JGI JOINT GENOME INSTITUTE
A DOE OFFICE OF SCIENCE USER FACILITY

Approved Proposals FY25

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

FY 2025 CSP Large Scale Proposals

Name	Institution	Proposal Title	Proposal Description
Barnhart, Elliott	U.S. Geological Survey	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. 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	Saturated soils are characterized as waterlogged soils, rich in organic matter, with low concentrations of

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		cycling across saturated soils	porewater oxygen. Anoxic microbial decomposition of this soil organic matter leads to the production of greenhouse gasses such as carbon dioxide and methane. 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 E.	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. This project will

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			develop a “super pangenome” research platform 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.
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.
Damashek, Julian	Hamilton College	Genome-resolved and activity-based archaeal ecology in a euxinic meromictic lake (Fayetteville Green Lake, NY, USA)	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

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			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 (Netherlands)	Revealing the diversity of primary carbon metabolism across the fungal kingdom	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

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			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.

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John, Uwe	Alfred Wegener Institute for Polar and Marine Research (Germany)	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. 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). 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. 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

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			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	Plant-plant interactions mediated by rhizosphere microbiota using the	Broomrape is a significant pest in the US and Europe, infesting many crops, and

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	Biologie et pathologie Végétales (France)	model: Arabidopsis thaliana (L.) Heynh — Phelipanche ramosa (L.) Pomel	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, Alex	University of Duisburg-Essen (Germany)	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

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			Earth's carbon and nitrogen cycles.
Sullivan, Matt	The Ohio State University	Ecogenomics and biogeochemical modeling of DNA and RNA viruses across terrestrial-marine interfaces	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 variations across the seasons

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			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 University	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

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			is the group that the common ornamentals African violets and Cape primroses come from. It also has unusually 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. 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) Proposals (back to top)

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. The proposed work explores the metabolic basis of CUE through stable isotope-based measurements of microbial growth and assessments of corresponding ecophysiological microbial phenotypes. 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 hydrobiogeo-chemical 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. 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.

FY 2025 CSP Functional Genomics Proposals (*back to top*)

Name	Affiliation	Proposal Title	Description
Chen, Hao	Auburn University	Unraveling the crosstalk in poplar's transcriptional regulatory network for drought tolerance and wood formation using DAP-seq technology	This research maps how genes control drought tolerance and wood production in poplar trees, a key bioenergy crop. By understanding the genetic switches (transcription factors) that regulate these traits, scientists can develop poplars that survive drought while maintaining high biomass production. This directly supports BER's mission to create resilient bioenergy feedstocks through genome-level plant engineering.
Cope-Arguello, Matthew	University of California, Davis	Unraveling the gene regulation necessary for bacterial survival using DAP-seq and RNA-seq	This project investigates how bacteria survive starvation by controlling their genes during nutrient-poor conditions. Understanding these survival mechanisms will enable scientists to engineer resilient microbes that persist in soil between crop plantings, supporting bioenergy feedstock growth. The research also reveals how bacteria drive nutrient cycling at low metabolic rates. This advances BER's mission to manipulate microbiomes for improved bioenergy crop production and understanding of environmental nutrient processes.
Isimikalu, Theophilus Olufemi	University of Maryland Eastern Shore	Elucidating soil carbon stabilization in switchgrass cutting systems: Influence of root exudation and microbial fingerprints	This project examines how switchgrass root compounds and soil microbes interact under different mowing schedules to optimize biofuel yields. By understanding these plant-microbe relationships and their effects on soil processes, scientists can reduce production inputs while maximizing biomass production. This advances BER's mission to develop bioenergy feedstocks through improved understanding of

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			plant-microbe interactions and how management practices influence nutrient cycles in terrestrial ecosystems.
Oakley, Todd H.	University of California, Santa Barbara	Exploring the evolutionary trade-offs of cyanobacterial rhodopsins for broad-spectrum energy capture	Scientists will test millions of rhodopsin protein variants from cyanobacteria to understand how they capture energy from different colors of light. Using machine learning to predict protein function from gene sequences, researchers can design microbes optimized for specific light wavelengths for bioenergy applications. This advances BER's mission to understand microbial metabolism for bioenergy development and build predictive models of biological systems, enabling engineered organisms for enhanced energy production.
Philmus, BJ	Oregon State University	Cyanobacterial secondary metabolites: Linking biosynthetic gene clusters to secondary metabolite structures and function	This research identifies compounds produced by cyanobacteria gene clusters to understand their role in freshwater ecosystem interactions. By linking genes to the chemicals they produce, scientists can determine how these compounds affect community dynamics—whether inhibiting competitors, preventing predation, or controlling fungal growth. This advances BER's mission to understand microbe-microbe interactions in freshwater systems and develop predictive models of microbial behavior in terrestrial-aquatic interfaces.
Rashotte, Aaron M.	Auburn University	Deciphering cytokinin signaling cascades to prolong photosynthesis and boost yield	This project investigates how the plant hormone cytokinin delays leaf aging, maintaining photosynthesis longer for increased biomass production. Using machine learning to analyze gene expression data, researchers identify key genetic regulators controlling leaf lifespan. DNA synthesis enables testing these genes to develop bioenergy crops with extended photosynthetic capacity. This advances BER's

