

PARP12

Sequences :

>NP_073587.1 protein mono-ADP-ribosyltransferase PARP12 [Homo sapiens]
MAQAQGVVGEVTQVLCAGGALELPRLRRRLRMGLSADALERLLRQGRFVAVRAGDAAAAPERVVLAAS
PLRLCRAHQGSKPGCVGLCAQLHLCRFMVYGACKFLRAGKNCNRNHSLSLTTTEHNLVSLRTHGVDHLSYNEL
CQLLFQNDPWLLEPICQHYNKGDPHGSCAFQKQCIKLHICQYFLQGECKFGTSCRRSHDFSNSENLEKL
EKLGMSSDLVSRLLPTIYRNAHDIKNKSSAPSRVPLFVPQGTSEKKDSGSGVSPNTLSQEEGDQICLYHI
RKSCSFQDKCHRHFHFLPYRWQFLDRGKWEDLDNMLEIEEAYCNPKIERILCSSESASTFHSHCLNFNAMT
YGATQARRLSTASSVTKPPHFILTTDWIYWMSDEFGSWQEYGRQGTVHPVTTVSSSDVEKAYLAYCTPGS
DGQAATLKFQAGKHNYELDFKAFVQKNLVYGTTKVCRPRPKYVSPQDVTMTQTCNTKFPGPKSIPTYWDS
SALPDPGFGKITLSSSEEEYQKVNLFNRTLFFYFVQKIERVQNLALWEVYQWQGMQKQNGGKAVER
QLFHGTSAIFVDAICQQNFDWRVCGVHGTSYKGKSYFARDAAYSHHYSKSDTQTHMTFLARVLVGEFVRG
NASFVRPPAKEGWSNAFYDSCVNSVSDPSIFVIFEKHQVYPEYVIQYTTSSKPSVTPSILLALGSLFSSR
Q

>XP_024106109.1 poly [ADP-ribose] polymerase 12 [Pongo abelii]
MAQAQGVVGEVTQVLCAGGALELPRLRRRLRMGLSADALERLLRQGRFVAVRAGDAAAAPERVVLAAS
PLRLCRAHQGSKPGCVGLCAQLHLCRFMVYGACKFLRAGKNCNRNHSLSLTTTEHNLVSLRTHGVDHLSYNEL
CQLLFQNDPWLLEPICQHYNKGDPHGSCAFQKQCIKLHICQYFLQGECKFGTSCRRSHDFSNSENLEKL
EKLGMSSDLVSRLLPTIYRNAHDIKNKSSAPSRVPPFVPQGTSEKKDSGSGVSPNTLSQEEGDQICLYHI
RKSCSFQDKCHRHFHFLPYRWQFLDRGKWEDLDNMLEIEEAYCNPKIERILCSSESASTFHSHCLNFNAMT
YGATQARRLSTASSVTKPPHFILTTDWIYWMSDEFGSWQEYGRQGTVAHPVTTVSSSDVEKAYLAYCTPGS
DGQAATLKFQAGKHNYELDFKAFVQKNLVYGTTKVCRPRPKYMSPODVTMTQTCNTKFPGPKSIPTYWDS
SALPDPGFGKITLSSSEEEYQKVNLFNRTLFFYFVQKIERVQNLALWEVYQWQGMQKQNGGKAVER
QLFHGTSTIFVDSICQQNFDWRVCGVHGTSYKGKSYFARDAAYSHHYSKSDTQTHMTFLARVLVGEFVRG
NASFVRPPAKEGWSNAFYDSCVNSVSDPSIFVIFEKHQVYPEYLIQYSTSSKPSVTPSILLALGSLFSRQ

>NP_766481.2 protein mono-ADP-ribosyltransferase PARP12 [Mus musculus]
MAQAQAVAAEVTQLLCAAGGALELAELRRRLRTSLGTDALERLLRDCGRFVVASRAVVAVGAGREAAAAA
SERLVLAVASSRLCRAHQGPKPGCTGLCAQLHLCKFLIYGNCKFLKTGKNCNRGNHLKTDHNLVSLRTHG
VDHLITYELCQLLLQNDPSLLPDICLHYNKGDPFGSCSFQKQCIKLHICQYFLQGECKFGTSCRRSHEF
TNESLSQLERLGLSSDLVSRLLSTYRNAYDIKNKSALSKVSPSPAGPQGSERKDSGSGVSPGTSPQ
ESEQICILYIRKSCSFQEKCHRHFHFLPYRWQFLDGGKWEDLDNMLEIEEAYSNPKSDRIVYTESAAGFH
FDNLDFNMKFGNTLARRLSTASSVTKPPHFILTTDWIYWMDDEFGSWQEYGRQSGHVPVTTISSSDVER
