

# Package ‘BiocHubsShiny’

July 23, 2025

**Type** Package

**Title** View AnnotationHub and ExperimentHub Resources Interactively

**Version** 1.8.1

**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.

**License** Artistic-2.0

**Encoding** UTF-8

**Depends** R (>= 4.3.0), shiny

**Imports** AnnotationHub, ExperimentHub, DT, htmlwidgets, rclipboard, S4Vectors, shinyAce, shinyjs, shinythemes, shinytoast, 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** 7.3.2

**Date** 2025-05-21

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

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**Author** Marcel Ramos [aut, cre] (ORCID:  
[<https://orcid.org/0000-0002-3242-0582>](https://orcid.org/0000-0002-3242-0582)),  
 Vincent Carey [ctb]

**Maintainer** Marcel Ramos <marcel.ramos@sph.cuny.edu>

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| BiocHubsShiny | <i>Initialize the shiny application for Bioconductor Hub resources</i> |
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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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