

PEX14

Homo sapiens:

>O75381 PEX14 [Homo sapiens]
MASSEQAEQPSQPSSTPGSENVLPREPLIATAVKFLQNSRVRQSPLATRRAFLKKKGLTD
EEDIMAFQSGTADEPSSLGPATQVVVPQPHLISQPYSPAGSRWRDYGALAIIMAGIA
FGFHQLYKKYLLPLILGGREDRKQLERMEAGLSELSGSVAQTVTQLQTTLASVQELLIQQ
QQKIQELAHELAAAKATTSTNWILESQNINELKSEINSLKGLLLNRRQFPSPSPAKIPS
WQIPVKSPSPSSPAAVNHHSSSDISPVSNESTSSSPGKEGHSPEGSTVTYHLLGPQEEGE
GVVDVKGVQV**RMEVQGE**EKKREDKEDEEDEDVSHVDEEDCLGVQRED**RGSGSG**NEQ
VEKLRRPEGASNESESD

Pongo abelii:

>XP_024109019.1 peroxisomal membrane protein PEX14 isoform X1 [Pongo abelii]
MASSEQAEQPSQPSSTPGSENVLPREPLIATAVKFLQNSRVRQSPLATRRAFLKKKGLTDEEIDMAFQQS
GTAADEPSSLGPATQVVVPQPHLVSQPYSPAGSRWRDYGALAIIMAGIAFGFHQLYKKYLLPLILGGRE
DRKQLERMEAGLSELSGSVAQTVTQLQTTLASVQELLIQQQQKIQELAHELAAAKATTSTNWILESQNIN
ELKSEINSLKGLLLNRRQFPSPSPAKIPSWOIPVKSPSPSSPAAVNHHSSSDISPVSNESTSSSPGKEG
HSPGSGTVTYHLLGPQEEGEGGVVDVKGV**RMEVQGE**EKKREDKEDEEDEDVSHVDEEDCLGVQRED**RGSGSG**NEQVEKLRRPEGASNESESD

Mus musculus:

>NP_062755.1 peroxisomal membrane protein PEX14 [Mus musculus]
MASSEQAEQPNQPSSPPGSENVVPREPLIATAVKFLQNSRVRQSPLATRRAFLKKKGLTDEEIDLAFQQS
GTAADEPSSLGPATPVVPQPHLTPQPYSPRGSWRDYGALAIIMAGIAFGFHQLYKRYLLPLILGGRE
DRKQLERMAASLSELSGTVAQTVTQVTTLASVQELLRQQQQKQVQELAHELATAKATTSTNWILESQNIN
ELKSEINSLKGLLLNRRQFPSPSPAKIPSWOIPVKSSSPSSPAAVNHHSSSDISPVSNESTSSSPGKDS
HSPGSGTATYHLLGPQEEGEGVLGVKGV**RMEVQGE**EKKREDKEDEEDEDVSHVDEEDVLGVQRED**RGSGSG**NEQVEKLRRPEGASNETERD

Gallus gallus:

>XP_001234697.3 peroxisomal membrane protein PEX14 [Gallus gallus]
MASSEQAEQPSQAGSSPATENAAAREPLIVTAVKFLQNPVRVQSPATRRAFLKKKGLTDEEIDLAFQQS
GTSADEPSPGFPSSQLVPAQPAHPVYVNPFGSRWRDYGALAIIMAGIAFGFHQLYKKYLLPLIMGKEDR
KQLQRIESNIAEMSGSVTQTQVTLQTLAAVQEMLIQQQQKIQELTQELAAKATTSTNWILESQNINEL
KSEIYSIKGLLLNRRQFPSPSPAKIPSWOIPVKSPSPSNPVVANHHSSSDISPVSNESTTSPVKENHS
PEGSKVCHLLSTEEGNKAVIDKSGV**RMEVQGE**EKKRENKRNEEEDEDEDVSHVDEEECMGVQTED
RGSGSGNEQVEKLRRPEGASNENEID

