

## SUPPORTING INFORMATION

# Mobilization of Iron Stored in Bacterioferritin is Required for Metabolic Homeostasis in *Pseudomonas aeruginosa*

Achala N. D. Punchi Hewage <sup>1</sup>, Leo Fontenot <sup>2</sup>, Jessie Guidry <sup>3</sup>, Thomas Weldeghiorghis <sup>2</sup>, Anil K. Mehta <sup>4</sup>, Fabrizio Donnarumma <sup>2</sup>, and Mario Rivera <sup>2,\*</sup>

<sup>1</sup> Department of Chemistry, University of Kansas, 2030 Becker Dr., Lawrence, KS, 66047, USA; achala@ku.edu

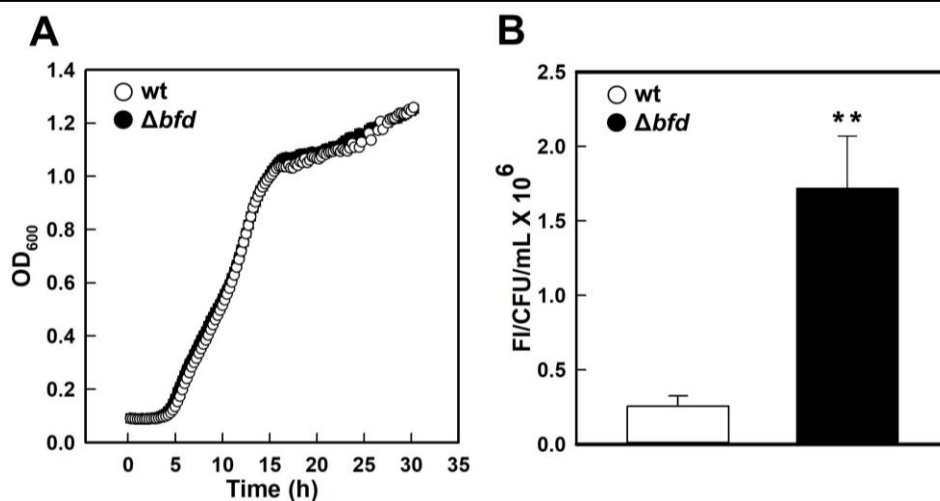
<sup>2</sup> Department of Chemistry, Louisiana State University, 232 Choppin Hall, Baton Rouge, LA, 70803, USA; lfont39@lsu.edu (L.F); thomaskw@lsu.edu (T.W); fabrizio@lsu.edu (F.D)

<sup>3</sup> Department of Biochemistry and Molecular Biology, Louisiana State University Health Science Center, 1901 Perdido Street, New Orleans, LA, 70112, USA; jjguid@lsuhsc.edu

<sup>4</sup> National High Magnetic Field Laboratory, University of Florida, 1149 Newell Drive, Gainesville, FL, 32610, USA; anil.mehta@ufl.edu.

\*Corresponding author. E-mail: [mrivera@lsu.edu](mailto:mrivera@lsu.edu)

ORCID: 0000-0002-5692-5497



**Figure S1.** Growth curves and levels of pyoverdine secreted by wt and  $\Delta bfd$  *P. aeruginosa* cells. **(A)** *P. aeruginosa* cells (wt and  $\Delta bfd$ ) were cultured in PI media supplemented with 10  $\mu$ M Fe at 37 °C and shaking at 220 rpm. For the purpose of all the analyses reported in this work, the cells were harvested by centrifugation 30 h post inoculation. **(B)** Pyoverdine secreted by the cells was measured in the cell-free supernatants by acquiring fluorescence emission spectra (430-550 nm) with excitation at 400 nm (10 nm slit width) and emission at 460 nm (10 nm slit width). Fluorescence intensity normalized to viable cell count (CFU/mL) shows that the  $\Delta bfd$  cells secrete approximately sixfold more pyoverdine than the wt cells.  $p < 0.01$  denoted by \*\* relative to wt.

**Table S1:** Proteins exhibiting significant abundance differences between wt and  $\Delta bfd$  cells.

| Protein ID              | Name | Function                                                 | Metal binding | FC = $\Delta bfd/wt$ | p value |
|-------------------------|------|----------------------------------------------------------|---------------|----------------------|---------|
|                         |      |                                                          |               | $log_2FC$            |         |
| Pyoverdine biosynthesis |      |                                                          |               |                      |         |
| PA2385                  | PvdQ | Acyl-homoserine lactone acylase                          |               | 3.14                 | 3.9E-10 |
| PA2386                  | PvdA | L-ornithine N(5)-monooxygenase                           |               | 3.02                 | 1.2E-15 |
| PA2388                  | FpvR |                                                          |               | -2.18                | 1.7E-03 |
| PA2389                  | PvdR |                                                          |               | 2.81                 | 2.8E-06 |
| PA2390                  | PvdT | Macrolide export ATP-binding/permease protein            |               | 2.73                 | 2.0E-10 |
| PA2391                  | OpmQ | Probable outer membrane protein                          |               | 2.00                 | 1.5E-04 |
| PA2392                  | PvdP |                                                          |               | 4.11                 | 5.2E-10 |
| PA2393                  | PvdM | Probable dipeptidase                                     |               | 3.22                 | 1.3E-13 |
| PA2394                  | PvdN |                                                          |               | 3.61                 | 2.3E-11 |
| PA2395                  | PvdO |                                                          |               | 3.48                 | 7.9E-16 |
| PA2396                  | PvdF | Pyoverdine synthetase F                                  |               | 3.25                 | 1.1E-10 |
| PA2397                  | PvdE | Pyoverdine biosynthesis protein                          |               | 3.16                 | 1.6E-12 |
| PA2398                  | FpvA | Ferripyoverdine receptor                                 |               | 1.72                 | 3.3E-07 |
| PA2399                  | PvdD | Pyoverdine synthetase D                                  |               | 2.75                 | 1.8E-13 |
| PA2400                  | PvdJ | Probable non-ribosomal peptide synthetase                |               | 2.87                 | 1.4E-12 |
| PA2402                  | PvdI | Pyoverdine peptide synthetase                            |               | 2.87                 | 4.6E-18 |
| PA2403                  | FpvG | Uncharacterized protein                                  |               | 2.90                 | 6.8E-12 |
| PA2404                  | FpvH | Uncharacterized protein                                  |               | 2.52                 | 1.8E-04 |
| PA2405                  | FpvJ | Probable adhesion protein                                |               | 2.94                 | 1.6E-11 |
| PA2407                  | FpvC | Probable ATP-binding component of ABC transporter        |               | 2.97                 | 1.6E-09 |
| PA2408                  | FpvD | Uncharacterized protein                                  |               | 1.20                 | 1.1E-03 |
| PA2410                  | FpvF | Probable thioesterase                                    |               | 2.44                 | 1.9E-09 |
| PA2411                  |      | MbtH domain-containing protein                           |               | 2.73                 | 6.3E-10 |
| PA2412                  |      | L-2,4-diaminobutyrate:2-ketoglutarate 4-aminotransferase |               | 1.20                 | 4.5E-03 |
| PA2413                  | PvdH | L-sorbose dehydrogenase                                  |               | 3.10                 | 6.2E-19 |
| PA2424                  | PvdL |                                                          |               | 2.76                 | 6.2E-20 |
| PA2425                  | PvdG |                                                          |               | 1.75                 | 6.3E-05 |
| PA2426                  | PvdS | Sigma factor                                             |               | 0.91                 | 4.8E-03 |
| PA4168                  | FpvB | Second ferric pyoverdine receptor FpvB                   |               | 0.67                 | 2.9E-01 |
| Pyochelin biosynthesis  |      |                                                          |               |                      |         |
| PA4218                  | FptX | Probable transporter                                     |               | 3.14                 | 2.1E-08 |
| PA4219                  | YfpB | Uncharacterized protein                                  |               | 2.83                 | 9.1E-11 |
| PA4221                  | FptA | Fe(3+)-pyochelin receptor (Fe(III)-pyochelin receptor)   |               | 2.50                 | 2.9E-10 |
| PA4222                  | PchI | Probable ATP-binding component of ABC transporter        |               | 3.36                 | 8.1E-19 |
| PA4223                  | PchH | Probable ATP-binding component of ABC transporter        |               | 3.32                 | 1.8E-11 |
| PA4224                  | PchG | Pyochelin biosynthetic protein                           |               | 2.74                 | 3.2E-21 |
| PA4225                  | PchF | Pyochelin synthetase                                     |               | 2.38                 | 9.0E-23 |
| PA4226                  | PchE | Dihydroaeruginosic acid synthetase                       |               | 2.79                 | 9.9E-17 |
| PA4227                  | PchR | Regulatory protein                                       |               | 1.19                 | 4.1E-06 |

|                                                       |       |                                                              |    |       |         |
|-------------------------------------------------------|-------|--------------------------------------------------------------|----|-------|---------|
| PA4228                                                | PchD  | Pyochelin biosynthesis protein                               |    | 2.84  | 3.4E-17 |
| PA4229                                                | PchC  | Pyochelin biosynthetic protein                               |    | 1.14  | 1.0E-07 |
| PA4230                                                | PchB  | Isochorismate pyruvate lyase                                 |    | 3.10  | 6.1E-18 |
| PA4231                                                | PchA  | Salicylate biosynthesis isochorismate synthase               |    | 1.93  | 1.2E-05 |
| Heme iron acquisition                                 |       |                                                              |    |       |         |
| PA0672                                                | HemO  | Heme oxygenase                                               |    | 1.49  | 6.9E-13 |
| PA4708                                                | PhuT  | Heme-transport protein                                       |    | 1.42  | 2.3E-04 |
| PA4709                                                | PhuS  |                                                              |    | 1.23  | 3.6E-04 |
| PA4710                                                | PhuR  | Heme/Hemoglobin uptake outer membrane receptor               |    | 2.59  | 1.5E-14 |
| Other iron acquisition and transport related proteins |       |                                                              |    |       |         |
| PA0471                                                | FiuR  | Probable transmembrane sensor                                | Fe | 0.66  | 5.0E-02 |
| PA2466                                                | FoxA  | Ferrioxamine receptor FoxA                                   |    | 0.56  | 7.5E-04 |
| PA3901                                                | FecA  | Fe(III) dicitrate transport protein FecA                     |    | 0.81  | 1.2E-01 |
| PA4514                                                | PiuA  | Probable outer membrane receptor for iron transport          |    | 1.02  | 1.6E-04 |
| PA4675                                                | OptH  | Probable TonB-dependent receptor                             |    | 0.53  | 4.8E-01 |
| Quorum sensing                                        |       |                                                              |    |       |         |
| PA0996                                                | PqsA  | Anthranilate--CoA ligase                                     |    | 1.71  | 1.4E-03 |
| PA0997                                                | PqsB  | Hypothetical protein                                         |    | 2.06  | 1.6E-06 |
| PA0998                                                | PqsC  | Hypothetical protein                                         |    | 2.28  | 1.1E-04 |
| PA0999                                                | PqsD  | 3-oxoacyl-ACP synthase                                       |    | 2.39  | 7.2E-11 |
| PA1000                                                | PqsE  | Thioesterase PqsE                                            |    | 2.08  | 9.6E-03 |
| PA1871                                                | LasA  | Protease LasA (Staphylolytic protease)                       |    | 0.55  | 8.2E-02 |
| PA2569                                                |       | Uncharacterized protein                                      |    | 0.78  | 4.3E-02 |
| PA2570                                                | LecA  | PA-I galactophilic lectin (PA-IL) (Galactose-binding lectin) |    | 1.53  | 1.3E-02 |
| PA3476                                                | RhII  | Acyl-homoserine-lactone synthase                             |    | -0.54 | 9.5E-02 |
| PA3478                                                | RhIB  | Rhamnosyltransferase chain B                                 |    | 0.71  | 1.8E-12 |
| PA3479                                                | RhIA  | 3-(3-hydroxydecanoyloxy)decanoate synthase                   |    | 0.70  | 2.3E-08 |
| PA3724                                                | LasB  | Elastase (Neutral metalloproteinase) (PAE) (Pseudolysin)     |    | -0.80 | 1.1E-01 |
| Phenazine biosynthesis                                |       |                                                              |    |       |         |
| PA1899                                                | PhzA2 | Phenazine biosynthesis protein PhzA                          |    | 1.94  | 1.2E-03 |
| PA1900                                                | PhzB2 | Phenazine biosynthesis protein PhzB                          |    | 0.99  | 7.2E-03 |
| PA1904                                                | PhzF2 | Probable phenazine biosynthesis protein                      |    | 0.61  | 2.2E-01 |
| PA1905                                                | PhzG2 | Pyridoxamine 5'-phosphate oxidase                            |    | 1.22  | 2.1E-03 |
| PA4213                                                | PhzD1 | Phenazine biosynthesis protein PhzD                          |    | 1.47  | 1.2E-10 |
| PA4214                                                | PhzE1 | Phenazine biosynthesis protein PhzE                          |    | 0.95  | 1.3E-10 |
| Carbon metabolism and amino acid metabolism           |       |                                                              |    |       |         |
| PA0400                                                | MetB  | Probable cystathionine gamma-lyase                           | Fe | 0.57  | 7.2E-07 |
| PA0792                                                | PrpD  | Propionate catabolic protein                                 |    | 0.95  | 1.1E-13 |
| PA0794                                                |       | Probable aconitate hydratase                                 |    | -0.65 | 3.9E-08 |
| PA0865                                                | Hpd   | 4-hydroxyphenylpyruvate dioxygenase (4HPPD)                  |    | 0.56  | 2.4E-03 |

