

# Dr. Yaqiang Cao *Curriculum Vitae*

National Heart, Lung, and Blood Institute/ NIH  
Bethesda, Maryland, U.S.A

[Google Scholar](#) | [GitHub](#)

[yaqiang.cao@nih.gov](mailto:yaqiang.cao@nih.gov) | [caoyaqiang0410@gmail.com](mailto:caoyaqiang0410@gmail.com) | Phone: (571)-267-0983

---

## **Education**

- **2019 Ph.D. in Computational Biology**, CAS-MPG Partner Institute for Computational Biology, University of Chinese Academy of Sciences, Shanghai, China
- **2012 B.S. in Bioengineering**, East China University of Science and Technology, Shanghai, China

## **Experience**

- **2024- Curr. Research Fellow**, NHLBI/NIH, with Dr. Keji Zhao
- **2019-2024 Visiting Fellow**, NHLBI/NIH, with Dr. Keji Zhao

## **Research Summary**

- **Focus:** Epigenome and 3D genome regulation in immunity, leukemia, and aging.
- **Methods:** Computational tools (cLoops2, vince) and experimental techniques (Hi-TrAC, iscMNase-seq) to map enhancer–promoter interactions and nucleosomes.
- **Discoveries:** Chromatin loops/histone modifications/transcription factors driving T-cell differentiation, leukemia, B-cell aging.
- **Collaborations:** Cross-disciplinary partnerships bridging basic science and clinical applications.
- **Impact:** Open, user-friendly software for reproducible epigenomic and 3D genomic research.

## **Manuscript under Review**

1. Tao Zhen \*, **Yaqiang Cao** \*, Tongyi Dou, Yun Chen, Guadalupe Lopez, Ana Catarina Menezes, Xufeng Wu, John A. Hammer, Jun Cheng, Lisa Garrett, Stacie Anderson, Martha Kirby, Stephen Wincovitch, Bayu Sisay, Abdel G. Elkahoul, Di Wu, Lucio Castilla, Wei Yang, Jiansen Jiang, Keji Zhao, Pu Paul Liu#: Enhancing RUNX1-DNA binding affinity is a critical step for leukemogenesis by CBF $\beta$ -SMMHC
2. Guangzhe Ge \*, **Yaqiang Cao** \*, Danping Wei \*, Mary Attaway, Barbara L Kee, Jinfang Zhu, and Keji Zhao #: Deciphering chromatin priming of T cell lineage by single-cell micrococcal nuclease sequencing

\* co-first author # correspondence.

## **First or Co-first Publications (13 out of 29 total publications)**

2024

Ma, F. \*, **Cao, Y. \***, Du, H., Braikia, F., Zong, L., Ollikainen, N., Bayer, M., Qiu, X., Park, B., Roy, R., Nandi, S., Sarantopoulou, D., Ziman, A., Bianchi, A., Beerman, I., Zhao, K., Grosschedl, R., Sen, R. #. (2024) Three-dimensional chromatin reorganization regulates B cell development during ageing. **Nat Cell Biol.** 1-12.

Liu, S. \*, **Cao, Y. \***, Cui, K\*, Ren, G., Zhao, T., Wang, X., Wei, D., Chen, Z., Gurram, R.K., Liu, C. and Wu, C., Zhu, J., & Zhao, K. # (2024) Regulation of T helper cell differentiation by the interplay between histone modification and chromatin interaction. **Immunity.** 57(5), 987-1004.

2023

**Cao, Y. \***, Liu, S. \*, Cui, K. \*, Tang, Q., & Zhao, K. # (2023). Hi-TrAC detects active sub-TADs and reveals internal organizations of super-enhancers. **Nucleic Acids Research,** 51(12), 6172-6189.

Cui, K. \*, Chen, Z. \*, **Cao, Y. \***, Liu, S. \*, Ren, G., Hu, G., Fang, D., Wei, D., Liu, C., Zhu, J., Wu, C. #, & Zhao, K. # (2023). Restraint of IFN- $\gamma$  expression through a distal silencer CNS-28 for tissue homeostasis. **Immunity,** 56(5), 944-958 (selected as cover, preview by Immunity)

2022

**Cao, Y. \***, Liu, S. \*, Ren, G. \*, Tang, Q., & Zhao, K. # (2022). cLoops2: a full-stack comprehensive analytical tool for chromatin interactions. **Nucleic Acids Research,** 50(1), 57-71.

