

Package ‘JASPAR2022’

December 10, 2025

Type Package

Title Data package for JASPAR database (version 2022)

Version 0.99.8

Description JASPAR is an open-access database containing manually curated, non-redundant transcription factor (TF) binding profiles for TFs across six taxonomic groups. In this 9th release, we expanded the CORE collection with 341 new profiles (148 for plants, 101 for vertebrates, 85 for urochordates, and 7 for insects), which corresponds to a 19% expansion over the previous release. To search thisdatabases, please use the package TFBSTools (>= 1.31.2).

Depends R (>= 4.1.0), methods, BiocFileCache, utils

License GPL-2

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

NeedsCompilation no

biocViews AnnotationData, FunctionalAnnotation, AnnotationHub

LazyData no

RoxygenNote 7.1.2

Suggests knitr, rmarkdown, BiocStyle, TFBSTools (>= 1.31.2)

VignetteBuilder knitr

git_url <https://git.bioconductor.org/packages/JASPAR2022>

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JASPAR2022-class	<i>JASPAR2022 object class</i>
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Description

The JASPAR2022 object class is a thin class for storing the path of JASPAR2022 style SQLite file.

Slots

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

Author(s)

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Examples

```
library(TFBSTools)
opts <- list()
opts[["species"]] <- 9606
opts[["type"]] <- "SELEX"
opts[["all_versions"]] <- TRUE
PFMatrixList <- getMatrixSet(JASPAR2022, opts)

opts2 <- list()
opts2[["type"]] <- "SELEX"
PFMatrixList2 <- getMatrixSet(JASPAR2022, opts2)
```

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