

Resource Summary Report

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[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: data processing software, data analysis software, software application, software resource

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

Keywords: phylogeny, bio.tools

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: 20260801T190304+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 12473 mentions in open access literature.

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

Markkanen M, et al. (2026) Sulfonamide resistance gene sul4 is hosted by common wastewater sludge bacteria and found in various newly described contexts and hosts. *Microbiology spectrum*, 14(1), e0085725.

Chen Z, et al. (2026) Evaluating Probe Design for Phylogenomics Across Taxonomic Scales: First Steps for Applying Ultraconserved Elements in an Understudied Class (Mollusca: Polyplacophora). *Molecular ecology resources*, 26(1), e70076.

Li C, et al. (2026) A cell-type-specific regulon controlling monoterpene indole alkaloid biosynthesis with feedback and feedforward activation loops. *The New phytologist*, 249(2), 945.

Cleveland ME, et al. (2026) Toward the Bioremediation of Nylon Waste Materials: Genome Mining Leads to the Identification of a Thermostable Laurolactamase From *Thermopolyspora flexuosa*. *ChemSusChem*, 19(1), e202501964.

Wang YH, et al. (2026) Insights into dill (*Anethum graveolens*) flavor formation via integrative analysis of chromosomal-scale genome, metabolome and transcriptome. *Journal of advanced research*, 79, 847.

Pourmahdi Borujeni M, et al. (2026) First Detection and Phylogenetic Analysis of Equine Hepacivirus (EqHV) in Iran. *Veterinary medicine and science*, 12(1), e70737.

Viruel J, et al. (2026) Phylogenomic Barcoding of Soil Seed Bank-Persistent and Wind-Dispersed Non-Native Plant Species in South Georgia. *Molecular ecology resources*, 26(1), e70068.

Stryko J, et al. (2026) Carbapenem-resistant *Acinetobacter baumannii* at a hospital in Botswana: detecting a protracted outbreak using whole genome sequencing. *Microbiology spectrum*, 14(1), e0176825.

Wang G, et al. (2025) Genomic evidence for hybridization and introgression between blue peafowl and endangered green peafowl and molecular foundation of leucistic plumage of blue peafowl. *GigaScience*, 14.

Terpis KX, et al. (2025) Multiple plastid losses within photosynthetic stramenopiles revealed by comprehensive phylogenomics. *Current biology : CB*, 35(3), 483.

Chen M, et al. (2025) The genome of *Hippophae salicifolia* provides new insights into the sexual differentiation of sea buckthorn. *GigaScience*, 14.

Yuan S, et al. (2025) Multiomic Analyses Reveal the Molecular Mechanisms of Arid Adaptation in a Desert Rodent Species. *Molecular biology and evolution*, 42(10).

Ren L, et al. (2025) Genomes reveal pervasive distant hybridization in nature among cyprinid fishes. *GigaScience*, 14.

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. *GigaScience*, 14.

Záhonová K, et al. (2025) Diplonemid protists possess exotic endomembrane machinery, impacting models of membrane trafficking in modern and ancient eukaryotes. *Current biology : CB*, 35(7), 1508.

Cuevas Zuviría B, et al. (2025) Structural evolution of nitrogenase over 3 billion years. *eLife*, 14.

Unitt A, et al. (2025) *Neisseria gonorrhoeae* LIN codes provide a robust, multi-resolution lineage nomenclature. *eLife*, 14.

Kariyayama H, et al. (2025) Hagfish olfactory repertoire illuminates lineage-specific diversification of olfaction in basal vertebrates. *iScience*, 28(12), 114118.

Scadden J, et al. (2025) The nisin O cluster: species dissemination, candidate leader peptide proteases and the role of regulatory systems. *Microbiology (Reading, England)*, 171(2).

Qi Z, et al. (2025) Telomere-to-telomere genome assembly of *Electrophorus electricus* provides insights into the evolution of electric eels. *GigaScience*, 14.