Package 'JASPAR2014'

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Version 1.48.0

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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

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JASPAR2014-package *Data package for JASPAR 2014*

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")
```

JASPAR2014-class *JASPAR2014 object*

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)
```

JASPAR2014SitesSeqs *Sites sequences*

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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