

## SUPPLEMENTARY INFORMATION

Belonging to the manuscript:

**Production of ammonia as a low-cost and long-distance antibiotic strategy by**

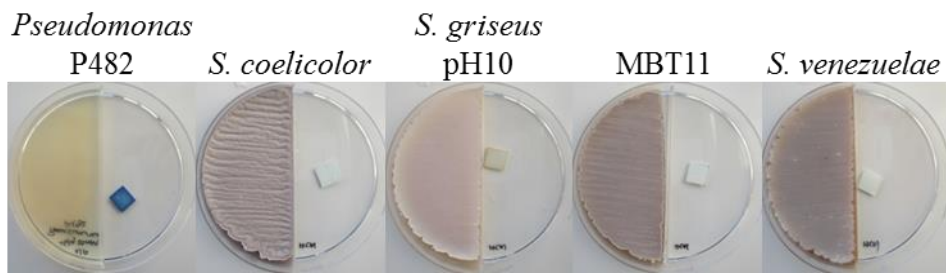
***Streptomyces* species**

Mariana Avalos<sup>1</sup>, Paolina Garbeva<sup>2</sup>, Jos M. Raaijmakers<sup>1, 2</sup>, Gilles P. van Wezel<sup>1, 2\*</sup>.

<sup>1</sup>Institute of Biology, Leiden University, Sylviusweg 72, 2333 BE Leiden, The Netherlands.

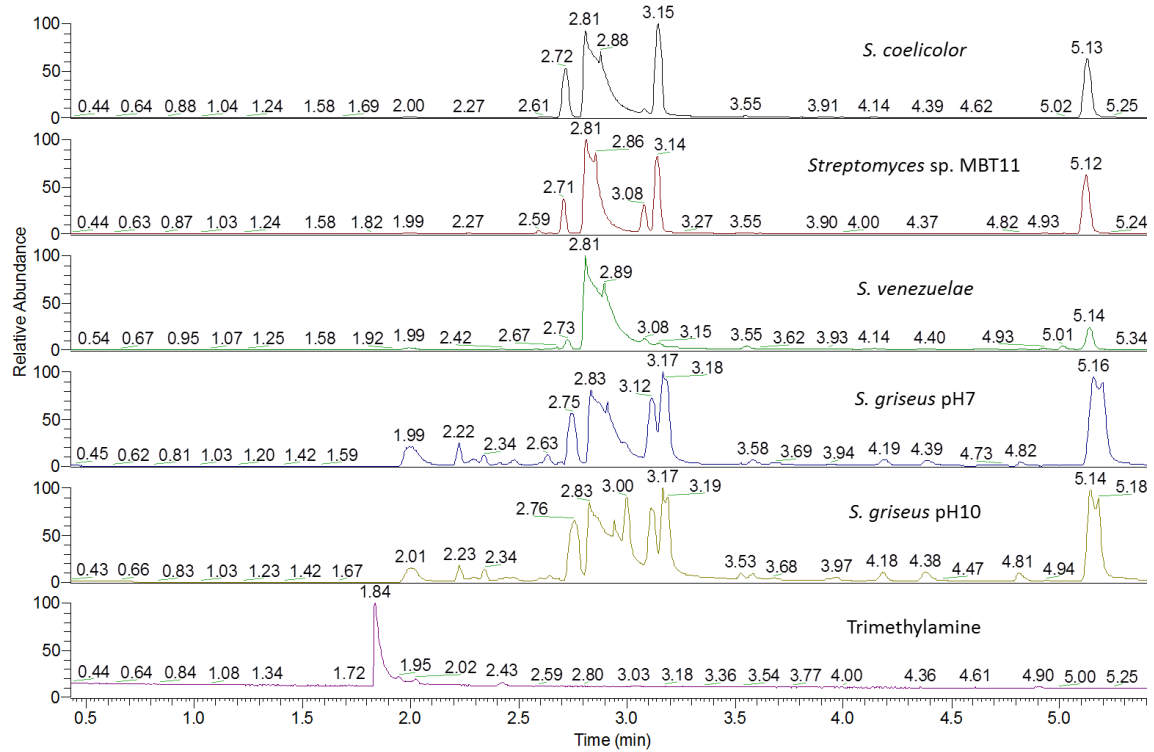
<sup>2</sup>Netherlands Institute of Ecology, Department of Microbial Ecology, Droevendaalsesteeg 10, 6708 PB Wageningen, The Netherlands.

