

# TxDB.Dmelanogaster.UCSC.dm3.ensGene

January 15, 2025

---

TxDB.Dmelanogaster.UCSC.dm3.ensGene

*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 18:15:53 +0000 (Wed, 07 Oct 2015) and based on the dm3 genome based on the ensGene table

## Author(s)

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

## See Also

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

## Examples

```
## load the library
library(TxDB.Dmelanogaster.UCSC.dm3.ensGene)
## list the contents that are loaded into memory
ls('package:TxDB.Dmelanogaster.UCSC.dm3.ensGene')
## show the db object that is loaded by calling it's name
TxDb.Dmelanogaster.UCSC.dm3.ensGene
```

# Index

**\* data**

`Txdb.Dmelanogaster.UCSC.dm3.ensGene,`  
[1](#)

**\* package**

`Txdb.Dmelanogaster.UCSC.dm3.ensGene,`  
[1](#)

`transcripts,` [1](#)

`transcriptsBy,` [1](#)

`Txdb.Dmelanogaster.UCSC.dm3.ensGene,` [1](#)

`Txdb.Dmelanogaster.UCSC.dm3.ensGene-package`  
`(Txdb.Dmelanogaster.UCSC.dm3.ensGene),`  
[1](#)