

## CURRENT

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<b>Branco Weiss Fellow</b>	October 2024 – 2029
<b>Lewis-Sigler Theory Scholar</b> , Princeton University	Princeton, NJ
<b>Fellow</b> , Center for the Physics of Biological Function, City University of New York	New York, NY
	September 2021 – present

## EDUCATION

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<b>Harvard University</b>	Cambridge, MA
Ph.D., Biophysics	May 2021
National Defense Science and Engineering Graduate (NDSEG) Fellowship	
<b>Princeton University</b>	Princeton, NJ
A.B., Physics; Graduated with Highest Honors	May 2016
Certificates: Quantitative & Computational Biology; Applied & Computational Mathematics	

## SELECTED FELLOWSHIPS, HONORS AND AWARDS

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<b>Branco Weiss Fellowship</b> <i>Supports postdoc/faculty transition</i>	2024 – 2029
<i>Awarded to 7/360 applicants worldwide across sciences, engineering, humanities</i>	
<b>Quantitative Biology Ph.D. Fellowship</b> <i>Harvard University</i>	2019 – 2021
<b>Certificates of Distinction in Teaching</b> <i>Harvard University</i>	March 2018, September 2018
<b>DBIO Graduate Student Travel Award</b> <i>to present at APS March Meeting</i>	January 2017
<b>National Defense Science and Engineering Graduate Fellowship</b>	June 2016
<b>Princeton Kusaka Memorial Prize in Physics</b>	June 2016
<b>Princeton Applied and Computational Mathematics Independent Project Prize</b>	June 2016
<b>Princeton Quantitative and Computational Biology Award</b>	June 2016
<b>Member, Phi Beta Kappa Society; Society of Sigma Xi</b>	June 2016
<b>Princeton Allen G. Shenstone Prize in Physics</b>	May 2015
<b>2015 Education Committee Travel Award</b> <i>to present at Biophysical Society Meeting</i>	February 2015
<b>Princeton Shapiro Prize for Academic Excellence</b>	December 2014
<b>Presidential Scholar Semifinalist; National Merit Scholarship Finalist</b>	January 2012

## PUBLICATIONS

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**O. Kimchi**, Y. Meir, N. S. Wingreen. *Lytic and temperate phage naturally coexist in a dynamic population model*. ISME Journal 18(1), wrae093 (2024).

**O. Kimchi**<sup>\*</sup>, B. B. Larsen<sup>\*</sup>, O. R. S. Dunkley, A. J. W. te Velthuis, C. A. Myhrvold. *RNA structure modulates Cas13 activity and enables mismatch detection*. bioRxiv 560533 (2023).

**O. Kimchi**<sup>†</sup>, E. M. King, M. P. Brenner. *Uncovering the mechanism for aggregation in repeat expanded RNA reveals a reentrant transition*. Nature Communications 14 (2023).

A. I. Curatolo, **O. Kimchi**, C. P. Goodrich, R. K. Krueger, M. P. Brenner. *A computational toolbox for the assembly yield of complex, heterogeneous structures*. Nature Communications 14 (2023).

T. Chiang, **O. Kimchi**, H. K. Dhaliwal, D. A. Villarreal, F. F. Vasquez, M. P. Brenner, V. Manoharan, R. Garmann. *Measuring intramolecular connectivity in long RNA molecules using two-dimensional DNA patch-probe arrays*. bioRxiv 532302 (2023).

**O. Kimchi**<sup>†</sup>, M. P. Brenner, L. J. Colwell. *RNA structure prediction including pseudoknots through direct enumeration of states: A user's guide to the LandscapeFold algorithm*. RNA structure prediction, Methods in Molecular Biology Springer (2022).

**O. Kimchi**<sup>†</sup>, C. P. Goodrich, A. Courbet, A. I. Curatolo, N. B. Woodall, D. Baker, M. P. Brenner. *Self-assembly based post-translational protein oscillators*. Science Advances 6(51) (2020).

J. Kames, D.D. Holcomb, **O. Kimchi**, M. DiCuccio, N. Hamasaki-Katagiri, T. Wang, A. A. Komar, A. Alexaki, C. Kimchi-Sarfaty. *Sequence analysis of SARS-CoV-2 genome reveals features important for vaccine design*. Scientific Reports 10, 15643 (2020).

**O. Kimchi**<sup>†</sup>, T. Cragolini, M. P. Brenner, L. J. Colwell<sup>†</sup>. *A polymer physics framework for the entropy of arbitrary pseudoknots*. Biophysical Journal 117(3):520-532 (2019).

