

Package ‘xcoredata’

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Type Package

Title data package for xcore

Version 1.15.0

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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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

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_db 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_db 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()
```

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](#)