

Approved Proposals FY17

Following are the approved user proposals for fiscal year 2017, including CSP, [CSP Small-Scale](#), [Synthesis](#), [JGI-EMSL FICUS](#), and [JGI-NERSC FICUS](#).

Community Science Program (CSP)

PI	Affiliation	Project Description
Aitken, Karen	CSIRO (Australia)	Understanding polyploidy through the generation of the first sugarcane genome sequence
Attwood, Graeme	AgResearch Ltd (New Zealand)	Defining gene function in rumen microbes
Bohlmann, Joerg	University of British Columbia (Canada)	Exploring the G3 “Gymnosperm Giga-Genomes” for Carbon Sequestration, Biofuels, and Bioproducts
Bonito, Gregory	Michigan State University	Functional gene network regulation in tripartite plant-fungal-bacterial mutualisms of bioenergy plants and algae
Bruns, Thomas	University of California, Berkeley	Functional genomics of pyrophilous fungi – determining the fate of pyrolyzed carbon in post-fire soils

Buchan, Alison	University of Tennessee Knoxville	<u>Geo-metabolomics of a saltmarsh: Combining <i>in situ</i>, bulk, genomic, transcriptomic, and DOMEomic data streams</u>
Coleman-Derr, Devin	USDA-ARS	<u>Exploring the role of drought-induced plant associated microbes in promoting plant fitness in <i>Sorghum bicolor</i> and <i>Oryza sativa</i></u>
Cox, Michael	University of Wisconsin-Madison	<u>Defining the Molecular Basis of Extreme Resistance to Ionizing Radiation</u>
Crowe, Sean	University of British Columbia (Canada)	<u>Mapping the global methanome</u>
Cullen, Daniel	Forest Products Laboratory	<u>Metatranscriptome analysis of fungal decay of <i>Pinus contorta</i></u>
Cushman, John	University of Nevada	<u>Ice plant gene atlas resource development for <i>Mesembryanthemum crystallinum</i>, a facultative crassulacean acid metabolism (CAM) model for improved water-use efficiency of bioenergy feedstocks.</u>
Des Marais, David	Harvard University	<u>Perenniality, abiotic stress tolerance, and biomass allocation in <i>Brachypodium</i>, a model grass genus for bioenergy</u>
Dijkstra, Paul	Northern Arizona University	<u>Stress in Microbial Communities in Response to Changes in Carbon and Nitrogen Availability</u>

Dopson, Mark	Linnaeus University (Sweden)	Exploring deep biosphere microbial communities by single-cell DNA sequencing
Doty, Sharon	University of Washington	Functional genomics of poplar endophytes for elucidation of mechanisms of improved plant growth under challenging conditions
Dudycha, Jeffry	University of South Carolina	Unlocking the photosynthetic diversity of cryptophyte algae through whole-genome sequencing.
Francis, Christopher	Stanford University	Spatiotemporal Characterization of Microbial Communities Controlling Estuarine Nitrogen and Carbon Cycling in the San Francisco Bay-Delta
Göker, Markus	DSMZ (Germany)	The One Thousand Microbial Genomes Phase 4 Project (KMG-4) – sequencing the most valuable type-strain genomes for metagenomic binning, comparative biology and taxonomic classification
Harris, Steven	University of Nebraska – Lincoln	Fungal interaction networks in biological soil crusts
Heyduk, Karolina	University of Georgia	Genome sequencing of C3 and CAM Yucca species
Johnson, Matthew	Woods Hole Oceanographic Institute	The role of acquired phototrophy in phytoplankton blooms: Insights from the <i>Mesodinium rubrum</i> genome
Kellogg, Elizabeth	Donald Danforth Plant Science Center	Pan-genomics of big bluestem, a broadly adapted dominant grass

