FICUS JGI-EMSL FY27 Call

The Facilities Integrating Collaborations for User Science (FICUS) program provides an exciting opportunity to advance collaborative science while utilizing the world-class experimental capabilities at U.S. Department of Energy (DOE)-supported Office of Science (SC) user facilities and collaborating institutions. The FICUS program is seeking collaborative research proposals that leverage and integrate capabilities in multiple facilities in a single project focused on advancing the knowledge and understanding of systems aligned with our focus areas.

The FICUS program, established in 2014, is designed to encourage and enable ambitious multidisciplinary research projects by integrating the expertise, experimental capabilities, data, and samples of multiple DOE Office of Science user facilities and the National Ecological Observatory Network (NEON). Proposals must request resources from at least two of the participating facilities, and principal investigators (PIs) will be limited to not more than two submissions per call.

The eligible SC user facilities and other entities for this FICUS call include:

- Joint Genome Institute (JGI) at Lawrence Berkeley National Laboratory (LBNL)
- Environmental Molecular Sciences Laboratory (EMSL) at Pacific Northwest National Laboratory (PNNL)
- Bio-SANS beamline through the Center for Structural Molecular Biology (CSMB) at Oak Ridge National Laboratory (ORNL)
- Advanced Photon Source (APS) at Argonne National Laboratory (ANL) via the eBERlight program.
- Applicants can also request access to archived biological, genomic, and geological samples and specimens from terrestrial and aquatic sites through the National Ecological Observatory Network (NEON) supported by the National Science Foundation (NSF).

Successful proposals should be designed to address high-risk, high-payoff research activities within the program's focus topic areas and aim to generate datasets that go beyond what can be achieved through individual efforts using capabilities at a single facility, with a completion timeline of 24 months. Applicants are strongly encouraged to contact facility staff (see contact

information below) prior to submitting a letter of intent (LOI), as this early consultation can help tailor research designs and inform decisions about available capabilities.

For a submission to be considered for review, the following template must be used:
FY27 FICUS Research LOI template

For awarded proposals, researchers should plan to ship samples to EMSL as close to the project start date as possible. All year-two samples must be received by EMSL no later than May 1, 2028, unless an exception is made by the project manager and the host Integrated Research Platform Leader. Data generated from FICUS projects are made available in accordance with each user facility's data policies.

Use of AI/ML

It is recognized that AI/machine learning (ML) and large language models (LLMs) are widely used in the modern workplace, including in science. To help ensure scientific integrity, submitters are discouraged from utilizing AI or LLMs to wholly generate proposals or create significant portions of proposals. Proposers are responsible for the accuracy and integrity of the content of their submission.

DOE Mission

The following topics are not within scope for this call for proposals: human health, pharmaceuticals, and cosmetics; food, feed, animal agriculture or aquaculture, and related production systems (including coffee beans, wheat, and other crops); invasive plant species; and first-generation biofuel targets (i.e., corn).

Also excluded are projects focused on environmental treatment, mitigation, or pollution, including biogas, greenhouse gas mitigation, climate change, wastewater treatment, sewage, solid or liquid waste, bioremediation of organic contaminants, per- and polyfluoroalkyl substances (PFAS), and harmful algal blooms.

Projects focused on fundamental science of animal and insect microbiomes or non-bioenergy plant pathogens are also out of scope, as are marine-focused projects (more than 185 km from land).

Focus Topic Areas

Bioeconomy and Biomanufacturing

We are seeking proposals for research aimed at advancing the part of the economy that uses biological resources, such as plants, fungi, algae, bacteria, archaea, microbial communities, viruses, and their byproducts, along with biological knowledge, tools, and processes to produce goods, services, and energy. Such projects would accelerate discoveries that drive synthetic

fuels, biomaterials, and bioproducts using the integrated approaches offered in the FICUS portfolio to characterize biochemical pathways important for conversion.

- Biological processes (including pathways generated by synthetic biology approaches) that are relevant to biofuel, biomaterial, and bioproduct production. Functional genomics and synthetic biology resources (mutant libraries, pathway optimization) to connect genotype to function for traits relevant to biomanufacturing.
- Structural and functional characterization 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.
- Multiomics data integration (metagenomics, metatranscriptomics, metaproteomics, metabolomics) to identify novel enzymes and biocatalysts for industrial applications.
- High-throughput single-cell and small sample size omics for accessing uncultivated microbial dark matter with potential for new biosynthetic capacities.

