	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	Q61464	ZN638_MOUSE	Mus musculus	Zinc finger protein 638	26.222628	NaN	S128;S288;S298;S367;S381;S418;S554;S606;S615;S637;S1099;S1400;S1635;S1661;S1864	24788674	MSRPRFNPRGTFPLQRPRAPNPPG MRPPGPFVRPGSMGLPRFYPAGRAR GIPHRFPGHGSYQNMGPQRMNVQV TQHRTDPRLTKEKLDFPEAQQKKGK PHGSRWDDESHITPPVEVKQSSVTQ VTEQSPKVQSRYTKESASSILASFGL SNEDLEELSRYPDEQLTPENMPLIL RDIRMRKMSRRLPNLPSHSRNKETL SNETVSSNVIDYGHASKYGYTEDPLE VRIYDPEIPTDEVKNEFQPQQSISAT VSTPNVICNSVFPGGDMFRQMDFP GESSSQSFFPVESGTKMSGLHISGQ SVLEPVKSISQSISQTVSQTTSQSLNP PSMNQVPFTFELDAVLRQQERISQK SVISSADAHGGPTESKKDYQSEADLP IRSPFGIVKASWLPKFTQAGAQKMK RLPTPSMMNDYYAASPRIFPHLCSL CNVECSHLKDWIQHQNTSTHIESCR QLRQQYPDWNPEILPSRRNESNRKE NETPRRRSHSPSPRHSRRSSSGHRI RRSRSPVRYIYRPRSRSPRICHRFISK YRSRSRSRSRSRSPYRSRNLLRRSPK SYRSASPERTSRKSVRSDRKKALED GGQRSVHGTEVTKQKHTETVDKGLS PAQKPKLASGTKPSAKSLSSVKSDSH LGAYSAHKSENLEDDTLPEGKQESG KSALAQRKPQKDQSLSSNSILLVSEL PEDGFTEEDIRKAFLPFGKISDVLLV PCRNEAYLEMELRKAVTSIMKYIET MPLVIKGKSVKVCVPGKKKPQNKEM KKKPSDIKKSSASALKKETDASKTME TVSSSSSAKSGQIKSSTVKVNKCAGK SAGSVKSVVTVAAKGKASIKTAKSGK KSLEAKKSGNIKNKDSNKPVTVPAN SEIKASSEDKATGKSAEESPSGTLEA TEKEPVNKESEEMSVVFISNLPNKG YSTEEIYNLAKPFGALKDILVLSSHK KAYIEINKKSADSMVKFYTCFPISMD GNQLSISMAPEHVDLKDEEALFTTLI QENDPEANIDKIYNRFVHLDNLPED GLQCVLCVGHQFGKVDRYMFMSNK NKVILQLESPESALSMYNFLKQNPQ NIGEHVLTCTLSPKTDSEVQRKNDL ELGKGSTFSPDLKNSPVDESEVQTA ADSSSVKPSEVEEETTSNIGTETSVH QEELGKEEPKQALCESDFAIQTLELE AQGAEVSIEIPLVASTPANIELFSENI DESALNQQMYTSDFEKEEAEVTNPE TELAVSDSVFIEERNIKGIIEDSPSET EDIFSGIVQPMVDAIAEVDKHETVSE VLPSACNVTQAPGSYIEDEKVVSKKD IAEKVILDEKEEDEFNVKETRMDLQ VKTEKAEKNEAIIFKEKLEKIIAAIRE KPIESSVIKADPTKGLDQTSKPDETG KSSVLTVSNVYSSKSSIKATVVSSPK AKSTPSKTESHSTFPKPVLREQIKAD KKVSAKEFGLLKNTRSGLAESNSKS KPTQIGVNRGCSGRISALQCKDSKV DYKDITKQSQETETKPPIMKRDDSN NKALALQNTKNSKSTTDRSSKSKEE PLFTFNLDEFVTVDEVIEEVNPSQAK QNPLKGKRKEALKISPSPELNLKKKK GKTSVPHSVEGELSFVTLDEIGEEED ATVQALVTVDEVIDEEELNMEEMVK NSNSLLTLDELIDQDDCIPHSGPKDV TVLSMAEEQDLQQERLVTVDEIGEV EESADITFATLNAKRDKRDSIGFISS QMPEDPSTLVTVDEIQDDSSDFHLM TLDEVTEEDENSLADFNNLKEELNF VTVDEVGDEEDGDNDSKVELARGKI EHHTDKKGNRKRRAVDPKKSKLDS FSQVGPGSETVTQKDLKTMPERHLA AKTPMKRVRLGKSSPSQKVAEPTKG EEAFQMSEGVDDAELKDSEPDEKR RKTQDSSVGKSMTSDVPGDLDFLVP KAGFFCPICSLFYSGEKAMANHCKS TRHKQNTEKFMAKQRKEKEQNETE ERSSR	None	None	None	None	None	None	None	None	None