Appendix D. GTL Meetings, Workshops, and Participating Institutions

GTL Meetings and Workshops
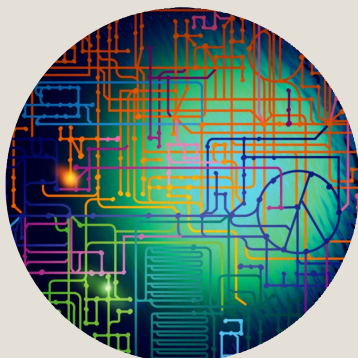
2000–2004 Totals

Participants:	1486
Unique participants:	792
Meetings:	46
Institutions:	235

2005

- June 19–22 Biotech Industry Organization (BIO) GTL Symposium, Philadelphia, Pennsylvania
- June 13–14 Plant Genomics for Biofuels, DOE-BP Joint Meeting; Washington, D.C.
- Feb. 6–9 Contractor-Grantee Workshop III; Washington, D.C.*

2004

- June 14–16 Roadmap Planning Phase II: Technology Deep Dive; Arlington, Virginia
- June 6–9 Biotech Industry Organization (BIO) GTL Symposium; San Francisco, California
- June 4–6 AAM Colloquium on Systems Microbiology; Portland, Oregon
- April 21–23 World Congress on Industrial Biotechnology GTL Workshop and Symposium, Orlando, Florida
- March 3–4 Planning Study I, Program Science and Capability Needs for DOE Missions; Washington, D.C.
- Feb 29–March 2 Contractor-Grantee Workshop II; Washington, D.C.*

2003

- Sept. 10–11 GTL and Beyond: Data Standards Workshop; Berkeley, California
- Sept. 3 Genomes to Life Milestones Workshop; Crystal City, Virginia
- July 22–24 Data Management, Protein Folding, and Modeling and Simulation Workshops; Gaithersburg, Maryland*
- June 17–18 Characterization and Imaging of Molecular Machines Facility Workshop; Atlanta, Georgia*

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*Workshop reports followed by an asterisk are on the web: www.doegenomestolife.org/pubs.shtml

GTL Meetings, Workshops, Participating Institutions

- June 2–3 Facility User Interactions Workshop (Portals); Gaithersburg, Maryland
- May 29–30 Protein Production and Characterization Workshop; Argonne, Illinois*
- May 12–14 Bioinformatics Workshop for Proteomics; La Jolla, California*
- April 1–2 Global Proteomics Workshop; Santa Fe, New Mexico*
- Feb. 9–12 Contractor-Grantee Workshop I; Arlington, Virginia*
- Feb. 3 Scientific Workshop on Affinity Reagent Needs for Facility I; Chicago, Illinois

2002

- Dec. 3–4 Biological and Environmental Advisory Committee (BERAC); Washington, D.C.
- Oct. 14–15 Facilities Planning; Gaithersburg, Maryland
- Aug. 16–17 Facilities Planning; Chicago, Illinois
- June 19–22 Facilities Planning; San Francisco, California
- April 16–19 Computing Strategies; Oak Ridge, Tennessee
- April 16–18 Imaging Workshop; Charlotte, North Carolina*
- April 2 Keck Institute Meeting; Claremont, California
- March 18–19 Mathematics Workshop; Gaithersburg, Maryland*
- March 6–7 Computer Science Workshop; Gaithersburg, Maryland*
- Jan. 22–23 Computational Infrastructure Workshop; Gaithersburg, Maryland*

2001

- Dec. 10–11 Technology Assessment for Mass Spectrometry; Washington, D.C.*
- Nov. 27 BERAC Presentation and Discussion of GTL Payoffs; Washington, D.C.
- Oct. 24–25 Energy and Climate Mission Payoffs; Chicago, Illinois
- Sept. 9–10 Science Mission Payoffs; Washington, D.C.
- Sept. 6– 7 Visions for Computational and Systems Biology Workshop; Washington, D.C.*
- Aug. 7–8 Computational Biology Workshop; Germantown, Maryland*
- June 23 Role of Biotechnology in Mitigating Greenhouse Gas Concentrations; Arlington, Virginia*
- Jan. 25–27 Genomes to Life Roadmap Planning; Germantown, Maryland

2000

- Dec. 1 Preliminary Report to BERAC on Roadmap; Washington, D.C.
- Nov. 30 Roadmap Drafting; Oak Ridge, Tennessee
- Nov. 14–15 Microbial Cell Project Workshop; Chicago, Illinois
- Nov. 7 Roadmap Strategy Meeting; San Diego, California
- Oct. 29–Nov. 1 Roadmap Planning; San Diego, California
- Oct. 6 Roadmapping Meeting; Denver, Colorado
- June 1 Subcommittee Report Approved by BERAC; Washington, D.C.
- March 2 BERAC Subcommittee; Washington, D.C.
- Jan. 1 BERAC Subcommittee; Washington, D.C.

Participating Institutions*

Abbott Laboratories
Advanced Life Sciences
Affymetrix
Agilix Corporation
Alfred P. Sloan Foundation
American Association for the Advancement of Science
American Type Culture Collection
Ames Laboratory
ApoCom Genomics
Applied Biosystems
Argonne National Laboratory
Arizona Court of Appeals
Arizona State University
Athenix
Baylor College of Medicine
Beckman Research Institute, City of Hope
Bell Labs
BIATECH
Bio-Technical Resources
Boston University
Brookhaven National Laboratory
California Institute of Technology
Carnegie Mellon University
Celera Genomics
CNRS UMR Ecologie Microbienne
Colin Gordon and Associates
Columbia University
Conkling Fiskum and McCormick, Inc.
Cornell College of Veterinary Medicine
Cornell University
Courant Institute
Dalhousie University
Dana-Farber Cancer Institute
Defense Advanced Research Projects Agency

Diversa Corporation
Duke University
DuPont Central Research and Development
Ehime University
Energy Sciences Network
Environmental Protection Agency
Fellowship for Interpretation of Genomes
Flad and Associates
Florida State University
Food and Drug Administration
Fred Hutchinson Cancer Center
Gene Logic, Inc.
Gene Network Sciences
General Electric
geneticXchange
GeneXPress
Genomatica, Inc.
GENOSCOPE
Georgetown University
Georgia Institute of Technology
GlaxoSmithKline
Harvard Medical School
Harvard University
HDR Inc.
Hebrew University
Howard Hughes Medical Institute
IBM Corporation
Indiana University
Inovise Medical
InPharmix Incorporated
Institute for Biological Energy Alternatives
Institute for Systems Biology
Institute for Genomic Research, The
Integrated Genomics, Inc.
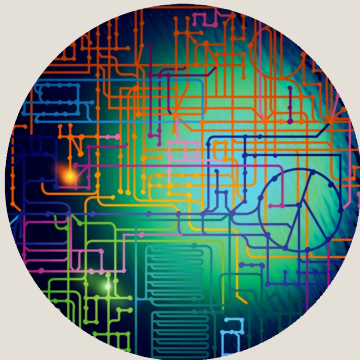J. Craig Venter Science Foundation

*2000–2004

Jackson Laboratory
Johns Hopkins University
Joint Genome Institute
Keck Graduate Institute
Keio University
Kosan Biosciences Incorporated
Lawrence Berkeley National Laboratory
Lawrence Livermore National Laboratory
Linus Pauling Institute
Los Alamos National Laboratory
Louisiana State University
Marine Biological Laboratory
Marshfield Medical Research Foundation
Massachusetts Institute of Technology
McGill University
Medical University of South Carolina
Merck Research Laboratories
Metrigen, Inc.
Michigan State University
Microsoft Corporation
MITRE Corporation
Molecular Sciences Institute
Monsanto Company
Montana State University
Monterey Bay Aquarium Research Institute
MP Biomedicals, Inc.
National Academies
National Academy of Sciences
National Cancer Institute
National Cancer Institute, Center for Cancer Research
National Center for Genome Research
National Center for Supercomputing Applications, Keck Genome Center
National Energy Research Scientific Computing Center
National Heart, Lung, and Blood Institute
National Institute of Environmental Health Sciences
National Institute of General Medical Sciences
National Institute of Standards and Technology
National Institutes of Health
National Renewable Energy Laboratory
National Science Foundation
National Water Research Institute (Canada)

Natural Resources Defense Council
Naval Surface Warfare Center, Dahlgren Division
NeoGenesis
New England Complex Systems Institute
New York University
NimbleGen Systems Inc.
North Carolina State University
Northern Arizona University
Northwestern University
Novagen
Novartis Research Foundation
Novation Biosciences
Oak Ridge Institute for Science and Education
Oak Ridge National Laboratory
Office of Management and Budget
Office of Naval Research
Ohio State University
Old Dominion University
Oregon Health Sciences University
Oregon State University
Oxford GlycoSciences
Pacific Northwest National Laboratory
Pennsylvania State University
Perkins and Will
Pfizer Inc.
Pittsburgh Supercomputing Center
PolyLC Inc.
Protometrix (Invitrogen)
Purdue University
Quantum Intelligenece
RIKEN
Roche
Rockefeller University
Rutgers University
Salk Institute
San Diego Supercomputer Center
Sandia National Laboratories
Sanger Centre
Science
Scripps Institution of Oceanography
Scripps Research Institute
SmithKline Beecham Pharmaceutical
Software Technology Group, Inc.

SoundVision Productions
Southwest Parallel Software
SRI International
St. Jude Children's Research Hospital
Stanford University
Stanford University School of Medicine
State University of New York, Stony Brook
Stony Brook University
Structural Genomics Consortium
Teranode Corporation
Texas Tech University
Thomas Jefferson National Accelerator Facility
U. S. Department of Agriculture
U. S. Department of Energy
U. S. House of Representatives, Science Committee
U. S. Senate, Energy and Natural Resources Committee
Uniformed Services University of the Health Sciences
University of Buffalo
University of California, Berkeley
University of California, Davis
University of California, Los Angeles
University of California, San Diego
University of California, San Francisco
University of California, Santa Barbara
University of California, Santa Cruz
University of Chicago
University of Cincinnati College of Medicine
University of Colorado
University of Connecticut
University of Connecticut Health Center
University of Delaware
University of Florida
University of Georgia
University of Illinois
University of Illinois, Chicago
University of Illinois, Urbana-Champaign
University of Iowa
University of Maryland

University of Maryland Biotech Institute
University of Massachusetts
University of Massachusetts, Amherst
University of Miami
University of Minnesota
University of Missouri, Columbia
University of North Carolina
University of Notre Dame
University of Pennsylvania
University of Pittsburgh
University of Southern California
University of Southern Mississippi
University of Tennessee
University of Tennessee Health Science Center
University of Tennessee, Knoxville
University of Texas
University of Texas, Austin
University of Texas, Houston
University of Texas Medical School
University of Utah
University of Virginia
University of Washington
University of Wisconsin, Madison
University of Wyoming
Uppsala University
Utah State University
Vanderbilt University
Vertex Pharmaceuticals
Virginia Tech
VizX Labs
Wadsworth Center
Washington State University
Washington University (St. Louis)
Wayne State University
Weyerhauser
Whitehead Institute for Biomedical Research
Whitehead Institute/MIT Center for Genome Research
Windber Research Institute

Appendix E. GTL-Funded Projects

GTL-Funded Projects*

Program Projects

Harvard Medical School

- Microbial Ecology, Proteogenomics, and Computational Optima

J. Craig Venter Institute

- Reconstruction of a Bacterial Genome from DNA Cassettes and Sargasso Sea Metagenomics

Joint Genome Institute

- DNA Sequencing for Genomics:GTL

Lawrence Berkeley National Laboratory

- Rapid Detection of Stress Response Pathways in Metal- and Radionuclide-Reducing Bacteria; with Sandia National Laboratories (SNL), Lawrence Livermore National Laboratory (LLNL), and Oak Ridge National Laboratory (ORNL)

Oak Ridge National Laboratory and Pacific Northwest National Laboratory

- Genomics:GTL Center for Molecular and Cellular Systems; with SNL, LLNL, and Argonne National Laboratory (ANL)

Sandia National Laboratories

- Carbon Sequestration in *Synechococcus sp.*: From Molecular Machines to Heirarchical Modeling; with ORNL

Shewanella Federation

- The *Shewanella* Federation: Environmental Sensing, Metabolic Response, and Regulatory Networks in the Respiratory Versatile Bacterium *Shewanella;* with Pacific Northwest National Laboratory (PNNL); BIATECH; Boston University; University of California, Los Angeles (UCLA); ORNL; Michigan State University; University of Southern California; Baylor University; and Genomatica

*Projects funded between GTL's 2002 inception and July 2005. Some listed projects are not funded currently, and GTL-supported workshops and conferences are not included.

