

# SH3BP2

## Homo sapiens:

>sp|P78314|3BP2\_HUMAN SH3 domain-binding protein 2 OS=Homo sapiens OX=9606 GN=SH3BP2 PE=1 SV=2  
MAAEEMHWVPVPMKAIGAQNLLTMPGGVAKAGYLHKKGGTQLQLLKWPLRFVIIHKRCVYY  
FKSSTSASPGAFSLSGYNRMRAAEETTSNNVFPFKIIHISKKHRTWFFSASSEERKS  
WMALLRREIGHFHEKKDLPLDTSDDSSDTSDFYGAVERPVDISLSPYPTDNEDYEHDDED  
DSYLEPDSPEPGRLEDALMHPAYPPPPVPTPRKPAFSDMPRAHSFTSKGPGPLLPFPFPP  
KHGLPDVGLAAEDSKRDPLCPRAEPCPRVPATPRRMSDPPPLSTMPTAPGLRKPPCFRES  
ASPSPEPWTPGHGACSTSSAAMATATSRNCDKLKSFHLSPRGPPTSEPPVPANKPKFL  
KIAEEDPPREAMPGLFVFPVAPRPALKLPVPEAMARPAVLPRPEKQPLPHLQ**RSPTG**  
**GR**FRSFSFEKPRQPSQADTGGDDSDEDIYKVLPLNSVFVNTTESCEVERLFKATSPRGEF  
QDGLYCIRNSTKSGKVLVVMDETSNKRNYRIFEKDSKFYLEGEVLFVSVGSMVEHYHT  
HVLPSHQSLLLRHYPGYTGPR

## Pongo abelii:

>PNJ23454.1 SH3BP2 isoform 3 [Pongo abelii]  
MASLGPRTPALSRSGRRAMCWSTISFMAAEETHWVPVPMKAIGAQNLLTMPGGVAKAGYLHKKGGTQLQ  
LLKWPLRFVIIHKRCVYYFKSSTSASPGAFSLSGYNRMRAAEETTSNNVFPFKIIHISKKHRTWFFSA  
SSEDERKSNMALLRREIGHFHEKKDLPLDTSDDSSDTSDFYGAVERPVDISLSPYPTDNEDYEHDDEDS  
YMEPDSPEPGRLEDALMHPAYPPPPVPTPRKPAFSDMPRAHSFTSKGPGPLLPFPFPPKHGLPDVGLAAE  
DSKRDPLCPRAEPCPRVPATPRRMSDPPPLSTMPTAPGLRKPPCFRESASPSPSPEPWTPGHGACSTSSA  
AIMATATSRNCDKLKSFHLSPRGPPTSQPPVPVANKPKFLKTAEEDPPREAMPGLFVSPVAPRPALKL  
PVPEATARPAVLPRPEKQPLPHLQ**RSPTGGR**FRSFSFEKPRQPLPADTGGDDSDEDIYKVLPLNSVFIN  
TTESCEVERLFKATSPRGEFQDGLYCIRNSTKSGKVLVVMDETSNKRNYRIFEKDSKFYLEGEVLFVS  
VSGMVEHYHTHVLPSHQSLLLRHYPGYTGPR

## Mus musculus:

>NP\_001139330.1 SH3 domain-binding protein 2 isoform c [Mus musculus]  
MSGGCRQLQSLLIAPELNSLSGFKDTCPQQVTGSCTMCWVSAMSFMAAEEMQWVPVPMKAIGAQNLLTMPGG  
VAKAGYLHKKGGTQLQLLKWPLRFVIIHKRCIYYFKSSTSASPGAFSLSGYNRMRAAEETTSNNVFPF  
KIIHISKKHRTWFFSASSEDERKSNMALLRREIGHFHEKKELPLDTSDDSSDTSDFYGAVERPIDISLS  
YMDNEDYEHDDEDDSYLEPDSGPGMKLEDALTYPPAYPPPPVVPVRKPAFSDLPRAHSFTSKSPSPLP  
PPPKRGLPDGTSAPEDAKDALGLRRVEPGLRVPAVTPRRMSDPPMSNVPTVNLRRKHCFRDSVNPGLPE  
WTPGHGTSVSSSTTMVAVATSRNCDKLKSFHLSRGPPTSEPPVPVANKPKFLKIAEEDPPREAAFAFPV  
PPVAPRPFPQKMPMEATVPRPAVLPRPENTPLPHLQ**RSPTGGR**FRGFSFEKARQPSQADTGEEDSDEDI  
YKVLPLNSVFVNTTESCEVERLFKATDPRGEFQDGLYCIRNSTKSGKVLVVMDESSNKRNYRIFEKDS  
KFYLEGEVLFASVSGMVEHYHTHVLPSHQSLLLRHYPGYAGPR

