	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	A0A140LIW3	A0A140LIW3_MOUSE	Mus musculus	NaN	25.775171	NaN	NaN	34678516	MQEESANDMECVQLPAETLRQVTI HRDPIYGFGFVAGSERPVVVRSVRP GGPSEDKLLAGDQIVAINEEDVSEAP RERFIELIRSAKESIVLTVLHTHQSPK SAFISAAKKAKLRSNPVKVRFSEQVT IGETDAKMMKKEALLLIPNVLKVFLE NGQIKSFTFDGRTTVKDVMATLQDR LSLRSIEHFALVLEYTGPEQNHKFLI LQDKQPLAYVVQRTHYHGMKCLFRI SFFPKDPVELLRRDPAAFEYLYIQSR NDVIRERFGMEPKPEMLLGLAALHI YITVSATRPSQKITLKNVEKEWGLEP FLPPSLLQGIKEKNLRKSLSQQLKAH QMHPSSSTKGSAIQAKLQYLRILNEL PTFTGVLFNTVGLDEKHSATTLLVGP RHGISHVIDLKTNLTTVLSEFSKISKI QLFRENQGVARVETSIMDAKPLVLL MEWPEATNFACLIAGYCRLLLDSRK MVFSRPASQPLPPPMIKADHMHSA HRPVTGGHLGKKESSYVGSVGTSPR KSSRCTTPPADSELVSFCYLHMREQ RKEQESRTDVNENLIFFEETRPRTKS DPTSKSSGQGYEVIPDDFDAASLDH EPCASRARSYTLDNSLGAEALNFYC DSCKVKLQEQMGPRKGGRPGSSRD NMVDLMSLPPPGSEEEEEEEDETTS LLPAIAAPPPGFRDNSSDEDDPKRRA VQSQEQGRHLRGLLYDEIPVTLIDSV QTRTVRDHAQELDDALVSTLQALEA LAASEDGPHPPPPQTAGLIVLATITPE SSLDSGHETNSSELTDMSEMMSAM KQHQNTTYFLAQHLNKDSLLARKDL PFRIQSCAAQAVLTAPYALGPPDPNP SPQPAVTGQSPAPTGARRKIPQSEVQ VQGDRPYSLAVHPALSPQLSEQKNL SLLPPVPEDRGPGHSRAGLEMSLRS ATPSLSEEQVSELRENLPKEVRLSPK LILDPKGNVTPAIISAALQQVVHSKSL ATPGTALATPSNRGERRLEASMGRP EVTMSRPEVSVMSSSVSKNLKFKM SPGAPETTRNSQQQLGPEVSASPRA STGSRADNLHLSPPEDRFPVQSFPP KSYLSRVSRDSMGKQATGEVAGKGG PEGAKPPPNKQSVVSGQGDKGQLES LSKSSKLEETSLVPRAGYPMALQSPS CQPRSHSPSCQPRGPSPSSQSRGQS PSCQPRSQSPLRPLATSRQVSTMPS RKLETTLDGAHSASEGPTKPKSSRG PFRLRNLFSATFPTRQKKETDERQA QLQKVKQYELEFLEELLKPPSQGELP GTEYLQPPAPGRCSCQLRSSPVQQG PGMSREQRRSCDCKRICRGGRPQAA QTPAPGLRERERVPPTQRQPEAGPG LSLNSPINVQRIRSTSLESRECRSDP ESGVSCLTTCASGGECLGDPNYRKL MRHYSISELDQGDTVSLTSDVYPHP PLGMLPREVKEIESGFPVGLGPKSKC AESPTLGEPSYVQVAPESKGPRQMA VFSLPEEVYRRPADLDEDSESSKCCS IRYCFYYRKCDMADDASDGKDELSY SIPMKILPGMKLDEQVVPVVSRTLQV LDAATCSSSPEVPHTQEIDLRVSTFE GSLAKINALRAHAYGLPDGFLAARL DTNELLTVLRQCVASPEARAPKPYVS QISEYKLELALKFKELRASCRRVANV DKSPTHMLAAITGSFQVLSSLIETFV RLVFIVRSEAQRQELLAKVEEVVRNY TFLLRAAEESTARNLNQQQQLQQQ QQQQQQQQQQPLPPPPLPAATGHH PPDSPSSTVMSTFTRSLKTLIK	None	None	None	None	None	None	None	None	None