

James LaFemina

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RESEARCH SUMMARY

Third-year PhD student in Biomolecular Engineering & Bioinformatics at UC Santa Cruz, seeking a research home for the final phase of my graduate training. My graduate work spans two labs and two systems: chromatin biochemistry in the Boeger Lab, where I studied how H3K56 acetylation regulates nucleosome dynamics, genome stability, and aneuploidy in budding yeast using reverse genetics, single-molecule chromatin analysis, and quantitative modeling; and iPSC-derived midbrain organoid electrophysiology in the Sharf Lab at the Genomics Institute, where I built computational pipelines for high-density multielectrode array recordings, developed neurotoxin dose-response protocols for Parkinson's disease modeling, and worked across wet lab and computational domains. The common thread: how multiple layers of governance produce higher-order biological function, i.e. chromatin modifications that stabilize gene expression programs, and neural circuits that generate coherent network behavior. I came to graduate school after a career in business development, because research is my vehicle for making a meaningful contribution to society.

EDUCATION

Ph.D. Student, Biomolecular Engineering & Bioinformatics	2023 – Present
University of California, Santa Cruz	Santa Cruz, CA
B.S. Biochemistry & Molecular Biology, Highest Honors in the Major	2023
University of California, Santa Cruz	Santa Cruz, CA

RESEARCH EXPERIENCE

Genomics Institute (Sharf Lab), Department of Biomolecular Engineering

University of California, Santa Cruz

Sept 2024 – Apr 2026

Interdisciplinary investigation to decode how human brain circuits emerge, interact, and transmit information to give rise to the hierarchy of emergent functions known as the human brain. The core model consisted of stem-cell derived replicas of human brain regions, HD electrophysiology, and computational techniques to capture circuit-level activity at single-neuron resolution.

Graduate Student Researcher

Sept 2024 – Apr 2026

Research focused on how neurons collectively transform dopaminergic signals into organized network activity, with the goal of better understanding the early drivers of neurodegeneration and the computational basis for learning and attention.

Selected achievements:

- Optimized midbrain organoid differentiation protocols (including neurotoxic lesioning with 6-OHDA and rotenone) to develop late-stage Parkinson's disease in vitro models.
- Developed and executed immunohistochemistry workflows to visualize and quantify dopaminergic neuron depletion in organoids.
- Performed high-density microelectrode array (HD-MEA) experiments on midbrain organoids and fused midbrain-thalamic organoids (assembloids) using Maxwell MaxOne/MaxTwo platforms.

- Constructed a custom Python data analysis pipeline on the National Research Platform Kubernetes cluster, in collaboration with TJ van der Molen (computational mentor): adaptive RMS-based burst detection algorithms, hierarchical caching, S3-based data management, and statistical methodology including linear mixed-effects models for hierarchical experimental designs.
- Adapted the protosequences framework (van der Molen et al., Nature Neuroscience 2025), under the mentorship of TJ van der Molen, for midbrain organoid network analysis, characterizing backbone unit fragmentation under chemical neurotoxin lesioning.
- Collaborated with fabrication, electrophysiology, and computational teams within the Braingeneers consortium to iteratively refine experimental design, data-analysis approaches, and interpretation of results.
- Developed detailed mechanistic companion guides for human midbrain, thalamic, and cortical organoid protocols, integrating cell biology rationale with literature citations.

Boeger Lab, Department of Molecular, Cell, and Developmental Biology

University of California, Santa Cruz

June 2023 – Sept 2024

The Boeger Lab investigates how stochastic transcriptional bursts and ATP-dependent chromatin remodeling together shape gene regulation specificity. The core approach uses theoretical modeling, yeast genetics, and single-molecule analyses to reveal how dynamic chromatin states resolve molecular noise into precise cellular outcomes.

Graduate Student Researcher

June 2023 – Sept 2024

Research focused on how disrupted histone modification and nucleosome dynamics destabilize chromatin architecture and lead to chromosome abnormalities that promote disease states. My approach used reverse genetics, chromatin biochemistry, quantitative single-cell analysis, and statistical modeling to dissect the relationship between nucleosome-level modifications and large-scale genomic instability.

Selected achievements:

- Designed experiments to test whether improper H3K56 acetylation induces re-replication rather than chromosomal missegregation as the primary driver of aneuploidy, supporting the Memory Hypothesis of replication control.
- Applied mutant yeast strains mimicking constitutive H3K56 hypo- and hyperacetylation to test their impact on genome stability.
- Employed a fluorescent reporter system to infer chromosomal copy number variations via flow cytometry, enabling real-time tracking of aneuploidy in single cells.
- Adapted and modernized the Luria-Delbrück fluctuation test to quantify mutation rates under different acetylation states.
- Applied topological assays using DNA supercoiling and topoisomerases to quantify nucleosome occupancy under various genetic perturbations.
- Performed MNase digestion and nanoNOME (single-molecule chromatin accessibility and methylation sequencing on Oxford Nanopore) to analyze chromatin structure and accessibility at base resolution.
- Applied inducible anchor-away systems to acutely deplete key regulatory proteins (e.g., TBP) and assess nucleosome dynamics in real time.

