

D. Allan Drummond

Gordon Center for Integrative Science, University of Chicago
GCIS W234, 929 E. 57th St., Chicago, IL 60637
dadrummond@uchicago.edu (773) 834-2017
<http://drummondlab.org>

ACADEMIC POSITIONS

University of Chicago	2011–	Chicago, IL
Assistant Professor, 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. <i>cum laude</i> in Mechanical and Aerospace Engineering.		

HONORS & AWARDS

W.J. Youden Award (with 3 coauthors), American Statistical Association, 2015.
Pew Scholar in the Biomedical Sciences, 2012–2016.
Sloan Research Fellow, 2012–2014.
Ellison Medical Foundation New Scholar in Aging, 2012 (declined).
Pritzker Scholar, University of Chicago (three awarded; sole junior awardee), 2012.
Symposium Fellow, 74th CSHL Symposium on Quantitative Biology (*Evolution: The Molecular Landscape*), 2009.
Postdoctoral Fellow Poster Award, Society for Molecular Biology & Evolution annual meeting, 2008.
Bauer Fellowship, FAS Center for Systems Biology, Harvard University, 2006–2011.
Milton and Francis Clauser Doctoral Prize (Caltech thesis prize, all fields), 2006.
Demetriades-Tsafka Prize in Bioengineering or Related Fields (best thesis, publication or discovery), 2006.
Everhart Distinguished Graduate Student Lecturer Award (Caltech-wide, three awarded), 2006.
Graduate Student Poster Award, Society for Molecular Biology & Evolution annual meeting, 2006.
Star Award and Recruiting Gem, Trilogy Software, 2000.

SUPPORT

Catalyst award, Chicago Biomedical Consortium, “Asymmetric retention of a regulatory memory by organelle tethering,” 2016–2017, PI: Drummond (multi-PI with Laura Lackner, NWU).
Chicago Biomedical Consortium, “Tracking mRNA localization and translation under heat stress,” 2015–2016, PI: Drummond.
US ARO W911NF-14-1-0411, “Mechanisms of prokaryotic evolution,” 2014–2019, PI: Michael Lynch, IU; role: co-I.
NIGMS 1-U54-GM105816, “Interactions regulating translation and protein biogenesis *in vivo*,” 2013–2018, PI: Patricia Clark, Notre Dame; role: co-I.
Pew Charitable Trust, Pew Scholar in the Biomedical Sciences, 2012–2016, PI: Drummond.

COMPLETED SUPPORT

Big Ideas Generator, Seed Award, “Evolving adaptive protein assembly,” 2014–2015, PI: Drummond.
Alfred P. Sloan Foundation, Sloan Research Fellowship, 2012–2014, PI: Drummond.
NIGMS 1-R01-GM088344, “The biophysical basis of translational selection,” 2009–2013, PI Claus Wilke, role co-I.

INVITED SPEAKING

FASEB *Protein Folding in the Cell*. Saxton’s River, VT. July 2016.
Physical Basis of Cellular Adaptation and Memory, Bellairs Institute, Barbados, April 2016.
Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany, April 2016.

Marquette University, March 2016.
Stanford University, February 2016.
Scripps Research Institute, December 2015.
Gordon Research Conference, *Stress Proteins in Growth, Development & Disease*. Lucca, Italy. July 2015.
Fred Hutchinson Cancer Research Center, June 2015.
University of Texas Medical School at Houston, November 2014.
1st HSF workshop, Paris, France, April 2014.
Columbia University, March 2014.
Causes of Genome Evolution (SMBE satellite meeting), Mishima, Japan, March 2014.
Princeton University, October 2013.
Kavli Israeli-American Frontiers of Science Symposium, June 2013.
Stony Brook University, December 2012.
U. Wyoming, October 2012.
VIB Student Symposium, Ghent, Belgium, August 2012.
KU Leuven, Belgium, August 2012.
Computations in Science seminar, University of Chicago, June 2012.
Midwest Conference on Protein Folding, April 2012 (closing plenary speaker).
Rochester University, Biology Seminar Series, April 2012.
Chicago Mass Spectrometry Discussion Group, Northwestern University, March 2012.
Phylomedicine Symposium, ASU, March 2012.
ASCB Symposium on Protein Balance, December 2011.
SMBE annual meeting, Kyoto, Japan 2011.
Experimental Approaches to Evolution and Ecology using Yeast, Heidelberg, Germany, 2010.
Frontiers in Genomics Seminar Series, UNAM, Cuernavaca, Mexico, 2009 (academic talk and public lecture).
Genome Informatics, Cold Spring Harbor, NY 2005.
USC Biol. Sci. seminar, 2004.

