

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
Q5SSW2	PSME4_MOUSE	Mus musculus	Proteasome activator complex subunit 4	37.816643	NaN	S1121;S1614;S1746	22645316;39627609	MEAPERAGGGEPPEPGRPVLGPR FVQKEIVYNKLLPYAERLDAESDQ LAQIKSNLGRAVQLQELWPGGLFWT RKLSTYIRLYGRKFSKEDHVLFIKLLY ELVSIPKLEISM MQGFARLLINLLKK KELLSRDDLELPWRPLYDLVERILYS KTEHLRLNSFPNSIENVLKTLVKS PYFPADSTAEMLEEWRLMCPFDVT MQKAISYFEIFLPTSLPELHHKGF LWFDELIGLWVSVQNLQWEGQLV NLFARLATDNIGYIDWDPYVPKIFTRI LRSLNLPVGSQVLPFRFLTAYDIG HAVIWITAMMGGPSKLVQKHLGLF NSITSFYHPSNNGRWLNKLMKLLQ RLPNSVVRRLHRERFKKPSWLT PVP ESHKLTDEDVDFVQCIIQPVLLAMF SKTGSLEAAQALQNLALMRPELVIPP VLERTYPALETLEPHQLTATLNCVI GVARSLVSGSKWFPEGPTHMLPLL MRALPGVDPNDFSKCMITFQFIGTF STLVPLVDCSSVLQERNDLTEIEKEL CSATAEFEDFVLFQFMDRCFGLIESS TLEQTREETETEKMTHELSVELGL SSTFTILTQCSDIFMVALQVFN SVSHIFETRVAGRMVADMCRAAVKC CPEESKLVPHCYGVITQTMND VLNEEELDKELLWNQLLSEITRVD GKKLLYREQLVKILQRTLHLCCKQG YTLSCNLLHLLRSTLLIYPTCYSV PGGFNKPPEYFPVKDWGKPGDLW NLGIQWHVPSSEEVSAFYLLDSFL QPELIKLCQCGDELEMSRDDILQS LTIVHSLIGSNNLPLKGEAVTNL VPSMVSLEETKLYTGLEHDLRENY REVIASVIRKLLSHLDNSEDDTKSLF LIKIIGDLLHFQGSKHHEFDSRWKS FNLVKKSMENRHLHGKKQHIRALLID RVMLQHELRLTVEGCEYKIHQD MIRDLLRLSTSSYSQVRNKAQOTFF AALGAYNFCCRDIPLVLEFLRPDRK DVTQQQFKGALYCLLGNHSGVCLA NLHDWDCIVQWPAVSSGLSQAM SLEKPSIVRLFDDLAEKIHRQYETIGL DFTIPKSCAAIAELLQSKNPSISQTL LSPEKIKGQKRQDKNADALRNYE CLVNTLLDQVEQRNLPWKFEHIGIG LLSLLLRDDRVLPLRAIRFFVENLNH DAIVVRKMAISAVAGILKQKLRTHKK LTINPYEISGCPKPTKILAGDRPDNH WLHYDSKNIPRTKKEWESSCFVEKT HWGYYNWPKNMVYAGVEEQPKLG RSREDMIEAEQIYDRFSDPKFVEQL ITFLSEDRKGRDKFSRRFCLFKGI FRNFDDAFLPVLKPHLERLVADSHE STQRCAEIIAGLIRGSKHWTFEKVE KLWELLCPPLRTALSNMTVETYND WGTCIATSCESRDPRKLHWFELL ESPLSGEGGSFVDACRLVYVQGLA QEWVRPELLHRLKYLEPKLTQVY KNVRERIGSVLTYIFMIDVSLPNTAP TTSPCIPEFTARVLEKPKPLTDVDEEI QNHVMEENGIGEDERTQGKLLKT ILKWL MASAGRSFSTAVKEQLQLLP LFFKIAPVENDNSYDELKRDACLCS LMSQGLLYPQQVPLILQVLSQTARSS SWHARYTVLTYLQTMVFYNFLFIFLN NEDAVKDIRWLIICLLEDEQLEVRE MAATTL SGLQCNFLTMSAMQIH FEQLCKTKPKKRKRDGPGSVGDTIPS AELVKRHAGVGLGACVLSSPYDVP TWMPQLLMNLSAHLNDPQPIEMTV KKTLSNFRRTHHDNWQEHKQQT DQLLVLTDLVSPCYA	True	False	5.0	5.0	1.261	1.021	False	0.675	0.849