Hydrobiogeochemistry

We seek proposals for research focused on understanding coupled biogeochemical processes and cycles in terrestrial systems and at terrestrial–aquatic interfaces, across spatial (molecular to kilometers) and temporal (milliseconds to decades) scales, that support the development of more secure and reliable energy systems. We solicit proposals that investigate naturally and anthropogenically driven interactions and feedbacks between biological, mineralogical, and geochemical components, and their associated uncertainties within Earth and environmental systems. Investigations of biotic–abiotic interactions are in scope. Proposals must clearly relate to the development of more secure and reliable energy systems.

- Community and functional profiling using large-scale metagenomes, metatranscriptomes, metaproteomes, metabolomes, and stable isotope probing (SIP) to connect microbial identity with active hydrobiogeochemical transformations.
- Hydrological, chemical, mineralogic, and metabolomic imaging of microbe–mineral–organic matter associations and hotspots to understand the molecular-to-pore-scale mechanisms by which hydrology, microbes, geochemical reactions, and viruses shape organic matter–mineral interactions.
- Impacts of major disturbances, such as wildfire, permafrost thaw, or extreme floods on hydrobiogeochemical processes.
- Microbial traits (e.g., dormancy, stress response, redox plasticity) and soil processes that confer resilience to ecosystem disturbance.
- Under what conditions do microbial interactions generate biogeochemical “hot spots and hot moments.”

Critical Minerals and Materials

We are seeking proposals for research focused on plants, algae, fungi, bacteria, archaea, microbial communities, and hydrobiogeochemical processes involved in the liberation and recovery of critical minerals and materials (CMMs) including rare earth elements (REEs). Such projects can include using integrated approaches offered in the FICUS portfolio to accelerate research on biological and bio-inspired recovery, cycling, and processing of CMMs from various sources.

- Functional characterization of biomining microorganisms that mobilize or accumulate REEs and other critical minerals.
- Metagenome-resolved discovery and multiomics (metabolomics, metaproteomics) based the characterization of microbial pathways involved in REE cycling and biosorption.
- Identification of novel biomolecules (e.g., metallophores, nanomaterials, biopolymers) with potential applications in novel materials for CMM and REE recovery.
- Synthetic biology-enabled enzyme discovery and optimization for selective extraction, recovery, and valorization of critical minerals.
- Biological processes (including pathways generated by synthetic biology approaches) that are relevant to DOE-relevant CMMs.
- Biogeochemical processes in soils and sediments (including aboveground heaps) important to recovering CMMs from unconventional sources.

Highlighted Capabilities

Proposals should make use of capabilities from two or more of the participating user facilities/entities.

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 the 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 (laser capture microdissection [LCM], fluorescence-activated cell sorting [FACS], nanodispensing) as well as split-pool ligation-based single-cell transcriptomics. (Contacts: Alex Beliaev, James Fulcher, or Sarai Williams)
- Chemical biology tools that emphasize the application of activity-based probes to characterize metabolic pathways, identify enzymatic signatures, capture small molecule–protein interactions, and visualize the movement and localization of metabolites. (Contacts: Sankar Krishnamoorthy or Alex Beliaev)

