

Resource Summary Report

Generated by T1D on Aug 2, 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, software resource, data processing software, software application

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: 20260803T040737+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 790 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

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.

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

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

Hägglund E, et al. (2026) Origin and Evolution of Key Enzymes in the Anammox Pathway Revisited. Genome biology and evolution, 18(1).

Vernié T, et al. (2025) Conservation of symbiotic signaling since the most recent common ancestor of land plants. Proceedings of the National Academy of Sciences of the United States of America, 122(1), e2408539121.

Darin E, et al. (2025) MyD88 knockdown by RNAi prevents bacterial stimulation of tubeworm metamorphosis. Proceedings of the National Academy of Sciences of the United States of America, 122(23), e2505805122.

Suetsugu K, et al. (2025) Integrated peloton and fruiting body isotope data shed light on mycoheterotrophic interactions in *Gastrodia pubilabiata* (Orchidaceae). Mycorrhiza, 35(3), 43.

Onetto CA, et al. (2025) Genetic and phenotypic diversity of wine-associated *Hanseniaspora* species. FEMS yeast research, 25.

Tanimura MW, et al. (2025) Comprehensive cDNA cloning and putative feature analysis of endogenous cellulases possessed by the Pacific oyster, *Crassostrea gigas*. PloS one, 20(2), e0313246.

Coelho MA, et al. (2025) Tracing the evolution and genomic dynamics of mating-type loci in *Cryptococcus* pathogens and closely related species. bioRxiv : the preprint server for biology.

Wang Z, et al. (2025) Biodegradation of high-molecular-weight polycyclic aromatic hydrocarbons by a novel species of the genus *Devosia* isolated from the deep-sea region of the Kermadec Trench. *Frontiers in microbiology*, 16, 1584496.

Howden K, et al. (2025) Applying Field and Genomic Epidemiology Methods to Investigate Transmission Networks of Highly Pathogenic Avian Influenza A (H5N1) in Domestic Poultry in British Columbia, Canada (2022-2023). *Transboundary and emerging diseases*, 2025, 4099285.

Bednarikova S, et al. (2025) Filariasis of parti-colored bats: phylogenetic analysis, infection prevalence, and possible vector mite identification. *Frontiers in veterinary science*, 12, 1546353.

Möhring J, et al. (2025) Increased phenotypic diversity as a consequence of ecological opportunity in the island radiation of Sulawesi ricefishes (Teleostei: Adrianichthyidae). *BMC ecology and evolution*, 25(1), 19.

Gonçalves C, et al. (2025) Stable hypermutators revealed by the genomic landscape of DNA repair genes among yeast species. *bioRxiv : the preprint server for biology*.

Liang Y, et al. (2025) The molecular basis of octocoral calcification revealed by genome and skeletal proteome analyses. *GigaScience*, 14.

Zhang RG, et al. (2025) SOI: robust identification of orthologous synteny with the Orthology Index and broad applications in evolutionary genomics. *Nucleic acids research*, 53(7).

Wu K, et al. (2025) *Methanosuratincola petrocarbonis* gen. nov., sp. nov., a methyl-reducing methanogen isolated from Shengli oil field, and proposal of *Methanosuratincolaceae* fam. nov., *Methanosuratincolales* ord. nov. and *Methanosuratincolia* classis nov. in the phylum Thermoproteota. *International journal of systematic and evolutionary microbiology*, 75(7).

Liu G, et al. (2025) The complete mitochondrial genome and phylogenetic analysis of a leaf insect *Cryptophyllum oyae* Cumming & Le Tirant, 2020 (Phasmatodea: Phylliidae) in China. *Mitochondrial DNA. Part B, Resources*, 10(8), 698.

Yun S, et al. (2025) The mitochondrial genome data of the *Capsicum annuum* cv. Dempsey (Solanaceae). *Data in brief*, 60, 111640.