

PARP4

Sequences :

>NP_006428.2 protein mono-ADP-ribosyltransferase PARP4 [Homo sapiens]
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IANPDIWKSIREKRLLDVKNYDPYKPLDITPPDQKASSSEVKTEGLCPDSATEEDTVELTEFGQNV
EIPHLPDQDFEVAKYNTLEKVGMEGGQEAUVVLEQCSRSDRCFFLISSHFLLDGGMTRRQFAIKKTS
ASEYFENYIEELKKQGFLRREHFTPEATQLASEQLQALLLEEVMNSSTLSQEVSDLVEMIMAEALGHLEH
MLLKPVNRISLNDVSKAEGILLVKAALNGETAEQLQKMTEFYRLIPHKGTMPEKVNGLGLAKKADLC
QLIRDMNVNVCETNLSKPNPFLAKYRALRCKIEHVEQNTTEFLRVKKEVLQNHHSKSPVDVLQIFRVGRV
NETTEFLSKLGNVRPLLHGSPVQNIIVGILCRGLLLPKVVEDRGVQRTDVGNLGSgiYFSDSLSTSIKYSH
PGETDGTLLLCDVALGKCMDLHEKDFSLTEAPPGYDSVHGVSQTASVTTDFEDDEFVYKTNQVKMKY
IIKFSMFGQIKDFHPSDHTLEEYRPEFSNFSKVEDYQLPDAKTSSTKAGLQDASGNLVPLEDVHIK
RIIDTVAQVIVFQTYTNKSHVPTEAKYIFPLDDKAAVCGFEAFINGKHIIVGEIKEKEEAQQEYLEAVTQG
HGAYLMSQADPVDVTVSGNLPKPAKVLIKITYITELSLGTVGVFMPATVAPWQQDKALNENLQD
TVEIKICKEIGTKQSFSLTMSIEMPVYIELFSDTHELKQKRTDCKAVISTMEGSSLDSSGFSLHIGLSAAYL
PRMWVEKHPEKESEACMLVFQPDLDVLPDLASESEVILCLDCSSSMEGVTFLLQAKQIALHALSLVGEKQ
KVNIIQFGTGYKELFSYPKHIITNTMAAEFIMSATPTMGNTDFWKTLRYLSLLYPARGSRNILLVSDGHL
QDESILTQLVKRSRPHTRLFACGIGSTANRHLRLILSQCGAGVFEYFNAKSKHSWRKQIEDQMTRLCPS
TCHSVSVWQQLNPDVPEALQAPAQVPSLFRNDRLLVYGFIPHCTQATLCALIQEKEFRCTMVSTTELQKTT
GTMIHKLAARALIRDYEDGILHENETSHEMKKQTLKSLIIKLKSNLSLTQFTSFVAVEKRDENESFP
IPKVSLLIAKEDVDVFLPYMSWQGEPOGAIVNRQSLASSEWPELRLSKRKHKKIPFSKRMKELSQPEV
SEDFEEDGLGVLPAPTSNLERGGVEKLLDLSWTESCKPTATEPLFKKVS PWETSTSSFFPIALAPVGSYLPPT
ARAHSPASLSFASYRQVASFSGAAPPQGFDAQSQGVPGTCADWIPQASACPTGPPQNPPSPCYGIV
FSGSLSASQASAPLQHPGGFTTRPSAGTFPELDSQPLHFSLPTDPIRGFGSYHPSASSPHFGPSAAS
LTANLRLPMASALPEALCSQSRTTPVDLLCEESVGSLEGSRCPVFAFGSDTESDELSEVLQDS
CFLQIKCOTDKDLSILCFLEVKEEDEIVCIQHWDAPVWTELLSLQTEDGFWKLTPELGLILNLTNGLHSLFKQK
GIGSLGKVGRECLLDLIATMLVLQFIRTRLEKEGIVFKSLMKMDASISRNIPWAFEAIKQASEWVRRT
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>NP_001125927.1 protein mono-ADP-ribosyltransferase PARP4 [Pongo abelii]
MMMGIFANCIFCLKVKVLPQOQKKKLQTDIKENGKGKFSFSLNPQCTHILNDADVLSQYQLNSIQKNHVH
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EIPHLPDQDFEVAKYNTLEKVGMEGGQEAUVVLEQCSRSDRCFFLISSHFLLDGGMTRRQFAIKKTS
ASEYFENYIEELKKQGFLRREHFTPEATQLASEQLQALLLEEVMNSSTLSQKVS
DLVEMIMAEALGHLEHMLLKPVNRISLNDVSKAEGILLVKAALNGETAEQLQKMMAEFYRLIPHKGTTMPKEVNGLGLAKKADLC
QLIRDMNVNVCETNLSKSPSPFLAKYQALRCKIEHVEQNTTEFLRVKKEVLQNHHSKSPVDVLQIFRVGRV
NETTEFLSKLGNVRPLLHGSPVRNIIVGILCRGLLLPKVVEDHGVQRTDVGNLGSgiYFSDSLSTSIKYSH
PGETDGTLLLCDVALGKCMDLHKKDFSLTEAPPGYDSVHGVSQTASVTTDFEDDEFVYKTNQVKMKY
IIKFSMFGQIKDFHPSDHTLEEYRPEFSNFSKVEDYQLPDAKTSSTKAGLQDASGNLVPLEDVHIK
RIIDTVAQVIVFQTYTNKSHVPTEAKYIFPLDDKAAVCGFEAFINGKHIIVGEIKEKEEAQQEYREAVTQG
HGAYLMSQADPVDVTVSGNLPKPAKVLIKIAYITELSLGTVGVFMPATVAPWQQDKALNENLQD
TVEIKICKEIGTKQSFSLTMSIEMPVYIELFSDTHELKQKRTDCKAVISTMEGSSLDSSGFSLHIGLSAAYL
PRMWVEKHPEKESEACMLVFQPDLDVLPDLANESEVILCLDCSSSMEGVTFLLQAKQIALHALSLVGEKQ
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QDESILTQLVKRSRPHTRLFACGIGSTANRHLRLILSQCGAGVFEYFNAKSKHSWRKQIEDQMTRLCPS
TCHSVSVWQQLNPDGPEALQAPAQVPSLFRNDRLLVYGFIPHCTQATLCALIQEKEFRCTMVSTTELQKTT
GTMIHKLAARALIRDYEDGILHENETSHEMKKQTLKSLIIKLKSNLSLTQFTSFVAVEKRDENESFP
IPKVSLLIAKEDVDVFLPYMSWQGEPOGAIVNRQSLASSEWQKLYSSKPKLAKRKKKLSQPEVSEDFEED
GLGVLPAPTSNLERGGVEKLSDLWTESCKPTATEPLFKKVS PWETSTSSLFVGSPPVVGSLYRPTAHAP
RAASMPFASYCQAASFSGAAPPQGFDAQPQSPAPGSCADWIPQASACPTGPPQNLSFAPFCGIAFSGS
SLSPQTLPFPQFPFGGCTTRPSAGTSPELDSQPLLFSLPTDPIRGFGSYHLSASSPHFGPSAASLTAN
LRLPIASALPEALCSQSQTTPVDLLCQESVGSLEGSRCPVFVRSSDTESEDELSEVLQDSRI
LKICOTDKDIPCFLEVI EDEIVCTQHWDAPVWTELLSLQTEDGFWKLTPELGLILNLTNGLHSLFKQKIGS
LGIGRERLLDLIATMLVLQFIRTRLEKEGIVFKSLMKMDPSISRNIPWAFEAIKKASEWVRRT
EQYPSICPRLELGDWDSATKQLLGLQPVNTVSPLHRVLHYSQG

>EDL36193.1 mCG130836, isoform C_a [Mus musculus]
MTLGI FANCIFCLKVKVLPQOQKKKLQTDIKENGKGKFSFLNPQCTHIVIVDSADVLSRCHLSIQKNDVQ
IANPAFIQDSVQRRLLDVKNYDPLSPAPAAPPAERSRSEVQSEYLPDNTPEKENTEVTEVSAENVEIP
PFIQDFEVVKYNIILEKVGGPETVVVELQSSQDPESC
PFVITAHFLADQKTRESTGKQTEGAEIYYES
YVEDLKQGGFLQEHFTAEATQLASEKLQALLLEEIVSSGALSQEVSDLLEVIWTEALGHLENTLLKPVN
MSLNDVSKAEGILLVKTALKNGDSPGLQKTMAEFYRLIPHRHPASEEVRNRLLLAQKEDLCQLVRDMV
NVCETNLSKPNPFLAKYRALRCKIEHVDQNTTEFSRVKKEVLQNNRSEQPV
DILQIFRVGRVNEATEFLSKLGNVRLLFHHGSPVRNIIIGILSRGLLLPKVAEDRGVQRTDVGNLGSgiYFSDSLSTSIKYAHAGETDGS
RLLVCCDVALGKCVNLFFKDFSLTEAPPGYDSVHGVSSETTSVP
TFDQDEFFVYKTNQVKMKYIVKFC
TPEGDIKEPHPHENTEEVEQRAEPSSVPEAGDFQLPDIKPFPTNIKAGLQDASANPVPLDSVHIKGRVDFVA
QVIVFQTYTNQSHVPTEAKYIFPLDDKAAVCGFEAFINGKHIIVGEIKEKEEARQEYREAVSQGHGAYLMD
QDTPDVTTVSGNLPFRRAKVLIKITYITELSIQSPVAIFFIPGTVAPWQQDKALNENLQD
TVEIRIKEI GAEQSFSLAMSIEMPYMEIETSSDTHELRKQSTDCKAVSTVEGSSLDSSGFSLHIGLRDAYLPRMWVEK
HPEKESEACMLVFQPELADVLPDLRGKNEVILCLDCSSSMEGVTFLLQAKQVALYALSLLGEEQKVNIMQF
GTGYKELFSYPKCIITDSKMATEFIMSAAPSMGNTDFWKVRLYLSLLYSEGFNRILLISDGHLQSES
LTLQLVKRNIQHTRVFTCAVGSTANRHLRLILSQCGAGVFEYFNSKSKHSWKKQIEAQMTIRIRSPCHSVSVK
WQQLSRDAPEPLQAPAMVPSLFRNDRLLVYGFIPHCTQATLQAFIQEKEFRCTMVSTTELQKTTGTMIHKL
AARALIRDYEDGILHDETNEHEMKNMKSLIELKSNLSLTQFTSFVAVEKRDVNEIPFANVPNIS
SELVAKEDVDVFLPYMSWQGEQPEASISQTEIDSSRLKHNLSDGHGVLQLSHSPNLSEIPTIHSEPEPLLP
KDLCSRDMGFSCGTAFGSFASSKDFDPGKFSQGPNNISFSPKAPMGVHLQSPFCSPKPPSAPPLVTN
VILCSSEAPQSYFLNLQSAAVHQSPNNRVSEIIMESVLESSLPSDYSSRDASSYLALGAEDSLLGSSS
FETDTEAAATPANDLLTSIETSSDEEACFDEQESPVWASLFA
LQTENGFWKLTPELGLILNLTNGLHSLFKQKIGS
LLEEKGIRSLGTGKERLLDLIATMLVLQFLYTKLEQGMVAKSLIKMDDAFISRNIPWAFENIKKAREWA
RKTEGQYPSICQRLGLGDWESATKQLLGIQPAQNTSLHRLIYYSGQ

>XP_046764289.1 protein mono-ADP-ribosyltransferase PARP4 isoform X1 [Gallus gallus]
MTIFANCVFFIKLKYSSIQKNSLKACIEENGGAIDFVLNNKCTHVLVDNANVLSHHNLKITQKYQLPVL
YADFPVMSVENGKLLVTDAFEVNTSQGNISNQWPGGHGLEDLSSENKIATNQNESNDSNLTVIGESDKR
IEFPKVGTLRPHSENASVPQDFEVAKYNVLEKINSKGSKDFVIELHCSQEYELFRLCAHFSASNGTK
KDKQFPI NKTADEIRENYDILVANLKSQDFLLRETFFPEAECLASTKLQKLLLEESINSSAICQEVSD
FVLEIWAELAGHLDSLLLESVNNISLNDVSKAEGILLQVKNALNEGANE
TALQEMMEFYQLIRHKTEIDYE VTKRLLSRQDLQLMRMDLNI
RETSMSCPNPSSLAKYQALRCKIDAVDPMSDEFLQVERQVLKNYNGC
SVRIILQVYIRIGRVSETAEFLGLSGNVRSLFHASSVRNMGILSRGLLMPKVVVEDHGVERTD
TGNLGSgiYFSDYSASVYSSPSEMDGTRLLAVCDVALGSCDLDERDFS
LNAAPSGYNSVHGVRKATADVSSDFEDDEFVYKTTQVKIRIVVKFLCAEDQIKQFP
GTEVEIEQDNTPESQCHLQNESYELPSRANISDTVTKTGLQ
DRVGNVPLESVHIKARIDFVAQVMFQTYTNQNSPTEAKVFPFLDDKAAVCGFEAFVGRHIIIGQK
EKKQAHREYKAIISEGDAYLMQDADPIVITVGNICFNSYLIKITYITELSLCNGCITFFHMPASV
SPWQDKALNENTQDTTIKKICVQKQVETLKKFSLDMSIEMPYSIESIHSWTHKLKIKTECKAVIKTVENS
SLDSSGFGDLWISHAYLPRMWVEKHPNKNSEACMLVFQPEFAAFDEEQLSSEIIILLDCSNMAGS
ALLQAKQIALHALKQFSRRQNVNLIKFGTGNFSEFSSFSKNTSKDLASL
TEPTSATATMGNTDLMKTLRYLSLLFPQSGHRNILLISDGHLQNESVTFQLVKNVHHTRL
TECGVSTANRHLRLSLSQYGAGAFEYFDSKSKYNWEAKIQNVQSRIFSPGCS
SVSIKWOQFDINAPKPMQAPAIQSLFTNERLLVYGVPHCTQATLRAILIN
DQELQTVVSTTELQKTTGTVTLHKLTARAFIRDYEDGILHENETHEHEMKQILKNMI
IHLSMENSIITQFTSFIAIEKRKDANEICSANVPNILEIIAQEDVDVFLPYM
NWEQKPMGSGTLFSGEPIGPPFDVALQSDAQS DCTFTKRC
TEGLQLQPEDLTVTKESIQSEVIPQDYGFHDDDIATVKFAAAMPFVCKP
PFVMSYCNTAPLFGSAGAAVMTQKNSFPTPALASSGAHLRLCGSPVYSPSP
PLVGMKYDNSFVDHINPTIMFGSCASTYSSDKTNAEKQVTHNSPV
PQHHKTKLKAKYRKMVTLGLQDATASEQFERPKRLLQSPCFITTEKERSQ
QKLELTPVMWEEIFDLQNGQSGWNLSPLQGLKILKFDVYLIINHFLIRNGI
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VHWAFFESIKKATEWVKRVEGQFPFICYRLELGDWDSATKMLG
IKCN

