# sysptm.db

October 16, 2009

## R topics documented:

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| sysptm_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

```
sysptm_dbconn()
sysptm_dbfile()
sysptm_dbschema(file="", show.indices=FALSE)
sysptm_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.

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**Details**

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

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

sysptm_dbschema prints the schema definition of the package annotation DB.

sysptm_dbInfo prints other information about the package annotation DB.

**Examples**

```
## Show the first three rows.
dbGetQuery(sysptm_dbconn(), "select * from sysptm limit 3")

## The connection object returned by sysptm_dbconn() was created with:
dbConnect(SQLite(), dbname=sysptm_dbfile(), cache_size=64000, synchronous=0)

sysptm_dbschema()

sysptm_dbInfo()
```

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sysptm.db *annotation data package*

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**Description**

Welcome to the sysptm.db annotation Package. The annotation package was built using a download-able R package - PAnnBuilder (download and build your own). The purpose is to provide detailed information about the protein pos-tranlational modifications from SysPTM database: http://www.biosino.org/papers/SysPTM/Current/ptm;http://www.biosino.org/papers/SysPTM/Current/name;http://www.biosino.org/papers/SysPTM/Current/Protein_ID_equal v1.1, 2008-11-20

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:sysptm.db")
```

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sysptmDE                 *Maps SysPTM protein identifier to textural descriptions*

---

### Description

sysptmDE maps SysPTM protein identifiers to their descriptive information.

### Details

Mappings were based on data provided by: SysPTM (http://www.biosino.org/papers/
SysPTM/Current/ptm;http://www.biosino.org/papers/SysPTM/Current/name;
http://www.biosino.org/papers/SysPTM/Current/Protein_ID_equal) on v1.1,
2008-11-20

### Examples

```
xx <- as.list(sysptmDE)
if(length(xx) > 0){
        # Get the value of the first key
        xx[[1]]
        # Get the values for a few keys
        if(length(xx) >= 3){
                xx[1:3]
        }
}
```

---

sysptmGENEID             *Map SysPTM protein identifier to Entrez gene identifier*

---

### Description

sysptmGENEID maps SysPTM protein identifiers to Entrez Gene identifiers.

### Details

Mappings were based on data provided by: SysPTM (http://www.biosino.org/papers/
SysPTM/Current/ptm;http://www.biosino.org/papers/SysPTM/Current/name;
http://www.biosino.org/papers/SysPTM/Current/Protein_ID_equal) on v1.1,
2008-11-20

### Examples

```
xx <- as.list(sysptmGENEID)
if(length(xx) > 0){
        # Get the value of the first key
        xx[[1]]
        # Get the values for a few keys
        if(length(xx) >= 3){
                xx[1:3]
        }
}
```

---

sysptmGN                          *Map SysPTM protein identifier to Gene Name*

---

## Description

sysptmGN maps SysPTM protein identifier to the corresponding gene names.

## Details

Each protein identifier maps to a vector containing the gene name or alias.

Mappings were based on data provided by: SysPTM ([http://www.biosino.org/papers/](http://www.biosino.org/papers/SysPTM/Current/ptm;http://www.biosino.org/papers/SysPTM/Current/name;http://www.biosino.org/papers/SysPTM/Current/Protein_ID_equal)
[SysPTM/Current/ptm;http://www.biosino.org/papers/SysPTM/Current/name;](http://www.biosino.org/papers/SysPTM/Current/ptm;http://www.biosino.org/papers/SysPTM/Current/name;http://www.biosino.org/papers/SysPTM/Current/Protein_ID_equal)
[http://www.biosino.org/papers/SysPTM/Current/Protein_ID_equal](http://www.biosino.org/papers/SysPTM/Current/Protein_ID_equal)) on v1.1,
2008-11-20

## Examples

```
# Convert to a list
xx <- as.list(sysptmGN)
# Remove protein that do not map to any GENENAME
xx <- xx[!is.na(xx)]
if(length(xx) > 0){
    # Gets the gene names for the first five probe identifiers
    xx[1:5]
    # Get the first one
    xx[[1]]
}
```

---

sysptmIDs                         *Map SysPTM protein identifiers to external identifiers*

---

## Description

sysptmIDs maps SysPTM protein identifiers to external protein identifiers.

