Package ‘biodbMirbase’

July 14, 2023

Title biodbMirbase, a library for connecting to miRBase mature database

Version 1.5.0

Description The biodbMirbase library is an extension of the biodb framework package, that provides access to miRBase mature database. It allows to retrieve entries by their accession number, and run specific web services.

Description: The biodbMirbase library provides access to the miRBase Database, using biodb package framework.

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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)

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Collate 'MirbaseMatureConn.R' 'MirbaseMatureEntry.R' 'package.R'

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`biodbMirbase-package`  
*biodbMirbase: biodbMirbase, a library for connecting to miRBase mature database*

**Description**

The `biodbMirbase` library is an extension of the `biodb` framework package, that provides access to miRBase mature database. It allows to retrieve entries by their accession number, and run specific web services. **Description:** The `biodbMirbase` library provides access to the miRBase Database, using `biodb` package framework.

**Details**

See vignette `biodbMirbase`:

```r
vignette('biodbMirbase', package='biodbMirbase')
```

**Author(s)**

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**See Also**

- `MirbaseMatureConn`

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`MirbaseMatureConn`  
*miRBase mature database connector class.*

**Description**

Connector class for miRBase mature database.

**Super classes**

`biodb::BiodbConnBase` -> `biodb::BiodbConn` -> `MirbaseMatureConn`
MirbaseMatureEntry

Methods

Public methods:

• MirbaseMatureConn$clone()

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

Usage:
MirbaseMatureConn$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('mirbase.mature')

# Get the first entry
e <- conn$getEntry('MIMAT0000433')

# Terminate instance.
mybiodb$terminate()
Usage:
MirbaseMatureEntry$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 MirbaseMatureConn:
conn <- mybiodb$getFactory()$createConn('mirbase.mature')

# Get the first entry
e <- conn$getEntry('MIMAT0000433')

# Terminate instance.
mybiodb$terminate()
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