Rattus.norvegicus

January 17, 2024

Rattus.norvegicus  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 Rattus.norvegicus. 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(Rattus.norvegicus)

Examples

Rattus.norvegicus
cls <- columns(Rattus.norvegicus)
cls
cls <- cls[c(1,19,45)]
ks <- head(keys(Rattus.norvegicus, keytype=kts[2]))
res <- select(Rattus.norvegicus, keys=ks, columns=cls, keytype=kt)
head(res)
Index

* datasets
  Rattus.norvegicus, 1

Rattus.norvegicus, 1