Resource Summary Report

Generated by NIF on Apr 25, 2025

CheckM

RRID:SCR_016646

Type: Tool

Proper Citation

CheckM (RRID:SCR_016646)

Resource Information

URL: http://ecogenomics.github.io/CheckM/

Proper Citation: CheckM (RRID:SCR_016646)

Description: Software tool to assess the quality of microbial genomes recovered from isolates, single cells, and metagenomes by using a broader set of marker genes specific to the position of a genome within a reference genome tree and information about the collocation of these genes.

Resource Type: software resource, software application, data analysis software, software toolkit, data processing software

Defining Citation: DOI:10.1101/gr.186072.114

Keywords: assess, quality, microbial, genome, recovered, bio.tools

Funding:

Availability: Free, Available for download, Freely available

Resource Name: CheckM

Resource ID: SCR_016646

Alternate IDs: biotools:checkm

Alternate URLs: https://github.com/Ecogenomics/CheckM, https://bio.tools/checkm

License: GNU General Public License

Record Creation Time: 20220129T080331+0000

Record Last Update: 20250425T060156+0000

Ratings and Alerts

No rating or validation information has been found for CheckM.

No alerts have been found for CheckM.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 121 mentions in open access literature.

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

Campos-Avelar I, et al. (2025) Bacillus cabrialesii subsp. cabrialesii Strain TE5: A Promising Biological Control Bacterium Against the Causal Agent of Spot Blotch in Wheat. Plants (Basel, Switzerland), 14(2).

Keuleyan E, et al. (2025) Characterization of Streptococcus pyogenes Strains from Tonsillopharyngitis and Scarlet Fever Resurgence, 2023-FIRST Detection of M1UK in Bulgaria. Microorganisms, 13(1).

Facimoto CT, et al. (2025) Hindguts of Kyphosus sydneyanus harbor phylogenetically and genomically distinct Alistipes capable of degrading algal polysaccharides and diazotrophy. mSystems, 10(1), e0100724.

Iliev I, et al. (2025) Characterization and Probiotic Potential of Levilactobacillus brevis DPL5: A Novel Strain Isolated from Human Breast Milk with Antimicrobial Properties Against Biofilm-Forming Staphylococcus aureus. Microorganisms, 13(1).

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.

Wajima T, et al. (2024) Molecular characterization of a novel putative pathogen, Streptococcus nakanoensis sp. nov., isolated from sputum culture. Microbiology spectrum, 12(10), e0135424.

Ghezzi H, et al. (2024) PUPpy: a primer design pipeline for substrain-level microbial detection and absolute quantification. mSphere, 9(7), e0036024.

Salgado JFM, et al. (2024) Unveiling lignocellulolytic potential: a genomic exploration of bacterial lineages within the termite gut. Microbiome, 12(1), 201.

Gao Y, et al. (2024) Different artificial feeding strategies shape the diverse gut microbial communities and functions with the potential risk of pathogen transmission to captive Asian small-clawed otters (Aonyx cinereus). mSystems, 9(12), e0095424.

Feng C, et al. (2024) Dynamic Changes of the Gut Microbiota and Its Functional Metagenomic Potential during the Development of Non-Small Cell Lung Cancer. International journal of molecular sciences, 25(7).

Bivona D, et al. (2024) Generation and Characterization of Stable Small Colony Variants of USA300 Staphylococcus aureus in RAW 264.7 Murine Macrophages. Antibiotics (Basel, Switzerland), 13(3).

Kapse N, et al. (2024) Unveiling the Probiotic Potential of Streptococcus thermophilus MCC0200: Insights from In Vitro Studies Corroborated with Genome Analysis. Microorganisms, 12(2).

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

Schiml VC, et al. (2024) Microbial consortia driving (ligno)cellulose transformation in agricultural woodchip bioreactors. Applied and environmental microbiology, 90(12), e0174224.

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

Zhang L, et al. (2024) Spatiotemporal dynamics of giant viruses within a deep freshwater lake reveal a distinct dark-water community. The ISME journal, 18(1).

Thanwisai A, et al. (2024) Xenorhabdus bharatensis sp. nov., Xenorhabdus entomophaga sp. nov., Xenorhabdus siamensis sp. nov., and Xenorhabdus thailandensis sp. nov. Isolated from Steinernema Entomopathogenic Nematodes. Current microbiology, 82(1), 10.

Katahira K, et al. (2024) Mobile genetic element-driven genomic changes in a community-associated methicillin-resistant Staphylococcus aureus clone during its transmission in a regional community outbreak in Japan. Microbial genomics, 10(7).

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).

Atkins H, et al. (2024) Evidence of Lactobacillus strains shared between the female urinary and vaginal microbiota. Microbial genomics, 10(7).