

9/20/2023

Gabriel J. Rocklin Ph.D.

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EDUCATION

2013-2019 Senior Fellow, Department of Biochemistry, University of Washington. Advisor: David Baker
2013 Ph.D. in Biophysics, University of California, San Francisco. Advisors: Brian Shoichet, Ken Dill
Thesis: Predicting charged protein-ligand binding affinities using free energy calculations
2007 B.A. in Biology-Chemistry & History, Claremont McKenna College, *summa cum laude*

ACADEMIC APPOINTMENTS

2019-Now Assistant Professor, Department of Pharmacology, Northwestern University
Core Member, Center for Synthetic Biology
Chemistry of Life Processes Institute
Robert H. Lurie Cancer Research Center

HONORS AND AWARDS

2023 Symposium Speaker, Biophysical Society Annual Meeting
2020 NIH New Innovator (DP2) Award
2019 Symposium Speaker, Biophysical Society Annual Meeting
2017 Rising Stars Symposium, University of Utah
2014-2017 Merck Postdoctoral Fellow of the Life Sciences Research Institute
2009-2012 National Defense Science and Engineering Graduate Fellowship
2008-2013 National Science Foundation Graduate Research Fellowship

INSTITUTIONAL SERVICE

DEI & Training Service

2021-Now Co-Director, Northwestern Synthetic Biology NSF REU
2020-Now Key Personnel, Northwestern NIH R25 PREP Program

Committee Service

2023 Internal Program Review committee, Department of Pharmacology
2022-Now Steering committee, Biotechnology Training Program
2022 Proposal reviewer, Lurie Cancer Center Translational Bridge Postdoctoral Fellowship Program
2020-2023 Member, DGP Admissions Committee
2020 Co-Organizer, Northwestern Center for Synthetic Biology Annual Retreat

Ph.D. Thesis Committees

2021-Now Alex Lee (DGP)
2020-Now Marija Milisavljevic (Chemical & Biological Engineering)
2020-2023 Kosuke Seki (Chemical & Biological Engineering)
2019-2022 Walter Thavarajah (Chemical & Biological Engineering)

Qualifying Exam Committee

2022 Jacqueline Trujillo (Driskill Graduate Program)
2021 Alex Lee (Driskill Graduate Program)
2021 Megan Larmore (Driskill Graduate Program)
2020 Hanyin Wang (Driskill Graduate Program)

PARTICIPATION IN PROFESSIONAL SOCIETIES AND EXTRAMURAL ORGANIZATIONS

A. Professional Society Memberships

2019-Now Rosetta Commons Core PI
2013-Now Biophysical Society
2013-2020 American Chemical Society

B. Leadership and Service

2022 Rosetta Commons REU Admissions Committee
2021 Organizing Committee, Central US Synthetic Biology Workshop
2020 Session Organizer & Chair, American Chemical Society Biochemical Technology Division National Meeting
"Use of Big Data and Modeling"
2019 Session Organizer & Chair, American Chemical Society Biochemical Technology Division National Meeting
"Therapeutic Protein Discovery"
2017 Group discussion leader on community diversity and inclusion, RosettaCON
2015-2017 Code of Conduct Committee, RosettaCON

EDITORIAL AND MANUSCRIPT REVIEW RESPONSIBILITIES

Reviewer for: *Science*, *Nature*, *Nature Methods*, *Nature Chemical Biology*, *Nature Communications*, *Proceedings of the National Academy of Sciences*, *ACS Synthetic Biology*, *PLoS Computational Biology*, *Journal of Molecular Biology*, *Journal of Chemical Physics*, *Journal of Chemical Theory and Computation*

GRANTS AND SPONSORED AWARDS

A. Current

NSF DBI-2150269 "REU Site: Synthetic Biology at Northwestern: From Molecules to Society (SynBREU 2.0)"
\$420,295 total costs, project period 4/2022-3/2025
Role: Co-PI

NIH DP2 GM140927-01 "High-throughput discovery of protein energy landscapes in natural and designed proteomes"
\$2,347,906 total costs (\$1,500,000 direct), project period 2020-09-30 – 2025-05-31
Role: PD/PI

B. Previous

NIH R01 GM127585 "Cell Penetration Profiling for Biotherapeutics"
\$102,278 to Northwestern, project period 3/2022-2/2026 (Terminated 3/2023)
Role: Co-I

