

Package ‘rpx’

October 12, 2016

Type Package

Title R Interface to the ProteomeXchange Repository

Version 1.8.3

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

Depends methods

Imports XML, 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

R topics documented:

pxannounced	2
PXDataset-class	2
pxnodes	4
Index	5

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/proteomexchange/>

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, ...): 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 in the working directory. Unless force is set to TRUE, files are not downloaded if already present in the working 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")
```

pxnodes	<i>Return the nodes of a PXDataset</i>
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Description

Returns the node names of the underlying XML content of an PXDataset object, available in the Data slot. This function is meant to be used if additional parsing of the XML structure is needed.

Usage

```
pxnodes(pxdata, name, all = FALSE)
```

Arguments

pxdata	An instance of class PXDataset.
name	The name of a node.
all	Should node from all levels be returned. Default is FALSE.

Value

A character with XML node names.

Author(s)

Laurent Gatto

Index

*Topic **classes**

PXDataset-class, [2](#)

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

download.file, [3](#)

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](#)

pxnodes, [4](#)

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](#)