Package ‘xcoredata’

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Type Package
Title data package for xcore
Version 1.6.0
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), GenomeInfoDb (>= 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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**chip_atlas_meta**

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```

**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 corresponds to promoters names, column names are formatted as TranscriptionFactor-Origin_Cell_ExperimentID (eg. PARK7_Neural_SH-SY5Y_DRX000550, MLL-AF6_Blood_ML-2_DRX001460).

**Examples**

`chip_atlas_promoters_f5()`

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_genencode  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**  Promoter 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_core()

---

remap_meta

ReMap2020 metadata

Description

Metadata associated with remap_promoters.

Usage

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

remap_meta()
remap_promoters_f5  ReMap2020 and FANTOM5 promoters intersection matrix

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
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
remap_promoters_f5()

symbol2fantom  Gene symbols to FANTOM5 core promoters names mappings

Description
Vector mapping gene symbols to FANTOM5 core promoters names.

Usage
symbol2fantom

Format
A named character vector of length 14222.

Examples
symbol2fantom()
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