

Approved Proposals FY14

Following are the approved user proposals for fiscal year 2014 including CSP and [JGI-EMSL “Facilities Integrating Collaborations for User Science” \(FICUS\) initiative projects.](#)

Community Science Program (CSP) Plans

Proposer	Affiliation	Project Description
Banfield, Jillian	UC Berkeley, LBNL	Community metagenomic and transcriptomic analyses of microbial carbon turnover in grassland soil profiles under two rainfall regimes
Bonito, Gregory	Duke University	Comparative genomics of early diverging terrestrial fungi and their bacterial endosymbionts
Brem, Rachel	UC Berkeley	Pioneering fungal mutagenesis using Tn-seq
Brutnell, Thomas	Donald Danforth Plant Science Center	Doubling the number of Panicoideae genome sequences
Canovas, David	University of Seville, Spain	Global genomic consequences of the deletion of the <i>Aspergilli</i> non-homologous end joining DNA repair mechanism employed as a genetic tool worldwide
Chen, Jay	Oak Ridge National Laboratory	RNA-seq-Enabled Expression Quantitative Trait Locus (eQTL) in Populus

Coleman, Jeffrey	Alpert Medical School of Brown University/Rhode Island Hospital	<u>Exploring the supernumerary chromosomes of the <i>Fusarium solani</i> and <i>Fusarium oxysporum</i> species complexes: Reservoirs for functional genetic diversity</u>
Duplessis, Sébastien	INRA, France	<u>Combined population genomics and transcriptomics to decipher the molecular bases of virulence and host adaptation in the poplar leaf rust fungus <i>Melampsora larici-populina</i></u>
Goodwin, Stephen	Purdue University	<u>Stress responses of fungal saprobes and plant pathogens of the Dothideomycetes</u>
Hammond, Ming	UC Berkeley	<u>Synthesis and parallel construction of a library of large binary vectors for the screening of suicide exons for multi-gene pathway engineering in plants</u>
Hazen, Samuel	University of Massachusetts	<u>Synthesis of grass transcription factors for functional characterization in the energy crop model system <i>Brachypodium distachyon</i></u>
Isaacs, Farren	Yale University	<u>Harvesting recombinases from metagenomes to develop multiplex genome engineering technologies in microorganisms</u>
Konstantinidis, Kostas	Georgia Institute of Technology	<u>The microbiome of the upper troposphere and its role in the chemistry of the atmosphere.</u>
Libault, Marc	University of Oklahoma	<u>Use of a single cell type model, the root hair cell, to advance our understanding of the soybean and sorghum transcriptomic and epigenomic responses to various environmental stresses</u>

Lilleskov, Erik	USDA Forest Service, Northern Research Station	Fungal, bacterial, and archaeal communities mediating C cycling and trace gas flux in peatland ecosystems subject to climate change
Mockler, Todd	Donald Danforth Plant Science Center	From sequence to function: Predicting physiological responses in <i>Brachypodium</i> to facilitate engineering of biofuel crops
Molnar, Istvan	University of Arizona	Leveraging the JGI MycoCosm to functionally characterize orphan polyketide synthase clusters and their predicted bioactive small molecule natural products using comparative metaparvomics and synthetic biology
Mullet, John	Texas A&M University	Sorghum GENCODE Project
Nelson, Rebecca	Cornell University	MetaMaize: Characterizing Aboveground Maize-Endophyte Associations Influenced By Host Genotype, Climatic Region, Seed Source, and Tissue Type
Pelletier, Dale	Oak Ridge National Laboratory	Defining the functional diversity of the Populus root microbiome
Pett-Ridge, Jennifer	Lawrence Livermore National Laboratory	Unraveling the rhizosphere carbon cycle: Using comparative metatranscriptomics to identify key processes involved in root-enhanced decomposition of organic matter
Schmitz, Robert	University of Georgia	Harnessing epigenomic reprogramming to improve bioenergy trait performance
Shaw, Jonathan	Duke University	Development of a Comparative Genomics Resource for <i>Sphagnum magellanicum</i>
Stepanauskas, Ramunas	Bigelow Laboratory for Ocean Sciences	Microbial Dark Matter project phase II – stepping deeper into unknown territory

Stewart, Frank	Georgia Institute of Technology	<u>Microbial and viral regulation of community carbon cycling across diverse low-oxygen zones</u>
Taylor, John	UC Berkeley	<u>Fungal response to global change: Adaption to global change and determination of rates of mutation and recombination</u>
Wagner, Michael	University of Vienna, Austria	<u>Raman-based microcolony genomics and transcriptomics for studying microevolution and ecology of nitrifiers</u>
Whitman, William	University of Georgia	<u>Genomic Encyclopedia of Bacterial and Archaeal Type Strains, Phase III: the genomes of soil and plant-associated and newly described type strains</u>

JGI-EMSL Facilities Integrating Collaborations for User Science (FICUS) Plans

Proposer	Affiliation	Project Description
Firestone, Mary Kathryn	UC Berkeley	<u>Mapping soil carbon from cradle to grave: using comparative transcriptomics, proteomics and metabolite analysis to identify the microbial blueprint for root-enhanced decomposition of organic matter</u>
Hansel, Colleen	Woods Hole Oceanographic Institution	<u>Genome-enabled Investigations of the Role of Secreted Proteins and Reactive Metabolites in Carbon Degradation by Pure and Mixed Ascomycete Fungal Communities</u>
Harris, Steven	University of Nebraska-Lincoln	<u>Engineering morphology and secretion to enhance the productivity of fungal fermentations</u>

Hess, Matthias	Washington State University Tri-Cities	<u>FECB: A Functional Encyclopedia of Cyanobacteria – Building the knowledge framework for an enhanced understanding of carbon and nitrogen cycling</u>
Hofmockel, Kirsten	Iowa State University	<u>Development of novel approaches to target microbial drivers of C cycling in soil aggregates</u>
Kistler, Harold	USDA ARS Cereal Disease Laboratory	<u>Organelles promoting high level terpenoid biosynthesis in filamentous fungi</u>
O'Malley, Michelle Ann	UC Santa Barbara	<u>Identification and Regulation of Cellulases within Novel Anaerobic Gut Fungi</u>
Weyman, Philip	J. Craig Venter Institute	<u>Functional genomics of moss-cyanobacteria interactions in boreal forest ecosystems</u>