

# Mus.musculus

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**Mus.musculus**

*Annotation package that collates several annotation resources.*

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## 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=kt))
ks
res <- select(Mus.musculus, keys=ks, columns=cls, keytype=kt)
head(res)
```

# Index

## \* datasets

[Mus.musculus, 1](#)

[Mus.musculus, 1](#)