

# 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

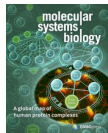
## Grants / Fellowships

- **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

- Drew, K., Marcotte, E.M. *Hu.MAP2.0: Integration of over 15,000 proteomic experiments builds a global compendium of protein assemblies. In Prep.*
- Drew, K.\*, Lee, C.\*, Cox, R.M., Dang, V., Devitt, C.C., Papoulas, O., Huizar, R.L., Marcotte, E.M. and Wallingford, J.B. *A systematic, label-free method for identifying RNA-associated proteins in vivo provides insights into vertebrate ciliary beating. **BioRxiv** <https://doi.org/10.1101/2020.02.26.966754> \*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.\*, 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.*

## Publications (cont.)

### Additional Publications

- 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. *A pan-plant protein complex map reveals deep conservation and novel assemblies.* **Cell (accepted)**
- 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.
- 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.

## Publications (cont.)

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

## Presentations

### Talks

- Winter RosettaCon 2020, New York, NY
- 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

- 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

## References

Edward Marcotte, Ph.D. ( *Postdoc Advisor* )

Professor

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John Wallingford, Ph.D. ( *Postdoc co-Advisor* )

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## References (cont.)

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Department of Computer Science  
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