

Resource Summary Report

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SPATA2

RRID:SCR_026167

Type: Tool

Proper Citation

SPATA2 (RRID:SCR_026167)

Resource Information

URL: <https://themilolab.github.io/SPATA2/>

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Description: Software package provides framework of functions and shiny-applications to work with spatial expression data. Used for spatial transcriptomics analysis.

Resource Type: software toolkit, source code, software resource

Defining Citation: [DOI:10.1038/s41467-024-50904-x](https://doi.org/10.1038/s41467-024-50904-x)

Keywords: Spatial transcriptomics analysis, spatial expression data, spatial transcriptomics,

Funding: German Cancer Consortium ;
German Research Foundation ;
German Ministry of Education and Research ;
European Innovation Council ;
Joachim Herz Foundation

Availability: Free, Available for download, Freely available

Resource Name: SPATA2

Resource ID: SCR_026167

Alternate URLs: <https://github.com/theMILOlab/SPATA2>

License: GNU GPL

Record Creation Time: 20241211T053244+0000

Record Last Update: 20260815T042912+0000

Ratings and Alerts

No rating or validation information has been found for SPATA2.

No alerts have been found for SPATA2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 29 mentions in open access literature.

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

Feng C, et al. (2026) Spatial tumor evolution panorama of ovarian cancer. Cell reports. Medicine, 7(3), 102666.

Petitprez F, et al. (2026) Local Tumor Microenvironment Niches Correlate With Survival And Immunotherapy Response In Human Glioblastoma. bioRxiv : the preprint server for biology.

Gao F, et al. (2026) Spatial transcriptomics reveals the mechanistic role of lactate metabolism in the pancreatic ductal adenocarcinoma microenvironment. Frontiers in immunology, 17, 1743187.

Chanoch-Myers R, et al. (2026) A blueprint for local and distal invasion programs in glioblastoma. Nature communications, 17(1).

Heezen LG, et al. (2026) Unraveling the spatial landscape of dystrophinopathies: a transcriptomic approach to Becker and Duchenne muscular dystrophies. The Journal of pathology, 269(3), 363.

Maas SLN, et al. (2026) A microenvironment-determined risk continuum refines subtyping in meningioma and reveals determinants of machine learning-based tumor classification. Nature genetics, 58(2), 341.

Hou D, et al. (2025) Dual $\alpha\text{V}\beta 8$ Integrin and PD-1 Blockade Overcomes TGF β -Mediated B-Cell Suppression to Enhance Anti-Tumor Immunity. Neuro-oncology, 27(9), 2355.

Wu W, et al. (2025) Multi-Transcriptomic Analysis Reveals GSC-Driven MES-Like Differentiation via EMT in GBM Cell-Cell Communication. Biomedicines, 13(6).

Liu X, et al. (2025) Investigation of the cytotoxic effects and mechanisms of the SLC39A6-targeting ADC drug BRY812 in CRC. Scientific reports, 15(1), 18275.

Nejo T, et al. (2025) Glioma-neuronal circuit remodeling induces regional immunosuppression. Nature communications, 16(1), 4770.

Solel E, et al. (2025) Gasdermin E in glioblastoma -pyroptosis resistance and tumor-promoting functions. Cell death discovery, 11(1), 284.

Salviano-Silva A, et al. (2025) Extracellular Vesicles Carrying Tenascin-C are Clinical Biomarkers and Improve Tumor-Derived DNA Analysis in Glioblastoma Patients. *ACS nano*, 19(10), 9844.

Drexler R, et al. (2025) Serotonergic neuron-glioma interactions drive high-grade glioma pathophysiology. *bioRxiv* : the preprint server for biology.

Jimenez-Macias JL, et al. (2025) Modulation of blood-tumor barrier transcriptional programs improves intratumoral drug delivery and potentiates chemotherapy in GBM. *Science advances*, 11(9), eadr1481.

Deng Y, et al. (2025) Single-cell transcriptomic profiling reveals liver fibrosis in colorectal cancer liver metastasis. *Experimental & molecular medicine*, 57(11), 2517.

Bastola S, et al. (2025) Endothelial-secreted Endocan activates PDGFRA and regulates vascularity and spatial phenotype in glioblastoma. *Nature communications*, 16(1), 471.

Ritter M, et al. (2025) Spatially resolved transcriptomics and graph-based deep learning improve accuracy of routine CNS tumor diagnostics. *Nature cancer*, 6(2), 292.

Fagiani F, et al. (2025) Spatially-restricted inflammation-induced senescent-like glia in multiple sclerosis and patient-derived organoids. *Nature communications*, 16(1), 8477.

Yan K, et al. (2024) Spatial transcriptomics reveals prognosis-associated cellular heterogeneity in the papillary thyroid carcinoma microenvironment. *Clinical and translational medicine*, 14(3), e1594.

Yao J, et al. (2024) Integration of multi-omics data revealed the orphan CpG islands and enhancer-dominated cis-regulatory network in glioma. *iScience*, 27(10), 110946.