	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
0	F8VQ93	F8VQ93_MOUSE	Mus musculus	NaN	25.385059	NaN	NaN	28528544	MSRERKGLSELRSELYFLIARFLEDG PCQQAAQVLIREVAEKELLPRRTDW TGKEHPRTYQNLVKYYRHLAPDHLL QICHRLGPLLEQEIPQSVPGVQTLLG AGRQSLLRTNKSCKHVVWKGSALAA LHCGRPPESPVNYGSPPSIADTLFSR KLNGKYRLERLVPTAVYQHMKMHK RILGHLSSVYCVTFDRTGRRIFTGSD DCLVKIWATDDGRLLATLRGHAAEIS DMAVNYENTMIAAGSCDKMIRVWC LRTCAPLAVLQGHSASITSLQFSPLC SGSKRYLSSTGADGTICFWLWDAGT LKINPRPTKFTERPRPGVQMICSSFS AGGMFLATGSTDHIIRVYFFGSGQPE KISELEFHTDKVDSIQFSNTSNRFVS GSRDGTARIWQFKRREWKSILLDMA TRPAGQNLQGIEDKITKMKVTMVAW DRHDNTVITAVNNMTLKVWNSYTG QLIHVLMGHEDEVFVLEPHPFDPRV LFSAGHDGNVIVWDLARGVKVRSYF NMIEGQGHGAVFDCKCSPDGQHFA CTDSHGHLLIFGFGSSSKYDKIADQ MFFHSDYRPLIRDANNFVLDEQTQQ APHLMPPPFLVDVDGNPHPSRYQRL VPGRENCREEQLIPQMGVTSSGLNQ VLSQQANQDISPLDSMIQRLQQEQD LRRSGEAGVSNASRVNRGSVSSTSE VHSPPNIGLRRSGQIEGVRQMHSNA PRSEIATERDLVAWSRRVVVPELSAG VASRQEEWRTAKGEEEIKSYRSEEK RKHLTVAKENKILTVSKNHAHEHFL DLGDSKKQQANQHNYRTRSALEETP RPLEELENGTSSSDEGEVLAVSGGT SEEEERAWHSDGSSSDYSSDYSDW TADAGINLQPPKKVPKHKTKKPESSS DEEEESENQKQKHIKKERKKANEEK DGPTSPKKKKPKERKQKRLAVGELT ENGLTLEEWLPSAWITDTLPRRCPF VPQMGDEVYYFRQGHEAYVEMARK NKIYSINPKKQPWHKMELREQELM KIVGIKYEVGLPTLCCLKLAFLDPDT GKLTGGSFTMKYHDMPDVIDFLVLR QQFDDAKYRRWNIGDRFRSVIDDA WWFGTIESQEPLQPEYPDSLFQCYN VCWDNGDTEKMSPWDMELIPNNA VFPEELGTSVPLTDVECRSLIYKPLD GEWGANPRDEECERIVGGINQLMTL DIASAFVAPVDLQAYPMYCTVVAYPT DLSTIKQRLENRFYRRFSSLMWEVR YIEHNTRTFNEPGSPIVKSAKFVTDL LLHFIKDQTCYNIIPLYNSMKKKVLS DSEEEEKDADVPGTSTRKRKDHQPR RRLRNRAQSYDIQAWKKQCQELLNL IFQCEDSEPFRQPVDLLEYPDYRDIID TPMDFATVRETLEAGNYESPMELCK DVRLIFSNSKAYTPSKRSRIYSMSLR LSAFFEEHISSVLSDYKSALRFHKRN TISKKRKKRNRSSSLSSSAASSPERK KRILKPQLKSEVSTSPFSIPTRSVLPR HNAAQMNGKPESSSVVRTRSNRVA VDPVVTEQPSTSSATKAFVSKTNTSA MPGKAMLENSVRHSKALSTLSSPDP LTFSHATKNNSAKENMEKEKPVKR KMKSSVFSKASPLPKSAAVIEQGECK NNVLIPGTIQVNGHGGQPSKLVKRG PGRKPKVEVNTSSGEVTHKKRGRKP KNLQCAKQENSEQNNMHPIRADVL PSSTCNFLSETNAVKEDLLQKKSRG GRKPKRKMKTHNLDSELIVPTNVKV LRRSNRKKTDDPIDEEEEFEELKGS EPHMRTRNQGRRTAFYNEDDSEEE QRQLLFEDTSLTFGTSSRGRVRKLTE KAKANLIGW	None	None	None	None	None	None	None	None	None