Package: annotables (via r-universe)

October 20, 2026

Type Package

Title Ensembl Annotation Tables

Version 0.3.0

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)

Config/roxygen2/version 8.1.0

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

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`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

bdgp654 *Fruitfly annotation data*

Description

Fruitfly (*Drosophila melanogaster*) annotations based on genome assembly BDGP654 from Ensembl.

Usage

```
bdgp654
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 28759 rows and 9 columns.

Details

Variables:

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

Source

http://ensembl.org/drosophila_melanogaster

Examples

```
head(bdgp654)
```

bdgp654_tx2gene *Fruitfly transcripts to genes*

Description

Lookup table for converting Fruitfly (*Drosophila melanogaster*) Ensembl transcript IDs to gene IDs based on genome assembly BDGP654 from Ensembl.

Usage

```
bdgp654_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(bdgp654_tx2gene)
```

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
```

`grcg7b` *Chicken annotation data*

Description

Chicken (*Gallus gallus*) annotations based on genome assembly GRCG7B from Ensembl.

Usage

```
grcg7b
```

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(grcg7b)
```

grcg7b_tx2gene *Chicken transcripts to genes*

Description

Lookup table for converting Chicken (*Gallus gallus*) Ensembl transcript IDs to gene IDs based on genome assembly GRCG7B from Ensembl.

Usage

```
grcg7b_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(grcg7b_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 91743 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 670670 rows and 2 columns.

Details

Variables:

- enstxp
- ensgene

Source

http://ensembl.org/homo_sapiens

Examples

```
head(grch38_tx2gene)
```

grcm39 *Mouse annotation data*

Description

Mouse (*Mus musculus*) annotations based on genome assembly GRCM39 from Ensembl.

Usage

```
grcm39
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 78718 rows and 9 columns.

Details

Variables:

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

Source

http://ensembl.org/mus_musculus

Examples

```
head(grcm39)
```

---

grcm39_tx2gene *Mouse transcripts to genes*

Description

Lookup table for converting Mouse (*Mus musculus*) Ensembl transcript IDs to gene IDs based on genome assembly GRCM39 from Ensembl.

Usage

```
grcm39_tx2gene
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 481956 rows and 2 columns.

Details

Variables:

- enstxp
- ensgene

Source

http://ensembl.org/mus_musculus

Examples

```
head(grcm39_tx2gene)
```

`grcr8` *Rat annotation data*

Description

Rat (*Rattus norvegicus*) annotations based on genome assembly GRCR8 from Ensembl.

Usage

```
grcr8
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 57760 rows and 9 columns.

Details

Variables:

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

Source

http://ensembl.org/rattus_norvegicus

Examples

```
head(grcr8)
```

grcr8_tx2gene *Rat transcripts to genes*

Description

Lookup table for converting Rat (*Rattus norvegicus*) Ensembl transcript IDs to gene IDs based on genome assembly GRCR8 from Ensembl.

Usage

```
grcr8_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(grcr8_tx2gene)
```

grcz11 *Zebrafish annotation data*

Description

Zebrafish (*Danio rerio*) annotations based on genome assembly GRCZ11 from Ensembl.

Usage

```
grcz11
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 92137 rows and 9 columns.

Details

Variables:

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

Source

http://ensembl.org/danio_rerio

Examples

```
head(grcz11)
```

---

grcz11_tx2gene *Zebrafish transcripts to genes*

Description

Lookup table for converting Zebrafish (*Danio rerio*) Ensembl transcript IDs to gene IDs based on genome assembly GRCZ11 from Ensembl.

Usage

```
grcz11_tx2gene
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 65905 rows and 2 columns.

Details

Variables:

- enstxp
- ensgene

Source

http://ensembl.org/danio_rerio

Examples

```
head(grcz11_tx2gene)
```

`mmul10` *Macaque annotation data*

Description

Macaque (*Macaca mulatta*) annotations based on genome assembly MMUL10 from Ensembl.

Usage

```
mmul10
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 37169 rows and 9 columns.

Details

Variables:

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

Source

http://ensembl.org/macaca_mulatta

Examples

```
head(mmul10)
```

mmul10_tx2gene *Macaque transcripts to genes*

Description

Lookup table for converting Macaque (*Macaca mulatta*) Ensembl transcript IDs to gene IDs based on genome assembly MMUL10 from Ensembl.

Usage

```
mmul10_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(mmul10_tx2gene)
```

roscfam1 *Dog annotation data*

Description

Dog (*Canis lupus familiaris*) annotations based on genome assembly ROSCFAM1 from Ensembl.

Usage

```
roscfam1
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 34012 rows and 9 columns.

Details

Variables:

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

Source

http://ensembl.org/canis_lupusfamiliaris

Examples

```
head(roscfam1)
```

---

roscfam1_tx2gene *Dog transcripts to genes*

Description

Lookup table for converting Dog (*Canis lupus familiaris*) Ensembl transcript IDs to gene IDs based on genome assembly ROSCFAM1 from Ensembl.

Usage

```
roscfam1_tx2gene
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 55335 rows and 2 columns.

Details

Variables:

- enstxp
- ensgene

Source

http://ensembl.org/canis_lupusfamiliaris

Examples

```
head(roscfam1_tx2gene)
```

`sscrofa111` *Pig annotation data*

Description

Pig (*Sus scrofa*) annotations based on genome assembly SSCROFA111 from Ensembl.

Usage

```
sscrofa111
```

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(sscrofa111)
```

sscrofa111_tx2gene *Pig transcripts to genes*

Description

Lookup table for converting Pig (*Sus scrofa*) Ensembl transcript IDs to gene IDs based on genome assembly SSCROFA111 from Ensembl.

Usage

```
sscrofa111_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(sscrofa111_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 46926 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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