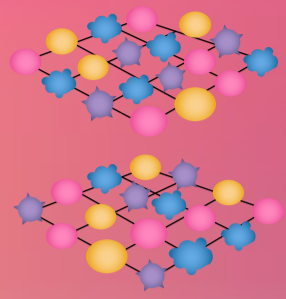


Publication Highlights for Multiomic Spatial Sequencing

Next-generation sequencing (NGS) based spatial analysis allows researchers to capture transcriptomic and proteomic information from cells within their native tissue environment, offering a multidimensional approach to understand gene expression and regulatory pathway mechanisms.

Spatial analysis



See spatial context of tissue architecture

Why choose an NGS-based approach to spatial analysis?

Study native cell-cell interactions

Powerful & integrated unbiased discovery tools

Gain more information about complex mechanisms

One platform, any omic

Review Paper

Williams, C.G. *et al.*

An introduction to spatial transcriptomics for biomedical research¹

Using RNA sequencing (RNA-Seq) technology powered by next-generation sequencing (NGS), spatial transcriptomics provides a comprehensive roadmap of transcriptional activity within intact tissue sections with high sensitivity. Regardless of the method, spatial transcriptomics allows you to accurately resolve mRNA expression at the cellular level in structurally preserved tissues.

Neurobiology

Ratz, M. *et al.*

Clonal relations in the mouse brain revealed by single-cell and spatial transcriptomics²

Mammalian brains have complex tissue architecture and relationships between various cells types are often not well understood. A combination of in vivo barcoding of early progenitors, single-cell and spatial transcriptomics can be used to demonstrate how complex cellular diversity develops in the brain using a significantly lower number of animal specimens.



Cancer Biology

Ben-Chetrit, N. *et al.*

Integration of whole transcriptome spatial profiling with protein markers³

Spatial transcriptomics and proteomics provide complementary information that independently transformed our understanding of complex biological processes. However, experimental integration of these modalities is limited. To overcome this, the authors developed Spatial Protein and Transcriptome Sequencing (SPOTS) for high-throughput simultaneous spatial transcriptomics and protein profiling. Compared with unimodal measurements, SPOTS substantially improves signal resolution and cell clustering and enhances the discovery power in differential gene expression analysis across tissue regions which is demonstrated using solid tumor models in this study.

Cardio: Heart Cell Atlas

Kazumasa, K. *et al.*

Spatially resolved multiomics of human cardiac niches⁴

Using an integrated multiomic approach, combining single-cell and spatial transcriptomic data, enabled unbiased discovery of cellular tissue microenvironment within novel cardiac niches to characterize cardiac structural microanatomy. Spatially-resolved transcriptomics provided information that is lost in single-cell analysis, across eight regions of the human heart, for additional insights into cell interactions, co-location and spatial organization. These data represent the largest, finely annotated healthy human heart cell providing a valuable resource to the research community.

- Williams, C.G. *et al.* An introduction to spatial transcriptomics for biomedical research. *Genome Med* 14, 68 (2022). <https://doi.org/10.1186/s13073-022-01075-1>
- Ratz, M. *et al.* Clonal relations in the mouse brain revealed by single-cell and spatial transcriptomics. *Nat Neurosci* 25, 285–294 (2022). <https://doi.org/10.1038/s41593-022-01011-x>
- Ben-Chetrit, N. *et al.* Integration of whole transcriptome spatial profiling with protein markers. *Nat Biotechnol* (2023). <https://doi.org/10.1038/s41587-022-01536-3>
- Kazumasa, K. *et al.* Spatially resolved multiomics of human cardiac niches. (2023). bioRxiv preprint doi: <https://doi.org/10.1101/2023.01.30.526202>