

# org.Tgondii.eg.db

November 7, 2017

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

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## Description

org.Tgondii.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: Tue Jan 31 17:06:38 2012

## Examples

```
x <- org.Tgondii.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]]
}
```

---

org.Tgondii.egALIAS2EG

*Map between Common Gene Symbol Identifiers and Entrez Gene*

---

## Description

org.Tgondii.egALIAS is an R object that provides mappings between common gene symbol identifiers and entrez gene identifiers.

## Details

Each gene symbol maps to a named vector containing the corresponding entrez gene identifier. The name of the vector corresponds to the gene symbol. Since gene symbols are sometimes redundantly assigned in the literature, users are cautioned that this map may produce multiple matching results for a single gene symbol. Users should map back from the entrez gene IDs produced to determine which result is the one they want when this happens.

Because of this problem with redundant assignment of gene symbols, is it never advisable to use gene symbols as primary identifiers.

This mapping includes ALL gene symbols including those which are already listed in the SYMBOL map. The SYMBOL map is meant to only list official gene symbols, while the ALIAS maps are meant to store all used symbols.

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: Tue Jan 31 17:06:38 2012

## References

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

## Examples

```
# Convert the object to a list
xx <- as.list(org.Tgondii.egALIAS2EG)
# 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.Tgondii.eg.db      *Bioconductor annotation data package*

---

### Description

Welcome to the org.Tgondii.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.Tgondii.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.Tgondii.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.Tgondii.eg.db")
```

---

org.Tgondii.egCHR      *Map Entrez Gene IDs to Chromosomes*

---

### Description

org.Tgondii.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: Tue Jan 31 17:06:38 2012

### Examples

```
x <- org.Tgondii.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.Tgondii.egGENENAME

*Map between Entrez Gene IDs and Genes*

---

### Description

org.Tgondii.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: Tue Jan 31 17:06:38 2012

### Examples

```
x <- org.Tgondii.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.Tgondii.egGO

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

---

### Description

org.Tgondii.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: blast2GO <http://www.blast2go.de/> With a date stamp from the source of: Tue Jan 31 17:06:36 2012 and Entrez Gene <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA/>

With a date stamp from the source of: Tue Jan 31 17:06:38 2012 and Gene Ontology <ftp://ftp.geneontology.org/pub/go/go>

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.Tgondii.egGO2ALLEGS](http://org.Tgondii.egGO2ALLEGS).

**Examples**

```

x <- org.Tgondii.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.Tgondii.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.Tgondii.egGO2ALLEGS

*Map Between Gene Ontology (GO) Identifiers and all Entrez Gene Identifiers in the subtree*

---

**Description**

org.Tgondii.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.Tgondii.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: blast2GO <http://www.blast2go.de/> With a date stamp from the source of: Tue Jan 31 17:06:36 2012 and Entrez Gene <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA> With a date stamp from the source of: Tue Jan 31 17:06:38 2012 and Gene Ontology <ftp://ftp.geneontology.org/pub/go/go> With a date stamp from the source of: 20110910

## References

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

## Examples

```
# Convert to a list
xx <- as.list(org.Tgondii.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.Tgondii.egMAPCOUNTS

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

---

## Description

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

```

---

```
org.Tgondii.egORGANISM
```

*The Organism for org.Tgondii.eg*

---

**Description**

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

**Details**

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

**Examples**

```
org.Tgondii.egORGANISM
```

---

```
org.Tgondii.egPMID
```

*Map between Entrez Gene Identifiers and PubMed Identifiers*

---

**Description**

org.Tgondii.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: Tue Jan 31 17:06:38 2012



## References

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

## Examples

```
x <- org.Tgondii.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.Tgondii.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.Tgondii.egREFSEQ *Map between Entrez Gene Identifiers and RefSeq Identifiers*

---

## Description

org.Tgondii.egREFSEQ is an R object that provides mappings between entrez gene identifiers and RefSeq identifiers.

## Details

Each entrez gene identifier is mapped to a named vector of RefSeq identifiers. The name represents the entrez gene identifier and the vector contains all RefSeq identifiers that can be mapped to that entrez gene identifier. The length of the vector may be one or greater, depending on how many RefSeq identifiers a given entrez gene identifier can be mapped to. An NA is reported for any entrez gene identifier that cannot be mapped to a RefSeq identifier at this time.

RefSeq identifiers differ in format according to the type of record the identifiers are for as shown below:

NG\\_XXXXX: RefSeq accessions for genomic region (nucleotide) records

NM\\_XXXXX: RefSeq accessions for mRNA records

NC\\_XXXXX: RefSeq accessions for chromosome records

NP\\_XXXXX: RefSeq accessions for protein records

XR\\_XXXXX: RefSeq accessions for model RNAs that are not associated with protein products

XM\\_XXXXX: RefSeq accessions for model mRNA records

XP\\_XXXXX: RefSeq accessions for model protein records

Where XXXXX is a sequence of integers.

