

TNKS2

Sequences :

>NP_079511.1 poly [ADP-ribose] polymerase tankyrase-2 [Homo sapiens]
MSGRRCAGGAACASAAAEAVEPAARELFEACRNGDVERVKRLVTPEKVNSRDTAGRKSTPLHFAAGFGR
KDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAENVNLLLRHGADPNARDNNWYTPLHEAAIKGKIDVC
IVLLQHGAEP TIRNTDGR TALDLADPSAKAVLTGEYKKDELLESARSNGNEEKMMALLTPLNVNCHASDGR
KSTPLHLAAGYNRVKIVQLLQLQHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMD LWQFT
LHEAASKNRVEVCSLLLSYGADPTLLNCHNKS AIDLAPTQPKERLAYEFKGHSL LQAAREADVTRIKKH
LSLEMVNFKHPQTHETALHCAAASPYPKRKQICE LLRRKGANINEKTKEFLTPLHVASEKAHNDVVEVV
KHEAKVNALDNLGQTS LHRAAYCGHLQTCRLLLSYGC DPNI I SLQGFTALQMGNE NVQQLLQEGISLGNS
EADRQLLEAAKAGDVETVKKLC TVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGL
VPLHNACSYGHYEAELLVKHGAVVNADLWKFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLD
LVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQ
HGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKGR TQLCALLLAHGAD
PTLKNQEGQTPLDLVSADDVSALLTAAMPSPSALPSCYKQV LNVGRSPGATADALSSGSPSSLSAASS
LDNLSSGSFSELSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLM DIFEREQITLDVLVEMGHK
ELKEIGINAYGHRHKLKIGVERLISGQQGLNPYLTANTSSG GTI LIDLSPDDKEFQSVEEEMQSTVREHR
DGGHAGGI FNRYN I LKIQKVCNKKLWERYTHRRKEVSEENHNHANERMLFHGSPFFVNAI I HKGFDERHAY
IGGMFGAGIYFAENSSKSNQVYVYGIGGTGCPVHKDRSCYICHRQLLFCRVTLGKSF LQFSAMKMAHSPF
GHSVTVGRPSVNGLALAEYVIYRGEQAYPEYLITYQIMRPEGMVDG

>XP_024109627.1 tankyrase-2 [Pongo abelii]
MSGRRCAGGAACASAAAEAVEPAARELFEACRNGDVERVKRLVTPEKVNSRDTAGRKSTPLHFAAGFGR
KDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAENVNLLLRHGADPNARDNNWYTPLHEAAIKGKIDVC
IVLLQHGAEP TIRNTDGR TALDLADPSAKAVLTGEYKKDELLESARSNGNEEKMMALLTPLNVNCHASDGR
KSTPLHLAAGYNRVKIVQLLQLQHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMD LWQFT
LHEAASKNRVEVCSLLLSYGADPTLLNCHNKS AIDLAPTQPKERLAYEFKGHSL LQAAREADVTRIKKH
LSLEMVNFKHPQTHETALHCAAASPYPKRKQICE LLRRKGANINEKTKEFLTPLHVASEKAHNDVVEVV
KHEAKVNALDNLGQTS LHRAAYCGHLQTCRLLLSYGC DPNI I SLQGFTALQMGNE NVQQLLQEGISLGNS
EADRQLLEAAKAGDVETVKKLC TVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGL
VPLHNACSYGHYEAELLVKHGAVVNADLWKFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLD
LVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQ
HGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKGR TQLCALLLAHGAD
PTLKNQEGQTPLDLVSADDVSALLTAAMPSPSALPSCYKQV LNVGRSPGATADALSSGSPSSLSAASS
LDNLSSGSFSELSVVSSSGTEGTSLEKKEVPGVDFSITQFVRNLGLEHLM DIFEREQITLDVLVEMGHK
ELKEIGINAYGHRHKLKIGVERLISGQQGLNPYLTANTSSG GTI LIDLSPDDKEFQSVEEEMQSTVREHR
DGGHAGGI FNRYN I LKIQKVCNKKLWERYTHRRKEVSEENHNHANERMLFHGSPFFVNAI I HKGFDERHAY
IGGMFGAGIYFAENSSKSNQVYVYGIGGTGCPVHKDRSCYICHRQLLFCRVTLGKSF LQFSAMKMAHSPF
GHSVTVGRPSVNGLALAEYVIYRGEQAYPEYLITYQIMRPEGMVDG

>NP_001157107.1 poly [ADP-ribose] polymerase tankyrase-2 [Mus musculus]
MSGRRCAGGAACASAGAEAVEPSARELFEACRNGDVERVKRLVTPEKVNSRDTAGRKSTPLHFAAGFGR
KDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAENVNLLLRHGADPNARDNNWYTPLHEAAIKGKIDVC
IVLLQHGAEP TIRNTDGR TALDLADPSAKAVLTGDYKKDELLESARSNGNEEKMMALLTPLNVNCHASDGR
KSTPLHLAAGYNRVKIVQLLQLLHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMD LWQFT
LHEAASKNRIVEVCSLLLSYGADPTLLNCHNKS AIDLAPTQPKERLSYEFKGHSL LQAAREADVTRIKKH
LSLEMVNFKHPQTHETALHCAAASPYPKRKQICE LLRRKGANTNEKTKEFLTPLHVASENAHNDVVEVV
KHEAKVNALDNLGQTS LHRAAHCGHLQTCRLLLSYGC DPNI I SLQGFTALQMGNE NVQQLLQEGASLGHS
EADRQLLEAAKAGDVETVKKLC TVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGL
VPLHNACSYGHYEAELLVKHGAVVNADLWKFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLD
LVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQ
HGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKGR TQLCALLLAHGAD
PTLKNQEGQTPLDLVSADDVSALLTAAMPSPSALPSCYKQV LNVGRSPGATADALSSGSPSSLSAASS
LDNLSSGSFSELSA VSSAAEGATGQRKEDSGIDFSITQFVRNLGLEHLM DIFEREQITLDVLVEMGHK
ELKEIGINAYGHRHKLKIGVERLISGQQGLNPYLTANNSSG GTI LIDLSPDDKEFQSVEEEMQSTVREHR
DGGHAGGVFNRYN I LKIQKVCNKKLWERYTHRRKEVSEENHNHANERMLFHGSPFFVNAI I HKGFDERHAY
IGGMFGAGIYFAENSSKNQVYVYGIGGTGCPVHKDRSCYICHRQLLFCRVTLGKSF LQFSAMKMAHSPF
GHSVTVGRPSVNGLALAEYVIYRGEQAYPEYLITYQIVRPEGMVDG

