

Supplementary Table 1. Peptide mass fingerprinting identification of cell wall-associated proteins of *S. pyogenes* isolate 5448, and percent identity of cell wall-associated proteins with human homologs.

Spot	Protein ^a	Function or pathway	Accession no. ^b	Molecular mass (kDa) ^c	pI ^c	Peptide matches ^d	Coverage (%) ^e	Human homolog ^f	
								Accession no. ^{b, g}	Identity (%) ^h
1	Enolase*	Glycolysis; Virulence factor	P69950	47.2	4.74	24	68.9	P09104	49
2	GAPDH	Glycolysis; Virulence factor	Q5XDW3	35.8	5.34	19	57.0	P04406	44
3	Chaperone protein DnaK (HSP70)	Chaperone	Q5XAD6	64.8	4.62	22	47.4	P38646	51
4	Putative carbamate kinase	Amino acid biosynthesis; arginine metabolism; pyrimidine nucleotide biosynthesis	Q8K6Q9	33.2	4.71	17	57.9	n/a	0
5	Putative alkyl hydroperoxidase	Peroxidase activity	Q7CEM3	20.5	4.65	11	58.1	P32119 ^o	39
6	General stress protein, Gls24 family	Stress protein	Q5XBW8	17.5	4.65	11	92.6	n/a	0
7	Putative thioredoxin	Electron transport	Q5XA57	13.6	5.06	8	45.8	B4DZQ3 ^d	41
8	LSU ribosomal protein L12P	Protein biosynthesis	Q5XCB4	12.9	4.42	9	77.0	n/a	0
9	Triosephosphate isomerase	Involved in several metabolic pathways	P69888	26.5	4.57	16	69.3	P60174	40
10	Fructose-bisphosphate aldolase	Glycolysis; sixth step	Q5XA12	31.0	4.91	16	52.1	n/a	0
11	Ribosome recycling factor	Protein synthesis	P68904	20.6	5.68	11	64.3	Q96E11	28
12	Putative phosphotransferase system (PTS), enzyme II component B	Protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	Q7CN95	17.9	6.13	14	78.5	n/a	0
13	Trigger factor	Protein folding and transport	Q5XA08	50.6	4.47	20	46.9	Q02790 ⁺	23
14	60 kDa chaperonin (GroEL)	Chaperone	Q8K5M5	56.9	4.75	28	62.4	P10809	47
15	Putative dipeptidase	Proteolysis and peptidolysis	Q99ZU1	51.3	4.87	17	46.1	Q96KP4 ^{tt}	43
16	Ornithine carbamoyltransferase	Arginine degradation; arginine deiminase pathway; second step	P65609	37.8	5.19	22	70.5	P00480	40
17	6-phosphofructokinase	Key control step of glycolysis	Q8P0S6	35.7	5.34	22	57.6	Q01813	37
18	Arginine deiminase	Virulence factor	Q5XAY2	46.2	4.99	26	68.5	n/a	0
19	Purine nucleoside phosphorylase	Purine-nucleoside phosphorylase activity	Q5XCL3	28.8	4.98	12	39.0	P00491 ^{tt}	45

20	Superoxide dismutase (Mn)	Virulence factor	Q8P0D4	22.5	4.87	9	57.0	P04179	50
21	Putative transketolase	Calcium ion binding; transketolase activity	Q8K670	77.5	4.98	16	29.5	P29401 ^d	33
22	10 kDa chaperonin (GroES)	Chaperone	P63771	10.3	4.79	8	86.5	P61604	32
23	30S ribosomal protein S6	Transcription	P66600	11.1	4.97	6	74.0	B9ZVW4 ^d	25
24	Phosphoenolpyruvate-protein phosphotransferase	Carbohydrate active-transport system	Q5XBI4	63.1	4.60	20	33.4	n/a	0
25	Putative NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	Metabolic enzyme	Q99Z67	50.4	5.06	23	50.1	P47895 ^d	32
26	Putative 2-dehydropantoate 2-reductase	Pantothenate biosynthesis	P65667	33.8	4.84	16	52.1	n/a	0
27	Protein phosphatase 2C	Phosphoprotein phosphatase activity	Q5XAP6	27.0	4.60	17	76.8	Q8N819	23
28	Adenylate kinase	Essential for maintenance and cell growth	P69882	23.7	4.83	18	84.0	P54819	39
29	Transcription elongation factor GreA	Transcription elongation	Q5XDQ7	19.7	5.08	12	77.8	n/a	0
30	M protein type 1*	Virulence factor	Q10372	54.2	6.53	14	33.3	Q15149 [†]	21
31	Chaperone protein DnaK (HSP70) fragment	Chaperone	Q8K624	64.8	4.61	9	15.0	P38646	51

^a GAS proteins implicated in human autoimmune complications are denoted by an asterisk (*).

^b Swiss-Prot/TrEMBL accession number.

^c Theoretical values obtained from Swiss-Prot/TrEMBL database.

^d Number of tryptic peptides detected by MALDI-TOF MS that could be matched to the protein.

^e Percentage of protein sequence covered by the matched peptides.

^f Top match identified by BLAST-P searches of the *Homo sapiens* database (using an E threshold of 1) at the Expasy/SIB BLAST network service (<http://au.expasy.org/tools/blast/>).

^g n/a (not applicable) indicates a human homolog of similar function was not identified.

^h GAS proteins without a known human homolog have zero percent identity.

[†] Human homolog identified using BLAST-P search does not have the same function as GAS protein.

[□] GAS or human protein has unknown function.