Kimberly A. Reynolds, PhD

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SUMMARY OF RESEARCH INTERESTS AND ACCOMPLISHMENTS

Proteins function in the context of cellular systems. Whether they assemble into larger physical complexes, exchange intermediates in a metabolic pathway, or activate one another in a signaling cascade, protein-protein interactions form the basis for cells to grow, divide, and respond to the environment. My goal is to design synthetic protein systems that function efficiently and appropriately when placed in this interaction-rich cellular context. I bring a combination of expertise in statistical protein sequence analysis, comparative genomics, and high-throughput protein functional characterization to this problem. My laboratory has engineered synthetic light-sensing allosteric proteins [*2,7*], used co-evolutionary information to rewire cell signaling in yeast [*11,14*], and developed high-throughput experimental tools for deeply characterizing the *in vivo* constraints on protein activity and abundance [*4,5,9,10*]. As a junior faculty member, my ability to do innovative, interdisciplinary work was recognized by a Data-Driven Discovery Investigator Award (one of 14 nation-wide from the Gordon and Betty Moore Foundation), a Scialog Fellow Award from the Research Corporation for Scientific Advancement, a NSF CAREER award, and a Young Faculty Award from the Biopolymers-in-Vivo subgroup of the Biophysical Society. I received a UT Southwestern Outstanding Graduate Educator award for my leadership in creating a new Computational Biology graduate curriculum.

POSITIONS AND SCIENTIFIC APPOINTMENTS

Associate Research Professor **July 2025**
Department of Biophysics
Johns Hopkins University, Baltimore, MD

Chair – Graduate Track in Computational Biology **2024-present**
UT Southwestern Medical Center, Dallas, TX

Associate Professor **2023-present**
Lyda Hill Dept. of Bioinformatics - Green Center for Systems Biology, and Dept. of Biophysics
UT Southwestern Medical Center, Dallas, TX

Assistant Professor **2014-2023**
Lyda Hill Dept. of Bioinformatics - Green Center for Systems Biology, and Dept. of Biophysics
UT Southwestern Medical Center, Dallas, TX

Postdoctoral Fellow **2008-2014**
Green Center for Systems Biology, UT Southwestern Medical Center, Dallas, TX
Advisor: Dr. Rama Ranganathan

Postdoctoral Fellow **2007-2008**
Department of Molecular Biology, The Scripps Research Institute, La Jolla
Advisors: Dr. Ruben Abagyan and Dr. Ed Roberts

Adjunct Professor **Fall 2007**
Department of Chemistry, University of San Diego, CA
mentored teaching fellowship as part of the Scripps JUST program

EDUCATION

Ph.D in Biophysics **Dec. 2006**
University of California, Berkeley. Advisor: Dr. Tracy M. Handel

B.A. in Biochemistry **May 2001**
Rice University, Houston, TX.

HONORS AND OTHER APPOINTMENTS

Chair, Annual Meeting of the NSF National Synthesis Center for Emergence In the Molecular and Cellular Sciences (NCEMS)	**2024**
Thematic lead, NSF National Synthesis Center for Emergence In the Molecular and Cellular Sciences (NCEMS)	**2024**
Biophysical Society - Biopolymers in Vivo subgroup Program Co-Chair	**2023**
Biophysical Society – Biopolymers in Vivo subgroup Young Faculty Award	**2022**
Outstanding Graduate Educator – UT Southwestern Academy of Teachers	**2020**
National Science Foundation CAREER award	**2020**
Scialog Fellow, Molecules Come to Life Program	**2016**
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. Dokwal, P.M. Brown, K. Filipowska, **K.A. Reynolds** (2025). Considering metabolic context in enzyme evolution and design. Biochemistry (64):3495.
2. J.W. McCormick, J.C. Dinan, M.A.X. Russo, **K.A Reynolds** (2024). Local disorder is associated with enhanced catalysis in an engineered photoswitch. [*preprint*] bioRxiv doi: 10.1101/2024.11.26.625553
3. Y. Zhao, T.P. Wytock, **K.A. Reynolds**, A.E. Motter (2024). Irreversibility in bacterial regulatory networks. Science Advances (10):eado3232.
4. T.N. Nguyen, C. Ingle, S. Thompson, **K.A. Reynolds** (2024). The genetic landscape of a metabolic interaction. Nature Communications (15):3351.
5. R.M. Otto, A. Turska-Nowak, P.M. Brown, **K.A. Reynolds** (2024). A continuous epistasis model for predicting growth rate given combinatorial variation in gene expression and environment. Cell Systems (15):134-148.e7

