

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P32862	RGT1_YEAST	Saccharomyces cerevisiae	Glucose transport transcription regulator RGT1	9.365641	NaN	S202;S205;S208;S229;S283;S284;S410;S414;S1130	33229814	MNELNTVSTNSSDSTKNGGTSNSP DDMDSAAAASHAIKKRTKASRACDQ CRKKKIKCDYKDEKGVCSNCQRNG DRCSFDRVPLKRGPSKGYTRSTSHP RTNEIQDHNNRSYNTFDNSNNTL NNNTGNSGDNGINSNTVPSTPSRS NSVLLPPLTQYIPQAGGIPPSFQNP QSTMPAGNIGQQQFWKVPYHEFQH QRKGSIDSLQSDISVRTLNPNEQLSY NTVQOSPITNKHTNDSGNANGSVT GSGSASGSGGYWSFIRTSGLLAPTD DHNGEQTRRSSIPSLLRNTSNLLLL GGQPQLPPPQQSQPQAHQQKLQQ GQNLYSYSQFSQQQPYNPSISSFGQ FAANGFHSRQGSVASEAMSPSAPA MFTSTSTNPVNVAQQTQRPOGQOV PQFSELGDKRRQSAPVSVTLSTD RLNGNENNNGEINNNNGSNNSGS SKDTSQHSQESVTPAALASSPGST PQRSTKKRRKSYVSKKTKPKRDS ITSKDSAHPMTTSSTIAYGQISVDLI DTYYEFIHVGFPIIPLNKTTLSDLLL VNTQPISNIHEVNSYVILWFRNSLEL LVRVALKQKPGGKFFDNIVGVALSPS NDNNKAGFTTATARDDAEKTRRDS HNEVQDTLEVQSVFIAALNECFQKI VDIHPKFRENNDQISPKIKVIYLSFI LLNYILAFVGYDNSFVLGMSVTIFNE FKLYKLLLFPEPDINDVKPPVDEEVS TGNGNTKTSEFEIGSESAGHMNPSN SPNSMDENISHYSVLFKRLYLVSFV DSLQSCAFGGPKLLNISIQGSTERFF SNDLGSKWCLEQSQLRLKSVLQSLK LGELMSELTRNRISMNGNRKPGFDI TNSSSLLSEYVETQPLSVAQLFCKLL IGKHNFINCLLSLYDSEAGVYSDTL DLSSKIADSLCSLISILQVLTILRLN PTNSIDFNYPNPPANNPTVQEGP SAMGSSPVAGNLSAAPPSEGNPDFY KKLLGLKQDTGTILSDLCRGIISPF AILHEVYNITELVKQMPTSLISIMMT ATTTQNTQDTKKSQDLVMKLSNSM NEVVQITSVLTMIKPFKIFEHELNKPI MSLTGGLSSTTRNDVMWPKSGOGL RESSVMKTLDERRTSGTQPTTAPV AAEPRLENVALENFVSIGWKLDD SELGWY