

Package ‘bronchialIL13’

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Version 1.30.0

Title time course experiment involving il13

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Description derived from CNMC (pepr.cnmcresearch.org)
http://pepr.cnmcresearch.org/browse.do?action=list_prj_exp&projectId=95
Human Bronchial Cell line A549

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biocViews ExperimentData, MicroarrayData

URL <http://www.biostat.harvard.edu/~carey>

git_url <https://git.bioconductor.org/packages/bronchialIL13>

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R topics documented:

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

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* **data**

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