

# Package ‘minfiDataEPIC’

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**Version** 1.30.0

**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

**git\_url** <https://git.bioconductor.org/packages/minfiDataEPIC>

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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)
```

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RGsetEPIC	<i>An example dataset for the Illumina's Human Methylation EPIC platform.</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.

**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 comparion preprocessed data.

**Examples**

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

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