

# PARP1

## Sequences :

>NP\_001609.2 poly [ADP-ribose] polymerase 1 [Homo sapiens]  
MAE5SDKLYRYEYAKSGRASCKKCSSESIPKDSLRLMAIMVQSPMFDGKVPWHYHPSCFWKVGHSIRHPDVE  
VDGFSLELRWDDQQKVKKTAEAGGVGTGKGQDGGISKAETLGDFAAEYAKSNRSTCKGCMKEIKKGQVRLS  
KMMVDPEKPQLGMI DRWYHPGCFVKNREELGFRPEYSASQLKGFSLLATDEK EALKKQLPGVSGEGRKG  
DEV DGVDEVAKKKSKKEKDKDSKLEKALKAQNLDLWN IKDELKKVCS TNDLKELLIFNKQQVPSGESAIL  
DRVADGMVFGALLPCEECSSGQLVFKSDAYYCTGDVTAWTKCMVKTQTPNKRKEWVTPKEFREISYLLKKLV  
KKQDRIFFPETSASVAATPPPSTASAPAAVNSSASADKPLSNMKILTLGKLSRNKDEVKAMIEKLGKLT  
GTANKASLCISTKKEVEKMNMKMEEVKEANIRVVSEDFLQDVSASTKSLQELFLAHLILSPWGAEVKAEPV  
EVVAPRGKSGAALSKKSKGQVKEEGINKSEKRMKLT LKGGAAVDPDSGLEHSAHVLEKGGKVSATLGLV  
DIVKGTNSYYKLQ LLEDDKENRYWIFRSWGRVGTVIGSNLKEQMPSKEDAEIHFPMKLYEEKTGNAMWSKN  
FTKYPKFPYPLEIDYGQDEEA VKKLT VNP GTKSKLPKP VQDLIKMIFDVE SMKKAMVEY EIDLQKMP LKG  
LSRRQIQAAYSILSEVQQA VSGSSDSQILDL SNRFYTLIPHDFGMKKPPLLNNADSVQAKVEMLDNLDD  
IEVAYSLLRGGSDSSKDPIDVNYEKLKTDIKVVD RDSEEA EIRKYVKNTHATTHNAYDLEVIDIFKIE  
REGEQYRKYPFKQLHNRRL LWHGSRRTTNFAGILSQGLRIAPPEAPVTGYMFGKGIYFADMVSKSANYCHT  
SQGDPIGLILLGEVALGNMYELKHASHISKLPKGKHSVKLGKTTDPDSANISLDGDEVPLGTGISSGVN  
DTSLLYNEYIVYDIAQVNLKYLKLLKFNFKTSLW

>Xp\_024101750.1 poly [ADP-ribose] polymerase 1 [Pongo abelii]  
MAE5SDKLYRYEYAKSGRASCKKCSSESIPKDSLRLMAIMVQSPMFDGKVPWHYHPSCFWKVGHSIRHPDVE  
VDGFSLELRWDDQQKVKKTAEAGGVGTGKGQDGGISKAETLGDFAAEYAKSNRSTCKGCMKEIKKGQVRLS  
KMMLDPEKPQLGMI DRWYHPGCFVKNREELGFRPEYSASQLKGFSLLATDEK EALKKQLPGVSGEGRKG  
DEV DGVDEVAKKKSKKEKDKDSKLEKALKAQNLDLWN IKDELKKVCS TNDLKELLIFNKQQVPSGESAIL  
DRVADGMVFGALLPCEECSSGQLVFKSDAYYCTGDVTAWTKCMVKTQTPNKRKEWVTPKEFREISYLLKKLV  
KKQDRIFFPETSAPVAATPPPSTASAPAAVNSSASADKPLSNMKILTLGKLSRNKDEVKAMIEKLGKLT  
GTANKASLCISTKKEVEKMNMKMEEVKEANIRVVSEDFLQDVSASTKSLQELFLAHLILSPWGAEVKAEPV  
EVVAPRGKSGAALSKKSKGQVKEEGINKSEKRMKLT LKGGAAVDPDSGLEHSAHVLEKGGKVSATLGLV  
DIVKGTNSYYKLQ LLEDDKENRYWIFRSWGRVGTVIGSNLKEQMPSKEDAEIHFPMKLYEEKTGNAMWSKN  
FTKYPKFPYPLEIDYGQDEEA VKKLT VNP GTKSKLPKP VQDLIKMIFDVE SMKKAMVEY EIDLQKMP LKG  
LSRRQIQAAYSILSEVQQA VSGSSDSQILDL SNRFYTLIPHDFGMKKPPLLNNADSVQAKVEMLDNLDD  
IEVAYSLLRGGSDSSKDPIDVNYEKLKTDIKVVD RDSEEA EIRKYVKNTHATTHNAYDLEVIDIFKIE  
REGEQYRKYPFKQLHNRRL LWHGSRRTTNFAGILSQGLRIAPPEAPVTGYMFGKGIYFADMVSKSANYCHT  
SQGDPIGLILLGEVALGNMYELKHASHISKLPKGKHSVKLGKTTDPDSASISLDGDEVPLGTGISSGVN  
DTCLLYNEYIVYDIAQVNLKYLKLLKFNFKTSLW

>BAE39743.1 unnamed protein product [Mus musculus]  
MAEASERLRYEYAKSGRASCKKCSSESIPKDSLRLMAIMVQSPMFDGKVPWHYHPSCFWKVGHSIRQPDVE  
VDGFSLELRWDDQQKVKKTAEAGGVGTGKGQDGGISKAETLGDFAAEYAKSNRSMCKGCELEKIEKGQMLRS  
KMMVDPEKPQLGMI DRWYHPTCFVKKRDDELGFRPEYSASQLKGFSLLSAEDKEALKKQLPAIKNKEGRKG  
DEV DGTDEVAKKKSKKGKDKDSKLEKALKAQNELIWN IKDELKKACSTNDLKELLIFNQQVPSGESAI  
LDRVADGMVFGALLPCKECSGQLVFKSDAYYCTGDVTAWTKCMVKTQNP SRKEWVTPKEFREISYLLKKLV  
VKQDRIFFPESAPAPLALPSVTSAPTAVNSSAPADKPLSNMKILTLGKLSQNKDEAKAVIEKLGKLT  
TGSAANKASLCISTKKEVEKMNMKMEEVKAANRVVSEDFLQDVSASTKSLQELLSAHSLSLWGAEVKAEP  
GEVVASGKSAAPSKKSGAVKEEGVKNSEKRMKLT LKGGAAVDPDSGLEHSAHVLEKGGKVSATLGLV  
DIVKGTNSYYKLQ LLEDDKESRYWIFRSWGRVGTVIGSNLKEQMPSKEDAEVHFPMKLYEEKTGNAMWSKN  
FTKYPKFPYPLEIDYGQDEEA VKKLT VNP GTKSKLPKP VQELVGMIFDVE SMKKALVEY EIDLQKMP LKG  
LSRRQIQAAYSILSEVQQA VSGSSDSQILDL SNRFYTLIPHDFGMKKPPLLNNADSVQAKVEMLDNLDD  
IEVAYSLLRGGSDSSKDPIDVNYEKLKTDIKVVD RDSEEA EIRKYVKNTHATTHNAYDLEVIDIFKIE  
REGEQYRKYPFKQLHNRRL LWHGSRRTTNFAGILSQGLRIAPPEAPVTGYMFGKGIYFADMVSKSANYCHT  
SQGDPIGLILLGEVALGNMYELKHASHISKLPKGKHSVKLGKTTDPDSASITLEGVEVPLGTGIPSGVN  
DTCLLYNEYIVYDIAQVNLKYLKLLKFNFKTSLW

