

# TxDB.Scerevisiae.UCSC.sacCer3.sgdGene

April 4, 2014

---

TxDB.Scerevisiae.UCSC.sacCer3.sgdGene

*Annotation package for TranscriptDb object(s)*

---

## Description

This package loads one or more TranscriptDb objects. Such TranscriptDb 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 TranscriptDb 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 2013-09-19 00:32:49 -0700 (Thu, 19 Sep 2013) and based on the sacCer3 genome based on the sgdGene table

## Author(s)

Marc Carlson

## 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

\*Topic **data**

`TxDb.Scerevisiae.UCSC.sacCer3.sgdGene,`

[1](#)

\*Topic **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](#)