

# USP25

## Homo sapiens:

>Q9UHP3 [Homo sapiens]  
MTVEQNVLQSSAAQKHQQTFLNQLREITGINDTQILQQALKDSNGNLELAVAFLTAKNAK  
TPQOEETTTYQTALPGNDRIYISVGSQADTNVIDLTGDDKDDLQRAIALSLAESNRAFRET  
GITDEEQAISRVLEASIAENKACLKRTPTTEVWRDSRNPYDRKRQDKAPVGLKNVGNTCWF  
SAVIQSLFNLLEFRRLVLNYPSPNAQDLPRNQKEHRNLPFMRLERLYFALLVGTTRKRYV  
DPSRAVEILKDAFKSNDSSQQQDVSEFTHKLLDWLEDAFQMAEEETDEEKPKNPMVELFY  
GRFLAVGVLEGGKFENTEMFGQYPLQVNGFKDLHECLEAAMIEGIESLHSENSGKSGQE  
HWFTELPFVLTFFELSRFENQALGRPEKIHNNKLEFPQVLYLDRYMHRNREITRIKREEIK  
RLKDYLVTLQQRLELYLSYSGGPKRFPPLVDVLQYALEFASSKPVCTSPVDDIDASSPPSG  
SIPSTLPSTTEQQGALSSEL PSTSPSSVAAISSRSVIHKPFTQSRIPDLPMPHPAPRHI  
TEEELSVLSECLHRWRTIEINTDRDQESISRIHRTIELMYSDKSMIQVPYRLHAVLVHE  
GQANAGHYWAYIFDHRESRWMKYNDIAVTKSWEELVRDSFGGYRNASAYCLMYINDKAQ  
FLIQEEFNKETGGPLVGIETLPPDLRDFVEEDNQRFKELEEWDAQLAQKALQEKLLASQ  
KLRESETSVTTAAAGDPEYLEQPSRSDFSKHLKEETIQITKASHEHEDKSPETVLQSA  
IKLEYARLVKLAQEDTPPETDYRLHHVVVYFIQNQAPKKIIEKTLLEQFGDRNLSFDERC  
HNIMKVAQAKLEMIKPEEVNLEEYEEWHQDYRKFRETTMYLIIIGLENFQRESYIDSLLFL  
ICAYQNNKELLSKGLYRGHDEELISHYRRECLLKLNQAAELFESGDEGVNNGLIIMNE  
FIVPFLPLLVDMEEEKDILAVEDMNRNWCYSYLGQEMEPHLQEKLTDFLPKLLDCSMEIK  
SFHEPPKLPYSYTHELCERFARIMLSLS

## Pongo abelii:

>XP\_024095245.1 ubiquitin carboxyl-terminal hydrolase 25 isoform X3 [Pongo abelii]  
MTVEQNVLQSSAAQKHQQTFLNQLREITGINDTQILQQALKDSNGNLELAVAFLTAKNAKTPQOEETTTY  
QTALPGNDRIYISVGSQADTNVIDLTGDDKDDLQRAIALSLAESNRAFRETGITDEEQAISRVLEASIAEN  
KACLKRTPTAEVWRDSRNPYDRKRQDKAPVGLKNVGNTCWFSAVIQSLFNLLEFRRLVLNYPSPNAQDL  
RNQKEHRNLPFMRLERLYFALLVGTTRKRYVDPSRAVEILKDAFKSNDSSQQQDVSEFTHKLLDWLEDAFQ  
MAEEETDEEKPKNPMVELFYGRFLAVGVLEGGKFENTEMFGQYPLQVNGFKDLHECLEAAMIEGIESLH  
SENSGKSGQEHWFTELPFVLTFFELSRFENQALGRPEKIHNNKLEFPQVLYLDRYMHRNREITRIKREEIK  
RLKDYLVTLQQRLELYLSYSGGPKRFPPLVDVLQYALEFASSKPVCTSPVDDIDASSPPSGSIPSTLPST  
TEQQGAPSSSEL PSTSPSSVAAISSRSVIHKPFTQSRIPDLPMPHPAPRHI  
TEEELSVLSECLHRWRTIEINTDRDQESISRIHRTIELMYSDKSMIQVPYRLHAVLVHEGQANAGHYWAYIFDHRESRWMKYNDIAVT  
KSWEELVRDSFGGYRNASAYCLMYINDKAQFLIQEEFNKETGGPLVGIETLPPDLRDFVEEDNQRFKE  
LEEWDAQLAQKALQEKLLASQKLRESETSVTTAAAGDPEYLEQPSRSDFSKHLKEETIQITKASHEHED  
KSPETVLQSAIKLEYARLVKLAQEDTPPETDYRLHHVVVYFIQNQAPKKIIEKTLLEQFGDRNLSFDERC  
HNIMKVAQAKLEMIKPEEVNLEEYEEWHQDYRKFRETTMYLIIIGLENFQRESYIDSLLFLICAYQNNKGL  
LSKGLYRGHDEELISHYRRECLLKLNQAAELFESGDEGVNNGLIIMNEFIVPFLPLLVDMEEEKDIL  
AVEDMNRNWCYSYLGQEMEPHLQEKLTDFLPKLLDCSMEIKSFHEPPKLPYSYTHELCERFARIMLSLS

## Mus musculus:

>NP\_038946.2 ubiquitin carboxyl-terminal hydrolase 25 [Mus musculus]  
MTVEQNVLQSSAAQKHQQTFLNQLREITGINDAQILQQALKDSNGNLELAVAFLTAKNAKTPQOEETGY  
QTALPGNDRIYISVGSQADANVIDLTGDDKDDLQRAIALSLAESNRAFRETGITDEEQAISRVLEASIAEN  
KACLKRTPTIEVWRDSRNPYDRKRQDKAPVGLKNVGNTCWFSAVIQSLFNLLEFRRLVLNYPSPNAQDL  
RNQKEHRNLPFMRLERLYFALLVGTTRKRYVDPSRAVEILKDAFKSNDSSQQQDVSEFTHKLLDWLEDAFQ  
MAEEETDEEKPKNPMVELFYGRFLAMGVLEGGKFENTEMFGQYPLQVNGFKDLHECLEAAMIEGIESLH  
SDNSGKSGQEHWFTELPFVLTFFELSRFENQALGRPEKIHNNKLEFPQVLYLDRYMHRNREITRIKREEIK  
RLKDYLVTLQQRLELYLSYSGGPKRFPPLVDVLQYALEFASSKPVCTSPVDDIDASSASGPLSPQSLPST  
TEQQGPCASDLPSSSPASGAALPLRSVIHKPFTQSRIPDLPMPHPAPRHI  
TEEELCVLESCLHRWRTIEINTDRDQESISRIHRTIELMYSDKSMIQVPYRLHAVLVHEGQANAGHYWAYIFDHRESRWMKYNDIAVT  
KSWEELVRDSFGGYRNASAYCLMYIDDKAQFLIQEEFNKETGQALVGMETLPPDLRDFVEEDNQRFKE  
LEEWDTQLAQRSLQEKLLAAPKLREAEASATTAAQGGADYLEQPSRSDLSKHWKEETLRVIAKASHDLED  
KGPETVLQSAIKLEYARLVKLAQEDTPPETDYRLHHVVVYFIQNQAPKKIIEKTLLEQFGDRNLSFDERC  
HNIMKVAQAKLEMIKPEEVNLEEYEEWHQDYRKFRETTMYLIIIGLENFQRESYIDSLLFLICAYQNNKGL  
LSKGLYRGHDEELISHYRRECLLKLNQAAELFESGDEGVNNGLIIMNEFIVPFLPLLVDMEEEKDIL  
AVEDMNRNWCYSYLGQMEANLQEKLTDFLPKLLDCSTEIKGFHEPPKLPYSYSAHELCEERFARIMLSLS

