

# Package: PhyloProfileData (via r-universe)

October 10, 2026

**Type** Package

**Version** 1.26.1

**Date** 2025-09-14

**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>

**License** MIT + file LICENSE

**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

**Config/roxygen2/version** 8.1.0

**Config/pak/sysreqs** cmake make libicu-dev libpng-dev libuv1-dev libssl-dev zlib1g-dev

**Repository** Bioconductor 3.23

**Date/Publication** 2026-09-14 17:51:47 UTC

**RemoteUrl** <https://github.com/bioc/PhyloProfileData>

**RemoteRef** RELEASE\_3\_23

**RemoteSha** cd383e1bef19b62f40283b73a592adfe0db18b98

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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 datas can be found in the vignette "PhyloProfileData" using `browseVignettes("PhyloProfileData")`.

**Author(s)**

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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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