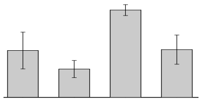
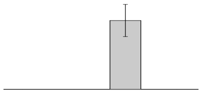
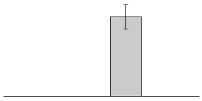
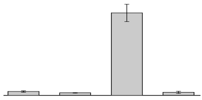
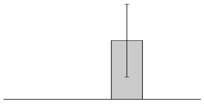
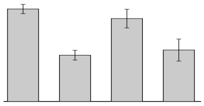
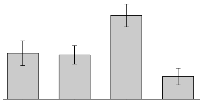
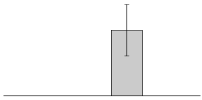
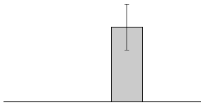
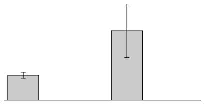
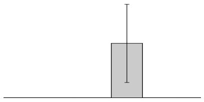
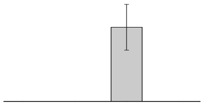
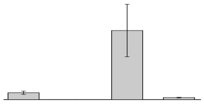
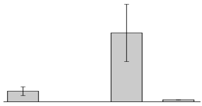
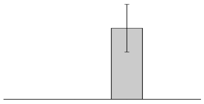
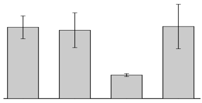
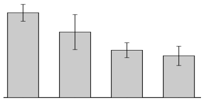
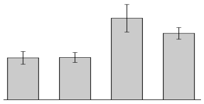
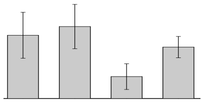
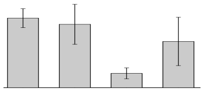
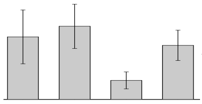
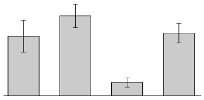
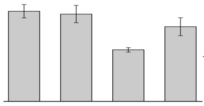
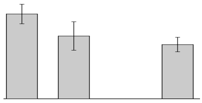
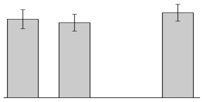
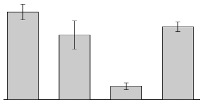
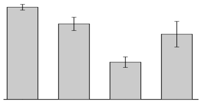
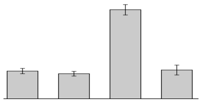
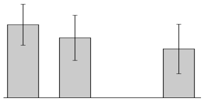
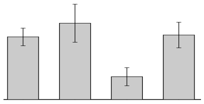
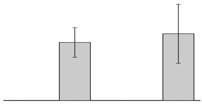
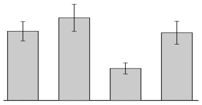
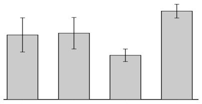
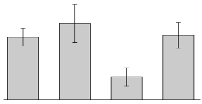
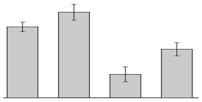
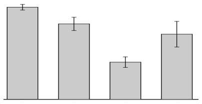
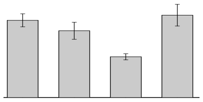
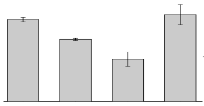
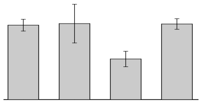
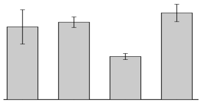
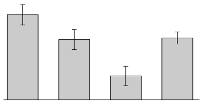
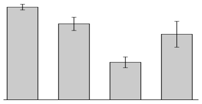
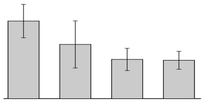
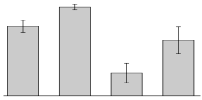
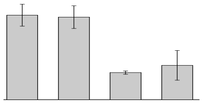
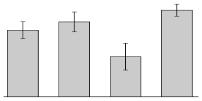
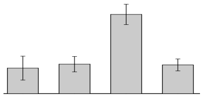
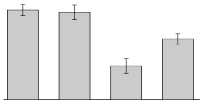
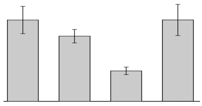
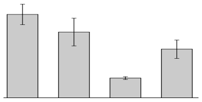
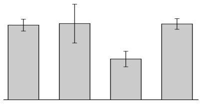
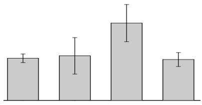
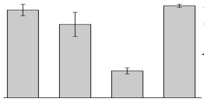
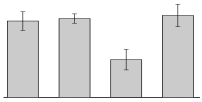
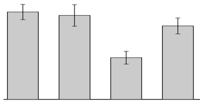
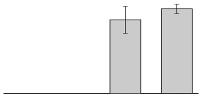
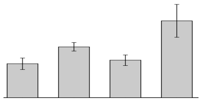
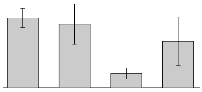
Table S1. Iron-responsive proteins in *A. baumannii* ATCC 19606^T identified via PMF.

