

<b>Table 3. <i>Salmonella typhimurium</i> proteins identified in flight and ground total cell samples from STS-115 using MudPIT analysis (251 proteins total)</b>				
<b>Protein name</b>	<b>Accession number</b>	<b>Protein molecular weight (Daltons)</b>	<b>Ground total cell protein ID probability*</b>	<b>Flight total cell protein ID probability*</b>
aspartate ammonia-lyase	gi 16767575	52268.1	100%	100%
translation elongation factor EF-Tu.A	gi 96718	43233.6	100%	100%
elongation factor G	gi 16766735	77582	100%	100%
putative hydrogenase membrane component precursor	gi 16764429	37497.2	100%	100%
GroEL protein	gi 16767579	57267.8	100%	100%
30S ribosomal protein S1	gi 16764341	61154.4	100%	100%
L-asparaginase	gi 16766407	36908.5	100%	100%
phosphoenolpyruvate carboxykinase	gi 16766788	59559.8	100%	100%
enolase	gi 16766258	45468	100%	100%
glyceraldehyde 3-phosphate dehydrogenase A	gi 16764641	35568.6	100%	100%
periplasmic glycerophosphodiester phosphodiesterase	gi 16765609	40407.8	100%	100%
molecular chaperone DnaK	gi 16763402	69241.2	100%	100%
30S ribosomal protein S3	gi 16766723	25965.5	100%	100%
formate acetyltransferase 1	gi 16764333	84989.4	100%	100%
50S ribosomal subunit protein L7/L12	gi 16767406	12281	100%	100%
ribosomal protein S7	gi 16766736	17572.5	100%	100%
histone like DNA-binding protein HU-alpha (NS2) (HU-2)	gi 16767424	9503.1	100%	100%
glycerol kinase	gi 16767352	56046.2	100%	100%
dihydrodipicolinate dehydrogenase	gi 16763544	50621.8	100%	100%
sn-glycerol-3-phosphate dehydrogenase	gi 16766813	56908.5	100%	100%
trigger factor	gi 16763828	48048.1	100%	100%
cold shock protein	gi 16765178	7384.3	100%	100%
DNA-binding protein HLP-II	gi 16765095	15525	100%	100%
ATP synthase beta subunit	gi 16767149	50265.5	100%	100%
phosphoglycerate kinase	gi 16766370	41115.1	100%	100%
iron-dependent alcohol dehydrogenase AdhE	gi 16765093	96199.8	100%	100%
50S ribosomal subunit protein L1	gi 16767404	24710.5	100%	100%
30S ribosomal protein S4	gi 16766705	23467.7	100%	100%
50S ribosomal subunit protein L13	gi 16766640	16000.7	100%	100%
putative outer membrane porin precursor	gi 16764916	39662.7	99%	99%
FKBP-type peptidyl-prolyl cis-trans isomerase	gi 16766742	28928.6	100%	100%
transketolase 1 isozyme	gi 16766377	72117	100%	100%
50S ribosomal subunit protein L5	gi 16766717	20300.6	100%	100%
DNA-directed RNA polymerase beta' subunit	gi 16767408	15522.0	100%	100%
30S ribosomal protein S13	gi 16766707	13144.1	100%	100%
alkyl hydroperoxide reductase C22 subunit	gi 16763985	20729.7	100%	100%
30S ribosomal subunit protein S5	gi 16766712	17585	100%	100%
50S ribosomal protein L24	gi 16766718	11298.3	100%	100%
DNA protection during starvation protein	gi 16764193	18699.8	100%	100%
ribosomal protein L19	gi 16765988	13112	100%	100%
acyl carrier protein	gi 16764551	8621.4	100%	100%
isocitrate dehydrogenase	gi 16764593	45771	100%	93%
triosephosphate isomerase	gi 16767347	26899	100%	100%
50S ribosomal subunit protein L3	gi 16766729	22228.7	100%	100%
30S ribosomal protein S2	gi 16763606	26741.2	100%	100%
lysine decarboxylase	gi 16765879	81220.5	100%	100%
putative universal stress protein	gi 16763991	15882.8	100%	100%
putative thiol-alkyl hydroperoxide reductase	gi 16763782	22299	100%	100%
