

EpiTxDb.Sc.sacCer3

October 8, 2025

EpiTxDb.Sc.sacCer3 *Annotation package for EpiTxDb objects*

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")
---------	--

Value

a [EpiTxDb](#) object

Author(s)

Felix G M Ernst [aut]

See Also

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

Examples

`EpiTxDb.Sc.sacCer3.tRNAdb()`

Index

EpiTxDb, [/](#)

EpiTxDb.Sc.sacCer3, [1](#)

modifications, [/](#)

modificationsBy, [/](#)

modifiedSeqsByTranscript, [/](#)

snoRNA.targets.sacCer3

(EpiTxDb.Sc.sacCer3), [1](#)