

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q9UPN3	MACF1_HUMAN	Homo sapiens	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	9.865057	T542;S4324;T5621;S6545;T6715;T6717;T6777;S6786;T6791;S7222;S7225	S4;S35;S57;S280;S814;S1122;S1367;S1376;S2006;S2051;S2077;S3122;S3331;S3927;S4495;S4496;S4521;S4836;S4962;T5435;S5808;S6032;S6967;T7254;S7279;S7292;S7330;S7333	29351928;35254053;30379171;34725712	MSSSDEETLSERSCRSERSRSERSERSYRSERSGSLSPCPGDTLPWNLPLHEQKKRKSQDSVLDPAERAVVRVAEDRDRVQKKTFTKWVNKHLMKVRKHI NDLYEDLRDGHNLISLLEVLSGIKLP REKGRMRFHRLQNVQIALDFLKQR QVKLVNIRNDDITDGNPKLTLGLIWT IILHFQISDIYISGESGDMSAKEKLLL WTQKVTAGYTGIKCTNFSSCWSDGK MFNALIHRYRPDLVDMERVQIQSNR ENLEQAFEVAERLGVTRLLDAEDVD VPSPDEKSVITYVSSIYDAFPKVPEGG EGISATEVDSRWQEYQSRVDSLIPWI KOHTILMSDKTFPQNPVELKALYNQ YIHFKETEILAKEREKGRIEELYKLE VWIEFGRIKLPQGYHPNDVEEEWGK LIIEMLEREKSLRPAVERLELLIQIAN KIQNGALNCEEKLTAKNTLQADAA HLESGQPVCESDVIMYIQECEGLIR QLQVDLQILRDENYYQLEELAFRVM RLQDELVTLRLECTNLYRKGHFTSL ELVPPSTLTTTHLKAEP LTKATHSSS TSWFRKPMTRAE LVAISSSEDEGNL RFVYELLSWVEEMQMKLERA EWGN DLPSVELQLETQQHIHTSVEELGSSV KEARLYEGKMSQNFHTSYAETLGKLE ETQYCKLKETSSFRMRHLQSLHKFV SRATAELIWLNEKEEEEELAYD WSDN NSNISAKRNYFSELTMELEEKQDVF RSLQDTAELLSLENHPAKQTVEAYS AAVQSQLQWMKQLCVCVEQHVKEN TAYFQFFSDARELESFLRN LQDSIKR KYSCDHNTSLSRLEDLLQDSMDEKE QLIQSKSSVASLVGRSKTIVQLKPRS PDHVLKNTISVKAVCDYRQIEITICK NDECVLEDNSQRTKWKVISPTGNEA MVPSVCFLIPPPNKDAIEMASRVEQ SYQKVMALWHQLHVNTKSLISWNY LRKDDLVLVQTNLEKLRSSAPGECH QIMKNLQAHYEDFLQDSRDSVLF SV ADRLRLEEEVEACKARFQHLMKSM ENEDKEETVAKMYISELKNIRLRLEE YEQRVVKRIQSLASSRTDRDAWQDN ALRIAEQEHTQEDLQQLRSDLD AVS MKCDSFLHQSPSSSSVPTLRSELNL LVEKMDHVYGLSTVYLNK LKTVDVI VRSIQDAELLVKGYEIKLSQEEVLA DLSALEAHWSTLRHWLSDVKDKNS VFSVLDEEIAKAKVVAEQMSRLTPER NLDLERYQEKGSQ LQERWHRVIAQL EIRQSELESIQEVLGDYRACHGTLIK WIEETTAQQEMMKPGQAEDSRVLS EQLSQQTALFAEIERNQTKLDQCQK FSQOYSTIVKDYELQLMTYKAFVESQ QKSPGKRRRMLSSSDAITQEFMDLR TRYTALVTLTTQHVKYISDALRRLEE EEKVVEEEKQEHVEKVKELLGWVST LARNTQ GKATSSSETKESTDIEKAILE QQVLSEELTTKKEQVSEAIKTSQIFL AKHGHKLSEKEKKQISEQLNALNKA YHDLCDGSANQLQQLQSLAHQTE QKECRAVAGVIDLGTVEIFPIFKAMQ KGLLDQDTGLVLLESQVIMSGLIAPE TGENLSLEEGIARNLINPQMYQQLR

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								QPVHGDDLVMNLMDAHKVFQKEL GKRTGTVQLKRSGRELIENSRDDT TWVKGQLQELSTRWDTVCCLSVSK QSRLEQALKQAEVFRDTHVHMLLEW LSEAEQTLRFRGALPDDTEALQSLID THKEFMKKVEEKRVNNSAVAMGE VILAVCHPDCITTIKHWITIRARFEE VLTWAKQHQQRLETALSELVANAEL LEELLAWIQWAETTILIQRDQEPIQON IDRVKALIAEHQTFMEEMTRKQPDV DRVTKTYKRKNIEPTHAPFIEKSRSG GRKSLSQPTPPMPILSQSEAKNPRI NQLSARWQQVWLLALERQRKLNDA LDRLEELKEFANFDFDVWRKKYMR WMNHKKSVMDFFRIDKDQDGKI TRQEFIDGILASKFPPTKLEMTAVAD IFDRDGDGYIDYEFVAALHPNKDAY RPTTDADKIEDEVTRQVAQCKCAKR FQVEQIGENKYRFGDSQQRLRLVRLR STVMVRVGGGWMALDEFVLKNDPC RARGRTNIELREKFILPEGASQGMTP FRSRGRRSKPSSRAASPTRSSSSASQ SNHSCTSMPPSPATPASGTKVIPSSG SKLKRPTPTFHSSRTSLAGDTSNSSS PASTGAKTNRADPKKSASRPGSRAG SRAGSRASSRRGSDASDFDLETQS ACSDTSESSAAGGQNSRRGLNKPS KIPTMSKKTITASPRTPGPKR
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