

Resource Summary Report

Generated by NIF on May 2, 2025

RAxML

RRID:SCR_006086

Type: Tool

Proper Citation

RAxML (RRID:SCR_006086)

Resource Information

URL: <https://github.com/stamatak/standard-RAxML>

Proper Citation: RAxML (RRID:SCR_006086)

Description: Software program for phylogenetic analyses of large datasets under maximum likelihood.

Abbreviations: RAxML

Synonyms: Randomized Axelerated Maximum Likelihood

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

Defining Citation: [PMID:24451623](#), [PMID:16928733](#), [PMID:15608047](#),
[DOI:10.1093/bioinformatics/btu033](#)

Keywords: phylogeny, bio.tools

Funding:

Availability: GNU General Public License

Resource Name: RAxML

Resource ID: SCR_006086

Alternate IDs: biotools:raxml, OMICS_02242

Alternate URLs: <https://bio.tools/raxml>, <https://sources.debian.org/src/raxml/>

Record Creation Time: 20220129T080234+0000

Record Last Update: 20250502T055620+0000

Ratings and Alerts

No rating or validation information has been found for RAxML.

No alerts have been found for RAxML.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11525 mentions in open access literature.

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

Magyar LB, et al. (2025) Pore-Forming Toxin-Like Proteins in the Anti-Parasitoid Immune Response of *Drosophila*. *Journal of innate immunity*, 17(1), 10.

Han J, et al. (2025) Catalytic mechanism underlying the regiospecificity of coumarin-substrate transmembrane prenyltransferases in Apiaceae. *Plant & cell physiology*, 66(1), 1.

Weldegebreal F, et al. (2025) Relationship between vaginal and gut microbiome and pregnancy outcomes in eastern Ethiopia: a protocol for a longitudinal maternal-infant cohort study (the EthioOMICS study). *BMJ open*, 15(1), e092461.

Witharana EP, et al. (2025) Subfamily evolution analysis using nuclear and chloroplast data from the same reads. *Scientific reports*, 15(1), 687.

Zhu W, et al. (2025) Origin, pathogenicity, and transmissibility of a human isolated influenza A(H10N3) virus from China. *Emerging microbes & infections*, 14(1), 2432364.

Guo F, et al. (2025) Insight into the codon usage patterns and adaptation of Tembusu Virus. *Poultry science*, 104(1), 104651.

Kress WJ, et al. (2025) Phylogenomics and a new classification of the tropical genus *Heliconia* L. (Monocots, Zingiberales, Heliconiaceae). *PhytoKeys*, 251, 37.

Cantatore DMP, et al. (2025) Intraspecific Morphometric Variation in a New Species of Ceratomyxa Thélohan 1892 (Cnidaria) from the South Atlantic Ocean: An Ecomorphological Study Using Geometric Morphometrics. *Biology*, 14(1).

Wen J, et al. (2025) Complete Mitochondrial Genome of King Threadfin, *Polydactylus macrochir* (Günther, 1867): Genome Characterization and Phylogenetic Analysis. *Genes*, 16(1).

Yacoub E, et al. (2025) A sweeping view of avian mycoplasmas biology drawn from comparative genomic analyses. *BMC genomics*, 26(1), 24.

Delavaux CS, et al. (2025) Uncovering Diversity within the Glomeromycota: Novel Clades, Family Distributions, and Land Use Sensitivity. *Ecology and evolution*, 15(1), e70597.

Schenk JJ, et al. (2025) Comparative diversification analyses of Hydrangeaceae and Loasaceae reveal complex evolutionary history as species disperse out of Mesoamerica. *American journal of botany*, 112(1), e16455.

Russell D, et al. (2025) Seed banking impacts native *Acacia ulicifolia* seed microbiome composition and function. *Environmental microbiome*, 20(1), 4.

Zeng X, et al. (2025) The complete mitochondrial genome of *Gyrodactylus pseudorasborae* (Platyhelminthes: Monogenea) with a phylogeny of Gyrodactylidae parasites. *BMC genomics*, 26(1), 34.

Gregory CL, et al. (2025) Utilizing a novel fecal sampling method to examine resistance of the honey bee (*Apis mellifera*) gut microbiome to a low dose of tetracycline. *PLoS one*, 20(1), e0317129.

Ramanujam H, et al. (2025) Recovery of *Mycobacterium tuberculosis* Complex Isolates Including Pre-Extensively Drug-Resistant Strains From Cattle at a Slaughterhouse in Chennai, India. *Open forum infectious diseases*, 12(1), ofae733.

Yu X, et al. (2025) Super pan-genome reveals extensive genomic variations associated with phenotypic divergence in *Actinidia*. *Molecular horticulture*, 5(1), 4.

Coomber AL, et al. (2025) A pangenome analysis reveals the center of origin and evolutionary history of *Phytophthora infestans* and 1c clade species. *PLoS one*, 20(1), e0314509.

Öztoprak H, et al. (2025) Chromosome-scale genome dynamics reveal signatures of independent haplotype evolution in the ancient asexual mite *Platynothrus peltifer*. *Science advances*, 11(4), eadn0817.

Rick JA, et al. (2025) Admixture and environmental fluctuations shape the evolutionary history of a predator radiation in East Africa's Lake Tanganyika. *bioRxiv : the preprint server for biology*.