

# org.At.tair.db

October 16, 2018

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org.At.tairARACYC

*Mappings between TAIR identifiers and KEGG pathway identifiers*

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## Description

AraCyc <http://www.arabidopsis.org/tools/aracyc/> maintains pathway data for Arabidopsis thaliana. org.At.tairARACYC maps TAIR identifiers to the common names of the pathways in which the genes represented by the tair identifiers are involved. Information is obtained from AraCyc.

## Details

Annotation based on data provided by: Tair [ftp://ftp.plantcyc.org/Pathways/Data/\\_dumps/PMN10\\_June2015/aracyc/\\_pa](ftp://ftp.plantcyc.org/Pathways/Data/_dumps/PMN10_June2015/aracyc/_pa)  
With a date stamp from the source of: 2015-Apr07

## References

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

## 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:
x <- org.At.tairARACYC
# Get the tair identifiers that are mapped to pathways
mapped_tairs <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_tairs])
if(length(xx) > 0) {
  # Get the pathways for the first five tairs
  xx[1:5]
  # For the first tair
  xx[[1]]
}
```

---

org.At.tairARACYCENZYME

*Map between TAIR IDs and Enzyme Names from ARACYC*

---

## Description

org.At.tairARACYCENZYME is an R object that provides mappings between TAIR identifiers and Enzyme Names from ARACYC.

## Details

Each TAIR identifier maps to a named vector containing the Enzyme name for that gene according to the ARACYC database. If this information is unknown, the vector will contain an NA.

Mappings between tair identifiers and enzyme identifiers were obtained using files provided by: Tair ftp://ftp.plantcyc.org/Pathways/Data\\_dumps/PMN10\\_June2015/aracyc\\_pathways.20150608 With a date stamp from the source of: 2015-Apr07

## 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:
x <- org.At.tairARACYCENZYME
# Get the tair identifiers that are mapped to an Enzyme Name
mapped_tairs <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_tairs])
if(length(xx) > 0) {
  # Get the ENZYME name for the first five tairs
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

org.At.tair.db

*Bioconductor annotation data package*

---

## Description

Welcome to the org.At.tair.db annotation Package. The purpose of this package is to provide detailed information about the org.At.tair platform. This package is updated biannually.

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(org.At.tair.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:org.At.tair.db")
```

---

 org.At.tairCHR

---

*Map TAIR IDs to Chromosomes*


---

**Description**

org.At.tairCHR is an R object that provides mappings between a TAIR identifier and the chromosome that contains the gene of interest.

**Details**

Each TAIR identifier maps to a vector of chromosomes. Due to inconsistencies that may exist at the time the object was built, the vector may contain more than one chromosome (e.g., the identifier may map to more than one chromosome). If the chromosomal location is unknown, the vector will contain an NA.

Mappings were based on data provided by: Tair ftp://ftp.arabidopsis.org/home/tair/Genes/TAIR10\genome\\_release/TAIR10.1.1. With a date stamp from the source of: 2015-Apr07

**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:
x <- org.At.tairCHR
# Get the tair identifiers that are mapped to a chromosome
mapped_tairs <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_tairs])
if(length(xx) > 0) {
  # Get the CHR for the first five tairs
  xx[1:5]
  # Get the first one
```

```

    xx[[1]]
  }

```

---

org.At.tairCHRENGTHS *A named vector for the length of each of the chromosomes*

---

### Description

org.At.tairCHRENGTHS 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.

### 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:
tt <- org.At.tairCHRENGTHS
# Length of chromosome 1
tt["1"]

```

---

org.At.tairCHRLOC *Map Manufacturer IDs to Chromosomal Location*

---

### Description

org.At.tairCHRLOC is an R object that maps manufacturer identifiers to the starting position of the gene. The position of a gene is measured as the number of base pairs.

The CHRLOCEND mapping is the same as the CHRLOC mapping except that it specifies the ending base of a gene instead of the start.

**Details**

Each manufacturer identifier maps to a named vector of chromosomal locations, where the name indicates the chromosome. Due to inconsistencies that may exist at the time the object was built, these vectors may contain more than one chromosome and/or location. If the chromosomal location is unknown, the vector will contain an NA.