Undergraduate Researcher

Mar 2023 – June 2023

Senior Thesis: ASF1-Mediated Histone H3K56 Regulation in Yeast Chromatin Stability

Advisor: Professor Hinrich Boeger

TECHNICAL SKILLS

Chromatin biology and biochemistry: Yeast genetics and strain construction, reverse genetics, MNase digestion, single-molecule chromatin accessibility sequencing (nanoNOME / Oxford Nanopore), DNA topology assays, anchor-away depletion systems, fluorescent reporter design.

Stem cell and organoid biology: iPSC culture and maintenance, midbrain/thalamic/cortical organoid differentiation, assembloid generation, neurotoxin lesioning (6-OHDA, rotenone), immunohistochemistry, confocal microscopy, dopamine ELISA.

Electrophysiology and neural systems: High-density multielectrode array recording (Maxwell MaxOne, MaxTwo), spike sorting (Kilosort2), burst detection and characterization, network-level activity analysis, backbone unit and protosequence analysis.

Computational and statistical methods: Python programming, pipeline development on Kubernetes (National Research Platform), S3-based data management, hierarchical caching architectures, linear mixed-effects models, hidden Markov models, PCA / UMAP / t-SNE, permutation testing, RNA-seq differential expression analysis, statistical genomics methodology.

Sequencing-based methods: Bulk RNA-seq (Plasmidsaurus 3' end counting submission workflow), single-molecule nanopore sequencing, ChIP-seq analytical methodology, RNA extraction (Maxwell RSC instrument).

Structural biology foundation: Completed Caltech cryo-electron microscopy curriculum (Grant Jensen) as part of undergraduate quantum mechanics and instrumentation coursework.

RELEVANT GRADUATE COURSEWORK

Bioinformatics & Computational Biology: Computational Genomics (PCA/NMF, permutation testing, HMM-based methods, Wright-Fisher and coalescent simulations), Statistical Genomics, RNA-seq Differential Expression Analysis, Algorithms for Bioinformatics.

Biomolecular Engineering: Advanced Biochemistry, Eukaryotic Gene Expression, Quantum Mechanics and Instrumentation (including Caltech cryo-EM curriculum), Bioethics, Dissertation Proposal Development (BME201).

TEACHING AND MENTORSHIP

Teaching Assistant, University of California, Santa Cruz

- Biochemistry III (Spring 2023, Spring 2024)
- Eukaryotic Molecular Biology (Winter 2024)

Undergraduate Research Mentorship

- Mentored six undergraduate researchers at the bench in the Boeger Lab, training them in yeast genetics, chromatin biochemistry, and reverse-genetics experimental design.
- Mentored undergraduate students through MEA data analysis (BME Lab 6) and neural clustering projects in the Sharf Lab.

AWARDS AND HONORS

- Highest Honors in the Major, Biochemistry & Molecular Biology, UC Santa Cruz (2023)

• PRIOR PROFESSIONAL EXPERIENCE

Prior to returning to academia in 2019, I built a 20-year career in business development, sales leadership, and executive consulting, working with Fortune 500 finance and marketing teams. I left this career because the desire to tackle more pressing problems for humanity became all-consuming.

Sales & Leadership Consultant, Experience to Lead / The Conference Board *Aug 2014 – Sept 2018*

New York City Metropolitan Area

- Led enterprise sales of experiential leadership development programs delivered at NASA, US Olympic Training Center, and other unique locations, targeting director-level and above intact leadership teams and high-potential cohorts at Fortune 500 companies.
- Developed a scalable, repeatable revenue generation process around 3-day experiential programs designed to address pressing organizational challenges and promote adaptive team leadership.

Independent Contractor, Business Development & Sales *May 2013 – Aug 2016*

New York City Metropolitan Area

- Built and executed strategic business development initiatives for emerging technology firms transitioning from venture funding to durable revenue generation.

Consultant, Analytics Sales & Product Development, American Express *Apr 2010 – May 2013*

- Product development, strategic positioning, and sales of a marketing analytics product for mid-sized AMEX businesses, interfacing directly with portfolio accounts to inform product innovation, marketing, and business development.

Business Development Manager, Experian Hitwise *Oct 2006 – Jan 2010*

- Online competitive intelligence and marketing analytics. Secured six-figure deals with Fortune 500 marketing executives.