

Resource Summary Report

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CheckM

RRID:SCR_016646

Type: Tool

Proper Citation

CheckM (RRID:SCR_016646)

Resource Information

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

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

Defining Citation: [DOI:10.1101/gr.186072.114](https://doi.org/10.1101/gr.186072.114)

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

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: 20260731T043011+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 184 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Mahajan S, et al. (2026) Molecular insights into the antimicrobial and cardiometabolic functions of *Lactobacillus crispatus* isolated from the reproductive tract microbiota of Indian women. *Journal of biomedical science*, 33(1), 7.

Viver T, et al. (2025) Comparative metagenomics indicates metabolic niche differentiation of benthic and planktonic Woeseiaceae. *Environmental microbiome*, 20(1), 74.

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).

Slosser T, et al. (2025) Novel hot spring Thermoproteota support vertical inheritance of ammonia oxidation and carbon fixation in Nitrososphaeria. *Access microbiology*, 7(4).

Gao F, et al. (2025) Genomic epidemiology and the evolution of erm(B)-mediated macrolide resistance in *Campylobacter*. *Microbial genomics*, 11(10).

Kruasuwan W, et al. (2025) Clinical long-read metagenomic sequencing of culture-negative infective endocarditis reveals genomic features and antimicrobial resistance. *BMC infectious diseases*, 25(1), 1299.

Chan Y-X, et al. (2025) Antimicrobial susceptibility and genomic characterization of *Lactococcus formosensis*, *Lactococcus garvieae*, and *Lactococcus petauri* in Hong Kong. *Microbiology spectrum*, 13(10), e0010125.

Scadden J, et al. (2025) The nisin O cluster: species dissemination, candidate leader peptide proteases and the role of regulatory systems. *Microbiology (Reading, England)*, 171(2).

Shao Z, et al. (2025) Genomic insights into host-Endozoicomonadaceae cophylogeny. *Microbial genomics*, 11(4).

Tucker SJ, et al. (2025) Habitat-specificity in SAR11 is associated with a few genes under high selection. *The ISME journal*, 19(1).

He J, et al. (2025) Multi-Habitat Landscape Promotes Microbial Diversity: Insights from the Traditional Agricultural Heritage and the Global Trend. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(46), e06402.

Abu Sabah E, et al. (2025) Phylogenomics, evolution and origin of multidrug-resistant *Acinetobacter baumannii* ST15. *Microbial genomics*, 11(7).

Zhou G, et al. (2025) Whole-genome probe capture sequencing reveals genomic diversity and characteristics of *Mycoplasma pneumoniae* in Nanjing, China. *Frontiers in microbiology*, 16, 1589971.

Piotr D, et al. (2025) Genomic and functional characterization of a lipopeptide-producing endophytic *Bacillus velezensis* EL isolated from *Euphorbia cyparissias* L. *Microbial cell factories*, 24(1), 250.

Patarapuwadol S, et al. (2025) Whole-genome sequencing of *Burkholderia glumae* strains from Thailand reveals potential horizontal gene transfer with *Burkholderia pseudomallei*. *PloS one*, 20(12), e0340071.

Jeilu O, et al. (2025) Metagenomic profiling of airborne microbial communities from aircraft filters and face masks. *Microbiome*, 13(1), 249.

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.

Dantas K, et al. (2025) Emergent *Escherichia coli* of the highly virulent B2-ST1193 clone producing KPC-2 carbapenemase in ready-to-eat vegetables. *Journal of global antimicrobial resistance*, 41, 105.

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).

Woods PH, et al. (2025) Identification of key steps in the evolution of anaerobic methanotrophy in *Candidatus Methanovorans* (ANME-3) archaea. *Science advances*, 11(25), eadq5232.