

TNKS1

Sequences :

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>NP_003738.2 poly [ADP-ribose] polymerase tankyrase-1 [Homo sapiens]
MAASRRSQHHHHHHQQQLQAPAGASAPPPPPPPPLSPGLAPGTTPASPTASGLAPFASPRHGIALPEGGD
SRDPDFRPRSPDPVDGTSCCSTTSTICTVAAAPVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSSSS
SSPSSPGSLSAESPEAAGVSTAPLPGAAGPGTGVPVAVSGALRELLAEACRNGDVSVRKRLVDAANVNAK
DMAGRKSSPLHFAAGFGRKDVVEHLLQMGANVHARDGGGLIPLHNACSFGHAEEVVSLLLCQGADPNARDN
WNYTFLHEAAIKGKIDVCIVLLQHGADPNIRNTDGKSALDLADPSAKAVLTGEYKKDELLEAARSNGEEK
LMALLTFLNVNCHASDGRKSTPLHLAAGYNRVRIVQLLQLHGADVHAKDKGGLVPLHNACSYGHYEVTEL
LLKHGACVNAMDLMQFTPLHEAASKNRVEVCSLLLSHGADPTLVNCHGKSAVDMAPTPELRERLTYEFKG
HSLLQAAREADLAKVKKTLALEIINFKQPQSHETALHCAVASLHPKRKQVTELLLRKGANVNEKNKDFMT
PLHVAERAHNDVMEVLHKKHAKMNALDTLGTQALHRAALAGHLQTCRLLLSYGS DPSII SLQGFTAAQM
GNEAVQQILSESTPIRTSDVDYRLLEASKAGDLETIVKQLCSSQNVCNCRDLEGRHSTPLHFAAGYNRVSVV
EYLLHHGADVHAKDKGGLVPLHNACSYGHYEAELLVRHGASVNVADLWKFTPLHEAAAKGKYEICKLLL
KHGADPTKKNRDNPTPLDLVKEGDTDIQDLLRGDAALLDAAKKGCLARVQKLCCTPENINCRDTQGRNSTP
LHLAAGYNNLEVAEYLLEHGADVNAQDKGGLIPLHNAASYGHV DIAALLIKYNTCVNATDKWAFTPHEA
AQKGR TQLCALLLAHGADPTMKNQEGQTPLDLATADDIRALLIDAMPPEALPTCFKQATVVSASLISPA
STPSCLSAASSIDNLTGPLAE LAVGASNAGDGAAGTERKEGEVAGLDMNISQFLKSLGLEHLRDI FETE
QITLDVLADMGHEELKEIGINAYGHRHKLIGKVERLLGGQQGTNPYLT FHCVNQGTILLDLAPEDKEYQS
VEEEMQSTIREHRDGNAGGIFNRYNVIRIQKVNNKLRERFCHRKQEVSEENHNHNHNERMLFHGSPFFIN
AI IHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVIGGGTGCTPHKDRSCYICHRQMLFCRVTLGKSF
LQFSTMKMAHAPPGHHSVIGRPSVNGLAYAEYVIYRGEQAYPEYLITYQIMKPEAPSQTATAAEQKT

>XP_024106876.1 tankyrase-1 [Pongo abelii]
MAASRRSQHHHHHHQQQLQAPAGASAPPPPPPPPLSPGLAPGTTPASPTASGLAPFASPRHGIALPEGGD
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SSPSSPGSLSAESPEAAGVSTAPLPGAAGPGTGVPVAVSGALRELLAEACRNGDVSVRKRLVDAANVNAK
DMAGRKSSPLHFAAGFGRKDVVEHLLQMGANVHARDGGGLIPLHNACSFGHAEEVVSLLLCQGADPNARDN
WNYTFLHEAAIKGKIDVCIVLLQHGADPNIRNTDGKSALDLADPSAKAVLTGEYKKDELLEAARSNGEEK
LMALLTFLNVNCHASDGRKSTPLHLAAGYNRVRIVQLLQLHGADVHAKDKGGLVPLHNACSYGHYEVTEL
LLKHGACVNAMDLMQFTPLHEAASKNRVEVCSLLLSHGADPTLVNCHGKSAVDMAPTPELRERLTYEFKG
HSLLQAAREADLAKVKKTLALEIINFKQPQSHETALHCAVASLHPKRKQVTELLLRKGANVNEKNKDFMT
PLHVAERAHNDVMEVLHKKHAKMNALDTLGTQALHRAALAGHLQTCRLLLSYGS DPSII SLQGFTAAQM
GNEAVQQILSESTPIRTSDVDYRLLEASKAGDLETIVKQLCSQNVCNCRDLEGRHSTPLHFAAGYNRVSVV
EYLLHHGADVHAKDKGGLVPLHNACSYGHYEAELLVRHGASVNVADLWKFTPLHEAAAKGKYEICKLLL
KHGADPTKKNRDNPTPLDLVKEGDTDIQDLLRGDAALLDAAKKGCLARVQKLCCTPENINCRDTQGRNSTP
LHLAAGYNNLEVAEYLLEHGADVNAQDKGGLIPLHNAASYGHV DIAALLIKYNTCVNATDKWAFTPHEA
AQKGR TQLCALLLAHGADPTMKNQEGQTPLDLATADDIRALLIDAMPPEALPTCFKQATVVSASLISPA
STPSCLSAASSIDNLTGPLAE LAVGASNAGDGAAGTERKEGEVAGLDMNISQFLKSLGLEHLRDI FETE
QITLDVLADMGHEELKEIGINAYGHRHKLIGKVERLLGGQQGTNPYLT FHCVNQGTILLDLAPEDKEYQS
VEEEMQSTIREHRDGNAGGIFNRYNVIRIQKVNNKLRERFCHRKQEVSEENHNHNHNERMLFHGSPFFIN
AI IHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVIGGGTGCTPHKDRSCYICHRQMLFCRVTLGKSF
LQFSTMKMAHAPPGHHSVIGRPSVNGLAYAEYVIYRGEQAYPEYLITYQIMKPEAPSQTATAAEQKT

>NP_780300.2 poly [ADP-ribose] polymerase tankyrase-1 [Mus musculus]
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SRDPDFRPRSPDPVDGAVCTVAAAPAAVPAASAAGVAPTAPAGGGGGGNNSSASSSPTSSSSSSSPSSPG
SPLAESPEAAGVSGTATLGAGAAGLPGVPAVSGALRELLAEACRNGDVSVRKRLVDAANVNAKDMAGRKSS
PLHFAAGFGRKDVVEHLLQMGANVHARDGGGLIPLHNACSFGHAEEVVSLLLCQGADPNARDNWNYYTFLH
EAATKGKIDVCIVLLQHGADPNIRNTDGKSALDLADPSAKAVLTGEYKKDELLEAARSNGEEKLMALLTFL
LVNCHASDGRKSTPLHLAAGYNRVRIVQLLQLHGADVHAKDKGGLVPLHNACSYGHYEVTELLLKHGAC
VNAMDLMQFTPLHEAASKNRVEVCSLLLSHGADPTLVNCHGKSAVDMAPTPELRERLTYEFKGSLLQAA
READLAKVKKTLALEIINFKQPQSHETALHCAVASLHPKRKQVAELLRLRKGANVNEKNKDFMTPLHVAE
RAHNDVMEVLHKKHAKMNALDSLGQALHRAALAGHLQTCRLLLSYGS DPSII SLISQGFTAAQMNEAVQQ
ILSESTPIRTSDVDYRLLEASKAGDLETIVKQLCSSQNVCNCRDLEGRHSTPLHFAAGYNRVSVVEYLLHHG
ADVHAKDKGGLVPLHNACSYGHYEAELLVRHGASVNVADLWKFTPLHEAAAKGKYEICKLLLKHGADPT
KKNRDNPTPLDLVKEGDTDIQDLLRGDAALLDAAKKGCLARVQKLCCTPENINCRDTQGRNSTPLHLAAGY
NNLEVAEYLLEHGADVNAQDKGGLIPLHNAASYGHV DIAALLIKYNTCVNATDKWAFTPHEAAQKGRGTQ
LCALLLAHGADPTMKNQEGQTPLDLATADDIRALLIDAMPPEALPTCFKQATVVSASLISPASTPSCLS
AASSIDNLTGPLTDLAVGASNAGDGAAGTERKEGEVAGLDMNISQFLKSLGLEHLRDI FETE QITLDVL
ADMGHEELKEIGINAYGHRHKLIGKVERLLGGQQGTNPYLT FHCVNQGTILLDLAPEDKEYQSVEEEMQS
TIREHRDGNAGGIFNRYNVIRIQKVNNKLRERFCHRKQEVSEENHNHNHNERMLFHGSPFFINAI IHKGF
DERHAYIGMFGAGIYFAENSSKSNQVYVIGGGTGCTPHKDRSCYICHRQMLFCRVTLGKSF LQFSTMK
MAHAPPGHHSVIGRPSVNGLAYAEYVIYRGEQAYPEYLITYQIMKPEAPSQTATAAEQKT

