Nathan J. Hillson

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EDUCATION

Stanford University School of Medicine, Stanford CA
Postdoctoral Fellowship, Microbiology, 2009

Harvard Medical School, Boston MA
Ph.D., Biophysics, 2004

Rice University, Houston TX
B.A., Physics; Computational and Applied Mathematics, *cum laude*, 1999

Selected Course Work:
Macromolecular X-ray Crystallography; Chemical Biology; Simulation of Macromolecules; Single-molecule Biophysics; Molecular Approaches to Drug Action, Discovery, and Design; Proteins: Structure, Function and Catalysis; Genomics and Computational Biology; Molecular Biology and Genetics; Numerical Analysis; Partial Differential Equations; High Performance and Parallel Computing; Algorithms and Data Structures; Statistical Mechanics and Thermodynamics; Quantum Mechanics.

EXPERIENCE

Joint BioEnergy Institute (JBEI), Emeryville CA — 2009-present
DOE Joint Genome Institute (JGI), Walnut Creek CA
Lawrence Berkeley National Labs (LBNL), Berkeley CA
SynBERC, Emeryville CA

Title:
Director of Synthetic Biology Informatics, JBEI
Program Lead, Synthetic Biology Informatics, JGI
Staff Scientist, Biological Systems & Engineering Division, LBNL
BioDesign Department Head, Biological Systems & Engin. Div., LBNL
Co-Deputy Director, Biological Systems & Engineering Div., LBNL
Affiliate Investigator, SynBERC

Responsibilities: To develop and demonstrate experimental wetware, software, and laboratory automation devices that facilitate, accelerate, and standardize the engineering of microbes. To provide and participate in the strategic and operational leadership of the Biological Systems & Engineering Division and more broadly the LBNL Biosciences Area.

TeselaGen Biotechnologies, Inc., San Francisco CA — 2011-present
Title: *Founder and Chief Scientific Officer*
Responsibilities: To lead the design of TeselaGen's DNA design and assembly bioCAD/CAM platform, and provide software development quality assurance and control.

Stanford University School of Medicine, Stanford CA 2004-2009

Title: *Postdoctoral Research Fellow*

Research Advisor: *Lucy Shapiro, Department of Developmental Biology*

Research topics: Engineered the bacterium *Caulobacter cresentus* into a whole-cell Uranium biosensor. Developed a high-throughput microscopy screen to identify mutant strains of *Caulobacter* that mislocalize the polar histidine kinases DivJ/PleC, or the cell-division protein ZapA. Protein-engineered a chimera of the essential histidine kinase CckA to generate a colorimetric reporter of CckA activity. Utilized the CckA chimera reporter system in a high-throughput screen to identify *Caulobacter* mutant strains that fail to activate CckA.

Harvard Medical School, Boston MA 2000-2004

Title: *Graduate Thesis Student*

Research Advisor: *Prof. Christopher T. Walsh*
Department of Biological Chemistry and Molecular Pharmacology

Dissertation topics: Studied the enzymatic activity of VibF, a six domain non-ribosomal peptide synthetase utilized in the biosynthesis of vibriobactin, an iron chelating siderophore (virulence factor) of the cholera causing pathogen *Vibrio cholerae*. Mapped catalytic activity to individual domains of VibF. Demonstrated that VibF functionally operates as a dimer, via biochemical mutant domain activity regain and by ultracentrifugation studies. Utilized correlated-mutation computational analysis to assist the chimeric-engineering of glycosyltransferases to decorate the peptide scaffold of the antibiotic vancomycin with alternative sugar moieties.

Harvard University, Cambridge MA 2000

Title: *Graduate Rotation Student*

Research Advisor: *Prof. Eugene Shakhnovich*
Department of Chemistry and Chemical Biology

Rotation topic: Adapted an existing all-atom protein folding model/program to study protein-peptide interactions in the MHC-II/10-mer peptide recognition system. Implemented the Perceptron learning device to cyclically refine the intra- and inter-molecular potentials to guarantee the lowest energy of the native (crystal structure) state of the protein-peptide complex when challenged with generated decoy structures.

Harvard University, Boston MA 2000

Title: *Graduate Rotation Student*

Research Advisor: *Prof. Christopher T. Walsh*
Department of Biological Chemistry and Molecular Pharmacology

Rotation topic: Studied the enzymatic activity of two previously uncharacterized proteins (YbtU and YbtT) implicated in the biosynthesis of yersiniabactin, an iron chelating siderophore necessary for the virulence of the plague causing pathogen *Yersinia pestis*. Attempted to measure cofactor binding and detect novel chemical species produced by YbtU, a protein predicted to be a putative reductase. Assayed for increased hydrolysis rates of a subtrate analog mediated by YbtT, assigned as a putative external thioesterase.

