

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
P97445	CAC1A_MOUSE	Mus musculus	Voltage-dependent P/Q-type calcium channel subunit alpha-1A	29.185005	NaN	T411;S450;S453;S752;S755;S792;S1038;S1042;S1051;T1935;S1998;S2016;S2028;S2030;S2071;S2091	22645316	MARFGDEMPGRYGAGGGGSGPAAG VVVGAAGGRGAGGSRQGGQPGAQR MYKQSMQAQRARTMALYNPIPVRQN CLTVNRSFLFSEDNVVRKYAKKITE WPPFEYMLATIIANCIVLALQHLPL DDDKTPMSERLDDTEPYFIGIFCFEA GKIVALGFAGFKGYSYLRNGWNVMD FVVVLTGILATVGTDFDLRTRAVRV LRPLKLVSGIPSLQVVLKSIKAMIP LLQIGLLFFAILFAIIGLEFYMGKF HTTCFEEGDDIQGESAPACGTEEP ARTCPNGTKCQPYWEGPNNGITQFD NILFAVLTVFQCITMEGWTDLLYNS NDASGNTWNWLYFIPLIIGSFFMLN LVLGVLGSEFAKERERVENRRAFLK LRRQQQIERELNGYMEWISKAEEVI LAEDTDVEQRHPFDGALRRATLKK SKTDLLNPEEAEDQLADIASVGSPPFA RASIKSAKLENSTFFHKKERRMRFYI RRMVKTQAFYWTVLSLVALNTLCVA IVHYNQPEWLSDFLYAEFIFLGLFM SEMFIKMYGLGTRPYFHSFNCFCDC GVIIGSIFEVIWAVIKPGTSFGISVLA RLLRLRFKVTKYWASLRNLVVSLLNS MKSIIISLLFLFLFIVV FALLGMQLFG GQFNFDGTPPTNFDTPFAAIMTVF QILTGEDWNEVMYDGIKSQGGVQG GMVFSIYFIVLTLFGNYTLNVLFAIA VDNLANAQELTKDEQEEEEAAANQK LALQKAKEVAEVSPLSAANMSIAVK EQQKNQKPTKSVWEQRTSEMRKQN LLASREALYGDAERWPTPYARPLRP DVKTHLDRPLVDPQENRNNNTNK SRAPEALRPTARPRESARDPDARRA WPGSPERAPGREGPYGRESEPPQRE HAPPREHAPWDADTERAKAGDAPR RHTHRPAEGEPRRHRARRRRPGDE PDDRPERPRPRDATTRPARAADGEG DDGERKRRHRHGPPAHDDRERRHR RRKENQSGVPSVGNLSTTRPIQQ DLGRQDLPLAEDLDNMKNKLATG EPASPHDSLGHSLPPSPAKIGNST NPGPALATNPQNAASRRTPNPNPN PSNPGPKTPENSLIVTNPSSQPNNS AKTARKPEHMAVEIPPACPLNHTV VQVNKNANPDPLPKKEEKEEKEE DPGEDGPKMPPYSSMFIILSTTNPL RRLCHYILNRYFEMCILMVIAMSSI ALAAEDPVQPNAPRNNVLRVFDYVF TGVFTFEMVIKMLDGLVLHQGAYF RDLWNILD FIVVSGALVAFATGNSK GKDINTIKSLRVLRLRPLKTIKRLPK LKAVFDCVVNSLKNVFNILIVYMLF MFIFAVAVQLFKGKFFHCTDESKE FERDCRGKYLLEYEKNEVKARDREW KKYEFHYDNVLWALLTLFTVSTGEG WPQVLKHSVDATFENQGPSGYRM EMSIYVYVYVFPFFVNFVALIIT FQEQGDKMMEEYSLEKNERACIDF AISAKPLTRHMPONKQSFQYRMWQ FVVSPPFEYTIMAMIALNTIVLMMKF YGASVAYENALRVFNIVFTSLFSLC VLKVMAGILNYFRDAWNIFDFVTV LGSITDILVTEFGNNFINLSFLRFR ARLIKLLRQGYTIRILLWTFVQSKAL PYVCLLIAMLFFIYAIHGQVFGNIGI DGEDEDSDEDEFQITEHNNFRFFQ ALMLLFRSATGEAWHNIMLSCLSGK PCDKNSGILTADCGNEFAYFYVFSFI FLCSFLMLNLFVAVIMDNFEYLTRD SSILGPHHLDEYVRVWAEYDPAACG RIHYKDMYSLLRVISPLGLGKKCPH RVACKRLLRMDLPVADDNTVHFNS TLMALIRTALDIKAKGGADKQQMD AELRKEMMAIWPNLSQKTLDLLVTP HKSTDLTVGKIYAAMMIMEYYRQSK AKKLQAMREEQNRTPLMFQRMPEP SPTQEGGSPQNALPSTQLDPPGGGLM AHEGGMKESPSWVTQRAQEMFQKT GTWSPERGGPIDMPNSQPNSQSVE	False	True	2.218	2.403	2.173	2.385	1.619	5.0	2.407

								MREMGTDGYSDSEHYLPMEGQTRA								
								ASMPRLPAENQRRGRPRGNDLSTI								
								SDTSPMKRSASVLPKARRLDDYSL								
								ERVPPEENQRYHQRRDRGHRTSE								
								RSLGRYTDVDTGLGTDLSMTTQSGD								
								LPSKDRDQDRGRPKDRKHPHHHH								
								HHHHHHPPAPDRDYAQERPDTRG								
								ARAREQRWSRSPSEGREHTTHRQG								
								SSSVSGSPAPSTSGTSTPRRGRRQLP								
								QTPCTPRPLVSYSPARRPAARRMA								
								GPAAPPGGSPRGCRRAPRWPAHAPE								
								GPRPRGADYTEPDSPREPPGGAHDP								
								APRSPRTPRAAGCASPRHGRRLPNG								
								YYAGHGAPRPRTARRGAHDAYSESE								
								DDWC								