Title  Human macrophage immune response
Version  1.20.0
Author  Michael Love
Maintainer  Michael Love <michaelisaiahlove@gmail.com>
Description  This package provides the output of running Salmon
on a set of 24 RNA-seq samples from Alasoo, et al. “Shared genetic
effects on chromatin and gene expression indicate a role for enhancer
For details on version numbers and how the samples were processed
see the package vignette.
biocViews  ExperimentData, SequencingData, RNASeqData
License  GPL (>= 2)
Depends  R (>= 3.5.0)
Suggests  knitr, markdown
VignetteBuilder  knitr
NeedsCompilation  no
git_url  https://git.bioconductor.org/packages/macrophage
git_branch  RELEASE_3_19
git_last_commit  95c66a8
git_last_commit_date  2024-04-30
Repository  Bioconductor 3.19
Date/Publication  2024-05-02

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**Description**

This package provides the output of running Salmon on a set of 24 RNA-seq samples from Alasoo, et al. (2018). For more details on the data and steps used to generate the quantification files, please refer to the package vignette.

**References**


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**gse**  
*Macrophage dataset - Salmon quantification*

**Description**

Estimated counts, abundance and effective length per gene for macrophage RNA-Seq experiment

**Usage**

`data("gse")`

**Format**

`RangedSummarizedExperiment`

**Details**

This package provides the output of running Salmon on a set of 24 RNA-seq samples from Alasoo, et al. (2018). For more details on the data and steps used to generate the quantification files, please refer to the package vignette. For the script used to build the gse object, see the gse_create.R script in the scripts directory.

**Source**

FASTQ files from ENA

**References**

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