

Resource Summary Report

Generated by [ASWG](#) on Sep 1, 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 analysis resource, data analysis software, data processing software, sequence analysis software, software application, software resource

Defining Citation: [PMID:22688413](#), [DOI: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: 20260829T182217+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 645 mentions in open access literature.

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

Zhou Z, et al. (2026) Integrative analysis of the mouse cecal microbiome across diet, age, and weight in the diverse BXD population. *Microbiome*, 14(1).

Moiseyenko A, et al. (2026) *Faecalibacterium prausnitzii*, depleted in the Parkinson's disease microbiome, improves motor deficits in α -synuclein overexpressing mice. *NPJ Parkinson's disease*, 12(1).

Werner L, et al. (2026) Antibiotic disruption of the gut microbiome triggers IBD-like proteolytic activity. *Cell reports*, 45(6), 117478.

Hattori-Muroi K, et al. (2026) Dietary soy shapes the microbiome to induce commensal-specific T follicular helper cells and IgA production. *Immunity*, 59(6), 1616.

Rashidi A, et al. (2026) Cohesive modules of engraftment in fecal microbiota transplantation. *iScience*, 29(6), 116025.

Moosavi D, et al. (2025) Stability and Variability of the Human Fecal Microbiome over 2 Years in the Multiethnic Cohort Study: A Metagenomic Analysis. *Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology*, 34(8), 1386.

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

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).

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.

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.

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.

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

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

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

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.

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

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.

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