## Gallus gallus:

>XP\_015141266.1 SH3 domain-binding protein 2 isoform X1 [Gallus gallus]  
MPERGYQLMALSSQKRLSYGESVSRRTMCRLGTVTRKMASEEQVWVPVPMKAIGAQNLLTMPGGVTKSGY  
LHKKGGTQLQLLKWPLRFVIIHEGCIYYFKTSTSASPGAFSLNGYNRMRAAEETTSNNVFPFKLVHIS  
KKHRTWFFSASSEDERKNMMLSLRREIDHYHDKKETVTEFSDSGSDADSFYGSVERPIDIKYSHHSADNE  
DYQKEEDDESYLEQPDTSIDVKKDFMPLPAYPPPPVPHVRKAAYSESRSHSFSGKTAGSTPPPPPPKRS  
LPEIKTEDFDGVREPQLCPRAEPNLKIQSSSRPSEQPPVPVPLPLFKKPFVCVKEPSSLPELPLSHVLTT  
TEGCEKLTNLNSPRTPPPLPSNPKLSQI~~TEK~~TVENKVPREHGKPLGFVPPVLKPPFPVPGHQHSVLKPR  
PEKPS~~CQ~~LQ**RSPTGGR**FRSFSFEKPA~~L~~PSKNQVNDSDDDY~~EK~~VELPTSIFLNTSESLEVERIFKAT  
SPKGQFQNGLYCIRNSTKAGKVLVVMVDQSAEKVRNYRIFEKDKFYLDADIMFLNMGSLVEYYSTHVLP  
SHGSLILRCPGYGSKPR

## Xenopus laevis:

>XP\_041443552.1 SH3 domain-binding protei~~n~~ 2 isoform X3 [Xenopus laevis]  
MASDESWEPTPMKAIGAQNLLTMPGGVAISGYLHKKGGTQLQIMKWPLRFVIIHKGCVVYFKTSTSATSQ  
GAFSLNGYNRMRAAEETTSNNVFPFKMVHISKKQRTWYFSAASEERKXWMLSLRKEIDHYHEKKEVT  
DLSDPDSDSDFYGSVERPVPIN~~Y~~THNPADDSYEDDDDDDDYVKGADENAPTYPPPPVPRNPRNGND  
SVKPR~~T~~MSDGLPYRPPPPPTPLIKTLP~~H~~LSDAQKESAIHQGFSCGPPPHKIEEFTPKLPPHKKTSFD  
LIGKEFPRREDLIGSSDSVGYDLCGPTIKFPSLSLQLGARHVPDPAFFPVSYPKKNGSSCKPMTNPSTQ  
LISNTVSKELTDKFRMMFPVSPAPPKPSFLSPVVKPSSSSNAPPPPPVKPSIPSTPSPVSTIASISPP  
VVP~~I~~KPRMLNDQKAERIPQKPPPIPRQPGRKSES~~D~~KLESPSKI**RSPTGGR**FRGLSTEGPAHP~~I~~KPKRKL  
TRNDSDEYKVLPLPVSVFVDNDSVEVERIFKAASPGGTPQNGLCFIRNSAKAGKVLVVMVDTATEKTRN  
YRIFEKDSKYFLAEALLFPDVESLVEHYITNKLPSHSTLVLQHAYGCSFPR

