

RNF146

Homo sapiens:

>sp|Q9NTX7|RN146_HUMAN E3 ubiquitin-protein ligase RNF146 OS=Homo sapiens OX=9606 GN=RNF146 PE=1 SV=1
MMAGCGEIDHSINMLPTNRKANESCNTAPSLTVPECAICLQTCVHPVSLPCKHVFCYLCVKGASWLKKRC
VKGASWLKKRCALCRQEIPEDFLDKPTLLSPEELKAASRGNGEYAWYYEGRNGWQYDER
TSRELEDAFSKGGKNTLEIAGFLYVADLENMVQYRRNEHGRRRRIKRDIIIDIPKKGAVAG
LRLDCDANTVNLA**RESSADGAD**SVSAQSGASVQPLVSSVRPLTSVDGQLTSPATPSPDAS
TSLEDSFAHLQLSGDNTAE**RSHRGE**EDHESPSSGRVPAPDTSIEETESDASSDSEDVS
AVVAQHSLTQQRLVSNANQTVPDRSDRSGTD**RSVA**GGGTVSVSV**RSRRPDGQC**TVTEV

Pongo abelii:

>NP_001128751.1 E3 ubiquitin-protein ligase RNF146 [Pongo abelii]
MAGCGEIDHSINMLPTNRKANESCNTAPSLTVPECAICLQTCVHPVSLPCKHVFCYLCVKGASWLKKRC
ALCRQEIPEDFLDKPTLLSPEELKAASRGNGEYAWYYEGRNGWQYDERTSRELEDAFSKGGKNTLEIAG
FLYVADLENMVQYRRNEHGRRRRIKRDIIIDIPKKGAVAGLRLDCDANTVNLA**RESSADGAD**SVSAQSGAS
VQPLVSSVRPLTSVDGQLTSPATPSPDASTSLEDSFAHLQLSGDNTAE**RSHRGE**EDHESPSSGRVPAP
DTSIEETESDASSDSEDVAVVAQHSLTQQRLVSNANQTVPDRSDRSGTD**RSVA**GGGTVSVSV**RSRRPD**
GQCTVTEV

Mus musculus:

>BAE31549.1 unnamed protein product [Mus musculus]
MEMAGCGEIDHSINMLPTNRKANESCNTAPSLTVPECAICLQTCVHPVSLPCKHVFCYLCVKGASWLKKRC
ALCRQEIPEDFLDKPTLLSPEELKAASRGNGEYAWYYEGRNGWQYDERTSRELEDAFSKGGKNTLEIAG
FLYVADLENMVQYRRNEHGRRRRIKRDIIIDIPKKGAVAGLRLDCDNTNVNLA**RESSADGAD**SGSAQTG
ASVQLAVPSSSTRPLTSVDGQLTSPVTPSPDAGISLEDSFAHLQLSGDSIAE**RSHRGE**EDHESPSSGRV
PDTSEETESDASSDSEDAPVVVAQHSLTQQRLVPLVFNQNTVADQSDRSGTD**RSVA**GGGTVMSVNV**RSRRP**
DGQCTVTEV

Gallus gallus:

>XP_015139929.3 E3 ubiquitin-protein ligase RNF146 [Gallus gallus]
MAGCGEIDHSINMLPTNRKNTNESCANAAAPSLTVPECAICLQTCVHPVSLPCKHVFCYLCVKGASWLKKRC
ALCRQEIPEDFLDKPTLLSPEELKAASRGNGEYAWYYEGRNGWQYDERTSRELEDAFSKGGKSTLEMLIA
GFLYIADLENMVQYRRNEHGRRRRIKRDIIIDIPKKGAVAGLRLDCDNTNVNLA**RESSADGAD**SLTGGAAA
VQPLVPVPSARPLPSLDGQLMSPSTPSPDASTSLENSFAHLQINGDSMAE**RSHRGE**EDHESSSSGRVPAP
PDTSEETESDASSDSEDVSAFLQQHPSSAQQRHLNANANQSGAD**RSVA**GGGANASV**RSRRPDGQC**TVT
EV

Xenopus laevis:

>XP_018118669.1 E3 ubiquitin-protein ligase rnf146 [Xenopus laevis]
MAGCGEVSHSANMLPTNKKLGPECSNAPSSSVPECAICLQICVHPVSLPCKHIFCYLCVKGASWLKKRC
ALCRQEIPEDFLDKPTLLSPEELKSASRGNGEYAWYYEGRNGWQYDERTSRELEDAFTKGGKSTLEMLIA
GFLYIADLENMVQYRRNEHGRRRRIKRDIVDIPKKGAVAGLRLCEDPANLNLA**RESSADGAD**NMAALGASS
SQPAPVLPARLHTSLTTASQVLSHSDVTNSLENSFAELQIGDPVIC**RNNIGE**EGGQPLINPRMPFPNA
VLEEPEPSSDSNDHGSFALQHHSFLGNP

