

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasm meml
P34926	MAP1A_RAT	Rattus norvegicus	Microtubule-associated protein 1A	44.386008	NaN	S114;S117;S118;S121;S155;T177;S319;S322;S384;T504;S526;S527;S604;S611;S643;T663;S666;S677;S690;S785;S872;S875;S876;S889;T892;S894;S898;S907;S980;S990;S998;S1007;S1013;S1022;S1029;S1037;S1061;S1132;S1134;S1148;S1160;S1178;S1188;S1191;S1197;S1206;S1209;S1252;S1280;S1301;S1304;S1307;S1504;S1568;S1574;S1594;S1622;S1643;S1715;S1742;S1757;S1763;S1767;T1772;S1778;S1784;S1897;T1923;S1988;T2026;S2043;S2077;S2204;S2221;S2225;S2228;S2229;S2260;S2424;S2620;S2635	18683930;8647865;38843836	MDGVAEFSEYVSETVDVPSPFDDLE PPTSGGFLKLSKPCCYFFPGRGDSA LFAVNGFNILVDGGSDRRKSCFWKLV RHLDRIDSVLLTHIGADNLPINGLL QRKVALEEEEQSQGSSSYSDVWVKNL ISPGLGVVFFNVDPDKLRLPDASRKA RSIEEACLTLQHLNRLGQAEPLYRV VSNITIEPLTLFHKMGVGRLDMYVLN PVKDSKEMQFLMQKWAGNSKAKTG IVLANGKEAEISVPLYTSITALVWLP ANPTEKIVRVLPFGNAPQNKILEGLE KLRHLDFLRYPVATQKDLAAGAVPA NLKPSKIKHRADSKESLKAAPKTAVS KLAKREEVLEEGAKEARSELAKELA KTEKKAKEPSEKPPPEKPSKSERVRG ESSEALKAERRLIKDKAGKKHLKE KISKLEEKDKKKEIKKERKELKKE EGRKEEKDAKDEKRRDKTKPEVKK LSKPDLPFTPEVRKTLTKAKAPGRV KVDKGRAARGEKELSSSEPRTPPAQK GAAPPAVSGHRELALSSPEDLTQD FEELKREERGLLAEQORDTGLGEKPL PADATEQGHPSAAIQVTQPSGPVLE GEHVEREKEVVPDSPGDKGSTNRGP DSGAEVEKEKETWEERKQREAEALGP ENTAAREESEAEVKEDVIEKALEE MEETHPSDEEGEETKAESFYQKHTQ EALKASPKSREALGGRDLGFOGKAP EKETASFLSSLATPAGATEHVSIQD ETIPGYSETEQTSDEEIHDEPDERPA PPRFPTSTYDLSGPEGPGPEASQAA DSAVPASSSKTYGAPETELTYPPNMV AAPLAEEHVSSATSITECDKLSSFA TSVAEDQSVASLTAPQTEETGKSSLL LDTVTSIPSSRTEATQGLDYVPSAGTI SPTSSLEEDKGFKSPCEDFSVTGES EKKGETVGRGLSGEKAVGKEEKYVV TSEKLSGQYAAVFGAPGHTLPPGEP ALGEVEERCLSPDDSTVKMASPPPS GPPSAAHTPFHQSPVEDKSEPRDFQ EDSWGETHKHSFGVSKEDSEEQTVKP GPEETS EEGKGPTRSPQAQDMPV SIAGGTGCTIQLLPEQDKAIVFETG EAGSNLGAGTLPGEVRTSTEATEP QKDEVLRFTDQSLSPEDAESLSVLSV VSPDITKQEAATPRSPCSLKEQPPHK DLWPMVSPEDTQSLSFSEESPSKET SLDISSKQLSPESLGTLOFGELNLGK EERGPVMKAEDDSCHLAPVSIPEPH RATVSPSTDETPAGTLPGGSFHSAL SVDRKHSPGEITGPGGHFMTSDSSL TKSPELSSPAMEDLAVEWEGKAPG KEKEPELKSETRQKQKQILPEKVAVV EQDLIIHQKDGALDEENKPGRQDDK TPEQKGRDLDEKDTAAELDKGPEPK EKDLREDQQRAGPPAEKDKASE QRDTDLQQTQATEPRDRAQERRDSE EKDKSLELRDRTPPEEKDRILVQEDR APEHSIPEPTQTDRAPRDKGTDDEKE QKEEASEEKEQVLEQKDWALGKEG ETLDQEAETAEQKDETLKEDKTQGG KSSFVEDKTTTSKETVLDQKSAEKA DSVEQDGAALKETRALGLEESPAE GSKAREQEKKYWKEDVQVQGWRET SPTRGEPVGGQKEPVPWEGKSPEQ EVRYWRDRDITLQQDAYWRELSADR KVWFPHELDGQGARPRYCEERESTF LDEGPDEQEITPLQHTPRSPWTSDF KDFQELPQKGLVERWLAESPVGL PPEEDKLTRSPFEIISPPASPPMETG QRVPSAPGQESVVPDTESTAPMRNE PTTPSWLAEIPWVVKDRPLPPAPLS PAPAPPTPAPEPHTPVPPVSWGLAEYD SVVAAVQEGAALEGGPYSPLGKDY RKAEGERECEGGAGAPDSSSFSPKV PEAGESLATRDTEQTEPEQREPTYPY DERSFQYADIYEQMMLTGLGPACPT REPPLGASGDWPHLSTKEEAAGCN TSAEKETSSPASPQNLQSDTPAFSYA SLAGPAVPPRQEPDGPVNEPSITPP	True	False	4.688	3.622	2.81	2.548	1.974	2.261

AVPPRAPISLSKDLSPPLNGSTVSCS  
PDRRTPSPKETGRGHWDDGTNDSD  
LEKGAREQPEKETRSPSPHHPMPM  
GHSSLWPETEAYSSLSSDSLGSVR  
PSLDFPASAFGFSSLQFAPPQLPSPA  
EPRSAPCGSLAFSGDRALALVPGTPT  
RTRHDEYLEVTKAPSLDSSLPQLPSP  
SSPGGLLSNLPRPASPALSEGSSSE  
ATTPVISSVAERFPPGLEAAEQSAEG  
LGSGKESAAHSLWDLTPLSPAPSAS  
LDLAPAPAPAPAPAGLPGDLGDGTL  
PCRPECTGELTKKPSFPLSPSGDHEA  
NGPGETSLNPPGFVTATAEKEEAEA  
PHAWERGSWPEGAERSRPDTLLSS  
EQPLRPGKSSGGPPCSLSSEVEAGP  
QGCATDPRPHCGELSPSFLNPPLPP  
STDDSDLSTEERLAGKGGRRRVGR  
PGATGGPCMADETPPTSASDSGSS  
QSDSDVPPETECCPSITAEALDSDE  
DGDFLPVDKAGGVSGTHHPRPGHD  
PPPTLPDPRPSPRPDVCMADEPEG  
LSSESGRVERLREKGRPRRAPGRA  
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VYVDLAYIPNHCSGKTADQFFRRV  
RASYYVVSNDPANGEPSRAVLDAL  
LEGKAQWGENLQVTLPHTHTEVTR  
EWYQQTHEQQQLNLVLAASSSTV  
VMQDESFPACKIEF