

# TAB182

## Homo sapiens:

>NP\_203754.2 182 kDa tankyrase-1-binding protein [Homo sapiens]  
MKVSTLTRESSAMASPLPREMEEELVPTGSEPGDTRAKPPVKPKPRALPAKPALPAKPSLLVPVGP RP PPRG  
PLAELPSARKMMMLAGPQPYGGSKRPLPFAPRP AVEASTGGEATQETGKEEAGKEEPPPLTPPARCAAPG  
GVRKAPAPFRPASERFAATTVEEILAKMEQPRKEVLASPDRLWGSRLTFNHDGSSRYGPRTYGTTTAPRD  
EDGSTLFRGWSQEGPVKSPAECREEHSKTPEERSLPSDLAFNGDLAKAASSELPADISKPWIPSSPAPSS  
ENGGPASPLGPAEASGSGPGSPHLHPPDKSSPCHSQLLEAQTPEASQASPCPAVTPSPAS AALPDEGSRH  
TPSPGLPAEGAPEAPRFPSSPPPEVLEPHSLDQPATSPRPLIEVGELLDLTRTFPSSGEEEEAKGDAHLRP  
TSLVQRRFSEGLVQSPSQDQEKLGGS LAALPQGGQS QALDRPFGAESNWSLSQSFEWTFPTRPSGLGVW  
RLDSPPPSPITEASEAAEAAEAGNLAVSSREEGVSQQGAGSAPSGSGSSWVGDDPSMSLTQKGDGES  
QPQPPAVPLEPLPTTETGTPGLPLQQAEEERYESQEPLAGQESPLPLATREAAALPILEPVLGQE QPAAPDQP  
CVLPADAPEPGQALPVEEEAVTLARAETTQARTEAQDLCRASPEPPGPESSSRWLDDLASPPPSGGGAR  
RGAGAE LKDTQSPSTCSEGLLGWSQKDLQSEFGITGDPQPSSFSPPSWCQGASQDYGLGGASPRGDPGLG  
ERDWT SKYQGAGEGSTREWASRCGIGQEEMEASSSQDQSKVSAPGVLTAQDRVVGKPAQLGTQRSQEAD  
VQDWEFRKRDSQGTYSRRDAELQDQEFKGRDSLGTYSRRDVS LGDWEFGKRDSL GAYASQDANEQGQDLG  
KRDHHGRYSSQDADEQDWEFQKR DVS LGTYGSRAAE PQEFGKSAWIRDYSSGSSSRTLDAQDRSFGTR  
PLSSGFSPEEAQQQDEEFKKI PSVEDSLGEGSRDAGRPERGSGGLFSPSTA HVPD GALGQRDQSSWQN  
SDAQSEVGGHQERQAGAGPGGSADLEDGEMGKRGVWGEFSLSVGPQREAAFPSPGQDWSRDFCIEASER  
SYQFGIIGNDRVSGAGSPSSKMEGGHFVPPGKTTAGSV DWTQDLGLRNLEVSSCVSGSGSSEARENAV  
QMGWSGGLSLRDMNLTGCLSESGGSEEPGGIGVGEKDWTS DNVNKS KDLAEVGE GGGHSQARES GVGQTDW  
SGVEAGEFLKSRERGVGQADWTPDLGLRNMAPGAVCSPGEHKLGVGQMDWGNLGLRDL E VTCDDPSGG  
SQGLRGCGVGQMDWTQDLAPRNVELFGAPSEAREHGVGVSQCPEPGLRHNGSLSPGLEARDPLEARELG  
VGETS GPE TQGEDYSSSSLEPHPADPGMETGEALSFGASPGRCPARPPSPSGQLLEEMLAASSSKAVAR  
RESAASGLGGLLEEEGAGAGAAQEEVLEPGRDSPPSW **RQCPDGEAS**QTEDVDGTWSSAARWSDQGPAQT  
SRRPSQGP PARSPQDPSFIEDTEILDSAMYRSRANLGRKRGHRAPIRPGGTLGLSEADSDAHLFQDS  
TEPRASRVSSDEEVVEEPQSRRTMSLGTKGLKVNLPFGLSPSALKAKLRPNRNSAEEGELAESKSSQK  
ESA VQRSKCKVPGLGKPLTLPPKPEKSSGSESSPNWLQALKLKKKKV

