

# TxDb.Hsapiens.UCSC.hg19.knownGene

November 24, 2023

---

TxDb.Hsapiens.UCSC.hg19.knownGene

*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 18:11:28 +0000 (Wed, 07 Oct 2015) and based on the hg19 genome based on the knownGene table

## Author(s)

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

## See Also

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

## Examples

```
## load the library
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
## list the contents that are loaded into memory
ls('package:TxDb.Hsapiens.UCSC.hg19.knownGene')
## show the db object that is loaded by calling it's name
TxDb.Hsapiens.UCSC.hg19.knownGene
```

# Index

**\* data**

`TxDb.Hsapiens.UCSC.hg19.knownGene,`

[1](#)

**\* package**

`TxDb.Hsapiens.UCSC.hg19.knownGene,`

[1](#)

`transcripts,` [1](#)

`transcriptsBy,` [1](#)

`TxDb.Hsapiens.UCSC.hg19.knownGene,` [1](#)

`TxDb.Hsapiens.UCSC.hg19.knownGene-package`  
`(TxDb.Hsapiens.UCSC.hg19.knownGene),`

[1](#)