6. J.C. Dinan, J.W. McCormick, **K.A. Reynolds** (2023). Engineering proteins using statistical models of coevolutionary sequence information. Perspectives on Machine Learning for Protein Science and Engineering, Cold Spring Harb Perspect Biol. (Ed. Peter K. Koo, Christian Dallago, Ananthan Nambiar, and Kevin K. Yang.) (16):a041463.
7. J. McCormick, M.A.X. Russo, S. Thompson, A. Blevins, **K.A. Reynolds** (2021). Structurally distributed surface sites tune allosteric regulation. Elife (10):e68346.
8. **K.A. Reynolds**, E. Rosa-Molinar, R.E. Ward, H. Zhang, B.R. Urbanowicz, A.M. Settles (2021). Accelerating biological insight for understudied genes. Integr Comp Biol (icab029).
9. A.D. Mathis, R.M. Otto, **K.A. Reynolds** (2021). A simplified strategy for titrating gene expression reveals new relationships between genotype, environment, and bacterial growth. Nucleic Acids Research (49):e6.
10. S. Thompson, Y. Zhang, C. Ingle, **K.A. Reynolds**, and T. Kortemme (2020). Altered expression of a quality control protease in E. coli reshapes the *in vivo* mutational landscape of a model enzyme. Elife (9):e53476.
11. J.W. McCormick, D. Pincus, O. Resnekov, and **K.A. Reynolds** (2019). Strategies for engineering and rewiring kinase regulation. Trends Biochem Sci (19):30234.
12. A.F.Schober, A.D. Mathis, C.Ingle, J.O. Park, L. Chen, J.D. Rabinowitz, I. Junier, O. Rivoire, and **K.A. Reynolds** (2019). A two-enzyme adaptive unit within bacterial folate metabolism. Cell Reports (27):3359.
13. Y.T. Tamer, I.K. Gaszek, H. Abdizadeh, T. Batur, **K. Reynolds**, A.R. Atilgan, C. Atilgan, E. Toprak (2019). High-order epistasis in catalytic power of dihydrofolate reductase gives rise to a rugged fitness landscape in the presence of trimethoprim selection. Molecular Biology and Evolution (36):1533.
14. D. Pincus, J. Pandey, Z.A. Feder, P. Creixell, O. Resnekov, and **K.A. Reynolds** (2018**)**. Engineering allosteric regulation in protein kinases. Science Signaling (11):555.
15. C. Rosensweig, **K.A. Reynolds,** P. Gao, Y. Shan, R. Ranganathan, J.S. Takahashi, C.B Green (2018). An evolutionary hotspot defines functional differences between CRYPTOCHROMES. Nature Communications (9):1138.
16. 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.
17. D. Pincus, O. Resnekov, **K.A. Reynolds** (2017). An evolution-based strategy for engineering allosteric regulation. Physical Biology (14): 025002.
18. O. Rivoire, **K.A. Reynolds**, R. Ranganathan (2016**).** Evolution-based functional decomposition of proteins. PLoS Comp Biol (12): e1004817.
19. **K.A. Reynolds** (2015). A new test of computational protein design: predicting posttranslational modification specificity for the enzyme SMYD2. Structure (23):11.
20. **K.A. Reynolds** (2014). Finding a common path: predicting gene function using inferred evolutionary trees. Developmental Cell (30):4.
21. **K.A. Reynolds**, W. P. Russ, M. Socolich, R. Ranganathan (2013). Evolution based design of proteins. Methods in Enzymology (523):213.
22. **K.A. Reynolds**, R.N.McLaughlin, R. Ranganathan (2011). Hotspots for allosteric regulation on protein surfaces. Cell (147):1564.