Harvard University, Boston MA 1999
Title: *Graduate Rotation Student*
Research Advisor: *Prof. Gerhard Wagner*
Department of Biological Chemistry and Molecular Pharmacology
Rotation topic: Used NMR spectroscopy to study the BID protein, a pro-apoptotic factor in the cell-death signaling pathway which becomes 100 times more potent after truncation by caspase-8. Conducted an experiment to collect a novel HSQC spectra of truncated BID. Analyzed differences in the spectra of truncated and full-length protein to identify residues whose chemical environments where changed due to the cleavage.

Los Alamos National Laboratories, Los Alamos NM 1996-1998
Title: *Undergraduate Summer Research Associate*
Research Advisor: *Angel Garcia, Ph.D.*
Theoretical Division (T-10): Theoretical Biology and Biophysics
Area of study: Composed Monte Carlo code to study minimalist off-lattice protein folding models. Investigated pressure effects on folding thermodynamics and kinetics of the theoretical Thirumalai protein. Optimized numerical Lambda Repressor protein model to best fit experimental B-factor data.

TEACHING

Teaching fellow, Biochemistry and Protein Structure, Harvard University 2001
Taught weekly session of 15 undergraduates and led review sessions.
Graded exams and weekly problem sets.

Teaching assistant, General Physics I and II, Rice University 1996-1999
Taught weekly class recitation sessions and review sessions.

HONORS

NSF Bay Area Regional I-Corps Summer 2015, Trailblazer Award
Berkeley Lab Director's Awards for Exceptional Achievement: Technology Transfer 2013
Emerging Leaders in Biosecurity 2013 Fellow
Synthetic Biology Leadership Accelerator Program 2012 Fellow
Joint BioEnergy Institute 2012 Entrepreneur Award
Damon Runyon Cancer Research Foundation Postdoctoral Research Fellow
National Defense Science and Engineering Predoctoral Fellowship
National Science Foundation Graduate Research Fellow
Harvard University Distinction in Teaching Award
Sigma Pi Sigma Physics Honor Society

PATENTS

Hillson, N.J. (2012) Scar-Less Multi-Part DNA Assembly Design Automation.
U.S. Patent Application No. US20120259607

Chang, C., Bharadwaj, R., Singh, A., Chandrasekaran, A., and Hillson, N.J.
(2012) Microfluidic Platform for Synthetic Biology Applications.
U.S. Patent Application No. US20120258487

Hillson, N.J., Shapiro, L., Hu, P., and Andersen, G.L. (2008) Heavy Metal Biosensor.
U.S. Patent Application No. US20110117590

RESEARCH

Gregory Linshiz, Erik Jensen, Nina Stawski, Changhao Bi, Nick Elsbree, Hong Jiao, Jungkyu Kim, Richard Mathies, Jay D. Keasling and Nathan J. Hillson. (2016) End-to-end automated microfluidic platform for synthetic biology: from design to functional analysis. *Journal of Biological Engineering* 10:3 DOI: 10.1186/s13036-016-0024-5

Philip Charles Gach, Steve C.C. Shih, Jess Sustarich, Jay D Keasling, Nathan J Hillson, Paul D. Adams, and Anup K Singh. (2016) A Droplet Microfluidic Platform for Automating Genetic Engineering. *ACS Synthetic Biology* DOI:10.1021/acssynbio.6b00011

Steve C. C. Shih, Garima Goyal, Peter W. Kim, Nicolas Koutsoubelis, Jay D. Keasling, Paul D. Adams, Nathan J. Hillson, and Anup K. Singh. (2015) A Versatile Microfluidic Device for Automating Synthetic Biology. *ACS Synthetic Biology* Article ASAP. DOI: 10.1021/acssynbio.5b00062

Simirenko L, Harmon-Smith M, Visel A, Rubin EM, and Hillson NJ. (2015) The Joint Genome Institute's synthetic biology internal review process. *Journal of Responsible Innovation*. DOI: 10.1080/23299460.2014.1002058

Alonso-Gutierrez J, Kim E.M., Batth TS, Cho N, Hu Q, Chan LJD, Petzold CJ, Hillson NJ, Adams PD, Keasling JD, Garcia-Martin H, and Lee TS. (2014) Principal component analysis of proteomics (PCAP) as a tool to direct metabolic engineering. *Metabolic Engineering*. doi:10.1016/j.ymben.2014.11.011

Lee S, Geller JT, Torok T, Wu CH, Singer M, Reid FC, Tarjan DR, Hazen TC, Arkin AP, and Hillson NJ. (2014) Characterization of Wastewater Treatment Plant Microbial Communities and the Effects of Carbon Sources on Diversity in Laboratory Models. PLoS ONE 9(8): e105689. doi:10.1371/journal.pone.0105689

