

Electronic Supplementary Information

Exploring the microbial metalloproteome using MIRAGE

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Figure S1. Autoradiogram of native 2D-PAGE of soluble protein extract of *E. coli*. Extracts were obtained from cells grown in (A) 6 μM Fe and in (B) 40 μM Fe (575 μg protein). The protein identities for the different spots are given in tables S1 and S2.

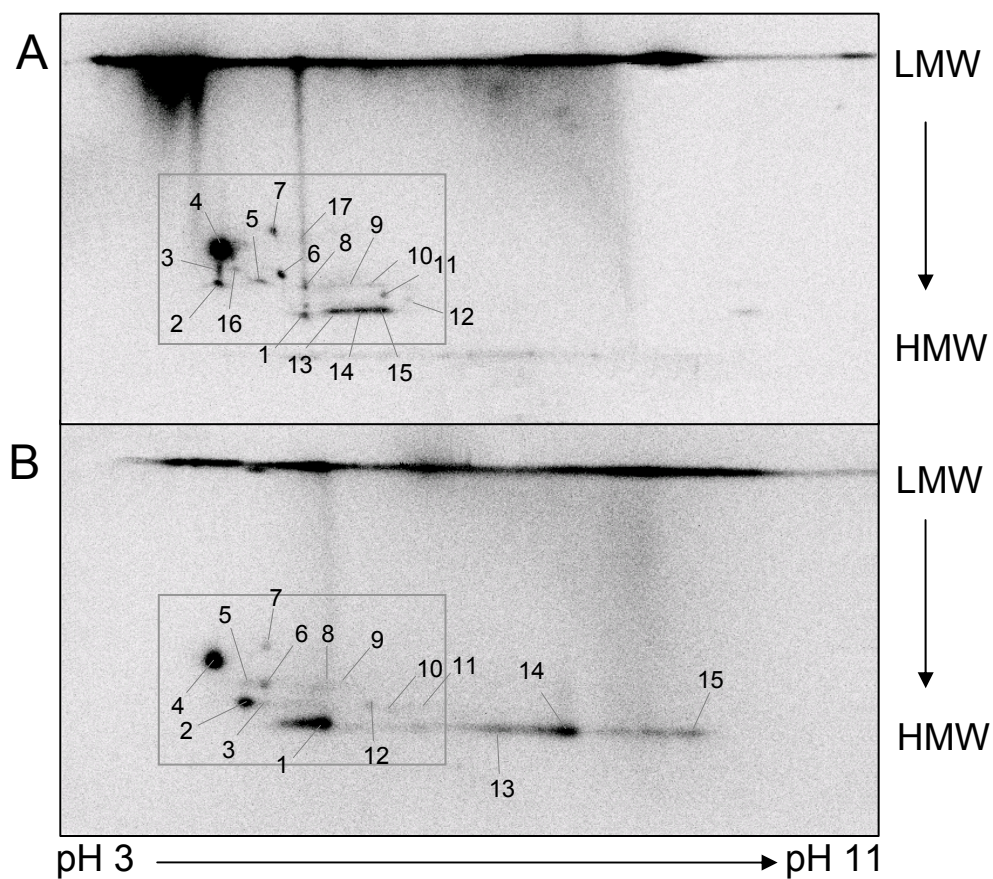


Table S1 Protein identification by LC MS/MS after native–native 2D–PAGE separation of *E. coli* soluble protein extract obtained from growth in LB medium containing 6 μ M Fe.

Spot #	Gene ^a	Protein	Mascot protein score ^b	emPAI ^c	Unique peptides	
1	Ftn	Ferritin	733	6.31	9	
	NmpC	Outer membrane porin protein nmpC precursor	250	0.56	5	
	Pgk	Phosphoglycerate kinase	163	0.30	3	
	Bfr	Bacterioferritin	133	0.76	3	
	YghZ	Aldo–keto reductase	66	0.20	2	
	GlyA	Serine hydroxymethyltransferase	57	0.17	2	
	2	KatE	Hydroperoxidase HPII (catalase)	1 675	2.64	22
CodA		Cytosine deaminase	448	0.83	7	
NmpC		Outer membrane porin protein nmpC precursor	272	0.56	5	
FliD		Flagellar filament capping protein	218	0.35	4	
FucU		Protein of fucose operon	204	1.45	3	
AldA		Aldehyde dehydrogenase A, NAD–linked	184	0.32	4	
FucI		L–fucose isomerase	129	0.18	3	
GadB		Glutamate decarboxylase isozyme	106	0.23	3	
GapA		Glyceraldehyde–3–phosphate dehydrogenase	88	0.35	3	
OmpC		Outer membrane porin protein C	72	0.19	2	
3		Dps	DNA protection protein	451	4.43	7
		SodB	Superoxide dismutase, iron	376	0.64	2
		NmpC	Outer membrane porin protein nmpC precursor	265	0.71	6
	YciF	Hypothetical protein b1258	209	1.12	3	
	OsmF	Predicted transporter subunit: periplasmic–binding component of ABC superfamily	194	0.73	5	
	SodA	Superoxide dismutase, Mn	139	0.84	4	
	IadA	Isoaspartyl dipeptidase	122	0.41	4	
	OppA	Oligopeptide transporter subunit	110	0.27	4	
	YghA	Oxidoreductase	103	0.40	3	
	MglB	Methyl–galactoside transporter subunit	81	0.22	2	
	AnsB	Periplasmic L–asparaginase II	77	0.21	2	
	4	SodB	Superoxide dismutase, iron	6 347	13.10	9
		Pck	Phosphoenolpyruvate carboxykinase	2 121	5.87	22
Gnd		Gluconate–6–phosphate dehydrogenase, decarboxylating	1 683	7.12	17	
CysK		Cysteine synthase A, O–acetylserine sulfhydrylase A	1 192	6.93	13	
AspC		Aspartate aminotransferase, PLP–dependent	1 086	4.59	17	
FliC		Flagellar filament structural protein (flagellin)	836	1.32	10	
AckA		Acetate/propionate kinase	705	1.69	7	
YgeY		Hypothetical protein Z4211	647	1.39	10	
FlgK		Flagellar hook–filament junction protein 1	496	0.65	7	
TalB		Transaldolase	382	0.83	5	
YcdX		Predicted zinc–binding hydrolase	306	0.93	5	
WrbA		Predicted flavoprotein in Trp regulation	300	1.75	6	
SpeB		Agmatinase	272	0.70	5	
Agn43		CP4–44 prophage; antigen 43 (Ag43) phase–variable biofilm formation autotransporter	262	0.19	4	
GlpQ		Periplasmic glycerophosphodiester phosphodiesterase	258	0.69	5	
Tpx		Thiol peroxidase	210	1.18	3	
FlgL		Flagellar hook–filament junction protein	148	0.23	2	
PotD		Polyamine transporter subunit	147	0.45	4	

	OsmC	Osmotically inducible, stress-inducible membrane protein	82	0.58	2
	AhpC	Alkyl hydroperoxide reductase, C22 subunit; detoxification of hydroperoxides	63	0.40	2
	RpL	50S ribosomal protein L7/L12	53	0.75	2
5	AldA	Aldehyde dehydrogenase A, NAD-linked	2 619	13.62	23
	CodA	Cytosine deaminase	1 130	3.32	15
	GapA	Glyceraldehyde-3-phosphate dehydrogenase	1 085	4.51	13
	PepP	Proline aminopeptidase P II	1 004	3.21	17
	DnaK	Molecular chaperone DnaK	344	0.52	8
	FliD	Flagellar filament capping protein	338	0.56	5
	SodB	Superoxide dismutase, iron	212	0.64	2
	AhpC	Alkyl hydroperoxide reductase, C22 subunit; detoxification of hydroperoxides	172	0.66	3
	GrpE	Heat shock protein	132	0.38	2
	Pgk	Phosphoglycerate kinase	104	0.19	2
	GadB	Glutamate decarboxylase isozyme	89	0.15	2
	Tuf	Elongation factor Tu	83	0.18	2
	HyaA	NiFe hydrogenase 1	54	0.11	2
6	PepQ	Proline dipeptidase	2 628	9.63	21
	GadB	Glutamate decarboxylase isozyme	1 273	3.44	14
	DapA	Dihydrodipicolinate synthase	938	3.35	8
	AcnA	Aconitate hydratase 1	625	0.62	13
	LysS	Lysyl-tRNA synthetase	604	1.25	12
	Eno	Phosphopyruvate hydratase	587	1.37	8
	DeoD	Purine nucleoside phosphorylase	568	4.82	9
	FusA	Elongation factor EF-2	521	0.59	9
	FliY	Cystine transporter subunit	425	1.67	7
	GlnS	Glutamyl-tRNA synthetase	417	0.76	10
	KdsA	3-deoxy-D-manno-octulosonate 8-phosphate synthase	368	1.50	7
	PotD	Polyamine transporter subunit	354	1.29	8
	DnaK	Molecular chaperone DnaK	344	0.44	7
	TalB	Transaldolase	323	0.83	6
	Tuf	Elongation factor Tu	252	0.51	5
	FliC	Flagellar filament structural protein (flagellin)	245	0.42	5
	AstD	Succinylglutamic semialdehyde dehydrogenase	223	0.40	5
	YbiB	Predicted transferase/phosphorylase	219	0.66	5
	Moab	Molybdopterin biosynthesis, protein B	211	1.55	5
	GapA	Glyceraldehyde-3-phosphate dehydrogenase	207	0.83	6
	LysS	Lysine tRNA synthetase, constitutive	200	0.37	5
	Eda	Keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase	197	0.96	4
	AhpC	Alkyl hydroperoxide reductase, C22 subunit; detoxification of hydroperoxides	189	0.96	4
	Pgk	Phosphoglycerate kinase	173	0.36	5
	SodB	Superoxide dismutase, iron	165	1.29	4
	UshA	Bifunctional UDP-sugar hydrolase/5'-nucleotidase	156	0.19	3
	UxaC	Uronate isomerase	149	0.22	3
	GroES	C-chaperonin GroES	148	1.65	3
	Fmt	10-formyltetrahydrofolate:L-methionyl-tRNA(fMet) N-formyltransferase	147	0.37	3
	Pgi	Glucose-6-phosphate isomerase	124	0.19	3
	AldA	Aldehyde dehydrogenase A, NAD-linked	89	0.15	2
	AspA	Aspartate ammonia-lyase	86	0.23	3
	Icd	E14 prophage; isocitrate dehydrogenase, specific for NADP+	64	0.17	2
7	DprA	Dihydropteridine reductase, NAD(P)H-dependent, oxygen-insensitive	1 068	28.81	17
	Bfr	Bacterioferritin	931	23.89	11
	gi 15832699	Putative formate acetyltransferase	712	17.20	9