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			mission to understand plant metabolism at the genome level for improved bioenergy feedstock development.
Scesa, Paul	University of South Florida	Animal genomes as a source of hydrocarbon feed stocks and biocatalysts	This project uses soft coral genes as blueprints to produce advanced biofuels and biomaterials. By understanding how corals synthesize defensive compounds, researchers can engineer microbes to manufacture these molecules for energy applications. Gene synthesis enables rapid testing of coral genetic pathways in laboratory systems. This advances BER's mission by developing new biological routes to produce fuels and materials.
Scott, Kathleen	University of South Florida	Functional expression of carbonic anhydrases that play key roles in cellular metabolism and the global carbon cycle	This project studies carbonic anhydrase enzymes that convert CO2 to bicarbonate, a critical process in all life forms. By synthesizing 50 genes encoding two understudied enzyme types common in industrial microbes, scientists can understand factors controlling their activity. This advances BER's mission by revealing microbial metabolism mechanisms essential for engineering organisms to produce biofuels and bioproducts, while improving understanding of how microbes drive nutrient cycles.
Taylor, Tiffany	University of Bath (UK)	Characterising the transcriptional regulon of plant growth promoting bacterium Pseudomonas fluorescens (SWB25) related to environmental persistence and flexibility to inform sustainable use in agriculture	This project investigates how *Pseudomonas fluorescens*, a beneficial soil bacterium, regulates genes to survive environmental changes while supporting plant growth. By studying proteins controlling gene expression, plasmids, and dormant gene activation, scientists can engineer more resilient microbes for agriculture. This advances BER's mission to understand and manipulate microbiomes to enhance bioenergy crop productivity through improved

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			nutrient availability and pathogen suppression.
Wakao, Setsuko	Lawrence Berkeley National Laboratory	Mapping the transcriptional regulators of silica biomineralization in diatoms	Diatoms produce intricate glass-like cell walls that could inspire new biomaterials. This project identifies genes and regulatory proteins controlling silica formation in these microscopic algae. Using DNA synthesis and sequencing, researchers will map how diatoms regulate biomineralization processes. This advances BER's mission to understand biological systems for biomaterial production, with findings applicable to engineering organisms that produce critical minerals and materials for energy applications.
Woolston, Benjamin	Northeastern University	Expanding the product range of anaerobic methanol fermentation	This project will engineer *Eubacterium limosum* bacteria to transform methanol into valuable chemicals like succinate and isobutanol — key ingredients for fuels and industrial products. By testing multiple genetic pathway variations, researchers aim to create the first anaerobic system for this conversion. This advances BER's mission to develop microbial metabolism for converting feedstocks into biofuels and bioproducts, establishing a new platform for energy-efficient chemical production.

FY 2025 CSP New Investigator Proposals (back to top)

Name	Affiliation	Proposal Title	Description
Baker, Bill J.	University of South Florida	Cold-adapted Polyketide Megaenzyme synthesis and expression	This project will study how cold-adapted genes and proteins from an Antarctic organism are synthesizing bioactive metabolites. Researchers seek to learn not only how to produce these metabolites in alternative biological systems, but how that synthetic pathway differs from warmer-water synthetic pathways — ultimately to enhance biosynthesis and reduce energy use in bioproducts.
Barrick, Jeff	University of Texas, Austin	Tempo and mode of changes in gene expression in the Escherichia coli long-term evolution experiment	This project will analyze E. coli from the frozen "fossil" record of a 25+-year laboratory evolution experiment to understand how mutations have caused changes in gene expression that improved bacterial fitness over time. Specifically, it will characterize how regulation and production of different bacterial genes has changed over 75,000 generations of bacterial evolution, helping to develop new models to understand microbial evolution and diversity.
Gilman, Ian	Michigan State University	The genomics of rapidly evolving CAM photosynthesis in Pelargonium	Pelargonium, “wild geraniums” or “Pellies”, are economically important ornamental plants native to arid southern Africa. By comparing the genomes of multiple Pelargonium species, we will describe the genetic elements responsible for crassulacean acid metabolism (CAM), an adaptation that increases drought resilience by enhancing the water use efficiency of photosynthesis. Dissecting the recent emergence of CAM in Pelargonium will, for the first time, illuminate critical steps in CAM evolution and facilitate the genetic engineering of CAM into other systems, while providing a model for the evolution of plant stress responses.
Graf, Louis	Sorbonne University (France)	Genomic and transcriptomic diversification in	The green algae of the order Chlamydomonadales have successfully colonized the polar

