Package 'curatedAdipoChIP'

November 10, 2026

Type Package

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

Version 1.28.0

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 RELEASE_3_23

git_last_commit a2e8f9a

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-10

Author Mahmoud Ahmed [aut, cre] (ORCID: <https://orcid.org/0000-0002-4377-6541>)

Maintainer Mahmoud Ahmed <mahmoud.s.fahmy@students.kasralainy.edu.eg>

Contents

curatedAdipoChIP 2

Index **3**

`curatedAdipoChIP` `curatedAdipoChIP` *package*

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)
```

Index

curatedAdipoChIP, 2
curatedAdipoChIP-package
        *(*curatedAdipoChIP*)*, 2