

Kevin Drew, Ph.D.

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Education

New York University School of Medicine, New York, NY	
Ph.D. in Biology -- Molecular Biophysics	February 2013
University of Chicago, Chicago, IL	
Master of Science in Computer Science	June 2005
University of Iowa, Iowa City, IA	
Bachelor of Science in Computer Science	May 2003

Research Experience

Assistant Professor University of Illinois at Chicago, Chicago, IL	2021 to Present
• The Drew Lab studies macromolecular assemblies in cells. These assemblies, made up of mostly proteins and nucleic acids, are responsible for most biological functions. We are specifically interested in learning how these assemblies function mechanistically and how they relate to human disease. We do this using biochemical, statistical, machine learning, computational, and proteomic approaches. We aim to uncover the identities of assembly components, determine their 3D structure, and modulate their activity.	
NIH K99/R00 Pathway to Independence Fellow University of Texas at Austin, Austin, TX Advisors: Dr. Edward M. Marcotte & Dr. John Wallingford	2013 to 2020
• Integrated heterogeneous protein interaction datasets using machine learning to build the most comprehensive and accurate human protein complex map • Developed computational tools to calculate structural models of protein complexes • Developed high throughput proteomic experiments to identify ribonucleoprotein complexes	
Ph.D. Student New York University School of Medicine, New York, NY Advisor: Dr. Richard Bonneau	2008 to 2013
• Computationally designed helical mimetic inhibitor of the MDM2 P53 protein interaction • Developed protocol for inhibitor design using Rosetta structure modeling software • Ran quantum simulations to validate Rosetta scoring function on non-peptidic backbones	
Research Assistant New York University, New York, NY Advisor: Dr. Richard Bonneau	2006 to 2008
• Developed a grid based computational pipeline to structurally and functionally annotate proteins from over 100 genomes using Rosetta <i>de novo</i> structure predictions	

Research Experience (cont.)

Bioinformatics Researcher DePaul University, Chicago, IL Advisor: David Angulo	2005 to 2006
<ul style="list-style-type: none">Analyzed mass spectrometry data containing post translational modifications	
Student Appointment Argonne National Laboratories, Argonne, IL Advisor: Dr Gregor von Laszewski and David Angulo	Summer 2004/2005
<ul style="list-style-type: none">Developed software to analyze mass spectrometry hydrogen deuterium exchange experimentsMentored undergraduates participating in the NSF REU program	

Grants / Fellowships

Current Funding

- BBSRC-NSF/BIO Research Infrastructure** 2023-27 \$412,219 (total costs)
 - UniPlex - Genome-Wide Protein Complex Prediction and Validation

Previous Funding

- RosettaCommons MiniGrant** 2022-2025 \$40,000 (total costs)
 - Utilization of a derivative-free evolution based minimizer for non-convex optimization problems in Rosetta
- NIH R00 Pathway to Independence Award (NICHD)** 2021-24 \$732,623 (total costs)
 - Discovery and characterization of novel ciliopathy protein complexes
- NIH LRP Loan Repayment Program (NICHD)** 2021-22 \$19,252
- NIH K99 Pathway to Independence Fellowship (NICHD)** 2018-20 \$193,816 (total costs)
 - Discovery and characterization of novel ciliopathy protein complexes
- NIH F32 Postdoctoral Fellowship (NIGMS)** 2014-17 \$101,404 (total costs)
 - Structural characterization of protein complexes involved in embryogenesis.
- NIH LRP Loan Repayment Program (NICHD)** 2018-19 \$19,252

Publications

Lead and/or Corresponding Author

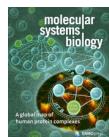
- Drew, K. (2026) Proteome-wide AlphaFold pool party (News & Views) *Mol Syst Biol* (2026). <https://doi.org/10.1038/s44320-026-00198-6> **corresponding author**
- Claussen, E.R., Woodcock-Girard, M.D., Fischer, S.N., Drew, K. (2025) *DirectContacts2: A network of direct physical protein interactions derived from high-throughput mass spectrometry experiments*. **BioRxiv** doi: <https://doi.org/10.1101/2025.07.17.665435> **corresponding author**
- Fischer, S. N., Claussen, E. R., Kourtis, S., Sdelci, S., Orchard, S., Hermjakob, H., Kustatscher, G., Drew, K. (2025) *hu.MAP3.0: Atlas of human protein complexes by integration of > 25,000 proteomic experiments*. **Molecular Systems Biology** 21: 911-943 **corresponding author**
- Fredrick, A.S., Claussen, E.R., Fischer, S.N., Balasanyants, S, Rajaraman, A., Rosner, A.C., and Drew, K. (2024) *Identifying Ciliary Proteins in Mammalian Retinas using a Gentle Extraction Method* **microPublication** doi: [10.17912/micropub.biology.001218](https://doi.org/10.17912/micropub.biology.001218). **corresponding author**

Publications (cont.)

