

**Expression analysis of a highly adherent and cytotoxic
small colony variant of *Pseudomonas aeruginosa* isolated from
a cystic fibrosis lung**

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Supplemental material

Table 3. Differential expression of genes in *P. aeruginosa* 20265 SCV, wildtype and revertant during exponential and stationary growth.

Figure 6. Genes of *P. aeruginosa* PAO1 not included in the genome of *P. aeruginosa* 20265 (shown are gene clusters of at least 3 genes).

TABLE 3. Differentially regulated genes¹ in *P. aeruginosa* 20265 SCV, wildtype and revertant during exponential and stationary growth.

Gene Name / GenBank Accession Number ²	Exponential phase			Stationary phase			Protein Name / GenBank definition ²	Confidence class ²	Function ²
	SCV/WT	SCV/REV	WT/REV	SCV/WT	SCV/REV	WT/REV			
PA0039		4.1 (0.2)	2.9 (0.4)			2.2 (0.1)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA0044_ <i>exoT</i>	67.1 (27.0)	4.2 (1.5)	-15.3 (7.7)				exoenzyme T	Class 1	Secreted Factors (toxins, enzymes, alginate)
PA0046		3.6 (0.9)					hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA0047		6.3 (2.1)					hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA0059_ <i>osmC</i>			3.1 (0.4)				osmotically inducible protein OsmC	Class 2	Adaptation, protection
PA0070	-16.7 (2.0)		24.4 (8.1)				hypothetical protein	Class 4	Hypothetical, unclassified, unknown;Membrane proteins
PA0073	-4.7 (0.2)						probable ATP-binding component of ABC transporter	Class 3	Transport of small molecules
PA0075	-11.3 (6.6)		4.7 (2.2)				probable phosphoprotein phosphatase	Class 3	Putative enzymes
PA0076	-25.2 (12.4)						hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA0077	-7.5 (3.2)						hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA0082	-15.4 (7.1)		30.1 (17.7)				hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA0083	-20.6 (3.1)		15.8 (3.8)			8.6 (6.8)	conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA0084	-10.8 (3.7)		5.6 (1.1)				conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA0085	-15.5 (1.9)		30.3 (26.3)				conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA0086	-4.9 (0.7)		4.3 (0.5)				hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA0088	-8.4 (3.9)						hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA0090	-12.5 (4.5)						probable ClpA/B-type chaperone	Class 3	Translation, post-translational modification, degradation
PA0102	2.4 (0.3)	5.4 (0.6)					probable carbonic anhydrase	Class 3	Central intermediary metabolism
PA0126	-4.9 (1.0)						hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA0146				-2.8 (0.8)			conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA0176				-2.2 (0.2)			probable chemotaxis transducer	Class 3	Adaptation, protection;Chemotaxis
PA0187				-2.3 (0.1)		2.3 (0.3)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA0194		-2.8 (0.6)					hypothetical protein	Class 4	Hypothetical, unclassified, unknown;Putative enzymes
PA0316_ <i>serA</i>	3.0 (0.2)						D-3-phosphoglycerate dehydrogenase	Class 2	Amino acid biosynthesis and metabolism
PA0427_ <i>oprM</i>						-2.3 (0.2)	major intrinsic multiple antibiotic resistance efflux outer membrane protein OprM precursor	Class 1	Membrane proteins;Transport of small molecules;Antibiotic resistance and susceptibility
PA0443						2.5 (0.3)	probable transporter	Class 3	Membrane proteins;Transport of small molecules
PA0444				-2.4 (0.2)			N-carbamoyl-beta-alanine amidohydrolase	Class 2	Nucleotide biosynthesis and metabolism
PA0460	4.3 (0.7)		-3.4 (0.3)				hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA0471	-5.1 (0.8)						probable transmembrane sensor	Class 3	Membrane proteins;Transcriptional regulators;Two-component regulatory systems
PA0472	-3.4 (1.0)						probable sigma-70 factor, ECF subfamily	Class 3	Transcriptional regulators
PA0537	-2.6 (0.2)						conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA0538_ <i>dsbB</i>	-24.6 (11.1)		6.2 (1.2)			7.1 (3.6)	disulfide bond formation protein	Class 2	Chaperones & heat shock proteins;Translation, post-translational modification, degradation
