

# AMOT

## Homo sapiens:

>Q4VCS5 [Homo sapiens]  
MRNSEEQPSGGTTVLQRLLQEQLRYGNPSENRSLLAIHQQATGNGPPFPSSGSGNPGPQSD  
VLSPQDHHQQLVAHAA**QSEFGQGE**IQSENLMIMEKQLSPRMQNNELPTYEEAKVQSQYFR  
GQQHASVGAAFYVTGVTNQMRTEGRPSVQRLNPGKMHQDEGLRDLKQGHVRSLSERLMQ  
MSLATSGVKAHPVTSAPLSPFPQNDLYKNPTSSSEFYKAQGPLPNQHSLKGMHRGPP  
EYFPKGMPQSVVCKPQEPGHFYSEHRLNQPGRTEGQLMRYPHPPEYGAARPAQDISLPL  
SARNSQPHSPSSSLTSGGSLPLLQSPSPSTRLSPARHPLVFNQGDHSAHLPRPQQHFLPNQ  
AHQGDHYRLSQPGLSQQQQQQQQHHHHHHHQQQQQQQPPQQQGEAYSAMPRAQPSSASY  
QPVPADYFAIVSRAQMQMVEILSDENRNLRQLEGGCYEKVARLQKVETEIQRVSEAYENLV  
KSSSKREALEKAMRNKLEGEIRRMHDFNRDLRERLETANKQLAEKEYEGSEDTRKTIISQL  
FAKNKESQREKLEIRRMHDFNRDLRERLETANKQLAEKEYEGSEDTRKTIISQL  
DKVEKMQQALVQLQAACEKREQLEHRLRTRLERELESRLRIQQRGNCQPTNVSEYNAAAL  
MELLREKEERILALEADMTKWEQKYLEENVMRHFALDAAATVAAQRDRTTVISHSPNTSYD  
TALEARIQKEEEEILMANKRCLDMEGRIKTLHAQIIIEKDAMIKVLQQRSRKEPSKTEQLS  
CMRPAKSLMSISNAGSGLLSHSSSTLTGSPIMEEKRDDKSWKGLGILLGGDYRAEYVPS  
TSPVFPSTPLLSAHSKTGSRDCTQTERTGESNKTAAVAPISVPAPVAAAAATAAITATA  
ATITTTMVAAPVAVAAAAAPAAAAAPSATAAATAAAVSPAAGQIPAAAAVASAAAAVA  
PSAAAAAAVQVAPAAPVFPAPALVFPVAPAAAQASAPAQTAPTSAPAVAPTPTPTPT  
AVAQAEVPASPATGPGPHRLSIPSLTCNPDKTGPFVFSNTLERKTIPIQLGQEPDAEMV  
EYLI

## Pongo abelii:

>XP\_009233461.1 angiomotin isoform X1 [Pongo abelii]  
MRNSEEQPSGGTTVLQRLLQEQLRYGNPSENRSLLAIHQQATGNGPPFPSSGSGNPGPQSDVLSPQDHHQQ  
LVAAHAA**QSEFGQGE**IQSENLMIMEKQLSPRMQNNELPTYEEAKVQSQYFRGQQHASVGAAFYVTGVTNQK  
MRTEGRPSVQRLNPGKMHQDEGLRDLKQGHVRSLSERLMQMSLATSGVKAHPVTSAPLSPFPQNDLYKN  
PTSSSEFYKAQGPLPNQHSLKGMHRGPPPEYFPKGMPQSVVCKPQEPGHFYSEHRLNQPGRTEGQLMR  
YQHPPEYGAARPAQDISLPLSARNSQPHSPSSSLTSGGSLPLLQSPSPSTRLSPARHPLVFNQGDHSAHL  
PRPQQHFLPNQAHQGDHYRLSQPGLSQQQQQQQQHHHHHHHQQQQQQQPPQQQGEAYSAMPRAQPSSASY  
QPVPADYFAIVSRAQMQMVEILSDENRNLRQLEGGCYEKVARLQKVETEIQRVSEAYENLVKSSSKREALEK  
AMRNKLEGEIRRMHDFNRDLRERLETANKQLAEKEYEGSEDTRKTIISQLFAKNKESQREKLEAEALATA  
RSTNEDQRRHIEIRDQALSNAAQAVVLEELKKQVYVVDKVEKMQQALVQLQAACEKREQLEHRLRTRL  
ERLELESRLIQQRQNCQPTNVSEYNAAALMELLREKEERILALEADMTKWEQKYLEENVMRHFALDAAAT  
VAAQRDRTTVISHSPNTSYDTALEARIQKEEEEILMANKRCLDMEGRIKTLHAQIIIEKDAMIKVLQQRSRK  
EPSKTEQLSCMRPAKSLMSISNAGSGLLSHSSSTLTGSPIMEEKRDDKSWKGLGILLGGDYRAEYVPS  
TSPVFPSTPLLSAHSKTGSRDCTQTERTGESNKTAAVAPISVPAPVAAAAATAAITATAATITTTMVAAP  
PVAAAAAPAAAAAAAPSPATAAAIAAAVSPAAGQIPAAASVASAAVAPFAAAAAAVQVAPAAP  
APVFPAPALVFPVAPAAAQASAPAQTAPTSAPAVAPTPTPTPTPAVAQAEVPASPATGPGPHRLSVPSLT  
CNPDKTGPFVFSNTLERKTIPIQLGQEPDAEMVEYLI

