

PROTEOMICS

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**Proteomic analysis of Mrr1p- and Tac1p-associated differential protein
expression in azole-resistant clinical isolates of *Candida albicans***

Table S1. Description of the differentially expressed proteins identified in clinical isolate F5 and mutant strain SCzcf36MK3A by PMF and MALDI-TOF MS

Protein	Systematic Name	Function	Mr pl	Z (kDa)	Protein score	Matched coverage	Matched peptides	Fold changes			Student's <i>t</i> -test		
								(F5/F1)	(F5MRR1M4B/F1)	(SCzcf36MK3A/SC5314)	F5/F1	F5MRR1M4B	SCzcf36MK3A
Eno1p	orf19.395	Enolase (2-Phosphoglycerate dehydratase)	5.5	47.2	2.4	21	7	2.1 ± 0.5	2.7 ± 0.9	0.8 ± 0.8	0.04	0.03	0.21
Tdh3p	orf19.6814	Glyceraldehyde-3-phosphate dehydrogenase	6.6	35.8	2.4	45	9	2.0 ± 1.9	1.4 ± 0.1	1.0 ± 0.4	0.21	0.32	0.40
Gpx1p	orf19.86	Glutathione peroxidase	6.6	18.1	2.4	35	7	3.7 ± 1.0	0.8 ± 0.4	34.2 ± 8.5	0.00	0.22	0.05
Grp2p	orf19.4309	Reductase	6	37.6	2.4	31	9	4.1 ± 0.9	1.0 ± 0.2	10.0 ± 7.0	0.00	0.36	0.15
Grp2p	orf19.4309	Reductase	6	37.6	2.3	28	8	5.5 ± 2.3	1.2 ± 0.6	4.7 ± 0.3	0.07	0.26	0.07
lfd1p	orf19.1048	Putative aryl-alcohol dehydrogenase	5.6	39.1	2.4	42	15	10 ± 6.2	1.1 ± 0.6	11.6 ± 3.8	0.11	0.37	0.00
lfd4p	orf19.4477	Putative aryl-alcohol dehydrogenase	6	38.3	2.4	37	15	10.1 ± 4.7	1.1 ± 0.1	35.2 ± 11.8	0.08	0.10	0.02
lfd5p	orf19.1048	Putative aryl-alcohol dehydrogenase	5.4	39.2	2.2	31	9	4.4 ± 1.9	1.3 ± 0.4	4.2 ± 1.6	0.11	0.28	0.01
lfd6p	orf19.4476	Putative aryl-alcohol dehydrogenase	5.9	39.1	2.2	26	8	5.1 ± 4.9	1.1 ± 0.1	190.1 ± 274	0.15	0.10	0.07
lpf5987p	orf19.7306	Aldo-keto reductase	5.5	39.0	2.3	43	9	4.7 ± 0.8	0.9 ± 0.1	102.6 ± 80	0.02	0.07	0.04
Oye32p	orf19.3131	Putative NADPH-dependent flavin oxidoreductase	5.9	47.5	2.4	30	10	7.3 ± 2.5	1.1 ± 0.1	No spot	0.00	0.40	N/A
Adh4p	orf19.271	2,4-dienoyl-coenzyme A reductase	7	28.1	2.4	28	8	25.2 ± 5.3	1.0 ± 0.2	2.7 ± 0.6	0.02	0.36	0.00
lpf17186p	orf19.251	Heat shock protein 31 of DJ-1/Pfpl family	4.7	25.8	2.3	20	5	6.1 ± 0.6	1.3 ± 0.2	3.5 ± 1.3	0.00	0.04	0.06
lpf17186p	orf19.251	Heat shock protein 31 of DJ-1/Pfpl family	4.7	25.8	2.1	25	9	7.9 ± 0.2	1.4 ± 0.1	2.6 ± 1.1	0.04	0.02	0.08
Gnd1p	orf19.5024	6-Phosphogluconate dehydrogenase	6.1	56.9	2.4	18	8	0.4 ± 0.1	1.3 ± 0.2	1.3 ± 0.8	0.00	0.07	0.34
Hxk2p	orf19.542	Hexokinase II, 3-prime end	5.1	47.5	2.3	26	11	2 ± 0.7	1.6 ± 1.1	0.9 ± 1.4	0.06	0.30	0.36
Tkl1p	orf19.5112	Transketolase 1	5.5	73.8	1.7	13	6	1.8 ± 0.7	1.3 ± 0.5	1.2 ± 1.4	0.01	0.33	0.44
Sam2p	orf19.657	S-Adenosylmethionine synthetase	5.6	42.2	1.7	23	8	1.5 ± 0.4	1.3 ± 0.4	1.0 ± 0.4	0.08	0.09	0.38
Aco1p	orf19.6385	Aconitate hydratase	6	84.2	1.6	10	7	0.5 ± 0.1	0.9 ± 0.3	1.1 ± 0.7	0.04	0.10	0.21
Ura5p	orf19.2555	Orotate phosphoribosyltransferase	5.9	23.5	1.8	25	5	0.6 ± 0.3	0.7 ± 0.3	1.1 ± 0.8	0.063	0.08	0.47
Pgk1p	orf19.3651	Phosphoglycerate kinase	6.1	45.2	2.4	34	12	1.6 ± 1.1	1.5 ± 0.5	1.3 ± 0.4	0.09	0.13	0.13