AYLAFCAPGADAQAATLKFQAGKHNYELHFKAFILQKNLVYGTIRKVCRRPKYVSPQDVMQKQSCNTKLHG
PKSIPDYWDPAALPDLGFKKITLSSSEEEYQKVNINFNRTLFFYFVQKIERIQNMLWEVYQWQCKQMK
QNGGKEVDERQLFHGTSAINFVDAICQQNFDWRVCGLHGTSYKGKSYFARDAAYSHHYSKSDTHSHMFLA
RVLVGDVFRGSTSFVRPPAKEGQSNAFYDSCVNSMSDPTIFVVEKHQVYPEYLIQYSTSSKFPASPISIF
VALGNLFTSRQ

>XP_416333.5 protein mono-ADP-ribosyltransferase PARP12 isoform X1 [Gallus gallus]
MRAMRAAQRAQCLPGRQGRMTAIPAEPGALRSSRRGRDRSRAARPFPLARPSRRQFRFRFLAQEAERWR
RRSRFRARPAGSGSAGGKQPGPAMVLPTQVLRLVCAGGGSLELEELLRLRPRPTAEQLAAVLDRPQRFT
LVRTPDEAAGGAAAAAAAEETVLVVAVTSSSLRLCLHEHAGCGRGCGRLLHLCYHLKGVCRNQOQARKEC
KFVHDFYSPHNHVSLRQGLDSTFSNDELRLQLLLQNDPTLLPEVCLHYNKGDPYGSCFTFKMCTKLHVC
QYFLRGCRFGSSCKRSHDFSCKPECCKELRQGMSSDIQKLPISYRNMYAIQNSKSGKHDTEDNKSLPC
KERKHSSSQESTSTSNVEVQICLYNLYTSCIFEDKCIETHFLPYRWQISDGTWTKDLESMEIEKEEYCD
PNNIRSSKPISESGFIFPYISFVMDQSGFKVRRLSTASSVTKPPHFILTTTEWIYWKDEHGVWREYKKG
DSRAAATVSSDDLEKAYTVGNSAKLNFKAGVHEYELDFGAMTQKNLRYKTERKVCRRPKFVQSSEVERI
RKRGFKNTEELRIIPSHWDKSALPEGLFKLIELDSSSEYNNKVKGDQRTMPKTHIKRICIQNPISLWEL
YQWQKEQMGKSNGGKTDERFLFHGTSSKKHIDAICHQNFDWIRICGLNGTVYKGKSYFARDAASYDAYCREG
SCSKTMFQARVLVGEFTVGRSSVVRPPLKDNQNFYDSCVNSSSNPSIFVIFEKQVYPEYLIIEYLDQACA
RML

>XP_018096331.1 protein mono-ADP-ribosyltransferase PARP12 [Xenopus laevis]
MWTNQLIMVHTARLSRRLCAGGSMELQQLGHSGLGNQQLERLVEVEGSLVLRVQEGDQKVAVYSD
LRLCQTFPKCAGCQQLHLCRYFLGSCNRSPCKFNHICIRNGHNLVSLQKFLDSMPIDELRQLLLQNDP
LLPDICSHYNRGDPHGSCCTYNNKNLHVCQHFLQGDCKGKEKCKRCHDLSSEETLKLKTKWQLSDSLL
PGLLETYYNAHTLKKSCDRPPRNVYKSAEKKTKPGPSKSGTSQEIEEICLYFIIRNSCSFKKECKVREHFL
PYRWQYVNTGQTKDLDNMEMIEKSYCDPNSRAVLNLDFAEMYQSNKVKRLSTPSSASKPPHFVFTTDW
KWWYMDENKWWVEYGTESDRHANSTICSSDLENFYQSNQTAADVFKPAGKHXYLSLSPKMMVQRNLQVETKR
RVCRPRFVYSGKDVKKKRSSTSEPSKEDKNTPEHWDKQTPDLGYKLVLLSPLSEEYSKIEMAFRCRTLRT
IRTHSERTIQNLALWEVYQWQEKQMKLNEGKDPERQLFHGTQVKLIDAICQQNFDWIRICGVHGTAYGK
GSYFARDSYSHNYCKRSSSQANIMFVARVLVGNFTRGHSSYLRRPSPKSEFRSTSFYDSCVDSKSNPSIF
VIFEKHQIYPEYLIKYSK

>XP_014003371.1 protein mono-ADP-ribosyltransferase PARP12 [Salmo salar]
MSSIYSYQYVTIKLCGNQGCLDFKRLDQIVGQKFTVADDVLLGILCDREKYAISKGEGKASRLAMSQNSVI
VAKTSLRVQSPGECLEHCENLHLCRYFVCGNCRFGNCKNAHSLDSPHNTAVIRLSLGHLDGEAELFPL
