	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi appara
0	Q9Y5S2	MRCKB_HUMAN	Homo sapiens	Serine/threonine-protein kinase MRCK beta	12.324105	S414	S221;S233;T239;T423;T954;S1680;S1682;S1686;S1690;S1693	37217939;38253038;38665916	MSAKVRLKKLEQLLLDGPWRNESAL SVETLLDVLVCLYTECSHSALRRDKY VAEFLEWAKPFTQLVKEMQLHRED FEIIKVIGRGAFGEVAVVKMKNTERI YAMKILNKWEMLKRAETACFREER DVLVNGDCQWITALHYAFQDENHL YLVMDYYVGGDLLTLLSKFEDKLPE DMARFYIGEMVLAIDSIHQLHYVHR DIKPDNVLLDVNGHIRLADFGSCLK MNDDGTVQSSVAVGTPDYISPEILQA MEDGMGKYGPECDWWSLGVCMYE MLYGETPFYAESLVETYGKIMNHEE RFQFPSHVTDVSEEAKDLIQRLICSR ERRLGQNGIEDFKKHAFFEGLNWE NIRNLEAPYIPDVSSPSDTSNFDVDD DVLRNTEILPPGSHTGFSGLHLPFIG FTFTTESCFSDRGSLKSIMQSNTLTK DEDVQRDLEHSLQMEAYERRIRRLE QEKLELSRKLQESTQTVQSLHGSSR ALSNSNRDKEIKKLNEEIERLKNKIA DSNRLERQLEDTVALRQEREDSTQR LRGLEKQHRVVRQEKEELHKQLVEA SERLKSQAKELKDAHQQRKLALQEF SELNERMAELRAQKQKVSRQLRDK EEEMEVATQKVDAMRQEMRRAEKL RKELEAQLDDAVAEASKERKLREHS ENFCKQMESELEALKVKQGGRGAG ATLEHQQEISKIKSELEKKVLFYEEE LVRREASHVLEVKNVKKEVHDSESH QLALQKEILMLKDKLEKSKRERHNE MEEAVGTIKDKYERERAMLFDENKK LTAENEKLCSFVDKLTAQNRQLEDE LQDLAAKKESVAHWEAQIAEIIQWV SDEKDARGYLQALASKMTEELEALR SSSLGSRTLDPLWKVRRSQKLDMSA RLELQSALEAEIRAKQLVQEELRKVK DANLTLESKLKDSEAKNRELLEEME ILKKKMEEKFRADTGLKLPDFQDSIF EYFNTAPLAHDLTFRTSSASEQETQ APKPEASPSMSVAASEQQEDMARPP QRPSAVPLPTTQALALAGPKPKAHQ FSIKSFSSPTQCSHCTSLMVGLIRQG YACEVCSFACHVSCKDGAPQVCPIPP EQSKRPLGVDVQRGIGTAYKGHVKV PKPTGVKKGWQRAYAVVCDCKLFLY DLPEGKSTQPGVIASQVLDLRDDEFS VSSVLASDVIHATRRDIPCIFRVTASL LGAPSKTSSLLILTENENEKRKWVGI LEGLQSILHKNRLRNQVVHVPLEAY DSSLPLIKAILTAAIVDADRIAVGLEE GLYVIEVTRDVIVRAADCKKVHQIEL APREKIVILLCGRNHHVHLYPWSSL DGAEGSFDIKLPETKGCQLMATATL KRNSGTCLFVAVKRLILCYEIQRTKP FHRKFNEIVAPGSVQCLAVLRDRLC VGYPSGFCLLSIQGDGQPLNLVNPN DPSLAFLSQQSFDALCAVELESEEYL LCFSHMGLYVDPQGRRARAQELMW PAAPVACSCSPTHVTVYSEYGVDVFD VRTMEWVQTIGLRRIRPLNSEGTLN LLNCEPPRLIYFKSKFSGAVLNVPDT SDNSKKQMLRTRSKRRFVFKVPEEE RLQQRREMLRDPELRSKMISNPTNF NHVAHMGPGDGMQVLMDLPLSAV PPSQEERPGPAPTNLARQPPSRNKP YISWPSSGGSEPSVTVPLRSMSDPD QDFDKEPDSDSTKHSTPSNSSNPSG PPSPNSPHRSQLPLEGLEQPACDT	True	False	4.19	1.373	0.903	0.639	0.846