\*Author for correspondence. Tel: +31 71 5274310; Email: g.wezel@biology.leidenuniv.nl

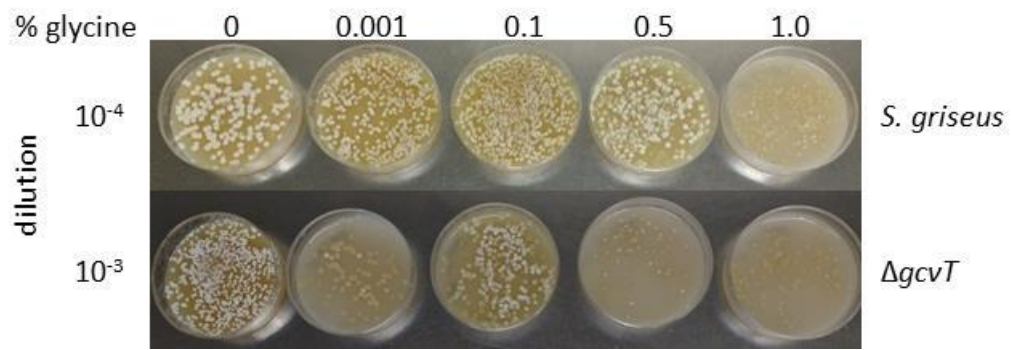


**Figure S1. HCN determination from different *Streptomyces* strains.** *Pseudomonas donghuensis* P482 was used as positive control<sup>28</sup>. Blue coloration is developed from the oxidation product from HCN + copper(II) ethyl acetoacetate and 4,4'-methylenebis-(N,N-dimethylaniline). none of the *Streptomyces* strains gave a positive reaction showing that the toxicity of the VCs from *Streptomyces* against *E. coli* is not due to the production of the toxic volatile HCN.

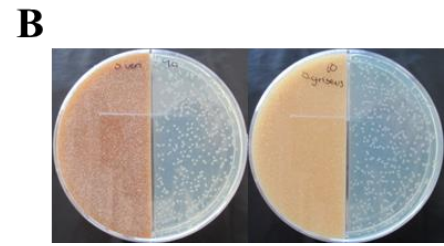
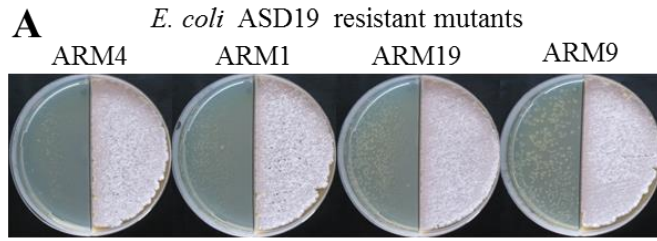
RT: 0.43 - 5.44



**Figure S2.** GC-chromatogram showing the absence of TMA in the headspace of *S. coelicolor* (black), *Streptomyces* sp. MBT11 (red), *S. venezuelae* (green), *S. griseus* grown at pH 7 (blue), *S. griseus* grown at pH 10 (yellow-green). Chromatogram of a TMA standard (RT 1.8 min.) is shown below (purple).



**Figure S3.** Colonies of *Streptomyces* recovered from the soil suspensions with different glycine concentrations using serial dilutions.



**Figure S4. A.** Colonies from *E. coli* strain ASD19 resistant to VCs produced by *Streptomyces* sp. MBT11. **B.** *E. coli* suppressor mutant ARM9 is resistant against VCs produced by *S. venezuelae* and *S. griseus* grown at pH 10 (buffered with glycine).

**Table S1.** Bacterial strains used in the present study.

Strains	Description	Reference
<i>E. coli</i> AS19- <i>rlmA::aph</i>	Hypersusceptible, KAN <sup>R</sup> resistant	Liu and Douthwaite, 2002
<i>E. coli</i> BREL606	Parent strain of <i>E. coli</i> AS19	<i>E. coli</i> Genetic stock center
<i>B. subtilis</i> 168	Wild-type strain	Barbe <i>et al.</i> , 2016
<i>S. coelicolor</i> A3(2) M145	SCP1-SCP2 <sup>-</sup> wild-type strain	Bentley, 2002
<i>S. lividans</i> 1326	Wild-type strain	Hopwood <i>et al.</i> , 1985
<i>S. griseus</i> DSM40236	Wild-type strain	Krainsky, 1914
<i>S. venezuelae</i> ATCC 15439	Wild-type strain	Song <i>et al.</i> , 2016
<i>Streptomyces</i> sp. MBT11	<i>Streptomyces</i> isolates	Zhu <i>et al.</i> , 2014
<i>Streptomyces</i> sp. MBT21		
ΔUTR-T	<i>S. griseus</i> IFO13350 with deletion of 5'-untranslated region of <i>gcvTH</i>	Tezuka and Ohnishi, 2014
GAL61	M145 Δ <i>gcvP</i> (::aac(3)IV)	Zhang, Le, 2015 (PhD Thesis)
MBT strains	Actinomycetes collection	Zhu, H. <i>et al.</i> , 2014

**Table S2. Volatile antimicrobial activity of streptomyces under different growth conditions.**

Growth (+) or inhibition (-) of indicator strains *E. coli* or *B. subtilis* is indicated, whereby (+/-) means poor growth, i.e. producing very small colonies.