LLQNDPILMPEICSHYNGVGEHGSKFKTSCTSLHLCLHFLQGDCKFGAGCKRAHTDATMTKILNLRG
FSQENIRILDKIYNKFIIGQGHEEKPSVVVPSASAIEPVGKERSRKPSSRSISETDRNEICLFFIRR
HCSFKEKCVRIHYHLPYKWQILERDGVTWRLDPNVEEIEKAYCIPGKDTSGGIQPVNFLTMTCGRSPVRR
LSTVSSVTKPPHFILTTEWLMYWSGELGQWIEYQYETIDGKERVASVTSKLTENVYQADPDSEIPFGSGH
NQYILRFKEMIQQNVRFKTKREVARRPCFLSGQDVEAKLKSQSPSTSSSTSVSPHWDKGAALPDFTYKL
VPLLDQMTHEYQWQSLFKTKMSTSTHKNIRIQNPISLWVRVTFQWQKEQMKVKNGKLVDERHLFHGTPESI
VDAICEQNFDWRVCGIHGSHYKGKSYFARDALYNRPFKSSSVSGKKIMFVALVLVGEFTKGNRDIYLRPPQ
KGTKRLLYDSCVDSSENPALFVVFKEQQIYPEFVIEYS

>XP_032833032.1 protein mono-ADP-ribosyltransferase PARP12 [Petromyzon marinus]
MQSSTYPQEQQQQEKPLPLDRALDTHLSDGALPLSALASALGFFDSALLAALRSKPELFALVEGSGSS
SSSLSGGQQQPERGSLDMRVLAVSALRVCPRYRERTGCPDGEGCAKLHVCRRFVLGSKCFGPDCKFSHD
FRDGNHRLCYKSGVEALPFDPMQTLQLLQNDPTLLPQICKTYKVLDAAGECKYGNKCARLHLCRPFVLGV
CKFGDKCRNHGLSDAGLRLLKHQGVCAWPDAAALLGLLRREQIHAAAGGADAADDGATIAPLGFAAR
AAARGKAGSGSGDGPAGAGRDGEGEICLYHLLSKCHYKDRCLKSHAALPYRWQERSHGGGAWQDLP
TEAMERHYCDPASVSHDSVDFIHMKSVMGTVRRLSTANAVAMPDNFLTTRWSWYQECVGTWIKYGDEA
TTNDRAKSNVSSDLEKAYHEDKEGSFKTAGRFYSRLDFKDMQTNLNEVGTTRCVRRRRPLLVTARDVEV
ARERHASLRTGVGVSVAHWDRASLSDVDISLVELVNTTSEYKEVATLFKNTLSQPSINILNVKRVQNL
LWDAFQRKREWMRKNDGVEVEERKLPHGTRPKHVVPICQQNIDWRLRGAHGTAYGEGSYFARDAASYST
YSKGRKGTAPASAAAMFLARVLVGRYTCGKAGYVRPAIKASPSTSAQGAPEVYFVYDSCVNTIEDPSIFV
FERDQIYPEYVIEYQF

>XP_019640190.1 PREDICTED: poly [ADP-ribose] polymerase 12-like [Branchiostoma belcheri]
MKFATNQDQSGSPNGGAGAFSCSPRGRGNGRGRGRGGRFGKPSPSDPAGRGGRGGAGRGRGMDRGRG
RGFGYSPQVPPASGPMVANEAKFSMNDVMQLMQAMHGAAPMPQQAQPEAAMVHPQAAPPSPSGARS
RSRQRTAHDNNDPPVPAKLQACQTYWYNNRQRCQTKGDACTFLHVCGRVLYGGCICFDKQGCQESHNILTQ
NKLQKFGIPCNSEKAVIDIFKRDVFNKRKAEQGDVKPEKLDEICFNIRQRCSYKTLCERMWCRMPYQ
WQYRAPAADRWRFHGLDNNVWEAYCKVTEDSYSPVRLDGKTCVAVNTDMKAVATDGSIGDTRQEFV
RLGTSSSVKSAAPHGLFVTEWLYWHVDVGTWVEYQGMNKSGEVKGTSLSLTSRDIEDRYQDQRDADVFTST
SHQVYVLRLLDMCQENTRVGTRDRVRKPKFVSEEDVKNPKPKPASRAKSARSASAWDESAPAHWS
DDEDFVKVDVGTSAEYRNKTLFEQGGMAGTAIAGVKRVQNAFLWASAYNRKKAQLKQNGKQDAEERLL
FHGTQDAVDAICQQNFDWRLSGSRVGLYGGQTYFSASAQYSHSYAQASNGRRYMFVVRVLVGYATQG
DAGIRRRPVPNPGEPYGRMYDSCVNDTANPNIFVIFDNAAQCYPEHIEY

