

# Package ‘ChIPDBData’

November 6, 2025

**Title** ChIP-seq Target Databases for TFEA.ChIP

**Version** 1.1.0

**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

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|            |                                                                       |
|------------|-----------------------------------------------------------------------|
| ChIPDBData | <i>ChIPDBData: A package for curated ChIP-seq TF target databases</i> |
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Description

The ChIPDBData package provides curated ChIP-seq transcription factor target databases designed for use with TFEA.ChIP

Package contents

- Functions provided: getChIPDB (for loading the dataset)

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See Also

Useful links:

- <https://github.com/yberda/ChIPDBData>
- Report bugs at <https://github.com/yberda/ChIPDBData/issues>

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|           |                                                   |
|-----------|---------------------------------------------------|
| getChIPDB | <i>Retrieve ChIPDB dataset from ExperimentHub</i> |
|-----------|---------------------------------------------------|

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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")
```

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