

## KAIA MATTIOLI

Postdoctoral Fellow  
NHGRI K99/R00 Awardee

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## EDUCATION

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- Postdoctoral Fellow • Brigham & Women's Hospital • Boston, MA** Nov. 2019 – present  
*Faculty mentor:* Prof. Martha Bulyk, Department of Medicine, Division of Genetics  
*Projects:* Methods for systematic assessment of the functions and DNA-binding patterns of transcription factor isoforms
- Ph.D. in Biomedical Sciences • Harvard University • Cambridge, MA** Aug. 2014 – Nov. 2019  
*Advisor:* Prof. John Rinn, Department of Stem Cell & Regenerative Biology  
*Co-advisors:* Prof. Frank Slack, Department of Pathology at Beth Israel Deaconess Medical Center  
 Dr. Marta Melé, Life Sciences Department at Barcelona Supercomputing Center  
*Dissertation:* High-throughput characterization of lncRNA regulation, evolution, and function
- B.S. cum laude • Stanford University • Stanford, CA** Sept. 2007 – June 2011  
*Major:* Biological Sciences

## EMPLOYMENT

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- Postdoctoral Researcher • Brigham and Women's Hospital • Boston, MA** Nov. 2019 – present
- Interested in understanding how the complexities of gene regulatory processes may be altered across species, individuals, and in diseases—particularly cancer—at both the *cis* level (via perturbations in regulatory elements) and the *trans* level (via perturbations in TFs and co-factors).
  - Developing methods to assess the functions of transcription factor isoforms in breast cancer in high-throughput as a 50/50 computational/experimental postdoc in Prof. Martha Bulyk's lab.
  - July 2020-January 2022 funded via a Harvard Medical School NIH T32 grant (selected two independent times, each after a competitive internal search).
  - January 2022-July 2023 funded via an NHGRI F32 award.
  - February 2024-February 2026 funded via an NHGRI K99/R00 award.
- Ph.D. Candidate • Harvard University • Cambridge, MA** Aug. 2014 – Nov. 2019
- Designed and analyzed high-throughput experimental screens to study the regulation, evolution, and function of lncRNAs as a 100% computational student in Prof. John Rinn's lab.
  - After Prof. Rinn moved institutions in 2017 and I remained at Harvard, additionally advised by Dr. Marta Melé (previously at Harvard, now at Barcelona Supercomputing Center) and Prof. Frank Slack (Beth Israel Deaconess Medical Center and Harvard Medical School).
  - Work included: analyzing functional genomics datasets (including RNA-seq, ChIP-seq, DNase-seq), mapping transcription factor motifs in DNA sequences, designing massively parallel reporter assay (MPRA) libraries and analyzing MPRA experiment sequencing results, designing CRISPR interference/activation (CRISPRi/a) libraries and analyzing CRISPR screen sequencing results, collaborating closely with experimentalists performing screen(s).
- Strategic Operations Analyst • Google, Inc. • Mountain View, CA** May 2013 – July 2014
- Business analyst for the wider Product Quality Operations (PQO) team, which works to ensure the safety of Google users across a variety of products.
  - Helped to set and track core business metrics & targets and provide actionable business intelligence to leadership.
  - Gained substantial experience with SQL databases & data visualization as well as strategic presentations
  - Performed a variety of independent analysis projects, including analyses of the effectiveness of certain Google advertising policies, the efficiency of team staffing, and promotion rates.
- Ads Quality Operations Associate • Google, Inc. • Mountain View, CA** July 2011 – May 2013
- Operations specialist tasked with ensuring the safety of Google AdWords users and the compliance of AdWords customers.
  - Worked with teams across the globe and interfaced with software engineers, sales, and legal stakeholders.
  - Promoted after demonstrating substantial independence and project management, presentation, and analysis skills.
- Research Assistant • Stanford University • Palo Alto, CA** Sep. 2010 – June 2011

- Worked under Prof. Ingmar Riedel-Kruse (now at University of Arizona) to study the relationship between perturbations in the Delta-Notch pathway and zebrafish ionocyte differentiation.
- Completed an undergraduate honors thesis titled "Quantitative gene perturbation and mathematical modeling to understand tissue patterning dynamics in zebrafish embryos."
- Work included zebrafish handling and mating, treating embryos with chemical inhibitors, genotyping, gel electrophoresis, and microscopy.

**Engineering Intern • Cobalt Biofuels •** Mountain View, CA June 2010 – June 2011

- Worked closely with members of the engineering, bioprocessing, and microbiology teams to make the production of bio-butanol more efficient.
- After a summer internship in college, asked to stay on part-time during the school year by senior executives after demonstrating efficient and effective problem-solving skills.

