Resource Summary Report

Generated by <u>NIF</u> on Apr 26, 2025

quicktree

RRID:SCR_024205 Type: Tool

Proper Citation

quicktree (RRID:SCR_024205)

Resource Information

URL: https://github.com/khowe/quicktree/

Proper Citation: quicktree (RRID:SCR_024205)

Description: Software application as implementation of Neighbor-Joining algorithm, capable of reconstructing phylogenies from huge alignments.

Resource Type: software toolkit, software library, software resource

Defining Citation: PMID:3447015

Keywords: Neighbor-Joining algorithm, reconstructing phylogenies from huge alignments,

Funding:

Availability: Free, Available for download, Freely available,

Resource Name: quicktree

Resource ID: SCR_024205

Alternate URLs: https://sources.debian.org/src/quicktree/

License: Apache-2.0 license

Record Creation Time: 20230824T050212+0000

Record Last Update: 20250426T061007+0000

Ratings and Alerts

No rating or validation information has been found for quicktree.

No alerts have been found for quicktree.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

Petroll R, et al. (2025) Enhanced sensitivity of TAPscan v4 enables comprehensive analysis of streptophyte transcription factor evolution. The Plant journal : for cell and molecular biology, 121(1), e17184.

Silva EC, et al. (2024) Molecular Characterization and Genome Mechanical Features of Two Newly Isolated Polyvalent Bacteriophages Infecting Pseudomonas syringae pv. garcae. Genes, 15(1).

Islam MI, et al. (2023) Ancestral reconstruction of the MotA stator subunit reveals that conserved residues far from the pore are required to drive flagellar motility. microLife, 4, uqad011.

Saber S, et al. (2022) Mutation, selection, and the prevalence of the Caenorhabditis elegans heat-sensitive mortal germline phenotype. G3 (Bethesda, Md.), 12(5).

So J, et al. (2022) VSGs Expressed during Natural T. b. gambiense Infection Exhibit Extensive Sequence Divergence and a Subspecies-Specific Bias towards Type B N-Terminal Domains. mBio, 13(6), e0255322.

Schniete JK, et al. (2021) ActDES - a curated Actinobacterial Database for Evolutionary Studies. Microbial genomics, 7(1).

Zhang X, et al. (2021) Cluster-specific gene markers enhance Shigella and enteroinvasive Escherichia coli in silico serotyping. Microbial genomics, 7(12).

Fenske GJ, et al. (2021) Analysis of 56,348 Genomes Identifies the Relationship between Antibiotic and Metal Resistance and the Spread of Multidrug-Resistant Non-Typhoidal Salmonella. Microorganisms, 9(7).

Purswani J, et al. (2017) BSocial: Deciphering Social Behaviors within Mixed Microbial Populations. Frontiers in microbiology, 8, 919.

Carré-Eusèbe D, et al. (2009) OVEX1, a novel chicken endogenous retrovirus with sex-

specific and left-right asymmetrical expression in gonads. Retrovirology, 6, 59.