

D. Allan Drummond

Biochemistry & Molecular Biology, The University of Chicago
GCIS W234, 929 E. 57th St., Chicago, IL 60637
dadrummond@uchicago.edu | <http://drummondlab.org>

Academic Positions

The University of Chicago 2011– Chicago, IL
Associate Professor, 2018–, Dept. of Biochemistry & Molecular Biology
and Dept. of Medicine, Section of Genetic Medicine.
Member: Committee on Genetics, Genomics & Systems Biology; Institute for Biophysical Dynamics.
Assistant Professor, 2011–2018
Harvard University 2006–2011 Cambridge, MA
Bauer Fellow (PI), 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 (selected)

John H. Blaffer Lecturer, MD Anderson Cancer Center, 2022.
Irvin Isenberg Memorial Lecturer, Marine Biological Laboratories, 2022.
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 Fellow in Computational & Evolutionary Molecular Biology, 2012.
Milton and Francis Clauser Doctoral Prize (Caltech thesis prize, all fields), 2006.

Publications (selected)

1. Glauninger HG*, Bard JAM*, Hickernell CJW*, Airolidi EM, Li W, Singer RH, Paul S, Fei J, Sosnick TR, Wallace EWJ, Drummond DA, “Transcriptome-wide mRNA condensation precedes stress granule formation and excludes stress-induced transcripts,” *bioRxiv* (2024).
2. Bard, J.A.M.B., Drummond, D.A., “Chaperone regulation of biomolecular condensates,” *Frontiers in Biophysics* 2 :1342506 (2024).
3. Keyport Kik, S., Christopher, D., Glauninger, H., Wong Hickernell, C., Bard, J.A.M., Lin, K.M., Squires, A.H. Ford, M., Sosnick, T.R., **Drummond, D.A.**, “An adaptive biomolecular condensation response is conserved across environmentally divergent species,” *Nature Communications* 15 :3127 (2024).
4. Triandafillou, C.G., Pan, R., Dinner, A.R., **Drummond, D.A.**, “Pervasive, conserved structure in highly charged protein regions,” *PLOS Computational Biology* 19(10): e1011565 (2023).
5. Glauninger, H., Wong Hickernell, C.J., Bard, J.A.M., **Drummond, D.A.**, “Stressful steps: progress and challenges in understanding stress-induced mRNA condensation and stress granule accumulation,” *Molecular Cell* 82(14):2544–2556 (2022). [review]
6. Yoo, H., Bard, J.B., Pilipenko, E.V., **Drummond, D.A.**, “Chaperones directly and efficiently disperse stress-triggered biomolecular condensates,” *Molecular Cell* 82(4):741–755 (2022).

7. Triandafillou, C.G., Katanski, C.D., Dinner, A.R., and **Drummond, D.A.** “Transient intracellular acidification regulates the core transcriptional heat shock response.” *eLife* 9 (August) (2020).
8. Pattanayak, G.K., Liao, Y., Wallace, E.W.J., Budnik, B.A., **Drummond, D.A.**, and Rust, M.J. “Daily cycles of reversible protein condensation in cyanobacteria.” *Cell Reports* 32 (7): 108032 (2020).
9. Yoo, H., Triandafillou, C.G., and **Drummond, D.A.** “Cellular sensing by phase separation: Using the process, not just the products.” *The Journal of Biological Chemistry* 294 (18): 7151–59 (2019). [review]
10. 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).
11. 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).
12. 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).
13. 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).
14. 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).
15. 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).
16. 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).
17. Wilke, C.O. & **Drummond, D.A.**, “Signatures of protein biophysics in coding sequence evolution,” *Curr. Opin. Struct. Bio.* 20(3):385–9 (2010). [review]
18. **Drummond, D.A.** and Wilke, C.O., “The evolutionary consequences of erroneous protein synthesis.” *Nature Reviews. Genetics* 10 (10): 715–24 (2009). [review]
19. **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).
20. Wilke, C.O. and **Drummond, D.A.**, “Population genetics of translational robustness,” *Genetics* 173:473–81 (2006).
21. **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).
22. **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).
23. **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).
24. **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).

Perspectives

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).

