

PA2449	MRIHVSFIDRVGITQEVLLALLGGRNLNLDAVEM---VPPNVYIDAPTLSPVLEELRAAL	57
PhhR	MRIKVHCQNRVGIIRDILNLLVDYGINVNRGEVGGDQGNAYLLCPNMINLQLOSLRPKL	60
TyrR	MRLEVFCEDRGLGTRELLDLLVLRGIDLRGIEI--DPIGRILYNFAELEFESFSSLMAEI	58
PA2449	LGIRGVQAMTVVDILPGORRLQLDALLAAMADPVLAVDGKGLVLLANPAFSERCGR---	114
PhhR	EAVPGVFGVKRVGLMPSEERRHLELNALLAALDFPVLSDVMGGQIVAAANRAAQLLGVVVD	120
TyrR	RRRAGVTDVRTVPWMPSEEREHLALSALLEALPEPVLSDVMKSKVDMANPASCQLFGOKLD	118
PA2449	DPAGERLASLFDDETLEDALVEQGFRLPLREVTFMGQALLDATP-ITEGPGEGERHLAG	173
PhhR	EVPGIPLSRYVEDLDLPELVRANKARINGLRVKVKGDFVLADIAP--LQSEHDESEALAG	178
TyrR	RLRNHTAAQLINGFNFLRWLESEPOQDSHNEHVVINGQNFLMEITPVYLOENDQ-HVLTG	177
PA2449	GLLTLVEPNRIGERLAALHHDHAEGFEMLLGDSQPIRTLKTRAORVAALDAPLLIHGETG	233
PhhR	AVLTLHRADRVGERIYHVRKQELRGFDSIFQSSRVMAAVVREARRMAPLDAPLLIEGETG	238
TyrR	AVVMRSTIRMGRLQONVAAQDVSAFSQIVAVSPKMKHVVEQAQKLAAPLLITGDTG	237
PA2449	TGKELVARGCHALSARHNSPFLALNCAALPENLAESELFQYAPGAFTGAQRGGKPGLEL	293
PhhR	TGKELLARACHLASPRGQSPFMALNCAGLPESMAETELFGYGFQAFEGARPEGKLGLEL	298
TyrR	TGKDLFAYACHQASPRAGKPYLALNCASIPEDAVESELFQHAP-----EGKKGFREQ	289
PA2449	AHQGTVFLDEIGEMSPYLQAKLLRFLSDGSFRRVGGDREVRVDVIRLSATHRNLEKMAE	353
PhhR	TAGGTLFLDGVGEMSPRLQAKLLRFLQDGCFRVGSDEEVLDVVRVICATQVDLSELCAK	358
TyrR	ANGGSVLLDEIGEMSPRMQAKLLRFLNDGTFRRVGEDHEVHVDVVRVICATQKNLVELVQK	349
PA2449	GSFREDLFYRLNVLSLEVPPLRERGHDIILLARHFMOQACAQIQRPVCR LAPGTYPALLS	413
PhhR	GEFRQDLYHRLNVLSLHIPPPLRECLDGLAPLAEHFLDQASRQIGCGLPKLSAQALERLER	418
TyrR	GMFREDLYYRLNVLTNLNPLRDCPDIMPLTELFVARFADEQGVPRPKLAADLNTVLR	409
PA2449	NRWPGNVRQLQNVIFRAAAICSSLVLDIGDLEIAGTAVARQNDGE---VGSLEEAVEGF	470
PhhR	YHWPGNVRQLENVLFQAVSLCEGGTVKAEHIRLPDYGAP-QPLGDFSLEGDLDAIVGRFE	477
TyrR	YAWPGNVRQLKNAIYRALTQLDGYELRPQDILLPDYDAATVAVGEDAMEGLSDEITSRFE	469
PA2449	KALLEKLYVSYSTRQLAARLQTSHTAIAHRLRKYGIGPRA---	511
PhhR	KAVLERLFREHPSSRQLGKRLGVSHHTAANKLRQHGVGQSEG--	519
TyrR	RSVLTQLYRNYPSTRKLAKRLGVSHHTAIAANKLREYGLSQKNEE	513

FIG S1 Alignment of PA2449 of *P. aeruginosa* PAO1 with PhhR (*P. aeruginosa* PAO1) and TyrR (*E. coli*). Proteins were aligned using Clustal X 2.1 with default settings. The predicted RpoN-interaction domains are overlaid with a heavy bar. A ~ 8 amino acid residue stretch (enclosed by a rectangle) is conserved in both PA2449 and PhhR but not TyrR.

