Package 'rpx'

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Type Package

Title R Interface to the ProteomeXchange Repository

Version 1.22.0

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Description The rpx package implements an interface to proteomics data submitted to the ProteomeXchange consortium.

Depends methods

Imports xml2, RCurl, utils

Suggests MSnbase, Biostrings, BiocStyle, testthat, knitr

License GPL-2

URL `https://github.com/lgatto/rpx`

BugReports `https://github.com/lgatto/rpx/issues`

VignetteBuilder knitr

biocViews ImmunoOncology, Proteomics, MassSpectrometry, DataImport, ThirdPartyClient

RoxygenNote 6.1.0

git_url https://git.bioconductor.org/packages/rpx

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R topics documented:

`pxannounced` *Return recent PX announcements*

Description

Queries the PX rss feed file for the latest PX dataset announcements.

Usage

```
pxannounced()
```

Value

A `data.frame` with announcements data set identifiers, publication dates and annoucement messages.

Author(s)

Laurent Gatto

Examples

```
pxannounced()
```

`PXDataset-class` *Class* `"PXDataset"`

Description

An S4 class to store and access information about ProteomeXchange (PX) data sets. Schema versions 1.0, 1.1 and 1.2 are supported and are documented on the PX code repository: https://code.google.com/p/proteomex

Objects from the Class

Objects can be created with the constructor `PXDataset`.

Slots

`id`**:** Object of class `"character"` storing the datasets unique identifier. Can be accessed with `pxid()`.

`formatVersion`**:** Object of class `"character"` storing the version of the ProteomeXchange schema.

`Data`**:** Object of class `"XMLNode"` storing the ProteomeXchange description as XML node tree.

Methods

- **pxfiles** `signature(object = "PXDataset")`: return a `character` of all available files.
- **pxget** `signature(object = "PXDataset",list,force = FALSE,destdir = getwd(),...)`: downloads the files from the ProteomeXchange repository. If `list` is missing, the file to be downloaded can be selected from a menu. If `list = "all"`, all files are downloaded. The file names, as returned by `pxfiles` can also be used. Alternatively, a `logical` or `numeric` indices can be used. All files will be downloaded into the directory specified by `destdir` (default is the current working directory). Unless `force` is set to `TRUE`, files are not downloaded if already present in the `destdir` directory. Additional parameters can be passed to `download.file` via `...`. Invisibly returns the names of the downloaded files.

  On Windows, the error

  ```
  In download.file(urls[i], toget[i], ...) :
      InternetOpenUrl failed: 'The login request was denied'
  ```

  had been reported when downloading files. In such cases, the `method` argument to `download.file` can be set. If `libcurl` is available (try `capailities("libcurl")` to check this), using `pxget(...,method = "libcurl")` has proven successful. See `?download.file` for more details.
- **pxid** `signature(object = "PXDataset")`: returns the unique ProteomeXchange identifier.
- **pxref** `signature(object = "PXDataset")`: returns the reference associcated with the `object`.
- **pxtax** `signature(object = "PXDataset")`: returns the scientic taxonomic name of `object`.
- **pxurl** `signature(object = "PXDataset"`: returns the base url on the ProteomeXchange server where `pxfiles(object)` reside.
- **show** `signature(object = "PXDataset")`: textual representation of `object`.

Author(s)

Laurent Gatto

References

Vizcaino J.A. et al. 'ProteomeXchange: globally co-ordinated proteomics data submission and dissemination', Nature Biotechnology 2014, 32, 223 – 226, doi:10.1038/nbt.2839.

Source repository for the ProteomeXchange project: https://code.google.com/p/proteomexchange/

Examples

```
px <- PXDataset("PXD000001")
px
pxtax(px)
pxurl(px)
pxref(px)
pxfiles(px)
fnm <- pxget(px, "PXD000001_mztab.txt")
library("MSnbase")
readMzTabData(fnm, "PEP")
unlink("PXD000001_mztab.txt")
```

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