50S ribosomal protein L9	gi 16767640	15765.8	100%	100%
50S ribosomal subunit protein L10	gi 16767405	17782.8	100%	100%
30S ribosomal subunit protein S16	gi 16765991	9216.7	100%	100%
50S ribosomal protein L20	gi 16764687	13479.6	100%	100%
pyruvate kinase	gi 16764728	50639.5	100%	98%
6-phosphogluconate dehydrogenase	gi 16765411	51379.2	100%	93%
inorganic pyrophosphatase	gi 16767660	19658.8	100%	100%
50S ribosomal protein L4	gi 16766728	22068.6	100%	100%
50S ribosomal protein L11	gi 16767403	14857.5	100%	100%
50S ribosomal subunit protein L17	gi 16766703	14377.2	100%	100%

succinyl-CoA synthetase beta chain	gij 16764108	41462.8	100%	100%
50S ribosomal subunit protein L6	gij 16766714	18841.3	100%	100%
fructose 1,6-bisphosphate aldolase	gij 16766369	39138.4	100%	100%
aconitate hydratase 2	gij 16763548	93513.7	100%	100%
iron superoxide dismutase	gij 16764779	21290.4	100%	100%
50S ribosomal protein L22	gij 16766724	12208.6	100%	100%
sn-glycerol-3-phosphate dehydrogenase large subunit	gij 16765611	59039.6	100%	100%
RNA polymerase, alpha subunit	gij 16766704	36494.1	100%	100%
30S ribosomal protein S10	gij 16766730	11748.8	100%	100%
RNA polymerase, beta subunit	gij 16767407	150586.6	100%	99%
polynucleotide phosphorylase	gij 16766580	77020.9	100%	100%
Lpp1 murein lipoprotein	gij 16764727	8373.6	100%	93%
malate dehydrogenase	gij 16766654	32457.8	100%	100%
citrate synthase	gij 16764100	48089.9	100%	100%
GroES protein	gij 16767578	10300.1	100%	100%
putative glutamic dehydrogenase-like protein	gij 16765136	48020.6	100%	100%
succinyl-CoA synthetase alpha subunit	gij 16764109	29757.8	99%	100%
transaldolase B	gij 16763397	35154.5	100%	100%
glycine dehydrogenase	gij 16766354	104270.1	93%	100%
transcription elongation factor NusA	gij 16766585	55408.3	100%	100%
flagellar biosynthesis filament structural protein	gij 16766083	52518.5	100%	100%
elongation factor Ts	gij 16763607	30339.6	100%	100%
N-acetylneuraminatase lyase	gij 16766634	32437.7	100%	100%
50S ribosomal subunit protein L32	gij 16764546	6428.4	100%	100%
ATP synthase alpha subunit	gij 16767151	5509.6	100%	97%
50S ribosomal subunit protein L14	gij 16766719	13550.2	99%	100%
phosphate acetyltransferase	gij 16765792	82305.8	100%	100%
50S ribosomal subunit protein L15	gij 16766710	14948.9	100%	100%
ribose-phosphate pyrophosphokinase	gij 16765121	34198.6	100%	88%
hydrogenase-2 large subunit	gij 16766447	62420.6	100%	100%
cytoplasmic ferritin	gij 16765276	19262.5	100%	100%
riboflavin synthase subunit beta	gij 16763797	15990.5	100%	97%
50S ribosomal subunit protein L29	gij 16766721	7242.6	100%	93%
putative universal stress protein	gij 16764996	15696.7	93%	100%
periplasmic nitrate reductase	gij 16765587	92856.9	100%	93%
hyperosmotically-inducible periplasmic protein	gij 16767802	21430.3	93%	93%
ornithine carbamoyltransferase	gij 16767710	36798.4	100%	100%
30S ribosomal protein S11	gij 16766706	13812.8	100%	100%
formate dehydrogenase alpha subunit	gij 16767302	112357.4	100%	100%
nucleoside diphosphate kinase (ndk)	gij 16765846	15503.7	100%	100%
putative pyruvate-flavodoxin oxidoreductase	gij 16764995	128563.7	55%	100%
glycoprotein/polysaccharide metabolism protein	gij 16763846	19458.9	100%	100%
O-acetyl serine sulfhydrylase	gij 11514514	34414.7	93%	100%