Alignment

XP_019640190.1[B.belcheri]	MKPATNGQDGSPNGGGARG--AFSCSPRGRGGNRGRGRGRGRGSPSPDPDA-----	51
XP_032833032.1[P.marinus]	-----	0
XP_014003371.1[S.salar]	-----	0
XP_018096331.1[X.laevis]	-----	0
XP_416333.5[G.gallus]	MRAMRAAQRAQCPLGRQRGMTAIPAEPGALRSSRGRDRSRAARPFPLARPSRRQFFR	60
NP_766481.2[M.musculus]	-----	0
NP_073587.1[H.sapiens]	-----	0
XP_024106109.1[P.abelii]	-----	0
XP_019640190.1[B.belcheri]	-----GRGGRGGARGGR-----GMDRGRGRGGFYSPQQV----	80
XP_032833032.1[P.marinus]	-----MQS---SYPEGQQQKEKPFPLDRLALDLDHSGCALPLSALASAL	43
XP_014003371.1[S.salar]	-----MSSIVSQVYTKILCGNQCLDFKRLDQIV	29
XP_018096331.1[X.laevis]	-----TNQLIMVHTARLSRRLCSAGGSMEQLGHS	34
XP_416333.5[G.gallus]	FLAQEAERWRRSRFRFRPAGSGSAGGKPGPAMVLPQTQVLRVLCAGGSGLELELLRRL	120
NP_766481.2[M.musculus]	-----MAQAAVAIAEVTQLLCAAGGALELAELRRL	31
NP_073587.1[H.sapiens]	-----MA-QAGVVGEVTQVLCAGGALELPRLRRL	30
XP_024106109.1[P.abelii]	-----MA-QAGVVGEVTQVLCAGGALELPRLRRL	30
XP_019640190.1[B.belcheri]	-----PPPA-SGPMVANEAKFSM-----NDVM-----	101
XP_032833032.1[P.marinus]	GF----PDSALLAALRSKPELFALVEGSGSSSSSLSGGQQ-QQPERGSLDWRVLAVSALR	98
XP_014003371.1[S.salar]	GQKFTVADDVLLG-ILCDREKYAI-----S---KGECKASRLAMSQNSVIVAKTSLR	77
XP_018096331.1[X.laevis]	G-LN--GQQLER-LVEVEGRSL-----VLRVQEGDQKVAVVRSDLR	72
XP_416333.5[G.gallus]	FCRPT--AEQLAA-VLRDQRFPLVTPDEAEA---GGAATAAAAEETVLVIVATSSLR	174
NP_766481.2[M.musculus]	RTSLG--TDALER-LLRDGGRFVVASRAVAVG---AGREA---AAAASERVLVAVSSLR	82
NP_073587.1[H.sapiens]	RMGLS--ADALER-LLRQGRFVVAVRAG-----G---AAAAPERVVLAVSPLR	73
XP_024106109.1[P.abelii]	RMGLS--ADALER-LLRQGRFVVAVRAG-----D---AAAAPERVVLAVSPLR	73
XP_019640190.1[B.belcheri]	-----QLMQAMHMGAAPOMPQAQPEAAVMHPQAPPFS-----G	134
XP_032833032.1[P.marinus]	VCPRYRE-RTGCPDGECAKLVCRRFVLSGCK-F---GPDCFKSHDFRGNHRLCYKS	153
XP_014003371.1[S.salar]	VQSP---PGE---CLHCENLHLCRYFVCGNCR-F---GNCKRNAHLSDPHNTAVIRSL	127
XP_018096331.1[X.laevis]	LCQT---PKC---AGDCGQLHLCRFYILGSCN-----RSPCKFNHCIRNGHNSVLQKF	120
XP_416333.5[G.gallus]	LCLHG---AGC---RGGCGRHLCKYHLKGVCVR-NQARKECKFVHDFFYSPHNSVLRLQ	228
NP_766481.2[M.musculus]	LCRAHQGKPGC---TGLCAQLHLCKFLIYGNCR-FLTKGNCRNGHNLKTDHNLVLRTH	139
