Resource Summary Report

Generated by dkNET on May 21, 2025

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

Funding:

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: 20250519T205016+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 62 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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

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.

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

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

Liao R, et al. (2024) Integrated metabolomic and metagenomic strategies shed light on interactions among planting environments, rhizosphere microbiota, and metabolites of tobacco in Yunnan, China. Frontiers in microbiology, 15, 1386150.

Takei S, et al. (2024) Identification of Mycobacterium abscessus using the peaks of ribosomal protein L29, L30 and hemophore-related protein by MALDI-MS proteotyping. Scientific reports, 14(1), 11187.

Huang P, et al. (2024) Gut microbial genomes with paired isolates from China illustrate probiotic and cardiometabolic effects. Cell genomics, 4(6), 100559.

Pinchart PE, et al. (2024) The genus Limnospira contains only two species both unable to

produce microcystins: L. maxima and L. platensis comb. nov. iScience, 27(9), 110845.

Santamarina-García G, et al. (2024) Shotgun metagenomic sequencing reveals the influence of artisanal dairy environments on the microbiomes, quality, and safety of Idiazabal, a raw ewe milk PDO cheese. Microbiome, 12(1), 262.

Zepeda-Rivera M, et al. (2024) A distinct Fusobacterium nucleatum clade dominates the colorectal cancer niche. Nature, 628(8007), 424.

Feng Y, et al. (2024) Population genomics uncovers global distribution, antimicrobial resistance, and virulence genes of the opportunistic pathogen Klebsiella aerogenes. Cell reports, 43(8), 114602.

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

Schvarcz CR, et al. (2024) The genome sequences of the marine diatom Epithemia pelagica strain UHM3201 (Schvarcz, Stancheva & Steward, 2022) and its nitrogen-fixing, endosymbiotic cyanobacterium. Wellcome open research, 9, 232.

Abadikhah M, et al. (2024) Viral diversity and host associations in microbial electrolysis cells. ISME communications, 4(1), ycae143.

Riesco R, et al. (2024) Update on the proposed minimal standards for the use of genome data for the taxonomy of prokaryotes. International journal of systematic and evolutionary microbiology, 74(3).

Carasso S, et al. (2024) Inflammation and bacteriophages affect DNA inversion states and functionality of the gut microbiota. Cell host & microbe, 32(3), 322.

Dede B, et al. (2024) Bacterial chemolithoautotrophy in ultramafic plumes along the Mid-Atlantic Ridge. The ISME journal, 18(1).

Huang KD, et al. (2024) Establishment of a non-Westernized gut microbiota in men who have sex with men is associated with sexual practices. Cell reports. Medicine, 5(3), 101426.

Peng S, et al. (2024) Metagenomic insights into jellyfish-associated microbiome dynamics during strobilation. ISME communications, 4(1), ycae036.

Bustos-Caparros E, et al. (2024) Ecological success of extreme halophiles subjected to recurrent osmotic disturbances is primarily driven by congeneric species replacement. The ISME journal, 18(1).