org.Hbacteriophora.eg.db

November 11, 2026

`org.Hbacteriophora.eg.db`

Bioconductor annotation data package

Description

Welcome to the org.Hbacteriophora.eg.db annotation Package. This is an organism specific package. The purpose is to provide detailed information about the species abbreviated in the second part of the package name org.Hbacteriophora.eg.db. This package is updated biannually.

To learn more about this package, users are encouraged to learn about the select, columns, keys and keytypes methods. These are described in a walkthrough on the bioconductor website as well as in the manual pages and vignettes in the AnnotationDbi package.

Examples

```
library(AnnotationHub)
ah <- AnnotationHub()
orgdb <- ah[["AH121717"]]
keytypes(orgdb)
head(keys(orgdb, keytype = "KEGGPATHWAY"))
```

`org.Hbacteriophora.egGENENAME`

Retrieve Gene Names for Given Symbols

Description

Provides full gene names for given gene symbols.

Value

A data frame of gene symbols and full gene names.

Examples

```
library(AnnotationHub)
ah <- AnnotationHub()
orgdb <- ah[["AH121717"]]
symbols <- head(keys(orgdb, keytype = "SYMBOL"))
select(orgdb, keys = symbols, columns = "GENENAME", keytype = "SYMBOL")
```

`org.Hbacteriophora.egGID`

Retrieve All Internal Gene IDs (GID)

Description

Internal database-assigned gene IDs used for consistent internal referencing.

Value

A character vector of gene IDs.

Examples

```
library(AnnotationHub)
ah <- AnnotationHub()
orgdb <- ah[["AH121717"]]
head(keys(orgdb, keytype = "GID"))
```

`org.Hbacteriophora.egGO`

Map Genes to GO Terms (Direct Annotations)

Description

Retrieves directly annotated Gene Ontology terms.

Value

A data frame of GO terms, ontology, and evidence.

Examples

```
library(AnnotationHub)
ah <- AnnotationHub()
orgdb <- ah[["AH121717"]]
gids <- head(keys(orgdb, keytype = "GID"))
select(orgdb, keys = gids, columns = "GO", keytype = "GID")
```

org.Hbacteriophora.egGOALL

Map Genes to GO Terms (Including Ancestors)

Description

Retrieves all GO terms including hierarchical ancestors.

Value

A data frame with GOALL terms, ONTOLOGYALL, and EVIDENCEALL.

Examples

```
library(AnnotationHub)
ah <- AnnotationHub()
orgdb <- ah[["AH121717"]]
gids <- head(keys(orgdb, keytype = "GID"))
select(orgdb, keys = gids, columns = "GOALL", keytype = "GID")
```

org.Hbacteriophora.egKEGGPATHWAY

Map Genes to KEGG Pathways

Description

KEGG pathways represent functional modules and metabolic pathways.

Value

A data frame mapping genes to KEGG pathways.

Examples

```
library(AnnotationHub)
ah <- AnnotationHub()
orgdb <- ah[["AH121717"]]
gids <- head(keys(orgdb, keytype = "GID"))
select(orgdb, keys = gids, columns = "KEGGPATHWAY", keytype = "GID")
```

`org.Hbacteriophora.egONTOLOGY`

List GO Ontology Categories (Direct)

Description

Ontology categories for directly assigned GO terms (BP, MF, CC).

Value

A character vector of ontology types.

Examples

```
library(AnnotationHub)
ah <- AnnotationHub()
orgdb <- ah[["AH121717"]]
gids <- head(keys(orgdb, keytype = "GID"))
select(orgdb, keys = gids, columns = "ONTOLOGY", keytype = "GID")
```

`org.Hbacteriophora.egONTOLOGYALL`

List GO Ontology Categories (All Terms)

Description

Ontology types associated with all GO terms (direct + ancestors).

Value

A character vector of ontology types.

