

# Package ‘ChIPDBData’

May 26, 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)

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**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)

### Author(s)

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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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