

# PARP6

## Sequences :

>NP\_001310451.1 protein mono-ADP-ribosyltransferase PARP6 isoform 1 [Homo sapiens]  
MDIKGQFWNDSDSGDNESEEFLYGVQGSCAADLYRHPQLDADIEAVKEIYSENSVSIREYGTIDDDVID  
LHNISFLDEEVSTAWKVLRTPEIVLRLRFSLSQYLDGPEPSIEVFQPSNKEGFGGLGLQKKILGMFTSQ  
QWKHLSNDFLKTQQEKRHSWFKASGTIKKFRAGLSIFSPIPKSPSPFPIQDSMLKGKLGVPPELRVGRLMN  
RSISCTMKNPKVEVFQYPPSPQAGLLCPQHVLGPPPARTSPLVSGHCKNIPITLEYGFVLQIMKYAEQRIP  
TLNEYCVVCDQHVFNQGSMLKPAVCTREL CVFSFYTLGVMSGAAEEVATGAEEVDLLVAMCRAALES  
PRKSIIFEPYPSVVDPTDKPTLAFNPKKNYERLQKALDSVMSIREMTQGSYLEIKKQMDKLDPLAHPLLQW  
IISNRSRHIVKLP LSR LKFMHTSHQFLLSSPPAKEARFRTAKKLYGSTFAFHGSHIENWHSILRNLGLVN  
ASYTKLQLHGAAYGKGIYLSPISSISFGYSGMGKGQHRMPSKDELVQRYNRMNTIPQTRS IQSRFLQSRN  
LNCIALCEVITSKDLQKHGNIWVCPVSDHVCTRFFVYEDGQVGDANINTQDPKIQKEIMRVIGTQVYTN

>XP\_024087899.1 poly [ADP-ribose] polymerase 6 isoform X2 [Pongo abelii]  
MDIKGQFWNDSDSGDNESEEFLYGVQGSCAADLYRHPQLDADIEAVKEIYSENSVSIREYGTIDDDVID  
LHNISFLDEEVSTAWKVLRTPEIVLRLRFSLSQYLDGPEPSIEVFQPSNKEGFGGLGLQKKILGMFTSQ  
QWKHLSNDFLKTQQEKRHSWFKASGTIKKFRAGLSIFSPIPKSPSPFPIQDSMLKGKLGVPPELRVGRLMN  
RSISCTMKNPKVEVFQYPPSPQAGLLCPQHVLGPPPARTSPLVSGHCKNIPITLEYGFVLQIMKYAEQRIP  
TLNEYCVVCDQHVFNQGSMLKPAVCTREL CVFSFYTLGVMSGAAEEVATGAEEVDLLVAMCRAALES  
PRKSIIFEPYPSVVDPTDKPTLAFNPKKNYERLQKALDSVMSIREMTQGSYLEIKKQMDKLDPLAHPLLQW  
IISNRSRHIVKLP LSR LKFMHTSHQFLLSSPPAKEARFRTAKKLYGSTFAFHGSHIENWHSILRNLGLVN  
ASYTKLQLHGAAYGKGIYLSPISSISFGYSGMGKGQHRMPSKDELVQRYNRMNTIPQTRS IQSRFLQSRN  
LNCIALCEVITSKDLQKHGNIWVCPVSDHVCTRFFVYEDGQVGDANINTQDPKIQKEIMRVIGTQVYTN

>NP\_001192168.1 protein mono-ADP-ribosyltransferase PARP6 isoform 1 [Mus musculus]  
MDIKGQFWNDSDSGDNESEEFLYGVQGSCAADLYRHPQLDADIEAVKEIYSENSVSIREYGTIDDDVID  
LHNISFLDEEVSTAWKVLRTPEIVLRLRFSLSQYLDGPEPSIEVFQPSNKEGFGGLGLQKKILCMFTSQ  
QWKHLSNDFLKTQQEKRHSWFKASGTIKKFRAGLSIFSPIPKSPSPFPIQDSMLKGKLGVPPELRVGRLMN  
RSISCTMKNPKVEVFQYPPSPQAGLLCPQHVLGPPPARTSPLVSGHCKNIPITLEYGFVLQIMKYAEQRIP  
TLNEYCVVCDQHVFNQGSMLKPAVCTREL CVFSFYTLGVMSGAAEEVATGAEEVDLLVAMCRAALES  
PRKSIIFEPYPSVVDPTDKPTLAFNPKKNYERLQKALDSVMSIREMTQGSYLEIKKQMDKLDPLAHPLLQW  
IISNRSRHIVKLP LSR LKFMHTSHQFLLSSPPAKEARFRTAKKLYGSTFAFHGSHIENWHSILRNLGLVN  
ASYTKLQLHGAAYGKGIYLSPISSISFGYSGMGKGQHRMPSKDELVQRYNRMNTIPQTRS IQSRFLQSRN  
LNCIALCEVITSKDLQKHGNIWVCPVSDHVCTRFFVYEDGQVGDANINTQDPKIQKEIMRVIGTQVYTN

