

# Package ‘JASPAR2016’

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**Version** 1.40.0

**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 (>= 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

**git\_url** <https://git.bioconductor.org/packages/JASPAR2016>

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JASPAR2016-class      *JASPAR2016 object*

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**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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\* **classes**

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