

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P14873	MAP1B_MOUSE	Mus musculus	Microtubule-associated protein 1B	23.732978	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	34418053;34678516;28528544;33300544;22517741	MATVVVEATEPEPSGSIGNPAASTSP SLSHRFLDSKFYLLVVVGETVTEEHL RRAIGNIELGIRSWDTNLI ECNLDQE LKL FVSRHSARFSPEVPGQKILHHR DVLETVVLINPSDEAVSTEVRLMITD AARHKLLVLTGQCFENTGELILQSG SFSFQNFIEIFTDQEI GELLSTTHPA NKASLTLFCPEEGDWKNSNLDHRN LQDFINIKLNSASILPEMEGLSEFTE YLSSESVEVPSPPFDILEPPTS GGGFLKS KPCCYIFPGGRGDSALFAVNGFNML INGGSERKSCFWKLRHLDRVDSILL THIGDDNLPGINSMLQRKIAELEEE RSQGSTNSDWMKNLISPDLGVVFL NVPENLKDPEPNIKMKRSIEEACFT LQYLNKLSMKPEPLFRSVGNTIEPVI LFQKMGVKGLEMYVLNPKSSKEM QYFMQQWTGTNKDKAELILPNGQE VDIPISYLTSVSSLIVWHPANPAEKII RVLFPGNSTQYNILEGLEKCLKHLDFL KQPLATQKDLTGQVPTPPVKQVKLK QRADSRESLKPATKPVASKSVRKES KEETPEVTKTSQVEKTPKVESKEKVL VKKDKPVKTESKPSVTEKEVSSKEE QSPVKA EVAEKQATESKPKVTKDKV VKKEIKTKLEEKKEEKPKKEVVKKED KTPLKKDEKPRKEEVKKEIKKEIKKE ERKELKKEVKKETPLKDAKKEVKKE EKKEVKKEEKEPKKEIKKISKDIKKS TPLSDTKKPSALKPKVAKKEESTKKE PLAAGKCLKDKGKVKVIKKEGKTTEAA ATAVGTAAATTAAVVAAAGIAASGPVK ELEAERSLMSSPEDLTKDFEELKAE EIDVAKDIKPQLELIEDEEKLKETQP GEAYVIQKETEVSKGSAESPDEGITT TEGEGECEQTPEELEPVEKQGVDDI EKFEDEGAGFEESSETGDYEEKAET EEAEPEEDGEDNASGSASKHSPT DDESAKAEADVHLKEKRESVSVGDD RAEEDMDDVLEKGEAEQSEEEGEE EDKAEDAREEGYEPDKTEAEDYVMA VADKAAEAGVTEEQYGYLGTSAKQP GIQSPSREPASSIHDETLPGGSESEA TASDEENREDQPEEFTATSGYTQSTI EISSEPTPMDMSTPRDVMDET NEETESPSQEFVNITKYESSLYSQEY SKPAVASFNGLSEGSKTATDYGKDY NASASTISPPSSMEEDKFSKLSALRDA YCSEEKELKASAELDIKDVSDERLSP AKSPSLSPSPSPIEKTPLGERSVNF LTPNEIKVSAEGEARVSPGVTQAVV EEHCASPEEKTLEVSPSPSVTGS GHTPYYQSPTDEKSSHLPTVTEKP QAVPVSF EFSEAKDENERASLSPMD EPVPDSESPVEKVLSPRLSPPLGSE SPYEDFLSADSKVLGRRSESPFEGK NGKQGFDPRESVSDLTSTGLYQDK QEEKSTGFIPIKEDFGPEKTS DVET

MSSQSALALDERKLGGDVSPTQIDV  
SQFGSFKEDTKMSISEGTVSDKSATP  
VDEGVAEDTYSHMEGVASVSTASVA  
TSSFPEPTDDVSPSLHAEVGSPhST  
EVDDSLSVSVVQTPTTFQETEMSPS  
KEECPRPMSISPPDFSPKTAksRTPV  
QDHRSEQSSMSIEFGQESPEHSLA  
MDFSRQSPDHPTLGASVLHITENGP  
TEVDYSPSDIQDSSLSHKIPTEEPSY  
TQDNDLSELISVSQVEASPSTSSAHT  
PSQIASPLQEDTLSDVVPREMSLYA  
SLASEKVQSLEGEKLSPKSDISPLTP  
RESSPLYSPGFSDSTSAAKETAAAHQ  
ASSSPPIDAATAEPYGFRRSMLFDTM  
QHHLALNRDLTSSVEKDSGGKTPG  
DFNYAYQKPENAAAGSPDEEDYDYES  
QEKTIrTHDVGGYYEKTERTIKSPC  
DSGYSYETIEKTIKTPEDGGYTCEITE  
KTTRTPEEGGYSYEISEKTTTRTPEVS  
GYTYEKTERRRLDDISNGYDDTED  
GGHTLGDCSYSYETTEKITSFPESES  
YSYETSTKTRSPDTSAYCYETMEKI  
TKTPQASTYSYETSDRCYttekkSPS  
EARQDVdLCLVSSCEFKHPKTELSP  
SFINPNPLEWFAGEEPTEESEKPLTQ  
SGGAPPPSGGKQQGRQCDETPPTSv  
SESAPSQTDSVPPETEECPSITADA  
NIDSEDESETIPTDKTVTYKHMDPPP  
APMQDRSPSPRHPDVSMVDPDALA  
VDQNLGKALKKDLKEKTKKKPGTK  
TKSSSPVKKGDGKSKPLAASPkgAL  
KESsdKvSRVASPKKKEsVEKATKTT  
TTPEVKATRGEEDKETKNAANASA  
SKSAKTATAGPGTTKAKSSTVPPGL  
PVYLDLCYIPNHSNSKNVDVEFFKR  
VRSSYYVvSGNDPAAEePSRAVLDAL  
LEGKAQWGSNMQVTLIPThDSEVM  
REWYQETHekQQDLNIMVlASSTV  
VMQDESFPACKIEL