

UniprotKB ID	Entry name	organism	full name	oglnaccscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion
P49792	RBP2_HUMAN	Homo sapiens	E3 SUMO-protein ligase RanBP2	42.604235	S248;S255;T561;T867;T870;T871;S874;T969;S970;T982;S993;T1021;T1026;S1039;T1045;S1047;S1048;T1053;S1061;S1063;S1065;T1071;S1072;S1118;T1396;T1399;S1400;S1509;T1513;S1514;S1583;S1592;S1613;T1638;T1757;S1768;S1869;S1884;T1885;S1890;S1894;S1912;T1941;S1953;T2192;S2199;S2263;T2480;T2492;S2499;S2835	T19;S21;T779;S781;S788;S837;S948;S955;T1098;S1103;S1107;S1110;T1144;S1160;S1249;T1396;T1412;S1443;S1450;S1456;S1509;S1520;S1573;S1833;S1835;S1869;S1871;T2005;S2008;T2153;S2246;S2251;S2270;S2280;S2290;T2293;S2297;S2462;S2493;S2510;S2526;T2613;T2666;S2668;S2741;T2743;S2805;S2900;S3207	28657654;31492838;35083852;34846842;23301498;34019948;34725712;25367160;22121020;32574038;36240223;28411811;35254053;29237092;33465208;28510447;29351928;20068230;31373491;30620550;3059200;30379171;34931806;22661428;35132862;33214551;27655845;35289036;38253038;32119511;38665916	MRRSKADVERYIASVQGSTPSPRQKSMKGFYFAKLYEAEKYDYLAKYICTYINVQERDPKAHRFLGLLYELEENTDKAVECYRRSVELNPTQKDLVLKIAELLCCKNDVTDGRAKYWLERAALKLFPGPSPAIYKLEQQLLDCEGEDGWNKLFDLIQSELYVRPDDVHVNIIRLVEVYRSTKRLKDAVAHCEAERNIALRSSLEWNSCVVQTLKEYLESLOCLESDDKSDWRATNTDLLAYANMLLTLSTRDVQESRELLQSFDSALQSVKSLGGNDEL SATFLEMKGHFYMHAGSLLLKMGQHSSNVQWRALSELAALCYLIAFOVPRPKIKLKGAGQNLLEMMACDRLSQSGHMLNLSRCKQDFLKEIVETFA NKSGQSALYDALFSSQSPKDTSFGLSDDIGNIDVREPELEDLTRYDVGAI RAHNGSLQHLTWLGLQWNSLPALPG IRKWLKQLFHHLPHETSRLETNAPE SICILDLEVFLLGVVYTSHLQLKEKCN SHHSSYQPLCLPLVCKQLCTERQKSWWDVAVCTLIHRKAVPGNVAKLRL LVQHEINTLRAQEKHGLQPALLVHW AECLQKTGSGLNSFYDQREYIGRSV HYWKVLPPLKIIKKNSIPEPIDPLF KHFSVDIQASEIVEYEEADAHITFAIL DAVNGNIEDAVTAFESIKSVVSYWN LALIFHRKAEDIENDALSPEEQEACK NYLRKTRDYLIKIIDSDSNLSVVK LPVPLESVKEMLSVMQELEDYSEG GPLYKNGSLRNADSEIKHSTPSPTRY SLSPSKSYKSPKTPRWAEDQNSLL KMICQQVEAIKEMQELKLNSSNSA SPHRWPTENYGPDSVPDGYQGSQTF HGAPLTVATTGPSVYYSQSPAYNSQY LLRPAANVTPTKGPVYGMNRLPPQQ HIYAYPQQMHTPPVQSSSACMFSEQ MYGPPALRFESPATGILSPRGDDYFN YNVQQTSTNPLPEPGYFTKPPIAAH ASRSAESKTIEFGKTNFVQMPGEG LRPSLPTQAHTTQPTPFKFNFNFKS NDGDFTFSSPQVVTQPPAAYSNSE SLLGLLTSKPLQGDGYSGAKPIPGG QTIGPRNTFNFGSKNVSGISFTENM GSSQKNSGFRSDDMFTFHGPGK SVFGTPTLETANKNHETDGGSAHGD