## Gallus gallus:

>XP\_040518387.1 ubiquitin carboxyl-terminal hydrolase 25 isoform X5 [Gallus gallus]  
MTVEQNVLQPGGAQKHQQTFLNQLREITGINDIQVLQQALKDSNGNLELAVAFLTAKNAKVPQOEETYYQ  
QTALPGNDRIYISVGSQADTNVIDLTGDDKDDLQRAIALSLEESNRAFRETGITDEEQAISRVLEASIAEN  
KASLKRTHTPEVMSDSPNPYDRKRQDNCVPGLKNVGNTCWFSAVIQSLFNLLEFRRLVLNFPSPANAQDL  
RNQKEHRNLPFMRLERLYFALLVGSKRKYVDPSRAVEILKDAFKSNDSSQQQDVSEFTHKLLDWLEDAFQ  
IAEEERDGEKPKNPMVELFYGRFLAVGVLEGGKFENTEMFGQYPLQVNGFKDLHECLEAAMIEGIESLH  
SENSAKSGQEHWFTELPFVLTFFELSRFENQALGRPEKIHNNKLEFPPILYLDRYMHNKREITRIKREIK  
RLKEYLVTLQQRLELYLSYSGGPKRFPPLVDVLQYALEFASSKPVCTSPVDDL GASAPSSGTLPAQTSPST  
IEQQGSSSDVPSTSPVQSRISVIHKPFTQSRIPDLPMPHPAPRHI  
TEEELSVLGCLHRWRTIEVNDTRDLQESISRIHRTIELMYFDKTMIQVPYRLHAVLVHEGQANAGHYWAYIYDHHQNRWMKYNDISVTKSTWEE  
ERDSFGGYRNASAYCLMYINDKEQYLIEEEFNKETGGIIVGMDTLPSDLRDYVKEDNKRFEKELEEWDAE  
LAQKAEQEKLLSQIFRAPAFSPAPFQAGEPPEYLEQPSRTDLSKHLKEDSVQAINKALASEQDRGPEAVLQ  
MIAIKLEYARLVKLAQEDTPPETDYRLHHVVVYFIQNQAPKKIIEKTLLEQFGDRNLSFDERC  
HNIMKVAQAKLEMIKPEEVNLEEYEEWHQDYRNFRETTMYLIIIGLENFQRESYIDSLLFLICAYQNNKGL  
LSKGLYRGHDEELISHYRRECLLKLNQAAELFESGDEGVNNGLIIMNEFIVPFLPLLVDMEEEKDIL  
AVEDMNRNWCYSYLGQEMEPNLQEKLTDFLPKLLDCSTEIKGFNDPPKLPYSYTHELCERYARIMLSLS

## Xenopus laevis:

>OCT93923.1 hypothetical protein XELAEV\_18011587mg [Xenopus laevis]  
MTVEQNVLQONSQKHQQTFLNQLREITGINDLQVLQQALKDSNGNLELAVAFLTAKNAKLPQOEETYYQ  
TALPNNDRYISVGSQADTNVIDLTVDKDDLQRAIALSLEESNRTFRETGITDEEQAISRVLEASIAENK  
ACKLRTHTPEVMSDSPNPYDRKRQDNCVPGLKNVGNTCWFSAVIQSLFNLLEFRRLVLNYPSPSAQDVPR  
NQKEHRNLPFMRLERLYFSLMVSSKRKYVDPSRAVEILKDAFKSNDSSQQQDVSEFTHKLLDWLEDAFQIK  
AEERDGEKPKNPMVELFYGRFLAVGVHEGGKFENTEMFGQYPLQVNGFKDLHECLEAAMIEGIESLH  
SENSGKSGQEHWFTELPFVLTFFELSRFENQALGRPEKIHNNKLEFPCLYDRYMHNKREITRLKREIKR  
LKDHLVTVLQQRLELYLSYSGGPKRFPPLADVLQYALEFASSKPVCTSPVEDIDVSAPSSGCVATQTMQSTT  
EHQGSASASETLPTQSRISVIHKPFTQSRIPDLPMPHPAPRNI  
TDEELSVLGCLHRWRTIEVNDTRDLQDSIGRIHRTIELMYSDKQMQVPYKLVHAVLVHEGQANAGHYWAYIFDHHEQRWMKYNDISVTKSWEELER  
DSFGGYRNASAYCLMYINDEEKLMAQEEYDKETGGQVLKGMIDILPLDREYIKEDNKRFEKELEAWDEQL  
RKAEQAEKLLSQIFRAPAFSPAPFQAGEPPEYLEQPSRTDLSKHLKEDSVQAINKALASEQDRGPEAVLQ  
MIAIKLEYARLVKLAQEDTPPETDYRLHHVVVYFIQNQAPKKIIEKTLLEQFGDRNLSFDERC  
HNIMKVAQAKLEMIKPEEVNLEEYEEWHQDYRNFRETTMYLIIIGLENFQRESYIDSLLFLICAYQNNKGL  
LSKGLYRGHDEELISHYRRECLLKLNQAAELFESGDEGVNNGLIIMNEFIVPFLPLLVDMEEEKDILAVEDMNRN  
WCYSYLGQEMEPNLQEKLTDFLPKLLDCSTEIKGLNDPPKLPNFSTHELCEERFARIMLSLS

