

SH3BP5

Homo sapiens:

>sp|O60239|3BP5_HUMAN SH3 domain-binding protein 5 OS=Homo sapiens OX=9606 GN=SH3BP5 PE=1 SV=2
MDAALKRSRSEEPAEILPPARDEEEEEEEGMEQGLEEEEEVDPRIQGELEKLNQSTDDIN
RRETELEDARQKFRSVLVEATVKLDELVKKIGKAVEDSKPYWEARRVARQAQLEAQKATQ
DFQRATEVLRAAKETISLAEQRLLEDDKRFDSAWQEMLNHATQRMVEAEQTKTRSELVH
KETAARYNAAMGRMRQLEKKLKRAINKSKPYFELKAKYVYVQLEQLKKTVDLQAKLTLAK
GEYKMAKNLEMISDEIHERRRSSAMGPF**RGCGVCGAL**GSSTSVEDLPGSKPEPDAISVASE
AFEDDSCSNFVSEDDSETQSVSSFSSSGPTSPSEMPDQFFAVVRPGSLDLPSPVLSSEFGM
MFPVLGP**SEFCSGAG**SPCEVERGDRAGEAENKTSKANNNRGLSSSSSGSGSSKSQSST
SPEGQALENRMKQLSLQCSKGRDGIADIKMWQIG

Pongo abelii:

>XP_002814083.1 SH3 domain-binding protein 5 [Pongo abelii]
MDAALKRSRSEEPAEILPPARDEEEEEEEGMEQGLEEEEEVDPRIQGELEKLNQSTDDINRRETELEDAR
QKFRSVLVEATVKLDELVKKIGKAVEDSKPYWEARRVARQAQLEAQKATQDFQRATEVLRAAKETISLAE
QRLLEDDKRFDSAWQEMLNHATQRMVEAEQTKTRSELVHKETAARYNAAMGRMRQLEKKLKRAINKSKP
YFELKAKYVYVQLEQLKKTVDLQAKLTLAKGEYKMAKNLEMISDEIHERRRSSAMGPF**RGCGVCGAL**GSST
SVEDLPGSKPEPDAISVASEAFEDDSCSNFVSEDDSETQSVSSFSSSGPTSPSEMPDQFFAVVRPGSLDLPS
SPVLSSEFGMMFPVLGP**SEFCSGAG**SPCEVERGDRAGEAENKTSKANNNRGLSNSSGSGSSKSQSSI
SPEGQALENRMKQLSLQCSKGRDGIADIKMWQIG

Mus musculus:

>NP_036024.2 SH3 domain-binding protein 5 isoform 1 [Mus musculus]
MDTALKRSRSDPEAELPPPAREVEEKEEEEEERMEQGLEEEEEVDPRIQGELEKLNQSTDDINRRETELE
DARQKFRSVLVEATVKLDELAKKIGKAVEDSKPYWEARRVARQAQLEAQKATQDFQRATEVLRAAKETIS
LAEQRLLEDDKRFDSAWQEMLNHATQRMVEAEQTKTRSELVHKETAARYNAAMGRMRQLEKKLKRAINK
SKPYFELKAKYVYVQLEQLKKTVDLQAKLALAKGEYKAALKSLERISDEIHERRRSSAMGPF**RGCGVCGAL**
SLSAVENLFPVKPEPDALSVASEAFEDDNCNLVSEDDSETQSVSSFSSSGPTSPSEMPDQFFAVARFGSL
DLPSFVLSSEFGMMFPVLGP**SEFCSGAG**SPCEVERGDRAGEAENKMSDKANNNRVLGSTNGSGGRSRSQ
SSTSLESQALETRMKQLSLQCSKGRDGIADIKMWQIG

Gallus gallus:

>NP_001026160.3 SH3 domain-binding protein 5 [Gallus gallus]
MEPGRGRGARAEEAPREEEEVDPRIQGELEKLNQSTDVINRRETELEDARQKFRSVLVEATVKLDELVK
KIGKAVEDSKPYWEARRVARQAQLEAQKATQDFQRATEVLRAAKETISLAEQRLLEDDKRFDSAWQEM
LNHATQRMVEAEQTKTRSELVHKETAARYNAAMGRMRQLEKKLKRAINKSKPYFELKAKYVYVQLEQLKKT
VDLQAKLSLAKGEYKTALKNLEMISDEIHERRRSSAMGPF**RGCGVCGAL**GSNTSVEDLSTSKPELDAVSMAS
EVFEDDNGSSFVSEEDSETQSVSSFSSSGPTSPSEVPAPFFPATRPGTLDLPSPVLSSEFGAIFPILGP**RG**
FCSCGASSPCEAERGDRAEGAENKASDRVNKNRSSNRSGSTEGALDNRMKQLSLQCMKIKEGICAGRKA
AQIG