Salmo salar:

>NP_001167373.1 E3 ubiquitin-protein ligase rnf146 [Salmo salar]
MASCGEVDHSVSLPSSKSGSDSACSGSSSPALPVEPECAICLQSCVHPVQLPCRHVFCFLVKGASW
QSKRCALCRQEVPEDFLEHPTLLSPEELKTGGRGATGDNAWYYEGRNGWQYDERTSRELEDAFTKGGKKT
AEMLIAGFLYVADLENMVQYRRNEHGRRRRIKRDIVDIPKKGAVAGLRLDEGGVQGSAAAG**RNSADGAD**
TSAAAVQAAAAAATTVLSAPARPPTSLGGQPGSPTSPLEDTALLHISPTDAPE**AEVGE**EEEAATA
TPSMSSSPNTYADGSGDWSDDDEGDGEAVPEPQRLRLGESLVDRSPPGAEESSSSSV**RSRRPDGQC**TEV

Petromyzon marinus:

>tr|S4R4W7|S4R4W7_PETMA E3 ubiquitin-protein ligase OS=Petromyzon marinus OX=7757 PE=4 SV=1
VPDCAICLQPCVHPARLPCRHVFCFLCAKGVALQSRRCALCRSEIPPDFLERPTLLCSTS
DGVPLKPRTANAWYYEGRNGWQYDERTSAELEAFARGSTTMEMLIAGLYVADLEAMV
QYRRSEPSRRRRMKRDLLSAPKKGVAGLRLDLTAPAVSPAHASGVGDVDRAVAGTSSGSG
SVVAGGLLASAGPSTITVASPSPVSVATSSTLSVDPLFDSGATSSFPSPRPATFAPQHQ
MRAVVGPPSPADSDSDRDEEDQYEDNEGAASISRQLAGM**RLGRSGAV**IDTAAEQQSS
AAPRSATLHVRS**RDGRPDGQY**TVTDV

Branchiostoma belcheri:

>XP_019623976.1 PREDICTED: E3 ubiquitin-protein ligase rnf146-like [Branchiostoma belcheri]
MAESRSVASAETSLSQSSAKKRREKEMABTATGQKPGGEMIPCAVCLQTCVQPVRLPCTHIFCYLCV
KVAVQSKRCALCRQEIPIEYLERPELVKPIKVTEQEGEEEEVYCWFEYGRNGWQYDERTNABLEDA
YTKKSGSCELLLAGFLYIIDFVNMLQFRRNDPSRRRIKRDLTNTPKKGAVAGVRLPAPAP**MAPADGVE**
GANEAGTGGSRSAVTSRATKSTRGPADHEDDSNEDTNRAEEDSTSIEDVTDQSARGNARQSPDSLQHQ
TPTQEEDDGDGTNSTGGAEMSEVMRL**RSRLGRGSH**SSRSGLVLAVLQGQVSSVANVMA**REEIFGDS**
DESD

Drosophila melanogaster:

>tr|B7Z078|B7Z078_DROME E3 ubiquitin-protein ligase OS=Drosophila melanogaster OX=7227 GN=Rnf146 PE=2 SV=1
MSQQRSTEQIAASNNNTSDVIALDDDEDTDVQVFAALRPTAPVIDLCVSPSTSAAAAA
AAAAHSGGGSGEDPAVGASGASGAASDSDSLASSPDEGALATGVDAAAAVSGEDSPSAAAA
ALECPICLQTCIHPARLPCGHIFCFLCVKGAVAYKNRRCAKCRREIPAFLDHPQLVNGIE
DICTT**RATEDGQY**WYYEGRNGWQYDDRTSQDIEDAFKGDKSCITILVAGVYIYVDLEQL
VQQRQNEPTRCRVRKDLATIPKKGAVAGLRIEGNQVTSDTVFSRPTNTANPTTVAAAASS
FISTIAATDAARIASDIIGSTLAHADELTRGLTASNLDLSSGQSNSNTNSNDAGRS
PASSPASSMQDLITRDLRNTQQVIAHNQHTIDLFEQALNDFQALAMRNYVSSDSEENN
QDQEHRLRE**REQLAGGQY**QPSNDNPQR

Hydra vulgaris:

