Supplemental Table 5. Proteins Increased in Blood Medium at 37 °C and 25 °C

Table 5A. Proteins Increased in Spores Produced on Blood at 37 °C over 25 °C

quasi.fdr	Protein ID	Protein Class/Name	KEGG Pathways	Pathway Names or Function (if found in KEGG)
		Amino Acid Metabolism		
1.46E-07	BAS0160	glucosamine--fructose-6-phosphate aminotransferase	bat00250, bat00520, bat01110	Alanine, aspartate and glutamate metabolism, Amino sugar and nucleotide sugar metabolism, Biosynthesis of secondary metabolites
7.33E-14	BAS2095	asparagine synthetase, glutamine-hydrolyzing	bat00250, bat01110	Alanine, aspartate and glutamate metabolism, Biosynthesis of secondary metabolites
2.92E-08	BAS2268	aspartate-semialdehyde dehydrogenase	bat00260, bat00270, bat00300, bat01110, bat01210	Glycine, serine and threonine metabolism, Cysteine and methionine metabolism, Lysine biosynthesis, Biosynthesis of secondary metabolites, 2-Oxocarboxylic acid metabolism
0.000557	BAS4253	phenylalanine 4-monooxygenase	bat00360, bat00400	Phenylalanine metabolism, Phenylalanine, tyrosine and tryptophan biosynthesis
4.38E-08	BAS4269	O-acetylserine lyase	bat00270	Cysteine and methionine metabolism
6.13E-09	BAS4271	hypothetical protein	bat00270	Cysteine and methionine metabolism
2.01E-05	BAS0331	5-methylribose kinase	bat00270	Cysteine and methionine metabolism
0.012818	BAS1876	amine oxidase, flavin-containing	bat00260, bat00330, bat00340, bat00350, bat00360, bat00380	Glycine, serine and threonine metabolism, Arginine and proline metabolism, Histidine metabolism, Tyrosine metabolism, Phenylalanine metabolism, Tryptophan metabolism
1.46E-07	BAS0160	glucosamine--fructose-6-phosphate aminotransferase	bat00250, bat00520, bat01110	Alanine, aspartate and glutamate metabolism, Amino sugar and nucleotide sugar metabolism, Biosynthesis of secondary metabolites
		Membrane, Wall or Surface Proteins		
1.55E-10	BAS5038	preprotein translocase subunit SecA		
0.00087	BAS0838	preprotein translocase subunit SecA		
4.78E-10	BAS3642	sugar ABC transporter, ATP-binding protein		
3.25E-09	BAS4334	ABC transporter, ATP-binding protein		
8.74E-06	BAS0248	ABC transporter, ATP-binding protein		
0.040258	BAS4723	ABC transporter, ATP-binding protein		
8.65E-08	BAS5137	UDP-N-acetylglucosamine 1-carboxyvinyltransferase		
1.55E-10	BAS5038	preprotein translocase subunit SecA		
		Other Enzymes and Proteins		
8.50E-05	BAS2680	acetyltransferase		
0.000148	BAS1263	acetyltransferase		
5.21E-12	BAS0197	aldo/keto reductase family oxidoreductase		Oxidoreductases
5.20E-09	BAS0329	alkyl hydroperoxide reductase, F subunit		Oxidoreductases
4.93E-07	BAS0314	aminopeptidase AmpS		Hydrolases
0.004355	BAS2448	cytochrome P450	bat00363, bat00624, bat00627, bat00903, bat01110	Bisphenol degradation, Polycyclic aromatic hydrocarbon degradation, Aminobenzoate degradation, Limonene and pinene degradation, Biosynthesis of secondary metabolites
4.59E-08	BAS2374	enoyl-CoA hydratase		