NIH R21 GM143560-01 "Developing cell-penetrating miniproteins as a new class of therapeutics"
\$422,873 total costs (\$275,000 direct), project period 2021-08-01 – 2023-07-31
Role: PD/PI

INVITED LECTURES

A. International/National

2023 Linderstrom-Lang Symposium, University of Copenhagen, Copenhagen Denmark
Global analysis of protein conformational dynamics in natural and designed domains
2023 University of Massachusetts Amherst Biochemistry Seminar, Amherst MA
Mega-scale Experimental Analysis of Protein Folding Stability in Biology and Design
2023 RosettaCON 2023, Leavenworth WA
Mega-scale Experimental Analysis of Protein Folding Stability in Biology and Design
2023 Van Andel Institute Bioinformatics Workshop, Grand Rapids MI
Mega-scale Experimental Analysis of Protein Folding Stability in Biology and Design

- 2023 DeepMind, London, United Kingdom
Mega-scale Experimental Analysis of Protein Folding Stability in Biology and Design
- 2023 Mutational Scanning Symposium, Hinxton, United Kingdom
Mega-scale Experimental Analysis of Protein Folding Stability in Biology and Design
- 2023 Proteins Gordon Research Conference, Holderness NH
Mega-scale Experimental Analysis of Protein Folding Stability in Biology and Protein Design (from abstracts)
- 2023 Computational Design and Modeling of Biomolecules Keystone Symposium, Banff, Alberta Canada
Mega-scale Experimental Analysis of Protein Folding Stability in Biology and Protein Design (from abstracts)
- 2023 Biophysical Society 2023, San Diego CA
“Predicting Protein Fold Symposium” Symposium
Mega-scale Experimental Analysis of Protein Folding Stability in Biology and Protein Design
- 2023 University of Michigan Biophysics Seminar
Mega-scale Experimental Analysis of Protein Folding Stability in Biology and Protein Design
- 2022 University of North Carolina Biochemistry & Biophysics Seminar
High-throughput studies of protein stability and conformational dynamics
- 2021 Illinois Institute of Technology Chemistry Colloquium
Massively parallel experiments to investigate protein stability and dynamics
- 2021 Amazon Bio-colloquium
Massively parallel experiments to investigate protein stability and dynamics
- 2021 University of Oregon Institute for Molecular Biology Seminar
The structural basis for protein energy landscapes in a de novo designed proteome
- 2021 11th International Conference on Biomolecular Engineering (ICBE) (remote due to Covid-19)
The structural basis for protein energy landscapes in a de novo designed proteome
- 2021 PepTalk 2021 Virtual Conference and Expo
High-throughput investigation of protein energy landscapes in non-antibody scaffolds
- 2020 Washington University in St. Louis Dept. of Biochemistry and Molecular Biophysics
The structural basis for protein energy landscapes in a de novo designed proteome
- 2020 PEGS (Protein Engineering Summit) Boston, Boston MA
High-throughput investigation of protein energy landscapes in non-antibody scaffolds
- 2019 International Conference on Hydrogen-Deuterium Exchange Mass Spectrometry, Banff Canada
The structural basis for protein energy landscapes in a de novo designed proteome
- 2019 PEGS (Protein Engineering Summit) Boston, Boston MA
New High-Throughput Technologies to Design and Optimize Non-Antibody Scaffolds
- 2019 Biophysical Society 2019, Baltimore MD
“Proteins: Exploring Sequence Space via Computation and Experiment” Symposium
The structural basis for protein energy landscapes in a de novo designed proteome
- 2018 RosettaCON 2018, Leavenworth WA
The structural basis for protein energy landscapes in a de novo designed proteome
- 2018 Genentech. Invited seminar, South San Francisco CA
Massively parallel design and testing of new protein folds and targeted inhibitors
- 2018 Chemistry and Biology of Peptides Gordon Research Conference 2018, Ventura CA
Massively parallel design and testing of new protein folds and targeted inhibitors
- 2018 Just. biotherapeutics for all. Invited seminar, Seattle WA
Massively parallel design and testing of new protein folds and targeted inhibitors
- 2018 PepTalk 2018, Keynote Presentation for Higher-Throughput Protein Production & Characterization
Massively parallel design and testing of new protein folds and targeted inhibitors