Liu, S. \*, **Cao, Y. \***, Cui, K., Tang, Q., & Zhao, K. # (2022). Hi-TrAC reveals division of labor of transcription factors in organizing chromatin loops. **Nature communications,** 13(1), 1-17.

2020

**Cao, Y. \***, Chen, Z. \*, Chen, X. \*, Ai, D. \*, Chen, G., McDermott, J., Huang, Y., Guo, X., & Han, J. # (2020). Accurate loop calling for 3D genomic data with cLoops. **Bioinformatics,** 36(3), 666-675.

Zhen, T. \*, **Cao, Y. \***, Ren, G., Zhao, L., Hyde, R. K., Lopez, G., Feng, D., Alemu, L., Zhao, K., & Liu, P. P. # (2020). RUNX1 and CBF $\beta$ -SMMHC transactivate target genes together in abnormal myeloid progenitors for leukemia development. **Blood,** The Journal of the American Society of Hematology, 136(21), 2373-2385. (selected as Plenary Paper)

Han, M. \*, Li, J. \*, **Cao, Y. \***, Huang, Y., Li, W., Zhu, H., Zhao, Q., Han, J., Wu, Q., Li, J., Feng, J., & Wong, J. (2020). A role for LSH in facilitating DNA methylation by DNMT1 through enhancing UHRF1 chromatin association. **Nucleic Acids Research,** 48(21), 12116-12134.

Zeng, Y. \*, **Cao, Y. \***, Halevy, R. S. \*, Nguyen, P., Liu, D., Zhang, X., Ahituv, N., & Han, J. (2020). Characterization of functional transposable element enhancers in acute myeloid leukemia. **Science China Life Sciences**, 1-13.

Huang, F. \*, **Cao, Y. \***, Wu, G., Chen, J., Lin, W., Lan, R., Wu, B., Xie, X., Hong, J., & Fu, L. (2020). BMP2 signaling activation enhances bone metastases of non-small cell lung cancer. **Journal of Cellular and Molecular Medicine**, 24(18), 10768-10784.

2019

**Cao, Y. \***, Chen, G. \*, Wu, G. \*, Zhang, X. \*, McDermott, J., Chen, X., Xu, C., Jiang, Q., Chen, Z., Zeng, Y., Ai, D., Huang, Y., & Han, J. # (2019). Widespread roles of enhancer-like transposable elements in cell identity and long-range genomic interactions. **Genome research**, 29(1), 40-52.

2016

Wang, L. \*, Xu, X. \*, **Cao, Y. \***, Li, Z., Cheng, H., Zhu, G., Duan, F., Na, J., Han, J., & Chen, Y. G. (2016). Activin/Smad2-induced H3K27me3 reduction is crucial to initiate mesendoderm differentiation of human embryonic stem cells. **Journal of Biological Chemistry**, jbc-M116.

## **Other Publications**

For a full list of publications: [Google Scholar](#)

2025

Khateb, M., Jung, R., Leibou, S., Hadley, P., Yu, Z., Dinerman, A. J., Dulemba, V., Gasmi, B., Levin, N., Kim, P., Bhasin, A., Bhat, D., Sindiri, S., Gartner, J. J., Prickett, T. D., Benzine, T., Farid, S. S., Parkhurst, M. R., Halas, H., **Cao, Y.**, Zhao, K., Yang, J. C., Robbins, P. F., Lowery, F., Krishna, S., Heller, T., McVicar, D., Rosenberg, S. A. & Klemen, N. D. (2025). Rapid enrichment of progenitor exhausted neoantigen-specific CD8 T cells from peripheral blood. **bioRxiv**, 2025-05.

2024

Zhu, X., Chen, X., **Cao, Y.**, Liu, C., Hu, G., Ganesan, S., Veres, T. Z., Fang, D., Liu, S., Chung, H., Germain, R. N., Schwartzberg, P. L., Zhao, K., & Zhu, J. (2024). Optimal CXCR5 Expression during Tfh Maturation Involves the Bhlhe40-Pou2af1 Axis. **bioRxiv**, 2024-05.

2022

Zhang, X., Jiang, Q., Li, J., Zhang, S., **Cao, Y.**, Xia, X., Cai, D., Tan, J., Chen, J., & Han, J. D. J. (2022). KCNQ1OT1 promotes genome-wide transposon repression by guiding RNA–DNA triplexes and HP1 binding. **Nature Cell Biology**, 1-13.

