

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P46821	MAP1B_HUMAN	Homo sapiens	Microtubule-associated protein 1B	10.070073	T1236;S1782;T1898;S1965	S336;S339;S343;T527;S541;S544;S561;S614;S828;S831;S832;S891;T899;T908;S936;S937;T948;S970;S977;S992;S995;S1016;S1144;S1154;S1156;S1187;S1190;S1208;S1211;S1212;S1229;S1247;S1252;S1256;S1258;S1260;S1262;S1265;S1276;S1280;T1282;S1298;S1312;S1322;S1324;S1326;T1328;S1330;S1339;S1376;S1378;S1387;S1389;S1396;S1400;S1408;T1410;S1427;S1438;S1443;S1501;S1512;S1520;S1522;T1525;S1527;S1618;S1620;S1625;S1653;S1663;S1666;S1690;S1772;S1779;S1782;S1785;T1788;S1792;S1793;T1796;S1797;S1801;S1819;S1881;S1899;S1915;S1917;S1919;T1932;S1939;T1949;S1965;T2034;S2209;S2271;S2289;T2305;S2414	34019948;34725712;37217939;25367160;35008409;35254053;26853435;28657654;23301498;30379171	MATVVVEATEPEPSGSIANPAASTSP SLSHRFLDSKFYLLVVVGEIVTEEHL RRAIGNIELGIRSWDTNLIENCLDQE LKL FVSRHSARFSPVPGQKILHHR DVLETVVLINPSDEAVSTEVRLMITD AARHKLLVLTGQC FENTGELILQSG SFSFQNFIEIFTDQEIGELLSTTHPA NKASLT LFCPEEGDWKNSLDRHN LQDFINIKLNSASILPEMEGLSEFTE YLSSEVVPSPFDILEPPTSGGFLKLS KPCCYIFPGGRGDSALFAVNGFNML INGGSEKSCFWKLRHLRDRVDSILL THIGDDNLP GINSMLQRKIAELEEE QSOGSTTNSDWMKNLISPD LGVVF NVPENLKNPEPNIKMKSRIEACFT LQYLNKLSMKPEPLFRSVGNTIDPVI LFQKMGV GKLEMYVLNPVKSSKEM QYFMQQTGTN KDKA EFILPNGQE VDLPISYLTSVSSLI VWH PANPAEKII RVLFPGNSTQYNILEGLEK LKHLDFL KQPLATQKDLTGQVPTPVVKQTKLK QRADSRESLKPAAKPLPSKSVRKESE EETPEVTKVNHVEKPPKVESKEKVM VKKDKPIKTETKPSVTEKEVPSKEEP SPVKA EVAEKQATDVKPKAAKEKTV KKETKVKPEDKKEEKEKPKKEVAKK EDKTPIKKEEKPKKEEVKKEVKKEIK KEEKKEPKKEVKKETPPKEVKKEVK KEEKKEVKKEEKEPKKEIKKLPKDAK KSSTPLSEAKKPAALPKVPKKEESV KKDSVAAGKPKKEGKIKVIKKEGKAA EAVAAA VGTGATTA AVMAAAGIAAIG PAKELEAERSLMSSPEDLT KDFEEL KAEVDVT KD IKPQLELIEDEEKLKE TEPVEAYVIQKEREVT KGAESPDEG ITTTEGECEQTPEELEPV EKQGV D DIEKFEDEGAGFEESSETGDYEEKA ETEEAEEPEEDGEEHVCSASKHSP TEDEESAKAEADAYIREKRESVASGD DRAEEDMDEAIEKGEAEQSEEEADE EDKAEDAREEEYEPEKMEAEDYVM AVVDKAAEAGGAEQYGF LTTPTKQ LGAQSPGREPASSIHDETLPGGSESE ATASDEENREDQPEEFTATSGYTQS TIEISSEPTMDEMSTPRDVMSDET NNEETESPSQEFVNITKYESSLYSQE YSKPADVTPLNGFSEGSKTDATDGK DYNASASTISPPSSMEEDKFSRSALR DAYCSEVKASTTLDIKDSISAVSSEK VSPSKSPSLSPSPSPLEKTPLGERS VNFSLTPNEIKVSAEAEVAPVSPEVT QEVVEHCASPEDKTLEVVSPSQSV TGSAGHTPYYSPTDEKSSHLPTTEVI EKPPAVPVSFEFSDAKDENERASVS PMDEPVPDSESPIEKVLSP LRSPLI GSESAYESFLSADDKASGRGAESPF EEKSGKQGS PDQVSPVSEMTSTSLY QDKQEGKSTDFAPIKEDFGQEKKTD DVEAMSSQPALALDERKLG DVSP TQ IDVSQFGSFKEDTKMSISEGTVSDKS ATPVDEGVAEDTYSHMEGVASVSTA

SVATSSFPEPTDDVSPSLHAEVGS  
HSTEVDSDLVSVVQTPPTTFQETEM  
SPSKEECPRPMSISPPDFSPKTA  
TPVQDHRSEQSSMSIEFGQESPEQ  
LAMDFSRQSPDHPTVGAGVLHITEN  
GPTFVDYSPSDMQDSSLHKIPPME  
EPSYTQDNDLSELISVQVEASPSTS  
SAHTPSQIASPLQEDTLDVAPPRD  
MSLYASLTSEKVQSLGEKLSPKSDI  
SPLTPRESSPLYSPTFSDSTSAVKEK  
TATCHSSSSPPIDAASAEPYGFRA  
LFDTMQHHLALNRDLSTPGLEKDS  
GGKTPGDFSYAYQKPEETTRSPDEE  
DYDYESYEKTRTSDVGGYIEKIER  
TTKSPSDSGYSYETIGKTTKTPEDGD  
YSYIEKTRTPEEGGYSYDISEKTT  
SPPEVSGYSYEKTERSRRLLDDISNG  
YDSEDGGHTLGDPSYSYETTEKITS  
FPESEGYSYETSTKTTRTPDTSTYCY  
ETAEKITRTPQASTYSYETSDLCYTAE  
KKSPSEARQVDLCLVSSCEYKHPK  
TELSPSFINPNLEWFASEEPTEESE  
KPLTQSGGAPPPGGKQGRQCDDET  
PPTSVESAPSQTDSVPPETECCPS  
ITADANIDSEDESETIPTDKTVYKH  
MDPPPAPVQDRSPSPRHPDVSMVD  
PEALAEQNLGKALKKDLKEKTKKK  
PGTKTKSSSPVKKSDGSKPLAASPK  
PAGLKESDKVSRVASPKKESVEK  
AAKPTTTPEVKAARGEKDKETKNA  
ANASAKSAKTATAGPGTTKTKSSA  
VPPGLPVYLDLCYIPNHSNSKNVDV  
EFFKRVRSYVVVSGNDPAAEPSR  
AVLDALLEGKAQWGSNMQVTLIPTH  
DSEVMREWYQETHEKQDLNIMVL  
ASSSTVVMQDESFPACKIEL