>XP_041440458.1 protein mono-ADP-ribosyltransferase PARP4 isoform X2 [Xenopus laevis]
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IVDSHF1WKCLEEKCLILDYQYLTAGVTPSEKEPQSQWADPEKTVF PENVPTLQNKDELWDRDYSEFDS
TFTDPPTDEVAKYSFFHKGSNVAFLELLCFPESSSFLFKISKVICSNGAEPDSSSQFANTAEASCQKYE
KCTEALKEQGFKRVKRIPPKVALLTSEALQKVLEEA1NATKLSPVVGYFVESVWTEALGHDKILSRPV
NSISLNDVSKAEGILLQVRKALDTGTPEGDISKAMAEFYRLIPHKKPMLVNIINKLLSTKQDLCLQILRDM
VSVCTENLSKNPFSILAKQALRCQIEHVESDTEEFHQVVSQQIRENKHCEESIKLKI FRVGKLSEATGF
QNLGNVKSLLHSAHSPHFVGLSKGILLPKNVEDDLGERTDIGNLGSQIYFSDSISTGVKYSEPSVTN
GARLLLVCDVALGNCKDLKYKDRFSLTEAPNGDFS VHGVRQVFGRKSDFEDEFEVYYSKDQVVMKYVQVFC
TAKDQVMEHDKLPVWVEPTEDVGEEPVQAEDPMLENIPEFRS1KGGLSQVQGNQIPLENIHVKGRMD
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LMQDADDDITFVSVGNLPNATV1IKITYITELNLEYETVDFS1PGTVASWQDKALKENTQDTEVKICV
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CTSASVWVQFSENDPEFVQAPAH1PALFKNSCLLVYGFAPRCTQAKLQALIDDKELDTMASTTELTQKTT
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VPMNLE11SAEVD1L1PYMTWETENKKK1GVDFPGWKENFCGCGGVPVSDERASLDEEESLFFSFAPP
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PFPSPAPPPPPPLALGMPFSFAPPPPPPL1PAAKSHSTDEVYSLDVALLGAQQVSVCAPPPPPPPGSGIC
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SRRCRVGEAEVALSQKRERAPPVFNALLDLQCEGSVCAPP1R1R1SVTPPVVALSQKRGRALPAFNALLDLQ
CEEGYLLNEELGCLLNMNVN1LIEVFLSKNGIQSLGKKGEDELKLIATLLVLQ1TCTYELVNVTFKNL
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ES1V

>XP_014020296.2 protein mono-ADP-ribosyltransferase PARP4 isoform X1 [Salmo salar]
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KKHQTPVVVGYEYVSRCLEKGVL1LPVEDYCLPPPPSTSL1PRPASP1P1SLV1LKGTSQPAEYQIQTVNAV
NQAESAGNQERTY1LKGFRVYTESDNDLPTYPTNFQVAKYSIFGKANSTWSVLELQSGSTEGGQQYRVV
RYWRDEHGAKSAAVQDKQVFLSMSEEAEEVYQTLRKLELQVRGL1TRTTLTPPEAPY1LGSAS1QLLLEEL
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LLVY1TELLQDRQV1LQV1LRVNRGVELQMFREDLGNV1KPL1HSSSPSS1FV1G1LSRGLL1PRVGVHEH1GE
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SCKN1LEE1TAGLLDCS1GQ1PL1PQAV1HVAR1LMD1LSQV11FQTY1NTQSTAP1EAKYV1FPLD1SAAV1CGF
EAF1NGKH1VMGQVKEKQARKEYQAI1ERGHGAY1LMDQAD1P1VFT1SVGN1LPAGATV1L1KVT1FVTE1LVV
EGL1NFS1LPGSVAP1WQSS1ALNQRTQV1LEKVCV1TNLDSQGEF1SLDMS1IEMPN1E11NLHCL1THKV1IKRT
DCAV1NR1TCPGET1LPGD1LGF1VCS1LAQ11HL1PRMW1EKHPDKDSQACMLV1FY1DFDE1F1CPTSS1PMS1GSS1EVI
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VQGSTEL1WRFL1RSL1LLP1PSQV1RNL1LLSD1GHV1NQAL1TL1QLV1RQHA1QSRL1F1TCL1G1SPTAN1RML1AL
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YGV1PHCT1QAT1L1GDL1SQGN1E1TW1SVTE1LQ1KTR1GT1LHK11TARAV1RDYED1GSL1HTEAE1HEGKK1SVK1
SF1IELSEK1FS1LSQFT1SFVA1EERD1SEQ1PNV1GFTD1VPK1LS1DEVD1FLPY1LSW1LEE1YEGD1GMD1LSNS
MSN1LD1GG1PVR1LCN1I1CEE1MVME1GEEH1SV1LQ1VQD1DE1SWE1GLN1SY1L1MGS1MVF1GSP1VTV1SAAT1K1PP1DM
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QLK1SCAVAD1ALL1PP1AS1VVG1SGP1PP1PAS1V1SS1PGP1PSRL1Q1SFAA1VSD1AL1P1PP1FAV1LS1SGP1PP1S
RLQ1SFSAT1VS1DAL1P1PT1PAS1V1SS1PGP1PSRL1Q1SFSAT1VS1DAL1P1PP1FAV1LS1SGP1PSRL1Q1SFSAT1VS
DAL1P1PT1PAS1V1SS1PGP1PSRL1Q1SFS1DAV1SD1L1P1PS1AL1V1SNE1FRA1KH1MRG1HP1K1PGV1GAI1SHT1AT1FPK
1LQAG1DLL1LSK1PRE1YP1VEL1CET1SKMW1TD1NS1EDK1CGL1VEM1DHW1QPSV1V1PAS1V1SGP1SGF1GGGR1VGS
QSSQ1HSG1WFG1DTAN1ACY1PGL1FEASS1AG1SLFG1PTL1PYL1GSS1GR1SMGL1SFEAP1LT1GGH1LNS1PL1TTH1GFN
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1LQHS1EGW1ECS1AS1GLS1LLG1VDY1FAN1VL1KNRG1IS1SLG1VRAH1ADI1L1RLVAS1LL1VLQ1MRV1RLE1EGK1LL
1LS1FLR1DL1DHS1PQ1RCR1EWA1VR1RAV1DMV1CWAD1REY1PVC1SRLE1FGW1DES1STR1QLL1G1D1P1P1PL1SL1L
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>XP_032828733.1 protein mono-ADP-ribosyltransferase PARP4 isoform X1 [Petromyzon marinus]
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VDDDED1NR1PAF1PEEF1EMV1RSA1FCKT1SEKEQ1TKEQYMAV1VEQAA1PHSS1GL1VRVA1YAH1ATCKNS1DKYT
SRL1TK1RMA1GSG1REAE1VFLGH1ACE1VLT1GER1CMV1KVDQ1LPGDL1QLG1SRMF1QQAQ1TES1MAN1FHL1SKEV1GR
FVSTVW1SEAL1GHL1SLQV1ILL1EPK1QVTKAE1ILL1QLK1KAV1SKDV1HDEGAL1ERLS1NEFYK1IPQKHV
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C1LL1HLE1PNS1DFNS1IRN1QLL1QSS1HGR1LDG1FK1IK1FRVDR1PAE1IGQ1FRSE1VGN1TRSL1FHAF1APR1SLL1GI
LSRGL1LL1PKTV1VGE1FQV1ERT1D1GML1CG1YFSD1S1STS1VKY1ARRAA1RDG1GRV1LAV1DC1VAL1GRCH1LVR1RR
DRSLA1AP1QGH1DSL1HGARA1TPG1ASE1FED1EFV1YD1PRQ1K1RY1IVQ1FCL1SDV1K1EENS1DAEE1FYEA1P
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IEAKY1T1P1DEMA1A1VCS1FEAF1NGKH1V1GV1KEKE1TAHQY1RNAV1SQGH1AY1LMD1QES1PDV1FV1SVGN1LP
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1I1NVT1P1THAIR1KRT1ACKAV1LEASS1D1SLG1SE1FQL1LV1FPAQ1I1HEPR1MW1VE1QN1PETS1QAC1IL1TFY1PE
AP1SHS1EGVD1IV1LDC1SASMT1Q1PLTDV1KR1L1FAL1RHL1PPG1SR1FNV1L1KFG1HYKEL1FPV1FRESS1PNS1IA
TAVS1F1KR1HAD1AGN1ELMR1PLRS1VALL1AGG1VGS1RDA1AAP1PV1SVLL1TDG1VAQ1SEAR1ATREAK1ENVR1LL
RVL1AC1GVGET1PN1RY1FLN1ALARN1SG1GACE1FFTAKNR1STWT1DKM1ALMEKAT1QV1CRDV1T1VEW1QR1FDR1GAL1G
GDR1VEM1QAP1R1ISV1FCG1TRL1V1VY1G1VPHCT1QAT1L1HAI1NNQ1E1FT1MV1STN1LQ1TRG1MK1HLR1L1TAHA1I1
Q1VED1GN1LHP1DE1TQHEV1IAEM1KSR1L1EL1SKE1YS1I1TP1T1SFVA1VER1SD1T1ADEAT1G1PAL1DELL1SKE1SV
D1PL1YV1GW1VEE1KARKK1GSG1MFL1RAB1K1K1P1V1G1GRG1GLAS1SK1IKY1KTR1PAC1SL11PEK1TQ1PE1EF
GSA1ERAN1L1S1PTE1EAA1DAS1QV1PS1EQPK1FAH1SAVE1AP1CNS1NEG1P1NL1SRD1VKD1HG1VSAS1R1TMSA
SSRF1GER1HL1LHRA1PV1L1KEAF1ECRR1SQ1GCG1FS1AYAPR1SV1VH1Q1LNSA1ET1PV1L1RAQ1AF1L1T1FND1VQ
PGV1SLG1V1I1MET1PSR1TPPY1QD1TER1GQARR1QSD1R1FNS1AY1P1FK1QK1LAR1VKK1PP1PL1LC1TAR1SPSS
AAL1MPD1VELH1RAAG1LSRV1PECAK1RDV1CAL1Q1PNR1D1SP1PTD1PE1P1R1L1P1PP1PAQ1HAS1RG1QPM1HDD1FQS
ST1CQAAS1RL1CEE1SP1GG1SN1LSE1FSD1GYM1PF1ESC1LM1FHT1SPGV1SLCG1SG1SSE1SD1TT1PWQ1HAD1LS
KIT1CT1QNK1DGS1WDG1VEL1SSL1GWS1PDH1TV1ILK1QGI1QSL1GLR1MEE1A1VRL1VW1TL1VL1QL1RL1RML1GAS
SLNE1FV1LLL1RRD1VST1AEL1DMF1G1SAD1AFARA1SW1R1STES1VCP1CVCT1R1EL1G1PNW1QAAT1CS1LL1GVA

>XP_019636962.1 PREDICTED: poly [ADP-ribose] polymerase 4-like [Branchiostoma belcheri]
MIFQPPEASSKEK1WKEGEK1GPDGAFKHPD1MEG1SVSD1PLLVD1GRF1EVARY1VFLQKDHCKV1TKKGAAAP1VV
QVLELQV1ASG1D1PDSK1GE1FKY1R1VMT1QETG1KA1EY1YMQ1TAGE1AVQV1G1LYDR1CTKH1PHS1YSRLAP1DGD1T
PWT1VGS1QL1HQML1REVEAR1PSS1V1PRVL1G1VDS1LMEET1LGN1SH1LTG1DV1LN1LDQ1EKA1E1LL1QLK1Q
AVERK1APNDEL1QKLS1EFF1SAI1PHRP1DHKDT11KNK1RE1ARK1QDMC1QL1RDM1SVSEAT1GWT1SHPS1AVARY
HAL1RCN1QSLAR1DSE1DYRT1LESM1HSS1QENG1TP1K1KVES1FVR1C1R1SMEET1GFT1SAI1GN1QT1KFHSS1QAQ1N
FV1G1LSR1GL1MLPK1VV1DDF1GG1TR1D1AGM1LGH1Y1FSD1AST1SAK1Y1SSPSK1TRGR1K1Y1MV1SEVAL1GKCK1D1VY
QQD1TSL1Q1PP1Q1G1NSV1HG1VNR1TDD11P1SE1FKDNE1Y1V1NNQ1Q1K1MY1L1VE1FL1SP1DQ1Q1TV1P1VDEA1YL1HL1LT
F1VE1IE1ED1Q1D1NK11S1LED1VQ1N1AD1PL1DK1V1K1G1L1SK1SGEEM1P1VL1K1SV1HV1RAK1LD1LAQ1V1VL1Q1SK1NE
NNVA1EAK1V1F1FL1DMA1V1GV1PEAF1NGKH1V1GV1K1E1K1E1AH1REY1QAI1SEGH1AY1LMD1EET1FV1F1TV1SV1G
N1FL1PRAS1VL1KIT1Y1SEL1AVE1G1EN1IC1FL1PG1SVAP1WQ1K1D1S1EE11QK1D1ETV1KY1G1K1D1AG1KE1F1SLQ1VAME
MP1D1RT1T1Q1SP1SHK1IR1VKT1ASKAV1LE1EKN1CML1GD1GFL1LQ1GLAE1IH1VR1MW1VER1HP1DKDS1QACML1TFY
PE1QAE1VM1QGHEV1ILL1DAS1N1MR1GS1PLEA1AKK1VALL1CL1SH1LPKE1CS1FN1VAF1GT1GYE1EL1FV1S1Q1PRIKS
NVS1K1EA1NF1Q1DLK1ASK1GNT1DAWR1PL1HG1FLL1P1SPG1KTR1NV1FL1SDGH1V1NAD1Q1TSL1D1IAH1YLE1TRV1FS
CGV1G1ST1SNK1HLL1RA1IAR1VGG1GAF1EY1FDD1K1SK1WER1K1VKS1QLM1KAA1Q1GLT1SV1SV1D1WQ1QDD1D1APP1VQ1A
PNQ1IV1SL1FNG1SRQ1VV1GYV1PHCT1QAT1L1KAV1NNR1E1STM1V1ST1SELS1ITAG1K1L1HQL1TARAV1R1DME1DGT1L
HYDR1THE1TK1MGL1K1PY11S1LS1KEY1S1VT1QFT1SFVA1VEK1RE1Q1GED1LT1GDG1PT1KEL1VQK1ESVD1ILSYMG
WQ1QDE1GL1D1STEL1FEV1K1VGL1GLSD1GRD1PE1VR1VQL1TDD1SLV1LQ1RE1TVY1GNS1LAA1SS1QVNN1FD1SN
RERS1V1LR1QK1SGGL1GLS1IMG1AE1HN1P1VLL1S1IVK1D1QAAD1T1GQL1FV1GDA1IK1VGN1VNEH1STHDD1VQ1
HLK1NS1PDD1VK1LTV1RY1RAAT1PY1LAPAK1WS1RY1SSE1Q1CNG1NAS1PAD1NETT1SSEW1KAE1V1TDY1EDMS1CEMT1V
E1MT1L1GY1SEG1VQ1RMAG1ILD1SS1VE1LEE1SE1D1EME1FGL1FQ1EGWMA1A1DEE1KE11LAK1PEME1KK1V1ALLEK
CS1RLAS1PMS1RS1AVAT1STAY1S1PTS1TKL1VAYS1V1SKPS1QK1MAL1KRAE1KE1EAP1R1PET1DEV1TV1DT1LKAS
LDG1I1QAR1DR1LE1DL1EKS1DTL1SAA1PV1FFQAST1A1SEEL1FAATA1EPT1VHEAT1LESK1PAVL1RKS1GRAP1PK
GAR1FV1RE1PE1PV1SE1VAQ1SAP1SAAS1RAP1AGF1IP1PGAS1FGK1SAG1LVGG1PPT1AEET1K1KE1VAF1GGQ
FGSD1AV1SQ1GAG1GAT1PFGAP1L1DAT1PFGAP1PFGAP1Q1GAP1Q1GAAK1TK1QE1AQ1RGS1DAV1SQ1GAG1GAT1P
FGAP1L1GAT1PFGAP1L1GAT1PFGAP1Q1GAAK1KTQEAA1FGQ1GSSNAV1SRGAD1V1TFF1PGAT1SGAT1PS1A

