

# Package ‘JASPAR2014’

May 16, 2024

**Version** 1.40.0

**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

**git\_url** <https://git.bioconductor.org/packages/JASPAR2014>

**git\_branch** RELEASE\_3\_19

**git\_last\_commit** 4f3eb19

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

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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 the 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:	<a href="http://jaspardev.genereg.net/">http://jaspardev.genereg.net/</a>
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 DNAStrngSet 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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