**Salmo salar:**

>XP\_013993323.1 PREDICTED: ubiquitin carboxyl-terminal hydrolase 25-like isoform X9 [Salmo salar]  
MTVEQNVLQQHSQKHQQTLNQLREVVTGTTDVQLLQQALQVSNGLDAEAVAFLTEKNAKVPQQDEAAYYQ  
TTQVGNDRYISVGSQADTNVIDLTGDDKDDLQRAIALSLEESSRAFRETGITDEEQAISRVLEASIAENK  
ASLKRTHTEVWSDSPNPHDRKRMCNCPVGLKNVGNTCWFSFSAVQSLEFNLLFQRLVLHYSPPARVQDLPR  
NQKEHRNLPFQJELRNLFSLMVGSKRKYVDPSRAVEILKDAFKSSESQQQDVSEFTHKLLDWLEDAFMK  
AEDREGEKFPKNFMVELFGRFQAVGVLEGGKFENTEMFGQPLQVNGFKDLHECLEAMIEGEIESLSHS  
SAENSASKQGEHWFTELPVLTFFELSRTEFQVALGRPEKIHNNKLEFPFMLYMDRYMDNRNIEATIKREI  
RRLKEQILLQQRLERYLSYSGSGPKRFLADVLYAMEPASSKPVCTSPLEDIDTSAPPGGTTGQILLPAL  
STAEQGPSCTLPEGLAAAPTQAPSTQQRVPVHKPFTHSRLPDPDPMHPAPRHITHEELRVLEGCLHRWRS  
EVENOTHDLQGSISRIRHTIELMYSDKSMQVPPRLHAVLVHEGQANAGHYWAYIDPHQQRWMMKYNDIS  
VTKSWEELVRDSFGGYRNASAYCLMYINDKKPFLIEEFDKETGQMLSGLDKLPDLKAVVKEDNGLFD  
KEMEEWDKLQARKAQEKLALAAAAAATAETTTSHQPMSTESPSPDSWGPDQDPEYMEQSPSTDSDKHLQ  
EDTERAISKAAAEQGEERSPEGLLTAAIKVETRLRLRFAQEDTAPENDYRLQHVIYVYIHNQAPKKILER  
TLIMQFADRNLSFDERCKSIMKVARAKLDLVKPEEVNMEEYEMWHQDYRNFRETTFIMIGLELFQKKCF  
VEALMYLITYSYQYNRELLVKGLYRGHNDELIGHYRRECLLKLNENAARMFESGEEPEVCNGLSIMNELVV  
PCPIPLLVDHTEKDLLAVEDMNRNWCYSLGQEMEPNLQEKLTDFLPKLLDCSTEIKSFHDPFKLPTYSTL  
ELVERYGRVMASLCRVADGS

**Petromyzon marinus:**

>XP\_032826770.1 ubiquitin carboxyl-terminal hydrolase 25-like isoform X3 [Petromyzon marinus]  
MADRQMTVMTVEHRETAGIPSRNNQIILNQLREITGNSDVIALQQALQAAQGDVSQAVALLTETPNQNA  
GCALSSSQSHRSLFNQSQNSTGVIDLTGDDKDDLQRAIALSLQETSERAVRADLTTEEQDISRVLEESLA  
EASGPGGVKRRKSDPCACSCPRGEGDASGGGAEEGEVAVSAVRAGAPVGLKNVGNTCWFSAVVQSLFHL  
PQFRRLILGFTLPDSRLQNFQSENERVGLCFKRELRLVLFALMVGSVRGFVPSPAVHILKGAFRGADTQQ  
DYSSEFTHKLLDWLEDAFRISABESRAKLLDVKPEEVNMEEYEMWHQDYRNFRETTFIMIGLELFQKKCF  
HDLHECLEHAHTAGDIEQQQSQPPACASSQQLWFSELPVLTLELSRFNFTEVGRPEKIHRSLEFPDT  
IYMDRYMESNKKEVTRIKRDEIRRLSEQQSHLQQTLARYQSYSGSPQRYPLVDILSCALQFASTPTATVLL  
PPTSVLNHHGPPSSAAKPPCTLSNHHVTTSPVTSSSQVVSNNIALFPPIVESTPIPTSNHHVSSSAASP  
VLTHNHSDLSSTVPPPTMQSTNRVLSPTSLEPIPVPLTNHVAPSCATTSTPTTINSHTAPSPAFLIHIA  
STNHVAPPTVVKSPADRALLVDDTGPVLINGVAELGVALPPSDESSQPKAEALDINGDLSSESTAA  
PGCVVADGEVHQLRQQQPPSAAAAVACSAPEPHHTQERHGARARQEVPAQKSGEQNRTGDPFPFGQRT  
ADSQASVSLQQGSLQGEAMQVDTLQENVQGEEEGSGQKQDITQQQGLAQGESNQQTETQQRFDLQSEAN  
QVSLIQDMQQQHHRGNVQQEHVQGGNPQQGNFQQENSEQCKEQEGSTQQCDVQRVQAVEARQEGGRLEW  
HGPCAPQAVTALELVRVLSRWNSQVQRELQDLQDSICRIKRTIDLMYTDKTRFQLPYRLHAVLVHDG  
QMAAGHYWAYVREHARLPAASASSSSSSSGNSASSNSVSGASDESSGSDSCWRKFNDRVSRASWEL  
VRDSYGGGARSASAYCLVYVNARAHDTSELAGAVGDLSSLSPALRDLVAKDNHRFLSEMAMRNGNGPER  
PAEPDADAREPGQRAEPREHEQEERRHEHGGEQAPARAAPAAAAAASREGEESGAAREQERADKHSQ  
TNSLQGEAEPTREVRVDGRARAGEREETRVHEGRAPDVASISETQRQGEADGSASLPGREGTSAPSPSPS  
GTEEYMKVGPDTTEKPKRVERVVEVSIPIDVGTIVVQAEEHGYNDEVMLTPAMQGVLMAVARARLVREAQ  
PEATLIEAFKVEYARLRTLAQESYPDASSPASPPAPAGASGAAATAWRGREERLEHVVIYLFQNEAPNR  
VVERALLEQFADRNLSYDEQLIKIMVAQAKLQEISPEDMDPAEYQKWHQEYELFRQVCVYLVMGIEKYQ  
EGRYTEALPCTMHAAHNEELLARQKRRGVRRDVLARYRRVVRVNEACALFTGTGDVAQATRLSLAAMT  
ELVLVPMALLAPLQSSCGGDAAGEAAVARESOLCAVELMERDWCYSYLGRDMSSELQELLDFLPRLD  
YQPEPAPPTQLTTPPLQGGPPPPPPPPSETKCESSGGENWRGLRAPRLKAYSPHTLAERKMAEVLVRNRP  
EA

