Antimicrobial Resistance Panel 3: *Pseudomonas aeruginosa,* Strain Z-61 Restoration of Key Mutations (*oprM, ampC, lptE*) to Wild Type

Catalog No. NR-55642

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Manufacturer:
BEI Resources

Product Description:
Pseudomonas aeruginosa (P. aeruginosa) strain Z61 (ATCC® 35151™) also known as strain K 799/61, is a drug-hypersusceptible strain generated by chemical mutagenesis of the parent wild-type strain *P. aeruginosa* ATCC® 12055™.[1] *P. aeruginosa* Z61 has been extensively used in studies of antibiotic susceptibility and drug discovery. Although the genetic basis of its hyper susceptibility is not fully understood, mutations in *oprM* (outer membrane efflux pump), *ampC* (inducible β-lactamase) and *lptE* (lipopolysaccharide transporter) genes have been characterized and predicted to be involved.[2] Antimicrobial Resistance Panel 3 consists of 14 strains with varying combinations of wild-type and mutant genes in the strain Z61 or ATCC® 12055™ backgrounds. Seven strains are derived from ATCC® 12055™, in which the wild-type sequences for *oprM*, *ampC* and *lptE* are exchanged for the Z61 mutation, individually or in combination. The remaining seven strains are derived from Z61 by genomic restoration of the wild-type sequences of these gene targets, individually or in combination. The strains comprising this panel are listed in Table 1.

NR-51954 was created by introducing *P. aeruginosa*, strain Z61-specific defect in *lptE,* to the chromosome of ATCC® 12055™.

NR-51955 was created by the chromosomal deletion of *oprM*, and the introduction of *P. aeruginosa,* strain Z61-specific defect in *lptE* to the chromosome of ATCC® 12055™.

NR-51956 was created by chromosomal deletion of *ampC*, and the introduction of *P. aeruginosa*, strain Z61-specific defect in *lptE* to the chromosome of ATCC® 12055™.

NR-51957 was created by the chromosomal deletion of *oprM* and *ampC*, and the introduction of *P. aeruginosa*, strain Z61-specific defect in *lptE* to the chromosome of ATCC® 12055™.

NR-51958 was created by the chromosomal deletion of *ampC* in the parent wild-type strain ATCC® 12055™.

NR-51959 was created by the chromosomal deletion of *oprM* in the parent wild-type strain ATCC® 12055™.

NR-51960 was created by the chromosomal deletion of *oprM* and *ampC* in the wild-type strain ATCC® 12055™.

NR-51961 was created by correcting the *oprM* mutation in the hypersusceptible *P. aeruginosa*, strain Z61 to the wild-type sequence. Wild-type *oprM* sequence derived from *P. aeruginosa,* strain PAO1 was used to carry out the genome correction.

NR-51962 was created by correcting the *ampC* mutation in the hypersusceptible *P. aeruginosa*, strain Z61 to the wild-type sequence. Wild-type *ampC* sequence derived from *P. aeruginosa*, strain PAO1 was used to carry out the genome correction.

NR-51963 was created by correcting the *lptE* mutation in the hypersusceptible *P. aeruginosa*, strain Z61 to the wild-type sequence. Wild-type *lptE* sequence derived from *P. aeruginosa*, strain PAO1 was used to carry out the genome correction.

NR-51964 was created by correcting *lptE* and *ampC* mutations in the hypersusceptible *P. aeruginosa*, strain Z61 to wild-type sequences. Wild-type *lptE* and *ampC* sequences derived from *P. aeruginosa*, strain PAO1 were used to carry out the genome corrections.

NR-51965 was created by correcting *lptE* and *oprM* mutations in the hypersusceptible *P. aeruginosa*, strain Z61 to wild-type sequences. Wild-type *lptE* and *oprM* sequences derived from *P. aeruginosa*, strain PAO1 were used to carry out the genome corrections.

NR-51966 was created by correcting *lptE*, *oprM* and *ampC* mutations in the hypersusceptible *P. aeruginosa*, strain Z61 to wild-type sequences. Wild-type *lptE*, *oprM* and *ampC* sequences derived from *P. aeruginosa*, strain PAO1 were used to carry out the genome corrections.

NR-51967 was created by correcting *ampC* and *oprM* mutations in the hypersusceptible *P. aeruginosa*, strain Z61 to wild-type sequences. Wild-type *lptE* and *oprM* sequences derived from *P. aeruginosa*, strain PAO1 were used to carry out the genome corrections.

