

# Package ‘scTHI.data’

May 14, 2024

**Type** Package

**Title** The package contains examples of single cell data used in vignettes and examples of the scTHI package; data contain both tumor cells and immune cells from public dataset of glioma

**Version** 1.16.0

**Description** Data for the vignette and tutorial of the package scTHI.

**License** GPL-2

**Depends** R (>= 4.0)

**Encoding** UTF-8

**LazyData** false

**RoxygenNote** 6.1.1.9000

**biocViews** ExperimentData, SingleCellData

**git\_url** <https://git.bioconductor.org/packages/scTHI.data>

**git\_branch** RELEASE\_3\_19

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**Repository** Bioconductor 3.19

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H3K27

*Example expression matrix for scTHI.*

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**Description**

A 21673 x 5527 matrix patient PatientBCH836 form Filbin, M. G., Tirosh, I., Hovestadt, V., Shaw, M. L., Escalante, L. E., Mathewson, N. D., ... & Haberler, C. (2018). Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. *Science*, 360(6386), 331-335. H3K27

**Usage**

H3K27

**Format**

An object of class `matrix` with 21673 rows and 527 columns.

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H3K27.meta*Annotation for the H3K27 e expression matrix for scTHI.*

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**Description**

A dataframe 527x9 for the matrix of patient PatientBCH836 form Filbin, M. G., Tirosh, I., Hovestadt, V., Shaw, M. L., Escalante, L. E., Mathewson, N. D., ... & Haberler, C. (2018). Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. *Science*, 360(6386), 331-335. H3K27.annotation

**Usage**

H3K27.meta

**Format**

An object of class `data.frame` with 527 rows and 9 columns.

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MGH45	<i>Example expression matrix for scTHI.</i>
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**Description**

A 17584 x 608 matrix patient PatientBCH836 form Venteicher AS, Tirosh I, Hebert C, Yizhak K et al. Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. Science 2017 Mar 31;355(6332) MGH45

**Usage**

MGH45

**Format**

An object of class `matrix` with 17584 rows and 608 columns.

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MGH45.annotation	<i>Annotation for Example expression matrix for scTHI.</i>
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**Description**

A 608 x 2 dataframe with the annotation for the MGH4 matrix Venteicher AS, Tirosh I, Hebert C, Yizhak K et al. Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. Science 2017 Mar 31;355(6332) MGH45.annotation

**Usage**

MGH45.annotation

**Format**

An object of class `data.frame` with 608 rows and 2 columns.

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`scExample`*Example expression matrix for scTHI.*

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**Description**

A 2000 x 100 matrix from the wiki manual to showcase the use of scTHI `scExample`

**Usage**

```
scExample
```

**Format**

An object of class `matrix` with 2000 rows and 100 columns.

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