FICUS JGI-EMSL FY26 Call (Open 1/16/25)

Timeline

January 16, 2025: Call opens
March 6, 2025: Letters of intent due
March 31, 2025: Invitations of proposals
May 1, 2025: Full proposals due
July 31, 2025: Project decisions sent
October 1, 2025: Project starts

Call Overview

The Joint Genome Institute (JGI), a DOE Office of Science User Facility at Lawrence Berkeley National Laboratory (Berkeley Lab), and the Environmental Molecular Sciences Laboratory (EMSL), a DOE Office of Science User Facility at the Pacific Northwest National Laboratory (PNNL) are seeking collaborative research proposals through the Facilities Integrating Collaborations for User Science (FICUS) program. The FICUS program, originally established in 2014 to encourage and enable ambitious multidisciplinary research projects, integrates expertise and experimental capabilities of multiple DOE-supported user facilities.

The FY2026 FICUS proposal call will include access to expanded capabilities available at DOE-supported user facilities, including the Bio-SANS beamline through the Center for Structural Molecular Biology (CSMB) at Oak Ridge National Laboratory, and the Advanced Photon Source at Argonne National Laboratory via the eBERlight program. Additionally, applicants can also request access to archived biological, genomic, and geological samples and specimens from terrestrial and aquatic sites through the National Science Foundation's (NSF) National Ecological Observatory Network (NEON).

Successful proposals will address high-risk/high-payoff activities within the focus topic areas that can be completed in 24 months, utilize a variety of available capabilities across two or more user facilities, and generate datasets that go beyond what can be produced through individual projects at each of these facilities. Applicants are strongly encouraged to contact facility staff (see contact information below) before submitting a Letter of Intent, to receive guidance on available capabilities and designs for analyses that are tailored to their research goals.

Focus Areas

Proposals submitted to this call should be responsive to one or more of the following focus area topics aligned to the Biological and Environmental Research (BER) program.

Biofuels, biomaterials, and bioproducts: Proposals should be aimed at characterizing biological processes (including pathways generated by synthetic biology approaches) that are relevant to biofuels, biomaterials, and bioproducts production, and connecting these processes to omics-based analyses for DOE-relevant plants, microbes, and microbial communities including viruses. Topics of interest include: generation and use of structural elucidation of proteins of unknown function; use of omics and structural biology data to refine and constrain genome-scale metabolic models; discovery, characterization, and engineering of enzymes and metabolic pathways for biomass decomposition and/or conversion to biofuels, biomaterials, and bioproducts; utilization of C1 substrates; microbially-mediated recycling and upcycling of plastics; secure biosystems design and biocontainment; genome-enabled organic and inorganic material synthesis; and investigations into organisms and/or biological products involved in plant-microbial interactions that impact biofuel and bioproduct feedstock productivity.

Hydro-biogeochemistry: Proposals should focus on the cycling and transport of key elements (especially carbon and nitrogen), nutrients, and other compounds within terrestrial ecosystems. Study systems could include soils, vegetation, microbial communities, the atmosphere, the subsurface, and land/aquatic/atmospheric interfaces, including but not limited to river/stream systems, coastal zones, terrestrial wetlands, and/or urban to rural ecosystems. Proposals should seek to elucidate key hydro-biogeochemical processes through which microorganisms and their metabolic processes: (i) influence soil carbon and nitrogen persistence, turnover, and sequestration, (ii) respond to hydrologic and environmental perturbations, (iii) facilitate the resilience of a given system following a significant disturbance event, and (iv) influence the biogeochemical cycling of critical elements, nutrients, colloids, and other compounds under baseline or disturbance conditions. Understanding the regulatory/metabolic processes of plants, microbes, and microbial communities, including viruses, is of particular interest. Proposals should seek to link microbial populations, genes, and traits to molecular biogeochemistry and to forcings in the surrounding environment. Emphasis is also placed on tracking biological processes across time and space to better understand how micro-scale changes translate into macro-scale effects.

Inter-organismal interactions: Proposals should explore the exchange of metabolites, signals and/or nutrients (carbon, nitrogen, and other elements) among plant roots to shoots, microbes, and viruses in below- and above-ground ecosystems and across associated interfaces (e.g., terrestrial-aquatic and land-atmosphere interfaces), as well as investigate signaling, cooperation, or competition via physical or chemical means under environmental stresses (e.g., flooding, drought, salinity). Proposals focused on the impacts of biological diversity and root structure within plant populations, on plant-associated microbial communities, and plant-microbial interactions are also encouraged. These investigations can include metabolite exchange, structural or functional characterization of transporters, surface proteins, exudates, and VOCs for example carbon transformations and plant mediated CH4 transport, foliar uptake of nutrients. Investigations that focus on the enzymes, pathways, proteins and metabolites involved in secondary metabolism that affect multi-organismal and organism-environment interactions are also encouraged.

