

Package: ListerEtAlBSseq (via r-universe)

October 10, 2026

Title BS-seq data of H1 and IMR90 cell line excerpted from Lister et al. 2009

Version 1.45.1

Date 2015-04-02

Description Base resolution bisulfite sequencing data of Human DNA methylomes

Depends R (>= 3.1.1), methylPipe

Suggests BSgenome.Hsapiens.UCSC.hg18

License Artistic 2.0

biocViews ExperimentData, Homo_sapiens_Data, SequencingData

PackageStatus Deprecated

Config/pak/sysreqs cmake make libbz2-dev libicu-dev libjpeg-dev liblzma-dev libpng-dev libuv1-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

Repository <https://bioc.r-universe.dev>

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H1.WGBS

BS-seq data of H1 cell line

Description

BS-seq data of H1 cell line from Lister et al. 2009

Details

This is the BS-seq dataset of H1 cell line (Lister et al. 2009). The dataset has been stored in BSdata class of package methylPipe and can directly be used for further analysis using the package.

Examples

```
library(BSgenome.Hsapiens.UCSC.hg18)
h1data <- system.file('extdata', 'mc_h1_tabix.txt.gz', package='ListerEtAlBSseq')
h1uncov <- system.file('extdata', 'uncov_GR_h1.Rdata', package='ListerEtAlBSseq')
load(h1uncov)
H1.WGBS <- BSdata(file=h1data, uncov=uncov_GR_h1, org=Hsapiens)
```

IMR90.WGBS

BS-seq data of IMR90 cell line

Description

BS-seq data of IMR90 cell line from Lister et al. 2009

Details

This is the BS-seq dataset of IMR90 cell line (Lister et al. 2009). The dataset has been stored in BSdata class of package methylPipe and can directly be used for further analysis using the package.

Examples

```
library(BSgenome.Hsapiens.UCSC.hg18)
imr90data <- system.file('extdata', 'mc_i90_tabix.txt.gz', package='ListerEtAlBSseq')
imr90uncov <- system.file('extdata', 'uncov_GR_imr90.Rdata', package='ListerEtAlBSseq')
load(imr90uncov)
IMR90.WGBS <- BSdata(file=imr90data, uncov=uncov_GR_imr90, org=Hsapiens)
```

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