CURRICULUM VITAE

PERSONAL INFORMATION

Name:	**Yaqiang Cao**
Organization:	System Biology Center, National Heart, Lung, and Blood Institute (NHLBI), National Institutes of Health (NIH)
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EDUCATION

2019 **Ph.D. in Computational Biology**
Chinese Academy of Sciences (CAS)- Max Planck Society (MPG) Partner Institute for Computational Biology, University of Chinese Academy of Sciences (UCAS), Shanghai, China.
Mentor: Prof. Jing-Dong Jackie Han

2012 **B.S. in Bioengineering**
East China University of Science and Technology, Shanghai, China.

RESEARCH EXPERIENCE

2024-Curr. **Research Fellow**
System Biology Center, National Heart, Lung, and Blood Institute (NHLBI), National Institutes of Health (NIH), Bethesda, MD, USA.
Mentor: Dr. Keji Zhao

2019-2024 **Visiting Fellow**
NHLBI/NIH, Bethesda, MD, USA.
Mentor: Dr. Keji Zhao

2011-2018 **Graduate Research Assistant**
CAS-MPG Partner Institute for Computational Biology, Shanghai, China.
Mentor: Prof. Jing-Dong Jackie Han

RESEARCH SUMMARY

Focus:	Chromatin regulation in immunity, leukemia, and aging.
Methods:	Created computational tools and experimental techniques to map high-resolution enhancer–promoter interactions and single-cell nucleosomes.
Discoveries:	Chromatin loops/histone modifications/transcription factors driving T-cell differentiation, acute myeloid leukemia, B-cell aging.
Collaborations:	Cross-disciplinary partnerships bridging basic science and clinical applications, involving biologists, physicians, and data scientists.
Impact:	User-friendly software for epigenomic and 3D genomic research; mechanism understandings for chromatin and clinical translations.

FIRST/CO-FIRST PUBLICATIONS (14 out of 31)

***** co-first author **#** correspondence.

2025 Zhen, T. *, ***Cao, Y.*** *, Dou, T., Chen, Y., Lopez, G., Menezes, A.C., Wu, X., Hammer, J., Cheng, J., Garrett, Anderson, S., Kirby, M., Wincovitch, S., Sisay, B., Elkahloun, A. G., Wu, D., Castilla, L., Yang, W., Jiang, J., Zhao, K., Liu, P. P.**#** (2025). CBFβ-SMMHC-driven leukemogenesis requires enhanced RUNX1-DNA binding affinity in mice. ***J Clin Invest***. 10.1172/jci192923.

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-γ 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 CBFβ-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

2025 Zhu, X., Chen, X., ***Cao, Y.***, Liu, C., Kline, Z. J., Hu, G., Ganesan, S., Veres, T. Z., Fang, D., Liu, S., Wei, D., Shibata, H., Golec, D. P., Chung, H., Germain, R. N., Schwartzberg, P. L., Zhao, K., & Zhu, J. (2025). Optimal CXCR5 expression during Tfh maturation involves the Bhlhe40–Pou2af1 axis. ***Cell Reports***, *44*(11), 116470.

Roy, S., Ren, M., Li, P., Cui, K., ***Cao, Y.***, Fisk, B., Markowitz, T. E., Redekar, N., Sakamoto, K., Nagao, K., Oh, J., Spolski, R., Liao, W., Dubois, S. P., Kelsall, B. L., Zhao, K., Phelan, J. D., & Leonard, W. J. (2025). BLIMP1 negatively regulates IL-2 signaling in T cells. ***Science Advances***, 11(29), eadx8105.

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.

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.

SOFTWARES

2022-Curr. astroBoy
An automated, AI-assisted platform for large-scale next-generation sequencing data analysis, supporting both in-house and publicly deposited datasets on a single-node server. Deployed at NHLBI/NIH, it has efficiently processed over 370 billion reads from more than 8,000 samples across 700+ analysis jobs since December 2022.

2023-Curr glitter
A custom-built, in-house web application for the analysis and visualization of single-cell RNA-seq data, developed to support collaborative research.

2023-Curr VINCE
A de novo Python package designed for nucleosome data analysis from single-cell MNase-seq, currently under active development and optimization.

2025 Ryder
A Python package for epigenome data normalization with internal reference and variable feature detection (manuscript submitting).

