### Virulence Factors (Iron Acquisition / Secreted Factors / Oxidative Stress)

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**Translation, Post-Translational Modification and Chaperones**

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| AES_1693 | PA0895 | PA14_52720 | N-Succinylglutamate S-Semialdehyde Dehydrogenase | gabD | 1.8451 | 0.0096 | 25 | 47.83 |
| AES_2388 | PA1293 | PA14_47940 | Putative Enzyme | rplA | 1.8103 | 0.0068 | 10 | 32.29 |
| AES_2682 | PA1589 | PA14_43940 | Succinyl-CoA Synthetase Alpha Chain | fabG | 3.3974 | 0.0164 | 9 | 32.39 |
| AES_2706 | PA1609 | PA14_43690 | Beta-Ketoacyl-ACP Synthase I | fabB | 2.4873 | 0.0022 | 14 | 36.05 |
| AES_1056 | PA2605 | PA14_30400 | Putative Sulfur Reductase Protein | yheN | 3.3556 | 0.0006 | 6 | 22.14 |
| AES_4015 | PA2640 | PA14_29980 | NADH Dehydrogenase I Chain E | nuoE | 3.1253 | 0.0169 | 4 | 17.47 |
| AES_4422 | PA2967 | PA14_25660 | 3-Oxoacyl-[Acyl-Carrier Protein] Reductase | fabG | 3.3974 | 0.0164 | 9 | 32.39 |
| AES_3765 | PA4602 | PA14_60890 | Glycine/Serine Hydroxymethyltransferase | glyA3 | 2.4338 | 0.0018 | 13 | 15.35 |
| AES_0239 | PA0143 | PA14_01760 | Non-specific Ribonucleoside Hydrolase | nus | 2.0180 | 0.0061 | 12 | 32.83 |
| AES_0533 | PA0265 | PA14_03430 | Succinate-Semialdehyde Dehydrogenase | gabD | 1.8451 | 0.0096 | 25 | 47.83 |
| AES_0679 | PA0330 | PA14_04310 | Ribose 5-Phosphate Isomerase | rplA | 1.8103 | 0.0068 | 10 | 32.29 |
| AES_0927 | PA0865 | PA14_53070 | 4-Hydroxyphenylpyruvate Dioxygenase | hpd | 1.6770 | 0.0030 | 68 | 56.58 |
| AES_3758 | PA2442 | PA14_33040 | Glycine Cleavage System Protein T2 | gcvT2 | 4.0371 | 0.0088 | 5 | 14.75 |
| AES_4099 | PA2709 | PA14_29110 | Cysteine Synthase A | cysK | 2.1305 | 0.0033 | 5 | 19.75 |
| AES_4399 | PA2952 | PA14_25860 | Electron Transfer Flavoprotein Beta Subunit Putative Electron Transfer Flavoprotein-Ubiquinone Oxidoreductase | etfB | 1.5572 | 0.0059 | 28 | 48.59 |
| AES_4400 | PA2953 | PA14_25840 | Electron Transfer Flavoprotein Beta Subunit | etfB | 1.5572 | 0.0059 | 28 | 48.59 |
| AES_5108 | PA3639 | PA14_17270 | Acetyl-CoA Carboxylase Alpha Subunit | accA | 1.6853 | 0.0001 | 35 | 50.95 |
| AES_5588 | PA4079 | PA14_11130 | Putative Short Chain Dehydrogenase | 1.5061 | 0.0083 | 5 | 20.52 |