>NP_989672.2 poly [ADP-ribose] polymerase tankyrase-2 [Gallus gallus]
MAARRCAGGAALAEAPGCSAVEPARELFEACRNGDVERVKRLVNPENVNSRDTAGRKSSPLHFAAGFG
KDVVEYLLQSGANVHARDDGGLIPLHNACSFGHAENVNLLLRHGADPNARDNNWYTPLHEAAIKGKTVD
CIVLLQHGAEP TIRNTDGR TALDLADPSAKAVLTGEYKKDELLESARSNGNEEKMSLLTPLNVNCHASDG
RKSTPLHLAAGYNRVKIVQLLQLQHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMD LWQFT
PLHEAASKNRVEVCSLLLSYGADPTLLNCHNKS TIDLAPTQPKERLAYEFKGHSL LQAARESDVARIKK
HLSLETNVNFKHPQTHETALHCAAASPYPKRKQVCELLRRKGANINEKTKDFLPLHVASEKAHNDVVEVV
VKHEAKVNALDNLGQTS LHRAAHCGHLQTCRLLLSGCDPSIVSLQGFTALQMGNE SVQQLLQEGIP LIGN
SDADQLLEAAKAGDVTVKKLC TVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGG
LVPLHNACSYGHYEAELLVKHGAVVNADLWKFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLD
LVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSPDNVNCRD TQGRHSTPLHLAAGYNNLEVAEYLLQ
HGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKGR TQLCALLLAHGA
DPTLKNQEGQTPLDLVTADDVSALLTAAMPSPSALPSCYKQVIVSVQTSSTADPLSSVSPSSLSAAS
SLDNLSSGSFSELP SVVTGNSAEAGATVLEKKEVSGVDFSINQFVRNLGLEHLIDIFEREQITLDVLVEMGH
KELKEIGINAYGHRHKLKIGVERLISGQQGLNPYLTANTSSG GTI LIDLSPDDKEFQSVEEEMQSTVREHR
DGGHAGGVFNRYN I LKIQKVCNKKLWERYTHRRKEVSEENHNHANERMLFHGSPFFVNAI I HKGFDERHAY
IGGMFGAGIYFAENSSKNQVYVYGIGGTGCPVHKDRSCYICHRQLLFCRVTLGKSF LQFSAMKMAHSP
PGHHSVTVGRPSVNGLALAEYVIYRGEQAYPEYLITYQIVKPEATTEA

>XP_018082988.1 poly [ADP-ribose] polymerase tankyrase-2 [Xenopus laevis]
MSGRRCAGASGAASHGNIGAGGEPAARELFEACRNGDVERVKRLVNSDNVNSRDTAGRKSTPLHFAAGFG
KDVVEHLLQSGANVHARDDGGLIPLHNACSFGHAENVSLLLRHGADPNARDNNWYTPLHEAAIKGKTIDV
CIVL FQHGAEP TIRNTDSR TALDLS DPSAKAVLTGEYKKDELLESARSNGNEEKMMALLTPLNVNCHASDG
RKSTPLHLAAGYNRVKIVQLLQLQHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGASVNAMD LWQFT
SLHEAASKNRVEVCSLLLSYGADPTMLNCHNKS AIDLAPTQPKERLSYEFKGHSL LQAAREADLTRIKK
HLSLETNVNFKHPQTHDTALHCAAASPYPKRKQVCELLFRKGANVNEKTKDFLPLHTASDKAHNDIVELL
IKHEAKVNALDNLGQTS LHRAAHCGHLQTCRLLLSGCDPSIVSLQGFTALQMGNE SVQQLLQEGLPFSN
SDADQLLEAAKAGDLDVVKLC TSQSVNCRDVEGRQSTPLHFAAGYNRAVVEYLLQHGADVHAKDKGG
LVALHNACSYGHYEVTELLVKHGAVINADLWKFTPLHEAAAKGKYEICKLLLHGADSTKKNRDGNTPLD
LVKDGDTDIQDLLRGDAALLDAAKKGCVSRVKKLC TPNVNCRD TQGRHSTPLHLAAGYNNLEVAEYLLQ
HGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNANDKWAFTPLHEAAQKGR TQLCALLLAHGA
DPALKNQEGQAPLDLVTADDVRALLTAAMP PAALPTPYKFLNVPQSTTAIAALSSVSPSSLSAAS
SLDNLSSGSFSETTSVSGAEGASGLDKKQGVDLNINQFLRN LGLEHLIDIFEREQITLDVLVEMGHKE
FKEIGISAYGHRHKLKIGVERLISGQQGLNPYLTANTSSG GTI LIDLSPDDKEFQSVEEEMQSTVREHR
DGGHAGGVFTKYN I LKIQKVCNKKLWERYTHRRKEVSEENHNHANERMLFHGSPFFVNAI I HKGFDERHAY
IGGMFGAGIYFAENSSKNQVYVYGIGGTGCPVHKDRSCYVCHRQLLFCRVTLGKSF LQFSAMKMAHSPG
HHSVTVGRPSVNGLALAEYVIYRGEQAYPEYLITYQIMKPEAVAE G

>XP_014034742.2 poly [ADP-ribose] polymerase tankyrase-2 isoform X1 [Salmo salar]
MASVAFRWGSA NTSKLYIYENTTFLMSTRQCSRV LGGVSPGVDT PRSGEPNREIFEACRNGDVERVR
RLVRPENVNSRDTAGRKSTPLHFAAGFGR RDVVDYLLQNGANVHARDEGGLVSLHNACSFHSEVVNLLR
RHGADANSRDNWSYTPLHEAAIKGSEV CIVLQHGAEP TIRNTDGR TALDLAEASTKAVLTGEYKDDL
LESARSGNEEDKIMALLTPLNVNCHASDGRKSSPLHLAAGYNRVKTVQLLLKHGADVHAKDKGDLVPLHNA
CSYGHYEVTDILVKQGACVNAMD LWQFTPLHEAASKNRVDVCSLLSVSYGADPTFLNCHNQSAIDLSPTPQ
LKERLAYEFRGHALLQAAREADL PRLKHL SLETTITFKHPLTHETALHCAATSPYPKRKQVCELLRRKGA
NVNEKTKDFLPLHLASEKSHNDI TEVLVKHEAKVNALDNLGQ TALHRAAHCGHLQTCRLL LKAGCDPLV
MSLQGFSPSQMGNE SVQEILHEGT LIGNSVDVQ LLEASKSGDLEIVKKLCTMQNVNCRDVEGRQSTPLH

FAAGYNRVSVVEYLLHGGADVHAKDKGGLVPLHNACSYGHYEAELLVHGAVVNIADLWKFTPLHEAAAA
KGKYEICKLLLQHGADPTKKNRDGSTPLDLVKDGTMDQDLLRGDAALLDAAKKGCLARVEKLCSPDNVN
CRDAQGRHSTLLHLAAGYNNLEVAEYLLQHGAEVNSQDKGGLPLHNAASYGHVDVAALLIKYDACVNAT
DKWAFTPLHEAAQKGRQTLCALLLAHGADPALRNQEGQSPDLVTVDVVRALLTAAMPSPALPGCYKPKQV
ISMSFSPGVVVVPPSLASASTPLSTLASRNSLDNQATASTCTAFPELALLGPSGAVGTDNKEVPGVDLSI
QGFLNNLQLEHLLIEFEREQITLDVLVEMGHKELKEIGINAYGHRHKIKGVKERLISGQPSLNPYTLTANT
ANSGTILIDLVSDDKEFQLVEEELQSTIREHRDGLAGGVFNRYNIVKIQKVNCKKLWERYTHRRKEVSE
EENHNHNERMLFHGSPFFVNAIHKGFDERHAYIGMGFAGIYFAENSSKSNQIVYIGGGTGCPHLKDRS
CYVCQRHLLFCRVTLGKSLFQFSAMKMAHSPPGHHSVTGRPSVNGLSLAEVVIYRGEQAYPEYLITYQIL
KPDASVDG