NP_073587.1[H.sapiens]	LCRAHQGKPGC---VGLCAQLHLCRFMYVGACK-FLRAGKNCRNSHSLTEHNLVLRTH	130
XP_024106109.1[P.abelii]	LCRAHQGKPGC---VGLCAQLHLCRFMYVGACK-FLRAGKNCRNSHSLTEHNLVLRTH	130
XP_019640190.1[B.belcheri]	GARS-RFRSRQRTAHNNDNPPVPAKLPQACTWYNNRQ---RGCTKGDACTFLHVCGRYLV	190
XP_032833032.1[P.marinus]	GVEA-LFFDPMQTL---LLQNDPTLLPQICKTYKVLV--AAGECKYGNKCARLHLGRFVL	208
XP_014003371.1[S.salar]	GHHG-LGEAEFLPL---LLQNDPYLMEITCSHYNKGCGEHSCKFKTSCITSLHLHLFQ	183
XP_018096331.1[X.laevis]	HLDS-MPIDELRQL---LLQNDPNLLPDICSHYNRGDCPHGSCITYNKNKMLHVCOHFLQ	176
XP_416333.5[G.gallus]	GLDSTFSNDELRLQL---LLQNDPTLLPEVCLHYNKGDPYGSCTFKMKCTKLHVCOYFLR	285
NP_766481.2[M.musculus]	GVDH-LTYTELQQL---LLQNDPSLLPDICLHYNKGDPFGSCSFQKQCIKLHIQOYFLQ	195
NP_073587.1[H.sapiens]	GVDH-LSYNELCQL---LFQNDPWLLPEICQHYNKGDPHGSCAFQKQCIKLHIQOYFLQ	186
XP_024106109.1[P.abelii]	GVDH-LSYNELCQL---LFQNDPWLLPEICQHYNKGDPHGSCAFQKQCIKLHIQOYFLQ	186
XP_019640190.1[B.belcheri]	GGCIFDKGQCEFSHNILTQQNGKILQKFGIPCNSEKAVIDIFKRDFVNKRKAEQ-----	244
XP_032833032.1[P.marinus]	GVCKFGD-KCRRNHGLSDAGLRRLKQHGVCAWPDAAALLGLLRREQIHAAAGGGADAAD	267
XP_014003371.1[S.salar]	GDCKPGA-GCKRAHTFDAT-TMKILNNGRGFSQENIRILDKIYNNKFIIIGQGEHEKPSVV	241
XP_018096331.1[X.laevis]	GDCKPGE-KCKRCHDLSEETLKKLTKWQLSDSLPLGLLETYTNAHTLKSSCDR--PPRN	233
XP_416333.5[G.gallus]	QCCRFPS-SCKRSHDFSPKECEKLERQGMSSDIQKLPSTYRNMVATQNSKGS--KHDT	342
NP_766481.2[M.musculus]	GECKFGT-SCKRSHEFTNSESLEQLERLGLSSDLVSRLLSTYRNAYDIKNKGA--LSKV	252
NP_073587.1[H.sapiens]	GECKFGT-SCKRSHDFSNSENLEKLEKLGMSDLVSRLLPTIYRNAHDIKNKSSA--PSRV	243
XP_024106109.1[P.abelii]	GECKFGT-SCKRSHDFSNSENLEKLEKLGMSDLVSRLLPTIYRNAHDIKNKSSA--PSRV	243
XP_019640190.1[B.belcheri]	-----GDKVPEKLDEICFINIRQRCSEYTKLCERW	273
XP_032833032.1[P.marinus]	DGATIALPGFAARAAARGRKAGSGGDGMPAGAAGRDGEGEICLYHLLSKCHYKDRCLKS	327
XP_014003371.1[S.salar]	VPSPASALIEPVGKERSRK-----PSSRSISETORNEICLFFIRRHCSFPEKCVRI	291
XP_018096331.1[X.laevis]	V----V---KSAEKKTTPGP-----S-KSGTSGQEIEICLYFIRNSCSFPEKCVRE	276
XP_416333.5[G.gallus]	EDNKLSPC--KERKHSS-----QESTSTNSEVEQICLYNLYTSCIFEDKCIRT	389
NP_766481.2[M.musculus]	SPSPAGQPGSGSERKDDSSGP-----VSPGTSPQSESEQICLYHIRKSCSFQEKCHRV	303
