Certificate of Analysis for NR-55642

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

Catalog No. NR-55642

Product Description:

NR-55642 consists of 14 strains with varying combinations of wild-type and mutant genes in the *Pseudomonas aeruginosa (P. aeruginosa)*, strain Z61 or *P. aeruginosa* ATCC® 12055™ backgrounds. Each component was produced by inoculation of the deposited material into Tryptic Soy broth and grown for 1 day at 37°C in an aerobic atmosphere. Broth inoculum was added to Tryptic Soy agar kolles, which were grown for 1 day at 37°C in an aerobic atmosphere to produce each lot. Quality control testing was completed under propagation conditions unless otherwise noted.

BEI Resources is committed to ensuring digital accessibility for people with disabilities. This Certificate of Analysis contains complex tables and may not be fully accessible. Please let us know if you encounter accessibility barriers and a fully accessible document will be provided: E-mail: Contact@BEIResources.org. We try to respond to feedback within 24 hours.

Table 1: Kit Components

COMPONENT NUMBER	DESCRIPTION	BACKGROUND STRAIN	GENE VARIANT(S)	LOT NUMBER	DATE OF MANUFACTURE
NR-51954	*P. aeruginosa*, strain NB52041-CDY0170	*P. aeruginosa* ATCC® 12055™	*lptE*^{D}	70044553	19MAY2021
NR-51955	*P. aeruginosa*, strain NB52041-CDY0171	*P. aeruginosa* ATCC® 12055™	*lptE*^{D}Δ*oprM*	70044555	19MAY2021
NR-51956	*P. aeruginosa*, strain NB52041-CDY0172	*P. aeruginosa* ATCC® 12055™	*lptE*^{D} Δ*ampC*	70044557	19MAY2021
NR-51957	*P. aeruginosa*, strain NB52041-CDY0173	*P. aeruginosa* ATCC® 12055™	*lptE*^{D} Δ*oprM* Δ*ampC*	70044559	19MAY2021
NR-51958	*P. aeruginosa*, strain NB52041-CDY0174	*P. aeruginosa* ATCC® 12055™	Δ*ampC*	70044561	21MAY2021
NR-51959	*P. aeruginosa*, strain NB52041-CDY0175	*P. aeruginosa* ATCC® 12055™	Δ*oprM*	70044563	21MAY2021
NR-51960	*P. aeruginosa*, strain NB52041-CDY0176	*P. aeruginosa* ATCC® 12055™	Δ*oprM* Δ*ampC*	70044565	04JUN2021
NR-51961	*P. aeruginosa*, strain NB52040-CDY0025	*P. aeruginosa* strain Z61	*oprM*	70044537	21MAY2021
NR-51962	*P. aeruginosa*, strain NB52040-CDY0082	*P. aeruginosa* strain Z61	*ampC*	70044539	21MAY2021
NR-51963	*P. aeruginosa*, strain NB52040-CDY0083	*P. aeruginosa* strain Z61	*lptE*	70044541	26MAY2021
NR-51964	*P. aeruginosa*, strain NB52040-CDY0084	*P. aeruginosa* strain Z61	*ampC*, *lptE*	70044543	21MAY2021
NR-51965	*P. aeruginosa*, strain NB52040-CDY0085	*P. aeruginosa* strain Z61	*oprM*, *lptE*	70044545	26MAY2021
NR-51966	*P. aeruginosa*, strain NB52040-CDY0086	*P. aeruginosa* strain Z61	*oprM*, *lptE*, *ampC*	70044547	19MAY2021
NR-51967	*P. aeruginosa*, strain NB52040-CDY0087	*P. aeruginosa* strain Z61	*ampC*, *oprM*	70044549	19MAY2021

BEI Resources
www.beiresources.org

E-mail: contact@beiresources.org
Tel: 800-359-7370
Fax: 703-365-2898

Table 2: *Pseudomonas aeruginosa*, strain NB52041-CDY0170 (NR-51954)

TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis		
Cellular morphology	Gram-negative rods	Gram-negative rods
Colony morphology	Report results	Circular, low convex, entire, smooth and cream
Motility (wet mount)	Report results	Motile
Hemolysis	Report results	Beta-hemolytic
VITEK® MS (MALDI-TOF)	*P. aeruginosa*	*P. aeruginosa* (99.9%)
Antibiotic Susceptibility Profile[1]		
Etest® antibiotic test strips 1 day at 35°C in an aerobic atmosphere on Mueller Hinton agar		
Ampicillin	Report results	48 µg per mL
Aztreonam	Report results	Sensitive (0.094 µg per mL)
Ciprofloxacin	Report results	Sensitive (0.094 µg per mL)
Gentamycin	Report results	Sensitive (1 to 1.5 µg per mL)
Rifampin	Report results	2.0 µg per mL
Tetracycline	Report results	4 to 6 µg per mL
Genotypic Analysis		
Digital DNA-DNA hybridization (dDDH)[2]	≥ 70% for species identification	*P. aeruginosa* (95.3%)
lptE mutation	*lptE* mutation present	Pending
Purity 7 days at 37°C in an aerobic atmosphere with 5% CO_2 on Tryptic Soy agar with 5% defibrinated sheep blood	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
Viability	Growth	Growth

[1]Minimum Inhibitory Concentration (MIC); MIC Interpretation Guideline: CLSI M100-S28 (2018)
[2]Relatedness between bacterial strains has traditionally been determined using DDH. For additional information, refer to Auch, A. F., et al. "Digital DNA-DNA Hybridization for Microbial Species Delineation by Means of Genome-to-Genome Sequence Comparison." Stand. Genomic Sci. 2 (2010): 117-134. PubMed: 21304684.

Table 3: *Pseudomonas aeruginosa*, strain NB52041-CDY0171 (NR-51955)

TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis		
Cellular morphology	Gram-negative rods	Gram-negative rods
Colony morphology	Report results	Circular, low convex, undulate, smooth and cream
Motility (wet mount)	Report results	Motile
Hemolysis	Report results	Beta-hemolytic
VITEK® MS (MALDI-TOF)	*P. aeruginosa*	*P. aeruginosa* (99.9%)
Antibiotic Susceptibility Profile[1]		
Etest® antibiotic test strips 1 day at 35°C in an aerobic atmosphere on Mueller Hinton agar		
Ampicillin	Report results	8 µg per mL
Aztreonam	Report results	Sensitive (≤ 0.016 µg per mL)
Ciprofloxacin	Report results	Sensitive (0.047 µg per mL)
Gentamycin	Report results	Sensitive (0.25 µg per mL)
Rifampin	Report results	1.0 µg per mL
Tetracycline	Report results	0.5 µg per mL
Genotypic Analysis		
Digital DNA-DNA hybridization (dDDH)[2]	≥ 70% for species identification	*P. aeruginosa* (95.3%)
oprM deletion	*oprM* deletion present	Pending

TEST	SPECIFICATIONS	RESULTS
lptE mutation	*lptE* mutation present	Pending
Purity 7 days at 37°C in an aerobic atmosphere with 5% CO_2 on Tryptic Soy agar with 5% defibrinated sheep blood	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
Viability	Growth	Growth

[1]Minimum Inhibitory Concentration (MIC); MIC Interpretation Guideline: CLSI M100-S28 (2018)
[2]Relatedness between bacterial strains has traditionally been determined using DDH. For additional information, refer to Auch, A. F., et al. "Digital DNA-DNA Hybridization for Microbial Species Delineation by Means of Genome-to-Genome Sequence Comparison." Stand. Genomic Sci. 2 (2010): 117-134. PubMed: 21304684.