>XP\_015134546.2 protein mono-ADP-ribosyltransferase PARP6 isoform X9 [Gallus gallus]  
MGTRQGAARPHSRHGADGRDGSFEGVPAVTSPPARRCRATEARGPDVKARWPPARPAAMRRQGRGQA  
AGSAREMDLKGQHWTTDDSDGDNSEEFLYGVQGTCAADLYRHPQLDADIEAVKEIYSENAVSVREYGTID  
DVIDLDLHNISFLDEEVATAMKVLRTPEIVLRLRFSLSQYLDGPEPSIEVFQPSNKEGFGGLGLQKKILG  
MFTSQWKHLSNDFLKTQQEKRHSWFKTSGTIKKFRAGLSIFSPIPKSPSPFPIQDSMLKGKLGVAPEVRV  
NRLMNRVSCTVRNPKGEVFGYTPSTQAGVAFNVLVGHCKNVPITLEYGFVLQIMKYAEQRIP TLNEYC  
VVCDEQHVFNQGSMLKPAVCTREL CVFSFYTLGVMSGAAEEVATGAEEVDLLVAMCRAALES  
PRKSIIFEPYPSVVDNDPKPTLAFNPKKNYERLQKALDSVMSIREMTQGSYLEIKKQMDKLDPLAHPLLQW  
IISNRSRHIVKLP LSR LKFMHTSHQFLLSSPPAKEARFRTAKKLYGSTFAFHGSHIENWHSILRNLGLVN  
ASYTKLQLHGAAYGKGIYLSPISSISFGYSGMGKGQHRMPSKDELVQRYNRMNTIPQTRS IQSRFLQSRN  
LNCIALCEVITSKDLQKHGNIWVCPVSDHVCTRFFVYEDGQVGDANINTQDPKIQKEIMRVIGTQVYTN

>XP\_041444306.1 protein mono-ADP-ribosyltransferase PARP6 isoform X2 [Xenopus laevis]  
MDIKGHNWPEEDSDGDNECEFLYGVQGTCCADLYRHPQLDADIEAVKEIYSENAVSVREYGTIDDDVID  
LHNIGFLDEEVATAMKVLRTPEIVLRLRFSLSQYLDGPEPTIDVFQPSNRDAFGLGILQKKIVSLFSSH  
QWRYLSNEVLRSQEERRLRVLKRVSGSIKFRAGLSIFSVPVKSPSPFPVQDVSVRSGLTGSDLRSLGTS  
DLRGPRLMNRVSCTLRNPKSELYGSHNPTQPLSSIQVSGHCKNVPITLEYGFVLQIMKYAEQRLPTLNE  
YCVVCDQHVFNQGSMLKPAVCTREL CVFSFYTLGVMSGAAEEVATGAEEVGLLVAMCRAALES  
PRKSIIFEPYPSVVDNDPKPTLAFNPKKNYERLQKALDSVMSIREMTQGSYLEIKKQMDKLDPLAHPLLQW  
IISNRSRHIVKLP LSR LKFMHTSHQFLLSSPPAKEARFRTAKKLYGSTFAFHGSHIENWHSILRNLGLVN  
ASYTKLQLHGAAYGKGIYLSPISSISFGYSGMGKGQHRMPSKDELVQRYNRMNTIPQTRCLQSRFLQSRN  
LNCIALCEVITSKDLQKHGNIWVCPVSDHVCTRFFVYEDGQVGDANINTQDPKIQKEIMRVIGTQVYSG