|        |       |                                                                     |        |       |         |
|--------|-------|---------------------------------------------------------------------|--------|-------|---------|
| PA1254 | LhpC  | Probable dihydrodipicolinate synthetase                             |        | -0.74 | 4.6E-04 |
| PA1255 | LhpK  | Probable trans-3-hydroxy-L-proline dehydratase (T3LHyp dehydratase) |        | -0.90 | 2.6E-02 |
| PA1260 | LhpP  | Amino acid ABC transporter periplasmic binding protein              |        | -0.52 | 6.9E-02 |
| PA1261 | LhpR  | Probable transcriptional regulator                                  |        | 0.68  | 3.9E-01 |
| PA1311 | PhnX  | Phosphonoacetaldehyde hydrolase (Phosphonatase)                     |        | -0.54 | 4.6E-01 |
| PA1422 | GbuR  | GbuR                                                                |        | 0.87  | 1.2E-01 |
| PA1562 | AcnA  | Aconitate hydratase 1                                               | Fe     | -0.98 | 6.2E-15 |
| PA2015 | LiuA  | Putative isovaleryl-CoA dehydrogenase                               |        | -0.78 | 2.1E-02 |
| PA2152 |       | Probable trehalose synthase                                         |        | 0.54  | 2.0E-01 |
| PA2300 | ChiC  | Chitinase                                                           |        | 0.76  | 1.6E-05 |
| PA2416 | TreA  | Periplasmic trehalase                                               |        | 0.81  | 4.2E-02 |
| PA3120 | LeuD  | 3-isopropylmalate dehydratase small subunit                         |        | -0.76 | 3.3E-03 |
| PA3121 | LeuC  | 3-isopropylmalate dehydratase large subunit                         | Fe     | -0.83 | 2.1E-07 |
| PA3236 | BetX  | Probable glycine betaine-binding protein                            |        | -0.68 | 5.0E-03 |
| PA3374 | PhnM  | Amidohydro_3 domain-containing protein                              |        | -0.94 | 9.0E-05 |
| PA3375 | PhnL  | Probable ATP-binding component of ABC transporter                   |        | -0.56 | 1.2E-01 |
| PA3376 | PhnK  | Probable ATP-binding component of ABC transporter                   |        | -0.60 | 4.2E-03 |
| PA3377 | PhnJ  | Alpha-D-ribose 1-methylphosphonate 5-phosphate C-P lyase            |        | -0.76 | 6.4E-02 |
| PA3378 | PhnI  | Uncharacterized protein                                             |        | -0.97 | 4.9E-03 |
| PA3379 | PhnH  | Uncharacterized protein                                             |        | -0.80 | 6.3E-04 |
| PA3380 | PhnG  | Uncharacterized protein                                             |        | -1.09 | 4.6E-03 |
| PA3417 | PdhA  | Pyruvate dehydrogenase E1 component subunit alpha                   |        | -0.54 | 9.5E-02 |
| PA3430 |       | Putative aldolase class 2 protein PA3430                            |        | -0.86 | 3.5E-02 |
| PA3459 |       | Probable glutamine amidotransferase                                 |        | -0.66 | 2.7E-06 |
| PA3506 |       | Probable decarboxylase                                              | Mn     | -0.62 | 3.3E-01 |
| PA3524 | GloA1 | Lactoylglutathione lyase                                            | Zn, Ni | -0.67 | 1.2E-02 |
| PA3896 |       | Probable 2-hydroxyacid dehydrogenase                                |        | 0.49  | 3.5E-01 |
| PA4150 | AcoA  | Probable dehydrogenase E1 component                                 |        | -0.53 | 4.0E-01 |
| PA4151 | AcoB  | Acetoin catabolism protein                                          |        | -0.72 | 2.5E-04 |
| PA4152 | AcoC  | Probable hydrolase                                                  |        | -0.67 | 5.0E-02 |
| PA4333 | FumA  | Probable fumarase                                                   | Fe     | -2.08 | 8.5E-13 |
| PA4470 | FumC1 | Fumarate hydratase                                                  | Mn     | 3.11  | 8.0E-16 |
| PA4628 | LysP  | Lysine-specific permease                                            |        | 0.65  | 2.1E-01 |
| PA5354 | GlcE  | Glycolate oxidase subunit GlcE                                      |        | -0.61 | 2.2E-01 |
| PA5376 | CbcV  |                                                                     |        | -0.53 | 4.7E-01 |
| PA5398 | DgcA  | Dimethylglycine catabolism                                          |        | -1.40 | 9.0E-05 |
| PA5410 | GbcA  | Glycine betaine catabolism protein                                  | Fe     | -1.41 | 1.3E-07 |
| PA5415 | GlyA1 | Serine hydroxymethyltransferase                                     |        | -0.79 | 2.3E-06 |
| PA5416 | SoxB  | Sarcosine oxidase beta subunit                                      |        | -0.69 | 2.7E-01 |
| PA5417 | SoxD  | Sarcosine oxidase delta subunit                                     |        | -0.66 | 2.0E-02 |
| PA5418 | SoxA  | Sarcosine oxidase alpha subunit                                     | Fe     | -0.60 | 5.7E-03 |
| PA5421 | FdhA  | Glutathione-independent formaldehyde dehydrogenase (FALDH) (FDH)    | Zn     | -0.61 | 7.3E-09 |
| PA5445 | PsecA | Probable coenzyme A transferase                                     |        | -0.62 | 3.2E-01 |

| Sulfur assimilation         |       |                                                         |    |       |         |
|-----------------------------|-------|---------------------------------------------------------|----|-------|---------|
| PA0280                      | CysA  | Sulfate transport protein                               |    | 1.17  | 1.2E-06 |
| PA0282                      | CysT  | Sulfate transport protein                               |    | 1.28  | 5.5E-06 |
| PA0283                      | Sbp   | Sulfate-binding protein precursor                       |    | 2.05  | 2.8E-19 |
| PA0500                      | BioB  | Biotin synthase                                         | Fe | 0.79  | 3.4E-02 |
| PA0916                      | YliG  | Ribosomal protein S12 methylthiotransferase             | Fe | -0.85 | 8.9E-02 |
| PA1192                      | YdaO  | tRNA-cytidine(32) 2-sulfurtransferase                   | Fe | -0.78 | 1.8E-01 |
| PA1505                      | MoaA2 | Molybdenum cofactor biosynthesis protein A 2            | Fe | -0.61 | 3.7E-01 |
| PA1838                      | CysI  | Sulfite reductase                                       | Fe | 0.68  | 2.0E-14 |
| PA2062                      |       | Probable pyridoxal-phosphate dependent enzyme           | Fe | 3.05  | 3.9E-05 |
| PA2566                      |       | Conserved hypothetical protein                          |    | -0.75 | 1.7E-01 |
| PA2594                      |       | Conserved hypothetical protein                          |    | 1.54  | 4.0E-05 |
| PA3445                      |       | Conserved hypothetical protein                          |    | 2.87  | 9.1E-06 |
| PA3938                      | TauA  | Probable periplasmic taurine-binding protein            |    | 2.47  | 4.1E-04 |
| PA3980                      | MiaB  | tRNA-2-methylthio-N(6)-dimethylallyladenine synthase    | Fe | -1.74 | 5.8E-06 |
| PA3996                      | LipA  | Lipoate synthase (Sulfur insertion protein LipA)        | Fe | -0.63 | 1.7E-01 |
| PA4442                      | CysN  | ATP sulfurylase GTP-binding subunit/APS kinase          |    | 0.83  | 5.3E-10 |
| PA4443                      | CysD  | ATP sulfurylase small subunit                           |    | 1.03  | 3.9E-03 |
| PA4973                      | ThiC  | Phosphomethylpyrimidine synthase                        | Fe | -0.56 | 4.0E-02 |
| PA5025                      | MetY  | Homocysteine synthase                                   |    | 0.86  | 9.1E-03 |
| Respiration                 |       |                                                         |    |       |         |
| PA0527                      | Dnr   | Transcriptional regulator                               |    | -0.94 | 1.5E-02 |
| PA1173                      | NapB  | Periplasmic nitrate reductase                           | Fe | -0.99 | 7.1E-03 |
| PA1174                      | NapA  | Periplasmic nitrate reductase                           | Fe | -1.31 | 1.2E-12 |
| PA1175                      | NapD  | NapA signal peptide-binding chaperone                   |    | -0.72 | 1.4E-02 |
| PA1176                      | NapF  | Ferredoxin-type protein                                 | Fe | -0.88 | 2.0E-02 |
| PA1544                      | Anr   | Transcriptional activator protein                       | Fe | 0.69  | 3.4E-05 |
| PA2266                      |       | Probable cytochrome c                                   | Fe | -0.56 | 4.6E-01 |
| PA3331                      |       | Cytochrome P450                                         | Fe | -0.67 | 7.6E-04 |
| PA3872                      | NarI  | Respiratory nitrate reductase gamma chain               | Fe | -0.58 | 3.6E-02 |
| PA4133                      | CcoN  | Cytochrome c oxidase subunit (Cbb3-type)                | Fe | -1.11 | 1.2E-02 |
| Anr regulon                 |       |                                                         |    |       |         |
| PA1546                      | HemN  | Oxygen-independent coproporphyrinogen III oxidase (CPO) | Fe | -1.63 | 2.6E-06 |
| PA1673                      |       | Bacteriohemerythrin                                     | Fe | -0.95 | 5.3E-06 |
| PA3049                      | Rmf   | Ribosome modulation factor                              |    | 0.74  | 3.8E-03 |
| PA3126                      | IbpA  | Heat-shock protein IbpA                                 |    | -0.60 | 2.5E-04 |
| PA3572                      |       | Hypothetical protein                                    |    | -0.52 | 2.5E-03 |
| PA3919                      | YlaK  | PINc domain-containing protein                          |    | -0.77 | 5.5E-02 |
| PA4587                      | CcpR  | Cytochrome c551 peroxidase                              | Fe | -0.52 | 1.3E-04 |
| PA4880                      |       | Probable bacterioferritin                               | Fe | -2.95 | 8.1E-16 |
| PA5475                      |       | Acetyltransferase                                       |    | -0.61 | 4.1E-02 |
| Oxidative stress regulation |       |                                                         |    |       |         |

