

# int.mppi.db

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## R topics documented:

int.mppi_dbconn	1
int.mppi.db	2
int.mppiMAPCOUNTS	2
int.mppiPPI	3

<b>Index</b>	<b>4</b>
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int.mppi_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

```
int.mppi_dbconn()  
int.mppi_dbfile()  
int.mppi_dbschema(file="", show.indices=FALSE)  
int.mppi_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.mppi\_dbconn returns a connection object to the package annotation DB. **IMPORTANT:** Don't call `dbDisconnect` on the connection object returned by `int.mppi_dbconn` or you will break all the `AnnDbObj` objects defined in this package!

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

int.mppi\_dbschema prints the schema definition of the package annotation DB.

int.mppi\_dbInfo prints other information about the package annotation DB.

### Examples

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

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

int.mppi_dbschema()

int.mppi_dbInfo()
```

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

Welcome to the int.mppi.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 mammalian protein-protein interactions from MPPI database: <http://mips.gsf.de/proj/ppi/data/mppi.gz>

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.mppi.db")
```

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int.mppiMAPCOUNTS	<i>Number of mapped keys for the maps in package int.mppi.db</i>
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### Description

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

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int.mppiPPI	<i>Protein-Protein interaction</i>
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**Description**

int.mppiPPI gives protein-protein interactions from MPPI database.

**Details**

Protein is given as Uniprot protein accession number.

Mappings were based on data provided by: MPPI (<http://mips.gsf.de/proj/ppi/data/mppi.gz>) on

**Examples**

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

# Index

## \*Topic **datasets**

`int.mppiMAPCOUNTS`, 2

`AnnDbObj`, 1

`checkMAPCOUNTS`, 2

`count.mappedkeys`, 2

`dbDisconnect`, 1

`int.mppi.db`, 2

`int.mppi_dbconn`, 1

`int.mppi_dbfile`  
(`int.mppi_dbconn`), 1

`int.mppi_dbInfo`  
(`int.mppi_dbconn`), 1

`int.mppi_dbschema`  
(`int.mppi_dbconn`), 1

`int.mppiMAPCOUNTS`, 2

`int.mppiPPI`, 3

`mappedkeys`, 2