## Salmo salar:

>XP\_013984441.1 PREDICTED: SH3 domain-binding protein 2-like isoform X1 [Salmo salar]  
MASAENWVPVPMRAIGAQNLLTMPGGVCHSGYLHKKGGSQFSLMKWPLRYIIHRCGVYYFKSSTSAPFQ  
GAFSLNGYNRMRAAEETTSNNVFPFKIVHFSKKHRTYCFSAANEERKXWMLRKEIDHYNDRRDSHI  
PNDS~~S~~DADSFYGSIECPMDITYAHDDPGDNVMLEDEDDDEDDY~~EK~~PDSPPTYKGRLTVPPSYHPP  
LPQCFRQESMSGCKGLPQPAFVPNRNTLSPLPKKMSPLLPKPLKGEVGHNNHGHKDVPNKDSPE~~S~~VRG  
PKAPHPTIASLQKQMMMGKTSISTLPGGDHRDKKPHAPVTLKSPATLPICINLERQMLNPSPPGCHGN  
TSPHSIVSVPNYCHSTRPTDPLPQPSPALNHKLGPYKPLLTKPCPCPATMPKRP~~R~~GSAC**RSPTGGR**SQT  
SVQDQVPASLRKNRDP~~S~~KYIDDDSDEDIYENVQLPDSVFVDITETSSVEKMFMESSSSPDGLYCFRNSAK  
TSKVLVVMVDLCKARNYRLFEDSRVLEFEMTFASLSALVEHYHSHPLPNHDSLCLQQPYRYHMPR

## Petromyzon marinus:

>XP\_032800705.1 SH3 domain-binding protein 2-like [Petromyzon marinus]  
MSAACRDWPLPMRSVGAQSIIITMPGGVHAHSGYLHKKGGTQVSFFAWPLRYVVLHAGCLYYKSS~~T~~ATIPR  
GSPSLRNGYNRMALQETSMGNVYFPKLVHNVHRHTWIFSAANEGERKXWMSAIRSEIENYLRPQSSNE  
RRNSSSSD~~S~~DFYEQVEMPLPLLDTSWGS~~G~~QDADEYDESDGDDDDGDGYLQPD~~D~~YLT~~H~~LES~~G~~TGGGSLSPQ  
PKQQQQPPPPQLLLASSPSPSPANKFTATTATT~~K~~RPALMPKPPPKPPQPPQQQQPQQQQPQQHHHQ  
ELGYFKRPIAGTIGPQQRSPPLFWAAVAAAAA~~A~~STTTTTTATTTTTTARGKALMPAA~~T~~TTTTTTKAP  
PRPLS**RSPTGGR**HKLIQIDSDSDYIQPEDAMPSTIFLD~~T~~TS~~G~~DEAEWRMKNAGLTHGLYCIRNSASSD  
QQVLVVMVDGECRKL~~R~~NFKIFRAGPLVSLDVS~~D~~GAPHFKLLSGLLDHYRVAPLPRQSSSLRLTQPLV

## Branchiostoma belcheri:

>XP\_019631975.1 PREDICTED: SH3 domain-binding protein 2-like [Branchiostoma belcheri]  
MISIALALPHPLRMAGAKDSKNRLSLSAGLGGVKSFLSALGQDDKHVIPGVTEPHITISAQELLSDGKA  
IFYGWLARKGNDVLSQRFMIKKHRYI~~L~~KDGCVVYFKNETSEKPCGAFSLSNYTKIMRAVDVETTELFWP  
FLLVGRFFQMRTWYFSASNEQDMQHMLNMKNEMDAVNSSVQAGHGGRSNPEVIVDPAYGDDSLPP  
IYQDTDEEHYYEDPDEHLQEEEDYLQVLEDGPRVTPVGAEAAGDVGA~~F~~REMLPPTPTSKMASPSKGY

GQEGAARPPVPLPKKQSSFFT~~KPLPAT~~QEGTRSPKKALVPPHMRGVSTSPPHQTESKGKVPSPPWKELK  
GPGVKKASEPINITSPGWTAGKTVGQRETGEGRGRDVKDEKKEKSGMARALAAEMTQKFGSNWQAAGGTA  
KPRT~~PDKPV~~PAAKPGLHPPK~~PGLAPKPGTS~~PKPG~~LAPKPGHPSRQGMKPLV~~PPHKPQVEVQGIMEDRYEHE  
EEEEPVEDPGIR~~KTFPGG~~FFSKKNFNENPESETDDVMPADVSDVDVEKAESCLRSGQVNGKYFLRPSK  
QDKGRMVLVVYDCAGQKCRKFKMYGLGSQLYLHKGAPTFSSMSDLLRHYQYHNL~~PVTDGVEIRL~~TEPYQG  
H

**Drosophila melanogaster:**

No homolog found.