## Pongo abelii:

>XP\_002821835.2 182 kDa tankyrase-1-binding protein [Pongo abelii]  
MKVSTLTRESSAMASPLPREMEEELVPTGSEPGDTRAKPPVKPKPRALPAKPALPAKPSLLVPVGP RP PPRG  
PLAELPSARKMMMLAGPQPYGGSKRPLPFAPRP AVEASTGGEATQETGKEEAGKEEPPPLTPPARCAAPG  
GVRKAPAPFRPASERFAATTVEEILAKMEQPRKEVPASPDRLWGSRLTFNHDGSSRYGPRTYGTTTAPRD  
EDGSTLSRGWSQEGPVKSPAECQE EHRKTP EERSLPSDLAFNGDLAKAASSELPADISKPWIPSSPAPSS  
ENGGPASPLGPAEASGSGPGSPHLHSPDKSSPCHSQLLEAQSP EASQASPCSPVTPTAPSAALPDEGSRH  
TPSPGLPAEGAPEAPRFPSSPPPEVLEPHSLDQPATSPQPIEVGELLDLTRTFPSSGEEEEAKGDAHLRP  
TSLVQRRFSEGLVQSPSQDQEKLGGS LAALPQGGQS QALDRPFGAESNWSLSSESFEWTFPTRPSGLGVW  
RLDSPPPSPITEASEAAEAAEAGNLAVSSGEEGVSQQGAGSAPSGSGSSWVGDDPSMSLTQKGDGES  
QPQPPAVPLEPLPTTETGTPGLPLQQAEEERYESQEPLAGQESPLPLATREAAALPILEPVLGQE QPAAPDQP  
CVLPADVP EPGQALPVEEAMTLDR AETTQPRTEAQDLCRASPEPPGPESSSRWLDDLASPPPSGGGAR  
RGAGSELKDAQSPSTCSEGLLGWSQKDLQSEFGITGDPQPSSFSPPSWCQGASQDYGLGGASPRGDPGLG  
ERDWT SKYQGAGEGSTRDWASRCGIGQEEMEASSSQDQSEVSAPGALTAQDRVVGKPAQLGTQRSQEAD  
VQDWEFRKRDSQGTYSRRDAELQDQEFKGRDSLGTYSRRDVS LGDWEFGKRDSL GTYASQDVNEQGQDLG  
KRDHRGRYSSQDADEQDWKFQKR DVS LGTYGSRGAEPQE QEFGKSAWIRDYSSGSSSRTLDAQDRSFGTR  
PLSSGFSPEEAQQQDEEFKKI PSVEDSLGEGSRDAGRPERESGGLFSPSTA HVPD GALGQRDQSSWQN  
SDAQSEVGGHQERQAGAGPGGSADLEDGEMGKRGVWGEFSLSVGPRREAAFPSPGQDWSRDFCIEASER  
SYQFGIIGNDRVSGAGSPSSKMEGGHFVPPGKTTAGSV DWTQDLGLRNLEVSSCVSGSGSSEARENAV  
QMGWSGGLSLRDMNLTGCLSESGGSEEPGGIGVGEKDWTS DNVNKS KDLAEVGE GGGHSQARES GVGQTDW  
SGVEAGEFLKSRERGVGQADWTPDLGLRNMAPGAVCSPGEHKLGVGQMDWGNLGLRDL E VTCDDPSGD  
SQGLRGCGVGQMDWTQDLAPRNVELFGAPSEAREHGVGVSQCPEPGLRHNGSLSPGLEARDPLEARELG  
VGETS GPE TQGEDDSSFSLEPHPADPGMETGEALSFGASPGRRPARPPSPSGQLLEEMLAASSSKAVAQ  
RESAASGLGGLLEEEGAGAGAAQEEVLEPGRDSPPSW **RQCPDGEAS**QTEDVDGTWSSAARWSDQGPAQT  
SRRPSQGP PARSPQDPSFIEDTEILDSAMYRSRANLGRKRGHRAPIRPGGTLGLSEADSDARLFQDS  
TEPRASRVSSDEEVVEEPQSRRTMSLGTKGLKVNLPFGLSPSALKAKLRPNRNSAEEGEPAESKSSQK  
ESA VQRSKCKVSGLGKPLTLPPKPEKSSGSESSPNWLQALKLKKKKV