	0.8% peptone		1% starch		MM	
	<i>E. coli</i>	<i>B. subtilis</i>	<i>E. coli</i>	<i>B. subtilis</i>	<i>E. coli</i>	<i>B. subtilis</i>
<i>S. coelicolor</i>	+	+	+	+	+	+
<i>S. lividans</i>	+	-	+	+	+	+
MBT11	-	+/-	-	+	+	+
<i>S. venezuelae</i>	-	+/-	+	+	+	+
<i>S. griseus</i>	-/+	-	+	+	+	+

Minimal media (MM) used: L-asparagine 0.5g/L, K<sub>2</sub>HPO<sub>4</sub> 0.5g/L, MgSO<sub>4</sub>(7H<sub>2</sub>O) 0.2g/L, FeSO<sub>4</sub>(7H<sub>2</sub>O) 0.01g/L, Glucose 10g/L, Agar 10g/L.

0.8% peptone or 1% starch were added to MM instead of glucose.

**Table S4.** RNAseq data comparing suppressor ARM9 to its parent *E. coli* ASD19. RNA was extracted from cells at mid-log (OD<sub>600</sub> =0.5). Only fold-changes above 2.0 or below -2.0 are shown.

Feature ID	ARM9 vs ASD19 fold change	GeneID	Protein Product	UniProt/SwissProt Accession
<b>DOWN-REGULATED</b>				
<i>envZ</i>	-16.43	947272	sensory histidine kinase in two-component regulatory system with OmpR	P0AEJ4
<i>omrA</i>	-15.86	2847746	N.A.	N.A.
<i>yhdV</i>	-15.86	947767	putative outer membrane protein response regulator in two-component	P64622
<i>ompR</i>	-14.84	947913	regulatory system with EnvZ	P0AA16
<i>yrhB</i>	-8.96	947948	stable heat shock chaperone	P46857
<i>yfcV</i>	-6.55	949109	putative fimbrial-like adhesin protein D-alanyl-D-alanine	P77288
<i>dacD</i>	-6.47	946518	carboxypeptidase, penicillin-binding protein 6b	P33013
<i>yqhH</i>	-6.20	946832	outer membrane lipoprotein, Lpp paralog	P65298
<i>hlyE</i>	-5.52	945745	hemolysin E	P77335
<i>oweS</i>	-5.52	947403	N.A.	P0AD35
<i>phnE</i>	-5.52	948625	N.A.	P16683
<i>ycjO</i>	-5.52	945888	putative sugar ABC transporter permease Ethanolamine catabolic microcompartment shell protein	P0AFR7
<i>eutN</i>	-5.17	946945	putative MFS transporter, membrane protein	P0AEJ8
<i>ydiM</i>	-4.83	946196	TPM domain protein, putative phosphatase multicopy suppressor of bamB, outer	P55140
<i>ycgG</i>	-4.83	945247	membrane lipoprotein	P37665
<i>yiaD</i>	-4.54	948075	putative lipoprotein and C40 family peptidase	Q47151
<i>yafL</i>	-4.48	944899	putative transporter	P77726
<i>yajR</i>	-4.37	945058	regulator of the transcriptional regulator FhIA	P0AEV4
<i>hycA</i>	-4.14	947193	N.A.	P76692
<i>yzgL</i>	-4.14	947933	N.A.	P76692
<i>hofP</i>	-3.96	947900	DNA catabolic protein	P45750
<i>fucA</i>	-3.94	947282	L-fucose-1-phosphate aldolase putative ethanol utilization	P0AB87
<i>eutS</i>	-3.91	946936	carboxysome structural protein	P63746
<i>ybgP</i>	-3.79	945110	putative periplasmic pilin chaperone	P75749
<i>yceO</i>	-3.79	945629	uncharacterized protein	P64442
<i>ykfJ</i>	-3.79	944924	N.A.	P75675
<i>yiaY</i>	-3.77	948102	L-threonine dehydrogenase	P37686
<i>ybdN</i>	-3.71	945205	PAPS reductase-like domain protein	P77216
<i>rybB</i>	-3.68	2847774	N.A.	N.A.
<i>pheV</i>	-3.56	947463	N.A.	N.A.
<i>yfbM</i>	-3.56	946745	DUF1877 family protein	P76483
<i>valV</i>	-3.52	946170	N.A.	N.A.
<i>csgB</i>	-3.45	947391	curlin nucleator protein, minor subunit in curli complex	P0ABK7
<i>yjjQ</i>	-3.45	948896	putative transcriptional regulator	P0ADD7
<i>ykgQ</i>	-3.45	5625557	N.A.	N.A.