Xenopus laevis:

>XP_018122983.1 SH3 domain-binding protein 5 [Xenopus laevis]
METTLINNTGQQENEQLKEEEEEVDPRIQGELEKLNQSTDDINRREIELEDARQKFRSVLVEATLKLDE
MVKKIGKAVEDSKPYWEARKVARQAQLEAQKATQDFQRATEVLRAAKETISLAEQRLLEDDKRFDSAWQ
EMLNHATQRMVEEEQKTRSELHKEATAAKYNAAMGRMRQLEKKLKRTINKSKPYFELKAKYVYVQLEQLK
KTYVDLQAKLSLAKGEYKTALKNLEMISDEIHEKRRSSAMGPF**RGCGVCGAL**GSNNLEDLACKLSDSNISM
TSEVFDDNLSLVSSEDDSETQSMSSPSVPTSPAETPSFPFNVPFRGSLDLSSPLSLSDPGLISFILGP
RGSGSGASSPECDLERGNRAEGSENSAAQDRINNNSKNSNRKAMALPVLDNKIKQITLECTKTNGNTNER
KKCSRSQSLASTLLVNAV

Salmo salar:

>XP_014056350.2 SH3 domain-binding protein 5 [Salmo salar]
MDNLKENRSDSDSEYEEEEVDPRIQGELEKLNQSTDDINRCETQLEDARQKFRTVLVEATVKLDELVKK
IGKAVESKPYWEARRVARQAQLEAQKATQDFQRATEVLRAAKETIALAEQRLLEEDTRQFDSAWQEMLN
HATQRMVEAEHTKTRSELVHKETAAKYTAAMGRMRQLEKKLKRTINKSKPYFELKAKYVYVQLEHLKKNVD
ELQAKLSQAKEGYKTALRNLEVISDEIHERRRNSAMGPF**RGCGVCGAL**SDSASVDDISSFKMESDGISMTSE
SFEDETCSSAMSEEDSETRSTCSPQDLPSPCPSASSSSPAPSSSSPAPSSRRCSDLPSPVLSLDFGL
ISPVLGP**SEFCSGAG**SPECDLERGDRAGEGELDNTVNNNSTTVPNTNKTTGLEVRLSFLSLRRSRNDS
TNNTKRERQSRSQTPQTPTVVLINGL

Petromyzon marinus:

>Xp_032831288.1 SH3 domain-binding protein 5-like [Petromyzon marinus]
MYWTKMIKMMIMMMQVMTMMCLQVMKAEDQKGRSELVHKQTAERYSVTMVHMQLERKLLKRTIKKSRP
YIELKAKYVYLEHQKQVAEGLQEAVTATTKGQYRAALDSLERSDEIHARRKASAVEEP**RGSGVCGAL**ITG
AFSMELGFFSMGDGDSFVSADACESDACSLMAKSDDNVLES CSPAGGAVPPAPLPTRPALQLAASEPG
SGRSRSGSSGSGSRSSSGGADPDSGFFSPVQDERLGP**RGSGVCGAL**SPCEGLPLPTGAGSSLPSPSEAEA
EPAEKTAAETGREGFCVDSVTPRGEEEEEDGSDAASGASGTHTAIDGCVGGGERERDMRAARERQE
EEEDGADSGEATAKESGDGQVAEGEGRSVSGTDGGAAMHEASPEEPEAAAWAVRAEDLSVGGVVKLEQKDE
EVEDEGEVEKVEVEVEEVEDEEVDLQGDIDRGGEVAGAGFTAGALGASVRDVAL

Branchiostoma belcheri:

