

Package ‘RforProteomics’

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Type Package

Title Companion package to the ‘Using R and Bioconductor for proteomics data analysis’ publication

Version 1.0.13

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Imports R.utils, Biobase

Suggests mzR, MSnbase, xcms, msdata, isobar, MALDIquant, MALDIquantForeign, readBrukerFlexData, rTAN-DEM, synapter, synapterdata, IPPD, Rdisop, OrgMassSpecR, BRAIN, rols, hpar, GO.db, org.Hs.eg.db, biomaRt, RColorBrewer, ggplot2, reshape2, knitr, biocViews, xtable

Enhances cleaver

Description This package contains code to illustrate the ‘Using R and Bioconductor for proteomics data analysis’ manuscript. The vignette describes the code and data needed to reproduce the examples and figures described in the paper as well as functions to download the PXD000001 data files.

URL <http://lgatto.github.com/RforProteomics/>

biocViews ExperimentData, MassSpectrometry, Proteomics, MassSpectrometryData

License Artistic-2.0

VignetteBuilder knitr

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getPXD000001mzData *Download the PXD000001 mzTab file*

Description

Unless already present, downloads the PXD000001 mzData file in the `destdir` directory. The resulting file is named `PRIDE_Exp_Complete_Ac_22134.xml`

Usage

```
getPXD000001mzData(destdir = ".")
```

Arguments

`destdir` A character with the destination folder.

Value

Invisibly returns the name of the downloaded file.

Author(s)

Laurent Gatto

getPXD000001mzTab *Download the PXD000001 mzTab file*

Description

Unless already present, downloads the PXD000001 mzTab file in the `destdir` directory. The resulting file is named `F063721.dat-mztab.txt`.

Usage

```
getPXD000001mzTab(destdir = ".")
```

Arguments

`destdir` A character with the destination folder.

Value

Invisibly returns the name of the downloaded file.

Author(s)

Laurent Gatto

getPXD000001mzXML *Download the PXD000001 mzXML file*

Description

Unless already present, downloads the PXD000001 mzXML file in the destdir directory. The resulting file is named TMT_Erwinia_1uLSike_Top10HCD_isol2_45stepped_60min_01.mzXML.

Usage

```
getPXD000001mzXML(destdir = ".")
```

Arguments

destdir A character with the destination folder.

Value

Invisibly returns the name of the downloaded file.

Author(s)

Laurent Gatto

RforProteomics *Opens RforProteomics vignettes*

Description

Opens the package vignettes.

Usage

```
RforProteomics()
```

Value

An instance of class vignette, as returned by [vignette](#)

Author(s)

Laurent Gatto

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