

Table S1. Genes whose transcription is controlled by HHQ, PQS and/or PqsE

PA number ^a	Gene name ^a	HHQ ^b	PQS ^c	PqsE ^d	Product name ^a
PA0051	<i>phzH</i>			3.2	Potential phenazine-modifying enzyme
PA0083	<i>tssB1</i>			-5.1	TssB1
PA0084	<i>tssC1</i>			-3.5	TssC1
<u>PA0129</u>	<i>bauD</i>		-5.5		Amino acid permease
<u>PA0130</u>	<i>bauC</i>		-5.5		3-oxopropanoate dehydrogenase
<u>PA0131</u>	<i>bauB</i>		-7.5		BauB
<u>PA0132</u>	<i>bauA</i>		-6.9		Beta-alanine:pyruvate transaminase
PA0187 [‡]				6.0	Hypothetical protein
PA0243 [‡]				3.2	Probable transcriptional regulator
<u>PA0263</u>	<i>hcpC</i>		-4.3		Secreted protein Hcp
PA0269 [‡]				3.3	Conserved hypothetical protein
PA0270 [‡]				2.8	Hypothetical protein
PA0271 [‡]				3.4	Hypothetical protein
PA0298	<i>spuB</i>			-2.8	Glutamylpolyamine synthetase
PA0299	<i>spuC</i>			-2.6	Polyamine:pyruvate transaminase
PA0303	<i>spuG</i>			-2.8	Polyamine transport protein PotH
PA0328	<i>aaaA</i>			-3.7	arginine-specific autotransporter, AaaA
<u>PA0423</u>	<i>pasP</i>		2.5		PasP
PA0431				2.7	Hypothetical protein
PA0432	<i>sahH</i>			2.9	S-adenosyl-L-homocysteine hydrolase
PA0471	<i>fiuR</i>		2.7		FiuR
PA0472	<i>fiuI</i>		2.5		FiuI
PA0480 [‡]				2.7	Probable hydrolase
<u>PA0509</u>	<i>nirN</i>		-16.0	-16.0	NirN
<u>PA0510</u>	<i>nirE</i>		-18.8	-13.1	NirE
<u>PA0511</u>	<i>nirJ</i>		-50.3	-22.1	Heme <i>d1</i> biosynthesis protein NirJ
<u>PA0512</u>	<i>nirH</i>		-22.4	-14.4	NirH
<u>PA0513</u>	<i>nirG</i>		-17.2	-13.5	NirG
<u>PA0514</u>	<i>nirL</i>		-27.2	-16.1	Heme <i>d1</i> biosynthesis protein NirL
<u>PA0515</u>	<i>nirD</i>		-75.3	-26.8	Probable transcriptional regulator
<u>PA0516</u>	<i>nirF</i>		-27.3	-12.8	Heme <i>d1</i> biosynthesis protein NirF
<u>PA0517</u>	<i>nirC</i>		-87.7	-21.5	Probable <i>c</i> -type cytochrome precursor
<u>PA0518</u>	<i>nirM</i>		-109.9	-28.6	Cytochrome <i>c551</i> precursor
<u>PA0519</u>	<i>nirS</i>		-101.2	-41.9	Nitrite reductase precursor
<u>PA0520</u>	<i>nirQ</i>		-4.7	-3.0	Regulatory protein NirQ
<u>PA0521</u>	<i>nirO</i>		-3.6	-3.2	Probable cytochrome <i>c</i> oxidase subunit
<u>PA0523</u>	<i>norC</i>		-32.4	-25.6	Nitric-oxide reductase subunit C
<u>PA0524</u>	<i>norB</i>		-41.0	-34.3	Nitric-oxide reductase subunit B
<u>PA0525</u>	<i>norD</i>		-7.2	-7.4	Probable denitrification protein NorD
<u>PA0526</u>			-20.1	-12.4	Hypothetical protein
PA0546	<i>metK</i>			3.0	Methionine adenosyltransferase
PA0746				-2.6	Probable acyl-CoA dehydrogenase

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<u>PA0792</u>	<i>prpD</i>		2.9		Propionate catabolic protein PrpD
<u>PA0794</u>			-3.7	-3.2	Probable aconitate hydratase
PA0795	<i>prpC</i>			-3.5	Citrate synthase 2
PA0796	<i>prpB</i>			-4.6	Carboxyphosphoenolpyruvate phosphonmutase
PA0848 [§]	<i>aphB</i>			2.5	alkyl hydroperoxide reductase, AhpB
PA0852	<i>cbpD</i>			4.1	Chitin-binding protein CbpD precursor
<u>PA0918</u>			-14.3		Cytochrome <i>b561</i>
PA0931	<i>pirA</i>		2.6		Ferric enterobactin receptor PirA
