

# Package ‘methylockData’

October 18, 2022

**Title** Data for methylock package

**Description** Collection of 9 datasets, andrews and bakulski cord blood, blood gse35069, blood gse35069 chen, blood gse35069 complete, combined cord blood, cord blood gse68456, gervin and lyle cord blood, quintivano dlpc 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 methylation with estimators to use with different methylation clocks

**Version** 1.4.0

**BugReports** <https://github.com/isglobal-brge/methylockData/issues>

**URL** <https://github.com/isglobal-brge/methylockData>

**biocViews** SpecimenSource, ExperimentHub, Tissue, OrganismData, Homo\_sapiens\_Data

**Imports** ExperimentHubData, ExperimentHub, utils

**Suggests** knitr, rmarkdown

**License** MIT + file LICENSE

**NeedsCompilation** no

**Encoding** UTF-8

**RoxygenNote** 7.1.2

**VignetteBuilder** knitr

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

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get_coefBLUP	<i>coefBLUP</i>
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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()
```

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<code>get_coefBohlin</code>	<i>coefBohlin</i>
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**Description**

`get_coefBohlin` returns the Bohlin's clock coefficients

**Usage**

`get_coefBohlin()`

**Value**

`coefBohlin` dataset

**Examples**

`get_coefBohlin()`

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<code>get_coefEN</code>	<i>coefEN</i>
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**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()
```

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<code>get_coefMayneGA</code>	<i>coefMayneGA</i>
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**Description**

`get_coefMayneGA` returns the Mayne's clock coefficients

**Usage**

`get_coefMayneGA()`

**Value**

`coefMayneGA` dataset

**Examples**

`get_coefMayneGA()`

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<code>get_coefPedBE</code>	<i>coefPedBE</i>
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**Description**

`get_coefPedBE` returns the PedBE's clock coefficients

**Usage**

`get_coefPedBE()`

**Value**

`coefPedBE` dataset

**Examples**

`get_coefPedBE()`

---

get_coefSkin	<i>coefSkin</i>
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**Description**

get\_coefSkin returns the Horvath's skin+blood clock coefficients

**Usage**

```
get_coefSkin()
```

**Value**

coefSkin dataset

**Examples**

```
get_coefSkin()
```

---

get_coefTL	<i>coefTL</i>
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---

**Description**

get\_coefTL returns the Telomere Length clock coefficients

**Usage**

```
get_coefTL()
```

**Value**

coefTL dataset

**Examples**

```
get_coefTL()
```



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get_coefWu	<i>Wu</i>
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**Description**

get\_coefWu returns the Wu's clock coefficients

**Usage**

get\_coefWu()

**Value**

Wu dataset

**Examples**

get\_coefWu()

---

get_cpgs_bn	<i>cpgs_bn</i>
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**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*

---

**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
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---

## 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	<i>TestDataset</i>
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**Description**

get\_TestDataset returns TestDataset

**Usage**

```
get_TestDataset()
```

**Value**

TestDataset dataset

**Examples**

```
get_TestDataset()
```

---

references.rda	<i>'references' data</i>
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---

**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**

```
data("references")
```

**Format**

A list with different data frame.

blood gse35069 complete methylation profiles from @reinius2012differential for purified blood cell types. It includes CD4T, CD8T, Mono,

blood gse35069 methylation profiles from @reinius2012differential for purified blood cell types. It includes CD4T,CD8T, Mono, Bcell, NK and Gran.

blood gse35069 chen methylation profiles from @chen2017epigenome blood cell types. It includes CD4T, CD8T, Mono, Bcell, NK, Neu and Eos.

andrews and bakulski cord blood Cord blood reference from @bakulski2016dna. It includes Bcell, CD4T, CD8T, Gran, Mono, NK and nRBC.

cord blood gse68456 Cord blood methylation profiles from @de2015nucleated. 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 @sliker2013identification. It includes Buccal, CD4T, CD8T, Mono, Bcell, NK, Gran.

### Examples

```
data(references)
## maybe str(references) ; plot(references) ...
```

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