

# Package ‘affydata’

June 4, 2026

**Version** 1.61.0

**Date** 2011-10

**Title** Affymetrix Data for Demonstration Purpose

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**URL** <https://bioconductor.org/packages/affydata>

**BugReports** <https://github.com/rafalab/affydata/issues>

**Depends** R (>= 2.4.0), affy (>= 1.23.4)

**Imports** methods

**Suggests** hgu95av2cdf, hgu133acdf

**Description** Example datasets of a slightly large size. They represent 'real world examples', unlike the artificial examples included in the package affy.

**License** GPL (>= 2)

**biocViews** ExperimentData, Tissue, MicroarrayData, TissueMicroarrayData

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

**git\_branch** devel

**git\_last\_commit** d3df454

**git\_last\_commit\_date** 2026-04-28

**Repository** Bioconductor 3.24

**Date/Publication** 2026-06-04

## Contents

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

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Dilution	<i>AffyBatch instance Dilution</i>
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**Description**

This [AffyBatch-class](#) object represents part of a dilution experiment dataset.

**Usage**

```
data(Dilution)
```

**Format**

An [AffyBatch-class](#) object containing 4 arrays.

**Source**

Two sources of cRNA A (human liver tissue) and B (Central Nervous System cell line) have been hybridized to human array (HGU95A) in a range of proportions and dilutions. This data set is taken from arrays hybridized to source A at 10.0 and 20  $\mu$ g. We have two replicate arrays for each generated cRNA. Three scanners have been used in this study. Each array replicate was processed in a different scanner.

For more information see Gautier et al., *affy - Analysis of Affymetrix GeneChip data at the probe level* <http://bioinformatics.oxfordjournals.org/content/20/3/307.full.pdf> *Bioinformatics*, 2004

# Index

\* **datasets**

Dilution, [2](#)

Dilution, [2](#)