	FliY	Cystine transporter subunit	637	4.58	10
	PepQ	Proline dipeptidase	455	0.54	4
	YbiB	Predicted transferase/phosphorylase	426	1.75	8
	HchA	Hsp31 molecular chaperone	190	0.41	3
	Def	Peptide deformylase	168	1.06	4
	GpmM	Phosphoglycerate mutase III, cofactor-independent	155	0.21	3
	RpiA	Ribose-5-phosphate isomerase A	148	0.59	3
	MogA	Molybdenum cofactor biosynthesis protein	147	0.64	3
	AhpC	Alkyl hydroperoxide reductase, C22 subunit; detoxification of hydroperoxides	140	0.54	4
	Rpe	Ribulose-phosphate 3-epimerase	138	0.54	3
	YjbJ	Hypothetical protein Z5644	134	2.32	3
	SpeE	Spermidine synthase (putrescine aminopropyltransferase)	126	0.24	2
	gi 38704245	FKBP-type 22KD peptidyl-prolyl cis-trans isomerase	110	0.37	2
	Pgk	Phosphoglycerate kinase	106	0.19	2
	DapA	Dihydrodipicolinate synthase	89	0.25	2
	RplL	50S ribosomal protein L7/L12	56	0.75	2
8	KatE	Hydroperoxidase HP11 (catalase)	1 972	3.32	25
	CpdB	2':3'-cyclic-nucleotide 2'-phosphodiesterase	1 935	4.38	21
	AnsB	Periplasmic L-asparaginase II	1 480	4.72	13
	GadB	Glutamate decarboxylase isozyme	1 346	2.88	10
	PflB	Pyruvate formate lyase I	967	1.76	21
	ArtI	Arginine transporter subunit	767	4.54	7
	gi 75209368	COG0371: Glycerol dehydrogenase and related enzymes	728	2.01	8
	ArgT	Lysine/arginine/ornithine transporter subunit	643	3.57	9
	YgfN	Xanthine dehydrogenase like protein, Mo and FeS containing subunit	467	0.32	7
	IadA	Isoaspartyl dipeptidase	467	1.00	7
	NmpC	Outer membrane porin protein nmpC precursor	464	1.23	6
	GapA	Glyceraldehyde-3-phosphate dehydrogenase	452	2.02	9
	FliC	Flagellar filament structural protein (flagellin)	447	0.75	7
	UshA	Bifunctional UDP-sugar hydrolase/5'-nucleotidase	404	0.70	9
	DnaK	Molecular chaperone DnaK	399	0.44	5
	GroEL	Chaperonin GroEL	360	0.65	8
	OmpC	Outer membrane porin protein C	353	0.86	6
	FolE	GTP cyclohydrolase I	306	1.03	4
	FsaA	Fructose-6-phosphate aldolase 1	301	1.15	3
	NagB	Glucosamine-6-phosphate deaminase	270	1.04	5
	YgfM	Predicted oxidoreductase; possible component of selenate reductase	190	0.85	5
	PanC	Pantothenate synthetase	179	0.57	4
	TktA	Transketolase 1, thiamin-binding	174	0.11	2
	PanB	3-methyl-2-oxobutanoate hydroxymethyltransferase	168	0.46	3
	FliD	Flagellar filament capping protein	165	0.25	3
	LamB	Maltose outer membrane porin (maltoporin)	163	0.16	2
	gi 15833050	Fructose-bisphosphate aldolase	150	0.20	2
	Prr	Medium chain aldehyde dehydrogenase	136	0.15	2
	Agp	Glucose-1-phosphatase/inositol phosphatase	136	0.17	2
	DeoD	Purine nucleoside phosphorylase	132	0.50	3
	Pgk	Phosphoglycerate kinase	130	0.30	3
	Tuf	Elongation factor Tu	125	0.28	3
	YgeW	Ornithine carbamoyltransferase	106	0.18	2
	AspC	Aspartate aminotransferase, PLP-	105	0.28	3

		dependent			
	PykA	Pyruvate kinase II	103	0.23	3
	YjbJ	Hypothetical protein Z5644	88	1.23	2
	FucU	Protein of fucose operon	85	0.96	2
	AtoB	Acetyl-CoA acetyltransferase	81	0.16	2
	MoaC	Molybdenum cofactor biosynthesis protein C	60	0.49	2
9	DapD	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	1 346	12.54	16
	Mdh	Malate dehydrogenase	1 214	6.21	14
	gi 89108341	Hypothetical protein	890	1.51	12
	gi 16132194	Periplasmic protein	639	2.81	7
	LysS	Lysyl-tRNA synthetase	597	1.55	14
	MglB	Methyl-galactoside transporter subunit	546	2.67	11
	FusA	Elongation factor EF-2	497	0.67	11
	DnaK	Molecular chaperone DnaK	482	0.78	8
	PurH	Fused IMP cyclohydrolase/phosphoribosylaminoimidazolecarboxamide formyltransferase	480	1.12	11
	RfaD	ADP-L-glycero-D-mannoheptose-6-epimerase	464	2.08	10
	MoaB	Molybdopterin biosynthesis, protein B	382	4.38	8
	NrfA	Periplasmic nitrite reductase	375	0.70	7
	FumB	Fumarase B	345	0.71	9^d
	Agp	Glucose-1-phosphatase/inositol phosphatase	323	0.73	7
	LysS	Lysine tRNA synthetase, constitutive	312	0.65	7
	gi 146196	Citrate synthase	307	0.56	6
	Eno	Phosphopyruvate hydratase	304	0.73	5
	Tuf	Elongation factor Tu	265	0.64	6
	FumA	Fumarase A	262	0.35	5^d
	Zwf	Glucose-6-phosphate dehydrogenase	242	0.57	7
	gi 15834295	Single-strand DNA-binding protein	204	0.74	2
	GroEL	Chaperonin GroEL	190	0.37	5
	AspA	Aspartate ammonia-lyase	160	0.31	4
	PepT	Peptidase T	145	0.27	3
	gi 146011	5,10-methylene-tetrahydrofolate dehydrogenase/5, 10-methenyl-tetrahydrofolate cyclo-hydrolase	92	0.26	2
	AroG	3-deoxy-7-phosphoheptulonate synthase	84	0.21	2
	RpsA	30S ribosomal protein S1	78	0.19	3
	gi 49176017	Bacterial alkaline phosphatase	74	0.16	2
* FumA has 3 unique peptides in common with FumB					
10	PflB	Pyruvate formate lyase I	1 984	4.44	30
	IadA	Isoaspartyl dipeptidase	1 759	6.34	15
	FliC	flagellar filament structural protein (flagellin)	1 282	2.54	11
	Prr	Medium chain aldehyde dehydrogenase	1 275	2.31	11
	ArtI	Arginine transporter subunit	1 153	8.83	11
	NmpC	Outer membrane porin protein nmpC precursor	1 070	2.18	9
	gi 75209368	COG0371: Glycerol dehydrogenase and related enzymes	970	3.34	9
	CpdB	2':3'-cyclic-nucleotide 2'-phosphodiesterase	787	0.75	11
	KatE	Hydroperoxidase HPII (catalase)	775	1.08	14
	Eno	Phosphopyruvate hydratase	773	1.78	9
	AspA	Aspartate ammonia-lyase	767	2.18	12
	OmpC	Outer membrane porin protein C	763	1.66	8
	LysS	Lysyl-tRNA synthetase	758	1.89	16
	ClpP	ATP-dependent Clp protease proteolytic subunit	729	1.89	4
	DnaK	Molecular chaperone DnaK	600	0.78	8
	AnsB	Periplasmic L-asparaginase II	578	1.39	5
	GapA	Glyceraldehyde-3-phosphate dehydrogenase	498	1.73	8

	LysS	Lysine tRNA synthetase, constitutive	393	0.87	10
	Tuf	Elongation factor Tu	382	0.78	6
	Asd	Aspartate–semialdehyde dehydrogenase	315	1.23	8
	RfaD	ADP–L–glycero–D–mannoheptose–6–epimerase	291	1.05	5
	LamB	Maltose outer membrane porin (maltoporin)	277	0.43	4
	OmpF	Outer membrane porin 1a (1a;b;F)	275	0.73	6
	GroEL	Chaperonin GroEL	273	0.46	6
	AtoB	Acetyl–CoA acetyltransferase	219	0.42	4
	RpoA	DNA–directed RNA polymerase alpha subunit	204	0.63	5
	ProA	Gamma–glutamylphosphate reductase	203	0.38	4
	GadB	Glutamate decarboxylase isozyme	199	0.23	3
	OmpW	Outer membrane protein W	183	0.59	2
	TdcE	Pyruvate formate–lyase 4/2–ketobutyrate formate–lyase	162	0.18	4
	DeoD	Purine nucleoside phosphorylase	157	0.72	4
	GcvP	Glycine decarboxylase, PLP–dependent, subunit (protein P) of glycine cleavage complex	142	0.11	3
	YebC	Hypothetical protein b1864	132	0.31	2
	RplI	50S ribosomal protein L9	109	0.55	2
	GrpE	Heat shock protein	107	0.38	2
	PanC	Pantothenate synthetase	94	0.08	2
	FsaA	Fructose–6–phosphate aldolase 1	71	0.36	2
	MinE	Cell division topological specificity factor MinE	64	0.93	2
	FusA	Elongation factor EF–2	50	0.10	2
11	YgfN	Xanthine dehydrogenase like protein, Mo and FeS containing subunit	1 366	1.74	23
	KatE	Hydroperoxidase HP11 (catalase)	1 310	2.19	20
	NmpC	Outer membrane porin protein nmpC precursor	619	1.91	9
	GapA	Glyceraldehyde–3–phosphate dehydrogenase	295	1.02	6
	SodB	Superoxide dismutase, iron	278	0.94	3
	YgfM	Predicted oxidoreductase; possible component of selenate reductase	253	1.10	5
	OmpC	Outer membrane porin protein C	138	0.31	3
	CodA	Cytosine deaminase	127	0.16	2
	IadA	Isoaspartyl dipeptidase	81	0.19	2
12	YgfN	Xanthine dehydrogenase like protein, Mo and FeS containing subunit	1 470	1.84	23
	IadA	Isoaspartyl dipeptidase	1 094	3.36	15
	YgfM	Predicted oxidoreductase; possible component of selenate reductase	527	2.03	8
	NmpC	Outer membrane porin protein nmpC precursor	424	1.23	8
	GapA	Glyceraldehyde–3–phosphate dehydrogenase	156	0.65	5
	KatE	Hydroperoxidase HP11 (catalase)	101	0.09	2
13	Bfr	Bacterioferritin	578	5.62	7
	Ftn	Ferritin	398	2.54	6
	gi 38704050	Fructose–bisphosphate aldolase	338	0.93	7
	NmpC	Outer membrane porin protein nmpC precursor	322	0.71	6
	GroEL	Chaperonin GroEL	251	0.46	6
	Tuf	Elongation factor Tu	136	0.28	3
	GuaB	Inositol–5–monophosphate dehydrogenase	128	0.23	3
	YghZ	Aldo–keto reductase	128	0.32	3
	GlnH	Glutamine ABC transporter periplasmic–binding protein	93	0.30	2
	gi 147461	Aspartate transcarbamoylase catalytic chain	85	0.23	2
	FabI	Enoyl–(acyl carrier protein) reductase	62	0.29	2

