

# Resource Summary Report

Generated by RRID on Apr 28, 2025

## 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:** source code, software application, software resource

**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:** 20250428T054354+0000

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## Ratings and Alerts

No rating or validation information has been found for VeryFastTree.

No alerts have been found for VeryFastTree.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 4 mentions in open access literature.

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

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.

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.

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