Chromosomal locations on both the sense and antisense strands are measured as the number of base pairs from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Chromosomal locations on the antisense strand have a leading "-" sign (e. g. -1234567).

Mappings were based on data provided by: Tair ftp://ftp.arabidopsis.org/Maps/seqviewer\\_data/sv\\_gene.data  
With a date stamp from the source of: 2015-Apr07

**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:
x <- org.At.tairCHRLOC
# Get the tair identifiers that are mapped to chromosome locations
mapped_tairs <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_tairs])
if(length(xx) > 0) {
  # Get the CHRLOC for the first five tairs
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

org.At.tairENTREZID    *Map TAIR identifiers with Entrez Gene identifiers*

---

**Description**

org.At.tairENTREZID is an R object that contains mappings between TAIR accession numbers and NCBI Entrez Gene identifiers.

**Details**

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

Mappings were based on data provided by: <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA>

**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:
x <- org.At.tairENTREZID
# Get the ORF IDs 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 Entrez gene IDs for the first five genes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

org.At.tairENZYME

*Map between TAIR IDs and Enzyme Commission (EC) Numbers*

---

## Description

org.At.tairENZYME is an R object that provides mappings between TAIR identifiers and EC numbers.

## Details

Each TAIR identifier maps to a named vector containing the EC number that corresponds to the enzyme produced by that gene. The name corresponds to the manufacturer 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.At.tairENZYME2TAIR, 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/jcbn/index.html#6>

Mappings between TAIR identifiers and enzyme identifiers were obtained using files provided by: Tair ftp://ftp.plantcyc.org/Pathways/Data\\_dumps/PMN10\\_June2015/aracyc\\_pathways.20150608 With a date stamp from the source of: 2015-Apr07

## 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:
x <- org.At.tairENZYME
# Get the TAIR identifiers that are mapped to an EC number
mapped_tairs <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_tairs])
if(length(xx) > 0) {
  # Get the ENZYME for the first five tairs
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

org.At.tairENZYME2TAIR

*Map between Enzyme Commission Numbers and TAIR Identifiers*

---

## Description

org.At.tairENZYME2TAIR is an R object that maps Enzyme Commission (EC) numbers to TAIR identifiers.

## Details

Each EC number maps to a named vector containing all of the TAIR identifiers that correspond to the gene that produces that enzyme. The name of the vector corresponds to the EC number.

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.At.tairENZYME2TAIR, 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/jcbn/index.html#6>

Mappings were based on data provided by: Tair [ftp://ftp.plantcyc.org/Pathways/Data\\_dumps/PMN10\\_June2015/aracyc/](ftp://ftp.plantcyc.org/Pathways/Data_dumps/PMN10_June2015/aracyc/)  
With a date stamp from the source of: 2015-Apr07

## References

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

## Examples

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

## Bimap interface:
# Convert to a list
xx <- as.list(org.At.tairENZYME2TAIR)
if(length(xx) > 0){
  # Gets the tair identifiers for the first five enzyme
  #commission numbers
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

org.At.tairGENENAME     *Map between TAIR IDs and Genes*

---

## Description

org.At.tairGENENAME is an R object that maps TAIR identifiers to the corresponding gene name.

## Details

Each TAIR identifier maps to a named vector containing the gene name. The vector name corresponds to the TAIR 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: Tair [ftp://ftp.arabidopsis.org/home/tair/Genes/TAIR10\\_genome\\_release/TAIR10\\_genes.txt](ftp://ftp.arabidopsis.org/home/tair/Genes/TAIR10_genome_release/TAIR10_genes.txt)  
With a date stamp from the source of: 2015-Apr07

## 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:
x <- org.At.tairGENENAME
# Get the TAIR identifiers that are mapped to a gene name
mapped_tairs <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_tairs])
if(length(xx) > 0) {
  # Get the GENENAME for the first five tairs
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

 org.At.tairGO

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


---

**Description**

org.At.tairGO is an R object that provides mappings between TAIR 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 TAIR 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 TAIR Gene id. Some of 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

A more complete listing of evidence codes can be found at:

<http://www.geneontology.org/GO.evidence.shtml>

Mappings between TAIR gene identifiers and GO information were obtained through their mappings to TAIR gene identifiers. NAs are assigned to TAIR 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: 2018-Mar28

