

# Package ‘ProteomicsAnnotationHubData’

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**Title** Transform public proteomics data resources into Bioconductor  
Data Structures

**Version** 1.16.0

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**Description** These recipes convert a variety and a growing number of  
public proteomics data sets into easily-used standard  
Bioconductor data structures.

**Depends** AnnotationHub (>= 2.1.45), AnnotationHubData,

**Imports** mzR (>= 2.3.2), MSnbase, Biostrings, GenomeInfoDb, utils,  
Biobase, BiocManager, RCurl

**Suggests** knitr, BiocStyle, rmarkdown, testthat

**biocViews** DataImport, Proteomics

**VignetteBuilder** knitr

**License** Artistic-2.0

**URL** <https://github.com/lgatto/ProteomicsAnnotationHubData>

**BugReports** <https://github.com/lgatto/ProteomicsAnnotationHubData/issues>

**Collate** ProteomicsAnnotationHubData.R utils.R PAHD.R zzz.R

**RoxygenNote** 5.0.1

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

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identicalRemLoc	<i>Are the remote and local instances identical</i>
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**Description**

This function compares the metadata of a remote object `rem` available on AnnotationHub and a local PAHD object. If these are identical, TRUE is returned, FALSE otherwise.

**Usage**

```
identicalRemLoc(rem, loc)
```

**Arguments**

<code>rem</code>	An instance of class AnnotationHub
<code>loc</code>	An instance of class AnnotationHubMetadata

**Value**

A logical

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makeAnnotationHubMetadata	<i>Make an AnnotationHubMeta resource</i>
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**Description**

Takes a list of PAHD instances and returns a subset matching the requested resource.

**Usage**

```
makeAnnotationHubMetadata(x, resource = proteomicsAnnotationHubDataResources)
```

**Arguments**

<code>x</code>	A list of PAHD instances.
<code>resource</code>	A character of length 1 with the desired resource. See <code>proteomicsAnnotationHubDataResources</code> for a list of available resources.

**Value**

A list of PAHD instances, matching resource.

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 PAHD

*Prepare data for inclusion into AnnotationHub*


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### Description

Reads ProteomicsAnnotationHubData dcf files and prepares them for inclusion into AnnotationHub. See ProteomicsAnnotationDataHub{ } for details and an example.

### Usage

```
PAHD(x, resourceDir)
```

### Arguments

x	One of multiple ProteomicsAnnotationHubData dcf files.
resourceDir	A character containing the directory holding the files (for instance PRIDE). If missing, will be inferred from the first RDataPath field of x.

### Details

Note: Current limitation is that all the files are expected to reside in a single resource directory.

### Value

A list of PAHD objects that can be used to prepare and submit data to AnnotationHub. See ProteomicsAnnotationHub() for details.

### Author(s)

```
Laurent Gatto ## example file for the PXD000001 data f <- list.files(system.file("extdata", package
= "ProteomicsAnnotationHubData"), full.names = TRUE) PXD000001 <- PAHD(f) length(PXD000001)
PXD000001[[1]]
```

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 PAHD-class

*An S4 class for ProteomicsAnnotationHubData objects*


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### Description

This class is a simple temporary container that extends the AnnotationHubMetadata. Please read that documentation for details. This class is likely to evolve in the future. See [PAHD](#) for to construct these objects from dcf files.

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ProteomicsAnnotationHubData

*Get started with ProteomicsAnnotationHubData*

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### Description

Read the ProteomicsAnnotationHubData vignette to get started with using Proteomics data from AnnotationHub and writing new recipes. Use availableProteomicsAnnotationHubData() to get a vector of available experiments. Use proteomicsAnnotationHubDataResources() to get a vector of available resources.

### Usage

```
ProteomicsAnnotationHubData()
```

```
availableProteomicsAnnotationHubData
```

```
proteomicsAnnotationHubDataResources
```

### Format

An object of class character of length 1.

### Value

Used for its side-effect of opening the package vignette. A vector of experiment identifiers.

### Author(s)

Laurent Gatto

### Examples

```
availableProteomicsAnnotationHubData
```

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readPahdFiles

*Reads one or multiple PAHD template files*

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### Description

Reads one or multiple ProteomicsAnnotationHubData dcf files into a matrix that can be processed with PAHD. Comment lines starting with # will be removed. See ProteomicsAnnotationDataHub() for details.

### Usage

```
readPahdFiles(file)
```

### Arguments

file            A character with one of multiple file names.

**Value**

A matrix containing

**Author(s)**

Laurent Gatto

**Examples**

```
## example file for the PXD000001 data
f <- list.files(system.file("extdata", package = "ProteomicsAnnotationHubData"),
               full.names = TRUE, pattern = "PXD000001.dcf")
readPahdFiles(f)
```

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writePahdTemplate	<i>Write a ProteomicsAnnotationHubData template</i>
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**Description**

Writes a simple template in dcf format (like an R package DESCRIPTION file) that, once completed (see `ProteomicsAnnotationHub()` for details), can be imported with [readPahdFiles](#) or directly processed with [PAHD](#). Note that these dcf files support comments (as opposed to DESCRIPTION files). Lines starting with # will be removed when parsed by [readPahdFiles](#).

**Usage**

```
writePahdTemplate(filename = "")
```

**Arguments**

filename	The name of the file to write the template in. Default is "", i.e. write output to the console.
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**Value**

Use for its side effect of preparing a annotation template.

**Author(s)**

Laurent Gatto <lg390@cam.ac.uk>

**Examples**

```
writePahdTemplate()
```

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