

Homo sapiens:

Pongo abelii:

Mus musculus:

[illegible]

AQVAHADQQLRDLGKFQVATDALKSREPQVKPQLDLSIDSLDLSLEEGLPCSVASKLPR**TQPDGTS**VPGE
PASPSISQRLPPKVESLESLEYFTPTPARGQAPLETSLDLSGDAFPDSGRKTRSARRRTTQIINITMTKKLE
LEEPDSANSSSYSTQSPASPAQANLRATSSSTQSLARLGSDDGNSALLSLPGYRPTTRSSARRSQARMS
APQGRNSFYMGTCQDEPEQLDDWNRIAEQLQQRNVCPPHLKTCTYPLESRPTLSLATITDEEMKTGDPRET
LRRASMQPQAIAGVGVIITTRQQRKVSSETHQGPPTPESKKATSCFPFRPMTPRDRHEGRKQSTADTKK
AAPVLKQADRQSMAFSILNTPKKLGNSLLRRGASKKTPAKVSPNPRSGTRRSPRIATTTGTATVATTP
RAKGKVKH

Gallus gallus:

>CBN80053.1 nuclear mitotic apparatus protein [Gallus gallus]
MPLHTTRATALLAWNSTKACAEPLGDLSQLQDCRVFIQIINKIHRTTEGESVLEQSLAERAAFICGFLQ
KLCKHKSATENLVS AQKLLGEGELELAKVAVLLLYHSSMSKSPDWNNEFDYQIQVELATILKFLVDHEE
SLSENLEVFLORRAPLSSPGTSSSSSEERSPGLSHFPQVRFLELQKIASSSSSMNMNLPGTSPASVPGDVLQ
TPQFQLRRLKKQLAITERENRDELEMELAENRKLITEKEAQITMMQHRIDRIALLNLEKQAADQLEPREMEE
LRERNESLLVRLHEALKQCQDLKTEKGQMDRKINQLSEENGDSL FKLREIASHLVQLQDALNELSEEHNS
ALMQSQAQAQLEGE LRAVLQEKKCLEEKVEITLQGKISLLEDQLVKLGD CSTQEKGEVMGDVLKLEELQ
EVSSITTTKGIELQASVLRLEEEKSQRDAALQAERNHFEMEKLQLGTHISNLQSSVSELHLAKEKLEQELR
AQEAHLTAQADALTAEVGKLSGFLQQQKEAAELRMQAEQERAQAEELRHRRDMSQEALSELSRVRVQLG
ASLKHSSEELVVRVTQAEAGKARQLGAEHKAVQERDAALQQQLQHLQQAKEKQLAALSSQLQSELAASKAS
SMEMQKEKAELNQVQELQARVLELSAQCCQSSAQGASETLRAQLRELEGLKDKDSQOKLADKVKAKEN
TRQERLLPLEESVRNTEGILEDEKRRAAESLEGNLARIAELEAEKQQLVQRGEQALQQHSEELARRQAL
ETRLQQVAEERREETAALQRQLAEVAKGEEGGERGLKRLQELSRHHGQAQRQLQAEQERVAELEARVAR
MASEQQQLAALQDLARAKEKEGKEQEKLASAERVGKLEAEVRKASEALEAVSKELSEERLKFKELEAV
ATQEAASEVARLSAALAEAAEHQGE LARKEEAAKRLQKELEDAKADCAAEKARKKVELEVQLQNSINEQRV
ERSAHQQLARSLLEIEKEGELEDELRLKNVSRGEELRDQLQTVSKLKGELASVEAVKERASKMDSLQG
FLAARSRDAEMDSIKAVYAKEASLKNLEEKIRHREQESGSSQDLIQEKLKEAQMLSVEVERLEQKCRFQ
QDTIAGLEKAVAEESQQAQAELEALQREAVRHRETAABLQRLLDASKSAQALQDGTVESLRKELQOKSKE
LAQSKMAVAAAEKEVASLRAAAEKGHLEEGWKELSQCTQELERNKSLGSLSEHVSILIHQLTEKKEG
SKELKRLIMAESEKSKLEERLVLQTEMATAASRAAERCSLMKVEVQRCQEEMEKQMTIEALKRDRHC
QSEREELRQEVKVCQDKFFQKEQLLSSILQQLGSAQAALAGEVVP LKHLCCQLQAERASLESKHREDLEQ
RAKATTALQAELARARVEVAELPALRDRAAEQERALQRLQKETASSERLAAQAANSRLAEENRALSES
VSRGQQLRDAELQAREKHRTRELECVRLAEAKAMASSRQEAEEAARKLEAMSNKYENTKVKVLEERQKFO
EEQKLMQAVEQLEVFQKEQAQKVEELNKKLVQHEKATR SQQVRKVLEGE LQSEATRQOEERVALEELQ
AQKEQAAEHYKAQMEKAKTHYDAKQONQDLAEKLKAMEQLQKENAELRTESERLAKELQQSVLQAEAE
LSCRELSGGVRSLETQLEFADQQLRELGKFPAPKATLKEPESFRQNPSDLTSDLSLSDGEGPLNSTRK
ATRRHSGDGAAPPGTTEPRASQRLPRKVESLESLEYFTPIASRTQPKLESSAGSLADVLSLESGRTRSGRRR
TTQITINITMTKKTETTEEPGGADASFSSILSEQPKAAPARARLRSARSLASFPSQDLSLKLDTSSPQEP
SGHAALLSLPGYRPATRSSLRRSQAGSSSSLGRSSIYLGTQDEPEQLDDWNRIAEQLQQRNACPPHLKT
CYPLESRPDSVLGTTITDEEMKTGDPETTLRRASMQPQIAEGAATRRGTLGGGWAHGGITTRQQRKRLSD
ESHQGDPTPESKKPVSCFPRPQTPRERRSSHLRRSEEQAPSQKPERRQSMAFSILNTPKKLGNSLLRRA
ANRKTTPKNSPRGTARRSPRIASTKSPKGAGRRALKDTKF

Xenopus laevis:

>XP_018103294.2 nuclear mitotic apparatus protein 1 isoform X3 [Xenopus laevis]
MALHSQKMEALICWNSLKVDEPVERFSQLQDILNLLKVVVGLSGNLEETTSVLQONPEQRINFLQSLQ
KYCRPGSSAEMLVQWQKILQGENLELEFSKVIIVLLFPYYS TMSKNPKKSEDPDHKTQTELASILRFLVDM
EESLCLDDKLINFLQRKARFPSSGDDASGSDAMS PYSMHRRKTEVRFLELHRVASSTIKSLPADAPSS
PMIEVLVHTPQFQMRRLKKQLSEVRECRDELEVALQNHKHLAEKEAQISLQQQIEHLIRLENQAELEQ
PKELEELREKNESLMMRLRDTLKCQDMKTDKKQLERKNDQWAEENGELTYKVRDLNRLAQQLAEALYET
TEEHERSLSNMQQKQNLSELSGAVGEKKYLEEHDILQGGKISMLEDQLKMGEREVEQETGDCMGDILK
LDLDAQEVAHVHSTQCLSLKEQIRQLEEEKSIAEVEMEAQRSRSESEKAQLQEIVTNLQTSLEITTFQKER
LDNEARAQQEHLMCQMTTKLLEISKIKSSLMHKDELKDIIHHKVEEERSEKNQLLENLKMLEESEKKDRQ
ELIHQVEHLDSSSLKVSSEGNLVGITQQLSESKTKEADYLR EEQQKICERDSSSLTLENEYKCKKDEEFIALN
GTLR TMEQDHQTSLSVIEELKREKAELASKVQELDATIIDLIAKQNLDSENDSQSKSHAITVESLKAQL
SEQESQVKIYQKKLSNLELVSKENSQ LKBEQLLSMEESVRNLSHELDKERMKFAASLDGDSKRKISHLEEM
KKLTESRDAALRNLDERTAGKKIESQLKNLEEEYHRSNESQHAQLAESCAAIKQREEREDELSKVVDIWK
KARYGEQQKIAQNSCHMQEQIEELKKT HSDVYQQLGERSKVLMI EAKASETKSSQLEKINQLEGELSA
ANACIKEREAEKKVL SALHSABEKLKIAYQGESERLSHLETALSNAKQDLDLAKLESD EKKYKA EFEA
MVVKLKGNSERIASLESELKNSLAVVKERKCESEKLSGEVEHLKRQLDDSSSQHKHEALAQNINIEIKQLI
DAKEKATSDLAITSEMGALQKQAVDTHKSEFSAQNLENSRSLDPIALKEGEVERINKEAALRQEEIQQQQ
QTMVKLTEELTALAALKERVALQEKEIKQQVQATKGAEEMEAMLKSIISEKSKRIECLEQDINKQKTDLS
SIEGQIQSKLSEAGHQHALIADLEKKCKEQKELICEAQNKAAEAKT LASEKASMEKQLKGIQTLENEIQ
KEBQKCDLQKQLELQAEKQETELRLKKELFHFKVQELQESQKSPDSSNRELSMSLSEVQEQQAIT
EAKEQABQYQKVIDMKNKEVNSLQAEINILSSKVTSEEVASDFEQRLQETSKSAKLEELKKLHTEVE
VYSKELVEKNCAVDILRTEAQTFKGEADEQRMADVCLQKQLSSQAE TNNNLQEQEQSQWQKNCAEKQKIC
SLQONLNSNQSLEEFASLKRYSQETLAERGLMQQKHQEILLSHKNLTERFOAELEKTKEDMAEIVLLKE
KLNNQELQLHLKQSENSDQSSQISLNQVNSRLLGENQSLSQITSDQDAKKLSTEMSTLKEQHEEEMKTLR
LQYEKTQREGNEQVQDLSRLRETATSKYDHVKSVKLQDKQTFQEEKQMLLRVELEAAAKEQSEQVQEL
NQKLQEQEKTLSQSQQKLKQREGETHEEAETHKRVIELESQLEQQTQAVEHYKAQMEKAKVHYDAKKQ
NSLELSDLELQSHIREQEHLRKENADLKAESQSLKELQHSLLQSKAEABQCNKLN SNRVRSLEAQVEYSDRQ
LQDLGKFLATDSTKRRDTFCVPRETRSHADVIDSIDLSDFEEDQLLNTSKNGRCNQEPATSSVHASL
DSPASSQLPKVESLESLEYFTPIPTRAQSKLESSIGSIDGLSDLSKKTRSARRRTTQIINITMTKTKTE
EREPESANTSFYSLRSAPSYQNLHQONPKRAARQAAISTPALASLP SQESLAKTEHFSSDDSLNNSVLM
NLPGRYAPARRSSRLSQTGRRSSFY MSTCQDEPD PQEDWTRIAELQARNKTCPPHLKTSYPLESKSLFS
STLTDEEVKLGDPKETLRRATMLPSQIQDSTTSTRLLTAGSGAEHLKGHGISTRQMKRVSEESHYGPD
TPEGKATCTCFPRPMTPKDKHDARRLSTMSKASSSHQQVQPTRRQTSAFSIFNTPKKLGSSLLKGLNKK
KTPPKNSPRGRGTNSSASSTSSKSPHLSLRKSPRRS PRVSTA KSPKASNKVQEEQIQFERKKQQRNK

Salmo salar:

