

Resource Summary Report

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Dendroscope3

RRID:SCR_024003

Type: Tool

Proper Citation

Dendroscope3 (RRID:SCR_024003)

Resource Information

URL: <https://github.com/danielhuson/dendroscope3>

Proper Citation: Dendroscope3 (RRID:SCR_024003)

Description: Software Java program for analyzing and visualizing rooted phylogenetic trees and networks.

Synonyms: dendroscope, dendroscope3

Resource Type: software application

Defining Citation: [PMID:22780991](#)

Keywords: analyzing and visualizing rooted phylogenetic trees and networks,

Availability: Free, Available for download, Freely available

Resource Name: Dendroscope3

Resource ID: SCR_024003

Alternate IDs: OMICS_04266

Old URLs: <https://sources.debian.org/src/dendroscope/>

License: GPL-3.0 license

Record Creation Time: 20230824T050211+0000

Record Last Update: 20260815T182744+0000

Ratings and Alerts

No rating or validation information has been found for Dendroscope3.

No alerts have been found for Dendroscope3.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Blanchard I, et al. (2026) Phylogeny-driven pangenome analysis uncovers the genomic landscape of domesticated and wild *Armeniaca* species. *Horticulture research*, 13(7), uhag104.

Yadav HK, et al. (2025) Telomere-to-telomere genome assembly of linseed (*Linum usitatissimum* L.) for functional genomics and accelerated genetic improvement. *Plant biotechnology journal*, 23(9), 3919.

Rocha ST, et al. (2025) The prevalence of motility-related genes within the human oral microbiota. *Microbiology spectrum*, 13(1), e0126424.

Grossman AS, et al. (2025) *Saccharibacteria* deploy two distinct type IV pili, driving episymbiosis, host competition, and twitching motility. *The ISME journal*, 19(1).

Kim KM, et al. (2025) Genetic isolation and metabolic complexity of an Antarctic subglacial microbiome. *Nature communications*, 16(1), 7501.

Selvaraj M, et al. (2024) Activation of plant immunity through conversion of a helper NLR homodimer into a resistosome. *PLoS biology*, 22(10), e3002868.

Zhao J, et al. (2023) Transcriptome-Based Study on the Phylogeny and Hybridization of Marattialean Ferns (Marattiaceae). *Plants (Basel, Switzerland)*, 12(12).

Kim JS, et al. (2022) The evolution and competitive strategies of *Akkermansia muciniphila* in gut. *Gut microbes*, 14(1), 2025017.

Gentile B, et al. (2020) A Retrospective Whole-Genome Sequencing Analysis of Carbapenem and Colistin-Resistant *Klebsiella pneumoniae* Nosocomial Strains Isolated during an MDR Surveillance Program. *Antibiotics (Basel, Switzerland)*, 9(5).

Garcia K, et al. (2020) Fungal Shaker-like channels beyond cellular K⁺ homeostasis: A role in ectomycorrhizal symbiosis between *Hebeloma cylindrosporum* and *Pinus pinaster*. *PloS one*, 15(11), e0242739.

Fasciana T, et al. (2019) Co-existence of virulence factors and antibiotic resistance in new *Klebsiella pneumoniae* clones emerging in south of Italy. *BMC infectious diseases*, 19(1), 928.

Gasperotti AF, et al. (2018) Identification of two different chemosensory pathways in representatives of the genus *Halomonas*. *BMC genomics*, 19(1), 266.

Bagnato C, et al. (2017) Analysis of triglyceride synthesis unveils a green algal soluble diacylglycerol acyltransferase and provides clues to potential enzymatic components of the chloroplast pathway. *BMC genomics*, 18(1), 223.

Rimoldi SG, et al. (2017) Whole genome sequencing for the molecular characterization of carbapenem-resistant *Klebsiella pneumoniae* strains isolated at the Italian ASST Fatebenefratelli Sacco Hospital, 2012-2014. *BMC infectious diseases*, 17(1), 666.

Campo S, et al. (2016) Small RNA-Based Antiviral Defense in the Phytopathogenic Fungus *Colletotrichum higginsianum*. *PLoS pathogens*, 12(6), e1005640.

Hassold S, et al. (2016) DNA Barcoding of Malagasy Rosewoods: Towards a Molecular Identification of CITES-Listed *Dalbergia* Species. *PloS one*, 11(6), e0157881.

Cardona T, et al. (2016) Origin of Bacteriochlorophyll *a* and the Early Diversification of Photosynthesis. *PloS one*, 11(3), e0151250.

Yoon MY, et al. (2016) A single gene of a commensal microbe affects host susceptibility to enteric infection. *Nature communications*, 7, 11606.

Papanicolaou A, et al. (2016) The whole genome sequence of the Mediterranean fruit fly, *Ceratitidis capitata* (Wiedemann), reveals insights into the biology and adaptive evolution of a highly invasive pest species. *Genome biology*, 17(1), 192.

Ure AE, et al. (2014) Characterization of human papillomavirus type 154 and tissue tropism of gammapapillomaviruses. *PloS one*, 9(2), e89342.