

# FDb.UCSC.tRNAs

April 2, 2025

---

FDb.UCSC.tRNAs

*Annotation package for FeatureDb object(s)*

---

## Description

This package loads one or more FeatureDb objects. Such FeatureDb 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 2012-09-10 13:15:01 -0700 (Mon, 10 Sep 2012) and based on the hg19 genome based on the tRNAs table

## Author(s)

Marc Carlson

## See Also

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

## Examples

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

# Index

\* **data**

FDb.UCSC.tRNAs, [1](#)

\* **package**

FDb.UCSC.tRNAs, [1](#)

FDb.Hsapiens.UCSC.hg18.tRNAs  
(FDb.UCSC.tRNAs), [1](#)

FDb.Hsapiens.UCSC.hg19.tRNAs  
(FDb.UCSC.tRNAs), [1](#)

FDb.Mmusculus.UCSC.mm9.tRNAs  
(FDb.UCSC.tRNAs), [1](#)

FDb.Rnorvegicus.UCSC.rn4.tRNAs  
(FDb.UCSC.tRNAs), [1](#)

FDb.UCSC.tRNAs, [1](#)

FDb.UCSC.tRNAs-package  
(FDb.UCSC.tRNAs), [1](#)

transcripts, [1](#)

transcriptsBy, [1](#)