30S ribosomal subunit protein S21	gij 16766509	8482.1	100%	100%
ornithine decarboxylase isozyme	gij 16764071	82432.6	100%	99%
fumarate reductase	gij 16767591	27157.3	100%	100%
anaerobic glycerol-3-phosphate dehydrogenase subunit B	gij 16765612	45653.3	100%	100%
glucose-specific PTS system enzyme IIA component	gij 16765753	18229.5	100%	100%
DNA-directed RNA polymerase omega subunit	gij 16767026	10218.3	100%	100%
FKBP-type peptidyl-prolyl cis-trans isomerase	gij 16766744	20767.9	100%	100%
pyruvate dehydrogenase E1 component	gij 16763542	99564	100%	97%
phosphate acetyltransferase	gij 16765665	77261.1	100%	93%
glucose-6-phosphate isomerase	gij 16767471	61412.3	100%	93%
putative oxidase	gij 16764715	113118.3	93%	99%
50S ribosomal subunit protein L16	gij 16766722	15176.6	100%	100%
enterobactin synthetase component F	gij 16763965	141727.2	78%	99%
50S ribosomal subunit protein L2	gij 16766726	29802.2	93%	100%
acetyl-coenzyme A carboxylase subunit alpha	gij 16763622	35327.3	100%	59%
pyruvate kinase	gij 16765230	51369.5	100%	93%
serine hydroxymethyltransferase	gij 16765875	45437	100%	93%
50S ribosomal subunit protein L28	gij 16767013	9032.6	93%	93%
isoaspartyl dipeptidase	gij 16767756	40306.8	100%	93%
sensory histidine kinase	gij 16765598	106264.3	100%	79%
putative inner membrane lipoprotein	gij 16765852	179631.1	87%	87%
Initiation factor IF-3	gij 16419853	16619.9	100%	100%

putative protease	gij 16764427	65586.3	99%	97%
thiosulfate reductase electron transport protein PhsB	gij 16765394	21300.7	93%	100%
dihydrolipoamide acetyltransferase	gij 16764107	43839.8	100%	100%
protein-export protein SecB	gij 16766986	17227	100%	100%
cytochrome d terminal oxidase polypeptide subunit I	gij 16764110	58299.5	100%	100%
putative detox protein in ethanolamine utilization	gij 16765785	9824.4	100%	100%
galactose transport protein	gij 16765520	35796.1	100%	99%
putative translation initiation inhibitor	gij 16767703	13557.2	100%	93%
dihydrolipoamide acetyltransferase	gij 16763543	66121.5	100%	93%
glutamine ABC transporter periplasmic-binding protein	gij 16764192	27245.6	93%	93%
putative selenocysteine synthase	gij 16767692	39874.5	47%	93%
30S ribosomal protein S20	gij 16763433	9637.9	100%	93%
NADH dehydrogenase I chain G	gij 16420864	100254.5	100%	100%
acetyl-CoA carboxylase	gij 16766675	49245.8	99%	100%
RNase E	gij 16764541	119381.7	100%	100%
fructose-1,6-bisphosphatase	gij 16767661	36781.5	100%	100%
phosphoenolpyruvate synthase	gij 16764700	87191.6	100%	100%
putative formate acetyltransferase	gij 16765966	14326.2	100%	93%
lipoprotein	gij 16765808	36919.8	100%	93%
sensory transduction histidine kinase	gij 16764736	65221.8	93%	54%
sensory kinase in two-component system with CreB	gij 16767830	51666.7	93%	59%
agmatinase	gij 16766379	33585.5	100%	100%
aminoacyl-histidine dipeptidase	gij 16763698	52419.9	93%	100%
30S ribosomal subunit protein S19	gij 16766725	10398.5	100%	93%
glucose-1-phosphate adenyllyltransferase	gij 16766822	48444.5	100%	83%
acetate kinase	gij 16765664	43240.3	100%	92%
ABC superfamily peptide transport protein	gij 16765039	30654.8	48%	100%
potassium-transporting ATPase subunit B	gij 16764075	72125	99%	74%
adenylosuccinate synthetase	gij 16767612	47359.7	100%	100%
ATP synthase delta subunit	gij 16767152	19394.2	97%	100%
