Certificate of Analysis for NR-4

Escherichia coli, Strain H10407

Catalog No. NR-4
(Derived from ATCC® 35401™)

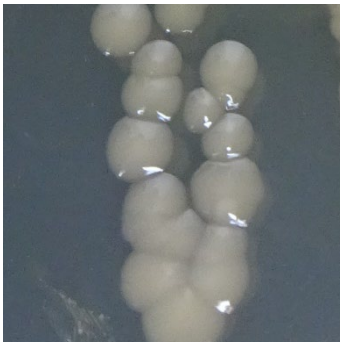
Product Description:
Escherichia coli (*E. coli*), strain H10407 was isolated from the feces of a patient with diarrhea in Bangladesh. NR-4 was produced by inoculation of BEI Resources seed lot 3561953 into Tryptic Soy broth and grown for 1 day at 37°C in an aerobic atmosphere. Broth inoculum was added to Tryptic Soy agar kolles, which were grown for 1 day at 37°C in an aerobic atmosphere with 5% CO_2 to produce this lot. Quality control testing was completed under propagation conditions unless otherwise noted.

Lot: 70058605 **Manufacturing Date: 08FEB2023**

TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis		
Cellular morphology	Gram-negative rods	Gram-negative rods
Colony morphology	Report results	Circular, convex, entire, smooth and cream (Figure 1)
Motility (wet mount)	Report results	Motile
VITEK® MS (MALDI-TOF)	*E. coli*	*E. coli* (99.9%)
Genotypic Analysis		
Next-Generation Sequencing (NGS) of Complete Genome[1]	≥ 99% sequence identity to *E. coli*, strain H10407 (GenBank: FN649414.1)	100% sequence identity to *E. coli*, strain H10407 (GenBank: FN649414.1)
Digital DNA-DNA hybridization (dDDH)[2,3]	≥ 70% for species identification	*Shigella boydii* (85.4%) *Shigella sonnei* (85.2%) *Shigella flexneri* (84.1%) *Shigella dysenteriae* (81.2%) *E. coli* (74.7%)
Purity (post-freeze) 8 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 (post-freeze)	Growth	Growth

[1]The whole genome of *E. coli,* strain H10407 (~ 5.1 megabase pairs) was sequenced using the Illumina® MiSeq® system and was analyzed and assembled with Kraken version 2.1.2 and Unicycler v0.4.8.
[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. dDDH analysis was performed using the Type (Strain) Genome Server.
[3]*Escherichia coli* and *Shigella* spp. are genetically related and cannot be differentiated by DDH. (Dif, G., et al. "In-Depth Genome-Based Analysis of *Shigella* spp. and *Escherichia* spp.: Resolving Ambiguities and Unveiling Phylogenetic Relationships." Curr. Microbiol. 82 (2025): 170. PubMed: 40045049.)

Figure 1: Colony Morphology



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/Sonia Bjorum Brower/
Sonia Bjorum Brower 16 JUN 2025
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 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.

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