

Locus Tag	Gene name	Description
PA14_44340	ccoN	Putative cytochrome oxidase subunit (Cbb3-type)
PA14_62400	yfdZ	Putative aminotransferase
PA14_00780		Putative carbonic anhydrases
PA14_58070		Putative tldD protein
PA14_33990		Probable ClpA/B-type protease
PA14_00940		Putative uncharacterized protein
PA14_52420	rimO	Ribosomal protein S12 methylthiotransferase RimO (S12 M)
PA14_42230	bglX	Periplasmic beta-glucosidase
PA14_01540		Putative uncharacterized protein
PA14_54180		Putative uncharacterized protein
PA14_39960	phzB2	Probable phenazine biosynthesis protein
PA14_64480	osmE	Osmotically inducible lipoprotein OsmE
PA14_28340		Putative peroxidase
PA14_00440	trpA	Tryptophan synthase alpha chain (EC 4.2.1.20)
PA14_38530	fahA	Fumarylacetoacetase
PA14_07280	yhiN	Putative periplasmic protein
PA14_53040		Putative uncharacterized protein
PA14_25160	lexA	LexA repressor (EC 3.4.21.88)
PA14_60890	glyA	Serine hydroxymethyltransferase (SHMT) (Serine methyla
PA14_34050		Putative uncharacterized protein
PA14_02810	pcaT	Dicarboxylic acid transporter PcaT
PA14_36020		Paraquat-inducible protein B
PA14_67350	hutU	Urocanate hydratase (Urocanase) (EC 4.2.1.49) (Imidazole
PA14_53950	prpC	Citrate synthase
PA14_51670	queC	7-cyano-7-deazaguanine synthase (EC 6.3.4.20) (7-cyano-
PA14_61700	prfA	Peptide chain release factor 1 (RF-1)
PA14_58250		Putative membrane protein
PA14_27370	deaD	Putative ATP-dependent RNA helicase, DEAD box family
PA14_38590	bdhA	3-hydroxybutyrate dehydrogenase
PA14_57720	cysD	Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4) (ATP-su
PA14_60830	mexD	Multidrug efflux RND transporter MexD
PA14_34030		Putative uncharacterized protein
PA14_50570		Putative uncharacterized protein
PA14_16180		Putative uncharacterized protein
PA14_47190	cyoB	Cytochrome o ubiquinol oxidase subunit I
PA14_38660	scoA	Putative CoA transferase, subunit A
PA14_03800	oprE	Anaerobically-induced outer membrane porin OprE
PA14_11340	trx-1	Putative thioredoxin
PA14_57780	hisD	Histidinol dehydrogenase (HDH) (EC 1.1.1.23)
PA14_00510		Putative hemagglutinin
PA14_26700		Putative acyl-CoA dehydrogenase
PA14_21020		Putative non-ribosomal peptide synthetase
PA14_67320	hutH	Histidine ammonia-lyase (Histidase) (EC 4.3.1.3)
PA14_41420		Putative uncharacterized protein
PA14_71650	aspA	Aspartate ammonia-lyase
PA14_03610	ycaL	Putative putative Zn-dependent protease with chaperone
PA14_68120	opmG	Putative outer membrane protein
PA14_07530	dnaG	DNA primase (EC 2.7.7.-)