>KAI8492211.1 SH3 domain-binding protein 5 [Branchiostoma belcheri]
MSEQQGPETSSSGDEGLDPRIQEELERLNAASNEINKLEAELDEARALFRQTLTESTQKLNLSKKRMGKSV
QKARPYIDAKKMAKQVQAEQKAAVEYQRANGIHRAARETISLAEQRLFSDADEKRFDSAWQEMLNHAT
MKVMEAEQMRKSEHDHQKQAEAYNTANHKQLQLEKSLKKVIAKTKPYFDVKTSLFELQLLQKQKQNVEDLQ
KAVSASKVKYREALKNLESISDEIHRNRQLLKEPF**RGSGVCGAL**ADRDLDLPEINLDDVDCSQSYSLDDDGNS
LDDTSTDDASMIATDDASLSRRDRGGSFTHSSSSVGESVSSSSAVGAACSQDVVEKTAEGGCTNEGTA
TESGQAVEGGSYTEGTAPAVQAVEGGLTEKVTAGDGDKAEDSMVAGTVTCREEEQHRMEEIQMLTEGNS
QNTSQNADTTEIETDKTDKEDIDVHVQAEAVDDVEKSFEDVVEEGYKEDMSHNADVPTPVAIPGNVNAEE
VVEQQVPTPEVVAESESFPFLKNEGDRMTNPNVAVACDPSLKDEYKVSRECREVIEQKVGQDEVKFES
VVGSALENQEPKVAFEVDVVKETVEALEESQTAGSVTCGRNDEEDNAKREEGTEVRSVESQETSVPDTPVE
AVNSASIEVSNVSTEEKPPEIRQTDKSSSVKEIRGSDNS

Drosophila melanogaster:

>NP_611010.4 parcas [Drosophila melanogaster]
MSSAEDGELDPQIQIELENLSATDEINKLEIELEEANSTFRILLNESTRRLKVSSSKKLGNCIEKARPY
EALDKAREAQIECQKAAVKFQRANEIHAAAKETVALAEQRFMNSHEWQFDNAWQEMLNHATQKVMDAET
QKADCHAEHRLTKLFNAAEQKLQQLLEDRFRRSINKSRPYFEEKQVCQDLQTQKNRIQELQQQVAGAKS
TYSTALNLERISEDHHRQRGDFPTPPGP: **KEGVCS** LNSPTSSALPSLPDFQLELEKCDYPSIAGSQMS
LGAKTPQAAATEDEEDACDYDETGADELRGVVDERDLEALRQVKILAVRFIEGGDQQQNDVWEHELK
ATVDKLDHLMMLKETAKRQQTNRLKSTEQRPDSLGAELKRHCDVVEVKVTSCATTASLPVTFHHQLNHL
APPTPIKKLQQQLAPLPSVNVSMRELPLLARLSNELLDRSSAAGGVKRTLRRRSLE

Hydra vulgaris:

>XP_047136805.1 SH3 domain-binding protein 5-like isoform X1 [Hydra vulgaris]
MYDSLVLLEMISKENEARQKSKYNNVEENEEEEELDPRIKCELERLNAATDGINHLETEFGEAQALFQQLM
QDAAFNLKVMHQKLGKAVDKSRPYEALKCAKISHSELHEALKFEQAQTRHFNAKKLIVTDTERIVFSSST
DRKLDPALQEMLNQATVEVMEAAATQSQKAWEVHRNASVEFEKKNKVALDLYDSLKKHIVKSRPYFDLKSS
FNQQLDLQKTRLEKVQEGLVQSKNEYAKILHNLELISDDIHQSREMKRKCSEM**KEGVCS** SQSNNNVL
VYKDVEKQEEKNNSNLVLNQRDDNIGDKENLDKNLSQVSGQTELVNLGESLSQSSDLFLNQNDENIGCNE
NLGESLSQVSGPTLVKIRKQVQSLLETSAEQKSKNRLSQTERLINVNKTLIENCFDKSYDVITSHSIPF
SHPQEEFVDSSINIEYHNISKFLKKSFILPEFEIIPRRHTISGEKDSFQLLNHNKKLFCCKSSSALI

Nematostella vectensis:

