org.At.tair.db

November 11, 2026

`org.At.tairARACYC` *Mappings between TAIR identifiers and KEGG pathway identifiers*

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/pmn/Pathways/Data_dumps/PMN15.5_January2023/pathv
With a date stamp from the source of: 2025-09-24

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/pmn/Pathways/Data_dumps/PMN15.5_January2023/pathways/aracyc_pathways.20230103 With a date stamp from the source of: 2025-09-24

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
## bimaps. 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 https://www.arabidopsis.org/api/download-files/download?filePath=Genes/T
With a date stamp from the source of: 2025-09-24

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

Description

org.At.tairCHRLENGTHS 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.tairCHRLENGTHS
# 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 https://www.arabidopsis.org/api/download-files/download?filePath=Maps/se
With a date stamp from the source of: 2025-09-24

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/pmn/Pathways/Data_dumps/PMN15.5_January2023/pathways/aracyc_pathways.20230103
With a date stamp from the source of: 2025-09-24

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/pmn/Pathways/Data_dumps/PMN15.5_January2023/p
With a date stamp from the source of: 2025-09-24

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 https://www.arabidopsis.org/api/download-files/download?filePath=Genes/T
With a date stamp from the source of: 2025-09-24

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 an Gene Ontology terms and other information are available in a separate data package named GO.

Mappings were based on data provided by: Gene Ontology http://current.geneontology.org/ontology/go-basic.obo With a date stamp from the source of: 2025-07-22

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 3nd 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 http://current.geneontology.org/ontology/go-basic.obo With a date stamp from the source of: 2025-07-22

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.tairGO2ALLTAIRS)
if(length(xx) > 0){
    # Gets the tair identifiers for the top 2nd and 3nd 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 https://www.arabidopsis.org/api/download-files/download?filePath=Public_
With a date stamp from the source of: 2025-09-24

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 https://www.arabidopsis.org/api/download-files/download?filePath=Public_
With a date stamp from the source of: 2025-09-24

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 https://www.arabidopsis.org/api/download-files/download?filePath=Public_
With a date stamp from the source of: 2025-09-24

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 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.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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