

Package ‘BiocHubsShiny’

April 5, 2026

Type Package

Title View AnnotationHub and ExperimentHub Resources Interactively

Version 1.10.0

Description A package that allows interactive exploration of AnnotationHub and ExperimentHub resources. It uses DT / DataTable to display resources for multiple organisms. It provides template code for reproducibility and for downloading resources via the indicated Hub package.

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Encoding UTF-8

Depends R (>= 4.3.0), shiny

Imports AnnotationHub, ExperimentHub, DT, htmlwidgets, rclipboard, S4Vectors, shinyAce, shinybiocloader, shinyjs, shinythemes, utils

Suggests BiocManager, BiocStyle, curl, glue, knitr, rmarkdown, sessioninfo, shinytest2

biocViews Software, ShinyApps

BugReports <https://github.com/Bioconductor/BiocHubsShiny/issues>

URL <https://github.com/Bioconductor/BiocHubsShiny>

VignetteBuilder knitr

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

Date 2025-09-22

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

git_branch RELEASE_3_22

git_last_commit 2adb511

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2026-04-05

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Description

The shiny app will allow the user to view a table of either [AnnotationHub](#) or [ExperimentHub](#) resources depending on the sidebar selection. It provides example code for downloading the selected resources.

Usage

```
BiocHubsShiny(...)
```

Arguments

... Further arguments to the runApp function

Details

Note. The code here was adapted from `interactiveDisplayBase` and `'display,Hub-method'` which are now deprecated.

Value

Mainly called for the side effect of displaying the shiny app in a browser

Examples

```
if (interactive()) {
  BiocHubsShiny()
}
```

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