PEER-REVIEWED PUBLICATIONS

- 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).
- 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).
- 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). (Accompany *Synopsis* by R. Robinson.)
- Franks, A.M., Csardi, G, **Drummond, D.A.**, and Airoidi, E.M., “Estimating a structured covariance matrix from multi-lab measurements in high-throughput biology,” *J. Am. Stat. Assoc.* 110(509):27–44 (2014).
- Geiler-Samerotte, K.A., Hashimoto, T., Dion, M.F., Budnik, B.A., Airoidi, E.M., and **Drummond, D.A.**, “Quantifying condition-dependent intracellular protein levels enables high-precision fitness estimates,” *PLOS One*, 8(9): e75320 (2013).
- 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). (*Faculty of 1000* recommended.)
- Agashe, D., Martinez-Gomez, N.C., **Drummond, D.A.**, and Marx, C.J., “Good codons, bad transcript: large reductions in gene expression and fitness arising from synonymous mutations in a key enzyme,” *Molecular Biology & Evolution*, 30(3):549–60 (2013).

8. 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).
9. **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). (Accompanying *Preview* by Powers & Balch; *Faculty of 1000* rated.)
10. Zhou, T., **Drummond, D.A.**, and Wilke, C.O., “Contact density affects protein evolutionary rate from bacteria to mammals,” *J. Mol. Evol.* 66(4):395–404 (2008).
11. Li, Y., **Drummond, D.A.**, Sawayama, A.M., Snow, C.S., Bloom, J.D., and Arnold, F.H., “A diverse family of thermostable cytochrome P450s created by recombination of stabilizing fragments,” *Nat. Biotech.* 25(9):1051–6 (2007). (*Faculty of 1000* rated.)
12. Bloom, J.D., **Drummond, D.A.**, Arnold, F.H., and Wilke, C.O., “Structural determinants of the rate of protein evolution in yeast,” *Molecular Biology & Evolution* 23(9):1751–61 (2006).
13. Wilke, C.O. & **Drummond, D.A.**, “Population genetics of translational robustness,” *Genetics* 173:473–81 (2006).
14. **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, 2013; *Faculty of 1000* rated.)
15. **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; *Faculty of 1000* rated.)
16. Wilke, C.O., Bloom, J.D., **Drummond, D.A.**, and Raval, A., “Predicting the tolerance of proteins to random amino acid substitution,” *Biophysical Journal* 89(6):3714–20 (2005).
17. **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). (*Faculty of 1000* rated.)
18. **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).
19. Bloom, J.D., Silberg, J.J., Wilke, C.O., **Drummond, D.A.**, Adami, C., and Arnold, F.H., “Thermodynamic prediction of protein neutrality,” *PNAS* 102(3):606–11 (2005). (*Faculty of 1000* rated.)

REVIEWS & COMMENTARY

20. Wallace, E.W.J. and **Drummond, D.A.** “Dying mRNA tells a story of its life,” *Cell* 161(6): 1246–1248 (2015).
21. **Drummond, D.A.**, “How infidelity creates a sticky situation,” *Molecular Cell* 48(5): 663–664 (2012).
22. Wilke, C.O. and **Drummond, D.A.**, “Signatures of protein biophysics in coding sequence evolution,” *Curr. Opin. Struct. Bio.* 20(3):385–9 (2010).
23. **Drummond, D.A.** and Wilke, C.O., “The evolutionary consequences of erroneous protein synthesis,” *Nature Reviews Genetics* 10(10):715–24 (2009).
24. **Drummond, D.A.**, “Protein evolution: innovative chaps,” *Current Biology* 19(17):R740–2 (2009).

SERVICE

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

Invited Perspectives: *Cell*, *Molecular Cell*; *Current Biology*

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

MEMBERSHIP

American Society for Biochemistry and Molecular Biology (ASBMB), 2014–present

American Society for Cell Biology (ASCB), 2011–present

Society for Molecular Biology and Evolution (SMBE), 2006–present

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.