6/6/2024

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
2024 Young Scientist Plenary Keynote, PEGS Boston: The Essential Protein & Antibody Engineering Summit
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)
2020-2024 Marija Milisavljevic (Chemical & Biological Engineering)
2020-2023 Kosuke Seki (Chemical & Biological Engineering)
2019-2022 Walter Thavarajah (Chemical & Biological Engineering)

Qualifying Exam Committee
2024 Assa Magassa (Chemistry)
2023 Tucker Shriver (Driskill Graduate Program)
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
2024   Co-Chair, RosettaCon 2024
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, Cell Systems, Cell Reports Methods, ACS Synthetic Biology, PLoS Computational Biology, Protein Engineering Design and Selection, Biochemistry, 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
2024   Young Scientist Plenary Keynote, PEGS Boston: The Essential Protein & Antibody Engineering Summit
           High-throughput discovery of protein stability and dynamics
2024   Johns Hopkins University Biophysics Seminar, Baltimore MD
           High-throughput discovery of protein folding stability and dynamics
2024   Lauffer Center for Physical and Quantitative Biology, Stony Brook University, Stony Brook NY
           High-throughput discovery of protein folding stability and dynamics
2023   Linderstrøm-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.

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/fHzUl

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

4. Wang H, Feng S, Tsuboyama K, Liu S, **Rocklin GJ**, Ovchinnikov S. Disentanglement of Evolutionary Constraints in Statistical Models of Proteins. PRX Life **2**, 023005 (2024)

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, Coutsias 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*

10. 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*

11. 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)

12. 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)

13. 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)

14. Olshefsky A, Benasutti H, Sylvestre M, Butterfield GL, Rocklin GJ, Richardson C, Hicks DR, Lajoie MJ, Song K, Leaf E, Treichel C, Decarreau J, Ke S, Kher G, Carter L, Chamberlain JS, Baker D, King NP, Pun SH. In vivo selection of synthetic nucleocapsids for tissue targeting. *Proceedings of the National Academy of Sciences* 120:46 (2023)

B. Patents

Before Northwestern

1. **Rocklin GJ**, Baker D. Folded and protease-resistant polypeptides. International patent application filed by the University of Washington, Application PCT/US2018/029904, Publication WO2018201020A1.

2. 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

3. 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

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

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)
          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
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

<u>Postdoctoral Fellows</u>
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   Vasili Kalas, Northwestern Physician Scientist Training Program Fellow
2023-2023   Tae-Eun Kim, Postdoctoral Fellow
2023-Now   Ted Litberg, Postdoctoral Fellow
2024-Now   Sara Volz, Postdoctoral Fellow

<u>Ph.D. Students</u>
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)
            National Defense Science and Engineering Graduate Fellowship (2024-2027)
2023-Now   Mario Garcia, Driskill Graduate Program (DGP) Ph.D. student
            Molecular Biophysics Training Program T32 Fellow (2023-2025)
2024-Now   Adun Obisesan, Driskill Graduate Program (DGP) Ph.D. Student

<u>Master's in Biotechnology Students</u>
2020-2021   Jonathan Chen, Master of Science in Biotechnology Student
2021-2021   Kyrollos Shenouda, Master of Science in Biotechnology Student
2024-Now   Ridhima Manocha, Master of Science in Biotechnology Student

<u>Postbaccalaureate Fellows</u>
2020-2021   Radhika Dalal, Rosetta Commons Postbaccalaureate Fellow
2021-2022   Andres Lira, Rosetta Commons Postbaccalaureate Fellow
2023-Now   Carlos Merlos, Rosetta Commons Postbaccalaureate Fellow

<u>Undergraduate Researchers</u>
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, 2024 Vani Lorish (Northwestern Synthetic Biology Summer REU, Rosetta Commons Summer REU)
2023-Now Pranav Doradla (2x Northwestern Summer Undergraduate Research Grant Recipient)
2023-Now Elle Jung (Northwestern Summer Undergraduate Research Grant Recipient)
2024-Now Carlos Lazo (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
2024   Karen Gomez, Driskill Graduate Program (DGP) Ph.D. Student