>XP_01255516.1 E3 ubiquitin-protein ligase rnf146 [Hydra vulgaris]

MTYCWVDSNPDCAVCLQQCLQPVQLPCKHIFCFLCLKGFAYRSKRCALCRSVIELEYFNNPIIHKVREKE
DVSSSTSNKVSVNLSPTSITYNWFYEGRNGWQYDERASLILEKAFSNSKKNCIELIAGFLYVVDFERMV
QYRKDNLARLRKVKRDSDDTLKGVAGIKLPKEIENKPD SKNVINKKELLTNTSDQLNNNQETLATERP
FINLASDLSQNSSGVNEVLYGIQQVALKD

Nematostella vectensis:

>XP_048581887.1 E3 ubiquitin-protein ligase rnf146 isoform X1 [Nematostella vectensis]
MAEGPENVKERQSDISSSKEDVSDSAEPVKNAVVVHLSTPRYLVSYCCIFGDTSEEEVLQNI FELDYQPD
CPVCLQQA SYFVRLPCGHMFCFLCIKGVALKSRKCAICRQPISPDYLDKPTLVKVVSGQSSSDKAPSDP
PADEVVWFYEGRNGWQYDTRKTSKEVESAFKGGKRSC TLLIAGFLYLIDFENMFQMRNEFGRRRIKRD
KPNAD **RKGAGITL** LKGLTVSELADLKNQTTETSTADNQW TSTEDVSVQALSGSPTEAANRD CDD SASSTS
DKESAPDETTFEACFMLMQPLIAHSESYHNSPVLGDVNAPS

Amphimedon queenslandica:

>XP_003383131.1 PREDICTED: E3 ubiquitin-protein ligase RNF146-like [Amphimedon queenslandica]
MADSENSKKQGQYGD SKSLEEKKKKSES LDKEGDRVVQVEKDLSKLKIKEDIVPFDMKCPICQDKSRHP
LTLPCGHTFCYLCIKGVYARQKV CALCRQAIPQH CIVSPPGTGE **REEEEGRK**TCWY YEA KSGGWWEYEE R
VRQELEIHYQSLQINNEDNQDQGQFVIYVSGFPYVVDFAKMIQYRQDKPNRSRRRIKREKGVAAEEGELVR
GVAGIPIAPSI RQDDN

