

# Package ‘MethylAidData’

May 5, 2026

**Type** Package

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

**Version** 1.45.0

**Date** 2018-03-24

**Author** Davy Cats, Tyler J. Gorrie-Stone, Bastiaan T. Heijmans, John  
W. Holloway, BIOS Consortium, Maarten van Iterson, Faisal I. Rezwam,  
Leonard Schalkwyk

**Maintainer** M. van Iterson <[mviterson@gmail.com](mailto:mviterson@gmail.com)>

**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

**git\_last\_commit** bd179ce

**git\_last\_commit\_date** 2026-04-28

**Repository** Bioconductor 3.24

**Date/Publication** 2026-05-05

## Contents

exampleDataLarge . . . . .	2
MethylAidDataEPIC . . . . .	2

<b>Index</b>	<b>4</b>
--------------	----------

---

exampleDataLarge      *summarizedData object on 2800 450k Human Methylation samples*

---

**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 used 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)
```

# Index

## \* datasets

exampleDataLarge, [2](#)

MethylAidDataEPIC, [2](#)

exampleDataLarge, [2](#)

MethylAidDataEPIC, [2](#)