

# Package ‘MethylAidData’

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**Type** Package

**Title** MethylAid-summarized data for 2800 Illumina 450k array samples and 2620 EPIC array samples

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**Description** A data package containing summarized Illumina 450k array data on 2800 samples and summarized EPIC data for 2620 samples. The data can be use as a background data set in the interactive application.

**License** GPL (>= 2)

**VignetteBuilder** knitr

**biocViews** ExperimentData, TechnologyData, MicroarrayData, MethylationArrayData

**Depends** MethylAid, R (>= 3.2)

**Suggests** BiocParallel, BiocStyle, knitr, minfiData, minfiDataEPIC

**NeedsCompilation** no

**RoxygenNote** 6.0.1

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

**git\_branch** devel

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exampleDataLarge	<i>summarizedData object on 2800 450k Human Methylation samples</i>
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### Description

Summarized 450K data on 2800 samples. The data can be used as a background data set in the interactive application.

### Usage

```
exampleDataLarge
```

### Format

```
summarizedData-object
```

### Value

Pre-summarizedData object on 2800 450k Human Methylation samples.

### Examples

```
library(MethylAid)
data(exampleDataLarge)
data(exampleData)
## Not run: visualize(exampleData, background=exampleDataLarge)
library(minfiData)
baseDir <- system.file("extdata", package="minfiData")
targets <- read.metharray.sheet(baseDir)
data <- summarize(targets)
## Not run: visualize(data, background=exampleDataLarge)
```

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MethylAidDataEPIC      *summarizedData object for 2620 EPIC Human Methylation samples*

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**Description**

Summarized EPIC data for 2620 samples. The data can be use as a background data set in the interactive application.

**Usage**

```
MethylAidDataEPIC
```

**Format**

```
summarizedData-object
```

**Value**

Pre-summarizedData object for 2620 EPIC Human Methylation samples.

**Examples**

```
data(MethylAidDataEPIC)
library(minfiDataEPIC)
baseDir <- system.file("extdata", package="minfiDataEPIC")
targets <- read.metharray.sheet(baseDir)
data <- summarize(targets)
## Not run: visualize(data, background=MethylAidDataEPIC)
```

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