>NP_989671.2 poly [ADP-ribose] polymerase tankyrase-1 [Gallus gallus]
MAAPPRRSQHHHHHHQQPPPGPASPAAASPPRPSLAPAEGLPAAQRHSLAGPEAGEAPDAERPPAPE
CSGGAAGPFPFGSGSSSGSSASSSSSSSTSSSVASSPAAESPEAAGSAGFRELLEACRNGDTRVKRL
VDAGNVNAKDMAGRKSTPLHFAAGFGRKDVVEHLLQTGANVHARDGGGLIPLHNACSFGHAEEVVSLLLCQ
GADPNARDNWNYYTFLHEAAIKGKIDVCIVLLQHGADPNIRNTDGKSALDLADPSAKAVLTGEYKKDELLE
AARSNGEEKLMALLTFLNVNCHASDGRKSTPLHLAAGYNRVRIVQLLQLHGADVHAKDKGGLVPLHNACSY
GHYEVTELLLKHGACVNAMDLMQFTPLHEAASKNRVEVCSLLLSHGADPTLVNCHGKSAVDMAPTPELR
ERLTYYEFKGSLLQAAREADLAKVKKTLALEIINFKQPQSHETALHCAVAHVPKRKQVTELLLRKGANV
NEKNKDFMTPLHVAERAHNDVMEVLHKKHAKMNALDTLGTQALHRAALAGHLQTCRLLNLSYGS DPSII S
LQGFTAAQIGNEAVQQILSESTPIRTSDVDYRLLEASKAGDLETIVKQLCSSQNVCNCRDLEGRHSTPLHFA
AGYNRVSVVEYLLHHGADVHAKDKGGLVPLHNACSYGHYEAELLVRHGASVNVADLWKFTPLHEAAAGK
KYEICKLLLKHGADPTKKNRDNPTPLDLVKEGDTDIQDLLRGDAALLDAAKKGCLARVQKLCCTQENINCR
DTQGRNSTPLHLAAGYNNLEVAEYLLEHGADVNAQDKGGLIPLHNAASYGHV DIAALLIKYNTCVNATDK
WAFTPHEAAQKGR TQLCALLLAHGADPTMKNQEGQTPLDLATADDIRALLIDAMPPEALPTCFKQATV
VSASLISPASTPSCLSAASSIDNLTGPLAE LAVGASNTDGAAGTERKEGEVSGGLDMNITQFLKSLGLE
HLRDI FETE QITLDVLADMGHEELKEIGINAYGHRHKLIGKVERLLGGQQGTNPYLT FHCVSQGTILLDL
APDDKEYQSVEEEMQSTIREHRDGNAGGIFNRYNVIRIQKVNNKLRERFCHRKQEVSEENHNHNHNERM
LFHGSPFFINAI IHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVIGGGTGCTPHKDRSCYICHRQMLF
CRVTLGKSF LQFSTMKMAHAPPGHHSVIGRPSVNGLAYAEYVIYRGEQAYPEYLITYQIVKPEAPSQGT
AAEQKT

>XP_018099068.1 poly [ADP-ribose] polymerase tankyrase-1 isoform X2 [Xenopus laevis]
MAAPSRRSQQQQVPTAAAGQSSQPPSPASPPSPSSRRRAASCCLSPCSPNETNALSLSREGPDSEPEGEAAS
QPGITPFRPLSPPPGEAANILSPTSSLPPAPAPSSGSSSSSSSPSSNSLCTGGSPAESPESGIVGGVSSVG
ITGGDPDLSAVSGAFRELFACRNGDVSVRKRLLEPANVNAKDMAGRKSTPLHFAAGFGRKDVVEHLLQTG
ANVHARDGGGLIPLHNACSFGHAEEVVTLLLCQGADPNARDNWNYYTFLHEASIKGKIDVCIVLLQHGADPN
IRNTDGKSALDLADPSAKAVLTGEYKKDELLEAARSNGEEKLMALLTFLNVNCHASDGRKSTPLHLAAGY
NRVQIVQLLQLHGADVHAKDKGGLVPLHNACSYGHYEVTELLLKHGACVNAMDLMQFTPLHEAASKNRVE
VCSLLLSHGADPTLVNCHGKSAVDMAPTPELKERLSYEFKGSLLQAAREADLAKVKKTLALEIINFKQPQ
SHETALHCAVASLHPKRKQITTELLLRKGASVNEKNKDFMTPLHVAERAHNDVVEVLHKKHAKMNALDT
LGQ TALHRAALGGHLQTCRLLSFGSDASIVSLQGFTAAQMNEAVQQILNESTPVRTSDVDYRLLEASK
AGDLDIKVQLCSSQNVCNCRDLEGRHSTPLHFAAGYNRVSVVEYLLHHGADVHAKDKGGLVPLHNACSYGH
YEAELLVRHGASVNVADLWKFTPLHEAAAKGKYEICKLLLKHGADPTKKNRDNPTPLDLVKEGDTDIQD
LLRGDAALLDAAKKGCLARVQKLCCTQENINCRDTQGRNSTPLHLAAGYNNLEVAEYLLEHGADVNAQDKG
GLIPLHNAASYGHV DIAALLIKYNTCVNATDKWAFTPHEAAQKGR TQLCALLLAHGADPTMKNQESQTP
LDLATADDIRALLIDAMPPEALPTCFKQATVVSASISPPSTPSCLSAASSIDNLTGPLAE LAVGVSN
AGDGAAGTERKEGEVTVLDININQFLKSLGLEHLRDI FETE QITLDVLADMGHEELKEIGINAYGHRHKL
IGKVERLLGGQQGTNPYLT FHCVSQGTVLLDLSADDDKEYQSVEEEMQNSIREHRDGNAGGVFNRYNVIR
IQKVNNKLRERFCHRKQEVSEENHNHNHNERMLFHGSPFFINAI IHKGFDERHAYIGMFGAGIYFAENSS
KSNQVYVIGGGTGCTPHKDRSCYICHRQMLFCRVTLGKSF LQFSTMKMAHAPPGHHSVIGRPSVNGLAY
AEYVIYRGEQAYPEYLITYQIMKPETPLQAATTAEQKT
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>XP_014017013.1 poly [ADP-ribose] polymerase tankyrase-1-like isoform X4 [Salmo salar]
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GSSTSPSTTTTSGGGSSSVSSPGSGGTTPGDGGSGIGGAFRELFEACRNGDVRVKRLVDSVNVNAKDMAGR
KSTPLHFAAGFGRRKDVVHLLQTGANVHARDGGGLIPLHNACSFGHAEVVSLLLCQGADPNARDNNWYTP
LHEAAIKGKIDVCIVLLQHGADPNIRNTDGSALDLADPSAKAVLTGEYKDELLEAARSGNEEKIMALL
TFLNVNCHASDGRKSTPLHAAAGYNRVIRVQLLLQHGADVHAKDGGGLVPLHNACSYGHFEVTELLLKHG
ACVNAIDLWQFTPLHEAASKNRVEVCSLLLSHGADPTLLNCHSKSAIDAAPTRELKRLITVEFKHGSLAQ
AAREADMAKVKKTALLETISFKHPQTGTALHCAVASHPHKKQVTELLLRKGANINEKNDKFTALHVA
SERAHNDILEVLQKHGAKVNAVDTLGGTALHRAALAGHQTICRLLLSYGADPAIVSLQGFTASQMGNEAV
QQILANENVPTNSDVYRFLAAKAGDLDTVQQLCTPQNVNCRDLEGRHSTPLHFAAGYNRVAVVEYLLH
HGADVHAKDGGGLVPLHNACSYGHFEVTELLVHSGASVNVADLWKFTPLHEAAAKGKYEICKLLKHGAD
PTKKNRGNMPLDMVKDGDITDIDLGRDAALLDAAKKGCLARVQKLCSPENINCRDTQGRNSTPLHLAA
GYNNLEVAEYLLHGGADVNAQDKGGLIPLHNAASYGHVDIAALLIKFNTCVNATDKWAFTPHEAAQKGR
TQLCALLAHGADPTMKNQEGQTDALDLATADDIRALLMDAMPDALPSCFKPQATVVSAGSVISPASTPS
CLSAASSIDNLAGFINELGAAGTSGVADGATGSDRKEGELVMDMNISQFKLGLLEHLRDIIFEREQISL
DVLADMGEELKEIGINAYGHRHKLIGKVERLLGGQQGANPYLTFHCANQGTVIDLAPDDKEGQSVVEE
MQSTIREHRDGGNAGGVFSRYNIIKIQKVVNKKLRERYTHRQKEISDENNNHNNRMLFHGSPFFINAIH
KGFDERHAYIGMGFGAGIYFAENSSKSNQYVYIGGGTGCPTHKDRSCYLCRQMLFCRVTLGKSFQFS
AMKMAHAPPGHHSVIGRPSVNGLAYAEYVIYRGEQAYPEYLITYQILKPESTATSAAGEDQKS