Alignment

Q9NTX7 [H.sapiens]	-----MMAGC-----	5
NP_001128751.1 [P.abelii]	-----MAGC-----	4
BAE31549.1 [M.musculus]	-----MEMAGC-----	6
XP_015139929.3 [G.gallus]	-----MAGC-----	4
XP_018118669.1 [X.laevis]	-----MAGC-----	4
NP_001167373.1 [S.salar]	-----MASC-----	4
XP_032825805.1 [P.marinus]	-----MSGC-----	4
XP_019623976.1 [B.belcheri]	MAESRS-----VASAETSLRQSSAK-----KR-----	22
AAI48063.1 [D.melanogaster]	MSQQRSTEQIAASNNTSDVIALDDD-----ED-TDVQFVAALRPTAPVIDLCVSPSTSA	54
XP_012555516.1 [H.vulgaris]	-----	0
XP_048581887.1 [N.vectensis]	MAEGPENVK-----ERQSDISSSKEDVSDSAEPVKNAVYVY-LSTPRYLVSYC-----	47
XP_003383131.1 [A.queenslandica]	-----MA-----	2
Q9NTX7 [H.sapiens]	-----GEIDHSINMLPTNRK-----ANES-----CSN-----	27
NP_001128751.1 [P.abelii]	-----GEIDHSINMLPTNRK-----ANES-----CSN-----	26
BAE31549.1 [M.musculus]	-----GEIDHSINMLPTNKK-----ANES-----CSN-----	28
XP_015139929.3 [G.gallus]	-----GEIDHSINMLPTNRK-----TNES-----CAN-----	26
XP_018118669.1 [X.laevis]	-----GEVSHSANMLPTNKK-----LGEP-----CSN-----	26
NP_001167373.1 [S.salar]	-----GEVDHSVSSLPSKK-----GSGDSACSGSSG-----	31
XP_032825805.1 [P.marinus]	-----RVLTGDEP--P-----SAGVGPGEA-----	22
XP_019623976.1 [B.belcheri]	-----REKEEMA-----ETATGQK-----	36
AAI48063.1 [D.melanogaster]	AAAAAAAAAHSGGGSGEDPAVGSASGAAASDTSLASSPDEGALATGVDAAAVSGEDS	114
XP_012555516.1 [H.vulgaris]	-----MT-----	2
XP_048581887.1 [N.vectensis]	-----CIFGDTE-----EEEVQN-----	61
XP_003383131.1 [A.queenslandica]	-----DSENSKKGQYGDSSKLEE--KEKKRKSESL---DKEGDRVVQVEKD-LSKLKIK	50
Q9NTX7 [H.sapiens]	TAPSLTVPECAICLQTCVHPVSLPCKHVFICYLCVKGASWLGRKRCALCRQEIPEDFLDKPT	87
NP_001128751.1 [P.abelii]	TAPSLTVPECAICLQTCVHPVSLPCKHVFICYLCVKGASWLGRKRCALCRQEIPEDFLDKPT	86
BAE31549.1 [M.musculus]	TAPSLTVPECAICLQTCVHPVSLPCKHVFICYLCVKGASWLGRKRCALCRQEIPEDFLDKPT	88
XP_015139929.3 [G.gallus]	AAPSLTVPECAICLQTCVHPVSLPCKHVFICYLCVKGASWLGRKRCALCRQEIPEDFLDKPT	86
XP_018118669.1 [X.laevis]	SAPSSSVPECAICLQTCVHPVSLPCKHVFICYLCVKGASWLGRKRCALCRQEIPEDFLDKPT	86
NP_001167373.1 [S.salar]	SSPALVPPECAICLQSCVHPVQLPCRHFVFCFLCVKGASWQSKRCALCRQEVPEDFLEHPT	91
XP_032825805.1 [P.marinus]	PPARPVVPECAICLQSCVHPARLPCRHFVFCFLCAKGVALQSRRCALCRSEIIPDFLERPT	82
XP_019623976.1 [B.belcheri]	PGGEDMIPECAVCLQTCVQVPRLPCTHIFCYLCVKGVANQSKRCALCRQEIPIEYLERPE	174
AAI48063.1 [D.melanogaster]	PSAAAALECPICLQTCIHPARLPCGHIFCFLCVKGAVYNRRRCAMCRREIPAEFLDHPQ	96
XP_012555516.1 [H.vulgaris]	YCWVDSNPDCAVCLQCCQLPVQLPCKHIFCFLCLKGFAYSKRRCALCRSVIELEYFNNPI	62
XP_048581887.1 [N.vectensis]	IFELDYQDPCVCLQQASYVPRVLP CGHMFCLCIKGVALSRKCAICRQPISPDYLDKPT	121