0.007344	BAS0227	fumarylacetoacetate hydrolase family protein		Secondary metabolites biosynthesis, transport and catabolism
4.00E-06	BAS3326	glyoxalase family protein		Secondary metabolites biosynthesis, transport and catabolism
4.59E-05	BAS3885	HAD superfamily hydrolase		Haloacid dehalogenase-like hydrolases
0.008603	BAS2017	HEAT repeat-containing PBS lyase		Virulence factor
3.01E-14	BAS2106	HSP20 family protein		
8.50E-05	BAS2680	acetyltransferase		
7.37E-12	BAS3072	isochorismatase family protein		
6.96E-05	BAS1014	LacI family sugar-binding transcriptional regulator		
0.000607	BAS4013	LacI family sugar-binding transcriptional regulator		
8.30E-06	BAS4005	lolS protein		Glyoxylase or a related metal-dependent hydrolase
0.017035	BAS4593	metallo-beta-lactamase family protein	bat00630	Glyoxylate and dicarboxylate metabolism
0.002565	BAS0557	molybdopterin oxidoreductase family protein		
1.51E-10	BAS0567	neutral protease		
0.008044	BAS0591	NorQ protein, putative		
1.09E-14	BAS5310	oligoendopeptidase F, putative		
1.40E-10	BAS3588	peptidase T		
9.56E-08	BAS5178	peptide chain release factor 1		
3.12E-07	BAS3707	phosphatase, putative		
3.93E-06	BAS4102	proline dipeptidase	bat03060	Protein export
1.93E-07	BAS3696	signal recognition particle protein		
2.36E-11	BAS3050	TPR domain-containing protein		
		Fatty Acid Biosynthesis and Degredation		
0.001326	BAS1017	lipoate-protein ligase A, putative	bat00785	Lipoic acid metabolism
0.002848	BAS4089	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	bat00061, bat00620, bat00640	Fatty acid biosynthesis, Pyruvate metabolism, Propanoate metabolism
		Glycolysis-Pyruvate metabolism-TCA cycle-Oxidative phosphorylation		
9.32E-11	BAS1176	dihydrolipoamide succinyltransferase	Citrate cycle (TCA cycle), Lysine degradation	Citrate cycle (TCA cycle), Lysine degradation, Biosynthesis of secondary metabolites
0.000197	BAS1177	2-oxoglutarate dehydrogenase E1 component	bat00020, bat00310, bat00380	Citrate cycle (TCA cycle), Lysine degradation, Tryptophan metabolism
0.000109	BAS2188	citrate synthase 3	bat00020, bat00630, bat01210	Citrate cycle (TCA cycle), Glyoxylate and dicarboxylate metabolism, 2-Oxocarboxylic acid metabolism
3.76E-05	BAS4773	gluconate 2-dehydrogenase	bat00030	Pentose phosphate pathway
		Nucleotide Metabolism		
0.040258	BAS3398	anaerobic ribonucleoside triphosphate reductase	bat00230, bat00240	Purine metabolism, Pyrimidine metabolism
0.005691	BAS4325	quinolinate synthetase	bat00760	Nicotinate and nicotinamide metabolism
		Transcription and Protein translation		
1.98E-13	BAS4472	threonyl-tRNA synthetase		
1.58E-14	BAS4936	tyrosyl-tRNA synthetase		
0.011693	BAS3670	prolyl-tRNA synthetase		
0.003931	BAS4836	transcriptional activator tipA, putative		

0.012427	BAS0976	transcriptional regulator Hpr		
1.34E-06	BAS0241	S1 RNA-binding domain-containing protein		
0.012427	BAS1601	TetR family transcriptional regulator		
0.000146	BAS4291	tRNA-specific 2-thiouridylase MnmA		
1.98E-13	BAS4472	threonyl-tRNA synthetase		
		Sporulation-Germination Proteins		
1.37E-08	BAS5185	stage 0 sporulation protein F		
0.000118	BAS5332	stage 0 sporulation protein J		
		Vitamin Metabolism		
2.92E-08	BAS4023	biotin synthase	bat00780	Biotin metabolism
9.92E-05	BAS4328	cysteine desulfurase	bat00730	Thiamine metabolism
		Hypothetical Proteins		
9.18E-11	BAS2803	hypothetical protein		
7.14E-12	BAS1431	hypothetical protein		
5.13E-11	BAS1255	hypothetical protein		
2.17E-05	BAS3621	hypothetical protein		
6.35E-05	BAS0394	hypothetical protein		
2.27E-05	BAS0915	hypothetical protein		
3.77E-07	BAS1468	hypothetical protein		
0.004289	BAS2664	hypothetical protein		
0.004248	BAS1250	hypothetical protein		
0.000272	BAS4426	hypothetical protein		
0.021434	BAS2158	hypothetical protein		
0.001927	BAS4448	hypothetical protein		
0.001865	BAS1377	hypothetical protein		
0.040258	BAS1643	hypothetical protein		
0.040258	BAS2081	hypothetical protein		
0.005272	BAS0997	hypothetical protein		
0.005272	BAS2284	hypothetical protein		
0.022284	BAS3328	hypothetical protein		
9.18E-11	BAS2803	hypothetical protein		

