

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extrac region
P14922	CYC8_YEAST	Saccharomyces cerevisiae	General transcriptional corepressor CYC8	24.475439	NaN	S429;T475;S710;S741;S768;S815;S817;S866;S943	33229814	MNPGGEQTIMEQPAQQQQQQQQQ QQQQQQAAVPPQPLDPLTQSTAET WLSIASLAETLGDGDRAAMAYDATL QFNPSAKALTSLAHLYRSRDMFQR AAELYERALLVNPPELSDVWATLGH YLMDDDLQRAYNAYQQALYHLSNP NVPKLWHGIGLYDRYGSGLDYAEAF AKVLELDPHFEKANEIYFRLGIIYKH QGWKSWALECFRYILPQPAPLQEW DIWFQLGSVLESMGEWQGAKEAYE HVLAQNQHAKVLQQLGCLYGMNS VQFYDPQKALDYLLKSLPADPSDATT WYHLGRVHMIRTDYTAAYDAFQQAV NRDSRNPIFWCSIGVLYYQISQYRDA LDAYTRAIRLNPYISEVWYDLGLTYE TCNNQLSDALDAYKQAARLDVNNV HIRERLEALTKLENPGNINKSNGA PTNASPAPPVILQPTLQPNQGNPL NTRISAQSANATASMVQQQHPAQ TPINSSATMYSNGASPOLQAQAQA AQAQAQAQAQAQAQAQAQAQAQA AQAQAQAQAQAQAQAQAQAQAQA AQAQAQAQAQAQAQAQAQAQAQA QQQQQQQQQQQQQQQQQQQQQ QQQQQQQQQQQQQQQQQQQQQ QQLQKGVSVQMLNPQQGQPYITQ PTVIQAHLQPFSTQAMEHPQSSQL PPQQQLQSVQHPQQLGQPQAQA PQLIQHNVEQNVLPRKRYMEGAIH TLVDAVSSSTHTENNTKSPRQPTH AIPTQAPATGITNAEPQVKKQLNSP NSNINKLVNTATSIENAKSEVSNQ SPAVVESNTNNTSQEEKPVKANSIP SVIGAQEPPEASPAEEATKAASVSP STKPLNTEPESSSVQPTVSESSTTK ANDQSTAETIELSTATVPAEASPVED EVRQHSKEENGTEASAPSTEEAEP AASRDAEKQQDETAATTITVIKPTLE TMETVKEEAKMREEEQTSQEKSPQ ENTLPRENVVRQVEEDENYDD	None	None	None	None	None	None	None	None	

0