

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane
Q9QYR6	MAP1A_MOUSE	Mus musculus	Microtubule-associated protein 1A	35.313349	NaN	S114;S117;S118;S121;S155;T177;S319;S322;S384;T504;S526;S527;S604;S611;T633;S644;S667;S678;S786;S873;S876;S877;S890;T893;S895;S899;S908;S981;S991;S999;S1008;S1014;S1023;S1062;T1068;S1131;S1133;S1147;S1159;S1177;S1187;S1190;S1196;S1205;S1208;S1251;S1289;S1310;S1313;S1316;S1516;S1580;S1606;S1634;S1648;S1720;S1747;S1762;S1768;S1772;T1777;S1783;S1789;S1902;T1928;S1993;T2031;S2048;S2082;S2209;S2226;S2230;S2233;S2234;S2425;S2623;S2637	35822049;22645316	MDGVAEFSEYVSETVDVPSPFDDLE PPTSGGFLKLSKPCCYIFPFGGRGDSA LFAVNGFNILVDGGSDRRCFKWKL RHLDRIDSVLLTHIGADNLPINGLL QRKVAEEEEQSQGSSSYSDWVKNL ISPGLGVVFFNVDPDKRLRDPASRKA RSIEEACLTQLHLNRLGIAEPLYRV VSNTIEPLTLFHKMGVGRDMDMYLN PVKDSKEMQFLMQKWAGNSKAKTG IVLANGKEAEISVPYLTISITAVVWLP ANPTEKIVRVLPFGNAPQNKILEGLE KLRHLDFLRYPVATQKDLAAGAVPA NLKPSKIKHRADSKESLKAAPKTAM SKLAKREEVLEEGAKEARSELAKEL AKSEKKAKEPSEKPEKPSKPERVRT ESSEALKAEKRKLIKDKVGGKHLKE KISKLEEKRDKEKKEIKKERKELKE EGRKEEKDAKKDEKRDTKPELKK FSKPDLPFTPEVRKTYLAKAPGRL KVDKGRAARGEKELSSPRTPPAQK GAAPPPAASGHRELALSSPEDLTQD FEELKREERGLLAEPDTELGEKPLP ADASEQGRPSTAIQVTOPPASVLEQE QVEREKVVPDFPEDKGSKNRAPDS GAEVEREKETWEERKPREAELTPEN IAAAREESEPEVKEDVIEKAELEEME EVHPSDEEEETKAESFYQKHMQE ALKVIPKGREALGGRELGFQKKAPE KETASFLSSLATPAGAAEHVSIQIDE TIPGYSETEQTSDEEIHDEPDERPAP PRFPSTYDLGSGPEGPGPFASQSAE SAVPASSKTYGAPETELTYPPNMVA APLAEHVVSSATSITECDKLSFAT SVAEDQSVASLTAPQTEETGKSSLLL DTVTSIPSSRTEATQGLDYVPSAGTIS PTSSLEEDKGFKSPCEDFSVTGESE KKGESVGRGLTGEKAVGKEEKNVTT SEKLSSQYAAVFGAPGHALHPGEP LGEVEERCLSPDDSTVKMASPPPSG PPSAAHTPFHQSPVEEKSEPDFQE DSWGDTKHAPGVSKEDAEEQTVKP GPEEAMSEEGKVLRSRSPQAQDTLG SLAGGQTGCTIQLLPEQDKAVVFET GEAGAASGAGSLPGEVVRTQEPAPQ KDELLGFTDQSFSPEDAESLVSLSV SPDTAKQEATPRSPCTPKEQLHKD LWPMVSPEDTQSLFSFSESPSKETS LDISSKQLSPESLGTQLQFGLSLGKE EKGPLVKAEDNSCHLAPVSIPEPHTA TVSPPTDEAAGEAGLTDESPAGNLP GSSFHSHALS GDRKHSPGEITGPGG HFMTSDSSLTKSPESLSPAMEDLA MEWGGKAPGSEDRATEQKEKELER KSETLQKQDQILSEKAALVQRDSVM HQKDEALDEENKPGGQDQKTSEOK GRDLDKKDTAVELGKGPPEPKGDLY LEDQGLAEKDKALEQRGAALQQTQA PEPRARAQEHDRDLQKDEHLELRDK TPEEKDKVLVLEDRAPEHIIPQPTQT DRAPEHRKVDKEQKDEASEEKEQV LEQKDWAREKEGAALDQDNRAAGQ KDGTLKEDKTQGQKSSFLEDKSTTP KEMTLQKSPEKAKGVEQQDQAVP EKTRALGLEESPEEKGKAREQEEKY WKEQDVVQGWRETSPTTRGEPVPAW EGKSPEQEVRYWRDRDITLQQDAY WKELSCERKVVFPHELDGQGARPR YSEERESTFLDEGPNEQETPLQHTP RSPWASDFKDFQEPPLPQKGLVER WLAESPVGLPPEEDKLTRSPFEIHS PPASPPMETGQRVPSAPGQESVPPD TKSTPPTRNEPTTPSWLAEIPWVPK DRPLPAPLSPAPAPPTPAPDPHAPA PFSWGIAEYDSVVAAVQEGAALEG GPYSPLGKDYRKAEGERE GEGGAGA PDSSSFSSKVPVETESHTRDAEQTE PEQREPTYPDERSFYADIYEQMM LTGLGPACPTREPLGASGDWPPHL STKEEAAGRNKSAEKELSSAVSPPN LHSDTPTFSYASLAPGPTIPRQPEPEP	None	None	None	None	None	None	None	

GPNVEPSFTPPAVPPRAPSISLSDPS  
PPLNGSTTSCGPDRTTPSPKEAGRS  
HWDDGTNDSLEKGAPEKQETQ  
SPSPHHMPVGHPSLWPETAHSSL  
SSDSHLGPVRPSLDFPASAFGFSLQ  
PAPPQLSPAEPSPAPCGSLAFSGDR  
ALALVPGTPTRTRHDEYLVTKAPSL  
DSSLPLQLPSPSSPGAPLLSNLPRPAS  
PALSEGSSSEATTPVISSVAERFPPGL  
EVAEQSSGELGPGNEPAAHSLWDLT  
PLSPAPLASRDLAPAPAPAPAPSLPG  
NLGDGTLSCRPECSGELTKKPSFSL  
HSGDHEANGPGETSLNPPGFATATA  
EKEEAEALHAWERGSWPEGAERSS  
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PPLPSTDDSDLSTEERLAGKGGRR  
RRAGRPGATGGPCPMADETPPTSAS  
DSGSSQSDSDVPEETECPSTAEAA  
LSDDEDGDFLPVDKAGVSGTHHPR  
PGHDPPPAPLPDPRPPPPRPDVCMA  
DPEGLSSESGRVERLREKVQGRPGR  
KAPGRAKSPARRLDIRGKRSPTPG  
KGPVDRTSRALPRRSTPSQVTSEEK  
DGHSPMSKGLVNLKAGSTALGSK  
GSSGPPVYVDLAYIPNHCSGKTADQ  
DFFRRVRASYVVSGNDPANGEPSR  
AVLDALLEGKAQWGENLQVTLIPTH  
DTEVTREWYQQTHEQQQLNLVVL  
ASSSTVVMQDESFPACKIEF