

Resource Summary Report

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GTDB-Tk

RRID:SCR_019136

Type: Tool

Proper Citation

GTDB-Tk (RRID:SCR_019136)

Resource Information

URL: <https://github.com/Ecogenomics/GtdbTk>

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Description: Open source software tool for assigning objective taxonomic classifications to bacterial and archaeal genomes based on Genome Database Taxonomy. Designed to work with recent advances that allow metagenome assembled genomes to be obtained directly from environmental samples. Can also be applied to isolate and single cell genomes.

Synonyms: GTDB-Tk v1.3.0, Genome Database Taxonomy-Tk

Resource Type: software resource, software toolkit

Keywords: Assigning objective taxonomic classifications, bacterial genome, archaeal genome, Genome Database Taxonomy, metagenome assembled genome, environmental sample, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: GTDB-Tk

Resource ID: SCR_019136

Alternate IDs: biotools:Gtdb-tk

Alternate URLs: <https://bio.tools/GTDB-Tk>

License: GNU GPL v3

Record Creation Time: 20220129T080343+0000

Record Last Update: 20260919T195818+0000

Ratings and Alerts

No rating or validation information has been found for GTDB-Tk.

No alerts have been found for GTDB-Tk.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 98 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Wang Y, et al. (2026) A Genomic Catalog of Migratory Microbiomes from Wild Birds across China's Habitats. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(26), e74581.

Kousar A, et al. (2026) Biological control of *Botrytis cinerea* in tomato and *Fusarium graminearum* in wheat using the novel species *Burkholderia mycopellens* and *Burkholderia crassaminum*. *Frontiers in microbiology*, 17, 1776517.

Yu L, et al. (2026) Systematic characterization of PBP2 as the primary siderophore recognizer in Actinomycetes and other Gram-positive bacteria. *Microbial genomics*, 12(4).

Sun Y, et al. (2026) Incomplete denitrifying bacteria drive N₂O fluxes in ancient Siberian permafrost microcosms. *FEMS microbiology ecology*, 102(5).

Campos-Madueno EI, et al. (2026) Gut microbiota and resistome profiles of Swiss expatriates in Africa revealed by Nanopore metagenomics. *Scientific reports*, 16(1), 7016.

Yasuda S, et al. (2026) Potential survival strategies of novel comammox and nitrite-oxidizing *Nitrospira* synthesizing osmoprotectants in a wastewater microbiome treating high-ammonia brackish landfill leachate. *Microbiome*, 14(1).

Radzieta M, et al. (2026) Anaerobe-associated microbial shifts at infection onset in diabetes-related foot ulcers revealed by longitudinal metagenomics. *Frontiers in cellular and infection microbiology*, 16, 1812721.

Valen??a CAS, et al. (2026) Genome-guided antimicrobial potential of *Bacillus stercoris* from coastal sand with activity against multidrug-resistant bacteria, including MRSA. *International microbiology : the official journal of the Spanish Society for Microbiology*, 29(5), 713.

Wunderer M, et al. (2026) Comparative phenotypic and genomic analysis of the methanogen *Methanomethylovorans thermophila* L2FAW and its phylogenomic placement within the Genome Taxonomy Database. *Access microbiology*, 8(5).

Sousa EG, et al. (2025) The research on the identification, taxonomy, and comparative genomics analysis of nine *Bacillus velezensis* strains significantly contributes to

microbiology, genetics, bioinformatics, and biotechnology. *Frontiers in microbiology*, 16, 1544934.

Liu Y, et al. (2025) Serial nitrogen-phosphate co-limitation controls the primary productivity in the transitional waters of northern South China Sea and the Pearl River Estuary. *Frontiers in microbiomes*, 4, 1655960.

Lu JN, et al. (2025) DNA viral community enhances microbial carbon fixation capacity via auxiliary metabolic genes in contaminated soils. *Nature communications*, 16(1), 9984.

Liu Y, et al. (2025) Reconstruction of 2,965 Microbial Genomes from Mangrove Sediments across Guangxi, China. *Scientific data*, 13(1), 125.

Bird E, et al. (2025) BALROG-ISO: a high-throughput pipeline for Bacterial Antimicrobial Resistance annotation of Genomes-ISOLate whole genome. *microPublication biology*, 2025.

Yao XQ, et al. (2025) Gut microbiota contribute to cold adaptation in mammals-primates and ungulates. *iScience*, 28(4), 112245.

Chandola U, et al. (2025) Non-cyanobacterial diazotrophs support the survival of marine microalgae in nitrogen-depleted environment. *Genome biology*, 26(1), 146.

Liang H, et al. (2025) Efficiently constructing complete genomes with CycloneSEQ to fill gaps in bacterial draft assemblies. *GigaByte (Hong Kong, China)*, 2025, gigabyte154.

Lin X, et al. (2025) Natural-selected plastics biodegradation species and enzymes in landfills. *PNAS nexus*, 4(3), pgaf066.

Chen Y, et al. (2025) Microbial response under sulfate stress in a sulfur-based autotrophic denitrification system. *Frontiers in microbiology*, 16, 1615317.

Villette R, et al. (2025) Human gut microbiome gene co-expression network reveals a loss in taxonomic and functional diversity in Parkinson's disease. *NPJ biofilms and microbiomes*, 11(1), 142.