

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
P97445	CAC1A_MOUSE	Mus musculus	Voltage-dependent P/Q-type calcium channel subunit alpha-1A	46.058797	S998	T411;S450;S453;S752;S755;S792;S1038;S1042;S1051;T1935;S1998;S2016;S2028;S2030;S2071;S2091	22645316;40885482	MARFGDEM PGRYGAGGGGSGPAAG VVVGAAAGGRGAGGSRQGGQPGAQR MYKQSMQAQRARTMALYNPIVRQN CLTVNRSFLFSEDNVVRKYAKKITE WPPFEYMLATHIANCIVLALQHLPL DDDKTPMSERLDDTEPYFIFGFCFEA GIKIVALGF AFHKGSYLRNGWNVMD FVVVLTGILATVGTDFDLRTRLRAVRV LRPLKLVSGIPSLQVVLK SIMKAMIP LLQIGLLFFAILFAIIGLEFYMGKF HTTCFEEGTD DIQGESAPCGTEEP ARTCPNGTKCQPYWEGPNNGITQFD NILFAVLT VFCITMEGWTDLLYNS NDASGNTWNWLYFIPLIIIGSFFMLN LVLGVLSGEFAKERERVENRRAFLK LRRQQQIERELNGYMEWISKAEEVI LAEDTDVEQRHPFDGALRRATLKK SKTDLLNPEEAEDQLADIASVGSPPFA RASIKSAKLENSTFFHKKERRMRFYI RRMVKTQAFYWTVLSLVALNTLCVA IVHYNQPEWLSDFLYAEFIFLGLFM SEMFIKMYGLGTRPYFHSSFNCFDC GVIIGSIFEVIWAVIKPGTSFGISVLA RLLRIFKVTKYWASLRNLVSVLLNS MKSISLLFLLFLFIVVFALLGMQLFG GQNFNDEGTPPTNFDTFPAAIMTVF QILTGEDWNEVMYDGIKSQGGVQG GMVFSIYFIVLTLFGNYTLLNVFLAIA VDNLANAQELTKDEQEEEEANQK LALQKAKEVAEVSPLSAANNMSIAVK EQQKNQKPTKSVWEQRTSEMRKQN LLASREALYGDAERWPTPYARPLRP DVKTHLDRPLVDPQENRNNNTNK SRAPEALRPTARPRESARDPDARRA WPGSPERAPGREGPGYGRESEPOORE HAPPREHAPWDADTERAKAGDAPR RHTHRPVAEGEPRRHRARRRPGDE PDDRPERRRPRDARPARAADGEG DDGERKRRHRHGPPAHDDRERRHR RRKENQSGVPVSGPNLSTTRPIQQ DLGRQDLPLAEDLDNMKNKLATG EPASPHDSLGHSGLPPSPAKIGNST NPGPALATNPQNAASRRTPNPNPGN PSNPGPKTPENSLIVTNPSSTPQNS AKTARKPEHMAVEIPPACPLNHTV VQVNKNANPDPLPKKEEKKKEEEEA DPGEDGPKMPPYSSMFILSTTNPL RRLCHYLNLRYFEMCILMVIAMSSI ALAEDPVQPNAPRNNVLRVFDYVF TGVFTFEMVIKIDLGLVLHQGAYF RDLWNILD FIVVSGALVAFVFTGNSK GKDINTIKSLRVLRLPKTKIKRLPK LKAVFDCVNSLKNVFNILIVYMLF MFIFAVVAVQLFKGKFFHCTDESKE FERDCRGKYLLEYKNEVKARDREW KKYEFHYDNVLWALLTLFTVSTGEG WPQVLKHSVDATFENQGPSGYRM EMSIFVYVYFVVPFFVFNIFVALIIT FQEQQDKMEEYSLEKNERACIDF AISAKPLTRHMPQNKQSFQYRMWQ FVVSPPFEYTIMAMIALNTIVLMMKF YGASVAYENALRVFNIVFTSLFLEC VLKVMAFGILNYFRDAWNIFDFVTV LGSITDILVTEFGNNFINLSFLRLFRA ARLIKLLRQGYTIRILLWTFVQSFKAL PYVCLLIAMLFFIYAIIGMQVFNGNI DGEDEDSDEDEFQITEHNNFRITFFQ ALMLLFRSATGEAWHNIMLSCLSGK PCDKNSGILTADCGNEFAYFYFVFSFI FLCSFMLNLFVAVIMDNFEYLTRD SSILGPHHLDEYVRVWAEYDPAACG RIHYKDMYSLLRVISPLGLGKCCPH RVACKRLLRMDLPVADDNTVHFNS TLMALIRTALDIKIAKGGADKQOMD AELRKEMMAIWPNL SOKTLDLLVTP HKSTD LTVGKIYAAMMIMEYYRQSK AKKLQAMREEQNRTPLMFQRMPEP SPTQEGGPSQNALPSTQLDPGGGLM AHEGGMKESPSWVTQRAQEMFQKT GTWSPERGPPIDMPNSQNSQSVE	False	True	2.219	2.4	2.172	2.391	1.621	5.0	2.

