

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
E9PZP8	E9PZP8_MOUSE	Mus musculus	NaN	33.218136	NaN	NaN	37507081;22645316	MATMVPVPPVKLKWLEHLNSSWITED SESIATREGVTVLYSKLISNKEVVP QQVLCCKGPPQPDFERESLSSDEQD HYLDALLSSQLALAKMVCSDSPFAG ALRKRLLVLRVYFALS NKYHDKGK VKQQHSPSSSGSADVHSVSRPR SSTDALIEMGVRTGLSLLFALLRQS WMMPVSGPLSLCNDVIHTAIEVVS SLPPLSLANESKIPPMGLDCLSQVTT FLKGVTIPNSGADTLGRRLASSELLG LAAQRGSLRYLLEWIEMALGASAVV YTMEKNKLLSSQEGMISFDCFMAL MQMRRSLGSSADRSQWREPTRTSE GLCSLYEAALCLFEEVCRMADYSR TCASPD SIQTGDPIVSETCEVYVWG SNSSHQLVEGTQEKILOPKLAPSFSD AQTI EAGQYCTFVISTDGSVRACGKG SYGRLGLGDSNNQSTLKKLTFEPHR SIKKVSSSKGSDGHTLAFTTEGEVFS WGDGDYGKLGHGNSSTQKYPKLIQ GPLQGVVVCVSAGYRHSAAVTEG ELYTWEGEDFGRLGHGDSNSRNIPT LVKDISNVGEVSCGSSHTIALSKDGR TVWSFGGGDNGKLGHDTRRVYKP KVIEALQGMFIRKVCAGSQSSLALTS TGQVYAWGCGACLGCSSEATALRP KLIEELAATRIVDISIGDSHCLSLSD NEVYAWGNNSMGQCGQGNSTGPIT KPKKVSGLDGIAIQQISAGTSHSLAW TALPRDRQVVAWHRPYCVDLEESTF SHLRSFLERYCDKINSEIPLPFSSR EHHNFKLCLKLLSNHLALALAGGV ATSILGRQAGPLRNLFRMLDSTVP DEIQEVVETLSVGATMLLPPLRERM ELLHSLLPQGPDRWESLSKQGRMQ LDIILTSLODHTHVASLLGYSSPSDA ADLSTVCMGYGNLSDQPYGSOICHP DTHLAEILMKTLRLNLFYTDQAFG ELEKNSDKYLLGTSSSENSQPAHLH ELLCSLQQLLAFCHINNVTESSS VALLHKHLQLLPHATDIYSRSANLL KESPWNGSVGEKLRDVIYVSAAGSM LCQIVNSLLLPVSVARPLLSYLLDLL PPLDCLNRLPAAALEDQELQWPL HGGPEVIDPAGVPLPQAQSWVWL DLERTIALLIGRCLGGM LQGSVPVPE EQDTAYWMKTPLFSDGVEMDTPQL DKCMSCLLEVALSGNEEQKPFDYKL RPEVAVYVDLALGCSKEPARSLWIS MQDYAVSKDWD SATLSNESLLDTV RFVLAALLKHTNLLSQACGESRYQP GKSLSEVYRCVYKVRSLACKNLEL IQTRSSSRDRWITDNQDSADVDPQE HSFTRTIDEAEMEELAERDREDGH PEPEDEEEEREHEVMTAGKIFQCFL SAREVARSRDRDRMNSGAGSGVRA DDPPPSQQERRVSTDLPEGQDVYT AACNSVIHRCALLILGVSPVIDELQK RREGQLQQPSVSASEGTGLMTRSE SLTAESRLVHASPSYRLIKRSSESDL SQPESDEEGYALSGRNVDLASS HRKRGPMSHQSLESLSDSWTRLKHT RDWVFNSSYFESDFDLTKSLGVHT LIENVVSVSGDVG NAPGFKEPEES MSTSPQASIIAMEQQQLRAELRLEAL HQILTLLSGMEEKGNVLLTGSRSSS GFQSTLLTSVRLQFLAGCFGLGTV GHTGTKGESGRLHHYQDGIRAAKR NIOVEIQVAVHKIYQQLSATLERALQ ANKHHIEAQRLLLVTVFALSVHYQ PVDVSLAISTGLLNVLSQLCGTDTML GOPLQLLTKTGVSQLSTALKVASTRL LQILAITGTYADKLSPKVQSLDLLL CSQLKNLLSQTGVLFMASFGEGEGE EEEEKVDSSGEAEKRDFRAALRKQ HAAELHLGDFLVFLRRVSSKAIQSK MASPKWTEVLLNIASQKCSSGIPLVG	False	False	2.791	2.311	1.257	0.93	0.702	2.047	1.025

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