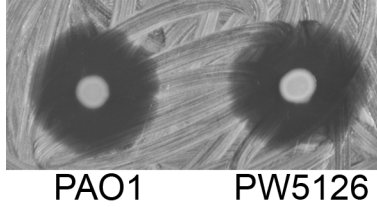


FIG S2 Killing of *S. aureus* ATCC 25923 by a transposon-insertion PA2449 mutant of *P. aeruginosa* PAO1 (PW5126). Strains were grown in peptone broth at 37 °C to an OD₆₀₀ of 0.7. Cultures were spotted onto LB plates that were freshly swabbed with *S. aureus*. As shown, there were no differences in the killing of *S. aureus* between both strains following a 24 h incubation at 37 °C.

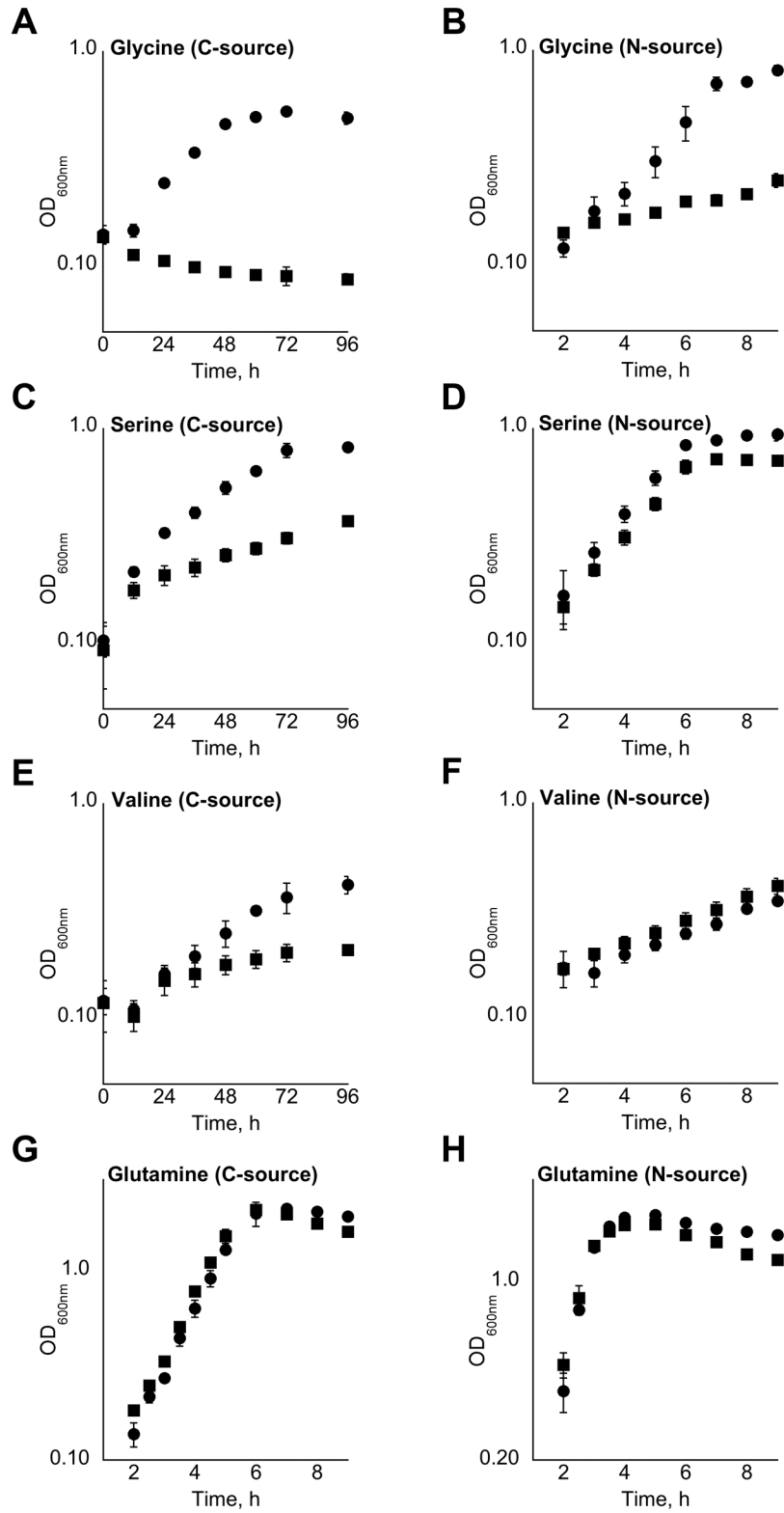


FIG S3 *P. aeruginosa* PAO1 (circles) and PW5126 (squares) were grown with indicated amino acids as sole sources for carbon (C-source) or nitrogen (N-sources).

TABLE S1 The strains used in this study were obtained from the *P. aeruginosa* PAO1 transposon mutant library (1).

