

# Package ‘LRBaseDbi’

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**Title** DBI to construct LRBase-related package

**Description** Interface to construct LRBase package (LRBase.XXX.eg.db).

**Version** 2.0.0

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**Suggests** RUnit, BiocGenerics, BiocStyle

**VignetteBuilder** utils

**biocViews** Infrastructure

**License** Artistic-2.0

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columns	<i>A function to return the columns of LRBase that user can retrieve</i>
---------	--

---

**Description**

This function returns the columns of LRBase that user can retrieve.

**Usage**

```
columns(x)
```

**Arguments**

x                   LRBaseDb object such as LRBase.Mmu.eg.db

**Value**

The columns of sqlite database

**Author(s)**

Koki Tsuyuzaki

**Examples**

```
showMethods("columns")
```

---

dbconn	<i>A function to return the connection to sqlite3 file</i>
--------	--

---

**Description**

This function returns the connection to sqlite file.

**Usage**

```
dbconn(x)
```

**Arguments**

x                   LRBaseDb object such as LRBase.Mmu.eg.db

**Value**

The database connection to sqlite3 file

**Author(s)**

Koki Tsuyuzaki

**Examples**

```
showMethods("dbconn")
```

---

dbfile	<i>A function to return the directory that the sqlite3 file stored</i>
--------	--

---

**Description**

This function returns the directory that the sqlite file stored.

**Usage**

```
dbfile(x)
```

**Arguments**

x                   LRBaseDb object such as LRBase.Mmu.eg.db

**Value**

The directory path to the sqlite3 file

**Author(s)**

Koki Tsuyuzaki

**Examples**

```
showMethods("dbfile")
```

---

dbInfo	<i>A function to return the database information</i>
--------	--

---

**Description**

This function returns the database information, which is METADATA table in sqlite file.

**Usage**

```
dbInfo(x)
```

**Arguments**

x                   LRBaseDb object such as LRBase.Mmu.eg.db

**Value**

The information of LRBase.XXX.eg.db-type package

**Author(s)**

Koki Tsuyuzaki

**Examples**

```
showMethods("dbInfo")
```

---

 dbschema

*A function to return the schema of sqlite-database*


---

**Description**

This function returns the schema of sqlite-database.

**Usage**

```
dbschema(x, file = "", show.indices = FALSE)
```

**Arguments**

x	LRBaseDb object such as LRBase.Mmu.eg.db
file	LRBaseDb file
show.indices	LRBaseDb show.indices

**Value**

The schema for constructing sqlite database file

**Author(s)**

Koki Tsuyuzaki

**Examples**

```
showMethods("dbschema")
```

---

 FANTOM5

*Data to construct user's original LRBaseDb package*


---

**Description**

Correspondance between Ligand Entrez Gene ID and Receptor Entrez Gene ID of FANTOM5 project used for demo data. This is to demonstrate how to construct user's original LRBaseDb package.

**Usage**

```
data(FANTOM5)
```

**Details**

- 1st Column: Ligand Entrez gene ID
- 2nd Column: Receptor Entrez gene ID
- 3rd Column: Source ID. In this case, PMID is used.
- 4th Column: Source Database. In this case, FANTOM5

**Value**

The test data is loaded

**Examples**

```
data(FANTOM5)
head(FANTOM5)
```

---

keys

*A function defined by AnnotationDbi to return the keys*

---

**Description**

This function returns the keys.

**Usage**

```
keys(x, keytype, ...)
```

**Arguments**

x	LRBaseDb object such as LRBase.Mmu.eg.db
keytype	LRBaseDb What kind of key user want to specify
...	LRBaseDb Other parameter

**Value**

The keys for using select functions

**Author(s)**

Koki Tsuyuzaki

**Examples**

```
showMethods("keys")
```

---

keytypes	<i>A function to return the columns that user can specified in select function</i>
----------	--

---

### Description

This function returns the columns that user can specified in select function.