**Branchiostoma belcheri:**

>XP\_019624636.1 PREDICTED: ubiquitin carboxyl-terminal hydrolase 25-like [Branchiostoma belcheri]  
MSEFILDHAYQAGKGDIAEVVSIITNQNSVSLVTNNRNDEVQVQVQVRNAQRPSQAGRPDGRANTQEPAGV  
IDLTADTEDKDQEDLQRAIALSLQEAQTANTANRPGCECRPKRRKSSVSDNVQETPREPGWVGLKNVG  
NTCWFSAVQSLEFHLPVFRDLVLGFRFFPKDPANPSRESLVLHFMQJELRCLFARMQGSNRKYIDPCTCVVK  
SLRELIFFRAGETQQDVSEFTHKLLDLLEEAFTIVQRRQSTQPGSSASANTSSENGDKKSNPMLDLFYGR  
IQAEGMHAGKMFTNQQTVGQYTLQVNGFKDLHESLEGATAGQIEITGHEEGATKSGLEHWFTHLPVLT  
ELSRFEFNQKLGKAEKIHKKLEFPKFLYMDRYLVNKKELTRLKREEMKMKKEEMDTLQAKLDSFNLYSGS  
YKRLPLPLDKYTLTEFAEKSTVQTVDGQVRSNGSGSSKAANGNHNGSEKKTDEEDGSSDDFEVISAV  
HSADSLACLSSKKTLDAVATKKAAPVPTSEEMAIPSKVHPCPHVTKHEELAVLQTLRRWRHEAEKEVKG  
LQDRILLYLQAKIENLYEDNSLKQVPYQLHAVLVHEGQASAGHYWAYVRDHTQNRLKFNVDVTVTGMSWGE  
LLRESEGGYHHASAYCLMYIDITRKDLVEVKLQWSQYDELKMLVLAENERFIAQQRDLESKQRRTMVRE  
EDPPANHRGGQTTSESSSGEVADQPIQGEHRVVDVQRKQFPQVKPFVTTETQQGVRLGRTSQQSTPLD  
HSGHVLQAMKMTLLEVSNGVDGYEGNRFNSNIETFGACPLQVQGYSNLHDSLEGMAARELEPANHGDTQNSG  
QEHWFTELPVLTFFMLSPFLNQSGRAEKIHEKLFQKCTYMDRYMERKELSRAREEVKTLKRRHL  
LKSSLDRYNTYSGSAKRSPIQDILDSALNFVRSTPPSDSTDVEMHTPIPGSPVTFGTTSAGPSTLSDRT  
PSLHAPRVYTESELETIATSLRRWRTEVEQVDLIDSTLSLKEVEEAISVMYNDEEMKTIPIRYLVAVLVHE  
QANGGHYWAYINDPLDRWRKFNIDITVSEVTWEEVERESLGGVRNVSAVCLLYCDARREEVIRAGNTE  
VLSAELQQVMNEDNASFEQLRDWDEKQAKAAKEAKSQALVVARPDLVDAEASCAVSPRAHSPAARASE  
SVLTANGLVPSLVDSGKLTIDEAITQWCNNEKTRLDKLAREYPEYPGDVRLLEHLGIYLMRCSAPDF  
TVECALIESVIDEVKAKDQSLMPYRKRVPQELEREKGTDRAADYKRKWEYMTFKLINSCFLTGLEHFHS  
QKYKSELPYLVHAYELNRLSDPTNNARMSDQRLLAHCRVCFKLKNELAISLFESDDYKTLCEGLDLVS  
EQVVPCTPQLVTSFYAEDREAEHMRNNWFTYLGKTVDEKREQELQDFLPKLLDGSDTGNFEEMRPPFVY  
RPTNSKDLCERFTRAMEIVHANMPPAAKA

**Drosophila melanogaster:**

No homolog found.

**Hydra vulgaris:**

No homolog found.

**Nematostella vectensis:**

>XP\_032229076.1 ubiquitin carboxyl-terminal hydrolase 25 [Nematostella vectensis]  
MTVEYPPSSMKKVTQENEAIHQCEITGVSIIEAQNAFAAGNYNVDEAISILTQSNLKSSTTHHVKKTFPV  
EQEEVILDTKDDKDDDDLEKAIALSLSQESQAGQPGGITAEEQDISRVLEASLIENKPGQKKRRKGDPMWM  
FVDPVNYPIDRKKVEGTPVGVGNVGNTCWFSFSAVQALFHLFVFRKLVLYGYPQPAANEQKDAHQLLFMLELR  
KLFALLVASRKKYVDPDKAIEILKEALQYNGSDSNPGNQQDVSEFTHKLEWLEDTFNTSEKEEEKSQAN  
SSSSNPFVELFFGQSKVDGYEGNRFNSNIETFGACPLQVQGYSNLHDSLEGMAARELEPANHGDTQNSG  
QEHWFTELPVLTFFMLSPFLNQSGRAEKIHEKLFQKCTYMDRYMERKELSRAREEVKTLKRRHL  
LKSSLDRYNTYSGSAKRSPIQDILDSALNFVRSTPPSDSTDVEMHTPIPGSPVTFGTTSAGPSTLSDRT  
PSLHAPRVYTESELETIATSLRRWRTEVEQVDLIDSTLSLKEVEEAISVMYNDEEMKTIPIRYLVAVLVHE  
QANGGHYWAYINDPLDRWRKFNIDITVSEVTWEEVERESLGGVRNVSAVCLLYCDARREEVIRAGNTE  
VLSAELQQVMNEDNASFEQLRDWDEKQAKAAKEAKSQALVVARPDLVDAEASCAVSPRAHSPAARASE  
SVLTANGLVPSLVDSGKLTIDEAITQWCNNEKTRLDKLAREYPEYPGDVRLLEHLGIYLMRCSAPDF  
TVECALIESVIDEVKAKDQSLMPYRKRVPQELEREKGTDRAADYKRKWEYMTFKLINSCFLTGLEHFHS  
QKYKSELPYLVHAYELNRLSDPTNNARMSDQRLLAHCRVCFKLKNELAISLFESDDYKTLCEGLDLVS  
EQVVPCTPQLVTSFYAEDREAEHMRNNWFTYLGKTVDEKREQELQDFLPKLLDGSDTGNFEEMRPPFVY  
RPTNSKDLCERFTRAMEIVHANMPPAAKA

**Amphimedon queenslandica:**

>XP\_019852971.1 PREDICTED: ubiquitin carboxyl-terminal hydrolase 25-like isoform X2 [Amphimedon queenslandica]  
MTSTAEVMSDKAKQDIMQLQEIFGITSTEAENSYQYKNSLSDAIVGLSSLQENGRVSLLEAAIKSPHS  
SESTSGDTSGLVATCANPNPMAAPAGGGGMAADSDQPTGSTNTNPIDLTQESQDDLDQALALSIGQMQH  
QGGGTSLEQJELKALASIAETHTEYGVPSRVDPDLNPHERKKIEGFLGLKNIGNTCWFSFSAVQSLEN  
TPAFRDSLHFNKTSQTEEDLPHCVLFVLELQKLFALLLESHQRYIDPKQAIDLNASFQTLGNHMQ  
QDVSEFKHLLLEWIEDAFNYQDKTKNNPIELFTGECVTEGKINETSFVNRSQGAFPVQIEGHAHLHDS

LEAATVNTEMEQETWFTHLPPVLVLELSRFKYNQLTGQAEKIHDSLSFDKTLYLDRYLHSNASQTRLLRK  
EMGLLRQPMRKIEETLKSSRLEGLVGAEGASPNVQEEGRSPSRSGSKEEVEFVRKWLEQWRSEMDTEISE  
LKSSLSATRESLDAVYSDPSMNRTSYHLHSVLVHQQASRGHYWAYVRKKKTKKKRKATREMGIQASYLDD  
EQTEEEGVDKSSSEKREEGEGHEDMEVTTTGGDTDVETFSPLSSCEPSSGPASVAPPEVKREEGSKED  
EEEEIWLKYNDVSVTTVDWEEVKRESFGRRGGESACNSNGPGTNTSAYCLLYVNSEAAKTWREEVHLLSLG  
LQRYIAYHNLAFERELKAYDLKVQLQQLTSSEGKELIKPAKAVRFEYPKGEEDPGASTNGGHDMMALAS  
DAKRARAGSPSNLEDMQIDLDNLPPVDPALNLQLSMRLSDKLQMFIQDVPGTIIESRLLTDFHYAHACQT  
SEKVRQAILLYEHVIQDLKRENDLNMSLLARKYFVEICKDPQIYQELQDVRLLYSRFCSCCYHFIQSVNEA  
KRN5WCLSLAHLINCPLYN5SISAQAGDKYSLDQQLGRFRCKALLMVSEIGTVAFTSGEVSSIVIGND  
YIVPGLKAFSLHPPFGDD5ILEKVREWCQCILDQSSLTEDDSKXLADLLMKIVEDYSKAPNIKIPQAFPSN  
FDTQRLAAQYTTAYKTLTSEILL

