

Resource Summary Report

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[ape](#)

RRID:SCR_017343

Type: Tool

Proper Citation

ape (RRID:SCR_017343)

Resource Information

URL: <https://CRAN.R-project.org/package=ape>

Proper Citation: ape (RRID:SCR_017343)

Description: Software R package for analysis of phylogenetics and evolution. Environment for modern phylogenetics and evolutionary analyses in R.

Synonyms: ape 3.0, ape 5.0, Analysis of Phylogenetics and Evolution

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

Defining Citation: [PMID:30016406](#), [PMID:14734327](#), [PMID:22495750](#)

Keywords: analysis, phylogenetics, evolution, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: ape

Resource ID: SCR_017343

Alternate IDs: biotools:ape

Alternate URLs: <https://cran.r-project.org/web/packages/ape/ape.pdf>, <http://ape-package.ird.fr/>, <https://bio.tools/ape>

License: GPLv3

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260728T043537+0000

Ratings and Alerts

No rating or validation information has been found for ape.

No alerts have been found for ape.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 42 mentions in open access literature.

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

Ma H, et al. (2025) Microbial profile of the appendix niche in acute appendicitis: a novel sampling approach. *FEBS open bio*, 15(12), 2001.

Ma H, et al. (2025) Spatially Resolved Tumor Ecosystems and Cell States in Gastric Adenocarcinoma Progression and Evolution. *Cancer discovery*, 15(4), 767.

Moshiri N, et al. (2025) CompactTree: a lightweight header-only C++ library and Python wrapper for ultra-large phylogenetics. *GigaByte (Hong Kong, China)*, 2025, gigabyte152.

Bertinetti C, et al. (2025) Phenotypic plasticity in visual opsin gene expression: a meta-analysis in teleost fish. *The Journal of experimental biology*, 228(13).

Dempsey E, et al. (2025) Protective Properties of the White Button Mushroom, *Agaricus bisporus*, in a Mouse Model of Colitis. *Molecular nutrition & food research*, e70133.

Christmas MJ, et al. (2025) Interpreting mammalian synonymous site conservation in light of the unwanted transcript hypothesis. *Nature communications*, 16(1), 2007.

Krueger ME, et al. (2025) Comparative analysis of Parkinson's and inflammatory bowel disease gut microbiomes reveals shared butyrate-producing bacteria depletion. *NPJ Parkinson's disease*, 11(1), 50.

Wilken AT, et al. (2025) Avian cranial kinesis is the result of increased encephalization during the origin of birds. *Proceedings of the National Academy of Sciences of the United States of America*, 122(13), e2411138122.

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

Menozzi E, et al. (2025) Exploring the relationship between GBA1 host genotype and gut microbiome in the GBA1 L444P/WT mouse model: implications for Parkinson's disease pathogenesis. *Frontiers in neuroscience*, 19, 1546203.

Youk J, et al. (2024) Quantitative and qualitative mutational impact of ionizing radiation on normal cells. *Cell genomics*, 4(2), 100499.

Wang M, et al. (2024) HIF α 1 and macrophage activation signalling pathways are potential biomarkers of invasive aspergillosis. *Experimental and therapeutic medicine*, 27(2), 86.

Weibel CA, et al. (2024) The protein domains of vertebrate species in which selection is more effective have greater intrinsic structural disorder. *eLife*, 12.

Tian WH, et al. (2024) Phylogenetic Insights Reveal New Taxa in Thyridariaceae and Massarinaceae. *Journal of fungi (Basel, Switzerland)*, 10(8).

Qin S, et al. (2024) Predicting the sequence-dependent backbone dynamics of intrinsically disordered proteins. *eLife*, 12.

Tian WH, et al. (2024) New and Interesting Pine-Associated Hyphomycetes from China. *Journal of fungi (Basel, Switzerland)*, 10(8).

Liu H, et al. (2024) Integrative molecular and spatial analysis reveals evolutionary dynamics and tumor-immune interplay of in situ and invasive acral melanoma. *Cancer cell*, 42(6), 1067.

Schall PZ, et al. (2023) Genome-wide methylation patterns from canine nanopore assemblies. *G3 (Bethesda, Md.)*, 13(11).

Olkkonen E, et al. (2023) Analysis of population structure and genetic diversity in low-variance Saimaa ringed seals using low-coverage whole-genome sequence data. *STAR protocols*, 4(4), 102567.

Türk Dermastia T, et al. (2023) Evaluation of the rbcL marker for metabarcoding of marine diatoms and inference of population structure of selected genera. *Frontiers in microbiology*, 14, 1071379.