glycerol dehydrogenase	gij 16767374	38723.5	100%	96%
succinate dehydrogenase catalytic subunit	gij 16764105	26847.2	100%	93%
FkbP-type peptidyl-prolyl cis-trans isomerase	gij 16767643	23719.2	100%	93%
putative sigma(54) modulation protein	gij 16765980	12634.6	100%	93%
ATP synthase epsilon subunit	gij 16767148	15046.6	100%	93%
putative cytoplasmic protein	gij 16765717	10269.4	100%	93%
needle complex major subunit PrgI	gij 16766179	8839.3	93%	100%
cytochrome o ubiquinol oxidase subunit I	gij 16763823	74265.7	93%	100%
fumarate reductase, flavoprotein subunit	gij 16767592	65473.9	93%	100%
putative lipoprotein	gij 16764058	12218.6	72%	96%
phase 1 flagellin	gij 16765297	51594.5	100%	100%
transcription termination factor Rho	gij 16767192	46977.2	100%	100%
arginine deiminase	gij 16767712	45544.5	99%	100%
serine endoprotease	gij 16766643	47310.1	93%	100%
putative fructose-1,6-bisphosphate aldolase	gij 16767344	31725.2	93%	100%
NADH dehydrogenase I chain F	gij 16765651	49229.2	100%	93%
small membrane protein A	gij 16766000	12327	93%	100%
single-strand DNA-binding protein	gij 16767506	19055.5	93%	100%
aldehyde oxidoreductase	gij 3885918	49239.5	93%	100%
PilQ ATP-binding protein	gij 32470257	58267.7	98%	86%
BipA GTPase	gij 16767274	67359.4	100%	66%
TrpR binding protein Wrba	gij 16764477	20849.7	100%	93%
catalase HPII	gij 16764669	83610.2	93%	100%
ethanolamine utilization protein EutL	gij 16765776	22678	100%	81%
nikB plasmid protein	gij 20521580	103992.3	79%	100%
thioredoxin	gij 16767191**	11789.4	100%	0
aldose 1-epimerase	gij 16764640	32541.6	100%	0
phosphopentomutase	gij 16767810	44227.1	100%	0
D-ribose-binding protein	gij 1070661	28512.8	93%	0
oriT nickase/helicase	gij 16445291	191664	100%	0
DNA polymerase I	gij 16767264	103114.9	93%	0
ATPase subunit	gij 7594817	46171.1	100%	0
phosphoglyceromutase	gij 16766989	56237.5	100%	0
putative periplasmic protein	gij 16765796	38706.3	100%	0
inositol-5-monophosphate dehydrogenase	gij 16765831	51930.1	100%	0

putative ATP-dependent helicase	gij 16765162	70268.1	93%	0
hydrogenase 3 large subunit	gij 16766155	65003.1	100%	0
mannose-specific enzyme IIAB	gij 16765171	34969.2	100%	0
30s ribosomal protein S6	gij 16767637**	15154.9	100%	0
dipeptide transport protein	gij 16766917	60202.5	100%	0
D-fructose-6-phosphate amidotransferase	gij 16767145	66860.7	100%	0
tetrathionate reductase subunit A (TtrA)	gij 16764733	110976.9	97%	0
uridine phosphorylase	gij 16422527	27205.9	100%	0
anaerobic dimethyl sulfoxide reductase chain B	gij 16764326**	22761.6	100%	0
virulence-associated protein mkfB	gij 7443056	62570.6	100%	0
prolyl-tRNA synthetase	gij 16763631	63522.6	100%	0
cytosine deaminase	gij 16766629	47608	100%	0
ribosome recycling factor	gij 16763609	20538	100%	0
dihydrodipicolinate synthase	gij 16765809**	31276.4	100%	0
putative dehydrogenase	gij 16765715	77238.8	99%	0
outer membrane-bound fatty acid transporter	gij 16765718	47688.5	93%	0
putative cytoplasmic protein	gij 16763672**	79560.5	99%	0
2-dehydro-3-deoxyphosphooctonate aldolase	gij 16765113	30777.4	93%	0
periplasmic maltose-binding protein	gij 16767479	43468	100%	0
chemotactic response protein	gij 16765257**	23902.4	100%	0
putative acetyltransferase	gij 16765805	74000	100%	0
