SUPPLEMENTARY Table S1

Experimental design of DIGE experiments

Gel	Cy2	Cy3	Cy5
1	pooled internal standard	0.1 #1	0.3 #1
2	pooled internal standard	0.6 #1	0.1 #2
3	pooled internal standard	0.3 #2	0.6 #2
4	pooled internal standard	0.1 #3	0.6 #3
5	pooled internal standard	0.6 #4	0.3 #3
6	pooled internal standard	0.3 #4	0.1 #4

The experimental design for the DIGE comparison of 0.1 vs. 0.3 vs. 0.6 h^{-1} dilution rate of *E. coli* MG1655 extracts, each with four replicates. The extracts were labeled with three fluorescent labels (Cy2, 3, 5) as shown and the pooled internal standard included a mix of extracts from all 3x4 replicates of this experiment (n=12).

SUPPLEMENTARY Table S2

Peptide fragment identification data for protein spots in Fig. 1 / Table 1

Spot	Protein ID	Name	Function		Score	Hits	Coverage
85	P06129	**BtuB**	Outer membrane cobalamin/Vit. B12 translocator	OM	183	7/16	54%
86	P06129	**BtuB**	Outer membrane cobalamin/Vit. B12 translocator	OM	131	5/20	47%
15	P10384	**FadL**	Long-chain fatty acid transport protein	OM	134	11/20	31%
70	P05825	**FepA**	Enterobactin outer-membrane receptor	OM	108	4/18	25%
69	P06971	**FhuA**	Ferric hydroxamate receptor	OM	119	13/18	18%
23	Q1REC0	**Fiu**	Catecholate siderophore receptor	OM	55	6/13	7%
24	Q1REC0	**Fiu**	Catecholate siderophore receptor	OM	199	9/21	52%
33	P02943	**LamB**	Maltoporin	OM	174	15/35	47%
25	P45464	**LpoA**	Penicillin-binding protein activator	OM	5	6/14	10%
26	P45464	**LpoA**	Penicillin-binding protein activator	OM	34	12/17	21%
13	P28635	**MetQ**	D-methionine-binding lipoprotein	OM	31	9/17	50%
14	P28635	**MetQ**	D-methionine-binding lipoprotein	OM	22	8/14	43%
16	P28635	**MetQ**	D-methionine-binding lipoprotein	OM	18	7/17	42%
38	P0A903	**NlbP**	Lipoprotein 34	OM	143	13/39	51%
51	P0A910	**OmpA**	Outer membrane protein A	OM	130	13/32	47%
63	P0A910	**OmpA**	Outer membrane protein A	OM	131	8/37	42%
64	P0A910	**OmpA**	Outer membrane protein A	OM	42	8/37	34%
88	P0A910	**OmpA**	Outer membrane protein A	OM	69	6/14	42%
32	P0A910	**OmpC**	Outer membrane protein C	OM	108	12/43	46%
38	P06996	**OmpC**	Outer membrane protein C	OM	171	15/47	47%
34	P02931	**OmpF**	Outer membrane protein F	OM	86	5/11	66%
37	P02931	**OmpF**	Outer membrane protein F	OM	25	8/32	28%
57	P02931	**OmpF**	Outer membrane protein F	OM	200	7/18	63%
58	P02931	**OmpF**	Outer membrane protein F	OM	143	5/21	19%
59	P02931	**OmpF**	Outer membrane protein F	OM	120	5/21	16%
60	P02931	**OmpF**	Outer membrane protein F	OM	136	8/27	41%
61	P02931	**OmpF**	Outer membrane protein F	OM	121	5/15	54%
62	P02931	**OmpF**	Outer membrane protein F	OM	99	4/9	37%
84	P02931	**OmpF**	Outer membrane protein F	OM	121	5/15	29%
11	P09169	**OmpT**	Protease 7; Omptin	OM	69	13/24	43%
31	P09169	**OmpT**	Protease 7; Omptin	OM	353	19/21	84%
68	P09169	**OmpT**	Protease 7; Omptin	OM	111	12/24	42%
73	P09169	**OmpT**	Protease 7; Omptin	OM	85	4/11	31%
1	P0A917	**OmpX**	Outer membrane protein X	OM	104	5/10	51%
65	P0A912	**Pal**	Peptidoglycan-associated lipoprotein	OM	7	5/13	29%
8	P37194	**Slp**	Lipid anchor protein	OM	42	5/27	38%
39	P02930	**TolC**	Outer membrane protein	OM	195	14/32	41%
43	P46130	**YbhC**	Putative acyl-CoA thioester hydrolase	OM	108	13/37	33%
71	P46130	**YbhC**	Putative acyl-CoA thioester hydrolase	OM	114	4/19	38%
4	P75818	**YbjP**	Uncharacterized lipoprotein	OM	20	6/14	50%
9	P64451	**YdcL**	Uncharacterized lipoprotein	OM	17	7/17	43%
45	P76576	**YfgM**	Uncharacterised membrane protein	OM	8	4/21	22%
48	P0AC02	**YfiO**	Uncharacterized lipoprotein	OM	209	8/24	63%
7	P0ADE6	**YgaU**	Uncharacterized lipoprotein	OM	77	10/22	65%
81	P0ADE4	**YtfM**	Uncharacfterized protein	OM	78	5/10	15%
21	P23847	**DppA**	Periplasmic dipeptide transport protein	P	18	10/17	19%
87	P0AEE5	**GgbP**	Glucose galactose periplasmic binding protein	P	83	10/19	34%
40	P0AEX9	**MalE**	Maltose-binding periplasmic protein	P	31	9/28	28%
94	P0AEX9	**MalE**	Maltose-binding periplasmic protein	P	90	4/11	35%
47	P0AEE5	**MglB**	D-galactose-binding periplasmic protein	P	21	8/36	29%
84	P37329	**ModA**	Molybdate periplasmic binding protein	P	7	6/16	24%
67	P23843	**OppA**	Periplasmic oligopeptide-binding protein	P	134	5/17	26%
97	P18472	**TraW**	Involved in F-pilus assembly	P	65	2/6	15%
18	P39172	**ZnuA**	High-affinity zinc uptake system protein	P	7	6/16	24%
29	P0ABB4	**AtpB**	ATP synthase subunit beta	IM	12	7/7	18%
90	C4ZZ10	**AtpD**	ATP synthase subunit beta	IM	83	3/9	18%
6	B1IX02	**AtpF**	ATP synthase subunit b	IM	70	9/24	58%
10	P77268	**DdbP**	Possibly D,D-dipeptide transport ATP-binding protein	IM	187	20/43	39%
20	P0AC42	**DhsA**	Succinate dehydrogenase flavoprotein subunit	IM	45	10/26	19%
30	P09127	**HemX**	Putative uroporphyrinogen-III C- methyltransferase	IM	10	6/12	19%
52	P69797	**ManX**	PTS system mannose-specific EIIAB component	IM	103	14/39	41%
3	P0AE18	**Map**	Methionine aminopeptidase; membrane associated	IM	90	3/9	21%

The differentially expressed spots were subject to MALDI-TOF analysis. Spot numbers are identical to Figure 2a. The p
Protein ID of best match protein was from E. coli (K12) identified through CBRG (Uniprot/SwissProt release Release 57.12) or MASCOT.
The **score** values were from from CBRG and MASCOT and values >60-90 are highly significant matches.
Hits are the positively identified peptide masses out of all resolved peptides masses per protein.
The **coverage** means the percentage of the protein sequence covered by the positively identified peptides.