Supplementary Information

Physiological and proteomic responses of continuous cultures of *Microcystis aeruginosa* PCC 7806 to changes in iron bioavailability and growth rate

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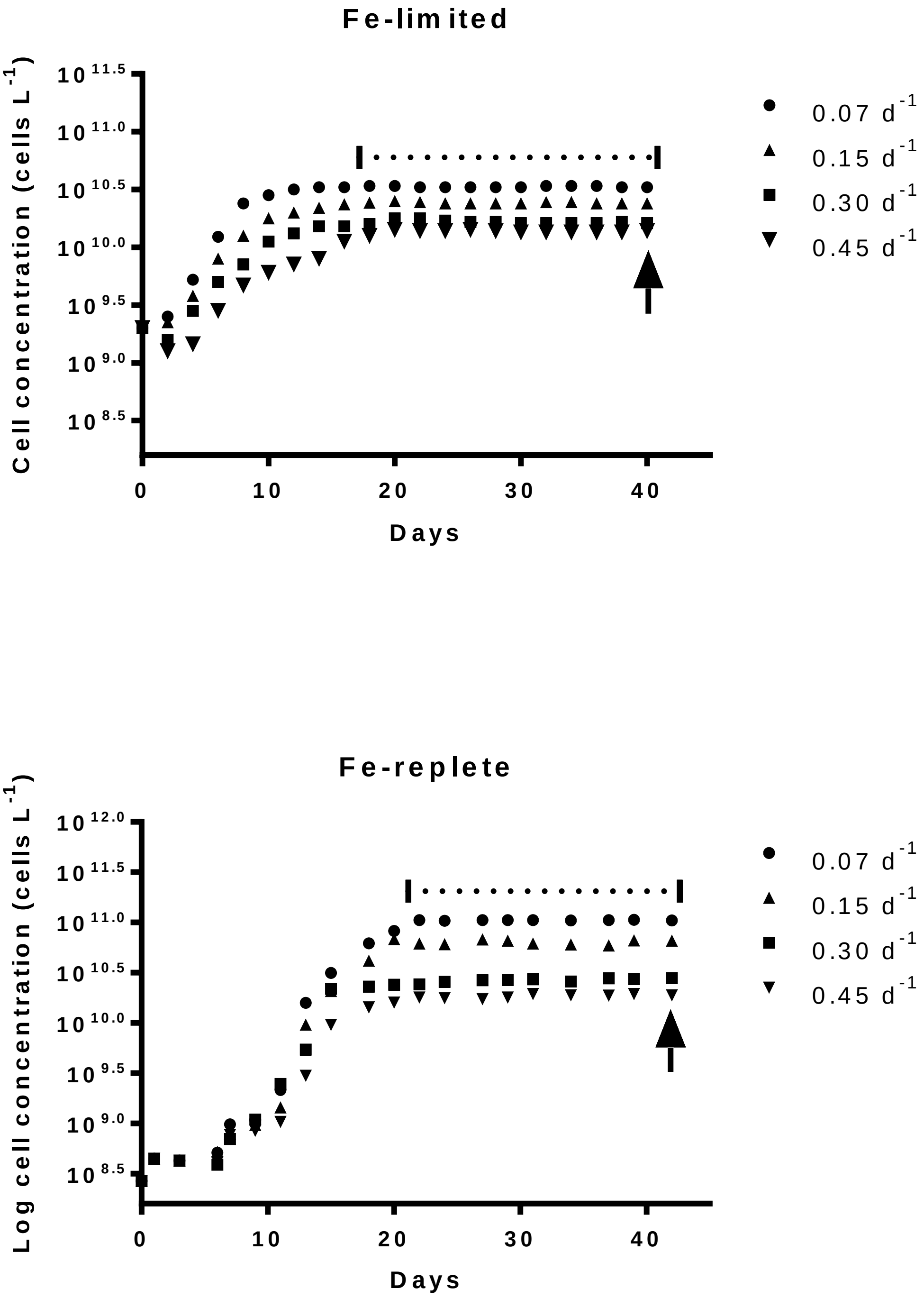

Figure S1. Growth of *M. aeruginosa* PCC 7806 in Fe-limited (top) and Fe-replete (bottom) chemostats. The dotted lines on the graph represent steady state where cell counts at subsequent samplings were within the 95% CI. The arrows mark the days when chemostat cultures were harvested (Fe-limited: Day 40, Fe-replete: Day 42) for physiological and proteomic analyses.

