Package ‘biodbExpasy’

May 9, 2024

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

**Version**  1.8.0

**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'

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biodbExpasy-package  biodbExpasy: biodbExpasy, a library for connecting to Expasy ENZYME database.

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)
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See Also
ExpasyEnzymeConn.

ExpasyEnzymeConn  Expasy ENZYME database. connector class.

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**:

```r
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**:

```r
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**:

```r
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.
ExpasyEnzymeEntry

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 Expasy ENZYME database. entry class.

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()
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