

int.intact.db

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int.intact_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

```
int.intact_dbconn()  
int.intact_dbfile()  
int.intact_dbschema(file="", show.indices=FALSE)  
int.intact_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.intact_dbconn returns a connection object to the package annotation DB. **IMPORTANT:** Don't call `dbDisconnect` on the connection object returned by `int.intact_dbconn` or you will break all the `AnnDbObj` objects defined in this package!

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

int.intact_dbschema prints the schema definition of the package annotation DB.

int.intact_dbInfo prints other information about the package annotation DB.

Examples

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

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

int.intact_dbschema()

int.intact_dbInfo()
```

```
int.intact.db      annotation data package
```

Description

Welcome to the int.intact.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 protein-protein interactions from IntAct database: <ftp://ftp.ebi.ac.uk/pub/databases/intact/current/psimitab/intact.txt>

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.intact.db")
```

```
int.intactMAPCOUNTS
      Number of mapped keys for the maps in package int.intact.db
```

Description

int.intactMAPCOUNTS provides the "map count" (i.e. the count of mapped keys) for each map in package int.intact.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.intactMAPCOUNTS
mapnames <- names(int.intactMAPCOUNTS)
int.intactMAPCOUNTS[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.intact.db
checkMAPCOUNTS("int.intact.db")
```

int.intactPPI *Protein-Protein interaction*

Description

int.intactPPI gives protein-protein interactions from IntAct database.

Details

Protein is given as Uniprot protein accession number.

Mappings were based on data provided by: IntAct (<ftp://ftp.ebi.ac.uk/pub/databases/intact/current/psimitab/intact.txt>) on

Examples

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

int.intactTAXID	<i>Taxonomy identifier</i>
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Description

int.intactTAXID map Uniprot protein accession number to its taxonomy identifier.

Details

Mappings were based on data provided by: IntAct (<ftp://ftp.ebi.ac.uk/pub/databases/intact/current/psimitab/intact.txt>) on

Examples

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

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