Package 'JASPAR2016'

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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 (>= 1.8.1).

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Depends R (>= 3.2.2), methods

License GPL-2

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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