>XP_032806710.1 poly [ADP-ribose] polymerase tankyrase-2 [Petromyzon marinus]
MAARRAHLASPPSSSSSLSPSSGSLDTTTAAAAAAATTTAAAAATTTAAVSATSPSTPTAAA
AAAVAAAAATGSGPGSGQDSSADGGDAGKELFEACRNGDVRGVKRLVPLNVNARDTTGRKSTPLHFAAG
FGRKDVVEHLLQNGANVHARDGGGLIPLHNACSFGHAEEVNNLLRQGADPNARDNNWYTPLEHAAIKGKI
DVCIVLLQHGADPGIRNTDGTALDLAEPATAKAVLTGEYKDELLEAARSNEEKLMAILLPLNVNCHAS
DGRKSTPLHLAAGYNRVRIVQLLQHGADVHAKDKGGLVPLHNACSYGHYEVTELLVKHGASVNAMDLMQ
FPLHEAASKNRVEVCSLLSYGADPTLLNCHSKSAIDLAPTSSELKERLVYEFRGHSLQAAREADVTRV
KKHLGLDINFKHPQTHETALHCAVASPYPKRKQVSELLRRKGANVNEKTKDLLPLHVASDKAHNDVID
VLLKHGAKINVTDSLQGTSLHRAAHAGHLTTCRLLLSHGCDPNLPSLQGGTAAQLGNEVSQQILHESSLP
VRNSDVEHQLLEAAKAGDLDTVKQLCTTQTVNCRDMEGRHSTPLHFAAGYNRVSVVEYLLQHGADVHAKD
KGGLVPLHNACSYGHYEAELLVKRGAVVNVDLWKFTPLHEAATAKGYEICKLLLKHGADPTKKNRDGN
TPDLIVKEGDDTDQDLLRGDAALLDAAKKGCLARVQKLCSENVNCRDSQGRNSTPLHLAAGYNNLEVAE
YLLHGGADVNAQDKGGLIPLHNAASYGHVDIAALLIKYSACVNATDKWAFTPLEHAAQKGRQTLCALLLA
HGADSPMKHQEGQTPLDLATADDVRALLIDAMPPEALPVTHKPPSIPTIAATSAATAALAGTTPALAS
LAPSPVPSGASAGAGVPLLASPSVPASLSAASSMDSLTGACGVAPSPVAGAIAGAAGDGTLLGAC
GVSAAGATGPAKDPKRSADFEIPGLDMNINMFKGLGLDHLRDIPEKEQITLDVLADMGHEELKEIGIN
AYGHRHKLKGVRELLGAQGGLAYPGANFYLSYHTTAQGTLLIDLPPDKVEQSVDEMQSTIREHKDG
GQAGGVFNRYNVIKIQKVNCKKLWERYTHRRKEVTEENHNHNERMLFHGSPFFINAINKGFDERHAYIG
MGFAGIYFAENSSKSNQIVYIGGGTGCPVHKDRSCYICQRQMLFCRVTLGKSLFQFSAMKMAHSPPGH
HSVIGRPSVNGLAFAEVVIYRGEQAYPEYLITYQILKPECTPDLTSAAGQKS

>XP_019641281.1 PREDICTED: tankyrase-1-like isoform X1 [Branchiostoma belcheri]
MAGRRAMLSDDRIHCDESSGCRELFEACRNGDVARVKKLITPQNVDNARDTAGRKTPLHFAAGFGRKDVV
EHLNQNGANVHARDGGGLIPLHNACSFGHAEEVNTLLRNGADPNARDNNWYTPLEHAAIKGKIDVCIVLL
QNQADPSIRNTDGTALDLAEPASAKTVLTGDYKDELLEAARSGNEDKLMALLPLNVNCHASDGRKSTP
LHLAAGYNRVRIVQLLQHGADVHAKDKGGLVPLHNACSYGHFEVTELLKHGASVNAMDLMQFTPLHEA
ASKSRIEVCSSLLSHGADPTLLNCHSKSAIDVASTPELQEKLSYEFKGHCLLDGARQTDMAKVKHLLQLD
IVNFKPHYTHDTALHCAALSPYPKRRQITELLIRKGANLDKNKEFTPLPHVASDKCYIDVMEVLLKHGA
KVNALDSLQTALHRGAHCGHVQACRLLLSFGVDPSIVSLQGVTAQMATEAVQQLMHEDPPSGPADECD
QLLEAAKAGDLEAVKVLNCPHTVNCRDVNRHSTPLHFAAGYNRVAVVEYLLQHGADVHAKDKGGLVPLH
NACSYGHYEVCELLKHGAVVNVDLWKFTPLHEAATAKGYEICKLLLKHGADPNKNRDGNTPDLIVDR
GDDTDQDLLRGDAALLDAAKGNLARVQKLATPENINCRDQTQGRNSTPLHLAAGYNNVVAEFLLENGAD
VNAQDKGGLIPLHNACSYGHVEIAQLLIKYGTCVNATDRWNFTPLHEAAQKGRQTLCALLAHGADPTMK
NOEQGTPLDLATAEDVRALLVDAMPQPSLPAAITAAVTKAASPISSPTTSPSTFQVLSITASMSDHLVGA
VGAGQGGDGAIDRSVAGESELDMDTISSFLQGLGLNQLLDINFKQITLDILBEMGHEELKEIGINAYGH
RHKLIKGVREILGGTGTTLNPLYTPALGSHGTILLDLSDDKEYQSVVEEVQSTIRQHKDQQQAGGIFNR
YNNVIKIQKVNCKKLWRYVHRKEVSEENHNQSNERMFLFHGSPFFINAINKGFDERHAYIGMGFAGIYF
AENSSKSNQIVYIGGGTGCPHKDRSCYICQRQMLFCRVTLGKAFQLQFSAMKMAHAPPGHHSVIGRPSV
GGLNFAEYVIYRGEQAFPEYLITYQIVKPEAPASPDPQK

>NP_651410.1 tankyrase, isoform A [Drosophila melanogaster]
MANSRSRAILSVNLDAVMANDPLRELFACKTGEIAKVKKLITPQTVNARDTAGRKTPLHFAAGYGRR
EVVEFLLNSGASIQACDEGGLHPLHNCCSFGHAEEVRLLLKAGASPNNTDNWNYTPLEHAAASKGVDDVCL
ALLQHGANTIRNSEQKTPLELADAEATRPVLTEYRKDELLEAARSGAEDRLALLTPLNVNCHASDGRR
STPLHLAAGYNRIGIVEILLANGADVHAKDKGGLVPLHNACSYGHFDVTKLLIQAGANVNANDLWAFTP
LEHAAASKRVEVCSSLLSRGADPTLLNCHSKSAIDAAPTELRLERIAFEYKGHCLLDACRCKDVSRAKKVL
CAEIVNVPHPYTGDTPLHLAVVSPDGKRRQIMELLTRKGLSLENEKNKAFPLTPLHAAELLLHYDAMEVLLK
QQAKNALDSLGGTPLHRCARDEQAVRLLLSYAADTNIVSLEGLTAAQLASDSVLKLLKNPDPSETHLLE
AARAGHDLTVRRIVLAMPISVNCRDLDGRHSTPLHFAAGFNRVPVVGQFLLEHGAENVYAADKGGVPLHNA
CSYGHYEVTELLVHGANVNSVDLWKFTPLHEAATAKGYDICKLLLKHGADPMKNRDGATPADIVKESD
HDVAELLRGPALLDAAKGNLARVQRLVTPESINCRDAQGRNSTPLHLAAGYNNFECAEYLLLENGADVN
AQDKGGLIPLHNACSYGHLDIAALLIKHKTVVNATDKWGTPLHEAAQKGRQTLCSSLLAHGADVAMNQ
EGQTPIELATADDVKCLLDAMATSLSQQALSASTQSLTSSSPADPATAAAPGTSSSSSSAILSPFTTET
VLLPTGASMILSVVPFLPSSSTRISPAQGAEEANGAEGSSDDLLPDADTTNVSGFPLSSQQLHHLIELF
EREQITLDILAEMGHDDLKQGVSAYGRHKILKGIAQLRSTTIGINNVLCTLLVDLPDDKEFVAVEE
EMQATIREHRDNGQAGGYETRYNIRVQVKQNRKLWERYAHRQEBIAEENFLQSNERMFLFHGSPFFINAIV
QRGFDERHAYIGMGFAGIYFAHSSKSNQIVYIGGGTGCPSHKDRSCYVCPRQLLLCRVALGKSLFYQ
SAMKMAHAPPGHHSVIGRPSAGGLHFAEYVIYRGEQSYPEYLITYQIVKPDSSSGSTEDTR