>XP_001637874.3 SH3 domain-binding protein 5-like [Nematostella vectensis]
MSSLTLSTDDTKLSHKFSDDVDSEESLDPRVKGELERLNSATTEINCLEKALEEMHALFRQTLTESAFV
LKSHANRYGKSINQSRPYEALERSKKAQIATQKAALKYERACCTHQAAKEMVARAEKLVSTKEHKVL
DPTWQDMLNKAVMKVMESEQEKCHAEKEHLETAHLFTKAGKELQDLTKLTAINKSRVYFDLTKTKMDQ
LEAHKKKEVISLQGKLKVAKKDYMSLRKLEGISDETHEVRQSRISLCLPS**KEGVCS**CPGHQAQPSGRT
ARDWDEGMMVLPDGRCDDSDKSTTDTSTRGDTSESIPDAVCNDTSKPIPDGVCNDTSKSIIPDAVCNDTSK
SIPDAVCNDTSKSIIPDPVCNLDSEPKISTMDRASDVSPAGACNDTAESALDAVCGDLGELPSEGTIDD
FSEST

Amphimedon queenslandica:

No homolog found.

Alignment

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O60239[H.sapiens]          MDAALKRSRSEEPAEILPPARDEEE-----EEEEEMQGLEE-EEEVDPRIQGELEKL 52
XP_002814083.1[P.abeli]i  MDAALKRSRSEEPAEILLPPARDEEE-----EEEEEMQGLEE-EEEVDPRIQGELEKL 52
NP_036024.2[M.musculus]   MDTALKRSRSEDEPAELPPAREVEE-----KEEEEERMEQGLEEEEEVDPRIQGELEKL 55
NP_001026160.3[G.gallus]  -----MEPG-----GRRGRAAEAPRPEEEVDPRIQGELEKL 33
XP_018122983.1[X.laavis]  ME-----TILI-----KNTGQENEQLKEEEEEVDPRIQGELEKL 36
XP_014056350.2[S.salar]   -----MD-----NLEKENRSDEDSVEEEVDPRIQGELEKL 32
XP_032831288.1[P.marinus] -----0-----0 0
KAT8492211.1[B.belcher]i -----MSEQGQPETSSGDEGLDPRIQEELERL 27
NP_611010.4[D.melanogaster] -----MSSADEGLDPQIQIETLENL 20
XP_047136805.1[H.vulgaris] -----MYDSLVLLEMISKENEARQKSKYNNVNEEEEEELDPRIKCELERL 45
XP_001637874.3[N.vectensis] -----MSS-LTLSTD-----DTKLSHKFSDDVEDSEESLDPRVKGELERL 39

O60239[H.sapiens]          NQSTDDINRKRETELEDARQKFRSVLVEATVKLDELVKKIGKAVEDSKPYWEARRVARQAA 112
XP_002814083.1[P.abeli]i  NQSTDDINRKRETELEDARQKFRSVLVEATVKLDELVKKIGKAVEDSKPYWEARRVARQAA 112
NP_036024.2[M.musculus]   NQSTDDINRKRETELEDARQKFRSVLVEATVKLDELAKKIGKAVEDSKPYWEARRVARQAA 115
NP_001026160.3[G.gallus]  NQSTDVINRKRETELEDARQKFRSVLVEATVKLDELVKKIGKAVEDSKPYWEARRVARQAA 93
XP_018122983.1[X.laavis]  NQSTDDINRKRETELEDARQKFRSVLVEATVKLDEMVKKIGKAVEDSKPYWEARRVARQAA 96
XP_014056350.2[S.salar]   NQSTDDINRCETQLEDAARQKFRVTLVEATVKLDELVKKIGKAVEESKPYWEARRVARQAA 92
XP_032831288.1[P.marinus] -----0-----0 0
KAT8492211.1[B.belcher]i  NAASNEINKLEAELEDEARALFQRTLTESTQKILNLSKKMGKSVQKARPYDAKKMAKQAA 87
NP_611010.4[D.melanogaster] NSATDEINKLEIELEEA NSTFRILLNESTRRLKLVSSKKLGNCIEKARPYEALDKAKAEAA 80
XP_047136805.1[H.vulgaris] NAATDGINHLETEFGEAQALFQQLMQDAAFNLKVMHQKLGKAVDSKSRPYEALKCAKISH 105
XP_001637874.3[N.vectensis] NSATTINCLEKALEEMHALFRQTLTESAFVLNKSHPANRQKSIQSRPYEALERSKKAQ 99