**Research Assistant • Stanford Hopkins Marine Station •** Pacific Grove, CA June 2009 – Sep. 2009

- Worked under Prof. George Somero to study the effect of temperature variation on gene expression within two species of mussels (genus *Mytilus*).
- Work included mussel dissections, gel electrophoresis, and colorimetric enzyme assays.

#### FUNDING AND FELLOWSHIPS

**Transition to Independence Parent K99/R00 Award • NIH NHGRI •** 1K99HG13345-01 Feb 2024 – Feb 2026

Project Title: Functional genomics approaches to decode the roles of transcription factor isoforms

**Ruth L. Kirschstein F32 Postdoctoral Fellowship Award • NIH NHGRI •** 1F32HG012318-01 Jan 2022 – June 2023

Project Title: Decoding the role of transcription factor isoforms

**Ruth L. Kirschstein T32 Training Grant in Genetics Awardee • NIH NIGMS •** T32-GM007748-42 July 2020 – Jan 2022

*selected after a competitive internal search of HMS-affiliated postdocs awarded independently 2 years in a row (2020 and 2021)*

**XSEDE Grant • National Science Foundation •** MCB170112 Aug. 2017 – Aug. 2018

*awarded \$1,091 of compute time on NSF servers*

**Graduate Research Fellowship (GRFP) • National Science Foundation •** DGE1144152 July 2016 – July 2019

#### PUBLICATIONS AND PREPRINTS (IN REVERSE CHRONOLOGICAL ORDER)

Oliveros W, Delfosse K, Lato DF, Kiriakopoulos K, Mokhtaridoost M, Said A, McMurray BJ, Browning JW, **Mattioli K**, Meng G, Ellis J, Mital S, Melé M, Maass PG. "Systematic characterization of regulatory variants of blood pressure genes." **Cell Genomics**; May 2023.

- Open Access Article: <https://doi.org/10.1016/j.xgen.2023.100330>

Schade AE, Kuzmickas R, Rodriguez CL, **Mattioli K**, Enos M, Gardner A, Cichowski K. "Combating castration-resistant prostate cancer by co-targeting the epigenetic regulators EZH2 and HDAC." **PLoS Biology**; April 2023.

- Open Access Article: <https://doi.org/10.1371/journal.pbio.3002038>

Lesurf R, Said A, Akinrinade O, Breckpot J, Delfosse K, Liu T, Yao R, McKenna F, Noche RR, Oliveros W, **Mattioli K**, Miron A, Yang Q, Meng G, Chan Seng Yue M, Sung WWL, Thiruvahindrapuram B, Genomics England Research Consortium, Loughheed J, Oechslein E, Bergin L, Smythe J, Mondal T, Melé M, Maass PG, Ellis J, Scherer SW, Mital S. "Whole genome sequencing delineates regulatory and novel genic variants in childhood cardiomyopathy." **npj Genomic Medicine**; March 2022.

- Open Access article: <https://www.nature.com/articles/s41525-022-00288-y>

Haswell JR\*, **Mattioli K\***, Gerhardinger C, Foster DJ, Fernandez PP, Maass PG, Rinn JL, Slack FJ. "Genome-wide CRISPR interference screen identifies lncRNA loci required for pluripotency and differentiation." **PLoS ONE**; November 2021.

(\* = equal contribution).

- Open Access article: <https://doi.org/10.1371/journal.pone.0252848>

**Mattioli K**, Gerhardinger C, Andergassen D, Maass PG, Rinn JL, Melé M. "Cis and trans effects differentially contribute to the evolution of promoters and enhancers." **Genome Biology**; August 2020.

- Open Access article: <https://genomebiology.biomedcentral.com/articles/10.1186/s13059-020-02110-3>

Bourges C, Groff AF, Burren OS, Gerhardinger C, **Mattioli K**, Hu T, Anand T, Epping MW, Smith KGC, Rinn JL, Lee JC. "Resolving mechanisms of immune-mediated disease in primary CD4 T cells." **EMBO Molecular Medicine**; April 2020.

- Open Access article: <https://doi.org/10.15252/emmm.202012112>

**Mattioli K**, Volders PJ, Gerhardinger C, Lee JC, Maass PG, Melé M, Rinn JL. "High-throughput functional analysis of lncRNA core promoters elucidates rules governing tissue-specificity." *Genome Research*; March 2019.

- Open Access article: <https://genome.cshlp.org/content/29/3/344>

Melé M, **Mattioli K**, Mallard W, Shechner DM, Gerhardinger C, Rinn JL. "Chromatin environment, transcriptional regulation, and splicing distinguish lincRNAs and mRNAs." *Genome Research*; January 2017.

