

# Haining Chen

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## BACKGROUND

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<b>Cornell University</b> , Ithaca, NY <i>Postdoctoral Fellow in Molecular Biology and Genetics</i>	2025 - present
<b>Cornell University</b> , Ithaca, NY <i>Ph.D. program in The Graduate Field of Biochemistry, Molecular and Cell Biology (BMCB)</i>	2020 - 2024
<b>Penn State University</b> , State College, PA <i>Ph.D. program in Department of Molecular, Cellular, and Integrative Biosciences (MCIBS)</i>	2018-2020
<b>Shandong University</b> , Jinan, China <i>Bachelor of Science in Microbiology</i>	2014-2018

## SKILLS

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- Biochemistry Labs Skills
  - Library construction and sequencing assays: ChIP-seq, ChIP-exo, and other next-generation sequencing (NGS) assays
  - Cell culture
  - Protein synthesis
  - X-ray crystallography
  - Isothermal Titration Calorimetry
  - Western blotting
  - Yeast two-hybrid assay
  - CRISPR and other gene editing technique
- Computer Skills
  - Pipeline design: development of reproducible workflows for NGS analysis, including genome annotation, regulatory element identification from ChIP-seq/ChIP-exo, RNA-seq data
  - Bioinformatics tools: Bioconductor, Bioconda, Picard tools, UCSC Genome Browser, SAMtools, BWA, STAR
- Programming languages: Python, Shell scripting, R
- Language Skills: Chinese, English.

## GRADUATE RESEARCH EXPERIENCE

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<b>Translational and rotational setting of nucleosomes across a human genome</b>	2018 – 2024
<ul style="list-style-type: none"><li>• Eukaryotic DNA is wrapped around a complex of histones, such that one side of the helix is accessible, and the other is buried. Yet, The rotational setting of genomic DNA on nucleosomes in human cells is still unknown.</li><li>• We developed a new ChIP-exo assay combining Lambda exonuclease and Benzonase to map a TF's binding site and its translational and rotational relationship with an adjacent nucleosome on the same DNA molecule.</li><li>• Using ChIP-exo, we identified rotational and/or translational setting on nucleosomes of CTCF, FoxA and NFIA sites.</li></ul>	
<b>Genome-wide protein molecular architecture of human promoters</b>	2018 – present

- During the process of transcription initiation, transcription factors (TFs) and cofactors interact with promoter or enhancer regions to regulate chromatin accessibility and transcription levels. However, the precise positioning of the pre-initiation complex (PIC), TFs, cofactors, and nucleosomes in vivo on a genomic scale, as well as their interplay, has not been thoroughly addressed.
- Using ChIP-exo, we showed that different GTFs exhibited precise and distinct exonuclease stop patterns at TATA-like or TATA-less core promoters, that are ~30 bp upstream of genome-wide TSSs. Distinct mechanisms of PIC assembly on TATA-like and TATA-less core-promoters were explored.
- Genome-wide TSSs have specific translational and rotational settings relative to the +1 nucleosome. We attribute the in-vivo architecture of the +1 nucleosome to nucleosome positioning sequence (NPS) patterns that are rotationally exposed.

## UNDERGRADUATE RESEARCH EXPERIENCE

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### Structure analysis of a protein containing a pzp domain and functional interaction with histone substrates

Sponsor Dr. Li Haitao. Tsinghua University.

Jul 2017 - May 2018

### Functional Assignment of Multiple ESCRT-III Homologs in Cell Division and Budding in *Sulfolobus Islandicus*.

Sponsor Dr. Yulong Shen. Shandong University.

May 2016 - Apr 2017

### The Target Signals of Msp1 in Yeast

Sponsor Dr. Jiang Hui. National Institute of Biological Sciences Beijing.

Jul 2016- Aug 2016

### Panda Feeder in Jinan Zoo

Shandong Province, China.

Jul 2015 - Aug 2015

## PROFESSIONAL TRAINING

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- Biology 598 – Experiential Teaching in Biology: improve teaching skills (Penn State 2018).
- BIOL 602: Supervised Experience in College Teaching : TA one semester in Biology 110 Lab section (Penn State 2018).
- Mentoring three rotation students in applying ChIP-exo 6.1 in yeast (Cornell 2022).
- Mentoring a rotation student in designing assays for ChIP-exo at single cell resolution (Cornell 2023).
- CVG mentoring program: providing additional informal support on the “soft skills” of academic science to two graduate students (Cornell 2023 - 2024).
- Mentoring a rotation student in a protein purification (Cornell 2024).

## PUBLICATIONS

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### Under review

- **Chen, H.**, Lang, O., Lai, W. K. M., Pugh, B. F. (2024). An integrated genome-wide mechanism of RNA polymerase II initiation complex assembly. *Under review, Nature*.
- **Chen, H.**, Krebs, E. J., Lai, W. K. M., Pugh, B. F. (2024). ChIP-exo 6: A protocol for high resolution genome-wide mapping of protein-DNA interactions in context with nucleosomes. *Under review, Nature protocol*.