>XP_032806710.1 poly [ADP-ribose] polymerase tankyrase-2 [Petromyzon marinus]
MAARAHLASPSSSSSLSPSSGSLDTTTAAAAAAATTTAAAAAATTTAAAVSATSSPSTTAAA
AAAAAAAATGSGPGSGQDSSADGGDAGKELFEACRNGDVRVKRLVSPLVNWARDTTGRKSTPLHFAAG
FGRRDVEHLLQNGANVHARDGGGLIPLHNACSFGHAEVNVNLLRQGDADPNARDNNWYTPHEAAIKGKI
DVCIVLLQHGADPGIRNTDGKTALDLAEPTAKAVLTGEYKDELLEAARSGNEEKIMALLTFLNVNCHAS
DGRKSTPLHAAAGYNRVIRVQLLLQHGADVHAKDGGGLVPLHNACSYGHFEVTELLVKHGASVNAIDLWQ
FTPLHEAASKNRVEVCSLLLSYGADPTLLNCHSKSAIDLAPTSELKERVYEFKRGHSLQAAREADVTRV
KKHLGLDINFKHPQTHETALHCAVASPYPKRKQVSELLLRKANVNEKTKDLLTFLHVASDKAANDVID
VLLKHGAKINVTDSLQGTSLHRAAHAGHLTTICRLLSHGCDPNLSLQGTAAQLGNEVSQQILHESSLP
VRNSDVEHQLLEAAKAGDLDTVQKLCCTTQTVNCRDMDEGRHSTPLHFAAGYNRVSVVEYLLQHGADVHAKD
KGLVPLHNACSYGHFEVTELLVKGAVNVNADLWKFTPLHEAAAKGKYEICKLLKHGADPTKKNRGN
TFLDLVKEGDTDIDLGRDAALLDAAKKGCLARVQKLCSENVNCRDSQGRNSTPLHAAAGYNNLEVAE
YLLEHGADVNAQDKGGLIPLHNAASYGHVDIAALLIKYSACVNATDKWAFTPHEAAQKGRGTQLCALLLA
HGADPSMKNQEGQTPDLATADDVRALLIDAMPPEALFVTHKPPSIPTIAATSAATAALALGPTPALAS
LAPSPVPSGASAGAGVPLLASPSSTPASLSAASSMDSLTGACGVAPSPVPAGAIAGAAGDGLTGAC
GVSAAADGATGPADKPDRAADFEIPLDMNINMFLKGLGLDHLRDIFEKEQITLDVLADMGEELKEIGIN
AYGHRHKLIGKVERLLGAQGGGLAYPGANPYLSYHTTAQGTLLIDLPPDDKEYQSVEDEMQSTIREHKDQ
GQAGGVFNRYNVIKIQKVRNKKLWERYTHRRKEVTEENNNHNNRMLFHGSPFFINAIKNGFDERHAYIG
MGFGAGIYFAENSSKSNQYVYIGGGTGCPVHKDRSCYICRQMLFCRVTLGKSFQFSAMKMAHSPPGH
HSVIGRPSVNGLAFAEYVIYRGEQAYPEYLITYQILKPECTPDLTSAAGQKS

>XP_019641281.1 PREDICTED: tankyrase-1-like isoform X1 [Branchiostoma belcheri]
MAGFRAMLSRDRTHCESGCRELFEACRNGDVARVKKLTTPQNVNWARDTAGRKSTPLHFAAGFGRRKDVV
EHLLLQGANVHARDGGGLIPLHNACSFGHAEVVTLLLRNGADPNARDNNWYTPHEAAIKGKIDVCIVLL
QNGADPSIRNTDGKTALDLAEPSAKTVLTGDYKDELLEAARSGNEEKIMALLTFLNVNCHASDGRKSTP
LHAAAGYNRVIRVQLLLQHGADVHAKDGGGLVPLHNACSYGHFEVTELLKHGASVNAIDLWQFTPLHEA
ASKSRIVEVCSLLLSHGADPTLLNCHSKSAIDVASTPELQEKLSYEFKGHCLLDGARQTDMAKVKHKLQD
IVNFKHPYTHDTALHCAALSYPKRRQITELLIRKGANLNDKNEFLTPLHVASDKCYIDVMEVLLKHGA
KNVALDLSLQGTALHRAAGHGVQACRLLLSFGVDPSIVSLQGVTAQAQMTEAVQMLHEDPPSGPADECD
QLLEAAKAGDLEAVKVLNPFHTVNCRDVNGRSTPLHFAAGYNRVAVVEYLLQHGADVHAKDGGGLVPLH
NACSYGHFEVTELLKHGASVNVADLWKFTPLHEAAAKGKYEICKLLKHGADPNKKNRDNPTFLDLVRD
GDTDIDLGRDAALLDAAKGNLARVQKLTATPENINCRDTQGRNSTPLHAAAGYNNLEVAEFLLENGAD
VNAQDKGGLIPLHNACSYGHVEIAQLLIKYGTCVNATDRWNFTPLHEAAQKGRGTQLCALLAHGADPTMK
NQEGQTPDLATAEDVRALLVDAMPQSLPAATIAATVKAASPISSPSTTPSGVLSTASSMDHLVGA
VGGAGQGDGAIDRSASVEGESLDMTISSSLQQLGLNQLLDIFNKEQITLDILGEMGEELKEIGINAYGH
RHKLILKGVIRILGGTGTTLNPLYLTPALGSHGTILTDLSPPDDKEYQSVEEVEQSTIRQHKDQQAGGIFNR
YNYVIKIQKVRNKKLRDRIYHRRKEVSEENNHQSNERMFLFHGSPFFINAIKNGFDERHAYIGMGFGAGIY
AENSSKSNQYVYIGGGTGCPHKKDRSCYICRQMLFCRVTLGKAFQFSAMKMAHAPPGHHSVIGRPSV
GGNLFAEYVIYRGEQAFPEYLITYQIVKPEAAPSPDQK

