

Package ‘PhyloProfileData’

April 7, 2026

Type Package

Version 1.25.0

Date 2025-06-25

Title Data package for phylogenetic profile analysis using
PhyloProfile tool

Description Two experimental datasets to illustrate running and analysing phylogenetic profiles with PhyloProfile package.

URL <https://github.com/BIONF/PhyloProfileData>

BugReports <https://github.com/trvinh/PhyloProfileData/issues>

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Depends R (>= 4.5.0)

Encoding UTF-8

biocViews ExperimentData, ReproducibleResearch, ExperimentHub

Imports ExperimentHub, Biostrings, BiocStyle

Suggests knitr, rmarkdown

VignetteBuilder knitr

LazyData false

NeedsCompilation yes

RoxygenNote 7.3.2

git_url <https://git.bioconductor.org/packages/PhyloProfileData>

git_branch devel

git_last_commit a0cd0b5

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Description

The PhyloProfileData package provides a collection of datasets to accompany the R package PhyloProfile, where they are used to illustrate how to run PhyloProfile and analyse its results. Briefly, it contains the phylogenetic profiles, the fasta sequences and the domain annotations for two experimental data sets, including human AMPK-TOR pathway proteins and BUSCO Arthropoda proteins.

Details

More details of the data can be found in the vignette "PhyloProfileData" using `browseVignettes("PhyloProfileData")`.

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See Also

Useful links:

- <https://github.com/BIONF/PhyloProfileData>
- Report bugs at <https://github.com/trvinh/PhyloProfileData/issues>

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