JGI JOINT GENOME INSTITUTE
A DOE OFFICE OF SCIENCE USER FACILITY

Approved Proposals FY12

Following are the approved user proposals for fiscal year 2012.

Community Science Program (CSP) Plans

Proposer	Affiliation	Project Description
Acinas, Silvia	ICM-CSIC, Spain	Microbial metagenomics and transcriptomics from a global deep-ocean expedition
Andresson, Olafur	University of Iceland	Sequencing of the three cultured partners of the lichen *Lobaria pulmonaria* and the sequencing of the transcriptomes from the natural tripartite lichen under selected and controlled conditions.
Banfield, Jill	University of California, Berkeley	Terabase sequencing for comprehensive genome reconstruction to assess metabolic potential for environmental bioremediation
Brodie, Eoin	DOE JGI	Mediterranean Grassland Soil Metagenome (MGSM): Enabling a systems view of soil carbon and nitrogen biogeochemistry under a changing climate.
Brutnell, Thomas	Boyce Thompson Institute for Plant Research	Development of sequence-based community tools for *Setaria viridis*-a model genetic system for C4 grasses

Bucking, Heike	South Dakota State University	Exploring the transcriptome of perennial grasses in association with beneficial microorganisms to increase biomass production and environmental sustainability of bioenergy production
Cary, Stephen	University of Delaware	Understanding terrestrial microbial biocomplexity in an Antarctic desert landscape: resolving universal drivers of community structure and function in a trophically simple system
Crouch, Jo Anne	USDA-ARS	Genomic signatures of pathogenicity and endophytism in five species of grass-associated *Colletotrichum* impacting the health and production of bioenergy feedstocks, agriculture and the environment
Dangl, Jeff	University of North Carolina at Chapel Hill	Plant associated metagenomes–Microbial community diversity and host control of community assembly across model and emerging plant ecological genomics systems.
DeAngelis, Kristen	University of Massachusetts	Microbial ecology and genomics of carbon-storing bacteria in rhizosphere soils
Dubilier, Nicole & Kleiner, Manuel	Max Planck Institute for Marine Microbiology, Germany	Understanding novel pathways for energy and carbon use in bacterial symbionts of gutless marine worms
Emerson, David	Bigelow Laboratory for Ocean Sciences	Single cell genome sequencing of biomineralizing bacteria
Fierer, Noah	University of Colorado	Cross-site metagenomic analyses to assess the impacts of experimental nitrogen additions on belowground carbon dynamics

Fredrickson, Jim	Pacific Northwest National Laboratory	Microbial Interactions in Extremophilic Mat Communities
Gilbert, Jack	Argonne National Laboratory	Creating a successional model for carbon remediation in the Gulf of Mexico
Gross, Stephen	DOE JGI	The Agave Microbiome: Exploring the role of microbial communities in plant adaptations to desert environments
Hazen, Samuel	University of Massachusetts	Creating a multi-functional library of grass transcription factors for the energy crop model system *Brachypodium distachyon*
Hess, Matthias	Washington State University	Expression profile of biomass-degrading fungi inhabiting the cow rumen
Kelly, William	AgResearch, New Zealand	The Hungate 1000. A catalogue of reference genomes from the rumen microbiome.
Kerfeld, Cheryl	DOE JGI	Enhancing Bacterial Carbon Capture and Sequestration: Synthesis of Building Blocks for the Carboxysome, A Metabolic Module for CO2 Fixation
Kyrpides, Nikos	DOE JGI	Genomic Encyclopedia of Type Strains, Phase I: the one thousand microbial genomes (KMG) project
Laplaze, Laurent	Institut de Recherche pour le Developpement (IRD), France	Transcriptome Analysis of Salt Tolerance in *Casuarina* trees
Martin, Francis	INRA, France	Metatranscriptomics of Soil Forest Ecosystems

McKay, Robert	Bowling Green State University	Metagenomics and metatranscriptomics of the Lake Erie ‘dead zone’: a seasonal source of greenhouse gases
McMahon, Katherine	University of Wisconsin, Madison	Dynamics of microbial carbon processing pathways across a decade in a freshwater eutrophic lake revealed through metagenomic sequencing
Mock, Thomas	University of East Anglia, UK	Sea of Change: Eukaryotic Phytoplankton Communities in the Arctic Ocean
Mohn, William	University of British Columbia, Canada	Metagenomic and metatranscriptomic analysis of forest soil communities across North America
Moran, Mary Ann	University of Georgia	The Genetic Basis for Heterotrophic Carbon Processing in the Sea
Murray, Alison	Desert Research Institute	Lake Vida brine microbial community (LVBMCo) genomics and transcriptomics – a window into diversity, adaptation and processes in extreme cold
Gerard Muyzer	Delft University of Technology	Genome sequencing of 100 strains of the haloalkaliphilic chemolithoautotrophic sulfur-oxidizing bacterium *Thioalkalivibrio*
Nealson, Kenneth	University of Southern California	Life at the edge: community cooperation and success in a very extreme (ultrabasic and ultra-reducing) environment
Ohm, Robin	DOE JGI	Towards functional genomics: development of *Schizophyllum commune* as a model system to study lignocellulose degradation
Pester, Michael	University of Vienna, Austria	Targeted metagenomics and metatranscriptomics of a sulfate-reducing rare biosphere member and potentially novel sulfate reducers that impact methane emission from peatlands

Powell, Amy	Sandia National Laboratories	A Phylogenomic Framework to Investigate Fungal Thermophily
Pukkila, Patricia	University of North Carolina at Chapel Hill	Functional genomics in the model mushroom *Coprinopsis cinerea*
Rodrigues, Jorge	University of Texas at Arlington	Profiling metagenomic consequences of Amazon deforestation at different spatial scales
Schadt, Christopher	Oak Ridge National Laboratory	Defining the *Populus* Microbiome: Role of Genotype by Environment Interactions in Shaping the Rhizosphere Microbiome of *Populus trichocarpa*
Schrenk, Matthew	East Carolina University	Metagenome-enabled Investigations of Carbon and Hydrogen Fluxes within the Serpentinite-hosted Subsurface Biosphere
Spatafora, Joseph	Oregon State University	1000 Fungal Genomes
Stepanauskas, Ramunas	Bigelow Laboratory for Ocean Sciences	Dark ocean microbial single cell genomics
Wing, Rod	University of Arizona	Empowering functional plant genomics with genomes and transcriptomes of the top 20 *Brassicales*