Package 'JASPAR2024'

December 10, 2025

Type Package

Title Data package for JASPAR database (version 2024)

Version 0.99.7

Description JASPAR (https://jaspar.elixir.no/) is a widely-used open-access database presenting manually curated high-quality and non-redundant DNA-binding profiles for transcription factors (TFs) across taxa. In this 10th release and 20th-anniversary update, the CORE collection has expanded with 329 new profiles. We updated three existing profiles and provided orthogonal support for 72 profiles from the previous release UNVALIDATED collection. Altogether, the JASPAR 2024 update provides a 20 percent increase in CORE profiles from the previous release. A trimming algorithm enhanced profiles by removing low information content flanking base pairs, which were likely uninformative (within the capacity of the PFM models) for TFBS predictions and modelling TF-DNA interactions. This release includes enhanced metadata, featuring a refined classification for plant TFs structural DNA-binding domains. The new JASPAR collections prompt updates to the genomic tracks of predicted TF-binding sites in 8 organisms, with human and mouse tracks available as native tracks in the UCSC Genome browser. All data are available through the JASPAR web interface and programmatically through its API and the updated Bioconductor and pyJASPAR packages. Finally, a new TFBS extraction tool enables users to retrieve predicted JASPAR TFBSs intersecting their genomic regions of interest.

Depends R (>= 4.3.0), methods, BiocFileCache, utils

License GPL-2

URL https://jaspar.elixir.no/

NeedsCompilation no

biocViews AnnotationData, FunctionalAnnotation, AnnotationHub

LazyData no

RoxygenNote 7.2.3

Suggests knitr, rmarkdown, BiocStyle, RSQLite

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```
VignetteBuilder knitr
BugReports https://github.com/da-bar/JASPAR2024
git_url https://git.bioconductor.org/packages/JASPAR2024
git_branch devel
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 db
                      Access database from JASPAR2024 object
Description
   The accessor function for retrieving the location of the database location slot from the JASPAR2024
   object
Usage
   db(object)
   ## S4 method for signature 'JASPAR2024'
   db(object)
Arguments
   object
                 JASPAR2024 class object
Value
   Returns the location of the JASPAR2024.sqlite file
Author(s)
   Damir Baranasic
```

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Examples

```
library(JASPAR2024)
JASPAR2024 <- JASPAR2024()
db(JASPAR2024)</pre>
```

JASPAR2024-class

JASPAR2024 object class

Description

The JASPAR2024 object class is a thin class for storing the path of JASPAR2024 style SQLite file.

Usage

JASPAR2024()

Value

JASPAR2024-class

Slots

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

Author(s)

Damir Baranasic

Examples

```
library(JASPAR2024)
library(RSQLite)

JASPAR2024 <- JASPAR2024()

JASPARConnect <- RSQLite::dbConnect(RSQLite::SQLite(), db(JASPAR2024))
RSQLite::dbGetQuery(JASPARConnect, 'SELECT * FROM MATRIX LIMIT 5')
dbDisconnect(JASPARConnect)</pre>
```

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