	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
0	Q6ZMW3	EMAL6_HUMAN	Homo sapiens	Echinoderm microtubule-associated protein-like 6	20.148807	S1091;T1557	NaN	30379171;38253038	MADRTAPRCQLRLEWVYGYRGHQC RNNLYYTAGKEVVYFVAGVGVVYNT REHSQKFFLGHNDDIISLALHPDKT LVATGQVGKEPYICIWDSYNVQTVSL LKDVHTHGVACLAFDSDGQRLASVG LDAKNTVCIWDWRKGKLLASATGHS DRIFDISWDPYQPNRVVSCGVKHIKF WTLCGNALTAKRGIFGKTGDLQTILC LACAKEDITYSGALNGDIYVWKGLN LVRTIQGAHSAGIFSMYACEEGFATG GRDGCIRLWDTDFKPITKIDLRETEQ GYKGLSIRSVCWKADRLLAGTQDSEI FEVIVRERDKPMLILQGHCEGELWA LALHPKKPLAVTGSDDRSVRLWSLA DHALIARCNMEEAVRSVAFSPDGSQ LALGMKDGSFIVLRVRDMTEVVHIK DRKEVIHEMKFSPDGSYLAVGSNDG PVDVYAVAQRYKKIGECSKSLSFITHI DWSLDSKYLQTNDGAGERLFYRMP SGKPLTSKEEIKGIPWASWTCVKGPE VSGIWPKYTEVTDINSVDANYNSSVL VSGDDFGLVKLFKFPCLKRGAKFRK YVGHSAHVTNVRWSHDFQWVLSTG GADHSVFQWRFIPEGVSNGMLETAP QEGGADSYSEESDSDLSDVPELDSD IEQEAQINYDRQVYKEDLPQLKQQS KEKNHAVPFLKREKAPEDSLKLQFI HGYRGYDCRNNLFYTQAGEVVYHIA AVAVVYNRQQHSQRLYLGHDDDILS LTIHPVKDYVATGQVGRDAAIHVWD TQTLKCLSLLKGQHQRGVCALDFSA DGKCLVSVGLDDFHSIVFWDWKKG EKIATTRGHKDKIFVVKCNPHHVDK LVTVGIKHIKFWQQAGGGFTSKRGT FGSVGKLETMMCVSYGRMEDLVFS GAATGDIFIWKDILLLKTVKAHDGPV FAMYALDKGFVTGGKDGIVELWDD MFERCLKTYAIKRSALSTSSKGLLLE DNPSIRAITLGHGHILVGTKNGEILEI DKSGPMTLLVQGHMEGEVWGLAAH PLLPICATVSDDKTLRIWELSAQHR MLAVRKLKKGGRCCAFSPDGKALAV GLNDGSFLVVNADTVEDMVSFHHR KEMISDIKFSKDTGKYLAVASHDNF VDIYNVLTSKRVGICKGASSYITHID WDSRGKLLQVNSGAREQLFFEAPR GKRHIIRPSEIEKIEWDTWTCVLGPT CEGIWPAHSDITDVNAASLTKDCSLL ATGDDFGFVKLFSYPVKGQHARFKK YVGHSAHVTNVRWLHNDSVLLTVG GADTALMIWTREFVGTQESKLVDSE ESDTDVEEDGGYDSDVAREKAIDYT TKIYAVSIREMEGTKPHQQLKEVSVE ERPPVSRAAPQPEKLQKNNITKKKK LVEELALDHVFGYRGFDCRNNLHYL NDGADIIFHTAAAGIVQNLSTGSQSF YLEHTDDILCLTVNQHPKYRNVVAT SQIGTTPSIHIWDAMTKHTLSMLRC FHSKGVNYINFSATGKLLVSVGVDP EHTITVWRWQEGAKVASRGGHLERI FVVEFRPDSDTQFVSVGVKHMKFW TLAGSALLYKKGVIGSLGAAKMQTM LSVAFGANNLTFTGAINGDVYVWKD HFLIRLVAKAHTGPVFTMYTTLRDGL IVTGGKERPTKEGGAVKLWDQEMK RCRAFQLETGQLVECVRSVCRGKGK ILVGTKDGEIIEVGEKNAASNILIDGH MEGEIWGLATHPSKDLFISASNDGT ARIWDLADKKLLNKVSLGHAARCAA YSPDGEMVAIGMKNGEFVILLVNSL KVWGKKRDRKSAIQDIRISPDNRFLA VGSSEHTVDFYDLTQGTNLNRIGYC KDIPSFVIQMDFSADGKYIQVSTGAY KRQVHEVPLGKQVTEAVVIEKITWAS WTSVLGDEVIGIWPRNADKADVNCA CVTHAGLNIVTGDDFGLVKLFDFPC TEKFAKHKRYFGHSAHVTNIRFSYD DKYVVSTGGDDCSVFVWRCL	None	None	None	None	None	None	None	None	None