

# Package ‘shinybiocloader’

October 13, 2025

**Title** Use a Shiny Bioconductor CSS loader

**Version** 0.99.1

**Description** Add a Bioconductor themed CSS loader to your shiny app. It is based on the shinycustomloader R package. Use a spinning Bioconductor note loader to enhance your shiny app loading screen. This package is intended for developer use.

**Depends** htmltools

**Imports** shiny

**Suggests** shinydashboard, tinytest, quarto

**VignetteBuilder** quarto

**SystemRequirements** quarto

**biocViews** Software, Infrastructure, GUI

**License** Artistic-2.0

**BugReports** <https://github.com/Bioconductor/shinybiocloader/issues>

**URL** <https://github.com/Bioconductor/shinybiocloader>

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

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

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## Description

Add a loader to a Shiny UI element

## Usage

```
withLoader(ui_element, loader = "biocspin", proxy.height = "400px")
```

## Arguments

|              |                                                                                                                                                                     |
|--------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ui_element   | A Shiny UI element (e.g., uiOutput, plotOutput, etc.) for which to wrap with the loader.                                                                            |
| loader       | character(1) A string specifying the loader type. Default is "biocspin".                                                                                            |
| proxy.height | character(1) A string specifying the height of the proxy element. Default is "400px". If the ui_element already has a height specified, this will be set to "100%". |

## Value

A Shiny UI element wrapped with the Bioconductor loader

## References

shinycustomloader <https://github.com/emitanaka/shinycustomloader>  
 dna spin <https://codepen.io/knut/pen/ZopMWW>

## Examples

```
library(shiny)
library(shinydashboard)
library(shinybiocloader)

waitHist <- function() {
  waiting <- faithful[["waiting"]]
  Sys.sleep(3) # Simulate loading
  hist(
    waiting, col = 'darkgray', border = 'white',
    main = 'Old Faithful Geyser Waiting Times Histogram',
    xlab = 'Waiting Time (min)'
  )
}

ui <- dashboardPage(
  dashboardHeader(title = "Bioconductor Loader"),
  dashboardSidebar(disable = TRUE),
  dashboardBody(
    h2("Bioconductor Spinning Loader"),
    HTML(
      paste0(
        "<pre><code class='language-r'>",
```

```
      "withLoader(plotOutput('distPlot'), loader='biocspin')",
      "</code></pre>"
    )
  ),
  fluidRow(
    box(
      title = "With Loader", status = "primary", solidHeader = TRUE,
      withLoader(plotOutput("distPlot"), loader = "biocspin")
    ),
    box(
      title = "Without Loader", status = "warning", solidHeader = TRUE,
      plotOutput("distPlot2")
    )
  )
)
)

server <- function(input, output) {
  output$distPlot <- renderPlot(waitHist())
  output$distPlot2 <- renderPlot(waitHist())
}

shinyApp(ui = ui, server = server)
```

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