

dName.db

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dName_dbconn	<i>Collect information about the package annotation DB</i>
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Description

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

Usage

```
dName_dbconn()  
dName_dbfile()  
dName_dbschema(file="", show.indices=FALSE)  
dName_dbInfo()
```

Arguments

<code>file</code>	A connection, or a character string naming the file to print to (see the file argument of the cat function for the details).
<code>show.indices</code>	The CREATE INDEX statements are not shown by default. Use show.indices=TRUE to get them.

Details

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

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

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

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

Examples

```
## Show the first three rows.
dbGetQuery(dName_dbconn(), "select * from kegg limit 3")

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

dName_dbschema()

dName_dbInfo()
```

dName.db

annotation data package

Description

Welcome to the dName.db annotation Package. The annotation package was built using a downloadable R package - PAnnBuilder (download and build your own). The purpose is to provide detailed information about the identifier and name in several public databases (KEGG, GO, Pfam, Interpro, Taxonomy): http://www.geneontology.org/ontology/gene_ontology_edit.obo on 09:03:2009 12:48 ; ftp://ftp.sanger.ac.uk/pub/databases/Pfam/current_release/Pfam_ls.gz on Release 23.0, 07/08 ; ftp://ftp.ebi.ac.uk/pub/databases/interpro/short_names.dat on Release 19.0, 29 January 2009 New features include: ; ftp://ftp.genome.jp/pub/kegg/pathway/map_title.tab on 2009 Feb 17 ; <ftp://ftp.ncbi.nih.gov/pub/taxonomy/taxdmp.zip> on 2009 Mar 10 ;

Each of these objects has their own manual page detailing where relevant data was obtained along with examples of how to use it. Many of these objects also have a reverse map available. When this is true, expect to usually find relevant information on the same manual page as the forward map.

Examples

```
# You can learn what objects this package supports with the following command:
ls("package:dName.db")
```

dNameGO2NAME *Map GO identifiers to name*

Description

dNameGO2NAME provides mappings of GO identifiers to its name.

Details

Mappings were based on data provided by GO: http://www.geneontology.org/ontology/gene_ontology_edit.obo on 09:03:2009 12:48

Examples

```
x <- dNameGO2NAME
# Get the GO identifiers that are mapped to descriptions.
mapped <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped])
if(length(xx) > 0){
  xx[2:3]
}
```

dNameINTERPRO2NAME *Map Interpro domain identifiers to name*

Description

dNameINTERPRO2NAME provides mappings of Interpro domain identifiers to its name.

Details

Mappings were based on data provided by Interpro: ftp://ftp.ebi.ac.uk/pub/databases/interpro/short_names.dat on Release 19.0, 29 January 2009 New features include:

Examples

```
x <- dNameINTERPRO2NAME
# Get the Interpro domain identifiers that are mapped to names.
mapped <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped])
if(length(xx) > 0){
  xx[2:3]
}
```

dNameMAPCOUNTS *Number of mapped keys for the maps in package dName.db*

Description

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

```
dNameMAPCOUNTS
mapnames <- names(dNameMAPCOUNTS)
dNameMAPCOUNTS[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 dName.db
checkMAPCOUNTS("dName.db")
```

dNamePATH2DE *Map KEGG pathway identifiers to description*

Description

dNamePATH2DE provides mappings of KEGG pathway identifiers to its description.

Details

Mappings were based on data provided by KEGG: ftp://ftp.genome.jp/pub/kegg/pathway/map_title.tab on 2009 Feb 17

Examples

```
x <- dNamePATH2DE
# Get the KEGG pathway identifiers that are mapped to descriptions.
mapped <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped])
if(length(xx) > 0){
  xx[2:3]
}
```

`dNamePFAM2DE`*Map Pfam domain identifiers to description*

Description

`dNamePFAM2DE` provides mappings of Pfam domain identifiers to its description.

Details

Mappings were based on data provided by Pfam: ftp://ftp.sanger.ac.uk/pub/databases/Pfam/current_release/Pfam_ls.gz on Release 23.0, 07/08

Examples

```
x <- dNamePFAM2DE
# Get the Pfam domain identifiers that are mapped to descriptions.
mapped <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped])
if(length(xx) > 0){
  xx[2:3]
}
```

`dNamePFAM2NAME`*Map Pfam domain identifiers to name*

Description

`dNamePFAM2NAME` provides mappings of Pfam domain identifiers to its name.

Details

Mappings were based on data provided by Pfam: ftp://ftp.sanger.ac.uk/pub/databases/Pfam/current_release/Pfam_ls.gz on Release 23.0, 07/08

Examples

```
x <- dNamePFAM2NAME
# Get the Pfam domain identifiers that are mapped to names.
mapped <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped])
if(length(xx) > 0){
  xx[2:3]
}
```

dNameTAXID2NAME *Map taxonomy identifiers to name*

Description

dNameTAXID2NAME provides mappings of taxonomy id to its name.

Details

Mappings were based on data provided by NCBI: <ftp://ftp.ncbi.nih.gov/pub/taxonomy/taxdmp.zip> on 2009 Mar 10

Examples

```
x <- dNameTAXID2NAME
# Get the taxonomy identifiers that are mapped to name.
mapped <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped])
if(length(xx) > 0){
  xx[2:3]
}
```

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