<i>yoaG</i>	-3.45	946314	uncharacterized protein	P64496
<i>insH1_5</i>	-3.42			
<i>leuT</i>	-3.34	948304	N.A.	N.A.
			cadmium and peroxide resistance protein,	
<i>yhcN</i>	-3.32	947835	stress-induced	P64614
<i>ydcJ</i>	-3.30	945991	putative metalloenzyme	P76097
<i>yeiW</i>	-3.22	4056031	UPF0153 cysteine cluster protein	P0AFT8
<i>yhfL</i>	-3.22	947879	small lipoprotein	P64627
<i>narU</i>	-3.10	945799	nitrate/nitrite transporter	P37758
<i>tfaX</i>	-3.10	945183	N.A.	P77087
<i>tfaX</i>	-3.10	945183	N.A.	P77087
<i>yeeH</i>	-3.10	5625565	N.A.	N.A.
<i>yoaF</i>	-3.07	946310	DUF333 family outer membrane lipoprotein	P64493
<i>ynjH</i>	-3.02	946279	DUF1496 family protein	P76227
<i>proL</i>	-2.94	946320	N.A.	N.A.
			putative general secretory pathway	
<i>gspJ</i>	-2.93	947832	component, cryptic	P45761
<i>yjfN</i>	-2.91	948709	DUF1471 family periplasmic protein	P0AF82
<i>yccE</i>	-2.90	947468	uncharacterized protein	P36661
<i>ivbL</i>	-2.87	948181	ilvB operon leader peptide	P03061
<i>ivbL</i>	-2.87	948181	ilvB operon leader peptide	P03061
<i>yfaZ</i>	-2.83	946739	outer membrane protein, putative porin	P76471
<i>ynjI</i>	-2.83	946239	inner membrane protein	P76228
<i>ybhB</i>	-2.79	945383	kinase inhibitor homolog, UPF0098 family	P12994
<i>ftnB</i>	-2.77	946407	ferritin B, putative ferrous iron reservoir	P0A9A2
<i>asnV</i>	-2.76	946509	N.A.	N.A.
<i>dicF</i>	-2.76	946140	N.A.	N.A.
<i>ssuE</i>	-2.76	945947	NAD(P)H-dependent FMN reductase	P80644
<i>ssuE</i>	-2.76	945947	NAD(P)H-dependent FMN reductase	P80644
<i>yadN</i>	-2.76	944841	putative fimbrial-like adhesin protein CP4-57 prophage, putative anti-restriction	P37050
<i>yfjX</i>	-2.76	947126	protein	P52139
<i>yhaC</i>	-2.76	947557	pentapeptide repeats-related protein	P11864
			putative Mg(2+) transport ATPase, inner	
<i>yhiD</i>	-2.76	948019	membrane protein	P0AFV2
<i>yjeV</i>	-2.76	7751630	uncharacterized protein	C1P621
<i>proM</i>	-2.76	948303	N.A.	N.A.
<i>yjHD</i>	-2.71	948809	N.A.	P39354
<i>mocA</i>	-2.68	947356	CTP:molybdopterin cytidyltransferase	Q46810
			chemotaxis regulator, protein-	
<i>cheR</i>	-2.67	946396	glutamate methyltransferase	P07364
<i>yjgN</i>	-2.67	948784	DUF898 family inner membrane protein	P39338
			ribophosphonate triphosphate synthase	
			subunit, putative ABC transporter-related	
<i>phnL</i>	-2.62	948612	ATPase	P16679
<i>yebB</i>	-2.62	946377	DUF830 family protein	P24238
			ribophosphonate triphosphate synthase	
<i>phnH</i>	-2.59	948619	subunit	P16686



