

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	extracellular region
P34228	SEF1_YEAST	Saccharomyces cerevisiae	Putative transcription factor SEF1	24.475439	NaN	S8;S263;S806	33229814	MVKDNRDSDQDQDFSSAHMKRQP EQQQLQQHQFPSSKKQRISHHDDSH QINHRPVTSCTHCRQHKKICDASQN FPHPCSRCEKIGLHCEINPOFRPKK GSQQLLLRQDVDEIKSKLDTLLAND SVFVHLLQIQIPMGNSLLNKLNLHPT PTPGTIIPNPDSSPSSGSPSSAAQRD SKVSVQTYLSREPQLLQANQGSNTN KFKANNEASSHMTLRASSLAQDSK GLVATEPNKLPPLLNDALPNSNKE SLPPALQMAFYKNNSAGNTPNGPFS PIQKTYSPHTTSTTVTTTTNQPPFAA TSHVATNNNADRKTTPVVATTTTTP LLPSPHANVDEFVLGDISISIEKANR LHHIFVTRYLPYFPIMYSNNATELYS QSQLLFWTVMLTACLSDPEPTMYCK LSSLIKQLAIETCWIRTPRSTHISQAL LILCIWPLPNQKVLDDCSYRFVGLAK SLSYQLGLHRGEFISEFTRTQTSMP NAEKWRTRTWLGIFFAELCWASILG LPPTSQTDYLLEKALSCGDEESEED NNSIDNNNNDKRNKKDEPHVESK YKLPGSFRRLSLANFQAKLSHIIGS STSSPDGLLEPKYRAETLSILGKELD LLAKTLNFSQDDTVNIYFLYVCLTVC CFAFLPETPPTDQIPYVTEAYLTATKI VTLNLLLETHQLIELPIYIRQAATFS ALILFKLQLTPLLPKYFDSARQSVV TIHRLYRNQLTAWATSVENDISRTAS MLEKLNFLVIMHPEVFEEDGIISR MRSHLTGSLFYDLVWCVEARRRE MDPEYNKQALEKAAKRRKFSSNGIY NGTSSSTGGITDRKLYPLPLYNHISR DFETVTKITPSGTTVTLVPTKNALK QAEKLAKTNNGSDSGSIMEINGIPL SMLGETGSVKFQSLFANTSNNSNDY NNNRLLDASNDISIPSNYIPVASV PASNNNPQSTKVDYYSNGPSVIPDL SMKRSVSTPVNHFPASVPGLRNHPV GNLSNNVTLGIDHPIPREHSNLQNV TMNYYNQFSNANAIGRSQSSMSHS RTPAASKSNMMDLHVSVDPGSSK STAYPPLSLFSSKNDINSNKTNRQFS TGTNTVTSNFFQIDNENNKTPGN KLTDFFQQSAGWIEGNSSNDFF GWFDMNMEQGF	None	None	None	None	None	None	None		