

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

[quikctree](#)

RRID:SCR_024205

Type: Tool

Proper Citation

quikctree (RRID:SCR_024205)

Resource Information

URL: <https://github.com/khowe/quikctree/>

Proper Citation: quikctree (RRID:SCR_024205)

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

Resource Type: software library, software resource, software toolkit

Defining Citation: [PMID:3447015](#)

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

Availability: Free, Available for download, Freely available,

Resource Name: quikctree

Resource ID: SCR_024205

Alternate URLs: <https://sources.debian.org/src/quikctree/>

License: Apache-2.0 license

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260905T133105+0000

Ratings and Alerts

No rating or validation information has been found for quikctree.

No alerts have been found for quikctree.

Data and Source Information

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

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.

Ryan K, et al. (2025) New Genome Assemblies for Poeciliidae: A Foundation for Adaptation Studies. *Genome biology and evolution*, 17(6).

Jivanji S, et al. (2025) Structural and epistatic regulatory variants cause hallmark white spotting in cattle. *Science advances*, 11(46), eadt5913.

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.