PA0563	-5.9 (0.4)		4.8 (1.9)				conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA0567						3.1 (1.1)	conserved hypothetical protein	Class 4	Membrane proteins;Hypothetical, unclassified, unknown
PA0633	-6.2 (2.5)						hypothetical protein	Class 4	Related to phage, transposon, or plasmid
PA0636	-5.4 (1.0)						hypothetical protein	Class 4	Related to phage, transposon, or plasmid
PA0639	-3.0 (0.7)						conserved hypothetical protein	Class 4	Related to phage, transposon, or plasmid
PA0659	-2.1 (0.1)						hypothetical protein	Class 4	Hypothetical, unclassified, unknown;Membrane proteins
PA0733		-2.9 (0.6)					probable pseudouridylylase synthase	Class 3	Transcription, RNA processing and degradation
PA0762_ <i>algU</i>	2.9 (0.6)						sigma factor AlgU	Class 1	Transcriptional regulators
PA0764_ <i>mucB</i>	-2.6 (0.5)		2.7 (0.3)				negative regulator for alginate biosynthesis MucB	Class 1	Cell wall / LPS / capsule;Transcriptional regulators;Secreted Factors (toxins, enzymes, alginate)
PA0795_ <i>prpC</i>						2.1 (0.2)	citrate synthase 2	Class 2	Carbon compound catabolism;Central intermediary metabolism
PA0805		5.5 (2.6)					hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA0833	4.8 (0.2)		-4.1 (0.4)				hypothetical protein	Class 4	Hypothetical, unclassified, unknown;Membrane proteins
PA0853	2.0 (0.1)						probable oxidoreductase	Class 3	Putative enzymes
PA0854_ <i>fumC2</i>			-2.7 (0.1)				fumarate hydratase	Class 2	Carbon compound catabolism;Energy metabolism
PA0867		3.3 (0.3)	2.7 (0.1)				hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA0869_ <i>pbpG</i>	-3.2 (0.3)						D-alanyl-D-alanine-endopeptidase	Class 1	Cell wall / LPS / capsule
PA0887_ <i>acsA</i>				10.0 (1.8)		-11.1 (2.1)	acetyl-coenzyme A synthetase	Class 2	Carbon compound catabolism;Central intermediary metabolism
PA0968	-2.4 (0.3)						conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1001_ <i>phnA</i>				-2.4 (0.3)			anthranilate synthase component I	Class 1	Adaptation, protection
PA1076		4.5 (2.9)					hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1079_ <i>flgD</i>						-2.9 (0.5)	flagellar basal-body rod modification protein FlgD	Class 2	Motility & Attachment;Cell wall / LPS / capsule
PA1080_ <i>flgE</i>		-5.5 (1.6)					flagellar hook protein FlgE	Class 2	Motility & Attachment;Cell wall / LPS / capsule
PA1082_ <i>flgG</i>		-4.4 (1.4)					flagellar basal-body rod protein FlgG	Class 2	Motility & Attachment;Cell wall / LPS / capsule
PA1095_ <i>flgJ</i>		-4.2 (0.8)					flagellar protein FlgJ	Class 2	Motility & Attachment;Cell wall / LPS / capsule
PA1096_ <i>flaS</i>						-2.6 (0.3)	two-component sensor	Class 1	Two-component regulatory systems
PA1099_ <i>flaR</i>						-2.5 (0.3)	two-component response regulator	Class 1	Transcriptional regulators;Two-component regulatory systems;Motility & Attachment
PA1101_ <i>flaF</i>		-5.2 (2.9)					flagellar M-ring outer membrane protein precursor	Class 1	Motility & Attachment;Cell wall / LPS / capsule
PA1137						-5.0 (2.9)	probable oxidoreductase	Class 3	Putative enzymes
PA1155_ <i>nrdB</i>				-2.4 (0.5)			ribonucleoside reductase, small chain	Class 2	Nucleotide biosynthesis and metabolism
PA1200	-3.4 (0.4)						conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1202	-9.6 (1.2)		9.7 (2.7)	-5.8 (2.2)		4.5 (0.5)	probable hydrolase	Class 3	Putative enzymes
PA1245				-5.4 (1.1)		4.2 (0.5)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown;Membrane proteins
PA1248_ <i>aprF</i>				-4.0 (2.1)			alkaline protease secretion protein AprF	Class 1	Protein secretion/export apparatus;Secreted Factors (toxins, enzymes, alginate)
PA1441		-3.6 (0.7)					hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1467	-3.2 (0.9)						hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1471				-3.0 (0.5)			hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1474						-3.9 (2.2)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1494	-3.6 (0.7)			-3.0 (0.6)		2.9 (0.4)	conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1545						-3.8 (1.4)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown

