# 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** curl

**VignetteBuilder** knitr

**Suggests** BiocStyle, knitr, rmarkdown, testthat

**Description** Use BridgeDb functions and load identifier mapping databases in R. It uses GitHub, Zenodo, and Figshare if you use this package to download identifier mappings files.

**biocViews** Software, Annotation, Metabolomics, Cheminformatics

**License** AGPL-3

**LazyLoad** yes

**URL** https://github.com/bridgedb/BridgeDbR

**BugReports** https://github.com/bridgedb/BridgeDbR/issues

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`BridgeDbR-package` *BridgeDbR Package.*

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## Description

R package for using BridgeDb directly from R.

## Author(s)

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`fullNameExists` *Determines if the full name corresponds to any known data source.*

---

## Description

Data sources are defined by a title and a short system code. This method determines if a data source is known with the given full name.

## Usage

```
fullNameExists(name)
```

### Arguments

| | |
|---|---|
| name | full name of the data source |

### Value

| | |
|---|---|
| exists | boolean that indicates if a data is known with the given name |

### Author(s)

Egon Willighagen

### Examples

```
exists <- fullNameExists("HMDB")
```

---

## getAttributes *Returns the attributes of the given identifier.*

---

### Description

Returns the attributes of the given identifier.

### Usage

```
getAttributes(mapper, source, identifier)
```

### Arguments

| | |
|---|---|
| mapper | loaded BridgeDb identifier mapper |
| source | system code of the data source |
| identifier | identifier to return the attributes for |

### Value

| | |
|---|---|
| mappings | a vector of attributes |

### Author(s)

Egon Willighagen

### Examples

```
## Not run:
location <- getDatabase("Homo sapiens")
mapper <- loadDatabase(location)
getAttributes(mapper, "L", "672")

## End(Not run)
```

`getBridgeNames` *Method to list the BridgeDb identifier mapping file names as available from the download site.*

## 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.

Occassionally, the ID mapping file download website changes the pattern of the file names. In that case, you can provide an alternative filename pattern to recognize files on the download site.

This method uses data from https://bridgedb.github.io/data/gene_database/.

## 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 *Downloads a identifier mapping database for the given organism.*

## 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.

This method extracts links from https://bridgedb.github.io/data/gene_database/ to identifier mapping databases hosted on Zenodo and Figshare, two public data archives.

## Usage

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

## Arguments

| | |
|---|---|
| organism | the organism name |
| location | optional parameter to indicate where the database should be saved |
| website | optional URL of the server where to look for BridgeDb identifier mapping databases |

## Value

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

## Author(s)

Egon Willighagen Christ Leemans

## Examples

```
## Not run: location <- getDatabase("Bacillus subtilis")
## Not run: location <- getDatabase("Homo sapiens")
```

getDataSource *Return a DataSource object based on either a name, Bioregistry.io prefix, or system code.*

## Description

Return a DataSource object based on either a name, Bioregistry.io prefix, or system code.

## Usage

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

### Arguments

| | |
|---|---|
| name | the name of the data source |
| code | the system code of the data source |
| prefix | the Bioregistry.io prefix of the data source |

### Value

| | |
|---|---|
| dataSource | a DataSource Java object |

### Author(s)

Egon Willighagen

### Examples

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

---

## getFullName *Return the name of a particular data source.*

---

### 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` *Return a list of data sources of which the identifier pattern matches the identifier given.*

## 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")
```

---

`getProperties` *BridgeDb database properties.*

---

## Description

Gets the properties of an BridgeDb ID mapping database.

## Usage

```
getProperties(mapper)
```

## Arguments

| | |
|---|---|
| `mapper` | loaded BridgeDb identifier mapper |

## Value

| | |
|---|---|
| `properties` | a data frame with the properties |

## Author(s)

Egon Willighagen

## Examples

```
## Not run:
location <- getDatabase("Bacillus subtilis")
mapper <- loadDatabase(location)
getProperties(mapper)

## End(Not run)
```

`getSystemCode` *Return the system code of a particular data source.*

## 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 |

## Value

| | |
|---|---|
| `systemCode` | the system code of the data source |

## Author(s)

Egon Willighagen Christ Leemans

## Examples

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

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

## 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

```
## Not run:
location <- getDatabase("Bacillus subtilis")
mapper <- loadDatabase(location)

## End(Not run)
```

---

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

---

## Description

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

## Usage

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

## 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) |
| compactIdentifier | the Bioregistry.io compact identifier to convert |

## Value

| | |
|---|---|
| mappings | a data frame of mapped identifiers for the target data source |

## Author(s)

Egon Willighagen

## Examples

```
## Not run:
location <- getDatabase("Bacillus subtilis")
mapper <- loadDatabase(location)
map(mapper, "En", "BSn5_00025", "S")
map(mapper, "En", "BSn5_00025")
location <- getDatabase("Homo sapiens")
mapper <- loadDatabase(location)
map(mapper, "En", "ENSG00000139618")
map(mapper, compactIdentifier="uniprot:P51587")

## End(Not run)
```

---

`maps` *Converts multiple identifiers into other identifiers for the given target data source.*

---

## Description

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

## Usage

```
maps(mapper, identifiers, target)
```

## Arguments

| | |
|---|---|
| `mapper` | loaded BridgeDb identifier mapper |
| `identifiers` | data frame with identifiers to be converted, with a source and a identifier column |
| `target` | system code of the target data source (optional) |

## Value

| | |
|---|---|
| `mappings` | a data frame of mapped identifiers for the target data source |

## Author(s)

Egon Willighagen

## Examples

```
## Not run:
location <- getDatabase("Bacillus subtilis")
mapper <- loadDatabase(location)
input = data.frame(
  source= c("L"),
  identifier= c("885041")
)
```

```
maps(mapper,input)

## End(Not run)
```

---

`registerDataSource` *Registers a new DataSource based on the given name or system code.*

---

## Description

Return a DataSource of the newly registered data source, based on either a name or system code.

## Usage

```
registerDataSource(code,name)
```

## Arguments

| | |
|---|---|
| `code` | the system code of the data source |
| `name` | the name of the data source |

## Value

| | |
|---|---|
| `dataSource` | a DataSource Java object |

## Author(s)

Egon Willighagen

## Examples

```
newDataSource <- registerDataSource(code="Cks", name="KNApSAcK")
```

---

`systemCodeExists` *Determines if the system code corresponds to any known data source.*

---

## Description

Data sources are defined by a title and a short system code. This method determines if a data source is known with the given system code.

## Usage

```
systemCodeExists(code)
```

## Arguments

| | |
|---|---|
| `code` | system code of the data source |

### Value

| | |
|---|---|
| exists | boolean that indicates if a data is known with the given system code |

### Author(s)

Egon Willighagen

### Examples

```
exists <- systemCodeExists("Ce")
```

---

## xrefExists *Checks if the given identifier exists*

---

### Description

Checks if the given identifier exists in the given mapping file

### Usage

```
xrefExists(mapper, source, identifier, compactIdentifier)
```

### Arguments

| | |
|---|---|
| mapper | loaded BridgeDb identifier mapper |
| source | system code of the data source |
| identifier | identifier to be searched |
| compactIdentifier | the Bioregistry.io compact identifier to check |

### Value

| | |
|---|---|
| boolean | true, if the given identifier is found in the mapping database |

### Author(s)

Egon Willighagen

### Examples

```
## Not run:
location <- getDatabase("Bacillus subtilis")
mapper <- loadDatabase(location)
xrefExists(mapper, "L", "885041")
xrefExists(mapper, compactIdentifier="ncbigene:885041")

## End(Not run)
```

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