>NP_651410.1 tankyrase, isoform A [Drosophila melanogaster]
MANSSRSRAILSVNLDVAMNDPLRELFEACKTGEIAKVKKLTTPQTVNARDTAGRKSTPLHFAAGYGRR
EVTEFLPLNSGASIQACDEGGLHPLHNCCSFGHAEVVRLLLKAGASPNTTNNWYTPHEAASKGVKDVCIL
ALLQGHGANHTIRNSEQKTPLELADEATRPVLTGEYKDELLEAARSGAEDRLLALLTFLNVNCHASDGRR
STPLHAAAGYNRIGIVEILLANGADVHAKDGGGLVPLHNACSYGHFDVTKLLIQAGANVNANDLWAFPTL
HEAASKSRVEVCSLLLSRGADPTLLNCHSKSAIDAAPTRELREERIAFEYKGHCLLDACRKCDEVSRACKLV
CAETVNVFHPYTGDTPLHLAVVSPDGKRRKQIMELLTRKGSLLNEKNKAFITPLHLAAELLHYDAMEVLLK
QGAKNALDLSLQGTPLHRCARDEQAVRLLLSYAADTNIVSLEGLTAAQLASDSVLKLLKNPFPDSETHLLE
AAKAGDGLTVRRIVLNNPISVNCRDLDGRHSTPLHFAAGFNRVVQVFLLEHGAEVYAADKGGGLVPLHNA
CSYGHFEVTELLVKHGASVNVSDLWKFTPLHEAAAKGKYEICKLLKHGADPMKKNRDNATPADLVKESD
HDVAELLRGPSTALLDAAKGNLARVQRLVTPESINCRDAQGRNSTPLHAAAGYNNFECAEYLLLENGADV
AQDKGGLIPLHNACSYGHLDTAALLIKHKTVVNATDKWGTFTPLHEAAQKGRGTQCLCSLLLAHGADAYMKNQ
EGQTPLELATADDVKCLLDAMATSLSQQALSASTQSLSSTSSPAPDATAAAGPTSSSSSSAILLSPTTET
VLLPTGASMILSVVPVPLTSSSSTRISPAQGAEEANGAEGSSSDLLPDADTITNVSGFLSSQQLHHLIELF
EREQITDILAEIMGHDDLKQGVSAFYGRHKILKGIAQLRSTTGIGNNVNLCITLLVDLLPDDKEFVAVEE
EMQATIREHRDNGAGGQYFTRYNIIRVKVQNRKKLWERYAHRQKEIAEENFLQSNERMFLFHGSPFFINAI
RQGFDERHAYIGMGFGAGIYFAEHSSKSNQYVYIGGGIGCPSHKDKSCYVCPRQLLLCRVALGKSFQY
SAMKMAHAPPGHHSVIGRPSAGGLHFAEYVIYRGEQAYPEYLITYQIVKPPDDSSSGTETDR

>XP_032220531.1 poly [ADP-ribose] polymerase tankyrase-1-like [Nematostella vectensis]
MPQARMAASKLASNPTFLSDPDVEGGRELFEACRNGDVRVKRLVNNNSVNVDRDTAGRKSSPLHFAA
FGRRKEVVEYLLQCGADVHARDGGGLIPLHNACSFGHAEVVRILLSHGADANARDNNWYTPHEAAVKKG
VDVCVVLLQHGADPNIRNTDGKTALDVAEAAKVLVTGDYKDELLEAGRSNEEKIMSLTFLNVNCHAS
SDGRKSTPLHAAAGYNRVGVQLLKHGADVHAKDGGGLVPLHNACSYGHFEVTELLIKHGASVNAIDLW
QFTPLHEAASKARVEVCALLLHGADPTLLNCHSKSAIDAAPTRELQEKLLSEFKHQILEAAKCGDCTAK
IKKLTITETINFQHPLTLDTPHLVAVASSPKKKGVETLLKKGADPNLQNKSSYAPLHVAAEKLFEAM
ELLLKHGAKVNAIDAGQTAHVAAIAGVQACRVLMNSGADPTCQTQFGYTAFAVEAPEFQVKVLHVNEE
SPSPVSDAEKQLLEAAKTGDLTEVKNLCTAQTVNCRDLDRGSTPLHFAAGYNRVVVEYLLNGADVHA
KDKGGLVPLHNACSYGHFEVTELLVHGAIVNVADLWKFTPLHEAAAKGKYEICQLLLKHGADPQKKNRD
GYTFLDLVKEGSDVADLLRGDAALLDAAKGNLIRITKLATPENINCRDTQGRNSTPLHAAAGYNNHLE
AEYLLLEHGADVNAQDKGGLIPLHNACSYGHVDIAALLIRYNTDVNATDRWLTPLHEAAQKGRGTQLCALL
LAHGAEPSMKNQEGQSPVDLATAEDVKCLLDAMLSTQTTSVSTAPVAKVPAPVATAGAATPATGPISG
MAPLSQANSSILLANSAGHGADGAFSNRSYEAQGEAVRSISAVHPGLDLDVVGQFLDGLQLNNLKEIFERE
QISWDVILVMGHEELKEIGINAYGHRHKLKAVKEKISGMGLGLGPFSTSQVGSVIQELSMVDKDFASV
ADEMQSTIREHRDNGAGGVTSYTILKIERVNVTKLWEKYVYRREIADSNHNNHANRMLFHGSPFFINA
IVQGFQDRHAYIGMGFGAGIYFAENSSKSNQYVYIGGGGCTPHKDRSCYSCERQLLLCRVALGKFPFY
QFSAVKMAHAPPGHHSVIGRPSGGLSFAEYVIYRGEQAYPEYLITYQIVKINKPDT

>XP_047128184.1 poly [ADP-ribose] polymerase tankyrase-2-like isoform X1 [Hydra vulgaris]
MALGRNRPAMPSPRRNSVASNFMQGVHENDSGRELFEACRTGDIVRVIRYLQNNWDVNMRTDAGRKSTPL
HFAAGFGRRKDIVYLLDAGADVHARDGGGLIPLHNACSFHGEVETLSLLRHADVARNARDNNWYTPHEAA
IKGKVEVCIALLQHGADPLIRNTDGKTARDLAEATAKAVLTGEYKKEELLEDSARSGCEEKMLSLITSLVN
NCHAGDGRKSTPLHAAAGYNRTRIVEILLKHGADVHAKDGGGLVPLHNACSYGHFEVTELLVKHGASVNA
MDLWQFTPLHEAASKMRIVECTLLSYGADPTVLNCHSKSAIDVAPVQELDKLLIYEGRHTYLEAVKSS
DLSKIKRIIAPDLVNVFPLTINSALHVCALSTSAKRDRVADFLIKKGCNMNFCNKQKLTPLHLCAIGNDN
VVVTEILIKAGADCNIVNESLQSPHLTAAQSGHAHICYLLMNGADPTIRNSSGYTPAQVGTESVQKIFQ
ARLEPMLKDVNDINLEASTGDFELIQSLCTPQNVNCRDVAGRMSTPLHFASGYNRMIDIVEHLLRCGADV
HAKDGGGLVPLHNACSYGHFEIAELIVRHGANVNAADYWKFTPLHEAAAKGKFDICKLLKHGADPKKKN
HEGYTFLDLVKEGFPDVADLLRGDAALLDAAKGNLAKVMKLVTHQININCRDTLGRNSTPLHAAAGYNH
VEAYLLEFGADVNAQDKGGLIPLHNACSYGHVDIAALLIKYKADVNTDRWLTPLHEAAQKGRGTQLCALL
LLLTHGANANMKNQEGQTPIDLATADDVQLLDQSMVSKSEVMQITSNCTSIKSPINSQVPLISNDLSP
QLEFPQGLTKPTANQILLSEPCNSDGLQTKRLRQAEGTNPDLIDIGTFLSSLQLEFLHEIFSRREQITMS
DVLIEMGPDQKEIGIVAYGHRHKLIGKVERLAGAGCTIVGEPFLSNINASGPNITLQELSMDEKDYQS

