

# Package ‘blimaTestingData’

February 14, 2019

**Type** Package

**Title** Data for testing of the package blima.

**Version** 1.2.0

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**Description** Experiment data package. The set were prepared using microarray images of human mesenchymal cells treated with various supplements. This package is intended to provide example data to test functionality provided by blima.

**License** GPL-3

**Depends** R(>= 3.0.0)

## Imports

**Suggests** blima, beadarray, illuminaHumanv4.db, BiocStyle

**URL** <https://bitbucket.org/kulvait/blima>

**biocViews** MicroarrayData, ExperimentData, GEO

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

**git\_branch** RELEASE\_3\_8

**git\_last\_commit** fe3ee6a

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`blimatesting`*blimatesting object for testing purposes of blima package*

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**Description**

This object is derived from the dataset of experiment on human mesenchymal cells. Experiment was performed using two Illumina arrays HumanHT-12 v4 Expression BeadChip Kit with total 24 array spots. For the testing purposes only 9 conditions were selected to be included to this object due to space reasons. We name the arrays used for downstream analysis A1,A2, A3, A4 for condition A (Group A) (cells grown in alfa-MEM medium with 10% fetal bovine serum) and E1, E2, E3, E4 for condition E (Group E) (cells grown in CellGro medium, with human serum and supplements FGF-2, EGF, M-CSF and insulin). In the set there is also included array labeled D4 for condition D(cells grown in CellGro medium, with human serum and supplements PDGF-BB, EGF, M-CSF and insulin).

These data has been deposited to NCBI Gene Expression Omnibus site as [GSE56129](#).

**Usage**

```
data(blimatesting)
```

**Author(s)**

Vojtech Kulvait

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