

Resource Summary Report

Generated by [ASWG](#) on Aug 26, 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: 20260821T194054+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 [ASWG](#) .

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

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.

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).

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.

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).

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.

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).

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).

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).

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.

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).

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.

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).

Dong L, et al. (2026) Genomic characterization of the multidrug-resistant IncP-2 plasmid pPAMS in a clinical isolate *Pseudomonas aeruginosa*. *BMC microbiology*, 26(1).

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).