

# EpiTxDb.Hs.hg38

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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.Hs.hg38.snoRNadb would be a EpiTxDb object of Homo sapiens data from snoRNadb build based on the hg38 genome.

## Usage

```
EpiTxDb.Hs.hg38.RMBase(version = "1")
```

```
EpiTxDb.Hs.hg38.snoRNadb(version = "1")
```

```
EpiTxDb.Hs.hg38.tRNadb(version = "1")
```

```
chain.rRNA.hg19Tohg38(version = "1")
```

```
chain.rRNA.hg38Tohg19(version = "1")
```

```
snoRNA.targets.hg38(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.Hs.hg38.snoRNadb()
```

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