

Package ‘EpiTxDb.Mm.mm10’

December 10, 2025

Title Annotation package for EpiTxDb objects

Description Exposes an annotation databases generated from several sources by exposing these as EpiTxDb object. Generated for Mus musculus/mm10.

Version 0.99.6

License Artistic-2.0

Encoding UTF-8

NeedsCompilation no

LazyData false

biocViews AnnotationHub, AnnotationData, Organism, Mus_musculus

Depends R (>= 4.0), AnnotationHub, EpiTxDb

Suggests BiocStyle, knitr, rmarkdown, testthat

Collate 'EpiTxDb.Mm.mm10.R'

organism Homo sapiens

species Homo sapiens

VignetteBuilder knitr

RoxygenNote 7.1.1

BugReports <https://github.com/FelixErnst/EpiTxDb.Mm.mm10/issues>

URL <https://github.com/FelixErnst/EpiTxDb.Mm.mm10>

git_url <https://git.bioconductor.org/packages/EpiTxDb.Mm.mm10>

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Description

This package loads one or more EpiTxDb objects. Such EpiTxDb objects are an R interface to prefabricated databases contained by this package.

The names of any objects exposed by this package indicate the origin and resources exposed. So for example EpiTxDb.Mm.mm10.tRNAdb would be a EpiTxDb object of Mus musculus data from tRNAdb build based on the mm10 genome.

Usage

```
EpiTxDb.Mm.mm10.RMBase(version = "1")

EpiTxDb.Mm.mm10.snoRNAdb(version = "1")

EpiTxDb.Mm.mm10.tRNAdb(version = "1")

snoRNA.targets.mm10(version = "1")
```

Arguments

version	a character value defining a version. Versions available: "1".(default: version = "1")
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Value

a [EpiTxDb](#) object

Author(s)

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See Also

- [modifications](#)
- [modificationsBy](#)
- [modifiedSeqsByTranscript](#)

Examples

```
EpiTxDb.Mm.mm10.tRNAdb()
```

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