

Package ‘JASPAR2016’

July 11, 2024

Version 1.32.0

Date 2015-11-04

Title Data package for JASPAR 2016

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

Author Ge Tan <ge_tan@live.com>

Maintainer Ge Tan <ge_tan@live.com>

Depends R ($\geq 3.2.2$), methods

License GPL-2

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

Type Package

biocViews ExperimentData, MotifAnnotation, GeneRegulation

NeedsCompilation no

LazyData no

git_url <https://git.bioconductor.org/packages/JASPAR2016>

git_branch RELEASE_3_19

git_last_commit 6ffd9c5

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-07-11

Contents

JASPAR2016-class	2
Index	3

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)
```

Index

* classes

JASPAR2016-class, [2](#)

JASPAR2016 (JASPAR2016-class), [2](#)

JASPAR2016-class, [2](#)