

Package: clustifyrdatahub (via r-universe)

October 10, 2026

Title External data sets for clustifyr in ExperimentHub

Version 1.22.0

Description References made from external single-cell mRNA sequencing data sets, stored as average gene expression matrices. For use with clustifyr <<https://bioconductor.org/packages/clustifyr>> to assign cell type identities.

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URL <https://rnabioco.github.io/clustifyrdatahub/>

Depends R (>= 4.0), ExperimentHub

Imports utils

Suggests clustifyr, Seurat, usethis, rmarkdown, knitr, tidy,
BiocStyle

VignetteBuilder knitr

Encoding UTF-8

LazyData true

RoxygenNote 7.2.1

biocViews SingleCellData, SequencingData, MicroarrayData,
ExperimentHub, RNASeqData, PackageTypeData, ExpressionData

BugReports <https://github.com/rnabioco/clustifyrdatahub/issues>

Config/Needs/website pkgdown, rnabioco/rbitemplate

Config/pak/sysreqs libicu-dev libpng-dev libssl-dev zlib1g-dev

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RemoteUrl <https://github.com/bioc/clustifyrdatahub>

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ref_cortex_dev	<i>Matrix of average gene detection on cortex development cell types</i>
----------------	--

Description

47 distinct annotated clusters of human neuronal subtypes

Usage

ref_cortex_dev

Format

An object of class function of length 1.

Source

<<https://cells.ucsc.edu/?ds=cortex-dev#>>

See Also

Other ref: [ref_MCA\(\)](#), [ref_hema_microarray\(\)](#), [ref_immgen\(\)](#), [ref_moca_main\(\)](#), [ref_mouse.rnaseq\(\)](#), [ref_mouse_atlas\(\)](#), [ref_pan_indrop\(\)](#), [ref_pan_smartseq2\(\)](#), [ref_tabula_muris_drop\(\)](#), [ref_tabula_muris_facs\(\)](#)

Examples

ref_cortex_dev(metadata = TRUE)

ref_hema_microarray	<i>Matrix of average gene detection by microarray on sorted immune cell populations</i>
---------------------	---

Description

38 distinct purified populations of human hematopoietic cells

Usage

```
ref_hema_microarray
```

Format

An object of class function of length 1.

Source

[<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE24759>]

See Also

Other ref: [ref_MCA\(\)](#), [ref_cortex_dev\(\)](#), [ref_immgen\(\)](#), [ref_moca_main\(\)](#), [ref_mouse.rnaseq\(\)](#), [ref_mouse_atlas\(\)](#), [ref_pan_indrop\(\)](#), [ref_pan_smartseq2\(\)](#), [ref_tabula_muris_drop\(\)](#), [ref_tabula_muris_facs\(\)](#)

Examples

```
ref_hema_microarray(metadata = TRUE)
```

ref_immgen	<i>Matrix of average gene expression from immgen data</i>
------------	---

Description

253 mouse immune cell types

Usage

```
ref_immgen
```

Format

An object of class function of length 1.

Source

```
["SingleR"]
```

See Also

Other ref: [ref_MCA\(\)](#), [ref_cortex_dev\(\)](#), [ref_hema_microarray\(\)](#), [ref_moca_main\(\)](#), [ref_mouse.rnaseq\(\)](#), [ref_mouse_atlas\(\)](#), [ref_pan_indrop\(\)](#), [ref_pan_smartseq2\(\)](#), [ref_tabula_muris_drop\(\)](#), [ref_tabula_muris_facs\(\)](#)

Examples

```
ref_immgen(metadata = TRUE)
```

ref_MCA

Matrix of average gene expression for single-cell RNA-seq.

Description

from mouse cell atlas project

Usage

```
ref_MCA
```

Format

An object of class function of length 1.

Source

<<https://figshare.com/s/865e694ad06d5857db4b>>

See Also

Other ref: [ref_cortex_dev\(\)](#), [ref_hema_microarray\(\)](#), [ref_immgen\(\)](#), [ref_moca_main\(\)](#), [ref_mouse.rnaseq\(\)](#), [ref_mouse_atlas\(\)](#), [ref_pan_indrop\(\)](#), [ref_pan_smartseq2\(\)](#), [ref_tabula_muris_drop\(\)](#), [ref_tabula_muris_facs\(\)](#)

Examples

```
ref_MCA(metadata = TRUE)
```

ref_moca_main	<i>Matrix of average gene expression per cluster from single-cell sci-RNA-seq3 from Mouse Organogenesis Cell Atlas.</i>
---------------	---

Description

100,000 cells

Usage

```
ref_moca_main
```

Format

An object of class function of length 1.

Source

<<http://atlas.gs.washington.edu/mouse-rna/>>

See Also

Other ref: [ref_MCA\(\)](#), [ref_cortex_dev\(\)](#), [ref_hema_microarray\(\)](#), [ref_immgen\(\)](#), [ref_mouse.rnaseq\(\)](#), [ref_mouse_atlas\(\)](#), [ref_pan_indrop\(\)](#), [ref_pan_smartseq2\(\)](#), [ref_tabula_muris_drop\(\)](#), [ref_tabula_muris_facs\(\)](#)

Examples

```
ref_moca_main(metadata = TRUE)
```

ref_mouse.rnaseq	<i>Matrix of average gene expression from general mouse cell type data</i>
------------------	--

Description

28 general cell types

Usage

```
ref_mouse.rnaseq
```

Format

An object of class function of length 1.

