Approved Proposals FY25

Following are the approved user proposals for Annual Community Science Program (CSP), FICUS JGI-EMSL, CSP Functional Genomics and CSP New Investigator calls.

FY 2025 Annual CSP Proposals

Proposer Name	Affiliation	Proposal Title	Proposal Description
Barnhart, Elliott	United States Geological Survey (USGS)	Exploring Fungal Contributions to Carbon Cycling in Deep Subsurface Organic-Rich Environments Across Depth and Salinity Gradients	Biogenic natural gas (BNG) is a valuable energy source that has typically been thought to form through the activities of specific bacteria and methanogens living deep underground. However, recent research suggests that fungi, which also live in these deep environments, may play an important role in the creation of this natural gas and in the cycling of carbon below the Earth's surface. This project aims to close this knowledge gap by studying and sequencing the DNA of fungi found in subsurface locations such as shale, petroleum deposits, and coal beds where BNG is present. This database will be a comprehensive resource, helping scientists across the country better understand the

			formation of BNG and the role of fungi play in underground carbon cycling.
Borton, Mikayla	Colorado State University	Decoding the Unifying Microbial Metabolic Controllers on Carbon Cycling Across Saturated Soils	Saturated soils are characterized as waterlogged soils, rich in organic matter, with low concentrations of porewater oxygen. Anoxic microbial decomposition of this soil organic matter leads to the production of greenhouse gasses such as carbon dioxide and methane. Likewise, these climatically important soils also store a substantial amount of soil organic carbon. Despite this climate relevance, the microbial communities and metabolic pathways driving carbon decomposition, along with their environmental controls, remain unresolved. A key outcome of this project will be development of the Multi-omics for Understanding Climate Change (MUCC) database, a necessary step for advancing knowledge of the interacting geochemical, ecological, and hydrological constraints on saturated soil microbiomes.

Carlson, John	Penn State University	Super-PanGenomes for Gene Discovery and Climate-Resiliency Research and Breeding in Eastern Oak Syngameons	Forests globally account for nearly 45% (900 pentagrams) of the carbon stored terrestrially and sequester 2.4 pentagrams of carbon annually, providing long-term carbon sequestration in above and below ground tree biomass and harvested wood products. Northern boreal and temperate forests are the most active terrestrial carbon sinks, despite facing many threats from invasive pests, changing land use, and rapidly changing climate. Prospects for achieving carbon neutrality and resilience to climate change rely in large part on forests and tree plantations continuing to efficiently sequester large amounts of carbon in biomass and forest products. For forests to fulfill that role, as climates change populations of trees in northern forests must either migrate with the shifting conditions or ‘adapt’ in place through replacement (mortality) of previously fit trees with seedlings with the genetic potential to survive and grow under the new climatic conditions. Oaks account for a substantial portion of the carbon storage of northern temperate forests. Oaks are also important to forest product-based industries and as keystone species providing essential ecosystem services to our communities. The past success of oaks in migration and

adaptation in response to new environmental conditions following the last ice age resulted in oaks becoming one of the most widespread, dominant, and species-rich groups of trees in northern hemisphere temperate forests. This has led to oaks becoming a focus of research into the genetic basis of adaptation to the environment in long-lived hardwood trees. It has long been observed that closely related oak species can produce hybrid offspring when they co-exist in natural forests. Has this ability to share genes among oaks species with different environmental adaptations contributed to the ability of oaks to adapt to past climate changes? What can we learn about hybridization among oaks to assist in conserving and improving their important roles in climate resiliency and bio-based products? This Community Science Program project will develop a ”super pangenome” research platform to answer those questions through detailed investigations of natural genetic exchange by hybridization within the two major sections of the oak genus – the white oaks and the red oaks. The research platform, consisting of newly sequenced and assembled genomes and genetic diversity data for 16 oak species in the eastern US, will enable