	ASQ[b]	Protein function/name[c]		NCBI	Theoretical[d]					
Spot[a]	A B C D	*Source is italicized*	Gene[c]	Accession #	M_r	pI	S[e]	M[f]	C[g]	F[h]
		Iron acquisition/Virulence								
22		Outer membrane receptor for ferrienterochelin and colicins *A. baumannii* ACICU	*fepA*	gi|184157262	82767	5.66	172	26	39	TC
27		Ferric aerobactin receptor protein *A. baumannii* ATCC 19606^T		gi|260555123	85609	7.55	346	42	74	TC
31		Ferric anguibactin receptor *A. baumannii* ATCC 19606^T	*bauA*	gi|260556700	82960	5.86	288	28	54	TC
33		Ferric aerobactin receptor protein *A. baumannii* ATCC 19606^T		gi|260555123	85609	7.55	138	25	38	OM
37		Ferric enterobactin receptor precursor *A. baumannii* AYE	*fepA*	gi|169796822	82746	5.66	146	23	42	OM
39		TonB-dependent vitamin B12 receptor *A. baumannii* ATCC 19606^T	*btuB*	gi|260557148	68121	5.22	277	28	57	OM
45		FhuE receptor *A. baumannii* ATCC 19606^T	*fhuE*	gi|260555105	80612	5.44	98	10	14	OM
46		FhuE receptor *A. baumannii* ATCC 19606^T	*fhuE*	gi|260555105	80612	5.44	226	25	42	OM
47		Ferric anguibactin receptor *A. baumannii* ATCC 19606^T	*bauA*	gi|260556700	82960	5.86	242	31	48	OM
48		Outer membrane receptor protein, mostly Fe transport *A. baumannii* ATCC 19606^T		gi|260557370	78171	5.47	339	33	58	OM
49		Ferric enterobactin receptor precursor *A. baumannii* AYE	*fepA*	gi|169796822	82746	5.66	113	19	28	OM
53		Ferric aerobactin receptor protein *A. baumannii* ATCC 19606^T		gi|260555123	85609	7.55	356	39	68	OM
54		Outer membrane receptor for ferrienterochelin and colicins *A. baumannii* ACICU	*fepA*	gi|184157262	82767	5.66	186	28	46	OM
55		Ferric aerobactin receptor protein *A. baumannii* ATCC 19606^T		gi|260555123	85609	7.55	405	48	73	OM
57		Ferric anguibactin receptor *A. baumannii* ATCC 19606^T	*bauA*	gi|260555123	85609	7.55	343	33	62	OM
		Porins								
32		Putative outer membrane protein W *A. baumannii* ATCC 19606^T	*ompW*	gi|260556338	23137	6.29	93	8	57	OM

34		Putative outer membrane protein *A. baumannii* ATCC 17978		gi|126640934	22471	9.30	93	11	53	OM
35		Carbapenem-associated resistance protein *A. baumannii* ATCC 19606^T	*carO*	gi|260556565	26855	4.66	133	12	76	OM
43		Putative outer membrane protein W *A. baumannii* ATCC 19606^T	*ompW*	gi|260556338	23137	6.29	83	8	57	OM
44		Outer membrane protein A *A. baumannii*	*ompA*	gi|129307154	36939	5.42	109	12	37	OM
56		Outer membrane protein Omp38 *A. baumannii* ATCC 19606^T	*omp38*	gi|260557183	38397	5.32	86	7	20	OM
58		Outer membrane protein Omp38 *Acinetobacter* sp. RUH2624	*omp38*	gi|260548855	37972	5.72	139	15	39	OM
		Adaptation/Stress tolerance								
5		Chaperonin GroEL *A. baumannii* SDF	*groEL*	gi|169632653	56886	4.92	273	34	55	TC
8		Superoxide dismutase (Fe) *A. baumannii* SDF	*sodB*	gi|169632935	22905	5.56	123	6	41	TC
9		Bacterioferritin *A. baumannii* ATCC 17978	*bfr*	gi|126640856	18023	5.02	137	17	70	TC
10		Superoxide dismutase (Fe) *A. baumannii* SDF	*sodB*	gi|169632935	22905	5.56	109	8	44	TC
24		Superoxide dismutase (Fe) *A. baumannii* SDF	*sodB*	gi|169632935	22905	5.56	83	8	44	TC
26		Fumarase C (fumarate hydratase class II) *A. baumannii* ATCC 19606^T	*fumC*	gi|260554730	50111	5.74	128	17	39	TC
38		Bacterioferritin *A. baumannii* ATCC 19606^T	*bfr*	gi|260410611	18137	5.02	106	14	72	OM
41		Bacterioferritin *A. baumannii* ATCC 19606^T	*bfr*	gi|260410611	18137	5.02	78	9	45	OM
42		Bacterioferritin *A. baumannii* ATCC 19606^T	*bfr*	gi|260410611	18137	5.02	100	12	66	OM
		TCA cycle								
14		Succinate dehydrogenase flavoprotein subunit *A. baumannii* ATCC 17978	*sdh*	gi|126642744	64049	6.07	92	6	18	TC
15		Aconitate hydratase 2 *A. baumannii* ATCC 19606^T	*acnB*	gi|260411150	95322	5.07	238	37	48	TC
19		Fumarate hydratase *A. baumannii* ATCC 17978	*fumA*	gi|193076292	54948	5.44	129	18	49	TC

