

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P14873	MAP1B_MOUSE	Mus musculus	Microtubule-associated protein 1B	24.088229	T794;T2027;S2285	S336;S339;S341;S343;T527;S541;S544;S561;S614;S825;S828;S829;S885;S888;T896;T905;S933;S934;T945;S960;S967;S974;S989;S992;S1013;S1141;S1151;S1153;S1183;S1186;S1204;S1207;S1208;S1225;S1242;S1247;S1251;S1253;S1255;S1257;S1260;S1271;S1275;T1277;S1293;S1307;S1317;S1319;S1321;T1323;S1325;S1334;S1371;S1373;S1382;S1384;S1391;S1395;S1403;T1405;S1422;S1438;S1497;S1508;S1516;S1518;T1521;S1523;S1614;S1616;S1621;S1649;S1659;S1662;S1686;S1768;S1775;S1778;S1781;T1784;S1788;S1789;T1792;S1793;S1797;S1815;S1877;S1911;S1915;T1928;T1945;S2030;S2205;S2267;S2285;T2301;S2410	33300544;34678516;22517741;35822049;34418053;28528544	MATVVVEATEPEPSGSIGNPAASTSP SLSHRFLDSKFYLLVVVGETVTEEHL RRAIGNIELGIRSWDTNLI ECNLDQE LKL FVSRHSARFSPEVPGQKILHHR DVLETVVLINPSDEAVSTEVRLMITD AARHKLLVLTGQCFENTGELILQSG SFSFQNFIEIFTDQEI GELLSTTHPA NKASLTLFCPEEGDWKNSNLDHRN LQDFINIKLNSASILPEMEGLSEFTE YLSSESVEVPSPPFDILEPPTSGGFLKLS KPCCYIFPGGRGDSALFAVNGFNML INGGSERKSCFWKLRHLDRVDSILL THIGDDNLPGINSMLQRKIAELEEE RSQGSTNSDWMKNLISPDLGVVFL NVPENLKDPEPNIKMKRSIEEACFT LQYLNKLSMKPEPLFRSVGNTIEPVI LFQKMGVVGKLEMYVLNPKSSKEM QYFMQQWTGTNKDKAELILPNGQE VDIPISYLTSVSSLIVWHPANPAEKII RVLFPGNSTQYNILEGLEKCLKHLDFL KQPLATQKDLTGQVPTPPVKQVKLK QRADSRESLKPATKPVASKSVRKES KEETPEVTKTSQVEKTPKVESKEKVL VKKDKPVKTESKPSVTEKEVSSKEE QSPVKA EVAEKQATESKPKVTKDKV VKKEIKTKLEEKKEEKPKKEVVKKED KTPLKKDEKPRKEEVKKEIKKEIKKE ERKELKKEVKKETPLKDAKKEVKKE EKKEVKKEEKEPKKEIKKISKDIKKS TPLSDTKKPSALKPKVAKKEESTKKE PLAAGKLDKDGKVKVIKKEGKTTEAA ATAVGTAAATTAAVVAAAGIAASGPVK ELEAERSLMSSPEDLTKDFEELKAE EIDVAKDIKPQLELIEDEEKLKETQP GEAYVIQKETEVSKGSAESPDEGITT TEGEGECEQTPEELEPVEKQGVDDI EKFEDEGAGFEESSETGDYEEKAET EEAEPEEDGEDNASGSASKHSPT DDESAKAEADVHLKEKRESVSVGDD RAEEDMDDVLEKGEAEQSEEEGEE EDKAEDAREEGYEPDKTEAEDYVMA VADKAAEAGVTEEQYGYLGTSAKQP GIQSPSREPASSIHDETLPGGSESEA TASDEENREDQPEEFTATSGYTQSTI EISSEPTPMDMSTPRDVMDET NEETESPSQEFVNITKYESSLYSQEY SKPAVASFNGLSEGSKTATDGDY NASASTISPPSSMEEDKFSKALRDA YCSEKELKASAELDIKDVSDERLSP AKSPSLSPSPSPIEKTPLGERSVNF LTPNEIKVSAEGEARVSPGVTQAVV EEHCASPEEKTLEVSPSQSVTGSA GHTPYYQSPTDEKSSHLPTVTEKP QAVPVSF EFSEAKDENERASLSPMD EPVPDSESPVEKVLSPRLSPPLGSE SPYEDFLSADSKVLGRRSESPFEGK NGKQGFDPRESVSDLTSTGLYQDK QEEKSTGFIPIKEDFGPEKTSVET

MSSQSALALDERKLGGDVSPTQIDV
SQFGSFKEDTKMSISEGTVSDKSATP
VDEGVAEDTYSHMEGVASVSTASVA
TSSFPEPTDDVSPSLHAEVGSPTHST
EVDDSLSVSVVQPTPTTFQETEMSPS
KEECPRPMSISPPDFSPKTAKSRTPV
QDHRSEQSSMSIEFGQESPEHSLA
MDFSRQSPDHPTLGASVLHITENGP
TEVDYSPSDIQDSSLSHKIPTEEPSY
TQDNDLSELISVSQVEASPSTSSAHT
PSQIASPLQEDTLDVVPREMSLYA
SLASEKVQSLEGEKLSPKSDISPLTP
RESSPLYSPGFSDSTSAAKETAAAHQ
ASSSPPIDAATAEPYGFRRSMLFDTM
QHHLALNRDLTSSVEKDSGGKTPG
DFNYAYQKPENAAAGSPDEEDYDYES
QEKTIIRTHDVGYYEKTERTIKSPC
DSGYSYETIEKTIKTPEDGGYTCEITE
KTTRTPEEGGYSYEISEKTTRTPEVS
GYTYEKTERRRLDDISNGYDDTED
GGHTLGDCSYSYETTEKITSFPESES
YSYETSTKTRSPDTSAYCYETMEKI
TKTPQASTYSYETSDRCYTTTEKKSPS
EARQDVLDCLVSSCEFHKPKTELSF
SFINPNPLEWFAGEEPTTESEKPLTQ
SGGAPPPSGGKQQGRQCDPTPPTSV
SESAPSQTDSVPPETEECPSITADA
NIDSEDESETIPTDKTVTYKHMDPPP
APMQDRSPSPRHPDVSMVDPDALA
VDQNLGKALKKDLKEKTKKKPGTK
TKSSSPVKKGDGKSKPLAASPKPGAL
KESSDKVSRSVSPKKKESVEKATKTT
TTPEVKATRGEEDKETKNAANASA
SKSAKTATAGPGTTKAKSSTVPPGL
PVYLDLCYIPNHSNSKNVDVEFFKR
VRSSYYVSGNDPAAEEPSRAVLDAL
LEGKAQWGSNMQVTLIPTHDSEVM
REWYQETHEKQDLNIMVLASSSTV
VMQDESFPACKIEL