

Package: TxDb.Athaliana.Ensembl.TAIR10 (via r-universe)

October 4, 2026

Title Transcripts Annotation Database for Arabidopsis thaliana

Version 0.99.5

Description TxDb.Athaliana.Ensembl.TAIR10 provides transcript, exon, CDS, and gene annotations for Arabidopsis thaliana based on the TAIR10 reference genome and Ensembl Plants release 63. The TxDb object is built from the Ensembl Plants GFF3 annotation and can be queried using GenomicFeatures accessors such as genes(), transcripts(), exonsBy(), and cdsBy().

Depends R (>= 4.5.0)

Imports stats, GenomicFeatures, GenomicRanges, AnnotationHub

Suggests BiocManager, BiocStyle, knitr, rmarkdown, testthat (>= 3.0.0)

VignetteBuilder knitr

License Artistic-2.0

Encoding UTF-8

URL <https://github.com/kabilanbio/TxDb.Athaliana.Ensembl.TAIR10>

BugReports <https://github.com/kabilanbio/TxDb.Athaliana.Ensembl.TAIR10/issues>

biocViews AnnotationData, TxDb, Arabidopsis_thaliana,
SequenceAnnotation, AnnotationHub

Config/testthat/edition 3

Config/roxygen2/version 8.1.0

Config/pak/sysreqs

make libbz2-dev libicu-dev liblzma-dev libpng-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

Repository <https://biocstaging.r-universe.dev>

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RemoteUrl <https://github.com/BiocStaging/TxDb.Athaliana.Ensembl.TAIR10>

RemoteRef HEAD

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Contents

TxDb.Athaliana.Ensembl.TAIR10	2
Index	3

TxDb.Athaliana.Ensembl.TAIR10
Annotation package for TxDb object(s)

Description

TxDb.Athaliana.Ensembl.TAIR10 provides transcript, exon, and CDS annotations for Arabidopsis thaliana based on the TAIR10 reference genome. It is a Bioconductor TxDb object built from the Ensembl Plants GFF3 annotation (release 63).

The package provides genomic coordinates and transcript models that can be accessed using GenomicFeatures accessors such as genes(), transcripts(), exonsBy(), and cdsBy().

Note

This data package was built from the Ensembl Plants GFF3 annotation (release 63) for Arabidopsis thaliana using the TAIR10 reference genome. The annotation includes the five nuclear chromosomes and the mitochondrial and plastid sequences.

Author(s)

Dwijesh Chandra Mishra (aut), Sharanbasappa D Madival (aut), Kabilan S (aut, cre) <kabilan151414@gmail.com>

See Also

[genes](#), [transcripts](#), [transcriptsBy](#), [exonsBy](#), [cdsBy](#)

Examples

```
## The TxDb object is downloaded from AnnotationHub, so this example is
## only run when AnnotationHub is installed and the resource is
## reachable.
if (requireNamespace("AnnotationHub", quietly=TRUE)) {
  txdb <- tryCatch({
    ah <- AnnotationHub::AnnotationHub()
    ah[["AH122287"]]
  }, error=function(e) NULL)

  if (!is.null(txdb)) {
    txdb
    ## retrieve all genes
    GenomicFeatures::genes(txdb)
  }
}
```

Index

* **data**

TxDB.Athaliana.Ensembl.TAIR10, [2](#)

* **package**

TxDB.Athaliana.Ensembl.TAIR10, [2](#)

cdsBy, [2](#)

exonsBy, [2](#)

genes, [2](#)

transcripts, [2](#)

transcriptsBy, [2](#)

TxDB.Athaliana.Ensembl.TAIR10, [2](#)

TxDB.Athaliana.Ensembl.TAIR10-package
(TxDB.Athaliana.Ensembl.TAIR10),
[2](#)

TxDB.Athaliana.Ensembl.TAIR10_dbconn
(TxDB.Athaliana.Ensembl.TAIR10),
[2](#)

TxDB.Athaliana.Ensembl.TAIR10_dbfile
(TxDB.Athaliana.Ensembl.TAIR10),
[2](#)

TxDB.Athaliana.Ensembl.TAIR10_dbInfo
(TxDB.Athaliana.Ensembl.TAIR10),
[2](#)

TxDB.Athaliana.Ensembl.TAIR10_dbschema
(TxDB.Athaliana.Ensembl.TAIR10),
[2](#)