- 2017 Biogen. Invited seminar, Cambridge MA
Massively parallel design and testing of new protein folds and targeted inhibitors
- 2017 Council of Scientific Society Presidents Winter Meeting, "Frontiers of Science", Washington D.C.
Massively parallel design of new protein folds and targeted inhibitors
- 2017 Rising Stars Symposium, University of Utah Biochemistry Department
Global analysis of protein folding using massively parallel design, synthesis, and testing
- 2015 RosettaCON 2015, Leavenworth WA
High throughput protein design at the edge of folding (Best Talk Award)
- 2014 Laufer Center for Physical and Quantitative Biology, Stony Brook University
Designing protein structures de novo the Rosetta way
- 2014 Free Energy Methods in Drug Design Workshop, Vertex Pharmaceuticals
Analytical corrections for charged compound binding affinities computed from periodic simulations
- 2013 5-College Chemistry Seminar, Claremont Colleges
Molecular dynamics simulations for drug discovery
- 2012 Free Energy Methods in Drug Design Workshop, Vertex Pharmaceuticals
Testing alchemical free energy calculations in a charged model site

B. Regional

- 2022 Midwest Protein Folding Meeting, South Bend IN
Faculty Keynote Talk: Lessons from millions of protein stability measurements
- 2019 Midwest Protein Folding Meeting, South Bend IN
The structural basis for protein energy landscapes in a de novo designed proteome
- 2019 Chan Zuckerberg Biohub, San Francisco CA
The structural basis for protein energy landscapes in a de novo designed proteome

C. Local

- 2022 Northwestern University, CLP Chalk Talk
High-throughput approaches to protein stability, design, and dynamics
- 2022 Northwestern University, Pharmacology Retreat
A Collaborative Approach to Protein Stability
- 2022 Northwestern University, Biotechnology Training Program
Massively parallel experiments to investigate protein stability and dynamics
- 2020 Northwestern University, Lurie Cancer Center Cancer and Physical Sciences Program
Massively parallel design of new protein folds and targeted inhibitors
- 2020 Northwestern University, Lurie Cancer Center Synthetic Biology and Cancer Mini-Symposium
Massively parallel design of new protein folds and targeted inhibitors
- 2020 Boston Protein Design and Modeling Club
Why designs fail, and how they move
- 2020 Northwestern University, Department of Urology Annual Retreat, Keynote Presentation
The structural basis for protein energy landscapes in a de novo designed proteome
- 2020 Northwestern University, Department of Biochemistry and Molecular Genetics
The structural basis for protein energy landscapes in a de novo designed proteome
- 2019 Chicago Mass Spectrometry Discussion Group
The structural basis for protein energy landscapes in a de novo designed proteome
- 2019 Northwestern University, Biophysics Training Grant Research in Progress Series
The structural basis for protein energy landscapes in a de novo designed proteome
- 2019 Northwestern University, Department of Medicine, Pulmonary Division

- The structural basis for protein energy landscapes in a de novo designed proteome*
- 2019 Northwestern University GeneMods (Student Synthetic Biology Society)
The structural basis for protein energy landscapes in a de novo designed proteome
- 2019 Northwestern University, Department of Pharmacology Annual Retreat
The structural basis for protein energy landscapes in a de novo designed proteome

PUBLICATIONS AND SCHOLARLY WORK

Google Scholar Profile: <http://goo.gl/fHzUI>

A. Peer-reviewed Original Investigations

At Northwestern

1. Peng X, Baxa M, Faruk N, Sachleben JR, Pintscher S, Gagnon IA, Houliston S, Arrowsmith CH, Freed KF, **Rocklin GJ**, Sosnick TR. Prediction and Validation of a Protein's Free Energy Surface Using Hydrogen Exchange and (Importantly) its Denaturant Dependence. *Journal of Chemical Theory and Computation* (2021)
2. Kim T-E*, Tsuboyama K*, Houliston S, Martell CM, Phoumyvong CM, Haddox HK, Arrowsmith CH, **Rocklin GJ**. Dissecting the stability determinants of a challenging de novo protein folding using massively parallel design and experimentation. *Proceedings of the National Academy of Sciences* 119:41 (2022) *contributed equally
3. Tsuboyama K, Dauparas J, Chen J, Laine E, Behbahani M, Weinstein JJ, Mangan NM, Ovchinnikov S, **Rocklin GJ**. Mega-scale experimental analysis of protein folding stability in biology and design. *Nature* 620, 434-424 (2023)
News Coverage: [Genetic Engineering & Biotechnology News](#), [Chemistry World](#)

