

# int.domine.db

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int.domine\_dbconn *Collect information about the package annotation DB*

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## Description

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

## Usage

```
int.domine_dbconn()  
int.domine_dbfile()  
int.domine_dbschema(file="", show.indices=FALSE)  
int.domine_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

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

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

`int.domine_dbschema` prints the schema definition of the package annotation DB.

`int.domine_dbInfo` prints other information about the package annotation DB.

## Examples

```
## Show the first three rows.
dbGetQuery(int.domine_dbconn(), "select * from domine limit 3")

## The connection object returned by int.domine_dbconn() was created with:
dbConnect(SQLite(), dbname=int.domine_dbfile(), cache_size=64000, synchronous=0)

int.domine_dbschema()

int.domine_dbInfo()
```

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int.domine.db	<i>annotation data package</i>
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## Description

Welcome to the int.domine.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 known and predicted protein domain (domain-domain) interactions from DOMINE database: <http://domine.utdallas.edu/domine-tables.zip> Version 1.1, February 2008

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:int.domine.db")
```

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int.domineDDI      *Domain-Domain interaction*

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### Description

int.domineDDI gives known and predicted domain-domain interactions from DOMINE database.

### Details

Domain identifier is given as Pfam identifier. Each domain identifier maps to a named vector containing interacted domains. The vector name corresponds to the abbreviation of the source of domain-domain interaction.

Mappings were based on data provided by: DOMINE (<http://domine.utdallas.edu/domine-tables.zip>) on Version 1.1, February 2008

### Examples

```
# Convert to a list
xx <- as.list(int.domineDDI)
if(length(xx) > 0){
  # Gets the first five interaction list
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

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int.domineMAPCOUNTS

*Number of mapped keys for the maps in package int.domine.db*

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### Description

int.domineMAPCOUNTS provides the "map count" (i.e. the count of mapped keys) for each map in package int.domine.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

```
int.domineMAPCOUNTS
mapnames <- names(int.domineMAPCOUNTS)
int.domineMAPCOUNTS[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 int.domine.db
checkMAPCOUNTS("int.domine.db")
```

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int.domineMETHOD    *Methods of getting domain-domain interaction*

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## Description

int.domineMETHOD gives known proof or prediction method about the source of domain-domain interaction.

## Details

Mappings were based on data provided by: DOMINE (<http://domine.utdallas.edu/domine-tables.zip>) on Version 1.1, February 2008

## Examples

```
# Convert to a list
xx <- as.list(int.domineMETHOD)
if(length(xx) > 0){
  # Gets the first five
  xx[1:5]
}
```

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