

Jeffrey Chang

jeffrey_chang@g.harvard.edu · Google Scholar · Personal Website

SUMMARY

I am a computational protein designer with extensive wet-lab and dry-lab experience and a strong background in statistical mechanics and biochemistry. In my Ph.D., I designed the first example of a fully de novo small-molecule-induced conformational change in a protein — a long-sought goal in molecular design with applications in biosensing. I am seeking a position that can integrate modern deep-learning tools, high-throughput experimental techniques, and classical biophysical intuition to continue advancing our understanding and design capabilities of the protein material, and/or to apply newfound design capabilities to tackle impactful and relevant problems.

EDUCATION

Ph.D. candidate in Physics

Harvard University

Sep. 2020 – Dec. 2026 (anticipated)

B.S. in Physics

Stanford University

GPA 4.03

2016 – 2020

TECHNICAL SKILLS

Computational protein design

RFdiffusion, LASErMPNN, AlphaFold3, PyMOL

Biochemistry

Protein expression and purification, NMR, CD, X-ray crystallography

Next-generation DNA sequencing

Library preparation and data analysis

Yeast display

Library design, cloning, transformation, and flow cytometry

Statistics

Bayesian inference, machine learning

Programming

Python, C++, and R

OTHER

Fluent Languages

English, French, Mandarin Chinese

Hobbies

Jazz melodica, classical piano, speed-cubing, Muay Thai, parkour, sewing

RESEARCH & PROFESSIONAL EXPERIENCE

Doctoral Researcher · Nicholas Polizzi Lab

2022 –

Harvard Medical School and Dana-Farber Cancer Institute

- Designed and experimentally validated a de novo protein with a lid that undergoes an open-to-closed conformational change upon binding the small-molecule cytotoxin exatecan [bioRxiv].
- Drove the project end-to-end as the primary contributor to all computations and experiments.
- Built and executed a computational design workflow involving scaffold generation, sequence design, structure prediction, biophysical filtering, and manual structural inspection in PyMOL.
- Performed comprehensive experimental characterization of the designed conformational switch, including fluorescence polarization, limited proteolysis, FRET, binding kinetics and affinity, circular dichroism, NMR, and X-ray crystallography.
- Devised a novel, rapid biophysical assay to quantify ligand-induced lid closure using limited proteolysis and a covalent fluorescent probe.

Textbook Author · with Steven Kivelson and Jack Jiang

2019 – 2024

Princeton University Press

- Collaborated with Prof. Kivelson and Dr. Jiang to write and publish an undergraduate textbook on the statistical mechanics of phases and phase transitions.
- Wrote initial drafts for 6 of 10 chapters, drew 73 full-color illustrations, created 31 problems with worked solutions, and jointly designed curriculum with co-authors.

Doctoral Researcher · Michael Desai Lab

2020 – 2022

Harvard Department of Organismic and Evolutionary Biology

- Worked in a four-person team during the COVID-19 pandemic to generate library-scale biophysical data mapping the evolutionary landscape of SARS-CoV-2 variants.
- Implemented a robust computational pipeline for inferring binding affinities from NGS data.
- Contributed to yeast-display experiments, NGS library preparation, and downstream data analysis and interpretation.

Ph.D. Rotation · Wesley Wong Lab

2021 – 2022

Wyss Institute, Boston Children's Hospital, and Harvard Medical School

- Developed a Bayesian nonparametric analysis method for inferring molecular subpopulations from single-molecule force-spectroscopy measurements.
- Applied the method to resolve molecular heterogeneity in force-spectroscopy datasets of polyclonal antibodies that were collected by previous Wong Lab members.

Biophysics and Statistical Modeling Consultant

2020 –

Manifold Biotechnologies, Inc.

- Formulated the theoretical framework that established the initial basis for the company's proprietary multiplexed protein-quantitation platform.
- Advised the experimental team on strategies to improve limit of detection, orthogonality, and dynamic range.

