

Locus Tag	Gene name	Description
PA14_18820		Putative uncharacterized protein
PA14_68440		Putative oxidoreductase, molybdopterin-binding
PA14_40070		Putative glutathione S-transferase
PA14_09240	pchD	Pyochelin biosynthesis protein PchD
PA14_07890		Putative permease of ABC transporter
PA14_11320		Putative uncharacterized protein
PA14_13170		Probable metal transporting P-type ATPase
PA14_09340	fptA	Fe(III)-pyochelin outer membrane receptor
PA14_39590	metE	5-methyltetrahydropteroyltriglutamate--homocysteine
PA14_57800	hisG	ATP phosphoribosyltransferase (ATP-PRT) (ATP-PRTase)
PA14_63100		Putative ferredoxin
PA14_05460	bioA	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
PA14_07870		Putative binding protein component of ABC transporter
PA14_01620	aptA	Beta-alanine--pyruvate transaminase
PA14_19350		Putative peptidase or cellulase
PA14_20200	nosZ	Nitrous-oxide reductase (EC 1.7.2.4) (N(2)OR) (N2O reductase)
PA14_39350	rbsB	Binding protein component of ABC ribose transporter
PA14_35330	kguT	Putative 2-ketogluconate transporter
PA14_04220		Putative binding protein component of ABC transporter
PA14_04090	fliY	Putative binding protein component of ABC transporter
PA14_47550		Glutathione peroxidase
PA14_07860		Putative ATP-binding component of ABC transporter
PA14_68260		Probable c4-dicarboxylate-binding protein
PA14_49330		Putative uncharacterized protein
PA14_35320	kguD	2-ketogluconate 6-phosphate reductase
PA14_40230		Putative secretion protein
PA14_65740	thiC	Phosphomethylpyrimidine synthase (EC 4.1.99.17) (Hydroxymethylpyrimidine synthase)
PA14_46990		Putative two-component response regulator
PA14_49250	napA	Periplasmic nitrate reductase (EC 1.7.99.4)
PA14_58870	ndh	NADH dehydrogenase
PA14_59840		Putative uncharacterized protein
PA14_27140		Putative ABC transporter, permease protein
PA14_63120	speE	Spermidine synthase (EC 2.5.1.16) (Putrescine aminopropyltransferase)
PA14_17960	glpK	Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)
PA14_33680	fpvA	Ferripyoverdine receptor
PA14_18630	eprS	Putative serine protease
PA14_59150		Single-stranded DNA-binding protein
PA14_06870	dnr	Transcriptional regulator Dnr
PA14_62350	phuR	Putative haem/haemoglobin uptake outer membrane protein
PA14_46960	ggt	Gamma-glutamyltranspeptidase
PA14_05510		UPF0312 protein PA14_05510
PA14_01580	gabP	Gamma-aminobutyrate permease
PA14_09490	phzM	Probable phenazine-specific methyltransferase
PA14_24330		Putative export protein
PA14_46970	ansB	Glutaminase-asparaginase
PA14_13140		Putative uncharacterized protein
PA14_25360	apbE	Putative thiamine biosynthesis lipoprotein
PA14_31030		Putative cation efflux system protein

