

# D. Allan Drummond

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

## ACADEMIC POSITIONS

<b>University of Chicago</b>	<b>2011–</b>	<b>Chicago, IL</b>
Assistant Professor, Depts. of Biochemistry & Molecular Biology and Human Genetics.		
<b>Harvard University</b>	<b>2006–2011</b>	<b>Cambridge, MA</b>
Bauer Fellow (PI with independent lab), FAS Center for Systems Biology.		

## EDUCATION

<b>California Institute of Technology</b>	<b>2002–2006</b>	<b>Pasadena, CA</b>
Ph.D. in Computation & Neural Systems, advised by Frances H. Arnold. Thesis: “Misfolding Dominates Protein Evolution”		
<b>Princeton University</b>	<b>1991–1995</b>	<b>Princeton, NJ</b>
B.S.E. <i>cum laude</i> in Mechanical and Aerospace Engineering.		

## HONORS & AWARDS

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, 74<sup>th</sup> 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

Big Ideas Generator, Seed Award, “Evolving adaptive protein assembly,” 2014–2015, 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

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 TALKS

TBA. Santa Barbara Advanced School of Quantitative Biology, Evolutionary Cell Biology, August 2015.  
“Molecular thermometers: mechanisms underlying the response to heat stress in budding yeast,” University of Texas Medical School at Houston, November 2014.  
“Revisiting HSF1 structure and function in yeast,” 1<sup>st</sup> HSF workshop, Paris, France, April 2014.  
“You err what you eat: evidence that a nutrient alters translational fidelity and genome-wide protein encoding,” Columbia University, March 2014.  
“Protein quality control and genome-wide signatures of purifying selection,” Causes of Genome Evolution, Mishima,

Japan, March 2014.

“Pervasive underestimation of transcriptional control,” Princeton University, October 2013.

“Selection on protein homeostasis,” Kavli Israeli-American Frontiers of Science Symposium, June 2013.

“Selection against protein aggregation at the proteome scale,” Stony Brook University, December 2012.

“Nutrient-driven coevolution of a tRNA modification with codon accuracy,” U. Wyoming, October 2012.

“Evolutionary and cellular responses to protein misfolding,” VIB Student Symposium, Ghent, Belgium, August 2012.

“Coevolution of codon accuracy with a eukaryotic tRNA modification,” KU Leuven, Belgium, August 2012.

“New biology or noisy data? The role of transcription in regulating steady-state protein levels in the world's best-studied eukaryote,” Computations in Science seminar, University of Chicago, June 2012.

“Global protein aggregation profiling in budding yeast,” Midwest Conference on Protein Folding, April 2012 (closing plenary speaker).

“A global protein aggregation map of budding yeast,” Rochester University, Biology Seminar Series, April 2012.

“Two problems in protein quantitation by mass spectrometry,” Chicago Mass Spectrometry Discussion Group, Northwestern University, March 2012.

“Evolutionary signatures of protein homeostasis,” Phylomedicine Symposium, ASU, March 2012.

“Protein balance and the failure rate of protein synthesis,” ASCB Symposium on Protein Balance, December 2011.

“Natural selection and translational fidelity in budding yeast,” SMBE annual meeting, Kyoto, Japan 2011.

“The fitness cost of protein misfolding in yeast,” EMBO Conference Series, Experimental Approaches to Evolution and Ecology using Yeast, Heidelberg, Germany, 2010.

“How mistakes in making proteins shape the evolution of genes,” Frontiers in Genomics Seminar Series, UNAM, Cuernavaca, Mexico, 2009 (academic talk and public lecture).

“Why highly expressed proteins evolve slowly,” Genome Informatics (Cold Spring Harbor), 2005.

“Error-prone mutants: solving a protein engineering mystery,” USC Biol. Sci. seminar, 2004.

## PEER-REVIEWED PUBLICATIONS

1. 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,” in revision (2014).
2. 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.)
3. 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.*, in press (2014).
4. 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).
5. 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).
6. 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).
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* 108(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). (Accompanying *Preview* by Powers & Balch; *Faculty of 1000* rated.)
9. 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).

10. 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.)
11. 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).
12. Wilke, C.O. & **Drummond, D.A.**, “Population genetics of translational robustness,” *Genetics* 173:473–81 (2006).
13. **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.)
14. **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.)
15. 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).
16. **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.)
17. **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).
18. 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

19. **Drummond, D.A.**, “How infidelity creates a sticky situation,” *Molecular Cell* 48(5): 663–664 (2012).
20. Wilke, C.O. and **Drummond, D.A.**, “Signatures of protein biophysics in coding sequence evolution,” *Curr. Opin. Struct. Bio.* 20(3):385–9 (2010).
21. **Drummond, D.A.** and Wilke, C.O., “The evolutionary consequences of erroneous protein synthesis,” *Nature Reviews Genetics* 10(10):715–24 (2009).
22. **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:** *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.