Xenopus laevis:

>XP_018081136.1 PREDICTED: peroxisomal membrane protein PEX14-like [Xenopus laevis]
MASSSQDQDSQGGSPSLINEKIVPRDQLIATAVKFLQNPVRVQSPVATRKEFLKKKGLSNEEIELAQQS
GTVHDDPGLVTHGTGIPHTPGSSQLAVQQFSPPGSRWREYALAIILAGIAFGFHQLYKRYLLPLILGGRE
SRKQLQRIESGVSEMSGSVTQTQVTLQTLAAVQELLIQQQQKIQELSELASAKASSSTNTILESQNIQ
ELKSEIYSIKGLLLNRRQFPSPSPASKIPAWOIPVKPPTLPSPAVLNHHSSSDISPVSNESGSSSPVKEI
HSPGTGKSSHHGLTTEESEIDVQTQV**RMEVQGE**EENEDDVQPDQDCIGVQTED**RGSGSG**NEQVQDK
LRRPEGASNEMDC

Salmo salar:

>XP_014001298.1 PREDICTED: peroxisomal membrane protein PEX14 [Salmo salar]
MASSQPDQDPQTQPRAPSRDDVAPREAMIATAVKFLQNHKVRQSPLETRKVFLLKKKGLTDKBIELAIQRSG
STDEPLALTVPVGQYVPLLDQQLAIPYSPRGYRWRDYGALTVIMMGMAFGHHLYKKYILPLIMGSKEDK
KHQRIESNIAEMSGTLTQTQVTLQTLATVQDLLVQQQKIHDLSELSTSEASSSTNRILDTQTIGDL
KAEISGLKGLLLGRRQFPASPSVPKIPSWQMPFLKPDITSTSSPINHTNHHSSSDISPVSNESASSSPIKDG
HHSPPQDALGPDGAGHLNGKNGVGLGGGATLPLDLKDQV**RMEVQGE**EKKKEEDVKEEKEEEEEEEDDVS
HVDEEHLVSPAED**RGSGSG**NEQVQDKLRRPEGASNESEVD

Petromyzon marinus:

>XP_032819505.1 peroxisomal membrane protein PEX14-like isoform X3 [Petromyzon marinus]
MADTEREVDVAVIGNASREHLVDTAFAKFLKNPRVAGSPPNIQRAFLRKKKGLTDVIEDVFLRAGVHRGTSL
AHAQHLAQSPAGPPASRHSWRWRDYGALSAVIAAIGFGINRLYKWLAAVRAAEAQRLTDVETVSAMAAS
LTHAVTQLQTSVAGTHELLSRQKQLERLTDDTAVSKASGPLLADLRTEIASIKGLMLGRKQFPFCPPNSA
AILPSWQLALKPSTSTGTTISSTMTSQDVNAATNKEQQLQPRENTDTLTGSSSENVSSSDISPSISHESASP
GLDSEVHTLKAEGKVNLSLQSLTQNGEVGGDFIHQHQDEDEVITEVCVLTKTVEAQGENEVD

Branchiostoma belcheri:

>XP_019628140.1 PREDICTED: LOW QUALITY PROTEIN: peroxisomal membrane protein PEX14-like [Branchiostoma belcheri]
MAAPDPKSSPKDEGSPSDVPLNPEPRQCMETAVKFLQNPVRVQSAFAQRAFLQKKGLTNEEIQLAIEK
SGTASDETNPPPPPPQAQSTAPVFLQPPVIVPVSPTSXKWRMGAVIVLVGGALYGLYRLFQAYLVPLW
KTRQEEQRRLERIEAAVTELSASVNYKTVGELQTSMGVVQQAALTKQSDRVQIEISMELAAGKSTARVFESQS
VSELKAEITSLKGLLLSRXYTKYLTDHYTFPPTPSPTPIIPSWQMEPVDSSASSSSKPAATTSSEVSPAEO
PLPADSNHAAETLDVAQNNGPSAQTVSTSESSEDTSSSIHVHNSNPLDDLSSGEMEAKGQMEVKGQMEV
KGEEVTAENVHQGEEDNREETVIKEA

