Package ‘xcoredata’

July 10, 2025

Type Package

Title data package for xcore

Version 1.13.0

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

git_url https://git.bioconductor.org/packages/xcoredata

git_branch devel

git_last_commit aa6c0d6

git_last_commit_date 2025-04-15

Repository Bioconductor 3.22

Date/Publication 2025-07-10

Author Maciej Migdał [aut, cre] (ORCID: <`https://orcid.org/0000-0002-8021-7263`>), Bogumił Kaczkowski [aut] (ORCID: <`https://orcid.org/0000-0001-6554-5608`>)

Maintainer Maciej Migdał <`mcjmigdal@gmail.com`>

Contents

`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 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 specifiying 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