Christopher H. Bohrer

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Education

- **National Cancer Institute, National Institutes of Health, Bethesda, MD** 2020–Present
  Postdoctoral Researcher
- **Johns Hopkins University, Baltimore, MD** 2020
  Ph.D., Biophysics and Biophysical Chemistry
- **Kent State University, Kent, OH** 2013
  B.S., Physics (magna cum laude)
  B.S., Education (magna cum laude)
  Minor, Biology

Research Experience

- **Chromatin and Transcription/Method Development, NCI, Bethesda, MD** May 2020–Present
  Advisor: Dr. Daniel R. Larson
  Utilized theory and experiment to investigate the link between chromatin organization and transcription regulation. Developed methods to improve the resolution of chromatin tracing data.
- **Super-Resolution Imaging/Method Development, JHU, Baltimore, MD** Jan 2014–Apr 2020
  Advisor: Dr. Jie Xiao
  Developed and applied novel methodologies to study the influence of chromosome structure on transcription with super-resolution microscopy.
- **Computational Biophysics/Bioinformatics, JHU, Baltimore, MD** Jan 2014–Apr 2020
  Advisor: Dr. Elijah Roberts
  Employed stochastic simulations to investigate the effects of local DNA structure on information propagation in bacteria.
- **Theoretical Molecular Biophysics, KSU, Kent, OH** Aug 2010–May 2013
  Advisor: Dr. John Portman
  Studied structural stability of various minor species of G-Quadruplex using computational techniques.
- **Single-Molecule Biophysics, KSU, Kent, OH** Aug 2010–May 2013
  Advisor: Dr. Hanbin Mao
  Worked with laser tweezers to study long-loop G-Quadruplexes and their kinetics.

In preparation Publications

**These authors contributed equally.*

1. **Bohrer CH**, Larson DR. Intra-chromosomal correlated nascent transcription over large physical distances.

   This work reveals two opposing regulatory regimes coexisting across the genome: strong cis-coordination that acts over hundreds of nanometers and a distinct mode of trans-competition. Using allele-resolved imaging and machine learning, we can classify which regime governs a specific gene pair with high accuracy. These findings establish a new framework for how genome organization and regulatory competition jointly shape transcriptional coupling on a global scale.

2. Fursova NA, **Bohrer CH**, Patange S, Sood V, Chow CC, Misteli T, Larson DR. Stochastic coupling of MYC gene and super-enhancer transcriptional dynamics via a shared enhancer network.

Publications

**These authors contributed equally.*

1. Messina O, Remini L, **Bohrer CH**, Fiche J-B, Walter J-C, Parmeggiani A, Nollmann M. Enhancer–promoter proximity predicts transcriptional competence but not transcriptional output in the *Drosophila* brain. *arXiv*. 2026 Sep 2. arXiv:2609.03058.
2. You DS, **Bohrer CH**, Rumde PH, Sanidas I, Swaffer MP, Larson DR, Elias JE, Lanz MC, Skotheim JM. Cell size-dependent mRNA transcription drives proteome remodeling. *Cell Reports*. 2026 Jun 23;45(6):117488. doi:10.1016/j.celrep.2026.117488.
3. Cho HJ, **Bohrer CH**, Trzaskoma P, Kim JM, Pekowska A, Casellas RC, Patro R, Chow CC, Larson DR. Highly constrained kinetic models for single-cell gene expression analysis. *bioRxiv*. 2026 May 25. doi:10.64898/2026.05.22.727214.
4. **Bohrer CH**, Larson DR. A methodology to reduce the localization error in multi-loci microscopy provides new insights into enhancer biology. PLOS Computational Biology. 2025 Dec 17;21(12):e1013796.

   We developed LEAR, a post-processing methodology that dramatically improves the resolution of multi-loci microscopy data without new experiments. Applying LEAR partially resolved a major discrepancy in the field, revealing for the first time a direct correlation between enhancer-promoter proximity and transcriptional bursting at the Sox2 locus. This work provides a vital tool for re-examining chromatin contact data and gives new physical insight into enhancer cooperation.
5. Yehya N*, **Bohrer CH***, Yu Q, Hathcock D, Goldberg BI, Leng S, Harris FE, Hendrix H, White M, Leng F, Meyer S, Tu Y, Xiao J. Chromosomal topological domain formation modulates transcription and the coupling of neighboring genes in *Escherichia coli*. *bioRxiv*. 2025 Nov 23. doi:10.1101/2025.11.23.690031.

