

# PARP3

## Sequences :

>NP\_001003931.4 protein mono-ADP-ribosyltransferase PARP3 isoform a [Homo sapiens]  
MAFKPKFWQTEGPEKKKGQAGREEDPFRSTAEALKAIPA EKRIIRVDPTCPLSSNPGTVVYEDYNCTL  
NQTNIEINNKKFYIIQLLQDSNRFFTWNWRGVRGVEVGQSKINHTRLEDAKKDFEKKFREKTKNNWAER  
DHVFSHPGKYTLIEVQAEDEAQEAVVKVDRGPVRTVTKRVQPCSLDPATQKLTINIFSKEMFKNTMALMD  
LDVKMPLGKLSKQIARGFEALEALEALKGPTDGGQSLLELSSHFYTVIPHNFGHSQPPPINSPELLQ  
AKKMDMLVLADIELAQAALQAVSEQEKTVVEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQTGSNNH  
RCPTLQHIWKVNQEGEEDRFQAHSKLGNRKLWWHGTNMAVVAAILTSGLRIMPHSGGRVKGKIYFASENS  
KSAGYVIGMKCAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIARGHTEPDPTQDTELELDGQ  
QVVVPQGPVPCPEFSSSTFSQSEYLIYQESQCRLRYLLEVHL

>XP\_002813722.3 poly [ADP-ribose] polymerase 3 isoform X1 [Pongo abelii]  
MSLLFLAMAPKKRPSVQTEGPEKKKGQAGREEDPFRSAAEALKAIPA EKRIIRVDPTCPLSSNPGTVVYE  
DYDCTLNQTNIGNNNKKFYIIQLLQDSDRFTCNWRGVRGVEVGQSKINHTRLEDAKKDFEKKFREKTKN  
NWAERDRFVSHPGKYTLIEVQAEDEAQEAVVKVGGPVRTVAKRVQPCSLDPATQKLTINIFSKEMFKNT  
MALMDLDVKMPLGKLSKQIARGFEALEALEALKGPTDGGQSLLELSSHFYTVIPHNFGRSQPPPINS  
PELLQAKKMDMLVLADIELAQAALQAASEQEKMVVEVPHPLDRDYQLLKCQLQLLDSGAPEYKVIQTYLEQ  
TGSNHRCPRTLQHIWKVNREGEEDRFQAHSKLGNRKLWWHGTNMAVVAAILTSGLRIMPHSGGRVKGKIYF  
ASENSKSAGYVTGMKCAHHVGYMFLGEVALGREHHINTDNPSLKSPPPGFDSVIARGHTEPDPTQDTELE  
ELDGGQVVVPQGPVPCPEFSSSTFSQSEYLIYQESQCRLRYLLEVHL

>EDL21147.1 poly (ADP-ribose) polymerase family, member 3, isoform CRA\_a [Mus musculus]  
MAPKKRASVQTGEGSKKQGTTEEDSFRSTAEALRAAPADNRVIRVDPSCPFSRNPQIQVHEDYDCTLNQ  
TNIGNNNKKFYIIQLLEEGSRFFCWNWRGVRGVEVGQSKMNHFTCLEDAKKDFEKKFREKTKNKNWEERDRF  
VAQPNKYTLIEVQGEAESQEAIVKVYSGPVRTVVKPCSLDPATQNLITNIFSKEMFKNAMTLMNLDVKRM  
PLGKLTQOIARGFEALEALEAMKNPTDGGQSLLELSSCFYTVIPHNFGSRSPPPINSFDVLQAKKMDML  
VLADIELAQTLLQAAPEEEEEKVVEVPHPLDRDYQLLRCQLQLLDSGESEYKAIQTYLKQTGNSYRCPNL  
RHWKVNREGEEDRFQAHSKLGNRKLWWHGTNMAVVAAILTSGLRIMPHSGGRVKGKIYFASENSKSAGY  
VTMTMCGGHQVGYMFLGEVALGKEHHITDDPSLKSPPPGFDSVIARGQTEPDPAQDIELELDGQPVVVV  
QGPVPQCPSPFKSSSFSQSEYLIYKESQCRLRYLLEIHL