Galdzicki M, Clancy KP, Oberortner E, Pocock M, Quinn JY, Rodriguez CA, Roehner N, Wilson ML, Adam L, Anderson JC, Bartley BA, Beal J, Chandran D, Chen J, Densmore D Endy D, Grünberg R, Hallinan J, Hillson NJ, Johnson JD, Kuchinsky A, Lux M, Misirli G, Peccoud J, Plahar HA, Sirin E, Stan GB, Villalobos A, Wipat A, Gennari JH, Myers CJ, Sauro HM. (2014) The Synthetic Biology Open Language (SBOL) provides a community standard for communicating designs in synthetic biology. *Nat Biotechnol*. 32(6):545-50. DOI: 10.1038/nbt.2891.

Lao J, Oikawa A, Bromley JR, McInerney P, Suttangkakul A, Smith-Moritz AM, Plahar H, Chiu TY, González Fernández-Niño SM, Ebert B, Yang F, Christiansen KM, Hansen SF, Stonebloom S, Adams PD, Ronald PC, Hillson NJ, Hadi MZ, Vega-Sánchez ME, Loqué D, Scheller HV, Heazlewood JL. (2014) The Plant Glycosyltransferase Clone Collection for Functional Genomics. *Plant J.* DOI: 10.1111/tpj.12577.

Golberg, A., Linshiz, G., Kravets, I., Stawski, N., Hillson, N.J., Yarmush, M.L., Marks, R.S., and Konry, T. (2014) Cloud-Enabled Microscopy and Droplet Microfluidic Platform for Specific Detection of Escherichia coli in Water. *PLoS ONE* 9(1): e86341. DOI:10.1371/journal.pone.0086341

Linshiz, G., Stawski, N., Goyal, G., Bi, C., Poust, S., Sharma, M., Mutalik, V., Keasling, J.D., and Hillson, N.J. (2014) PR-PR Cross-Platform Laboratory Automation System. *ACS Synthetic Biology* 3 (8), 515–524. DOI: 10.1021/sb4001728

Hillson, N.J. (2014) j5 DNA Assembly Design Automation. *DNA Cloning and Assembly Methods*, Valla S., and Lale, R. (Editors), *Humana Press*, 245-269.

Bi, C., Su, P., Müller, J., Yeh, Y.C., Chhabra, S.R., Beller, H.R., Singer, S.W., and Hillson, N.J. (2013) Development of a broad-host synthetic biology toolbox for ralstonia eutropha and its application to engineering hydrocarbon biofuel production. *Microbial Cell Factories 12:107*. DOI: 10.1186/1475-2859-12-107.

Golberg, A., Vitkin, E., Linshiz, G., Khan, S. A., Hillson, N. J., Yakhini, Z. and Yarmush, M. L. (2013) Proposed design of distributed macroalgal biorefineries: thermodynamics, bioconversion technology, and sustainability implications for developing economies. *Biofuels, Bioprod. Bioref*. DOI: 10.1002/bbb.1438.

Müller, J., MacEachran, D., Burd, H., Sathitsuksanoh, N., Bi, C., Yeh, Y.C., Lee, T.S., Hillson, N.J., Chhabra, S.R., Singer, S.W., and Beller, H.R. (2013) Engineering of Ralstonia eutropha H16 for Autotrophic and Heterotrophic Production of Methyl Ketones. *Appl. Environ. Microbiol. 79(14)*:4433-9. DOI: 10.1128/AEM.00973-13.
Linshiz, G., Goldberg, A., Konry, T., and Hillson, N.J. (2013) The Fusion of Biology, Computer Science, and Engineering – towards efficient and successful synthetic biology. *Perspectives in Biology and Medicine 55 (4)*, 503-520.

Yeh, Y.C., Müller, J., Bi, C., Hillson, N.J., Beller, H.R., Chhabra, S.R., and Singer, S.W. (2013), Functionalizing bacterial cell surfaces with a phage protein. *Chem Commun 49(9):*910-2.

Goldberg, A., Linshiz, G., Koudritsky, M., Chemodanov, A., and Hillson, N.J. (2012) Distributed marine biorefineries for developing economies. *Proceedings of the ASME 2012 International Mechanical Engineering Congress & Exposition*. IMECE2012-86051.

Linshiz, G., Stawski, N., Poust, S., Bi, C., Keasling, J.D., and Hillson, N.J. (2012) PaR-PaR Laboratory Automation platform. *ACS Synthetic Biology, 2 (5),* 216–222.

Ham, T.S., Dmytriv, Z. Plahar, H., Chen, J., Hillson, N.J., and Keasling, J.D. (2012) Design, Implementation and Practice of JBEI-ICE: An Open Source Biological Part Registry Platform and Tools. *Nucleic Acids Research 40 (18):*e141.

