

## Additional file 2. Annotation of antisense sRNAs.

Name	Start*	End*	Length*	Type of sRNA**	Antisense gene***	Direction	Gene name	Gene function	Gene pathway
asdnaA****	1320	1784	465	internal	PA0001	>	<i>dnaA</i>	chromosomal replication initiator protein DnaA	DNA replication, recombination, modification and repair
as4	35866	35974	109	end-span	PA0033	<	<i>hptC</i>	Histidine phosphotransfer protein HptC	
as5	40775	40925	151	end-span	PA0039	>		hypothetical protein	Hypothetical, unclassified, unknown
as6	182516	182617	102	end-span	PA0158	>	<i>trnC</i>	Resistance-Nodulation-Cell Division (RND) tricosan efflux transporter, TrnC	Antibiotic resistance and susceptibility; Transport of small molecules
as7	184720	184861	142	internal	PA0162	>	<i>opdC</i>	histidine porin OpdC	Membrane proteins; Transport of small molecules
as8	226915	226976	62	internal	PA0196	>	<i>pntB</i>	pyridine nucleotide transhydrogenase, beta subunit	Transport of small molecules; Energy metabolism
as9	263722	263909	188	internal	PA0234	>		hypothetical protein	Hypothetical, unclassified, unknown
as10	288493	288639	147	internal	PA0257	<		hypothetical protein	Related to phage, transposon, or plasmid
as11	290529	290665	137	internal	PA0259	<		hypothetical protein	Hypothetical, unclassified, unknown
as12	291428	291543	116	internal	PA0260	<		hypothetical protein	Hypothetical, unclassified, unknown; Membrane proteins
as13	299094	299181	88	internal	PA0264	<		hypothetical protein	Hypothetical, unclassified, unknown
as14	334305	334355	51	internal	PA0296	<	<i>spuL</i>	Glutamylpolyamine synthetase	Putative enzymes; Carbon compound catabolism
as15	338651	338736	86	internal	PA0300	<	<i>spuD</i>	polyamine transport protein	Transport of small molecules
as16	353325	353458	134	internal	PA0313	<		L-cysteine transporter of ABC system YecS	Membrane proteins; Transport of small molecules
as17	368517	368669	153	internal	PA0328	<		hypothetical protein	Hypothetical, unclassified, unknown
as18	379215	379350	136	internal	PA0337	>	<i>ptsP</i>	phosphoenolpyruvate-protein phosphotransferase PtsP	Transport of small molecules
as19	448929	449284	356	internal	PA0407	<	<i>gshB</i>	glutathione synthetase	Amino acid biosynthesis and metabolism; Biosynthesis of cofactors, prosthetic groups and carriers
as20	521726	521838	113	internal	PA0461	<		conserved hypothetical protein	Hypothetical, unclassified, unknown
as21	544658	544778	121	internal	PA0483	>		probable acetyltransferase	Putative enzymes
as22	554963	555078	116	internal	PA0495	>		hypothetical protein	Hypothetical, unclassified, unknown
as23	557312	557569	258	end-span	PA0498	>		hypothetical protein	Hypothetical, unclassified, unknown
as24	646779	646892	114	internal	PA0588	<		conserved hypothetical protein	Hypothetical, unclassified, unknown
as25	654775	654912	138	internal	PA0595	<	<i>ostA</i>	organic solvent tolerance protein OstA precursor	Adaptation, Protection
as26	659114	659270	157	internal	PA0599	<		hypothetical protein	Hypothetical, unclassified, unknown
as27	680736	680853	118	internal	PA0620	>		probable bacteriophage protein	Related to phage, transposon, or plasmid
as28	697609	697703	95	internal	PA0641	>		probable bacteriophage protein	Related to phage, transposon, or plasmid
as29	701233	701489	257	end-span	PA0645	>		hypothetical protein	Related to phage, transposon, or plasmid
as29	701233	701489	257	start-span	PA0646	>		hypothetical protein	Related to phage, transposon, or plasmid
