

# org.Ag.eg.db

February 8, 2012

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org.Ag.egACCNUM      *Map Entrez Gene identifiers to GenBank Accession Numbers*

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## Description

org.Ag.egACCNUM is an R object that contains mappings between Entrez Gene identifiers and GenBank accession numbers.

## Details

This object is a simple mapping of Entrez Gene identifiers <http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene> to all possible GenBank accession numbers.

Mappings were based on data provided by: Entrez Gene <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA> With a date stamp from the source of: 2011-Sep14

## Examples

```
x <- org.Ag.egACCNUM
# Get the entrez gene identifiers that are mapped to an ACCNUM
mapped_genes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_genes])
if(length(xx) > 0) {
  # Get the ACCNUM for the first five genes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
#For the reverse map ACCNUM2EG:
# Convert to a list
xx <- as.list(org.Ag.egACCNUM2EG)
if(length(xx) > 0){
  # Gets the entrez gene identifiers for the first five Entrez Gene IDs
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

org.Ag.eg.db

*Bioconductor annotation data package*

---

**Description**

Welcome to the org.Ag.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.Ag.eg.db. "Hs" is for Homo sapiens. This package is updated biannually.

You can learn what objects this package supports with the following command:

```
ls ("package:org.Ag.eg.db")
```

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**

```
ls ("package:org.Ag.eg.db")
```

---

org.Ag.egCHRENGTHS

*A named vector for the length of each of the chromosomes*

---

**Description**

org.Ag.egCHRENGTHS provides the length measured in base pairs for each of the chromosomes.

**Details**

This is a named vector with chromosome numbers as the names and the corresponding lengths for chromosomes as the values.

Total lengths of chromosomes were derived by calculating the number of base pairs on the sequence string for each chromosome.

**Examples**

```
tt <- org.Ag.egCHRENGTHS
# Length of chromosome 1
tt["1"]
```

---

 org.Ag.egCHR

*Map Entrez Gene IDs to Chromosomes*


---

### Description

org.Ag.egCHR is an R object that provides mappings between entrez gene identifiers and the chromosome that contains the gene of interest.

### Details

Each entrez gene identifier maps to a vector of a chromosome.

Mappings were based on data provided by: Entrez Gene ftp://ftp.ncbi.nlm.nih.gov/gene/DATA With a date stamp from the source of: 2011-Sep14

### Examples

```
x <- org.Ag.egCHR
# Get the entrez gene identifiers that are mapped to a chromosome
mapped_genes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_genes])
if(length(xx) > 0) {
  # Get the CHR for the first five genes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

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

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

org.Ag.eg\_dbschema prints the schema definition of the package annotation DB.

org.Ag.eg\_dbInfo prints other information about the package annotation DB.

**Value**

org.Ag.eg\_dbconn: a DBIConnection object representing an open connection to the package annotation DB.

org.Ag.eg\_dbfile: a character string with the path to the package annotation DB.

org.Ag.eg\_dbschema: none (invisible NULL).

org.Ag.eg\_dbInfo: none (invisible NULL).

**See Also**

`dbGetQuery`, `dbConnect`, `dbconn`, `dbfile`, `dbschema`, `dbInfo`

**Examples**

```
## Count the number of rows in the "genes" table:
dbGetQuery(org.Ag.eg_dbconn(), "SELECT COUNT(*) FROM genes")

## The connection object returned by org.Ag.eg_dbconn() was
## created with:
dbConnect(SQLite(), dbname=org.Ag.eg_dbfile(), cache_size=64000,
synchronous=0)

org.Ag.eg_dbschema()

org.Ag.eg_dbInfo()
```

---

```
org.Ag.egENSEMBLPROT
```

*Map Ensembl protein accession numbers with Entrez Gene identifiers*

---

**Description**

org.Ag.egENSEMBL is an R object that contains mappings between Entrez Gene identifiers and Ensembl protein accession numbers.

**Details**

This object is a simple mapping of Entrez Gene identifiers <http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene> to Ensembl protein accession numbers.

