

Nathan J. Hillson

Lawrence Berkeley National Lab
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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

DOE Agile BioFoundry, Emeryville CA **2016-present**
Title: *Principal Investigator*
Responsibilities: To lead the development and demonstration of the Agile BioFoundry.

DOE Joint BioEnergy Institute (JBEI), Emeryville CA **2009-present**
Title: *Director of Synthetic Biology Informatics* 2014-present
Director of Synthetic Biology 2009-2014
Responsibilities: To develop and demonstrate experimental wetware, software, and laboratory automation devices that facilitate, accelerate, and standardize the engineering of microbes.

DOE Joint Genome Institute (JGI), Walnut Creek CA **2012-present**
Title: *Program Lead, Synthetic Biology Informatics*
Responsibilities: To develop and demonstrate DNA screening biosecurity software and Synthetic Biology Institutional Review processes and software, and coordinate Synthetic Biology Informatics work at the JGI, JBEI, and the Agile BioFoundry.

Lawrence Berkeley National Lab (LBNL), Berkeley CA **2009-present**
Title: *BioDesign Dept. Head, Biological Systems & Engin. Div.* 2015-present
Staff Scientist, Biological Systems & Engin. Div. 2015-present
Co-Deputy Director, Biological Systems & Engin. Div. 2015-2016
Staff Scientist, Physical Biosciences Division 2011-2015
Research Scientist, Physical Biosciences Division 2009-2011
Responsibilities: In addition to Agile BioFoundry, JBEI, and JGI responsibilities (see above), provide and participate in the strategic and operational leadership of the Biological Systems & Engineering Division and more broadly the LBNL Biosciences Area.

Engineering Biology Research Center (EBRC), Emeryville CA 2016-present

Title: *Affiliate Investigator*

Responsibilities: To further develop and demonstrate the ICE repository platform towards achieving a “Web of Registries”.

TeselaGen Biotechnologies, Inc., San Francisco CA 2011-present

Title: *Co-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.

Synberc, Emeryville CA 2013-2016

Title: *Affiliate Investigator*

Responsibilities: To further develop and demonstrate the ICE repository platform towards achieving a “Web of Registries”, and to support and maintain Synberc’s ICE repository instance.

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 crescentus* 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 substrate 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 were 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
 Journal of Biological Engineering 2016 Publication of the Year
 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. (2016) Scar-Less Multi-Part DNA Assembly Design Automation. U.S. Patent No. 10,373,703. Issued August 6, 2019.

Hillson, N.J. (2012) Scar-Less Multi-Part DNA Assembly Design Automation. U.S. Patent No. 9,361,427. Issued June 7, 2016.

Chang, C., Bharadwaj, R., Singh, A., Chandrasekaran, A., and **Hillson, N.J.** (2012) Microfluidic Platform for Synthetic Biology Applications. U.S. Patent US10131903B2. Issued November 20, 2018.

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

RESEARCH

Chen Y, Guenther JM, Gin JW, Chan LJG, Costello Z, Ogorzalek TL, Tran HM, Blake-Hedges JM, Keasling JD, Adams PD, Garcia Martin H, **Hillson NJ**, Petzold CJ. (2019) "An automated 'cells-to-peptides' sample preparation workflow for high-throughput, quantitative proteomic assays of microbes". *J Proteome Res*. doi:10.1021/acs.jproteome.9b00455

Jesus F. Barajas, Ryan P. McAndrew, Mitchell G. Thompson, Tyler W. H. Backman, Bo Pang, Tristan de Rond, Jose H. Pereira, Veronica T. Benites, Héctor García Martín, Edward E. K. Baidoo, **Nathan J. Hillson**, Paul D. Adams, and Jay D. Keasling. (2019) "Structural insights into dehydratase substrate selection for the borrelidin and fluvirucin polyketide synthases" *J Ind Microbiol Biotechnol* <https://doi.org/10.1007/s10295-019-02189-z>

Paul Opgenorth, Zak Costello, Takuya Okada, Garima Goyal, Yan Chen, Jennifer Gin, Veronica T. Benites, Markus de Raad, Trent R. Northen, Kai Deng, Samuel Deutsch, Edward E.K. Baidoo, Christopher J. Petzold, **Nathan J Hillson**, Hector Garcia Martin, and Harry R Beller. (2019) "Lessons from two Design-Build-Test-Learn cycles of dodecanol production in Escherichia coli aided by machine learning". *ACS Synth. Biol.* DOI: 10.1021/acssynbio.9b00020

Nathan Hillson, Mark Caddick, Yizhi Cai, Jose A. Carrasco, Matthew Wook Chang, Natalie C. Curach, David J. Bell, Rosalind Le Feuvre, Douglas C. Friedman, Xiongfei Fu, Nicholas D. Gold, Markus J. Herrgård, Maciej B. Holowko, James R. Johnson, Richard A. Johnson, Jay D. Keasling, Richard I. Kitney, Akihiko Kondo, Chenli Liu, Vincent J. J. Martin, Filippo Menolascina, Chiaki Ogino, Nicola J. Patron, Marilene Pavan, Chueh Loo Poh, Isak S. Pretorius, Susan J. Rosser, Nigel S. Scrutton, Marko Storch, Hille Tekotte, Evelyn Travnik, Claudia E. Vickers, Wen Shan Yew, Yingjin Yuan, Huimin Zhao & Paul S. Freemont. (2019) "Building a global alliance of biofoundries". *Nature Communications*, 10:2040 <https://www.nature.com/articles/s41467-019-10079-2>