| AES_1705 | PA0904 | PA14_52580 | LysC | 2.7753 | 0.0046 | 7 | 10.68 |
| AES_2686 | PA1586 | PA14_44000 | Dihydrolipoamide Succinyltransferase (E2 Subunit) | 1.4973 | 0.0095 | 73 | 50.37 |
| AES_2252 | PA2069 | PA14_37745 | Probable Carbamoyl Transferase | 2.7935 | 0.0001 | 17 | 22.47 |
| AES_4432 | PA2966 | PA14_25670 | Acetyl-CoA Carboxylase Beta Subunit | 2.7753 | 0.0046 | 73 | 50.37 |
| AES_4653 | PA3112 | PA14_23860 | Aspartate Kinase Alpha and Beta Chain | 1.5712 | 0.0067 | 34 | 46.23 |
| AES_1668 | PA14_44000 | PA14_44000 | Dihydrolipoamide Succinyltransferase (E2 Subunit) | 1.4973 | 0.0095 | 73 | 50.37 |
| AES_3828 | PA4785 | PA14_63250 | Putative Acyl-CoA Thiolase | 2.1197 | 0.0000 | 23 | 41.61 |
| AES_1670 | PA5171 | PA14_68330 | Arginine Deiminase | 0.6954 | 0.0383 | 145 | 64.83 |
| AES_1377 | PA14_54640 | PA14_54640 | Probable Enoyl-CoA Hydratase/Isomerase | 0.6004 | 0.0000 | 30 | 46.32 |
| AES_3543 | PA14_35490 | PA14_35490 | Probable Enoyl-CoA Hydratase/Isomerase | 0.6004 | 0.0000 | 30 | 46.32 |
| AES_5105 | PA3636 | PA14_17310 | 2-Dehydro-3-Deoxyphosphoocotenate Aldolase | 0.5370 | 0.0068 | 18 | 17.08 |
| AES_0346 | PA2250 | PA14_21890 | Probable Enoyl-CoA Hydratase/Isomerase | 0.6004 | 0.0000 | 30 | 46.32 |
| AES_0073 | PA3366 | PA14_20560 | Aliphatic Amidase | 0.5070 | 0.0143 | 6 | 8.67 |
| AES_4991 | PA3366 | PA14_12130 | Lipoate Synthase | 0.6308 | 0.0004 | 3 | 5.20 |
| AES_5901 | PA4431 | PA14_57570 | Probable Enoyl-CoA Hydratase/Isomerase | 0.6004 | 0.0000 | 30 | 46.32 |
| AES_1669 | PA5172 | PA14_68340 | Ornithine Carbamoyltransferase | 0.5944 | 0.0002 | 242 | 58.33 |
| AES_1656 | PA5184 | PA14_68480 | Putative Periplasmic Chorismate Mutase | 0.6399 | 0.0032 | 3 | 23.24 |
| AES_6914 | PA5553 | PA14_73230 | Probable Periplasmic Chorismate Mutase | 0.6399 | 0.0032 | 3 | 23.24 |
| AES_0848 | PA0446 | PA14_05820 | Probable Periplasmic Chorismate Mutase | 0.6399 | 0.0032 | 3 | 23.24 |
| AES_0204 | PA0747 | PA14_54620 | Probable Aldehyde Dehydrogenase | 0.5939 | 0.0091 | 6 | 10.81 |
| AES_3906 | PA2540 | PA14_31720 | Probative Lysophospholipase | 0.6377 | 0.0063 | 4 | 9.96 |
| AES_5849 | PA4389 | PA14_57050 | Probable Short-Chain Dehydrogenase | 0.5798 | 0.0029 | 6 | 17.86 |

