

***Pseudomonas aeruginosa*, Strain MRSN 16383**

Catalog No. NR-51583

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Product Description:

Pseudomonas aeruginosa (*P. aeruginosa*), strain MRSN 16383 was isolated in 2013 from a human respiratory sample in the United States as part of a global surveillance program. *P. aeruginosa*, strain MRSN 16383 was deposited as multi-locus sequence type (MLST) ST 3006, sensitive to amikacin, aztreonam, ceftazidime, meropenem, piperacillin/tazobactam and tobramycin, intermediately resistant to gentamicin and imipenem and resistant to cefepime, ciprofloxacin and levofloxacin. NR-51583 was produced by inoculation of BEI Resources seed lot 70025073 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 this lot. Quality control testing was completed under propagation conditions unless otherwise noted.

Lot: 70074704

Manufacturing Date: 26MAR2025

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TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis Cellular morphology Colony morphologies ¹ Motility (wet mount) VITEK® MS (MALDI-TOF)	Gram-negative rods Report results Report results <i>P. aeruginosa</i>	Gram-negative rods Colony Type 1: Circular, convex, entire, smooth and cream (Figure 1) Colony Type 2: Circular, low convex, entire, smooth and cream (Figure 1) Motile <i>P. aeruginosa</i> (99.9%)
Antibiotic Susceptibility Profile^{2,3,4} Amikacin Cefazolin Cefepime Ceftazidime Ciprofloxacin Gentamicin Levofloxacin Meropenem Piperacillin/tazobactam Tobramycin	Sensitive Resistant Intermediate Sensitive Resistant Intermediate Resistant Sensitive Sensitive Sensitive	Sensitive (16 µg/mL) Resistant (≥ 64 µg/mL) Sensitive (8 µg/mL) ⁵ Sensitive (4 µg/mL) Resistant (≥ 4 µg/mL) Intermediate (8 µg/mL) Resistant (≥ 8 µg/mL) Sensitive (≤ 0.25 µg/mL) Sensitive (≤ 4 µg/mL) Sensitive (≤ 1 µg/mL)
Genotypic Analysis Sequencing of 16S ribosomal RNA gene (~ 1420 base pairs)	≥ 99% sequence identity to <i>P. aeruginosa</i> , strain MRSN 16383 (GenBank: RXVQ01000033.1)	100% sequence identity to <i>P. aeruginosa</i> , strain MRSN 16383 (GenBank: RXVQ01000033.1)
Purity 7 days at 37°C in an aerobic atmosphere with and without 5% CO ₂ on Tryptic Soy agar	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
Viability	Growth	Growth

¹Two colony types were observed. VITEK® MS (MALDI-TOF) analysis identified cells from both colony types as *P. aeruginosa*.

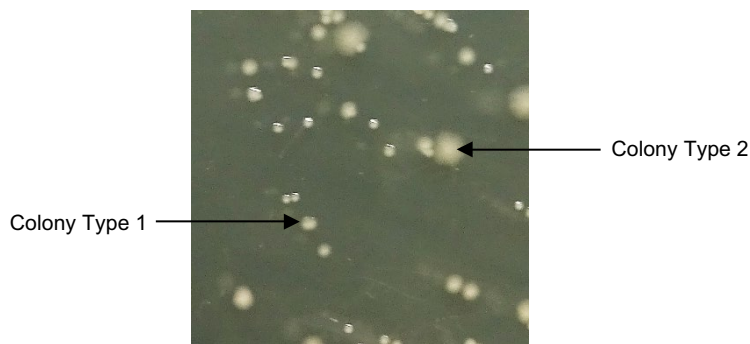
²Minimum Inhibitory Concentration (MIC); MIC interpretation was determined using VITEK® 2 software version 09.02 combined with the bioMérieux Advanced Expert System™ (AES) software using the interpretation standard CLSI M100-S28 (2018) and the interpretation guideline "Natural Resistance." For more information, please refer to Sanders, C. C., et al. "Potential Impact of the VITEK® 2 System and the Advanced Expert System on the Clinical Laboratory of a University-Based Hospital." *J. Clin. Microbiol.* 39 (2001): 2379-2385. PubMed: 11427542.

³Antibiotic susceptibility was tested using using a combination of bioMérieux VITEK® 2 GN81 and ETEST®.

⁴*P. aeruginosa* and other nonfermentative gram-negative bacteria are intrinsically resistant to penicillin, cephalosporins I, cephalosporin II, cephamycins, clindamycin, daptomycin, fusidic acid, glycopeptides, linezolid, macrolides, quinupristin-dalfopristin, and rifampin. These antibiotics were removed from the VITEK® 2 GN81 card and are no longer tested: ampicillin, amoxicillin, amoxicillin/clavulanic acid, ceftiofur, ceftriaxone, cefuroxime, ertapenem, tetracycline, tigecycline, trimethoprim/sulfamethoxazole, chloramphenicol and nitrofurantoin.

⁵*P. aeruginosa*, strain MRSN 16383 was deposited as resistant to cefepime, but showed an MIC of 16 µg/mL (interpreted as intermediately resistant) for lot 70025072 during QC testing. Testing was performed in duplicate. The susceptibility result of the current lot for this antibiotic is within one doubling dilution of specification, which is considered an equivalent result.

Figure 1: Colony Morphology



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