**O. Kimchi**, S. L. Veatch, B. B. Machta. *Ion channels can be allosterically regulated by membrane domains near a de-mixing critical point*. Journal of General Physiology 150(12):1769-1777 (2018). Accepted for cover.

M. Watts, J. Ha, **O. Kimchi**, A. Sherman. *Paracrine Regulation of Glucagon Secretion: The  $\beta$ - $\alpha$ - $\delta$  Model*. American Journal of Physiology—Endocrinology & Metabolism 310(8):E597-E611 (2016).

\*Co-first authors <sup>†</sup>Corresponding author

## SELECTED PRESENTATIONS

<b>Competition and coexistence in phage and bacteria</b> <i>Invited speaker, APS March Meeting</i>	2024
<b>RNA structure can inhibit Cas13 activity and enables SNP detection</b> <i>Poster, Soft condensed matter physics Gordon Research Conference, Winter Q-Bio conference, Biophysical Society Annual Meeting</i>	2023
<b>A reentrant transition in RNA aggregation</b> <i>Speaker &amp; session chair, APS March Meeting</i>	2023
<b>RNA hybridization in and out of equilibrium</b> <i>Invited speaker, Boston College Biology Seminar</i>	2021
<b>Towards a synthetic post-translational protein oscillator</b> <i>Selected oral presentation, 1<sup>st</sup> Annual Biodesign Research Conference Speaker &amp; session chair, APS March Meeting; Speaker &amp; poster, Harvard QBio symposium</i>	2020
<b>RNA structure and kinetics including pseudoknots through complete landscape enumeration</b> <i>Speaker, APS March Meeting; Poster, Stochastic Physics in Biology GRC</i>	2019
<b>A complete free energy landscape for RNA structure</b> <i>Speaker, APS March Meeting; Poster, Cargèse summer school</i>	2018
<b>Regulation by a Critical Membrane</b> <i>Speaker, APS March Meeting; Poster, Intracellular Phase Transitions Meeting</i>	2017

## RESEARCH EXPERIENCE

<b>Princeton University Lewis-Sigler Institute for Integrative Genomics</b> Independent postdoctoral fellow	<i>Princeton, NJ</i> Fall 2021 – Present
<ul style="list-style-type: none"> <li>• <i>How does RNA secondary structure affect Cas13 activity?</i> with Cameron Myhrvold <ul style="list-style-type: none"> <li>– Initiated experimental collaboration to probe effects of RNA structure on Cas13</li> <li>– Designed experiments and developed model to interpret results, driving new experimental directions</li> </ul> </li> <li>• <i>Why are homotypic RNA clusters so prevalent?</i> with Liz Gavis and Ned Wingreen <ul style="list-style-type: none"> <li>– Formulated hypothesis for the ubiquity of RNA homotypic clusters in <i>Drosophila</i> embryogenesis</li> <li>– Designed experiments to test hypothesis, currently being carried out by Gavis lab</li> </ul> </li> <li>• <i>How do lytic and lysogenic phage coexist?</i> with Ned Wingreen <ul style="list-style-type: none"> <li>– Coded and analyzed ODE-based model for ecological dynamics of lytic and lysogenic phage</li> </ul> </li> <li>• <i>Are homo- or hetero-polymers more prone to phase separation?</i> with Ned Wingreen <ul style="list-style-type: none"> <li>– Worked with student to write molecular dynamics simulations for polymeric phase separation</li> </ul> </li> <li>• <i>What drives phase separation for repeat RNA?</i> with Michael Brenner <ul style="list-style-type: none"> <li>– Constructed new analytical framework for RNA condensates based on multimer enumeration</li> <li>– Coded dynamic programming model to complement statistical mechanics theory</li> </ul> </li> </ul>	

**Google Research**

*Palo Alto, CA*

Summer Intern

Summer 2019

- *What information is encoded by continuous glucose monitors?*
  - Analyzed large time-series datasets of patient continuous glucose monitoring data
  - Employed machine learning, neural networks (LSTMs, CNNs, FCNs)
- *Are correlations in language truly long-range?* Advisor: Bill Bialek
  - Conducted large-scale dataset analysis on English text documents
  - Used information theory approaches to compare correlations to those expected by chance