NP_073587.1[H.sapiens]	PP-LFVPQGTSEKDDSSGS-----VSPNTLSQEEGDQICLYHIRKSCSFQDKCHRV	293
XP_024106109.1[P.abelii]	PP-PFVPQGTSEKDDSSGS-----VSPNTLSQESDQICLYHIRKSCSFQDKCHRV	293
XP_019640190.1[B.belcheri]	HCRMPYQWYRAPAADRWRFHGDLDNMVEEAYCKVTEDSYSPVRL--DGKTCVAVNFTDM	331
XP_032833032.1[P.marinus]	HAALPYRWQERSHGGGAQWDLPG--TEAMERHYCDPASVS-----HDSVDFIHM	374
XP_014003371.1[S.salar]	HYHLPYRWQILERDGVTRDLPN--VEEIEKAYCIPGKDTSGG-----IQPVNFLT	341
XP_018096331.1[X.laevis]	HFHLPYRWQVY--TNGTWKDLN--MEMIEKSYCDPNSRAV-----LVNLDFEAM	322
XP_416333.5[G.gallus]	HFHLPYRWQIS--DGTTWKDLN--MEEIEKEYCDPNNIRSSKPISESGFIPFYISFVDM	445
NP_766481.2[M.musculus]	HFHLPYRWQFL--DGGKWKDLN--MELIEEAYSNPKDRIVYTESAAGPHFDNLFNSM	359
NP_073587.1[H.sapiens]	HFHLPYRWQFL--DRGKWEDLN--MELIEEAYNPKIERILCESASFTFHSCLNFNAM	349
XP_024106109.1[P.abelii]	HFHLPYRWQFL--DRGKWEDLN--MELIEEAYNPKIERILCESASFTFHSCLNFNAM	349
XP_019640190.1[B.belcheri]	KAVATDGSIGDTRQEFVRLSTSSSVKSPAGHLVFTWMLWYHWDVGTWVEYQGMNKS	391
XP_032833032.1[P.marinus]	KSV-----HGTVRLSTANAVAMPDNFLTTRMSWYQECVGTWIKYGEAATTN	423
XP_014003371.1[S.salar]	TCG-----RSPVRLSTVSSVTKPPHFLTTEWMLWYSGELGQWIEYQGETYDG	390
XP_018096331.1[X.laevis]	TYQ-----SNKVRLSTPSSASKPPHFVFTTDMKWYMWDEYNKWVEYGTESDR-	370
XP_416333.5[G.gallus]	QSG-----FKVRLSTASSVTKPPHFLTTEWMLWYWKDEHGVWREYGGKDS-	493
NP_766481.2[M.musculus]	KFG-----NTLARRLSTASSVTKPPHFLTTEWMLWYMWDEFGSWQYGRQGS-	407
NP_073587.1[H.sapiens]	TYG-----ATQARRLSTASSVTKPPHFLTTEWMLWYMWDEFGSWQYGRQGTV-	397
XP_024106109.1[P.abelii]	TYG-----ATQARRLSTASSVTKPPHFLTTEWMLWYMWDEFGSWQYGRQGT-	397
XP_019640190.1[B.belcheri]	EVRGTSLSLRSRDIEDRYQD-----QRDADVTFSTSHHQVYLRRLDMQENTRVGTRRD	444
XP_032833032.1[P.marinus]	D-RAKSNVSSLDLEKAYHE-----DKEGSFKTAGRFSYRLDFKMDTQTNLEVGTRRC	475
XP_014003371.1[S.salar]	K-EKVASVTSKLTENYQA-----DPDSEIPFGSGHNNQYILRFKEMYQQNVRFKTKRE	442
XP_018096331.1[X.laevis]	---HANSTICSSDLENFYQS-----NQTAADVFKFAGKHKYSLSPKNNVQRNLQYETKRR	421
XP_416333.5[G.gallus]	---RAAATVSSDLEKAYTV-----GNSAKLNFKAGVHVELDFGAMTQKNRLVYETKRR	544
NP_766481.2[M.musculus]	--HPVTISSSDVEKAYLAFCAQADQAATLKFQAGKHNVELDFKAFQKNLIVYETKRR	465