**Hydra vulgaris:**

No homolog found.

**Nematostella vectensis:**

>XP\_032222077.1 SH3 domain-binding protein 2 isoform X3 [Nematostella vectensis]  
MSNGPTWRTC~~SMP~~TT~~RHNECS~~VPGN~~RIRS~~RTD~~TNITAPKH~~PEPYMSIPAQSLVQDECHIHC~~GT~~VRKENKY  
NMWQDRYLVLHKGCMYYK~~NYLDKSAKQ~~FSLSGYRVSTAPERAVKLPWVFKLTHLQPEKRTFYFAAKSE  
KELNEWMSKIKEDIDEYCEPLATSGFNPECEAT~~RQSSSGSSDDGDS~~FKYDYPLFAPEFALAKALTLEKLS  
ESQNSSASSEPEYCP~~PPS~~FDTLPNGSPPPPPARNQSSGKERAQPIGSVPTPVMMGKSGKSSVDISAVILG  
KAALKPVQDNSLPPLPKPRSKLRQSPRVHAGSH~~PSS~~SPPTKPKPSVHKYASDPELA~~CLP~~QQTSLPPAN  
PALVDSSDSEEDDYLKILPDEESTPNHGNNDEFIPRLSTLERLRPEGKSFRTPPEKEQI~~HID~~VL~~PATS~~  
VKLDIERTKAIAMLEGRNGMYILHKSRS~~GDIGQCL~~SVCIEDRVRHFLVFYSKEEGYALDRDAQRFPTLE  
EVIRHHYTTPLPKQQSATLEQPYRWPH

**Amphimedon queenslandica:**

No homolog found.

## Alignment

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XP_03222077.1[N.vectensis]      -MSGNTW-----RTC-SMPTTRHNECSVGNRIRSRDTNITAP 38
XP_019631975.1[B.belcheri]      MIS-----LALALPHPLRMAGAKDSKNRSLSAGLGGVKKSFLSAL-----GQQDKHVIP 50
XP_032800705.1[P.marinus]       -----MSAACR 6
XP_013984441.1[S.salar]         -----MSAEN 6
XP_041443552.1[X.laevis]        -----MASDEP 6
XP_015141266.1[G.gallus]        MPERGYQ-----LLMALSSQR-----KLSYGESVSRRTMCRIGTV-----TRKMASEBQ 44
NP_001139330.1[M.musculus]       -MSGGCRLLQSLLLAPELNSLSGFK-----DTCQQVGTSGCTMCWVSAM-----SFMAAEEM 50
P78314[H.sapiens]               -----MAAEEM 6
PNJ23454.1[P.abelii]            -----MASLGPR-----TPALSRSRGRRAMCWVSTI-----SFMAAEET 34

