

Resource Summary Report

Generated by [kravitz2](#) on Jul 30, 2026

MetaPhlAn

RRID:SCR_004915

Type: Tool

Proper Citation

MetaPhlAn (RRID:SCR_004915)

Resource Information

URL: <http://huttenhower.sph.harvard.edu/metaphlan2>

Proper Citation: MetaPhlAn (RRID:SCR_004915)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on February 28, 2023. Computational tool for profiling the composition of microbial communities from metagenomic shotgun sequencing data. It relies on unique clade-specific marker genes identified from reference genomes.

Synonyms: MetaPhlAn, Metagenomic Phylogenetic Analysis, MetaPhlAn version 2, MetaPhlAn - Metagenomic Phylogenetic Analysis, MetaPhlAn v2

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

Defining Citation: [PMID:22688413](https://pubmed.ncbi.nlm.nih.gov/22688413/), [DOI:10.1038/nmeth.3589](https://doi.org/10.1038/nmeth.3589)

Keywords: microbial community, microbial composition, microbial genome, microbial sequence

Resource Name: MetaPhlAn

Resource ID: SCR_004915

Alternate IDs: OMICS_02286

Alternate URLs: <http://huttenhower.sph.harvard.edu/metaphlan>
<https://bitbucket.org/nsegata/metaphlan/>, <https://sources.debian.org/src/metaphlan2/>

Record Creation Time: 20220129T080227+0000

Record Last Update: 20260731T042704+0000

Ratings and Alerts

No rating or validation information has been found for MetaPhlAn.

No alerts have been found for MetaPhlAn.

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 [kravitz2](#).

Zielińska K, et al. (2025) Healthy microbiome-moving towards functional interpretation. *GigaScience*, 14.

Yang Z, et al. (2025) *Veillonella* intestinal colonization promotes *C. difficile* infection in Crohn's disease. *Cell host & microbe*, 33(9), 1518.

Horvath M, et al. (2025) Species- and strain-specific microbial modulation of interferon, innate immunity, and epithelial barrier in 2D air-liquid interface respiratory epithelial cultures. *BMC biology*, 23(1), 28.

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.

Chen YC, et al. (2025) PreLect: Prevalence leveraged consistent feature selection decodes microbial signatures across cohorts. *NPJ biofilms and microbiomes*, 11(1), 3.

Bloom PP, et al. (2025) Safety and efficacy of a defined bacterial consortium, VE303, to treat HE. *Hepatology communications*, 9(3).

Gulyaeva A, et al. (2025) Identification and characterization of *Faecalibacterium* prophages rich in diversity-generating retroelements. *Microbiology spectrum*, 13(2), e0106624.

Heidrich V, et al. (2025) Newly identified species from the dog dental plaque microbiome highlight little overlap with humans. *NPJ biofilms and microbiomes*, 11(1), 30.

Vinogradova E, et al. (2025) *Enterococcus* dysbiosis as a mediator of vitamin D deficiency-associated memory impairments. *Heliyon*, 11(2), e41969.

Reddi S, et al. (2025) Fecal microbiota transplantation to prevent acute graft-versus-host disease: pre-planned interim analysis of donor effect. *Nature communications*, 16(1), 1034.

Jiang Y, et al. (2025) GutMetaNet: an integrated database for exploring horizontal gene transfer and functional redundancy in the human gut microbiome. *Nucleic acids research*,

53(D1), D772.

Banerjee G, et al. (2025) Deep sequencing-derived Metagenome Assembled Genomes from the gut microbiome of liver transplant patients. *Scientific data*, 12(1), 39.

Sampson TR, et al. (2025) Alpha synuclein overexpression can drive microbiome dysbiosis in mice. *Scientific reports*, 15(1), 4014.

Puller V, et al. (2025) Impact of simulation and reference catalogues on the evaluation of taxonomic profiling pipelines. *Microbial genomics*, 11(1).

Portlock T, et al. (2025) Interconnected pathways link faecal microbiota plasma lipids and brain activity to childhood malnutrition related cognition. *Nature communications*, 16(1), 473.

Nasr E, et al. (2025) PathoGFAIR: a collection of FAIR and adaptable (meta)genomics workflows for (foodborne) pathogens detection and tracking. *GigaScience*, 14.

Høyer KL, et al. (2025) Faecal microbiota transplantation for patients with diabetes type 1 and severe gastrointestinal neuropathy (FADIGAS): a randomised, double-blinded, placebo-controlled trial. *EClinicalMedicine*, 79, 103000.

Chin KTC, et al. (2025) Flagellin in blood and *Bifidobacterium pseudocatenulatum* in gut are associated with live birth upon IVF-frozen embryo transfer. *iScience*, 28(2), 111933.

Sun L, et al. (2025) Shallow-water mussels (*Mytilus galloprovincialis*) adapt to deep-sea environment through transcriptomic and metagenomic insights. *Communications biology*, 8(1), 46.

Nychas E, et al. (2025) Discovery of robust and highly specific microbiome signatures of non-alcoholic fatty liver disease. *Microbiome*, 13(1), 10.