

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 17, 2026

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: 20260912T195910+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 [SPARC SAWG](#) .

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

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.

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

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.

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.

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*.

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).

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).

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

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

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).

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.

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

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.

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.