	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	extracellula region
0	Q61290	CAC1E_MOUSE	Mus musculus	Voltage-dependent R-type calcium channel subunit alpha-1E	24.474581	NaN	S15;S20;S428;T441;S737;S746;S794;S816;S856;S948;S1099;S2054;S2073	33300544	MARFGEAVVVGRPGSGDGDSDQSR NRQGTPVPASGPAAAYKQSKAQRAR TMALYNPIPVRQNCFTVNRSLFIFGE DNIVRKYAKKLIDWPPFEYMILATIIA NCIVLALEQHLPEDDKTPMSRRLEK TEPYFIGIFCFEAGIKIVALGFIFHKGS YLRNGWNVMDFIVVLSGILATAGTH FNTHVDLRALRAVRVLRPLKLVSGIP SLQIVLKSIMKAMVPLLQIGLLLFFAI LMFAIIGLEFYSGKLHRACFMNNSG ILEGFDPPHPCGVQGCPAGYECKDW IGPNDGITQFDNILFAVLTVFQCITM EGWTTVLYNTNDALGATWNWLYFIP LIIIGSFFVLNLVLGVLSGEFAKERER VENRRAFMKLRRQQQIERELNGYRA WIDKAEEVMLAEENKNSGTSALEVL RRATIKRSRTEAMTRDSSDEHCVDIS SVGTPLARASIKSTKVDGASYFRHKE RLLRISIRHMVKSQVFYWIVLSVVAL NTACVAIVHHNQPQWLTHLLYYAEF LFLGLFLLEMSLKMYGMGPRLYFHS SFNCFDFGVTVGSIFEVVWAIFRPGT SFGISVLRALRLLRIFKITKYWASLRN LVVSLMSSMKSIISLLFLLFLFIVVFA LLGMQLFGGRFNFNDGTPSANFDT FPAAIMTVFQILTGEDWNEVMYNGI RSQGGVSSGMWSAIYFIVLTLFGNY TLLNVFLAIAVDNLANAQELTKDEQ EEEEAFNQKHALQKAKEVSPMSAP NMPSIERDRRRRHHMSMWEPRSS HLRERRRRHHMSVWEQRTSQLRRH MQMSSQEALNKEEAPPMNPLNPLN PLSPLNPLNAHPSLYRRPRPIEGLAL GLGLEKCEEERISRGGSLKGDIGGLT SALDNQRSPLSLGKREPPWLPRSCH GNCDPIQQEAGGGETVVTFEDRARH RQSQRRSRHRRVRTEGKDSASASRS RSASQERSLDEGVSVEGEKEHEPHS SHRSKEPTIHEEERTQDLRRTNSLM VPRGSGLVGALDEAETPLVQPQPEL EVGKDAALTEQEAEGSSEQALLGDV QLDVGRGISQSEPDLSCMTANMDK ATTESTSVTVAIPDVDPLVDSTVVNIS NKTDGEASPLKEAETKEEEEEVEKK KKQKKEKRETGKAMVPHSSMFIFST TNPIRRACHYIVNLRYFEMCILLVIAA SSIALAAEDPVLTNSERNKVLRYFDY VFTGVFTFEMVIKMIDQGLILQDGSY FRDLWNILDFVVVVGALVAFALANA LGTNKGRDIKTIKSLRVLRVLRPLKTI KRLPKLKAVFDCVVTSLKNVFNILIV YKLFMFIFAVIAVQLFKGKFFYCTDS SKDTEKECIGNYVDHEKNKMEVKG REWKRHEFHYDNIIWALLTLFTVST GEGWPQVLQHSVDVTEEDRGPSRS NRMEMSIFYVVYFVVFPFFFVNIFVA LIIITFQEQGDKMMEECSLEKNERA CIDFAISAKPLTRYMPQNRHTFQYRV WHFVVSPSFEYTIMAMIALNTVVLM MKYYTAPCTYELALKYLNIAFTMVFS LECVLKVIAFGFLNYFRDTWNIFDFI TVIGSITEIILTDSKLVNTSGFNMSFL KLFRAARLIKLLRQGYTIRILLWTFVQ SFKALPYVCLLIAMLFFIYAIIGMQVF GNIKLDEESHINRHNNFRSFFGSLM LLFRSATGEAWQEIMLSCLGEKGCE PDTTAPSGQNESERCGTDLAYVYFV SFIFFCSFLMLNLFVAVIMDNFEYLT RDSSILGPHHLDEFVRVWAEYDRAA CGRIHYTEMYEMLTLMSPPLGLGKR CPSKVAYKRLVLMNMPVAEDMTVH FTSTLMALIRTALDIKIAKGGADRQQ LDSELQKETLAIWPHLSQKMLDLLV PMPKASDLTVGKIYAAMMIMDYYKQ SKVKKQRQQLEEQKNAPMFQRMEP SSLPQEIIANAKALPYLQQDPVSGLS GRSGYPSMSPLSPQEIFQLACMDPA DDGQFQEQQSLVVTDPSSMRRSFST IRDKRSNSSWLEEFSMERSSENTYK SRRRSYHSSLRLSAHRLNSDSGHKS	None	None	None	None	None	None	None	None	None

									DTHRSGGRERGRSKERKHLLSPDVS RCNSEERGTQADWESPERRQSRSPS EGRSQTPNRQGTGSLSESSIPSISDT STPRRSRRQLPPVPPKPRPLLSYSSL MRHTGGISPPPDGSEGGSPLASQAL ESNSACLTESSNSLHPQQGQHPSPQ HYISEPYLALHEDSHASDCGEEETLT FEAAVATSLGRSNTIGSAPPLRHSW QMPNGHYRRRRWGAWAGMMCGA VSDLLSDTEEDDKC								