

Resource Summary Report

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MetaBAT

RRID:SCR_019134

Type: Tool

Proper Citation

MetaBAT (RRID:SCR_019134)

Resource Information

URL: <https://bitbucket.org/berkeleylab/metabat/src/master/>

Proper Citation: MetaBAT (RRID:SCR_019134)

Description: Software statistical framework for reconstructing genomes from metagenome data. Open source software tool for accurately reconstructing single genomes from complex microbial communities.

Synonyms: MetaBAT2

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

Defining Citation: [PMID:26336640](#)

Keywords: Genome bin, metagenome datasets, reconstructing single genomes, microbial communities, metagenome data

Availability: Free, Available for download, Freely available

Resource Name: MetaBAT

Resource ID: SCR_019134

Alternate URLs: <https://bitbucket.org/berkeleylab/metabat/wiki/CAMI>,
<https://sources.debian.org/src/metabat/>

Record Creation Time: 20220129T080343+0000

Record Last Update: 20260821T194140+0000

Ratings and Alerts

No rating or validation information has been found for MetaBAT.

No alerts have been found for MetaBAT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 761 mentions in open access literature.

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

Jourdain L, et al. (2026) Environmental selection constrains metabolic network architecture despite taxonomic turnover in anaerobic digestion communities. The ISME journal, 20(1).

Wang W, et al. (2026) Multiomics insights into the effects of prebiotics on physical function and metabolism in adults with obesity and knee osteoarthritis. Gut microbes, 18(1), 2679516.

Tow WK, et al. (2026) Metagenomic insights into urolithin formation from rambutan rind extract by rat faecal-derived microbiome. Applied microbiology and biotechnology, 110(1).

Liu Z, et al. (2026) Dietary regulation on gut resistome linked with microbial amino acid metabolism in pigs. Animal microbiome, 8(1).

Peña-Valencia MF, et al. (2026) Lignocellulose-mediated selection of potential halophilic PET-degrading enzymes from mangrove soil. Nature communications, 17(1).

Liu J, et al. (2026) Comprehensive profiling of antibiotic resistance, virulence genes, and mobile genetic elements in the gut microbiome of Tibetan antelopes. mSystems, 11(2), e0144325.

Kiran R, et al. (2026) Halophilic Anaerobic Cultures Enriched with CO₂:H₂ from Different Saline Environments Reveal Unknown Autotrophic Bacterial Diversity and Modular Carbon Fixation Pathways. Microbial ecology, 89(1), 40.

Kim DD, et al. (2026) Metagenomic strain tracking reveals patterns of bacterial spread and the impact of water chlorination. medRxiv : the preprint server for health sciences.

Liu Y, et al. (2026) Ultra-deep metagenomic sequencing enables reconstruction of diverse, high quality microbial genomes from human urine samples. BMC microbiology, 26(1).

Feng T, et al. (2026) A comprehensive ruminant microbial catalog (CRMC) reveals convergent selection for key vitamin-synthesizing pathways and genes across ruminants and human. GigaScience, 15.

Ahmad AA, et al. (2026) Integrative multi-omics analysis of dietary fibre-induced modulations in the composition and function of chicken caecal microbiota. *NPJ biofilms and microbiomes*, 12(1).

Warring SD, et al. (2026) Single-cell sequencing reveals unexpected genetic diversity among *Bodo* spp. flagellates and their bacterial endosymbionts. *Microbial genomics*, 12(3).

Wang J, et al. (2026) Earthworm gut microbiome promotes biodegradation of albendazole in soil. *Crop health*, 4(1).

Westmeijer G, et al. (2026) Exploring microbial diversity using cell-size fractionated enrichment incubations from subsurface aquifers at Äspö, Sweden. *Communications biology*, 9(1).

Bedoya-Urrego K, et al. (2026) Uncovering the hidden yeast diversity in fermented coffee: Insights from a shotgun metagenomic approach. *PloS one*, 21(2), e0332370.

Peterse IF, et al. (2026) Robust ammonia oxidation by "Candidatus Nitrosacidococcus tergens" across a broad pH range. *mBio*, 17(5), e0297525.

Lee HG, et al. (2026) metaFun: An analysis pipeline for metagenomic big data with fast and unified functional searches. *Gut microbes*, 18(1), 2611544.

Chen X, et al. (2026) Metagenomic expansion of *Joyebacterota* identifies *Cavimicrobium*, a dominant sulfide-producing lineage in anoxic marine ecosystems. *ISME communications*, 6(1), ycag137.

Guo J, et al. (2026) Mobile genetic elements shape microbial diversity and functions in thawing permafrost soils. *Nature microbiology*, 11(7), 1800.

Ricci F, et al. (2026) Chemosynthesis enables microbial communities to flourish in a marine cave ecosystem. *The ISME journal*, 20(1).