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Supporting Information
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Proteomics for the analysis of the *Candida albicans* biofilm lifestyle

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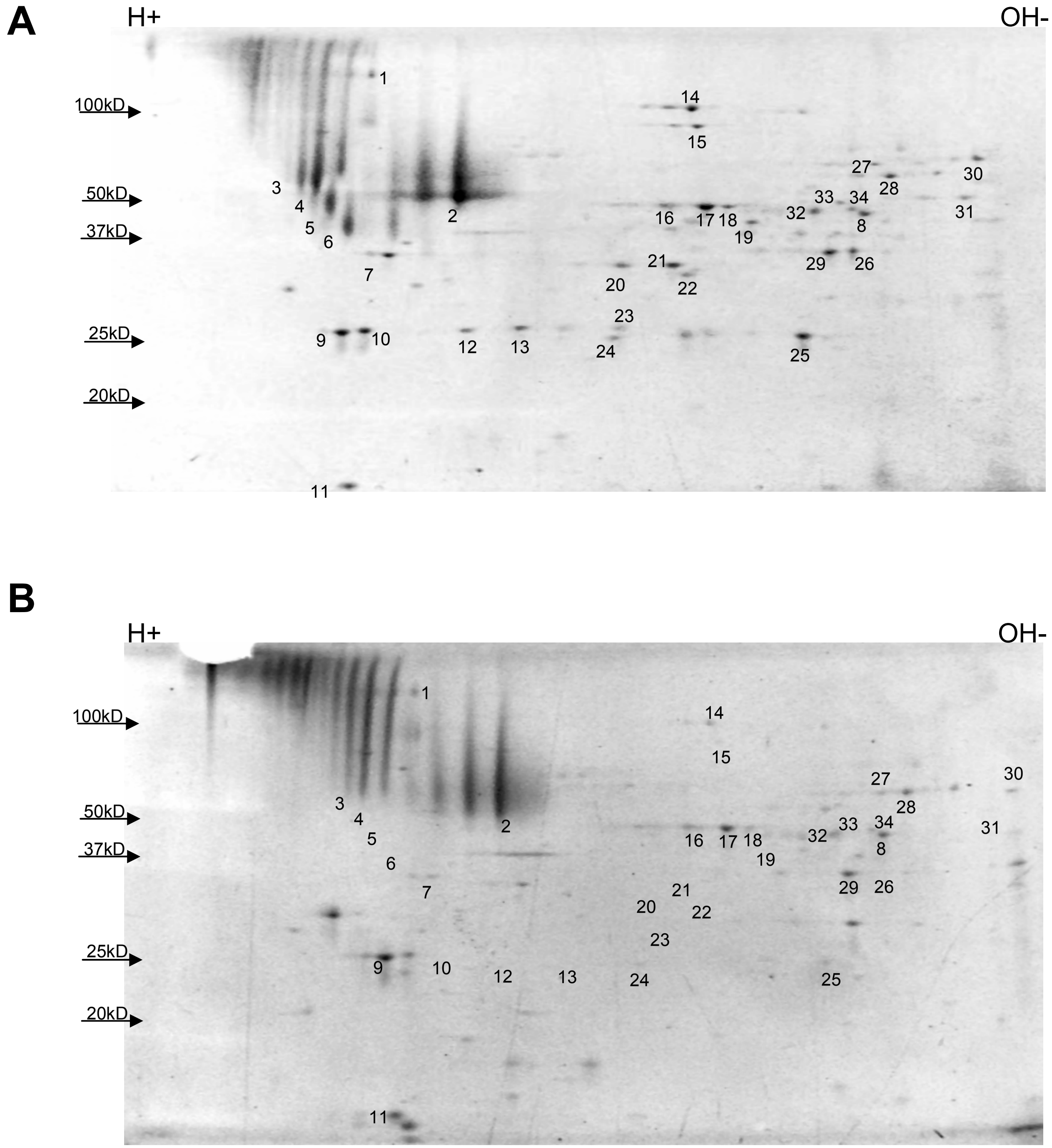
Supplementary Table 1. Proteins identified in the β-ME-extracts from biofilm and planktonic cells.