NP_073587.1[H.sapiens]	--HPVTISSSDVEKAYLAYCTPGSDQAATLKFQAGKHNVELDFKAFVQKNLIVYETTKK	455
XP_024106109.1[P.abelii]	--HPVTISSSDVEKAYLAYCTPGSDQAATLKFQAGKHNVELDFKAFVQKNLIVYETTKK	455
XP_019640190.1[B.belcheri]	VRRRPKFVSEEDVKNPPKPPASRAKSARSASAWDESAPAHWSPMSD--DDEFVKVDVVG	503
XP_032833032.1[P.marinus]	VRRRPPLLVTARDVEVARERHAS-----LSRTGVGVSFAHWDRASLSDVDISLVELVNT	528
XP_014003371.1[S.salar]	VRRRPCLSGQDVEAKLKGSGP-----ESTSSSTVSVPHPHWDKALPDTYKLVPLLDQ	496
XP_018096331.1[X.laevis]	VRRRPVFSVGDKVKKRSTSE-----P--SKEDKNTPEHWDKQTPDLGYKLVLVLSPL	473
XP_416333.5[G.gallus]	VRRPKFVSPQSEVERIRKRGFK-----N--TEELRRIPSHWDKALPDELFGKLTLDSS	596
NP_766481.2[M.musculus]	VRRPKFVSPQDVMQKSCNT-----K--LHGPKSIDPYWDPAALPDLGFKKITLSSS	516
NP_073587.1[H.sapiens]	VRRPKFVSPQDVTMTQTCNT-----K--FPGPKSIDPYWDSSALPDGFGKITLSSS	506
XP_024106109.1[P.abelii]	VRRPKFVSPQDVTMTQTCNT-----K--FPGPKSIDPYWDSSALPDGFGKITLSSS	506
XP_019640190.1[B.belcheri]	SAEYRNKVLTFEQGGM-AGTAIAGVKRVQNAFLMSAYNRKKAQLKKQNGKDAERLLFH	562

XP_032833032.1[P.marinus]	TSEYKEVATLKFNTLSQPSINILNVKRVQNLWDAPQKREWMRKNKGVEVEERKLFH	588
XP_014003371.1[S.salar]	MTEYQMVSLSFKRTMT--STIHKINRIQNPSLWRFQWQKEQMKVKNGKLVDERHLFH	554
XP_018096331.1[X.laavis]	SEESKIEAMFCRTLRT--IRIHSIERIQNLALWEVYQWQKEQMKKLNKGKDPEERQLFH	531
XP_416333.5[G.gallus]	SEYKNKVGDFQRTMPK--THIKRICRIQNPSLWELVQWQKEQMKQKNGGK-TDERFLFH	653
NP_766481.2[M.musculus]	SEYQKVNINIFNRTLPP--YFVQKIERIQNMGLWEVYQWQKQKQNGGKEVDERQLFH	574
NP_073587.1[H.sapiens]	SEYQKVNINIFNRTLPP--YFVQKIERVQNLALWEVYQWQKQKQNGGKAVDERQLFH	564
XP_024106109.1[P.abellii]	SEYQKVNINIFNRTLPP--YFVQKIERVQNLALWEVYQWQKQKQNGGKAVDERQLFH	564
	** : * . : : *:* ** : : : : * * :** **	
XP_019640190.1[B.belcheri]	GTQDAVVDAICQNFDMRLSGSRVGQLYGQGTYSASAQYSHSYAQQA--SNGRRYMFV	619
XP_032833032.1[P.marinus]	GTRPKHVVPICQNIQNDWRLRGA-HGTAYGEGSYFARDASYSHYSKGRGTAPASAAFL	647
XP_014003371.1[S.salar]	GTEPSIVDAICEQNFDMRVCGI-HGSHYKGGSYFARDALYSNRFSSKSS--VSGKKIMFV	610
XP_018096331.1[X.laavis]	GTRVKKHIDAICQNFDMRVICGV-HGTVYKGGSYFARDASSYSHNYCKRS--SSQANIMFV	587
XP_416333.5[G.gallus]	GTSKKHIDAICHQNFDMRVICGL-HGTVYKGGSYFARDASYSDAYCREG--SCSKTMMFQ	708
NP_766481.2[M.musculus]	GTSANFVDAICQNFDMRVICGL-HGTSYKGGSYFARDAAYSHHYSKSD---THSHMMFL	629
