

Kimberly A. Reynolds

Contact

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Education

- | | |
|---|-------------|
| Ph.D in Biophysics
University of California, Berkeley. Advisor: Dr. Tracy M. Handel | 2006 |
| B.A. in Biochemistry
Rice University, Houston, TX. | 2001 |

Research and Professional Experience

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|---|---------------------|
| Assistant Professor
Green Center for Systems Biology and Dept. of Biophysics
UT Southwestern Medical Center, Dallas, TX | 2014-present |
| Postdoctoral Researcher – <i>Advisor: Dr. Rama Ranganathan</i>
Green Center for Systems Biology, UT Southwestern Medical Center, Dallas, TX | 2008-2014 |
| Postdoctoral Researcher – <i>Advisors: Dr. Ruben Abagyan and Dr. Ed Roberts</i>
Department of Molecular Biology, The Scripps Research Institute, La Jolla | 2007-2008 |
| Adjunct Professor – <i>mentored teaching fellowship</i>
Department of Chemistry, University of San Diego, CA | Fall 2007 |

Awards and Fellowships

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|---|------------------|
| Scialog Fellow, Molecules Come to Life Program | 2016-2017 |
| Data Driven Discovery Investigator, Gordon and Betty Moore Foundation | 2014 |
| Alfred Gilman award for excellence in postdoctoral research, UTSW | 2011 |
| Scripps/USD JUST program mentored undergraduate teaching internship | 2007 |
| National Science Foundation Graduate Research Fellow | 2003-2006 |
| Achievement Rewards for College Scholars (ARCS) Graduate Fellow | 2001-2003 |

Publications

1. D. Pincus, J. Pandey, P. Creixell, O. Resnekov, and **K.A. Reynolds**. Evolution and engineering of allosteric regulation in protein kinases. *Manuscript submitted*. bioRxiv preprint: <https://doi.org/10.1101/189761>
2. A.F.Schober, C.Ingle, J.O. Park, L. Chen, J.D. Rabinowitz, I. Junier, O. Rivoire, and **K.A. Reynolds**. An evolutionary module in central metabolism. *Manuscript submitted*. bioRxiv preprint: <https://doi.org/10.1101/120006>

3. C. Rosensweig, **K.A. Reynolds**, P. Gao, Y. Shan, R. Ranganathan, J.S. Takahashi, C.B Green. An evolutionary hotspot defines functional differences between CRYPTOCHROMES. *Nature Communications* (9):1138. <http://dx.doi.org/0.1038/s41467-018-03503-6>
4. C. Narayanan, D. Gagné, **K.A. Reynolds**, N. Doucet (2017). Conserved amino acid networks modulate discrete functional properties in an enzyme superfamily. *Scientific Reports* (7):3207. <http://dx.doi.org/10.1038/s41598-017-03298-4>
5. D. Pincus, O. Resnekov, **K.A. Reynolds** (2017). An evolution-based strategy for engineering allosteric regulation. *Physical Biology* (14): 025002. <http://dx.doi.org/10.1088/1478-3975/aa64a4>
6. O. Rivoire, **K.A. Reynolds**, R. Ranganathan (2016). Evolution-based functional decomposition of proteins. *PLoS Comp Biol* (12): e1004817. <http://dx.doi.org/10.1371/journal.pcbi.1004817>
Associated software: <http://reynoldsk.github.io/pySCA/>
7. **K.A. Reynolds** (2015). A new test of computational protein design: predicting posttranslational modification specificity for the enzyme SMYD2. *Structure* (23): 11-12. <http://dx.doi.org/10.1016/j.str.2014.12.004>
8. **K.A. Reynolds** (2014). Finding a common path: predicting gene function using inferred evolutionary trees. *Developmental Cell* (30): 4-5. <http://dx.doi.org/10.1016/j.devcel.2014.06.029>
9. **K.A. Reynolds**, W. P. Russ, M. Socolich, R. Ranganathan (2013). Evolution based design of proteins. *Methods in Enzymology* (523): 213-235. <http://dx.doi.org/10.1016/B978-0-12-394292-0.00010-2>
10. **K.A. Reynolds**, R.N. McLaughlin, R. Ranganathan (2011). Hotspots for allosteric regulation on protein surfaces. *Cell* (147): 1564-1575. <http://dx.doi.org/10.1016/j.cell.2011.10.049>
11. M.S. Hanes, **K.A. Reynolds**, C. McNamara, P. Ghosh, R.A. Bonomo, J.F. Kirsch, T.M. Handel (2011). Specificity and cooperativity at β -lactamase position 104 in TEM-1/BLIP and SHV-1/BLIP interactions. *Proteins* (73): 1267-1276. <http://dx.doi.org/10.1002/prot.22961>
12. **K.A. Reynolds**, V. Katritch, R. Abagyan (2010). Structure and modeling of GPCRs: Implications for drug discovery. *Molecular Pharmacology and Drug Targeting: Shifting Paradigms and New Directions*, Ed. Annette Gilchrist, Chapter 15.
13. V. Katritch, **K.A. Reynolds**, V. Cherezov, M.A. Hanson, C.B. Roth, M. Yeager. R. Abagyan (2009). Analysis of full and partial agonists binding to β_2 -adrenergic receptor suggests a role of transmembrane helix V in agonist-specific conformational changes. *J. Molecular Recognition* (22): 307-318. <http://onlinelibrary.wiley.com/doi/10.1002/jmr.949/abstract>
14. **K.A. Reynolds**, V. Katritch, R. Abagyan (2009). Identifying conformational changes of the β_2 adrenoceptor that enable accurate prediction of ligand/receptor interactions and screening for GPCR modulators. *Journal of Computer Aided Molecular Design* (23): 273-288. <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2667566/?tool=pubmed>
15. **K.A. Reynolds**, M.S. Hanes, J.M. Thomson, A.J. Antczak, J.M. Berger, R.A. Bonomo, J.F. Kirsch and T.M. Handel (2008). Computational redesign of the SHV-1 β -lactamase/ β -

