Kirk MacKinnon

Post-doctoral Associate

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Center for Genomics and Systems Biology, NYU

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About me

Molecular and computational biologist studying gene regulatory networks using integrated genomic approaches (RNA-seq, DAP-seq, and related datasets). My work focuses on understanding transcriptional regulation while developing practical, reproducible approaches to analyzing complex biological data.

I am particularly interested in training students in applied bioinformatics, emphasizing clear biological interpretation alongside computational skills, and contributing to the development of collaborative, student-centered research and teaching programs.

My training spans end-to-end experimental and computational genomics, from DNA/RNA extraction and sequencing library preparation to high-throughput data analysis and modeling.

Education

2015–2021 Doctorate of Philosophy — UMass Amherst
Molecular & Cellular Biology
- Transcriptional regulation and gene regulatory networks; emphasis on genomic data analysis

2011–2015 Bachelor of Science — UMass Amherst
Biology

Research Experience

2022–Present Postdoctoral Associate — Coruzzi Lab
New York, NY
- Develop and analyze cell-specific gene regulatory networks using RNA-seq and DAP-seq datasets
- Integrate computational and experimental approaches to identify regulatory interactions and network structure
- Design reproducible analysis pipelines for high-throughput genomic data
- Mentor students in computational and biological data analysis

2015–2021 Ph.D. Researcher — Hazen Lab
Amherst, MA
- Investigated transcriptional regulation of growth in Brachypodium distachyon
- Analyzed RNA-seq and time-series datasets to identify regulatory patterns and environmental responses
- Contributed to multiple peer-reviewed publications
- Developed experience in experimental design and data interpretation

2013–2015 Research Assistant — Hazen Lab
Amherst, MA
- Performed time-lapse image analysis of plant growth under varying abiotic conditions
- Assisted in data collection and analysis for ongoing lab projects

Teaching

2020 Bioinformatics Workshop Instructor (Lab-based) — Hazen Lab
Amherst, MA
- Designed and delivered an introductory bioinformatics course for graduate researchers
- Taught foundational skills including Bash, R, and general computational workflows
- Developed structured lessons and assignments to support applied learning
- Mentored participants in applying computational methods to their research projects

2018–2020 Graduate Teaching Assistant – Introductory Biology I (BIO 151)
University of Massachusetts Amherst
Amherst, MA
- Led discussion sections and supported student learning in foundational biology concepts
- Assisted in grading and evaluation of student work
- Facilitated understanding of experimental design and data interpretation
- Mentored undergraduate students in academic and scientific development

Publications

In prep. — Landscape of Transcription Factor Regulatory Harmony in Arabidopsis
Kirk J.-M. MacKinnon et al.

Submitted — Genome-wide transcription factor binding reveals regulatory logic and evolutionary divergence in grasses — Nature Communications
Bahman Khahani, Leo A. Baumgart, Kirk R. Amundson, Ian W. McCahill, Greg A. Gregory, Kirk J.-M. MacKinnon, Xiaocheng Yu, Ritesh Mewalal, Anthony Bortolazzo, Yu Zhang, Madelaine E. Bartlett, John P. Vogel, Ian K. Blaby, Ronan C. O'Malley, Samuel P. Hazen

Submitted — Combinatorial effects of transcription factors functionally revealed by single cell TARGET-seq — Molecular Systems Biology
Amélie Emanuel, Jean-Baptiste Carluer, Will E. Hinckley, Baldwin Dumortier, Samantha Frangos, Kirk MacKinnon, Bruno Guillotin, Tim L. Jeffers, Yitao Long, Manpreet Katari, Dennis Shasha, Angelo Pasquino, Matthew D. Brooks, Stéphanie Pateyron, Myriam Boyer-Clavel, Stéphanie Boireau, Wojciech Szponarski, Hatem Rouached, Sandrine Ruffel, André Mas, Gloria Coruzzi, Bastiaan O. Bargmann, Etienne Delannoy

2024 — Mechanically induced localisation of SECONDARY WALL INTERACTING bZIP is associated with thigmomorphogenic and secondary cell wall gene expression — Quantitative Plant Biology
Joshua H. Coomey, Kirk J.-M. MacKinnon, Ian W. McCahill, Bahman Khahani, Pubudu P. Handakumbura, Gina M. Trabucco, Jessica Mazzola, Nicole A. Leblanc, Rithany Kheam, Miriam Hernandez-Romero, Kerrie Barry, Lifeng Liu, Ji E. Lee, John P. Vogel, Ronan C. O'Malley, James J. Chambers, Samuel P. Hazen
- https://doi.org/10.1017/qpb.2024.5

