

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
H9KV01	H9KV01_MOUSE	Mus musculus	NaN	26.09834	NaN	NaN	36064721	MAADIEQVFRSFVSVSKFREIQEQLSS GRSEQLNGETNPPIEGNQAGDTAA SARSLPNEEIVQKIEEVLDSGVLDTL RYKPDLKEASRKRCSVQTDPTDE VPTKSKKHKHKHKKHKKHKKKEKE KKYKRQPEESESKLSSHHDGNLESD SFLKFDSEPSAAALEHPVRAFGLSEA SETALVLEPPVVSMEVQESHVLETL KPKTKAAELSVVSTVISEQSEQPMP GMLEPSMTKILDSFTAAPVPMSTAA LKSPEPVVTVMSVEYQKSVLKSLETM PPETSKITLVELPIAKVVEPSETLTIV SETPTEVHPEPSPSTMDFPESSTTDV QRLPEQPVEAPSEIADSSMTRPQESL ELPKTTAVELQESTVASALELPGPPA TSILELQGGPVTVPPELPGPSATPVPE LSGPLSTPVPELPGPPATVVPELPGP SVTPVPQLSQELPGPPAPSMGLEPP QEVPEPPVMAQELSGVPAVSAAIELT GQPAVTVAMELTEQPVTITTEFEQPV AMTTVEHPGHPEVTTATGLLGOPEA AMVLELPGQPVATTALELSGQPSVT GVPELSGLPSATRALELSGQSVATGA LELPGQLMATGALEFSGQSGAAGAL ELGQPLATGVLELPGQPGAPELPG QPVATVALEISVQSVVTTSELSTMTV SQSLEVPSTTALESYNTVAQELPTTL VGETSVTVGVDPLMAQESHMLASN TMETHMLASNTMDSQMLASNTMD SQMLASNTMDSQMLASSTMDSQM LASSTMDSQMLATSTMDSQMLATS SMDSQMLATSSMDSQMLATSSMDS QMLATSSMDSQMLATSSMDSQML ATSSMDSQMLATSSMDSQMLATSS MDSQMLASGAMDSQMLASGTMDA QMLASGTMDAQMLASSTQDSAMM GSKSPDPYRLAQDPYRLAQDPYRLG HDPYRLGHDAYRLGQDPYRLGHDPY RLTPDPYRVSPRPYRIAPRSYRIAPRP YRLAPRPLMLASRRSMMMSYAAER SMMSSYERSMMSYERSMMSYMAE RSMMSAYERSMMSAYERSMMSYMAE AERSMMSAYERSMMSAYERSMMSY PMADRSMMMSGADRSMMSYSAA DRSMMSYSAADRSMMSSYTDRSM MSMAADSYTDSYTDYTEAYMVPPPL PPEEPPTMPPLPPEEPPMTPLPPEE PPEGPALSTEQSALTADNTWSTEV LSTGESLSQPEPPVSQSEISEPMAVP ANYSMSESETSMMLASEAVMTVPEPA REPESVTSAPVESAVVAEHMVPE RPMTYMVSETTMSVEPAVLTSEASV ISETSETYDSMRPSGHAISEVTMSLL EPAVTISQPAENSLLEPSMTVPAPST MTTTESPVVAVTEIPPVAVPEPPIMA VPELPTMAVVKTPAVAVPEPLVAAPE PPTMATPELCSLSVSEPPVAVSELPA LADPEHAITAVSGVSSLEPSVPILEPA VSVLQPVMIVSEPSVPVQEPVAVSE PAVIVSEHTQITSPEMAVESSPVIVDS SVMSSQIMKGMNLLGGDENLGPEV GMQETLLHPGEEPRDGGHLKSDLY ENEYDRNADLTVNSHLIVKDAEHNT VCATTVGPVGEASEEKILPISETKEIT ELATCAAVSEADIGRSLSSQLALELD TVGTSKGFVFTASALISESKYDVEV SVTTQDTEHDMVISTSPSGGSEADIE GPLPAKDIHLDLPSTNFKDVEDSL PIKESAQAVAVASPKESSEDETVPL PNKEIVPESGYSASIDEINEADLVRPL LPKDMERLTSLRAGIEGPLLASEVER DKSAASPVVISIPERASESSSEKDD YEIFVKVDTHEKSKKNKNRDKGEK EKKRDSSLRSRKRKSKSSEHKSRKR	None	None	None	None	None	None	None		

TSESRSRARKRSSKSKSHRSQTRS
SRSRRRRRSSRSRKSRRGRRSVSKE
KRKRSPKHRSKSRERKRKRSSSRDN
RKAARARSRTPSRRRSHTPSRRRR
SRVGRRRSFSISPSRRSRTPSRRSR
TPSRRSRTPSRRSRTPSRRSRTPSRR
RRRSASVRRRSFSISPVRLRRSRTPL
RRRFSRSPIRRKRSRSEGRSPKRL
TDLDKAQLLEIAKANAAAMCAKAGV
PLPPNLKPAPPTIEEKVAKKSGGATI
EELTEKCKQIAQSKEDDDVIVNKP
VSDEEEEEPPFYHHPFKLSEPKPIFF
NLNIAAAKPTPPKSQVTLTKEFPVSS
GSQHRKKEADSVYGEWVPVEKNGE
ESKDDDNVFSSSLPSEGRVKROGRV
KRQMKQPAASHLTVTRCNLCGTKP
QSEKHRIAESVITSLPNIGPSMHLW
EGSPRYNYLASRFASRLYSSRFWW