For the reverse map GO2TAIR, each GO term maps to a named vector of TAIR gene identifiers. A GO identifier may be mapped to the same TAIR 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.At.tairGO2ALLTAIRS](#).
- [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:
x <- org.At.tairGO
# Get the TAIR 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.At.tairGO2TAIR)
if(length(xx) > 0){
  # Gets the TAIR gene ids for the top 2nd and 3rd GO identifiers
  goids <- xx[2:3]
  # Gets the TAIR ids for the first element of goids
  goids[[1]]
  # Evidence code for the mappings
  names(goids[[1]])
}
```

---

org.At.tairGO2ALLTAIRS

*Map between Gene Ontology (GO) Identifiers and all TAIR Identifiers  
in the subtree*

---

## Description

org.At.tairGO2ALLTAIRS is an R object that provides mappings between a given GO identifier and all TAIR 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 manufacturer id corresponds to the evidence code for that GO identifier. This object org.At.tairGO2ALLTAIRS maps between a given GO identifier and all TAIR 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 TAIR 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: 2018-Mar28

For GO2ALL style mappings, the intention is to return all the genes that are the same kind of term as the parent term (based on the idea that they are more specific descriptions of the general term). However because of this intent, not all relationship types will be counted as offspring for this mapping. Only "is a" and "has a" style relationships indicate that the genes from the child terms would be the same kind of thing.

## References

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

**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:
# Convert to a list
xx <- as.list(org.At.tairG02ALLTAIRS)
if(length(xx) > 0){
  # Gets the tair identifiers for the top 2nd and 3rd GO identifiers
  goids <- xx[2:3]
  # Gets all the tair identifiers for the first element of goids
  goids[[1]]
  # Evidence code for the mappings
  names(goids[[1]])
}
```

---

org.At.tairMAPCOUNTS *Number of mapped keys for the maps in package org.At.tair.db*

---

**Description**

org.At.tairMAPCOUNTS provides the "map count" (i.e. the count of mapped keys) for each map in package org.At.tair.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:
org.At.tairMAPCOUNTS
mapnames <- names(org.At.tairMAPCOUNTS)
```

```

org.At.tairMAPCOUNTS[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.At.tair.db
checkMAPCOUNTS("org.At.tair.db")

```

---

org.At.tairORGANISM     *The Organism for org.At.tair*

---

### Description

org.At.tairORGANISM is an R object that contains a single item: a character string that names the organism for which org.At.tair was built.

### Details

Although the package name is suggestive of the organism for which it was built, org.At.tairORGANISM 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.At.tairORGANISM

```

---

org.At.tairPATH     *Mappings between TAIR identifiers and KEGG pathway identifiers*

---

### Description

KEGG (Kyoto Encyclopedia of Genes and Genomes) maintains pathway data for various organisms. org.At.tairPATH maps TAIR identifiers to the identifiers used by KEGG for pathways in which the genes represented by the TAIR identifiers are involved

### 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/>

## 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:
x <- org.At.tairPATH
# Get the TAIR 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]]
}
```

---

org.At.tairPATH2TAIR *Map between Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway identifiers and TAIR Identifiers*

---

## Description

org.At.tairPATH2TAIR is an R object that provides mappings between KEGG identifiers and TAIR identifiers.

## Details

Each KEGG identifier is mapped to a named vector of manufacturer identifiers. The name represents the KEGG identifier and the vector contains all TAIR identifiers that are found in that particular pathway. An NA is reported for any KEGG identifier that cannot be mapped to any TAIR identifiers.

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

**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:
# Convert the object to a list
xx <- as.list(org.At.tairPATH2TAIR)
# Remove pathway identifiers that do not map to any tair id
xx <- xx[!is.na(xx)]
if(length(xx) > 0){
  # The tair identifiers for the first two elements of XX
  xx[1:2]
  # Get the first one
  xx[[1]]
}
```

---

org.At.tairPMID

*Map between TAIR Identifiers and PubMed Identifiers*

---

**Description**

org.At.tairPMID is an R object that provides mappings between TAIR identifiers and PubMed identifiers.