O60239[H.sapiens]          LEAQKATQDFORATEVLRAAKETISLAEQRLL--DDKRQFDSAWQEMLNHATQRMVEAE 170
XP_002814083.1[P.abeli]i  LEAQKATQDFORATEVLRAAKETISLAEQRLL--DDKRQFDSAWQEMLNHATQRMVEAE 170
NP_036024.2[M.musculus]   LEAQKATQDFORATEVLRAAKETISLAEQRLL--DDKRQFDSAWQEMLNHATQRMVEAE 173
NP_001026160.3[G.gallus]  LEAQKATQDFORATEVLRAAKETISLAEQRLL--DDKRQFDSAWQEMLNHATQRMVEAE 151
XP_018122983.1[X.laavis]  LEAQKATQDFORATEVLRAAKETISLAEQRLL--DDKRQFDSAWQEMLNHATQRMVEAE 154
XP_014056350.2[S.salar]   LEAQKATQDFORATEVLRAAKETIALAEQRLL--EDTRQFDSAWQEMLNHATQRMVEAE 150
XP_032831288.1[P.marinus] -----MMVTMKIMMMIMMMVMVMMLQVMKAE 30
KAT8492211.1[B.belcher]i  VEAQKAAYEQRANGIHRARETISLAEQRLLFSDADEKQFDSAWQEMLNHATQRMVEAE 147
NP_611010.4[D.melanogaster] IECQKAAYKFORANEIHAAAKETVALAEQRFSNSH-EWQFDNAWQEMLNHATQRMVDAE 139
XP_047136805.1[H.vulgaris] SELHEAALKFEQAQTRHFNAKKLVTDTERIVFS--STDRKLDPALQEMLNATQVMEAA 163
XP_001637874.3[N.vectensis] IATQKAALKYERACCTHQAAKEMVARAEKLVSTSEKHKVLDPTWQDMLNKAVMKMESE 159
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O60239[H.sapiens]          QTKTRSELVHKETAARYNAAMGRMRQLEKKLKRAINKSKPYFELKAKYVVQLEQLKKTVD 230
XP_002814083.1[P.abeli]i  QTKTRSELVHKETAARYNAAMGRMRQLEKKLKRAINKSKPYFELKAKYVVQLEQLKKTVD 230
NP_036024.2[M.musculus]   QTKTRSELVHKETAARYNAAMGRMRQLEKKLKRAINKSKPYFELKAKYVVQLEQLKKTVD 233
NP_001026160.3[G.gallus]  QTKTRSELVHKETAARYNAAMGRMRQLEKKLKRAINKSKPYFELKAKYVVQLEQLKKTVD 211
XP_018122983.1[X.laavis]  QKTKRSELLHKETAARYNAAMGRMRQLEKKLKRTINKSKPYFELKAKYVVQLEQLKKTVD 214
XP_014056350.2[S.salar]   HTKTRSELVHKETAARYNAAMGRMRQLEKKLKRTINKSKPYFELKAKYVVQLEHLKKNVD 210
XP_032831288.1[P.marinus]  QDKGRSELVHKQTAERYSVTMVHMNQLEKRLKRTIKKSRPYELKAKYVLELEHQKQVRE 90
KAT8492211.1[B.belcher]i  QMRKSSEHDHQKAAEYNTANHKLQLEKLSKKVIKTKTPYFDVKTSFELQLLQKQNVRE 207
NP_611010.4[D.melanogaster] TQKADCHAEHQRLTKLFNAAEQKLQLEEDFRFRSINKSRPYFEKQVCQDQLQTKQNRQI 199
XP_047136805.1[H.vulgaris] TQSQKAWVEHNRNASVEFEKKNKVALDLYDSLLKXHVKSRYFDLKSFFNQQLDLQKTRLE 223
XP_001637874.3[N.vectensis] QEKCHAEKEHLETAHLFTKAGKELQDLTKTKLTAINKSRVYFDLTKTYMDQLEAHKKEVI 219
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O60239[H.sapiens]          DLQAKLTLAKGEYKMAKNLEMISDEIHERRRSS---AMGPRCCGVGAEGSSTSVE---D 284
XP_002814083.1[P.abeli]i  DLQAKLTLAKGEYKMAKNLEMISDEIHERRRSS---AMGPRCCGVGAEGSSTSVE---D 284
NP_036024.2[M.musculus]   DLQAKLALAKGEYKAALKSLERISDEIHERRRSN---AMGPRCCGVGAEGSIAVS---N 287
NP_001026160.3[G.gallus]  DLQAKLSLAKGEYKALKNLEMISDEIHERRRSA---AMGPRCCGVGAEGSNTSVE---D 265
XP_018122983.1[X.laavis]  DLQAKLSLAKGEYKALKNLEMISDEIHEKRRTS---SMGPRCCGVGAEGSNN--SLE---D 267
