

PROTEOMICS

Supporting Information for Proteomics

DOI 10.1002/pmic.200500100

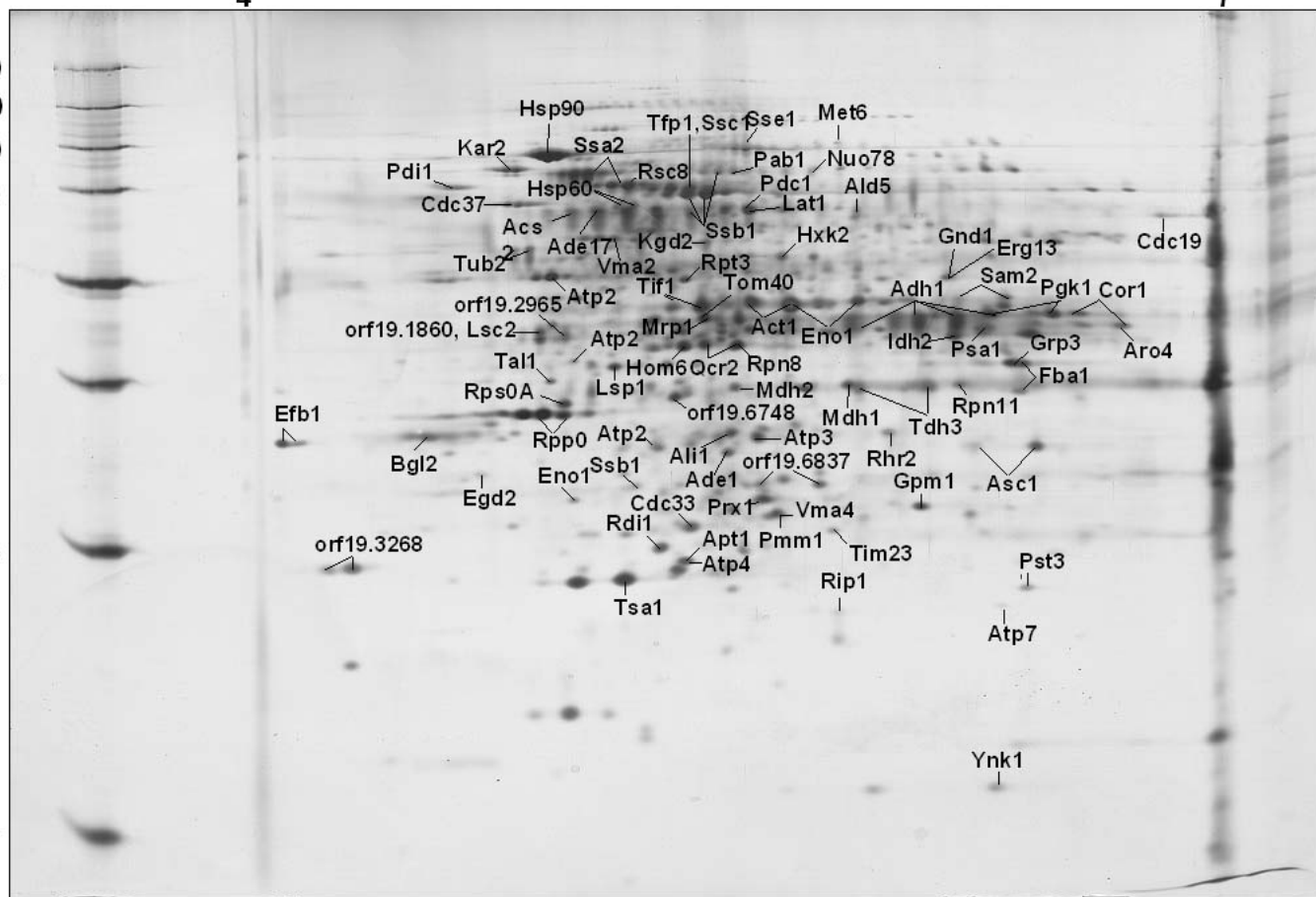
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**Proteomic analysis of *Candida albicans* yeast and
hyphal cell wall and associated proteins**

Supplemental Figure 1. Silver-stained two-dimensional electrophoresis gel showing all the proteins in the *C. albicans* hyphae cell wall-enriched fraction extracted with DTT/SDS. The proteins were separated in the first dimension using a pI 4-7 gradient immobilized strip followed by a 14 % SDS-PAGE gel.

kDa 250
150
100
75
50
37
25
15

M. Wt.



Supplemental Table 1. DTT/SDS-Extractible Proteins identified from *C. albicans* yeast and hyphal cell wall enriched fractions.

