

# Package ‘scRNAseq’

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**Title** A Collection of Public Single-Cell RNA-Seq Datasets

**Version** 1.0.0

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**Description** Gene-level read counts of three public scRNA-seq datasets.  
See vignette for details.

**License** CC0

**NeedsCompilation** no

**Depends** R (>= 3.3), SummarizedExperiment

**Suggests** BiocStyle, knitr, rmarkdown

**VignetteBuilder** knitr

**Encoding** UTF-8

**biocViews** ExperimentData, ExpressionData, SequencingData, RNASeqData

## R topics documented:

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scRNAseq-package      *A Collection of Public Single-Cell RNA-Seq Datasets*

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## Description

Gene-level read counts of three public scRNA-seq datasets. See vignette for details.

**Details**

This package contains a collection of three publicly available single-cell RNA-seq datasets.

The dataset `fluidigm` contains 65 cells from Pollen et al. (2014), each sequenced at high and low coverage.

The dataset `th2` contains 96 T helper cells from Mahata et al. (2014).

The dataset `allen` contains 379 cells from the mouse visual cortex. This is a subset of the data published in Tasic et al. (2016).

See the package vignette for details on the pre-processing of the data.

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**References**

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