

# Package ‘Prostar’

April 10, 2023

**Type** Package

**Title** Provides a GUI for DAPAR

**Version** 1.30.7

**Date** 2023-02-22

**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 (>= 4.2.0)

**Suggests** BiocStyle, BiocManager, testthat, shinyTree, knitr, colourpicker, gtools, XML, R.utils, RColorBrewer, DT, shinyWidgets, sass, rclipboard

**Imports** DAPAR (>= 1.30.6), DAPARdata (>= 1.28.0), rhandsontable, data.table, shiny, shinyBS, shinyAce, highcharter, htmlwidgets, webshot, shinythemes, later, shinycssloaders, future, promises, shinyjqui, tibble, ggplot2, gplots, shinyjs, vioplot

**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>

**git\_branch** RELEASE\_3\_16

**git\_last\_commit** 7981aa2**git\_last\_commit\_date** 2023-03-19**Date/Publication** 2023-04-10**Author** Thomas Burger [aut],  
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Samuel Wiczorek [cre, aut]**Maintainer** Samuel Wiczorek <samuel.wiczorek@cea.fr>

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### Description

Prostar

### Usage

Prostar()

### Value

A new window in the default internet browser

### Author(s)

Samuel Wiczorek

### Examples

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

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