Package: annotables (via r-universe)

June 8, 2026

Type Package

Title Ensembl Annotation Tables

Version 0.2.0

Description Provides tables for converting and annotating Ensembl Gene IDs.

URL https://github.com/stephenturner/annotables

BugReports https://github.com/stephenturner/annotables/issues

License GPL-3

LazyData TRUE

LazyDataCompression xz

Depends R (>= 3.1.2)

Imports tibble

Suggests devtools, dplyr, knitr, rlang, rmarkdown, whisker, yaml

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

Repository https://laleoarrow.r-universe.dev

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RemoteUrl https://github.com/stephenturner/annotables

RemoteRef HEAD

RemoteSha 5bf7dc053e88d850d9acdca943289e688f0a1d4f

Contents

`annotables-package` *annotables*

Description

Provides tables for converting and annotating Ensembl Gene IDs.

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See Also

Useful links:

- `https://github.com/stephenturner/annotables`
- Report bugs at `https://github.com/stephenturner/annotables/issues`

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bdgp6 *Fruitfly annotation data*

Description

Fruitfly (*Drosophila melanogaster*) annotations based on genome assembly BDGP6 from Ensembl.

Usage

```
bdgp6
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 26383 rows and 9 columns.

Details

Variables:

- ensgene
- entrez
- symbol
- chr
- start
- end
- strand
- biotype
- description

Source

http://ensembl.org/drosophila_melanogaster

Examples

```
head(bdgp6)
```

`bdgp6_tx2gene` *Fruitfly transcripts to genes*

Description

Lookup table for converting Fruitfly (*Drosophila melanogaster*) Ensembl transcript IDs to gene IDs based on genome assembly BDGP6 from Ensembl.

Usage

```
bdgp6_tx2gene
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 41600 rows and 2 columns.

Details

Variables:

- enstxp
- ensgene

Source

`http://ensembl.org/drosophila_melanogaster`

Examples

```
head(bdgp6_tx2gene)
```

`cfamiliaris` *Dog gene annotation table*

Description

Gene annotation table for Canis lupus familiaris (dog) from Ensembl.

Usage

```
cfamiliaris
```

Format

A data frame with gene annotation columns.

Details

Variables:

- ensgene
- entrez
- symbol
- chr
- start
- end
- strand
- biotype
- description

Source

Ensembl

`http://ensembl.org/canis_lupusfamiliaris`

Examples

```
head(cfamiliaris)
```

`cfamiliaris_tx2gene` *Dog transcript-to-gene table*

Description

Transcript-to-gene mapping for Canis lupus familiaris (dog) from Ensembl.

Usage

```
cfamiliaris_tx2gene
```

Format

A data frame with transcript and gene columns.

Source

Ensembl

`drerio` *Zebrafish gene annotation table*

Description

Gene annotation table for Danio rerio (zebrafish) from Ensembl.

Usage

```
drerio
```

Format

A data frame with gene annotation columns.

Details

Variables:

- ensgene
- entrez
- symbol
- chr
- start
- end
- strand
- biotype
- description

Source

Ensembl

`http://ensembl.org/danio_rerio`

Examples

```
head(drerio)
```

`drerio_tx2gene` *Zebrafish transcript-to-gene table*

Description

Transcript-to-gene mapping for Danio rerio (zebrafish) from Ensembl.

Usage

```
drerio_tx2gene
```

Format

A data frame with transcript and gene columns.

Source

Ensembl

`ensembl_version` *Ensembl version used for build*

Description

Ensembl version used for build

Usage

```
ensembl_version
```

Format

An object of class `character` of length 1.

Source

`http://www.ensembl.org/`

Examples

```
ensembl_version
```

`galgal5` *Chicken annotation data*

Description

Chicken (*Gallus gallus*) annotations based on genome assembly GALGAL5 from Ensembl.

Usage

```
galgal5
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 34332 rows and 9 columns.

Details

Variables:

- ensgene
- entrez
- symbol
- chr
- start
- end
- strand
- biotype
- description

Source

http://ensembl.org/gallus_gallus

Examples

```
head(galgal5)
```

`galgal5_tx2gene` *Chicken transcripts to genes*

Description

Lookup table for converting Chicken (*Gallus gallus*) Ensembl transcript IDs to gene IDs based on genome assembly GALGAL5 from Ensembl.

Usage

```
galgal5_tx2gene
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 72689 rows and 2 columns.

Details

Variables:

- enstxp
- ensgene

Source

http://ensembl.org/gallus_gallus

Examples

```
head(galgal5_tx2gene)
```

`grch37` *Human annotation data*

Description

Human (*Homo sapiens*) annotations based on genome assembly GRCH37 from Ensembl.

Usage

```
grch37
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 66978 rows and 9 columns.

Details

Variables:

- ensgene
- entrez
- symbol
- chr
- start
- end
- strand
- biotype
- description

Source

`http://ensembl.org/homo_sapiens`

Examples

```
head(grch37)
```

`grch37_tx2gene` *Human transcripts to genes*

Description

Lookup table for converting Human (*Homo sapiens*) Ensembl transcript IDs to gene IDs based on genome assembly GRCH37 from Ensembl.

Usage

```
grch37_tx2gene
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 215170 rows and 2 columns.