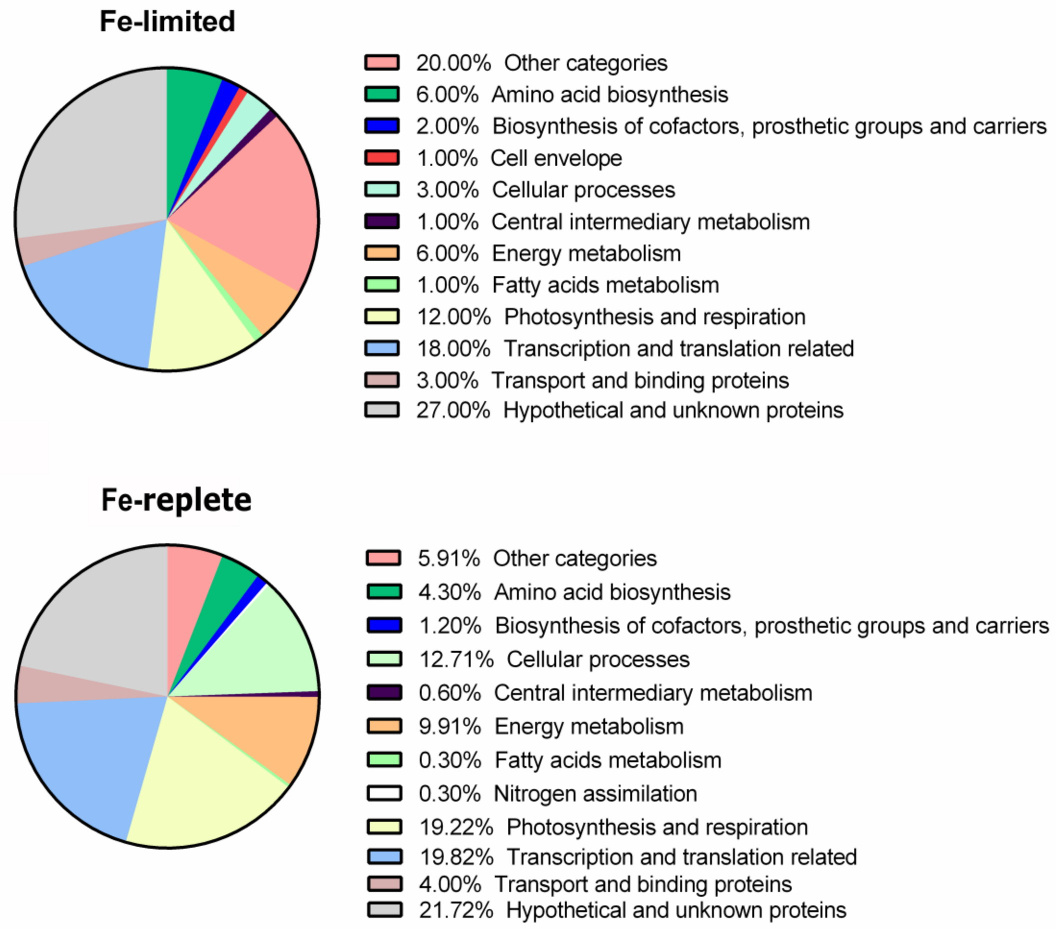

Figure S2. Core proteins identified in *M. aeruginosa* PCC 7806 under Fe-limited (top) and Fe-replete (bottom) chemostats. Proteins were assigned into functional groups according to CyanoBase (http://genome.microbedb.jp/cyanobase).