XP_03222077.1[N.vectensis]      KHPEFYMSIPAQSLVQ--DECHIHCGTVRKEN-----KYNMWQDRYLVLHKGCMYYKRY 91
XP_019631975.1[B.belcheri]      GVTEPHITISAQELLS-DGKAIFYGWLRRKKGNDVLSQRFMWKHRYVILKDGCVYYFKNE 109
XP_032800705.1[P.marinus]       DWPLPMRSVGAQSILTMPGGVAHSGYLHKKGGTQV---SFFAWPLRYVVLHAGCLYYKSS 64
XP_013984441.1[S.salar]         YWPVPMKAIGAQNLLTMPGGVCHSGYLHKKGGSQF---SLMKWPLRYVIIHRCGVYYFKSS 64
XP_041443552.1[X.laevis]        SWPTPMKAIGAQNLLTMPGGVAISGYLHKKGGTQL---QIMKWPLRFVIIHRCGVYYFKTS 64
XP_015141266.1[G.gallus]        WVPVPMKAIGAQNLLTMPGGVTKSGYLHKKGGTQL---QILKWPLRFVIIHEGCIYYFKTS 102
NP_001139330.1[M.musculus]      QWPVPMKAIGAQNLLTMPGGVAKAGYLHKKGGTQL---QLLKWPLRFVIIHKRCIYYFKSS 108
P78314[H.sapiens]               HWPVPMKAIGAQNLLTMPGGVAKAGYLHKKGGTQL---QLLKWPLRFVIIHKRCVYYFKSS 64
PNJ23454.1[P.abelii]            HWPVPMKAIGAQNLLTMPGGVAKAGYLHKKGGTQL---QLLKWPLRFVIIHKRCVYYFKSS 92
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XP_03222077.1[N.vectensis]      LDKSAKQFSLSGYRVS--TAPERAVKLPMVFKLTHLQPEKRTFFYPAKSEKEINEMWSK 149
XP_019631975.1[B.belcheri]      TSEKPCGAFSLSNYTKIMRAVDVETTELPMWFLVGRFPQMRTYFSAASNEQDMQHWMLN 169
XP_032800705.1[P.marinus]       TATIPRGSFSLRGYNRMRAAQETSMGNVYFVKLVHNNVRHRTWIFSAANEGERKWMMSA 124
XP_013984441.1[S.salar]         TSPAQGAFLSNGYNRMRAAEETTSNNVFPFKIVHFSKKHRTYCFSAANEERKWMRN 124
XP_041443552.1[X.laevis]        TSATSPQGAFLSNGYNRMRAAEETTSNNVFPFKVMHISKKHRTWFFSAASEERKWMMS 124
XP_015141266.1[G.gallus]        TSASPQGAFLSNGYNRMRAAEETTSNNVFPFKLVHISKKHRTWFFSASSEDERKWMMS 162
NP_001139330.1[M.musculus]      TSASPQGAFLSNGYNRMRAAEETTSNNVFPFKIIHISKKHRTWFFSASSEDERKWMMS 168
P78314[H.sapiens]               TSASPQGAFLSNGYNRMRAAEETTSNNVFPFKIIHISKKHRTWFFSASSEDERKWMMS 124
PNJ23454.1[P.abelii]            TSASPQGAFLSNGYNRMRAAEETTSNNVFPFKIIHISKKHRTWFFSASSEDERKWMMS 152
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XP_03222077.1[N.vectensis]      IKEDIYECEPLATSGFNPECEATRQSSSGSSDDGDSFKYDY----- 191
XP_019631975.1[B.belcheri]      MKNEMDAVNSSVQAGAGHGRGSNP-----EVIVDPDPAVGDDSLPPI-YQDTD-----EEE 219
XP_032800705.1[P.marinus]       IRSEIENYLRPQSNE--RRN-----SSSSDKFYEQVEMPLPLDSTWSSGSDQA 172
XP_013984441.1[S.salar]         LRKEIDHYNDRDRDSHI-PNDS-----ESDADSFYSGIECPMDITYAHDPPG---D 170
XP_041443552.1[X.laevis]        LRKEIDHYHEKKETVTDLSDP-----DSDSDSFYSGVERPVPINYNHNPAD---D 171
XP_015141266.1[G.gallus]        LRKEIDHYHDKKETVTTEFSDS-----GSDADSFYSGVERPIDIKYSHHSAD---N 209
NP_001139330.1[M.musculus]      LRREIGHFHEKKELPLDTSDS-----SSDTSFYGAVERPIDISLSSYFMD---N 215
P78314[H.sapiens]               LRREIGHFHEKKDLPLDTSDS-----SSDTSFYGAVERPVDISLSPYPTD---N 171