>XP\_040537823.1 protein mono-ADP-ribosyltransferase PARP3 [Gallus gallus]  
MAPKRRAPASQPADGGKKAKGGEEEEDAWSSALTALTAPREKPPATIDGQCPLSAGDPADKYVEDYDC  
TLNQTNISANNKKFYIIQLIEHGGTYSTWNWRGVRGVEVGQSKLLPFTSLAAAKDFEKKFREKTKNRMWA  
RDMFVAPQKGKTYTLIEVQPGAGQEAVALVDGAGDEKVSRRVLPALDETTQKLVALIFSSDMFRHAMQAM  
NLDVKRMPLGKLSKQIARGFEALEALEALGEGQPSMSRLEELSSRFYTVIPHNFGRARPPPIDSPPELL  
RAKKMDMLVLADIEVAQSQAQKVEEEVVAHPLDRDYALLCCQLTLLEDTSQBEVEMILNVAQTGGQVY  
VLNWRVAEGEDLFGADHLEHRRLLWHGTNMAVVAAILKNGLRIMPHSGGRVKGKIYFASENSKSAC  
YVGCTSKRVGLMFLTEVALGKPYCITRDEPTLQQPPNGYDSVQACGRTEPDPAQDVEVTLDDKKVLVCQG  
KPIMPAYKSSFFQSEYLIYQESQCRIRYLVQLHF

>XP\_018121381.1 poly (ADP-ribose) polymerase family member 3 L homeolog isoform X1 [Xenopus laevis]  
MAPKRRAAATKAKASGKIKTKVKEEVKEEEIEQPVKATDRFQSAVQALKAASGKKGKAKVDSCCHLSCGG  
DYEVYEDYDCLMNQTNIGSNNNKFYVILITSKKESYCNWRGVRGVELGQSKLSFPFNLAGAQKDFEKKF  
KDKTKNSWSERENFTAHPGKYTMIIEVQHNDDDDDGSGEATVYKADTVGTVQKVPCSLDKPTQDLMSLI  
FSSDMFEKAMQTMNLDIKKMPGKLSKAQIAGGFEALDELQAALDRKANKGVLSDLSRFYTVIPHNFG  
RTPPVIDTVEVLQAKKMDMLVLADIELAQTLLQADKVKKEEEEEKVQEVPHPLDVIDYGLLKCDSLSDLT  
EYKVINTVYKNTGPSYSPLKILNVMSVNREKEEERLNAHKDIDNRLLWHGTNIAVVVAILKSGLRIMP  
HSGGRVKGKIYFASENSKSAGYVGCTSKNLGIMFLNEVALGKEHHITMDDCSLKSPPKGYDSVVARGCTE  
PDPAKDRVLALDGRKITVPQGPPIKMEKYNCTFSQSEYLYVKESQARLRYLILLQF

>XP\_045560960.1 poly [ADP-ribose] polymerase 3 isoform X1 [Salmo salar]  
MAPKRRASSTKANKTGGKKVKQEPDTPKDAFTSAKEALKAAGPEVKGKKRADEHCLLSEQHSGRVHEDY  
DCLMNQTNIGNNNKFYVIVQLCIDDSYYCWTWRGVRGVEGTGQSNLSDLSNSPDKAIRDKEKKFKDKTKNS  
WKERDNFESHGPKYTLIEVQDQDAEVKVCVQKVIKGFPRNILLCTLSDPTQKLIQLIFSNMFKFEAME  
CNMLDIKKMPLGKLSKQIAGGFEVLEIEGAMNASRKLEELSSKFFTTIPHNFGTRPPIVDSSEIVE  
KKKMDMLVLADIEIAQNLKAEKTEKAQMEVEKVPHALDQNYLSLSCKLSLLQRTDQEKFVIERYLKATA  
CSHNQPKIIVMVEDRETEAERFENDGLENRLLWHGTNMAVVAAILKGGLRIMPQSGGRVGRGIYFAS  
ENSKSAAYVRTSKDRGVMLNEVALGKENTITMDDSLKEAPTYGNCVVARQLEPDSKDIFLTLDGKQ  
VAVPQGEPIKQPYQYKDSFFSNSEYLVYKENCQRIRYLLELKF

