

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
E9Q7N9	E9Q7N9_MOUSE	Mus musculus	NaN	25.875327	S1799	NaN	30059200	MAAQEEGTVLRLSPSEQEDEEDEEA AAARRVQRFALDPRVRFLLGRLRQA LRFPEETWGOYLESDDHROVLGDFL ESTGPASLVFVSATAGRLSASPEIPR DVKHKLVYFAKMTENMGESDFSQ TILFGEIPRLLTHVTAFLDEILVPVL SNKNNHTSWSCFISQDVEHHTVEM KNKMHIFRGKMSRRTHLPIPTIAENI DLDQHLYVTRPQSDERRILHAIESLV IKWSHQIEIIEKDSAHPLLSGLHPT PETELDFWTRHDNLKCIYSQLQAP IVLKMVKILRTROSSYLPALKGIFTTV ENALLEAQDVELHLRPLRRHIHSLO EAEFPQTRILAPLLHTICLIWSHSKF YNTPARVIVLLQEFNLFIDQARAYL SPEDLLKGEIEDALEKVQVAISVLKT FQNSFFKYRKGLTSYFTRNTEQRSW DFQSHLVFGRFNKFLDRLVKIEDMF VTILEFEKLERLEFGGSKGAVLNAQI HSTSEEFIECKVFFQOSTYDPSDCD DMEFESDYFKFKSRTLDFDRRLGTL LCEGLSNCSGLESFAFKLLTIFGNFLE KPVVMEMFSPHYSTLLNMFNAELD VCKQLYDEHMKQIEHGHEILNKNM PFTSGNIKWARMLLERLQMFWSNF TSLHYLFPDSPAEEAVCQKYAEMTT LLDQFESHYSEWRRNVDTECFENL NOPLVKFSPINGLLSVNFDPKLVAVL REVKYLLMLKKS DIPDSALGIFOKRN IILKYGNLELLVQGYNKKQTLLEVE YPLIEDELGAIDEQLRVAATWLTWQ DDFWVYMERVQVATAELECRVSQT QSNMLTIQQTMAWAWEWPLLPRE TRREAALTLDDKGLFAKYLKLIRED GCKIHNLVEENRKLFRADPSLDSWK IYVEFIDDIVVEGFFQAILHDLDFFLR NTEKQLKPTFFQAOQLMPPPEIVF KPPLEKEAGDGFYDLVEMLCGSFR VSAQMGRVAAHLADIADYQNDMDN MLGLAEVRQEIMNRVADVINKVLEF RSSLETYSYLWVDDRVEILRQFLLYG HAVPSEEMDAPASEDILQPPTLEQF KEQIDIYEALYIQMSKFDDFRVFNSW FKVDMRPFKLSLLNVIKKWSWMFQ EHLLRFVVDLSLSELGQFIKQTNAGL QRQLCEGDHDLVDIMGHLLAVRS RQRATDELFEPLKETIMLLESYGQK MPEQVYAQLEELPERWETTKKIAAM VRHEVSPLONAEVTLIRKCCILFDEK QAEFRERFRSYAPLGFKAENPYAVL DKANQELEALEEEMEOMQNSARLF EVALPEYKQMKQCRQEIRLLKGLWD VIYVRRSIDNWTETQWRQINVEQM DLELRRFAKEIWSLDAKAVRVWDAYS GLEGTVKDMTTSRLRAIAELQNPALR DRHWQQLMKAIGVRFVINDSTLSD LLAVQLHRVEDDVRDIVDQAVKELG TEKVITDVSHTWEALEFSYEAHHRT GTPLLKSDEQLFETLEHNQVQLQSL LQSKYVEYFIEQVLSWQNKLVADA VIFTWMQVQRTWSHLESIFVCSEDI RVQLVEDARRFDKVDAEFKELMFET AKVKNVLEATCRPHLYEKLKDFQHR LSLCEKALAEYLETKRVTFFPRFYFIS ADLLDILSKGAQPKQVTHHLVKLFD SISDLQFEDNLDVSTHKAVGMFSKE KEYVPFQAGCECIGHVESWLLQLEQ TMKDTVRLAITEAITAYEEKPRELWI FDFPAQVALTGSQIWWTTDVGIAFS RLEEGYETALKDFHKKQISQLNTLIT LLLGELSPGDRQKVMTICTIDVHAR DVVAKLISQKVVSPHAFTWLSQLRH EWEDSRKHCVNICDAHFQYFYEYL GNSPRLVITPLTDRCYITLTQSLHLT	False	False	2.015	2.463	1.651	0.808	0.694	1.793	2.828

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