

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 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: software application, software resource, data processing software, data analysis software

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: 20260728T043552+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 [nidm-terms](#) .

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.

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

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

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

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.

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

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

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

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

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).

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

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.

Purse C, et al. (2025) Intestinal microbiota profiles of captive-bred cynomolgus macaques reveal influence of biogeography and age. *Animal microbiome*, 7(1), 47.

Lei Y, et al. (2025) Deciphering functional landscapes of rumen microbiota unveils the role of *Prevotella bryantii* in milk fat synthesis in goats. *Genome biology*, 26(1), 311.

Rasmussen AN, et al. (2025) Floodplain nitrifiers harbor the genetic potential for utilizing a wide range of organic nitrogen compounds. *mSystems*, 10(11), e0082925.