

Supplementary Material

Table S1. *P. aeruginosa* PBP3 variants within the transpeptidase domain^a.

[illegible]

^aSequence variants in the transpeptidase domain of PBP3 in clinical isolates and experimentally evolved β -lactam-resistant mutants are listed. Variants predicted using the bioinformatics tool Provean^{1, 17, 18} to affect protein function are shown in red, and those predicted to not significantly affect protein function are in blue. The table is derived from a figure from¹.

Table S2. *P. aeruginosa* PBP3 variants outside the transpeptidase domain^a

PBP3 variants	A9T	W13R	R14L	A28T	D40V	G46S	A60V	G63S/D/C/R	I65T	R153S	R175H	G188A	G191E/D	N212T	P215L	G216S	R226C	
	Clinical Isolates																	Study
																		3
																		4
																		5
																		8
																		10
																		11
																		12
																		14

^aSequence variants in the cytoplasmic (yellow), membrane spanning alpha-helix (green) and domain likely involved in protein-protein interactions (Brown) of PBP3 in clinical isolates and experimentally evolved β -lactam-resistant mutants are listed. Variants predicted using the bioinformatics tool Provean ^{1, 17, 18} to affect protein function are shown in red, and those predicted to not significantly affect protein function in blue. Figure is derived from a figure from ¹.

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