XP_003383131.1 [A.queenslandica]	EDIVPFDMKCPICQDKSRHPLTGPCHTFCYLCIKGVYARQKVCALCRQAI PQHCVTSPP	110
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Q9NTX7 [H.sapiens]	LLSPEELK-----AASR-----G-NGEYAWYIEGR-NGWMQYDERTS	122
NP_001128751.1 [P.abelii]	LLSPEELK-----AASR-----G-NGEYAWYIEGR-NGWMQYDERTS	121
BAE31549.1 [M.musculus]	LLSPEELK-----AASR-----G-NGEYAWYIEGR-NGWMQYDERTS	123
XP_015139929.3 [G.gallus]	LLSPEELK-----AASR-----G-NGEYAWYIEGR-NGWMQYDERTS	121
XP_018118669.1 [X.laevis]	LLSPEELK-----SASR-----G-NGEYAWYIEGR-NGWMQYDERTS	121
NP_001167373.1 [S.salar]	LLSPEELK-----TGGR-----GATGDNAMYIEGR-NGWMQYDERTS	127
XP_032825805.1 [P.marinus]	LLCSTSDGQPLAQQQRRPSASMGVAGGASEGVPLKPRATANAMYIEGR-NGWMQYDERTS	141
XP_019623976.1 [B.belcheri]	LVKPIKVTEEQ-----E-----GEEEEVYCWYIEGR-NGWMQYDERTN	134
AAI48063.1 [D.melanogaster]	LVNGIEDICTT-----RATEDFGWYIEGR-NGWMQYDERTS	210
XP_012555516.1 [H.vulgaris]	LIKVKREKEDVSSSTSNKVSVN-----LSTPSITYNWFYIEGR-NGWMQYDERAS	109
XP_048581887.1 [N.vectensis]	LVKVVSGQSSSSD-----KAP-----SDPPADEYVWFYIEGR-NGWMQYDRTKS	163
XP_003383131.1 [A.queenslandica]	GTGERE-----EEEGRKTCWYIEAKSGGWYIEERVIR	142
	. : * : . * * * * * : * : * : * : * : . : *	
Q9NTX7 [H.sapiens]	RELEDAFSKG-----KKNTEMLIAGFLYVADLENMVQYRRNEHGRRRRIKRDIDI	173
NP_001128751.1 [P.abelii]	RELEDAFSKG-----KKNTEMLIAGFLYVADLENMVQYRRNEHGRRRRIKRDIDI	172
BAE31549.1 [M.musculus]	RELEDAFSKG-----KKNTEMLIAGFLYVADLENMVQYRRNEHGRRRRIKRDIDI	174
XP_015139929.3 [G.gallus]	RELEDAFSKG-----KKSTEMLIAGFLYVADLENMVQYRRNEHGRRRRIKRDIDI	172
XP_018118669.1 [X.laevis]	RELEDAFTKG-----KKSTEMLIAGFLYVADLENMVQYRRNEHGRRRRIKRDIVDI	172
NP_001167373.1 [S.salar]	RELEDAFSKG-----KKTAEMLIAGFLYVADLENMVQYRRNEHGRRRRIKRDIVDI	178
XP_032825805.1 [P.marinus]	AELEEAFAARG-----STTMEMLIAGFLYVADLEAMVQYRRSEPSRRRMKRDLLSA	192
XP_019623976.1 [B.belcheri]	AELDAYTKK-----KKSCCELLIAGFLYIIDFVNMQLFRNDPSRRRIKRDLTNT	185
AAI48063.1 [D.melanogaster]	QDIEDAFKKG-----DKSCTILVAGVYVVVDLEQLVQQRQNEPTRCRVRKRDLATI	261
XP_012555516.1 [H.vulgaris]	LILEKAFSNS-----KKNCEILIAGFLYVVDFERMVQYRKDNLARLKRVRKSDSDST	160
XP_048581887.1 [N.vectensis]	KEVESAFKGG-----KRSCTLLIAGFLYLIDFENFMQRRNEPGRRRRIKRDKPNA	214
XP_003383131.1 [A.queenslandica]	QLELIHYQSLQINNEDNQDQGQFVIYVSGFFVVDFAKMIQYRQDKPNRSRIKREKQVA	202
	. : * : . : * : * : * : * : * : . : * : * : * : * : . : *	
Q9NTX7 [H.sapiens]	P-----KKGVAGLRLCDANTVNL---ARESSADGADSVSAQS-----	208
NP_001128751.1 [P.abelii]	P-----KKGVAGLRLCDANTVNL---ARESSADGADSVSAQS-----	207
BAE31549.1 [M.musculus]	P-----KKGVAGLRLCDTNTVNL---ARESSADGADSGSAQT-----	209
XP_015139929.3 [G.gallus]	P-----KKGVAGLRLCDTNSVNL---ARESSADGADSTLTGG-----	207
