EpiTxDb.Sc.sacCer3

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`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)

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See Also

- `modifications`
- `modificationsBy`
- `modifiedSeqsByTranscript`

Examples

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