Mus.musculus

November 6, 2026

`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