Lacramioara Bintu

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Research Summary

My group studies the basic principles of **gene regulation** in human cells with a focus on: **transcription factors** (see: new method to measure tens of thousands of regulators and combinations in human cells, discovery of hundreds of new human transcriptional activators and repressors and their sequence rules, viral transcriptional activators and repressors), **chromatin** (see: spreading, chromatin structure and memory, oncohistones and memory), and **RNA regulators (**see high-throughput method to identify modular effector domains in RNA binding proteins). We **use high-throughput synthetic biology, single-cell imaging**, and **mathematical modeling**. We build new tools to measure, perturb, and model gene regulation.

Education

2010	**Ph.D. Physics** *Dissertation*: Dynamic Interactions and Molecular Rearrangements Occurring when RNA Polymerase II Meets the Nucleosome	**University of California, Berkeley**
2005	**B.S. Physics, Neuroscience, Mathematics**, *summa cum laude* *Thesis*: Statistical Mechanics of Gene Regulation	**Brandeis University**

Employment History

2017-current	**Associate Professor of Bioengineering, Stanford University, Bio-X and Biophysics member** Direct research on gene regulation and synthetic biology. Teach 2 courses/year.
2017-2025	**Assistant Professor of Bioengineering, Stanford University**
2011-2016	**Postdoctoral Fellow, California Institute of Technology** with ***Prof. Michael Elowitz*** Measured single-cell dynamics of gene expression in response to recruitment of chromatin regulators at a reporter gene, and developed a model of chromatin-mediated gene regulation.
2005-2010	**Graduate Student, University of California, Berkeley** with ***Prof. Carlos Bustamante*** Measured single-molecule transcription of RNA polymerase II through nucleosomes using optical tweezers and AFM, and developed models of transcription and histone transfer. **Graduate Teaching Assistant:** Molecular Biophysics, Physics for Scientists and Engineers
2004&2005 Summers	**Research Assistant, California Institute of Technology** with ***Prof. Rob Phillips*** Modeled how the mechanics of DNA looping between repressor binding sites influences transcriptional repression in the *lac* and *ara* operons.
2004-2005	**Undergraduate Student Researcher, Brandeis University** with ***Prof. Jané Kondev*** Developed a model of gene regulation at the level of transcription using the thermodynamics of polymerase and transcription factors binding to DNA in *Escherichia coli*.
2003	**Research Assistant, Brandeis University** with ***Prof. Karl Canter*** Studied the life cycle of multicellular magnetotactic prokaryotes using time-lapse microscopy.
2003	**Instructor, Teaching Opportunities in Physical Sciences (TOPS**) MIT & Harvard
2002	**Undergraduate Teaching Assistant:** Modern Physics, Brandeis University

Professional Experience

2025-present	Head of Graduate Admission for the Stanford Bioengineering PhD Program
2024	Conference Organizer Co-chair, EMBO Conference: Quantitative biology to molecular mechanisms, Heidelberg, Germany
2024	Conference Organizer Co-chair: Keystone Single-Cell Biology: Tissue Genomics, Technologies and Disease, Vancouver, Canada
2022-present	Co-Founder and Scientific Advisor, Stylus Medicine

2021-present	Co-Chair of Imaging Working Group, 4D Nucleome, Common Fund, NIH
2021-present	Member, Integrating Imaging and Omics Working Group, 4D Nucleome, NIH
2021-present	Member, Genome Technology Development Working Group, NHGRI, NIH
2021	Member of the Planning Committee for the 4D Nucleome NIH Annual Meeting
2019, 2022	Conference Organizer: International Mammalian Synthetic Biology Workshop
2020	Member, Grant Review Panel, National Institutes of Health
2019, 2023-24	Conference Organizer, International Mammalian Synthetic Biology Workshop
2018-2022	Conference Organizer: International Conference on Epigenetics and Bioengineering (EpiBio), co-chair of organizing committee 2018&2022

