Package 'ChIPDBData'

November 13, 2025

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

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RoxygenNote 7.3.2

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Contents

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

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`

`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