			geneticists to learn what genes and segments of chromosomes are shared among interbreeding oak species, how each species remains distinct genetically despite hybridization, and if diagnostic tests can be developed to assist in sustaining oak forests.
Conway, Jonathan	Princeton University	Promoter Discovery and Characterization to Enable Metabolic Engineering in Lignocellulosic Thermophiles	Anaerobic, lignocellulosic, thermophiles are a promising group of candidate microorganisms for lignocellulosic bioprocessing because of their native ability to degrade cellulose and hemicellulose in lignocellulosic biomasses. Consolidated BioProcessing schemes utilizing these organisms would enable the degradation of lignocellulose and conversion to product in one reactor, but require tools to genetically manipulate product pathways in these organisms. This project will enable the creation of a library of promoters that will be characterized in vivo for their ability to drive protein expression at known levels. We will utilize these characterized promoters to optimize the acetone production pathway in Caldicellulosiruptor bescii as a demonstration of the engineering necessary to improve the titer of a chemical product from a lignocellulosic thermophile. We will also pioneer the use of CRISPRi in

			C. bescii which will offer another level of transcriptional control in this organism for discovery and engineering.
Damashek, Julian	Hamilton College	Genome-resolved and activity-based archaeal ecology in a euxinic meromictic lake (Fayetteville Green Lake, NY, USA)	Though archaea are single cells like bacteria, they are more closely related to eukaryotes, the group including plants and animals. For this reason, there is wide interest in understanding the roles archaea played in the evolution of eukaryotic cells. This project aims to study one group of enigmatic archaea, the Woesearchaeota, in Fayetteville Green Lake (NY). Green Lake is “meromictic,” meaning that unlike most lakes, it never mixes. By using a variety of high-throughput sequencing techniques, we will analyze archaeal dynamics at many depths in Green Lake, with a specific interest in determining the activity of Woesearchaeota and the role they play in cycling carbon and nutrients in the lake. This unprecedented insight into some of their basic biological characteristics will not only teach us about this fascinating group of archaea, but will help understand their contribution to regional and global carbon and nutrient cycling.

de Vries, Ronald	Westerdijk Fungal Biodiversity Institute	Revealing the diversity of primary carbon metabolism across the fungal kingdom	Primary carbon metabolism enables fungi to convert sugars e.g., obtained from degradation of plant biomass, into the compounds and energy needed its growth and reproduction. With the availability of an increasing number of genome sequences it has become clear that the organization of primary carbon metabolism in fungi is highly diverse and that it is difficult to transfer knowledge between more distantly related fungi. In this project we aim to classify this diversity by making validated reference models for primary carbon metabolism for most main taxonomic groups of fungi. This will not only provide a better understanding of this central physiological process, but also provide insights into the potential role of individual fungi in their natural environment. It will also provide us with the in depth knowledge of metabolism to enable the generation of improved and novel fungal cell factory to produce a wide range of biochemicals to from sustainable resources to replace chemical synthesis from fossil resources.

Dieter, Emily	Gettysburg College	Investigation of Radical S-Adenosyl-L-methionine enzymes hypothesized to be involved in Methanogenic Archaea metabolism	A thorough understanding of methanogens is needed to mitigate or harness methane production, yet methanogens often inhabit extreme environments, making them extremely difficult to study in the laboratory. In this project, researchers will investigate biological processes of methanogens by expressing key methanogen proteins in organisms that are more amenable to growth in a laboratory environment. Proteins will be purified from the host, then functionally characterized outside of the organism. This research is ultimately expected to provide valuable insight into fundamental biological processes in methanogens.

Hord, Ashlynn	University of Tennessee, Knoxville	Are rear-edge or relict populations reservoirs for resilience genes? Biogeographic patterns of genetic variation and introgression in a riparian tree species	Introgression, or the movement of genes between species via interspecific hybridization, followed by backcrossing between hybrids and parental species, has been hypothesized to increase species' resilience to climate change. Our study proposes to use JGI-generated annotated genomes and resequencing for two ecologically and economically important species, Populus angustifolia (narrowleaf cottonwood) and P. fremontii (Fremont cottonwood). We aim to: 1) Understand how populations of these riparian, foundation tree species are adapting to climate change; and 2) Determine whether hybrid introgression is a prominent mechanism by which this adaptation occurs. Identifying the role of introgression and the genomic underpinnings of climate change adaptation in these natural populations will broaden the toolkit for sustainable production of the well-studied bioenergy feedstock candidate and congeneric species, Populus trichocarpa.