lactamase Inhibitor Protein interface. *JMB* (382): 1265-1275.
<http://dx.doi.org/10.1016/j.jmb.2008.05.051>

16. A.B. Chowdry, **K.A. Reynolds**, M.S. Hanes, M. Voorhies, N. Pokala, and T.M. Handel (2007). An object-oriented Library for Computational Protein Design. *Journal of Comp. Chem.* (28): 2378-2388. <http://onlinelibrary.wiley.com/doi/10.1002/jcc.20727/abstract>
17. **K.A. Reynolds**, J.M Thomson, K.D. Corbett, C.R. Bethel, J.M. Berger, J.F. Kirsch, R.A. Bonomo, and T.M. Handel (2006). Structural and Computational Characterization of the SHV-1 β -lactamase/ β -lactamase Inhibitor Protein (BLIP) interface. *JBC* (281): 26745-26753.
<http://www.jbc.org/content/281/36/26745.long>
18. M.A. Lovato, M.M. Meyer, **K.A. Foster**, W. K. Wilson, W. Gu, E. L. de Hostos, and S. P. T. Matsuda (2000). Cloning and characterization of the Dictyostelium discoideum cycloartenol synthase cDNA. *Lipids* (36): 249-255. <http://dx.doi.org/10.1007/s11745-000-0520-3>

Press and links.

1. J.M Perkel. (2015) Seize the moment: A successful leap from postdoc to lab head requires tight control over time and tasks. *Nature* (517): 517-519. [link](#)
2. Related to Data Driven Discovery Investigator award: *UTSW press release* - [link](#), Reddit Ask-me-anything forum - [link](#), *Genome Web* - [link](#), *BioNew Texas* - [link](#)
3. Google scholar: <https://scholar.google.com/citations?user=6bWFU7MAAAAJ&hl=en>

Funding

Gordon and Betty Moore Foundation, Data Driven Discovery Award 12/14-12/19
Decoding the genome using evolutionary statistics
\$1.5M, Role: PI

Gordon and Betty Moore Foundation, Scialog Grant 07/16 – 07/17
Conditional Gene Essentiality as a Function of Cell Metabolic State
\$56,250, Role: PI