NCBI <http://www.ncbi.nlm.nih.gov/RefSeq/> allows users to query the RefSeq database using RefSeq identifiers.

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: Tue Jan 31 17:06:38 2012

## References

<http://www.ncbi.nlm.nih.gov> <http://www.ncbi.nlm.nih.gov/RefSeq/>

## Examples

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

# For the reverse map:
x <- org.Tgondii.egREFSEQ2EG
# Get the RefSeq identifier that are mapped to an entrez gene ID
mapped_seqs <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_seqs])
if(length(xx) > 0) {
  # Get the entrez gene for the first five Refseqs
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

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

---

## Description

org.Tgondii.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: Tue Jan 31 17:06:38 2012

## References

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

## Examples

```
x <- org.Tgondii.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.Tgondii.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.Tgondii.egUNIGENE *Map between Entrez Gene Identifiers and UniGene cluster identifiers*

---

## Description

org.Tgondii.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: Tue Jan 31 17:06:38 2012

## References

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

## Examples

```
x <- org.Tgondii.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.Tgondii.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.Tgondii.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.Tgondii.eg_dbconn()
org.Tgondii.eg_dbfile()
org.Tgondii.eg_dbschema(file="", show.indices=FALSE)
org.Tgondii.eg_dbInfo()
```

## Arguments

file	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).
show.indices	The CREATE INDEX statements are not shown by default. Use <code>show.indices=TRUE</code> to get them.

## Details

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

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

`org.Tgondii.eg_dbschema` prints the schema definition of the package annotation DB.

`org.Tgondii.eg_dbInfo` prints other information about the package annotation DB.

## Value

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

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

`org.Tgondii.eg_dbschema`: none (invisible NULL).

`org.Tgondii.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.Tgondii.eg_dbconn(), "SELECT COUNT(*) FROM genes")

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

org.Tgondii.eg_dbschema()

org.Tgondii.eg_dbInfo()
```

# Index

## \*Topic **datasets**

- org.Tgondii.eg.db, [3](#)
- org.Tgondii.eg\_dbconn, [13](#)
- org.Tgondii.egACCNUM, [1](#)
- org.Tgondii.egALIAS2EG, [2](#)
- org.Tgondii.egCHR, [3](#)
- org.Tgondii.egGENENAME, [4](#)
- org.Tgondii.egGO, [4](#)
- org.Tgondii.egGO2ALLEGS, [6](#)
- org.Tgondii.egMAPCOUNTS, [7](#)
- org.Tgondii.egORGANISM, [8](#)
- org.Tgondii.egPMID, [8](#)
- org.Tgondii.egREFSEQ, [9](#)
- org.Tgondii.egSYMBOL, [11](#)
- org.Tgondii.egUNIGENE, [12](#)

## \*Topic **utilities**

- org.Tgondii.eg\_dbconn, [13](#)

AnnDbObj, [13](#)

cat, [13](#)

checkMAPCOUNTS, [7](#)

count.mappedkeys, [7](#)

dbconn, [13](#)

dbConnect, [13](#)

dbDisconnect, [13](#)

dbfile, [13](#)

dbGetQuery, [13](#)

dbInfo, [13](#)

dbschema, [13](#)

mappedkeys, [7](#)

org.Tgondii.eg (org.Tgondii.eg.db), [3](#)

org.Tgondii.eg.db, [3](#)

org.Tgondii.eg\_dbconn, [13](#)

org.Tgondii.eg\_dbfile  
(org.Tgondii.eg\_dbconn), [13](#)

org.Tgondii.eg\_dbInfo  
(org.Tgondii.eg\_dbconn), [13](#)

org.Tgondii.eg\_dbschema  
(org.Tgondii.eg\_dbconn), [13](#)

org.Tgondii.egACCNUM, [1](#)

org.Tgondii.egACCNUM2EG  
(org.Tgondii.egACCNUM), [1](#)

org.Tgondii.egALIAS2EG, [2](#)

org.Tgondii.egCHR, [3](#)

org.Tgondii.egGENENAME, [4](#)

org.Tgondii.egGO, [4](#)

org.Tgondii.egGO2ALLEGS, [5, 6](#)

org.Tgondii.egGO2EG (org.Tgondii.egGO),  
[4](#)

org.Tgondii.egMAPCOUNTS, [7](#)

org.Tgondii.egORGANISM, [8](#)

org.Tgondii.egPMID, [8](#)

org.Tgondii.egPMID2EG  
(org.Tgondii.egPMID), [8](#)

org.Tgondii.egREFSEQ, [9](#)

org.Tgondii.egREFSEQ2EG  
(org.Tgondii.egREFSEQ), [9](#)

org.Tgondii.egSYMBOL, [11](#)

org.Tgondii.egSYMBOL2EG  
(org.Tgondii.egSYMBOL), [11](#)

org.Tgondii.egUNIGENE, [12](#)

org.Tgondii.egUNIGENE2EG  
(org.Tgondii.egUNIGENE), [12](#)