XP_014056350.2[S.salar]   ELQAKLSQAKGEYKALTALNLEVISDEIHERRRSN---AMGPRCCGVGAEGSDASVD---D 264
XP_032831288.1[P.marinus]  GLQEAVTATKGQYRAALDSLERISDEIHARRKA---SAVEPRCCGVGAETTTGAFSM---E 145
KAT8492211.1[B.belcher]i  DLQKAVASAKVRYREALKNLESISDEIHRFRQ-L---LKEPRAGVGAADADRDLP---E 262
NP_611010.4[D.melanogaster] ELQGVVAGAKSTYSTALTALNLERISDEIHRQGD-FPTTPGPRVGAALNSPTSSALPS 258
XP_047136805.1[H.vulgaris] KVQEGLVQSKNEYAKILHNLELISDDIHQSRMRKRVCSSEMG-EGVAVSSQSNNVLYVK 283
XP_001637874.3[N.vectensis] SLQGLKVAKKYDYSMLRKLLEGISDEIHEVRQSRISLCLPS-ELSGVGA-SCPHQAP---S 276
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O60239[H.sapiens]          LPGSKPEP-----DAISVASEAFEDDSCSNF---VSEDDSET---QSVSSFSSGP 328
XP_002814083.1[P.abeli]i  LPGSKPEP-----DAISVASEAFEDDSCSNF---VSEDDSET---QSVSSFSSGP 328
NP_036024.2[M.musculus]   LPVSKPEP-----DAISVASEAFEDDSCSNL---VSEDDSET---QSVSSFSSGP 331
NP_001026160.3[G.gallus]  LSTSKPEL-----DAVSMASEVFEDDNGSSF---VSEDDSET---QSVSSFSSGP 309
XP_018122983.1[X.laavis]  LSACKLDS-----DNISMTSEVFDDNLSL---VSEDDSET---QSMSSFSSGP 311
XP_014056350.2[S.salar]   ISSFKMES-----DGISMTSESFEDTCCSS---AMSEEDSET---RSTCSPQDLP 309
XP_032831288.1[P.marinus]  LGFFSMDG-----DSFSVASDACESDACSLM---ASKDDNYLES CSPAGAVP 191
KAT8492211.1[B.belcher]i  INLDDVDS--CSQY--SDLDDGNSLDTSTD TDDA-SMI---AQTDASLRDRRDRGFTSHS 314
NP_611010.4[D.melanogaster] LPDPQLELEKCDY-P-SIAGSQMSLGAKT--PQAA---AEETDE---EDACDYD--- 302
XP_047136805.1[H.vulgaris] DVEKQEEKNNMNLNLRQDDNIG--DKNELDNLSQ---VSGQTFLV--- 325
XP_001637874.3[N.vectensis] EGRGARDW-----D--EDGMMVLPGDRCDSDSKSTTDSRGDTSESIPDAVCNDTSKP 327
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O60239[H.sapiens]          -T-----SPSEM-----PDQFPVAVRPGSLDLPSPV-----SLSEFG 359
XP_002814083.1[P.abeli]i  -T-----SPSEM-----PDQFPVAVRPGSLDLPSPV-----SLSEFG 359
NP_036024.2[M.musculus]   -T-----SPSEM-----PDQFPVAVRPGSLDLPSPV-----SLSEFG 362
NP_001026160.3[G.gallus]  -T-----SPSEV-----PAPFPVATRPGLTDLPSPV-----SLSEFG 340
XP_018122983.1[X.laavis]  -T-----SPAEL-----PSFPVNVRRPGSLDLSSPL-----SLSDFG 342
XP_014056350.2[S.salar]   -SPCPSASSSSPAPSSS-----S-SAPASSRPPCSLDLPSPV-----SLSDFG 349
XP_032831288.1[P.marinus]  PAPLPTR-----P-----PALQLAASEFGSGRSRSGSSSGSGRSRSGSGADPDSG 236
KAT8492211.1[B.belcher]i  -S-----SVGES-----VSSSSAVGAACSQDVVEKT-----A----- 340
NP_611010.4[D.melanogaster] -----NLGES-----LSQSSDL----- 302
XP_047136805.1[H.vulgaris] -----NLGES-----LSQSSDL----- 337
XP_001637874.3[N.vectensis] -IPDGVCDNDSKSI PDAVCNDTSKSI PDAVCDDTSKSI PDVPC-----DNLDESPKISTMD 382