Grants, Fellowships, and Awards

2018-2028	Maximizing Investigators' Research Award (MIRA) R35, NIGMS, NIH, Single-cell analysis and synthetic control of mammalian chromatin dynamics and gene regulation
2021-2025	R01 Award, NIH, NHGRI, High-throughput development and characterization of compact tools for transcriptional and chromatin perturbations, MPIs: Bintu and Bassik
2020-2025	U01 Award, 4DN Common Fund, NIH, Live-cell multiplex super-resolution imaging of chromatin state transitions, MPIs: Bintu and Boettiger; Co-Is: Greenleaf, Spakowitz, Wysocka
2015-2020	Career Award at the Scientific Interface, Borroughs Wellcome Fund
2011-2014	Jane Coffin Childs Postdoctoral Fellowship
2011-2014	Beckman Institute Fellowship, equipment research grant, California Institute of Technology
2011	Weintraub Graduate Student Award for outstanding achievement, Fred Hutchinson Center
2006	Outstanding Graduate Student Instructor Award, University of California, Berkeley
2005	Doris Brewer Cohen Endowment Award for best senior thesis, Brandeis University
2005	Molly W. and Charles K. Schiff Memorial Award in Science, Brandeis University
2004	Elihu A. Silver Prize for undergraduate research in science, Brandeis University
2001-2005	Wien International Scholarship, Brandeis University

Publications

† Co-corresponding authors. * Equal-contributing first authors. My trainees are indicated in bold face.

1. Wolfsberg E, Paul JS, **Tycko J**, Chen B, Bassik MC, **Bintu L**, Alizadeh AA, Gao XJ. Machine-guided dual-objective protein engineering for deimmunization and therapeutic functions. Cell Systems. 2025 Jun 3.
2. **Thurm AR, Janer Carattini GL, Bintu L.** Human Synthetic Biology and Programmable Gene Regulation Control. Annual Review of Genomics and Human Genetics. 2025 Apr 25;26.
3. Doughty BR*, **Hinks MM***, Schaepe JM*, Marinov GK, **Thurm AR**, **Rios-Martinez C**, Parks BE, Tan Y, Marklund E, Dubocanin D, **Bintu L**†, Greenleaf WJ†. Single-molecule chromatin configurations link transcription factor binding to expression in human cells. *Nature.* Epub Nov 20, 2024
4. **Tycko J*, Van M*,** Aradhana, **DelRosso N,** Yao D, Xu X, **Ludwig C,** Spees K, Liu K, Hess GT, Gu M., **Mukund AX**, **Suzuki PH**, Kamber RA, Qi LS, **Bintu L**†, Bassik MC†. Development of compact transcriptional effectors using high-throughput measurements in diverse contexts. *Nature Biotechnology*, doi: 10.1038/s41587-024-02442-6 Epub Nov 1 2024.
5. **Sinha J, Nickels JF**, **Thurm AR**, **Ludwig CH**, Archibald BN, **Hinks MM, *Wan J***, Fang D, **Bintu L**. The H3.3 K36M oncohistone disrupts the establishment of epigenetic memory through loss of DNA methylation, *Molecular Cell* 84(20):3899-3915, 2024
6. **Mukund AX, Tycko J, Allen SJ**, Robinson SA, Andrews C, **Ludwig CH**, Spees K, Bassik MC, **Bintu L**. “High-throughput functional characterization of combinations of transcriptional activators and repressors.” *Cell Systems*, 14(9):746–763, 2023
7. **Ludwig CH, Thurm AR,** Morgens DW, Yang KJ, **Tycko J,** Bassik MC, Glaunsinger BA, **Bintu L**. “High-Throughput Discovery and Characterization of Viral Transcriptional Effectors in Human Cells,” *Cell Systems*, 14(6):482-500, 2023

