SUPPLEMENTARY MATERIALS

Towards understanding the novel adhesin function of *Candida albicans* phosphoglycerate mutase at the pathogen cell surface: some structural analysis of the interactions with human host extracellular matrix proteins

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SUPPLEMENTARY FIGURES

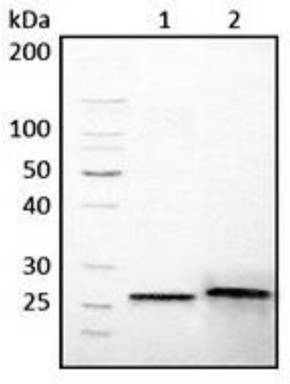

Figure S1. Electrophoretic characteristics of purified fungal proteins: (1) cell surface Gpm1 of *C. albicans* (2), recombinant Gpm1of *C. albicans*, obtained by heterologous overexpression in E. *coli*. Individual fungal proteins were analyzed by SDS-PAGE under reducing conditions in the Laemmli system with silver staining.

SUPPLEMENTARY TABLES

Table S1. Crosslinking between *C. albicans* Gpm1 and isolated *C. albicans* CWP – raw data of double repetition. MM range – a range of apparent molecular mass, estimated for protein bands excised from electrophoretic gels, based on the molecular mass standard sample, MM – theoretical molecular mass, Sc – scores, NP. – Number of peptides, SC – sequence coverage.

MM range (kDa)	**Swiss Prot protein database accession**	**Protein name**	**MM (kDa)**	**Sc**	**NP**	**S.C. (%)**
Samples with CWP repetition 1						
Above 200	ALS3_CANAL	Agglutinin-like protein 3	124.31	346	17	10
	RBT1_CANAL	Cell wall protein RTB1	74.49	68	1	5
120- 100	METE_CANAL	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	85.76	353	21	31
	PGK_CANAL	Phosphoglycerate kinase	45.27	114	8	22
	ALS3_CANAL	Agglutinin-like protein 3	124.31	73	4	5
70- 60	METE_CANAL	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	85.76	371	15	18
	PGK_CANAL	Phosphoglycerate kinase	45.27	173	9	21

	TSA1B_CANAL	Peroxiredoxin TSA1-B	21.96	118	4	22
	KPYK_CANAL	Pyruvate kinase	55.75	79	1	2
	EF2_CANAL	Elongation factor 2	93.86	66	5	7
40	PGK_CANAL	Phosphoglycerate kinase	45.27	714	32	69
	EF2_CANAL	Elongation factor 2	93.86	432	22	16
	METE_CANAL	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	85.76	335	12	19
	G6PI_CANAL	Glucose-6-phosphate isomerase	61.15	212	5	10
	TKT1_CANAX	Transketolase 1	73.84	210	6	12
	NNRD_CANAL	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	42.10	137	4	11
	SAHH_CANAL	Adenosylhomocysteinase	49.67	122	2	5
	TSA1B_CANAL	Peroxiredoxin	21.96	99	4	22
30-25	PGK_CANAL	Phosphoglycerate kinase	45.27	297	15	37
	EF2_CANAL	Elongation factor 2	93.86	296	18	20

	PMGY_CANAL	Phosphoglycerate mutase	27.44	152	12	31
	METE_CANAL	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	85.76	109	7	11
	TSA1B_CANAL	Peroxiredoxin	21.96	84	3	14
	SAHH_CANAL	Adenosylhomocysteinase	49.67	71	2	6
	TKT1_CANAX	Transketolase 1	73.84	68	2	3
25-20	PGK_CANAL	Phosphoglycerate kinase	45.27	278	12	29
	EF2_CANAL	Elongation factor 2	93.86	140	8	12
	RL10A_CANAL	60S ribosomal protein L10a	24.48	140	6	19
	PMGY_CANAL	Phosphoglycerate mutase	27.44	125	7	23
	SODM_CANAX	Superoxide dismutase [Mn], mitochondrial	26.21	91	1	5
	G6PI_CANAL	Glucose-6-phosphate isomerase	61.15	87	3	6
	TSA1B_CANAL	Peroxiredoxin	21.96	80	2	9
	SAHH_CANAL	Adenosylhomocysteinase	49.67	66	1	2

