

# TxDB.Cfamiliaris.UCSC.canFam3.refGene

December 18, 2024

---

TxDB.Cfamiliaris.UCSC.canFam3.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 2020-04-28 14:19:25 +0000 (Tue, 28 Apr 2020) and based on the canFam3 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.Cfamiliaris.UCSC.canFam3.refGene)
## list the contents that are loaded into memory
ls('package:TxDB.Cfamiliaris.UCSC.canFam3.refGene')
## show the db object that is loaded by calling it's name
TxDb.Cfamiliaris.UCSC.canFam3.refGene
```

# Index

**\* data**

TxDb.Cfamilaris.UCSC.canFam3.refGene,  
[1](#)

**\* package**

TxDb.Cfamilaris.UCSC.canFam3.refGene,  
[1](#)

transcripts, [1](#)

transcriptsBy, [1](#)

TxDb.Cfamilaris.UCSC.canFam3.refGene,  
[1](#)

TxDb.Cfamilaris.UCSC.canFam3.refGene-package  
(TxDb.Cfamilaris.UCSC.canFam3.refGene),  
[1](#)