Resource Summary Report

Generated by NIF on Apr 18, 2025

GraPhlAn

RRID:SCR_016130
Type: Tool

Proper Citation

GraPhlAn (RRID:SCR_016130)

Resource Information

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

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Description: Software tool for producing high-quality circular representations of taxonomic and phylogenetic trees. Used for concise, integrative, informative, and publication-ready representations of phylogenetically- and taxonomically-driven investigation as a high-resolution microbial tree of life with taxonomic annotations.

Synonyms: Graphlan

Resource Type: data processing software, data visualization software, software resource, software application

Keywords: circular, high, resolution, microbal, tree, taxonomy, annotation, phylogenetic, investigation

Funding:

Availability: Free, Available for download

Resource Name: GraPhlAn

Resource ID: SCR_016130

Alternate IDs: OMICS_11549

Alternate URLs: https://huttenhower.sph.harvard.edu/graphlan, https://sources.debian.org/src/graphlan/

License URLs:
https://bitbucket.org/nsegata/graphlan/src/17f32c8d85849d397884564680c145e5b8d28923/license.txt?
view-default

Record Creation Time: 20220129T080329+0000

Record Last Update: 20250418T055439+0000

Ratings and Alerts

No rating or validation information has been found for GraPhlAn.

No alerts have been found for GraPhlAn.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 171 mentions in open access literature.

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

Jiao J, et al. (2024) Ecological niches and assembly dynamics of diverse microbial consortia in the gastrointestine of goat kids. The ISME journal, 18(1).

Li J, et al. (2024) Microbial and metabolic profiles unveil mutualistic microbe-microbe interaction in obesity-related colorectal cancer. Cell reports. Medicine, 5(3), 101429.

Rozwalak P, et al. (2024) Ultraconserved bacteriophage genome sequence identified in 1300-year-old human palaeofaeces. Nature communications, 15(1), 495.

Lu X, et al. (2024) Metagenomic analysis reveals high diversity of gut viromes in yaks (Bos grunniens) from the Qinghai-Tibet Plateau. Communications biology, 7(1), 1097.

Lim C, et al. (2024) Evaluation of the cervical liquid-based cytology sample as a microbiome resource for dual diagnosis. PloS one, 19(12), e0308985.

Huang KD, et al. (2024) Establishment of a non-Westernized gut microbiota in men who have sex with men is associated with sexual practices. Cell reports. Medicine, 5(3), 101426.

Yoon KN, et al. (2024) Lactiplantibacillus argentoratensis AGMB00912 alleviates salmonellosis and modulates gut microbiota in weaned piglets: a pilot study. Scientific reports, 14(1), 15466.

Shi Z, et al. (2024) Multi-omics strategy reveals potential role of antimicrobial resistance and virulence factor genes responsible for Simmental diarrheic calves caused by Escherichia coli. mSystems, 9(6), e0134823.

Chang Y, et al. (2024) Integrated transcriptome and microbiome analyses of residual feed intake in ducks during high production period. Poultry science, 103(6), 103726.

Glendinning L, et al. (2024) Altitude-dependent agro-ecologies impact the microbiome diversity of scavenging indigenous chicken in Ethiopia. Microbiome, 12(1), 138.

Khan NA, et al. (2024) C/N ratio effect on oily wastewater treatment using column type SBR: machine learning prediction and metagenomics study. Scientific reports, 14(1), 22950.

Yoon KN, et al. (2024) Lactiplantibacillus argentoratensis AGMB00912 protects weaning mice from ETEC infection and enhances gut health. Frontiers in microbiology, 15, 1440134.

Xie D, et al. (2024) Anesthetics change the oral microbial composition of children and increase the abundance of the genus Haemophilus. Translational pediatrics, 13(12), 2097.

Lavallee JM, et al. (2024) Land management shapes drought responses of dominant soil microbial taxa across grasslands. Nature communications, 15(1), 29.

Su P, et al. (2024) Microbiome homeostasis on rice leaves is regulated by a precursor molecule of lignin biosynthesis. Nature communications, 15(1), 23.

Hsieh CC, et al. (2024) Amelioration of the brain structural connectivity is accompanied with changes of gut microbiota in a tuberous sclerosis complex mouse model. Translational psychiatry, 14(1), 68.

Han Y, et al. (2024) Longitudinal multi-omics analysis uncovers the altered landscape of gut microbiota and plasma metabolome in response to high altitude. Microbiome, 12(1), 70.

Pan Y, et al. (2024) Drought-induced assembly of rhizosphere mycobiomes shows beneficial effects on plant growth. mSystems, 9(7), e0035424.

Jeon BJ, et al. (2024) Plant growth-promoting effects of a novel Lelliottia sp. JS-SCA-14 and comparative genome analysis. Frontiers in plant science, 15, 1484616.

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).