

# LRBase.Dme.eg.db

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LRBase.Dme.eg.db	<i>Annotation package that provides correspondence between Ligand-Receptor genes as 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 LRBaseDbi package for more details.

## Usage

```
LRBase.Dme.eg.db
```

## Value

LRBase.XXX.eg.db-type package

## Author(s)

Koki Tsuyuzaki

## Examples

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

species(LRBase.Dme.eg.db)
dbInfo(LRBase.Dme.eg.db)
dbfile(LRBase.Dme.eg.db)
dbSchema(LRBase.Dme.eg.db)
```

```
dbconn(LRBase.Dme.eg.db)  
lrPackageName(LRBase.Dme.eg.db)  
lrNomenclature(LRBase.Dme.eg.db)  
lrListDatabases(LRBase.Dme.eg.db)  
lrVersion(LRBase.Dme.eg.db)
```

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