Gene Name / GenBank Accession Number ²	Exponential phase			Stationary phase			Protein Name / GenBank definition ²	Confidence class ²	Function ²
	SCV/WT	SCV/REV	WT/REV	SCV/WT	SCV/REV	WT/REV			
PA1546_hemN	2.7 (0.3)						oxygen-independent coproporphyrinogen III oxidase	Class 1	Biosynthesis of cofactors, prosthetic groups and carriers
PA1571	2.5 (0.2)	3.8 (0.5)					hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1589_sucD	2.3 (0.2)						succinyl-CoA synthetase alpha chain	Class 2	Energy metabolism
PA1592_i				-3.1 (1.1)			hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1597		5.4 (3.7)					hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1624						-2.5 (0.1)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1673	2.7 (0.7)						hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1692	9.6 (1.2)	3.4 (0.9)					probable translocation protein in type III secretion	Class 3	Protein secretion/export apparatus
PA1694_pscQ	57.1 (46.1)	3.8 (1.0)	-20.9 (19.2)				translocation protein in type III secretion	Class 2	Protein secretion/export apparatus
PA1695_pscP	7.1 (2.5)	2.6 (0.3)	-2.7 (0.9)				translocation protein in type III secretion	Class 2	Protein secretion/export apparatus
PA1696_pscO	40.1 (1.4)	4.2 (0.6)	-10.2 (2.2)				translocation protein in type III secretion	Class 2	Protein secretion/export apparatus
PA1697	10.6 (1.0)	3.4 (0.8)	-3.0 (0.5)				ATP synthase in type III secretion system	Class 2	Protein secretion/export apparatus
PA1699_popN	29.9 (16.1)	5.2 (1.0)	-6.0 (2.6)				outer membrane protein PopN	Class 1	Membrane proteins;Protein secretion/export apparatus
PA1699	79.4 (20.4)	4.7 (0.7)	-16.2 (7.6)				conserved hypothetical protein in type III secretion	Class 4	Hypothetical, unclassified, unknown;Protein secretion/export apparatus
PA1700	36.9 (13.6)	5.2 (1.7)	-7.2 (6.0)				conserved hypothetical protein in type III secretion	Class 4	Hypothetical, unclassified, unknown;Protein secretion/export apparatus
PA1701	34.9 (10.3)	4.9 (1.6)	-7.9 (3.4)				conserved hypothetical protein in type III secretion	Class 4	Hypothetical, unclassified, unknown;Protein secretion/export apparatus
PA1702	43.0 (2.8)	7.0 (1.7)					type III secretory apparatus protein PcrD	Class 1	Protein secretion/export apparatus
PA1703_pcrD	7.7 (1.1)	3.3 (0.6)					transcriptional regulator protein PcrR	Class 1	Transcriptional regulators
PA1704_pcrR	28.1 (4.5)	4.5 (0.6)					regulator in type III secretion	Class 1	Protein secretion/export apparatus
PA1705_pcrG	5.9 (2.5)						type III secretion protein PcrV	Class 1	Protein secretion/export apparatus
PA1706_pcrV	268.2 (173.3)	4.3 (1.0)	-54.7 (55.8)	26.0 (8.2)		-8.8 (3.4)	regulatory protein PcrH	Class 1	Protein secretion/export apparatus;Secreted Factors (toxins, enzymes, alginate)
PA1707_pcrH	42.7 (7.0)	4.2 (1.0)	-12.6 (3.0)	9.6 (5.4)			translocator protein PopB	Class 1	Protein secretion/export apparatus
PA1708_popB	137.7 (33.4)	3.4 (0.8)	-37.0 (10.7)	7.5 (1.3)		-4.2 (0.4)	translocator protein PopD	Class 1	Protein secretion/export apparatus
PA1709_popD	60.9 (4.0)	4.6 (1.1)	-12.0 (3.1)				exoenzyme S synthesis protein C precursor	Class 1	Protein secretion/export apparatus;Translation, post-translational modification, degradation
PA1710_exsC	13.1 (2.1)	4.0 (1.5)	-3.3 (0.6)	8.5 (1.5)		-5.6 (1.0)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1711	11.3 (0.6)	3.2 (0.8)	-3.5 (0.7)	8.2 (0.9)		-5.0 (0.9)	exoenzyme S synthesis protein B	Class 1	Protein secretion/export apparatus;Translation, post-translational modification, degradation
PA1712_exsB	5.3 (0.5)	2.8 (0.3)		8.2 (3.4)			hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1714	14.9 (0.0)	4.9 (1.1)	-3.4 (0.6)				type III export apparatus protein	Class 1	Protein secretion/export apparatus
PA1715_pscB	45.7 (7.3)	5.6 (1.0)	-13.2 (3.0)				type III secretion protein PscC	Class 1	Protein secretion/export apparatus
PA1716_pscC	9.0 (1.6)	3.2 (0.6)					type III export protein PscD	Class 1	Protein secretion/export apparatus
PA1717_pscD	24.2 (12.0)	5.6 (0.2)	-3.9 (0.9)				type III export protein PscE	Class 1	Protein secretion/export apparatus
PA1718_pscE	33.2 (2.2)	4.0 (0.2)	-8.5 (0.9)				type III export protein PscF	Class 1	Protein secretion/export apparatus
PA1719_pscF	42.3 (27.7)	3.6 (0.9)	-15.3 (11.0)				type III export protein PscG	Class 2	Protein secretion/export apparatus
