

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q8CJE3	Q8CJE3_RAT	Rattus norvegicus	NaN	23.439218	NaN	NaN	38843836	MVILQKGDYVWMDLKSQGEFDPVIG AMVKLCESGQIQVVDDEGNEHWISP QNATHIKPMHPTSVHGVEDMIRLG DLNEAGILRNLLIRYRDHLIYTYTCSI LVAVNPYQLLSIYSSEHIRQYTNKKI GEMPPHIFAIADNCFNMKRNNRD QCCIISGESGAGKTESTKLILQFLAAI SGQHSWIEQQVLEATPILEAFGNAK TIRNDNSSRFKGYIDIHFNKRGAIEG AKIEQYLLEKSRVCRQAPDERNYHV FYCMLGEMNEEEKKLGQQAADY NYLAMGNICITCEGRVDSQEYANIRS AMKVLMTDTENWEILKLLAAILHM GNLQYEARTFENLDACEVLFSPSLA TAASHLEVNPPDLMSCSLTSRTLITRG ETVSTPLSREQALDVRDAFVKGIYGR LFVWVIEKINAAIKPPSQEVTNSRR SIGLLDIFGFENFTVNSFEQLCINFA NEHLQOFFVRHVFKLEQEEYDLESI DWLHIEFTDNQEALDMIANRPMNVI SLIDEESKFPKGTDATMLHKLNSQH RLNANYVPPKNSHETQFGINHFAGI VYYESQGFLEKNRDTLHGDIQLVHS SRNKFVKQIFQADVAMGAETRRKSP TLSSQFKRSLELLMRTLGCQPPFFV RCIKPNEFKKPMFLDRHLCVRQLRY SGMMETIRIRHAGYPIRYSFVEFVER YRVLLPGVKPAYKQDDLQGTQORMA EAVLGTDDWQIGKTKIFLKDHHH MLLEVERDKAITDRVILLQKVIRGFK DRSNFLRLKSAATLIQRHWRGHHH RKNYELIRLGFRLQALHRSRKLHK QYRLARQRIIFQARCRAYLVRRAFR HRLWAVITVQAYARGMIARRLHRR RVEYWRRLEAERMRLAEEELRKE MSAKKAKEEAERKHQERLAQLARE DAERELKEKEEAARRKELLQOMERA RHEPINHSDMVDMFGFLGTSSGL PGQEQAPSGFEDLERGRREMVEE DVDAAALPLPDEDEEDLSEYKFAKFA ATYFQGTTHSYTRRPLKQPLLYHD DEGDQLAALAVWITILRFMGDLPEP KYHTAMSDGSEKIPVMTKIYETLTK KTYKRELQALQGEQAQLSEGQKKT SVKHKLVHLTLKKSCLTEEVTKRL HDGESMVQGNMLEDRPTS NLEKL HFIIINGILRPALRDEIYQISKQLTH NPSKSSYARGWILVSLCVGCFAPSEK FVKYLRNFIHGGPPGYAPYCEERLRR TFVNGTRTOPPSWLELQATKSKKPI MLPVTFMDGTTKLLADSATTAKEL CNALADKISLKDRFGFSLYALFDKV SSLGSGSDHVMDAISQCEQYAKEQG AQERNAPWRLFFRKEVFTPWHNPS EDNVATNLIYQQVVRGVKFGGEYRCE KEDDLAELASQQYFVDYGSEMILER LLSLVPTYIPDREITPLKNLEKWAQL AIAAHKGIYAQRRTDAQVKQDVV NYARFKWPLLFSRFYEAYKFGPPLP KSDVIVAVNWTGVYFVDEQEQLLE LSFPEIMAVSSRGAKLMAPSFTLAT IKGDEYTFSSNAEDIRDLVVTFLG LRKRSKYVVALQDNPNPAGEESGFL SFAKGLIILDHDTGEQVMNSGWA NGINERTKQRGDFPTDCVYVMPVT LPPREIVALVTMPDQRQDVVRLQL RTAEPEVRTKPYTLEEFYDYFRSPP KHTLSRVMVSKARGKDRLWSHTRE PLKQALLKKIVGSEELSQEACMSFIA VLKYMGDYPSKRTRSVNELTDQIFE WAVKAEPLKDEAYVQILKQLTDNHI RYSEEKGWELLWLCTGLFPPSNILL PHVQRFLQSRKHCLAI DCLORLQK	True	True	4.683	2.359	2.036	1.167	1.56	4.468	1.558