## Mus musculus:

>NP\_001074729.1 182 kDa tankyrase-1-binding protein [Mus musculus]  
MKGSTLTREGTAMASPLPREMEEELAPVGSEPCDPRAKPPVKPKPRGLPSKPALPAKPSLLVPVGP RP PPRG  
PLAELPSARKMMMLAGPQPYGVSKRPLPFAPRP SAEATAGGDVTVQESGKEDAGKEDLPPLTPPARCAALG  
GVRKAPAPFRPSSERFAACTVEEILAKMEQPRKEILASPDRLWGSRLTFNHDGSSRYGPRTYGA PCPREE  
DSKSPAKGRSQEGTA EIPAE CQE EHSKTPEERNLTSSPAMNGDLAKLACSEAPT DVS KTWVTSSADP VSE  
HGGSTSAVRLANI SV PASESPRLSSRPSPCHSQLSETQSPAASEASSICLPVTPASPSAVLP AEPFGHS  
PSELPAEAA PETLSPNSSPVETVSGHSP EQPPVLLPQLLTGAELPDITRTFP CGEEAAARGHTESRP  
SSLAQRRFSEGLVQPPSQDQEKLGGS LATLPQGQGSQALDRPFGSGTESNWSLSQSFEWTFPTRPSGLG  
WMRLDSPPPSPITEASEAAEAAEADSWAVSGRGEGVSVQVGPCTPPAPESPRKPI SGVQGNPDGISL PQRD  
DGESQRPSPALLPSTVEGPPGAPLLQAKENYEDQEPLVGHESPITLAAREAAPLVLEPALGQQQPTPSDQ  
PCILFVDVPDPEQALSTEEDVVTLGWAETTLPMTEAQEPCSVSP EPTGP ESSSRWLDDLASPPPNSSGA  
RRAAGAE LKDRQSPSTCSEGLLGWAQKDLQSEFGVATDSHSSFGSSWSQDTSQNYLSGGRSPVGD TGL  
GKR DWSKCGGSGEGSTREWASRHSLGQEVIGIGGSQDSEEVVPRERAVGRPAQLGAQGLEADAQQWEF  
GKRESQDPHSHIDKEIQDQEFKGRDSLGSFSTRDASLQDWEFGKRASVSTNQD TDENDQELGMKNLSRGY  
SSQDAEEQDREFEKRDVLIDHGRAT AQNQEF GKSAWFQDYSGGGGSRVLGSGQERGFGIRLSLSSGFS  
PEEAQQQDEEFKKTFVGEDRFCEASRDVGHLEEGASGGLLSPTSPHSRDGAARPKDEGSWQDGDSSQEI  
TRLQGRMQAESQSPTNVLDLKEREQRWAGEFSLGVAAQSEAAFPSPCRQDWSR DVCVEASESSYQFGIIGNDRVSGAGLSPSRKSGGGHFVPPGETKAGAVDWTQDLGLRNLEVSSCVSSEGPSEAREN VVGQMGWSDS  
LGLNNGDLARLQGTGESEEPRLSLVG EKDWTS SVEARNRDLPGQAEVGRHSQARES GVGPEPDWSGAEAGE  
FLKSRERGVGQADWTPDLGLRNMAPGAGCSPGEPRELGVGQVWDGDDLGLRNLEVSCDLESGGSRGCGVG  
QMDWAQDLGLRNRLRCGAPSEVRECGVRVGPDL ELDPKSSGSLSPGLETDPLEARELG VGEISGPE TQ  
GEDSSSPSFETPS EDTGMDTGEAPSLGASPS SCLTRSPPSGSQSLLEGIMTASSSKGAPQRESAASGSRV  
LLEEEGLAAGAGQGE PQFEPSPRAPLPS **RQCPDGEAS**QVEEVDGTWSLTGAARQNEQASAPPPRRPRPRL  
PSCPSED F S FIEDTEILDSAMYRSRANLGRKRGHRAPIRPGGTLGLSETADSDTRLFQDSTEPRASRV  
SSDEEVVEEPQSRRTMSLGTKGLKVNLPFGLSPSALKAKLRSRNSAE EGVTESKSSQKESSVQRSKS  
CKVPGLGKPLTLPPKPEKSSGSESSPNWLQALKLKKKKI