PA1720_pscG	21.1 (6.0)	6.0 (0.6)					type III export protein PscH	Class 1	Protein secretion/export apparatus
PA1721_pscH	9.9 (2.4)	4.5 (1.1)					type III export protein PscI	Class 1	Protein secretion/export apparatus
PA1722_pscI	11.5 (3.4)	3.9 (0.9)	-3.9 (1.0)				type III export protein PscJ	Class 1	Protein secretion/export apparatus
PA1723_pscJ	4.9 (0.7)	3.8 (0.3)					type III export protein PscK	Class 1	Protein secretion/export apparatus
PA1724_pscK	6.4 (1.4)	3.5 (0.8)					type III export protein PscL	Class 1	Protein secretion/export apparatus
PA1725_pscL	12.3 (4.3)	4.0 (0.7)					conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1730				-3.0 (0.5)		2.4 (0.3)	conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1731				-2.2 (0.2)			conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1732						2.2 (0.2)	conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1733				-2.5 (0.3)		2.6 (0.1)	conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1762	-2.5 (0.4)			-2.8 (0.9)			probable serine/threonine-protein kinase	Class 3	Adaptation, protection
PA1842	4.1 (0.9)						hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1852		4.5 (1.3)				2.8 (0.2)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1862_modB	9.7 (2.0)	4.3 (0.7)					molybdenum transport protein ModB	Class 2	Transport of small molecules
PA1863_modA	5.5 (0.8)	6.3 (3.1)					molybdate-binding periplasmic protein precursor ModA	Class 2	Transport of small molecules
PA1871_lasA				-2.3 (0.4)			LasA protease precursor	Class 1	Translation, post-translational modification, degradation;Secreted Factors (toxins, enzymes, alginate)
PA1901_phzC2				-9.1 (5.9)		8.9 (5.5)	phenazine biosynthesis protein PhzC	Class 1	Secreted Factors (toxins, enzymes, alginate)
PA1924							hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1967				-4.5 (1.3)	-3.7 (1.3)		hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA1984		-4.1 (1.7)	-10.5 (7.7)	8.7 (1.7)		-9.8 (1.5)	probable aldehyde dehydrogenase	Class 3	Putative enzymes
PA1999				-8.7 (0.8)		-8.3 (1.1)	probable CoA transferase, subunit A	Class 3	Amino acid biosynthesis and metabolism;Carbon compound catabolism
PA2000				-6.3 (1.0)		-4.4 (0.9)	probable CoA transferase, subunit B	Class 3	Amino acid biosynthesis and metabolism;Carbon compound catabolism
PA2001_atoB				-4.4 (0.9)		-3.9 (0.9)	acetyl-CoA acetyltransferase	Class 2	Central intermediary metabolism;Fatty acid and phospholipid metabolism
PA2003_bdhA				-3.9 (0.9)		16.7 (8.0)	3-hydroxybutyrate dehydrogenase	Class 2	Carbon compound catabolism
PA2025_gor				-4.4 (0.8)		4.5 (0.7)	glutathione reductase	Class 1	Biosynthesis of cofactors, prosthetic groups and carriers;Amino acid biosynthesis and metabolism
PA2027				-3.9 (0.9)			hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA2047	-7.2 (3.3)						probable transcriptional regulator	Class 3	Transcriptional regulators
PA2069				-2.1 (0.0)			probable carbamoyl transferase	Class 3	Putative enzymes
PA2166	-3.2 (0.4)		3.1 (0.5)				hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA2191_exoY	31.7 (10.6)	6.8 (2.7)				3.5 (1.0)	adenylate cyclase ExoY	Class 1	Secreted Factors (toxins, enzymes, alginate)
PA2193_hcnA							hydrogen cyanide synthase HcnA	Class 2	Central intermediary metabolism
PA2204		-2.2 (0.3)					probable binding protein component of ABC transporter	Class 3	Transport of small molecules
PA2233				-3.0 (0.6)			probable glycosyl transferase	Class 3	Putative enzymes
PA2235				-12.0 (1.5)			hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA2247_bkdA1				-3.2 (1.2)		5.3 (2.3)	2-oxoisovalerate dehydrogenase (alpha subunit)	Class 2	Amino acid biosynthesis and metabolism
PA2248_bkdA2				-3.8 (0.7)		4.0 (0.7)	2-oxoisovalerate dehydrogenase (beta subunit)	Class 2	Amino acid biosynthesis and metabolism
PA2249_bkdB				-6.8 (4.7)			branched-chain alpha-keto acid dehydrogenase (lipoamide component)	Class 2	Amino acid biosynthesis and metabolism
PA2259_ptxS	2.3 (0.1)						transcriptional regulator PtxS	Class 1	Transcriptional regulators;Secreted Factors (toxins, enzymes, alginate)
PA2270	-3.1 (0.5)						probable transcriptional regulator	Class 3	Transcriptional regulators
PA2300_chic						3.3 (0.6)	chitinase	Class 2	Carbon compound catabolism

