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Super-Resolution Three-Dimensional Spatial Biomolecule Identity And Abundance Assessment

Tech ID: 33760 / UC Case 2023-703-0

BRIEF DESCRIPTION

This technology offers a groundbreaking approach to map biomolecules in 3D space with subcellular resolution, revolutionizing our understanding of tissue organization and disease propagation.

FULL DESCRIPTION

Researchers at UCI have developed an innovative method for assessing biomolecule identity and abundance in tissue samples with unparalleled depth and high-resolution in three-dimensional space. It uniquely enables the spatial profiling of nucleic acids and proteins in whole-mount tissues, avoiding the limitations of tissue sectioning while achieving subcellular resolution. This facilitates a more accurate and comprehensive understanding of cellular organization, function, and interaction within tissues.

SUGGESTED USES

- » High-resolution 3D spatial profiling of biomolecules
- » Ability to analyze whole-mount tissues, increasing throughput and accuracy
- » Subcellular resolution enables precise cell differentiation
- » Multiomics capability allows for the examination of gene expression, phenotype, genotype, and epigenomics simultaneously
- » Facilitates understanding of spatial heterogeneity in tissues, crucial for organ function and disease development

ADVANTAGES

- » High-resolution 3D spatial profiling of biomolecules
- » Ability to analyze whole-mount tissues, increasing throughput and accuracy
- » Subcellular resolution enables precise cell differentiation
- » Multiomics capability allows for the examination of gene expression, phenotype, genotype, and epigenomics simultaneously
- » Facilitates understanding of spatial heterogeneity in tissues, crucial for organ function and disease development

PATENT STATUS

CONTACT

Ben Chu
ben.chu@uci.edu
tel: .



OTHER INFORMATION

CATEGORIZED AS

- » **Biotechnology**
 - » Genomics
 - » Proteomics
- » **Imaging**
 - » Molecular
- » **Medical**
 - » Diagnostics
 - » Research Tools
- » **Research Tools**
 - » Other

RELATED CASES

2023-703-0

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Additional Patent Pending

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5270 California Avenue / Irvine, CA
92697-7700 / Tel: 949.824.2683



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