

Package ‘PhyloProfileData’

November 27, 2025

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>

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git_last_commit a0cd0b5

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Author Vinh Tran [aut, cre] (ORCID: [<https://orcid.org/0000-0001-6772-7595>](https://orcid.org/0000-0001-6772-7595)),
Ingo Ebersberger [aut],
Hannah Mülbaier [ctb],
Arpit Jain [ctb]

Maintainer Vinh Tran <tran@bio.uni-frankfurt.de>

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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)

Maintainer: Vinh Tran <tran@bio.uni-frankfurt.de> ([ORCID](#))

Authors:

- Ingo Ebersberger <ebersberger@bio.uni-frankfurt.de>

Other contributors:

- Hannah Mülbaier <hannah.muelbaier@gmail.com> [contributor]
- Arpit Jain <arpitrb@gmail.com> [contributor]

See Also

Useful links:

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

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