Table 4: *Pseudomonas aeruginosa*, strain NB52041-CDY0172 (NR-51956)

TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis		
Cellular morphology	Gram-negative rods	Gram-negative rods
Colony morphology	Report results	Circular, low convex, undulate, smooth and cream
Motility (wet mount)	Report results	Motile
Hemolysis	Report results	Beta-hemolytic
VITEK® MS (MALDI-TOF)	*P. aeruginosa*	*P. aeruginosa* (99.9%)
Antibiotic Susceptibility Profile[1] Etest® antibiotic test strips 1 day at 35°C in an aerobic atmosphere on Mueller Hinton agar		
Ampicillin	Report results	2 µg per mL
Aztreonam	Report results	Sensitive (0.125 µg per mL)
Ciprofloxacin	Report results	Sensitive (0.094 to 0.125 µg per mL)
Gentamycin	Report results	Sensitive (1.0 to 1.5 µg per mL)
Rifampin	Report results	1.5 µg per mL
Tetracycline	Report results	4.0 µg per mL
Genotypic Analysis		
Digital DNA-DNA hybridization (dDDH)[2]	≥ 70% for species identification	*P. aeruginosa* (95%)
ampC deletion	*ampC* deletion present	Pending
lptE mutation	*lptE* mutation present	Pending
Purity 7 days at 37°C in an aerobic atmosphere with 5% CO_2 on Tryptic Soy agar with 5% defibrinated sheep blood	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
Viability	Growth	Growth

[1]Minimum Inhibitory Concentration (MIC); MIC Interpretation Guideline: CLSI M100-S28 (2018)
[2]Relatedness between bacterial strains has traditionally been determined using DDH. For additional information, refer to Auch, A. F., et al. "Digital DNA-DNA Hybridization for Microbial Species Delineation by Means of Genome-to-Genome Sequence Comparison." Stand. Genomic Sci. 2 (2010): 117-134. PubMed: 21304684.

Table 5: *Pseudomonas aeruginosa*, strain NB52041-CDY0173 (NR-51957)

TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis		
Cellular morphology	Gram-negative rods	Gram-negative rods
Colony morphology	Report results	Circular, convex, entire, smooth and cream
Motility (wet mount)	Report results	Motile
Hemolysis	Report results	Beta-hemolytic
VITEK® MS (MALDI-TOF)	*P. aeruginosa*	*P. aeruginosa* (99.9%)

TEST	SPECIFICATIONS	RESULTS
Antibiotic Susceptibility Profile[1]		
Etest® antibiotic test strips		
1 day at 35°C in an aerobic atmosphere on Mueller Hinton agar		
Ampicillin	Report results	0.023 to 0.032 µg per mL
Aztreonam	Report results	Sensitive (≤ 0.016 µg per mL)
Ciprofloxacin	Report results	Sensitive (0.003 to 0.008 µg per mL)
Gentamycin	Report results	Sensitive (0.16 to 0.25 µg per mL)
Rifampin	Report results	1.0 µg per mL
Tetracycline	Report results	0.25 µg per mL
Genotypic Analysis		
Digital DNA-DNA hybridization (dDDH)[2]	≥ 70% for species identification	*P. aeruginosa* (95.3%)
ampC deletion	*ampC* deletion present	Pending
oprM deletion	*oprM* deletion present	Pending
lptE mutation	*lptE* mutation present	Pending
Purity	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
7 days at 37°C in an aerobic atmosphere on Tryptic Soy agar with or without 5% CO_2		
Viability	Growth	Growth

[1]Minimum Inhibitory Concentration (MIC); MIC Interpretation Guideline: CLSI M100-S28 (2018)
[2]Relatedness between bacterial strains has traditionally been determined using DDH. For additional information, refer to Auch, A. F., et al. "Digital DNA-DNA Hybridization for Microbial Species Delineation by Means of Genome-to-Genome Sequence Comparison." Stand. Genomic Sci. 2 (2010): 117-134. PubMed: 21304684.