14	Bfr	Bacterioferritin	464	3.54	6
	gi 38704050	Fructose-bisphosphate aldolase	390	1.32	9
	MglB	Methyl-galactoside transporter subunit	354	0.82	6
	Ftn	Ferritin	339	1.47	5
	GroEL	Chaperonin GroEL	328	0.65	8
	NmpC	Outer membrane porin protein nmpC precursor	229	0.56	5
	YghZ	Aldo-keto reductase	139	0.44	4
	RpoA	DNA-directed RNA polymerase alpha subunit	118	0.34	3
	RpoA	DNA-directed RNA polymerase beta' subunit	92	0.05	2
	GlnH	Glutamine ABC transporter periplasmic-binding protein	82	0.30	2
	Tuf	Elongation factor Tu	81	0.18	2
	PykA	Pyruvate kinase II	78	0.15	2
15	Bfr	Bacterioferritin	262	3.50	6
	Tuf	Elongation factor Tu	244	0.50	5
	SodC	Superoxide dismutase precursor (Cu-Zn)	205	0.65	4
	GalU	Glucose-1-phosphate uridylyltransferase	202	0.52	3
	RfaD	ADP-L-glycero-D-mannoheptose-6-epimerase	102	0.46	3
	gi 75515034	COG0589: Universal stress protein UspA and related nucleotide-binding proteins	86	0.35	2
	YgiN	Hypothetical protein Z4380	82	0.35	3
16	SodB	Superoxide dismutase, iron	1 179	0.94	3
	NmpC	Outer membrane porin protein nmpC precursor	586	1.91	10
		Formate dehydrogenase-O, major subunit (Formate dehydrogenase-O subunit alpha) (FDH-Z subunit alpha) (Aerobic formate dehydrogenase major subunit)			6
	FdoG		287	0.21	
	OmpC	Outer membrane porin protein C	266	0.86	7
	YjgB	Predicted alcohol dehydrogenase, Zn-dependent and NAD(P)-binding	169	0.47	4
	GapA	Glyceraldehyde-3-phosphate dehydrogenase	155	0.65	5
	MoaB	Molybdopterin biosynthesis, protein B	87	0.45	2
	Pgi	Glucose-6-phosphate isomerase	77	0.12	2
	gi 146632	LS-BP precursor	76	0.20	2
	FdoH	Formate dehydrogenase-O, Fe-S subunit	35	0.11	1
17	IadA	Putative formate acetyltransferase	575	28.51	10
	AhpC	Alkyl hydroperoxide reductase, C22 subunit; detoxification of hydroperoxides	531	5.40	9
	NemA	N-ethylmaleimide reductase, FMN-linked	502	2.25	11
	FliC	Flagellar filament structural protein (flagellin)	467	0.64	6
	FliY	Cystine transporter subunit	412	1.36	6
	MogA	Molybdenum cofactor biosynthesis protein	389	3.40	6
	gi 38704245	FKBP-type 22KD peptidyl-prolyl cis-trans isomerase	352	2.04	4
	Fur	Ferric uptake regulator	342	2.43	4
	gi 89108648	Hypothetical protein	335	2.93	4
	RplL	50S ribosomal protein L7/L12	311	3.03	5
	Bfr	Bacterioferritin	268	1.13	4
	gi 75209368	COG0371: Glycerol dehydrogenase and related enzymes	236	0.58	5
	LuxS	S-ribosylhomocysteinase	227	0.71	3
	DeoD	Purine nucleoside phosphorylase	219	0.97	5
	Hns	DNA-binding protein HLP-II (HU, BH2, HD, NS); pleiotropic regulator	214	0.96	3
	TrxB	Thioredoxin reductase	202	0.67	4
	YbiB	Predicted transferase/phosphorylase	190	0.50	4
	Bcp	Bacterioferritin comigratory protein	180	0.48	2

YieF	Hypothetical protein Z5208	163	0.99	4
gi 15832673	Regulatory protein P-II for glutamine synthetase	150	1.29	3
gi 16129288	Predicted hydrolase	142	0.52	4
GpmM	Phosphoglycero mutase III, cofactor-independent	140	0.14	2
TpiA	Triosephosphate isomerase	135	0.30	2
gi 133976	30S ribosomal protein S6	134	0.95	3
Tig	Trigger factor	117	0.16	2
YdjA	Hypothetical protein Z2798	113	0.42	2
YniC	Predicted hydrolase	112	0.54	3
YeiG	Predicted esterase	110	0.40	3
YjbJ	Hypothetical protein Z5644	106	1.23	2
Ppa	Inorganic pyrophosphatase	85	0.43	2
FlgL	Flagellar hook-filament junction protein	82	0.23	2

^aGenes from Database *E. coli* K12 genome (www.ecocyc.com); ^bMascot identity threshold $p < 0.05$. Spot numbers correspond to numbered positions in Fig. 1A; ^cemPAI is a measure for the relative abundance of proteins in a spot; ^dThree unique peptides that were detected occur in both FumA and FumB and cannot be unambiguously assigned to either one of them. They have now been assigned to both FumA and FumB.

The position of spot number is indicated in Fig. S1A. This table contains just proteins with number of unique peptides ≥ 2 .

Table S2 Protein identification by LC MS/MS after native–native 2D–PAGE separation of *E. coli* soluble protein extract obtained from growth in LB medium containing 40 μ M Fe.

Spot #	Gene ^a	Protein	Mascot protein score ^b	emPAI ^c	Unique peptides	
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	PflB	Pyruvate formate lyase I	823	1.05	16	
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	GapA	Glyceraldehyde–3–phosphate dehydrogenase	377	1.02	5	
	NfsB	Nitroreductase A, NADPH–dependent, FMN–dependent	359	1.86	8	
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	AlaS	Alanyl–tRNA synthetase	211	0.25	5	
	PykA	Pyruvate kinase II	146	0.32	4	
	Rnr_Pfl	Putative formate acetyltransferase	135	1.07	3	
	Eda	Keto–hydroxyglutarate–aldolase/keto–deoxy–phosphogluconate aldolase	114	0.37	2	
	Tsf	Elongation factor Ts	107	0.26	2	
	XdhB	Xanthine dehydrogenase, FAD–binding subunit	91	0.25	2	
	AspC	Aspartate aminotransferase, PLP–dependent	78	0.18	2	
	Fbp	Fructose–biphosphate aldolase	76	0.20	2	
	SodB	Superoxide dismutase, iron	75	0.64	3	
	XdhA	Xanthine dehydrogenase, molybdenum binding subunit	73	0.09	1	
	Bfr	Bacterioferritin	65	0.46	2	
	GroEL	Chaperonin GroEL	61	0.13	2	
	TalB	Transaldolase	56	0.22	2	
	2	YgfK	Putative oxidoreductase, Fe–S subunit	3 967	5.25	45
PflB		Pyruvate formate lyase I	2 228	5.73	38	
GadB		Glutamate decarboxylase isozyme	1 097	2.17	13	
DnaK		Molecular chaperone DnaK	693	0.87	11	
GapA		Glyceraldehyde–3–phosphate dehydrogenase	627	1.73	8	
SodB		Superoxide dismutase, Fe	504	2.18	6	
PckA		Phosphoenolpyruvate carboxykinase	415	0.52	6	
Rnr_Pfl		Putative formate acetyltransferase	321	3.27	5	
FliC		Flagellar filament structural protein (flagellin)	282	0.52	5	
UshA		Bifunctional UDP–sugar hydrolase/5'–nucleotidase	269	0.27	4	
PanC		Pantothenate synthetase	247	1.20	5	
TalB		Transaldolase	195	0.35	3	
GrpE		Heat shock protein	183	0.91	4	
NmpC		Outer membrane porin protein nmpC precursor	176	0.31	3	
YfcZ		Hypothetical protein	163	1.60	3	
CodA		Cytosine deaminase	147	0.25	3	
3		CodA	Cytosine deaminase	1 703	5.71	17
		YgfK	Putative oxidoreductase, Fe–S subunit	944	1.04	21
		PflB	Pyruvate formate lyase I	896	1.43	20
		GapA	Glyceraldehyde–3–phosphate dehydrogenase	6.97	2.69	12
	DnaK	Molecular chaperone DnaK	657	0.97	11	
	GadB	Glutamate decarboxylase isozyme	635	1.26	11	
	FliC	Flagellar filament structural protein (flagellin)	470	1.17	9	
	SodB	Superoxide dismutase, iron	285	1.70	4	
	PckA	Phosphoenolpyruvate carboxykinase	238	0.52	6	
	GrpE	Heat shock protein	212	0.91	3	
	YfcZ	Hypothetical protein	180	2.58	3	

	PanC	Pantothenate synthetase	176	0.75	4
	Rnr_Pfl	Putative formate acetyltransferase	173	1.07	3
	UshA	Bifunctional UDP-sugar hydrolase/5'-nucleotidase	140	0.19	3
	NmpC	Outer membrane porin protein nmpC precursor	134	0.19	2
	YbiB	Predicted transferase/phosphorylase	122	0.36	3
	AldA	Aldehyde dehydrogenase A, NAD-linked	117	0.23	3
	AhpC	Alkyl hydroperoxide reductase, C22 subunit; detoxification of hydroperoxides	106	0.40	2
4	SodB	Superoxide dismutase, iron	3 928	9.13	7
	PckA	Phosphoenolpyruvate carboxykinase	2 702	8.86	24
	GorA	Glutathione oxidoreductase	1 762	3.34	15
	AckA	Acetate/propionate kinase	879	2.44	12
	Gnd	Gluconate-6-phosphate dehydrogenase, decarboxylating	841	1.85	11
	Icd	E14 prophage; isocitrate dehydrogenase, specific for NADP+	534	1.55	10
	AspC	Aspartate aminotransferase, PLP-dependent	289	0.93	8
	Mdh	Malate dehydrogenase	259	0.55	3
	Ftn	Ferritin	177	0.44	2
	YcdX	Predicted zinc-binding hydrolase	176	0.48	2
	CysK	Cysteine synthase A, O-acetylserine sulfhydrylase A	173	0.36	2
	AhpC	Alkyl hydroperoxide reductase, C22 subunit; detoxification of hydroperoxides	163	0.66	3
	SpeB	Agmatinase	151	0.37	3
	PepN	Aminopeptidase N	151	0.12	2
	TalB	Transaldolase	142	0.35	3
	GlpQ	Periplasmic glycerophosphodiester phosphodiesterase	91	0.19	2
	FliC	Flagellar filament structural protein (flagellin)	68	0.15	2
5	AcnA	COG1048: Aconitase A	4 900	13.93	47
	RihC	Ribonucleoside hydrolase 3	2 167	5.31	12
	DnaK	Molecular chaperone DnaK	2 118	4.06	22
	FliY	Cystine transporter subunit	1 904	30.18	17
	KdsA	3-deoxy-D-manno-oculosonate 8-phosphate synthase	1 851	13.00	15
	PepQ	Proline dipeptidase	1 131	3.19	15
	GapA	Glyceraldehyde-3-phosphate dehydrogenase	977	1.73	9
	SodB	Superoxide dismutase, iron	646	6.28	7
	HtpG	Heat shock protein 90	640	1.49	18
	YgfK	Putative oxidoreductase, Fe-S	557	0.45	13
	Rpe	Ribulose-phosphate 3-epimerase	541	2.65	7
	Pgi	Glucose-6-phosphate isomerase	473	0.60	7
	SodA	Superoxide dismutase, Mn	450	1.92	6
	GrpE	Heat shock protein	436	2.66	7
	SerS	Seryl-tRNA synthetase	313	1.26	12
	AtoB	Acetyl-CoA acetyltransferase	309	0.42	4
	GadB	Glutamate decarboxylase isozyme	270	0.40	5
	Mdh	Malate dehydrogenase	248	0.73	5
	RibH	Riboflavin synthase subunit beta	240	0.91	3
	PflB	Pyruvate formate lyase I	232	0.35	8
	TdcE	Pyruvate formate-lyase 4/2-Ketobutyrate formate-lyase	231	0.18	5
	DapA	Dihydrodipicolinate synthase	184	0.57	5
	FliC	Flagellar filament structural protein (flagellin)	180	0.32	6
	Eda	Keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase	168	1.20	6
	GroEL	Chaperonin GroEL	168	0.13	2
	Rnr_Pfl	Putative formate acetyltransferase	165	1.63	4
	YiiU	Hypothetical protein	150	1.01	2