NP_073587.1[H.sapiens]	GTSANFVDAICQNFDMRVICGV-HGTSYKGGSYFARDAAYSHHYSKSD---TQTHTMFL	619
XP_024106109.1[P.abellii]	GTSTIFVDSICQNFDMRVICGV-HGTSYKGGSYFARDAAYSHHYSKSD---TQTHTMFL	619
	** : **.*:*:* * * **.*:*:* : : ** . : : **	
XP_019640190.1[B.belcheri]	VRVLVGAYTQGDAGIRPPPPVNP-----EPYGRMYDSCVNDTANPNIFVIFDNAQCY	672
XP_032833032.1[P.marinus]	ARVLVGRYTCGKAGYVRPPPAIKASPSTAGQPAPEVYDSCVNTIEDPSIFVVFERDQIY	707
XP_014003371.1[S.salar]	ALVLVGEFTKGNRDYLRPPPKGKTK-----KRLYDSCVDSSENPALFVVFQKQIY	660
XP_018096331.1[X.laavis]	ARVLVGNFTKRGHSSYLRRPPSKSEF-----RSTSFYDSCVDSSENPALFVVFQKQIY	639
XP_416333.5[G.gallus]	ARVLVGEFTVGRSSYVRPPLKDN-----QNFYDSCVNSSENPALFVVFQKQVY	757
NP_766481.2[M.musculus]	ARVLVGDFVGRGTSFVRPPAKEGQ-----SNAFYDSCVNSMDSPTIFVVFQKQVY	680
NP_073587.1[H.sapiens]	ARVLVGEFVRGNASFVRPPAKEGW-----SNAFYDSCVNSVSDPSIFVVFQKQVY	670
XP_024106109.1[P.abellii]	ARVLVGEFVRGNASFVRPPAKEGW-----SNAFYDSCVNSVSDPSIFVVFQKQVY	670
	. **** :. * . *** :***** :* ***:*. * *	
XP_019640190.1[B.belcheri]	PEHIIY-----	679
XP_032833032.1[P.marinus]	PEYVIEYQF-----	716
XP_014003371.1[S.salar]	PEFVIEYS-----	668
XP_018096331.1[X.laavis]	PEYLIKYSK-----	649
XP_416333.5[G.gallus]	PEYLIYLDQACARML-----	773
NP_766481.2[M.musculus]	PEYLIQYSTSSKPPASPSIFVALGNLFTSRQ	711
NP_073587.1[H.sapiens]	PEYVIQYTTSSKPSVTPSILLALGSLFSSRQ	701
XP_024106109.1[P.abellii]	PEYLIQYSTSSKPSVTPSILLALGSLFSSRQ	700
	**.:*:*	

Percent identity matrix:

```
#
#
# Percent Identity Matrix - created by Clustal2.1
#
#
1: XP_019640190.1[B.belcheri] 100.00 33.28 34.61 33.98 32.97 31.43 33.04 32.87
2: XP_032833032.1[P.marinus] 33.28 100.00 37.08 39.00 38.62 38.58 39.63 39.63
3: XP_014003371.1[S.salar] 34.61 37.08 100.00 45.92 45.40 45.64 46.13 46.13
4: XP_018096331.1[X.laevis] 33.98 39.00 45.92 100.00 50.94 51.88 51.49 51.64
5: XP_416333.5[G.gallus] 32.97 38.62 45.40 50.94 100.00 54.20 54.41 54.41
6: NP_766481.2[M.musculus] 31.43 38.58 45.64 51.88 54.20 100.00 81.03 81.43
7: NP_073587.1[H.sapiens] 33.04 39.63 46.13 51.49 54.41 81.03 100.00 97.71
8: XP_024106109.1[P.abelii] 32.87 39.63 46.13 51.64 54.41 81.43 97.71 100.00
```