# Package 'ChIPDBData'

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

**Version** 1.0.0

**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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# Contents

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ChIPDBData                *ChIPDBData: A package for curated ChIP-seq TF target databases*

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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                *Retrieve ChIPDB dataset from ExperimentHub*

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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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