Detailed information for each mutant strain, including antibiotic susceptibility profile, is available on the Certificate of Analysis.

Material Provided:
Each panel contains one vial of each of the bacterial strains in the panel. Each vial contains approximately 0.5 mL of bacterial culture in Tryptic Soy broth supplemented with 10% glycerol.

Note: If homogeneity is required for your intended use, please purify prior to initiating work.

Packaging/Storage:
Each isolate was packaged aseptically in cryovials. The product is provided frozen and should be stored at -60°C or colder immediately upon arrival. For long-term storage, the vapor phase of a liquid nitrogen freezer is recommended. Freeze thaw cycles should be avoided.

Growth Conditions:
Media:
Tryptic Soy broth or equivalent
Tryptic Soy agar or equivalent
Incubation:
Temperature: 37°C
Atmosphere: Aerobic
Propagation:
1. Keep vial frozen until ready for use, then thaw.
2. Transfer the entire thawed aliquot into a single tube of broth.
3. Use several drops of the suspension to inoculate an agar slant and/or plate.
4. Incubate the tube, slant and/or plate at 37°C for 1 day.

Citation:
Acknowledgment for publications should read "The following reagent was obtained through BEI Resources, NIAID, NIH: Antimicrobial Resistance Panel 3: *Pseudomonas aeruginosa*, Strain Z-61 Restoration of Key Mutations (*oprM*, *ampC*, *lptE*) to Wild Type, NR-55642."

Biosafety Level: 2
Appropriate safety procedures should always be used with this material. Laboratory safety is discussed in the following publication: U.S. Department of Health and Human Services, Public Health Service, Centers for Disease Control and Prevention, and National Institutes of Health. Biosafety in Microbiological and Biomedical Laboratories. 6th ed. Washington, DC: U.S. Government Printing Office, 2020; see www.cdc.gov/biosafety/publications/bmbl5/index.htm.

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References:
1. Zimmermann, W. "Penetration of Beta-Lactam Antibiotics into their Target Enzymes in *Pseudomonas aeruginosa*: Comparison of a Highly Sensitive Mutant with its Parent Strain." Antimicrob. Agents Chemother. 18 (1980): 94-100. PubMed: 6774666.
2. Shen, X., et al. "Defects in Efflux (*oprM*), β-Lactamase (*ampC*), and Lipopolysaccharide Transport (*lptE*) Genes Mediate Antibiotic Hypersusceptibility of *Pseudomonas aeruginosa* Strain Z61." Antimicrob. Agents Chemother. 63 (2019): e00784-19. PubMed: 31036686.

Support Provided by NIAID

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Table 1: Panel Strains

Item Number	Stain	Background strain	Gene variant(s)
NR-51954	NB52041-CDY0170	*P. aeruginosa* ATCC® 12055™	*lptE*^{D}
NR-51955	NB52041-CDY0171	*P. aeruginosa* ATCC® 12055™	*lptE*^{D}Δ*oprM*
NR-51956	NB52041-CDY0172	*P. aeruginosa* ATCC® 12055™	*lptE*^{D} Δ*ampC*
NR-51957	NB52041-CDY0173	*P. aeruginosa* ATCC® 12055™	*lptE*^{D} Δ*oprM* Δ*ampC*
NR-51958	NB52041-CDY0174	*P. aeruginosa* ATCC® 12055™	Δ*ampC*
NR-51959	NB52041-CDY0175	*P. aeruginosa* ATCC® 12055™	Δ*oprM*
NR-51960	NB52041-CDY0176	*P. aeruginosa* ATCC® 12055™	Δ*oprM* Δ*ampC*
NR-51961	NB52040-CDY0025	*P. aeruginosa* strain Z61	*oprM*
NR-51962	NB52040-CDY0082	*P. aeruginosa* strain Z61	*ampC*
NR-51963	NB52040-CDY0083	*P. aeruginosa* strain Z61	*lptE*
NR-51964	NB52040-CDY0084	*P. aeruginosa* strain Z61	*ampC*, *lptE*
NR-51965	NB52040-CDY0085	*P. aeruginosa* strain Z61	*oprM*, *lptE*
NR-51966	NB52040-CDY0086	*P. aeruginosa* strain Z61	*oprM*, *lptE, ampC*
NR-51967	NB52040-CDY0087	*P. aeruginosa* strain Z61	*ampC*, *oprM*

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