SUPPLEMENTAL MATERIAL

MS/MS data acquired through WARP-LC were searched on MASCOT (Version 2.4.1) using ProteinScape (Version 3.0, Bruker Daltonics) with the search restricted to *Salmonella* on the UniProtKB/SwissProt database (status May 2013). This search was limited to tryptic peptides with variable methionine, histidine, and tryptophan oxidation, and MS/MS mass tolerance of ± 0.8 Da. The peptide mass tolerance was set to ± 100 ppm. The peptide charge was defined as +1 and two miscleavages were allowed. A peptide decoy database as well as percolator algorithm were used to improve significance of search results.

The analysis of the acquired data by searching the UniProtKB/SwissProt database yielded a number of proteins for each sample, ranging from 239 to 322 proteins. As a comparison, the number of protein peaks found by classical whole cell protein MALDI-TOF MS ranged only from 51 to 59.

Table S1 gives an overview of the biomarker peptides identified for the three subspecies *Salmonella enterica* subsp. *arizonae*, *S. enterica* subsp. *enterica*, and *S. enterica* subsp. *houtenae* which were assigned to *Salmonella* proteins in the MASCOT search on the UniProtKB/SwissProt database. Of note, no biomarker peptides could be annotated to *S. enterica* subsp. *houtenae*, since the UniProtKB/SwissProt database contained only two protein entries for this subspecies at the time of the analysis, namely the guanine nucleotide exchange factor SopE and the inositol phosphate phosphatase SopB, to none of which a biomarker peptide could be annotated.

***Salmonella* subspecies**	**Assigned protein**	**Protein mass (kDa)**	**Biomarker peptide mass (Da)**	**Amino acid exchange (subspecies)**	**Search parameters (± ppm)°**
S. arizonae	6-phospho-gluconolactonase	36.4	3,004.52 ± 0.03	A→C, Y→H, A→V (ent) A→C, Y→H, A→V, E→A (hou)	25 50 100
S. arizonae	60 kDa chaperonin	57.3	1,602.88 ± 0.01	N→T (ent*, hou*)	25
S. arizonae	ATP-dependent protease ATP-binding subunit HslU	49.6	2,889.48 ± 0.00	V→I, T→A (ent*, hou*)	25 50 100
S. arizonae	Cell division protein ZipA homolog	36.1	2,457.00 ± 0.02	DA→EE (ent*) S→A, DA→EE (hou*)	25
S. arizonae	Lysine-tRNA ligase	57.6	2,923.32 ± 0.05	Q→L (ent, hou)	50
S. arizonae	Molecular chaperone DnaK	69.3	2,464.23 ± 0.00	M→T (ent*, hou*)	25
S. enterica	50S ribosomal protein L17	14.4	2,551.20 ± 0.02	(–)→S, T→A (ari*, hou*)	25 50 100
			2,567.19 ± 0.02 (oxidized)	(–)→S, T→A (ari*, hou*)	25 50 100
S. enterica	Flagella synthesis protein FlgN	16.0	3,103.55 ± 0.01	D→N, S→A (ari) D→N (hou)	25 50 100
S. enterica	Glutamine-fructose-6-phosphate aminotransferase [isomerizing]	66.8	2,722.40 ± 0.02	A→S (ari, hou)	25 50 100
S. enterica	Glutaredoxin-1 Grx1	9.9	1,114.49 ± 0.01	K→N (ari, hou)	25
S. enterica	H-NS histone family	15.5	1,979.88 ± 0.01	MD→IN (ari) D→G (hou)	25
S. enterica	Nucleoside diphosphate kinase	15.5	2,424.11 ± 0.02	L→F (ari*, hou*)	25
S. enterica	Outer membrane protein A	38.4	3,540.76 ± 0.03	V→T, P→A, T→Y (ari) V→A, GP→(–)Y (hou)	25 50 100
			3,956.00 ± 0.04 (missed cleavage)	V→T, P→A, T→Y (ari) V→A, GP→(–)Y (hou)	25 50 100
S. enterica	Probable thiol peroxidase	18.0	2,379.23 ± 0.01	S→N (ari) T→A (hou)	25
S. enterica	Transaldolase 1	35.1	3,048.54 ± 0.02	H→N (ari, hou)	25 50 100

