.1[X.laevis]	TTSSKNIVLHSSGLHIIKASVLVNGG-----T-TMDAEVLEYPPFEEIAIIS	245
XP_424862.3[G.gallus]	TQVTKKIVLHSSGLNITKATITSTGG-----SQEKAVELLEYPHLDQIAVMA	247
NP_766415.1[M.musculus]	LQDTRDILHSTGHNISRVTFMSAVS-----SQEKQAEILEYYPHEQIAVVA	247
Q9UIQ6[H.sapiens]	LQVTWNIILHSTGHNISRVTFMSAVS-----SQEKQAEILEYAYHQQIAIVA	247
XP_024102718.1[P.abelii]	LQVTWNIILHSTGHNISRVTFMSAVS-----SQEKQAEILEYAYHQQIAIVA	247
NP_731786.1[D.melanogaster]	NALTNLIVLHAKELNVHSISLNMMA-----IRVATDSINLDESRELLLTIL	216
XP_003386159.1[A.queenslandica]	NQSTDLIVFHAKMDTLNVTSLTKGVRG-----DQLGTSRQFPFYSDNPVITQL	185
XP_019622707.1[B.belcheri]	VKKTDLVVHFHVKELNITQSSVKTMNVN-----SVPIV--KELEYTNGEQYCLRL	234
XP_012561211.1[H.vulgaris]	TEETDSVLLHIDKNISEVKCYHGSSAMSKHKGPEDSQQVPVKDHLISVEHEFLIMRMKE	169
XP_032239104.1[N.vectensis]	NEDTDYIFIAHKQMLTKFEVLNQGKE-----PLKIMETANCEKLEMFSIKV	213
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XP_032824577.1[P.marinus]	RKPLTQGGMYLLNITFTGRLSTSFLGFYRSTYRAEDG---SDRPLAVTQFEPTSARESF	391
XP_014016586.1[S.salar]	PEDLKVGQVCVLTLDYAASLSHTYDGFYNSSYNKDTG---AKRVLAATQFEPPQAARKAF	307
NP_001088429.1[X.laevis]	PESLLKGKCELLTIQYAANFSSTYYGFYKIDYMKDSN---K-RSLAATQFEPLAARKAF	300
XP_424862.3[G.gallus]	PESLLAGQNYTVNLEYSSNLSDTYYGFYRVSYKDENS---KQRWFAATQFEPLAARSAF	303
NP_766415.1[M.musculus]	PEPLLTGHNYTLKIEYSANISSYGFYGITVYTKDSN---EKKYFAATQFEPLAARSAF	303
Q9UIQ6[H.sapiens]	PEALLAGHNYTLKIEYSANISSYGFYGFSTYDESN---EKKYFAATQFEPLAARSAF	303
XP_024102718.1[P.abelii]	PEALLAGHNYTLKIEYSANMSRYFGFYGFSTYDESN---EKKYFAATQFEPLAARSAF	303
NP_731786.1[D.melanogaster]	REVLSMNKAYTILASFDCLDS-SLVGSYISNYTNADG---VDRSIISTKFEPTYARQAF	271
XP_003386159.1[A.queenslandica]	ADSLDTNDNLQINISFNVTLRDDLVGFPYKSSYLADN---EVHYLATTQFEPTDARRAF	241
XP_019622707.1[B.belcheri]	GGQLSAGQNTIVVHFSGELNDGLYGFYRSTYTLNKGKDGEESRLATTQFEAANARAAF	294
XP_012561211.1[H.vulgaris]	QHELEVKGQYTLFRFNRGLSNGLEGFYKSSYTTSGK---EKRYLATTTFEATQARAFA	225
XP_032239104.1[N.vectensis]	KGGLKKGESVVLQIDFNAVLAELKTGFYKSSYKDKDG---NTRYLATTTFEPTDARAFA	269
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XP_032824577.1[P.marinus]	PCFDEPDFKASFDISIVRD--AAHTLSLNMPLNETVTR-KDGLLEDTFKG-SVMMSTYLV	447