Mappings were based on data provided by: [ftp://ftp.ensembl.org/pub/current\\_fasta](ftp://ftp.ensembl.org/pub/current_fasta)  
<ftp://ftp.ncbi.nlm.nih.gov/gene/DATA>

**Examples**

```
x <- org.Ag.egENSEMBLPROT
# Get the entrez gene IDs that are mapped to an Ensembl ID
mapped_genes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_genes])
if(length(xx) > 0) {
  # Get the Ensembl gene IDs for the first five proteins
  xx[1:5]
  # Get the first one
  xx[[1]]
}
#For the reverse map ENSEMBLPROT2EG:
# Convert to a list
xx <- as.list(org.Ag.egENSEMBLPROT2EG)
if(length(xx) > 0){
  # Gets the entrez gene IDs for the first five Ensembl IDs
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

org.Ag.egENSEMBL     *Map Ensembl gene accession numbers with Entrez Gene identifiers*

---

**Description**

org.Ag.egENSEMBL is an R object that contains mappings between Entrez Gene identifiers and Ensembl gene accession numbers.

**Details**

This object is a simple mapping of Entrez Gene identifiers <http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene> to Ensembl gene Accession Numbers.

Mappings were based on data provided by BOTH of these sources: <http://www.ensembl.org/biomart/martview/> <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA>

This mapping is a combination of NCBI to ensembl IDs from BOTH NCBI and ensembl. Users who wish to only use mappings from NCBI are encouraged to see the ncbi2ensembl table in the appropriate organism package. Users who wish to only use mappings from ensembl are encouraged to see the ensembl2ncbi table which is also found in the appropriate organism packages. These mappings are based upon the ensembl table which is contains data from BOTH of these sources in an effort to maximize the chances that you will find a match.

Mappings were based on data provided by: Entrez Gene <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA> With a date stamp from the source of: 2011-Sep14

**Examples**

```
x <- org.Ag.egENSEMBL
# Get the entrez gene IDs that are mapped to an Ensembl ID
mapped_genes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_genes])
```

```

if(length(xx) > 0) {
  # Get the Ensembl gene IDs for the first five genes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
#For the reverse map ENSEMBL2EG:
# Convert to a list
xx <- as.list(org.Ag.egENSEMBL2EG)
if(length(xx) > 0){
  # Gets the entrez gene IDs for the first five Ensembl IDs
  xx[1:5]
  # Get the first one
  xx[[1]]
}

```

---

```
org.Ag.egENSEMBLTRANS
```

*Map Ensembl transcript accession numbers with Entrez Gene identifiers*

---

## Description

org.Ag.egENSEMBL is an R object that contains mappings between Entrez Gene identifiers and Ensembl transcript accession numbers.

## Details

This object is a simple mapping of Entrez Gene identifiers <http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene> to Ensembl transcript accession numbers.

Mappings were based on data provided by: [ftp://ftp.ensembl.org/pub/current\\_fasta](ftp://ftp.ensembl.org/pub/current_fasta)  
<ftp://ftp.ncbi.nlm.nih.gov/gene/DATA>

## Examples

```

x <- org.Ag.egENSEMBLTRANS
# Get the entrez gene IDs that are mapped to an Ensembl ID
mapped_genes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_genes])
if(length(xx) > 0) {
  # Get the Ensembl gene IDs for the first five proteins
  xx[1:5]
  # Get the first one
  xx[[1]]
}
#For the reverse map ENSEMBLTRANS2EG:
# Convert to a list
xx <- as.list(org.Ag.egENSEMBLTRANS2EG)
if(length(xx) > 0){
  # Gets the entrez gene IDs for the first five Ensembl IDs
  xx[1:5]
  # Get the first one
  xx[[1]]
}

```

---

org.Ag.egENZYME      *Map between Entrez Gene IDs and Enzyme Commission (EC) Numbers*

---

## Description

org.Ag.egENZYME is an R object that provides mappings between entrez gene identifiers and EC numbers.

## Details

Each entrez gene identifier maps to a named vector containing the EC number that corresponds to the enzyme produced by that gene. The name corresponds to the entrez gene identifier. If this information is unknown, the vector will contain an NA.

Enzyme Commission numbers are assigned by the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology <http://www.chem.qmw.ac.uk/iubmb/enzyme/> to allow enzymes to be identified.

An Enzyme Commission number is of the format EC x.y.z.w, where x, y, z, and w are numeric numbers. In org.Ag.egENZYME2EG, EC is dropped from the Enzyme Commission numbers.

Enzyme Commission numbers have corresponding names that describe the functions of enzymes in such a way that EC x is a more general description than EC x.y that in turn is a more general description than EC x.y.z. The top level EC numbers and names are listed below:

EC 1 oxidoreductases

EC 2 transferases

EC 3 hydrolases

EC 4 lyases

EC 5 isomerases

EC 6 ligases

The EC name for a given EC number can be viewed at <http://www.chem.qmul.ac.uk/iupac/jcfn/index.html#6>

Mappings between entrez gene identifiers and enzyme identifiers were obtained using files provided by: KEGG GENOME <ftp://ftp.genome.jp/pub/kegg/genomes> With a date stamp from the source of: 2011-Mar15

For the reverse map, each EC number maps to a named vector containing the entrez gene identifier that corresponds to the gene that produces that enzyme. The name of the vector corresponds to the EC number.

## References

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

## Examples