Table 6: *Pseudomonas aeruginosa*, strain NB52041-CDY0174 (NR-51958)

TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis		
Cellular morphology	Gram-negative rods	Gram-negative rods
Colony morphology	Report results	Circular, convex, entire, smooth and cream
Motility (wet mount)	Report results	Motile
Hemolysis	Report results	Beta-hemolytic
VITEK® MS (MALDI-TOF)	*P. aeruginosa*	*P. aeruginosa* (99.9%)
Antibiotic Susceptibility Profile[1]		
Etest® antibiotic test strips		
1 day at 35°C in an aerobic atmosphere on Mueller Hinton agar		
Ampicillin	Report results	48 µg per mL
Aztreonam	Report results	Sensitive (2 µg per mL)
Ciprofloxacin	Report results	Sensitive (0.38 to 0.75 µg per mL)
Gentamycin	Report results	Sensitive (3 to 4 µg per mL)
Rifampin	Report results	> 32 µg per mL
Tetracycline	Report results	32 to 48 µg per mL
Genotypic Analysis		
Digital DNA-DNA hybridization (dDDH)[2]	≥ 70% for species identification	*P. aeruginosa* (95%)
ampC deletion	*ampC* deletion present	Pending
Purity	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
7 days at 37°C in an aerobic atmosphere on Tryptic Soy agar with or without 5% CO_2		
Viability	Growth	Growth

[1]Minimum Inhibitory Concentration (MIC); MIC Interpretation Guideline: CLSI M100-S28 (2018)
[2]Relatedness between bacterial strains has traditionally been determined using DDH. For additional information, refer to Auch, A. F., et al. "Digital DNA-DNA Hybridization for Microbial Species Delineation by Means of Genome-to-Genome Sequence Comparison." Stand. Genomic Sci. 2 (2010): 117-134. PubMed: 21304684.

Table 7: *Pseudomonas aeruginosa*, strain NB52041-CDY0175 (NR-51959)

TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis		
Cellular morphology	Gram-negative rods	Gram-negative rods
Colony morphology	Report results	Circular, low convex, entire, smooth and cream
Motility (wet mount)	Report results	Motile
VITEK® MS (MALDI-TOF)	*P. aeruginosa*	*P. aeruginosa* (99.9%)
Antibiotic Susceptibility Profile[1]		
Etest® antibiotic test strips		
1 day at 35°C in an aerobic atmosphere on Mueller Hinton agar		
Ampicillin	Report results	> 256 µg per mL
Aztreonam	Report results	Sensitive (0.25 to 0.38 µg per mL)
Ciprofloxacin	Report results	Sensitive (1.0 µg per mL)
Gentamycin	Report results	Sensitive (0.5 µg per mL)
Rifampin	Report results	> 32 µg per mL
Tetracycline	Report results	2 µg per mL
Genotypic Analysis		
Digital DNA-DNA hybridization (dDDH)[2]	≥ 70% for species identification	*P. aeruginosa* (95.4%)
oprM deletion	*oprM* deletion present	Pending
Purity	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
7 days at 37°C in an aerobic atmosphere with 5% CO_2 on Tryptic Soy agar with 5% defibrinated sheep blood		
Viability	Growth	Growth

[1]Minimum Inhibitory Concentration (MIC); MIC Interpretation Guideline: CLSI M100-S28 (2018)
[2]Relatedness between bacterial strains has traditionally been determined using DDH. For additional information, refer to Auch, A. F., et al. "Digital DNA-DNA Hybridization for Microbial Species Delineation by Means of Genome-to-Genome Sequence Comparison." Stand. Genomic Sci. 2 (2010): 117-134. PubMed: 21304684.

Table 8: *Pseudomonas aeruginosa*, strain NB52041-CDY0176 (NR-51960)

TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis		
Cellular morphology	Gram-negative rods	Gram-negative rods
Colony morphology	Report results	Circular, convex, entire, rough and cream
Motility (wet mount)	Report results	Motile
Hemolysis	Report results	Beta-hemolytic
VITEK® MS (MALDI-TOF)	*P. aeruginosa*	*P. aeruginosa* (99.9%)
Antibiotic Susceptibility Profile[1]		
Etest® antibiotic test strips		
1 day at 35°C in an aerobic atmosphere on Mueller Hinton agar		
Ampicillin	Report results	Inconclusive[2]
Aztreonam	Report results	Sensitive (0.019 µg per mL)
Ciprofloxacin	Report results	Sensitive (0.075 to 1.0 µg per mL)
Gentamycin	Report results	Sensitive (0.25 µg per mL)
Rifampin	Report results	> 32 µg per mL
Tetracycline	Report results	1 µg per mL
Genotypic Analysis		
Digital DNA-DNA hybridization (dDDH)[3]	≥ 70% for species identification	*P. aeruginosa* (95.4%)
ampC deletion	*ampC* deletion present	Pending
oprM deletion	*oprM* deletion present	Pending

TEST	SPECIFICATIONS	RESULTS
Purity 7 days at 37°C in an aerobic atmosphere on Tryptic Soy agar with 5% defibrinated sheep blood	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
Viability	Growth	Growth

[1]Minimum Inhibitory Concentration (MIC); MIC Interpretation Guideline: CLSI M100-S28 (2018)
[2]Antibiotic susceptibility testing performed in duplicate determined that for *P. aeruginosa*, strain NB52041-CDY0176, the ampicillin MICs are 1.5 µg per mL and > 256 µg per mL.
[3]Relatedness between bacterial strains has traditionally been determined using DDH. For additional information, refer to Auch, A. F., et al. "Digital DNA-DNA Hybridization for Microbial Species Delineation by Means of Genome-to-Genome Sequence Comparison." Stand. Genomic Sci. 2 (2010): 117-134. PubMed: 21304684.

Table 9: *Pseudomonas aeruginosa*, strain NB52040-CDY0025 (NR-51961)

TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis		
Cellular morphology	Gram-negative rods	Gram-negative rods
Colony morphology	Report results	Circular, convex, entire, smooth and cream
Motility (wet mount)	Report results	Motile
Hemolysis	Report results	Beta-hemolytic
VITEK® MS (MALDI-TOF)	*P. aeruginosa*	*P. aeruginosa* (99.9%)
Antibiotic Susceptibility Profile[1]		
Etest® antibiotic test strips 1 day at 35°C in an aerobic atmosphere on Mueller Hinton agar		
Ampicillin	Report results	1.5 µg per mL
Aztreonam	Report results	Sensitive (0.047 µg per mL)
Ciprofloxacin	Report results	Sensitive (0.064 µg per mL)
Gentamicin	Report results	Sensitive (1.0 µg per mL)
Rifampin	Report results	1.0 to 1.5 µg per mL
Tetracycline	Report results	Inconclusive[2]
Genotypic Analysis		
Digital DNA-DNA hybridization (dDDH)[3]	≥ 70% for species identification	*P. aeruginosa* (95.3%)
Wild-type *oprM*	Wild-type *oprM* present	Pending
Purity 7 days at 37°C in an aerobic atmosphere on Tryptic Soy agar with and without 5% CO_2	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
Viability	Growth	Growth

[1]Minimum Inhibitory Concentration (MIC); MIC Interpretation Guideline: CLSI M100-S28 (2018)
[2]Antibiotic susceptibility testing performed in duplicate determined that for *P. aeruginosa*, strain NB52040-CDY0025, the ampicillin MICs are 6 µg per mL and 16 µg per mL.
[3]Relatedness between bacterial strains has traditionally been determined using DDH. For additional information, refer to Auch, A. F., et al. "Digital DNA-DNA Hybridization for Microbial Species Delineation by Means of Genome-to-Genome Sequence Comparison." Stand. Genomic Sci. 2 (2010): 117-134. PubMed: 21304684.