>XP\_014030859.1 protein mono-ADP-ribosyltransferase PARP6 isoform X4 [Salmo salar]  
MDIKGQSWTDEESDGENESEQFLYGIQGSAAADLYRHPQLDADIEAVKDIYTSADVSVREYGTIDDDVID  
LQNTNISFLDEEVATAMKVLRTPEIILRLRFSLSQYLDGPEPSVEVFQPSNKEGFGSLGLQKKILSTFTSQ  
QWKHLSNEFLKAQQEKRHSWFKAGGTIKKFRAGLSIFSPIPKSPSYPLIQDTVLVKGKLSVPELRVTRLMN  
RSISCTMKNPKGELFSYPNQSQTAVAPARAQAQITTRQLRIELFFSSQAGGHCKNIPITLEYGFVLQIMKY  
SEQRIP TLNEYCVVCDQHVFNQGSMLKPAVCTREL CVFSFYTLGVMSGAAEEVATGAEEVDLLVAMCRA  
ALES  
PRKSIIFEPYPSVVDNDPKPTLAFNPKKNYERLQKALDSVMSIREMTQGSYLEIKKQMDKLDPLA  
HPLLQW  
IISNRSRHIVKLP LSR LKFMHTSHQFLLSSPPAKEARFRTAKKLYGSTFAFHGSHIENWHSILRNLGLVN  
ASYTKLQLHGAAYGKGIYLSPISSISFGYSGMGKGQHRMPTKDELVQRYNRMNTIPQSRPIQS  
RFLQSRNLNCIALCEVITSKDLQKHGNIWVCPVSDHVCTRFFVYEDGQVGDANINTQEPKVIQKEIMRVI  
GTQIYSS

>XP\_032806551.1 protein mono-ADP-ribosyltransferase PARP6-like isoform X1 [Petromyzon marinus]  
MDQDLSAPKWTGEESDGETSEDEFPCGVQVQVADGETHRHPQLDADIESVREKYGDGAQVQIREYGAIDDVA  
VDLHINVGFLDEEIAATAMKVMRTEAVVLR LHFSLSQYLDGPEPSVDVFQPSNKDSFGIGLQKKVLKAFV  
SQQWKHLSNDCLQSQSHSKRLNLLKSSRNAKLRSP LLSHLHRSPSFLPHQDGGGRKRNLEQNGSSQQ  
GNATKTLPLIEHGFQVDTMLYGEQRIPTLNEFCVVCDEPHVFQMGPMKPAVCAARELCVFAFQTLCVMTQ  
AAAEVATGPEVVDLLAMCRSALES  
PRKSIIFDPYPSVVDNDPKALAFNPKKNYERLQKALDSIMSVR  
EMTQGSYLDIKKQMDKQDLSLAHPLLQW  
IISNRSRHIVKLSRQLKFMHTPHQFLLSSPPAKEARFRAA  
KKLYGSFSAFHGSHIENWHSILRNLGLVN  
ASYTKLQLHGAAYGKGIYLSPISSISFGYSGMGKGQHRMESK  
EKVLQNCNRVNTTPIQIKTMQSRFLQSRNLNCIALCEVITSKDLQKHGNIWCPMSDHVCTRFFVYEDGQ  
VGDANINTQDHHQVQAEILRLGMQSVSL

>XP\_019614591.1 PREDICTED: poly [ADP-ribose] polymerase 6-like isoform X5 [Branchiostoma belcheri]  
MHPQLDNDIKSVQRFGAHAINTRIFSSIDDVDAELNIDMSFLDEEIAKAWKNRQEPVIRLHLSFSQY  
LDANEPPKVEVFQPSNKETFGLMQIQKIMETFLSKEWKDLNDRVTAICVPLRPI SARSSSHSHKGASSH  
GKKLQLHEMSKSPQSLSVSSWKVRPKKIDHRHVAQLVDMGFTVEMARNALFMTNRNLEEAINLLLTQPE  
SCRPAAGGGAGSSSFRGTWTSALFLAPSAQQHVVLPAFPSQPLKPATIGDELHLVPCSTERGRTAKTI  
PLEYGFFLAQCLIIYARNRIPTLNEYCVVCDPHIFQNGAMKLPVVCEREVCVFAFQQLGVMRGAADIAT  
GAEEVDLLAMVAKASSHSPRKDLILDPFPSPVVDPDNAKEMVLSPKKKNYDRVNAILDSLMSVREMTQASV  
DMKKQDKDKYAWPFLSWISSNRSRHIVKLPESRRIKFMHTPHQFLLSSPPAKEQAFREAKRQHGSFL  
AFHGSHIENWHSILRNLGLINASGTQHQLHGAAYGSGIYLSPNSSVSFGYSCMGHSHKAARNKALLVTPH  
RKGFLQGCALGCTNQTTAASEKTKGKENTKRFLESDNLTCIALCEVISHKELRKHNNIWWPNPDHVCT  
RFFVYEDGQVGDSDVDTQEKEHQKELIRAIGNMTATD