	GroES	Co-chaperonin GroES	105	0.92	4
	UshA	Bifunctional UDP-sugar hydrolase/5'-nucleotidase	89	0.13	2
	AhpC	Alkyl hydroperoxide reductase, C22 subunit; detoxification of hydroperoxides	70	0.40	2
	AceE	Pyruvate dehydrogenase (decarboxylase component)	59	0.12	4
	ValS	Valyl-tRNA synthetase	42	0.03	2
6	DnaK	Molecular chaperone DnaK	4 146	12.67	32
	AcnA	COG1048: Aconitase A	4 006	9.70	39
	FliY	Cystine transporter subunit	2 271	20.57	17
	RihC	Ribonucleoside hydrolase 3	1 506	5.31	10
	AceA	Isocitrate lyase	1 415	4.25	16
	GroES	Co-chaperonin GroES	1 401	17.68	4
	AtoB	Acetyl-CoA acetyltransferase	1 234	3.90	14
	AldA	Aldehyde dehydrogenase A, NAD-linked	1 067	2.96	15
	KdsA	3-deoxy-D-manno-octulosonate 8-phosphate synthase	1 066	3.98	10
	SerS	Seryl-tRNA synthetase	1 040	3.40	15
	ValS	Valyl-tRNA synthetase	996	0.95	16
	PepQ	Proline dipeptidase	986	2.38	13
	SodB	Superoxide dismutase, iron	905	5.17	6
	GrpE	Heat shock protein	904	2.66	6
	Rpe	Ribulose-phosphate 3-epimerase	766	3.86	7
	GabT	4-aminobutyrate aminotransferase, PLP-dependent	740	1.55	12
	AhpC	Alkyl hydroperoxide reductase, C22 subunit; detoxification of hydroperoxides	638	6.58	9
	YgfK	Putative oxidoreductase, Fe-S subunit	611	0.64	13
	GapA	Glyceraldehyde-3-phosphate dehydrogenase	511	2.34	11
	IlvD	Dihydroxyacid dehydratase	501	1.03	12
	AstD	Succinylglutamic semialdehyde dehydrogenase	500	1.10	8
	PflB	Pyruvate formate lyase I	494	0.73	15
	GadB	Glutamate decarboxylase isozyme	473	0.72	8
	HtpG	Heat shock protein 90	453	0.75	12
	TktA	Transketolase 1, thiamin-binding	439	0.35	7
	Eda	Keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase	417	0.52	5
	SodA	Superoxide dismutase, Mn	411	1.51	4
	YcaC	Predicted hydrolase	287	0.84	3
	TdcE	Pyruvate formate-lyase 4/2-ketobutyrate formate-lyase	283	0.23	5
	IleS	Isoleucyl-tRNA synthetase	233	0.19	5
	CysK	Cysteine synthase A, O-acetylserine sulfhydrylase A	207	0.86	5
	Pgi	Glucose-6-phosphate isomerase	196	0.34	5
	YgeY	Hypothetical protein	195	0.49	6
	FabA	3-hydroxydecanoyl-ACP dehydratase	186	2.01	5
	Icd	E14 prophage; isocitrate dehydrogenase, specific for NADP+	162	0.48	5
	CysE	Serine acetyltransferase	136	0.44	3
	GroEL	Chaperonin GroEL	122	0.29	5
	Tig	Trigger factor	116	0.25	3
	gi 83587818	COG0281: Malic enzyme			
	gi 15803663	Putative dehydrogenase	91	0.26	5
	Tsf	Elongation factor Ts	91	0.42	3
	Adk	Adenylate kinase	82	0.16	2
	Mdh	Malate dehydrogenase	52	3	
7	GmM	Phosphoglycerate mutase III, cofactor-independent	993	3.10	14
	Bfr	Bacterioferritin	959	19.60	10
	HhA	Hsp31 molecular chaperone	695	2.92	9
	AhpC	Alkyl hydroperoxide reductase, C22 subunit; detoxification of hydroperoxides	657	4.41	7

	Fbp	Fructose-bisphosphate aldolase	598	1.72	7
	TreC	Trehalose-6-P hydrolase	571	0.86	10
	KdsA	3-deoxy-D-manno-octulosonate 8-phosphate synthase	434	1.23	5
	Rnr_Pfl	Putative formate acetyltransferase	423	3.27	4
	GapA	Glyceraldehyde-3-phosphate dehydrogenase	361	0.65	5
	RpiA	Ribose-5-phosphate isomerase A	329	1.95	6
	gi 75212202	COG0251: Putative translation initiation inhibitor, yjgF family	320	2.54	5
	Ddl	D-alanylalanine synthetase	315	0.89	6
	TrxB	Thioredoxin reductase	285	1.05	6
	YgeY	Hypothetical protein	249	0.49	4
	AcnA	Aconitase A	228	0.12	3
	YbiB	Predicted transferase/phosphorylase	211	0.66	5
	Pgi	Glucose-6-phosphate isomerase	190	0.26	3
	RihC	Ribonucleoside hydrolase 3	182	0.38	2
	Adk	Adenylate kinase	180	1.11	5
	CheY	Chemotaxis regulator transmits chemoreceptor signals to flagellar motor components	176	1.09	2
	Cmk	Cytidylate kinase	166	0.77	4
	PpiB	Peptidyl-prolyl cis-trans isomerase B (rotamase B)			
	Rpe	Ribulose-phosphate 3-epimerase	157	0.78	3
	PepE	Peptidase E	136	0.54	3
	NfsB	Nitroreductase A, NADPH-dependent, FMN-dependent	135	0.48	3
	DprA	Dihydropteridine reductase, NAD(P)H-dependent, oxygen-insensitive	124	0.34	2
	gi 75227401	COG0663: Carbonic anhydrases/acetyltransferases, isoleucine patch superfamily	121	0.41	2
	FliY	Cystine transporter subunit	115	0.28	2
	DnaK	Molecular chaperone DnaK			
	GltX	Glutamyl-tRNA synthetase	100	0.14	2
	SodB	Superoxide dismutase, iron	99	0.39	2
	PepQ	Proline dipeptidase	96	0.15	2
	Tig	Trigger factor	91	0.16	2
	Pgk	Phosphoglycerate kinase	82	0.19	2
	Tsf	Elongation factor Ts	80	0.26	2
	YgfK	Putative oxidoreductase, Fe-S subunit	80	0.06	2
	Apt	Adenine phosphoribosyltransferase	70	0.42	2
	TiaE	2-keto-D-gluconate reductase	68	0.35	3
	PhnA	Hypothetical protein	64	0.72	2
	Eno	Phosphopyruvate hydratase	63	0.17	2
	PrIC	Oligopeptidase A	61	0.10	2
	YcaR	Hypothetical protein	50	1.55	2
8	Mdh	Malate dehydrogenase	2 456	16.35	16
	DapD	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	1 208	11.03	14
	FumB	Fumarase B	1 187	3.71	21^d
	FumA	Fumarase A	839	1.59	14^d
	DnaK	Molecular chaperone DnaK	767	2.00	17
	SerS	Seryl-tRNA synthetase	584	2.04	11
	NrfA	Periplasmic nitrite reductase	509	1.37	9
	FusA	Elongation factor EF-2	437	0.75	9
	GlcB	Malate synthase G	433	0.71	11
	AspA	Aspartate ammonia-lyase	415	1.11	9
	IleS	Isoleucyl-tRNA synthetase	399	0.51	11
	purH	Fused IMP cyclohydrolase/phospho-ribosylaminoimidazolecarboxamide formyltransferase	367	0.87	9
	Eno	Phosphopyruvate hydratase	341	1.03	7
	AceE	Pyruvate dehydrogenase (decarboxylase component)	329	0.39	9

	LysS	Lysyl-tRNA synthetase	315	0.75	8
	HtpG	Heat shock protein 90	268	0.36	6
	ValS	Valyl-tRNA synthetase	243	0.26	6
	GroEL	Chaperonin GroEL	238	0.46	6
	FabI	Enoyl-(acyl carrier protein) reductase	231	1.43	6
	MglB	Methyl-galactoside transporter subunit	224	0.82	5
	GrpE	Heat shock protein	212	0.63	2
	Zwf	Glucose-6-phosphate dehydrogenase	208	0.47	6
	PdxB	Erythronate-4-phosphate dehydrogenase	204	0.68	6
	YceI	Hypothetical protein	204	0.96	4
	YgfK	Putative oxidoreductase, Fe-S subunit	203	0.24	7
	GshB	Glutathione synthetase	193	0.49	4
	LysS	Lysine tRNA synthetase, constitutive	180	0.46	5
	OsmY	Periplasmic protein	161	0.65	3
	NrdA	Ribonucleoside diphosphate reductase 1, alpha subunit	148	0.18	4
	RbsD	Membrane-associated component of D-ribose high-affinity transport system	145	0.97	2
	YebB	Hypothetical protein	145	0.89	5
	Agp	Glucose-1-phosphatase/inositol phosphatase	142	0.26	2
	TdcE	Keto acid formate-lyase	140	0.36	5
	PflB	Pyruvate formate lyase I	121	0.14	3
	InfB	Translation initiation factor IF-2	116	0.08	2
	MalE	Periplasmic maltose-binding protein	113	0.28	3
	Tdh	Threonine 3-dehydrogenase, NAD(P)-binding	108	0.33	3
	ThrS	Threonyl-tRNA synthetase	103	0.21	4
	TktA	Transketolase 1, thiamin-binding	100	0.11	2
	GltA	Citrate synthase	94	0.16	2
	gi 15832709	Heat shock protein	69	0.08	2
	FliC	Flagellar filament structural protein (flagellin)	63	0.15	2
	PanC	Pantothenate synthetase	57	0.25	2
d FumA has 9 unique peptides in common with FumB					
9	FabI	Enoyl-(acyl carrier protein) reductase	1 500	17.40	14
	FumB	Fumarase B	951	1.92	16^d
	Mdh	Malate dehydrogenase	888	6.21	14
	YebB	Hypothetical protein	847	5.05	11
	DapD	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	790	3.66	9
	MglB	Methyl-galactoside transporter subunit	539	2.01	10
	FumA	Fumarase A	482	0.61	8^d
	AspA	Aspartate ammonia-lyase	438	1.11	10
	DnaK	Molecular chaperone DnaK	407	0.60	8
	GrpE	Heat shock protein	281	1.35	4
	IleS	Isoleucyl-tRNA synthetase	277	0.27	7
	NrfA	Periplasmic nitrite reductase	265	0.30	4
	ValS	Valyl-tRNA synthetase	211	0.18	4
	FusA	Elongation factor EF-2	209	0.26	5
	Eno	Phosphopyruvate hydratase	187	0.37	4
	Agp	Glucose-1-phosphatase/inositol	172	0.26	2
	HtpG	Heat shock protein 90	164	0.22	4
	TktA	Transketolase 1, thiamin-binding	161	0.22	4
	LysS	Lysyl-tRNA synthetase	160	0.45	6
	PdxB	Erythronate-4-phosphate dehydrogenase	155	0.4	5
	SerS	Seryl-tRNA synthetase	152	0.34	4
	LysS	Lysine tRNA synthetase, constitutive	141	0.37	5
	KdsA	3-deoxy-D-manno-octulosonate 8-phosphate synthase	125	0.41	2
	TdcE	Keto acid formate-lyase	123	0.20	3
	PanC	Pantothenate synthetase	117	0.25	2
	GapA	Glyceraldehyde-3-phosphate dehydrogenase	114	0.22	2
	AcnA	Aconitase A	107	0.04	1
	GrxC	Glutaredoxin 3	98	1.95	3