University of Massachusetts, Amherst

- Analysis of the Genetic Potential and Gene Expression of Microbial Communities Involved in the In Situ Bioremediation of Uranium

- Harvesting Electrical Energy from Organic Matter; with ANL

Communication

- Genome Management Information System; ORNL

Bioinformatics, Modeling, and Computation

- A Conceptual and In Silico Model of the Dissimilatory Metal-Reducing Microorganism, *Geobacter sulfurreducens*; University of Massachusetts, Amherst

- Animal Gene Regulatory Networks; California Institute of Technology

- Cofunding for BioSpice Projects; Defense Advanced Research Projects Agency (DARPA)

- Computation Hypothesis Testing: Integrating Heterogeneous Data and Large-Scale Simulation to Generate Pathway Hypotheses; Gene Network Sciences

- Computational Resources for GTL; Keck Graduate Institute

- Computing Frontiers: Prospects from Biology; National Academy of Sciences

- Development of Advanced Tools for Data Management, Integration, Analysis, and Visualization Through a Comprehensive Systems Analysis of the Halophilic Archaeon; Institute for Systems Biology

- Development of Bioinformatics and Experimental Technologies for Identification of Prokaryotic Regulatory Networks; Brown University

- Identification and Characterization of Prokaryotic Regulatory Networks; Washington University

Environmental Genomics

- Application of High-Throughput Gel Microdroplet Culturing to Develop a Novel Genomics Technology Platform; Diversa Corp.

- Genome-Facilitated Analyses of Geomicrobial Processes; PNNL, LLNL, LBNL

- Growth of Uncultured Microorganisms from Soil Communities; Northeastern University and ORNL

- Proteogenomic Approaches for the Molecular Characterization of Natural Microbial Communities; University of California, Berkeley

Microbial Genomics

- Dynamics of Cellular Processes in *Deinococcus radiodurans*; Henry M. Jackson Foundation

- Genome-Wide Analysis of *Prochlorococcus marinus* Protein-Protein Interactions; LLNL

- Global Characterization of Genetic Regulatory Circuitry Controlling Adaptive Metabolic Pathways; Stanford University

- Metabolic Engineering of Light and Dark Biochemical Pathways in Wild-Type and Mutant Strains of *Synechocystis* PCC 6803 for Maximal, 24-Hour Production of Hydrogen Gas; Oregon State University

- Metabolic Functional Analysis of Bacteria Genomes; Oregon State University

- Molecular Basis for Metabolic and Energetic Diversity; University of Wisconsin

- Rapid Reverse Engineering of Genetic Networks Via Systematic Transcriptional Perturbations; Boston University

- *Rhodopseudomonas palustris* Microbial Cell Project; ORNL and Ohio State University

- Whole Genome Transcriptional Analysis of Environmental Stresses in *Caulobacter crescentus*; LBNL

Technology Development and Use

Imaging, Molecular, and Cellular Analysis

- Development of a Hybrid Electron Cryotomography Scheme for High-Throughput Protein Mapping in Whole Bacteria; Brookhaven National Laboratory (BNL)

- Dynamic Spatial Organization of Multiprotein Complexes Controlling Microbial Polar Organization, Chromosome Replication, and Cytokinesis; Stanford University

- Electron Tomography of Microbial Cells; LBNL

- Microscopies of Molecular Machines: Structural Dynamics of Gene Regulations in Bacteria; LBNL

- New, Highly Specific Vibrational Probes for Monitoring Metabolic Activity in Microbes and Microbial Communities; LLNL

- Probe of Single Microbial Proteins and Multi-protein Complexes with Bioconjugated Quantum Dots; Georgia Tech Research Corporation

- Real-Time Gene Expression Profiling of Live *Shewanella oneidensis* Cells; Harvard University and PNNL

- Single Cell Imaging of Macromolecular Dynamics in a Cell; LBNL

- Use of Near-Infrared Probes of Microscopic Functional Analysis of Microbial Consortia Including Hard-to-Culture Microbes; ANL

Protein Production and Molecular Tags

- Center for Genomics and Proteomics Research Program; UCLA

- Chemical Methods for the Production of Proteins and Protein and Peptide Reagents and for the Characterization of Protein Complexes; University of Chicago

- Combined Informatics and Experimental Strategy for Improving Protein Expression; University of Maryland Biotech Institute

- Development of Genome-Scale Expression Methods; ANL

- Development of Multipurpose Tags and Affinity Reagents for Rapid Isolation and Visualization of Protein Complexes; PNNL

- Functionalized Nanotubes of Enzyme Immobilization (Pilot Project); PNNL

- High-Throughput Biophysical Analyses of Purified Proteins; BNL

- Integrated Approach to Functional Genomics; Los Alamos National Laboratory (LANL)

Proteomics and Metabolomics

- Application of High-Throughput Proteomics Structural Studies of Essential Proteins from *D. radiodurans* and *S. oneidensis*; PNNL

- Development of High-Throughput Proteomics Production Operations; PNNL

- Growth and Metabolism of Individual Bacterial Cells Utilizing Nanosims; LLNL

- Metabolomic Functional Analysis of Bacterial Genomes; LANL

- Microbial Communities; PNNL

- New Technologies for Metabolomics; LBNL

- Technology for Ultrahigh-Resolution Localization of Gene Transfer; PNNL
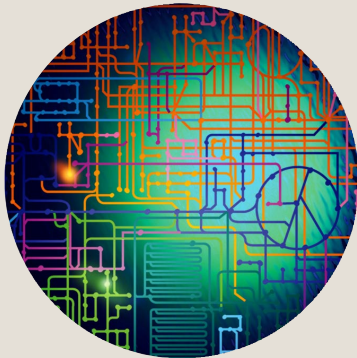
Ethical, Legal, and Social Issues

- DNA Files; SoundVision Productions

- Science Literacy Workshop; SoundVision

Computing and Education

- BACTER (Bringing Advanced Computational Resources to Environmental Research) Institute; University of Wisconsin, Madison

- Center for Computational Biology; University of California, Merced; Renssalear Polytechnic Institute; and LLNL

- Institute for Multiscale Modeling of Biological Interactions; Johns Hopkins University, University of Delaware, and LANL

Appendix F. Strategic Planning for CCSP and CCTP

Strategic Planning for CCSP and CCTP

Strategic planning for Climate Change Science Program (CCSP) and Climate Change Technology Program (CCTP) included analysis of hundreds of technologies and methods to meet national and global goals. Biological and environmental research studies (including those on the roles of microbes in ocean and terrestrial environments) are critical to understanding and predicting climate changes and developing technologies for biobased fuel production and climate mitigation and adaptation.

Knowledge from GTL research will be the foundation for developing microbial strategies that support CCSP and CCTP goals outlined below.

CCSP Goal

• **www.climatescience.gov**

Improve Quantification of the Climate-Changing Forces and Related Systems

• Improve understanding of key "feedbacks" and sensitivities of biological and ecological systems and accelerate incorporation into climate models to reduce uncertainty.

• Develop information on the carbon cycle to assist in evaluation of carbon-sequestration strategies and alternative response options.

CCTP Goals

• **www.climatetechnology.gov**

Reduce Emissions From the Energy Supply

• Use microbes or microbial enzymes in nanostructures for the photosynthetic production of hydrogen and other high-energy fuels.

• Use microbes for production of biofuels from biomass, in situ bioprocessing of fossil fuels, and design of improved biomass feedstocks.

Capture and Sequester Carbon Dioxide

- Understand the role of microbes in the cycling of carbon in terrestrial and marine environments.

- Use this understanding to determine efficacy and impacts of ocean and terrestrial sequestration strategies.

- Incorporate microbial processes into systems for capturing carbon dioxide from the atmosphere.

Reduce Emissions of Other Greenhouse Gases

- Understand microbial contributions to nitrous oxide and methane emissions from natural biogeochemical cycles.

- Understand the communities of microbes in the digestive systems of livestock that release methane.
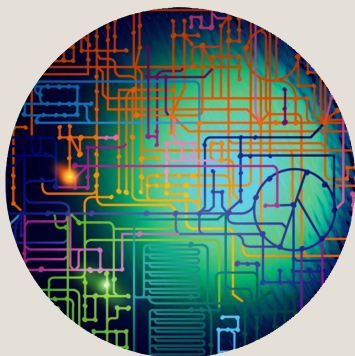
Enhance Capabilities to Measure and Monitor GHG Emissions

- Develop ecogenomic sensors for detecting changes in ocean and soil microbial communities.

- Quantify net emissions of GHGs from microbial processes.

Appendix G. Microbial Genomes Sequenced or in Process by DOE

Microbial Genomes Sequenced or in Process by DOE

Uncovering Potential Applications Relevant to DOE Missions

Microbes and microbial consortia sequenced or in process for various DOE missions include those listed below (last updated July 15, 2005).

Carbon Sequestration

‡*Aureococcus anophagefferens* (algae, ~32 Mb): Brown tide-forming pelagophyte, forms coastal blooms, reduces trace metals; can seques-ter substantial amounts of carbon.

†*Azotobacter vinelandii* **AvOP** (bacteria, 4.5 Mb): Aerobic, fixes nitrogen; found in soils worldwide; has nitrogenases incorporating molybdenum and vanadium (in addition to iron); relevant to energy use and carbon sequestration.

‡*Bradyrhizobium sp.* **strain BTAi** (bacteria, 9.2 Mb): Versatile photo-synthetic; carbon dioxide- and nitrogen-fixing symbiont of legumes; nodule-forming on roots and stems; aids plant in carbon processing.