### Alignment

[illegible]

XP_032826770.1[P.marinus]	ASTPPATVLLPPTSLVNHKGPPSSAAKPPCTLTSTNHVTTSPVSSSQVVSTNNIALFPIVE	540
XP_032229076.1[N.vectensis]	VRSTPP-----SDSTDVEMHT-----	466
XP_013993323.1[S.salar]	ASSKPV-----CTSPLEDIDT-----	475
OCT93923.1[X.laevis]	ASSKPV-----CTSPVEDIDV-----	473
XP_040518387.1[G.gallus]	ASSKPV-----CTSPVDDLGA-----	474
NP_038946.2[M.musculus]	ASSKPV-----CTSPVDDIDA-----	474
Q9UHP3[H.sapiens]	ASSKPV-----CTSPVDDIDA-----	474
XP_024095245.1[P.abelii]	ASSKPV-----CTSPVDDIDA-----	474
XP_019852971.1[A.queenslandica]	-----GVL-----	445
XP_019624636.1[B.belcheri]	-----GHNG-----	468
XP_032826770.1[P.marinus]	STPIPSTNHVSSSAASPIVLTTNHSDLSTVPPTPMQSTNKRVLSPSTSLPIPVPLTNH	600
XP_032229076.1[N.vectensis]	-----PIPGSP-----	472
XP_013993323.1[S.salar]	-----SAPPGGTTG-----	484
OCT93923.1[X.laevis]	-----SAPPSGCV-----	482
XP_040518387.1[G.gallus]	-----SAPSSGTL-----	483
NP_038946.2[M.musculus]	-----SSSASGPL-----	483
Q9UHP3[H.sapiens]	-----SSPPSGSIP-----	483
XP_024095245.1[P.abelii]	-----SSPPSGSIP-----	483
XP_019852971.1[A.queenslandica]	-----GAEG-----	449
XP_019624636.1[B.belcheri]	-----SEKKTDEEDGSSDDFEVI-----SAV-----	490
XP_032826770.1[P.marinus]	VAPSCATTSTPTTISINHAPSPAVLPPIHIASSTNHVAPPTVVKSPADRALLVDDTGPFVLIN	660
XP_032229076.1[N.vectensis]	-----VTFGTTSAGST-----	484
XP_013993323.1[S.salar]	-----QLPALSTAEQCPSTLP-----	502
OCT93923.1[X.laevis]	-----TQTMQSTTEHQGSSSAS-----	499
XP_040518387.1[G.gallus]	-----AQTSPSTIEQQGPSSSDV-----	501
NP_038946.2[M.musculus]	-----SQSLPSTTEQQGPCASDL-----	501
Q9UHP3[H.sapiens]	-----SQTLPSTTEQQGALSSEL-----	501
XP_024095245.1[P.abelii]	-----SQTLPSTTEQQGAPSSSEL-----	501
XP_019852971.1[A.queenslandica]	-----H-----	449
XP_019624636.1[B.belcheri]	-----H-----S-----	492
XP_032826770.1[P.marinus]	GVAELGVALPSSDESSKQPKAEALDINGDLSESESTAAPGCVVADGEVHQLRQQPQPSSA	720
XP_032229076.1[N.vectensis]	-----EGL-----	484
XP_013993323.1[S.salar]	-----EGL-----	505
OCT93923.1[X.laevis]	-----P-S-----	499
XP_040518387.1[G.gallus]	-----P-S-----	503
NP_038946.2[M.musculus]	-----P-S-----	503
Q9UHP3[H.sapiens]	-----P-S-----	503
XP_024095245.1[P.abelii]	-----P-S-----	503
XP_019852971.1[A.queenslandica]	-----ADSLACLSSKKT-----	449
XP_019624636.1[B.belcheri]	AAAVACSAPEPHHTQERHGARQEVPAQQKSGEQNRTGDPPPPTEQRTADSQQASVLQ	503
XP_032826770.1[P.marinus]	-----AAAPTQAP-----STQQRVPIH-----	780
XP_032229076.1[N.vectensis]	-----ETQ-----LPTQSRVPIH-----	484
XP_013993323.1[S.salar]	-----TSP-----VQSRVPIH-----	522
OCT93923.1[X.laevis]	-----SSSPASGA-----ALPLRSVPIH-----	511
XP_040518387.1[G.gallus]	-----T-SPSSVA-----AISRSVPIH-----	513
NP_038946.2[M.musculus]	-----T-SPSSVA-----AISRSVPIH-----	520
Q9UHP3[H.sapiens]	-----T-SPSSVA-----AISRSVPIH-----	519
XP_024095245.1[P.abelii]	-----T-SPSSVA-----AISRSVPIH-----	519
XP_019852971.1[A.queenslandica]	-----QGSLQEQEAMQVDTLQENVQQGEEEGSQQKIDITQQQQLAQGESNQQTQQRFDLQSEAN	449
XP_019624636.1[B.belcheri]	-----K-----	503
XP_032826770.1[P.marinus]	-----K-----	840
XP_032229076.1[N.vectensis]	-----K-----	484
XP_013993323.1[S.salar]	-----K-----	523
OCT93923.1[X.laevis]	-----K-----	512
XP_040518387.1[G.gallus]	-----K-----	514
NP_038946.2[M.musculus]	-----K-----	521
Q9UHP3[H.sapiens]	-----K-----	520
XP_024095245.1[P.abelii]	-----K-----	520
XP_019852971.1[A.queenslandica]	-----LDA-----VATKKAAPVP-----	449
XP_019624636.1[B.belcheri]	QVSLLLQDMQQQHRGNVQGEHVQQGNPQQGNFQQENSEQCKEQQEGSTQQCDVQRVQAVE	516
XP_032826770.1[P.marinus]	-----LSD-----	900
XP_032229076.1[N.vectensis]	-----PFTQ-----	487
XP_013993323.1[S.salar]	-----PFTQ-----	527
OCT93923.1[X.laevis]	-----PFTQ-----	516
XP_040518387.1[G.gallus]	-----PFTQ-----	518
NP_038946.2[M.musculus]	-----PFTQ-----	525
Q9UHP3[H.sapiens]	-----PFTQ-----	524
XP_024095245.1[P.abelii]	-----PFTQ-----	524
XP_019852971.1[A.queenslandica]	---ASPNVQEGRPSPRSGSKEEVFVRKWLQWRSEMDTEISELSSSLSATRESLDVAV	506
XP_019624636.1[B.belcheri]	TSEEMAIPSKVHIPCPHVHTKEELAVLQTCCLRWRHEAEKVKGLQDRILYLQAKIENLY	576
XP_032826770.1[P.marinus]	ARQEGGRLEWHGCPAPQAVTALELELRAVLRSRWNQVQRELQDLQDSICRIKRTIDILMY	960
XP_032229076.1[N.vectensis]	---T---RTPSLHPAPRYVTELELETIATSLSRWRTEVEQDVLQDLSLKEVEEASVMY	541
XP_013993323.1[S.salar]	---SRLPPDLPMHPAPRHITEELRVLEGCLHRWRSEVENDTHDLQDSISRIHRTIELMY	584
OCT93923.1[X.laevis]	---SRIPPDLPMPHPAPRHITEELSVLEGCLHRWRTEVETDTRDLQDSISRIHRTIELMY	573
XP_040518387.1[G.gallus]	---SRIPPDLPMPHPAPRHITEELSVLEGCLHRWRTEVENDTRDLQDSISRIHRTIELMY	575
NP_038946.2[M.musculus]	---SRIPPDLPMPHPAPRHITEELSVLEGCLHRWRTEVENDTRDLQDSISRIHRTIELMY	582
Q9UHP3[H.sapiens]	---SRIPPDLPMPHPAPRHITEELSVLEGCLHRWRTEVENDTRDLQDSISRIHRTIELMY	581
XP_024095245.1[P.abelii]	---SRIPPDLPMPHPAPRHITEELSVLEGCLHRWRTEVENDTRDLQDSISRIHRTIELMY	581
XP_019852971.1[A.queenslandica]	SDPSMNRSTYHLHSLVHQQASRGHYWAYVRKKTKKKRATREMGQIASYLDDEQTEEE	566
XP_019624636.1[B.belcheri]	EDNSLKQVPYQLHAVLVHEGQASAGHYWAYVRDHT-----S-----	611
XP_032826770.1[P.marinus]	TDKTFRQLPYRLHAVLVHDDGQAMAGHYWAYVREHARLPAAAASSSS-----	1008
XP_032229076.1[N.vectensis]	NOEEMKTIPIYRLHAVLVHEGQANAGHYWAYINDPL-----	576
XP_013993323.1[S.salar]	SDKSMQVVFRLHAVLVHEGQANAGHYWAYIYDPH-----	619
OCT93923.1[X.laevis]	SDKSMQVVPYRLHAVLVHEGQANAGHYWAYIFDHH-----	608
XP_040518387.1[G.gallus]	FDKSMIQVVPYRLHAVLVHEGQANAGHYWAYIYDHH-----	610
NP_038946.2[M.musculus]	SDKSMIQVVPYRLHAVLVHEGQANAGHYWAYIYDHR-----	617
Q9UHP3[H.sapiens]	SDKSMIQVVPYRLHAVLVHEGQANAGHYWAYIYDHR-----	616
XP_024095245.1[P.abelii]	SDKSMIQVVPYRLHAVLVHEGQANAGHYWAYIYDHR-----	616
XP_019852971.1[A.queenslandica]	GVDKSSSEKKEEGEGHEDMEVTTTGGDDTVETFSPLSSCEPSSGPASVAPPEVKKEEG	626
XP_019624636.1[B.belcheri]	-----SSGNSASSNSNSVSGASD-----	611
XP_032826770.1[P.marinus]	-----SSGNSASSNSNSVSGASD-----	1025
XP_032229076.1[N.vectensis]	-----	576
XP_013993323.1[S.salar]	-----	619
OCT93923.1[X.laevis]	-----	608
XP_040518387.1[G.gallus]	-----	610
NP_038946.2[M.musculus]	-----	617

