

Resource Summary Report

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[scvi-tools](#)

RRID:SCR_026673

Type: Tool

Proper Citation

scvi-tools (RRID:SCR_026673)

Resource Information

URL: <https://scvi-tools.org/>

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Description: Software Python library for deep probabilistic analysis of single-cell and spatial omics data. Used for probabilistic modeling and analysis of single-cell omics data, built on top of PyTorch and AnnData.

Synonyms: single-cell variational inference tools

Resource Type: software toolkit, software library, software resource, software application, source code, data analysis software, data processing software

Defining Citation: [PMID:35132262](#)

Keywords: probabilistic analysis, single-cell omics data, spatial omics data,

Funding: NIGMS R35GM124916;
Chan-Zuckerberg Foundation ;
NHGRI T32HG000047

Availability: Free, Available for download, Freely available

Resource Name: scvi-tools

Resource ID: SCR_026673

Alternate URLs: <https://github.com/scverse/scvi-tools>

License: BSD-3-Clause

Record Creation Time: 20250328T060315+0000

Record Last Update: 20260808T190749+0000

Ratings and Alerts

No rating or validation information has been found for scvi-tools.

No alerts have been found for scvi-tools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 58 mentions in open access literature.

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

Sirc N, et al. (2026) Functionally Characterizing the Renal Cell Carcinoma Tumor-Immune Microenvironment via Patient-Derived Ex Vivo Models. Cancer research communications, 6(2), 402.

Anilkumar Sithara A, et al. (2026) Composition and Functional State of T and NK Cells in the Extramedullary Myeloma Tumor Microenvironment. Blood cancer discovery, 7(2), 250.

Rius Rigau A, et al. (2026) Deep phenotyping of skin tissue remodeling in patients with systemic sclerosis treated with CD19-CAR T cells. Nature communications, 17(1).

Jin X, et al. (2026) Construction of a SEMA3 family-based model to predict prognosis and molecular subtypes in pancreatic ductal adenocarcinoma. Discover oncology, 17(1).

Kim S, et al. (2026) Bazedoxifene reverses sexually dimorphic autistic-like abnormalities in biallelic MDGA1-mutant mice. EMBO molecular medicine, 18(4), 1358.

Su Z, et al. (2026) Topographic structure and function of locus coeruleus norepinephrine neurons. bioRxiv : the preprint server for biology.

Du Z, et al. (2026) SMART: spatial multi-omic aggregation using graph neural networks and metric learning. Nature communications, 17(1).

Feng JX, et al. (2026) Single-cell lineage tracing identifies hemogenic endothelial cells in the adult mouse bone marrow. eLife, 15.

Rebboah E, et al. (2026) Systematic cell-type resolved transcriptomes of 8 tissues in 8 lab and wild-derived mouse strains capture global and local expression variation. Cell genomics, 6(4), 101108.

Cheng Y, et al. (2026) Aligned cross-modal integration and regulatory heterogeneity characterization of single-cell multiomic data with deep contrastive learning. Genome medicine, 18(1), 10.

Wang H, et al. (2026) Peripheral monocyte ratio as a predictive biomarker for metastasis-directed therapy in prostate cancer: insights from an exploratory study. BMC cancer,

26(1).

Acemel RD, et al. (2026) Flexibility of cell fates and functions across sex determination systems revealed by comparative single-cell analyses. *bioRxiv : the preprint server for biology*.

Sparre AA, et al. (2026) Batch correction for large-scale mass spectrometry imaging experiments. *Bioinformatics (Oxford, England)*, 42(6).

Li M, et al. (2026) SpatialCOC: an integrative framework for spatial continuous mapping and cross-omics correction in spatial multi-omics data. *Nature communications*, 17(1).

Díaz-Campos MÁ, et al. (2026) Single-Cell Transcriptomic Profiling Reveals Immunometabolic Reprogramming and Cell-Cell Communication in the Tumor Microenvironment of Human Hepatocellular Carcinoma. *International journal of molecular sciences*, 27(12).

Thompson JM, et al. (2026) Nuclei isolation from rat and cow white adipose tissues for single-nucleus RNA sequencing; rat WAT remains a challenge. *Frontiers in physiology*, 17, 1741037.

Koladiya A, et al. (2026) CellFuse Enables Multimodal Integration of Single-Cell and Spatial Proteomics Data for Systems-Level Analysis in Cancer. *Cancer research*, 86(14), 3379.

Gao Y, et al. (2026) Conserved Cell Type Signatures Across the Brainstem and Spinal Cord in the Mouse Central Nervous System. *bioRxiv : the preprint server for biology*.

Chen Y, et al. (2025) UCS: A Unified Approach to Cell Segmentation for Subcellular Spatial Transcriptomics. *Small methods*, 9(5), e2400975.

Yu H, et al. (2025) PerturbNet predicts single-cell responses to unseen chemical and genetic perturbations. *Molecular systems biology*, 21(8), 960.