Lin, X., Liu, Y., Liu, S., Zhu, X., Wu, L., Zhu, Y., Zhao, D., Xu, X., Chemparathy, A., Wang, H., **Cao, Y.**, Nakamura, M., Noordermeer, J., Russa, M., Wong, W., Zhao, K., & Qi, L. S. (2022). Nested epistasis enhancer networks for robust genome regulation. **Science**, 377(6610), 1077-1085.

Ren, G., Lai, B., Harly, C., Baek, S., Ding, Y., Zheng, M., **Cao, Y.**, Cui, K., Yang, Y., Zhu, J., Hager, G., Bhandoola, A., & Zhao, K. (2022). Transcription factors TCF-1 and

GATA3 are key factors for the epigenetic priming of early innate lymphoid progenitors toward distinct cell fates. ***Immunity***, 55(8), 1402-1413.

Pan, L., Ku, W. L., Tang, Q., **Cao, Y.**, & Zhao, K. (2022). scPCOR-seq enables co-profiling of chromatin occupancy and RNAs in single cells. ***Communications Biology***, 5(1), 1-9.

Fang, D., Cui, K., **Cao, Y.**, Zheng, M., Kawabe, T., Hu, G., Khillan, J., Li, D., Zhong, C., Jankovic, D., Sher, A., Zhao, K., & Zhu, J. (2022). Differential regulation of transcription factor T-bet induction during NK cell development and T helper-1 cell differentiation. ***Immunity***, 55(4), 639-655.

2021

Ku, W. L., Pan, L., **Cao, Y.**, Gao, W., & Zhao, K. (2021). Profiling single-cell histone modifications using indexing chromatin immunocleavage sequencing. ***Genome Research***, 31(10), 1831-1842.

Huang, F., **Cao, Y.**, Wang, C., Lan, R., Wu, B., Xie, X., Hong, J., Fu, L., & Wu, G. (2021). PNMA5 promotes bone metastasis of non-small-cell lung cancer as a target of BMP2 signaling. ***Frontiers in Cell and Developmental Biology***, 1400.

2020

Qiu, X., Ma, F., Zhao, M., **Cao, Y.**, Shipp, L., Liu, A., Dutta, A., Singh, A., Braikia, F.Z., De, S., Wood, W. H., Becker, K.G., Zhou, W., Ji, H., Zhao, K., Atchison, M.L., & Sen, R. (2020). Altered 3D chromatin structure permits inversional recombination at the IgH locus. ***Science Advances***, 6(33), eaaz8850.

Xia, X., Chen, X., Wu, G., Li, F., Wang, Y., Chen, Y., Chen, M., Wang, X., Chen, W., Xian, B., Chen, W., **Cao, Y.**, Xu, C., Gong, W., Chen, G., Cai, D., Wei, W., Yan, Y., Liu, K., Qiao, N., Zhao, X., Jia, J., Wang, W., Kennedy, B., Zhang, K., Cannistraci, C., Zhou, Y., & Han, J. (2020). Three-dimensional facial-image analysis to predict heterogeneity of the human ageing rate and the impact of lifestyle. ***Nature Metabolism***, 2(9), 946-957.

2019

Chen, X., Xu, C., Hong, S., Xia, X., **Cao, Y.**, McDermott, J., Mu, Y., & Han, J. (2019). Immune cell types and secreted factors contributing to inflammation-to-cancer transition and immune therapy response. ***Cell Reports***, 26(7), 1965-1977.

2018

Xu, C., Ai, D., Shi, D., Suo, S., Chen, X., Yan, Y., **Cao, Y.**, Zhang, R., Sun, N., Chen, W., McDermott, J., Zhang, S., Zeng, Y. & Han, J. (2018). Accurate drug repositioning through non-tissue-specific core signatures from cancer transcriptomes. ***Cell Reports***, 25(2), 523-535.

2015

Chen, W., Qian, W., Wu, G., Chen, W., Xian, B., Chen, X., **Cao, Y.**, Green, C.D., Zhao, F., Tang, K., & Han, J. (2015). Three-dimensional human facial morphologies as robust aging markers. ***Cell Research***, 25(5), 574-587.

Huang, Y., Yu, X., Sun, N., Qiao, N., **Cao, Y.**, Boyd-Kirkup, J. D., Shen, Q., & Han, J. (2015). Single-cell-level spatial gene expression in the embryonic neural differentiation niche. **Genome Research**, 25(4), 570-581.

