	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatu
0	P42345	MTOR_HUMAN	Homo sapiens	Serine/threonine-protein kinase mTOR	31.82577	S56	S567;T1162;S1261;S2159;T2164;T2173;T2446;S2448;S2478;S2481	39388284;32892442;39531497	MLGTGPAAATTAATTSSNVSVLQQF ASGLKSRNEETRAKAAKELQHYVTM ELREMSQEESTRFYDQLNHHIFELV SSSDANERKGGILAIASLIGVEGGNA TRIGRFANYLRNLLPSNDPVVMEMA SKAIGRLAMAGDTFTAEYVEFEVKR ALEWLGADRNEGRRHAAVLVLRELA ISVPTFFFQQVQPFFDNIFVAVWDPK QAIREGAVAALRACLILTTQREPKEM QKPQWYRHTFEEAEKGFDETLAKEK GMNRDDRIHGALLILNELVRISSME GERLREEMEEITQQQLVHDKYCKDL MGFGTKPRHITPFTSFQAVQPQQSN ALVGLLGYSSHQGLMGFGTSPSPAK STLVESRCCRDLMEEKFDQVCQWV LKCRNSKNSLIQMTILNLLPRLAAFR PSAFTDTQYLQDTMNHVLSCVKKEK ERTAAFQALGLLSVAVRSEFKVYLPR VLDIIRAALPPKDFAHKRQKAMQVD ATVFTCISMLARAMGPGIQQDIKELL EPMLAVGLSPALTAVLYDLSRQIPQL KKDIQDGLLKMLSLVLMHKPLRHPG MPKGLAHQLASPGLTTLPEASDVGSI TLALRTLGSFEFEGHSLTQFVRHCA DHFLNSEHKEIRMEAARTCSRLLTP SIHLISGHAHVVSQTAVQVVADVLSK LLVVGITDPDPDIRYCVLASLDERFD AHLAQAENLQALFVALNDQVFEIRE LAICTVGRLSSMNPAFVMPFLRKML IQILTELEHSGIGRIKEQSARMLGHL VSNAPRLIRPYMEPILKALILKLKDPD PDPNPGVINNVLATIGELAQVSGLE MRKWVDELFIIIMDMLQDSSLLAKR QVALWTLGQLVASTGYVVEPYRKYP TLLEVLLNFLKTEQNQGTRREAIRVL GLLGALDPYKHKVNIGMIDQSRDAS AVSLSESKSSQDSSDYSTSEMLVNM GNLPLDEFYPAVSMVALMRIFRDQS LSHHHTMVVQAITFIFKSLGLKCVQ FLPQVMPTFLNVIRVCDGAIREFLFQ QLGMLVSFVKSHIRPYMDEIVTLMR EFWVMNTSIQSTIILLIEQIVVALGGE FKLYLPQLIPHMLRVFMHDNSPGRI VSIKLLAAIQLFGANLDDYLHLLLPPI VKLFDAPEAPLPSRKAALETVDRLTE SLDFTDYASRIIHPIVRTLDQSPELRS TAMDTLSSLVFQLGKKYQIFIPMVN KVLVRHRINHQRYDVLICRIVKGYTL ADEEEDPLIYQHRMLRSGQGDALAS GPVETGPMKKLHVSTINLQKAWGAA RRVSKDDWLEWLRRLSLELLKDSSS PSLRSCWALAQAYNPMARDLFNAA FVSCWSELNEDQQDELIRSIELALTS QDIAEVTQTLLNLAEFMEHSDKGPL PLRDDNGIVLLGERAAKCRAYAKAL HYKELEFQKGPTPAILESLISINNKL QQPEAAAGVLEYAMKHFGELEIQAT WYEKLHEWEDALVAYDKKMDTNKD DPELMLGRMRCLEALGEWGQLHQ QCCEKWTLVNDETQAKMARMAAAA AWGLGQWDSMEEYTCMIPRDTHDG AFYRAVLALHQDLFSLAQQCIDKAR DLLDAELTAMAGESYSRAYGAMVSC HMLSELEEVIQYKLVPERREIIRQIW WERLQGCQRIVEDWQKILMVRSLVV SPHEDMRTWLKYASLCGKSGRLALA HKTLVLLLGVDPSRQLDHPLPTVHP QVTYAYMKNMWKSARKIDAFQHMQ HFVQTMQQQAQHAIATEDQQHKQE LHKLMARCFLKLGEWQLNLQGINE STIPKVLQYYSAATEHDRSWYKAWH AWAVMNFEAVLHYKHQNQARDEK KKLRHASGANITNATTAATTAATATT TASTEGSNSESEAESTENSPTPSPLQ KKVTEDLSKTLLMYTVPAVQGFFRSI SLSRGNNLQDTLRVLTLWFDYGHW PDVNEALVEGVKAIQIDTWLQVIPQL IARIDTPRPLVGRLIHQLLTDIGRYHP QALIYPLTVASKSTTTARHNAANKIL KNMCEHSNTLVQQAMMVSEELIRV	True	False	4.76	4.824	4.552	4.386	4.122

									AILWHEMWHEGLEEASRLYFGERN VKGMFEVLEPLHAMMERGPQTLKE TSFNQAYGRDLMEAQEWCRKYMKS GNVKDLTQAWDLYYHVFRRISKQLP QLTSLELQYVSPKLLMCRDLELAVP GTYDPNQPIIRIQSIAPSLQVITSKQR PRKLTLMGSNGHEFVFLLKGHEDL RQDERVMQLFGLVNTLLANDPTSLR KNLSIQRYAVIPLSTNSGLIGWVPHC DTLHALIRDYREKKKILLNIEHRIML RMAPDYDHLTLMQKVEVFEHAVNN TAGDDLAKLLWLKSPSSEVWFDRRT NYTRSLAVMSMVGYILGLGDRHPSN LMLDRLSGKILHIDFGDCFEVAMTR EKFPEKIPFRLTRMLTNAMEVTGLD GNYRITCHTVMEVLREHKDSVMAV LEAFVYDPLLNWRLMDTNTKGNKR SRTRTDSYSAGQSVEILDGVELGEPA HKKTGTTVPESIHSFIGDGLVKPEAL NKKAIQIINRVRDKLTGRDFSHDDTL DVPTQVELLIKQATSHENLCQCYIG WCPFW							