Garima Goyal, Zak Costello, Jorge Alonso Guitierrez, Aram Kang, Taek Soon Lee, Hector Garcia Martin, and **Nathan J. Hillson**. (2018) "Parallel Integration and Chromosomal Expansion of Metabolic Pathways" *ACS Synthetic Biology* DOI: 10.1021/acssynbio.8b00243

Thomas L. Ruegg, Jose H. Pereira, Joseph C. Chen, Andy DeGiovanni, Pavel Novichkov, Vivek K. Mutalik, Giovani P. Tomaleri, Steven W. Singer, **Nathan J. Hillson**, Blake A. Simmons, Paul D. Adams & Michael P. Thelen. (2018) "Jungle Express is a versatile repressor system for tight transcriptional control". *Nature Communications* 9, 3617. <https://doi.org/10.1038/s41467-018-05857-3>

Sebastian Palluk, Daniel H. Arlow, Tristan de Rond, Rathin Bector, Justine S. Kang, Hratch M. Baghdassarian, Alisa N. Truong, Peter W. Kim, Anup K. Singh, **Nathan J. Hillson**, Jay D. Keasling. (2018) "De novo DNA synthesis using polymerase-tethered nucleotides" *Nature Biotech* doi:10.1038/nbt.4173

Jesus F. Barajas, Amin Zargar, Bo Pang, Veronica T. Benites, Jennifer Gin, Edward E. K. Baidoo, Christopher J. Petzold, **Nathan J. Hillson**, and Jay D. Keasling. (2018) "Biochemical Characterization of β -Amino Acid Incorporation in Fluvirucin B2 Biosynthesis". *ChemBioChem* 10.1002/cbic.201800169

Mitchell G. Thompson, Nima Sedaghatian, Jesus F. Barajas, Maren Wehrs, Constance B. Bailey, Nurgul Kaplan, **Nathan J. Hillson**, Aindrila Mukhopadhyay & Jay D. Keasling. (2018) "Isolation and characterization of novel mutations in the pSC101 origin that increase copy number". *Scientific Reports* 8, 1590 doi:10.1038/s41598-018-20016-w

Dossani ZY, Reider Apel A, Szmidt-Middleton H, **Hillson NJ**, Deutsch S, Keasling JD, and Mukhopadhyay A. (2017). A combinatorial approach to synthetic transcription factor-promoter combinations for yeast strain engineering. *Yeast* 1–8. doi:10.1002/yea.3292

de Rond T, Stow P, Eigl I, Johnson RE, Chan LJG, Goyal G, Baidoo EEK, **Hillson NJ**, Petzold CJ, Sarpong R, and Keasling JD. (2017) "Oxidative cyclization of prodigiosin by an alkylglycerol monooxygenase-like enzyme". *Nature Chemical Biology* doi:10.1038/nchembio.2471

Morrell W, Birkel G, Forrer M, Lopez T, Backman T, Dussault M, Petzold C, Baidoo E, Costello Z, Ando D, Alonso Gutierrez J, George K, Mukhopadhyay A, Vaino I, Keasling J, Adams P, **Hillson NJ***, Garcia Martin H*. (2017) "The Experiment Data Depot: a web-based software tool for biological experimental data storage, sharing, and visualization" *ACS Synthetic Biology* DOI: 10.1021/acssynbio.7b00204

Gach PC*, Iwai K, Kim P, **Hillson NJ**, and Singh AK*. (2017) Droplet Microfluidics for Synthetic Biology. *Lab on a Chip*. DOI: 10.1039/C7LC00576H

Oberortner E, Cheng JF, **Hillson NJ**, and Deutsch S. (2016) Streamlining the Design-to-Build transition with Build-Optimization Software Tools (BOOST) *ACS Synth. Biol.*, DOI: 10.1021/acssynbio.6b00200

Apel AR, d'Espaux L, Wehrs M, Sachs D, Li R, Tong G, Garber M, Nnadi O, Zhuang W, **Hillson NJ**, Keasling JD, and Mukhopadhyay A. (2016) A Cas9-based toolkit to program gene expression in *Saccharomyces cerevisiae*. *Nucl. Acids Res.* doi:10.1093/nar/gkw1023

Nathan J. Hillson*, Hector A. Plahar, Jacob Beal*, and Ranjini Prithviraj. (2016) Improving Synthetic Biology Communication: Recommended Practices for Visual Depiction and Digital Submission of Genetic Designs. *ACS Synth. Biol.*, 5 (6), pp 449–451. DOI: 10.1021/acssynbio.6b00146

Javidpour P, Deutsch S, Mutalik VK, **Hillson NJ**, Petzold CJ, Keasling JD, et al. (2016) Investigation of Proposed Ladderane Biosynthetic Genes from Anammox Bacteria by Heterologous Expression in *E. coli*. *PLoS ONE* 11(3): e0151087. doi:10.1371/journal.pone.0151087

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

Jacqueline Y. Quinn, Robert Sidney Cox III, Aaron Adler, Jacob Beal, Swapnil Bhatia, Yizhi Cai, Joanna Chen, Kevin Clancy, Michal Galdzicki, **Nathan J. Hillson**, Nicolas Le Novère, Akshay J. Maheshwari, James Alastair McLaughlin, Chris J. Myers, Umesh P, Matthew Pocock, Cesar Rodriguez, Larisa Soldatova, Guy-Bart V. Stan, Neil Swainston, Anil Wipat, Herbert M. Sauro. (2015) SBOL Visual: A Graphical Language for Genetic Designs. *PLoS Biol* 13(12): e1002310. doi:10.1371/journal.pbio.1002310

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, Y E.M., Bath 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.

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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 JBEL-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*, Koepl 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.
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- 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.
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