>P26446.2 [Gallus gallus]  
MAETGDKFYRAEYAKSGRASCKKCGESIAKDSLRLALMVQSPMFDGKVPWHHHYSCFWKKRARIVSHTDID  
GFPELRWEDQEKIKKAIETGGAAAGAGGDSKGGKGEMTNDFAAEYAKSNRSTCKGCEQKIEKGQIRIS  
KMMVHPEKPQLGMI DRWYHPDCFVNSRAELGFLPAYGATQLLGPSILKAEKDETLLKQLPATKTEGRKG  
EEVDGNVAVAKKSRKEKESKQEQTELHWIKDELKKVCS TNDLKELLIANKQEVPSGENAILD  
RVADGMVFGALLPCEECSSGQVFKSDAYYCSGDITAWTKCVAKTQTPNKRKDWVTPKEFREIPLYLKKFFKK  
KQDRIFPPEAA TVNSAPPPASAPLTETVTA PQDKPLTNMKILTLGKLSKNKEEVKNIEELGGKMTTAT  
NKAATLCISTQKEVEKMNMKMEEVDAKVRVVSEFLDKVKSNNKGQFELLSLHAISPWGAEVKTEHGEVA  
VDGKCSKPNAMKSGAVKVEEQPSKSEKMKLT VKGGAAVDPDSGLEDSAHVFEKGGKIFSATLGLVDIV  
KGTNSYYKLQ LLEDDRESRYWIFRSWGRVGTVIGSNLKEQMPSKEDAEVHFLNLYEECTGNSWHSKNFTK  
YPKFPYPLEIDYGQDEEA VRKLT V SAGT SKLAKPIQDLIKMIFDVE SMKKAMVEFEIDLQKMP LGLSK  
RQIQSAYSILNEVQQA VSGGSESQILDL SNRFYTLIPHDFGMKKPPLL SNLEYIQAKVQMLDNLDDIEV  
AYSLLRGGNEGDGKDPIDVNYEKLRTDIKVV DKS EEA KIIQYVKNTHAATHNAYDLKVV EIFRIERE  
ESQRYKYPFKQLHNRQL LWHGSRRTTNFAGILSQGLRIAPPEAPVTGYMFGKGIYFADMVSKSANYCHTSQA  
DPIGLILLGEVALGNMYELKNASHITKLPKGKHSVKLGKTA PDPTATTTLDGVEVPLGNIGISTGINDTC  
LLYNEYIVYDIAQVNLKYLKLLKFNFKTSLW

>NP\_001081571.1 poly [ADP-ribose] polymerase 1 [Xenopus laevis]  
MAEASDKLYRAEYAKSGRASCKKCGDNIAKDSLRLAIMVQSPMFDGKVPWHHHYSCFWKKRARVLSQGDII  
GYTELWEDQEMIKKAIETGGAAAGAGGDSKGGKGEMTNDFAAEYAKSNRSACKGCEQKIEKGQIRISK  
KSVDEVFPQLGMI DRWYHPDCFVNSREELGFLPSYSASQLKGFTILSAEDKDSLKKLPAVKNEGKRMAD  
EVDGSAATKKKIKKEKESKLEKLLKEQTELWHIKDELKKVCS TNDLKELLIANKQVPSGETNIVD  
RVSDGMVFGALLPCEECSSGQVFKGDAYYCTGDLASATWKCVAKTQTPNKRKDWVTPKEFHEIPLYLKKFFKK  
RHDRAFPPCAAPTPI SPPAAPEPKPTVEETFE PKPLTNTKVL LIGKLSKNKDEVKTLIEGLGGKVAGSA  
KHANLCISTNKEVEKMNMKMEEVKAANRVVSDDFLKEVESGKSVQELLSQFGI SSWGAEIQEAVQPT  
KQPSGSGVAGKSSGKVKKEEGSNKSEKMKLT VKGGAVIDPDSLEDSCHVLETGGKIFSATLGLVDITR  
GTNSYYKLQ LLEHDRDSRYWIFRSWGRVGTVIGSKLLEEMSSKEDAEIHFNLVQDKTGNAMWSPNFTKY  
PKFPYPLEIDYGQDEEDVVKLSVGAGTKSLAKPVQELIKLIFDVE SMKKAMVEFEIDLQKMP LGLSKR  
QIQSAYSILSQVQA VSESLEARLLDL SNQFYTLIPHDFGMKKPPLL NLDYIQAKVQMLDNLDDIEVA  
YSLLRGAGDGEKDPIDVNYEKIKTDIKVVKDSEESRIICDVKNTHADTHNAYDLEVIDEIKFIDREGE  
YQRYKYPFKQLHNRQL LWHGSRRTTNFAGILSQGLRIAPPEAPVTGYMFGKGIYFADMVSKSANYCHAMPGS  
PIGLILLGEVALGNMHELKAASQITKLPKGKHSVKLGRTAPDPSATVQLDGDVPLGKGTSANISDTSLS  
LYNEYIVYDIAQVNLKYLKLLKFNFKGMMW

>XP\_014061166.1 poly [ADP-ribose] polymerase 1 isoform X1 [Salmo salar]  
MADAQEDKLYKAEYAKSGRASCKKCKENIAKDSLRLAIMVQSPMFDGKVPWHHHYSCFWLRASAQSPADI  
AGFSLELRWEDQEKYKKAIE TGGAAAGGKDGKGAKEKTLDNFAVEYAKSNRSTCKGCEQKIEKDQIRVRS  
KKTVDPEKPQLGLIDRWYHTACFVGRREELVFKPEYSAAQLKGFNTLRVEDKEELKRRLLPAVKS KGRKKT  
DEV DGEAGSKKKDEEEEEKKVELQMKEQSQLI WGIKDKLRQCFTSNDMKELLIANQGEVPSGESNVDS  
LGDCAAFGALKKECEQQLVFKSDAYYCTGDL SAWTKCVFKTQLPNRKDWVTPKEFHELP LKFFKK  
QDRVFPKVPAPAPPASSAAVPCASASAPSLPEGAFAADKPLTGMKLITVGLKLRQNKDELKA AVEELGGKII  
TGTAANKATLCISTKKEVEKMNMKMEEAEEVGRVRSSEDFLTDIKSSGKALQELVLSLHAISPWGAEVKLET  
QQAASA RSGAMAGKSTKRVKEEGVSKASKMKLT VKGGAAVDPDSGLENSAHVLDQNGKIFSATLGLV  
DIVKGTNSYYKLQ LLEDDHVHKRYWIFRSWGRVGTITGSKKLLDKFNDKNSAMDNFLGVYEERTGNAGWSSH  
FTKYPNRFYPLEIDYGQDEEA VKRLTASAGTNSLAKPVQELIRTIIFDVE SMKKAMVEFEIDLQKMP LKG  
LSRRQIQSAYALLSEVQQA VSDSSSESHILDL SNRFYTLIPHDFGMKKPPLL NLDYIQAKVQMLDNLDDIEVA  
YEVAYSLLKGAEDNKDPIDVNYEKLTKIEVV DKTKEAEIILQYVKNTHAATHNTYTLEVEIEFKIV  
REGEYQRYKYPFDL PNRQL LWHGSRATNYAGILSQGLRIAPPEAPVTGYMFGKVYFADMVSKSANYCHT  
SQSDPTGLLL LGEVALGNMHELKASHITKLPKGKHSVKLGRTAPDPSATVTLDGQVPLGKGNTNID  
DTSLLYNEYIVYDIAQVNLKYLKLLKFNQMSMW

>XP\_032819895.1 poly [ADP-ribose] polymerase 1 [Petromyzon marinus]  
MADKFFKAEYAKSSRASCKKCGNIEKDCLRLAVMVQSPRFDGKVPQWHHFQCFWKRARPLTQADVDGFS