### Usage

```
keytypes(x)
```

### Arguments

x                      LRBaseDb object such as LRBase.Mmu.eg.db

### Value

The columns that user can specify as key

### Author(s)

Koki Tsuyuzaki

### Examples

```
showMethods("keytypes")
```

---

LRBaseDb-class	<i>LRBaseDb objects</i>
----------------	-------------------------

---

### Description

LRBaseDb is the simple class for providing the relationship between Entrez gene IDs and LRBase IDs. It provides the database connection and easily accessible with columns, keytypes, keys and select. Some users may use additional functions such as dbconn, dbfile, dbschema, dbInfo, and species for much complex data acquisition.

columns shows which kinds of data can be returned for the LRBaseDb object.

keytypes allows the user to discover which keytypes can be passed in to select or keys and the keytype argument.

keys returns keys for the database contained in the LRBaseDb object . This method is already documented in the keys manual page but is mentioned again here because it's usage with select is so intimate. By default it will return the primary keys for the database, but if used with the keytype argument, it will return the keys from that keytype.

select will retrieve the data as a data.frame based on parameters for selected keys, columns, and keytype arguments.

dbconn returns the connection with database in the package.

dbfile returns the absolute path sqlite file is saved.

dbschema returns the database schema.

dbInfo returns the many meta information about the package.

species returns the species name.

### Usage

```
LRBaseDb
```

### Arguments

LRBaseDb            the LRBaseDb object. But in practice this will mean an object derived from an LRBaseDb object such as a LRBase.Hsa.eg.db, LRBase.Mmu.eg.db or many other LRBase.XXX.eg.db (XXX means abbreviation of species name).

### Value

the LRBaseDb object

### Author(s)

Koki Tsuyuzaki

### See Also

[dbConnect](#)

### Examples

```
ls("package:LRBaseDbi")
```

---

lrListDatabases

*A function to return the list of databases used in the package*

---

### Description

This function returns the list of databases used in the package.

### Usage

```
lrListDatabases(x)
```

### Arguments

x                    LRBaseDb object such as LRBase.Mmu.eg.db

### Value

The list of source databases

### Author(s)

Koki Tsuyuzaki

**Examples**

```
showMethods("lrListDatabases")
```

---

lrNomenclature	<i>A function to return the scientific name</i>
----------------	---

---

**Description**

This function returns the scientific name of species used in the package.

**Usage**

```
lrNomenclature(x)
```

**Arguments**

x                      LRBaseDb object such as LRBase.Mmu.eg.db

**Value**

The scientific name of organisms

**Author(s)**

Koki Tsuyuzaki

**Examples**

```
showMethods("lrNomenclature")
```

---

lrPackageName	<i>A function to return the package name</i>
---------------	--

---

**Description**

This function returns the package name

**Usage**

```
lrPackageName(x)
```

**Arguments**

x                      LRBaseDb object such as LRBase.Mmu.eg.db

**Value**

The name of LRBase.XXX.eg.db-type package



**Author(s)**

Koki Tsuyuzaki

**Examples**

```
showMethods("lrPackageName")
```

---

lrVersion

*A function to return the LRBase version of package*


---

**Description**

This function returns the version of LRBase used in the package.

**Usage**

```
lrVersion(x)
```

**Arguments**

x                   LRBaseDb object such as LRBase.Mmu.eg.db

**Value**

The version of LR database

**Author(s)**

Koki Tsuyuzaki

**Examples**

```
showMethods("lrVersion")
```

---

makeLRBasePackage

*Making LRBaseDb packages from corresponding table as single data frame.*


---

**Description**

makeLRBasePackage is a method that generates a package that will load an appropriate LRBaseDb object that will in turn point to existing annotation packages.