	Strain	Relevant genotype
<i>P. aeruginosa</i>	PAO1-UW	wild-type
	PW1069	PA0049-E09::ISphoA/hah
	PW1205	PA0122-A06::ISlacZ/hah
	PW4738	<i>hcnB</i> -D07::ISlacZ/hah
	PW5112	<i>gcvT2</i> -G08::ISlacZ/hah
	PW5114	<i>sdaA</i> -G08::ISlacZ/hah
	PW5121	<i>gcvH2</i> -G02-ISlacZ/hah
	PW5126	PA2449-E03::ISphoA/hah
	PW5183	<i>mexF</i> -B02::ISphoA/hah

TABLE S2 Plasmids generated and used in this study. Plasmids either encode for tetracycline (Tc^R), kanamycin (Km^R) or gentamicin (Gm^R) resistance.

Plasmid	Characteristics	Source
pBBR1MCS-5	Broad-host range expression plasmid; Gm ^R	(2)
pUCP-A2G2	<i>phzA2B2C2D2E2F2G2</i> in pUCP26; Tc ^R	(3)
pCR®-Blunt	<i>E. coli</i> cloning plasmid; Km ^R	Invitrogen
pET28b	<i>E. coli</i> expression plasmid	Novagen
pBRL407	<i>metE-lacZ</i> fusion in pCR®-Blunt	This study
pBRL408	PA2449 in pCR®-Blunt	This study
pBRL409	<i>E. coli metE</i> in pCR®-Blunt	This study
pBRL410	<i>E. coli lacZ</i> with RBS in pCR®-Blunt	This study
pBRL411	<i>phzB1</i> promoter in pCR®-Blunt	This study
pBRL413	<i>phzA2B2C2D2E2F2G2</i> in pBBR1MCS-5	This study
pBRL415	<i>metE-lacZ</i> fusion in pBBR1MCS-5	This study
pBRL416	<i>E. coli lacZ</i> with RBS in pBBR1MCS-5	This study
pBRL417	PA2449 ORF in pET28b	This study
pBRL418	<i>phzB1</i> promoter in pBRL416	This study
pBRL420	<i>phzB2</i> promoter in pCR®-Blunt	This study
pBRL421	<i>phzM</i> promoter in pCR®-Blunt	This study
pBRL422	<i>phzH</i> promoter in pCR®-Blunt	This study
pBRL423	<i>phzB2</i> promoter in pBRL416	This study
pBRL424	<i>phzM</i> promoter in pBRL416	This study
pBRL425	<i>phzH</i> promoter in pBRL416	This study
pBRL435	RBS-PA2449 in pBBR1MCS-5	This study
pBRL439	<i>hcnA-lacZ</i> fusion in pCR®-Blunt	This study
pBRL447	<i>hcnA-lacZ</i> fusion in pBBR1MCS-5	This study
pBRL453	<i>gcvP2-lacZ</i> fusion in pCR®-Blunt	This study
pBRL456	<i>gcvP2-lacZ</i> fusion in pBBR1MCS-5	This study
pBRL480	<i>E. coli metE</i> in pBBR1MCS-5	This study

TABLE S3 Oligonucleotides used in this study. Identifiers and sequences for each oligonucleotide are given. Restriction sites used for cloning purposes are shown in *italics*. Oligonucleotides used for generating fusion constructs between the *E. coli lacZ* ORF with the ‘DNA of interest’ are marked as “fusion” in the **Notes** column.

Identifier	Sequence	Gene Target	Notes
WT01.f	gcagcatatgcgcatccacgtctccttcat	PA2449 ORF	<i>Nde</i> I
WT02.r	gcaggaattcgcaagccggtgtattccagcg	PA2449 ORF	<i>EcoR</i> I
BL343.f	ttaggcctgaatgccggtg	<i>rplU</i>	–
BL343.r	atgtacgcagtgattgttaccg	<i>rplU</i>	–
BL393.f	gacggtagcaagaaggagatatacatgacctgattacggattcactg	<i>E. coli lacZ</i>	<i>Kpn</i> I
BL393.r	gacaagcttgacagttattttgacaccagaccaactggta	<i>E. coli lacZ</i>	<i>Hind</i> III
BL394.f	gacgcatgagcctgttccagagccttttc	<i>phzB1</i>	<i>Sph</i> I
BL394.r	gacggtagcagattggattgtcgtatcagggcat	<i>phzB1</i>	<i>Kpn</i> I
BL396.f	gttctccagtagacaacgacaacag	<i>metE</i>	fusion
BL396.r	gaatccgtaatcatggatcattgggtgttctccagtcgaaagg	<i>metE</i>	fusion
BL398.f	gacgcatgagcctgtcaactgaatcgac	<i>phzB2</i>	<i>Sph</i> I
BL398.r	gacggtagcaggaatggcattatcgagcat	<i>phzB2</i>	<i>Kpn</i> I
BL399.f	gacgcatgaggttagatgtcattcaagtggg	<i>phzM</i>	<i>Sph</i> I
BL399.r	gacggtagccttttattctctctcgttacacatttc	<i>phzM</i>	<i>Kpn</i> I
BL400.f	gacgcatgagtcgaacgttgccacgaaatc	<i>phzH</i>	<i>Sph</i> I
BL400.r	gacggtagcagggaaactcctataattgatgtttatc	<i>phzH</i>	<i>Kpn</i> I
BL408.f	gacctgcaacaccgacaag	<i>hcnA</i>	fusion
BL408.r	gaatccgtaatcatggatcattgccctttcatccgtgagag	<i>hcnA</i>	fusion
BL427.f	atgacctgattacggattcactg	<i>E. coli lacZ</i>	fusion
BL427.r	gcagttattttgacaccagaccaactggta	<i>E. coli lacZ</i>	fusion
BL429.f	ctgcagttctgcccgcagtg	<i>gcvP2</i>	fusion
BL429.r	gaatccgtaatcatggatcattgacgggatcctcagggcgtc	<i>gcvP2</i>	fusion

