

Resource Summary Report

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IQ-TREE

RRID:SCR_017254

Type: Tool

Proper Citation

IQ-TREE (RRID:SCR_017254)

Resource Information

URL: <http://www.iqtree.org/>

Proper Citation: IQ-TREE (RRID:SCR_017254)

Description: Software tool as stochastic algorithm for estimating maximum likelihood phylogenies. Used for phylogenomic inference.

Resource Type: software application, data analysis software, software resource, data processing software

Defining Citation: [PMID:25371430](#)

Keywords: stochastic, algorithm, estimate, maximum, likelihood, phylogeny, phylogenomic, inference, data, dataset, bio.tools

Funding Agency: Austrian Science Fund , University of Vienna

Availability: Free, Available for download, Freely available

Resource Name: IQ-TREE

Resource ID: SCR_017254

Alternate IDs: biotools:ufboot2

Alternate URLs: <https://bio.tools/ufboot2/>

Ratings and Alerts

No rating or validation information has been found for IQ-TREE.

No alerts have been found for IQ-TREE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 416 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Kennard AS, et al. (2024) An internally controlled system to study microtubule network diversification links tubulin evolution to the use of distinct microtubule regulators. bioRxiv : the preprint server for biology.

Li H, et al. (2024) The structure and assembly mechanisms of T4-like cyanophages community in the South China Sea. Microbiology spectrum, 12(2), e0200223.

Balboa RF, et al. (2024) African bushpigs exhibit porous species boundaries and appeared in Madagascar concurrently with human arrival. Nature communications, 15(1), 172.

Kogay R, et al. (2024) Defense systems and horizontal gene transfer in bacteria. bioRxiv : the preprint server for biology.

Li H, et al. (2024) Recurrent evolutionary switches of mitochondrial cytochrome c maturation systems in Archaeplastida. Nature communications, 15(1), 1548.

Flores-Alvarez LJ, et al. (2024) Sequencing and description of the genome of a strain of *Stenotrophomonas geniculata* isolated from a patient infected with COVID-19 at Hospital Regional No.1 de Charo, Michoacán, México. microPublication biology, 2024.

Tamura T, et al. (2024) Virological characteristics of the SARS-CoV-2 Omicron XBB.1.5 variant. Nature communications, 15(1), 1176.

Yu N, et al. (2024) Chromosome-level genome of spider *Pardosa pseudoannulata* and cuticle protein genes in environmental stresses. Scientific data, 11(1), 121.

Ling-Hu T, et al. (2024) Integration of individualized and population-level molecular epidemiology data to model COVID-19 outcomes. Cell reports. Medicine, 5(1), 101361.

Witte TE, et al. (2024) Debunking the Myth of *Fusarium poae* T-2/HT-2 Toxin Production. Journal of agricultural and food chemistry, 72(8), 3949.

Yi X, et al. (2024) ?Molecular and morphological evidence support a new species of

Rosaceae *Prunus* subg. *Cerasus* from Wuyishan National Park, southeast China. *PhytoKeys*, 237, 269.

Wu J, et al. (2024) A farnesyl-dependent structural role for CENP-E in expansion of the fibrous corona. *The Journal of cell biology*, 223(1).

Lin JY, et al. (2024) The complete mitochondrial genome of *Aphidius colemani* (Hymenoptera: Braconidae: Aphidiinae). *Mitochondrial DNA. Part B, Resources*, 9(2), 257.

Che Y, et al. (2024) Transmission dynamics of drug-resistant tuberculosis in Ningbo, China: an epidemiological and genomic analysis. *Frontiers in cellular and infection microbiology*, 14, 1327477.

Dieng I, et al. (2024) The Spatiotemporal Distribution and Molecular Characterization of Circulating Dengue Virus Serotypes/Genotypes in Senegal from 2019 to 2023. *Tropical medicine and infectious disease*, 9(2).

Kogay R, et al. (2024) Co-evolution of gene transfer agents and their alphaproteobacterial hosts. *Journal of bacteriology*, 206(2), e0039823.

Lin M, et al. (2024) ?*Camelliazijinica* (Theaceae), a new species endemic to Danxia landscape from Guangdong Province, China. *PhytoKeys*, 237, 245.

Sánchez-Busó L, et al. (2024) pyngoST: fast, simultaneous and accurate multiple sequence typing of *Neisseria gonorrhoeae* genome collections. *Microbial genomics*, 10(1).

Lan G, et al. (2024) Complete Mitochondrial Genome and Phylogenetic Analysis of *Tarsiger indicus* (Aves: Passeriformes: Muscicapidae). *Genes*, 15(1).

Xu Y, et al. (2024) Chromosome-level genome of the poultry shaft louse *Menopon gallinae* provides insight into the host-switching and adaptive evolution of parasitic lice. *GigaScience*, 13(1).