8. **DelRosso N, Tycko J, Suzuki P, Andrews C**, Aradhana, **Mukund A, Liongson I, Ludwig C**, Spees K, Fordyce P, Bassik MC, **Bintu L**. Large-scale mapping and mutagenesis of human transcriptional effector domains. *Nature*. Apr;616(7956):365-372, 2023

9. Dekker J, Alber F, Aufmkolk S, Beliveau BJ, Bruneau BG, Belmont AS, **Bintu L**, Boettiger A, Calandrelli R, Disteche CM, Gilbert DM, Gregor T, Hansen AS, Huang B, Huangfu D, Kalhor R, Leslie CS, Li W, Li Y, Ma J, William S. Noble WS, Peter J. Park PJ, Jennifer E. Phillips-Cremins JE, Katherine S. Pollard KS, Rafelski SM, Ren B, Ruan Y, Shav-Tal Y, Shen Y, Shendure K, Shu X, Strambio-De-Castillia C, Vertii A, Zhang H, Zhong S "Spatial and temporal organization of the genome: current state and future aims of the 4D Nucleome Project," *Molecular Cell* 83, 2023

10. Marinov GK, Kim SH, Bagdatli ST, Trevino AE, **Tycko J**, Wu T, **Bintu L**, Bassik MC, He C, Kundaje A, Greenleaf WJ. "Direct profiling of genome-wide dCas9 and Cas9 specificity using ssDNA mapping (CasKAS)," *Genome Biology*. Apr 21;24(1):85, 2023

11. **Hinks M,** Marinov GK, Kundaje A, **Bintu L**, Greenleaf WJ. "Single-Molecule Mapping of Chromatin Accessibility Using NOMe-seq/dSMF." *Methods Mol Biol*. 2611:101-119, 2023

12. Cabera A*, Edelstein HI*, Glykofrydis F*, Love KS*, Palacios S*, **Tycko J***, Zhang M, **Lensch S**, Shields CE, Livingston M, Weiss R, Zhao H, Haynes KA, Morsut L, Chen YY, Khalil AS, Wong WW, Collins JJ, Rosser SJ, Polizzi K, Elowitz MB, Fussenegger M, Hilton IB, Leonard JN, **Bintu L**, Galloway KE, Deans TL. "The sound of silence: Transgene silencing in mammalian cell engineering." *Cell Systems* 13(12): 950-973, 2022.

13. Durrant MG*, Fanton A*, **Tycko J***, **Hinks MM**, Chandrasekaran SS, Perry NT, Schaepe J, Du PP, Lotfy P, Bassik MC†, **Bintu L**†, Bhatt AS†, Hsu PD†. "Systematic discovery of recombinases for efficient integration of large DNA sequences into the human genome*," Nature Biotechnology*, Apr;41(4):488-499, 2023

14. **Lensch S**, **Herschl MH, Ludwig CH**, **Sinha J**, **Hinks MM**, **Mukund A**, **Fujimori T**, **Bintu L**. "Dynamic spreading of chromatin-mediated gene silencing and reactivation between neighboring genes in single cells," *eLife* 11:75115, 2022

15. **Mukund A**, **Bintu L**, "Temporal signaling, population control, and information processing through chromatin-mediated gene regulation," *Journal of Theoretical Biology* 535, 110977, ISSN 0022-5193, 2022

16. **Van MV**, **Fujimori T**, **Bintu L**, "Nanobody-mediated control of gene expression and epigenetic memory," *Nature Communications,* 12(1): 1-12, 2021

17. **Tycko J**, **DelRosso N**, Hess GT, Aradhana, Banerjee A, **Mukund A**, **Van MV**, Ego BK, Yao D, Spees K, **Suzuki P**, Marinov GK, Kundaje A, Bassik MC†, **Bintu L**†, "High-throughput discovery and characterization of human transcriptional effectors," *Cell,* 183(7): 2020-2035.e16, 2020