- Claussen, E.R., Renfrew, P.D., Müller, C.L., Drew, K. (2023) *Scaffold Matcher: A CMA-ES based algorithm for identifying hotspot aligned peptidomimetic scaffolds*. **Proteins** 2023;1–13. **corresponding author**
- Drew, K., Wallingford, J.B., Marcotte, E.M. (2021) *hu.MAP 2.0: Integration of over 15,000 proteomic experiments builds a global compendium of human protein assemblies*. **Molecular Systems Biology** 17: e10016. **corresponding author**

Pre-UIC

- Drew, K.*, Lee, C.*, Cox, R.M., Dang, V., Devitt, C.C., Papoulas, O., Huizar, R.L., Marcotte, E.M. and Wallingford, J.B. (2020) *A systematic, label-free method for identifying RNA-associated proteins in vivo provides insights into vertebrate ciliary beating*. **Developmental Biology** Sep 5;S0012-1606(20)30229-3. ***equal contribution**
- Mallam, A.L.* Sae-Lee, W., Schaub, J.M., Tu, F., Battenhouse, A., Jang, Y.J., Kim, J., Wallingford, J.B., Finkelstein, I.J., Marcotte, E.M., and Drew, K.* (2019) *Systematic discovery of endogenous human ribonucleoprotein complexes*. **Cell Reports** 29, 1351–1368 ***equal contribution, corresponding author**
- Drew, K., Müller, C.L., Bonneau, R., and Marcotte, E.M. (2017). *Identifying direct contacts between protein complex subunits from their conditional dependence in proteomics datasets*. **PLoS Computational Biology** 13, e1005625. **corresponding author**



- Drew, K., Lee, C., Huizar, R.L., Tu, F., Borgeson, B., McWhite, C.D., Ma, Y., Wallingford, J.B., and Marcotte, E.M. (2017). *Integration of over 9,000 mass spectrometry experiments builds a global map of human protein complexes*. **Molecular Systems Biology** 3, 932. **(Cover article, Highlighted in Cell Systems)**

- Lao, B.B.* Drew, K.*, Guerracino, D.A., Brewer, T.F., Heindel, D.W., Bonneau, R., and Arora, P.S. (2014). *Rational design of topographical helix mimics as potent inhibitors of protein-protein interactions*. **J. Am. Chem. Soc.** 136, 7877–7888. ***equal contribution**
- Drew, K.*, Renfrew, P.D.* Craven, T.W., Butterfoss, G.L., Chou, F.-C., Lyskov, S., Bullock, B.N., Watkins, A., Labonte, J.W., Pacella, M., et al. (2013). *Adding diverse noncanonical backbones to rosetta: enabling peptidomimetic design*. **PLoS One** 8, e67051. ***equal contribution (Rosetta Special Collection)**
- Drew, K., Winters, P., Butterfoss, G.L., Berstis, V., Uplinger, K., Armstrong, J., Riffle, M., Schweighofer, E., Bovermann, B., Goodlett, D.R., et al. (2011). *The Proteome Folding Project: proteome-scale prediction of structure and function*. **Genome Research** 21, 1981–1994. **(Recommended in F1000.com)**
- Drew, K., Chivian, D. and Bonneau, R. (2009) *De novo protein structure prediction: methods and application*. **Structural Bioinformatics** 2nd Edition. John Wiley & Sons, Inc **(Book Chapter)**
- Avila-Campillo, I.* Drew, K.*, Lin, J., Reiss, D.J., and Bonneau, R. (2007). *BioNetBuilder: automatic integration of biological networks*. **Bioinformatics** 23, 392–393. ***equal contribution**
- Drew, K. (2005) *Computationally Analyzing Mass Spectra of Hydrogen Deuterium Exchange Experiments*. **Masters Dissertation**, Tech-Report TR-2005-12, University of Chicago. April 10, 2005.