Novel applications of molecular techniques: Proposals should be aimed at re-defining the boundaries of scientific integration of experimental and data capabilities across the participating entities. Outcomes should have long-term benefits to DOE/BER goals involving biofuels, biomaterials, and bioproducts production, plastic bioprocessing and degradation, plant-microbe interactions, and nutrient exchange, ecosystem resilience or plasticity in response to significant environmental disturbance events, and land-atmosphere exchanges and feedback. Structural and functional characterization of novel proteins (e.g., enzymes), compounds (e.g., primary and secondary metabolites), or biomaterials produced by genes found in (meta)genomic data, as well as functional analysis of uncultivated organisms, are of particular interest. For high-risk, exploratory studies aimed at assessing the general feasibility or establishing proof of principle, the scope should be limited to a scale required to demonstrate novel results, with the possibility of expanded support after successful completion.

The following topics are not within scope for this call for proposals: *food, feed, pharmaceuticals, cosmetics, starch, marine (more than 185 km from land), human health related, wastewater treatment, and transport of plastics/microplastics.*

Highlighted Capabilities

Proposals should make use of capabilities from two or more of the participating user facilities/entities, where at least one of the facilities must be EMSL and/or JGI.

Environmental Molecular Sciences Laboratory

EMSL provides a wide range of unique and state-of-the-art omics, imaging, and computational capabilities that can be applied to proposals under this call. Applicants should especially consider emerging, cutting-edge capabilities that are available to users who coordinate their proposals with the EMSL scientists who lead their development. The capabilities include but are not limited to the following:

Advanced single-cell biology workflows for elucidating functional heterogeneity of multicellular/multispecies systems such as microbial communities and host-microbe systems. Approaches include small-sample omics (transcriptomics, proteomics, and metabolomics) analyses enabled by advanced cell separation techniques (LCM, FACS, nano-dispensing) as well as split-pool ligation-based single-cell transcriptomics. (Contact: Alex Beliaev, James Fulcher, or Sarai Williams)

Chemical biology tools that emphasize application of activity-based probes to characterize metabolic pathways, identify enzymatic signatures, capture small molecule-protein interactions, and visualize movement and localization of metabolites. (Contacts: Sankar Krishnamoorthy or Alex Beliaev)

Stable isotope probing and analysis platform that includes labeled CO2 plant growth facilities, NMR, IRMS, and NanoSIMS, which enables isotope ratio mapping with high resolution (50 nm). (Contact: Amir Ahkami, Mary Lipton, or Pubudu Handakumbura)

NanoSIMS analysis also enables imaging of isotopic labels and trace elements with high sensitivity (ppm). It is ideally suited for observing the fate of added isotopically enriched compounds in plant-microbe-soil systems. (Contact: Jeremy Bougoure)

Spatial metabolomics, used to investigate the spatial distribution of molecules within biological samples. (Contact: Chris Anderton, Dusan Velickovic, or Kristin Burnum-Johnson)

Structural biology approaches utilizing cell-free expression, native mass spectrometry, and/or NMR capabilities for characterization of proteins and protein complexes (Contact: James Evans, Lili Pasa-Tolić, or Garry Buchko)

High resolution cryo-TEM for atomic resolution structural analysis of proteins, protein complexes, and/or small molecule crystals or for high resolution tomographic analysis of whole cells and tissues. (Contact: James Evans or Amar Parvate)

Aquilos cryo-FIB/SEM for site-selective sample preparation for cryo-EM/tomography or serial section slice-and-view 3D imaging of large tissue or plant/microbe interactions. (Contact: James Evans or Trevor Moser)

Tender X-ray nanotomography system for 3D nanoscale imaging of cells and biological materials. (Contact: James Evans or Scott Lea)

High mass-resolution soil organic matter composition analysis using Fourier Transform Ion Cyclotron Resonance (FTICR) mass spectrometry, particularly proposals that include complementary NMR, LC-MS/MS, or LC-FTICR-MS metabolomics characterization. (Contact: Will Kew).

Transmission electron microscopy, scanning electron microscopy, and helium ion microscopy for chemical and morphological analysis of colloids, organo-mineral associations, and nanominerals. (Contact: Odeta Qafoku).

