

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q6ZU64	CFA65_HUMAN	Homo sapiens	Cilia- and flagella-associated protein 65	23.497111	T588	NaN	39302247;30379171	MFTLTGCRLEVKTKQVENPSVSFAS SFPLIPLLLRGRKSVQKKQAESKQIK LHTQSAPFGLCPKDMMLTQAPSSVV RSRNSRNHTVNSGGSCLSASTVAIP AINDSSAAMSACSTISAQPASSMDT QMHSPKKQERVNKRVIWIEVAEEL HWKGWELGKETTRNLVVKNSRLKL QKMKYRPPKTKFFFTVIPQIFLSPGI TLTLPIVFRPLEAKEYMDQLWFKA EGMFCVGLRATLPCRHLCRPPSLQ LPMCAVGDTEAFFCLDNVGDLPF FTWFEFSSPFQMLPATGLLEPGQASQ IKVTFQPLTAVIYEQATCWYGAGSR QRSSIQLAQAVAKCAQLLVSIKHKCPE DQDAEGFQKLLYFGSVAVGCTSERQ IRLHNPSAVNAPFRIEISPEDEAEDQ AFSCPTAHGIVLPGKCKVSVFFHPK TLDTRTVDYCSIMPSGCASKTLLKVV GFCRGPVSLQHYCVNFSWVNLGE RSEQLWIENQSDCTAHFQFAIDCL ESVFTIRPAFGTLVKGARMTLHCAF QPTHPIICFRRVACLIIHQDPLFLDL MGTCHSDSTKPAILKQHLTWYRTH LARGTLTYPPDILDAMLKEKKLAQD QNGALMIPIQDLEMPAPQYPIPP MTEFFFDGTSDFITFPPPISEVPEVD FGACPGPEAPNPVPLCLMNHKTGKI MVVWTRRSDCPFWVTPESCDVPPL KSMAMRLHFQPPHPNCLYVLEA FAIKVLQSYSNIEEDCTMCPSWCLT VRARGHSYFAGFEHHPQYSLDVPK LFPVAVSSGEPYRSLLLVKNKDKLLT FSLAPQRGSDVILRPTSGLVAPGAHQ IILICTYPEGSSWKQHTFYLCNASP QYLKEVSMYSREEPLQLKLDTHKSL YFKPTWVGCSSTSPFTFRNPSRLPL QFEWRVSEQHRKLLAVQPSRGLIQP NERLTLTWTFSPLEETKYLFOVGMW VWEAGLSPNANPAATTHYMLRLVG VGLTSSLSAKEKELAFGNLVNSKQ SRFLVLLNDGNCTLYRRLYLEQGGP EAVDNHPLALQDRTEGSMPPRSQ DTICLTACPKQRSQYSWTTITYSLLSH RDNKAGEKQELCCVSLVAVYPLLSIL DVSSMGSAEGITRKHWRFLSLDLL NSYLERDPTPCELTYKVPTRHSMSQI PPVLTPLRLDFNFGAAPFKAPPSVVF LALKNSGVVSLDWAFLLPSDQRIDV ELWAEQAEINSTEHLQMRVQDNCL FSISPKAGSLSPGQEQMVLYKSHLF IGTDHLPVLFKVSHGRELINFIGVT VKPEQKYVHFTSTTHQFIPIGDITLP PRQIYELYNGGVPVTYEVQTDVLSQ VQEKNFDPHPCCLNPKGEIQGST ARVLWIFSPIEAKTYTVDVPIHILGW NSALIHFGQVGYNPHMMGDTAPFH NISSWDNSSIHSRLVVPQNVFLSQ SHISLGNIPVQSKSRLLFLNNISKN EEIAFSWQPSPLDFGEVSVSPMIGVV APEETVPFVVTLRASVHASFYADLV CKLYSQQLMRQYHKELQEWKDEKV ROEVEFTITDMKVKKRTCTACEPA RKYKTLPPKNOQSVSRPASWKLQT PKEEVSWPQPSPGMLCLGLTAR AHATDYFLANFFSEFPCHFLHRELP KRKAPREESSETSEKSPNKWGPVSK QKKQLLVDLTTHIRGLLEDKNFHEA VDQSLVEQVYFRQFWNEQSTKFM DQKNSLYLMPILVPSSSWEDGK GK QPKEDRPEHYPLGKKEEGEEKGE EEEEEEEEEEEEEEEEELGKEEI EKEEERDEKKEKVSAGIGPTQP ESQESMQWQWQQQLNVMVKEEQE QDEKEAIRRLPAFANLQEALENMI QNILVEASRGEVLTSRPRVIALPPF CVPRSLTPDILLPTQAEVLHPVPL PTDLP	False	False	1.031	1.537	1.677	0.512	False	3.597	0.328