reactome.db

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`reactome.db` *Bioconductor annotation data package*

Description

Welcome to the reactome.db annotation Package. The purpose of this package is to provide detailed information about the latest version of the Reactome database. This package is updated biannually.

You can learn what objects this package supports with the following command:

`ls("package:reactome.db")`

Each of these objects has their own manual page detailing where relevant data was obtained along with some examples of how to use it.

Examples

```
ls("package:reactome.db")
```

`reactomeEXTID2PATHID` *An annotation data object that maps Entrez Gene identifiers to Reactome pathway identifiers*

Description

reactomeEXTID2PATHID maps Entrez Gene identifiers to Reactome pathway identifiers.

Details

This is an R object containing key and value pairs. Keys are Entrez Gene identifiers and values are the corresponding Reactome pathway identifiers. Values are vectors of length 1 or greater depending on whether a given external identifier can be mapped to only one or more Reactome pathway identifiers.

Reactome pathway identifiers are the identifiers used by Reactome for various pathways.

Mappings between Reactome pathway identifiers and pathway names can be obtained through another annotation data object named reactomePATHID2NAME.

Mappings were based on data provided by: Reactome http://reactome.org/download/current/NCBI2Reactome_All_Level & http://reactome.org/download/current/ReactomePathways.txt With a date stamp from the source that is the same as the time stamp of the package.

References

http://www.reactome.org/

Examples

```
xx <- as.list(reactomeEXTID2PATHID)
if(length(xx) > 0){
 # Get the value of the first key
 xx[[1]]
 # Get the values for multiget for a few keys
 if(length(xx) >= 3){
  xx[1:3]
 }
}
```

`reactomeGO2REACTOMEID` *An annotation data object that maps Gene Ontology (GO) identifiers to Reactome database identifiers*

Description

reactomeGO2REACTOMEID maps GO identifiers to Reactome database identifiers

Details

This is an R object containing key and value pairs. Keys are GO identifiers and values are Reactome database identifiers. Values are vectors of length 1.

Mappings were based on data provided by: Reactome wget http://reactome.org/download/current/gene_association.reacto With a date stamp from the source that is the same as the time stamp of the package.

References

http://www.reactome.org/

Examples

```
xx <- as.list(reactomeGO2REACTOMEID)
if(length(xx) > 0){
 # Get the value of the first key
 xx[[1]]
 # Get values for a few keys
 if(length(xx) >= 3){
  xx[1:3]
 }
}
```

`reactomeMAPCOUNTS` *Number of mapped keys for the maps in package reactome.db*

Description

reactomeMAPCOUNTS provides the "map count" (i.e. the count of mapped keys) for each map in package reactome.db.

Details

This "map count" information is precalculated and stored in the package annotation DB. This allows some quality control and is used by the `checkMAPCOUNTS` function defined in AnnotationDbi to compare and validate different methods (like `count.mappedkeys(x)` or `sum(!is.na(as.list(x)))`) for getting the "map count" of a given map.

See Also

`mappedkeys`, `count.mappedkeys`, `checkMAPCOUNTS`

Examples

```
reactomeMAPCOUNTS
mapnames <- names(reactomeMAPCOUNTS)
reactomeMAPCOUNTS[mapnames[1]]
x <- get(mapnames[1])
sum(!is.na(as.list(x)))
count.mappedkeys(x)   # much faster!

## Check the "map count" of all the maps in package reactome.db
checkMAPCOUNTS("reactome.db")
```

`reactomePATHID2EXTID` *An annotation data object that maps Reactome pathway identifiers to Entrez Gene identifiers.*

Description

reactomePATHID2EXTID maps Reactome pathway identifiers to Entrez Gene identifiers

Details

This is an R object containing key and value pairs. Keys are Reactome pathway identifiers and values are Entrez Gene identifiers. Values are vectors of length 1 or greater depending on whether a pathway identifier can be mapped to one or more Entrez Gene identifiers.

Reactome pathway identifiers are the identifiers used by Reactome for various pathways.

Mappings between Reactome pathway identifiers and pathway names can be obtained through another annotation data object named reactomePATHID2NAME.

Mappings were based on data provided by: Reactome http://reactome.org/download/current/NCBI2Reactome_All_Level & http://reactome.org/download/current/ReactomePathways.txt With a date stamp from the source that is the same as the time stamp of the package.

