

Package ‘rpx’

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Type Package

Title R Interface to the ProteomeXchange Repository

Version 1.26.2

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

Depends methods

Imports BiocFileCache, rappdirs, xml2, RCurl, utils

Suggests 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	2
PXDataset-class	2

Index	4
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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	<i>Class "PXDataset"</i>
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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.

Details

From version 1.99.1 on, rpx uses the Bioconductor BiocFileCache package to automatically cache all downloaded ProteomeXchange files. When a file is downloaded for the first time, it is added to the cache. When already available, the file path to the cached file is returned. The rpx cache is returned by `rpx:::get_cache()`. The user is asked to confirm its creation when data is first downloaded.

For more details on how to manage the cache (for example if some files need to be deleted), please refer to the BiocFileCache vignette.

Methods

- pxfiles** signature(object = "PXDataset"): return a character of all available files.
- pxget** signature(object = "PXDataset", list, ...): 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.
If not already cached, the files are downloaded and added to the package cache. The function then returns the names of the files in the cache directory.
- 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

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)

fas <- pxget(px, "erwinia_carotovora.fasta")
fas
library("Biostrings")
readAAStringSet(fas)
```

Index

* classes

PXDataset-class, [2](#)

class:PXDataset (PXDataset-class), [2](#)

pxannounced, [2](#)

PXDataset (PXDataset-class), [2](#)

PXDataset-class, [2](#)

pxfiles (PXDataset-class), [2](#)

pxfiles, PXDataset-method
(PXDataset-class), [2](#)

pxget (PXDataset-class), [2](#)

pxget, PXDataset-method
(PXDataset-class), [2](#)

pxid (PXDataset-class), [2](#)

pxid, PXDataset-method
(PXDataset-class), [2](#)

pxref (PXDataset-class), [2](#)

pxref, PXDataset-method
(PXDataset-class), [2](#)

pntax (PXDataset-class), [2](#)

pntax, PXDataset-method
(PXDataset-class), [2](#)

pxurl (PXDataset-class), [2](#)

pxurl, PXDataset-method
(PXDataset-class), [2](#)

show, PXDataset-method

(PXDataset-class), [2](#)