>XP\_019849465.1 PREDICTED: poly [ADP-ribose] polymerase 6-like [Amphimedon queenslandica]  
MLPEDRQLKSMQDTKYQFLLLSSPPAKEMAFQQAOKLKHGSTFAFHGSHIENWHSIMRKLGLINASGTQYQLN  
GAYAGSGIYLSPHAMTSFGYSNRYDDPSQKQSGSGKQLETLAGKLNITCIALCEVTSKELRRSGDIW  
VCSNSEHVWTRFFVYDTNSATSEASSLHETNRAFKQEIIMHVAVALAKMKLNDSTASKTK

## Alignment

XP_019849465.1[A.queenslandica]	-----	0
XP_019614591.1[B.belcheri]	-----	0
XP_032806551.1[P.marinus]	-----	0
XP_041444306.1[X.laevis]	-----	0
XP_014030859.1[S.salar]	-----	0
XP_015134546.2[G.gallus]	MGTQRGAAARPHSRHAGDRDGSFGFAGVPAVTSPPARRCRATEARGPDVKARMPPARPA	60
NP_001310451.1[H.sapiens]	-----	0
XP_024087899.1[P.abelii]	-----	0
NP_001192168.1[M.musculus]	-----	0
XP_019849465.1[A.queenslandica]	-----	0
XP_019614591.1[B.belcheri]	-----MHPQLNDNIK	10
XP_032806551.1[P.marinus]	-----MDQDLSAPKWTGEESDGETESDEFFCGVQVNADGETHRHPQLDADIE	47
XP_041444306.1[X.laevis]	-----MDIKGHNWPEEDSDGDNCEGFYLGVGQTCADLYRHPQLDADIE	45
XP_014030859.1[S.salar]	-----MDIKGQSWTDEESDGENESEGFYLGIGQSCAADLYRHPQLDADIE	45
XP_015134546.2[G.gallus]	AWRRQGRGQAAGSAEMDLKGQYWTDDSDGDNSEEFYLGVGQTCADLYRHPQLDADIE	120
NP_001310451.1[H.sapiens]	-----MDIKGFWNDDSDGDNSEEFYLGVGQSCAADLYRHPQLDADIE	45
XP_024087899.1[P.abelii]	-----MDIKGFWNDDSDGDNSEEFYLGVGQSCAADLYRHPQLDADIE	45
NP_001192168.1[M.musculus]	-----MDIKGFWNDDSDGDNSEEFYLGVGQSCAADLYRHPQLDADIE	45
XP_019849465.1[A.queenslandica]	-----	0
XP_019614591.1[B.belcheri]	SVEQRFGAAHINTRIFSSIDDVDAELNIDMSFLDEEIAKAWKVNREQPIVIRLHLSFSQY	70
XP_032806551.1[P.marinus]	SVREKYGQDAVQIREYGAIDDVAVDLHNIVGFLDEEATAWKVMRTEAVVLRHLHFSLSQY	107
XP_041444306.1[X.laevis]	AVKEIYSENNAVSVREYGTIDVDIDLHINIGFLDEEVATAWKVIRTEPIVLRFRSLSQY	105
XP_014030859.1[S.salar]	AVKDIYTSNAVSVREYGTIDVDIDLQINISFLDEEVATAWKVIRTEPIVLRFRSLSQY	105
XP_015134546.2[G.gallus]	AVKEIYSENNAVSVREYGTIDVDIDLHVNISFLDEEVATAWKVIRTEPIVLRFRSLSQY	180
NP_001310451.1[H.sapiens]	AVKEIYSENSVSIREYGTIDVDIDLHINISFLDEEVSTAWKVLRTPEIVLRFRSLSQY	105
XP_024087899.1[P.abelii]	AVKEIYSENSVSIREYGTIDVDIDLHINISFLDEEVSTAWKVLRTPEIVLRFRSLSQY	105
NP_001192168.1[M.musculus]	AVKEIYSENSVSIREYGTIDVDIDLHINISFLDEEVSTAWKVLRTPEIVLRFRSLSQY	105
XP_019849465.1[A.queenslandica]	-----	0
XP_019614591.1[B.belcheri]	LDANEPPKVEVFQPSNKEFTFLGMQIQKIMETFLSKWEKDLSDNRVTAICVPLRPISARS	130
XP_032806551.1[P.marinus]	LDGPE-PSVDVFQPSNKDSFGIGLQKVKLKAFFVSQQWKHLNSDCLQSQHSEKRLNL----	162
XP_041444306.1[X.laevis]	LDGPE-PTIDVFQPSNRDAFGLGQLKKIVLSFSSHQWRYLSNEVLRSQQERRLRW----	160
XP_014030859.1[S.salar]	LDGPE-PSVEVFQPSNKEGFSGLGLKKILSTFTSQQWKHLNSEFLKAQQEKKRHSW----	160