PA14_40010		Putative uncharacterized protein
PA14_36310	hcnC	Hydrogen cyanide synthase HcnC
PA14_38840	exaC	NAD ⁺ dependent acetaldehyde dehydrogenase
PA14_31510		Putative short-chain dehydrogenase
PA14_15350		Putative integrase
PA14_16190		Putative uncharacterized protein
PA14_01020		Putative uncharacterized protein
PA14_57710	cysN	ATP sulfurylase GTP-binding subunit/APS kinase
PA14_29420	ysgA	Putative diene lactone hydrolase
PA14_48610		Putative sparagine synthase
PA14_03050	pobA	p-hydroxybenzoate hydroxylase
PA14_61040	katB	Catalase (EC 1.11.1.6)
PA14_01010		Putative uncharacterized protein
PA14_47210	cyoA	Cytochrome o ubiquinol oxidase subunit II
PA14_00910		Putative uncharacterized protein
PA14_48560		Putative uncharacterized protein
PA14_20980		Putative short chain dehydrogenase
PA14_03650	cysA	Sulfate transport protein CysA
PA14_29230		Putative hydrolase
PA14_26750		Putative uncharacterized protein
PA14_00925		Putative uncharacterized protein
PA14_60850	mexC	Multidrug efflux RND membrane fusion protein
PA14_18120	mmsA	Methylmalonate-semialdehyde dehydrogenase
PA14_48570		Putative 2-isopropylmalate synthase
PA14_48590		Putative uncharacterized protein
PA14_40770	cysI	Sulfite reductase
PA14_72660		Putative amidase
PA14_42450	popB	Translocator protein PopB
PA14_36810	katE	Catalase (EC 1.11.1.6)
PA14_00820		Putative uncharacterized protein
PA14_01100	clpB	Putative ClpA/B-type chaperone
PA14_60190	clpB	ClpB protein
PA14_59220		Pyocin S5
PA14_00875	ppkA	Serine/threonine protein kinase PpkA
PA14_71560	fdhA	Glutathione-independent formaldehyde dehydrogenase
PA14_62940	dapB	4-hydroxy-tetrahydrodipicolinate reductase (HTPA reductase)
PA14_62960	dnaJ	Chaperone protein DnaJ
PA14_43840		Putative diene lactone hydrolase family protein
PA14_38640	scoB	Putative CoA transferase, subunit B
PA14_53070	hpd	4-hydroxyphenylpyruvate dioxygenase
PA14_54210		Lon protease (EC 3.4.21.53)
PA14_18140	mmsB	3-hydroxyisobutyrate dehydrogenase
PA14_62970	dnaK	Chaperone protein DnaK (HSP70) (Heat shock 70 kDa protein)
PA14_43850	htpG	Chaperone protein HtpG (Heat shock protein HtpG) (High temperature shock protein)
PA14_66790	hslU	ATP-dependent protease ATPase subunit HslU (Unfoldase)
PA14_62990	grpE	Protein GrpE (HSP-70 cofactor)
PA14_08070	gpFI	Putative phage tail sheath protein
PA14_66770	hslV	ATP-dependent protease subunit HslV (EC 3.4.25.2)
PA14_02790	pcaF	Beta-ketoadipyl CoA thiolase PcaF
PA14_02770	pcaJ	Putative CoA transferase, subunit B

PA14_53820		Putative uncharacterized protein
PA14_02760	catI	Putative CoA transferase, subunit A

Protein abundance ratios (P) and normalized mRNA reads (T) of the PA14 *tnprmC* tran

$\log_2((P(\text{tnprmC}) / P(\text{tnprmC}::\text{prmC})) / ((T(\text{tnprmC}) / T(\text{tnprmC}::\text{prmC})))$	Stop codon
0,73	TGA
0,73	TGA
0,74	TGA
0,74	TGA
0,75	TGA
0,76	TAA
0,76	TGA
0,77	TGA
0,78	TAA
0,78	TGA
0,78	TGA
0,78	TGA
0,79	TGA
0,80	TGA
0,80	TGA
0,83	TGA
0,83	TAG
0,83	TGA
0,83	TGA
0,83	TAA
0,84	TGA
0,85	TGA
0,86	TGA
0,86	TGA
0,88	TGA
0,89	TGA
0,91	TGA
0,92	TGA
0,93	TGA
0,94	TAG
0,94	TGA
0,94	TGA
0,96	TGA
0,98	TAG
1,02	TGA
1,02	TGA
1,03	TGA
1,03	TAA
1,03	TGA
1,07	TGA
1,08	TGA
1,14	TGA
1,15	TGA
1,15	TGA
1,15	TGA
1,16	TGA
1,17	TAA
1,17	TGA
1,18	TGA

1,19	TAA
1,21	TAG
1,24	TGA
1,28	TAA
1,30	TAA
1,30	TGA
1,31	TGA
1,32	TGA
1,33	TAG
1,33	TGA
1,36	TAG
1,36	TGA
1,41	TAA
1,44	TAA
1,45	TGA
1,46	TGA
1,48	TGA
1,50	TGA
1,54	TGA
1,54	TAA
1,59	TGA
1,60	TAA
1,60	TGA
1,65	TGA
1,67	TGA
1,68	TAA
1,71	TGA
1,76	TGA
1,81	TGA
1,82	TGA
1,84	TGA
1,87	TGA
1,90	TAA
1,92	TGA
1,92	TGA
2,12	TGA
2,18	TAA
2,18	TGA
2,20	TGA
2,22	TGA
2,28	TGA
2,28	TGA
2,49	TAA
2,51	TAA
2,61	TGA
2,63	TGA
2,65	TAA
2,72	TGA
2,81	TGA
3,32	TGA

3,45	TGA
3,53	TGA

sposon mutant complemented with pUCP20::EV (*tn_{pr}mC*) compared to the mutant complemented with pUCF

$\rho^{20}::prmC$ ($tnprmC::prmC$) were combined to PrmC-dependent protein to mRNA ratios: (P($tnprmC$),

$/P(\text{tnprmC}::\text{prmC})/T(\text{tnprmC})/T(\text{tnprmC}::\text{prmC})$). The 100 genes with the highest values (top 100 *h*

igh) were selected.