```
x <- org.Ag.egENZYME
# Get the entrez gene identifiers that are mapped to an EC number
mapped_genes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_genes])
```

```

if(length(xx) > 0) {
  # Get the ENZYME for the first five genes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
# For the reverse map:
# Convert to a list
xx <- as.list(org.Ag.egENZYME2EG)
if(length(xx) > 0){
  # Gets the entrez gene identifiers for the first five enzyme
  #commission numbers
  xx[1:5]
  # Get the first one
  xx[[1]]
}

```

---

org.Ag.egGENENAME *Map between Entrez Gene IDs and Genes*

---

## Description

org.Ag.egGENENAME is an R object that maps entrez gene identifiers to the corresponding gene name.

## Details

Each entrez gene identifier maps to a named vector containing the gene name. The vector name corresponds to the entrez gene identifier. If the gene name is unknown, the vector will contain an NA.

Gene names currently include both the official (validated by a nomenclature committee) and preferred names (interim selected for display) for genes. Efforts are being made to differentiate the two by adding a name to the vector.

Mappings were based on data provided by: Entrez Gene <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA> With a date stamp from the source of: 2011-Sep14

## Examples

```

x <- org.Ag.egGENENAME
# Get the gene names that are mapped to an entrez gene identifier
mapped_genes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_genes])
if(length(xx) > 0) {
  # Get the GENE NAME for the first five genes
  xx[1:5]
  # Get the first one
  xx[[1]]
}

```



---

org.Ag.egGO2ALLEGS *Map Between Gene Ontology (GO) Identifiers and all Entrez Gene Identifiers in the subtree*

---

## Description

org.Ag.egGO2ALLEGS is an R object that provides mappings between a given GO identifier and all Entrez Gene identifiers annotated at that GO term or one of its children in the GO ontology.

## Details

GO consists of three ontologies—molecular function (MF), biological process (BP), and cellular component (CC). All ontologies are structured as directed acyclic graphs (DAGs). Each node in each DAG (tree) is a GO term (id) associated with a named vector of manufacturer identifiers. The name associated with each Entrez Gene id corresponds to the evidence code for that GO identifier. This object org.Ag.egGO2ALLEGS maps between a given GO identifier and all Entrez Gene identifiers annotated at that GO term or one of its children in the GO ontology.

The evidence code indicates what kind of evidence supports the association between the GO and Entrez Gene identifiers. Evidence codes currently 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

A GO identifier may be mapped to the same Entrez Gene identifier more than once but the evidence code can be different. Mappings between Gene Ontology identifiers and Gene Ontology terms and other information are available in a separate data package named GO.

Mappings were based on data provided by: Gene Ontology <ftp://ftp.geneontology.org/pub/go/godatabase/archive/latest-lite/> With a date stamp from the source of: 20110910 and Entrez Gene <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA/> With a date stamp from the source of: 2011-Sep14

## References

<ftp://ftp.ncbi.nlm.nih.gov/gene/DATA/>

**Examples**

