

Resource Summary Report

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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: 20260829T183314+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 6279 mentions in open access literature.

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

Francette AM, et al. (2026) Evolutionary analysis of transcription elongation factors reveals conserved and lineage-specific regulatory domains. PLoS biology, 24(6), e3003855.

Black JJ, et al. (2026) The Legionella pneumophila effector SidL is an adenylyltransferase that modifies the glycolytic intermediate 3-phosphoglycerate. Molecular cell.

Suksa W, et al. (2026) Metagenomic analysis revealed the presence of novel Actinomycetota "Candidatus Solincola uaceae" sp. nov., obtained from a hot spring. Scientific reports, 16(1), 6922.

Gao MX, et al. (2026) Genome mining and functional characterization of four type I sesquiterpene synthases from the Tiger Milk Mushroom Lignosus rhinocerus. Natural products and bioprospecting, 16(1), 27.

Shin GY, et al. (2026) Comparative genomics of Pantoea allii lineages and distribution of ecologically relevant traits. Microbial genomics, 12(2).

Miao F, et al. (2026) Antimicrobial resistance and genomic characteristics of avian Pasteurella multocida. Poultry science, 105(4), 106524.

Song H, et al. (2026) Artificial lagoon project alters archaeal diversity, community assembly, and potential activity around a nearshore island: insights from an annual cycle. Applied and environmental microbiology, 92(1), e0149925.

Kallscheuer N, et al. (2026) Four novel Planctomicrobium species isolated from sewage sludge or leakage water of a compost heap in Northern Germany. Scientific reports, 16(1), 4347.

Fuentes-Alburquenque S, et al. (2026) Regional consistency in microbial community responses to hydrocarbon pollution in maritime Antarctic soils. BMC microbiology, 26(1).

Liu Z, et al. (2026) Listeria monocytogenes of two sequence types in a maternal-fetal listeriosis: clinical management and bacterial genomics. BMC infectious diseases, 26(1), 356.

Pappert FA, et al. (2026) Parental fasting effects on offspring immune gene expression, epigenetic patterns, and gut microbiota in a species with male pregnancy (Syngnathus typhle). BMC biology, 24(1), 24.

Dani M, et al. (2026) Species delimitation within the Achnanthidium minutissimum complex (Bacillariophyta), based on morphological, molecular, and ecophysiological approaches. Journal of phycology, 62(1), 25.

Geng X, et al. (2026) Comprehensive analysis of chloroplast genome evolution in Poaceae: codon usage patterns, selection pressures, and phylogenomic relationships. *BMC genomics*, 27(1), 217.

Ma H, et al. (2026) Cold-adapted carboxylesterases from Alcanivoracaceae active with a wide range of synthetic polyesters. *Applied microbiology and biotechnology*, 110(1), 59.

Zhao Y, et al. (2026) YamOmics: a comprehensive data resource on yam multi-omics. *BMC bioinformatics*, 27(1).

Kalinich CC, et al. (2026) A tiled amplicon protocol for culture-free whole-genome sequencing of *M. tuberculosis* from clinical specimens. *Journal of clinical microbiology*, 64(3), e0182325.

U??ur Aydin Z, et al. (2026) A clinical next-generation sequencing study on the microbial profiles of asymptomatic apical periodontitis in type 2 diabetic and systemically healthy individuals following adjuvant antimicrobial photodynamic therapy. *Clinical oral investigations*, 30(2), 75.

Fu L, et al. (2026) OsNAC10 negatively regulates salt tolerance by repressing OsHKT1;5 expression and reducing shoot-to-root Na⁺ recirculation in rice. *Plant communications*, 7(6), 101771.

Alvarenga DO, et al. (2026) Climate Change Impacts the Structure and Nitrogen-Fixing Activities of Subarctic Feather Moss Microbiomes Across a Precipitation Gradient. *Global change biology*, 32(2), e70718.

Hu Y, et al. (2026) The reference genome sequence of the scarlet follicle, *Sterculia lanceolata*, reveals a paleo-polyploidization and its impact on fruit quality and fruit dehiscence. *Functional & integrative genomics*, 26(1), 46.