XP_018118669.1 [X.laevis]	P-----KKGVAGLRLECDPANLNL---ARESSADGADNMALG-----	207
NP_001167373.1 [S.salar]	P-----KKGVAGLRLDTEGGVQGSAAACRGNSADGADTSAAAVQAAA-----	220
XP_032825805.1 [P.marinus]	P-----KKGVAGLRDLDTAPAVSPA---HASGVGDVDRAVAGTSSGSGSVVAGGFSMLSS	244
XP_019623976.1 [B.belcheri]	P-----KKGVAGVRLPAPAPRNAP---ADGVGEGAGEGATGSSRS---VAVTSRATKST	223
AAI48063.1 [D.melanogaster]	P-----KKGVAGLRLEQVTSDFVFS---RPTNTANPTTVAAASS-----FIST	304
XP_012555516.1 [H.vulgaris]	D-----LKGVAGIKLPKEIENKP-D---SKNVINKKELLTNTSDN-----	196
XP_048581887.1 [N.vectensis]	D-----RKGVAGIRLKLTVSRELAD---LKNQT---TETSTADN-----	247
XP_003383131.1 [A.queenslandica]	EEGEELVRGVAGIPIAPSIRQDDN-----	226
	. : * * * : .	
Q9NTX7 [H.sapiens]	-----GASVQPLV-SSVRPLTSSVDGQ---LTSFA-----	233
NP_001128751.1 [P.abelii]	-----GASVQPLV-SSVRPLTSSVDGQ---LTSFA-----	232
BAE31549.1 [M.musculus]	-----GASVQLAVPSSTRPLTSSVDGQ---LTSFV-----	235
XP_015139929.3 [G.gallus]	-----AAAVQPLVPVSARPLPLSLDGQ---LMSPS-----	233
XP_018118669.1 [X.laevis]	-----ASSSQPAPVLPARLHTSLT-T---TASQV-----	232
NP_001167373.1 [S.salar]	-----AAPAATTVLSAPARPPTSLGGQ---LCSPT-----	247
XP_032825805.1 [P.marinus]	AASVSSSGLSAAALGVSSAAGGVSASGGLLASAGPSTITVASPSSPVSSVATS---STLSV	302
XP_019623976.1 [B.belcheri]	RGPADHEDDSDNEDTNNR-----AE---EDSTSEDVTDQSARGN---ARQSP	272
AAI48063.1 [D.melanogaster]	IAA-----TDAAIRIASDIIGSTLAHADEL-T---RGLTASN-LNDDLSSSDSFSICT	352
XP_012555516.1 [H.vulgaris]	-----QLNNQET-----LA-----	206
XP_048581887.1 [N.vectensis]	-----QWTSTEDV-----SVQALSGS---PTEA-----	267
XP_003383131.1 [A.queenslandica]	-----	226
Q9NTX7 [H.sapiens]	TPSPDAST-----SLEDSFAHLQL-----SGDNTAE---RSH--RGELEE---DHESP-	273
NP_001128751.1 [P.abelii]	TPSPDAST-----SLEDSFAHLQL-----SGDNTAE---RSH--RGELEE---DHESP-	272
BAE31549.1 [M.musculus]	TPSPDAGI-----SLEDSFAHLQL-----SGDSIAE---RSH--RGELEE---DHESP-	275
XP_015139929.3 [G.gallus]	TPSPDAST-----SLENSFAHLQI-----NGDSMAE---RSH--RGELEE---DHESP-	273
XP_018118669.1 [X.laevis]	LSHSDVTN-----SLENSFAELQI-----GD-FVIG---RNN--IGELEE---GQPL--	270
NP_001167373.1 [S.salar]	S-----P-----SLEDTLALLHI-----SPTDAPE---RAE--VGELEE---EATAT-	281
XP_032825805.1 [P.marinus]	DPLPDSGATSSFP-SRPATFAPQHQMRAVFPSPADSDSSD-RDDEQDYEDNEGAA	359
XP_019623976.1 [B.belcheri]	D-----SL---RQ---HTPTQEEDDDGDTNSTGGAE-SE-----	302
AAI48063.1 [D.melanogaster]	PPLLLT-AKCVFVASLISTV-YLKLY-----	376
XP_012555516.1 [H.vulgaris]	-----T---ERFPFINASDLQNSSGVNEVLYG-----	231
XP_048581887.1 [N.vectensis]	-----A---NRDCDSASSTSDKESAPDETTHE-----	292
XP_003383131.1 [A.queenslandica]	-----	226

