Rongxin Fang

Assistant Professor of Neurosurgery and, by courtesy, of Genetics

Bio

BIO

Rongxin Fang received his Ph.D. in Bioinformatics and Systems Biology from the University of California, San Diego, under the mentorship of Bing Ren (2015–2019). During his doctoral training, he developed high-throughput genomic technologies and computational tools to map the structure and activity of the mammalian genome at large scale and single-cell resolution. He then applied these approaches to investigate how cis-regulatory elements - such as enhancers - control gene expression and drive the diverse transcriptional programs underlying cellular diversity in the mammalian brain. As an HHMI–Damon Runyon Postdoctoral Fellow at Harvard University (2019–2024), he worked with Xiaowei Zhuang. Rongxin developed and applied genome-scale, volumetric 3D transcriptome imaging methods to map the molecular and cellular architecture of the mammalian brain across evolution and aging. He also contributed to the collaboration with Adam Cohen and Catherine Dulac to integrate transcriptome imaging with functional neuronal imaging, identifying neuronal populations in the animal brain that underlie specific brain functions.

ACADEMIC APPOINTMENTS

- Assistant Professor, Neurosurgery
- Assistant Professor (By courtesy), Genetics
- Member, Bio-X
- Member, Maternal & Child Health Research Institute (MCHRI)
- Faculty Fellow, Sarafan ChEM-H
- Member, Wu Tsai Neurosciences Institute

HONORS AND AWARDS

- Damon Runyon-Dale F. Frey Award for Breakthrough Scientists, Damon Runyon Cancer Research Foundation (2024)
- Next Generation Leader, Allen Institute (2024)
- Winning Image, Beauty of the Brain Contest, Harvard University (2023)
- Rising Star in Health in Engineering, Johns Hopkins & Columbia University (2022)
- HHMI-Damon Runyon Postdoc Fellowship, HHMI / Damon Runyon Cancer Research Foundation (2020)
- Keystone Symposia Future of Science Fund Scholarship, Keystone (2019)
- Best Paper of the Year Award, Ludwig Institute Cancer Research (2018)
- Best Poster Award, Research in Computational Molecular Biology (RECOMB) (2013)
- National Scholarship of China, Ministry of Education, China (2012)

PROFESSIONAL EDUCATION

- Postdoc, Harvard University , Spatial Genomics (2024)
- Ph.D., University of California San Diego , Bioinformatics & System Biology (2019)

PATENTS

- Xiaowei Zhuang, Rongxin Fang, Aaron Halpern. "United States Patent 63506283 Three-dimensional single cell transcriptome imaging of thick tissues", Harvard University, HHMI, Jul 6, 0173
- Bing Ren, Miao Yu, Rongxin Fang. "United States Patent 16330002 Genome-wide identification of chromatin interactions.", Ludwig Institute for Cancer Research, Mar 7, 0172

LINKS

- Fang Lab: https://fanglabstanford.org
- X: https://x.com/RongxinFang

Teaching

STANFORD ADVISEES

Postdoctoral Faculty Sponsor

Ya Jiang, Zhiyuan Sun

Doctoral Dissertation Advisor (AC)

Eduardo Chaparro Barriera

Publications

PUBLICATIONS

- **Three-dimensional single-cell transcriptome imaging of thick tissues.** *eLife*
  Fang, R., Halpern, A., Rahman, M. M., Huang, Z., Lei, Z., Hell, S. J., Dulac, C., Zhuang, X.
  2024; 12
- **Conservation and divergence of cortical cell organization in human and mouse revealed by MERFISH.** *Science (New York, N.Y.)*
  Fang, R., Xia, C., Close, J. L., Zhang, M., He, J., Huang, Z., Halpern, A. R., Long, B., Miller, J. A., Lein, E. S., Zhuang, X.
  2022; 377 (6601): 56-62
- **Comprehensive analysis of single cell ATAC-seq data with SnapATAC.** *Nature communications*
  Fang, R., Preissl, S., Li, Y., Hou, X., Lucero, J., Wang, X., Motamedi, A., Shiau, A. K., Zhou, X., Xie, F., Mukamel, E. A., Zhang, K., Zhang, et al
  2021; 12 (1): 1337
- **Single-nucleus analysis of accessible chromatin in developing mouse forebrain reveals cell-type-specific transcriptional regulation.** *Nature neuroscience*
  Preissl, S., Fang, R., Huang, H., Zhao, Y., Raviram, R., Gorkin, D. U., Zhang, Y., Sos, B. C., Afzal, V., Dickel, D. E., Kuan, S., Visel, A., Pennacchio, et al
  2018; 21 (3): 432-439
- **A tiling-deletion-based genetic screen for cis-regulatory element identification in mammalian cells.** *Nature methods*
  Diao, Y., Fang, R., Li, B., Meng, Z., Yu, J., Qiu, Y., Lin, K. C., Huang, H., Liu, T., Marina, R. J., Jung, I., Shen, Y., Guan, et al
  2017; 14 (6): 629-635
- **Mapping of long-range chromatin interactions by proximity ligation-assisted ChIP-seq.** *Cell research*
  Fang, R., Yu, M., Li, G., Chee, S., Liu, T., Schmitt, A. D., Ren, B.
  2016; 26 (12): 1345-1348
- **Integrative analysis of the 3D genome and epigenome in mouse embryonic tissues.** *Nature structural & molecular biology*
  Yu, M., Zemke, N. R., Chen, Z., Juric, I., Hu, R., Raviram, R., Abnousi, A., Fang, R., Zhang, Y., Gorkin, D. U., Li, Y. E., Zhao, Y., Lee, et al