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	SCV/WT	SCV/REV	WT/REV	SCV/WT	SCV/REV	WT/REV			
PA2304	-6.0 (3.6)						hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA2305				-6.4 (4.9)			probable non-ribosomal peptide synthetase	Class 3	Putative enzymes
PA2384				-4.3 (0.4)		4.9 (0.8)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA2386_pvdA				-8.4 (5.8)		3.5 (1.1)	L-ornithine N5-oxygenase	Class 1	Adaptation, protection
PA2390	-10.4 (4.5)						probable ATP-binding/permease fusion ABC transporter	Class 3	Membrane proteins;Transport of small molecules
PA2398_fpvA				-2.4 (0.5)		2.6 (0.3)	ferripyoverdine receptor	Class 1	Transport of small molecules
PA2407						2.1 (0.1)	probable adhesion protein	Class 3	Motility & Attachment
PA2408				-9.1 (2.2)			probable ATP-binding component of ABC transporter	Class 3	Transport of small molecules
PA2409				-9.2 (5.9)			probable permease of ABC transporter	Class 3	Membrane proteins;Transport of small molecules
PA2411				-9.4 (4.6)			probable thioesterase	Class 3	Adaptation, protection;Putative enzymes
PA2412				-2.8 (0.3)		3.9 (1.0)	conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA2413				-4.9 (3.4)			probable class III aminotransferase	Class 3	Putative enzymes
PA2422						-3.1 (0.4)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA2424_pvdL						15.2 (8.8)	hypothetical protein	Class 1	Adaptation, protection
PA2432						4.6 (2.4)	PvdL	Class 3	Transcriptional regulators
PA2433	-21.6 (12.5)		16.1 (12.4)				probable transcriptional regulator	Class 4	Hypothetical, unclassified, unknown
PA2441	-3.4 (0.4)						hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA2442_gcvT2	5.0 (1.2)	15.4 (6.2)					hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA2450	-3.6 (1.2)						glycine cleavage system protein T2	Class 2	Amino acid biosynthesis and metabolism;Central intermediary metabolism
PA2450	-3.3 (1.0)						hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA2475	-18.3 (0.6)						probable cytochrome P450	Class 3	Adaptation, protection;Putative enzymes
PA2476_dsbG	-58.9 (5.0)		56.0 (6.3)	-11.7 (1.1)		11.4 (1.8)	thiol:disulfide interchange protein DsbG	Class 2	Chaperones & heat shock proteins;Translation, post-translational modification, degradation
PA2477	-41.1 (5.6)		132.8 (49.2)	-14.6 (11.7)		37.0 (12.3)	probable thiol:disulfide interchange protein	Class 3	Putative enzymes;Membrane proteins
PA2478	-111.7 (38.2)		217.0 (56.1)	-49.6 (5.2)		50.6 (22.9)	probable thiol:disulfide interchange protein	Class 3	Putative enzymes;Membrane proteins
PA2479	-13.9 (4.0)		9.2 (3.3)	-6.9 (1.7)		6.5 (2.0)	probable two-component response regulator	Class 3	Transcriptional regulators;Two-component regulatory systems
PA2480	-18.8 (4.8)		82.5 (52.3)	-3.8 (0.9)		6.5 (1.1)	probable two-component sensor	Class 3	Two-component regulatory systems
PA2506	-82.0 (9.8)		34.0 (9.1)	-18.6 (3.1)		15.6 (2.6)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA2537	-13.4 (6.7)						probable acyltransferase	Class 3	Fatty acid and phospholipid metabolism
PA2538	-7.5 (0.4)		2.8 (0.5)				hypothetical protein	Class 4	Hypothetical, unclassified, unknown;Membrane proteins
PA2540	-5.1 (1.8)						conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA2580	-3.9 (1.3)						conserved hypothetical protein	Class 4	Putative enzymes
PA2684	-4.4 (0.3)						conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA2694	-4.3 (0.8)						probable thioredoxin	Class 3	Energy metabolism
PA2711	-3.0 (0.3)						probable periplasmic spermidine/putrescine-binding protein	Class 3	Transport of small molecules
PA2747		5.1 (2.4)	3.7 (1.4)	4.4 (0.8)		-2.7 (0.1)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA2755_eco	-4.5 (1.1)		4.1 (0.1)				ecotin precursor	Class 2	Translation, post-translational modification, degradation
PA2780	-12.6 (6.8)		21.3 (13.7)	-23.6 (11.5)		85.3 (22.7)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA2781	-26.6 (9.4)		49.1 (49.9)	-14.3 (4.0)		22.9 (13.5)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA2805		4.2 (0.6)					hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA2827		3.4 (0.4)					conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA2853_oprI						2.3 (0.1)	outer membrane lipoprotein OprI precursor	Class 1	Membrane proteins
PA2883		4.4 (0.7)					hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3021			3.2 (1.3)				hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3031							hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3038						-3.2 (1.0)	probable porin	Class 3	Transport of small molecules
PA3049_rmf		6.7 (2.6)					ribosome modulation factor	Class 2	Translation, post-translational modification, degradation
PA3126_lbpA		5.3 (1.8)					heat-shock protein lbpA	Class 2	Chaperones & heat shock proteins
PA3161_himD		2.5 (0.1)					integration host factor beta subunit	Class 1	DNA replication, recombination, modification and repair;Transcription, RNA processing and degradation;Translation, post-translational modification, degradation
PA3205						2.9 (0.7)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3214		2.4 (0.3)					hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3234				-4.1 (2.0)			probable sodium:solute symporter	Class 3	Membrane proteins;Transport of small molecules
PA3235				-17.8 (9.5)			conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown;Membrane proteins
PA3245_minE		2.5 (0.3)					cell division topological specificity factor MinE	Class 2	Cell division
PA3250						2.2 (0.1)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3274						2.7 (0.4)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3286		3.0 (0.5)					hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3307	4.1 (0.1)	-2.4 (0.4)					hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3329						11.4 (8.7)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3330				-7.4 (6.1)			probable short chain dehydrogenase	Class 3	Putative enzymes
PA3331				-3.1 (0.6)		7.6 (1.6)	cytochrome P450	Class 2	Adaptation, protection;Carbon compound catabolism
PA3332						3.2 (0.8)	conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3369				6.5 (0.4)		-4.9 (0.3)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown;Membrane proteins
PA3370				4.5 (0.6)		-4.0 (0.2)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown;Membrane proteins
PA3371				-3.1 (0.2)			hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3407_hasAp				-8.2 (4.6)		6.0 (2.0)	heme acquisition protein HasAp	Class 1	Transport of small molecules
PA3445			-4.5 (1.9)				conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3517		-5.4 (2.7)					probable lyase	Class 3	Carbon compound catabolism
PA3530			10.8 (6.1)				conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3531_bfrB			-3.5 (0.6)				bacterioferritin	Class 2	Transport of small molecules;Adaptation, protection
PA3552	4.5 (1.3)						conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3611	-2.6 (0.5)						hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3631	-4.2 (0.6)						conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3662		-2.3 (0.2)					hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3691		-3.0 (0.5)					hypothetical protein	Class 4	Hypothetical, unclassified, unknown
		-2.0 (0.1)					hypothetical protein	Class 4	Hypothetical, unclassified, unknown