Details

Variables:

- enstxp
- ensgene

Source

http://ensembl.org/homo_sapiens

Examples

```
head(grch37_tx2gene)
```

`grch38` *Human annotation data*

Description

Human (*Homo sapiens*) annotations based on genome assembly GRCH38 from Ensembl.

Usage

```
grch38
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 91673 rows and 9 columns.

Details

Variables:

- ensgene
- entrez
- symbol
- chr
- start
- end
- strand
- biotype
- description

Source

http://ensembl.org/homo_sapiens

Examples

```
head(grch38)
```

`grch38_tx2gene` *Human transcripts to genes*

Description

Lookup table for converting Human (*Homo sapiens*) Ensembl transcript IDs to gene IDs based on genome assembly GRCH38 from Ensembl.

Usage

```
grch38_tx2gene
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 412044 rows and 2 columns.

Details

Variables:

- enstxp
- ensgene

Source

`http://ensembl.org/homo_sapiens`

Examples

```
head(grch38_tx2gene)
```

`grcm38` *Mouse annotation data*

Description

Mouse (*Mus musculus*) annotations based on genome assembly GRCM38 from Ensembl.

Usage

```
grcm38
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 78630 rows and 9 columns.

Details

Variables:

- ensgene
- entrez
- symbol
- chr
- start
- end
- strand
- biotype
- description

Source

http://ensembl.org/mus_musculus

Examples

```
head(grcm38)
```

`grcm38_tx2gene` *Mouse transcripts to genes*

Description

Lookup table for converting Mouse (*Mus musculus*) Ensembl transcript IDs to gene IDs based on genome assembly GRCM38 from Ensembl.

Usage

```
grcm38_tx2gene
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 278369 rows and 2 columns.

Details

Variables:

- enstxp
- ensgene

Source

http://ensembl.org/mus_musculus

Examples

```
head(grcm38_tx2gene)
```

`mmul801` *Macaque annotation data*

Description

Macaque (*Macaca mulatta*) annotations based on genome assembly MMUL801 from Ensembl.

Usage

```
mmul801
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 36086 rows and 9 columns.

Details

Variables:

- ensgene
- entrez
- symbol
- chr
- start
- end
- strand
- biotype
- description

Source

http://ensembl.org/macaca_mulatta

Examples

```
head(mmul801)
```

`mmul801_tx2gene` *Macaque transcripts to genes*

Description

Lookup table for converting Macaque (*Macaca mulatta*) Ensembl transcript IDs to gene IDs based on genome assembly MMUL801 from Ensembl.

Usage

```
mmul801_tx2gene
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 64228 rows and 2 columns.

Details

Variables:

- enstxp
- ensgene

Source

http://ensembl.org/macaca_mulatta

Examples

```
head(mmul801_tx2gene)
```

`rnor6` *Rat annotation data*

Description

Rat (*Rattus norvegicus*) annotations based on genome assembly RNOR6 from Ensembl.

Usage

```
rnor6
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 57961 rows and 9 columns.

Details

Variables:

- ensgene
- entrez
- symbol
- chr
- start
- end
- strand
- biotype
- description

Source

`http://ensembl.org/rattus_norvegicus`

Examples

```
head(rnor6)
```

`rnor6_tx2gene` *Rat transcripts to genes*

Description

Lookup table for converting Rat (*Rattus norvegicus*) Ensembl transcript IDs to gene IDs based on genome assembly RNOR6 from Ensembl.

Usage

```
rnor6_tx2gene
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 95472 rows and 2 columns.

Details

Variables:

- enstxp
- ensgene

Source

http://ensembl.org/rattus_norvegicus

Examples

```
head(rnor6_tx2gene)
```

`sscrofa` *Pig annotation data*

Description

Pig (*Sus scrofa*) annotations based on genome assembly SSCROFA from Ensembl.

Usage

```
sscrofa
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 35819 rows and 9 columns.

Details

Variables:

- ensgene
- entrez
- symbol
- chr
- start
- end
- strand
- biotype
- description

Source

http://ensembl.org/sus_scrofa

Examples

```
head(sscrofa)
```

`sscrofa_tx2gene` *Pig transcripts to genes*

Description

Lookup table for converting Pig (*Sus scrofa*) Ensembl transcript IDs to gene IDs based on genome assembly SSCROFA from Ensembl.

Usage

```
sscrofa_tx2gene
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 60440 rows and 2 columns.

Details

Variables:

- enstxp
- ensgene

Source

`http://ensembl.org/sus_scrofa`

Examples

```
head(sscrofa_tx2gene)
```

`wbcel235` *Roundworm annotation data*

Description

Roundworm (*Caenorhabditis elegans*) annotations based on genome assembly WBCEL235 from Ensembl.

Usage

```
wbcel235
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 49077 rows and 9 columns.

Details

Variables:

- ensgene
- entrez
- symbol
- chr
- start
- end
- strand
- biotype
- description

Source

`http://ensembl.org/caenorhabditis_elegans`

Examples

```
head(wbcel235)
```

`wbcel235_tx2gene` *Roundworm transcripts to genes*

Description

Lookup table for converting Roundworm (*Caenorhabditis elegans*) Ensembl transcript IDs to gene IDs based on genome assembly WBCEL235 from Ensembl.

Usage

```
wbcel235_tx2gene
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 60000 rows and 2 columns.

Details

Variables:

- enstxp
- ensgene

Source

http://ensembl.org/caenorhabditis_elegans

Examples

```
head(wbcel235_tx2gene)
```

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