
Yaqiang Cao, Ph.D., *Curriculum Vitae*

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EDUCATION

East China University of Science and Technology

Bachelor of Bioengineering

2008.09 - 2012.06

CAS-MPG Partner Institute for Computational Biology

Ph.D. of Computational Biology
(M.S. included)

2012.09 -2018.12

EXPERIENCES

Postdoc, visiting fellow, with Dr. Keji Zhao, NHLBI, NIH

2019.04-

RESEARCH INTEREST

Bioinformatics, chromatin 3D structures, single-cell epigenetics, T-cell immunology

PUBLICATIONS ([full list](#))

1. 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. (**co-first author**)
2. 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.
3. 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.
4. 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. (**co-first author**)
5. 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.
6. 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.
7. **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[J]. *Genome research*, 2019, 29(1): 40-52. (**first author**)
8. **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. (**first author**)
9. 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. (**co-first author**)
10. 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. (**co-first author**)
11. 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.
12. 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. (**co-first author**)

13. 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.
14. 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 β -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. (**co-first author, selected as Plenary Paper**)
15. 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**, (2021): 1400.
16. Ku, W. L., Pan, L., **Cao, Y.**, Gao, W., & Zhao, K. (2021). Profiling single-cell histone modifications using indexing chromatin immunocleavage sequencing. **Genome Research**, gr-260893.
17. **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. (**first author**)
18. 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.
19. 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.
20. 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.
21. 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.
22. 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.
23. 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. (**co-first author**)
24. 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 (**co-first author, selected as cover**)
25. **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**, gkad378. (**first author**)

ACADEMIC OPEN SOURCE SOFTWARES

1. [cLoops](#): accurate and flexible loops calling tool for 3D genomic data (released in 2017)
2. [cLoops2](#): full stack analysis tool for chromatin interaction data such as Hi-TrAC, HiChIP and Hi-C (released in 2021)

INVITED TALKS

1. **Epigenetics Retreat, November 2017, Ningbo, China**; Accurate loop calling for 3D genomic data with cLoops.
2. **DECODE Seminar Series, August 2023, NIH, Bethesda, USA**; Fine-scale dynamic chromatin loops and domains: beyond cohesin.
3. **Invited by Prof. Lei Hou, August 2023, Boston University, Boston, USA**; Fine-scale dynamic chromatin loops and domains: beyond cohesin.

POSTERS

1. **Otto Warburg Summer School, September 2015, Max Planck Institute for Molecular Genetics, Berlin, German**; Yaqiang Cao (2015) iDBSCAN: An improvement to density-based clustering method for ultrafast detection of chromosomal interactions
2. **The 3th International Symposium on 3D genomics, November 2016, Huazhong Agricultural University, Wuhan, China**; Yaqiang Cao (2016) Widespread Associated Retrotransposons MIR and L2 Function as Seeds of Cis-regulatory Units Marking Cell

Identities

3. **The First Chromatin Biology Conference of the Chinese Society for Cell Biology, April 2017, Shenzhen, China;** Yaqiang Cao (2017) Widespread Associated Retrotransposons MIR and L2 Function as Seeds of Cis-regulatory Units
 4. **Cold Spring Harbor Asia Conferences on Chromatin, Epigenetics & Transcription, April 2018, Suzhou, China;** Yaqiang Cao (2018) cLoops-A clustering-based loops calling method for ChIA-PET, HiChIP and Hi-C
 5. **4D Nucleosome Annual Meeting, December 2019, DC, USA;** Shuai Liu, Yaqiang Cao, Qingsong Tang, Keji Zhao (2019) TrAC-looping2 – A Highly Sensitive Technique for Detecting Multiple Levels of Chromatin Interactions
 6. **SCBA DC-Baltimore chapter annual scientific symposium, December 2022, University of Maryland, USA;** Yaqiang Cao (2022) Hi-TrAC reveals internal organizations of super-enhancers
 7. **NHLBI Fellow Festival, April 2023, NIH, Bethesda, USA;** Yaqiang Cao (2023) Hi-TrAC reveals internal organizations of super-enhancers
 8. **Gordon Research Conference, Genome Architecture in Cell Fate and Disease, June 2023, Ventura, California, USA;** Yaqiang Cao (2023) Hi-TrAC: Revealing Fine-Scale Dynamic Chromatin Loops and Domains
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REVIEW CONTRIBUTIONS

Frontiers in Immunology
Frontiers in Oncology
Frontiers in Pharmacology
Frontiers in Genetics
BMC Genomics
Cancer Control
Genes
Cells
Biomolecules