

# TxDB.Mmulatta.UCSC.rheMac8.refGene

June 11, 2025

---

TxDB.Mmulatta.UCSC.rheMac8.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 2020-10-11 17:32:17 +0000 (Sun, 11 Oct 2020) and based on the rheMac8 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.Mmulatta.UCSC.rheMac8.refGene)
## list the contents that are loaded into memory
ls('package:TxDB.Mmulatta.UCSC.rheMac8.refGene')
## show the db object that is loaded by calling it's name
TxDb.Mmulatta.UCSC.rheMac8.refGene
```

# Index

## **\* data**

TxDb.Mmulatta.UCSC.rheMac8.refGene,  
[1](#)

## **\* package**

TxDb.Mmulatta.UCSC.rheMac8.refGene,  
[1](#)

transcripts, [1](#)

transcriptsBy, [1](#)

TxDb.Mmulatta.UCSC.rheMac8.refGene, [1](#)

TxDb.Mmulatta.UCSC.rheMac8.refGene-package  
(TxDb.Mmulatta.UCSC.rheMac8.refGene),  
[1](#)