MeSH.Mga.eg.db
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Annotation package that provides correspondence between MeSH ID and Entrez Gene ID

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.Mga.eg.db

Author(s)
Koki Tsuyuzaki

Examples
library(MeSH.Mga.eg.db)
MeSH.Mga.eg.db

c <- columns(MeSH.Mga.eg.db)
c
kts <- keytypes(MeSH.Mga.eg.db)
kts <- kts[2]
kts
ks <- head(keys(MeSH.Mga.eg.db, keytype=kts[2]))
ks
res <- select(MeSH.Mga.eg.db, keys=ks, columns=c, keytype=kts)
head(res)
dbconn(MeSH.Mga.eg.db)
dbfile(MeSH.Mga.eg.db)
dbschema(MeSH.Mga.eg.db)
dbInfo(MeSH.Mga.eg.db)
species(MeSH.Mga.eg.db)
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