PNJ23454.1[P.abelii]            LRREIGHFHEKKDLPLDTSDS-----SSDTSFYGAVERPVDISLSPYPTD---N 199
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XP_03222077.1[N.vectensis]      -----PLFAPEFALAKALTLEKLSQSNNSSASSEPEYCPPPSFDTLFN-- 235
XP_019631975.1[B.belcheri]      HYYEDPEHLQEEEDYLQVLEDGPRVTPVGAAAG-DGVGA--FREMPLPTPTSK--M 272
XP_032800705.1[P.marinus]       DEYDEDSGDDDDGDYQLPDYDL--TTHLESGTG-GGLSPQPKQQQPPFPQLLASSPS 229
XP_013984441.1[S.salar]         NYMLEDEEDDEDDDYKPDSPF--TY-KGRLTVP-P-----PPSYHPPFLFCQFRQES 219
XP_041443552.1[X.laevis]        SY---EDDDDEDDDYVKPDGAD-E-----N-----APTYPFPVPFRNPRNGN 209
XP_015141266.1[G.gallus]        ED---YDQDEDDSYLQPDTS--IV-KDDFMV-L-----PPAYPPPPVPVHRKAAAY 254
NP_001139330.1[M.musculus]      ED---YEHEDEDDSYLEPDSPG--PMKLEDALT-Y-----PPAYPPPPVPVPRKPAF 261
P78314[H.sapiens]               ED---YEHEDEDDSYLEPDSPE--PGRLEDALM-H-----PPAYPPPPVPTPRKPAF 217
PNJ23454.1[P.abelii]            ED---YEHEDEDDSYMEPDSPE--PGRLEDALM-H-----PPAYPPPPVPTPRKPAF 245
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XP_03222077.1[N.vectensis]      -----GS-----PPPPPARN-QSGK-ERAQ-----PIGSVPTPVM 264
XP_019631975.1[B.belcheri]      ASPS-----KGWYQGEGAARPPVPLPKK--QSSFTKPLPATPQEGTRSPKKALVPPHMR 325
XP_032800705.1[P.marinus]       PSPANKFTATTATTKRPALMPKPPKPPFPQQFQ--QQQ-----QFQQQ 271
XP_013984441.1[S.salar]         S-----MSGCKLQCPAPVFNKTLSSFLPKKMSPLLR-----PKLG 256
XP_041443552.1[X.laevis]        D--SVKPRMTMSDVG-----LPYRPPPPPTPLIKTLPHLSDQARKE-----SAIHQG 254
XP_015141266.1[G.gallus]        S---E-SRSHSFGSKTAGSTPPPPPKR---SLPEIKTEDFFG-----VREPQ- 295
NP_001139330.1[M.musculus]      S---DLPRAHSFTSKSPSPLPPPPPKR---GLPDGTGSAPEDA-----KDAL- 302
P78314[H.sapiens]               S---DMPRAHSFTSKGPGPLPPPPPKH---GLPDVGLAAEDS-----KRDPL- 259
PNJ23454.1[P.abelii]            S---DMPRAHSFTSKGPGPLPPPPPKH---GLPDVGLAAEDS-----KRDPL- 287
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XP_03222077.1[N.vectensis]      GKSCKSSV-----DI-----SAVILGKAALK-----PV-----QDNLPLPL 296
XP_019631975.1[B.belcheri]      GVSTSPPHQTE-SKGKVPS-----GYFKRPIAGTA-----PPWK 347
XP_032800705.1[P.marinus]       QQQH--HHHQEL-----GYPKRPVIGTA----- 293
XP_013984441.1[S.salar]         E-VGHNHHGH---KDVPNKDSPEPSVRGPKAPHPTIASLQK---QMMMGKTSISTLP 307
XP_041443552.1[X.laevis]        FSCGPPPHKIEEFTPKLPHKKTSTFDLIGKEPPRRLEDIGSSDSVPGYDLGCTIKPPSP 314
XP_015141266.1[G.gallus]        LPCRAEP-----NLKIQSS-----SRKPS--EQ-----PP-PVPPPL 324
NP_001139330.1[M.musculus]      GLRRVEP-----GLRVPAT-----PRRMS--DP-----PMSNVPTVP 332
P78314[H.sapiens]               CPRRAEP-----CPRVPAT-----PRRMS--DP-----PLSTMTAP 289
PNJ23454.1[P.abelii]            CPRRAEP-----CPRVPAT-----PRRMS--DP-----PLSTMTAP 317