ELRSADQDRIKKHIEGSADGEGKSSGKANGAAASNTLPDFLVEYAKSNRSKCKGCDDEKDDVRISRK  
MINIEKPHLGMIDHWYHTNCFVEHRDTLGLSTYGANQIGGFTRLNANDKKAVELTLLGTVVVDGKRAED  
QVDEVAKKIKLESQQKEEEKMLKKQSNVWSFKDGLKSCSDIEDLKELLIANQAVPSGESAVLERLA  
DGMAFGALLPCAECQDQGLVCMSDAYRCSGNISGWTCKTFSTKTPKRNEWIIKPEFKDVPFLKKYKYKQR  
ERVFMSAQATTSPFRAATVATATVATAATKSGEAPGTSAGAVPGKLLAGKALCLVGKLQKSRDDIKALVE  
KLGGKMTSTVPKADFCISTKKEVEKMSKKIAEAQTCNVCVVAEDLLTEASGRPLAELVSAHRSLTWGAP I  
KVQEPTVKTPEVLEVPKEASAKSSKRRKSEGGKAENKLLTVKGRAAVDPLSNLVDVAHVLEDGRGMIYG  
AAMSILVYERGTNSYYKLQLLECDLNRKRWYFWSGRALGTTIGGTKLEMKKREDAVEHFQCLYDYDKTGN  
KWARNFYKYFNKFPYVETDYGQDDDIHDLKAWAGTNSKLAKEPQJELRLMIFDIDSMKMTVEFEIDLC  
KMPLGKLSRKQIQSAYSVLGDAQKLVSSEGLTSLIQDLNSKFYTLPHDPGMKKPTLLNDLDVYIKMKVDM  
LDNLMDIEVAYSLLNPKDETSGGKDLDDASYEKLHTTIEVLGKDTEEFVILLEYVNTNTHAHTDAYELE  
VEEVFKVSRDGEFORYPREFRLHNRQLLWHGSRMTNYAGILSKGLRIAPKEAPVTGYMFGKGVYFADMVS  
KSANYCHTSPSNPTGLILLAEVALGNMHELKQSESIITKLPGKTHSVKGVGTAPDPKKTVTLNGVQVPIG  
NPSATGINDTSLLYNEYIVYDVAQVNIKYLKLNFKYKMQLW

>XP\_019618726.1 PREDICTED: poly [ADP-ribose] polymerase 1-like isoform X1 [Branchiostoma belcheri]  
MLAYRVQEAAKISMADEGKAYKAEYAKSNRASCKLCKGNITKDSRLRLARMVQSPHFDGKVPNWFHYSCEF  
FKKCKPSSSTVEFSVGTGLRWDQDEKLKKTIGGEGSSAGADAGGDEVAPGVQVFSVEYAKSNRSACRGCS  
EKIDKLVRISSKVDEGDQWGPDKDLWHHVDCFVEKREELGFTTDMAPSVIQGYKKLSKDDQDILVKGLGS  
GTTGRRKAKGSGAAAKVKAEETEEKKLKEQSKLVNKRIDELSKSMSENDSLKELLANDQDIPSGESA  
LLDRDSGMAGFALQRCPECKHGQLFYRSDGYHCSGNLTETWKICIYTTREPKRKKWIIIPDDLKEEVFFLK  
KFKSKVAARVFAAHVAAASSTSDSPSSSSRADEKKPLHHVKVVLGKTKSKAEMTKAIEKLGGTVASKV  
DSTVACVISSEKEDVQMSKKIKDAKAADVHVVEDFVTVDEKGGAAALLMQKSIASWGSDDPHSRIATVEE  
KPSKSKSKSYEEMESGTEKKLMMVKGAADVDPDSGIEHSAHVLEDKGVYNAVLGLVDLVRGTNSYYKL  
QVLEADGNRWYVFRAMGRVGTTVGKNLETFHRSQGALEQFLNLYEKTGNEFGTKNFVKYPKRFYPLD  
TDYQGEEDLQKLIKPGSKSTLAREVQELIQMIFDIESMKKAMVEFEIDLKMPGLKLSRKQIESAYSIV  
LTELNGILTGERSATLILDAENRFYTLIPHDPGMKKPPLMDNEEVIKAKTMTLDNLLEIEVAYNLLKGGD  
DGEKGDPIDAHYEKLLCKMDEVKEKASDEFAMVQEVYKNTAKHTSHYTLVEVELFKIAREGEASRYRFPQ  
QLHNRQLLWHGSRVTNYAGILSQGLRIAPPEAPVTGYMFGKGLYFADMVSKSANYCATSTASPTGLLLLC  
EVALGNMYERKHAEVSKLPGKMSTKGLGATGPDGATKTLPNGTQVPIGHGVPSVSGSSLLLYNEYIV  
YDVAQVEMKYLRMKFNKYSKW

>NP\_001104452.1 Poly-(ADP-ribose) polymerase [Drosophila melanogaster]  
MDLELPYLAAYARTGRATCKGCKSTISKDTLRIAMVQSAFHDAKVPNWFHKTFFKNQRPSSVGDIQNI  
GNLRFAQKELTDLVENIQEVIISAQLGKKRSKAFNLALKDFGIEYAKSSRSTCRGCEQKINKDLVLRKT  
VYDTEVMGYGGQPLWHHLECFAQLRSELGWFSAGDEMPGFQSLADDDQAKVKNAIPPIKSEELPDKRA  
KMELSDNTEEGEKQLKLDQNDAYFRFRDDIKNMKKKDDIILLKFNQQPVTDTEKLFQDADLLTFG  
AIESCSCEKSCQFIVNKSQYICNGNHSEWTKCNKLLKEPTRSACIVPKELKALYNFLNTVKEIPSTRIFN  
NFPFNKSTFSRSLKTNKNNDVLRVPTIPRISPPPLYNLKFSIIGLKNQHKLKRRIENLGKKGFVEKISEN  
TIAISTELEIQKKSTRMKFAELGHIHIVPEFLDFVEADTEGAIKYINSTCICSWGTDPKSRIPKETTK  
SLNSNSYITKSMPSRTFKVKDGLADVPDPSGLEDIAHVYVDSNNKYSVVLGLTDIQRNKNNSYYKVQLLKA  
DKKEYMIFRSWGRIGTNIGNSKLEEDPSESAKRNFKELIYADKTGNEYEQRDNFVKRTGRMYPIEIQYD  
DDGKLVKHESHFFTSKLEISVQNLIKLI FDI DLSMKNKTLMEFHIDMDKMLGKLSAHQIQSAYRVVKEIYN  
VLECGSNTAKLIDATNRFYTLIPHNFVGVLPTLIEHQJEDLRQMLDSLAEIEVAYSIIKSEEDVDACN  
PLNDHYAQIKTQILVALDKNSEEFILLSQVKNTHASTHKSYDLKIVDVFKVSRQCEARARPKFPFKLHNRK  
LLWHGSRLTNFGILSHGLRIAPPEAPVTGYMFGKGLYFADMVSKSANYCCTSQQNSTGLMLLSEVALGD  
NMECTSAKYINKLSNNKHSFCGRGRTMPDPTKYSIRSDGVEIPYGETITDEHLKSSLLLYNEYIVYDVAQV  
NIQYLFMRFEKYSY