VAEEMQSTVVEHKDGGVAGGIFSRYSCLKIERVINKKLWDKYYYQRKQVADANHNHPNERMLFHGSPFVN
AIVQKGFDERHAYIGMGFAGIYFAEHSSKSNQYVYVYIGGGSGCPVHKDRSCYDCKRQIILCRVTLGKPF
FQNSAMKMAHAPPGHHSVIGRPNSSGLSYPEYVYVYRGEQAYPEYLITYKIERPNTLSSCQSAVD

>XP_019848937.1 PREDICTED: tankyrase-2-like [Amphimedon queenslandica]
MDTRDHQAKIPGDSRQTSQSIEEGESADKNTGDLARLFEACKNGDIDTVQNLIQQRQSSANERDLHGRKS
TPLHFAAGFGRRDIVKFLIEKGAHVDFRDEGGLIPLHNSCSFGHVDVVQQLLSNGANPNQAQDNWKFSPPLH
EAAIKGADVCIYLLQHGAUSSLLNTRKAPIDLANGQAREVLLGTYYRQDELLAAKVGDEQLLMQILTP
LNYNCHASDCRRSTPLHLAAGYNRTSIVQQLLKQGADVHAKDKGGLVPLHNACSYGHYVEAELLKYGAS
INVTDLMQFTPLQEAASKGRSDVCSLLLAHGANPSIANCHGKTAFNLLAPSEEFKKLDSYRGYQLLAAA
EDGGIILLKLLSSQLLKFOHHQTLDTLLHKAVLSKSSNRQSVIDALLKRGINLNIGNKENMTPLICAAK
KGILEVVEQLVQRGANINHODINGMTSLHWAVQNEHAQICRYLLSSGANPSIVNNQGTITYQLKTSDDTIQ
LILKNEPPVSQFBEIEQQLLEAARNSDLEILKKICTPQNVNCRDTRKRMSTPLHFAAGYNRVTVVEFLEN
GADVHAKDKGGLVPLHNACSYGHYVEAELLKYKANVNAMDLMKFTPLHEAAAKEKYDICKLLKNGANV
HSKNRDNLTPIDLVKDPKSDLADLLRGEFALLDAKKGEIERVKKLLTEDNVNCRDEYGRNSTPLHLAAG
YNHLDVVEYLLLENKADVNAKDKGLVPLHNASSYGHVDVASLLIRYNSVINATDRWNFTPLHEAAQKGR
QVCSLLIIHGADVYLKNQEQIPLDLATADDVIALQDAMMKDIPLTIPPAEKEAKSNIVNKGTLTAAGAS
LLASELVLGDGVDKNGMVTQRRGGPAGVGDGSDKGFMSYRGGDAPPPWHNVTVKDILTELELGHVLEL
FEREQITIDILIEMNGDDLQSIGITAFGVRHRLKRIRELVQGNNEEYPVGVTTTKPTQGTQLIELSSDD
KEFIDTADLMQSTICEHRDDGKAGGVFDSYEILKIERIVNTKVMERYKYRKEVAESNNNCANELMLFHG
SPFPVYIVHNGFDERHAYIGMGFAGIYFAEHSSKSNQYVYVYIGGGNGCPEHKNRSCYTCRLKLLCRVV
LGKPVYQYTAVRIAHPGHHSVIGRPSAGGLNYPEYVYVYRGEQAYPEYIITFRIKKPSATDSMSSSSSL
DMSNNT