Number	Function	Gene Name	Accession #	Expectation Probability	Matching Peptides	Percent Coverage
1	Heat shock protein 70	*SSA1*	EAL03541	1.40E-17	23	52
2	Pyruvate decarboxylase	*CaO19.10395*	EAK96569	9.00E-07	14	36
3	Inositil 1 phosphate synthase	*INO1*	EAL00459	1.20E-14	18	63
4	Enolase similar to *S.cerevisiae* ENO1	*ENO1*	EAK92704	1.40E-05	17	51
5	Enolase similar to *S.cerevisiae* ENO1	*ENO1*	EAK92704	5.10E-17	17	47
	O-acetylhomoserine O-acetylserine sulphydrylase	*MET15*	EAK94256	9.20E-10	17	65
6	Immunogenic alcohol dehydrogenase	*ADH1*	EAL03292	2.70E-08	15	60
7	Alcohol dehydrogenase 2	*ADH2*	CAA21988	7.10E-04	10	37
8	Inosine-5'-monophosphate dehydrogenase	*IMH3*	AAB51509	1.50E-05	15	55
9	Malate dehydrogenase	*MDH2*	EAK99723	1.20E-05	15	54
10	Homoserine dehydrogenase	*HOM6*	EAL02651	4.60E-09	15	66
11	Similar to heat shock protease protein; Hsp5	*CaO19.8442*	EAL02254	2.90E-03	8	43
12	Similar to heat shock protease protein; Hsp5	*CaO19.8442*	EAL02254	2.90E-03	8	43
13	mRNA cap-binding protein eIF4E	*CDC33*	EAL00500	7.70E-04	41	83
14	Potential Rho protein GDP dissociation inhibitor	*RDI1*	EAL04471	4.10E-18	16	75
15	Thiol specific antioxidant	*TSA1*	EAK97074	3.20E-07	10	55
16	Similar to both *S.cerevisiae* versions of hypusine-containing translation initiation factor eIF-5A	*TIF51*	EAK97745	1.50E-02	6	33
17	Hypothetical protein	*CaO19.3053*	EAL02753	2.60E-10	12	82
18	Potential alkyl hydroperoxide reductase	*AHP11*	EAL01672	4.60E-02	7	46
19	Potential alkyl hydroperoxide reductase	*AHP11*	EAL01672	2.40E-03	7	46
20	Likely HSP70 family chaperonin	*SSA2*	EAK94611	7.70E-03	15	32
21	Likely HSP70 family chaperonin	*SSA2*	EAK94611	2.90E-08	19	45
22	Elongation factor 1B	*EF1B*	CAA65366	ESI	3	15
23	Heat shock protein 70	*HSP70*	EAL03541	3.80E-02	27	67
24	Pyruvate decarboxylase	*CaO19.10395*	EAK96569	3.60E-03	15	34
25	Pyruvate decarboxylase	*CaO19.10395*	EAK96569	2.90E-08	17	54
	HSP70	*SSB1*	EAK97208	1.10E-08	12	24
26	HSP70	*SSB1*	EAK97208	2.00E-08	14	24
27	Co-chaperonin ST1-like orf, has 9 TPR repeats	*STI1*	EAK95695	7.60E-10	15	25
28	Co-chaperonin ST1-like orf, has 9 TPR repeats	*STI1*	EAK95695	1.10E-03	10	24

29	Similar to Human tumor protein, ortholog of *S. cerevisiae* Tma19p	*CaO19.3268*	EAK99010	ESI	5	38
30	Similar to Human tumor protein, ortholog of *S. cerevisiae* Tma19p	*CaO19.3268*	EAK99010	ESI	4	29
31	Inositil 1 phosphate synthase	*INO1*	EAL00459	6.80E-09	18	62
32	Potential nascent polypeptide-associated complex alpha subunit	*EGD2*	EAL04361	3.20E-02	9	48
