

Resource Summary Report

Generated by T1D on Aug 1, 2026

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: softwre application

Defining Citation: [PMID:22780991](https://pubmed.ncbi.nlm.nih.gov/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: 20260725T191035+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 22 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

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

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.

Grossman AS, et al. (2025) *Saccharibacteria* deploy two distinct type IV pili, driving episybiosis, 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.

Gasparotti 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.

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

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

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, *Ceratitis 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.

Barba M, et al. (2013) Identifying reaction modules in metabolic pathways: bioinformatic deduction and experimental validation of a new putative route in purine catabolism. BMC systems biology, 7, 99.