18. **Tycko J***, Wainberg M*, Marinov GK*, Ursu O, Hess GT, Ego BK, Aradhana, Li A, Truong A, Trevino AE, Spees K, Yao D, Kaplow IM, Greenside PG, Morgens DW, Phanstiel DH, Snyder MP, **Bintu L**, Greenleaf WJ, Kundaje A, Bassik MC, "Mitigation of off-target toxicity in CRISPR-Cas9 screens for essential non-coding elements", *Nature Communications*, 10(1): 1-14, 2019

19. **Ludwig CH**, **Bintu L**, "Mapping chromatin modifications at the single-cell level." *Development*, 146(12): dev170217, 2019

20. **Tycko J*, Van MV*,** Elowitz MB, & **Bintu L**, "Advancing towards a global mammalian gene regulation model through single-cell analysis and synthetic biology*," Current Opinion in Biomedical Engineering*, 4: 174-193, 2017

21. **Bintu L***, Yong J*, Antebi YE, McCue K, Kazuki Y, Uno N, Oshimura M, Elowitz MB, "Dynamics of epigenetic regulation at the single-cell level," *Science*, 351 (6274): 720-724, 2016

22. Dangkulwanich M, Ishibashi T, **Bintu L**, Bustamante C, "Molecular Mechanisms of Transcription through Single-Molecule Experiments," *Chemical reviews*, 114 (6): 3203-23, 2014

23. **Bintu L***, Ishibashi T*, Dangkulwanich M, Wu Y, Lubkowska L, Kashlev M, Bustamante C, Nucleosomal Elements that Control the Topography of the Barrier to Transcription. *Cell,* 151 (4): 738 (2012).

24. Zamft B, **Bintu L**, Ishibashi T, Bustamante C. Nascent RNA Structure Modulates the Transcriptional Dynamics of RNA Polymerases. *Proceedings of the National Academy of Sciences,* 109 (23): 8948-8953, 2012.

25. **<u>Bintu L*</u>**, Kopaczynska M*, Hodges C, Lubkowska L, Kashlev M, Bustamante C. The Elongation Rate of RNA Polymerase Determines the Fate of Transcribed Nucleosomes. *Nature Structural & Molecular Biology,* 18 (12): 1394-1399, 2011.
26. Hodges C*, **<u>Bintu L*</u>**, Lubkowska L, Kashlev M, Bustamante C. Nucleosomal Fluctuations Govern the Transcription Dynamics of RNA Polymerase II. *Science*, 325 (5940): 626, 2009.
27. **<u>Bintu L</u>**, Buchler N, Garcia H, Gerland U, Hwa T, Kondev J, Phillips R. Transcriptional Regulation by the Numbers 1: Models. *Current Opinion in Genetics & Development*, 15(2):116, 2005.
28. **<u>Bintu L</u>**, Buchler N, Garcia H, Gerland U, Hwa T, Kondev J, Kuhlman T, Phillips R. Transcriptional Regulation by the Numbers 2: Applications. *Current Opinion in Genetics & Development*, 15(2):125, 2005.

