

# 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** Immunology, Proteomics, MassSpectrometry, DataImport, ThirdPartyClient

**RoxygenNote** 6.1.0

**git\_url** <https://git.bioconductor.org/packages/rpx>

**git\_branch** RELEASE\_3\_10

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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()
```

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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/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 `capabilities("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 associated with the object.

**pntax** 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
pntax(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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