Protein Name	Assembly 19 orf	Description	Mascot Score $\Delta m=0.5$	Mascot #Peptides	Mass (kDa)		Isoelectric Point (pI)		Expression Ratio H / Y
					Observed	Predicted	Observed	Predicted	
ACS2	orf19.1064	acetyl-coenzyme A synthetase	180	4	78	74	5.1	6.05	589
ACT1	orf19.5007	actin	45	1	45	40	5.5	6.19	1.3
ACT1	orf19.5007	actin	261	5	45	40	5.8	6.19	1.4
ADE1	orf19.7484	phosphoribosyl-amidoimidazole- succinocarboxamide synthetase	334	7	33	33	5.4	5.14	1.0
ADE17	orf19.492	5- aminoimidazole-4-carboxamide ribonucleotide transformylase	146	4	69	65	5.0	6.52	665
ADH1	orf19.3997	alcohol dehydrogenase 1	432	6	41	46	6.0	8.19	
ADH1	orf19.3997	alcohol dehydrogenase 1	38	1	40	46	6.1	8.19	
ADH1	orf19.3997	alcohol dehydrogenase 1	339	5	42	46	6.2	8.19	4.5
ADH1	orf19.3997	alcohol dehydrogenase 1	68	2	43	46	6.3	8.19	
ALD5	orf19.5806	aldehyde dehydrogenase	211	4	67	54	5.8	5.37	1.0
ALI1	orf19.1710	mitochondrial NADH-ubiquinone oxidoreductase	533	8	34	33	5.4	6.53	0.8
APT1	orf19.1448	adenine phosphoribosyltransferase	583	9	25	21	5.3	4.95	0.8
ARO4	orf19.4060	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase isoenzyme	83	2	40	40	6.6	6.63	
ASC1	orf19.6906	WD repeat protein that interacts with the translational machinery	162	4	33	15	6.2	4.63	0.5
ASC1	orf19.6906	WD repeat protein that interacts with the translational machinery	393	7	33	15	6.4	4.63	0.7
ATP2	orf19.5653	F1F0-ATPase complex, F1 beta subunit	1220	18	51	56	4.8-4.9-	4.68	0.6
ATP2	orf19.5653	F1F0-ATPase complex, F1 beta subunit	502	9	38	56	4.9	4.68	1.0
ATP2	orf19.5653	F1F0-ATPase complex, F1 beta subunit	332	6	33	56	5.3	4.68	1.0
ATP3	orf19.3223	ATP synthase gamma subunit	320	6	34	31	5.5	5.11	0.8
ATP4	orf19.3579	ATP synthase F0 sector subunit 4	114	2	25	26	5.3	6.3	
ATP7	orf19.2785	ATP synthase d subunit	129	3	23	19	6.3	6.56	0.1
BGL2	orf19.4565	beta-1,3 glucan transferase	106	2	34	34	4.4-4.5	4.33	2.6
CDC19	orf19.3575	pyruvate kinase	98	2	68	55	6.8	7.00	91
CDC33	orf19.7626	mRNA cap-binding protein eIF4E, translation initiation	71	2	27	24	5.3	4.93	0.8
CDC37	orf19.5531	cell division control protein	455	9	71	59	4.7	4.43	0.8
COR1	orf19.4016	part of ubiquinol cyt-c reductase complex	332	6	43	48	6.4	6.98	0.8
COR1	orf19.4016	part of ubiquinol cyt-c reductase complex	386	6	40	48	6.6	6.98	0.7
EFB1	orf19.3838	translation elongation factor eEF1beta	276	4	33	26	4.2	4.16	0.6

