

Package: TxDb.Gmax.JGI.Gmv4 (via r-universe)

October 4, 2026

Title Transcripts Annotation Database for Soybean

Version 0.99.1

Description TxDb.Gmax.JGI.Gmv4 provides transcript, exon, and CDS annotations for soybean (Glycine max Wm82.a4.v1). It is a Bioconductor TxDb object built from the official JGI/Phytozome GFF3 annotation and is available via AnnotationHub (retrievable with AnnotationHub()); after loading you can use GenomicFeatures accessors (genes(), transcripts(), exonsBy(), cdsBy()) to extract gene models identified by JGI/Phytozome locus IDs.

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.Gmax.JGI.Gmv4>

BugReports <https://github.com/kabilanbio/TxDb.Gmax.JGI.Gmv4/issues>

biocViews AnnotationData, TxDb, Glycine_max, 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.Gmax.JGI.Gmv4>

RemoteRef HEAD

RemoteSha d6537e9eab880f40465224fcda3fad3eb1e2df46

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Description

TxDb.Gmax.JGI.Gmv4 provides transcript, exon, and CDS annotations for soybean (Glycine max Wm82.a4.v1). It is a Bioconductor TxDb object built from the official JGI/Phytozome GFF3 annotation and is available via AnnotationHub (retrievable with AnnotationHub()); after loading you can use GenomicFeatures accessors (genes(), transcripts(), exonsBy(), cdsBy()) to extract gene models identified by JGI/Phytozome locus IDs.

Note

This data package was built from the JGI/Phytozome GFF3 annotation of soybean (Glycine max Wm82.a4.v1).

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See Also

[transcripts](#), [transcriptsBy](#)

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[["AH122288"]]
  }, error=function(e) NULL)

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

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