>XP_032220531.1 poly [ADP-ribose] polymerase tankyrase-1-like [Nematostella vectensis]
MPQAKMASKKLASNPFTLSDPDCEGRELFEACRNGDVKVRKLVNNSNVNVRDTAGRKSPLHFAA
GFRKEVEVVEYLLQCGADVHAMDGGGLIPLHNACSFGHAEEVRIILSHGADANARDNNWYTPLEHAAVKGK
VDVCVLLQHGADPNIRNTDGTALDVAEAAKLVLTGDYKDELLEGARSGNEEKLMSLLTPLNVNCHA
SDGRKSTPLHLAAGYNRVGVVQLLLKHGADVHAKDKGGLVPLHNACSYGHFEVTELLKHGASVNAMDLMW
QFTPLHEAASKARVEVCALLHGGADPTLLNCHSKSAIDAAPTELQEKLLSEFGKHQILEAAKGDCTAK
IKKLTITETINFQHPLTDLTDLHVAVASSSPKKKGVIETLLKKGADPNQKNSSYAPLHVAAEKLFEAM
EELLKHAKKNAIDSAQGTALHVAAIAGQVQACRVLMNSGADPTCQTFGQYTAFEVAPFVQKVLHNEE
SPSPVSDAEKQLLEAAKTGDETVNKLTAQTVNCRDLGRCSTPLHFAAGYNNRVVVEYLLNAGAHVA
KMGKGLVPLHNACSYGHVKEIAYNVNVDLWKFTPLHEAATAKGYEICKLLLKHGADPMKNRD
GYTFLDLVKEGSDVADLLRGDAALLDAAKGNLIRITKLATPENINCRDQTQGRNSTPLHLAAGYNHVA
AEYLLHGGADVNAQDKGGLIPLHNACSYGHVDIAALLIRYNTDVNATDRWLFTPLHEAAQKGRQTLCALL
LAHGAESPKNQEGQSPVDLATAEDVKLLGDAMLSTQTTSVSTAPVAKVPAPVTATAGATPATGPISG
MAPLSQANSSLLANSPAGHDGAFSNRSVEAQGEAVRSISAVHPGLDVGVDVQGLDGLQLNKLKEIFERE
QISWDVLDVMGHEELKEIGIHAYGHRHKILKAVKEKISGMGLGLGPFSTSVQVQSVIQELSMVDKDFASV
ADEMQSTIVEHRDNGTAGGVTSYTIILKIERVNTKLWEKYVYRREIADSNHNHANERMLFHGSPFFINA
IVQKGFQDRHAYIGMGFAGIYFAHSSKSNQIVYIGGGTGCPCHKDRSCYVCPRQLLLCRVALGKSLFYQ
FSAVKMAHAPPGHHSVIGRPSGGLSFAEYVIYRGEQAYPEYLITYQIVKPDSSSGSTEDTR

>XP_047128184.1 poly [ADP-ribose] polymerase tankyrase-2-like isoform X1 [Hydra vulgaris]
MALGRPNRAMPSSRNVSASNFMDDGGVHENDSGRELFEACRTGDVIRVRYLIQNNVDNMRDTAGRKTPL
HFAAGFGRKDIVVEYLLDAGADVHARDGGGLIPLHNACSFHGEVTELLSLRHADVARNARDNNWYTPLEHAA
IKGKVEVCIALQHGADPLIRNTDGTARDLAEATAKAVLTGEYKKEELDSARSGCEEKMLSLITSLNV
NHAGDGRKSTPLHLAAGYNRTRIVEILLKHGADVHAKDKGGLVPLHNACSYGHYEVTELLVKHGASVNA
MDLMQFTPLHEAASKMREIVCTLLSYGADPTVLNCHSKTAIDVAPVQELKDKLLYEYRGHTYLEAVKSS
DLSKIKRIAPDVLNPFVHPLTLNSALHVCALSTSARDRVADFLIKKGCNMMFCNKRQKLTPLHLCAGNND
VVVEILLKAGADCNVNEESQSPHLIAAGSGHAHCYILLMGADPTIRNSGVTFAQVGTESVQKIFQ
ARLEPMKDVLDNLLEASKTGDFELIQSLCTPQVAKCRDVAGRSTPLHFAAGYNNRMDIVEHLLRGADV
HAKDKGGLVPLHNACSYGHFEIAELLVHGANVNAADYWKFTPLHEAATAKGFDCIKLLKHGADPKKKN
HEGYTFLDLVKEGFPDVADLLRGDAALLDAAKGNLAKVMKLVTHQNINCRDPTLGRNSTPLHLAAGYNHV
EYAEYLLLEFGADVNAQDKGGLIPLHNACSYGHVDIAALLIKYKADVNTARWLFTPLHEAAQKGRQTLCALL
LLTHGANANMKHQEGQTPIDLATADDVQVLLQDSMVSKEVMQITSNTCISKSPINSPQVLPISNDLSP
QLEFPQGLTKPSTANQNLLESPNCSDGLQTKRLRQAEGTNPLDIDIGTFLSSLQLEFLHEIFISREQITM
DVLIEMGPDQKLEIGIVAYGHRHKILKGVKERLAGAGCTIVGEPFLSNINASGPNTILQELSMDEKDYQS
VAEEMQSTVVEHKDGGVAGGISRSYSSSLKIERVINKKLWDKYYYQRKVADANHNHNERNMLFHGSPFFIN
AIVQKGFDERHAYIGMGFAGIYFAHSSKSNQIVYIGGGTGCPVHKDRSCYDCKRQIILCRVTLGKFF
FQNSAMKMAHAPPGHHSVIGRPSGGLSYPEYVYRGEQAYPEYLITYKIERPNTLSSCQSAVD

>XP_019848937.1 PREDICTED: tankyrase-2-like [Amphimedon queenslandica]
MDTRDHAQIPGDSRQTSQSIEEGESADKNTGDLARLFEACKNGDITVQNLIQQRQSSANERDLHGRKS
TPLHFAAGFGRRDIVKFLIEKGAHVDFRDEGGLIPLHNCSFQGHVDVVQLLNSGANPNQADNWKFSPLH
EAAIKGADVCI VLLQHGADSSLNTDRKAPIDLANGAREVLLGTYRQDELLEAAKVGEQLLMQILTP
LNVNCHASDGRKSTPLHLAAGYNRTSIVQLLLQGDADVHAKDKGGLVPLHNACSYGHYEAELLKYGAS
INVTDLQWFTPLQEAASKGRSDVCSLLLAHGANPSIANCHGKTAFNLPAPSEEFRRKLDSEYRGYQLAAA

EDGGIILLKKLLSSQLLKFHQHTLDTLLHKAVLSKSSNRQSVI DALLKRGINLNI GNKENMTPLICA AK
KGILEVVEQLVQRGANINHQDINGMTSLHWAVQNEHAQICRYLLSSGANPSIVNNQGQTIYQLKTSDTIQ
LILKNEPPVSQFEIEQQLLEAARNSDLEILKKICTPQNVNCRDTKGRMSTPLHFAAGYNRVTVVEFLEN
GADVHAKDKGGLVPLHNACSYGHYEAELLVKYKANVNAMDLMKFTPLHEAAAKEKYDICKLLLKNGANV
HSKNRDNLTPIDLVKDPKSDLADLLRGE PALLDAAKKGEIERVKKLLTEDNVNCRDEYGRNSTPLHLAAG
YNHLDVVEYLL ENKADVNAKDKGGLVPLHNASSYGHVDVASLLIRYNSVINATDRWNFTPLHEAAQKGRT
QVCSLLIIHGADVILKNQEGQIPLDLATADDVIALQDAMMKDIPLTIPPAEKEAKSNIVNKG LTAAGAS
LLASELVLGDGVDDKNCMVTQQRGGPAGVGDSKGFMSYRGGGDAPPWHNVTVKDLILELELGHVEL
FEREQITDILIEMNODDLSIGITAFGVHRLLKRIR ELVQGNNEEYFVGVTTKPTQTQLIELSSDD
KEPITDADLMQSTICEHRDDGKAGGVFDSYELKIERIVNTKVWERYKYRKEVAESNNNCANELMLFHG
SPFPVPIVHNGFDERHAYIGGMFGAGIYFAEHSKSNQVYVYIGGGNGCPEHKNRSCYTC LRKLLLCRVV
LGKPVQYTA VRIAHAPPGHHSVIGRPSAGGLNYPEVVIYRGEQAYPEYIITFRIKKPSATDSMSSSSSL
DMSNNT

