

Striatin

Homo sapiens:

>sp|O43815|STRN_HUMAN Striatin OS=Homo sapiens OX=9606 GN=STRN PE=1 SV=4
MDEQAGPGVFFSNHHFGAGGAKGLGPLAEAAAAAGDGAAGAAQAQYSLPGILHFLQHEW
ARFEVERAQWEVERAELQAQIAFLQGERKQGENLKDDLVRRIKMLEYALKQERAKYHKLK
YGTELNQGDMKPPSYDSDEGNETEVPQQNSQLMMWQGRQLLRQYLQEVGYTDTILDVKS
KRVRALLGFSSDVTDRDDKNQDSVNGTEAEVKETAMIAKSELTDSASVLDNFKFLESA
AADFSDDEDDDDVDGREKSVIDTSTIVRKKALPDSGEDRDTKEALKEFDLVTSEEGDNE
SAGDGCTGWEKEDQCLMPEAWNVDQGVITKLKEQYKKERKGGKVKRPNRSKLQDMLAN
LRDVELPQLPSVSGSPSRPSSSRLPEHEINRADEV EALTFFPSSGSKSFIMGADAEALESE
LGLGELAGLTVANEADSLTYDIANNKDALRKTWNPKFTLRSHFDGIRALAFHPIEPVLIT
ASDHTLKMWNLQKTAPAKKSTSLDVEPIYTFRAHKGPVLCVVMSSNGEQCYSGGTGDLI
QGWNTTNPNIIDPYDSYDPSVLRGAFVGHGTDAAVWGLAYSAAHQRLSCSADGTLRLWNTTE
VAPALSVFNDTKELGIPASVDLVSSDP SHVASFSKGYTISFNMETQQRILTLESNVDTT
ANSSCQINRVISHPTLPISITAHEDRHIKFYDNNNTGKLIHSMVAHLEAVTSLAVDPNGLY
LMSGSHDCSIRLWNLESKTCIQEFTAHRKKFEESIHDVAFHPSKCYIASAGADALAKVFV

Pongo abelii:

>XP_002812184.3 striatin isoform X1 [Pongo abelii]
MDEQAGPGVFFSNHHFGAGGAKGLGPLAEAAAAAGDGAAGAAQAQYSLPGILHFLQHEWARFEVERAQW
EVERAEILQAQIAFLQGERKQGENLKDDLVRRIKMLEYALKQERAKYHKLKYGTELNQGDMKPPSYDSDEG
NETEVPQQNSQLMMWQGRQLLRQYLQEVGYTDTILDVKSKVRALLGFSSDVTDRDDKNQDSVNGTE
AEVKETAMIGKSELTDSASVLDNFKFLESAADFSDEDEDDDDVDGREKSVIDTSTIVRKKALPDSGEDRD
TKEALKEFDLVTSEEGDNE**SAGDGCTG**WEKEDQCLMPEAWNVDQGVITKLKEQYKKERKGGKVKRPN
RSKLQDMLANLRDVELPQLPSVSGSPSRPSSSRLPEHEINRADEV EALTFFPSSGSKSFIMGADAEALESE
LGLGELAGLTVANEADSLTYDIANNKDALRKTWNPKFTLRSHFDGIRALAFHPIEPVLITASEDHTLKMW
NLQKTAPAKKSTSLDVEPIYTFRAHKGPVLCVVMSSNGEQCYSGGTGDLIQGWNTTNPNIIDPYDSYDPSV
LRGPELLGHGTDAAVWGLAYSAAHQRLSCSADGTLRLWNTTEVAPALSVFNDTKELGIPASVDLVSSDP SHM
VASFSKGYTISFNMETQQRILTLESNVDTTANSSCQINRVISHPTLPISITAHEDRHIKFYDNNNTGKLIH
SMVAHLEAVTSLAVDPNGLYLMSGSHDCSIRLWNLESKTCIQEFTAHRKKFEESIHDVAFHPSKCYIASA
GADALAKVFV

Mus musculus:

>NP_035630.2 striatin [Mus musculus]
MDEQAGPGVFFSNHHFGAGGAKGLGPLAEAAAAAGDGAAGAAQAQYSLPGILHFLQHEWARFEVERAQW
EVERAEILQAQIAFLQGERKQGENLKDDLVRRIKMLEYALKQERAKYHKLKYGTELNQGDMKPPSYDSDEG
NETEVPQQNSQLMMWQGRQLLRQYLQEVGYTDTILDVKSKVRALLGFSSDVTDRDDKNQDSVINGTE
AEVKETAMIGKSELTDSASVLDNFKFLESAADFSDEDEDDTDGRAKSVIDTSTIVRKKALPDTSEDRD
TKEALKEFDLVTSEEGDNE**SAGDGCTG**WEKEDQCLTPEAWNVDQGVISKLKEQYKKERKGGKVKRPN
RSKLQDMLANLRDVELPQLPSVSGSPSRPSSSRLPEQELSRADDEV EALTFFPSSGSKSFIMGADAEALESE
LGLGELAGLTVANEADSLAYDIANNKDALRKTWNPKFTLRSHFDGIRALAFHPIEPVLITASEDHTLKMW
NLQKTAPAKKSTSLDVEPIYTFRAHKGPVLCVVMSSNGEQCYSGGTGGRIQSWSTTNPNDVPYDAYDPSV
LRGPELLGHGTDAAVWGLAYSAAHQRLSCSADGTLRLWNTTEVAPALSVFNDNQELGIPASVDLVSSDP SHM
VASFSKGYTISFNMETQQRVLTLESNVDTSSSSCQINRVISHPTLPISITAHEDRHIKFYDNNNTGKLIH
SMVAHLEAVTSLAVDPNGLYLMSGSHDCSIRLWNLESKTCIQEFTAHRKKFEESIHDVAFHPSKCYIASA
GADALAKVFV

Gallus gallus:

>XP_040524727.1 striatin isoform X3 [Gallus gallus]
MDEQAGPGVFFSNNNNNALLPPTTGGPGLEPGEAAAAAAGGGGGGVSAGGAAAPVSASRAQYSV
PGILHFLQHEWRFEAERAWEAERAELQAQIAFLQGERKQGENLKDDLVRRIKMLEYALKQERAKYHKLK
KYGTLELNQGDMKPPNYDSDEGNETEIQPQNSQLIWQGRQLLRQYLQEVGYTDTILDVKSKQVRALLGL
SDSAEKENRNQPEMVNGTEGQIKENAMIGKPELTDSASLLETFFKFLENAAADFSDEEDEDEIEGREKTI
IDTATIVRKRVLSDSSEDRDT EALKEFDLVTSDSEGDES**SAGDGCTG**WEKEDQCLMPEAWNVDQGVIT
KLKEQYKKERKGGKVKRPNRSKLQDMLANLRDVEDDLPSLQPSVAPSSRPSSSRLIEHEINRTDEV EALT
FFPSSGSKSFIMGTDETLENELGGLGELAGLTVANEADSLTYDIGNNTDALRKTWNPKFTLRSHFDGIRGLA
FHIPIEPVLITASEDHTLKMWNLQKTAPAKKSASLDVEPIYTFRAHSGPVLCVVMSSNGEQCYSGGTGDLI
HGWNNTNPNIIDPYDSYDPSVLRGAFVGHGTDAAVWGLVYSGTHQRLLSCSADGTVRLWKATEVAPALNVFND
NQEMGIPSSVDLVSSDP SLMVASFNTGHTSIFNMETRQQRILTLESQVDNTVSTSCQINRVISHPTLPISI
TAHEDRHIKFYDNNNTGKLIHSMVAHLDAVTS LAVDPNGLYLMSGSHDCSIRLWNLESKTCIQEFTAHRKK
FDESIHDVAFHPSKCYIASAGADALAKVFV

Xenopus laevis:

>XP_041418671.1 striatin isoform X1 [Xenopus laevis]
MDEQAGPGVFFNNNNNSLLSAGTGCGGAGKGFEAGAADAASVAGGGGGGSAGRAQYQSIIPGILHFLQHEWA
RFEVERAQWEVERAEMQAQIAFLQGERKQGENLKDDLVRRIKMLEYALKQERAKYHKLKYGTELNQGDMK
PPNYDSDEANENIEIQPQNSQFTWKQSRQLLRQYLQEVGYTDTILDVKSKVRSLGLSADSDRLTDT
NPDMSVNGTETELPNPLVLGKPDMTDSASVLETFFKFLENAAAEFSDEDEEENESRKDTIIDSATIVRRR
IITDPSNDTTEALKEFDLFGSDDEGGES**SAGDGCTG**WEKEDQCCPITESWNVDQGVITKLKEQYKKERK
GKVKRPNRSKLQDMLANLRDEVDELPSLQPSVSVSSRPASSRSISEQEINRADEV EALTFFPSSGSKSFIMG
ADAEALENELGLGELAGLTVANEADSLTYDIANNKDALRKTWNPKFTLRSHFDGIRGLAFHPSPEVLITAS
EDHTLKMWNLQKTAPAKKSTSLDIEPIYTFRAHRGFPVLCVVMSTNGEQCYSGGTGCVISWNTPNNSNDP
YDSYDPTVLRGAYEGHGTDAVWGLVYSAVHQRLLSAAADGTRIWNATEVSPALSFNENQELGIPSSVDL
VSCDPAHLVASFNGGHTNIFNMETQKVLTLESCIDTAVNSTCQINRVISHPTLPISITAHEDRHIKFYD
NNTGKLIHSMVAHLDAVTS LAVDPNGLYLMSGSHDCSIRLWNLESKTCIQEFTAHRKKSDESIHDVAFHPS
SKCYIASAGADALAKVFV

Salmo salar:

>XP_045558221.1 striatin-like isoform X1 [Salmo salar]
MDEQAGPGVFFNNNNNSILAGGKVVLLPEGDAGEAARAPYSIPGILHFLQHEWARFEVERAQWEVQRAELQ
AQIAFLQGERKQGENLKDDLVRRIKMLEYALKQERAKYHKLKYGTELNQGDMKPPSYDSDEVNENETTGS
LNQLSWKQGRQLLRQYLQEVGYTDTILDVKSQRVKTLLAMAGDGGGRPGERTGSSETPLVNGTDTVPKGT
GTGGRKTEVSSSAVLDTFRFYCDDEDDDGAGLDRTIMEQTGTCGTVRKKPSSSSPALSLSMDTSED
FDABDALKGFDPLSSPDMMDTSPES**SAGDGCTG**WEKEEQSAMSEAWVDQGLITKLKEYEKKERKGGK
KRNKRSKLQDMLANLRQDEMSPREPSSSPQASNAPRNLNEHQQDNRTDEV EALTFFPSSGKAFIMGDE
NMEAEGLGELAGLTVANEADSLAYDMSNNKDALRKTWNPKFTLRSHFDGIRGLAFHPIEPVLITAS
EDHTLKMWNLQKTAPAKKSASVDEMPMYTFRAHQGAVLCVVMSTGEQCFSGGVDGTIQSWNTPNPNLIDPYDS
YEPYTVLRGALCGHTDLVWGLVYSGVHQRLLSGSGDGTVRLMDASNTKPALATFQNKEGFVSPSSVDLVCS
PAHMTVSTSGQIGLFNMETQQLVLVLSESAETGTGTCQINKVLSHPTLPITITAEEDRHIKFFDNNNTGKLI
HSMVAHLDAVTS LAVDPNGLYLMSGSHDCSIRLWNLETKTCIQEFTAHRKKNDESIHDVAFHPSKAYIA
SAGADALAKVFV

Petromyzon marinus:

>XP_032803414.1 striatin-3-like isoform X1 [Petromyzon marinus]
MDEHPALQVGS PGLKQLQQPSSGGSGQQQQQQQQQLLQQQLQMHQQQGGEGGESGRPHYSMPGILH
YIQHEWARFEMERASWDMERAELQARIAFLQGERKQENLKDDLVRRIKMLEYALKQERAKYHKLYGTE
LNQGDMPKPTTFDAEETNDTDTFPVVTSNSQLTWRQGRQLLRQYLQEVGYTDTILDVRSQRVRSLLGLSGPFP
DQNGAPDAKNIEQILNGRDIMSILKPEDDAKRRNGDKSRSEPLVPSVVDTFQFLQEEEDSDGDEDDDDDE
SVGLVDERFRASAKKAKIGNEGLAADLADDPDTEELAKEFDLFLVTTEDEGAGEAASGSDGQVWDKEEL
SPSGEEDWIDHGLTKLKEQYKKEKRNKKQAKRPNRSALQOMLANREVDBELSPLAASSPFRQPEEARAP
LPHDNARSDEGESPFPRGTGKMPISGPEEAMDTTGLGELADLTVTNDA DSPSYDIGANKDAFRKKTWNKPF
TLRSHFDGVRALAFHPSHEHVLVTASEDHTLKLWNLQKTI SGKKTASLDVEPIYTFRAHTGPVLSLAISTS
GEQCFSGGTDASIRCNWNPSPNIDPYDTFEASVLGQTLHGSDAVWGLAYSSLRRLSCSADGTVRLWD
PSCQDSPCLNTYNPDKEHGIPVSVDFVSDASHLVATFGGGDTLVFDMETAKPVITLESRIETDTPGLNQ
INRVVSHPTLPITVTAHEDRHIKFFDNNTGKQVHSMVAHLDAVTCCLAVDPNGLYILMSGSHDCSIRLWNLE
SKTCVQEITAHRRKKFDEA IHDVAFHPSKAFIASAGADALAKVFV

Branchiostoma belcheri:

>XP_019631056.1 PREDICTED: striatin-3-like [Branchiostoma belcheri]
MDGSTGNPHAVPGSNQPGMI PNKPQTLQDEQSQOTKYISIPGILHFIQHEWARFEMERAHWEVERAELQ
ARIAFLQGERKQENLKRDLVRIKMLEYALKQERAKYHKLYGTELNQGEMRPPTPPSDEERETDSPLS
QNSQVTWRQGRQLLRQYLQEIGYSDTILDVRSNRVRTLLGLTPNESTKQDGEAGEVLVNGQEEREARRDA
DRRPVEKKRAGIPEIDSEASVLATFDLFSSEAVDDEDEENLSDGEEDGGAADDESEEREQRRRRKEGKKA
LVQMENESLAGMEDVLADPETEEALAEFDLVSSEAGEGAGEAKSTDGAEWGLDKSPTEEWAMDKNLLN
KLKEEFFKKERKSKKGAKRPNRSTLQAMLANLGDDDIVMPASGPPRSAINNPDLGPLDEPRKEGGPEEQV
LGVGPFEESELEAALGLGDLAGLTVTNEAEPLQYDVAATKEAFRKTWNPKYTLRSHFDVRAALAFHP IEF
VLITASEDHTLKMWNLQKTVPAKKSASLDVEPIYTFRAHSGPVTCLCVSSNGQCYSGSTDSTIRCNWIP
SPNIDPYDAFDPFTVLQALVGHGDAIWGVTHISVKQQLLSCSADGTVRLWLSLQKSPLLNTYTAEKDGA
PTSVDFVRCEL SQMVAAYSSSVAVLYDLETAQVAKLDA RQCSDSGVSSQINRVVAHPTLPITITAHEDR
HIKFFDNNSGKMNTMVAHLDAVTS LAVDPNGLYLLSGSHDCSIRLWNLDSKTCVQEITSHRKKFDESIF
DVAFHPSKPYIASAGADALAKVFV

Drosophila melanogaster:

>NP_609177.1 connector of kinase to AP-1, isoform A [Drosophila melanogaster]
MGNTSGATAGINNKPVGGA TGAGVLVGGVGGSNSIGGVLNSLGGGGSGGLSISGLNAGGQNANVGGM
GNVGDDGNGMVGSGVNNQATTPTQYTI PGILHFIQHEWSRFELERSQWDVDRaelQARIAM LGERCK
LESLSKDLTRRIKMLEYALRQERAKFYRLKYGTDPFQLNEFKPNSDEAGLAGEVATDSEVPSYSSVNTTW
RQGRQMRLQYLAIEIGYTDNIIDVRSNRVRSILGNLNNAEHDGSGGLGGGLGGTGGENLSPNINGNESN
KRASITEGRHTPAKRVQQSIDEIIVDTEAAVMANFELGATEMSDDDEISDDLEMAVATDNDDTDVKLAKR
AKSGDMLTTEVDGSLGLGELAQLVTNNESD GAYDANSKDGTTGSGAGGAYRKTWNAKYTLRSHFDGVR
LI FHPEEPVLITASEDHTLKLWNLQKTVQAKKSASLDVEPIYTFRAHTGPVLC LGMSSSGETCYSGGLDG
NIECWLQPSNIDPYDCYDPNVHSGTLEGHGDAVWGLTTMQSNIVCSADGTVKLWSPYNKEPLLRTYTA
SEAEVGPSSVDFVRNEVDHIVVAAYS AHCIVYDTETGKQVVRLEAAQEMS GNTGKFINKVSHPTLPITIT
TAHEDRHIRFDWNTSGTLVHSMVAHLEPVTSLAVDAHGLYLLSGSHDCSIRLWNLDNKTVCQEITAHRRKK
FDESIFDVAFHATKPYIASAGADGLAKVFV

Hydra vulgaris:

>NP_001296588.1 striatin-3-like [Hydra vulgaris]
MEIDAKIINGVNKSNNGVSSSNPMVYSIPGILHYIQHEWARFIERAHWEVERAELQARIAFLQGERKG
QENLKRDILIRRIKMLEFALRKRQKFKHKLKYGTETLKL PDIKDDEDHDLANNEII SNKNHDLVFN YKQGRQ
LLRQYLQEIGFTDKVLEMR SARIRSLGITTDDLPTEASTKSKKNEKRQEDFTVSLNQEONCFNDPVDT
DSTEVIEDSVTKNSLESKKVEHETGDTFVLKDFDLGNEELNVDEASNIQNEEQDDMSNVNDESKLNKIK
QKNETKDRGKKKRNPNKDVKNMLQT FNAGEEELIPPPPQASTPSVPRVSGGVVDEIPVIGDITVLPSSG
YSRQVKLVAVNHSGVSDVTEVAMGLGD LADLSVSNELGNLDSKDDMRKTWGPKYTLRSHFDGVRSLCFH
PEAALITGSEDHTLKLWLSQKNVQGKRGNISDLEPVYTFRHS DGLVCCAINSNGTVCSYSGGLDFKIQC
WNLPSLNIIDLPGPYDPNVLDG DALIGHSDSVWMDLAYHIDTDFLLSCSADGTCKLWNPSIKSPLLETYKSPE
SGTPTSIVSVCTDGTGVAASYTSESCVYD IETAKPIVTFSPKTYGLSQINKVISHPTHPI LITAHEDR
HVRFDFLSSGKEVHSMVAHLDAVTS LIDPSGLYILSGSHDGSIRLWSMENKTCIQEITAHRRKKFDEAVF
DVAFHPSQPYIASAGADALAKVFV

Nematostella vectensis:

>XP_032221713.1 striatin [Nematostella vectensis]
WYSIDMDSDSGKLPQSSQNIENDSGTKFTIPGILHFIQHEWARFEMERAHWEVERAELQARIAFLQGER
KQENLKHDLIRRIKMLEFALKQERAKYHRKLYGTDLQGERSPKKEQEKKEEHPNEVTGSSNKPSPMWRQ
GRQLLRQYLQEVGYTDAILDVRSRVRSLILGSAAEPLAPAQMNQTS PRKPPDGPPEI REPSQSRFPVS
VQQAPSSHDVVAPNPIRRAPPHIPIPGKKPADEDFESEAAVMANDFDLENDIEDEEENEDEVDDGGSAD
DEDDERDVLKTERRIIKKPKTDSNEDLSPEEEALDEFK FVMGDDMDSDSTVIEVPTGKDLDEVNIHM
PDGEGEMAEQDHLHPDGT PKDEWDVDP SMLAKLKEQYKKERKSKKNVKRPPRSALQVMIANLGGDEEMP
QPQSTPAPATTGPPSVRLVGS RAMSEI PPPIGSVKIPTKTEAAPAASSPPKNEFFEDALGLGELAE LTVN
NEAEALSYEINKKDEFRKTWNPKFTLRSHFDSIRS VYFHPQEA AVITASEDHTMKLWNLQKTVPQKKSNI
LDVEPIYTFRHSAAVL SVVISSTSDMCFSGGADGTILCWNIPSLDLDPYGPYSPNVITGALLEVHTDAVM
GLAVQTNSLQLLSCSSDGTCLRNWPTLKSPLNTFILDKESSCTPTSIDFLRMDTSQMVASYSARA AIF
DLETAEA VNLDSAKTYNNPSTQINKVSHPTLPVTITAHEDRHIRFFDNNTGKQI HSMVAHLDAVTS L
AVDPNGLYLLSGSHDCSIRLWNLDSKTCVQEITSHRKKFDESIDYDAFHPHTKPYIASAGADGLAKVFV

Amphimedon queenslandica:

>XP_019858798.1 PREDICTED: striatin-3-like isoform X1 [Amphimedon queenslandica]
MSIEEAAAPVTRPFMMGPNGPSGPIPSDPGQPQAGYSVPGVLQFIKQEFGRFERERASWEVERAELQGKIA
FLQGERKGDHNLMDRLVRIKMLEFALKQERNKVYKLTHTGDSGLSLKPPQLDTETNPTVESSLSPLYN
QKESRQILRDYLREVGFPFWLEARVARNLNIRITLMSSTNQNEPLFP PPAVEAPSETYSKPPHPFPSS
TGGSIDIVNCTMQEQIGORRDTAESEDAVQVQWTFDPLSNEDSDDEEETEQVATKDLFQGLE
NTTEPAGLDKGAIMDGDIFYEDRYSKSDNPPDLPIGEEDNEWEFKQVVERQYQYKRKSNKSNISSRPPR
EQLRQLQQVANTNQPAEEMSSVMGLMGMPVRGHHDLEGVRSVPHRI PDERPEVYSLGIGELYSIANPSDFI
MNLSTSGSKRWEHKYTMRNHYDAVTCVQFHPMDMLVTGSEDATIKLWSIPKSKKSAI I DVEPAFTF
RGHTGPGVLSLAVSSDGEVYVSGSADGQLRMQTFPNLSDPFDIYDLDIQKGVLEGHGDAIWGLVFNQNSG
LLASASADGHCI LWDPVNSSQIKSIVSEEALGSPTSIDFLHGESI VVSYAKV VVYDVETGKPVVTLDS
ALTYNGTPTTQINKVLSHPTLPFIVITAHEDKYICFFDSKSGQVTHSMTAHMDAVTGLAIDPHGLYILSGS
HDGSLRFWSMETKTCVQEITAHRRKKFDESIYNVTC HLTKFPFASAGADGIKAVLL