TABLE S4 Complete list of genes having > 2-fold change in transcript levels in a transposon-insertion PA2449 mutant compared to wild-type *P. aeruginosa* PAO1 grown in peptone broth. Fold-changes represent mean values \pm standard deviation (SD). Gene ID, name and descriptions are based on information available from (www.pseudomonas.com).

Gene ID	Gene name	Fold-change (\pm SD)	Description
PA0048		- 3.56 \pm 0.45	probable transcriptional regulator
PA0049		- 10.3 \pm 3.04	hypothetical protein
PA0050		- 2.75 \pm 0.35	hypothetical protein
PA0052		- 3.41 \pm 1.01	hypothetical protein
PA0059	<i>osmC</i>	- 4.66 \pm 1.16	osmotically inducible protein
PA0105	<i>coxB</i>	- 2.64 \pm 0.25	cytochrome c oxidase, subunit II
PA0106	<i>coxA</i>	- 3.00 \pm 0.61	cytochrome c oxidase, subunit I
PA0107		- 2.62 \pm 0.28	hypothetical protein
PA0108	<i>collI</i>	- 2.64 \pm 0.52	cytochrome c oxidase, subunit III
PA0110		- 2.66 \pm 0.62	hypothetical protein
PA0111		- 2.52 \pm 0.23	hypothetical protein
PA0112		- 2.39 \pm 0.33	hypothetical protein
PA0113		- 2.17 \pm 0.09	probable cytochrome c oxidase assembly factor
PA0122	<i>rahU</i>	- 29.7 \pm 15.5	protein affecting pleiotropic properties
PA0144		- 2.86 \pm 0.50	hypothetical protein
PA0355	<i>pfpl</i>	- 4.88 \pm 1.78	protease
PA0431		- 2.74 \pm 0.63	hypothetical protein
PA0432	<i>sahH</i>	- 3.34 \pm 0.35	S-adenosyl-L-homocysteine hydrolase
PA0450		2.69 \pm 0.36	probable phosphate transporter
PA0546	<i>metK</i>	- 5.04 \pm 1.84	methionine adenosyltransferase
PA0547		- 4.34 \pm 1.03	probable transcriptional regulator
PA0674	<i>vreA</i>	2.33 \pm 0.17	TonB-related protein
PA0676	<i>vreR</i>	2.34 \pm 0.32	sigma factor regulator
PA0681	<i>hxcT</i>	3.82 \pm 1.07	pseudopilin
PA0682	<i>hxcH</i>	2.85 \pm 0.68	pseudopilin
PA0683		2.91 \pm 0.72	probable type II secretion system protein
PA0684		2.93 \pm 0.73	probable type II secretion system protein
PA0685		4.24 \pm 1.62	probable type II secretion system protein
PA0686		3.05 \pm 0.50	probable type II secretion system protein
PA0687		2.24 \pm 0.25	probable type II secretion system protein
PA0688		2.56 \pm 0.41	probable binding protein component of ABC transporter
PA0690		2.40 \pm 0.33	hypothetical protein
PA0691		3.06 \pm 0.43	hypothetical protein
PA0692		3.71 \pm 0.42	hypothetical protein
PA0693	<i>exbB2</i>	4.49 \pm 0.58	transport protein
PA0694	<i>exbD2</i>	3.24 \pm 0.46	transport protein
PA0695		2.87 \pm 0.42	hypothetical protein
PA0696		4.34 \pm 0.99	hypothetical protein
PA0697		4.03 \pm 0.37	hypothetical protein
PA0698		4.06 \pm 0.80	hypothetical protein