>XP\_032219514.1 poly [ADP-ribose] polymerase 1 isoform X1 [Nematostella vectensis]  
MSENVDVFFTEYAKSNRSSCKSKSNIGKDSLRVARMVQSPHFDGKVPNWFHSCFFFKQFKPKSLAEIA  
GIDGLRWDQDEKFRQAQVGGASDVDPDTAAATVSVVEQPDLLAEYAKSSRSTCKHCDEQIVKGELRLAKVM  
DGEKGVYVPKWHVPCFLKAMPDLDISGLTIAQHTFGQKLKGDQKLLIDKFGSQKQISKKKGGKKSLE  
ASAAAMPKVSASEEKEEQQLKQSEAIWKIRDELKTNCSLSELEMEDNEINFPQGGTTSVDFDRCDGMFLF  
GRLLPCECHCGMLVYRSDGYHCTGNVSGWTKCAFTTQDPKRTKWIVISKELKNTDFLTKTCKCKEMKRLF  
PKLTAIQGAIPGKPLNNMMAVIGKLRKTKADVASCVAGLGGTMDRVTSKVDCCSITQAEVSKSSSKRM  
KDAEKFINIPVVSSEFLDAIKDGEFNSNIAKHSLVSWGKIKALDIVDGPLRLRRKASDSKYLGAQPKPKV  
KLVSQGAADVPAASEMEDDCHVLEVKGVVYSATLGMVDISRGTSNYYKLQVLKDKKSSRCYLFRSWGVRG  
TTTIGSGKLEDGCSHNSAVQSFEELYREKTGNWSEKMDNVFKHPNRFYPLEIDYQGAHEDVVKAKIEMGS  
KSKLPSQIQELIKMIFDVESMKRTLIEFEILDKKMPLGLKTKRKQIEKAYSVLGEAQQLSEAAKSTAVLD  
VSNRFYTLIPHDFGMRKFPLLDNEELIKLIGMLDSLMEIEVAYNLIKGTKDNGAKDPIDLHYETLKTDIRVVD  
EVLDHKSABEGLISEVSNTHATHQYELLELDVFKIKRGEBAELFKFPQJLHNRQLLWHGSRRTNYAGIL  
ILSQGLRIAPPEAPVTGYMFGKGVYFADMVSKSANYCCTSPNNIQLLLCEVALGNMHELKHAFTPKVY  
PKGKHSVKLGKTAPDPSATHTFEDGTIVPGKKGCPAPVKDSSLLLYNEYIVYDVAQVNIKYLKTKFKYK  
YGW

>XP\_047140981.1 poly [ADP-ribose] polymerase 1 [Hydra vulgaris]  
MSEDLPYNAEYAKSGRAGCKSKCNIGKDSLRIAKVMQSPHFDGKIPQWYHYSCTFFKFKPLNVSDIKNF  
DSLRWDQDEKLRQIGCPQKKDVPDGPSTNVNKNDFIEYAKSGRAKCRCKEIEKDIIRIAKIMESSE  
SKFKGLIPFWYHVCFALSKSELEAQNLTSNEDGWGELSEEDQEKVGLIEIKFKKHGKLIKKGKNINIK  
DECKDEKKEIKDEKVEKFKLQNKVEYDMRDKLQKNVPNNVRLKLLDANNYNTTGENTLLERCADGICF  
GALLTCECKTGNLVYRTEGYCTGHVSGWTSCTFLTPTPKRKKWHIPKELLLENDFLSTIKPKVEERTF  
MTTTKMTMDIKESQKRPLENRKVIIVIGKLESKGVINENKIQLLGGTLSAAVSKSCYCCISTQDEIEKSTK  
RMGTQVITYNIPVVTENFLDAVQNGEIDALMKNSIAPWGTNREMLDDKMDNFKSMKRTSSSIESSKKAKV  
IMKGGAVVDPDPSGLEKCHILSVRGELFTAVLGLVDLLRGTSNYYKQALEHDTKKKYVFRSWGVRGVT  
IGGNKLEHFVNQEDAIENFKVEYGEKTGNTVSNRKKDFVKYPNKFYPLDIDYQGNDEMLQSSITPGSLSIL  
PNPVKELIKLIFDVEAMKHALVEFEIDMKMPLGLKSKKQIETAYGCLGDCQKFLANNPDGSKILDASNR  
FYTLIPHDFGMRKFPLLDNEELIKLIGMLDSLMEIEVAYNLIKGTKDNGAKDPIDLHYETLKTDIRVVD  
KESQDFELIVEYKNTAKHTSNYSLDIEVFSIERAGEKQRVFPKDLFNKLLWHGSRRTNYAGILSQ  
GLRIAPPEAPVTGYMFGKGLYFADMVSKSANYCCTSPNNIQLLLCEVALGNMHELKHAFTPKVY  
HSCKGLGSTSPDSMDKVIDGEVLVPLGKPISTNIKDSLTLLYNEYIVYDVAQVNIKYLQKLFNICY

>XP\_003385071.1 PREDICTED: poly [ADP-ribose] polymerase 1-like [Amphimedon queenslandica]  
MADDDPYRTEYAKSNRSSCKACRETIKADSLRARMVQAPNFAKIPHWYHYSCTFFGPKMKLVSVSIG  
GMGGLRWDQDQKIQAKIDGGGATAGKRRKKGSADGEENATKKQKRTSEPDKALREQNEMIKWIKRDL  
ESHLTKGELKDLLDANGQAIKPGESCILDACADGMVFGSLGLECEGGQLVRTHYSYSCAGFISDWTGCT  
NTTTEAKRRKRWIPKQLKEYDFLKSYYKVPRTVFFEAPPTFPSVSGSIASSSSQQPIDPSKPLSGFKIA  
SSGRLSKTKGELKKLIVLSGGEMSTVNRRNTLLISNEAEVEENSSTAICAASRYQIPVVYDIEYLDVSDAS  
GDALGKVKSHTISSTWASPHLEGSNGREETSADVEKVPPLTVKMKVKGGVVDPDGLDSSHIIYQSGE  
KYTAVLGLVDITKGTNSYYKLQLESDSKGSYYLFRAMGRVGTITGGNKLEDPGYLDLDALESEFLRLYQE  
KTGTSWHIRKHARKVPGKFPYPIDIDYGEEGPSLSLSGAGSNSKLAPEIQDLIKMIFDIQMKMDAMMEFE  
IDMKMPLGLKSKRQILSAYSVLNELQNELTGAKNPSRILDGSNRFYTLIPHDFGMAKPPLEETEEMIKS  
KILMLDNLKEIEIAYSLLKTEGEGSADKPLDIHYEKLKTNMSVLDKESEEFKRLVEYVANTHAATHNQY  
QLEVEQVFNLERHGEKKRYKPSKLENRMMLWHGSRLTNFGVILSQGLRIAPPEAPVTGYMFGKGVYFAD  
MVSKSANYCWTSPQSPVGLMLLCEVALGNMYEREHADIITSLPAGKHSHTKIGRTAPDPTSNVYSESGAI  
IPMGKGTSSSRSTSLLYNEYIVYDVAQVNIKYLKRNMFYKYYR