>XP\_032819077.1 protein mono-ADP-ribosyltransferase PARP3 [Petromyzon marinus]  
MAPKRRKAAAKGKRQKKVKAEPVPPAVDKVETRKALKTEPGSKAKAKIDSACNLANKTGLEVHEDY  
DCLMNQTNIGHNNKKFYIIQLIAGDGKFTYTRWRGVRGEGGQNAMKTFGNVAEAIKDFEKKFKDKTKNNW  
QQRDEFTAHPGKYTLIEHQHEDDEEEGEKPVVSVDAVDGSLTKKVIKPCSLPKQTDLMSLIFSNDMFKD  
AMKEMNLDVKMPLGKLSKAQIGRGFDALAEALRTAAGQRNLESLSTFFFTIIPHNFGMRPVPVINS  
QEIIRNKKMDMLVLADIVLAQSLQADKRAAAAAGEGDVGTVEVPHPLNADYDLKCELELLGENSH  
LAVIQVVAATAPSYMKNVNCVMKNREGECECFKAHEELSNRLLWHGTNIAVVVAILKSGLRIMPHSGG  
RVGRGIYFASQNEKSAQYMGYACDGRGVMLNEVVLNGEFTITKDDCSLKQAPAGYDSVVARGHVEPDK  
KDVILELDGKQVTVPGGRPVQAKFKQSNFSHSEYLVYNENQCRIRYLLVSNK

>XP\_019634302.1 PREDICTED: poly [ADP-ribose] polymerase 3-like [Branchiostoma belcheri]  
MPRAAKRKAATKGGDSASPOLSKMIVAQLKQECTKQGLTAGTKAVLLKRLQENTGAGGKKVTEDTAP  
TTAKAAAEKLLKADSPKTKKYVKVDSFCLNGRGVQDDYDCLMNQTNIGHNNKFYIIQLIRTAGVSPY  
YVNRWRGVRGEPQSGALKGPWDLTEAKKDFEKKFKDKTKNWSKRGSPVFPFKGKYTLLEMDTEETDEDEQ  
DTAEKIALLDQLDGPSKNVPLSSLSQTSLIKLIFDNDFEKMMAKMEIDVRKMPGKLSKAQIAGKFE  
VLDEIEEVLTKGRTSGLTELSRFYTVIPHDFGRVPVPIQNDQEKLRKKMDMLVLVLDGIEIAQAMQKDKD  
KDDGSEATDVKHPDLNLDLNCLELLKPSSEEFKVIKYEATKYSGWRDPKILNVKWDVRSGEGRDF  
KEHDHLENRKLWWHGTNMAVVAAILKTGLRIMPHSGGRVGRGIYFASENSKSAGYVGCASGNVGMFLNE  
VALGKEKRITRDDSSLTKAPSGFDSVVAVGHREPDPKKNTMTKLDGRTVVVPQGPINQTEGQSSSFSQS  
EYLVYKENCQRIRYLLKMKFGS

>AAM50807.1 LD31274p [Drosophila melanogaster]  
MKFAEELGHIVPIEFLDFVEADTEGAIKYINSTCICSWGTDPKSRIPKETTKSLSNSIYTKSMPVSRT  
FKVKDGLAVDPDSGLEDIAHVYVDSNNKYSVVLGLTDIQRNKNYSYKVLKADKADKEKYWIFRSWGRIGT  
NIGNSKLEEFDTSESARNFKIEIYADKTGNEYEQRDNFVKRTGRMYPIEIQYDDDKVLKHESHFTSKL  
EISVQNLIKLIFDIDSMNKTLMFEHIFDMDKMPLGKLSAHQIQSAYRVVKEIYNVLECGSNTAKLIDATNR  
FYTLIPHNFGVQLPTLIEHQIEDLRQMLDSLAEIEVAYSIIKSEDSVACNPLDNHYAQIKTLQVALD  
KNSEFEFSLSQYVKNTASTHKSVDLKIVDVFKVSRQGEARRFPFKFKLHNRKLWWHGSRLTNFVGILSH  
GLRIAPPEAPPTGYMFGKIYFADMVSKSANYCCTSQNSTGLMLLSEVALGDMMECTSAKYINKLSNNK  
HSCFGRGRMFPDFTKSYIRSDGVEIPYGETITDEHLSKSLLYNEHIVYDQVNIQYLFMEFKYSY

