CURRICULUM VITAE

Name: Gavin Schlissel
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ACADEMIC APPOINTMENTS

Assistant Professor (2026 – present)
Department of Chemical & Systems Biology
Stanford School of Medicine

Postdoctoral Researcher (2019 – 2025)
NIH K99 Postdoctoral Fellow (2023 – present)
Jane Coffin Childs Postdoctoral Fellow (2020-2023)
Whitehead Institute for Biomedical Research
Supervisor: Pulin Li

Graduate student researcher (2013 – 2019)
Graduate student instructor (2014 – 2016)
University of California, Berkeley
Supervisor: Jasper Rine

Undergraduate student researcher (2011-2013)
Princeton University
Supervisor: Leonid Kruglyak

TRAINING

Postdoctoral
Advisor – Pulin Li
Whitehead Institute for Biomedical Research
Funding – NIH K99 Pathway to Independence Award
Jane Coffin Childs Postdoctoral Fellowship
Research – Single-molecule understanding of Hedgehog diffusion

Graduate:
Ph.D. (Molecular Biology), May 2019
Designated emphasis in computational and genomic biology
University of California, Berkeley
Thesis: *Nucleosomes can transmit epigenetic memory*
August 2013 - September 2019
Thesis committee–
Jasper Rine, Chair
Barbara Meyer
Nick Ingolia
Oskar Hallatschek

Undergraduate:
Bachelor of Arts, 2013
Princeton University
Major in Molecular Biology

Thesis: *Gene level dissection of a complex trait*
Thesis advisor–Leonid Kruglyak

FINANCIAL SUPPORT

NIGMS K99/R00 Transition to Independence Award
$947,000 (2023-2028)
Jane Coffin Childs Fund Postdoctoral Fellow
$179,000 (2020-2023)

HONORS AND AWARDS

Postdoctoral – Whitehead Institute Service Award (2023)
Best Talk Award, EMBO workshop on long-distance cell-cell communication (2022)
Jane Coffin Childs Fund Postdoctoral Fellow (Awarded 2020)
Life Science Research Foundation Fellow (Declined, 2020)

Graduate – Best oral presentation – MCB Dept. joint retreat (2017)
Best poster – Genetics, Genomics & Development divisional retreat (2015)

Undergraduate – A.B., *Cum laude* (2013)
Award for outstanding undergraduate thesis (2013)
Elected, Sigma Xi scientific honor society (2013)

INSTITUTIONAL RESPONSIBILITIES

Teaching— MCB149, The Human Genome (2016)
MCB140, General genetics (2014-2015)
QB3 programming bootcamp (2014-2015)

Administrative— Co-chair of Whitehead Institute Postdoc Association (2021-2022)
Graduate student delegate to faculty meetings for Genetics, Genomics & Development (2015-2016)
UC Berkeley MCB Graduate Student Organization delegate, Genetics, Genomics & Development (2015-2016)
Princeton Priorities committee (2012-2013)
Princeton committee on admissions and financial aid (2011-2013)

COMMERCIAL ACTIVITIES

Venture capital— Scientific advisor to OMX Ventures (2020-present)
Technical diligence for new investments
Ongoing technical monitoring for portfolio companies in synthetic biology and AI
Freelance consultant for VC/PE diligence in biotech (2016-2019)

PRESENTATIONS

Oral— ASCB Annual meeting minisymposium: Physical Biology (selected)

Philadelphia, PA 2025
HHMI / Janelia: Biology and Engineering the Cell Surface (selected)
Ashburn, VA (2025)
CSHL Single Biomolecules (selected)
Cold Spring Harbor, NY (2024)
Virtual Gastrulation Zoom Talks (invited)
Boston, MA (2024)
Postdoctoral Rising Stars Symposium (invited)
Salt Lake City, UT (2024)
Santa Cruz Developmental Biology Meeting (selected)
Santa Cruz, CA 2024
Winter Q-Bio (selected)
Honolulu, HI 2024
Babraham Institute (invited)
Cambridge, UK 2024
Francis Crick Institute development group (invited)
London, UK 2024
ASCB Annual Meeting Minisymposium: Exploring Morphogenic Diversity (selected)
Boston, MA 2023
Jane Coffin Childs Foundation annual meeting
New York, NY 2023
Whitehead Institute Forum
Cambridge, MA 2023
EMBO workshop on long-distance cell-cell communication in development and disease (selected)
Exeter, UK 2022
Whitehead Institute Retreat
Waterville Valley, NH 2022
Genetics faculty meeting invited lunch speaker (invited)
Berkeley, CA 2019
GSA International Yeast Genetics Meeting (selected)
Stanford, CA 2018
MCB Departmental joint retreat
Tahoe City, CA 2017
Yeast subgroup, Calico Labs (invited)
South San Francisco, CA 2016
Undergraduate Health Sciences Symposium
Princeton NJ 2013