Alignment

XP_019858798.1[A.queenslandica]	-----MS--IEEA	6
NP_001296588.1[H.vulgaris]		0
NP_609177.1[D.melanogaster]	MTNSGATAGINNKPVGATGAGVLVGGGVGGANSSIGVLSNSLGGGSGGLSISGLNA	60
XP_032221713.1[N.vectensis]		0
XP_019631056.1[B.belcheri]	-----MDDGSTGN-----PHAVPPSGSQPMIP--NKPQ	27
XP_032803414.1[P.marinus]	-----MDEHPALQ---VGSFGL-----KQLQQQPSGGSGQQQ---QQQQ	33
XP_045558221.1[S.salar]	-----A-----GGKVLIP--E---	28
XP_041418671.1[X.laevis]	-----MDEQAGPGVFFNNNNNSL-----LSAGTGGGAGK--GFEA	34
XP_040524727.1[G.gallus]	-----MDEQAGPGVFFSNNNNNN-----ALLLPPTTGGPGLEP--GEAA	37
NP_035630.2[M.musculus]	-----MDEQAGPGVFFSNNHPG-----AGGAKGLGP--LAEA	30
043815[H.sapiens]	-----MDEQAGPGVFFSNNHPG-----AGGAKGLGP--LAEA	30
XP_002812184.3[P.abelii]	-----MDEQAGPGVFFSNNHPG-----AGGAKGLGP--LAEA	30
XP_019858798.1[A.queenslandica]	A---PVTRPFMMGP-----NGPSGPIPSDPGQQAQYSVPGVLQFIKQEFGRFERERA	56
NP_001296588.1[H.vulgaris]	-----MEIDAKI--INGVNKSGNVNESSNPMVYSIPGILHYIQHEWARFEIERA	48
NP_609177.1[D.melanogaster]	GGQN--AN--VGMGNGVGGDGGNGMVGGGVNNQATTTPQYTI PGILHFIQHEWSRFELERS	118
XP_032221713.1[N.vectensis]	-----MYSIDMDSSSGKLPQSSQNIENDSGTKFTI PGILHFIQHEWARFEMERA	50
XP_019631056.1[B.belcheri]	T-----LQDEQSQQTKYSIPGILHFIQHEWARFEMERA	60
XP_032803414.1[P.marinus]	QQQQLLQQQLQMHQQQGG-----EGGESGRPHYSMPGILHYIQHEWARFEMERA	84
XP_045558221.1[S.salar]	-----GDAGEAARAPYSIPGILHFIQHEWARFEVERA	60
XP_041418671.1[X.laevis]	G-----AADAASVAGGGGG-----SAGRAQYSIPGILHFIQHEWARFEVERA	77
XP_040524727.1[G.gallus]	A-----AAAAAAGGGGGV SAGGAAAPVSASRAQYSVPGILHFIQHEWRFEAERA	89
NP_035630.2[M.musculus]	A-----AAGDGAAGAAARAQYSLPGILHFIQHEWARFEVERA	68
043815[H.sapiens]	A-----AAGDGAAGAAARAQYSLPGILHFIQHEWARFEVERA	68
XP_002812184.3[P.abelii]	A-----AAGDGAAGAAARAQYSLPGILHFIQHEWARFEVERA	68
XP_019858798.1[A.queenslandica]	SWEVERAELQKIAFLQGERKGDNLMRDLVRRIKMLEFALKQERNKVYKLTGTD SGLS	116
NP_001296588.1[H.vulgaris]	HWEVERAELQARIAFLQGERKQENLKRDILRRIKMLEFALKRQERKQFHKLYGTDELKLP	108
NP_609177.1[D.melanogaster]	QWDVDRaelQARIAFLQGERKCLSELSKDLTRRIKMLEYALKQERAKFYRLKYGTDPQOL	178
XP_032221713.1[N.vectensis]	HWEVERAELQARIAFLQGERKQENLKHDILRRIKMLEFALKQERAKYHRLKYGTDLGQE	110
XP_019631056.1[B.belcheri]	HWEVERAELQARIAFLQGERKQENLKRDILVRRIKMLEYALKQERAKYHKLKYGTELNQG	120
XP_032803414.1[P.marinus]	SWDMERaelQARIAFLQGERKQENLKDLVRRIKMLEYALKQERAKYHKLKYGTELNQG	144
XP_045558221.1[S.salar]	QWEVQRAELQAQIAFLQGERKQENLKDLVRRIKMLEYALKQERAKYHKLKYGTELNQG	120
XP_041418671.1[X.laevis]	QWEVERAELQAQIAFLQGERKQENLKDLVRRIKMLEYALKQERAKYHKLKYGTELNQG	137
XP_040524727.1[G.gallus]	EWEAERaelQAQIAFLQGERKQENLKDLVRRIKMLEYALKQERAKYHKLKYGTELNQG	149
NP_035630.2[M.musculus]	QWEVERAELQAQIAFLQGERKQENLKDLVRRIKMLEYALKQERAKYHKLKYGTELNQG	128
043815[H.sapiens]	QWEVERAELQAQIAFLQGERKQENLKDLVRRIKMLEYALKQERAKYHKLKYGTELNQG	128
XP_002812184.3[P.abelii]	QWEVERAELQAQIAFLQGERKQENLKDLVRRIKMLEYALKQERAKYHKLKYGTELNQG	128
NP_019858798.1[A.queenslandica]	LKPPQLDTET-----NPVTESSLPSLVNQKESRQLRDRYREVGPDPNVLEARVAR	168
NP_001296588.1[H.vulgaris]	DIKDDH-----DLANNEIISNKHDLVFNKYQGRQLLRQYLQIGFTDKVLEMRASR	162
NP_609177.1[D.melanogaster]	NEFKPSNEDAGLAGEVATDSEV--PYSSVNTVTRQGRQMLRQYLAIEGYTDNI DVRSNR	237
XP_032221713.1[N.vectensis]	RSPPK--EQEQKE-----EHPNEVTGSSNKP SMMWRQGRQLLRQYLQEVGYTDAILDVRSNR	165
XP_019631056.1[B.belcheri]	EMRPP--TPPSDE-----ERETDSPL--SQNSQVTVTRQGRQLLRQYLQEVGYTDILDVRSNR	174
XP_032803414.1[P.marinus]	DMKPP--TFDAEE-----TNDDTTFVVTSSNQLTVRQGRQLLRQYLQEVGYTDITLDVRSQR	199
XP_045558221.1[S.salar]	DMKPP--SYDSDE-----VNENETTG--SLNNQLSWKQGRQLLRQYLQEVGYTDITLDVKSQR	174
XP_041418671.1[X.laevis]	DMKPP--NYDSDE-----ANENEIQPPQNSQFIWKQSRQLLRQYLQEVGYTDITLDVKSQR	192
XP_040524727.1[G.gallus]	DMKPP--NYDSDE-----GNETEIQP--QONSQLIWKQGRQLLRQYLQEVGYTDITLDVKSQR	203
NP_035630.2[M.musculus]	DMKPP--SYDSDE-----GNETEIQP--QONSQIMWKQGRQLLRQYLQEVGYTDITLDVKSQR	182
043815[H.sapiens]	DMKPP--SYDSDE-----GNETEIQP--QONSQIMWKQGRQLLRQYLQEVGYTDITLDVKSQR	182
XP_002812184.3[P.abelii]	DMKPP--SYDSDE-----GNETEIQP--QONSQIMWKQGRQLLRQYLQEVGYTDITLDVKSQR	182