23. 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.
24. **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.
25. 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. Journal of Molecular Recognition (22):307.
26. **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.
27. **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. Journal of Molecular Biology (382):1265.
28. 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 Computational Chemistry (28):2378.
29. **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. Journal of Biological Chemistry (281):26745.
30. 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.

FUNDING

Pending

NSF 10/2025-9/2028
EXPAND: Top-down analysis of metabolic and differentiation networks
Requested direct costs: $442,220 Role: Co-I

Current

Human Frontier Science Program (HFSP) 9/2025-8/2028
Mapping and modeling protein evolution on the abundance-activity-toxicity isoclines of fitness
Requested direct costs: $362,765 Role: Co-I

NIH 2R01GM136842 9/2024-7/2028
Mapping genetic variation in enzyme velocity to growth rate phenotype
direct costs: $860,000 Role: PI

NSF 2206974 8/2022-7/2026
Quantifying the prevalence and phenotypic consequences of transcriptional irreversibility in bacteria

direct costs: $822,068 ($461,128 to Reynolds, $360,940 to Co-PI) Role: PI

NSF 1942354 6/2020-5/2026
CAREER: Defining structural principles for the engineering and evolution of allostery
direct costs: $682,843 Role: PI

Completed

NIH 1R01GM136842 4/2020-3/2024
Mapping genetic variation in enzyme velocity to growth rate phenotype
direct costs: $800,000 Role: PI

Gordon and Betty Moore Foundation, Data Driven Discovery Continuation 12/2019-11/2021
Decoding the genome using evolutionary statistics
direct costs: $350,000, Role: PI

Gordon and Betty Moore Foundation, Data Driven Discovery Award 12/2014-11/2019
Decoding the genome using evolutionary statistics
direct costs: $1.5M, Role: PI

Gordon and Betty Moore Foundation, Scialog Fellow Grant 7/2016-7/2017
Conditional Gene Essentiality as a Function of Cell Metabolic State
direct costs: $56,250, Role: PI

TEACHING AND SERVICE

Classroom Instruction

Thread head, Core Course thread in Computational and Systems Biology	2018-pres
Lecturer, Quantitative Biology, UTSW	2018-pres
Lecturer, Core course thread in Protein biophysics	2019-2021
Course director, Mathematical Foundations of Quantitative Biology, UTSW	2016-pres
Lecturer, Molecular Microbiology graduate course, UTSW	2014-2018
Lecturer, Core Course thread in Computational and Systems Biology	2013-2017
Lecturer, Mathematics in Medicine (a course for MD students), UTSW	2017
Discussion leader, Core Course - Proteins thread, UTSW	2015
Discussion leader, Molecular Microbiology journal club, UTSW	2015
Discussion leader, Core Course thread in Computational and Systems Biology	2014-2021
Bioinformatics outreach talk, UTSW STARS program	2014

Teaching related service

Member: *Molecular Biophysics graduate program,*
Biomedical Engineering graduate program - Computational Biology track.
Affiliated with Molecular Microbiology graduate program, 2014-Fall 2018.