Drosophila melanogaster:

>NP_649253.1 peroxin 14 [Drosophila melanogaster]
MSSNNTDQDGTVMATATSVQNQDVEAGVDEQLPRESLITTAVSFLQNTKVRHTTLTIKQKQFLRSKGLTAH
BIQLACERAGVFTQDPNKNPNPNPTVISIGSQLHALQPQPTVLGRIREIIHSAALFSGVVYAVYIFWKQY
IAPYLFKGSKKKAVDEVLDIDKKVETRNDLNKEILAVRDLITTQQREHAQQLNREFSNFRSDDLDAIKG
LLNLRKQFAGPVAPIAVPSIPAWQLAGSPHHHHRHSGSDNEKGGDAGSGSGSSETVVTFNKSDSLEIM

Hydra vulgaris:

>XP_004208685.1 PREDICTED: peroxisomal membrane protein PEX14-like [Hydra vulgaris]
MKVDSNEEDVSKKVDVAVRFLSNPNVKSINKESEAFLSKGLNDEMELNAMQKASSECEIAESNRKWSIF
TYFKGIVILGAGILSAANYAYKAYILPPIVAHEIKDDGRIERLGEISVQAMKDDIKQHTVELSSTLKDIQTVL
EKQHKVIVILLQESIQNSPFDHTTLADIKAELSNVKTMMLSRKQFPKAPFTQQSNEIPAWQRVDNKKKTVDV

STDDTSSSETI

Nematostella vectensis:

>XP_032228851.1 peroxisomal membrane protein PEX14-like [Nematostella vectensis]
MADPKEANMEEATNADSKQKKIATAVKFLQNPRVRSTPMSQRRAFLEKKGLTKEEIDLAVEQSGTAGDVV
SVQAPSAITPYQTQVQRVAPLPYTWRGYLGAAVIGGSLGYIIVTVFKKFILPLITHKKQKDERLRAIENS
VGELSNVMDTVGGVQTTLDSVQKLLIEQQKQIICLSADLSSTQEKVEQLPTESYSVNDLKSEIISLKGL
LLNRKAFPSPLDNSTPAGIPSWQRAVTA GADSRITDSASTSFAASKRNDGGQITESGTYNSSRKKASYE
SEHKSMNGEISSEKKKKTPEKKETPPEVPQEMEHSNHNESDITDTNTVKSAITNENLDDAVLVDSQDI
SLQSNDTSSASSLSDMSANASFNEESIAFSSTCIKVPFAEASKSEELPSASAIEVD

Amphimedon queenslandica:

>XP_003385343.1 PREDICTED: peroxisomal membrane protein PEX14-like [Amphimedon queenslandica]
MAAMSSESTSAASSPEVNGASTDPIKGSFVPRDSSYSEFMRRLLPERQKLLDIAVKFLINPRVVNSNDDD
KIAFLNKKGLNEEEIYWVRQEAAASRPAPSLAVPAPPTSLALTTPTQATPTLTHLVIRGVLVGSMTGFIY
WIKGVVSKWFDLKVQQRHQVLEERVQEI RTTLETMTMQLQTTLSIKVLLERQQEQITQLSSTQSNVV
ASNELRTINSELSTLKGLLLNHRHQFPTPQKDNLSLPPGIPSWQRNTSLPPLNTNGSSKEQEASGDGGG
GGGESSTGTTVQQNSNNNDNDEEDDD

