

TxDB.Sscrofa.UCSC.susScr3.refGene

March 17, 2021

TxDB.Sscrofa.UCSC.susScr3.refGene

Annotation package for TxDb object(s)

Description

This package loads one or more TxDb objects. Such TxDb 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 TxDb.Hsapiens.UCSC.hg19.knownGene would be a TxDb object, of Homo sapiens data from UCSC build hg19 based on the knownGene Track.

Note

This data package was made from resources at UCSC on 2020-10-11 17:31:23 +0000 (Sun, 11 Oct 2020) and based on the susScr3 genome based on the refGene table

Author(s)

Bioconductor Core Team, Bioconductor Package Maintainer <maintainer@bioconductor.org> [cre]

See Also

[transcripts](#), [transcriptsBy](#)

Examples

```
## load the library
library(TxDB.Sscrofa.UCSC.susScr3.refGene)
## list the contents that are loaded into memory
ls('package:TxDB.Sscrofa.UCSC.susScr3.refGene')
## show the db object that is loaded by calling it's name
TxDb.Sscrofa.UCSC.susScr3.refGene
```

Index

*** data**

`TxDb.Sscrofa.UCSC.susScr3.refGene,`
[1](#)

*** package**

`TxDb.Sscrofa.UCSC.susScr3.refGene,`
[1](#)

`transcripts,` [1](#)

`transcriptsBy,` [1](#)

`TxDb.Sscrofa.UCSC.susScr3.refGene,` [1](#)

`TxDb.Sscrofa.UCSC.susScr3.refGene-package`
`(TxDb.Sscrofa.UCSC.susScr3.refGene),`
[1](#)