

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 17, 2026

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, data processing software, software application, software resource

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: 20260912T195850+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 [SPARC SAWG](#) .

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

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.

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

Olowo-Okere A, et al. (2026) Genomic and phylogenomic analyses reveal extensive diversity among soil-derived *Acinetobacter baumannii* isolates from Nigeria. *Scientific reports*, 16(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.

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).

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

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

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).

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.

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

Vassilieff H, et al. (2026) Endogenous viral elements trace the ancient origins and early evolution of the Caulimoviridae. *PLoS pathogens*, 22(6), e1014340.

Lin Y, et al. (2026) Genomic characterization of a Chinese bovine papillomavirus isolate and its L1-based phylogenetic placement in a global dataset. *Frontiers in veterinary science*, 13, 1839050.

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

Calvo EP, et al. (2026) Unexpected diversification of DENV2 genotype III in Colombia: New Insights and application of the globalized nomenclature. *PloS one*, 21(2), e0343528.

Alikhanova A, et al. (2026) Complete chloroplast genome sequence data of *Iris kuschakewiczii* B.Fedtsch., an endemic species of the Northern Tien Shan mountains. *Data in brief*, 65, 112563.

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

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).

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