

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	ex re
O55017	CAC1B_MOUSE	Mus musculus	Voltage-dependent N-type calcium channel subunit alpha-1B	35.498311	NaN	S411;S745;S748;S783;S1058;S2056;S2212;S2221;S2244	34678516;22645316	MVRFGDELGGRYGGTGGGERARGG GAGGAGGPGQGLPPGQRVLYKQSI AQRARTMALYNPIPVKQNCFTVNRS LFVFSEDNVVRKYAKRITEWPPFEY MILATHIANCIVLALEQHLDPGDKTP MSERLDDTEPYFIGIFCFEAGIKIAL GFVFHKGSYLRNGWNVMDFFVVVLT GILATAGTDFDLRTLRAVRVLRPLKL VSGIPSLQVVLKSIMKAMVPLLIQGL LLFFAILMFAIIGLEFYMGKFKACF PNSTDTEPVGDFPCGKDPARQCDG DTECREYWPFPNGITNFNDFNILFAIL TVFQCITMEGWTDLINTNDAAAGNT WNWLYFIPLIIGSFFMLNLVLGVL GEFAKERERVENRRRAFLKLRROQOI ERELNGYLEWIFKAEVMLAEEDKN AEEKSPDLVKRAATKSRNDLIHAE EGEDRFVDLCVGSPPFARASLKSGK TESSSYFRKKEKMFRRFIRRMVKAQ SFYVVVLCVVALNTLCVAMVHYNQ PQRLTTALYFAEFVLGLFLEMSLK MYGLGPRSYFRSSFNCDFGVI V GSI FEVVWAAIKPGTSFGISVLRALRLRI FKVTKYWNLSRLNVVSLLSMKSII LLFLFLFIVV FALLGMQLFGGQFNF QDETPTTNFDTPAAILTVFQILTGE DWNVAVMYHGIESQGGVSKGMFSSF YFIVLTLFGNYTLLNVFLAIAVDNLA NAQELTKDEEEMEEAANQKALQK AKEVAEVSPMSAANISIAARQNSA KARSVWEQRASQLRQLNLRASCEAL YSEMDPEERLRYASTRHVRPDMKT HMDRPLVVEGRDGLRGPVGSKSKP EGTEATESADLPRRHHRRDRDKTS ATAPAGGEQDRTESTETGAREERAR PRRSHSKETPGADTQVRCERSRRHH RRGSPEATEREPRRHRRAHRHAQD SSKEGTAPVLVPGERRARHRGPRT GPREAENNEEPTRRHRARHKVPPTL QPPEEAEEKESNAVEGDKETRNH QPKEPHCDLEAIAVTGVGPLHMLPS TCLQKVDEQPEDADNQRNVTRMGS QPSDPSTTVHVPVTLTGPPGETPVVP SGNMNLEGQAEKGKEAEADDVLR GPRPIVYSSMFLCSPTNLLRRFCFY IVTMRYFEMVILVIALSSIALAAEDP VRTDSFRNALKYMDYIFTGVFTFE MVIKIDLGLLLHPGAYFRDLWNIL DFIVVSGALVAFVAFSFMGSGKGD NTIKSLRVLRLRPLKTIKRLPKLAV FDCVVNSLKNVNLIVYMLFMFIFA VIAVQLFKGKFFYCTDESKELERDCR GQYLDYEKEEVEAQPROWKYDFH YDNVLWALLTLFTVSTGEGWPMVLK HSVDATYEEQGSPGFRMELSFIFY VYFVFPFFVNI FVALIITFQEQGD KVMSECSLEKNERACIDFAISAKPLT RYMPQNKQSFQYKTWTFVVSPPFEY FIMAMIALNTVLMMKFYDAPYEYE LMLKCLNIVFTSMFSMECLKIAFG VLNYFRDANNVDFVTVLGSITDILV TEIANNFINLSFLRLFRARLIKLLRQ GYTIRILLWTFVQSFKALPYVCLLIAM LFFIYAIIGMQVFGNIALDDTTSINR HNNFRFLQALMLLFRSATGEAWH EIMLSCLGNRACDPHANASECGSDF AYFYFVSFIFLCSFLMLNLFVAVIMD NFEYLTRDSSILGPHHLDEFIRVWAE YDPAACGRISYNDMFEMLKHMSPP LGLGKKCPARVAYKRLVRMNPISN EDMTVHFTSLMALIRTALEIKLAPA GTRQHQCDALRKEISSWANLPQK TLDLLVPPHKPDEMTVGKVYAALMI FDYKQNKTRDQTHQAPGGLSQM GPVSLFHPLKATLEQTQPAVLRGAR VFLRQKSATSLNNGGAIQTQESGIKE SLSWGTRTQDALYERAPLERGHS AEIPVQSGTLAVDVQMNMNTRLG PDGEPQPGLESQGRAASMPRLAAET QPAPNASPMKRSISTLAPRPHGTQL	False	True	1.973	1.968	1.728	2.117	1.287	5.0	2.