as30	718785	718934	150	internal	PA0667	<		conserved hypothetical protein	Hypothetical, unclassified, unknown
as31	748895	749047	153	internal	PA0689	>		hypothetical protein	Hypothetical, unclassified, unknown; Transport of small molecules
as32	749460	749562	103	internal	PA0689	>		hypothetical protein	Hypothetical, unclassified, unknown; Transport of small molecules
as33	761761	761823	63	internal	PA0690	>		hypothetical protein	Hypothetical, unclassified, unknown
as34	784213	784303	91	internal	PA0713	>		hypothetical protein	Hypothetical, unclassified, unknown
as35	795503	795648	146	internal	PA0727	>		hypothetical protein from bacteriophage PF1	Hypothetical, unclassified, unknown; Related to phage, transposon, or plasmid
as36	798624	798854	231	start-span	PA0730	<		probable transferase	Putative enzymes
as37	817964	818095	132	start-span	PA0750	<	<i>ung</i>	uracil-DNA glycosylase	DNA replication, recombination, modification and repair
as38	898637	898918	282	end-span	PA0823	<		lipopolysaccharide biosynthetic protein LpxO2	Hypothetical, unclassified, unknown
as38	898637	898918	282	start-span	PA0822	<		hypothetical protein	Hypothetical, unclassified, unknown
as39	921673	921840	168	end-span	PA0845	<		conserved hypothetical protein	Hypothetical, unclassified, unknown
as40	967079	967178	100	internal	PA0884	>		probable C4-dicarboxylate-binding periplasmic protein	Transport of small molecules
as41	967184	967283	100	internal	PA0884	>		probable C4-dicarboxylate-binding periplasmic protein	Transport of small molecules
as42	977508	977658	151	internal	PA0894	<		hypothetical protein	Hypothetical, unclassified, unknown
as43	990194	990309	116	internal	PA0904	<	<i>lysC</i>	aspartate kinase alpha and beta chain	Amino acid biosynthesis and metabolism
as44	1026460	1026563	104	internal	PA0936	<	<i>lpxO2</i>	lipopolysaccharide biosynthetic protein LpxO2	Putative enzymes; Cell wall / LPS / capsule
as45	1027896	1028083	188	end-span	PA0937	>		conserved hypothetical protein	Hypothetical, unclassified, unknown
as47	1056103	1056248	146	internal	PA0972	>	<i>tolB</i>	TolB protein	Transport of small molecules
as48	1060351	1060676	326	end-span	PA0977	<		hypothetical protein	Hypothetical, unclassified, unknown
as49	1066483	1066610	128	internal	PA0985	<	<i>pyoS5</i>	pyocin S5	Membrane proteins; Secreted Factors (toxins, enzymes, alginate)
as50	1073865	1074007	143	end-span	PA0992	>	<i>cupC1</i>	fimbrial subunit CupC1	Motility & Attachment
as50	1073865	1074007	143	start-span	PA0993	>	<i>cupC2</i>	chaperone CupC2	Motility & Attachment; Chaperones & heat shock proteins
as52	1098349	1098557	209	internal	PA1015	<		probable transcriptional regulator	Transcriptional regulators
as53	1119615	1119886	272	end-span	PA1032	<	<i>quiP</i>	QuiP	Carbon compound catabolism; Putative enzymes; Antibiotic resistance and susceptibility
as54	1135102	1135286	185	end-span	PA1047	>		probable esterase	Putative enzymes
as55	1135776	1135875	100	internal	PA1048	>		probable outer membrane protein precursor	Membrane proteins; Transport of small molecules
as56	1141250	1141364	115	start-span	PA1053	>		conserved hypothetical protein	Membrane proteins
as57	1207482	1207531	50	internal	PA1113	>		probable ATP-binding/permease fusion ABC transporter	Membrane proteins; Transport of small molecules
as58	1232028	1232169	142	start-span	PA1140	<		conserved hypothetical protein	Hypothetical, unclassified, unknown
