U.S. DEPARTMENT OF ENERGY

DOE/SC-0110

Joint Meeting

Genomics:GTL Awardee Workshop VII

and

USDA-DOE Plant Feedstock Genomics for Bioenergy Awardee Workshop 2009

Bethesda, Maryland
February 8–11, 2009

Prepared for the
U.S. Department of Energy
Office of Science
Office of Biological and Environmental Research
Office of Advanced Scientific Computing Research
Germantown, MD 20874-1290

http://genomicsgtl.energy.gov

Prepared by
Genome Management Information System
Oak Ridge National Laboratory
Oak Ridge, TN 37830
Managed by UT-Battelle, LLC
For the U.S. Department of Energy
Under contract DE-AC05-00OR22725

Contents

Introduction to Workshop Abstracts 1

Systems Biology for DOE Energy and Environmental Missions 3

Bioenergy

Biofuels > Bioenergy Research Centers

Joint Bioenergy Institute (JBEI)

Systematic Characterization of Glycosyltransferases Involved in Plant Cell Wall Biosynthesis 3
Henrik Vibe Scheller[1]* (hscheller@lbl.gov), Ai Oikawaa, Lan Yin,[1,2] Eva Knoch,[1,2] Naomi Geshi,[2] Carsten Rautengarten,[1] Yuzuki Manabe,[1] and Chithra Manisseri[1]

Analysis of Putative Feruloyltransferase Transcript Levels and Cell Wall Composition During Rice Development 3
Laura E. Bartley[1,2]* (LEBartley@lbl.gov), Chithra Manisseri,[2] Brian Williams,[1,2] Dawn Chiniquy,[1,2] Jesper Harholt,[2] Henrik Vibe Scheller,[2] and Pamela C. Ronald[1,2]

The Utilization of *Arabidopsis* Genetic Variants to Understand Cell Wall Structure and Biosynthesis 4
Joshua L. Heazlewood* (JLHeazlewood@lbl.gov), Katy M. Christiansen, Dominique Loque, and A. Michelle Smith

Selection, Cloning and Functional Characterization of Rice-Diverged, Cell Wall-Related Glycosyltransferases 4
Miguel Vega-Sánchez* (mevegasanchez@ucdavis.edu), Laura Bartley, Peijian Cao, and Pamela Ronald (pcronald@ucdavis.edu)

Monolignol Transporters and Cell Wall Oxidases Screens 5
Fan Yang* (Fyang@lbl.gov), Nakako Shibagaki, and Dominique Loque

Starting Point for Enzymatic Hydrolysis for Cellulose: Enzyme Engineering of Glycoside Hydrolase-5 Endoglucanases 5
Blake A. Simmons[1,2]* (basimmons@lbl.gov), Zhiwei Chen,[1,2] Supratim Datta,[1,2] Danielle T. Ercek,[1] Hanbin Liu,[1,2] Josh I. Park,[1,2] Huu Tran,[1,2] Swapnil R. Chhabra,[1] Masood Z. Hadi,[1,2] and Rajat Sapra[1,2]

A Comparative Study of Dilute Acid and Ionic Liquid Pretreatment of Biomass and Model Lignocellulosics 6
Chenlin Li[1,2]* (Cli@lbl.gov), Rohit Arora,[1,2] Chithra Manisseri,[1] Ken Vogel,[3] Blake Simmons,[1,2] and Seema Singh[1,2]

Understanding Ionic Liquid Pretreatment of Lignocellulosic Biomasses 6
Seema Singh[1]* (SSingh@lbl.gov), Rohit Arora,[1] Chithra Manisseri,[1] Chenlin Li,[1] Henrik Vibe Scheller,[1] Ken Vogel,[2] and Blake Simmons[1]

JBEI Microbial Communities Deconstruction Research Activities 7
Terry C. Hazen* (TCHazen@lbl.gov), Phil Hugenholtz, Steve Singer, Jean VanderGheynst, Patrik M. D'haeseleer, Michael P. Thelen, Kristin DeAngelis, Amitha Reddy, Martin Allgaier, Julian Fortney, Gary Andersen, Todd DeSantis, Eoin Brodie, Cindy Wu, Dara Goodheart, Mary Firestone, Whendee Silver, and Blake Simmons

Discovery and Optimization of Lignocellulolytic Bacteria From Puerto Rican Rainforest Soils 8
Kristen M. DeAngelis* (KDeAngelis@lbl.gov), Whendee L. Silver, Julian Fortney, and Terry C. Hazen

Metagenomic Characterization of Compost and Rain Forest Soil Microbial Communities 8
Martin Allgaier[1]* (MAllgaier@lbl.gov), Amitha Reddy,[1,2] Jean VanderGheynst,[2] Alex Copeland,[3] Victor Kunin,[3] Patrik D'haeseleer,[4] Kristen DeAngelis,[1,5] Julian Fortney,[1,5] Dylan Chivian,[1,5] Paramvir S. Dehal,[5] Blake Simmons,[1,6] Terry C. Hazen,[1,5] and Phil Hugenholtz[1,3] (PHugenholtz@lbl.gov)

The Fuels Synthesis Division of the Joint BioEnergy Institute (JBEI) 9
E. Baidoo, H.R. Beller, R. Chan, S. Chhabra* (SRChhabra@lbl.gov), H. Chou, R. Dahl, Z. Dmytriv, M. Dunlop, C. Fortman, D. Garcia, H. Garcia Martin, J. Gilmore, J. Gin, E.-B. Goh, J. Haliburton, T. Ham, C. Joshua, Y. Kang, R. Krupa, S.K. Lee, T.S. Lee, C. Liu, A. McKee, A. Mukhopadhyay, F. Nowroozi, M. Ouellet, P. Peralta-Yahya, N. Prasad, S. Rodriguez, B. Rutherford, E. Steen, and J.D. Keasling

Building a *de novo* Synthetic Metabolic Pathway for Producing Branched-C5 Alcohols 9
H.H. Chou[1,3,4]* (HHChou@lbl.gov) and J.D. Keasling[1,2,3,4]

Transcriptomic Studies of the Response to Exogenous Exposure and Endogenous Production of Biofuel Candidates in *E. coli* 10
R. Dahl[1,3]* (robdahl@berkeley.edu), B. Rutherford,[1,3] A. Mukhopadhyay,[2,3] and J.D. Keasling[1,2,3,4]*

Increasing Mevalonate Production by Engineering the Metabolism of *Escherichia Coli* 10
Yisheng (Connie) Kang* (srhconnie@gmail.com), Hector Garcia Martin, Peter Benke, Mario Ouellet, Jennifer Gin, and Jay D. Keasling

Microbial Production of Isoprenoid Biodiesel 11
Taek Soon Lee* (tslee@lbl.gov), Nilu Prasad, Rossana Chan, Clem Fortman, and Jay Keasling

Harnessing Genomic Recombination to Improve Microbial Metabolic Phenotypes 11
Adrienne E. McKee* (AEMcKee@lbl.gov), John Haliburton, Veronica Fok, Mario Ouellette, Jay D. Keasling, and Swapnil Chhabra

Optimizing Isoprenoid Biosynthesis 11
Farnaz Nowroozi* (FNowroozi@lbl.gov), David E. Garcia, Edward E. Baidoo, and Jay D. Keasling

Metabolic Engineering of *Saccharomyces cerevisiae* for the Production of n-Butanol 12
Eric J. Steen[1,2]* (EJSteen@lbl.gov), Rossana Chan,[1,3] Nilu Prasad,[1,3] Samuel Myers,[1,3] Christopher J. Petzold,[1,3] Alyssa Redding,[1,3] Mario Ouellet,[1,3] and Jay D. Keasling[1,2,3,4]

Omics Research at the Joint BioEnergy Institute (JBEI) 12
Paul D. Adams, Tanveer S. Batth, Peter I. Benke, Rob Dahl, Jay D. Keasling, Aindrila Mukhopadhyay* (amukhopadhyay@lbl.gov), Mario Ouellet, Alyssa M. Redding, Becky J. Rutherford, Chris J. Petzold, and Pramila Tamrakar

JBEI Computational Biology Core 13
Dylan Chivian[1,2,3]* (DCChivian@lbl.gov), Paramvir S. Dehal,[2,3] Marcin P. Joachimiak,[2,3] Keith Keller,[2,4] Morgan N. Price,[2,3] Jason K. Baumohl,[2,3] John T. Bates,[1,3] and Adam P. Arkin[1,2,3,4]

High Throughput Technologies to Break the Biological Barriers to Cellulosic Fuels 13
Masood Hadi[1,3]* (MZhadi@sandia.gov), H. Tran,[1,3] S. Morrison,[1,3] H.C. Chu,[1,3] A. DeGiovanni,[2,3] and P. Adams[2,3]

High Throughput Mass Spectrometry Based Enzymatic Assays for Biofuels Development 14
Trent R. Northen[1]* (trnorthen@lbl.gov), Jinq-Chyi Lee,[3] Chris Petzold,[2] Blake Simmons,[2] Paul Adams,[2] and Anup Singh[2]

* Presenting author

Multi-Mode Spectroscopic High Throughput Screening (HTS) of Phenols and Monolignols 14
Komandoor Achyuthan* (kachyut@sandia.gov), Blake Simmons, Paul Adams, and Anup Singh

Microfluidics for Protein Expression, Purification, and Screening 16
Rajiv Bharadwaj* (rbharadwaj@lbl.gov), Jim Brennan, and Anup K. Singh

Electron Microscopic Imaging at JBEI 16
Bernhard Knierim* (BKnierim@lbl.gov), Lina Prak, Seema Singh, Danielle Jorgens, Marcin Zemla, Kristen DeAngelis, Amitha Reddy, Jean Vandergheynst, Terry C. Hazen, Brad Holmes, Rajat Sapra, Blake Simmons, Paul Adams, and Manfred Auer

An MRM-based Mass Spectrometry Method for Optimization of Protein Expression to Increase Biofuel Production 17
Christopher J. Petzold[1]* (CJPetzold@lbl.gov), Alyssa M. Redding,[1] Sung Kuk Lee,[1] Farnaz F. Nowroozi,[2] Tanveer S. Batth,[1] Aindrila Mukhopadhyay,[1] Paul D. Adams,[1] and Jay D. Keasling[1,2]

Great Lakes Bioenergy Research Center (GLBRC)

Streamlined Method for Biomass Whole-Cell-Wall Structural Profiling 18
John Ralph[1]* (jralph@wisc.edu), Fachuang Lu,[2] Hoon Kim,[2] Xiaowen Fang,[2] Mark Norton,[2] James J. Ellinger,[2] John L. Markley,[2] Daniel Yelle,[3] Kenneth E. Hammel,[4] Sally A. Ralph,[4] Ronald D. Hatfield,[5] Paul F. Schatz,[5] Mattias Hedenström,[6] and Björn Sundberg[7]

Quantification of Whole Plant Cell Wall and Plant Metabolites Using Advanced 2D ^{1}H-^{13}C HMQC NMR Techniques 19
Xiaowen Fang,[1]* James Ellinger,[1] Mark Norton,[1] William M. Westler,[1] Michael Casler,[2] Shawn M. Kaeppler,[3] and John M. Markley[1] (markley@nmrfam.wisc.edu)

Endogenous Variation for Biofuel Quantity and Quality Traits in Maize and Switchgrass 20
Shawn Kaeppler* (smkaeppl@wisc.edu), Natalia de Leon (ndeleongatti@wisc.edu), Mike Casler (mdcasler@wisc.edu), Heidi Kaeppler (hfkaeppl@wisc.edu), Rajan Sekhon, James Johnson, and Candy Hansey

Discovery of Genes that Mediate and Regulate Hemicellulose Biosynthesis 20
Kenneth Keegstra* (Keegstra@msu.edu), Markus Pauly (Paulymar@msu.edu), Curtis Wilkerson (Wilker13@msu.edu), David Cavalier, Jean-Christoph Cocuron, Jacob Jensen, Nick Thrower, and Yan Wang

Biomass Trait Screening in a *Brachypodium* Mutant Population 21
Megan Galvin,[1] Sonali Nath,[1] Colleen Stephens,[1] Florian Kraemer,[2] Markus Pauly,[2] John Vogel,[3] and John Sedbrook[1]* (jcsedbr@ilstu.edu)

Understanding the Transcriptional Regulation of Secondary Wall Biosynthesis: A Step Toward Optimizing Lignocellulosic Feedstock for Biofuel Productivity and Processing 21
Jae-Heung Ko, Won-Chan Kim, Zhongnan Zhang, and Kyung-Hwan Han* (hanky@msu.edu)

Use of Proteomics Technologies for the Characterization of Proteins, Microbes and Microbial Communities Important for Bioenergy Production 22
Mary S. Lipton[1]* (mary.lipton@pnl.gov), Stephen J. Callister,[1] Kim K. Hixson,[2] Samuel O. Purvine,[2] Angela D. Norbeck,[1] Ronald J. Moore,[1] Therese R. Clauss,[1] and Carrie D. Nicora[1]

