**MeSH.Zma.eg.db**

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*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.Zma.eg.db`

**Author(s)**

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**Examples**

```r
library(MeSH.Zma.eg.db)
MeSH.Zma.eg.db

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

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