Preprints

1. **Wan J***, **Thurm AR*, Allen SJ, Ludwig CH, Patel AN, <u>Bintu L</u>**. High-throughput development and characterization of new functional nanobodies for gene regulation and epigenetic control in human cells. BioRxiv. 621523, November 03, 2024. Available from: https://www.biorxiv.org/content/10.1101/2024.11.01.621523v1
2. Valbuena R*, Nigam A*, **Tycko J**, **Suzuki P**, Spees K, Aradhana A, Arana S, Du P, Patel RA, **<u>Bintu L</u>**†, Kundaje A†, Bassik MC†. Prediction and design of transcriptional repressor domains with large-scale mutational scans and deep learning. BioRxiv 614253, September 21, 2024. Available from: https://www.biorxiv.org/content/10.1101/2024.09.21.614253
3. DelRosso N*, Suzuki PH*, Griffith D, Lotthammer JM, Novak B, Kocalar S, Sheth MU, Holehouse AS, Bintu L, Fordyce P**.** High-throughput affinity measurements of direct interactions between activation domains and co-activators. BioRxiv 608698, August 20, 2024. Available from: https://www.biorxiv.org/content/10.1101/2024.08.19.608698
4. **Thurm AR, Finkel Y**, **Andrews C, Cai XS**, Benko C, **<u>Bintu L</u>**. High-throughput discovery of regulatory effector domains in human RNA-binding proteins. BioRxiv. 604317, July 19, 2024. Available from: https://www.biorxiv.org/content/10.1101/2024.07.19.604317
5. **Fujimori T**, **Rios-Martinez C, Thurm AR**, **Hinks MM**, Doughty BR, **Sinha J**, Le D, Hafner A, Greenleaf WJ, Boettiger AN, **<u>Bintu L</u>**. Single-cell chromatin state transitions during epigenetic memory formation, BioRxiv 56061, October 03, 2023 Available from: https://doi.org/10.1101/2023.10.03.56061
6. Katz N, An C, Lee YJ, **Tycko J,** Zhang M, Kang J, **<u>Bintu L</u>**, Bassik MC, Huang WH, Gao XJ. Tunable, self-contained gene dosage control via proteolytic cleavage of CRISPR-Cas systems. BioRxiv 617463, October 09, 2024. Available from: https://www.biorxiv.org/content/10.1101/2024.10.09.617463
7. Vlahos AE, Call CC, Eckman N, Kadaba SE, Guo S, **Thurm AR**, Kang J, Appel EA, **<u>Bintu L</u>**, Gao XJ. A complete suite for compact programming of protein secretion. bioRxiv. 2023 Oct 4:2023-10. Available from: https://www.biorxiv.org/content/10.1101/2023.10.04.560774v2.abstract

Edited Works:

1. **DelRosso N, <u>Bintu L</u>,** Using High-Throughput Measurements to Identify Principles of Transcriptional and Epigenetic Regulators. Book chapter in *Epigenome Editing: Methods and Protocols* (pp. 79-101). New York, NY: Springer US, 2024.

Patents

Patents Issued

Bintu L, Yong J, Elowitz ME. 2016. Fractional Regulation of Transcription; US20160304872A1

Patents under consideration

1. Bhatt AS, Durrant MG, Tycko JC, Hsu PD, Fanton A, Bassik MC, Bintu L. 2021. Serine Recombinases. U.S. Provisional Application No.: 63/275,288
2. Bintu L, Van M, Wan J. 2021. Nanobodies Against Endogenous Chromatin Regulators for Transcriptional and Epigenetic Control in Human Cells. U.S. 2021. Provisional Application No.: 63/242,898

3. Bassik MC, Tycko J, Hess GT, and Bintu L. Compact transcriptional effector domains and combinations for regulating endogenous gene transcription. 2021. U.S. Provisional Application No.: 63/234,096
4. Bassik MC, Tycko J, Hess GT, and Bintu L. Compositions, Systems, And Methods For The Generation, Identification, And Characterization Of Effector Domains For Activating And Silencing Gene Expression. 2020. U.S. Provisional Application No.: 63/074,793

Selected Presentations

Invited Plenary Talks and Distinguished Lectures

1. Keynote Speaker: Systems Biology of Single Cells Conference, Irvine, CA, May 8-9, 2025.
2. Keynote Speaker: American Physical Society Global Physics Summit, Genome Organization Session, “Dissecting human gene regulation principles using single-cell measurements and statistical mechanics”, Anaheim, CA, March 16-21, 2025
3. Keynote Speaker: Integrative Training Symposium, North Carolina State University, “Distilling the rules of transcription factors functions in human cells using high-throughput synthetic biology”, Raleigh NC, February 9, 2024
4. Rising Stars Dahlem Colloquia in Molecular Genetics, Max Planck Institute for Molecular Genetics, , “High-throughput discovery and characterization of human and viral transcriptional regulators,” Berlin, Germany, November 14, 2022
5. Keynote Speaker: University of California, Berkeley, Biophysics Retreat, “High-throughput discovery and systematic sequence characterization of transcriptional activators and repressors in human cells”, Green Mountain Retreat, Santa Cruz, CA, September 30 - October 2, 2022