XP_014016586.1[S.salar]	PCFDEPAFKATFLVIRITRE--PGYITLSNMPEAKTTTL-PSGLLEDEFEQTAVNMSTYLV	364
NP_001088429.1[X.laevis]	PCFDEPAFKSTFQINIIIRN-DESMISLNMPEAKTSKT-SDGLLQDEYST-SVRMSTYLV	357
XP_424862.3[G.gallus]	PCFDEPAFKATFSIRIKRD--EKLSTLSNMPEKATTPV-TKGIVQDEFV-SLRKMSTYLV	359
NP_766415.1[M.musculus]	PCFDEPAFKATFIKITRN--EHHTALSNMPEKSSVPA-EEGLIQDEFSE-SVRKMSTYLV	359
Q9UIQ6[H.sapiens]	PCFDEPAFKATFIKIIIRD--EQYTALSNMPEKSSVVL-DDGLVQDEFSE-SVRKMSTYLV	359
XP_024102718.1[P.abelii]	PCFDEPAFKATFIIRIIRD--EQYTALSNMPEKSSVIL-EDGLVQDEFYE-SVRKMSTYLV	359
NP_731786.1[D.melanogaster]	PCFDEPALKAQFTITVARPSGDEYHVLNMPVASEYVD--GDITEVTFAE-TVPMMSTYLA	328
XP_003386159.1[A.queenslandica]	PCFDEPAMKANFSIELTHA--NRYNAVSNMPVARRVSK-ANDKATTSFNT-SYKMSSTYLV	297
XP_019622707.1[B.belcheri]	PCFDEPALKATQLHVMRE--GRHSTLFNMPKD-HIEDLLGLKMDVFK-SVAMSTYLV	350
XP_012561211.1[H.vulgaris]	PCFDEPALKALFEIIMVRE--PQHTALSNMPIVKTINR-TDGLKEDHFQK-SLMMSSTYLV	281
XP_032239104.1[N.vectensis]	PCFDEPALKAVFNMVIYRK--AEHVSLSNMPIKETFKDKESQVIDVFEP-SVRKMSTYLV	326
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XP_014016586.1[S.salar]	LMSQDWG---EEE-SVSRQELRSALLEMACSLGRQNCNDQATALYDQWTSNQTKQI-P	862
NP_001088429.1[X.laevis]	TLIKQTWM---DEG-TLAERQLRSSLLDFACSNPGFSCLEKATELFNSWRVKN--TRI-P	851
XP_0424862.3[G.gallus]	KIDQQNWT---DDG-TISERELRSMLLTFFACTHDIRNCRTAASKMFDEWMKSNGTMSL-P	855
NP_766415.1[M.musculus]	QIQQQTWT---DEG-TPSMRELRSALLEFACAHSLNCTTMAIPLFDSWMAASNGTQSL-P	856
Q9UIQ6[H.sapiens]	QIQQQTWT---DEG-TPSMRELRSALLEFACAHSLNCTTMAIPLFDDWMAASNGTQSL-P	856
XP_024102718.1[P.abelii]	QIQQQTWT---NEG-TPSMRELRSALLEFACIHNLCNCSTTAMKLFDDWMAASNGTQSL-P	856
NP_731786.1[D.melanogaster]	IVEKVTFT---VAA-DHLENRLRIKVLSSACSLGHESSLQQAATLFDNQWLASF--ETRFN	826
XP_003386159.1[A.queenslandica]	ITRKLSPN---KTGLSHLQILLRTYVLLSGYKIGDISIADTSLTMRFRNMWTDG---ISV-P	799
XP_019622707.1[B.belcheri]	TIGVEGWE---DQG-DQLTKFLRSTVLGAACDYGHEQSTQQAHTLIFANMKGT---QNV-A	856
XP_012561211.1[H.vulgaris]	IVDKLGWS---DEG-THLNRYLRGAALRSSVWMDNTDSVKRALBIFDRFNMNH--ESV-A	777
XP_032239104.1[N.vectensis]	IVRKLQWD---DKG-SHLQRYLRSYVLKLCARYGDVECATAVKSRFADWM-RG--ESL-P	833
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XP_032824577.1[P.marinus]	ADLMSTVLRVAVRD-GDRPTWDSVQEHYHRAKSSTEQAQKYLEALASTSDEDQQWSILENA	1003