Gene Name / GenBank Accession Number ²	Exponential phase			Stationary phase			Protein Name / GenBank definition ²	Confidence class ²	Function ²
	SCV/WT	SCV/REV	WT/REV	SCV/WT	SCV/REV	WT/REV			
PA3716	-2.7 (0.3)						hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3720						-10.0 (6.3)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3729	-5.6 (1.3)		3.1 (0.6)				conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3779						-5.3 (2.9)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3790_oprC	25.8 (11.3)	9.6 (7.5)					putative copper transport outer membrane porin OprC precursor	Class 1	Transport of small molecules
PA3813_iscU		-2.2 (0.2)					probable iron-binding protein IscU	Class 3	Biosynthesis of cofactors, prosthetic groups and carriers
PA3819	4.0 (0.0)	2.3 (0.2)					conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown;Membrane proteins
PA3841_exoS	90.6 (33.3)	3.9 (0.8)	-22.2 (11.2)	5.5 (1.9)			exoenzyme S	Class 1	Secreted Factors (toxins, enzymes, alginate)
PA3842	29.6 (11.6)	3.2 (0.8)	-8.6 (3.8)				probable chaperone	Class 3	Chaperones & heat shock proteins;Secreted Factors (toxins, enzymes, alginate)
PA3843	65.4 (6.4)	4.2 (0.9)	-16.8 (3.5)				hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3901_fecA	-22.2 (12.0)						Fe(III) dicitrate transport protein FecA	Class 2	Membrane proteins;Transport of small molecules
PA3931			-3.8 (1.7)				conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA3989_holA						-8.5 (2.7)	DNA polymerase III, delta subunit	Class 2	DNA replication, recombination, modification and repair
PA4031_ppa						-3.3 (1.2)	inorganic pyrophosphatase	Class 2	Central intermediary metabolism
PA4110_ampC			-4.6 (1.8)			2.8 (0.6)	beta-lactamase precursor	Class 1	Adaptation, protection
PA4139	16.2 (14.1)	11.9 (5.4)					hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA4148						-20.5 (2.8)	probable short-chain dehydrogenase	Class 3	Putative enzymes
PA4195			-2.8 (0.6)			21.8 (4.4)	probable binding protein component of ABC transporter	Class 3	Transport of small molecules
PA4217_phzS						-6.5 (1.9)	flavin-containing monooxygenase	Class 1	Putative enzymes
PA4218	19.0 (15.8)		-12.3 (7.2)				probable transporter	Class 3	Membrane proteins;Transport of small molecules
PA4220	21.3 (3.1)						hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA4221_fptA	15.1 (2.6)		-11.0 (1.0)			-17.7 (15.7)	Fe(III)-pyochelin receptor precursor	Class 1	Transport of small molecules
PA4223	5.6 (0.7)		-4.1 (0.8)			-2.9 (0.5)	probable ATP-binding component of ABC transporter	Class 3	Membrane proteins;Transport of small molecules
PA4224	3.9 (1.0)		-3.4 (0.9)			-4.1 (1.5)	pyochelin biosynthetic protein PchG	Class 1	Membrane proteins;Transport of small molecules
PA4225_pchF	37.0 (5.5)		-36.7 (20.2)				pyochelin synthetase	Class 1	Transport of small molecules;Secreted Factors (toxins, enzymes, alginate)
PA4226_pchE	37.4 (11.1)		-40.5 (16.9)				dihydroaeruginic acid synthetase	Class 1	Transport of small molecules;Secreted Factors (toxins, enzymes, alginate)
PA4228_pchD	14.2 (13.6)		-17.4 (16.7)				pyochelin biosynthesis protein PchD	Class 1	Transport of small molecules;Secreted Factors (toxins, enzymes, alginate)
PA4229_pchC	34.2 (6.5)		-40.0 (17.3)			-4.4 (0.9)	pyochelin biosynthetic protein PchC	Class 1	Transport of small molecules;Secreted Factors (toxins, enzymes, alginate)
PA4230_pchB	24.3 (1.9)		-28.3 (8.4)				salicylate biosynthesis protein PchB	Class 1	Transport of small molecules;Secreted Factors (toxins, enzymes, alginate)
PA4231_pchA	5.8 (0.4)						salicylate biosynthesis isochorismate synthase	Class 1	Secreted Factors (toxins, enzymes, alginate);Transport of small molecules
PA4290						-4.6 (2.0)	probable chemotaxis transducer	Class 3	Adaptation, protection;Chemotaxis
PA4309_pctA						-14.2 (10.7)	chemotactic transducer PctA	Class 1	Adaptation, protection;Chemotaxis
PA4317	-56.5 (28.1)		15.2 (9.5)				hypothetical protein	Class 4	Hypothetical, unclassified, unknown;Membrane proteins
PA4323	-2.2 (0.3)						hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA4326						-2.4 (0.1)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA4370_icmP	-2.7 (0.4)						Insulin-cleaving metalloproteinase	Class 1	Membrane proteins
PA4389	2.4 (0.2)	2.2 (0.3)					probable short-chain dehydrogenase	Class 3	Putative enzymes
PA4469						-2.4 (0.2)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA4470_fumC1						2.4 (0.2)	fumarate hydratase	Class 1	Energy metabolism
PA4471						-2.4 (0.3)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA4482_gatC		-2.7 (0.4)					Glu-tRNA(Gln) amidotransferase subunit C	Class 2	Translation, post-translational modification, degradation
PA4489	-2.8 (0.6)						conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA4490	-5.2 (0.8)						conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA4491	-5.5 (1.2)						conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA4495	-3.2 (0.6)					2.2 (0.1)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA4501						-4.3 (1.9)	probable porin	Class 3	Transport of small molecules
PA4513	-4.2 (0.4)						probable oxidoreductase	Class 3	Putative enzymes
PA4515	-3.2 (0.4)						conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA4523						-2.6 (0.5)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA4563_rpsT						2.8 (0.5)	30S ribosomal protein S20	Class 2	Translation, post-translational modification, degradation;Central intermediary metabolism
PA4570	-2.5 (0.3)					-4.4 (0.5)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA4607						-2.7 (0.7)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA4611	2.6 (1.0)	4.7 (2.9)				2.8 (0.3)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA4624			5.7 (1.8)				hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA4625		3.6 (0.9)					hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA4633						-6.1 (4.6)	probable chemotaxis transducer	Class 3	Adaptation, protection;Chemotaxis
PA4674		5.1 (2.4)					conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA4675	-2.3 (0.1)						probable TonB-dependent receptor	Class 3	Transport of small molecules
PA4764_fur		2.7 (0.4)					ferric uptake regulation protein	Class 1	Transcriptional regulators
PA4803	-9.4 (2.4)		14.9 (0.8)			-8.5 (1.6)	hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA4826			13.7 (0.5)				hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA4843		-5.4 (1.2)				-2.8 (0.4)	probable two-component response regulator	Class 3	Transcriptional regulators;Two-component regulatory systems
PA4847_accB						-2.6 (0.5)	biotin carboxyl carrier protein (BCCP)	Class 1	Fatty acid and phospholipid metabolism
PA4893_ureG						-2.5 (0.4)	urease accessory protein UreG	Class 2	Biosynthesis of cofactors, prosthetic groups and carriers
PA4909						-5.9 (1.8)	probable ATP-binding component of ABC transporter	Class 3	Transport of small molecules
PA5015_aceE						-2.4 (0.4)	pyruvate dehydrogenase	Class 1	Amino acid biosynthesis and metabolism;Energy metabolism
PA5016_aceF						2.3 (0.3)	dihydropyrimidinase	Class 1	Carbon compound catabolism;Energy metabolism
PA5061						-4.2 (1.3)	conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA5073	-2.5 (0.4)						hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA5095	-2.9 (0.7)						probable permease of ABC transporter	Class 3	Membrane proteins;Transport of small molecules
PA5113	-5.1 (1.6)		4.1 (0.8)				hypothetical protein	Class 4	Hypothetical, unclassified, unknown;Membrane proteins
PA5163_rmlA						-3.2 (0.4)	glucose-1-phosphate thymidyltransferase	Class 2	Cell wall / LPS / capsule
PA5174	2.2 (0.2)						probable beta-ketoacyl synthase	Class 3	Fatty acid and phospholipid metabolism
PA5178						-3.3 (0.5)	conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA5217			2.7 (0.4)			2.6 (0.3)	probable binding protein component of ABC iron transporter	Class 3	Transport of small molecules

