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# Joint Meeting

## Genomics:GTL Awardee Workshop V

and

## Metabolic Engineering Working Group
## Interagency Conference on Metabolic Engineering 2007

and

## USDA-DOE Plant Feedstock Genomics for Bioenergy Awardee Workshop 2007

**Bethesda, Maryland**
**February 11–14, 2007**

Prepared for the
U.S. Department of Energy
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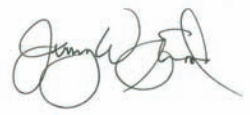
# Welcome

Welcome to the 2007 Joint Genomics:GTL Awardee Workshop, Metabolic Engineering Interagency Working Group Conference ,and the USDA-DOE Plant Feedstock Genomics for Bioenergy Joint Program Meeting. Attendees of this year's joint meeting represent a broad cross section of cutting-edge research disciplines, including microbiology, plant biology, genomics, proteomics, physiology, structural biology, metabolic engineering, ecology, evolutionary biology, bioinformatics, and computational biology. Uniting this diverse community of researchers is the shared goal to understand the complex genetic and metabolic systems supporting the life of microbes, plants, and biological communities. This approach is by definition integrative and multidisciplinary, and we applaud the collaborative spirit that brings you to this meeting and informs your research. This joint meeting provides unique opportunities to enhance collaboration and advance science beyond the boundaries of any of these individual research programs.

In May of 2006, the National Research Council of the National Academies completed an independent review of the Genomics:GTL program. The review committee enthusiastically endorsed the systems biology focus of the program, lauded the general excellence of research conducted by its grantees, and re-emphasized the critical importance of the program's core mission—to advance fundamental research on bioenergy solutions, bioremediation of environmental contaminants, and global carbon cycling and sequestration. The review also recommended that, in place of the previously proposed technology-oriented user facilities, the Genomics:GTL program should form interdisciplinary research centers focused on fundamental research addressing DOE mission needs, including bioenergy. DOE embraced this recommendation, and review of proposals for GTL Bioenergy Research Centers is under way.

This year's meeting features sessions that will be of broad interest to scientists funded by all three of the participating research programs—the Genomics: GTL program, the Metabolic Engineering Working Group, and the USDA-DOE Plant Feedstock Genomics for Bioenergy Joint Program. The goal of the Metabolic Engineering Working Group is the targeted and purposeful alteration of an organism's metabolic pathways to better understand and use cellular pathways for chemical transformation, energy transduction, and supramolecular assembly. The USDA-DOE Plant Feedstock Genomics for Bioenergy joint program focuses on genomics-based research leading to the improved use of biomass and plant feedstocks for the production of such fuels as ethanol or renewable chemical feedstocks. By bringing together these distinct but complementary research communities, we hope to foster the exchange of ideas, sharing of expertise, and formation of new partnerships among researchers.

We look forward to an exciting and productive meeting and encourage you to participate in discussions and build new relationships. We wish to thank the organizers of this year's meeting, especially members of the research community who have generously agreed to play a larger role in organizing this year's breakout sessions. Finally, we thank you for lending your knowledge, creativity, and vision to the represented research programs and wish you continued success in the coming year.



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# Agenda

## Sunday Evening, February 11th

**5:00-8:00 Registration and Poster Setup**

**6:00-8:00 Mixer**

## Monday, February 12th

**7:00-8:00 Continental Breakfast**

**8:00-8:45 Welcome**

State of Genomics:GTL Program, Vision for the Future
Mike Viola, David Thomassen, and Jim Fredrickson

**8:45-9:15 Systems Biology: An Overview**

Timothy Donohue – University of Wisconsin, Madison
"Systems Analysis of Solar Energy Stress Responses"

**9:15-12:00 Plenary Session**

Carbon Processing at Organismal, Community, & Global Scales
Moderator: Dan Drell

Session Objectives: This session will examine the global carbon cycle at various levels of resolution and from a variety of different research perspectives. The goal of the session is to promote discussion of potential contributions of GTL research towards more effectively modeling the global carbon budget and understanding the role of microbes and microbial communities in planetary scale processing and sequestration of carbon.

| | |
|---|---|
| 9:15-9:45 | Jae Edmonds – Pacific Northwest National Laboratory<br>"Biotech, Energy, and a Climate-Constrained World" |
| 9:45-10:15 | Bruce Hungate – Northern Arizona University<br>Title To Be Announced |
| 10:15-10:30 | Break |
| 10:30-11:00 | Mary Lidstrom – University of Washington<br>"Integrated Metabolism Studies of Methylotrophy" |
| 11:00-11:30 | Ramon Gonzalez – Rice University<br>"The Role of Metabolic Engineering and Systems Biology in Biofuel Production" |