TPFGGTPFASTISLFGHSTTAAKEPEAALFGPASSATPSGGGGFSGSTSSDIPLKDEDKSSVPIDSSKG
LKGPAPLEEKGTTTGFRRFGSSQAKMIPQGGGFI SHPQMQQQQQAQSNVDRARIPGRKAQSARKTTGGK
ALRPAADKVASDGVKADSPDVTVMFDESDDAKETKTPTSAKSPKLMIPATCCMCMVYDMPPLYYQQGSPFP
PAPSRGPPPLPPTSQQEPPPPPPPCAGPPLPAGAPPPPPQFRKSLLLALSQEKLGKSGSQSPTEMIQP
PPSRAPPPSMGRRPPPPPSMGRRPPPPMTRAPPNNMARLVRDADALYVYVLGETTKRMGARIGARIGAR
SLKAAELPKGEEEEPMEEVESPAICGEQVEESMDLKRKLKKKKVLELRAEFKKYSELFPVDEREERD
GRSSLLNQIMRGTSLRRGPGAYHSASPHTSDSAGYFSGTETVVVPVITTRSGSLTERTVDQLFALLKHT
DQGSWIEFSPELDQLLGISSSTCVQIFNTAGLRSLGAKVAKLLQLVATLLVLQLMLHLPLQFFPSSCSL
LHLDVMQVAEWRSAVQQVLAWAKGVDTMHPFSVSRLELGRKSWDDLTKKLIGVGVSLVHE

>XP_032219396.1 protein mono-ADP-ribosyltransferase PARP4 isoform X1 [Nematostella vectensis]

MSVTFPSGLLVLDSSGLPGFSFKQQLRSLKITSNGGTTSYILTKKTDYVLTSDGERTLSSYKGRATAAKL
GVVPVHIDFIDSLSSGLSAPDPTYILSETPEKQFSSGKIVITAPKGGCFNKKVSSSVQVLQADLSKI
RFFPYFKSGKPSYDEKSYEIAKHVLYQRRADAGEVLVFAIELHVIPPSTCFDGHYRVFHHHGNFKALK
EGNDAEQCTKECSYHGSSEALGTIYIALCAKVTQPPHNLTCCKWTLSSKIGSDMKKEESMDTRSSGEGES
VSQEVASLVLYLWTEAIGCLNSTLSVPLESIKLQKVQEAAILMSLKEEFNTQNKESIKSLMEEFDSLI
PHQIKIKDSTVNRGLIAEKQNLCLQIRDMVTISEATNMSTVSSHAKYKALRCHIEALHPFEEAEYKAIKE
LATIEEQTSNDIIVLNVFSLHRPVEDINRYHGLGRQKLLFHASRVNRFVGLSRGLLLPTIVVDDFGGQR
SDAGMLGHGIYFADRASTSAKYSPPGMLGSRFMLVNRKVALGKSEYRKFTKDLTRPPDGYNSVIGVKATE
TQPSDFKDDFVVYDTQQQMRYLEVFALPEDDI IARDNVSVDSGVVEEPLDNEDEIEVDLSDVMSIPDP
LLKVEAGLGKTDKADVPVLKAVHIRAKLLDLAAQVVMQAYCNNSDVPIEAKYVFLPDDMAAVCGFEAFIN
GKHIIGEVKEKEQARKEYREAI SAGHGAYLMDDEETPDVFTVNVGNLPPAAVSLIKITIYVAELTVEGELIC
FRLPGSAVPWQRQAADDVTQTDVDTICVDEENQSTNSVQVSEMPFEIRAILCPGHDVKVKRTSTKAVV
EMAPGGTLGSGFQLQIQLAELHVPFMMVERHDEADSGACMLAFYPEFESGPPHHVEVIFVLDASCSMGK
KALQEAARKLITMLCSLMEEEMAFNIVFVGSNYSELFTQSQKKDKETVARAAKFVKSVAKVGSTDLMRVL
RSLLYLLRNSADPNSNVFLFTDGHVTESETTLAIIRDILRLTRVFTFGVGTCTNRHFLRSMARVGAAGAY
ELFDSKYSKMERKVESQLSKAQPVLTLSVKVAMQQHDSYAKPVOAAPHIVSLFNGSKQVYVYGLVDNCT
QASLTAEDVGRVSVTWSLSELSITTKGVHLQJLARAARIOWEEGSLDPNHTKHMAKRDMDKPIISLSK
RFSIYVQFTSFVAIEHRKKDEKFDASLGPSIDELVSHEDVDVPIYVSWEEEPESRDVGKPESSSKSTGDRV
AGLVSEARVLERFSVLQAETLYKRACDTALSAESPONRATYKAFLSLAQFYVDVHGLQKAEALTMLHG
ALGGIEHDVSSRSRNFDDLLEHLRQDSSSYDEVGRIVAEFNPMKDKINKSKRVIASPPFNVDYPMWQTVVYN
KLFEACRSESTETGTSASSTSSSESEELSDNSEDSDWGSDEFYEDNIDDEVYQDAVGESEEEEGED
DVGCMLEAEAEVERSEAPTPLVIVDGSMMWKGFGAGDDAPKGVFPPIVGRPRHQGVMMGQMGKDSYVGM
EASHKRGILSLSTPQKREARPTPPLQDRPPPLQDRPPPEAMEGRALTDRVWIPFIEEAPLDHTASIDLEE
QEDLVVMDKGEVLDDGLFEAMCENNAQKAASLAMGKKRRQVDQLTLDSDYDIEHVLPSNTQVAATLDTD
DMVMDMNRATSSALKERAVSYDIQDLSCEVAEDAVKEEAEERPITAFGLDSCIARVSSSEKSSLYDEI
PSPNNRPFKKKVANIPSPKPRPPRASKIAAPPAAPSLQAVCIDLPEPPLKAGDSPLKRSVKAPLPPPPPPQ
ASRIIDYRASYGAAPAPSLQAVCIDLPEPPLKAGDSPLKRSVKPLPPPPPPQQAARIDYRASVGAAPLPP
KRGGGPPPLPKRGGGPPPLFGAMALRTGAPSKASKSPFGGRGQPVFATSAEILHPLARTPSELAPKGV
PSQTNDIEAPVMSRLQLLESIRAKKTKETDREDIMKQDSDGEADI LRREAHQHSMETLEADRNEAEMG
VRPFRKKGRKMLEKAAAEQKKEAMEEPSESLQNRMKRMWTADKLELFAHQNDGYWSEKELEVAFRDI
CSFLSRLLLNAGASLGDFAETILKMLTITII TLAILKTYLPDQFPVSLVQGVSSGLVTSSEWRNVQGRA
LSWLKMRMRKPSVCSRELGLPGDWIDVAKGIIIDDKVHLMI GVR

>XP_047129290.1 protein mono-ADP-ribosyltransferase PARP4 isoform X5 [Hydra vulgaris]

MFSGCIVTLDLITNASFREKEILRKAIIVNNGGVSYIITKSKTHVNVASKEFAQTSYRCERALKYGVFVV
TSDFTKSYEAGFLNHHESFLAFKIEKESVDLKSGLSTKSSNNNNCMKKVSEAEVLLNCRVMSDGKGP
WNNDLILFEPVKYFLLLSENSKDGNRPFCLIELHVSCDAGMARVMQVGNVTEKETSKNVCEYRAAKDAYE
CEITLFGACINQYKKEFQNKNELESEPLSKSYAIGSKYLYEWPGRNSEVTRTEMTNSHLNVNTIWAQAQNL
KDLLANSIHSYILADVRAEIGILLQICEFEEKDEKLTLEEYFYSIIKLKNNNVLDNAKII SRMFDLC
QVTKDVGVSSTNMKTIPIISNAKYKALGNIKELHYEALGELKTTISMSMEAKEIEVLSAFEINRISE
KGVDFVGFVFFHSTSTENLVGILSRGLLLPKVYVDQHGGERTDVGMNGYIFASAASTCIKYSKPSQTS
GSRFMLCELNLGKTKTYRKFKDLEAPAGYDSTHGKSTSNESPFDDEFCVYDVRQRITHIVEFK
LASDNVHHTLNNVDSEDEGISDFDSESELIKDVSVDQDPLSKVYVSLQSSNTQPVPLTAVHIRAKLQE
FSSEVVVLQAYRNDINPIEAKYVPLESSAAVCSFEAFINGKHIVGKVEKEQARKEYKEAIQQGHGAY
LMEEQESPDVFTVTVGNLPPNSDVLKITYVAELSLDDQISFSLPGCVAPVWKDQALATKMQNELETI
NVNNSGFEFSLEISLEMPCAIRSIVSPHTGNILIKKTATKAVVMKNDPLGTSFQLLIALAEIHVPRMMWQK
SPQDESQKACMLSPFFPEDGIDGHEVIFLIDASNSMKDHFIELQKLYLYTEKMPQSTKFNVMVFNFDY
KELFFYSRKFDESKQQVMSLLKLLKNCNGGTHLWSVLKMIEMLSCESTMKNVFLFSDGHI FDEISTLARI
RNLKNVRVLTFFGVGTTPNKHI LQKMACLGSGYFFEYFDNRNAKSKQKKVLELQLEKCCQPVLTNIKIHWIQ
HDEDAKPLQAPNEITTLFNGNRLVVGFPVPHCTMANLSAILNGKELNITVSTSELSTTVGLTIHRLAK
SVINDMDQMLHPOQYKHEAIIKARKKGLIQLSIEYSIVTKFTSFIAVEERKNKEGKVTAFTINELVIA
ETVDLIPMGFETKTSVPMQAKAFSLSEILDGMHMLKDELSLSEDDVDNDSLSLQSESEEEKLYKPK
IILDIGMAETKAGFAGCRAPKVIPTLVGRPRHQGVMMVGMQKDAYVNEALS KRGILLTLLSPTKLKDG
ETDSTPLQLIGDGTINIVKPTSKAINPKFKIAKCKREL SKGLSTLQHSVQQSINIDSDVDYQKSYIM
LTKQKECAEIEQTSDDFLSMQSDNLMMDYCEMLASKEIYLESDSVKDIHQFKLREKKSATPPSSSTRNV
SSLRKKQPFPEPMVSKVCLQAQMPLDMPMPPPQLMPLFGAKQPSAEPMMLKACSPAKMPDLPMPMPQLM
PLFGAKQPSAEPMMLKACSPGKTSFFSQPPPPPPAQSMYLFQAKQPLPEPTLSKDCPLGKTSFFSQPPPP
PPAQSMYLFQAKQPLPEPTLSKDCPLGMLGKKLAAAPPAQSVSLFGSNKSSLMFSRNCFSDDLGMFKR
EESHLDLDCDDLEMLADEKLSLDYRPAATGTISACHFVKPISCAYYEPCFLERKKTISIENGLSKSVDFCFFK
DEKFERFPLDGRSFVFLNKTSNEDLINTLEFLVENQHSDDGYWELEDIFDQDQSTISFDILFVDVCRKLA
LSLCEKYSSEIQRLIATIIIVCVI PKLASNDKALWSYPHYLRNESNKASDKLTSAPFFKGSYILHEDCK
FPSIHTRLGLGYSLEEMTFQVYRLASQSFDKRMELRL

>XP_019851276.1 PREDICTED: uncharacterized protein LOC100633591 isoform X2 [Amphimedon queenslandica]