Gene Name / GenBank Accession Number ²	Exponential phase			Stationary phase			Protein Name / GenBank definition ²	Confidence class ²	Function ²
	SCV/WT	SCV/REV	WT/REV	SCV/WT	SCV/REV	WT/REV			
PA5222							hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA5240_trxA	2.3 (0.1)	3.1 (0.7)					thioredoxin	Class 2	Nucleotide biosynthesis and metabolism; Translation, post-translational modification
PA5274_rnk							nucleoside diphosphate kinase regulator	Class 2	Transcriptional regulators
PA5287_amtB							ammonium transporter AmtB	Class 2	Membrane proteins; Transport of small molecules
PA5304_dadA							D-amino acid dehydrogenase, small subunit	Class 2	Amino acid biosynthesis and metabolism; Energy metabolism
PA5313							probable pyridoxal-dependent aminotransferase	Class 3	Putative enzymes
PA5316_rpmB							50S ribosomal protein L28	Class 2	Translation, post-translational modification, degradation
PA5317							probable binding protein component of ABC dipeptide transporter	Class 3	Transport of small molecules
PA5339	2.5 (0.4)						conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA5355_glcD	-6.5 (7.1)						glycolate oxidase subunit GlcD	Class 2	Central intermediary metabolism; Carbon compound catabolism
PA5424							conserved hypothetical protein	Class 4	Hypothetical, unclassified, unknown; Membrane proteins
PA5429_aspA							aspartate ammonia-lyase	Class 2	Amino acid biosynthesis and metabolism
PA5461	3.1 (0.7)	2.7 (0.3)					hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA5470							probable peptide chain release factor	Class 3	Translation, post-translational modification, degradation
PA5481	-2.9 (0.7)						hypothetical protein	Class 4	Hypothetical, unclassified, unknown
PA5482							TonB protein	Class 4	Hypothetical, unclassified, unknown; Membrane proteins
PA5531_tonB	-3.8 (0.1)						type IV pilin	Class 1	Transport of small molecules
L37109_pilA	7.5 (4.4)						type IV pilin	ND	Motility & Attachment; Cell wall / LPS / capsule
L81176_cds3_fliD	-3.0 (0.3)	-4.0 (0.5)					flagellar cap protein	ND	Motility & Attachment; Cell wall / LPS / capsule
L81176_cds5_fliS'		-2.8 (0.5)					hypothetical protein	ND	Motility & Attachment; Cell wall / LPS / capsule
L81176_cds6_fliP		-3.1 (0.6)					type IV pili length control protein	ND	Motility & Attachment; Cell wall / LPS / capsule
M57501_fliA_fliC	-6.2 (1.0)	-13.6 (2.0)	-2.4 (0.2)				flagellin type a	ND	Motility & Attachment; Cell wall / LPS / capsule
AF332547_orfB	-2.4 (0.3)	-3.7 (0.4)					putative acyl carrier protein – flagellin glycosylation	ND	Motility & Attachment; Cell wall / LPS / capsule
AF332547_orfC		-3.0 (0.5)					putative 3-oxoacyl (acyl carrier protein) synthase – flagellin glycosylation	ND	Motility & Attachment; Cell wall / LPS / capsule
AF332547_orfF		-3.2 (0.2)					large subunit aromatic dioxygenase – flagellin glycosylation	ND	Motility & Attachment; Cell wall / LPS / capsule
ig_5130767_5131427							Intergenic region between PA4639 and PA4640, 5130767-5131427, (+) strand		
ig_727608_721556	2.8 (0.4)	2.7 (0.3)					Intergenic region between PA0701 and PA0702, 721556-727608, (-) strand		

