

# Package ‘muSpaData’

February 10, 2026

**Version** 1.3.0

**Title** Multi-sample multi-group spatially resolved transcriptomic data

**Description** Data package containing a multi-sample multi-group spatial dataset in SpatialExperiment Bioconductor object format.

**URL** <https://github.com/peicai/muSpaData>

**BugReports** <https://github.com/peicai/muSpaData/issues>

**License** MIT + file LICENSE

**Depends** R (>= 4.5.0), ExperimentHub

**Suggests** SpatialExperiment, ggplot2, BiocStyle, knitr, rmarkdown, R.utils

**biocViews** ExperimentHub, ExperimentData, ExpressionData, SpatialData, SingleCellData

**VignetteBuilder** knitr

**RoxygenNote** 7.3.2

**Encoding** UTF-8

**NeedsCompilation** no

**git\_url** <https://git.bioconductor.org/packages/muSpaData>

**git\_branch** devel

**git\_last\_commit** cfc96e3

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.23

**Date/Publication** 2026-02-10

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|               |                              |
|---------------|------------------------------|
| Wei22_example | Wei22_example <i>dataset</i> |
|---------------|------------------------------|

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### Description

- A subset of the Wei22\_full dataset, focusing on fewer regeneration stages.
- It includes 2 (2 sections), 10 (2 sections), and 20 (2 sections) days post injury (DPI).
- The original data is deposited in the Spatial Transcript Omics DataBase (STOmics DB) under dataset id STDS0000056.

### Usage

```
Wei22_example(metadata = FALSE)
```

### Arguments

|          |                                                                                                                                                                       |
|----------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| metadata | A logical value indicating whether to return only the ExperimentHub meta-data, which describes the overall dataset, or to load the entire dataset. Defaults to FALSE. |
|----------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------|

### Details

**link to reference:** <https://www.science.org/doi/10.1126/science.abp9444>

**link to raw data:** <https://db.cngb.org/stomics/artista/download/>

### Value

an object of class SpatialExperiment.

### Author(s)

Peiying Cai <peiying.cai@uzh.ch>

### References

Wei et al. (2022). "Single-cell Stereo-seq reveals induced progenitor cells involved in axolotl brain regeneration", *Science*, **377**(6610).

### Examples

```
# load metadata only
Wei22_example(metadata = TRUE)

# load SpatialExperiment
Wei22_example(metadata = FALSE)
```

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Wei22\_full

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Wei22\_full dataset

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**Description**

- Single-cell Stereo-seq spatial transcriptomics data includes axolotl brain tissues collected from multiple sections across five regeneration stages (16 samples in total)
- The dataset contains 13890 features across 147432 cells, and preprocessing has been applied.
- The original data is deposited in the Spatial Transcript Omics DataBase (STOmics DB) under dataset id STDS0000056.

**Usage**

```
Wei22_full(metadata = FALSE)
```

**Arguments**

|          |                                                                                                                                                                       |
|----------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| metadata | A logical value indicating whether to return only the ExperimentHub meta-data, which describes the overall dataset, or to load the entire dataset. Defaults to FALSE. |
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**Details**

**link to reference:** <https://www.science.org/doi/10.1126/science.abp9444>

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**Value**

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**Author(s)**

Peiying Cai <peiying.cai@uzh.ch>

**References**

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**Examples**

```
# load metadata only
Wei22_full(metadata = TRUE)

# load SpatialExperiment
Wei22_full(metadata = FALSE)
```

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