   As co-first author, I designed and created a novel synthetic system in E. coli to precisely control local chromosome topology. Our single-cell measurements revealed that forming a topological domain represses transcription and alters the coupling between neighboring genes in a supercoiling-dependent manner. This work establishes chromosome topology as a major regulator of both gene expression levels and their coordination in bacteria.
6. McQuillen R, Perez AJ, Yang X, **Bohrer CH**, Smith EL, Chareyre S, Tsui HC, Bruce KE, Hla YM, McCausland JW, Winkler ME, Goley E, Ramamurthi K, Xiao J. Light-dependent modulation of protein localization and function in living bacteria cells. *Nature Communications*. 2024 Dec 30;15(1):10746. doi:10.1038/s41467-024-54147-8.
7. (**Review**) **Bohrer CH**, Fursova NA, Larson DR. Enhancers: a focus on synthetic biology and correlated gene expression. *ACS Synthetic Biology*. 2024 Sep 14;13(10):3093–108. doi:10.1021/acssynbio.4c00312.
8. Trzaskoma P, Jung S, Pekowska A, **Bohrer CH**, Wang X, Naz F, Dell'Orso S, Dubois WD, Olivera A, Vartak SV, Zhao Y, Nayak S, Overmiller A, Morasso M, Sartorelli V, Larson D, Chow C, Casellas, R, O'Shea J. 3D chromatin architecture, BRD4, and Mediator have distinct roles in regulating genome-wide transcriptional bursting and gene network. *Science Advances*. 2024 Aug 9;10(32):eadl4893. doi:10.1126/sciadv.adl4893.
9. Keikhosravi A, Almansour F, **Bohrer CH**, Fursova NA, Guin K, Sood V, Misteli T, Larson DR, Pegoraro G. High-throughput image processing software for the study of nuclear architecture and gene expression. *Scientific Reports*. 2024 Aug 8;14(1):18426. doi:10.1038/s41598-024-69426-2.
10. **Bohrer CH**, Larson DR. Synthetic analysis of chromatin tracing and live-cell imaging indicates pervasive spatial coupling between genes. *eLife*. 2023 Feb 15;12:e81861. doi:10.7554/eLife.81861.

    By developing a synthetic analysis that integrates fixed-cell chromatin tracing with live-cell imaging, we demonstrated that spatial proximity (<300 nm), not linear genomic distance, predicts coordinated transcriptional bursting. This finding establishes a fundamental spatial principle for enhancer-promoter communication.
11. Geng Y, **Bohrer CH**, Yehya N, Hendrix H, Shachaf L, Liu J, Xiao J, Roberts E. A spatially resolved stochastic model reveals the role of supercoiling in transcription regulation. *PLoS Computational Biology*. 2022 Sep 19;18(9):e1009788. doi:10.1371/journal.pcbi.1009788.
12. (**Review**) **Bohrer CH**, Larson DR. The stochastic genome and its role in gene expression. *Cold Spring Harbor Perspectives in Biology*. 2021 Oct 1;13(10):a040386. doi:10.1101/cshperspect.a040386.
13. **Bohrer CH**, Yang X, Thakur S, Weng X, Tenner B, McQuillen R, Ross B, Wooten M, Chen X, Zhang J, Roberts E, Xiao J. A pairwise distance distribution correction (DDC) algorithm to eliminate blinking-caused artifacts in SMLM. *Nature Methods*. 2021 Jun;18(6):669–77. doi:10.1038/s41592-021-01156-8.

    We developed the DDC algorithm to correct for blinking artifacts, a pervasive issue in super-resolution microscopy that creates false molecular clusters. The foundational principles of this method have been widely adopted and

integrated into other software like TARDIS, enabling more accurate quantification of molecular organization across the field.