	GroEL	Chaperonin GroEL	93	0.13	2
	SodB	Superoxide dismutase, iron	89	0.18	1
	Zwf	Glucose-6-phosphate dehydrogenase	86	0.21	3
	RbsB	D-ribose transporter subunit	84	0.26	2
	PflB	Pyruvate formate lyase I	81	0.14	3
	SucC	Succinyl-CoA synthetase subunit beta	66	0.09	1
	gi 15832709	Heat shock protein	66	0.08	2
	AceE	Pyruvate dehydrogenase (decarboxylase component)	52	0.04	1
	ThrS	Threonyl-tRNA synthetase	51	0.10	2
d FumA has 6 unique peptides in common with FumB					
10	AspA	Aspartate ammonia-lyase	2 862	9.83	20
	MglB	Methyl-galactoside transporter subunit	2 462	32.23	21
	FabI	Enoyl-(acyl carrier protein) reductase	1 423	15.21	15
	FumB	Fumarase B	932	1.59	13^d
	PflB	Pyruvate formate lyase I	783	1.05	16
	GcvP	Glycine decarboxylase, PLP-dependent, subunit (protein P) of glycine cleavage complex	782	0.62	13
	FumA	Fumarase A	638	0.92	10^d
	TktB	Transketolase 2, thiamin-binding	612	0.72	10
	TktA	Transketolase 1, thiamin-binding	568	0.73	11
	AceE	Pyruvate dehydrogenase (decarboxylase component)	498	0.49	9
	TdcE	Pyruvate formate-lyase 4/2-ketobutyrate formate-lyase	436	0.52	10
	AldA	Aldehyde dehydrogenase A, NAD-linked	422	0.73	6
	DapD	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	421	2.27	8
	PdxB	Erythronate-4-phosphate dehydrogenase	406	0.99	8
	DsbC	Protein disulfide isomerase II	393	2.00	6
	gi 15832709	Heat shock protein	342	0.30	6
	GapA	Glyceraldehyde-3-phosphate dehydrogenase	276	0.695	4
	YebB	Hypothetical protein	214	0.37	3
	YgfN	Xanthine dehydrogenase like protein, Mo and FeS containing subunit	204	0.11	3
	Udp	Uridine phosphorylase	202	0.48	2
	DnaK	Molecular chaperone DnaK	198	0.17	3
	GrxC	Glutaredoxin 3	198	3.23	3
	KatG	Catalase/hydroperoxidase HPI(I)	186	0.31	6
	FtsP	Repressor protein for FtsI	178	0.32	4
	YiiU	Hypothetical protein	164	1.01	2
	gi 75177918	COG3013: Uncharacterized conserved protein	164	1.04	3
	Mdh	Malate dehydrogenase	155	0.25	2
	KdsA	3-deoxy-D-manno-octulosonate 8-phosphate synthase	139	0.26	2
	NagA	N-acetylglucosamine-6-phosphate deacetylase	135	0.19	2
	AcnA	Aconitase A	77	0.04	1
	ModA	Molybdate transporter subunit	70	0.30	2
	SucC	Succinyl-CoA synthetase subunit beta	45	0.09	1
	SucD	Succinyl-CoA synthetase alpha subunit	40	0.13	1
d FumA has 7 unique peptides in common with FumB					
11	ThrS	Threonyl-tRNA synthetase	1 153	2.88	22
	Mdh	Malate dehydrogenase	857	3.65	9
	YgfN	Xanthine dehydrogenase like protein, Mo and FeS containing subunit	501	0.75	13
	YgfK	Putative oxidoreductase, Fe-S subunit	453	0.59	14
	gi 83585805	COG1185: Polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)	450	0.93	11
	gi 75177918	COG3013: Uncharacterized conserved protein	372	4.00	7
	PflB	Pyruvate formate lyase I	365	0.59	10

	gi 15832709	Heat shock protein	268	0.30	6
	AspA	Aspartate ammonia-lyase	260	0.61	6
	Eco	Ecotin, a serine protease inhibitor	253	2.81	5
	GcvP	Glycine decarboxylase, PLP-dependent, subunit (protein P) of glycine cleavage complex	236	0.32	7
	YgfM	Predicted oxidoreductase; possible component of selenate reductase	175	0.85	5
	PepT	Peptidase T	171	0.37	4
	YicC	Hypothetical protein	149	0.54	4
	PheA	Chorismate mutase-P	128	0.39	4
	Prr	Medium chain aldehyde dehydrogenase	125	0.33	3
	gi 15803317	Hypothetical protein	111	0.15	2
	AspS	Aspartyl-tRNA synthetase	94	0.12	2
	BetB	Betaine aldehyde dehydrogenase, NAD-dependent	91	0.15	2
	SucC	Succinyl-CoA synthetase subunit beta	91	0.19	2
	GltA	citrate synthase	88	0.16	2
	SucD	Succinyl-CoA synthetase alpha subunit	72	0.27	2
	LsrB	A12 transporter	66	0.22	2
	IadA	Isoaspartyl dipeptidase	64	0.19	2
	KdsD	D-arabinose 5-phosphate	63	0.22	2
	TdcE	Keto acid formate-lyase	57	0.13	2
	MenB	Dihydroxynaphthoic acid synthetase	55	0.25	2
12	YgfN	Xanthine dehydrogenase like protein, Mo and FeS containing subunit	1 309	1.65	20
	GcvP	Glycine decarboxylase, PLP-dependent, subunit (protein P) of glycine cleavage complex	1 256	1.46	18
	gi 83585805	COG1185: Polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)	1 192	2.55	19
	ThrS	Threonyl-tRNA synthetase	1 143	2.70	25
	gi 83587769	COG3131: Periplasmic glucans biosynthesis protein	916	2.30	14
	PflB	Pyruvate formate lyase I	873	1.43	21
	Prr	Medium chain aldehyde dehydrogenase	728	0.76	5
	OsmY	Periplasmic protein	728	3.50	7
	SucC	Succinyl-CoA synthetase subunit beta	661	2.07	9
	AspA	Aspartate ammonia-lyase	522	1.42	11
	YicC	Hypothetical protein	516	1.37	6
	gi 15832709	Heat shock protein	516	0.46	9
	YgfM	Predicted oxidoreductase; possible component of selenate reductase	496	1.68	7
	AspS	aspartyl-tRNA synthetase	394	0.47	7
	FumC	Fumarase C	363	0.64	6
	gi 15803317	Hypothetical protein	357	0.52	5
	KdsD	D-arabinose 5-phosphate isomerase	225	0.83	6
	GroES	Co-chaperonin GroES	210	1.65	2
	GapA	Glyceraldehyde-3-phosphate dehydrogenase	202	0.49	4
	OppA	Oligopeptide transporter subunit	194	0.27	3
	PurB	adenylosuccinate lyase	188	0.52	5
	SucD	Succinyl-CoA synthetase alpha subunit	183	1.04	6
	ModA	Molybdate transporter subunit	170	0.92	5
	PanC	Pantothenate synthetase	163	0.57	4
	YgfK	Putative oxidoreductase, Fe-S subunit	153	0.10	3
	GltA	citrate synthase	143	0.35	3
	BetB	Betaine aldehyde dehydrogenase, NAD-dependent	138	0.15	2
	SerA	D-3-phosphoglycerate dehydrogenase	137	0.27	3
	PdxJ	Pyridoxal phosphate biosynthetic protein	121	0.31	2
	UshA	Bifunctional UDP-sugar hydrolase/5'-nucleotidase	120	0.13	2
	Dcd	2'-deoxycytidine 5'-triphosphate deaminase	109	0.64	3

	PepT	Peptidase T	88	0.17	2
	TdcE	Pyruvate formate-lyase 4/2-ketobutyrate formate-lyase	71	0.13	3
	AppA	Phosphoanhydride phosphorylase	56	0.16	2
13	gi 1658028	Dehydrin	387	1.40	10
	Bfr	Bacterioferritin	364	7	9
	Mdh	Malate dehydrogenase	334	0.55	4
	RbsB	D-ribose transporter subunit	280	1.82	8
	Ftn	Ferritin	195	1.96	5
	XdhA	Xanthine dehydrogenase, molybdenum binding subunit	145	0.25	5
	YajQ	Hypothetical protein	127	0.74	2
	XdhB	Xanthine dehydrogenase, FAD-binding subunit	116	0.25	2
	Frr	Ribosome releasing factor	95	0.41	2
	AphA	Acid phosphatase/phosphotransferase, class B, non-specific	87	0.31	2
	YnjE	Predicted thiosulfate sulfur transferase	82	0.16	2
	YghZ	Aldo-keto reductase	81	0.20	2
	AccD	Acetyl-CoA carboxylase beta subunit	75	0.24	2
	GroEL	Chaperonin GroEL	67	0.13	2
	AccA	Acetyl-CoA carboxylase alpha subunit	55	0.22	2
14	Mdh	Malate dehydrogenase	238	0.55	4
	Ftn	Ferritin	171	1.06	3
	YajQ	Hypothetical protein	126	0.74	2
	AphA	Acid phosphatase/phosphotransferase, class B, non-specific	120	0.50	2
	CspC	Cold shock protein	83	1.43	2
	Bfr	Bacterioferritin	67	0.46	2
15	Mdh	Malate dehydrogenase	481	0.73	5
	SucB	Dihydrolipoamide acetyltransferase	297	0.77	7
	Ftn	Ferritin	238	1.96	5
	KatG	Catalase/hydroperoxidase HPI(I)	184	0.31	7
	AceF	Pyruvate dehydrogenase, dihydrolipoyltransacetylase component E2	171	0.39	6
	LacZ	Beta-D-galactosidase	107	0.26	3
	RbsB	D-ribose transporter subunit	107	0.26	2
	HtrA	Periplasmic serine protease Do; heat shock protein HtrA	63	0.16	3
	GlnH	Glutamine ABC transporter periplasmic-binding protein	61	0.30	2
	Eno	Phosphopyruvate hydratase	60	0.17	2
	YrbC	Predicted ABC-type organic solvent transporter	44	0.34	2

^aGenes from Database *E. coli* K12 genome (www.ecocyc.com); ^bMascot identity threshold $p < 0.05$. Spot numbers correspond to numbered positions in Fig. 1A; ^cemPAI is a measure for the relative abundance of proteins in a spot; ^dUnique peptides that were detected occur in both FumA and FumB and cannot be unambiguously assigned to either one of them. They have now been assigned to both FumA and FumB.

The position of spot number is indicated in Fig. S1B. This table contains just proteins with number of unique peptides ≥ 2 .

Figure S2 Coomassie brilliant blue (CBB) stained gels of native–native 2D–PAGE of soluble protein extract (μg protein) obtained from *E. coli* (575 μg) after growth on high iron. **A** without DNase; **B** with 0.1 mg/L DNase and 0.1 mg/L RNase.

