

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 20, 2026

VeryFastTree

RRID:SCR_023594

Type: Tool

Proper Citation

VeryFastTree (RRID:SCR_023594)

Resource Information

URL: <https://github.com/citiususc/veryfasttree>

Proper Citation: VeryFastTree (RRID:SCR_023594)

Description: Software tool for speeding up estimation of phylogenetic trees for large alignments through parallelization and vectorization strategies.

Resource Type: software application, software resource, source code

Defining Citation: [PMID:32573652](#), [DOI:10.1093/bioinformatics/btaa582](#)

Keywords: large alignments, phylogenetic tree, phylogenetic tree creation, bio.tools

Funding: ERDF ;
MICINN ;
Xunta de Galicia

Availability: Free, Available for download, Freely available

Resource Name: VeryFastTree

Resource ID: SCR_023594

Alternate IDs: biotools:veryfasttree

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

License: GNU GPL v3

Record Creation Time: 20230523T050222+0000

Record Last Update: 20260919T195739+0000

Ratings and Alerts

No rating or validation information has been found for VeryFastTree.

No alerts have been found for VeryFastTree.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Din NS, et al. (2026) Dynamics of a large multidrug-resistant plasmid encoding New Delhi metallo- β -lactamase-1 and oxacillinase-58 carbapenemases in *Acinetobacter baumannii* clinical isolates from a tertiary hospital in Malaysia. *Microbial genomics*, 12(2).

Egas RA, et al. (2026) Carbon monoxide metabolism in freshwater anaerobic methanotrophic archaea. *Nature communications*, 17(1).

Xu JT, et al. (2025) Diverse impacts of different *rpoB* mutations on the anti-tuberculosis efficacy of capreomycin. *EBioMedicine*, 117, 105776.

Khawaja T, et al. (2024) Deep sequencing of *Escherichia coli* exposes colonisation diversity and impact of antibiotics in Punjab, Pakistan. *Nature communications*, 15(1), 5196.

Piñeiro C, et al. (2024) Efficient phylogenetic tree inference for massive taxonomic datasets: harnessing the power of a server to analyze 1 million taxa. *GigaScience*, 13.

de Jonge PA, et al. (2024) Phylogeny and disease associations of a widespread and ancient intestinal bacteriophage lineage. *Nature communications*, 15(1), 6346.

Gorzalski A, et al. (2023) The use of whole-genome sequencing and development of bioinformatics to monitor overlapping outbreaks of *Candida auris* in southern Nevada. *Frontiers in public health*, 11, 1198189.

Pu L, et al. (2023) Dissecting the genetic landscape of GPCR signaling through phenotypic profiling in *C. elegans*. *Nature communications*, 14(1), 8410.