N/A-not applicable

Table S2. Description of the differentially expressed proteins identified in clinical isolate G5 by PMF and MALDI-TOF MS

Protein	Systematic ^a Name	Function	pI	Mr (kDa)	Z score	Protein coverage	Matched peptides	Fold change (G5/G1)	Student's t-test
Adh1p	orf19.3997	Alcohol dehydrogenase	8.6	46.1	2.4	36	15	1.7 ± 0.7	0.19
Cyp1p	orf19.6472	Cyclophilin (peptidylprolyl isomerase)	7.9	17.7	2.4	40	7	0.6 ± 0.1	0.00
Eno1p	orf19.395	Enolase (2-Phosphoglycerate dehydratase)	5.5	47.2	2.4	61	20	2.2 ± 0.7	0.04
Fba1p	orf19.4618	Fructose-bisphosphate aldolase	5.7	39.2	2.4	24	9	2.4 ± 0.6	0.02
Tdh3p	orf19.6814	Glyceraldehyde-3-phosphate dehydrogenase	6.6	35.8	2.4	25	9	1.9 ± 0.3	0.05
Gpx1p	orf19.86	Glutathion peroxidase	6.6	18.1	2.4	41	8	3.8 ± 0.3	0.04
Grp2p	orf19.4309	Reductase	6	37.6	2.4	22	9	4.4 ± 1.1	0.05
Grp2p	orf19.4309	Reductase	6	37.6	2.4	35	13	5.3 ± 0.9	0.02
lfd1p	orf19.1048	Putative aryl-alcohol dehydrogenase	5.6	39.1	1.8	28	8	3.9 ± 0.4	0.00
lfd4p	orf19.4477	Putative aryl-alcohol dehydrogenase	6	38.3	2.4	46	19	27.6 ± 16.2	0.19
lfd5p	orf19.1048	Putative aryl-alcohol dehydrogenase	5.4	39.2	2.4	33	12	13.9 ± 6.2	0.20
lfd6p	orf19.4476	Putative aryl-alcohol dehydrogenase	5.9	39.1	1.2	49	10	201 ± 46	0.00
lpf351p	orf19.7531	Unknown function	7.9	25.2	1.9	18	5	0.5 ± 0	0.00
lpf1621p	orf19.6585	Unknown function	9.6	14.4	2.2	44	5	0.5 ± 0	0.00
lpf5987p	orf19.7306	Aldo-keto reductase	5.5	39.0	1.8	21	6	5.4 ± 3.2	0.04
Oye32p	orf19.3131	Putative NADPH-dependent flavin oxidoreductase	5.9	47.5	1.8	21	6	4.8 ± 0.4	0.00
Adh4p	orf19.271	2,4-dienoyl-coenzyme A reductase	7	28.1	2.4	22	6	4.5 ± 0.5	0.00
lpf17186p	orf19.251	Heat shock protein 31 of DJ-1/Pfp1 family	4.7	25.8	2.3	35	7	10.8 ± 2.2	0.00
lpf17186p	orf19.251	Heat shock protein 31 of DJ-1/Pfp1 family	4.7	25.8	2.4	23	7	2 ± 0.6	0.08
Pdc11p	orf19.2877	Pyruvate decarboxylase	5.4	62.4	2.4	36	15	6.0 ± 0.4	0.00
Rpp2p	orf19.6403.1	Acidic ribosomal protein	3.9	10.8	2.25	55	4	0.5 ± 0.1	0.19
Tpi1p	orf19.6745	Triose phosphate isomerase	5.7	26.6	2.0	35	7	1.8 ± 0.1	0.13

