Resource Summary Report

Generated by NIF on Apr 25, 2025

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

Keywords: analyzing and visualizing rooted phylogenetic trees and networks,

Funding:

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: 20250420T015258+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 19 mentions in open access literature.

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

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

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.

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.

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.

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

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.

Deslandes V, et al. (2010) Transcriptional profiling of Actinobacillus pleuropneumoniae during the acute phase of a natural infection in pigs. BMC genomics, 11, 98.

Stonaker JL, et al. (2009) Diversity of Pol IV function is defined by mutations at the maize rmr7 locus. PLoS genetics, 5(11), e1000706.