Package 'bodymapRat'

February 27, 2025

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

License CC BY 4.0

VignetteBuilder knitr

RoxygenNote 6.1.1

Encoding UTF-8

git_url https://git.bioconductor.org/packages/bodymapRat

git_branch devel

git_last_commit 3ddf493

git_last_commit_date 2024-10-29

Repository Bioconductor 3.21

Date/Publication 2025-02-27

Author Stephanie Hicks [aut, cre] (ORCID:
<https://orcid.org/0000-0002-7858-0231>),
Kwame Okrah [aut]

Maintainer Stephanie Hicks <shicks19@jhu.edu>

Contents

---

bodymapRat   *Experimental dataset from the rat BodyMap project*

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 down-
loaded from ExperimentHub

Format

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

Examples

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

Index