MENLDSLFRGQITLELDSISPFKKKSAKQSVIQYGGIVSFIVTKKTHLVVNNVEKAQDSYKSRMAQK
WGIPVVVISKFIEDCIENKGLLEPDQFVVAGKTPSEELSSGKIVASMEDKSNDRKKRKPKNVNLNQIKV
WPMFHADGKMTPLFPEDGYEIVRHAFPKYKMSKLTSFVAIEIHVVPTSVTEDKPLYRVFVHKHGLEQR
LKTGELGTCECRIVETSLDAEAVIAYLQKQITSSPYSMERVQIQLSMIGSPGLRKLMSETWPRGVAGSRE
DLDBLVSKLYEYVSEALIEIGFPLTVLQNIKLQVEKEAEALMSIRKLLDEGRIGDDEDIKKTYKQYN
SALPNSKAPRIDSXKVIANRQEPFCQVIRDLVSVSESTNWSHKSGVPVAKYHALRCQMCPIDVPVSKEYSDVK
EHIMSSLTNDSNDPEILSIYSVQRVVEESQFSSHLSGNKRLFLHSSQLQNFVGLSLRGLLLPKVIVVDDPVG
SRSDPQMLGSGGIYFADSASLSVKFSQPKRHRGTRMLMNEVALGNVKEFTSYQKELLAAPNGFHSYKGV
KGTTEEPSDFKENEYVVYKTEQQRMRYLIEFRLPQDEEIQDQTESEKYEENEEIEDEESNIVTDGVSL
DVKNVTDPLSKVEAGLVKDGGVPLKAVHVKALQIDLAAKVIVLQSYKNESLVPTEAKYVFLDDMAAVC
GFEAFINGKHII GEVKEKEQAHREYQKAISEGHGAYLMDDEETPDVFTVSVGNLPPGASVLIKITIYVAELQ
AEGENVVFLSPGSVAPWKQEAALDETTQVDVEKVKRSDADLSVQISIDMPFTIRTIESPAHKIKMKKT
DTKATVELCPGEKLTGTGFQLLIGLAEIHVPRMVEENDKGHHACMLTFYEFEEAESIVENEIFLLDVSN
SMKGDALDNAAKVVLLLLLHHLPPKTYFNVFTFGAMFEIFFPSSVQINNETLSFATKQVQSCQAVMGNTDI
WRPLHSLYLLSEAASSSTGGLTNSSTLPPCSPFVIVSDGHMTEAPLSAIKDGAQNYRVFTFGVSSSTANR
HFLRSMARVGGCSEFFDSQKKSRRERKVKELSKAFQPALTGVGVQWQHEDENAPPIQAPKSIITSLFS
GSRQVYVGVPHCKQASLKAFI GRKEIQTMVSTSLDATTSGQTLHQLTAQALIRDWSEGLNDRDTEHEI
MKRDLKFTIINTSKEYSIVSQFTSFVAIEKREKDEKFDATKGPSIEDLVSKENVDKLYMGWEIQDQADP
VKIAAESIIDVVIASMAGETDVIKLDITAFNKNVSESTQNTLPNSHPARVKLLKMRLEVLLKMKDKLSDGQELL
EGLITDHLHRLGSDISTRILNVLEIGIRDGFSRMI DAKRKAEEAEAAARRSRMMI VAEAAKSLRQSTLETERD
GGIIEGARMEILKSRITAFKQKIEIESLESKLHLITRRRGRALKKDIIPAEERKASPKVPLKKKKAVAKNRGP
IRQESPEKDEISIVAEGRRSIRMEBEPDEEDIPVAVITDGMDTVAKGAGAGDGRSVFPAIVGRFRHQ
GVMMQMGKDSYVGEAKSKRGILLTKSPFERPSKPMMAASQPIVQYVEKEKESASVTEEDVNLNLFQ
YDGRNYESIDFSMAENYQVNEVLMDELEMDSELMQESLMVESAEIYEELEQOSEETIAYNQKELRSRKYK
KSIPGTSPTSLLLKGLGSKPEQEGQLGTGLAGFASKPPEGYLSLIDIEGLAMPANKETYSPLSQTYNPVSP
VYSPTSVTPSPAYSPTSPSYSPSLPSYVPTCTTSPAYNAPTNGKLSAPSVPGLTNRNSDKVSDSSSETSR
NLSQLSAYLGS GKSRFESVLSLEKSAPLSQPTAAPPSRSRIVRFEAGALTGSSSQAPLEVPVPPPLPP
RAVMTKSAPSEPIYPSFDGIPAFSVRNAISSSPGSPPELTWMSSPFKSPPLPRSAPLPGGPPAKPSRS
SGRALMQSGGPPPPPPPPGTGAPMQLSEKSPPPPPVPLRSRDRGPMVPQSTVLSGRPPPPPPPHFMLC
GEVPMPSGGPPPPPLPYLSRGIAQRLLPGGPPPPPPPPPGGAAGAPLPGSSKVA PKGKSKVSYAGLADKK
TTPQASPFSGAGGKKEPSGTGRGALLSSIKKGVSLQKVTEKKEEKSVASLMQALQSRKAPEAFNLKL
VDYSKWSVEMSDDDSDDDDEDDDEGGGGGGGRSLLVNEFFAFQDQERAEDKVQGESEEEEEESDNNMA
FGLFDSFDEEALSNASYSMSENAQESDGEKVI EVQNFVFINSSQIYMMYSLQKDDGSWLLSDLDITVIM
PGTGDRVLVNLNEAGAKSLGSRVYKELLSIATCTFVLRLLNLFNDAYKITFSPHFEIDMSNGDPGDIAT
PMKNSLVLCNKLHKQNPSVTRLELGYSLIDAVDKILKLA

Alignment

XP_047129290.1[H.vulgaris]	-----MFGSCIVTDLA--TNASFREKEILRKAINVNGGVSYIITKKSTHVVVA	48
XP_032828733.1[P.marinus]	-----MGLFSACFIVLDLP---SWPRQRRLQLKEQLTAHGAIIASHAVTSHCTHLVVS	49
XP_032219396.1[N.vectensis]	-----MSVIFSGLLFVLDDSSGLPGFSFKQKQLRSKITSNGGTISYILTKKTDYVLTS	53
XP_019851276.1[A.queenslandica]	----MENLDSLFRGCQTLELD--SSIPFKKKSALQSVTIQYGGIVSFIIVTKKTTHLVNV	54
XP_019636962.1[B.belcheri]	-----	0
XP_014020296.2[S.salar]	MDKSTYKSMAPFDCNCFVLELK---TLPYKEKKRKLKLAITENGSGISVYINKQCTLVVTI	57
XP_041440458.1[X.laevis]	-----MTVAIFSDCVFLKIN---DLSFKERKALKSTITSNNGVTSFVLNKKQCTHVNVN	51
XP_046764289.1[G.gallus]	-----MTIPANCVPFIKLK---YSSIQKKNLSKACIEENGGAIDFVLNNKCTHVLVD	49
EDL36193.1[M.musculus]	-----MTLGIFANCIFCLKVK---YLPQQKKKLLQTDIKENGKGFSLNLPQCTHIVID	51
NP_006428.2[H.sapiens]	-----MVMGIFANCIFCLKVK---YLPQQKKKLLQTDIKENGKGFSLNLPQCTHIIID	51
NP_001125927.1[P.abelii]	-----MMMGIANCIFCLKVK---YLPQQKKKLLQTDIKENGKGFSLNLPQCTHIIID	51
XP_047129290.1[H.vulgaris]	SKEFAQTSYRCERALKYGVVPTSDFITKSVEAGFLLNHESFLAFKIEKESVDE---LKS	105
XP_032828733.1[P.marinus]	AEG-AGSPSRLKLAAKHGVRVVCPEFLDRCFATGQLLEPALADDPADNNNIAGNEEREN	108
XP_032219396.1[N.vectensis]	DGERTLSYKGRATAAKLGVPVVIDFIDSCLSGGLSAPDPTYILSETPESKQFS-S---	109
XP_019851276.1[A.queenslandica]	NVEKAQDSYKSRMAQKWGIPVVSIKFIEDCIENGKLLPEDPQFVAGKTP-SEELS-S---	109
XP_019636962.1[B.belcheri]	-----	0
XP_014020296.2[S.salar]	SMS-SLSASRVRSIKKHQTPVVGVEYVSRCLEKGVLIPVEDYCLPPPPSTSLIPP--RPA	114
XP_041440458.1[X.laevis]	TIA-FLSASQLKTQKHQIQIVDSHFIMKCLEEKLLIDYQYLTAGVTPSEKEPQ-SWQA	109
XP_046764289.1[G.gallus]	NAN-VLSHHNKLTKQYQLPVLADFWKSVENGKLLVTDAFEV--NTSQGNISN-QWPG	105
EDL36193.1[M.musculus]	SAD-VLSRCHLNSIQKNDVQIANPAFIQDSVQRLLLDVRNYDP--LSPAPAAP---PA	104
NP_006428.2[H.sapiens]	NAD-VLSQYQLNSIQKNHVIANPDFIWSIREKRLLDVKNYDP--YKPLDITP----PP	104
NP_001125927.1[P.abelii]	NAD-VLSQYQLNSIQKNHVIANPDFIWESVREKRLLDVKNYDP--YKPLDIIIP----PP	104
XP_047129290.1[H.vulgaris]	GKLSLKSSNNNMCKKVS-----EAEVLLNCRVMSDGK-----GPMN	142
XP_032828733.1[P.marinus]	GV-VTSAIRT-KTRD-HKRGPPAEETFELNKNVKLVWDDD-----EDINRPA	151
XP_032219396.1[N.vectensis]	GKIVTAPKQG-GCFNKKYSVVQVLQADLSKIRFFPY-----KGSKGPSY	153
XP_019851276.1[A.queenslandica]	GKIVASMEDK-SNSDRKKRR--PKSNVNLIQIKVMPWPHA-----DGMKTPLF	154
XP_019636962.1[B.belcheri]	-----MIF-----Q-PPEA-----SSKEKVMKEGEGKPDGAFKHPDMEGSVSDPLL	40
XP_014020296.2[S.salar]	SPLPSLSVLK-GTSQ-PAEVQIQTVN-AVN--QAESAGNQERTYLGKFRVYTESDNDLFT	169
XP_041440458.1[X.laevis]	D--PEKTVF-----P-----E-----NVPTLQNKDELWDRDYSE---FDSETFT	143
XP_046764289.1[G.gallus]	G--HGLEDL-----S-SSENKIATNQNESDNSNLTVIGESDKRIEFKVGTLRFHSENASV	157
EDL36193.1[M.musculus]	E--R-----SR-----E-VQ--SE-----YLPSDNTEPEKENTEVTEVAENVEIPP	141
NP_006428.2[H.sapiens]	D--Q--KA-----S-SSEVK--TE-----GLCPDSATEEEDTVELTEFGMQNVEIPH	144
NP_001125927.1[P.abelii]	D--Q--KP-----S-SPEVK--TE-----GLCPDSATEQEDTVELTEFGTQNVEIPH	144
XP_047129290.1[H.vulgaris]	NDILFEVPKYFLLLENSKSDG----NRPFCLIELHVS CDG-----AMRWVCQYGN-	188
XP_032828733.1[P.marinus]	FPEEFEMVRSAIFCKTSEKQ---TKEQHMVAVVEVQAAPHS-----SGLVFRVAAYHATC	203
XP_032219396.1[N.vectensis]	DEKSYELAKHVLQRRADAQE---VLVFSALELHVIIPS---TCFDGHYRVFHHHGNF	206
XP_019851276.1[A.queenslandica]	PEDGVEIVMHAFFPKYKMKSK---LTSFVAIEIHVVPTS---VTECKPLRVFVHKHGL	207
XP_019636962.1[B.belcheri]	VDGRFEVARYVPLQKDHCCKYTKKGAAPVQVQLVQASGDPSSKGEFKYKVMT--QE-	97
XP_014020296.2[S.salar]	YPTNFQVAKYSIFGKANS-----STWSVLELQSGSTE-----GGQQYRVVRYWRE-	215
XP_041440458.1[X.laevis]	DPDDEFAKYSFFHK-----GSNVAFLELLCFPE-----SSSFLFKISKVICD-	186
XP_046764289.1[G.gallus]	FPQDFEVAKYNVLEKINSKG-----SKDFVVIELHCSQE-----QYEFRLFCAHFA-S-	205
EDL36193.1[M.musculus]	FLQDFEVVKYNILEKV---G-----GPETVVVELQSSQD-----PESCPFITAHFLL-	186
NP_006428.2[H.sapiens]	LPQDFEVAKYNTLEKVGMEG-----GQEAUVVELQCSRD-----SRDCPFLISSHFL-	192
NP_001125927.1[P.abelii]	LPQDFEVAKYNTLEKVGMEG-----GQEAUVVELQCSRD-----SRDCPFLISSHFL-	192
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XP_047129290.1[H.vulgaris]	--NVTEKETSKNVCEYRAAKDAYECEILFGACINQYKPEQNKNELSEPLSKSYAIGSK-	245
XP_032828733.1[P.marinus]	KNSDKV---TSRLTKVRMAGSGREAELVGHACEVLTGERCGMVKVDQ-LPGDLQLGSRM	259
XP_032219396.1[N.vectensis]	KALKEGNDAEQCTKECSYHGSSSEALGTYIALCAKVTQPPHNLTCWC--TLSSKIGS--	262
XP_019851276.1[A.queenslandica]	EQRKKTGEL--GTCECRYVETSLDAEAVYALCKQYTSSSPYSMERV-Q--YLSFMIGSPG	262
XP_019636962.1[B.belcheri]	---TGG-----AKERYMQTAGAEAVQVYIGLYDRCTKHPHYSKRLADGDTPTWVGSPQ	148
XP_014020296.2[S.salar]	---DHGAKSAAVQDKQVFLSMSEEAIVEYQTLRKLELQVRGLTLRTPL--PEAPYLGSA	270
XP_041440458.1[X.laevis]	---SNGAEP---DSSQFANTAEASQKYKECTEALQKQFKRVKRIIP--PKVALLTSEA	238
XP_046764289.1[G.gallus]	---SNCKKK---DKQFLINKTAEIRENYDILVANLKSQOFLIRETFP--PEACLASTK	257
EDL36193.1[M.musculus]	---ADQK-T---RESTCKQTSDEAIEYFESYVEDLKQOGLLQEHFT--AEATQLASEK	237
NP_006428.2[H.sapiens]	---DDGMEF---RRQFAIKTSEDASEYFENYIEELKKQGLLREHFT--PEATQLASEQ	244
NP_001125927.1[P.abelii]	---DDGMQT---RRQFAIKTSEDASEYFENYIEELKKQGLLREHFT--PEATQLASEQ	244
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XP_047129290.1[H.vulgaris]	---YLYEWPGRNSEVTRMTSNLSHLVNTIWADAQNLKDLLANSIHSYILADVVRAG	301
XP_032828733.1[P.marinus]	FQQAQTE-----ISMANFHLSKEVGRFVSTVWSEALGHLSQLQVPIILLIEPKQVTKAEA	314
XP_032219396.1[N.vectensis]	--DKMKESMDTRSSGEGESVQEVASLVVDYLWTEAIGCLNSTLVSPLIESIKLQKVQEAEA	321
XP_019851276.1[A.queenslandica]	LRKLMSETWPRGVAGSREDLPLVSKLVEYVWSEATGIEGLFTVPLQNKLEQVEKAEA	322
XP_019636962.1[B.belcheri]	LHQMLREVE-----ARPPSSVSPRVLGLVDSLMEETLGNLSHILTGVDVINLNDQIEKAEA	203
XP_014020296.2[S.salar]	LQQLLLEEK-----LSCSSLSQEVGVFVLLMAEALGCLDNVLKVPITSLSINDVSRAEG	325
XP_041440458.1[X.laevis]	LQKVLLLEA-----INATKLSPVGVGFVESVWTEALGHLDKILSRPVNSISLNDVSKAEG	293
XP_046764289.1[G.gallus]	LQKLLLEES-----INSSAICQEVSDFVELIWAELAGHLDSLLLESVNNSISLNDVSKAEG	312
EDL36193.1[M.musculus]	LQALLLEEV-----ISSGALSQEVSDLEVIWTEALGHLENTLLKPVNSMSISLNDVSKAEG	292
NP_006428.2[H.sapiens]	LQALLLEEV-----MNSSTLSQEVSDLVEMIWAELAGHLEHMLLKPVNRISLNDVSKAEG	299
NP_001125927.1[P.abelii]	LQALLLEEV-----MNSSTLSQEVSDLVEMIWAELAGHLEHMLLKPVNRISLNDVSKAEG	299
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XP_047129290.1[H.vulgaris]	ILLQIKCEFKKDD---EKLKTLSEFPYSIKLKKNNN-VLDNAKISRMPDLQCVIKD	355
XP_032828733.1[P.marinus]	ILLQLKKAVALSKDVH--DEGALERLSNEFPYKIPQKHVAVCPITGMASISAKLIDLQILRD	373
XP_032219396.1[N.vectensis]	IILMSLKEEFDNTQ---NKEKISKLWEEFDSLIPHQIKIKDSTVNGKLIAEQNLQCLIRD	378
XP_019851276.1[A.queenslandica]	ALMSIRKLLDEGRT--GDEDIKKYTKDYSALPNKS---APIDSKKVIANRQEFQCVIRD	379
XP_019636962.1[B.belcheri]	ILLQLQKAVERKA---PNDELQKLSSEFFSAIPHRPDHKDTINKNKEIARKQDMCQLIRD	260
XP_014020296.2[S.salar]	ILLQVQRKLRARQGEQPDTEVASIMEEVYTLPHKTDQSHLPLHTKLISSQLDLQCLIRD	385
XP_041440458.1[X.laevis]	ILLQVRKALDTGETF---GDISKAMAEFYRLPHKKFML-VNINKKLLSTQKDLQCLIRD	349
XP_046764289.1[G.gallus]	ILLQVKNALNEGANE---TALQEMMEFYQLIRHKTEID-YEVTKRLLSRKQDLQCLMRD	368
EDL36193.1[M.musculus]	ILLLVKTKALNGDSP---GQLQKTMAEFYRLPHRHPAS--EEVNLRLLAQKEDLCQLVRD	348
NP_006428.2[H.sapiens]	ILLLVKAALNGETA---EQLQKMMTEFYRLIPHKGTMP--KEVNLGLLAKKADLCQLIRD	355
NP_001125927.1[P.abelii]	ILLLVKAALNGETA---EQLQKMMAEFYRLIPHKGTTTP--KEVNLGLLAKKADLCQLIRD	355
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XP_047129290.1[H.vulgaris]	VVGVSSESTN-----WKTIPLSNARYKALGNIKELHYEAL--	390
XP_032828733.1[P.marinus]	VVDANEATNRKNKTGGDDSSMRKENLAKKLTASSHSAITLAQPTALRCSLHLHLEPNSSDF	433
XP_032219396.1[N.vectensis]	MVTISEATN-----MSTVSHLAKYKALRCCKIEALHPEEAAY	415
XP_019851276.1[A.queenslandica]	LVSVSSESTN-----WSHSGKGVAKYHALRCQMCPIDPVSKEY	416
XP_019636962.1[B.belcheri]	MVSVSEATG-----WTSHSAAVARYHALRCNQSILARDSBY	297
XP_014020296.2[S.salar]	VILNVSEATL-----RSPISPCGLKYKALRCSTIERVPPGPELL	422
XP_041440458.1[X.laevis]	MVSVCEATNL-----SKPNPSILAKYQALRCQIEHVESDTEEF	386
XP_046764289.1[G.gallus]	MINIRETSM-----SCPNPSSLAKYKALRCCKIDAVDPMSEF	405
EDL36193.1[M.musculus]	MVNVCEATNL-----SKPNPNSLAKYKALRCCKIEHVQDQNTTEF	385
NP_006428.2[H.sapiens]	MVNVCEATNL-----SKPNPSSLAKYKALRCCKIEHVQDQNTTEF	392
NP_001125927.1[P.abelii]	MVNVCEATNL-----SKPSPPSLAKYKALRCCKIEHVQDQNTTEF	392
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XP_047129290.1[H.vulgaris]	GELKKTISMS-SMEAKEIEVLSAFELNRISEKGG---VDFVGPFPHSTSTENLVGILSR	445
XP_032828733.1[P.marinus]	NSIRNQLQSSHGRLDGFKILKIFRVDRAPIQGFRSEVGNTRSLFHAFAPRSLLGILSR	493
XP_032219396.1[N.vectensis]	KAIKELATEE-QTGSNDIIVLVFSLHRPVEDINRYHGLGRQKLFLPHASRVNRFVILSR	474
XP_019851276.1[A.queenslandica]	SDVKEHIMSSLDNSNDPEILSIYSVQRPVVEESQFSHSLGNRKLFLHSSQLQNFVILSR	476
XP_019636962.1[B.belcheri]	RTLSEMIHSSQNGTTPPIKVESVFRVCRSMEEGTFTSAIGNIKTQFHSSQAQNFVILSR	357
XP_014020296.2[S.salar]	YVT-----EL-LQDRQVQILQVLRVNRGVELQMFRDLGNVKPFLHSSSPSSFGVILSR	445
XP_041440458.1[X.laevis]	HQVSQQIRENK-HCEESI KILKIFRVGLKSEATGQQRNLGNVKSLHLHASSPSHFVILSR	445