15	TSA1B_CANAL	Peroxiredoxin	21.96	330	14	48
	PMGY_CANAL	Phosphoglycerate mutase	27.44	103	9	33
	PGK_CANAL	Phosphoglycerate kinase	45.27	84	8	20
Control samples repetition 1						
Above 200	ALS3_CANAL	Agglutinin-like protein 3	124.31	374	18	10
	TSA1B_CANAL	Peroxiredoxin	21.96	83	3	20
120- 100	ALS3_CANAL	Agglutinin-like protein 3	124.31	66	6	5
70- 60	PGK_CANAL	Phosphoglycerate kinase	45.27	81	5	13
	METE_CANAL	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	85.76	68	7	13
40	EF2_CANAL	Elongation factor 2	93.86	239	15	14
	PGK_CANAL	Phosphoglycerate kinase	45.27	223	11	28
	G6PI_CANAL	Glucose-6-phosphate isomerase	61.15	201	7	13
	SAHH_CANAL	Adenosylhomocysteinase	49.67	98	2	6
	ENO1_CANAL	Enolase 1	47.20	70	1	2
30- 25	EF2_CANAL	Elongation factor 2	93.86	314	16	22

	G6PI_CANAL	Glucose-6-phosphate isomerase	61.15	220	10	20
	PGK_CANAL	Phosphoglycerate kinase	45.27	207	13	35
	SAHH_CANAL	Adenosylhomocysteinase	49.67	114	2	6
	METE_CANAL	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	85.76	91	3	5
	PMGY_CANAL	Phosphoglycerate mutase	27.44	73	4	10
25- 20	G6PI_CANAL	Glucose-6-phosphate isomerase	61.15	249	10	20
	PMGY_CANAL	Phosphoglycerate mutase	27.44	134	6	37
	PGK_CANAL	Phosphoglycerate kinase	45.27	129	8	23
	RL10A_CANAL	60S ribosomal protein L10a	24.48	128	7	35
	SAHH_CANAL	Adenosylhomocysteinase	49.67	118	4	10
	XYL1_CANAL	NAD(P)H-dependent D-xylose reductase I,II	36.67	106	5	18
	EF2_CANAL	Elongation factor 2	93.86	94	7	8

	SODM_CANAX	Superoxide dismutase [Mn], mitochondrial	26.21	78	1	5
	ENO1_CANAL	Enolase 1	47.20	68	1	2
15	TSA1B_CANAL	Peroxiredoxin	21.96	155	7	41
	SAHH_CANAL	Adenosylhomocysteinase	49.67	82	3	9
	TKT1_CANAX	Transketolase 1	73.84	78	3	5
	G6PI_CANAL	Glucose-6-phosphate isomerase	61.15	74	2	4
Samples with CWP repetition 2						
Above 200	ALS3_CANAL	Agglutinin-like protein 3	124310	266	16	7
	PMGY_CANAL	Phosphoglycerate mutase	27437	125	6	29
120	PMGY_CANAL	Phosphoglycerate mutase	27437	97	10	43
100	PGK_CANAL	Phosphoglycerate kinase	45266	189	11	32
	PMGY_CANAL	Phosphoglycerate mutase	27437	176	9	35
	METE_CANAL	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	85763	76	7	15
60-50	PGK_CANAL	Phosphoglycerate kinase	45266	254	11	31

	METE_CANAL	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	85763	240	10	16
	G6PI_CANAL	Glucose-6-phosphate isomerase	61148	224	8	16
	PMGY_CANAL	Phosphoglycerate mutase	27437	205	10	38
	KPYK_CANAL	Pyruvate kinase	55752	90	1	2
50	EF2_CANAL	Elongation factor 2	93865	507	25	23
	SAHH_CANAL	Adenosylhomocysteinase	49668	230	8	20
	TKT1_CANAX	Transketolase 1	73843	137	4	9
	ENO1_CANAL	Enolase 1	47202	114	3	9
	PGK_CANAL	Phosphoglycerate kinase	45266	111	7	20
	PMGY_CANAL	Phosphoglycerate mutase	27437	80	4	22
40	PGK_CANAL	Phosphoglycerate kinase	45266	867	39	77
	EF2_CANAL	Elongation factor 2	93865	513	24	19
	G6PI_CANAL	Glucose-6-phosphate isomerase	61148	222	12	28
	METE_CANAL	5-methyltetrahydropteroyltri	85763	118	6	11

		glutamate--homocysteine methyltransferase				
	TKT1_CANAX	Transketolase 1	73843	94	4	6
	SAHH_CANAL	Adenosylhomocysteinase	49668	93	2	6
30	PMGY_CANAL	Phosphoglycerate mutase	27437	448	24	58
	EF2_CANAL	Elongation factor 2	93865	250	11	13
	PGK_CANAL	Phosphoglycerate kinase	45266	91	5	13
30- 25	PMGY_CANAL	Phosphoglycerate mutase	27437	374	20	51
	PGK_CANAL	Phosphoglycerate kinase	45266	161	11	30
	EF2_CANAL	Elongation factor 2	93865	85	5	5
	TKT1_CANAX	Transketolase 1	73843	77		3
25	PMGY_CANAL	Phosphoglycerate mutase	27437	260	17	43
	RL10A_CANAL	60S ribosomal protein L10a	24477	204	9	29
	PGK_CANAL	Phosphoglycerate kinase	45266	185	10	24
	G6PI_CANAL	Glucose-6-phosphate isomerase	61148	94	3	6
	EF2_CANAL	Elongation factor 2	93865	91	4	5