as59	1323807	1323918	112	internal	PA1221	<		hypothetical protein	Hypothetical, unclassified, unknown
as60	1394817	1395002	186	internal	PA1284	<		probable acyl-CoA dehydrogenase	Putative enzymes
as62	1455941	1456046	106	internal	PA1342	<		probable binding protein component of ABC transporter	Transport of small molecules
as64	1484863	1485037	175	internal	PA1370	>		hypothetical protein	Hypothetical, unclassified, unknown
as65	1485541	1485595	55	internal	PA1370	>		hypothetical protein	Hypothetical, unclassified, unknown
as66	1499584	1499684	101	internal	PA1382	>		probable type II secretion system protein	Protein secretion/export apparatus
as67	1499690	1499742	53	internal	PA1382	>		probable type II secretion system protein	Protein secretion/export apparatus
as68	1502841	1502987	147	internal	PA1383	>		hypothetical protein	Hypothetical, unclassified, unknown
as69	1503570	1503696	127	internal	PA1384	>	<i>galE</i>	UDP-glucose 4-epimerase	Nucleotide biosynthesis and metabolism; Carbon compound catabolism; Central intermediary metabolism
as70	1503843	1503937	95	internal	PA1384	>	<i>galE</i>	UDP-glucose 4-epimerase	Nucleotide biosynthesis and metabolism; Carbon compound catabolism; Central intermediary metabolism
as71	1504553	1504676	124	end-span	PA1384	>	<i>galE</i>	UDP-glucose 4-epimerase	Nucleotide biosynthesis and metabolism; Carbon compound catabolism; Central intermediary metabolism
as71	1504553	1504676	124	start-span	PA1385	>		probable glycosyl transferase	Cell wall / LPS / capsule
as72	1504788	1504927	140	internal	PA1385	>		probable glycosyl transferase	Cell wall / LPS / capsule
as73	1506107	1506208	102	internal	PA1386	>		probable ATP-binding component of ABC transporter	Transport of small molecules
as74	1558500	1558752	253	internal	PA1430	>	<i>lasR</i>	transcriptional regulator LasR	Adaptation, Protection; Transcriptional regulators
as75	1588434	1588549	116	internal	PA1458	>		probable two-component sensor	Chemotaxis; Two-component regulatory systems
as76	1639661	1639805	145	end-span	PA1510	<		hypothetical protein	Hypothetical, unclassified, unknown
as76	1639661	1639805	145	start-span	PA1509	<		hypothetical protein	Hypothetical, unclassified, unknown
as77	1640773	1640948	176	internal	PA1510	<		hypothetical protein	Hypothetical, unclassified, unknown
as78	1698424	1698534	111	internal	PA1561	<	<i>aer</i>	aerotaxis receptor Aer	Adaptation, Protection; Chemotaxis
as79	1717615	1717930	116	end-span	PA1578	>		hypothetical protein	Hypothetical, unclassified, unknown
as80	1732127	1732265	139	end-span	PA1589	>	<i>sucD</i>	succinyl-CoA synthetase alpha chain	Energy metabolism
as81	1785747	1785881	135	internal	PA1640	<		conserved hypothetical protein	Hypothetical, unclassified, unknown
as82	1790530	1790650	121	internal	PA1645	<		hypothetical protein	Hypothetical, unclassified, unknown
as83	1838134	1838246	113	internal	PA1688	>		hypothetical protein	Hypothetical, unclassified, unknown
as84	1911985	1912118	134	internal	PA1767	<		hypothetical protein	Membrane proteins
as85	1912994	1913099	106	end-span	PA1769	<		conserved hypothetical protein	Hypothetical, unclassified, unknown
as86	1913728	1913919	192	start-span	PA1769	<		conserved hypothetical protein	Hypothetical, unclassified, unknown
as87	1916046	1916172	127	internal	PA1770	>	<i>ppsA</i>	phosphoenolpyruvate synthase	Energy metabolism; Carbon compound catabolism; Central intermediary metabolism
