

Package: ChIPDBData (via r-universe)

October 10, 2026

Title ChIP-seq Target Databases for TFEA.ChIP

Version 1.2.0

Description Provides curated gene target databases derived from ChIP-seq datasets, formatted as ChIPDB objects for use with TFEA.ChIP.

License GPL-3

Imports ExperimentHub

Suggests knitr, rmarkdown, BiocStyle, AnnotationHub, TFEA.ChIP, DESeq2, testthat (>= 3.0.0)

biocViews ExperimentData, ExperimentHub, Homo_sapiens_Data, ENCODE, SequencingData

VignetteEngine knitr::rmarkdown

VignetteBuilder knitr

URL <https://github.com/yberda/ChIPDBData>

BugReports <https://github.com/yberda/ChIPDBData/issues>

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

Config/testthat/edition 3

Config/pak/sysreqs libicu-dev libpng-dev libssl-dev zlib1g-dev

Repository Bioconductor 3.23

Date/Publication 2026-04-28 12:38:02 UTC

RemoteUrl <https://github.com/bioc/ChIPDBData>

RemoteRef RELEASE_3_23

RemoteSha bb6cf18332d0671967d26ebec8adfed389cc06a6

Contents

getChIPDB	2
Index	3

`getChIPDB`*Retrieve ChIPDB dataset from ExperimentHub*

Description

This function fetches ChIPDB objects (lists of transcription factor–target gene associations) for use with the TFEA.ChIP package. Available datasets include ENCODE, CREDB, and GeneHancer-derived collections.

Usage

```
getChIPDB(  
  name = c("ENCODE_rE2G", "ENCODE_rE2G_25score", "ENCODE_rE2G_50score",  
    "ENCODE_rE2G_75score", "ENCODE_rE2G_50depth", "ENCODE_rE2G_100depth",  
    "ENCODE_rE2G_200depth", "ENCODE_rE2G_300depth", "CREdb", "GeneHancer")  
)
```

Arguments

name	A character string naming the dataset to retrieve. Options: "ENCODE_rE2G", "ENCODE_rE2G_25score", "ENCODE_rE2G_50score", "ENCODE_rE2G_75score", "ENCODE_rE2G_50depth", "ENCODE_rE2G_100depth", "ENCODE_rE2G_200depth", "ENCODE_rE2G_300depth", "CREdb", "GeneHancer".
------	---

Value

A list object of class ChIPDB containing transcription factor–target gene mappings.

Examples

```
ChIPDB <- getChIPDB("ENCODE_rE2G_300depth")
```

Index

getChIPDB, [2](#)