

DYLAN CHIVIAN, Ph.D.

Computational Biology Research Scientist
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ACADEMIC AND RESEARCH

DOE Systems Biology Knowledgebase/LBNL, Berkeley, CA Research Scientist, Microbial Communities Co-Lead	2011-present
DOE Joint BioEnergy Institute/LBNL, Berkeley, CA Research Scientist, Computational Biology Lead	2008-2011
Lawrence Berkeley National Laboratory (LBNL), Berkeley, CA Post-doctoral Researcher, Environmental genomics Advisor: Prof. Adam Arkin	2005-2008
University of Washington, Seattle, WA Graduate Student, Protein structure homology modeling Advisor: Prof. David Baker Ph.D. 2005, Biochemistry and Biomolecular Structure and Design	1999-2005
University of California, Berkeley, CA B.S. 1994 Engineering Science: Bioengineering Emphases: Computer Science and Molecular Biology	1989-1994

INDUSTRY

Andromedia Inc. (now Adobe), San Francisco, CA Software Engineer	1998-1999
Novo Media Group Inc. (now ARC Worldwide), San Francisco, CA Software Engineer	1996-1998

SOFTWARE AUTHORED

metaMicrobesOnline	Microbial community genomics web server, meta.MicrobesOnline.org
Robetta	Protein tertiary structure prediction web server, www.Robetta.org
Ginzu	Protein homolog identification and domain parsing, www.Robetta.org
K*Sync	Protein sequence to structure alignment, www.Robetta.org

AWARDS AND DISTINCTIONS

Video Glossary definition of the word "Extremophile" Lawrence Berkeley National Laboratory	2009-ongoing
2008 Science News of the Year, "Community of One" <i>ScienceNews</i> , Jan. 3 rd , 2009	2008
PMMB Burroughs Wellcome National Fellowship Program in Mathematics and Molecular Biology (Burroughs Wellcome Fund)	2001-2003

ADVISORY AND REVIEW PANELS

“EarthCube Oceanography and Geobiology Environmental `Omics (ECOGEO) Research Coordination Network (RCN)”, U.S. National Science Foundation, Geosciences Directorate and Office of Cyberinfrastructure EarthCube Program, Steering Committee, Honolulu, HI August 2015

“Systems Biology Enabled Research on the Role of Microbial Communities on Carbon Cycling”, U.S. Department of Energy, Office of Science, Office of Biological and Environmental Research, Genomic Science program, Grant Proposal Review Panel, Gaithersburg, MD, June 2013

“Ten Thousand Genomes at a Time: Metagenome Assembly and Beyond”, U.S. Department of Energy Joint Genome Institute Workshop, Walnut Creek, CA, Oct 2011

“DOE Computational Biology & Bioinformatics for the Development of a Systems Biology Knowledgebase”, U.S. Department of Energy, Office of Science, Office of Biological and Environmental Research, Genomic Science program, Systems Biology Knowledgebase Grant Proposal Review Panel, Gaithersburg, MD, April 2010

“Large Scale Computing and Storage Requirements for Biological and Environmental Research”. U.S. Department of Energy, Office of Science, Office of Biological and Environmental Research, NERSC/ASCR/BER Workshop, Rockville, MD, May 2009

“Systems Biology Knowledgebase for a New Era in Biology”, U.S. Department of Energy Office of Science Genomic Sciences Systems Biology for Energy and the Environment Workshop, Washington, DC, May 2008

INVITED ORAL PRESENTATIONS

“Environmental genomics reveals a single-species ecosystem deep within Earth”, NPR’s “Talk of the Nation: Science Friday”, Oct 10th, 2008

“Environmental genomics reveals a single-species ecosystem deep within Earth”, Science Magazine Podcast, Oct 10th, 2008

“Environmental genomics reveals a single-species ecosystem deep within Earth”, 12th International Symposium on Microbial Ecology, Cairns, Australia, 2008

“Domain boundary prediction in CASP7”, Seventh Meeting on the Critical Assessment of Techniques for Protein Structure Prediction, Asilomar, Monterey, CA, 2006

“Environmental genomic characterization of the deep subsurface microorganism *Candidatus Desulforudis audaxviator*”, 11th International Symposium on Microbial Ecology, Vienna, Austria, 2006

“Prediction of CASP6 structures using automated Robetta protocols”, Sixth Meeting on the Critical Assessment of Techniques for Protein Structure Prediction, Gaeta, Italy, 2004

“Automated prediction of CASP-5 structures using the Robetta server” (with Rohl CA) Fifth Meeting on the Critical Assessment of Techniques for Protein Structure Prediction, Asilomar, Monterey, CA, 2002

PEER REVIEWED PUBLICATIONS (Google H-index = 20)

Labonté JM, Field EK, Lau M, **Chivian D**, Van Heerden E, Wommack KE, Kieft TL, Onstott TC, Stepanauskas R. (2015) "Single cell genomics indicates horizontal gene transfer and viral infections in a deep subsurface Firmicutes population" *Front Microbiol.* 6:349.