2021 — Mechanically induced localization of SECONDARY WALL INTERACTING bZIP is associated with thigmomorphogenic and secondary cell wall gene expression
Joshua H. Coomey, Kirk J.-M. MacKinnon, Ian W. McCahill, Bahman Khahani, Pubudu P. Handakumbura, Gina M. Trabucco, Jessica Mazzola, Nicole A. Leblanc, Rithany Kheam, Miriam Hernandez-Romero, Kerrie Barry, Lifeng Liu, Ji E. Lee, John P. Vogel, Ronan C. O'Malley, James J. Chambers, Samuel P. Hazen
- https://doi.org/10.1101/2021.02.03.429573

2020 — Changes in ambient temperature are the prevailing cue in determining Brachypodium distachyon diurnal gene regulation — New Phytologist
Kirk J-M. MacKinnon, Benjamin J. Cole, Chang Yu, Joshua H. Coomey, Nolan T. Hartwick, Marie-Stanislas Remigereau, Tomás Duffy, Todd P. Michael, Steve A. Kay, Samuel P. Hazen
- https://doi.org/10.1111/nph.16507

2018 — SECONDARY WALL ASSOCIATED MYB1 is a positive regulator of secondary cell wall thickening in Brachypodium distachyon and is not found in the Brassicaceae — The Plant Journal
Pubudu P. Handakumbura, Kathryn Brow, Ian P. Whitney, Kangmei Zhao, Karen A. Sanguinet, Scott J. Lee, Jennifer Olins, Sandra P. Romero-Gamboa, Michael J. Harrington, Carlisle J. Bascom, Kirk J-M. MacKinnon, Michael T. Veling, Lifeng Liu, Ji E. Lee, John P. Vogel, Ronan C. O'Malley, Magdalena Bezanilla, Laura E. Bartley, Samuel P. Hazen
- https://doi.org/10.1111/tpj.14047

2018 — Secondary Wall Regulating NACs Differentially Bind at the Promoter at a CELLULOSE SYNTHASE A4 Cis-eQTL — Frontiers in Plant Science
Jennifer R. Olins, Li Lin, Scott J. Lee, Gina M. Trabucco, Kirk J.-M. MacKinnon, Samuel P. Hazen
- https://doi.org/10.3389/fpls.2018.01895

2014 — Daily Changes in Temperature, Not the Circadian Clock, Regulate Growth Rate in Brachypodium distachyon — PLoS ONE
Dominick A. Matos, Benjamin J. Cole, Ian P. Whitney, Kirk J.-M. MacKinnon, Steve A. Kay, Samuel P. Hazen
- https://doi.org/10.1371/journal.pone.0100072

Awards

2021 Howard E. and Margaret E. Barr Bigelow Memorial Scholarship.
2021 Lotta M. Crabtree Fellowship in Production Agriculture.
2020 Center for Agriculture, Food and the Environment Fellowship.
2019 Lotta M. Crabtree Fellowship in Production Agriculture.
2018 Center for Agriculture, Food and the Environment Fellowship.
2015 Outstanding Biology Research Award.

Conference Presentations

Talks

2018 Exploring Diurnal Rhythmic Gene Expression in Brachypodium distachyon. ASPB Northeastern Section Meeting.

Posters

2019 Changes in ambient temperature are the prevailing cue in determining Brachypodium distachyon diurnal gene regulation. Annual Symposium in Plant Biology.
2019 Exploring Diurnal Rhythmic Gene Expression in Brachypodium distachyon. PAG XXVII.
2014 Daily Changes in Temperature, Not the Circadian Clock, Regulate Growth Rate in Brachypodium distachyon. UMass Undergraduate Research Symposium.

Mentoring & Outreach

Train and mentor undergraduate assistants in the Hazen Lab

2017–2021 Undergraduate Research Mentorship — Hazen Lab
University of Massachusetts Amherst

- Mentored undergraduate students in plant biology research projects
- Provided guidance in experimental design and data analysis
- Supported development of scientific reasoning and communication skills
- Students mentored: Sanyam Shilpakar; Chang Yu; Alden Nichols; Jacob Scott; Crysta Daniels

Creation of online tools for data exploration

2018–Present Development of Online Genomic Data Exploration Tools — Hazen Lab; Coruzzi Lab

- Developed interactive Shiny applications for exploration of RNA-seq datasets
- Designed tools to make complex genomic data accessible to researchers
- Built an online platform for exploring transcription factor regulatory harmony data
- Applications available at: kirkmackinnon.com