

Package ‘bronchialIL13’

April 14, 2020

Version 1.24.0

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_10

git_last_commit 5f7de2f

git_last_commit_date 2019-10-29

Date/Publication 2020-04-14

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

*Topic **data**

HAHrma, 1

HAH (HAHrma), 1

HAHrma, 1