Protein Expression Approaches to Cellulose Destruction 23
Nathaniel L. Elsen, Abolfazl Arabshahi, Allison Riederer, and Brian G. Fox* (bgfox@biochem.wisc.edu)

Engineering Cellulases with Improved Stability 23
George N. Phillips Jr.* (phillips@biochem.wisc.edu), Thomas J. Rutkoski, Robert W. Smith, and He Zhang

Simple Chemical Transformation of Lignocellulosic Biomass into Fuels and Chemicals 23
Joseph B. Binder[1,2,*] and Ronald T. Raines[1,2,3] (rtraines@wisc.edu)

Construction of a Consolidated Bioprocessor Derived from *Escherichia coli* 24
David H. Keating* (dkeating@glbrc.wisc.edu), Mary Tremaine, and Robert Landick

Molecular, Genetic and Genomic Approaches to Alleviate Bottlenecks in Cellulosic Ethanol Production by Yeast 24
Trey Sato[1]* (tksato@glbrc.wisc.edu), Jennifer Van Vleet,[1,2,3] Thomas Jeffries,[2,3] Jeffrey Lewis,[1,3] and Audrey Gasch[1,3]

Catalytic Processing of Carbohydrates for the Production of Liquid Fuels 25
Drew J. Braden[1]* (braden@wisc.edu), Elif I. Gurbuz,[1] Edward L. Kunkes,[1] Dante A. Simonetti,[2] Ryan M. West,[1] Juan Carlos Serrano-Ruiz,[1] Christian A. Gartner,[1] and James A. Dumesic[1]

Engineering *E. coli* for Production of Hydrocarbons 26
Brian Pfleger (pfleger@engr.wisc.edu) and Rebecca Lennen* (lennen@wisc.edu)

Networks Contributing to Photosynthetic Biohydrogen Production in *Rhodobacter sphaeroides* 26
Wayne S. Kontur[1]* (wskontur@wisc.edu), Eva C. Ziegelhoffer,[1] L. Safak Yilmaz,[2] Daniel R. Noguera[2] (noguera@engr.wisc.edu), and Timothy J. Donohue[1] (tdonohue@bact.wisc.edu)

Bacterial Communities in the Rhizosphere of Biofuel Crops as Evaluated by 16S rRNA Pyrosequencing ... 27
Ederson da Conceição Jesus* (ederson@msu.edu), Endang Susilawati (endangsusilawati@gmail.com), Qiong Wang (wangqion@msu.edu), Jorge Rodrigues (jorge@uta.edu) and James M. Tiedje (tiedjej@msu.edu)

BioEnergy Cropping Systems on Marginal Land 27
Stephanie Smith* (smith579@msu.edu) and Kurt Thelen (thelenk3@msu.edu)

Bioenergy Sciences Center (BESC)

The BioEnergy Science Center—An Overview 28
M. Keller,[1] L. Lynd,[2] A. Darvill,[3] and B. Davison[1]* (davisonbh@ornl.gov)

The Use of TAIL PCR to Identify Genes Controlling Extreme Phenotypes in a *Populus* Activation Tagged Population 28
G.A. Tuskan[1]* (gtk@ornl.gov), T. Tschaplinski,[1] U. Kalluri,[1] T. Yin,[1] L. Gunter,[1] M. Martin,[1] N. Engle,[1] S. Jawdy,[1] X. Yang,[1] Martin Keller,[2] V. Busov,[3] S. Strauss,[4] X. Ma,[4] M. Davis,[5] and R. Sykes[5]

The pANIC Vector Set for Overexpression of Transgenes and RNAi-Mediated Knockdown of Native Genes in Switchgrass (*Panicum virgatum* L) 29
David G.J. Mann[1]* (dmann1@utk.edu), Peter R. LaFayette,[2] Laura L. Abercrombie,[1] Wayne A. Parrott,[2] C. Neal Stewart Jr.,[1] and Martin Keller[3]

Genetic Modification of Lignin Biosynthesis in Switchgrass 30
Hiroshi Hisano,[1] Hui Shen,[2] Rangaraj Nandakumar,[1] Chunxiang Fu,[1] Xirong Xiao,[1] Yaxin Ge,[1] Tim Hernandez,[2] Fang Chen[2]* (fchen@noble.org), Richard A. Dixon,[2] Zeng-Yu Wang,[1] and Martin Keller[3]

New Insights on the Mechanism of Xylan Biosynthesis 30

Maria J. Peña[1]* (mpena@ccrc.uga.edu), Breeanna Urbanowicz,[1] Alan G. Darvill,[1,2] Malcolm O'Neill,[1] William S. York,[1,2] and Martin Keller[3]

Functional Identification and Characterization of Sugar-1-P Kinases in *Arabidopsis* 31

Ting Yang[1,2,3]* (goldfishting@gmail.com), Liron Bar-Peled,[2] Lindsay Gebhart,[2] John Glushka,[2] Maor Bar-Peled,[1,2,4] and Martin Keller[5]

GAUT12 (GAlactUronosylTransferase 12): A Putative Glycosyltransferase Involved in *Arabidopsis* Secondary Cell Wall Biosynthesis 31

Zhangying Hao[1,3]* (haozhangying@gmail.com), Staffan Persson,[4] Kyle David Hutcheson,[2,3] Debra Mohnen,[2,3] and Martin Keller[5]

Isolation of Novel Biofuel-Relevant Thermophiles and the Identification of Extracellular Cellulolytic Enzymes Using Multi-Dimensional LC-MS/MS 32

James G. Elkins* (elkinsjg@ornl.gov), Scott D. Hamilton-Brehm, Adriane Lochner, Richard J. Giannone, Tatiana Vishnivetskaya, Jennifer Mosher, Mircea Podar, Jennifer Morrell-Falvey, Steve Allman, Dawn Klingeman, Sue Carroll, Miriam Land, Steven D. Brown, Robert Hettich, Tommy Phelps, and Martin Keller

Degradation of Plant Biomass without Pretreatment by the Thermophilic Anaerobe, *Anaerocellum thermophilum* 33

Irina Kataeva[1]* (kataeva@uga.edu), Sung-Jae Yang,[1] Nick Sennett,[1] Aleksandar Cvetkovic,[1] Farris L. Poole II,[1] Scott D. Hamilton-Brehm,[1,3] Richard J. Giannone,[3] Robert L. Hettich,[3] Nancy E. Engle,[3] Timothy J. Tschaplinski,[3] Janet Westpheling,[1,2] Michael W.W. Adams,[1,2] and Martin Keller[3]

Integration of Genomics and Bioinformatics to Identify Genetic Differences in an Ethanol Tolerant *Clostridium thermocellum* ATCC27405 Strain 34

Steven D. Brown[1]* (brownsd@ornl.gov), Tatiana Karpinets,[1] Jonathan R. Mielenz,[1] Shihui Yang,[1] Dawn M. Klingeman,[1] Miriam L. Land,[1] Loren J. Hauser,[1] Babu Raman,[1] Miguel Rodriguez Jr.,[1] Tingfen Yan,[1] Tatiana A. Vishnivetskaya,[1] Herbert J. Strobel,[2] Maria V. Sizova,[3] Nicolai Panikov,[3] Ying Xu,[4] Phuongan Dam,[4] Lee Lynd,[3] and Martin Keller[1]

Advances in Microbial Cellulose Utilization: Methods Development and Kinetics 35

Nicolai Panikov[1]* (Nicolai.Panikov@Dartmouth.edu), Maria Sizova,[1] Evert Holwerda,[1] Julie Paye,[1] Lois St. Brice,[1] Lee Lynd,[1] and Martin Keller[2]

Metagenomics for Mining New Deconstructive Enzymes, Exploring Enzyme Diversity and Screening Cellulolytic Activities 35

Luen-Luen Li,[1] Sean M. McCorkle,[1] Denise C. Monteleone,[1] Susannah G. Tringe,[2] Tanja Woyke,[2] Shi-You Ding,[3] Michael Himmel,[3] Safiyh Taghavi,[1] Carl Abulencia,[4] Deborah Balch,[4] Ying Hefner,[4] Melisa Low,[4] Steven Truong,[4] Peter Luginbühl,[4] Steve Wells,[4] Joel Kreps,[4] Kevin Gray,[4] Daniel van der Lelie[1]* (vdlelied@bnl.gov), and Martin Keller[5]

The Improved Cellulosome: Computational Modeling to Minisomes 36

Yannick J. Bomble[1]* (yannick_bomble@nrel.gov), Michael F. Crowley,[1] Shi-you Ding,[1] Qi Xu,[1] Mark R. Nimlos,[2] Jiancong Xu,[3] Moumita Saharay,[3] Hong Guo,[4] John W. Brady,[5] David B. Wilson,[6] Jeremy C. Smith,[3] Michael E. Himmel,[1] and Martin Keller[7]

A Rapid Analytical Pyrolysis Method for Investigating Genetic Modification of the Lignin Pathway in Alfalfa (*Medicago sativa*) 37

A. Ziebell[1]* (angela_ziebell@nrel.gov), R. Sykes,[1] D. Astling,[1] K. Reichel,[1] C. Doeppke,[1] M. Davis,[1] and Martin Keller[2]

Integrated High Throughput Pretreatment and Enzymatic Hydrolysis in 96 Well Plates.....37
Michael H. Studer[1]* (michael.studer@ucr.edu), Jaclyn DeMartini,[1] Heather McKenzie,[1] Charles E. Wyman,[1] and Martin Keller[2]

Advanced Imaging Projects in the BioEnergy Science Center (BESC).....38
Shi-You Ding[1]* (shi_you_ding@nrel.gov), Yining Zeng,[1] Thomas Haas,[1] Yu-San Liu,[1] Mike Himmel,[1] X. Sunney Xie[2] (xie@chemistry.harvard.edu), and Martin Keller[3]

Analytical BESC Advances in Characterization of Biomass and Recalcitrance.....39
Y. Pu[1]* (Yunqiao.Pu@ipst.gatech.edu), N. Jiang,[1] H. Li,[1] M. Foston,[1] R. Samuel,[1] J. Seokwon,[1] A.J. Ragauskas,[1] and Martin Keller[2]

Computer Simulation of Lignocellulosic Biomass.....40
Loukas Petridis[1]* (petridisl@ornl.gov), Benjamin Lindner,[1] Jeremy C. Smith,[1] and Martin Keller[2]

The Plant Cell Wall Biosynthesis Related Galacturonosyltransferase (GAUT) and GAUT-Like (GATL) Genes Have a Different Origin than the Other Glycosyltransferase Family 8 Genes.....40
Yanbin Yin[1,3]* (yinyb@csbl.bmb.uga.edu), Huiling Chen,[1] Michael Hahn,[2,3] Debra Mohnen,[2,3,] Ying Xu,[1,3] and Martin Keller[3]

Computational Prediction of Golgi Resident Proteins in *Arabidopsis thaliana*.....41
Wen-Chi Chou[1,3]* (wcc@uga.edu), Maor Bar-Peled,[2,3] Ying Xu,[1,3] and Martin Keller[3]

The BioEnergy Science Center Laboratory Information Management System (LIMS).....41
Susan K. Holladay* (holladaysk@ornl.gov), Denise D. Schmoyer, Sheryl A. Martin, Edward C. Uberbacher, and Martin Keller

The BESC Knowledgebase: An Infrastructure for Biological Discovery.....42
Morey Parang[1,2]* (parangm@ornl.gov), Tatiana Karpinets,[1,2] Doug Hyatt,[1,2] Mike Leuze,[1] Honney Park,[1] Bob Cottingham,[1] Michael Galloway,[1] Loren Hauser,[1] Mustafa Syed,[1] Ed Uberbacher,[1] and Martin Keller[1]

BioEnergy Science Center Education and Outreach.....43
P. Doney[1,3]* (patdoney@uga.edu), S. Fowler,[2,3] B. Davison,[2,3] M. Keller,[2,3] J. Westpheling,[1,3] S. Kral,[4] J. Griffin,[4] and H. Schulson[4]

USDA–DOE Plant Feedstock Genomics for Bioenergy

Towards a Map of the *Populus* Biomass Protein-Protein Interaction Network.....44
Eric Beers[1]* (ebeers@vt.edu) Amy Brunner,[2] Allan Dickerman,[3] Xiaoyan Sheng,[2] Chengsong Zhao,[1] and Mingzhe Zhao[1]

Development of Genomic and Genetic Tools for Foxtail Millet, and Use of These Tools in the Improvement of Biomass Production for Bioenergy Crops.....45
Jeffrey L. Bennetzen[1]* (maize@uga.edu), Katrien M. Devos[2] (kdevos@uga.edu), Andrew Doust[3] (andrew.doust@okstate.edu), Janice Zale[4] (janicezale@comcast.net), and Ryan Percifield[1]

Identifying Genes Controlling Feruloylation in Grass Cell Walls.....45
M.M. de O. Buanafina* (mmb26@psu.edu) and D. Braun (dda10@psu.edu)