### **Gallus gallus:**

>XP\_040557690.1 182 kDa tankyrase-1-binding protein isoform X1 [Gallus gallus]  
MASQPQSLHPPPLPCASGGAGLAAGSPEKGSRPKPPVVRPKPRVLPKPAVPAKPCLPHPPPAPRHSRPELP  
SAEKINRLAGPQPYSGGGGAALRRPSFTIKSPETPNGKGLSPPPVLTPEDESCSTPSDEVPLAPSTPSRK  
GPAPFKVTPVVFVATKKLERFPGTVEEILAKMDSKEGLGSPDRARLSFFCPDSSSRFGSKTFTAFRRRRPSG  
EADGDSPCGEARQLLQQAEGELCTGGDRCLMVETSSSSPAGPSCAGDPGCLRRPPSPDLSLSLQLGPPGSP  
RPPACPPPGAFFQPSASAPGSPDAPPELLAPGSPTMAPESPESPAQRPTTELLATSIQAPGAPSSVAEPW  
LGASHSPGSPHTPSEGSPTPASPTPGTSQLSPKATCPPGSPESATEPSPPPSPPPELPARASCPPGSPG  
GPDDSLVSSQTPEGPDFSLPPSNRDSGLRRSSEGVLRPPPSEGQGMGLLGGSLGALPQPGDLPAEHLMSG  
ESSWSLSQSFEWTFPTRGVRGLPSPPRSPIQEAADSGLSEEDSDREGAATGSHGDSGDTDGPGLAVTSS  
WGAE GAPCPGGFVAQQEAESEEEEEEGEAE L D S T E L H I V E P S L D S A E P E P F V K A A P D P A P T E A D A S C E  
PTGDFPASLQGLGGFGQDEGSSKGPD A H T D P R W L T E L L A S P R A S G R D P L N T E E Q E G L L G W S R K D L C S E  
F G I G R S H Q A G A F D W S H K A V A R Q G D W P C E M E Q D Q K F R T N S S R N N S C G I S D M N Q Q D R A F G A A E R D W S S N Y K G  
T E L M G D T R L G S S D W S K S H G A G E S C L Q D Q D F S K P T W G T G Y G L D S A G S R E E V G S G K A E W S S P Y S V G H G Q Q Q D  
K E L S S R Q P G W A G K Y G S G D L E T H S G D A A P V W S S E Y G T G D A D I K D R E V T P D W A S K Y S S R D A E T K D K D F T L G W  
A G R S S T G D A G T L D K E F C S S R S A W D S K Y S T R D M E S Q D R E F S P S R P A W S G E Y S T Q D M E S Q D R E F S P S R L A E A  
S E Y S S R D M E I Q D R E F S P S R P A C A E E H S T S D M E S Q D R E F S T S R P T W H R E Y S S R D M E S Q D R E F S P S R P A C T N  
E Y S T S D A E T Q D R E F N P S R P T W H S E Y S S R D M E T Q D R E F S P S R P A C A D E Y I T K N M E S Q D R E F S P N R P A E A S E  
Y S A R D V E T Q D R E L K S N K P A W D D E Y I T K N M E S R D R E F G P S R S V W A S D Y D S M N T E K G E F S S R L S W A G E C S I  
G Q T Q L A N A F G V R K E D L P G L C A P S R P G Q E S S W G S T D Q Q E S G T R D W A E L H L G G A E H Q N Q F G I I G T E R V S D P  
S S T A A S A D G L M S W A N K M R S E V P Q E F R Q P L G D W H S D L S F S T S G I T G K A D E G E F S Q M A W D E G L A A V G S S A Q P  
Q Q A K V E E P G W S Q D L E E A G W S E E L R E A E A R R Q E W A S A F G A R C A A R S Q D F S A G E Q S L G G D G G S A D G N P E N I H  
L S E S S P L G D D A V A E P A A A E P I W G E S A T P R T D P M E Q Q D L P E L A A A P L P A E A A G E T P E T E S E E A P L D S P D G  
K T P V S W E E K R L S V S A S Q P E G L L D L S G Q D F T F L E D T E V L D S T M Y R S K A N L G R K R R H R A P V L R P G A T S E G D S  
W I F Q D S T E P R P A R A A A S S D E E A A E P K S R R V R A S P S G K G V K V L P F P G L T T S A L K A K L R G R N R S V E E G A S P  
V D S K A T P T K D P H V Q R S K S C K I P G L S G K P L A L P P K P E K S S G S D A S P P H W L Q A L K L K K K K S

### **Xenopus laevis:**

No homolog found.

### **Salmo salar:**

No homolog found.

### **Petromyzon marinus:**

No homolog found.

### **Branchiostoma belcheri:**

No homolog found.

### **Drosophila melanogaster:**

No homolog found.

### **Hydra vulgaris:**

No homolog found.

### **Nematostella vectensis:**

No homolog found.

### **Amphimedon queenslandica:**

No homolog found.

