

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P78559	MAP1A_HUMAN	Homo sapiens	Microtubule-associated protein 1A	11.071134	T873;S874;S877;S878;T2221	S114;S117;S118;S121;S155;T177;S319;S322;S384;T504;S526;S527;S605;S612;T616;S644;S667;S787;S874;S877;S878;S891;T894;S896;S900;S909;S986;S996;S1004;S1013;S1019;S1029;S1069;S1144;S1146;S1160;S1172;S1190;S1200;S1203;S1209;S1218;S1221;S1264;S1326;S1329;S1544;S1600;S1626;S1654;S1675;S1749;S1762;S1776;S1791;S1797;S1801;S1812;S1818;S1931;T1957;S2022;T2058;S2074;S2104;S2106;S2108;S2235;S2252;S2256;S2259;S2260;S2449;S2649;S2664	30379171;35132862;28657654	MDGVAEFSEYVSETVDVPSPFDLLE PPTSGGFLKLSKPCCYIFPGGRGDSA LFAVNGFNILVDGGSDRKSCFWKLV RHLDRIDSVLLTHIGADNLPINGLL QRKVAELEEEEQSGSSSYSDWVKNL ISPELGVVFFNVPEKLRLPDASRKAK RSIEEACLTLQHLNRLGIQAEPLYRV VSNITIEPLTLFHKMGVGRDMMYLV PVKDSKEMQFLMQKWAGNSKAKTG IVL.PNGKEAEISVPLYTSITALVWVLP ANPTEKIVRVLPFGNAPQNKILEGLE KLRHLDLFLRYPVATQKDLASGAVPT NLKPSKIKQRADSKESLKATTKTAVS KLAKREEVVEEGAKEARSELAKELA KTEKKAKESSEKPEKPAKPERVKTE SSEALKAEKRKLIKDKVGGKHLKEKI SKLEEKDKKEKKEIKKERKELKKDE GRKEEKDAKKEEKRKDTKPELKKI SKPDLKPFTEVVRKTLTKAKVPRVK IDRSRAIRGEKELSSPEQTPPAQKGT VPLPTISGHRELVLSSPEDLTQDFEE MKREERALLAEQRDTGLGDKPFPLD TAEEGPPSTAIQGTTPPSVPLGQEEH VMKEKELVPEVPVEEQGSKDRGLDSG AETEEKDTWEEKKQREARLPDRT EAREESEPEVKEDVIEKAELEEMEE VHPSDEEEEDATKAEGFYQKHMQE PLKVTPRSREAFGGRELGLQGKAP KETSFLSSLTTPAGATEHVSYIQDE TIPGYSETEQTISDEEIHDEPEERPAP PRFHTSTYDLPGPEGAGPFEASQPA DSAVPATSGKVYGTPELTYPTNIV AAPLAEEHVSSATSITECDKLSSFA TVAEDQSVASLTAPQTEETGKSSLL LDTVTSIPSSRTEATQGLDYVPSAGTI SPTSSLEEDKGFKSPCEDFSVTGES EKRGEEIIGKGLSGERAVEEEEEETAN VEMSEKLCQYGTVPVFSAPGHALHP GEPALGEAEERCLSPDDSTVKMASP PPSGPPSATHTPFHQSPVEEKSEPEQ DFQEADSWGDTKRTPGVGKEDAAE ETVKPGPEEGTLEKEEKVPPRSPQA QEAPVNIDEGLTGCTIQLLPAQDKAI VFEIMEAGEPTGPILGAEALPGLLRT LPQEPGKPKQKDEVLRYPDRSLSPED AESLSVLSVPSPTANQEPTPKSPCG LTEQYLHKDRWPEVSPEDTQSLSL EESPSKETS LDVSSKQLSPESLGTLO FGELNLGKEEMGHLMQAEDTSHHT APMSVPEPHAATASPPTDGTTRYSA QTDITDDSLDRKSPASSFSHSTPSGN GKYLPGAITSPEHILTPDSSFSKSPE SLPGPALEDIAIKWEDKVPGLKDRTS EQKKEPEPKDEVLQKDKTLEHKEV VEPKDTAIYQKDEALHVKNKAVKQO DKALEQKGRDLEQKDTALEQKDKAL EPKDKDLEEKDKALEQKDKIPEEKD KALEQKDTALEQKDKALEPKDKDLE QKDRVLEQKEKIPKDKALDQKVR SVEHKAPEDTVAEMKDRDLEQTDK

APEQKHQAQEQKDKVSEKKDQALE  
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LVQEGRAREQEEKYWRGQDVVQEW  
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RESTFLDEGPDDEQEVPLREHATRS  
PWASDFKDFQESSPQKLEVERWL  
AESPVGLPPEEEDKLTRSPFEIISPPA  
SPPEMVGQRVPSAPGQESPIPDPKL  
MPHMKNEPTTPSWLADIPPVWPKD  
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FSWGTAEYDSVVAVQEGAAELEGG  
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PEQREPTYPDERSFYADIYEQMM  
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GSSSEATTPVISSVAERFSPSLEAAE  
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QGCATEPRPHRGELSPSFLNPLPSS  
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SGAPVYVDLAYIPNHCSGKTADLDFP  
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DALLEGKAQWGENLQVTLIPTHDT  
VTREWYQQTHEQQQLNVLVLASS  
STVVMQDESFPACKIEF