Q9UHP3[H.sapiens]	-----	616
XP_024095245.1[P.abelii]	-----	616
XP_019852971.1[A.queenslandica]	SKEDDEEIIWLKYNDSVTTVDWEEVKRESFGRGESACNSNGPGTNTSAYCLLYVNSEA	686
XP_019624636.1[B.belcheri]	-----QNRWLKFNVDVVTGMSWGLLRESEGG-Y-----HHASAYCLMYIDITR	654
XP_032826770.1[P.marinus]	ESSGSDSCWRKFNDVRVSRASWELVRDSYGGGA-----RSASAYCLYVYNARA	1074
XP_032229076.1[N.vectensis]	-----DRWRKFNDDTVSEVTWEEVERESLGG-Y-----RNVSYAYCLLYCDARR	619
XP_013993323.1[S.salar]	-----QQRWKMKNYDISVTKSSWEEELVRDSFGG-Y-----RNASAYCLMYINDKK	662
XP_032229076.1[N.vectensis]	-----EQRWKMKNYDISVTKSSWEEELVRDSFGG-Y-----RNASAYCLMYINDEE	651
XP_040518387.1[G.gallus]	-----QNRWKMKNYDISVTKSSWEEELVRDSFGG-Y-----RNASAYCLMYINDKE	653
NP_038946.2[M.musculus]	-----ESRWKMKNYDIATVTKSSWEEELVRDSFGG-Y-----RNASAYCLMYIDDKA	660
Q9UHP3[H.sapiens]	-----ESRWKMKNYDIATVTKSSWEEELVRDSFGG-Y-----RNASAYCLMYINDKA	659
XP_024095245.1[P.abelii]	-----ESRWKMKNYDIATVTKSSWEEELVRDSFGG-Y-----RNASAYCLMYINDKA	659
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XP_019852971.1[A.queenslandica]	AKTWREE-----VHLLSLGLQRYIAYHNLAFERELKAYDLKVQLQQLTSS--E	733
XP_019624636.1[B.belcheri]	KDLVEVKLQW-----SQYDELKLMVLAENERFIAQQRDLESKQRRTMVVR----	699
XP_032826770.1[P.marinus]	HDFTSEL-----AGEAVGDLSSLSPALRDLVAKDNHRFLSEAMMRGNPGERPAEPADARE	1130
XP_032229076.1[N.vectensis]	EEVIRAGN-----TPEVLSAELQQMVEDNASFEQLRDWDEKQAKAAKEAKS----	667
XP_013993323.1[S.salar]	PFLIEEEFDKETGQMLSGLDKLPDSLDAKYVKEDNGLFDKMEEDWDLQARKAQEKL---	719
XP_032229076.1[N.vectensis]	KCLMQEEYDKETGQVLKGMIDILPLDLREYIKEDNRRFEKELEEDWDLQARKAQEKL---	708
XP_040518387.1[G.gallus]	QYLIEEEFNKETGQILVGMIDTLPDLRDFVEEDNRRFEKELEEDWDLQARKAQEKL---	710
NP_038946.2[M.musculus]	QFLIQEEFNKETGQALVGMETLPPDLRDFVEEDNRRFEKELEEDWDLQARKAQEKL---	717
Q9UHP3[H.sapiens]	QFLIQEEFNKETGQPLVGIEITLPPDLRDFVEEDNRRFEKELEEDWDLQARKAQEKL---	716
XP_024095245.1[P.abelii]	QFLIQEEFNKETGQPLVGIEITLPPDLRDFVEEDNRRFEKELEEDWDLQARKAQEKL---	716
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XP_019852971.1[A.queenslandica]	-G-----KEL-----IKPAKAVRFE-YPK-----	750
XP_019624636.1[B.belcheri]	-----EEDPPAN-----HGRGQGTSESSSSEVA--	723
XP_032826770.1[P.marinus]	PGQRAEPREHEQEERRHEGGEQAPARAAPAAAAAASREGGSGGAAREQERADKHSQ	1190
XP_032229076.1[N.vectensis]	-----QALVVARPDLVLA-----EA-----	683
XP_013993323.1[S.salar]	-----ALAAAA-----ATA-----ET-----	731
XP_032229076.1[N.vectensis]	-----ILAQKAL-----K-----	716
XP_040518387.1[G.gallus]	-----LSQIPR-----	716
NP_038946.2[M.musculus]	-----LAAPKLR-----E-----	725
Q9UHP3[H.sapiens]	-----LASQKLR-----E-----	724
XP_024095245.1[P.abelii]	-----LASQKLR-----E-----	724
XP_019852971.1[A.queenslandica]	-----	750
XP_019624636.1[B.belcheri]	-----DQPIQ-----GQEHVRDVQRKQ-----P	741
XP_032826770.1[P.marinus]	TNSLEQEAEPTRERVDGRARAGEREETRVHEGRAPDVASISSETQRQGSADGSASLPGR	1250
XP_032229076.1[N.vectensis]	-----SCAVSP-----	693
XP_013993323.1[S.salar]	-----TTSHQ-----MSTE-----	741
XP_032229076.1[N.vectensis]	-----	716
XP_040518387.1[G.gallus]	-----A-----	717
NP_038946.2[M.musculus]	-----A-----	726
Q9UHP3[H.sapiens]	-----S-----	725
XP_024095245.1[P.abelii]	-----S-----	725
XP_019852971.1[A.queenslandica]	GEEDPGASTNGGHDMMALASDAKRARAGSPSNLEDMQIDLDNLFPVDPALLNQ-----	803
XP_019624636.1[B.belcheri]	PQVKPKPVTTETQQGVRLGRSTQQSTP-----LD-----HSGH-----	774
XP_032826770.1[P.marinus]	GTSAPSPSPSGTEEYMKVGPDTPTTEKP-----RVERVVEV-----SIPDVGTVVQAEHGYND	1304
XP_032229076.1[N.vectensis]	AAAA-----SES-----VLTA-----NLGVL-----	710
XP_013993323.1[S.salar]	PSPDPSWGPQQDPEYMEQPSPTDDSKH-----LQED-----TERAI-----	777
XP_032229076.1[N.vectensis]	QAPLVAAAPNEPEYMEQPARADAPNE-----TSEE-----TTNVI-----	752
XP_040518387.1[G.gallus]	PAPSPAPVQAGEPEYLEQPSKRTDLSKH-----LKED-----SVQAI-----	753
NP_038946.2[M.musculus]	EASATTAAQA-GGADYLEQPSKSDLSKH-----WKEE-----TLRVI-----	761
Q9UHP3[H.sapiens]	ETSVTTAAQAAGDPEYLEQPSRSDFSKH-----LKEE-----TIQII-----	761
XP_024095245.1[P.abelii]	ETSVTTAAQAAGDPEYLEQPSRSDFSKH-----LKEE-----TIRII-----	761