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		Arctic and Antarctic green algal Chlamydomonadales	environments of the Arctic and Antarctic. Through genome sequencing and gene expression analysis of four strains of these algae, this study will identify genetic, biological and physiological adaptations supporting life in the poles and identify new biomarkers for the fragility and resilience of polar algae.
Guo, Yuxi	University of Florida	Unraveling physiological mechanisms driving variations in microbial carbon use efficiency: Insights from metagenomic data	This project will reveal how different agricultural management practices and rainfall patterns affect the genetic machinery of soil microbes at a working cattle ranch in Florida, helping to better manage grasslands for both agricultural productivity and carbon-use efficiency in the future.
He, Shaomei	University of Wisconsin, Madison	Depth-discrete metagenomics and metatranscriptomics to inform methane and redox cycling in humic lakes	Globally lakes are experiencing concurrent browning and deoxygenation caused by increased organic carbon inputs from catchment areas and decreased oxygen in the water. Humic lakes, also known as brown-water lakes, serve as a model system to study the ecological consequences and response to surface water-browning and deoxygenation. Researchers will investigate the key players, i.e. microorganisms, in such habitats, aiming to understand their functions and their interactions with each other and with the environment.
Hill-Maini, Vayu	Stanford University	Building Phanerochaete chrysosporium as a model for synthetic and systems biology in white-rot fungi	White-rot fungi are able to degrade recalcitrant materials such as wood and plastics — and produce sustainable materials, chemicals, and foods. Using Phanerochoate chrysosporium as a model, researchers will characterize the inner workings of these organisms' complex metabolism and build tools that enable the engineering of white rot fungi for bioenergy and bioproducts.
Lefler, Forrest	University of Florida	Linking microbial communities to biogeochemical	Stormwater ponds are engineered ecosystems in suburban areas which have recently been identified as

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		cycles in stormwater treatment ponds	biogeochemical (e.g., carbon, nitrogen, phosphorus) hotspots. In this study, researchers aim to evaluate the microbial communities present and their influence on biogeochemical cycling and how they relate to the ponds' ability to store and sequester nutrients.
Leung, Pok Man (Bob)	Monash University	Unveiling unique soil microbial adaptations and biogeochemical processes across drylands in seven continents	The diversity of soil microbes and their role in carbon and nutrient cycling in "dryland" ecosystems, which are characterised by a lack of water, is not well-understood. Through an in-depth study of genomic data of soil microbes and their nutrient cycling processes across time and space within major drylands from all seven continents, this project will substantially expand available genomic data of dryland soil microbes to uncover their unique ecosystem roles and adaptations.
Li, Huang	University of Nebraska, Lincoln	Transcriptomic profiling of mitochondrial respiratory mutants in Chlamydomonas and Camelina for bioenergetic research	By analyzing the gene expression level and network in modified green algae and oilseed crops that differ in the use of these pathways, researchers seek to identify promising genetic targets and components to improve their respiration and energy efficiency at the cellular level. Ultimately, our insights could lead to breakthroughs in optimizing biofuel crops, increasing their growth rates and yields while reducing energy loss and resource inputs.
Maurice, Sundy	University of Oslo	FunDecompo: Processes underlying the assembly of fungal communities and impact on wood decomposition	This project aims to untangle the genetic basis of assembly history and co-occurrences of species in dead wood. Understanding the interplay of saprotrophic fungi using transcriptomics approaches, is a first step toward untangling the decomposition process and consequently the ecosystem functioning.
McGivern, Bridget	University of Wisconsin, Eau Claire	Linking microbial gene expression to	Through the livestock enteric fermentation process, specialized communities of microorganisms

