	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	ext reg
0	A0A0B4K7J2	RBP2_DROME	Drosophila melanogaster	E3 SUMO-protein ligase RanBP2	28.06426	S1243;T1500;S1819;T1858;S1860;S1938	NaN	40245499	MFTTRKEVDAHVHKMLGKLQPGRE RDIKGLAVARLYMKVQEYPKAIEYLN GYLRVRDDAVGHNMIATCYSRLNPP DVTEALQHYQRSIQIDPRQSEVVIDA CELLVKENNASITECARYWLDQANS LDLSGNKQVFNLRMRVNLADSNGE RDDTSGGDGEQNTLEILMYKELQAR PQDVNIRIQLLRSYVEKMKIDQAFNY ALKTELESKNCTSQSNEWYEQIWM VLFKIEMAKDVKKNWRFWHFALHT LDRLVQLSLEGSGLADSSKQLFRLD QYLFKFSTSIERSGDAPQRDLHQACI DHFTGQLLLHAVTLIFKREVLANKN KWMSTLRSALPLLLLGYQVRPIDDS STNQWIKHCDAEQKQLIQMWRPQG AFRCAQLGRTLLGCLDRSQMEIKND RENAEFDENKNSGNSMPGLFADSE ELLASAHQQCLDKSWRSQIYQQLFT HAEHKLKDTSSHLVRNLRLQLPLFE WPNLAHIENYELQALVLPPHSLAQH VYLALGTDPNKLGDAPRVVFYEGFQ RDVKQNLNYCGQDSISQVDVDLYLY ATTIQTRRKLQIQREVYDSSNLGNR NAAARPHMMPFANLVGQLGAPEQS NWWDLVVRLNSNQLITEGNRAEQR AQLQHGLEAVRGVNGPKADAIIIFQL GKILNSRSDRSSLEARIDTLYRQGFSI LRHQHNQQMESYVRVFKYGSAGST AAWQDLQSLAEEAVTYFSEKMFRIG QYEQFLDEVRGLHLPMAYFLQSEAC HHLEESSKLPRTSRDRYSERRRECL QKTQKLIKNDDKHPLIAAMHRHQQ DRNSRGIDNSFGSPDVHNNSSAYED AEDDFYSHAAFSANRSRRQLEVTPV TPIVMAQPSQEMEQAVKQISKSLCV LKDDVSVGMEAMRQDIKVLTEKFTG LEDLLKKIKISSRDTPTRDVDPAAAL GLDDLFIIEDALAEHQQQQQHQQQQ SHNQGAIHPVVPNPYTSGFYNGMP NTPSAQERFLQGPYGSPMFNQNQM YNYYAAQAQAQAQAQFLRTPPAPGSI PPPNMFGPRNPNFGLPSMFPPPTVP SVAPYIDAMGNFTQPPPSLIPPPAQP AAPPAPLNILESKPVVALPTPGFFNT TTPVFGASPIQVPQSKPLTVPTVPIPS TAPAPPIAGTVNPPATTAVPPPVHIPQ VAPSVPAQPPAPAPVSVPSMFNRAL NNQPVEKEPPANVVITSSDPLPKPTT ASVQPTLSVTIPAQHIKPSLVQAPEQ PAQSAQPAQPSVSGVGSLSFNFGSK SSESPFSFKTQVAKAAAEKQKEQEE AEQNQSGATDPNKTLPQDTSADDYD PRPDFKPIIPLPDEVEVRTGEEGEDIK FTSRAKLFRYVDKEWKERGTGVIKIL CDKATGVSRVLMRRDQTHKVCANH TITADITINVANQDKDKKSLLWAAND FADEQVTLERFLVRFKTGELAEEFR VAFTKASEAAKSKETVKPTVNTAEK GSTATAPAAFKSFVTSTPAANSLINK PQEQTKTQPNPDPPATAAKSLFGTLS VSAAPATSAPASATPFASFSFTPNGS SGFGTSTASPFGNLSFGTASAVGSG NNTTLFTTALIKDNTVQGKTLQQES QLNKSNSSDAEEEYVPTAQFVPVIAL PDIVEVVTGEENEDVLFEHRAKLLR WDKEANEWKERGLGNMKLLRDRT DPNKVRLLMRREQVHKLCCNQRLL PETKFTYATNCKAAVTWGAQDYSDE ELTTALLAVRFKSQDICQQFLEAVQK AQQSIGNEPKKEEVPSAAGEKEKPIK GFGDAFKPKAGSWNCQACYTNNGQ DQLYCLACQEPKDATVPPKQSGLDQ GNALNLTTSSSNKFSFGFASSATLPA TGGFSFGGATQPKEKPAVAVVTASA SAPTSVQTAALGFGKSSMTSGFGDA FKPAVGSWSCSACYVNNPGESLYCS ACDAPKNDTVPQKEKSLGSGLNLPP TSKFSFGFGAAAAGDKDQAGDGATF NFAAMPAAVAPTTSIGSSSFTFSMTK PKPDQQQPNSTAAKEDEDNDSQEV	True	False	3.134	4.267	1.536	1.422	1.126	1.525	1.1

									EEEENNTYFSPVIPLPDKIDVKTGEE DEELLYVHKAKLYRLNESDWKERGL GDVKILRHRQTKKLRVVMRREQVFK ICLNHVLNENVVYREKTETSWMFAV HDFSEGESVLERFTLRFKNKEVAQG FMEAIKNALNETAKPIEDSPVVGSVS QSTEANKPSQKNDGAAKSRGGESEV LDVGKTSSVRPTTHEVIPPLPMTLPL LTLPQPLAKPNDYQTPATILFKGSSL SRNNSSASEASKTPSSAFIFGSTDKS EPGKDAGPLANLQKLASGEGQGNVL GSIFRSGSSNENSSDGSVKFFFGGG NKAAEQQKKDSSESVFGGNKADSQ SPATQEAPKLAFGGIAAPVFGDANPF GGHKVNLQKSDGKEEPKSIIGGTPLL FGGSNAFGIPKIETQSPAKDFVFGSA PAFGQMATFSFTAAKNEKEKDITSN NTTDLKAEGKEKKELVPETTSTFADL AKTGSTFADLASNPGGTFADLANKT GNDFANLSANSQGTTVGFNKSAGG GFYNLTHQNAFKNFESPQATEECD DDGDATTDDNYDPHYDAIVELPDEI VVTTGEENETKLFGERAKLYRYDAE SKQWKERGVGEIKVLEHPELQTFRLI MRQEQIHKLVLNMNISASLQMDYM NAQMKSFLWAGYNYAVDAEGKVDT EGVLERLACRFAKEEIASEFLNTVNS CIKRAKALQGDEENKNDDAPEEQAS S								