

# Homo.sapiens

April 11, 2018

---

Homo.sapiens

*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 Homo.sapiens. 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(Homo.sapiens)
```

## Examples

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

# Index

\*Topic **datasets**

Homo.sapiens, 1

Homo.sapiens, 1