

AGENDA

Sunday Evening, February 10, 2008

- 5:00-8:00 Registration and Poster Set Up
6:00-8:00 Mixer

Monday, February 11, 2008

- 7:00-8:00 Continental Breakfast

- 8:00-9:00 **Welcome, State of Genomics:GTL Program** Sharlene Weatherwax

- 9:00-11:30 **Plenary Session: DOE Bioenergy Research Centers** Moderator: John Houghton

9:00-9:45 Tim Donohue - University of Wisconsin
The Great Lakes Bioenergy Research Center

9:45-10:30 Martin Keller - Oak Ridge National Laboratory
The Bioenergy Science Center

10:30-10:45 Break

10:45-11:30 Jay Keasling - Lawrence Berkeley National Laboratory
The Joint Bioenergy Institute

- 11:30-12:00 **Joint Genome Institute Update** Eddie Rubin

12:00-2:00 Lunch

2:00-5:00 **Concurrent Breakout Sessions**

- 2:00-5:00 **Breakout Session 1: Metabolic Engineering Working Group (MEWG): Interagency Conference on Metabolic Engineering** Moderator: Fred Heineken, National Science Foundation

This breakout session, conducted jointly between the DOE Genomics:GTL program and the MEWG Inter-Agency Conference on Metabolic Engineering 2008, addresses how metabolic engineering facilitates the development of the biorefinery approach to chemical production. Biorefineries are a major focus of the drive to replace fossil fuels with sustainable biologically derived ones. The same biological feedstocks that can be used for fuel production can also be the starting materials for other value added chemical products, from acids to polymers. Biorefineries have the potential to produce multiple product lines at the same plant. To do so, however, often requires metabolic engineering of the organisms involved in the various production stages. This session, therefore focuses on work that addresses some of the issues associated with such chemical production, from modification of organisms for fuel and value added chemical production to techniques for measuring and manipulating the necessary metabolic networks.

2:00-2:25 Christina Smolke, Caltech
Foundational advances in RNA engineering applied to control biosynthesis

2:25-2:50 Dhinakar Kompala, University of Colorado, Boulder
*Kinetic modeling of metabolically engineered *Zymomonas mobilis* to maximize ethanol production from a mixture of glucose and xylose*

2:50-3:15 Terry Papoutsakis, University of Delaware
Development of tolerant and other complex phenotypes for biofuel production

- 3:15-3:40 Break
- 3:40-4:05 Roger Ely, Oregon State University
Metabolic engineering for maximal, 24-hour production of hydrogen gas by wild-type and mutant strains of Synechocystis PCC 6803
- 4:05-4:30 John Frost, Michigan State University/ Frost Chemical Laboratory
Supplanting the chemical legacy of Alfred Nobel: Creation of a pathway for the biosynthesis of 1,2,4-butanetriol
- 4:30-5:00 Group Discussion

- 2:00-5:00 **Breakout Session 2:
Nanoscience Technology** Moderator: Sharlene Weatherwax
Organizers:
Ron Zuckermann – Molecular Foundry, LBNL
Mike Simpson – Center for Nanophase
Materials Science, ORNL

This tutorial will highlight opportunities bridging between nanoscience technology and genomics research. In addition to describing the specific missions of the Molecular Foundry at LBNL and the Center for Nanophase Materials Sciences (CNMS) at ORNL, presentations will illustrate how members of the Genomics:GTL community can work with these unique DOE scientific user facilities.

- 2:00-3:15 Ron Zuckerman – Lawrence Berkeley National Laboratory
Carolyn Pearce – University of Manchester
Joseph Mougous – University of Washington
Kent Kirshenbaum – New York University
David Robinson – Sandia National Laboratory

- 3:15-3:30 Break
- 4:00-5:00 Mike Simpson – Oak Ridge National Laboratory
Mike McCollum – Miami University
Mitch Doktycz – Oak Ridge National Laboratory
Gary Saylor – University of Tennessee

- 2:00-5:00 **Breakout Session 3: Methods for Studying Proteins &
Protein Complexes** Moderator: Arthur Katz
Organizer: Jim Bruce,
Washington State University

Comprehensively analyzing the proteins and molecular complexes that perform life's most essential functions presents many challenges due to their large number, biochemical variations and dynamic nature. In this session, presentations will be made on a variety of advanced analytical approaches to the study of protein-protein interactions and molecular complexes. These will be followed by an open discussion period focusing on the application of new methodologies to the characterization complex molecular interactions.

- 2:00-2:25 Liang Shi – Pacific Northwest National Laboratory
Investigation of Protein-protein Interactions Related to Salmonella typhimurium Pathogenesis: in vivo cross-linking with formaldehyde, tandem affinity purification and mass spectrometry identification
- 2:25-2:50 Gareth Butland – Lawrence Berkeley National Laboratory
Title To Be Announced

- 2:50-3:15 Gary Siuzdak – Scripps Research Institute
A Novel Approach Toward Characterizing Protein-Metabolite Interactions
- 3:15-3:40 Greg Hurst – Oak Ridge National Laboratory
Analysis of Protein Complexes at the Genomics:GTL Center for Molecular and Cellular Systems
- 3:30-4:00 Break
- 4:00-5:00 Group Discussion
- 5:00-8:00 Poster Session Salon ABCD

