

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P15146	MTAP2_RAT	Rattus norvegicus	Microtubule-associated protein 2	25.147692	NaN	S28;S37;S136;S140;S143;S221;S224;S285;S348;S478;S498;S522;S552;S598;S605;S610;S628;S728;S732;T736;S739;S741;T748;S825;S884;S893;S939;S1051;S1140;S1141;S1146;T1161;S1162;S1166;S1353;T1359;S1541;S1562;S1594;T1608;T1611;T1622;T1625;T1652;S1656;S1682;S1816;S1821;S1824;S1829;S1842;S319;S350;S382	17496889;19322778;18683930;15340146	MADERKDEGKAPHWTSASLTEAAA HPHSPKMDQGGSGEGLSRANGF PYREEEGAFGEHGSQGTYSDTKEN GINGELTSADRETAEEVSARIVQVVT AEAVAVLKGEQEKEAQHKDQPAALP LAAETVNLPPSPPPSPASEQFAALE EDLLTASKMEFPEQKQLPSSFAEPL DKEETEFKMQSKPGEDEFHAALVPQ PDTSKTPQDKKDPQDMEGKSPASP FAQTFGTNLEDIKQITEPSITVPSIGL SAEPLAPKDQKDWFIEMPVSESKKDE WGLAAPISPGPLTPMREKDVLEDIPR WEGKQFDSMPSPPFHGGSFPLPLDT VKDERVTEGSQPFAPVFFQSDDKMS LQDTSGSATSKESSKDEEPQKDKAD KVADVPVSEATTVLGDVHSPAVEGF VGENISGEEKGTTDQEKKETSTPSV QEPTLTETEPQTKLEETSKVSIETV AKEEESLKLKDDKAGVIQTSTEQSF KEDQKQEQETIEALKQDSFPISLEQA VTDAAMATKTLEKVTSEPEAVSEKR EIQGLFEEDIADKSKLEGAGSATVAE VEMPFYEDKSGMSKYFETSALKEDV TRSTGLGSDYYELSDSRGNAQESLD TVSPKNQQDEKELLAKASQPSPPAH EAGYSTLAQSYTSDHPSLPEEPSSP QERMFTIDPKVYGEKRDHLHKNKDD LTLRSRLGLGGRSAIEQRSMSINLPM SCLDSIALGFNFGRGHDLSPASDIL TNTSGSMDEGDDYLPPTTPAVEKIP CFPIESKEEEDKTEQAKVTGGQTTQ VETSSSEPFPAKEYKNGTVMAPDL PEMLDLAGTRSRLASVSADAEVARR KVPSEAVVAESSTGLPPVADDSQPV KPDSQLEDMGYCVFNKYTVPLPSPV QDSENLSGESGSFYEGTDDKVRDL ATDLSLIEVKLAAAGRVKDEFTEAKE ASPPSSADKSGLSREFDQDRKANDK LDTVLEKSEEHVDSKEHAKSEEVG DKVELFGLGVTYEQTSAKELITTKET APERAEKGLSSVPEVAEVETTTKADQ GLDVAACKDDQSPLDIKVSDFGQMA SGMSVDAGKTIELKFEVDQQLTLSS EAPQETDSFMGIESSHVKDGAKVSE TEVKEKVAKPDLVHQEAVDKESYE SSGEHESLTMESLKPDEGKETSPE TSLIQDEVALKLSVEIPCPPPSEADS SIDEKAEVQMEFIQLPKEESTETPDI PAIPSDVTQPQPEAVVSEPAEVRGEE EEIEAEGEYDKLLFRSDTLQITDLLV PGSREEFVETCPGEHKGVVESVVTIE DDFITVVQTTTDEGELGSHSVRFAAP VQPEEERRPYPHDEELEVLMAAEAQ AEPKDGSPDAPATPEKEEVPFSEYKT

ETYYDDYKDETTIDDSIMDADSLWVD
TQDDDRSILTEQLETIPKEERAEKEA
RRPSLEKHRKEKPFKTGRGRISTPER
REVAKKEPSTVSRDEVRRKKAVYKK
AELAKESEVQAHSPSRKLILKPAIKYT
RPTHLSVCVKRKTATSGESAQAPSAF
KQAKDKVTDGITKSPEKRSSLPRPSS
ILPPRRGVSGDRENSFSLNSSISSA
RRTRRSEPIRRAGKSGTSTPTTPGST
AITPGTPPSYSSRTPGTPGTPSYPRTP
GTPKSGILVPSEKKVAIIRTPPKSPAT
PKQLRLINQPLPDLKNVSKIGSTDN
IKYQPKGGQVRILNKKMDFSKVQSR
CGSKDNIKHSAGGGNVQIVTKKIDLS
HVTSKCGSLKNIRHRPGGGRVKIES
VKLDFKEKAQAKVGSLDNAHHVPG
GGNVKIDSQKLNFRREHAKARVDHG
AEIITQSPSRSSVASPRRLSNVSSSGS
INLLESPQLATLAEDVTAALAKQGL