2014

Hong, S., Huang, Y., **Cao, Y.**, Chen, X., & Han, J. D. J. (2014). Approaches to uncovering cancer diagnostic and prognostic molecular signatures. **Molecular & Cellular Oncology**, 1(2), e957981.

## **Software Development**

- [\*\*astroBoy\*\*](#): An automated NGS data-analysis platform with AI assistant deployed at NIH, which has rapidly processed over 250 billion reads from 7,000+ samples across 600+ jobs since December 2022.
- [\*\*cLoops2\*\*](#): Full stack analysis tool for chromatin interaction data such as Hi-TrAC, HiChIP and Hi-C (released in 2021).
- [\*\*cLoops\*\*](#): Accurate and flexible loops calling tool for 3D genomic data (released in 2017).

## **Awards & Honors**

- **2024 NHLBI Director's Award for Innovation** – Discovery of a novel regulatory element for IFN- $\gamma$  expression (2023 Immunity paper work)

## **Mentoring**

- **2024 and 2023 Hannah Zhu**, NIH Summer Internship Program, University of Maryland; working together on STARR-seq analysis for enhancer-enhancer interactions and developing a 3D genome browser.
- **2024 Emily Yu**, High School Senior Project, The Bryn Mawr School (2024); working together on scRNA-seq analysis; currently attending Yale University.

## **Review Service**

Reviewer (directly from editors) for: *Bioinformatics*, *Communications Biology*, *BMC Genomics*, *F1000Research*, *Frontiers in Immunology*, *Frontiers in Bioinformatics*, *Genes*, *Cells* and etc.

## **Invited Talks**

2025 NIDDK TriLab Bioinformatics Core, NIDDK, Bethesda, USA

2024 NICHD Bioinformatics and Scientific Programming Core, NICHD, Bethesda, USA

2024 Invited by Dr. Gordon L. Hager, NCI, Bethesda, USA  
2023 Invited by Prof. Lei Hou, Boston University, Boston, USA  
2023 DECODE Seminar Series, NIH, Bethesda, USA  
2017 Epigenetics Retreat, Ningbo, China

## **Conference Presentations & Posters**

2024 NCI Histone Modifications and Chromatin Structure Symposium, Bethesda, Maryland, USA  
2024 Epigenetics & Chromatin, Cold Spring Harbor Laboratory, New York, USA  
2024 NHLBI Fellow Festival, NIH, Bethesda, USA  
2024 NIH/FDA Immunology Interest Group Retreat, Washington, DC, USA  
2023 Gordon Research Conference, Genome Architecture in Cell Fate and Disease, Ventura, California, USA  
2023 NHLBI Fellow Festival, NIH, Bethesda, USA  
2022 SCBA DC-Baltimore Chapter Annual Scientific Symposium, University of Maryland, USA  
2019 4D Nucleosome Annual Meeting, Washington, DC, USA  
2018 Cold Spring Harbor Asia Conference on Chromatin, Epigenetics & Transcription, Suzhou, China  
2017 First Chromatin Biology Conference, Shenzhen, China  
2016 3rd International Symposium on 3D Genomics, Huazhong Agricultural University, Wuhan, China  
2015 Otto Warburg Summer School, Max Planck Institute for Molecular Genetics, Berlin, Germany

## **Technical Skills**

- Epigenomic/Gene Expression Data Analysis (Hi-C, ATAC-seq, ChIP-seq, MNase-seq, Hi-TrAC, RNA-seq, 10x single-cell RNA-seq)
- Programming (Python, Bash)
- High-Performance Computing
- CPU/GPU Servers Setup and Maintenance
- Web-application Development
- Deep-learning
- Machine-learning

## **References**

- Dr. Keji Zhao (postdoc mentor), NIH Distinguished Investigator, NHLBI/NIH, [zhaok@nhlbi.nih.gov](mailto:zhaok@nhlbi.nih.gov) ,

- Dr. Paul P. Liu (collaborator), Senior Investigator, NHGRI/NIH, [pliu@nhgri.nih.gov](mailto:pliu@nhgri.nih.gov)
- Dr. Chuan Wu (collaborator) , Senior Investigator, NCI/NIH, [chuan.wu@nih.gov](mailto:chuan.wu@nih.gov)
- Dr. Jingfang Zhu (collaborator), Senior Investigator, NIAID/NIH, [jfzhu@niaid.nih.gov](mailto:jfzhu@niaid.nih.gov)