

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 1, 2026

PhyloPhlAn

RRID:SCR_013082

Type: Tool

Proper Citation

PhyloPhlAn (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., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

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

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

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: 20260725T190743+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 339 mentions in open access literature.

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

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

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

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

Tzlil G, et al. (2025) Structural insights into light harvesting by antenna-containing rhodopsins in marine Asgard archaea. *Nature microbiology*, 10(6), 1484.

Zhang Q, et al. (2025) Long-term metagenomic insights into the roles of antiviral defense systems in stabilizing activated sludge bacterial communities. *The ISME journal*, 19(1).

Rindi L, et al. (2025) Legacies of temperature fluctuations promote stability in marine biofilm communities. *Nature communications*, 16(1), 2442.

Li C, et al. (2025) Multiomic analysis of different horse breeds reveals that gut microbial butyrate enhances racehorse athletic performance. *NPJ biofilms and microbiomes*, 11(1), 87.

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

Kang X, et al. (2025) The Gut Microbiome of the Asiatic Toad (*Bufo gargarizans*) Reflects Environmental Changes and Human Activities. *Ecology and evolution*, 15(5), e71394.

Li P, et al. (2025) Anthropogenic climate change may reduce global diazotroph diversity. *Nature communications*, 16(1), 8208.

Sáenz JS, et al. (2025) Antiviral defense systems in the rumen microbiome. *mSystems*, 10(2), e0152124.

Lee MS, et al. (2025) *Aestuariibius violaceus* sp. nov., isolated from a marine limpet *Cellana toreuma*. International journal of systematic and evolutionary microbiology, 75(7).

Hitch TCA, et al. (2025) HiBC: a publicly available collection of bacterial strains isolated from the human gut. Nature communications, 16(1), 4203.

Keegstra JM, et al. (2025) Risk-reward trade-off during carbon starvation generates dichotomy in motility endurance among marine bacteria. Nature microbiology, 10(6), 1393.

Fernández-Fernández R, et al. (2025) Genomic Analysis of Bacteriocin-Producing *Staphylococci*: High Prevalence of Lanthipeptides and the Micrococцин P1 Biosynthetic Gene Clusters. Probiotics and antimicrobial proteins, 17(1), 159.

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.

Molina-Pardines C, et al. (2025) Extensive paralogism in the environmental pangenome: a key factor in the ecological success of natural SAR11 populations. Microbiome, 13(1), 41.

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

Haro-Moreno JM, et al. (2025) The hidden genetic reservoir: structural variants as drivers of marine microbial and viral microdiversity. Environmental microbiome, 20(1), 110.

Liu Q, et al. (2025) Multi-kingdom microbiota analysis reveals bacteria-viral interplay in IBS with depression and anxiety. NPJ biofilms and microbiomes, 11(1), 129.