EGD2	orf19.5858	GAL4 enhancer protein	215	3	31	20	4.6	4.43	0.1
ENO1	orf19.395	enolase I	243	4	45	47	5.6	5.52	1.4
ENO1	orf19.395	enolase I	1016	15	45	47	5.8	5.52	0.8
ENO1	orf19.395	enolase I	32	1	28	47	4.9	5.52	0.5
ERG13	orf19.7312	3-hydroxy-3-methylglutaryl coenzyme A synthase	349	7	51	50	6.1	5.75	1.2
FBA1	orf19.4618	fructose-bisphosphate aldolase	487	8	38	39	6.3	5.97	0.7
FBA1	orf19.4618	fructose-bisphosphate aldolase	77	2	37	39	6.3	5.97	0.8
GND1	orf19.5024	6-phosphogluconate dehydrogenase	199	3	51	57	6.1	6.53	
GPM1	orf19.903	phosphoglycerate mutase	536	7	28	28	6.0	6.05	0.7
GRP3	orf19.4309	induced by osmotic stress	79	1	38	38	6.3	6.39	
HOM6	orf19.2951	homoserine dehydrogenase	334	6	39	39	5.4	4.95	2.3
HSP60	orf19.717	mitochondrial groEL-type heat shock protein	899	15	71	60	5.1	4.95	0.5
HSP70	orf19.4980	heat shock protein 70	1046	15	82	70	4.9-5.0	4.79	
HSP70	orf19.4980	heat shock protein 70	1156	19	78	70	5.1-5.2	4.79	3.9
HSP90	orf19.6515	heat shock protein 90	1160	20	89	81	4.8-4.9	4.52	1.9
HXK2	orf19.542	hexokinase II	56	1	56	48	5.6	4.8	3.2
IDH2	orf19.5791	mitochondrial isocitrate dehydrogenase (NAD+) subunit 2	506	8	40	39	6.1	6.89	0.8
KAR2	orf19.2013	dnaK/HSP70/ BiP family ATPase & chaperone	803	13	84	75	4.7-4.8	4.56	3.2
KGD2	orf19.6126	2-oxoglutarate dehydrogenase complex E2 component	112	2	59	48	5.4	9.04	0.9
LAT1	orf19.6561	dihydrolipoamide acetyltransferase component	333	6	69	50	5.5	5.61	0.8
LSC2	orf19.710	succinate-CoA ligase beta subunit	506	8	40	22	4.8	4.57	1.9
LSP1	orf19.3149	Long chain base Stimulates Phosphorylation	275	4	38	36	5.1	4.61	9.1
MDH1	orf19.4602	mitochondrial malate dehydrogenase	711	10	37	35	5.8	5.97	0.4
MDH2	orf19.7481	malate dehydrogenase	329	7	37	36	5.5	5.25	1.5
MET6	orf19.2551	methionine-synthesizing 5-methyltetrahydropteroyltriglutamate	364	8	105	86	5.7	5.28	35
MRP1	orf19.1662	mitochondrial ribosomal small subunit protein	65	2	42	35	5.4	6.04	
NUO78	orf19.7590	NADH dehydrogenase (ubiquinone) 78K chain precursor, 5' end	629	9	84	59	5.7-5.8	5.12	0.9
orf19.1860	orf19.1860	hypothetical protein	78	1	40	9	4.8	9.47	1.9
orf19.2965	orf19.2965	pump-driving ATPase	117	3	40	40	4.9	4.63	2.8
orf19.3268	orf19.3268	translationally controlled tumor protein	75	1	24	19	4.2-4.3	4.06	0.9
orf19.6748	orf19.6748	translation initiation factor	186	3	36	37	5.3	4.9	1.8
orf19.6837	orf19.6837	corticosteroid 11-beta-dehydrogenase	109	2	30	23	5.5	4.49	0.7
orf19.6837	orf19.6837	corticosteroid 11-beta-dehydrogenase	439	8	30	23	5.7	4.49	0.5
PAB1	orf19.3037	3'-end RNA-processing complex component	193	4	80	70	5.7-5.8	4.95	2.7
PDC1	orf19.2877	pyruvate decarboxylase	766	13	69	62	5.5	5.26	1.0
PDI1	orf19.5130	protein disulfide isomerase	216	4	77	62	4.5-4.6	4.33	2.4

