

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
E9PWL1	E9PWL1_MOUSE	Mus musculus	Voltage-dependent T-type calcium channel subunit alpha	29.185005	NaN	NaN	22645316	MDEEEDGAGAEESGQPRSFTQLND LSGAGGRQGGSTKDPGSADSEAE GLPPYPALAPVVFFYLSQDSRPRSWCL RTVCNPWFERVSMVILLNCVTLGM FRPCEDIAQCSQRCLQAFDDFIFA FFAVEMVVKMVALGIFGKKCYLGD WNRLDFFVIAGMLEYSLDLQNVSF SAVRTVRLRPLRAINRVPSMRILVT LLDTPMLGNVLLCCFFVFFIFGIV GVQLWAGLLRNRCFLPENFSLPLSV DLEPYQTENEDESPPFCISQPRENG MRSCRSVPTLRGEGGGPPCGLDYE AYNSSNTTCVNWNYQYTNCSAGE HNPFKGAINFNDNIGYAWIAIFQVITL EGWVDIMYFVMDAHSFYNFYIFILLI IVGSSFFMINLCLVVIATQFSETKQRE SQLMREQRVRFSLNASTLASFSEPG SCYEELLKYLVYILRKAARRLAQVSR AVGVRAGLLSSPVARGGOEPQPSGS CSRSRRRLSVHHLVHHHHHHHHHH YHLGNGTLRVPRASPEIQDRDANGS RWLMLPPPSTPTPSGGPPRGAESVH SFYHADCHLEPVRCQAPPPRSPSEA SGRTVGSQKVVYPTVHTSPPPEMLKD KALVEVAPSPGPPTLTSFNIPPFPSS MHKLETTQSTGACHSSCKISSPCSK ADSGACGPDSCPYCARTGAGEPESA DHEMPDSDSEAVYEFQDAQHSDDL RDPHRRRRPSLGPDAEPSSVLAFWR LICDTRKIVDSKYFGRGIMAILVNT LSMGIEYHEQPEELTNAEISNIVFT SLFALEMMLKLLVYGPFGYIKNPYNI FDGVIVVISVWEIVGQGGGLSVLRT FRLMRVLRVLRFPALQRQLVVLMM TMDNVATFCMLLMLFIFIFSILGMH LFGCKFASERDGDTPDRKNFDSLL WAIVTVFQILTQEDWNKVLYNGMAS TSSWAALYFIALMTFGNYVLFNLLVA ILVEGQAEQDATKSESEPDFFSPSV DGDGDRKKRLALVALGEHSELRKSL LPPLIHTAATPMSLPKSSSTGVGEAL GSGSRRTSSSGSAEPTAHHEMKSP PSARSSPHSPWSAASSWTSRRSSRN SLGRAPSLKRRSPSGERRSLLSGEG QESQDEEESSEEDRASAPGSDHRH RGSLEREAKSSFDPDTPLOVPLHR TASGRSSASEHQDCNGKSASGRRLAR TLRADDPPLDGDDGDDEGNLSKGE RLRAWVRARLPACCRERDSWSAYIF PPQSRFRLLCHRIITHKMFHDHVVVI IFLNCITIAMERPKIDPHSAERIFLTL SNYIFTAVFLAEMTVKVALGWCFG EQAYLRSSWNVLDGLLVLISVIDILV SMVSDSGTKILGMLRVLRLRTRLRP LRVISRAQGLKLVVETLMSLKPIGN IVVICCAFFIIFGILGVQLFKGKFFVC QGEDTRNITNKSDCAEASRWRVRH KYNFDNLGQALMSLFLASKDGVV DIMYDGLDAVGVDQQPIMNHNPW MLLYFISFLLIVAFFVLNMFVGVVVE NFHKCRQHQQEEEARRREEKRLKR LEKKRRSKEKQADMLMLDDVIASGS SASAASEAQCKPYSDYSRFRLLVH HLCTSHYLDLDFITGVIGLVVVTMAM EHYQPPQILDALKICNYIFTVIFVLE SVFKLVAFGFRFFQDRWNQDLAI VLLSIMGITLEEIEVNASLPINPTIIRI MRVLRIRARVLKLLKMAVGMRALD VMQALPQVGNLGLLFFMFFIFAAL GVELFGDLECDETHPCEGLGRHATF RNFGMFLTLFRVSTGDNWNGIMK DTRLRDCQUESTCYNTVISPIYFVSVF LTAQFVLVNVVIAVLMKHLEESNKE AKEEALEAELEEMKTLSPQPHSP LGSPFLWPGVEGVNSPSPKPGAPH TTAHIGAASSGFSLEHPTMVPHTTE	None	None	None	None	None	None	None		

