

Resource Summary Report

Generated by RRID on Aug 2, 2026

IQ TREE

RRID:SCR_021163

Type: Tool

Proper Citation

IQ TREE (RRID:SCR_021163)

Resource Information

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

Proper Citation: IQ TREE (RRID:SCR_021163)

Description: Software tool for phylogenomic inference.

Resource Type: data processing software, data analysis 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: 20260801T190713+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 350 mentions in open access literature.

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

Li T, et al. (2025) Drift Drives Foraminiferal Community Assembly on a Carbonate Platform. *Ecology and evolution*, 15(6), e71604.

Lan R, et al. (2025) Continuous evolution of Eurasian avian-like H1N1 swine influenza viruses with pdm/09-derived internal genes enhances pathogenicity in mice. *Journal of virology*, 99(10), e0043025.

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.

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

Mottawea W, et al. (2025) Multi-level analysis of gut microbiome extracellular vesicles-host interaction reveals a connection to gut-brain axis signaling. *Microbiology spectrum*, 13(2), e0136824.

Elizondo-Reyna E, et al. (2025) Insights from a Genome-Wide Study of *Pantoea* agglomerans UADEC20: A Promising Strain for Phosphate Solubilization and Exopolysaccharides Production. *Current issues in molecular biology*, 47(1).

Li L, et al. (2025) Systematic metaproteomics mapping reveals functional and ecological landscapes of Ex vivo human gut microbiota responses to therapeutic drugs. *Nature communications*, 16(1), 9383.

Renaud EA, et al. (2025) The HCF101 protein is an important component of the cytosolic iron-sulfur synthesis pathway in *Toxoplasma gondii*. *PLoS biology*, 23(2), e3003028.

Trifone C, et al. (2025) Contribution of intact viral genomes persisting in blood and tissues during ART to plasma viral rebound in SHIV-infected rhesus macaques. *iScience*, 28(3), 111998.

Xiong C, et al. (2025) Mitochondrial Genomes from Fungal the Entomopathogenic *Moelleriella* Genus Reveals Evolutionary History, Intron Dynamics and Phylogeny. *Journal of fungi (Basel, Switzerland)*, 11(2).

Yuan M, et al. (2025) AaMYC3 bridges the regulation of glandular trichome density and artemisinin biosynthesis in *Artemisia annua*. *Plant biotechnology journal*, 23(2), 315.

Chen D, et al. (2025) Largest genome assembly in Brassicaceae: retrotransposon-driven genome expansion and karyotype evolution in *Matthiola incana*. *Plant biotechnology journal*, 23(9), 4109.

Singkum P, et al. (2025) Environmental Yeast Abundance and Diversity Assessment in Recreation Areas of Bangkok, Thailand. *Environmental microbiology reports*, 17(5), e70212.

Soares AP, et al. (2025) B-cell epitope mapping of Orthoflavivirus zikaense in mother-newborn immune interaction reveals postnatal immune signatures. *Scientific reports*, 15(1), 36530.

Yang J, et al. (2025) Analyzing the distribution of virulence factors of *Mycobacterium tuberculosis* and the impact of virulence gene mutations on treatment outcomes in different lineages using whole-genome sequencing in Urumqi. *Virulence*, 16(1), 2552875.

Karn RC, et al. (2025) A Broad Genome Survey Reveals Widespread Presence of Secretoglobins in Squamate and Archosaur Reptiles that Flowered into Diversity in Mammals. *Genome biology and evolution*, 17(3).

Bernardi V, et al. (2025) Yellow Fever Virus in Mosquitoes from Rainforest Bordering Manaus, Brazil, 2022. *Emerging infectious diseases*, 31(4), 851.

Strobel AG, et al. (2025) Meningococcal C Disease Outbreak Caused by Multidrug-Resistant *Neisseria meningitidis*, Fiji. *Emerging infectious diseases*, 31(1), 32.

Lambisia AW, et al. (2025) Identification of coxsackievirus A24 variant during an acute hemorrhagic conjunctivitis outbreak in coastal Kenya, 2024. *Wellcome open research*, 10, 28.

Tenrisau D, et al. (2025) Molecular epidemiological surveillance of monkeypox virus in Indonesia from 2023 to 2024. *Epidemiology and infection*, 153, e79.