LeBoldus, Jared	Oregon State University	RNAseq enabled metabolic modeling of disease resistance to Septoria canker in the DOE flagship <i>P. trichocarpa</i>
Lopez Peredo, Elena	Marine Biological Laboratory	Protecting photosynthesis during desiccation: do the genomes of desert-derived and aquatic <i>Scenedesmus</i> species hold the key to understanding extreme desiccation tolerance among green algae?
MacGregor, Barbara	University of North Carolina	Single-cell (meta-)genomics of uncultivable large sulfur bacteria and their epibionts: investigating host-microbe mediation of biogeochemical cycling
Mockler, Todd	Danforth Center	A Complete-Sequence Population for Pan-Genome Analysis of Sorghum
Moran, Mary Ann	University of Georgia	Dynamics of Bacterial Carbon and Sulfur Cycling in a Coastal Environment
Nguyen, Nhu	University of Hawai'i at Manoa	A genome atlas of the ectomycorrhizal genus <i>Suillus</i>: Phylogenetic diversity and population genomics of a keystone guild of symbiotic forest fungi
Nicholson, Wayne	University of Florida	Transcriptomic and methylomic responses of <i>Carnobacterium</i> species to extreme low pressure
Pett-Ridge, Jennifer	Lawrence Livermore National Laboratory	Microbial Carbon Transformations in Wet Tropical Soils: Effects of Redox Fluctuation

Raff, Jonathan	Indiana University	<u>Combined Flux Chamber and Genomics Approach to Understanding Soil Emissions of Reactive Nitrogen Oxides in a Forested Environment</u>
Shade, Ashley	Michigan State University	<u>Greater than the sum of its parts? A synthetic microbial community approach to untangle member interactions and exometabolite production</u>
Smart, Christine	Cornell University	<u>Genetic diversity of shrub willow pathogen <i>Melampsora americana</i> aided by genome sequence</u>
Stepanauskas, Ramunas	Bigelow Laboratory for Ocean Sciences	<u>Expanding the dark matter reference catalog by targeting taxonomic blind spots</u>
Whitman, William	University of Georgia	<u>Core and pangenomes of soil and plant-associated prokaryotes</u>
Yang, Xiaohan	Oak Ridge National Laboratory	<u>Gene atlas for <i>Kalanchoe laxiflora</i>, a obligate crassulacean acid metabolism (CAM) model for genetic improvement of water-use efficiency in bioenergy feedstocks</u>
Zhang, Chi	University of Nebraska – Lincoln	<u>Genome sequencing of Zygnematales, the closest algal lineage to land plants, as a foundation for comparative genomic, transcriptomic, epigenetic, evolutionary, and biochemical studies</u>

Small-Scale Microbial/Metagenome

PI	Affiliation	Project Description
Alvarez-Cohen, Lisa	University of California, Berkeley	Unraveling functional dynamics and regulation crucial for the stability of an anaerobic ammonium oxidizing (anammox) community via community metatranscriptomics and 16S rRNA sequencing
Andras, Jason	Mount Holyoke College	The effect of ecological restoration on the structure and function of soil microbial communities in coastal wetlands
Averill, Colin	Boston University	Molecular mechanisms of ectomycorrhizal interactions that stabilize soil carbon
Bell, Terrence	Pennsylvania State University	How interactions with soil microbiomes impact the survival and activity of a nitrogen-fixing soil surface consortium
Bowen, Jennifer	Northeastern University	Building a foundation for understanding carbon and nitrogen cycling in microbially diverse salt marsh sediments
Chistoserdova, Ludmila	University of Washington	Probing the role of electron transfer redox mediators in methane-oxidizing communities
Coleman, Maureen	University of Chicago	Teasing apart coexisting picocyanobacteria and their contributions to biogeochemistry
Cotner, James	University of Minnesota-Duluth	Translating stoichiometric diversity into genomic diversity: What elements are

		responsible for variability in bacterial biomass stoichiometry?
Craft, Chris	Indiana University	Microbial activity and community composition in a tidal freshwater marsh in response to sea level rise and saltwater intrusion: A field manipulation
D'Agostino, Paul	Technische Universität München (Germany)	Genome mining and synthetic biology of underrepresented organisms in the search for novel (bio-)chemistry
Dove, Nicholas	University of California, Merced	Immediate effects of prescribed fire on microbial communities, decomposition, and nitrification
Dynarski, Katherine	University of California, Davis	Microbial community composition and function throughout decomposition in temperate forests across a bedrock nitrogen gradient
Freedman, Zachary	West Virginia University	Assessing the recovery of microbial traits in bioenergy crop agroecosystems on reclaimed surface mines
Gutierrez, Tony	Heriot-Watt University (UK)	Genomic reconstruction to resolve the functional potential of oil-degrading bacteria in deep and surface waters of the Faroe-Shetland Channel
Hatzenpichler, Roland	Montana State University	Genomic characterization of cosmopolitan sediment-dwelling archaea hypothesized to be involved in anaerobic carbon cycling

