**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 2016-04-01 19:38:49 +0000 (Fri, 01 Apr 2016) 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**

```r
## 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

∗Topic data
  TxDB.Cfamiliaris.UCSC.canFam3.refGene,
  1

∗Topic package
  TxDB.Cfamiliaris.UCSC.canFam3.refGene,
  1

transcripts. /
transcriptsBy. /
TxDB.Cfamiliaris.UCSC.canFam3.refGene,
  1

TxDB.Cfamiliaris.UCSC.canFam3.refGene-package
  (TxDB.Cfamiliaris.UCSC.canFam3.refGene),
  1