XP_015134546.2[G.gallus]	LDGPE-PSIEVFQPSNKEGFGGLGLQKKILGMFTSQQWKHLNSDFLKTQQEKKRHSW----	235
NP_001310451.1[H.sapiens]	LDGPE-PSIEVFQPSNKEGFGGLGLQKKILGMFTSQQWKHLNSDFLKTQQEKKRHSW----	160
XP_024087899.1[P.abelii]	LDGPE-PSIEVFQPSNKEGFGGLGLQKKILGMFTSQQWKHLNSDFLKTQQEKKRHSW----	160
NP_001192168.1[M.musculus]	LDGPE-PSIEVFQPSNKEGFGGLGLQKKILCMFTSQQWKHLNSDFLKTQQEKKRHSW----	160
XP_019849465.1[A.queenslandica]	-----	0
XP_019614591.1[B.belcheri]	SHSHKGASSHGKLLQLHEMSKSFQSLVSSWK---VRPVYKIH-D-----RHAQVLVDMG	181
XP_032806551.1[P.marinus]	----LKSSRN-----A-----KKLRSPLSLLSHLRSFSLPHQDGGGGRKRN-----	201
XP_041444306.1[X.laevis]	----LRVSGS-----I-----KKFRAGLSIFSFPVKPSFPGVQDSVVRSGLTGSDLRSG	206
XP_014030859.1[S.salar]	----FKAGGT-----I-----KKFRAGLSIFSFPKSPSYPLIQDTVLKGGKLS-----	199
XP_015134546.2[G.gallus]	----FKTSGT-----I-----KKFRAGLSIFSFPKSPSFVPIQDSVLKGGKLG-----	274
NP_001310451.1[H.sapiens]	----FKASGT-----I-----KKFRAGLSIFSFPKSPSFPFIQDSMLKGGKLG-----	199
XP_024087899.1[P.abelii]	----FKASGT-----I-----KKFRAGLSIFSFPKSPSFPFIQDSMLKGGKLG-----	199
NP_001192168.1[M.musculus]	----FKASGT-----I-----KKFRAGLSIFSFPKSPSFPFIQDSMLKGGKLG-----	199
XP_019849465.1[A.queenslandica]	-----	0
XP_019614591.1[B.belcheri]	FTVEMARNALFMTNRNLEEAINLLLTQPESCRPGAGGGGAGSSSFRGTWTSALFLAPSVAQ	241
XP_032806551.1[P.marinus]	LTGSDLR-----GPRLMNRSVSCTLRNPKS-----ELYGSHNPTT	201
XP_041444306.1[X.laevis]	--VPELR-----VTRLMNRSISCTMKNPKG-----ELFSYPPNSQ	232
XP_014030859.1[S.salar]	----APEVR-----VNRLMNRSVSCVTKNPKG-----EVFGYTPSTQ	307
XP_015134546.2[G.gallus]	--VPELR-----VGRLMNRSISCTMKNPKV-----EVFGYPPSPQ	232
NP_001310451.1[H.sapiens]	--VPELR-----VGRLMNRSISCTMKNPKV-----EVFGYPPSPQ	232
XP_024087899.1[P.abelii]	--VPELR-----VGRLMNRSISCTMKNPKV-----EVFGYPPSPQ	232
NP_001192168.1[M.musculus]	--VPELR-----VGRLMNRSISCTMKNPKV-----EVFGYPPSPQ	232
XP_019849465.1[A.queenslandica]	-----	0
XP_019614591.1[B.belcheri]	QHQQVVLPARFSQPLKPATI-GDELHLVPCSTERGRKTAKTIPGLEYGFLAQCLYARNRIP	300
XP_032806551.1[P.marinus]	-----LEQNGSSQQGNATKTLPILEHGLVQTMLYGEQRIP	237
XP_041444306.1[X.laevis]	--Q-----PLSSIQVSGHCKTVPTELEYGFLVQIMKYAEQRIP	276
XP_014030859.1[S.salar]	--TVAVPAA-----RAPAQITTRQLIELFFSSQAGGHCKNIPTELEYGFLVQIMKYSEQRIP	286
XP_015134546.2[G.gallus]	--AGVA-----PFNIVGGHCKNVPTLEYGFLVQIMKYAEQRIP	344
NP_001310451.1[H.sapiens]	--AGLLCPQ-----HVG-----LPPPARTSPLVSGHCKNIPTELEYGFLVQIMKYAEQRIP	280
XP_024087899.1[P.abelii]	--AGLLCPQ-----HVG-----LPPPARTSPLVSGHCKNIPTELEYGFLVQIMKYAEQRIP	280