XP_019858798.1[A.queenslandica]	LNLYRTLMSSTNQNEPPL--P-----PPAVEAPSETYSKPPHPHPESSSTGGGS	215
NP_001296588.1[H.vulgaris]	IRSLLGITTTDDLPTEDASTKSK--KNEKRQEDFTVSLNAEQ--N-----	202
NP_609177.1[D.melanogaster]	VRSLGLNNNAEHDDGGSGGLGGGLGGGTGGENLSPNINGNE--SNKRASETE-----	287
XP_032221713.1[N.vectensis]	VRSLGLSAAELAPAQMNQTS--PRKFPDGG-----PZETREPS--QSREPFVSRQQAPSSHD	220
XP_019631056.1[B.belcheri]	VRTLLGLTPNESKQDEA--G-----EVLVNGEQ--EKLARR-----	208
XP_032803414.1[P.marinus]	VRSLGLSGPPDQNGAPDAKNI-----EQLINGRD--IMSIKP-----	235
XP_045558221.1[S.salar]	VKTLLAMAGDGGRRPGERTGSE-----TFLVNGTD--TVPKGT-----	210
XP_041418671.1[X.laevis]	VRSLGLSADSRLTDT--NQ-----DSMVNGTE--TELPNP-----	226
XP_040524727.1[G.gallus]	VRALLGLSSDASEKE--NR--NQ-----EPMVNGTE--GQIKEN-----	236
NP_035630.2[M.musculus]	VRALLGFSSDVTDREDDK--NQ-----DSVINGTE--AEVKET-----	216
043815[H.sapiens]	VRALLGFSSDVTDREDDK--NQ-----DSVINGTE--AEVKET-----	216
XP_002812184.3[P.abelii]	VRALLGFSSDVTDREDDK--NQ-----DSVINGTE--AEVKET-----	216
XP_019858798.1[A.queenslandica]	DIVPNGTD---MQEQIGGRRDTEASEDDAVKQVQNTFDLSNEDSDDEDETEWQQVA	271
NP_001296588.1[H.vulgaris]	-----GRHTP--AKKV--QQ--SIDEIIVDTAAV-----CFDNPVDT-----DS	312
NP_609177.1[D.melanogaster]	VVAVPNPIRRAPPHIPPI--GK--KPADEFSEAAVMANFDPLENDIEDEENDEVDVGG	277
XP_032221713.1[N.vectensis]	-----DADRRPVEKKRA--G-----IPEIDSEASVLATFDLSSEAVDDEENLSDGEE	256
XP_019631056.1[B.belcheri]	-----KEDDAKRN--G-----DKSRSEPLVPSVVDTFQFLEEEDSDGDEDDDDDES	281
XP_032803414.1[P.marinus]	-----GTG-----G-----RKTEVSESSALVDTFRFYC-----DEDDDEDGAG	243
XP_045558221.1[S.salar]	-----LVL-----G-----KPMTDASASVLETFKFLNAAEPFSDEDEEENES	265
XP_041418671.1[X.laevis]	-----AMI-----G-----KPELTDASASVLETFKFLNAAADFSDEDEDETEG	275
XP_040524727.1[G.gallus]	-----AMI-----G-----KSELTDASASVLDNFKFLESAADFSDEDEDETDG	255
NP_035630.2[M.musculus]	-----AMI-----A-----KSELTDASASVLDNFKFLESAADFSDEDEDDVDG	255
043815[H.sapiens]	-----AMI-----G-----KSELTDASASVLDNFKFLESAADFSDEDEDDVDG	255
XP_002812184.3[P.abelii]	-----AMI-----G-----KSELTDASASVLDNFKFLESAADFSDEDEDDVDG	255
XP_019858798.1[A.queenslandica]	T-----KDLFQGLENTT-----EPAGLDKGAIMDGFVYE	301
NP_001296588.1[H.vulgaris]	--TEVIEDS-----VTKNSL-----ESKKVEHETGDTFVLKDFDFLGN	248
NP_609177.1[D.melanogaster]	---SADDED--DERDVLKTERRIK-----KPK--TDSNEDLSPEEEALDEFKFMVG	323
XP_032221713.1[N.vectensis]	DGGAADDES--EERE--QRRRREK GKALVQMENESLAGMEDVLADPETEEALAEFDPLVS	314
XP_019631056.1[B.belcheri]	---VGLVDE-----RDRPRASKKA-----KIGNEGLAADLADDPTEALKEFDPLVT	326
XP_032803414.1[P.marinus]	LDRTIMEQTGPTGTMTVRKKPPSS-----SSPALSLSMDTSDPDADALKEFDPLSS	295
XP_045558221.1[S.salar]	RDKTIIDS-----ATIVRRK-----IIPSDN--DTEALKEFDPLGS	301
XP_041418671.1[X.laevis]	REKTIIDT---ATIVRRK-----VLSDSSEDRDTTEALKEFDPLVT	313
XP_040524727.1[G.gallus]	RAKSVIDT---STIVRRK-----ALPDSSEDRDTKEALKEFDPLVT	293
NP_035630.2[M.musculus]	REKSVIDT---STIVRRK-----ALPDSGEDRDTKEALKEFDPLVT	293
043815[H.sapiens]	REKSVIDT---STIVRRK-----ALPDSGEDRDTKEALKEFDPLVT	293
XP_002812184.3[P.abelii]	REKSVIDT---STIVRRK-----ALPDSGEDRDTKEALKEFDPLVT	293
XP_019858798.1[A.queenslandica]	DRYSSKSDN--P-----PDLPIGEEDNEMEFKQ--VER	331
NP_001296588.1[H.vulgaris]	EELNVDEASN-----IQNEEQDDW-----SNVDSEKLQNK	278
NP_609177.1[D.melanogaster]	TEMSDDDEI--S-----DDLE-----	334
XP_032221713.1[N.vectensis]	DDDDMDSSTVIEVPTGKDLDEVNIHMPDGEEGMAEQDHLHPDGTPKDEWDVDFSMIAKL	382
XP_019631056.1[B.belcheri]	EA--GEGAGE--AK--ST-----DGAEW-----GL--DKSPTEEEMAMDKNLLNKL	353
XP_032803414.1[P.marinus]	TEDGEAGE--AKSSG-----DGTW-----DKEELSPSGEEWDIDHGLITKL	367
XP_045558221.1[S.salar]	PDNMDTSP--SRSAG-----DGTW-----EKEEKSAMSAAWDVQGLITKL	336
XP_041418671.1[X.laevis]	DDSE--GGE--SRSAG-----DGTW-----EKEDQCPTITESWNVDQGVITKL	342
XP_040524727.1[G.gallus]	SDEG--DGE--SRSAG-----DGTW-----EKEDQCLMPEAWNVDQGVITKL	350
NP_035630.2[M.musculus]	SEEG--DNE--SRSAG-----DGTW-----EKEDQCLTEPAWNVDQGVISKL	332
043815[H.sapiens]	SEEG--DNE--SRSAG-----DGTW-----EKEDQCLMPEAWNVDQGVITKL	332
XP_002812184.3[P.abelii]	SEEG--DNE--SRSAG-----DGTW-----EKEDQCLMPEAWNVDQGVITKL	332