Medical Scientist Training Program (MSTP) Admissions Committee	2023-pres
Women in computational biology speaker, Komen Foundation Hackathon	2023
Director, STARS Python workshop for high school students	2022-pres
Reviewer, ABRCMS Annual meeting	2021-pres
Bioinformatics Recruitment and Engagement Committee (BREC)	2022-2025
DBS Graduate Student Admissions Committee	2020-2023
Chair, Computational Biology Curriculum Committee	2020-2021

Molecular Biophysics Steering Committee	2017-pres
Molecular Biophysics T32 Advisory Committee	2017-pres
SURF (summer undergraduate research fellowship) mentor, UTSW	2014-pres
Organizer, Comp/Sys Bio student WIPS series (w/ Jaqaman), UTSW	2015-2020
External reviewer, PhD thesis Matt Deyell, Paris Diderot, France	2018
Women in Science and Medicine (WISMAC) lunch panelist, UTSW	2017
Judge, Dallas Regional Science and Engineering Fair	2013-2017
Research mentor, Medical Student Summer Research Program	2015-2016
Research mentor, UT Dallas undergraduate senior thesis project	2011-2012
Women in Science and Engineering (WISE) mentor, SMU, Dallas TX	2008

As a member of the biomedical engineering and molecular biophysics graduate programs, I have served on 19 thesis committees and 11 qualifying exam committees.

Other Service

Panelist, NSF Chemical, Biological, Environmental, and Transport Systems (CBET)	2024
Panelist, NSF Molecular and Cell Biology (MCB)	2024
Lyda Hill Dept. of Bioinformatics Faculty Search Committee Chair	2023-2024
Biopolymers in vivo subgroup of Biophysical Society – program co-chair	2023
Ad hoc reviewer, NSF Chemistry of Life program, Molecular Biophysics program	2022
University Lecture Series Committee	2022
NIH ZRG1 GGG-P ML Member Conflict Genes, Genomes, and Genetics Study Section	2021
Meeting organizer and publication committee chair, Function Community of Special Interest (COSI) - Intelligent Systems for Molecular Biology (ISMB)	2019-2023
Reviewer, Human Frontier Science Program (HFSP)	2019
Panelist, Board Meeting of the Research Corporation for Scientific Advancement	2018
Green Center for Systems Biology Faculty Search Committee, UTSW	2015

Reviewer for: Science, eLife, PNAS, Journal of Molecular Biology, Biophysical Journal, Nature Ecology and Evolution, Molecular Systems Biology, Nature Communications, Cell Systems, Nature Biotechnology, Structure, Molecular Biology and Evolution, PLOS Biology, PLOS Computational Biology, Bioinformatics, Journal of Antimicrobial Chemotherapy, Genome Biology, Metabolic Engineering, and Protein Science

SCIENTIFIC TALKS

2025

04/01	Mapping and modeling the impact of protein biochemical variation on growth rate phenotype. Seminar, Department of Molecular and Human Genetics, Baylor College of Medicine. Houston, Texas.

2024

12/16	The genetic landscape of a biochemical interaction. Keynote speaker, PROTEO-Laval. Quebec City, Canada.
12/13	Mapping the relationship between gene expression variation and bacterial growth rate phenotype with CRISPRi. Seminar, Institute of Integrative Biology and Systems (IBIS), Université Laval. Quebec City, Canada.
11/13	Mapping and modeling the “design specifications” of cellular systems. Seminar, Department of Biochemistry, University of Kansas Medical Center. Kansas City, KS.
09/25	Mapping and modeling the “design specifications” of cellular systems. Seminar, Department of Biological Sciences, University of Texas Dallas. Dallas, TX.

09/13 Mapping and modeling the “design specifications” of cellular systems. Seminar, Department of Chemical and Biological Engineering, The University of Colorado Boulder. Boulder, CO.

04/25 Dissecting the genetic basis of bacterial growth phenotype with CRISPRi. Seminar, School of Pharmacy, University of Wisconsin. Madison, WI.

