Daniel Bryan Goodman

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Current position

Post-doctoral Fellow, Wyss Institute for Bioinspired Engineering

Areas of specialization

Synthetic Biology \cdot Genome Engineering \cdot Systems Biology \cdot Bioinformatics and Computational Biology \cdot Technology Development for Multiplex Molecular Biology \cdot Oligonucleotide Library Synthesis \cdot Pooled genetic selections and screens \cdot Comparative Genomics and Evolution \cdot Data Visualization

Education

- PHD in Bioinformatics and Integrative Genomics, Massachusetts Institute of Technology
 - Thesis: Understanding Genetic Systems through Multiplexed Design, Synthesis, and Measurement
 - NSF Graduate Research Fellow
- 2008 Whitaker International Bioengineering Fellow, University of Cambridge.
 - Project title: Image Recognition and Microfluidics for Bead-based DNA Sequencing
- BS in Bioengineering w/ specialization in Bioinformatics, University of California at San Diego
 - Senior Thesis: Viral Genome Rearrangements in Baculoviridae inform phylogeny and function

Honors & awards

- Martha Gray Prize, Harvard-MIT Division of Health Science and Technology
- SynBERC Practices Fellow, Six Parties Synthetic Biology Symposium

- National Science Foundation Graduate Research Fellowship
- 2008-2009 Whitaker International Bioengineering Fellow
- 2003-2007 Provost Honors, Eleanor Roosevelt College at UCSD
- Pacific Rim Undergraduate Experience (PRIME) Award Recipient
- 2005 Google Summer of Code Award

Publications & talks

JOURNAL ARTICLES

- Luhan Yang, Adrian Briggs, Wei Leong Chew, Prashant Mali, Marc Guell, John Aach, *Daniel B. Goodman*, David Cox, Yinan Kan, Emal Lesha, Venkataramanan Soundararajan, Feng Zhang, and George M. Church. Genome editing with targeted deaminases. *bioRxiv*, page 066597, 2016.
- Nili Ostrov*, Matthieu M. Landon*, Marc Guell, Gleb Kuznetsov, Jun Teramoto, Natalie Cervantes, Minerva Zhou, Kerry Singh, Michael G. Napolitano, Mark Moosburner, Ellen Shrock, Benjamin W. Pruitt, Nicholas Conway, *Daniel B. Goodman*, Cameron L. Gardner, Garry Tyree, Alexandra Gonzales, Barry L. Wanner, Julie E. Norville, Marc J. Lajoie, and George M. Church. Design, synthesis and testing towards a 57-codon genome. *Science (in press)*, 2016.
- Michael G. Napolitano*, Matthieu M. Landon*, Christopher J. Gregg*, Marc J. Lajoie*, Lakshmi N. Govindarajan, Joshua A. Mosberg, Gleb Kuznetsov, *Daniel B. Goodman*, Oscar Vargas-Rodriguez, Farren J. Isaacs, Dieter Söll, and George M. Church. Emergent rules for codon choice elucidated by editing rare arginine codons in escherichia coli. *Proceedings of the National Academy of Sciences (in press)*, 2016.
- Christopher J. Gregg, Marc J. Lajoie, Michael G. Napolitano, Joshua A. Mosberg, *Daniel B. Goodman*, John Aach, Farren J. Isaacs, and George M Church. Rational optimization of tolC as a powerful dual selectable marker for genome engineering. *Nucleic Acids Research*, 42(7):4779–4790, 2014.
- Daniel B. Goodman, George M. Church, and Sriram Kosuri. Causes and effects of N-terminal codon bias in bacterial genes. Science, 342(6157):475–479, 2013.
- Sriram Kosuri*, *Daniel B. Goodman**, Guillaume Cambray, Vivek K. Mutalik, Yuan Gao, Adam P. Arkin, Drew Endy, and George M. Church. Composability of regulatory sequences controlling transcription and translation in e. coli.trolling transcription and translation in escherichia coli. *Proceedings of the National Academy of Sciences*, 110(34):14024–14029, 2013.
- Marc J. Lajoie, Alexis J. Rovner, *Daniel B. Goodman*, Hans-Rudolf Aerni, Adrian D. Haimovich, Gleb Kuznetsov, Jaron A. Mercer, Harris H. Wang, Peter A. Carr, Joshua A. Mosberg, Nadin Rohland, Peter G. Schultz, Joseph M. Jacobson, Jesse Rinehart, George M.

