

# Package ‘rpx’

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**Type** Package

**Title** R Interface to the ProteomeXchange Repository

**Version** 1.2.0

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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, BiocGenerics, RUnit, knitr

**License** GPL-2

**VignetteBuilder** knitr

**biocViews** Proteomics, MassSpectrometry, DataImport, ThirdPartyClient

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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	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/teomexchan>

**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")
```

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