14. Gyparaki MT, Arab A, Sorokina EM, Santiago-Ruiz AN, **Bohrer CH**, Xiao J, Lakadamyali M. Tau forms oligomeric complexes on microtubules that are distinct from tau aggregates. *Proceedings of the National Academy of Sciences.* 2021 May 11;118(19):e2021461118. doi:10.1073/pnas.2021461118.
15. Tenner B, Getz M, Ross B, Ohadi D, **Bohrer CH**, Greenwald E, Mehta S, Xiao J, Rangamani P, Zhang J. Spatially compartmentalized phase regulation of a Ca2+-cAMP-PKA oscillatory circuit. *eLife.* 2020 Nov 17;9:e55013. doi:10.7554/eLife.55013.
16. (**Review**) **Bohrer CH**, Xiao J. Complex diffusion in bacteria. *Physical Microbiology.* 2020:15–43.
17. Weng X*, **Bohrer CH***, Bettridge K, Lagda AC, Cagliero C, Jin DJ, Xiao J. Spatial organization of RNA polymerase and its relationship with transcription in Escherichia coli. *Proceedings of the National Academy of Sciences.* 2019 Oct 1;116(40):20115–23. doi:10.1073/pnas.1903968116.

    As co-first author, I led the computational analysis of super-resolution imaging data to challenge the prevailing model of RNA polymerase (RNAP) organization. Our quantitative analysis revealed that while RNAP clusters are active transcription centers, their spatial organization is surprisingly independent of transcription activity and is instead dictated by the underlying nucleoid structure. This work fundamentally reframes the understanding of bacterial transcription by decoupling the mechanism of cluster formation from its function.
18. Fang X, Liu Q, **Bohrer CH**, Hensel Z, Han W, Wang J, Xiao J. Cell fate potentials and switching kinetics uncovered in a classic bistable genetic switch. *Nature Communications.* 2018 Jul 17;9(1):2787. doi:10.1038/s41467-018-05071-8.
19. **Bohrer CH***, Yang X*, Lyu Z, Wang SC, Xiao J. Improved single-molecule localization precision in astigmatism-based 3D superresolution imaging using weighted likelihood estimation. *bioRxiv.* 2018 Jan 1:304816. doi:10.1101/304816.

    As co-first author, I developed a weighted likelihood estimation framework to improve localization precision in astigmatism-based 3D super-resolution imaging. The work established the feasibility of this approach for more accurate 3D localization, though we did not continue its development after a similar method appeared in the literature.
20. Klein M, Sharma R, **Bohrer CH**, Avelis CM, Roberts E. Biospark: scalable analysis of large numerical datasets from biological simulations and experiments using Hadoop and Spark. *Bioinformatics.* 2017 Jan 15;33(2):303–5. doi:10.1093/bioinformatics/btw614.
21. **Bohrer CH**, Bettridge K, Xiao J. Reduction of confinement error in single-molecule tracking in live bacterial cells using SPICER. *Biophysical Journal.* 2017 Feb 28;112(4):568–74. doi:10.1016/j.bpj.2016.12.034.

    We developed an analysis method that reduces confinement-induced bias in single-molecule tracking in small bacterial cells by selectively using both long- and short-axis displacements. Validated with simulations and RNA polymerase tracking in live E. coli, SPICER improves estimates of diffusion coefficients and state-transition probabilities while remaining easy to integrate into existing SMT workflows.
22. **Bohrer CH**, Roberts E. A biophysical model of supercoiling dependent transcription predicts a structural aspect to gene regulation. *BMC Biophysics.* 2016 Dec;9(1):2. doi:10.1186/s13628-016-0027-1.

    We developed a biophysical model showing that transcription-generated supercoiling can couple the activity of neighboring genes within the same topological domain. The model predicts that nearby genes should exhibit correlated, temporally synchronized bursts of mRNA production, identifying chromosome topology as a physical mechanism for coordinated gene expression beyond promoter-specific regulation.
23. Roberts E, Be'er S, **Bohrer CH**, Sharma R, Assaf M. Dynamics of simple gene-network motifs subject to extrinsic fluctuations. *Physical Review* E. 2015 Dec 31;92(6):062717. doi:10.1103/PhysRevE.92.062717.
24. Koirala D, Ghimire C, **Bohrer CH**, Sannohe Y, Sugiyama H, Mao H. Long-loop G-quadruplexes are misfolded population minorities with fast transition kinetics in human telomeric sequences. *Journal of the American Chemical Society.* 2013 Jan 31;135(6):2235–41. doi:10.1021/ja309388b.

