

Barbosa et al (2016) The ceramide-activated protein phosphatase Sit4p controls lifespan, mitochondrial function and cell cycle progression by regulating hexokinase 2 phosphorylation. *Cell Cycle*

Supplemental Table S1. Identification of proteins differentially expressed in *sit4Δ* cells by MALDI-MS/MS.

Proteins were isolated from *S. cerevisiae* BY4741 and *sit4Δ* cells grown to exponential phase in YPD medium and separated by two-dimensional electrophoresis. Proteins were visualized by silver staining. Gel was scanned using a densitometer, images were converted to TIFF format and PDQuest v7.3 software was used for quantification of spot intensities. Proteins were identified by MALDI-TOF/TOF.

Gel spot	Accession no.	Protein name	Protein Function	MW	pI	Fold Change	S.D.
Proteins downregulated							
1	gi 6320846	Ntf2p	Nuclear Transport Factor 2	14444	4.5	0,19	0,18
2	gi 6323138	Ahp1p	Thiol-specific peroxiredoxin	19274	5.0	0,20	0,12
3	gi 6322794	Tma19p	Protein that associates with ribosomes	18786	4.4	0,36	0,09
4	gi 6319315	Efb1p	Translation elongation factor 1 beta	22670	4.3	0,53	0,03
5	gi 6323138	Ahp1p	Thiol-specific peroxiredoxin	19274	5.0	0,45	0,19
6	gi 6323138	Ahp1p	Thiol-specific peroxiredoxin	19274	5.0	0,29	0,01
7	gi 6323208	Ylr179cp	Protein of unknown function	22251	4.8	0,25	0,17
8	gi 6322707	Mrp8p	Putative mitochondrial ribosomal protein	25082	4.7	0,28	0,05
9	gi 6322531	Lia1p	Deoxyhypusine hydroxylase	36313	4.8	0,35	0,14
10	gi 6323077	Rps0bp	Protein component of the small (40S) ribosomal subunit	28002	4.7	0,54	0,05
11	gi 6319698	Pdb1p	E1 beta subunit of the pyruvate dehydrogenase (PDH) complex	40086	5.2	0,35	0,14

12	gi 6322565	Ado1p	Adenosine kinase	36520	4.9	0,39	0,07
13	gi 6323221	Hcr1p	Dual function protein involved in translation initiation as a substoichiometric component of eukaryotic translation initiation factor 3 (eIF3) and required for processing of 20S pre-rRNA	29546	5.0	0.30	0,05
14	gi 6320899	Hmf1p	Member of the p14.5 protein family with similarity to Mmf1p	14011	5.2	0,53	0,07
15	gi 6324907	Vma4p	Subunit E of the eight-subunit V1 peripheral membrane domain of the vacuolar H ⁺ -ATPase (V-ATPase)	26455	5.3	0,39	0.02
16	gi 14318474	Sec53p	Phosphomannomutase	29216	5.1	0,39	0,01
17	gi 6324120	Ssb2p	Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p	66668	5.4	0,1	0,01
18	gi 6325196	Ald6p	Cytosolic aldehyde dehydrogenase	54414	5.2	0,56	0,06
19	gi 6322564	Sod1p	Cytosolic superoxide dismutase	15959	5.6	0,41	0,13
20	gi 6324669	Rki1p	Ribose-5-phosphate ketol-isomerase	28355	5.6	0,40	0,05
21	gi 6319326	Ade1p	N-succinyl-5-aminoimidazole-4-carboxamide ribotide (SAICAR) synthetase	34508	5.7	0,27	0.04
22	gi 6321968	Eno2p	Enolase II	46942	5.7	0,46	0,02
23	gi 6321859	Dys1p	Deoxyhypusine synthase	43264	5.5	0,41	0,03
24	gi 6320359	Cpr1p	Cytoplasmic peptidyl-prolyl cis-trans isomerase (cyclophilin)	17494	6.9	0,41	0,01
27	gi 6320079	Ydl124wp	NADPH-dependent alpha-keto amide reductase	35595	5.8	0,28	0,23
29	gi 6320662	Guk1p	Guanylate kinase	20682	6.6	0,38	0,08

32	gi 6320359	Cpr1p	Cytoplasmic peptidyl-prolyl cis-trans isomerase (cyclophilin)	17494	6.9	0,47	0,06
33	gi 6324709	ldh2p	Subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase	39886	8.8	0,47	0.05
38	gi 6323087	Shm2p	Cytosolic serine hydroxymethyltransferase	52471	7.0	0,54	0,11
39	gi 45719888	Ura1p	Dihydroorotate dehydrogenase	34950	5.8	0,39	0,42
Proteins upregulated							
25	gi 6322468	Tdh2p	Glyceraldehyde-3-phosphate dehydrogenase	35939	6.5	6,9	2,0
26	gi 6321631	Tdh3p	Glyceraldehyde-3-phosphate dehydrogenase	35838	6.5	4,2	0,3
28	gi 6324486	Adh1p	Alcohol dehydrogenase	37282	6.2	>10	
30	gi 6321631	Tdh3p	Glyceraldehyde-3-phosphate dehydrogenase	35838	6.5	3,6	2,1
31	gi 6322468	Tdh2p	Glyceraldehyde-3-phosphate dehydrogenase	35939	6.5	2,8	0,1
34	gi 6321631	Tdh3p	Glyceraldehyde-3-phosphate dehydrogenase	35838	6.5	3,2	1,3
35	gi 6321693	Eno1p	Enolase I	46844	6.2	2,5	0,4
36	gi 6323886	Rps10bp	Protein component of the small (40S) ribosomal subunit	12731	9.1	>10	
37	gi 10383781	Pgk1p	3-phosphoglycerate kinase	44768	7.1	3,6	1,6