20		Aconitate hydratase 2 *A. baumannii* ATCC 19606^{T}	*acnB*	gi|260411150	95322	5.07	136	24	32	TC
21		Aconitate hydratase 1 *A. baumannii* ATCC 19606^{T}	*acnA*	gi|260556094	100503	5.28	410	36	44	TC
30		Succinate dehydrogenase flavoprotein subunit *A. baumannii* ATCC 17978	*sdh*	gi|126642744	64049	6.07	169	21	46	TC
		Lipid Metabolism								
3		Beta-ketoadipyl CoA thiolase *A. baumannii* ATCC 19606^{T}	*pcaF*	gi|260555473	43107	5.96	138	20	54	TC
18		Acyl-CoA dehydrogenase *A. baumannii* ATCC 19606^{T}		gi|260554863	42780	5.30	185	26	46	TC
25		2-ketocyclohexanecarboxyl-CoA hydrolase *A. baumannii* ATCC 19606^{T}		gi|260555475	29342	5.75	231	27	76	TC
29		2-hydroxycyclohexanecarboxyl-CoA dehydrogenase *A. baumannii* ATCC 19606^{T}	*fabG*	gi|260555032	27802	5.96	100	10	50	TC
		Regulatory								
2		Host factor I for bacteriophage Q beta replication hfq *A. baumannii* AYE	*hfq*	gi|169795564	16751	6.82	91	8	39	TC
50		30S ribosomal protein S6 *A. baumannii* SDF	*rpsF*	gi|169633238	14954	5.70	93	10	61	OM
51		50S ribosomal protein L3 *A. baumannii* AYE	*rplC*	gi|169794594	22523	9.87	108	10	63	OM
52		Peptidyl-prolyl cis-trans isomerase *A. baumannii* ATCC 17978	*surA*	gi|126641590	46526	5.75	197	19	47	OM
		Energy/Metabolisms								
1		Phenylacetate-CoA oxygenase subunit PaaB *A. baumannii* ATCC 17978	*paaB*	gi|126641383	11317	6.04	176	15	86	TC
4		Serine hydroxymethyltransferase *A. baumannii* AYE	*glyA*	gi|169795307	44967	5.44	107	11	36	TC
11		Putative flavohemoprotein (hemoglobin-like protein) *A. baumannii* ATCC 19606^{T}		gi|260409628	28814	4.91	188	15	60	TC
12		Phenylacetate-CoA oxygenase/ reductase PaaK subunit *A. baumannii* ATCC 17978	*paaK*	gi|193077015	39763	5.03	195	25	63	TC
16		Benzoate 1,2-dioxygenase, small subunit *A. baumannii* ATCC 19606^{T}		gi|260554867	18965	5.22	93	6	30	TC
28		Phenylacetate-CoA oxygenase subunit PaaB *A. baumannii* ATCC 17978	*paaB*	gi|126641383	11317	6.04	196	16	91	TC

36		F0F1 ATP synthase subunit alpha *A. baumannii* ATCC 17978	*atpA*	gi|162286757	55363	5.29	207	25	45	OM
		Unknown								
6		Putative 17-kDa surface antigen *A. baumannii* ACICU		gi|184157742	12424	4.70	87	8	83	TC
7		Signal peptide ydeN *A. baumannii* ATCC 19606^{T}	*ydeN*	gi|260556330	22987	4.75	92	7	34	TC
13		Hypothetical protein A1S_1295 *A. baumannii* ATCC 17978		gi|193076983	55265	5.07	129	17	39	TC
17		Short chain dehydrogenase *A. baumannii* SDF		gi|169632063	26998	5.18	135	14	55	TC
23		Hemerythrin HHE cation binding domain protein *A. baumannii* AB900		gi|239501928	17516	5.68	88	9	53	TC
40		Hypothetical protein A1S_1295 *A. baumannii* ATCC 17978		gi|193076983	55265	5.07	149	20	49	OM

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[a] The spot numbers correspond to the numbers given in Figures 2, 3 and 4.

[b] Average spot quantity per treatment group (n = 3); columns A, $^{-}$Fe/$^{-}$DIP; B, $^{+}$Fe/$^{-}$DIP; C, $^{-}$Fe/$^{+}$DIP; D, $^{+}$Fe/$^{+}$DIP.

[c] Protein function, name and gene were determined by http:/www.ncbi.nlm.nih.gov/BLAST/.

[d] Theoretical molecular mass (M_r) and isoelectric point (p*I*) were calculated by http:/www.expasy.org/.

[e] Mascot score.

[f] Number of matched peptide masses.

[g] Percent sequence coverage.

[h] Protein fraction, total cell (TC) or Outer membrane-enriched (OM) protein extracts.