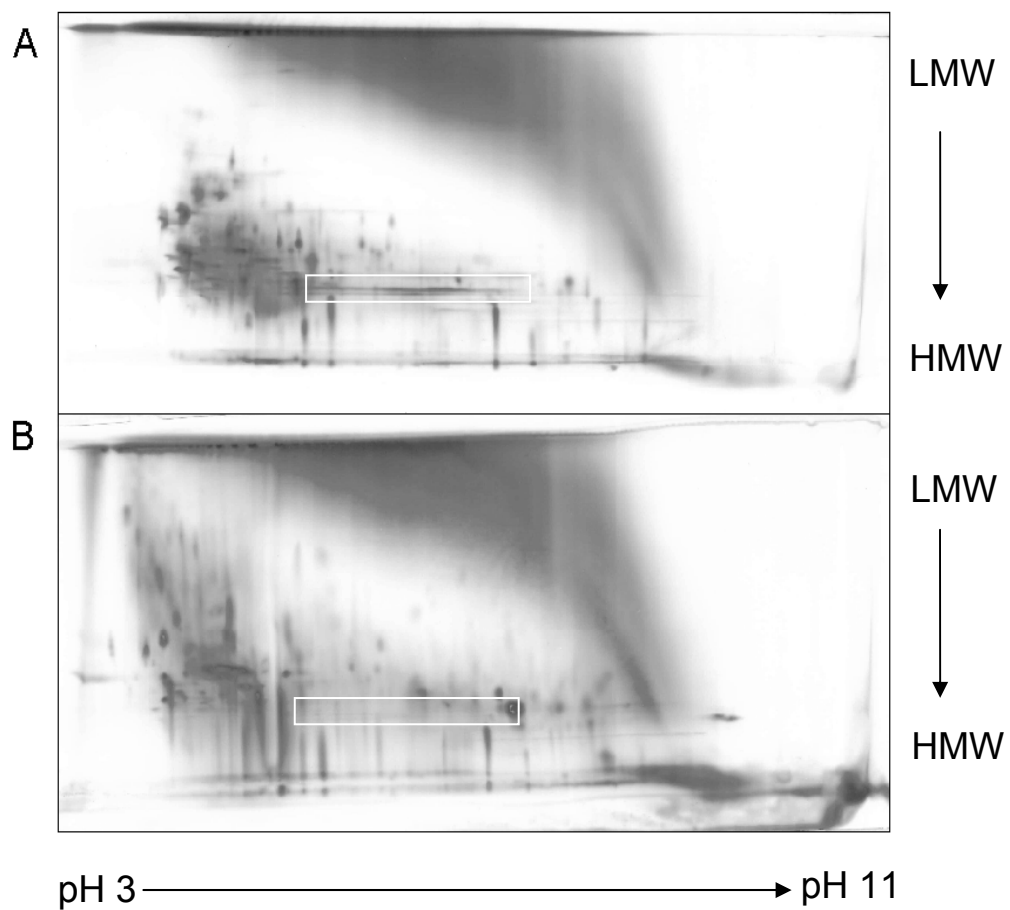


Figure S3 Autoradiogram of native 2D-PAGE of soluble protein extract of *E. coli* grown on 0.24 mM ^{69m}Zn . The spot positions are indicated with numbers.

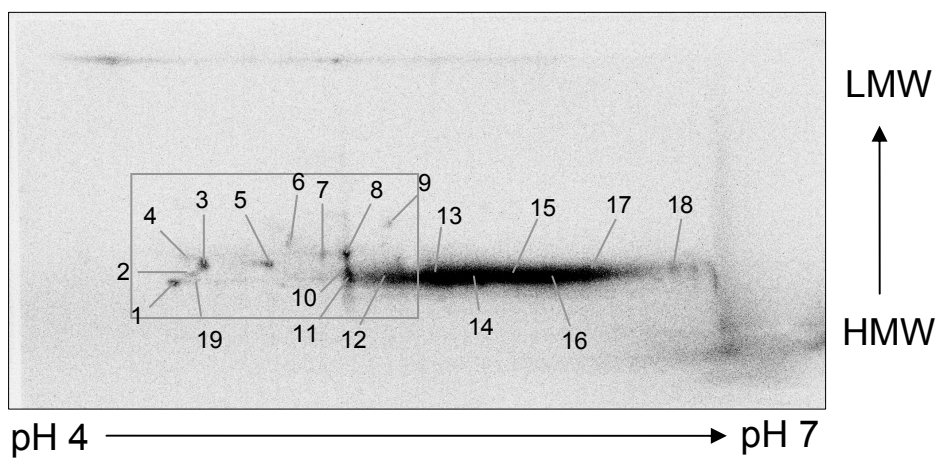


Table S3 Protein identification by LC MS/MS after native–native 2D–PAGE separation of *E. coli* soluble protein extract obtained from growth in LB medium containing 0.24 mM ^{69m}ZnCl₂. The predicted Zn-containing proteins according to the gene ontology database of *E. coli* (www.ecocyc.org) are in bold.

Spot #	Gene	Protein	Mascot protein score	emPAI	Unique peptides	
1	FliC	Flagellar filament structural protein (flagellin)	1183	3.37	18	
	YcaC	Predicted hydrolase	1010	3.59	9	
	GadB	Glutamate decarboxylase isozyme	866	1.96	14	
	LysS	lysyl–tRNA synthetase	252	0.55	7	
	DnaK	Molecular chaperone DnaK	224	0.30	5	
	Tig	trigger factor	164	0.25	3	
	SerS	seryl–tRNA synthetase	161	0.34	4	
	DapA	Dihydrodipicolinate synthase	149	0.57	4	
	Gnd	gluconate–6–phosphate dehydrogenase, decarboxylating	128	0.23	3	
	WrbA	Predicted flavoprotein in Trp regulation	104	0.40	2	
	PflD	Putative formate acetyltransferase	98	0.62	3	
	AdiA	Biodegradative arginine decarboxylase (ADC)	95	0.14	3	
	GroEL	Chaperonin GroEL	94	0.13	2	
	GroES	Co–chaperonin GroES	84	1.65	3	
	Eno	Phosphopyruvate hydratase	82	0.17	2	
	FusA	Elongation factor EF–2	77	0.15	3	
	2	UxaC	Uronate isomerase	5829	45.75	38
GadB		Glutamate decarboxylase isozyme	1334	2.88	15	
FliC		Flagellin	960	1.67	11	
WrbA		Predicted flavoprotein in Trp regulation	697	7.97	11	
Gnd		Gluconate–6–phosphate dehydrogenase, decarboxylating	573	1.01	9	
PckA		Phosphoenolpyruvate carboxykinase	502	0.72	9	
SodB		Superoxide dismutase, iron	449	3.43	7	
TalB		Transaldolase	362	1.03	7	
AspC		Aspartate transaminase	324	0.93	8	
NlpB		Lipoprotein 34 precursor	273	0.63	4	
YcaC		Predicted hydrolase	181	0.36	2	
LdhA		D–lactate dehydrogenase	175	0.34	3	
YhfA		Hypothetical protein b3356	133	0.61	2	
GroEL		Chaperonin groEL	124	0.13	2	
RpsA		Ribosomal protein S1	123	0.19	3	
DapA		Dihydrodipicolinate synthase	120	0.25	2	
GlpQ		Glycerophosphodiester phosphodiesterase precursor, periplasmic	118	0.30	3	
Moab		Molybdopterin biosynthesis, protein B	104	0.75	3	
3		SodB	Superoxide dismutase, iron	2738	7.58	8
		PckA	Phosphoenolpyruvate carboxykinase	1212	1.96	15
	GlpQ	Glycerophosphodiester phosphodiesterase precursor, periplasmic	400	0.55	5	
	Gnd	Gluconate–6–phosphate dehydrogenase, decarboxylating	387	0.63	6	
	Gor	Glutathione–disulfide reductase	341	0.55	6	
	TalB	Transaldolase	322	0.66	5	
	CysK	Cysteine synthase A	302	0.68	5	
	AckA	Acetate kinase	284	0.51	5	
	AhpC	Alkyl hydroperoxide reductase C22 subunit	269	1.33	5	
	WrbA	Predicted flavoprotein in Trp regulation	180	0.96	4	
	YcdX	Predicted zinc–binding hydrolase	176	0.48	3	
	HdhA	7 alpha–hydroxysteroid dehydrogenase	153	0.48	3	
	GmhA	Phosphoheptose isomerase	104	0.40	2	
	4	SodB	Superoxide dismutase, iron	2579	6.28	7
YgeY		Probable deacetylase	1603	4.30	18	
AckA		Acetate kinase	333	0.78	6	

	FliC	Flagellin	261	0.32	4
	CysK	Cysteine synthase A	241	0.86	6
	PckA	Phosphoenolpyruvate carboxykinase	211	0.27	4
	GrpE	Heat shock protein	199	0.91	4
	WrbA	Predicted flavoprotein in Trp regulation	143	0.66	3
	AhpC	Alkyl hydroperoxide reductase C22 subunit	137	0.66	4
	AspC	Aspartate transaminase	119	0.63	9
5	AdhC	Alcohol dehydrogenase C	1740	5.62	18
	SodB	Superoxide dismutase, iron	1462	3.43	6
	PckA	Phosphoenolpyruvate carboxykinase	1271	2.34	17
	Gor	Glutathione–disulfide reductase	1066	2.48	13
	Gnd	Gluconate–6–phosphate dehydrogenase, decarboxylating	894	2.05	15
	HdhA	7 alpha–hydroxysteroid dehydrogenase	840	6.21	11
	WrbA	Predicted flavoprotein in Trp regulation	781	5.40	10
	YcdX	Predicted zinc–binding hydrolase	610	2.26	8
	AckA	Acetate kinase	514	0.93	6
	OsmC	Protein C, osmotically inducible	481	2.94	4
	GadB	Glutamate decarboxylase isozyme	333	0.50	6
	CysK	Cysteine synthase A	277	0.68	5
	PotD	Spermidine/putrescine–binding protein precursor	248	0.59	5
	YchN	Conserved protein	234	1.94	4
	GpmA	Phosphoglyceromutase 1	203	0.65	4
	PepD	X–His dipeptidase	159	0.23	3
	PmbA	Protease involved in Microcin B17 maturation	133	0.34	3
	IpxD	Hypothetical protein b0177	125	0.13	3
	SspA	Stringent starvation protein	121	0.34	2
	MoaB	Molybdopterin biosynthesis, protein B	120	0.75	3
	DnaK	Molecular chaperone DnaK	109	0.11	2
	Icd	Isocitrate dehydrogenase (NADP)	106	0.26	3
	YDJA	Putative NAD(P)H nitroreductase ydjA	106	0.69	3
	Rne	Ribonuclease E	89	0.06	2
6	SpeE	Spermidine synthase	947	1.40	6
	SodB	Superoxide dismutase, iron	632	0.94	4
	Tsf	Translation elongation factor EF–Ts	547	2.21	9
	GloB	Probable hydroxyacylglutathione hydrolase	512	2.45	9
	Bfr	Bacterioferritin	428	2.76	6
	RutE	Predicted nitroreductase	343	1.81	7
	MdaB	Modulator of drug activity B	293	1.63	5
	FklB	Predicted hydrolase	263	1.21	5
	YgfK	Putative oxidoreductase Fe–S subunit	260	0.20	6
	MtlD	Mannitol–1–phosphate 5–dehydrogenase	246	0.55	4
	YjgF	Predicted hydrolase	234	1.75	3
	GldA	Glycerol dehydrogenase	227	0.58	5
	YchN	Conserved protein	187	0.71	2
	YjbJ	Hypothetical protein ECs5028	178	2.32	3
	YieF	Hypothetical protein b3713	162	0.99	3
	YiiM	Predicted hydrolase	144	0.32	2
	GlnB	Nitrogen regulatory protein P–II.1	143	1.29	3
	YbjW	Hydroxylamine reductase	138	0.19	3
	RplL	Ribosomal protein L7/L12	138	0.16	2
	MogA	Molybdopterin biosynthesis protein mog	110	0.39	2
	OsmC	Protein C, osmotically inducible	110	0.58	2
	TdcF	Predicted hydrolase	106	0.63	2
	DeoB	Phosphopentomutase	88	0.17	2
	AhpC	Alkyl hydroperoxide reductase C22 subunit	84	0.40	2
	NemA	Probable N–ethylmaleimide reductase	77	0.20	2
	HtpG	Heat shock protein C62.5	71	0.11	2
	AcpD	[acyl–carrier–protein] phosphodiesterase	70	0.39	2
	YcjY	Conserved hypothetical protein b1327	63	0.23	2

