# Package 'ListerEtAlBSseq'

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

**Version** 1.44.0

**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

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**Author** Mattia Pelizzola [aut], Kamal Kishore [aut], Mattia Furlan [ctb, cre]

**Maintainer** Mattia Furlan <mattia.furlan@iit.it>

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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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