TABLE S1 Complete list of biomarker peptides assigned to *Salmonella* proteins in the MASCOT search on the UniProtKB/SwissProt database. The peptide masses are given as the arithmetic mean calculated from the values of the three replicates of the subspecies with the according standard deviation. All numbers were rounded to the second digit after the coma.

*: Sequence analogous to biomarker peptide observed. (–): missing amino acid. °: for all searches S/N = 10. ari: *S*. *enterica* subsp. *arizonae*, ent: *S*. *enterica* subsp. *enterica*, hou: *S*. *enterica* subsp. *houtenae*.

***Salmonella* subspecies**	**Assigned protein**	**Protein mass (kDa)**	**Biomarker peptide mass (Da)**	**Amino acid exchange (subspecies)**	**Search parameters (± ppm)°**
S. arizonae	6-phospho-gluconolactonase	36.4	3,004.52 ± 0.03	A→C, Y→H, A→V (ent) A→C, Y→H, A→V, E→A (hou)	25 50 100
S. arizonae	60 kDa chaperonin	57.3	1,602.88 ± 0.01	N→T (ent*, hou*)	25
S. arizonae	Aminoacyl-histidine dipeptidase	52.5	2,704.27 ± 0.03	K→T (ent*, hou)	25 50 100
S. arizonae	Arsenate reductase	13.4	1,420.81 ± 0.00	E→D (ent*) E→D, G→S (hou*)	25
S. arizonae	ATP-dependent protease ATP-binding subunit HslU	49.6	2,889.48 ± 0.00	V→I, T→A (ent*, hou*)	25 50 100
S. arizonae	Cell division protein DamX	45.3	2,643.06 ± 0.01	V→D (ent*, hou*)	25 50 100
S. arizonae	Chromosomal replication initiation protein	49.9	2,235.13 ± 0.01	P→S (ent, hou)	25
S. arizonae	DNA-binding transcriptional regulator PhoP	25.7	1,482.89 ± 0.01	L→S (ent*, hou*)	25
S. arizonae	Ferric uptake regulator	17.0	3,291.42 ± 0.01	Q→H (ent) E→D, Q→H (hou)	25 50
S. arizonae	Fructose-bisphosphate aldolase	38.1	2,914.46 ± 0.01	S→A (ent, hou*)	25 50 100
S. arizonae	Heat shock protein	17.7	2,955.56 ± 0.01	S→L (ent, hou)	25 50 100
S. arizonae	Hydrogenase nickel incorporation protein HypB	31.4	3,764.78 ± 0.11	K→N, T→A (ent•, hou)	100
S. arizonae	Hypothetical protein SARI_01500	34.0	3,305.78 ± 0.00	I→V (ent*, hou*)	25 50
S. arizonae	Hypothetical protein SARI_03463	10.5	2,231.05 ± 0.00	H→Y (ent*, hou)	25
S. arizonae	Isoprenoid biosynthesis protein	22.9	2,747.45 ± 0.02	E→D, A→S (ent*) A→S (hou*)	25
			3,117.72 ± 0.01 (missed cleavage)	E→D, A→S (ent*) A→S (hou*)	25