Before Northwestern

1. DerMardirossian C, **Rocklin G**, Seo JY, Bokoch GM. Phosphorylation of RhoGDI by Src Regulates RhoGTPase Binding and Cytosol-Membrane Cycling. *Mol Biol Cell* 17, 4760-8 (2006)
2. Teotico DG*, Babaoglu K*, **Rocklin GJ**, Ferreira RS, Giannetti AM, Shoichet BK. Docking for fragment inhibitors of AmpC beta-lactamase. *Proc Natl Acad Sci U S A* 106, 7455-60 (2009) *contributed equally
3. Boyce SE*, Mobley DL*, **Rocklin GJ**, Graves AP, Dill KA, Shoichet BK. Predicting ligand binding affinity with alchemical free energy methods in a polar model binding site. *J Mol Biol* 394, 747-63 (2009) *contributed equally
4. **Rocklin GJ†**, Mobley DL, Dill KA. Separated Topologies – a Method for Relative Binding Free Energy Calculations using Orientational Restraints. *J Chem Phys* 138, 085104 (2013) †corresponding author
5. **Rocklin GJ†**, Mobley DL, Dill KA. Calculating the Sensitivity and Robustness of Binding Free Energy Calculations to Force Field Parameters. *J Chem Theory Comput* 9:7, 3072-83 (2013) †corresponding author
6. **Rocklin GJ***, Boyce SE*, Fischer M*, Fish I, Mobley DL, Shoichet BK, Dill KA. Blind prediction of charged ligand binding affinities in a model binding site. *J Mol Biol* 425, 4569-83 (2013) *contributed equally
[Recommendation on Faculty of 1000 Prime](#)
7. **Rocklin GJ**, Mobley DL, Dill KA, Hünenberger PE. Calculating the binding free energies of charged species based on explicit-solvent simulations employing lattice-sum methods: An accurate correction scheme for electrostatic finite-size effects. *J Chem Phys* 139, 184103 (2013)
[Featured Cover Article](#). [Recommendation on Faculty of 1000 Prime](#).
8. Bhardwaj G*, Mulligan VK*, Bahl CD*, Gilmore JM, Harvey PJ, Cheneval O, Buchko GW, Pulavarta SVSRK, Kass Q, Eletsky A, Huang P-S, Johnsen WA, Greisen PJ, **Rocklin GJ**, Song Y, Linsky TW, Watkins A, Rettie SA, Xu X, Carter LP, Bonneau R, Olson JM, Coutsiyas E, Correnti CE, Szyperski T, Craik DJ, Baker D. Accurate de novo design of hyperstable constrained peptides. *Nature* 538, 329-35 (2016) *contributed equally
9. **Rocklin GJ**, Chidyausiku TM, Goreshnik I, Ford A, Houliston S, Lemak A, Carter L, Ravichandran R, Mulligan VK, Chevalier A, Arrowsmith CH, Baker D. Global analysis of protein folding using massively parallel design, synthesis, and testing. *Science* 357, 168-75 (2017)
[Perspective by Woolfson et al.](#)
[Recommendations on Faculty of 1000 Prime](#)

Research highlights: *Nature Chemical Biology*, *Nature Methods*

News coverage: *Chemical & Engineering News* (with my cover art), *Chemistry World*, *ACCN (Canadian Chemical News)*, *Genetic Engineering & Biotechnology News*, *The Scientist*

- Chevalier A*, Silva D-A*, **Rocklin GJ***, Hicks DR, Vergara R, Murapa P, Bernard S, Zhang L, Lam K-H, Yao G, Bahl CD, Miyashita S-I, Goreshnik I, Fuller JT, Koday MT, Jenkins C, Colvin T, Carter L, Bohn A, Bryan CM, Fernandez-Velasco DA, Stewart L, Dong M, Huang X, Jin R, Wilson IA, Fuller DH, Baker D. Massively parallel de novo protein design for targeted therapeutics. *Nature* 550, 74-79 (2017) *contributed equally
Research highlights: *Cell*, *Biochemistry*
News coverage: *The New York Times*, *Chemical & Engineering News*, *In the Pipeline*
- Guttman M, Padte NN, Huang Y, Yu J, **Rocklin GJ**, Weitzner BD, Scian M, Ho DD, Lee KK. The influence of proline isomerization on potency and stability of anti-HIV antibody 10E8. *Scientific Reports* 10, 14313 (2020)
- Bryan CM, **Rocklin GJ**, Bick MJ, Ford A, Majri-Morrison S, Kroll AV, Miller CJ, Carter L, Goreshnik I, Kang A, DiMaio F, Tarbell KV, Baker D. Computational design of a synthetic PD-1 agonist. *Proceedings of the National Academy of Sciences* 118 (2021)
- Singer JM, Novotney S, Strickland D, Haddox HK, Leiby N, **Rocklin GJ**, Chow CM, Roy A, Bera AK, Motta FC, Cao L, Strauch E-M, Chidyausiku TM, Ford A, Ho E, Zaitzeff A, Mackenzie CO, Eramian H, DiMaio F, Grigoryan G, Vaughn M, Stewart LJ, Baker D, Klavins E. Large-scale design and refinement of stable proteins using sequence-only models. *PloS one* e0265020 (2022)