Awards and Honors

- Selected as Judge, *Fellows Award for Research Excellence*, NIH Office of Intramural Training and Education (2024)
- *Retinal Disease Interest Group Award*, National Eye Institute, NIH (2024)
- *Fellows Award for Research Excellence*, NIH Office of Intramural Training and Education (2023)
- *Director's Innovation Award*, National Cancer Institute, NIH (2022)
- Nominee, *Harold M. Weintraub Graduate Student Award*, Fred Hutchinson Cancer Center, Selected as sole departmental nominee recognizing exceptional graduate research (2020)
- *Addison-Wesley Award in Physics*, Kent State University (2013)

- *John Wiley Award in Physics*, Kent State University (2011)

Oral Presentations

- CCR Center of Excellence in Chromosome Biology (CECB) Workshop, NIH, Bethesda, MD (2026): "When Genes Coordinate—and When They Compete: Nascent Transcription in the 3D Genome."
- Department Colloquium, University of Texas Medical Branch, Galveston, TX (2026). "Dissecting the Relationship Between Genome Organization and Transcription Regulation."
- Department Colloquium, Carnegie Mellon University, PA (2026). "Dissecting the Relationship Between Genome Organization and Transcription Regulation."
- Department Colloquium, The Ohio State University, OH (2026). "Dissecting the Relationship Between Genome Organization and Transcription Regulation."
- International Asilomar Chromatin Chromosomes and Epigenetics Conference, CA (2024): "Widespread correlated gene expression and action at a distance."
- Genome Organization and Nuclear Function, CSHL (2024): "A methodology to reduce the localization error of multi-loci microscopy data provides new insights into enhancer dynamics and correlated transcriptional bursts."
- Retinal Disease Interest Group, MD (2024): "Widespread correlated gene expression and action at a distance."
- Systems Biology SIG Symposium, MD (2024): "Widespread correlated gene expression and action at a distance."
- DECODE Chromatin Series, MD (2023): "Synthetic analysis of chromatin tracing and live-cell imaging indicates pervasive spatial coupling between genes."
- Cell Bio 2022 ASCB, DC (2022): "Synthetic analysis of chromatin tracing and live-cell imaging indicates pervasive spatial coupling between genes."
- NIH Chromatin and Transcription Interest Group, NIH (2022): "Synthetic analysis of chromatin tracing and live-cell imaging indicates pervasive spatial coupling between genes."
- Genome Organization and Nuclear Function, CSHL (2022): "Transcription modulates the distances between genes on individual chromosomes and distance dictates correlated transcriptional bursts."
- Institute for Biomedical Research Annual Retreat, MD (2019): "Correcting for blinking in superresolution microscopy."
- Single Molecule Meeting, Biochemical Society, Oxford (2018): "The chromosome's fight against disorder in E. coli."
- Lectures in Computational Biophysics, MD (2016): "The chromosome's fight against disorder in E. coli."

Teaching

- Teaching Assistant, Johns Hopkins University Department of Biophysics, Baltimore, MD 2016
  Course: Protein Engineering Biological Laboratory, Professor Carolyn Fitch
- Teaching Assistant, Johns Hopkins University Department of Biophysics, Baltimore, MD 2015
  Course: Introduction to Computing, Professor Greg Bowman
- Student Teacher, Kent Ohio High School, Kent, OH 2013
  Subjects: Chemistry and Environmental Science
- Student Teacher, Akron Ohio Middle School, Akron, OH 2012
  Subject: Chemistry
- Head Math Tutor, Kent State University, Kent, OH 2010–2014

Mentorship

- Hyeon Jin Cho, University of Maryland Graduate Student 2022–2024
  Current Position: Postdoc
- Yuncong Geng, Hopkins Graduate Student 2018–2019
  Current Position: PhD Student at Illinois Urbana-Champaign
- Nicolás Yehya, Hopkins Graduate Student 2018–2019
  Current Position: Postdoc
- Maxwell T. White, Hopkins Undergraduate 2016–2018
  Current Position: MD-PhD Student at Johns Hopkins University

- Yiwen Zhang, Peking University Visiting Undergrad 2017
  Current Position: PhD Student at Harvard
- Logan Qiao, High School Student, 2016
  Current Position: Data Science Consultant at Ekimetrics

Outreach and Service

- Instructor for inner city Baltimore students at the Fun with Science Summer Camp, a week-long camp where participants work with real scientists from Johns Hopkins (from 2016 to 2019).
- Invited Reviewer for eLife
- Invited Reviewer for Communications Biology
- Invited Reviewer for Epigenetics & Chromatin
- Invited Reviewer for Nucleic Acids Research
- Invited Reviewer for Journal of the Royal Society Interface
- Invited Reviewer for Biophysical Journal
- Invited Reviewer for PeerRef