S. arizonae	Membrane protein	15.7	3,051.48 ± 0.02	L→I, T→A (ent*) L→I, M→V, T→A (hou*)	25 50 100
S. arizonae	Molecular chaperone DnaK	69.3	2,464.23 ± 0.00	M→T (ent*, hou*)	25
S. arizonae	N-acetyltransferase	18.6	1,011.45 ± 0.00	R→K (ent, hou)	25
S. arizonae	N-ethylmaleimide reductase	39.5	2,590.17 ± 0.02	K→E, E→A (ent*) E→A (hou*)	25
			2,789.30 ± 0.01 (missed cleavage)	K→E, E→A (ent*) E→A (hou*)	25
S. arizonae	NADH dehydrogenase subunit G	100.0	3,009.44 ± 0.01	H→Q (ent) A→T, D→G, H→Q (hou)	25 50 100
S. arizonae	Outer-membrane lipoprotein carrier protein	22.5	2,725.27 ± 0.01	S→A (ent, hou)	25 50 100
S. arizonae	Outer membrane porin protein C	41.2	2,433.06 ± 0.01	N→S (ent*, hou*)	25
S. arizonae	Outer membrane protein A	38.6	1,221.67 ± 0.00	N→D (ent*, hou*)	25
S. arizonae	Peptidyl-prolyl cis-trans isomerase SurA	47.2	3,771.96 ± 0.03	N→S, G→E (ent, hou*)	25 50 100
S. arizonae	Phosphoenolpyruvate-protein phosphotransferase	63.3	3,073.57 ± 0.01	FI→YL (ent*, hou*)	25 50 100
S. arizonae	Pyruvate dehydrogenase subunit E1	99.6	2,649.29 ± 0.03	V→I (ent*, hou*)	25 50 100
S. arizonae	Ribonuclease E	120.0	3,602.85 ± 0.04	T→V, I→V (ent*) T→A, I→V (hou) T→A, T→A, I→V (hou*)	25 50
S. enterica	Cell division protein DamX	45.5	3,153.62 ± 0.03	TT→AP, TA→KV (ari•) A→T, T→K, A→T (hou)	25 50 100
S. enterica	CRISPR system CASCADE complex protein CasC	38.7	2,377.21 ± 0.03	not found (ari) YE→FQ, ING→VRD, LNV→IPA, VK→IT (hou)	25 50 100
S. enterica	Flagella synthesis protein FlgN	16.0	3,103.55 ± 0.01	D→N, S→A (ari) D→N (hou*)	25 50 100
S. enterica	Formate acetyltransferase 1	85.0	2,250.99 ± 0.01	D→E, K→T (ari, hou)	25
S. enterica	Fumarate hydratase	51.8	2,460.30 ± 0.01	P→S (ari) L→M (hou*)	25 50 100
S. enterica	Glutaredoxin-1 Grx1	9.9	1,114.49 ± 0.01	K→N (ari•, hou)	25

S. enterica	Glycogen phosphorylase	84.1	2,666.28 ± 0.03	K→E (ari*, hou)	25
S. enterica	H-NS histone family	15.5	1,979.88 ± 0.01	MD→IN (ari*) D→G (hou*)	25
S. enterica	Isoprenoid biosynthesis protein	22.8	2,749.45 ± 0.01	D→E, S→A (ari*) D→E (hou*)	25 50 100
S. enterica	N-ethylmaleimide reductase	39.4	2,860.34 ± 0.01	E→K, A→E (ari) E→K (hou)	25 50
S. enterica	NlpB/DapX lipoprotein	36.9	2,843.33 ± 0.01	N→S (ari, hou*)	25 50
S. enterica	Nucleoside diphosphate kinase	15.5	2,424.11 ± 0.02	L→F (ari*, hou*)	25
S. enterica	Outer membrane protein A	38.4	3,540.76 ± 0.03	V→T, P→A, T→Y (ari*) V→A, GP→(–)Y (hou*)	25 50 100
S. enterica	Peptidyl-prolyl cis-trans isomerase PpiD	58.2	2,187.04 ± 0.00	V→A, V→T (ari*) V→T (hou*)	25
S. enterica	Probable thiol peroxidase	18.0	2,379.23 ± 0.01	S→N (ari*) T→A (hou*)	25
S. enterica	Protease specific for phage lambda cII repressor	45.6	2,736.21 ± 0.02	N→K (ari, hou)	25
			2,892.31 ± 0.02 (missed cleavage)	N→K (ari, hou)	25
S. enterica	Putative outer membrane protein	12.8	3,224.54 ± 0.02	L→F, S→R, S→I, N→Y (ari•) S→T (hou*)	25 50 100
S. enterica	Ribonuclease E	119.3	2,706.37 ± 0.00	S→T (ari*) P→T, S→T (hou*)	25 50 100
			3,046.42 ± 0.02	T→A, S→T (ari*) T→A, H→Y (hou*)	25 50 100
			3,586.85 ± 0.02	V→T, V→I (ari*) V→A (hou) V→A, T→A (hou*)	25
S. houtenae	2,3,4,5-tetrahydropyridine-2,6-carboxylate N-succinyltransferase	29.8	972.40 ± 0.00	D→E (ari*, ent*)	25
S. houtenae	60 kDa chaperonin	57.2	2,980.25 ± 0.04	A→G (ari*, ent*)	25
			3,336.50 ± 0.02 (missed cleavage)	A→G (ari*, ent*)	25 50 100