Alignment

XP_019848937.1 [A. queenslandica]		0
NP_651410.1 [D. melanogaster]		0
XP_047128184.1 [H. vulgaris]		0
XP_032220531.1 [N. vectensis]		0
XP_032806710.1 [P. marinus]		0
XP_019641281.1 [B. belcheri]		0
XP_014017013.1 [S. salar]	MAVSRSSSQQQGN-----LLSPF	19
XP_018099068.1 [X. laevis]	MAAPSRSSQ---QQVFATAAGQSPPPSASPFLSPSS---RR---AASCLSPPCSP	48
NP_989671.2 [G. gallus]	MAAPPRR---SQ-HHHHHHGPPPPPGPASPPAAASPPSPSLAPAEGL-PAQ	58
NP_003738.2 [H. sapiens]	MAASRRSQNHNNHHHQQLQPAGGASAPPPPPPPLSPGLAAGTTP-ASTASGLAFASP	49
XP_024106876.1 [P. abelii]	MAASRRSQNHNNHHHQQLQPAGGASAPPPPPPPLSPGLAAGTTP-ASTASGLAFASP	59
NP_780300.2 [M. musculus]	MAASRRSQNHNNHHHQQLQPAGGASAPPPPPPPLSPGLAAGTTP-ASTAGGLAFASP	59
-----MAGR		
XP_019848937.1 [A. queenslandica]		0
NP_651410.1 [D. melanogaster]		0
XP_047128184.1 [H. vulgaris]		0
XP_032220531.1 [N. vectensis]		0
XP_032806710.1 [P. marinus]		0
XP_019641281.1 [B. belcheri]		0
XP_014017013.1 [S. salar]	-----MAARRAHLASPSSSSSLSPSGSLDTTAAAAAAAATTTAAAAAAT	46
XP_018099068.1 [X. laevis]	RNGSLSVSPFGSPSLNL-----VTATLVFPDGERGCSTG-	53
NP_989671.2 [G. gallus]	ETNALSSLREGPDSEPEGEAASQGTFTRFLSPFPPEGAANIL-	90
NP_003738.2 [H. sapiens]	RHS-----LAGPEGA--FPDAERFFAPE-	70
XP_024106876.1 [P. abelii]	RHG-----LALPEGDGSRDPDFRPSPDPVDGTSCCSTTSITCTVAAPVPVAVST	110
NP_780300.2 [M. musculus]	RHG-----LALPEGDGSRDPDFRPSPDPVDGTSCCSTTSITCTVTAAPVPVAVST	110
	RHG-----LALPEGDGSRDPDFRPSPDPVDGVACTVA--APAAPFAA---	100
-----MANSRS		
XP_019848937.1 [A. queenslandica]		0
NP_651410.1 [D. melanogaster]		0
XP_047128184.1 [H. vulgaris]		0
XP_032220531.1 [N. vectensis]		0
XP_032806710.1 [P. marinus]		0
XP_019641281.1 [B. belcheri]		0
XP_014017013.1 [S. salar]	-----MENPL--ASFDLQTALSLSGGSTPTTTTSGGGSSSVSPGS	93
XP_018099068.1 [X. laevis]	SPTSLSLPAPAFPSSSGSSSS---SS---PSSNSLCGTGPSAESPVIGVSGSVG	140
NP_989671.2 [G. gallus]	-CSEGAAFPFGPGSSSGSSSGSSSSSS---SSTS SVSPSPAEPESV-	143
NP_003738.2 [H. sapiens]	SSAAGVAPNPAGS---GSNNPSSSSSSPTSSSSSSPSSPSSGLAESPEAAGVSSTAPLGP	167
XP_024106876.1 [P. abelii]	SSAAGVAPNPAGS---GSNNPSSSSSSPTSSSSSSPSSPSSGLAESPEAAGVSSTAPLGP	167
NP_780300.2 [M. musculus]	SAAGVAPTTPAGGGGGNNASSASPTSSSSSSPSSPSSGLAESPEAAGVGSTATLGA	160
-----MQ-CARMAKSKLA		
XP_019848937.1 [A. queenslandica]		0
NP_651410.1 [D. melanogaster]		0
XP_047128184.1 [H. vulgaris]		0
XP_032220531.1 [N. vectensis]		0
XP_032806710.1 [P. marinus]		0
XP_019641281.1 [B. belcheri]		0
XP_014017013.1 [S. salar]	-----TTAAAMT-----TTAAVSATSSSFTT-----AAAAA VAAAAATGS	12
XP_018099068.1 [X. laevis]	-----MENPL--ASFDLQTALSLSGGSTPTTTTSGGGSSSVSPGS	93
NP_989671.2 [G. gallus]	SPTSLSLPAPAFPSSSGSSSS---SS---PSSNSLCGTGPSAESPVIGVSGSVG	140
NP_003738.2 [H. sapiens]	SSAAGVAPNPAGS---GSNNPSSSSSSPTSSSSSSPSSPSSGLAESPEAAGVSSTAPLGP	167
XP_024106876.1 [P. abelii]	SSAAGVAPNPAGS---GSNNPSSSSSSPTSSSSSSPSSPSSGLAESPEAAGVSSTAPLGP	167
NP_780300.2 [M. musculus]	SAAGVAPTTPAGGGGGNNASSASPTSSSSSSPSSPSSGLAESPEAAGVGSTATLGA	160
-----MALGRPNRAMPSSRN-----S----		
XP_019848937.1 [A. queenslandica]		0
NP_651410.1 [D. melanogaster]		0
XP_047128184.1 [H. vulgaris]		0
XP_032220531.1 [N. vectensis]		0
XP_032806710.1 [P. marinus]		0
XP_019641281.1 [B. belcheri]		0
XP_014017013.1 [S. salar]	-----TTAAAMT-----TTAAVSATSSSFTT-----AAAAA VAAAAATGS	12
XP_018099068.1 [X. laevis]	-----MENPL--ASFDLQTALSLSGGSTPTTTTSGGGSSSVSPGS	93
NP_989671.2 [G. gallus]	SPTSLSLPAPAFPSSSGSSSS---SS---PSSNSLCGTGPSAESPVIGVSGSVG	140
NP_003738.2 [H. sapiens]	SSAAGVAPNPAGS---GSNNPSSSSSSPTSSSSSSPSSPSSGLAESPEAAGVSSTAPLGP	167
XP_024106876.1 [P. abelii]	SSAAGVAPNPAGS---GSNNPSSSSSSPTSSSSSSPSSPSSGLAESPEAAGVSSTAPLGP	167
NP_780300.2 [M. musculus]	SAAGVAPTTPAGGGGGNNASSASPTSSSSSSPSSPSSGLAESPEAAGVGSTATLGA	160
-----MDTRDHQAIPGDS-----RQ-T		
XP_019848937.1 [A. queenslandica]		0
NP_651410.1 [D. melanogaster]		0
XP_047128184.1 [H. vulgaris]		0
XP_032220531.1 [N. vectensis]		0
XP_032806710.1 [P. marinus]		0
XP_019641281.1 [B. belcheri]		0
XP_014017013.1 [S. salar]	-----MENPL--ASFDLQTALSLSGGSTPTTTTSGGGSSSVSPGS	93
XP_018099068.1 [X. laevis]	SPTSLSLPAPAFPSSSGSSSS---SS---PSSNSLCGTGPSAESPVIGVSGSVG	140
NP_989671.2 [G. gallus]	-CSEGAAFPFGPGSSSGSSSGSSSSSS---SSTS SVSPSPAEPESV-	143
NP_003738.2 [H. sapiens]	SSAAGVAPNPAGS---GSNNPSSSSSSPTSSSSSSPSSPSSGLAESPEAAGVSSTAPLGP	167
XP_024106876.1 [P. abelii]	SSAAGVAPNPAGS---GSNNPSSSSSSPTSSSSSSPSSPSSGLAESPEAAGVSSTAPLGP	167
NP_780300.2 [M. musculus]	SAAGVAPTTPAGGGGGNNASSASPTSSSSSSPSSPSSGLAESPEAAGVGSTATLGA	160
-----MANSRS		
XP_019848937.1 [A. queenslandica]		0
NP_651410.1 [D. melanogaster]		0
XP_047128184.1 [H. vulgaris]		0
XP_032220531.1 [N. vectensis]		0
XP_032806710.		

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*****: : : * : ** ***** : : :
XP_019848937.1[A.queenslandica] NCHGKTAFNLPASEFEKRLDSEYRGYQLAAAEDEGGIIILKKLLSSQLLKQHHQTLD
XP_651410.1[D.melanogaster] NCHSKSAIDAAPTRELRIIAFEYKHGLCDLCKRCKDVSRAKKIVCAEIVNVPHTYGD
XP_047128184.1[H.vulgaris] NCHSKTADIVAPVQLDKLIDYFEGHYTHLEAVKSGSDLSKIKRIIAPDLVNVFPLTLN
XP_032220531.1[N.vectensis] XP_032220531.1[N.vectensis] NCHSKTADIVAPTELQKLLSEFQKGLDGAARQCDTAKIKLITITETINQPHLTD
XP_032806710.1[P.marinus] NCHSKSAIDLAPTSELKRLYFVFGHSLQQAAREADLVTRVKHGLGDIINFKPHQTHE
XP_01641281.1[B.belcheri] NCHSKSAIDVASTPEKQLSEYFKGHCLLDGARQTDMAKVKVHGLDQIVNFKPHYTHD
XP_014017013.1[S.salar] NCHSKGSVDMAPPTPELKRLLTFEFGHSLQQAAREADMAKVKVHTLALIEINFKPHQTHE
XP_01899068.1[L.laevis] NCHGKSADVMAPTPELKRSEYFKGHSLQQAAREADLAKVKTTLALIEINFKPQOSHE
XP_989671.2[G.gallus] NCHGKSADVMAPTPELKRLLTFEFGHSLQQAAREADLAKVKTTLALIEINFKPQOSHE
XP_003738.2[H.sapiens] NCHGKSADVMAPTPELKRLLTFEFGHSLQQAAREADLAKVKTTLALIEINFKPQOSHE
XP_024106876.1[P.abellii] NCHGKSADVMAPTPELKRLLTFEFGHSLQQAAREADLAKVKTTLALIEINFKPQOSHE
XP_780300.2[M.musculus] NCHGKSADVMAPTPELKRLLTFEFGHSLQQAAREADLAKVKTTLALIEINFKPQOSHE

