Package ‘TransOmicsData’

April 2, 2026

Title A collection of trans-omics datasets across various biological systems

Version 1.6.0

Date 2024-01-29

Description Contains a collection of trans-omics datasets generated using various sequencing technologies such as RNA-seq, Mass spectrometry and ChIP-seq.
Modalities include the bulk profiling of the phosphoproteome, proteome, transcriptome and epigenome.
Data reflects the timecourses of different developmental systems from the mouse or human.

Imports S4Vectors, utils

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BugReports https://support.bioconductor.org/t/TransOmicsData

URL https://github.com/PYangLab/TransOmicsData

VignetteBuilder knitr

Suggests BiocStyle, knitr, rmarkdown, RefManageR, sessioninfo, testthat, ExperimentHub

biocViews ExperimentHub, MassSpectrometryData, RNASeqData, ChIPSeqData, Tissue, SequencingData

Encoding UTF-8

LazyData false

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.1

Config/testthat/edition 3

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

git_branch RELEASE_3_22

git_last_commit 848dce3

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2026-04-02

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Contents

`listDatasets` *List all datasets*

Description

This lists the summary information for all available datasets in the **TransOmicsData** package.

Usage

```
listDatasets()
```

Details

This package contains datasets spanning various biological contexts such as in vitro embryonic and tissue-specific development in mouse and human extracted from different sequencing technologies.

Value

A DataFrame, containing the following fields

- `Title`, short name of this data.
- `Description`, description of the data.
- `Omics`, omic layers profiled in the data.
- `Species`, species of the data.
- `RDataPath`, the corresponding rds files in this package.

Author(s)

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Examples

```
listDatasets()
```

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