- Open Access article: <https://genome.cshlp.org/content/27/1/27>

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## PRESENTATIONS

### Invited Talks

- "Decoding the effects of alternative isoforms on the transcriptome at single-cell resolution." NHGRI Advances in Genomic Technologies Annual Meeting, Jackson Laboratories, CT. *July 2022*.
- "Decoding the role of transcription factor isoforms in breast cancer." University of Utah Rising Stars in Genetics and Genomics Symposium, Salt Lake City, UT. *May 2022*.
- "Long-read RNA-sequencing of human breast cancer cell lines reveals novel cancer-specific transcription factor isoforms." NCI Cancer Systems Biology Consortium Annual Junior Investigator Meeting, virtual conference. *August 2021. (virtual)*
- "High-throughput characterization of lncRNA regulation, evolution, and function." Severo Ochoa Invited Research Seminar, Barcelona, Spain. *November 2019*.
- "High-throughput analysis of lncRNA core promoters elucidates rules governing tissue-specificity." Gene Expression and RNA Series (GEARS) Talk, Cambridge, MA. *April 2019*.

### Invited Outreach

- Introduction and moderation of the "Analyses of genome structure and function" session and panel. NHGRI Advances in Genomic Technologies Outreach Meeting, virtual event. *July 2022*.

### Contributed Talks

- "Widespread variation in molecular interactions and regulatory properties among transcription factor isoforms." Genetics Research in Progress Departmental Seminar, Brigham and Women's Hospital Division of Genetics / Department of Medicine, Boston, MA. *October 2023. (virtual)*
- "Decoding the role of transcription factor isoforms in breast cancer." Genetics Research in Progress Departmental Seminar, Brigham and Women's Hospital Division of Genetics / Department of Medicine, Boston, MA. *May 2022. (virtual)*
- "Rewiring of gene regulatory networks by transcription factor isoforms." co-presented with Dr. Luke Lambourne. Cancer Biology Departmental Seminar, Dana Farber Cancer Institute, Boston, MA. *November 2021. (virtual)*
- "Decoding the role of transcription factor isoforms in breast cancer." Genetics Research in Progress Departmental Seminar, Brigham and Women's Hospital Division of Genetics / Department of Medicine, Boston, MA. *May 2021. (virtual)*
- "High-throughput analysis of gene expression evolution." Departmental Seminar, Barcelona Supercomputing Center Life Sciences Department, Barcelona, Spain. *March 2019*.
- "High-throughput analysis of lncRNA core promoters elucidates rules governing tissue-specificity." Biological & Biomedical Sciences Ph.D. Program Annual Retreat, Provincetown, MA. *September 2018*.

### Poster Presentations

- "Multi-dimensional rewiring of molecular interaction networks by transcription factor isoforms in differentiation and breast cancer." NCI Cancer Systems Biology Consortium Annual Meeting, Denver, CO. *March 2023*.
- "Long-read RNA-sequencing of human breast cancer cell lines reveals novel cancer-specific transcription factor isoforms." NCI Cancer Systems Biology Consortium Annual Meeting, virtual conference. *September 2021. (virtual)*
- "Using massively parallel reporter assays to dissect the tissue-specificity of long non-coding RNAs." ASBMB Conference on Transcriptional Regulation, Snowbird, UT. *October 2018*.
- "Using massively parallel reporter assays to dissect the tissue-specificity of long non-coding RNAs." Keystone Conference on Non-Coding RNAs, Keystone, CO. *February 2018*.
- "Uncovering the functional implications of the transcriptional regulation of long non-coding RNAs." Gordon Research Conference on Post-Transcriptional Gene Regulation, Stowe, VT. *July 2016*.
- "Charting the landscape of DNA sequence and chromatin structure at ultraconserved elements." Harvard Epigenetics Symposium, Boston, MA. *December 2015*.

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## TEACHING EXPERIENCE

**Teaching Assistant • Harvard University • Cambridge, MA**  
 Course: Bootcamp in Quantitative Methods (NEUROBIO 306QC)

Aug. 2017 & Aug. 2018

- Assisted Professors Michael Springer & Rick Born in teaching a MATLAB programming course (2 week intensive bootcamp) to first year Ph.D. students.
- Provided assistance to students during in class coding exercises, graded assignments, and held office hours.
- No student evaluations available for this course.

**Teaching Assistant • Harvard University • Cambridge, MA**

Sept. 2016 – Dec. 2016

*Course:* Biological Data Analysis (MCB 112)

- Assisted Professor Sean Eddy in teaching Python and biological data analysis methods in advanced semester-long course intended for upper level undergraduates and graduate students.
- Attended lectures, graded problem sets & provided code answer keys, and held weekly office hours.
- Student evaluations (Harvard Q-score): 5/5.

**Teaching Assistant • Harvard Medical School • Boston, MA**

Sept. 2015 – Dec. 2015

*Course:* Principles of Molecular Biology (BCMP 200)

- Assisted Professor Joe Loparo in teaching molecular biology survey course intended for first year Ph.D. students.
- Attended lectures, held weekly sections, and graded problem sets & chalk talks.
- Student evaluations (Harvard Q-score): 5/5.

