

# Package ‘TransOmicsData’

February 3, 2026

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

**Version** 1.7.0

**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

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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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