John, Uwe	Alfred Wegener Institute for Polar and Marine Research	The role of niche adaptability in the evolution of the harmful alga, Alexandrium catenella: Dinophyceae	Harmful algal blooms (HABs), in particular those caused by toxic dinoflagellates, have devastating impacts on fisheries and the aquaculture industry, resulting in a global annual loss of ~$7.5 billion. HABs pose significant human health risks through seafood poisoning and are becoming more frequent in warming oceans due to climate change. However, the molecular and evolutionary mechanisms that result in HABs are poorly understood due to a lack of genomic data from the dinoflagellate species that cause these events. This project will address this crucial knowledge gap by generating high-quality genomic and transcriptomic resources from the globally distributed, HAB-causing dinoflagellate, Alexandrium catenella (genome size ~50 Gbp). This dinoflagellate is responsible for HABs across these regions worldwide, resulting in detrimental impacts to local fisheries and aquaculture. Genes, functions, and candidate biomarkers identified from the A. catenella data will of high societal relevance by helping guide risk-mitigation, prevention, and management strategies of harmful algal blooms.

Khare, Sagar	Rutgers University	Targeted high-throughput design of biocatalysts for degrading selected polymers	We are being inundated by large quantities of polymeric materials, directly or indirectly anthropogenic, often made with carbon derived from petroleum sources. For example, the great pacific garbage patch contains human-made plastics, and brown algal blooms are devastating the economies of many communities in the Atlantic ocean. Nature has developed fledgling catalysts – enzymes – that can degrade these polymers and large-scale metagenome sequencing efforts have made the genetic sequences of these enzymes available. However, these molecules have evolved in specific environmental niches (e.g. ocean floor) and generally remain unavailable to us as these proteins are not robust to production conditions in common recombinant production strains and the conditions required for industrial biocatalysis. This work will discover the protocols for high-throughput design and optimization that enable the routine and rapid development of highly active biocatalysts from diverse environmental niches.

Manzitto-Tripp, Erin	University of Colorado-Boulder	Engineering drought-tolerant pennycress via loss-of-function alleles observed in an aridity extremophile	The Namib and Kaokoveld Deserts are two of the oldest and driest deserts on Earth. The average precipitation in the region is <100 mm/yr and because inter-annual rainfall is highly variable, many plants in these deserts survive for years to decades with little or no precipitation. Despite this extreme aridity, these deserts harbor some very interesting plant lineages. Pennycress (Thlaspi arvense) is emerging as a new oilseed crop with great potential as a cover crop as well. Closely related to the model plant Arabidopsis, it is ideal to translate specific discoveries to the field. We propose to expedite pennycress crop improvement – specifically drought tolerance – using a gene knockout strategy in which pennycress target loci are identified based on Petalidium loss-of-function (LoF) alleles. LoF alleles encode premature stop codons, frameshifts, splice site disruptions, or point mutations that render encoded proteins non-functional.

Poulin, Lucie	Université de Nantes, Laboratoire de Biologie et pathologie Végétales	Plant – plant interactions mediated by rhizosphere microbiota using the model: Arabidopsis thaliana (L.) Heynh – Phelipanche ramosa (L.) Pomel	Plants are essential to modern society, providing numerous ecological benefits. It’s crucial to understand how plants interact within ecosystems, including their relationships with other organisms and with each other. Over the last decade, scientists have discovered that microbes play a vital role in these interactions, potentially offering solutions to contemporary challenges. Broomrape is a significant pest in the US and Europe, infesting many crops, and current solutions to control it are not very effective. We aim to understand the complex molecular communication that happens in the soil between parasitic plants, their host plants, and the soil microbes that can influence these interactions and the resulting parasitism. This project explores how soil microbes affect the signaling molecules in the vicinity of the host plant and, in turn, how this influences the growth of branched broomrape. By understanding how parasitic plants like broomrape operate in their complex environment, we hope to develop better agricultural strategies.

