

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

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

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: 20260905T132812+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 238 mentions in open access literature.

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

Parween S, et al. (2026) Desert Plant Endophyte Genome Database: a curated repository of endophytic bacterial genomes across arid ecosystems. Database : the journal of biological databases and curation, 2026.

Meinen-Jochum J, et al. (2026) Sequencing and Analysis of Chicken Segmented Filamentous Bacteria Genome Revealed Unique Avian-Specific Features. Microorganisms, 14(2).

Heng YC, et al. (2026) Metagenomic insights into the global wild boar faecal microbiome reveal novel taxa and carbohydrate degraders distinguishing wild and domesticated Sus. Microbiome, 14(1).

Rios Galicia B, et al. (2026) Legionella stuttgartensis sp. nov. and Legionella nigrisilvae sp. nov., two new species isolated from a re-cooling plant and from a drinking water house installation in southern Germany. International journal of systematic and evolutionary microbiology, 76(6).

Das R, et al. (2026) Microbial community structure, functional potential, probiotic signatures, and MAG reconstruction of fermented bamboo shoots from Northeast India. FEMS microbes, 7, xtag032.

Montgomery A, et al. (2026) Tracking active heterotrophic microbial communities in the Guaymas Basin deep biosphere with BONCAT-FACS. ISME communications, 6(1), ycag111.

She Q, et al. (2026) Rapid dissemination of Staphylococcus aureus in the neonatal intensive care unit is associated with invasive infection. Nature communications, 17(1).

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.

Ayzanoa B, et al. (2026) Genomic surveillance of multidrug-resistant Escherichia coli and Klebsiella in clinical and wastewater isolates from a paediatric hospital in Lima, Peru. Access microbiology, 8(1).

Aja-Macaya P, et al. (2026) Emergence of New Delhi Metallo- β -Lactamase 14-Producing *Klebsiella pneumoniae* Sequence Type 147 Clone in Spain and Outbreak in the Canary Islands. *Emerging infectious diseases*, 32(1), 63.

Aziz T, et al. (2026) Genomic insights into probiotic potential and metabolic adaptability of food derived *Lactiplantibacillus plantarum* and *Pediococcus acidilactici*. *Frontiers in microbiology*, 17, 1847858.

Dai W, et al. (2026) Genome-Scale Metabolic Models Guided Improvement of Fermented Milk Quality and Flavor by *Lactocaseibacillus paracasei* subsp. *paracasei* 63. *Foods* (Basel, Switzerland), 15(11).

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.

Hao Y, et al. (2026) Metagenomic insights into the influence of goose farming on the gut microbiome and antibiotic resistome of workers. *Poultry science*, 105(4), 106487.

Zhang Y, et al. (2026) Integrative profiling of *Helicobacter pylori* clinical isolates: virulence genes, antimicrobial susceptibility and genetic diversity in gastric cancer risk stratification. *Microbial genomics*, 12(3).

Kerek Á, et al. (2026) Integrated Phenotypic and Genomic Profiling of Antimicrobial Resistance and Virulence-Associated Determinants in Poultry-Derived *Enterococcus* spp. from Hungary. *Veterinary sciences*, 13(2).

Song Y, et al. (2026) Ecology-guided *Bacillus* SynCom from a rice-duckweed core reveals division of labor for concurrent growth promotion and sheath blight suppression. *Microbiome*, 14(1).

Colombini L, et al. (2026) The novel pseudo-compound transposon Tn7086 carries aminoglycoside resistance genes in *Enterococcus faecalis*. *Microbial genomics*, 12(4).

Zhou J, et al. (2026) *Ornithinibacillus liuyingii* sp. nov.: a novel multidrug-resistant and potentially pathogenic bacterium isolated from *Apodemus chevrieri* lung tissue. *BMC microbiology*, 26(1).

Meyer J, et al. (2026) Pandemic SHV-106-producing *Klebsiella pneumoniae* ST231 isolated from Brazilian hedgehog (*Coendou spinosus*) reveals an emerging environmental circulation of a high-risk multidrug-resistant lineage. *Antonie van Leeuwenhoek*, 119(5).