- **Chen, H.**, Krebs, E. J., Lang, O., Lai, W. K. M., Pugh, B. F. (2024). Translational and rotational setting of nucleosomes across a human genome. *Under review, Molecular Cell*

## Published

- Liu, J., Gao, R., Li, C., Ni, J., Yang, Z., Zhang, Q. **Chen, H.**, Shen, Y. (2017). Functional assignment of multiple ESCRT-III homologs in cell division and budding in *Sulfolobus islandicus*. *Molecular microbiology*, 105(4), 540-553.
- **Chen, H.**, & Pugh, B. F. (2021). What do transcription factors interact with?. *Journal of Molecular Biology*, 166883.
- Zheng, S., Bi, Y., **Chen, H.**, Gong, B., Jia, S., & Li, H. (2021). Molecular basis for bipartite recognition of histone H3 by the PZP domain of PHF14. *Nucleic acids research*, 49(15), 8961-8973.

## CONFERENCE PRESENTATIONS/POSTERS

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- Poster: "Protein molecular architecture of human promoter" - Mechanisms of Eukaryotic Transcription, Cold Spring Harbor, NY, Aug. 26 – Aug. 30, 2025.
- Poster: "Protein molecular architecture of human promoter" - 2024 ASBMB Transcriptional Regulation by Chromatin and RNA Polymerase Conference, Alexandria, Sept. 26- Sept. 29, 2024.
- Poster: "Protein molecular architecture of human promoter" - 2024 MBG+ Recruitment, Cornell University, Aug. 21, 2024.
- Research presentation: "Same-molecule rotational relationship between transcription factors and nucleosomes" - Mechanisms of Eukaryotic Transcription, Cold Spring Harbor, NY, Aug. 29 – Sep. 2, 2023.
- Research presentation: "Same-molecule rotational relationship between transcription factors and nucleosomes" - Summer Symposium on Chromatin and Epigenetic Regulation of Transcription, State College, PA, Aug. 6-9, 2023.
- Research presentation: "Protein molecular architecture of human promoters" - BMCB Student Seminar, Cornell University, Nov. 14, 2022.
- Research presentation: "Protein molecular architecture of human promoter" - BMBB GGD symposium, Cornell University, Oct. 10, 2022.
- Poster: "Protein molecular architecture of human promoter" - 2022 ASBMB Conference, Snowbird, UT, Sep. 28-Oct. 2, 2022.
- Research presentation: "Protein molecular architecture of human promoter" - MBG Retreat, Cornell University, Aug. 16, 2022.
- Research presentation: "High-throughput ChIP-exo by nuclei barcoding" - BMBB Student Seminar, Cornell University, Feb. 14, 2022.
- Event: "2021 Mechanisms of Eukaryotic Transcription" - Cold Spring Harbor virtual meeting, Aug. 31, 2021 - Sep. 3, 2021.
- Research presentation: "High-throughput ChIP-exo by nuclei barcoding" - BMBB Student Seminar, Cornell University, Mar. 8, 2021.
- Event: "High-throughput ChIP-exo by nuclei barcoding" - Annual Center for Eukaryotic Gene Regulation retreat, Penn State University, Oct. 17, 2020.
- Research presentation: "High-throughput ChIP-exo by nuclei barcoding" - Megameeting in Center for Eukaryotic Gene Regulation, Penn State University, Jun. 10, 2020.
- Research presentation: "High-throughput Chip-exo by nuclei barcoding" - Megameeting in Center for Eukaryotic Gene Regulation, 4th Floor Frear Bridge at Penn State University, Mar. 3, 2020.

- Poster Presentation: "Bar-Chip-exo: High-throughput Chip-exo for large-scale DNA-binding proteins studies" - Annual Center for Eukaryotic Gene Regulation retreat at 310 Elks Club Rd., Boalsburg, PA, Dec. 10, 2019.
- Event: "Mechanisms of Eukaryotic Transcription" at Cold Spring Harbor Laboratory, Aug. 27, 2019 - Aug. 31, 2019.
- Poster Presentation: "Bar-Chip-exo: High-throughput Chip-exo for large-scale DNA-binding proteins studies" - MCIBS and Pathobiology Retreat at Toftrees Resort, State College, PA, Aug. 20, 2019.
- Event: "Summer Symposium on Chromatin and Epigenetic Regulation of Transcription" at Penn State University, Jul. 30, 2019 - Aug. 2, 2019.
- Research Presentation: "Bar-Chip-exo: High-throughput Chip-exo for large-scale DNA-binding proteins studies" - Megameeting in Center for Eukaryotic Gene Regulation, 4th Floor Frear Bridge at Penn State University, May 11, 2019.

## PERSONAL WEBSITE

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- [HeninChen.github.io](https://heninchengithub.io)