|                                                |       |                                                          |    |       |         |
|------------------------------------------------|-------|----------------------------------------------------------|----|-------|---------|
| PA0140                                         | AhpF  | Alkyl hydroperoxide reductase subunit F                  |    | -0.60 | 2.1E-06 |
| PA0849                                         | TrxB2 | Thioredoxin reductase                                    |    | -0.77 | 4.2E-04 |
| PA2185                                         | KatN  | Non-heme catalase KatN                                   | Mn | -0.91 | 1.2E-01 |
| PA2580                                         | MdaB  | Flavodoxin_2 domain-containing protein                   |    | -0.55 | 1.0E-02 |
| PA3450                                         | LsfA  | Probable antioxidant protein                             |    | 2.49  | 1.2E-21 |
| PA3533                                         | GrxD  | Glutaredoxin                                             |    | -0.81 | 3.6E-08 |
| PA4236                                         | KatA  | Catalase                                                 | Fe | -1.08 | 1.4E-08 |
| PA4366                                         | SodB  | Superoxide dismutase [Fe]                                | Fe | -0.96 | 7.1E-03 |
| PA4468                                         | SodA  | Superoxide dismutase [Mn]                                | Mn | 2.81  | 2.6E-14 |
| <b>Nucleotide synthesis and metabolism</b>     |       |                                                          |    |       |         |
| PA0441                                         | Dht   | D-hydantoinase/dihydropyrimidinase (DHPase)              | Zn | -0.71 | 2.2E-02 |
| PA1155                                         | NrdB  | Ribonucleoside-diphosphate reductase subunit beta        | Fe | -0.61 | 2.0E-02 |
| PA1156                                         | NrdA  | Ribonucleoside-diphosphate reductase                     |    | -0.62 | 1.9E-06 |
| PA1932                                         |       | Probable hydroxylase molybdopterin-containing subunit    |    | -0.89 | 9.0E-02 |
| <b>Lipid metabolism</b>                        |       |                                                          |    |       |         |
| PA0347                                         | GlpQ  | Glycerophosphoryl diester phosphodiesterase, periplasmic |    | -1.06 | 2.6E-11 |
| PA2862                                         | LipA  | Triacylglycerol lipase                                   |    | -0.52 | 2.1E-01 |
| PA3092                                         | FadH1 | 2,4-dienoyl-CoA reductase FadH1                          |    | -1.11 | 2.0E-04 |
| PA3319                                         | PlcN  | Non-hemolytic phospholipase C (PLC-N)                    |    | -0.84 | 3.6E-14 |
| PA3333                                         | FabH  | 3-oxoacyl-[acyl-carrier-protein] synthase 3              |    | -0.85 | 4.6E-06 |
| PA4350                                         | OlsB  | Uncharacterized protein                                  |    | -0.55 | 5.0E-02 |
| PA4353                                         | YajB  | Uncharacterized protein                                  |    | -0.56 | 6.0E-03 |
| PA4661                                         | PagL  | Lipid A deacylase PagL                                   |    | 0.51  | 6.1E-02 |
| <b>Secreted proteins and secretion systems</b> |       |                                                          |    |       |         |
| PA0572                                         | ImpA  | Immunomodulating metalloprotease                         | Zn | 0.71  | 1.1E-02 |
| PA0688                                         | PhoA  | Alkaline phosphatase L (L-AP)                            |    | -0.74 | 5.8E-09 |
| PA1245                                         | AprX  | Uncharacterized protein                                  |    | 3.02  | 3.9E-10 |
| PA1246                                         | AprD  | Alkaline protease secretion ATP-binding protein AprD     |    | 2.25  | 2.2E-09 |
| PA1247                                         | AprE  | Alkaline protease secretion protein AprE                 |    | 2.11  | 3.1E-03 |
| PA1249                                         | AprA  | Serralysin (Alkaline metalloproteinase) (AP)             | Zn | 1.82  | 1.4E-10 |
| PA1250                                         | AprI  | Proteinase inhibitor (Aprin)                             | Zn | 0.96  | 1.0E-03 |
| PA3099                                         | XcpV  | Type II secretion system protein I                       |    | 0.79  | 1.4E-01 |
| <b>Oxidation-reduction processes</b>           |       |                                                          |    |       |         |
| PA0785                                         | AzoR1 | FMN-dependent NADH-azoreductase 1                        |    | -0.69 | 2.3E-01 |
| PA0840                                         |       | Probable oxidoreductase                                  |    | -0.51 | 1.3E-02 |
| PA2033                                         |       | FAD-binding FR-type domain-containing protein            |    | 1.72  | 5.8E-10 |
| PA2158                                         |       | Probable alcohol dehydrogenase (Zn-dependent)            | Zn | 0.75  | 1.4E-01 |
| PA2378                                         |       | Probable aldehyde dehydrogenase                          |    | -0.93 | 8.1E-05 |
| PA2379                                         |       | Probable oxidoreductase                                  | Fe | -1.03 | 1.4E-03 |
| PA5150                                         |       | Probable short-chain dehydrogenase                       |    | 1.45  | 1.0E-09 |
| PA5187                                         |       | Probable acyl-CoA dehydrogenase                          |    | -0.61 | 2.8E-01 |

|                                    |        |                                                                                    |  |       |         |
|------------------------------------|--------|------------------------------------------------------------------------------------|--|-------|---------|
| PA5188                             |        | Probable 3-hydroxyacyl-CoA dehydrogenase                                           |  | -0.63 | 1.4E-02 |
| <b>Other cellular transporters</b> |        |                                                                                    |  |       |         |
| PA2203                             |        | Probable amino acid permease                                                       |  | 1.74  | 6.8E-03 |
| PA2491                             | MexS   | Probable oxidoreductase                                                            |  | -1.06 | 1.2E-09 |
| PA2493                             | MexE   | Resistance-Nodulation-Cell Division (RND) multidrug efflux membrane fusion protein |  | -0.81 | 2.3E-07 |
| PA2494                             | MexF   | Efflux pump membrane transporter                                                   |  | -0.75 | 3.2E-07 |
| PA3280                             | OprO   | Porin O                                                                            |  | -1.02 | 8.4E-07 |
| PA3931                             |        | Uncharacterized protein                                                            |  | 1.54  | 1.8E-22 |
| PA5103                             | PuuR   | OpuAC domain-containing protein                                                    |  | 0.71  | 1.2E-01 |
| PA5217                             |        | Probable binding protein component of ABC iron transporter                         |  | 0.50  | 8.7E-02 |
| <b>Others</b>                      |        |                                                                                    |  |       |         |
| PA0168                             | YigZ   | Uncharacterized protein                                                            |  | 0.56  | 2.9E-01 |
| PA0225                             |        | Probable transcriptional regulator                                                 |  | 0.78  | 1.0E-01 |
| PA0277                             |        | Peptidase_M48 domain-containing protein                                            |  | -0.58 | 3.6E-02 |
| PA0284                             |        | Uncharacterized protein                                                            |  | 2.35  | 3.5E-07 |
| PA0312                             |        | DUF523 domain-containing protein                                                   |  | -1.44 | 3.1E-02 |
| PA0321                             | AphB   | Acetylputrescine amidohydrolase 2                                                  |  | -0.53 | 1.7E-03 |
| PA0423                             | PasP   | UPF0312 protein PA0423                                                             |  | 0.61  | 3.8E-06 |
| PA0540                             |        | Uncharacterized protein                                                            |  | 0.82  | 6.5E-03 |
| PA0622                             |        | Probable bacteriophage protein                                                     |  | 0.62  | 1.3E-03 |
| PA0623                             |        | Probable bacteriophage protein                                                     |  | 0.68  | 1.0E-02 |
| PA0633                             |        | Uncharacterized protein                                                            |  | 1.19  | 3.0E-02 |
| PA0634                             |        | Uncharacterized protein                                                            |  | 0.52  | 2.8E-02 |
| PA0641                             |        | Probable bacteriophage protein                                                     |  | 0.96  | 4.1E-02 |
| PA0757                             |        | Probable two-component sensor                                                      |  | 0.58  | 5.6E-01 |
| PA0807                             | AmpDh3 | AmpDh3                                                                             |  | 0.51  | 1.6E-03 |
| PA0929                             | PirR   | Two-component response regulator                                                   |  | -1.24 | 6.0E-05 |
| PA0981                             |        | Uncharacterized protein                                                            |  | -0.97 | 9.2E-05 |
| PA0984                             |        | Colicin immunity protein                                                           |  | 0.52  | 1.0E-01 |
| PA0985                             | PyoS5  | Pyocin S5                                                                          |  | 0.91  | 6.7E-07 |
| PA1017                             | PauA   | Pimeloyl-CoA synthetase                                                            |  | 1.23  | 5.2E-01 |
| PA1026                             |        | Uncharacterized protein                                                            |  | -0.80 | 4.2E-02 |
| PA1484                             |        | Probable transcriptional regulator                                                 |  | 0.62  | 1.3E-01 |
| PA1522                             |        | Uncharacterized protein                                                            |  | -0.55 | 1.5E-01 |
| PA1727                             | MucR   | Uncharacterized signaling protein PA1727                                           |  | -0.71 | 5.7E-02 |
| PA1784                             |        | Alginate_lyase2 domain-containing protein                                          |  | 1.36  | 1.9E-02 |
| PA1837                             |        | Uncharacterized protein                                                            |  | 1.10  | 6.2E-02 |
| PA2034                             |        | Methyltransf_25 domain-containing protein                                          |  | 2.07  | 1.3E-09 |
| PA2048                             |        | ABM domain-containing protein                                                      |  | -0.71 | 1.0E-03 |
| PA2066                             |        | DUF218 domain-containing protein                                                   |  | 0.99  | 3.2E-02 |
| PA2086                             |        | Probable epoxide hydrolase                                                         |  | 3.48  | 1.6E-17 |
| PA2161                             |        | Uncharacterized protein                                                            |  | 0.62  | 3.7E-01 |
| PA2171                             |        | Hemerythrin domain-containing protein                                              |  | -2.46 | 1.4E-01 |