XP_03222077.1[N.vectensis]      KPR-----S 300
XP_019631975.1[B.belcheri]      ELKGGGVKKASEFINITSPGWTAGKTVGQRETGEGRGRDVKDEKKEKSGMARALAAEMTQ 407
XP_032800705.1[P.marinus]       ---IGQQQRSP-----PLPWAAVAASAASTTTTT-----TTATTTTT 328
XP_013984441.1[S.salar]         GG---DHRDKKP-----HAPVTLKSP-----ATLPICI 332
XP_041443552.1[X.laevis]        SLQLGARHVDPAPPVPVSPKNGSSCKPMTNPTQ-----LISNTVSKELTD 362
XP_015141266.1[G.gallus]        LFKKPFPCVKFPSSLPEL-----PL-----SHVLTTEGCE 355
NP_001139330.1[M.musculus]      NLRKHPCFRDSVNP--GLEPWTFGHGTSSVSSST-----TMAVATSRNCD 375
P78314[H.sapiens]               GLRKPPCFRESASP--SPEPWTFGHGACSTSSAA-----IMATATSRNCD 332
PNJ23454.1[P.abelii]            GLRKPPCFRESASPSPEPWTFGHGACSTSSAA-----IMATATSRNCD 362

XP_03222077.1[N.vectensis]      KLRQSPRVHA-GSHPPSSPSPTKPKPKSVHKYASDPDEL-----ACL PQ-- 342
XP_019631975.1[B.belcheri]      KFGSNWQAAGGTAKPRTPDKPVPAKPLGLHPK-----PGLAPKPG-- 447
XP_032800705.1[P.marinus]       NLERQMGMLNP-SP-----PGCHGNTPSHLPSVPNYCH-STRP-----TPDLPPQPS- 377
XP_013984441.1[S.salar]         KP-RMPVY-----PSPAPFSPFLSPVKVFKSSSSNAPPPPPVKKSIPTSTFPS 411
XP_041443552.1[X.laevis]        KL-KTLNLS-PT-----PLPSNKKLKSQITEKTVE---AKVPREH----- 393
XP_015141266.1[G.gallus]        KL-KSFHLS-SP-----E-----EPSPREA----- 414
NP_001139330.1[M.musculus]      KL-KSFHLS-SP-RGPPTSEPPVPVANKPKFLKIA-----E-----EDDPREA- 371
P78314[H.sapiens]               KL-KSFHLS-SP-RGPPTSEPPVPVANKPKFLKIA-----E-----EDDPREA- 401
PNJ23454.1[P.abelii]            KL-KSFHLS-SP-RGPPTSEPPVPVANKPKFLKIA-----E-----EDDPREA- 401