Poster—

Gordon Research Conference: Developmental Biology (2023)
Santa Cruz Developmental Biology meeting (2022)
Gordon research conference: Chromosome Dynamics (2019)
Gordon research conference: Chromatin Structure & Function (2018)
Cold Spring Harbor Symposium on Quantitative Biology: Chromatin Segregation & Structure (2017)
GSA Allied Genetics Conference (2016)
UC Berkeley genetics, genomics & development

divisional retreat (2015)
UC Berkeley joint divisional retreat (2014)
GSA international yeast meeting (2014)
UC Berkeley genetics, genomics & development divisional retreat (2013)
Princeton undergraduate research symposium (2013)
Princeton summer research symposium (2012)

MENTORSHIP

Rotation— 6 rotation students, MIT (2020 – 2024)
4 rotation students, UC Berkeley (2015 – 2019)

Ad Hoc— 1 Undergraduate student, MIT (2020 – 2024)
3 graduate students, MIT (2021 – 2024)
2 Technicians, Li lab (2019-2020)
2 Postdocs transitioning from physics, Rine lab (2016-2019)

PATENTS AND PATENT APPLICATIONS

1. Corn JE, Yang AS, **Schlissel GS**. Compositions and methods for tagging target proteins in proximity to a nucleotide sequence of interest. U.S. Patent Application no. 62503779. May 9, 2017
2. **Schlissel GS**, Li P. Hydrophobic Modifications to proteins. Provisional patent, filed Sept. 2024.

PUBLICATIONS

(peer reviewed research papers numbered in bold)

1. Bothma JP, Garcia HG, Esposito E, **Schlissel G**, Gregor T, Levine M. 2014. Dynamic regulation of eve stripe 2 expression reveals transcriptional bursts in living Drosophila embryos. PNAS. 111(29):10598-603. PMID 24994903

   Brief Description – This paper reported the results of my first graduate rotation, in which we discovered that transcription from the Eve stripe 2 enhancer was "bursty," and that the Eve strip 2 pattern is rapidly refined within the first ~25 minutes of the 14th nuclear division cycle. Additionally, this was among the first papers to use MS2/MCP tagging to measure RNA transcription rates in live embryos.

2. **Schlissel G***, Kryzanowski MK,* Caudron F, Barral Y, Rine J. 2017. Aggregation of the Whi3 protein, not loss of heterochromatin, causes sterility in old yeast cells. Science. 355(6330):1184-87. PMID 28302853

   Commentary – Gitler AD, Jarosz DF. Old moms say, no Sir. Science. 355(6330):1126-27. PMID 28302810

   Brief Description – This paper established that yeast aging did not correspond to a loss of heterochromatin, in conflict with widely-cited reports in the literature. Furthermore, this work

established that protein aggregation was responsible for the canonical observation in the yeast aging field, that old yeast cells do not respond to mating pheromone.

3. **Schlissel G**, Rine J (2019) The nucleosome core particle remembers its position through DNA replication and RNA transcription. PNAS. 116(41):20605-611. PMID 31511420

   Commentary – Henikoff S, Ahmad K. Nucleosomes remember where they were. PNAS; DOI:10.1073/pnas.1914581116. PMID 31511423

   Brief Description – We established that nucleosomes present at given locus prior to DNA replication re-occupied the exact same locus after DNA replication, suggesting that nucleosomes can store and transmit epigenetic memory. Additionally, this paper established that transcription did not cause nucleosomes to "slide" locally. This work required us to build a novel biotin ligase, which we used to label and track single nucleosomes with unprecedented accuracy. This paper represents my core thesis work during my time at Berkeley.

4. **Schlissel G**, Li P (2020) Synthetic Developmental Biology: understanding through reconstitution. Annual Review of Cell and Developmental Biology 2020 36:1, 339-357

   Brief Description – This paper reviewed developmental biology literature that relied on reconstitution as a strategy to probe developmental questions. The literature we surveyed range from classic biochemistry to modern embryoid technologies, connected by a common conceptual reliance on "understanding through reconstitution."

5. **Schlissel G**, Meziane M, Narducci D, Hansen AS, Li P. Diffusion barriers imposed by tissue topology shape Hedgehog morphogen gradients. PNAS. 2024 Sep 3;121(36):e2400677121. PMID: 39190357.

   Brief Description – This is my most complex paper to date – both technologically and intellectually – and this is the paper I am most proud of. We discovered that Hedgehog gradients form by extracellular diffusion of Hedgehog monomers, which slide along cell membranes and occasionally jump from cell-to-cell. We found that the "jump" probability is sufficient to control the Hedgehog range, suggesting novel biochemical mechanisms that evolution can use to regulate morphogen gradient length scales. To build this model, we developed a novel approach to track single molecules of Hedgehog in live cells. This paper disproved several legacy ideas in the Hedgehog signaling field, and unified many ideas in the morphogen signaling field that were previously thought to be at odds. The paper represents the core work I've done as a postdoc.