## Alignment

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NP_001104452.1[D.melanogaster] -----MDIELPYLAERYARTGRATCKGCKSTISKDTLRIAMVMQSAFHDAK 45
XP_003385071.1[A.queenslandica] -----MADDDPPRYTEYAKSNRSCCKACRETIAKDSLRLMARVMQAPNFDK 46
XP_032819895.1[P.marinus] -----MADKPFKAEYAKSSRASCKKCGNIKEDCLRLAMVMQSPRFDGK 44
XP_014061166.1[S.salar] -----MADAQEDKLKYAEYAKSSGRASCKCKENIAKDSLRLMAIMVQSPMFDGK 48
NP_001081571.1[X.laevis] -----MAEASDKLYPAEYAKSSGRASCKKCGNIAKESLRLAIMVQSPMFDGK 47
P26446.2[G.gallus] -----MAETGDKPYPAEYAKSSGRASCKKCGESIAKDSLRLAIMVQSPMFDGK 47
BAE39743.1[M.musculus] -----MAEASERLYRYEYAKSSGRASCKKCSIESIPKDSLRLMAIMVQSPMFDGK 47
NP_001609.2[H.sapiens] -----MAESSDKLYRYEYAKSSGRASCKKCSIESIPKDSLRLMAIMVQSPMFDGK 47
XP_024101750.1[P.abelii] -----MAESSDKLYRYEYAKSSGRASCKKCSIESIPKDSLRLMAIMVQSPMFDGK 47
XP_047140981.1[H.vulgaris] -----MSEDLPYNAEYAKSSGRASCKKCKNIGKDSLRLIAKMVQSPHFDGK 45
XP_019618726.1[B.belcheri] MLAYRVQEAAKISMADEGKAYKAEYAKSNRASCCKLCKGNITKDSLRLIARMVQSPHFDGK 60
XP_032219514.1[N.vectensis] -----MSENDVPFKTEYAKSNRSCCKSKCNIGKDSLRLIARMVQSPHFDGK 46
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NP_001104452.1[D.melanogaster] VPNIWFHKTCFFKN-QRPSSVG--DIQNIIGNLRFADQKELTDLVENIQEVISAIQLGK-KRS 101
XP_003385071.1[A.queenslandica] IPHWYHFSFCFFGPKMKLVSV--SQIGMGGLRWDQKQIAKIDGGGGATAG--KKR--- 99
XP_032819895.1[P.marinus] VPQWHHFQCFWKR-ARPLTQA--DVDGFSELRSADQDRIKKHIEGSADGEGKSSSGKANG 101
XP_014061166.1[S.salar] VPHWHHFSFCFWLR-ASAQSP--ADIAGFSLRWEDQEKVKKAIETGGAAGGK-GD-VKGG 103
NP_001081571.1[X.laevis] VPHWHHYSFCFWKR-ARVLSQG--DIYGYTELRWEDQEMIKKAIETGGAAGA-GG-DSKG 102
P26446.2[G.gallus] VPHWHHYSFCFWKR-ARIVSHT--DIDGFELRWEDQEKIKKAIETGALQEER-GGTRKEV 103
BAE39743.1[M.musculus] VPHWHHYSFCFWKV-GHSIRQPDVEVDGFSSELRWDDQKVKKTAAGGVAGK---GQDGSG 103
NP_001609.2[H.sapiens] VPHWHHYSFCFWKV-GHSIRHPDVEVDGFSSELRWDDQKVKKTAAGGVATG---GQDGIG 103
XP_024101750.1[P.abelii] VPHWHHYSFCFWKV-GHSIRHPDVEVDGFSSELRWDDQKVKKTAAGGVATG---GQDGIG 103
XP_047140981.1[H.vulgaris] IPQWHYHFSFCFFK-FKPLNV--SDIKNFDLSLWDDQEKLEQIGCFQKKVDV---D---G 96
XP_019618726.1[B.belcheri] VPHWHHYSFCFFKK-CKPSST--VEFSQVTLRWDDQEKLKKTIGGEGSAGA---DAGGD 114
XP_032219514.1[N.vectensis] VPNIWFHFSFCFFKKQFKPKSL--AEIAGIDGLRWDDQEKFRQAQVYGGASDVPD---TTAAA 101
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NP_001104452.1[D.melanogaster] KAFNLALKDFGIEYAKSSRSTCRGCEQKINKDLVRLKRTVYDTEVMGYGGQPLWHHLEC 161
XP_003385071.1[A.queenslandica] ----- 99
XP_032819895.1[P.marinus] AAASNTLPDFLVEYAKSNRSCCKGDDKIEKDDVRISRKMINIE-KPHLGMDHWHYTNC 160
XP_014061166.1[S.salar] AKGECTLNDFAVEYAKSNRSTCKGCEQKIEKQIRVSKKTVDPE-KPQLGLDRWYHTAC 162
NP_001081571.1[X.laevis] KGEMTLNDFAAEYAKSNRSCCKGCEQKIEKQIRISKKSVDE-KPQLGMDRWYHPDC 161
P26446.2[G.gallus] GKAESKTLGDFAAEYAKSNRSTCKGCEQKIEKQIRISKKMVHPE-KPQLGMDRWYHPDC 162
BAE39743.1[M.musculus] GKAECTLGDFAEYAKSNRSCCKGCEKIEKQGMRLSKMVDE-KPQLGMDRWYHPTC 162
NP_001609.2[H.sapiens] SKAECTLGDFAEYAKSNRSTCKGCEKIEKQVRLSKMVDE-KPQLGMDRWYHPGC 162
XP_024101750.1[P.abelii] SKAECTLGDFAEYAKSNRSTCKGCEKIEKQVRLSKMMLDE-KPQLGMDRWYHPGC 162
XP_047140981.1[H.vulgaris] PSNSTVKNKDFCIEYAKSGRAKCRKCEEKIEKDIRIAKIMESBE-SKFGGLIPFWYHVKC 171
XP_019618726.1[B.belcheri] EVDAPGVQVSVEYAKSNRSCRCGCEKIDKGLVRISKKVDE---GDQWGPGLWHHVDC 155
XP_032219514.1[N.vectensis] TVS-VEQPDLLAEYAKSSRSTCKHCEQIVKGELRLAK-VMD---GEKYPVPKWHHVPC 156

NP_001104452.1[D.melanogaster] FAQLRSELGMWFA--SGEDMPFGQS LADDQAKVKNAIPPIKSEELPDTKRA----- 210
XP_003385071.1[A.queenslandica] -----KKGKSADGENAT 112
XP_032819895.1[P.marinus] FVEHRDITGLFSTYGANQIGGFTRLNANDKKAVETLLGTVVVDGKR--KAEDQVDEVA-- 216
XP_014061166.1[S.salar] FVGRREELVFKPEYSAQQLKGFTNLRVEDKEELKRLPAVKSKGKR--KTDEVDGEGASK 220
NP_001081571.1[X.laevis] FVSSREELGFLPYSYASQLKGFTLSAEDKDSLKKLPAVKNEGKR--KADEVGHSAAT 219
P26446.2[G.gallus] FVSRRAELGFLPAYGATQLLGFSLKAEDKETLKKQLPATKTEGKR--KGEEVDGNVV-A 219
BAE39743.1[M.musculus] FVSKRDELGFRPEYASQLKGFTLSAEDKEALKKQLPAIKNEGKR--KGDEVGDTDEVA 220
NP_001609.2[H.sapiens] FVKNREELGFRPEYASQLKGFTLLATEDKEALKKQLPGVKSEGRK--KGDEVGDVEVA 220
XP_024101750.1[P.abelii] FVKNREELGFRPEYASQLKGFTLLATEDKEALKKQLPGVKSEGRK--KGDEVGDVEVA 220
XP_047140981.1[H.vulgaris] FALSKELEAQ-NLTSNEIDGWGELSEEDQEKVGLIEFKFKHGKLIKKNKINIKDECK 214
XP_019618726.1[B.belcheri] FVKREELGFTTDMAPSVIQGYKLSKDDQDILVKLLSGTGTGKRK--AKG---SNG-AA 225
XP_032219514.1[N.vectensis] FLKAMPDLDISGITLAQHFTGQFKLGDDQKLLIDKFGSQKQISKK--KGGKKSLEASAA 214