PA0699		3.84 ± 0.64	probable peptidyl-prolyl isomerase
PA0700		2.81 ± 0.54	hypothetical protein
PA0701		2.97 ± 0.43	probable transcriptional regulator
PA0744		- 2.46 ± 0.53	probable enoyl-CoA hydratase
PA0745		- 2.81 ± 0.60	probable enoyl-CoA hydratase
PA0746		- 2.52 ± 0.19	probable acyl-CoA dehydrogenase
PA0747		- 2.56 ± 0.33	probable aldehyde dehydrogenase
PA0802		2.84 ± 0.59	hypothetical protein
PA0844	<i>plcH</i>	2.45 ± 0.36	hemolytic phospholipase C
PA0852	<i>cpdD</i>	- 7.46 ± 3.36	chitin-binding protein
PA0958	<i>oprD</i>	- 2.46 ± 0.42	basic amino acid/peptide outer membrane porin
PA1130	<i>rhIC</i>	- 7.22 ± 1.15	rhamnosyltransferase 2
PA1131		- 3.42 ± 0.50	probable major facilitator superfamily transporter
PA1211		- 4.10 ± 1.23	hypothetical protein
PA1212		- 5.58 ± 1.98	probable major facilitator superfamily transporter
PA1213		- 6.91 ± 1.27	hypothetical protein
PA1214		- 6.64 ± 1.51	hypothetical protein
PA1215		- 12.4 ± 4.27	hypothetical protein
PA1216		- 57.1 ± 15.3	hypothetical protein
PA1217		- 39.5 ± 11.6	probable 2-isopropylmalate synthase
PA1218		- 18.4 ± 3.82	hypothetical protein
PA1219		- 5.39 ± 1.41	hypothetical protein
PA1220		- 7.44 ± 2.56	hypothetical protein
PA1221		- 8.50 ± 3.40	hypothetical protein
PA1323		- 3.27 ± 0.91	hypothetical protein
PA1324		- 3.60 ± 0.61	hypothetical protein
PA1332		2.83 ± 0.32	hypothetical protein
PA1333		6.23 ± 2.45	hypothetical protein
PA1404		- 3.89 ± 1.28	hypothetical protein
PA1743		2.52 ± 0.30	hypothetical protein
PA1744		3.17 ± 0.93	hypothetical protein
PA1784		- 3.38 ± 0.67	hypothetical protein
PA1800	<i>tig</i>	2.32 ± 0.20	trigger factor
PA1869		- 9.21 ± 2.77	probable acyl carrier protein
PA1871	<i>lasA</i>	- 9.94 ± 1.45	protease
PA1874		- 6.09 ± 0.82	hypothetical protein
PA1875		- 5.06 ± 1.93	probable outer membrane protein
PA1876		- 4.10 ± 1.15	probable ATP-binding fusion ABC transporter
PA1877		- 3.32 ± 0.82	probable secretion protein
PA1888		- 2.27 ± 0.24	hypothetical protein
PA1892		- 2.08 ± 0.09	hypothetical protein
PA1894		- 5.77 ± 0.95	hypothetical protein
PA1895		- 3.86 ± 0.40	hypothetical protein
PA1896		- 3.09 ± 0.53	hypothetical protein
PA1897		- 4.16 ± 0.75	hypothetical protein
PA1901 ^a	<i>phzC2</i>	- 30.7 ± 9.04	phenazine biosynthesis
PA1902 ^a	<i>phzD2</i>	- 27.5 ± 4.87	phenazine biosynthesis
PA1903 ^a	<i>phzE2</i>	- 45.7 ± 9.59	phenazine biosynthesis
PA1904 ^a	<i>phzF2</i>	- 46.8 ± 12.3	phenazine biosynthesis
PA1905 ^a	<i>phzG2</i>	- 58.6 ± 7.83	phenazine biosynthesis
PA1914		- 18.8 ± 4.97	hypothetical protein