>XP_045580741.1 nuclear mitotic apparatus protein 1 isoform X1 [Salmo salar]
MHLWLDKEHALLEWVNHNLVDLPVRSINDLQDVLMLKLVYLRKKEEPANSYLDQHVRKLVVSDFLQ
DCRCSTTERGALISWDNINSGLNLEVELSKVLVLLYHVSVINNHVDNLQLEYKFEVELASMLRFLVDNNS
LYLSENLEKYLRKKPLPFSFNSDISSTSSSSLFNDDSPVFQRRKMGVSQFLLDQTVASSSVSSPLQDVM
NTPQFQLKLQRLQRQERDMRDELEKDLTTSATTLTQRESQICQLQHRIEKLLRQAEQEQEPREDELQEL
HSKNEGRLRTLHEVLKECQALKTNSSQMERKVDSLTEENGTLSAQMREVVARIASAEAEVDRLIEAQDSA
QGEWSSRHCHLQDELNRATAQKECLSEQMLILQSKISSELEDELSKAKMQEKGVMGPILEWEQLKQELAD
ATLRLHAECCTIARLKGKEQAAALHAQERASLQAESQRLQVIVTELQEALSALRADREALELASKEERE
SLTAQLHTLTAEVASLTQTVQOREQEVKALGEEVQEQECMRGELN LAMERQDREAREIEQELTSHVDTMG
ASLRAREEEVQVREKQLTKQQESALQREV LQEEMAASEKALKELKKQEEAVREAEATLRHQEITTHVTDL
CSLRQEHQALQELARQEEIE SLEKEAQAAHREKAEVAEALSRLQEEVRSLEGEQMAQLEEAQREKERLL
LQSTENMETLQTERAAASSLAEAKDLELSILREEVRAEEQLAMQEEYRLRQEEQLAEAAQENENNM
RERLAGLLDQISLLKVEQCQGNKMEALREEHAAQLEQLRLVKEQVEVQERNEETS AALREKESLSREKE
SSRLREKESLRGLEEELQSTTSLASQRQEE LTSLKEEVILQEEVEERRAAEALAVEAREALEESVSAL
QQQLDSAIQDNMGRKCERLEQDLERQGTLVEELRQQEH SARLEATRLRQEISTHLSRLVEVQREKEEL
RGEVSLHQQRAAVLQSSLEEQEVAMRVLKEQKESIREETTVTKIEALQAQLEVVSSLAAAKDLQLSTLREE
ATALQELQAKREQEISLQKEV LQEAHREKESLEALREELARQEE LREELILQQQRAQSLQSLSEEQEEA
KLELTLKEERAREEATQLRQIISTHLSRLVEVQRGKEELREQEAKAREETTVKMEALQAQLEVVSSLAAA
KDLQSLTAREASSLLCQNTKRAADLKQVLEKTLRELSLSEBHALKEDLAKQQEBELRGEVSLHQQRAA
ELQLSLEEKQEA LRELKQQLVQQEDSS LQKVLQEAQAALQQAEDALRGEVSLHQQRAE LQHQAAL
REQEKSTTEATLKM EALKAAKDLQLSALTEKATALQELQAKREQEISLQKEV LQEAHREKESVREALRE
LARQQELREELILQQQRAQSLQSLSEEQEALKELTLKEERAREEATQLRQISTHLSRLVEVQRGKEE
LRQEKEKAREETTVKMEALQAQLEVVSSLAAAKDLQLSTLREEASLLCQENTKRAADLKQVLEKIRLES
LLSEBHALKEDLAKQQEBELRGEVSLHQQRAAE LQHQAALRQE EKSTTEATLKM EALKAAKDLQLSAL
TEKATALQELQAKREQEISLQKEV LQEAHREKESLEALREELARQEE LREELILQQQRAQSLQSLSEEQ
QEALKEITLKEERAREEATLKMVALQA AKDLLESLTRQEATQLRQEISTHVS HLEEVKSEGFLPREHTHAL
QVQLAKQEE NSLQKGLLEQVQATV LQEREAKEALRGEVSLHQQSLSEEQQAVARETLARQKEEGQAAGV
QKELMEQFV LQQEK EALLTRALQAEQNSQSELEGSMAELRAQAESRESGQRQLDALLLEKERLTEGHQV
LEMKCSAQRLEAVLLEELALLRQEMGTEWEKQITRLREQLAANTEVVEHYKQTQVEKAKSHSYGKKQQL

VESQEQVTELQRSLEVREHEVNAVTTTEMKLLQKELEKARNKEKSLSSKVNLTLEAQLAFTDRHLREQSQVR
PERGGIGIEKMRGGRESVYLKVPQSQTHQETSGSDSLDSDSDSLNTTRPLGPDESSPTPLVRSSERVAAK
RRALGGESLETLYFTPMNNRQINRTSTERRLESSITCLGELALDSARKRPPPTSSARRRRRTQVIVNITMSK
TTPGRGGAGGSDSNEMFYSLSSVRSHPNITGSTHTARPLISMEVFHTPGKPAVASDQLLSLPGYRRSTVH
VAAPQSTGQFCVGAENEPDHAADDWLRIAELQARNQSCPLHLKSSYPLESRPSLGPSEFFETDDDLRMGDP
TETIRRASVMPGQIQESLSSHRLSLHPGQADSTTASRPAYGSHRLSLMPPKPKASSTLANQNTNHLRGSN
LSLKRSKADQEPDTEVVRMEAKRMATSCFPRPLTPKGGRFSSSNNRQFPSPAERRQSMVFSIDNTPRKAA
KSGGLQRMGNKIRSSSTRKSPANKISRVPRSGDVKSFPQGGKAQRKSPRTNSSKSPKNFTSARKEPEVLV
GKPIHLRS

Petromyzon marinus:

>XP_032819484.1 nuclear mitotic apparatus protein 1-like [Petromyzon marinus]
MVNGRKSAAALISWVMCMCAEKTESLWDLKDLSTYLHIQTIKASVDVKPLLKSSSEYEGKNYIREFLHQFF
QKNACLTQTVDMDALTVGEHVELELAKLTVAFLLCAAVSTETIQSRMKFLDPDTQIQLHEILKFVMDNEESP
QLQVNLLELLNNGCVVRSPGVFSIATEETSGRFSSPLSSLPLGHTAGVRFRLQRIASSSMNNLLSSPGS
PSSPMLSPFFDQPAVEVRRLLKQQLRQEWBQQEKLLEGELSSKSQLLKQSEQEVAEELGRVERLVQLTQTRPP
SPLPSELAELHEKTQRLSVTVKQCQELKKEINELMEKRLTLQAEENGELSSKVRESCTHAECSRSLFEES
RSAGQRHAAEVRIRHLEALGEALNSKASLEETVRILQGLKALAEKASLEQRNLPFGVEVMSEVLQM
BEWHMCQKARERADVGLPPLAKAHTNTTHGHDPTTSREEQSAFPNNVSDNDSSTLIVKDRKYLMPNEST
MELEGSMVDQYNVTFREELDGHESKQTGVSQDKCEATRARSSALKQNSLEGSSSTSRRREMGARGVEN
PEFKNNHGRDRTLQGGRTLLQQERVALSKERDILERERAALEKEQMAVIAMGAGNRSILMGHMLTTEASIA
QQRAILDQEKNNILNEKAALKAMEDEININLRQKSRLLDQEKRRLEQDMMILKQKWNVCVEQDNLVKER
AIEDQSKASFTKEIITYLKASLEETSGMKARVEQERVLLENEREKIQSITANQNDTASLQREIRIAMQOE
VDVREQARSALICVVAALEKIEVMPGNEKGSVICALEEGMTTLKAILGLDKGIACEGTHIDMADNGVIAQ
AVLQQRTEPEAQDNYFISVGRHGMGHRERDRTLQEKDKNTIEETTWGERSLSQRESLVSLDQSDNVLDR
DQADLETVRVLLKADTKMAVLAPQESAANKVQPMEDQCSPLQDESDSATVRQKAFTPAETVRVLQVQANL
DHEQIVFRDQLQHEVAVLEQKRTTTLTASLEQERNRLCELEQASMSVMEA DSLKAALQLEEVFVFRATLNR
ERTVLEEMKFKVQDNTLLQDQEKVKLQRDRDILLEDEKVSIERERVALLDKMKTALAEKMAIERERVILVA
PLQEERTVLKRELAALHQERAKWTTESERLVQEQALLEQQRVALQQERESLDQHRGNLKVKSEQERAAQS
ETMYVKQENACRLTEQKTLIHDMAELRTTVDEEEMSWARKRVALDKEKAENERVKSNLDRMAVIKKQK
SLDQSGMAKFALERTDFLHKAMINENKSNLKTILIEDCIVLEQKQTPGPKVKGILLDESATAKQERDVCK
AKQAANTLTLQRRAAEALSSSVVERHSVLEQEMYDAVPAKPRQAATQHHETEDTAPPGKVNAAALKALQDLE
TDTEIQEMSSPGAEDRKRTARSEIRRENVNSSFDQEKHGLEKNALEKGENFREDDIMAAATMEENLDT
MTQYEVSTDVARSIDIVTETGMAPSNTIFTKEECATLQANVSEIEDHFNTPGVENTRILSKENLEQTPSEDG
RRHSMVTRSARKRSRYSQETLYFTPLQTRPSLVGGQAPALDWSLNSLEDLVIDSAKKKPRTSSTRRTM
HVIDITILNKKVESCRDRSVSSASTMRSSTTTAYELRSHGDRPTPVQSSNWSLGFPASSAFVTLDFTTS
QNSLQLEDMRSGRLSDASRLSPGYRPLPGHPTDGRNLQQLAPPTRRRKGNASYMSCVDEPDPEAEW
DELEQGLGAHALPRRQPRAALGTACYTEGLQENQPPVNCVKVDFSEKSDTRNDHLRQEELGKRNRQATL
PHLRSCYPLKVEFTMPGEDLCTAKPEMTARRMFLPALADANAMRKRKSGIGHNTECSPESKKSATMCF
VVPATPRERPPFRASPRDDHPQRSWPIIRRLQSMRSRKKSPSSKASKP

Branchiostoma belcheri:

>XP_019634543.1 PREDICTED: LOW QUALITY PROTEIN; nuclear mitotic apparatus protein 1-like [Branchiostoma belcheri]
MFNRGKLDALLGWNVLLGVGTVESLKLRLGNILVRIVLQIDPKLIEAEADPAGRVEVKSFLGFGHVTS
LGDDTVVRWHLLIQANVAVLAKAAITLVTAFVSDAREGQPMGKMDGRMKAEVVTIKDILLQPNITNBERK
GRRPDPADILLKEQSMVSPDAICNGGGGRDGLSTHTNRHVSVATPMSGPGVVVTRLFDSPMSFVRNLMSQSP
QMOKYKIALTKAQQVQQLKIELGTKKHIIIDENDVQLRKMQRALQEKSESEMRLSARLDGLRALQDENDAL
QARESERKKLQQRCEKLTKALHIEYEVYKTECQELKKQNDRLFEERHGMEDAMKRCQDQMALQVQELQTELH
CTGQQLQALRDSLKAKDQALQHMQQEKALLEQARHTEERLRETQLELQETMHSSGME SMGESLGSIVEK
RAQELQELQAYTQENWTKPEEAAKLVESLAAARANAASLEDNIRLSIAEGDKQKDLTEHLDNAVQKYQT
AEQLSNEEMARHKAIEIQHQQEQEYQALKTDAAMEREALRSKLGAVSSTKTALTEVLTLENERWTFKAKEAYR
EETLSTEKKLEGAQKQVAQLEEENSVTMAVMQDEKDALERQKLEVSAAAQKCLQINDQVSLQEEKAAY
VANLEGVYKARVEAEMTLGQKELEQTLHDKTSAESALHNTKEQLTAVSQEKAITSALEQVVKQKEEEAAG
LDQLVLTAATENSLSAADLESKAKLCRTLAEAKMLADAIGKLGAASSEKESSELQSLMSDLQTERDSLQG
QLEDLQQQKEDLTQQNSDLHTLELDEHSKDKGAALSKIKEVATSNTELTSLKHSQKRLDSISDCLDILLS
CQEKAMDSLHQEHTELSLENRDLTSKVSLEKQLEESTQGLTHVTEEKESQVINLEGLRLDQASLDKAE
QEKWSMQAEISQRERAAAVLQEQHAKRLQHLESSESRQLERAEALRVQLLESNSRAAAAEQSGCKLQAE
QTLQQTQADREAEETEKQAADMQTELFQVQDRLLISESAKNRAEAQNADLCNELQTMKEQVLSLEADSKAQ
QQQLDRREAAAMAAANKAGKELGQGLEISQVEREAVQQQLDMVHAALDQAEASKDLKGQLSTAQQGLEQS
KSGSEELRQLGTAQQLQLEEMKTSRDDLQSHLQTAQEQQLQKQDAVQGEQLQKQLQTAQVNLQSEATRNDL
QNHQLTAQGTAPFTKGQVCRVNRQKQLQTVLEANLQQTAEATKNDLQSHLQTAQEQQLQQRNTAQAEQLKQLQTA
QANVQQTAEARNDLQSHLQTAQEQQLKLDOTALGELQNLQTAQASLQHTAEATRNDLQSHLQTAQEHQKQ
DTAQVBLQKQLQTAQNLQNTQNLQTAQEQQLQKQDTQVSELQKQLQAAQANLQQTAEATRNDL
QQQLTAQEHQKQKQDADLQNLQTAQAEKGLHSEAVRNDLQSQVLQAMQEQLNKNDAAQVLIQTALKALAN
LQETEAATSNLQSQQLQTAQQLQKQCTAHDGLQVQLQSSMAKLEQSEASRSDLQGLQTAQEQQLQKEAA
VGLCNSLQLEASQVLEKAEAGRNDLQSQVDLVQAQVMQSQNSDDETVAEALRVQAAHFEQECSSQLQEEKQ
LLQWEMDMAYKVRVQCCSTLQRELGEAAHSSQQLLENNAQLCSQQQEMAKEKSYRQKEVAMQOHFEE
QLRGLKELQGAMEEVQGRKNMLEEQLKMSQSQQELSEQLHSYQMHYORKKETIQDLEKSLQKQENAHES
VKQLQTVQQERNKLLKENSLSLTDVKTAEKLEKEEATTKKLYQQVRSLEAQVDLANRLRQKQHVSF
ATPAARSINTSDSIDETADETFDLEPSRQRHSTSRDDLRTLSNSQVAGEEEDGKNKNTISTDSLEGD
SLDTSIFSRTSQDSGMSTRSQRRRTTVSIEMVQTESDRRLSRTSTEHVLDGSSISGASSWRGAAPRFVVS
ECEEEPEQYDWRLSLQRRNLTQPRHLQSCYPTETQGTALREETDLSKTLRRTLRSQQAATFSITPG
KKRRHEADENSASRKKTVMPSTPSKTPSVFKTPKKIASAAAGIFKKPTGKTPSSRRRSRLQGRGKSPA
GRNLKAKTPTKTPNKHQAKQDPRRQSIAFNIGFSLPGKFRKSARKAKEKREQAQKPEQSRMSIANVKSFL
SVNNSKTNKTKAARKPLGRNNAQTGV

Drosophila melanogaster:

No homolog found.

Hydra vulgaris:

No homolog found.

Nematostella vectensis:

>XP_032223093.1 nuclear mitotic apparatus protein 1 isoform X1 [Nematostella vectensis]
MNNERVATLLEWINSVSGNVNLPFRDSTVENVKLLVKTILHLIDKSDDEVLPGYDDATVEGLVGPFISSL
EGYVRQKLDGIVINPNLITVDADEVEIGKVIALMLSAAVQECENANYFVKIKQSFEESVQYQIKEIITELL
QQVEHGLGDSASAITKLLKHTTGKNKEKQELPAGTDVCVESPLFGKSPTETLFSSSPFLSLMSSPQLKTKQH
QFTMNKHLQKVSKQLSLDAQMHMQATLEELADCKCEIDVDKTKMKLEKNKDVLHLMKVIDELESTQHYK
ADYEKLERSERMKQRVAELEAFREQSCNLDERMADFLKKAMFKKSVEDMEQLKTKCERYKSQLEHEEF
KASELKAALERRVKDVERLEKERDEALFAASEAMELWKARKSVEIDEEERLDGDSFPVDTQHTNLSRI
IELEPTNEKLRAQLASAIIDPSEVQRLNDALEDAEQSKRSYEASYVEAKCKILELSDSVCKTETQFKVREK
ELNSRLLEELTKNVLSQEKLTNHRKELSRQLSELSARGEVEAHAIASEKQATASKALDELLDERKAAE
QAACTRYNELRRREMEKERRAEKVEEIRDCDHKIRHVTEELHGIETQQRQEMRQKRDEFPSTREDELKA
AVERVTEERDAVKNAIEEMVGDLTLELNEVKSrvLLLESLQQASTSWESAEAAALTEAKAILEKELVSLK
ESQALLNEDNASLNKELVAMCEKEKYIISVNKELAQISNLKMRREEEKKREASRQIADLEEKLAGMVQEI
GRLESNTKGWEEANVWEEKAQIGKEVACLKDAFSTEMYTEKQSLAKHSRDIEGMTKINEELKAKLCS
QKQSLDEVQNTQNGRLQREMCATEDKLLQITTLRNKILEQLLAEQQQGEERAARQAEMDHKADHAKAMQ
EATLLNBERDAFKASLELERAQCQLVAGDEIEGFKRSQNETQELLIEKHRAKQMEELQGLQDF
TKQNLNYEDTKQYQVQREYEMERAWKKKLTANEELVKLKGEMFENSQKHSABLCLRRQTOEKEDE
MEGEKKNMQEHTRQTOEKLQTSETIIKGLRADIKQLEIVKKTLEVEKGQLKSICEDFAKKEKDRLLEVEK
MTDKHEEKIAKINENQRALALKDEDAQKLMEKTEELKARMEDEHQKALGLKDEDIQKLMKEOTELKAKM
EDEHQKALGLKDEDAQRLIKETEELKARMAEIEEARKGEVAMAEERRQKAEQKKSMDAIEHLKRLKE
QSEESLIKESDAKFTKTNDLEKVKKALETTQESWKEKETEMAAKLAQSEQLCEDMKDDQELIERLQDEIA

KMEEQVNVINEEKGLLEEQLLEEQDTNKRLLGMQVNSLEAQVKHADMTIREQKAKMQSFENQSEKVKKTRK
MLIEVEKVLFPVQEAQELLDESTTESDDSEMRVDDLKLTRQGSSVSFASVNGTDFGKSLSTSSISRTSLR
STVRPSASRRQSAMYVKGSTPPTRRTTSSAAFFIVGDEFANNMEQSEYEFDWDRLAELERRNTICPPHL
KTSYPVETQTRPSEGNGLHAARSETALTRKRKPEDTLTSSVKERKDMTTSKSEGQIKRSRKRITDMVSS
KINSLRPSKSNENIKEKQKSGNSLAFEITPPKKRKAEPKAASDTPRRESTKKETVAFTIENSPPKKCKV
QRTRTINRSTATTQLVRDKDRETFKREKKLETKNRIPLRSSNRKIAK

Amphimedon queenslandica:

No homolog found.