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NCHGKTAFNLAPEEPRFGRDSEYRGYQLAAEDCGGILLKKLLSQQLFQHHQTJDT	371
NCHSKSADIDVAPTELRRERIAFEYGHGQLDAACDKRCKIVAAQNVFVPHYTDG	372
NCHSKTADIDVAPQELKMLLYVRGHQYLEAGKCTSDLSKIKRIAPDLVNFVHFLTNS	373
NCHSKSADIDAAPTELQEKLSLEFGHGYLEAAKVTDAKCTKKRILITFNFQHFLTLD	374
NCHSKSADIDVAPTELSEIKRLVYFPGKHSLLQAAREADVTRVKKHQLDILINFKHQPTHT	375
NCHSKSADIDVASTPELQEKLSYFPGKCHLDGGRQTDMAKYVKKHQLDILINFKHQPTHT	376
NCHSKGSAVDMAPTPELKERLITYFPGKHSLLQAAREADMAKVKTTLALELISFKHQPTNET	377
NCHSKGSAVDMAPTPELKERLSYFPGKHSLLQAAREADLAKVKTTLALELINFKQPSHET	378
NCHSKGSAVDMAPTPELKERLITYFPGKHSLLQAAREADMAKVKTTLALELINFKQPSHET	379
NCHSKGSAVDMAPTPELKERLITYFPGKHSLLQAAREADLAKVKTTLALELINFKQPSHET	380
NCHSKGSAVDMAPTPELKERLITYFPGKHSLLQAAREADLAKVKTTLALELINFKQPSHET	381
NCHSKGSAVDMAPTPELKERLITYFPGKHSLLQAAREADLAKVKTTLALELINFKQPSHET	382
NCHSKGSAVDMAPTPELKERLITYFPGKHSLLQAAREADLAKVKTTLALELINFKQPSHET	383
NCHSKGSAVDMAPTPELKERLITYFPGKHSLLQAAREADLAKVKTTLALELINFKQPSHET	384
NCHSKGSAVDMAPTPELKERLITYFPGKHSLLQAAREADLAKVKTTLALELINFKQPSHET	385
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NCHSKGSAVDMAPTPELKERLITYFPGKHSLLQAAREADLAKVKTTLALELINFKQPSHET	389
NCHSKGSAVDMAPTPELKERLITYFPGKHSLLQAAREADLAKVKTTLALELINFKQPSHET	390
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NCHSKGSAVDMAPTPELKERLITYFPGKHSLLQAAREADLAKVKTTLALELINFKQPSHET	393
NCHSKGSAVDMAPTPELKERLITYFPGKHSLLQAAREADLAKVKTTLALELINFKQPSHET	394
NCHSKGSAVDMAPTPELKERLITYFPGKHSLLQAAREADLAKVKTTLALELINFKQPSHET	395
NCHSKGSAVDMAPTPELKERLITYFPGKHSLLQAAREADLAKVKTTLALELINFKQPSHET	396
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NCHSKGSAVDMAPTPELKERLITYFPGKHSLLQAAREADLAKVKTTLALELINFKQPSHET	399
NCHSKGSAVDMAPTPELKERLITYFPGKHSLLQAAREADLAKVKTTLALELINFKQPSHET	400

XP_019489337.1[*A.queenslandica*] GHVDAIALLIRYNSVNTDKRWFTLPLEAAAGKRGQTQVCSLLITHGADVLYNKGQEQIPL
NP_651410.1[*D.melanogaster*] GHVDAIALLIKRYTVMNATDKRWFTLPLEAAAGKRGQTQVCSLLIHAAGDAPVMYNNQEQGTPL
XP_047126184.1[*H.vulgaris*] GHVDAIALLIKRYADNVNATDRLWFTLPLEAAAGKRGQTQVCSLLITHGANAMNNKQEQGTPL
XP_032205231.1[*N.vectensis*] GHVDAIALLIKYQNTDVMNATDRLWFTLPLEAAAGKRGQTQVCSLLIHAAGDAPFSMNKQEQGSP
XP_032806710.1[*P.marinus*] GHVDAIALLIKYSCAVNATDKRWFTLPLEAAAGKRGQTQVCSLLIHAAGDAPFSMNKQEQGTPL
XP_019641281.1[*B.belcheri*] GHVEIAQLLIKYGTCVNATDKRWFTLPLEAAAGKRGQTQVCSLLIHAAGDAPTMKNQEQGTPL
XP_014017013.1[*S.salar*] GHVDAIALLIKFYNTCVNATDKWFTLPLEAAAGKRGQTQVCSLLIHAAGDAPTMKNQEQGTPL
XP_018099068.1[*X.laenig*] GHVDAIALLIKYKTCVNATDKWFTLPLEAAAGKRGQTQVCSLLIHAAGDAPTMKNQEQGTPL
NP_989671.2[*G.gallus*] GHVDAIALLIKYNTCVNATDKWFTLPLEAAAGKRGQTQVCSLLIHAAGDAPTMKNQEQGTPL
NP_003738.2[*H.sapiens*] GHVDAIALLIKYNTCVNATDKWFTLPLEAAAGKRGQTQVCSLLIHAAGDAPTMKNQEQGTPL
XP_024106876.1[*P.abellii*] GHVDAIALLIKYNTCVNATDKWFTLPLEAAAGKRGQTQVCSLLIHAAGDAPTMKNQEQGTPL
NP_780300.2[*M.musculus*] GHVDAIALLIKYNTCVNATDKWFTLPLEAAAGKRGQTQVCSLLIHAAGDAPTMKNQEQGTPL