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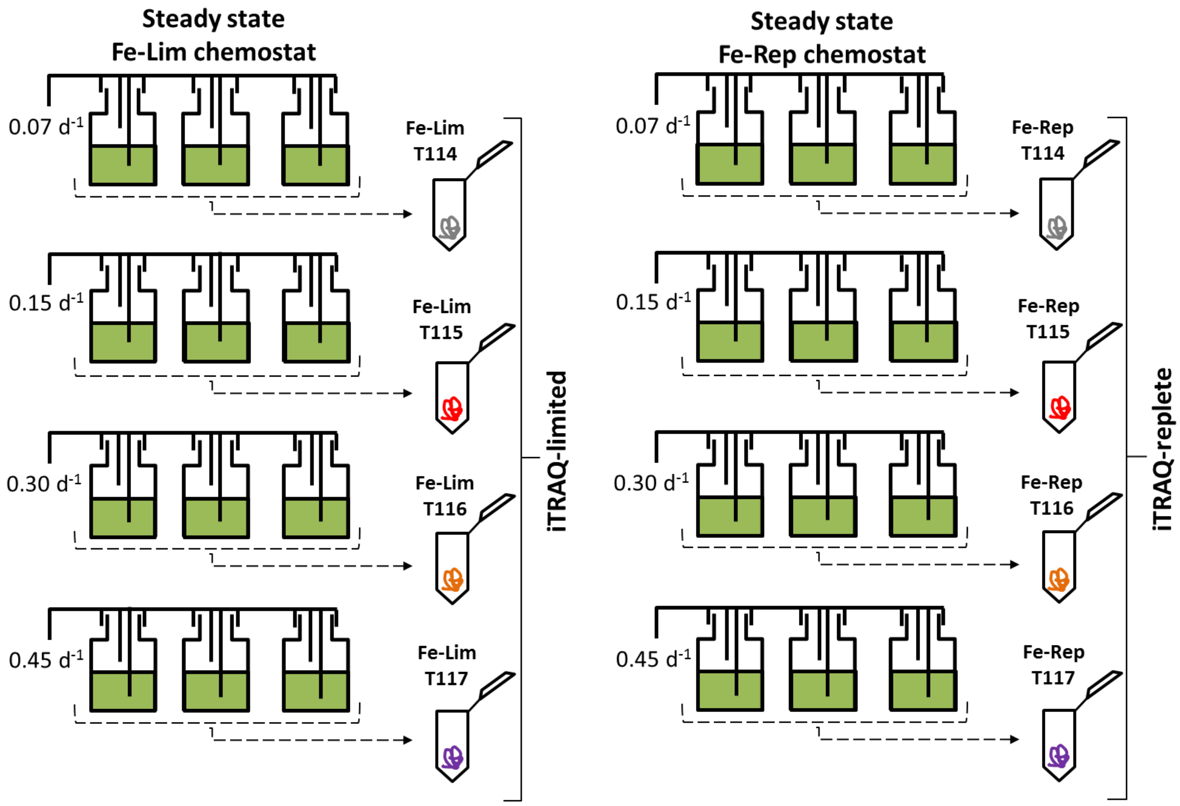

Figure S3 Summary of iTRAQ experimental design *M. aeruginosa* were cultured in chemostats to steady-state under Fe-limited (100 nM Fe) and Fe-replete (1,000 nM Fe) conditions at four dilution rates. Cells were harvested and protein extraction was carried out on each culture. Biological replicates were pooled for iTRAQ labeling and technical replicates were run for each iTRAQ analysis. The highest dilution rate (0.45 d^{-1}; T117) was used as the reference condition for each chemostat.

Table S1. Retention time and optimal compound dependent parameters for MCYST analysis by tandem MS

Compounds	RT (min)	MRM transitions	MRM Ratio	DP	CE	CXP
ENK	8	570.2 --> 136.1* 570.2 --> 120.1 570.2 --> 91.1	1 0.95 0.9	86	73 75 129	24 20 14
[D-Asp3]MCYST-RR	8.7	512.9 --> 135.1* 512.9 --> 103 512.9 --> 127.1	1 0.7 0.3	91	43 93 67	24 18 22
MCYST-RR	8.8	519.9 --> 135.1* 519.9 --> 103.1 519.9 --> 127.1	1 0.75 0.3	81	43 95 65	24 18 22
NOD	9.7	825.4 --> 135.3* 825.4 --> 103.1 825.4 --> 227	1 1 0.4	136	83 129 71	22 18 22
[D-Asp3]MCYST-LR	10	981.4 --> 135.1* 981.4 --> 127.2 981.4 --> 103.1	1 0.5 0.3	136	101 127 129	22 20 16
MCYST-YR	10.1	1045.4 --> 135.1* 1045.4 --> 127.1 1045.4 --> 213	1 0.4 0.25	156	103 125 83	22 22 22
MCYST-LR	10.2	995.5 --> 135.2* 995.5 --> 127 995.5 --> 213.1	1 0.55 0.5	161	101 129 87	8 22 12
MCYST-LA	16.4	910.5 --> 776.3* 910.5 --> 135.3 910.5 --> 213.1	1 0.65 0.3	96	29 87 67	12 22 18
MCYST-LW	18.9	1025.3 --> 135.2* 1025.3 --> 891.4 1025.3 --> 213.1	1 0.75 0.5	116	93 33 77	22 28 12
MCYST-LF	19.9	986.4 --> 135.1* 986.4 --> 852.4 986.4 --> 213.1	1 0.7 0.2	111	95 31 75	24 26 12

*Main MRM transition for quantitative determination. Retention time (RT); Collision energy (CE)

Table S2. Mobile phase gradient for LC analysis of MCYST samples

Total time (min)	Mobile phase A (%)	Mobile phase B (%)
5*	95	5
0	95	5
0.2	95	5
12	30	70
14	25	75
21	15	85
23	95	5

