

## Approved Proposals FY16

Following are the approved user proposals for fiscal year 2016 including CSP, [CSP Small-Scale](#), [Synthesis](#), and [FICUS projects](#).

### FY 2016 Community Science Program (CSP) Plans

| PI                  | Affiliation  | Project Description   |
|---------------------|--|---|
| Catcheside, David   | Flinders University (Australia)                          | <a href="#">Acquisition of the sequestrate (truffle like) habit by basidiomycete macrofungi</a>   |
| Cooper, Elizabeth   | Clemson University                                       | <a href="#">Comparative transcriptomics of sweet and grain sorghum to understand the mechanism and timing of sugar accumulation in an important bioenergy crop</a>        |
| de Vries, Ronald    | CBS-KNAW Fungal Biodiversity Centre (Netherlands)        | <a href="#">Dissecting the different approaches of ascomycete fungi to degrade plant biomass</a>  |
| DeLong, Ed          | University of Hawaii at Manoa                            | <a href="#">Going long and going deep: Comprehensive open ocean community single cell genome sequencing at the model open ocean time series study site, station ALOHA</a> |
| Dollhofer, Veronika | Bavarian State Research Center for Agriculture (Germany) | <a href="#">Anaerobic fungi and assessment of their potential for biogas production</a>   |

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| Duplessis, Sebastien | INRA (France)                           | <a href="#"><u>Sequencing a reference genome for <i>Phakopsora pachyrhizi</i>, the fungal pathogen responsible for the Asian Soybean Rust</u></a>   |
| Francis, Christopher | Stanford University                     | <a href="#"><u>Metagenomic characterization of nitrogen-cycling microbial communities impacting uranium release in the Upper Colorado River Basin</u></a>   |
| Hamelin, Richard     | University of British Columbia (Canada) | <a href="#"><u>Pathobiome of bioenergy trees</u></a>  |
| Hibbett, David       | Clark University                        | <a href="#"><u>Comparative and functional genomics of shiitake mushrooms: an international collaboration to resolve evolutionary relationships, substrate specificity, growth profiles, and routes to domestication in the amphi-Pacific genus <i>Lentinula</i></u></a> |
| Juenger, Tom         | University of Texas at Austin           | <a href="#"><u>Exploring natural genetic diversity in switchgrass (<i>Panicum virgatum</i>) and its microbiome</u></a>  |
| Kalyuzhnaya, Marina  | University of Washington                | <a href="#"><u>Systems level insights into methane cycling in arid and semi-arid ecosystems via community metagenomics and metatranscriptomics</u></a>  |
| Lorito, Matteo       | University of Naples (Italy)            | <a href="#"><u>Supporting the development of microbial probiotics for grasses useful in sustainable bioenergy production</u></a>  |
| Martin, Francis      | INRA (France)                           | <a href="#"><u>1KFG: Deep sequencing of ecologically-relevant Dikarya</u></a>   |
| Mayali, Xavier       | Lawrence Livermore National Laboratory  | <a href="#"><u>Influence of phycosphere-associated bacteria on microalgal biofuel production</u></a>  |

