# Package 'curatedAdipoRNA'

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Type Package

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

Version 1.23.0

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

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adipo\_counts

Gene counts in differentiating adipocytes

## 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 cura

# 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, preprocessing 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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