

Package ‘curatedAdipoRNA’

October 24, 2025

Type Package

Title A Curated RNA-Seq Dataset of MDI-induced Differentiated Adipocytes (3T3-L1)

Version 1.25.0

Year 2019

Description A curated dataset of RNA-Seq samples. The samples are MDI-induced pre-phagocytes (3T3-L1) at different time points/stage of differentiation. The package document the data collection, pre-processing and processing. In addition to the documentation, the package contains the scripts that was used to generated the data.

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URL <https://github.com/MahShaaban/curatedAdipoRNA>

BugReports <https://github.com/MahShaaban/curatedAdipoRNA/issues>

Encoding UTF-8

RoxygenNote 6.1.1

LazyData TRUE

Depends R (>= 3.6), SummarizedExperiment

Suggests knitr, rmarkdown, DESeq2, fastqcr, devtools, testthat, readr, dplyr, tidyr, ggplot2, S4Vectors

VignetteBuilder knitr

biocViews ExperimentData, GEO, RNASeqData, SequencingData

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

git_branch devel

git_last_commit 7977992

git_last_commit_date 2025-04-15

Repository Bioconductor 3.23

Date/Publication 2025-10-24

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adipo_counts	<i>Gene counts in differentiating adipocytes</i>
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Description

Gene counts in differentiating adipocytes

Usage

adipo_counts

Format

A RangedSummarizedExperiment object contains:

- assay** The gene counts matrix.
- colData** The phenotype data and quality control data of the samples.
- rowRanges** The feature data at gene level.
- metadata** The study level metadata which contains one object called studies. This is a data.frame of bibliography information of the studies from which the samples were collected.

Examples

```
# load the data object
data('adipo_counts')

# print the object
adipo_counts
```

curatedAdipoRNA	curatedAdipoRNA <i>package</i>
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Description

A Curated RNA-Seq Dataset of MDI-induced Differentiated Adipocytes (3T3-L1)

Details

A curated dataset of RNA-Seq samples. The samples are MDI-induced pre-phagocytes (3T3-L1) at different time points/stage of differentiation. The package document the data collection, pre-processing and processing. In addition to the documentation, the package contains the scripts that was used to generated the data. The datasets and the pipeline used to process it are documented in [adipo_counts](#) and the package vignette.

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* **datasets**

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