Table S3. Description of the differentially expressed proteins identified in clinical isolate 6299 by PMF and MALDI-TOF MS

Protein	Systematic ^a Name	Function	pI	Mr (kDa)	Z score	Protein coverage	Matched peptides	Fold change 6299/5833	Student's t-test
Adh1p	orf19.3997	Alcohol dehydrogenase	8.6	46.1	2.3	42	13	1.7 ± 0.1	0.01
Eno1p	orf19.395	Enolase (2-Phosphoglycerate dehydratase)	5.5	47.2	2.4	53	16	2.4 ± 0.7	0.00
Tdh3p	orf19.6814	Glyceraldehyde-3-phosphate dehydrogenase	6.6	35.8	1.8	38	10	1.8 ± 0.4	0.09
Gnd1p	orf19.5024	6-Phosphogluconate dehydrogenase	6.1	56.9	2.4	33	18	0.4 ± 0.1	0.05
Gpx1p	orf19.86	Glutathione peroxidase	6.6	18.1	2.4	39	8	3.1 ± 0.6	0.00
Grp2p	orf19.4309	Reductase	6	37.6	2.4	18	5	11.6 ± 0.8	0.01
Grp2p	orf19.4309	Reductase	6	37.6	2.4	55	22	13.4 ± 3.9	0.04
lfd1p	orf19.1048	Putative aryl-alcohol dehydrogenase	5.6	39.1	2.2	21	9	6.4 ± 1.3	0.01
lfd4p	orf19.4477	Putative aryl-alcohol dehydrogenase	6	38.3	2.3	31	8	2.1 ± 1.1	0.06
lfd5p	orf19.1048	Putative aryl-alcohol dehydrogenase	5.4	39.2	2.4	33	8	6.9 ± 1.1	0.01
lpf5987p	orf19.7306	Aldo-keto reductase	5.5	39.0	2.4	44	11	3.2 ± 0.3	0.00
Oye32p	orf19.3131	Putative NADPH-dependent flavin oxidoreductase	5.9	47.5	1.3	16	4	1.7 ± 0.3	0.01
Adh4p	orf19.271	2,4-dienoyl-coenzyme A reductase	7	28.1	2.4	25	7	21.8 ± 7.5	0.00
lpf17186p	orf19.251	Heat shock protein 31 of DJ-1/Pfp1 family	4.7	25.8	2.4	48	9	5.2 ± 0.6	0.00
lpf17186p	orf19.251	Heat shock protein 31 of DJ-1/Pfp1 family	4.7	25.8	2.4	36	7	7.7 ± 1.2	0.01
Pdc11p	orf19.2877	Pyruvate decarboxylase	5.4	62.4	2.3	17	7	2.5 ± 1.7	0.16
Rpl10Ep	orf19.7015	Ribosomal protein L10	4.7	33.3	1.6	36	4	1.6 ± 0.2	0.04
Ntf2p	orf19.4879.2	Nuclear transport factor	4.6	14.69	2.15	42	4	0.6 ± 0.2	0.04
Guk1p	orf19.1115	Guanylate kinase	5.6	21.3	1.5	17	4	0.5 ± 0.0	0.00

Table S4. Description of the differentially expressed proteins identified in clinical isolate 5674 and mutant strain SZY91 by PMF and MALDI-TOF MS

