

Package ‘bronchialIL13’

January 12, 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
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 2022-01-12

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

Examples

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

Index

* **data**

HAHrma, [1](#)

HAH (HAHrma), [1](#)

HAHrma, [1](#)