Additional Publications

- Vazquez, N., Lee, C., Valenzuela, I., Phan, T.P., Derderian, C., Chávez, M., Mooney, N.A., Demeter, J., Aziz-Zanjani, M.O., Cusco, I., Codina, M., Martínez-Gil, N., Valverde, D., Solarat, C., Buel, A., Thauvin-Robinet, C., Steichen, E., Filges, I., Joset, P., De Geyter, J., Vaidyanathan, K., Gardner, T.P., Toriyama, M., Marcotte, E.M., Drew, K., Roberson, E.C., Jackson, P.K., Reiter, J.F., Tizzano, E.F., Wallingford, J.B. (2025) *The human ciliopathy protein RSG1 links the CPLANE complex to transition zone architecture*. **Nature Communications**. 16, 5701.

Publications (cont.)

- Balu, S., Huget, S., Medina Reyes, J.J., Ragueneau, E., Panneerselvam, K., Fischer, S.N., Claussen, E.R., Kourtis, S., Combe, C.W., Meldal, B.H.M., Perfetto, L., Rappaport, J., Kustatscher, G., Drew, K., Orchard, S., Hermjakob, H. (2024) *Complex portal 2025: predicted human complexes and enhanced visualisation tools for the comparison of orthologous and paralogous complexes*. **Nucleic Acids Research**. 2024 Nov 18:gkae1085.
- Cox, R. M., Papoulas, O., Shril, S., Lee, C., Gardner, T., Battenhouse, A. M., Lee, M., Drew, K., McWhite, C. D., Yang, D., Leggere, J.C., Durand, D., Hildebrandt, F., Wallingford, J. B., Marcotte, E. M. (2024) *Ancient eukaryotic protein interactions illuminate modern genetic traits and disorders*. **BioRxiv** <https://doi.org/10.1101/2024.05.26.595818>
- Sepehri, B., Drew, K., and Villegas, J.A. *Come for the atmosphere, stay for the interactions: Deciphering small molecule partitioning into biomolecular condensates*. **Cell Chemical Biology** Volume 30, Issue 11, P1337-1339, November 16, 2023
- Sae-Lee, W., McCafferty, C.L., Verbeke, E.J., Havugimana, P.C., Papoulas, O., McWhite, C.D., Houser, J.R., Vanuytsel, K., Murphy, G., Drew, K., Emili, A., Taylor, D.W., Marcotte, E.M. (2022) *The protein organization of a red blood cell* **Cell Reports**. Volume 40, Issue 3, 19 July 2022, 111103
- McWhite, C.D., Papoulas, O., Drew, K., Dang, V., Leggere, J.C., Sae-Lee, W., Marcotte, E.M. (2021) *Co-fractionation/mass spectrometry to identify protein complexes*. **STAR protocols** Vol.2(1), p.100370
- Floyd, B.M., Drew, K., Marcotte, E.M. (2021) *Systematic Identification of Protein Phosphorylation-Mediated Interactions* **Journal of Proteome Research** 20 (2), 1359-1370

