

Package ‘ObMiTi’

July 15, 2025

Type Package

Title Ob/ob Mice Data on Normal and High Fat Diet

Version 1.16.0

Year 2021

Description The package provide RNA-seq count for 2 strains of mus mus-clus; Wild type and Ob/Ob. Each strain was divided into two groups, and each group received either chow diet or high fat diet. RNA expression was measured after 20 weeks in 7 tissues.

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URL <https://github.com/OmarElAshkar/ObMiTi>

BugReports <https://github.com/OmarElAshkar/ObMiTi/issues>

Encoding UTF-8

RoxygenNote 7.1.1

Depends R (>= 4.1), SummarizedExperiment, ExperimentHub

Suggests knitr, rmarkdown, BiocManager, GenomicFeatures, S4Vectors, devtools, testthat

VignetteBuilder knitr

biocViews ExperimentHub, GEO, RNASeqData

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

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Description

Title: Ob/ob Mice Data on Normal and High Fat Diet The package provide RNA-seq count for 2 strains of mus musclus; Wild type and Ob/Ob. Each strain was divided into two groups, and each group received either chow diet or high fat diet. RNA expression was measured after 12 weeks in 7 tissues.

Details

The dataset can be accessed through the ExperimentHub as a RangedSummarizedExperiment object contains:

- assay** The read counts matrix.
- colData** The phenotype data of the samples
- rowRanges** The feature data and annotation of the peaks.
- metadata** extra details about the sample and associated phenotype studies. This is a data.frame of bibliography information of the studies from which the samples were collected for.

Examples

```
# load the data object
library(ExperimentHub)

# query package resources on ExperimentHub
eh <- ExperimentHub()
query(eh, "ObMiTi")

# load data from ExperimentHub
ob_counts <- query(eh, "ObMiTi")[[1]]

# print object
ob_counts
```

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