NP_001192168.1[M.musculus]	--AGLLCPQ-----HVG-----LPPPARTSPLVSGHCKNIPTELEYGFLVQIMKYAEQRIP	280
XP_019849465.1[A.queenslandica]	-----	0
XP_019614591.1[B.belcheri]	TLNEYCVVCDEPHIFQNGAMLKPVVCCEREVCVFAFQQLGVMRGAADDIATGAEVVDLLLA	360
XP_032806551.1[P.marinus]	TLNEFCVVCDEPHVFQNGPMLKPAVCARELCVFAQTQLGVMTGAAAEVATGPEVVDLLLA	297
XP_041444306.1[X.laevis]	TLNEYCVVCDEQHVFNQASMLKPAVCTRELCVFSFYTLGVMSGAAEEVATGAEVVGLLVA	336
XP_014030859.1[S.salar]	TLNEYCVVCDEQHVFNQGSMLKPAVCTRELCVFSFYTLGVMSGAAEEVATGAEVVDLLVA	346
XP_015134546.2[G.gallus]	TLNEYCVVCDEQHVFNQGSMLKPAVCTRELCVFSFYTLGVMSGAAEEVATGAEVVDLLVA	404
NP_001310451.1[H.sapiens]	TLNEYCVVCDEQHVFNQGSMLKPAVCTRELCVFSFYTLGVMSGAAEEVATGAEVVDLLVA	340
XP_024087899.1[P.abelii]	TLNEYCVVCDEQHVFNQGSMLKPAVCTRELCVFSFYTLGVMSGAAEEVATGAEVVDLLVA	340
NP_001192168.1[M.musculus]	TLNEYCVVCDEQHVFNQGSMLKPAVCTRELCVFSFYTLGVMSGAAEEVATGAEVVDLLVA	340
XP_019849465.1[A.queenslandica]	-----	0
XP_019614591.1[B.belcheri]	MVKASSHSPRKDLILDPPFSSVVDPNAKEMVLSPKKKNYDRVNAI LDSLMSVREMTQAS-	419
XP_032806551.1[P.marinus]	MCRSALESPRKSIIFDPYPSSVVDPNDPKALAFNPKKKNYERLQALDLSMSVREMTQGSY	357
XP_041444306.1[X.laevis]	MCRAALESPRKSIIFEPYPSSVVDPNDPKTLAFNPKKKNYERLQKALDSVMSIREMTQGSY	396
XP_014030859.1[S.salar]	MCRAALESPRKSIIFEPYPSSVVDPNDPKTLAFNPKKKNYERLQKALDSVMSIREMTQGSY	406
XP_015134546.2[G.gallus]	MCRAALESPRKSIIFEPYPSSVVDPNDPKTLAFNPKKKNYERLQKALDSVMSIREMTQGSY	464
NP_001310451.1[H.sapiens]	MCRAALESPRKSIIFEPYPSSVVDPTDPKTLAFNPKKKNYERLQKALDSVMSIREMTQGSY	400
XP_024087899.1[P.abelii]	MCRAALESPRKSIIFEPYPSSVVDPTDPKTLAFNPKKKNYERLQKALDSVMSIREMTQGSY	400
NP_001192168.1[M.musculus]	MCRAALESPRKSIIFEPYPSSVVDPTDPKTLAFNPKKKNYERLQKALDSVMSIREMTQGSY	400
XP_019849465.1[A.queenslandica]	-----MLPEDRQLKSMDTKYQFLLLSSPPAKEMAF	30
XP_019614591.1[B.belcheri]	VDMMKQLDKKDYAWPFLSWISSNRSHIVKLPESSRIKFMHTPHQFLLSSPPAKEQAF	479
XP_032806551.1[P.marinus]	LDIKKQMDKQDLSLAHPLLQWISSNRSHIVKLQSSRQLKFMHTPHQFLLSSPPAKEARF	417
XP_041444306.1[X.laevis]	LEIKKQMDKDLPLAHLPLQWISSNRSHIVKLPLSR-LKFMHTSHQFLLSSPPAKEARF	455
XP_014030859.1[S.salar]	LEIKKQMDKDLPLAHLPLQWISSNRSHIVKLPLSRQLKFMHTSHQFLLSSPPAKEARF	466
XP_015134546.2[G.gallus]	LEIKKQMDKDLPLAHLPLQWISSNRSHIVKLPLSR-LKFMHTSHQFLLSSPPAKEARF	523
NP_001310451.1[H.sapiens]	LEIKKQMDKDLPLAHLPLQWISSNRSHIVKLPLSR-LKFMHTSHQFLLSSPPAKEARF	459
XP_024087899.1[P.abelii]	LEIKKQMDKDLPLAHLPLQWISSNRSHIVKLPLSR-LKFMHTSHQFLLSSPPAKEARF	459
NP_001192168.1[M.musculus]	LEIKKQMDKDLPLAHLPLQWISSNRSHIVKLPLSR-LKFMHTSHQFLLSSPPAKEARF	459
XP_019849465.1[A.queenslandica]	QQAKLKHGSTFAPFHGSSSIENWHSIMRKLINASGTKYQLNGAAYGSGIYLSPHAMTSFGY	90

