

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	extracell region
Q810W7	MAST1_RAT	Rattus norvegicus	Microtubule-associated serine/threonine-protein kinase 1	23.439218	NaN	S90;S139;S167;S346;T351;S689;S895;S954;S1414	38843836	MSDSLWTALSNFMSPSFPGGSMFR RTKSCRTSNRKSLLITSTSPTLPRPH SPLPGHGLSSPLDSPRNFSPNTPAH FSFASSRRADGRRWLSLALPSSGYG TNTPSSSTVSSSCSSQERLHQLPYQPT VDELHFLSKHFGSTESITDEDGRRR SPAVRPRSRLSPGRSPSSYDNEIVM MNHVYKERFFKATAQMEKLRDFA RAYEPDSVLPLADGVLSFIHHQIIELA RDCLTKSRDGLITTVYFELQENLEK LLQDAYERSESELEVAFTQLVKLLII ISRPARLLECLEFNPEEFYHLLAEAE GHAKEGHLVKTDIRYIIRQLGLTRD PFDPVVRLEEQDSSGGSNTPEQDDTS EGRSSTS KAKKPPGESDFDTIKLISN GAYGAVYLVRHRDTRQRFAMKKINK QNLILRNQIQAFVERDILTFAPENPF VVGMFCSFETRRHLCVMMEYVEGG DCATLLKNIGALPVEMARMYFAETV LALAYLHNYGIVHRDLKPDNLLITSM GHIKLDFGLSKMGLMSLITNLYEG HIEKDAREFLDKQVCGTPEYIPEVI LRQGYKPVDDWAMGIIYEFLVGC VPPFGDTPEELFGQVSDILWPEGD EALPTDAQLLISLLQTNPLVRLGAG GAFEVKQHSFRDLDTGLLRQKA EFIPHESEDSTSYFDTRSDRYHHV NSYDEDDTTEEEVPEIRQFSSCSPRF SKVYSSMEQLSQHEPKTPVSASGAS KRDPNAKGPEEKVAGKREGLGGLTL REKTWRGGSPKIKRFSASEASFLEG EASPPGARRRFSALLEPSRFTAPQE DEDEARLRPRRPSDDPPSSLDTRVP KEAAQOEGTSTPGEPEATERSHPGD FCPPSKDGDPSGPRATNDLVLRRAR HQQLSGDLSVEKRPSRTGGKVIKSA SATALSVMIPAVDPHGGSPLASPMS PRSLSSNPSSRDSSPSRDYSPAVSGL RSPITIQRSQKYGFTLRIRVYMGD SDVYSVHHIVVHVEEGGPAQEAGLC AGDLITHVNGEPVHGMVHPEVVVELI LKSGNKVAVTTTPEFNTSIRIGPARR SSYKAKMARRNRPSAKDGOESKK RSSLFRKITKQSNLLHTSRSLSLNR SLSSSDSLPGSPTHGLPARSPTHSYR STPDSAYLGASSQSSPASSTPNSPA SSASHHIRPSTLHGLSPKLHROYRSA RCKSAGNIPLSPLAHTPSPTQASPPP LPGHTVGSHTTQSFPKHLHSSPPIV RPRPKSAEPPRSPLLKRVQSAEKLGA SLGADKKGALRKHSLEVGHPDFRDK FHGELALHSLAESDGETPPIEGPGAT RQVAMRRLGRQESPLSLGADPLLPD GVORPMASGKEDSAGGTEACTPPRA TTPGSRTLERDLGCTRHSQSVQTEDG PGGVARALAKAALSPVQEHETGRRS SSGEAGTPPVIVVEPARPGVKTQTP QPLGTDKGLKEPVAQIPLVPDAPRV RERWVLEEEERTTLGPRSKPASP KLSPPDQTPTVAPTKNVPRSAAPPVP PASLMVPGTKPEAGNSRCPAEGVA SAGLTKTGAPSPASLGP	True	False	2.795	5.0	0.656	False	False	3.448	0.687