Package ‘xcoredata’

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Type Package
Title data package for xcore
Version 1.8.0
Description Provides data to use with xcore package.
Depends R (>= 4.2)
Imports ExperimentHub (>= 2.2.0), utils (>= 4.2.0)
Suggests BiocGenerics (>= 0.40.0), data.table (>= 1.14.2),
    GenomInfoDb (>= 1.30.0), GenomicRanges (>= 1.46.1), IRanges
    (>= 2.28.0), knitr (>= 1.37), rmarkdown (>= 2.11), Matrix (>=
    1.3.4), stringr (>= 1.4.0), S4Vectors (>= 0.32.3),
    TxDb.Hsapiens.UCSC.hg38.knownGene (>= 3.14.0), xcore
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Contents

chip_atlas_meta .......................................................... 2
chip_atlas_promoters_f5 .................................................. 3
entrez2fantom .............................................................. 3
promoters_f5 ................................................................. 4
promoters_f5_core .......................................................... 4
remap_meta ................................................................. 5
remap_promoters_f5 ....................................................... 6
symbol2fantom .............................................................. 6

Index.............................................................................. 7

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chip_atlas_meta  ChIP-Atlas metadata

Description

Metadata associated with chip_atlas_promoters.

Usage

chip_atlas_meta

Format

A data.frame with 13891 rows and 5 columns.

id  Character giving internal experiment ID.

.tf  Character giving transcription factor name.

tf_dbd  Character giving transcription factor DNA binding domain family, as per CIS BP database.

biotype  Character giving experiment biological origin.

study  Character giving study ID.

Examples

chip_atlas_meta()
**chip_atlas_promoters_f5**

*ChIP-Atlas FANTOM5 promoters intersection matrix*

**Description**

An intersection matrix describing overlaps between ChIP-Atlas’s ChIP-seq tracks and *promoters_f5*. To find overlapping regions promoters were extended by 500bp in both directions.

**Usage**

chip_atlas_promoters_f5

**Format**

A matrix with 209911 rows and 13891 columns. Row names correspond to promoters names, column names are formatted as TranscriptionFactor_Origin_Cell_ExperimentID (e.g. PARK7_Neural_SH-SY5Y_DRX000550, MLL-AF6_Blood_ML-2_DRX001460).

**Examples**

chip_atlas_promoters_f5()

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**entrez2fantom**

*ENTREZ IDs to FANTOM5 core promoters names mappings*

**Description**

Vector mapping ENTREZ IDs to FANTOM5 core promoters names.

**Usage**

entrez2fantom

**Format**

A named character vector of length 14214.

**Examples**

entrez2fantom()
promoters_f5  

Promoters GenomicRanges object

Description

FANTOM5’s hg38 promoters annotated with nearest features in GENCODE ver. 38 annotation and UCSC hg38 knownGene annotation ver. 3.13.0.

Usage

promoters_f5

Format

A GenomicRanges object of length 209911, with 11 metadata columns:

- name  Promotor name.
- score  Numeric vector.
- gene_type_gencode  Gene type of associated gene as defined by GENCODE annotation.
- ENTREZID  ENTREZ ID of associated gene as defined by all three annotation sources. Prevalence of annotations: UCSC > GENCODE > FANTOM5.
- SYMBOL  Gene symbol of associated gene as defined by all three annotation sources. Prevalence of annotations: UCSC > GENCODE > FANTOM5.

Examples

promoters_f5()

promoters_f5_core  

Core promoters GenomicRanges object

Description

Core promoters selected from promoters_f5. Selection criteria were GENCODE confirmation and ENCODE ROADMAP confirmation. Further for each gene single promoter with highest FANTOM5 score was selected.

Usage

promoters_f5_core
Format

A GenomicRanges object of length 14191, with 16 metadata columns:

- **name** Promotor name.
- **score** Numeric vector.
- **gene_type_gencode** Gene type of associated gene as defined by GENCODE annotation.
- **ENTREZID** ENTREZ ID of associated gene as defined by all three annotation sources. Prevalence of annotations: UCSC > GENCODE > FANTOM5.
- **SYMBOL** Gene symbol of associated gene as defined by all three annotation sources. Prevalence of annotations: UCSC > GENCODE > FANTOM5.

Examples

```r
promoters_f5_core()
```

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remap_meta  ReMap2020 metadata

Description

Metadata associated with remap_promoters.

Usage

```r
remap_meta
```

Format

A `data.table` with 5798 rows and 6 columns.

- **id** Character giving internal experiment ID.
- **tf** Character giving transcription factor name.
- **tf_dbd** Character giving transcription factor DNA binding domain family, as per CIS BP database.
- **biotype** Character giving experiment biological origin.
- **study** Character giving study ID.
- **condition** Character specifying experiment conditions or treatment.

Examples

```r
remap_meta()
```
### remap_promoters_f5

**Description**

An intersection matrix describing overlaps between ReMap2020's ChIP-seq tracks and promoters_f5. To find overlapping regions promoters were extended by 500bp in both directions.

**Usage**

```r
remap_promoters_f5
```

**Format**

A Matrix with 209911 rows and 5728 columns. Row names corresponds to promoters names, column names are formatted as ExperimentID.TranscriptionFactor.Biotype.

**Examples**

```r
remap_promoters_f5()
```

### symbol2fantom

**Description**

Gene symbols to FANTOM5 core promoters names mappings.

**Usage**

```r
symbol2fantom
```

**Format**

A named character vector of length 14222.

**Examples**

```r
symbol2fantom()
```
Index

* datasets
  chip_atlas_meta, 2
  chip_atlas_promoters_f5, 3
  entrez2fantom, 3
  promoters_f5, 4
  promoters_f5_core, 4
  remap_meta, 5
  remap_promoters_f5, 6
  symbol2fantom, 6

chip_atlas_meta, 2
chip_atlas_promoters_f5, 3

entrez2fantom, 3

promoters_f5, 3, 4, 6
promoters_f5_core, 4

remap_meta, 5
remap_promoters_f5, 6

symbol2fantom, 6