Alignment

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XP_019848937.1[A.queenslandica] -----
NP_651410.1[D.melanogaster] -----
XP_047128184.1[H.vulgaris] -----
XP_032220531.1[N.vectensis] -----
XP_014034742.2[S.salar] MA-----SVARFWGS-----ANT-----NSKLYIYE
XP_018082988.1[X.laevis] -----
NP_989672.2[G.gallus] -----
NP_001157107.1[M.musculus] -----
NP_079511.1[H.sapiens] -----
XP_024109627.1[P.abelii] -----
XP_032806710.1[P.marinus] -----
XP_019641281.1[B.belcheri] MAARRAHLASPPSSSSSLSPSSGSLDTTAAAAAAAATTTAAAAAATTTAAAMTTTAAVSA

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XP_019848937.1[A.queenslandica] -----MDTRDHQAKIPGDSRQTSQSIEEGESADKNTGDLARLFEACKNGDIDTVQNLIQQ
NP_651410.1[D.melanogaster] -----MANSSRSR--ALLSVNLDAVMANDPLRELFEACKTGEIAKVKKLIT-
XP_047128184.1[H.vulgaris] -----MALGRPNRAMPSPR--RNS--VASNFMDDGVHENDSGRELFEACRTGVDVIRVYLIQN
XP_032220531.1[N.vectensis] -----MPCQAKMAS--KKL--ASNPTFLSDPDVCEGGRELFEACRNGDVSKVRKLVTN
XP_014034742.2[S.salar] NTPPLMSTRQCSR-----VLGL--GVVSPGVDTPRSQEPNREIFEACRNGDVERVRKLV-
XP_018082988.1[X.laevis] -----MSGRRACG-----ASGS--AASHG--NIGAGGEPARELFEACRNGDVERVRKLVN-
NP_989672.2[G.gallus] -----MAARRCAG-----GAAA--LAEAF--GCGSAVEPARELFEACRNGDVERVRKLV-
NP_001157107.1[M.musculus] -----MSGRRACG-----GGAA--CAS--A--GAEAVEPARELFEACRNGDVERVRKLV-
NP_079511.1[H.sapiens] -----MSGRRACG-----GGAA--CAS--A--AAEAVEPARELFEACRNGDVERVRKLV-
XP_024109627.1[P.abelii] -----MSGRRACG-----GGAA--CAS--A--AAEAMEPARELFEACRNGDVERVRKLV-
XP_032806710.1[P.marinus] TSSPSTTAAAAAAVAAAAATGS--GPSGQDSADGDGAKELFEACRNGDVRVRKLV-
XP_019641281.1[B.belcheri] -----MAGRR--AMLSSDRICHDESSGCRELFEACRNGDVARVKKLIT-

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XP_019848937.1[A.queenslandica] RQSSANERDLHGRKSTPLHFAAGFGRRDIVKFLIEKGAVHDFRDEGLIPLHNSCSFGHV
NP_651410.1[D.melanogaster] P-QTVNARDTAGRKSTPLHFAAGYGRREVVEFLNLSGASTQACDEGLHPLHNCSSFHGA
XP_047128184.1[H.vulgaris] N-WDVNMRDTAGRKSTPLHFAAGFGRKDIVEYLLDAGADVHARDGGILIPLHNACSFHGV
XP_032220531.1[N.vectensis] N-SNVNVRDTAGRKSSPLHFAAGFGRKEVVEYLLQCGADVHAMDGGILIPLHNACSFHGA
XP_014034742.2[S.salar] P-ENVNSRDTAGRKSTPLHFAAGFGRRDVVEYLLQNGANVHARDEGLVSLHNACSFGHS
XP_018082988.1[X.laevis] S-DNVNSRDTAGRKSTPLHFAAGFGRKDVVEHLLQSGANVHARDGGILIPIHNACSFHGA
NP_989672.2[G.gallus] P-ENVNSRDTAGRKSSPLHFAAGFGRKDVVEYLLQSGANVHARDGGILIPLHNACSFHGA
NP_001157107.1[M.musculus] P-EKVNSRDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDGGILIPLHNACSFHGA
NP_079511.1[H.sapiens] P-EKVNSRDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDGGILIPLHNACSFHGA
XP_024109627.1[P.abelii] P-EKVNSRDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDGGILIPLHNACSFHGA
XP_032806710.1[P.marinus] P-LNVNARDTTGRKSTPLHFAAGFGRKDVVEHLLQNGANVHARDGGILIPLHNACSFHGA
XP_019641281.1[B.belcheri] P-QNVNARDTAGRKSTPLHFAAGFGRKDVVEHLLQNGANVHARDGGILIPLHNACSFHGA

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XP_019848937.1[A.queenslandica] DVVQLLLSNGANPNAQDNWKFSPLEHAAIKGKADVCIVLLQHGADSSLLNTRDKAPIDLA
NP_651410.1[D.melanogaster] EVVRLLLKAGASPTNTDNNWYTPLHEAAISKGKDVDCVIALLQGHANHTIRNSEQKTPLELA
XP_047128184.1[H.vulgaris] EVTLSSLRHADVNARDNNWYTPLHEAAIKGKVEVCIALLQHGADPLIRNTDGTARTDLA
XP_032220531.1[N.vectensis] EVVRILLSHGADANARDNNWYTPLHEAAVKGKDVDCVIVLLQHGADPNIRNTDGTALDVA
XP_014034742.2[S.salar] EVVNLLLRHGADANSRDNNWYTPLHEAAIKGKSEVCIVLLQHGAEPTIRNTDGR TALDLA
XP_018082988.1[X.laevis] EVVSLLLRHGADPNARDNNWYTPLHEAAIKGKIDVCIVLFQHGADPTIRNTDGR TALDLS
NP_989672.2[G.gallus] EVVNLLLRHGADPNARDNNWYTPLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGR TALDLA
NP_001157107.1[M.musculus] EVVNLLLRHGADPNARDNNWYTPLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGR TALDLA
NP_079511.1[H.sapiens] EVVNLLLRHGADPNARDNNWYTPLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGR TALDLA
XP_024109627.1[P.abelii] EVVNLLLRHGADPNARDNNWYTPLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGR TALDLA
XP_032806710.1[P.marinus] EVVNLLLRQGADPNARDNNWYTPLHEAAIKGKIDVCIVLLQHGADPGIRNTDGTALDLA
XP_019641281.1[B.belcheri] EVVTLTLRNGADPNARDNNWYTPLHEAAIKGKIDVCIVLLQNGADPSIRNTDGTALDLA