|          |      |                                                                   |    |       |         |
|----------|------|-------------------------------------------------------------------|----|-------|---------|
| PA2184   | YciE | DUF892 domain-containing protein                                  |    | 0.63  | 1.3E-03 |
| PA2204   |      | Probable binding protein component of ABC transporter             |    | 1.82  | 4.9E-23 |
| PA2309   |      | Uncharacterized protein                                           |    | 1.50  | 9.9E-04 |
| PA2328   |      | Uncharacterized protein                                           |    | 1.15  | 1.8E-05 |
| PA2384   |      | Uncharacterized protein                                           |    | 2.81  | 2.6E-12 |
| PA2414   |      | L-sorbose dehydrogenase                                           |    | 0.75  | 1.1E-01 |
| PA2448   |      | Amidohydro_3 domain-containing protein                            |    | 0.60  | 2.6E-04 |
| PA2531   |      | Probable aminotransferase                                         |    | 2.63  | 1.7E-07 |
| PA2535   |      | Probable oxidoreductase                                           |    | -0.53 | 3.6E-08 |
| PA2599   |      | PBPb domain-containing protein                                    |    | 0.79  | 2.7E-02 |
| PA2603   |      | Probable thiosulfate sulfurtransferase                            |    | 0.58  | 2.5E-02 |
| PA2635   |      | Uncharacterized protein                                           |    | -1.18 | 2.3E-04 |
| PA2765   |      | Uncharacterized protein                                           | Fe | -0.92 | 3.2E-09 |
| PA2786   |      | GAF domain-containing protein                                     |    | 3.91  | 1.2E-17 |
| PA2804   |      | HD_domain domain-containing protein                               |    | -1.16 | 1.1E-05 |
| PA2821   |      | Probable glutathione S-transferase                                |    | -1.06 | 4.5E-07 |
| PA2831   |      | Uncharacterized protein                                           | Zn | -0.57 | 3.7E-08 |
| PA2915   |      | Lactamase_B domain-containing protein                             |    | -0.64 | 1.2E-02 |
| PA2956   |      | Elp3 domain-containing protein                                    | Fe | -0.97 | 7.2E-02 |
| PA3009   |      | Uncharacterized protein                                           |    | -0.76 | 8.7E-02 |
| PA3010   |      | Uncharacterized protein                                           |    | -0.54 | 8.3E-03 |
| PA3022   |      | MOSC domain-containing protein                                    | Mo | -0.63 | 6.0E-03 |
| PA3067   |      | Probable transcriptional regulator                                |    | -1.20 | 3.2E-01 |
| PA3124   |      | Probable transcriptional regulator                                |    | -1.20 | 6.7E-02 |
| PA3219   |      | Metallophos_2 domain-containing protein                           |    | -0.98 | 2.0E-08 |
| PA3240   |      | Putative quercetin 2,3-dioxygenase PA3240 (Putative quercetinase) |    | -0.63 | 1.0E-01 |
| PA3277   |      | Probable short-chain dehydrogenase                                |    | 0.57  | 2.4E-01 |
| PA3321   |      | Probable transcriptional regulator                                |    | -0.82 | 4.2E-02 |
| PA3327   |      | Probable non-ribosomal peptide synthetase                         |    | -1.48 | 2.3E-04 |
| PA3328   |      | Probable FAD-dependent monooxygenase                              |    | -1.01 | 1.1E-02 |
| PA3329   |      | Condensation domain-containing protein                            |    | -0.79 | 6.8E-09 |
| PA3330   |      | Probable short chain dehydrogenase                                |    | -1.20 | 1.8E-05 |
| PA3332   |      | Uncharacterized PhzA/B-like protein PA3332                        |    | -0.64 | 2.4E-02 |
| PA3441   | SsuF | Probable molybdopterin-binding protein                            |    | 3.04  | 3.2E-09 |
| PA3815   | IscR | HTH-type transcriptional regulator IscR                           |    | -0.56 | 8.9E-02 |
| PA3844   |      | GST N-terminal domain-containing protein                          |    | -0.88 | 6.7E-09 |
| PA3846   |      | Isochorismatase domain-containing protein                         |    | -0.95 | 3.9E-03 |
| PA3865.1 |      | Pyocin S4 immunity protein                                        |    | 2.14  | 2.8E-02 |
| PA3866   |      | Pyocin protein                                                    |    | 1.67  | 2.2E-12 |
| PA3932   |      | Probable transcriptional regulator                                |    | 2.24  | 6.1E-07 |
| PA4131   |      | Probable iron-sulfur protein                                      | Fe | -1.29 | 3.8E-03 |
| PA4165   |      | Probable transcriptional regulator                                |    | 0.60  | 3.0E-02 |
| PA4195   |      | Probable binding protein component of ABC transporter             |    | 2.01  | 2.0E-03 |
| PA4197   | BfiS |                                                                   |    | -1.20 | 1.8E-01 |
| PA4325   |      | DUF4124 domain-containing protein                                 |    | -0.87 | 2.7E-01 |

|        |      |                                                                     |    |       |         |
|--------|------|---------------------------------------------------------------------|----|-------|---------|
| PA4370 | IcmP | Insulin-cleaving metalloproteinase outer membrane protein           |    | 1.12  | 1.1E-14 |
| PA4371 |      | Uncharacterized protein                                             | Fe | 0.64  | 2.8E-08 |
| PA4373 |      | Uncharacterized protein                                             |    | 0.73  | 2.4E-01 |
| PA4384 |      | Uncharacterized protein                                             |    | 0.50  | 1.6E-01 |
| PA4390 |      | Uncharacterized protein                                             |    | 1.05  | 1.3E-01 |
| PA4573 |      | Uncharacterized protein                                             |    | 1.95  | 1.9E-01 |
| PA4664 | PrmC | S-adenosylmethionine-dependent methyltransferase                    |    | -0.75 | 1.2E-02 |
| PA4674 | VapI | Antotoxin HigA                                                      |    | -0.64 | 1.6E-01 |
| PA4692 | MsrP | Protein-methionine-sulfoxide reductase catalytic subunit MsrP       |    | -0.71 | 1.1E-01 |
| PA4704 | CbpA | cAMP-binding protein A                                              |    | -0.55 | 2.9E-01 |
| PA4728 | FolK | 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase |    | 0.96  | 5.4E-02 |
| PA4792 |      | GP-PDE domain-containing protein                                    |    | 1.61  | 1.2E-11 |
| PA4875 |      | MOSC domain-containing protein                                      | Mo | -1.06 | 1.7E-04 |
| PA4928 | YgiR | UPF0313 protein                                                     | Fe | -1.31 | 6.7E-03 |
| PA4943 | HflX | GTPase HflX (GTP-binding protein HflX)                              |    | -0.55 | 3.3E-01 |
| PA5081 |      | Nudix hydrolase domain-containing protein                           |    | 0.69  | 3.1E-02 |
| PA5189 |      | Probable transcriptional regulator                                  |    | 0.50  | 4.4E-01 |
| PA5506 |      | Uncharacterized protein                                             |    | -0.66 | 2.2E-01 |

Proteins exhibiting significant abundance differences between wt and  $\Delta bfd$  cells were functionally categorized using the Kyoto Encyclopedia of Genes and Genomes (KEGG) Orthology classification [1], the Pseudomonas Genome Database [2], and the UniProt database [3].

**Table S2:** Proteins exhibiting significant abundance differences between wt and  $\Delta bfd$  cells are compared to proteins exhibiting significant abundance differences between wt cells cultured in high vs. low iron conditions

| Protein ID              | Name | Function                                                 | Metal binding | This study<br>FC = $\Delta bfd/wt$ |           | Low vs High Fe<br>ref [4] |           |         |
|-------------------------|------|----------------------------------------------------------|---------------|------------------------------------|-----------|---------------------------|-----------|---------|
|                         |      |                                                          |               | $log_2FC$                          | $p$ value | $log_2FC$                 | $p$ value |         |
| Pyoverdine biosynthesis |      |                                                          |               |                                    |           |                           |           |         |
| PA2385                  | PvdQ | Acyl-homoserine lactone acylase                          |               | 3.14                               | 3.9E-10   | 2.67                      | 1.5E-05   |         |
| PA2386                  | PvdA | L-ornithine N(5)-monooxygenase                           |               | 3.02                               | 1.2E-15   | 3.00                      | 1.2E-05   |         |
| PA2388                  | FpvR |                                                          |               | -2.18                              | 1.7E-03   | ND                        |           |         |
| PA2389                  | PvdR |                                                          |               | 2.81                               | 2.8E-06   | 2.07                      | 3.6E-05   |         |
| PA2390                  | PvdT | Macrolide export ATP-binding/permease protein            |               | 2.73                               | 2.0E-10   | 2.18                      | 1.9E-04   |         |
| PA2391                  | OpmQ | Probable outer membrane protein                          |               | 2.00                               | 1.5E-04   | 1.77                      | 6.2E-04   |         |
| PA2392                  | PvdP |                                                          |               | 4.11                               | 5.2E-10   | 2.67                      | 6.6E-05   |         |
| PA2393                  | PvdM | Probable dipeptidase                                     |               | 3.22                               | 1.3E-13   | 3.05                      | 9.0E-06   |         |
| PA2394                  | PvdN |                                                          |               | 3.61                               | 2.3E-11   | 3.15                      | 1.0E-06   |         |
| PA2395                  | PvdO |                                                          |               | 3.48                               | 7.9E-16   | 1.76                      | 4.6E-03   |         |
| PA2396                  | PvdF | Pyoverdine synthetase F                                  |               | 3.25                               | 1.1E-10   | 2.30                      | 1.8E-04   |         |
| PA2397                  | PvdE | Pyoverdine biosynthesis protein                          |               | 3.16                               | 1.6E-12   | 2.98                      | 3.1E-05   |         |
| PA2398                  | FpvA | Ferripyoverdine receptor                                 |               | 1.72                               | 3.3E-07   | 3.83                      | 1.8E-07   |         |
| PA2399                  | PvdD | Pyoverdine synthetase D                                  |               | 2.75                               | 1.8E-13   | ND                        |           |         |
| PA2400                  | PvdJ | Probable non-ribosomal peptide synthetase                |               | 2.87                               | 1.4E-12   | 1.22                      | 7.1E-04   |         |
| PA2402                  | PvdI | Pyoverdine peptide synthetase                            |               | 2.87                               | 4.6E-18   | ND                        |           |         |
| PA2403                  | FpvG | Uncharacterized protein                                  |               | 2.90                               | 6.8E-12   | 0.47                      | 3.4E-01   |         |
| PA2404                  | FpvH | Uncharacterized protein                                  |               | 2.52                               | 1.8E-04   | 4.38                      | 7.9E-06   |         |
| PA2405                  | FpvJ | Probable adhesion protein                                |               | 2.94                               | 1.6E-11   | ND                        |           |         |
| PA2407                  | FpvC | Probable ATP-binding component of ABC transporter        |               | 2.97                               | 1.6E-09   | 1.97                      | 9.9E-04   |         |
| PA2408                  | FpvD | Uncharacterized protein                                  |               | 1.20                               | 1.1E-03   | infinit<br>y              | 1.9E-07   |         |
| PA2410                  | FpvF | Probable thioesterase                                    |               | 2.44                               | 1.9E-09   | 2.62                      | 4.5E-04   |         |
| PA2411                  |      | MbtH domain-containing protein                           |               | 2.73                               | 6.3E-10   | 1.97                      | 2.1E-04   |         |
| PA2412                  |      | L-2,4-diaminobutyrate:2-ketoglutarate 4-aminotransferase |               | 1.20                               | 4.5E-03   | 3.66                      | 5.8E-05   |         |
| PA2413                  | PvdH | L-sorbose dehydrogenase                                  |               | 3.10                               | 6.2E-19   | 3.40                      | 1.9E-05   |         |
| PA2424                  | PvdL |                                                          |               | 2.76                               | 6.2E-20   | ND                        |           |         |
| PA2425                  | PvdG |                                                          |               | 1.75                               | 6.3E-05   | ND                        |           |         |
| PA2426                  | PvdS | Sigma factor                                             |               | 0.91                               | 4.8E-03   | 1.70                      | 4.5E-04   |         |
| PA4168                  | FpvB | Second ferric pyoverdine receptor FpvB                   |               | 0.67                               | 2.9E-01   | 2.56                      | 5.2E-06   |         |
| Pyochelin biosynthesis  |      |                                                          |               |                                    |           |                           |           |         |
| PA4218                  | FptX | Probable transporter                                     |               |                                    | 3.14      | 2.1E-08                   | 2.71      | 9.9E-05 |
| PA4219                  | YfpB | Uncharacterized protein                                  |               |                                    | 2.83      | 9.1E-11                   | ND        |         |
| PA4221                  | FptA | Fe(3+)-pyochelin receptor (Fe(III)-pyochelin receptor)   | 2.50          |                                    | 2.9E-10   | 4.07                      | 3.5E-06   |         |
| PA4222                  | PchI | Probable ATP-binding component of ABC transporter        | 3.36          |                                    | 8.1E-19   | 2.49                      | 4.1E-04   |         |