<i>pinR</i>	-2.59	948973	Rac prophage, putative site-specific recombinase	P0ADI0
<i>pinR</i>	-2.59	948973	Rac prophage, putative site-specific recombinase	P0ADI0
<i>yehL</i>	-2.59	946656	putative hexameric AAA+ MoxR family ATPase	P33348
<i>yneK</i>	-2.59	946080	uncharacterized protein	P76150
<i>yhfG</i>	-2.58	947871	putative antitoxin for Fic	P0ADX5
<i>ytfK</i>	-2.56	948736	DUF1107 family protein	P0ADE2
<i>bluF</i>	-2.55	947592	anti-repressor for YcgE, blue light-responsive, FAD-binding, inactive c-di-GMP phosphodiesterase-like EALdomain protein	P75990
<i>yecD</i>	-2.53	946384	isochorismatase family protein	P0ADI7
<i>ttdA</i>	-2.53	947565	L-tartrate dehydratase, alpha subunit	P05847
<i>ygbE</i>	-2.53	947268	DUF3561 family inner membrane protein	P46141
<i>yhfX</i>	-2.50	947889	putative pyridoxal 5'-phosphate binding protein	P45550
<i>yecE</i>	-2.44	946382	UPF0759 family protein	P37348
<i>ypdK</i>	-2.44	7751622	inner membrane protein	C1P610
<i>leuU</i>	-2.43	947505	N.A.	N.A.
<i>eptB</i>	-2.42	948068	KDO phosphoethanolamine transferase, Ca(2+)-inducible	P37661
<i>eaeH</i>	-2.41	944957	N.A.	P36943
<i>yehP</i>	-2.41	946652	VMA domain putative YehL ATPase stimulator	P33352
<i>ygeQ</i>	-2.41	947344	N.A.	Q46797
<i>ydeM</i>	-2.39	945981	putative YdeN-specific sulfatase-maturing enzyme	P76134
<i>greB</i>	-2.38	2847706	transcript cleavage factor	P30128
<i>leuP</i>	-2.37	948875	N.A.	N.A.
<i>mepM</i>	-2.37	946376	murein DD-endopeptidase, space-maker hydrolase, septation protein	P0AFS9
<i>ycgG</i>	-2.36	945738	putative membrane-anchored cyclic-di-GMP phosphodiesterase	P75995
<i>yfdX</i>	-2.36	949108	uncharacterized protein	P76520
<i>yneL</i>	-2.36	946063	N.A.	P76138
<i>glnX</i>	-2.35	945257	N.A.	N.A.
<i>arcZ</i>	-2.34	2847690	N.A.	N.A.
<i>yncl</i>	-2.33	5061503	stress-induced small inner membrane enterobacterial protein	A5A615
<i>araG</i>	-2.32	946408	L-arabinose ABC transporter ATPase	P0AAF3
<i>tnaB</i>	-2.32	948220	tryptophan transporter of low affinity	P23173
<i>ygjQ</i>	-2.32	947598	DUF218 superfamily protein	P42598
<i>yeaV</i>	-2.31	947326	putative transporter	P0ABD1
<i>alaX</i>	-2.30	946859	N.A.	N.A.
<i>cadB</i>	-2.30	948654	putative lysine/cadaverine transporter	P0AAE8
<i>istR</i>	-2.30	5061525	N.A.	N.A.
<i>istR</i>	-2.30	5061525	N.A.	N.A.
<i>rclC</i>	-2.30	944974	reactive chlorine species (RCS) stress-resistance inner membrane protein	P75685
<i>ybgO</i>	-2.30	947550	putative fimbrial protein	P75748
<i>acrE</i>	-2.28	947706	cytoplasmic membrane lipoprotein	P24180

