

Escherichia coli, Strain H288

Catalog No. NR-15830

Product Description:

Escherichia coli (*E. coli*), strain H288 was isolated in 2001 from a human feces sample collected in Canberra, Australian Capital Territory, Australia. NR-15830 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 this lot. Quality control testing was completed under propagation conditions unless otherwise noted.

Lot: 70003321

Manufacturing Date: 17MAR2017

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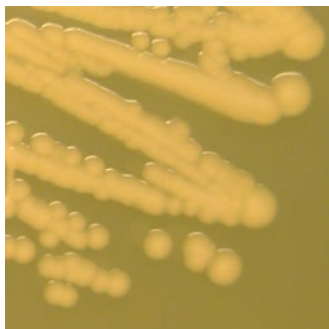
TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis Cellular morphology Colony morphology Motility Thermo Scientific™ Motility Test Medium with TTC Indicator for 1 day at 37°C in an aerobic atmosphere VITEK® MS (MALDI-TOF)	Gram-negative rods Report results Report results <i>E. coli</i>	Gram-negative rods Circular, convex, entire, smooth and cream (Figure 1) Non-motile <i>E. coli</i> (99.9%)
Genotypic Analysis Digital DNA-DNA hybridization (dDDH) ¹	≥ 70% for species identification	<i>Shigella sonnei</i> (85.5%) ^{2,3} <i>Shigella boydii</i> (84.9%) <i>Shigella flexneri</i> (84.7%) <i>Shigella dysenteriae</i> (81.7%) <i>E. coli</i> (75.1%)
Purity (post-freeze) 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 (post-freeze)	Growth	Growth

¹Relatedness 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.

²Reclassification of *Shigella sonnei*, *Shigella boydii*, *Shigella flexneri* and *Shigella dysenteriae* as subspecies of *E. coli* (*E. coli* subsp. *shigella* subsp. nov.) has been proposed [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.].

³The whole genome of *E. coli*, strain H288 (Total Contig Length ~ 4.9 megabase pairs) was sequenced using the Illumina® MiSeq™ platform and was analyzed and assembled using CLC Genomics Workbench software.

Figure 1: Colony Morphology



/Sonia Bjorum Brower/
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29 SEP 2026

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