

# KEGG.db

October 16, 2018

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KEGG.db

*Bioconductor annotation data package*

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## Description

Welcome to the KEGG.db annotation Package. The purpose of this package was to provide detailed information about the latest version of the KEGG pathway databases. But a number of years ago, KEGG changed their policy about sharing their data and so this package is no longer allowed to be current. Users who are interested in a more current pathway data are encouraged to look at the KEGGREST or reactome.db packages.

Objects in this package are accessed using the `select()` interface. See `?select` in the `AnnotationDbi` package for details.

## See Also

- [AnnotationDb-class](#) for use of `keys()`, `columns()` and `select()`.

## Examples

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

## Bimap interface:
## The 'old style' of interacting with these objects is manipulation as
## bimap. While this approach is still available we strongly encourage the
## use of select().
ls("package:KEGG.db")
```

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KEGGENZYMEID2GO	<i>An annotation data object that maps Enzyme Commission numbers to Gene Ontology identifiers</i>
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### Description

KEGGENZYMEID2GO maps Enzyme Commission numbers to Gene Ontology (GO) identifiers

### Details

This is an R object containing key and value pairs. Keys are Enzyme Commission numbers and values are GO identifiers. Values are vectors of length 1. Enzyme Commission numbers that can not be mapped to a GO term are assigned a value NA.

Mappings were based on data provided by: Gene Ontology External Link <http://www.geneontology.org/external2go>  
With a date stamp from the source of: 2015-Sepec2go27

### References

<ftp://ftp.genome.ad.jp/pub/kegg/pathways>

### 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:
xx <- as.list(KEGGENZYMEID2GO)
if(length(xx) > 0){
  # Get the value of the first key
  xx[[1]]
  # Get values for a few keys
  if(length(xx) >= 3)
    xx[1:3]
}
```

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KEGGEXTID2PATHID	<i>An annotation data object that maps Entrez Gene or Open Reading Frame identifiers to KEGG pathway identifiers</i>
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### Description

KEGGEXTID2PATHID maps Entrez Gene (for human, mouse, and rat) and Open Reading Frame (for yeast) identifiers to KEGG pathway identifiers.

**Details**

This is an R object containing key and value pairs. Keys are Entrez Gene identifiers for human, mouse, and rat and Open Reading Frame (ORF) identifiers for yeast and values are the corresponding KEGG pathway identifiers. Values are vectors of length 1 or greater depending on whether a given external identifier can be mapped to only one or more KEGG pathway identifiers. NAs are assigned to Entrez Gene or ORF identifiers that can not be mapped to any pathway identifier.

KEGG pathway identifiers are the identifiers used by KEGG for various pathways.

Mappings between KEGG pathway identifiers and pathway names can be obtained through another annotation data object named KEGGPATHID2NAME.

Mappings were based on data provided by: KEGG GENOME <ftp://ftp.genome.jp/pub/kegg/genomes> With a date stamp from the source of: 2011-Mar15

**References**

<ftp://ftp.genome.ad.jp/pub/kegg/pathways>

**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:
xx <- as.list(KEGGEXTID2PATHID)
if(length(xx) > 0){
  # Get the value of the first key
  xx[[1]]
  # Get the values for multiget for a few keys
  if(length(xx) >= 3){
    xx[1:3]
  }
}
```

---

KEGGGO2ENZYMEID

*An annotation data object that maps Gene Ontology (GO) identifiers to Enzyme Commission numbers*

---

**Description**

KEGGGO2ENZYMEID maps GO identifiers to Enzyme Commission numbers

**Details**

This is an R object containing key and value pairs. Keys are GO identifiers and values are Enzyme Commission numbers. Values are vectors of length 1. GO identifiers can not be mapped to any Enzyme Commission number are assigned NAs.

Mappings are based on data provided by: Gene Ontology External Link <http://www.geneontology.org/external2go> With a date stamp from the source of: 2015-Sepec2go27

## References

<ftp://ftp.genome.ad.jp/pub/kegg/pathways>

## 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:
xx <- as.list(KEGGG02ENZYMEID)
if(length(xx) > 0){
  # Get the value of the first key
  xx[[1]]
  # Get values for a few keys
  if(length(xx) >= 3){
    xx[1:3]
  }
}
```

