

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>

Proper Citation: GTDB-Tk (RRID:SCR_019136)

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: 20260801T191103+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 79 mentions in open access literature.

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

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.

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

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

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.

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.

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.

Kasmanas JC, et al. (2025) Integrating comparative genomics and risk classification by assessing virulence, antimicrobial resistance, and plasmid spread in microbial communities with gSpreadComp. GigaScience, 14.

Teng T, et al. (2025) Microbiota alterations leading to amino acid deficiency contribute to depression in children and adolescents. Microbiome, 13(1), 128.

Zeng Z, et al. (2025) Oxidative adaptations in prokaryotes imply the oxygenic photosynthesis before crown-group Cyanobacteria. PNAS nexus, 4(2), pgaf035.

Kieninger B, et al. (2025) Development and validation of a core genome multilocus sequence typing scheme for Citrobacter freundii: application in outbreak investigations

and comparative analysis across the *Citrobacter* genus. *Journal of clinical microbiology*, 63(10), e0086025.

Xiao LF, et al. (2025) Comprehensive metagenomic analysis of the giant panda's oral microbiome reveals distinct taxonomic and functional characteristics. *Animal microbiome*, 7(1), 114.

Pan S, et al. (2025) A holistic genome dataset of bacteria and archaea of mangrove sediments. *GigaScience*, 14.

Villette R, et al. (2025) Integrated multi-omics highlights alterations of gut microbiome functions in prodromal and idiopathic Parkinson's disease. *Microbiome*, 13(1), 200.

Takei S, et al. (2024) Isolation and identification of *Wickerhamiella tropicalis* from blood culture by MALDI-MS. *Frontiers in cellular and infection microbiology*, 14, 1361432.

Duarte VdS, et al. (2024) Host DNA depletion methods and genome-centric metagenomics of bovine hindmilk microbiome. *mSphere*, 9(1), e0047023.

Nanetti E, et al. (2024) The Alpine ibex (*Capra ibex*) gut microbiome, seasonal dynamics, and potential application in lignocellulose bioconversion. *iScience*, 27(7), 110194.

Zheng B, et al. (2024) MBCN: A novel reference database for Efficient Metagenomic analysis of human gut microbiome. *Heliyon*, 10(18), e37422.

Kim EJ, et al. (2024) *Sphingomonas longa* sp. nov., *Sphingomonas mollis* sp. nov. and *Sphingomonas aurea* sp. nov.: three novel *Sphingomonas* species isolated from soil. *International journal of systematic and evolutionary microbiology*, 74(12).

Banerjee G, et al. (2024) Protocol for the construction and functional profiling of metagenome-assembled genomes for microbiome analyses. *STAR protocols*, 5(3), 103167.