

# Resource Summary Report

Generated by [ASWG](#) on Aug 4, 2026

## FastTree

RRID:SCR\_015501

Type: Tool

### Proper Citation

FastTree (RRID:SCR\_015501)

### Resource Information

**URL:** <http://www.microbesonline.org/fasttree/>

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**Description:** Source code that infers approximately-maximum-likelihood phylogenetic trees from alignments of nucleotide or protein sequences. It uses the Jukes-Cantor or generalized time-reversible (GTR) models of nucleotide evolution and the JTT, WAG, or LG models of amino acid evolution.

**Resource Type:** software resource, source code

**Defining Citation:** [PMID:19377059](https://pubmed.ncbi.nlm.nih.gov/19377059/), [DOI:10.1371/journal.pone.0009490](https://doi.org/10.1371/journal.pone.0009490)

**Keywords:** phylogenetic tree, phylogenetic tree creation, bio.tools

**Resource Name:** FastTree

**Resource ID:** SCR\_015501

**Alternate IDs:** biotools:fasttree, OMICS\_14703

**Alternate URLs:** <https://bio.tools/fasttree>, <https://sources.debian.org/src/fasttree/>

**Record Creation Time:** 20220129T080326+0000

**Record Last Update:** 20260804T043559+0000

### Ratings and Alerts

No rating or validation information has been found for FastTree.

No alerts have been found for FastTree.

### Data and Source Information

## Usage and Citation Metrics

We found 5774 mentions in open access literature.

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

Sebastian PJ, et al. (2026) Apparent expansion of virulent *Vibrio parahaemolyticus* in humans and sea otters. *Virulence*, 17(1), 2603698.

Hu Y, et al. (2026) Global epidemiological and genetic characteristics of carbapenem-resistant *Escherichia coli* carrying blaIMP. *Microbiology spectrum*, 14(1), e0324425.

Yanez Ortuno D, et al. (2026) Predicting bacterial-mediated entomopathogenicity through comparative genomics and statistical modeling. *Microbiology spectrum*, 14(1), e0310825.

H??gglund E, et al. (2026) Origin and Evolution of Key Enzymes in the Anammox Pathway Revisited. *Genome biology and evolution*, 18(1).

Shi T, et al. (2026) Revisiting ancient whole-genome duplications in the seed and flowering plants through the lens of dosage-sensitive genes. *Science advances*, 12(1), eaea9797.

Levine J, et al. (2026) Microbial signature of pediatric Crohn's disease: Differentiation from functional gastrointestinal disorders and relationship with increased disease activity. *Physiological reports*, 14(1), e70665.

Baldelli V, et al. (2026) The *Pseudomonas aeruginosa* sirB2 gene is a fitness determinant of anaerobic growth and its inactivation affects virulence and rugose small colony variants emergence. *Virulence*, 17(1), 2605800.

Markkanen M, et al. (2026) Sulfonamide resistance gene sul4 is hosted by common wastewater sludge bacteria and found in various newly described contexts and hosts. *Microbiology spectrum*, 14(1), e0085725.

Wang X-Y, et al. (2026) Genomic epidemiology and plasmid characterization of antimicrobial resistance and virulence in cattle *Escherichia coli* from China. *Microbiology spectrum*, 14(1), e0325625.

Inieta M, et al. (2025) Impact of toothpaste use on the subgingival microbiome: a pilot randomized clinical trial. *BMC oral health*, 25(1), 854.

Garsmeur O, et al. (2025) The genomic footprints of wild *Saccharum* species trace domestication, diversification, and modern breeding of sugarcane. *Cell*, 188(25), 7252.

Xu CCY, et al. (2025) Pre-exposure to stress reduces loss of community and genetic diversity following severe environmental disturbance. *Current biology : CB*, 35(5), 1061.

Liu C, et al. (2025) A chromosome-scale genome assembly of the pioneer plant *Stylosanthes angustifolia*: insights into genome evolution and drought adaptation.

GigaScience, 14.

Xue J, et al. (2025) An HIV fusion-inhibitory lipopeptide provides robust post-exposure prophylaxis and prevents viral reservoir seeding in macaques. *Cell reports*, 44(9), 116228.

Froschauer K, et al. (2025) Complementary Ribo-seq approaches map the translome and provide a small protein census in the foodborne pathogen *Campylobacter jejuni*. *Nature communications*, 16(1), 3078.

Unitt A, et al. (2025) *Neisseria gonorrhoeae* LIN codes provide a robust, multi-resolution lineage nomenclature. *eLife*, 14.

Nath R, et al. (2025) Lineage-Specific Class-A GPCR Dynamics Reflect Diverse Chemosensory Adaptations in Lophotrochozoa. *Molecular biology and evolution*, 42(3).

Rakesh S, et al. (2025) Unveiling the structural and functional implications of uncharacterized NSPs and variations in the molecular toolkit across arteriviruses. *NAR genomics and bioinformatics*, 7(2), lqaf035.

Saticioglu IB, et al. (2025) Phylogenomic characterization of *Flavobacterium psychrophilum* isolates retrieved from Turkish rainbow trout farms. *Journal of fish diseases*, 48(8), e13961.

Kerlikowsky F, et al. (2025) Distinct Microbial Taxa Are Associated with LDL-Cholesterol Reduction after 12 Weeks of *Lactobacillus plantarum* Intake in Mild Hypercholesterolemia: Results of a Randomized Controlled Study. *Probiotics and antimicrobial proteins*, 17(3), 1086.