S. houtenae	Cell division protein DamX	45.6	1,925.13 ± 0.01	VA→AT, RP→ST, PAA→(–) (–) (–) (ari*) P→T (ent)	25 50
S. houtenae	Cell division protein MukB	170.0	1,453.78 ± 0.01	T→S (ari, ent)	25
S. houtenae	Cytochrome d ubiquinol oxidase subunit 3	15.0	1,812.85 ± 0.01	G→S (ari*, ent*)	25
S. houtenae	DNA-binding transcriptional regulator KdgR	29.9	1,881.78 ± 0.01	E→A (ari*, ent*)	25 50
S. houtenae	Elongation factor G	77.4	3,062.52 ± 0.02	D→E (ari, ent*)	25 50 100
S. houtenae	Flagella synthesis protein FlgN	16.0	3,102.61 ± 0.05	S→A (ari) N→D (ent*)	50 100
S. houtenae	Hydrogenase formation protein HypD	41.1	2,240.03 ± 0.01	H→R (ari*, ent)	25
S. houtenae	Isoprenoid biosynthesis protein	22.9	2,763.46 ± 0.02	S→A (ari*) E→D (ent*)	25
S. houtenae	NAD(P)H:quinone oxidoreductase, type IV	20.9	2,703.34 ± 0.04	E→D (ari*, ent*)	50 100
S. houtenae	NlpB/DapX lipoprotein	36.9	2,504.25 ± 0.01	D→E, V→P (ari) V→A (ent*)	25
S. houtenae	Outer membrane protein A	38.4	3,521.70 ± 0.02	A→T, Y→GA, T→Y (ari*) A→V, Y→GP (ent*)	25 50 100
S. houtenae	Sigma-E factor negative regulatory protein	24.2	2,662.39 ± 0.01	L→Q (ari*, ent*)	25 50 100
S. houtenae	Universal stress protein G	15.8	1,090.67 ± 0.00	S→T (ari*, ent*)	25
S. houtenae	Valyl-tRNA synthetase	108.1	1,056.65 ± 0.00	V→I (ari, ent*)	25

TABLE S2 Complete list of biomarker peptides assigned to *Salmonella* proteins in the MASCOT search on the NCBI database. The peptide masses are given as the arithmetic mean calculated from the values of the three replicates of the subspecies with the according standard deviation. All numbers were rounded to the second digit after the coma.

*: Sequence analogous to biomarker peptide observed. •: shorter or longer peptide sequence containing at least one relevant amino acid exchange was observed. (–): missing amino acid. °: for all searches S/N = 10. ari: *S. enterica* subsp. *arizonae*, ent: *S. enterica* subsp. *enterica*, hou: *S. enterica* subsp. *houtenae*.