

# 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>

**git\_url** <https://git.bioconductor.org/packages/BridgeDbR>

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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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fullNameExists	<i>Determines if the full name corresponds to any known data source.</i>
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### 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	<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.

Occasionally, 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/](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
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### 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.

This method extracts links from [https://bridgedb.github.io/data/gene\\_database/](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	<i>Return a DataSource object based on either a name, Bioregistry.io prefix, or system code.</i>
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---

**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
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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
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**Value**

systemCode	the full name of the data source
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**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	<i>BridgeDb database properties.</i>
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**Description**

Gets the properties of an BridgeDb ID mapping database.

**Usage**

```
getProperties(mapper)
```

**Arguments**

mapper	loaded BridgeDb identifier mapper
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**Value**

properties	a data frame with the properties
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**Author(s)**

Egon Willighagen

**Examples**

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



---

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
------	-------------------------

**Value**

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

**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**

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

## End(Not run)
```

---

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

---

**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	<i>Converts multiple identifiers into other identifiers for the given target data source.</i>
------	---

---

**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>code</code>	the system code of the data source
<code>name</code>	the name of the data source

**Value**

<code>dataSource</code>	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>code</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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