Package: Prostar (via r-universe)

October 7, 2024

Type Package

Title Provides a GUI for DAPAR

Version 1.37.0

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 7.3.2

Encoding UTF-8

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

BugReports https://github.com/edyp-lab/Prostar/issues

VignetteBuilder knitr

Repository https://bioc.r-universe.dev

RemoteUrl https://github.com/bioc/Prostar

RemoteRef HEAD

RemoteSha b001e02d181647111f0f79a450e1aa477498c0ee

Contents

`BuildColorStyles` *xxxx*

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

```
## Not run:
    Prostar()

## End(Not run)
```

Index