

Package ‘Prostar’

September 29, 2022

Type Package

Title A GUI for DAPAR package

Version 1.28.5

Date 2022-09-22

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 ($\geq 4.1.0$)

Suggests BiocStyle, BiocManager, testthat, shinyTree, knitr, future, sass, R.utils, gplots, ggplot2, vioplot, promises, colourpicker, tibble, DAPARdata ($\geq 1.22.2$), webshot, shinythemes, XML, gtools, compiler, shinyjs, DT

Imports DAPAR ($\geq 1.28.5$), rhandsontable, data.table, shiny, shinyBS, shinyAce, highcharter, MSnbase, shinyWidgets, shinycssloaders, htmlwidgets, RColorBrewer, shinyjqui, later

NeedsCompilation no

RoxygenNote 7.2.1

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>

git_branch RELEASE_3_15

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Prostar

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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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