	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	ex re
0	Q03833	GIS1_YEAST	Saccharomyces cerevisiae	Transcriptional activator/repressor GIS1	24.475439	NaN	S70;S343;S690;S694;S696;S734;S747	33229814	MEIKPVEVIDGVPVFKPSMMEFANF QYFIDEITKFGIENGIVKVIPPKEWLE LLEGSPPAESLKTIQLDSPIQQQAKR WDKHENGVFSIENEYDNKSYNLTQ WKNLAESLDSRISQGDFNDKTLKEN CRVDSQQDCYDLAQLQILESDFWKT IAFSKPFYAVDENSSIFPYDLTLWNL NNLPDSINSSNRRLLTGQSKCIFPW HLDEQNKCSINYLHFGAPKQWYSIP SANTDQFLKILSKEPSSNKENCPAFI RHQNIITSPDFLRKNNIKFNRVVQF QHEFIITFPYCMYSGFNYGYNFGESI EFILDQQAVVRKQPLKCGCGNKKEE RKSGPFSNLSYDSNESEQRGSITDN DNDLFQKVRSFDELLNHSSQELQN LEDNKNPLFSNINMNRPQSSSLRST TPNGVNQFLNMNQTTISRISSPLLSR MMDLSNIVEPTLDDPGSKFKRKVLT PQLPQMNIPSNSSNFGTPSLTNTNS LLSNITATSTNPSTTTNGSQNHNNV NANGINTSAAASINNNISSTNNSAN NSSSNNNVSTVPSSMMHSSTLNGT SGLGGDNDDNMLALSLATLANSAT ASPRLTLPPLSSPMNPNGHTSYNGN MMNNNSGNGSNGSNSYSNGVTTA AATTTSAPHNLSIVSPNPTYSPNPLS LYLTNSKNPLNSGLAPLSPSTSNIPF LKRNNVVTLNISREASKSPISSFVND YRSPLGVSNPLMYSSTINDYSNGTGI RQNSNNINPLDAGPSFSPLHKKPKIL NGNDNSNLDSNNFDYSFTGNKQES NPSILNNNTNNNDNYRTSSMNNN GNNYQAHSSKFGENEVIMSDHGKIY ICRECNRQFSSGHHLTRHKKSVHSG EKPHSCPRCGKRFKRRDHVLQHLN KKIPCTQEMENTKLAES	None	None	None	None	None	None	None	None	No