Table 5B. Proteins Increased in Spores Produced on Blood at 25 ^{o}C over 37 ^{o}C

quasi.fdr	Protein ID	Protein Class/Name	KEGG Pathways	Pathway Names or Function (if found in KEGG)
		Amino Acid Metabolism		
0.02597	BAS0228	homogentisate 1,2-dioxygenase, putative	bat00350, bat00643	Tyrosine metabolism, Styrene degradation
1.59E-10	BAS4070	leucine dehydrogenase	bat00280, bat00290	Valine, leucine and isoleucine degradation, Valine, leucine and isoleucine biosynthesis
		Membrane, Wall or Surface Proteins		
7.33E-14	BAS0638	immune inhibitor A metalloprotease		
2.46E-12	BAS1022	wall-associated protein, putative		
5.13E-11	BAS1048	S-layer protein, putative		
1.00E-11	BAS1197	immune inhibitor A metalloprotease	bat00650	Butanoate metabolism

2.08E-12	BAS1683	N-acetylmuramoyl-L-alanine amidase		
7.21E-13	BAS2277	N-acetylmuramoyl-L-alanine amidase		
9.39E-13	BAS3463	N-acetylmuramoyl-L-alanine amidase		
2.36E-11	BAS3140	ABC transporter, ATP-binding protein		Oxidoreductases
5.20E-10	BAS3377	oligopeptide ABC transporter, oligopeptide-binding protein, putative	bat00450	Selenocompound metabolism
1.40E-07	BAS2657	oligopeptide ABC transporter, oligopeptide-binding protein, putative		
0.00173	BAS4853	ABC transporter, substrate-binding protein, putative - 100% homology to methionine transporter in *B. cereus*	bat00362, bat00622	Benzoate degradation, Xylene degradation
9.13E-07	BAS2964	adhesion lipoprotein	bat00480	Glutathione metabolism
0.002512	BAS3747	cell-division initiation protein DivIVA	bat00860	Porphyrin and chlorophyll metabolism
7.28E-12	BAS2084	penicillin-binding protein 3		
6.23E-09	BAS4865	putative lipoprotein		
		Other Enzymes and Proteins		
0.001551	BAS0066	Hsp33-like chaperonin		
1.01E-06	BAS0405	general stress protein 26		
0.02597	BAS4914	general stress protein 20U		
7.43E-09	BAS0641	alcohol dehydrogenase, zinc-containing		
9.80E-06	BAS0687	CBS domain-containing protein		
5.97E-15	BAS1054	cold shock protein CspA		
6.13E-09	BAS2094	HSP20 family protein		
3.98E-12	BAS4537	thiol peroxidase		
3.98E-12	BAS4849	aminotransferase, class V		
0.001381	BAS4177	superoxide dismutase, Mn		
0.02597	BAS5226	4-oxalocrotonate tautomerase		
0.000102	BAS4792	leucyl aminopeptidase		
0.000196	BAS4359	delta-aminolevulinic acid dehydratase		
0.02597	BAS1287	D-alanine--poly(phosphoribitol) ligase subunit 1	bat00650	Butanoate metabolism
0.000102	BAS4753	DksA/TraR family DNA-binding protein		
3.23E-05	BAS4419	electron transfer flavoprotein, beta subunit		
1.44E-06	BAS4612	glucose-1-dehydrogenase		
0.001381	BAS4214	GrpE protein		Oxidoreductases
1.04E-08	BAS4467	M42 family peptidase	bat00450	Selenocompound metabolism
3.50E-06	BAS1045	M48 family peptidase		
2.52E-09	BAS5169	PTS system, glucose-specific IIA component, putative	bat00362, bat00622	Benzoate degradation, Xylene degradation
0.00173	BAS2658	NLP/P60 family protein	bat00480	Glutathione metabolism
1.31E-05	BAS4202	putative metalloprotease	bat00860	Porphyrin and chlorophyll metabolism
0.02597	BAS0350	Rieske 2Fe-2S iron-sulfur protein, putative		
0.02597	BAS0712	short chain dehydrogenase		
4.59E-08	BAS0288	SPFH domain-containing protein/band 7 family protein		
		Fatty Acid Biosynthesis and Degredation		

