

# Package ‘ObMiTi’

January 2, 2025

**Type** Package

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

**Version** 1.15.0

**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 ei-  
ther chow diet or high fat diet. RNA expression was measured after 20 weeks in 7 tissues.

**License** GPL-3

**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>

**git\_branch** devel

**git\_last\_commit** 78f6179

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**Repository** Bioconductor 3.21

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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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