Mössbauer spectroscopy for analysis of nano-Fe minerals and Fe-organic matter assemblages. (Contact: Ravi Kukkadapu).

Integration of spatial soil structure, organic matter, and elemental composition approaches (above) with omics capabilities provided by the JGI. High-risk/reward proposals are encouraged. (Contact: Emily Graham, Odeta Qafoku, Tamas Varga, or Emiley Eloe-Fadrosh at JGI)

Noninvasive root imaging platform for monitoring and characterizing plant root systems in transparent growth medium. (Contact: Amir Ahkami or Vimal Kumar Balasubramanian)

Optical Coherence Tomography for a non-invasive approach for in situ, 3D imaging of living tissues. The approach can be applied to static samples or deployed in various growth chambers to provide time-series imaging of plants or other systems. (Contact: Amir Ahkami)

Liquid and Solid state NMR-based metabolomics to define the metabolite profile in a biological system, including primary and secondary metabolites and plant cell wall components. (Contact: David Hoyt or Andrew Lipton)

Interactive data visualization tools that support the exploration of complex natural organic matter or proteomics data, and comparison of data across treatment groups. (Contact: Satish Karra or Kelly Stratton)
Tahoma, BER's heterogeneous (CPU/GPU) computing system for highly parallel modeling/simulation and data processing needs. (Contact: Satish Karra)
A suite of TerraForms platforms to measure the impact of target soil parameters on ecological interactions, including pore scale micromodels, mineral-amended TerraForms, RhizoChip, and Bioprinted Synthetic Soil Aggregates.2 These TerraForms platforms are ideal for multiomics characterization and multimodal imaging of the spatial organization of soil and rhizosphere communities (plant, bacteria, and fungi) and mapping molecular exchanges between organisms. (Contact: Amir Ahkami, Arunima Bhattacharjee, or Jayde Aufrecht)

Other capabilities that offer opportunities for novel and exciting experimental data include a variety of in-situ probes for NMR, advanced electron microscopy in a specialized "quiet" facility, high-resolution mass spectrometry, including a 21 Tesla FTICR, and Atom Probe Tomography. Learn more about these and other EMSL capabilities.

Joint Genome Institute

The JGI employs both next-generation short-read sequencing platforms and 3rd generation single-molecule/long-read capabilities, along with DNA synthesis and mass spectrometry-based metabolomics. The capabilities available for this call are listed below. More details about JGI products, including expected cycle times, can be found here. FICUS proposals should request no more than 3 Tb of sequencing, 500 kb of synthesis, and up to 200 samples for metabolomics polar analysis and 500 samples for nonpolar analysis. Requests for Pacific Biosciences long-read sequencing is capped at 1 Tb and 50 samples (up to 500 samples for bacterial/archaeal isolate genomes). Requests for DAP-seq should include a minimum of 92 transcription factors. For EcoFAB experiments, up to 50 EcoFAB devices can be requested per proposal. Researchers are encouraged to review JGI's sample submission guidelines to obtain additional information about the amounts of material that are required for various product types. Individual proposals may draw from one or more of these capabilities as needed to fulfill project goals. Successful proposals often leverage a combination of these capabilities.

De novo sequencing and annotation of plant, algal, fungal, bacterial, archaeal, and viral genomes.
Resequencing for variation detection.
Fluorescence-activated cell sorting for targeted metagenomics and single-cell genomics, e.g. genome sequencing of metabolically active microbes labeled via Bio-Orthogonal Non-Canonical Amino acid Tagging (BONCAT).
Imaging (light and fluorescence microscopy), laser microdissection, and metagenomic sequencing of microbial aggregates and particle-attached bacteria (on a very limited basis pending discussion with JGI. (Contact: Rex Malmstrom)
Microbial and/or viral community DNA/RNA sequencing and annotation (i.e., metagenomes and metatranscriptomes).

Stable isotope probing-enabled metagenomics.
Transcriptome analysis including coding transcript annotation and expression profiling.
Prokaryotic whole genome DNA methylation analysis.
Transcription factor binding site discovery with DAP-seq.
Gene and pathway DNA synthesis.
Whole genome gRNA library construction and QC.
Organism engineering.
LC-MS/MS based metabolomic and exometabolomic analysis of polar (e.g., amino acids, organic acids, sugars, nucleobases, etc.) and non-polar metabolites (e.g., secondary metabolites, lipids, etc.).
Integrated metabolomic and genomic analyses.
Investigations using EcoFAB devices and, if desired, mutant/diverse natural accessions of Brachypodium distachyon supplied by JGI to conduct non-destructive root imaging and growth media sampling experiments to uncover the mechanisms underlying the interactions between plants and their root microbiomes.

