

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

FastTree

RRID:SCR_015501

Type: Tool

Proper Citation

FastTree (RRID:SCR_015501)

Resource Information

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

Proper Citation: FastTree (RRID:SCR_015501)

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: source code, software resource

Defining Citation: [PMID:19377059](#), [DOI: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: 20260801T191238+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 [RRID](#) .

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

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

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

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.

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

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

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.

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.

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.

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.

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

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.

Zheng J, et al. (2025) Genome mining and OSMAC strategies unveil diverse secondary metabolites from the endophytic fungus *Diaporthe kyushuensis* ZMU-48-1 with antifungal activity. *Frontiers in microbiology*, 16, 1604639.