

# D. Allan Drummond

Biochemistry & Molecular Biology, The University of Chicago  
GCIS W234, 929 E. 57th St., Chicago, IL 60637  
dadrummond@uchicago.edu | (773) 834-2017 | drummondlab.org

## Academic Positions

*The University of Chicago* 2011– Chicago, IL  
Associate Professor with tenure (effective July 1, 2018), Depts. of Biochemistry & Molecular Biology and Human Genetics.

*Harvard University* 2006–2011 Cambridge, MA  
Bauer Fellow (PI with independent lab), FAS Center for Systems Biology.

## Education

*California Institute of Technology* 2002–2006 Pasadena, CA  
Ph.D. in Computation & Neural Systems, advised by Frances H. Arnold.  
Thesis: “Misfolding Dominates Protein Evolution”

*Princeton University* 1991–1995 Princeton, NJ  
B.S.E. *cum laude* in Mechanical and Aerospace Engineering.

## Honors & Awards (5 most recent)

Junior Faculty Award, Biopolymers In Vivo subgroup, Biophysical Society, 2018.  
Distinguished Faculty Award, The University of Chicago Biological Sciences Division, 2017.  
W.J. Youden Award (with 3 coauthors), American Statistical Association, 2015.  
Pew Scholar in the Biomedical Sciences, 2012–2016.  
Sloan Research Fellow, 2012–2014.

## Selected Peer-Reviewed Publications (of 22 total, *h*-index: 19)

1. Riback, J.A.\* , Katanski, C.D.\* (co-first authors), Kear-Scott, J.L., Pilipenko, E.V., Rojek, A.E., Sosnick, T.R., and **Drummond, D.A.**, “Stress-triggered phase separation is an adaptive, evolutionarily tuned response,” *Cell* 168(6):1028–1040 (2017).
2. Wallace, E.W.J., Kear-Scott, J.L., Pilipenko, E.V., Schwartz, M.H., Laskowski, P.R., Rojek, A.E., Katanski, C.D., Riback, J.A., Dion, M.F., Franks, A.M., Airoidi, E.M., Pan, T., Budnik, B.A., and **Drummond, D.A.**, “Reversible, specific, active aggregates of endogenous proteins assemble upon heat stress,” *Cell* 162(6):1286–1298 (2015).
3. Csárdi, G, Franks, A.M., Choi, D.S., Airoidi, E.M., and **Drummond, D.A.**, “Accounting for experimental noise reveals that mRNA levels, amplified by post-transcriptional processes, largely determine steady-state protein levels in yeast,” *PLOS Genetics* 11(5):e1005206 (2015).
4. Zaborske, J., Bauer DuMont, V.L., Wallace, E.W.J., Pan, T., Aquadro, C.F., and **Drummond, D.A.**, “A nutrient-driven tRNA modification alters translational fidelity and genome-wide protein coding across an animal genus,” *PLOS Biology* 12(12):e1002015 (2014).
5. Franks, A.M., Csárdi, G., **Drummond, D.A.**, and Airoidi E.M., “Estimating a structured covariance matrix from multi-lab measurements in high-throughput biology,” *Journal of the American Statistical Association* 110 (509) :27–44 (2014).
6. Wallace, E.W.J., Airoidi, E.M., and **Drummond, D.A.**, “Estimating selection on synonymous codon usage from noisy experimental data,” *Molecular Biology & Evolution* 30(6):1438–53 (2013).