Developing Association Mapping in Polyploidy Perennial Biofuel Grasses: Establishing the Baseline on Genome-Size Variation 46
Denise E. Costich,[1]* Bernd Friebe,[2] Michelle E. Denton,[3] Elhan Ersoz,[3] Michael D. Casler,[4] Jerome H. Cherney,[5] and Edward S. Buckler[1] (dc58@cornell.edu)

Computational Resources for Biofuel Feedstock Species 46
Kevin L. Childs* (kchilds@plantbiology.msu.edu) and C. Robin Buell (buell@msu.edu)

Translational Genomics for the Improvement of Switchgrass 47
Bryan W. Penning, Anna T. Olek, Maureen C. McCann, and Nicholas C. Carpita* (carpita@purdue.edu)

Genomic Knowledgebase for Facilitating the Use of Woody Biomass for Fuel Ethanol Production 47
Vincent Chiang (Vincent_Chiang@ncsu.edu), Ron Sederoff, Ho-min Chang, Ying-Hsuan Sun,* Ting-Feng Yeh, Shanfa Lu, Quanzi Li, and Rui Shi

Systematic Modification of Monolignol Pathway Gene Expression for Improved Lignocellulose Utilization 48
Richard A. Dixon* (radixon@noble.org), Fang Chen, Rui Zhou, Lisa Jackson, Gail Shadle, and Qiao Zhou

Genetic Dissection of the Lignocellulosic Pathway of Wheat to Improve Biomass Quality of Grasses as a Feedstock for Biofuels 49
W. Li[1]* (wli@ksu.edu), C. Bi,[1] S.K. Sehgal,[1] N. Rothe,[1] H. Trick,[1] F. Chen,[2] R.A. Dixon,[2] and B.S. Gill[1] (bsgill@ksu.edu)

Development of Genomic Tools for the Improvement of Prairie Cordgrass (*Spartina pectinata*), a Highly Productive Bioenergy Feedstock Crop 50
Jose L. Gonzalez* (jose.gonzalez@sdstate.edu), Arvid Boe, and Vance Owens

Profiling the Small RNAs of *Brachypodium distachyon* 50
Matthias Ganssmann,* Marcelo German, Blake C. Meyers, and Pamela J. Green (green@dbi.udel.edu)

Transcription Factor Protein Interactions with Cell Wall Gene *cis*-Regulatory Regions and Their Overall Role in Bioenergy Feedstock Properties 51
Naomi Young,[1] Ghislain Breton,[2] Todd C Mockler,[3] Steve A Kay,[2] and Samuel P Hazen[1]* (hazen@bio.umass.edu)

Biochemical Genomics of Wood Formation: *O*-acylesterification for Alteration of Lignocellulosic Property 51
Chang-Jun Liu* (cliu@bnl.gov), Xiao-Hong Yu, and Jin-Ying Gou

Characterization of Pectin Acetylesterase Reveals Critical Roles of Cell Wall Acylesterification in Plant Growth and Development 52
Jin-Ying Gou* and Chang-Jun Liu (cliu@bnl.gov)

***Brachypodium* Transcriptomics** 53
Henry D. Priest[1]* (priesth@onid.orst.edu), Samuel Fox,[1] Wenqin Wang,[2] Todd P. Michael,[2] and Todd C. Mockler[1] (tmockler@cgrb.oregonstate.edu)

Identification of Cell Wall Synthesis Regulatory Genes Controlling Biomass Characteristics and Yield in Rice (*Oryza sativa*) 53
Zhaohua Peng[1]* (zp7@BCH.msstate.edu), Pamela Ronald,[2] and Guo-liang Wang[3]

NIRS Prediction of Corn Stover Cell Wall Composition and Conversion Potential, and Relationships among these Traits 53

H.G. Jung[1,2]* (Hans.Jung@ars.usda.gov), M.L. Lewis,[2] R.E. Lorenzana,[2] and R. Bernardo[2] (bernardo@umn.edu)

Epigenomics of Development in *Populus* 55

Kyle R. Pomraning,[2] Palitha D. Dharmawardhana,[3] Henry D. Priest,[4] Olga Shevchenko,[3] Caiping Ma,[3] Elizabeth Etherington,[3] Larry Wilhem,[4] Todd Mockler,[1,4] Michael Freitag,[1,2] and Steven Strauss[1,3]*

An EST-Microsatellite Linkage Map of Switchgrass (*Panicum Virgatum* L.) and Comparison Within the Poaceae 55

Christian Tobias[1] (christian.tobias@ars.usda.gov), Miki Okada[1]* (miki.okada@ars.usda.gov), Christina Lanzatella-Craig,[1] Brindha Narasimhamoorthy,[2] Malay Saha,[2] and Joe Bouton[2]

Fast Detection of Improved Hydrolysis in Plants with Genetically Modified Lignin 56

C. Chapple[1] (chapple@purdue.edu), R. Meilan,[2] X. Li,[1] E.A. Ximenes,[3,4] Y. Kim,[3,4] and M.R. Ladisch[3,4]*

Genome-Enabled Discovery of Carbon Sequestration Genes 57

Gerald A. Tuskan[1] (tuskanga@ornl.gov), Timothy J. Tschaplinski[1]* (tschaplinstj@ornl.gov), Udaya Kalluri,[1] Tongming Yin,[1] Xiaohan Yang,[1] Xinye Zhang,[1] Nancy Engle,[1] Priya Ranjan,[1] Manojit Basu,[1] Lee Gunter,[1] Sara Jawdy,[1] Madhavi Martin,[1] Alina Campbel,[1] Stephen DiFazio,[2] John Davis,[3] Maud Hinchee,[8] Christa Pinnacchio,[6] Rick Meila,[4] Victor Buso,[7] and Steve Strauss[5]

Genetic Dissection of Bioenergy Traits in Sorghum 58

Wilfred Vermerris[1]* (wev@ufl.edu), Ana Saballos,[1] Zhanguo Xin,[2] Jeffery Pedersen,[3] Scott Sattler,[3] William Rooney,[4] Seth Murray,[4] and Stephen Kresovich[5]

Insertional Mutagenesis of *Brachypodium distachyon* 58

John Vogel* (john.vogel@ars.usda.gov), Jennifer Bragg, Jiajie Wu, Yong Gu, Gerard Lazo, and Olin Anderson

Identification of Genes That Control Biomass Production Using Rice as a Model System 59

Jan E. Leach[1]* (jan.leach@colostate.edu), Daniel R. Bush[2,3] (dbush@colostate.edu), Hei Leung[3] (h.leung@cgiar.org), and John McKay[1,3] (jkmckay@lamar.colostate.edu)

Resource Development in Switchgrass, a Polyploid Perennial Biofuel Grass 60

Katrien M. Devos[1,2]* (kdevos@uga.edu), Jeffrey L. Bennetzen,[3] Joe H. Bouton,[4] E. Charles Brummer,[1] and Malay C. Saha[4]

Identification of Genes that Regulate Phosphate Acquisition and Plant Performance During Arbuscular Mycorrhizal Symbiosis in *Medicago truncatula* and *Brachypodium distachyon* 60

S. Karen Gomez,[1] Nathan Pumplin,[1] Aynur Cakmak,[1] Jeon Hong,[1] Ying Li,[2] Matthew E. Hudson,[2] and Maria J. Harrison[1]* (mjh78@cornell.edu)

Biofuels > Analytical and Imaging Technologies for Studying Lignocellulosic Material Degradation

Three-Dimensional Spatial Profiling of Lignocellulosic Materials by Coupling Light Scattering and Mass Spectrometry 61

P.W. Bohn[1]* (pbohn@nd.edu) and J.V. Sweedler[2] (sweedler@scs.uiuc.edu)

Visualization of Acid-Pretreatment Effects on Lignocellulose by Integration of Neutron Scattering and Computer Simulation 62

Barbara R. Evans[1]* (evansb@ornl.gov), Jeremy C. Smith,[2,3] Loukas Petridis,[2] Volker Urban,[1,4] Sai Venkatesh Pingali,[1,4] Dean A. Myles,[1,4,5] William T. Heller,[1,4] Hugh M. O'Neill,[1,4] Joseph McGaughey,[1] Art Ragauskas,[6] Marcus Foston,[6] and Ida Lee[1,7]

Synchrotron Infrared Spectromicroscopy of Cellulose Degradation Strategies of Living Cellulolytic Bacteria 63

Hoi-Ying N. Holman[1]* (hyholman@lbl.gov), Zhao Hao,[1] Ping Hu,[1] Robin Miles,[2] Albert Pisano,[3] Inkyu Park,[3] and Sun Choi[3]

A New Solution-State NMR Approach to Elucidate Fungal and Enzyme/Mediator Delignification Pathways 64

Kenneth E. Hammel[1]* (kehammel@wisc.edu), Daniel J. Yelle,[1] John Ralph,[2] Dongsheng Wei,[1] and Alexander N. Kapich[1]

In Vivo Mapping of ROS Produced by Wood Decay Fungi during Early Colonization 64

Christopher G. Hunt[1]* (cghunt@fs.fed.us), Kenneth E. Hammel[1,2] (kehammel@wisc.edu), and Don Carl Jones[1]

Stimulated Raman Scattering as an Imaging Tool for Lignocellulosic Biomass Conversion 65

Brian G. Saar, Yining Zeng, Christian W. Freudiger, Marcel G. Friedrich, Gary R. Holtom, Shi-you Ding, and X. Sunney Xie* (xie@chemistry.harvard.edu)

Probing the Architecture of the Plant Cell Wall during Deconstruction in Single Cells from *Zinnia elegans* 65

C.I. Lacayo[1]* (lacayo2@llnl.gov), H.-Y. Holman,[2] M. Hwang,[1] A. Hiddessen,[1] A.J. Malkin,[1] and M.P. Thelen[1] (mthelen@llnl.gov)

Integrated Nondestructive Spatial and Chemical Analysis of Lignocellulosic Materials during Pretreatment and Bioconversion to Ethanol 66

Gary Peter* (gfpeter@ufl.edu), Choong Heon Lee, Kyle Lundsford, Steve Blackband, Lonnie Ingram, and Richard Yost

Single-Molecule Studies of Cellulose Degradation by Celluosomes 67

Haw Yang* (hyang@lbl.gov), Jamie Cate (jcate@lbl.gov), Chang-Li Chen, Padma Gunda, Dan Montiel, and Hu Cang

Systems Biology and Metabolic Engineering Approaches for Biological Hydrogen Production

Metabolic Modeling for Maximizing Photobiological H_2 Production in Cyanobacteria 68

Alexander S. Beliaev[1]* (alex.beliaev@pnl.gov), Grigoriy E. Pinchuk,[1] Oleg V. Geydebrekht,[1] Michael H. Huesemann,[2] Elizabeth H. Burrows,[3] Trang Vu,[4] Jennifer L. Reed,[4] Andrei L. Osterman,[5] John R. Benemann,[6] and Jim K. Fredrickson[1]

A High-Throughput Genetic Screen for Large Subunit Hydrogenase (*hoxH*) Enzyme Presence in Cyanobacteria Using Whole-Cell Duplex PCR and Novel Amplification Parameters 69

Nicholas J. Skizim (nskizim@princeton.edu), Derrick R.J. Kolling,* Diana Chien, and G. Charles Dismukes

Probing the Interdependence of Hydrogenase- and Nitrogenase-Dependent Hydrogen Production in *Cyanothece* sp. Miami BG043511 by Genetic Deletion and Mutant Analysis 69

Nicholas J. Skizim[1]* (nskizim@princeton.edu), Randall Kerstetter,[2] Todd Michael,[2] and G. Charles Dismukes[1]

Microalgal Biomass as Feedstock for Production of Hydrogen and Methane Fuels 70
Mark B. Smith[1]* (mbsmith@princeton.edu), Damian Carrieri[1] (carrieri@princeton.edu), Jun Cheng[2] (juncheng@zju.edu.cn), Gennady Ananyev[1] (anayev@princeton.edu), and G. Charles Dismukes[1] (dismukes@princeton.edu)

Development of Biologically-Based Assays to Study Rate-Limiting Factors in Algal Hydrogen Photoproduction 70
Alexandra Dubini,[1] Matthew Wecker,[2] and Maria L. Ghirardi[1]* (maria_ghirardi@nrel.gov)

Novel Hydrogen Production Systems Operative at Thermodynamic Extremes 71
Michael J. McInerney,[1] Jesscia Seiber,[1] Ralph S. Tanner,[1] and Robert P. Gunsalus[2]* (robg@microbio.ucla.edu)

Mechanism of Post-Translational Control of Nitrogenase is Revealed by Analysis of Constitutive Hydrogen-Producing Mutants of *Rhodopseudomonas palustris* 71
Erin K. Heiniger* (erinkh@u.washington.edu), Yasuhiro Oda, and Caroline S. Harwood

Systems Biology of Hydrogen Regulation in *Methanococcus maripaludis* 72
Erik L. Hendrickson,[1] Qiangwei Xia,[1] William B. Whitman,[2] Murray Hackett,[1] John A. Leigh[3]* (leighj@u.washington.edu), and Nitin Baliga[4]

