

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P20357	MTAP2_MOUSE	Mus musculus	Microtubule-associated protein 2	23.375343	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;22645316;35822049	MADERKDEGKAPHWTSASLTEAAA HPHSPMKDQGGAGEGLSRNANGF PYREEEEGAFGEHRSQGTYSDTKEN GINGELTSADRETAEV SARIVQVVT AEAVAVLKGEQEKEAQHKDQPAALP LAAEETANLPPSPPPSPASEQATATVE EDLLTASKMEFPEQEKFPSFAEPL DKGEMEFKMPKPKGDFEHAALVP DTSKTPQDKKDLQGMERGEKLPVVPF AQTFGTNLEDRKQSTEP SIVMPSIGL SAEPPAPKEPKDWFIE MPTE SKKDE WGLAAPISPGPLTPMREKDVLEDIPR WEGKQFDSPMPSPFHGG SFTLPLDT MKNERVSEGPRPFAPVFFQ SDDKVS LQDPSALATSKESKDEEPLKDKAD KVADVSISEVTLLGNVHSPVVEGYV GENISGEVKVTTDQEKKETSAPSVQ EPTLTETEPQTKLDEKSTV SIEEAVA KKEESFKLRDDKTGVIQTSTEQSF SK EDQKQGEHTIDELKQDSFPISLEQAV TDAAMTSKTLGKVTSEPEAVSERREI OGLFEEKTADKNKLEGAGSATIAEV EMPFYEDKSGMSKYFETSALKEDM TRSTELGSDYYELSDSRGSAQESLDT ISPKNQHDEKELQAKASQPSPPAQE AGYSTLAQSYTPDHPSELPEEPSSPQ ERMFTIDPKVYGEKRD LHSKNKDDL TLRSRLGLGGRSAIEQRSM SINLPMS CLDSIALGFNFGRGHDL SPLASDILT NTSGSMDEGDDYLPPTTPAVEKMPC FPIESKEEEDKAEQAKVTGGQTIQVE TSSESPFPAKEYYKNGTVMAPDLPE MLDLAGTRSRLASVSADAEVARRKS VPSEAMLAESSTSLPPVADESPVTVK PDSQLEDMGYCVFNKYTVPLPSPVQ DSENLSGESGSFYEGTDDKVRRDLA TDL SLIEVKLAAAGRVKDEF TAEKEA SPPTSADKSRLSREFD HDRKANDKL DTVLEKSEEHIDSKEHAKES EEMGG KVELFGLGITYDQASTKELITTKDTSP EKTEKGLSSVPEVAEVEPTTKADQG LDFAATKAEPSQLDIKVSDFGQMAS GMNVDAGKAIELKFEVAQELT LSSE APQEADSFMGVESGHIKEGGKVNET EVKEKVTKPD LVHQEAVDK EESYES SGEHESLTMESLKPDEGKKETS PET SLIQDEVALKLSVEIPC PVPVSEADLS TDEKGEVQMEFIQLPKEESTETPDIP AIPSDVTQPQPEAIVSEPAEVPSEEE EIEAGGEYDKLLFRSDTLQISDLLVS ESREEFVETCPGELKGVVESVVTIED DFITVVQTTTDEGESGSHSVRFAAPA QPPEERRRPRPHDEELEIEMAEEAQA

EPKDGSPDAPATPEKEEVAFSEYKTE
TYDDYKDETTIDDSIMDADSLWVDT
QDDDRSILTEQLETIPKEERAEKDAR
RPSLEKHRKEKPFKTGRGRISTPERK
VAKKEPSTVSRDEVRRKKAVYKKA
LAKKSEVQAHSPSRKLILKPAIKYTRP
THLSCVKRKTTAASGDLAQAPGAFK
QAKDKVTDGISKSPKRSSLPRPSSI
LPPRRGVSGDRENSFSLNSSISSAR
RTTRSEPIRRAGKSGTSTPTTPGSTAI
TPGTPPSYSSRTPGTGTPSYPRTPG
TPKSGILVPSEKKVAIIRTPPKSPATP
KQLRLINQPLPDLKNVKSIGSTDNI
KYQPKGQVQIVTKKIDLSHVTSKCG
SLKNIRHRPGGGRVKIESVKLDFKEK
AQAKVGSLDNAHHVPGGGNVKIDS
QKLNFRHAKARVDHGAEIITQSPS
RSSVASPRRLSNVSSSGSINLLESPQ
LATLAEDVTAALAKQGL