# Package 'curatedAdipoRNA'

**Type** Package

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

**Version** 1.15.0

**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.

**License** GPL-3

**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** master

**git_last_commit** e190740

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# R **topics documented:**

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  adipo_counts *Gene counts in differentiating adipocytes*

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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 *package* |
|---|---|

## 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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