XP_03222077.1[N.vectensis]      -----QTSLPFANPALVDSSDSEDDYL-KILPDEESTPN-----HGNNDDEFIRLSTL 391
XP_019631975.1[B.belcheri]      -----TSPKPGIAPKPGHPSRQGMKPLVPPHKKQVEVQIGMEDRYEHEEEEEPEVDPGI 501
XP_032800705.1[P.marinus]       ---TARGKA-----LMPAAT-----TTTTTTKAPPRFL 354
XP_013984441.1[S.salar]         ALNHLGLPYKPLLTTKPPCP-----ATM-----PKRPRGSA 408
XP_041443552.1[X.laevis]        VTIASISPPVPPIKPRMLNDQKAERIPQKPPPIPR--QP-----GRKSESDDKLESPK 462
XP_015141266.1[G.gallus]        ---GKGLFVFPVPLPKPP-----VPGH-----QHS-----VLKPRPEKPSCPQL 429
NP_001139330.1[M.musculus]      ---AKF-APVPVPVAPRPP-----VQKMPMEATVRP-----AVLPRPENTPLPHL 455
P78314[H.sapiens]               ---AMPGLFVFPVAPRPP-----ALKLVPEAMARP-----AVLPRPEKPLPHL 413
PNJ23454.1[P.abelii]            ---AMPGLFVSPVAPRPP-----ALKLVPEAMARP-----AVLPRPEKPLPHL 443
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XP_03222077.1[N.vectensis]	ERLRPEGKSRFTPPDEKEQ-----IHIDVLPATSVKLDIE	426
XP_019631975.1[B.belcheri]	RRTPFEGNSFSKKNFNENPES-----ETDD-----VMP-----ADVSDVDVDE	539
XP_032800705.1[P.marinus]	SRPQPEGESEFHKLQID-----SDSDYIQPEDAMPSTIFLDTTSGDEAE	398
XP_013984441.1[S.salar]	QRSPPDGLSSQTSVDQVPASLRKNRDPISKYIDDDSDDE-DYENVQLPDSVFVDITETSVE	467
XP_041443552.1[X.laavis]	LRSPFDGQSFRLSTEGPAHP--IKPKRKLTRNDSDE-DYEKVLPLVSVFVDTNDSVEVE	519
XP_015141266.1[G.gallus]	QRSPPDQGSFRSFSFEKPPALP--SKPN--QVNDSDDE-DYEKVELPTSIFLNTSESLEVE	484
NP_001139330.1[M.musculus]	QRSPPDQGSFRGFSFEKARQP--SQAD--TGEEDSDE-DYEKVELPNSVVFVNTTESCEVE	510
P78314[H.sapiens]	QRSPPDQGSFRSFSFEKPRQP--SQAD--TGGDSDDE-DYEKVLPLNSVVFVNTTESCEVE	468
PNJ23454.1[P.abelii]	QRSPPDQGSFRSFSFEKPRQP--LPAD--TGGDSDDE-DYEKVLPLNSVVFVNTTESCEVE	498
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XP_03222077.1[N.vectensis]	RTKAIAM--LEGRNGMYILHKSRSGDIGQCLS--VCIEDRVRHFLVFYSKEEGGYALDRD	482
XP_019631975.1[B.belcheri]	K--AESCLRSQQVNGKYFLRPSKQDKGKMWLVVYDCAGQCKRKFMYGLGSQLYLH--KG	595
XP_032800705.1[P.marinus]	WRMENA----GLTHGLYCIRNSASSDQ-QVLVWVDGECRKLRFKIFRAGPLVSLDVSDG	453
XP_013984441.1[S.salar]	KMFMESS--SSPDGLYCFRNSASKTS-KVLVWVDVLCARNYRIFEEDSRVFLE---F	521
XP_041443552.1[X.laavis]	RIFKAASPGGTPQNGLYCIRNS-AKAG-KVLVWVDVLCARNYRIFEEDSKFYLE---A	574
XP_015141266.1[G.gallus]	RIFKATSPKGGTPQNGLYCIRNSSTKAG-KVLVWVDQSAEKVRNYRIFEKDSKYFLE---A	540
NP_001139330.1[M.musculus]	RLFKATDPRGEPQDGLYCIRNSSTKSG-KVLVWVDESSNKVRNYRIFEKDSKYFLE---G	566
P78314[H.sapiens]	RLFKATSPRGEPPQDGLYCIRNSSTKSG-KVLVWVDETSNKVRNYRIFEKDSKYFLE---G	524
PNJ23454.1[P.abelii]	RLFKATSPRGEPPQDGLYCIRNSSTKSG-KVLVWVDETSNKVRNYRIFEKDSKYFLE---G	554
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XP_03222077.1[N.vectensis]	AQRPFTELEVIRHHYTTPLPKQQSATLEQPYRWPH--	517
XP_019631975.1[B.belcheri]	APTFSSMSDLLRHYQHNLVPTDGVIEIRLTEPYQG--	631
XP_032800705.1[P.marinus]	APHFKLLSGLLDHYRVAPLPRQSSLRLTQPLVV---	486
XP_013984441.1[S.salar]	EMTFASLSALVEHYHSHPLPNHDSLLCQQPYRYIMPR	558
XP_041443552.1[X.laavis]	ELLFPDVESLVEHYHTNKLPSHSTLVLLQAHYGCSPFR	611
XP_015141266.1[G.gallus]	DIMFLNMGSLVEYYSTHVLPSHGSLLLRCPYGYGSKPR	577
NP_001139330.1[M.musculus]	EVLFSVSGSMVEHYHTHVLPSHQSLLLRHPYGYAGPR	603
P78314[H.sapiens]	EVLFSVSGSMVEHYHTHVLPSHQSLLLRHPYGYTGPR	561
PNJ23454.1[P.abelii]	EVLFSVSGSMVEHYHTHVLPSHQSLLLRHPYGYTGPR	591
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