

Resource Summary Report

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GraPhlAn

RRID:SCR_016130

Type: Tool

Proper Citation

GraPhlAn (RRID:SCR_016130)

Resource Information

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

Proper Citation: GraPhlAn (RRID:SCR_016130)

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

Synonyms: Graphlan

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

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

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

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.view-default>

Record Creation Time: 20220129T080329+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 183 mentions in open access literature.

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

Zhou M, et al. (2025) Identification and characterization of a novel human adenovirus type HAdV-D116. *Frontiers in microbiology*, 16, 1566316.

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.

Wang Y, et al. (2025) Dietary and environmental factors affecting the dynamics of the gut bacteria in Tibetan Awang sheep (*Ovis aries*) across divergent breeding models. *Frontiers in microbiology*, 16, 1502898.

Zheng YM, et al. (2025) Retrospective review: single- and multidonor washed microbiota transplantation have equivalent efficacy in the treatment of autism. *Frontiers in cellular and infection microbiology*, 15, 1606417.

Lu X, et al. (2025) Metagenomic analysis reveals the diversity of the vaginal virome and its association with vaginitis. *Frontiers in cellular and infection microbiology*, 15, 1582553.

Li YL, et al. (2025) Roles of oral and gut microbiota in acute myocardial infarction. *Journal of advanced research*, 74, 319.

Wang H, et al. (2025) Reduced maternal SCFAs in GDM diminish GPR43 signaling and induce offspring CAKUT. *Communications biology*, 8(1), 1063.

Kumar ST, et al. (2025) Breed-specific differences of gut microbiota and metabolomic insights into fat deposition and meat quality in Chinese Songliao Black Pig and Large White ?? Landrace Pig Breeds. *BMC microbiology*, 25(1), 334.

Liu F, et al. (2025) *Escherichia coli* is implicated in the development and manifestation of host susceptibility to the roundworm *Trichostrongylus colubriformis* infections in sheep. *Veterinary research*, 56(1), 133.

Abuzahrah SS, et al. (2025) Exploring the microorganisms biodiversity associated with sponge species in the red sea through 18S ribosomal RNA gene sequencing. *AMB Express*, 15(1), 60.

Chen CC, et al. (2025) Temperature-dependent shifts in gut microbiota and metabolome of olive flounder (*Paralichthys olivaceus*): implications for cold-water aquaculture expansion and probiotic applications. *Animal microbiome*, 7(1), 49.

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.

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.

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.

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.

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

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

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

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.

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