|                                                              |       |                                                              |    |       |         |       |         |
|--------------------------------------------------------------|-------|--------------------------------------------------------------|----|-------|---------|-------|---------|
| PA4223                                                       | PchH  | Probable ATP-binding component of ABC transporter            |    | 3.32  | 1.8E-11 | 2.71  | 1.0E-04 |
| PA4224                                                       | PchG  | Pyochelin biosynthetic protein                               |    | 2.74  | 3.2E-21 | 2.00  | 5.9E-03 |
| PA4225                                                       | PchF  | Pyochelin synthetase                                         |    | 2.38  | 9.0E-23 | 0.87  | 8.4E-03 |
| PA4226                                                       | PchE  | Dihydroaeruginosic acid synthetase                           |    | 2.79  | 9.9E-17 | 2.60  | 9.7E-04 |
| PA4227                                                       | PchR  | Regulatory protein                                           |    | 1.19  | 4.1E-06 | 2.93  | 3.1E-04 |
| PA4228                                                       | PchD  | Pyochelin biosynthesis protein                               |    | 2.84  | 3.4E-17 | 1.83  | 1.0E-03 |
| PA4229                                                       | PchC  | Pyochelin biosynthetic protein                               |    | 1.14  | 1.0E-07 | ND    |         |
| PA4230                                                       | PchB  | Isochorismate pyruvate lyase                                 |    | 3.10  | 6.1E-18 | 4.50  | 1.8E-04 |
| PA4231                                                       | PchA  | Salicylate biosynthesis isochorismate synthase               |    | 1.93  | 1.2E-05 | ND    |         |
| <b>Heme iron acquisition</b>                                 |       |                                                              |    |       |         |       |         |
| PA0672                                                       | HemO  | Heme oxygenase                                               |    | 1.49  | 6.9E-13 | 2.51  | 1.0E-04 |
| PA4708                                                       | PhuT  | Heme-transport protein                                       |    | 1.42  | 2.3E-04 | 2.62  | 4.4E-06 |
| PA4709                                                       | PhuS  |                                                              |    | 1.23  | 3.6E-04 | 2.34  | 4.1E-06 |
| PA4710                                                       | PhuR  | Heme/Hemoglobin uptake outer membrane receptor               |    | 2.59  | 1.5E-14 | 3.35  | 1.4E-06 |
| <b>Other iron acquisition and transport related proteins</b> |       |                                                              |    |       |         |       |         |
| PA0471                                                       | FiuR  | Probable transmembrane sensor                                |    | 0.66  | 5.0E-02 | 2.52  | 3.8E-06 |
| PA2466                                                       | FoxA  | Ferrioxamine receptor FoxA                                   |    | 0.56  | 7.5E-04 |       |         |
| PA3901                                                       | FecA  | Fe(III) dicitrate transport protein FecA                     | Fe | 0.81  | 1.2E-01 | 2.87  | 3.3E-05 |
| PA4514                                                       | PiuA  | Probable outer membrane receptor for iron transport          |    | 1.02  | 1.6E-04 | 1.28  | 1.5E-04 |
| PA4675                                                       | OptH  | Probable TonB-dependent receptor                             |    | 0.53  | 4.8E-01 |       |         |
| <b>Quorum sensing</b>                                        |       |                                                              |    |       |         |       |         |
| PA0996                                                       | PqsA  | Anthranilate--CoA ligase                                     |    | 1.71  | 1.4E-03 |       |         |
| PA0997                                                       | PqsB  | Hypothetical protein                                         |    | 2.06  | 1.6E-06 |       |         |
| PA0998                                                       | PqsC  | Hypothetical protein                                         |    | 2.28  | 1.1E-04 |       |         |
| PA0999                                                       | PqsD  | 3-oxoacyl-ACP synthase                                       |    | 2.39  | 7.2E-11 | 1.42  | 5.2E-05 |
| PA1000                                                       | PqsE  | Thioesterase PqsE                                            |    | 2.08  | 9.6E-03 |       |         |
| PA1871                                                       | LasA  | Protease LasA (Staphylolytic protease)                       |    | 0.55  | 8.2E-02 |       |         |
| PA2569                                                       |       | Uncharacterized protein                                      |    | 0.78  | 4.3E-02 |       |         |
| PA2570                                                       | LecA  | PA-I galactophilic lectin (PA-IL) (Galactose-binding lectin) |    | 1.53  | 1.3E-02 |       |         |
| PA3476                                                       | RhlI  | Acyl-homoserine-lactone synthase                             |    | -0.54 | 9.5E-02 | -1.08 | 2.8E-03 |
| PA3478                                                       | RhlB  | Rhamnosyltransferase chain B                                 |    | 0.71  | 1.8E-12 |       |         |
| PA3479                                                       | RhlA  | 3-(3-hydroxydecanoyloxy) decanoate synthase                  |    | 0.70  | 2.3E-08 |       |         |
| PA3724                                                       | LasB  | Elastase (Neutral metalloproteinase) (PAE) (Pseudolysin)     |    | -0.80 | 1.1E-01 | 1.01  | 2.2E-02 |
| <b>Phenazine biosynthesis</b>                                |       |                                                              |    |       |         |       |         |
| PA1899                                                       | PhzA2 | Phenazine biosynthesis protein                               |    | 1.94  | 1.2E-03 |       |         |
| PA1900                                                       | PhzB2 | Phenazine biosynthesis protein                               |    | 0.99  | 7.2E-03 | -2.66 | 7.6E-05 |
| PA1904                                                       | PhzF2 | Probable phenazine biosynthesis protein                      |    | 0.61  | 2.2E-01 | -1.15 | 9.6E-04 |
| PA1905                                                       | PhzG2 | Pyridoxamine 5'-phosphate oxidase                            |    | 1.22  | 2.1E-03 |       |         |

|                                                    |           |                                                                     |        |       |         |       |         |
|----------------------------------------------------|-----------|---------------------------------------------------------------------|--------|-------|---------|-------|---------|
| PA4213                                             | PhzD1     | Phenazine biosynthesis protein                                      |        | 1.47  | 1.2E-10 | -1.91 | 3.2E-03 |
| PA4214                                             | PhzE1     | Phenazine biosynthesis protein                                      |        | 0.95  | 1.3E-10 |       |         |
| <b>Carbon metabolism and amino acid metabolism</b> |           |                                                                     |        |       |         |       |         |
| PA0400                                             | MetB      | Probable cystathionine gamma-lyase                                  |        | 0.57  | 7.2E-07 | 1.66  | 2.0E-04 |
| PA0792                                             | PrpD      | Propionate catabolic protein                                        | Fe     | 0.95  | 1.1E-13 | 2.10  | 7.5E-06 |
| PA0794                                             |           | Probable aconitate hydratase                                        |        | -0.65 | 3.9E-08 | -2.13 | 1.9E-05 |
| PA0865                                             | Hpd       | 4-hydroxyphenylpyruvate dioxygenase (4HPPD)                         |        | 0.56  | 2.4E-03 | 1.61  | 1.1E-03 |
| PA1254                                             | LhpC      | Probable dihydrodipicolinate synthetase                             |        | -0.74 | 4.6E-04 |       |         |
| PA1255                                             | LhpK      | Probable trans-3-hydroxy-L-proline dehydratase (T3LHyp dehydratase) |        | -0.90 | 2.6E-02 |       |         |
| PA1260                                             | LhpP      | Amino acid ABC transporter Periplasmic binding protein              |        | -0.52 | 6.9E-02 |       |         |
| PA1261                                             | LhpR      | Probable transcriptional regulator                                  |        | 0.68  | 3.9E-01 |       |         |
| PA1311                                             | PhnX      | Phosphonoacetaldehyde hydrolase (Phosphonatase)                     |        | -0.54 | 4.6E-01 |       |         |
| PA1422                                             | GbuR      | GbuR                                                                |        | 0.87  | 1.2E-01 |       |         |
| PA1562                                             | AcnA      | Aconitate hydratase 1                                               | Fe     | -0.98 | 6.2E-15 | -2.59 | 3.5E-05 |
| PA2015                                             | LiuA      | Putative isovaleryl-CoA dehydrogenase                               |        | -0.78 | 2.1E-02 | 1.37  | 4.0E-05 |
| PA2152                                             |           | Probable trehalose synthase                                         |        | 0.54  | 2.0E-01 |       |         |
| PA2300                                             | ChiC      | Chitinase                                                           |        | 0.76  | 1.6E-05 |       |         |
| PA2416                                             | TreA      | Periplasmic trehalase                                               |        | 0.81  | 4.2E-02 |       |         |
| PA3120                                             | LeuD      | 3-isopropylmalate dehydratase small subunit                         |        | -0.76 | 3.3E-03 |       |         |
| PA3121                                             | LeuC      | 3-isopropylmalate dehydratase large subunit                         | Fe     | -0.83 | 2.1E-07 | -1.94 | 2.2E-04 |
| PA3236                                             | BetX      | Probable glycine betaine-binding protein                            |        | -0.68 | 5.0E-03 |       |         |
| PA3374                                             | PhnM      | Amidohydro_3 domain-containing protein                              |        | -0.94 | 9.0E-05 |       |         |
| PA3375                                             | PhnL      | Probable ATP-binding component of ABC transporter                   |        | -0.56 | 1.2E-01 |       |         |
| PA3376                                             | PhnK      | Probable ATP-binding component of ABC transporter                   |        | -0.60 | 4.2E-03 |       |         |
| PA3377                                             | PhnJ      | Alpha-D-ribose 1-methylphosphonate 5-phosphate C-P lyase            |        | -0.76 | 6.4E-02 |       |         |
| PA3378                                             | PhnI      | Uncharacterized protein                                             |        | -0.97 | 4.9E-03 |       |         |
| PA3379                                             | PhnH      | Uncharacterized protein                                             |        | -0.80 | 6.3E-04 |       |         |
| PA3380                                             | PhnG      | Uncharacterized protein                                             |        | -1.09 | 4.6E-03 |       |         |
| PA3417                                             | PdhA      | Pyruvate dehydrogenase E1 component subunit alpha                   |        | -0.54 | 9.5E-02 |       |         |
| PA3430                                             |           | Putative aldolase class 2 protein                                   |        | -0.86 | 3.5E-02 | -8.45 | 6.2E-04 |
| PA3459                                             |           | Probable glutamine amidotransferase                                 |        | -0.66 | 2.7E-06 |       |         |
| PA3506                                             |           | Probable decarboxylase                                              | Mn     | -0.62 | 3.3E-01 |       |         |
| PA3524                                             | GloA1     | Lactoylglutathione lyase                                            | Zn, Ni | -0.67 | 1.2E-02 | -1.73 | 7.7E-04 |
| PA3896                                             |           | Probable 2-hydroxyacid dehydrogenase                                |        | 0.49  | 3.5E-01 |       |         |
| PA4150                                             | AcoA      | Probable dehydrogenase E1 component                                 |        | -0.53 | 4.0E-01 |       |         |
| PA4151                                             | AcoB      | Acetoin catabolism protein                                          |        | -0.72 | 2.5E-04 |       |         |
| PA4152                                             | AcoC      | Probable hydrolase                                                  |        | -0.67 | 5.0E-02 |       |         |
| PA4333                                             | FumA      | Probable fumarase                                                   | Fe     | -2.08 | 8.5E-13 | -3.96 | 7.2E-06 |
| PA4470                                             | FumC<br>1 | Fumarate hydratase                                                  | Mn     | 3.11  | 8.0E-16 | 4.95  | 3.2E-08 |
| PA4628                                             | LysP      | Lysine-specific permease                                            |        | 0.65  | 2.1E-01 |       |         |