XP_032223093.1[N.vectensis]	--MNNERVLTALLENISVSNVGNVLFRDFTSVNKKLVKTHLHDKDSDEVLPGYDDAT	58	
XP_019634543.1[B.belcherii]	--MFNGKGLADALQWNLILG--V-CTVESLEKLDENVNRILVRVQLIDPK-----	51	
XP_032819484.1[P.marinus]	--MVNGRKSAALIWNCNM--CA-EKTESLWDLDKLSYLHIHLITQTIKAS-VDVK-PLKSSA	54	
XP_045580741.1[s.salar]	MVLRLLDEKHAELWENHNIN-LVD-LPVSRIINDQQGVLMKMLVKIRLEKE-FPAN-SYLDQH	56	
XP_01803294.2[X.laevis]	MAHHSKGMEALKWCNSJLK--EPVDFRFSQLQDINILLKVVGVLSNGLEETT--SVLQON	57	
CBN80053.1[G.gallus]	MLPHTTTRATALLAWNSNTKACA-EPLGRSLSQLQDCRVFVIQTIINKIHT--EEGE-SVLQGS	57	
NP_001304073.1[M.musculus]	MTLHATRAATLLSWNSLSH-LVA-DPVETVLQDQCISFIKIINTIHT--KEGO-QILQOF	57	
Q14980[H.sapiens]	MTLHATRGAAILLSWSNLSH-LVA-DPVEAVLQDQCISFIKIINDIHT--KEGO-QILQOF	56	
XP_002822235.1[P.abellii]	MTLHATRGAAILLSWSNLSH-LVA-DPVEAVLQDQCISFIKIINDIHT--KEGO-QILQOF	56	
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XP_032223093.1[N.vectensis]	VEGLVGVTISSLESIGYRQKLID--GIVINPNLITTVDADEVIEIKRVIAIMLSAAVQECENANY	116	
XP_019634543.1[B.belcherii]	PAGRVVEVSGSLFLGFHVTLSDGDTYVRWMLIRIQANED--EIAAKATLLTIFAFVSDARQE	109	
XP_032819484.1[P.marinus]	EYEGKNYIREFLHQFFQFN-AQLQTVDFGVHELELAACITVFLCACVASFTEIGS	113	
XP_045580741.1[s.salar]	VQERKLKVVSDFLQCDRCRSTGERALISVDNINSINGLINEVELSKVILVLYSHYSVIN--NHV	PEQRNFGLGSFLQKVRCPGSSAANSQWIKLGENLELEFSKVFIVLLPYSTMSSKNRP	117
XP_01803294.2[X.laevis]	LAEAPAFICGFLQKCHKASTENLVASAQKLECEL--ELAKVAILLHSMSSSKSPR	115	
CBN80053.1[G.gallus]	PERLFDFVCSFLQKRKHHPSPCTCVSVQKVIWGESM--ELAKMMLFLYGOSTMSSRNLR	114	
NP_001304073.1[M.musculus]	VSERLDFVCSFLQKRKHHPSPSPECVLASQKVLGSEL--ELAKMTMLLYHSTMSSKSFR	114	
Q14980[H.sapiens]	VSERLDFVCSFLQKRKHHPSPSPECVLASQKVLGSEL--ELAKMTMLLYHSTMSSKSFR	114	
XP_002822235.1[P.abellii]	VSERLDFVCSFLQKRKHHPSPSPECVLASQKVLGSEL--ELAKMTMLLYHSTMSSKSFR	114	
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XP_032223093.1[N.vectensis]	FVKKI-QSFSESVQYQIKEIETILTQQVHEGGDLASAITKLKHT-----TGK-----	163	
XP_019634543.1[B.belcherii]	RMSXMDGMGKAWEVTDIKQIINFNTINNERKGRPRFDLILLEGMSVMPT-ACINGG----	165	
XP_032819484.1[P.marinus]	RMKFLL-----DPDPTQILHELKFMVDNEESPQLQNVILLELNGVCVPSGPVGSIAETE	169	
XP_045580741.1[s.salar]	DINQL-----EYKFVEELASMRFLVDNENSILYSENLEYKRLKPFLLSPFSDISSTS--S	KSEDF-----DHKTQTELASTIRFLVDNESCILDCKDINFLQKRRFPSSGD-----	165
XP_01803294.2[X.laevis]	DWNEF-----DYQIQVELATILFKVLDDHEELS--ENLEVFORRRALPPSPGT-----	161	
CBN80053.1[G.gallus]	DWQEF-----EYGVQAEIALVILKFLMDHEESINITDELDESFEKVP-PY--THA-----	159	
NP_001304073.1[M.musculus]	DWQEF-----EYKQAEIALVILKFLVDHEGINLINDELLENFLQA-PVPSTCS-----	161	
Q14980[H.sapiens]	DWQEF-----EYKQAEIALVILKFLVDHEGINLINDELLENFLQA-PVPSTCS-----	161	
XP_002822235.1[P.abellii]	DWQEF-----EYKQAEIALVILKFLVDHEGINLINDELLENFLQA-PVPSTCS-----	161	
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XP_032223093.1[N.vectensis]	---NKEQGELP-----AGTCVDESPLPKSP--TET-----LFSSSPFLSLMSSPOLKTK	208	
XP_019634543.1[B.belcherii]	---GGRDGSLT-----HTNRHRSVATPM-SGPVPIVTRLDFSMSVPMNLMSPOMQY	215	
XP_032819484.1[P.marinus]	SGRFSPPLSL--PLCHTAGVRFRDIQRIASSMNLLNSLPSSMFLSQFPAVEVR	227	
XP_045580741.1[s.salar]	SALFNDDSPFVQKRRHGQSVOQLDITQVASSS-----VSSPLSDMIPTFOQL	218	
XP_01803294.2[X.laevis]	DSGSSDAMSYPVSRHRRTKTEVRFLELHVRASS--TIKSLPADAPSPMIEVLHTPQFQMR	224	
CBN80053.1[G.gallus]	SSSSSES-P--GLSHPOVRFLELQIASSSSSMMNLMPGTASPVPDGLVLTPOFQRL	217	
NP_001304073.1[M.musculus]	ST-LSEELS-P-PSHOTKRIREFLEQRIASSS--SENNFLGSSPSPMGDILQTPQFQMR	215	
Q14980[H.sapiens]	ST-FPEELS-P-PSHOAKREIRFLELQVASSS--SENNFLGSSPASMGDILQTPQFQMR	217	
XP_002822235.1[P.abellii]	ST-FPEELS-P-PSHOAKREIRFLELQVASSS--SENNFLGSSPASMGDILQTPQFQMR	217	
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XP_032223093.1[N.vectensis]	QHQFTMNKLHKQVSKQLSLDAQMHQMHTALEELDCKCEIDVYKTRMKRSLNDVVHLM	268	
XP_019634543.1[B.belcherii]	TA----LTKAQOQVQQLKITELGTGKIIIDENDVQLRRQRALEQEKSMRELISARDLDGRA	272	
XP_032819484.1[P.marinus]	K-----LQKQLQEWQEQCKLEGLSSSKQLSQSQBEVALRQGVKRLVQ	273	
XP_045580741.1[s.salar]	R-----LQRLQKRDMDRELELQTLTSATTITQRESQITQOLHRIKLE	263	
XP_01803294.2[X.laevis]	R-----LKKQLSEVRECREDLEVELAQNHKHAKEASQIAMSLQOOEHILRI	270	
CBN80053.1[G.gallus]	R-----LKKOLAERNRDELELAENRKLITEKAOITAMQORQIDRLAL	263	
NP_001304073.1[M.musculus]	R-----LKKQLADERSNRDLELELAENRKLITEKDAOITAMQORQIDRLAL	263	
Q14980[H.sapiens]	R-----LKKQLADERSNRDLELELAENRKLITEKDAOITAMQORQIDRLAL	263	
XP_002822235.1[P.abellii]	R-----LKKQLADERSNRDLELELAENRKLITEKDAOITAMQORQIDRLAL	263	
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XP_032223093.1[N.vectensis]	VIDELETSTQHYKADYEKLERESERMKQVIAELEAFREQS-----CNLDERMADFLEKK	321	
XP_019634543.1[B.belcherii]	LQDENADLQARESERRKQCEKCEKITQALHEVEYVYTEQELKKQNDR-----LFEER	325	
XP_032819484.1[P.marinus]	LITOTFRPS-PLPSELAELEHKTQ-----RLSV--TQEQCLBKLNEMLEKRLITQALEAN	319	
XP_045580741.1[s.salar]	-REQEQEQEPREDLEQLHSNKNEGLRTLRLH--VLKEQCADKTNSSQMERKVDLSSTEEN	325	
XP_01803294.2[X.laevis]	LENREQA-ELQEPKELELREKNESSLMRLRL--TLKQCDMKTDKQLKERKNDQWAZEN	326	
CBN80053.1[G.gallus]	INEKQAADQLQEPREMEELERNESLIVRLHE--LTKQCDMLTEKQGMDDRKNQLSEEN	320	
NP_001304073.1[M.musculus]	INEKQAASSQEPKELEEELRGNESLITVRLHE--LTKQCDMLTEKQGMDDRKNQLSEEN	318	
Q14980[H.sapiens]	INEKQAASSPLEKELEEELRDNESLITMRHE--LTKQCDMLTEKQGMDDRKNQLSEEN	320	
XP_002822235.1[P.abellii]	INEKQAASSPLEKELEEELRDNESLITMRHE--LTKQCDMLTEKQGMDDRKNQLSEEN	320	
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XP_032223093.1[N.vectensis]	AMFKKSVEDMEQKDKTKERYKSLQHEH-----EFKAS	353	
XP_019634543.1[B.belcherii]	HGME-----DAMKRCQDMALQVQELQTEHLTCTGQQLQALRDSLKAKQDALQHWQEKA	378	
XP_032819484.1[P.marinus]	GELS-----SKVRESCTILAECRS--LFEERSASAQRHAEAVRH	359	
XP_045580741.1[s.salar]	GTLSS-----AQMEVVARLASAEA--EVDRISTEAQDSQAGEWSSRFX	359	
XP_01803294.2[X.laevis]	GELTF-----YKVRDLSNRALQLOE--ALYETTEEHSRLSNWOQ		

XP_032223093.1[N.vectensis]	QSKRSYEAS-----YVEAKCKILEEDSVCKTETQPKVREKELNSRL	496
XP_019634543.1[B.belcheri]	QEYQALKTDAAEMERALSRLGAV-----SSTKT--ALEVTLENERWTFKAKEEAYREEI	563
XP_032819484.1[P.marinus]	-----DQYNVTFR-----EEL	509
XP_045580741.1[S.salar]	QEVKALGEEVQCEMQRGELNLAMERQDREAREEIQELTSHVDTMGASLRRAE--EEV	570
XP_018103294.2[X.laavis]	KEVKDIIHHKVEERSEKQNLLENKMLEESSKKDRQELIHQVEHLDSLVKSE--GNL	580
CBN80053.1[G.gallus]	KEAAELRMQAEQERAQAEELRH-----RDMASQEALESLSRRVEQLGASLKHSE--EEL	570
NP_001390473.1[M.musculus]	QELASLKEQAKKEQAQMLQTMQ-----EQEQAAGQLRQQVEQLSSSLKLKE--QQL	561
Q14980[H.sapiens]	QELAGLKQQAQKEKQAQLAQLTQ-----QQEQASQGLRHQVEQLSSSLKQKE--QQL	567
XP_002822235.1[P.abelii]	QELAGLKQQAQKEKQAQLAQLTQ-----QQEQASQGLRHQVEQLSSSLKQKE--QQL	567
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XP_032223093.1[N.vectensis]	EELTKNVE-----	504
XP_019634543.1[B.belcheri]	LSTKKLEGAKQKVAQLEENSVTMAVMQDEK-----DALERQLKEVSAAAEQKCLQL	616
XP_032819484.1[P.marinus]	DGHESKQTGVSDKDC-----VEATRARSALKQNSLEGSS--TSSR	548
XP_045580741.1[S.salar]	QVREKQLTKQQQESA-----LQREVLQEEMA--ASEKALKELKQEEAVREAEATR	618
