

# Package ‘bronchialIL13’

April 13, 2022

**Version** 1.32.0

**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\_14

**git\_last\_commit** 8c12d49

**git\_last\_commit\_date** 2021-10-26

**Date/Publication** 2022-04-13

## R topics documented:

HAHrma . . . . . 1

**Index** . . . . . 3

---

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

---

## 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$time, HAhrma$strt)
```

# Index

\* **data**

HAHrma, [1](#)

HAH (HAHrma), [1](#)

HAHrma, [1](#)