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		variations in rumen methane emissions	living in rumen convert organic matter from feed into hydrogen gas and smaller organic compounds that are used by the animal for energy. This process generates methane as a byproduct, which is then released into the atmosphere. In this project, researchers aim to understand the rumen microbial mechanisms underlying variable methane emissions in cattle by first building a census of microbial genomes inhabiting cattle rumen, and then examining the gene expression of those genomes related to the carbon cycle.
McRose, Darcy	Massachusetts Institute of Technology	Identifying microbial secondary metabolites that solubilize phosphorus in the rhizospheres of native grasses	This proposal focuses on specific types of secondary metabolites, those with redox activity, which can help make the critical nutrient phosphorus more available in soils. We isolated bacteria from the roots of native grasses collected across the US and used newly developed high-throughput chemical screens to identify bacteria that are making secondary metabolites of interest. This work will help us understand how plants and microbes interact and provide tools to help manipulate plant microbiomes for enhanced crop yields.
Murali, Ranjani	University of Nevada, Las Vegas	Investigating novel denitrification pathways in hot and cold springs	By mining the large sequence datasets that became available after the genomics sequencing revolution, novel nitrogen-cycling enzymes were identified. In this study, researchers aim to understand the impact of these novel pathways on nitrogen cycling in hot and cold springs, using sequencing technologies, laboratory cultures and biochemical analyses. The results from this study will provide insight into how microbial adaptation to extreme environments can lead to the development of biochemical novelty.
Osburn, Ernie	University of Kentucky	Exploring the role of viruses in soil carbon	This research focuses on how viruses found in soil ecosystems

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		cycling through stable isotope probing	contribute to carbon cycling, which is essential for maintaining soil health and addressing climate change. To accomplish this goal, researchers aim to develop a new method where "heavy" labelled carbon sources are traced into the DNA of soil viruses, which will allow the identification and characterization of the viruses by sequencing their genomes.
Patel, Ravikumar	The Connecticut Agricultural Experiment Station	The role of phytohormones in bacteria, protist, and plant interactions in the rhizosphere	This project explores how plants, protists, and bacteria interact through signaling molecules like plant hormones to shape the rhizosphere ecosystem. By uncovering these interactions, researchers aim to reveal new mechanisms that promote plant growth and soil health, with potential applications in sustainable agriculture.
Polturak, Guy	Hebrew University of Jerusalem	Discovery of defense-related biosynthetic gene clusters in sugarcane	This study seeks to explore chemical defense mechanisms in sugarcane, a major biofuel and food crop. By investigating the genes and associated metabolites that are induced in sugarcane in response to biotic stress, researchers aim to provide insights into how sugarcane naturally combats pests and pathogens by producing specialized defense molecules.
Reich, Marlis	University of Bremen	Decoding the genetic mechanisms of fungal roles in carbon transformation within the aquatic microbial carbon pump	This project aims to unravel the intricate mechanisms through which aquatic fungi contribute to carbon transformation processes, both in present conditions and under future climate scenarios. By employing advanced transcriptomic and meta-transcriptomic analyses, the project aims to uncover how fungi, through their degradation activity and interactions with other microbes, shape the overall carbon transformation processes within the microbial community.
RoyChowdhury, Taniya	Woodwell Climate Research Center	Pathways of carbon metabolism under cover crops	This study will use a highly-resolved metabolomics approach to quantifying the chemically diverse carbon substrates available for

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			microbial uptake in the cover crop rhizosphere, using data mining techniques to predict the impacts of such chemical diversity on the active soil microbiome by using metatranscriptomics.
Schmidt, Mar	Cornell University	Decoding the metabolic network that sustains Lake Ontario	Microbes are essential to the health of the Great Lakes, which harbor roughly 2 octillion microbial genes — an immense genetic potential currently underexplored, with their diversity and role in the ecosystem largely unknown. This study will explore how microbial communities in Lake Ontario — a vital drinking water source for ~9 million people — adapt and influence water quality, helping to understand how microbial communities regulate nutrient cycling in this vital freshwater ecosystem.
Spiegel, Cody	University of California, San Diego	Integrating metatranscriptomics and metabolomics to reveal key microbial metabolic traits underlying aquatic ecosystem function	This study explores how the mixing of terrestrial and aquatic microbial communities influences leaf litter decomposition in river systems, by linking bacterial gene expression to changes in litter chemistry. Researchers aim to better understand how these microbes interact and adapt to environmental shifts, contributing to ecosystem resilience in the face of climate and land-use change.
Tan, James	Ohio State University	Integrating ecogenomics, a novel viral-host linkage method, and functional genomics to study biogeochemically critical phage-host interactions in a coastal time-series	To understand how coastal microbiomes, particularly viral communities, support ecosystem health and biogeochemical processes in the Gulf of the Naples, researchers will sequence viral and bacterial communities across a comprehensive monthly time-series. In conjunction with novel single-cell techniques and functional genomics, they will explore how viruses impact their host metabolisms, providing insight into how they modulate coastal biogeochemistry.
Timmins-Schiffman, Emma	University of Washington	Antarctic Sea ice and snow metagenomes to	Antarctic sea ice is home to diverse micro-organisms, including bacteria and algae. The goal of this project is

