

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	12.289763	S981;S986	S1058	35254053	MAESASPPSSSAAAPAAEPGVTTEQP GPRSPSSPPGLEEPLDGADPHVPH PDLAPIAFFCLRQTTSPRNWCIMV CNPWFECVSMVLVILLNCVTLGMYQP CDDMDCLSDRCKILQVDFDFIFIFFA MEMVLKMVALGIFGKKCYLGDTWN RLDFFIVMAGMVEYSLDLQINLSAI RTVRVLRPLKAINRVPSMRILVNLLL DTLPMLGNVLLLCFFVFFIFGIIGVQ LWAGLLRNRCFLEENFTIQGDVALP PYYQPEEDDEMPFICSLSGDNGIMG CHEIPPLKEQGRECCLSKDDVYDFG AGRQDLNASGLCVNWNRYNVCRT GSANPHKGAINFDNIGYAWIVIFQVI TLEGWVEIMYYVMDAHSFYNFYFIL LIIVGSFFMINLCLVVIATQFSETKQR EHRMLEQRQRYLSSTVASYAEPG DCYEEIFQYVCHILRKARRALGLYQ ALQSRQALGPEAPAPAKPGPHAKE PRHYHGKTKGQGDEGRHLGSRHCQ TLHGPA SPGNDHSGRELC PQHSPLD ATPHTLVQIPATLASDPASCPCQHQ EDGRRPSGLGSTDSGQEGSGSGSSA GGEDEADGDGARSSD GASSELGKE EEEEEQADGAVWLCGDVWRETRAK LRGIVDSKYFNRGIMMAILVNTVSM GIEHHEQPEELTNILEICNVVFTSMF ALEMILKLA AFG LFDYLRNPNYIFDS IIVIISIWEIVGQADGGLSVLRTFLLR VLKLVRFMPALRRQLVVLKTMMDN VATFCMLLMLFIFIFSILGMHIFGCK FSLRTDTGDTV PDRKNFDSLLWAIV TVFQILTQEDWNV VLYNGMASTSP WASLYFVALMTFGNYVLFNLLVAIL VEGFQAEGDANRSYSD EDQSSS NIE EFDKLEGLDSSGDPKLCPIPMTPN GHLDP SLPLGGHLGPAGAAGPAPRL SLQDPMLVALGSRKSSVMSLGRM SYDQRSLSSSRSSYYGPWGRSAAWA SRRSSWNSLKHKPPSAEHESLLSAE RGGGARVCEVA ADEGPPRAAPLHTP HAHHIHGPHLAHRHRHRRRTLSL DNRDSVDLAELVPAVGAHPRAAWR AAGPAPGHEDCNGRMP SIAKDVFTK MGDRGDRGEDEE EIDYTL CFRVRK MIDVYKPDWCEVREDWSVYLFSPE NRFRVLCQTIIAHKLFDYVVLAFIFL NCITIALERPQIEAGSTERIFLTVSNIY FTAIFV GEMTLKVVSLGLYFGEQAYL

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