Pre-UIC

- Lee, C., Cox, R.M., Papoulas, O., Horani, A., Drew, K., Devitt, C.C., Brody, S.L., Marcotte, E.M., Wallingford, J.B. (2020) *Functional partitioning of a liquid-like organelle during assembly of axonemal dyneins* **eLife** 2020;9:e58662 doi: 10.7554/eLife.58662
- McWhite, C.D., Papoulas, O., Drew, K., Cox, R.M., Oldfield-June, V., Dong, O.X., Kwon, T., Wan C., Salmi, M.L., Roux, S.J., Browning, K.S., Chen, Z.J., Ronald, P.C., Marcotte, E.M. (2020) *A pan-plant protein complex map reveals deep conservation and novel assemblies*. **Cell** 181, 460–474, April 16, 2020
- Verbeke, E.J., Mallam, A.L., Drew, K., Marcotte, E.M., and Taylor, D.W. (2018). *Classification of Single Particles from Human Cell Extract Reveals Distinct Structures*. **Cell Reports** 24, 259-268.e3. (**Highlighted in Nature Methods, Recommended in F1000.com**)
- Jiang, T., Renfrew, D., Drew, K., Youngs, N., Butterfoss, G., Bonneau, R., and Shasha, D. (2018). *An Adaptive Geometric Search Algorithm for Macromolecular Scaffold Selection*. **Protein Engineering, Design and Selection**, gzy028
- Huizar, R., Lee, C., Boulgakov, A., Horani, A., Tu, F., Drew, K., Marcotte, E., Brody, S., and Wallingford, J. (2017). *A phase separated organelle at the root of motile ciliopathy*. **BioRxiv** <https://doi.org/10.1101/213793>
- Toriyama, M., Lee, C., Taylor, S.P., Duran, I., Cohn, D.H., Bruel, A.-L., Tabler, J.M., Drew, K., Kelly, M.R., Kim, S., et al. (2016). *The ciliopathy-associated CPLANE proteins direct basal body recruitment of intraflagellar transport machinery*. **Nature Genetics** 48, 648–656.
- Phanse, S., Wan, C., Borgeson, B., Tu, F., Drew, K., Clark, G., Xiong, X., Kagan, O., Kwan, J., Bezginov, A., et al. (2016). *Proteome-wide dataset supporting the study of ancient metazoan macromolecular complexes*. **Data in Brief** 6, 715–721.
- Wan, C., Borgeson, B., Phanse, S., Tu, F., Drew, K., Clark, G., Xiong, X., Kagan, O., Kwan, J., Bezginov, A., et al. (2015). *Panorama of ancient metazoan macromolecular complexes*. **Nature** 525, 339–344.
- Butterfoss, G.L., Drew, K., Renfrew, P.D., Kirshenbaum, K., and Bonneau, R. (2014). *Conformational preferences of peptide-peptoid hybrid oligomers*. **Biopolymers: Peptide Science** 102, 369–378.

Publications (cont.)

- Kilambi, K.P., Pacella, M.S., Xu, J., Labonte, J.W., Porter, J.R., Muthu, P., Drew, K., Kuroda, D., Schueler-Furman, O., Bonneau, R., et al. (2013). *Extending RosettaDock with water, sugar, and pH for prediction of complex structures and affinities for CAPRI rounds 20-27*. **Proteins** 81, 2201–2209.
- Lyskov, S., Chou, F.-C., Conchúir, S.Ó., Der, B.S., Drew, K., Kuroda, D., Xu, J., Weitzner, B.D., Renfrew, P.D., Sripakdeevong, P., et al. (2013). *Serverification of molecular modeling applications: the Rosetta Online Server that Includes Everyone (ROSIE)*. **PLoS One** 8, e63906.
- Youngs, N., Penfold-Brown, D., Drew, K., Shasha, D., and Bonneau, R. (2013). *Parametric Bayesian priors and better choice of negative examples improve protein function prediction*. **Bioinformatics** 29, 1190–1198.
- Baltz, A.G., Munschauer, M., Schwanhäusser, B., Vasile, A., Murakawa, Y., Schueler, M., Youngs, N., Penfold-Brown, D., Drew, K., Milek, M., et al. (2012). *The mRNA-bound proteome and its global occupancy profile on protein-coding transcripts*. **Molecular Cell** 46, 674–690.
- Pentony, M.M., Winters, P., Penfold-Brown, D., Drew, K., Narechania, A., DeSalle, R., Bonneau, R., and Purugganan, M.D. (2012). *The plant proteome folding project: structure and positive selection in plant protein families*. **Genome Biology & Evolution** 4, 360–371.
- Poultney, C.S., Butterfoss, G.L., Gutwein, M.R., Drew, K., Gresham, D., Gunsalus, K.C., Shasha, D.E., and Bonneau, R. (2011). *Rational design of temperature-sensitive alleles using computational structure prediction*. **PLoS One** 6, e23947.
- Wang, K.H., Isidro, A.L., Domingues, L., Eskandarian, H.A., McKenney, P.T., Drew, K., Grabowski, P., Chua, M.-H., Barry, S.N., Guan, M., et al. (2009). *The coat morphogenetic protein SpoVID is necessary for spore encasement in *Bacillus subtilis**. **Molecular Microbiology** 74, 634–649.
- Konieczka, J.H., Drew, K., Pine, A., Belasco, K., Davey, S., Yatskievych, T.A., Bonneau, R., and Antin, P.B. (2009). *BioNetBuilder2.0: bringing systems biology to chicken and other model organisms*. **BMC Genomics** 10 Suppl 2, S6.
- Boxem, M., Maliga, Z., Klitgord, N., Li, N., Lemmens, I., Mana, M., de Lichtenfelde, L., Mul, J.D., van de Peut, D., Devos, M., Simonis, N., Schlaitz, A.L., Cokol, M., Yildirim, M.A., Hao, T., Fan, C., Lin, C., Tipsword, M., Drew, K., et al. (2008). *A protein domain-based interactome network for *C. elegans* early embryogenesis*. **Cell** 134, 534–545.
- Parker, L., Engel-Hall, A., Drew, K., Steinhardt, G., Helseth, D.L., Jr, Jabon, D., McMurry, T., Angulo, D.S., and Kron, S.J. (2008). *Investigating quantitation of phosphorylation using MALDI-TOF mass spectrometry*. **Journal of Mass Spectrometry** 43, 518–527.