NP_001104452.1[D.melanogaster] --KMELSDTNEEGEKQRLKQNDQDAYFRFRDDIKNMKKKIDIDILLKFNNQPVFTGDTCK 268
XP_003385071.1[A.queenslandica] K-----KQKTESPEDKALREQNEMIMWIKDKLESHLTGKELKDLLDANGQAI PKGE-SC 166
XP_032819895.1[P.marinus] -KKTKLESMQKEEKEEMLKQKSNVMSFPGDLKSCSDIEDLKELLIANQAVPSGE-SA 274
XP_014061166.1[S.salar] KKKQ---EEEEKKVLQMKRQSQLIWGIKKLQKCFSTNDMKELLIANQEVPSGE-SN 276
NP_001081571.1[X.laevis] KKKIKKEKEK-ESKLEKLLKEQTELIIWHIKDELKKVCSTNDLKELLIANQQVPSGE-TN 277
P26446.2[G.gallus] KKKSRKEKEK-ESKQEKQLKEQTELIIWIKDELKKVCSTNDLKELLIANQQEVPSGE-NA 277
BAE39743.1[M.musculus] KKKSKKGKDKSSLEKALKAQNELIWNIKDELKKACSTNDLKELLIFNQQVPSGE-SA 279
NP_001609.2[H.sapiens] KKKSKKEKDKD-SKLEKALKAQNDLIWNIKDELKKVCSTNDLKELLIFNQQVPSGE-SA 278
XP_024101750.1[P.abelii] KKKSKKEKDKD-SKLEKALKAQNDLIWNIKDELKKVCSTNDLKELLIFNQQVPSGE-SA 278
XP_047140981.1[H.vulgaris] D-----EEKKIEKDEKVEKFLQNKQEYWMRDKLQKNVNNVRLKLLDANNYNTTGE-NT 269
XP_019618726.1[B.belcheri] A-----KKVKAETEKEKLEKQSKLVWKIRDELKSKMENSDLKELLANDQDIPSGE-SA 280
XP_032219514.1[N.vectensis] M-----PVKSASEEKEEQKLEQSEAIWKIRDELKTNCSLSELREMLDNEINFPQGE-TS 269
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NP_001104452.1[D.melanogaster] LFDQTADLLTFGATIESCECNQCQFVNVKSGYICNGNHSEWTKCNKLLKEPTRSACIVPK 328
XP_003385071.1[A.queenslandica] ILDACADGMVFGSLGLCEECG-GQLRVRTHSYSCAGFISDWTKCTNTTAEKRRKRWIPK 225
XP_032819895.1[P.marinus] VLERLADGMAGFALLPCECKGQGLVCMDSAYRCSGNISGWTCTFTSKTPKRNEMIPK 334
XP_014061166.1[S.salar] VVDSLGDGMAGFALLPCEECG-GQLVFKSDAYYCTGDSLAWTKCVFKTQLPNRKDMVTPK 336
NP_001081571.1[X.laevis] IVDRVSDGMAGFALLPCEECG-GQVFVKGDAYYCTGDSLAWTKCVAKTQTPNKKDMVTPK 336
P26446.2[G.gallus] ILDRVADGMAGFALLPCEECG-GQVFVFKSDAYYCSGDTIATWTKCVAKTQTPNKKDMVTPK 336
BAE39743.1[M.musculus] ILDRVADGMAGFALLPCECKS-GQLVFKSDAYYCTGDTIATWTKCMVKQTQPNRSKEMVTPK 338
NP_001609.2[H.sapiens] ILDRVADGMAGFALLPCEECG-GQLVFKSDAYYCTGDTIATWTKCMVKQTQPNRSKEMVTPK 337
XP_024101750.1[P.abelii] ILDRVADGMVFGALLPCECKS-GQLVFKSDAYYCTGDTIATWTKCMVKQTQPNRKEMVTPK 327
XP_047140981.1[H.vulgaris] LLERCADGICPGALLTCECKTGNLVVRTEGYCTGHVSGWTSCTFLTQTQPKKKWHIIPK 339
XP_019618726.1[B.belcheri] LLDRSLDGMAGFALLQRCPECKHGQLFYRSDGYHCSGNLTETWTKCIYITREPKRKKMIPD 340
XP_032219514.1[N.vectensis] VFDRCS DGMGLFGRLLPCHCHGMLVYRSDGYHCTGNVSGWTKCAFTTQDPKRTKMVISK 329
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NP_001104452.1[D.melanogaster] ELKALYNFLNTVKEIPSTRIFNFFPNKSTFSRSLKLTNK-----NNNDVLRVPTIPRI 381
XP_003385071.1[A.queenslandica] QLK-EYDFLKSYYKVPRTVFPEAPPTSPSVGS-----IASSSSQQIDP 270
XP_032819895.1[P.marinus] EFK-DVPLFKKYYKQRRVFMASQATTSPPPRAATVATATVATAATKSGEAPGTSAGAVP 393
XP_014061166.1[S.salar] EFH-ELPFLKKFKFRQDRVFPKVPAPAPPASSAAVPCAS-----SAPSIPLPEGAPA 387
NP_001081571.1[X.laevis] EFH-EIPLYKKFKFRHRAFPPCAAPT-PI S-----PPAA-----PEPKPTVEETFPE 383
P26446.2[G.gallus] EFR-EIPLYKKFKCKQDRIFPPEAATVNSAP---PPP-----ASAPLTETVTAQ 383
BAE39743.1[M.musculus] EFR-EISYLKKLVKKQDRIFPPESPAPLA---LPLSV-----TSAPTAVNSSAPA 387
NP_001609.2[H.sapiens] EFR-EISYLKKLVKKQDRIFPPETSASVAAT---PPPST-----ASAPAAVNSSASA 386
XP_024101750.1[P.abelii] EFR-EISYLKKLVKKQDRIFPPETSAPVAAT---PPPST-----ASAPAAVNSSASA 387
XP_047140981.1[H.vulgaris] ELLLENDFLSTIKPKVEERTFTMTTMMNT-----DIKESQ 364
XP_019618726.1[B.belcheri] DLKEEVPLFKKFSKVAARVFSAAHVAASSES-----TDSFSSSSRADE 364
XP_032219514.1[N.vectensis] ELKKTNDPLKTFCKCKEMKRLFPKLTAIQPG-----AIP 382
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NP_001104452.1[D.melanogaster] SPPLYNLKFSIIGL-KNQHKELRKRIENLGGKFEVKISENTIAIISTELEIQKKS-TRMK 439
XP_003385071.1[A.queenslandica] SKPLSGFKFIASSGRLSKTKGELKLLVLGGEMSTVNRTNLTLLISNEAEVEENSTAIC 330
XP_032819895.1[P.marinus] GKLLAGKALCLVGLQKSRDDIKALVEKLGKMTSTVP-KADFCISTKKEVEKMS-KKIA 445
XP_014061166.1[S.salar] DKPLTGMKLLTVGKLQNKDELKAAVEELGGKITGTAN-KATLCLSTKKEVEKMS-KKME 445
NP_001081571.1[X.laevis] GKPLTNTKVLTLIGKLSKNKDEVKTLIEGLGGKVAGSAH-KANLCISTNKEVEKMS-KKME 445
P26446.2[G.gallus] DKPLTNMKILTLGKLSKNKEEVKNIVIEELGGKMTTAN-KATLCISTQKEVEKMS-KKME 441
BAE39743.1[M.musculus] DKPLSNMKILTGLKLSKNKDEAKAVIEKLGGLKLTGSAN-KASLCISTKKEVEKMS-KKME 445
NP_001609.2[H.sapiens] DKPLSNMKILTGLKLSRNKDEVKAMIEKLGGLKLTGTAN-KASLCISTKKEVEKMN-KKME 444
XP_024101750.1[P.abelii] DKPLSNMKILTGLKLSRNKDEVKAMIEKLGGLKLTGTAN-KASLCISTKKEVEKMN-KKME 444
XP_047140981.1[H.vulgaris] KRPLENRKVIIVGKLKESKGVIENKQLLGGTLAAVSKSCYCCISTQDEIEKST-KRMQ 423
XP_019618726.1[B.belcheri] KKLPLH-HVKVVLGKTKSKAEMTKAIEKLGTVASKVDSTVACVISKEDVQMS-KKIK 442
XP_032219514.1[N.vectensis] GKPLSNMMAVIGKLRKTADVASCVAGLGGTMDRVTSKVDCCISTQAEVSKSS-KRKM 421
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NP_00104452.1 [D.melanogaster]	FAEELGHIGVIEPIEFLDVFADTEGAIKYINSTICISWGTDPKPSRIPEKTTKS-----	491
XP_003385071.1 [A. queenslandica]	AAASRYQIPVVDIEFLDVFADG-----DALGQKVKHSTIISSWTASPHLESGNGREET-----	490
XP_032819895.1 [P. marinus]	EAEQTCNVCVVDFDLDT-----ASGRFLAEIYSAHRLSTWGAPIVKEQTEPTVPEVLVPEK	503
XP_014061166.1 [S. salar]	EAEVEGVVDFEEDFLDTDKSSGKALQELVSLHLAISFWGAEVKLETPAQQA-----SRSGAMA	509
NP_001081571.1 [X. laevis]	EVKAAENVRVVSEDFLKEFVES-----GKSVQELLSQFGIISWGAEVKLEQAVQFTEKQ-----PSSGGA	499
P26446.2 [G. gallus]	EVKDACKVRVVEEFPLDKVDSNNKGFLVSLHLSISFWGAEVKLETPAQQA-----SRSGAMA	509
BAB39743.1 [M. musculus]	EVKEANIRVVSEDFLQDVQVASTKSLQELLSAHLSSWGAEVKLEPGEVAVSKSGKAA-----PS	504
NP_01609.2 [H. sapiens]	EVKEANIRVVSEDFLQDVQVASTKSLQELFLAHLISLPSWGAEVKLEPGEVAVPRGKSGAALS	504
XP_024101750.1 [P. abelii]	EVKEANIRVVSEDFLQDVQVASTKSLQELFLAHLISLPSWGAEVKLEPGEVAVPRGKSGAALS	504
XP_047140981.1 [H. vulgaris]	TKTYNTYIPVVTENFLDAVQNG-----EIDA-LMKNISIPAGVNRNREMLDKKDN-----F	471
XP_019618726.1 [B. belcheri]	DAKAADVHVEQDFVTDVDEKG-----GAALLIMKRSIASWGSDPHSRATVIE-----K	490
XP_032219514.1 [N. vectensis]	DAEKNFIPVVEEFLDAVDEK-----EFNSNIAKHLSISWGKILATIDVDEL-----P	471
NP_00104452.1 [D.melanogaster]	-----LNSNSIYTKSMFVSRTFKVKDGLVDPDSGLIEDIAHVYSDNSNNKSVLVGLDTIQ	546
XP_003385071.1 [A. queenslandica]	-----DSAVFEFLTVTKMKVKGGAUVDPDSGLNDSHHIYVEQGEKYVATGLVGDIT	432
XP_032819895.1 [P. marinus]	ASAKSSKRKSGEQKAENKLLITVKGAADVDPDSGLNDSHHIYEDLRDMGRIYGAAMSLDVE	469
XP_014061166.1 [S. salar]	GKSTKRKVEEGESGKASKMKMLITVKGAAVDPDSGLENSAHVLELDNQNGKISATLGLVDIV	563
NP_001081571.1 [X. laevis]	GKSSGKVGKEEGSKSMKKMLITVKGAAADIPDSDELENSCHVLTDEGKGFISATLGLVDIV	563
P26446.2 [G. gallus]	MKASAGVKEEGQPSKSEKKMLITVKGAAVDPDSGLESAHVLEKGGKGFISATLGLVDIV	563
BAB39743.1 [M. musculus]	KKSGAV-----KEEGNKSEKKMLITVKGAAVDPDSGLESAHVLEKGGKGFISATLGLVDIV	563
NP_01609.2 [H. sapiens]	KKSKGQV-----KEEGNKSEKKMLITVKGAAVDPDSGLESAHVLEKGGKGFISATLGLVDIV	563
XP_024101750.1 [P. abelii]	KKSKGQV-----KEEGNKSEKKMLITVKGAAVDPDSGLESAHVLEKGGKGFISATLGLVDIV	563
XP_047140981.1 [H. vulgaris]	K-----SMKRKTSYIESSKAAVMKMGGAUVDPDSGLESHCHILSVRGELITAVLGLVDIV	521
XP_019618726.1 [B. belcheri]	PKSSKSKTSYIEMSEGTKLKMMVKGAAVDPDSGLESAHVLEKGGKGFISATLGLVDIV	521
XP_032219514.1 [N. vectensis]	LRKASDSKYELGASQPKVKVLISVKGGAUVDPASEMEDDCHVLEKGGVYSATLGLVDIVS	530
NP_00104452.1 [D.melanogaster]	RNKNISYKQQLLADKADKEKYVIFRWSGRIGTINISKLEPDT-----SEAKRNFIYADKT	605
XP_003385071.1 [A. queenslandica]	RGNTSYKQQLLESDSKYGLVYFRWGRVGTITIGNKLEFDGYDITLSEFFRLYQKRT	622
XP_032819895.1 [P. marinus]	RGNTSYKQQLLEDDHKNRYKVVFRSGRGLTITIGTKLEKMS-----REDAVEHFCQLVYDKT	622
XP_014061166.1 [S. salar]	RGNTSYKQQLLEDDHKNRYKVVFRSGRGLTITIGTKLEKMS-----REDAVEHFCQLVYDKT	622
NP_001081571.1 [X. laevis]	RGNTSYKQQLLEDDHKNRYKVVFRSGRGLTITIGTKLEKMS-----REDAVEHFCQLVYDKT	622
P26446.2 [G. gallus]	RGNTSYKQQLLEDDHKNRYKVVFRSGRGLTITIGTKLEKMS-----REDAVEHFCQLVYDKT	622
BAB39743.1 [M. musculus]	RGNTSYKQQLLEDDHKNRYKVVFRSGRGLTITIGTKLEKMS-----REDAVEHFCQLVYDKT	622
NP_01609.2 [H. sapiens]	RGNTSYKQQLLEDDHKNRYKVVFRSGRGLTITIGTKLEKMS-----REDAVEHFCQLVYDKT	622
XP_024101750.1 [P. abelii]	RGNTSYKQQLLEDDHKNRYKVVFRSGRGLTITIGTKLEKMS-----REDAVEHFCQLVYDKT	622
XP_047140981.1 [H. vulgaris]	RGNTSYKQQLLEDDHKNRYKVVFRSGRGLTITIGTKLEKMS-----REDAVEHFCQLVYDKT	622
XP_019618726.1 [B. belcheri]	RGNTSYKQQLLEDDHKNRYKVVFRSGRGLTITIGTKLEKMS-----REDAVEHFCQLVYDKT	622
XP_032219514.1 [N. vectensis]	RGNTSYKQQLLEDDHKNRYKVVFRSGRGLTITIGTKLEKMS-----REDAVEHFCQLVYDKT	622
NP_00104452.1 [D.melanogaster]	GNEYEQDRNFVRRTRGMVPIELIQQDDQKLVKHES-----HFFTSKLEISVQNLIKLFIDFS	563
XP_003385071.1 [A. queenslandica]	CTSNHRRKHAKNVKCEPPIELIQQDEEGPGLS-----LSGASGKLAFIEIQLIKMIFDQK	651
XP_032819895.1 [P. marinus]	GKNKWA-----RNFYKVPKNFYPLDIQQDEEAGVLEHDLKAMAGNSKALQELIRHMFIDQK	681
XP_014061166.1 [S. salar]	GNAMWS-----SHTFYKPNFYPLDIQQDEEAVKRLTASAGTNSLAKPVQELITFDVES	677
NP_001081571.1 [X. laevis]	GNAMWS-----SHTFYKPNFYPLDIQQDEEAVKRLTASAGTNSLAKPVQELITFDVES	677
P26446.2 [G. gallus]	GNAMWS-----SHTFYKPNFYPLDIQQDEEAVKRLTASAGTNSLAKPVQELITFDVES	677
BAB39743.1 [M. musculus]	GNAMWS-----SHTFYKPNFYPLDIQQDEEAVKRLTASAGTNSLAKPVQELITFDVES	677
NP_01609.2 [H. sapiens]	GNAMWS-----SHTFYKPNFYPLDIQQDEEAVKRLTASAGTNSLAKPVQELITFDVES	677
XP_024101750.1 [P. abelii]	GNAMWS-----SHTFYKPNFYPLDIQQDEEAVKRLTASAGTNSLAKPVQELITFDVES	677
XP_047140981.1 [H. vulgaris]	GNAMWS-----SHTFYKPNFYPLDIQQDEEAVKRLTASAGTNSLAKPVQELITFDVES	677
XP_019618726.1 [B. belcheri]	GNAMWS-----SHTFYKPNFYPLDIQQDEEAVKRLTASAGTNSLAKPVQELITFDVES	677
XP_032219514.1 [N. vectensis]	GNAMWS-----SHTFYKPNFYPLDIQQDEEAVKRLTASAGTNSLAKPVQELITFDVES	677
NP_00104452.1 [D.melanogaster]	GNTWSNRKDFVKYKPNFYPLDIQQDEEAGVLEHDLKAMAGNSKALQELIRHMFIDQK	681
XP_003385071.1 [A. queenslandica]	GNTWSNRKDFVKYKPNFYPLDIQQDEEAGVLEHDLKAMAGNSKALQELIRHMFIDQK	681
XP_032819895.1 [P. marinus]	GNTWSNRKDFVKYKPNFYPLDIQQDEEAGVLEHDLKAMAGNSKALQELIRHMFIDQK	681
XP_014061166.1 [S. salar]	GNTWSNRKDFVKYKPNFYPLDIQQDEEAGVLEHDLKAMAGNSKALQELIRHMFIDQK	681
NP_001081571.1 [X. laevis]	GNTWSNRKDFVKYKPNFYPLDIQQDEEAGVLEHDLKAMAGNSKALQELIRHMFIDQK	681
P26446.2 [G. gallus]	GNTWSNRKDFVKYKPNFYPLDIQQDEEAGVLEHDLKAMAGNSKALQELIRHMFIDQK	681
BAB39743.1 [M. musculus]	GNTWSNRKDFVKYKPNFYPLDIQQDEEAGVLEHDLKAMAGNSKALQELIRHMFIDQK	681
NP_01609.2 [H. sapiens]	GNTWSNRKDFVKYKPNFYPLDIQQDEEAGVLEHDLKAMAGNSKALQELIRHMFIDQK</	