‡*Calyptogena magnifica* (clam) proteobacterial symbiont (bacteria, est. ~ 4 Mb): Isolated from deep sea vents, sulfur oxidizing, nitrogen fixing; fixes carbon dioxide via possibly novel pathway; carbon sequestration.

†*Chlamydomonas reinhardtii* (eukaryotes, ~100 Mb): Green alga, photosynthetic, widespread in environment, 17 chromosomes, widely used model system.

Photosynthetic Green Sulfur Bacteria: Sequester carbon via photo-synthesis; produce hydrogen when cocultured with sulfate-reducing bacteria.

- ‡*Chlorobium limicola* **DSMZ 245(T)** (2.4 Mb): Nonmotile, rod shaped; type strain for all green sulfur bacteria.

- ‡*Chlorobium phaeobacteroides* **DSMZ 266T** (~2.2 Mb): Rod shaped; does not use nitrogen or sulfide.

- ‡*Chlorobium phaeobacteroides* **MN1 Black Sea** (2.2 Mb): Photo-synthetic in very low light, with chlorophylls that absorb 1 photon every 5 hours.

- **Chlorobium tepidum* (2.1 Mb): Photosynthetic; may play impor-tant role in earth's overall carbon cycle.

- ‡*Chlorobium vibrioforme f. thiosulfatophilum* **DSMZ 265(T)** (2.5 Mb): Curved rod shape.

- †*Chloroflexus aurantiacus* **J-10-fl** (3 Mb): Modern version of organism; needs no oxygen for photosynthesis; uses unique pathway to fix carbon dioxide.

- ‡*Chloroherpeton thalassium* (~3 to 3.5 Mb): Most taxonomically divergent of green sulfur bacteria.

Chloroflexi **Bacteria (7 Strains, est. ~5 Mb each):** Gram-negative, filamentous anoxygenic phototrophs; useful in carbon sequestration, biofuels.

- ‡*Candidatus Chlorothrix halophila*: Marine and hypersaline biofilms; produces bacterial chlorophylls (BChl) a and c and chlorosomes.

- ‡*Chloroflexus aggregans* **DSMZ 9485:** Motile, grows at 55°C in both light and dark.

- ‡*Chloronema sp.* **strain UdG9001**: Motile, photoautotrophic; isolated from Little Long Lake, Wis.; grows in iron-rich environments.

- ‡*Heliothrix oregonensis*: Bright orange colored, motile; grows optimally at 45° to 55°C; forms monolayers on top of microbial biofilms.

- ‡*Herpetosiphon aurantiacus* **DSM 785**: Orange colored, isolated from Birch Lake, Minn.; hydrolyzes starch, does not produce BChls.

- ‡*Roseiflexus castenholzii* **DSM 13941**: Motile, red to reddish-brown colored; has BChl-a but not BChl-c or chlorosomes.

- ‡*Roseiflexus sp.* **strain RS-1**: Isolated from high-temperature biofilms in Octopus Spring, Yellowstone.

◊*Colwellia* **34H** (bacteria, 5.3 Mb): Psychrophile, important in carbon and nutrient cycling in polar marine environments.

‡*Crocosphaera watsonii* **WH8501** (cyanobacteria, 3.6 to 5 Mb): Marine, unicellular; confined to waters from 26 to 32°C; temporally segregates carbon-dioxide fixation from nitrogen fixation.

‡*Emiliania huxleyi* **1516** (marine algae, ~5 Mb): Marine coccolithophorids; plays role in global carbon cycling and sulfur transformation.

‡*Frankia* **Cc13** (bacteria, ~8 to 10 Mb): Actinomycetes, Group II, fixes nitrogen; forms major nitrogen-fixing symbiosis in temperate soils; promotes formation of woody-biomass energy source.

‡*Frankia sp.* **EAN1pec** (bacteria, ~10 Mb): Group III, ubiquitous, fixes nitrogen, forming major nitrogen-fixing symbiosis in temperate soils; promotes formation of woody-biomass energy source; grows well, shows metal resistance.

‡*Jannaschina sp.* **CCS1** (bacteria, 4.5 to 5 Mb): Member of *Roseobacter* clade; contributes to oceanic anoxygenic phototrophy, a mode of light-driven energy acquisition.

Micromonas pusilla ssp. **Eukarya (2 strains, ~15 Mb each):** Abundant in oceans, very small (1 to 3 microns in length); significant planktonic primary producers (carbon-dioxide fixers) in size class; carbon sequestration.

- ‡*M. pusilla* **NOUM17(RCC 299)**: Equatorial Pacific isolate.

- ‡*M. pusilla* **CCMP1545**: England West Coast isolate.

‡*Moorella thermoacetica* ATCC39073 (bacteria): Fixes carbon dioxide in absence of oxygen; can grow on hydrogen, carbon dioxide, or carbon monoxide as sole carbon source; acetogenic.

Bacteria Involved in Nitrification Affecting Climate Change: Oxidize ammonia; can degrade chlorinated aliphatic hydrocarbons; give insight into basis of biogeochemical nitrogen cycle.

- ‡*Nitrobacter hamburgensis* (~3 Mb): Found in soil; model organism for biochemical, structural, and molecular investigations; has carboxysomes.

- ‡*Nitrobacter winogradskyi* **Nb-255** (~3 Mb): Widely distributed, also nitrite oxidizing; can grow with several metabolic modes and anoxically by denitrification; can fix carbon dioxide.

- ‡*Nitrosococcus oceani* (~3 Mb): Gamma proteobacterium that oxidizes ammonia (others are beta proteobacteria).

- *Nitrosomonas europaea* **ATCC19718** (2.2 Mb): Aids incorporation of carbon dioxide into biomass.

- ‡*Nitrosomonas eutropha* (~3 Mb): Physiologically diverse; can oxidize nitrous oxide while reducing either ammonia or hydrogen; important in wastewater treatment systems; potential for remediation of high ammonia concentrations in waters.

- *‡Nitrosospira multiformis* **Surinam** (~3 Mb): Well-studied, typical of those seen in soil environments.

‡*Nostoc punctiforme* **ATCC29133 (bacteria, 10 Mb): Fixes carbon dioxide and nitrogen; produces hydrogen; survives acidic, anaerobic, and low-temperature conditions.

‡*Ostreococcus* (eukaryotes, est. 8 to 10 Mb): Fast-growing, ubiquitous; important in marine carbon fixation.

‡*Pelodictyon luteolum* **DSMZ 273(T)** (bacteria, 3.0 Mb): Rod-shaped photosynthetic GSB cells that can form yellow-green hollow microcolonies.

‡*Pelodictyon phaeoclathratiforme* **BU-1, DSMZ 5477** (bacteria, 3 Mb): Gas vesicle containing green sulfur bacterium cells that can form 3D net-like microcolonies.

‡*Prochlorococcus isolate* **NATL2 (prokaryotes, 1.7 to 2.4 Mb): Ocean carbon sequestration.

Prochlorococcus marinus **MED4** (bacteria, 1.7 Mb), *Prochlorococcus marinus* **MIT9313** (bacteria, 2.4 Mb), and **‡*Prochlorococcus marinus* **MIT9312** (bacteria, ~2.4 Mb): All ecotypes abundant in temperate and tropical oceans; important in ocean carbon cycling; absorb blue light efficiently; **MIT9313** is adapted to lower-light conditions (lower ocean depths) and **MIT9312** to higher-light conditions nearer the surface.

‡*Prosthecochloris aestuarii* **SK413, DSMZ 271(t)** (bacteria, 2.5 Mb): Nonmotile, spherical to ovoid green sulfur bacteria; nitrogen-fixing marine strain; high salt requirement.

Rhodopseudomonas palustris **Bacteria (5 strains, ~5.5 Mb each):** Metabolically versatile, can produce hydrogen, fix carbon dioxide, biodegrade organic pollutants and plant biomass; biofuels.

- ‡*R. palustris* **BisA53:** Isolated from Dutch site; grows well on benzoate, tends to aggregate.

- ‡*R. palustris* **BisB5:** Isolated from Dutch contaminated site; smaller, more motile form; fewer rosettes than sequenced **CGA009.**

- ‡*R. palustris* **BisB18:** Isolated from Dutch site; slower growing than **CGA009.**

- **‡*R. palustris* **CGA0009**: Biodegrades under both aerobic and anaerobic conditions.

- ‡*R. palustris* **HaA2**: Unable to grow on benzoate; isolated from Haren site.

‡*Rhodospirillum rubrum* **ATCC11170 (bacteria, 3.4 Mb): Phototrophic; grows in various conditions, including aerobic and anaerobic; fixes nitrogen, grows on hydrogen; model for photosynthesis.

‡*Roseobacter* **strain TM1040** (bacteria, ~4.5 Mb each): Isolated from dinoflagellate; fixes carbon in marine surroundings.

‡*Sphingopyxis alaskensis* **RB2256** (bacteria, 3.2 Mb): Makes up large proportion of oceanic biomass; major contributor to global carbon flux; can bioconcentrate trace metals.

‡*Synechococcus elongates* **PCC7 942 (cyanobacteria, 2.4 to 2.7 Mb): Carbon fixation; photosynthesis in fresh waters.

‡*Synechococcus sp.* **C9902 (coastal)** and **Cc9605 (oligotrophic)** (bacteria, ~2.4 Mb each): Fixes carbon dioxide; globally distributed; important in carbon fluxes in marine environment.

Synechococcus **WH8102** (bacteria, 2.4 Mb): Photosynthetic; important to ocean carbon fixation; genetically tractable.

†*Thalassiosira pseudonana* (eukarya, ~25 Mb): Ocean diatom, major participant in biological "pumping" of carbon to ocean depths.

‡*Thiobacillus denitrificans* **ATCC23644 (bacteria, ~2 Mb): Fixes carbon; oxidizes sulfur and iron; involved in bioremediation.

‡*Thiomicrospira crunogena* (bacteria, 2 Mb): Marine gamma proteobacterium isolated from East Pacific; found in deep sea vents; grows rapidly (doubling time, ~1 hour); carbon-concentrating mechanism similar to cyanobacteria; sulfur oxidizing; fixes carbon dioxide; can grow in low to absent oxygen conditions; desulfurylates coal; strips sour gas (hydrogen sulfide) from petroleum.

‡*Thiomicrospira denitrificans* (~1.6 Mb): Marine epsilon proteo-bacterium found in hydrothermal vents but also in oxygen-containing, anoxic ocean-transition regions; uses reverse TCA cycle for carbon fixation; sulfur oxidizing; fixes CO_2; can grow in low to absent oxygen conditions; desulfurylates coal; strips sour gas (HS) from petroleum.

†*Trichodesmium erythraeum* **IMS101** (bacteria, 6.5 Mb): Key nitrogen-fixing microbe; plays major role in tropical and subtropical oceans.

Energy Production

Anabaena variabilis **ATCC29413 (cyanobacteria, 7 to 10 Mb): Filamentous heterocyst-forming; fixes nitrogen and carbon dioxide; produces hydrogen.

