Package ‘LRBaseDbi’

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Title DBI to construct LRBase-related package

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

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Suggests testthat, BiocStyle, AnnotationHub

VignetteBuilder utils

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Contents

`LRBaseDb-class` *LRBaseDb objects*

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, species, lrNomenclature, lrListDatabases, and lrVersion 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.

lrNomenclature returns the scientific name.

lrListDatabases returns the list of databases to correspond Gene ID of ligend gene and Gene ID of receptor gene.

lrVersion returns the version of LRBaseDb.

Usage

```
columns(x)
keytypes(x)
keys(x, keytype, ...)
select(x, keys, columns, keytype, ...)
dbconn(x)
dbfile(x)
dbschema(x, file = "", show.indices = FALSE)
dbInfo(x)
species(object)
lrNomenclature(x)
lrListDatabases(x)
lrVersion(x)
```

Arguments

x	the LRBaseDb object converted by LRBaseDbi::LRBaseDb.
object	same as x
keys	the keys to select records for from the database. All possible keys are returned by using the keys method.
columns	the columns or kinds of things that can be retrieved from the database. As with keys, all possible columns are returned by using the columns method.

`keytype` the keytype that matches the keys used. For the `select` methods, this is used to indicate the kind of ID being used with the keys argument. For the `keys` method this is used to indicate which kind of keys are desired from `keys`

`...` other arguments.

`file` The `file` argument must be a connection, or a character string naming the file to print to (see the `file` argument of the `cat` function for the details).

`show.indices` The CREATE INDEX statements are not shown by default. Use `show.indices=TRUE` to get them.

Value

`keys`, `columns`, `keytypes`, `dbfile`, `dbInfo`, `species`, and `lrNomenclature` each return a character vector or possible values. `select`, `dbschema`, `lrListDatabases`, and `lrVersion` each return a data.frame. dbconn returns database connection.

Author(s)

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See Also

`dbConnect`

Examples

```
# library("LRBaseDbi")
# library("AnnotationHub")

# # Data retrieval from AnnotationHub
# ah <- AnnotationHub()
# dbfile <- query(ah, c("LRBaseDb", "Sus scrofa", "v001"))[[1]]

# # Constructor
# LRBase.Ssc.eg.db <- LRBaseDbi::LRBaseDb(dbfile)

# # show
# LRBase.Ssc.eg.db

# # dbconn
# dbconn(LRBase.Ssc.eg.db)

# # dbfile
# dbfile(LRBase.Ssc.eg.db)

# # dbschema
# dbschema(LRBase.Ssc.eg.db)

# # dbInfo
# dbInfo(LRBase.Ssc.eg.db)

# # species
# species(LRBase.Ssc.eg.db)

# # lrNomenclature
# lrNomenclature(LRBase.Ssc.eg.db)
# # lrListDatabases
# lrListDatabases(LRBase.Ssc.eg.db)

# # lrVersion
# lrVersion(LRBase.Ssc.eg.db)

# # columns
# cols <- columns(LRBase.Ssc.eg.db)

# # keytypes
# kts <- keytypes(LRBase.Ssc.eg.db)

# # keys
# ks <- keys(LRBase.Ssc.eg.db, keytype="GENEID_L")[seq(10)]

# # select
# out <- select(LRBase.Ssc.eg.db,
#     columns=cols,
#     keys=ks,
#     keytype="GENEID_L")
```

Index