**Hypothetical proteins**
Proteins were identified by 2-DLC-MS/MS and quantitated by iTRAQ labelling. AES No., PAO1 No. and PA14 No. refer to translated ORF number from AES-1, PAO1 and PA14 genome sequence. No. Pept. refers to number of identified and iTRAQ labeled peptides used to perform quantitation and statistical analysis; Seq. Cov. (%), % of the sequence covered by matching peptides; AES-1R v PA14 (PAO1), n-fold difference

| AES_7165   | -     | -     | Hypothetical Protein | 4.1526 | 0.0308 | 5 | 24.07 | 4.8960 | 0.0013 | 3 | 24.07 |
| AES_0637   | PA0315 | PA14_04100 | Conserved Hypothetical Protein | 1.5228 | 0.0041 | 10 | 36.55 | 2.5466 | 0.0207 | 5 | 36.55 |
| AES_1536   | PA0833 | PA14_53500 | Hypothetical Protein | 1.6175 | 0.0256 | 13 | 46.41 | 3.1256 | 0.0002 | 6 | 41.35 |
| AES_5488   | PA4005 | PA14_12030 | Conserved Hypothetical Protein | 2.3688 | 0.0050 | 5 | 23.73 | 1.6222 | 0.0007 | 5 | 23.73 |
| AES_0883   | PA0460 | PA14_06010 | Conserved Hypothetical Protein | 1.8659 | 0.0063 | 14 | 41.15 | 1.2685 | 0.0447 | 14 | 41.15 |
| AES_6165   | PA4735 | PA14_62650 | Conserved Hypothetical Protein | 1.7217 | 0.0044 | 9 | 6.89 | 1.3444 | 0.0412 | 9 | 6.89 |
| AES_6169   | PA4738 | PA14_62680 | Conserved Hypothetical Protein | 1.5007 | 0.0020 | 27 | 33.85 | 0.7070 | 0.0378 | 16 | 33.85 |
| AES_0680   | PA0329 | PA14_04300 | Conserved Hypothetical Protein | 2.4904 | 0.0004 | 16 | 37.07 |
| AES_3524   | PA2235 | PA14_35690 | Hypothetical Protein | 1.6654 | 0.0272 | 26 | 18.13 |
| AES_5515   | PA4015 | PA14_11910 | (R)-Specific Enoyl-CoA Hydratase | 2.0609 | 0.0000 | 16 | 51.66 |
| AES_5858   | PA4395 | PA14_57130 | Conserved Hypothetical Protein | 1.785 | 0.0089 | 20 | 42.77 |
| AES_3210   | PA4441 | PA14_57690 | Conserved Hypothetical Protein | 2.8918 | 0.0001 | 13 | 47.97 |
| AES_1176   | PA0565 | PA14_07355 | Hypothetical Protein | 0.6567 | 0.0002 | 7 | 18.75 |
| AES_1757   | PA0943 | PA14_52060 | Conserved Hypothetical Protein | 0.5491 | 0.0063 | 6 | 6.30 |
| AES_2192   | PA1216 | PA14_48590 | Conserved Hypothetical Protein | 0.6678 | 0.0038 | 5 | 17.74 |
| AES_3134   | PA1913 | PA14_39790 | Conserved Hypothetical Protein | 0.4476 | 0.0062 | 2 | 10.62 |
| AES_5217   | PA3729 | PA14_16180 | Conserved Hypothetical Protein | 0.6722 | 0.0014 | 16 | 17.49 |
| AES_6297   | PA5494 | PA14_72500 | Conserved Hypothetical Protein | 0.5483 | 0.0004 | 5 | 9.38 | 1.3341 | 0.0121 | 3 | 9.38 |
| -         | -     | PA14_53590 | Hypothetical Protein | 0.1846 | 0.0002 | 3 | 4.49 |
| AES_0804   | PA0418 | PA14_05440 | Hypothetical Protein | 0.6617 | 0.0100 | 3 | 5.94 |
| AES_2373   | PA1324 | PA14_47120 | Hypothetical Protein | 0.5786 | 0.0004 | 9 | 31.18 |
| AES_1751   | PA0938 | PA14_52130 | Hypothetical Protein | 0.6989 | 0.0005 | 17 | 17.65 |
| AES_0226   | PA0141 | PA14_01730 | Conserved Hypothetical Protein | 0.7398 | 0.0084 | 9 | 28.19 |

-Proteins were identified by 2-DLC-MS/MS and quantitated by iTRAQ labelling. AES No., PAO1 No. and PA14 No. refer to translated ORF number from AES-1, PAO1 and PA14 genome sequence. No. Pept. refers to number of identified and iTRAQ labeled peptides used to perform quantitation and statistical analysis; Seq. Cov. (%), % of the sequence covered by matching peptides; AES-1R v PA14 (PAO1), n-fold difference
in abundance in AES-1R compared to PA14 and PAO1. Proteins with a ratio >1.5 (shaded red; p<0.05, shaded light green) or <0.67 (shaded blue; p<0.05), or >1.3 (also shaded red; p<0.01, shaded dark green) or <0.77 (p<0.01; also shaded blue) were considered to be statistically significantly altered in abundance. Proteins meeting the fold change criteria but not the accepted p-values are shaded in yellow. Proteins not meeting the fold criteria but for which acceptable p-values were obtained (providing statistical evidence of a small fold change) are not shaded.