

# Package ‘Prostar’

October 18, 2022

**Type** Package

**Title** A GUI for DAPAR package

**Version** 1.28.6

**Date** 2022-10-17

**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 (>= 4.1.0)

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

**Imports** DAPAR (>= 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

**git\_last\_commit** d212650

**git\_last\_commit\_date** 2022-10-17

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### Description

Prostar

### Usage

Prostar()

### Value

A new window in the default internet browser

### Author(s)

Samuel Wieczorek

### Examples

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

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