XP_04764289.1 [G.gallus]	LVQVERVQLKNN--YNGCSVRILQVVRIGVRSVTEAFGLSGLNVRSLFPHASVVRNFMGILSR	444
EDL36193.1 [M.musculus]	SRVKEVQLQNN--RSEQPVDFVIGVYFSDSISTSVKYARRAARADGRGLVAVCDVALGR	504
NP_006428.2 [H.sapiens]	LRVKEVQLQNN--HKSFPVDVLQVFRVGRVNETTEFLSKLGNVRFLHSGSPQVQNVGILCR	451
NP_00125927.1 [P.abelii]	LRVKEVQLQNN--HKSFPVDVLQVFRVGRVNETTEFLSKLGNVRFLHSGSPQVQNVGILCR	451

XP_047129290.1 [H.vulgaris]	GLLLPKVVVDVQHGGERTDVGMLGNGIYFASAASSTCIKYSKSPST--SGSRFMLLCELNLNGK	504
XP_032828733.1 [P.marinus]	GLLLPKTVGVGEFVERTDITMGLGCGYIFSDSISTSVKYARRAARADGRGLVAVCDVALGR	504
XP_032219396.1 [N.vectensis]	GLLLPTIVVDVQGGSRSDAGMLGHGIVFADRASTAKYSSPGM--LGSFRMLKNVAKVALG	536
XP_019851276.1 [A.queenslandica]	GLLLPKPIVVDVDFGGRSDPMLGSGSIVFADSSASLVSFKSGPGKKRRHTRMLNVEALNG	532
XP_019636662.1 [B.belcheri]	GLMLPKVVVDVDFGGRITDAGMLGSGIYFSDA--TSAKYSKSPST--RGRMYVSEVALGK	515
XP_014020296.2 [S.salar]	GLLLPKVGVGEHGIERTDITNGLNGGIVYFSDAMTSLKYSKSPST--DGSRLLVCDVALGR	445
XP_01440458.1 [X.laevis]	GLLLPKNVEDDLGLERTDITNGLNGGIVYFSDISTGVKYSSEPSV--NGARLLVCDVALNG	504
EDL36193.1 [M.musculus]	GLMLPKVVDVDFGGRSDPMLGSGSIVFADSSASLVSFKSGPGKKRRHTRMLNVEALNG	502
XP_04764289.1 [G.gallus]	GLLLPKV--AEDRGVQRTDVGNLGSGIYFSDSLTSLIKYAHAGET--DGSRLVVCVDAKLG	523
NP_006428.2 [H.sapiens]	GLLLPKV--VEDRGVQRTDVGNLGSGIYFSDSLTSLIKYSHPGET--DGTRLLLICVDAKLG	509
NP_00125927.1 [P.abelii]	GLLLPKV--VEDHGVQRTDVGNLGSGIYFSDSLTSLIKYSHPGET--DGTRLLLICVDAKLG	509

XP_047129290.1 [H.vulgaris]	TKTYRKQFKDNLAEAPAGSDSHTGKVSSTNEPSDDDDDEFVYDVSRQRTITHIVEFKLASD	616
XP_032828733.1 [P.marinus]	HLVRRRRDSLAAAPGSDSHLGHARTLTGSSEFFDEFCVYDVRQKRLYIVQFCSLE	613
XP_032219396.1 [N.vectensis]	SKKEYRKFTKDLTRPPDGNSYVIGKATETQPSDFDKDEFVYVTKQQMRVLYIEFALPDE	592
XP_019851276.1 [A.queenslandica]	VKEFTSYQKELLAAANGFHSKVGKVGITTEPDSGLSPFENEYVYVTKQQMRVLYIEFALPQ	596
XP_019636662.1 [B.belcheri]	CKDVYQQDTSLTQTPGNSYVHVGKVTNDITSEFEEKDNEVYVYVNNQQMRVLYIEFALPQ	475
XP_014020296.2 [S.salar]	CTDLQKRDTSLTQPEGSHVHVGVRHPTPKKPSFEDNEVYVYVSPQMRVLYIEFALPQ	594
XP_01440458.1 [X.laevis]	CRDLYKRDFTSLTEANGPDSVHVGVRTPGFRKGSDFDEFCVYVYVSKQDQMRVLYVQFCTAKD	564
XP_04764289.1 [G.gallus]	CLDLYVERDTSILMAAPSGNSVHVGKRTADNDSFDEFCVYVYVTKQVIRVYVQFCTAED	583
EDL36193.1 [M.musculus]	CYNLFKPKDFTSLTPGNSYVHVGKSETTSVTPGNSYVHVGKSETTSVTPGNSYVHVGKSETTSV	562
NP_006428.2 [H.sapiens]	CMDLHEKDFSLTEAPGSDSHVHVGSTASVTTTDFDEFCVYVYVTKQVIRVYVQFCTAED	569
NP_00125927.1 [P.abelii]	CMDLHKDFTSLTEAPGSDSHVHVGSTASVTTTDFDEFCVYVYVTKQVIRVYVQFCTAED	569

XP_047129290.1 [H.vulgaris]	NVHHTLNDVDSED-----EGIESDFTSESLISKDVSVDQPSKSVYQSQSTNQ--P	616
XP_032828733.1 [P.marinus]	VVKEENSDAVEEYFPEATPAD-ER-IL-PEPNI-PELPGQEGFQRLSGHSGVGS--P	618
XP_032219396.1 [N.vectensis]	DIARINVNDVSGFVEEPLDN-----EDEIVLSDVMISIPDLLKVEAGLKGDTADK--P	645
XP_019851276.1 [A.queenslandica]	EEIDQDDETESEK--YENEEIEDEESNIVDTGVSLSKDNVDTPLSKVEAGLKVDD--GG--V	652
XP_019636662.1 [B.belcheri]	QVTPVDVEAYLLH--LTPVEIEEDQDLN-ILKSLEDQNIADPLDKVKGLLKSQGEEMP	530
XP_014020296.2 [S.salar]	QLKDQFPTDITDTS--TEPLPVPSPDSLSCGEAEEDVGSKNPLEEVATGLLDCSQG--P	652
XP_01440458.1 [X.laevis]	QVMNEHDKLPFWV--EPTDEED--GEFV--QAEDEPMLENIPEFRSILKGGLSVQGN--Q	616
XP_04764289.1 [G.gallus]	QIKQFQPTCEVEI--EQDNTEPEFSQCHL-----QNEDESPANSINIVDTGVSLSKQDRLGN--P	636
EDL36193.1 [M.musculus]	QIKQFHPHSDHTEL--EYRPREFSN--FS--KVEDYQLPDAKTSSTSSKAGLQDASGN--L	613
NP_006428.2 [H.sapiens]	QIKDHPHSDHTEL--EYRPREFSN--FS--KVEDYQLPDAKTSSTSSKAGLQDASGN--L	620
NP_00125927.1 [P.abelii]	QIKDHPHSDHTEL--EYRPREFSN--FS--KVEDYQLPDAKTSSTSSKAGLQDASGN--L	620
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XP_047129290.1 [H.vulgaris]	VPLTAVHIVRAKLLQEYFSEVVVLQAYRNDNISNPIEAKYVFFLESAACVGSFEAFINGKHV	726
XP_032828733.1 [P.marinus]	VPLKAVHVRANILDTQAIVVQYENDNSTPEVIEAKYVFFLEDAEAAVCSFEAFINGKHV	678
XP_032219396.1 [N.vectensis]	VPLKAVHIVRAKLLDLAAQVVMVQACNNSDVPIEAKYVFFLDDMAAVCGFEAFINGKHV	705
XP_019851276.1 [A.queenslandica]	VPLKAVHVVQAQLDLIAAKVILVQSYKENSELVPVIEAKYVFFLDDMAAVCGFEAFINGKHV	712
XP_019636662.1 [B.belcheri]	VPLKSVHVRKALLDLIAAQVILVQSYKNNENVAIEAKYVFFLDDMAAVCGFEAFINGKHV	710
XP_014020296.2 [S.salar]	VLQQAIVHVARILMDLSQVILFQTYTNKSSVPIEAKYVFFLDDMAAVCGFEAFINGKHV	592
XP_01440458.1 [X.laevis]	PLENIHIVGRMDILVMEVIFQTYTNKSSVPIEAKYVFFLDDMAAVCGFEAFINGKHV	596
XP_04764289.1 [G.gallus]	VPLSVHVIKARIIDTFAVQVVFQTYTNKSHVPIEAKYVFFLDDMAAVCGFEAFINGKHV	676
EDL36193.1 [M.musculus]	VPLSVHVIKARIIDTFAVQVVFQTYTNKSHVPIEAKYVFFLDDMAAVCGFEAFINGKHV	713
NP_006428.2 [H.sapiens]	VPLSVHVIKARIIDTFAVQVVFQTYTNKSHVPIEAKYVFFLDDMAAVCGFEAFINGKHV	680
NP_00125927.1 [P.abelii]	VPLSVHVIKARIIDTFAVQVVFQTYTNKSHVPIEAKYVFFLDDMAAVCGFEAFINGKHV	680

