

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
D4AA77	D4AA77_RAT	Rattus norvegicus	NaN	23.439218	NaN	NaN	38843836	MDCGRGLHGAAPGLSAPESGRGA GAGGRRGQEAAPRGPPASRRLLR APGSRPRRAPCTRRAAQPALAWMAP RAAGGAPPSARAAAAVPLPPRSHSR CPGLLPPLLLLLGAARAGALEIQRR FPSPTPTNNFALDGTAGTVYLAAVN RLYQLSGANLSLEAEATVGPVPSPL CHAPQLPQASCEHPRLTDNYNKIL QLDPGQGLVVACGSIYQGLCQLRRR GNISALAVSFPPAAPTAEPTVFPSPM LNVAANHPNASTVGLVLPASGTGG SRLLVGATYTYGSAFFPRNRSLED HRFENTPEISIRSLDARGDLAKLFTF DLNPSDDNILKIKQGAKEQHKLGFV RAFLHPAVPPHSAHPYAYLALNSEA RAGDKDSQARSLLARICLPRGAGGD AKKLTESIYQLGLQCAGGAGRGDLYS RLVSVFPAREQFFAVFERPQGTPGA RNAPAALCAFRFADVQAAIRAARTA CFVEPAPDVVAVLDSVVQGTGPACE SKRNIQLQPEQLDCGAAHLQHPLTIL QPLRASPVFRAPGLTAVAVANANNY TAVFLGTATGRLLKISLNESMQVVS RVLTVAYGEPVHHVMQFDPMDPGY LYLMTSHQMARVKAACEVHSTCG DCVGAADAYCGWCTLETRCTFKQD CANSLSLPHWTSASEGPSRCPAMTV LPSEIDVHRDVTGMILQISGLPPLS GMEMACDYNGVRTVARVPGPAYG HQIAYCNLLPRAQFPFPAGQDHVT VEMSVRVKGNIVSANFTIYDCSRIG QVYPHTACTSCLSTQWPCSWCQLH SCVSNQSRQCDSNPNTSPQDCQIV PSPLAPVPTGGSQDILVPLTKAAFFH GTSLQCSFGLENFVAVWANDSLVR CNQVVLHTTQKSQVFPLSLKLGPP DRFLDSPNPMTVVYNCAMGSPDC SQCLGREDLGHLCVWWDGCRLRGP LQPLSGTCPAPEIRAIEPLSGPLNGG TLLTIRGKNLGRRLSDVAHGVWIGN VACEPLADRYTVSEEIVCATGPAPGA FSDVVTNVNSKEGRSREQFSYVLP VHSLPESMGPKAGGTRITIHGSDLN VGSMLQVLVNDTDPCTDLTRTATS TCTVPRGTLPSVPVCFVRESRGCV HGNTLFWYMQNPVITAISPGRSPVS GGRTITVAGERFHMVQNVSMVHH IGREPTFCVLNSTLIICSPGALSNA SAPVDFPINGRAYADEAAEELDPAE AQRGSRFRLDYLNPQFSTAKREKW IKHHPGEPLTLVIHKEQDSLGLSHE YHIKIGQVSCDIQHSRVIHCSVNES LGTAEGLPITIQVGNFNQTIATLQL GGSETAIVSVIVCSVLLLLSVVALFV FCTKSRAERYWQKTLQMEEMES QIREEIRKGFaelQtdmtdltkELN RSQGIPFLEYKHfVtrtffpkcSSLY EERYVLPskTLNSQGSPPQETHPL LGEWNIPEHCRPSMEEGISLFSLL NNKHFLIVFVHALEQQKDFAVRDRC SLASLLTIALHGKLEYYSIMKELLV DLIDASAANKPKMLRRTESVVEKM LTNWSMICMYGCLRETVGEPFFLLL CAIKQQINKGSIDAITGKARYTLNEE WLLRENIEAKPRNLNVSFQCGGMD SLSVRAMDtdTLtQVKEKILEAFCK NVPYSQWPRAEDVDLEWFASSTQSY VLRDLDDTSVVEDGRKKNLTLAHYK IPEGASLAMSLTDKKDNTLGRVKDL DTEKYFHLVLPtDELVEPKSHRQS HRKKVLPeiYlTrLLStKgtLQkFLD DLFKAILSIREDKPPLAVKYFFDFLEE QAEKRGISDPDLHIWKTNSLPLRF	False	True	1.022	1.953	1.88	0.789	0.596	4.677	1.618