|                            |         |                                                                  |    |       |         |       |         |
|----------------------------|---------|------------------------------------------------------------------|----|-------|---------|-------|---------|
| PA5354                     | GlcE    | Glycolate oxidase subunit GlcE                                   |    | -0.61 | 2.2E-01 |       |         |
| PA5376                     | CbcV    |                                                                  |    | -0.53 | 4.7E-01 |       |         |
| PA5398                     | DgcA    | Dimethylglycine catabolism                                       |    | -1.40 | 9.0E-05 | 1.31  | 1.2E-03 |
| PA5410                     | GbcA    | glycine betaine catabolism protein                               | Fe | -1.41 | 1.3E-07 |       |         |
| PA5415                     | GlyA1   | Serine hydroxymethyltransferase                                  |    | -0.79 | 2.3E-06 |       |         |
| PA5416                     | SoxB    | Sarcosine oxidase beta subunit                                   |    | -0.69 | 2.7E-01 |       |         |
| PA5417                     | SoxD    | Sarcosine oxidase delta subunit                                  |    | -0.66 | 2.0E-02 |       |         |
| PA5418                     | SoxA    | Sarcosine oxidase alpha subunit                                  | Fe | -0.60 | 5.7E-03 |       |         |
| PA5421                     | FdhA    | Glutathione-independent formaldehyde dehydrogenase (FALDH) (FDH) | Zn | -0.61 | 7.3E-09 |       |         |
| PA5445                     | Pseco A | Probable coenzyme A transferase                                  |    | -0.62 | 3.2E-01 |       |         |
| <b>Sulfur assimilation</b> |         |                                                                  |    |       |         |       |         |
| PA0280                     | CysA    | Sulfate transport protein                                        |    | 1.17  | 1.2E-06 |       |         |
| PA0282                     | CysT    | Sulfate transport protein                                        |    | 1.28  | 5.5E-06 |       |         |
| PA0283                     | Sbp     | Sulfate-binding protein precursor                                |    | 2.05  | 2.8E-19 |       |         |
| PA0500                     | BioB    | Biotin synthase                                                  | Fe | 0.79  | 3.4E-02 | -0.61 | 4.7E-03 |
| PA0916                     | YliG    | Ribosomal protein S12 methylthiotransferase                      | Fe | -0.85 | 8.9E-02 | 1.11  | 1.8E-03 |
| PA1192                     | YdaO    | tRNA-cytidine(32) 2-sulfurtransferase                            | Fe | -0.78 | 1.8E-01 |       |         |
| PA1505                     | MoaA 2  | Molybdenum cofactor biosynthesis protein A 2                     | Fe | -0.61 | 3.7E-01 |       |         |
| PA1838                     | CysI    | Sulfite reductase                                                | Fe | 0.68  | 2.0E-14 | -1.46 | 5.6E-05 |
| PA2062                     |         | Probable pyridoxal-phosphate dependent enzyme                    | Fe | 3.05  | 3.9E-05 |       |         |
| PA2566                     |         | Conserved hypothetical protein                                   |    | -0.75 | 1.7E-01 |       |         |
| PA2594                     |         | Conserved hypothetical protein                                   |    | 1.54  | 4.0E-05 |       |         |
| PA3445                     |         | Conserved hypothetical protein                                   |    | 2.87  | 9.1E-06 | -1.87 | 3.6E-02 |
| PA3938                     | TauA    | Probable periplasmic taurine-binding protein                     |    | 2.47  | 4.1E-04 |       |         |
| PA3980                     | MiaB    | tRNA-2-methylthio-N(6)-dimethylallyl-adenosine synthase          | Fe | -1.74 | 5.8E-06 |       |         |
| PA3996                     | LipA    | Lipoate synthase (Sulfur insertion protein LipA)                 | Fe | -0.63 | 1.7E-01 |       |         |
| PA4442                     | CysN    | ATP sulfurylase GTP-binding subunit/APS kinase                   |    | 0.83  | 5.3E-10 | -1.60 | 2.7E-04 |
| PA4443                     | CysD    | ATP sulfurylase small subunit                                    |    | 1.03  | 3.9E-03 | -2.09 | 6.1E-06 |
| PA4973                     | ThiC    | Phosphomethylpyrimidine synthase                                 | Fe | -0.56 | 4.0E-02 | -0.84 | 2.5E-03 |
| PA5025                     | MetY    | Homocysteine synthase                                            |    | 0.86  | 9.1E-03 |       |         |
| <b>Respiration</b>         |         |                                                                  |    |       |         |       |         |
| PA0527                     | Dnr     | Transcriptional regulator                                        |    | -0.94 | 1.5E-02 |       |         |
| PA1173                     | NapB    | Periplasmic nitrate reductase                                    | Fe | -0.99 | 7.1E-03 |       |         |
| PA1174                     | NapA    | Periplasmic nitrate reductase                                    | Fe | -1.31 | 1.2E-12 | -1.58 | 2.5E-04 |
| PA1175                     | NapD    | NapA signal peptide-binding chaperone                            |    | -0.72 | 1.4E-02 |       |         |
| PA1176                     | NapF    | Ferredoxin-type protein                                          | Fe | -0.88 | 2.0E-02 |       |         |
| PA1544                     | Anr     | Transcriptional activator protein                                | Fe | 0.69  | 3.4E-05 |       |         |
| PA2266                     |         | Probable cytochrome c                                            | Fe | -0.56 | 4.6E-01 |       |         |
| PA3331                     |         | Cytochrome P450                                                  | Fe | -0.67 | 7.6E-04 | -2.73 | 1.9E-02 |
| PA3872                     | NarI    | Respiratory nitrate reductase gamma chain                        | Fe | -0.58 | 3.6E-02 |       |         |
| PA4133                     | CcoN    | Cytochrome c oxidase subunit (Cbb3-type)                         | Fe | -1.11 | 1.2E-02 | -2.63 | 1.9E-03 |

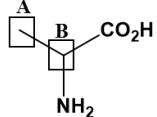
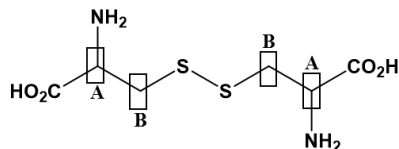
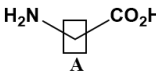
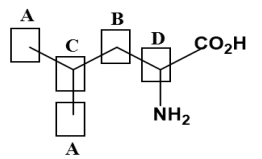
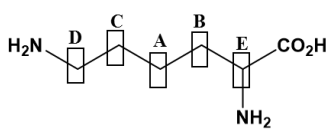
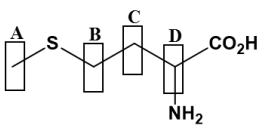
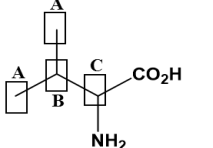
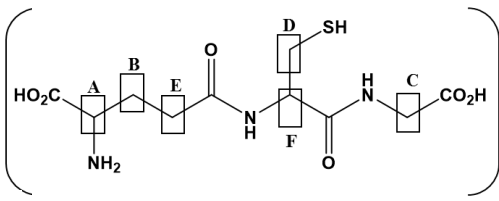
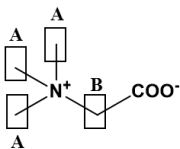
| Anr regulon                             |       |                                                          |    |       |         |       |         |
|-----------------------------------------|-------|----------------------------------------------------------|----|-------|---------|-------|---------|
| PA1546                                  | HemN  | Oxygen-independent coproporphyrinogen III oxidase (CPO)  | Fe | -1.63 | 2.6E-06 | -1.33 | 4.8E-04 |
| PA1673                                  |       | Bacteriohemerythrin                                      | Fe | -0.95 | 5.3E-06 | -2.13 | 1.1E-03 |
| PA3049                                  | Rmf   | Ribosome modulation factor                               |    | 0.74  | 3.8E-03 | 1.42  | 3.3E-03 |
| PA3126                                  | IbpA  | Heat-shock protein IbpA                                  |    | -0.60 | 2.5E-04 |       |         |
| PA3572                                  |       | Hypothetical protein                                     |    | -0.52 | 2.5E-03 |       |         |
| PA3919                                  | YlaK  | PINc domain-containing protein                           |    | -0.77 | 5.5E-02 |       |         |
| PA4587                                  | CcpR  | Cytochrome c551 peroxidase                               | Fe | -0.52 | 1.3E-04 |       |         |
| PA4880                                  |       | Probable bacterioferritin                                | Fe | -2.95 | 8.1E-16 | -3.54 | 4.5E-06 |
| PA5475                                  |       | Acetyltransferase                                        |    | -0.61 | 4.1E-02 | -2.96 | 2.3E-04 |
| Oxidative stress regulation             |       |                                                          |    |       |         |       |         |
| PA0140                                  | AhpF  | Alkyl hydroperoxide reductase subunit F                  |    | -0.60 | 2.1E-06 |       |         |
| PA0849                                  | TrxB2 | Thioredoxin reductase                                    |    | -0.77 | 4.2E-04 |       |         |
| PA2185                                  | KatN  | Non-heme catalase KatN                                   | Mn | -0.91 | 1.2E-01 |       |         |
| PA2580                                  | MdaB  | Flavodoxin_2 domain-containing protein                   |    | -0.55 | 1.0E-02 |       |         |
| PA3450                                  | LsfA  | Probable antioxidant protein                             |    | 2.49  | 1.2E-21 |       |         |
| PA3533                                  | GrxD  | Glutaredoxin                                             |    | -0.81 | 3.6E-08 | -3.28 | 2.9E-04 |
| PA4236                                  | KatA  | Catalase                                                 | Fe | -1.08 | 1.4E-08 | -3.06 | 7.4E-06 |
| PA4366                                  | SodB  | Superoxide dismutase [Fe]                                | Fe | -0.96 | 7.1E-03 | -4.28 | 4.2E-06 |
| PA4468                                  | SodA  | Superoxide dismutase [Mn]                                | Mn | 2.81  | 2.6E-14 | 3.91  | 4.4E-05 |
| Nucleotide synthesis and metabolism     |       |                                                          |    |       |         |       |         |
| PA0441                                  | Dht   | D-hydantoinase/ dihydropyrimidinase (DHPase)             | Zn | -0.71 | 2.2E-02 |       |         |
| PA1155                                  | NrdB  | Ribonucleoside-diphosphate reductase subunit beta        | Fe | -0.61 | 2.0E-02 |       |         |
| PA1156                                  | NrdA  | Ribonucleoside-diphosphate reductase                     |    | -0.62 | 1.9E-06 |       |         |
| PA1932                                  |       | Probable hydroxylase molybdopterin-containing subunit    |    | -0.89 | 9.0E-02 |       |         |
| Lipid metabolism                        |       |                                                          |    |       |         |       |         |
| PA0347                                  | GlpQ  | Glycerophosphoryl diester phosphodiesterase, periplasmic |    | -1.06 | 2.6E-11 |       |         |
| PA2862                                  | LipA  | Triacylglycerol lipase                                   |    | -0.52 | 2.1E-01 |       |         |
| PA3092                                  | FadH1 | 2,4-dienoyl-CoA reductase FadH1                          |    | -1.11 | 2.0E-04 |       |         |
| PA3319                                  | PlcN  | Non-hemolytic phospholipase C (PLC-N)                    |    | -0.84 | 3.6E-14 |       |         |
| PA3333                                  | FabH  | 3-oxoacyl-[acyl-carrier-protein] synthase 3              |    | -0.85 | 4.6E-06 | -1.67 | 6.7E-04 |
| PA4350                                  | OlsB  | Uncharacterized protein                                  |    | -0.55 | 5.0E-02 |       |         |
| PA4353                                  | YajB  | Uncharacterized protein                                  |    | -0.56 | 6.0E-03 |       |         |
| PA4661                                  | PagL  | Lipid A deacylase PagL                                   |    | 0.51  | 6.1E-02 |       |         |
| Secreted proteins and secretion systems |       |                                                          |    |       |         |       |         |
| PA0572                                  | ImpA  | Immunomodulating metalloprotease                         | Zn | 0.71  | 1.1E-02 |       |         |
| PA0688                                  | PhoA  | Alkaline phosphatase L (L-AP)                            |    | -0.74 | 5.8E-09 |       |         |
| PA1245                                  | AprX  | Uncharacterized protein                                  |    | 3.02  | 3.9E-10 | 3.29  | 1.1E-01 |