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		reveal community biogeochemical function in a changing environment	to understand how these microbes impact the movement of chemical compounds and nutrients in their ice habitat that connects the seawater below with the atmosphere above.
Venturini, Andressa M.	American University	Amazonian forest degradation: Impacts on soil microorganisms	The Amazon rainforest is rapidly changing: 20% has been cleared, and nearly 40% of what remains is degraded by fires, timber extraction, droughts, and/or habitat fragmentation; yet the impact on soil microbes — key regulators of nutrient and greenhouse gas cycling — remains poorly understood. This research will investigate how Amazonian land-use change and forest degradation affect microbial diversity and function, providing insights to inform environmental policies in the region and its implication for bioenergy production.
Waschulin, Valentin	University of Vienna	Understanding the effect of recurrent drought on growth and function of a grassland soil microbial community	This project is focused on understanding the effect of drought on soil bacteria. Droughts are big stress events for all soil organisms, including bacteria, and recurrent drought significantly changes which bacteria found in a soil. Using a 17-year data set from an experimental site in the Austrian Alps, researchers will analyse the genes of the bacteria that are present in the different plots — which range from no drought treatment to 17 years of drought treatment — to find out how some bacteria continue to thrive when others quite literally "dry up."
Winck, Flavia Vischi	Universidade de São Paulo	Omics analysis of the interplay of amino acids in the regulation of the arginine metabolism and lipids accumulation in Chlamydomonas reinhardtii	This project will investigate how specific amino acids can enhance the production of oils in the microalgae Chlamydomonas reinhardtii, a promising organism for biofuel production. Further research will focus on how these amino acids impact the metabolism of C. reinhardtii to identify specific biological mechanisms that control oil production. By uncovering how these pathways work, the study aims to

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			provide insights for developing new methods to increase oil production in algae, making it a more viable source for renewable energy.
Wisecaver, Jen	Purdue University	Transcriptional characterization of toxin biosynthesis pathways in Prymnesium parvum, a growing algal threat to freshwater ecosystems	Many algal species produce a diverse array of toxins and other specialized bioproducts. Identifying the genes that make these toxins would enable new investigation into how these toxins are synthesized and open new doors for natural product research. This study aims to create a gene expression atlas for the golden alga Prymnesium parvum, surveying 30 unique culture conditions known to perturb toxin production and other traits associated with toxicity.
You, Yaqi	SUNY College of Environmental Science and Forestry	Understanding biochar-induced rhizosphere reprogramming for greenhouse gas mitigation and sustainable bioenergy crop production	Understanding biochar-induced rhizosphere reprogramming for greenhouse gas mitigation and sustainable bioenergy crop production This project will investigate biochar-induced changes in the rhizosphere, with a focus on the microbial mechanisms associated with shifts in plant-microbe interactions, to enhance bioenergy crop production while mitigating human impact through improved microbial interactions and nutrient cycling.
Zhang, Yong	Georgia Southern University	Exploring genomic dynamics and gene regulatory networks underlying the biofuel producing capability of Fusarium oxysporum	F. oxysporum is one of the few filamentous fungal species able to break down biomass and convert monosaccharides to ethanol. Although numerous F. oxysporum have been sequenced as pathogens, its bioenergy production potential has not been comprehensively studied using the cutting edge genomic and functional approaches. This proposed work aims to bridge the gap by sequencing of F. oxysporum with inter-species variation in producing bioethanol from plant biomass. These data will be used to understand the genes and regulatory

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			mechanisms that contribute to bioconversion efficacy.
Zhong, Zhiping	Ohio State University	Illuminating microbial responses to climate change at decadal-to-millennial scales archived in the largest tropical glacier	This proposal requests sequencing of environmental DNA from glacier materials (snow, firn, and ice) and surrounding soils from the world's largest tropical glacier. These samples have been characterized by paleoclimatologist members of this team for date, climate proxies, dust, and chemistry. The sequencing will be used to understand the relationship between climate variation and microbial and viral community response.