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

NIH K99/R00 Pathway to Independence Fellow   2013 to Present
University of Texas at Austin, Austin, TX
Advisors: Dr. Edward M. Marcotte & Dr. John Wallingford

- 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   2008 to 2013
New York University School of Medicine, New York, NY
Advisor: Dr. Richard Bonneau

- 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   2006 to 2008
New York University, New York, NY
Advisor: Dr. Richard Bonneau

- Developed a grid based computational pipeline to structurally and functionally annotate proteins from over 100 genomes using Rosetta *de novo* structure predictions

Bioinformatics Researcher   2005 to 2006
DePaul University, Chicago, IL
Advisor: David Angulo

- Analyzed mass spectrometry data containing post translational modifications

Student Appointment   Summer 2004/2005
Argonne National Laboratories, Argonne, IL
Advisor: Dr Gregor von Laszewski and David Angulo

- Developed software to analyze mass spectrometry hydrogen deuterium exchange experiments
- Mentored undergraduates participating in the NSF REU program

Grants / Fellowships

- **NIH K99/R00** Pathway to Independence Fellowship (**NICHD**) 2018-23 $935,278 (direct costs)
  - Discovery and characterization of novel ciliopathy protein complexes

- **NIH F32** Postdoctoral Fellowship (**NIGMS**) 2014-17 $101,404 (direct costs)
  - Structural characterization of protein complexes involved in embryogenesis.

- **NIH LRP** Loan Repayment Program (**NICHD**) 2018-19 $19,252

Publications

Lead Author

- Mallam, A.L.*****, Sae-Lee, W., Schaub, J.M., Tu, F., Battenhouse, A., Jang, Y.J., Kim, J., Finkelstein, I.J., Marcotte, E.M., and Drew, K.***** *Systematic discovery of endogenous human ribonucleoprotein complexes.* **BioRxiv** https://doi.org/10.1101/480061 ****equal contribution***

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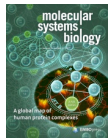
- Drew, K., Lee, C., Huizar, R.L., Tu, F., Borgeson, B., McWhite, C.D., Ma, Y., Wallingford, J.B., and Marcotte, E.M. (2017). *Integration of over 9,000 mass spectrometry experiments builds a global map of human protein complexes.* **Molecular Systems Biology** *3*, 932. (***Cover article, Highlighted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

- Lao, B.B.*, Drew, K.*, Guarracino, 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.

Supporting Author

- 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

- 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**)

Publications (cont.)

- 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.

- 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 Lichtervelde, 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., <u>Drew, K.</u> (2016)
- *Oxopiperazine helix mimetics as inhibitors of the p53-MDM2 interaction*, WO 2015160914 A1, Arora, P.S., Lao, B.B., Guarracino, D., Bonneau, R., <u>Drew, K.</u> (2015)

Presentations

Talks

- 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
- 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

- 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
- 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 and Extracurriculars

- Intelligent Systems for Molecular Biology (ISMB)
- Society for Developmental Biology (SDB)
- Human Proteome Organization (HUPO)
- Palm Elementary, Austin, Texas - UT Outreach Organizer
- Lee Elementary, Austin, Texas - Science Fair Judge
- The American Association for the Advancement of Science (AAAS)
- The New York Academy of Sciences (NYAS)
- Brothers and Sisters in Science (BASIS), middle school mentoring program

Teaching

- 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

References

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