PA14_39780	hvn	Putative halovibrin
PA14_11810		Putative aldehyde dehydrogenase
PA14_34640	gntK	Gluconokinase
PA14_70080	lrp	Leucine responsive regulatory protein
PA14_17930	glpD	Glycerol-3-phosphate dehydrogenase
PA14_58060		UPF0307 protein PA14_58060
PA14_13190		Putative uncharacterized protein
PA14_68070		Putative ABC transporter, periplasmic amino acid-binding protein
PA14_58410		Putative outer membrane porin
PA14_01320	colI	Cytochrome c oxidase, subunit III
PA14_24310		Putative BNR/Asp-box repeat protein
PA14_73120		Putative periplasmic transport protein
PA14_24790	opdQ	Putative outer membrane porin
PA14_57810	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (E
PA14_25760	holB	DNA polymerase III, delta prime subunit
PA14_58390		Putative binding protein component of ABC transporter
PA14_63090	lldD	L-lactate dehydrogenase [cytochrome] (EC 1.1.2.3)
PA14_72450	dsbA	Thiol:disulfide interchange protein DsbA
PA14_13130		Putative uncharacterized protein
PA14_71030		Putative glycine betaine/L-proline ABC transporter, periplasmic
PA14_61740	lolB	Outer-membrane lipoprotein LolB
PA14_67400		Putative ABC transporter, periplasmic substrate-binding protein
PA14_58730	pilA	Type IV pilin structural subunit
PA14_34140		Putative uncharacterized protein
PA14_57840	ttg2D	Putative toluene tolerance protein
PA14_68340	arcB	Ornithine carbamoyltransferase, catabolic (OTCase) (EC 2.3.1.15)
PA14_63160	pmrB	Two-component sensor
PA14_29090	potF4	Putative periplasmic spermidine/putrescine-binding protein
PA14_43740		Putative 5-oxo-L-prolinase
PA14_00690		Putative metallo-beta-lactamase
PA14_13110		Probable medium-chain acyl-CoA ligase
PA14_23090	edaA	2-keto-3-deoxy-6-phosphogluconate aldolase
PA14_68210	rmlC	dTDP-4-dehydrorhamnose 3,5-epimerase
PA14_09760		Putative transcriptional regulator, GntR family
PA14_11310		Putative ABC transporter, ATP-binding protein
PA14_46910	ybeJ	Putative binding protein component of ABC transporter
PA14_58350		Putative binding protein component of ABC transporter
PA14_05540	mexB	RND multidrug efflux transporter MexB
PA14_14100	yhdW	Putative amino-acid ABC transporter binding protein
PA14_14390		Putative ABC-type transport protein, periplasmic component
PA14_64980	nadE	NH(3)-dependent NAD(+) synthetase (EC 6.3.1.5)
PA14_21960		Putative ABC transporter, periplasmic substrate-binding protein
PA14_35290	gnd	Gluconate dehydrogenase
PA14_71580		Putative uncharacterized protein
PA14_53230		Probable oxidoreductase
PA14_68900	fbpA	Putative iron ABC transporter, periplasmic iron-binding protein
PA14_66120		Putative uncharacterized protein
PA14_22450	ppiA	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)
PA14_68060		Putative amino acid ABC transporter, ATP-binding protein
PA14_04010		Putative uncharacterized protein

PA14_18350	arnA	Bifunctional polymyxin resistance protein ArnA [Includ
PA14_46240		Putative mechanosensitive ion channel family protein

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

$\log_2((P(\text{tnprmC}) / P(\text{tnprmC}::\text{prmC})) / ((T(\text{tnprmC}) / T(\text{tnprmC}::\text{prmC})))$	Stop codon
-3,06	TGA
-2,57	TGA
-2,51	TGA
-2,51	TGA
-2,48	TAG
-2,47	TAG
-2,41	TGA
-2,31	TGA
-2,29	TGA
-2,27	TGA
-2,23	TAG
-2,22	TGA
-2,19	TAA
-2,15	TGA
-1,92	TGA
-1,78	TGA
-1,71	TGA
-1,66	TGA
-1,66	TGA
-1,62	TGA
-1,62	TGA
-1,62	TGA
-1,56	TAA
-1,55	TGA
-1,48	TGA
-1,48	TGA
-1,48	TAG
-1,45	TAG
-1,44	TGA
-1,43	TGA
-1,42	TGA
-1,40	TGA
-1,38	TGA
-1,38	TGA
-1,37	TGA
-1,35	TGA
-1,33	TAG
-1,33	TGA
-1,29	TGA
-1,23	TGA
-1,22	TAA
-1,22	TGA
-1,22	TGA
-1,20	TGA
-1,20	TGA
-1,19	TGA
-1,18	TGA
-1,17	TGA

-1,16	TGA
-1,14	TAG
-1,12	TGA
-1,12	TGA
-1,10	TGA
-1,08	TAG
-1,05	TAA
-1,04	TGA
-1,04	TAA
-1,03	TGA
-1,03	TAA
-1,02	TGA
-1,00	TAA
-1,00	TAG
-1,00	TAG
-0,99	TGA
-0,99	TGA
-0,99	TAG
-0,98	TGA
-0,97	TAG
-0,97	TGA
-0,97	TAA
-0,97	TAA
-0,97	TAG
-0,97	TGA
-0,96	TGA
-0,95	TGA
-0,92	TGA
-0,91	TAA
-0,91	TGA
-0,91	TGA
-0,91	TGA
-0,91	TGA
-0,89	TAG
-0,89	TGA
-0,88	TAA
-0,88	TAG
-0,88	TGA
-0,87	TGA
-0,87	TAA
-0,86	TGA
-0,85	TGA
-0,85	TGA
-0,85	TAG
-0,84	TAG
-0,84	TGA
-0,84	TGA
-0,84	TGA
-0,84	TAA
-0,84	TAA

-0,83	TGA
-0,83	TGA

ransposon mutant complemented with pUCP20::EV (*tnprmC*) compared to the mutant complemented with pl







JCP20::*prmC* (*tnprmC* ::*prmC*) were combined to PrmC-dependent protein to mRNA ratios: (P(*tnprm*





$iC)/P(\text{tnprmC}::\text{prmC})/(\text{T}(\text{tnprmC})/\text{T}(\text{tnprmC}::\text{prmC}))$ . The 100 genes with the lowest values (top100)





) low ) were selected.