For general questions, please contact Christa Pennacchio, Project Management Office. For questions about the appropriateness of projects or experimental design, please contact Tanja Woyke, Deputy for User Programs. Technical and Scientific Leads will also be available to answer any questions prior to proposal submission.

Center for Structural Molecular Biology

CSMB supports the user access and science program of the Biological Small-Angle Neutron Scattering (Bio-SANS) instrument at the High-Flux Isotope Reactor located at Oak Ridge National Laboratory. Neutrons provide unique structural information due to their sensitivity to hydrogen and deuterium that is unattainable by other means. Through this FICUS partnership, CSMB is providing access to resources listed below for studies of hierarchical and complex biological systems.

Small-angle neutron scattering at Bio-SANS provides structural information about a range of biological systems across length scales from 1 – 100 nm. Examples include biomacromolecules and their complexes in solution, biomembranes, and hierarchical and complex systems such as plant cell walls and soils.
Deuterium labeling of biological macromolecules including proteins, lipids, nucleic acids, biopolymers.

These tools help researchers understand how macromolecular systems are formed and how they interact with other systems in living cells. For further information about the CSMB and Bio-SANS please visit https://www.ornl.gov/facility/csmb and/or contact Hugh O’Neill).

Advanced Photon Source

APS at Argonne National Laboratory (ANL) has recently been upgraded with new transformative accelerator technology, significantly increasing the brightness of the produced X-ray beams. The new design of the storage ring, the beamline improvement program and new feature beamlines will offer a wide range of X-ray – based tools that will provide novel opportunities for research pertinent to the BER mission, including biological, geological, geochemical, and environmental sciences, to address existing and new scientific challenges. The eBERlight program serves as a liaison between the user community and the APS, offering an integrated platform enhancing user science through focused communication with users and coordinated activities among the relevant APS beamlines.

In addition to enhanced APS X-ray beamlines and techniques, eBERlight offers expertise and additional infrastructure available at ANL that includes (i) Advanced Protein Characterization Facility (APCF, sector 84 of APS, sample preparation), (ii) Advanced Leadership Computing Facility (ALCF, exascale computing for data processing using supercomputers), (iii) APS cryolab (sample preparation), and (iv) Molecular Environmental Science and Biogeochemical Process Group (MESBPG) laboratories (sample preparation).

Specific capabilities/resources include:

Protein production and structural characterization resources/services in the Advanced Protein Characterization Facility for gene cloning, recombinant protein expression, purification, characterization, crystallization (access to the lab to perform the work or mail-in service for gene-to-structure pipeline). (Contact: Karolina Michalska)

Macromolecular crystallography for determination of 3D structures of macromolecules: proteins, nucleic acids and their complexes. (Contact: Karolina Michalska)

Full-field X-ray imaging for micro- and nano-computed X-ray tomography (CT) to enable 3D visualization of soil cores or aggregates, plant structures, etc. Sample size ranges from µm to cm. (Contact: Xiaoyang Liu)

X-ray microscopy for visualization and quantification of elemental distributions (X-Ray Fluorescence (XRF)) in 2D/3D and structural information (X-ray ptychography) in 2D/3D. XRF approaches are applicable for mapping elements with an atomic number of 14 (silicon) and higher. X-ray ptychography is a computational scanning microscopy technique for acquiring structural information with resolutions beyond the limits of X-ray focusing optics. Both techniques can be applied to a variety of samples in both biological and environmental research, such as soils, plants, rhizosphere, aerosol particles, and microorganisms. Sample size ranges for XRF are from µm to cm with spatial resolution ranges from 50 nm to 30 µm. The highest achievable spatial resolution for ptychography is 5 nm. (Contact: Gosia Korbas)

For general questions, please contact Karolina Michalska.