DDDDGPHFEPVPLPKIEVKTGEE DEEEFFCNRAKLFKRFVDESKEWKER GIGNVKILRHKTSGKIRLLMRREQVL KICANHYISPMKLTNAGSDRSFV WHALDYADELPKPEQLAIRFKTPEE AALFKCKFEEAQSILKAPGNTVAMA SNQAVRIVKEPTSHDNKDICKSDAG NLNFEFQVAKKEGSWWHCNSCSLK NASTAKKCVSCQNLNPSNKLGVGP LAETVFTPKTSPENVQDRFALVTPKK EGHWDCSI CLRNEPTVSRACIQN TKSANKSGSSFVHQASFQKQGDLP KPINSDFRSVFTKEGQWDCSACL VQNEGSSTKCAACQNP RKQSLPATSI PTPASFQKFTSESKTLKSGFEDMF AKKEGQWDCSSCLRNEANATRCV ACQNPDKPSPSTVPPAPASFQKFTSE TSKAPKSGFEGMFTKKEGQWDCSV CLRNEASATKCIACQNP GKQNTT SAVSTPASSETSKAPKSGFEGMFTK KEGQWDCSVCLRNEASATKCIACQ NPGKQNTTSAVSTPASSETSKAPK SGFEGMFTKKEGQWDCSVCLRNE ASATKCIACQCPKQNTTSAVSTPAS SEISKAPKSGFEGMFTKKEGQWDCSV CCVQNESSSLKCVACDASKPHTKPI AEAPSAFTLGSSEMKLHDSGSGVGT GFKSNFSEKASKFGNTEQGFKFGHV DQENSPSFMFQSSNTEFKSTKEGF SIPVSADGFKFGISEPGNQEKSEKP LENGTFQAQDISGQKNRGRVIFGQ TSSTFTFADLAKSTSGEGFQFGKDDP NFKGFSGAGEKLFSSQYGMANKA NTSGDFEKDDDAYKTEDSDDIHFEP	True	False	4.732	5.0	1.943

VVQMPEKVELVTGEEDEKVLYSQRV  
KLFRRFDAEVSQWKERGLGNLKILKN  
EVNGKLRMLMRREQVLKVCANHWI  
TTTMINLKPLSGSDRAWMWLASDFS  
DGDAKLEQLAAKFKTPELAEFFKQK  
FEECORLLLDIPLQTPHKLVDTRAA  
KLIQRAEEMKSGLKDFKTFLTNDQT  
KVTEENKSGSGTGAAGASDPTTIKPN  
PENTGPTLEWDNYDLREDALDDSVS  
SSSVHASPLASSPVRKNLFRFGESTT  
GFNFSEKLSALSPKSPAKLNQSGTS  
VGTDEESDVTQEEERDGOYFEPVVP  
LPDLVEVSSGEENEQVVFSHRAKLY  
RYDKDVGQWKERGIKILQNYDN  
KQVRIVMRRDQVLKLCANHRITPDM  
TLQNMKGTERVWLWTACDFADGER  
KVEHLAVRFLQDVADSFKKIFDEA  
KTAQEKDSLITPHVSRSTPRESPCG  
KIAVAVLEETTRERTDVIQDDVADA  
TSEVEVSSTSETTPKAVVSPPKFVFG  
SESVKSIFSSSEKSPFAFGNSSATGS  
LFGFSFNAPLKSNNSETSSVAQSGS  
ESKVEPKKCELSKNSDIEQSSDSKVK  
NLFASFPTSESSINYFKTPEKAKEK  
KKPEDSPSDDDLVLYELTPTAEQKA  
LATKCLKLPPTFFCYKNRPDYVSEEEE  
DDEDFTAVKKNGLYLDGSEKCR  
PLEENTADNEKECIIVWEKKPTVEEK  
AKADTLKLPPTFFCGVCSDDTDEDNG  
NGEDFQSELQKVQEAQKSQTEEITS  
TTDSVYTGTEVMVPSFCKSEEPDSI  
TKSISPSVSSSETMDKPVDLSTRKEI  
DTDSTSQGESKIVSFCFGSSTGLSFA  
DLASSNSGDFAFGSKDNFQWANT  
GAAVFGTQSVGTQSAGKVGEDDGS  
DEEVVHNEDIHFEPVSLPEVEVKS  
EEDDEILFKERAKLYRWDRDVSQWK  
ERGVGDIKILWHTMKNYRILMRRD  
QVFKVCANHVITKTMELKPLNVSN  
ALVWTASDYADGEAKVEQLAVRFT  
KEVADCFKTFECCQNLMLKQKG  
HVSLAAELSKETNPVVFFDVCADGE  
PLGRITMELFNSNIVPRTAENFRALCT  
GKGFVGFKNVIFHRVIPDFVCGGDI  
TKHDGTGGQSIYGDKFEDENFDVKH  
TGPGLLSMANQONTNNSQFVITLK  
KAEHLDFKHVVFVKGMDTVKKI  
ESFGSPKGSVCCRITITECGQI