Resource Summary Report

Generated by RRID on Apr 19, 2025

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, sequence analysis software, data analysis software, software application, software resource, data processing software

Defining Citation: PMID:22688413, DOI:10.1038/nmeth.3589

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

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

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: 20250419T055004+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 624 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

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.

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

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

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.

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.

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

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.

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.

Park HA, et al. (2025) Metagenomic Analysis Identifies Sex-Related Gut Microbial Functions and Bacterial Taxa Associated With Skeletal Muscle Mass. Journal of cachexia, sarcopenia and muscle, 16(1), e13636.

Fackelmann G, et al. (2025) Gut microbiome signatures of vegan, vegetarian and omnivore diets and associated health outcomes across 21,561 individuals. Nature microbiology, 10(1), 41.

Guccione C, et al. (2025) Community assembly modeling of microbial evolution within Barrett's esophagus and esophageal adenocarcinoma. bioRxiv : the preprint server for biology.

Yunusbayev B, et al. (2025) Gut dysbiosis narrative in psoriasis: matched-pair approach identifies only subtle shifts correlated with elevated fecal calprotectin. Microbiology spectrum, 13(1), e0138224.

Fahur Bottino G, et al. (2025) Early life microbial succession in the gut follows common patterns in humans across the globe. Nature communications, 16(1), 660.

McReynolds E, et al. (2025) An ecological-evolutionary perspective on the genomic diversity and habitat preferences of the Acidobacteriota. Microbial genomics, 11(1).

Shimizu H, et al. (2025) Sucrose-preferring gut microbes prevent host obesity by producing exopolysaccharides. Nature communications, 16(1), 1145.