Table 10: *Pseudomonas aeruginosa*, strain NB52040-CDY0082 (NR-51962)

TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis		
Cellular morphology	Gram-negative rods	Gram-negative rods
Colony morphology	Report results	Circular, convex, entire, smooth and cream
Motility (wet mount)	Report results	Motile
Hemolysis	Report results	Beta-hemolytic
VITEK® MS (MALDI-TOF)	*P. aeruginosa*	*P. aeruginosa* (99.9%)

TEST	SPECIFICATIONS	RESULTS
Antibiotic Susceptibility Profile[1]		
Etest® antibiotic test strips		
1 day at 35°C in an aerobic atmosphere on Mueller Hinton agar		
Ampicillin	Report results	4 µg per mL
Aztreonam	Report results	Sensitive (0.016 µg per mL)
Ciprofloxacin	Report results	Sensitive (0.125 µg per mL)
Gentamicin	Report results	Sensitive (0.38 µg per mL)
Rifampin	Report results	1.5 µg per mL
Tetracycline	Report results	1 µg per mL
Genotypic Analysis		
Digital DNA-DNA hybridization (dDDH)[2]	≥ 70% for species identification	*P. aeruginosa* (95.2%)
Wild-type *ampC*	Wild-type *ampC* present	Pending
Purity	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
7 days at 37°C in an aerobic atmosphere on Tryptic Soy agar with and without 5% CO_2		
Viability	Growth	Growth

[1]Minimum Inhibitory Concentration (MIC); MIC Interpretation Guideline: CLSI M100-S28 (2018)
[2]Relatedness between bacterial strains has traditionally been determined using DDH. For additional information, refer to Auch, A. F., et al. "Digital DNA-DNA Hybridization for Microbial Species Delineation by Means of Genome-to-Genome Sequence Comparison." Stand. Genomic Sci. 2 (2010): 117-134. PubMed: 21304684.

Table 11: *Pseudomonas aeruginosa*, strain NB52040-CDY0083 (NR-51963)

TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis		
Cellular morphology	Gram-negative rods	Gram-negative rods
Colony morphology	Report results	Circular, low convex, entire, smooth and cream
Motility (wet mount)	Report results	Motile
Hemolysis	Report results	Beta-hemolytic
VITEK® MS (MALDI-TOF)	*P. aeruginosa*	*P. aeruginosa* (99.9%)
Antibiotic Susceptibility Profile[1]		
Etest® antibiotic test strips		
1 day at 35°C in an aerobic atmosphere on Mueller Hinton agar		
Ampicillin	Report results	0.50 µg per mL
Aztreonam	Report results	Sensitive (0.19 µg per mL)
Ciprofloxacin	Report results	Sensitive (0.38 to 0.75 µg per mL)
Gentamicin	Report results	Sensitive (0.5 µg per mL)
Rifampin	Report results	> 32 µg per mL
Tetracycline	Report results	3 µg per mL
Genotypic Analysis		
Digital DNA-DNA hybridization (dDDH)[2]	≥ 70% for species identification	*P. aeruginosa* (95.3%)
Wild-type *lptE*	Wild-type *lptE* present	Pending
Purity	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
7 days on Tryptic Soy agar at 37°C in an aerobic atmosphere with and without 5% CO_2		
Viability	Growth	Growth

[1]Minimum Inhibitory Concentration (MIC); MIC Interpretation Guideline: CLSI M100-S28 (2018)
[2]Relatedness between bacterial strains has traditionally been determined using DDH. For additional information, refer to Auch, A. F., et al. "Digital DNA-DNA Hybridization for Microbial Species Delineation by Means of Genome-to-Genome Sequence Comparison." Stand. Genomic Sci. 2 (2010): 117-134. PubMed: 21304684.

Table 12: *Pseudomonas aeruginosa*, strain NB52040-CDY0084 (NR-51964)

TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis		
Cellular morphology	Gram-negative rods	Gram-negative rods
Colony morphology	Report results	Circular, flat, entire, smooth and cream
Motility (wet mount)	Report results	Motile
VITEK® MS (MALDI-TOF)	*P. aeruginosa*	*P. aeruginosa* (99.9%)
Antibiotic Susceptibility Profile[1]		
Etest® antibiotic test strips 1 day at 35°C in an aerobic atmosphere on Mueller Hinton agar		
Ampicillin	Report results	1 to 4 µg per mL
Aztreonam	Report results	Sensitive (0.38 to 0.50 µg per mL)
Ciprofloxacin	Report results	Sensitive (0.38 µg per mL)
Gentamicin	Report results	Sensitive (0.5 µg per mL)
Rifampin	Report results	> 32 µg per mL
Tetracycline	Report results	4 µg per mL
Genotypic Analysis		
Digital DNA-DNA hybridization (dDDH)[2]	≥ 70% for species identification	*P. aeruginosa* (95.2%)
Wild-type *ampC*	Wild-type *ampC* present	Pending
Wild-type *lptE*	Wild-type *lptE* present	Pending
Purity 7 days on Tryptic Soy agar with 5% sheep blood at 37°C in an aerobic atmosphere with 5% CO_2	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
Viability	Growth	Growth

[1]Minimum Inhibitory Concentration (MIC); MIC Interpretation Guideline: CLSI M100-S28 (2018)
[2]Relatedness between bacterial strains has traditionally been determined using DDH. For additional information, refer to Auch, A. F., et al. "Digital DNA-DNA Hybridization for Microbial Species Delineation by Means of Genome-to-Genome Sequence Comparison." Stand. Genomic Sci. 2 (2010): 117-134. PubMed: 21304684.

Table 13: *Pseudomonas aeruginosa*, strain NB52040-CDY0085 (NR-51965)

TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis		
Cellular morphology	Gram-negative rods	Gram-negative rods
Colony morphology	Report results	Circular, convex, entire, smooth and cream
Motility (wet mount)	Report results	Motile
VITEK® MS (MALDI-TOF)	*P. aeruginosa*	*P. aeruginosa* (99.9%)
Antibiotic Susceptibility Profile[1]		
Etest® antibiotic test strips 1 day at 35°C in an aerobic atmosphere on Mueller Hinton agar		
Ampicillin	Report results	48 µg per mL
Aztreonam	Report results	Sensitive (3 µg per mL)
Ciprofloxacin	Report results	Sensitive (0.75 to 1.0 µg per mL)
Gentamicin	Report results	Sensitive (2 to 3 µg per mL)
Rifampin	Report results	> 32 µg per mL
Tetracycline	Report results	Inconclusive[2]
Genotypic Analysis		
Digital DNA-DNA hybridization (dDDH)[3]	≥ 70% for species identification	*P. aeruginosa* (95.1%)
Wild-type *lptE*	Wild-type *lptE* present	Pending
Wild-type *oprM*	Wild-type *oprM* present	Pending

BEI Resources
www.beiresources.org

E-mail: contact@beiresources.org
Tel: 800-359-7370
Fax: 703-365-2898

TEST	SPECIFICATIONS	RESULTS
Purity 37°C on Tryptic Soy agar with 5% sheep blood in an aerobic atmosphere with 5% CO_2	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
Viability	Growth	Growth

[1]Minimum Inhibitory Concentration (MIC); MIC Interpretation Guideline: CLSI M100-S28 (2018)
[2]Antibiotic susceptibility testing performed in duplicate determined that for *P. aeruginosa*, strain NB52040-CDY0085, the tetracycline MICs are 16 to 24 µg per mL and > 256 µg per mL.
[3]Relatedness between bacterial strains has traditionally been determined using DDH. For additional information, refer to Auch, A. F., et al. "Digital DNA-DNA Hybridization for Microbial Species Delineation by Means of Genome-to-Genome Sequence Comparison." Stand. Genomic Sci. 2 (2010): 117-134. PubMed: 21304684.