Protein	Systematic Name	Function	pI	Mr (kDa)	Z score	Protein coverage	Matched peptides	Fold changes			Student's t-test		
								(5674/5457)	(SZY31/5457)	(SZY91/SC5314)	(5674/5457)	SZY31/5457	SZY91/SC5314
Eno1p	orf19.395	Enolase (2-Phosphoglycerate dehydratase)	5.5	47.2	2.3	40	15	2.2 ± 0.4	1.2 ± 0.3	0.7 ± 0.5	0.00	0.17	0.16
Tdh3p	orf19.6814	Glyceraldehyde-3-phosphate dehydrogenase	6.6	35.8	2.1	46	10	2 ± 0.5	0.9 ± 0.2	0.9 ± 0.3	0.03	0.43	0.26
Gpx1p	orf19.86	Glutathione peroxidase	6.6	18.1	2.4	26	6	8.5 ± 1.5	1.2 ± 0.2	103 ± 102.7	0.01	0.11	0.03
lpf4065p	orf19.1862	Unknown function	5.2	13.1	2.2	50	4	2.2 ± 0.2	1.1 ± 0.1	1.5 ± 0.7	0.01	0.14	0.15
lpf15297p	orf19.3053	Unknown function	4.3	20.3	2.3	59	8	1.6 ± 0.1	1.0 ± 0.1	4.0 ± 2.6	0.01	0.44	0.12
Pdc11p	orf19.2877	Pyruvate decarboxylase	5.4	62.4	2.4	35	11	2.3 ± 0.6	1.5 ± 0.2	1.4 ± 1.0	0.00	0.00	0.1
Ssb1p	orf19.6367	Heat shock protein 70	5.3	66.4	2.4	40	24	1.6 ± 0.3	2.5 ± 1.7	1.1 ± 0.6	0.06	0.14	0.37
Ino1p	orf19.7585	Myoinositol-1-phosphate synthase	5.3	57.8	2.4	25	11	2.6 ± 0.9	1.0 ± 0.2	No spot	0.02	0.39	N/A
Ssb1p	orf19.6367	Heat shock protein 70	5.3	66.4	1.6	14	8	0.5 ± 0	0.7 ± 0.3	No spot	0.00	0.14	N/A
Snz1p	orf19.2947	Stationary phase protein	5.8	31.8	1.7	15	5	0.5 ± 0	0.9 ± 0.1	2.3 ± 0.4	0.00	0.11	0.11
Adh1p	orf19.3997	Alcohol dehydrogenase	8.6	46.1	2.4	53	20	1.5 ± 0	1.0 ± 0.3	1.5 ± 0.6	0.00	0.32	0.10
Ado1p	orf19.5591	Adenosine kinase	5	38.2	2.3	35	10	0.5 ± 0.1	1.0 ± 0.1	0.9 ± 0.1	0.01	0.46	0.13
Apt1p	orf19.1448	Adenine phosphoribosyltransferase	5.2	20.9	2.3	52	7	0.5 ± 0.1	1.1 ± 0.2	1.2 ± 0.2	0.02	0.31	0.13
Tif1p	orf19.3324	Translation initiation factor (eIF4B)	5.2	44.6	2.4	39	14	2.3 ± 0.2	1.2 ± 0.6	1.0 ± 0.2	0.01	0.29	0.37
Ura5p	orf19.2555	Orotate phosphoribosyltransferase	5.9	23.5	1.7	22	4	0.6 ± 0.0	0.8 ± 0.2	1.3 ± 0.2	0.00	0.13	0.05
Imh3p	orf19.18	Inosine monophosphate dehydrogenase	6.7	39.8	2.4	22	6	0.5 ± 0	1.1 ± 0.1	1.9 ± 0.7	0.00	0.16	0.06
Guk1p	orf19.1115	Guanylate kinase	5.6	21.3	2.3	23	5	0.6 ± 0.1	1.1 ± 0.1	1.9 ± 0.4	0.02	0.20	0.02
Rpl10Ep	orf19.7015	Ribosomal protein L10	4.7	33.3	2.3	31	9	0.6 ± 0.2	1.2 ± 0.1	1.3 ± 0.6	0.02	0.09	0.28
Gpm1p	orf19.903	Phosphoglycerate mutase	5.8	27.4	2.24	35	7	2.5 ± 0.8	1.2 ± 0.3	3.0 ± 2.6	0.0	0.15	0.08

N/A-not applicable

Table S5. Description of the differentially expressed proteins identified in clinical isolate Gu5 by PMF and MALDI-TOF MS

