

# Package ‘bodymapRat’

December 12, 2024

**Title** Experimental dataset from the rat BodyMap project

**Version** 1.23.0

**Description** This package contains a SummarizedExperiment from the Yu et al. (2013) paper that performed the rat BodyMap across 11 organs and 4 developmental stages. Raw FASTQ files were downloaded and mapped using STAR. Data is available on ExperimentHub as a data package.

**Depends** R (>= 3.6.0), SummarizedExperiment, ExperimentHub

**Imports** utils

**Suggests** rmarkdown, knitr, BiocStyle, testthat

**biocViews** SequencingData, RNASeqData, ExpressionData, ExperimentData, ExperimentHub

**NeedsCompilation** no

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**VignetteBuilder** knitr

**RoxygenNote** 6.1.1

**Encoding** UTF-8

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

**git\_branch** devel

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**Repository** Bioconductor 3.21

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bodymapRat

*Experimental dataset from the rat BodyMap project*

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### Description

This package contains a SummarizedExperiment from the Yu et al. (2013) paper that performed the rat BodyMap across 11 organs and 4 developmental stages. Raw FASTQ files were downloaded and mapped using STAR. FlowSorted.DLPFC.450k data set from Bioconductor. The purpose is to create an example object for the man pages and vignette in this package.

The SummarizedExperiment object was created using the `/inst/scripts/make-data.Rmd` and is downloaded from ExperimentHub

### Format

A SummarizedExperiment object with 652 RNA-seq samples (columns).

### Examples

```
library(ExperimentHub)
bm_rat <- bodymapRat()
dim(bm_rat)
```

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