PA0997* [‡] [◊]	<i>pqsB</i>	6.7	17.5		PqsB
PA0998* [‡] [◊]	<i>pqsC</i>	5.5	16.1		PqsC
PA0999* [‡] [◊]	<i>pqsD</i>	5.8	15.7		3-oxoacyl-[acyl-carrier-protein] synthase III
PA1000* [‡] [◊]	<i>pqsE</i>			22.8	Quinolone signal response protein
PA1001* [‡] [◊]	<i>phnA</i>			26.2	Anthranilate synthase component I
PA1002* [‡] [◊]	<i>phnB</i>			22.4	Anthranilate synthase component II
PA1070	<i>braG</i>			-3.5	Branched-chain amino acid transport protein BraG
PA1071	<i>braF</i>			-3.1	Branched-chain amino acid transport protein BraF
PA1072	<i>braE</i>			-4.0	Branched-chain amino acid transport protein BraE
PA1073	<i>braD</i>			-5.3	Branched-chain amino acid transport protein BraD
PA1134			3.3		Hypothetical protein
<u>PA1172</u>	<i>napC</i>		-5.7		Cytochrome <i>c</i> -type protein NapC
<u>PA1173</u>	<i>napB</i>		-8.9		Cytochrome <i>c</i> -type protein NapB precursor
<u>PA1174</u> [§]	<i>napA</i>		-6.5		Periplasmic nitrate reductase protein NapA
<u>PA1195</u>			-3.4		Hypothetical protein
PA1212 [‡]				2.8	Probable MFS transporter
PA1213 [‡]				3.7	Hypothetical protein
PA1214				3.6	Hypothetical protein
PA1215				4.1	Hypothetical protein
PA1216*				4.9	Hypothetical protein
PA1217				5.8	Probable 2-isopropylmalate synthase
PA1218 [‡]				5.5	Hypothetical protein
PA1245 ^{§‡}	<i>aprX</i>		3.9		AprX
PA1300			11.1		Probable sigma-70 factor, ECF subfamily
PA1301 [‡]			6.1		Probable transmembrane sensor
PA1318 [‡]	<i>cyoB</i>		2.9		Cytochrome <i>o</i> -ubiquinol oxidase subunit I
<u>PA1551</u>	<i>fixG</i>		-3.7		Probable ferredoxin
<u>PA1562</u>	<i>acnA</i>		-2.6		Aconitate hydratase 1
<u>PA1565</u>	<i>pauB2</i>		-9.7	-3.8	FAD-dependent oxidoreductase
<u>PA1583</u>	<i>sdhA</i>		-2.6		Succinate dehydrogenase (flavoprotein subunit)
<u>PA1602</u>			-2.7		Probable oxidoreductase
<u>PA1659</u>	<i>hsiF2</i>		-2.5		HsiF2
<u>PA1706</u>	<i>pcrV</i>		2.7		Type III secretion protein PcrV
<u>PA1707</u>	<i>pcrH</i>		3.1		Regulatory protein PcrH
<u>PA1708</u>	<i>popB</i>		5.6		Translocator protein PopB
<u>PA1709</u>	<i>popD</i>		3.0		Translocator outer membrane protein PopD precursor

PA number ^a	Gene name ^a	HHQ ^b	PQS ^c	PqsE ^d	Product name ^a
<u>PA1710</u>	<i>exsC</i>		3.5		ExsC exoenzyme S synthesis protein C precursor
<u>PA1711</u>	<i>exsE</i>		3.1		ExsE
<u>PA1712</u>	<i>exsB</i>		2.6		Exoenzyme S synthesis protein B
<u>PA1718</u>	<i>pscE</i>		4.3		Type III export protein PscE
PA1869				2.8	Probable acyl carrier protein
PA1888				2.8	Hypothetical protein
<u>PA1897</u>			-3.1		Hypothetical protein
PA1901 ^l	<i>phzC2</i>			5.5	Phenazine biosynthesis protein PhzC
PA1902 [§]	<i>phzD2</i>			7.5	Phenazine biosynthesis protein PhzD
PA1903 ^l	<i>phzE2</i>			8.8	Phenazine biosynthesis protein PhzE
PA1904	<i>phzF2</i>			10.3	Probable phenazine biosynthesis protein
PA1905	<i>phzG2</i>			9.7	Probable pyridoxamine 5'-phosphate oxidase
<u>PA1912</u>	<i>femI</i>		3.6		ECF sigma factor, FemI
PA1946	<i>rbsB</i>			-2.6	Binding protein component precursor of ABC ribose transporter
