**Rattus.norvegicus**

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| Rattus norvegicus | 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 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**

```r
library(Rattus.norvegicus)
```

**Examples**

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