Source

```
["SingleR"]
```

See Also

Other ref: [ref_MCA\(\)](#), [ref_cortex_dev\(\)](#), [ref_hema_microarray\(\)](#), [ref_immgen\(\)](#), [ref_moca_main\(\)](#), [ref_mouse_atlas\(\)](#), [ref_pan_indrop\(\)](#), [ref_pan_smartseq2\(\)](#), [ref_tabula_muris_drop\(\)](#), [ref_tabula_muris_facs\(\)](#)

Examples

```
ref_mouse.rnaseq(metadata = TRUE)
```

ref_mouse_atlas	<i>Atlas matrix of average gene expression aggregated from scRNA-seq data of mouse organisms</i>
-----------------	--

Description

Data aggregated from NCBI Gene Expression Omnibus

Usage

```
ref_mouse_atlas
```

Format

An object of class function of length 1.

Source

```
<https://github.com/rnabioco/scRNA-seq-Cell-Ref-Matrix/blob/master/atlas/musMusculus/MouseAtlas.rds>
```

See Also

Other ref: [ref_MCA\(\)](#), [ref_cortex_dev\(\)](#), [ref_hema_microarray\(\)](#), [ref_immgen\(\)](#), [ref_moca_main\(\)](#), [ref_mouse.rnaseq\(\)](#), [ref_pan_indrop\(\)](#), [ref_pan_smartseq2\(\)](#), [ref_tabula_muris_drop\(\)](#), [ref_tabula_muris_facs\(\)](#)

Examples

```
ref_mouse_atlas(metadata = TRUE)
```

ref_pan_indrop	<i>Matrix of average gene expression per cluster from single-cell RNA-seq pancreas data using indrop method.</i>
----------------	--

Description

A sample of 8569 pancreas cells

Usage

```
ref_pan_indrop
```

Format

An object of class function of length 1.

Source

<<https://hemberg-lab.github.io/scRNA.seq.datasets/human/pancreas/>>

See Also

Other ref: [ref_MCA\(\)](#), [ref_cortex_dev\(\)](#), [ref_hema_microarray\(\)](#), [ref_immgen\(\)](#), [ref_moca_main\(\)](#), [ref_mouse.rnaseq\(\)](#), [ref_mouse_atlas\(\)](#), [ref_pan_smartseq2\(\)](#), [ref_tabula_muris_drop\(\)](#), [ref_tabula_muris_facs\(\)](#)

Examples

```
ref_pan_indrop(metadata = TRUE)
```

ref_pan_smartseq2	<i>Matrix of average gene expression per cluster from single-cell RNA-seq pancreas data using smartseq2 method.</i>
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Description

A sample of 2209 pancreas cells

Usage

```
ref_pan_smartseq2
```

Format

An object of class function of length 1.

Source

<<https://hemberg-lab.github.io/scRNA.seq.datasets/human/pancreas/>>

See Also

Other ref: [ref_MCA\(\)](#), [ref_cortex_dev\(\)](#), [ref_hema_microarray\(\)](#), [ref_immgen\(\)](#), [ref_moca_main\(\)](#), [ref_mouse.rnaseq\(\)](#), [ref_mouse_atlas\(\)](#), [ref_pan_indrop\(\)](#), [ref_tabula_muris_drop\(\)](#), [ref_tabula_muris_facs\(\)](#)

Examples

```
ref_pan_smartseq2(metadata = TRUE)
```

ref_tabula_muris_drop *Matrix of average gene expression per cluster from single-cell RNA-seq from Tabula Muris (10x genomics).*

Description

422,803 droplet libraries, 55,656 of which passed a QC cutoff of 500 genes and 1000 UMI

Usage

```
ref_tabula_muris_drop
```

Format

An object of class function of length 1.

Source

<<https://tabula-muris.ds.czbiohub.org/>>

See Also

Other ref: [ref_MCA\(\)](#), [ref_cortex_dev\(\)](#), [ref_hema_microarray\(\)](#), [ref_immgen\(\)](#), [ref_moca_main\(\)](#), [ref_mouse.rnaseq\(\)](#), [ref_mouse_atlas\(\)](#), [ref_pan_indrop\(\)](#), [ref_pan_smartseq2\(\)](#), [ref_tabula_muris_facs\(\)](#)

Examples

```
ref_tabula_muris_drop(metadata = TRUE)
```

ref_tabula_muris_facs *Matrix of average gene expression per cluster from single-cell RNA-seq from Tabula Muris (SMART-Seq2).*

Description

53,760 cells from 20 tissues from 8 mice

Usage

```
ref_tabula_muris_facs
```

Format

An object of class function of length 1.

Source

<<https://tabula-muris.ds.czbiohub.org/>>

See Also

Other ref: [ref_MCA\(\)](#), [ref_cortex_dev\(\)](#), [ref_hema_microarray\(\)](#), [ref_immgen\(\)](#), [ref_moca_main\(\)](#), [ref_mouse.rnaseq\(\)](#), [ref_mouse_atlas\(\)](#), [ref_pan_indrop\(\)](#), [ref_pan_smartseq2\(\)](#), [ref_tabula_muris_drop\(\)](#)

Examples

```
ref_tabula_muris_facs(metadata = TRUE)
```

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