PA1927	<i>metE</i>	- 25.7 ± 2.09	methionine synthase
PA1930		- 2.75 ± 0.69	probable chemotaxis transducer
PA1970		45.6 ± 18.9	hypothetical protein
PA1978	<i>erbR</i>	2.92 ± 0.71	response regulator
PA1983	<i>exaB</i>	8.73 ± 1.78	cytochrome c550
PA2000	<i>dhcB</i>	- 2.30 ± 0.15	dehydrocarnitine CoA transferase
PA2014	<i>liuB</i>	- 2.48 ± 0.37	methylcrotonyl-CoA carboxylase
PA2015	<i>liuA</i>	- 2.36 ± 0.18	putative isovaleryl-CoA dehydrogenase
PA2017		2.72 ± 0.54	hypothetical protein
PA2021		- 3.76 ± 0.72	hypothetical protein
PA2066		- 3.38 ± 0.71	hypothetical protein
PA2067		- 5.56 ± 1.09	probable hydrolase
PA2068		- 6.10 ± 2.06	probable major facilitator superfamily transporter
PA2069		- 11.2 ± 3.88	probable carbamoyl transferase
PA2110		- 5.06 ± 1.27	hypothetical protein
PA2111		- 4.06 ± 0.47	hypothetical protein
PA2112		- 4.24 ± 1.41	hypothetical protein
PA2114		- 4.41 ± 1.20	probable major facilitator superfamily transporter
PA2116		- 5.03 ± 0.64	hypothetical protein
PA2143		- 3.06 ± 0.66	hypothetical protein
PA2166		- 7.16 ± 2.23	hypothetical protein
PA2170		- 2.84 ± 1.31	hypothetical protein
PA2171		- 4.29 ± 0.68	hypothetical protein
PA2176		- 2.92 ± 0.30	hypothetical protein
PA2193	<i>hcnA</i>	- 38.2 ± 5.10	hydrogen cyanide synthase
PA2194	<i>hcnB</i>	- 11.9 ± 4.02	hydrogen cyanide synthase
PA2195	<i>hcnC</i>	- 9.10 ± 2.19	hydrogen cyanide synthase
PA2204		- 2.55 ± 0.50	probable binding protein component of ABC transporter
PA2232	<i>pslB</i>	- 2.44 ± 0.23	mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase
PA2234	<i>pslD</i>	- 2.19 ± 0.19	protein involved in polysaccharide export
PA2235	<i>pslE</i>	- 2.36 ± 0.27	protein involved in exopolysaccharide biosynthesis
PA2240	<i>pslJ</i>	- 2.45 ± 0.33	protein involved in exopolysaccharide biosynthesis
PA2274		- 10.8 ± 2.48	hypothetical protein
PA2300	<i>chiC</i>	- 3.35 ± 0.70	chitinase
PA2317		5.43 ± 0.58	probable oxidoreductase
PA2318		5.19 ± 1.48	hypothetical protein
PA2384		- 4.08 ± 0.84	hypothetical protein
PA2405		- 2.59 ± 0.55	hypothetical protein
PA2414		- 2.85 ± 0.66	L-sorbose dehydrogenase
PA2415		- 2.56 ± 0.29	hypothetical protein
PA2433		- 5.00 ± 1.12	hypothetical protein
PA2442	<i>gcvT2</i>	- 12.6 ± 2.34	glycine cleavage system protein T2
PA2443	<i>sdaA</i>	- 11.7 ± 1.32	L-serine dehydratase
PA2444	<i>glyA2</i>	- 54.4 ± 6.04	serine hydroxymethyltransferase
PA2445	<i>gcvP2</i>	- 37.5 ± 4.58	glycine cleavage system protein P2
PA2446	<i>gcvH2</i>	- 59.3 ± 25.1	glycine cleavage system protein H2
PA2486		14.9 ± 8.70	hypothetical protein
PA2491	<i>mexS</i>	12.4 ± 4.20	probable oxidoreductase

PA2493	<i>mexE</i>	139 ± 16.6	multidrug efflux membrane fusion protein
PA2494	<i>mexF</i>	115 ± 16.5	multidrug efflux transporter
PA2495	<i>oprN</i>	43.1 ± 8.70	multidrug efflux outer membrane protein
PA2564		- 4.60 ± 0.83	hypothetical protein
PA2565		- 4.97 ± 0.85	hypothetical protein
PA2566		- 7.10 ± 1.29	hypothetical protein
PA2570	<i>lecA</i>	- 26.0 ± 6.95	PA-IL lectin
PA2588		- 2.99 ± 0.49	probable transcriptional regulator
PA2592		- 3.02 ± 0.85	probable periplasmic spermidine/putrescine-binding protein
PA2635		3.03 ± 0.52	hypothetical protein
PA2747		- 17.6 ± 9.28	hypothetical protein
PA2754		- 4.32 ± 1.52	hypothetical protein
PA2759		16.3 ± 1.93	hypothetical protein
PA2788		- 2.70 ± 0.38	probable chemotaxis transducer
PA2811		6.43 ± 1.05	probable permease of ABC-2 transporter
PA2812		5.07 ± 0.72	probable ATP-binding component of ABC transporter
PA2813		6.26 ± 0.37	probable glutathione S-transferase
PA2939		- 3.84 ± 0.42	probable aminopeptidase
PA3023		- 2.43 ± 0.32	hypothetical protein
PA3032	<i>snr1</i>	- 3.71 ± 0.58	cytochrome c Snr1
PA3041		- 2.47 ± 0.40	hypothetical protein
PA3229		124 ± 17.2	hypothetical protein
PA3258		2.47 ± 0.27	hypothetical protein
PA3273		- 2.62 ± 0.55	hypothetical protein
PA3296	<i>phoA</i>	2.83 ± 0.32	alkaline phosphatase
PA3319	<i>plcN</i>	4.01 ± 0.22	non-hemolytic phospholipase C
PA3326	<i>clpP2</i>	- 7.84 ± 1.12	ATP-dependent Clp protease
PA3327		- 4.08 ± 0.89	probable non-ribosomal peptide synthetase
PA3328		- 6.40 ± 1.91	probable FAD-dependent monooxygenase
PA3329		- 7.12 ± 1.84	hypothetical protein
PA3330		- 7.06 ± 1.67	probable short chain dehydrogenase
PA3331		- 18.6 ± 4.04	cytochrome P450
PA3332		- 12.5 ± 3.82	hypothetical protein
PA3333	<i>fabH2</i>	- 9.48 ± 1.78	3-oxoacyl-acyl-carrier-protein synthase III
PA3334		- 17.6 ± 5.50	probable acyl carrier protein
PA3335		- 6.48 ± 0.96	hypothetical protein
PA3336		- 4.77 ± 0.94	probable major facilitator superfamily transporter
PA3361	<i>lecB</i>	- 34.5 ± 7.81	fucose-binding lectin PA-IIL
PA3362		- 3.67 ± 0.88	hypothetical protein
PA3363	<i>amiR</i>	- 6.70 ± 1.97	aliphatic amidase regulator
PA3364	<i>amiC</i>	- 4.52 ± 0.90	aliphatic amidase expression-regulating protein
PA3365		- 12.0 ± 2.18	probable chaperone
PA3366	<i>amiE</i>	- 8.70 ± 1.67	aliphatic amidase
PA3397	<i>fpr</i>	- 3.08 ± 1.09	ferredoxin reductase
PA3465		- 2.33 ± 0.31	hypothetical protein
PA3476	<i>rhIL</i>	- 3.59 ± 1.28	autoinducer synthesis protein
PA3478	<i>rhIB</i>	- 27.4 ± 3.70	rhamnosyltransferase chain B
PA3479	<i>rhIA</i>	- 38.4 ± 6.35	rhamnosyltransferase chain A
PA3520		- 6.35 ± 2.78	hypothetical protein

