	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
0	E7EVA0	E7EVA0_HUMAN	Homo sapiens	Microtubule-associated protein	25.886613	NaN	NaN	35008409	MADLSLADALTEPSPDIEGEIKRDFI ATLEAEAFDDVVGETVGKTDYIPLLD VDEKTGNSESKKKPCSETSQIEDLPL PPHPASLSFHLPLDTPSSKPTLLANG GHGVEGSDTTGSPTEFLEEKMAYQE YPNSQNWPEDTNFCFQPEQVVDPIQ TDPFKMYHDDDLADLVFPSSATADT SIFAGQNDPLKDSYGMSPCNTAVVP QGWSVEALNSPHSESFVSPEAVAEP PQPTAVPLELAKEIEMASEERPPAQA LEIMMGLKTTDMAPSKETEMALAK DMALATKTEVALAKDMESPTKLDVT LAKDMQPSMESDMALVKDMELPTE KEVALVKDVRWPTETDVSSAKNVVL PTETEVAPAKDVTLLKETERASPIKM DLAPSKDMGPPKENKKETERASPIK MDLAPSKDMGPPKENKIVPAKDLVL LSEIEVAQANDIISSTEISSAEKVALS SETEVALARDMTLPPETNVILTKDKA LPLEAEVAPVKDMAQLPETEIAPAKD VAPSTVKEVGLLKDMSPLSETEMAL GKDVTPPPETEVVLIKNVCLPPEMEV ALTEDQVPALKTEAPLAKDGVLTLA NNVTPAKDVPPLSETEATPVPIKDM EIAQTQKGISEDSHLESLQDVGQSAA PTFMISPETVTGTGKKCSLPAEEDSV LEKLGERKPCNSQPSELSSETSANF MYCGTPPTQAKQVCRPSDRRSTRPK PARVPPELLGGSPPWKTLDHRLGHC SLSESGWVSGSSSCGGPGNQRKSIH VDSLEPQRDLGREAWDIESTPIMMK KKKKKPKQKRYSQPRAGGPSDDDNA DKPKGHPFAADTQKSGVLPSQPTTM GTEYGLVSGENLKRECLVNSSAARL VAENFVSESLRIPLYPSEEAPKTAISS QSKLRVEEESKSNKSVLQNQDKKLL KQHEYKPQPAPHLKTPVDKSQSVGP LNLKGPLAEVSAYNVETPLDIRLKEG CSPFLDQEVMGVVSKPTAAKEIPNL VPTLIASNPLECNLKEGNNESKMTK LQNVKLKEFPEGAEEDKELKKEAFP NERQEISIFTSEQLQGQVLVQVPGVE NEPFKRMAGDGKSRKGRGSSGKMR TDSGKVKAKSELPFLLDSQKDGRAV LIPSEPVSKTEGMTTQDKSEELGLNS SKQPGTKADLTEAVVMGEPKEMTQ PKVAGTMQALIPLESGSGMTQTSGV STETGDVVKDMGVNNQSKEGRCPW KDHEAAPWISEKPKKRGNEGKSKKF KNNYSTQPARMERKEEILNPPFEGK DGDTGSIPHKSKEIGFTFPKMHDSS FSHTPDTPTVEAVDRKGGNFQVNFV ELGTLGENKISTVKASTVTEPPAKVT DVSCQEQIQGAGFVPSVVSEENKTD AANRYTAVADKPSKRSNDGKSKKVK NSSPEKHILENKIDATKIHVPMETTG DQGIEGMAYMDENRNITFTCPRTPS ELINKSSPLEVLESAACEKLPTPTPQ VVKEGDSFPDTLAKNGQEIAPAQISK SLMVDNYTKDGVPGQERPKGPSAVV PSTSTGGVALPITTAIETVNIHGDHSL KNKAELADSMKNEAGIDEGHVIGES ESVHSGASKHSVEKVTELAKGHLLP GVPVEDQSLPGEARALEGYADRGNF PAHPVNEEKETKEGSVAVQIPDLLE DKAQKLSFCEDQNAQDRNSKGSDS LNKKVDLTLLSPKSENDKLKEISLAC KITELESVSLPTPEIQSDFLHSKVEAP PSEVADTLVIMTASKGVRLPEPKDKI LETPQKMTEKSESKTPGEGKKEDKS RMAEPMKGYMRPTKSRGLTPLLPKS TIQEQERHKQLKSAGIARPEEGRPVV SGTGNDITTPPNKELPPSPEKKTKPL ATTQPAKTSTSKAKTQPTSLPKQPAP TTIGGLNKKPMSLASGLVPAAPPKRP AVASARPSILPSKDVKPKPIADAKAPE	None	None	None	None	None	None	None	None	None

								KRASPSKPASAPASRSGSKSTQTVAK TTTAAAVASTGPSSRSPSTLLPKKPT AIKTEGKPAEVKKMTAKSVPADLSRP KSTSTSSMKKTTTLSGTAPAAGVVPS RVKATPMPSRPSTTPFIDKKPTSAKP SSTTPRLSRLATNTSAPDLKNVRSKV GSTENIKHQPGGGRAKVEKKTEAAA TTRKPESNAVTKTAGPIASAQKQPAG KVQIVSKKVSYSHIQSKCGSKDNIKH VPGGGNVQIQNKKVDISKVSSKCGS KANIKHKPGGGDVKIESQKLNFKEK AQAKVGSLDNVGHLPAGGAVKTEG GGSEAPLCPGPPAGEEPAISEAAPEA GAPTSASGLNGHPTLSGGGDQREAQ TLDSQIQETSI								