

# MeSH.Sau.USA300TCH1516.eg.db

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MeSH.Sau.USA300TCH1516.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.USA300TCH1516.eg.db
```

## Author(s)

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## Examples

```
library(MeSH.Sau.USA300TCH1516.eg.db)  
MeSH.Sau.USA300TCH1516.eg.db
```

```
cls <- columns(MeSH.Sau.USA300TCH1516.eg.db)  
cls  
kts <- keytypes(MeSH.Sau.USA300TCH1516.eg.db)  
kt <- kts[2]  
kts  
ks <- head(keys(MeSH.Sau.USA300TCH1516.eg.db, keytype=kts[2]))  
ks  
res <- select(MeSH.Sau.USA300TCH1516.eg.db, keys=ks, columns=cls, keytype=kt)  
head(res)
```

```
dbconn(MeSH.Sau.USA300TCH1516.eg.db)  
dbfile(MeSH.Sau.USA300TCH1516.eg.db)  
dbschema(MeSH.Sau.USA300TCH1516.eg.db)  
dbInfo(MeSH.Sau.USA300TCH1516.eg.db)  
species(MeSH.Sau.USA300TCH1516.eg.db)
```

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