|                                      |        |                                                            |    |       |         |       |         |
|--------------------------------------|--------|------------------------------------------------------------|----|-------|---------|-------|---------|
| PA1246                               | AprD   | Alkaline protease secretion ATP-binding protein AprD       |    | 2.25  | 2.2E-09 | 3.43  | 5.1E-04 |
| PA1247                               | AprE   | Alkaline protease secretion protein AprE                   |    | 2.11  | 3.1E-03 | -0.17 | 9.0E-02 |
| PA1249                               | AprA   | Serralysin (Alkaline metalloproteinase) (AP)               | Zn | 1.82  | 1.4E-10 | 0.83  | 1.0E-02 |
| PA1250                               | AprI   | Proteinase inhibitor (Aprin)                               | Zn | 0.96  | 1.0E-03 |       |         |
| PA3099                               | XcpV   | Type II secretion system protein I                         |    | 0.79  | 1.4E-01 |       |         |
| <b>Oxidation-reduction processes</b> |        |                                                            |    |       |         |       |         |
| PA0785                               | AzoR1  | FMN-dependent NADH-azoreductase 1                          |    | -0.69 | 2.3E-01 |       |         |
| PA0840                               |        | Probable oxidoreductase                                    |    | -0.51 | 1.3E-02 |       |         |
| PA2033                               |        | FAD-binding FR-type domain-containing protein              |    | 1.72  | 5.8E-10 | 2.42  | 4.1E-05 |
| PA2158                               |        | Probable alcohol dehydrogenase (Zn-dependent)              | Zn | 0.75  | 1.4E-01 |       |         |
| PA2378                               |        | Probable aldehyde dehydrogenase                            |    | -0.93 | 8.1E-05 | -1.64 | 2.7E-03 |
| PA2379                               |        | Probable oxidoreductase                                    | Fe | -1.03 | 1.4E-03 | -2.15 | 2.5E-03 |
| PA5150                               |        | Probable short-chain dehydrogenase                         |    | 1.45  | 1.0E-09 | 2.53  | 7.4E-05 |
| PA5187                               |        | Probable acyl-CoA dehydrogenase                            |    | -0.61 | 2.8E-01 |       |         |
| PA5188                               |        | Probable 3-hydroxyacyl-CoA dehydrogenase                   |    | -0.63 | 1.4E-02 | -2.62 | 5.8E-05 |
| <b>Other cellular transporters</b>   |        |                                                            |    |       |         |       |         |
| PA2203                               |        | Probable amino acid permease                               |    | 1.74  | 6.8E-03 |       |         |
| PA2491                               | MexS   | Probable oxidoreductase                                    |    | -1.06 | 1.2E-09 | -1.05 | 3.0E-05 |
| PA2493                               | MexE   | RND multidrug efflux membrane fusion protein               |    | -0.81 | 2.3E-07 |       |         |
| PA2494                               | MexF   | Efflux pump membrane transporter                           |    | -0.75 | 3.2E-07 |       |         |
| PA3280                               | OprO   | Porin O                                                    |    | -1.02 | 8.4E-07 |       |         |
| PA3931                               |        | Uncharacterized protein                                    |    | 1.54  | 1.8E-22 |       |         |
| PA5103                               | PuuR   | OpuAC domain-containing protein                            |    | 0.71  | 1.2E-01 |       |         |
| PA5217                               |        | Probable binding protein component of ABC iron transporter |    | 0.50  | 8.7E-02 | 1.86  | 2.3E-05 |
| <b>Others</b>                        |        |                                                            |    |       |         |       |         |
| PA0168                               | YigZ   | Uncharacterized protein                                    |    | 0.56  | 2.9E-01 |       |         |
| PA0225                               |        | Probable transcriptional regulator                         |    | 0.78  | 1.0E-01 |       |         |
| PA0277                               |        | Peptidase_M48 domain-containing protein                    |    | -0.58 | 3.6E-02 |       |         |
| PA0284                               |        | Uncharacterized protein                                    |    | 2.35  | 3.5E-07 | -2.90 | 1.9E-03 |
| PA0312                               |        | DUF523 domain-containing protein                           |    | -1.44 | 3.1E-02 | -1.63 | 1.3E-03 |
| PA0321                               | AphB   | Acetylpolymine amidohydrolase 2                            |    | -0.53 | 1.7E-03 |       |         |
| PA0423                               | PasP   | UPF0312 protein PA0423                                     |    | 0.61  | 3.8E-06 | 1.21  | 3.4E-04 |
| PA0540                               |        | Uncharacterized protein                                    |    | 0.82  | 6.5E-03 |       |         |
| PA0622                               |        | Probable bacteriophage protein                             |    | 0.62  | 1.3E-03 |       |         |
| PA0623                               |        | Probable bacteriophage protein                             |    | 0.68  | 1.0E-02 |       |         |
| PA0633                               |        | Uncharacterized protein                                    |    | 1.19  | 3.0E-02 |       |         |
| PA0634                               |        | Uncharacterized protein                                    |    | 0.52  | 2.8E-02 |       |         |
| PA0641                               |        | Probable bacteriophage protein                             |    | 0.96  | 4.1E-02 |       |         |
| PA0757                               |        | Probable two-component sensor                              |    | 0.58  | 5.6E-01 |       |         |
| PA0807                               | AmpDh3 | AmpDh3                                                     |    | 0.51  | 1.6E-03 |       |         |

|        |       |                                                                   |    |       |         |       |         |
|--------|-------|-------------------------------------------------------------------|----|-------|---------|-------|---------|
| PA0929 | PirR  | Two-component response regulator                                  |    | -1.24 | 6.0E-05 | ND    |         |
| PA0981 |       | Uncharacterized protein                                           |    | -0.97 | 9.2E-05 |       |         |
| PA0984 |       | Colicin immunity protein                                          |    | 0.52  | 1.0E-01 |       |         |
| PA0985 | PyoS5 | Pyocin S5                                                         |    | 0.91  | 6.7E-07 |       |         |
| PA1017 | PauA  | Pimeloyl-CoA synthetase                                           |    | 1.23  | 5.2E-01 |       |         |
| PA1026 |       | Uncharacterized protein                                           |    | -0.80 | 4.2E-02 |       |         |
| PA1484 |       | Probable transcriptional regulator                                |    | 0.62  | 1.3E-01 |       |         |
| PA1522 |       | Uncharacterized protein                                           |    | -0.55 | 1.5E-01 |       |         |
| PA1727 | MucR  | Uncharacterized signaling protein PA1727                          |    | -0.71 | 5.7E-02 |       |         |
| PA1784 |       | Alginate_lyase2 domain-containing protein                         |    | 1.36  | 1.9E-02 |       |         |
| PA1837 |       | Uncharacterized protein                                           |    | 1.10  | 6.2E-02 | -3.18 | 1.7E-04 |
| PA2034 |       | Methyltransf_25 domain-containing protein                         |    | 2.07  | 1.3E-09 | 2.45  | 1.1E-04 |
| PA2048 |       | ABM domain-containing protein                                     |    | -0.71 | 1.0E-03 |       |         |
| PA2066 |       | DUF218 domain-containing protein                                  |    | 0.99  | 3.2E-02 |       |         |
| PA2086 |       | Probable epoxide hydrolase                                        |    | 3.48  | 1.6E-17 |       |         |
| PA2161 |       | Uncharacterized protein                                           |    | 0.62  | 3.7E-01 | 3.92  | 1.1E-04 |
| PA2171 |       | Hemerythrin domain-containing protein                             |    | -2.46 | 1.4E-01 | -1.93 | 3.4E-03 |
| PA2184 | YciE  | DUF892 domain-containing protein                                  |    | 0.63  | 1.3E-03 |       |         |
| PA2204 |       | Probable binding protein component of ABC transporter             |    | 1.82  | 4.9E-23 |       |         |
| PA2309 |       | Uncharacterized protein                                           |    | 1.50  | 9.9E-04 |       |         |
| PA2328 |       | Uncharacterized protein                                           |    | 1.15  | 1.8E-05 |       |         |
| PA2384 |       | Uncharacterized protein                                           |    | 2.81  | 2.6E-12 | 3.59  | 8.3E-05 |
| PA2414 |       | L-sorbose dehydrogenase                                           |    | 0.75  | 1.1E-01 |       |         |
| PA2448 |       | Amidohydro_3 domain-containing protein                            |    | 0.60  | 2.6E-04 |       |         |
| PA2531 |       | Probable aminotransferase                                         |    | 2.63  | 1.7E-07 | 1.57  | 5.1E-05 |
| PA2535 |       | Probable oxidoreductase                                           |    | -0.53 | 3.6E-08 |       |         |
| PA2599 |       | PBPb domain-containing protein                                    |    | 0.79  | 2.7E-02 |       |         |
| PA2603 |       | Probable thiosulfate sulfurtransferase                            |    | 0.58  | 2.5E-02 |       |         |
| PA2635 |       | Uncharacterized protein                                           |    | -1.18 | 2.3E-04 |       |         |
| PA2765 |       | Uncharacterized protein                                           | Fe | -0.92 | 3.2E-09 | -1.20 | 8.3E-03 |
| PA2786 |       | GAF domain-containing protein                                     |    | 3.91  | 1.2E-17 |       |         |
| PA2804 |       | HD_domain domain-containing protein                               |    | -1.16 | 1.1E-05 |       |         |
| PA2821 |       | Probable glutathione S-transferase                                |    | -1.06 | 4.5E-07 |       |         |
| PA2831 |       | Uncharacterized protein                                           | Zn | -0.57 | 3.7E-08 | -1.68 | 6.4E-04 |
| PA2915 |       | Lactamase_B domain-containing protein                             |    | -0.64 | 1.2E-02 |       |         |
| PA2956 |       | Elp3 domain-containing protein                                    | Fe | -0.97 | 7.2E-02 | -2.56 | 6.8E-04 |
| PA3009 |       | Uncharacterized protein                                           |    | -0.76 | 8.7E-02 | -3.55 | 2.2E-02 |
| PA3010 |       | Uncharacterized protein                                           |    | -0.54 | 8.3E-03 |       |         |
| PA3022 |       | MOSC domain-containing protein                                    | Mo | -0.63 | 6.0E-03 | -1.50 | 1.1E-03 |
| PA3067 |       | Probable transcriptional regulator                                |    | -1.20 | 3.2E-01 |       |         |
| PA3124 |       | Probable transcriptional regulator                                |    | -1.20 | 6.7E-02 |       |         |
| PA3219 |       | Metallophos_2 domain-containing protein                           |    | -0.98 | 2.0E-08 |       |         |
| PA3240 |       | Putative quercetin 2,3-dioxygenase PA3240 (Putative quercetinase) |    | -0.63 | 1.0E-01 |       |         |
| PA3277 |       | Probable short-chain dehydrogenase                                |    | 0.57  | 2.4E-01 |       |         |