33	Enolase similar to *S.cerevisiae* ENO1	*ENO1*	EAK92704	9.20E-10	17	65
34	Immunogenic alcohol dehydrogenase	*ADH1*	EAL03292	7.40E-05	8	27
35	29 kDa IgE-binding protein similar to *S. cerevisiae* YDR533C, GATase1	*CaO19.251*	EAL01090	2.20E-02	7	44
36	Transaldolase	*TAL1*	EAK96114	2.90E-12	18	61
37	Similar to *Pichia stipitis* xylitol dehydrogenase (XYL2)	*XYL2*	EAL00550	1.10E-07	14	61
38	Likely S-adenosylmethionine synthetase	*SAM2*	EAK94727	1.00E-04	12	35
39	Immunogenic alcohol dehydrogenase	*ADH1*	EAL03292	7.30E-08	14	49
40	Similar to *S.cerevisiae* 3 phosphoglycerate kinase	*PGK1*	EAK92141	7.30E-06	10	31
41	Similar to *S.cerevisiae* 3 phosphoglycerate kinase	*PGK1*	EAK92141	5.10E-07	13	35
42	Inorganic pyrophosphatase	*IPP1*	EAK95370	7.50E-04	9	51
43	Likely Coproporphyrinogen III oxidase	*HEM13*	EAK91775	2.00E-10	12	41
44	Fructose bisphosphate aldolase	*FBA1*	EAL04108	1.50E-04	9	26
45	Fructose bisphosphate aldolase	*FBA1*	EAL04108	1.40E-09	17	65
46	Fructose-bisphosphate aldolase	*FBA1*	EAL04108	8.10E-13	16	62
47	Potential oxidoreductase	*GRE22*	EAL01915	0.00013	11	38
48	Stationary-phase-induced protein	*SNZ99*	EAL02647	2.60E-12	15	45
49	Likely phosphomannomutase	*PMM1*	EAL02637	2.10E-10	13	44
50	Triosephophate isomerase	*TPI1*	CAB77631	1.30E-02	10	50
51	Triosephophate isomerase	*TPI1*	CAB77631	8.00E-02	10	47
52	Likely phosphoglycerate mutase	*GPM1*	EAL02334	6.80E-07	14	59
53	Likely guanylate kinase	*GUK1*	EAK91949	2.90E-08	12	44
54	Similar to Protoplasts-SecreTed protein (PST2)	*PST2*	EAK91104	1.50E-02	11	94
55	Potential nascent polypeptide-associated complex beta subunit	*EGD1*	EAK93932	7.40E-04	6	71
56	Cu,Zn-superoxide dismutase	*SOD1*	AAC12872	8.10E-07	8	62
57	Nucleoside diphosphate kinase-like orf	*YNK1*	EAL01916	3.80E-04	9	52
58	Likely cobalamin-independent methionine	*MET6*	EAK99386	2.90E-26	30	62

	synthase					
59	Transketolase 1	*TKT1*	CAA21989	1.80E-08	12	23
60	Transketolase 1	*TKT1*	CAA21989	1.70E-09	12	22
61	Likely cobalamin-independent methionine synthase, Met6p	*MET6*	EAK99386	4.40E-04	9	13
62	Hypothetical protein CaO19.5112, transketolase 1	*TKT1*	EAK98686	3.90E-07	10	20
63	Inorganic pyrophosphatase	*IPP1*	EAK95370	4.60E-06	11	49
64	Mannose-6-phosphate isomerase	*PMI1*	CAA57548	7.70E-05	10	35
65	Potential stress response protein	*DDR48*	EAK95180	3.00E-02	6	51
66	29 kDa IgE-binding protein similar to *S. cerevisiae* YDR533C, GATase1	*CaO19.7882*	EAL01225	8.10E-03	6	30
67	Pyruvate kinase	*CDC19*	EAK95958	5.80E-02	7	19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