<i>asr</i>	-2.28	945103	acid shock-inducible periplasmic protein	P36560
<i>viaK</i>	-2.27	948096	2,3-diketo-L-gulonate reductase, NADH-dependent	P37672
<i>ryjB</i>	-2.27	5061532	N.A.	N.A.
<i>cbtA</i>	-2.26	946534	CP4-44 prophage, toxin of the YeeV-YeeU toxin-antitoxin system	P64524
<i>yobB</i>	-2.25	948329	C-N hydrolase family protein	P76280
<i>glcC</i>	-2.25	947466	glycolate-inducible glc operon transcriptional repressor, autorepressor	P0ACL5
<i>gatY</i>	-2.25	946636	D-tagatose 1,6-bisphosphate aldolase 2, catalytic subunit	POC8J6
<i>nrfB</i>	-2.25	948573	nitrite reductase, formate-dependent, penta-hemocytochrome c	POABL1
<i>nrfB</i>	-2.25	948573	nitrite reductase, formate-dependent, penta-hemocytochrome c	POABL1
<i>dtpB</i>	-2.24	948006	dipeptide and tripeptide permease B	P36837
<i>arpA</i>	-2.24	944933	ankyrin repeat protein	P23325
<i>chiX</i>	-2.24	5061500	N.A.	N.A.
<i>hchA</i>	-2.24	946481	glyoxalase III and Hsp31 molecular chaperone	P31658
<i>malG</i>	-2.24	948530	maltose transporter subunit	P68183
<i>prfH</i>	-2.24	947374	N.A.	P28369
<i>proK</i>	-2.24	948061	N.A.	N.A.
<i>yeiL</i>	-2.24	946670	putative transcriptional regulator	POA9E9
<i>yfdF</i>	-2.24	946819	uncharacterized protein	P76505
<i>bsmA</i>	-2.24	948708	bioflm peroxide resistance protein	P39297
<i>yoeG</i>	-2.23	5625566	N.A.	N.A.
<i>araF</i>	-2.23	946409	L-arabinose ABC transporter periplasmic binding protein	P02924
<i>ydjJ</i>	-2.23	946292	putative Zn-dependent NAD(P)-binding oxidoreductase	P77280
<i>yjhX</i>	-2.23	1450297	UPF0386 family protein	Q2EEU2
<i>tnaC</i>	-2.21	948223	tryptophanase leader peptide	P0AD89
<i>prpR</i>	-2.21	944987	propionate catabolism operon regulatory protein	P77743
<i>fadA</i>	-2.20	948324	3-ketoacyl-CoA thiolase (thiolase I)	P21151
<i>leuL</i>	-2.20	946072	leu operon leader peptide	P0AD79
<i>uhpT</i>	-2.20	948201	hexose phosphate transporter	P0AGCO
<i>fadB</i>	-2.19	948336	fused 3-hydroxybutyryl-CoA epimerase /delta(3)-cis-delta(2)-trans-enoyl- CoA isomerase/enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase	P21177
<i>argX</i>	-2.19	945107	N.A.	N.A.
<i>glnV</i>	-2.18	945255	N.A.	N.A.
<i>astA</i>	-2.17	946261	arginine succinyltransferase	P0AE37
<i>fumC</i>	-2.15	946147	fumarate hydratase (fumarase C), aerobic ClassII	P05042
<i>astE</i>	-2.14	946256	succinylglutamate desuccinylase	P76215
<i>fadH</i>	-2.14	947594	2,4-dienoyl-CoA reductase, NADH and FMN-linked	P42593
<i>yhjH</i>	-2.13	948042	cyclic-di-GMP phosphodiesterase, FlhDC-regulated	P37646

<i>astC</i>	-2.13	946255	succinylornithine transaminase, PLP-dependent	P77581
<i>putP</i>	-2.13	945602	proline:sodium symporter	P07117
<i>hscC</i>	-2.12	945218	Hsp70 family chaperone Hsc62, RpoD-binding transcription inhibitor	P77319
<i>fic</i>	-2.12	947872	stationary phase-induced protein, putative toxin	P20605
<i>mcbR</i>	-2.12	946014	colanic acid and biofilm gene transcriptional regulator, MqsR-controlled	P76114
<i>asnW</i>	-2.12	946494	N.A.	N.A.
<i>yqjI</i>	-2.12	947530	DUF1449 family inner membrane protein	P76657
<i>nikC</i>	-2.11	947990	nickel ABC transporter permease	P0AFA9
<i>ulaA</i>	-2.09	948717	L-ascorbate-specific enzyme IIC permease component of PTS	P39301
<i>mliC</i>	-2.09	946811	inhibitor of c-type lysozyme, membrane-bound, putative lipoprotein	P28224
<i>astB</i>	-2.09	946259	succinylarginine dihydrolase	P76216
<i>aspA</i>	-2.09	948658	aspartate ammonia-lyase	P0AC38
<i>csgF</i>	-2.07	945622	curli nucleation outer membrane protein	P0AE98
<i>fimI</i>	-2.07	948841	fimbrial protein involved in type 1 pilus biosynthesis	P39264
<i>glnK</i>	-2.07	945087	nitrogen assimilation regulatory protein for GlnL, GlnE, and AmtB	P0AC55
<i>hycB</i>	-2.07	948002	hydrogenase 3, Fe-S subunit	P0AAK1
<i>nrfG</i>	-2.07	948592	heme lyase (NrfEFG) for insertion of heme in toc552, subunit NrfG	P32712
<i>nrfG</i>	-2.07	948592	heme lyase (NrfEFG) for insertion of heme intoc552, subunit NrfG	P32712
<i>prpB</i>	-2.07	944990	2-methylisocitrate lyase	P77541
<i>ralA</i>	-2.07	20160642	N.A.	N.A.
<i>rhmR</i>	-2.07	944752	putative DNA-binding transcriptional regulator for the rhm operon	P77732
<i>rzpQ</i>	-2.07	946101	Rz-like protein, Qin prophage	P76158
<i>selC</i>	-2.07	948167	N.A.	N.A.
<i>selC</i>	-2.07	948167	N.A.	N.A.
<i>selC</i>	-2.07	948167	N.A.	N.A.
<i>torC</i>	-2.07	946252	trimethylamine N-oxide (TMAO) reductase I, cytochrome c-type subunit	P33226
<i>wcaD</i>	-2.07	946550	putative colanic acid polymerase	P71238
<i>ybeR</i>	-2.07	945249	uncharacterized protein	P77627
<i>ybfB</i>	-2.07	947566	putative membrane protein	P0AAU5
<i>ybiY</i>	-2.07	945445	putative pyruvate formate lyase activating enzyme	P75794
<i>ycgY</i>	-2.07	945761	uncharacterized protein	P76012
<i>yciE</i>	-2.07	946871	putative rubrerythrin/ferritin-like metal-binding protein	P21363
<i>ydfK</i>	-2.07	947451	cold shock protein, function unknown, Qin prophage	P76154
<i>yehK</i>	-2.07	4056035	uncharacterized protein	P33347
<i>yghS</i>	-2.07	947476	putative ATP-binding protein	Q46843
<i>yhaB</i>	-2.07	947705	uncharacterized protein	P11865
<i>yhdU</i>	-2.07	947700	putative membrane protein	P64619

