

Package ‘EpiTxDb.Hs.hg38’

January 28, 2026

Title Annotation package for EpiTxDb objects

Description Exposes an annotation databases generated from several sources by exposing these as EpiTxDb object. Generated for Homo sapiens/hg38.

Version 0.99.7

License Artistic-2.0

Encoding UTF-8

NeedsCompilation no

LazyData false

biocViews AnnotationHub, AnnotationData, Organism, Homo_sapiens

Depends R (>= 4.0), AnnotationHub, EpiTxDb

Suggests BiocStyle, knitr, rmarkdown, testthat, Modstrings,
rtracklayer

Collate 'EpiTxDb.Hs.hg38.R'

organism Homo sapiens

species Homo sapiens

VignetteBuilder knitr

RoxygenNote 7.1.1

BugReports <https://github.com/FelixErnst/EpiTxDb.Hs.hg38/issues>

URL <https://github.com/FelixErnst/EpiTxDb.Hs.hg38>

git_url <https://git.bioconductor.org/packages/EpiTxDb.Hs.hg38>

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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.Hs.hg38.snoRNadb would be a EpiTxDb object of Homo sapiens data from snoRNadb build based on the hg38 genome.

Usage

```
EpiTxDb.Hs.hg38.RMBase(version = "1")

EpiTxDb.Hs.hg38.snoRNadb(version = "1")

EpiTxDb.Hs.hg38.tRNadb(version = "1")

chain.rRNA.hg19Tohg38(version = "1")

chain.rRNA.hg38Tohg19(version = "1")

snoRNA.targets.hg38(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.Hs.hg38.snoRNAdb()
```

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