XP_003385071.1[A.queenslandica]	LLCEVALGNMYEREHADYITSLPAGKHSTKGIGRTAPDPTSNYVSESGAII PMGKGTSS	850
XP_032819895.1[P.marinus]	LLAEVALGNMHELKQSESI TKLPKGTHSVKVGKRTAPDPKKT VTL-NGVQVP IGNPSATG	986
XP_014061166.1[S.salar]	LLGEVALGNMHELKKAASHITKLPKGKHSVKGLGRNAPDPSATVTL-DGVQVPLGKGNTN	978
NP_001081571.1[X.laevis]	LLGEVALGNMHELKKAASQITKLPKGKHSVKGLGRTAPDPSATVQL-DGVDVPLGKGTSAN	974
P26446.2[G.gallus]	LLGEVALGNMYELKNASHITKLPKGKHSVKGLGRTAPDPTATTTL-DGVEVPLNGISTG	975
BAE39743.1[M.musculus]	LLGEVALGNMYELKNASHISKLPKGKHSVKGLGKTTPDPSASITL-EGVEVPLGTGIPSG	978
NP_001609.2[H.sapiens]	LLGEVALGNMYELKNASHISKLPKGKHSVKGLGKTTPDPSANISL-DGVDVPLGTGISSG	978
XP_024101750.1[P.abelii]	LLGEVALGNMYELKNASHISKLPKGKHSVKGLGKTTPDPSASISL-DGVEVPLGTGISSG	978
XP_047140981.1[H.vulgaris]	LLCEVALGNMYELKQSEHISKLPKGKHSVKGLGSTSPDPSMDKVIDCEVLVPLGKPISTN	944
XP_019618726.1[B.belcheri]	LLCEVALGNMYERKHAIEYVSKLPKGKHSVKGLGATGPDGATKTL PNGTQVPIGHGVPSG	967
XP_032219514.1[N.vectensis]	LLCEVALGNMHELKHA SFIKKVPGKHSVKGLGRTAPDPSATHTFEDGTIVPKGKGCPAP	948
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NP_001104452.1[D.melanogaster]	HLKSSLLYNEYIVYDVAQVNIQYLFRMEFKYSY----	994
XP_003385071.1[A.queenslandica]	SRSTSLLYNEYIVYDVAQINMKYLIKMFYKYYR----	883
XP_032819895.1[P.marinus]	INDTSLLYNEYIVYDVAQVNIKYLKLNFKYKQLW----	1022
XP_014061166.1[S.salar]	IDDTSLLYNEYIVYDVAQVNLKYLKIKFNKYQMSMW----	1014
NP_001081571.1[X.laevis]	ISDTSLLYNEYIVYDIAQVNLKYLKLNFKYKGMWM----	1011
P26446.2[G.gallus]	INDTCLLYNEYIVYDVAQVNLKYLKLNFKFNKTSLW----	1011
BAE39743.1[M.musculus]	VNDTCLLYNEYIVYDIAQVNLKYLKLNFKFNKTSLW----	1014
NP_001609.2[H.sapiens]	VNDTSLLYNEYIVYDIAQVNLKYLKLNFKFNKTSLW----	1014
XP_024101750.1[P.abelii]	VNDTCLLYNEYIVYDIAQVNLKYLKLNFKFNKTSLW----	1014
XP_047140981.1[H.vulgaris]	IKDSTLLYNEYIVYDVAQVNIKYLVLQLFNICY----	977
XP_019618726.1[B.belcheri]	VSGSSLLYNEYIVYDVAQVEMKYLI RMKFNKYSLW----	1002
XP_032219514.1[N.vectensis]	VKDSSLLYNEYIVYDIAQINMKYLLKTKFKYKYGW----	983
	: ***** **::: **.: ::::	

