

# Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

## IQ TREE

RRID:SCR\_021163

Type: Tool

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### Proper Citation

IQ TREE (RRID:SCR\_021163)

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### Resource Information

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

**Proper Citation:** IQ TREE (RRID:SCR\_021163)

**Description:** Software tool for phylogenomic inference.

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

**Keywords:** phylogenomic inference, tree of life, data analysis

**Funding:** Austrian Science Fund FWF ;  
University of Vienna

**Availability:** Free, Available for download, Freely available

**Resource Name:** IQ TREE

**Resource ID:** SCR\_021163

**Alternate IDs:** OMICS\_11543

**Alternate URLs:** <https://sources.debian.org/src/iqtree/>

**License:** GNU GPL

**Record Creation Time:** 20220129T080354+0000

**Record Last Update:** 20260905T132935+0000

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### Ratings and Alerts

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

No alerts have been found for IQ TREE.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 450 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

Huang G, et al. (2026) The architecture and energy transfer pathways of PSI-LHCI-LHCII in the phototrophic flagellate *Euglena gracilis*. *Nature communications*, 17(1).

Filho CG, et al. (2026) Guillain-Barr?? Syndrome and Visual Impairment Associated with Emerging Oropouche Virus Lineage, Brazil, 2024. *Emerging infectious diseases*, 32(4), 644.

Maqbool M, et al. (2026) Exploration of the genomic diversity of third-generation cephalosporin-resistant *Escherichia coli* in Australian clinical settings. *Microbial genomics*, 12(1).

Mbwana JR, et al. (2026) Molecular characterisation of extended-Spectrum-Beta-lactamase-producing *Klebsiella pneumoniae* among children and chicken in the rural Korogwe District, Tanzania. *One health (Amsterdam, Netherlands)*, 23, 101472.

Ohama Y, et al. (2026) Whole-Genome Analysis of *Treponema pallidum* Subspecies endemicum among Men Who Have Sex with Men, Japan, 2020-2023. *Emerging infectious diseases*, 32(4), 636.

Mihalca AD, et al. (2026) First imported case of New World leishmaniasis in Romania: diagnostic and therapeutic challenges in a non-endemic country. *Infectious diseases of poverty*, 15(1).

Novikova D, et al. (2026) AGP and EXO-LIKE genes promote brassinosteroid-dependent anisotropic growth. *The New phytologist*, 250(4), 2384.

Xiao Q, et al. (2026) Insights into the Cytochrome P450 Monooxygenase Superfamily in *Kadsura heteroclita* (Xuetong). *Molecules (Basel, Switzerland)*, 31(12).

Li S, et al. (2026) Genomic dissection of the clonal background and global dissemination of hypervirulent *Klebsiella pneumoniae* CG23-KL57 lineage. *Nature communications*, 17(1), 1451.

Duan M, et al. (2026) Genomic Signatures Underlying Environmental Adaptation and Reproductive Traits in the Tibetan Pig. *Animals : an open access journal from MDPI*, 16(3).

Obeng BM, et al. (2026) Regional Variations of Rates and Determinants of Drug Resistance Mutations in People Failing First-line Therapy for HIV-1: A Substudy from the

D2EFT Phase 3b/4 Clinical Trial. Clinical infectious diseases : an official publication of the Infectious Diseases Society of America, 82(4), e693.

Yi D, et al. (2026) Computational analysis and expression profiling of the Sulfate Transporter gene family in tomato under selenium and abiotic stress treatment. BMC plant biology, 26(1).

Zhang Y, et al. (2026) Haemaphysalis longicornis HSP20 inhibits Rickettsia heilongjiangensis replication by targeting the pathogen 50S ribosomal protein. Parasites & vectors, 19(1).

Andreani J, et al. (2026) Severe Respiratory Illness and Death Associated with Outbreak of Human Rhinovirus B14 among Older Adults, France, 2024. Emerging infectious diseases, 32(5), 768.

Ryckman M, et al. (2026) Occurrence and subtyping of the intestinal protozoan Blastocystis sp. in French oyster areas reveal potential fecal contamination routes and associated risks to consumer health. Food and waterborne parasitology, 43, e00332.

Shi X, et al. (2026) Chloroplast genomes provide new insights into the phylogeny and evolution of the genus Hibiscus L. BMC plant biology, 26(1).

Idoudi F, et al. (2026) Decoding antibody response to MERS-CoV in wild dromedary camels. Proceedings of the National Academy of Sciences of the United States of America, 123(7), e2513716123.

Lai DN, et al. (2026) Dynamic auxin maxima regulate male-to-hermaphrodite conversion and de novo meristem formation in the fern Ceratopteris gametophytes. PLoS biology, 24(1), e3003592.

Citu C, et al. (2025) Identification and catalog of viral transcriptional regulators in human diseases. iScience, 28(3), 112081.

Ndiaye AJS, et al. (2025) Whole Genome Sequencing and Genetic Diversity of Respiratory Viruses Detected in Children With Acute Respiratory Infections: A One-Year Cross-Sectional Study in Senegal. Journal of medical virology, 97(4), e70342.