phosphoglucosamine mutase	gij 16766590	47424.2	100%	0
ATP-dependent RNA helicase	gij 16765963	50040.2	100%	0
glutamine synthetase	gij 16767272	51768.7	100%	0
outer membrane protein Tsx	gij 16763793	32761.5	100%	0
ribonuclease R (RNase R)	gij 16767614	92033.1	99%	0
DNA-binding protein HU-beta	gij 16763832	9222	99%	0
putative zinc-binding dehydrogenase	gij 16764887	37229	100%	0
transcriptional repressor for rbs operon (GalR/LacI family)	gij 16767170	36702.1	100%	0
ubiquinone/menaquinone methyltransferase UbiE	gij 16767240	28118.9	100%	0
phosphoheptose isomerase	gij 16763693	20878.5	100%	0
ClpB ATP-dependent protease	gij 16765976	95421.8	99%	0
putative pyrophosphatase	gij 16766260	30812.9	99%	0
putative GTP-binding protein	gij 16766597	43086.7	99%	0
putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase	gij 16767370	56560	98%	0
hypothetical ABC transporter ATP-binding protein	gij 16763887	24467.3	98%	0
putative glycosyl transferase	gij 16765625	36500	98%	0
citrate lyase alpha chain	gij 56967225	54561.7	97%	0
arginine-binding periplasmic protein 1 precursor	gij 16764251	26979.4	0	93%
cold shock-like protein cspE	gij 16764006	7433.5	0	93%
outer membrane protein C	gij 16765595**	41222.1	0	93%
lysine decarboxylase 2	gij 16763624	80747.8	0	93%
putative integral membrane protein	gij 16764196	59589.3	0	93%
aminopeptidase B	gij 16765856	46339	0	93%
glycerate kinase II	gij 16763905	39003.1	0	99%
ecotin precursor	gij 16765590	18199.7	0	100%
3,4-dihydroxy-2-butanone 4-phosphate synthase	gij 16766495	23292.3	0	86%
2-oxoglutarate dehydrogenase	gij 16764106	104805.9	0	100%
D-ribose-binding periplasmic protein	gij 16767168	30944.8	0	99%
flagellar hook-associated protein	gij 16765298	49818.7	0	87%
cysteine desulfurase	gij 16765863	45075.7	0	83%
hydrogenase-3 accessory protein	gij 16766161**	31375.2	0	99%
putative imidazolonepropionase or amidohydrolase	gij 16767659	42408	0	100%
asparagine synthetase B	gij 16764050	62555.9	0	100%
50S ribosomal subunit protein L30	gij 16766711**	6495.8	0	100%
50S ribosomal subunit protein L23	gij 16766727**	11194.9	0	100%
membrane-bound ATP synthase, epsilon-subunit	gij 6625704	14848.1	0	100%
hydrogenase-2 small chain protein	gij 16766450	39604.2	0	100%
ATP synthase subunit C	gij 16767150	31538	0	100%
precorrin-8X methylmutase	gij 16765363	23016.8	0	99%
translation initiation factor IF-2	gij 16766584	97383.5	0	99%
ethanolamine ammonia-lyase heavy chain	gij 16765778	49432	0	99%
putative copper-transporting ATPase	gij 16763878	87893	0	99%

\*Peptide samples obtained from MudPIT were analyzed using Sequest and X!Tandem software, and the data was organized using the Scaffold program. To be considered a positive identification in Scaffold, the following parameters were used: a minimum of 2 peptides from a given protein identified with peptide and protein thresholds of 80% to give an overall protein identification (ID) probability of at least 80%. Note that a protein ID probability of greater than 80% in at least one of the samples warranted inclusion in the table so as to allow identification of possible differential expression of a given protein.

\*\*Proteins identified via MuDPIT analysis as differentially expressed that also displayed differential expression via microarray analysis.