

# Package ‘xcoredata’

October 12, 2023

**Type** Package

**Title** data package for xcore

**Version** 1.4.0

**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** RELEASE\_3\_17

**git\_last\_commit** 7cc9a13

**git\_last\_commit\_date** 2023-04-25

**Date/Publication** 2023-10-12

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

**Maintainer** Maciej Migdał <[mcjmigdal@gmail.com](mailto:mcjmigdal@gmail.com)>

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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()
```

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chip_atlas_promoters_f5	<i>ChIP-Atlas FANTOM5 promoters intersection matrix</i>
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### 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*

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**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	<i>ReMap2020 metadata</i>
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**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

*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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