

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q8VDR9	DOCK6_MOUSE	Mus musculus	Dedicator of cytokinesis protein 6	33.453389	T16	S178;S870;S878;S882;S1341;T2064;S2065;S2069	36084651	MAASERRAFAHKINRTVAAEVRKQV SRERSGSPHSSRRSSSSSLGVPLTEVI EPLDFEDVLLSRPPEVEPEGPLRDLIE FPVDDLELLKQPRECRRTESGVPEDE GQLDAQVRAAVEMYSIEDWVIVRRRY QHLSTAYSPITTETQREWQKGLTCQ VFEQDTPGDERTGPEVDVDDPQHCS GSPEDTPRSSGASGIFSLRNLAADSL LPTLLEQAAPEDVDRRNEALRRQHR APTLTLYPAPDEDEAVERCSRPEPP REHFGQRILVKCLSLKFEIEIEPIFGT LALYDVREKKKISENFYFDLNSDSVK GLLRAHGTHPAISTLARSATFSVTYPS PDIFLVVLEKVLQGGDISECCPEPYM VMKEADTAKNKEKLEKLRLAEEQFC TRLGRYRMPFAWTAVHLANIVSRPQ DRDSDEGERRPTWAERRRRGPDQ RGYSGDDACSFSSFRPATLTVTNFF KQEAERLSEDLFKFLADMRRPSSL LRLRPVTAQLKLDISPAPENLHFCL SPDLLHVKPYDPRGRPTKEILEFPA REVVAPHSCYRNLLFVYPSLNFSS RQGSVRNLAVRIQYMAGEDQSQALP VIFGKSSCSEFTREAFTPVVYHNKSP EFYEEFKRLRPACVTENHHLFFTFY HVSCQPRPGTALETPVGFTWIPLLQ HGRLRTGPFCLPVSVDQPPSYSVLT PDVALPGRWVDGHKGVFSVELTA VSSVHPQDPHLDKFFTLVHVLEEGI FPPRLKETVLESGTMEQELRASLAA LRLASPEPLVAFSHLVLKLVRLVVR PPICGQMVNLGRGAFEMAHVASL VHRNLEAVQDSRGHCPLASVHYA FRLPGGDLSPGEAPPATVQAATLAR GSGRPASLYLARSKISSSNPD LAVV PGSVDDVSRILASKGVDRSHSWVN SAYAPGGSKAVLRRVPPYCGADPRQ LLHEELALQWVSGSAVRELVLQHA WFFFQLMVKSMELHLLGQRLDTP RKLRFPGRFLDDIAALVASVGLVIT RVHKDMKLAERLNASLAFFLSDLLS IADRGYIFSLVRAHYQVATRLQASAP NPTALLTLMDFTRILCSHEHYVTL NLPCCPLSPPASPSVSTTSQSST FSSQAPDPKVTSMFELSGPFRQHF LSGLLLTELALALDPEAEGASLLHKK AISAVHSLLCSDVDVSRYAEATVKAK VAELYPLLSLARDTLPLQHGFAEGS GORSRLASMLDSDTEGEGDIGSTIN PSVAMAAGGPLAPGSRTSISQGPST AARSGCPLSAESSRLLVCVLWVWK NAEPTLLQRWAADLALPQLGRLLDL LYLCLAAFYKGGKAFERINSLTFKK SLDMKARLEAILGTIGARQEMVRR SRERSPFCNQENVRWRKSATHWRQ TSDRVDTKDEMEHEALVDGNLAT EASLVLDLTLTIVQTVMLSEARES LSAVLVVLYSLGSAQSALFLQHGGLA TQRALVSKFPPELLFEEDTEL CADLCL RLLRHCGSRISTIRMHASASLYLLMR QNFEIGHNFARVKMLVTMSLSLVG TTQNFSEHLRKSLLTILTYAEDIG LRDSTFAEQVQDLMFNLHMILTDTV KMKEHQEDPEMLMDLMIYRIARGYQ GSPDLRLTWLQNMAGKHAELGNHA EAAQCMVHAAALVAEYLALLEDSRH LPVGCVSFQNVSSNVLEESAISDDIL SPDEEGFCSGKNFTLGLVGLLEQA AGYFTMGGLYEAVNEVYKNLPILEA HRDYKLAAVHGKLEAFTKIMHQ SGWERVFGTYFRVGFYGRFGDLDE QEFVYKEPSITKLAEISHRLEEFYTER FGDDVVEIKDSNPVDSKSLDPQKAY IQITYVEPHFDTYELKDRVTFDRNY GLRAFLFCTPFTPDGRAHGELAEQ KRKTLTSTEHAFPIKTRIRVCHREE TVLTPVEVAIEDMQKKTRELAFAEQ DPPDAKMLQMVLGSGVPTVNGQP LEVAQVFLSEIPEDPKLFRHNNKRL CFKDFCKCEDALRNKALIGPDQK	None	None	None	None	None	None	None		