Teaching and outreach

Thread head, Core Course thread in Computational and Systems Biology	2018
Lecturer, Quantitative Biology, UTSW	2018
Lecturer, Mathematics in Medicine (a course for MD students), UTSW	2017
Organizer, Comp/Sys Bio student WIPS series (w/ Jaqaman), UTSW	2015-2017
Women in Science and Medicine (WISMAC) lunch panelist, UTSW	2017
Course director, Mathematical Foundations of Quantitative Biology, UTSW	2016-2017
Research mentor, Medical Student Summer Research Program	2015-2016
Discussion leader, Computational and Systems Biology thread, UTSW	2014-2017
Discussion leader, Core Course - Proteins thread, UTSW	2015
Discussion leader, Molecular Microbiology journal club, UTSW	2015
Lecturer, Molecular Microbiology graduate course, UTSW	2014-2017
Lecturer, Quantitative Biology thread, graduate core course, UTSW	2013-2017
Judge, Dallas Regional Science and Engineering Fair	2013-2017
SURF (summer undergraduate research fellowship) mentor, UTSW	2009-2015
Bioinformatics outreach talk, UTSW STARS program	2014
Research mentor, UT Dallas undergraduate senior thesis project	2011-2012
Women in Science and Engineering (WISE) mentor, SMU, Dallas TX	2008

Service

Panelist, Board Meeting Research Corporation for Scientific Advancement	2018
Thesis committee (<i>Leigh Manley, Lin lab</i>)	2018
Qualifying exam committee (<i>Michael Cotten, Rosen lab, Biophysics</i>)	2018
Qualifying exam committee chair (<i>Paul Blazek, Lin lab, MSTP</i>)	2018
Molecular Biophysics Steering Committee	2017-pres
Molecular Biophysics T32 Advisory Committee	2017-pres
Thesis committee chair (<i>Paul Blazek, Lin lab, MSTP</i>)	2017-pres
Thesis committee chair (<i>Yusuf Tamer, Toprak lab, Biophysics</i>)	2016-pres
Qualifying exam committee chair (<i>Yusuf Tamer, Biophysics</i>)	2016
Qualifying exam committee (<i>Bradley Quade, Biophysics</i>)	2015
Green Center for Systems Biology Faculty Search Committee, UTSW	2014-2015
<i>Reviewer for:</i> Cell Systems, Nature Biotechnology, Structure, Molecular Biology and Evolution, and Protein Science	

Talks

2018

- 07/18 Using evolutionary information to understand cellular systems. Keynote speaker, Function COSI – ISMB annual meeting, Chicago, IL
- 06/18 Evolution and engineering of allosteric regulation in protein kinases. Invited speaker, Protein Engineering Canada, Vancouver, CA
- 03/18 Using genomic data to identify modularity in cell systems. Invited speaker, Biology seminar series, Texas A&M University, College Station, TX
- 01/18 Genotype, phenotype. Gordon and Betty Moore Investigator Symposium, Monterey, CA

2017

- 10/17 Decoding the genome with evolutionary statistics. Keynote speaker, Australasian Genomic Technologies Association (AGTA) Conference, Hobart, Tasmania.
- 10/17 Using evolutionary information to decode the genome. Invited speaker, BioResearch Conference, UT Dallas, Dallas, TX
- 09/17 Hotspots for the evolution and engineering of new allostery. MSTP works in progress talk, UTSW, Dallas, TX
- 07/17 Hotspots for the evolution and engineering of allosteric regulation. Invited speaker, Workshop on designing biomolecular switches, Telluride Science Research Center, Telluride, CO
- 06/17 Using genomic data to identify modularity in cell systems. QP SURF lunch talk, UTSW, Dallas, TX
- 04/17 Conditional gene essentiality as a function of cell metabolic state. Funding awardee, Scialog Molecules-Come to-Life meeting, Tuscon, AZ
- 03/17 Evolutionary modularity. Invited speaker, Quantitative Biosciences Institute Spring Mutations meeting, UCSF, San Francisco, CA
- 03/17 An evolutionary module in central metabolism. Invited speaker, qBio seminar series, UCSD, San Diego, CA
- 02/17 Evolution of regulatory diversity in the kinase superfamily. Platform Talk, Biophysical Society Annual Meeting, New Orleans.
- 01/17 An evolutionary module in central metabolism. Student-invited speaker, Bioinformatics Biophysics and Chemistry (BBC) seminar. University of California, San Francisco.

2016

- 10/16 Statistical Genomics. Gordon and Betty Moore Investigator Symposium, New York, NY.