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XP_019848937.1[A.queenslandica] NGQAREVLLGTGYRQDELLEAAKVGEQLLMQILTPLNVNCHASDGRRSTPLHLAGYNNRT
NP_651410.1[D.melanogaster] DEATRPVLTGEYRKDELLEAARSGAEDRLLALLTPPLNVNCHASDGRRSTPLHLAGYNNRI
XP_047128184.1[H.vulgaris] EATAKAVLTGEYKDELLEDSARSNGEEKMALLTPPLNVNCHADGRKSTPLHLAGYNNRT
XP_032220531.1[N.vectensis] EAAKVLVTGDYKDELLEDSARSNGEEKLMSLLTPPLNVNCHADGRKSTPLHLAGYNNRV
XP_014034742.2[S.salar] EASTKAVLTGEYKDELLEDSARSNGEEDKLMALLTPPLNVNCHASDGRKSSPLHLAGYNNRV
XP_018082988.1[X.laevis] DPSAKAVLTGEYKDELLEDSARSNGEEKMALLTPPLNVNCHASDGRKSTPLHLAGYNNRV
NP_989672.2[G.gallus] DPSAKAVLTGEYKDELLEDSARSNGEEKMALLTPPLNVNCHASDGRKSTPLHLAGYNNRV
NP_001157107.1[M.musculus] DPSAKAVLTGDYKDELLEDSARSNGEEKMALLTPPLNVNCHASDGRKSTPLHLAGYNNRV
NP_079511.1[H.sapiens] DPSAKAVLTGEYKDELLEDSARSNGEEKMALLTPPLNVNCHASDGRKSTPLHLAGYNNRV
XP_024109627.1[P.abelii] DPSAKAVLTGEYKDELLEDSARSNGEEKMALLTPPLNVNCHASDGRKSTPLHLAGYNNRV
XP_032806710.1[P.marinus] EPTAKAVLTGEYKDELLEAARSNGEEKLMALLTPPLNVNCHASDGRKSTPLHLAGYNNRV
XP_019641281.1[B.belcheri] EPSAKTVLTGDYKDELLEAARSNGEEDKLMALLTPPLNVNCHASDGRKSTPLHLAGYNNRV

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XP_019848937.1[A.queenslandica] SIVQLLLKQGDVHAKDKGGLVPLHNACSYGHYVEAELLKYGASINVTDLWQFTPLQEA
NP_651410.1[D.melanogaster] GIVEILLANGADVHAKDKGGLVPLHNACSYGHFVDVTKLLIQAGANVNANDLWQFTPLHEA
XP_047128184.1[H.vulgaris] RIVEILLKHGADVHAKDKGGLVPLHNACSYGHYEVTELLVKHGASVNAMD LQWFTPLHEA
XP_032220531.1[N.vectensis] GVVQLLLKHGADVHAKDKGGLVPLHNACSYGHFEVTELLIKHGASVNAMD LQWFTPLHEA
XP_014034742.2[S.salar] KTVQLLLKHGADVHAKDKGDLVPLHNACSYGHYEVTDILVKQGCACVNAMD LQWFTPLHEA
XP_018082988.1[X.laevis] KIVQLLLKHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGASVNAMD LQWFTSLHEA
NP_989672.2[G.gallus] KIVQLLLKHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMD LQWFTPLHEA
NP_001157107.1[M.musculus] KIVQLLLKHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMD LQWFTPLHEA
NP_079511.1[H.sapiens] KIVQLLLKHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMD LQWFTPLHEA
XP_024109627.1[P.abelii] KIVQLLLKHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMD LQWFTPLHEA
XP_032806710.1[P.marinus] RIVQLLLKHGADVHAKDKGGLVPLHNACSYGHYEVTELLVKHGASVNAMD LQWFTPLHEA
XP_019641281.1[B.belcheri] RIVQLILQHGADVHAKDKGGLVPLHNACSYGHFEVTELLIKHGASVNAMD LQWFTPLHEA

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XP_019848937.1[A.queenslandica] ASKGRSDVCSLLLAHGAFNPSIANCHGKTAFNAPSEEFKKKLDSEYRGYQLLAAEDGGI
NP_651410.1[D.melanogaster] ASKSRVEVCSLLLSRGADPTLLNCHSKSAIDAPATRELRIEAFYKGCILLDACRKCVD
XP_047128184.1[H.vulgaris] ASKMRIEVCITLLLSYGADPTVLNCHSKSAIDVAPVQELKDKLLIYEGHTYILEAVKSSDL
XP_032220531.1[N.vectensis] ASKARVEVCALLLGHGADPTLLNCHSKSAIDAPATKELQEKLLSEFKGHQILEAAKGCDT
XP_014034742.2[S.salar] ASKNRVDCVCSLLSVSYGADPTFLNCHNQSAIDLSPTPQLKERLAYEPRFGHALLQAAREADL
XP_018082988.1[X.laevis] ASKNRVEVCSSLLLSYGADPTMLNCHNKS AIDLAPTPQLKERLSYEFKGHSL LQAAREADL
NP_989672.2[G.gallus] ASKNRVEVCSSLLLSYGADPTLLNCHNKSITIDLAPTPQLKERLAYEPRFGHSL LQAARESDV
NP_001157107.1[M.musculus] ASKNRVEVCSSLLLSYGADPTLLNCHNKS AIDLAPTAQLKERLSYEFKGHSL LQAAREADV
NP_079511.1[H.sapiens] ASKNRVEVCSSLLLSYGADPTLLNCHNKS AIDLAPTPQLKERLAYEPRFGHSL LQAAREADV
XP_024109627.1[P.abelii] ASKNRVEVCSSLLLSYGADPTLLNCHNKS AIDLAPTPQLKERLAYEPRFGHSL LQAAREADV
XP_032806710.1[P.marinus] ASKNRVEVCSSLLLSYGADPTLLNCHSKSAIDLAPTSELKERLAYEPRFGHSL LQAAREADV
XP_019641281.1[B.belcheri] ASKSRVEVCSSLLLSHGADPTLLNCHSKSAIDVASTPELQEKLSYEFKGCILLDGAARQTD

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XP_019848937.1[A.queenslandica] ILLKKLLSSQLLKFOHQHTLDTLLHKAIVLSKSNRQSVIDALLKRGINLIGNKENMTPL
NP_651410.1[D.melanogaster] SPAKKLVCAEIVNVPHPYTGDTPLHLAVVSPDGKRQKQIMELLTRKGSLLNEKNKAF LTP
XP_047128184.1[H.vulgaris] SKIKRIIAPDLNVFHP LTNLSALHVCALSTS AKRDVADFLIKKGCNMFNCQK LTP
XP_032220531.1[N.vectensis] AKIKKLTITTEINFQHPLTDLTPHLVAVASSPPKKRGVITELLKKGADPNLQNKSSYAPL
XP_014034742.2[S.salar] PRLLKHL SLEITITFKHPLTHETALHCAASTPYPKRKQVCELLLRKGANVNEKT KDFLTP
XP_018082988.1[X.laevis] TRIKKHLSLEIVNFKHPQTHETALHCAASPPYPKRKQVCELLFRKGANVNEKT KDFLTP
NP_989672.2[G.gallus] ARIKKHLSLEIVNFKHPQTHETALHCAASPPYPKRKQVCELLLRKGANIN EKT KDFLTP
NP_001157107.1[M.musculus] TRIKKHLSLEMVNFKHPQTHETALHCAASPPYPKRKQICELLLRKGANIN EKT KDFLTP
NP_079511.1[H.sapiens] TRIKKHLSLEMVNFKHPQTHETALHCAASPPYPKRKQICELLLRKGANIN EKT KDFLTP
XP_024109627.1[P.abelii] TRIKKHLSLEMVNFKHPQTHETALHCAASPPYPKRKQICELLLRKGANIN EKT KDFLTP
XP_032806710.1[P.marinus] TRVKKHLGLDINFKHPQTHETALHCAVASPPYPKRKQVSELLLRKGANVNEKT KDLLTP
XP_019641281.1[B.belcheri] AKVKKHLGLDINFKHPQTHETALHCAALSPYPKRKQITELLIRKGANLNDKNKEFLTP

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[illegible]