‡**Caldicellulosiruptor saccharolyticus** (bacteria, 4.3 Mb): Versatile biomass-degrading, hydrogen-producing thermophile; biofuels.

◊**Carboxydothermus hydrogenoformans** (bacteria, 2.10 Mb): Gram positive; converts carbon monoxide and water to carbon dioxide and hydrogen.

‡**Clostridium phytofermentans** (bacteria, ~5 Mb): Degrades plant polymer cellulose, pectin, starch, and xylan to produce ethanol and hydrogen.

‡**Clostridium beijerinckii** **NCIMB 8052** (bacteria, 6.7 Mb): Produces solvent; converts biomass to fuels and chemicals; potential for alternate energy production.

***Methanobacterium thermoautotrophicum** **Delta H** (archaea, 1.7 Mb): Produces methane; plays role in earth's overall carbon cycle.

†**Methanococcoides burtonii** **DSM6242** (archaea, 3 Mb): Extremophile adapted to cold (less than 5°C); produces methane.

***Methanococcus jannaschii** **DSM2661** (archaea extremophile, 1.7 Mb): May identify high-temperature, high-pressure enzymes; produces methane.

‡**Methanosaeta thermophila** P_T(**DSM6194**) (archaea, ~ 3Mb): Widely distributed in environment; metabolizes acetates into methane; potential producer of biofuel.

†**Methanosarcina barkeri** **Fusaro** (archaea, 2.8 Mb): Lives in cattle rumen; digests cellulose and other polysaccharides to produce methane; very oxygen sensitive; grows in variety of substrates.

‡**Methanospirillum hungateii** **JF1** (bacteria, 2.8 Mb): Methanogen; system for studying multispecies microbial assemblage composed of metabolically diverse microorganisms functioning as a single catalytic unit.

‡**Methylobacillus flagellatus** **KT** (proteobacteria, 3.1 Mb): Bioremediation; cycling of one-C compounds; environmentally benign bioprocessing into feedstocks.

‡**Pichia stipitis** **CBS 6054** (fungi, 12 Mb): Ferments xylose to ethanol; potential to oxidize products of lignin degradation and play a role in cellulose degradation as endosymbiont of beetles; converts biomass to ethanol.

‡**Syntrophomonas wolfei** **Göttingen DSM 2245B** (bacteria, 4.5 Mb): Methanogenic and syntrophic; potential hydrogen producers; useful in bioremediation; system for studying multispecies microbial assemblage of metabolically diverse microorganisms functioning as single catalytic unit.

‡**Syntrophobacter fumaroxidans** **MPOB** (bacteria, 3.3 Mb): Methanogenic proprionate oxidizer; uses fumarate as electron acceptor; can produce hydrogen and formate; syntrophic (i.e., part of bacteria community).

◊**Thermotoga neopolitana** **ATCC49045** (bacteria, ~1.8 Mb): Combines with oxygen to produce hydrogen.

Bioremediation

‡**Acidiphilium cryptum** **JF 5** (bacteria, 2.46 Mb): Reduces iron and iron oxides in very acid conditions (pH 2.2 to 5); possible bioremediation of metals in acid environments.

†**Acidithiobacillus ferrooxidans** (bacteria, 2.9 Mb): Used in mining industry to sequester iron and sulfide.

‡**Acidobacterium sp.** (bacteria, two Group 1 strains, one Group 3 strain, est. ~4 Mb each): Ubiquitous in soil, including those contaminated with chromium, zinc, other metals, and PCBs.

‡**Alkaliphillus metalliredigenes** (bacteria, ~4 Mb): Reduces iron, other metals, uranium under alkaline conditions (optimal growth, pH 9.6).

‡**Anaeromyxobacter delahogenans** **2CP-C** (bacteria, 3.38 Mb): Reduces metal (iron, uranium, others); degrades aromatic and halogenated hydrocarbons.

‡**Arthrobacter sp.** **strain FB24** (bacteria, ~2.4 Mb): Resists metal (reduces chromium, lead); degrades hydrocarbon; resists radiation; widely distributed in soils.

‡**Burkholderia ambifaria** (bacteria, 4.7 Mb): Genomovar VII; smallest *Burkholderia* genome, biocontrol agent.

‡*Burkholderia ambifaria* **AMMD** (bacteria, ~7.2 Mb): Ubiquitous rhizosphere colonizer and member of the *Burkholderia cepacia* complex; nitrogen fixer, organic-pollutant degrader; bioremediation.

†*Burkholderia xenovorans (formerly Burkholderia fungorum)* **LB400** (bacteria, 8 Mb): Outstanding degrader of polychlorinated biphenyls (PCBs).

‡*Burkholderia vietnamiensis* **G4** (bacteria, ~8 to 10 Mb): Genomovar V; degrades trichloroethylene; colonizes rhizosphere.

**Caulobacter crescentus* (bacteria, 4.01 Mb): Potential for heavy-metal remediation in waste-treatment plant wastewater.

‡*Chromohalobacter salexigens* **DSM 3043** *(*formerly *Halomonas elongatee)* (bacteria, 4 Mb): Most-halotolerant eubacteria known; displays metal resistance; degrades aromatic hydrocarbons and toxic organics; high halotolerance, suggesting applications in extreme environments.

†*Dechloromonas* RCB (bacteria, 2 Mb): Oxidizes iron. Converts perchlorate to chloride; anaerobically oxidizes benzene to carbon dioxide.

**Dehalococcoides ethenogenes* (bacteria, 1.5 Mb): Degrades dangerous solvent trichloroethene to benign products.

‡*Dehalococcoides sp.* **strain BAV1** (bacteria, 2 Mb): Detoxifies many dichloroethene isomers; potential for bioremediating organic-compound contamination; isolated from Michigan site.

‡*Dehalococcoides sp*. **strain VS** (bacteria, 1.5 Mb): Detoxifies many dichloroethene isomers; potential for bioremediation of organic-compound-contaminated sites, isolated from site in Texas.

‡*Deinococcus geothermalis* **DSM11300** (bacteria, ~3 Mb): Resists radiation; can bioremediate radioactive mixed waste at temperatures up to 55°C.

Deinococcus radiodurans* **R1 (bacteria, 3 Mb): Survives extremely high levels of radiation; possesses DNA-repair capabilities for radioactive waste cleanup.

†*Desulfitobacterium hafniense* **DCB-2** (bacteria, 4.6 Mb): Degrades pollutants such as chlorinated organic compounds that include some pesticides.

‡*Desulfotomaculum reducens* **MI-1** (bacteria, 4 Mb): Gram-positive, spore-forming, metabolically versatile sulfate and metal (iron, manganese, uranium, chromium) reducer. Can reduce uranium and nitrate simultaneously; bioremediation.

***Desulfovibrio desulfuricans* **G20** (bacteria, 3.1 Mb): Anaerobic; reduces sulfate, uranium, and toxic metals; corrodes iron piping; "sours" petroleum with hydrogen sulfide.

Desulfovibrio vulgaris* **Hildenborough (bacteria, 3.2 Mb): High potential for bioremediation through metal and sulfate reduction and sulfate utilization.

†*Desulfuromonas acetoxidans* (bacteria, 4.1 Mb): Marine microbe; reduces iron; oxidizes acetate to carbon dioxide under anoxic conditions via process coupled to sulfur reduction or iron (III).

†*Ferroplasma acidarmanus* **fer1** (archaea, 2 Mb): Lives in most acidic conditions on earth; oxidizes iron; transforms sulfide in metal ores to sulfuric acid, leading to contamination of mining sites.

†*Geobacter metallireducens* (bacteria, 6.8 Mb): Widespread in freshwater sediments; gains energy by reducing iron, manganese, uranium, and other metals; oxidizes toluene and phenol.

‡*Geobacter sp*. **strain FRC-32** (bacteria, ~5 Mb): Iron and uranium reducer, isolated from uranium-contaminated subsurface at U.S. DOE-NABIR Field Research Center; bioremediation.

◊*Geobacter sulfurreducens* (bacteria, 2.5 Mb): Reduces a variety of metals, including iron and uranium.

‡*Glomus intraradices* (fungi, ~11 to 12 Mb): Forms spores to establish a functional symbiotic (and pathogenic) relationship with plant roots.

‡*Kineococcus radiotolerans* **nov** (bacteria, 4.3 to 4.6 Mb): Highly radioresistant; degrades organic pollutants.

‡*Laccaria bicolor* (fungi, ~40 Mb): Commonly found mushroom; stimulates root formation, differentiation in various plants.

†*Mesorhizobium* **BNC1** (bacteria, 5 Mb): Fixes nitrogen with leguminous plants; agriculturally important.

***Methylobium petroleophilum* **PM1** (bacteria, 4.6 Mb): Degrades diverse hydrocarbons, including MTBE (methyl tertiary butyl ether, a common fuel additive), benzene, toluene, xylene, and phenol; biodegradation.

◊*Methylococcus capsulatus* (bacteria, 4.6 Mb): Uses methane as single carbon and energy source; generates pollutant-oxidizing enzymes; used commercially to produce biomass and other proteins.

Mycobacteria (5 isolates, est. ~5 Mb each): Fast growing, nonpathogenic; degraders of polycyclic aromatic hydrocarbons (PAH); found in soils.

- ‡*Mycobacterium flavescens*: Isolated from PAH-contaminated site in Indiana.
- ‡*Mycobacterium vanbaalenii*: Isolated from PAH-contaminated site in Texas.
- ‡*Mycobacterium sp.* **KMS**: Isolated from remediated superfund site, Libby, Montana.
- ‡*Mycobacterium sp.* **JLS**: Isolated from remediated superfund site, Libby, Montana.
- ‡*Mycobacterium sp.* **MCS**: Isolated from remediated superfund site, Libby, Montana.

‡*Nectria haematococca* **MPVI** (fungi, ~40 Mb): Member of *Fusarium solani* species complex; ubiquitous; degrades lignins, hydrocarbons, plastics, some pesticides; useful in biorediation.

‡*Nocardioides* **strain JS614** (bacteria, ~4.5 Mb): Grows aerobically and efficiently on vinyl chloride (VC) and ethene. If starved of VC for more than 1 day, will not recover for more than 40 days; 300-Kb plasmid containing VC- and ethene-degradation pathways.

†*Novosphingobium aromaticivorans* **F199** (bacteria, 3.8 Mb): Degrades aromatic compounds in soil, including toluene, xylene, naphthalene, and fluorine.

Bacteria Involved in Microbial Arsenic Transformation (~2 to 4 Mb each)

- ‡*Bacillus selenitireducens* **MLS-10**: Haloalkaliphile, respires toxic selenium, argon, sulfur, nitrates.
- ‡*Bacillus selenitireducens* **MLMS-1**: Respires argon, fixes carbon dioxide in apparent absence of RuBisCo.
- ‡*Clostridium sp.* **OhILAs**: Strict anaerobe, spore forming; respires argon, nitrates, sulfur, and selenium.
- ‡*Clostridium sp.* **MLHE-1**: Oxidizes arsenite, potentially can fix carbon dioxide via Form 1 RuBisCo.

‡*Paracoccus denitrificans* (bacteria, 3.66 Mb): Bioremediates various pollutants; involved in carbon sequestration and denitrification; may be closely related to evolutionary precursor of mitochondria.