Invited Conference Presentations

1. EMBL International Conference: Gene regulation: one molecule at a time, Heidelberg, Germany, July 15-18, 2025
2. Gordon Research Conference: Genome Architecture in Cell Fate and Disease, Ventura Beach Marriott, CA, June 15-20, 2025
3. Keystone Symposia on Epigenetics in Development and Disease / Interplay of Chromatin Architecture and Transcription Regulation. Banff, Canada, March 29- April 2, 2025
4. EMBL International Conference: Quantitative biology to molecular mechanisms, “Dynamics and mechanisms of bifunctional transcriptional effectors in human cells,” EMBL Heidelberg, Germany, November 19 – 22, 2024
5. International Epigenetics and Bioengineering Conference (EpiBio2024), “Development of compact transcriptional effectors using high-throughput measurements in diverse contexts,” Amsterdam, Netherlands, October 3-5, 2024
6. Single-Cell Genomics 2024, “Bifunctional Transcriptional Effectors that Switch from Activators to Repressors”, Corinthia, Greece, September 16-18, 2024
7. Gordon Research Conference: Chromatin Structure and Function, “Using Single-Molecule Footprinting and Chromatin Tracing to Understand Gene Regulation and Epigenetic Memory Principles”, Smithfield, RI, July 7-12, 2024
8. 15th International Conference on Genomics and Systems Biology of Human Disease and Aging, “Bifunctional Effectors that Switch from Activators to Repressors: Dynamics and Mechanisms”, Chania, Greece, June 22-26, 2024
9. Advances in Genomic Technology Development Annual Meeting, Farmington, “High-throughput measurements of gene expression and chromatin state changes upon targeted gene activation”, Farmington, CT, June 11-13, 2024
10. Genome Technology Forum organized by the National Human Genome Research Institute (NHGRI) and the Technology Development Coordinating Center (TDCC) at Jackson Laboratory, “Chromatin Structure and Gene Regulation”, Farmington, CT, June 10, 2024
11. Cold Spring Harbor Labs, Systems Biology: Global Regulation of Gene Expression, “Dynamics and mechanisms of bifunctional transcriptional effectors”, Cold Spring Harbor, NY, March 13-16, 2024

