

# Resource Summary Report

Generated by T1D on Aug 5, 2026

## MetaPhlAn

RRID:SCR\_004915

Type: Tool

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### Proper Citation

MetaPhlAn (RRID:SCR\_004915)

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### 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 software, software resource, sequence analysis software, software application, data analysis resource

**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:** 20260805T044115+0000

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### Ratings and Alerts

No rating or validation information has been found for MetaPhlAn.

No alerts have been found for MetaPhlAn.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 637 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#).

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.

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

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

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.

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.

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.

Bhosle A, et al. (2025) Response of the gut microbiome and metabolome to dietary fiber in healthy dogs. *mSystems*, 10(1), e0045224.

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.

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.