XP_047129290.1 [H.vulgaris]	GKVKVEKQKAEYKEAYKIQGGHGYALMEEQEESPVDFTVTVGNLPSNDSVLIKITYVLAELS	736
XP_032828733.1 [P.marinus]	GKVKKEKETHAQQYRNAYVSGHGYALMQD--ESPVDFTVTVGNLPSNDFACRVLKITYVLCELA	786
XP_032219396.1 [N.vectensis]	GEVKEKEQKAEYKEAYKISAGHGYALMDE--ETPDFTVTVGNLPSNDFACRVLKITYVLCELA	763
XP_019851276.1 [A.queenslandica]	GEVKEKEQKAEYKEAYKISAGHGYALMDE--ETPDFTVTVGNLPSNDFACRVLKITYVLCELA	770
XP_019636662.1 [B.belcheri]	GEVKEKEAHEAYKEAYKISAGHGYALMDE--ETPDFTVTVGNLPSNDFACRVLKITYVLCELA	

XP_01936962.1 [B. belcheri]	-----KCESFNVVAPGTGYEELFAVSPRIKSNVSKAEFMFDQLKASKSGNTDAMWPLHGFFLLP	872
XP_014002096.2 [S. salar]	HHSVRVNIVSPGSDQKAFLLDANPLVE-ALQPAKKFMSSPVGGSTLWRLPRLVLSLSP	878
XP_041440458.1 [X. laevis]	-----SWLSINIIISPTGSPKFCEVCVCKPENNI-LIPELVQFTMKFPMGMNGLTWLKLQSLCLLA	963
XP_046764289.1 [G. gallus]	-----SRQNVNLIKFGTNSSEDFSSFKNTSK-DLASLTFEFTTSATMTGMDLWKLTRYLSLFL	981
EDL36193.1 [M. musculus]	-----EEQKVNIIQGGTGYKELFSPYKCIOTD-----SKMATFEMSAAFSMGNTDFWKLRYLSLly	957
NP_006428.2 [H. sapiens]	-----EKQKVINI1QGGTGYKELFSPYKHITH-----NTMAAEFIMSATPTMGNTDFWKLTRYLSLly	964
NP_001125927.1 [P. abelii]	-----EKQKVINI1QGGTGYKELFSPYKHITH-----NTMAAEFIMSATPTMGNTDFWKLTRYLSLly	964
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XP_047129290.1 [H. vulgaris]	CES-----TMKNVFLFSDGHI DEISTLARINRLKKNVRLTFPGVGTTPNKH	1001
XP_032828733.1 [P. marinus]	GGV-----G-GSRDAAAPSVSVLLLTLDGVAQSEARATREARNVRLTLRVLCAGGETPNRY	1037
XP_032219396.1 [N. vectensis]	-----TADYPSVFLFTDGHVTEESTTLAYLRIDRLKTRTFVFGVGTTCNRH	1064
XP_019851276.1 [A. queenslandica]	EAASSSTGGTLNSTSLTLLFVGVYISDGHVTEESLTAISLKGAGVRYVTEFGVSTANRH	1051
XP_019636962.1 [B. belcheri]	PSP-----GKTNVNLI1DGHVWDAQPLTSDIHAHLETRVSPGCVGSTSNKH	920
XP_014002096.2 [S. salar]	PSQ-----GV-RNLLLSDDGHVQNALTLQVLRQHAQSRLTFCGLSTANRH	1045
XP_041440458.1 [X. laevis]	PSS-----GTMQNVLLISDGHQENNRVFLQILKNAGKVRLETCGVGATANRH	1011
XP_046764289.1 [G. gallus]	PSQ-----GH-RNLLISDGHQENSVTFVQKSDRNVHTRTLCTCGVSTANRH	1028
EDL36193.1 [M. musculus]	PSE-----GF-RNLLISDGHQESLTLQVVKRNIQHTRTFVTCVAGSTANRH	1004
NP_006428.2 [H. sapiens]	PAR-----GS-RNLLISDGHQESLTLQVVKRNIQHTRTFVTCVAGSTANRH	1004
NP_001125927.1 [P. abelii]	PAR-----GS-RNLLISDGHQESLTLQVVKRNIQHTRTFVTCVAGSTANRH	1004
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XP_047129290.1 [H. vulgaris]	ILQKMACLSGSGYEYFDKNAKSKWKQKVELQLEKCCQPVLTNIKIHIHQHDEDA---PK	1057
XP_032828733.1 [P. marinus]	FLNALARNAGGAEFFFTKARNRSTDRMLALMEKATPVPCVRDTVWQQRFDAGLGDGRV	1023
XP_032219396.1 [N. vectensis]	FLRSMARVGGAGAYELFDFKSKSRWKERVKSLSKARQVDRVSTMVSTSELSITTGVLVHLQ	1194
XP_019851276.1 [A. queenslandica]	PK FLRSMARVGGCGSEFFDSQKRSRWRKVEGLSKAFQALGTGVDVQWQHQHDEDA-----PP	1107
XP_019636962.1 [B. belcheri]	LLRAARVKGVEGKFDOTKTSKWRKVEGLSKAFQALGTGVDVQWQHQHDEDA-----PP	1107
XP_014002096.2 [S. salar]	MLLAQAGGAGAYEFFDTKTHKTRWEKVAQVRSIMSPGCSVSVYKQGFNPSA	1071
XP_041440458.1 [X. laevis]	PMRLCLAQYGAGFEFFEDKSKNWEKIMEAQLEKMSNPACTSASVVKQGFSEND-----PE	1067
XP_046764289.1 [G. gallus]	MLRSLSGYAGAGFEYFDKSKSYNNAEKIQNVQSRISFVCKSSVYIKWQGFINDA-----PK	1084
EDL36193.1 [M. musculus]	ILRLTSLQCCGAGVEYFNNAKSKHSWKQIEAQQTRISFSPSCHSVYKWKQGLSRDA-----PE	1060
NP_006428.2 [H. sapiens]	VLRILSLQCCGAGVEYFNNAKSKHSWKQIEDQMTRLCSFSPSCHSVYKWKQGLNPDV-----PE	1067
NP_001125927.1 [P. abelii]	ILRLSLQCCGAGVEYFNNAKSKHSWKQIEDQMTRLCSFSPSCHSVYKWKQGLNPDG-----PE	1067
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XP_047129290.1 [H. vulgaris]	PLQAPNEITTTLPNGNRLLVYGVFPHCTMANLSALINLNGELNLTIVSTSELSTVTLTIHRL	1117
XP_032828733.1 [P. marinus]	EMQAPRMIRSVFCGTRLVYGVFPHCTQATLHAIIINNQEFTSMVSTSNLTQITRGMRLVHL	1184
XP_032219396.1 [N. vectensis]	PVQAPHDVISFNGSRQVYGVLDVNCQTQASLTAEVDRVSTMVSTSELSITTGVLVHLQ	1153
XP_019851276.1 [A. queenslandica]	PIQAPKSIITSLFSGSRQVYGVFPHCTQASLRAIFGRKIEIQTMVSTSELDLTTSGTLLQHL	1107
XP_019636962.1 [B. belcheri]	PVQAPHQVSLFNGSRQVYGVFPHCTQATLKAIVNNRISITMVSTSELSITAGTLLIHL	1036
XP_014002096.2 [S. salar]	PVQAPQIHALFDLFIHLYGVFPHCTQATLLOGLSDQVSTSELTQITKTGTFHLK	1161
XP_041440458.1 [X. laevis]	PVQAPAHIPALFKNSSLVYGVFPHCTQAKIQLIDDKELDTMASTTELTQITKTGTMHLK	1127
XP_046764289.1 [G. gallus]	PMQAPAGIQLSLFNNRLLVYGVFPHCTQATLRAIINDQBLQTVSTTELTQITGTVLHLK	1144
EDL36193.1 [M. musculus]	PLQAPAMVPSLFFNNRLLVYGVFPHCTQATQAFIQKEKFTMVSTTELTQITGTGMHLK	1120
NP_006428.2 [H. sapiens]	ALQAPAGVSLFFNNRLLVYGVFPHCTQATLQALIQKEKFTMVSTTELTQITGTGMHLK	1127
NP_001125927.1 [P. abelii]	ALQAPAGVSLFFNNRLLVYGVFPHCTQATLQALIQKEKFTMVSTTELTQITGTGMHLK	1127
	**** : : * : : * : * * : * : * : * : * : * : * : *	
XP_047129290.1 [H. vulgaris]	AAKSVINDDNGMLHQQQKHEAIAKEMKGIQLISLEYISVTFKTSFIAVEERKEKNG	1176
XP_032828733.1 [P. marinus]	TAHAIIQDYEDGNLPHDQTEQHEVI1AEMKRSI1LISKEYSI1PTPYSFVAVERDSTLA	1243
XP_032219396.1 [N. vectensis]	TARAI1RDWEEGSLDPNHTKHEMAKRMKDPI1LSLKRFS1VSQFTSFVAIEHRKKDEKF	1213
XP_019851276.1 [A. queenslandica]	TAQALI1RDWEEGSLDNDTHEIMKRLDTP1INTSKEYSI1VSQFTSFVAIEHRKKDEKF	1297
XP_019636962.1 [B. belcheri]	TARAVIRDDGTLIVDRTHETKMGMLKPKFI1LSKEYSI1VTFKTSFIAVEERKEQEDL	1026
XP_014002096.2 [S. salar]	TARAVIRDDGTLIVDRTHETKMGMLKPKFI1LSKEYSI1VTFKTSFIAVEERDSE-Q	1026
XP_041440458.1 [X. laevis]	TAQALIRDDGTLFHEHEHEHEMKQKTLKSI1LTSKYSI1VTFKTSFIAVEERKDAEK	1186
XP_046764289.1 [G. gallus]	TARAFIRDDGTLIHENETHEMKKQTLKXNMI1LTSKYSI1VTFKTSFIAVEERKDAE1	1203
EDL36193.1 [M. musculus]	AARALIRDDGTLIHDDENHEMKKINMKS1LITLKSNSI1TQFTSFVAVEKRDNEI1	1179
NP_006428.2 [H. sapiens]	AARALIRDDGTLIHENETHEMKKQTLKSI1LITLKSNSI1TQFTSFVAVEKRDENES	1186
NP_001125927.1 [P. abelii]	AARALIRDDGTLIHENETHEMKKQTLKSI1LITLKSNSI1TQFTSFVAVEKRDENES	1186
	**** : * : * : * : * : * : * : * : * : * : * : *	
XP_047129290.1 [H. vulgaris]	KDVTAPTINELVLMETVDILPYMGFEFTKTSVPMOKAR-----FSLSEILD-----	1222
XP_032828733.1 [P. marinus]	DEATGPALDELILSKESVDPLPYVWVEEKAARKKKGSMQF-----HLR-----	1286
XP_032219396.1 [N. vectensis		

