

Package ‘biodbExpasy’

March 31, 2023

Title biodbExpasy, a library for connecting to Expasy ENZYME database.

Version 1.2.0

Description The biodbExpasy library provides access to Expasy ENZYME database, using biodb package framework. It allows to retrieve entries by their accession number. Web services can be accessed for searching the database by name or comments.

License AGPL-3

biocViews Software, Infrastructure, DataImport

VignetteBuilder knitr

Encoding UTF-8

Depends R (>= 4.1)

Imports biodb (>= 1.3.1), R6, stringr, chk

Suggests roxygen2, BiocStyle, testthat (>= 2.0.0), devtools, knitr, rmarkdown, covr, lgr

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.2

Collate 'ExpasyEnzymeConn.R' 'ExpasyEnzymeEntry.R' 'package.R'

git_url <https://git.bioconductor.org/packages/biodbExpasy>

git_branch RELEASE_3_16

git_last_commit ef6c7ee

git_last_commit_date 2022-11-01

Date/Publication 2023-03-31

Author Pierrick Roger [aut, cre] (<<https://orcid.org/0000-0001-8177-4873>>)

Maintainer Pierrick Roger <pierrick.roger@cea.fr>

R topics documented:

biodbExpasy-package	2
ExpasyEnzymeConn	2
ExpasyEnzymeEntry	4

Index**6**

biodbExpasy-package	<i>biodbExpasy: biodbExpasy, a library for connecting to Expasy ENZYME database.</i>
---------------------	--

Description

The biodbExpasy library provides access to Expasy ENZYME database, using biodb package framework. It allows to retrieve entries by their accession number. Web services can be accessed for searching the database by name or comments.

Details

See vignette biodbExpasy:

```
vignette('biodbExpasy', package='biodbExpasy')
```

Author(s)

Maintainer: Pierrick Roger <pierrick.roger@cea.fr> ([ORCID](#))

See Also

[ExpasyEnzymeConn](#).

ExpasyEnzymeConn	<i>Expasy ENZYME database. connector class.</i>
------------------	---

Description

Expasy ENZYME database. connector class.

Expasy ENZYME database. connector class.

Details

Connector class for Expasy ENZYME database.

This is a concrete connector class. It must never be instantiated directly, but instead be instantiated through the factory [BiodbFactory](#). Only specific methods are described here. See super classes for the description of inherited methods.

Super classes

[biodb::BiodbConnBase](#) -> [biodb::BiodbConn](#) -> ExpasyEnzymeConn

Methods

Public methods:

- [ExpasyEnzymeConn\\$new\(\)](#)
- [ExpasyEnzymeConn\\$wsEnzymeByName\(\)](#)
- [ExpasyEnzymeConn\\$wsEnzymeByComment\(\)](#)
- [ExpasyEnzymeConn\\$clone\(\)](#)

Method `new()`: New instance initializer. Connector classes must not be instantiated directly. Instead, you must use the `createConn()` method of the factory class.

Usage:

```
ExpasyEnzymeConn$new(...)
```

Arguments:

... All parameters are passed to the super class initializer.

Returns: Nothing.

Method `wsEnzymeByName()`: Calls enzyme-byname web service and returns the HTML result. See <http://enzyme.expasy.org/enzyme-byname.html>.

Usage:

```
ExpasyEnzymeConn$wsEnzymeByName(  
  name,  
  retfmt = c("plain", "request", "parsed", "ids")  
)
```

Arguments:

`name` The name to search for.

`retfmt` The format to use for the returned value. 'plain' will return the raw result from the server, as a character value. 'request' will return a `BiodbRequest` instance containing the request as it would have been sent. 'parsed' will return an XML object, containing the parsed result. 'ids' will return a character vector containing the IDs of the matching entries.

Returns: Depending on `retfmt`.

Method `wsEnzymeByComment()`: Calls enzyme-bycomment web service and returns the HTML result. See <http://enzyme.expasy.org/enzyme-bycomment.html>.

Usage:

```
ExpasyEnzymeConn$wsEnzymeByComment(  
  comment,  
  retfmt = c("plain", "request", "parsed", "ids")  
)
```

Arguments:

`comment` The comment to search for.

`retfmt` The format to use for the returned value. 'plain' will return the raw result from the server, as a character value. 'request' will return a `BiodbRequest` instance containing the request as it would have been sent. 'parsed' will return an XML object, containing the parsed result. 'ids' will return a character vector containing the IDs of the matching entries.

Returns: Depending on retfmt.

Method clone(): The objects of this class are cloneable with this method.

Usage:

```
ExpasyEnzymeConn$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

See Also

[BiodbConn](#).

Examples

```
# Create an instance with default settings:
mybiodb <- biodb::newInst()

# Get a connector:
conn <- mybiodb$getFactory()$createConn('expasy.enzyme')

# Get the first entry
e <- conn$getEntry('1.1.1.1')

# Terminate instance.
mybiodb$terminate()
```

ExpasyEnzymeEntry	<i>Expasy ENZYME database. entry class.</i>
-------------------	---

Description

Entry class for Expasy ENZYME database.

Super classes

[biodb::BiodbEntry](#) -> [biodb::BiodbTxtEntry](#) -> ExpasyEnzymeEntry

Methods

Public methods:

- [ExpasyEnzymeEntry\\$clone\(\)](#)

Method clone(): The objects of this class are cloneable with this method.

Usage:

```
ExpasyEnzymeEntry$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

See Also[BiodbTxtEntry](#).**Examples**

```
# Create an instance with default settings:
mybiodb <- biodb::newInst()

# Get a connector that inherits from ExpasyEnzymeConn:
conn <- mybiodb$getFactory()$createConn('expasy.enzyme')

# Get the first entry
e <- conn$getEntry('1.1.1.1')

# Terminate instance.
mybiodb$terminate()
```

Index

`biodb::BiodbConn`, [2](#)
`biodb::BiodbConnBase`, [2](#)
`biodb::BiodbEntry`, [4](#)
`biodb::BiodbTxtEntry`, [4](#)
`BiodbConn`, [4](#)
`biodbExpasy` (`biodbExpasy-package`), [2](#)
`biodbExpasy-package`, [2](#)
`BiodbFactory`, [2](#)
`BiodbTxtEntry`, [5](#)

`ExpasyEnzymeConn`, [2](#), [2](#)
`ExpasyEnzymeEntry`, [4](#)