## Mus musculus:

>NP\_695231.3 angiomotin isoform 1 [Mus musculus]  
MRSSDDQPSGGTTVLQRLLQEQLRYGNPSENRSLLAIHQQATGNSSPFSTGSGNQGPQNDVLSSQDHHQQ  
QLVAHP**QSEFGQGE**IQSENGVMEKQLSPRMQNNELPTYEEAKVQSQYFRGQQHASVGAAFYVTGVTNQK  
KMRTEGRPSVQRLTPGKMHQDEGLRDLKQGHVRSLSERLMQMSLATSGVKAHPVTSAPLSPFPQNDLYKN  
NATSSSEFYKAQGPPFSGHSLKGMHRGPPPEYFPKGVPQSQSVVCKPQEPGHFYSEHRLNQPGRTEGQLMR  
RYQHPPEYGAARPAQDISLPLSARNSQPHSPSSSLTAGASSLLPLLQSPSPSTRLPQGHLSVQGDHSAH  
LSRHQQHLLSSQSHQGDHYRHQAQSLTSAQQQGEAYSAMPRAQGSASQVPMADPFAMVSRQAQMQMVEIL  
SDENRNLRQLEGGCYEKVARLQKVETEIQRVSEAYENLVKSSSKREALEKAMRNKLEGEIRRMHDFNRDL  
RDLRETANKQLAEKEYEGSEDTRKTIISQLFAKHKNQREKLEAEALATARSTNEDQRRHIEIRDQALSN  
AQAKVVLEELKKQVYVVDKVEKMQQALVQLQAACEKREQLEHRLRTRLERELESRLIQQRQNSQPTN  
ASRYNAAALMELLREKEERILALEADMTKWEQKYLEENVMRHFALDAAATVAAQRDRTTVISHSPNTSYDT  
ALEARIQKEEEEILMANKRCLDMEGRIKTLHAQIIIEKDAMIKVLQQRSRKEPSKTEQLSSMRPAKSLMSI  
SNAGSGLLSHSSSTLTGAPIMEEKRDDKSWKGLGVLLGGDYRVEVPVPTSPVFPSTPLLSAHSKTGSRD  
CTQTERTGESTTAAVTPISAPMAGPVAAAAPAAAINATAATNTATATAATNTIMVAAAPVAVAAAAAPA  
AAAAATPSNAAALAAAAAPATSVSAATSVSAANSISPAAPVAPAAVPPAAPVSPAAPVIPAASALTP  
ATVSPATAATAAVAAATTAATAAAAAATTAIQVAPATSAVPVSPASIPAPATAQASAPTPTQASTPAP  
TEPSPVPVPTPALVQTEGPANPAGSSGPRRLSTPNLMCNPKDPDAPAFHSSTLERKTIPIQLGQEPDAE  
MVEYLI