Protein	Systematic ^a Name	Function	pI	Mr (kDa)	Z score	Protein coverage	Matched peptides	Fold change Gu5/Gu2	Student's t-test
Eno1p	orf19.395	Enolase (2-Phosphoglycerate dehydratase)	5.5	47.2	2.4	49	18	2.0 ± 0.3	0.05
Tdh3p	orf19.6814	Glyceraldehyde-3-phosphate dehydrogenase	6.6	35.8	2.4	29	8	1.7 ± 0.3	0.00
Gpx1p	orf19.86	Glutathione peroxidase	6.6	18.1	2.4	37	7	4.2 ± 1.3	0.00
lpf4065p	orf19.1862	Unknown function	5.2	13.1	2.3	56	6	2.0 ± 0.3	0.01
lpf15297p	orf19.3053	Unknown function	4.3	20.3	1.8	25	5	1.8 ± 0.2	0.00
Pdc11p	orf19.2877	Pyruvate decarboxylase	5.4	62.4	2.4	31	14	2.2 ± 0.8	0.00
Ssb1p	orf19.6367	Heat shock protein 70	5.3	66.4	2.4	29	15	1.7 ± 0.4	0.00
Adh1p	orf19.3997	Alcohol dehydrogenase	8.6	46.1	2.3	20	7	2.0 ± 0.4	0.01
Atp2p	orf19.5653	F1F0 ATPase complex, beta subunit	4.9	55.7	2.4	51	18	1.8 ± 0.3	0.05
Ino1p	orf19.7585	Myoinositol-1-phosphate synthase	5.3	57.8	2.3	28	9	2.7 ± 0.5	0.01
Ssb1p	orf19.6367	Heat shock protein 70	5.3	66.4	2.4	56	28	0.5 ± 0.3	0.08
Snz1p	orf19.2947	Stationary phase protein	5.8	31.8	2.3	24	7	0.5 ± 0.1	0.00
Apt1p	orf19.1448	Adenine phosphoribosyltransferase	5.2	20.9	2.1	49	6	0.2 ± 0.3	0.02
Ssa1p	orf19.4980	Heat shock protein 70	4.9	70.1	2.3	17	11	3.7 ± 3.1	0.05
ldh2p	orf19.5791	Isocitrate dehydrogenase	6.4	39.3	1.7	21	6	0.5 ± 0.0	0.01
Gnd1p	orf19.5024	6-Phosphogluconate dehydrogenase	6.1	56.9	2.3	18	7	0.4 ± 0.1	0.03
Ilv5p	orf19.88	Keto-acid reducto-isomerase	6.2	44.8	2.3	24	11	1.5 ± 0.2	0.01
Rps5p	orf19.4336	Ribosomal protein S5	9	25.3	2.3	20	7	2.2 ± 0.9	0.06
Rpl10Ep	orf19.7015	Ribosomal protein L10	4.7	33.3	1.6	18	5	1.8 ± 0.5	0.05
Sap8p	orf19.242	Aspartic protease	5.9	43.0	1.7	16	4	1.7 ± 0.4	0.04

Table S6. Description of the differentially expressed proteins identified in clinical isolate C56 by PMF and MALDI-TOF MS

Protein	Systematic ^a Name	Function	pI	Mr (kDa)	Z score	Protein coverage	Matched peptides	Fold change C56/C43	Student's t-test
Eno1p	orf19.395	Enolase (2-Phosphoglycerate dehydratase)	5.5	47.2	2.0	21	7	1.6 ± 0.6	0.11
Tdh3p	orf19.6814	Glyceraldehyde-3-phosphate dehydrogenase	6.6	35.8	2.3	18	6	2.1 ± 1.1	0.08
Gpx1p	orf19.86	Glutathione peroxidase	6.6	18.1	2.0	23	5	12 ± 8	0.05
lpf4065p	orf19.1862	Unknown function	5.2	13.1	1.7	47	4	3.9 ± 1.5	0.01
lpf15297p	orf19.3053	Unknown function	4.3	20.3	1.9	39	5	6.1 ± 2.5	0.01
Pdc11p	orf19.2877	Pyruvate decarboxylase	5.4	62.4	2.4	34	14	1.6 ± 0.2	0.04
Ssb1p	orf19.6367	Heat shock protein 70	5.3	66.4	2.3	39	14	2.2 ± 0.1	0.03
Adh1p	orf19.3997	Alcohol dehydrogenase	8.6	46.1	2.4	50	16	510 ± 456	0.01
Atp2p	orf19.5653	F1F0 ATPase complex, beta subunit	4.9	55.7	2.4	52	16	1.8 ± 0.5	0.00
Ssb1p	orf19.6367	Heat shock protein 70	5.3	66.4	1.7	19	7	0.5 ± 0	0.03
Snz1p	orf19.2947	Stationary phase protein	5.8	31.8	2.4	24	7	0.4 ± 0.2	0.02
Ado1p	orf19.5591	Adenosine kinase	5	38.2	2.4	43	11	0.5 ± 0.0	0.04
Car2p	orf19.5641	Ornithine aminotransferase	5.9	47.3	2.3	41	13	9.2 ± 3.6	0.00
Aco1p	orf19.6385	Aconitate hydratase	6	84.2	2.4	36	26	0.5 ± 0.2	0.02
Tsa1p	orf19.7417	Similar to <i>S.cerevisiae</i> thiol-specific antioxidant-like protein	5	21.8	2.3	37	7	2.4 ± 1.1	0.07
Tal1p	orf19.4371	Transaldolase	4.9	35.7	2.4	23	8	0.6 ± 0.1	0.04
Asr2p	orf19.7284	Unknown function	5.4	27.8	2.2	29	7	24.3 ± 16.9	0.01