

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P15205	MAP1B_RAT	Rattus norvegicus	Microtubule-associated protein 1B	25.149868	NaN	S336;S339;S341;S343;T527;S541;S544;S561;S614;S821;S824;S825;S881;S884;T892;T901;S929;S930;T941;S956;S963;S985;S988;S1009;S1148;S1150;S1180;S1183;S1201;S1204;S1205;S1239;S1244;S1248;S1250;S1252;S1254;S1257;S1268;S1272;T1274;S1291;S1305;S1315;S1317;S1319;T1321;S1323;S1332;S1369;S1371;S1380;S1382;S1389;S1393;S1401;T1403;S1420;S1436;S1494;S1505;S1513;S1515;T1518;S1520;S1611;S1613;S1618;S1646;S1656;S1659;S1683;S1765;S1772;S1775;S1778;T1781;S1785;S1786;T1789;S1790;S1794;S1812;S1870;S1874;S1908;S1912;T1925;S1932;T1942;S2027;S2202;S2264;S2282;T2298;S2407	8647865;18683930;15340146	MATVVVEATEPEPSGSIGNPAATTSP SLSHRFLDSKFYLLVVVGETVTEEHL RRAIGNIELGIRSWDTNLIECNLDQE LKLFSRHSARFSPEVPGQKILHHS DVLETVVLINPSDEAVSTEVRLMITD AARHKLLVLTGQCFENTGELILQSG SFSFQNFIEIFTDQEIGELLSTTHPA NKASLTLCPEEGDWKNSNLDHRN LQDFINIKLNSASILPEMEGLSEFTE YLSSESVEVPSFPDILEPPTSGGFLKLS KPCCYIFPGGRGDSALFAVNGFNML INGGSRKSCFWKLIRHLDRVDSILL THIGDDNLPGINSMLQRKIAELEEE RSQGSTSNSDWMKNLISPDLGVVFL NVPENLKNPEPNIKMKRSTEEACFT LQYLNKLSMKPEPLFRSVGNAIEPVI LFQKMGVKGLEMYVLPVKSSEKEM QYFMQQWTGTNKDKAELILPNGQE VDIPISYLTSSVSLIVWHPANPAEKII RVLFPGNSTQYNILEGLEKCLKHLDLFL KQPLATQKDLTGQVSTPPVKQVKLK QRADSRESLKPATKPLSSKSVRKESK EEAPEATKASQVEKTPKVESKEKVIV KKDKPGKVESKPSVTEKEVPSKEEQ SPVKAEVAEKAATESKPKVTKDKVV KKEIKTKPEEKKEEKPKKEVAKKEDK TPLKKDEKPKKEEAKKEIKKEIKKEE KKELKKEVKKETPLKDAKKEVKKDE KKEVKKEEKPKKEIKKISKDIKKSTP LSDTKKPAALKPKVAKKEEPTKKEPI AAGKCLKDKGKVKVIKKEGKTTEAAAT AVGTAAVAAAAGVAASGPAKELEAE RSLMSSPEDLTKDFEELKAAEIDVAK DIKPQLELIEDEEKLKETEPGEAYVIQ KETEVS KGSAESPDEGITTTEGEGEC EQTPEELEPVEKQGVDDIEKFEDEG AGFEESSEAGDYEEKAETEEAEEPE EDGEDNVSGSASKHSPTEDDEEIIAKA EADVHIKEKRESVASGDDRAEEDMD EALEKGEAEQSEEEGEEEDKAEDA REEDHEPDKTEAEDYVMAVVDKAA EAGVTEDQYGFLGTPAKQPGVQSPS REPASSIHDETLPGGSESEATASDEE NREDQPEEFTATSGYTQSTIEISSEP TPMDEMSTPRDVMSDETNNETES PSQEFVNITKYESSLYSQEYSKPVVA SFNGLSDGSKTDATDGRDYNASAST ISPPSSMEEDKFSKSALRDAYRPEET DVKTGAELDIKDVSDERLSPAKSPSL SPSPPSPIEKTPLGERSVNFSLTPNEI KASAEGEATAVVSPGVTQAVVEEHC ASPEEKTLEVVSQSVTGSAGHTPY

YQSPTDEKSSHLPTTEVTEKPAVAVPV
FETFEAKDENERSSISPMDEPVPDS
ESPIEKVLSPLRSPPLIGSEAYEDFL
SADDKALGRRSESPFEGKNGKQGF
DKESPVSDLTSDLYQDKQEEKSAGFI
PIKEDFSPEKKASDAEIMSSQSALAL
DERKLGGDGSPTQVDVSQFGSFKED
TKMSISEGTVSDKSATPVDEGVAED
TYSHMEGVASVSTASVATSSFPPTT
DDVSPSLHAEVGSVPHSTEVDDSLSV
SVVQTPPTTFQETEMSPSKEECPRPM
SISPPDFSPKTAKSRTPVQDHRSEQS
SMSIEFGQESPEHSLAMDFSRQSPD
HPTVGAGMLHITENGPTEVDYSPSD
IQDSSLSHKIPTEEPSYTQDNDLSE
LISVSQVEASPSTSSAHTPSQIASPLQ
EDTLSDVVPPRDMSLYASLASEKVQ
SLEGEKLSPKSDISPLTPRESSPTYSP
GFSDDSTSGAKESTAAYQTSSSPIDA
AAAEPYGFRRSMLFDTMQHHLALS
RDLTSSVEKDNGGKTPGDFNYAYQ
KPESTTESPDEEDYDYESHEKTIQAH
DVGYYEKTERTIKSPCDSGYSYETI
EKTTKTPEDGGYSCEITEKTRTPEE
GGYSYEISEKTRTPEVSGYTYEKTE
RSRRLDDISNGYDDTEDGGHTLGD
CSYSYETTEKITSFPESESYSYETTTK
TTRSPDTSAYCYETMEKITKTPQAST
YSYETSDRCYTPERKSPSEARQDVDL
CLVSSCEFHKHPKTELSPSFINPNPLE
WFAGEEPTEESEKPLTQSGGAPPPS
GGKQQRQCDETPPTSVMSESAPSQT
DSDVPPETECCPSITADANIDSEDES
ETIPTDKTVTYKHMDPPPAPMQDRS
PSPRHPDVSMVDPEALAEQNLGKA
LKKDLKEKAKTKKPGTKTKSSSPVKK
GDGKSKPSAASPKPGALKESSDKVS
RVASPKKESVEKAMKTTTTTPEVKA
TRGEEKDKETKNAANASASKSVKTA
TAGPGTTKTAKSSTVPPGLPVYLDLC
YIPNHSNSKNVDVEFFKRVRSSYYV
VSGNDPAAEEPSRAVLDALEGKAQ
WGSNMQVTLIPTHDSEVMREWYQE
THEKQQDLNIMVLASSSTVVMQDES
FPACKIEL