**Harvard University Departments of Applied Mathematics and Physics**

Cambridge, MA

Ph.D. Researcher; Advisor: Michael Brenner

Fall 2016 – May 2021

- *How can we leverage hybridization to improve structure prediction for large RNA?*
  - Developed new collaborations on DNA/RNA hybridization with Manoharan lab (Harvard)
  - Worked closely with collaborators to design high throughput microarray-based hybridization experiments
  - Developed novel analysis method employing automatic differentiation of microarray data
- *How can we optimize the yields of de novo designed protein assemblies?*
  - Formulated equilibrium statistical mechanics theory for yield of asymmetric protein self-assembly
  - Worked in team of 6 students/postdocs to develop theory, simulations, and experiments concurrently
- *Can current protein design tools enable the construction of a synthetic post-translational protein oscillator?*
  - Developed new collaborations on protein self-assembly with Baker lab (UW)
  - Constructed differential equation-based models for experimentally realizable protein oscillators
- *Enumerating RNA free energy landscapes including pseudoknots*
  - Constructed Feynman diagram formalism for entropies of complex RNA structures (pseudoknots)
  - Developed algorithm to predict complete energy landscape of arbitrary RNA sequences
- *The epistatic landscape of compensatory evolution in *S. cerevisiae**; Advisor: Michael Desai Winter 2017
  - Conducted collaborative experimental rotation project
  - Techniques used include: PCR, gel electrophoresis, cell culturing, transfections, Illumina sequencing

**Princeton University Lewis-Sigler Institute for Integrative Genomics and Dept. of Physics** Princeton, NJ

Undergraduate Researcher

Summer 2014 – Spring 2016

- *How are ion channels affected by the nearly-critical cell membrane?* Advisor: Ben Machta
  - Developed large-scale algorithm to simulate Ising model dynamics with embedded lattice channel
  - Analyzed results using statistical mechanics scaling laws to demonstrate biological relevance of model
- *How does a 30S ribosome find its target on an mRNA?* Advisor: Ned Wingreen
  - Formulated and probed feasibility of testable quantitative theories for ribosome search
- *Monte Carlo analysis of the Potts Model phase transition.* Advisor: David Huse
  - Performed Monte Carlo simulations on fractal-dimensional lattice to probe phase transition order

**National Institutes of Health Laboratory of Biological Modeling**

Bethesda, MD

Summer Intern

Summer 2013

- *What leads to anti-synchronous pancreatic insulin/glucagon oscillations?* Advisor: Arthur Sherman
  - Developed and numerically solved large ODE system predicting biological  $\alpha/\beta$  cell coupling

**TEACHING, MENTORSHIP, AND COMMUNITY ACTIVITIES**

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**Conference organizer**

January 2024

- Co-organized workshop “Bacteria vs. Phage: The Main Event” at Princeton Center for Theoretical Science.
- Recruited speakers, emphasizing diversity across different axes; led discussions throughout workshop

**DEI community service**

Winter 2024 – present

- Member, LSI Climate Committee, Princeton University

**Research advisor**

Fall 2021 – present

- Provided mentorship on experimental design and presentations to graduate and post-bac students
- Wrote recommendation letter for post-bac student, who started graduate school at Stanford in Fall 2023

**Preceptor and course instructor**

Fall 2021, Summer 2022

- Co-led precepts for Integrated Science, an intensive Freshman course
- Organized discussion group for Princeton Summer Undergraduate Program about scientific presentations

#### **Research advisor**

Summer 2020

- Provided thought leadership and technical mentorship to undergraduate researchers
- Research topics focused on developing synthetic dynamical systems and covid-19 modeling

#### **Course developer and instructor**

Summer 2020

- Developed and taught quantitative biology course about how to read and understand scientific papers
- Course aimed at 12 minority and underrepresented students performing summer research at Harvard

#### **Seminar leader**

Fall 2019-Spring 2021

- Ran Kavli seminar: weekly seminar series with diverse speakers fostering intra-Harvard collaborations
- Shepherded seminar into virtual space in March 2020, maintaining high attendance and engagement

#### **Teaching fellow**

- Graduate student teaching fellow Fall 2017, Spring 2018, Fall 2020
  - Constructed problem sets, led recitations, and mentored students in independent projects
  - Courses were at both graduate and undergraduate level in mathematical modeling
- QuantLab tutor at Princeton University Freshman Scholars Institute Summers 2014-2015
  - Mentored students in problem sets and labs to make quantitative majors more accessible
  - Program was for incoming freshmen to Princeton from minority, low-income backgrounds