National Ecological Observatory Network

NEON, a large facility project funded by the National Science Foundation (NSF), is a continental-scale platform for ecological research. It comprises terrestrial, aquatic, atmospheric, and remote sensing measurements and cyberinfrastructure that deliver standardized, calibrated data to the scientific community through a single, openly accessible data portal. In addition to its openly available data products NEON provides access to hundreds of thousands of archived biological, genomic, and geological samples and specimens from terrestrial and aquatic sites. NEON infrastructure is geographically distributed across the United States and will generate data for ecological research over a 30-year period. The network is designed to enable the research community to ask and address their own questions on a regional to continental scale around a variety of environmental challenges. Requests for large numbers of samples or that require additional sample processing may incur a service fee. Additional information about the network is available below:

NEON Field Sites
NEON Research Support and Assignable Assets
NEON Letters of support
Biorepository website
NEON Megapit Archive
NEON Metagenomic sequencing

For general questions, please contact Michael SanClements.

National Microbiome Data Collaborative (NMDC) and DOE Systems Biology Knowledgebase (KBase)

Applicants are encouraged to interface with NMDC and KBase, as appropriate, for the registration, standardization of their data, and multi-omics data integration (NMDC) and advanced analysis (KBase).

The National Microbiome Data Collaborative (NMDC) is an integrated microbiome data ecosystem hosting high-quality, consistently processed multi-omics microbiome data to enable data sharing, management, and cross-comparison across studies in accordance with the FAIR (Findable, Accessible, Interoperable, Reusable) data principles. Applicants interested in collaborating with the NMDC team and using the NMDC Submission Portal for coordinated data capture and sharing across EMSL and the JGI should indicate so in their proposal.

The Department of Energy Systems Biology Knowledgebase (KBase) is a free, open-source data analysis platform for system biology research that supports the FAIR data principles, reproducible analysis workflows, and sharing and publishing of data sets and knowledge generated from your analysis. Please explore the analyses supported by KBase, available at www.kbase.us/learn, and reach out to the KBase staff to discuss how they can support your project.

Data Policies

EMSL: https://www.emsl.pnnl.gov/basic/data-management-policy/1243
JGI: https://jgi.doe.gov/Data-Policy-Support
CSMB: https://www.ornl.gov/content/data-management-plan
APS: https://www.aps.anl.gov/Users-Information/Help-Reference/Data-Management-Retrieval-Practices
NEON: https://www.neonscience.org/data-samples/data-policies-citation

Review Criteria

FICUS proposals are reviewed for technical feasibility by scientific staff at each facility. Proposals also undergo external peer review against four scientific criteria. For each criterion, the reviewer rates the proposal “extraordinary, excellent, good, fair, or poor” and provides detailed comments on the quality of the proposal to support each rating. The reviewer also provides overall comments and recommendations to support the ratings given, noting specifically the proposal’s strengths and weaknesses. These scores and comments serve as the starting point for Proposal Review Panel (PRP) discussions. The PRP is responsible for the final score and recommendation to the facilities’ management.

Criterion 1: Scientific merit and quality of the proposed research (50%)

Potential Considerations: How important is the proposed activity to advancing knowledge and understanding within its own field or across different fields? To what extent does the proposed activity suggest and explore creative and original concepts? How well conceived and organized is the proposed activity?

Criterion 2: Qualifications of the proposed research team to achieve proposal goals and contribute to high-impact science (15%)

Potential Considerations: Does the proposal team, combined with relevant staff expertise from the appropriate facilities, possess the appropriate breadth of skill/knowledge to successfully perform the proposed research and drive progress in this science area? Proposals will be evaluated on whether scientists with expertise and the necessary skills will be ready to perform follow-up research and publications. If successful, would the proposed research deliver high-impact products (for example, be publishable in high-impact journals or contribute to the establishment of a unique high-quality reference dataset)? The size and productivity of the user community will also be considered.

Note: Impact factors are a measure of the average number of citations per published article. Journals with higher impact factors reflect a higher average of citations per article and are considered more influential within their scientific field.

Criterion 3: Relevance of the proposed research to FICUS call (20%)

Potential Considerations: What is the relationship of the proposed research to DOE missions? Does the research project significantly advance the mission goals? Proof of concept proposals for the demonstration of a technology that would be applicable to a DOE mission are acceptable. How well does the project plan represent a unique or innovative demonstration and to what extent does it advance the mission area?

Criterion 4: Appropriateness and reasonableness of the request for resources for the proposed research (15%)

Potential Considerations: Are capabilities requested from at least 2 institutions essential to performing this research? Does the project generate a dataset unique to these facilities and beyond what each could generate by itself? Are the proposed methods/approaches optimal for achieving the scientific objectives of the proposal? Are the requested resources reasonable and appropriate for the proposed research? Does the complexity and/or scope of effort justify the duration of the proposed project? Is the specified work plan practical and achievable within the specified project timeframe (e.g., shorter than JGI's CSP projects)?