

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
E9Q2C0	E9Q2C0_MOUSE	Mus musculus	NaN	25.875327	T19	NaN	30059200	MDLIITQELARARNQDATALRRAY ELIKSANLGKSELDPTESFSPDLFVL CAEQALKMKEPEISEDICQMYFKVK APITQFLGRAHL CRAQLCAPQSEEN VEEFENCVTQYMKAINFAKGEPRYY FLVFNASVLYWNMVRPFLKPGYHH LVIPLSLQIITVLNQTEEDKEWRAE LMLELLECYLQAGRKEDATKFCFTA APFVRTQVPHKYRQMFSTMVRYEVL DDLMLREDKQQSILSITYHINSLKA KLDKNNLPENLEQILRKMRYRDLSSQY HDQHVPTIREEKILLFELGRLCLTL KNEPIASDCLQYLKKMETEDTGKLL EMEGLECELDALRLGSKLKMVLRGA VEEQLLHKRMDNILQRAIRLGNPTTI HVLCTAQNICLPLLQHNLRHHLR KPLTNIAEILEKVDLSMILLRCOVHM EMAYIEQDDDRVEPAIEHMQKAMR LDSLGIYRDKIKITYRRQLQGTMLYQ SPDRPEDKATMAIEQAKKATPKDSA RKKRAILVNAGLALAPDTFQIVLSE NESKVSIGKIKGRFTYLCAKARHHIL SVDKAAGHLRRLGYENDKDRIVIWA ELAKVAWQQDWDVCR TASRFCLL YDNVKAKRSTKLKRGRKKVIEGSM SDWAPSDMAMHKQMPDLLRRIAK VLFISAEATVHLLRSEGVLNNQAIP PEDLSQHPAGYVPEPPESNSEWITY RTWIENLSQYAMNNWMRAAEIGQE LGSWIVQNAVVVLNHNRLHLAG RQKELVESLFFLSIHKVGYTEDSV MLVMLCNALARGLIMSWIPTQTPEK SKKNVRPTLVHGPLESSTLSDIRA EVCEFALNLTNGNVPEDIVPTNVRQ HLIATVWKAKQLLQQQIGRLGTDE QSTNEDISSVTRVLVALEMYSNGL GLMDFTVPLVQVVKMASECNWSD HLVELQTLRLTHFAYMAHDHEVT MACSQNATQMGKHLRSFEPSSNAK LAAEMLCMVSCIQGRSIMEENLKGK QLRLAAAKAFVESARFGGLANSNSL VMMAARHYWNTWLP LLS PANRKK AKASLQRHISINKTENKKQETDKTLP LHQWPSADFQTGGTGPEIPFLPGAE DDLTLRAALYTLFNSHADRNDE MGLKVLDEAVQVLPRTAHRLLIFKH MVIVKAKLGQNFTMEIQKFKDEKES YLASMWYRLAQNSKTVCGELSICYQ NAIQALQKPENNWQKVDYIMEFSE WMYKQFPLDDVFDHLDWAIEILLS MKPNEDALEPEPKKEGQASPAQSLT ESTVPSNQASLDQFRSVRQLEALA RVHILRALMASPSASSYEDDCLMAY SFFKHILQISLTEGVKLIPEKNLQAVS SQLLLTKKEKEKEKEKEKEREKKEK EKKEKKEKKEKKEKKEKKEKKEEKE EKEKKEKKEKKEKKEKKEEKEKKEK EKKEKKEKKEKEREKKEKVKDTK QISTSASNKPPDEIPTSIGEWASYS EDLLHVFKQDKSDCTINSSSFQKPT YSLYIDHLAKALQKMFHLHEL SIPIL QLGVLIAEAVVESKSLADLYHLRLQ VCSDLRLHYAATHHEEVIGQAYFGD MEQASCRKEIAFKKEKNKEPEMEDY LPTLHEQLTSDSVEVKALIAQDKIL KINGETGKLEGTSYPQLWLLKGEV LLELELHQPARLLSQAQWAFQELG DICSEAQSLLLAELANKEKNHAQA MLMVERAQQLGAAEEFWYKSTLTL AEAILSSDDRKEISVCSLQKIDTF RALQNERPNRVSLEFLIMELEARC VKLRIQFACNLTDDEFNEHPFLRE LEDHLLVEQNLIFFGGYKKNYVDLK LDHAKIKRLCAQKEKDEEQKTAYYL	None	None	None	None	None	None	None		

EMYSLSQKAVSEEEVFHRIQALLSL
HDLQNINSPVMRRRLARLKLSLAETC
LDLLQLVCKEALDLQMEQGSFEKLL
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LAGKALHLLYVQTDVVPYSPFCWEE
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KTMPSPKGKLIITVGGYCKVTRVATSP
TAISDLLTSIQWFQRQTRVKEQALCT
QSLSSILEHMEDYLPITPQLTFPES
RNQMPTAVGDAGKNKGREKERKISL
PSGQPDPEYLILIVDKFLELPLEGLS
MLNEVTLSRDFSLQMLWNRLHKE
EREGSMKKEVKSDDLKKTTPGKKAL
KSIMTRIIPPECNLIDSDTIKFVVDY
EEARGTELMRPIEITQEILEKYRDTF
TGRWMGHLGNHNFPSQADWEQLL
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GVESIVDNQWPTLMQDNMLRATIL
WDNLLAIGKPLGKTVRLIHKLCNEP
GSQDEKQVSKNEPSELQPHHPES
LTTALNWWLYGLPHQAIV