

Package ‘BridgeDbR’

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Type Package

Title Code for using BridgeDb identifier mapping framework from within R

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Depends R (>= 3.3.0), rJava

Imports RCurl

Suggests testthat

Description Use BridgeDb functions and load identifier mapping databases in R

biocViews Software, Annotation

License AGPL-3

LazyLoad yes

URL <https://github.com/bridgedb/BridgeDb>,
<https://github.com/BiGCAT-UM/bridgedb-r>

BugReports <https://github.com/BiGCAT-UM/bridgedb-r/issues>

NeedsCompilation no

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BridgeDbR-package	<i>BridgeDBR Package.</i>
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Description

R package for using BridgeDB directly from R.

Author(s)

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getBridgeNames	<i>Method to list the BridgeDb identifier mapping file names as available from the download site.</i>
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Description

This method returns a list of file names of BridgeDb identifier mapping files as they are available from the mapping file download site. The optional code parameter can be used to restrict the list to a specific organism.

Usage

```
getBridgeNames(code, website, pattern)
```

Arguments

code	the organism code
website	optional parameter that allows you to provide a different location to download BridgeDb Derby files from.
pattern	optional parameter to change the filename pattern of the BridgeDb Derby files.

Value

list	the list of available BridgeDb mapping files
------	--

Author(s)

Egon Willighagen Christ Leemans

Examples

```
files <- getBridgeNames("Hs")
## Not run:
prereleases <- getBridgeNames(
  website="http://bridgedb.org/data/gene_database/pre-release/",
  pattern="metabolites_\\d*.bridge"
)
## End(Not run)
```

getDatabase	<i>Downloads a identifier mapping database for the given organism.</i>
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Description

Downloads a identifier mapping database for the given organism. The optional location parameter can be used to indicate where the file should be stored. If not give, it will save it in a temporary folder.

Usage

```
getDatabase(organism, location)
```

Arguments

organism	the organism name
location	optional parameter to indicate where the database should be saved

Value

location	the location where the database was saved
----------	---

Author(s)

Egon Willighagen Christ Leemans

Examples

```
location <- getDatabase("Mycobacterium tuberculosis")  
## Not run: location <- getDatabase("Homo sapiens")
```

getDataSource	<i>Return a DataSource object based on either a name or system code.</i>
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Description

Return a DataSource object based on either a name or system code.

Usage

```
getDataSource(name, code)
```

Arguments

name	the name of the data source
code	the system code of the data source

Value

dataSource	a DataSource Java object
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Author(s)

Egon Willighagen

Examples

```
dataSource <- getDataSource(code="Ce")
```

getFullName	<i>Return the name of a particular data source.</i>
-------------	---

Description

Data sources are defined by a title and a short system code. This method converts a system code into a full name.

Usage

```
getFullName(syscode)
```

Arguments

syscode the system code of the data source

Value

systemCode the full name of the data source

Author(s)

Egon Willighagen Christ Leemans

Examples

```
name <- getFullName("Ce")
```

getMatchingSources	<i>Return a list of data sources of which the identifier pattern matches the identifier given.</i>
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Description

This method runs through all data sources it knows about, and looks for sources of which the identifier pattern matches the given identifier.

Usage

```
getMatchingSources(identifier)
```

Arguments

identifier identifier to test

Value

list list of matching data sources

Author(s)

Egon Willighagen Christ Leemans

Examples

```
list <- getMatchingSources("555")
```

`getOrganismCode` *Return the code of a particular organism.*

Description

This method converts a organism latin name into a code.

Usage

```
getOrganismCode(name)
```

Arguments

name latin name of an organism

Value

systemCode the code of the organism

Author(s)

Egon Willighagen Christ Leemans

Examples

```
systemCode <- getOrganismCode("Mus musculus")
```

getSystemCode	<i>Return the system code of a particular data source.</i>
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Description

Data sources are defined by a title and a short system code. This method converts a name into a system code.

Usage

```
getSystemCode(name)
```

Arguments

name	name of the data source
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Value

systemCode	the system code of the data source
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Author(s)

Egon Willighagen Christ Leemans

Examples

```
systemCode <- getSystemCode("ChEBI")
```

loadDatabase	<i>Loads a BridgeDb identifier mapping database (.bridge file) as an IDMapper Java-Object.</i>
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Description

Loads a BridgeDb identifier mapping database (.bridge file) as an IDMapper Java-Object.

Usage

```
loadDatabase(location)
```

Arguments

location	location on the hard disk of the BridgeDb file
----------	--

Details

The return Java-Object is a Java class implementing the BridgeDb IDMapper interface. It is the required mapper class that is used as input for other methods that need an IDMapper.

Value

mapper an IDMapper object

Author(s)

Egon Willighagen

Examples

```
location <- getDatabase("Mycobacterium tuberculosis")
mapper <- loadDatabase(location)
```

map	<i>Converts one identifier into other identifiers for the given target data source.</i>
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Description

Converts one identifier into other identifiers for the given target data source.

Usage

```
map(mapper, source, identifier, target)
```

Arguments

mapper	loaded BridgeDb identifier mapper
source	system code of the data source
identifier	identifier to be converted
target	system code of the target data source (optional)

Value

mappings a vector of mapped identifiers for the target data source

Author(s)

Egon Willighagen

Examples

```
location <- getDatabase("Mycobacterium tuberculosis")
mapper <- loadDatabase(location)
map(mapper, "L", "885041", "X")
map(mapper, "L", "885041")
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