

# Package ‘lumiBarnes’

July 2, 2024

**Type** Package

**Title** Barnes Benchmark Illumina Tissues Titration Data

**Version** 1.44.0

**Date** 2010-10-12

**Author** Pan Du

**Maintainer** Pan Du <dupan@northwestern.edu>

**Description** The Barnes benchmark dataset can be used to evaluate the algorithms for Illumina microarrays. It measured a titration series of two human tissues, blood and placenta, and includes six samples with the titration ratio of blood and placenta as 100:0, 95:5, 75:25, 50:50, 25:75 and 0:100. The samples were hybridized on Human-Ref-8 BeadChip (Illumina, Inc) in duplicate. The data is loaded as an LumiBatch Object (see documents in the lumi package).

**License** LGPL

**Depends** R (>= 2.0), Biobase (>= 2.5.5), lumi (>= 1.1.0)

**biocViews** ExperimentData, Tissue, MicroarrayData, ChipOnChipData

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

**git\_branch** RELEASE\_3\_19

**git\_last\_commit** 267696c

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.19

**Date/Publication** 2024-07-02

## Contents

lumiBarnes . . . . .	2
<b>Index</b>	<b>3</b>

---

`lumiBarnes`*Barnes Benchmark Illumina Tissues Titration Data*

---

**Description**

The Barnes data set measured a titration series of two human tissues, blood and placenta. It includes six samples with the titration ratio of blood and placenta as 100:0, 95:5, 75:25, 50:50, 25:75 and 0:100. The samples were hybridized on HumanRef-8 BeadChip (Illumina, Inc) in duplicate. See (Barnes, et al., 2005) for details. The data is saved as a LumiBatch object and should be use together with lumi package.

Because the Barnes data utilized the pre-released version of HumanRef-8 version 1 BeadChip, some probes on the chip do not exist in the public released HumanRef-8 version 1 BeadChip. For annotation consistence, these probes was removed in the lumiBarnes package. For the interested users, the raw data can be downloaded from the paper companion website: <http://www.bioinformatics.ubc.ca/pavlidis/lab/platformCom>

**Usage**

```
data(lumiBarnes)
```

**Format**

lumiBarnes is a [LumiBatch-class](#) object.

**Source**

Barnes, M., Freudenberg, J., Thompson, S., Aronow, B. and Pavlidis, P. (2005) Ex-perimental comparison and cross-validation of the Affymetrix and Illumina gene expression analysis platforms, Nucleic Acids Res, 33, 5914-5923.

**Examples**

```
data(lumiBarnes)
lumiBarnes
```

# Index

\* **datasets**

lumiBarnes, [2](#)

lumiBarnes, [2](#)