	SODM_CANAX	Superoxide dismutase [Mn], mitochondrial	26214	88	1	5
	SAHH_CANAL	Adenosylhomocysteinase	49668	76	1	2
15	TSA1B_CANAL	Peroxiredoxin	21960	353	16	42
	PMGY_CANAL	Phosphoglycerate mutase	27437	219	12	38
Control samples repetition 2						
60-50	METE_CANAL	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	85763	72	5	9
	G6PI_CANAL	Glucose-6-phosphate isomerase	61148	66	5	10
50	EF2_CANAL	Elongation factor 2	93865	360	23	21
	SAHH_CANAL	Adenosylhomocysteinase	49668	152	7	19
	TKT1_CANAX	Transketolase 1	73843	128	6	11
	G6PI_CANAL	Glucose-6-phosphate isomerase	61148	113	5	10
	PGK_CANAL	Phosphoglycerate kinase	45266	77	4	11
40	EF2_CANAL	Elongation factor 2	93865	342	21	20

	PGK_CANAL	Phosphoglycerate kinase	45266	326	19	48
	G6PI_CANAL	Glucose-6-phosphate isomerase	61148	288	13	28
	METE_CANAL	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	85763	147	7	11
	SAHH_CANAL	Adenosylhomocysteinase	49668	117	3	8
	TKT1_CANAX	Transketolase 1	73843	70	1	2
30	EF2_CANAL	Elongation factor 2	93865	301	18	18
	PGK_CANAL	Phosphoglycerate kinase	45266	243	11	27
	SAHH_CANAL	Adenosylhomocysteinase	49668	119	4	7
	G6PI_CANAL	Glucose-6-phosphate isomerase	61148	117	4	9
30- 25	G6PI_CANAL	Glucose-6-phosphate isomerase	61148	177	6	11
	PGK_CANAL	Phosphoglycerate kinase	45266	165	11	31
	EF2_CANAL	Elongation factor 2	93865	161	10	11
	PMGY_CANAL	Phosphoglycerate mutase	27437	148	9	30

	TKT1_CANAX	Transketolase 1	73843	67	2	3
25	G6PI_CANAL	Glucose-6-phosphate isomerase	61148	183	7	14
	PGK_CANAL	Phosphoglycerate kinase	45266	167	8	18
	SAHH_CANAL	Adenosylhomocysteinase	49668	158	5	12
	EF2_CANAL	Elongation factor 2	93865	111	4	5
	RL10A_CANAL	60S ribosomal protein L10a	24477	84	5	19
	SODM_CANAX	Superoxide dismutase [Mn], mitochondrial	26214	81	1	5
	PMGY_CANAL	Phosphoglycerate mutase	27437	70	5	21
	ENO1_CANAL	Enolase 1	47202	69	2	6
15	TSA1B_CANAL	Peroxiredoxin	21960	187	10	41

Table S2. List of peptide matches from the MassMatrix PC server. For the underlined amino acids, mass shifts due to the sulfo-SDAD junction are indicated.

	Score	pp	pp$_2$	pp$_{\text{tag}}$
Peptides of *C. albicans* Gpm1				
$_{138}$Y$\underline{\text{A}}$DVDPA$\underline{\text{V}}$VPLTESLALVIDR$_{158}$	63	15.9	12.9	8.6
$_{116}$SFDVPPPKI$\underline{\text{D}}$PKDEYSQ$\underline{\text{V}}$GDR$_{136}$	57	9.1	8.5	5.1
$_{116}$SFDVPPP$\underline{\text{K}}_{123}$	47	14.4	9.6	4.7
$_{61}$AIQTANIA$\underline{\text{L}}$DAADQLYVPVK$_{80}$	58	23.9	10.1	4.1
$_{159}$L$\underline{\text{L}}$PYWQ$\underline{\text{D}}$EIAGDLLAGK$_{175}$	46	12.7	6.4	10.3
Peptides of human VTR				
$_{354}$IYISGMAP$\underline{\text{R}}$PSLAK$_{367}$	64	12.7	11.7	5.9
Peptides of human FN				
$_{904}$SDTVP$\underline{\text{S}}$PRDLQFVEVTD$\underline{\text{V}}$K$_{922}$	50	5.2	6.4	5.7
$_{1117}\underline{\text{L}}$GVRPSQGGEAPR$_{1129}$	61	18.2	8.0	5.5