

Package ‘EpiTxDb.Sc.sacCer3’

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 *Saccharomyces cerevisiae*/sacCer3.

Version 0.99.5

License Artistic-2.0

Encoding UTF-8

NeedsCompilation no

LazyData false

biocViews AnnotationHub, AnnotationData, Organism,
Saccharomyces_cerevisiae

Depends R (>= 4.0), AnnotationHub, EpiTxDb

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

Collate 'EpiTxDb.Sc.sacCer3.R'

organism Saccharomyces cerevisiae

species Saccharomyces cerevisiae

VignetteBuilder knitr

RoxygenNote 7.1.1

BugReports <https://github.com/FelixErnst/EpiTxDb.Sc.sacCer3/issues>

URL <https://github.com/FelixErnst/EpiTxDb.Sc.sacCer3>

git_url <https://git.bioconductor.org/packages/EpiTxDb.Sc.sacCer3>

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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.Sc.sacCer3.tRNadb would be a EpiTxDb object for Saccharomyces cerevisia data from tRNadb build based on the sacCer3 genome build.

Usage

```
EpiTxDb.Sc.sacCer3.RMBase(version = "1")
```

```
EpiTxDb.Sc.sacCer3.tRNadb(version = "1")
```

```
EpiTxDb.Sc.sacCer3.snoRNadb(version = "1")
```

```
snoRNA.targets.sacCer3(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.Sc.sacCer3.tRNadb()
```

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