

# TxDB.Scerevisiae.UCSC.sacCer3.sgdGene

April 12, 2023

---

TxDB.Scerevisiae.UCSC.sacCer3.sgdGene

*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 2015-10-07 18:20:42 +0000 (Wed, 07 Oct 2015) and based on the sacCer3 genome based on the sgdGene table

## Author(s)

Marc Carlson, Bioconductor Package Maintainer <maintainer@bioconductor.org> [cre]

## See Also

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

## Examples

```
## load the library
library(TxDB.Scerevisiae.UCSC.sacCer3.sgdGene)
## list the contents that are loaded into memory
ls('package:TxDB.Scerevisiae.UCSC.sacCer3.sgdGene')
## show the db object that is loaded by calling it's name
TxDB.Scerevisiae.UCSC.sacCer3.sgdGene
```

# Index

**\* data**

`TxDB.Scerevisiae.UCSC.sacCer3.sgdGene,`

[1](#)

**\* package**

`TxDB.Scerevisiae.UCSC.sacCer3.sgdGene,`

[1](#)

`transcripts,` [1](#)

`transcriptsBy,` [1](#)

`TxDB.Scerevisiae.UCSC.sacCer3.sgdGene,`

[1](#)

`TxDB.Scerevisiae.UCSC.sacCer3.sgdGene-package`

`(TxDB.Scerevisiae.UCSC.sacCer3.sgdGene),`

[1](#)