XP_014016586.1[S.salar]	GDLQRVVFVSAQS---NLGWLSLMEAYSSTTYDSEKRKILQALASTQDPQSIWILSTG	919
NP_001088429.1[X.laevis]	TDVMKVVFVKVGART---TEGWTLRLSTYDSSIYEAERKILQALASTDNAKILQWLMQES	908
XP_0424862.3[G.gallus]	SDLMKAITFGAKT---NDGWELFLKMYSSFPVEAEKSKMIEALASTEDVRKMMWLMQNS	912
NP_766415.1[M.musculus]	TDVMVTVPKVGART---EKGWFLFLFSMYSMGSEAEKNKILEALASSEDVHKLYWLMKSS	913
Q9UIQ6[H.sapiens]	TDVMTVPKVGART---DKGWSFLLGKYISIGSEAEKNKILEALASSEDVRKLYWLMKSS	913
XP_024102718.1[P.abelii]	TDVMTVPKVGART---DKGWSFLLGKYISIGSEAEKNKILEALASSEDVRKLYWLMKSS	913
NP_731786.1[D.melanogaster]	PDIRLVVYYGLQQVNTAAWDQVWKLYLDESDAQEKLKIMNCLTAVQVPWLLQRYINWA	886
XP_003386159.1[A.queenslandica]	PDLRLVVYVAIAA--GGETEWNYLWSWYKNTNPYEKQICLSALAQSKKEYWILSRYLEYS	858
XP_019622707.1[B.belcheri]	ANLKTVVYTSVGQH--GGEENWFCWQYTSATVAEAKRLLYALANTRDNKLVTKLLRYT	915
XP_012561211.1[H.vulgaris]	PNLRSTVYLAGIKY--GGKEQWEFMLANKYLPFPPEQRKMLPALADSSDESILKLYLSWS	836
XP_032239104.1[N.vectensis]	PNLRSVIYDTGVHL--GGEKEFKYMYEQYKNSYVAAEKRKLLFAMSATQNPALMKGLLDS	892
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XP_032824577.1[P.marinus]	MAGVEVRSQELPRIVGVMARTSWTGRLLTWDFLRKRWSLLVEKFSLSGFSALSNMWSVTS	1063
XP_014016586.1[S.salar]	LEGGIQTQELPLVITMSD-GFAGHLFWDFVKENWDKIKKFPVGSYPIQSIKSTTS	978
NP_001088429.1[X.laevis]	LDGGSIRSQELPAVIGFICK-RSPGYLLAWNFIKQNWDLITQKFMPSGFPQINIVSKTTH	967
XP_0424862.3[G.gallus]	LEGEVIRTQELSHIATISH-SLPGHLLAWDFVKENWEKLTTRKPHLGSYTIQNISSSTS	971
NP_766415.1[M.musculus]	LDGDIIRTQKLSLIIRTVGR-HFPGHLLAWDFVKENWNKLVHKFHLGSYTIQNIIVAGSTH	972
Q9UIQ6[H.sapiens]	LNGDNFRFQKLSFIIRTVGR-HFPGHLLAWDFVKENWNKLVHKFHLGSYTIQNIIVAGSTY	972
XP_024102718.1[P.abelii]	LNGDNFRFQKLSFIIRTVSR-HFPGHLLAWDFVKENWNKLVHKFHLGSYTIQNIIVAGSTY	972
NP_731786.1[D.melanogaster]	WDESNVRRQDYFTLLGYIST-NPVGQSLVWDVRENWEKLVDRFGINERTLGRILPTITA	945
XP_003386159.1[A.queenslandica]	MSQ--VRSQDTLYVIRSVAR-NVNGRYLAWNVRDNYDTIFPKYGGSGSFSRLIRISITG	915
XP_019622707.1[B.belcheri]	LDSTKIRSQDVTRTITYVSR-TAVGYQLAWNFKVSNWQTFPLDRYGGSGSFNMAELAKIPAH	974
XP_012561211.1[H.vulgaris]	MNTSIIRTQDTCGVIEHIST-NIKGTMADDFVKNWEKLFERYKGSGFDMSSSLIKTVFA	895
XP_032239104.1[N.vectensis]	MSTQ-IRSQDTSVITSVAS-NCKGRNLAWDFVKENWNKLVHKFHLGSYTIQNIIVAGSTH	950