XP_018103294.2[X.laavis]	VGITQQLESKTKE-----ADYLREEQKKIICERDSSLSTLNEYKC-----	620
CBN80053.1[G.gallus]	VRVTQEAEKG-----ARQLGAHEKAVQERDAALQQLQHLQO-----	607
NP_001390473.1[M.musculus]	EEAAKEQEAATRDHA-----QQLAIVAEAREASLRERDARQQLLETVEK-----	605
Q14980[H.sapiens]	KEVAEKQEAATRDHA-----QQLATAAEEREASLRERDAALKQLEALEK-----	611
XP_002822235.1[P.abelii]	KEVVEKQEAATRDHA-----QQLATAAEEREASLRERDAALKQLEALEK-----	611
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XP_032223093.1[N.vectensis]	----LSQEKLT-----HNRKELSRLQSELSLARGEVE-----A	533
XP_019634543.1[B.belcheri]	NQQVSLQEEKAADVANL-----EGYKARVEAEMTGLQKELEQTLHDKTSAESALHNTKE	671
XP_032819484.1[P.marinus]	-----REMGIARGVQENFEFKNNGHRDTLEQGRILLQQERVALSKER-----	590
XP_045580741.1[S.salar]	-----LHQEITTHVTDLC-----SLRQEHQALQELARQQEEI-----SLEKE	656
XP_018103294.2[X.laavis]	-----KQDEEPIALNGTLRTMQDH-----QTSLS	645
CBN80053.1[G.gallus]	-----AKKQLAALSSQLQSLEAAS-----KA	629
NP_001390473.1[M.musculus]	-----EKDAKLESLQQQLQAANDAR-----DNAQT	630
Q14980[H.sapiens]	-----EKAAKLEILQQQLQVANEAR-----DSAQT	636
XP_002822235.1[P.abelii]	-----EKAAKLETLQQQLQAANEAR-----DSAQT	636
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XP_032223093.1[N.vectensis]	HAIASEKQRATASKALDELDERKAAEQAACTRY-----	567
XP_019634543.1[B.belcheri]	QLTAVSQKEAAITSALEQVQKQ-----	693
XP_032819484.1[P.marinus]	--DILERERAALKE--QMA-VIAMGAGN-----	614
XP_045580741.1[S.salar]	AQAAMHREKAEVAELSRQLQEE-VRSLSGEQMAQLEEAQREKERLLQLSTENMETLQTERA	715
XP_018103294.2[X.laavis]	VTEELKREKAELASKVQELDAT-ILDLIACQNLD--	680
CBN80053.1[G.gallus]	SSMEMQKEKAELNKKVQELQAR-VLELSAQCCQSSA-----	664
NP_001390473.1[M.musculus]	SVTQAQKEKAELSQRKIGELHAC-IEASH-----	657
Q14980[H.sapiens]	SVTQAQKEKAELSRKVEELQAC-VETAR-----	663
XP_002822235.1[P.abelii]	SVTQAQKEKAELSRKVEELRAC-VETAR-----	663
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XP_032223093.1[N.vectensis]	-----K-----	568
XP_019634543.1[B.belcheri]	-----K-----EEEAGQLQDQIVTANTENSS	714
XP_032819484.1[P.marinus]	--RSIIMGHMLTTEASIAQORA---ILD--QE---KNNKNLEKA---ALKMADEIN-	658
XP_045580741.1[S.salar]	AASSLAAEKDLELSLREEVRAREEQQLAMQEEV-----RLRQEELEQELAAQENIN-	768
XP_018103294.2[X.laavis]	ENDSQSKSHAITVESLKAQLSEQESQVKIYQKKLLSSNELSVSKENSQKLEQLLSMEESVR-	739
CBN80053.1[G.gallus]	QAG-----SAETLRAQLRELEGLKDSQKGLADKEKVAKENLRLQERLLFLEESVR-	715
NP_001390473.1[M.musculus]	--Q-----EQRVQARVTELEAQLKAEQKKTTEREKVQVQEAQLEQLRALEESLK-	706
Q14980[H.sapiens]	--Q-----EQHEAQAQVALEQLRSEQQKATEKERVQAEKQDQLEQLQALKEESLK-	712
XP_002822235.1[P.abelii]	--Q-----EQHEAQAQVALEFQLRSEQQKATEKERVQAEKQDQLEQLRALKESLK-	712
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XP_032223093.1[N.vectensis]	-----ELRREMESKERRAEKEV-----EIRRDCHK-----IRHV-----	599
XP_019634543.1[B.belcheri]	LAADLESKAKLRTLEAEKAMLADAI-----GKLGAASSEKESKELQSL-----	757
XP_032819484.1[P.marinus]	-----INLR-----QKSRLLDQEKRLQDMITL-----KQKWNVCE-QEQ-DNL-----	696
XP_045580741.1[S.salar]	-----NMRE-----RLAGLLDQISLLKEVCQE-GKNMREALREHAAQLEQ	807
XP_018103294.2[X.laavis]	-----NLSEHLDEKMKFAASLDGDSKRIHLEE--E-----MKKL-----	773
CBN80053.1[G.gallus]	-----NTEGILEDEKKRAAESLEGNLARIAELEA--E-----KQOL-----	749
NP_001390473.1[M.musculus]	-----ITKGSLEEKKRAADALKEQQCRATEMEA--E-----TRSL-----	740
Q14980[H.sapiens]	-----VTKGSLEEKKRAADALEEQRCISELKA--E-----TRSL-----	746
XP_002822235.1[P.abelii]	-----VTKGSLEEKKRAADALEEQRCISELKA--E-----TRSL-----	746
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XP_032223093.1[N.vectensis]	----TEELH-----GILETQRQEMQRKDEFSTREDELKAAVERVTEERDA----	641
XP_019634543.1[B.belcheri]	-----MSDLQTERDSLQQLDELQOQ-----	778
XP_032819484.1[P.marinus]	-----VKE---RAIEDQS	706
XP_045580741.1[S.salar]	LRLVKEQVEQVQERNEETSAAALREKESSLREKESSLREKESSLRGLEELQSTTSLASQR	867
XP_018103294.2[X.laavis]	-----TESRDAALRNLEDEERTAGKKIESQL	798
CBN80053.1[G.gallus]	-----VORGEQALQHSSEELARRQALETRL	774
NP_001390473.1[M.musculus]	-----MEQREEREKELEQEKAGRGKLEARI	765
Q14980[H.sapiens]	-----VEQHKREKELEERAGRGKLEARL	771
XP_002822235.1[P.abelii]	-----VEQHKREKELEERAGRGKLEARL	771
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XP_032223093.1[N.vectensis]	-----V-----KNAYEEMVGDKLTELENEVK-----	662
XP_019634543.1[B.belcheri]	-----KEDLTQQNSDLHTELDEHSKDKGAALSK	806
XP_032819484.1[P.marinus]	K-----ASPTKEIYYLKA-----SLEETSGMK-----	729
XP_045580741.1[S.salar]	QOELTSLKEEVIYSLQEVEVRRRAAEALAVEAEAREELVESVALQDDAQDNDMKRQK	927
XP_018103294.2[X.laavis]	KN-----L-----EEEYHRSNESQHAQLAESCAITKQREEE	829
CBN80053.1[G.gallus]	QQ-----V-----AEERREETAALQRLAEVAKGEGERGR	805
NP_001390473.1[M.musculus]	QQ-----L-----EEAHQAEETALRHLEAATAAQHRAESE	796
Q14980[H.sapiens]	QQ-----L-----GEAHQAEETVLRRLAEAMAAQHTAESE	802
XP_002822235.1[P.abelii]	QQ-----L-----GEAHQAEETVLRRLAEAMAAQHTAESE	802
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XP_032223093.1[N.vectensis]	-----SRVLEEESLQQAQSTSWESA-EAALTEAKAILEKELVSLKESQ-----	703
XP_019634543.1[B.belcheri]	I-----KEVAT-----SNTLTKTSLKHSGRKRLDSISDC	834
XP_032819484.1[P.marinus]	-----ARVEQERVLLN-----EREKIQTISITANQ-----	754
XP_045580741.1[S.salar]	CERLEQDLEQRTGLVEELRQHEHS-----ARLEATRLRQESTHLSRLLEVQRE	976
XP_018103294.2[X.laavis]	RDELSKVVDIWKARYGESQKQIAQNSCHMQEQIEELKKTSHDQVQQLGERSKVLMEAK	889
CBN80053.1[G.gallus]	LEKRLQE-----LSREHGQACQRLQAEQERVALEAR	837
NP_001390473.1[M.musculus]	CERLIREVESRQKRFARQEQEARYGAMFQEQLMALKGEXTGQ--EVQ-----EEAVEIH	849
Q14980[H.sapiens]	CBLVLKEVAWVRERYEDSQEEAQYGAMFQEQLMTLKEECEKARQELQAEKQVAGIESH	862
XP_002822235.1[P.abelii]	CBLVLKEVAWVRERYEDSQEEAQYGAMFQEQLMTLKEECEKARQELQAEKQVAGIESH	862
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XP_032223093.1[N.vectensis]	-----ALLNEDNASLNKELVAMCE-----KEK	725
XP_019634543.1[B.belcheri]	LDILLSCQEKAMDSLHQHETELS-----LENRLDTSKVSKELEKQLEE-----STG	879
XP_032819484.1[P.marinus]	-----NDTASLQREIRIAMQO-EVDVREQARSALICVAA-LEKIEV---MPGNE-	798
XP_045580741.1[S.salar]	KEELRG-----EVSLLHQQRAAVLQOSLEEQEVAMRVLEKQKESSTREETTVTKTEALQAQLE	1031
XP_018103294.2[X.laavis]	ASETKSSQLEKINQLEGLSAANA-CIKEREAEKKVLSALHSAEKLKIA---YQGESE	945
CBN80053.1[G.gallus]	VARMASEQQQLAALQDLQARAKE-K-----EGKE-----QEKI-A-----SAE	874
NP_001390473.1[M.musculus]	SEGQPGQQQSQAQLHASLAKAIQ-QVQEKEVRAQKLVDLSALQEKMAA-----TNK	901
Q14980[H.sapiens]	SELQISRQQNELAELHANLALALQ-QVQEKEVRAQKLADDLSTLQEKMAA-----TSK	914
XP_002822235.1[P.abelii]	SELQISRQQNELAELHANLALALQ-QVQEKEVRAQKLADDLSTLQEKMAA-----TSK	914
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XP_032223093.1[N.vectensis]	YIISVNKELEAQISNLKMR-----EEEKREASRQIADLEE---KLGMVQEI	771
XP_019634543.1[B.belcheri]	QLTHVTEEKESQVNLNLEGLRDLQASLDKAEQKWSMQAEISQRERAAVLEQHAQLRLQ	939
XP_032819484.1[P.marinus]	-----KGSV-----ICALLEGMTTLKAIL-----GLDKGIACEGTH-----ID-----	831
XP_045580741.1[S.salar]	VVSSLAAAKDLQLSTLREAEATLQELAKREQ--EISLQKREVLQEAHREKESLEAL-----	1085

