

Resource Summary Report

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phytools

RRID:SCR_015502

Type: Tool

Proper Citation

phytools (RRID:SCR_015502)

Resource Information

URL: <https://cran.r-project.org/web/packages/phytools/index.html>

Proper Citation: phytools (RRID:SCR_015502)

Description: Software R package for phylogenetic comparative biology. The package contains various functions for phylogenetic analysis of comparative data from species.

Resource Type: software resource, source code

Defining Citation: [DOI:10.1111/j.2041-210X.2011.00169.x](https://doi.org/10.1111/j.2041-210X.2011.00169.x)

Keywords: r package, phylogenetic comparison, phylogenetic analysis

Availability: Available for download, Acknowledgement requested

Resource Name: phytools

Resource ID: SCR_015502

Alternate IDs: OMICS_12499

Alternate URLs: <https://github.com/liamrevell/phytools>, <https://sources.debian.org/src/r-cran-phytools/>

License: GPL-2, GPL-3

Record Creation Time: 20220129T080326+0000

Record Last Update: 20260912T200357+0000

Ratings and Alerts

No rating or validation information has been found for phytools.

No alerts have been found for phytools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 718 mentions in open access literature.

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

Szablińska-Piernik J, et al. (2026) Giant chromosomes of a tiny plant-the complete telomere-to-telomere genome assembly of the simple thalloid liverwort *Apopellia endiviifolia* (Jungermanniopsida, Marchantiophyta). *GigaScience*, 15.

Nawae W, et al. (2026) Genome Assembly of Three Shrub Mangroves in the Genus *Acanthus* Reveals Two Polyploidy Events and Expansion of Genes Linked to Root Adaptation in Coastal Habitats. *GigaScience*, 15.

Bittlingmaier M, et al. (2026) Plant and soil biodiversity sustain root mycorrhizal fungal richness under drought stress. *The ISME journal*, 20(1).

Adden A, et al. (2026) The evolution of lepidopteran brain morphology. *Journal of comparative physiology. A, Neuroethology, sensory, neural, and behavioral physiology*, 212(2), 409.

Li B, et al. (2026) Phylogenomics, ecomorphological evolution, and historical biogeography in *Deuterocohnia* (Bromeliaceae: Pitcairnioideae). *American journal of botany*, 113(2), e70153.

Cai L, et al. (2026) Recombination and Retroprocessing in Broomrapes Reveal RNA-Mediated Gene Transfer Mechanism and a Generalizable Model for Mitochondrial Evolution in Heterotrophic Plants. *Genome biology and evolution*, 18(2).

Wang W, et al. (2026) Comparative genomics reveals evolutionary signatures of genes associated with jumping in beetles. *Zoological research*, 47(1), 88.

Humberto AC, et al. (2026) The Repeatome in the Mega-Genus *Epidendrum* L. (*Epidendroideae*, *Orchidaceae*): An In Silico Comparative Analysis. *Genes*, 17(2).

Satoh S, et al. (2026) Repeated evolution of cooperative breeding and life history traits in Lake Tanganyika cichlids. *Communications biology*, 9(1).

Wang H, et al. (2026) Integrative chloroplast genomics of *Polygonaceae*: evolutionary dynamics, codon optimization, and phylogenetic resolution. *BMC plant biology*, 26(1).

Jallow MM, et al. (2026) Epidemiology, Genomic Diversity, and Evolutionary Dynamics of Human Metapneumovirus Over 7 Years of Integrated Community- and Hospital-Based Sentinel Surveillance in Senegal, 2018-2024. *Influenza and other respiratory viruses*, 20(7), e70290.

Osnes MN, et al. (2026) Genomic epidemiology of *Streptococcus pneumoniae* GPSC6: post-vaccine expansion of β -lactam-susceptible serotype 24F in Europe. *Microbial genomics*, 12(5).

Zhang R, et al. (2026) HiFi-Assembled Mitogenomes of Four Pygmy Grasshoppers Reveal Mito-Nuclear Discordance in *Zhengitettix transpicula* and Lineage-Specific Mitochondrial Intergenic Length Variation. *Life (Basel, Switzerland)*, 16(6).

Muthu G G, et al. (2026) Evolutionary Analysis of Trehalose Breakdown Pathways. *Genome biology and evolution*, 18(6).

Wang J, et al. (2026) Exploring differences in the human gut microbiome between Han Chinese and non-Chinese populations. *Genome biology*, 27(1), 34.

Hale CO, et al. (2026) Widespread turnover of a conserved cis-regulatory code across 589 grass species. *Molecular biology and evolution*, 43(1).

Tör?-Sziogyártó V, et al. (2026) Inconsistent relationships detected between seed size, shape and persistence for different plant functional groups in the Pannonian flora. *Annals of botany*, 137(4), 1026.

Wei J, et al. (2026) Convergent genome evolution shaped the emergence of terrestrial animals. *Nature*, 649(8097), 638.

Alfsen A, et al. (2026) Broadening the semiaquatic scene: Quantification of long bone microanatomy across pinnipeds. *Anatomical record (Hoboken, N.J. : 2007)*, 309(8), 2124.

Labella-Ortega M, et al. (2026) Uncovering the genome evolutionary dynamics of the Mediterranean endemic palm *Chamaerops humilis*. *BMC plant biology*, 26(1).