

Package ‘Prostar’

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Type Package

Title Provides a GUI for DAPAR

Version 1.34.6

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Description This package provides a GUI interface for the DAPAR package. The package Prostar (Proteomics statistical analysis with R) is a Bioconductor distributed R package which provides all the necessary functions to analyze quantitative data from label-free proteomics experiments. Contrarily to most other similar R packages, it is endowed with rich and user-friendly graphical interfaces, so that no programming skill is required.

biocViews Proteomics, MassSpectrometry, Normalization, Preprocessing, Software, GUI

License Artistic-2.0

Depends R (>= 4.3.0)

Suggests BiocStyle, BiocManager, testthat

Imports DAPAR (>= 1.34.6), DAPARdata (>= 1.27.3), rhandsontable, data.table, shiny, shinyBS, shinyAce, highcharter, htmlwidgets, webshot, shinythemes, later, shinycssloaders, future, promises, shinyjqui, tibble, ggplot2, gplots, shinyjs, vioplot, shinyTree, knitr, colourpicker, gtools, XML, R.utils, RColorBrewer, DT, shinyWidgets, sass, rclipboard, markdown

NeedsCompilation no

RoxygenNote 7.2.3

Encoding UTF-8

URL <http://www.prostar-proteomics.org/>

BugReports <https://github.com/prostarproteomics/Prostar/issues>

VignetteBuilder knitr

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

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R topics documented:

BuildColorStyles	2
getDataForExprs	3
Prostar	3

Index	4
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BuildColorStyles	xxxx
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Description

xxxx

Usage

BuildColorStyles(obj)

Arguments

obj xx

getDataForExprs *xxxx*

Description

xxxx

Usage

getDataForExprs(obj, digits = NULL)

Arguments

obj xx
 digits xxx

Prostar *Prostar*

Description

Prostar

Usage

Prostar()

Value

A new window in the default internet browser

Author(s)

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Examples

```
if (interactive()) {
  Prostar()
}
```

Index

BuildColorStyles, [2](#)

getDataForExprs, [3](#)

Prostar, [3](#)