PA3568		- 4.01 ± 0.46	probable acetyl-CoA synthetase
PA3569	<i>mmsB</i>	- 3.42 ± 0.40	3-hydroxyisobutyrate dehydrogenase
PA3570	<i>mmsA</i>	- 2.86 ± 0.42	methylmalonate-semialdehyde dehydrogenase
PA3602		2.22 ± 0.18	hypothetical protein
PA3629	<i>adhC</i>	2.42 ± 0.32	alcohol dehydrogenase
PA3691		- 5.02 ± 1.05	hypothetical protein
PA3692	<i>lptF</i>	- 5.42 ± 1.40	lipotoxon F
PA3710		- 3.38 ± 0.41	probable GMC-type oxidoreductase
PA3724	<i>lasB</i>	- 17.7 ± 2.69	elastase
PA3734		- 5.96 ± 1.88	hypothetical protein
PA3788		- 2.77 ± 0.39	hypothetical protein
PA3925		2.40 ± 0.26	probable acyl-CoA thiolase
PA4070		2.86 ± 0.69	probable transcriptional regulator
PA4072		4.87 ± 0.78	probable amino acid permease
PA4073		6.20 ± 1.53	probable aldehyde dehydrogenase
PA4078		- 3.09 ± 0.67	probable nonribosomal peptide synthetase
PA4091	<i>hpaA</i>	6.97 ± 2.00	4-hydroxyphenylacetate 3-monooxygenase
PA4092	<i>hpaC</i>	5.35 ± 1.11	4-hydroxyphenylacetate 3-monooxygenase
PA4100		2.95 ± 0.79	probable dehydrogenase
PA4121		18.0 ± 3.21	hypothetical protein
PA4122		7.80 ± 1.28	hypothetical protein
PA4123	<i>hpcC</i>	12.9 ± 2.34	5-carboxy-2-hydroxymuconate semialdehyde dehydrogenase
PA4124	<i>hpcB</i>	6.39 ± 1.30	homoprotocatechuate 2,3-dioxygenase
PA4125	<i>hpcD</i>	10.9 ± 1.11	5-carboxymethyl-2-hydroxymuconate isomerase
PA4126		2.84 ± 0.86	probable major facilitator superfamily transporter
PA4127	<i>hpcG</i>	3.54 ± 0.94	2-oxo-hept-3-ene-1,7-dioate hydratase
PA4128		3.15 ± 0.61	hypothetical protein
PA4129		- 11.3 ± 1.30	hypothetical protein
PA4130		- 16.1 ± 4.16	probable sulfite or nitrite reductase
PA4131		- 21.0 ± 4.91	probable iron-sulfur protein
PA4132		- 6.31 ± 0.91	conserved hypothetical protein
PA4133		- 9.05 ± 2.30	cytochrome c oxidase
PA4134		- 3.89 ± 0.50	hypothetical protein
PA4141		- 31.4 ± 6.26	hypothetical protein
PA4175	<i>piv</i>	- 4.68 ± 0.65	protease IV
PA4205	<i>mexG</i>	- 18.2 ± 4.98	hypothetical protein
PA4206	<i>mexH</i>	- 15.6 ± 3.45	resistance-nodulation-dell division efflux membrane fusion protein
PA4207	<i>mexI</i>	- 15.0 ± 1.15	resistance-nodulation-dell division efflux transporter
PA4208	<i>opmD</i>	- 11.5 ± 2.34	probable outer membrane protein
PA4209	<i>phzM</i>	- 22.7 ± 2.79	phenazine-specific methyltransferase
PA4210 ^a	<i>phzA1</i>	- 24.3 ± 4.69	phenazine biosynthesis protein
PA4211 ^a	<i>phzB1</i>	- 113 ± 16.8	phenazine biosynthesis protein
PA4217	<i>phzS</i>	- 68.9 ± 8.75	flavin-containing monooxygenase
PA4218	<i>ampP</i>	3.25 ± 0.51	siderophore transporter
PA4219	<i>ampO</i>	2.68 ± 0.39	iron-regulated membrane protein
PA4220		4.08 ± 1.42	hypothetical protein
PA4221	<i>fptA</i>	4.24 ± 0.47	iron-pyochelin outer membrane receptor
PA4222		2.84 ± 0.70	probable ATP-binding component of ABC