**Usage**

```
makeLRBasePackage(pkgname, data, metadata, organism,
  pkgtitle="An annotation package for the LRBaseDb object",
  pkgdescription=paste("Contains the LRBaseDb object",
    "to access data from several related annotation packages."),
  version, maintainer, author, destDir, license="Artistic-2.0")
```

**Arguments**

pkgname	The package name. We highly recommend that the name is ABC.XXX.eg.db-type, where ABC is some character and XXX is a abbreviation of organisms such as Hsa: Homo sapiens
data	Data frame contains Ligand GENEID (e.g., 100036770), Receptor GENEID (e.g., 100036770), SOURCEID (PMID), and SOURCEID (e.g., FANTOM5)
metadata	Data frame contains metadata of the package
organism	The name of the organism this package represents
pkgtitle	The title of this package written in DESCRIPTION file
pkgdescription	The description of this package written in DESCRIPTION file
version	The version number of this package
maintainer	The maintainer who creates the package (must include email to be valid)
author	The creator of the package
destDir	A path where the package source should be assembled.
license	The license and it's version

**Details**

The purpose of this method is to create a special package that will depend on existing annotation packages and which will load a special LRBaseDb object that will allow proper dispatch of special select methods. These methods will allow the user to easily query across multiple annotation resources via information contained by the LRBaseDb object. Because the end result will be a package that treats all the data mapped together as a single source, the user is encouraged to take extra care to ensure that the different packages used are from the same build etc.

**Value**

A special package to load an [LRBaseDb](#) object.

**Author(s)**

Koki Tsuyuzaki

**See Also**

[LRBaseDb](#)

**Examples**

```
if(interactive()){
  ## makeLRBasePackage enable users to construct
  ## user's own custom LRBase package
  data(FANTOM5)
  head(FANTOM5)

  # We are also needed to prepare meta data as follows.
  data(metaFANTOM5)
  metaFANTOM5

  ## sets up a temporary directory for this example
  ## (users won't need to do this step)
```

```
tmp <- tempfile()
dir.create(tmp)

## makes an Organism package for human called Homo.sapiens
makeLRBasePackage(pkgname = "FANTOM5.Hsa.eg.db",
  data = FANTOM5,
  metadata = metaFANTOM5,
  organism = "Homo sapiens",
  pkgtitle="An annotation package for the LRBaseDb object",
  pkgdescription=paste("Contains the LRBaseDb object",
    "to access data from several related annotation packages."),
  version = "0.99.0",
  maintainer = "Koki Tsuyuzaki <k.t.the-answer@hotmail.co.jp>",
  author = "Koki Tsuyuzaki",
  destDir = tmp,
  license="Artistic-2.0")
}
```

---

metaFANTOM5

*Metadata to construct user's original LRBaseDb package*

---

## Description

Meta data to construct user's custom LRBaseDb

## Usage

```
data(metaFANTOM5)
```

## Details

- SOURCEDATE: The date the source data is retrived
- SOURCENAME: Type of source data
- SOURCEURL: The URL of source data
- DBSCHEMA: Database schema
- DBSCHEMAVERSION: The version of database schema
- ORGANISM: The scientific name
- SPECIES: The common name of the species
- package: The pacakge name
- Db type: The type of name (or class name)
- LRVERSION: The version for numbering of ligand-receptor data

## Value

The test data is loaded

## Examples

```
data(metaFANTOM5)
head(metaFANTOM5)
```

---

select	<i>select function defined by AnnotationDbi-class</i>
--------	---

---

**Description**

This function returns the corresponding rows that user specified

**Usage**

```
select(x, keys, columns, keytype, ...)
```

**Arguments**

x	LRBaseDb object such as LRBase.Mmu.eg.db
keys	LRBaseDb keys vector
columns	LRBaseDb columns the user want to retrieve
keytype	LRBaseDb What kind of key the user want to specify
...	LRBaseDb Other parameter

**Value**

select function defined by AnnotationDbi package

**Author(s)**

Koki Tsuyuzaki

**Examples**

```
showMethods("select")
```

---

species	<i>A function to return the name of organism</i>
---------	--

---

**Description**

This function returns the name of organism.

**Usage**

```
species(object)
```

**Arguments**

object	LRBaseDb object such as LRBase.Mmu.eg.db
--------	--

**Value**

The common name of organisms

*species*

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**Author(s)**

Koki Tsuyuzaki

**Examples**

```
showMethods("species")
```

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