

# Package ‘JASPAR2014’

December 18, 2025

**Version** 1.47.0

**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** devel

**git\_last\_commit** d27e6eb

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.23

**Date/Publication** 2025-12-18

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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 | <i>JASPAR2014 object</i> |
|------------------|--------------------------|

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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 | <i>Sites sequences</i> |
|---------------------|------------------------|

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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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