B. Patents

Before Northwestern

- Rocklin GJ**, Baker D. Folded and protease-resistant polypeptides. International patent application filed by the University of Washington, Application PCT/US2018/029904, Publication WO2018201020A1.
- Baker D, Chevalier AA, **Rocklin GJ**, Bahl CD, Stewart LJ, Silva Manzano D-A, Fuller DL, Treants Koday M, Gilmore J. De novo designed hemagglutinin binding proteins. US Patent 10,766,929
- Bryan C, Baker D, Rocklin G. De Novo Stable, Modular PD-1 Binding Protein (LGM.3) & Oligomeric Variants. US patent application filed by the University of Washington, USPTO 62/967,093

TEACHING

At Northwestern

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| 2023 | IBiS 409 Biophysical Methods. Two sessions on Structural Proteomics, Fall 2023 |
| 2023 | IGP 401 Biochemistry I. Two lectures on Protein Engineering, Fall 2023 |
| 2023 | DGP Journal Club Discussion Leader (two discussions) |
| 2022 | DGP Journal Club Discussion Leader (two discussions) |
| 2022 | IGP 401 Biochemistry I. Two lectures on Protein Engineering, Fall 2022 |
| 2021 | IBiS 409 Biophysical Methods. Two sessions on Structural Proteomics, Fall 2021 |
| 2021 | IGP 401 Biochemistry I. Two lectures on Protein Engineering, Fall 2021 |
| 2021 | Harvard University Science Olympiad Seminar |
| 2021 | DGP Journal Club Discussion Leader (two discussions) |
| 2020 | IGP 401 Biochemistry I. Two lectures on Protein Engineering, Fall 2020 |
| 2020 | DGP Journal Club Discussion Leader (two discussions) |
| 2019 | DGP Journal Club Discussion Leader (one discussion) |

Before Northwestern

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| 2017 | Skype a Scientist discussion with 4th Grade Class, Lake Pointe Elementary, Austin TX |
| 2017 | Instructor, BIS 285 B "An Ounce of Prevention: Vaccines in Science and Society" (3 credit seminar) Winter 2017 term, University of Washington (Bothell campus)
<i>Co-designed and co-taught undergraduate seminar course with two other postdocs, with faculty mentorship provided through the University of Washington Science Teaching Experience for Postdocs Fellowship</i> |

- 2017 Keynote Lecture, Washington Jr. Science & Humanities Symposium
Computational protein design on a massive scale: Big molecules meet big data
- 2014 Guest Lecture, Lynbrook High School Science Club
- 2012 Guest Lecture, Lynbrook High School Science Club
- 2011 Career fair presentation, Homestead High School Career Fair
- 2008-2011 Teaching Assistant, UCSF Biophysics Bootcamp
Led small group discussions. Lectured on computational biophysical methods. Assisted with Python classes.
- 2010 Guest Lecture, U.C. Berkeley E39B Introduction to Computational Engineering
- 2009 Teaching Assistant, UCSF NSF Graduate Research Fellowship Program Application Workshop
Guided first-year graduate students through fellowship applications; edited and revised proposals
- 2009 Teaching Assistant, UCSF BP204B Macromolecular Interactions
Assisted first-year Ph.D. students in theory and methods of macromolecules, preparing a research proposal
- 2003-2005 Volunteer Debate Coach, Alta Loma High School

