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3D spatial single cell omics by jetlet barcoding

Stanford researchers have developed a powerful new method for 3D spatial single-cell omics with cellular resolution using jetlet molecular barcoding.

Current spatial omics tools are limited to thin, 2D tissue slices and cannot achieve cellular resolution in three-dimensional samples. Imaging-based approaches target only a limited set of genes and are unable to capture full-transcriptome or multiomic data.

This platform overcomes those limitations by injecting unique spatial barcodes into intact cells across multiple tissue layers, enabling mapping of each cell's 3D position alongside its molecular profile. Arrays of high-precision fluidic injectors ("jetlets") deliver barcodes from multiple angles without disrupting cell integrity. The platform integrates seamlessly with single-cell sequencing workflows and supports untargeted transcriptomic, proteomic, or multiomic analyses. When paired with confocal microscopy, it also enhances cell boundary and morphology mapping.

This innovation enables deep 3D exploration of tissue architecture, cell–cell interactions, and disease mechanisms, advancing new applications in biomedical research, organoid modeling, drug discovery, and precision diagnostics.

Applications

- 3D spatial single-cell multiomics for complex tissues and organoids
- Whole-transcriptome or multiomic mapping in intact 3D samples
- Integration with standard single-cell sequencing platforms for spatial analysis

Advantages

- Enables true 3D spatial mapping at single-cell resolution
- Compatible with untargeted transcriptomic, proteomic, and multiomic analyses
- Outperforms microscopy-based methods (e.g., seqFISH, GeoMX) limited to small gene panels
- Preserves cell integrity and spatial structure during jetlet-based barcode delivery
- Links molecular profiles to precise cell locations for downstream analysis

Patents

- Published Application: [WO2025024701](WO2025024701)

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