KEGG.db

April 2, 2013

KEGG.db   *Bioconductor annotation data package*

Description

Welcome to the KEGG.db annotation Package. The purpose of this package is to provide detailed information about the latest version of the KEGG pathway databases. This package is updated biannually.

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

ls("package:KEGG.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:KEGG.db")

KEGG_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

```
KEGG_dbconn()
KEGG_dbfile()
KEGG_dbschema(file="", show.indices=FALSE)
KEGG_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

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

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

KEGG_dbschema prints the schema definition of the package annotation DB.

KEGG_dbInfo prints other information about the package annotation DB.

Value

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

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

KEGG_dbschema: none (invisible NULL).

KEGG_dbInfo: none (invisible NULL).

See Also

dbGetQuery, dbConnect, dbconn, dbfile, dbschema, dbInfo

Examples

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

## The connection object returned by KEGG_dbconn() was
## created with:
dbConnect(SQLite(), dbname=KEGG_dbfile(), cache_size=64000,
synchronous=0)

KEGG_dbschema()

KEGG_dbInfo()
```

KEGGENZYMEID2GO	*An annotation data object that maps Enzyme Commission numbers to Gene Ontology identifiers*

Description

KEGGENZYMEID2GO maps Enzyme Commission numbers to Gene Ontoloty (GO) identifiers

Details

This is an R object containing key and value pairs. Keys are Enzyme Commission numbers and values are GO identifiers. Values are vectors of length 1. Enzyme Commission numbers that can not be mapped to a GO term are assigned a value NA.

Mappings were based on data provided by: Gene Ontology External Link http://www.geneontology.org/external2go With a date stamp from the source of: 2012-Junec2go19

References

ftp://ftp.genome.ad.jp/pub/kegg/pathways

Examples

```
xx <- as.list(KEGGENZYMEID2GO)
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]
}
}
```

KEGGEXTID2PATHID *An annotation data object that maps Entrez Gene or Open Reading Frame identifiers KEGG pathway identifiers*

Description

KEGGEXTID2PATHID maps Entrez Gene (for human, mouse, and rat) and Open Reading Frame (for yeast) identifiers to KEGG pathway identifiers.

Details

This is an R object containing key and value pairs. Keys are Entrez Gene identifiers for human, mouse, and rat and Open Reading Frame (ORF) identifiers for yeast and values are the corresponding KEGG 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 KEGG pathway identifiers. NAs are assigned to Entrez Gene or ORF identifiers that can not be mapped to any pathway identifier.

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

Mappings between KEGG pathway identifiers and pathway names can be obtained through another annotation data object named KEGGPATHID2NAME.

Mappings were based on data provided by: KEGG GENOME ftp://ftp.genome.jp/pub/kegg/genomes With a date stamp from the source of: 2011-Mar15

References

ftp://ftp.genome.ad.jp/pub/kegg/pathways

Examples

```
xx <- as.list(KEGGEXTID2PATHID)
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]
}
}
```

KEGGGO2ENZYMEID   *An annotation data object that maps Gene Ontology (GO) identifiers*
                   to Enzyme Commission numbers

Description

KEGGGO2ENZYMEID maps GO identifiers to Enzyme Commission numbers

Details

This is an R object containing key and value pairs. Keys are GO identifiers and values are Enzyme Commission numbers. Values are vectors of length 1. GO identifiers can not be mapped to any Enzyme Commission number are assigned NAs.

Mappings are based on data provided by: Gene Ontology External Link http://www.geneontology.org/external2go With a date stamp from the source of: 2012-Junec2go19

References

ftp://ftp.genome.ad.jp/pub/kegg/pathways

Examples

```
xx <- as.list(KEGGGO2ENZYMEID)
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]
}
}
```

KEGGMAPCOUNTS   *Number of mapped keys for the maps in package KEGG.db*

Description

KEGGMAPCOUNTS provides the "map count" (i.e. the count of mapped keys) for each map in package KEGG.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

```
KEGGMAPCOUNTS
mapnames <- names(KEGGMAPCOUNTS)
KEGGMAPCOUNTS[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 KEGG.db
checkMAPCOUNTS("KEGG.db")
```

KEGGPATHID2EXTID *An annotation data object that maps KEGG pathway identifiers to Entrez Gene or Open Reading Frame identifiers.*

Description

KEGGPATHID2EXTID maps KEGG pathway identifiers to Entrez Gene (for human, mouse, and rat) or Open Reading Frame (for yeast) identifiers

Details

This is an R object containing key and value pairs. Keys are KEGG pathway identifiers and values are Entrez Gene identifiers for human, mouse, and rat or Open Reading Frame (ORF) identifiers for yeast. Values are vectors of length 1 or greater depending on whether a pathway identifier can be maapped to one or more Entrez Gene or ORF identifiers. NAs are assigned to KEGG pathway identifiers that can not be mapped to any Entrez Gene or ORF identifiers.

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

Mappings between KEGG pathway identifiers and pathway names can be obtained through another annotation data object named KEGGPATHID2NAME.

Mappings were based on data provided by: KEGG GENOME ftp://ftp.genome.jp/pub/kegg/genomes
With a date stamp from the source of: 2011-Mar15

References

ftp://ftp.genome.ad.jp/pub/kegg/pathways

Examples

```
xx <- as.list(KEGGPATHID2EXTID)
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]
}
}
```

KEGGPATHID2NAME   *An annotation data object that maps KEGG pathway identifiers to KEGG pathway names*

Description

KEGGPATHID2NAME maps KEGG pathway identifiers to pathway names used by KEGG for various pathways

Details

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

Mappings were based on data provided by: KEGG PATHWAY ftp://ftp.genome.jp/pub/kegg/pathway
With a date stamp from the source of: 2011-Mar14

References

ftp://ftp.genome.ad.jp/pub/kegg/pathways

Examples

```
xx <- as.list(KEGGPATHID2NAME)
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]
}
}
```

KEGGPATHNAME2ID *An annotation data object that maps KEGG pathway names to identifiers for the corresponding pathway names used by KEGG*

Description

KEGGPATHNAME2ID maps KEGG pathway names to pathway identifiers used by KEGG for various pathways

Details

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

Mappings were based on data provided by: KEGG PATHWAY ftp://ftp.genome.jp/pub/kegg/pathway With a date stamp from the source of: 2011-Mar14

References

ftp://ftp.genome.ad.jp/pub/kegg/pathways

Examples

```
xx <- as.list(KEGGPATHNAME2ID)
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]
}
}
```

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