

Resource Summary Report

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[ggtree](#)

RRID:SCR_018560

Type: Tool

Proper Citation

ggtree (RRID:SCR_018560)

Resource Information

URL: <https://bioconductor.org/packages/ggtree/>

Proper Citation: ggtree (RRID:SCR_018560)

Description: Software R package for visualization and annotation of phylogenetic trees with their covariates and other tree like structures with their annotation data. Can import evolutionary data from different tree file formats and analysis programs as well as other associated data from experiments so that various sources and types of data can be displayed on tree for comparison and further analyses.

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

Defining Citation: [DOI:10.1111/2041-210X.12628](https://doi.org/10.1111/2041-210X.12628)

Keywords: Phylogenetic tree visualization, phylogenetic tree annotation, data, bio.tools

Funding: Seed Funding Programme for Basic Research

Availability: Free, Available for download, Freely available

Resource Name: ggtree

Resource ID: SCR_018560

Alternate IDs: biotools:ggtree

Alternate URLs: <https://bio.tools/ggtree>

License: Artistic-2.0

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260903T235500+0000

Ratings and Alerts

No rating or validation information has been found for ggtree.

No alerts have been found for ggtree.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 61 mentions in open access literature.

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

Bassiouni R, et al. (2026) Integrated Single-Cell Whole-Genome Sequencing and Spatial Transcriptomics Reveal Intratumoral Heterogeneity in Ovarian Cancer. Cancer research communications, 6(5), 1020.

Paoli JE, et al. (2026) One Health Genomic Surveillance at Human-Animal Interfaces in Rural Ghana Reveals Underreported Viruses of Zoonotic and Economic Concern. Viruses, 18(6).

Fouch?? S, et al. (2026) Recurrent Chromosome Destabilization Through Repeat-Mediated Rearrangements in a Fungal Pathogen. Genome biology and evolution, 18(3).

Wild C, et al. (2026) Restoring structural complexity in temperate forests increases bat and bird diversity. Current biology : CB, 36(11), 2840.

Nakamoto JA, et al. (2026) Structural and functional diversity of toxin-antitoxin-chaperone systems. Cell reports, 45(3), 117024.

Lan G, et al. (2026) Dynamic economic-entropy regulation of community-scale green hydrogen supply chains with carbon-microgrid coupling. iScience, 29(4), 115504.

Nickles GR, et al. (2026) Tracing the origins of crmA megasynthase through lichen genomes. Current biology : CB, 36(13), 3354.

Serna C, et al. (2025) Global dissemination of npmA mediated pan-aminoglycoside resistance via a mobile genetic element in Gram-positive bacteria. Nature communications, 16(1), 6360.

Newstead L, et al. (2025) Genomic characterization of Pseudomonas aeruginosa from canine otitis highlights the need for a One Health approach to this opportunistic pathogen. Microbial genomics, 11(5).

Webb J, et al. (2025) Multi-strain carriage and intrahost diversity of Staphylococcus aureus among Indigenous adults in the USA. Microbial genomics, 11(3).

Xie D, et al. (2025) Deciphering genomic evolution of metastatic organotropism with 535 paired primary lung cancers and metastases. *Cell reports*, 44(10), 116449.

Sia CM, et al. (2025) Distinct adaptation and epidemiological success of different genotypes within *Salmonella enterica* serovar Dublin. *eLife*, 13.

Immonen TT, et al. (2024) No evidence for ongoing replication on ART in SIV-infected macaques. *Nature communications*, 15(1), 5093.

Ding X, et al. (2024) Transmission restriction and genomic evolution co-shape the genetic diversity patterns of influenza A virus. *Virologica Sinica*, 39(4), 525.

Kennedy SJ, et al. (2024) Culture-dependent identification of rare marine sediment bacteria from the Gulf of Mexico and Antarctica. *bioRxiv : the preprint server for biology*.

Tamura T, et al. (2024) Virological characteristics of the SARS-CoV-2 Omicron XBB.1.5 variant. *Nature communications*, 15(1), 1176.

Joseph R, et al. (2024) Isolation of a Novel *Pythium* Species, *P. thermoculicivorax*, and *Trichoderma* sp. from Natural Enzootic Mosquito Larval Infections. *Journal of fungi (Basel, Switzerland)*, 10(3).

Yajima H, et al. (2024) Structural basis for receptor-binding domain mobility of the spike in SARS-CoV-2 BA.2.86 and JN.1. *Nature communications*, 15(1), 8574.

Atre M, et al. (2024) Origin, evolution, and maintenance of gene-strand bias in bacteria. *Nucleic acids research*, 52(7), 3493.

Kyriacou RG, et al. (2024) GC Content Across Insect Genomes: Phylogenetic Patterns, Causes and Consequences. *Journal of molecular evolution*, 92(2), 138.