

# Package ‘JASPAR2014’

October 18, 2017

**Version** 1.12.0

**Date** 2014-03-10

**Title** Data package for JASPAR

**Description**

Data package for JASPAR 2014. To search this databases, please use the package TFBSTools.

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**Depends** R (>= 3.0.1), methods, Biostrings (>= 2.29.19)

**License** GPL-2

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

**Type** Package

**biocViews** ExperimentData, SequencingData

**NeedsCompilation** no

**LazyData** yes

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JASPAR2014-package     *Data package for JASPAR 2014*

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## Description

Data package for JASPAR 2014. To search this databases, please use th e package TFBSTools.

**Details**

Package: JASPAR2014  
Version: 0.99.2  
Date: 2013-10-07  
Depends: R (>= 3.0.1), methods, Biostrings (>= 2.29.19)  
License: GPL-2  
URL: <http://jaspardev.genereg.net/>  
Type: Package  
NeedsCompilation: no  
LazyData: yes

**Author(s)**

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**References**

See <http://jaspardev.genereg.net/> for more details about JASPAR.

**Examples**

```
## load the library
library(JASPAR2014)
## list the contents that are loaded into memory
ls("package:JASPAR2014")
```

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JASPAR2014-class      *JASPAR2014 object*

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**Description**

The JASPAR2014 object class is a thin class for storing the path of JASPAR2014 style SQLite file.

**Slots**

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

**Author(s)**

Ge Tan

**See Also**

[JASPAR2014SitesSeqs](#),

**Examples**

```
## Not run:  
  library(JASPAR2014)  
  JASPAR2014  
  
## End(Not run)
```

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JASPAR2014SitesSeqs    *Sites sequences*

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**Description**

A list of DNASTringSet storing transcription factor binding sites sequences from JASPAR 2014 release with JASPAR IDs as names

**Source**

<http://jaspar.binf.ku.dk/html/DOWNLOAD/sites/>

**Examples**

```
## Not run:  
  library(JASPAR2014)  
  JASPAR2014SitesSeqs  
  
## End(Not run)
```

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