Chen, J., Densmore, D., Ham, T.S., Keasling, J.D. and Hillson, N.J. (2012) DeviceEditor visual biological CAD canvas. *Journal of Biological Engineering 6*:1.

Hillson, N.J.*, Rosengarten, R.D., and Keasling, J.D. (2012)
j5 DNA Assembly Design Automation Software. *ACS Synthetic Biology 1 (1)*, 14-21.

Mukhopadhyay, A., Hillson, N.J., and Keasling, J.D. (2012) Microbial stress tolerance: from genomics to biofuels. *Microbial Stress Tolerance for Biofuels*, Liu, Z.L. (Editor), *Springer-Verlag, 1st Edition*, 209-238.

Hillson, N.J. (2011) DNA Assembly Method Standardization for Synthetic Biomolecular Circuits and Systems. *Design and Analysis of Bio-molecular Circuits*, Koeppl H., Densmore, D., di Bernardo, M., and Setti, G. (Editors), *Springer-Verlag, 1st Edition,* 295-314.

Iniesta, A.A.*, Hillson, N.J.*, and Shapiro, L. (2010) Polar Remodeling and Histidine Kinase Activation, Which Is Essential for Caulobacter Cell Cycle Progression, Are Dependent on DNA Replication Initiation. *J. Bacteriol. 192,* 3893-3902.

Iniesta, A.A.*, Hillson, N.J.*, and Shapiro, L. (2010) Cell pole-specific activation of a critical bacterial cell cycle kinase. *Proc. Natl. Acad. Sci. U.S.A. 107,* 7012-7.

Christen, B.*, Fero, M.J.*, Hillson, N.J., Bowman, G., Hong, S., Shapiro, L., and McAdams, H.H. (2010) High-throughput identification of protein localization dependency networks. *Proc. Natl. Acad. Sci. U.S.A. 107*, 4681-6.
Hillson, N.J., Hu, P., Andersen, G.L., and Shapiro, L. (2007) Caulobacter crescentus as a whole cell uranium biosensor. *Appl. Environ. Microbiol. 73*, 7615-7621.

McGrath, P.T., Lee, H., Zhang, L., Iniesta, A.A., Hottes, A.K., Tan, M.H., Hillson, N.J., Hu, P., Shapiro, L., and McAdams, H.H. (2007) High-throughput identification of transcription start sites, conserved promoter motifs and predicted regulons. *Nat. Biotechnol. 25*, 584-592.

Hicks, L.M.*, Balibar, C.J.*, Walsh, C.T., Kelleher, N.L., and Hillson, N.J. (2006) Probing intra- versus interchain kinetic preferences of L-Thr acylation on dimeric VibF with mass spectrometry. *Biophys. J. 91*, 2609-2619.

Kelly, W.L., Hillson, N.J., and Walsh, C.T. (2005) Excision of the epothilone synthetase B cyclization domain and demonstration of in trans condensation/cyclodehydration activity. *Biochemistry 44*, 13385-133393.

Pacholec, M., Hillson, N.J., and Walsh, C.T. (2005) NovJ/Novk catalyze benzylic oxidation of a beta-hydroxyl tyrosyl-S-pantetheinyl enzyme during aminocoumarin ring formation in novobiocin biosynthesis. *Biochemistry 44*, 12819-12826.

Hillson, N.J., Balibar, C.J. and Walsh, C.T. (2004) Catalytically Inactive Condensation Domain C1 Is Responsible for the Dimerization of the VibF Subunit of Vibriobactin Synthetase. *Biochemistry 43*, 11344-11351.

Hillson, N.J., Walsh, C.T. (2003) Dimeric Structure of the Six-Domain VibF Subunit of Vibriobactin Synthetase: Mutant Domain Activity Regain and Ultracentrifugation Studies. *Biochemistry 41*, 766-775.

Sieber, S.A., Linne, U., Hillson, N.J., Roche, E., Walsh, C.T., Marahiel, M.A. (2002) Evidence for a monomeric structure of nonribosomal peptide synthetases. *Chemistry & Biology 9*, 997-1008.

Marshall, C.G., Hillson, N.J., Walsh, C.T. (2002) Catalytic mapping of the vibriobactin biosynthetic enzyme VibF. *Biochemistry 41*, 244-250.

Miller, D.A., Luo, L., Hillson, N., Keating T.A., Walsh, C.T. (2002) Yersiniabactin synthetase: a four-protein assembly line producing the nonribosomal peptide/polyketide hybrid siderophore of *Yersinia pestis*. *Chemistry & Biology 9*, 333-44.

Hillson, N., Onuchic, J.N., Garcia, A.E. (1999) Pressure-induced protein-folding/unfolding kinetics. *Proc. Natl. Acad. Sci. U.S.A. 96*, 14848-14853.