

Package ‘bronchialIL13’

September 4, 2025

Version 1.46.0

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
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_21

git_last_commit effb992

git_last_commit_date 2025-04-15

Repository Bioconductor 3.21

Date/Publication 2025-09-04

Contents

HAHrma	2
Index	3

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

Examples

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

Index

* **data**

HAHrma, [2](#)

HAH (HAHrma), [2](#)

HAHrma, [2](#)