Patents

- *Oxopiperazine helix mimetics for control of hypoxia-inducible gene expression*, WO 2015179547 A3, Arora, P.S., Lao, B.B., Bonneau, R., Drew, K. (2016)
- *Oxopiperazine helix mimetics as inhibitors of the p53-MDM2 interaction*, WO 2015160914 A1, Arora, P.S., Lao, B.B., Guaraccino, D., Bonneau, R., Drew, K. (2015)

Presentations

Talks

- UCLA Biochemistry, Molecular, and Structural Biology Department, 2026, Los Angeles, CA
- HUPO World Congress 2025, Toronto, Canada
- HUPO World Congress 2024, Dresden, Germany
- ISMB 2024, Montreal, Canada
- HUPO-PSI 2024, Virtual (2x)
- Summer RosettaCon 2023, Leavenworth, WA (Covid decline)

Presentations (cont)

- Keystone Computational Design and Modeling of Biomolecules 2023, Banff, CA
- US HUPO 2023, Chicago, IL
- ISMB 2022, Madison, IL
- Summer RosettaCon 2022, Leavenworth, WA
- Summer RosettaCon 2021, Virtual
- HUPO 2021, Virtual
- Keystone Proteomics in Cell Biology and Disease 2020, Virtual
- Summer RosettaCon 2020, Virtual
- Winter RosettaCon 2020, New York, NY
- Keystone RNA-Protein Interactions Conference 2019, Whistler, BC, CA
- Human Proteome Organization World Congress 2018, Orlando, FL
- International Xenopus Conference 2018, Seattle, WA
- Society for Developmental Biology (Hilde Mangold Postdoctoral Symposium) 2018, Portland, OR
- New York University Langone Health Institute for Systems Genetics (ISG) 2018, New York, NY
- Flatiron Institute 2018, New York, NY
- BioDynamics 2018, London, UK
- Keystone Omics Strategies to Study the Proteome 2017, Breckenridge, CO
- The Simons Center for Data Analysis (SCDA) 2016, New York, NY
- ISMB 2016, Orlando, FL
- MiniRosettaCon 2013, New York, NY (**organizer**)
- RosettaCon 2012, Leavenworth, WA
- Second Annual Molecular Biophysics Graduate Student Symposium, 2012, New York, NY
- RosettaCon 2008, Leavenworth, WA
- NYC Area Microbial Evolution & Genomics Workshop 2008, New York, NY

Posters

- US HUPO 2026, St. Louis, MO
- HUPO World Congress 2024, Dresden, Germany
- Summer RosettaCon 2024, Cle Elum, WA
- US HUPO 2024, Portland, OR
- Society of Developmental Biology 2023, Chicago, IL
- HUPO World Congress 2022, Cancun, Mexico
- Inner Modeller 2022, Chicago, IL
- Summer RosettaCon 2021, Virtual
- FASEB Biology of Cilia and Flagella 2017, Scottsdale, AZ
- 3D-SIG 2016, Orlando, FL
- Winter q-bio 2016, Oahu, HI
- Hybrid Methods in Structural Biology 2015, Tahoe City, CA
- RosettaCon 2014, Leavenworth, WA
- RosettaCon 2013, Leavenworth, WA
- RosettaCon 2011, Leavenworth, WA
- ISMB 2011, Vienna, Austria
- RosettaCon 2009, Leavenworth, WA
- RosettaCon 2007, Leavenworth, WA
- RosettaCon 2006, Leavenworth, WA

Additional Awards

- International Xenopus Conference Travel Award 2018
- Hilde Mangold Postdoctoral Symposium Travel Award 2018
- UT MBS Postdoctoral Travel Fellowship 2018
- UT MBS Retreat 2018 Presentation Award 2nd Place

Additional Awards (cont.)