## Gallus gallus:

>XP\_004940856.2 angiomotin [Gallus gallus]  
MRNSEEQAATTVLQRLLQEQLRYGNPNDRNLLALHQQATGNAPPFNSTGNPASQNEGLSSQDHLVTHA  
V**QSEFGQGE**IQVONSIMEKQLSPRLQNSDELPTYEEAKVQSQYFRGQPHASVGAAFYVTGVTNQMRTEG  
RPTVQRYVSPKVKHQDEGLKDLKQGHVRSLSERLMQLSLATSGVKAHAPVTSAPLSPLSPQSSDPYK  
NSGSSSEFYKNSVQPPSPQSMKGMQGRGPPPEYPKYKNVSTPSMCKPQDSGHFYSDHRVSQQGRSDGPMWR  
YQHPPEYGSVRQNFVQLQQRPPHHSPSSSLTSLGSLTLQSPPPSRLSPSQHQQLPTPSQGDGPIGL  
PRTQQPFLSNQVHQDGLYRLCQPFLLGPOQQGDSYSVMSRAQQIPSPYQMQQVDPFAIVSRAQMQMVEILS  
EENRSLRQELDGCYEKVARLQKLETEIQQVSEAYKNLEKSSSKRDALKAMRNKLEGEIRRLHDFNRDLR  
ERMETANKQLAEKEFEGSEDNRKTIISQLFAQNKETQREKEKLEIELAAARSTNEDQRRHIEIRDQALNNA  
QAKVKVLEELKKQVYVVEKVEKMQQALVQLQAACEKREQLEHRLRTRLERELESRLMQQRQGTQAANV  
SEYNATALMELLREKEERILALEADMTKWEQKYLEESVMRQFALDAAATVAAQRDRTTVISHSPNPSYDTS  
LEARIQKEEEEILLANRRCLDMEGRIKTLHAQIIIEKDAMIKVLQQRSRKEPGKTDQLSSMRPAKSLMSI  
NAGSGLLSHSSSTLSSTPIIEEKRDDKSWKGLGVLLGTEYRSESIPTSPSPVLPTPLLSAHSKTGSRDCT  
STQTRDNGEQSKAAPSPAAPTGRPLTASLPYADKTGDLFHSSTLERKAPVQTMGQDLPDGEMVEYLI

## Xenopus laevis:

>XP\_018085358.1 PREDICTED: angiomotin-like isoform X1 [Xenopus laevis]  
MRTSEEQAATTVLQRLLQEQLRYGNPNENRNLLALHQQATGNVPSYGGGQGSQNEGLTLQDPQLVPHA**QSEFGQGE**IQVENLMKQIPLRSQNSDELPTYEEAKVQSQYFRGQPHTSVGAAFYVTGVTNQMRTEGRPT  
VQVRVSPGKVHQDGLKDLKHGHVRSLSERLMQLSLATSGVKAHAPITSAPLSFQGPDPFKNSDNDMFKN  
FPQGGQGVTEHRGQVYVVEKVNISPLTQCKSEVEFGPHYGEHRGSLQNSDGDGPMRYQHPPEYGAARQ  
QDVQQQIQHRPSHYHSTSSLTSLGSMQLQSPITMSPSQQHPFSPSHGDFYTVPSRAHHIPIVYNVVFQ  
QDVKRSPOSQFGQQQMDPVLRLPPVPSPYQMQNDPPTIVSRAQNMVSLSEENRSLRKELEDYDKV  
ARFQKMEMEIQRISEAYENLVKSSSKRETLEKAMRTLEELIRRIHDFNRDLRERDNTANKQLAAKEFEG  
SEDNKRTIISQLLAQNKETQREKEKLEIEISSRLSTNQDQRRHIEIRDQALNNAQAKVVLEELKKQVY  
VDVKVEKMQQALVQLQAACEKREQLEHRLRTRLERELESRLRIQQRGQNSQSSNVSEYSAATIMELLREKEE  
RVLALAEADMTKWEQKYLEESVMRQFALDAAATVATQRTASISHSPSGSFDTSLEARIQKEEEEILLANR  
RCLVDEGRKIKTLHAQIIIEKDAMIKVLQQRSRKDPKTDQSSTMRPSKSLMSISNAGSGLLSHSSALSSTP  
LIEDKREDKSWKGLGVLLATEYRSESASSTSPSIRPSTPLLCGHSKTGSKDCTQTRGAEQNKPPSVS  
ASPGPGRLATPSPMYNSERTAETVFSSTLDRKNPLPLPLGQDLTDGELVEYLI

Salmo salar:

[illegible]

