

TxDB.Scerevisiae.UCSC.sacCer2.sgdGene

April 4, 2014

TxDB.Scerevisiae.UCSC.sacCer2.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 00:32:21 -0700 (Thu, 19 Sep 2013) and based on the sacCer2 genome based on the sgdGene table

Author(s)

Marc Carlson

See Also

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

Examples

```
## load the library
library(TxDB.Scerevisiae.UCSC.sacCer2.sgdGene)
## list the contents that are loaded into memory
ls('package:TxDB.Scerevisiae.UCSC.sacCer2.sgdGene')
## show the db object that is loaded by calling it's name
TxDB.Scerevisiae.UCSC.sacCer2.sgdGene
```

Index

*Topic **data**

`Txdb.Scerevisiae.UCSC.sacCer2.sgdGene,`

[1](#)

*Topic **package**

`Txdb.Scerevisiae.UCSC.sacCer2.sgdGene,`

[1](#)

`transcripts, 1`

`transcriptsBy, 1`

`Txdb.Scerevisiae.UCSC.sacCer2.sgdGene,`

[1](#)

`Txdb.Scerevisiae.UCSC.sacCer2.sgdGene-package`

`(Txdb.Scerevisiae.UCSC.sacCer2.sgdGene),`

[1](#)