

Resource Summary Report

Generated by [RRID](#) on Aug 2, 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 processing software, data analysis 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: 20260801T190628+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 637 mentions in open access literature.

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

Kimbrel JA, et al. (2026) High-quality Acinetobacter genomes recovered from combat wounds via metagenomic sequencing resemble cultured isolate genomes. Microbiology spectrum, 14(1), e0187625.

Huang C, et al. (2026) The High-Altitude Adaptation Characteristics of Microbiota-Host Cross-Talk in Yak Gastrointestinal Track. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(1), e14862.

Xu CCY, et al. (2025) Pre-exposure to stress reduces loss of community and genetic diversity following severe environmental disturbance. Current biology : CB, 35(5), 1061.

Pan S, et al. (2025) A holistic genome dataset of bacteria and archaea of mangrove sediments. GigaScience, 14.

Feng Y, et al. (2025) Regional antimicrobial resistance gene flow among the One Health sectors in China. Microbiome, 13(1), 3.

Qu Q, et al. (2025) Population-level gut microbiome and its associations with environmental factors and metabolic disorders in Southwest China. NPJ biofilms and microbiomes, 11(1), 24.

Middelboe M, et al. (2025) Prophage-encoded chitinase gene supports growth of its bacterial host isolated from deep-sea sediments. The ISME journal, 19(1).

Foysal MJ, et al. (2025) The impact of anthropogenic activities on antimicrobial and heavy metal resistance in aquatic environments. Applied and environmental microbiology, 91(4), e0231724.

Fang Y, et al. (2025) Genome-resolved year-round dynamics reveal a broad range of giant virus microdiversity. mSystems, 10(1), e0116824.

Kang X, et al. (2025) The Gut Microbiome of the Asiatic Toad (Bufo gargarizans) Reflects Environmental Changes and Human Activities. Ecology and evolution, 15(5), e71394.

Bergauer K, et al. (2025) Dark ocean archaeal and bacterial chemoautotrophs drive vitamin B1 production in oxygen minimum zones. ISME communications, 5(1), ycaf077.

Zheng J, et al. (2025) Cellulose-functionalized magnetic nanoparticle-mediated isolation of novel cellulolytic bacteria. *Applied and environmental microbiology*, 91(10), e0078825.

Robes JMD, et al. (2025) Inverse stable isotope probing-metabolomics (InverSIP) identifies an iron acquisition system in a methane-oxidizing bacterial community. *Proceedings of the National Academy of Sciences of the United States of America*, 122(36), e2507323122.

Ormaasen I, et al. (2025) Tracing of streptococcal strains from infant stools across human body sites links site-specific prevalence to adhesins. *Applied and environmental microbiology*, 91(9), e0019625.

Quijada NM, et al. (2025) The food-associated resistome is shaped by processing and production environments. *Nature microbiology*, 10(8), 1854.

Peng S-X, et al. (2025) Biogeography and ecological functions of underestimated CPR and DPANN in acid mine drainage sediments. *mBio*, 16(6), e0070525.

Liao H, et al. (2025) Harnessing phage consortia to mitigate the soil antibiotic resistome by targeting keystone taxa *Streptomyces*. *Microbiome*, 13(1), 127.

Sereika M, et al. (2025) Genome-resolved long-read sequencing expands known microbial diversity across terrestrial habitats. *Nature microbiology*, 10(8), 2018.

Echeveste Medrano MJ, et al. (2025) Physiological Stress Response to Sulfide Exposure of Freshwater Anaerobic Methanotrophic Archaea. *Environmental science & technology*, 59(21), 10262.

Fortin SG, et al. (2025) Microplastic biofilms as potential hotspots for plastic biodegradation and nitrogen cycling: a metagenomic perspective. *FEMS microbiology ecology*, 101(5).