XP_040557690.1[G.allus]	---MASQPQSLHPLPCASGGAGLAAGSPKESGSPRPKPPVRPKPVLVLP-KPAVPAKPCF	55
NP_001074729.1[M.musculus]	MKGSTLREGTAMASPLPDQME-EELAPVGSSEPGDPRAPKPPVKPKPGLPSKPAKPAKPSL	59
NP_203754.2[H.sapiens]	MKVSTLRESSAMASPLPREME-EELVPTGSEPGDTRAKPPVPKPRPALPAKPAKPAKPSL	59
XP_002821835.2[P.abellii]	MKVSTLRESSAMASPLPREME-EELVPTGSEPGDTRAKPPVPKPRPALPAKPAKPAKPSL	59
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XP_040557690.1[G.allus]	P---HPPAPAPRHSPRPELPSAEKINRLAGQPYSGGGSGAALR-RPSFTIK-----SPETP	106
NP_001074729.1[M.musculus]	LVPVGPFRPPRGPLAELPSARKMMNLGAGPYGVSKRPLFPFAPRPSAEATAGGDVTDQESGK	119
NP_203754.2[H.sapiens]	LVPVGPFRPPRGPLAELPSARKMMNLGAGPYGVSKRPLFPFAPRPAVEASTGGEATQETGK	119
XP_002821835.2[P.abellii]	LVPVGPFRPPRGPLAELPSARKMMNLGAGPYGVSKRPLFPFAPRPAVEASTGGEATQETGK	119
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XP_040557690.1[G.allus]	NGKGLSPSPVVLTPEDSCSTPSDEVPLAPSTPSRKGPAPKFPVLPVPVATKLERFPFGTVEE	166
NP_001074729.1[M.musculus]	EDGKAGDLPLPTTPARCAALG-----GVRKAPAPFRPSSERFAACTVVE	163
NP_203754.2[H.sapiens]	EEAGKEEPPPLTPPARCAAG-----GVRKAPAPFRPSPASERFAATTVEE	163
XP_002821835.2[P.abellii]	EEAGKEEPPPLTPPARCAAG-----GVRKAPAPFRPSPASERFAATTVEE	163
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XP_040557690.1[G.allus]	ILAKMDS--KEGLGSPDRARL---SPFCPDSSSRFSGKSTFTAFRRRPSGEADGDSGPEARQ	222
NP_001074729.1[M.musculus]	ILAKMEQPRKEILASPDRLWGSRLTFNHDGSSRYGPRTYGTTAPR-CPRE--EDSKSPAKRG-	219
NP_203754.2[H.sapiens]	ILAKMEQPRKEVLASPDRLWGSRLTFNHDGSSRYGPRTYGTTAPRD--EDGSTLSRGRW-	220
XP_002821835.2[P.abellii]	ILAKMEQPRKEVPASPDRLWGSRLTFNHDGSSRYGPRTYGTTAPRD--EDGSTLSRGRW-	220
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XP_040557690.1[G.allus]	LLQQAEGELGTGGDRCLMVE----TSSSSPAGPSGAGDCPGLRRPSPSPDLSLQLGPPG	278
NP_001074729.1[M.musculus]	-SQ--EGTAELI-PAECQEEHKSPTPEERNLTSSPAMNGDLAKLACSEAPTDVSKTWTWSSA	275
NP_203754.2[H.sapiens]	-SQ--EGVPKS-PAECREHESKTPTEERSLPSDLAFNGDLAKAASSELPAISKWPISSP	276
XP_002821835.2[P.abellii]	-SQ--EGVPKF-PAECQEEHKTPEERSLPSDLAFNGDLAKAASSELPAISKWPISSP	276
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XP_040557690.1[G.allus]	SPRPP--ACPPPGAPFQPSASAGSPDAPPELLAPGSTPTMAPESPESPAQRPTTELL---	333
NP_001074729.1[M.musculus]	DPVSEHGGSSTAVRLANS-----VPASESPL--SSRPSSPCHSOLSETQSPA	322
NP_203754.2[H.sapiens]	APSENGGSPASGLPAEAS-----GSGPSCPHLHPDKSSPCHSOLLEAQTPE	324
XP_002821835.2[P.abellii]	APSENGGSPASGLPAEAS-----GSGPSCPHLHPDKSSPCHSOLLEAQSPE	324
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XP_040557690.1[G.allus]	---ATSIQ---APGAPSSVAEPWLGASHSPGSPHTPSEGSPTPASSTPGTSLSPKATC	387
NP_001074729.1[M.musculus]	ASEASSICLVTPASPASAV-LP-----AEPGHSPSSSPLPAEAAETPLSPNNSPVE-	372