XP_018103294.2[X.laavis]	RLSHL-----ETALSNKQDLDCIAKELSDKEYKKA-EFEAM----	981
CBN80053.1[G.gallus]	RVGKL-----EAEVRKASEALEAVSKELSEE-----	900
NP_001390473.1[M.musculus]	EVACL-----KTLVLRKAGEQQTASLELLKEPPRAA-NRA-----	935
Q14980[H.sapiens]	EVARL-----ETLVRKAGEQQTASRELVKPEPARAG-DRQ-----	948
XP_002822235.1[P.abelii]	EVARL-----ETLVRKAGEQQTASRELVKPEPARAG-DGQ-----	948
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XP_032223093.1[N.vectensis]	RLSESNKGWEEFANV-----WVEEK-----	791
XP_019634543.1[B.belcheri]	HLESSESRQLER-AEALRVQLLESNSRAAAAEQSCGKLQAEQLTQQTADREAETEKQA	998
XP_032819484.1[P.marinus]	-----MADNGIVAQAVLQQQRTPE-----	850
XP_045580741.1[S.salar]	-----REELARQQEELREELILQQQRAQSLQESLEEQQEALKEL-----T-----LKE	1128
XP_018103294.2[X.laavis]	-----VKVLKEQNS-----ERIASLESELKNSLAVVKER-----K-----CES	1014
CBN80053.1[G.gallus]	-----SDQLGEQQG-----RPF-----SSTHAIVKAM-----E-----REA	961
NP_001390473.1[M.musculus]	-----PEWLEEQQG-----RQF-----CSTQAALQAM-----E-----REA	974
Q14980[H.sapiens]	-----PEWLEEQQG-----RQF-----CSTQAALQAM-----E-----REA	974
XP_002822235.1[P.abelii]	-----PEWLEEQQG-----RQF-----CSTQAALQAM-----E-----REA	974
XP_032223093.1[N.vectensis]	AQIGKEVACLKDAFSTEMQTEKQSLEA-----KHSRDI-----	824
XP_019634543.1[B.belcheri]	ADMQTELQFVQDRLILSESASN-----RAEAQNADLQNELQTMKEQVLSLEADSKAQQQQL	1054
XP_032819484.1[P.marinus]	-----A-----QDNYFISVGKHGM-----GHRE-----RDTLQCEKDKT-----NI-----E-----	882
XP_045580741.1[S.salar]	ERAREATQLRQOIST-----HLSRL-----E-----	1150
XP_018103294.2[X.laavis]	EKLGSVEHLKRQLDDSSQKHKEALAKNIEIKQLIDAKEKATSDI-----	1060
CBN80053.1[G.gallus]	TQEAASEVARLSAALEEAAREHGEALARRREEAKRLQKELEDAKADC-----A-----	958
NP_001390473.1[M.musculus]	EQMGLELERLAALIKSQGQQQEEERGQQEREVARLTQERGQAQADL-----A-----	1008
Q14980[H.sapiens]	EQMGLELERLAALMESQGGQQQEEERGQQEREVARLTQERGQAQADL-----A-----	1021
XP_002822235.1[P.abelii]	EQMGLELERLAALMESQGGQQQEEERGQQEREVARLTQERGQAQADL-----A-----	1021
XP_032223093.1[N.vectensis]	-----EGMTKINEELKAKL-----CSQKQSLDEVITQNYGRQLQREMCATEDKLL---	867
XP_019634543.1[B.belcheri]	RDRSEAMAAANKAGKELQGLLEISQVEREAVQQQLDMVHAALDQAEASKCDLKGQLS---	1111
XP_032819484.1[P.marinus]	-----ETWGDERSLSQ-----RESLVS-----LDQNSDVLDRDQ-----	912
XP_045580741.1[S.salar]	-----EVQ-----RGKEELREQEKEAREETTVMKEALQAQLVVSLSAAAKDLQSLTREAESLLC	1206
XP_018103294.2[X.laavis]	-----AIKSEMGALQKAVDTHKSEFSALQNELSRSLDFITAKEGEVERLINKEAA---	1110
CBN80053.1[G.gallus]	-----AEK-----ARKVELEVQLQNSINEQVERSAHQELARSLEETEEKEGDELRLKNNV---	1011
NP_001390473.1[M.musculus]	-----QEK-----AKAELEMRLQNTLINEQRVEFAALQEAALAHALTEKEGTDQELAKLRGQEA---	1061
Q14980[H.sapiens]	-----LEK-----AARAELEMRLQNALNEQRVEFATLQEAALAHALTEKEGKDQELAKLRGLEA---	1074
XP_002822235.1[P.abelii]	-----LEK-----AARAELEMRLQNALNEQRVEFATLQEAALAHALTEKEGKDQELAKLRGLEA---	1074
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XP_032223093.1[N.vectensis]	-----QITRERNKIEBQLL-----A-----EQQGGEERAAR	893
XP_019634543.1[B.belcheri]	-----TAQQQLEQ-----SKSGSEELRRQLGTAAQ	1136
XP_032819484.1[P.marinus]	-----ADLETVRDVLKADTKMAVLAPMQESAARKVDFMEEDCSPLDQEDS-----	957
XP_045580741.1[S.salar]	QENTKRAADLKDVQLEKIRLESLLS-----E-----EHRALK-----EDLAKQEEELRGEVSLHQ	1257
XP_018103294.2[X.laavis]	-----LQEEETQQQQQTMKLTTEILT-----ALAAALK-----EKVALQEBEKQVQVATKG	1156
CBN80053.1[G.gallus]	-----SRGEELRLQKQTVSKLKGELA-----SVEAVK-----ERASKMDSRLQCFLEAARS	1057
NP_001390473.1[M.musculus]	-----AQRTLEKELQQTLEQLKIQLV-----KKEKEH-----PAGASGEDASG-----	1100
Q14980[H.sapiens]	-----AQIKELEELRQTVKQLKEQLA-----KKEKEH-----A-----SG-----	1104
XP_002822235.1[P.abelii]	-----AQIKELEELRQTVKQLKEQLA-----KKEKEH-----A-----SG-----	1104
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XP_032223093.1[N.vectensis]	QAEEMDHIAKHAK-----A-----MQEATDLLNRERDAFKAQSLERLERA	933
XP_019634543.1[B.belcheri]	QLEEMKT-----SRDDLQSHLQTAQEQLQKQDAVGELQKQLQTAQV-----NLQQ-----	1182
XP_032819484.1[P.marinus]	-DATVRNQKAFTPA-----ETVRLVQANLDHEQI-----VF-----RDSLQHEVAVLEQK	1001
XP_045580741.1[S.salar]	RAAELQ-----LSLEEKQEAELRELKEQLVQQQE-DSSL-----	1289
XP_018103294.2[X.laavis]	AEEMEANKLSITSEKSKRIECLQEDIKNQKTDLSITQEQYQSKSLSEAQGHQALADLEKK	1216
CBN80053.1[G.gallus]	RDAEMDSIKAVYAK-EASLKNLEEKIRHREQESGSDQLYQKEKLQAQMLSVEVERLEQK	1161
NP_001390473.1[M.musculus]	-----PGTQSET-----AG-----KTDAPGPELQALRAEISKLEQQ	1131
Q14980[H.sapiens]	-----SGAQSEA-----AG-----RTEPTGPKLEALRAEVSKLEQQ	1135
XP_002822235.1[P.abelii]	-----SGAQSEA-----AG-----RTEPTGPKLEALRAEVSKLEQQ	1135
XP_032223093.1[N.vectensis]	CQGLKVAGDEIEGF-----KRSQNETQELLIHE	961
XP_019634543.1[B.belcheri]	-----SEATRNDLQNLHQTAAQTAPTQKGVCRVQKQLQTVANLQQTATKNDLQSHLQTA	1239
XP_032819484.1[P.marinus]	R-----QKVLQEA-----QAAALQOEAVDALRGVESLHQRAAELQHQAAL	1026
XP_045580741.1[S.salar]	CKEKQELICEAQNKAAEAKTLASEKASMEKLGKIQTLTLENIQKQERQKTCDLQKQLEVS	1276
XP_018103294.2[X.laavis]	CREQDDITAGLEKAVAEG-----SQQQQAELALQREAVRHRETAALQRLLDAS	1166
CBN80053.1[G.gallus]	CQQQQQVEGLTHS-----LKSE	1149
NP_001390473.1[M.musculus]	CQKQEQEADSLERS-----LEAE	1153
Q14980[H.sapiens]	CQQQQQADSLERS-----LEAE	1153
XP_002822235.1[P.abelii]	CQQQQQADSLERS-----LEAE	1153
XP_032223093.1[N.vectensis]	K-----HRAKQMEEELEQLRQDFSTKQKNLYEDTTK	992
XP_019634543.1[B.belcheri]	-----QEQLOQKN-----TAQAEQLQKQ	1256
XP_032819484.1[P.marinus]	RME-----ADSLKAA-----LQLEEI-----VFRATL-----NEERTV	1054
XP_045580741.1[S.salar]	RQEKEKSTEEATLKMEALKAAKDLQLSALTEKATALQELQAKRQEELSLQKEVLQEAHRE	1390
XP_018103294.2[X.laavis]	R-----ALQAEKETEL-----EALKKELFHHVQELQESQSKSFSDSNRE	1314
CBN80053.1[G.gallus]	R-----SAQALQDGTV-----ESLRKELQDKSKELAQSKMAVAVAAREE	1204
NP_001390473.1[M.musculus]	R-----ACRAEQDKAL-----ETLQGLQLEKAKELGHQQAASASAQRE	1187
Q14980[H.sapiens]	R-----ASRAERDSAL-----ETLQGLQLEKAKELGHQQSALASAQRE	1191
XP_002822235.1[P.abelii]	R-----ASRAERDSSL-----ETLQGLQLEKAKELGHQQSALASAQRE	1191
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XP_032223093.1[N.vectensis]	K-----QTQVRQEYEMERAAMKKLETANEEL-----	1019
XP_019634543.1[B.belcheri]	LQTAQANVQQTAAARNDLQSHLQIAQEQLKLDKDTALGELQNLQTAQASLQHTAETR--	1313
XP_032819484.1[P.marinus]	LEEMKFKVQDNTLLQDQEKVK-----LQRDRDLLEDEKVSIERERV--	1095
XP_045580741.1[S.salar]	KESVEALREELARQEEELREELIL-----QQQRAQSLQESLEEQQEALKELTKEERAREEA	1447
XP_018103294.2[X.laavis]	LSSMLSEVQERQALTEAKEQAEQYQKVIDMKNKEVNSLQAEINILSSKVTSKEEVS---	1371
CBN80053.1[G.gallus]	VASLRAAAQEKGHLEEGWKEQLSQCIQELERKNSLLGSLSEEVSIILHRQLTEKEGES---	1261
NP_001390473.1[M.musculus]	LAAFRKAKAQDHSKAEDEWKAQVARGQEAERKNSLSSLEEVSILNRQVLEKEGES---	1244
Q14980[H.sapiens]	LAAFRKTKVDHSKAEDEWKAQVARGQEAERKNSLSSLEEVSILNRQVLEKEGES---	1248
XP_002822235.1[P.abelii]	LAAFRKTKVDHSKAEDEWKAQVARGQEAERKNSLSSLEEVSILNRQVLEKEGES---	1248
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XP_032223093.1[N.vectensis]	-----NDLQSHLQTAQ-----EHL-QQKDTAQVEL-----QKQLQT-AQVNLQQAEC	1019
XP_019634543.1[B.belcheri]	-----ALDK-----MKA-----TLEMKATWKEKRVVLVAFLEQ	1353
XP_032819484.1[P.marinus]	TQLRQQISTHLSRLSEVQRKKEELREQEKEAREETTVMKEALQAQLEV-----VSSLAAAKDL	1125
XP_045580741.1[S.salar]	-----ADFEQ-----RLQGETSKSAKLEKLLKHLTEVEV-----SSKELVEKNK	1505
XP_018103294.2[X.laavis]	-----KELKR-----LVMAESEKSKLEERLRLVLTQEMAT--AASRAAER--	1411
CBN80053.1[G.gallus]	-----KELKR-----LVMAESEKSKLEERLRLVLTQEMAT--AASRAAER--	1299
NP_001390473.1[M.musculus]	-----KELKR-----LVMAESEKSKLEERLRLVLTQEMAT--NSARAAER--	1282
Q14980[H.sapiens]	-----KELKR-----LVMAESEKSKLEERLRLVLTQEMAT--NSARAAER--	1286
XP_002822235.1[P.abelii]	-----KELQ-----LVMAESEKSKLEERLRLVLTQEMAT--NSARAAER--	1286
XP_032223093.1[N.vectensis]	-----VKLRGEMFENSQK-----HSAELICLRQT-----QEKEDEME	1052
XP_019634543.1[B.belcheri]	TRNDLQSHLQTAQEQLQKQDQTV-----QGE-----LQKQLQAAQANLQQTATRNLIQ	1401
XP_032819484.1[P.marinus]	-RVTLKRELAALHGERAKWTTE-----SERLVQEQALLEQQRVALQEQERESLD-----QHR	1175
XP_045580741.1[S.salar]	QLSTLREEASLQCQENTKRAADLKDVQLEKIRL-ESLSEEHRALKEDL-----AKQQEELR	1561
XP_018103294.2[X.laavis]	AVDILRTAEQTFKGEADEQRMA-----VD-----CLQKLLSQAEITNNLIQ	1452
CBN80053.1[G.gallus]	-CSLMKVEVQRQCEEMEKQRTM-----IE-----ALKRDRHQCEREELR	1339
NP_001390473.1[M.musculus]	-SSALREEVQSLREEVEKQRVV-----SE-----NSRQELASQAERAELG	1322
Q14980[H.sapiens]	-SSALREEVQSLREEAEKQVVA-----SE-----NLQELTSQAERAELG	1326

