**Mus.musculus**

April 26, 2017

---

**Mus.musculus**  
*Annotation package that collates several annotation resources.*

---

**Description**

This data object was automatically created by Bioconductor Core Team. It represents a collection of annotation packages that can be used as a single object named Mus.musculus. This object can be used with the standard four accessor method for all AnnotationDbi objects. Namely: cols, keytype, keys and select. Users are encouraged to read the vignette from the `OrganismDbi` package for more details.

**Usage**

```r
library(Mus.musculus)
```

**Examples**

```r
Mus.musculus
cls <- columns(Mus.musculus)
cls
cls <- cls[c(1,19,45)]
kt <- keytypes(Mus.musculus)
kt <- kts[2]
kt
ts <- head(keys(Mus.musculus, keytype=kt))
ts
res <- select(Mus.musculus, keys=ks, columns=cls, keytype=kt)
head(res)
```
Index

«Topic datasets
   Mus.musculus, 1

Mus.musculus, 1