NP_203754.2[H.sapiens]	ASQA-SPCPAVTSPASFAA-LP-----DEGSRHTPSGLPAEGAPEAPRPSPPPE-	373
XP_002821835.2[P.abellii]	ASQA-SPCSPVTPATPASA-LP-----DEGSRHTPSGLPAEGAPEAPRPSPPPE-	373
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XP_040557690.1[G.allus]	PPGSPESATEPSPPPSPPELPARASCPPGSPGGDDSLVSSQTEGPDFS-----LPPSN	443
NP_001074729.1[M.musculus]	-----TVSGHHSPEQPPVLLPQLLT-----EGAEVL-DITRTFFCGEEAAAGHTESLR	420
NP_203754.2[H.sapiens]	-----VL-EPHSLDQPPATSPRPLI-----EVGELL-DLTRTFPSGEEEEAKGDAHLRP	420
XP_002821835.2[P.abellii]	-----VL-EPHSLDQPPATSPQFVI-----EVGELL-DLTRTFPSGEEEEAKGDAHLRP	420
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XP_040557690.1[G.allus]	RDSGLRRSSEGVLRPPPEGGGMGLLGGSLGALPQPGDL---PAEHLSSGESSWSLSQS	499
NP_001074729.1[M.musculus]	SSLAQRRFSEGVLPQPSQD---QEKLGGSLATLPQGGQSALDRPFGSGTESNWSLSQS	477
NP_203754.2[H.sapiens]	TSLVQRRFSEGVLPQPSQD---QEKLGGSALALPQGGQSALALDRPFG--AESNWSLSQS	475
XP_002821835.2[P.abellii]	TSLVQRRFSEGVLPQPSQD---QEKLGGSALALPQGGQSALALDRPFG--AESNWSLSQS	475
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XP_040557690.1[G.allus]	FEWTFPTTR---GVRGLPSPRPSPIQEAADSGLSEEDSD-----REGAAT-----	541
NP_001074729.1[M.musculus]	FEWTFPTTRPSGLGVWRDLSPPPSPITEASEAAEAADSWAVSGRGESVQVGQPTTAP	537
NP_203754.2[H.sapiens]	FEWTFPTTRPSGLGVWRDLSPPPSPITEASEAAEAAGNLAIVSSREEGVQSQGAGSAP	535
XP_002821835.2[P.abellii]	FEWTFPTTRPSGLGVWRDLSPPPSPITEASEAAEAAGNLAIVSSGEEGVQSQGAGSAP	535
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XP_040557690.1[G.allus]	-----GSHGDSGTDGPGLAVTSSWGAEG-----APCPGPGVAQQEAESS	581
NP_001074729.1[M.musculus]	ESPRKPSIGVQG--NDPGISLPQRDDGESQSPRSPALLP---STVEGPPGAPILLQAKENYE	592
NP_203754.2[H.sapiens]	SGS--GSSWVQG--DDPMSMLTKQGDGSEQQPFPVAPVLEPLPTTEGTGFLPLQQAERYE	591
XP_002821835.2[P.abellii]	SGS--GSSWVQG--DDPMSMLTKQGDGSEQQPFPVAPVLEPLPTTEGTGFLPLQQAERYE	591
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XP_040557690.1[G.allus]	EEEEEEGE-----AELDSTELHIVEPSLDSAEPEPPVKAAPDPAPTEADASCEPTGDFP	636
NP_001074729.1[M.musculus]	DQEPVLVGHESPIITLAAREALPVLEPALQGGQPTFS-----DQPCILFVDVP	639
NP_203754.2[H.sapiens]	SQEPPLAGQESPLPLATREAAFLPLEVLVGLQEQPAP-----DQPCVLFDAP	638
XP_002821835.2[P.abellii]	SQEPPLAGQESPLPLATREAAFLPLEVLVGLQEQPAP-----DQPCVLFDAPV	638
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XP_040557690.1[G.allus]	ASLQGLGG-----PGQDEGSSKGPDAHTDPRWLTELLASPRARASG	677
NP_001074729.1[M.musculus]	DPEQALSTEDDVTLGWAETTLPTMTAEPQCPSPVEPTGESSRWLDDLASSPPNNGS	698
NP_203754.2[H.sapiens]	EPQALPVVEEAVALTARAETQTARTEAQDLCRASPEPPGPESSRWLDDLASSPPSGGG	699
XP_002821835.2[P.abellii]	EPQALPVVEEAAMTLARAETQTARTEAQDLCRASPEPPGPESSRWLDDLASSPPSGGS	698