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| McMahon, Katherine | University of Wisconsin-Madison          | <a href="#"><u>Diel cycles of gene expression in oligotrophic, dystrophic, and eutrophic lakes to identify new gene functions and dissect carbon cycling metabolisms</u></a>             |
| Merchant, Sabeeha  | University of California, Los Angeles    | <a href="#"><u>Comparative genomics and expression profiling of snow algae <i>Chlamydomonas cribrum</i> and <i>Chloromonas nivalis</i></u></a>   |
| Niyogi, Kris       | University of California, Berkeley       | <a href="#"><u>Functional genomics of photosynthesis in <i>Chlamydomonas</i>, JGI's flagship alga</u></a>  |
| O'Malley, Michelle | University of California, Santa Barbara  | <a href="#"><u>Genomic basis for syntrophic interactions between anaerobic gut fungi and methanogenic archaea</u></a>  |
| Pires, J. Chris    | University of Missouri-Columbia          | <a href="#"><u>Investigating the diversity of mycorrhizal fungi to understand the evolution and function of symbiosis with orchids</u></a>   |
| Plett, Jonathan    | University of Western Sydney (Australia) | <a href="#"><u>Exploring the genomic basis for the global diversification by the ectomycorrhizal genus <i>Pisolithus</i></u></a>   |
| Poland, Jesse      | Kansas State University                  | <a href="#"><u>The Intermediate Wheatgrass Genome: A resource for understanding mechanisms of perenniality and accelerating the development of perennial crops</u></a>                   |
| Rappe, Michael     | University of Hawaii at Manoa            | <a href="#"><u>Metagenomics of viral and microbial communities inhabiting warm, anoxic fluids of the sediment-buried deep ocean crust</u></a>  |
| Schachtman, Daniel | University of Nebraska                   | <a href="#"><u>Systems analysis of the physiological and molecular mechanisms of Sorghum nitrogen use efficiency, water use efficiency and interactions with the soil microbiome</u></a> |

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| Spatafora, Joey | Oregon State University              | <a href="#">Genomics of the early diverging lineages of fungi and their transition to terrestrial, plant-based ecologies</a>     |
| Umen, James     | Donald Danforth Plant Science Center | <a href="#">Single cell and population dynamics of chromatin across the diurnal cycle in the model alga <i>Chlamydomonas</i></a> |
| Walsh, David    | Concordia University (Canada)        | <a href="#">Microbial metagenomics of carbon cycling communities in northern aquatic ecosystems</a>                              |
| Wrighton, Kelly | Ohio State University                | <a href="#">Life in the extreme deep terrestrial subsurface: microbial metabolism before and after shale gas extraction</a>      |

## Small-Scale Proposals

| Proposer               | Affiliation                          | Project Description   |
|------------------------|--------------------------------------|---|
| Beman, J Michael       | University of California, Merced     | Metagenomics of methane production and oxidation in high altitude lakes of Yosemite National Park   |
| Chistoserdova, Ludmila | University of Washington             | Understanding methane cycling through manipulation of synthetic methane-oxidizing communities   |
| Cullings, Ken          | NASA Ames                            | Extreme endosymbiosis: An investigation into a unique fungal microbiome found in geothermal ecosystems in Yellowstone National Park and New Zealand |
| DeAngelis, Kristen     | University of Massachusetts, Amherst | Expanding genomic diversity of terrestrial bacteria: linking genes to metabolism in the   |

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|                     |   | slower-growing members of forest soil bacterial communities   |
| Kostka, Joel        | Georgia Institute of Technology         | The role of the Sphagnum microbiome in carbon and nutrient cycling in peatlands   |
| McMahon, Katherine  | University of Wisconsin-Madison         | Reference genomes for abundant freshwater taxa – <i>Actinobacteria</i> and <i>Verrucomicrobia</i> phase 2                   |
| Meredith, Laura     | Stanford University                     | Microbial, chemical, and physical drivers of COS fluxes and 18O-CO <sub>2</sub> exchange rates in soils                     |
| Miller, Christopher | University of Colorado, Denver          | Developing a systems-level understanding of biotic and abiotic controls on microbial methane cycling in freshwater wetlands |
| Redmond, Molly      | University of North Carolina, Charlotte | Metagenomic sequencing of methane-oxidizing mesocosms from the Gulf of Mexico and Hudson Canyon                             |
| Rich, Jeremy        | Brown University                        | Metagenomic sequencing of an uncultivated bacterial phylum in marine sediments amended with organic carbon and nitrate      |
| Saito, Mak          | Woods Hole Oceanographic Institution    | Characterizing <i>Synechococcus</i> dominated populations from the Costa Rica dome and surrounding waters                   |
| Shade, Ashley       | Michigan State University               | Response and recovery of surface soil microbial communities to an ongoing underground coalmine fire                         |
| Simister, Rachel    | University of British Columbia          | Linking microbial genomic capacity to geochemical process in the deep terrestrial biosphere                                 |

