

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

Defining Citation: [PMID:25371430](#)

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

Funding: 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/>

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260807T042904+0000

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 1007 mentions in open access literature.

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

Jing X, et al. (2026) Phylogenetic and pathogenic analyses of circulating infectious bursal disease virus strains in China. Poultry science, 105(1), 106108.

Angélica Maya M, et al. (2026) Adenovirus Genotypes Associated With Severe Acute Respiratory Infections Outbreak in Children, in Antioquia, Colombia, 2022-2023. The Pediatric infectious disease journal, 45(2), 112.

Steinfurth A, et al. (2026) Investigating high pathogenicity avian influenza virus incursions to remote islands: detection of H5N1 on Gough Island in the South Atlantic Ocean. Emerging microbes & infections, 15(1), 2627076.

Sound JK, et al. (2026) Mass spectrometry reveals the evolutionary conservation of phycobiliprotein complexes. Nature communications, 17(1).

Martínez-Alvarez L, et al. (2026) Diversity and evolution of archaeal immune strategies. Nucleic acids research, 54(5).

Zhang JY, et al. (2026) Demographic history and identification of threats under climate and anthropogenic activity provide insights into conservation for *Cypripedium palangshanense*. BMC plant biology, 26(1), 213.

Maurstad MF, et al. (2026) The green lacewing venom system and the complex mechanisms underlying its evolution. Molecular biology and evolution, 43(1).

Bowerman KL, et al. (2026) A molecular inventory of the faecal microbiomes of 23 marsupial species. Microbial genomics, 12(1).

Fiaz N, et al. (2026) Distinct mutational landscapes and phylogenomic insights of the SARS-CoV-2 delta variant in Pakistan and India: Regional evolution, novel mutations, and epidemiological implications. PloS one, 21(2), e0340704.

Kim S, et al. (2026) Chromosome-Scale Reference Genome Assemblies for Two Anoplophora Longhorned Beetle Species (Coleoptera: Cerambycidae). Genome biology and evolution, 18(3).

Perez VP, et al. (2026) Dairy Farm *Streptococcus agalactiae* in a Region of Northeast Brazil: Genetic Diversity, Resistome, and Virulome. *Pathogens* (Basel, Switzerland), 15(2).

Wang JX, et al. (2026) Re-Examination: No True *Tabidia Snellen*, 1880 (Lepidoptera: Crambidae) in China, with Descriptions of Two New Genera and Three New Species. *Insects*, 17(2).

Raza Abbas S, et al. (2026) Phylogenomics to structure: evolutionary and clinical signals in the TP53 DNA-binding core through LOOCV-validated ensemble learning. *Briefings in bioinformatics*, 27(1).

Zhao R, et al. (2026) The effect of hyper-induced SOS response on evolution in *Escherichia coli*. *BMC microbiology*, 26(1).

Feinauer IS, et al. (2026) Whole genomes reveal subpopulations and isolation-by-distance patterns in the Norwegian lemming. *BMC biology*, 24(1).

Mahnert A, et al. (2026) Cultivation and molecular profiling reveal ammonia-oxidizing archaea as skin commensals. *The ISME journal*, 20(1).

Shi J, et al. (2026) Transcriptome Analysis and Identification of Chemosensory Genes in *Leguminivora glycinivorella*. *Biology*, 15(6).

Bianchini G, et al. (2026) AliFilter: a machine learning approach to alignment filtering. *Molecular biology and evolution*, 43(4).

Declerck C, et al. (2026) Spread of extended-spectrum β -lactamase-producing Enterobacterales (ESBL-E) in the community living spaces of patients identified as ESBL-E carriers: impact of the housing density in an African context. *Tropical medicine and health*, 54(1).

Cacciabue M, et al. (2026) The whole genome analysis of four Orf virus strains from Europe and South America. *Virus evolution*, 12(1), veag004.