

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus
P08775	RPB1_MOUSE	Mus musculus	DNA-directed RNA polymerase II subunit RPB1	34.742345	S651	S27;S217;T1840;S1843;S1845;S1847;S1849;S1850;T1854;S1857;T1860;S1861;T1863;S1864;T1867;S1868;T1870;T1874;S1875;T1877;S1878;T1881;S1882;T1885;T1894;S1896;S1899;S1906;T1909;T1912;S1913;T1915;T1916;S1917;T1919;S1920;T1923;T1926;S1927;T1929;T1930;S1931;T1933;S1934	29187734;24968300;34418053;39627609	MHGGGPPSGDSACPLRTIKRVQFGV LSPDELKRMSTVTEGGIKYPETTEGG RPKLGGLMDPRQGVIERGRCQTCFA GNMTECPGHFGHIELAKPVFHVGF VKTMKVLRCVCFCSKLLVDSNNPK IKDILAKSKGQPKRRLTHVYDLCKGK NICEGGEEMDNKFGVEQPEGDEDL TKEKGHGGCGRYQPRIRRSGLLEYA EWKHVNEDESQEKILLSPERVHEIF KRISDEECFVLGMEPRYARPEWMIV TVLPVPPLSVRPAVVMQGSARNQDD LTHKLADIVKINNQLRRNEQNGAAA HVIAEDVKLLQFHVATMVDNELPGL PRAMQKSGRPLKSLKQRLKGGKEGRV RGNLMGKRVDFAARTVITPDPNLSI DQVGVPRSIANMTFAEIVTPFNIDR LQELVRRGNSQYPGAKYIIRDNGDRI DLRFHPKPSDLHLQGTGYKVERHMC DGDIVIFNRQPTLHKMSMMGHRVRI LPWSTFRLNLSVTTTPYNADFDGDEM NLHLQSQLETRAEIQELAMVPRMIV TPQSNRPVMGIVQDILTAVRKFTKR DVFLERGEVMNLLMFLSTWDGKVP QPAILKPRPLWTGKQIFSLIPGHINC IRTHSTHPDDEDSGPKHISPGDTKV VVENGELIMGILCKKSLGTSAGSLVH ISYLEMGHDITRLFYSNIQTVINNWL LIEGHTIGIGDSIADSKTYQDIQNTIK KAKQDVIEVIEKAHNNELEPTPGNT LRQTFENQVNRILNDARDKTGSSAQ KSLSEYNNFKSMVVS GAKGSKINIS QVIAVVGQONVEGKRIPFGKHRTL PHFIKDDYGPESRGFVENSYLAGLTP TEFFFFHAMGGREGLIDTAVKTAETG YIQRRLIKSMESVMVKYDATVRNSIN QVVQLRYGEDGLAGESVEFQNLATL KPSNKAFEKKFRFDYTNERALRRTL QEDLVKDVLSNAHIQNELEFERM REDREVLRVIFPTGDSKVVLPCLLLR MIWNAQKIFHINPRLPSDLHPKVVVE GVKELSKKLVIVNGDDPLSRQAQEN ATLLFNHILRSTLCSRRAEEFRLSG EAFDWLLGEIESKFNQAIHPGEMV GALAAQSLGEPATQMTLNTFHYAGV SAKNVTLGVPRLKELINISKKPKTPS LTVFLLGQSARDAERAKDILCRLEHT TLRKVTANTAIYYDPNPOSTVVAEDQ EWNVYVYEMPDFDVARISPWLLRVE LDRKHMTRDKLTMEQIAEKINAGFG DDLNCIFNDDNAEKLVRIRIMNSD ENKMQEEEEVVDMDDDVFLRCIE SNMLTDMTLQGIEQISKVYMHLPQT DNKKKIITEDGEFKALQEWILETDG VSLMRVLSKEDVDPVRTTSNDIVEIF TVLGIEAVRKALERELYHVISFDGSY VNYRHLALLCDTMTCRGHLMAITR HGVMNRQDTGPMKCSFEETVDVLM EAAAHGSDPMKGVSENI MLGQLA PAGTCGFLLLLDAEKCKYGMIEPTNI PGLGAAGPTGMFFGSAPSPMGGISP AMTPWNQGATPAYGAWSPSVSGSM TPGAAGFSPSAASDASGFSPGYS WSPTPGSPGSPGSSPYIPSPGGAMS PSYSPTSPAYEPRSPGGYTPQSPSYS PTSPSYSPTSPSYSPTSPNYSPTSPSY SPTSPSYSPTSPSYSPTSPSYSPTSPS YSPTSPSYSPTSPSYSPTSPSYSPTSP SYSPTSPSYSPTSPSYSPTSPSYSPTSP PSYSPTSPSYSPTSPSYSPTSPNYSPT SPNYTPTSPSYSPTSPSYSPTSPNYTP TSPNYSPTSPSYSPTSPSYSPTSPSYS PSSPRYTPQSPTYTPSSPSYSPSSPSY SPTSPKYTPSPSYSPPSPEYTPASPK YSPTSPKYSPTSPKYSPTSPYSPYTP KYSPTSPYTPSPVYTPSPKYSPTSP PTYSPYTPKYSPTSPYTPSPKYSTY SPTSPGYSPYTPYTPSPYTPSPYTP EEN	True	False	2.686	5.0	1.863	1.598	1.032