PA2014	<i>liuB</i>			-2.6	Methylcrotonyl-CoA carboxylase, beta-subunit
PA2030				3.7	Hypothetical protein
PA2031*				3.7	Hypothetical protein
PA2033 ^l			17.6		Hypothetical protein
PA2034			5.5		Hypothetical protein
PA2041				-4.7	Amino acid permease
PA2066 [‡]				3.0	Hypothetical protein
PA2068 ^l				2.7	Probable MFS transporter
PA2069* ^l				3.9	Probable carbamoyl transferase
PA2193*	<i>hcnA</i>			3.6	Hydrogen cyanide synthase HcnA
PA2194*	<i>hcnB</i>			3.1	Hydrogen cyanide synthase HcnB
PA2195*	<i>hcnC</i>			3.0	Hydrogen cyanide synthase HcnC
<u>PA2264</u>			-3.4		Conserved hypothetical protein
<u>PA2265</u>			-3.7		Gluconate dehydrogenase
PA2274* ^l				5.4	Hypothetical protein
PA2300* ^l ^o	<i>chiC</i>			18.7	Chitinase
PA2383			4.5		Probable transcriptional regulator
PA2384 [§]			42.2		Hypothetical protein
PA2385	<i>pvdQ</i>		29.1		3-oxo-C ₁₂ -homoserine lactone acylase PvdQ
PA2386	<i>pvdA</i>		113.8		L-ornithine N5-oxygenase
PA2389	<i>pvdR</i>		7.3		PvdR
PA2390	<i>pvdT</i>		4.1		PvdT
PA2391	<i>opmQ</i>		3.3		Probable outer membrane protein precursor
PA2392	<i>pvdP</i>		7.9		PvdP
PA2393			55.0		Probable dipeptidase precursor
PA2394	<i>pvdN</i>		45.6		PvdN
PA2395	<i>pvdO</i>		27.3		PvdO
PA2396	<i>pvdF</i>		49.0		Pyoverdine synthetase F
PA2397	<i>pvdE</i>		48.2		Pyoverdine biosynthesis protein PvdE
PA2398	<i>fpvA</i>		16.4		Ferripyoverdine receptor

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PA2399	<i>pvdD</i>		18.2		Pyoverdine synthetase D
PA2400	<i>pvdJ</i>		21.9		PvdJ
PA2402			23.1		Probable non-ribosomal peptide synthetase
PA2403			4.7		Hypothetical protein
PA2404			3.6		Hypothetical protein
PA2405 [§]			3.9		Hypothetical protein
PA2406			3.4		Hypothetical protein
PA2407			4.6		Probable adhesion protein
PA2408			3.7		Probable ATP-binding component of ABC transporter
PA2409			3.5		Probable permease of ABC transporter
PA2410			3.0		Hypothetical protein
PA2411			30.2		Probable thioesterase
PA2412 ^{§l}			70.7		Conserved hypothetical protein
PA2413 ^l	<i>pvdH</i>		43.1		L-2,4-diaminobutyrate:2-ketoglutarate 4-aminotransferase
PA2424	<i>pvdL</i>		26.2		PvdL
PA2425	<i>pvdG</i>		11.6		PvdG
PA2426	<i>pvdS</i>		43.9		Sigma factor PvdS
PA2427			21.3		Hypothetical protein
PA2444	<i>glyA2</i>			-3.9	Serine hydroxymethyltransferase
PA2448 [‡]				3.7	Hypothetical protein
PA2451			5.1		Hypothetical protein
PA2452			48.2		Hypothetical protein
<u>PA2481</u>			-2.9		Hypothetical protein
<u>PA2482</u>			-2.7		Probable cytochrome <i>c</i>
PA2509 ^{l‡}	<i>catB</i>			4.3	Muconate cycloisomerase I
PA2511 [‡]	<i>antR</i>			3.2	AntR
PA2531			3.2		Probable aminotransferase
PA2554				-2.7	Probable short-chain dehydrogenase
PA2555				-2.8	Probable AMP-binding enzyme
PA2557				-3.3	Probable AMP-binding enzyme
PA2564	<i>tam</i>			4.6	Hypothetical protein
PA2565				3.5	Hypothetical protein
PA2570 ^{*l‡}	<i>lecA</i>			26.3	LecA lectin
PA2588				2.7	Probable transcriptional regulator
PA2682				3.0	Conserved hypothetical protein
<u>PA2765</u>			-2.9		Hypothetical protein
