

Package ‘rpx’

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Type Package

Title R Interface to the ProteomeXchange Repository

Version 1.14.0

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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 Proteomics, MassSpectrometry, DataImport, ThirdPartyClient

RoxygenNote 5.0.1

NeedsCompilation no

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pxannounced	<i>Return recent PX announcements</i>
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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 announcement messages.

Author(s)

Laurent Gatto

Examples

```
pxannounced()
```

PXDataset-class	Class "PXDataset"
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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/teomex/>

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.

pxid signature(object = "PXDataset"): returns the unique ProteomeXchange identifier.

pxref signature(object = "PXDataset"): returns the reference associated with the object.

pxtax signature(object = "PXDataset"): returns the scientific 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 <lg390@cam.ac.uk>

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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