

# Package ‘tissueTreg’

November 19, 2024

**Title** TWGBS and RNA-seq data from tissue T regulatory cells from mice

**Version** 1.27.0

**Author** Charles Imbusch [aut, cre],  
Michael Delacher [aut],  
Markus Feuerer [aut],  
Benedikt Brors [aut]

**Maintainer** Charles Imbusch <c.imbusch@dkfz.de>

**Description** The package provides ready to use epigenomes (obtained from TWGBS) and transcriptomes (RNA-seq) from various tissues as obtained in the study (Delacher and Imbusch 2017, PMID: 28783152).

Regulatory T cells (Treg cells) perform two distinct functions: they maintain self-tolerance, and they support organ homeostasis by differentiating into specialized tissue Treg cells. The underlying dataset characterises the epigenetic and transcriptomic modifications for specialized tissue Treg cells.

**Depends** R (>= 3.5)

**License** GPL (>= 2)

**Encoding** UTF-8

**LazyData** true

**Suggests** BiocStyle, knitr, rmarkdown, testthat, ExperimentHub, bsseq, SummarizedExperiment, ggplot2, reshape2

**VignetteBuilder** knitr

**biocViews** ExperimentData, Tissue, Mus\_musculus\_Data, SequencingData, RNASeqData

**URL** <https://github.com/cimbusch/tissueTreg>

**RoxygenNote** 6.0.1

**git\_url** <https://git.bioconductor.org/packages/tissueTreg>

**git\_branch** devel

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### Description

The package provides ready to use epigenomes (obtained from TWGBS) and transcriptomes (RNA-seq) from various tissues. Regulatory T cells (Treg cells) perform two distinct functions: they maintain self-tolerance, and they support organ homeostasis by differentiating into specialized tissue Treg cells. The underlying dataset characterises the epigenetic and transcriptomic modifications for specialized tissue Treg cells.

### Source

Delacher, M, Imbusch, CD, Weichenhan, D, Breiling, A, Hotz-Wagenblatt, A, Träger, U, Hofer, AC, Kägebein, D, Wang, Q, Frauhammer, F, Mallm, JP, Bauer, K, Herrmann, C, Lang, PA, Brors, B, Plass, C, Feuerer, M (2017). Genome-wide DNA-methylation landscape defines specialization of regulatory T cells in tissues. *Nat. Immunol.*, 18, 10:1160-1172.

### Examples

```
eh <- ExperimentHub::ExperimentHub()

# RNA-seq RPKM data:
se_rpkms <- eh[["EH1074"]]

# Whole genome bisulfite sequencing data as bsseq objects:
tregs_per_sample <- eh[["EH1072"]]
tregs_per_tissue <- eh[["EH1073"]]
```

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\* **datasets**

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