

# 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

Postdoctoral Fellow 2013 to Present  
University of Texas at Austin, Austin, TX  
Advisor: Dr. Edward M. Marcotte

- Integrated heterogeneous protein interaction datasets to build a human protein complex map
- Developed computational tools to calculate structural models of protein complexes

PhD 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

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

## Publications

- Michinori Toriyama, Chanjae Lee, S. Paige Taylor, Ivan Duran, Daniel H. Cohn, Ange-Line Bruel, Jacqueline M. Tabler, **Kevin Drew**, Marcus R. Kelley, Sukyoung Kim, Tae Joo Park, Daniella Braun, Ghislaine Pierquin, Armand Biver, Kerstin Wagner, Anne Malfroot, Inusha Panigrahi, Brunella Franco, Hadeel Adel Al-lami, Yvonne Yeung, Yeon Ja Choi, University of Washington Center for Mendelian Genomics, Yannis Duffourd, L Faivre, JB Rivière, Jiang Chen, Karen J. Liu, Edward M. Marcotte, Friedhelm Hildebrandt, Christel Thauvin-Robinet, Deborah Krakow, Peter K. Jackson, and John B. Wallingford *The ciliopathy-associated CPLANE proteins direct basal body recruitment of intraflagellar transport machinery*. Nature Genetics, In Press
- Phanse S, Wan C, Borgeson B, Tu F, **Drew K**, Clark G, Xiong X, Kagan O, Kwan J, Bezginov A, Chessman K, Pal S, Cromar G, Papoulas O, Ni Z, Boutz DR, Stoilova S, Havugimana PC, Guo X, Maly RH, Sarov M, Greenblatt J, Babu M, Derry WB, R Tillier E, Wallingford JB, Parkinson J, Marcotte EM, Emili A, *Proteome-wide dataset supporting the study of ancient metazoan macromolecular complexes*, Data in Brief, 6:715-21 (2015)
- Cuihong Wan, Blake Borgeson, Sadhna Phanse, Fan Tu, **Kevin Drew**, Greg Clark, Xuejian Xiong, Olga Kagan, Julian Kwan, Alexandr Bezginov, Kyle Chessman, Swati Pal, Graham Cromar, Ophelia Papoulas, Zuyao Ni, Daniel R Boutz, Snezana Stoilova, Pierre C Havugimana, Xinghua Guo, Ramy H Maly, Mihail Sarov, Jack Greenblatt, Mohan Babu, W Brent Derry, Elisabeth R Tillier, John B Wallingford, John Parkinson, Edward M Marcotte, Andrew Emili *Panorama of ancient metazoan macromolecular complexes* Nature 525, 339–344 17 September 2015 doi:10.1038/nature14877
- Glenn L. Butterfoss, **Kevin Drew**, P. Douglas Renfrew, Kent Kirshenbaum and Richard Bonneau *Conformational Preferences of Peptide-Peptoid Hybrid Oligomers*. Biopolymers: Peptide Science. 2014 Jun 11. doi: 10.1002/bip.22516.
- Brooke Bullock Lao,\* **Kevin Drew**,\* Danielle A. Guarracino, Thomas F. Brewer, Daniel Heindel, Richard Bonneau and Paramjit S. Arora *Rational Design of Topographical Helix Mimics as Potent Inhibitors of Protein–Protein Interactions*. J. Am. Chem. Soc., 2014, 136 (22), pp 7877–7888. \*shared first authors
- Krishna Praneeth Kilambi, Michael Pacella, Jianqing Xu, Jason Labonte, Justin Porter, Pravin Muthu, **Kevin Drew**, Daisuke Kuroda, Ora Schueler-Furman, Richard Bonneau, and Jeffrey J. Gray *Extending RosettaDock with water, sugar and pH for prediction of complex structures and affinities for CAPRI rounds 20-27*. Proteins. 2013 Dec;81(12):2201-9.
- **Kevin Drew**\*, P. Douglas Renfrew\*, Tim Craven, Glenn Butterfoss, Fang-Chieh Chou, Brooke N. Bullock, Andrew Watkins, Sergey Lyskov, Andrew Leaver-Fay, Brian Kuhlman, Jeffrey J. Gray, Philip Bradley, Kent Kirshenbaum, Paramjit S. Arora, Rhiju Das, Richard Bonneau *Peptidomimetics in Rosetta: Noncanonical Backbones for Drug and Foldamer Design*. PLoS ONE 8(7): e67051. \*shared first authors
- Lyskov S, Chou F-C, Conchúir SÓ, Der BS, **Drew K**, et al. (2013) Serverification of Molecular Modeling Applications: The Rosetta Online Server That Includes Everyone (ROSIE). PLoS ONE 8(5): e63906. doi:10.1371/journal.pone.0063906
- Noah Youngs, Duncan Penfold-Brown, **Kevin Drew**, Dennis Shasha, Richard Bonneau. *Parametric Bayesian Priors and Better Choice of Negative Examples Improve Protein Function Prediction*. Bioinformatics 29 (9), 1190-1198
- Baltz AG, Munschauer M, Schwanhäusser B, Vasile A, Murakawa Y, Schueler M, Youngs N, Penfold-Brown D, **Drew K**, Milek M, Wyler E, Bonneau R, Selbach M, Dieterich C, Landthaler M. *The mRNA-bound proteome and its global occupancy profile on protein-coding transcripts*. Mol Cell. 2012 Jun 8;46(5):674-90.
- Melissa M. Pentony, Patrick Winter, Duncan Penfold-Brown, **Kevin Drew**, Apurva Narechania, Rob DeSalle, Richard Bonneau, Michael D. Purugganan (2012) *The plant proteome folding project: structure and positive selection in plant protein families*. Genome Biol Evol. 2012;4(3):360-71. Epub 2012 Feb 16.
- Christopher S. Poultney, David Gresham, Nathan J. Brandt, Glenn L. Butterfoss, Michelle R. Gutwein, **Kevin Drew**, Kristin C. Gunsalus, Dennis E. Shasha, Richard Bonneau (2011) *Rational design of temperature-sensitive alleles using computational structure prediction*. PLoS One. 2011;6(9):e23947. Epub 2011 Sep 2.

