Package 'curatedAdipoChIP'

May 16, 2024

Type Package

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

Version 1.21.0

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

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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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