	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	Q06337	EAF1_YEAST	Saccharomyces cerevisiae	Chromatin modification-related protein EAF1	24.475439	NaN	S841;T971	33229814	MSSRPSSAVPNSASLSEDQSSDRSK FPKADDLIDERDRKLTELYCVSRLNQ LLELTDENKLRKEIDAFLKKNDIRRG IRFDEASLPKLLHTAATPITKKKLKDV NLINVPNQRLSDSKMSRELPENSEN VSVKSESHFVPSHDNSIRENMMDS LRPAEKTGGMWNKRPLESTMGGEE ERHEKRQKMQSQSLESSNNSEMAS LPISPRPPVPNALAHYTYYENIEYPPA DPTEVQPAVKFKDPLIKNIMAKEIDT SDHYNENNVDALETVFLLMNDYIPS KIPQALPLAELKYMSQTLPLINLIPRA HKALTTNIINNALNEARITVVGSRIE ELRRLGLWSLRQPKRFIDPWKQHNT HQNILLEEAKWMQADFKEGHKYKV AICTAMAQAIKDYWTYGEICCVKRKT LLPGKENKLSDDGRISEKSGRPSDTS RNDSDISIAGKDDIGIIANVDDITEKE SAAANDNDENGKNEAGAKSDFDFA DGLLSQEGAHDQIISSIDTKLLLKKP SSSSEVVLIQHEVAASSALIETEESKK ELAPPFKLSIFVDELNTFEKTLIQDLP LYNGINEERPKKDDSLPFIPISKSVVS LDDNGFYKLLERQLIDEEPSISQLSK RRGMFYGNRRNHYLRPPAVPSLRYL QNRTPTIWLSEDDQELVKNINTYGY NWELISAHMTHRLTYSYLSNIERRT PWQCFERFVQLNERFNFSDLKGPR AHSAQQWLIEAHKFQQRQNRRISPL GVNTESIQRGHRRLRWASMFEAIRK CMKKRENTPRPNPTQPRKPLDCKN MKVPTPAEMSLLKAQRDEALRRDIQ LRRTVKNRLQQRQQQSQQAHSSRA QSPIPSNGKSSSNLARNGQASAPRP NQKQYTEQDIIESYSRKLLEQKPDIG PEMALKAAKNYYRTLREQQQQLKQ HQIQQQRQQLQEESSHVQQLQQLQ PGSQAPPPKSSPSQSSLSNISNINSA PRIKSPTPQEILQRFQKQ	None	None	None	None	None	None	None	None	None