02/29 Mapping and modeling the impact of protein biochemical variation on growth rate phenotype. Seminar, Department of Biophysics, Johns Hopkins University. Baltimore, MD

2023

10/23 The genetic landscape of a metabolic interaction. Invited speaker, Gibbs Society for Biological Thermodynamics. Carbondale, IL

09/23 Quantifying and predicting the relationship between enzyme biochemistry and cell growth rate. Telluride Science Research Center Workshop on Plasticity in Biological Organization. Telluride, CO

09/23 On the evolvability of new allosteric regulation. Invited speaker, Center for the Physics of Evolved Systems, University of Chicago. (virtual)

03/23 The genetic landscape of a metabolic interaction. Seminar, Institute of Molecular Biology (IMB), University of Oregon. Eugene, OR

2022

11/22 The genetic landscape of a metabolic interaction. Seminar, Department of Chemistry and School of Pharmacy, University of North Carolina. Chapel Hill, NC

09/22 A continuous epistasis model for predicting growth rate given combinatorial variation in gene expression and environment. Telluride Science Research Center Workshop on Emergent Simplicity in Biophysical Dynamics. Telluride, CO

09/22 The genetic landscape of a metabolic interaction. Seminar, Department of Biochemistry and Biophysics, Texas A&M University. College Station, TX

03/22 The genetic landscape of a metabolic interaction. Seminar, Department of Chemistry, University of Washington. Seattle, WA

02/22 Mapping the sequence determinants of protein regulation. Invited talk, Biopolymers *in vivo* subgroup, Biophysical Society. San Francisco, CA

2021

11/21 Mapping the sequence determinants of protein function and regulation. Harvard Systems Biology Theory Lunch (virtual)

11/21 Quantifying (and modeling) the relationship between gene expression and bacterial growth rate. Seminar, Department of Microbiology, UTSW Medical Center

09/21 Challenges in synthesizing Deep Mutational Scanning data. Invited speaker and panelist, NSF workshop: Challenges and Opportunities in Synthesizing Massively Parallel Assays (virtual)

09/21 Understanding and using SCA. Invited workshop for the Herschlag and Fordyce labs, Stanford, CA (virtual)

07/21 Emergent simplicity in epistasis. Telluride Science Research Center workshop – Emergent simplicity in Biophysical Dynamics, Telluride, CO (virtual)

04/21 Mapping sequence constraints in an essential metabolic enzyme. Keynote speaker, Mutational Scanning Symposium, Center for the Multiplex Assessment of Phenotype, University of Washington (virtual)

03/21 Evolution inspired engineering of allostery. Seminar, Systems Biology, Universite Laval, Quebec CA (virtual)

2020

10/20	Structurally distributed surface sites tune allosteric regulation. Seminar, Biological Physics, Arizona State University, Tempe AZ (virtual)
02/20	Mapping and modeling functional constraints on an essential metabolic enzyme. Invited speaker, Winter Q-Bio Annual Meeting, Waikoloa, HI

2019

11/19	A two-enzyme adaptive unit within bacterial folate metabolism. Seminar, Center for Physics of Evolving Systems, University of Chicago, IL
07/19	Rewiring how cells respond to the environment, using protein sequence information. QP SURF lunch talk, UTSW, Dallas, TX
06/19	Hotspots for the evolution and engineering of allosteric regulation. Invited speaker, Molecular mechanisms in evolution Gordon Research Conference, MA
05/19	A two-enzyme adaptive unit within bacterial folate metabolism. UC Irvine, CA
04/19	Comprehensively mapping the mutations influencing allostery in a model enzyme. Stanford University, CA
04/19	Rewiring how cells respond to the environment, using protein sequence information. Gordon and Betty Moore Investigator Symposium, San Francisco, CA
03/19	Hotspots for the evolution and engineering of allosteric regulation. Invited speaker, Biophysical Society, Baltimore, MD

2018

12/18	Hotspots for the evolution and engineering of allosteric regulation. Invited speaker, ASCB annual meeting, San Diego, CA
10/18	Hotspots for the evolution and engineering of allosteric regulation. Invited speaker, Northeastern Structure Symposium, Farmington, CT
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 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 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 Colombia, 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, 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, Mol. 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, Intriniscally 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	Hotpots for allosteric regulation on a protein surface. Seminar, Dept of Systems Biology, Harvard Medical School (Boston, MA).