

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane
B1AWN6	SCN2A_MOUSE	Mus musculus	Sodium channel protein type 2 subunit alpha	37.975063	T1964;T1967	S4;S468;S471;S484;S526;S528;S531;S553;S554;S558;S573;S576;S589;S610;S623;S687;S688;S722;S1507;S1931;T1944;T1964;T1967;S1972	33300544;40885482	MAQSVLVPVPPGPDSEFRFFFTRESLAAIE QRIAEKAKRKPQKERKDEDDENGPK PNSDLEAGKSLPFIYGDIPPEMVSSE LEDLDPYYINKKTFIVLNKGKAIKSRFS ATSALYILTPFNPPIKLAIKILVHSLFN VLIMCTILTNCVFMVMTMSNPPDWTK NVEYTFGTGIYTFESLIKILARGFCLED FTFLRDPWNWLDFTVITFAYVTEFV NLGNVSALRTRFVLRALKTISVIPGL KTIVGALIQSVKCLSDVMILTVFCLSV FALIGLQLFMGNLRNKLQWPPDN STFEINITSFNNSLDWNGTAFNRT MNMFNWDEYIEDKSHFYFLEGQND ALLCGNSSDAGQCPEGYICVKAGR PNYGYTSFDTFSWAFLSLFRLMTQD FWENLYQLTLRAAGKTYMIFVVLVIF LGSFYLINLILAVVAMAYEEQNAATL EEAEQKEAEFQOMLEQLKKQEEEA QAAAAAASAESEDRDFSGAGGIGVFSE SSVASKLSKSEKELKNRRKKKKQK EQAGEEEKEDAVRKSASEDSIRKKG FRFSLEGSRLTYEKRFSSPHQSLLSI RGSLSFPRRNSRASLFSFKGRVKDIG SENDFADDEHSTFEDNDSRRDSL PHRHGERRPSNVSQASRASRGIP PMNGKMHSVAVDCNGVSVLVGGPSA LTSVPGQLLEGGITTEIRKRRSS YHVSMDLLEDPTSQRORAMSMASILT NTMEELESRQKCPKPCWYKFANMC LIWDCCPKWLKVKHVNLVVMDF VDLAIITICIVLNTLFMAMEHYPMTE QFSSVLSVGNLVFTGIFTAEMFLKHA MDPYFYFOEGWNIQDFIVLSLME LGLANVEGLSVLRSFRLRVFKLAKS WPTLNMLIKIIGNSVGLGNLTLVLA IIVFIFAVVGMQLFGKSYKECVCKIS NDCLEPRWHMHDFFHSFLIVFRVL CGEWIETMWDCEVAGQTMCLTVF MMVMVIGNLVVNLFLALLSSFS DNLAATDDDNEMNNLQIIVGRMQK GIDFVKKIREFIQKAFVRKQKALDEI KPLEDLNKKDCISNHTTIEIGKDL NYLKDNGTTSIGISSVEKYVDES DYMSPFINNPSLTVTVPIAVGESDFEN LNTEEFSSSESDMEESKEKLNATSSS EGSTVDIGAPAEQPEAEPEESLEP EACFTEDCVRKFKCCQISIEEGKGL WWNLKTCYKIVEHNWFETVIFVMI LLSSGALAFEDIYEQRTIKTMLEYA DKVFTYIFILEMLLKWVAYGFQMYF TNAWCWLDLFLVDVSLVSLTANALG YSELGAIKSLRTRALRPLRALS RFE GMRVVVNALLGAIPSIMNVLVCLIF WLIFSIMGVNLFAKGFYHCINYYTGE MFDVSVVNNYSECALIESNQAR WKNVKVNFNVGLGYLSLLQVATF KGWMDIMYAAVDSRNVLPQPKYED NLYMYLYFVIFIFGFFTLNLFIVGII DNFNQKKKFGGQDIFMTEEQKKY YNAMKKGSKKPKPIPRPANKFQG MVFDVTKQVFDISIMILICLNMVT MMVETDDQSOEMTNILYWINLVFIV LFTGECVLKLSLRHYFTIGWNIFD FVVVLSIVGMFLAELIEKYFVSPTLF RVIRLARIGRILRLIKGAKGIRTLFAL MMSLPALFNIGLLFLVMFIYAIIFGM SNFAYVKREVGIDDMFNFTFGNS MICLFQITTSAGWDGLLAPILNSGPP DCDPEKDHGSSVKGDCGNPSVGIF FFVSYIIISFLVVNMYIAVILENFSVA TEESAEPLEDDFEMFYEVWEKFD DATQFIEFKLSDFAAALDPPLLIAKP NKVQLIAMDLPMVSGDRHICLIDILF AFTKRVLGESGEMDALRIQMEERF MASNPSKVSYEPITTLKRRQEVSA IVIQRAYRRYLLKQKVKVSSYKDK GKEDEGTPKEDIITDKLNENSTPEK TDVTPSTTSPPSYDSVTKPEKEKPEK DKSEKEDKGDIRESKK	False	True	2.105	1.972	1.698	1.672	1.304	5.0