

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q9P0X4	CAC1I_HUMAN	Homo sapiens	Voltage-dependent T-type calcium channel subunit alpha-1I	8.666114	S981;S986	S1058	35254053	MAESASPPSSSAAAPAAEPGVTTEQP GPRSPSSPPGLEEPLDGADPHVPH PDLAPIAFFCLRQTTSPRNWCIMV CNPWFECVSMVLVILLNCVTLGMYQP CDDMDCLSDRCKILQVDFDFIFIFFA MEMVLKMVALGIFGKKCYLGDTWN RLDFFIVMAGMVEYSLDLQINLSAI RTVRVLRPLKAINRVPSMRILVNLLL DTLPMLGNVLLLCFFVFFIFGIIGVQ LWAGLLRNRCFLEENFTIQGDVALP PYYQPEEDDEMPFICSLSGDNGIMG CHEIPPLKEQGRECCLSKDDVYDFG AGRQDLNASGLCVNWNRYYNVCRT GSANPHKGAINFDNIGYAWIVIFQVI TLEGWVEIMYYVMDAHSFYNFYFIL LIIVGSFFMINLCLVVIATQFSETKQR EHRMLEQRQRYLSSTVASAEPG DCYEEIFQYVCHILRKARRALGLYQ ALQSRRALGPEAPAPAKPGPHAKE PRHYHGKTKGQGDEGRHLGSRHCQ TLHGPA SPGNDHSGRELC PQHSPLD ATPHTLVQIPATLASDPASCPCQHQ EDGRRPSGLGSTDSGQEGSGSGSSA GGEDEADGDGARSSD GASSELGKE EEEEEQADGAVWLCGDVWRETRAK LRGIVDSKYFNRGIMMAILVNTVSM GIEHHEQPEELTNILEICNVVFTSMF ALEMILKLA AFG LFDYLRNPNYIFDS IIVIISIWEIVGQADGGLSVLRTFRLLR VLKLVRFMPALRRQLVVLKTMMDN VATFCMLLMLFIFIFSILGMHIFGCK FSLRTDTGDTV PDRKNFDSLLWAIV TVFQILTQEDWNV VLYNGMASTSP WASLYFVALMTFGNYVLFNLLVAIL VEGFQAEGDANRSYSD EDQSSS NIE EFDKLEGLDSSGDPKLCPIPMTPN GHLDP SLPLGGHLGPAGAAGPAPRL SLQDPMLVALGSRKSSVMSLGRM SYDQRSLSSSRSSYYGPWGRSAAWA SRRSSWNSLKHKPPSAEHESLLSAE RGGGARVCEVA ADEGPPRAAPLHTP HAHHIHHGPHLAHRHRHRRRTLSL DNRDSVDLAELVPAVGAHPRAAWR AAGPAPGHEDCNGRMP SIAKDVFTK MGDRGDRGEDEE EIDYTL CFRVRK MIDVYKPDWCEVREDWSVYLF SPE NRFRVLCQTIIAHKLFDYVVLAFIFL NCITIALERPQIEAGSTERIFLTVSNIY FTAIFV GEMTLKVVSLGLYFGEQAYL

RSSWNVLGFLVFSIIDIVVSLASA  
GGAKILGVLRLRLLRTLRLRPLRVISRA  
PGLKLVVETLISSLKPIGNIVLICCAF  
FIIFGILGVQLFKGKFYHCLGVDTRNI  
TNRSDCMAANYRWWHHKYNFDNL  
GQALMSLFLVASKDGWVNIMYNGL  
DAVAVDQQPVTNHNPWMLLYFISFL  
LIVSFFVLNMFVGVVVENFHKCRQH  
QEAEEARREEKRLRRLEKKRRKAQ  
RLPYATYCHTRLLIHSMTSHYLDI  
FITFIICLVVTMSLEHYNQPTSLET  
ALKYCNMFTTVFVLEAVLKLVAFG  
LRRFFKDRWNQLDLAIVLLSVMGIT  
LEEIEINAALPINPTIIRIMRVLRIARV  
LKLLKMATGMRALLDTVVQALPQVG  
NLGLLFMLLFFIYAALGVELFGKLCV  
NDENPCEGMSRHATFENFGMAFLT  
LFQVSTGDNWNGIMKDTLRDCTHD  
ERSCLSSLQFVSPLYFVSFVLTAQFV  
LINVVAVLMKHLDDSNKEAQEDAE  
MDAELELEMAHGLGPGPRLPTGSP  
GAPGRGPGGAGGGGDTEGGLCRRC  
YSPAQENLWLDVSLIHKDSLEGELTI  
IDNLSGSIFHHYSSPAGCKKCHHDK  
QEVQLAETEAFSLNSDRSSILLGDD  
LSLEDPTACPPGRKDSKGELDPPEP  
MRVGDLGECFFPLSSTAVSPDPENF  
LCEMEEIPFNPVRSWLKHDSSQAPP  
SPFSPDASSPLLPMPAEFFHPAVSAS  
QKGPEKGTGTGTLPKIALQGSWASL  
RSPRVNCTLLRQATGSDTSLDASPSS  
SAGSLQTTLEDSTLSDSPRRALGPP  
APAPGPRAGLSPAARRRLSLRGRGLF  
SLRGLRAHQRSRSSGGSTSPGCTHH  
DSMDPSDEEGRGGAGGGGAGSEHS  
ETLSSLSTSLFCPPPPPPAPGLTPAR  
KFSSTSSLAAPGRPHAAALAHGLAR  
SPSWAADRSKDPPGRAPLPMGLGPL  
APPPQPLPGELEPGDAASKRKR