7. Geiler-Samerotte, K.A., Dion, M.F., Budnik, B.A., Hartl, D.L., and **Drummond, D.A.**, “Misfolded proteins impose a dosage-dependent fitness cost and trigger a cytosolic unfolded protein response in yeast,” *Proc. Nat’l. Acad. Sci. USA* 180(2):680–685 (2011).
8. **Drummond, D.A.** and Wilke, C.O., “Mistranslation-induced protein misfolding as a dominant constraint on coding-sequence evolution,” *Cell* 134(2):341–52 (2008).
9. Wilke, C.O. and **Drummond, D.A.**, “Population genetics of translational robustness,” *Genetics* 173:473–81 (2006).
10. **Drummond, D.A.**, Raval, A., and Wilke, C.O., “A single determinant dominates the rate of yeast protein evolution,” *Molecular Biology & Evolution* 23(2):327–37 (2006). (*MBE* Early Citation Classic.)
11. **Drummond, D.A.**, Bloom, J.D., Adami, C., Wilke, C.O., and Arnold, F.H., “Why highly expressed proteins evolve slowly,” *Proc. Nat’l. Acad. Sci. USA* 102(40):14338–43 (2005). (Nature Research Highlights and J. Cell Biol. Research Roundup; #1 most-read PNAS paper, Oct. 2005)
12. **Drummond, D.A.**, Iverson, B.L., Georgiou, G.G., and Arnold, F.H., “Why high-error-rate mutagenesis libraries are enriched in functional and improved proteins,” *J. Mol. Biol.* 350(4):806–16 (2005).
13. **Drummond, D.A.**, Silberg, J.J., Meyer, M.M., Wilke, C.O., and Arnold, F.H., “On the conservative nature of intragenic recombination,” *Proc. Nat’l. Acad. Sci. USA* 102(15):5380–5 (2005).

### **Selected Reviews & Commentary (of 6 total)**

1. Triandafillou, C.G. & **Drummond, D.A.** “Heat Shock Factor 1: from fire chief to crowd-control specialist,” *Molecular Cell* 63(1):1–2 (2016).
2. Wallace, E.W.J. & **Drummond, D.A.** “Dying mRNA tells a story of its life,” *Cell* 161(6) (2015).
3. **Drummond, D.A.**, “How infidelity creates a sticky situation,” *Molecular Cell* 48(5): 663–664 (2012).
4. Wilke, C.O. & **Drummond, D.A.**, “Signatures of protein biophysics in coding sequence evolution,” *Curr. Opin. Struct. Bio.* 20(3):385–9 (2010).

### **Invited Speaking (most recent)**

1. Research seminar, UT Southwestern, 2017.
2. Professor Mariam Hasson Memorial Lecture, Purdue University, 2017.
3. Research seminar, Stowers Institute for Medical Research, 2017.
4. Research Seminar, UCSF (Biochemistry & Biophysics), 2017.
5. Protein Aggregation in Health & Disease, FASEB Science Research Conference, 2017.
6. Stress Proteins in Growth, Development, and Disease, Gordon Research Conference, 2017.

### **Support**

NIGMS 1-R01-GM126547-01, “Determining the molecular basis of adaptive stress-triggered protein phase separation,” 2018–2021, PI: Drummond (co-PI Tobin Sosnick).

Catalyst Award, Chicago Biomedical Consortium, “Asymmetric retention of a regulatory memory by organelle tethering,” 2016–2017, PI: Drummond (multi-PI with Laura Lackner, NWU).

US ARO W911NF-14-1-0411, “Mechanisms of prokaryotic evolution,” 2014–2019, PI: Lynch.

NIGMS 1-U54-GM105816, “Interactions regulating translation and protein biogenesis in vivo,” 2013–2018, PI: Clark.

### **Service**

Program co-organizer, 2018 Biopolymers In Vivo subgroup meeting, Biophysical Society

Co-organizer, 2016 Midwest Stress & Molecular Chaperones meeting, Northwestern University

Guest Editor: *PNAS*; *PLOS Genetics*; *PLOS Computational Biology*

Reviewer: *Science*; *Nature*; *Cell*; *PNAS*; *eLife*; *PLOS Biology*; *PLOS Genetics*; *Molecular Cell*; and others.

## **Membership**

American Society for Biochemistry and Molecular Biology  
American Society for Cell Biology  
Biophysical Society  
Society for Molecular Biology and Evolution

## **Industry Experience**

1995–2002

Trilogy Software, Inc.

Austin, TX

Multiple positions; finished as Director, Trilogy University (180-person organization). Responsible for research direction, curriculum, external relations for nationally known corporate university and R&D incubator (subject of April 2001 *Harvard Business Review* feature “No Ordinary Boot Camp”). Led leadership development program.