

org.Hs.bf.db

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org.Hs.bfBF2IPI	<i>Map body fluid to protein IPI identifiers</i>
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Description

org.Hs.bfBF2IPI is an R environment that provides mappings body fluid to protein IPI identifiers in this body fluids.

Details

The name of body fluids in use include: Amniotic fluid; Bronchoalveolar lavage fluid; Cerebrospinal fluid; Milk; Nipple aspiration fluid; Plasma/Serum; Saliva; Seminal Fluid; Synovial Fluid; Tear; Urine.

Mappings were based on data provided by: Sys-BodyFluid (http://www.biosino.org/papers/Sys-BodyFluid/Current/experiment_protein.txt) on Version 1.1 2008-11-22

Examples

```
# Convert to a list
xx <- as.list(org.Hs.bfBF2IPI)
xx <- xx[!is.na(xx)]
if(length(xx) > 0){
  # Get the first one
  xx[[1]]
}
```

org.Hs.bfBF

Map Protein identifiers to body fluids

Description

org.Hs.bfBF is an R environment that provides mappings between protein identifiers and involved body fluids.

Details

The name of body fluids in use include: Amniotic fluid; Bronchoalveolar lavage fluid; Cerebrospinal fluid; Milk; Nipple aspiration fluid; Plasma/Serum; Saliva; Seminal Fluid; Synovial Fluid; Tear; Urine.

Mappings were based on data provided by: Sys-BodyFluid (http://www.biosino.org/papers/Sys-BodyFluid/Current/experiment_protein.txt) on Version 1.1 2008-11-22

Examples

```
# Convert to a list
xx <- as.list(org.Hs.bfBF)
xx <- xx[!is.na(xx)]
if(length(xx) > 0){
  # Get the first one
  xx[[1]]
}
```

org.Hs.bf_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

```
org.Hs.bf_dbconn()
org.Hs.bf_dbfile()
org.Hs.bf_dbschema(file="", show.indices=FALSE)
org.Hs.bf_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

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

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

`org.Hs.bf_dbschema` prints the schema definition of the package annotation DB.

`org.Hs.bf_dbInfo` prints other information about the package annotation DB.

Examples

```
## Show the first three rows.
dbGetQuery(org.Hs.bf_dbconn(), "select * from sysbodyfluid limit 3")

## The connection object returned by org.Hs.bf_dbconn() was created with:
dbConnect(SQLite(), dbname=org.Hs.bf_dbfile(), cache_size=64000, synchronous=0)

org.Hs.bf_dbschema()

org.Hs.bf_dbInfo()
```

org.Hs.bf.db *annotation data package*

Description

Welcome to the org.Hs.bf.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 Human body fluid proteins from Sys-BodyFluid database: http://www.biosino.org/papers/Sys-BodyFluid/Current/experiment_protein.txt <http://www.biosino.org/papers/Sys-BodyFluid/Current/paper.txt> Version 1.1 2008-11-22

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:org.Hs.bf.db")
```

org.Hs.bfMAPCOUNTS *Number of mapped keys for the maps in package org.Hs.bf.db*

Description

org.Hs.bfMAPCOUNTS provides the "map count" (i.e. the count of mapped keys) for each map in package org.Hs.bf.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

```
org.Hs.bfMAPCOUNTS
mapnames <- names(org.Hs.bfMAPCOUNTS)
org.Hs.bfMAPCOUNTS[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 org.Hs.bf.db
checkMAPCOUNTS("org.Hs.bf.db")
```

org.Hs.bfORGANISM *The Organism for org.Hs.bf.db*

Description

org.Hs.bfORGANISM is an R object that contains a single item: a character string that names the organism for which org.Hs.bf.db was built.

Details

Although the package name is suggestive of the organism for which it was built, org.Hs.bfORGANISM provides a simple way to programmatically extract the organism name.

Examples

```
org.Hs.bfORGANISM
```

org.Hs.bfPMID2BF *Map published paper to body fluid*

Description

org.Hs.bfPMID2BF is an R environment that provides mappings between public peer-reviewed papers collected in Sys-BodyFluid and involved body fluids.

Details

The name of body fluids in use include: Amniotic fluid; Bronchoalveolar lavage fluid; Cerebrospinal fluid; Milk; Nipple aspiration fluid; Plasma/Serum; Saliva; Seminal Fluid; Synovial Fluid; Tear; Urine.

Mappings were based on data provided by: Sys-BodyFluid (<http://www.biosino.org/papers/Sys-BodyFluid/Current/paper.txt>) on Version 1.1 2008-11-22

Examples

```
## Convert to a list
xx <- as.list(org.Hs.bfPMID2BF)
if(length(xx) > 0){
  ## Get the first one
  xx[[1]]
}

## For the reverse map org.Hs.bfBF2PMID
xx <- as.list(org.Hs.bfBF2PMID)
if(length(xx) > 0){
  ## Get the first one
  xx[[1]]
}
```

org.Hs.bfPMID2ENGINE
Map published paper to search engine

Description

org.Hs.bfPMID2ENGINE is an R environment that provides mappings between public peer-reviewed papers collected in Sys-BodyFluid and protein search engines.

Details

Frequently used search engines include SEQUEST, Mascot, and so on.

Mappings were based on data provided by: Sys-BodyFluid (<http://www.biosino.org/papers/Sys-BodyFluid/Current/paper.txt>) on Version 1.1 2008-11-22

Examples

```
# Convert to a list
xx <- as.list(org.Hs.bfPMID2ENGINE)
xx <- xx[!is.na(xx)]
if(length(xx) > 0){
  # Get the first one
  xx[[1]]
}
```

org.Hs.bfPMID2PLATFORM

Map published paper to experimental platform

Description

org.Hs.bfPMID2PLATFORM is an R environment that provides mappings between public peer-reviewed papers collected in Sys-BodyFluid and mass spectrometry experimental platforms.

Details

Mappings were based on data provided by: Sys-BodyFluid (<http://www.biosino.org/papers/Sys-BodyFluid/Current/paper.txt>) on Version 1.1 2008-11-22

Examples

```
# Convert to a list
xx <- as.list(org.Hs.bfPMID2PLATFORM)
xx <- xx[!is.na(xx)]
if(length(xx) > 0){
  # Get the first one
  xx[[1]]
}
```

org.Hs.bfPMID2SAMPLE

Map published paper to experimental sample

Description

org.Hs.bfPMID2SAMPLE is an R environment that provides mappings between public peer-reviewed papers collected in Sys-BodyFluid and experimental sample.

Details

Mappings were based on data provided by: Sys-BodyFluid (<http://www.biosino.org/papers/Sys-BodyFluid/Current/paper.txt>) on Version 1.1 2008-11-22

Examples

```
# Convert to a list
xx <- as.list(org.Hs.bfPMID2SAMPLE)
xx <- xx[!is.na(xx)]
if(length(xx) > 0){
  # Get the first one
  xx[[1]]
}
```

org.Hs.bfPMID2TITLE

Map published paper to search engine

Description

org.Hs.bfPMID2TITLE is an R environment that provides mappings between public peer-reviewed papers collected in Sys-BodyFluid and their titles.

Details

Mappings were based on data provided by: Sys-BodyFluid (<http://www.biosino.org/papers/Sys-BodyFluid/Current/paper.txt>) on Version 1.1 2008-11-22

Examples

```
# Convert to a list
xx <- as.list(org.Hs.bfPMID2TITLE)
xx <- xx[!is.na(xx)]
if(length(xx) > 0){
  # Get the first one
  xx[[1]]
}
```

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