12. Winter qBio, “How do human transcription factors work and interface with chromatin?”, Oahu, Hawaii, February 19-23, 2024
13. Biophysical Society Meeting, “Biophysical principles of transcriptional activators and repressors using high-throughput and single-molecule measurements in human cells”, Philadelphia, PA, February 12-13, 2024
14. Keystone Single-Cell Conference, “The Control of Gene Regulation at Single-Cell Resolution,” Vancouver, BC, Canada, January 21-24, 2024
15. 4D Nucleome Consortium NIH Annual Meeting, FISH-OMICS Data Formats and Standards, Imaging Working Group Update, Boston, MA, Dec 9-11, 2023
16. Rules of Protein-DNA Recognition International Conference, Cancun, Mexico, “How do transcriptional activators and repressor domains work: high-throughput and single-cell measurements”, Oct 10-13, 2023
17. The Conceptual Power of Single-cell Biology, Cell Press Symposium, “Single-cell dynamics of gene silencing, epigenetic memory and chromatin structure,”, San Diego, CA, USA, Aug 28-30, 2023
18. Synthetic Biology Gordon Research Conference: Transforming Biology into a Technology to Solve Global Challenges, “The sequence determinants of human transcriptional activators and repressors: high-throughput discovery and systematic perturbations,” Newry, ME, USA, July 16-21, 2023
19. Advances in Genomic Technology Development Annual Meeting, NHGRI-NIH, “High-throughput identification and characterization of human and viral transcriptional activation and repression domains, San Diego, CA, USA, June 6-8, 2023
20. Synthetic Biology: Engineering, Evolution & Design (SEED), “Fundamental components of mammalian synthetic biology circuits: activators, repressors, insulators, terminators,” Los Angeles, CA, USA, May 31-June 1, 2023
21. ELRIG Research and Innovation 2023 – Accelerating Future Drug Discovery, Wellcome Trust Sanger Institute, “Development of compact gene control tools using high-throughput measurements,” Cambridge, UK, March 29-30, 2023
22. EMBO International Conference: Functional Genomics to Systems Biology, EMBL Heidelberg, “High-throughput discovery and systematic sequence characterization of human transcriptional regulators,” Heidelberg, Germany, November 15-18, 2022
23. 5th International Conference on CRISPR Technologies, “Development of compact and potent transcriptional repression and activation tools using high-throughput measurements in different genomic and cell contexts,”, Claremont, CA, USA, October 31-November 2, 2022
24. Advances in Genomic Technology Development Meeting, National Human Genome Research Institute, “New compact tools for transcriptional activation and repression in human cells: systematic development and testing with high-throughput methods,”, Farmington, CT, USA, July 12-14, 2022
25. 14th International Conference on Genomes, Pathways, and Systems Medicine , “The sequence determinants of human transcriptional domains: large-scale discovery and systematic perturbations,” Rhodos, Greece, June 16-21, 2022
26. Learning Meaningful Representations of Life Workshop, Thirty-fifth Conference on Neural Information Processing Systems (NeurIPS), “High-throughput discovery and characterization of human transcriptional repressor and activator domains,”, virtual, December 14, 2021
27. 4D Nucleome Consortium Annual Meeting, NIH Common Fund, “Thoughts and Tips for the Assistant Professor Job Search,” virtual, December 9, 2021
28. International Epigenetics and Bioengineering Conference (EpiBio2021), “High-throughput development of nanobodies for transcriptional and epigenetic control,” virtual, November 4, 2021
29. Cold Spring Harbor Genome Engineering: CRISPR Frontiers, “A high-throughput approach for developing compact tools for transcriptional and chromatin perturbations,” virtual, August 18-21, 2021
30. Epigenetics Consortium of South Australia (EpiCSA), Groundbreaking Epigenetic Discoveries Seminar Series, “Developing compact tools for transcriptional and chromatin perturbations”, virtual, August 15, 2021
31. International Mammalian Synthetic Biology Workshop (mSBW2021), “High-throughput discovery and characterization of human transcriptional repressor and activator domains,” virtual, July 19-21, 2021

32. Cold Spring Harbor Meeting on Cellular Dynamics & Models, “Chromatin-mediated gene control: single-cell and high-throughput measurements,”, virtual, May 20, 2021
33. Riken BDR Symposium, “High-throughput discovery and characterization of human transcriptional effectors,” Japan, virtual, March 1-3, 2021
34. 2020 4DN Phase II Kickoff Meeting, Live-cell multiplex super-resolution imaging of chromatin state transitions, , virtual, organized by NIH, December 2-4, 2020
35. Protein-DNA Interactions: from Biophysics to Cancer Biology, “Controlling and measuring epigenetic regulation dynamics”, Houston, Texas, December 5-6, 2019
36. Current Methods in Cell Biology, “Single-cell imaging and synthetic biology for dissecting epigenetic regulation”, , EMBL Heidelberg, Germany September 8-17, 2019
37. Frontiers in Biophysics - Eleftheria Foundation, “Spreading of epigenetic silencing and activation in single cells”, Paros, Greece, June 10-13, 2019
38. International Epigenetics and Bioengineering Conference (EpiBio 2018), “Dynamic control of multiple genes using chromatin regulators”, , San Francisco, October 4-5, 2018
39. Biology and Mathematics in the Bay Area (BaMBA 12), “The effects of chromatin on the dynamics of gene expression: measurements and models”, Stanford, November 3, 2018
40. American Society for Cell Biology Annual Meeting (ASCB|EMBO 2018), “Spreading of epigenetic silencing and activation in single cells ”, San Diego, December 8-12, 2018
41. Principles of Gene Circuit Design, “Chromatin enables fractional gene regulation and epigenetic memory”, Oaxaca, Mexico, September 10-15, 2017
42. Single Cell Analysis Course, Cold Spring Harbor Laboratory, Invited Lecture, Cold Spring Harbor, NY, July 5th, 2017
43. Physiology Course, Marine Biological Laboratory, Invited Lecture, Woods Whole, MA, July 3, 2017
44. Fourth International Mammalian Synthetic Biology Workshop (mSBW), “Single-cell dynamics of chromatin-mediated gene regulation”, Boston, May 6-7, 2017

