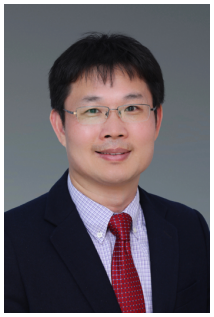
Chaoyong Yang, Professor



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2008- Present Professor, Xiamen University
2017-Present Professor, Institute of Molecular Medicine, Shanghai Jiao Tong University
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Research Interests:
Chemical Biology of Nucleic Acids, Microfluidics, Single Cell Biology, Spatial Multi-Omics

Selected Publications:

1. Li, K., Lu, X., Liao, J., Chen, H., Lin, W., Zhao, Y., Tang, D., Li, C., Tian, Z., Zhu, Z., Jiang, H., Sun, J., Zhang, H*., **Yang, C*.**, DNA-DISK: Automated end-to-end data storage via enzymatic single-nucleotide DNA synthesis and sequencing on digital microfluidics. ***Proc. Natl. Acad. Sci. U. S. A.*** **2024**, *121*, e2410164121.

2. Cao, J., Zheng, Z., Sun, D., Chen, X., Cheng, R., Lv, T., An, Y., Zheng, J*., Song, J*., Wu, L*., **Yang, C***. Dendrimeric DNA Coordinate Barcoding Design for Spatial RNA Sequencing. ***Nat. Biotechnol.*** **2024**, *doi.org/10.1038/s41587-023-02086-y*.

3. Lin, S., Yin, K., Zhang, Y., Lin, F., Chen, X., Zeng, X., Guo, X., Zhang, H., Song, J*., **Yang, C*.** Well-TEMP-seq as a microwell-based strategy for massively parallel profiling of temporal dynamics in single-cells. ***Nat. Commun.*** **2023**, *14*, 1272.

4. Guo, X., Lin, F., Yi, C., Song, J., Sun, D., Lin, L., Zhong, Z., Wu, Z., Wang, X., Zhang, Y., Li, J., Zhang, H*., Liu, F*., **Yang, C*.,** Song, J*., Deep transfer learning enables lesion tracing of circulating tumor cells. ***Nat. Commun***. **2022**, *13*, 7687.

5. Sun, M[#]., Liu, S[#]., Song, T., Chen, F., Zhang, J., Huang, J., Wan, S., Lu, Y., Chen, H*., Tan, W*., Song, Y*., **Yang, C***., Spherical Neutralizing Aptamer Inhibits SARS-CoV-2 Infection and Suppresses Mutational Escape. ***J. Am. Chem. Soc.*** **2021**, *143,* 21541-21548.

Decoder-FFPE-Seq Enables Sensitive Spatial Transcriptomic Analysis in Archival Tissues with Single Cell Resolution

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Abstract

Spatial transcriptomics serves as a powerful tool for dissecting spatial organization and molecular features of tumor microenvironment. However, current methods are largely limited to assaying polyA-tailed transcripts in fresh frozen samples with unsatisfactory sensitivity and resolution. Considering formalin-fixed and paraffinembedded (FFPE) tissues are the most common in clinical histopathology, we herein reported a blotting-assisted DNA coordinate barcoding design for spatial RNA sequencing of FFPE samples (Decoder-FFPE-Seq). Through targeted hybridization and ligation, fragmented or polyA tail degraded mRNA, and non-A-tailed RNAs, could be comprehensively transformed to DNA probes which contained PCR index, RNA definition sequence, and polyA tail, extending the scope of spatial transcriptomics to wider RNA species and sample types. By blotting ligased poly-A-tailed probes from tissue onto spatially barcoded substrates of 8 μm resolution with high-density polyT tail DNAs
, Decoder-FFPE-Seq achieved spatial profiling of transcripts and long non-coding RNA in FFPE tissues with single cell resolution, whose sensitivity is much higher than existing methods. Finally, Decoder-FFPE-Seq revealed heterogenous tumor microenvironment of archival oral squamous cell carcinoma samples from 12 patients of immunotherapy response and non-response. Decoder-FFPE-Seq is versatile and compatible to uncover various RNA types in archival sample with high sensitivity and resolution, which would accelerate discoveries in disease pathology and clinical translational research.