

# Package ‘PhyloProfileData’

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**Type** Package

**Version** 1.6.0

**Date** 2019-05-30

**Title** Data package for phylogenetic profile analysis using  
PhyloProfile tool

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**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 (>= 3.6.0)

**Encoding** UTF-8

**biocViews** ExperimentData, ReproducibleResearch, ExperimentHub

**Imports** ExperimentHub, Biostrings

**Suggests** knitr

**VignetteBuilder** knitr

**LazyData** false

**NeedsCompilation** yes

**RoxygenNote** 6.1.1

**git\_url** <https://git.bioconductor.org/packages/PhyloProfileData>

**git\_branch** RELEASE\_3\_13

**git\_last\_commit** 69c5d89

**git\_last\_commit\_date** 2021-05-19

**Date/Publication** 2021-06-12

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PhyloProfileData

*Data package for phylogenetic profile analysis using PhyloProfile tool*

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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")`.

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