

# Package ‘minfiDataEPIC’

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**Version** 1.35.0

**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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**License** Artistic-2.0

**Depends** R (>= 3.3), minfi (>= 1.21.2),  
IlluminaHumanMethylationEPICmanifest,  
IlluminaHumanMethylationEPICanno.ilm10b2.hg19

**LazyData** yes

**biocViews** Homo\_sapiens\_Data, MethylationArrayData, MicroarrayData

**NeedsCompilation** no

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MsetEPIC

*An example dataset for Illumina's Human Methylation EPIC dataset, after preprocessing.*

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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)
```

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RGsetEPIC

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

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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.

### 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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