PA2862	<i>lipA</i>			-8.7	Lactonizing lipase precursor
<u>PA2953</u>			-2.9		Electron transfer flavoprotein-ubiquinone oxidoreductase
PA3032 [§]	<i>snr1</i>			5.4	Cytochrome <i>c</i> Snr1
<u>PA3120</u>	<i>leuD</i>		-2.5		3-isopropylmalate dehydratase small subunit
<u>PA3121</u>	<i>leuC</i>		-3.6		3-isopropylmalate dehydratase large subunit
PA3190	<i>gltB</i>			-3.3	Probable binding protein component of ABC sugar transporter
PA3192	<i>gltR</i>			-2.6	Two-component response regulator GltR
PA3195 [*]	<i>gapA</i>			-4.6	Glyceraldehyde 3-phosphate dehydrogenase

PA number ^a	Gene name ^a	HHQ ^b	PQS ^c	PqsE ^d	Product name ^a
PA3300	<i>fadD2</i>			-2.5	Long-chain-fatty-acid-CoA ligase
PA3361* ^o	<i>lecB</i>			8.5	Fucose-binding lectin LecB
PA3369*				3.1	Hypothetical protein
<u>PA3391</u>	<i>nosR</i>		-4.6	-4.1	Regulatory protein NosR
<u>PA3392*</u>	<i>nosZ</i>		-72.7	-58.8	Nitrous-oxide reductase precursor
<u>PA3393</u>	<i>nosD</i>		-8.8	-9.0	NosD protein
<u>PA3394</u>	<i>nosF</i>		-6.3	-5.8	NosF protein
<u>PA3395</u>	<i>nosY</i>		-3.9	-3.2	NosY protein
<u>PA3396</u>	<i>nosL</i>		-3.4	-2.7	NosL protein
PA3407	<i>hasAp</i>		76.6		Heme acquisition protein HasAp
PA3408	<i>hasR</i>		6.4		Heme uptake outer membrane receptor HasR precursor
PA3410	<i>hasI</i>		7.6		HasI
<u>PA3441</u>	<i>ssuF</i>		10.2		Probable molybdopterin-binding protein
<u>PA3444</u>	<i>ssuD</i>		4.2		Conserved hypothetical protein
<u>PA3452</u>	<i>mqaA</i>		2.6		Malate:quinone oxidoreductase
PA3478*	<i>rhlB</i>			3.6	Rhamnosyltransferase chain B
PA3479	<i>rhlA</i>			3.6	Rhamnosyltransferase chain A
PA3484	<i>tse3</i>			-2.6	Tse3
PA3520* ^s				4.0	Hypothetical protein
<u>PA3524</u>	<i>gloA1</i>		-2.7		Lactoylglutathione lyase
PA3530	<i>bfd</i>		18.6		Bacterioferritin-associated ferredoxin Bfd
PA3568	<i>ymmS</i>			-8.9	Probable acetyl-CoA synthetase
PA3569	<i>mmsB</i>			-5.3	3-hydroxyisobutyrate dehydrogenase
PA3570	<i>mmsA</i>			-3.9	Methylmalonate-semialdehyde dehydrogenase
<u>PA3600</u>	<i>rpl36</i>		3.0		Conserved hypothetical protein
<u>PA3601</u>	<i>ykgM</i>		2.7		Conserved hypothetical protein
<u>PA3602</u>	<i>yerD</i>		-6.4		Conserved hypothetical protein
PA3709				-6.4	Probable MFS transporter
PA3710				-5.0	Probable GMC-type oxidoreductase
PA3734				4.8	Hypothetical protein
<u>PA3784</u>			-6.0		Hypothetical protein
<u>PA3785</u>			-7.0		Conserved hypothetical protein
<u>PA3790</u>	<i>oprC</i>		-3.7		Putative copper transport outer membrane porin OprC
<u>PA3841</u>	<i>exoS</i>		2.6		Exoenzyme S
<u>PA3842</u>	<i>spcS</i>		3.9		Specific <i>Pseudomonas</i> chaperone for ExoS, SpcS
<u>PA3866</u>			2.6		Pyocin protein
<u>PA3870</u>	<i>moaA1</i>		-2.7		Molybdopterin biosynthetic protein A1
<u>PA3872</u>	<i>narI</i>		-7.0	-5.0	Respiratory nitrate reductase gamma chain
<u>PA3873</u>	<i>narJ</i>		-3.6	-3.1	Respiratory nitrate reductase delta chain
<u>PA3874</u>	<i>narH</i>		-6.5	-3.8	Respiratory nitrate reductase beta chain
PA3899	<i>fecI</i>		3.4		FecI
