	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	P23201	SPA2_YEAST	Saccharomyces cerevisiae	Protein SPA2	24.475439	NaN	S182;S183;T220;S254;S274;S301;S585;S599;S646;S817;S820;S865;S883;S910;S937;S961;S979;S1053;S1056;S1080;S1173;T1179;S1180;T1251;S1263	33229814	MGTSSEVSLAHHRDIFHYYVSLKTF FEVTGENRDRSNSTRAQKARAKLLK LSSSQFYELSTDVSDELQRRIGEDAN QPDYLLPKANFHMKRNQARQKLAN LSQTRFNDLLDDILFEIKRRGFDKDL DAPRPPLPQPMKQEVSKDSDDTART STNSSSVTQVAPNVSVQPSLVIPKMA SIDWSSEEEEEEQVKEKPNEPEGKQ TSMDEKKEAKPALNPIVTDSDLPDS QVLARDITSMARTPTTTHKNYWDVN DSPIIKVDKDIDNEKGPEQLKSPEVQ RAENNNPNSEMEDKVKELTDLNSD LHLQIEDLNAKLASLTSEKEKEKKEE KEEKEKEKNLKINYTIDESFQKELLS LNSQIGELSIENENLKQKISEFELHQ KKNDNHNDLKITDGFISKYSSADGLI PAQYILNANNLIIQFTTRLSAVPIGDS TAISHQIGEELFQILSQLSNLISQLLL SADLLQYKDQVILLKASLSHAITSIRY FSVYGPVLIPKITVQAAVSEVCFAMC NLIDSAKIKSDSNGESTTSNEGNRQ VLEYSSPTATTPMTPTFPSTSGINMK KGFINPRKPASFLNDVEEEESPVKPL KITQKAINSPIIRPSSSNGVPTTSRKP SGTGLFSLMIDSSIAKNSSHKEDND KYVSPIKAVTSASNSASSNISEIPKLT LPPQAKIGTVIPPSENQVPNIKIENTE EDNKRSDITNEISVKPTSSIADKLKQ FEQSSEKKSSPKENPIAKEEMDSKP KLSNKFITSMNDVSTDDSSSDGNEN DDADDDDDFTYMALKQTMKREGSK IEKNNDSKLPANIVELDLHESPESVK IESPESIKEITSSEMSSEMPSSSLPKR LVEDVEPSEMPEKGASVESVRKKNF QEPLGNVESPDMTQKVKSLGMTGK AVGPESDSRVESPGMTGQIKSLNMA GKVVGPEADSRVESPGMKEQIKSLG MTGKITAQESIKSPEAARKLASSGEV DKIESPRMVRESESLEAVGNTIPSN MTVKMESPNLKGNTVSEPQEIRRDI ASSEPIENVDPPKVLKKIVFPKAVNR TGSPKSVEKTPSSATLKKSGLPEPNS QIVSPELAKNSPLAPIKKNVELRETN KPHTETITSVEPTNKDANTSWRDAD LNRTIKREEEDEDFDRVNHNIQITG AYTKTGKIDYHKIPVDRKAKSEAEVH TSEEDIDESNNVNGKRADAQIHITER KHAFVNPTENSQVKKTSHSPFLNSK PVQYENSESNGGINNHIKIKNTGET TAHDEKHYSDDDDSSYQFVPMKHE EQEQEQNRSEEEESEDDDEEEEDS DFDVDTFDIENPDNTLSELLLYLEH QTMDVISTIQSLLTSIKKPQVTKGNL RGESNAINQVIGQMVDATSISMEQS RNANLKKHGDWVVQSLRDCSRRMT ILCQLTGDGILAKEKSDQDYADKNFK QRLAGIAFDVAKCTKELVKTVEEASL KDEINYLNSKLK	None	None	None	None	None	None	None	None	None