## Publications (cont.)

- **Kevin Drew**, Patrick Winters, Glenn L. Butterfoss, Viktors Berstis, Keith Uplinger, Jonathan Armstrong, Michael Riffle, Erik Schweighofer, Bill Bovermann, David R. Goodlett, Trisha N. Davis, Dennis Shasha, Lars Malmström, Richard Bonneau *The Proteome Folding Project: proteome-scale prediction of structure and function*. Genome Res. 2011 Nov;21(11):1981-94. Epub 2011 Aug 8.
- Wang KH, Isidro AL, Domingues L, Eskandarian HA, McKenney PT, **Drew K**, Grabowski P, Chua MH, Barry SN, Guan M, Bonneau R, Henriques AO, Eichenberger P. (2009) *The coat morphogenetic protein SpoVID is necessary for spore encasement in Bacillus subtilis*. Mol Microbiol. 2009 Nov;74(3):634-49. Epub 2009 Sep 22
- Konieczka JH, **Drew K**, Pine A, Belasco K, Davey S, Yatskievych TA, Bonneau R, Antin PB. BioNetBuilder2.0: bringing systems biology to chicken and other model organisms. BMC Genomics. 2009 Jul 14;10 Suppl 2:S6.
- **Kevin Drew**, Dylan Chivian and Richard Bonneau (2009) *De novo protein structure prediction: methods and application*. Structural Bioinformatics 2nd Edition. John Wiley & Sons, Inc (Book Chapter)
- Mike Boxem, Zoltan Maliga, Niels J. Klitgord, Na Li, Irma Lemmens, Miyeko Mana, Lorenzo De Lichertervelde, Joram Mul, Diederik van de Peut, Maxime Devos, Nicolas Simonis, Anne-Lore Schlaitz, Murat Cokol, Muhammed A. Yildirim, Tong Hao, Changyu Fan, Chenwei Lin, Mike Tipsword, **Kevin Drew**, Matilde Galli, Kahn Rhrissorakrai, David Drechsel, David E. Hill, Richard Bonneau, Kristin C. Gunsalus, Frederick P. Roth, Fabio Piano, Jan Tavernier, Sander van den Heuvel, Anthony A. Hyman, Marc Vidal. *A Protein Domain-Based Interactome Network for C. elegans Early Embryogenesis*. (2008) Cell, 134(3) pp. 534 - 545.
- Laurie Parker, Aaron Engel-Hall, **Kevin Drew**, George Steinhardt, Donald L. Helseth, Jr., David Jabon, Timothy McMurtry, David S. Angulo and Stephen J. Kron. (2007) *Quantitation of phosphorylation using MALDI-TOF mass spectrometry*. Journal of Mass Spectrometry 2008 Apr;43(4):518-27.
- Iliana Avila-Campillo\*, **Kevin Drew\***, John Lin, David J. Reiss and Richard Bonneau (2006) *BioNetBuilder: automatic integration of biological networks*. Bioinformatics 2007 23(3):392-393. \*shared first authors
- **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.

## Presentations

- RosettaCon 2012, Leavenworth, WA
- Second Annual Molecular Biophysics Graduate Student Symposium, 2012, New York, NY
- Poster, ISMB 2011, Vienna, Austria
- RosettaCon 2008, Leavenworth, WA
- NYC Area Microbial Evolution & Genomics Workshop 2008, New York, NY

## Fellowships / Awards

- NIH F32 Postdoctoral Fellowship
- ISMB/ECCB 2011 Travel Fellowship
- T32 Training Fellowship, New York University, School of Medicine
- University of Chicago Computer Science Department Commendation Letter
- Midwest Software Engineering Conference Best of Conference Student Poster
- University of Iowa Dean's List

## Organizations and Extracurriculars

- Intelligent Systems for Molecular Biology (ISMB)
- 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 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* )  
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The University of Texas at Austin  
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Associate Professor  
New York University  
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