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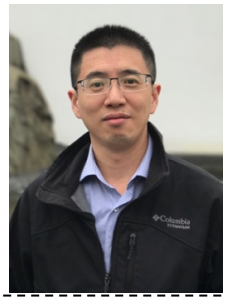

2006- Present	Professor, Peking University
2005-2006	Postdoctoral Scholar, Stanford University
2002-2005	Postdoctoral Scholar, Caltech
2002 ScD	Peking University
1997 BS	Peking University

Research Interests:
Sequencing, Microfluidics

Selected Publications:

1. Wenbo Sun, Tingyu Yang, Fengming Sun, Panhong Liu, Ji Gao, Xianmei Lan, Wei Xu, Yuhong Pang, Tong Li, Cuifeng Li, Qingtai Liang, Haoze Chen, Xiaohang Liu, Wenting Tan, Huanhuan Zhu, Fang Wang, Fanjun Cheng, Weiwei Zhai, Han-Na Kim, Jengren Zhang, Linqi Zhang, Lu Lu,* Qiaoran Xi,* Guohong Deng,* Yanyi Huang,* Xin Jin,* Xiangjun Chen,* Wanli Liu.* An IGHG1 variant exhibits polarized prevalence and confers enhanced IgG1 antibody responses against life-threatening organisms. ***Nature Immunology*** 2023, in press.
2. Tianyi Chang,# Wuji Han,# Mengcheng Jiang,# Jizhou Li,# Zhizhao Liao, Mingchuan Tang, Jianyun Zhang, Jie Shen, Zitian Chen, Peng Fei, Xianwen Ren, Yuhong Pang, Guanbo Wang, Jianbin Wang,* and **Yanyi Huang***. Rapid and Signal Crowdedness-Robust In-Situ Sequencing through Hybrid Block Coding. ***PNAS*** 2023, 120(47), e2309227120.
3. Yueying He, Yue Xue, Jingyao Wang, Yupeng Huang, Lu Liu, **Yanyi Huang**,* Yi Qin Gao*. Diffusion-enhanced characterization of 3D chromatin structure reveals its linkage to gene interactome. ***Genome Res.*** 2023, 33(8), 1354-1368.
4. Lu Liu,# He Chen,# Cheng Sun,# Jianyun Zhang,# Juncheng Wang, Meijie Du, Jie Li, Lin Di, Jie Shen, Shuang Geng, Yuhong Pang, Yingying Luo, Chen Wu, Yusi Fu,* Zhe Zheng,* Jianbin Wang,* **Yanyi Huang***. Low frequency somatic copy number alterations in normal human lymphocytes revealed by large scale single-cell whole genome profiling. ***Genome Res.*** 2022, 32, 44-54.
5. Ruoyan Li,# Lin Di,# Jie Li,# Wenyi Fan,# Yachen Liu, Wenjia Guo, Weiling Liu, Lu Liu, Qiong Li, Liping Chen, Yamei Chen, Chuanwang Miao, Hongjin Liu, Yuqian Wang, Yuling Ma, Deshu Xu, Dongxin Lin*, **Yanyi Huang***, Jianbin Wang*, Fan Bai*, Chen Wu*. A body map of somatic mutagenesis in morphologically normal human tissues. ***Nature*** 2021, 597 (7876), 398-403.

PRISM: Multiplexed Profiling of RNA In-Situ through Single-round of Imaging in Three-Dimensional Tissue

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Abstract

To resolve many RNA species in situ, cyclic reactions are typically necessary to increase the multiplexity since conventional fluorescence microscopy is often limited to five channels. Therefore, sophisticated instrumentation is needed to perform in-situ sequencing or sequential fluorescence insitu hybridization imaging, restricting the widespread adoption of spatial RNA imaging methods among biological research communities. Here, we present 'Profiling of RNA In-situ through Single-round of iMaging' (PRISM), which leverages the spectral intensity levels to expand the coding capacity. With a radius vector coding strategy to ensure the orthogonality of codewords, PRISM can reach up to 64-plex RNA imaging in a single imaging shot with conventional microscopes. As a panel-based spatial transcriptomic imaging approach, the entire experimental process can be completed within one day. We verified PRISM's versatility on various tissues, such as mouse brains, mouse embryos, and human hepatocellular carcinoma (HCC) samples, generating more than 5.7 million annotated cells. We performed quasi-3D spatial landscapes to track major cell types in different organs during embryonic development from E12.5 to E14.5. We also revealed the critical role of cancer-associated fibroblasts (CAFs) on immune infiltration and immune response heterogeneity within and between tumor microenvironments. We extended PRISM to 100-μm thick mouse brain slices to generate accurate 3D cell atlas and subcellular RNA localization landscapes. PRISM is robust and easy to operate, with a fast turnaround time and sub-cellular resolution, offering a new transcriptomic imaging toolbox for all biologists.