**Petromyzon marinus:**

XP\_032827792.1 a.giomotin-like protein 1 [Petromyzon marinus]  
 MFDGVRERALERMRAEDNSKGVLRILQIQELRYGVQDNRGLLALQQQATAGSPPTAANAATGAGASHG  
 ALSIAPTS'GAVSLGGAPAAQSSSISTSESLVDLRSEA [redacted] HQSSETPEKQARLALLQQQQ  
 QQQQY'QQQQQ'QQQQQY'QQQQQY'QHHTALEP'LYSEAA'HYSSYSS'LSQGGQGT'VHQRMSSNTGPA  
 FYVTAT'GAGKRGTEGRAVOTPS'PLPMDGGLKQGHVRS'LSERMLQ'TLENGKAGALPLGSSPSS  
 VSSPQSSADFCRLQNGSPQ'PFRDLPGRPFPEY'PFKHIAA'APQGS'PLQLQNTFALQHGHVYFGAEQH  
 LLRYQ'FPPEYNMARTQ'QGMQPMQ'VSSFSASQSGAGSLIS'QMSGAGL'GPMQNLGSMTL'VTAQQT'  
 PMYTGLOGS'SMAHTGAG'GEEELHMLLRSGQ'VELLTENM'LRSESLSEYCGED'KIQKMERVIRISEA  
 VLENKTS'KRLET'ALAKMTKMS'ERLHDFNRDRLDKLRS'NQLKASLR'VEKSEENDKLTAKI'KLKQ  
 AKCKE'RGRLPT'LELELETL'RAQQGAPGAPPT'GEHAAP'AMELLRLKREKRVLEAD'LEADWQKY  
 LEESAPQ'FAMDAANAAT'ERTDT'INANSNP'ASEEY'FLMASRCHDM'RGKINLHQA'ITEKDMIKY  
 LQSRSE'QKQGTSSAT'SLPKSPKSV'PTAANAAS'GPGGLAGLAAK'PMAASP'LEERLQAGTGSF  
 GLVSTELA'EGGSTAVGLSFLR'VSP'PPSPHIFV'KSSKSDSTQ'ETRGAEQ'VSSSHPMPPAAERK  
 KSNLT'PRGSKML'LDVSDRADDRADMMAGAEKLLDGR'PLHMSG'PDQEDQVNMVEHLLI

Branchiostoma belcheri:

No homolog found.

**Drosophila melanogaster:**

No homolog found.

### Hydra vulgaris:

No homolog found.

**Nematostella vectensis:**

No homolog found.

*Amphimedon queenslandica*:

No homolog found.

