	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplas reticulun
0	P11137	MTAP2_HUMAN	Homo sapiens	Microtubule-associated protein 2	29.925637	S199;T241;T335;S502;T522;T851;S1082	S136;S140;S143;S285;S498;S601;S605;S610;S629;S725;S729;T733;S736;S738;T745;S821;S881;S890;S936;S1133;S1134;S1139;T1154;S1155;S1159;S1347;S1353;S1534;S1555;S1588;T1602;T1605;T1616;T1619;T1649;S1653;S1679;S1782;S1787;S1790;S1795;S1808;T67;S323;S354;S386	28657654;29485866	MADERKDEAKAPHWTSAPLTEASA HSHPPEIKDQGGAGEGLVRSANGFP YREDEEGAFGEHGSQGTYSNTKEN GINGELTSADRETAEEVSARIVQVVT AEAVAVLKGEQEKEAQHKDQTAALP LAAEETANLPPSPPPSPASEQTVTVE EDLLTASKMEFHDQQELTPSTAEPS DQKEKESEKQSKPGEDLKHAALVSQ PETTKTYPDKKDMQGTEEEKAPLAL FGHTLVASLEDMKQKTEPSLVVPGI DLPKEPPTPKEQKDWFIEMPTEAKK DEWGLVAPISPGPLTPMREKDVFDD IPKWEGKQFDSPMPSPFQGGSFTLP LDVMKNEIVTETSPFAPAFLQPDDK KSLQQTSGPATAKDSFKIEEPHEAKP DKMAEAPPSEAMTLPKDAHIPVVEE HVMGKVLEEEKEAINQETVQQRDTF TPSGQEPILTEKETELKLEEKTTISDK EAVPKESKPPKPADEEIGIIQTSTEHT FSEQKDQEPTTDMLKQDSFPVSLEQ AVTDSAMTSKTLEKAMTEPSALIEKS SIQELFEMRVDDKDKIEGVGAATSA ELDMPFYEDKSGMSKYFETSALKEE ATKSIEPGSDYYELSDTRESVHESID TMSPMHKNGDKEFQTGKESQPSPP AQEAGYSTLAQSYPSDLPEEPSSPQE RMFTIDPKVYGEKRDLHSKNKDDLT LSRSLGLGGRSAIEQRSMSINLPMS CLDSIALGFNFGRGHDLSPLASDILT NTSGSMDEGDDYLPATTPALEKAPC FPVESKEEEQIEKVKATGEESTQAEI SCESPFLAKDFYKNGTVMAPDLPEM LDLAGTRSRLASVSADAEVARRKSVP SETVVEDSRTGLPPVTDENHVIVKTD SQLEDLGYCVFNKYTVPLPSPVQDS ENLSGESGTFYEGTDDKVRRDLATD LSLIEVKLAAAGRVKDEFSVDKEASA HISGDKSGLSKEFDQEKKANDRLDT VLEKSEEHADSKEHAKKTEEAGDEI ETFGLGVTYEQALAKDLSIPTDASSE KAEKGLSSVPEIAEVEPSKKVEQGLD FAVQGQLDVKISDFGQMASGLNIDD RRATELKLEATQDMTPSSKAPQEAD AFMGVESGHMKEGTKVSETEVKEK VAKPDLVHQEAVDKEESYESSGEHE SLTMESLKADEGKKETSPESSLIQDE IAVKLSVEIPCPPAVSEADLATDERA DVQMEFIQGPKEESKETPDISITPSD VAEPLHETIVSEPAEIQSEEEEIEAQG EYDKLLFRSDTLQITDLGVSGAREEF VETCPSEHKGVIESVVTIEDDFITVV QTTTDEGESGSHSVRFAALEQPEVE RRPSPHDEEEFEVEEAAEAQAEPKD GSPEAPASPEREEVALSEYKTETYDD YKDETTIDDSIMDADSLWVDTQDDD RSIMTEQLETIPKEEKAEKEARRSSL EKHRKEKPFKTGRGRISTPERKVAK KEPSTVSRDEVRRKKAVYKKAELAK KTEVQAHSPSRKFILKPAIKYTRPTH LSCVKRKTTAAGGESALAPSVFKQA KDKVSDGVTKSPEKRSSLPRPSSILP PRRGVSGDRDENSFSLNSSISSSAR RTTRSEPIRRAGKSGTSTPTTPGSTAI TPGTPPSYSSRTPGTPGTPSYPRTPH TPGTPKSAILVPSEKKVAIIRTPPKSP ATPKQLRLINQPLPDLKNVKSKIGST DNIKYQPKGGQVQIVTKKIDLSHVTS KCGSLKNIRHRPGGGRVKIESVKLD FKEKAQAKVGSLDNAHHVPGGGNV KIDSQKLNFREHAKARVDHGAEIITQ SPGRSSVASPRRLSNVSSSGSINLLE SPQLATLAEDVTAALAKQGL	None	None	None	None	None	None