

# Mus.musculus

May 15, 2024

---

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

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

## Examples

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

# Index

\* **datasets**

Mus.musculus, [1](#)

Mus.musculus, [1](#)