|          |      |                                                                     |    |       |         |       |         |
|----------|------|---------------------------------------------------------------------|----|-------|---------|-------|---------|
| PA3321   |      | Probable transcriptional regulator                                  |    | -0.82 | 4.2E-02 |       |         |
| PA3327   |      | Probable non-ribosomal peptide synthetase                           |    | -1.48 | 2.3E-04 |       |         |
| PA3328   |      | Probable FAD-dependent monooxygenase                                |    | -1.01 | 1.1E-02 |       |         |
| PA3329   |      | Condensation domain-containing protein                              |    | -0.79 | 6.8E-09 |       |         |
| PA3330   |      | Probable short chain dehydrogenase                                  |    | -1.20 | 1.8E-05 |       |         |
| PA3332   |      | Uncharacterized PhzA/B-like protein PA3332                          |    | -0.64 | 2.4E-02 | -1.04 | 1.9E-04 |
| PA3441   | SsuF | Probable molybdopterin-binding protein                              |    | 3.04  | 3.2E-09 |       |         |
| PA3815   | IscR | HTH-type transcriptional regulator IscR                             |    | -0.56 | 8.9E-02 | 1.04  | 2.6E-02 |
| PA3844   |      | GST N-terminal domain-containing protein                            |    | -0.88 | 6.7E-09 |       |         |
| PA3846   |      | Isochorismatase domain-containing protein                           |    | -0.95 | 3.9E-03 | -1.09 | 7.2E-03 |
| PA3865.1 |      | Pyosin S4 immunity protein                                          |    | 2.14  | 2.8E-02 |       |         |
| PA3866   |      | Pyocin protein                                                      |    | 1.67  | 2.2E-12 | 2.08  | 1.4E-04 |
| PA3932   |      | Probable transcriptional regulator                                  |    | 2.24  | 6.1E-07 |       |         |
| PA4131   |      | Probable iron-sulfur protein                                        | Fe | -1.29 | 3.8E-03 | -2.62 | 2.8E-06 |
| PA4165   |      | Probable transcriptional regulator                                  |    | 0.60  | 3.0E-02 |       |         |
| PA4195   |      | Probable binding protein component of ABC transporter               |    | 2.01  | 2.0E-03 | -2.29 | 6.4E-03 |
| PA4197   | BfiS |                                                                     |    | -1.20 | 1.8E-01 |       |         |
| PA4325   |      | DUF4124 domain-containing protein                                   |    | -0.87 | 2.7E-01 |       |         |
| PA4370   | IcmP | Insulin-cleaving metalloproteinase outer membrane protein           |    | 1.12  | 1.1E-14 | 1.85  | 1.2E-03 |
| PA4371   |      | Uncharacterized protein                                             | Fe | 0.64  | 2.8E-08 |       |         |
| PA4373   |      | Uncharacterized protein                                             |    | 0.73  | 2.4E-01 |       |         |
| PA4384   |      | Uncharacterized protein                                             |    | 0.50  | 1.6E-01 |       |         |
| PA4390   |      | Uncharacterized protein                                             |    | 1.05  | 1.3E-01 | 1.12  | 3.0E-04 |
| PA4573   |      | Uncharacterized protein                                             |    | 1.95  | 1.9E-01 |       |         |
| PA4664   | PrmC | S-adenosylmethionine-dependent methyltransferase                    |    | -0.75 | 1.2E-02 |       |         |
| PA4674   | VapI | Antotoxin HigA                                                      |    | -0.64 | 1.6E-01 |       |         |
| PA4692   | MsrP | Protein-methionine-sulfoxide reductase catalytic subunit MsrP       |    | -0.71 | 1.1E-01 |       |         |
| PA4704   | CbpA | cAMP-binding protein A                                              |    | -0.55 | 2.9E-01 |       |         |
| PA4728   | FolK | 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase |    | 0.96  | 5.4E-02 |       |         |
| PA4792   |      | GP-PDE domain-containing protein                                    |    | 1.61  | 1.2E-11 |       |         |
| PA4875   |      | MOSC domain-containing protein                                      | Mo | -1.06 | 1.7E-04 |       |         |
| PA4928   | YgiR | UPF0313 protein                                                     | Fe | -1.31 | 6.7E-03 |       |         |
| PA4943   | HflX | GTPase HflX (GTP-binding protein HflX)                              |    | -0.55 | 3.3E-01 |       |         |
| PA5081   |      | Nudix hydrolase domain-containing protein                           |    | 0.69  | 3.1E-02 |       |         |
| PA5189   |      | Probable transcriptional regulator                                  |    | 0.50  | 4.4E-01 |       |         |
| PA5506   |      | Uncharacterized protein                                             |    | -0.66 | 2.2E-01 |       |         |

**Table S3:** Resonance assignments for  $^1\text{H}$  and  $^{13}\text{C}$  chemical shifts of amino acids and other metabolites identified by NMR spectroscopy in the wt and  $\Delta bfd$  cells.

| Metabolite           | Structure                                                                           | Group                                                                                            | $\delta_{\text{H}}$ (ppm)                    | $\delta_{\text{C}}$ (ppm)                          | $^1\text{H}$ Multiplicity                                             |
|----------------------|-------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------|----------------------------------------------|----------------------------------------------------|-----------------------------------------------------------------------|
| Alanine              |    | A-CH <sub>3</sub><br>B-CH                                                                        | 1.471<br>3.771                               | 18.83<br>53.29                                     | <i>d</i><br><i>q</i>                                                  |
| Cystine              |    | A-CH<br>B-CH <sub>2</sub>                                                                        | 4.103<br>3.180, 3.378                        | 56.14<br>40.55                                     | <i>dd</i><br><i>dd</i>                                                |
| Glycine              |    | A-CH <sub>2</sub>                                                                                | 3.545                                        | 44.13                                              | <i>s</i>                                                              |
| Leucine              |    | A-CH <sub>3</sub><br>B-CH <sub>2</sub><br>C-CH<br>D-CH                                           | 0.949<br>1.701<br>1.701<br>3.719             | 24.75, 23.59<br>42.53<br>26.87<br>56.11            | <i>t</i><br><i>m</i><br><i>m</i><br><i>m</i>                          |
| Lysine               |   | A-CH <sub>2</sub><br>B-CH <sub>2</sub><br>C-CH <sub>2</sub><br>D-CH <sub>2</sub><br>E-CH         | 1.465<br>1.716<br>1.895<br>3.012<br>3.745    | 24.15<br>29.14<br>32.63<br>41.75<br>57.19          | <i>m</i><br><i>quint</i><br><i>m</i><br><i>t</i><br><i>t</i>          |
| Methionine           |  | A-CH <sub>3</sub><br>B-CH <sub>2</sub><br>C-CH <sub>2</sub><br>D-CH                              | 2.122<br>2.629<br>2.183, 2.122<br>3.850      | 16.64<br>31.51<br>32.40<br>56.58                   | <i>m</i><br><i>t</i><br><i>m</i><br><i>dd</i>                         |
| Valine               |  | A-CH <sub>3</sub><br>B-CH<br>C-CH                                                                | 0.981, 1.034<br>2.266<br>3.599               | 19.37, 20.70<br>31.83<br>63.08                     | <i>d</i><br><i>m</i><br><i>d</i>                                      |
| Oxidized glutathione |  | A-CH <sub>2</sub><br>B-CH <sub>2</sub><br>C-CH <sub>2</sub><br>D-CH <sub>2</sub><br>E-CH<br>F-CH | 2.16<br>2.53<br>3.77<br>3.14<br>3.77<br>4.75 | 28.98<br>34.10<br>46.18<br>41.39<br>56.80<br>55.30 | <i>m</i><br><i>m</i><br><i>m</i><br><i>dd</i><br><i>m</i><br><i>q</i> |
| Glycine-betaine      |  | A-CH <sub>3</sub><br>B-CH <sub>2</sub>                                                           | 3.255<br>3.895                               | 56.08<br>68.86                                     | <i>s</i><br><i>s</i>                                                  |

Chemical shift assignments were made in reference to the publicly accessible Human Metabolome and BioMagResBank databases [5,6]. Assignments were corroborated with the aid of  $^1\text{H}$ - $^{13}\text{C}$ -HSQC and TOCSY spectra, as presented in Materials and Methods.

## References

1. Kanehisa, M.; Goto, S.; Sato, Y.; Kawashima, M.; Furumichi, M.; Tanabe, M. Data, information, knowledge and principle: back to metabolism in KEGG. *Nucleic acids research* **2014**, *42*, D199-D205, doi:10.1093/nar/gkt1076.
2. Winsor, G.L.; Griffiths, E.J.; Lo, R.; Dhillon, B.K.; Shay, J.A.; Brinkman, F.S. Enhanced annotations and features for comparing thousands of *Pseudomonas* genomes in the *Pseudomonas* genome database. *Nucleic Acids Res* **2016**, *44*, D646-653, doi:10.1093/nar/gkv1227.
3. Apweiler, R.; Bairoch, A.; Wu, C.H.; Barker, W.C.; Boeckmann, B.; Ferro, S.; Gasteiger, E.; Huang, H.; Lopez, R.; Magrane, M., et al. UniProt: the Universal Protein knowledgebase. *Nucleic Acids Res* **2004**, *32*, D115-119, doi:10.1093/nar/gkh131.
4. Nelson, C.E.; Huang, W.; Brewer, L.K.; Nguyen, A.T.; Kane, M.A.; Wilks, A.; Oglesby-Sherrouse, A.G. Proteomic Analysis of the *Pseudomonas aeruginosa* Iron Starvation Response Reveals PrrF Small Regulatory RNA-Dependent Iron Regulation of Twitching Motility, Amino Acid Metabolism, and Zinc Homeostasis Proteins. *J Bacteriol* **2019**, *201*, doi:10.1128/JB.00754-18.
5. Wishart, D.S.; Feunang, Y.D.; Marcu, A.; Guo, A.C.; Liang, K.; Vazquez-Fresno, R.; Sajed, T.; Johnson, D.; Li, C.; Karu, N., et al. HMDB 4.0: the human metabolome database for 2018. *Nucleic Acids Res* **2018**, *46*, D608-D617, doi:10.1093/nar/gkx1089.
6. Ulrich, E.L.; Akutsu, H.; Doreleijers, J.F.; Harano, Y.; Ioannidis, Y.E.; Lin, J.; Livny, M.; Mading, S.; Maziuk, D.; Miller, Z., et al. BioMagResBank. *Nucleic Acids Res* **2008**, *36*, D402-408, doi:10.1093/nar/gkm957.