

Package: JASPAR2016 (via r-universe)

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Title Data package for JASPAR 2016

Description Data package for JASPAR 2016. To search this databases,
please use the package TFBSTools ($\geq 1.8.1$).

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Depends R ($\geq 3.2.2$), methods

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URL <http://jaspar.genereg.net/>

Type Package

biocViews ExperimentData, MotifAnnotation, GeneRegulation

NeedsCompilation no

LazyData no

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JASPAR2016-class

JASPAR2016 object

Description

The JASPAR2016 object class is a thin class for storing the path of JASPAR2016 style SQLite file.

Slots

db: Object of class "character": a character string of the path of SQLite file.

Author(s)

Ge Tan

Examples

```
## Not run:
library(JASPAR2016)
JASPAR2016

library(TFBSTools)

opts <- list()
opts[["species"]] <- 9606
opts[["type"]] <- "SELEX"
opts[["all_versions"]] <- TRUE
PFMatrixList <- getMatrixSet(JASPAR2016, opts)

opts2 <- list()
opts2[["type"]] <- "SELEX"
PFMatrixList2 <- getMatrixSet(JASPAR2016, opts2)

## End(Not run)
```

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