

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: 20260821T194045+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 [ASWG](#) .

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.

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

Liu H, et al. (2026) Molecular characterization of a clinical ST145 Klebsiella oxytoca strain co-producing KPC-2 and IMP-96 carbapenemases. mSystems, 11(1), e0152925.

Kok CR, et al. (2026) Microbiome dynamics in the congregate environment of U.S. Army Infantry training. Microbiology spectrum, 14(2), e0047425.

Deng Y, et al. (2026) Molecular epidemiology of drug resistance and transmission of Mycobacterium tuberculosis in Meigu County, Sichuan Province, China. Microbiology spectrum, 14(2), e0268525.

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.

Jiao Z, et al. (2026) Unidirectional genomic introgression facilitates the colonization of an invasive orchid in arid, metal-enriched sedimentary habitats. Plant communications, 7(1), 101561.

Wang Y, et al. (2026) GeneFamily: a comprehensive mammalian gene family database with extensive annotation and interactive visualization. Nucleic acids research, 54(D1), D419.

Protic IA, et al. (2026) Comparative genomic analyses shed light on the introduction routes of rice-pathogenic Burkholderia gladioli strains into Bangladesh. BMC genomics, 27(1), 121.

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.

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.

Ge G, et al. (2026) Isolation, identification and genomic analysis of *Mycobacterium caprae* strain SY-1 from Chinese sika deer (*Cervus nippon*). *BMC genomics*, 27(1), 184.

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

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.

Xia P, et al. (2026) Genomic analysis of *Enterococcus faecium* co-carrying *optrA* and *poxA* from a swine farm: dissemination across the human-animal-environment interface. *BMC microbiology*, 26(1), 125.

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.

Lee H, et al. (2026) Diverse bacterial pattern recognition receptors sense the conserved phage proteome. *bioRxiv* : the preprint server for biology.