

Package ‘minfiDataEPIC’

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Version 1.0.0

Title Example data for the Illumina Methylation EPIC array

Description Data from 3 technical replicates of the cell line GM12878 from the EPIC methylation array.

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Depends R (>= 3.3), minfi (>= 1.18.2),
IlluminaHumanMethylationEPICmanifest,
IlluminaHumanMethylationEPICanno.ilm10b2.hg19

LazyData yes

biocViews Homo_sapiens_Data, MethylationArrayData, MicroarrayData

NeedsCompilation no

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MsetEPIC	<i>An example dataset for Illumina’s Human Methylation EPIC dataset, after preprocessing.</i>
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Description

This contains the raw data for 3 technical replicates of the cell line GM12878 from the Illumina’s Human Methylation EPIC platform. The data has been preprocessed with preprocessRaw.

Usage

```
data(MsetEPIC)
```

Format

An object of class “MethylSet”

Details

Scripts for creating the object is found in the `scripts` directory of the package and `extdata` contains the IDAT files. The data has been preprocessed using `preprocessRaw`.

See Also

[MethylSet](#) for the class definition, [preprocessRaw](#) for the preprocessing function, [RGsetEPIC](#) for the companion raw data.

Examples

```
data(MsetEPIC)
pData(MsetEPIC)
```

RGsetEPIC

An example dataset for the Illumina's Human Methylation EPIC platform.

Description

This contains the raw data for 3 technical replicates of the cell line GM12878 from the Illumina's Human Methylation EPIC platform.

Usage

```
data(RGsetEPIC)
```

Format

An object of class "RGChannelSet"

Details

Scripts for creating the object is found in the `scripts` directory of the package and `extdata` contains the IDAT files.

See Also

[RGChannelSet](#) for the class definition, [MsetEPIC](#) for the companion preprocessed data.

Examples

```
data(RGsetEPIC)
pData(RGsetEPIC)
```

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