

# Package ‘bronchialIL13’

April 16, 2024

**Version** 1.40.0

**Title** time course experiment involving il13

**Author** Vince Carey <stvjc@channing.harvard.edu>

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

**Maintainer** Vince Carey <stvjc@channing.harvard.edu>

**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>

**git\_branch** RELEASE\_3\_18

**git\_last\_commit** 7499106

**git\_last\_commit\_date** 2023-10-24

**Repository** Bioconductor 3.18

**Date/Publication** 2024-04-16

## R topics documented:

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

---

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

---

**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)
```

# Index

\* **data**

HAHrma, [2](#)

HAH (HAHrma), [2](#)

HAHrma, [2](#)