

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
O00555-2	CAC1A_HUMAN	Homo sapiens	Isoform 2 of Voltage-dependent P/Q-type calcium channel subunit alpha-1A	19.817031	T2120 (O00555-2)	T409;S447;S450;S749;S752;S789;S1084;S1093;T1983;S2046;S2064;S2076;S2078;S2119;S2139	30379171;35254053	MARFGDEMPARYGGGGSGAAAGVV VSGGGGRGAGGSRQGGQPQAORMY KQSMARARTMALYNPIPVQRNCLT VNRSLFLFSEDNVVRKYAKKITEWP PFEYMILATHIANCIVLALQHLPPDD KTPMSERLDDTEPYFIGIFCFEAGIKI IALGFAFHKGYSYLRNGWNVMDVAV VLTGILATVGTFFDLRTRRAVRLRP LKLVSIGPSLQVVLKSIKAMIPLLQI GLLFFAILFAHGLEFYMGKFHTTC FEEGTDIQQGESPAPCGTEEPARTCP NGTKCQPYWEGPNNGITQFDNLFA VLTVFQCITMEGWTDLLYNSNDASG NTWNWLYFIPLIIGSFFMLNLVLGV LSGEFAKERERVENRRRAFLKLRQQ QIERELNGYMEWISKAEEVILAEDET DGEQRHPFDGALRRRTIKKSKTDLL NPPEAEDQLADIASVGSPPFARASIKS AKLENSTFFHKKERRMRFYIRRMVK TQAFYWTVLSLVALNLTCAIVHYN QPEWLSDFLYAEFIFLGLFMSEMF KMYGLGTRPYFHSFFNCFDCGVIIG SIFEVIWAVIKPGTSFGISVLRALRLL RIFKVTKYASLRNLVSVLLNSMKS ISLLFLFLFIVVFALLGMQLFGGQF NFDEGTPPTNFDTFPAAIMTVFQILT GEDWNEVMYDGIKSGGGVQGGMV FSIYFIVLTLFGNYTLLNVFLAIAVDN LANAQELTKVEADEQEEEEAANQKL ALQKAKEVAEVSPLSAANMSIAVKE QQKNQKPAKSVWEQRTSEMRKQNL LASREALYNEMDPDERWKAAYTRH LRPDMKTHLDRPLVVDQENRNNN TNKSRAAEPTVDORLQQRRAEDFLR KQARYHDRARDPSGSAGLDARRPW AGSQEAELSRGPGYGRESDDHAREG SLEQPGFWEGEAERGKAGDPHRRH VHRQGSRSRSGSPRTGADGEHR RHRARRRPGEEGPEKKAERRARHR EGSRPARGEGEGEGPDGGERRRR HRHGAPATYEGDARREDKERRHRR RKENQSGVVPVSPNLSTTRPIQDD LGRQDPPLAEDIDNMKNNKLATAES AAPHGSLGHAGLPQSPAKMGNSTD PGPMLAIPAMATNPQNAASRRTPNN PGNPSNPGPPKTPENSLIVTNPSTGTQ TNSAKTARKPDHTTVDIPACPPPLN HTVVQVNKNANPDPLPKKEEEKKEE EEDDRGEDGPKMPPYSSMFI NPLRRLCHYILNLYFEMCILMVA MSSIALAAEDPVQPNAPRNNVLRYP DYVFTGVFTFEMVIKIDLGLVLHQ GAYFRDLWNILDFIVVSGALVAF GNSKGDINTIKSLRVLRLRPLKTI KRLPKLAVFDCVNSLKNVFNILIV YMLFMFIFAVVAVQLFKGKFFHCTD ESKEFEKDCRGKYLLEYKNEVKARD REWKKYEFHYDNVLWALLTLFTVST GEGWPQVLKHSDVATFENQGPS YRMEMSIFVYVYVVFVFFVFNIFVA LIIITFOEQGDKMMEEYSLEKNERA CIDFAISAKPLTRHMPQNKQSFQYR MWQFVVSPPFEYTIMAMIALNTIVL MMKFYGASVAYENALRVFNIVFTSL FSLECVLKVMAFGILNYFRDAWNIF DFVTVLGSITDILVTEFGNPNFINL SFLRLFRAARLIKLLRQGYTIRILLWT FVQSFKALPVCLLIAMLFFIYAIIGM QVFGNIGIDVEDEDSDEDEFQITEH NNFRFTFFQALMLLFRSATGEAWHNI MLSCLSGKPCDKNSGILTRECGNEF AYFYFVSFIFLCSFLMLNLFVAVIMD NFEYLTRDSSILGPHHLDEYVVRWA EYDPAAWGRMPYLDMYQMLRHMS PPLGLGKKCPARVAYKRLLRMDLPV ADDNTVHFNSTLMALIRTALDIKIAK GGADKQQMDAELRKEMMAIWP SQKTLDLLVTPHKSTDLTVGKIYAA MIMEYYRQSKAKKLQAMREEQDRT PLMFQRMPEPPTQEGGPGQNALP	None	None	None	None	None	None	None	