Alignment

NP_649253.1[D.melanogaster]	MSSNNTD-----TG-D-----TTVMATATSVQNDVEAGVDEQLPRESLITTAVSF	44
XP_003385343.1[A.queenslandica]	MAAMSSSESTSAASSPEVNGASTDPIKGSFVPRDSS---YSEFMRRLLPERQKLLDIAVKF	57
XP_032819505.1[P.marinus]	MADT-----ER-----E-----VDVIGNASREHLVDTAFAKF	27
XP_004208685.1[H.vulgaris]	MADP-----KEA-----N-----MKEVSDNEDVDSKKVDVAVRF	20
XP_032228851.1[N.vectensis]	MAAP-----DPKSSPKDEGSP-----MEEATNADSKQKQIATAVKF	28
XP_019628140.1[B.belcheri]	MASS-----EQP--DPOTQP-R-----SDVPLNPEFRQQMIIATAVKF	36
XP_014001298.1[S.salar]	MASS-----DQT--DQSVQCGP-----APSRDDVAPREMIATAVKF	34
XP_018081136.1[X.laevius]	MASS-----EQA-EQPSQAGS-----SPATENAAAREPLIVTAVKF	35
XP_001234697.3[G.gallus]	MASS-----EQA-EQPSQPS--TPGSENVLPREPLIATAVKF	35
075381[H.sapiens]	MASS-----EQA-EQPSQPS--TPGSENVLPREPLIATAVKF	35
XP_024109019.1[P.abelii]	MASS-----EQA-EQNPQPS--PPGSENVVPREPLIATAVKF	35
NP_062755.1[M.musculus]	. : * . *	
NP_649253.1[D.melanogaster]	LQNTKVRHTTLIQKQFLRSKGLTAHEIQLACERAGVFTQDPNKPFPNPNFTVISIGSQLH	104
XP_003385343.1[A.queenslandica]	LINPRVVNSNDDDKIAFLNKKGLNEEIIYWRQEASRPAPSIAVPAPPTSLALT--PTQ	116
XP_032819505.1[P.marinus]	LKNPRVAGSPPNIQRAFLRKKGLTDVEIEDVFLRAGVHRGTSLAHAQH-----LAQSP	80
XP_004208685.1[H.vulgaris]	LSNPNVKSTNKESKEAFLKSKGLNDMEILNAMQKASSECEIA-----	62
XP_032228851.1[N.vectensis]	LQNPRVKRSTPMSQRRAFLEKKGLTKEEIDLAVEQSGTAGDVSVQAPS-----A	77
XP_019628140.1[B.belcheri]	LQNPRVRQSAFAQRRRAFLKKGTLNEEIQLAIEKSGTASDETNPPTPPPAQVASTAPVP	96
XP_014001298.1[S.salar]	LQNHKVRQSPLETRKVFLLKKGLTDKEIELAQRSGST--DEPLALTPV-----GPQYP	86
XP_018081136.1[X.laevius]	LQNPVRVRQSPVATRKFEFLKKGLSNEEIELAQSGSGTVHDDPGLVTHT-----GIPHT	88
XP_001234697.3[G.gallus]	LQNSRVVRQSPLATRAFLKKKGLTDEEIDLAFQSGSGTSADEPQSPGPS-----SQLVP	88
075381[H.sapiens]	LQNSRVVRQSPLATRAFLKKKGLTDEEIDMAFQSGSGTAADEPSSLGPA-----TQVVP	88
XP_024109019.1[P.abelii]	LQNSRVVRQSPLATRAFLKKKGLTDEEIDMAFQSGSGTAADEPSSLGPA-----TQVVP	88
NP_062755.1[M.musculus]	* * . * : : * . * . * . * . * . *	
NP_649253.1[D.melanogaster]	ALQ-----PQPTVLGRIREIISHAALFSGVVYAVYIFWKQYIAPYLF-GKSKK----KA	153
XP_003385343.1[A.queenslandica]	ATP-----TLTH--LVIRGVLVSGMFGIYFIWKGVVSKWFDLSKVQOERHOV	162
XP_032819505.1[P.marinus]	AGP-----PASRHSWRWRDVGALSAVIAAGFGINRKYKWL-----A-VRAEAQRLTD	129
XP_004208685.1[H.vulgaris]	-----ESNKWSIF--TYFKGIVIGAGISAAANYKAYILPVYA-HEIKDDGRIER	110
XP_032228851.1[N.vectensis]	ITPYQTQVQRVAPLPYTWRGYLGAAVIGGSLGYIIVTVFKKFIPLIT-HKKQKDERLRA	136
XP_019628140.1[B.belcheri]	LQPPPVIV-----PVSPWSKWRDMGAVILVGGALYGLYRLFQAYILPWK--TRQEEQRLER	152
XP_014001298.1[S.salar]	LDDPQLAPIPYSPRGYRWRYDGAITVIMGMAGFPHHLYKKYILPLIM-GSKEDKKHLQR	145
