

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	gol apj
Q9NSI6	BRWD1_HUMAN	Homo sapiens	Bromodomain and WD repeat-containing protein 1	21.658119	S6;S1786;S2218	T687;S696;S701;S710;S1289;S1475;T1477;S1479;S1605;S1607;S1678;S1683;S1686;S1755;S1756;S1786;S1788;S1793;S1820;T1867;S1871;S1904;S1905;S1907;S1910;S1943;T1955;S2018;S2020;S2052;T2164;S2166;S2214	28411811;30379171;29485866	MAEPSSARRPVLIESELYFLIARYLS AGPCRRAAQOVLVQELEQYQLPKRL DWEGNEHNRSYEELVLSNKHVAPD HLLQICQIRIGPMLDKEIPPSISRVTSL LGAGRQSLRLRTAKDCRHTVWVGSAF AALHRGRPPEMPVNYGSPNLVEIHH RGKQLTGCSTFSTAFPQGTMYQHMK HRRILGHLSAVYCVAFDRTGHRIFTG SDDCLVKIWRSTHNGRLLSTLRGHS EISDMAVNYENTMIAAGSCDKIIRV WCLRTCAPVAVLQGHGTSITSLQFS PMAKGSQRYMVSTGADGTVCVFWQ WDLESLKFSRPLKFKTEKPRPGVQM LCSSFSVGGMFLATGSTDHVMIRMYF LGFEAPEKIAELESHTDKVDSIQFCN NGDRFLSGSRDGTARIWRFEQLEW RSILLDMATRISGDLSEEEERFMKPK VTMIAWNQNDIVVAVNDHVLKV WNSYTGQLLHNLMGHADEVFVLET HPFDSTRIMLSAGHDGSIFIWDITKGT KMKHYFNMIIEGQGHGAVFDCKFSQ DGOHFACTDSHGHLIFGFGCSKPY EKIPDQMFHFDYRPLIRDSNYYVL DEQTQQAPHLMPPLVDVGNPH PTKYQRLVPGRENSADEHLIPQLGYV ATSDGEVIEQIISLQTNNDERSPE SILDGMIRLQOQQDQRMGADQDTI PRGLSNGEETPRRGFRRLSDIQSPP NIGLRRSGVEGVRQMHQNAFRSQI ATERDLQAWKRRVVPEVPLGIFRK LEDFRLEKGEERNLYIGRKRKTLQ LSHKSDSVLVVSQSRQRTCRKYPN YGRNRNSWRELSGNSSESSSVRHET SCDQSEGGSGSEDEWRSRDKSESY SESSSDSSRYSDWTADAGINLQPLP RTSCRRTTRFCSSSEDEISTENLSP PKRRRKRKKNKPKKENLRRMTPA ELANMEHLYEFHPPVWITDTLTKS PFVPMGDEVIYFRQGHEAYIEAVR RNNIYELNPNKEPWRKMDLRDOEL VKIVGIRYEVGPPTLCLLAFIDPAT GKLMKSFISIRYHDMPPVIDFLVLR QFYDEARQNRWQSCDRFRSIIDDAW WFGTVLSQEPYQPQYPSHFQCYIV RWDNTEIEKLSPWDMPIPDNDVPP EELGASISVTTDELEKLLYKQAGEW GOKSRDEECDRIHSGIDQLLNLDAIA AFAGPVDLCTYPKYCTVVAYPTDLYT IRMLVNRFRRLSALVWEVRYIEH NARTFNPEPESVIARSAKKIDQLLFI KNQHCTNISELSNTSENDEQNAED LDDSDLPKTSSGRRRVHDGKKSIRA TNYVESNWKQCKELVNLIFQCEDSD EPFRQPVLDVEYDPYRDIIDTPMDFG TVRETLDAGNYDSPLEFCCKDIRLIFS NAKAYTPNKRSKIYSMTLRLSALFEE KMKKISSDFKIGQKFNELRRSQRF KQRQNCCKGDSQPNKSIRNLKPKRLK SQTKIPELVGSPQTSSRTAYLGH KTSAGISSGVTSGDSSDAESSERRK RNRPIITNGSTLSESEVEDSLATSLSS SASSSEESKESRRARESSSRGLSR SSNLRVTRRAAQRKTGPVSLANGC GRKATRRVYLSDDNNSETGEIL KARAGNRRKVLKCAAVAANKIKLM SDVEENSSSESVCSGRKLPNRNASA VARKLLHNSEDEQSLKSEIEEEL KDENQLLPVSSHTAOSNVDESEN DSESEDLRVARKNWHANGYKSH PAPSKTKFLKIESSEEDSKSHSDHA CNRTAGPSTSVQKLKAEISIEEADSE PGRSGGRKYNTFFKNASFFKTKIL SDSEDESEEQDREDGKCHKMEMN PISGNLNCPIAMSQCSDDHGCETD LSDDDKIEKPNFMKDSASQDNG LSRKISRKRVCSSDSDSLQVVKSS KARTGLLRTRRCAATAANKIKLMSD VEDVLENVHTRSKNGRKKPLHLAC TTAKKLSDCGEGSVHCEVPSEQYAC EGKPPDPDSEGSTKVLSQLNGSD	True	False	4.604	5.0	0.794	0.721	0.5