*Pre-equilibrium time before injection

Table S3. Optimal MS operating parameters for MCYST analysis

Instrument Model	AB Sciex Instruments 4000Q TRAP LC-MS/MS
Parameter	Setting Value
Curtain Gas (CUR)	12 (psig)
Temperature (TEM)	600 (^{o}C)
Nebuliser gas (GS1)	40 (pisg)
Turbo gas (GS2)	35 (psig)
Interface Heater (ihe)	ON
Collision Gas (CAD)	High Mode
IonSpray Voltage (IS)	4500 (kV)
Entrance Potential (EP)	10
MRM Scan Window	360 (sec)
Target Scan Time*	1.6 (sec)

*Target scan time should be set at somewhat value so that each analyte peak comprises 9-14 data points

Table S4. Summary of ANOVA statistics for MCYST comparisons between dilution rates.

	Compare each cell mean with the other cell mean in that row.				
	Number of families	1			
	Number of comparisons per family	4			
	Alpha	0.05			
	Sidak's multiple comparisons test	Mean Diff.	95% CI of diff.	Summary	Adjusted P Value
Total Q_{MCYST}	Control vs. Fe-limited				
	0.45	-44.61	-69.43 to -19.80	***	0.0005
	0.30	-44.02	-68.83 to -19.20	***	0.0006
	0.15	-22.04	-46.85 to 2.770	ns	0.093
	0.07	-21.94	-46.75 to 2.874	ns	0.0952
Fe-Replete $\mathrm{MCYST}_{\mathrm{int}}$	[D-Asp3]MCYST-LR vs. MCYST-LR				
	0.45	-11.97	-24.10 to 0.1513	ns	0.0537
	0.30	-16.24	-28.37 to -4.119	**	0.0069
	0.15	-22.99	-35.12 to -10.86	***	0.0003
	0.07	-27.7	-39.82 to -15.57	****	< 0.0001
Fe-Limited $\mathrm{MCYST}_{\mathrm{int}}$	[D-Asp3]MCYST-LR vs. MCYST-LR				
	0.45	-26.78	-43.88 to -9.684	**	0.0018
	0.30	-34.8	-51.90 to -17.70	***	0.0001
	0.15	-32.44	-49.54 to -15.34	***	0.0003
	0.07	-29.62	-46.72 to -12.52	***	0.0007
Fe-Limited $\mathrm{MCYST}_{\mathrm{ext}}$	[D-Asp3]MCYST-LR vs. MCYST-LR				
	0.45	-0.2533	-0.7143 to 0.2076	ns	0.4603
	0.30	-0.3133	-0.7743 to 0.1476	ns	0.2673
	0.15	-0.59	-1.051 to -0.1290	**	0.0098
	0.07	-0.9667	-1.428 to -0.5057	****	< 0.0001

Table S5. Differentially expressed proteins in *M. aeruginosa* under Fe-limitation at different dilution rates. Values highlighted in red represent down-regulation while those highlighted in green represent up-regulation of the protein relative to the 0.45 d^{-1} (control) condition.

Accession	**Protein ID**	**0.07 d^{-1}**	***P* val**	**Log2 fold**	**0.15 d^{-1}**	***P* val**	**Log2 fold**	**0.30 d^{-1}**	***P* val**	**Log2 fold**
Energy metabolism (Photosynthesis)										
MAE_10270	Allophycocyanin subunit alpha (*apcA*)	0.912	0.0377	-0.133						
MAE_10260	Allophycocyanin subunit beta (*apcB*)				0.215	0.0348	-2.219			
MAE_10240	Phycobilisome small core linker polypeptide (*apcC*)	0.209	0.0107	-2.259	0.146	0.0182	-2.771			
MAE_49370	Phycobilisome core-membrane linker polypeptide (*apcE*)	0.209	0.0001	-2.259	0.256	0.0001	-1.967	0.483	0.0001	-1.050
MAE_21640	Phycobilisome core component (*apcF*)				0.497	0.0266	-1.010			
MAE_24460	Phycocyanin alpha subunit PCA (*cpcA1*)	0.840	0.0430	-0.253						
MAE_48340	Phycobilisome rod-core linker polypeptide (*cpcG*)				0.302	0.0204	-1.727	2.249	0.0003	1.169
MAE_10220	Photosystem II protein D1 Precursor (*psbA1*)	0.107	0.0195	-3.229	0.194	0.0118	-2.365			
MAE_32990	Photosystem II core light harvesting protein (*psbB*)				0.078	0.0003	-3.681			
MAE_44250	Photosystem II manganese-stabilizing polypeptide (*psbO*)	0.030	0.0011	-5.076						
MAE_50080	Photosystem II extrinsic protein (*psbQ*)				4.055	0.0116	2.020			
MAE_36490	Photosystem II complex extrinsic protein U (*PsbU*)				3.802		1.927			
MAE_47560	Photosystem I P700 chlorophyll a apoprotein A1 (*psaA*)	0.145	0.0010	-2.790	0.132	0.0003	-2.923			
MAE_47570	Photosystem I P700 chlorophyll a apoprotein A2 (*psaB*)	0.082	0.0048	-3.601				0.328	0.0422	-1.608

