org.Hs.pep.db

February 3, 2010

---

org.Hs.pep_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.pep_dbconn()
org.Hs.pep_dbfile()
org.Hs.pep_dbschema(file="", show.indices=FALSE)
org.Hs.pep_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.pep_dbconn returns a connection object to the package annotation DB. IMPORTANT: Don't call dbDisconnect on the connection object returned by org.Hs.pep_dbconn or you will break all the AnnDbObj objects defined in this package!

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

org.Hs.pep_dbschema prints the schema definition of the package annotation DB.

org.Hs.pep_dbInfo prints other information about the package annotation DB.

1

Examples

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

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

org.Hs.pep_dbschema()

org.Hs.pep_dbInfo()
```

---

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

Description

Welcome to the org.Hs.pep.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 peptides identified by mass spectrometry from PeptideAtlas database: http://www.peptideatlas.org/builds/human/HumanP0.9/200704/APD_Hs_all. fasta;http://www.peptideatlas.org/builds/human/HumanP0.9/200704/coordinate_ mapping.txt Human April 2007

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.pep.db")
```

---

org.Hs.pepMAPCOUNTS

                    Number of mapped keys for the maps in package org.Hs.pep.db

---

Description

org.Hs.pepMAPCOUNTS provides the "map count" (i.e. the count of mapped keys) for each map in package org.Hs.pep.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.pepMAPCOUNTS
mapnames <- names(org.Hs.pepMAPCOUNTS)
org.Hs.pepMAPCOUNTS[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.pep.db
checkMAPCOUNTS("org.Hs.pep.db")
```

`org.Hs.pepPEP2CHR`   *Map peptide identifier to the its chromosome location*

Description

org.Hs.pepPEP2CHR provides mappings between a PeptideAtlas peptide identifier and the its location on the chromosome, including chromosome, strand, start position on the chromosome, end position on the chromosome.

Details

Mappings were based on data provided by: PeptideAtlas (http://www.peptideatlas.org/builds/human/HumanP0.9/200704/APD_Hs_all.fasta; http://www.peptideatlas.org/builds/human/HumanP0.9/200704/coordinate_mapping.txt) on Human April 2007

Examples

```
    # Convert to a list
    xx <- as.list(org.Hs.pepPEP2CHR)
# Get the values for a few keys
if(length(xx) >= 3){
xx[1:3]
}
```

`org.Hs.pepPEP2PROTEIN`
                        Map peptide identifier to the its portien location

---

Description

org.Hs.pepPEP2PROTEIN provides mappings between a PeptideAtlas peptide identifier and the its location on the protein, including protien identifier, start position on the protein, end position on the protein.

Details

Mappings were based on data provided by: PeptideAtlas (http://www.peptideatlas.org/builds/human/HumanP0.9/200704/APD_Hs_all.fasta; http://www.peptideatlas.org/builds/human/HumanP0.9/200704/coordinate_mapping.txt) on Human April 2007

Examples

```
    # Convert to a list
    xx <- as.list(org.Hs.pepPEP2PROTEIN)
# Get the values for a few keys
if(length(xx) >= 3){
xx[1:3]
}
```

---

org.Hs.pepSEQ   *Map peptide identifier to the its sequence*

Description

org.Hs.pepSEQ provides mappings between a PeptideAtlas peptide identifier and the its sequence.

Details

Mappings were based on data provided by: PeptideAtlas ([http://www.peptideatlas.org/](http://www.peptideatlas.org/builds/human/HumanP0.9/200704/APD_Hs_all.fasta) [builds/human/HumanP0.9/200704/APD_Hs_all.fasta;](http://www.peptideatlas.org/builds/human/HumanP0.9/200704/APD_Hs_all.fasta) [http://www.peptideatlas.](http://www.peptideatlas.org/builds/human/HumanP0.9/200704/coordinate_mapping.txt) [org/builds/human/HumanP0.9/200704/coordinate_mapping.txt](http://www.peptideatlas.org/builds/human/HumanP0.9/200704/coordinate_mapping.txt)) on Human April 2007

Examples

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

Index