

Kimberly A. Reynolds

Contact

Green Center for Systems Biology
University of Texas Southwestern Med. Center
6001 Forest Park Blvd, ND11.120D,
Dallas, TX 75390

214-645-6157 (office)
214-645-8123 (laboratory)
kimberly.reynolds@utsouthwestern.edu
<https://reynolds-lab.net>

Education

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

Research and Professional Experience

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

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. J. McCormick, M.A.X. Russo, S. Thompson, A. Blevins, **K.A. Reynolds** (2021). Structurally distributed surface sites tune allosteric regulation. *Elife* (10):e68346. <https://doi.org/10.7554/elife.68346>
2. **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). <https://doi.org/10.1093/icb/icab029>
3. 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. <https://doi.org/10.1093/nar/gkaa1073>
4. 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. <https://doi.org/10.7554/eLife.53476>
5. J.W. McCormick, D. Pincus, O. Resnekov, and **K.A. Reynolds** (2019). Strategies for engineering and rewiring kinase regulation. *Trends Biochem Sci* (19):30234. <https://doi.org/10.1016/j.tibs.2019.11.005>
6. 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. <https://doi.org/10.1016/j.celrep.2019.05.030>
7. 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. <https://doi.org/10.1093/molbev/msz086>
8. 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. <https://doi.org/10.1126/scisignal.aar3250>
9. 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. <http://dx.doi.org/10.1038/s41467-018-03503-6>
10. 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>
11. 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>
12. 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/>

13. **K.A. Reynolds** (2015). A new test of computational protein design: predicting posttranslational modification specificity for the enzyme SMYD2. *Structure* (23):11. <http://dx.doi.org/10.1016/j.str.2014.12.004>
14. **K.A. Reynolds** (2014). Finding a common path: predicting gene function using inferred evolutionary trees. *Developmental Cell* (30):4. <http://dx.doi.org/10.1016/j.devcel.2014.06.029>
15. **K.A. Reynolds**, W. P. Russ, M. Socolich, R. Ranganathan (2013). Evolution based design of proteins. *Methods in Enzymology* (523):213. <http://dx.doi.org/10.1016/B978-0-12-394292-0.00010-2>
16. **K.A. Reynolds**, R.N.McLaughlin, R. Ranganathan (2011). Hotspots for allosteric regulation on protein surfaces. *Cell* (147):1564. <http://dx.doi.org/10.1016/j.cell.2011.10.049>
17. 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. <http://dx.doi.org/10.1002/prot.22961>
18. **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.
19. 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. <http://onlinelibrary.wiley.com/doi/10.1002/jmr.949/abstract>
20. **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. <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2667566/?tool=pubmed>
21. **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. <http://dx.doi.org/10.1016/j.jmb.2008.05.051>
22. 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. <http://onlinelibrary.wiley.com/doi/10.1002/jcc.20727/abstract>
23. **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. <http://www.jbc.org/content/281/36/26745.long>
24. 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. <http://dx.doi.org/10.1007/s11745-000-0520-3>

Funding

Current

NSF CAREER 6/2020 – 5/2025
CAREER: Defining structural principles for the engineering and evolution of allostery
\$1,099,999, Role: PI

NIH R01 4/2020 – 3/2024
Mapping genetic variation in enzyme velocity to growth rate phenotype
\$1,269,837, Role: PI

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