

# 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 <code>show.indices=TRUE</code> 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()
```

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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](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](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](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](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](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](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](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](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](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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