

Package ‘MethylAidData’

April 30, 2026

Type Package

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

Version 1.44.0

Date 2018-03-24

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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 RELEASE_3_23

git_last_commit ad0ba75

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-04-30

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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)
```

MethylAidDataEPIC *summarizedData object for 2620 EPIC Human Methylation samples*

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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* **datasets**

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