	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extra regio
0	Q13698	CAC1S_HUMAN	Homo sapiens	Voltage-dependent L-type calcium channel subunit alpha-1S	19.817031	S346;T349	S393;S397;S687;S1575;S1617	30379171;35254053	MEPSSPQDEGLRKKQPKKPVPEILP RPPRALFCLTLENPLRKACISIVEWK PFETIILLTIFANCVALAVYLPMPEDD NNSLNLGLEKLEYFFLIVFSIEAAMK IIAYGFLFHQDAYLRSGWNVLDFTIV FLGVFTVILEQVNVIQSHTAPMSSKG AGLDVKALRAFRVLRPLRLVSGVPSL QVVLNSIFKAMLPLFHIALLVLFMVII YAIIGLELFKGKMHKTCYFIGTDIVAT VENEEPSPCARTGSGRRCTINGSEC RGGWPGPNHGITHFDNFGFSMLTV YQCITMEGWTDVLYWVNDAIGNEW PWIYFVTLILLGSFFILNLVLGVLSGE FTKEREKAKSRGTFQKLREKQQLDE DLRGYMSWITQGEVMDVEDFREGK LSLDEGGSDTESLYEIAGLNKIIQFIR HWRQWNRIFRWKCHDIVKSKVFYW LVILIVALNTLSIASEHHNQPLWLTR LQDIANRVLLSLFTTEMLMKMYGLG LRQYFMSIFNRFDCFVVCSGILEILL VESGAMTPLGISVLRCIRLLRIFKITK YWTSLSNLVASLLNSIRSIASLLLLLF LFIVIFALLGMQLFGGRYDFEDTEVR RSNFDNFPQALISVFQVLTGEDWTS MMYNGIMAYGGPSYPGMLVCIYFIIL FVCGNYILLNVFLAIAVDNLAEAESL TSAQKAKAEEKKRRKMSKGLPDKSE EEKSTMAKKLEQKPKGEGIPTTAKL KIDEFESNVNEVKDPYPSADFPGDD EEDEPEIPLSPRPRPLAELQLKEKAV PIPEASSFFIFSPTNKIRVLCHRIVNA TWFTNFILLFILLSSAALAAEDPIRAD SMRNQILKHFDIGFTSVFTVEIVLKM TTYGAFLHKGSFCRNYFNMLDLLVV AVSLISMGLESSAISVVKILRVLRVLR PLRAINRAKGLKHVVQCMFVAISTIG NIVLVTTLLQFMFACIGVQLFKGKFF RCTDLSKMTEEECRGYYYVYKDGDP MQIELRHREWVHSDFHFDNVLSAM MSLFTVSTFEGWPQLLYKAIDSNAE DVGPIYNNRVEMAIFFIIYIILIAFFM MNIFVGFVIVTFQEQGETEYKNCEL DKNQRQCVQYALKARPLRCYIPKNP YQYQVWYIVTSSYFEYLMFALIMLNT ICLGMQHYNQSEQMNHISDILNVAF TIIFTLEMILKLMAFKARGYFGDPWN VFDFLIVIGSIIDVILSEIDTFLASSGG LYCLGGGCGNVDPDESARISSAFFR LFRVMRLIKLLSRAEGVRTLLWTFIK SFQALPYVALLIVMLFFIYAVIGMQM FGKIALVDGTQINRNNNFQTFPQAV LLLFRCATGEAWQEILLACSYGKLCD PESDYAPGEEYTCGTNFAYYYFISFY MLCAFLVINLFVAVIMDNFDYLTRD WSILGPHHLDEFKAIWAEYDPEAKG RIKHLDVVTLLRRIQPPLGFGKFCPH RVACKRLVGMNMPLNSDGTVTFNA TLFALVRTALKIKTEGNFEQANEELR AIIKKIWKRTSMKLLDQVIPPIGDDEV TVGKFYATFLIQEHFRKFMKRQEEY YGYRPKKDIVQIQAGLRTIEEEAAPEI CRTVSGDLAAEEELERAMVEAAME EGIFRRTGGLFGQVDNFLERTNSLP PVMANQRPLQFAEIEMEEMESPVFL EDFPQDPRTNPLARANTNNANANV AYGNSNHSNSHVFSSVHYEREFPEE TETPATRGRALGQPCRVLGPHSKPC VEMLKGLLTQRAMPRGQAPPAPCQ CPRVESSMPEDRKSSTPGSLHEETP HSRSTRENTSRCSAPATALLIQKALV RGGLGTLAADANFIMATGQALADAC QMEPEEVEIMATELLKGREAPEGMA SSLGCLNLGSSLGSLDQHQGSQETL IPPRL	False	True	2.037	1.881	1.859	3.501	0.919	5.0	2.168