			putative Hcp1 family polymorphic toxin protein ,putative colicin-like DNase/tRNase activity	P46855
<i>yhhZ</i>	-2.07	947952		
<i>ylcG</i>	-2.07	1450240	uncharacterized protein, DLP12 prophage	Q47272
<i>ynfN</i>	-2.07	946097	Qin prophage, cold shock-induced protein	P76157
<i>yoeF</i>	-2.07	1450273	N.A.	Q2EES3
			peptidyl-prolyl cis-trans isomerase A (rotamaseA)	P0AFL3
<i>ppiA</i>	-2.05	947870		
<i>ligB</i>	-2.05	948164	DNA ligase, NAD(+)-dependent	P25772
			putative membrane-anchored cyclic-di-GMP phosphodiesterase	P75800
<i>yliE</i>	-2.04	945462		
<i>hisR</i>	-2.03	948305	N.A.	N.A.
<i>secG</i>	-2.03	947720	preprotein translocase membrane subunit	P0AG99
<i>secG</i>	-2.03	947720	preprotein translocase membrane subunit	P0AG99
<i>secG</i>	-2.03	947720	preprotein translocase membrane subunit	P0AG99
<i>feaR</i>	-2.02	945941	transcriptional activator for <i>tynA</i> and <i>feaB</i>	Q47129
<i>alaW</i>	-2.02	946860	N.A.	N.A.
			bifunctional prepilin leader	
<i>gspO</i>	-2.02	947840	peptidase/methylase	P25960
<i>ymfA</i>	-2.02	945684	DUF3592 family inner membrane protein	P75962
<i>yebQ</i>	-2.01	946048	putative transporter	P76269
<i>dgcZ</i>	-2.0	946075	diguanylate cyclase, zinc-sensing	P31129

Feature ID	ARM9 vs AS19 fold change	GeneID	Protein Product	UniProt/SwissProt Accession
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#### UP-REGULATED

			toxin of GhoTS toxin-antitoxin pair, membrane-lytic protein, stimulator of persister cell formation	P64646
<i>ghoT</i>	7.25	1450308		
<i>xisD</i>	7.25	5625559	N.A.	N.A.
<i>yciG</i>	5.80	947489	KGG family protein	P21361
			antitoxin of GhoTS toxin-antitoxin pair,	
<i>ghoS</i>	5.32	948646	endonuclease for <i>ghoT</i> mRNA	P0AF61
<i>ylcI</i>	5.32	5061499	DUF3950 family protein, DLP12 prophage	A5A607
<i>rrfD</i>	5.08	947769	N.A.	N.A.
<i>ymgA</i>	4.46	948991	RcsB connector protein for regulation of biofilm	P75992
<i>ppdD</i>	4.35	945817	putative prepilin peptidase-dependent pilin	P36647
<i>rrsC</i>	3.93	948270	N.A.	N.A.
<i>grcA</i>	3.89	947068	autonomous glycyl radical cofactor	P68066
<i>ydeQ</i>	3.87	946050	putative fimbrial-like adhesin protein	P77588
<i>ibpB</i>	3.74	948192	heat shock chaperone	POC058
<i>rrfG</i>	3.55	947070	N.A.	N.A.
<i>sstT</i>	3.42	947605	sodium:serine/threonine symporter	POAGE4
<i>sstT</i>	3.42	947605	sodium:serine/threonine symporter	POAGE4
<i>rrfH</i>	3.38	944898	N.A.	N.A.
<i>rrfB</i>	3.32	948471	N.A.	N.A.