MAE_23300	Photosystem I subunit II (*psaD*)	0.078	0.0001	-3.681	0.083	0.0001	-3.588			
MAE_47290	Photosystem I subunit III (*psaF*)	0.066	0.0050	-3.920	0.387	0.0475	-1.369			
MAE_43690	Photosystem I subunit XI (*psaL*)	6.138	0.0441	2.618						
MAE_09490	Photosystem I subunit XII (*psaM*)	0.209	0.0148	-2.259	0.047	0.0011	-4.398			
MAE_19230	Apocytochrome f (*petA*)				2.128	0.0270	1.090			
MAE_12570	Ferredoxin-NADP oxidoreductase (*petH*)	0.177	0.0033	-2.498	0.387	0.0058	-1.369			
MAE_50160	F0F1 ATP synthase subunit alpha (*atpA*)				0.189	0.0004	-2.405			
MAE_50150	F0F1 ATP synthase subunit delta (*atpD*)	0.347	0.0307	-1.528						
MAE_50130	F0F1 ATP synthase subunit B' (*atpG*)	0.120	0.0015	-3.056						
Energy metabolism (C-fixation and carbohydrate metabolism)										
MAE_47890	Ribulose bisphosphate carboxylase large chain (RubisCo large subunit) (*rbcL*)	0.069	0.0001	-3.867	0.108	0.0062	-3.242	0.506	0.0029	-0.983
MAE_47870	Ribulose bisphosphate carboxylase small subunit (RubisCo small subunit) (*rbcS*)	0.055	0.0002	-4.186				0.492	0.0284	-1.023
MAE_25030	NAD(P)-dependent glyceraldehyde-3-phosphate dehydrogenase	0.409	0.0134	-1.289	0.147	0.0001	-2.764	0.479	0.0089	-1.063
MAE_38450	Phosphoribulokinase (*prK*)				0.126	0.0092	-2.990			
MAE_47930	Carbon dioxide concentrating mechanism protein K (*ccmK1*)				4.488	0.0051	2.166			
MAE_47910	Carbon dioxide concentrating mechanism protein (*ccmM*)	0.215	0.0433	-2.219						
MAE_50050	PHA-specific acetoacetyl-CoA reductase (*phaB*)	5.346	0.0438	2.418	6.668	0.0146	2.737			
MAE_02620	Phosphoenolpyruvate synthase (*ppsA*)	2.535	0.0084	1.342	1.380	0.0241	0.465	1.294	0.0276	0.372
MAE_54130	4-alpha-glucanotransferase							0.347	0.0332	-1.528
MAE_20180	Glycogen phosphorylase (*glgP*)				0.187	0.0001	-2.418	0.575	0.0158	-0.797
MAE_35090	Enolase phosphopyruvate hydratase (*eno*)							1.923	0.0021	0.943
MAE_34890	Glyceraldehyde 3-phosphate dehydrogenase, type 1 (*gap1*)	0.308	0.0069	-1.701	0.075	0.0000	-3.747			