O60239[H.sapiens]          MMFP-----VLGP-SEC-SGAS-----SPECEVERGDRAEGAENKTSIDKAN----- 399
XP_002814083.1[P.abeli]i  MMFP-----VLGP-SEC-SGAS-----SPECEVERGDRAEGAENKTSIDKAN----- 399
NP_036024.2[M.musculus]   MMFP-----ILGP-SEC-SGAS-----SPECEVERGDRAEGAENKMSIDKAN----- 402
NP_001026160.3[G.gallus]  AIFP-----ILGP-SEC-SGAS-----SPECEVERGDRAEGAENKASIDRVN----- 380
XP_018122983.1[X.laavis]  LISP-----ILGP-SEC-SGAS-----SPECDLERGDRAEGAEGELDNVTN----- 389
XP_014056350.2[S.salar]   LISP-----VLGP-SEC-SGAS-----SPECDLERGDRAEGAEGELDNVTN----- 389
XP_032831288.1[P.marinus]  FFSVPVDERLGP-SEC-SGAS-----SPECEGLPPLTGAGSLPPSEAEAEPAEKTRAETG 292
KAT8492211.1[B.belcher]i  -----EGGCTNEGTA-TESGQAVEGGSYTGTAFAVQAVE----- 374
NP_611010.4[D.melanogaster] -----ETGAGELRGVVDERDLEALRQKVK----- 326
XP_047136805.1[H.vulgaris] -FLN-----QNDENIGCNENLGESLSQVSGPT-----ELVKIRKQVQ----- 373
XP_001637874.3[N.vectensis] RASD-----VSPSAGACNDTAESALDAVCGDLGELPSEGTIDDFSEST----- 425