>XP\_047143363.1 protein mono-ADP-ribosyltransferase PARP3 [Hydra vulgaris]  
MPKRRKVAQKASSIEETLPIKFSDLKVPKELKAECLRNLEDGKKKADLIERLEEYENQSNTSTKKVK  
KEEKEDEKPVITKDKLALAEKEKADKKMFKVDSLCTLASNASVDDYDCLMNQTNVGHNNKFYVILQ  
TCSGAGYVVMNRGVRGEAGANAIGKPFNDQQYAIKEFTKFKFEKTKNNWEDKNFQPVAGKYTLLEMDG  
EDEPFGYTEKNLDAVDSPLTVKVKTRPCKLDKPTESLILKIFDNDFEKAEMANNIDVKMPLGKLSKSQ  
IAGKFEVLEEIQVEINKNKSSKQLDLSRFFFTLIPHNFGRQRPPTISDQETLQMKMDMLTVLGDIEIAQS  
LQNVVVKKEEVEDHPLDTNYGLLKCDLKHIDCKSDTFKIINNYIEQTKSSYGNIKLLDVWEVDVRMGE  
RFSAHNIDKNRKLWWHGTNMAVVAILKSGLRIMPHSGGRVGRGIYFASEHAKSAGYVGTARDGTGIMFL  
NEVALGKHIIITQDSSSLKAPPKGYDSVLAKRGREPDPMSMTSLIINGNTVTVPGQKPVETDAHSSSFHQ  
SEYLIYKESQNRIRYLLKMKFH

>XP\_019856101.1 PREDICTED: poly [ADP-ribose] polymerase 3-like [Amphimedon queenslandica]  
MPFKRQRKRTAAAKEDEPTTSAVAPLNPAAITVTQLRAELSKGLDITGKKALLVQRLTDSLKSSDEPS

TTKKAKTEDPAEDEGEEDTTEGELTYSKAAAALRQADKKKEGKRQRTVDTHIPWYTNIEVVDDWDCML  
NQTNIHNNKFFYIQLLSNKNNGYFHVWNRWGRVGEFGMNMKGPFHAMDAATKEFAKKFKDKTKNDWS  
DRDSFTPHAGKYTLIEMGGDDDEPMDVIEDVDTGKPKKIKPCTLDKPTQNLVKLIFDNDMFREAMKTL  
EIDTKMPLGKLSKAQIAKGFEALEALESALQSKASRAKLSLSKFFYTIIPHDFGRRIPPPVIDNQEHLQ  
KKFDMLTVLGDIEIAQSLQKDKIKTEQPDIEEVPHFEDVNYASLKAKLEHVKKEDSDYKIIETYLQTEP  
SYRKLEIVDIWRVSRDGEAERFSVHDSIENRLLMHGTNAVVAAILKSGLRIMPHSGGRVGRGIYFASE  
NSKSAGYVGCANNIGIMFLNEVALGKEHSITRDDSSLVKAPAGHDSVVARGHTEPDPALDTTITIDGKT  
TVFQGGPKSQKYSTSSFSQTEYLIYKESQNRIRYLLKLFGGHSFFF

[illegible]

