	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	extracell region
0	Q91YE5	BAZ2A_MOUSE	Mus musculus	Bromodomain adjacent to zinc finger domain protein 2A	38.223321	NaN	T499;S501;T540;S605;S1042;S1174;S1374;S1377;S1383;S1545;S1733;T1738;S1755;S1767	40997131	MEMEANDHFNFTGLPPAPAASGLK PSPSSGEGLYTNGSPMNFPQQGKSL NGDVNVNGLSTVSHTTTSGILNSAP HSSSTSHLHHPNVAYDCLWNYSQY PSANPGNNLKDPPLLSQFPGGQYPL NGILGGNRQPSSPSHNTNLRAGSQE FWANGTQSPMGLNFDSQELYDSFP DQNFEVMPNGPPSFFTSPQTSPML GSSIQTFAPSQDVSSDIHPDEAAEKE LTSVVAENGTGLVGSLELEEEQPEL KMCGYNGSVSSVESLHQEVSVLVPD PTVSCLDDPSHLPDQLEDTPILSEDS LEPFDSLAAEPVSGSLYGIDDAELMG AEDKLPLEGNPVISALDCPALSNAN AFSLLADDSQTSASIFVSPTSPPVLG ESVLQDNSFGLNSCSDSEQEEIETQ SSNFQRPLTEPAPDQPPSTQLHPAV SPTASPAASLTASAEISPAVSPVASSP VPPEVFVAVSPASSPALPAISLEASM TTPVTSPQGSPEPSPAAAFQTVSPAR KNVSSAPKARADREETTGGAVAVSG SGDVLKRRIATPEEVRLPLQHGWRR EVRIKKGSHRWQGETWYYGPCGKR MKQFPEVIKYLSRNVVHSVRREHFS FSPRMPVGDFFEERDTPEGLQWVQ LSAEEIPSRIQAITGKRGRPRNNEKA KNKEVPKVKRGRGRPPKIKMPELLN KTDNRLPKKLETQEILSEDDKAKMT KNKKKMRQKVQRGESQTPVQGQAR NKRKQDTKSLKQKDTKKKLKAEKEK MKTKQEKLKEKVKREKKEKVKAKG KEGPRARPSCRADKTLATQKRLEEQ QRQQAILEEMKKPTEGMCLSDHQP LPDFTRIPGLTLSSRAFSDCLTIVEFL HSFGKVLGFDLTKDVPSLGVLQEGL LCQGDSLDKVQDLLVRLLKAALHDP GLPPYCQSLKILGEKMSEIPLTRDNV SEILRCFLMAYRVEPPFCDSLRTQPF QAQPPQQKAAILAFLVHELNSSTIIIN EIDKTLESVSSCRKNKWIVEGRLRRL KTALAKRTGRPEVMMEGAEDGLGR RRSSRIMEETSGIEEEEEEENTTAVH GRRGRKEGEIDVAASSIPELERHIEK LSKRQLFFRKKLLHSSQMLRAVSLG QDRYRRHYWVLPYLAGIFVEGSEGS TVTEDEIKQETESLMEVVTSTPSSAR ASVKRELTGSNASTSPARSRGRPRK PKPGSLQPQHLQSTIRECDSEQAQT QVHPEPQPQLQAPTQPHLQPSSGFL EPEGSPFSLGQSQHDLSQSAFLSWL SQTQSHNSLLSSSVLTPDSSPGKLD SAPSQSLEEPEPDEAQSCPGPQGPW FNFSAQIPCDAAPTPPPAVSEDQPTP SLQLLASSKPMNTPGAANPCSPVQL SSTHLPGGTPKRLSGDSEEMSQSPT GLGQPKRRGRPPSKFFKQVEQHYLT QLTAQPIPPEMCSGWWWIRDPETLD VLLKALHPRGIREKALHKHLSKHKD FLQEVCLQPLTDPIFEPNELPALEEG VMSWSPKEKTYETDLAVLQWVEEL EQRVVLSDLQIRGWTCPTPDSTRED LTYCEHLPDSPEDIPWRGRGREGTV PQRQNNNPLDLAVMRLAVLEQNVE RRYLREPLWAAHEVVVEKALLSTPN GAPDGTSTEISYEITPRVRVWRQTLE RCRSAAQVCLCMGQLERSIAWEKSV NKVTCLVCRKGDNDEFLLLCDGCD RGCHIYCHRPKMEAVPEGDWFCAV CLSQQVEEEYTQRPGFPKRGQKRKS SFPLTFPEGDSRRRMLSRSRDSPAV PRYPEDGLSPPKRRRHSMRSHHSDL TFCEIILMEMESHDAAWPFLEPVNP RLVSGYRRVIKNPMDFSTMRERLLR GGYTSSEEFAADALLVFDNCQTFNE DDSEVGKAGHVMRRFFESRWEEFY QGKQANL	True	False	3.277	5.0	0.907	0.751	False	0.793	0.921