XP_032827792.1[P.marinus]		-MGDPYARERALAEEMRAEE-----DMSGKV	23
XP_014052684.1[S.salar]	MFRKXASSLRMPRISEENRNWIDRGSSSFHEVRGLRETEMRVADETSSTSNNSNTTV		60
NP_695231.3[M.musculus]		--MRSDDPPSGGTTV	14
Q4VC55[H.sapiens]		--MRNSEEPSGGTIV	14
XP_009233461.1[P.abellii]		--MRNSEEPSGGTIV	14
XP_004940856.2[G.gallus]		--MTNSEEQ--AATTI	12
XP_018085358.1[X.laevis]		--MTNSEEQ--AATTI	12
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XP_032827792.1[P.marinus]	LQRLLQEQLRYRGTVDNRGLLATQQOATAGSPTPANAAATGAGAHSALSLAPTSLGAVS		83
XP_014052684.1[S.salar]	LQRLLQEQLRMGRYGSRNVQLAMQHQQQQQQRRQOE-GVGASQG-YPGHV-		107
NP_695231.3[M.musculus]	LQRLLQEQLRYGNPNSENRLAIHQATNGSPFSTGSNGNQGP-QNDVL		62
Q4VC55[H.sapiens]	LQRLLQEQLRYGNPNSENRLAIHQATNGPFPPFGSGSGNPFP-QSDVI		62
XP_009233461.1[P.abellii]	LQRLLQEQLRYGNPNSENRLAIHQATNGPFPPFGSGSGNPFP-QSDVI		62
XP_004940856.2[G.gallus]	LQRLLQEQLRYGNPNDRNLRLAHQAATGNAPPFN-TGGPAS-ONEGI		59
XP_018085358.1[X.laevis]	LQRLLQEQLRYGNPNDRNLRLAHQAATGNVPYSY-GTPGS-ONEGI		57
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XP_032827792.1[P.marinus]	LOGAPAAAAGSSIISTESLVQDRQSACPLAQHQPMSSETPEKAQQLALLQQALQQQ		146
XP_014052684.1[S.salar]	GPDNRHDHMVMPIHAIAAFANLQDSGVCKEKSRRGG-		146
NP_695231.3[M.musculus]	--SQNDHQQLVAHFADCPQTIGLSQENGWEKO		96
Q4VC55[H.sapiens]	--SQDHMQ-QLVAHAACPQTIGLSIQENSELMEO		95
XP_009233461.1[P.abellii]	--SQDHMQ-QLVAHAACPQTIGLSIQENSELMEO		95
XP_004940856.2[G.gallus]	--SQDHP-QLVTFAAACCFPCCTIGVS-LNMKEO		87
XP_018085358.1[X.laevis]	TLDQP-QLVFHAACPFCCTIGVEN-LMEKO		90
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XP_032827792.1[P.marinus]	QYYQQQQCQQQQQQYYQQQQYQQHHHTAPELPYEERAKVHSQYSSLQSGGGGT-VHQA		202
XP_014052684.1[S.salar]	--SSGGGMSSGGGGSSGQNPFDELPTYEAARKVGHQPHGFPHHGQHQQHQQQQQ		199
NP_695231.3[M.musculus]	--LSPFMQNNELPTYEAARKVQSYFYRQGOH		125
Q4VC55[H.sapiens]	--LSPFMQNNELPTYEAARKVQSYFYRQGOH		124
XP_009233461.1[P.abellii]	--LSPFMQNNELPTYEAARKVQSYFYRQGOH		124
XP_004940856.2[G.gallus]	--LSPFLQNNEDLTPLYEARVKVQSYFYRFQOPH		119
XP_018085358.1[X.laevis]	--ILPRSQNNEDLTPLYEARVKVQSYFYRFQOPH		116
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XP_032827792.1[P.marinus]	MSNTGPSAAFVVYTATVGAQKGRTGRPAVRTSP-LPIMQDGDLKKELKHGHRVSLSERLMQ		261
XP_014052684.1[S.salar]	LFPSVGAAFFVTAITNGKRVTRTGRTVQRLSTGGKVHGDGDKLKDKGHVRVSLSERLMQ		259
NP_695231.3[M.musculus]	--ASVGAAFFVTVGT-NQMKTIEGRFSVQRLTP-GMHMDCEGLRDLDKGHRVSLSERLMQ		181
Q4VC55[H.sapiens]	--ASVGAAFFVTVGT-NQMKTIEGRFSVRQRP-GMHMDCEGLRDLDKGHRVSLSERLMQ		180
XP_009233461.1[P.abellii]	--ASVGAAFFVTVGT-NQMKTIEGRFSVRQRP-GMHMDCEGLRDLDKGHRVSLSERLMQ		180