Table 14: *Pseudomonas aeruginosa*, strain NB52040-CDY0086 (NR-51966)

TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis		
Cellular morphology	Gram-negative rods	Gram-negative rods
Colony morphology	Report results	Irregular, flat, undulate, smooth and cream
Motility (wet mount)	Report results	Motile
Hemolysis	Report results	Beta-hemolytic
VITEK® MS (MALDI-TOF)	*P. aeruginosa*	*P. aeruginosa* (99.9%)
Antibiotic Susceptibility Profile[1]		
Etest® antibiotic test strips 1 day at 35°C in an aerobic atmosphere on Mueller Hinton agar		
Ampicillin	Report results	> 32 µg per mL
Aztreonam	Report results	Sensitive (1 µg per mL)
Ciprofloxacin	Report results	Sensitive (0.05 µg per mL)
Gentamicin	Report results	Sensitive (4 µg per mL)
Rifampin	Report results	> 32 µg per mL
Tetracycline	Report results	24 µg per mL
Genotypic Analysis		
Digital DNA-DNA hybridization (dDDH)[2]	≥ 70% for species identification	*P. aeruginosa* (95.3%)
Wild-type *ampC*	Wild-type *ampC* present	Pending
Wild-type *lptE*	Wild-type *lptE* present	Pending
Wild-type *oprM*	Wild-type *oprM* present	Pending
Purity 7 days at 37°C in an aerobic atmosphere on Tryptic Soy agar with 5% defibrinated sheep blood	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
Viability	Growth	Growth

[1]Minimum Inhibitory Concentration (MIC); MIC Interpretation Guideline: CLSI M100-S28 (2018)
[2]Relatedness between bacterial strains has traditionally been determined using DDH. For additional information, refer to Auch, A. F., et al. "Digital DNA-DNA Hybridization for Microbial Species Delineation by Means of Genome-to-Genome Sequence Comparison." Stand. Genomic Sci. 2 (2010): 117-134. PubMed: 21304684.

Table 15: *Pseudomonas aeruginosa*, strain NB52040-CDY0087 (NR-51967)

TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis		
Cellular morphology	Gram-negative rods	Gram-negative rods
Colony morphology	Report results	Circular, low convex, entire, smooth and cream
Motility (wet mount)	Report results	Motile
Hemolysis	Report results	Beta-hemolytic
VITEK® MS (MALDI-TOF)	*P. aeruginosa*	*P. aeruginosa* (99.9%)

Certificate of Analysis for NR-55642

TEST	SPECIFICATIONS	RESULTS
Antibiotic Susceptibility Profile[1]		
Etest® antibiotic test strips		
1 day at 35°C in an aerobic atmosphere on Mueller Hinton agar		
Ampicillin	Report results	2 to 3 µg per mL
Aztreonam	Report results	Sensitive (0.047 µg per mL)
Ciprofloxacin	Report results	Sensitive (0.094 µg per mL)
Gentamicin	Report results	Sensitive (2 µg per mL)
Rifampin	Report results	1 µg per mL
Tetracycline	Report results	3 µg per mL
Genotypic Analysis		
Digital DNA-DNA hybridization (dDDH)[2]	≥ 70% for species identification	*P. aeruginosa* (95.2%)
Wild-type *lptE*	Wild-type *lptE* present	Pending
Wild-type *oprM*	Wild-type *oprM* present	Pending
Purity	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
7 days at 37°C in an aerobic atmosphere on Tryptic Soy agar with 5% defibrinated sheep blood		
Viability	Growth	Growth

[1]Minimum Inhibitory Concentration (MIC); MIC Interpretation Guideline: CLSI M100-S28 (2018)
[2]Relatedness between bacterial strains has traditionally been determined using DDH. For additional information, refer to Auch, A. F., et al. "Digital DNA-DNA Hybridization for Microbial Species Delineation by Means of Genome-to-Genome Sequence Comparison." Stand. Genomic Sci. 2 (2010): 117-134. PubMed: 21304684.

/Sonia Bjorum Brower/
Sonia Bjorum Brower 28 OCT 2022
Technical Manager or designee, ATCC Federal Solutions

ATCC®, on behalf of BEI Resources, hereby represents and warrants that the material provided under this certificate has been subjected by ATCC® and the contributor to the tests and procedures specified and that the results described, along with any other data provided in this certificate, are true and accurate to the best of ATCC®'s knowledge.

Support Provided by NIAID

BEI Resources
www.beiresources.org
E-mail: contact@beiresources.org
Tel: 800-359-7370
Fax: 703-365-2898