Systems Level Approaches to Understanding and Manipulating Heterocyst Differentiation in *Nostoc punctiforme*: Sites of Hydrogenase and Nitrogenase Synthesis and Activity 73
Harry Christman,[1] Elsie Campbell,[1] Brett Phinney,[2] Wan-Ling Chiu,[3] and John C. Meeks[1]* (jcmeeks@ucdavis.edu)

***Thermotoga maritima* Sugar Kinome** 74
Irina Rodionva,[1] Xiaoqing Li,[1] Chen Yang,[1] Ying Zhang,[1] Ines Thiele,[2] Bernhard O. Palsson,[2] Dmitry Rodionov[1] (rodionov@burnham.org), and Andrei Osterman[1,3]* (osterman@burnham.org)

Conservation and Variations in *Shewanella* Transcriptional Regulatory Network 74
Dmitry Rodionov[1]* (rodionov@burnham.org), Irina Rodionova,[1] Xiaoqing Li,[1] Pavel Novichkov,[2] Margaret Romine,[3] Mikhail Gelfand,[4] and Andrei Osterman[1,5] (osterman@burnham.org)

Development of *Cyanothece* as a New Model Organism for Biological Hydrogen Production 75
Anindita Banerjee,[1] Michelle Liberton,[1] Hanayo Sato,[1] Jana Stöckel,[1] Lawrence Page,[1] Rick Huang,[2] Yinjie Tang,[2] Hogtao Min,[3] Louis A. Sherman,[3] Stephen J. Callister,[4] Richard D. Smith,[4] and Himadri B. Pakrasi[1,2]*

Systems-Level Understanding of Hydrogen Production by *Thermotoga maritima* 76
Vasiliy Portnoy[1]* (vasiliy.portnoy@gmail.com), Karsten Zengler,[1] Ines Thiele,[1] Ying Zhang,[2] Andrei Osterman,[2] and Bernhard O. Palsson[1] (palsson@ucsd.edu)

Systems-Level Kinetic Flux Profiling Elucidates a Bifurcated TCA Cycle in *C. acetobutylicum* 77
Daniel Amador-Noguez* (damador@princeton.edu), Jing Fan (jingfan@princeton.edu), Nathaniel Roquet (nroquet@Princeton.EDU), Xiao-Jiang Feng, Herschel Rabitz, and Joshua D. Rabinowitz (joshr@princeton.edu)

Systems Approach to Probing Hydrogen Regulation (SAPHyRe): The SurR Redox-Switched Transcriptional Regulator Controlling Hydrogen Production in *Pyrococcus furiosus* 78
Gina L. Lipscomb,[1]* Hua Yang,[1,3] Annette Keese,[2] Gerrit J. Schut,[1] B.C. Wang,[1] Michael Thomm,[2] Janet Westpheling,[1] Michael W.W. Adams,[1] and Robert A. Scott[1] (rscott@uga.edu)

Filling Knowledge Gaps in Biological Networks: Integrated Global Approaches to Understand H_2 Metabolism in *Chlamydomonas reinhardtii* 78

Christopher H. Chang,[1] Alexandra Dubini,[1] Florence Mus,[2] Venkataramanan Subramanian,[1,3] David M. Alber,[1] Peter A. Graf,[1] Glenn Murray,[3] Kwiseon Kim,[1] Arthur R. Grossman,[2] Matthew C. Posewitz,[3] and Michael Seibert[1]* (mike_seibert@nrel.gov)

Examining the Molecular Basis for the Utilization of Alternative Redox Systems to Maximize Hydrogen Production in RubisCO-Compromised Mutants of Nonsulfur Purple Bacteria 80

Rick A. Laguna* (laguna.2@osu.edu) and F. Robert Tabita

Pathways and Regulatory Network of Hydrogen Production from Cellulose by *Clostridium thermocellum* 81

Jonathan Millen[1]* (jonathan_millen@hotmail.com), Matthew Heckman,[1] Hsin-Yi Tsai,[1] Pin-Ching Maness,[2] Mary Lipton,[3] and J.H. David Wu[1] (davidwu@che.rochester.edu)

Inference and Integration of Regulatory Dynamics in Metabolic Network Models 81

William J. Riehl[1]* (briehl@bu.edu), Hsuan-Chao Chiu[1]* (hcchiu@bu.edu), and Daniel Segrè[1,2] (dsegre@bu.edu)

Effects of Mutational Modification of Electron Pathways of *Desulfovibrio* Strains 82

Kimberly L. Keller[1,2]* (kellerkl@missouri.edu), Steve D. Brown,[3] Iris Porat,[3] and Judy D. Wall[1,2] (WallJ@missouri.edu)

Modeling Electron Flow in *Rhodobacter sphaeroides* for the Identification of Potential Approaches to Maximize Hydrogen Production 83

L. Safak Yilmaz[1,*] (yilmaz@cae.wisc.edu), Alison P. Sanders, Rodolfo Perez,[1] Wayne S. Kontur,[2] Timothy J. Donohue[2] (tdonohue@bact.wisc.edu), and Daniel R. Noguera[1] (noguera@engr.wisc.edu)

SBIR Bioenergy Research

Consolidated Bioelectrochemical Processing of Cellulosic Biomass to Ethanol and Hydrogen 84

T. Shimotori[1]* (shimo@mfctech.net), M. Nelson,[1] and H. May[2]

***Clostridium phytofermentans*: Genome Sequence of a Model System for the Direct Conversion of Plant Biomass to Fuels** 85

E. Petit,[1] T. Warnick,[1] W. Latouf,[1,3] A. Tolonen,[4] N. Ivanova,[5] A. Lykidis,[5] M. Land,[6] L. Hauser,[6] N. Kyrpides,[5] B. Henrissat,[7] G. Church,[4] D. Schnell,[2] S. Leschine,[1] and J. Blanchard[1]* (blanchard@microbio.umass.edu)

A Genome-Wide Perspective on the Regulation of Plant Carbohydrate Conversion to Biofuels in *Clostridium phytofermentans* 85

E. Petit,* T. Warnick, S. Leschine, and J. Blanchard (blanchard@microbio.umass.edu)

Systems Environmental Microbiology

The Virtual Institute of Microbial Stress and Survival VIMSS:ESPP

ESPP Functional Genomics and Imaging Core (FGIC): Cell Wide Analysis of Metal-Reducing Bacteria 86

Aindrila Mukhopadhyay,[1,6]* Edward Baidoo,[1,6] Kelly Bender[5,6] (bender@micro.siu.edu), Peter Benke,[1,6] Swapnil Chhabra,[1,6] Elliot Drury,[3,6] Masood Hadi,[2,6] Zhili He,[4,6] Jay Keasling[1,6] (keasling@.berkeley.edu), Kimberly Keller,[3,6] Eric Luning,[1,6] Francesco Pingitore,[1,6] Alyssa Redding,[1,6] Jarrod Robertson,[3,6] Rajat Sapra,[2,6] Anup Singh[2,6] (aksingh@sandia.gov), Judy Wall[3,6] (wallj@missouri.edu), Grant Zane,[3,6] Aifen Zhou,[4,6] and Jizhong Zhou[4,6] (jzhou@rccc.ou.edu)

Analysis of a *Desulfovibrio vulgaris* Small RNA and Its Target Under Various Stress Conditions 87
Andrew S. Burns[1,2] and Kelly S. Bender[1,2]* (bender@micro.siu.edu)

Functional Characterization of Microbial Genomes by Tagged Transposon Mutagenesis.....87
Adam Deutschbauer[1,4]* (AMDeutschbauer@lbl.gov), Julia Oh,[2] Morgan Price,[1,4] Jennifer Kuehl,[1,4] Paramvir Dehal,[1,4] Corey Nislow,[3] Ronald W. Davis,[2] and Adam P. Arkin[1,4]

The Development and Application of an Integrated Functional Genomics Platform in *Desulfovibrio desulfuricans* G20 88
Adam Deutschbauer,[1,2] Jennifer Kuehl[1,2]* (JVKuehl@lbl.gov), Morgan Price,[1,2] Paramvir Dehal,[1,2] Terry C. Hazen,[1,2] and Adam P. Arkin[1,2]

A Phylogenomic Approach to the Evolutionary Origins of Microbial Metabolisms 89
Lawrence David[1]* (ldavid@mit.edu) and Eric Alm[1,2]

Resource for the Exploration of Regulons Accurately Predicted by the Methods of Comparative Genomics 89
Pavel S. Novichkov[1]* (PSNovichkov@lbl.gov), Mikhail S. Gelfand,[2] Inna Dubchak,[1,4] and Dmitry A. Rodionov[2,3]

Expression Profiling of Hypothetical Genes in *Desulfovibrio vulgaris* Leads to Improved Functional Annotation 90
Dwayne A. Elias* (eliasd@missouri.edu) Elliott C. Drury, Alyssa M. Redding, Aindrila Mukhopadhyay, Marcin Joachimiak, Huei-Che B.Yen, Matthew W. Fields,[3] Terry C. Hazen,[1] Adam P. Arkin (APArkin@lbl.gov), Jay D. Keasling,[1] and Judy D. Wall[2]

Impact of Elevated Nitrate on Sulfate-Reducing Bacteria: Implications of Inhibitory Mechanisms in Addition to Osmotic Stress.....90
Qiang He,[1,2]* Zhili He,[3,13] Dominique C. Joyner,[4,13] Marcin Joachimiak,[5,13] Morgan N. Price,[5,13] Zamin K. Yang,[6,13] Huei-Che Bill Yen,[7,13] Christopher L. Hemme,[3,13] Romy Chakraborty,[4,13] Wenqiong Chen,[8,13] Matthew M. Fields,[9,13] David A. Stahl,[12,13] Jay D. Keasling,[5,11,13] Martin Keller,[6,13] Adam P. Arkin[5,10,13] (APArkin@lbl.gov), Terry C. Hazen,[4,13] Judy D. Wall,[7,13] and Jizhong Zhou[3,13]

A Role of CO and a CO Sensor Protein in the Energy Metabolism of *D. vulgaris* Hildenborough.....91
Lara Rajeev[1]* (lrajeev@u.washington.edu), Sergey Stolyar,[1] David A Stahl,[1] Grant Zane,[2] and Judy Wall[2]

Comparison of the Sulfate-Reducing Capacity of *Desulfovibrio vulgaris* Hildenborough Deleted for the Operon Containing *qmoABC* and a Hypothetical Protein (DVU0851) versus Deletion of the Hypothetical Protein Alone 91
Grant M. Zane,* Dwayne A. Elias, Huei-Che Yen, and Judy D. Wall

The Molecular Mechanism of Adaptation to Salt Stress Revealed by the Long-Term Evolution of *Desulfovibrio vugaris* Hildenborough.....92
Aifen Zhou,[1,6]* Zhili He,[1,6] Marcin P. Joachimiak,[2,6] Paramvir S. Dehal,[2,6] Adam P. Arkin[2,6] (APArkin@lbl.gov), Kristina Hillesland,[4,6] David Stahl,[4,6] Judy Wall,[5,6] Terry C. Hazen,[3,6] and Jizhong Zhou[1,6]

***Desulfovibrio vulgaris* Hildenborough Responses to Salt and H_2O_2 Stresses**.....92
Zhili He,[1,10]* Aifen Zhou,[1,10] Qiang He,[2,10] Aindrila Mukhopadhyay,[3,10] Edward Baidoo,[3,10] Marcin Joachimiak,[3,10] Christopher L. Hemme,[1,10] Peter Benke,[3,10] Alyssa M. Redding,[3,10] Matthew M. Fields,[4,11] David A. Stahl,[5,10] Jay D. Keasling,[3,6,10] Adam P. Arkin[3,7,10] (APArkin@lbl.gov), Terry C. Hazen,[8,10] Judy D. Wall,[9,10] and Jizhong Zhou[1,10]

Analysis of an Intact Dissimilatory Sulfite Reductase Protein Complex from *Desulfovibrio vulgaris* Using an Ion Mobility QTOF Analyzer 93

Ming Dong,[1] Michael Daly,[2] Haichuan Liu,[3] Simon Allen,[3] Evelin Szakal,[3] Steven C. Hall,[3] Susan J. Fisher,[1,3] Terry C. Hazen,[1] Jil T. Geller,[1] Mary E. Singer,[1] Lee L. Yang,[1] Jian Jin,[1] H. Ewa Witkowska,[2*] and Mark D. Biggin[1] (mdbiggin@lbl.gov)

Microbes Online: An Integrated Portal for Comparative Functional Genomics 94

Paramvir S. Dehal[1,2*] (PSDehal@lbl.gov), Jason K. Baumohl,[1,2] Dylan Chivian,[1,2,3] Katherine H. Huang,[1,2] Marcin P. Joachimiak,[1,2] Keith Keller,[1,2] Morgan N. Price,[1,2] and Adam P. Arkin[1,2,3,4]

