

Supplementary material

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-Manuscript Title: *Harnessing Paenarthrobacter ureafaciens YL1 and Pseudomonas koreensis YL2 interactions to improve degradation of sulfamethoxazole*

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Table S1 The CARD analysis⁵³ of the strain YL2: the Resistance Gene Identifier (RGI) for perfect and strict hits to known resistance genes.

RGI Criteria	ARO Term	Detection Criteria	AMR Gene Family	Drug class	Resistance Mechanism	% Identity of Matching Region	% Length of Reference Sequence
Strict	adeF	protein homolog model	resistance-nodulation-cell division (RND) antibiotic efflux pump	fluoroquinolone antibiotic, tetracycline antibiotic	antibiotic efflux	66.6	100.28
Strict	adeF	protein homolog model	resistance-nodulation-cell division (RND) antibiotic efflux pump	fluoroquinolone antibiotic, tetracycline antibiotic	antibiotic efflux	43.1	97.45
Strict	FosA	protein homolog model	fosfomycin thiol transferase	fosfomycin	antibiotic inactivation	69.12	102.22
Strict	Pseudomonas aeruginosa soxR	protein homolog model	ATP-binding cassette (ABC) antibiotic efflux pump, major facilitator superfamily (MFS) antibiotic efflux pump, resistance-nodulation-cell division (RND) antibiotic efflux pump	fluoroquinolone antibiotic, cephalosporin, glycylycine, penam, tetracycline antibiotic, acridine dye, rifamycin antibiotic, phenicol antibiotic, triclosan, disinfecting agents and intercalating dyes	antibiotic target alteration, antibiotic efflux	68.79	95.51
Strict	Acinetobacter baumannii AbaQ	protein homolog model	major facilitator superfamily (MFS) antibiotic efflux pump	fluoroquinolone antibiotic	antibiotic efflux	72.81	101.38