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   2012.09 -2018.12
(M.S. included)

EXPERIENCES

Postdoc, visiting fellow, with Dr. Keji Zhao, NHLBI, NIH   2019.04-

RESERCH INTEREST

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

SELECTED PUBLICATIONS

1. ***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.
2. ***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.
3. 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. (**co-first author, selected as Plenary Paper**)
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. 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**)
6. 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**)
7. ***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.

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.

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

REVIEW CONTRIBUTIONS

Frontiers in Immunology
Frontiers in Oncology
Frontiers in Pharmacology
Frontiers in Genetics
BMC Genomics
F1000Research
Cancer Control
Genes
Cells
Biomolecules