MAE_30020	Fructose-1,6-/sedoheptulose-1,7-bisphosphatase (*glpX*)	0.258	0.0003	-1.953						
MAE_32470	Fructose-1,6-bisphosphate aldolase (*fbaA)*	0.340	0.0266	-1.555	0.322	0.0036	-1.634			
MAE_52710	6-phosphofructokinase (*pfkA1*)	0.054	0.0370	-4.212						
MAE_14970	Transketolase with thiamine and pyrimidine binding domains	0.132	0.0001	-2.923	0.466	0.0016	-1.103			
MAE_61820	Transketolase with TktA domain	0.179	0.0146	-2.485	0.114	0.0010	-3.136	0.570	0.0377	-0.811
MAE_34870	D-xylulose 5-phosphate/D-fructose 6-phosphate phosphoketolase family protein	0.191	0.0203	-2.392						
MAE_43640	Glucose 6-phosphate dehydrogenase (*zwf*)				0.084	0.0068	-3.574			
MAE_14900	NADH-dependent glutamate synthase small subunit (*gltD*)				0.325	0.0390	-1.621			
MAE_09050	Glutamate--ammonia ligase (*glnN*)	0.096	0.0083	-3.375						
MAE_07560	NADH-dependent glutamate synthase large subunit (*gltB*)	0.116	0.0012	-3.109	0.1960	0.0042	-2.352			
Amino acid metabolism										
MAE_59440	Diaminopimelate epimerase (dapF)	0.847	0.0053	-0.239	0.705	0.0180	-0.505			
MAE_01980	Aldehyde dehydrogenase (*aldH*)				0.189	0.0473	-2.405			
MAE_50250	S-adenosyl-L-homocysteine hydrolase adenosylhomocysteinase	0.175	0.0000	-2.511	0.215	0.0000	-2.219			
MAE_45970	S-adenosylmethionine synthetase (*metK*)	0.097	0.0322	-3.362						
MAE_50420	Carbamoyl phosphate synthase large subunit (*carB*) pyrA?				0.461	0.0093	-1.116	0.766	0.0254	-0.385
MAE_35390	Aspartate aminotransferase (*aspC*)				5.702	0.0000	2.511	1.995	0.0463	0.997
MAE_15720	Acetylornithine aminotransferase (*argD*)				4.131	0.0023	2.046			
MAE_60310	Cysteine syntase (*cysK*)				6.310	0.0144	2.656			
MAE_62000	Leucyl aminopeptidase (*pepA*)				2.630	0.0055	1.395			
MAE_32670	Glycine cleavage system protein H (*gcvH*)				5.916	0.0499	2.565			

MAE_39110	Branched-chain amino acid aminotransferase (*ilvE*)				7.379	0.0026	2.883			
MAE_28670	Dihydroxy-acid dehydratase (*ilvD*)				5.346	0.0000	2.418	1.871	0.0440	0.904
Cellular processes										
MAE_46050	CP12 polypeptide fused with CBS domain							0.2560	0.0048	-1.967
MAE_62780	Putative peroxiredoxin	0.053	0.0450	-4.239						
MAE_36510	Peroxiredoxin	0.157	0.0009	-2.671						
MAE_48380	Universal stress protein UspA homolog	0.121	0.0452	-3.043						
MAE_02790	Thioredoxin (*trxA*)				3.133	0.0014	1.648			
MAE_22850	Delta-aminolevulinic acid dehydratase (*hemB*)				8.472	0.0152	3.083			
MAE_62840	DNA starvation/stationary phase protection protein Dps / DNA-binding ferritin-like protein				5.650	0.0038	2.498			
MAE_60930	Bacterioferritin comigratory protein				3.162	0.0001	1.661			
MAE_53990	Iron/manganese superoxide dismutase (*sodB*)				5.248	0.0016	2.392			
MAE_16920	Superoxide dismutase (*sodB*)				13.062	0.0197	3.707			
gi|159028112	Flavodoxin (*isiB*)	3.162	0.0006	1.661				2.421	0.0057	1.276
Transport and binding proteins										
MAE_39210	Chloroplastic outer envelope membrane protein homolog	3.531	0.0442	1.820	7.586	0.0013	2.923	4.246	0.0097	2.086
MAE_14800	Nitrate/nitrite transport protein (*nrtA*)	3.373	0.0002	1.754	7.586	0.0000	2.923	2.377	0.0121	1.249
MAE_06220	ABC-type urea transport system substrate-binding protein				15.704	0.0000	3.973			
MAE_56680	Iron transport system substrate-binding protein	5.754	0.0000	2.525	8.551	0.0000	3.096	1.754	0.9975	0.811
MAE_47420	Extracellular solute-binding protein				2.911	0.0081	1.541			
Genetic information processing - Transcription and translation proteins										

