

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
B5DEJ9	B5DEJ9_RAT	Rattus norvegicus	NaN	23.439218	NaN	NaN	38843836	MARLADYFIVVGYDHEKPGPEGGLG KIIQRFPPQQDWDTPFPQGIELGTTK EEIEGEEVSALIQPAEVFAPKSLVLVS RLDYPEIFRACLGLIYTVYVDSLVSLS ESLIANLCACLVPAAGGSQKLFSLGA GDRQLIQTPLHDSLPTGTSTVALLFQ QLGIQNVNLNLFCAVLTKVLFHSA SFQRLSDACRALESMLFPLKYSYPYI PILPAQLLEVLSSPTPFIIGVHSIFKTD VHELLDVIIADLDGGTIKIPECIHLSS LPEPLLHQTQAALSILHPDLEVADH AFPPPRTALSHSKMLDKEVRVAVFLR LFAQLFQGYRSCLQLIRIHAEPVIHF HKTAFLGQRGLVENDFLTQVNLNGM AFAGFVSEKPPYRACDLFDELVAE EVERIKVEENNPLKMIKHIRELAEQL FKNENPNPHMAFQKVPRTGESH RVHILPFPKINEARVQELIQENLAKN QNATPATRTEKKCIVPAGPPVVSIMD KVITVFNSAQRLEVVNRNCISFIFENK TLETETLPAALRALKGAARQCLTD ELGLHVQNRAILDHQQFDYIIRMM NCTLQDCSSLEEYNIAAALLPLTSAF YRRAPGVSQFAYTCVQDHPWITNQ QFWETTFYSAVQEQVRSLYLSAKED NHTPHQKQKELPDGQYQERTAMD AAEQRLWPTLSKATQQLVQHEES TVFSQAIHFANLMVNLVPLDTSKN KLLRASAPGDWESGNSIVTNSIAGS VAESFDTESGFEDSENNDVANSVVR FIARFIDKVCESGVTQDHIRSLHCM IPGIVAMHIETLEAVHRESRRLPPIQK PKILRPALLPGEIIVCEGLRVLLDPD GREATGGLLGGPQLLPAEGALFLT YRILFRGTPHDQLVGEQTVVRSFPIA SITKEKKITMQNQLQQNMQEGLOIT SASFQLIKVAFDEEVSPVVDIFKKQ LMKFRYPQSIFSTFAAAGQTTPOIIL PKQKEKNTSFRTFSTIVKGAKKAGK MTIGRQYLLKKRTGTIVEERANRPG WNEEDDISVDDCELPTSTTLKASE KSTMEQLVEKACFRDYQRLGLGTIS GSSSRKPEYFRVTASNRLYSLCRSY PGLLVIPQAVQDSSLPRVARYRHN RLPVVCWKNRSRGTLLLRSGGFHGK GVVGLFKSQNSPQAVSTSSLESSSI EQEKYLQALLTAVIVHQKLRGNSTLT VRPTLALSPVHGYRDKCFTQSNKSKS SAKEPVHNQGVWASLRSSTRLISSP TSLIDVGARLAGKDHSASFNSTYLO NQLSKRQAALYIFGEKSQLRSSKVEF AFNCFVVPVEFHEIRQVKASFKKLM RACIPSTIPTDSEVTFLKALEDSEWF PQLHRIMQLAVVSEVLENGSSVWV CLEEGWDITTQVTSVLQLLSDPFYRT IEGFRMLVEKEWLSFGHKFSQRSSL ALNSQSGFAPIFLQFLDCVHQVHN QYPTFEFNLYYLKFALFHVSNRFK TFLLDSDYERLEHGTFFDDKGDKHA KKGVCIWECIDKMHKRSVFFNYLY SPVEIEALKPNVNVSSLKWDYDYTEE TLAGPSYDWMMLTPKHFPEESDV AGGAGPQSQKRTVWPCYDDVTCSTQ PDALTRLFSEIEKLEHKLNTPEKW HQLWEKITMDLKEPRTDHSRHS RSPGIASTNVPSYQKRPALHALHRSP TEDQSTTTAPSNVGEHRAATLYSQY TSKNDENRSFEGTLYKRGALLKGWK PRWFVLDVTKHQLRYDSGEDTSCK GHIDLAEVEMVVPAGPSMGAPKYTS DKAFFDLKTSKRVYNFCAQDQGSQAQ QWMDRIQSCISDA	False	False	3.253	2.503	0.93	1.003	1.157	1.112	0.848