# **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 resource, data analysis software, software application, data processing software

Defining Citation: PMID:30016406, PMID:14734327, PMID:22495750

Keywords: analysis, phylogenetics, evolution, bio.tools

Funding:

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: 20250509T060243+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 31 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

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

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) New and Interesting Pine-Associated Hyphomycetes from China. Journal of fungi (Basel, Switzerland), 10(8).

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

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

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

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.

Yao Y, et al. (2023) Limitations of principal components in quantitative genetic association models for human studies. eLife, 12.

Sedah P, et al. (2023) Impact of Seed Origin and Genetic Drift of Improved Rice Variety

IR841 in Benin. Rice (New York, N.Y.), 16(1), 48.

Turk 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.

Pan J, et al. (2023) Metagenomic analysis of herbivorous mammalian viral communities in the Northwest Plateau. BMC genomics, 24(1), 568.

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

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

Leighton J, et al. (2023) Reconstructing mutational lineages in breast cancer by multi-patient-targeted single-cell DNA sequencing. Cell genomics, 3(1), 100215.

Howard-McCombe J, et al. (2023) Genetic swamping of the critically endangered Scottish wildcat was recent and accelerated by disease. Current biology : CB, 33(21), 4761.

Ledda A, et al. (2022) Hospital outbreak of carbapenem-resistant Enterobacterales associated with a blaOXA-48 plasmid carried mostly by Escherichia coli ST399. Microbial genomics, 8(4).

Gulyaeva A, et al. (2022) Discovery, diversity, and functional associations of crAss-like phages in human gut metagenomes from four Dutch cohorts. Cell reports, 38(2), 110204.

Wang Z, et al. (2022) A chromosome-level reference genome of Ensete glaucum gives insight into diversity and chromosomal and repetitive sequence evolution in the Musaceae. GigaScience, 11.

Nan J, et al. (2022) Genome resequencing reveals independent domestication and breeding improvement of naked oat. GigaScience, 12.

Nojiri T, et al. (2021) Embryonic evidence uncovers convergent origins of laryngeal echolocation in bats. Current biology : CB, 31(7), 1353.