7	FbaA	Fructose-bisphosphate aldolase II	2154	4.63	16
	HchA	H-NS-repressed protein, 30K	1372	7.71	13
	YgeY	Probable deacetylase	1234	4.73	17
	HtpG	Heat shock protein C62.5	763	0.93	15
	Tsf	Translation elongation factor EF-Ts	639	4.13	14
	OsmC	Protein C, osmotically inducible	492	8.81	8
	WrbA	Predicted flavoprotein in Trp regulation	342	1.75	6
	SspA	Stringent starvation protein	305	1.40	6
	YjgF	Predicted hydrolase	303	1.14	3
	Bfr	Bacterioferritin	274	1.13	3
	TreC	Alpha,alpha-phosphotrehalase	271	0.66	10
	SerC	Phosphoserine transaminase	245	0.71	7
	YbiB	Predicted transferase/phosphorylase	231	0.66	5
	AhpF	Alkyl hydroperoxide reductase subunit F	228	0.38	5
	PdxK	Pyridoxal kinase	221	0.58	4
	SpeE	Spermidine synthase	217	0.55	3
	PepE	Peptidase E	203	1.05	5
	TpiA	Triose-phosphate isomerase	185	0.48	3
	HdhA	7 alpha-hydroxysteroid dehydrogenase	184	0.69	3
	RpiA	Ribosephosphate isomerase	163	0.59	3
	CysK	Cysteine synthase A	156	0.23	2
	RbsK	Ribokinase	150	0.39	5
	SodB	Superoxide dismutase, iron	142	0.64	4
	AlaS	Alanine-tRNA ligase	137	0.08	2
	OmpX	Outer membrane protein X	135	0.76	3
	AhpC	Alkyl hydroperoxide reductase C22 subunit	126	0.66	4
	NfsA	Drug activity modulator A	104	0.30	2
	GshA	Glutamate-cysteine ligase	97	0.28	4
	YahK	Probable alcohol dehydrogenase (NADP)	82	0.20	2
	ClpB	Endopeptidase Clp, ATP-binding chain clpB	81	0.08	3
	Rpe	D-ribulose-5-phosphate 3-epimerase	66	0.33	3
ZapB	Hypothetical protein ECs4853	63	0.42	2	
8	FbaA	Fructose-bisphosphate aldolase II	3930	8.72	19
	YgeY	Probable deacetylase	1886	6.27	20
	HtpG	Heat shock protein C62.5	728	1.03	13
	HchA	H-NS-repressed protein, 30K	591	1.79	7
	ManA	Mannose-6-phosphate isomerase	529	0.65	5
	YbiB	Predicted transferase/phosphorylase	490	1.25	7
	Def	Peptide deformylase	416	1.96	6
	WrbA	Predicted flavoprotein in Trp regulation	402	2.26	6
	PepE	Peptidase E	383	1.74	6
	FabF	3-oxoacyl-[acyl-carrier-protein] synthase II	382	0.65	6
	TrxB	Thioredoxin-disulfide reductase	355	0.85	6
	SerC	Phosphoserine transaminase	321	0.57	5
	CysK	Cysteine synthase A	312	0.51	4
	AhpC	Alkyl hydroperoxide reductase C22 subunit	289	1.75	5
	YfiD	Probable glycyl radical protein yfiD	274	3.27	6
	Tsf	Translation elongation factor EF-Ts	261	0.42	3
	Gor	Glutathione-disulfide reductase	248	0.25	3
	YdgS	Probable pyridoxal kinase	235	0.40	3
	OsmC	Protein C, osmotically inducible	232	0.98	2
	NfsA	Drug activity modulator A	196	0.30	2
	Gnd	Gluconate-6-phosphate dehydrogenase, decarboxylating	194	0.23	3
	HdhA	7 alpha-hydroxysteroid dehydrogenase	173	0.30	2
	YghU	Predicted hydrolase	169	0.55	4
	YahK	Probable alcohol dehydrogenase (NADP)	153	0.20	2
	GcvT	Aminomethyltransferase	150	0.20	2
	Hns	DNA-binding protein H-NS	130	0.56	2
	YciD	YciD protein precursor	95	0.36	3

	KdsC	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase	93	0.42	2
	TreC	Alpha, alpha-phosphotrehalase	81	0.06	2
	SodB	Superoxide dismutase, iron	80	0.18	2
9	FbaA	Fructose-bisphosphate aldolase II	540	1.07	8
	MsrB	Hypothetical protein b1778	291	2.76	6
	YgeY	Probable deacetylase	117	0.17	2
	SodB	Superoxide dismutase, iron	104	0.39	2
	DeoD	Purine-nucleoside phosphorylase	94	0.31	2
10	Tsf	Translation elongation factor EF-Ts	3117	13.67	18
	Gnd	Gluconate-6-phosphate dehydrogenase, decarboxylating	1782	6.57	25
	DeoC	Deoxyribose-phosphate aldolase	1212	8.86	17
	WrbA	Predicted flavoprotein in Trp regulation	1155	9.62	12
	Gor	Glutathione-disulfide reductase	1150	2.48	13
	HtpG	Heat shock protein C62.5	725	1.14	15
	HdhA	7 alpha-hydroxysteroid dehydrogenase	663	3.86	11
	GmhA	Phosphoheptose isomerase	606	5.34	10
	YbiB	Predicted transferase/phosphorylase	599	2.73	11
	PmbA	Protease involved in Microcin B17 maturation	580	1.26	11
	YgeY	Probable deacetylase	546	0.89	8
	CysK	Cysteine synthase A	541	1.29	8
	TldD	Protease involved in Microcin B17 maturation	541	0.75	8
	YqjG	Hypothetical 37.4 kD protein in exuR-tdcC intergenic region	453	0.77	6
	FbaA	Fructose-bisphosphate aldolase II	429	1.07	7
	Ppa	Inorganic diphosphatase	417	3.96	8
	TreC	Alpha, alpha-phosphotrehalase	350	0.57	8
	YdhF	Predicted hydrolase	350	1.33	7
	GadB	Glutamate decarboxylase isozyme	331	0.40	5
	YghU	Predicted hydrolase	305	0.73	4
	NfsA	Drug activity modulator A	305	0.69	4
	PckA	Phosphoenolpyruvate carboxykinase	302	0.44	6
	SodB	Superoxide dismutase, iron	284	1.29	5
	DnaK	Molecular chaperone DnaK	277	0.23	4
	YgeW	Hypothetical protein ygeW	251	0.62	6
	YajF	Fructokinase	246	0.54	4
	HchA	H-NS-repressed protein, 30K	244	0.41	3
	Asd	Aspartate-semialdehyde dehydrogenase	240	0.43	4
	TpiA	Triose-phosphate isomerase	235	0.30	2
	YadF	Carbonic anhydrase 2	221	0.75	3
	KdsC	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase	218	1.01	4
	YggS	Hypothetical protein b2951	218	0.51	3
	GlpQ	Glycerophosphodiester phosphodiesterase precursor, periplasmic	216	0.28	2
	DapB	Dihydrodipicolinate reductase	208	0.28	2
	EutL	Hypothetical protein b2439	207	0.59	3
	DeoD	Purine-nucleoside phosphorylase	206	0.72	4
	YbeK	Purine nucleosidase-related protein ybeK	195	0.52	3
	GshA	Glutamate-cysteine ligase	194	0.20	3
	AckA	Acetate kinase	176	0.28	3
	YncB	Putative NADP-dependent oxidoreductase yncB	172	0.33	3
	BglA	6-phospho-beta-glucosidase	165	0.29	4
	ZraP	Zinc resistance-associated protein	160	0.98	2
	YjhH	Uncharacterized protein	159	0.39	3
	MoaB	Molybdopterin biosynthesis, protein B	149	0.75	3
	MgsA	Methylglyoxal synthase	125	0.51	2
	SspA	Stringent starvation protein	124	0.34	2
	GpmA	Phosphoglyceromutase 1	120	0.45	3
	HemF	Coproporphyrinogen oxidase III	116	0.36	3
	GuaA	GMP synthase (glutamine-hydrolyzing)	99	0.13	2
	YjgF	Predicted hydrolase	94	0.66	2

	Mdh	Malate dehydrogenase	93	0.25	2
	Def	Peptide deformylase	92	0.44	2
	DapE	Succinyl–diaminopimelate desuccinylase	92	0.19	2
	RplL	Ribosomal protein L7/L12	79	0.75	2
11	Tsf	Elongation factor Ts	3889	22.40	19
	DeoD	Purine nucleoside phosphorylase	1932	37.77	24
	GadB	Glutamate decarboxylase isozyme	1643	2.63	13
	YgeW	ornithine carbamoyltransferase	1548	4.45	18
	BglA	6–phospho–beta–glucosidase A	1104	1.99	15
	HtpG	Heat shock protein 90	905	1.25	16
	Dcp	Dipeptidyl carboxypeptidase II	889	0.75	11
	GuaA	GMP synthetase (glutamine aminotransferase)	882	1.35	13
	DnaK	Molecular chaperone DnaK	766	0.78	10
	Gnd	Gluconate–6–phosphate dehydrogenase, decarboxylating	727	0.87	8
	DapA	Dihydrodipicolinate synthase	685	2.47	8
	Ybgl	Hypothetical protein Z0861	624	1.20	5
	YadF	Carbonic anhydrase	621	4.33	10
	LdhA	Fermentative D–lactate dehydrogenase, NAD–dependent	529	0.79	6
	SpeB	Agmatinase	410	1.10	6
	Pgi	Glucose–6–phosphate isomerase	363	0.34	5
	WrbA	Predicted flavoprotein in Trp regulation	354	1.33	5
	AcnB	Bifunctional aconitate hydratase 2/2–methylisocitrate dehydratase	337	0.31	7
	YhhX	Predicted oxidoreductase with NAD(P)–binding Rossmann–fold domain	333	0.58	5
	UxaC	Uronate isomerase	328	0.59	7
	LeuS	Leucyl–tRNA synthetase	326	0.25	5
	YgeY	Probable deacetylase	291	0.37	4
	DeoC	2–deoxyribose–5–phosphate aldolase, NAD(P)–linked	276	0.66	4
	ZraP	Zinc resistance–associated protein	250	1.49	3
	Tig	Trigger factor	243	0.35	4
	YbiB	Predicted transferase/phosphorylase	235	0.66	5
	Moab	Molybdopterin biosynthesis, protein B	226	1.11	4
	Eda	Keto–hydroxyglutarate–aldolase/keto–deoxy–phosphogluconate aldolase	207	0.88	3
	PotD	Polyamine transporter subunit	201	0.59	5
	RbsD	D–ribose pyranase	199	0.36	3
	PurH	Fused IMP cyclohydrolase/phosphoribosylaminoimidazolecarboxamide formyltransferase	180	0.28	4
	NadE	NAD synthetase, NH ₃ /glutamine–dependent	177	0.42	3
	GroES	Co–chaperonin GroES	176	2.67	3
	RplL	50S Ribosomal protein L7/L12	158	1.31	3
	YqhD	Alcohol dehydrogenase, NAD(P)–dependent	144	0.29	3
	PfkA	6–phosphofructokinase	141	0.50	4
	Tuf	Elongation factor Tu	140	0.18	2
	NanA	N–acetylneuraminase lyase	132	0.24	2
	OmpW	Outer membrane protein W	125	0.36	2
	LysS	Lysyl–tRNA synthetase	120	0.21	3
	Asd	Aspartate–semialdehyde dehydrogenase	120	0.20	2
	GmhA	Phosphoheptose isomerase	119	0.40	2
	GldA	Glycerol dehydrogenase	118	0.20	2
	FbaA	Fructose–biphosphate aldolase II	99	0.20	2
	MetK	S–adenosylmethionine synthetase	84	0.19	2
	YhfA	Hypothetical protein Z4717	76	0.61	2
	Ppa	Inorganic pyrophosphatase	74	0.43	2
	PflB	Pyruvate formate lyase I	73	0.09	2
12	DnaK	DnaK–typeMolecular chaperone DnaK	2395	3.80	27
	GadB	Glutamate decarboxylase isozyme	1371	2.39	14