Undergraduate Researcher · Steven Boxer Lab

2017 – 2019

Stanford Department of Chemistry

- Carried out an X-ray crystallographic study that established structural evidence for photoisomerization pathways in fluorescent proteins.
- Worked largely independently with guidance from a graduate mentor.

HONORS & AWARDS

Harvard NSF-Simons Quantitative Biology Award	2022
NSF Graduate Research Fellowship	2020
Harvard Dept. of Physics James Mills Peirce Fellowship	2020
Stanford Deans' Award for Academic Achievement	2020
Stanford Bio-X Undergraduate Fellow	2018

TEACHING

Harvard Life Sciences 50: Integrated Science	Winter 2022 – 23
Harvard Applied Math 104: Complex and Fourier Analysis	Autumn 2021 – 22
Stanford Physics 216: Back of the Envelope Physics	Autumn 2019 – 20
Stanford Physics 63: Electricity, Magnetism, and Waves	Winter 2019 – 20

★ favorite works ‡ equal contribution

PREPRINTS

- 2026** ★ De novo design of small-molecule–induced conformational change
J. Chang, N. F. Polizzi
bioRxiv. doi:10.64898/2026.08.03.742366. [\[link\]](#)

PUBLICATIONS

- 2023** Serial femtosecond crystallography reveals that photoactivation in a fluorescent protein proceeds via the hula twist mechanism
A. Fadini, C. D. M. Hutchison, D. Morozov, J. Chang, K. Maghlaoui, S. Perrett, F. Luo, J. C. X. Kho, M. G. Romei, R. M. L. Morgan, C. M. Orr, V. Cordon-Preciado, T. Fujiwara, N. Nuemket, T. Tosha, R. Tanaka, S. Owada, K. Tono, S. Iwata, S. G. Boxer, G. Groenhof, E. Nango, J. van Thor
Journal of the American Chemical Society **145**(29), 15796–15808 (2023). [\[link\]](#)
- 2023** ★ Resolving Molecular Heterogeneity with Single-Molecule Centrifugation
Y. Luo‡, J. Chang‡, D. Yang‡, J. S. Bryan IV, M. MacIsaac, S. Pressé, W. P. Wong
Journal of the American Chemical Society **145**(6), 3276–3282 (2023). [\[link\]](#)
- 2023** The landscape of antibody binding affinity in SARS-CoV-2 Omicron BA.1 evolution
A. Moulana‡, T. Dupic‡, A. M. Phillips‡, J. Chang‡, A. A. Roffler, A. J. Greaney, T. N. Starr, J. D. Bloom, M. M. Desai
eLife **12**, e83442 (2023). [\[link\]](#)
- 2022** Torsional Diffusion for Molecular Conformer Generation
B. Jing‡, G. Corso‡, J. Chang, R. Barzilay, T. Jaakkola
Advances in Neural Information Processing Systems **35**, 24240–24258 (2022). [\[link\]](#)
- 2022** Compensatory epistasis maintains ACE2 affinity in SARS-CoV-2 Omicron BA.1
A. Moulana‡, T. Dupic‡, A. M. Phillips‡, J. Chang‡, S. Nieves, A. A. Roffler, A. J. Greaney, T. N. Starr, J. D. Bloom, M. M. Desai
Nature Communications **13**, 7011 (2022). [\[link\]](#)
- 2021** Binding affinity landscapes constrain the evolution of broadly neutralizing anti-influenza antibodies
A. M. Phillips, K. R. Lawrence, A. Moulana, T. Dupic, J. Chang, M. S. Johnson, I. Cvijovic, T. Mora, A. M. Walczak, M. M. Desai
eLife **10**, e71393 (2021). [\[link\]](#)
- 2019** ★ Structural Evidence of Photoisomerization Pathways in Fluorescent Proteins
J. Chang, M. G. Romei, S. G. Boxer
Journal of the American Chemical Society **141**(39), 15504–15508 (2019). [\[link\]](#)

BOOKS

- 2024** ★ Statistical Mechanics of Phases and Phase Transitions
Steven A. Kivelson, Jack M. Jiang, Jeffrey Chang
Princeton University Press (2024). [\[website\]](#)