Department Seminars

45. California Institute of Technology, Biology and Bioengineering Division Seminar, “Distilling the rules of transcriptional activators and repressors using high-throughput and single-cell methods”, Pasadena, CA October, 22, 2024
46. Stanford Frontiers in Biology Seminar Series, “How do human transcriptional activators and repressors work with chromatin: emerging principles from high-throughput and single-cell measurements”, Stanford, CA, May 8, 2024
47. Stanford SciCube Symposium, Stanford University, January 31, 2024
48. Broad Institute of MIT and Harvard, “Systematic dissection of transcription factors using high-throughput and single-molecule methods in human cells”, Cambridge, MA, Dec 8, 2023
49. MIT Biology and Whitehead Institute, “Distilling the rules of transcriptional activators and repressors using high-throughput and single-cell methods”, Cambridge, MA, Dec 7, 2023
50. Harvard Medical School, Systems Biology Department, “Distilling the rules of transcriptional activators and repressors using high-throughput and single-cell methods”, Boston, MA, Dec 4, 2023
51. Genentech, Translational Genomics Speaker Seminar Series, “High-throughput development of tools for gene regulation,”, San Francisco, CA, USA, September 19, 2023
52. Washington University in Saint Louis, Genetics Department, “The sequence determinants of human transcriptional activators and repressors: high-throughput discovery and systematic perturbations”, St. Louis, MO, USA, May 23, 2023
53. University of California Berkeley, Molecular and Cellular Biology Department Seminar, “Human transcriptional effectors: high-throughput and single-cell measurements”, Berkeley, CA, USA, May 5, 2023
54. Vienna BioCenter Seminar, Vienna BioCenter, “High-throughput discovery and sequence

characterization of human and viral transcriptional regulators," Vienna, Austria, November 19, 2022

55. Broad Institute of MIT and Harvard, Broad Institute Cell Circuits & Epigenomics Seminar Series, "Human transcriptional activators and repressors: high-throughput discovery, protein sequence determinants, and compact tool development," virtual, September 12, 2022
56. Rockefeller University, Rockefeller Anderson Cancer Center Seminar, "The KRAB domains: high-throughput characterization, single-cell dynamics, and tool development," virtual, March 3, 2022
57. University of California Berkeley, Bioengineering Department Seminar, "Compact tools for transcriptional and chromatin perturbations: high-throughput development and single-cell characterization," December 1, 2021
58. Massachusetts Institute of Technology, Biological Engineering Department Virtual Seminar, "Compact tools for transcriptional and chromatin perturbations: high-throughput development and single-cell characterization," October 14, 2021
59. University of California, Davis, Genetics Seminar, "Spreading of silencing and activation upon recruitment of chromatin regulators", November 18, 2019
60. University of Washington, Seattle, "Molecular Engineering Seminar, Controlling, measuring, and modelling epigenetic regulation dynamics", December 3, 2019
61. University of California Santa Cruz, Biomolecular Engineering Department Seminar, "Characterizing epigenetic control tools at the single-cell level", June 7, 2018