MAE_46070	10 kDa chaperonin, co-chaperonin GroES (*groS*)				1.787	0.0431	0.837			
gi|159027173	Metallothionein (*smtA*)				15.996	0.0014	4.000			
MAE_02510	RNA-binding protein	8.954	0.0262	3.163	17.378	0.0028	4.119			
MAE_45870	RNA-binding region protein (*rbpF*/A2)	14.859	0.0272	3.893	19.953	0.0190	4.319	9.550	0.0442	3.256
MAE_30540	Ribosome recycling factor (*frr*)				2.291	0.0256	1.196			
MAE_03930	Aspartyl/glutamyl-tRNA amidotransferase subunit B (*gatB*)				0.123	0.0146	-3.030			
MAE_62700	Trigger factor (*tig*)				0.227	0.0381	-2.139			
MAE_61840	ClpB protein				0.738	0.0368	-0.439	0.718	0.0230	-0.478
MAE_57190	ATP-dependent Clp protease-like protein				0.139	0.0041	-2.844			
MAE_46080	60 kDa chaperonin GroEL1 (*groEL1*)	0.146	0.0313	-2.777	0.425	0.0373	-1.236			
MAE_03410	60 kDa chaperonin GroEL2 (*groEL2*)	0.229	0.0063	-2.126						
MAE_62320	Bifunctional phosphoribosyl aminoimidazole carboxy formyl formyltransferase / inosinemonophosphate cyclohydrolase (*purH*)				0.297	0.0437	-1.754			
MAE_13690	Transcriptional regulator (AbrB family)	0.223	0.0196	-2.166						
MAE_54500	DNA-directed RNA polymerase beta subunit (*rpoB*)				0.143	0.0352	-2.804			
MAE_11110	DNA-directed RNA polymerase subunit gamma (*rpoC1*)				0.116	0.0358	-3.109			
MAE_42760	Elongation factor (*tuf*)	0.227	0.0187	-2.139	0.061	0.0000	-4.034	0.515	0.0248	-0.957
MAE_43910	30S ribosomal protein S1	0.311	0.0146	-1.688	0.194	0.0023	-2.365			
MAE_57370	30S ribosomal protein S3 (*rpsC*)				0.077		-3.694			
MAE_32430	30S ribosomal protein S4 (*rpsD*)				0.286	0.0031	-1.807			
MAE_57270	30S ribosomal protein S5 (*rpsE*)	0.281	0.0073	-1.834	0.095	0.0009	-3.402			
MAE_11310	30S ribosomal protein S6	0.313	0.0078	-1.674	0.182	0.0030	-2.458			
MAE_57300	30S ribosomal protein S8 (*rpsH*)				0.207	0.0025	-2.272			

MAE_52500	30S ribosomal protein S9 (*rpsI*)				0.087	0.0024	-3.521			
MAE_06280	30S ribosomal protein S15	0.041	0.0000	-4.611						
MAE_57595	30S ribosomal protein S16				0.236	0.0126	-2.086			
MAE_48050	30S ribosomal protein S18	0.219	0.3709	-2.193	0.069	0.0042	-3.853	0.718	0.3355	-0.478
MAE_43885	50S ribosomal protein L7/L12							0.328	0.0306	-1.608
MAE_36630	50S ribolsomal protein L1 (*rplA*)	0.080	0.0021	-3.641						
MAE_57430	50S ribosomal protein L3				0.060	0.0032	-4.066			
MAE_57420	50S ribosomal protein L4				0.203	0.0224	-2.299			
MAE_43870	50S ribosomal protein L10	0.063	0.0015	-4.000	0.550	0.0500	-0.864	0.291	0.0324	-1.781
MAE_36590	50S ribosomal protein L19	0.302	0.0285	-1.727	0.075	0.0013	-3.734	0.655	0.0455	-0.611
MAE_52530	50S ribosomal protein L17 (*rplQ*)	0.136	0.0049	-2.883						
MAE_57330	50S ribosomal protein L14	0.261	0.0127	-1.940	0.175	0.0361	-2.511			
MAE_57260	50S ribosomal protein L15 (*rplO*)	0.071	0.0009	-3.827	0.261	0.0036	-1.940			
MAE_57320	50S ribosomal protein L24				0.067	0.0323	-3.893			
Other categories										
MAE_04080	Heat shock protein (*grpE*)				2.249	0.0147	1.169			
MAE_21600	Putative thylakoid-associated protein	3.565	0.0085	1.834	2.965	0.0098	1.568	4.920	0.0005	2.299
MAE_62060	Cell division protein FtsH (*ftsH3*)	7.244	0.0308	2.857						
MAE_42350	Subtilisin-like protein peptidase S8 and S53	2.938	0.0161	1.555						
MAE_50430	Putative modulator of DNA gyrase peptidase U62	7.047	0.0128	2.817						
MAE_37620	Gas vesicle structural protein (*gvpC*)				1.803	0.0001	0.850	1.393	0.0019	0.478
MAE_61940	Plasma membrane protein with phage shock protein PspA domain				3.105	0.0080	1.634	1.977	0.2859	0.983
MAE_38380	Tic22-like protein	0.097	0.0153	-3.362	2.399	0.0018	1.262	0.745	0.4004	-0.425
MAE_54380	FKBP-type peptidyl-prolyl cis-trans isomerase (*ytfC*)				1.660	0.0315	0.731			
MAE_18910	Orange carotenoid-binding protein /water-soluble carotenoid protein	0.520	0.0173	-0.943	0.2109	0.0001	-2.246	0.497	0.0071	-1.010