Probst, Alexander	University of Duisburg-Essen	Genomic expansion of freshwater algae and their interacting bacteria and viruses	Algae are important organisms on planet Earth as they transform carbon dioxide into organic matter fueling the food chain in freshwater ecosystems. They are extremely diverse in nature and often associate with other organisms like bacteria that help them to acquire nutrients like nitrogen compounds. Beyond the fact that some need other organisms to make a living, some algae have evolved capabilities to acquire carbon from other sources like carbohydrates. The evolution of the acquisition of these capabilities is little understood as is the interaction of algae with other organisms. This multi-faceted project will harness a wide-ranging collaborative effort to reveal genetic treasures kept within algal genomes that shape their important contributions to Earth's carbon and nitrogen cycles.

Sullivan, Matthew	The Ohio State University	Ecogenomics and biogeochemical modeling of DNA and RNA viruses across terrestrial-marine interfaces	Microbes drive most of the natural processes (like nutrient cycling) that keep our planet running and ecosystem healthy and in balance. However, in recent years it has been found that viruses that infect these environmentally-important microbes play a crucial role in influencing these microbial activities. This proposal aims to examine virus communities and their hosts in less-studied areas where land and ocean meet: terrestrial-marine interfaces located at two major ‘ocean features’ – the Benguela Upwelling off the coast of southern Africa and the Amazon River plume, which seed gigatons of carbon into the ocean currents. Our research will provide a detailed and comprehensive resource that will help improve our understanding of how microbes and viruses impact climate-sensitive environments. This knowledge is vital for predicting how these ecosystems might change in the future and how they can be managed to support a healthy planet.

Sumner, Dawn	University of California Davis	Seasonal Metabolism Changes Across Redox Gradients in Photosynthetic Mats, Lake Fryxell, Antarctica	Rocky desert valleys in Antarctica commonly host ice-covered lakes with microbial communities living on the lake floors. When enough light penetrates the ice cover, photosynthetic bacteria and algae convert carbon into biomass to support unusual, cold adapted ecosystems. Due to the high latitude of the lakes, photosynthesis can only occur part of the year. Similarly, researchers can only study these communities during spring and summer. Thus, little is known about how these communities change during the >4 month long winter when no oxygen is produced. By studying tvariations across the seasons and at different depths in the lake, which have different amounts of light and oxygen, we will gain insights into how photosynthesis supports these ecosystems and how the communities may respond to changes in lake level and ice cover associated with climate change.

Ward, Christopher	Bowling Green State University	Opening the floodgates: how hydroelectric dam removal led to reshuffling of downstream microbial plankton community and biogeochemical potentials in a freshwater estuary	Many hydroelectric dams are being removed from rivers throughout the world in order to restore water flow and access to critical fish habitat. While conducting a long-term time series in Sandusky Bay (Ohio), we discovered that dam removal coincided with the disappearance of harmful cyanobacterial bloom, overall improved water quality and restructured microbial community in the downstream water body. By improving our understanding of nutrient cycling and functional diversity in a freshwater estuary, we can clarify the connections between energy and environmental genomics, supporting stewardship of US and global natural resources.
Willoughby, Andrew	Duke Univeristy	Gesneriaceae genomes to unlock novel biology for plant regeneration	The ability to regrow plants from cuttings, or plant regeneration, is essential to plant research and the biotech industry. The difficulty in getting important crop plants (especially bioenergy crops) to regenerate is a bottleneck in these fields that this research is aimed at addressing. To understand the limitations on plant regeneration, we are establishing a new model system, the genus Streptocarpus. Streptocarpus is the group that the common ornamentals African violets and Cape primroses come from. It

			also has unsually flexible development that promotes regeneration.
Young, Kristina	U.S. Department of Agriculture	Investigating microbial gene expression and metabolite profiles in response to varying resource levels in dryland soils.	This project aims to explore how the availability of nutrients affects the processes in dryland soils, which are areas with low moisture levels. By understanding these processes, we hope to gain insights into how these soils contribute to the broader environment, especially in terms of how they process and release carbon, a key element that influences climate change. Our study will focus on three key nutrients: carbon, nitrogen, and phosphorus. We will experiment by adding different amounts of these nutrients to bare soil samples and observe how the microbial communities in these soils respond. These tiny organisms play a crucial role in breaking down organic material and cycling nutrients. By studying how different microbial species react to nutrient changes, we can better understand which microbes are more active and how they contribute to soil health and carbon cycling.