2024

- **Integrated analysis of single-cell chromatin state and transcriptome identified common vulnerability despite glioblastoma heterogeneity.** *Proceedings of the National Academy of Sciences of the United States of America*

  Raviram, R., Raman, A., Preissl, S., Ning, J., Wu, S., Koga, T., Zhang, K., Brennan, C. W., Zhu, C., Luebeck, J., Van Deynze, K., Han, J. Y., Hou, et al

  2023; 120 (20): e2210991120

- **Single nucleus multi-omics identifies human cortical cell regulatory genome diversity.** *Cell genomics*

  Luo, C., Liu, H., Xie, F., Armand, E. J., Siletti, K., Bakken, T. E., Fang, R., Doyle, W. I., Stuart, T., Hodge, R. D., Hu, L., Wang, B. A., Zhang, et al

  2022; 2 (3)

- **A multimodal cell census and atlas of the mammalian primary motor cortex** *NATURE*

  Callaway, E. M., Dong, H., Ecker, J. R., Hawrylycz, M. J., Huang, Z., Lein, E. S., Ngai, J., Osten, P., Ren, B., Tolias, A., White, O., Zeng, H., Zhuang, et al

  2021; 598 (7879): 86-102

- **Comparative cellular analysis of motor cortex in human, marmoset and mouse.** *Nature*

  Bakken, T. E., Jorstad, N. L., Hu, Q., Lake, B. B., Tian, W., Kalmbach, B. E., Crow, M., Hodge, R. D., Krienen, F. M., Sorensen, S. A., Eggermont, J., Yao, Z., Aevermann, et al

  2021; 598 (7879): 111-119

- **An atlas of gene regulatory elements in adult mouse cerebrum.** *Nature*

  Li, Y. E., Preissl, S., Hou, X., Zhang, Z., Zhang, K., Qiu, Y., Poirion, O. B., Li, B., Chiou, J., Liu, H., Pinto-Duarte, A., Kubo, N., Yang, et al

  2021; 598 (7879): 129-136

- **A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex.** *Nature*

  Yao, Z., Liu, H., Xie, F., Fischer, S., Adkins, R. S., Aldridge, A. I., Ament, S. A., Bartlett, A., Behrens, M. M., Van den Berge, K., Bertagnolli, D., de Bézieux, H. R., Biancalani, et al

  2021; 598 (7879): 103-110

- **Single-cell chromatin accessibility identifies pancreatic islet cell type- and state-specific regulatory programs of diabetes risk.** *Nature genetics*

  Chiou, J., Zeng, C., Cheng, Z., Han, J. Y., Schlichting, M., Miller, M., Mendez, R., Huang, S., Wang, J., Sui, Y., Deogaygay, A., Okino, M. L., Qiu, et al

  2021; 53 (4): 455-466

- **Chromothripsis drives the evolution of gene amplification in cancer.** *Nature*

  Shoshani, O., Brunner, S. F., Yaeger, R., Ly, P., Nechemia-Arbely, Y., Kim, D. H., Fang, R., Castillon, G. A., Yu, M., Li, J. S., Sun, Y., Ellisman, M. H., Ren, et al

  2021; 591 (7848): 137-141

- **Spatiotemporal DNA methylome dynamics of the developing mouse fetus.** *Nature*

  He, Y., Hariharan, M., Gorkin, D. U., Dickel, D. E., Luo, C., Castanon, R. G., Nery, J. R., Lee, A. Y., Zhao, Y., Huang, H., Williams, B. A., Trout, D., Amrhein, et al

  2020; 583 (7818): 752-759

- **Joint profiling of DNA methylation and chromatin architecture in single cells.** *Nature methods*

  Li, G., Liu, Y., Zhang, Y., Kubo, N., Yu, M., Fang, R., Kellis, M., Ren, B.

  2019; 16 (10): 991-993

- **Transcriptionally active HERV-H retrotransposons demarcate topologically associating domains in human pluripotent stem cells.** *Nature genetics*

  Zhang, Y., Li, T., Preissl, S., Amaral, M. L., Grinstein, J. D., Farah, E. N., Destici, E., Qiu, Y., Hu, R., Lee, A. Y., Chee, S., Ma, K., Ye, et al

  2019; 51 (9): 1380-1388

- **MAPS: Model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP experiments.** *PLoS computational biology*

  Juric, I., Yu, M., Abnousi, A., Raviram, R., Fang, R., Zhao, Y., Zhang, Y., Qiu, Y., Yang, Y., Li, Y., Ren, B., Hu, M.

  2019; 15 (4): e1006982

- **Hyper-Editing of Cell-Cycle Regulatory and Tumor Suppressor RNA Promotes Malignant Progenitor Propagation.** *Cancer cell*

  Jiang, Q., Isquith, J., Zipeto, M. A., Diep, R. H., Pham, J., Delos Santos, N., Reynoso, E., Chau, J., Leu, H., Lazzari, E., Melese, E., Ma, W., Fang, et al

2019; 35 (1): 81-94.e7

- **Analysis of Genetically Diverse Macrophages Reveals Local and Domain-wide Mechanisms that Control Transcription Factor Binding and Function.** *Cell*

  Link, V. M., Duttke, S. H., Chun, H. B., Holtman, I. R., Westin, E., Hoeksema, M. A., Abe, Y., Skola, D., Romanoski, C. E., Tao, J., Fonseca, G. J., Troutman, T. D., Spann, et al

  2018; 173 (7): 1796-1809.e17