as88	1949036	1949142	107	internal	PA1797	<		hypothetical protein	Hypothetical, unclassified, unknown
as89	1953270	1953371	102	internal	PA1800	>	<i>tig</i>	trigger factor	Cell division; Chaperones & heat shock proteins
as90	1954335	1954415	81	internal	PA1801	>	<i>clpP</i>	ClpP	Chaperones & heat shock proteins; Cell wall / LPS / capsule



as196	5071970	5072154	185	internal	PA4527	>	<i>pilC</i>	still frameshift type 4 fimbrial biogenesis protein PilC	Motility & Attachment
as197	5101107	5101200	94	internal	PA4554	>	<i>pilY1</i>	type 4 fimbrial biogenesis protein PilY1	Motility & Attachment
as198	5101511	5101611	101	internal	PA4554	>	<i>pilY1</i>	type 4 fimbrial biogenesis protein PilY1	Motility & Attachment
as199	5141781	5141969	189	end-span	PA4591	<		probable hypothetical protein	Hypothetical, unclassified, unknown
as200	5148538	5148668	131	start-span	PA4595	<		probable ATP-binding component of ABC transporter	Transport of small molecules
as201	5274032	5274193	162	internal	PA4696	<	<i>ilvI</i>	acetolactate synthase large subunit	Biosynthesis of cofactors, prosthetic groups and carriers; Amino acid biosynthesis and metabolism
as202	5296232	5296293	62	internal	PA4717	>		conserved hypothetical protein	Hypothetical, unclassified, unknown
as203	5296311	5296538	228	internal	PA4717	>		conserved hypothetical protein	Hypothetical, unclassified, unknown
as204	5301771	5301838	68	internal	PA4722	<		probable aminotransferase	Putative enzymes
as205	5356355	5356495	141	internal	PA4770	>	<i>lldP</i>	L-lactate permease	Transport of small molecules
as206	5375454	5375529	76	end-span	PA4786	>		probable short-chain dehydrogenase	Putative enzymes
as207	5380813	5380919	107	internal	PA4793	>		hypothetical protein	Hypothetical, unclassified, unknown
as208	5382370	5382497	128	end-span	PA4796	>		hypothetical protein	Hypothetical, unclassified, unknown
as209	5408036	5408137	102	internal	PA4818	<		conserved hypothetical protein	Membrane proteins
as210	5473394	5473504	111	internal	PA4877	<		hypothetical protein	Hypothetical, unclassified, unknown
as211	5522339	5522410	72	start-span	PA4923	<		conserved hypothetical protein	Hypothetical, unclassified, unknown
as212	5532791	5532916	126	internal	PA4929	<		hypothetical protein	Membrane proteins
as214	5545002	5545131	130	internal	PA4941	<	<i>hflC</i>	protease subunit HflC	Translation, post-translational modification, degradation; Cell division
as216	5580862	5581109	248	start-span	PA4972	>		hypothetical protein	Hypothetical, unclassified, unknown
as217	5584935	5585163	229	internal	PA4974	>		probable outer membrane protein precursor	Protein secretion/export apparatus
as218	5585580	5585652	73	end-span	PA4975	<		NAD(P)H quinone oxidoreductase	Energy metabolism
as219	5602759	5602870	112	internal	PA4986	<		probable oxidoreductase	Putative enzymes
as220	5617657	5617793	137	internal	PA5000	<	<i>wapR</i>	alpha-1,3-rhamnosyltransferase WapR	Putative enzymes; Cell wall / LPS / capsule
as221	5618584	5618634	51	internal	PA5001	<		hypothetical protein	Hypothetical, unclassified, unknown
as222	5655041	5655112	72	internal	PA5024	<		conserved hypothetical protein	Hypothetical, unclassified, unknown
as223	5678557	5678652	96	internal	PA5042	<	<i>pilO</i>	type 4 fimbrial biogenesis protein PilO	Motility & Attachment
asponA****	5680819	5681167	349	start-span	PA5045	<	<i>ponA</i>	penicillin-binding protein 1A	Cell wall / LPS / capsule
as225	5684803	5684910	108	end-span	PA5047	<		hypothetical protein	Hypothetical, unclassified, unknown
