# Package 'methylclockData'

November 10, 2026

**Title** Data for methylclock package

**Description** Collection of 9 datasets, andrews and bakulski cord blood, blood gse35069, blood gse35069 chen, blood gse35069 complete, combined cord blood, cord bloo d gse68456, gervin and lyle cord blood, guintivano dlpfc and saliva gse48472". Data downloaded from [meffil](https://github.com/perishky/meffil/). Data used to estimate cell counts using Extrinsic epigenetic age acceleration (EEAA) method Collection of 12 datasets to use with MethylClock package to estimate chronological and gestational DNA methylationwith estimators to use wit different methylation clocks

**Version** 1.20.0

**BugReports** https://github.com/isglobal-brge/methylclockData/issues

**URL** https://github.com/isglobal-brge/methylclockData

**biocViews** SpecimenSource, ExperimentHub, Tissue, OrganismData, Homo_sapiens_Data

**Imports** ExperimentHubData, ExperimentHub, utils

**Suggests** knitr, BiocStyle, rmarkdown

**License** MIT + file LICENSE

**NeedsCompilation** no

**Encoding** UTF-8

**RoxygenNote** 7.1.2

**VignetteBuilder** knitr

**git_url** https://git.bioconductor.org/packages/methylclockData

**git_branch** RELEASE_3_23

**git_last_commit** c5eeb1b

**git_last_commit_date** 2026-04-28

**Repository** Bioconductor 3.23

**Date/Publication** 2026-11-10

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`get_coefBLUP` *coefBLUP*

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## Description

`get_coefBLUP` returns the Best Linear Unbiased Prediction (BLUP) clock coefficients

## Usage

```
get_coefBLUP()
```

## Value

coefBLUP dataset

## Examples

```
get_coefBLUP()
```

## get_coefBohlin *coefBohlin*

### Description

get_coefBohlin returns the Bohlin's clock coefficients

### Usage

```
get_coefBohlin()
```

### Value

coefBohlin dataset

### Examples

```
get_coefBohlin()
```

## get_coefEN *coefEN*

### Description

get_coefEN returns the Elastic Net (EN) clock coefficients

### Usage

```
get_coefEN()
```

### Value

coefEN dataset

### Examples

```
get_coefEN()
```

## get_coefEPIC *coefEPIC*

### Description

`get_coefEPIC` returns the EPIC clock coefficients

### Usage

```
get_coefEPIC()
```

### Value

coefEPIC dataset

### Examples

```
get_coefEPIC()
```

## get_coefHannum *coefHannum*

### Description

`get_coefHannum` returns the Hannum's clock coefficients

### Usage

```
get_coefHannum()
```

### Value

coefHannum dataset

### Examples

```
get_coefHannum()
```

## get_coefHorvath *coefHorvath*

### Description

get_coefHorvath returns the Hobarth's clock coefficients

### Usage

```
get_coefHorvath()
```

### Value

coefHorvath dataset

### Examples

```
get_coefHorvath()
```

## get_coefKnightGA *coefKnightGA*

### Description

get_coefKnightGA returns the Knight's clock coefficients

### Usage

```
get_coefKnightGA()
```

### Value

coefKnightGA dataset

### Examples

```
get_coefKnightGA()
```

## get_coefLeeGA *coefLeeGA*

### Description

get_coefLeeGA returns the Lee's Gestational Age clock coefficients

### Usage

```
get_coefLeeGA()
```

### Value

coefLeeGA dataset

### Examples

```
get_coefLeeGA()
```

## get_coefLevine *coefLevine*

### Description

get_coefLevine returns the Levine's clock coefficients

### Usage

```
get_coefLevine()
```

### Value

coefLevine dataset

### Examples

```
get_coefLevine()
```

## get_coefMayneGA *coefMayneGA*

### Description

get_coefMayneGA returns the Mayne's clock coefficients

### Usage

```
get_coefMayneGA()
```

### Value

coefMayneGA dataset

### Examples

```
get_coefMayneGA()
```

## get_coefPedBE *coefPedBE*

### Description

get_coefPedBE returns the PedBE's clock coefficients

### Usage

```
get_coefPedBE()
```

### Value

coefPedBE dataset

### Examples

```
get_coefPedBE()
```

## get_coefSkin *coefSkin*

### Description

get_coefSkin returns the Horvath's skin+blood clock coefficients

### Usage

```
get_coefSkin()
```

### Value

coefSkin dataset

### Examples

```
get_coefSkin()
```

## get_coefTL *coefTL*

### Description

get_coefTL returns the Telomere Length clock coefficients

### Usage

```
get_coefTL()
```

### Value

coefTL dataset

### Examples

```
get_coefTL()
```

## get_coefWu *Wu*

### Description

get_coefWu returns the Wu's clock coefficients

### Usage

```
get_coefWu()
```

### Value

Wu dataset

### Examples

```
get_coefWu()
```

## get_cpgs_bn *cpgs_bn*

### Description

get_cpgs_bn returns data to use Horvath's CpGs to train a Bayesian Neural Network (BNN)

### Usage

```
get_cpgs_bn()
```

### Value

cpgs_bn dataset

### Examples

```
get_cpgs_bn()
```

---

`get_MethylationDataExample` *MethylationDataExample55*

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## Description

`get_MethylationDataExample` MethylationDataExample55 for vignette

## Usage

```
get_MethylationDataExample()
```

## Value

MethylationDataExample55 dataset

## Examples

```
get_MethylationDataExample()
```

---

`get_probeAnnotation21kdatMethUsed` *probeAnnotation21kdatMethUsed*

---

## Description

`get_probeAnnotation21kdatMethUsed` returns probeAnnotation21kdatMethUsed

## Usage

```
get_probeAnnotation21kdatMethUsed()
```

## Value

probeAnnotation21kdatMethUsed dataset

## Examples

```
get_probeAnnotation21kdatMethUsed()
```

get_references *references*

## Description

The methylclockData package is a repository of a few public datasets that needs the *methylclock* package to estimate chronological and gestational DNA methylation (DNAm) age as well as biological age using different methylation clocks.

## Usage

```
get_references()
```

## Format

A list with different data frame.

`blood gse35069 complete` methylation profiles from Reinius 2012 for purified blood cell types. It includes CD4T, CD8T, Mono,

`blood gse35069` methylation profiles from Reinius 2012 for purified blood cell types. It includes CD4T,CD8T, Mono, Bcell, NK and Gran.

`blood gse35069 chen` methylation profiles from Chen 2017 blood cell types. It includes CD4T, CD8T, Mono, Bcell, NK, Neu and Eos.

`andrews and bakulski cord blood` Cord blood reference from Bakulski 2016. It includes Bcell, CD4T, CD8T, Gran, Mono, NK and nRBC.

`cord blood gse68456` Cord blood methylation profiles from De 2015. It includes CD4T, CD8T, Mono, Bcell, NK, Neu, Eos and RBC.

`gervin and lyle cord blood` Cord blood reference generated by Kristina Gervin and Robert Lyle, available at 'miffil' package. It includes CD14, Bcell, CD4T, CD8T, NK, Gran.

`saliva gse48472` Reference generated from the multi-tissue pannel from Slieker 2013. It includes Buccal, CD4T, CD8T, Mono, Bcell, NK, Gran.

## Details

`get_references` returns the file with references data

## Value

references dataset

## Examples

```
get_references()
```

`get_TestDataset` *TestDataset*

## Description

`get_TestDataset` returns TestDataset

## Usage

```
get_TestDataset()
```

## Value

TestDataset dataset

## Examples

```
get_TestDataset()
```

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