**Rattus.norvegicus**

November 18, 2016

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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  
c1s <- columns(Rattus.norvegicus)  
c1s  
c1s <- c1s[c(1,19,45)]  
kts <- keytypes(Rattus.norvegicus)  
kts <- kts[2]  
kts  
ks <- head(keys(Rattus.norvegicus, keytype=kts[2]))  
ks  
res <- select(Rattus.norvegicus, keys=ks, columns=c1s, keytype=kts)  
head(res)
```
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