
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 -2019.01

EXPERIENCES

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

2019.04-2024.04

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

2024.04-

RESERCH INTEREST

bioinformatics, chromatin organization, single-cell epigenetics, T-cell immunology

SELECTED PUBLICATIONS

1. 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*.
2. **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.
3. 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**)
4. **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.
5. 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. (**selected as Plenary Paper**)
6. **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.
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.

* co-first author # correspondence

OTHER 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. 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)
8. 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)
9. 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)
10. 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.
11. 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.
12. 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.
13. 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.
14. 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.
15. 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.
16. 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.
17. 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.
18. 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.
19. 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).

ACADEMIC 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)

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3. [astroBoy](#): streamlined NGS data automatic processing web service for in-house data and public data (GEO database), in-house service within NIH since December 2022
 4. [Ranger iGenome Browser](#): a lightweight efficient genome browser for hosting in-house chromatin interaction 3D data and epigenome data tracks, in developing
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AWARDS

1. **2024 NHLBI Director's Awards of Innovation:** For discovering the first negative regulatory element for interferon-gamma expression and elucidating its mechanism of function in preventing enhancer-promoter interaction through long-distance chromatin interactions.
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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.
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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
 9. **NIH/FDA IMMUNOLOGY INTEREST GROUP 2024 RETREAT, January 2024, DC, USA:** Yaqiang Cao (2024) T Helper Cell Fate Orchestrated by H3K4me1–Chromatin Loop–GATA3 Tangos
 10. **NHLBI Fellow Festival, March 2024, NIH, Bethesda, USA:** Yaqiang Cao (2024) T Helper Cell Fate Orchestrated by H3K4me1–Chromatin Loop–GATA3 Tangos
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REVIEW CONTRIBUTIONS

Frontiers in Immunology
Frontiers in Bioinformatics
Frontiers in Oncology
Frontiers in Pharmacology
Frontiers in Genetics
Communication Biology
BMC Genomics
F1000Research
Cancer Control
Genes
Cells

Biomolecules

Journal of Personalized Medicine

International Journal of Molecular Sciences