Q9NTX7 [H.sapiens]		
NP_001128751.1 [P.abelii]	--SS-----GR-----VPA-PD--TSIEETESDASSDSE--D-VSA	301
BAE31549.1 [M.musculus]	--SS-----GR-----VPA-PD--TSIEETESDASSDSE--D-VSA	300
XP_015139929.3 [G.gallus]	--SS-----GR-----VP---D--TSVEETESDASSDSE--D-APV	301
XP_018118669.1 [X.laavis]	--SS-----GR-----VPA-PD--TSVEETESDASSDSE--D-VSA	301
NP_001167373.1 [S.salar]	--IN-----FR-----MPP-FN--AVLEEPEPSDSND-----HGS	295
XP_032825805.1 [P.marinus]	--PS-----MS-----SS-FN--TYAD--GSGDWSDDDEG--D-GEA	307
XP_019623976.1 [B.belcheri]	SISRQLAGMRLGRSGQISLAGEGGGSSRAVYAA-PH--LAEDDGSRLLGRRRTNMPPFP	416
AAL48063.1 [D.melanogaster]	--MVRMLQKSRLLGRGSDSSRSGLQAVLQQVSSVANVAMAREEIPGDSSDSED-----	354
XP_012555516.1 [H.vulgaris]	-----IQQVALK-----D-----	376
XP_048581887.1 [N.vectensis]	FACFMLMQPLTAHSESYHNSPVLG-----DVNA-----P-----S-----	239
XP_003383131.1 [A.queenslandica]	-----	322
	-----	226
Q9NTX7 [H.sapiens]		
NP_001128751.1 [P.abelii]	VV-AQHSLTQQRLLVSN-----ANQTVFDRSDRSGTDRSV-A-----	336
BAE31549.1 [M.musculus]	VV-AQHSLTQQRLLVSN-----ANQTVFDRSDRSGTDRSV-A-----	335
XP_015139929.3 [G.gallus]	VV-AQHSLTQQRPLVFN-----GNQTVADQSDRSGTDRSV-A-----	336
XP_018118669.1 [X.laavis]	PL-QQHPSSAQQR-----HLNANANQSGADRPV-A-----	329
NP_001167373.1 [S.salar]	PA-LQHHSFLGNP-----	307
XP_032825805.1 [P.marinus]	VEPREQRLRLGES-----LVDRSPPG-----	328
XP_019623976.1 [B.belcheri]	PPPHRQPALLPDSLAARQDSGTGRPLRASERLTAHQHGAHGAESSGGGGTGGAVIDT	476
AAL48063.1 [D.melanogaster]	-----	354
XP_012555516.1 [H.vulgaris]	-----	376
XP_048581887.1 [N.vectensis]	-----	239
XP_003383131.1 [A.queenslandica]	-----	322
	-----	226
Q9NTX7 [H.sapiens]		
NP_001128751.1 [P.abelii]	-----GGGTVSVSVRSRRPDGQCTVTEV-----	359
BAE31549.1 [M.musculus]	-----GGGTVSVSVRSRRPDGQCTVTEV-----	358
XP_015139929.3 [G.gallus]	-----GGRTMSVNVRSRRPDGQCTVTEV-----	359
XP_018118669.1 [X.laavis]	-----GGGVANASVRSRRPDGQCTVTEV-----	352
NP_001167373.1 [S.salar]	-----AEASSSSSVRSRRPDGQCTEV-----	307
XP_032825805.1 [P.marinus]	AEAQQQSAAPRSATLHVRSRDGRPDGQCTVTDVVNSAIIILLYMWVLGEPLGTQRGARAA	349
XP_019623976.1 [B.belcheri]	-----	536
AAL48063.1 [D.melanogaster]	-----	354
XP_012555516.1 [H.vulgaris]	-----	376
XP_048581887.1 [N.vectensis]	-----	239
XP_003383131.1 [A.queenslandica]	-----	322
	-----	226
Q9NTX7 [H.sapiens]		
NP_001128751.1 [P.abelii]	-----	359
BAE31549.1 [M.musculus]	-----	358
XP_015139929.3 [G.gallus]	-----	359
XP_018118669.1 [X.laavis]	-----	352
NP_001167373.1 [S.salar]	-----	307
XP_032825805.1 [P.marinus]	SSYRRVRGGGLCTYTFVIFPDLACASLAQSMRDADPDEEDSDRIHNKDRTRSPDRKGDLE	349
XP_019623976.1 [B.belcheri]	-----	596
AAL48063.1 [D.melanogaster]	-----	354
XP_012555516.1 [H.vulgaris]	-----	376
XP_048581887.1 [N.vectensis]	-----	239
XP_003383131.1 [A.queenslandica]	-----	322
	-----	226
Q9NTX7 [H.sapiens]		
NP_001128751.1 [P.abelii]	-----	359
BAE31549.1 [M.musculus]	-----	358
XP_015139929.3 [G.gallus]	-----	359
XP_018118669.1 [X.laavis]	-----	352
NP_001167373.1 [S.salar]	-----	307
XP_032825805.1 [P.marinus]	AASPVDGVDVSKDLDETSERIQQLESALGNATLRLHKLESADVREAGGARGHSGITRSLQK	349
XP_019623976.1 [B.belcheri]	-----	656
AAL48063.1 [D.melanogaster]	-----	354
XP_012555516.1 [H.vulgaris]	-----	376
XP_048581887.1 [N.vectensis]	-----	239
XP_003383131.1 [A.queenslandica]	-----	322
	-----	226
Q9NTX7 [H.sapiens]		
NP_001128751.1 [P.abelii]	-----	359
BAE31549.1 [M.musculus]	-----	358
XP_015139929.3 [G.gallus]	-----	359
XP_018118669.1 [X.laavis]	-----	352
NP_001167373.1 [S.salar]	-----	307
XP_032825805.1 [P.marinus]	KVLEQARNIQTQLQHSNRHLERKVTELESREPREVTRRKILNRQPYTSTTTNDDDDGDDDDDED	349
XP_019623976.1 [B.belcheri]	-----	716
AAL48063.1 [D.melanogaster]	-----	354
XP_012555516.1 [H.vulgaris]	-----	376
XP_048581887.1 [N.vectensis]	-----	239
XP_003383131.1 [A.queenslandica]	-----	322
	-----	226
Q9NTX7 [H.sapiens]		
NP_001128751.1 [P.abelii]	-----	359
BAE31549.1 [M.musculus]	-----	358
XP_015139929.3 [G.gallus]	-----	359
XP_018118669.1 [X.laavis]	-----	352
NP_001167373.1 [S.salar]	-----	307
XP_032825805.1 [P.marinus]	DEDDNDDDDDEEDDAHDDDDDKNNEVSRHQSSDEAQPKNRLHGGKSGHNTTAVQGRAR	349
XP_019623976.1 [B.belcheri]	-----	776
AAL48063.1 [D.melanogaster]	-----	354
XP_012555516.1 [H.vulgaris]	-----	376
XP_048581887.1 [N.vectensis]	-----	239
XP_003383131.1 [A.queenslandica]	-----	322
	-----	226
Q9NTX7 [H.sapiens]		
NP_001128751.1 [P.abelii]	-----	359
BAE31549.1 [M.musculus]	-----	358
XP_015139929.3 [G.gallus]	-----	359
XP_018118669.1 [X.laavis]	-----	352
NP_001167373.1 [S.salar]	-----	307
XP_032825805.1 [P.marinus]	GAQVITRELRGATASAEETGRDTTAAGVPAGPGGPYQDCAEYRSQGTSGIYVLHVFNTSH	349
XP_019623976.1 [B.belcheri]	-----	836
AAL48063.1 [D.melanogaster]	-----	354
XP_012555516.1 [H.vulgaris]	-----	376
XP_048581887.1 [N.vectensis]	-----	239
XP_003383131.1 [A.queenslandica]	-----	322
	-----	226
Q9NTX7 [H.sapiens]		
	-----	359

