

UniprotKB ID	Entry name	organism	full name	oglcnaScore	oglcna sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q8WYB5	KAT6B_HUMAN	Homo sapiens	Histone acetyltransferase KAT6B	22.770101	NaN	S355;S647;S1048	34019948;28314751	MVKLANPLYTEWILEAIQKIKKQKQR PSEERICHAVSTSHGLDKKTVSEOLE LSVQDGSVLKVTNKGSLASYKDPDNP GRFSSVKPGTFPKSAKSGRSGCNDL RNVVDWKNLLRRAIEGLEEPNGSSLK NIEKYLRSDLTSTTNNPAFQQRL RLGAKRAVNNGRLLKDGPOQYRVNY GSLDGKGAPOQPSAFPSSLPPVSLLP HEKDQPRADPIPICSFCLGTKESNRE KKPEELLSCADCGSSGHPSCCLKFCP ELTTNVKALRWQCIECKTCSACRVQ GRNADNMLFCDSCDRGFHMECCD PPLSRMPKGMWICQVCRPKKKGRK LLHEKAAQIKRRYAKPIGRPKNKLKQ RLLSVTSDEGSMNAFTGRCSPPGRGQ KTKVCTTPSSGHAASGKSSSRLAV TDPTRPGATTKITTTSTYISASTLKVN KKTGLIDGLTKFFTPSPDGRRSRGE IIDFSKHYRPRKKVSKQKQCTSHVLA TGTTQKLKPPSSLPPTPIISGQSPSS QKSSSTATSSPQSSSSQCSVPSLSS LTTNSQLKALFDGLSHIYTTQGQSRK KGHPYAPPKRMRRKTELSSTAKSK AHFFGKDIRSRFISHSSSSWGMA RGSIFKAIHFKRTTFLKKHRMLGRL KYKVPQMGTPSPGKSLTDGRIKP DQDDDEIKINIKQESADVNVIGNKD VVTEEDLDVFKQAQELWSEKIECES GVEDCGRYPSVIEFGKYEIQTWYSSP YPQYARLPKLYLCEFCCLKYMKSKNI LLRHSKCKGWFHPPANEIYRRKDL VFEVDGNMSKIYCNLCLLAKLFLD HKTLYYDVEPFLFYVLTKNDEKGGCH LVGYFSKEKLCQKYNVSCIMIMPO HORQGFGRFLIDFSYLLSRREGQAG SPEKPLSDLGRLSYLAYWKSVILEYL YHHHERHISIKAISRATGMCPHDIA TLQHLHMIDKRDGRFVIIRREKLIL HMEKLTCSRANELDPDSLRTWPIL ISNAAVSEEREAEKEAERLMEQAS CWEKEEQEILSTRANSRQSPAKVQS KNKYLHSPESRPVTGERGQLELLESK ESSEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEENIQSSPPRLTKPQ SVAIKRKRPFVKKRGRKRRRINSS VTTETISETTEVLNEPFDNSDEERP MPQLEPTCEIEVEEDGRKPVLRKAF QHQP GKKRQTEEEEGKDNHCFKNA DPCRNNMNDSSNLKEGSKDNPEP LKCKQVWPKGTKRGLSKWRQNKER KTGFKNLYTPPETPMEPDEQVTVE EQKETSEKTSPPSPIREVEVKETGE ALLPQEEENRREETCAPVSPNTSPGE KPEDDLIKPEEEEEEEEEEEEEEEEE EGEEFEGGNVEKDPDGAKSQEKE EPEISTEKEDSARLDDHEEEEEDE EPSHNEDHDADDEDDSHMESAEVE KEELPRESFKEVLENQETFLDLNVQ PGHNSPEVLMDCGVDLTASCNSEP KELAGDPEAVPESDEEPPPGEQAQK QDQKNSKEVDTEFKEGNPATMEIDS ETVQAVQSLTQESSEODDTFQDCAE TQEACRSLQNYTRADQSPQIATLTD DCQQSDHSSPVSSHSPGQSVRSV NSPSVPALENSYAQISPDQSAISVPS LQNMETSPMMDVPSVDHSSQVVD SGFSDLGSIESTTENYENPSSYDSTM GGSICGNGSSQNSCSYSLTSSSLT QSSCAVTOQMSNIGSCSMLQQTISI SSPPTCSVKSPQGCVVERPPSSSQQL AQCSMAANFTPPMQLAEIPETSNAN IGLYERMGQSDFGAGHYPOPSATFS LAKLQQLTNTLIDHSLPYSHSAAVTS YANSASLSTPLSNTGLVQLSQSPHSV PGGPOAQTMTPPPNTLPPMNLPP PLLQRNMAASNIGISHSQRLQTOIAS KGHISMRTKSASLSPAATHSQSIYG RSQTAMQGPARTLTMQRGMNMS VNLMPAPAYNVNSVNMNMNTLNA MNGYSMSQPMNSGYSHNHGYM	True	False	2.853	5.0	2.034	1.453	1.107	1.61	1.512