```

# Convert to a list
xx <- as.list(org.Ag.egGO2ALLEGS)
if(length(xx) > 0){
  # Gets the Entrez Gene identifiers for the top 2nd and 3rd GO identifiers
  goids <- xx[2:3]
  # Gets all the Entrez Gene identifiers for the first element of goids
  goids[[1]]
  # Evidence code for the mappings
  names(goids[[1]])
}

```

---

 org.Ag.egGO

---

*Map between Entrez Gene IDs and Gene Ontology (GO)*


---

**Description**

org.Ag.egGO is an R object that provides mappings between entrez gene identifiers and the GO identifiers that they are directly associated with. This mapping and its reverse mapping do NOT associate the child terms from the GO ontology with the gene. Only the directly evidenced terms are represented here.

**Details**

Each Entrez Gene identifier is mapped to a list of lists. The names on the outer list are GO identifiers. Each inner list consists of three named elements: GOID, Ontology, and Evidence.

The GOID element matches the GO identifier named in the outer list and is included for convenience when processing the data using 'lapply'.

The Ontology element indicates which of the three Gene Ontology categories this identifier belongs to. The categories are biological process (BP), cellular component (CC), and molecular function (MF).

The Evidence element contains a code indicating what kind of evidence supports the association of the GO identifier to the Entrez Gene 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 between entrez gene identifiers and GO information were obtained through their mappings to Entrez Gene identifiers. NAs are assigned to entrez gene identifiers that can not be mapped

to any Gene Ontology information. Mappings between Gene Ontology identifiers and Gene Ontology terms and other information are available in a separate data package named GO.

Mappings were based on data provided by: Gene Ontology <ftp://ftp.geneontology.org/pub/go/godatabase/archive/latest-lite/> With a date stamp from the source of: 20110910

For the reverse map GO2EG, each GO term maps to a named vector of entrez gene identifiers. A GO identifier may be mapped to the same entrez gene identifier more than once but the evidence code can be different. Mappings between Gene Ontology identifiers and Gene Ontology terms and other information are available in a separate data package named GO.

## References

<ftp://ftp.ncbi.nlm.nih.gov/gene/DATA/>

## See Also

[org.Ag.egGO2ALLEGS.](#)

## Examples

```
x <- org.Ag.egGO
# Get the entrez gene identifiers that are mapped to a GO ID
mapped_genes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_genes])
if(length(xx) > 0) {
  # Try the first one
  got <- xx[[1]]
  got[[1]][["GOID"]]
  got[[1]][["Ontology"]]
  got[[1]][["Evidence"]]
}
# For the reverse map:
# Convert to a list
xx <- as.list(org.Ag.egGO2EG)
if(length(xx) > 0){
  # Gets the entrez gene ids for the top 2nd and 3rd GO identifiers
  goids <- xx[2:3]
  # Gets the entrez gene ids for the first element of goids
  goids[[1]]
  # Evidence code for the mappings
  names(goids[[1]])
}
```

---

org.Ag.egMAPCOUNTS *Number of mapped keys for the maps in package org.Ag.eg.db*

---

## Description

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

---

org.Ag.egORGANISM *The Organism for org.Ag.eg*

---

**Description**

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

**Details**

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

**Examples**

```
org.Ag.egORGANISM
```

---

org.Ag.egPATH *Mappings between Entrez Gene identifiers and KEGG pathway identifiers*

---

**Description**

KEGG (Kyoto Encyclopedia of Genes and Genomes) maintains pathway data for various organisms. org.Ag.egPATH maps entrez gene identifiers to the identifiers used by KEGG for pathways

## Details

Each KEGG pathway has a name and identifier. Pathway name for a given pathway identifier can be obtained using the KEGG data package that can either be built using AnnBuilder or downloaded from Bioconductor <http://www.bioconductor.org>.

Graphic presentations of pathways are searchable at url <http://www.genome.ad.jp/kegg/pathway.html> by using pathway identifiers as keys.

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

<http://www.genome.ad.jp/kegg/>

## Examples

```
x <- org.Ag.egPATH
# Get the entrez gene identifiers that are mapped to a KEGG pathway ID
mapped_genes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_genes])
if(length(xx) > 0) {
  # Get the PATH for the first five genes
  xx[1:5]
  # Get the first one
  xx[[1]]
}

# For the reverse map:
# Convert the object to a list
xx <- as.list(org.Ag.egPATH2EG)
# Remove pathway identifiers that do not map to any entrez gene id
xx <- xx[!is.na(xx)]
if(length(xx) > 0){
  # The entrez gene identifiers for the first two elements of XX
  xx[1:2]
  # Get the first one
  xx[[1]]
}
```

---

org.Ag.egPMID

*Map between Entrez Gene Identifiers and PubMed Identifiers*

---

## Description

org.Ag.egPMID is an R object that provides mappings between entrez gene identifiers and PubMed identifiers.

## Details

Each entrez gene identifier is mapped to a named vector of PubMed identifiers. The name associated with each vector corresponds to the entrez gene identifier. The length of the vector may be one or

greater, depending on how many PubMed identifiers a given entrez gene identifier is mapped to. An NA is reported for any entrez gene identifier that cannot be mapped to a PubMed identifier.

Titles, abstracts, and possibly full texts of articles can be obtained from PubMed by providing a valid PubMed identifier. The `pubmed` function of `annotate` can also be used for the same purpose.

Mappings were based on data provided by: Entrez Gene <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA> With a date stamp from the source of: 2011-Sep14

## References

<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=PubMed>

## Examples