O60239[H.sapiens]          -NNRGLSSSSSGSGSSKSSQSSSTSPG-----QALENRMKQLSLQCSKGRDGI--IAD--- 448
XP_002814083.1[P.abeli]i  -NNRGLSSSSSGSGSSKSSQSSSTSPG-----QALENRMKQLSLQCSKGRDGI--IAD--- 448
NP_036024.2[M.musculus]   -NNRVLGSTNGSGSGRSRQSSSTLES-----QALETRMKQLSLQCSKGRDGI--IAD--- 451
NP_001026160.3[G.gallus]  -KNRSSNR-----SGSTEG-----LALDNRMKQLSLQCSKMKIKEGI--CAG--- 417
XP_018122983.1[X.laavis]  -NNSKSN-----RKAMAL-----PVLDNKIKQITLECTKTGNGT--NTE--- 419
XP_014056350.2[S.salar]   -NNSTTVPTNK-----T-----TGLEVRLSFSLRRSRNDSTN--NTK--- 425
XP_032831288.1[P.marinus]  REGFCVDVTPRGEEDGSDAAASGA-----SGT-----HTAI-ADGG-----VGGGE 336
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KAI8492211.1[B.belcheri]	--GG-LTEKVTAGDGDKAED-SMVVAGTVTCREEEQHRMEEIQMLTEGNSQNTSQNADTTE	431
NP_611010.4[D.melanogaster]	--ILAVRPiEGGDGQQQNDVWE---HEL---KATVDKLDHMLMKETAKRQQTNRLKSTE	378
XP_047136805.1[H.vulgaris]	-SL-L-----ET--SAEQKSKNRLSQTERLINVNKTLIENCDF---	407
XP_001637874.3[N.vectensis]	-----	425
O60239[H.sapiens]	IKM----VQIG-----	455
XP_002814083.1[P.abelii]	IKM----VQIG-----	455
NP_036024.2[M.musculus]	IKM----VQIG-----	458
NP_001026160.3[G.gallus]	RKA----AQIG-----	424
XP_018122983.1[X.laavis]	RKK----CSRS-QSLA-----S-T-LLVNA	437
XP_014056350.2[S.salar]	RER----QSRG-QTPT-----QT-V-VLING	444
XP_032831288.1[P.marinus]	RERDMRAAERRE-QEEDDGADSGEATKESGDGQVAEGEGRSVSG-----TDG	384
KAI8492211.1[B.belcheri]	IETDKTKEDID-VHVQGEAVDDVEKSF---EDVVEEGYKEDMSHNDVPT-P-VAIPG	484
NP_611010.4[D.melanogaster]	QRP-----DSLQ-AEALKRHC-----DVVEVKVTS-CATTASLPVTPHHQLNH	419
XP_047136805.1[H.vulgaris]	KSYDVITSHSIPFSPQEEFVDSSINEY---HN-----ISK	440
XP_001637874.3[N.vectensis]	-----	425
O60239[H.sapiens]	-----	455
XP_002814083.1[P.abelii]	-----	455
NP_036024.2[M.musculus]	-----	458
NP_001026160.3[G.gallus]	-----	424
XP_018122983.1[X.laavis]	V-----	438
XP_014056350.2[S.salar]	L-----	445
XP_032831288.1[P.marinus]	GAAMHFAEPREE---PAAA-----WAVRAEDLSVGGV	413
KAI8492211.1[B.belcheri]	NNVAEE-VVEQQQVTPTTEVKAESFPTLKNEGDRTNMPNVAACDPSLKDE-VKVSEC	542
NP_611010.4[D.melanogaster]	LAPPTPIKKLQQQLAPLPSVNVSMRELPLLARLSN-----ELDRSSAAFQGV	467
XP_047136805.1[H.vulgaris]	FLKKSPILEFEFIIIPRHTISGEKDSFQLLNHNKK-----LFCKSS-----	481
XP_001637874.3[N.vectensis]	-----	425
O60239[H.sapiens]	-----	455
XP_002814083.1[P.abelii]	-----	455
NP_036024.2[M.musculus]	-----	458
NP_001026160.3[G.gallus]	-----	424
XP_018122983.1[X.laavis]	-----	438
XP_014056350.2[S.salar]	-----	445
XP_032831288.1[P.marinus]	KLEQKDEEVEDEGEVE-----KVEVEE-VEEDEEVDLQGDIGDRGGE	455
KAI8492211.1[B.belcheri]	REEVIEQKVGQDEVKFESTEGSALENQEPKAFEDVVVKETVEAIEESQTAGSVTGRNDE	602
NP_611010.4[D.melanogaster]	RKTLRRRS-----LE-----	477
XP_047136805.1[H.vulgaris]	-SALI-----	485
XP_001637874.3[N.vectensis]	-----	425
O60239[H.sapiens]	-----	455
XP_002814083.1[P.abelii]	-----	455
NP_036024.2[M.musculus]	-----	458
NP_001026160.3[G.gallus]	-----	424
XP_018122983.1[X.laavis]	-----	438
XP_014056350.2[S.salar]	-----	445
XP_032831288.1[P.marinus]	GVAGAGFTAGALGASVRDVAL-----	476
KAI8492211.1[B.belcheri]	EDN----AKREEGTEVRSVESQETSVPDTPVEAVSNASIEEVSNTSTEEKPPEIRQTDKS	658
NP_611010.4[D.melanogaster]	-----	477
XP_047136805.1[H.vulgaris]	-----	485
XP_001637874.3[N.vectensis]	-----	425
O60239[H.sapiens]	-----	455
XP_002814083.1[P.abelii]	-----	455
NP_036024.2[M.musculus]	-----	458
NP_001026160.3[G.gallus]	-----	424
XP_018122983.1[X.laavis]	-----	438
XP_014056350.2[S.salar]	-----	445
XP_032831288.1[P.marinus]	-----	476
KAI8492211.1[B.belcheri]	SSVEKIRGRNDS-----	670
NP_611010.4[D.melanogaster]	-----	477
XP_047136805.1[H.vulgaris]	-----	485
XP_001637874.3[N.vectensis]	-----	425