

Table S1. Characterization of antibacterial activity of *P. putida* BW11M1. Homology of genes disrupted in *P. putida* BW11M1 plasposon mutants lacking antibacterial activity using *X. alfalfae* subsp. *alfalfae* LMG 497 as indicator strain.

Mutant	Homology				
	Protein name	Accession nr	Function of gene product	Identity ^a	Reference [*]
CMPG2178, CMPG2179, CMPG2180, CMPG2181, CMPG2182, CMPG2183, CMPG2184	EtIA (PSEEN3332)	YP_608877	Entolysin synthetase A	75%	[1]
CMPG2185, CMPG2186, CMPG2187, CMPG2188, CMPG2189, CMPG2190, CMPG2191, CMPG2192, CMPG2193, CMPG2194	EtIB (PSEEN3045)	YP_608606	Entolysin synthetase B	69%	[1]
CMPG2195, CMPG2196, CMPG2197, CMPG2198, CMPG2199, CMPG2200	EtIC (PSEEN3044)	YP_608605	Entolysin synthetase C	72%	[1]
CMPG2201	EtIR (PSEEN3335)	YP_608878	Entolysin transcriptional regulator (LuxR family)	75%	[1]
CMPG2202	FahA (PSEEN4611)	YP_610068	Fumarylacetoacetase (homogentisate catabolism)	97%	[2]
CMPG2203	CysG (PSEEN2217)	YP_607840	Siroheme synthase	96%	[3]
CMPG2204	RecB (PSEEN0692)	YP_606434	Exonuclease V, beta subunit	90%	[4]
CMPG2205	ClpB (PSEEN4678)	YP_610130	ATP-dependent Clp protease, ATP-binding subunit	99%	[5]
CMPG2206	PSEEN0141	YP_605934	Surface adhesion protein LapA homologue	96%	[6]
CMPG2207	PSEEN3459	YP_608995	Alginate <i>O</i> -acetylation protein (AlgJ-like)	84%	[7]
CMPG2208	PA3156	NP_251846	LPS <i>N</i> -acetyltransferase WbpD homologue	84%	[8]
CMPG2209	PyrE (PSEEN5436)	YP_610831	Orotate phosphoribosyl-transferase	100%	[9]
CMPG2210	LeuS (PSEEN4813)	YP_610252	Leucyl-tRNA synthetase	98%	[10]
CMPG2211	PSEEN4860	YP_610295	Hypothetical protein	80%	[11]

^a Amino acid sequence identity of the predicted full-length gene product deduced from the corresponding gene identified in the *P. putida* BW11M1 draft genomic sequence (unpublished data). For all mutants genes, highest homology was found for *Pseudomonas entomophila* L48 gene products [12], except for CMPG2208 with a disrupted gene encoding a homologue of *Pseudomonas aeruginosa* PAO1 WbpD.

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