

# TxDb.Sscrofa.UCSC.susScr3.refGene

April 16, 2019

---

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 2018-10-19 16:56:08 +0000 (Fri, 19 Oct 2018) 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

\*Topic **data**

`TxDb.Sscrofa.UCSC.susScr3.refGene,`

[1](#)

\*Topic **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](#)