XP_019614591.1[B.belcheri]	REAKRQHGSLFAPFHGSHIENWHWSILRLHGLINASGTQHQLHGAAYGSGIYLSPNSVSFGY	539
XP_032806551.1[P.marinus]	RAAKKLGYGSFAPFHGSHIENWHWSILRLNGVLNASYTKYQLHLGAAYGKGIYLPSSISIFGY	539
XP_041444306.1[X.laevis]	RTAKKLYGSTFAFHGSHIENWHWSILRLNGVLNASYTKYQLHLGAAYGKGIYLPSSISIFGY	539
XP_0414430859.1[S.salar]	RTAKKLYGSTFAFHGSHIENWHWSVLRNLGNLNASYTKYQLHLGAAYGKGIYLPSSISIFGY	526
XP_015134546.2[G.gallus]	RTAKKLYGSTFAFHGSHIENWHWSILRLNGVLNASYTKYQLHLGAAYGKGIYLPSSISIFGY	583
NP_001310451.1[H.sapiens]	RTAKKLYGSTFAFHGSHIENWHWSILRLNGVLNASYTKYQLHLGAAYGKGIYLPSSISIFGY	519
XP_024087899.1[P.abelii]	RTAKKLYGSTFAFHGSHIENWHWSILRLNGVLNASYTKYQLHLGAAYGKGIYLPSSISIFGY	519
NP_001192168.1[M.musculus]	RTAKKLYGSTFAFHGSHIENWHWSILRLNGVLNASYTKYQLHLGAAYGKGIYLPSSISIFGY : ** :***** :*:**:*** ***:***** : ***	519
XP_019849465.1[A.quenslandica]	SNRYIYDPSSQKK-----GSSGKQLETLAGKLNI	119
XP_019614591.1[B.belcheri]	SCMGHSGHKAARNKALLVTPPHRGFLQGCKALCTGNTTAASEKGTKKKTRFRLESNDL	599
XP_032806551.1[P.marinus]	SGMGKGQRHMESEKLV-----QCNRVNITP-----QIKTMGRSFLQSRLN	519
XP_041444306.1[X.laevis]	SGMGKGQRHMFSDLV-----QRYNRMTIP-----QTKCLSRFLQSRLN	557
XP_0414430859.1[S.salar]	SGMGKGQRHMPTDKELV-----QRYNRMTIP-----QSRPIQSRFLQSRLN	568
XP_015134546.2[G.gallus]	SGMGKGQRHMRPKDELV-----QRYNRMTIP-----QTSRIQSRFLQSRLN	625
NP_001310451.1[H.sapiens]	SGMGKGQRHMRPKDELV-----QRYNRMTIP-----QTSRIQSRFLQSRLN	621
XP_024087899.1[P.abelii]	SGMGKGQRHMRPKDELV-----QRYNRMTIP-----QTSRIQSRFLQSRLN	618
NP_001192168.1[M.musculus]	SGMGKGQRHMRPKDELV-----QRYNRMTIP-----QTSRIQSRFLQSRLN * . : . . . *	561
XP_019849465.1[A.quenslandica]	TCIALCEVVTSKELRRSGDIWVCNSEHVTVRFVFVYTNSATSEASSLHTEINRAFKQE	179
XP_019614591.1[B.belcheri]	TICALCEVITSKELRKHNIVVFNPDHCVTRFFVFVEDGVGDGMSV---DTQEKYQAE	656
XP_032806551.1[P.marinus]	NCIALCEVITSKDLQKHGINVWCPMSDHCVTTRFFVFVEDGVGDGDI---NTQDPKIQAE	616
XP_041444306.1[X.laevis]	NCIALCEVITSKDLQKHGINVWCPVDHCVTRFFVFVEDGVGDGDI---NTQDPKIQAE	574
XP_0414430859.1[S.salar]	NCIALCEVITSKDLQKHGINVWCPVDHCVTRFFVFVEDGVGDGDI---NTQEPKVIQE	625
XP_015134546.2[G.gallus]	NCIALCEVITSKDLQKHGINVWCPVDHCVTRFFVFVEDGVGDGDI---NTQDPKIQKE	682
NP_001310451.1[H.sapiens]	NCIALCEVITSKDLQKHGINVWCPVDHCVTRFFVFVEDGVGDGDI---NTQDPKIQKE	618
XP_024087899.1[P.abelii]	NCIALCEVITSKDLQKHGINVWCPVDHCVTRFFVFVEDGVGDGDI---NTQDPKIQKE	618
NP_001192168.1[M.musculus]	NCIALCEVITSKDLQKHGINVWCPVDHCVTRFFVFVEDGVGDGDI---NTQDPKIQKE ***** :*:**:*** ***:***** : . . . *	618
XP_019849465.1[A.quenslandica]	IMHAVALKAMKMLDNSASTKT 201	
XP_019614591.1[B.belcheri]	ILRAIGNTADT----- 668	
XP_032806551.1[P.marinus]	ILRLGMQSVSL----- 588	
XP_041444306.1[X.laevis]	IMRVIGTQVYS----- 626	
XP_0414430859.1[S.salar]	IMRVIGTQIYS----- 637	
XP_015134546.2[G.gallus]	IMRVIGTQVYTN----- 694	
NP_001310451.1[H.sapiens]	IMRVIGTQVYTN----- 630	
XP_024087899.1[P.abelii]	IMRVIGTQVYTN----- 630	
NP_001192168.1[M.musculus]	IMRVIGTQVYTN----- 630 **:	

