

# EpiTxDb.Mm.mm10

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*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.Mm.mm10.tRNAdb would be a EpiTxDb object of Mus musculus data from tRNAdb build based on the mm10 genome.

## Usage

```
EpiTxDb.Mm.mm10.RMBase(version = "1")
```

```
EpiTxDb.Mm.mm10.snoRNAdb(version = "1")
```

```
EpiTxDb.Mm.mm10.tRNAdb(version = "1")
```

```
snoRNA.targets.mm10(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.Mm.mm10.tRNAdb()`

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