Pgi	Glucose-6-phosphate isomerase	1309	2.23	18	
LeuS	Leucine-tRNA ligase	1104	1.10	19	
PflB	Formate C-acetyltransferase 1	967	1.14	15	
SerS	Serine-tRNA ligase	939	1.82	13	
TktA	Transketolase 1, thiamin-binding	772	0.82	12	
YgeW	Hypothetical protein ygeW	708	1.43	11	
AtoB	Acetyl-CoA C-acetyltransferase	686	1.64	9	
FusA	Translation elongation factor EF-G	677	0.45	7	
PurH	PurH bifunctional enzyme	660	0.76	9	
GshB	Glutathione synthase	557	1.46	8	
TnaA	Tryptophanase	521	1.11	11	
Tig	Trigger factor	520	0.96	9	
RplL	Ribosomal protein L7/L12	510	2.05	3	
HtpG	Heat shock protein C62.5	509	0.84	11	
LysU	Lysine-tRNA ligase thermoinducible	491	0.99	10	
GrpE	Heat shock protein	447	1.65	5	
Rpe	D-ribulose-5-phosphate 3-epimerase	446	1.37	5	
ArgH	Argininosuccinate lyase	435	0.64	7	
BglA	6-phospho-beta-glucosidase	407	0.67	8	
Tsf	Translation elongation factor EF-Ts	382	1.26	7	
ValS	Valine-tRNA ligase	373	0.35	9	
AldA	Lactaldehyde dehydrogenase	364	0.73	8	
GroES	Chaperonin groES	315	4.08	4	
YqhD	Alcohol dehydrogenase, NAD(P)-dependent	303	0.67	5	
PepP	X-Pro aminopeptidase II	295	0.43	4	
AspA	Aspartate ammonia-lyase	286	0.61	7	
FabA	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase	229	1.51	5	
GlcG	Protein glcG	222	1.12	2	
KdgA	2-dehydro-3-deoxy-phosphogluconate aldolase	217	0.88	4	
TktB	Transketolase 2, thiamin-binding	215	0.22	4	
RbsD	Hypothetical protein ECs4690	214	0.57	2	
Gnd	Gluconate-6-phosphate dehydrogenase, decarboxylating	216	0.32	4	
Dcp	Peptidyl-dipeptidase Dcp	209	0.15	3	
Agp	Glucose-1-phosphatase precursor	190	0.26	3	
YgeY	Probable deacetylase	187	0.27	3	
YfiD	Probable glycyl radical protein yfiD	186	2.35	5	
WrbA	Predicted flavoprotein in Trp regulation	180	0.40	2	
DeoD	Purine-nucleoside phosphorylase	164	0.50	3	
YlbA	Hypothetical protein b0515	154	0.28	2	
TufB	Translation elongation factor EF-Tu.B	154	0.28	3	
AceA	Isocitrate lyase	151	0.25	3	
Asd	Aspartate-semialdehyde dehydrogenase	149	0.20	2	
SpeB	Agmatinase	147	0.24	2	
IleS	Isoleucine-tRNA ligase	139	0.15	4	
GapA	Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) A	131	0.35	3	
YbiB	Predicted transferase/phosphorylase	123	0.36	3	
Moab	Molybdopterin biosynthesis, protein B	110	0.45	2	
YjgB	Predicted hydrolase	103	0.21	2	
DapA	Dihydrodipicolinate synthase	83	0.25	2	
GlcB	Malate synthase isoenzyme G	76	0.09	2	
TdcE	Keto acid formate-lyase	67	0.13	2	
13	GlcB	Malate synthase G	2012	4.25	32
	Agp	Glucose-1-phosphatase/inositol phosphatase	1585	9.46	24
	FliY	Cystine transporter subunit	649	3.94	13
	MglB	Methyl-galactoside transporter subunit	630	2.32	11
	DapD	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	525	1.90	9
	ClpB	Protein disaggregation chaperone	500	0.46	9
	ZraP	Zinc resistance-associated protein	310	2.94	4
	LysS	Lysyl-tRNA synthetase	308	0.65	8

	DnaK	Molecular chaperone DnaK	307	0.37	6
	YgeW	Ornithine carbamoyltransferase	304	0.76	7
	PurH	Fused IMP cyclohydrolase/phosphoribosylaminoimid azolecarboxamide formyltransferase	204	0.28	4
	YqhD	Alcohol dehydrogenase, NAD(P)- dependent	176	0.29	3
	Mdh	Malate dehydrogenase	168	0.39	3
	AlnB	Alanine racemase 2, PLP-binding	135	0.44	4
	TktA	Transketolase 1, thiamin-binding	131	0.11	2
	PflB	Pyruvate formate lyase I			
	Efp	Elongation factor P	94	0.41	2
	NikA	Nickel transporter subunit	88	0.13	2
	Hns	DNA-binding protein HLP-II (HU, BH2, HD, NS); pleiotropic regulator	82	0.56	2
	Eno	Phosphopyruvate hydratase	71	0.17	2
14	FumB	Anaerobic class I fumarate hydratase (fumarase B)	361	0.61	8
	ZraP	Zinc resistance-associated protein	352	3.95	5
	LysS	Lysyl-tRNA synthetase	347	0.75	9
	Mdh	Malate dehydrogenase	151	0.55	4
	LysS	Lysine tRNA synthetase, constitutive	137	0.21	3
	YkgC	Predicted pyridine nucleotide-disulfide oxidoreductase	98	0.25	3
	ProA	Gamma-glutamylphosphate reductase	92	0.17	2
	EbgR	DNA-binding transcriptional repressor	92	0.22	2
	DapD	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	90	0.27	2
	Eno	Phosphopyruvate hydratase	77	0.17	2
	MdoD	Periplasmic glucan biosynthesis protein	76	0.12	2
	RbsB	D-ribose transporter subunit	74	0.26	2
	ClpB	Protein disaggregation chaperone	72	0.08	2
	GlgB	1,4-alpha-glucan branching enzyme	71	0.09	2
15	ZraP	Zinc resistance-associated protein	403	2.94	5
	LysS	Lysyl-tRNA synthetase	357	0.99	11
	YjjV	Predicted deoxyribonuclease	260	0.84	5
	RpoA	DNA-directed RNA polymerase alpha subunit	209	0.63	5
	RbsB	D-ribose transporter subunit	167	0.41	3
	GlgB	1,4-alpha-glucan branching enzyme	162	0.19	4
	OmpA	Outer membrane protein 3a (II*;G;d)	152	0.33	3
	LpdA	Dihydrolipoamide dehydrogenase	142	0.24	3
	Mdh	Malate dehydrogenase	140	0.39	3
	PykF	Pyruvate kinase	88	0.15	2
	OsmY	Periplasmic protein	87	0.40	2
	MdoD	Periplasmic glucan biosynthesis protein	69	0.12	2
16	TalA	Transaldolase	569	3.47	14
	ZraP	Zinc resistance-associated protein	464	5.22	6
	Mdh	Malate dehydrogenase	290	1.16	7
	MdoD	Periplasmic glucan biosynthesis protein	287	0.50	7
	SpoR	Guanylate kinase	242	1.46	6
	RfaD	ADP-L-glycero-D-mannoheptose-6- epimerase	159	0.67	5
	TktB	Transketolase 2, thiamin-binding	125	0.16	3
	LysS	Lysyl-tRNA synthetase	124	0.28	4
	PaxA	2'-deoxycytidine 5'-triphosphate deaminase	122	0.39	2
	YebB	Hypothetical protein Fpla041 [Plasmid F]	114	0.37	3
	YgaU	Hypothetical protein b2665	99	0.91	3
17	ZraP	Zinc resistance-associated protein	315	2.94	6
	TalA	Transaldolase	171	0.49	4
	YhbH	Putative yhbH sigma 54 modulator	137	1.24	3
	TesB	Acyl-CoA thioesterase II	126	0.40	3
	IspF	2-C-methyl-D-erythritol 2,4- cyclodiphosphate synthase	125	0.51	2

	YgiW	Hypothetical protein Z4376	62	0.63	2
18	RbsB	D-ribose transporter subunit	332	1.24	7
	ZraP	Zinc resistance-associated protein	303	2.13	4
	YaeH	Putative structural protein	133	0.99	3
	FabG	3-oxoacyl-[acyl-carrier-protein] reductase	107	0.52	3
	GadB	Glutamate decarboxylase isozyme	104	0.15	2
	RbfA	Ribosome-binding factor A	83	0.58	2
	YgiW	Hypothetical protein Z4376	59	0.63	2
	YlaD	Maltose O-acetyltransferase	57	0.41	2
19	NanA	N-acetylneuraminatase lyase	576	2.68	10
	TalB	Transaldolase	550	2.36	11
	GapA	Glyceraldehyde-3-phosphate dehydrogenase	357	0.49	3
	Agn	CP4-44 prophage; antigen 43 (Ag43) phase-variable biofilm formation autotransporter	331	0.31	7
	GadB	Glutamate decarboxylase isozyme	326	0.84	9
	PckA	Phosphoenolpyruvate carboxykinase	323	0.62	8
	DeoD	Purine nucleoside phosphorylase	283	1.58	7
	YdgA	Hypothetical protein b1614	225	0.49	6
	DnaK	Molecular chaperone DnaK	211	0.30	5
	Eno	Phosphopyruvate hydratase	202	0.48	5
	UxaC	Uronate isomerase	188	0.30	4
	HisD	Bifunctional histidinol dehydrogenase/histidinol dehydrogenase	180	0.36	4
	YcaC	Predicted hydrolase	172	0.58	3
	LivK	high-affinity leucine-specific transport system; periplasmic binding protein	160	0.44	4
	WrbA	Predicted flavoprotein in Trp regulation	133	0.66	3
	FliC	Flagellar filament structural protein (flagellin)	133	0.23	3
	LysS	Lysyl-tRNA synthetase	129	0.21	3
	GabT	4-aminobutyrate aminotransferase, PLP-dependent	125	0.17	2
	Pgk	Phosphoglycerate kinase	116	0.42	4
	Rpe	Ribulose-phosphate 3-epimerase	106	0.54	3
	PotD	Polyamine transporter subunit	91	0.32	3
	RplL	50S Ribosomal protein L7/L12	91	1.31	3
	DapA	Dihydrodipicolinate synthase	75	0.25	2
	FusA	Elongation factor EF-2	56	0.10	2
	AhpC	Alkyl hydroperoxide reductase, C22 subunit; detoxification of hydroperoxides	52	0.40	2

The position of spot number is indicated in Fig. S3. This table contains just proteins with number of unique peptides ≥ 2 .