XP_019858798.1 [A. queenslandica]	YQEYKRSKNKSNKSIIRSPPEQLRQQLQVANTYQPAEEMS-----SVMLGMGMPVRGH	383
NP_001296588.1 [H. vulgularis]	LKQFNENKTRDKGRKSRPNKMMKLQPTFNAG-----EELIPPPQASTPVS-----PRVSGG	384
XP_609177.1 [D. melanogaster]	-----MVAATNDND-----TDVVK-L-----AKR-----	385
XP_032221713.1 [N. vectensis]	KEQYKKERKSKKNVKRPSRALQVMIANLGGD-----EEMP-PQGSTPAPATGPPSGPVLV	386
XP_01631056.1 [B. belcheri]	KEEFPKKERKSKKGAKNRNSLTQAMLANLGGD-----DDLVP-MPA-SGPPRSAINPNLDG--	387
XP_032803414.1 [P. marinus]	KEQYKKERNKKKGVKPNRSKQDMLANLRV-----DDLS-PLAASSPFR-QPEERAAPLF	388
XP_04558221.1 [S. salar]	KEEYKRCERKGGKGGKPNRSKQDMLANLRQ-----EDMS-PREFFSSPQARSNAPRLNEQ	389
XP_04148671.1 [X. laevis]	KEQYKKERKGGKGVKPNRSKQDMLANLRV-----DELP-SLPQSVSPSSSPASSRISPE	390
XP_04054727.1 [G. gallus]	KEQYKKERKGGKGVKPNRSKQDMLANLRV-----DDLP-SLPQSVAPSSSPSSSRSLIEH	391
NP_035630.2 [M. musculus]	KEQYKKERKGGKGVKPNRSKQDMLANLRV-----DELP-SLPQSVSPSSSPSSSRSLPEQ	392
043815 [H. sapiens]	KEQYKKERKGGKGVKPNRSKQDMLANLRV-----DELP-SLPQSVSPSSSPSSSRSLPEH	393
XP_002812184.3 [P. abelii]	KEQYKKERKGGKGVKPNRSKQDMLANLRV-----DELP-SLPQSVSPSSSPSSSRSLPEH	394
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XP_019858798.1 [A. queenslandica]	HDLEGV-----RVSHRIPDEREVSIGLIGELVIANPS	417
NP_001296588.1 [H. vulgularis]	---YVDDEIPVIGDTLPSSGGVSQRVK---LVAIVNIGSGVDTVEAMGLDADLSDVNS	418
XP_609177.1 [D. melanogaster]	-----A-----KSGKMDLITEVDSGLIGELAGLTVNN	376
XP_032221713.1 [N. vectensis]	-----GSR-----AMSEIIPPGISVKPIPTKEAAPASPKPNKEFPEDALGIGELAEITVNN	491
XP_01631056.1 [B. belcheri]	-----PLDEP-RKEGGEPGQV-----LVGGVPEESLEAALGGLAGLTVTN	497
XP_032803414.1 [P. marinus]	HDNARSDD-E-GESEFPFGTG-----KMFISGPEEAMD-TTGLGELADLTVTN	466
XP_04558221.1 [S. salar]	HQDNRTDEV-E-GESEFPFGTG-----KAFIMGPNEMAEELGIGELAGLTVAN	438
XP_04148671.1 [X. laevis]	---EINRADEV-EALTFPPSSG-----KSFIMGADEALENELLGIGELAGLTVAN	443
XP_04054727.1 [G. gallus]	---EINRTDEV-EALTFPPSSG-----KSFIMGTDTELENELGIGELAGLTVAN	451
NP_035630.2 [M. musculus]	---ELSRDEV-EALTFPPSSG-----KSFIMGDAEALSELGIGELAGLTVAN	433
043815 [H. sapiens]	---EINRADEV-EALTFPPSSG-----KSFIMGDAEALSELGIGELAGLTVAN	433
XP_002812184.3 [P. abelii]	---EINRADEV-EALTFPPSSG-----KSFIMGDAEALSELGIGELAGLTVAN	433
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XP_019858798.1 [A. queenslandica]	--D---FIMN-----PSTSGSKSWEHKYKTMRNHYDAVTCVGFHPHMDMLVGSEDA	464
NP_001296588.1 [H. vulgularis]	ELGNL-----DSKDMQKSGWPKYKTLRSHFDGVRSLCFHPEYAAILTGSEHD	433
XP_609177.1 [D. melanogaster]	ESDGA-YDANSKDGDTGGSGAGGYKTKWAKYTLRSHFDGVRSLCFHPEYAAILTASEHD	437
XP_032221713.1 [N. vectensis]	EAEALSVEYN-----KDEKFPKTNKFKTLRSHFDGVRSLCFHPEYAAILTASEHD	442
