org.Hs.goa.db

February 3, 2010

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

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

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

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

Examples

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

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

org.Hs.goa_dbschema()

org.Hs.goa_dbInfo()
```

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

Description

Welcome to the org.Hs.goa.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 gene ontology annoation from GOA database: `ftp://ftp.ebi.ac.uk/pub/databases/GO/goa/proteomes/25.H_sapiens.goa` Tue Mar 10 14:32:26 2009

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.goa.db")
```

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org.Hs.goaDE   *Maps protein to textural descriptions*

Description

org.Hs.goaDE maps Swiss-Prot protein accession number to their descriptive information.

Details

Mappings were based on data provided by: GOA (`ftp://ftp.ebi.ac.uk/pub/databases/GO/goa/proteomes/25.H_sapiens.goa`) on Tue Mar 10 14:32:26 2009

Examples

```
xx <- as.list(org.Hs.goaDE)
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]
}
}
```

`org.Hs.goaGO`   *Maps protein to gene ontology*

Description

org.Hs.goaGO maps Swiss-Prot protein accession number to their gene ontology annotation.

Details

The Evidence element contains a code indicating what kind of evidence supports the association of the GO id to the protein id. The evidence codes in use include: IMP: inferred from mutant phenotype IGI: inferred from genetic interaction IPI: inferred from physical interaction ISS: inferred from sequence similarity IDA: inferred from direct assay IEP: inferred from expression pattern IEA: inferred from electronic annotation TAS: traceable author statement NAS: non-traceable author statement ND: no biological data available IC: inferred by curator

Mappings were based on data provided by: GOA (`ftp://ftp.ebi.ac.uk/pub/databases/GO/goa/proteomes/25.H_sapiens.goa`) on Tue Mar 10 14:32:26 2009

Examples

```
xx <- as.list(org.Hs.goaGO)
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]
}
}

  # For the reverse map org.Hs.goaGO2SPAC:
  xx <- as.list(org.Hs.goaGO2SPAC)
  if(length(xx) > 0){
      xx[2:3]
  }
```

`org.Hs.goaMAPCOUNTS`

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

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Description

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

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org.Hs.goaORGANISM *The Organism for org.Hs.goa.db*

Description

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

Details

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

Examples

```
org.Hs.goaORGANISM
```

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org.Hs.goaSPID   *Maps protein to Swiss-Prot identifiers*

Description

org.Hs.goaSPID maps Swiss-Prot protein accession number to Swiss-Prot protein identifiers.

Details

Mappings were based on data provided by: GOA (ftp://ftp.ebi.ac.uk/pub/databases/GO/goa/proteomes/25.H_sapiens.goa) on Tue Mar 10 14:32:26 2009

Examples

```
xx <- as.list(org.Hs.goaSPID)
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]
}
}

## For the reverse map org.Hs.goaSPID2SPAC
xx <- as.list(org.Hs.goaSPID2SPAC)
xx[[1]]
```

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