‡*Polaromonas naphthalenivorans sp.* **strain nov CJ2** (bacteria, ~6 Mb): Degrades PAHs, naphthalene in situ in contaminated environment; bioremediation.

‡*Beta proteobacterium sp.* **JS666** (bacteria, ~4.5 Mb): Only aerobic bacterium reported to grow on *cis*-dichloroethene (cDCE, a common contaminant at DOE sites); yellow, nonmotile; devoid of vacuoles; prefers 20°C but will not grow at 30°C or on vinyl chloride or ethene.

‡*Pseudoalteromonas atlantica* (bacteria, 3.5 Mb): Marine, gram-negative, motile, biofilm forming, secretes degradative enzymes, polysaccharides that bind metals; bioremediation.

†*Pseudomonas fluorescens* **PFO-1** (bacteria, 5.5 Mb): Metabolically diverse; degrades pollutants such as styrene, TNT, and polycyclic aromatic hydrocarbons; useful in applications requiring bacteria release and survival in soil.

*Pseudomonas putida (bacteria, 6.1 Mb): High potential for bioremediation by reducing metal and pollutants.

‡*Pseudomonas putida* **F1** (bacteria, 6.2 Mb): Grows well on a variety of aromatic hydrocarbons including benzene, toluene, ethylbenzene; bioremediation of organics.

‡*Ralstonia eutropha* **JMP-134** (bacteria, 7.24 Mb): Gram negative; degrades chloroaromatic compounds and chemically related pollutants; potential for bioremediation.

†*Ralstonia metallidurans* **CH34** (bacteria, 5 Mb): Contains two "mega" plasmids; resistant to wide variety of heavy metals, which accumulate on the cell surface; strong potential for bioremediation of metals.

Rhodobacter sphaeroides **2.4.1 (bacteria, 4.4 Mb): Metabolically diverse, grows in wide variety of conditions; photosynthetic, providing fundamental insights into light-driven, renewable-energy production; can detoxify metal oxides, useful in bioremediation.

Metal-Reducing *Shewanella* Bacteria: Affect metals including uranium, technetium, and chromium; important in carbon cycling in anaerobic environments; thrive in redox gradient environments; produce energy by generating weak electrical current; display metabolic diversity, potential for bioremediation.

- ‡*Shewanella amazonensis* (4.3 Mb): Isolated from sediments in Amazon River delta; active in reduction of iron, manganese, and sulfur compounds; optimal growth at 35°C, with 1% to 3% salt.

- ‡*Shewanella baltica* **OS195** (est. ~5 Mb): Second *S. baltica* strain, ~69% DNA homology with **OS155.**

- ‡*Shewanella baltica* **OS1155** (3.6 Mb): Isolated from Gotland Deep in central Baltic Sea, predominantly low- and zero-oxygen regions; can use glycogen, cellobiose, and sucrose as sole sources of carbon and energy.

- ‡*Shewanella denitrificans* **OS220** (3.1 Mb): Denitrifies vigorously; isolated from Gotland Deep in central Baltic Sea; uses nitrate, nitrite, and sulfite as electron acceptors.

- ‡*Shewanella frigidimarina* **NCMB400** (2.1 Mb): Isolated from North Sea off coast of Aberdeen; rich in *c*-type cytochromes, with increased cytochrome synthesis during growth in low- to zero-oxygen conditions when iron is present.

- **Shewanella oneidensis* **MR-1** (bacteria, 4.5 Mb): May degrade organic wastes and reduce or sequester a range of toxic metals.

- ‡*Shewanella putrefaciens* **CN-32** (3.22 Mb): Isolated from uranium-bearing subsurface formation in northwestern New Mexico; reduces array of metals and radionuclides, including solid-phase iron and manganese oxides, uranium (VI), technetium (VII), and chromium (VI) with hydrogen, formate, or lactate; has unusual membrane sugars.

- ‡*Shewanella putrefaciens* **ML-S2** (est. ~5 Mb): Hypersaline, pH ~10 environment; isolated from Mono Lake, Calif.

- ‡*Shewanella putrefaciens* **p200** (3.2 Mb): Isolated from corroding oil pipeline in Canada; among most genetically characterized metal-reducing *Shewanellae;* degrades carbon tetrachloride under low- to zero-oxygen conditions.

- ‡*Shewanella putrefaciens* **W3-6-1** (est. ~5 Mb): Marine; forms magnetite at 0°C.

- ‡*Shewanella sp.* **ANA-3** (est. ~5 Mb): Fast-growing, unique As(V) respiratory mechanism.

- ‡*Shewanella sp.* **MR-4** (est. ~5 Mb): Isolated from 5-M depth (oxic) of Black Sea.

- ‡*Shewanella sp.* **MR-7** (est. ~5 Mb): Isolated from 60-M depth (anoxic) of Black Sea.

- ‡*Shewanella sp.* **PV-4** (4 to 4.5 Mb): Most diverse of *Shewanellae;* prefers cold temperatures; produces magnetite at 0°C; reduces cobalt at –4°C.

‡*Xanthobacter autotrophicus* **Py2** (bacteria, 5 Mb): Ubiquitous, nutritionally versatile; degrades chlorinated hydrocarbons, fixes nitrogen, synthesizes biodegradable plastics; bioremediation.

Cellulose Degradation

†*Clostridium thermocellum* ATCC27405 (bacteria, ~5 Mb); Degrades cellulose; potentially useful for conversion of biomass (cellulose) to energy.

****Cytophaga hutchinsonii* ATCC33406 (bacteria, 4 Mb): Very abundant in nature; decomposes cellulose, lacks cellulosomes.

‡*Flavobacterium johnsoniae* (bacteria, 4.8 Mb): Common in soils and freshwaters; degrades chitin and numerous other macromolecules via direct contact; possible use in biomass conversion.

****Microbulbifer degradans* 2-40 (bacteria, 6 Mb): Marine microbe; degrades and recycles insoluble complex polysaccharides via protruding membrane structures called hydrolosomes; potential for conversion of complex biomass to energy.

*Phanerochaete chrysosporium (eukarya, ~30 Mb): "White rot" fungus; aerobic and degrades both celluloses and lignins; can also degrade polyaromatic hydrocarbons.

‡*Postia placenta* **MAS 698** (eukaryote, ~40 Mb): "Brown-rot fungus" degrades cellulose and hemicellulose, secretes oxalic acid, detoxifies certain metals.

‡*Rubrobacter xylanophilus* (actinobacteria, ~2.6 Mb): Thermophile, highly radioresistant; degrades hemicellulose, xylan.

†*Thermobifida fusca* YX (bacteria, 3.6 Mb): Major degrader of organic materials.

‡*Trichoderma reesei* **RUT-C30, ATCC56765** (fungi, 33 Mb): Efficiently degrades cellulose.

Biotechnology and Applied Microbiology

‡*Acidothermus cellulolyticus* **ATCC 43068** (bacteria, ~6 Mb): Thermophile isolated from acid hot spring in Yellowstone; degrades cellulose, source of high-temperature enzymes; biotechnology.

‡*Actinobacillus succinogenes* **130Z (ATCC 55618)** (bacteria, ~2 Mb): From biomass, produces large amounts of succinate; intermediate for production of various chemicals; biotechnology.

*Aquifex aeolicus **VF5** (bacteria extremophile, 1.5 Mb): Potential for identifying high-temperature enzymes.

*Archaeoglobus fulgidus **DSM4304** (archaea extremophile, 2.1 Mb): Potential for identifying high-temperature and high-pressure enzymes; useful in oil industry.

‡*Aspergillus niger* (fungi, ~32 Mb): Common in soils; model for microbial fermentation and bioproduction of organic acids, enzymes, processing and secretion of proteins; biotechnology.

†*Bifidobacterium longum* **DJO10A** (bacteria, 2.1 Mb): Anaerobic, gram-positive prokaryote; key component in promoting healthy human gastrointestinal tract.

†*Brevibacterium linens* **BL2** (bacteria, 3 Mb): Applications in industrial production of vitamins, amino acids for fine chemicals, and cheese; survives high salt, carbohydrate starvation, and extended drying conditions.

*Clostridium acetobutylicum (bacteria, 4.1 Mb): Produces acetone, butanol, and ethanol; useful for industrial enzymology.

†*Ehrlichia chaffeensis* **Sapulpa** (bacteria, 1 Mb): Intracellular, tick-transmitted rickettsia endemic in wild deer populations; causes human monocytic ehrlichiosis.

**Ehrlichia canis* **Jake (bacteria, 1 Mb): Closely related to *E. chaffeensis*; causes tick-borne disease in dogs (canine monocytic ehrlichiosis).

◊*Gemmata obscuriglobus* **UQM 2246** (bacteria, 9 Mb): Planctomycete; widely distributed in freshwater environments; displays a membrane-bound, DNA-containing nucleoid (possibly presaging the nucleus).

*Halobacterium halobium **plasmid** (archaea, 2.3 Mb): Potential for identifying high-salinity enzymes.

‡*Halorhodospira halophila* (bacteria, ~ 4 Mb): Photosynthetic (fixes carbon dioxide), tolerant of high salt concentrations and high pH; biotechnology.

†*Lactobacillus brevis* **ATCC367** (bacteria, 2 Mb): Vital in fermentation of food, feed, and wine.

†*Lactobacillus casei* **ATCC334** (bacteria, 2.5 Mb): Used as starter culture in dairy fermentations and for bulk lactic acid production; found in plant, milk, and sourdough environments as well as human intestinal tract, mouth, and vagina.

†*Lactobacillus delbrueckii* **bulgaricus ATCCBAA365** (bacteria, 2.3 Mb): Classic example of obligate homofermentative pathway for bulk production of lactic acid.

†*Lactobacillus gasseri* **ATCC33323** (bacteria, 1.8 Mb): Naturally inhabits gastrointestinal tract of man and animals. Important for healthy intestinal microflora.

†*Lactococcus lactis cremoris* **SK11** (bacteria, 2.3 Mb): Used extensively in food fermentation, especially cheese.

†*Leuconostoc mesenteroides* (bacteria, 2 Mb): Important role in several industrial and food fermentations.

†*Magnetococcus* **MC-1** (bacteria, 4.5 Mb): Requires limited oxygen; reduces iron; produces magnetite, which has many practical commercial uses.

†*Magnetospirillum magnetotacticum* **MS-1 ATCC31632** (bacteria, 4.5 Mb): Requires limited oxygen; reduces iron, produces magnetite; possible model for biomineralization and evolutionary responses; may serve as a geomagnetic tracer.

†*Oenococcus oeni* **PSU1** (bacteria, 8 Mb): Lactic acid microbe occurring naturally in fruit mashes; used in wineries for fermentation; acid and alcohol tolerant.

†*Pediococcus pentosaceus* **ATCC25745** (bacteria, 2 Mb): Gram positive; facultatively anaerobic lactic acid microbe; acid tolerant; used as starter culture in sausage, cucumber, green bean, and soya milk fermentations; ripening agent of cheeses.