XP_002822235.1[P.abelii]	-SCALREEVQSLREEAEKQVRA-----SE-----NLRQELTSQAERAELG	1326
XP_032223093.1[N.vectensis]	GE--KKNMQEHTR-----QTQEKLQT-----SE-TIIKGLRADIKQLEIVKKTLE	1094
XP_019634543.1[B.belcheri]	GQ--LHTAQEHL-----QKQDADLQNLQTAAG--KLE--HSEAVRN-----	1437
XP_032819484.1[P.marinus]	GNLKVKSEQERAAQSETMYKVQENACLR-----EQKTLI-HDMAELRTT-----	1220
XP_045580741.1[S.salar]	GE--VSLHQQRAA-----ELQHQAALRQEKEKSTEEATLKMEALKAAKDLQLSAL----	1610
XP_018103294.2[X.laavis]	QE--IQSWQKNCA-----EKEQKICSLQ--QNLNSNQ--SLL-EEFASLKRS-----	1492
CBN80053.1[G.gallus]	QE--KVKQCKFF-----KQEQLSSLQ--QELGSAQ--ALA-GEVPLKHL-----	1379
NP_001390473.1[M.musculus]	QE--LKAWQEKFF-----KQEALQALQ--LEHTSTQ--ALV-SELLPAKHL-----	1362
Q14980[H.sapiens]	QE--LKAWQEKFF-----KQEALQALQ--LEHTSTQ--ALV-SELLPAKHL-----	1366
XP_002822235.1[P.abelii]	QE--LKAWQEKFF-----KQEALQALQ--LEHTSTQ--ALV-SELLPAKHL-----	1366
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XP_032223093.1[N.vectensis]	VEKGQLKSICEDFAKKEKDRLLVEKMTKDHEEKIAKIKNENQRALAKDEDAQKLMKET	1154
XP_019634543.1[B.belcheri]	-----DLQ--SQL-----QAMQEQLNKKDAAGV-LQIQLKTALANLQET	1474
XP_032819484.1[P.marinus]	-----VD--EEM-----SWARKRVALDKKAENER-VKSNLDRE-----	1252
XP_045580741.1[S.salar]	--TEKAIALQEQAKREQEISLQKEVLQEAH-----REKESLEA-LREELARQQUEELREE	1662
XP_018103294.2[X.laavis]	-----YQETLAERGLMQKHQELLSHKNLTER-FQAELEKTKEDMAEI	1535
CBN80053.1[G.gallus]	-----CQQLQAERASLESKHXEDLEQRAKATTA-LQAEILARARVEVAEL	1422
NP_001390473.1[M.musculus]	-----CQQLQAEQAAAEKRFRELEQSKQAAGG-LQAEILMQAQLREL	1405
Q14980[H.sapiens]	-----CQQLQAEQAAAEKRFRELEQSKQAAGG-LRAELLRQAQLREL	1409
XP_002822235.1[P.abelii]	-----CQQLQAEQAAAEKRFRELEQSKQAAGG-LRAELLRQAQLREL	1409
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XP_032223093.1[N.vectensis]	EELKAKM-----E-----	1162
XP_019634543.1[B.belcheri]	EATKSNL-----	1481
XP_032819484.1[P.marinus]	MAVIKQKSLLDQSM-----	1269
XP_045580741.1[S.salar]	LTLQQRASQLSLEQSLQEEQKALKELTKEERAREEATLKMVALQAQKDELSTLRQEATQ	1722
XP_018103294.2[X.laavis]	VLLKEKL-----NNQELQLH-----K	1551
CBN80053.1[G.gallus]	PALDRRA-----AEQERALQ-----R	1438
NP_001390473.1[M.musculus]	GSLSRQK-----VEQERAAQ-----Q	1421
Q14980[H.sapiens]	IPLRQKV-----AEQERTAQ-----Q	1425
XP_002822235.1[P.abelii]	IPLRQKV-----AEQERTAQ-----Q	1425
	: :	
XP_032223093.1[N.vectensis]	-----D-EH-----QKALGLKDEDIQKLMKETDELKARMEDE-----	1193
XP_019634543.1[B.belcheri]	-----QSOL-----QTAQGLQLE-----KCTAHDGLQVQLQSSMAKLEQSE	1517
XP_032819484.1[P.marinus]	FALERTDFLHKAMENKSNLKTLETDCIVLE-----Q--EKTGPQK--VK-----	1312
XP_045580741.1[S.salar]	LQKEISTHVSHLEEV-----KSEGPLRE-----EHTALQVQLAKQQ-----	1758
XP_018103294.2[X.laavis]	LQSENSDQSSQISNL-----QVNSRLG-----ENQSLQSISDQDA-----	1588
CBN80053.1[G.gallus]	LQKETSASSERLAAL-----QAANSRLAE-----ENRALSSESVRGQ-----	1475
NP_001390473.1[M.musculus]	LRAEKASYAEQLSML-----KKAHGLLAE-----ENRGLGERANLGR-----	1458
Q14980[H.sapiens]	LRAEKASYAEQLSML-----KKAHGLLAE-----ENRGLGERANLGR-----	1462
XP_002822235.1[P.abelii]	LRAEKASYAEQLSML-----KKAHGLLAE-----ENRGLGERANLGR-----	1462
	: :	
XP_032223093.1[N.vectensis]	-----HQKALGLKDE-----DAQRLIKEETEELKA-----KMAIEEAR--KGEVA	1231
XP_019634543.1[B.belcheri]	ASRSDLQGLQTAQEQ-----LQKQEAAGVCLNSQLEASQVQLEKAEAGRNDLQ	1566
XP_032819484.1[P.marinus]	---GLLDLESATAKQERDVCKAKQASNTLTQRRAAEALSSSVRHSVVLQEQ-----	1361
XP_045580741.1[S.salar]	---EENSILQKGLLQE-----VQ--ATVLQEREAKALRGVSLHQSSL--EE--QQVA	1802
XP_018103294.2[X.laavis]	---KKLSIEMSTLKE-----Q-----HEEEMKTLRLQYEKTQREGNEQV--QDLS	1628
CBN80053.1[G.gallus]	---QRLDAELGQARE-----K-----HTRELCVRLAEAKMASSRQEA--EEAA	1515
NP_001390473.1[M.musculus]	---QFLEVELDQARE-----K-----YVQELAAVTRDAETHLAEMRQEA--QSTS	1498
Q14980[H.sapiens]	---QFLEVELDQARE-----K-----YVQELAAVTRDAETHLAEMRQEA--QSTA	1502
XP_002822235.1[P.abelii]	---QFLEVELDQARE-----K-----YVQELAAVTRDAETHLAEMRQEA--QSTA	1502
	: :	
XP_032223093.1[N.vectensis]	MAEEERRQKAE-----	1249
XP_019634543.1[B.belcheri]	SQVLDVQAQYMQSQNSSDETVAELRVQAAHFQECSQLQEEKQQLLKQWEDMAYKVRVE	1626
XP_032819484.1[P.marinus]	-----MYDA-----VPKPRQAATQHHETE	1381
XP_045580741.1[S.salar]	VBETLARQKEEQ-----AAGV--QKELMEQFVSLQKEKALLTRALQAEQNSQSELE	1853
XP_018103294.2[X.laavis]	LRLETATSKYDH-----V--KSKVLLQKTFQEEKQMLLIRBELAAAKKEQS	1674
CBN80053.1[G.gallus]	RKLEAMSNKYEN-----T--KVKVLEERQKFOEERQKILMAQVQLELVFQKEQA	1561
NP_001390473.1[M.musculus]	RELEVMTAKYEG-----A--KVKVLEERQKFOEERQKILTAQVQLELVFQREQT	1544
Q14980[H.sapiens]	RELEVMTAKYEG-----A--KVKVLEERQKFOEERQKILTAQVQLELVFQREQT	1548
XP_002822235.1[P.abelii]	RELEVMTAKYEG-----A--KVKVLEERQKFOEERQKILTAQVQLELVFQREQT	1548
	: :	
XP_032223093.1[N.vectensis]	AEIHCLKRKLEQSEESLK---ESDAKFTKTND-----ELDKV-----	1283
XP_019634543.1[B.belcheri]	QQCSTLQRELGEAAHSSQQLLENNALQCSQQQ-----EMAKEKSYRQKVEAMQHFEEQ	1681
XP_032819484.1[P.marinus]	-----DTAPPKGVN--AALKALQDLETTDIQEMSSP-----	1411
XP_045580741.1[S.salar]	GSMAELRAQAE--SRESGQRQLD--ALLLEKERLTGHQVLEMKCSAAQRLAVAL--EE	1908
XP_018103294.2[X.laavis]	EQVQE-----LN--KQLRQKEKTL-----SQQKRLKQR-----	1701
CBN80053.1[G.gallus]	KQVEE-----LN--KKLVQHEKATR-----SQQQRVKVL-----	1588
NP_001390473.1[M.musculus]	KQVEE-----LS--KKLTEHDQASK-----VQQQKLKAFQA--Q--	1574
Q14980[H.sapiens]	KQVEE-----LS--KKLADSDQASK-----VQQQKLKAVQA--Q--	1578
XP_002822235.1[P.abelii]	KQVEE-----LS--KKLVESDQASK-----VQQQKLKAVQA--Q--	1578
	: : :	
XP_032223093.1[N.vectensis]	---KKALETTQESWKEKETEMAAKLAQSEQLCEDMKDD-----Q-----	1319
XP_019634543.1[B.belcheri]	LRGLKELQGAEEVQKQGNMLEEQKMSQSQQQLSEQLHSYQMHYQRKKTETIDLEKSL	1741
XP_032819484.1[P.marinus]	---GA--TEDRKARSEIRRENVNSSFDQEKGHLEKNALEKGENFREDDIMAAEMEENL	1468
XP_045580741.1[S.salar]	LALL--REQMEGTEMEKQIRDLREQLAANTEVVEHYKTVQVEKASHYSKKQQLVSEQEV	1967
XP_018103294.2[X.laavis]	---EG--ETHEEAETHKRVIELESQLEQQTQAVEHYKQMEKAKVHYDAKKQNQELSDEL	1758
CBN80053.1[G.gallus]	---EG--ELQSEATRQQERVALEELQAEQQAEEHYKQMEKAKTHYDAKKQNQQLAEKL	1645
NP_001390473.1[M.musculus]	---RG--ESQEQVQRLQTLNELQAQLSQKEQAAEHYKLQMEKAKTHYDAKKQNQQLQEQL	1631
Q14980[H.sapiens]	---GG--ESQQAQRLQAQLNELQAQLSQKEQAAEHYKLQMEKAKTHYDAKKQNQQLQEQL	1635
XP_002822235.1[P.abelii]	---GG--ESQQAQRLQAQLNELQAQLSQKEQAAEHYKLQMEKAKTHYDAKKQNQQLQEQL	1635
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XP_032223093.1[N.vectensis]	-----ELLERLQDEIARKMEEQVNV--LNEEKGLLEEQLLEEQDTNKR	1359
XP_019634543.1[B.belcheri]	QKQENAHESVKNLQLTQVQERNKLKKNSS-----LSTDVKTAEIKLEKEEATTKK	1792
XP_032819484.1[P.marinus]	D-----TIM-----QYE--VSTDVARSIVTETGMAPSNTIFTKEECAT	1505
XP_045580741.1[S.salar]	T-----ELQRSLEVRHEHVNAVTTMEKL--LQKELEK-----ARNKEKS	2004
XP_018103294.2[X.laavis]	Q-----SHIREQEHRLKRENAIDLKAESEQ--LSKELQHSLLQSKEAEQCNKN	1802
CBN80053.1[G.gallus]	-----KAMEQLQKENALRTESER--LAKELQSVLQAKAEALSCE	1685
NP_001390473.1[M.musculus]	-----QDLEELQKENKELRSEAEER--LGRELQAQGLKTKKAEQTCTRH	1671
Q14980[H.sapiens]	-----RSLEQLQKENKELRAEAEER--LGHELQAQGLKTKKAEQTCTRH	1675
XP_002822235.1[P.abelii]	-----RSLEQLQKENKELRAEAEER--LGHELQAQGLKTKKAEQTCTRH	1675
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XP_032223093.1[N.vectensis]	LGMQVNSLEAQVKHADMTIREQKAKMQSFENQS--EKVKK--TR-----	1399
XP_019634543.1[B.belcheri]	LYQQVRSLEAQVDLANRQLRQKQHVSPATPA-----RSLNTSTD	1833
XP_032819484.1[P.marinus]	LQANVSEIED-----	1515
XP_045580741.1[S.salar]	LSSKVNTELAQLAFTDRHLREQSQVRPERGGIETKMRGGRESVYLKVPQSQTHQETSGD	2064
XP_018103294.2[X.laavis]	LSNRVRSLEAQVEYSDRQLQDLGKFQLATDS-----TKRRDTFCVPRETRSHADVSID	1855
CBN80053.1[G.gallus]	LSGVRSLETLQLEFADQQLRELKGFPAKPAT-----LKEPESTRFN-----PSDLSTD	1733
NP_001390473.1[M.musculus]	LTAQVRSLEAQVAHADQQLRDLGKFQVATDA-----LKSREPQVKP-----QLDLSID	1719
Q14980[H.sapiens]	LTAQVRSLEAQVAHADQQLRDLGKFQVATDA-----LKSREPQAKP-----QLDLSID	1723
XP_002822235.1[P.abelii]	LTAQVRSLEAQVAHADQQLRDLGKFQVATDA-----LKSREPQAKP-----QLDLSID	1723
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XP_032223093.1[N.vectensis]	KMLIEVEKVLVPVQEAQELLDESTTESDD--SEMR-----V----DDLKLTRQGS	1442