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XP_032824577.1[P.marinus]	GFSSTYHLDQVEEFVASLRDSSGELRVFKEARDTIRANHHWLATNRVALHKWLTEQS---	1120
XP_014016586.1[S.salar]	QFSTQTHLEEVQGFSSSLKERGSGMRSVQEALETIRLAQLWMDRNLPTLRILWL-----	1031
NP_001088429.1[X.laevis]	QFSTDVHLENEVIAPFNSTQEKSRGEMCVKEAVETIKLNIEMWNNFDSLATWLLPSQ---	1024
XP_0424862.3[G.gallus]	QFAFKVHLLLEVKTFFESKESKLRVKKEAIDTQLNIQWMEITLAKLQEWL-----	1024
NP_766415.1[M.musculus]	LFSTKTHLSEVQAFQENQSEATLKLRCVQEALEVIQLNIQWMEITLAKLQEWL-----	1025
Q9UIQ6[H.sapiens]	LFSTKTHLSEVQAFQENQSEATFLRLRCVQEALEVIQLNIQWMEITLAKLQEWL-----	1025
XP_024102718.1[P.abelii]	LFSTKTHLSEVQAFQENQSEATFLRLRCVQEALEVIQLNIQWMEITLAKLQEWL-----	1025
NP_731786.1[D.melanogaster]	RFSTETKLEEMQFFAKYPEAGAGTAARQQAQALEAVKANIKWLAANKAQVGEWLANVYQQS	1005
XP_003386159.1[A.queenslandica]	SFATSWMELQEVESFFQKV-DVGSASLALQQSKEIVRGNIAWLDDNESVIGEMWNLVSGA	974
XP_019622707.1[B.belcheri]	RFSTRQLEEVKSFQSH-DISAAARAQTIETIQSNIFWLEKNKDKVKTKWIKNYFMFP	1033
XP_012561211.1[H.vulgaris]	RMKTKEDLKKVSEI-----	910
XP_032239104.1[N.vectensis]	HFSTPQKLKEIQEFFKKH-ELGSGKLASKQAEEGISSNIDWMKNNIEVALKWLEHTQAE	1009
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XP_032824577.1[P.marinus]	-----	1120
XP_014016586.1[S.salar]	-----	1031
NP_001088429.1[X.laevis]	-----	1024
XP_0424862.3[G.gallus]	-----	1024
NP_766415.1[M.musculus]	-----	1025
Q9UIQ6[H.sapiens]	-----	1025
XP_024102718.1[P.abelii]	-----	1025
NP_731786.1[D.melanogaster]	SVTNRIQ-----	1012
XP_003386159.1[A.queenslandica]	MSA-----	977
XP_019622707.1[B.belcheri]	---EGGKARSSEI-----	1043
XP_012561211.1[H.vulgaris]	-----	910
XP_032239104.1[N.vectensis]	SKPADGDLGVANVERLENILAPEGFQEEYQDRENQEKPYQNKRYSNQHYGRDDQDRRF	1069
XP_032824577.1[P.marinus]	-----	1120
XP_014016586.1[S.salar]	-----	1031
NP_001088429.1[X.laevis]	-----	1024
XP_0424862.3[G.gallus]	-----	1024
NP_766415.1[M.musculus]	-----	1025
Q9UIQ6[H.sapiens]	-----	1025
XP_024102718.1[P.abelii]	-----	1025
NP_731786.1[D.melanogaster]	-----	1012
XP_003386159.1[A.queenslandica]	-----	977
XP_019622707.1[B.belcheri]	-----	1043
XP_012561211.1[H.vulgaris]	-----	910
XP_032239104.1[N.vectensis]	SNEYNDDDYEPERRGYEQ	1088