

Package: minfiDataEPIC (via r-universe)

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Version 1.38.0

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 (>= 1.21.2),
IlluminaHumanMethylationEPICmanifest,
IlluminaHumanMethylationEPICanno.ilm10b2.hg19

LazyData yes

biocViews Homo_sapiens_Data, MethylationArrayData, MicroarrayData

NeedsCompilation no

Config/pak/sysreqs make libbz2-dev libicu-dev liblzma-dev libpng-dev libxml2-dev libssl-dev libx11-dev xz-utils zlib1g-dev

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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	<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 comparison preprocessed data.

Examples

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

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