NP_651410.1[D.melanogaster] GASMLSPVPVPLPLSSSTRISPAQG-----AEANGAEGSSSD---DLLPADDTITN 893
XP_047128184.1[H.vulgaris] -----K--PSTANQNLL-----LSEPCNSDGLQTKRLRDQAEQTNPLDID 886
XP_032220531.1[N.vectensis] -----S--PAGHGDGAFSNRSV-SEA-----QGEAVRSISAVHPGLDVD 890
XP_014034742.2[S.salar] TASTCTAFPELPAL-----LGPSSGAV-----GTDNKEVPGVDLS 909
XP_018082988.1[X.laervis] ----ASSFSETTSVSS-----GGAEGAS-----GLDK-KDEGVLDLN 876
NP_989672.2[G.gallus] ----SGSFSELPVVG-----TNSAEGAT-----VLEKKEVSGVDPS 878
NP_001157107.1[M.musculus] ----SGSFSELSAVVS-----SSAAEGAT-----GLQRKEDSGIDFS 877
NP_079511.1[H.sapiens] ----SGSFSELSVVVS-----SGTEGAS-----SLEKKEVPGVDPS 877
XP_024109627.1[P.abeli] ----SGSFSELSVVVS-----SSGTEGTS-----SLEKKEVPGVDPS 877
XP_032806710.1[P.marinus] GACGVAPSPVPAGAIG--AGAAGDGTLLGACGVSAADGATGPADKPDRSADFEYPLGLDMN 1009
XP_019641281.1[B.belcheri] GAVGGA-----CQGDGA-----IDRSAGESELDMT 865

XP_019848937.1[A.queenslandica] VKDILTELELGHVLEFEREQITDILIEMNNGDDLQSIGITAFGVRHRLKRIRELVQGN 954
NP_651410.1[D.melanogaster] VSGFLSSQQLHHLIELFEREQITLDILAEMGHDDLKQVGSAYGFRHKILKGIAQLRSTT 953
XP_047128184.1[H.vulgaris] IGTFLSSLQLEFLHEIFEREQITMDVLTEMGPDLKEIGIVAYGHRHKILKGVKERLAGA 946
XP_032220531.1[N.vectensis] VGQFLDGLQLNNLKEIFEREQISWDVLVMGHEELKEIGIHAYGHRHKILKAVKEKISGM 950
XP_014034742.2[S.salar] IQGFLNNLGLLEHLEIFEREQITLDVLVEMGHKEKEIGINAYGHRHKILKGVRLISGP 969
XP_018082988.1[X.laervis] INQFLRNLGLEHLIDVFEREQITLDVLVEMGHKEKEIGINAYGHRHKILKGVRLISGQ 936
NP_989672.2[G.gallus] INQFVRNLGLEHLIDVFEREQITLDVLVEMGHKEKEIGINAYGHRHKILKGVRLISGQ 938
NP_001157107.1[M.musculus] ITQFIRNLGLEHLMIDFEREQITLDVLVEMGHKEKEIGINAYGHRHKILKGVRLISGQ 937
NP_079511.1[H.sapiens] ITQFVRNLGLEHLMIDFEREQITLDVLVEMGHKEKEIGINAYGHRHKILKGVRLISGQ 937
XP_024109627.1[P.abeli] ITQFLRNLGLEHLMIDFEREQITLDVLVEMGHKEKEIGINAYGHRHKILKGVRLISGQ 937
XP_032806710.1[P.marinus] INMFLKGLGLDHLRIDFEKEQITLDVLADMGHEELKEIGINAYGHRHKILKGVRLISGQ 1069
XP_019641281.1[B.belcheri] ISSFLQQLGLNQLLDIFNKEQITLDILGEMGHEELKEIGINAYGHRHKILKGVRELGGT 925
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XP_019848937.1[A.queenslandica] NEEY-----PVGWTTKPTQGTQLIELSSDDKEFIDTADLMQSTICEHRDDGKAGGVFDS 1009
NP_651410.1[D.melanogaster] GIGN-----NVNLCITLVDLLPDDKEFVAVEEEMQATIREHRDNGQAGGVFTR 1001
XP_047128184.1[H.vulgaris] GCTIV--GEPFLSNINASGNTILQELSMDEKDYQSVAAEEMQSTVVEHKDGGVAGGIFSR 1004
XP_032220531.1[N.vectensis] GLG-----LGPFTST--SQVQGSVIQELSMVDKFAVVADEEMQSTVEHRDSDTAGGVFTS 1003
XP_014034742.2[S.salar] Q-----GLNPYLTINTANSSTILIDLVSDDKEFQVLEVEELQSTIREHRDGLAGGVFNR 1023
XP_018082988.1[X.laervis] H-----GLNPYLTINTSNSSTILIDLAPDDKEFLSVEEEMQSTVREHRDGGHAGGVFTK 990
NP_989672.2[G.gallus] Q-----GLNPYLTINTSSSGTLLIDLSSEKFEQSVSEEMQSTVREHRDGGHAGGVFNR 992
NP_001157107.1[M.musculus] Q-----GLNPYLTINTSSSGTLLIDLSPPDDKEFQSVSEEMQSTVREHRDGGHAGGVFNR 991
NP_079511.1[H.sapiens] Q-----GLNPYLTINTSSSGTLLIDLSPPDDKEFQSVSEEMQSTVREHRDGGHAGGIFNR 991
XP_024109627.1[P.abeli] Q-----GLNPYLTINTSSSGTLLIDLSPPDDKEFQSVSEEMQSTVREHRDGGHAGGIFNR 991
XP_032806710.1[P.marinus] QGGLAYPGANPYLSYHTTAQGTLLIDLPPDDKEQSVSEEMQSTIREHKDGGQAGGVFNR 1129
XP_019641281.1[B.belcheri] GT-----TLNPYLTALGSGHTLITDLSPPDDKEQSVSEVEEQSTIRQHKKDQAGGIFNR 980
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XP_019848937.1[A.queenslandica] YEILKIERIVNTKWERYKYRRKEVAEENNNNCANELMLFHGSPFPVYIVHNGFDERHAYI 1069
NP_651410.1[D.melanogaster] YNIRVQKVQNRKLWERYAHRQELAEENFLQSNERMFLFHGSPFFINAVIQRGFDERHAYI 1061
XP_047128184.1[H.vulgaris] YSSLKIERIVNKKLWERYQRRQVADANNNHNERMLFHGSPFFINAVIQRGFDERHAYI 1064
XP_032220531.1[N.vectensis] YTLIKIERIVNTKWERYKYRRKEVAEENNNNCANELMLFHGSPFFINAVIQRGFDERHAYI 1063
XP_014034742.2[S.salar] YNIVIKIQKVNKKLWERYTHRRKEVSEENNNHNSNERMLFHGSPFFINAVIHKGFERHAYI 1083
XP_018082988.1[X.laervis] YNILKIQKVNKKLWERYTHRRKEVSEENNNHNSNERMLFHGSPFFINAVIHKGFERHAYI 1050
NP_989672.2[G.gallus] YNILKIQKVNKKLWERYTHRRKEVSEENNNHNERMLFHGSPFFINAVIHKGFERHAYI 1052
NP_001157107.1[M.musculus] YNILKIQKVNKKLWERYTHRRKEVSEENNNHNERMLFHGSPFFINAVIHKGFERHAYI 1051
NP_079511.1[H.sapiens] YNILKIQKVNKKLWERYTHRRKEVSEENNNHNERMLFHGSPFFINAVIHKGFERHAYI 1051
XP_024109627.1[P.abeli] YNILKIQKVNKKLWERYTHRRKEVSEENNNHNERMLFHGSPFFINAVIHKGFERHAYI 1051
XP_032806710.1[P.marinus] YNVIKIQKVNKKLWERYTHRRKEVSEENNNHNERMLFHGSPFFINAVIHKGFERHAYI 1189
XP_019641281.1[B.belcheri] YNVIKIQKVNKKLWERYTHRRKEVSEENNNHNSNERMLFHGSPFFINAVIHKGFERHAYI 1040
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XP_019848937.1[A.queenslandica] GGMFGAGIYFAEHSSSKSNQYVYVIGGGNGCPEHKNRSCYTCLRKLLRCRVVLGKPFVEQYT 1129
NP_651410.1[D.melanogaster] GGMFGAGIYFAEHSSSKSNQYVYVIGGGIGCPSHKDRSCYVCPRQLLLRCRVLGRKSLQYS 1121
XP_047128184.1[H.vulgaris] GGMFGAGIYFAEHSSSKSNQYVYVIGGGSGCPCVHKDRSCYDCKRQILLCRVTLGKPFQNS 1124
XP_032220531.1[N.vectensis] GGMFGAGIYFAEHSSSKSNQYVYVIGGGSGCPTHKDRSCYSCERQQLLLRCRVLGRKPFYQFS 1123
XP_014034742.2[S.salar] GGMFGAGIYFAEHSSSKSNQYVYVIGGGTGCPPLHKDRSCYVCQRHLLFCRVTLGKSLFQFS 1143
XP_018082988.1[X.laervis] GGMFGAGIYFAEHSSSKSNQYVYVIGGGTGCPPLHKDRSCYVCHRQLLFCRVTLGKSLFQFS 1110
NP_989672.2[G.gallus] GGMFGAGIYFAEHSSSKSNQYVYVIGGGTGCPPLHKDRSCYVCHRQLLFCRVTLGKSLFQFS 1112
NP_001157107.1[M.musculus] GGMFGAGIYFAEHSSSKSNQYVYVIGGGTGCPPLHKDRSCYVCHRQLLFCRVTLGKSLFQFS 1111
NP_079511.1[H.sapiens] GGMFGAGIYFAEHSSSKSNQYVYVIGGGTGCPVHKDRSCYVCHRQLLFCRVTLGKSLFQFS 1111
XP_024109627.1[P.abeli] GGMFGAGIYFAEHSSSKSNQYVYVIGGGTGCPVHKDRSCYVCHRQLLFCRVTLGKSLFQFS 1111
XP_032806710.1[P.marinus] GGMFGAGIYFAEHSSSKSNQYVYVIGGGTGCPVHKDRSCYVCHRQLLFCRVTLGKSLFQFS 1249
XP_019641281.1[B.belcheri] GGMFGAGIYFAEHSSSKSNQYVYVIGGGTGCPPLHKDRSCYVCHRQLLFCRVTLGKSLFQFS 1100
*****:***** :* :*: :* :.: :*: :* :. :.

