| | UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence | intracellular | extracellular | cytosol | nucleus | mitochndrion | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 0 | P49792 | RBP2_HUMAN | Homo sapiens | E3 SUMO-protein ligase RanBP2 | 33.618334 | S248;S255;T561;S858;T860;T867;T870;T871;S874;T969;S970;T982;S991;S993;T1021;T1026;S1039;T1045;S1047;S1048;T1053;S1061;S1063;S1065;T1071;S1072;S1118;T1396;T1399;S1400;S1509;T1513;S1514;T1517;S1573;S1583;S1592;S1613;T1638;T1639;T1644;T1757;S1768;S1869;S1884;T1885;S1890;S1894;S1912;T1941;T1944;T1946;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 | 27655845;23301498;30379171;31492838;34725712;40914422;20068230;33465208;25367160;29237092;40596516;32574038;22661428;38665916;34931806;34846842;30059200;30620550;39534244;39302247;34019948;28510447;29351928;39531497;40307207;22121020;28657654;35289036;35132862;35083852;33214551;31373491;36240223;35254053;32119511;28411811;38253038 | MRRSKADVERYIASVQGSTPSPRQKSMKGFYFAKLYYEAKEYDLAKKYICTYINVQERDPKAHRFLGLLYELEENTDKAVECYRRSVELNPTQKDLVLKIAELLCKNDVTDGRAKYWLERAAKLFPGSPAIYKLKEQLLDCEGEDGWNKLFDLIQSELYVRPDDVHVNIRLVEVYRSTKRLKDAVAHCHEAERNIALRSSLEWNSCVVQTLKEYLESLQCLESDKSDWRATNTDLLLAYANLMLLTLSTRDVQESRELLQSFDSALQSVKSLGGNDELSATFLEMKGHFYMHAGSLLLKMGQHSSNVQWRALSELAALCYLIAFQVPRPKIKLIKGEAGQNLLEMMACDRLSQSGHMLLNLSRGKQDFLKEIVETFANKSGQSALYDALFSSQSPKDTSFLGSDDIGNIDVREPELEDLTRYDVGAIRAHNGSLQHLTWLGLQWNSLPALPGIRKWLKQLFHHLPHETSRLETNAPESICILDLEVFLLGVVYTSHLQLKEKCNSHHSSYQPLCLPLPVCKQLCTERQKSWWDAVCTLIHRKAVPGNVAKLRLLVQHEINTLRAQEKHGLQPALLVHWAECLQKTGSGLNSFYDQREYIGRSVHYWKKVLPLLKIIKKKNSIPEPIDPLFKHFHSVDIQASEIVEYEEDAHITFAILDAVNGNIEDAVTAFESIKSVVSYWNLALIFHRKAEDIENDALSPEEQEECKNYLRKTRDYLIKIIDDSDSNLSVVKKLPVPLESVKEMLNSVMQELEDYSEGGPLYKNGSLRNADSEIKHSTPSPTRYSLSPSKSYKYSPKTPPRWAEDQNSLLKMICQQVEAIKKEMQELKLNSSNSASPHRWPTENYGPDSVPDGYQGSQTFHGAPLTVATTGPSVYYSQSPAYNSQYLLRPAANVTPTKGPVYGMNRLPPQQHIYAYPQQMHTPPVQSSSACMFSQEMYGPPALRFESPATGILSPRGDDYFNYNVQQTSTNPPLPEPGYFTKPPIAAHASRSAESKTIEFGKTNFVQPMPGEGLRPSLPTQAHTTQPTPFKFNSNFKSNDGDFTFSSPQVVTQPPPAAYSNSESLLGLLTSDKPLQGDGYSGAKPIPGGQTIGPRNTFNFGSKNVSGISFTENMGSSQQKNSGFRRSDDMFTFHGPGKSVFGTPTLETANKNHETDGGSAHGDDDDDGPHFEPVVPLPDKIEVKTGEEDEEFFCNRAKLFRFDVESKEWKERGIGNVKILRHKTSGKIRLLMRREQVLKICANHYISPDMKLTPNAGSDRSFVWHALDYADELPKPEQLAIRFKTPEEAALFKCKFEEAQSILKAPGTNVAMASNQAVRIVKEPTSHDNKDICKSDAGNLNFEFQVAKKEGSWWHCNSCSLKNASTAKKCVSCQNLNPSNKELVGPPLAETVFTPKTSPENVQDRFALVTPKKEGHWDCSICLVRNEPTVSRCIACQNTKSANKSGSSFVHQASFKFGQGDLPKPINSDFRSVFSTKEGQWDCSACLVQNEGSSTKCAACQNPRKQSLPATSIPTPASFKFGTSETSKTLKSGFEDMFAKKEGQWDCSSCLVRNEANATRCVACQNPDKPSPSTSVPAPASFKFGTSETSKAPKSGFEGMFTKKEGQWDCSVCLVRNEASATKCIACQCPSKQNQTTAISTPASEISKAPKSGFEGMFIRKGQWDCSVCCVQNESSSLKCVACDASKPTHKPIAEAPSAFTLGSEMKLHDSSGSQVGTGFKSNFSEKASKFGNTEQGFKFGHVDQENSPSFMFQGSSNTEFKSTKEGFSIPVSADGFKFGISEPGNQEKKSEKPLENGTGFQAQDISGQKNGRGVIFGQTSSTFTFADLAKSTSGEGFQFGKKDPNFKGFSGAGEKLFSSQYGKMANKANTSGDFEKDDDAYKTEDSDDIHFEP | True | False | 4.732 | 5.0 | 1.944 | |

| | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | VVQMPEKVELVTGEEDEKVLYSQRV<br>KLFRFDAEVSQWKERGLGNLKILKN<br>EVNGKLRMLMRREQVLKVCANHWI<br>TTTMNLKPLSGSDRAWMWLASDFS<br>DGDAKLEQLAAKFKTPELAEEFKQK<br>FEECQRLLLDIPLQTPHKLVDTGRAA<br>KLIQRAEEMKSGLKDFKTFLTNDQT<br>KVTEEENKGSGTGAAGASDTTIKPN<br>PENTGPTLEWDNYDLREDALDDSVS<br>SSSVHASPLASSPVRKNLFRFGESTT<br>GFNFSFKSALSPSKSPAKLNQSGTS<br>VGTDEESDVTQEEERDGQYFEPVVP<br>LPDLVEVSSGEENEQVVFSHRAKLY<br>RYDKDVGQWKERGIGDIKILQNYDN<br>KQVRIVMRRDQVLKLCANHRITPDM<br>TLQNMKGTERVWLWTACDFADGER<br>KVEHLAVRFKLQDVADSFKKIFDEA<br>KTAQEKDSLITPHVSRSSTPRESPCG<br>KIAVAVLEETTRERTDVIQGDDVADA<br>TSEVEVSSTSETTPKAVVSPPKFVFG<br>SESVKSIFSSEKSKPFAFGNSSATGS<br>LFGFSFNAPLKSNNSETSSVAQSGS<br>ESKVEPKKCELSKNSDIEQSSDSKVK<br>NLFASFPTEESSINYTFKTPEKAKEK<br>KKPEDSPSDDDVLIVYELTPTAEQKA<br>LATKLKLPPTFFCYKNRPDYVSEEEE<br>DDEDFETAVKKLNGKLYLDGSEKCR<br>PLEENTADNEKECIIVWEKKPTVEEK<br>AKADTLKLPPTFFCGVCSDTDEDNG<br>NGEDFQSELQKVQEAQKSQTEEITS<br>TTDSVYTGGTEVMVPSFCKSEEPDSI<br>TKSISSPSVSSETMDKPVDLSTRKEI<br>DTDSTSQGESKIVSFGFGSSTGLSFA<br>DLASSNSGDFAFGSKDKNFQWANT<br>GAAVFGTQSVGTQSAGKVGEDEDGS<br>DEEVVHNEDIHFEPIVSLPEVEVKSG<br>EEDEEILFKERAKLYRWDRDVSQWK<br>ERGVGDIKILWHTMKNYYRILMRRD<br>QVFKVCANHVITKTMELKPLNVSNN<br>ALVWTASDYADGEAKVEQLAVRFKT<br>KEVADCFKKTFEECQQNLMKLQKG<br>HVSLAAELSKETNPVVFFDVCADGE<br>PLGRITMELFSNIVPRTAENFRALCT<br>GEKGFGFKNSIFHRVIPDFVCQGGDI<br>TKHDGTGGQSIYGDKFEDENFDVKH<br>TGPGLLSMANQGQNTNNSQFVITLK<br>KAEHLDFKHVVFGFVKDGMDTVKKI<br>ESFGSPKGSVCRRITITECGQI | | | | | |