

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
Q01668	CAC1D_HUMAN	Homo sapiens	Voltage-dependent L-type calcium channel subunit alpha-1D	23.777946	NaN	NaN	28411811;37217939	MMMMMMMKMQHQROQQADHANEANYARGTRLPLSGEGPTSQPNSSKOTVLSWQAAIDAAARQAKAAQTMST SAPPVGSLSQORKRQYAKSKKQGN SSNSRPARALFCLSLNPPIRACISIV EWKPFDFILLAI FANCVALAIYIPFPE DDSNSTNHNLEKVEYAFLLIIFTVETF LKIIAYGLLLHPNAYVRNGWNLLDF VIVVGLFSVILEQLTKETEGGNHSS GKSGGFVDKALRAFRVLRPLRLVSG VPSLQVVLNSHIKAMVPLLHIALLVLF VIIIYAIIGLELFIGKMHKTCFFADSDI VAEEDPAPCAFSGNGRQCTANGTEC RSGWVGPNGGITNFDNFAMFLT V FOCITMEGWTDVLYWMNDAMGFE LPWVYFVSLVIFGSFFVLNLVGVLS GEFKEREKAKARGDFOKLREKQQL EEDLKGYLDWITQAEDIDPENEEEG GEEGKRNTSMPTSETESVNTENVSG EGENRGCCGSLCQAISKSLRRWR RWNRFNRRRCRAAVKSVTFYWLIV LVFLNLTLSSEHYNQPDWLTQIQDI ANKVLALFTCEMLVKMYSGLQAY FVSLFNRFDVFCVCGGITETILVELEI MSPLGISVFRVRLRIFKVRHWTS LSNLVALLSNMKSIASLLLLFLFIII FSLLGMQLFGGKFNFDQTQKRSTF DNFPQALLTVFQILTGEDWNAVMYD GIMAYGGPSSGMIVCIYFIILFICGN YILLNVFLAIAVDNLADAESLNTAQK EEAEERKARKESLENKKNKP EVNQIANSDNKVTIDDYREDEDDK PYPDCDVPVGEDEDEDEPEVPA GPRRRISELNMKEKIAPIEGSAFFI LSKTNPVIRVGCCHLHHHIFTNLIV FIMLSSAALAEEDPIRSHSFRNTILG YFDYAFTAIFTVEILLKMTTFGAFH KGAFCRNYFNLLDMLVVGSLVSG IQSSAISVVKILRVLRLRPLRAINRA KGLKHVVQCVFAIRTIGNIMIVTTL LQFMFACIGVQLFKGFYRCTDEAK SNPEECRGLFILYKGDVDSPVVRE RIWQNSDFNFDNLSAMMALFTVS TFEQWVALLYKAIDSDNGENIGPIYNH RVEISIFHHIIVAFMMNIFVGFVIV TFQEQEKEYKNCDELKQNRQCV E YALKARPLRRYPKNPYQYKFWYV V N SSPFEYMMFVLMNLCLAMQHY EQSKMFNDAMDILNMVFTGVFVE MVLKVI AFKPKGYFSDAWN TFD SLIV IGSIIDVALSEADPTESENVVPTATP GNSEESNRISITFFRLFRVRLVKLL SRGEGIRTLWTFIKSFQALPYVALLI AMLFFIYAVIGMQMFGKVAMRDNN QINRNNNFQTFPQAVLLLFRCATGE AWQEI MLACLPGKLCDPESDYNPGE EYTCGSNFAIVYFISFYMLCAFLIINL FVAVIMDNFDYLTRDWSILGPHHLD EFKRIWSEYDPEAKGRIKHLDVVTL RRIQPPLGFGKLCPHRVACKRLVAM NMPLNSDGTVMFNATL FALVRTAL KIKTEGNLEQANEELRAVKKIWKKT SMKLLDQVVPAGDDEVTVGKFYAT FLIQDYFRKFKRKEQGLVGKYPK NTTIALQAQLRTLHDIGPEIRRAISCD LQDDEPEETKREEDDVFKRNGALL GNHVNHVNSDRRDSLQQTNTTHRP LHVQRPSIPPASDTEKPLFPAGNSV CHNHHNHNSIGKQVPTSTNANLNN ANMSKAAHGKRPSIGNLEHVSENG HHSSHKHDREPQRSSVKRTRYET YIRSDSGEQLP TICREDPEIHGYFR DPHCLGEQYFSEECYEDDSSPTW SRQNYGYSRYPRNIDSERPRGYH HPQGFLEDDSPVCYDSRRSPRRRL LPPTPASHRRSSFNFECLRRQSSQE EVPSSPIFPHRTALPLHLMQQQIMA VAGLDSSKAQYSPSHSTRSWATPP ATPPYRDWTPCYTPLIQVEQSEALDQ	False	True	2.276	2.213	2.214	2.355	1.37	5.0	2.279