- Church, and Farren J. Isaacs. Genomically recoded organisms expand biological functions. *Science*, 342(6156):357–360, 2013.
- Farren J. Isaacs, Peter A. Carr, Harris H. Wang, Marc J. Lajoie, Bram Sterling, Laurens Kraal, Andrew C. Tolonen, Tara A. Gianoulis, *Daniel B. Goodman*, Nikos B. Reppas, Christopher J. Emig, Duhee Bang, Samuel J. Hwang, Michael C. Jewett, Joseph M. Jacobson, and George M. Church. Precise manipulation of chromosomes in vivo enables genome-wide codon replacement. *Science*, 333(6040):348–353, 2011.
- Irene Tiemann-Boege, Christina Curtis, Deepali N. Shinde, Daniel B Goodman, Simon Tavare, and Norman Arnheim. Product length and dye choice and and detection chemistry in the bead-emulsion amplification of millions of single dna molecules in parallel. Analytical Chemistry, 81(14):5770-5776, 2009.
- Nitin Gupta, Jamal Benhamida, Vipul Bhargava, *Daniel B. Goodman*, Elisabeth Kain, Ian Kerman, Ngan Nguyen, Noah Ollikainen, Jesse Rodriguez, Jian Wang, Mary S. Lipton, Margaret Romine, Vineet Bafna, Richard D. Smith, and Pavel A. Pevzner. Comparative proteogenomics: combining mass spectrometry and comparative genomics to analyze multiple genomes. *Genome Research*, 18(7):1133–1142, 2008.
- Daniel B. Goodman, Noah Ollikainen, and Chris Sholley. Baculovirus phylogeny based on genome rearrangements. In *Comparative Genomics*, pages 69–82. Springer Berlin Heidelberg, 2007.

Conference papers

- Gleb Kuznetsov*, *Daniel B. Goodman**, Marc J. Lajoie*, and George M. Church. Mill-stone: Software for iterative genome engineering. In 7th International Workshop on Bio-Design Automation, 2015.
- Daniel B. Goodman*, Casper Enghuus*, and George M Church. Design and characterization of genetic circuits using multiplex dna synthesis. In 7th International Workshop on Bio-Design Automation, 2015.
- J. Collins, D. Lavigne, Y. Lin, D. Goodman, P. Irwan, and A. P. Lee. Automated multiplexed multidensity microfluidic (m₃) cell sensing based on electrical gain measurements. In *IEEE EMBS Special Topic Conference on Microtechnologies in Medicine and Biology*, 2005.
- J. Collins, D. Goodman, and P. Delhaesand A.P. Lee. Nanofluidic channel engineering using laminar flow layer-by-layer deposition of polyelectrolytes. In ASME Integrated Nanosystems & Nanotechnology Showcase, 2004.

Conferences & Talks

- Gleb Kuznetsov*, *Daniel B. Goodman**, Marc J. Lajoie*, and George M. Church. Millstone: Software for iterative genome engineering. In 7th International Workshop on Bio-Design Automation, 2015.
- Daniel B. Goodman. Millstone: A cloud-based genome engineering platform. Synthetic Biology Engineering Research Council 2014 Spring Retreat. UC Berkeley, Berkeley, CA, USA, 2014.

- Daniel B. Goodman. Design and interrogation of genetic elements using megabase-scale dna synthesis. Wyss Institute Annual Retreat. Boston, MA, USA, 2013.
- Daniel B. Goodman, Sri Kosuri, Guillaume Cambray, Vivek K. Mutalik, Yuan Gao, Adam P. Arkin, Drew Endy, and George M. Church. Composability of regulatory sequences controlling transcription and translation in e. coli. Synthetic Biology 6.0 Conference, University College London, London, UK, 2013.
- Daniel B. Goodman. Multiplex synthesis and characterization of transcriptional and translational regulatory elements in e. coli. Synthetic Biology Engineering Research Council 2012 Spring Retreat. UC Berkeley, Berkeley, CA, USA, 2012.
- L. Boettger, *D. Goodman*, E. O'Neill, and X. Yan. Cambridge iBrain: Foundations for an artificial nervous system using organizing electrical patterning. iGEM Jamboree 2008. Cambridge, MA, USA, 2008.
- L. Xie, J. Wang, J. Chung, D. Goodman, N. Ollikainen, and P. E. Bourne. Genome wide identification of off-site protein targets for major pharmaceuticals using functional site similarity and protein-ligand docking. Intelligent Systems for Molecular Biology 2007. Vienna, Austria, 2007.
- D. Goodman, N. Ollikainen, and C. Sholley. Genome rearrangements in baculovirus genomes. Algorithmic Biology 2006. La Jolla, CA, USA, 2006.
- D. Goodman and M. Levesque. High-throughput virtual screening of a novel kinase on the grid: Homology modeling and template-based techniques. Supercomputing 2006. Tampa Bay, FL, USA, 2006.

Press/Media

- Kristy Hamilton. Science magazine podcast. September 27, 2013.
- Nicholas Wade. Synthetic Biology at the megabase scale. GetSynBio.com. October 22, 2013.
- Nicholas Wade. Genetic code of E. coli is hijacked by biologists. New York Times. July 14, 2011.
- Geoff Watts. BBC Radio: Leading Edge. National Radio Program. Broadcast November 8, 2008.

Teaching

- Judge, International Genetically Engineered Machines (iGEM), World Finals, Boston,
 MA
- Lecturer, ENG-SCI 222: Advanced Cellular Engineering, School of Engineering and Applied Sciences, Harvard University
- 2013-current Mentored PhD student Max Schubert, Harvard University

| 2013-2015 | Mentored MS student Casper Enghuus, Harvard University Currently graduate student at MIT, Microbiology |
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| 2012-2014 | Mentored research intern Gleb Kuznetsov, Harvard University Currently graduate student at Harvard, Biophysics |
| 2011 | Head Teaching Fellow, International Genetically Engineered Machines (iGEM) Team, Harvard University |
| 2007-2008 | Salk Mobile Science Laboratory |
| 2007 | Biology Teaching Assistant, University of California at San Diego. |