XP_004940856.2[G.gallus]	--ASVGAAFFVTVGT-NQMKTIEGRFTVQRVSP-KGVHQDEGLRKDKGHVRVSLSERLMQ		175
XP_018085358.1[X.laevis]	--TSVGAFFVTVGT-NQMKTIEGRFTVQRVSP-KGVHQDGLDKLKHGHRVSLSERLMQ		172
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XP_032827792.1[P.marinus]	LTLKNKGAQAKPLPLGSSPPSVF-----QSSADFCLRNQJSPF---QRPDY		305
XP_014052684.1[S.salar]	LSLATSGVKAHAPTSAPLSPQLFP-PGPFDDGYKFS-----GQ		297
NP_695231.3[M.musculus]	MSLATSGVKAHPPVTSAPSPLP-----PNDLYLNKNTSSSEFYKAQGPLNHSHSKLGE		235
Q4VC55[H.sapiens]	MSLATSGVKAHPPVTSAPSPLP-----PNDLYLNKNTSSSEFYKAQGPLNHSHSKLGE		234
XP_009233461.1[P.abellii]	MSLATSGVKAHPPVTSAPSPLP-----PNDLYLNKNTSSSEFYKAQGPLNHSHSKLGE		234
XP_004940856.2[G.gallus]	LSLATSGVKAHAPTSAPLSPPLSPSQSSSDYPKYNSG-SSEFYKSNVPPPSPSMKMG		221
XP_018085358.1[X.laevis]	LSLATSGVKAHAPTSAPLSPQ-----PGDFYNKD-SDNMFKN---PPQCQGQKYTE		234
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XP_032827792.1[P.marinus]	PRGPPPEYFFPKHAKAAPQSGPLQNLQFTALQHQQHHHVPGAQBHLRYQPPEYNMARQ		365
XP_014052684.1[S.salar]	HRTGPPPYDFPNKMGSFKSQPOHQEGGHYQEHRRFDPRDQGRNEVPHVRYQPPVEYGSFS		357
NP_695231.3[M.musculus]	HRGPPPEYFFPGKFQSPQSV---CKSGEPGHIFYSEHRLNQGRTEGQLMKRVQHPPEYGAARA		293
Q4VC55[H.sapiens]	HRGPPPEYFFPGKFQSPQSV---CKFPEGPHYSEHRLNQGRTEGQLMKRVQHPPEYGAARP		292
XP_009233461.1[P.abellii]	HRGPPPEYFFPGKFQSPQSV---CKFPEGPHYSEHRLNQGRTEGQLMKRVQHPPEYGAARP		292
XP_004940856.2[G.gallus]	RGCPEPEYFKMVYSTPMSC-CFKQSDGHIFTSEHRVLSQRSQCSDCMBRWQHPPEYGSARG		292
XP_018085358.1[X.laevis]	HRGPPPEYFKMITNSTPLFQ-GKSEKVGFBHYGEHGLSKNRSDBGMMRWQHPPEYGSARG		279
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XP_032827792.1[P.marinus]	TQQGM----QPMQNYSHSPASQSGSAGSLSQMS-GAGALGP-----PMQNLGSMITLT		413
XP_014052684.1[S.salar]	NKESS---VHQSRVHHHTPTSSITSVGLSRAQSTISLNSLASHPSTTHPPQCGDPYAS		412
NP_695231.3[M.musculus]	TDITSSLISLARNSQPHSTPTSSLTAGASSLPLQLQSPSPSTRLPQGP-H-LVSNQGDHSAH		350
Q4VC55[H.sapiens]	AQDIS-LPLSANRQPHSTPTSSLTSGG-SLPLQSPSPSTRLSPAR-H-HPLVNQGDHSAH		348
XP_009233461.1[P.abellii]	AQDIS-LPLSANRQPHSTPTSSLTSGG-SLPLQSPSPSTRLSPAR-H-HPLVNQGDHSAH		348
XP_004940856.2[G.gallus]	NPDVQ-LQLQORRPHHHSPTSSLTSLG-SLTLQSPSPSTRLSRQHOQPLTFPSQGDGPLL		334
XP_018085358.1[X.laevis]	NPDVQ-QQIQHRPSHYHSPTSSLTSLG-SMLSQLSPTI-MSPSQ-OHPFPSHGDGYFTV		334
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XP_032827792.1[P.marinus]	TA-----VAQPTMY		423
XP_014052684.1[S.salar]	TGPRS---PQGGSGHGDIYLCGATHPLPQRGHGPFMDHDPYESTSRMHQQQCHHGFQOOQ		472
NP_695231.3[M.musculus]	LS-RHQDLLSSQSQGHGDIRHRAQ-----ASLT		377
Q4VC55[H.sapiens]	LP-RPQGHFLPNQAQGHGDIRLSQ-----PGLSQQQQQQQQQHHHH-H		