XP_019634543.1[B.belcheri]	SIETDAETFDLEPRSRQRHS---TSRDDLDRTLSNSQVAGEEEDKKNRTISTDSLEGD	1890
XP_032819484.1[P.marinus]	HPNTGVENTRILSKENLEQTP---SEDG---R-RHSMVT-----RSARKRSSRY	1557
XP_045580741.1[S.salar]	SLDLSLDDSLNNTTRPLGPDE---SS-----TPLVRSSERV---AAKRRALGGE	2107
XP_018103294.2[X.laavis]	SLDLSFEEDQLLNSTSKNGRC---NQEP---A-TSSVHASSLDSP---ASSQLPKKVE	1903
CBN80053.1[G.gallus]	SLDLSLDEGQPLNSTRKATRS---HSDG---SAAPGTEPR---ASQRLPRKVE	1778
NP_001390473.1[M.musculus]	SLDLSLEEGTPCSVASKLPRT---QPDG---TVVGPGEFASP---ISQRLPPKVE	1764
Q14980[H.sapiens]	SLDLSCEEGLPLSITSKLPRT---QPDG---TVVGPGEFASP---ISQRLPPKVE	1768
XP_002822235.1[P.abelii]	SLDLSCEEGLPLSITSKLPRT---QPDG---TVVGPGEFASP---ISQRLPPKVE	1768
	: :.	
XP_032223093.1[N.vectensis]	---SVSFASVNGTD-----FGKSLSTSSISRTSL-----	1469
XP_019634543.1[B.belcheri]	SLDTSIFS-----RTSQDSGMSTR---SQRRRTTVSIEMV	1922
XP_032819484.1[P.marinus]	SQETLYFTPLQTRPSLVGGQAPALDWSLNSLEDLVDSAKKKPR-TSSTRRTTHVIDIT	1616
XP_045580741.1[S.salar]	SLETLFTPMNNRQINRTSTERRLESSITCLGELALDSARKRPPPTSSARRRTTQVINIT	2167
XP_018103294.2[X.laavis]	SLESLYFTPIPTRA-----QSKLESSIGSGLDLSLDSKKTTR---SARRRTTQIINIT	1953
CBN80053.1[G.gallus]	SLESLYFTPIASRT-----QPKLESSAGSLADVLESgcRTR---SRRRTTQIINIT	1828
NP_001390473.1[M.musculus]	SLESLYFTTTPARG-----QAPLETSLDLSGLDAFPDsgRKTTR---SARRRTTQIINIT	1814
Q14980[H.sapiens]	SLESLYFTTPIPARS-----QAPLESSLDSLGDVFLDsgRKTTR---SARRRTTQIINIT	1818
XP_002822235.1[P.abelii]	SLESLYFTTPIPARS-----QAPLESSLDSLGDVFLDsgRKTTR---SARRRTTQIINIT	1818
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XP_032223093.1[N.vectensis]	---EDSRRL-----RSTVRPSA-----	1477
XP_019634543.1[B.belcheri]	QT---EDSRRL-----	1930
XP_032819484.1[P.marinus]	LNKVKVSCRDSVSSSASTMRSTTTAYELRSHGDRPTPVQSSNWSLGFPPASSASFTLD	1676
XP_045580741.1[S.salar]	MSKTTTPGRGGAGGDS---NEMFYSLSSVRSHPNITGSTH---TARPIS-----	2210
XP_018103294.2[X.laavis]	MTKTKTEERE---PESA-----NTSFYSLRAPSQNLHQQNPRAARPAQAISTPALA	2004
CBN80053.1[G.gallus]	MTKTKETTEE---PGQA-----DASFSSILSEGPQKAAPAKAR-----LRASRLA	1871
NP_001390473.1[M.musculus]	MTYKLEL-EE---PDSA-----NSSFYSTQSAPAS---QAN-----LRAT----	1847
Q14980[H.sapiens]	MTYKLDV-EE---PDSA-----NSSFYSTRSAPAS---QAS-----LRAT----	1851
XP_002822235.1[P.abelii]	MTYKLDV-EE---PDSA-----NSSFYSTRSAPAS---QAS-----LRAT----	1851
XP_032223093.1[N.vectensis]	-----SRQSAMVVKGSTPPTRRTTSSA-----AFFIVG	1506
XP_019634543.1[B.belcheri]	-----SRTSTEHDVLGSS-----IGSASSWRGAAP	1955
XP_032819484.1[P.marinus]	TFTQNSLQLEDMR---SGRLSDASLRLSLPGYRPLGPHGTGDRNLEQLQAPPTTRRRKGNA	1734
XP_045580741.1[S.salar]	-----MEVFHTPGKPAVAVDQLLSLPGYRSTVHV-----AAPQSTG	2248
XP_018103294.2[X.laavis]	SLPQESLAKTEHFSDDSLNNSVLMNLPGYRAPARRSSRLSQ-----T-----GGRS	2052
CBN80053.1[G.gallus]	SFPQDSLSKLDTSPPQEPSPGHAALLSLPGYRPTATRSSLRKS---AGSSS---SLGRS	1924
NP_001390473.1[M.musculus]	---SSTQSLARLG---SPDDGNSALLSLPGYRPTTRSSARRSQ---ARMSSGAPQGRN	1896
Q14980[H.sapiens]	---SSTQSLARLG---SPDYGNSALLSLPGYRPTTRSSARRSQ---AGVSSGAPPGRN	1900
XP_002822235.1[P.abelii]	---SSTQSLARLG---SPDYGNSALLSLPGYRPTTRSSARRSQ---AGVSSGAPPGRN	1900
XP_032223093.1[N.vectensis]	DEFANNMEQSEYEFPDWD-----	1524
XP_019634543.1[B.belcheri]	RFFVSECEEBEQ-YDWD-----	1972
XP_032819484.1[P.marinus]	SYVM-SCVDEPDPEAEWDELERQGLGAHALPRRQFPAALGTSACYTEGLQENQPPVNCV	1793
XP_045580741.1[S.salar]	QFCVGAENEPDHAADDWL-----	2266
XP_018103294.2[X.laavis]	SFYMSTCQDEPDQDEWT-----	2070
CBN80053.1[G.gallus]	SIYLGTCQDEPEQLDDWN-----	1942
NP_001390473.1[M.musculus]	SFYMGTQDEPEQLDDWN-----	1914
Q14980[H.sapiens]	SFYMGTQDEPEQLDDWN-----	1918
XP_002822235.1[P.abelii]	SFYMGTQDEPEQLDDWN-----	1918
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XP_032223093.1[N.vectensis]	-----RLAELERRNTICPHLKTSPVETQTRPSEGNGLHAARSETALTRK	1570
XP_019634543.1[B.belcheri]	-----RLSELQRRNTLQPRHLQSCYPTETQGTALAE-----T	2004
XP_032819484.1[P.marinus]	DFSEKSDTRNDHLLRQEELGKRNQATLPHLRKSPYPLKVETP-----MPGEDLC---T	1842
XP_045580741.1[S.salar]	-----RIAEQARNQSCPLHLKSSYPLESRPSLGSPFEFTDDDLR---M	2307
XP_018103294.2[X.laavis]	-----RIAEQARNKTCPPHLKTSYPLESKPSLFS--TLTDEEVK-----L	2110
CBN80053.1[G.gallus]	-----RIAEQQRNRACPPHLKTCYPLESRPSDLVG-TITDEEMK-----T	1982
NP_001390473.1[M.musculus]	-----RIAEQQRNRVCPPHLKTCTYPLESRPTLSLA-TITDEEMK-----T	1954
Q14980[H.sapiens]	-----RIAEQQRNRVCPPHLKTCTYPLESRPSLSLG-TITDEEMK-----T	1958
XP_002822235.1[P.abelii]	-----RIAEQQRNRVCPPHLKTCTYPLESRPSLSLG-TITDEEMK-----T	1958
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XP_032223093.1[N.vectensis]	RKPEDTLTSS-----VKERKDMTTSKS-EQGIKR-----SRSKRITDMVSSK----	1611
XP_019634543.1[B.belcheri]	EDLSKTLRRTTLRSSQAAKTFSITPGKKRRHEADENSA-----SRKKTVMVMPSTPS----	2055
XP_032819484.1[P.marinus]	AKPEMTARRMFLRPALADANADM-----	1865
XP_045580741.1[S.salar]	GDPTETIRRASVMPQIQESLSHRLSLHPGQADSTTASRPAYGSHRLSLMPFKPASST	2367
XP_018103294.2[X.laavis]	GDPKETLRRATMLPSQIQDSTTSTRLLTLAGSGAEH-----LKHGISTRQQ-----	2157
CBN80053.1[G.gallus]	GDPTETLRRASMQPLQIAEGAATRRG-TLG---GG-----WAHGGITRQQ-----	2024
NP_001390473.1[M.musculus]	GDPRETLRRASMQPIQIAEGV-----GITTTRQQ-----	1982
Q14980[H.sapiens]	GDQPETLRRASMQPIQIAEGT-----GITTTRQQ-----	1986
XP_002822235.1[P.abelii]	GDQPETLRRASMQPIQIAEGT-----GITTTRQQ-----	1986
	. *	
XP_032223093.1[N.vectensis]	-----INSLRPSKSNENIKEQKQ---SGNSLAFEI---TPPKKR--	1644
XP_019634543.1[B.belcheri]	-----K-RTPSVFKTPKKIASAAAGIFKKPTGKTPSSRRRS	2089
XP_032819484.1[P.marinus]	-----RKRKSGIGHNTEC-SPE---SKK---SATMCFVVA---TPPREP--	1900
XP_045580741.1[S.salar]	LNQNTNHLNRLGNSLSKRSKQJEPD-TPEVMEAKR---KATSCFPRL---TPKGGR--	2419
XP_018103294.2[X.laavis]	-----MKRVSESHYGPD-TPEQ---K---MTATCFPRM---TPKDKH--	2191
CBN80053.1[G.gallus]	-----RKRKLSDESHQGD-TPEQ---K---KPVSCFPRQ---TPRER--	2058
NP_001390473.1[M.musculus]	-----RKRVSSETHQGP-TPEQ---K---KATSCFPRM---TPDRH--	2016
Q14980[H.sapiens]	-----RKRVSLEPHQGP-TPEQ---K---KATSCFPRM---TPDRH--	2020
XP_002822235.1[P.abelii]	-----RKRVSLEPHQGP-TPEQ---K---KATSCFPRM---TPDRH--	2020
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XP_032223093.1[N.vectensis]	-----KAEPKAASDTPPRESTKKTVAFTIENSPPKKCKVQR---TRTI	1686
XP_019634543.1[B.belcheri]	PRLQGRGKSPAGRLNKAKTPTKTPNKHQAKQDPRQSIAPNIGFSLKGRKSA--RKAK	2147
XP_032819484.1[P.marinus]	-----PPRASPRRDDH---PQRSWPIIRR-----LRQSM	1926
XP_045580741.1[S.salar]	-----FSSS-----NNRQPPSPAERRQSMVFSIDNTPRKAASKSGFLQRM	2460
XP_018103294.2[X.laavis]	-----DARRLSTMESK-ASSSHQVQPTRRQTSAFSIFNTPKKLGS---SLLKRGL	2238
CBN80053.1[G.gallus]	-----SSHLSRR---SEQQAPSQKQPERQSMAFSILANTPKKLGN---SLLRRAA	2101
NP_001390473.1[M.musculus]	-----EGRKQSTADTQKKAAPVLKQADRQSMAFSILANTPKKLGN---SLLRRAA	2064
Q14980[H.sapiens]	-----EGRKQSTTEAQKKAAPASTQADRQSMAFSILANTPKKLGN---SLLRRAA	2068
XP_002822235.1[P.abelii]	-----EGRKQSTTEAQKKAAPASTQADRQSMAFSILANTPKKLGN---SLLRRAA	2068
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XP_032223093.1[N.vectensis]	NRSTATTO-----LV---RDKDRETFKREKLTENRILPRSSNRKIAK-----	1727
XP_019634543.1[B.belcheri]	EKREA---QKEPSQRRMSI---ANVKSF-LSV-----NNSKT-NKTKAARKPLGTRNA	2193
XP_032819484.1[P.marinus]	SKRKSPPSKASKP-----	1939
XP_045580741.1[S.salar]	NKIRSSTRKSPAN-KISRVPRSGDVKSPO---PGGKAQRKSPRT-NSSKSPKNFTSARKEP	2516
XP_018103294.2[X.laavis]	NKKTTPKN-SPRGRGTNNSASSTSSKSPHLSLRKSPSRKSPRV-STAKSPKASNKV-GQ	2294
CBN80053.1[G.gallus]	NKKTTPKN-SP-RGTAR-----RSPRI-ASTKSPKGAKGRALK	2137
NP_001390473.1[M.musculus]	SKKTPAKV-SPNPRSGTR-----RSPRI-ATTTTGTA---TVATT	2099
Q14980[H.sapiens]	SKKALSKA-SPNTRSGTR-----RSPRI-ATTTASAATAAIGAT	2106
XP_002822235.1[P.abelii]	SKKALSKA-SPNTRSGTR-----RSPRI-ATTTASAATAAIGAT	2105
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XP_032223093.1[N.vectensis]	-----	1727
XP_019634543.1[B.belcheri]	QTGV-----	2197
XP_032819484.1[P.marinus]	-----	1939
XP_045580741.1[S.salar]	EVLVGKPIHLR-----	2528
XP_018103294.2[X.laavis]	-----EEQIQFFERKQQRNK	2309

CBN80053.1[G.gallus]	D-----TKF-----	2141
NP_001390473.1[M.musculus]	PRAKGKVKH-----	2108
Q14980[H.sapiens]	PRAKGKAKH-----	2115
XP_002822235.1[P.abelii]	PRAKGKAKH-----	2114