

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 7, 2026

[scimap](#)

RRID:SCR_024751

Type: Tool

Proper Citation

scimap (RRID:SCR_024751)

Resource Information

URL: <https://scimap.xyz>

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Description: Software toolkit for analyzing spatial molecular data. Underlying framework is generalizable to spatial datasets mapped to XY coordinates. Package uses anndata framework making it easy to integrate with other popular single-cell analysis toolkits. It includes preprocessing, phenotyping, visualization, clustering, spatial analysis and differential spatial testing. Python based implementation efficiently deals with large datasets of millions of cells.

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

Keywords: Python, spatial single cell analysis, spatial datasets, analyzing spatial molecular data,

Funding: NCI K99 CA256497

Availability: Free, Available for download, Freely available

Resource Name: scimap

Resource ID: SCR_024751

Alternate URLs: <https://github.com/labsyspharm/scimap>

Record Creation Time: 20231204T190629+0000

Record Last Update: 20260905T133440+0000

Ratings and Alerts

No rating or validation information has been found for scimap.

No alerts have been found for scimap.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Vallius T, et al. (2025) Spatial determinants of tumor cell dedifferentiation and plasticity in primary cutaneous melanoma. bioRxiv : the preprint server for biology.

Leivonen SK, et al. (2025) Characterization of cancer-associated fibroblasts and their spatial architecture reveals heterogeneity and survival associations in classic Hodgkin lymphoma. HemaSphere, 9(5), e70145.

Shi Y, et al. (2025) Mechanisms of tumor persistence in metastatic melanoma following successful immunotherapy. bioRxiv : the preprint server for biology.

Autio M, et al. (2025) Spatial Analysis of the Tumor Microenvironment in Diffuse Large B-cell Lymphoma Reveals Clinically Relevant Cell Interactions and Recurrent Cellular Neighborhoods. Cancer immunology research, 13(10), 1674.

Smith D, et al. (2025) Spatial and single cell mapping of castleman disease reveals key stromal cell types and cytokine pathways. Nature communications, 16(1), 6009.

Naei VY, et al. (2025) Spatial interaction mapping of PD-1/PD-L1 in head and neck cancer reveals the role of macrophage-tumour barriers associated with immunotherapy response. Journal of translational medicine, 23(1), 177.

Williams JB, et al. (2025) Regulatory T cells inhibit CD8+ TRM-like cells during the early stages of tumor immune escape. bioRxiv : the preprint server for biology.

Aung TN, et al. (2025) Spatial signatures for predicting immunotherapy outcomes using multi-omics in non-small cell lung cancer. Nature genetics, 57(10), 2482.

Nirmal AJ, et al. (2024) SCIMAP: A Python Toolkit for Integrated Spatial Analysis of Multiplexed Imaging Data. Journal of open source software, 9(97).

Donovan ML, et al. (2024) Protocol for high-plex, whole-slide imaging of human formalin-fixed paraffin-embedded tissue using PhenoCycler-Fusion. STAR protocols, 5(3), 103226.

Smith D, et al. (2024) Spatial and Single Cell Mapping of Castleman Disease Reveals Key Stromal Cell Types and Cytokine Pathways. bioRxiv : the preprint server for biology.

Sundaram S, et al. (2022) Deciphering the Immune Complexity in Esophageal Adenocarcinoma and Pre-Cancerous Lesions With Sequential Multiplex Immunohistochemistry and Sparse Subspace Clustering Approach. *Frontiers in immunology*, 13, 874255.

Park J, et al. (2022) Spatial omics technologies at multimodal and single cell/subcellular level. *Genome biology*, 23(1), 256.