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| Slonczewski, Joan | Kenyon College        | Cyanobacterial communities of Antarctic Lake Fryxell littoral mats and glacier meltwater  |
| Tolar, Bradley    | Stanford University   | Monitoring the transcriptional response of a representative low-salinity ammonia-oxidizing thaumarchaeote to shifts in environmental conditions |
| Walsh, David      | Concordia University  | Metagenomics of western Arctic Ocean microbial communities  |
| Wilkins, Michael  | Ohio State University | Seasonal sulfur cycling as a control on methane flux in carbon-rich prairie pothole sediment ecosystems   |
| Wrighton, Kelly   | Ohio State University | Identifying key genomes and metabolisms responsible for near-surface methane cycling in freshwater wetlands                                     |

## Synthesis Proposals

| Proposer       | Affiliation                                   | Project Description   |
|----------------|---|---|
| Chang, Jui-Jen | Biodiversity Research Center, Academia Sinica | Designer Operons-A biomimic approach to the regulation of an enzyme cocktail for an artificial enzyme complex |
| Chen, Brandon  | Genomatica, Inc.                              | Engineering efficient methanol utilization for renewable chemicals  |
| McCourt, Peter | University of Toronto                         | Exploring the perception landscape of the strigolactone receptor  |

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| Prather, Kristala | Massachusetts Institute of Technology | Combinatorial assembly, screening and functional characterization of a recombinant glucaric acid pathway in <i>S. cerevisiae</i>   |
| Shen, Ben         | The Scripps Research institute        | Construction of bacterial artificial chromosome (BAC) vector libraries for comparative genomics, elucidation of gene functions and heterologous expression of targeted genes |
| Smanski, Mike     | University of Minnesota               | Towards a mechanistic understanding of disease suppressive soils: Refactoring natural product gene clusters  |
| Wang, Clay        | University of Southern California     | Identification of fungal secondary metabolites with novel structures   |
| Zimmer, Jochen    | University of Virginia                | Synthesis of cellulose synthase genes implicated in primary and secondary plant cell wall formation for structural and functional analyses of plant cellulose biosynthesis   |

## FY 2016 Facilities Integrating Collaboration for User Science (FICUS) JGI-EMSL Plans

| Proposer               | Affiliation                  | Project Description   |
|------------------------|------------------------------|---|
| Bell-Pedersen, Deborah | Texas A&M University         | Specialized Ribosomes: A New Frontier in Gene Regulation  |
| Cardon, Zoe            | Marine Biological Laboratory | 3D Reality Check: Developing Structural Support for Predicting Microbial Function and Interpreting Microbial "Omics" Data |

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| Doty,<br>Sharon     | University of<br>Washington              | Nitrogen fixation in <i>Populus</i> : Identification and localization of the key diazotrophs in planta   |
| Duhaime,<br>Melissa | University of<br>Michigan                | Building the phage-host-environment interaction data to scale from genes-to-ecosystems: Towards predictive modeling of wild microbial and viral community dynamics |
| Eastwood,<br>Dan    | Swansea<br>University (UK)               | Genomes to dynamic decay communities: Understanding fungal interactions during early decomposition events in natural lignocellulosic substrate                     |
| Neumann,<br>Rebecca | University of<br>Washington              | A Rhizosphere-Scale Investigation of the Relationship Between Plant Productivity and Methane Emissions from Wetlands   |
| Orphan,<br>Victoria | California<br>Institute of<br>Technology | Fluorescence-based cell sorting and targeted proteomic analysis of active methane-oxidizing syntrophic consortia from environmental samples                        |
| Pan,<br>Chongle     | Oak Ridge<br>National<br>Laboratory      | Integrated Omics Analyses of a <i>Populus</i> Pedigree for Crop Improvement  |