## Details

Each SysPTM protein identifier maps to a named vector containing protein identifiers from public
databases, such as Swiss-Prot, IPI, NCBI RefSeq, and so on. The vector name corresponds to the
public database.

Mappings were based on data provided by: SysPTM ([http://www.biosino.org/papers/](http://www.biosino.org/papers/SysPTM/Current/ptm;http://www.biosino.org/papers/SysPTM/Current/name;http://www.biosino.org/papers/SysPTM/Current/Protein_ID_equal)
[SysPTM/Current/ptm;http://www.biosino.org/papers/SysPTM/Current/name;](http://www.biosino.org/papers/SysPTM/Current/ptm;http://www.biosino.org/papers/SysPTM/Current/name;http://www.biosino.org/papers/SysPTM/Current/Protein_ID_equal)
[http://www.biosino.org/papers/SysPTM/Current/Protein_ID_equal](http://www.biosino.org/papers/SysPTM/Current/Protein_ID_equal)) on v1.1,
2008-11-20

### Examples

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

---

sysptmMAPCOUNTS          *Number of mapped keys for the maps in package sysptm.db*

---

### Description

sysptmMAPCOUNTS provides the "map count" (i.e. the count of mapped keys) for each map in package sysptm.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

```
sysptmMAPCOUNTS
mapnames <- names(sysptmMAPCOUNTS)
sysptmMAPCOUNTS[mapnames[1]]
x <- get(mapnames[1])
sum(!is.na(as.list(x)))
count.mappedkeys(x)    # much faster!
```

---

sysptmORGANISM          *Map SysPTM protein identifiers to organism*

---

### Description

sysptmORGANISM map SysPTM protein identifiers to the name the organism.

### Details

Mappings were based on data provided by: SysPTM (http://www.biosino.org/papers/SysPTM/Current/ptm; http://www.biosino.org/papers/SysPTM/Current/name; http://www.biosino.org/papers/SysPTM/Current/Protein_ID_equal) on v1.1, 2008-11-20

## Examples

```
 # Convert to a list
xxx <- as.list(sysptmORGANISM)
# randomly display 10 proteins
sample(xxx, 10)
```

---

sysptmPTMTYPE          *Map site to the type of posttranslational modifications*

---

## Description

sysptmPTMTYPE maps a site to the type of posttranslational modifications (PTMs). The site is consisted of SysPTM protein identifer, start position of PTM, and end position of PTM.

## Details

Mappings were based on data provided by: SysPTM (http://www.biosino.org/papers/SysPTM/Current/ptm;http://www.biosino.org/papers/SysPTM/Current/name; http://www.biosino.org/papers/SysPTM/Current/Protein_ID_equal) on v1.1, 2008-11-20

## Examples

```
# Convert to a list
xx <- as.list(sysptmPTMTYPE)
# Get the values for a few keys
if(length(xx) >= 3){
  xx[1:3]
}

## For the reverse map sysptmPTMTYPE2SITE
xx <- as.list(sysptmPTMTYPE2SITE)
if(length(xx) > 0){
    ## Get the first one
    xx[[1]]
}
```

---

sysptmSEQ          *Map protein identifier to the protein sequence*

---

## Description

sysptmSEQ provides mappings between a SysPTM protein identifier and the protein Sequence.

## Details

Mappings were based on data provided by: SysPTM (http://www.biosino.org/papers/SysPTM/Current/ptm;http://www.biosino.org/papers/SysPTM/Current/name; http://www.biosino.org/papers/SysPTM/Current/Protein_ID_equal) on v1.1, 2008-11-20

## Examples

```
# Convert to a list
xx <- as.list(sysptmSEQ)
 # Get the values for a few keys
 if(length(xx) >= 3){
   xx[1:3]
 }
```

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