Hatzinikolaou, Dimitris	University of Athens (Greece)	Genome sequencing of lignin and cellulose degrading isolates from Greek habitats
Hunt, Dana	Duke University	Seasonal and disturbance-related alterations in the biogeochemical cycling of estuarine carbon
Jensen, Paul	University of California, San Diego	Extracellular electron shuttles: A mechanism for obligate aerobes to survive anaerobic conditions
Kelly, Charlene	West Virginia University	Quantifying ecosystem changes following American chestnut restoration: From microbes to ecosystem function
Konstantinidis, Konstantinos	Georgia Institute of Technology	Real-time identification of horizontal gene transfer events using series metagenomes
Lebeis, Sarah	University of Tennessee	Characterizing functional chemotaxis receptors in different root zones
Lindemann, Steve	Purdue University	Identifying genome properties and environmental conditions governing the assembly of stable cyanobacterial-heterotroph consortia
Lindow, Steven	University of California, Berkeley	Trait-driven assembly of the leaf surface microbiome in an agricultural context
Maresca, Julia	University of Delaware	Light-induced gene expression in cosmopolitan freshwater Actinobacteria
Martens-Habbena, Willm	Fort Lauderdale Research and Education Center	Biogeochemistry of carbon and nitrogen cycling in subsiding subtropical soils

Mavrodi, Dmitri	University of Southern Mississippi	Transcriptomic responses of beneficial <i>Pseudomonas</i> rhizobacteria to <i>Brachypodium</i> root exudates
McMahon, Katherine	University of Wisconsin-Madison	Reference Genomes for Freshwater Bacteria – Alpha- and Beta-Proteobacteria
Müller, Henry	Graz University of Technology (Austria)	Elucidating the relevance of DNA methylation of strain-specific plant-microbe interactions
Myroid, David	Oregon State University	The metagenome of DIRT: How 20 years of altered carbon inputs have altered the functional potential of soil microbial communities
Oliveira, Rafael	State University of Campinas (Brazil)	Unravelling microbial communities associated with native plant species from P-impooverished soils of a global biodiversity hotspot
Ottesen, Elizabeth	University of Georgia	The genetic drivers and metabolic consequences of pelagic stream microbial community assembly
Pan, Chongle	Oak Ridge National Laboratory	Multi-cycle Selection of Sorghum Microbiomes for Biological Nitrogen Fixation
Richardson, Ruth	Cornell University	Metatranscriptomic responses of a butyrate-to-methane enrichment culture to sulfate and iron availability: elucidating the identities and strategies of metabolically versatile sulfate and iron reducing populations

Samuel, Buck	Baylor College of Medicine	Genomic analyses of the natural microbiome of <i>Caenorhabditis elegans</i>
Schmer, Marty	USDA-ARS	Nitrogen effects on soil microbial communities and soil organic carbon in a resilient bioenergy cropping system
Seyfferth, Angelia	University of Delaware	Impacts of rice cultivation practices on carbon and iron cycling: Unraveling functional microbial diversity in rice paddy rhizocompartments subject to silica-rich rice residue amendment
Valentine, David	University of California, Santa Barbara	Metagenomic reconstruction of novel archaeal genomes from energy-limited hypersaline sediments.
Veley, Kira	Donald Danforth Plant Science Center	Epigenetic and transcriptional changes that occur in populations of bacteria colonizing plant hosts.
Venturi, Vittorio	International Centre of Genetic Engineering and Biotechnology (ICGEB) (Italy)	Sequencing of a set of identified and characterized rice bacterial endophytes

Synthesis

PI	Affiliation	Project Description
Baker, David	University of Washington	Large scale <i>de novo</i> enzyme design for next generation metabolic engineering
Beisel, Chase	North Carolina State University	Profiling the functional diversity of CRISPR-Cas systems using cell-free transcription-translation systems