Ramsay BD, Hwang C, Woo HL, Carroll SL, Lucas S, Han J, Lapidus AL, Cheng JF, Goodwin LA, Pitluck S, Peters L, Chertkov O, Held B, Detter JC, Han CS, Tapia R, Land ML, Hauser LJ, Kyrpides NC, Ivanova NN, Mikhailova N, Pagani I, Woyke T, Arkin AP, Dehal P, **Chivian D**, Criddle CS, Wu W, Chakraborty R, Hazen TC, Fields MW. (2015) "High-Quality Draft Genome Sequence of *Desulfovibrio carbinophilus* FW-101-2B, an Organic Acid-Oxidizing Sulfate-Reducing Bacterium Isolated from Uranium(VI)-Contaminated Groundwater" *Genome Announc.* 3(2). pii: e00092-15.

Heins RA, Cheng X, Nath S, Deng K, Bowen BP, **Chivian DC**, Datta S, Friedland GD, D'Haeseleer P, Wu D, Tran-Gyamfi M, Scullin CS, Singh S, Shi W, Hamilton MG, Bendall ML, Sczyrba A, Thompson J, Feldman T, Guenther JM, Gladden JM, Cheng JF, Adams PD, Rubin EM, Simmons BA, Sale KL, Northen TR, Deutsch S. (2014) "Phylogenomically guided identification of industrially relevant GH1 β -glucosidases through DNA synthesis and nanostructure-initiator mass spectrometry" *ACS Chem Biol.* 9(9):2082-91.

Deangelis KM, D'Haeseleer P, **Chivian D**, Simmons B, Arkin AP, Mavromatis K, Malfatti S, Tringe S, Hazen TC. (2013) "Metagenomes of tropical soil-derived anaerobic switchgrass-adapted consortia with and without iron" *Stand Genomic Sci.* 7(3):382-98.

Chivian D*, Dehal PS, Keller K, Arkin AP*. (2013) "MetaMicrobesOnline: phylogenomic analysis of microbial communities" *Nucleic Acids Res.* 41(Database issue):D648-54.

McKee AE[†], Rutherford BJ[†], **Chivian DC**[†], Baidoo EK[†], Juminaga D, Kuo D, Benke PI, Dietrich JA, Ma SM, Arkin AP, Petzold CJ, Adams PD, Keasling JD, Chhabra SR. (2012) "Manipulation of the Carbon Storage Regulator System for Metabolite Remodeling and Biofuel Production in *Escherichia coli*" *Microb Cell Fact.* 11(1):79.

Chen Z, Friedland GD, Pereira JH, Reveco SA, Chan R, Park JI, Thelen MP, Adams PD, Arkin AP, Keasling JD, Blanch HW, Simmons BA, Sale KL, **Chivian D***, Chhabra SR*. (2012) "Tracing determinants of dual substrate specificity in glycoside hydrolase family 5" *J Biol Chem.* 287(30):25335-43.

Deangelis KM, D'Haeseleer P, **Chivian D**, Fortney JL, Khudyakov J, Simmons B, Woo H, Arkin AP, Davenport KW, Goodwin L, Chen A, Ivanova N, Kyrpides NC, Mavromatis K, Woyke T, Hazen TC. (2011) "Complete genome sequence of 'Enterobacter lignolyticus' SCF1" *Stand Genomic Sci.* 5(1):69-85.

Ma SM, Garcia DE, Redding-Johanson AM, Friedland GD, Chan R, Batth TS, Haliburton JR, **Chivian D**, Keasling JD, Petzold CJ, Lee TS, Chhabra SR. (2011) "Optimization of a heterologous mevalonate pathway through the use of variant HMG-CoA reductases" *Metab Eng.* 13(5):588-97.

Bates JT, **Chivian D***, Arkin AP*. (2011) "GLAMM: Genome-Linked Application for Metabolic Maps" *Nucleic Acids Res.* 39(Web Server issue):W400-5.

Dehal PS, Joachimiak MP, Price MN, Bates JT, Baumohl JK, **Chivian D**, Friedland GD, Huang KH, Keller K, Novichkov PS, Dubchak IL, Alm EJ, Arkin AP. (2010) "MicrobesOnline: an integrated portal for comparative and functional genomics" *Nucleic Acids Res.* 38(Database issue):D396-400.

Walker CB, Stolyar S, **Chivian D**, Pinel N, Gabster JA, Dehal PS, He Z, Yang ZK, Yen HC, Zhou J, Wall JD, Hazen TC, Arkin AP, Stahl DA. (2009) "Contribution of mobile genetic elements to *Desulfovibrio vulgaris* genome plasticity" *Environ Microbiol.* 11(9):2244-52.