- ISMB/ECCB 2011 Travel Fellowship
- T32 Training Fellowship, New York University, School of Medicine
- University of Chicago Computer Science Department Commendation Letter 2005
- Midwest Software Engineering Conference Best of Conference Student Poster
- University of Iowa Dean's List

Organizations

- RosettaCommons Member
- UIC Center for Bioinformatics and Quantitative Biology Affiliate Member
- UIC Honors College
- Intelligent Systems for Molecular Biology (ISMB)
- Society for Developmental Biology (SDB)
- Human Proteome Organization (HUPO)
- The American Association for the Advancement of Science (AAAS)
- The New York Academy of Sciences (NYAS)

Outreach

- Illinois Math & Science Academy (IMSA) High School Mentor (2021-2025)
 - Host high school student in lab weekly
- Oak Park Education Foundation (OPEF) Science Alliance (2024 - 2025)
 - Ran "Molecules of Biology" Workshop for 4-5th graders (strawberry DNA extraction, microscopy of jellyfish, FoldIT protein folding computer game)
- Oak Park Education Foundation (OPEF) STEM Fest (2024 - 2025)
 - Ran "Molecules of Biology" Workshop (2x) for 4-5th graders (strawberry DNA extraction, potato enzyme demonstration, microscopy of jellyfish)
 - Scientific booth (computer visualization of 3D protein structures, 3D printed protein models, FoldIT protein folding computer game)

Pre-UIC

- Palm Elementary, Austin, Texas - UT Outreach Organizer
- Lee Elementary, Austin, Texas - Science Fair Judge
- Brothers and Sisters in Science (BASIS), middle school mentoring program

Teaching

- Biochemistry (BIOS/CHEM-352) Spring 2026
- Biochemistry (BIOS/CHEM-352) Fall 2025
- Concepts in Biochemistry and Molecular Biology (BIOS-524) Fall 2025
- Biochemistry (BIOS/CHEM-352) Spring 2025
- Biochemistry (BIOS/CHEM-352) Fall 2024
- Concepts in Biochemistry and Molecular Biology (BIOS-524) Fall 2024
- Biochemistry (BIOS/CHEM-352) Spring 2024
- Independent Research (BIOS-399) Spring 2024
- Biochemistry (BIOS/CHEM-352) Fall 2023
- Concepts in Biochemistry and Molecular Biology (BIOS-524) Fall 2023
- Biochemistry (BIOS/CHEM-352) Spring 2023
- Concepts in Biochemistry and Molecular Biology (BIOS-524) Fall 2022
- Biochemistry (BIOS/CHEM-352) Spring 2022
- Concepts in Biochemistry and Molecular Biology (BIOS-524) Fall 2021
- Biology Colloquium (BIOS-196) Fall 2021

Teaching (cont.)

Pre-UIC

- Physical Methods for Biochemistry Guest Lecture October 2019
- Systems Biology / Bioinformatics Guest Lecture March 2019
- Systems Biology / Bioinformatics Guest Lecture March 2018
- Systems Biology / Bioinformatics Guest Lecture March 2017
- Biochemistry Guest Lecture Oct 2016
- Systems Biology / Bioinformatics Guest Lecture Feb 2016
- Biochemistry Guest Lecture Oct 2015
- Rosetta Workshop May 2015
- Systems Biology / Bioinformatics Guest Lecture Feb 2015
- Rosetta Workshop May 2014