‡*Phytophthera ramorum* **UCD Pr4** (fungi, 24 to 40 Mb): Pathogen of California oak.

‡*Phytophthora sojae* **P6497** (fungi, 62 to 90 Mb): Soybean pathogen.

‡*Psychromonas ingrahamii (*bacteria, ~ Mb): Grows in Arctic sea ice at –12°C; large, rod shaped; doubles every 10 days; will promote studies of low-temperature enzymes.

Pseudomonas syringae B728a (bacteria, 5.6 Mb): Pathogenic to a variety of plant species, severely impacting both food and biomass production.

Pyrobaculum aerophilum (archaea extremophile, 2.2 Mb): May identify high-temperature enzymes.

Pyrococcus furiosus (archaea extremophile, 2.1 Mb): May identify high-temperature enzymes.

†*Streptococcus thermophilus* LMD-9 (bacteria, 1.8 Mb): Used as starter in cheese and yogurt fermentations; thermotolerant; noted for exopolysaccharide production.

Thermotoga maritima M5B8 (bacteria extremophile, 1.8 Mb): Potential for identifying high-temperature, high-pressure enzymes; metabolizes many simple and complex carbohydrates; possible source of renewable carbon and energy.

Microbial Consortia

‡**Acid mine drainage communities (Iron Mountain, Calif.):** Main site is very acidic (pH <0.5) but geochemically well characterized, with six major species (including *F. acidarmanus*); this site, as well as other nearby sites being sampled, is heavily contaminated with metals; insights into "simple" communities and metal bioremediation.

‡**Active methylotroph community:** Dominant members of Lake Washington, Seattle, one-carbon compound metabolizing bacterial population; carbon cycling, bioremediation.

‡**Anaerobic bioreactor granule samples** (some 200 BACs from Hanford PNNL site): Potential for methane and hydrogen production; exhibit archetypical systems for metabolic-interaction studies among microbes; relatively simple complex microcosm of organic matter's methanogenic degradation in environment.

‡**Boiling thermal pool** (Yellowstone National Park): Characterization of complete communities making up extreme environments; relevance for bioremediation, carbon management.

Chlorochromatium aggregatum (green sulfur bacteria, plus epibiont, 2 to 10 Mb): Two-component culturable consortium; utilizes hydrogen, sulfur, as electron donors for carbon fixation.

‡**Environmental** *Geobacteraceae*: Samples from former uranium mining sites and marine and freshwater sediments.

‡**Microbial population from The Cedars (Calif.)**: Site with pH ~12, low-salt, high-metal concentrations; limited population diversity, high-carbonate deposition; carbon processing.

‡**Obsidian hot spring (Yellowstone)**: Community genomic sampling of microbes from 74°C pool; carbon management, bioremediation.

‡**PAH-degrading mycobacteria:** Mycobacteria from three sites where pollutants (polycyclic aromatic hydrocarbons) are degraded; bioremediation.

‡**Picoplankton BACs** [Hawaii Ocean Time Series (HOTS) site]: Oceanic picoplankton affecting global carbon cycle, energy production, and geochemical and elemental cycling.

‡**Sargasso Sea community**: Catalogue of marine microbial diversity in a low-nutrient environment.

‡**Uncultured microbes in soil environments:** Being sequenced by JGI-Diversa collaboration.

‡**Viruses infecting globally distributed microalgae**: Pathogens of phytoplankton; may regulate phytoplankton populations and therefore carbon-dioxide fixation in oceans.

Technology Development, Pilot Projects

Borrelia burgdorferi B31 (bacteria, 1.4 Mb): Human pathogen that causes Lyme disease; one linear chromosome (915 kb) supported by DOE; entire genome published by TIGR.

Brucella melitensis 16M (bacteria, 3.3 Mb): Pathogenic to animals and humans; biothreat agent.

†*Enterococcus faecium* (bacteria, 2.8 Mb): Pathogenic to many organisms, including humans; tolerates relatively high salt and acid concentrations.

†*Exiguobacterium* **255-15** (bacteria, 3 to 4 Mb) (NASA): Isolated from 2- to 3-million-year-old Siberian permafrost sediment; grows well at –2.5°C; associated with infections in humans.

***Haemophilus somnus* **129PT** (bacteria, ~2.5 Mb): Vaccine strain of *H. somnus,* which causes systemic diseases in cattle; lacks surface-binding protein for immunoglobulins.

Mycoplasma genitalium* **G-37 (bacteria, 580 kb): Human pathogen; serves as model for minimal set of genes sufficient for free living.

Psychrobacter **273-4 (bacteria, 2.5 Mb) (NASA): Isolated from 20,000- to 40,000-year-old Siberian permafrost sediment; grows well at –2.5°C; radiation resistant.

†*Streptococcus suis* **1591** (bacteria, 2.2 Mb): Pathogenic to pigs and humans; causes meningitis, especially in tropical regions.

†*Xylella fastidiosa* **Dixon** (almond) (bacteria, 2.6 Mb): Pathogenic to economically important plants such as orange and almond trees.

†*Xylella fastidiosa* Ann1 (oleander) (bacteria, 2.6 Mb): Pathogenic to plants, particularly oleanders**.**

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†Draft sequence by the DOE Joint Genome Institute (JGI).

‡New microbes being sequenced by JGI.
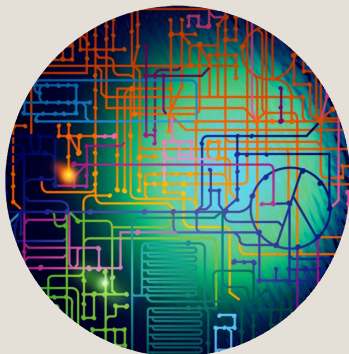
◊Sequenced by the The Institute for Genomic Research.

*Completed and published (see www.genomesonline.org).

**Completed, not published (as of July 15, 2005).

Appendix H. Programs Complementary to GTL Research

Programs Complementary to GTL Research

Introduction

This section details some governmental research complementary to GTL. Because of the centrality of genomics to the study of all life, GTL can benefit other life sciences programs, and GTL progress can be accelerated by synergies attained through data and resources from others. Although vastly different in focus, scope, and scale of research, the projects listed here are united by their underlying study of DNA and its corresponding technologies. Breakthroughs in one can lead to innovations in another.

DOE already cooperates with other federal agencies on numerous complementary programs. BER coordinates its GTL microbial research with other federal agencies through the National Science and Technology Council's Interagency Working Group on Microbial Genomics. The initial report of this group can be found at www.ostp.gov/html/microbial/start.htm. BER also participates in GTL-related interagency research solicitations that provide additional opportunities to coordinate complementary research programs across agencies. Examples can be viewed on the web (www.nsf.gov/pubs/2004/nsf04607/nsf04607.pdf). Coordination of GTL with those programs may include shared technology development, computing and information tools and standards, databases, and use of resources and facilities.

The information below was taken from web resources and may be incomplete. URLs are provided for further information and exploration. Updates to the online version of this list are encouraged (contact: millsmd@ornl.gov).

DOE Office of Science (SC) Programs

SC Office of Biological and Environmental Research (BER)

www.sc.doe.gov/ober/ober_top.html

BER supports basic biological and environmental research relevant to DOE missions. Biological discoveries are needed to clean and protect the environment, offer new energy alternatives, and understand the impacts of energy use on climate change. BER consists of four divisions: Climate Change Research Division, Environmental Remediation Sciences Division, Life Sciences Division, and Medical Sciences Division. GTL is a Life Sciences Division program jointly supported by BER and the Advanced Scientific Computing Research program in DOE's Office of Science. GTL is complementary to other BER research programs.

Environmental Remediation Sciences Division (ERSD)

www.sc.doe.gov/ober/ersd_top.html

See sidebar, Environmental Remediation Sciences Division Activities Complementary to GTL, p. 223.

- **Natural and Accelerated Bioremediation Research (NABIR) (www.lbl.gov/nabir/)**
  NABIR concentrates on field- and laboratory-based studies of natural microbial communities and their interactions with heavy-metal and radionuclide contaminants. NABIR focuses on understanding and enhancing natural microbial activities that remove contaminants from groundwater and transform them into chemical forms that pose less risk to humans and the environment. Interactions between GTL and NABIR will be important for providing the scientific foundation to develop more effective microbe-based remediation strategies.

Climate Change Research Division (CCRD)

www.sc.doe.gov/ober/ccrd_top.html

CCRD fosters research on understanding the basic chemical, physical, and biological processes of the earth's atmosphere, land, and oceans and how these processes may be affected by energy production and use, primarily the emission of carbon dioxide from fossil-fuel combustion. CCRD modeling aims to quantify sources and sinks of greenhouse gases, especially carbon dioxide; accurately predict and assess the potential consequences of climate change; and evaluate the benefits and costs of alternative response options. GTL-related programs include:

- **Program for Ecosystem Research (PER; http://per.ornl.gov)**
  PER supports research that aims to understand and predict impacts of energy-related environmental changes on the processes and component organisms of terrestrial ecosystems.

- **Ocean Science (OS; www.sc.doe.gov/ober/ccrd/oceans.html)**
  OS focuses on understanding ocean-atmosphere carbon exchange and evaluating ocean-based carbon-sequestration strategies.

- **Terrestrial Carbon Processes (TCP; www.sc.doe.gov/ober/ccrd/tcp.html)**
  TCP's goal is to understand terrestrial carbon cycling and evaluate the potential of long-term carbon sequestration in terrestrial environments.

- **Carbon Sequestration Research (http://cdiac2.esd.ornl.gov)**
  BER's carbon-sequestration research program includes both CCRD and Life Sciences Division research that could lead to strategies to improve the use of trees within the genus *Populus* (poplar) or other trees for long-term sequestration of meaningful amounts of atmospheric carbon in terrestrial ecosystems. Research also emphasizes strategies to use the poplar and microbial genomic sequences to enhance partitioning of carbon into quantitatively important recalcitrant components of trees or soil organic matter that could lead to enhanced carbon sequestration.

SC Office of Basic Energy Sciences (BES)

www.sc.doe.gov/bes/bes.html

BES supports research that provides a scientific foundation for developing new and improved energy technologies and for understanding and mitigating the environmental impacts of energy use. GTL-related programs:

- **Energy Biosciences (EB) (www.sc.doe.gov/bes/eb/ebhome.html)**
  Energy Biosciences is part of the Chemical Sciences, Geosciences, and Biosciences Division

at BES. This program supports basic research to understand the processes of plants and microorganisms that could be used to develop future energy-related biotechnologies. EB emphasizes understanding biological principles rather than optimizing biological processes. Research topics include mechanistic studies of photosynthetic solar-energy capture; mechanisms and regulation of carbon fixation and carbon or energy storage; regulation of plant growth and development; and examination of metabolic pathways relevant to the production of useful chemicals and fuels.

