

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	extracellular region
Q02294	CAC1B_RAT	Rattus norvegicus	Voltage-dependent N-type calcium channel subunit alpha-1B	23.439218	NaN	S411;S746;S749;S784;S1067;S2065;S2221;S2230;S2253	38843836	MVRFGDELGGRYGGTGGGERARGG GAGGAGCGPGGGLPVGGQVLYKQSI AQRARTMALYNPIPVKQNCFTVNR LFVFEEDNVVRKYAKRITWPPFEY MILATIIANCIVLALQHLDPGDKTP MSERLDDTEPYFIFGFCFEAGIKIAL GFVFKGYSYLRNGWNVMDVFFVLT EILATAGTDFDLRTRAVRVLRLK VSGIPSLQVVLKSIKAMVPLLQIGL LLFFAILMFAIIGLEFYMGKFKKACF PNSTDAEPVGDVPCGKEAPARLDCS DTECREYWPGNFGITNFDNLFIL TVFQCITMEGWTDILYNTNDAAGNT WNWLYFIPLIIGSFMLNLVLGVLS GEFAKERERVENRRAFLKLRQQQI ERELNGYLEWIFKAEVMLAEEDKN AEEKSPLDAVLKRAATKKSRNDLIHA EEGEDRFVDLCAAGSPFARASLKSG KTESSSYFRKKEKMFRLIRRMVKA QSFYVWVLCVVALNTLCVAMVHYN QPORLTALYFAEFVFLGLFTEMSL KMYGLGPRSYFRSSFCDFGVIVG SIFEVWAAIKPGTSFGISVLRALRL RIFKVTKYWNSLRNLVSLNSMK IISLLFLFLFVVFALLGMQLFGGQF NFQDETPTTNFDTPFAAILTVFQILT GEDWNAVMYHGIESQGGVSKGMFS SFYFIVLTLFGNYLLNVFLAIAVDNL ANAQELTKDEEMEEANQKLLAQ KAKEVAEVSPPMSAANISIAARQNS AKARSVWEQRASQLRQLNLRASCEA LYSEMDPEERLRYASTRHVRPDMKT HMDRPLVVEPGRDGLRGPAGNKSK PEGTEATEGADPPRRHRRDRDK TSASTPAGGEQDRDTCPKAESTETG AREERARPRRSHSKEAPGADTVRC ERSRRHRRRGSPEEATERPRRHRA HRHAQDSSKEGEGTAPVLPKGER RARHRGPRTGPRETENSEPTRRHR AKHKVPPTLEPPERVAEKESNVVE GDKETRNHQKPEPRCDLEAIAVTGV GSLHMLPSTCLQKQVDEQPEDADNQ RNVTRMGSQSPDPTTVHVPTLTG PPGEATVPSANTDLEGGAEKKEA EADDVLRGRPRVYSSMFLSPTN LLRRFCHYVTMRYFEMVILVIALS SIALAAEDPVRTDSFRNNALKYMDYI FTGVFTFEMVIKIDLGLLHPGAYF RDLWNILDVIVSGALVAFVSSFM GGSKGKDINTIKSLRVLRLPLKTIK RLPKLKAVFDCVNSLKNVNLIVY MLFMFIVAVIQLFKGKFFYCTDES KELERDCRGOYLDYEKEEVEAOPRO WKYDFHYDNLWALLTLFTVSTGE GWPMVLKHSVDATYEEQGSPGFR MELSFYVYVYVFFVFFVNFVALIII TFQEQGDKVMSECSLEKNERACIDF AISAKPLTRYMPQNKQSFQYKTWTF VVSPPFEYFIMAMIALNTVLMMKF YDAPYEYELMLKCLNIVFTSMFSL CILKIIAFGLNYFRDAWNVDFVTV LGSITDILVTEIANNFNLSFLRLFRA ARLIKLCRQGYTIRILLWTFVQSKAL PYVCLLIAMLFFIYAIIGMQVFGNIAL DDGTSINRHNFRFTLQALMLLFRS ATGEAWHEIMLSCLGNRACDPHAN ASECGSDFAYFYVFSFIFLCSFLMLN LFVAVIMDNFEYLTRDSSILGPHHLD EFIRVWAEYDPAACGRISYNDMFEM LKHMSPLGLGKPCPARVAYKRLVR MNMPISNEDMTVHFTSTLMALIRTA LEIKLAPAGTKQHQCDAELRKEISSV WANLPQKTLDLLVPPHKPDEMTVG KVYAAALMIFDFYKQNKTRDQTHQA PGGLSQMGVSLFHPLKATLEQTQP AVLRGARVFLRQKSATSLNNGGAIQT QESGIKESLSWGTQRTQDVLVEARA PLERGHSAEIPVGOFGALAVDVQMO NMTLRGPDGEPQGLSQGRAASM PRLAETQPAPNASPMKRSISTLAPR	False	True	1.1	1.35	1.106	1.2	False	4.432	1.379

