

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitoch
Q9UPN3	MACF1_HUMAN	Homo sapiens	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/4/5	14.499112	T542;S4324;T4646;S4664;T5621;S6545;T6715;T6717;T6777;S6786;T6791;S6878;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;30379171;40596516;38665916;34725712;35254053;40914422;39302247;38253038	MSSSDEETLSERSCRSERSCRSERSYRSERSGSLSPCPPGDTLPWNLPLHEQKKRKSQDSVLDPAERAVRVAEDRDRVQKKTFTKWVNHKLMKVRKHI NDLYEDLRDGHNLISLLEVLVSGIKLP REKGRMRFRHLQNVQIALDFLKQR QVKLVNIRNDDITDGNPKLTLGLIWT ILHFQISDIYISGESGDMSAKEKLLL WTQKVTAGYTGIKCTNFSSCWSDGK MFNALIHRYRPDLVDMERVQIQSNR ENLEQAFEVAERLGVTRLLDAEDVD VPSPDEKSVITYVSSYDAFPKVPPEGG EGISATEVDSRWQEQYQSRVDSLIPWI KQHTILMSDKTFPQNPVELKALYNQ YIHFKETEILAKEREKGRIEELYKLE VWIEFGRIKLPQGYHPNDVEEHWGK LIEMLEREKSLRPAVERLELLLQIAN KIQNGALNCEEKLTAKNTLQADAA HLESGQPVOCESDVIMYIQECEGLIR QLQVDLQILRDENYQLEELAFRVM RLQDELVTLRLECTNLYRKGHFTSL ELVPPSTLTTTHLKAEP LTKATHSS TSWFRKPMTRAE LVAISSEDEGNL RFVYELLVWVEEMQMKLERAEWGN DLPVVELQLETQHHIHTSVEELGSSV KEARLYEGKMSQNFHTSYAETLGKL ETQYCKLKETSFRMRHLQSLHKFV SRATAELIWLNEKEEELAYDWSDN NSNISAKRNYFSELTMELEEKQDVF RSLQDTAELLLENHPAKQTV EAYS AAVQSQLQWМКQCLCVCVEHQVKEN TAYFQFFSDARELESFLRNLQDSIKR KYSCDHNTLSLRLEDLLQDSMDEKE QLIQSKSSVASLVGRSKTIVQLKPRS PDHVLKNTISVKA VCDYRQIEITICK NDECVLEDNSQRTKWKVISPTGNEA MVPSVCF LIPPNKDAIEMASRVEQ SYQVМALWHLHVNTKSLISWNY LRKDLDLVQTNWLEKLRSSAPGECH QIMKNLQAHYEDFLQDSRDSVLFV ADRLRLEEEVEACKARFQHLMKSM ENEDKEETVAKMYISELKNIRLLEE YEQRVVKRIQSLASSRTDRDAWQDN ALRIAEQEHTQEDLQQLRSDDLDAVS MKCDSFLHQSPSSSVPTLRSELNL LVEKMDHVYGLSTVYLNKLTVDVI VRSIQDAELLVKGYEIKLSQEEVVL DL SALEAHWSTLRHWLSDVKDKNS VFSVLDEEIAKAKVVAEQMSRLTPER NLDLERYQEKGSQ LQERWHRVIAQL EIROSELESIQEVLGDYRACHGTLIK WIEETTAQQEMMKPGQAEDSRVLS EQLSQQTALFAEIERNQTKLDQCCK FSQQYSTIVKDYELQLMTYKAFVESQ QKSPGKRRRMLSSSDAITQEFMDLR TRYTALVTLTTQHVKYISDALRRLEE EEKVVEEEKQEHVEKVKELGWVST LARNTQ GKATSSETKESTDIEKAILE QQVLSEELTTKKEQVSEAIKTSQIFL AKHGHLSEKEKKQISEQLNALNKA YHDLCDGSANLQQLQS QLAHQTE QKECRAVACVIDLGTVEIFPIFKAMQ KGLLDQDTGLVLESQVIMSGLIAPE TGENLSLEEGIARNLINPQMYQQLR ELQDALALISRLTESRGPLSVVEAIEK RIISETVGLKILEAHLATGGFSLSPSE NCINLEEA FHQGLISAWLHSVLESY LRTSKNLIDPNTAEKIGLLDLMQRCI VHQESGFKLLPVKQLAGGMVSLKSG RKVSIFRAVQEG LIDRQVTVRLEAQ LFAGGIVDPRTGHRLTVEEAVRHNL DQDMACAILIRQLQTGGIHDVTGQR LTIDEAVSNDLVAAKIALVILESLWFS MGLLWPESGEILPITDALEQGVSTE LAHKILSNRQHIKALFLPATTEILSW KKAIESGILDRDLANNLKSICIPDVM PHMQLADSAEQNINPGAAVLPCKSKS HPKATASQSENLLFQLMTHSYINVQ NGORLLLDKELMETLTSRDEYQTS PPKVEIGHQRQKTPPELQESANVKI	False	True	3.241	2.101	1.99

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