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XP_019852971.1[A.queenslandica]	-----LSMRLSDKLMQFIQDVPGTIIIESRLL-----	829
XP_019624636.1[B.belcheri]	-----VL-----QATMKITILEVSNIEQEQGPEK-----ALIKAVNIEYHRLSLVEKIGISR-----	820
XP_032826770.1[P.marinus]	EVMLTPAMQGVLMVAVARARLVREAQGPAA-----TLIEAFRVEYARLRLTAQESYPDASSP	1360
XP_032229076.1[N.vectensis]	-----P-S-----LVDSGSKLTIIDEAITQWNCNEKTRLDKLAREYPPY-----	749
XP_013993323.1[S.salar]	-----S-KAAAEQEEERSPEG-----LLTAAIKVEYTRLLRFAQEDTA-P-----	815
XP_032229076.1[N.vectensis]	-----T-QAATE-SEDKGPEA-----VLQMAIKTEYARLVKLQEDPL-P-----	789
XP_040518387.1[G.gallus]	-----N-KALAE-QEDRGPEA-----IMDTAIKLEYTRLLKLQEDPP-P-----	790
NP_038946.2[M.musculus]	-----A-KASHD-LEDKGPET-----VLQSAIKLEYARLVKLQEDTP-P-----	798
Q9UHP3[H.sapiens]	-----T-KASHE-HEDKSPET-----VLQSAIKLEYARLVKLQEDTP-P-----	798
XP_024095245.1[P.abelii]	-----T-KASHE-HEDKSPET-----VLQSAIKLEYARLVKLQEDTP-P-----	798
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XP_019852971.1[A.queenslandica]	-----TDFHYAHACQTSSEKVRQAILYEHVIQD-LKR-EN	861
XP_019624636.1[B.belcheri]	-----QYDPRLEHCVVYLIINGAARVIVERTLVEQFADRGLSGDSK	861
XP_032826770.1[P.marinus]	ASPPPLAPAGASGAATWAGREERLEHVYIYLFQNEAPNRVVERALLEQFADRNLSYDEQ	1420
XP_032229076.1[N.vectensis]	-----PGDVRLEHLGTYLMLKCSAPDFTYVECALLESYDEVHAKDQS	790
XP_013993323.1[S.salar]	-----ENDYRLQHVIVYFTHNQAPKKIIEKTLLEQFADRNLSDFER	856
XP_032229076.1[N.vectensis]	-----EIDYRLQHAIVYFIQSQAPKKIIEKTLLEQFADRNLSDFER	830
XP_040518387.1[G.gallus]	-----ECDYRLRHAIVYFIQSQAPKKIIEKTLLEQFADRNLSDFER	831
NP_038946.2[M.musculus]	-----ETDYRLHHVYFIQSQAPKKIIEKTLLEQFADRNLSDFER	839
Q9UHP3[H.sapiens]	-----ETDYRLHHVYFIQSQAPKKIIEKTLLEQFADRNLSDFER	839
XP_024095245.1[P.abelii]	-----ETDYRLHHVYFIQSQAPKKIIEKTLLEQFADRNLSDFER	839
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XP_019852971.1[A.queenslandica]	DLNMSLIARKYFVEICKDPQIYQELQDVRLLYSRFSCCYHFQISVNEAKRNSWCLSLAH	921
XP_019624636.1[B.belcheri]	STIEMKVAQSKLIMQLSEENLKAYEKWHADYGLFQKTVMLLGLGIEFFHQERFPEALTY	921
XP_032826770.1[P.marinus]	LKIMKVAQAKLQEISPEDMDPAEYQKWHQYELFRQVCVYLVMGIEKYQGRVTEALPC	1480
XP_032229076.1[N.vectensis]	LMPYRKVKQVEFLERE-KGTDRADYKRWKEMMTYFKLINSCLFTGLEHFSQKYKESLPY	849
XP_013993323.1[S.salar]	CKSIMKVARAKLDLVKPEEVNMEYEMHQDYRNFRETTTIFIMIGLELFGKKCFVEALMY	916
XP_032229076.1[N.vectensis]	CRNIMKVAQAKLEMIKPEDEVNMEYERKWHQDYRNFRETTTIILIGLELFGQNSYVEALLY	890
XP_040518387.1[G.gallus]	CRNIMKVAQAKLEMIKPEDEVNMEYERKWHQDYRNFRETTTIILIGLELFGQNSYVEALLY	891
NP_038946.2[M.musculus]	CHNIMKVAQAKLEMIKPEEVNLEEYEEWHADYKFRETTTIILIGLENFQRESYIDSLLF	899
Q9UHP3[H.sapiens]	CHNIMKVAQAKLEMIKPEEVNLEEYEEWHADYKFRETTTIILIGLENFQRESYIDSLLF	899
XP_024095245.1[P.abelii]	CHNIMKVAQAKLEMIKPEEVNLEEYEEWHADYKFRETTTIILIGLENFQRESYIDSLLF	899
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XP_019852971.1[A.queenslandica]	IINCIFYLNSISAAQAGDK-YSLDQQLLGRFRCKALLMVSIEGTVAFTSGEVS---SSIVI	977
XP_019624636.1[B.belcheri]	LVHAWTYNQQLLGEKKNYIMADSSLTTHYRTQCLKLSLSEQACSLFESGDTEVDEGLQL	981
XP_032826770.1[P.marinus]	LMHAHVAEENELAR-QOR-RGVRRDVLARYRVVCRVRNVEACALFTGTGDVAQATSLAV	1538
XP_032229076.1[N.vectensis]	LVHAYELNRKLSDPNTNA-RSMDQRLLAHCRVCFCLKLNELASLFSDDYKTLCEGLDL	908
XP_013993323.1[S.salar]	LIYSYQYNKELLVK-GLY-RGHDELISHYRRECLLKLNENAMFESGEEPEVNCGLSI	974
XP_032229076.1[N.vectensis]	LIYGYQYNKELLVK-GLY-RGHDELISHYRRECLLKLNENAMFESGEEPEVNCGLSI	948
XP_040518387.1[G.gallus]	LIYAYQNNKELLVK-GPY-RGHDEELISHYRRECLLKLNENAMFESGDDQEVNNGLI	949
NP_038946.2[M.musculus]	LIYAYQNNKELLVK-GPY-RGHDEELISHYRRECLLKLNENAMFESGDDQEVNNGLI	957
Q9UHP3[H.sapiens]	LICAYQNNKELLVK-GLY-RGHDEELISHYRRECLLKLNENAMFESGDDQEVNNGLI	957
XP_024095245.1[P.abelii]	LICAYQNNKELLVK-GLY-RGHDEELISHYRRECLLKLNENAMFESGDDQEVNNGLI	957
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XP_019852971.1[A.queenslandica]	GNDIYIVPGLKAFSLHP-----FPFGDSILEKVRREWCQCLDQSSLETDDSD	1022
XP_019624636.1[B.belcheri]	MVELVVPQCMALQELG-----GTDSQDAIEAIEIRSNWCYDLQG-DLPDWCQ	1026

