

# Package ‘JASPAR2016’

June 20, 2024

**Version** 1.33.0

**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** devel

**git\_last\_commit** 8284586

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.20

**Date/Publication** 2024-06-20

## Contents

JASPAR2016-class . . . . .	2
<b>Index</b>	<b>3</b>

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](#)