

Resource Summary Report

Generated by [NIF](#) on Jul 31, 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 resource, software application, source code

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

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

Funding: MICINN ;
Xunta de Galicia ;
ERDF

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: 20260731T043138+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 5 mentions in open access literature.

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

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.

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

Pi??eiro 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.

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