PGK1	orf19.3651	phosphoglycerate kinase	305	7	43	45	6.3	6.43	2.7
PGK1	orf19.3651	phosphoglycerate kinase	211	5	43	45	6.5	6.43	1.5
PMM1	orf19.2937	phosphomannomutase	211	3	27	29	5.6	5.41	1.0
PRX1	orf19.5180	regulation of redox homeostasis	33	1	29	25	5.5	5.34	1.9
PSA1	orf19.6190	GDP-mannose pyrophosphorylase	46	1	40	40	6.2	6.25	2.1
PST3	orf19.5285	flavodoxin	245	5	23	21	6.4	6.23	0.5
QCR2	orf19.2644	ubiquinol--cytochrome-c reductase 40KD chain II	922	14	39	40	5.5	5.27	1.0
QCR2	orf19.2644	ubiquinol--cytochrome-c reductase 40KD chain II	398	8	39	40	5.4	5.27	0.7
RDI1	orf19.5968	Rho GDP dissociation inhibitor	111	2	25	23	5.2	4.91	1.9
RHR2	orf19.5437	DL-glycerol-3-phosphatase	54	1	34	28	5.9	5.6	3.5
RIP1	orf19.5893	component of ubiquinol cytochrome- c reductase complex	153	3	23	17	5.8	5	0.1
RPN11	orf19.7264	multicatalytic endopeptidase	34	1	37	35	6.2	6.23	2.4
RPN8	orf19.3168	component of 19S proteasome regulatory particle	393	6	39	37	5.5	5.14	
RPP0	orf19.7015	ribosomal protein P0 (A0) (L10E)	457	8	35	33	4.8-4.9	4.46	0.9
RPP0	orf19.7015	ribosomal protein P0 (A0) (L10E)	217	4	36	33	4.9	4.46	0.6
RPS0A	orf19.6975	ribosomal protein S0A	265	5	36	26	4.9	4.49	0.6
RPT3	orf19.5793	26S proteasome regulatory subunit	349	7	50	46	5.3	4.98	1.3
RSC8	orf19.7234	eighth largest subunit of RSC	46	1	78	64	5.1	4.83	
SAM2	orf19.657	S- adenosylmethionine synthetase	159	2	46	42	6.3	5.83	0.9
SAM2	orf19.657	S- adenosylmethionine synthetase	120	2	45	42	6.2	5.83	0.6
SSA2	orf19.1065	chaperonin of the HSP70 family	1285	19	82	70	4.9-5.0	4.68	1.8
SSA2	orf19.1065	chaperonin of the HSP70 family	878	14	78	70	5.0-5.2	4.68	
SSB1	orf19.6367	heat shock protein of the HSP70 family	236	4	28	66	4.9	5.01	0.4
SSB1	orf19.6367	heat shock protein of the HSP70 family	557	9	77	66	5.2-5.3	5	
SSB1	orf19.6367	heat shock protein of the HSP70 family	1368	19	75	66	5.2-5.4	5	0.8
SSB1	orf19.6367	heat shock protein of the HSP70 family	28	1	83	66	5.4	5	
SSB1	orf19.6367	heat shock protein of the HSP70 family	692	12	68	66	5.3	5.01	10
SSC1	orf19.1896	mitochondrial heat shock protein of the HSP70 family	707	13	77	70	5.2-5.3	5.25	1.1
SSE1	orf19.2435	heat shock protein of HSP70 family	835	15	83	79	5.4	4.95	142
TAL1	orf19.4371	transaldolase	276	5	37	36	4.9	4.63	0.6
TDH3	orf19.6814	GLYCERALDEHYDE 3- PHOSPHATE DEHYDROGENASE	116	2	37	36	5.8	7.14	8.4
TDH3	orf19.6814	GLYCERALDEHYDE 3- PHOSPHATE DEHYDROGENASE	162	3	37	36	6.1	7.14	3.5
TFP1	orf19.1680	vacuolar ATPase V1 domain catalytic subunit A	258	6	77	63	5.2-5.3	5	
TIF1	orf19.3324	translation initiation factor 4A	843	15	44	45	5.3	4.99	1.8
TIF1	orf19.3324	translation initiation factor 4A	121	2	42	45	5.4	4.99	
TIF1	orf19.3324	translation initiation factor 4A	169	5	44	45	5.3	4.99	2.2

TIM23	orf19.1361	mitochondrial inner membrane import translocase subunit	252	5	26	23	5.8	5.7	0.2
TOM40	orf19.6524	translocase of outer mitochondrial membrane	610	11	42	42	5.4	5.17	2.1
TSA1	orf19.7417	thiol-specific antioxidant protein	674	11	24	22	5.1	4.7	1.3
TUB2	orf19.6034	beta- tubulin	324	6	58	48	4.8	4.35	2.1
VMA2	orf19.6634	vacuolar ATPase V1 domain subunit B	847	13	61	57	5.0-5.1	4.66	1.8
VMA4	orf19.2598	vacuolar H+- ATPase V1 domain subunit	99	2	27	24	5.6	5.16	
YNK1	orf19.4311	nucleoside diphosphate kinase	328	5	17	17	6.3	6.53	0.2