as226	5699012	5699062	51	internal	PA5058	<	<i>phaC2</i>	poly(3-hydroxyalkanoic acid) synthase 2	Central intermediary metabolism
as228	5725557	5725795	239	internal	PA5087	<		hypothetical protein	Hypothetical, unclassified, unknown
as229	5739066	5739203	138	internal	PA5097	<		probable amino acid permease	Membrane proteins; Transport of small molecules
as230	5785777	5785905	129	internal	PA5136	<		hypothetical protein	Hypothetical, unclassified, unknown
as231	5799079	5799208	130	internal	PA5150	<		probable short-chain dehydrogenase	Putative enzymes
as232	5817430	5817493	64	internal	PA5167	>		probable c4-dicarboxylate-binding protein	Membrane proteins; Transport of small molecules
as233	5824524	5824599	76	internal	PA5172	>	<i>arcB</i>	ornithine carbamoyltransferase, catabolic	Amino acid biosynthesis and metabolism
as234	5844451	5844527	77	end-span	PA5192	<	<i>pckA</i>	phosphoenolpyruvate carboxykinase	Carbon compound catabolism; Energy metabolism
as235	5863452	5863719	268	start-span	PA5208	<		conserved hypothetical protein	Hypothetical, unclassified, unknown
as236	5868209	5868408	200	internal	PA5213	<	<i>gcvP1</i>	glycine cleavage system protein P1	Central intermediary metabolism; Amino acid biosynthesis and metabolism
as237	5896925	5897003	79	internal	PA5238	<		probable O-antigen acetylase	Putative enzymes; Membrane proteins; Cell wall / LPS / capsule
as238	5897008	5897057	50	internal	PA5238	<		probable O-antigen acetylase	Putative enzymes; Membrane proteins; Cell wall / LPS / capsule
as239	5926819	5926963	145	internal	PA5264	<		hypothetical protein	Hypothetical, unclassified, unknown; Membrane proteins
as240	6059529	6059600	72	internal	PA5380	>	<i>gbdR</i>	GbdR	Transcriptional regulators
as241	6090655	6090800	146	start-span	PA5412	<		hypothetical protein	Hypothetical, unclassified, unknown
as242	6135711	6135789	79	internal	PA5446	>		hypothetical protein	Hypothetical, unclassified, unknown
as243	6141133	6141239	107	internal	PA5451	<	<i>wzm</i>	membrane subunit of A-band LPS efflux transporter	Cell wall / LPS / capsule; Membrane proteins; Transport of small molecules
as244	6157855	6157964	110	internal	PA5468	>		probable citrate transporter	Transport of small molecules
as245	6158032	6158203	172	end-span	PA5468	>		probable citrate transporter	Transport of small molecules
as245	6158032	6158203	172	start-span	PA5469	>		conserved hypothetical protein	Membrane proteins
as246	6171684	6171915	232	start-span	PA5480	>		hypothetical protein	Hypothetical, unclassified, unknown
as247	6183216	6183389	174	internal	PA5492	>		conserved hypothetical protein	Hypothetical, unclassified, unknown
as248	6218749	6219078	330	end-span	PA5525	>		probable transcriptional regulator	Transcriptional regulators
as249	6245830	6245973	144	internal	PA5551	<		hypothetical protein	Hypothetical, unclassified, unknown
as250	6247796	6247909	114	end-span	PA5553	<	<i>atpC</i>	ATP synthase epsilon chain	Energy metabolism

\* Coordinates and length of the sRNAs predicted by RNA-Seq data.

\*\*The antisense sRNAs were categorized depending on their position with respect to the opposite gene as "start-span" (the asRNA spans over the start of the antisense gene), "internal" (the asRNA start and end within the antisense gene), or "end-span" (the asRNA spans over the end of the gene).

\*\*\*Some asRNAs overlap with 2 genes.

\*\*\*\*Coordinates validated by 5' and 3'-RACE experiments.