

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
H9KV00	H9KV00_MOUSE	Mus musculus	NaN	25.775171	NaN	NaN	34678516	MAADIEQVFRSFVSVSKFREIQEQLSS GRSEQLNGETNPPIEGNQAGDTAA SARSLPNEEIVQKIEEVLDSGVLDTL RYKPDLKEASRKRCSVSVQTDPTDE VPTKSKKHKHKHKHKKKKKKEKE KKYKRQPEESESKLSSHHDGNLESD SFLKFDSEPSAAALEHPVRAFGLSEA SETALVLEPPVVSMEVQESHVLETL KPKTKAAELSVVSTVISEQSEQPMP GMLEPSMTKILDSFTAAPVPMSTAA LKSPEPVVTVMSVEYQKSVLKSLETM PPETSKITLVELPIAKVVEPSETLTIV SETPTEVHPEPSPSTMDFPESSTTDV QRLPEQPVEAPSEIADSSMTRPQESL ELPKTTAVELQESTVASALELPGPPA TSILELQGGPVTPVPELPGPSATPVPE LSGPLSTPVPELPGPPATVVPELPGP SVTPVPQLSQELPGPPAPSMGLEPP QEVPEPPVMAQELSGVPAVSAAIELT GQPAVTVAMELTEQPVTITTEFEQPV AMTTVEHPGHPEVTTATGLLGOPEA AMVLELPGQPVATTALELSGQPSVT GVPELSGLPSATRALELSGQSVATGA LELPGQLMATGALEFSGQSGAAGAL ELGQPLATGVLELPGQPGAPELPG QPVATVALEISVQSVVTTSELSTMTV SQSLEVPSTTALESYNTVAQELPTTL VGETSVTVGVDPPLMAQESHMLASN TMETHMLASNTMDSQMLASNTMD SQMLASNTMDSQMLASSTMDSQM LASSTMDSQMLATSTMDSQMLATS SMDSQMLATSSMDSQMLATSSMDS QMLATSSMDSQMLATSSMDSQML ATSSMDSQMLATSSMDSQMLATSS MDSQMLASGAMDSQMLASGTMDA QMLASGTMDAQMLASSTQDSAMM GSKSPDPYRLAQDPYRLAQDPYRLG HDPYRLGHDAYRLGQDPYRLGHDPY RLTPDPYRVSPRPYRIAPRSYRIAPRP YRLAPRPLMLASRRSMMMSYAAER SMMSSYERSMMSYERSMMSMPMAE RSMMSAYERSMMSAYERSMMSMPM AERSMMSAYERSMMSAYERSMMS PMADRSMMMSGADRSMMSYSAA DRSMMSYSAADRSMMSSYTDRSM MSMAADSYTDSYTDYTEAYMVPPPL PPEEPPTMPPLPPEEPPMTPLPPEE PPEGPALSTEQSALTADNTWSTEV LSTGESLSQPEPPVSQSEISEPMAVP ANYSMSESETSMMLASEAVMTVPEPA REPESVTSAPVESAVVAEHMVPE RPMTYMVSETTMSVEPAVLTSEASV ISETSETYDSMRPSGHAISEVTMSLL EPAVTISQPAENSLLEPSMTVPAPST MTTTESPVVAVTEIPPVAVPEPPIMA VPELPTMAVVKTPAVAVPEPLVAAPE PPTMATPELCSLSVSEPPVAVSELPA LADPEHAITAVSGVSSLEPSVPILEPA VSVLQPVMIVSEPSVPVQEPVAVSE PAVIVSEHTQITSPEMAVESSPVIVDS SVMSSQIMKGMNLLGGDENLGPEV GMQETLLHPGEEPRDGGHLKSDLY ENEYDRNADLTVNSHLIVKDAEHNT VCATTVGPVGEASEEKILPISETKEIT ELATCAAVSEADIGRSLSSQLALELD TVGTSKGFVFTASALISESKYDVEV SVTTQDTEHDMVISTSPSGGSEADIE GPLPAKDIHLDLPSTNPFCKDVEDSL PIKESAQAVAVALSPKESSEDETVPL PNKEIVPESGYSASIDEINEADLVRPL LPKDMERLTSLRAGIEGPLLASEVER DKSAASPVVISIPERASESSSEKDD YEIFVKVDTHEKSKKNKNRDKGEK EKKRDSSLRSRKRKSKSSEHKSRKR	None	None	None	None	None	None	None		

TSESRSRARKRSSKSKSHRSQTRSR
SRSRRRRRSSRSRKS SRGRRSVSKE
KKRSPKHRSKSRERKRKRSSSRDN
RKAARARSRTPSRRRSHTPSRRRR
SRVGRRRSFSISPSRRSRTPSRRSR
TPSRRSRTPSRRSRTPSRRSRTPSRR
RRRSASVRRRSFSISPVRLRRSRTPL
RRRFSRSPIRRKRSSSERGRSPKRL
TDLDKAQLEIAKANAAAMCAKAGV
PLPPNLKPAPPPTIEEKVAKKSGGATI
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VSDEEEEEPPFYHHPFKLSEPKPIFF
NLNIAAAKPTPPKSQVTLTKEFPVSS
GSQHRKKEADSVYGEWVPVEKNGE
ESKDDDNVFSSSLPSEPVDISTAMS
ERALAQRLENAFDLEAMSMMLNR
AQERIDAWAQLNSIPGQFTGSTGVO
VLTQEQLANTGAQAWIKKDQFLRAA
PVTGGMGAVLMRKMGWREGEGLG
KNKEGNKEPILVDFKTRKGLVAVG
ERAQKRSGNFSAAMKDLGKHPVS
ALMEICNRRWQPPEFLLVHDSGPD
HRKHFLFRVLINGSAYQPSFASP
KHAKATAATVVLQAMGLVPKDLMA
NATCFRSASRR