	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	Q7Z5N4	SDK1_HUMAN	Homo sapiens	Protein sidekick-1	21.909316	S2176;T2187	NaN	39531497;37217939	MARGARPSAAGGGGGGAEPPERAG PGRPRGSPPGRARPSLAPRPGPEPSR PRAAPETSGGDTAGAGRCGGRRAAK LGPGRRGWWALLALQLHLLRALAQ DDVAPYFKTEPGLPQIHLEGNRLVLT CLAEGSWPLEFKWMRDDSELTTYSS EYKYIIPSLQKLDAGFYRCVVRNRMG ALLQRKSEVQVAYMGSFMDTDQRK TVSQGRAAILNLLPITSYPRPQVTWF REGHKIIPSNRIAITLENQLVILATTT SDAGAYYVQAVNEKNGENKTSPFIH LSIARDVGTPETMAPTIVVPPGNRSV VAGSSETTLECIASARPVEDLSVTWK RNGVRITSGLHSFGRRLTISNPTSAD TGPYVCEAALPGSAFEPARATAFLFII EPPYFTAEPESRISAEVEETVDIGCQ AMGVPLPTLQWYKDAISISRLQNPRY KVLASGGLRIQKLRPEDSGIFQCFAS NEGGEIQTHTYLDVTNIAPVFTQRPV DTTVTDGMTAILRCEVSGAPKPAITW KRENHILASGSVRIPRFMLLESGGL QIAPVFIQDAGNYTCYAANTEGSLNA SATLTVWNRTSIVHPPEDHVVIKGTT ATLHCGATHDPRVSLRYVWKKDNV ALTPSSTSRIVVEKDGSLLISQTWSG DIGDYSCEIVSEGGNDSRMARLEVIE LPHSPQNLLVSPNSSHSHAVVLSWV RPFDGNSPILYYIVELSENNSPWKVH LSNVGPEMTGVTVSGLTPARTYQFR VCAVNEVGRGQYSAETSRLMLPEEP PSAPPKNIVASGRTNQSIMVQWQPP PETEHNGVLRGYILRYRLAGLPGEYQ QRNITSPEVNYCLVTDLIIWTQYEIQ VAAYNGAGLGVFSRAVTEYTLQGVP TAPPQNVQTEAVNSTTIQFLWNPPP QQFINGINQGYKLLAWPADAPEAVT VVTIAPDFHGVHHGHITNLKKFTAYF TSVLCFTTPGDGPPSTPQLVWTQED KPGAVGHLSFTEILDTSLKVSWQEPL EKNGIITGYQISWEVYGRNDSRLTHT LNSTTHEYKIQGLSSLTTYTIDVAAVT AVGTGLVTSSTISSGVPPDLPGAPSN LVISNISPRSATLQFRPGYDGKTSISR WIVEGQVGAIGDEEEWVTLYEEENE PDAQMLEIPNLTPYTHYRFRMKQVN IVGPSPYSPSSRVIQTLQAPPDVAPTS VTVRTASETSLRLRWVPLPDSQYNG NPESVGYRIKYWRSDLQSSAVAQVV SDRLEREFTIEELEEWMEYELQMQA FNAVGAGPWSEVVRGRTRESVPSAA PENVSAEAVSSTQILLTWTSVPEQD QNGLILGYKILFRAKDLDPEPRSHIV RGNHTQSALLAGLRKFVLYELQVLA FTRIGNGVPSTPLILERTKDDAPGPP VRLVFPEVRLTSVRIVWQPPEEPNGI ILGYQIAYRLASSSPHTFTTVEVGATV RQFTATDLAPESAYIFRLSAKTRQGW GEPLEATVITTEKRERPAPPRELLVP QAEVTARSLRLQWVPGSDGASPIRY FTMQVRELPRGEWQTYSSSISHEAT ACVVDRLRPFTSYKLRLKATNDIGDS DFSSETEAVTTLQDVPGEPPGSVSAT PHTTSSVLIQWQPPRDESLNGLLQG YRIYYRELEYEAGSGTEAKTLKNPIAL HAELTAQSSFKTVNSSSTSTMCELT HLKKYRRYEVIMTAYNIIGESPASAP VEVFVGEAAPAMAPQNVQVTPLTAS QLEVTWDPPPPESQNGNIQGYKIYY WEADSQNETEKMKVLFLPEPVVRLK NLTSHTKYLVSISAFNAAGDGPKSDP QQGRTHQAAPGAPSFLAFSEITSTTL NVSWGEPAAANGILQGYRVVYEPLA PVQGVSKVVTVEVRGNWQRWLKVR DLTKGVTYFFRVQARTITYGPELQAN ITAGPAEGSPGSPRDVLVTKSASELT LQWTEGHSGDTPTTGYVIEARPSDE GLWDMFVKDIPRSATSYTLSLDKLR QGVTYEFRVVAVNEAGYGEPSNPST AVSAQVEAPFYEEWWFLLVMALSSL	False	False	2.53	1.306	0.188	0.188	False	4.346	0.234

								IVILLVVFALVLHGQNKKYKNCSTGK GISTMEESVTLDNGGFAALELSSRH LNVKSTFSKKNGTRSPPRPSPGGLH YSDEDICNKYNGAVLTESVSLKEKSA DASESEATDSDYEDALPKHSFVNHY MSDPTYYNSWKRRAQGRAPAPHRY EAVAGSEAGAQLHPVITTQSAGGVYT PAGPGARTPLTGFSSFV									