

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	gol app
P45481	CBP_MOUSE	Mus musculus	Histone lysine acetyltransferase CREBBP	37.127146	S138;S147;T319	S120;S1031;S1077;S1383;S1387;S1764;S2064;S2077;S2080;S2350	36852467;34678516;22645316	MAENLLDGPNNPKRAKLSPPGFSAN DNTDFGSLFDLENDLPDELLPNEGEL SLLNSGNLVPDAASKHKQSELLRG GSGSSINPGIGNVSASSPVQQLGG QAQQPNNSTNMAISLGMGKSPLNQ GDSSTPNLPKQAAASTSGPTPPASQAL NPQAQKQVGLVTSSPATSQTGPVIC MNAFNQTHPGLLNSNSGHSMLMN QAQQGQAQVMNGSLGAAGRGRGA GMPYPAPAMQGATSSVLAETLTQVS PQMAGHAGLNTAQAGGMTKMGMT GTTSPFGQPFSSQTGGQMGATGVN PQLASKQSMVNSLPAFPTDIKNTSV TTVPNMSQLQTSVGVPTQAIATGPT ADPEKRKLIQQQLVLLLHAHKCQRR EQANGEVRACSLPHCRTMKNVLNH MTHCQAGKACQVAHCASSRQIISH WKNCTRHDPCVCLPLKNASDKRNQ QTILGSPASGIQNTIGSVGAGQONAT SLSNPNPIDPSSMORAYAAALGLPYM NQPQTQLQPQVPGQQAQPPAHQQ MRTLNALGNNPMSIPAGGITDQOP PNLISESALPTSLGATNPLMNDGSN SGNIGSLSTIPTAAPSSSTGVRKGWH EHTVQDLRSHLVHKLVAIFPTDP AALKDRRMENTLVAYAKKVEGDMYE SANSRDEYYHLLAEIKYKIQKELEEK RRSRLHKQIGLGNQPALPASGAQPP VIPPAQSVRPPNGPLPLPVNRMQVS QGMNSFNPMISLGNVQLPQAPMGP RAASPMNHSVQMNMSASVPGMAIS PSRMPQPPNMMGTANNIMAQAPT QNQLPQNPQFPSSSGAMSVNSVGM GQPAQAQAGVSQGVPGAALPNPLN MLAPQASQLPCPPVTQSPHPTPPP ASTAAGMPSLQHTAPGMTPPQAAA PTQPSTPVSSGQTPTPTPGSVPSAAQ TQSTPTVQAAAQAQVTPQPQTPVQP PSVATPQSSQQQPTPVHTQPPGTPLS QAAASIDNRVTPSSVTSAAETSSQQP GPDVPMLEMKTEVQTDAAEPEPTES KGEPRSEMMEEDLQSSQVKEETD TTEQKSEPMVEEKKPEVKVEAKEE EENSSNDTASQSTSPSQPRKIKFKPE ELRQALMPTLEALYRQDPESLPRFQ PVDPQLLGIQDYFDIVKNPMDLSTIK RKLDTGQYQEPWQYVDDVWLMFN NAWLYNRKTSRVYKFCSKLAEVFEQ EIDPVMQSLGYCCGRKYEFSPOTLC CYGKQLCTIPRDAAYSYQNRVHFC EKCFTEIQGENVTLGDDPSQPQTIS KDQFEKKKNDTLDPEPFVDCKECGR KMHQICVLHYDIIWPSGFVCDNCLK KTGRPRKENKFSAKRLQTRRLGNHL EDRVNKFLLRQNHPEAGEVFVRVV ASSDKTVEVKPGMKSRFVDSGEMS ESFPYRTKALFAFEIDGVDVCFEG MHVQNTALIAHQIQGRVYISYLDI HFFRPRCLRTAVYHEILIGLEYVVK LGYVTGHIWACPPSEGDDYIFHCHP PDQKIPKPKRLQEWYKMLDKAFEA RIINDYKIDIFKQANEDRLTSAKELPY FEGDFWPNVLEESIKELEQEEERK KEESTAASETPEGSQDGSKNAKKN NKKTNKSSISRANKKKPSMPNVS NDLSQKLYATMEKHKEVFFVIHLHA GPVISTQPPIVDPDPLLSCDLMDGRD AFLTLARDKHWFSSLRRSKWSTLC MLVELHTQGDREVFVTCNECKHHV ETRWHTVCEDYDLGNCYNTKSHT HKMVKWGLGLDDESSQGEPOSKS PQESRRLSIQRICISLVHACQCRNA NCSLSPCQKMKRVVQHTKGCKRKT NGGCPVCKQLIALCCYHAKHCOENK CPVPFLNIKHKLROQQIOHRLQQA QLMRRMATMNTNRNVQQSLPSPT SAPPGTPTQQPSTPQTPPPAQPPQS PVNMSAPGFPNVARTQPPPTVSAGK PTNQVPAPPPPAQPPAAVEAARQIE REAQQQQHLYRANINNGMPPGRAG	None	None	None	None	None	None	