XP_01631056.1 [B. belcheri]	EAEPLQDVVA-----ATKEAFKTKWNKFKTLRSHFDGVRSLCFHPEYAAILTASEHD	449
XP_032803414.1 [P. marinus]	EADSPSYDYG-----ANKDAFKTKWNKFKTLRSHFDGVRSLCFHPEYAAILTASEHD	518
XP_04558221.1 [S. salar]	EADSLAYDMS-----NNKDALKRTWNKFKTLRSHFDGVRSLCFHPEYAAILTASEHD	493
XP_04148671.1 [X. laevis]	EADSLAYDIA-----NNKDALKRTWNKFKTLRSHFDGVRSLCFHPEYAAILTASEHD	493
XP_04054727.1 [G. gallus]	EADSLTYDIG-----NNTDALKRTWNKFKTLRSHFDGVRSLCFHPEYAAILTASEHD	505
NP_035630.2 [M. musculus]	EADSLAYDIA-----NNKDALKRTWNKFKTLRSHFDGVRSLCFHPEYAAILTASEHD	485
043815 [H. sapiens]	EADSLTYDIG-----NNTDALKRTWNKFKTLRSHFDGVRSLCFHPEYAAILTASEHD	485
XP_002812184.3 [P. abelii]	EADSLTYDIA-----NNKDALKRTWNKFKTLRSHFDGVRSLCFHPEYAAILTASEHD	485
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XP_019858798.1 [A. queenslandica]	TIKLWSIPKSS-QKKSALIDVEPAITFRGHGTGVPVLSLSSGDEVGVYSGSGADQLRMWNT	523
NP_001296588.1 [H. vulgularis]	TIKLWSLQKSGQKGRGNIISDLVEPYTFRAGHGSDGLVCAANSNGTGYSGGDLRCQWNL	493
XP_609177.1 [D. melanogaster]	TIKLWNLQKTKTQAKKSASLDVEPLYITFFRAHGTVPLVLSGMSSTGTYSGGDLRCQWNL	497
XP_032221713.1 [N. vectensis]	TMKLNWLQKTKPQKSNLIDVEPLYITFFRAHSAALVLSITSDMCSFGDAGTILCWNI	602
XP_01631056.1 [B. belcheri]	TIKLWNLQKTKTQAKKSASLDVEPLYITFFRAHSGPVTCLVSVNSGDTGQSGSDTIRCWNI	559
XP_032803414.1 [P. marinus]	TIKLWNLQKTKSGKTASLDVEPLYITFFRAHGPVLSIASSTGQCSGSDTIRCWNI	578
XP_04558221.1 [S. salar]	TIKLWNLQKTKPAKKSASLDVEPLYITFFRAHQGANLVLCVMSNGEQCSGSDTIRGQSWNT	553
XP_04148671.1 [X. laevis]	TIKLWNLQKTKPAKKSASLDVEPLYITFFRAHSGPVLVCMVSNBQCSGSDTIRGQSWNT	563
XP_04054727.1 [G. gallus]	TIKLWNLQKTKPAKKSASLDVEPLYITFFRAHSGPVLVCMVSNBQCSGSDTIRGQSWNT	545
NP_035630.2 [M. musculus]	TIKLWNLQKTKPAKKSASLDVEPLYITFFRAHSGPVLVCMVSNBQCSGSDTIRGQSWNT	545
043815 [H. sapiens]	TIKLWNLQKTKPAKKSASLDVEPLYITFFRAHSGPVLVCMVSNBQCSGSDTIRGQSWNT	545
XP_002812184.3 [P. abelii]	TIKLWNLQKTKPAKKSASLDVEPLYITFFRAHSGPVLVCMVSNBQCSGSDTIRGQSWNT	545
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XP_019858798.1 [A. queenslandica]	PNDLSDPFDYIDLQKGVLEGHTDAIWGLVFNQSNGLASASADGHCLIDWPV---NSSQ	581
NP_001296588.1 [H. vulgularis]	PSLNIDLPYDQGVPNVGLDGLIGHSDSVMDLAYHITDITFLDSCADGTCKLNPVS---IKSP	551
XP_609177.1 [D. melanogaster]	PSPNIDPYDGVPNVHSGTLGHTDAIWGLVIT---MQSNVLSGADGTCKLNPVS---NKPE	553
XP_032221713.1 [N. vectensis]	PSLDDLPYDQGVPNVGTALVIEHTDAIWGLVQTNLSQLLSCSSDGTCLRLNPT---LKSP	617
XP_01631056.1 [B. belcheri]	PSPNIDPYDAFDPTLVQALGVIEHTDAIWGLVITHSVKQLLSCADGTCLRLNPT---NKSP	610
XP_032803414.1 [P. marinus]	PSPNIDPYDTEFAEVLQGLTLGHSADWGLVAYSSLRRLRLSCADGTCLRLNPTSDQSPF	638
XP_04558221.1 [S. salar]	PNNLNDPYDTEFVLRGALGCHTDLWGLVYSGVGHQSNGLASASADGTCLRLNPTAS---NTPK	608
XP_04148671.1 [X. laevis]	PNNLNDPYDSDVPTVLRGAYEG	