

# org.Hbacteriophora.eg.db

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org.Hbacteriophora.eg.db

*Bioconductor annotation data package*

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## 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"))
```

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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")
```

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`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")
```

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`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 <a href="#">cat</a> 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")
```

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