Bokinsky, Gregory	Delft University of Technology (Netherlands)	Plug adapters for biology: Activating heterologous iron-sulfur enzymes to fully exploit Nature's catalytic potential
Chistoserdova, Ludmila	University of Washington	Establishing lanthanides as new life metals and understanding redox properties of lanthanide enzymes in metabolism of methane
Dueber, John	University of California, Berkeley	Identification of novel D-altronate dehydratases in the enolase superfamily enabling pectin utilization in <i>S. cerevisiae</i>
Huang, Possu	Stanford University	New protein platform for secondary metabolite detection
Jewett, Michael	Northwestern University	Reframing combinatorial assembly and rapid prototyping of biosynthetic pathways with cell-free systems
Juminaga, Alex	LanzaTech, Inc.	Advancing understanding of acetogenic CO ₂ fixation by generating a gene knock-out library to accelerate design of commercial strains for autotrophic production of fuels and bioproducts
Mead, David	Varigen Biosciences	Metagenomic mining for next generation DNA polymerases
Philmus, Benjamin	Oregon State University	Linking cyanobacterial orphan biosynthetic gene clusters to secondary metabolites
Redding, Kevin	Arizona State University	Chloroplastic CO ₂ reduction to formate supporting synthetic carbon fixation

Schmeing, Thomas	McGill University	Synthetic DNA to facilitate structural and functional understanding of nonribosomal peptide synthetase production of secondary metabolites
Scott, Kathleen	University of South Florida	Creation of constructs for functional expression of recently described inorganic carbon transporters widespread among sulfur- and iron-oxidizing chemolithoautotrophic microorganisms
Subramanian, Venkatamaranan	National Renewable Energy Laboratory	Molecular engineering of <i>Trichoderma reesei</i> for improved cellulase production
Welander, Paula	Stanford University	Expression of novel triterpenoid biosynthesis proteins from environmental metagenomes

FY 2017 Facilities Integrating Collaboration for User Science (FICUS) JGI-EMSL Plans

Proposer	Affiliation	Project Description
Baldrian, Petr	Institute of Microbiology ASCR (Czech Republic)	The impacts of nitrogen availability and seasonal dynamics on plant-microbial interactions affecting C and N cycling in coniferous forest soils
Bartley, Laura	University of Oklahoma	Systems analysis of grass secondary cell wall development and regulation for biofuel production

Bianchi, Thomas	University of Florida	<u>The role of priming effects on the conversion of blue carbon to CO₂ in the coastal zone</u>
Blanchard, Jeffrey	University of Massachusetts Amherst	<u>Molecular mechanisms underlying changes in the temperature sensitive respiration response of forest soils to long-term experimental warming</u>
Cattolico, Rose Ann	University of Washington	<u>Global warming induced salinity shifts: metabolic responses by algal-bacterial consortia</u>
Fendorf, Scott	Stanford University	<u>Metabolic Constraints on Organic Matter Decomposition and Metal Cycling in Sediment Deposits</u>
Liao, Hui-Ling	Duke University	<u>Combined 'omics approaches for the study of ectomycorrhizal symbiosis between <i>Suillus</i> and <i>Pinaceae</i>, with emphasis on their role in nutrient cycling</u>
Rich, Virginia	The Ohio State University	<u>Something old, something new: systems-level insights into plant-microbial-permafrost carbon dynamics by parallel high-resolution organic matter and microbial meta-omics</u>
Skerker, Jeffrey	University of California, Berkeley	<u>Understanding conversion of biomass-derived carbon into lipids and terpenoids in the oleaginous yeast <i>Rhodospiridium toruloides</i></u>
Wrighton, Kelly	The Ohio State University	<u>Deciphering controls on plant decomposition in Arctic ecosystems: Identifying unknown microbial</u>

[condensed tannin degradation pathways](#)

FY 2017 Facilities Integrating Collaboration for User Science (FICUS) JGI-NERSC Plans

Proposer	Affiliation	Project Description
Babbitt, Patricia	University of California, San Francisco	Environmental Profiling of Enzyme Superfamilies for Function Prediction
Baker, David	University of Washington	Eukaryotic Protein Structure Determination Using Metagenome and Metatranscriptome Sequence Data
Brooks, Phillip	University of California, Davis	Advancing Metagenome Classification and Comparison by MinHash Fingerprinting of IMG/M Data Sets
DeLong, Edward	University of Hawaii at Manoa	Quantitative Analyses of Naturally Occurring Small RNAs in Global Metagenomic and Metatranscriptomic Datasets
Hallam, Steven	University of British Columbia (Canada)	Charting Global Biogeochemical Cycles using Fast Phylogenetic Mapping of Functional Anchor Genes
Konstantinidis, Konstantinos	Georgia Institute of Technology	Assessing Microbiomes at the Individual Population Level: Tool Development and Applications to Soil Carbon Cycling