MAE_27460	Cyanophycin synthetase (*cphA*)				0.236	0.0020	-2.086			
MAE_31270	S-layer region-like precursor protein	0.395	0.0198	-1.342	0.120	0.0031	-3.056			
gi|169788458	Actin				0.076	0.0330	-3.721			
Hypothetical proteins										
gi|159027829	Hypothetical protein	0.089	0.0032	-3.495	0.402	0.0032	-1.316	0.560	0.0045	-0.837
gi|159027827	Hypothetical protein				2.188	0.0022	1.130	1.820	0.0183	0.864
gi|159030339	Hypothetical protein	0.053	0.0000	-4.239						
gi|159029460	Hypothetical protein	11.803	0.0282	3.561						
gi|159030907	Hypothetical protein				4.966	0.0081	2.312			
gi|159029624	Hypothetical protein	2.780	0.0265	1.475						
MAE_37770	Hypothetical protein	0.117	0.0028	-3.096						
MAE_06000	Hypothetical protein				10.093	0.0000	3.335			
MAE_47530	Hypothetical protein	18.880	0.0002	4.234				15.417	0.0004	3.947
MAE_11600	Hypothetical protein	0.068	0.0010	-3.880	0.425	0.011	-1.236	0.692	0.0254	-0.532
MAE_11610	Hypothetical protein	0.168	0.0441	-2.578	0.215	0.0035	-2.219			
MAE_61990	Hypothetical protein				7.798	0.0015	2.963			
MAE_15680	Hypothetical protein	0.247	0.0024	-2.020						
MAE_46700	Hypothetical protein				6.792	0.0023	2.764			
MAE_07350	Hypothetical protein	4.875	0.0202	2.286	5.012	0.0037	2.325			
MAE_11840	Hypothetical protein				0.281	0.0412	-1.834			
MAE_07360	Hypothetical protein	7.871	0.0093	2.976	5.808	0.0293	2.538			
MAE_36690	Hypothetical protein				4.699	0.0250	2.232			
MAE_02150	Hypothetical protein	5.861	0.0408	2.551	4.613	0.0444	2.206			
MAE_44430	Hypothetical protein	5.395	0.0255	2.432						
MAE_41180	Hypothetical protein				9.818	0.0204	3.295	5.346	0.1626	2.418
MAE_35080	Hypothetical protein	0.686	0.0428	-0.545	16.904	0.0084	4.079	3.631	0.0367	1.860
MAE_19620	Hypothetical protein	5.395	0.0425	2.432						

Table S6. Differentially expressed proteins in *M. aeruginosa* under Fe-repletion at different dilution rates. Values highlighted in red represent down-regulation while those highlighted in green represent up-regulation of the protein relative to the 0.45 d^{-1} (control) condition.

Accession	**Protein ID**	**0.07 d^{-1}**	***P* val**	**Log2 fold**	**0.15 d^{-1}**	***P* val**	**Log2 fold**	**0.30 d^{-1}**	***P* val**	**Log2 fold**
Genetic information processing -Transcription and translation proteins										
MAE_42760	Elongation factor Tu (*tuf*)							0.273	0.0419	-1.874
MAE_54740	AbrB family transcriptional regulator	0.263	0.0415	-1.927						
MAE_49450	Molecular chaperone (*dnaK*)	9.638	0.0045	3.269				10.186	0.0182	3.349
gi|488826847	DNA-binding protein	0.334	0.0223	-1.581	0.227	0.0182	-2.139			
MAE_44930	30S ribosomal protein S2				0.809	0.0306	-0.306			
Transport and binding proteins										
gi|488836772	Iron uptake protein A1	2.858	0.0297	1.515						
Energy metabolism										
MAE_07560	NADH-dependent glutamate synthase large subunit (*gltB*)	0.299	0.0246	-1.741						
MAE_10260	Allophycocyanin subunit beta (*apcB*)				0.453	0.0096	-1.143			
MAE_50150	ATP synthase (*atpD*)				0.114	0.0044	-3.136			
gi|488830534	Putative thylakoid-associated protein	0.196	0.0038	-2.352						
Other categories										
MAE_37620	Gas vesicle structural protein, GvpC	3.436	0.0049	1.781						
Hypothetical proteins										
gi|159030339	Hypothetical protein				0.092	0.0023	-3.442			
gi|159030973	Hypothetical protein	0.242	0.0030	-2.0463	0.084	0.0118	-3.574	0.461	0.0410	-1.116