	ALRSTNQDQRRIHEIRQDLNNAQAQKVVLKLEELKKQVYVEKVERMQQALQLQAACE	712
NP_695231.3[M.musculus]	TARSTNDNRQHRIEIRDQALSNAQQRVVKLKEELKKQVYVDVKVEQMQUALVQLQAACE	598
Q4VC55[H.sapiens]	TARSTNDQRRIHEIRDQALSNAQAQVVVLKLEELKKQVYVDVKVEQMQUALVQLQAACE	618
XP_009233461.1[P.abellii]	TARSTNDNRQHRIEIRDQALSNAQAQVVVLKLEELKKQVYVDVKVEQMQUALVQLQAACE	619
XP_004940856.2[G.gallus]	AARSTNDQRRIHEIRDQALSNAQAQVVVLKLEELKKQVYVEKVERMQQALQLQAACE	597
XP_018085358.1[X.laevis]	SIRSTNQDQRRIHEIRDQALNNAAQAQVVVLKLEELKKQVYVDVKVEQMQUALVQLQAACE	580
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XP_032827792.1[P.marinus]	REQLERLRITRLERELETETRAQQRGAPPFGA-TSEHAAPALMELLEKEERVLAADM	693
XP_014052684.1[S.salar]	REQLEHLRLTRLERELESLSRMQQRGVQSQQSSSGQEYSATAMHLEHRKEERILALEAD	772
NP_695231.3[M.musculus]	REQLEHLRLTRLERELESLSRTQQRGQNCPFT-ASEYNAAALMELLEKEERILALEAD	657
Q4VC55[H.sapiens]	REQLEHLRLTRLERELESLSRTQQRGQNCPFT-VSEYNAAALMELLEKEERILALEAD	678
XP_009233461.1[P.abellii]	REQLEHLRLTRLERELESLSRTQQRGQNCPFT-VSEYNAAALMELLEKEERILALEAD	677
XP_004940856.2[G.gallus]	REQLEHLRLTRLERELESLSRMQQRGVQSQAAN-VSEYNATALEMLEKEERILALEAD	666
XP_018085358.1[X.laevis]	REQLEHLRLTRLERELESLSRTQQRGVQSSSN-VSEYSAATLMELLEKEERVLAADM	639
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XP_032827792.1[P.marinus]	MWWEQKYLVESAMRFQFMDAAAATAATERDT---TIANSFNASFS-----EEEEF	832
XP_014052684.1[S.salar]	TKWEQKYLVESVFQPDALDAASVAATQTDSLVSIVSHSPSFSESQGLSVEARIQKEEBI	772
NP_695231.3[M.musculus]	TKWEQKYLEENWMRHFDALDAATAVAAGRDT--TVISHSPNTSYDT--ALEARIQKEEBI	713
Q4VC55[H.sapiens]	TKWEQKYLEENWMRHFDALDAATAVAAGRDT--TVISHSPNTSYDT--ALEARIQKEEBI	734
XP_009233461.1[P.abellii]	TKWEQKYLEENWMRHFDALDAATAVAAGRDT--TVISHSPNTSYDT--ALEARIQKEEBI	733
XP_004940856.2[G.gallus]	TKWEQKYLVESWMRHFDALDAATAVAAGRDT--TVISHSPNSPYDT--SLEARIQKEEBI	712
XP_018085358.1[X.laevis]	TKWEQKYLVESVMRFQDALDAATAVTGRDT--ASTISHSPNSPYDT--SLEARIQKEEBI	695
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XP_032827792.1[P.marinus]	MLASRRCHDMEGRIKNLHAQIIIEKDAMIKVLQRSKRKEQGKGTESSATSLRPAKSVPSIA	800
XP_014052684.1[S.salar]	LMANRRCLDMESRIKNLHAQIIIEKDAMIKVLHQRSRKDP-NKRDRAQAIMRPFKSLSMTA	791
NP_695231.3[M.musculus]	LMAINKRCLDMEGRIKTLLHAQIIIEKDAMIKVLQQRSKPE-SKTE-QLSMRPFAKSLMSIS	871
Q4VC55[H.sapiens]	LMAINKRCLDMEGRIKTLLHAQIIIEKDAMIKVLQQRSKPE-SKTE-QLSCMRPAKSLMSIS	792
XP_009233461.1[P.abellii]	LMAINKRCLDMEGRIKTLLHAQIIIEKDAMIKVLQQRSKPE-SKTE-QLSMRPFAKSLMSIS	791
XP_004940856.2[G.gallus]	LLANRRCLDMEGRIKTLLHAQIIIEKDAMIKVLQQRSKPE-GKTD-QLSMRPFAKSLMSIS	770
XP_018085358.1[X.laevis]	LLANRCVDMEGRIKTLLHAQIIIEKDAMIKVLQQRSKRP-SKTD-QSSMTRPKSLMSIS	753
	:::.* ** * *:*****:*****:*****:~::~:::~::~:** :	
XP_032827792.1[P.marinus]	AASGSPGGGLASGLAARKPPMAASPSEELEGA--RTGSFSLGYSTELAEGETASVGL	858
