

# MeSH.Sau.MRSA252.eg.db

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MeSH.Sau.MRSA252.eg.db

*Annotation package that provides correspondence between MeSH ID and Entrez Gene ID*

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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

```
MeSH.Sau.MRSA252.eg.db
```

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## Examples

```
library(MeSH.Sau.MRSA252.eg.db)
MeSH.Sau.MRSA252.eg.db

cls <- columns(MeSH.Sau.MRSA252.eg.db)
cls
kts <- keytypes(MeSH.Sau.MRSA252.eg.db)
kt <- kts[2]
kts
ks <- head(keys(MeSH.Sau.MRSA252.eg.db, keytype=kts[2]))
ks
res <- select(MeSH.Sau.MRSA252.eg.db, keys=ks, columns=cls, keytype=kt)
head(res)

dbconn(MeSH.Sau.MRSA252.eg.db)
```

```
dbfile(MeSH.Sau.MRSA252.eg.db)  
dbschema(MeSH.Sau.MRSA252.eg.db)  
dbInfo(MeSH.Sau.MRSA252.eg.db)  
species(MeSH.Sau.MRSA252.eg.db)
```

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