Progress in the Development of the RegTransBase Database and the Comparative Analysis System 95

Michael J. Cipriano,[1] Pavel Novichkov,[1,4] Alexei E. Kazakov,[2] Dmitry Ravcheev,[2] Adam P. Arkin[1,3,4] (APArkin@lbl.gov), Mikhail S. Gelfand,[2,5] and Inna Dubchak[1,4,6*] (ILDubchak@lbl.gov)

Applied Environmental Microbiology Core Research on Stress Response Pathways in Metal-Reducers VIMSS: ESPP 95

Terry C. Hazen[1,2*] (TCHazen@lbl.gov), Gary Anderson,[1,2] Sharon Borglin,[1,2] Eoin Brodie,[1,2] Steve van Dien,[8] Matthew Fields,[1,7] Julian Fortney,[1,2] Jil Geller,[1,2] E. Hendrickson,[5] Kristina L Hillesland,[1,6] Hoi-Ying Holman,[1,2] J. Leigh,[1,6] T. Lie,[1,6] Janet Jacobsen,[1,2] Dominique Joyner,[1,2] Romy Chakraborty,[1,2] Martin Keller,[1,3] Aindrila Mukhopadhyay,[1,2] Christopher Schadt,[1,3] David Stahl,[1,6] Sergey Stolyar,[1,6] Chris Walker,[1,6] Judy Wall,[1,5] Zamin Yang,[1,3] Huei-che Yen,[1,5] Grant Zane,[1,5] and Jizhong Zhou[1,9]

Microfluidic Tools for Single-Cell Genomic Analysis of Environmental Bacteria 97

Robert J. Meagher,[1,3] Masood Z. Hadi,[1,3] Yooli K. Light,[1,3] Paramvir Dehal,[2,3] Terry Hazen,[2,3] Adam Arkin[2,3] (aparkin@lbl.gov), and Anup K. Singh[1,3*] (aksingh@sandia.gov)

Applications of GeoChip for Analysis of Different Microbial Communities 98

Joy D. Van Nostrand,[1,2*] Liyou Wu,[1] Patricia Waldron,[1] Ye Deng,[1] Zhili He,[1,2] Weimin Wu,[3] Sue Carroll,[4] Chris Schadt,[4,2] Anthony Palumbo,[4] Dave Watson,[4] Craig Criddle,[3] Phil Jardine,[4] Terry C. Hazen,[5,2] and Jizhong Zhou[1,2]

Temporal and Spatial Organization within a Syntrophic Bacterial-Archaeal Biofilm 99

K. Brileya,[1] C. Walker,[2] S. Stolyar,[2] D.A. Stahl,[2] A. Arkin[3] (AParkin@lbl.gov), T.C. Hazen,[3] and M.W. Fields[1*] (matthew.fields@erc.montana.edu)

Evolution and Stability in a Syntrophic Community 99

Kristina L Hillesland* (hilleskl@u.washington.edu) and David A Stahl

Development and Analysis of Multispecies Consortia to Study Microbial Community Stress and Survival 100

L.D. Miller,[1] A. Venkateswaran,[1] J. Mosher,[1] M. Drake,[1] Z.K. Yang,[1] M. Rodriguez,[1] S.D. Brown,[1] T.J. Phelps,[1] M. Podar,[1] A.V. Palumbo,[1] C.W. Schadt,[1] M. Keller,[1] D.C. Joyner,[2] T.C. Hazen,[2] S. Stolyar,[3] K. Hillisland,[3] and D.A. Stahl[3]

Characterization of Metal-Reducing Communities and Isolates from Uranium-Contaminated Groundwater and Sediments 101

B. Ramsay,[1,8] C. Hwang,[1,8] S. Carroll,[2] A. Lapidus,[3] J.C. Detter,[3] C. Han,[3] M. Land,[3] L. Hauser,[3] T.C. Hazen,[4,8] A. Arkin[4,8] (APArkin@lbl.gov), A. Belieav,[5] R. Sanford,[6] F. Löeffler,[7] and M.W. Fields[1,8*] (matthew.fields@erc.montana.edu)

Changing Patterns of Selection on γ-Proteobacteria Revealed by the Ratio of Substitutions in Slow:Fast-Evolving Sites 102

Jesse Shapiro[1] and Eric Alm[1,2*] (ejalm@mit.edu)

Natural Diversity and Experimental Evolution of Environmental Stress Tolerance in Marine Bacteria 102
A.C. Materna,[1]* S.A. Clarke,[1] C. Cruz,[1] X. Gao,[1] and E.J. Alm[1,2,3] (ejalm@mit.edu)

The *Shewanella* Federation

Constraint-Based Metabolic Modeling Reveals High Maintenance Energy Requirement for Growth of *Shewanella oneidensis* MR-1 Under Elevated O_2 Tensions 103
Grigoriy E. Pinchuk[1]* (grigoriy.pinchuk@pnl.gov), Jennifer L. Reed,[2] Oleg V. Geydebrekht,[1] Eric A. Hill,[1] Alexander S. Beliaev,[1] and Jim K. Fredrickson[1]

Phylogenetic Footprinting in the *Shewanellae* 103
Lee Ann McCue[1]* (leeann.mccue@pnl.gov), William A. Thompson,[2] Lee A. Newberg,[3,4] and Charles E. Lawrence[2]

Constraint-Based Modeling of Metabolism in *Shewanella oneidensis* MR-1 104
Jennifer L. Reed[1]* (reed@engr.wisc.edu), Sharon J. Wiback,[2] Iman Famili,[2] Jessica De Ingeniis,[3] and Grigoriy Pinchuk[4]

Progress in Identification of the 'Mobilome' Associated with 21 Sequenced *Shewanella* sp. 105
Margaret Romine* (Margie.romine@pnl.gov)

Adenylate Cyclases and Anaerobic Respiration in *Shewanella oneidensis* MR-1 106
M. Charania[1]* (charania@uwm.edu), E. Biddle,[1] Y. Zhang,[2] G. Pinchuk,[2] A. Beliaev,[2] and D. Saffarini[1] (daads@uwm.edu)

Experimental and Computational Analysis of Growth-Phase Dependent Transcriptional Programs in *Shewanella oneidensis* 106
Qasim K. Beg[1]* (qasimbeg@bu.edu), Niels Klitgord,[2] Mattia Zampieri,[2,3] Timothy S. Gardner,[1,4] and Daniel Segrè[1,2,5] (dsegre@bu.edu)

Metabolic Optimality and Trade-Offs Under Combinatorial Genetic and Nutrient Modifications 107
David K. Byrne[1]* (Dbyrne@Bu.Edu), Timothy S. Gardner,[2,4] and Daniel Segrè[1,2,3]

Comparative Analyses Across an Evolutionary Gradient Within the *Shewanella* Genus 107
Margrethe H. Serres[1]* (mserres@mbl.edu), Kostas Konstantinidis,[2] Margaret F. Romine,[3] Jorge L.M. Rodrigues,[4] Anna Y. Obraztsova,[5] Mary S. Lipton,[3] LeeAnn McCue,[3] James K. Fredrickson,[3] and James M. Tiedje[6]

Evolution of Signal Transduction in a Bacterial Genus 108
Harold Shanafield* (hshanafi@utk.edu), Luke E. Ulrich, and Igor B. Zhulin

Investigating Environmental Specialization in a Population of *Shewanella baltica* Strains 108
Jie Deng,[1] Jennifer M. Auchtung[1]* (blackjen@msu.edu), Konstantinos Konstantinidis,[2] and James M. Tiedje[1] (tiedjej@msu.edu)

Characterization of *C*-type Cytochromes and Their Role in Anaerobic Respiration in *Shewanella oneidensis* and *S. putrefaciens* 109
Haichun Gao,[1] Jingrong Chen,[1] Yili Liang,[1]* Soumitra Barua,[1,2] Dongru Qiu,[1] Zhili He[1] (zhili.he@ou.edu), Alexander S. Beliav,[3] Margaret F. Romine,[3] Samantha Reed,[3] Dave Culley,[3] David Kennedy,[3] Yunfeng Yang,[2] James M. Tiedje,[4] James K. Fredrickson,[3] Kenneth H. Nealson,[5] and Jizhong Zhou[1,2] (jzhou@ou.edu)

The NapC- and CymA-Dependent Nitrate Reduction in *Shewanella oneidensis* MR-1 and *S. putrefaciens* W3-18-1 110

Dongru Qiu[1]* (qiu@ou.edu), Haichun Gao,[1] Yili Liang,[1] Jingrong Chen,[1] Zhili He,[1] Margaret F. Romine,[2] Kenneth H. Nealson,[4] James M. Tiedje,[3] James K. Fredrickson,[2] and Jizhong Zhou[1] (jzhou@ou.edu)

The *Shewanella* Knowledgebase 110

Tatiana Karpinets[1,2] (karpinetstv@ornl.gov),[3] Margaret Romine,[1] Denise Schmoyer,[1,2] Guruprasad Kora,[1] Mike Leuze,[1] Mustafa Syed,[4] Erich Baker,[1] Byung Park,[3] Andrey Gorin,[1,5] Nagiza Samatova,[1] and Ed Uberbacher[1]* (ube@ornl.gov)

Geobacter Systems Understanding

Experimental Genome Annotation of *Geobacter sulfurreducens* 112

Karsten Zengler,[1] Byung-Kwan Cho[1]* (bcho@ucsd.edu) Yu Qiu,[1] Christian Barrett,[1] Young-Seoub Park,[1] Mary Lipton,[2] Derek Lovley[3] (dlovley@microbio.umass.edu), and Bernhard O. Palsson[1]

Novel Approaches for Genome-Scale Spatial Analysis of Gene Transcription in Biofilms: Elucidation of Differences in Metabolism Throughout *Geobacter sulfurreducens* Biofilms Producing High Current Densities 112

Ashley E. Franks* (aefranks@microbio.umass.edu), Kelly P. Nevin, Kengo Inoue, Richard H. Glaven, and Derek R. Lovley

Genome-Wide Mapping of Transcriptional Start Sites of *Geobacter sulfurreducens* using High-Throughput Sequence Methodologies 114

Katy Juárez[1]* (katy@ibt.unam.mx), Alfredo Mendoza,[1] Leticia Vega-Alvarado,[2] Blanca Taboada,[2] Verónica Jimémez,[3] Leticia Olvera,[1] Maricela Olvera,[1] Ana L. Tirado,[1] Julio Collado-Vides,[3] Enrique Morett,[1] and Derek R. Lovley[4] (dlovley@microbio.umass.edu)

Genome Resequencing Reveals that Current-Harvesting Electrodes Select for Rare Variant of *Geobacter sulfurreducens* Capable of Enhanced Current Production 114

Anna Klimes[1]* (aklimes@microbio.umass.edu), Kelly P. Nevin,[1] Hana Yi,[1] Jessica E. Butler,[1] Trevor L. Woodard,[1] Christian L. Barrett,[2] Karsten Zengler,[2] Bernhard Palsson,[2] Barbara Methe,[3] Yuan Gao,[4] Bin Xie,[4] Chen Liang,[5] and Derek R. Lovley[1]

Bioinformatic Analysis of Gene Regulation in *Geobacter sulfurreducens:* an Integration of Transcriptome and Sequence Information, Molecular Evolutionary Studies, and Database Management 116

Julia Krushkal[1]* (jkrushka@utmem.edu), Yanhua Qu,[1] Peter Brown,[2] Sreedhar Sontineni,[1] Toshiyuki Ueki,[2] Katy Juarez,[3] Ching Leang,[2] Enrique Merino,[3] Jeanette Peeples,[1] Jose F. Barbe,[1] Ronald M. Adkins,[1] and Derek R. Lovley (dlovley@microbio.umass.edu)

Dynamic Genome-Scale Modeling of *Geobacter* Species in Subsurface Environments 117

R. Mahadevan,[2]* Jun Sun,[1] Kai Zhuang,[2] Yilin Fang,[3] Tim Scheibe,[3] Hanno Richter,[4] Carla Risso,[4] Paula Mouser,[4] Ashley Franks,[4] and Derek Lovley[4]

The Application of Metagenomic and Metatranscriptomic Approaches to the Study of Microbial Communities in a Uranium-Contaminated Subsurface Environment 119

Barbara Methé[1]* (bmethe@jcvi.org), Robert Deboy,[1] Qinghu Ren,[1] Michael Geimer,[1] Jamison McCorrison,[1] Dawn Holmes,[2] and Derek Lovley[2]

New Insights into *Rhodoferax ferrireducens* Through Genome Annotation and Genome-Based *in silico* Metabolic Modeling 120

Carla Risso[1]* (crisso@microbio.umass.edu), Jun Sun,[2] Kai Zhuang,[3] Radhakrishnan Mahadevan,[3] Olivia Bui,[2] Robert DeBoy,[4] Wael Ismael,[1] Christophe H. Schilling,[2] Barbara A. Methé,[4] and Derek Lovley[1] (dlovley@microbio.umass.edu)

