

S4 Table. Identification of proteins in spots that exhibit significant RuBPS staining intensity changes in the absence of CaPpz1

Protein Name ¹	Protein ID ¹	Systemic gene name ²	Standard gene name ¹	Protein abbreviation ²	Spot ID [#]	Fold change	p value
14-3-3 protein homolog	O42766	<i>C1_03220C</i>	<i>BMH1</i>	Bmh1	47	-1.97	0.006
40S ribosomal protein S0	O42817	<i>C3_05370C</i>	<i>YST1</i>	Yst1	22	-2.35	0.042
60S ribosomal protein L20	A0A1D8PLC9	<i>C4_01520C</i>	<i>RPL20B</i>	Rpl20B	10	-2.21	0.021
Adenylosuccinate synthetase	P0CH96	<i>C1_09640W</i>	<i>ADE12</i>	Ade12	46	2.60	0.045
Deoxyhypusine hydroxylase	Q59Z14	<i>C2_07290W</i>	<i>LIA1</i>	Lia1-like**	18	-1.59	0.019
Elongation factor 1-beta	A0A1D8PM35	<i>C4_04480C</i>	<i>EFB1</i>	Efb1	43	-2.37	0.002
Elongation factor 3*	P25997	<i>C5_01580C</i>	<i>CEF3</i>	Cef3	44	-7.08	0.004
					27	-3.63	0.020
Heat shock protein SSA1	P41797	<i>C1_13480W</i>	<i>HSP70</i>	Hsp70/Ssa1	32	-1.52	0.042
Isocitrate dehydrogenase [NAD] subunit 1 (mitochondrial)	A0A1D8PEM5	<i>C1_09630W</i>	<i>IDH1</i>	Idh1	45	2.76	0.017
Peptidyl-prolyl cis-trans isomerase	Q5ALM6	<i>C2_02320C</i>	<i>CPR3</i>	Cpr3	02	-2.20	0.006
Peroxiredoxin TSA1	Q9Y7F0	<i>C3_06180C</i>	<i>TSA1</i>	Tsa1	16	-2.23	0.002
Protein URE2	Q96WL3	<i>C2_04710C</i>	<i>URE2</i>	Ure2	48	1.95	0.0004
Transketolase 1	Q5A750	<i>C1_08320W</i>	<i>TKL1</i>	Tkl1	29	1.84	0.012
Ubiquitin-activating enzyme E1	A0A1D8PKJ3	<i>C3_06500W</i>	<i>UBA1</i>	Uba1	30	1.59	0.029

Based on ¹<http://www.uniprot.org/> and ² <http://www.candidagenome.org/>.

*The protein was identified in two separate spots.

** The abbreviation is based on the name of the *S. cerevisiae* ortholog.

Phosphoprotein containing spots (see S3 Table) are highlighted in bold face.