Chivian D^{*}, Brodie EL, Alm EJ, Culley DE, Dehal PS, DeSantis TZ, Gihring TM, Lapidus A, Lin LH, Lowry SR, Moser DP, Richardson P, Southam G, Wanger G, Pratt LM, Andersen GL, Hazen TC, Brockman FJ, Arkin AP, Onstott TC. (2008) "Environmental genomics reveals a single-species ecosystem deep within Earth" *Science* 322:275-8.

Das R, Qian B, Raman S, Vernon R, Thompson J, Bradley P, Khare S, Tyka MD, Bhat D, **Chivian D**, Kim DE, Sheffler WH, Malmstrom L, Wollacott AM, Wang C, Andre I, Baker D. (2007) "Structure prediction for CASP7 targets using extensive all-atom refinement with Rosetta@home" *Proteins* 69:118-28.

Tress M, Cheng J, Baldi P, Joo K, Lee J, Seo JH, Lee J, Baker D, **Chivian D**, Kim D, Ezkurdia I. (2007) "Assessment of predictions submitted for the CASP7 domain prediction category" *Proteins* 69:137-51.

Haft RJ, Gachelet EG, Nguyen T, Toussaint L, **Chivian D**, Traxler B. (2007) "In vivo oligomerization of the F conjugative coupling protein TraD" *J Bacteriol* 189:6626-34.

Malmstrom L, Riffle M, Strauss CE, **Chivian D**, Davis TN, Bonneau R, Baker D. (2007) "Superfamily Assignments for the Yeast Proteome through Integration of Structure Prediction with the Gene Ontology" *PLoS Biol* 5:e76

Deutschbauer AM[†], **Chivian D**[†], Arkin AP. (2006) "Genomics for environmental microbiology" *Curr Opin Biotechnol* 17:229-35

Chivian D, Baker D. (2006) "Homology modeling using parametric alignment ensemble generation with consensus and energy-based model selection" *Nucleic Acids Res* 34:e112

Misura KM, **Chivian D**, Rohl CA, Kim DE, Baker D. (2006) "Physically realistic homology models built with ROSETTA can be more accurate than their templates" *Proc Natl Acad Sci USA* 103:5361-6

Chivian D[†], Kim DE[†], Malmstrom L, Schonbrun, J, Rohl CA, Baker D. (2005) "Prediction of CASP6 structures using automated Robetta protocols" *Proteins* 61:157-66

Kim DE[†], **Chivian D**[†], Malmstrom L, Baker D. (2005) "Automated prediction of domain boundaries in CASP6 targets using Ginzu and RosettaDOM" *Proteins* 61:193-200

Bradley P, Malmstrom L, Qian B, Schonbrun J, **Chivian D**, Kim DE, Meiler J, Misura KM, Baker D. (2005) "Free modeling with Rosetta in CASP6" *Proteins* 61:128-34

Kim DE[†], **Chivian D**[†], Baker D. (2004) "Protein structure prediction and analysis using the Robetta server" *Nucleic Acids Res* 32(Web Server issue):W526-31

Rohl CA, Strauss CE, **Chivian D**, Baker D. (2004) "Modeling structurally variable regions in homologous proteins with rosetta" *Proteins* 55:656-77

Chivian D, Kim DE, Malmstrom L, Bradley P, Robertson T, Murphy P, Strauss CE, Bonneau R, Rohl CA, Baker D. (2003) "Automated prediction of CASP-5 structures using the Robetta server" *Proteins* 53:524-33

Bradley P[†], **Chivian D**[†], Meiler J[†], Misura KM[†], Rohl CA[†], Schief WR[†], Wedemeyer WJ[†], Schueler-Furman O, Murphy P, Schonbrun J, Strauss CE, Baker D. (2003) "Rosetta predictions in CASP5: successes, failures, and prospects for complete automation" *Proteins* 53:457-68

Bonneau R, Strauss CE, Rohl CA, **Chivian D**, Bradley P, Malmstrom L, Robertson T, Baker D. (2002) "De novo prediction of three-dimensional structures for major protein families" *J Mol Biol* 322:65-78

Bonneau R, Tsai J, Ruczinski I, **Chivian D**, Rohl CA, Strauss CE, Baker D. (2001) "Rosetta in CASP4: progress in ab initio protein structure prediction" *Proteins Suppl* 5:119-26

BOOK CHAPTER

Chivian D, Robertson T, Bonneau R, Baker D. (2003) "Ab initio methods" Chapter 27 of "Structural Bioinformatics" (ed: Bourne & Weissig), John Wiley & Sons, Inc.

DISSERTATION

Chivian D, Baker D. (2005) "Application of information from homologous proteins for the prediction of protein structure" University of Washington

† contributed equally

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