**12:00-2:00 Lunch**

**2:00-4:30 Breakout Session A**

USDA-DOE Plant Feedstock Genomics for Bioenergy Joint Program Meeting
Moderators: Ed Kaleikau (USDA) & Sharlene Weatherwax (DOE)

| | |
|---|---|
| 2:00-2:15 | Program Overview: Chavonda Jacobs-Young - USDA |
| 2:15-2:30 | Vincent Chiang – North Carolina State University |
| 2:30-2:45 | Clint Chapple – Purdue University |
| 2:45-3:00 | Chang-Jun Liu – Brookhaven National Laboratory |
| 3:00-3:15 | Bikram Gill – Kansas State University |
| 3:15-3:30 | Richard Dixon – The Nobel Foundation |
| 3:30-4:00 | Break |
| 4:00-4:15 | William Rooney – Texas A&M University |
| 4:15-4:30 | Charles Brummer – University of Georgia |
| 4:30-4:45 | John Ralph - USDA-ARS, University of Wisconsin |
| 4:45-5:00 | Chris Somerville – Carnegie Institute of Washington |

**2:00-5:00 Breakout Session B**

Data Management & Sharing Tutorial

| | |
|---|---|
| Organizers: | Ed Uberbacher – Oak Ridge National Laboratory<br>Jeff Grethe – University of California, San Diego |
| Moderator: | John Houghton |
| 2:00-3:30 | Panel Discussion (Participants To Be Announced) |
| 3:30-4:00 | Break |
| 4:00-5:00 | Group Discussion |

**2:00-5:00 Breakout Session C**

Cultivation Methodology Tutorial
Moderator: Joe Graber
Organizers: Slava Epstein & Hans Scholten

| | |
|---|---|
| 2:00-2:20 | Slava Epstein – Northeastern University |
| 2:20-2:40 | Hans Scholten – Pacific Northwest National Laboratory |
| 2:40-2:55 | Martin Keller – Oak Ridge National Laboratory |
| 2:55-3:10 | Chris Belnap – University of California, Berkeley |
| 3:10-3:25 | Judy Wall – University of Missouri, Columbia |
| 3:30-4:00 | Break |
| 4:00-5:00 | Group Discussion |

**5:00-8:00 Poster Session**

# Tuesday, February 13th

## 7:00-8:00 Continental Breakfast

## 8:00-10:00 Plenary Session

Environmental Sensing & Response In Contaminated Habitats
Moderator: Joe Graber

Session Objectives: This session will examine the means by which microorganisms sense environmental conditions and process the acquired information to form an adaptive response. Emphasis will be placed on the role of GTL research in understanding organismal and community dynamics in relevant habitats and how this information can be integrated into the study of contaminant fate and transport.

8:00-8:30 Derek Lovley – University of Massachusetts, Amherst
"Adaptive Evolution and Adaptive Responses in Gene Expression of *Geobacter* Species During Uranium Bioremediation and in Microbial Fuel Cells"

8:30-9:00 Tim Gardner, Boston University
"Genome-scale mapping of transcription networks in *Shewanella oneidensis*: identification of carbon and metal-respiratory regulation"

9:00-9:30 Jill Banfield - University of California, Berkeley
Title To Be Announced

9:30-10:00 Adam Arkin – Lawrence Berkely National Laboratory
Title To Be Announced

## 10:00-10:15 Break

## 10:15-10:45 Information Representation, Integration, & Sharing Working Group Report

Genomics:GTL Data & Information Sharing Policy
Jim Fredrickson & Roland Hirsch

## 10:45-11:15 Report of the Joint Genome Institute

Edward Rubin - Joint Genome Institute

## 11:15-12:15 Keynote Lecture on Systems Biology

Marc Vidal – Harvard University
"Interactome Networks"

## 12:15-2:00 Lunch

## 2:00-5:00 Breakout Session D

Metabolic Engineering Interagency Working Group Conference: Methods to Examine Biochemical & Metabolic Networks
Organizers: Gail McLean (USDA) & Sharlene Weatherwax (DOE)
Moderators: Mark Segal (EPA) & Fred Heineken (NSF)

2:00-3:30 Presentations:
Bernhard Palsson – University of California, San Diego
George Bennett – Rice University
James Liao – University of California, Los Angeles
Jackie Shanks – Iowa State University

3:30-4:00 Break

4:00-5:00 Group Discussion

## 2:00-5:00 Breakout Session E

Tools for the Prediction & Validation of Gene Function
Organizers: Margaret Romine – Pacific Northwest National Laboratory
Andrei Osterman – The Burnham Institute
Moderator: Marvin Stodolsky

