

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
P13586	ATC1_YEAST	Saccharomyces cerevisiae	Calcium-transporting ATPase 1	26.164835	NaN	S227	38179648	MSDNPFNASLLDEDSNREREILDAT AEALSKPPSLEYCTLSVDEALEKLD TDKNGGLRSNEANNRRSLYGPNEI TVEDDESLFKKFLSNFIEDRMILLI GSAVVSFLFMGNIDDAVSIITLAIIVVT VGFVQEYRSEKSLEALNKLVPAECH LMRCGQESHVLASTLVPDGLVHFRI GDRIPADRIIEAIDLSDSENLTGEN EPVHKTSQTIEKSSFNDQPNISIVPIS ERSCIAYMGTLVKEGHGKIVVGTG TNTSFGAVFEMMNNIEKPKTLPQLT MDKLGKDLSLVSFIVIGMICLVGIIQ GRSWLEMFQISVSLAAIIEPEGLPIIV TVTLALGVLRMAKRKAIVRRLPSVET LGSVNVICSDKTGTLSNHMTVSKL WCLDSMSNKLNVLSLDKNKKTNS NGNLKNYLTEDVRETLTIGNLCNNA SFSQEHAIFLGNPTDVALLEQLANF EMPDIRNTVQKVQELPFNSKRKRLMA TKILNPVDNKCTVYVKGAFERILEYS TSYLKSKGKTEKLEAQKATINECA NSMASEGLRVFGFAKLTLSDSSTPL TEDLIKDLTFTGLIGMNDPPRPNVKF AIEQLQGGVHIIMITGSENTAVNI AKQIGIPVIDPKLSVLSGDKLDEMSE DQLANVIDHVNI FARATPEHKLNIVR ALRRGDVVAMTGDGVNDAPALKL SDIGVSMGRIGTDVAKEASDMVLT DDFSTILTAIEEGKIFNNIQNFLTF QLSTSVAALSLVALSTAFKLPNPLNA MQILWINILMDGPPAQSLGVEPVDH EVMKKPPRKRTDKILTHDVMKRLLT TAACIIVGTVYIFVKEMAEDGKV TAR DTTMTFTCFVFFDMFNALACRHNT KSIFEIGFFT NKMFN YAVGLSLLGQ MCAIYIPFFQSIFKTEKLGISDILLLL ISSSVFIVDELRLKLRKLNTRKNEEDSTY FSNV	None	None	None	None	None	None	None		

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