<u>PA3938</u>	<i>tauA</i>		2.7		Probable periplasmic taurine-binding protein precursor
PA4023	<i>eutP</i>			-4.5	Probable transport protein
PA4024	<i>eutB</i>			-2.8	Ethanolamine ammonia-lyase large subunit

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PA4078*				12.1	Probable nonribosomal peptide synthetase
<u>PA4131</u> §			-5.8		Probable iron-sulfur protein
<u>PA4132</u>			-3.1		Conserved hypothetical protein
<u>PA4133</u>	<i>ccoN</i>		-5.2		Cytochrome c oxidase subunit (cbb3-type)
<u>PA4134</u> ‡			-6.1		Hypothetical protein
<u>PA4140</u> ‡			5.3		Hypothetical protein
<u>PA4141</u> *§‡			4.4	5.2	Hypothetical protein
<u>PA4142</u> ‡			4.3	4.8	Probable secretion protein
PA4168	<i>fpvB</i>		4.0		Second ferric pyoverdine receptor FpvB
PA4175	<i>prpL</i>		3.7		PrpL, protease IV
PA4205* ¹⁰	<i>mexG</i>			25.0	Hypothetical protein
PA4206* ¹⁰	<i>mexH</i>			16.4	Probable RND efflux membrane fusion protein precursor
PA4207* ¹⁰	<i>mexI</i>			18.5	Probable RND efflux transporter
PA4208* ¹⁰	<i>opmD</i>			11.6	Probable outer membrane protein precursor
PA4209* ¹⁰	<i>phzM</i>			4.1	Probable phenazine-specific methyltransferase
PA4210 ⁰	<i>phzA</i>			10.2	Probable phenazine biosynthesis protein
PA4211* ⁰	<i>phzB</i>			5.6	Probable phenazine biosynthesis protein
PA4217* ⁰ §	<i>phzS</i>			9.0	Flavin-containing monooxygenase
PA4218 § ¹	<i>ampP</i>		22.6		AmpP
PA4219	<i>yfpB</i>		10.7		AmpO
PA4220 §	<i>fptB</i>		30.3		Hypothetical protein
PA4221 § ¹ ‡	<i>fptA</i>		23.6		Fe(III)-pyochelin outer membrane receptor precursor
PA4222 § ¹ ‡	<i>pchI</i>		13.8		Probable ATP-binding component of ABC transporter
PA4223 §	<i>pchH</i>		13.7		Probable ATP-binding component of ABC transporter
PA4224 §	<i>pchG</i>		40.1		Pyochelin biosynthetic protein PchG
PA4225 § ¹ ‡	<i>pchF</i>		37.0		Pyochelin synthetase
PA4226 § ¹ ‡	<i>pchE</i>		28.0		Dihydroaeruginosic acid synthetase
PA4227 ‡	<i>pchR</i>		11.2		Transcriptional regulator PchR
PA4228 § ¹ ‡	<i>pchD</i>		34.1		Pyochelin biosynthesis protein PchD
PA4229 § ¹	<i>pchC</i>		31.5		Pyochelin biosynthetic protein PchC
PA4230 § ¹	<i>pchB</i>		47.3		Salicylate biosynthesis protein PchB
PA4231 § ¹ ‡	<i>pchA</i>		44.0		Salicylate biosynthesis isochorismate synthase
<u>PA4236</u> §	<i>katA</i>		-5.5		Catalase
<u>PA4333</u>	<i>fumA</i>		-3.4		Probable fumarase
<u>PA4366</u>	<i>sodB</i>		-3.8		Superoxide dismutase
PA4370	<i>icmP</i>		2.6		Insulin-cleaving metalloproteinase outer membrane protein
PA4384				3.0	Hypothetical protein
<u>PA4429</u>			-2.9		Probable cytochrome <i>cI</i> precursor
<u>PA4430</u>			-3.1		Probable cytochrome <i>b</i>
<u>PA4431</u>			-2.8		Probable iron-sulfur protein
PA4467			12.9		Hypothetical protein
PA4468 §	<i>sodA</i>		89.4		Superoxide dismutase
PA4469 § ¹	<i>orfX</i>		136.5		OrfX
PA4470 § ¹	<i>fumC1</i>		114.7		Fumarate hydratase

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PA4471 [§]	<i>fagA</i>		58.6		FagA
PA4500				-2.6	Probable binding protein component of ABC transporter
PA4501	<i>opdD</i>			-5.4	Glycine-glutamate dipeptide porin OpdP