TRAINEES

Postdoctoral Fellows

- 2019-2023 Sugyan Dixit, Postdoctoral Fellow
After Rocklin Lab: Senior Research Associate, Discovery Partners Institute
- 2020-2023 Kotaro Tsuboyama, Postdoctoral Fellow
Cross-border Postdoctoral Fellow (CPD) fellow of the Japanese Science Promotion Society (2019-2021)
Human Frontiers Science Program Long-Term Postdoctoral Fellowship (2021-2023)
JST PRESTO Award (2021)
After Rocklin Lab: Lecturer, University of Tokyo Institute for Industrial Science (Independent PI position)
- 2021-Now Jane Thibeault, Postdoctoral Fellow
- 2021-Now Állan Ferrari, Postdoctoral Fellow
BEPE fellow of the São Paulo Research Foundation (2021-2022)
- 2023-Now Tae-Eun Kim, Postdoctoral Fellow

Ph.D. Students

- 2019-2023 Tae-Eun Kim, Driskill Graduate Program (DGP) Ph.D. Student
Julius B. Kahn Fellowship to an outstanding graduate student in Pharmacology (2021-2022)
- 2020-Now Cydney Martell, Driskill Graduate Program (DGP) Ph.D. Student
Chemistry of Life Processes Institute Chemistry-Biology Interface T32 Fellow (2020-2022)
PhRMA Predoctoral fellowship in Drug Delivery (2023-2025)
- 2020-Now Will Corcoran, Interdisciplinary Biological Sciences Program (IBiS) Ph.D. Student
Biotechnology Training Program T32 Fellow (2020-2022)
(co-advised with Prof. Josh Leonard, Dept. of Chemical & Biological Engineering)
- 2021-Now Claire Phoumyvong, Driskill Graduate Program (DGP) Ph.D. student
Synthetic Biology Across Scales (SynBAS) NSF NRT Fellow (2021-2023)
NIH Ruth L. Kirschstein Predoctoral Individual National Research Service Award (2023-2025)
- 2022-Now Tanu Priya, Driskill Graduate Program (DGP) Ph.D. student
Biotechnology Training Program Cluster Member (2022-2023)
Julius B. Kahn Fellowship to an outstanding graduate student in Pharmacology (2023-2024)
- 2023-Now Andra Campbell, Driskill Graduate Program (DGP) Ph.D. student
Biotechnology Training Program T32 Fellow (2023-2025)
- 2023-Now Mario Garcia, Driskill Graduate Program (DGP) Ph.D. student
Molecular Biophysics Training Program T32 Fellow (2023-2025)

Master's in Biotechnology Students

- 2020-2021 Jonathan Chen, Master of Science in Biotechnology Student
- 2021-2021 Kyrollos Shenouda, Master of Science in Biotechnology Student

Postbaccalaureate Fellows

2020-2021 Radhika Dalal, Rosetta Commons Postbaccalaureate Fellow

2021-2022 Andres Lira, Rosetta Commons Postbaccalaureate Fellow

2023-Now Carlos Merlos, Rosetta Commons Postbaccalaureate Fellow

Undergraduate Researchers

2020 Jordan Gewing-Mullins (Scripps College Summer Fellowship)

2020 Nahtalee Lomeli (California Alliance for Minority Participation Summer Research Scholars Program)

2021 William Howe (Rosetta Commons Summer REU)

2021 Matthew Jin (Northwestern Synthetic Biology Summer REU)

2022 Sarah Fahlberg (Rosetta Commons Summer REU)

2022 Cassandra Chrisman (Northwestern Synthetic Biology Summer REU)

2022-Now Yulia Gutierrez (Northwestern Summer Undergraduate Research Grant Recipient)

Northwestern CLP CAURS Undergraduate Research Award

Rosetta Commons Summer REU fellow at AI Proteins, Boston MA

2023 Hannah Ma (Northwestern Undergraduate Research Grant Recipient)

2023 Darcy Kim (Rosetta Commons Summer REU)

2023 Vani Lorish (Northwestern Synthetic Biology Summer REU)

2023-Now Pranav Doradla (Northwestern Summer Undergraduate Research Grant Recipient)

2023-Now Elle Jung (Northwestern Summer Undergraduate Research Grant Recipient)

Former Ph.D. Rotation Students

2019 Aishwarya Ramamurthy, Driskill Graduate Program (DGP) Ph.D. Student

2019 Katiannah Moise, Driskill Graduate Program (DGP) Ph.D. Student

2019 Junlong "Jack" Chi, Driskill Graduate Program (DGP) Ph.D. Student

2021 Edric Choi, Driskill Graduate Program (DGP) Ph.D. Student

2021 Estefany Guzman, Driskill Graduate Program (DGP) Ph.D. Student

2022 Austin Klein, Driskill Graduate Program (DGP) Ph.D. Student