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**MENTORSHIP**

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**Brent Carroll • Research Technician**

July 2022 – present

*Project:* analyzing the role of alternative isoforms on the transcriptome at single-cell resolution using a variety of experimental techniques, including mammalian cell culture, flow cytometry, RT-qPCR, and single-cell RNA-seq as a technician in the Bulyk Lab; currently applying to PhD programs**Octavia Huang • Masters Student**

May 2022 – present

*Project:* investigating differences in 5' and 3' untranslated regions (e.g. RNA-binding protein motifs) across breast cancer cell lines using PacBio long-read RNA-seq data; for Master's Thesis in Biostatistics at Harvard T.H. Chan School of Public Health  
*Outcomes:* currently a PhD student**Shay Iyer • Undergraduate Student**

2021 Summer

*Project:* worked on analyzing differences in protein domains among transcription factor isoforms using long read RNA-seq data, as part of the virtual-only 2021 Harvard Summer Honors Undergraduate Research Program (SHURP)  
*Outcomes:* oral presentation at SHURP end-of-summer programming and Leadership Alliance National Symposium (LANS)**Anisa Prasad • Undergraduate Student**

Aug. 2020 – present

*Project:* currently analyzing differences in DNA binding between alternative isoforms of transcription factors, as assessed via protein-binding microarrays, and performing literature review of assessed TFs, as an undergraduate at Harvard College  
*Outcomes:* presented at Bulyk Lab meeting, awarded a Harvard Program for Research in Science and Engineering (PRISE) funded summer research position in the lab in 2022; currently in medical school**Violet Kimble • Undergraduate**

2020 Summer

*Project:* worked on analyzing differences in DNA binding between alternative isoforms of transcription factors, as assessed via protein-binding microarrays, as part of the virtual-only 2020 Harvard Summer Honors Undergraduate Research Program (SHURP)  
*Outcomes:* oral presentations at Leadership Alliance National Symposium (LANS) conference and SHURP end-of-summer programming, poster presentation at Society for Advancement of Chicanos/Hispanics and Native Americans in Science (SACNAS) Conference, for which she was awarded a Student Presentation Award; currently a PhD student

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**SELECTED AWARDS & HONORS**

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- Transition to Independence K99/R00 (awardee), 2024
- University of Utah "Rising Stars in Genetics and Genomics", 2022
- Ruth L. Kirschstein F32 Postdoctoral Fellow (awardee), 2021
- NCI Cancer Systems Biology Consortium Junior Investigator Podium Presentation Award (awardee), 2021
- Ruth L. Kirschstein T32 Postdoctoral Fellow (awardee x2), 2020, 2021
- Severo Ochoa Mobility Support Grant from Barcelona Supercomputing Center (awardee), 2019
- Harvard Data Science Postdoctoral Fellowship (finalist), 2018
- Harvard Distinction in Teaching Award (awardee), 2017
- National Science Foundation Graduate Research Fellow (awardee), 2016
- National Merit Scholar (awardee), 2007
- National AP Scholar (awardee), 2007

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**SERVICE & OUTREACH**

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**Mentor • Harvard Graduate Women in Science & Engineering • Cambridge, MA**

Sep. 2020 – 2023

- Serving as a mentor to a group of 3 first year graduate student women at Harvard, with whom I meet once every 6 weeks.
- Participated as a mentor for academic years of 2020, 2021, and 2022.

- Content Consultant • Oklahoma Science Project • Cambridge, MA** Feb. 2019 – May 2019
- Provided guidance regarding computational biology lesson content geared towards high schoolers residing in Oklahoma.
- Volunteer Tutor • Cambridge Rindge & Latin High School • Cambridge, MA** Jan. 2017 – May 2017
- Tutored 2-3 high school students in math, chemistry, and English once a week.
- Exec. Board • Harvard Graduate Women in Science & Engineering • Cambridge, MA** Jan. 2015 – Jan. 2018
- Elected to the executive board as Communications Chair during my first year of graduate school. Ran the organization's email accounts, organized professional & social events, and performed social media outreach.
  - Passionate about increasing gender parity in STEM & academia and making these spaces more inclusive for minoritized individuals.
- Volunteer Mentor • Pathfinders' Digital Literacy Project • Boston, MA** Sept. 2015 – Dec. 2015
- Taught a local 6th grade student Javascript as part of an opt-in school program; also provided career/school mentorship and goal discussions.

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PEER REVIEWS PERFORMED

**Solo Reviews**

- *PLoS Computational Biology*, 2023.
- *Nucleic Acids Research*, 2023.
- *Cell Systems*, 2022.
- *BMC Genomics*, 2021.
- *Cellular and Molecular Neurobiology*, 2020.

**Co-Reviews (with an advisor)**

- *Science*, 2021.
- *Genome Biology*, 2019.