References

http://www.reactome.org/

Examples

```
xx <- as.list(reactomePATHID2EXTID)
if(length(xx) > 0){
 # Get the value of the first key
 xx[[1]]
 # Get the values for multiget for a few keys
 if(length(xx) >= 3){
  xx[1:3]
 }
}
```

`reactomePATHID2NAME` *An annotation data object that maps Reactome pathway identifiers to Reactome pathway names*

Description

reactomePATHID2NAME maps Reactome pathway identifiers to pathway names used by Reactome for various pathways

Details

This is an R object containing key and value pairs. Keys are Reactome pathway identifiers and values are pathway names. Values are vectors of length 1.

Mappings were based on data provided by: Reactome http://reactome.org/download/current/ReactomePathways.txt With a date stamp from the source that is the same as the time stamp of the package.

References

http://www.reactome.org/

Examples

```
xx <- as.list(reactomePATHID2NAME)
if(length(xx) > 0){
 # get the value for the first key
 xx[[1]]
 # Get the values for a few keys
 if(length(xx) >= 3){
  xx[1:3]
 }
}
```

`reactomePATHNAME2ID` *An annotation data object that maps Reactome pathway names to identifiers for the corresponding pathway names used by Reactome*

Description

reactomePATHNAME2ID maps Reactome pathway names to pathway identifiers used by Reactome for various pathways

Details

This is an R object containing key and value pairs. Keys are Reactome pathway names and values are pathway identifiers. Values are vectors of length 1.

Mappings were based on data provided by: Reactome http://reactome.org/download/current/ReactomePathways.txt With a date stamp from the source that is the same as the time stamp of the package.

References

`http://www.reactome.org/`

Examples

```
xx <- as.list(reactomePATHNAME2ID)
if(length(xx) > 0){
 # get the value for the first key
 xx[[1]]
 # Get the values for a few keys
 if(length(xx) >= 3){
  xx[1:3]
 }
}
```

`reactomeREACTOMEID2GO` *An annotation data object that maps Reactome database identifiers to Gene Ontology identifiers*

Description

reactomeREACTOMEID2GO maps Reactome database identifiers to Gene Ontoloty (GO) identifiers

Details

This is an R object containing key and value pairs. Keys are Reactome database identifiers and values are GO identifiers. Values are vectors of length 1.

Mappings were based on data provided by: Reactome http://reactome.org/download/current/gene_association.reactome With a date stamp from the source that is the same as the time stamp of the package.

References

`http://www.reactome.org/`

Examples

```
xx <- as.list(reactomeREACTOMEID2GO)
if(length(xx) > 0){
 # Get the value of the first key
 xx[[1]]
               # Get values for a few keys
 if(length(xx) >= 3){
  xx[1:3]
 }
}
```

`reactome_dbconn` *Collect information about the package annotation DB*

Description

Some convenience functions for getting a connection object to (or collecting information about) the package annotation DB.

Usage

```
reactome_dbconn()
reactome_dbfile()
reactome_dbschema(file="", show.indices=FALSE)
reactome_dbInfo()
```

Arguments

`file`	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.

Details

`reactome_dbconn` returns a connection object to the package annotation DB. IMPORTANT: Don't call `dbDisconnect` on the connection object returned by `reactome_dbconn` or you will break all the `AnnDbObj` objects defined in this package!

`reactome_dbfile` returns the path (character string) to the package annotation DB (this is an SQLite file).

`reactome_dbschema` prints the schema definition of the package annotation DB.

`reactome_dbInfo` prints other information about the package annotation DB.

Value

`reactome_dbconn`: a DBIConnection object representing an open connection to the package annotation DB.

`reactome_dbfile`: a character string with the path to the package annotation DB.

`reactome_dbschema`: none (invisible `NULL`).

`reactome_dbInfo`: none (invisible `NULL`).

See Also

`dbGetQuery`, `dbConnect`, `dbconn`, `dbfile`, `dbschema`, `dbInfo`

Examples

```
library(RSQLite)
## Count the number of rows in the "pathway2name" table:
dbGetQuery(reactome_dbconn(), "SELECT COUNT(*) FROM pathway2name")

## The connection object returned by reactome_dbconn() was
## created with:
dbConnect(SQLite(), dbname=reactome_dbfile(), cache_size=64000,
synchronous="off")

reactome_dbschema()

reactome_dbInfo()
```

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