XP_019848937.1[A.queenslandica] AVRIAHAPFGHHSVIGRPSAGGLNYPEYVYIRGEQAYPEYIITFRIKKPSATDSMSSSSS 1189
NP_651410.1[D.melanogaster] AMKMAHAPPGHHSVIGRPSAGGLHFAEYVYIRGEQAYPEYLITYQIVKPDSSSGTEDTR 1181
XP_047128184.1[H.vulgaris] AMKMAHAPPGHHSVIGRPSAGGLSYPEYVYIRGEQAYPEYLITYKIERPNTLSSCQSAVD 1184
XP_032220531.1[N.vectensis] AVKMAHAPPGHHSVIGRPSAGGLSFAEYVYIRGEQAYPEYLITYKINKPDT----- 1174
XP_014034742.2[S.salar] AMKMAHSPPGHHSVIGRPSVNGLSLAEYVYIRGEQAYPEYLITYQILKPDASVDG----- 1198
XP_018082988.1[X.laervis] AMKMAHSPPGHHSVIGRPSVNGLSLAEYVYIRGEQAYPEYIITYQIMKPEAVAE----- 1165
NP_989672.2[G.gallus] AMKMAHSPPGHHSVIGRPSVNGLSLAEYVYIRGEQAYPEYLITYQIVKPEATTEA----- 1167
NP_001157107.1[M.musculus] AMKMAHSPPGHHSVIGRPSVNGLSLAEYVYIRGEQAYPEYLITYQIVRPEGMVDG----- 1166
NP_079511.1[H.sapiens] AMKMAHSPPGHHSVIGRPSVNGLSLAEYVYIRGEQAYPEYLITYQIMRPEGMVDG----- 1166
XP_024109627.1[P.abeli] AMKMAHSPPGHHSVIGRPSVNGLSLAEYVYIRGEQAYPEYLITYQIMRPEGMVDG----- 1166
XP_032806710.1[P.marinus] AMKMAHSPPGHHSVIGRPSVNGLSLAEYVYIRGEQAYPEYLITYQILKECTPDLTSAAG 1309
XP_019641281.1[B.belcheri] AMKMAHAPPGHHSVIGRPSVGLNFAEYVYIRGEQAYPEYLITYQIVKPEAPAPSPDQK 1160
.: :: :*: :* :. :. :. :*: :*: :*: :* :.

XP_019848937.1[A.queenslandica] LDMSNNNT 1196
NP_651410.1[D.melanogaster] ----- 1181
XP_047128184.1[H.vulgaris] ----- 1184
XP_032220531.1[N.vectensis] ----- 1174
XP_014034742.2[S.salar] ----- 1198
XP_018082988.1[X.laervis] ----- 1165
NP_989672.2[G.gallus] ----- 1167
NP_001157107.1[M.musculus] ----- 1166
NP_079511.1[H.sapiens] ----- 1166
XP_024109627.1[P.abeli] ----- 1166
XP_032806710.1[P.marinus] QKS----- 1312
XP_019641281.1[B.belcheri] ----- 1160

Percent identity matrix:

```
#
#
# Percent Identity Matrix - created by Clustal2.1
#
#
1: XP_019848937.1[A.queenslandica] 100.00 56.09 56.91 60.57 56.97 58.58 59.06 58.93 58.93 59.02 57.73 58.79
2: NP_651410.1[D.melanogaster] 56.09 100.00 60.07 65.63 64.35 66.16 66.55 66.52 66.34 66.34 65.70 68.40
3: XP_047128184.1[H.vulgaris] 56.91 60.07 100.00 67.19 63.13 64.35 65.11 65.26 65.08 65.26 63.82 65.67
4: XP_032220531.1[N.vectensis] 60.57 65.63 67.19 100.00 67.66 69.42 70.76 70.21 70.21 70.12 70.17 71.87
5: XP_014034742.2[S.salar] 56.97 64.35 63.13 67.66 100.00 81.77 84.71 83.23 83.92 83.92 76.38 73.16
6: XP_018082988.1[X.laevis] 58.58 66.16 64.35 69.42 81.77 100.00 88.76 87.29 87.97 87.97 80.43 77.10
7: NP_989672.2[G.gallus] 59.06 66.55 65.11 70.76 84.71 88.76 100.00 92.80 93.65 93.40 82.26 78.00
8: NP_001157107.1[M.musculus] 58.93 66.52 65.26 70.21 83.23 87.29 92.80 100.00 97.26 97.00 81.56 78.43
9: NP_079511.1[H.sapiens] 58.93 66.34 65.08 70.21 83.92 87.97 93.65 97.26 100.00 99.66 81.90 78.16
10: XP_024109627.1[P.abelii] 59.02 66.34 65.26 70.12 83.92 87.97 93.40 97.00 99.66 100.00 81.90 78.25
11: XP_032806710.1[P.marinus] 57.73 65.70 63.82 70.17 76.38 80.43 82.26 81.56 81.90 81.90 100.00 80.00
12: XP_019641281.1[B.belcheri] 58.79 68.40 65.67 71.87 73.16 77.10 78.00 78.43 78.16 78.25 80.00 100.00
```