

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

[spatiAlign](#)

RRID:SCR_024828

Type: Tool

Proper Citation

spatiAlign (RRID:SCR_024828)

Resource Information

URL: <https://github.com/STOmics/Spatialign.git>

Proper Citation: spatiAlign (RRID:SCR_024828)

Description: Software tool as unsupervised contrastive learning model that employs expression of all measured genes and spatial location of cells, to integrate multiple tissue sections. Enables joint downstream analysis of multiple datasets in low-dimensional embeddings and also in reconstructed full expression space. Used for integrative analysis of time-series brain sections, including spatial clustering, differential expression analysis, and particularly trajectory inference that requires corrected gene expression matrix.

Resource Type: data processing software, software application, data analysis software, software resource

Defining Citation: [DOI:10.1101/2023.08.08.552402](https://doi.org/10.1101/2023.08.08.552402)

Keywords: integrative analysis, time-series brain sections, multiple datasets, spatial clustering, differential expression analysis, trajectory inference,

Availability: Free, Available for download, Freely available

Resource Name: spatiAlign

Resource ID: SCR_024828

License: MIT License

Record Creation Time: 20240104T050329+0000

Record Last Update: 20260815T042906+0000

Ratings and Alerts

No rating or validation information has been found for spatiAlign.

No alerts have been found for spatiAlign.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Zhang C, et al. (2024) spatiAlign: an unsupervised contrastive learning model for data integration of spatially resolved transcriptomics. GigaScience, 13.