## Percent identity matrix:

```
#
#
# Percent Identity Matrix - created by Clustal2.1
#
#
1: NP_001104452.1[D.melanogaster] 100.00 45.19 40.18 41.21 42.21 42.13 41.10 41.66 41.76 43.42 42.96 43.56
2: XP_003385071.1[A.queenslandica] 45.19 100.00 49.08 51.72 51.15 54.02 50.46 51.21 51.09 49.59 53.75 52.20
3: XP_032819895.1[P.marinus] 40.18 49.08 100.00 59.56 58.58 59.76 57.07 56.67 56.47 48.76 53.02 50.57
4: XP_014061166.1[S.salar] 41.21 51.72 59.56 100.00 72.14 73.63 69.18 69.88 69.68 50.16 54.22 52.52
5: NP_001081571.1[X.laevis] 42.21 51.15 58.58 72.14 100.00 77.98 73.66 74.06 73.66 50.47 55.10 52.94
6: P26446.2[G.gallus] 42.13 54.02 59.76 73.63 77.98 100.00 77.86 78.95 78.95 51.40 55.09 53.34
7: BAE39743.1[M.musculus] 41.10 50.46 57.07 69.18 73.66 77.86 100.00 92.40 92.60 50.31 54.93 52.87
8: NP_001609.2[H.sapiens] 41.66 51.21 56.67 69.88 74.06 78.95 92.40 100.00 99.41 51.29 54.38 53.24
9: XP_024101750.1[P.abelii] 41.76 51.09 56.47 69.68 73.66 78.95 92.60 99.41 100.00 51.19 54.18 53.24
10: XP_047140981.1[H.vulgaris] 43.42 49.59 48.76 50.16 50.47 51.40 50.31 51.29 51.19 100.00 51.71 52.38
11: XP_019618726.1[B.belcheri] 42.96 53.75 53.02 54.22 55.10 55.09 54.93 54.38 54.18 51.71 100.00 55.38
12: XP_032219514.1[N.vectensis] 43.56 52.20 50.57 52.52 52.94 53.34 52.87 53.24 53.24 52.38 55.38 100.00
```