**org.Mxanthus.db**

January 17, 2024

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**exampleGene**  
*Example Genes for Myxococcus xanthus*

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**Description**

A set of genes (in the SYMBOL keytype) randomly obtained to perform enrichment analysis with clusterProfiler and org.Mxanthus.db

**Examples**

```
gene = exampleGene
```

---

**loadOldData**  
*The loadOldData(v) function*

---

**Description**

This is a function that generates a OrgDv object that stores old versions stored in AnnotationHub

**Usage**

```
loadOldData(v)
```

**Arguments**

- `v`  
  This value must be a character. It must be the two first numbers of the package version that uses the database that the user want to download. For example: "1.0"

**Value**

An OrgDb object
Examples

```r
old_version = loadOldData("1.0.0")
```

---

**loadOrgMxanthusDb**  
*The loadOrgMxanthusDb(value) function*

---

**Description**

This is a function that generates the object org.Mxanthus.db (an OrgDb object) when the package is loaded.

**Usage**

```r
loadOrgMxanthusDb(value)
```

**Arguments**

- **value**
  
  This value must be NULL

**Value**

An OrgDb object called org.Mxanthus.db

**Examples**

```r
function (value)
{
  stopifnot(missing(value))
  if (is.null(ah75133)) {
    ah <- AnnotationHub::AnnotationHub()
    ah75133 <<- ah["AH75133"]
  }
  ah75133
}
```

---

**org.Mxanthus.db**  
*The Data for org.Mxanthus.db*

---

**Description**

org.Mxanthus.db is an OrgDb object that stores the data from Annotation Hub that links each gene of the Genome with its corresponding GO terms and other biological identifiers.

**See Also**

- `AnnotationDb-class` for use of the `select()` interface.
Examples

```r
## Obtain the columns stored in org.Mxanthus.eg.db

columns(org.Mxanthus.db)

## This is a query to obtain the SYMBOL and the GO terms related to the GID 2000

select(org.Mxanthus.db, keys="2000", columns=c("SYMBOL", "GO"))
```

---

**Description**

Welcome to the `org.Mxanthus.db` annotation Package. This is an organism specific package. The purpose is to provide detailed information about the species abbreviated in the second part of the package name `org.Mxanthus.db`. This package is updated biannually.

To learn more about this package, users are encouraged to learn about the select, columns, keys and keytypes methods. These are described in a walkthrough on the bioconductor website as well as in the manual pages and vignettes in the AnnotationDbi package.

Examples

```r
## Obtain the keytypes supported by org.Mxanthus.eg.db

keytypes(org.Mxanthus.db)

## Show the metadata information about the database

show(org.Mxanthus.db)
```

---

**Description**

`org.Mxanthus.dbORGANISM` is an R object that contains a single item: a character string that names the organism for which `org.Mxanthus.db` was built.

**Details**

Although the package name is suggestive of the organism for which it was built, `org.Mxanthus.dbORGANISM` provides a simple way to programmatically extract the organism name.
See Also

- **AnnotationDb-class** for use of the select() interface.

Examples

```r
## select() interface:
## Objects in this package can be accessed using the select() interface
## from the AnnotationDbi package. See ?select for details.

## Bimap interface:
name <- org.Mxanthus.dbORGANISM
```

---

### versions

<table>
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<tr>
<th>versions</th>
<th>Old Versions for the Dataset stored in AnnotationHub</th>
</tr>
</thead>
</table>

Description

An environment in which the AnnotationHub code of the different versions of the database is stored in each entry. At the moment only support the old version 1.0.0

Examples

```r
ah = suppressMessages(AnnotationHub::AnnotationHub())
old_version = ah[[versions["1.0.0"]], verbose=FALSE]]
```
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