

# Package ‘bronchialIL13’

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**Version** 1.28.0

**Title** time course experiment involving il13

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**Depends** R(>= 2.10.0), affy (>= 1.23.4)

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**Description** derived from CNMC (pepr.cnmcresearch.org)  
[http://pepr.cnmcresearch.org/browse.do?action=list\\_prj\\_exp&projectId=95](http://pepr.cnmcresearch.org/browse.do?action=list_prj_exp&projectId=95)  
Human Bronchial Cell line A549

**License** GPL-2

**biocViews** ExperimentData, MicroarrayData

**URL** <http://www.biostat.harvard.edu/~carey>

**git\_url** <https://git.bioconductor.org/packages/bronchialIL13>

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## R topics documented:

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HAHrma	<i>data on Affymetrix U133a chips regarding time course response of human bronchial cell line A549 to IL13</i>
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## Description

data on Affymetrix U133a chips regarding time course response of human bronchial cell line A549 to IL13

## Usage

```
data(HAHrma)  
data(HAH)
```

**Format**

The format is a Biobase `exprSet` structure. `phenoData` variables are `id`, `trt` and `time` (hours). HAH is derived from a `ReadAffy` of 15 CEL files, and HAHrma is derived from `rma(HAH)`, with manual construction of the `phenoData` based on the filenames. The CEL files are in `inst/cel/dataoq.zip`.

**Source**

[http://pepr.cnmcresearch.org/browse.do?action=list\\_prj\\_exp&projectId=95](http://pepr.cnmcresearch.org/browse.do?action=list_prj_exp&projectId=95)

**Examples**

```
data(HAHrma)
table(HAHrma$time, HAHrma$trt)
```

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**\* data**

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