

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
A0A087WS16	A0A087WS16_MOUSE	Mus musculus	NaN	22.380232	NaN	NaN	37507081	MRKRRHLPLVAVFSLLSGIATTHA QQHGVMVEVNRDIVFLVDGSSSLGP SNFNAIRDVTRVIRLEIGQDLVQV SVAQYADTVKPEFYLSYTNKRDAIT AVRKMALNGSALYTGSSLDVFRNN LFTSSAGHRAAEGVPKLLVLITGGKS LDEVSPQAQELKRGSIMALAVGSKA ADEDELKEIAFSSLVFPAEFRPAPL QNMLPSLMAPLRLLTGTTESKRDI LFLFDGSVNVLGQFPVAVRDFLYRIE ELDVKPDGTRVAIAQFSDDVRLSRF SEHQTKAEILNLVKKMKLKTGKALN LGYALDYALRNIFVRSAGSRIEDNVQ QFLVLLVAGRSSDAVAGPASSLKOR GVVPPFIQAKNANPSELEQIVLSPAFI LAAESLPKIGDLQSQIVSLLKAEQGS GPVSGEKDVVFLIDGSEGVRSGFPLL KDFVQRVVESLDVGPRVVALVQY SDRTRPEFYLSHMDQQGVSAIRR LTLGGPTPNTGAALFVLRNLTSS TGSRIAEGVQLLIVLTAEPGDDVDR GPSVVLKQGGAVPIGIGIGNADISEM QTISFIPDFAVAITFRELGTIQQVISE RVIQLNREELSSLKPIPTSTGAGVG SKKDVVFLIDGSRNAGPEFQYIRTLI ERIVEYLDIGFDTRVAIQFSEDSK MEFPLNAHFSKDEVQNAVRRRLRPK GGSQVYIGNALEYVLKNIFQRPLGSR IEEGVPQFLVLISSGKSDDEVDDSAV ELKQFGVAPLTARHTDQEELVKISL SPEYVYSVTFRELPRLEQKLLTPITT LTSQQIHQILASTRYPPSVVESDAADI VFLIDSDAVKPDGIAHIRDFVSRIVR RLNIGPSKVRIGVVQFSNDVFPFYL KTHKSQSSVLEAIRRLRFKGGSPNLT GRALEFVARNLFFVKSAGSRIEDGVP QHLVFLGGKSDVARHAQVISSS GIVSLGIGDRNIDRTDLQITINDPRL VFTVREFRELPNIEERVMLSFPGSGA TPQPPGVDLPSRPEKKKADIVFLL DGSINFRDRSFQEVLRFASEIVTVY EDGDSIRVGLVQYNSDPTDEFFLRD FSTKRQIIDAINVVYKGGRHANTRV GIEHLLRNHFVPEAGSRLDERVPOIA FVITGGKSVEDAQDVSLALTQKGVK VFAVGVRNIDSEEVGKIASNSATAFR VGSVQELSELSETVLETLHDAMHET LCPGVTDVSKACNLEVLGFDGSRD QNVFVSQKGLSKVDIILNRISQIQRI SCSGNQLPTVVRVSMANTPSGPVEA FDFAEYQPELFEKFRNMRSQRPYVL TADTLKLYQNKFRQSSPDTVKVVIHF TDGADGMADLYRASEELRQAGAQ ALILVGLERVANLERLMHLEFGRGF MYDRPLRLNLLDLYELAEQLDNIA EKACCGVPCKCSGERGDRGPIGSIGP KGISGEDGYRGPDEGGPGERGPP GVNGTQGFQCGPQGVKGRGSRGFP GEKGEIGLDGLDGEEDKGLPG SSGEKSGPGRRGDKGPKGDKGERG DVGIRGDPGDSGRDSQQRGPKGETG DIGPMGLPGRDGIPGSPGDPKDG SGRRGPAGAKNRGGPGQPFEGE QTRGSQGPPIGPPGLIGEQQIGP PRGGGGTAGAPGERGRTGPLGRKGE PGEPGPKGSIGNRGRGETGDDGRD GVSEGRRGKKGGERGFPYGPYKGT PGEPGADGPPGPKGIRRRGNSGPP GATGQKGDPGYPGSGHKGNRGDS VDQCALIQSIRDKCPCCYGPLECPVF PTELAFALDTSEGVTDTFSRMREV LLGIVGDLTIAESNCPRGARVAVVTY NNEVTTEIRFADSKKKSALLDSIQNL QVALTSKQSLTAMSFVARNTFKR VRSGFLMRKVAVFFSNKPTRASQQL REAVLKLSDAGITPLFLTSQEDRQLI	None	None	None	None	None	None	None		

NALQINNTAVGHALVLPARRDLTDF  
LKNVLTCHVCLDICNIDPSCGFGSW  
RPSFRDRRAAGSDVDIDLAFILDSSE  
ATTLFQFNEMKKYGYVIRQLDLSPD  
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VPPVKVEFSLTDYGAKKLLDFLSRR  
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EVYSFASEPNDVFFKFVDKSTELNE  
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RKQCDWFQGDQPVKNGVKFGHKQI  
NPPHTANSLSKVVITMKPVTTTK  
PTAIVNLPPAKPAPARPAPAQPVLAK  
PDPAKPAQARPAPAKPASAKLVPPQP  
VHVQPAPAQTASVRPAPAKPAPPQP  
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VPAKPAVPAQPAPPQAAAAPVPAK  
AVPAQAAAQMPAQPVLTKSAAVK  
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VQVSEVTENSARLHWERPEPSSSFF  
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NLMVNTTEPLFLTKTDICKLSRDAGT  
CVDFKLLWHYDLESKSKCRFWYGG  
CGGENRFRHSQECEKMCSPDLLV