

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	p n
P20357	MTAP2_MOUSE	Mus musculus	Microtubule-associated protein 2	35.309632	S472	S28;S136;S140;S143;S283;S333;S346;S476;S496;S520;S550;S596;S599;S603;S608;S626;S726;S730;T734;S737;S739;T746;S823;S883;S892;S938;S1050;S1139;S1140;S1145;T1160;S1161;S1165;S1352;T1358;S1539;S1560;S1592;T1606;T1609;T1620;T1623;T1650;S1654;S1680;S1783;S1788;S1791;S1796;S1809	33300544;35822049;22645316	MADERKDEGKAPHWTSASLTEAAA HPHSPPEMKDQGGAGEGLSRNANGF PYREEEEGAFGEHRSQGTYSDTKEN GINGELTSADRETAEEVSARIVQVVT AEAVAVLKGEQKEAQHKDQPAALP LAAEETANLPPSPPPSPASEQTATVE EDLLTASKMEFPEQEFKFPSSFAEPL DKGEMEFKMPKPKGEDFEHAALVP DTSKTPQDKKDLQGMEDGEKLPVVPF AQTFGTNLEDRKQSTEPSIVMPSIGL SAEPPAPKEPKDWFIEMPTESKKDE WGLAAPISPGPLTPMREKDVLEDIPR WEGKQFDSMPSPFHHGGSFTLPLDT MKNERVSEGRPFAPVFFQSDDKVS LQDPSALATSKESKDEEPLKDKAD KVADVSISEVTLLGNVHSPVVEGYV GENISGEVKVTTDQEKKETSAPSVQ EPTLTETEPQTKLDEKSTVSIEEA KKEESFKLRDDKTGVIQTSTEQSF EDQKGOEHTIDELKQDSFPISLEQAV TDAAMTSKTLGKVTSEPEAVSERREI QGLFEEKTADKNKLEGAGSATIAEV EMPFYEDKSGMSKYFETSALKEDM TRSTELGSDYYELSDSRGSAQESLDT ISPKNQHDEKELQAKASQSPPAQE AGYSTLAQSYTPDHPSELPEEPSQP ERMFTIDPKVYGEKRDLSKKNKDDL TLRSRLGLGGRSAIEQRSMSINLPM CLDSIALGFNFRGHDLSPASDILT NTSGSMDEGDDYLPPTTPAVEKMP FPIESKEEEDKAEQAKVTGGQTIQVE TSSESPFPAKEYYKNGTVMADLPE MLDLAGTRSLASVSADAEVARRKS VPSEAMLAESSTSLPPVADESPVTVK PDSQLEDMGYCVFNKYTVPLPSVQ DSENLGSESGSFYEGTDDKVRRLA TDLSLIEVKLAAAGRVKDEFTA SPPTSADKSRSLREFDHRKANDKL DTVLEKSEEHIDSKEHAKSEEMGG KVELFGLGITYDQASTKELITKDTSP EKTEKGLSSVPEVAEVEPTKADQG LDFAATKAEPQLDKVSDFCQMAS GMNVDAKAIELKFEVAQELTSLSE APQEADSFMGVESHGHIKEGGVNET EVKEKVTKPDLVHQEAVDKKEESY SGEHESLTMESLKPDEGKKETSPET SLIQDEVALKLSVEIPCPPVSEADLS TDEKGEVQMEFIQLPKEESTETPDIP AIPSDVTQPPQPEAVSEPAEVPSE EIEAGGEYDKLLFRSDTLQISDLL ESREEFVETCPGELKGVVESVVTIED DFITVVQTTTDEGESGSHSVRFAAPA QPEEERRRPHDEELEIEMAAEAQA EPKDGSPDAPATPEKEEVAFSEYKTE TYDDYKDETTIDDSIMDADSLWVDT QDDRSILTEQLETIPKEERAEKDAR RPSLEKHRKEKPFKTGRGRISTPERK VAKKEPSTVSRDEVRRKAVYKKA LAKKSEVQAHSRKLILKPAIKYTRP THLSCVRRKTTAASGDLAQAPGAFK QAKDKVTDGISKSPKRSLSLPRPSSI LPRRGGVSGDREENSFSLNSSISSAR RTRTRSEPIRRAGKSGTSTPTTPGSTAI TPGTPPSYSSRTPGTGPSTPSYRTPG TPKSGILVPSEKKVAIIRTTPKSPATP KQLRLINQPLPDLKNVKSKIGSTDNI KYQPKGGQVQIVTKKIDLSHVTSCCG SLKNIRHRPGGGRVKIESVLDFKEK AQAKVGLDNAHHVPGGGNVKIDS QKLNFRHAKARVDHGAIEHTQSPS RSSVASPRRLSNVSSGSINLLESPQ LATLAEDVTAALAKQGL	True	True	2.96	5.0	2.319	1.829	1.587	4.