

# Package ‘CLLmethylation’

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**Title** Methylation data of primary CLL samples in PACE project

**Version** 1.26.0

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**Description** The package includes DNA methylation data for the primary Chronic Lymphocytic Leukemia samples included in the Primary Blood Cancer Encyclopedia (PACE) project. Raw data from the 450k DNA methylation arrays is stored in the European Genome-Phenome Archive (EGA) under accession number EGAS0000100174. For more information concerning the project please refer to the paper “Drug-perturbation-based stratification of blood cancer” by Dietrich S, Oles M, Lu J et al., J. Clin. Invest. (2018) and R/Bioconductor package BloodCancerMultiOmics2017.

**Depends** R (>= 3.5.0)

**Encoding** UTF-8

**VignetteBuilder** knitr

**Imports** SummarizedExperiment, ExperimentHub

**Suggests** BiocStyle, ggplot2, knitr, rmarkdown

**License** LGPL

**biocViews** ExperimentData, DiseaseModel, CancerData, LeukemiaCancerData

**LazyData** true

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

**git\_branch** RELEASE\_3\_20

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meth

*DNA methylation data*

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### **Description**

The data was produced with the use of either 450k or 850k methylation arrays. Preprocessing of raw IDAT files was made using minfi R/Bioconductor package version 1.19.16. Intensities were normalized using the functional normalization algorithm. CpG sites containing SNPs inside the probe body were removed. Data is a subset of CpG sites present in 450k methylation arrays.

### **Format**

"[RangedSummarizedExperiment](#)" object with Features 435155 and Samples 196.

### **Author(s)**

Andreas Mock, Malgorzata Oles

### **Examples**

```
library("SummarizedExperiment")
library("ExperimentHub")
eh = ExperimentHub()
meth = eh[["EH1071"]]
colData(meth)
assay(meth)[1:5,1:5]
head(rowData(meth))
```

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\* **datasets**

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