DOE Office of Fossil Energy (FE) Programs

www.fossil.energy.gov

FE supports research and development that address technological challenges of the nation's energy and environmental initiatives. GTL scientific insights could spur R&D in the following FE programs:

Bioprocessing and Biotechnology Research

www.fossil.energy.gov/programs/powersystems/ advresearch/advresearch-bioprocessing.html

Bioprocessing and biotechnology activities are part of FE's Advanced Research Programs for Coal and Natural Gas Power Systems. Research is directed toward using biology to develop applications for generating clean, efficient electric power and producing clean fuels from coal. Some research topics include biomodification of coal to reduce mercury emissions; bioremediation of waste streams from power plants; use of microbial toxins to reduce fouling of cooling water intake and discharge systems; investigation of marine microalgae for carbon dioxide biofixation potential; and use of biological systems to produce hydrogen from coal and coal-waste products.

Carbon Sequestration

www.fossil.energy.gov/programs/sequestration/

Carbon Sequestration Core R&D is developing technologies that can capture and permanently store greenhouse gases. GTL will be a scientific foundation for technology development in the following areas:

- **Ocean Sequestration Research (www.fossil. energy.gov/programs/sequestration/ocean/)**
- **Carbon Capture Research (www.fossil.energy. gov/programs/sequestration/capture/)**
- **Terrestrial Sequestration Research (www.fossil. energy.gov/programs/sequestration/terrestrial/)**
- **Novel Carbon Sequestration Concepts (www. fossil.energy.gov/programs/sequestration/ novelconcepts/)**

DOE Office of Energy Efficiency and Renewable Energy (EERE)

www.eere.energy.gov
See sidebar, DOE Activities Complementary to GTL Research, p. 203.

Biomass Program

www.eere.energy.gov/biomass

The Biomass Program supports the research and development of advanced technologies that transform biomass into biofuels, biopower, and high-value bioproducts. GTL will play an important role in providing a better understanding of current microbial processes and discovering new microbial capabilities relevant to the Sugar Platform and Products research areas.

Hydrogen Production

www.eere.energy.gov/hydrogenandfuelcells/ hydrogen_production.html

Hydrogen Production, within EERE's Hydrogen, Fuel Cells, and Infrastructure Technologies Program, aims to research and develop low-cost, highly efficient hydrogen-production technologies from diverse domestic sources. GTL science could benefit two Hydrogen Production research areas: (1) Biological and Biomass-Based Production, for improving efficiencies of anaerobic fermentation systems; and (2) Photolytic Hydrogen, for photobiological production of hydrogen by green algae.

National Science Foundation (NSF) Programs

www.nsf.gov

- **Biochemical Engineering and Biotechnology (BEB; www.nsf.gov/funding/pgm_summ.jsp?pims_id=13368)**
  BEB supports basic engineering research that aims to understand and achieve quantitative assessments of biomolecular processes (in vivo, in vitro, and ex vivo) that can be used to develop practical biotechnological applications. BEB projects cover a wide range of biotechnological research areas: Fermentation, enzyme studies, recombinant DNA technology, bioprocess control and optimization, metabolic-pathway engineering, cell culturing, tissue engineering, food processing, and relevant information-technology development.

- **Biocomplexity in the Environment (BE): Integrated Research and Education in Environmental Systems (www.nsf.gov/funding/pgm_summ.jsp?pims_id=5532)**
  BE promotes new approaches to studying the dynamic nature of biological systems and their impact on physical and chemical processes of the environment. All environments (including natural ecosystems and agricultural and urban lands) and organisms from microbes to humans fall within the BE framework.

- **Biological Databases and Informatics (BD&I) Program (www.nsf.gov/funding/pgm_summ.jsp?pims_id=5444&org=BIO)**
  BD&I supports new approaches to the management, analysis, and dissemination of biological knowledge that will benefit the scientific community and the general public. BD&I will explore theoretical research on data structures; develop new types of databases with architectures better suited to the complexity of biology; and design easy-to-use interfaces and tools for data analysis and use.

- **Biological Oceanography Program (www.nsf.gov/funding/pgm_summ.jsp?pims_id=11696)**
  This program supports the study of marine organisms and their interactions with each other and with elements in their environment. Subfields in this program include ecosystem and biogeochemical processes; community and population ecology; behavioral, reproductive, and life-history ecology; physiological and chemical ecology; and evolutionary ecology.

- **Biomolecular Systems Cluster (www.nsf.gov/funding/pgm_summ.jsp?pims_id=12771)**
  The Biomolecular Systems Cluster supports research to develop technologies and computational and experimental approaches for the study of biomolecular complexes, mechanistic studies of biomolecular activity, and characterization of higher-order biochemical processes by which organisms acquire and use energy.

- **Catalysis and Biocatalysis (www.nsf.gov/funding/pgm_summ.jsp?pims_id=13360)**
  This program fosters fundamental and applied research in the following areas: Kinetics and mechanisms of chemical reactions important to the production of fuels, chemicals, and specialized materials; characterization of chemical reactions at or near solid surfaces; electrocatalytic processes with industrial or commercial importance; green chemistry or use of biorenewable resources; kinetic modeling and theory of biocatalysis; reactive deposition and processing for thin-film materials; and the use of chemical reaction or transport knowledge to design or control chemical reactors.

- **Cellular Systems Cluster (www.nsf.gov/funding/pgm_summ.jsp?pims_id=12772)**
  This program focuses on the structure, function, and regulation of plant, animal, and microbial cells and their interactions with the environment and with one another. Microbial Observatories (MO) and Microbial Interactions and Processes (MIP) are included in this cluster. MO's goal is to establish a network of sites for observing and understanding microbial diversity in different habitats over long time periods. MIP supports shorter-term, smaller-scale microbial-diversity research that is not site based.

- **Ecological Biology Cluster (EBC; www.nsf.gov/funding/pgm_summ.jsp?pims_id=12823)**
  EBC supports experimental, observational, theoretical, and modeling studies on the structure and function of complex biological associations in natural and managed ecological systems. This program includes the National Center for Ecological Analysis and Synthesis, which analyzes ecological information, tests ecological theories,

examines sociological issues relevant to ecology, supports education and outreach, and informs science policy and management decisions.

- **Ecosystem Science Cluster (ESC) (www.nsf. gov/funding/pgm_summ.jsp?pims_id=12822)**
  ESC supports investigations of terrestrial, aquatic, and wetland ecosystems. Projects that use new or existing quantitative or conceptual models to synthesize and integrate knowledge are encouraged. ESC research includes Ecosystem Studies, which concentrate on whole-system processes and relationships in ecosystems, spanning a wide range of spatial and temporal scales; and Long-Term Ecological Research (LTER), which involves studies at a network of more than a dozen field sites.

- **Environmental Engineering and Technology (www.nsf.gov/funding/pgm_summ.jsp?pims_ id=13370)**
  The Environmental Engineering and Technology program supports research on the use of innovative biological, chemical, and physical processes to remediate polluted land, water, and air resources and the development of principles for pollution avoidance.

- **Frontiers in Integrative Biological Research (FIBR; www.nsf.gov/funding/pgm_summ. jsp?pims_id=6188)**
  FIBR supports large interdisciplinary research to seek answers to important, understudied, nondisease-related biological questions. By encouraging research that creatively applies science concepts and strategies with research tools that span a broad range of disciplinary and intellectual boundaries, FIBR supports collaborative projects that may not fit readily into existing programs.

- **Genes and Genome Systems Cluster (GGSC; www.nsf.gov/funding/pgm_summ.jsp?pims_ id=12780)**
  GGSC supports research on the genetic mechanisms and genome organization, expression, and regulation of all organisms (prokaryote, eukaryote, phage, and virus).

- **Geobiology and Environmental Geochemistry (GEG; www.nsf.gov/funding/pgm_summ. jsp?pims_id=13410)**
  GEG fosters research on (1) biological factors in geophysical and geochemical processes; (2) rates and mechanisms of inorganic and organic geo-

chemical processes; (3) natural and anthropogenic impacts on biogeochemical cycles; (4) geochemical phenomena, widely ranging spatially from planetary and regional to mineral surface and supramolecular; and (5) development of tools, methods, and models for low-temperature geochemistry and geobiological research. GEG encourages the use of new bioanalytical tools to study terrestrial environments.

- **Instrument Development for Biological Research (IDBR; www.nsf.gov/funding/pgm_ summ.jsp?pims_id=9187)**
  IDBR supports research that will develop new and improved instrumentation, software for operating instrumentation, and data-analysis methods to advance the study of biological systems at any level. Proof-of-concept development for entirely novel instrumentation is encouraged.

- **Mathematical Biology (www.nsf.gov/funding/ pgm_summ.jsp?pims_id=5690)**
  This program supports research on mathematics important to the biological sciences that does not involve statistics or probability. NSF programs in statistics and probability may include research specific to other areas of science and engineering.

- **Research in Biogeosciences 2005 (BioGeo; www.nsf.gov/funding/pgm_summ.jsp?pims_ id=5508)**
  BioGeo fosters research that explores the interactions of microbes with earth materials (including minerals, rocks, hydrates, soils, and dust). Research should elucidate past and present roles of microbial communities in earth processes, microbial strategies for deriving energy and nutrients, and how these strategies alter earth materials and the environment.

National Institutes of Health (NIH)

www.nih.gov

- **Bioinformatics and Computational Biology (BCB) Roadmap Initiatives (www.nihroadmap. nih.gov/bioinformatics/)**
  Four National Centers for Biomedical Computing (NCBC) established in 2004 are the key programmatic initiatives of the NIH BCB Roadmap. These centers aim to develop and implement the core of a universal computing infrastructure urgently needed to speed progress in biomedical research.

The centers will create innovative software programs and other tools that will enable the biomedical community to integrate, analyze, model, simulate, and share data on human health and disease.

- **Biomedical Information Science and Technology Initiative (BISTI; www.bisti.nih.gov)**
Launched in 2000, BISTI's goal is to make optimal use of computer science and technology to address problems in biology and medicine. A BISTI consortium serves as the focus of biomedical computing issues at NIH and facilitates implementation of BISTI recommendations. The consortium is composed of representatives from NIH centers and institutes and other federal agencies concerned with bioinformatics and computational applications. The consortium's mission is to make optimal use of computer science and technology to address problems in biology and medicine by fostering new basic understandings, collaborations, and initiatives between the disciplines of computational and biomedical sciences.

- **Complex Biological Systems Initiative (www.nigms.nih.gov/funding/complex_summary.html)**
This National Institute for General Medical Sciences (NIGMS) program promotes quantitative, interdisciplinary approaches to problems of biomedical significance, particularly those that involve the complex, interactive behavior of many components. Three classes of initiatives are supported: Interdisciplinary research to attract investigators trained in mathematically based disciplines to the study of biomedical problems; mechanisms to train biomedical scientists in quantitative approaches and to acquaint nonbiologists with biological problems; and interdisciplinary training for scientists at the pre- and postdoctoral levels.

- **National Institute of Allergy and Infectious Diseases (NIAID) Microbial Sequencing Centers (www.niaid.nih.gov/dmid/genomes/mscs/overview.htm)**
NIAID's Microbial Sequencing Centers (MSCs) sequence microorganisms and invertebrate vectors of disease that are considered agents of bioterrorism or responsible for emerging and reemerging diseases.

