

Package ‘Prostar’

April 24, 2024

Type Package

Title Provides a GUI for DAPAR

Version 1.35.2

Date 2024-01-17

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 (>= 4.4.0)

Suggests BiocStyle, BiocManager, testthat, knitr

Imports DAPAR (>= 1.35.1), DAPARdata (>= 1.30.0), rhandsontable, data.table, shiny, shinyBS, shinyAce, highcharter, htmlwidgets, webshot, shinythemes, later, shinycssloaders, future, promises, shinyjqui, tibble, ggplot2, gplots, shinyjs, vioplot, Biobase, DT, R.utils, RColorBrewer, XML, colourpicker, gtools, markdown, rclipboard, sass, shinyTree, shinyWidgets

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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BuildColorStyles	xxx
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Description

xxxx

Usage

BuildColorStyles(obj)

Arguments

obj	xx
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getDataForExprs	xxx
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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()  
}
```

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