

# Package ‘macrophage’

April 16, 2024

**Title** Human macrophage immune response

**Version** 1.18.0

**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 priming in immune response”, published in Nature Genetics, January 2018. 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\_18

**git\_last\_commit** 16aec9c

**git\_last\_commit\_date** 2023-10-24

**Repository** Bioconductor 3.18

**Date/Publication** 2024-04-16

## R topics documented:

macrophage-package . . . . .	2
gse . . . . .	2
<b>Index</b>	<b>3</b>

---

macrophage-package      *Salmon quantifications for human macrophage immune response*

---

### 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

Alasoo, et al. "Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response", Nature Genetics, January 2018 doi: 10.1038/s41588-018-0046-7.

---

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

Alasoo, et al. "Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response", Nature Genetics, January 2018 doi: 10.1038/s41588-018-0046-7.

# Index

\* **datasets**

gse, [2](#)

\* **package**

macrophage-package, [2](#)

gse, [2](#)

macrophage-package, [2](#)