- 04/16 A conserved evolutionary module in central metabolism. Invited speaker, Biophysics seminar, ESPCI Paris Tech, Paris, France.
- 03/16 An evolutionary module in central metabolism. Invited speaker, Biophysics seminar, University of Illinois, Urbana-Champaign
- 03/16 An evolutionary module in central metabolism. Invited speaker, Biochemistry and molecular biology graduate student hosted seminar, University of British Columbia, Vancouver, Canada.
- 2015**
- 11/15 A statistical genomics approach to understanding cellular systems. Mathematics and biology seminar series, Southern Methodist University, Dallas, TX.
- 10/15 Decoding the genome: Relating sequence variation to function and phenotype. Gordon and Betty Moore Investigator Symposium, Seattle, WA.
- 08/15 An evolutionary module in central metabolism. Endowed scholars WIPS, UTSW (Dallas, TX)
- 08/15 Hotspots for allosteric regulation on a protein surface. Evolutionary Cell Biology Program, Kavli Institute for Theoretical Physics, UCSB (Santa Barbara, CA)
- 08/15 Decomposing complex systems. Evolutionary Cell Biology Program, Kavli Institute for Theoretical Physics, UCSB (Santa Barbara, CA)
- 05/15 Decomposing complex systems. Guest lecturer, Howard Berg lab, Harvard (Boston, MA)
- 2014**
- 12/14 Using evolutionary statistics to find functional modules. Invited talk, MIT (Boston, MA)
- 12/14 Finding evolutionary “design principles” for cellular systems. Special biophysics seminar, Boston University (Boston, MA)
- 11/14 Using evolutionary statistics to find functional modules. Microbiology seminar, UTSW (Dallas, TX)
- 09/14 Using evolutionary statistics to find functional modules. Molecular Biophysics discussion group, UTSW (Dallas, TX)
- 09/14 Understanding Cellular Systems Using Genome Data. UTSW STARS program – public science talks for educators (Dallas, TX)
- 09/14 Decoding the genome. New Faculty Research Forum, UTSW (Dallas, TX)
- 07/14 Decoding the genome. Invited talk, Gordon and Betty Moore Foundation data driven discovery finalist symposium (San Jose, California)
- 06/14 Principles of function in cellular protein networks. Invited talk, Protein Engineering Canada Conference (Ottawa, Ontario)
- 2013**
- 12/13 Principles of function in cellular protein networks. Graduate student invited seminar, UTHSC (Houston, TX)
- 09/13 Evolution, engineering and epistasis: mapping functional coupling between proteins. Seminar, MRC Laboratory of Molecular Biology (Cambridge, England).
- 02/13 Principles of function in cellular protein networks. Special seminar, Dept. of Bioengineering, California Institute of Technology (Pasadena, CA).
- 02/13 Principles of function in cellular protein networks. Special seminar, Dept. of Biochemistry, Molecular Biology and Biophysics, University of Minnesota (St. Paul, MN).
- 02/13 Principles of function in cellular protein networks. Special seminar, FAS Center for Systems Biology, Harvard University (Cambridge, MA).
- 02/13 Principles of function in cellular protein networks. Special seminar, Dept. of Systems Biology, Harvard Medical School (Boston, MA).

01/13 Principles of function in cellular protein networks. Special seminar, Green Center for Systems Biology, UTSW Medical Center (Dallas, TX)

2012

12/12 Principles of function in cellular protein networks. Earl Stadtman Symposium on genetics, genomics and systems biology, NIH (Bethesda, MD)

11/12 Principles of function in cellular protein networks. Special seminar, Dept. of Biology, Amherst College (Amherst, MA).

07/12 A structural model for the emergence of allosteric control in proteins. Gordon Research Conference, Intrinsically Disordered Proteins (Mount Snow, VT)

02/12 Hotspots for allosteric regulation on a protein surface. Finalist interview talk, UTSW award for excellence in postdoctoral research (Dallas, TX).

01/12 Hotspots for allosteric regulation on a protein surface. Seminar, Dept of Systems Biology, Harvard Medical School (Boston, MA).

2009-2011

07/11 Hotspots for allosteric regulation on a protein surface. Gordon Research Conference, Mechanisms of Cell Signaling (Bates College, ME).

03/11 A structural model for the emergence of allosteric control in proteins. Annual Meeting of the American Physical Society. (Dallas, TX)

02/11 A mechanism for the evolution of regulation in proteins. Invited talk, Biophysics group, CNRS (Grenoble, France)

10/10 A mechanism for the evolution of allosteric control in proteins. Dutch meeting on Molecular and Cellular Biophysics (Veldhoven, Netherlands).

03/10 Evolution of Allosteric Regulation in Proteins. Protein allostery meeting, UCSD. (San Diego, CA)

10/09 Evolution-based engineering of allosteric regulation in proteins. Society for Neuroscience (Chicago, IL).