PA4502				-2.8	Probable binding protein component of ABC transporter
PA4519	<i>speC</i>			2.7	Ornithine decarboxylase
PA4570			57.4		Hypothetical protein
<u>PA4587</u> ^{*§}	<i>ccpR</i>		-12.3		Cytochrome <i>c55I</i> peroxidase precursor
PA4613 ^{§‡}	<i>katB</i>			2.7	Catalase
PA4623				2.5	Hypothetical protein
PA4648	<i>cupE1</i>			3.0	Pilin subunit CupE1
PA4708	<i>phuT</i>		4.2		Heme-transport protein, PhuT
PA4709	<i>phuS</i>		4.5		PhuS
PA4710	<i>phuR</i>		9.2		Heme/Haemoglobin uptake outer membrane receptor PhuR
PA4774				-2.5	Hypothetical protein
<u>PA4810</u>	<i>fdnI</i>		-3.0		Nitrate-inducible formate dehydrogenase, gamma subunit
<u>PA4811</u> [§]	<i>fdnH</i>		-4.5		Nitrate-inducible formate dehydrogenase, beta subunit
<u>PA4812</u> [§]	<i>fdnG</i>		-5.3		Formate dehydrogenase-O, major subunit
<u>PA4880</u> [§]			-10.4		Probable bacterioferritin
PA4896			3.5		Probable sigma-70 factor, ECF subfamily
PA5058	<i>phaC2</i>			2.5	Poly(3-hydroxyalkanoic acid) synthase 2
PA5082	<i>dguC</i>			-13.2	DguC
PA5098	<i>hutH</i>			-3.5	Histidine ammonia-lyase
PA5100	<i>hutU</i>			-3.2	Urocanase
PA5153				-2.6	Amino acid ABC transporter periplasmic binding protein
PA5154				-4.5	Probable permease of ABC transporter
PA5167	<i>dctP</i>			-3.4	DctP
PA5168	<i>dctQ</i>			-5.6	DctQ
PA5169	<i>dctM</i>			-7.0	DctM
<u>PA5300</u>	<i>cycB</i>		-3.4		Cytochrome <i>c5</i>
<u>PA5355</u>	<i>glcD</i>		-3.5		Glycolate oxidase subunit GlcD
<u>PA5380</u>	<i>gbdR</i>		-2.6		GbdR
<u>PA5396</u>			-4.3		Hypothetical protein
<u>PA5397</u>			-4.6		Hypothetical protein
<u>PA5410</u>	<i>gbcA</i>		-5.7		GbcA
PA5460 [§]				3.7	Hypothetical protein

^a PA number, gene name and product name are from the *Pseudomonas* Genome Database [13]. Genes previously reported controlled by iron-starvation are in bold characters [40,41]; genes controlled by PQS via a PqsR-independent and iron starvation-independent signalling pathway(s) are underlined. *, genes whose transcription was altered in the $\Delta pqsR$ mutant with respect to the wild type strain [10]; §, genes whose transcription was altered upon exogenous PQS provision [28]; ¶, genes whose transcription was altered in the $\Delta pqsA$ mutant with respect to the wild type strain [11]; ‡, genes whose transcription was altered upon PqsE overexpression [11]; ◇, genes whose transcription was altered in the $\Delta pqsH$ mutant with respect to the wild type strain [23]. RND, Resistance-Nodulation-Cell division; MFS, major facilitator superfamily.

- ^b Fold change in gene expression in *P. aeruginosa* PAO1 Δ 4AQ grown in LB supplemented with 40 μ M HHQ with respect to the same strain grown in LB.
- ^c Fold change in gene expression in *P. aeruginosa* PAO1 Δ 4AQ grown in LB supplemented with 40 μ M PQS with respect to the same strain grown in LB.
- ^d Fold change in gene expression in *P. aeruginosa* PAO1 Δ 4AQ grown in LB supplemented with 1 mM IPTG (to induce PqsE expression) with respect to the same strain grown in LB.