NF_001074729.1[M.musculus]	CGQSGEGS-----TREWASRHSLGQ-----EVIGIGSQDESEV-----P---VRERA	819
NF_203754.2[H.sapiens]	YGQGAGEGS-----TREWASRCGIGQ-----EEMEASSSQDQSKVS-APGVLT---AQDRV	824
XP_002821835.2[P.abelii]	YGQGAGEGS-----TRDWASRCGIGQ-----EEMEASSSQDQSEVS-APGALT---AQDRV	824
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XP_040557690.1[G.gallus]	PGWAGKYGSGDLETHSGDAAPVWSSEYGTGDADIKDREVT-PDWASKYSSRDAETKDKDF	906
NF_001074729.1[M.musculus]	VGRPAQLGA-----QG-LEADAQQWFGKRESQDPHSIHDKELQDQEF	861
NF_203754.2[H.sapiens]	VGKPAQLGT-----QRSQEAADVQDWEFRKRDSQGTYSRRDAELQDQEF	867
XP_002821835.2[P.abelii]	VGKPAQLGT-----QRSQEAADVQDWEFRKRDSQGTYSRRDAELQDQEF	867
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XP_040557690.1[G.gallus]	TLGWAGRSSTGDAGTLDKEFCSSRSASWDSKYSTRDMESQDREFSPSRPAWSGEYSTQDME	966
NF_001074729.1[M.musculus]	GKR-----DSL-----GSFSTRDASLQDWEFGKR--ASVSTN--QDTE	895
NF_203754.2[H.sapiens]	GKR-----DSL-----GTYSRRDVS LGDWEFGKR--DSL GAYASQDAN	903
XP_002821835.2[P.abelii]	GKR-----DSL-----GTYSRRDVS LGDWEFGKR--DSL GTYASQDVN	903
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XP_040557690.1[G.gallus]	SQDREFSPSRLAEASEYSSRDMEIQDREFSPSRPACAEHSTSDMESQDREFSTSRPTWH	1026
NF_001074729.1[M.musculus]	ENDQELGMK--NLSRGYSSQDAEEQDREFEKRDSV-LDIHGSRAQAQQNQE--GKSAWF	950
NF_203754.2[H.sapiens]	EQGQDLGKR--DHHGRYSSQDAEQDWEFQKRDSV-LGTYGSRAAEPQE--GKSAWI	958
XP_002821835.2[P.abelii]	EQGQDLGKR--DHRGRYSSQDAEQDWKFQKRDSV-LGTYGSRGAEPQE--GKSAWI	958
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XP_040557690.1[G.gallus]	REYSSR----DMESQDREFSPSRPACTNEYSTDAETQDREFNFSRPTWHSEYSSRDME	1081
NF_001074729.1[M.musculus]	QDYSSGGGSRVLGSGERGFGRS--LSSGFSPEEAQQQDEEFKKT FVGEDRFCEASRD	1008
NF_203754.2[H.sapiens]	RDYSSGG--SSRTLDAQDRSFGTRP--LSSGFSPEEAQQQDEEFKKTIPSVEDSLGEGSRD	1015
XP_002821835.2[P.abelii]	RDYSSGG--SSRTLDAQDRSFGTRP--LSSGFSPEEAQQQDEEFKKTIPSVEDSLGEGSRD	1015
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XP_040557690.1[G.gallus]	-----TQDREFSPSRPACADEYITKNMESQ--DREFSPN--R---PAEASEYSARDVE	1127
NF_001074729.1[M.musculus]	VGHLEEGASGGLLSPSTPHSRDGAARPKDEGSWQDGDSSQETRLQGRMQAESQSPTNVD	1068
NF_203754.2[H.sapiens]	AGRPGERGGGLFSPSTAHVPD GALQRDQSSWQNSDASQEVGGHQRQAGAGPGSAD	1075
XP_002821835.2[P.abelii]	AGRPGERESGGLFSPSTAHVPD GALQRDQSSWQNSDASQEVGGHQRQAGAGPGSAD	1075
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XP_040557690.1[G.gallus]	TQDRELKSNKPANDDEYITKNMESRDREFGFSRSVWASDYDSMNTKEGFSSSRLSWAGE	1187
NF_001074729.1[M.musculus]	LED--KEREQRGWAGEFSLGVAAQSEAAFS PG-----	1098
NF_203754.2[H.sapiens]	LED--GEMGKRGWVGFSLSVGPQREAAFS PG-----	1105
XP_002821835.2[P.abelii]	LED--GEMGKRGWVGFSLSVGPQREAAFS PG-----	1105
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XP_040557690.1[G.gallus]	CSIGQTQLANAFGVRKEDLPGLCAPSRPGQESSWGSTDQQESGTRDWAEELHLGAEHQN	1247
NF_001074729.1[M.musculus]	-----RQDWSRDVCVEASESSY	1115
NF_203754.2[H.sapiens]	-----QQDWSRDFCIEASERSY	1122
XP_002821835.2[P.abelii]	-----QQDWSRDFCIEASERSY	1122
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XP_040557690.1[G.gallus]	QFGIIGTERVSDPSSTA-----	1264
NF_001074729.1[M.musculus]	QFGIIGNDRVSGAGLSPSRKSGGGHFVPPGKTKAGAVDWTDLGLRNLEVSSCVSGSGPS	1175
NF_203754.2[H.sapiens]	QFGIIGNDRVSGAGFSPSSKMEGGHFVPPGKTTAGSVDWTDQLGLRNLEVSSCVSGSGSS	1182
XP_002821835.2[P.abelii]	QFGIIGNDRVSGAGFSPSSKMEGGHFVPPGKTTAGSVDWTDQLGLRNLEVSSCVSGSGSS	1182
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XP_040557690.1[G.gallus]	---ASADGLMSWANKMRS-----EVPQEPRQPLGDWHSDFSSTSGITGKA	1307
NF_001074729.1[M.musculus]	EARENVVGQMGWSDSLGLNNDLARRLTGSESEEPRLGVGEKDWTSVSEARNRDLPGQA	1235
NF_203754.2[H.sapiens]	EARESAVGQMGWGGGLSLRDMNLTGCLSGSGSEEPGGIVGGEKDWTSVNVKSKDLAEVG	1242
