	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	P38198	STU1_YEAST	Saccharomyces cerevisiae	Protein STU1	24.475439	NaN	S997;S1018;T1047;S1063;S1167	33229814	MSSFNNETNNNSNTNTHPDDSFPL YTVFKDESVPIEEKMALLTRFKGHV KKELVNESSIQAYFAALLFISGHYAY RSYPRLIFLSHSSLCYLIKRVAMQSP VQFNDTLVEQLLNHLIFELPNEKKF WLASIKAIEAIYLVNPSKIQAILANFL RRPSENQNGDYLNRIKSTLLTIDELI QINEKNNSNHLQLLRFFMLSFTNLL NNNLNEHANDDNNNVIIELIFDIMY KYLKMDDENSQDLIDGFINDLEVEK FKQKFISLAKSQDQHGSQEDKSTLF DEEYEFQLLLAEAKLPQLSNNLSSK DPAMKKNYESLNQLQQDLENLLAP FQSVKETEQNWKLRQSNIIELDNIIS GNIPKDNPEEFVTVIKEVQLIELISRA TSSLRTTLSLTALLFLKRLIHILNDQL PLSILDQIFVIFKNLLSSTKKISSQTAF HCLITLIIDINHFHNKLFQLSFLLINE KTVTPRFCSAILLRSFLIKFNDSNLSL NNSNTTSPTSKLENNIIYIEEWLKKG ISDSQTTVREAMRLTFWYFYKCYPT NAKRLLSSSFSPQLKKATELAIPAHL NINYQVSRVSSTASASSATSRLYSHS SNNSSRKTSLLEQKRNYPSYAQPTQ SSSTSLLNAPAVTAGGSVIASKLSNK LKTNLRSTSEYSSKENEKRARHHDS MNSVSNSNTKDNNNVTKRKVSAPP SSTAATKVSENYTNFDDFPSNQIDLT DELSNSYSNPLIKKYMDKNDVSMSS SPISLKGSNKLGEYETLYKKFNDASF PAQIKDALQYLQKELLLTSQQSSSAP KFEFPMIMKKLRQIMIKSPNDFKPF LSIEKFTNGVPLNYLIELYSINSFDYA EILKNRMNPEKPYELTNLIITIADLFN FLNANNCPNDFKLYYMKYKTTFFNY NFKLLLEIFRNLNIKHDNTLRSGTN DLMPKISMILFQIYGKEFDYTCYFNL IFEIYKFDNNRFNKLLADFDIVSTKM KICHELEKKDANFKVEDIISRESSVS FTPIDNKKSEGDEESDDAVDENDVK KCMEMTMINPFKNLETDKTLELKN NVGKRTSSTDSVVIHDDNDKDKKLS EMTKIVSVYQLDQPNPAKEEDDIDM ENSQKSDLNLSEIFQNSGENTERKL KDDNEPTVKFSTDPPKIINEPEKLIG NGNENEKPDLETMSPIKINGDENM GQKQRITVKRERDVALTEQDINSKK MKLVNNKKSEKMHLLIMDNFPRDS LTVYEISHLLMVDSNGNTLMDFDVY FNHMSKAINRIKSGSFTMKHINYLIE PLITCFQNQKMTDWLTNENGFDEL LDVAIMLLKSTDDTPSIPSKISSKSIIL VHCLLVWKKFLNTLSENADDDGVS VRMCFEEVWEQILLMLNKFSDYGN EIYKLAQEFRDSLMLSHFFKKHSAT RILSMLVTEIQPDTAGVKETFLIETL WKMLQSPTICQQFKKSNISEIIQTMS YFIMGTDNTSWNFTSAVVLARCLRV LQTTPDYTEQETERLFDCLPKNVFK MIMFIASNE	None	None	None	None	None	None	None	None	None