¹ For all genes with a significant differential expression (Wilcoxon Rank Test of Affymetrix Microarray Suite Software) in a magnitude of at least 2 fold in all 4 pairings of each comparison, the arithmetic average and the SD were calculated. Upregulated genes have positive values, downregulated genes are given as negative values.

[†] Gene annotations imposed on the 8/10/2003 by the *P. aeruginosa* Sequencing and Community Annotation Project (<http://www.pseudomonas.com>) (1). For non-PAO 1 genes the GenBank entries are given, genes of the flagella apparatus are annotated as proposed by Dasgupta *et al.* (2003).

1. Stover, C. K., X. Q. Pham, A. L. Erwin, S. D. Mizoguchi, P. Warren, M. J. Hickey, F. S. Brinkman, W. O. Hufnagle, D. J. Kowalik, M. Lagrou, R. L. Garber, L. Goltry, E. Tolentino, S. Westbrook-Wadman, Y. Yuan, L. L. Brody, S. N. Coulter, K. R. Folger, A. Kas, K. Larbig, R. Lim, K. Smith, D. Spencer, G. K. Wong, Z. Wu, I. T. Paulsen, J. Reizer, M. H. Saier, R. E. Hancock, S. Lory, and M. V. Olson. 2000. Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen. *Nature* 406:959-964.

2. Dasgupta, N., M. C. Wolfgang, A. L. Goodman, S. K. Arora, J. Jyot, S. Lory, and R. Ramphal. 2003. A four-tiered transcriptional regulatory circuit controls flagellar biogenesis in *Pseudomonas aeruginosa*. *Molecular Microbiology* 50:809-824.

FIGURE 6. Genes of *P. aeruginosa* PAO1 not included in the genome of *P. aeruginosa* 20265 (shown are gene clusters of at least 3 genes).

