Package ‘TransOmicsData’

July 25, 2024

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

**Version**  1.0.1

**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**  RELEASE_3_19

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**Repository**  Bioconductor 3.19
listDatasets

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

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