Resource Summary Report

Generated by NIF on Apr 27, 2025

PhyD3

RRID:SCR_015892
Type: Tool

Proper Citation

PhyD3 (RRID:SCR_015892)

Resource Information

URL: https://phyd3.bits.vib.be/

Proper Citation: PhyD3 (RRID:SCR_015892)

Description: Web application that is a phylogenetic tree viewer based on d3.js. It was developed as an alternative to Archaeopteryx inspired by d3.phylogram.js.

Abbreviations: PhyD3

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

Defining Citation: PMID:28525531

Keywords: javascript, visualization, toolkit, phylogeny, program, phylogenetic data, bio.tools

Funding:

Availability: Open source, Demo available

Resource Name: PhyD3

Resource ID: SCR_015892

Alternate IDs: biotools:phyd3

Alternate URLs: https://github.com/vibbits/phyd3, https://bio.tools/phyd3

License: GNU General Public License v3.0

Record Creation Time: 20220129T080328+0000

Record Last Update: 20250426T060515+0000

Ratings and Alerts

No rating or validation information has been found for PhyD3.

No alerts have been found for PhyD3.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 39 mentions in open access literature.

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

Paredes Contreras BV, et al. (2025) Enhanced UV-B photoprotection activity of carotenoids from the novel Arthrobacter sp. strain LAPM80 isolated from King George Island, Antarctica. Heliyon, 11(1), e41400.

Hamed SM, et al. (2025) Pseudocitrobacter cyperus, a novel bacterial species recovered from Cyperus alternifolius in Egypt. BMC microbiology, 25(1), 20.

Petakh P, et al. (2024) Exploring Leptospira interrogans FDAARGOS_203: Insights into AMR and Anti-Phage Defense. Microorganisms, 12(3).

Maguvu TE, et al. (2024) Pathogenicity, phylogenomic, and comparative genomic study of Pseudomonas syringae sensu lato affecting sweet cherry in California. Microbiology spectrum, 12(10), e0132424.

Erban T, et al. (2024) Mixta mediterraneensis as a novel and abundant gut symbiont of the allergen-producing domestic mite Blomia tropicalis. Experimental & applied acarology, 92(2), 161.

Olanrewaju OS, et al. (2024) Genomic diversity, antibiotic resistance, and virulence in South African Enterococcus faecalis and Enterococcus lactis isolates. World journal of microbiology & biotechnology, 40(10), 289.

Aguilar C, et al. (2024) Actinomycetota bioprospecting from ore-forming environments. Microbial genomics, 10(5).

Olanrewaju OS, et al. (2024) Genome mining of Escherichia coli WG5D from drinking water

source: unraveling antibiotic resistance genes, virulence factors, and pathogenicity. BMC genomics, 25(1), 263.

Maguvu TE, et al. (2024) Phylogenomic analyses and comparative genomics of Pseudomonas syringae associated with almond (Prunus dulcis) in California. PloS one, 19(4), e0297867.

Pentekhina I, et al. (2023) Chitinolytic and Fungicidal Potential of the Marine Bacterial Strains Habituating Pacific Ocean Regions. Microorganisms, 11(9).

Widada J, et al. (2023) Marine-Derived Streptomyces sennicomposti GMY01 with Anti-Plasmodial and Anticancer Activities: Genome Analysis, In Vitro Bioassay, Metabolite Profiling, and Molecular Docking. Microorganisms, 11(8).

Zaghloul HAH, et al. (2023) Whole genome analyses of toxicants tolerance genes of Apis mellifera gut-derived Enterococcus faecium strains. BMC genomics, 24(1), 479.

Alghamdi AK, et al. (2023) Complete genome sequence analysis of plant growth-promoting bacterium, Isoptericola sp. AK164 isolated from the rhizosphere of Avicennia marina growing at the Red Sea coast. Archives of microbiology, 205(9), 307.

Mavroidi A, et al. (2023) Comprehensive Analysis of Virulence Determinants and Genomic Islands of blaNDM-1-Producing Enterobacter hormaechei Clinical Isolates from Greece. Antibiotics (Basel, Switzerland), 12(10).

Ilnitskiy IS, et al. (2022) OrthoQuantum: visualizing evolutionary repertoire of eukaryotic proteins. Nucleic acids research, 50(W1), W534.

Nusrin S, et al. (2022) Multiple Mechanisms Confer Resistance to Azithromycin in Shigella in Bangladesh: a Comprehensive Whole Genome-Based Approach. Microbiology spectrum, 10(4), e0074122.

Saini MK, et al. (2021) Genomic and Phenotypic Characterization of Chloracidobacterium Isolates Provides Evidence for Multiple Species. Frontiers in microbiology, 12, 704168.

Wang Y, et al. (2021) Considerations on the Identity and Diversity of Organisms Affiliated with Sphingobacterium multivorum-Proposal for a New Species, Sphingobacterium paramultivorum. Microorganisms, 9(10).

Maguvu TE, et al. (2021) Whole Genome Sequencing Based Taxonomic Classification, and Comparative Genomic Analysis of Potentially Human Pathogenic Enterobacter spp. Isolated from Chlorinated Wastewater in the North West Province, South Africa. Microorganisms, 9(9).

Gutierrez-Albanchez E, et al. (2021) Pseudomonas palmensis sp. nov., a Novel Bacterium Isolated From Nicotiana glauca Microbiome: Draft Genome Analysis and Biological Potential for Agriculture. Frontiers in microbiology, 12, 672751.