

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q9C0C2	TB182_HUMAN	Homo sapiens	182 kDa tankyrase-1-binding protein	19.217476	S422;T819;T1154	S14;T131;S178;S221;S228;T239;S287;S301;S429;S435;S437;S494;S498;T501;S601;S672;S691;S695;S712;S724;S744;S762;S806;T833;S836;S851;S872;S877;S882;S893;T897;S899;S920;S936;S976;T979;S983;S987;S1004;S1008;S1013;S1024;S1029;S1054;S1073;S1091;S1103;S1133;S1138;S1158;S1178;S1248;S1253;T1282;S1297;S1328;S1331;S1383;S1385;S1435;S1439;S1450;S1452;S1473;S1476;S1503;S1506;T1518;S1533;S1545;S1558;T1563;S1620;S1621;S1631;S1652;S1666;S1715	28411811;31637018;28657654;31373491;34019948;30620550;23301498;30397120	MKVSTLRESSAMASPLPREMEEELV PTGSEPGDTRAKPPVKPKPRALPAKP ALPAKPSLLVVPVGRPPRGPLAELPS ARKMNMLAGPQPYGGSKRPLPFAP RPAVEASTGGEATQETGKEEAGKEE PPPLTPPARCAAPGGVRKAPAPFRPA SERFAATTVEEILAKMEQPRKEVLAS PDRLWGSRLTFNHDGSSRYGPRTYG TTTAPRDEGSTLFRGWSQEGPVKS PAECREEHSKTPEERSLPSDLAFNG DLAKAASSELPADISKWPSSPAPSS ENGGPASPGLPAEASGSGPGSPHLH PPDKSSPCHSQLLEAQTPEASQASP CPAVTPSAPSAALPDEGSRHTPSPGL PAEGAPEAPRPSSPPEVLEPHSLDQ PPATSPRPLIEVGELLDLTRTFPSGG EEEAKGDAHLRPTSLVQRRFSEGLV QSPSQDQEKLGSLAALPQGQGSQ ALDRPFGAESNWSLSQSFWEWTFPTR PSGLGVWRLDSPPPSPITEASEAAEA AEAGNLAVSSREEGVSQQGQGAGSA PSGSGSSWVQDDPSMSLTQKGDG ESQPQFPVPLEPLPTTEGTPGLPLQ QAEERYESQEPLAGQESPLPLATREA ALPILEPVLGQEQAAPDQPCVLFAD APEPGQALPVEEEAVTLARAETTQAR TEAQDLCRASPEPPGPESSSRWLDD LLASPPPSGGGARRGAGAEKDTQS PSTCSEGLLQWSQKDLQSEFGITGD PQPSSFSPSSWCQGASQDYGLGGAS PRGDPGLGERDWTSKYGQGAGEGS TREWASRCGIGQEEMEASSSQDQS KVSAPGVLTAAQDRVVGKPAQLGTQR SQEADVQDWEFRKRDSQGTYSRRD AELQDQEFGKRDSLGTYSRRDVS LG DWEFGKRDSLQAYASQDANEQGGQD LGKRDHGGYSSQDADEQDWEFQK RDVSLGTYSRAAEQEQEFGKSAW IRDYSSGGSSRTLDAQDRSFGTRPLS SGFSPPEAAQQQDEEFKIPSVEDSL GEGSRDAGRPGERGSGGLFSPSTAH VPD GALGQRDQSSWQNSDASQEVG GHQERQQAGAQQPGSADLEDGEMG KRGWVGEFSLSVGPQREAAFPSPGQQ DWSRDFCIEASERSYQFGIIGNDRVS GAGFSPSSKMEGGHFVPPGKTTAGS VDWTDQLGLRNLEVSSCVGSGGSSE ARESAVGQMGWSGGLSLRDMNLTG CLESGGSEEPGGIGVGEKDWTSVDN VKSKDLAEVGEVGGGHSQARESGVG QTDWSGVEAGEFLKSRERGVGQAD WTPDLGLRNMAPGAVCSPGESKEL GVGQMDWGNLGLRDLEVTCDPDS GGSQGLRGCQVGMQMDWTQDLAPQ NVELFGAPSEAREHGVGGVSQCPEP GLRHNGSLSPGLEARDPLEARELGV GETSGPETQGEDYSSSSLEPHPADP

