

# EpiTxDb.Sc.sacCer3

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

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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") |
|---------|----------------------------------------------------------------------------------------|

## Value

a [EpiTxDb](#) object

## Author(s)

Felix G M Ernst [aut]

**See Also**

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

**Examples**

```
EpiTxDb.Sc.sacCer3.tRNAdb()
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