XP_002821835.2[P.abelii]	EARENAVGQMGWGGGLSLRDMNLAGCLSGSGSEEPGGIVGGEKDWTSVNVKSKDLAEVG	1242
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XP_040557690.1[G.gallus]	DEGEPSQMAWDEGLAAGVSSAQPPQAKVEEPGWSQD-----LEEAGWSEEL--	1353
NF_001074729.1[M.musculus]	EVG-----RHSQARES GVGEPDWSGAEAGEFLKSRERGVQADWTPDLGL	1280
NF_203754.2[H.sapiens]	EGG-----GHSQARES GVGQTDWSGVEAGEFLKSRERGVQADWTPDLGL	1287
XP_002821835.2[P.abelii]	EGG-----GHSQARES GVGQTDWSGVEAGEFLKSRERGVQADWTPDLGL	1287
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XP_040557690.1[G.gallus]	-----REAEARRQEWASAFGARCAARSQDFSAG-EQSLGGDGGS-----AD	1393
NF_001074729.1[M.musculus]	RNMAPGAGCSPGEPRELGVQDWDGDLGLRNLEVSCDLES GGS---RGCVGQMDWAQD	1337
NF_203754.2[H.sapiens]	RNMAPGAVCSPGESKELGVGQMDWGNLGLRLDLEVTCDPDSGGSQGLRGCGVGQMDWTQD	1347
XP_002821835.2[P.abelii]	RNMAPGAVCSPGEHKELGVGQMDWGNLGLRLDLEVTCDPESGDSQGLRGCGVGQMDWTQD	1347
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XP_040557690.1[G.gallus]	GNPENIHLSE-----SSPPL-----GDDAVAEP	1416
NF_001074729.1[M.musculus]	LGLRNRLCGAPSEVRECGVGRVGPDLGLDPKSSGSLSPGLETDPLEARELGVGETSGP	1397
NF_203754.2[H.sapiens]	LAPQNVFLFGAPSEAREHVGVGVSQCPEPGLRHNGSLSPGLEARDPLEARELGVGETSGP	1407
XP_002821835.2[P.abelii]	LAPRNVFLFGAPSEAREHVGVGVSQCPEPGLRHNGSLSPGLEARDPLEARELGVGETSGP	1407
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XP_040557690.1[G.gallus]	A-----AAEPIWGESA---TPRTDPMEQDLP-LAAAP----	1446
NF_001074729.1[M.musculus]	ETQGEDSSSPSFETPSEDGTGEAPSLGASPPSCLTRSPSGSQSLLEGIMTASSSKG	1457
NF_203754.2[H.sapiens]	ETQGEDYSSSSLEPHPADPGMETGEALSFGASPGRCFARPPPSGSGQLLEMLAASSSKA	1467
XP_002821835.2[P.abelii]	ETQGEDSSFSLEPHPADPGMETGEALSFGASPGRRPARPPPSGSGQLLEMLAASSSKA	1467
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XP_040557690.1[G.gallus]	-----LPAAEA--G-----E-----TPETESEAPLSDPDGK--	1471
NF_001074729.1[M.musculus]	APQRESAASGSRVLLLEEGLAAGAGQGEPOEPSRAPLPSS--RQPDGEASQVEVDGTWSL	1517
NF_203754.2[H.sapiens]	VARRESAASGLGGLLEEGAGAGAAQEEVLEPGRDSPSPSW--RQPDGEASQTEDVDGTWSG	1527
XP_002821835.2[P.abelii]	VAQRESAASGLGGLLEEGAGAGAAQEEVLEPGRDSPSPSW--RQPDGEASQTEDVDGTWSG	1527
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XP_040557690.1[G.gallus]	-TPVSWEEKRLSV-SASQPEGL-LDLSGQDFTFLEDTEVLDSTMYRSKANLGRKRRHRAP	1528
NF_001074729.1[M.musculus]	TGAARQNEQASAPPPRRPRLGLPSCPSDFSFIEDTEILDSAMYRSRANLGRKRGHRAP	1577
NF_203754.2[H.sapiens]	SAA-RWSDQGPACTSRPSQGP PARSPSQDPSFIEDTEILDSAMYRSRANLGRKRGHRAP	1586
XP_002821835.2[P.abelii]	SAA-RWSDQGPACTSRPSQGP PARSPSQDPSFIEDTEILDSAMYRSRANLGRKRGHRAP	1586
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XP_040557690.1[G.gallus]	VLRPGAT-----SEGDSWIFQDSTEPRPARAAASDEEAAEPPKSRVRASPSKGVKV	1582
NP_001074729.1[M.musculus]	AIRPGGTLGLSETADSDTRLFQDSTEPRASRV-PSSDEEVVEEPQSRRTMSLGTGKGLKV	1636
NP_203754.2[H.sapiens]	VIRPGGTLGLSEAADSDAHLFQDSTEPRASRV-PSSDEEVVEEPQSRRTMSLGTGKGLKV	1645
XP_002821835.2[P.abelii]	AIRPGGTLGLSEAADSDARLFQDSTEPRASRV-PSSDEEVVEEPQSRRTMSLGTGKGLKV	1645
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XP_040557690.1[G.gallus]	PLFPGLTTSALKAKLRGRNRSVEEGASPVDSKATPTKDPHVQRSKSKIPGLSGKPLALP	1642
NP_001074729.1[M.musculus]	NLFPGLSPSALKAKLRSRNRSAEEGEVTE--SKSSQKESVQRSKSKVPGL-GKPLTLP	1693
NP_203754.2[H.sapiens]	NLFPGLSPSALKAKLRPNRNSAEEGELAE--SKSSQKESAVQRSKSKVPGL-GKPLTLP	1702
XP_002821835.2[P.abelii]	NLFPGLSPSALKAKLRPNRNSAEEGEPAE--SKSSQKESAVQRSKSKVSGL-GKPLTLP	1702
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XP_040557690.1[G.gallus]	PKPEKSSGSDASPPHWLQALKLKKKKS	1669
NP_001074729.1[M.musculus]	PKPEKSSGSEGSSPNWLQALKLKKKKI	1720
NP_203754.2[H.sapiens]	PKPEKSSGSEGSSPNWLQALKLKKKKV	1729
XP_002821835.2[P.abelii]	PKPEKSSGSEGSSPNWLQALKLKKKKV	1729
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