

# org.MeSH.Hsa.db

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org.MeSH.Hsa.db	<i>Annotation package that provides correspondence between MeSH ID and Entrez Gene ID</i>
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## Description

This data represents a collection of annotation packages that can be used as a single object named as package name. This object can be used with the standard four accessor method for all AnnotationDbi objects. Namely: columns, keytypes, keys and select. Users are encouraged to read the vignette from the MeSHdbi package for more details.

## Usage

```
org.MeSH.Hsa.db
```

## Author(s)

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## Examples

```
library(org.MeSH.Hsa.db)
org.MeSH.Hsa.db

cls <- columns(org.MeSH.Hsa.db)
cls
kts <- keytypes(org.MeSH.Hsa.db)
kt <- kts[2]
kts
ks <- head(keys(org.MeSH.Hsa.db, keytype=kts[2]))
ks
res <- select(org.MeSH.Hsa.db, keys=ks, columns=cls, keytype=kt)
head(res)

dbconn(org.MeSH.Hsa.db)
dbfile(org.MeSH.Hsa.db)
```

```
dbschema(org.MeSH.Hsa.db)  
dbInfo(org.MeSH.Hsa.db)  
species(org.MeSH.Hsa.db)
```

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