NP_001128751.1[P.abelii]	-----	358
BAE31549.1[M.musculus]	-----	359
XP_015139929.3[G.gallus]	-----	352
XP_018118669.1[X.laavis]	-----	307
NP_001167373.1[S.salar]	-----	349
XP_032825805.1[P.marinus]	TLKVYCDMQTGGGWTVPQRREDGHINFNRPWQDYKLGFGSADREYWLGNAAVHVLTSRR	896
XP_019623976.1[B.belcheri]	-----	354
AAL48063.1[D.melanogaster]	-----	376
XP_012555516.1[H.vulgaris]	-----	239
XP_048581887.1[N.vectensis]	-----	322
XP_003383131.1[A.queenslandica]	-----	226
Q9NTX7[H.sapiens]	-----	359
NP_001128751.1[P.abelii]	-----	358
BAE31549.1[M.musculus]	-----	359
XP_015139929.3[G.gallus]	-----	352
XP_018118669.1[X.laavis]	-----	307
NP_001167373.1[S.salar]	-----	349
XP_032825805.1[P.marinus]	PQALRILLWDWDENQAYASYARFTLRGEAARYRLLVSGFSGTAGRYSSLAQSGAEFSTRD	956
XP_019623976.1[B.belcheri]	-----	354
AAL48063.1[D.melanogaster]	-----	376
XP_012555516.1[H.vulgaris]	-----	239
XP_048581887.1[N.vectensis]	-----	322
XP_003383131.1[A.queenslandica]	-----	226
Q9NTX7[H.sapiens]	-----	359
NP_001128751.1[P.abelii]	-----	358
BAE31549.1[M.musculus]	-----	359
XP_015139929.3[G.gallus]	-----	352
XP_018118669.1[X.laavis]	-----	307
NP_001167373.1[S.salar]	-----	349
XP_032825805.1[P.marinus]	QDHDRCQCKCAQLSSGGWWEACGSPNLNGQFFPKGSHYGHFNGIKWHYWRGASYSLKAS	1016
XP_019623976.1[B.belcheri]	-----	354
AAL48063.1[D.melanogaster]	-----	376
XP_012555516.1[H.vulgaris]	-----	239
XP_048581887.1[N.vectensis]	-----	322
XP_003383131.1[A.queenslandica]	-----	226
Q9NTX7[H.sapiens]	-----	359
NP_001128751.1[P.abelii]	-----	358
BAE31549.1[M.musculus]	-----	359
XP_015139929.3[G.gallus]	-----	352
XP_018118669.1[X.laavis]	-----	307
NP_001167373.1[S.salar]	-----	349
XP_032825805.1[P.marinus]	TMMIRPADF	1025
XP_019623976.1[B.belcheri]	-----	354
AAL48063.1[D.melanogaster]	-----	376
XP_012555516.1[H.vulgaris]	-----	239
XP_048581887.1[N.vectensis]	-----	322
XP_003383131.1[A.queenslandica]	-----	226