XP_032828733.1[P.marinus]	-----ACFS-----	1316
XP_032219396.1[N.vectensis]	---KLFEACRSSESTETGTSASSTSSSESSSEELSDNSDSDWGS-----	1444
XP_019851276.1[A.queenslandica]	LESKLHLITRR-----RGKALKKD---IPPAEER--KASPKVPLKKK-----	1461
XP_019636962.1[B.belcheri]	-----QCN-----GNAS-----PADN-----ETSSSEWKAETDYEDMSCEMVT-----	1330
XP_014020296.2[S.salar]	-----QCN-----GNAS-----PADN-----DESWEGL-----NYSYLM-----	1310
XP_041440458.1[X.laervis]	-----FPGWKEN-----FCGKY-----	1234
XP_046764289.1[G.gallus]	-----GEFFY-----	1245
EDL36193.1[M.musculus]	-----SSRLK-----	1224
NP_006428.2[H.sapiens]	-----SSEWPEL-----RLSKRK-----	1239
NP_001125927.1[P.abelii]	-----SSEWQKL-----YSSKPK-----	1239
XP_047129290.1[H.vulgaris]	-----NDDSSLRQES-----EEKKKL-----	1256
XP_032828733.1[P.marinus]	-----LIPEKTEQTPEIEFGSAAER-----A-----	1337
XP_032219396.1[N.vectensis]	-----EFYEDNIDDEV-YQDAVGEEEEEGEDDVY---GMCLEEAEEVERSE-----	1487
XP_019851276.1[A.queenslandica]	-----KAVAK-----NRGPIREQESPEKDEDISVAEEGRRSIRMEEEPEEE-----	1502
XP_019636962.1[B.belcheri]	EIMTLGYSEGVMKAGKILD-----SSVELEEESEDEMEFGLFDQEGW-MAADEEKE-----	1383
XP_014020296.2[S.salar]	GSMVFGSPVTVSAA-TKPPDMLTKSEG-AVTDEEMECFNDMYFGLQE-SEH-----	1358
XP_041440458.1[X.laervis]	-----GGPVSV-----ERASLDEEEE-----S---LP-----	1254
XP_046764289.1[G.gallus]	-----IPPFDAVLQ-----DSDAQSDCFTTKRCETE-----GLQLQPEDLT-----	1281
EDL36193.1[M.musculus]	H---NKL-----SD-----GHGVLQLSHS-----	1240
NP_006428.2[H.sapiens]	H---RKIPFSKRKM-----EL---SQPEVSEDFEED-----GLGVLPAFTS-----	1274
NP_001125927.1[P.abelii]	L---R---AKRKK---KL---SQPEVSEDFEED-----GLGVLPAFTS-----	1270
XP_047129290.1[H.vulgaris]	YKKPILLIDIGMAETKAGFAGCRAPKVVITLVGRPRHQGVVMGMGQKDAYVNEALSKRG-----	1316
XP_032828733.1[P.marinus]	NLSPPFEIAAAD-----TASQYPSSEIQPKFAHAS-----	1366
XP_032219396.1[N.vectensis]	APTPLVIDVGSMMKVGFPAGDDAPKGVFFPIVGRPRHQGVVMGMGQKDSYVGEAHSKRG-----	1547
XP_019851276.1[A.queenslandica]	DIPVAVIDTGMDTVKAGFAGDGRPSVFPALVGRPRHQGVVMGMGQKDSYVGEAKSKRG-----	1562
XP_019636962.1[B.belcheri]	ILAKPEM-----E---KKKVALLEKCSRLASPVMSRS-----AVATSTAYSPTSPTKLVA-----	1430
XP_014020296.2[S.salar]	PLRGSVI-----MHSEALTSFYSPTLHTI-----TGQSSTPVTPLYATKMLA-----	1400
XP_041440458.1[X.laervis]	-----FSFAPPPFDE-----EEE-----	1268
XP_046764289.1[G.gallus]	V-----TK-----ESISQ-----	1289
EDL36193.1[M.musculus]	PINLSEI-----PTI-H-----	1251
NP_006428.2[H.sapiens]	NLERGGV-----EKL-LDLSWTESCKPTA-----TEPLFKKVPWETST-----	1312
NP_001125927.1[P.abelii]	NLERGGV-----EKL-LDLSWTESCKPTA-----TEPLFKKVPWETST-----	1308
XP_047129290.1[H.vulgaris]	I--LTLSPFKLDKGSSETD--STKPLQLI-----GDTG--NIVKPE-----	1351
XP_032828733.1[P.marinus]	--VEAVP-----CSNEGPNLSRRDV-----KDHGV--SASR-----	1394
XP_032219396.1[N.vectensis]	I--LSLSTPQKREARPTPLQDRPPPPPLQDRPP-----FAMEGRA-----LTKDR-----	1590
XP_019851276.1[A.queenslandica]	I--LTLKSPFERPSKPMAMSYSQPIVQVEEKE-----KESSATVEEDVNDLFGYDYG-----	1613
XP_019636962.1[B.belcheri]	YSVYSKPSPOKMAALKRAE-KELEAPRPETDEVTVDTLKASLDGIQAQRDLLEDLIEKSD-----	1489
XP_014020296.2[S.salar]	MTVETD-----	1406
XP_041440458.1[X.laervis]	-----SL-----	1270
XP_046764289.1[G.gallus]	-----	1289
EDL36193.1[M.musculus]	-----	1251
NP_006428.2[H.sapiens]	-----SS-----	1314
NP_001125927.1[P.abelii]	-----SS-----	1310
XP_047129290.1[H.vulgaris]	TSKAINPKFKIAKCKRE---LSKGLST-LQHSSVQQSI-----N-----	1386
XP_032828733.1[P.marinus]	-ITMS-----ASSRFRGERHLLHRAAP-----V-----	1416
XP_032219396.1[N.vectensis]	VIMPIE-EAPLDHTASI-----DLEE-----QEDL-----YVDMKGEV-----	1623
XP_019851276.1[A.queenslandica]	RNYEIS-DFSMENYQVNEVLMDELEM-----DESL-----MEQSLM-----	1649
XP_019636962.1[B.belcheri]	TLSAEAPVFFQASTAISEELFAATAEPTVHEATLVESKPAVLKRSKSGRA--PPKGARFVRE-----	1547
XP_014020296.2[S.salar]	-----PIPELSETI-----QSLPEIVRHAKSRQGDFRADRHRK-----	1440
XP_041440458.1[X.laervis]	-----IYN--SPAV--A-----	1278
XP_046764289.1[G.gallus]	-----EVIPQDYGPHDD-----	1302
EDL36193.1[M.musculus]	-----DSEPLLGLFKD-----	1262
NP_006428.2[H.sapiens]	-----FFPILAPAV-----GSYLPPTARAHS-----	1335
NP_001125927.1[P.abelii]	-----LFGVSPFVV-----GSYLRPTAHAPR-----	1331
XP_047129290.1[H.vulgaris]	IDSDSV---DYQK-----S---YIMLTQKQKCAEIEQTS-----	1415
XP_032828733.1[P.marinus]	-----ILKEAFECRRS-----	1427
XP_032219396.1[N.vectensis]	LDDDLGFEAMCNAQKAA-----SL--AMGKRQRQDVQDLT-----	1656
XP_019851276.1[A.queenslandica]	VESAELYEELQOSEETIAVNQKELRSRKVKKSIPGTSPTSLKGLGSKEPQEGQLGTG-----	1709
XP_019636962.1[B.belcheri]	VEPEPVSEEVQASAPSAS-----RSAPAFGPIPPGAS-----FGKKS-----	1586
XP_014020296.2[S.salar]	VCADPAFDVTETQK--KSL-----SVA-DVPRPPPSVL-----QLKSCA-----	1476
XP_041440458.1[X.laervis]	-----F-----SFAPPPP--PPPL-----S-----	1291
XP_046764289.1[G.gallus]	-----I--ATV-----KFAAAMPFVPCPKPF-----VMSYCN-----	1326
EDL36193.1[M.musculus]	-----LCSR-----MGFSCG-----	1273
NP_006428.2[H.sapiens]	-----PASLS-----FASYRQ-----	1346
NP_001125927.1[P.abelii]	-----AASMP-----FASYCQ-----	1342
XP_047129290.1[H.vulgaris]	--DFLSMQ-----SDNL-----	1425
XP_032828733.1[P.marinus]	-----QQFGSSAYAPRSV-----VHQLNSAET-----	1450
XP_032219396.1[N.vectensis]	L-----DSYD-----P---I---HEVLPSNTQVATLDDT-----DD-----	1681
XP_019851276.1[A.queenslandica]	LAFGASKPREGYL-----SLDI-EGLAMPANKETYSLSQTYNPVSP-----	1750
XP_019636962.1[B.belcheri]	---GLVGGPPTTAEETKTKEVAFQGGFGSDAVSQAGFATPFAGAPPLDATPFAGPPFGA-----	1644
XP_014020296.2[S.salar]	VADALLPPAS-----VVGs-----PGPPPPPSVLSSPG-----	1506
XP_041440458.1[X.laervis]	VAKT-----FDS-----PTPAVPFSPFAP--PP-----	1311
XP_046764289.1[G.gallus]	TAPL-----FGS-----AVGAAYMTQKN--SF-----	1346
EDL36193.1[M.musculus]	TA-F-----SGS-----FASSKDFDPGKFSQG-----	1294
NP_006428.2[H.sapiens]	VA-S-----FGS-----AAPPRQFDASQFSQG-----	1367
NP_001125927.1[P.abelii]	AA-S-----FGS-----AAPPRQFDAPQFSQS-----	1363
XP_047129290.1[H.vulgaris]	-----MMDYCEMIASKES-----	1438
XP_032828733.1[P.marinus]	-----PVP-----LIRAQAFAP-----	1462
XP_032219396.1[N.vectensis]	-----MYVDMKN-----RATSSALKE-----RAVSYDI-----QDSLCEV-----	1711
XP_019851276.1[A.queenslandica]	-----VYSPT-----SVTSPAYSP-----TSPSYSP-----SLPSYVPTCTSPAYNAP-----	1788
XP_019636962.1[B.belcheri]	PQFGAPQFGAAKTKTQEAQRFGSDAVSQAGGATPFAGAPPLGATPFAGPLGATPFAGAP-----	1704
XP_014020296.2[S.salar]	-----PPPS-----	1510
XP_041440458.1[X.laervis]	-----PPP-----	1314
XP_046764289.1[G.gallus]	-----PTT-----	1349
EDL36193.1[M.musculus]	-----PNN-----	1297
NP_006428.2[H.sapiens]	-----PVP-----	1370
NP_001125927.1[P.abelii]	-----PAP-----	1366
XP_047129290.1[H.vulgaris]	-----IYLESDSVK-----DIHQ-----	1451
XP_032828733.1[P.marinus]	-----AEDAVK-----	1462
XP_032219396.1[N.vectensis]	TVNGKLSAPSVPLTFNRSSDKVS-----	1717
XP_019851276.1[A.queenslandica]	QFGAAKIKTQEAAGQGFSSNAVSRGADVSTTPFGATSFGATPSIATPFPGTTFFASTISL-----	1812
XP_019636962.1[B.belcheri]	-----RLQS-----	1764
XP_014020296.2[S.salar]	-----	1514
XP_041440458.1[X.laervis]	-----	1314
XP_046764289.1[G.gallus]	-----	1349
EDL36193.1[M.musculus]	-----	1297
NP_006428.2[H.sapiens]	-----	1370
NP_001125927.1[P.abelii]	-----	1366

XP_047129290.1[H.vulgaris]	FKL-----REKKSATPPPSST-RNV--SSLRKKQPFPEPMVS-----	1485
XP_032828733.1[P.marinus]	-----L--TIFDNV-QPPG--VSLGVIAMETP-----SR	1486
XP_032219396.1[N.vectensis]	-----EEEAEPIAIFGLDSCIARVS-----SS-EEKSSLYDEI--PSPNRPFFKKK	1761
XP_019851276.1[A.queenslandica]	-----SDSSETSRNIIQLSSAYLGSGKS--RRFESVLSLEKSAPLSQPT--AAPPNSRSRIVR	1864
XP_019636962.1[B.belcheri]	FGHSTTAAKEPEAALFGPASSATPSGGGFSFGSTS--SDIPLKDEDKSSVPIDSSKGLK	1822
XP_014020296.2[S.salar]	FSAAVSDALPPPPFAVFLSSGPPFPSRL-QSFSATV-----	1549
XP_041440458.1[X.laavis]	-----FSAFPPPPPLA-L-----	1328
XP_046764289.1[G.gallus]	-----AL-ASSGAHLRLC-G-----	1362
EDL36193.1[M.musculus]	-----ISFSPKAPEMGVIL-H-----	1311
NP_006428.2[H.sapiens]	-----GTCADWIPQSASC-P-----	1384
NP_001125927.1[P.abelii]	-----GSCADWIPQSASC-P-----	1380
XP_047129290.1[H.vulgaris]	-----KV-----CLQAKMP-----	1494
XP_032828733.1[P.marinus]	FTPPYQDTFERGQARRQS-----	1504
XP_032219396.1[N.vectensis]	-----VA--NI-----PSPKPRPPFRASKI	1778
XP_019851276.1[A.queenslandica]	-----FEAGALTFGSSSQAPLEP-----VPPPLPPRAVMT	1895
XP_019636962.1[B.belcheri]	FGAPLEEKGGTTGFRFGGSSQAKMIQQGGFISHPQMQQQQQAQSNVPRDRIRPGRKAQS	1882
XP_014020296.2[S.salar]	-----	1549
XP_041440458.1[X.laavis]	-----	1328
XP_046764289.1[G.gallus]	-----	1362
EDL36193.1[M.musculus]	-----	1311
NP_006428.2[H.sapiens]	-----	1384
NP_001125927.1[P.abelii]	-----	1380
XP_047129290.1[H.vulgaris]	-----DLPMPPPQIMPL-----	1507
XP_032828733.1[P.marinus]	-----DRFT-----NSAY-----	1512
XP_032219396.1[N.vectensis]	--AA-----PPAPSLQAV-----	1789
XP_019851276.1[A.queenslandica]	--KSAPSEPIYPSFDGIPAFSVRNAISSSPGSPPELTPWSS--PSFKSPPLPSAPL	1949
XP_019636962.1[B.belcheri]	ARKTTGGKALRPAADKVASDGVK-----ADSSPDTVVFMDESADKAKETKTPTSAKSPL	1935
XP_014020296.2[S.salar]	-----SDALPFTPPA-----	1559
XP_041440458.1[X.laavis]	-----G-----	1329
XP_046764289.1[G.gallus]	-----Q-----	1362
EDL36193.1[M.musculus]	-----T-----	1312
NP_006428.2[H.sapiens]	-----T-----	1385
NP_001125927.1[P.abelii]	-----T-----	1381
XP_047129290.1[H.vulgaris]	FGAKQPSAEPMLLKACSPAKMPDLPMP--PPQ-----LMPLFGAKQPSAEPM---LLK-	1556
XP_032828733.1[P.marinus]	FF--KP---QKCL---ARVKKPPP-----LLC--FTARSFSSAALMPDVHEL	1550
XP_032219396.1[N.vectensis]	CI--DLPEPLKAGDSPLKRSVKAPLF-PPPPQQA---SRI---	1829
XP_019851276.1[A.queenslandica]	PG--GPPAKFSKSGRALMQSGGPPPPPPFTGT---APMQLSEKS-PPPPVPV---LRS	2001
XP_019636962.1[B.belcheri]	KM--IPATCCMVCYDMPLPYQQGSPPPP--PAPSRGPPPLPPTSQEQEPPIPPPPP	1984
XP_014020296.2[S.salar]	-----SVLSSPGPPPS-R-----LQSFSAITVDALPPPPPA	1589
XP_041440458.1[X.laavis]	-----MPFSFAPPPPP-P-----PLALGMFSPFAPPPPPPP	1359
XP_046764289.1[G.gallus]	-----SPVYSPPS-----PLVGMKYDNSFV-----	1382
EDL36193.1[M.musculus]	-----SPFCSPPKPPS-A-----PPLVTNVLCS-	1335
NP_006428.2[H.sapiens]	-----G--PPQNPPS-S-----PYCGIVFSGSSL-----	1406
NP_001125927.1[P.abelii]	-----G--PPQNLSF-A-----PFCGIAFSGSSL-----	1402
XP_047129290.1[H.vulgaris]	-----ACSPGKTSFFSQPPPPPAQSMYLFAGAKPLPEPTLSKD--CLPGKTSFFSQPP	1608
XP_032828733.1[P.marinus]	RAAGLM-----SRVPECAK--RDVCAQLP--NRDSPTD--FPEP	1585
XP_032219396.1[N.vectensis]	-----YGAAPPAPSLQAVCID--LPEPLK--AGDSPKRSVKKPLP	1867
XP_019851276.1[A.queenslandica]	RDRGPMMPVQSTVSSGRPPPPPHFMLCGE--VPMS-----G-----GPP	2041
XP_019636962.1[B.belcheri]	-----CPAGPPLPAGAPPPPPQFRKSL--LALSQEKLGKSGQSPTMT--QPPP	2032
XP_014020296.2[S.salar]	-----FVLS-----SPGPPPSRLQ-SFS-----ATVSDA--LPP	1615
XP_041440458.1[X.laavis]	-----LPAA-----KSH-STDEVY-SLD--VALL-----GAQQVSVC--APPP	1391
XP_046764289.1[G.gallus]	-----DH--IP-----	1386
EDL36193.1[M.musculus]	-----	1335
NP_006428.2[H.sapiens]	-----SS--AQSA-----	1412
NP_001125927.1[P.abelii]	-----SP--TQLP-----	1408
XP_047129290.1[H.vulgaris]	PPPPAQ-SM---YLFGA-----KQPLPEPTLS-----KD	1633
XP_032828733.1[P.marinus]	PRLPPP-----PPAQHASR--FGQP-----MHD-----	1606
XP_032219396.1[N.vectensis]	PPPPQQAARDYRASYGAPPLPKRGGGPPLPKRGGGPPLFGAMALR--TGAPSKASKP	1925
XP_019851276.1[A.queenslandica]	PPLPYLSRGIAQRRLPGGPPPP--PPPPPPGAAGAPLPGSSKVA--PKGKSKV--S	2091
XP_019636962.1[B.belcheri]	SRAPPP-----SMGRRPPPPSMGRRPPPPMTRAPPP-----NMARLRVDAD	2075
XP_014020296.2[S.salar]	--TPPA-----SVLSSPGPPPSRLQSFSDAVSDSLPPPSALVSNEFRAIKHKMRG--H	1664
XP_041440458.1[X.laavis]	PPPPPG-----SICA--PPPPGFCAP-----SPPAFDELLQV-----	1422
XP_046764289.1[G.gallus]	-----N-----TIMF--GCASTYSSD-----KTNAEQV-----	1409
EDL36193.1[M.musculus]	-----APQSYFLNL-----QSAAVHQS-----	1352
NP_006428.2[H.sapiens]	PLQHGP-----GFTT--RPSAGTFFEL-----DSPQLHFSLPTDPD	1446
NP_001125927.1[P.abelii]	PPQFPG-----GCTT--RPSAGTSPEL-----DSPQLHFSLPTDPD	1442
XP_047129290.1[H.vulgaris]	CLPGLMGKKLAAPPAQSVSLFGSN-----KSSLMFSRNSCFSS-----	1672
XP_032828733.1[P.marinus]	-----DFQSSSTC-----	1613
XP_032219396.1[N.vectensis]	SFGGRGQPOVFAT--SASEILHPRLA--RTPSEL-----A-----	1956
XP_019851276.1[A.queenslandica]	YYAGLADKKT--T--QASPPSKAGGK--KEPSGP-----TGRGAL--LSSI-----	2129
XP_019636962.1[B.belcheri]	A-----L-----	2077
XP_014020296.2[S.salar]	PKPGVGAI--SHT--ATFFKLQAGKD-LLLSKPREPYVELCETSKMWTVDNSLSEDKDC	1719
XP_041440458.1[X.laavis]	-----LEQ-----TQLAVS-----MIETE-----	1436
XP_046764289.1[G.gallus]	-----T--HNSPVPQHKKTKLKAKYRKK-----MVTGL-----	1436
EDL36193.1[M.musculus]	-----PNN-RVSEIIMES-----VESSL-----	1369
NP_006428.2[H.sapiens]	PIRFGGSY--HPS--ASSPFHFQPSAASLTANLRLP-----MASAL-----	1483
NP_001125927.1[P.abelii]	PIRFGGSY--HLS--ASSPFHFQPSAASLTANLRLP-----IASAL-----	1479
XP_047129290.1[H.vulgaris]	-----DDL-----GMPKREE-----	1682
XP_032828733.1[P.marinus]	-----PKGVP-----SQ-----TNDEAP-----	1614
XP_032219396.1[N.vectensis]	-----KKGVS--LQ--KYTVKKKEEKS-----	1969
XP_019851276.1[A.queenslandica]	-----YYVGLGETTKRMGARIGARIGARSLKKAELPKGEEEP-----	2116
XP_019636962.1[B.belcheri]	GLVEMDHQPSVVPASVPPSGFSFGGRVSGSQSSQHHGSMFGDTAN--ACYIPGLFEASS	1777
XP_014020296.2[S.salar]	-----PE-----KAEHEGADFPVRPAR--KKKIYNTVEEP-----	1464
XP_041440458.1[X.laavis]	-----P-----SDYSSRDA--SS-----	1436
XP_046764289.1[G.gallus]	-----P-----EALCSQSR--TTPVDLCLLEES-----	1380
EDL36193.1[M.musculus]	-----P-----EALCSQSQ--TTPVDLCLLQES-----	1504
NP_006428.2[H.sapiens]	-----P-----	1500
NP_001125927.1[P.abelii]	-----P-----	1500
XP_047129290.1[H.vulgaris]	-----HSLDLCDDL-----EMLADEKLSL-----DYRPAATG	1709
XP_032828733.1[P.marinus]	-----AASRLCEESFPGSSNLS-----ESF-----SSED-----	1639
XP_032219396.1[N.vectensis]	VFMSRLQLLESTR--AK-----KKTETDRED--I--MKQDSS-----	2001
XP_019851276.1[A.queenslandica]	VSASLMQALQSRK-----APEAFNLKLVDSYKWSVEMSDDD--SWDDDEEDDEGGGG	2200
XP_019636962.1[B.belcheri]	M-----EVEESPAICGEQVEESMDLKRLLKKKKVLELRAEFKKYESLPVDER--EE	2168
XP_014020296.2[S.salar]	A-----GSLFGPTLPYLGGSSGRSMGLS-----FEAPLT-----	1805
XP_041440458.1[X.laavis]	M-----GRLGHSRRCVRGEEVA--LS-----QK-----	1485
XP_046764289.1[G.gallus]	-----QDATASEQ-----E-----F-----	1446