Students

- Miles Woodcock-Girard - Graduate Student - MCDBN
- Samantha Fischer - Graduate Student - MCDBN
- Andi Rosner - Graduate Student - MCDBN
- Akshaya Rajaraman - Graduate Student / **American Heart Association Fellow** - MCDBN
- Nathaniel Thomas - Undergraduate Student (UCLA) - Summer REU-Rosetta Student 2024
- Karen Garcia - Undergraduate Student (ColumbiaU) - Summer REU-Rosetta Student 2025
- James Zhu - Undergraduate Student (Pomona College) - Summer REU-Rosetta Student 2026
- Vibhav Prabhakar - Undergraduate Student - LAS/Honors
- Carlos Merlos - Undergraduate Student - L@s GANAS Fellow
- Adeline Fredrick - Undergraduate Student - LAS/Honors
- Elizabeth Stierle - Biomedical Visualization Master's program
- Vedanti Joshi - Daniel Wright Junior High School / IMSA
- Folashade (Gloria) Olorunfemi - Graduate Student - MCDBN (rotation)
- Garry Lewis - Graduate Student - MCDBN (rotation)
- Samson Balasanyants - Graduate Student - MCDBN (rotation)
- Samson Adejumo - Graduate Student - MCDBN (rotation)
- Maryam Behzadi - Graduate Student - MCDBN (rotation)
- Hamida Mahmood - Graduate Student - MCDBN (rotation)
- Sangita Ghimire - Graduate Student - MCDBN (rotation)
- Sourav Chakraborty - Graduate Student - MCDBN (rotation)
- Paul Urban - Graduate Student - MCDBN (rotation)
- Eunseo Kim - Graduate Student - MCDBN (rotation)
- Jill Pan - Graduate Student - MCDBN (rotation)
- Yu-Ting Lu - Graduate Student - MCDBN (rotation)
- Kaitlyn Watson - Graduate Student - MCDBN (rotation)
- Amara Victoria - Graduate Student - MCDBN (rotation)

Service

UIC

- MCDBN Graduate Admissions (2021 - Present, **Chair** 2023 - 2025)
- Mass Spectrometry Core Advisory Committee (2021- Present)
- PhD Committee Member - Mandisa Timba (2026 - Present)
- PhD Committee Member - Eleus Bhuiya (2025 - Present)
- PhD Committee Member - Hamida Mahmood (2025 - Present)
- PhD Committee Member - Samson Balasanyants (**Chair** 2024 - Present)
- PhD Committee Member - Sourav Chakraborty (2024 - Present)
- PhD Committee Member - Tomi Jacobs (2024 - Present)

Service (cont.).

- PhD Committee Member - Cliff Yerby (2024 - Present)
- PhD Committee Member - Gloria Olorunfemi (2023 - Present)
- PhD Committee Member - Nicole Curtis (2022 - Present)
- PhD Committee Member - Egor Syroegin (2022 - 2025)
- Masters Committee Member - Joseph Lombardo (2021 - 2022)
- UIC Honors College Faculty Mentor - Isabella Andrade (2025-Present)
- UIC Honors College Faculty Mentor - Zachary Natsheh (2024-Present)
- UIC Honors College Faculty Mentor - Disha Sharma (2023-2025)
- UIC CBQB Research Day Oral Presentation Award Committee (2022-2024)
- UIC Honors College Research Grant Review (2023-2024)
- UIC Honors College Faculty Mentor - Adeline Fredrick (2022-2023)

Global

- Summer RosettaCon 2025 Conference **Chair**
- Cell Systems Reviewer (2025)
- Protein Science Reviewer (2025)
- Molecular Systems Biology Reviewer (2025)
- Journal of Molecular Biology Reviewer (2025)
- Nature Communications Reviewer (2021-2025)
- ISMB Great Lakes Bioinformatics Conference Abstract Reviewer (2024)
- Summer RosettaCon Conference Abstract Reviewer (2024)
- Scientific Data Journal Reviewer (2024)
- PLOS Computational Biology Reviewer (2022-2024)
- Bioinformatics Reviewer (2024)
- Summer RosettaCon Career Panelist (2024)
- Summer RosettaCon Scientific Group Discussion - “Learning from Experimental Data” (2024)
- Summer RosettaCon Small Group Discussion Leader (2024)
- Nature Computational Science Reviewer (2022)
- Summer RosettaCon 2022 Poster Award Committee (2022)
- Summer RosettaCon Session Chair (2021)
- PLOS Biology Reviewer (2020)
- Keystone RNA-Protein Interactions Conference Session Chair (2019)

References

Edward Marcotte, Ph.D. (*Postdoc Advisor*)
Professor
The University of Texas at Austin
Institute for Cellular and Molecular Biology
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Center for Computational Biology and Bioinformatics
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John Wallingford, Ph.D. (*Postdoc co-Advisor*)
Professor
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References (cont.)

Richard Bonneau, Ph.D. (*Ph.D. Advisor*)
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