```
x <- org.Ag.egPMID
# Get the entrez gene identifiers that are mapped to any PubMed ID
mapped_genes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_genes])
if(length(xx) > 0){
  # The entrez gene identifiers for the first two elements of XX
  xx[1:2]
  # Get the first one
  xx[[1]]
  if(interactive() && !is.null(xx[[1]]) && !is.na(xx[[1]]))
    && require(annotate){
      # Gets article information as XML files
      xmls <- pubmed(xx[[1]], disp = "data")
      # Views article information using a browser
      pubmed(xx[[1]], disp = "browser")
    }
}
# For the reverse map:
# Convert the object to a list
xx <- as.list(org.Ag.egPMID2EG)
if(length(xx) > 0){
  # The entrez gene identifiers for the first two elements of XX
  xx[1:2]
  # Get the first one
  xx[[1]]
  if(interactive() && require(annotate){
    # Gets article information as XML files for a PubMed id
    xmls <- pubmed(names(xx)[1], disp = "data")
    # Views article information using a browser
    pubmed(names(xx)[1], disp = "browser")
  }
}
```

---

org.Ag.egREFSEQ

*Map between Entrez Gene Identifiers and RefSeq Identifiers*

---

## Description

`org.Ag.egREFSEQ` is an R object that provides mappings between entrez gene identifiers and Ref-Seq identifiers.



---

org.Ag.egSYMBOL      *Map between Entrez Gene Identifiers and Gene Symbols*

---

## Description

org.Ag.egSYMBOL is an R object that provides mappings between entrez gene identifiers and gene abbreviations.

## Details

Each entrez gene identifier is mapped to the a common abbreviation for the corresponding gene. An NA is reported if there is no known abbreviation for a given gene.

Symbols typically consist of 3 letters that define either a single gene (ABC) or multiple genes (ABC1, ABC2, ABC3). Gene symbols can be used as key words to query public databases such as Entrez Gene.

Mappings were based on data provided by: Entrez Gene <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA> With a date stamp from the source of: 2011-Sep14

## References

<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene>

## Examples

```
x <- org.Ag.egSYMBOL
# Get the gene symbol that are mapped to an entrez gene identifiers
mapped_genes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_genes])
if(length(xx) > 0) {
  # Get the SYMBOL for the first five genes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
# For the reverse map:
x <- org.Ag.egSYMBOL2EG
# Get the entrez gene identifiers that are mapped to a gene symbol
mapped_genes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_genes])
if(length(xx) > 0) {
  # Get the entrez gene ID for the first five genes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```



---

org.Ag.egUNIGENE     *Map between Entrez Gene Identifiers and UniGene cluster identifiers*

---

## Description

org.Ag.egUNIGENE is an R object that provides mappings between entrez gene identifiers and UniGene identifiers.

## Details

Each entrez gene identifier is mapped to a UniGene identifier. An NA is reported if the entrez gene identifier cannot be mapped to UniGene at this time.

A UniGene identifier represents a cluster of sequences of a gene. Using UniGene identifiers one can query the UniGene database for information about the sequences.

Mappings were based on data provided by: Entrez Gene <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA> With a date stamp from the source of: 2011-Sep14

## References

<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene>

## Examples

```
x <- org.Ag.egUNIGENE
# Get the Unigene identifiers that are mapped to an entrez gene id
mapped_genes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_genes])
if(length(xx) > 0) {
  # Get the UNIGENE for the first five genes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
# For the reverse map:
x <- org.Ag.egUNIGENE2EG
# Get the entrez gene identifiers that are mapped to a Unigene id
mapped_genes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_genes])
if(length(xx) > 0) {
  # Get the entrez gene for the first five genes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

org.Ag.egUNIPROT    *Map Uniprot accession numbers with Entrez Gene identifiers*

---

### Description

org.Ag.egUNIPROT is an R object that contains mappings between Entrez Gene identifiers and Uniprot accession numbers.

### Details

This object is a simple mapping of Entrez Gene identifiers <http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene> to Uniprot Accession Numbers.

Mappings were based on data provided by: Entrez Gene <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA> With a date stamp from the source of: 2011-Sep14

### Examples

```
x <- org.Ag.egUNIPROT
# Get the entrez gene IDs that are mapped to a Uniprot ID
mapped_genes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_genes])
if(length(xx) > 0) {
  # Get the Uniprot gene IDs for the first five genes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

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