Tuesday, February 12, 2008

- 7:00-8:00 Continental Breakfast
- 8:00-9:00 **Keynote Speaker - Jo Handelsman, University of Wisconsin - Madison**
Molecules of War & Conversation and the Soil Metagenome
- 9:00-9:30 Data Management & Sharing Policy – Susan Gregurick & Jim Fredrickson
- 9:30-10:00 Break
- 10:00-12:00 **Plenary Session: Advances in Genomic Technology** Moderator: Marvin Stodolsky
- 10:00-10:40 Daniel Gibson - J. Craig Venter Institute
Mycoplasma Genome Synthesis and Transplantation: Progress on Constructing a Synthetic Cell
- 10:40-11:20 George Church - Harvard University
Genome-wide Reprogramming and Accelerated Evolution
- 11:20-12:00 Daphne Preuss - University of Chicago, Chromatin Inc.
Developing Synthetic Chromosomes for Crops: Applications for Agriculture and Energy
- 12:00-2:00 Lunch
- 2:00-5:00 **Concurrent Breakout Sessions**
- 2:00-5:00 **Breakout Session 4: Advanced Characterization and Imaging of Lignocellulose Materials** Moderator: Roland Hirsch
- Lignocellulosic materials are difficult to break down into components that are easy to process into fuels and other products. They also are very difficult to characterize sufficiently to understand in real time how they are affected by physical, chemical and biological treatments. Yet these materials are the starting point for much planned research in the Genomics:GTL program. This session will provide an overview of four analytical technologies and how they may overcome the obstacles to characterizing lignocellulosic materials. The presentations will be by scientists who have recently initiated research projects to study the application of the technologies to GTL-relevant materials. The focus will be on the capabilities of the technologies and the session will be appropriate for attendees unfamiliar with them.

- 2:00-2:25 Barbara Evans - Oak Ridge National Laboratory
Dynamic Visualization of Lignocellulose Degradation by Integration of Neutron Scattering Imaging and Computer Simulation
- 2:25-2:50 Gary Peter - University of Florida
Title To Be Announced
- 2:50-3:15 Hoi-Ying Holman - Lawrence Berkeley National Laboratory
Synchrotron Infrared (SIR) SpectroMicroscopy of Living Microbial Cells
- 3:15-3:40 Paul Bohn - Notre Dame University
Three-Dimensional Spatial Profiling of Lignocellulosic Materials by Coupling Light Scattering and Mass Spectrometry
- 3:40-4:00 Break
- 4:00-5:00 Group Discussion

2:00-5:00 **Breakout Session 5: Microbial Growth Technologies for Systems Biology** Moderator: Joe Graber

Understanding the systems biology of microorganisms requires not only advanced molecular tools but also increasingly sophisticated cultivation techniques that allow subtle manipulation of environmental variables and microbial growth states. This session will focus on advanced cultivation approaches used to study and model regulatory control of complex behaviors by microbes and microbial communities. A series of presentations will be followed by an open discussion period to discuss new methodologies, identify technical hurdles, and exchange ideas on cultivation strategies relevant to systems biology research.

- 2:00-2:25 Jeff McLean, J. Craig Venter Institute
Cultivation and Analytical Approaches for Systems Biology of Biofilms
- 2:25-2:50 Mary Lidstrom, University of Washington
Coupling Function to Genomics in Microbial Communities Via Single-Cell Analysis
- 2:50-3:15 Nitin Baliga, Institute for Systems Biology
Culturing Technologies for Constructing Predictive Systems- Scale Models of Microbial Behavior
- 3:15-3:40 Dave Emerson, Bigelow Research Laboratory
The Way Life Should Be: Using Gradients to Capture Microbes and Study Their Behavior
- 3:30-4:00 Break
- 4:00-5:00 Group Discussion

2:00-5:00 **Breakout Session 6: Web-Based Resources for Microbial Genomics** Moderators: Dan Drell and Sharlene Weatherwax

Recent advances in genome and metagenome sequencing technology have yielded not only exciting new insights on the fundamental properties of organisms and communities, but also an intimidating volume of data that is increasingly difficult to organize and study. In this session, tutorials will be provided on three web-based resources that facilitate data management and provide bioinformatics tools for the analysis of large genomic and metagenomic data sets. In addition to providing overviews of available resources, these presentations will focus on the practical application of these resources to demonstration sets of common data.

- 2:00-2:30 Microbes Online

- Paramvir Dehal, Lawrence Berkeley National Laboratory
- 2:30-3:30 Integrated Microbial Genomes (IMG)
Phil Hugenholtz, Joint Genome Institute
- 3:30-4:00 Break
- 4:00-5:00 CAMERA Metagenomics Database
Rekha Seshdari, J. Craig Venter Institute
- 5:00-8:00 Poster Session Salon ABCD

Wednesday, February 13, 2008

- 7:00-8:00 Continental Breakfast
- 8:00-10:00 **Plenary Session: Protein Interactions, Complexes, & Networks**
Moderator: Arthur Katz
- 8:00-8:40 Michelle Buchanan - Oak Ridge National Laboratory
The Center for Molecular and Cellular Systems: Biological Insights from Large Scale Protein-Protein Interaction Studies
- 8:40-9:20 Mark Biggin - Lawrence Berkeley National Laboratory
*High Throughput Identification and Characterization of Protein Complexes in *Desulfovibrio vulgaris**
- 9:20-10:00 John Tainer - Lawrence Berkeley National Laboratory
Molecular Assemblies, Genes, and Genomics Integrated Efficiently (MAGGIE): Integrating Combined Methods and Comparative Systems to Connect Genes to Functional Networks
- 10:00-10:30 Break
- 10:30-11:00 Zan Luthey-Schulten, University of Illinois at Urbana-Champaign
Title To Be Announced
- 11:00-11:30 Rick Stevens, Argonne National Laboratory
Presentation on the Joint Report BERAC/ASCAC Joint Report on Computational Modeling in the Genomics:GTL Program
- 11:30-12:00 Closing Remarks