Adaptive Evolution of *Geobacter sulfurreducens* under Likely Subsurface Bioremediation Conditions Revealed with Genome Resequencing 121

Zarath M. Summers[1]* (zsummers@microbio.umass.edu), Pier-Luc Tremblay,[1] Toshiyuki Ueki,[1] Wael Ismail,[1] Jennifer K. Hart,[1] Bernhard Palsson,[2] Christian Barrett,[2] Karsten Zengler,[2] Yuan Gao,[3] Bin Xie,[3] Chen Liang,[3] and Derek R. Lovley[1]

Novel Mechanisms Regulating the Expression of Genes in *Geobacter* species Important for Metal Reduction, Electricity Production, and Growth in the Subsurface 123

Toshiyuki Ueki* (tueki@microbio.umass.edu), Byoung-Chan Kim, and Derek R. Lovley (dlovley@microbio.umass.edu)

Nitrogen Metabolism in the *Geobacteraceae*: The Role of RpoN 124

Karsten Zengler[1]* (kzengler@ucsd.edu), Yu Qiu,[1] Jessica De Ingeniis,[2] Derek Lovley[3] (dlovley@microbio.umass.edu), and Bernhard Ø. Palsson[1]

Structures and Redox Potentials of Periplasmic Cytochromes from *Geobacter sulfurreducens* 125

P. Raj Pokkuluri[1]* (rajp@anl.gov), Yuri Y. Londer,[1] Norma E.C. Duke,[1] Miguel Pessanha,[2] Leonor Morgado,[2] Ana P. Fernandes,[2] Carlos A. Salgueiro,[2] and Marianne Schiffer[1] (mschiffer@anl.gov)

Caulobacter Systems Understanding

Automatic Segmentation and Structural Study of the Bacterial Cell Wall in Cryo-Electron Tomography 126

Farshid Moussavi[1]* (farshid1@stanford.edu), Fernando Amat,[1] Luis R. Comolli,[2] Kenneth H. Downing,[2] Mark Horowit,[2] and Harley McAdams[3] (hmcadams@stanford.edu)

Control Mechanisms for Chromosome Orientation and Dynamics in *Caulobacter crescentus* 127

Esteban Toro,[1] Grant R Bowman,[1] Luis R Comolli,[2] Sun-Hae Hong,[1] Jian Zhu,[2] Michael Eckart,[1] Marcelle Koenig,[1] Kenneth H. Downing,[2] W.E. Moerner,[1] Thomas Earnest,[2] Harley McAdams,[1] and Lucy Shapiro[1]* (shapiro@stanford.edu)

Optimizing the Detection of Specific Protein Complexes in *Caulobacter crescentus* at the Electron Microscopic Level 128

Guido M. Gaietta[1]* (ggaietta@ncmir.ucsd.edu), Ying Jones,[1] Julie Lee,[1] Masako Terada,[1] Grant Bowman,[2] Monica Schwartz,[2] Lucy Shapiro,[2] and Mark H. Ellisman[1] (mellisman@ucsd.edu)

Generating, Implementing and Refining of a Custom Algorithm to Localize Ribosomes in Tomographic Reconstructions of *Caulobacter crescentus* 129

Rick Giuly,[1] James Obayashi,[1] Ying Jones,[1] Guido M. Gaietta[1]* (ggaietta@ncmir.ucsd.edu), Lucy Shapiro,[2] and Mark H. Ellisman[1] (mellisman@ucsd.edu)

AMD Community Systems Understanding

Whole Community Proteomic Approaches to Decipher Protein Information from Natural Microbial Communities 130

Robert L. Hettich[1]* (hettichrl@ornl.gov), Nathan VerBerkmoes,[1] Brian Erickson,[1] Alison Russell,[1] Paul Abraham,[1] Chongle Pan,[1] Manesh Shah,[1] Doug Hyatt,[1] Denise Schmoyer,[1] Paul Wilmes,[2] Ryan Mueller,[2] Vincent Denef,[2] Steve Singer,[3] Michael Thelen,[3] and Jillian Banfield[2]

Insights into the Ecology and Evolution of a Natural Microbial Ecosystem from Acid Mine Drainage using Community Genomics and Proteomics 131

R.S. Mueller[1]* (rmueller@berkeley.edu), V.J. Denef,[1] S.L. Simmons,[1] D. Goltsman,[1] P. Wilmes,[1] C. Belnap,[1] A.P. Yelton,[1] G.J. Dick,[1] B.J. Baker,[1] L. Comolli,[3] B.C. Thomas,[1] B. Dill,[2] L. Hauser,[2] M. Land,[2] S.W. Singer,[3] L. Kalnejais,[1] M. Shah,[2] N.C. VerBerkmoes,[2] M.P. Thelen,[3] R.L. Hettich,[2] and J.F. Banfield[1]

Community Proteogenomic Analysis of Virus-Host Interactions in a Natural System 132

Christine Sun[1]* (christine_sun@berkeley.edu), Christopher Belnap,[1] Brian Thomas,[1] Kimberly Pause,[2] Paul Wilmes,[1] Daniela Goltsman,[1] Chongle Pan,[3] Anders Andersson,[1] Robert Hettich,[3] Nathan VerBerkmoes,[3] Mya Breitbart,[2] and Jill Banfield[1]

Shotgun Proteomics and *De Novo* Sequencing for the Detection of Viral Signatures in Natural Microbial Communities 133

Nathan VerBerkmoes[1]* (nve@ornl.gov), Chongle Pan,[1] Brian Dill,[1] Patricia Carey,[1] Jacque Young,[1] Doug Hyatt,[1] Manesh Shah,[1] Kim Pause,[2] Christine Sun,[3] Brian Thomas,[3] Paul Wilmes,[3] Robert L. Hettich,[1] Mya Breitbart,[2] and Jillian Banfield[3] (jbanfield@berkeley.edu)

Characterization of Viruses from an Acid Mine Drainage System 135

Kimberly C. Pause[1]* (kpause@marine.usf.edu), Christine L. Sun,[2] Paul Wilmes,[2] Robert Hettich,[3] Nathan VerBerkmoes,[3] Luis Comolli,[4] Jillian F. Banfield,[2] and Mya Breitbart[1]

Microbially Mediated Transformation of Metal and Metal Oxide Nanoparticles 136

M.J. Doktycz[1]* (doktyczmj@ornl.gov), D.A. Pelletier,[1] C.K. McKeown,[1] S.D. Brown,[1] B. Gu,[2] W. Wang,[2] D.P. Allison,[1,3] D.C. Joy,[3,4] and T.J. Phelps[1]

Systems Biology Strategies and Technologies for Understanding Microbesand Microbial Communities 137

Genomic and Proteomic Strategies

Profiling Microbial Identity and Activity: Novel Applications of NanoSIMS and High Density Microarrays 137

Eoin Brodie[1]* (elbrodie@lbl.gov), Jennifer Pett-Ridge[2] (pettridge2@llnl.gov), Peter Weber,[2] Gary Andersen,[1] Meredith Blackwell,[3] Nhu Nguyen,[4] Katherine Goldfarb,[1] Stephanie Gross,[3] and Paul Hoeprich[2] (hoeprich2@llnl.gov)

NanoSIP: Functional Analysis of Phototrophic Microbial Mat Community Members Using High-Resolution Secondary Ion Mass Spectrometry 138

Luke Burow,[1,2]* Dagmar Woebken,[1,2]* Lee Prufert-Bebout,[2] Brad Bebout,[2] Tori Hoehler,[2] Jennifer Pett-Ridge,[3] Steven W. Singer,[3] Alfred M. Spormann,[1] and Peter K. Weber[3] (weber21@llnl.gov)

NanoSIP: Linking Microbial Phylogeny to Metabolic Activity at the Single Cell Level Using Element Labeling and NanoSIMS Detection 138

J. Pett-Ridge[1]* (pettridge2@llnl.gov), S.W. Singer,[1]* S. Behrens,[2] T. Lösekann,[3] W.-O. Ng,[2] Dagmar Woebken,[2] Rick Webb,[4] B. Stevenson,[5] D. Relman,[3] A.M. Spormann,[2] and P.K. Weber[1] (weber21@llnl.gov)

Production of Extracellular Polymeric Substances by a Natural Acidophilic Biofilm 139

Y. Jiao,[1]* (jiao1@llnl.gov), M. Shrenk,[2] G. Cody,[2] J.F. Banfield,[3] and M.P. Thelen[1]

Soil Community Metagenomics at the DOE's Climate Change Research Sites 140

Cheryl Kuske[1]* (kuske@lanl.gov) and the FACE soil metagenomics working group: Gary Xie,[1] John Dunbar,[1] Larry Ticknor,[1] Yvonne Rogers,[1] Shannon Silva,[1] La Verne Gallegos-Garcia,[1] Stephanie Eichorst,[1] Shannon Johnson,[1] Don Zak,[2] Rytas Vilgalys,[3] Chris Schadt,[4] Dave Evans,[5] Patrick Megonigal,[6] Bruce Hungate,[7] Rob Jackson,[3] David Bruce,[1,8] and Susannah Tringe[8]

Flow Sorting and Whole Genome Amplification of Individual Microbes 141

Sébastien Rodrigue[1]* (s_rod@mit.edu), Rex R. Malmstrom,[1]* Aaron Berlin,[2] Matthew Henn,[2] and Sallie W. Chisholm[1,3] (chisholm@mit.edu)

Viruses Hijacking Cyanobacterial Carbon Metabolism 141

Luke R. Thompson[1]* (luket@mit.edu), JoAnne Stubbe,[1,2] and Sallie W. Chisholm[1,3]

Quantitative Proteomics of *Prochlorococcus*: Towards an Integrated View of Gene Expression and Cellular Stoichiometry 142

Jacob R. Waldbauer[1]* (jwal@mit.edu) and Sallie W. Chisholm[2] (chisholm@mit.edu)

Bacterioplankton Community Transcriptional Response to Environmental Perturbations 142

Jay McCarren* (mccarren@mit.edu), Rex Malmstrom, Yanmei Shi, Sebastien Rodrigue, Sallie W. Chisholm, and Edward DeLong

Grand Challenge in Membrane Biology: A Systems Biology Study of the Unicellular Diazotrophic Cyanobacterium *Cyanothece* sp. ATCC 51142 143

Michelle Liberton[1]* (mliberton@biology2.wustl.edu), Jana Stöckel[1], Alice C. Dohnalkova[2], Galya Orr[3], Jon M. Jacobs[3], Thanura Elvitigala[1], Eric A. Welsh[1], Hongtao Min[4], Jörg Toepel[4], Thomas O. Metz[3], Hans Scholten[3], Michael A. Kennedy[3], Garry W. Buchko[3], Nicole M. Koropatkin[5], Rajeev Aurora[6], Bijoy K. Ghosh[1], Teruo Ogawa[7], Jason E. McDermott[3], Katrina M. Waters[3], Christopher Oehmen[3], Gordon A. Anderson[3], Thomas J. Smith[5], Richard D. Smith[3], Louis A. Sherman[4], David W. Koppenaal[2,3], and Himadri B. Pakrasi[1] (pakrasi@wustl.edu)

Functional Analysis of Trace Nutrient Homeostasis in *Chlamydomonas* using Next Generation Sequencers 144

Sabeeha Merchant[1,2] (sabeeha@chem.ucla.edu), Madeli Castruita,[2] David Casero,[3] Janette Kropat,[2] Steven Karpowicz,[2] Shawn Cokus,[3] and Matteo Pellegrini[1,3]*

Whole-Genome Comparative Analyses Across an Environmental Gradient Reveal Surprisingly Rapid Bacterial Adaptation Mediated by Horizontal Gene Transfer 144

Alejandro Caro,[1] Jie Deng,[2] Jennifer Auchtung,[2] James Tiedje,[2] and Konstantinos Konstantinidis[1]*(kostas@ce.gatech.edu)

A Laboratory Scientist Encounters Genome Sequences 145

F. William Studier* (studier@bnl.gov)

Coupling Function to Phylogeny via Single-Cell Phenotyping 145
Michael C. Konopka[1]* (mkonopka@u.washington.edu), Sarah C. McQuaide,[2] Samuel Levine,[1] Ekaterina Latypova,[3] Tim J. Strovas,[4] Marina G. Kalyuzhnaya,[3] and Mary E. Lidstrom[1,3] (lidstrom@u.washington.edu)

Proteomics Driven Analysis of Microbes, Plants and Microbial Communities 147
Mary S. Lipton[1]* (mary.lipton@pnl.gov), Stephen J. Callister,[1] Joshua E. Turse,[1] Thomas Taverner,[1] Margaret F. Romine,[1] Kim K. Hixson,[2] Samuel O. Purvine,[2] Angela D. Norbeck,[1] Matthew E. Monroe,[1] Xuixia Du,[1] Feng Yang,[1] Brain M. Ham,[1] Carrie D. Nicora,[1] Richard D. Smith,[1] and Jim K. Fredrickson[1]

