

Package ‘xcoredata’

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Type Package

Title data package for xcore

Version 1.16.0

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

License GPL-2

Encoding UTF-8

RoxygenNote 7.1.2

VignetteBuilder knitr

biocViews ExperimentHub, ExperimentData, Homo_sapiens_Data

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chip_atlas_meta	<i>ChIP-Atlas metadata</i>
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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_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

```
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	<i>ReMap2020 and FANTOM5 promoters intersection matrix</i>
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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	<i>Gene symbols to FANTOM5 core promoters names mappings</i>
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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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