

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracel region
Q921C3	BRWD1_MOUSE	Mus musculus	Bromodomain and WD repeat-containing protein 1	25.019509	T1691	T687;S697;S702;S711;S1291;S1481;S1609;S1611;S1682;S1686;S1689;S1751;S1752;S1782;S1784;S1789;S1810;S1830;T1853;S1857;S1889;S1890;S1927;T1939;S2004;S2040;T2151;S2153	34418053	MAEFPSPARRPVPLIESELYFLIARYLS AGPCRRAAQVLVQLEEQYQLLPKRL DWEGNEHNRSYEELVLSNKHVAPD HLLQICQRIGPMLDKEVPPSISRVT LLGAGRQSLLRATAKDCRHTVWKGSA FAALHRGRPEMPVNYGPPPSLVEI HRGRQLTGCSTFTAFPGTMYQHIK MHRRILGHL SAVYCVAFDRTGHRIF TGSDDCLVKIWSHNGRLLSTLRGH SAEISDMAVNYENTLIAAGSCDKIR VWCLRTCAPVAVLQGTGTSITSLQF SPMAKGPQRYMVSTGADGTVCFWQ WDLESKFSPRPLKFTEKPRPGVQM LCSFSVGGMFLATGSTDHVIRMYF LGFDAPEKIAELESHTDKVDSIQFCN NGDRFLSGSRDGTARIWRFEQLEW RSILLDMSARISGDTSEEEERFMKPK VTMIAWNQDDSTVAVNDHVLKV WSSYTGQLLHNLGHAEVFLVLETH PFDSRIMLSAGHDGSIFIWDITKGIK MKHYFNMIEGQGHGAVFDCKFSQD GOHFACTDSHGHLIFGFGCSKPYE KIPDQMFHTDYRPLRDSNNYVLD EQTQQAPHLMPPPFLVDVGNPHF TKFQRLVPGRENSADEHLVPLGYV ATSDGEVIEQHLSHTNDSGDASPES SVLDGMIRQLQQQDQRLGVDQDG TANGLPSGEGTPRRGSFRRLSLDIQS PPNIGLRRSGQVEGVRQMHQNA SQIATERDLQAWKRRVVVPEAPGM FRRLDIRIERGEEERNLYVIGRKKK TFQVPQKSNMVLVSQSRQRTCRRK YANYSRRNADQCELSGNESSGSRV HETSYDQSEGCSEDEDEWRNDRR SGSDSDSSSSQYSDWTADTGIN LQPPLRMSRRRVTRFCSTSEDEMS MENISPPKRRRRRRESKPKRESLR RMTPAELANMEHLYEFHPPVWITDT TLRKSFPVPMGDEVMYFRQGHEA YIEAVRRNNIYELNPHKEPWRKMDL RDQELVKIVGLRYEVGPPTLCLCLLA FIDPATGRLTDKSFIRYHDMFDPVID FLVLRQFYDEARQNRWQPCDRFRSI IDDAWWFGTVLSQEPYQPQYPSHF QCYIVRWDNTETEKLSPWDMPIPD NVDPPPEELGASISVTSDELEKLLYK QEGEWQRRSRDEECDRISGIDQLL NLDIAAAFAGPVDLCTYPKYCTVVAY PTDLYTIRMRLVNRFYRRLSALIWEV RYIEHNARTFNPEPVIARSAKKTD QLLKFIKNQDCTNISELCNTSDNDE DDSADDLDDSDLPKTSSGRKRVHN WKRRSRASGCIESDWRROCKALLILI FQCEDSEPFRRQPVLDLDEYPDYRDIID TPMDFGTVRETLEAGNYDSPVEFCK DIRLIFSNAKAYTPNKRSKIYMTLR LSALFEEMKKISFDKIGQKFKKEL RRSQRFKQRQNCNGAVPGDRRRRN VKQKQFKSQTKVIPQLMCPSSQSTS SKVPLSATRKTSAVSSGFTSGDSSD SAGSLERVRRQRPEVLRSGSVLFGS EMEDFLATSSSSASNSSEESKASP GARESSLRSGVLRGSNLGVTRTRAA RRKAGSVSLENGCGRKATRKRVYLS DSDNNSVETDENLKNRKCSSSRKV LRKCAAVAASKIKLMSDAEDSSSESP CSGRKLPHRNASAVARKLLHNSD DQSLKSETEELKDQNSLLISGPHS VHNSISDESSEDLRATRTWNANG CTSHTAATCKTKSRPIESSEEDSRCH GSDHGPSSTGDPSTSGQKLRA EADSEPESSVLCNTHLCKKAKILS DSEDCEEKCGERRGPEVEGSPVSEA LREAILAPOCLSHRGSETDSDG AVREKSYNSENGVSLENGQRRKVS RKSSDKESNLQVTQKSPKDRSSPS RITQRASVATDKMMLTSDAEDLSLES VCTRSKRRRKKPARFACTPAKTALSS EKKHAHCEVPEAQPACRNKLEPEPEH QDSAENPSQAASADLNSGGGSSFEQ	None	None	None	None	None	None	None		