FY 2025 Facilities Integrating Collaboration for User Science (FICUS) JGI-EMSL Proposals

Proposer	Affiliation	Proposal Title	Proposal Description
Frank, Margaret	Cornell University	Multi-omics discovery of long-distance mobile signals involved in vascular plant carbon partitioning	Intercellular communication in vascular plants is fundamental to understanding biomass allocation, particularly in the context of carbon accumulation and partitioning between root and shoot systems. Despite significant advancements, a comprehensive view of the molecular signals governing this process is still lacking. Our project addresses this gap by employing a multidisciplinary, multi-omics approach integrating genomics, proteomics, and advanced imaging techniques. Our proposal and research involve identifying and functionally characterizing mobile signals, including RNAs, proteins, and hormones. The significance of our research lies in its potential to revolutionize our understanding of intercellular communication in plants and its implications for biomass accumulation.

Hallam, Steven	University of British Columbia	Targeted multi-omics of metabolically active microbial populations in anaerobic digesters bioaugmented with carbon-based conductive materials	Metabolic interactions are integral to renewable natural gas (RNG) production from different biomass inputs in anaerobic digestion (AD) environments. One of the most important sets of interactions involves syntrophic acetate oxidizing bacteria (SAOB) and methanogenic archaea ultimately responsible for converting acetate into methane and carbon dioxide, thus driving the production of RNG. Here, we aim to leverage this approach to evaluate SAOB activity and interactions in the context of an incubator reactor system utilizing conductive carbon cloth. We will do this in the context of an emerging bioinformatics workflow that leverages multi-omic datasets to construct genome-resolved microbial correlation networks in which active microbial consortia involved in bioenergy production will be mapped. The resulting activity-dependent genome-resolved correlation network will provide foundational insights into the AD environment understudy and will inform strategies for optimizing bioenergy production.

Howard-Varona, Cristina	The Ohio State University	Environmental virus-microbe interactions: Regulation, functions, and ecosystem footprints of diverse virocells	Microbes are well recognized to dominate most biomes on Earth, but their fate is intertwined with that of viruses. Viral infection transforms cells into completely new entities called ‘virocells’ which are fundamentally different from their uninfected counterparts, as their main objective is viral reproduction rather than cell growth. Because of that, in the very few environmental virus-bacteria model systems investigated, virocells drastically alter (1) intracellular transcripts, proteins, and metabolites, (2) interactions with other organisms, and (3) interactions with the environment. Despite these efforts, environmental virocell understanding still has knowledge gaps. We propose to close these knowledge gaps through investigating both (i) transcriptional regulatory landscapes of diverse virus-microbe interactions, and (ii) biomolecules,functions, and ecosystem outputs of variably phage-resistant microbes.

Hultman, Jenni	University of Helsinki	Illuminating the role and function of soil microbes in Arctic greenhouse gas cycling through systems biology multiomics approaches	Global warming is more pronounced in the Arctic regions than the rest of the globe, with recent estimates predicting the Arctic warming four times faster compared to the global average. Arctic soils contain more than half of the global soil organic carbon stock and the role of tundra soils to greenhouse gas (GHG) emissions, particularly methane (CH4), carbon dioxide (CO2) and nitrous oxide (N2O), are predicted to increase in the future. However, it is still unclear how such fundamental changes will influence these ecosystems and the high latitudes have the potential for further substantial positive feedbacks to climate warming. A better understanding of Arctic microbial communities and their function as well as considering changes in below- and above-ground microclimatic conditions together with microbial activity, is crucial for increased recognition of the cycling of GHG in the northern hemisphere and their impact on climate change on a global scale.

Kohl, Lukas	University of Eastern Finland	Growth efficiency and carbon allocation in the peatland methane cycle	The goal of this proposal is to link process rates in the methane cycle to microbial growth rates and carbon allocation(e.g. necromass formation). Microbial growth efficiency and carbon use efficiency are key parameters in biogeochemical models, however, so far these growth rates have not been measured for individual microbial processes. Similarly, the formation rates of secondary microbial compounds, as a function of microbial growth and transformation, is a crucial parameter for understanding the formation of both stabilized organic matter and easily decomposable/leachable, dissolved organic matter. In this project, we will conduct a pioneering experiment that addresses these questions for methane oxidation, a central process in the peatland methane cycle.

