Docket #: S24-450

SPatial Assay for Accessible chromatin, Cell lineages, and gene Expression with sequencing (SPACE-seq)

Stanford scientists have developed SPACE-seq, a novel technology that integrates spatial epigenomics and transcriptomics into a single platform. This approach addresses the challenge of analyzing complex tissues by providing a unified workflow that combines chromatin accessibility and gene expression analysis using commercially available systems.

SPACE-seq adapts ATAC-seq to generate polyA-tailed epigenomic libraries, allowing for the simultaneous investigation of multiple data modalities using standard spatial transcriptomics reagents. This simplifies spatial multiomics by eliminating the need for bespoke slides and capture chemistries, making it more accessible and efficient for researchers.

Stage of Development
Pre-clinical

Applications

- **Biomedical research:** studying tissue organization and disease mechanisms.
- **Clinical diagnostics:** understanding spatially organized somatic clones and disease progression.

Advantages

- Simplifies spatial multiomics.

- Facilitates unbiased and high-throughput analysis of complex tissues.
- Utilizes and is compatible with existing commercial systems, reducing the need for custom devices.

Publications

- Y. Huang, J.A. Belk, R. Zhang, N.E. Weiser, Z. Chiang, M.G. Jones, P.S. Mischel, J.D. Buenrostro, & H.Y. Chang (2025). "Unified molecular approach for spatial epigenome, transcriptome, and cell lineages." *Proc. Natl. Acad. Sci. U.S.A.* 122 (16) e2424070122.

Patents

- Published Application: WO2026136221

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