

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	extracellular region
A0A2R8VHF9	A0A2R8VHF9_MOUSE	Mus musculus	NaN	22.380232	NaN	NaN	37507081	MAQKGQLSDDEKFLFVDFKDFMNSP MAQADWWAKLWVWVPEKQGFEEA SIKEEKGDVVVVELVENGKVTVGK DDIQKMNPPKFSKVEDMAELTCLN EASVLHNLREYFSGLIYTYSGLFV VVNPYKYLPIYSEKIVDMYKGGKRHE MPPHIYAIADTAYRSMQLDREDQSIL CTGESGAGKTENTKKVIQYLAVVASS HKGKDDSSITGELEKQLQANPILEA FGNAKTVKNDNSSRFGKFINRFDV TGYIVGANIETYLLEKSRAIRQARDE RTFHIFYLLAGAKEKMKSDLLESF NSYTFLSNGFVPIAAQDDEMFQET LEAMSIMGFNEEEQLAILKVSSVL QLGNIVFKKERNTDQASMPDNTAA QKVCHLVGINVDFTRAILTPRIKVG RDVVQKAQTKAQADFAIEALAKATY ERLFRWILSRVKNALDKTRHQGASF LGILDIAGFIFEVNSFEQLCINYTNE KLQQLFNHTMFILEQEEYQREGIEW NFIDFGLDLQPCIELIERPNNPPGVL ALLDEECWFPKATDKSFVEKLCSEQ GNHPKFQPKQLKDKTEFSIIHYAG KVDYNASAWLTKNMDPLNDNVTSL LNASSDKFVADLWKDVRIVGLDQ MAKMTESLPSASKTKKGMFRTVG QLYKEQLGKMLTLRNTTPNFVRCII PNHEKRSGLDAFLVLEQLRCNGVL EGIRICRQGFNRRIVQEFRQRYEILA ANAIKGFMDGKQACILMIKALELD PNLYRIGQSKIFFRTGVLAHLEEEED LKITDVIMAFQAMCRGYLARKAFTK RQQQLTAMKVIQRNCAAYLKLNRW QWWRLFTKVKPLLQVTRQEEEMQA KEEEMQKIKERQQAETELKELEOK HTQLAEKTLLEQLQAETELYAEA EEMRVRLAAKKQEELEIHEMEARL EEEEERDQQLQAERKKMAQQMLDL EEQLEEEEAARQKLOLEKVTAAEKIK KLEDDILVMDDQNSKLSKERKLEE RVSDLTNLAEEEEKAKNLTCLKSK HESMISELEVRLLKKEEKSRQELEKL KRKLEGDASDFHEQIADLQAIQIEL KMQLAKKEEELQAALARLDEEIAQK NNALKKIRELEGHISDLQEDLDSER AARNKAEKQRDLGEELEALKTELE DTLDSTATQQLRAKREQEVTVLKK ALDEETRSHEAQVOEMRQKHTQAV EELTEQLEQFKRAKANLDSKQTLLE KENADLAGELRVLGQAKQVEVHKK KKLEVLQDLQSKCSDGERARAELS DKVHKLQNEVESVTGMLNEAEGKAI KLAKDVASLGSQLODTEQLLEQETR QKLNVSTKLROLEDERNSLQDQLDE EMEAKQNLERHVSTLNIQLSDSKKK LQDFASTIEVMEEGKRLQKEMEGL SQYYEKAAYDKLEKTKNRLQOQL DDLVDLDNRQQLVSNLEKKQKFF DQLLAEEKNISKYADERDRAEAEA REKETKALSLARALEEAEKEELER TNKMLKAEMEDLVSSKDDVGNVH ELEKSKRALETQMEEMKTQLEELED ELQATEDAKLRLEVMQALKGQFE RDLQARDEQNEEKRRQLQRQLHEY ETELERKQRALAAAANKKLEGDL KDLELQADSAIKGEEAIKQLRKLQA QMKDFQRELDARASRDEIFATSKE NEKKAKSLEADLMQLQEDLAAEERA RKQADLEKEELAEELASSLSGRNTL QDEKRRLEARIAQLEEELEEEQGNM EAMSDRVRKATLQAEQLSNELATER STAQKNESARQQLERQNKELRSKLO EVEGAVKAKLKSTVAALAKIAQLEE QVEQEAEREQAATKSLKQDKKLLKE VLLQVEDERKMAEQYKEQAEKGNT KVKQLKRQLEEEESQRINANRRK	False	False	3.649	2.702	2.192	1.93	1.326	2.181	2.307

