	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	extracellular region
0	Q9NY46	SCN3A_HUMAN	Homo sapiens	Sodium channel protein type 3 subunit alpha	19.994096	NaN	S484;S485;S486;S1501	37217939	MAQALLVPPGPESFRLFTRESLAAIE KRAAEEKAKKPKKEQDNDDENKPK PNSDLEAGKNLPFIYGDIPPEMVSEP LEDLDPYYINKKTFIVMNKGKAIFRF SATSALYILTPLNPVRKIAIKILVHSLF SMLIMCTILTNCVFMTLSNPPDWTK NVEYTFTGIYTFESLIKILARGFCLED FTFLRDPWNWLDFSVIVMAYVTEFV SLGNVSALRTFRVLRALKTISVIPGLK TIVGALIQSVKKLSDVMILTVFCLSVF ALIGLQLFMGNLRNKCLQWPPSDSA FETNTTSYFNGTMDSNGTFVNVTM STFNWKDYIGDDSHFYVLDGQKDPL LCGNGSDAGQCPEGYICVKAGRNPN YGYTSFDTFSWAFLSLFRLMTQDYW ENLYQLTLRAAGKTYMIFFVLVIFLG SFYLVNLILAVVAMAYEEQNQATLE EAEQKEAEFQQMLEQLKKQQEEAQ AVAAASAASRDFSGIGGLGELLESSS EASKLSSKSAKEWRNRRKKRRQRE HLEGNNKGERDSFPKSESEDSVKRS SFLFSMDGNRLTSDKKFCSPHQSLL SIRGSLFSPRRNSKTSIFSFRGRAKD VGSENDFADDEHSTFEDSESRRDSL FVPHRHGERRNSNVSQASMSSRMV PGLPANGKMHSTVDCNGVVSLVGG PSALTSPTGQLPPEGTTTETEVRKRR LSSYQISMEMLEDSSGRQRAVSIASI LTNTMEELEESRQKCPPCWYRFAN VFLIWDCCDAWLKVKHLVNLIVMDP FVDLAITICIVLNTLFMAMEHYPMTE QFSSVLTVGNLVFTGIFTAEMVLKIIA MDPYYYFQEGWNIFDGIIVSLSLMEL GLSNVEGLSVLRSFRLLRVFKLAKS WPTLNMLIKIIGNSVGALGNLTLVLA IIVFIFAVVGMQLFGKSYKECVCKIN DDCTLPRWHMNDFFHSFLIVFRVLC GEWIETMWDCMEVAGQTMCLIVFM LVMVIGNLVVLNLFLALLLSSFSSDN LAATDDDNEMNNLQIAVGRMQKGI DYVKNKMRECFQKAFFRKPKVIEIH EGNKIDSCMSNNTGIEISKELNYLR DGNGTTSGVGTGSSVEKYVIDENDY MSFINNPSLTVTVPIAVGESDFENLN TEEFSSESELEESKEKLNATSSSEGS TVDVVLPREGEQAETEPEEDLKPEA CFTEGCIKKFPFCQVSTEEGKGKIW WNLRKTCYSIVEHNWFETFIVFMIL LSSGALAFEDIYIEQRKTIKTMLEYAD KVFTYIFILEMLLKWVAYGFQTYFTN AWCWLDFLIVDVSLVSLVANALGYS ELGAIKSLRTLRALRPLRALSRFEGM RVVVNALVGAIPSIMNVLLVCLIFWL IFSIMGVNLFAGKFYHCVNMTTGN MFDISDVNNLSDCQALGKQARWKN VKVNFDNVGAGYLALLQVATFKGW MDIMYAAVDSRDVKLQPVYEENLY MYLYFVIFIIFGSFFTLNLFIGVIIDNF NQQKKKFGGQDIFMTEEQKKYYNA MKKLGSKKPQKPIPRPANKFQGMVF DFVTRQVFDISIMILICLNMVTMMV ETDDQGKYMTLVLSRINLVFIVLFTG EFVLKLVSLRHYYFTIGWNIFDFVVV ILSIVGMFLAEMIEKYFVSPTLFRVIR LARIGRILRLIKGAKGIRTLLFALMMS LPALFNIGLLLFLVMFIYAIFGMSNF AYVKKEAGIDDMFNFETFGNSMICL FQITTSAGWDGLLAPILNSAPPDCDP DTIHPGSSVKGDCGNPSVGIFFFVSY IIISFLVVVNMYIAVILENFSVATEES AEPLSEDDFEMFYEVWEKFDPDATQ FIEFSKLSDFAAALDPPLLIAKPNKV QLIAMDLPMVSGDRIHCLDILFAFTK RVLGESGEMDALRIQMEDRFMASN PSKVSYEPITTTLKRKQEEVSAAIIQR NFRCYLLKQRLKNISSNYNKEAIKGR	False	False	1.625	1.851	1.644	1.483	0.992	4.215	2.038

									IDLPIKQDMIIDKLNGNSTPEKTDGS SSTTSPPSYDSVTKPDKEKFEKDKPE KESKGKEVRENQK										