

# org.HsMm.ortholog.db

February 3, 2010

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org.HsMm.ortholog\_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.HsMm.ortholog_dbconn()
org.HsMm.ortholog_dbfile()
org.HsMm.ortholog_dbschema(file="", show.indices=FALSE)
org.HsMm.ortholog_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.HsMm.ortholog_dbconn` returns a connection object to the package annotation DB. **IMPORTANT: Don't call `dbDisconnect` on the connection object returned by `org.HsMm.ortholog_dbconn` or you will break all the `AnnDbObj` objects defined in this package!**

`org.HsMm.ortholog_dbfile` returns the path (character string) to the package annotation DB (this is an SQLite file).

`org.HsMm.ortholog_dbschema` prints the schema definition of the package annotation DB.

`org.HsMm.ortholog_dbInfo` prints other information about the package annotation DB.

**Examples**

```
## Show the first three rows.
dbGetQuery(org.HsMm.ortholog_dbconn(), "select * from ortholog limit 3")

## The connection object returned by org.HsMm.ortholog_dbconn() was created with:
dbConnect(SQLite(), dbname=org.HsMm.ortholog_dbfile(), cache_size=64000, synchronous=0)

org.HsMm.ortholog_dbschema()

org.HsMm.ortholog_dbInfo()
```

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```
org.HsMm.ortholog.db
      annotation data package
```

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**Description**

Welcome to the org.HsMm.ortholog.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 ortholog protein from Inparanoid eukaryotic ortholog database: <http://inparanoid.sbc.su.se/download/current/sequences/processed/ensHOMSA.fa>; <http://inparanoid.sbc.su.se/download/current/sequences/processed/modMUSMU.fa>; <http://inparanoid.sbc.su.se/download/current/sqltables/sqltable.ensHOMSA.fa-modMUSMU.fa> Release 6.0, 09/07

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.HsMm.ortholog.db")
```

---

```
org.HsMm.orthologMAPCOUNTS
      Number of mapped keys for the maps in package
      org.HsMm.ortholog.db
```

---

**Description**

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

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```
org.HsMm.orthologORGANISM
```

*The Organism for org.HsMm.ortholog.db*

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**Description**

org.HsMm.orthologORGANISM is an R object that contains a single item: a character string that names the organism for which org.HsMm.ortholog.db was built.

**Details**

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

**Examples**

```
org.HsMm.orthologORGANISM
```

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```
org.HsMm.orthologORTHOLOG
```

*Map protein identifier to its ortholog*

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**Description**

org.HsMm.orthologORTHOLOG map protein identifier to its ortholog identifier.

**Details**

Mappings were based on data provided by: Inparanoid (<http://inparanoid.sbc.su.se/download/current/sequences/processed/ensHOMSA.fa>; <http://inparanoid.sbc.su.se/download/current/sequences/processed/modMUSMU.fa>; <http://inparanoid.sbc.su.se/download/current/sqltables/sqltable.ensHOMSA.fa-modMUSMU.fa>) on Release 6.0, 09/07

**Examples**

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

## For the reverse map org.HsMm.orthologORTHOLOG2PROTEIN
## Convert to a list
xxx <- as.list(org.HsMm.orthologORTHOLOG2PROTEIN)
## randomly display 10 proteins
sample(xxx, 10)
```

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org.HsMm.orthologSEQ

*Map protein identifier to the protein sequence*

---

**Description**

org.HsMm.orthologSEQ provides mappings between a protein identifier and the protein Sequence.

**Details**

Mappings were based on data provided by: Inparanoid (<http://inparanoid.sbc.su.se/download/current/sequences/processed/ensHOMSA.fa>; <http://inparanoid.sbc.su.se/download/current/sequences/processed/modMUSMU.fa>; <http://inparanoid.sbc.su.se/download/current/sqltables/sqltable.ensHOMSA.fa-modMUSMU.fa>) on Release 6.0, 09/07

**Examples**

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

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