**Details**

Each TAIR identifier is mapped to a named vector of PubMed identifiers. The name associated with each vector corresponds to the TAIR identifier. The length of the vector may be one or greater, depending on how many PubMed identifiers a given TAIR identifier is mapped to. An NA is reported for any TAIR 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: Tair [ftp://ftp.arabidopsis.org/home/tair/User\\_Requests/Locus\\_Published\\_2015-Apr07](ftp://ftp.arabidopsis.org/home/tair/User_Requests/Locus_Published_2015-Apr07)  
With a date stamp from the source of: 2015-Apr07

**References**

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

**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:
x <- org.At.tairPMID
# Get the tair 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 tair 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")
  }
}
```

---

org.At.tairPMID2TAIR *Map between PubMed Identifiers and TAIR Identifiers*

---

**Description**

org.At.tairPMID2TAIR is an R object that provides mappings between PubMed identifiers and TAIR identifiers.

**Details**

Each PubMed identifier is mapped to a named vector of TAIR identifiers. The name represents the PubMed identifier and the vector contains all TAIR identifiers that are represented by that PubMed identifier. The length of the vector may be one or longer, depending on how many TAIR identifiers are mapped to a given 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: Tair ftp://ftp.arabidopsis.org/home/tair/User\Requests/Locus\_Published\_2015-Apr07  
With a date stamp from the source of: 2015-Apr07

**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:
# Convert the object to a list
xx <- as.list(org.At.tairPMID2TAIR)
if(length(xx) > 0){
  # The tair 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.At.tairREFSEQ

*Map between TAIR Identifiers and RefSeq Identifiers*


---

## Description

org.At.tairREFSEQ is an R object that provides mappings between TAIR identifiers and RefSeq identifiers.

## Details

Each TAIR identifier is mapped to a named vector of RefSeq identifiers. The name represents the TAIR identifier and the vector contains all RefSeq identifiers that can be mapped to that TAIR identifier. The length of the vector may be one or greater, depending on how many RefSeq identifiers a given TAIR identifier can be mapped to. An NA is reported for any TAIR 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 <https://www.ncbi.nlm.nih.gov/RefSeq/> allows users to query the RefSeq database using RefSeq identifiers.

Mappings were based on data provided by: <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA>

## References

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

## 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:
x <- org.At.tairREFSEQ
# Get the TAIR 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.At.tairREFSEQ2TAIR
# Get the RefSeq identifier that are mapped to an TAIR ID
mapped_seqs <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_seqs])
if(length(xx) > 0) {
  # Get the TAIR ID for the first five Refseqs
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

org.At.tairSYMBOL

*Map between TAIR Identifiers and Gene Symbols*

---

## Description

org.At.tairSYMBOL is an R object that provides mappings between TAIR identifiers and gene abbreviations.

## Details

Each TAIR identifier is mapped to an 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: Tair ftp://ftp.arabidopsis.org/home/tair/Genes/gene\_aliases\_20140331.txt  
With a date stamp from the source of: 2015-Apr07

## References

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

## 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:
x <- org.At.tairSYMBOL
# Get the tair 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 SYMBOL for the first five genes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

org.At.tair\_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.At.tair_dbconn()
org.At.tair_dbfile()
org.At.tair_dbschema(file="", show.indices=FALSE)
org.At.tair_dbInfo()
```

## Arguments

file	A connection, or a character string naming the file to print to (see the file 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.At.tair\_dbconn returns a connection object to the package annotation DB. **IMPORTANT:** Don't call `dbDisconnect` on the connection object returned by `org.At.tair_dbconn` or you will break all the `AnnDbObj` objects defined in this package!

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

org.At.tair\_dbschema prints the schema definition of the package annotation DB.

org.At.tair\_dbInfo prints other information about the package annotation DB.

## Value

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

org.At.tair\_dbfile: a character string with the path to the package annotation DB.

org.At.tair\_dbschema: none (invisible NULL).

org.At.tair\_dbInfo: none (invisible NULL).

## See Also

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

## Examples

```
library(DBI)
## Count the number of rows in the "genes" table:
dbGetQuery(org.At.tair_dbconn(), "SELECT COUNT(*) FROM genes")

org.At.tair_dbschema()

org.At.tair_dbInfo()
```

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