Nuccio, Erin	Lawrence Livermore National Laboratory	Illuminating the contribution of plant-associated fungi to enhanced rock weathering	Mutualistic associations between plants and mycorrhizal fungi can enhance plant productivity, resilience to stress, and carbon (C) allocation belowground. The most ancient and common plant symbionts are arbuscular mycorrhizal fungi (AMF), which colonize 72% of plant species globally and are key contributors to plant nutrition and the soil C cycle. A recent estimate suggests that synergistic interactions between AMF and soil microbes may contribute 70 Tg of assimilated plant N annually. We propose to investigate context-dependent resource exchange of C and nitrogen (N)between a bioenergy grass—Sorghum bicolor, a DOE bioenergy flagship plant—and two AMF guilds. We hypothesize that AMF guilds have distinct effects on the N cycling microbes and resource flux, where their two exploration strategies will have tradeoffs for N recovery depending on N availability.

Rempfert, Kaitlin	Pacific Northwest National Laboratory	Unpacking the metabolic basis of carbon use efficiency to understand and predict soil organic carbon accumulation	Microbial carbon use efficiency (CUE) is a metric that describes the microbial community’s gross biomass production per unit substrate taken up over short time scales. As soil organic carbon (SOC) is highly influenced by microbial growth and biomass accumulation, CUE is important for understanding and predicting soil-climate feedbacks. CUE is a complex metric based largely on the balance of metabolic investments for building biomass relative to other cellular functional attributes in response to environmental conditions. The proposed work explores the metabolic basis of CUE through stable isotope-based measurements of microbial growth and assessments of corresponding ecophysiological microbial phenotypes. We aim to pair multi-omic (transcriptomic and metabolomic)profiling with substrate-agnostic quantification of microbial CUE as a function of soil depth, seasonality, and soil moisture to identify the metabolic mechanisms driving CUE and its sensitivity to environmental change. This work will generate a range of CUE values under varying environmental conditions which can be incorporated by the modeling community to improve predictions of C-cycling.

Rippner, Devin	United States Department of Agriculture	Long term crop rotations alter soil function and prairie carbon dynamics to depth in midwestern cropping systems	Over the past 150 years, the tallgrass prairie biome of central North America has been rapidly replaced by annual cropping systems, transforming the region into one of the world's most productive grain areas. The productivity of this region is in large part attributed to the nutrient rich soil organic matter (SOM) that accumulated from millenia of prairie growth. However, much of this native SOM has been lost over the last 150 years, raising concerns about the sustainability of current agricultural practices. The proposed project will link long-term agricultural management practices and hydrobiogeochemical functions above and below the typical plow layer at macro and microscales.

Thompson, Luke	Cornell University	Single-cell analysis of Symbiont physiology and development using fluorescent protein-tagged cell identity lines to optimize therapeutic molecule delivery to economically important tree crops.	Our lab has developed a new biotechnology based on the gall-forming bacteria Agrobacterium tumefaciens. Our technology combines target gene expression with just the plant growth regulator genes from the bacteria. When our modified A. tumefaciens applied to a plant stem, the result is the formation of a non-pathogenic cluster of plant cells, referred to as a Symbiont, that are transgenic as opposed to the host plant. Symbiont technology is of course based on a bacterial gene manipulation system, but it can also be loaded with molecular products from other microbes. Therapeutics, growth regulating molecules, antibiotics or biopesticides can be produced within the Symbiont system and delivered directly to the host plant reducing user and environmental costs. Symbiont technology grown in vitro has also shown promise as a biofactory for larger scale production of these molecules; this project focuses on optimizing this promising technology.

Van Doren, Steven	University of Missouri	Visualization of the Regulation of the Enzyme that Launches Oil Synthesis in a New Biofuel Crop	The oilseed crop pennycress is being developed for sustainable biofuel production. This project will further develop ongoing research for rational engineering of fatty acid synthesis in pennycress to “open the tap” for oil biosynthesis. The central questions of this project address the structural mechanisms of acceleration and slowing of the biotin carboxylase (BC) activity that launches oil synthesis in the plastid. This will provide structural and functional insight into inhibition and activation of plant oil biosynthesis.