EDL36193.1[M.musculus]	Y-----LALEGAEDSLGGSSF---ET-----D-----	1400
NP_006428.2[H.sapiens]	V-----GSLEGRCPVFVAFQSS---DT-----E-----	1524
NP_001125927.1[P.abelii]	V-----GSLEGRCPVFVFRSS---DT-----E-----	1520
XP_047129290.1[H.vulgaris]	TISACHFVKP-----ISCAYYE-PCF	1729
XP_032828733.1[P.marinus]	-----DYGMPF-----ESCIMFH---	1652
XP_032219396.1[N.vectensis]	--GEADILRREAHQH-----SMETEL-----EADRNEAMGVRPVPRKRGRKMLE-KK-	2046
XP_019851276.1[A.queenslandica]	GGGRSRLLVNEFFAPQDQERAEKVVQQEEEEESDDNMAFGLPDSF--DEALSN-ASY	2257
XP_019636962.1[B.belcheri]	RDGRSLLNQIMRGTSL-----RGRPGAYHSASF	2197
XP_014020296.2[S.salar]	-GGHLNSPLPTTHGFNLTH-----FLGASLGSSLFQ-SSL	1838
XP_041440458.1[X.laervis]	-----RERAPPVF--NAL	1496
XP_046764289.1[G.gallus]	-----PERPKRLLPSCF	1459
EDL36193.1[M.musculus]	-----TDEAAFIANDLL	1413
NP_006428.2[H.sapiens]	-----SDELSEVLQDSCF	1537
NP_001125927.1[P.abelii]	-----SDELSEVLQDSRI	1533
XP_047129290.1[H.vulgaris]	LERKKTSIENG-----LKSVDCCFFKDEKFERPFLDGRSFVFLNKTSNEDLINNTLEFL	1783
XP_032828733.1[P.marinus]	--TS-----PGVSLCGSSG-----SSEFSDTTPWQ--HADLSKI	1682
XP_032219396.1[N.vectensis]	--AA-----EQK-----KEAMEEPS-----ESLQNRMRKWMATDKLLEL	2078
XP_019851276.1[A.queenslandica]	YSMS-----ENA-----QESDGKVV-----IEVQNQF-PVINSSQIYMM	2290
XP_019636962.1[B.belcheri]	HPTS-----DSAGYPSGTETVVVPI-----VTRGSGSLTEKTVDQLFAL	2236
XP_014020296.2[S.salar]	RTLQQHHLVQAQKPLDIKKNIQKLVGDSER-REG-----LEFRKNLT--DVVKWTEI	1888
XP_041440458.1[X.laervis]	LDLQC-----EGSVCAPPPPIRFI-SVTP--PV-----ALSQKRGR--ALPAFNAL	1536
XP_046764289.1[G.gallus]	ITT-----EK-E-----RSQKLEL-----TPVMWEEI	1481
EDL36193.1[M.musculus]	TSI-----E-TSSD-EBC-----AFCDDEQE--SPVFWASL	1440
NP_006428.2[H.sapiens]	LQIKC-----DTKD--DSLCLFL-EVKE-EDE-----IVCIQHWQ--DAVPWTEL	1576
NP_001125927.1[P.abelii]	LQIKC-----DTKD--DSIPCFLE-VEIE-EDE-----IVCTQHWQ--DAVPWTEL	1572
XP_047129290.1[H.vulgaris]	VENQHSDGYWELEDIFQDQOSTISFDILFVDVCRKLALSLCGEYSSEIQRLIATIIVCV	1843
XP_032828733.1[P.marinus]	TCLQNKDGSDGGVELSSL-VGWSPDH-ITVILKKQGIQSLGLRMEEAIVRLVMTLLVLQ	1740
XP_032219396.1[N.vectensis]	FASQHNDGYWSEK-ELEVA-FRI-DCSFLSRLLVNAGAQLGDEAFETILKMLTTIITLA	2135
XP_019851276.1[A.queenslandica]	YSLQKDDGWSLLS-DLDTI-VMPGTGDRVLKVLNEAGAKSLGRVYKELSLIATCFVLR	2348
XP_019636962.1[B.belcheri]	LKHTDQSGYWEFSPELDQL-LGISSSTCVQ-IFNTAGLSLGAKVAKQLLVLATLLVLQ	2294
XP_014020296.2[S.salar]	FALQHSSEGYWECSASLGLS-LGVVDVYFANVFLKNRGISSLGVRRAHADLRLVASLLVLQ	1947
XP_041440458.1[X.laervis]	LDLQCEEGYWLNLNEELGCL-LNMNVNYLIEVFLSKNGIQSLGKRGKDEVKLKIATLLVLQ	1595
XP_046764289.1[G.gallus]	FDLQNGDGSWNLSPLGKI-LKFDVDYLINHFLIRNGIQSLGKRGKDEVKLKIATLLVLQ	1540
EDL36193.1[M.musculus]	FALQTENGFWKLTPELGLI-LNLNVNALL-TSLEEKGIRSLGTGRERLLDIATLLVLQ	1498
NP_006428.2[H.sapiens]	LSLQTEDGFWKLTPELGLI-LNLNTNGLH-SFLKQKGIQSLGVKGRECLLDLIATMLVLQ	1634
NP_001125927.1[P.abelii]	FSLQTEDGFWKLTPELGLI-LNLNTNALH-SFLKQKGIQSLGKGRERLLDIATMLVLQ	1630
XP_047129290.1[H.vulgaris]	IFKLALSNDKALWSY--P-YHLRESNLKA-----SDKLTSAFFKGYSYLHEDCKFPSIHT	1896
XP_032828733.1[P.marinus]	ILRLRMGLASSINEFVLLLLRRDVSSTAELDMFMGSADAFARAASWIRSTESVCPVCVT	1800
XP_032219396.1[N.vectensis]	ILKTYLPDQFPVSLV--QQVSEGE--LV-----TSEWRNQVGRALSWLRKMDRKMPSVCS	2186
XP_019851276.1[A.queenslandica]	LLNLNFPDAYKITFS--PHFEIDMSNGD-----PGDIATKMKNLSVLCKNLHKQNPVSVT	2401
XP_019636962.1[B.belcheri]	LIMLHLPLQFPSCSS--L-LHLDVMQVA-----AE-WRSAVQQVLAWAKGVDTHMPSVYS	2345
XP_014020296.2[S.salar]	LMRVRLLEEGKLLLS--L-FRLDLHSP--QPRCERWEAVRRAVDWVKWADREYPCVCS	2002
XP_041440458.1[X.laervis]	TI-CTYELVNVTFKN--L-MKLDESFT--SP---FYETIEKSMKWARCKDKQYPGICY	1645
XP_046764289.1[G.gallus]	FIRCANELQGIVFKS--L-MKLDNLTT--SGVHWAFESIKKATEWVKRTEGQYPSICY	1594
EDL36193.1[M.musculus]	FLYTKLEQEGMVAKS--L-IMDDAFIS---RNIPWAFENIKKAREWARKTEGQYPSICQ	1552
NP_006428.2[H.sapiens]	FIRTRLEKEGIVFKS--L-MKMDASIS---RNIPWAFENIKKASEWVRTEGQYPSICP	1688
NP_001125927.1[P.abelii]	FIRTRLEKEGIVFKS--L-MKMDPSIS---RNIPWAFENIKKASEWVRTEGQYPSICP	1684
XP_047129290.1[H.vulgaris]	RLGLGYSLEEMTFQVYRLASQSFDKRMELRL-----	1927
XP_032828733.1[P.marinus]	RLELGPNNQAAATCSLLGVA-----	1819
XP_032219396.1[N.vectensis]	RLELGPMDVVAAGIIDDKVHLMIGVR-----	2213
XP_019851276.1[A.queenslandica]	RLELGYSLIDAVDKILKL---CA-----	2421
XP_019636962.1[B.belcheri]	RLELGKSWDDLTKLIGVGVSLVHE-----	2370
XP_014020296.2[S.salar]	RLEFQWDMESSRQLLGTDPPHPLSLPLILGT--TGGVRAQ	2041
XP_041440458.1[X.laervis]	RLGLGKDWDSATRKLLSIDPVDPSDLFFAVESVESIV--	1684
XP_046764289.1[G.gallus]	RLELGKDWDSATKMLIGIKCN-----	1615
EDL36193.1[M.musculus]	RLELGKDWDSATKQLLGIQPOAN-TSLHRLIYYSQG----	1587
NP_006428.2[H.sapiens]	RLELGNDWDSATKQLLGLPISTVSLPHRVLHYSQG----	1724
NP_001125927.1[P.abelii]	RLELGKDWDSATKQLLGLQPVNTVSLPHRVLHYSQG----	1720
	** : * . : :	

Percent identity matrix:

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#
#
# Percent Identity Matrix - created by Clustal2.1
#
#
1: XP_047129290.1[H.vulgaris] 100.00 32.26 38.59 36.70 35.72 31.35 33.51 32.90 32.98 31.27 31.01
2: XP_032828733.1[P.marinus] 32.26 100.00 35.34 33.67 38.19 37.01 37.08 36.52 37.52 35.76 35.56
3: XP_032219396.1[N.vectensis] 38.59 35.34 100.00 40.86 39.21 34.87 34.69 35.85 35.81 33.82 33.88
4: XP_019851276.1[A.queenslandica] 36.70 33.67 40.86 100.00 37.82 33.09 35.17 34.30 34.63 31.77 31.83
5: XP_019636962.1[B.belcheri] 35.72 38.19 39.21 37.82 100.00 37.25 39.20 38.54 38.25 35.98 35.56
6: XP_014020296.2[S.salar] 31.35 37.01 34.87 33.09 37.25 100.00 41.80 43.30 41.68 40.36 39.81
7: XP_041440458.1[X.laevis] 33.51 37.08 34.69 35.17 39.20 41.80 100.00 48.16 47.33 47.32 46.94
8: XP_046764289.1[G.gallus] 32.90 36.52 35.85 34.30 38.54 43.30 48.16 100.00 52.14 53.34 53.41
9: EDL36193.1[M.musculus] 32.98 37.52 35.81 34.63 38.25 41.68 47.33 52.14 100.00 70.25 70.02
10: NP_006428.2[H.sapiens] 31.27 35.76 33.82 31.77 35.98 40.36 47.32 53.34 70.25 100.00 94.36
11: NP_001125927.1[P.abelii] 31.01 35.56 33.88 31.83 35.56 39.81 46.94 53.41 70.02 94.36 100.00
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