

Resource Summary Report

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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

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: 20260731T042957+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 47 mentions in open access literature.

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

Qi J, et al. (2026) Integrated genomic and metabolomic analysis reveals the biocontrol potential of endophytic *Bacillus velezensis* NS13 against *Fusarium* species in *Lonicera macranthoides*. *BMC microbiology*, 26(1), 5.

Prole JR, et al. (2025) Identification of four novel *Streptomyces* isolated from machair grassland soil using a culture-based bioprospecting strategy: *Streptomyces caledonius* sp. nov., *Streptomyces machairae* sp. nov., *Streptomyces pratisoli* sp. nov. and *Streptomyces achmelvichensis* sp. nov. *International journal of systematic and evolutionary microbiology*, 75(4).

Ranesan AC, et al. (2025) Whole genome surveying and metabolomic profiling aided navigation of therapeutic plethora of *Streptomyces melanogenes* WPF1 isolated from *Pinus patula* rhizosphere. *Bioresources and bioprocessing*, 12(1), 149.

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.

Ali MS, et al. (2025) 'Candidatus *Pseudomonas auctus*' sp. nov. JDE115 isolated from nodules on soybean (*Glycine max*). *PloS one*, 20(9), e0331920.

Zaman SAU, et al. (2025) Whole genome of petroleum hydrocarbon degrading *Rhodococcus indonesiensis* isolated from Nacharam, Hyderabad, India. *Scientific reports*, 16(1), 165.

Diricks M, et al. (2025) Global lineages of non-tuberculous mycobacteria in residential water samples from Germany. *BMC microbiology*, 25(1), 792.

Shu W, et al. (2025) Description of *Streptomyces explomaris* sp. nov., isolated from the coastal soil rhizosphere of *Juniperus excelsa* and reclassification of *Streptomyces libani* as a later heterotypic synonym of *Streptomyces nigrescens*. *International journal of systematic and evolutionary microbiology*, 75(5).

Doh??l M, et al. (2025) Diagnostics, resistance and clinical relevance of non-tuberculous mycobacteria unidentified at the species level by line probe assays: a bi-national study. *Annals of clinical microbiology and antimicrobials*, 24(1), 14.

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

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.

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

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.

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

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.

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).

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.

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).