

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membr
Q9JLN9	MTOR_MOUSE	Mus musculus	Serine/threonine-protein kinase mTOR	30.048722	NaN	S567;T1162;S1261;S2159;T2164;T2173;T2446;S2448;S2478;S2481	39388284;33300544	MLGTGPAVATASAAATSSNVSVLQOF ASGLKSRNEETRAKAAKELQHYVTM ELREMSQEESTRFYDQLNHHIFELV SSSDANERKGGILAIASLIGVEGNS TRIGRFANYLRNLLPSSDPVVMEMA SKAIGRLAMAGDTFTAAYVEFEVVKR ALEWLGADRNEGRRHAAVLVLR ISVPTFFFOQVQPFDFNIFVAVWDPK QAIREGAVAALRACLILTTQREP KQPQWYRHTFEAEKGFDETLAKEK GMNRDDRIHGALLILNELVRISSE GERLREEMEEITQQQLVHDKYCKDL MGFGTKPRHITPFTSFQAVQPQPN ALVGLLGYSSPQGLMGFGTSPSPAK STLVESRCCRDLMEEKFDQVCQWV LKCRSSKNSLIQMTILNLLPRLA PSAFTDTQYLQDTMNHVLSVCVKEK ERTAAAFQALGLLSVAVRSEFKVYL VLDIIRAALPPKDFAHKRQKTQV TVFTCISMLARAMGPGIQDIDELLE PMLAVGLSPALTAVALYDLSRQIP KDIQDGLLKMLSLVLMHKPLRHPG MPKGLAHQLASPLTTLPEASDVASI TLALRTLGSFEFEGHSLTQFVRHCA DHFLNSEHKEIRMEAAARTCSRL SIHLISGHAAVVSQTAVQVAVD LLVVGITDPPDIRYCVLASLDER AHLAQAEENLQALFVALNDQVFE LAICTVGRSSMNPFAVMPFLRKML IQILTEHSGIGRIKESARMGLGHL VSNAPRLRIPYMEPIKALILKLD PDPNPGVINNVLATIGELAQVSG MRKWVDELFIHMDMLQDSSLLAKR QVALWTLGQLVASTGYVVEPYRKY TLLEVLLNFKTEQNGTRREAIRV GLLALDPYKHKVNIQDQSRDAS AVLSSEKSSQDSSDYSTSEMLVNM GNLPLDEFYPAVSMVALMRIFR LSHHHTMVVQAITFIKSLGKCVQ FLPOVMPFNLNVRVCDGAIREFL QLGMLVSFVKSHIRPYMDEIVTL EFVWMTSISQSTIILLIEQIVVAL FKLYLPQIPHMLRVFMHDNSQGR VSIKLLAAIQLFGANLDDYHLHLL VKLFDAPVPLPSRKAALETVDR SLDFTDYASRIHPVIRTLQSP TAMDTLSSLVFQLGKKYQIFIP KVLVRHRINHORYDVLICRIVK ADEEEDPLIYQHRMLRSSQGDAL GPVETGPMKHLHVSTINLQKAWG RRVSKDDWLEWLRRLSLELLKDS PSLRSCWALAQAYNPMARDLFNA FVSCWSELNEDQDELIRSIELAL QDIAEVTQTLNLAEFMEHSDKGP PLRDDNGIVLLGERAAKCRAYAK HYKELEFQKGPPTAILESISIN QQPEAASGVLEYAMKHFGELEIQ WYEKLHEWEDALVAYDKMDTNKE DPELMLGRMRCLEALGEWQQLHQ QCCEKWTLVNDQAKMARMMAAAA AWGLGQWDSMEEYTCMIPRDTHD AFYRAVLALHQDLFSLAQQCIDK DLLDAELTAMAGESYSRAYGAMV HMLSELEEVQYKLVPERREIRQW WERLQCCQRIVEDWQKILMVRSLV SPHEDMRTWLKYASLCGKSGRLA HKTLVLLGVDPSRQLDHPLPTAHP QVTYAYMKNMWKSARKIDAFQHM HFVQTMQQAQHAIAATEDQHKQ LHKLMARCFKLGWQLNLQGINE STIPKLVQYSAATEHDSRWYKAWH AWAVMNFVAVLHYKHQNAARDEK KCLRHASGANITNATTAATAASAA ATSTEGSNSESEAESNENSPSP QKQVTEDESKTLLLYTVPVAVQGF ISLSRGNLQDTRLVTLWFDYGHV PDVNEALVEGVKAIQIDTWLQVIP IARIDTPRPLVGRLIHQLLTDIGR YHPQALYPLTVASKSTTARHNAANK KILKNCMEHSNTLVQAMMVSEELIRV	True	False	5.0	5.0	4.572	4.381	4.114	4.213