PA4223		3.20 ± 0.84	transporter probable ATP-binding component of ABC transporter
PA4224	<i>pchG</i>	3.48 ± 0.64	pyochelin biosynthesis protein
PA4225	<i>pchF</i>	3.85 ± 1.02	pyochelin synthetase
PA4226	<i>pchE</i>	3.92 ± 1.56	dihydroaeruginic acid synthetase
PA4228	<i>pchD</i>	3.50 ± 0.40	pyochelin biosynthesis protein
PA4229	<i>pchC</i>	3.36 ± 1.21	pyochelin biosynthesis protein
PA4230	<i>pchB</i>	2.96 ± 0.47	salicylate biosynthesis protein
PA4231	<i>pchA</i>	2.88 ± 0.64	isochorismate synthase
PA4293	<i>pprA</i>	- 3.17 ± 0.64	two-component sensor
PA4294		- 3.84 ± 0.92	hypothetical protein
PA4297	<i>tadG</i>	- 2.61 ± 0.43	probable membrane protein
PA4298		- 3.46 ± 1.07	hypothetical protein
PA4299	<i>tadD</i>	- 2.74 ± 0.12	Flp pilus assembly protein
PA4300	<i>tadC</i>	- 2.60 ± 0.22	Flp pilus assembly protein
PA4301	<i>tadB</i>	- 2.55 ± 0.25	Flp pilus assembly protein
PA4302	<i>tadA</i>	- 3.03 ± 1.03	Flp pilus assembly protein
PA4303	<i>tadZ</i>	- 2.65 ± 0.22	Flp pilus assembly protein
PA4304	<i>rcpA</i>	- 2.78 ± 0.71	Flp pilus assembly protein
PA4305	<i>rcpC</i>	- 2.77 ± 0.31	Flp pilus assembly protein
PA4306	<i>flp</i>	- 3.73 ± 1.63	Type IVb pilin
PA4311		- 2.29 ± 0.16	hypothetical protein
PA4333		2.50 ± 0.33	probable fumarase
PA4354		7.27 ± 4.43	hypothetical protein
PA4356	<i>xenB</i>	5.84 ± 1.63	xenobiotic reductase
PA4590	<i>pra</i>	- 5.13 ± 1.31	protein activator
PA4623		19.9 ± 10.1	hypothetical protein
PA4648	<i>cupE1</i>	- 4.64 ± 1.27	Pilin subunit
PA4649	<i>cupE2</i>	- 3.03 ± 0.41	Pilin subunit
PA4650	<i>cupE3</i>	- 3.13 ± 0.56	Pilin subunit
PA4651	<i>cupE4</i>	- 5.29 ± 1.02	Pilin assembly chaperone
PA4653	<i>cupE6</i>	- 2.66 ± 0.50	Adhesin-like protein
PA4738		- 12.3 ± 4.18	hypothetical protein
PA4739		- 16.8 ± 4.97	hypothetical protein
PA4781		- 2.35 ± 0.34	cyclic di-GMP phosphodiesterase
PA4844		2.54 ± 0.37	probable chemotaxis transducer
PA4880		- 5.08 ± 2.64	probable bacterioferritin
PA4881		109 ± 15.6	hypothetical protein
PA4925		- 3.56 ± 0.75	hypothetical protein
PA5219		- 2.97 ± 0.83	hypothetical protein
PA5220		- 13.6 ± 2.23	hypothetical protein
PA5415	<i>glyA1</i>	- 10.4 ± 2.36	serine hydroxymethyltransferase
PA5481		- 16.6 ± 2.00	hypothetical protein
PA5482		- 17.6 ± 4.51	hypothetical protein
PA5506		- 12.3 ± 3.58	hypothetical protein
PA5507		- 19.4 ± 4.68	hypothetical protein
PA5508	<i>pauA7</i>	- 3.62 ± 0.84	Glutamylpolyamine synthetase
PA5509		- 7.28 ± 1.58	hypothetical protein
PA5510		- 2.68 ± 0.42	probable transporter

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