2:00-3:30 Panel Discussion:
Scott Lesley - Scripps Research Institute
Tom Squier - Pacific Northwest National Laboratory
Tim Gardner - Boston University

3:30-4:00 Break

4:00-5:00 Group Discussion

## 2:00-5:00 Breakout Session F

Imaging Techniques Tutorial
Organizers: Eva Nogales - University of California, Berkeley
Gang Bao – Georgia Institute of Technology
Moderator: Arthur Katz

2:00-2:20 Eva Nogales - Lawrence Berkeley National Laboratory and University of California, Berkeley

2:20-2:40 Grant Jensen - California Institute of Technology

2:40-2:55 David Spector - Cold Spring Harbor Laboratory

2:55-3:10 Hedi Mattoussi - Naval Research Laboratory

3:10-3:25 Guido Gaietta - University of California, San Diego

3:30-4:00 Break

4:00-5:00 Group Discussion

## 5:00-8:00 Poster Session

# Wednesday, February 14th

**7:00-8:00 Continental Breakfast**

**8:00-10:45 Plenary Session**

Protein Structure & Function
Moderator: Roland Hirsch

Session Objective: This session will discuss the critical role of protein structural determination in understanding the functional capabilities of gene products. The goal of this session is to promote discussion of new advances in structural biology of proteins and ways in which the GTL community can incorporate these approaches into new research directions.

| | |
|---|---|
| 8:00-8:30 | David Eisenberg – University of California, Los Angeles<br>"Stuctural Biology: An Overview of Activities at the UCLA-DOE Institute for Genomics & Proteomics" |
| 8:30-9:00 | Sunney Xie – Harvard University<br>"Single-Molecule Approach to Bacterial Molecular Biology: From In Vitro to In Vivo Studies" |
| 9:00-9:30 | J.H. David Wu – University of Rochester<br>Structural Biology of the Cellulosome |
| 9:30-10:00 | Keith Hodgson - Stanford Linear Accelerator Center<br>"Studying Biocomplexity at Nano to Subnanometer Resolution: The Role of Synchrotron Radiation and the DOE National User Facilities" |
| 10:00-10:15 | Break |
| 10:15-10:45 | Himadri Pakrasi - Washington University<br>"Membrane Biology Grand Challenge: Engagement of a DOE National User Facility for Integrative Studies of an Energy Producing Photosynthetic Bacterium" |

**10:45-11:15 Reports on Tutorial Sessions (10 minutes each)**

**11:15-11:30 Closing Remarks**

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# Workshop Abstracts

The Genomics:GTL Program abstracts and posters are organized according to the Milestones set forth in the GTL Roadmap and as shown below [*DOE Genomics:GTL Roadmap: Systems Biology for Energy and Environment*; October 2005; GenomicsGTL.energy.gov]. Some of the research projects are pilots or proof-of-principle studies for sysems biology, technology and methods development, and computing.

Abstracts associated with the Metabolic Engineering Working Group (MEWG) are identified as such and intermixed with GTL abstracts in relevant categories.

Abstracts from the Plant Feedstock Genomics Joint Program (PFGJG) are in their own subsection beginning on page 201.

## Genomics:GTL Overarching Scientific Goal

Achieve a predictive, systems-level understanding of biological systems to help enable biobased solutions to DOE mission challenges.

### Science and Technology Milestones

**Milestone 1: Develop Techniques to Determine the Genome Structure and Functional Potential of Microbes and Microbial Communities**

1.1 Organism Sequencing, Annotation, and Comparative Genomics

1.2 Microbial-Community Sequencing and Analysis

1.3 Protein Production and Characterization

1.4 Molecular Interactions

**Milestone 2: Develop Methods and Concepts Needed to Achieve a Systems-Level Understanding of Microbial Cell and Community Function, Regulation, and Dynamics**

2.1 Omics: Systems Measurements of Plants, Microbes, and Communities

2.2 Metabolic Network Experimentation and Modeling

2.3 Regulatory Processes

**Milestone 3: Develop the Knowledgebase, Computational Methods, and Capabilities to Advance the Understanding and Prediction of Complex Biological Systems**

3.1 Computing Infrastructure, Bioinformatics, and Data Management

### Communication

### Ethical, Legal, and Societal Issues

### USDA-DOE Abstracts

The following table is a simple summation of how GTL science and DOE missions align (GTL Roadmap p. 40).

## Summary Table. GTL Science Roadmap for DOE Missions

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