# Package ‘curatedAdipoChIP’

July 24, 2025

**Type** Package

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

**Version** 1.25.0

**Year** 2019

**Description** A curated dataset of publicly available ChIP-sequencing of transcription factors, chromatin remodelers and histone modifications in the 3T3-L1 pre-adipocyte cell line. The package document the data collection, pre-processing and processing of the data. 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/curatedAdipoChIP

**BugReports** https://github.com/MahShaaban/curatedAdipoChIP/issues

**Encoding** UTF-8

**RoxygenNote** 6.1.1

**Depends** R (>= 3.6), SummarizedExperiment, ExperimentHub

**Suggests** knitr, rmarkdown, GenomicFeatures, ChIPseeker, AnnotationDbi, S4Vectors, DESeq2, fastqcr, devtools, testthat, readr, dplyr, tidyr, ggplot2

**VignetteBuilder** knitr

**biocViews** ExperimentData, ExperimentHub, GEO, ChIPSeqData, SequencingData

**git_url** https://git.bioconductor.org/packages/curatedAdipoChIP

**git_branch** devel

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## `curatedAdipoChIP` `curatedAdipoChIP` *package*

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### Description

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

### Details

A curated dataset of publicly available ChIP-sequencing of transcription factors, chromatin remodelers and histone modifications in the 3T3-L1 pre-adipocyte cell line. The package document the data collection, pre-processing and processing of the data. In addition to the documentation, the package contains the scripts that was used to generated the data.

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

**assay** The read counts `matrix`.

**colData** The phenotype data and quality control data of the samples.

**rowRanges** The feature data and annotation of the peaks.

**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

```
## Not run:
# load the data object
library(ExperimentHub)

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

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

# print object
peak_counts

## End(Not run)
```

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