	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	extracellu region
0	Q03016	GIP3_YEAST	Saccharomyces cerevisiae	GLC7-interacting protein 3	24.475439	NaN	S68;T99;S103;S143;S260;T264;S269	33229814	MITNTEFDVPVDWLYKGKSRRKTNT KPSRPSTSPASSSSTSSSKNGDNSTS GNRSSNDKPRARSSSVSNAALCNTE KPDLKRNDGNTSASDTDNIPLLTPIN SGNRSDSADIDNPATVDAIDLIDNDD NGSSTQFVRKKRSTSISNAVVSSKPR LASSAINATASSSVGKGKHPPISSPS NATLKRSNSTSGEKTKRSIFGSLFSK RSTSSSASTAKKPLPVVNTSTTENES GGIKAVATPDPRVKEISSPMRGVAPT ASKPQTPILPSPALAVKDLSTVSLKR VSFAVDKFESDPPQQLPSRTPKKGNI LIPDDMISEVPSISVGISSSNQSAKST NSNIKGPLYTKKSKEYILALENQKLA LREAAKHQQEAHFAANRIAFEVANF KTASDAGGKLTEKSSEGTITKQREEV SPPNVEADRELENNKLAENLSKAGI DKPIHMHEHYFKEPDQDKYQDGHSI ENNEVTLDVIYTRCCHLREILPIPSTL RQVKDKTAPLQILKFLNPKPTLIDILS FCDFITIAPIHTIVFDNVALNQDMFRI IISALVNSTVLDKLSLRNVRIDQDGW KLLCKFLLLNKSLNKLDISQTKIKSD LAESLYRHNMDWNLFTDVLSQRSH KPIEELLFNGIQFSKIPYSCFARLLTS FATQKNFPESGIRLGLAGATTSNISQ DCLKFIFNWMSQYNVQGVDLAFND LSTMIKPMVGKLSALSYDNLRYFILN STNISTSYDLALLLKYLSKLPNLIFLD LSNLSQCFPDILPYMYKYLPRFPNLK RIHLDSNNLTLKELAVVCNILIKCKS LSHVSMTNQNVENFYLMNGTDSPV QQTNTDGDLDSSSTLDVKGQFAKNS FSSTLYAFARDSPNLIGLDFDYDLISE EIQSRIALCLMRNMKRTMDSTFQLD ELDSQDDLLFDGSLVTMTAESVLEK LNLLSDKSTKVKKDTTKRYLLKKYIE KFHILHHNVQHTIDTMFEKRKSGEL PLQEKENLVRLLLLEQNLCNILELFS HNPNLNDVLGSSRDDSKESVDSSE DSKLPALKHVESGYHVPEEKIQPEN DVITARPHLMATDSGKTIDVFTGKPL VFKHTSSSTSVGCKKQEEEEGELHK WGFFVQQQRSLYPENESTRQTPFAS GDTPINTETAGKSTSSPSVSTSNNET ATTSLFSPANPKILPKIPSGAVLRSAI MKAKGIDSIDDLIQNVNSNNIELENI YGESIQNSASTFTPGVDSDVSAPNTD KGSVETLPAVSTDDPNCEVKVTATY DKLLNNLSMERSIRL	None	None	None	None	None	None	None	None	None