XP_018081136.1[X.laevius]	GPSSQLAVQQFSPGSRWREYGALAIIMAGIAGFGHQLYKKYLLPLII-GGREDRKQLQR	147
XP_001234697.3[G.gallus]	AQPAHPV---VYNPPGSRWRDYDALAIIMAGIAGFGHQLYKKYLLPLIM-GGREDRKQLQR	145
075381[H.sapiens]	VQPPHLISQPYSPAGSRWRDYDALAIIMAGIAGFGHQLYKKYLLPLII-GGREDRKQLQR	147
XP_024109019.1[P.abelii]	VQPPHLVSPQYSPAGSRWRDYDALAIIMAGIAGFGHQLYKKYLLPLII-GGREDRKQLQR	147
NP_062755.1[M.musculus]	VQPPHLTPQPYSPGSRWRDYDALAIIMAGIAGFGHQLYKKYLLPLII-GGREDRKQLQR	147
NP_649253.1[D.melanogaster]	VDEVLDIDKKVETRTNDLNKEILAVRDLITQQREHAQQIL-----N	195
XP_003385343.1[A.queenslandica]	LEERVQEIIRTTLETTMQRLQQTLLSIKVLLEQQEQIT--TQLSSQT-----SNVVAS	212
XP_032819505.1[P.marinus]	VESTVSAMAASLTTHAVTQLQTSVAGTHELLSRQKQL-ERLTDTDVATSKAS-----G	180
XP_004208685.1[H.vulgaris]	LGESVQAMKDDIKQHTYELSELSTLKDQITVLEKQHKVI-VLLQES-----IQNSPFDH	161
XP_032228851.1[N.vectensis]	IENSUVGELSNSVMDTVGGVQTTLDSVKLLLEQQQKI-ICLSADLSSTQEK-VEQLPTES	194
XP_019628140.1[B.belcheri]	IEAAVTELSASVNKTVGELQTSMGVVQQALTQKSDRV-QEISMELAAKG---STARVFES	208
XP_014001298.1[S.salar]	IESNIAEMSGTLTQTVTQLQOTLAIVQDLLVQQQKI-HDLSQELSTSEASSTNRI-LDT	204
XP_018081136.1[X.laevius]	IESGVSEMSGSVTQTVTQLQOTTLAAVQELLIQQQKI-QELSLELSASKASSNTNILES	206
XP_001234697.3[G.gallus]	IESNIAEMSGSVTQTVTQLQOTTLAAVQELMIQQQKI-QELTQELAASKATTSTNWILES	204
075381[H.sapiens]	MEAGLSELSGSVAQTVTQLQOTTLASVQELLIQQQKI-QELAHELAAAKATTSTNWILES	206
XP_024109019.1[P.abelii]	MEAGLSELSGSVAQTVTQLQOTTLASVQELLIQQQKI-QELAHELAAAKATTSTNWILES	206
NP_062755.1[M.musculus]	MAASLSSELGTVQTVTQVQOTTLASVQELLRQQQKV-QELAHELATAKATTSTNWILES	206
NP_649253.1[D.melanogaster]	REFSNFRSLDAIKGLLLNRR-----QFAGPVAP---IAVPSIPAWQLAGSPHHHHR	244
XP_003385343.1[A.queenslandica]	NELRTINSELSTLKGILLNRR-----QFPTPKQDNLSLPPGISWQRNTSLPLPNT	263
XP_032819505.1[P.marinus]	PLLADLRTEIASIKGLMLGRK-----QFPC--PP--NSAAILPWSQLALKFPSTSTG	227
XP_004208685.1[H.vulgaris]	TTLADIKAEILSNVKTMMLSRK-----QFFKAPRT--QGSNELPAWQRVDNKKVTDV	210
XP_032228851.1[N.vectensis]	YSVNDLKSEIISLKGILLNRR-----AFPSBLDN--STPACTIPSWQRVATGADSR	243
XP_019628140.1[B.belcheri]	QSVSELKAEIISLKGILLSRXVTKYKLTDHVTFPP--TP--SPTPIPSWQMEFVDSASSS	264
XP_014001298.1[S.salar]	QTIGDLKAEIISLKGILLGR--O-----OFFA--SP--SVKPIPSWQMLPKFDTI-S	249
XP_018081136.1[X.laevius]	QNIQELKSEIYSLKGILLNRR-----QFPP--SP--S-ASKIPAWQIPVKPPTL--	248
XP_001234697.3[G.gallus]	QVINELKSEIYSLKGILLNRR-----QFPP--SP--S-APKIPSWQIPVKPSSP--	250
075381[H.sapiens]	QVINELKSEINSLKGILLNRR-----QFPP--SP--S-APKIPSWQIPVKPSSP--	250
XP_024109019.1[P.abelii]	QVINELKSEINSLKGILLNRR-----QFPP--SP--S-APKIPSWQIPVKPSSP--	250