High Throughput Comprehensive Quantitative Proteomics and Metabolomics for Genomics:GTL 148
Gordon A. Anderson* (gordon@pnl.gov) Ronald J. Moore, David J. Anderson, Kenneth J. Auberry, Mikhail E. Belov, Stephen J. Callister, Therese R.W. Clauss, Kim K. Hixson, Gary R. Kiebel, Mary S. Lipton, Thomas O. Metz, Matthew E. Monroe, Heather M. Mottaz, Carrie D. Nicora, Angela D. Norbeck, Daniel J. Orton, Ljiljana Paša-Tolić, Kostantinos Petritis, David C. Prior, Samuel O. Purvine, Yufeng Shen, Anil K. Shukla, Aleksey V. Tolmachev, Nikola Tolić, Karl Weitz, Rui Zhang, Rui Zhao, and Richard D. Smith (rds@pnl.gov)

A New Platform for Much Higher Throughput Comprehensive Quantitative Proteomics 149
Richard D. Smith* (rds@pnl.gov), Gordon A. Anderson, Erin Baker, Mikhail E. Belov, William F. Danielson III, Yehia M. Ibrahim, Ryan Kelly, Andrei V. Liyu, Matthew E. Monroe, Daniel J. Orton, Jason Page, David C. Prior, Keqi Tang, and Aleksey V. Tolmachev

Live-Cell Visualization of Tagged Bacterial Protein Dynamics and Turnover 150
Thomas Squier* (thomas.squier@pnl.gov), M. Uljana Mayer, and Yijia Xiong

Identification of All Engineering Interventions Leading to Targeted Overproductions 151
Sridhar Ranganathan* (sur152@psu.edu), Patrick F. Suthers, and Costas D. Maranas (costas@psu.edu)

Automated Construction of Genome-Scale Metabolic Models: Application to *Mycoplasma genitalium* 152
Patrick F. Suthers[1]* (suthers@engr.psu.edu), Vinay Satish Kumar,[2] and Costas D. Maranas[1] (costas@psu.edu)

Synthetic Lethality Analysis Based on the *Escherichia coli* Metabolic Model 152
Alireza Zomorrodi* (auz107@psu.edu), Patrick F. Suthers, and Costas D. Maranas (costas@psu.edu)

Molecular Interactions and Protein Complexes

The MAGGIE Project

High Throughput Structural Characterization of Protein Complexes in Solution using Small Angle X-ray Scattering (SAXS) Combined with Mass Spectrometry (MS) 153
John A. Tainer[1,3]* (jat@scripps.edu), Greg L. Hura,[1] Steven M. Yannone,[1] Stephen R. Holbrook,[1] Jane Tanamachi,[1] Mike Adams,[2] Gary Siuzdak,[3] and Nitin S. Baliga[4]

Define the Metalloproteome by Letting Metals Take the Lead: A Component of the MAGGIE Project ... 154
Aleksandar Cvetkovic[1]* (alcv@uga.edu), Angeli Lal Menon,[1] Farris L. Poole II,[1] Sarat Shanmukh,[1] Michael Thorgersen,[1] Joseph Scott,[1] Jeremy Praissman,[1] Ewa Kalisiak,[2] Sunia Trauger,[2] Steven M. Yannone,[3] John A. Tainer,[3] Gary Siuzdak,[2] and Michael W.W. Adams[1]

The MAGGIE Project: Production and Isolation of Native and Recombinant Multiprotein Complexes and Modified Proteins from Hyperthermophilic *Sulfolobus solfataricus* 155

Robert Rambo,[1] Trent Northen,[1] Adam Barnebay,[1] Kenneth Stedman,[2] Michael W.W. Adams,[3] Gary Siuzdak,[4] Nitin S. Baliga,[5] Steven R. Holbrook,[1] John A. Tainer,[1,6] and Steven M. Yannone[1]* (SMYannone@lbl.gov)

Technologies for Robust and Rational Reengineering of Microbial Systems 155

W.L. Pang,[1]* T. Koide,[1] D.J. Reiss,[1] C. Bare,[1] K. Beer,[1] R. Bonneau,[2] S. Coesel,[1] M.T. Facciotti,[3] A. Kaur,[1] F.Y. Lo,[1] K. Masumura,[4] D. Miller,[1] M. Orellana,[1] M. Pan,[1] A.K. Schmid,[1] P. Shannon,[1] D. Tenenbaum,[1] P.T. Van,[1] K. Whitehead,[1] and N.S. Baliga[1] (nbaliga@systemsbiology.org)

Dynamic Assembly of Functional Transcriptional Complexes Inside Genes and Operons 156

David J. Reiss* (dreiss@systemsbiology.org), Tie Koide, W. Lee Pang, J. Christopher Bare, Marc T. Facciotti, Amy K. Schmid, Min Pan, Bruz Marzolf, Phu T. Van, Fang-Yin Lo, Abhishek Pratap, Eric W. Deutsch, Amelia Peterson, Dan Martin, and Nitin S. Baliga (nbaliga@systemsbiology.org)

Protein Complex Analysis Project (PCAP)

Protein Complex Analysis Project (PCAP): Automated Particle Picking in Electron Microscopy Images 156

Pablo Arbelaez[1]* (arbelaez@eecs.berkeley.edu), Bong-Gyoon Han,[2]* (bghan@lbl.gov), Robert M. Glaeser,[2] and Jitendra Malik[1]

A High Throughput Pipeline for Identifying Protein-Protein Interactions in *Desulfovibrio vulgaris* using Tandem-Affinity Purification 157

Swapnil Chhabra,[1] Gareth Butland[1]* (GPButland@lbl.gov), Dwayne Elias,[2] Veronica Fok,[1] Ramadevi Prathapam,[1] Thomas Juba,[2] John Marc Chandonia,[1] Ewa Witkowska,[3] Mark Biggin[1] (MDBiggin@lbl.gov), Terry Hazen,[1] Judy Wall,[2] and Jay Keasling[1,4]

Protein Complex Analysis Project (PCAP): Protein Complex Purification and Identification by "Tagless" Strategy 157

Ming Dong,[1]* Haichuan Liu,[2] Lee Yang,[1] Megan Choi,[1] Evelin D. Szakal,[2] Simon Allen,[2] Steven C. Hall,[2] Susan J. Fisher,[1,2] Gareth Butland,[1] Terry C. Hazen,[1] Jil T. Geller,[1] Mary E. Singer,[1] Peter Walian,[1] Bing Jap,[1] Jian Jin,[1] John-Marc Chandonia,[1] H. Ewa Witkowska,[2] and Mark D. Biggin[1] (mdbiggin@lbl.gov)

Protein Complex Analysis Project (PCAP): Localization of Multi-Protein Complexes through SNAP-Tag Labeling 158

Manfred Auer,[1,3]* Mark D. Biggin[1,3] (MDBiggin@lbl.gov), Gareth Butland,[1,3] Swapnil Chhabra,[1,3] Dwayne A. Elias[2,3] (eliasd@missouri.edu), Afolami Fagorala,[3] Terry Hazen,[1,3] Danielle Jorgens,[1,3] Dominique C. Joyner,[3] Thomas R. Juba,[2,3] Melissa Perez,[1,3] Jonathan P. Remis,[1,3] Andrew Tauscher,[1,3] and Judy D. Wall[2,3]

Protein Complex Analysis Project (PCAP): Survey of Large Protein Complexes in *Desulfovibrio vulgaris* Reveals Unexpected Structural Diversity 159

Bong-Gyoon Han[1]* (bghan@lbl.gov), Ming Dong,[1] Mark D. Biggin,[1] and Robert M. Glaeser[1]

Protein Complex Analysis Project (PCAP): Introduction of Iterative MS/MS Acquisition (IMMA) to the MALDI LC MS/MS Workflow To Enable High Throughput Protein Complex Identification using Tagless Strategy 159

Haichuan Liu,[1]* Lee Yang,[2] Nikita Khainovski,[2] Ming Dong,[2] Evelin D. Szakal,[1] Megan Choi,[2] Simon Allen,[1] Terry C. Hazen,[1] Jil T. Geller,[1] Mary E. Singer,[1] Peter Walian,[1] Bing Jap,[1] Steven C. Hall,[1] Susan J. Fisher,[1,2] H. Ewa Witkowska,[1] Jian Jin,[2] and Mark D. Biggin[2] (mdbiggin@lbl.gov)

Protein Complex Analysis Project (PCAP): Isolation and Identification of Membrane Protein Complexes from *D. vulgaris* 160

Peter J. Walian[1]* (PJWalian@lbl.gov), Simon Allen,[2] Lucy Zeng,[1] Evelin Szakal,[2] Eric Johansen,[2] Steven C. Hall,[2] Susan J. Fisher,[1,2] Mary E. Singer,[1] Chansu Park,[1] Terry C. Hazen,[1] H. Ewa Witkowska,[2] Mark D. Biggin,[1] and Bing K. Jap[1]

Protein Complex Analysis Project (PCAP): Reconstruction of Multiple Structural Conformations of Macromolecular Complexes Studied by Single-Particle Electron Microscopy 161

Maxim Shatsky[1,2]* (maxshats@compbio.berkeley.edu), Richard J. Hall,[2] Jitendra Malik,[2] and Steven E. Brenner[1,2]

Protein Complex Analysis Project (PCAP): High Throughput Identification and Structural Characterization of Multi-Protein Complexes During Stress Response in *Desulfovibrio vulgaris* : Data Management and Bioinformatics Subproject 162

Adam P. Arkin,[1,2] Steven E. Brenner,[1,2] Max Shatsky,[1,2] Ralph Santos,[1] Jason Baumohl,[1] Keith Keller,[1] and John-Marc Chandonia[1,2]* (jmchandonia@lbl.gov)

Protein Complex Analysis Project (PCAP): Towards Localization of Functionality in *Desulfovibrio vulgaris* by Electron Microscopy 162

David A. Ball* (DABall@lbl.gov), Jonathan Remis, Manfred Auer, and Kenneth H. Downing

Protein Complex Analysis Project (PCAP): High Throughput Identification and Structural Characterization of Multi-Protein Complexes During Stress Response in *Desulfovibrio vulgaris:* Microbiology Subproject 163

Terry C. Hazen[1,4]* (tchazen@lbl.gov), Hoi-Ying Holman,[1,4] Jay Keasling,[1,2,4] Aindrila Mukhopadhyay,[1,4] Swapnil Chhabra,[1,4] Jil T. Geller,[1,4] Mary Singer,[1,4] Dominique Joyner,[1,4] Lauren Camp,[1,4] Tamas Torok,[1,4] Judy Wall,[3,4] Dwayne Elias,[3,4] and Mark D. Biggin[1,4]

The Center for Molecular and Cellular Systems

An Integrative Strategy for the Determination of the Modular Structure of Functional Networks of *Rhodopseudomonas palustris* 164

William R. Cannon[2]* (William.Cannon@pnl.gov), Don Daly,[2] Mudita Singhal,[2] Lee Ann McCue,[2] Ronald Taylor,[2] Dale A. Pelletier,[1] Gregory B. Hurst,[1] Denise D. Schmoyer,[1] Jennifer L. Morrell-Falvey,[1] Brian S. Hooker,[2] Chongle Pan,[1] W. Hayes McDonald,[1,3] Michelle V. Buchanan,[1] and H. Steven Wiley[2]

An Imaging-Based Assay with High Sensitivity for Confirming and Characterizing Protein Interactions 165

Jennifer L. Morrell-Falvey* (morrelljl1@ornl.gov), A. Nicole Edwards, Jason D. Fowlkes, Robert F. Standaert, Dale A. Pelletier, Mitchel J. Doktycz, and Michelle V. Buchanan

Functional Characterization of Protein Complexes and Cellular Systems in *Rhodopseudomonas palustris* using Stable Isotopic Labeling and Quantitative Proteomics 165

Chongle Pan[1]* (panc@ornl.gov), W. Judson Hervey IV,[1,2] Michael S. Allen,[1,3] Dale A. Pelletier,[1] Gregory B. Hurst,[1] and Michelle V. Buchanan[1]

Protein-Protein Interactions in *Rhodopseudomonas palustris* at the Genomics:GTL Center for Molecular and Cellular Systems 166
Dale A. Pelletier[1]* (pelletierda@ornl.gov), Kevin K. Anderson,[2] William R. Cannon,[2] Don S. Daly,[2] Brian S. Hooker,[2] H. Steven Wiley,[2] Lee Ann McCue,[2] Chongle Pan,[1] Manesh B. Shah,[1] W. Hayes McDonald,[1] Keiji G. Asano,[1] Gregory B. Hurst,[1] Denise D. Schmoyer,[1] Jenny L. Morrell-Falvey,[1] Mitchel J. Doktycz,[1] Sheryl A. Martin,[1] Mudita Singhal,[2] Ronald C. Taylor,[2] and Michelle V. Buchanan[1]