- **National Technology Centers for Networks and Pathways (www.nihroadmap.nih.gov/buildingblocks/)**
As part of the NIH Roadmap for Medical Research, two National Technology Centers for Networks and Pathways were established and several more are planned. The primary goal of these centers is to develop new technologies to study the dynamics of molecular interactions within cells. Such capabilities are crucial for expanding the identification of biological pathways and developing treatments for diseases involving such pathways. The awards are administered by the National Center for Research Resources, an NIH component that supports primary research to create and develop critical resources, models, and technologies.

- **Protein Structure Initiative (PSI; www.nigms.nih.gov/psi/)**
PSI is a 10-year project funded largely by NIGMS to determine the three-dimensional (3D) shapes of a wide range of proteins. These structures are expected to shed light on protein function in many life processes and could lead to the development of new medicines. The long-range goal of PSI is to make 3D atomic-level structures of most proteins easily obtainable from knowledge of their corresponding DNA sequences. The first half of this project—a pilot phase that started in 2000—has centered on developing new tools and processes that enable researchers to determine quickly, cheaply, and reliably the shapes of many proteins found in nature. PSI projects are in federal, university, and industry laboratories.

- **Systems Biology Initiative (SBI; www.nigms.nih.gov/funding/systems.html)**
This NIGMS program supports systems biology research for areas central to its mission of supporting basic biomedical research and developing new computational approaches to biomedical complexity. SBI's goal is to establish national centers for systems biology that develop pioneering research, training, and outreach programs focused on quantitative, systems-level analysis of biomedically important phenomena within the NIGMS mission. High priority is given to projects that integrate multi-investigator, multidisciplinary approaches with a high degree of interplay between computational and experimental approaches. Innovation is critical for design of

both research projects and infrastructure with the mission of serving communities beyond participating investigators, institutions, and collaborators.

Department of Agriculture (USDA): Cooperative State Research, Education, and Extension Service (CSREES)

www.csrees.usda.gov/about/about.html

- **Agricultural Plant Biochemistry (www.csrees. usda.gov/fo/fundview.cfm?fonum=1115)** The aim is to characterize the biochemical processes and pathways in the cell and the genes and proteins involved in them.

- **Biobased Products and Bioenergy Production Research Program (www.csrees.usda.gov/fo/ fundview.cfm?fonum=1073)** This program supports the tripling of U.S. use of biobased products by 2010 and more research on biomass processing and conversion.

- **Biology of Plant-Microbe Associations (www. csrees.usda.gov/fo/fundview.cfm?fonum=1120)** This program supports fundamental and mission-linked research on interactions among plants and their associated microbes, including fungi and fungal-like microbes, bacteria, viruses, viroids, and mycoplasma-like organisms.

Department of Defense (DoD): Defense Advanced Research Projects Agency (DARPA)

www.darpa.mil/

- **BioCOMP Program (www.darpa.mil/ipto/ programs/biocomp/)** BioCOMP develops a computational framework to enable construction of sophisticated models of intracellular processes that can be used to predict and control the behavior of living cells. In addition, BioCOMP generates new computational paradigms and engineering applications that use biomolecules as information-processing, sensing, or structural components.

- **Biological Input/Output Systems Program (BIOS; www.darpa.mil/dso/thrust/biosci/ bios.htm)**

BIOS will develop robust technologies for designing DNA-encoded "plug-and-play" modules that will enable use of organisms (e.g., plants, microbes, lower eukaryotes) as remote sentinels for reporting the presence of chemical or biological analytes.

- **BioSPICE (https://users.biospice.org/)** BioSPICE is a set of open-source software tools that can be used by biological researchers to model the processes of living cells. It is being used to study several different biological systems: Bacterial systems to investigate such phenomena as sporulation, chemotaxis, and bacterial metabolism; viral systems to understand Lambda-phage, HIV-1, and host-pathogen interactions; eukaryotic systems to model cell cycles, cellular differentiation, immunological function, and cell signaling; and synthetic systems such as minimal cells. Some mathematical models developed using BioSPICE include pathway and interaction networks, models of gene expression, and probabilistic modeling for sequence analysis. BioSPICE is the product of a collaboration involving DARPA, NSF, academic institutions, and other federal agencies.

- **Defense Against Chemical, Biological, Radiological Weapons Program (DACBRW; www.darpa.mil/ spo/programs/cbr.htm)** This program seeks to protect building inhabitants from an indoor release of chemical or biological agents and from radiological attack. DACBRW includes research into sensing of bioaerosols and triangulation identification for genetic evaluation of risks (biosensors).

Other Programs

- **HUPO Proteomics Standards Initiative (http://psidev.sourceforge.net/)**

- **National Aeronautics and Space Administration (NASA) Ames Genome Research Facility (www.phenomorph.arc.nasa.gov)** Research at the facility includes the Nanopore Project and functional genomics.

- **NASA Fundamental Space Biology Program (FSB; www.fundamentalbiology.arc.nasa.gov)** FSB has increased emphasis on cell and molecular biology and developmental biology, as well as on the growing disciplines of evolutionary biology and genomics. Part of the program's purpose is to

increase visibility and funding for molecular biology research.

- **National Institute of Standards and Technology (NIST) Biotechnology Division (www.cstl.nist.gov/biotech/)**
The mission of the NIST Biotechnology program is to advance the commercialization of biotechnology by developing the scientific and engineering technical base, reliable measurements, standards, data, and models to enable U.S. industry to quickly and economically produce biochemical products with appropriate quality control. The division is organized into four groups: DNA Technologies; Bioprocess Measurements; Structural Biology; and Cell and Tissue Measurements.

- **National Oceanic and Atmospheric Administration (NOAA) Office of Global Programs (OGP) Climate and Global Change Program (www.ogp.noaa.gov)**
OGP assists NOAA by sponsoring scientific research aimed at understanding climate variability and predictability. Through studies in these areas, researchers coordinate activities that jointly contribute to improved predictions and assessments of climate change over a continuum of time scales from season to season, year to year, and throughout a decade and beyond.

- **United Nations Educational, Scientific and Cultural Organization (UNESCO) Microbial Resources Centres (MIRCEN; www.portal. unesco.org/sc_nat/ev.php?URLID=2491& URL_DO=DO_TOPIC)**
MIRCEN comprises 34 academic and research institutes in developed and developing countries involved in a global collaborative effort to harness microbiological research and biotechnological applications for the benefit of humankind. The global MIRCEN network's research and training activities aim to (1) provide a global infrastructure incorporating national, regional, and international cooperating laboratories geared to the management, distribution, and use of the microbial gene pool; (2) reinforce use of the rhizobial gene pool in developing countries with an agrarian base; (3) foster development of new inexpensive technologies native to specific regions; (4) promote economic and environmental applications of microbiology; and (5) serve as the network's focal centers for training.

- **U.S. Geological Survey (USGS) Biological Resource Division (http://biology.usgs.gov)**
The USGS Biological Resource Division works with others to provide the scientific understanding and technologies needed to support the sound management and conservation of U.S. biological resources. USGS is committed to data and information sharing and has established the National Biological Information Infrastructure, a network of distributed databases and information sources on biological resources.

Interagency Cooperation

For more information on the following programs, see the web site for current and archived solicitations after each entry.

- **Environmental Molecular Science Institutes (EMSI; www.nsf.gov/funding/pgm_summ. jsp?pims_id=5294)**
EMSI is a partnership between NSF and DOE for collaborative, interdisciplinary research to attain a fundamental, molecular-level understanding of natural and anthropogenic processes in the environment. An institute typically supports a group of six or more investigators from academic institutions, nonprofit organizations, industry, or national laboratories with complementary research interests.

- **Interagency Microbial Genome Sequencing Program (USDA with NSF) (www.csrees.usda. gov/fo/fundview.cfm?fonum=1108)**
This program supports high-throughput sequencing of the genomes of a wide range of microorganisms (including viruses, bacteria, archaea, fungi, oomycetes, protists, and agriculturally important nematodes).

- **Interagency Modeling and Analysis Group (No web site available; see last call for proposals at www.nsf.gov/pubs/2004/nsf04607/nsf04607.pdf)**
This group is a collaboration among NSF, NIH, NASA, and DOE to encourage the integrative systems engineering approach to multiscale modeling, combining theoretical and computational approaches. This collaboration aims to formulate and validate novel computational and statistical methods and relationships for spanning multiple scales, broaden and expand currently established levels of modeling expertise and

multiscale modeling activities, and produce models of practical utility to the community at large. The group also plans to form a consortium of investigators for information exchange on critical issues including model intraoperability and evaluation and open-source software sharing.

- **Joint DMS/BIO/NIGMS Initiative to Support Research in the Area of Mathematical Biology (www.nsf.gov/funding/pgm_summ.jsp?pims_id=5300)**
  This initiative supports research on mathematical and statistical problems related to the biological sciences, including conferences, educational research experiences, postdoctoral research fellowships, and acquisition of computational equipment. It involves the NSF Directorate for Mathematical and Physical Sciences' Division of Mathematical Sciences, the NSF Directorate for Biological Sciences, and NIH NGMIS.

- **Mathematical Sciences: Innovations at the Interface of the Sciences and Engineering (www.nsf.gov/funding/pgm_summ.jsp?pims_id=9673)**
  The Mathematical Sciences Priority Area (MSPA) cuts across multiple NSF directorates and supports the integration of mathematical and statistical research with a wide range of science disciplines. Initially, MPSA interdisciplinary projects are focusing on mathematical challenges associated with handling large data sets, managing and modeling uncertainty, and modeling complex nonlinear systems.

- **Metabolic Engineering Working Group (MEWG; www.metabolicengineering.gov)**
  MEWG is a collaboration among eight agencies and departments to provide research funding and agency in-kind support (e.g., equipment, lab space, and materials) to gain a better understanding of metabolic pathways and metabolic engineering in living systems. Conceptual and technical approaches necessary to understand the integration and control of genetic, catalytic, and transport processes will be valuable as fundamental research and also will provide the underpinning for many applications of immediate value. Participating institutions include the Department of Commerce, Environmental Protection Agency, DoD, DOE, NASA, NIH, NIGMS, NSF, and USDA.

- **Microbial Genome Sequencing Program (www.nsf.gov/funding/pgm_summ.jsp?pims_id=5688)**
  This program is a collaboration between NSF and USDA CSREES. It supports high-throughput genome sequencing of microorganisms (e.g., viruses, bacteria, archaea, fungi, oomycetes, protists, and agriculturally important nematodes) that have fundamental biological interest or relevance to such national priorities as productivity and sustainability of agricultural and natural resources and food-supply safety and quality.

- **Nanoscale Science and Engineering (www.nsf.gov/funding/pgm_summ.jsp?pims_id=7169)**
  This program brings together engineering and various scientific disciplines to advance the emerging field of nanotechnology. Research areas include nanoscale investigations of biosystems; environmental processes; nanostructures and devices; multiscale multiphenomena theory, modeling, and simulation; and manufacturing processes; as well as research on societal and educational implications of nanoscale research and technology development.

- **National Science and Technology Council Interagency Working Group on Microbial Genomics (www.ostp.gov/html/microbial/aboutus.htm)**
  This working group consists of representatives from all federal agencies that support or conduct microbial research.