2021 cLoops2
A Python package for full stack analysis tool for chromatin interaction data such as Hi-TrAC, HiChIP and Hi-C (*Nucleic Acids Research*, 2022).

2019 TOWN
A Python package built on Keras for high-throughput, deep learning–augmented bright-field microscopy to automatically count live *C. elegans* worms. Developed for in-house use in drug screening to identify compounds that extend worm survival curves.

2017 cLoops
A Python package for accurate and flexible loops calling tool for 3D genomic data (*Bioinformatics*, 2020).

UNDER REVIEW/REVISE

2025
1. 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
2. ***Yaqiang Cao*** *#, Guangzhe Ge *, and Keji Zhao #: Ryder: Epigenome Normalization and Variable Feature Identification

AWARDS and HONORS

2024 **NHLBI Director's Award for Innovation**
Discovery of a novel regulatory element for IFN-γ expression (*Immunity*, 2023).

MENTORING

2025- Tuan Vinh
NIH Oxford-Cambridge Scholars Program Ph.D. student
Co-mentoring in bioinformatics and nucleosomes.

2024,2023 Hannah Zhu
University of Maryland; NIH Summer Internship Program.
Collaborated on STARR-seq and Hi-TrAC data analysis to study enhancer–enhancer interactions.

2024 Emily Yu
The Bryn Mawr School; High School Senior Project.

Currently Yale University; mentored on single-cell RNA-seq analysis.

2019-2020 Jonathan Perrie
NIH Postbac Program. Co-mentored in bioinformatics.
Successfully enrolled into the bioinformatics Ph.D. program at UCLA.

2015-18 Yingying Zeng
Partner Institute for Computational Biology; Junior master's student. Co-mentored in bioinformatics and collaborated on research investigating the epigenetic features of MIR retrotransposons. Co-first-authored a publication and successfully enrolled into the Ph.D. program at Nanyang Technological University (Singapore).

2016-18 Zhaoxiong Chen
Partner Institute for Computational Biology; Junior Ph.D. student. Co-mentored in bioinformatics and collaborated on research optimizing the cDBSCAN algorithm and cLoops. Co-first-authored a publication.

2016-18 Daosheng Ai
Partner Institute for Computational Biology; intern. Co-mentored in bioinformatics.
Co-first-authored a publication. Successfully enrolled into the Ph.D. program at Peking University (China).

PEER REVIEWER

Nature Communications, Bioinformatics, Communications Biology, BMC Bioinformatics, BMC Genomics, F1000Research, Frontiers in Immunology, Frontiers in Bioinformatics, Genes, Cells etc.

EDITORIAL SERVICES

Frontiers in Immunology, Frontiers in Medicine

TALKS

2025 TriLab Bioinformatics Core, NIDDK, Bethesda, USA
2024 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 & POSTERS

2025 NIH/FDA Immunology Interest Group Retreat, DC, USA
2024 NCI Histone Modifications and Chromatin Structure Symposium, Bethesda, 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, DC, USA
2023 Genome Architecture in Cell Fate and Disease, Ventura, California, USA
2023 NHLBI Fellow Festival, Bethesda, USA
2022 SCBA DC-Baltimore Chapter Annual Scientific Symposium, University of Maryland, USA
2019 4D Nucleosome Annual Meeting, DC, USA
2018 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, 3D Genome, and single-cell data analysis (Hi-C, HiChIP, ATAC-seq, ChIP-seq, MNase-seq, Hi-TrAC, RNA-seq, Micro-C, 10x single-cell RNA-seq, 10x single-cell multiomics, STARR-seq, RRBS, EM-seq, WES), with expertise in customized and sophisticated data mining approaches
- Proficient in Python programming and package development
- Experienced CPU/GPU servers setup and maintenance
- Web-application development
- Application and development of deep-learning and machine-learning algorithms

REFERENCE

Dr. Keji Zhao	Distinguished Investigator, NHLBI/NIH	zhaok@nhlbi.nih.gov	301-496-2098
Dr. Paul P. Liu	Senior Investigator, NHGRI/NIH	pliu@nhgri.nih.gov	301-402-2529
Dr. Jinfang Zhu	Senior Investigator, NIAID/NIH	jfzhu@niaid.nih.gov	301-402-6662