<i>yccT</i>	3.16	945577	UPF0319 family protein	P0A8X4
<i>nirD</i>	3.08	947881	nitrite reductase (NADH) small subunit	P0A9I8
<i>cstA</i>	3.06	945213	carbon starvation protein involved in peptide utilization, APC peptide transporter family protein	P15078
<i>aaeX</i>	2.90	947751	DUF1656 family putative inner membrane efflux pump associated protein	P46478
<i>esrE</i>	2.90	14678511	N.A.	N.A.
<i>hokA</i>	2.90	2847732	toxic polypeptide, small	P37305
<i>insl1_2</i>	2.90			
<i>rutF</i>	2.90	946594	flavin:NADH reductase	P75893
<i>wcaB</i>	2.90	946573	putative acyl transferase	P0ACC9
<i>ydeO</i>	2.90	945922	UV-inducible global regulator, EvgA-,GadE-dependent	P76135
<i>yfbK</i>	2.90	946743	Von Willebrand factor domain putative lipoprotein	P76481
<i>yohP</i>	2.90	7751636	uncharacterized protein	C1P609
<i>ompT</i>	2.89	945185	DLP12 prophage, outer membrane protease VII, outer membrane protein 3b	P09169
<i>phnK</i>	2.74	948611	carbon-phosphorus lyase complex subunit,putative ATP transporter ATP-binding protein	P16678
<i>bglH</i>	2.69	948228	carbohydrate-specific outer membrane porin, cryptic	P26218
<i>yhjE</i>	2.50	948032	putative MFS transporter, membrane protein	P37643
<i>ycgZ</i>	2.47	945885	RcsB connector protein for regulation of biofilmand acid-resistance	P75991
<i>fimC</i>	2.42	948843	periplasmic chaperone	P31697
<i>yegR</i>	2.42	946613	uncharacterized protein	P76406
<i>yigG</i>	2.42	948344	PRK11371 family inner membrane protein	P27843
<i>ybdD</i>	2.36	949021	DUF466 family protein	P0AAS9
<i>ibpA</i>	2.31	948200	heat shock chaperone	P0C054
<i>ariR</i>	2.28	945340	RcsB connector protein for regulation of biofilm and acid-resistance	P75993
<i>chaA</i>	2.28	945790	calcium/sodium:proton antiporter	P31801
<i>citG</i>	2.18	946395	2-(5''-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase	P77231
<i>dicC</i>	2.18	946120	Qin prophage, DNA-binding transcriptional regulator for DicB	P06965
<i>gfcC</i>	2.18	944978	ionperiplasmic protein	P75883
<i>rrfC</i>	2.18	948273	N.A.	N.A.
<i>tfaD</i>	2.18	945171	N.A.	P77699
<i>tfaD</i>	2.18	945171	N.A.	P77699
<i>ttdB</i>	2.18	947568	L-tartrate dehydratase, beta subunit	P0AC35
<i>yafF</i>	2.18	1450235	N.A.	Q2EEP9
<i>ydeR</i>	2.18	946049	putative fimbrial-like adhesin protein	P77294
<i>ydiL</i>	2.18	946181	putative HTH domain DNA-binding protein	P76196
<i>yjiC</i>	2.18	948850	uncharacterized protein	P39374
<i>ymjC</i>	2.18	1450258	N.A.	Q2EER5
<i>ompF</i>	2.11	945554	outer membrane porin 1a (Ia,b,F)	P02931
<i>ybfA</i>	2.11	947452	DUF2517 family protein	P0AAU2
<i>ydiB</i>	2.10	946200	quinat/shikimate 5-dehydrogenase,NAD(P)-binding	P0A6D5
<i>fimF</i>	2.05	948845	minor component of type 1 fimbriae	P08189
<i>caiD</i>	2.05	948995	carnitinyI-CoA dehydratase	P31551

*ydfU*

2.03

946108

Qin prophage, uncharacterized protein

P76162