NP_062755.1[M.musculus]	QVINELKSEINSLKGILLNRR-----QFPP--SP--S-APKIPSWQIPVKSSSP--	250
NP_649253.1[D.melanogaster]	HSGSDDNEKG-----DDAGSGS	261
XP_003385343.1[A.queenslandica]	TNGSSKE--SQDVNAATNKEQQLQPRENTDTLGSSENVSSSDISPISHESASPLDSEVH	283
XP_032819505.1[P.marinus]	TTISSMTQSDVNAATNKEQQLQPRENTDTLGSSENVSSSDISPISHESASPLDSEVH	287
XP_004208685.1[H.vulgaris]	STDDTS--SQDVNAATNKEQQLQPRENTDTLGSSENVSSSDISPISHESASPLDSEVH	221
XP_032228851.1[N.vectensis]	TTDSAST-----SPAAS-----KRNKDDG	262
XP_019628140.1[B.belcheri]	SSKPAT-----TSSEVSPAQPL----PADSN-	287
XP_014001298.1[S.salar]	TSSPSIN-----HTNSSSDISPVSNEASASSSPKKG-	280
XP_018081136.1[X.laevius]	-PSPAVL-----NHHSSSDISPVSNEASASSSPKKEI-	280
XP_001234697.3[G.gallus]	-SSPAV-----NHHSSSDISPVSNESTSSSPGKEG-	278
075381[H.sapiens]	-SSPAV-----NHHSSSDISPVSNESTSSSPGKEG-	280
XP_024109019.1[P.abelii]	-SSPAV-----NHHSSSDISPVSNESTSSSPGKEG-	280
NP_062755.1[M.musculus]	-SSPAV-----NHHSSSDISPVSNESTSSSPGKDS-	280
NP_649253.1[D.melanogaster]	GSSETEVVTKNSDS-SL-----EIM-----	280
XP_003385343.1[A.queenslandica]	ESSTGTTVQQNSNN-----KVNSLQSLTQNGEVGD-	297
XP_032819505.1[P.marinus]	TLKAEG-----KVNSLQSLTQNGEVGD-	309
XP_004208685.1[H.vulgaris]	QITESG---TYNSS-RK-----KASYESEHKSMNGEISSEKKKKTPPEK	221
XP_032228851.1[N.vectensis]	HAAETLDVAQNGPSAQKTVSTSESSEDTSSIVHVSNDLDSGGEEMA--KGQMEVK	345
XP_019628140.1[B.belcheri]	HHSQDQALG---GPDGA-----HGLNGKNGVGLGG-GAT--LPPLDLK	305
XP_014001298.1[S.salar]	HSPEGT-----KGSSHHLLGLTEE-----ESEIDVQ	317
XP_018081136.1[X.laevius]	HSPEGS-----KVSCHLLSTEEG---N--KAVIDVK	304
XP_001234697.3[G.gallus]	HSPEGS-----TVTYHLLGPQEE---G--EGVVDVK	306
075381[H.sapiens]	HSPEGS-----TVTYHLLGPQEE---G--EGVVDVK	306
XP_024109019.1[P.abelii]	HSPEGS-----TATYHLLGPQEE---G--EGVLDVK	306
NP_062755.1[M.musculus]	HSPEGS-----TATYHLLGPQEE---G--EGVLDVK	306
NP_649253.1[D.melanogaster]	-----DN-----NDEEDDD	280
XP_003385343.1[A.queenslandica]	-----GFI--HQHOD-----EDEDVI-	306
XP_032819505.1[P.marinus]	-----GFI--HQHOD-----EDEDVI-	323
XP_004208685.1[H.vulgaris]	KETPPEVVPQEMEH--SHHSNESSDPTNTVKSAITNENLDDAVLDSQDISLQNDTSA	221
XP_032228851.1[N.vectensis]	G--QMEVKGEEVTAENVHQQ--E-----EDNREETVI-	359
XP_019628140.1[B.belcheri]	DQVRMEVQGEEEKKEEDVKEEKEE-----EEEEEDDVS	373
XP_014001298.1[S.salar]	TQVRMEVQGEENEDD-----V-----	322
XP_018081136.1[X.laevius]	SQVRMEVQGEEEKRENK-RNEEEE-----EDEDDDVS	336
XP_001234697.3[G.gallus]	GQVRMEVQGEEEKREDK-ED--E-----EDEDDDVS	335
075381[H.sapiens]	GQVRMEVQGEEEKREDK-ED--E-----EDEDDDVS	335
XP_024109019.1[P.abelii]	GQVRMEVQGEEEKREDK-ED--E-----D-DEDDVS	335
NP_062755.1[M.musculus]	GQVRMEVQGEEEKREDK-ED--E-----D-DEDDVS	334

