

# Package ‘Prostar’

September 12, 2024

**Type** Package

**Title** Provides a GUI for DAPAR

**Version** 1.36.2

**Date** 2024-056-10

**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 (>= 1.36.2), DAPARdata (>= 1.34.0), 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>

**git\_branch** RELEASE\_3\_19

**git\_last\_commit** 0b46101  
**git\_last\_commit\_date** 2024-06-10  
**Repository** Bioconductor 3.19  
**Date/Publication** 2024-09-11  
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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

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Prostar

*Prostar*

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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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