

UniprotKB ID	Entry name	organism	full name	oglcnaScore	oglcna sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
P38065	AP2A_YEAST	Saccharomyces cerevisiae	AP-2 complex subunit alpha	24.475439	NaN	T727;S733	33229814	MDRKKTLINSSVSNNNSTIKGLQLFI ADLRSAAQQAQEQEKRIQSEIVKIKQH FDAAKKKQGNHDLRGGYQRKKYVA KLAYIYTSNTTKLNEILFGLQTVEL LKSSIFSEKFIGYMTLELLYERSEVVA KVNDEVNYQLMKDLSSDDNFVML ALNFVGVVGGELTNRLAYNDDITTV FKILRSPTSSIYLKKSALSFLALLK NHSILTEDLQRKQLWQIRILSLDDT ENYRLTLATIPLIEFIKIDPSYCTRL LPQLTEILYNCVVVGTSRSSDNQFPL EYTFANMPNPWLITKVVSLLSILIAS PTERDSGSLQTNINIDNELLNKLK CVSVAIELGTRQAQDPMERIVQNTV LFSLINFASKLDPSEAISNSVTALC SLLTSKEINIRYLTLDLVLKCSSSGK PAIDAVRYKNLDMIFHLLNTERDSSI VRKVVDLLYFTFDVENVKIIVDGLLQ YILSPKNLAEPQIKSDIAVKIAILTEKY ATDINWFVHSLQLLSLTSNTTINDDE IWQRLCQIVVNNPSLHRITCERLVDY LCKKQASEAIKAAAFLLGEYSSLITD RISSANLFTLFAEKYFSAPNVAKAMI LTTMIKLYKTSPEIGSNVIKFFQLELN SLDIELQTRSFEYLNIIQLAKVNGNT DILQILFEPMPFFNSKSNPLLKRLGS LPASAGSTTLINTPSEASSSTPDLLSK RANSSRSIMVMPPPSRRTIDDVN SKISSSEDFSGKDSYYSRQILAPNWR EGFTRMISHKQGVLFSSLMKVFYR ITTPDAQQPYVFHISLAFINLWEWIT GLSTQIIPSKTQGNPEYLMNINTPST ATIGPHKRAEQSYEV/SIRKPFVDEDS PILAIHFCKGGSTNTINLKAIGMTT LISSDVNPSMHLNLAQFISRWKTLS DALGKEGEYQKSGIKLNKDFRKYVETI SLEDGLLLLTQTVKRLGFDIVDQTSV RSTLFVSGIIHTKSEGNFGCLMKIQY QVNGTVNVTKTTTAGPLAKYIVECI KNVLTk	None	None	None	None	None	None	None		

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