---

KEGGMAPCOUNTS

*Number of mapped keys for the maps in package KEGG.db*

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## Description

KEGGMAPCOUNTS provides the "map count" (i.e. the count of mapped keys) for each map in package KEGG.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](#)
- [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:
KEGGMAPCOUNTS
mapnames <- names(KEGGMAPCOUNTS)
KEGGMAPCOUNTS[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 KEGG.db
checkMAPCOUNTS("KEGG.db")
```

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KEGGPATHID2EXTID	<i>An annotation data object that maps KEGG pathway identifiers to Entrez Gene or Open Reading Frame identifiers.</i>
------------------	---

---

## Description

KEGGPATHID2EXTID maps KEGG pathway identifiers to Entrez Gene (for human, mouse, and rat) or Open Reading Frame (for yeast) identifiers

## Details

This is an R object containing key and value pairs. Keys are KEGG pathway identifiers and values are Entrez Gene identifiers for human, mouse, and rat or Open Reading Frame (ORF) identifiers for yeast. Values are vectors of length 1 or greater depending on whether a pathway identifier can be mapped to one or more Entrez Gene or ORF identifiers. NAs are assigned to KEGG pathway identifiers that can not be mapped to any Entrez Gene or ORF identifiers.

KEGG pathway identifiers are the identifiers used by KEGG for various pathways.

Mappings between KEGG pathway identifiers and pathway names can be obtained through another annotation data object named KEGGPATHID2NAME.

Mappings were based on data provided by: KEGG GENOME <ftp://ftp.genome.jp/pub/kegg/genomes>  
With a date stamp from the source of: 2011-Mar15

## References

<ftp://ftp.genome.ad.jp/pub/kegg/pathways>

## 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:
xx <- as.list(KEGGPATHID2EXTID)
if(length(xx) > 0){
  # Get the value of the first key
  xx[[1]]
  # Get the values for multiget for a few keys
  if(length(xx) >= 3){
    xx[1:3]
  }
}
```

---

KEGGPATHID2NAME	<i>An annotation data object that maps KEGG pathway identifiers to KEGG pathway names</i>
-----------------	---

---

**Description**

KEGGPATHID2NAME maps KEGG pathway identifiers to pathway names used by KEGG for various pathways

**Details**

This is an R object containing key and value pairs. Keys are KEGG pathway identifiers and values are pathway names. Values are vectors of length 1.

Mappings were based on data provided by: KEGG PATHWAY <ftp://ftp.genome.jp/pub/kegg/pathway>  
 With a date stamp from the source of: 2011-Mar15

**References**

<ftp://ftp.genome.ad.jp/pub/kegg/pathways>

**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:
xx <- as.list(KEGGPATHID2NAME)
if(length(xx) > 0){
  # get the value for the first key
  xx[[1]]
  # Get the values for a few keys
  if(length(xx) >= 3){
```

```
    xx[1:3]
  }
}
```

---

KEGGPATHNAME2ID	<i>An annotation data object that maps KEGG pathway names to identifiers for the corresponding pathway names used by KEGG</i>
-----------------	---

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### Description

KEGGPATHNAME2ID maps KEGG pathway names to pathway identifiers used by KEGG for various pathways

### Details

This is an R object containing key and value pairs. Keys are KEGG pathway names and values are pathway identifiers. Values are vectors of length 1.

Mappings were based on data provided by: KEGG PATHWAY <ftp://ftp.genome.jp/pub/kegg/pathway>  
With a date stamp from the source of: 2011-Mar15

### References

<ftp://ftp.genome.ad.jp/pub/kegg/pathways>

### 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:
xx <- as.list(KEGGPATHNAME2ID)
if(length(xx) > 0){
  # get the value for the first key
  xx[[1]]
  # Get the values for a few keys
  if(length(xx) >= 3){
    xx[1:3]
  }
}
```

---

KEGG\_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

```
KEGG_dbconn()  
KEGG_dbfile()  
KEGG_dbschema(file="", show.indices=FALSE)  
KEGG_dbInfo()
```

## Arguments

<code>file</code>	A connection, or a character string naming the file to print to (see the <code>file</code> argument of the <code>cat</code> function for the details).
<code>show.indices</code>	The CREATE INDEX statements are not shown by default. Use <code>show.indices=TRUE</code> to get them.

## Details

KEGG\_dbconn returns a connection object to the package annotation DB. **IMPORTANT:** Don't call `dbDisconnect` on the connection object returned by `KEGG_dbconn` or you will break all the `AnnDbObj` objects defined in this package!

KEGG\_dbfile returns the path (character string) to the package annotation DB (this is an SQLite file).

KEGG\_dbschema prints the schema definition of the package annotation DB.

KEGG\_dbInfo prints other information about the package annotation DB.

## Value

KEGG\_dbconn: a `DBIConnection` object representing an open connection to the package annotation DB.

KEGG\_dbfile: a character string with the path to the package annotation DB.

KEGG\_dbschema: none (invisible NULL).

KEGG\_dbInfo: none (invisible NULL).

## See Also

[dbGetQuery](#), [dbConnect](#), [dbconn](#), [dbfile](#), [dbschema](#), [dbInfo](#)



**Examples**

```
library(DBI)
## Count the number of rows in the "pathway2name" table:
dbGetQuery(KEGG_dbconn(), "SELECT COUNT(*) FROM pathway2name")
```

```
KEGG_dbschema()
```

```
KEGG_dbInfo()
```

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