

# Package ‘TransOmicsData’

May 14, 2026

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

**Version** 1.9.0

**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

**License** GPL-3 + file LICENSE

**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** devel

**git\_last\_commit** 2bc8e51

**git\_last\_commit\_date** 2026-04-28

**Repository** Bioconductor 3.24

**Date/Publication** 2026-05-14

**Author** Carissa Chen [aut] (ORCID: <<https://orcid.org/0000-0003-2419-7840>>),  
Di Xiao [aut, cre] (ORCID: <<https://orcid.org/0000-0002-9225-7086>>),  
Pengyi Yang [aut] (ORCID: <<https://orcid.org/0000-0003-1098-3138>>)

**Maintainer** Di Xiao <d.xiao@sydney.edu.au>

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listDatasets	<i>List all datasets</i>
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### 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)

Carissa Chen

### Examples

```
listDatasets()
```

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