Homo.sapiens

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`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)
```

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