	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	Q06836	SYT1_YEAST	Saccharomyces cerevisiae	Arf guanine nucleotide exchange factor SYT1	24.475439	NaN	T277;S369	33229814	MNQSISSLIKLKFLQSHSNDKNGNK KGGSNVSTGIDKLRESESYRSPFLQL AEIQEHTNNDDDKLDVKECEPTKKH SKLSRIRRKMGRLDLNFRSANEKGS EDDEILVAQHLRNGQDPEEMPFKSE NNIDSIEKVPKPDGERVTLTSSGSDN VKRNSKHAPFIPVKPALEKFPSSNRL SRDYRKSQEPTLFNGDRLVPTLPTVS RISTSSSVGSSTAASRYFNPSKRAVV ASSSSSSSSIKFNSLHAIPLDATPQIE LAKQQDEISKRRFGRRRSRTVDVFD YINKNNTAKNKPPLSPSSFIRTIDEK NTNSLMQDPMGSRGPLLPDDANIIS NDTDGAEASHPDHQVLSRSRSQSTS FVQGKGGKRKSIEDEGYHNKLGLPH GSGPTSVYNNKSNANSTITGMSRRS SSIVNALSSFVNLRSSSLSSSRQQHL QQQQQLQQKLDVSLEDLPPVPAPEF SDSCKDFLIKLAPYGKFIGIILTEKDD EFKKNCLNYLLTNCFEFKNDPLDIA LRKLLMFLELPKETQQIDRLIMAFSF AYYKAQKSYSKKKGIECPWSNADQV YFIAFSLLMLHTDYFNPNNKSKMTK HDFVDLVHNDKYSGGNEIPMAVLTY FYENVTAKESPKFNYFLMSPMALDD SILDKDAFDTNFAITLSSNSMYSPID MIKRGSIIPKEASLSPIFYPLTNSISAS GIAPSTAASCPPSTSGTINGANLGTA NSNSNRPASNSISSYFSYNPSSSSSG NATLVQDDINVYSHIINDTLNEVNLF PEVSKYWNKNALKANLLRNEEHKY EKYYSIMNDTKGGYLRFHKSQLNKL NLPNFEILNDNSRSGCKNSDYKYCK ILQMGAIMNLGMPSRKFSIVNSAKI HWKKEFAILTSLGLLICDKMDWINP QMMKDPKSGTTNYIIDFKSGFSFVP GSTIDVYNGLFADRERDSLGKSHFA SLVLAYTEHHSTGSHTSNTTAASSSA KHNEGVFEPSSDEEDSITNSTDGTS SVSNGESDNDSVSSSDNQLSSNDS NEDYHSIKDEYPIFEDENADCLLYLH TCHRNFIWKCANKYERDNWIDSINL FSAYDGCYVEIGSIANTICNKRKLTIL QRMERLRSIKSAKWEKLKKFESTLM LMGKCVPISTKTKTDMINRIRQLAVR MDWLIYEIKRSELFVSIIKEVTRKQA EKNILEHGKGEEEGQGNNDDSDGI DDIEESFLFNENSLQVCVSDSSYDE YSNE	None	None	None	None	None	None	None	None	None