

Package ‘biodbMirbase’

April 7, 2023

Title biodbMirbase, a library for connecting to miRBase mature database

Version 1.2.2

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

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biodbMirbase-package	<i>biodbMirbase: biodbMirbase, a library for connecting to miRBase mature database</i>
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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:

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

Author(s)

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See Also

[MirbaseMatureConn](#).

MirbaseMatureConn	<i>miRBase mature database connector class.</i>
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Description

Connector class for miRBase mature database.

Super classes

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

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()
```

MirbaseMatureEntry *miRBase mature database entry class.*

Description

Entry class for miRBase mature database.

Super classes

```
biodb::BiodbEntry -> biodb::BiodbTxtEntry -> MirbaseMatureEntry
```

Methods

Public methods:

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

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

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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