### Percent identity matrix:

```
#
#
# Percent Identity Matrix - created by Clustal2.1
#
#
1: XP_019849465.1[A.queenslandica] 100.00 52.13 48.66 50.54 50.80 50.54 50.54 50.54 50.54
2: XP_019614591.1[B.belcheri] 52.13 100.00 59.15 54.22 56.35 56.79 55.90 55.90 55.90
3: XP_032806551.1[P.marinus] 48.66 59.15 100.00 73.58 74.57 74.66 74.02 74.02 74.02
4: XP_041444306.1[X.laevis] 50.54 54.22 73.58 100.00 84.60 87.50 86.55 86.55 86.39
5: XP_014030859.1[S.salar] 50.80 56.35 74.57 84.60 100.00 90.47 89.21 89.21 89.05
6: XP_015134546.2[G.gallus] 50.54 56.79 74.66 87.50 90.47 100.00 95.15 95.15 94.83
7: NP_001310451.1[H.sapiens] 50.54 55.90 74.02 86.55 89.21 95.15 100.00 100.00 99.68
8: XP_024087899.1[P.abelii] 50.54 55.90 74.02 86.55 89.21 95.15 100.00 100.00 99.68
9: NP_001192168.1[M.musculus] 50.54 55.90 74.02 86.39 89.05 94.83 99.68 99.68 100.00
```