org.Mxanthus.db

November 11, 2026

`exampleGene` *Example Genes for Myxococcus xanthus*

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

```
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

```
loadOrgMxanthusDb(value)
```

Arguments

`value`	This value must be NULL

Value

An OrgDb objecto called org.Mxanthus.db

Examples

```
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

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

columns(org.Mxanthus.db)

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

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

---

org.Mxanthus.dbBASE *Bioconductor annotation data package*

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

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

keytypes(org.Mxanthus.db)

## Show the metadata information about the database

show(org.Mxanthus.db)
```

---

org.Mxanthus.dbORGANISM *The Organism for 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

```
## 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 *Old Versions for the Dataset stored in AnnotationHub*

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

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

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