

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P49792	RBP2_HUMAN	Homo sapiens	E3 SUMO-protein ligase RanBP2	36.945258	S248;S255;T561;T867;T870;T871;S874;S970;T982;S993;T1026;S1039;T1045;S1047;S1048;T1053;S1061;S1063;S1065;T1071;S1072;S1118;T1396;T1399;S1400;T1513;S1514;S1583;S1592;S1613;T1638;T1757;S1768;S1869;S1884;T1885;S1890;S1894;S1912;S1953;T2192;S2199;S2263;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	30379171;33214551;27655845;31492838;32119511;30620550;20068230;30059200;25367160;33465208;28657654;29351928;31373491;29237092;34019948;22121020;28411811;22661428;32574038;23301498;28510447	MRRSKADVERYIASVQGSTPSPRQK SMKGFYFACKLYEAKYDLAKKYICT YINVQERDPKAHRFLGLLYELEENT DKAVECYRRSVELNPTQKDLVLKIAE LLCKNDVTDGRAKYWLERAALKLFPG SPAIFYKLKEQLLDCGEDGWNKLFDF LIQSELYVRPDDVHVNRILVEVYRST KRLKDAVAHCEAERNIALRSSLEW NSCVVQTLKEYLESLOCLESDKSDW RATNTDLLLAYANLMLLTLSTRDVO ESRELLQSFDSALQSVKSLGGNDEL SATFLEMKGHFYMHAGSLLLKMGQ HSSNVQWRALSELAALCYLIAFQVP RPKIKLIKGEAGQNLLEMMACDRLS QSGHMLLNLSRGKQDFLKEIVETFA NKSGQSALYDALFSSQSPKDTSFGL SDDIGNIDVREPELEDLTRYDVGAI AHNGSLQHLTWLGLQWNSLPALPG IRKWLKQLFHHLPHETSRLETNAPE SICILDLEVFLLGVVYTSHLQLKEKC NSHHSSYQPLCLPLPVCKQLCTERQ KSWWDVAVCTLIHRKAVPGNVAKLRL LVQHEINTLRAQEKHGLQPALLVHW AECLQKTGSGLNSFYDQREYIGRSV HYWKKVPLLLKIIKKNSIPEPIDPLF KHFHSDVIQASEIVEYEEADAHITFAIL DAVNGNIEDAVTAFESIHSVSYWN LALIFHRKAEDIENDALSPEEQEACK NYLRKTRDYLIKIIDSDSNLSVVKK LPVPLESVKEMLSVMQLEDYSEG GPLYKNGSLRNADSEIKHSTPSPTRY SLSPSKSYKYSKPTPPRWAEDQNSLL KMICQQVEAIKKEMQELKLNSSNSA SPHRWPTENYGPDSVPDGYQGSQTF HGAPLTVATTGPSVYYSQSPAYNSQY LLRPAANVTPTKGPVYGMNRLPPQQ HIYAYPQQMHTPPVQSSACMFSQE MYGPPALRFESPATGILSPRGDDYFN YNVQQTSTNPPLEPGYFTKPIIAAH ASRSAESKTIEFGKTNFVQMPGEG LRPSLPTQAHTTQPTPFKFN SNFKS NDGDFTFSSPQVVTQPPAAYSNSE SLLGLLTSDKPLQGDGYSGAKPIPGG QTIGPRNTFNGSKNVSGISFTENM GSSQQKNSGFRSDDMFTFHGPGK SVFGTPTLETANKNHETDGGSAHGD DDDDGPHFEPVVPLPDKIEVKTGEE DEEEFFCNRAKLFRFDVESKEWKER GIGNVKILRHKTSGKIRLLMRREQVL KICANHYISPDMLTPNAGSDRSFV WHALDYADELPKPEQLAIRFKTPEE AALFKCKFEEAQSILKAPGTNVAMA SNQAVRIVKEPTSHDNKDICKSDAG NLNFEFQVAKKEGSWWHCNSCLK NASTAKKCVSCQNLNPSNKELVGPP LAETVFTPKTSPENVQDRFALVTPKK EGHWDCSICLVRNEPTVSRACIQN TKSANKSGSSFVHQASFQFGQDLP KPINSDFRSVFSTKEGQWDCSACLV QNEGSSTKCAACQNPRKQSLPATSI PTPASFKFGTSETSKTLKSGFEDMF

AKKEGQWDCSSCLVRNEANATRCV
 ACQNPDKPSPSTSVAPASFKEFGTSE
 TSKAPKSGFEGMFTKKEGQWDCSV
 CLVRNEASATKCIACQNPQKQNTT
 SAVSTPASSETSKAPKSGFEGMFTK
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 NPGKQNTTSAVSTPASSETSKAPK
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 LENGTFQAQDISGQKNGRQVIFGQ
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 EVNGKLRMLMRREQVLKVCANHWI
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 KIAVAVLEETTRETQVQDDVADA
 TSEVEVSSTSETTPKAVVSPPKFVFG
 SESVKSIFSSEKSKPFAFGNSSATGS
 LFGFSFNAPLKSNNSETSSVAQSGS
 ESKVEPKKCELSKNSDIEQSSDSKVK
 NLFASFPTEESSINYFTKPEKAKEK
 KKPEDSPSDDDLIVYELTPTAEQKA
 LATKLKLPPTFFCYKNRPDYVSEEEE
 DDEFETAVKKNLNGKLYLDGSEKCR
 PLEENTADNEKECIVVEKKPTVEEK
 AKADTLKLPPTFFCGVCSDTDEEDNG
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 TKSISPSVSSETMDKPVLDSTRKEI
 DTDSTSQGESKIVSFGFGSSTGLSFA
 DLASSNSGDFAFGSKDNFQWANT
 GAAVFGTQSVGTQSAGKVEDEDGS
 DEEVVHNEDIHFEPVSLPEVEVKSG
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 ERGVGDIKILWHTMKNYRILMRRD
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 ALVWTASDYADGEAKVEQLAVRFKT
 KEVADCFKKTFECCQNLMLKQKG
 HVSLAAELSKETNPVFFDVCADGE
 PLGRITMELFSNIVPRTAENFRALCT
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 TKHDGTGGQSIYGDKFEDENFDVKH
 TGPGLLSMANQQQNTNNSQFVITLK

