

# org.Hs.goa.db

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org.Hs.goa\_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

```
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()
```

---

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](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")
```

---

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](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](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*

---

### 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")

```

---

```
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
```

---

org.Hs.goaSPID	<i>Maps protein to Swiss-Prot identifiers</i>
----------------	-----------------------------------------------

---

## 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](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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