Validation of Genome Sequence Annotation

Toward a High Throughput Functional Annotation Pipeline for Fungal Glycoside Hydrolases 167
Scott E. Baker[1]* (scott.baker@pnl.gov), Ellen A. Panisko,[1] Deanna Auberry,[1] Beth Hofstad,[1] Jon K. Magnuson,[1] Barbara Robbertse[2], Adrian Tsang[3], and Frank Collart[4]

Annotation of the *Clostridium phytofermentans* ORFome by Proteogenomic Mapping 167
Andrew Tolonen*

Protein Functional Assignment Using a Fluorescence-Based Thermal Shift Assay 168
Ashley M. Frank[1]* (afrank@anl.gov), Sarah E. Giuliani,[1] William Studier,[2] and Frank Collart[1]

Assignment of Enzymatic Function for Core Metabolic Enzymes 168
Elizabeth Landorf,[1]* Vincent Lu,[1] Gopi Podila,[2] Michael Proudfoot,[3] Alexander Yakunin,[3] and Frank Collart[1] (fcollart@anl.gov)

Quality Improvement Process for JGI-ORNL Microbial Annotation Pipeline 169
Miriam Land[1]* (landml@ornl.gov), Loren Hauser,[1] Janet Chang,[1] Cynthia Jefferies,[1] Gwo-Liang Chen,[1] Frank Larimer,[1] Natalia Mikhailova,[2] Natalia Ivanova,[2] Athanasios Lykidis,[2] Galina Ovchinnikova,[2] Amrita Pati,[2] Nikos Kyrpides,[2] and Bob Cottingham[1]

Phylogenomics-Guided Validation of Function for Conserved Unknown Genes 170
Valérie de Crécy-Lagard[1]* (vcrecy@ufl.edu) and Andrew D. Hanson[2] (adha@ufl.edu)

Comparative Genomics and Experimental Validation to Find Universal, Globally Missing Genes: The Universal Families COG009 and CO0533 171
Basma El Yacoubi[1]* (basma@ufl.edu) and Valérie de Crécy-Lagard[1] (vcrecy@ufl.edu)

Genome Annotation: Coupling the Power of Plant-Prokaryote Comparative Genomics to Experimental Validation, COG0720 and COG3404 172
Anne Pribat[1]* (pribat@ufl.edu), Linda Jeanguenin,[1] Valérie de Crécy-Lagard[2] (vcrecy@ufl.edu), and Andrew D. Hanson[1] (adha@ufl.edu)

Use of Modern Chemical Protein Synthesis Techniques to Experimentally Validate the Functional Annotation of Microbial Genomes 174
Stephen Kent* (skent@uchicago.edu) and Youhei Sohma

Towards Annotation of the Unannotated—A Dissection of Unannotated Proteins in *Clostridium thermocellum* 175
Y.J. Chang,* Loren J. Hauser, Gwo-liang Chen, Frank Larimer, Pavan Ghatty, and Miriam Land (ml3@ornl.gov)

An Integrated Approach to Experimental Validation of Putative Gene Functions in *M. acetivorans* 175
Ethel Apolinario,[1] Yihong Chen,[2] Zvi Kelman,[2] Zhuo Li,[2] Basil J. Nikolau,[3] Kevin Sowers,[1] Eric Testroet,[3] and John Orban[2,]* (orban@umbi.umd.edu)

Transcriptome Analysis of *Chlamydomonas reinhardtii* using Ultra-High-Throughput Sequencing.....176
David Casero Díaz-Cano,[1] Madeli Castruita,[2] Sabeeha Merchant,[2] and Matteo Pellegrini[1]* (matteop@mcdb.ucla.edu)

Transcript Verification Coupled with Metabolic Network Modeling for *Chlamydomonas reinhardtii*.....177
Ani Manichaikul,[1]* Lila Ghamsari,[2,3] Chenwei Lin,[2,3] Erik F.Y. Hom,[4] Ryan R. Murray,[2,3] Roger L. Chang,[5] Arvind K. Chavali,[1] Yun Shen,[2,3] Xinping Yang,[2,3] Ines Thiele,[5] Jason A. Papin[1] (papin@virginia.edu), and Kourosh Salehi-Ashtiani[2,3] (Kourosh_Salehi-ashtiani@DFCI.harvard.edu)

Genemap-MS: High Throughput Mass Spectrometry Approaches to Microbial Gene Annotation Validation.....178
Trent R. Northen* (trnorthen@lbl.gov), Benjamin Bowen, Steven M. Yannone, Jill Fuss, John Tainer, and Gary Siuzdak (siuzdak@scripps.edu)

Novel Mass Spectrometry Based Platforms for the Investigation of Model Organisms.....178
Sunia A. Trauger[1]* (strauger@scripps.edu), Trent Northen,[2] Nitin Baliga,[3] Steven M. Yannone,[2] Michael W.W. Adams,[3] and Gary Siuzdak[1]

Annotation of Translation Initiation Sites Using Prodigal.....179
Doug Hyatt, Miriam Land (ml3@ornl.gov), and Loren Hauser*

Computing Resources and Databases

Release of Taxomatic and Refinement of the SOSCC Algorithm.....180
J. Fish[1]* (fishjord@msu.edu), Q. Wang,[1] S.H. Harrison,[1] T.G. Lilburn,[2] P.R. Saxman,[3] J.R. Cole,[1] and G.M. Garrity[1]

NamesforLife Semantic Resolution Services for the Life Sciences.....182
Charles T. Parker,[1] Sarah Wigley,[1] Nicole Osier,[2] Jordan Fish,[1] Qiong Wang,[1] Donna McGarrel,[1] James R. Cole,[1,2] Catherine Lyons,[1] and George M. Garrity[1,2]* (garrity@names4life.com)

Standards in Genomic Sciences: an Open-Access, Standards-Supportive Publication that Rapidly Disseminates Concise Genome and Metagenome Reports in Compliance with MIGS/MIMS Standards183
Scott H. Harrison[1]* (harris41@msu.edu), Sam V. Angiuoli,[2] Patrick S.G. Chain,[1,3,4,5] Dawn Field,[6] Frank-Oliver Glöckner,[7] Lynette Hirschman,[8] Eugene Kolker,[9,10] Nikos Kyrpides,[4] Susanna-Assunta Sansone,[11] Lynn M. Schriml,[2] Peter Sterk,[6,11] David W. Ussery,[12] Owen White,[2] and George M. Garrity[1,5]

The Ribosomal Database Project: Tools and Sequences for rRNA Analysis.....184
J.R. Cole* (colej@msu.edu), Q. Wang, B. Chai, J. Fish, E. Cardenas, R.J. Farris, D.M. McGarrell, G.M. Garrity, and J.M. Tiedje (tiedjej@msu.edu)

Communication

.....187

Genome Management Information System: A Multifaceted Approach to DOE Systems Biology Research Communication and Facilitation.....187
Anne E. Adamson, Shirley H. Andrews, Jennifer L. Bownas, Sharon Burris, Kris Christen, Holly Haun, Sheryl A. Martin, Marissa D. Mills, Kim Nylander, Judy M. Wyrick, Anita J. Alton, and Betty K. Mansfield* (mansfieldbk@ornl.gov)

Ethical, Legal, and Societal Issues 189

Intellectual Property and U.S. Public Investments in Research on Biofuel Technologies 189
Kerri Clark* (kleclark@ucdavis.edu), Rohan Patel, Kyle Jensen, and Alan Bennett

Implications of Alternative Intellectual Property Rights Management Approaches 189
David J. Bjornstad* (bjornstaddj@ornl.gov) and Amy K. Wolfe (wolfeak@ornl.gov)

The Biofuels Revolution: Understanding the Social, Cultural, and Economic Impacts of Biofuels Development on Rural Communities 190
Theresa Selfa[1]* (tselfa@ksu.edu), Richard Goe,[1] Laszlo Kulcsar,[1] Gerad Middendorf,[1] and Carmen Bain[2]

Analysis of Global Economic and Environmental Impacts of a Substantial Increase in Bioenergy Production 191
Wallace E. Tyner (wtyner@purdue.edu), Thomas W. Hertel, Farzad Taheripour,* and Dileep K. Birur

Issues Associated with the Transition from Science to Application in a Fundamental Nanoscience User Center 192
Amy K. Wolfe* (wolfeak@ornl.gov) and David J. Bjornstad (bjornstaddj@ornl.gov)

Global Net Primary Production and Bioenergy Potentials and the Environmental Consequences: An Analysis with a Process-Based Terrestrial Ecosystem Model 193
Qianlai Zhuang (qzhuang@purdue.edu), Kai Xu, and Yanyu Lu*

Appendix 1: Participants ..... not available

Appendix 2: Websites 203

Program Websites

Bioenergy Research Center Websites

Project and Related Websites

Author Index 205

Institutional Index 213

Addendum of late abstracts available page 215. Late abstracts not indexed.

Introduction to Workshop Abstracts

Genomics:GTL Goal and Objectives

Ultimate Scientific Goal
Achieve a predictive, systems-level understanding of plants, microbes, and biological communities, via integration of fundamental science and technology development, to enable biological solutions to DOE mission challenges in energy, environment, and climate.

Objective 1: Determine the genomic properties, molecular and regulatory mechanisms, and resulting functional potential of microbes, plants, and biological communities central to DOE missions.

Objective 2: Develop the experimental capabilities and enabling technologies needed to achieve a genome-based, dynamic systems-level understanding of organism and community functions.

Objective 3: Develop the knowledgebase, computational infrastructure, and modeling capabilities to advance the understanding, prediction, and manipulation of complex biological systems.

Abstract Organization

Genomics:GTL program abstracts and posters are organized according to the following research areas important to achieving the ultimate GTL scientific goal and objectives.

Systems Biology for DOE Energy and Environmental Missions

Bioenergy

- Biofuels: Bioenergy Research Centers
- Biofuels: USDA–DOE Plant Feedstock Genomics for Bioenergy
- Biofuels: Analytical and Imaging Technologies for Studying Lignocellulosic Material Degradation
- Systems Biology and Metabolic Engineering Approaches for Biological Hydrogen Production
- SBIR Bioenergy Research

Systems Environmental Microbiology

Systems Biology Strategies and Technologies for Understanding Microbes and Microbial Communities

Genomic and Proteomic Strategies

Molecular Interactions and Protein Complexes

Validation of Genome Sequence Annotation

Computing Resources and Databases

Communication

Ethical, Legal, and Societal Issues

The following table is a summation of how GTL science and DOE missions align (*DOE Genomics:GTL Roadmap: Systems Biology for Energy and Environment*; October 2005, p. 40). (GenomicsGTL.energy.gov)

Summary Table. GTL Science Roadmap for DOE Missions

		DOE Mission Goals		GTL Science Roadmaps
Selected Processes	Biofuels	**Processes to convert cellulose to fuels** • Understanding and improving cellulase activity • Improving sugar transportation and fermentation to alcohols • Integrated processing **Microbial processes to convert sunlight to hydrogen fuels** • Understanding photolytic fuel production • Designing photosynthetic biofuel systems	Science Objectives	▸ **Characterize genes, proteins, machines, pathways, and systems** • Conducting genomic surveys and comparisons • Mining natural systems for new functions • Producing and characterizing proteins • Analyzing interactions, complexes, and machines ▸ **Understand functions and regulation** • Measuring molecular responses: Inventories • Performing functional assays ▸ **Develop predictive mechanistic models** • Conducting experimental design • Designing and manipulating molecules • Using cellular and cell-free systems
Selected Processes	Environmental Remediation	**Microbial processes to reduce toxic metals** • Understanding microbe-mineral interactions • Devising restoration processes	Mission Outputs	**Systems engineering** • System-design strategies for deployment • Living and extracellular systems • Validation and verification analyses
Natural Systems' Behavior	Environmental Remediation	**Subsurface microbial communities' role in transport and fate of contaminants** • Understanding fate and effects • Supporting remediation decisions	Science Objectives	▸ **Analyze communities and their genomic potential** • Sequencing and comparing genomes • Screening natural systems for processes • Producing and characterizing proteins ▸ **Understand community responses, regulation** • Comparing CO_2, nutrients, biogeochemistry cycles • Producing cellular and community molecular inventories • Performing community functional assays ▸ **Predict responses and impacts** • Building interactive and predictive models • Applying natural and manipulated scenarios
Natural Systems' Behavior	Carbon Cycling and Sequestration	**Ocean microbial communities' role in the biological CO_2 pump** • Understanding C, N, P, O, and S cycles • Predicting climate responses • Assessing impacts of sequestration **Terrestrial microbial communities' role in global carbon cycle** • Understanding C, N, P, O, and S cycles • Predicting carbon inventories and climate responses • Assessing sequestration concepts	Mission Outputs	**Robust science base for policy and engineering** • Model ecosystem response to natural events • Efficacy and impacts of intervention strategies **Sensor development** • Community dynamics • Environmental and functional assays

A capsule summary of systems being studied, mission goals that drive the analysis, generalized science roadmaps, and outputs to DOE missions. To elucidate design principles, each of these goals entails the examination of thousands of natural primary and ancillary pathways, variants, and functions, as well as large numbers of experimental mutations.