XP_014052684.1[S.salar]	NIG----G---SGLLSHSLLGSSSPIETE-RKDSXMGWSLLGLCGDYREP---L--	936
NP_695231.3[M.musculus]	NA----G---SGLLSHSSTLTGFIMEEKDRDKSWKSGLLGLLGVDYREP---V-	816
Q4VC55[H.sapiens]	NA----G---SGLLSHSSTLTGFSPIEEKDRDKSWKSGLLGLLGVDYRAEY---V-	837
XP_009233461.1[P.abellii]	NA----G---SGLLSHSSTLTGFSPIEEKDRDKSWKSGLLGLLDYRAEY---V-	836
XP_004940856.2[G.gallus]	NA----G---SGLLSHSSTLSTPTILEEKREDKSWKSGLLGLVLTGYRES---I-	815
XP_018085358.1[X.laevis]	NA----G---SGLLSHSSTLSTPTILEEKREDKSWKSGLLGLVLTGYRES---A-	798
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XP_032827792.1[P.marinus]	SPMKRALPLPPPSPH-FTHVXSXXSDSTQTGERAQGEQSSPHMDPAAERKKNTLP	917
XP_014052684.1[S.salar]	RTEISSSSPVFLPTLGHSGTSGSRDCSTQTDKGQSQGQEAASSKPSTPAL--QSMTLPS	993
NP_695231.3[M.musculus]	PST--PSPVPPTPLLASAHTSGSRDCSTQTERGSTKTAATVPISPAP-----MAG	866
Q4VC55[H.sapiens]	APT--PSPVPPTPLLASAHTSGSRDCSTQTERGSTKTAATVPISPAP-----AP	866
XP_009233461.1[P.abellii]	PST--PSPVPPTPLLASAHTSGSRDCSTQTERGSTKTAATVPISPAP-----AP	865
XP_004940856.2[G.gallus]	PST--PSPVLPTPLLASAHTSGSRDCSTQTDARGNEQKAAPSAPA--P-----TPG	883
XP_018085358.1[X.laevis]	SST--PSPPIRPTPLLCGSGKDDCCTQTDARGEQNKPRPSVAS--P-----PG	846
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XP_032827792.1[P.marinus]	GSKM-LPSLHVLRVDARDRA-----DMKMAAGE-----	944
XP_014052684.1[S.salar]	RLSS-----	997
NP_695231.3[M.musculus]	FVAAAAATAAINATAATTNTATTTTMM/VAAAFVAVAAVAAAAA-----TPSPAANA	923
Q4VC55[H.sapiens]	-VAAAAATAAI-----TATAATITTTTTMM/VAAAAAFVAAAAA-----AAPSPAANA	937
XP_009233461.1[P.abellii]	-VAAAAATAAI-----TATAATITTTTTMM/VAAAFVAAAAAATAAAAAAAAAPATAA	937
XP_004940856.2[G.gallus]	RLPT-----	867
XP_018085358.1[X.laevis]	RLAT-----	850
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XP_032827792.1[P.marinus]	-----	944
XP_014052684.1[S.salar]	-----	997
NP_695231.3[M.musculus]	LAAAAAPATSVAANTSVAANSISPAAPVAAVVPAAFPVPAAPVPAAPAAVQIPAAASLTPTAV	983
Q4VC55[H.sapiens]	TA-----AAVSPAAAGQIPAAASVAS--	955
XP_009233461.1[P.abellii]	TA-----AAVSPAAAGQIPAAASVAS--	958
XP_004940856.2[G.gallus]	-----	867
XP_018085358.1[X.laevis]	-----	850
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XP_032827792.1[P.marinus]	-----	944
XP_014052684.1[S.salar]	-----	997
NP_695231.3[M.musculus]	SPTAATAATAVAAATTAITAAAAAATTAIVQAPATAPAVPASVPSIPA-----PATAQASPT	104
Q4VC55[H.sapiens]	-----AAAVPAS-AAAAAAAVQVPAAPAFPVALVPPVPAAPAAQAQSPA	999
XP_009233461.1[P.abellii]	-----VAAPVAPAAAAAAVQVPAAPAFPVALVPPVPAAPAAQAQSPA	100
XP_004940856.2[G.gallus]	-----	867
XP_018085358.1[X.laevis]	-----	850
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XP_032827792.1[P.marinus]	-----	944
XP_014052684.1[S.salar]	-----	997
NP_695231.3[M.m		