XP_032826770.1[P.marinus]	MTLVLPLAMALLAPLGSSCEGGDAGDEAAVARES	DLCAVELMRDRWCSYLGRDDMASELQ	1598
XP_032229076.1[N.vectensis]	VSEQVVPCIPQLVTSP-----	Y-AEDREAVEHMRNNWFTYLGQ-TVDEKRQ	952
XP_013993323.1[S.salar]	MNELVVPCIPLLLVHD-----	T-EKDLLAVEDMRNRWCSYLGQ-EMEPNLQ	1018
OCT93923.1[X.laevis]	MNELIVPCIPLLLVDD-----	MEEKDIVAVEDMRNRWCSYLGQ-EMEPNLQ	993
XP_040518387.1[G.gallus]	MNELIVPCIPLLLVDE-----	MEEKDIVAVEDMRNRWCSYLGQ-EMEPNLQ	994
NP_038946.2[M.musculus]	MNEFIVPFPLPLLVDD-----	MEEKDILAVEDMRNRWCSYLGQ-EMEANLQ	1002
Q9UHP3[H.sapiens]	MNEFIVPFPLPLLVDE-----	MEEKDILAVEDMRNRWCSYLGQ-EMEPHLQ	1002
XP_024095245.1[P.abelii]	MNEFIVPFPLPLLVDE-----	MEEKDILAVEDMRNRWCSYLGQ-EMEPHLQ	1002
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XP_019852971.1[A.queenslandica]	DKLADLLMKIVEDYSKAPNIK-----	IPQA	1047
XP_019624636.1[B.belcheri]	EKLQDFLPQLLDCSGD-----	LQQLRTPPA	1051
XP_032826770.1[P.marinus]	ELLTDFLPRLLDYQPE-PAPPTQLTPPLQGPPPPPPPPSE	PKCESSGENWRGLRAPPR	1657
XP_032229076.1[N.vectensis]	EKLQDFLPKLLDGGTD-----	GNFEEMRPPPV	979
XP_013993323.1[S.salar]	EKLTDFLPKLLDCSTE-----	IKSFHDPPK	1043
OCT93923.1[X.laevis]	EKLTDFLPKLLDCSTE-----	IKGLNDPPK	1018
XP_040518387.1[G.gallus]	EKLTDFLPKLLDCSTE-----	IKGFNDPPK	1019
NP_038946.2[M.musculus]	EKLTDFLPKLLDCSTE-----	IKGFHEPPK	1027
Q9UHP3[H.sapiens]	EKLTDFLPKLLDCSME-----	IKSFHEPPK	1027
XP_024095245.1[P.abelii]	EKLTDFLPKLLDCSME-----	IKSFHEPPK	1027
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XP_019852971.1[A.queenslandica]	PSNFDTQRLAAQYTTAYKTLTSEILL----	1073	
XP_019624636.1[B.belcheri]	V--WPSQHIAEFSTVMQAVVLAEPDITVD--	1078	
XP_032826770.1[P.marinus]	LKAYSPHTLAERMAEVLVRNR--	PREA--	1682
XP_032229076.1[N.vectensis]	MRPTNSKDLCEFRFRAMEIVHANMFFAANKA	1009	
XP_013993323.1[S.salar]	LPTYSTLELVERYGRVMASLC--	WFAALGR	1071
OCT93923.1[X.laevis]	LPNFSHELCECFARIMLSLSR--	MFALGR	1046
XP_040518387.1[G.gallus]	LPSYSTHELCECFARIMLSLSR--	TFALGR	1047
NP_038946.2[M.musculus]	LPSYSTHELCECFARIMLSLSR--	TFALGR	1055
Q9UHP3[H.sapiens]	LPSYSTHELCECFARIMLSLSR--	TFALGR	1055
XP_024095245.1[P.abelii]	LPSYSTHELCECFARIMLSLSR--	TFALGR	1055
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