9.39E-13	BAS3932	acetyl-CoA acetyltransferase	bat00071, bat00280, bat00310, bat00362, bat00380, bat00620, bat00630, bat00640, bat00650, bat00900, bat01110	Fatty acid degradation, Valine, leucine and isoleucine degradation, Lysine degradation, Benzoate degradation, Tryptophan metabolism, Pyruvate metabolism, Glyoxylate and dicarboxylate metabolism, Propanoate metabolism, Butanoate metabolism, Terpenoid backbone biosynthesis, Biosynthesis of secondary metabolites
1.19E-10	BAS5116	(3R)-hydroxymyristoyl-ACP dehydratase	bat00061, bat00780	Fatty acid biosynthesis, Biotin metabolism
		Glycolysis-Pyruvate metabolism-TCA cycle-Oxidative phosphorylation		
1.62E-05	BAS3179	putative translaldolase	bat00030, bat01110	Pentose phosphate pathway, Biosynthesis of secondary metabolites
0.02597	BAS0637	putative translaldolase	bat00030, bat01110	Pentose phosphate pathway, Biosynthesis of secondary metabolites
0.02597	BAS3965	N-acetylglucosamine-6-phosphate deacetylase		
9.79E-09	BAS4414	succinate dehydrogenase, cytochrome b558 subunit	bat00020, bat00190, bat00650, bat01110	Citrate cycle (TCA cycle), Oxidative phosphorylation, Butanoate metabolism, Biosynthesis of secondary metabolites
6.35E-06	BAS4492	pyruvate kinase	bat00010, bat00230, bat00620, bat01110	Glycolysis / Gluconeogenesis, Purine metabolism, Pyruvate metabolism, Biosynthesis of secondary metabolites
0.000132	BAS4493	6-phosphofructokinase	bat00010, bat00030 , bat00051, bat00052	Glycolysis / Gluconeogenesis, Pentose phosphate pathway, Fructose and mannose metabolism, Galactose metabolism
0.02597	BAS1784	L-lactate dehydrogenase	bat00010, bat00270, bat00620, bat00640	Glycolysis / Gluconeogenesis, Cysteine and methionine metabolism, Pyruvate metabolism, Propanoate metabolism
		Nucleotide Metabolism		
3.51E-07	BAS0137	DNA-directed RNA polymerase subunit alpha	bat00230, bat00240	Purine metabolism, Pyrimidine metabolism
0.02597	BAS4270	5prime-methylthioadenosine/S-adenosylhomocysteine nucleosidase	bat00230, bat00240, bat00760	Purine metabolism, Pyrimidine metabolism, Nicotinate and nicotinamide metabolism
0.001381	BAS4009	5prime-nucleotidase family protein	bat00230, bat00240, bat00760	Purine metabolism, Pyrimidine metabolism, Nicotinate and nicotinamide metabolism
0.000102	BAS1372	purine nucleoside phosphorylase	bat00230, bat00240, bat00760	Purine metabolism, Pyrimidine metabolism, Nicotinate and nicotinamide metabolism
0.000132	BAS5320	adenylosuccinate synthetase		bat00230, bat00250
0.02597	BAS2301	DEAD-box ATP dependent DNA helicase		
6.12E-06	BAS3658	polynucleotide phosphorylase/polyadenylase		
		Transcription and Protein translation		
4.24E-12	BAS3559	RNA-binding protein Hfq		RNA degradation
6.35E-12	BAS0099	50S ribosomal protein L10		
4.84E-07	BAS0126	50S ribosomal protein L18		
3.38E-07	BAS4275	transcription elongation factor GreA		
9.13E-07	BAS4471	translation initiation factor IF-3		
		Sporulation-Germination Proteins		
1.50E-06	BAS1192	spore coat-associated protein		

9.37E-14	BAS3653	dipicolinate synthase subunit B		
		Vitamin metabolism		
		Hypothetical Proteins		
7.05E-06	BAS2320	hypothetical protein		
0.02597	BAS1349	hypothetical protein		
0.02597	BAS3647	hypothetical protein		
0.001452	BAS4087	hypothetical protein		
0.02597	BAS3081	hypothetical protein		
0.02597	BAS1620	hypothetical protein		
0.002512	BAS1302	hypothetical protein		
0.000102	BAS1467	hypothetical protein		
0.000132	BAS0289	hypothetical protein		
0.000132	BAS4281	hypothetical protein		
5.61E-06	BAS4283	hypothetical protein		
2.17E-07	BAS4755	hypothetical protein		
1.07E-06	BAS0820	hypothetical protein		
2.40E-11	BAS4934	hypothetical protein		
8.82E-11	BAS3372	hypothetical protein		
7.05E-06	BAS2320	hypothetical protein		