

# org.Hs.bf.db

February 3, 2010

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org.Hs.bfBF2IPI      *Map body fluid to protein IPI identifiers*

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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](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]]
}
```

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org.Hs.bfBF      *Map Protein identifiers to body fluids*

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## 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](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/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]]
}
```

# Index

## \*Topic **datasets**

- org.Hs.bfMAPCOUNTS, 3
- AnnDbObj, 2
- checkMAPCOUNTS, 3
- count.mappedkeys, 3
- dbDisconnect, 2
- mappedkeys, 3
- org.Hs.bf.db, 3
- org.Hs.bf\_dbconn, 2
- org.Hs.bf\_dbfile
  - (org.Hs.bf\_dbconn), 2
- org.Hs.bf\_dbInfo
  - (org.Hs.bf\_dbconn), 2
- org.Hs.bf\_dbschema
  - (org.Hs.bf\_dbconn), 2
- org.Hs.bfBF, 1
- org.Hs.bfBF2IPI, 1
- org.Hs.bfBF2PMID
  - (org.Hs.bfPMID2BF), 4
- org.Hs.bfMAPCOUNTS, 3
- org.Hs.bfORGANISM, 4
- org.Hs.bfPMID2BF, 4
- org.Hs.bfPMID2ENGINE, 5
- org.Hs.bfPMID2PLATFORM, 5
- org.Hs.bfPMID2SAMPLE, 6
- org.Hs.bfPMID2TITLE, 6