Resource Summary Report

Generated by dkNET on Apr 29, 2025

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 analysis software, data processing software, software resource,

software application

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: 20250429T060048+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 301 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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).

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.

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

Zhang Y, et al. (2025) Morphological Characteristics, Mitochondrial Genome, and Evolutionary Insights Into a New Sea Squirt From the Beibu Gulf. Ecology and evolution, 15(1), e70639.

Pidgeon R, et al. (2025) Diet-derived urolithin A is produced by a dehydroxylase encoded by human gut Enterocloster species. Nature communications, 16(1), 999.

Ren H, et al. (2025) MixtureFinder: Estimating DNA Mixture Models for Phylogenetic Analyses. Molecular biology and evolution, 42(1).

Badar N, et al. (2024) Evolutionary analysis of seasonal influenza A viruses in Pakistan 2020-2023. Influenza and other respiratory viruses, 18(2), e13262.

da Costa Castilho M, et al. (2024) Evidence of Zika Virus Reinfection by Genome Diversity and Antibody Response Analysis, Brazil. Emerging infectious diseases, 30(2), 310.

Izadi M, et al. (2024) Discovering conserved epitopes of Monkeypox: Novel immunoinformatic and machine learning approaches. Heliyon, 10(3), e24972.

Liénard MA, et al. (2024) TRPA5 encodes a thermosensitive ankyrin ion channel receptor in a triatomine insect. iScience, 27(4), 109541.

Reyes JIL, et al. (2024) Detection and quantification of natural Wolbachia in Aedes aegypti in Metropolitan Manila, Philippines using locally designed primers. Frontiers in cellular and infection microbiology, 14, 1360438.

Choi CH, et al. (2024) Genomic Analysis of Monkeypox Virus During the 2023 Epidemic in Korea. Journal of Korean medical science, 39(18), e165.

Carvalho APS, et al. (2024) Comprehensive phylogeny of Pieridae butterflies reveals strong correlation between diversification and temperature. iScience, 27(4), 109336.

Isaac SL, et al. (2024) Genome mining of Lactiplantibacillus plantarum PA21: insights into its antimicrobial potential. BMC genomics, 25(1), 571.

Khatun MS, et al. (2024) Genome-wide identification and characterization of FORMIN gene family in potato (Solanum tuberosum L.) and their expression profiles in response to drought stress condition. PloS one, 19(8), e0309353.

Blom MPK, et al. (2024) Hybridization in birds-of-paradise: Widespread ancestral gene flow despite strong sexual selection in a lek-mating system. iScience, 27(7), 110300.

Lambisia AW, et al. (2024) Multispecies Cocirculation of Adenoviruses Identified by Next-Generation Sequencing During an Acute Gastroenteritis Outbreak in Coastal Kenya in 2023. Open forum infectious diseases, 11(9), ofae505.

Yu L, et al. (2024) Prevalence, antimicrobial resistance, and genomic characterization of Salmonella strains isolated in Hangzhou, China: a two-year study. Annals of clinical microbiology and antimicrobials, 23(1), 86.

Heng YC, et al. (2024) Expanding the biosynthesis spectrum of hydroxy fatty acids: unleashing the potential of novel bacterial fatty acid hydratases. Biotechnology for biofuels and bioproducts, 17(1), 131.

Cueva DF, et al. (2024) Evidence of population genetic structure in Ecuadorian Andean bears. Scientific reports, 14(1), 2834.