XP_020103931.1[H.sapiens]	LGNRKLWLHGHGTMMAVVAAILTSLGLRMIPH----	SGGRVGKGVIYFASENSKSAGYVIGMKC	431
XP_020813722.3[P.abellii]	LGNRKLWLHGHGTMMAVVAAILTSLGLRMIPH----	SGGRVGKGVIYFASENSKSAGYVIGMKC	436
XP_01812381.1[X.laevis]	IDNRLLWGHGTHIAVVVAALKSLGLRMIPH----	SGGRVGKGVIYFASENSKSAGYV--GC	445
XP_032819077.1[P.marinus]	LSNRKLWLHGHGTHIAVVVAALKSLGLRMIPH----	SGGRVGKGVIYFASQNEKSAGYVM--GY	441
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AAM50807.1[D.melanogaster]	QQNSTLMLLESEVALGDMMECTSAK-YINKLSNNHKSCFGRGRTMDFPTKSY-----IRSDG	512	
XP_047143363.1[H.vulgaris]	ARDGTGIMFLNVAIGKQHITITQDDSLSLAKPPKGYSIVAAKGRPEPDMSTSLIINGNT	520	
XP_019634302.1[B.belcherii]	ASGVNGIMFLNVALGEKKRITRDDSSLTKAPSGDVSVAVHGHEPDPKKNTMKLDGRT	538	
XP_019856101.1[A.jenlandica]	-ANNIGIMFLNVALGKEHSITRDDSSLTKAPAGHDSVAVARGTEPPDALDTITIDGKT	559	
XP_045506960.1[S.salar]	TSKDRGMFLNVALGKENITITMDSSLSKEATPGYTCNVARGQLPEPDPKDIFLTLDGKQ	490	
XP_040537823.1[G.gallus]	TSKRQGMFLTEVALGKYPCYTIREDTPLTKQPPNGDYVSQAQGRETPEDPAQDEVTLDGKK	484	
BDJ21147.1[M.musculus]	GHHQGVYMFLEVALGKEHNHITITDPSLSKPPGFDYSIARGTEPFPDAQDILEELDGQ	486	
XP_01003931.4[H.sapiens]	GAHHGVYMFLEVALGREHNHTINDPSLSKPPGFDYSIARGTEPFPDQTDELTLEDGGQ	491	
XP_020813722.3[P.abellii]	GAHHGVYMFLEVALGREHNHTINDPSLSKPPGFDYSIARGTEPFPDQTDELTLEDGGQ	496	
XP_01812381.1[X.laevis]	TSKNLGMFLNVALGKEHNITMDPSLSKPPGKVDYSVARGTEPFPDKDRVLALDGRK	505	
XP_032819077.1[P.marinus]	ACDGRGVFMFLNVLGNFTITDKDCSLKQAFAGDYSVARGHVTEPFPKKDVILELDGKQ	501	
	: *:*****::: ...*, **** :	* :*:***** ** *	
AAM50807.1[D.melanogaster]	VEIPYGTEITIDEHLK-SSLIYNLYIVDYDAQNRIYLFRMEFKYSY----	557	
XP_047143363.1[H.vulgaris]	VTVFQGKFVETDA-HSSSPHQSEYILYKESQNIIRYLLKMKFH-----	582	
XP_019634302.1[B.belcherii]	VTVFQGQFINQIQSQSSSFQSQEYLVYKENQCIRRYLLKMKFGS-----	582	
XP_019856101.1[A.jenlandica]	VTVFQGQSQKQYKYSTSSFSQEYILYKESQNIIRYLLKMKFGHSHFFF	608	
XP_045506960.1[S.salar]	VAVFQGEPIKQFQKDSFFSNSEYLVYKENQCIRRYLLELKFI-----	532	
XP_040537823.1[G.gallus]	VLVCQKGFIMPAYKDDSSFFQSQEYILYKESQNIIRYLVQLHF-----	526	
BDJ21147.1[M.musculus]	VTVFQGPVPVQCFKFSKSSSFQSQEYILYKESQCLRLYLELHL-----	528	
XP_01003931.4[H.sapiens]	VTVFQGPVPVCFEFSSTTSFSQEYILYKESQCLRLYLELVHL-----	538	
XP_020813722.3[P.abellii]	VTVFQGPVPVCFEFSSTTSFSQEYILYKESQCLRLYLELVHL-----	538	
XP_01812381.1[X.laevis]	ITVFQGPVKMEKYNCSTFSQSQEYLVYKESQARLYLLLLLF-----	547	
XP_032819077.1[P.marinus]	VTVFQGRPVQVAKFKQNSFHSHEYLVYNEQCNIIRYLLVLSNK-----	544	
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## Percent identity matrix:

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#
# Percent Identity Matrix - created by Clustal2.1
#
#
1: AAM50807.1[D.melanogaster] 100.00 31.67 33.52 30.97 33.13 33.81 31.64 31.39 31.21 33.67 31.72
2: XP_047143363.1[H.vulgaris] 31.67 100.00 57.27 55.57 54.05 51.47 51.87 50.59 50.77 56.98 53.58
3: XP_019634302.1[B.belcheri] 33.52 57.27 100.00 56.89 57.89 55.21 54.31 54.76 55.19 57.12 56.12
4: XP_019856101.1[A.queenslandica] 30.97 55.57 56.89 100.00 55.34 52.91 52.91 50.67 51.52 57.60 53.99
5: XP_045560960.1[S.salar] 33.13 54.05 57.89 55.34 100.00 57.14 57.45 55.09 56.43 61.98 60.04
6: XP_040537823.1[G.gallus] 33.81 51.47 55.21 52.91 57.14 100.00 63.44 61.30 62.38 60.99 55.77
7: EDL21147.1[M.musculus] 31.64 51.87 54.31 52.91 57.45 63.44 100.00 81.40 82.70 62.19 57.34
8: NP_001003931.4[H.sapiens] 31.39 50.59 54.76 50.67 55.09 61.30 81.40 100.00 97.18 59.13 56.62
9: XP_002813722.3[P.abelii] 31.21 50.77 55.19 51.52 56.43 62.38 82.70 97.18 100.00 60.38 57.20
10: XP_018112381.1[X.laevis] 33.67 56.98 57.12 57.60 61.98 60.99 62.19 59.13 60.38 100.00 61.50
11: XP_032819077.1[P.marinus] 31.72 53.58 56.12 53.99 60.04 55.77 57.34 56.62 57.20 61.50 100.00
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