NP_649253.1[D.melanogaster]	-----	280
XP_003385343.1[A.queenslandica]	-----	306
XP_032819505.1[P.marinus]	-----TEVCVLTKVEAQGENEVD-----	341
XP_004208685.1[H.vulgaris]	-----	221
XP_032228851.1[N.vectensis]	SSLSDMSANASFNEESIAFSSTCIKVPAAASKSEELPSAS-----AIEVD	404
XP_019628140.1[B.belcheri]	-----K--EA-----	376
XP_014001298.1[S.salar]	-----HVDEEEHLSVPAEDSRGGDGGQNEQVDKLRPPEGASNESEVD	392
XP_018081136.1[X.laevis]	-----VQPEDCIGVQTEDSRGGDGGQNEQVDKLRPPEGASNEMDC-	363
XP_001234697.3[G.gallus]	-----HVDEEECMGVQTEDSRGGDGGQNEQVEKLRPPEGASNENEID	378
O75381[H.sapiens]	-----HVDEEDCLGVQREDSRGGDGGQNEQVEKLRPPEGASNESERD	377
XP_024109019.1[P.abelii]	-----HVDEEDCLGVQREDSRGGDGGQNEQVEKLRPPEGASNESERD	377
NP_062755.1[M.musculus]	-----HVDEEDVLGVQREDSRGGDGGQNEQVEKLRPPEGASNETERD	376