

Resource Summary Report

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BMTagger

RRID:SCR_014619

Type: Tool

Proper Citation

BMTagger (RRID:SCR_014619)

Resource Information

URL: http://hmpdacc.org/resources/tools_protocols.php

Proper Citation: BMTagger (RRID:SCR_014619)

Description: A tool that discriminates between human reads and microbial reads without performing an alignment of all reads to the human genome.

Synonyms: Best Match Tagger

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

Keywords: microbiome, human reads, metagenomics, microbial reads, human genome

Availability: Available as files

Resource Name: BMTagger

Resource ID: SCR_014619

Alternate URLs: <ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/bmtagger/>

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260829T182849+0000

Ratings and Alerts

No rating or validation information has been found for BMTagger.

No alerts have been found for BMTagger.

Data and Source Information

Usage and Citation Metrics

We found 93 mentions in open access literature.

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

Cheng G, et al. (2026) Intratumoral Parvimonas micra promotes esophageal squamous cell carcinoma via p-cresol-induced Treg differentiation. Science advances, 12(8), eady1644.

Ulloa MA, et al. (2026) Bacterial genome reconstruction and community profiling in Neotropical Drosophila. Scientific reports, 16(1), 6601.

González-Pinto L, et al. (2026) Genetic and biochemical characterization of OXA-1054, a carbapenem-hydrolyzing class D β -lactamase conferring broad-spectrum β -lactam resistance in Pseudomonas aeruginosa. Antimicrobial agents and chemotherapy, 70(7), e0180525.

Kiran S, et al. (2026) Segmented filamentous bacteria are worldwide human gut commensals. Nature communications, 17(1).

Lee SC, et al. (2026) Functional divergence of the gut microbiome associated with lifestyle and helminth infection in Indigenous Peninsular Malaysian. Research square.

Matoba R, et al. (2026) Metabolic and functional pathways of gut microbiota in patients with gastric cancer. Scientific reports, 16(1).

Parizadeh M, et al. (2026) Impact of maternal, infant, and household factors on early-life gut microbiome development in a rural setting. The ISME journal, 20(1).

Guo Y, et al. (2026) Dietary iron overload exacerbates intestinal damage induced by Eimeria tenella infection in broilers via impaired barrier integrity and gut microbiota dysbiosis. Poultry science, 105(5), 106664.

Xu J, et al. (2026) Limosilactobacillus mucosae attenuates hyperlipidemic periodontitis via the gut-oral axis. Gut microbes, 18(1), 2617699.

Pellegrinetti TA, et al. (2026) Pseudogenization of the chaperonin system in 'Candidatus Phytoplasma pruni' revealed by genome sequencing and comparative genomics. Microbial genomics, 12(6).

Bodkhe RL, et al. (2026) Multi-cohort Analysis Reveals Microbiome Signatures Associated with Drug Response in New-Onset Rheumatoid Arthritis. bioRxiv : the preprint server for biology.

Zhang X, et al. (2026) Dietary Lonicera japonica supplementation modulates cecal gut microbial composition and metabolomic profiles in weaned piglets. Frontiers in veterinary science, 13, 1804735.

Liu C, et al. (2026) Integrative multi-omics analysis reveals microbiota alterations and clinical indicators predictive of pulmonary fibrosis progression following SARS-CoV-2 infection. *Briefings in bioinformatics*, 27(2).

Dong J, et al. (2026) Buyang Huanwu Decoction promotes neurorepair after spinal cord injury through a *Lactobacillus johnsonii*-indole-3-lactic acid-AhR-PI3K/Akt axis. *Chinese medicine*, 21(1).

Saidi F, et al. (2025) Effect of initiation of antiretroviral drugs for HIV prevention or treatment on the vaginal microbiome of pregnant women in Malawi. *NPJ biofilms and microbiomes*, 11(1), 67.

Huang H, et al. (2025) Multi-omics dataset of individual variations in growth performance of large yellow croaker. *Scientific data*, 12(1), 90.

Peña-López Y, et al. (2025) Joint fluid multi-omics improves diagnostic confidence during evaluation of children with presumed septic arthritis. *Pediatric rheumatology online journal*, 23(1), 9.

Zhang X, et al. (2025) Biochanin A improves nitrogen utilization efficiency by regulating ruminal microbial community in dairy goats. *Microbiome*, 14(1), 13.

Trepka KR, et al. (2025) Shifts in the human gut microbiome during cancer chemotherapy are diet-dependent. *bioRxiv : the preprint server for biology*.

Lee G, et al. (2025) Distinct gut microbiome features characterize *Fasciola hepatica* infection and predict triclabendazole treatment outcomes in Peruvian patients. *Frontiers in cellular and infection microbiology*, 15, 1555171.