Examples

```
library(AnnotationHub)
ah <- AnnotationHub()
orgdb <- ah[["AH121717"]]
gids <- head(keys(orgdb, keytype = "GID"))
select(orgdb, keys = gids, columns = "ONTOLOGYALL", keytype = "GID")
```

org.Hbacteriophora.egORGANISM

The Organism for org.Hbacteriophora.eg

Description

org.Hbacteriophora.egORGANISM is an R object that contains a single item: a character string that names the organism for which org.Hbacteriophora.eg was built.

Details

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

See Also

- AnnotationDb-class for use of the select() interface.

Examples

```
## select() interface:
## Objects in this package can be accessed using the select() interface
## from the AnnotationDbi package. See ?select for details.

## Bimap interface:
org.Hbacteriophora.egORGANISM
```

org.Hbacteriophora.egSYMBOL

Retrieve All Gene Symbols

Description

Gene symbols are standardized short-form identifiers used in biological studies.

Value

A character vector of gene symbols.

Examples

```
library(AnnotationHub)
ah <- AnnotationHub()
orgdb <- ah[["AH121717"]]
head(keys(orgdb, keytype = "SYMBOL"))
```

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

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

org.Hbacteriophora.eg_dbschema prints the schema definition of the package annotation DB.

org.Hbacteriophora.eg_dbInfo prints other information about the package annotation DB.

Value

org.Hbacteriophora.eg_dbconn: a DBIConnection object representing an open connection to the package annotation DB.

org.Hbacteriophora.eg_dbfile: a character string with the path to the package annotation DB.

org.Hbacteriophora.eg_dbschema: none (invisible NULL).

org.Hbacteriophora.eg_dbInfo: none (invisible NULL).

See Also

dbGetQuery, dbConnect, dbconn, dbfile, dbschema, dbInfo

Examples

```
library(DBI)
library(AnnotationHub)

# Retrieve OrgDb from AnnotationHub
ah <- AnnotationHub()
orgdb <- ah[["AH121717"]]

# Count rows in "genes" table
dbGetQuery(dbconn(orgdb), "SELECT COUNT(*) FROM genes")

# List tables and fields
dbListTables(dbconn(orgdb))
dbListFields(dbconn(orgdb), "genes")
```

Index

∗ **datasets**
org.Hbacteriophora.eg.db, 1
org.Hbacteriophora.eg_dbconn, 6
org.Hbacteriophora.egGENENAME, 1
org.Hbacteriophora.egGID, 2
org.Hbacteriophora.egGO, 2
org.Hbacteriophora.egGOALL, 3
org.Hbacteriophora.egKEGGPATHWAY, 3
org.Hbacteriophora.egONTOLOGY, 4
org.Hbacteriophora.egONTOLOGYALL, 4
org.Hbacteriophora.egORGANISM, 5
org.Hbacteriophora.egSYMBOL, 5
∗ **utilities**
org.Hbacteriophora.eg_dbconn, 6

AnnDbObj, *6*

cat, *6*

dbconn, *6*
dbConnect, *6*
dbDisconnect, *6*
dbfile, *6*
dbGetQuery, *6*
dbInfo, *6*
dbschema, *6*

org.Hbacteriophora.eg (org.Hbacteriophora.eg.db), 1
org.Hbacteriophora.eg.db, 1
org.Hbacteriophora.eg_dbconn, 6
org.Hbacteriophora.eg_dbfile (org.Hbacteriophora.eg_dbconn), 6
org.Hbacteriophora.eg_dbInfo (org.Hbacteriophora.eg_dbconn), 6
org.Hbacteriophora.eg_dbschema (org.Hbacteriophora.eg_dbconn), 6
org.Hbacteriophora.egGENENAME, 1
org.Hbacteriophora.egGID, 2
org.Hbacteriophora.egGO, 2
org.Hbacteriophora.egGOALL, 3
org.Hbacteriophora.egKEGGPATHWAY, 3
org.Hbacteriophora.egONTOLOGY, 4
org.Hbacteriophora.egONTOLOGYALL, 4
org.Hbacteriophora.egORGANISM, 5
org.Hbacteriophora.egSYMBOL, 5