## **Resource Summary Report**

Generated by dkNET on Apr 29, 2025

# **PhyloPhlAn**

RRID:SCR\_013082

Type: Tool

## **Proper Citation**

PhyloPhIAn (RRID:SCR\_013082)

#### **Resource Information**

URL: https://bitbucket.org/nsegata/phylophlan/wiki/Home

**Proper Citation:** PhyloPhlAn (RRID:SCR\_013082)

**Description:** Software pipeline for reconstructing highly accurate and resolved phylogenetic trees based on whole-genome sequence information. Pipeline is scalable to thousands of genomes and uses the most conserved 400 proteins for extracting the phylogenetic signal. PhyloPhlAn also implements taxonomic curation, estimation, and insertion operations.

Abbreviations: PhyloPhlAn

Synonyms: PhyloPhlAn: microbial Tree of Life using 400 universal proteins

**Resource Type:** software resource

**Defining Citation:** PMID:23942190

**Keywords:** phylogenetic tree, whole-genome sequence, genome, protein

**Funding:** 

Resource Name: PhyloPhlAn

Resource ID: SCR\_013082

Alternate IDs: OMICS\_01525

Alternate URLs: https://sources.debian.org/src/phylophlan/

**Record Creation Time: 20220129T080314+0000** 

Record Last Update: 20250420T014632+0000

## **Ratings and Alerts**

No rating or validation information has been found for PhyloPhlAn.

No alerts have been found for PhyloPhlAn.

#### Data and Source Information

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 301 mentions in open access literature.

**Listed below are recent publications.** The full list is available at <u>dkNET</u>.

Ni M, et al. (2025) Epigenetic phase variation in the gut microbiome enhances bacterial adaptation. bioRxiv: the preprint server for biology.

Sanchez VA, et al. (2025) Genome evolution following an ecological shift in nectar-dwelling Acinetobacter. mSphere, 10(1), e0101024.

Feng Y, et al. (2025) Regional antimicrobial resistance gene flow among the One Health sectors in China. Microbiome, 13(1), 3.

Gu S, et al. (2025) Siderophore synthetase-receptor gene coevolution reveals habitat- and pathogen-specific bacterial iron interaction networks. Science advances, 11(3), eadq5038.

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

Su G, et al. (2025) Gut mycobiome alterations and network interactions with the bacteriome in patients with atherosclerotic cardiovascular disease. Microbiology spectrum, 13(1), e0218224.

Li Q, et al. (2025) Reductive acetogenesis is a dominant process in the ruminant hindgut. Microbiome, 13(1), 28.

Hu H, et al. (2025) Metagenome-assembled microbial genomes (n?=?3,448) of the oral microbiomes of Tibetan and Duroc pigs. Scientific data, 12(1), 141.

Mills KB, et al. (2024) Staphylococcus aureus skin colonization is mediated by SasG lectin variation. Cell reports, 43(4), 114022.

Ma L, et al. (2024) Clostridium butyricum and carbohydrate active enzymes contribute to the reduced fat deposition in pigs. iMeta, 3(1), e160.

Huang L, et al. (2024) A multi-kingdom collection of 33,804 reference genomes for the human vaginal microbiome. Nature microbiology, 9(8), 2185.

Klimek D, et al. (2024) Comparative genomic analysis of Planctomycetota potential for polysaccharide degradation identifies biotechnologically relevant microbes. BMC genomics, 25(1), 523.

Wang Y, et al. (2024) Metagenomic comparison of gut communities between wild and captive Himalayan griffons. Frontiers in veterinary science, 11, 1403932.

Gaspari M, et al. (2024) Decoding Microbial Responses to Ammonia Shock Loads in Biogas Reactors through Metagenomics and Metatranscriptomics. Environmental science & technology, 58(1), 591.

Hu W-f, et al. (2024) Characteristics and immune functions of the endogenous CRISPR-Cas systems in myxobacteria. mSystems, 9(6), e0121023.

Ridley RS, et al. (2024) Potential routes of plastics biotransformation involving novel plastizymes revealed by global multi-omic analysis of plastic associated microbes. Scientific reports, 14(1), 8798.

Liu D, et al. (2024) Anaerostipes hadrus, a butyrate-producing bacterium capable of metabolizing 5-fluorouracil. mSphere, 9(4), e0081623.

Duan Z, et al. (2024) Nosocomial surveillance of multidrug-resistant Acinetobacter baumannii: a genomic epidemiological study. Microbiology spectrum, 12(2), e0220723.

Nickols WA, et al. (2024) Evaluating metagenomic analyses for undercharacterized environments: what's needed to light up the microbial dark matter? bioRxiv: the preprint server for biology.

Branck T, et al. (2024) Comprehensive profile of the companion animal gut microbiome integrating reference-based and reference-free methods. The ISME journal, 18(1).