XP_019848937.1 [A. queenslandica]	DLATADDVALLQDAMMKPLIT-IPPAEKAKSN-----I-----V	830
NP_651410.1 [D. melanogaster]	ELATADDVKLLQDAMATLSLQALASASTQSLTSS-----SPADP	816
XP_047128184.1 [H. vulgaris]	DLATADDVQVLLQDSMSVSKSEMQITSNICS-----	821
XP_032220531.1 [N. vectensis]	DLATAEDVKLLQDAMDLSQTQTSVSTAPVAKVPA-----PV	824
XP_032806710.1 [P. marinus]	DLATADDVALLIDAMPPEALPVTHKPFSSITPITSAATAAATAALAGPTPALASLPSPV	916
XP_019641281.1 [B. belcheri]	DLATAEDVRLLDVAMPQPSQLPAATTAAT-VKAA-	812
XP_014017013.1 [S. salar]	DLATADDIRALLMDAMPPEALPSCFKPQATVVSAG-----	900
XP_018099068.1 [X. laevis]	DLATADDIRALLIDAMPPEALPSCFKPQATVVA-----	945
NP_989671.2 [G. gallus]	DLATADDIRALLIDAMPPEALPTCFKPQATVVA-----	913
NP_003738.2 [H. sapiens]	DLATADDIRALLIDAMPPEALPTCFKPQATVVA-----	974
XP_024106876.1 [P. abelii]	DLATADDIRALLIDAMPPEALPTCFKPQATVVA-----	967
NP_780300.2 [M. musculus]	DLATADDIRALLIDAMPPEALPTCFKPQATVVA-----	974
	*****: ** *	
XP_019848937.1 [A. queenslandica]	NKGLTAAGA-----SLLAS-----ELVLGDGVDDKNMGVT-----	860
NP_651410.1 [D. melanogaster]	ATAAAAPGTSSSSSSSALSPSTTIVLTPGAS-----MILSVFVPLPLSSST	863
XP_047128184.1 [H. vulgaris]	-----LKSIPNSQVLPISNDLSQLEPQE-----GLTKPSTANQN	856
XP_032220531.1 [N. vectensis]	TATA-----GAATPATGTISGMAPLSQAN-----S	849
XP_032806710.1 [P. marinus]	PSGASASGA-----GVPLLASPSSTPASLSAASMDSLTGACCVAPSPVAGAIAGAGAAGD	97
XP_019641281.1 [B. belcheri]	-----PTSSPSTPTSSPTGVLSTASSMDHLVAGVG-----GA-----	84
XP_014017013.1 [S. salar]	-----VISPASTPSCLSAASDINLGLPMAELGAA-----GTS-----	934
XP_018099068.1 [X. laevis]	-----S-----IISPSTPSCLSAASDINLGLPMAELAVG-----GVS-----	979
NP_989671.2 [G. gallus]	-----S-----LISPASTPSCLSAASDINLGLPMAELAVG-----GAS-----	947
NP_003738.2 [H. sapiens]	-----S-----LISPASTPSCLSAASDINLGLPMAELAVG-----GAS-----	1008
XP_024106876.1 [P. abelii]	-----S-----LISPASTPSCLSAASDINLGLPMAELAVG-----GAS-----	1008
NP_780300.2 [M. musculus]	-----S-----LISPASTPSCLSAASDINLGLPMAELAVG-----GAS-----	1001
	*****: ** *	
XP_019848937.1 [A. queenslandica]	-QRRGGPAGVGDGSDKGFMS-----YRGGDAPFPWHNVTVRIGLTELGLHVLVEFR	913
NP_651410.1 [D. melanogaster]	-RISPAQGAENAGEGSSS-----D-----DLDPADPTFNVGSLFSSQQHHLIELFER	912
XP_047128184.1 [H. vulgaris]	-LLSEP-CNSDCLQ-----TKRLDRAGQTNPLDIDGTFTSLAQLEPHETFSR	905
XP_032220531.1 [N. vectensis]	SLLANSAPHGDDGAPGASVNRSEVAGAVRSISAVHPLGLDVVDQFLDGLNNHLKEIFER	909
XP_032806710.1 [P. marinus]	TLLGACGVSAADGATGPA-----DKDPSRADPELGLDMMNMFRLKGLDHLRDLFEF	1028
XP_019641281.1 [B. belcheri]	-----QQGDGAADR-----SAVEGE-SLDMTISSPFLQGLDHLIDFNK	884
XP_014017013.1 [S. salar]	-----GVADGAGTS-----DRKEGELVLMDDMINQFPLKSLGLEHLRDLIFET	975
XP_018099068.1 [X. laevis]	-----NAGDGAAGT-----ERKEGVELVDININQFPLKSLGLEHLRDLIFET	1020
NP_989671.2 [G. gallus]	-----NTGDGAAGT-----ERKEGEVGLDDMINQFPLKSLGLEHLRDLIFET	988
NP_003738.2 [H. sapiens]	-----NAGDGAAGT-----ERKEGEVGLDDMINQFPLKSLGLEHLRDLIFET	1049
XP_024106876.1 [P. abelii]	-----NAGDGAAGT-----ERKEGELGLDDMINQFPLKSLGLEHLRDLIFET	1049
NP_780300.2 [M. musculus]	-----NAGDGAAGA-----ERKEGEVGLDDMINQFPLKSLGLEHLRDLIFET	1042
	: * : : : : * : : : *	
XP_019848937.1 [A. queenslandica]	EQITLDILAEHGMDDLQSGVITAFVGRHRLIKGIRIELVQGNNE-----YPVGVTTTKP	967
NP_651410.1 [D. melanogaster]	EQITLDILAEHGMDDLQSGVITAFVGRHRLIKGIRIELVQGNNTGIGN-----NV	959
XP_047128184.1 [H. vulgaris]	EQITMDVLVEMDGLQKEIGIVAYGHRHRLIKGVERLQAGACGTG--G--EPPFLSNINAS	962
XP_032806710.1 [P. marinus]	EQSGSVLVDMGHGHKELKEIGINAYGHRHRLIKGVERLQAGACGTG--G--EPPFLSNINAS	961
XP_032806710.1 [P. marinus]	EQSGSVLVDMGHGHKELKEIGINAYGHRHRLIKGVERLQAGACGTG--G--EPPFLSNINAS	1087
XP_019641281.1 [B. belcheri]	EQITLDILAEHGMDDLQSGVITAFVGRHRLIKGIRIELVQGNNE-----YPVGVTTTKP	938
XP_014017013.1 [S. salar]	EQITLDILAEHGMDDLQSGVITAFVGRHRLIKGIRIELVQGNNE-----YPVGVTTTKP	1028
XP_018099068.1 [X. laevis]	EQITLDILAEHGMDDLQSGVITAFVGRHRLIKGIRIELVQGNNE-----YPVGVTTTKP	1073
NP_989671.2 [G. gallus]	EQITLDILAEHGMDDLQSGVITAFVGRHRLIKGIRIELVQGNNE-----YPVGVTTTKP	1041
NP_003738.2 [H. sapiens]	EQITLDILAEHGMDDLQSGVITAFVGRHRLIKGIRIELVQGNNE-----YPVGVTTTKP	1102
XP_024106876.1 [P. abelii]	EQITLDILAEHGMDDLQSGVITAFVGRHRLIKGIRIELVQGNNE-----YPVGVTTTKP	1102
NP_780300.2 [M. musculus]	EQITLDILAEHGMDDLQSGVITAFVGRHRLIKGIRIELVQGNNE-----YPVGVTTTKP	1095
	***: * : : : * : : : * : : : *	
XP_019848937.1 [A. queenslandica]	TQGTQLIELSSDDKEFIDTADLMQSTICEHRDNGKAGGVDSVEILKIRIVNMTKWERY	1027
NP_651410.1 [D. melanogaster]	NLCTLLVDLLPDKDEFFVAEEEMQATIREHRDNGKAGGVYFTRNIRIVQVKNMKLREY	1019
XP_047128184.1 [H. vulgaris]	GPNTLLQELSSDDEKQSVAAEEMQSTVEHRDNGKAGGVFTRSYSLKIRIVNMTKWERY	1022
XP_032220531.1 [N. vectensis]	VQGSVQLSVMQDKFASVDEEMQSTVEHRDNGKAGGVFTRSYSLKIRIVNMTKWERY	1022
XP_032806710.1 [P. marinus]	QGTLLDILAEHGMDDLQSGVITAFVGRHRLIKGIRIELVQGNNE-----YPVGVTTTKP	1147
XP_019641281.1 [B. belcheri]	SHTGILLDILAEHGMDDLQSGVITAFVGRHRLIKGIRIELVQGNNE-----YPVGVTTTKP	998
XP_014017013.1 [S. salar]	NQGTLLDILAEHGMDDLQSGVITAFVGRHRLIKGIRIELVQGNNE-----YPVGVTTTKP	1088
XP_018099068.1 [X. laevis]	SGQTVLLDILAEHGMDDLQSGVITAFVGRHRLIKGIRIELVQGNNE-----YPVGVTTTKP	1133
NP_989671.2 [G. gallus]	SGQTVLLDILAEHGMDDLQSGVITAFVGRHRLIKGIRIELVQGNNE-----YPVGVTTTKP	1101
NP_003738.2 [H. sapiens]	SGQTVLLDILAEHGMDDLQSGVITAFVGRHRLIKGIRIELVQGNNE-----YPVGVTTTKP	1162
XP		

Percent identity matrix:

```
#
#
# Percent Identity Matrix - created by Clustal2.1
#
#
1: XP_019848937.1[A.queenslandica] 100.00 56.61 56.26 60.24 58.20 58.78 57.98 57.87 58.99 58.15 58.24 58.33
2: NP_651410.1[D.melanogaster] 56.61 100.00 60.37 64.62 65.53 68.43 66.78 66.17 67.32 66.70 66.78 66.87
3: XP_047128184.1[H.vulgaris] 56.26 60.37 100.00 68.01 64.65 65.41 64.30 63.79 65.21 64.59 64.68 64.77
4: XP_032220531.1[N.vectensis] 60.24 64.62 68.01 100.00 70.41 71.77 71.65 70.27 71.72 71.42 71.42 71.50
5: XP_032806710.1[P.marinus] 58.20 65.53 64.65 70.41 100.00 79.64 81.58 80.45 83.01 80.58 80.50 81.23
6: XP_019641281.1[B.belcheri] 58.78 68.43 65.41 71.77 79.64 100.00 78.66 79.04 80.28 79.44 79.53 79.53
7: XP_014017013.1[S.salar] 57.98 66.78 64.30 71.65 81.58 78.66 100.00 86.51 87.95 86.97 87.05 86.47
8: XP_018099068.1[X.laevis] 57.87 66.17 63.79 70.27 80.45 79.04 86.51 100.00 90.73 89.50 89.35 88.67
9: NP_989671.2[G.gallus] 58.99 67.32 65.21 71.72 83.01 80.28 87.95 90.73 100.00 93.42 93.42 93.04
10: NP_003738.2[H.sapiens] 58.15 66.70 64.59 71.42 80.58 79.44 86.97 89.50 93.42 100.00 99.70 97.72
11: XP_024106876.1[P.abelii] 58.24 66.78 64.68 71.42 80.50 79.53 87.05 89.35 93.42 99.70 100.00 97.80
12: NP_780300.2[M.musculus] 58.33 66.87 64.77 71.50 81.23 79.53 86.47 88.67 93.04 97.72 97.80 100.00
```