- Stable isotope probing and analysis platform that includes labeled CO2 plant growth facilities, nuclear magnetic resonance (NMR), and isotope ratio mass spectrometry (IRMS). (Contact: Amir Ahkami)
- Nanoscale secondary ion mass spectrometry (NanoSIMS) imaging of isotope ratios, isotopic labels, and trace elements with high sensitivity (ppm) at high spatial resolution (50 nm). This is highly relevant for stable isotope probing (previous bullet) and well suited for observing the fate of added isotopically enriched compounds in plant–microbe–soil systems. (Contact: Jeremy Bougoure)
- Spatial multiomics (metabolomics, lipidomics, and/or proteomics), used to investigate the spatial distribution of molecules within biological samples. (Contacts: Chris Anderton, Dusan Velickovic, or Paul Piehowski)
- High-throughput proteomics approaches including post-translational modification analysis (ubiquitination, phosphorylation, acetylation, carbamylation) for large-scale bacterial, fungal, or algal phenotyping. (Contacts: Paul Piehowski or Marina Gritsenko)
- Structural biology approaches utilizing cell-free expression and/or native mass spectrometry capabilities for the characterization of proteins and protein complexes. (Contact: James Evans)
- High-resolution cryo-electron microscopy (cryo-EM) for the atomic resolution structural analysis of proteins, protein complexes, and/or small-molecule crystals or for high-resolution tomographic analysis of whole cells and tissues. (Contacts: James Evans or Amar Parvate)
- Aquilos cryo-focused ion beam/scanning electron microscopy (cryo-FIB/SEM) instrument for site-selective sample preparation for cryo-EM/tomography or serial section slice-and-view 3-D imaging of large tissue or plant/microbe interactions. (Contacts: James Evans or Trevor Moser)
- High mass-resolution molecular analysis using Fourier-transform ion cyclotron resonance (FTICR) mass spectrometry (MS), particularly proposals that include complementary NMR, liquid chromatography–tandem mass spectrometry (LC-MS/MS), or LC-FTICR-MS metabolomics characterization. (Contact: Will Kew)
- Compositional analysis of dissolved and extracted organic matter (high mass resolution) from model systems, sediments, and soils: FTICR-MS, LC-MS/MS, or LC-FTICR-MS. (Contact: Will Kew)
- Chemical imaging and microanalysis of critical minerals and other biogeochemical components in sediments and soils, including colloids, organo-mineral associations, and nanominerals. Methods include transmission electron microscopy and scanning electron microscopy (Contact: Odeta Qafoku), secondary ion mass spectrometry (Contact: Zihua Zhu), NanoSIMS (Contact: Jeremy Bougoure), matrix-assisted laser desorption/ionization (MALDI) MS imaging (Contact: Dusan Velickovic), 3-D X-ray computed tomography (CT) imaging down to 40 µm (Contact: Tamas Varga), atom-probe tomography for 3-D atom-by-atom maps and simultaneous MS at part per million elemental sensitivity (Contact: Danny Perea).
- Integration of spatial soil structure, organic matter, and elemental composition approaches (above) with omics capabilities provided by the JGI. (Contacts: Emily Graham, Odeta Qafoku, Tamas Varga, or Emiley Eloe-Fadrosh at JGI)

- Optical coherence tomography for a noninvasive approach for *in situ*, 3-D 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. (Contacts: Amir Ahkami or Vimal Balasubramanian)
- 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. (Contacts: 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. (Contacts: Satish Karra or Kelly Stratton)
- Tahoma, the Biological and Environmental Research (BER) program'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. These 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. (Contacts: Arunima Bhattacharjee or Jayde Aufrecht)

Learn more about 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. The capabilities available for this call are listed below. More details about JGI products, including expected cycle times, can be found on the JGI Products web page. FICUS proposals should request no more than 3 Tb of sequencing, 500 kb of synthesis. Requests for Pacific Biosciences long-read sequencing are capped at 1 Tb and 50 samples (up to 2,000 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, protist, 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 noncanonical amino acid tagging (BONCAT). (Contact: Rex Malmstrom)

- 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 for the linkage of microbial identity and function. (Contact: Rex Malmstrom)
- Transcriptome analysis including coding transcript annotation and expression profiling.
- Prokaryotic whole genome DNA methylation analysis.
- Transcription factor binding site discovery with DAP-seq. (Contact: Leo Baumgart)
- Gene and pathway DNA synthesis. (Contact: Ian Blaby)
- Whole genome gRNA library construction and quality control (QC). (Contact: Ian Blaby)
- Organism engineering. (Contact: Ian Blaby)
- Investigations using EcoFAB devices and, if desired, mutant/diverse natural accessions of *Brachypodium distachyon* supplied by JGI to conduct nondestructive root imaging and growth media sampling experiments to uncover the mechanisms underlying the interactions between plants and their root microbiomes. (Contact: Trent Northen or John Vogel).

For general questions, contact Christa Pennacchio, Project Management Office.

For questions about the appropriateness of projects or experimental design, 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

The 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, the CSMB provides access to the 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, visit the CSMB website and/or contact Hugh O'Neill.

Advanced Photon Source

The 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 APCF 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 the determination of 3-D 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 3-D visualization of soil cores or aggregates, plant structures, etc. Sample size ranges from micrometers to centimeters. (Contact: Xiaoyang Liu)
- X-ray fluorescence microscopy (XFM) for the visualization and quantification of elemental distributions in two or three dimensions and X-ray ptychography for 2-D or 3-D structural information. XFM is suitable for mapping elements with atomic numbers higher than that of magnesium. Sample sizes for XFM range from micrometers to centimeters, with spatial resolutions ranging from 50 nanometers to 30 micrometers. X-ray ptychography is a computational scanning microscopy method used to obtain structural information with resolutions exceeding the limits of X-ray focusing optics. The maximum achievable spatial resolution for ptychography is 5 nanometers. Both techniques can be applied to various samples in biological and environmental research, such as soils, plants, the rhizosphere, and microorganisms (Contact: Gosia Korbas)

- X-ray absorption spectroscopy (XAS) is a technique used to investigate the local atomic and electronic structure of materials at the elemental level. XAS provides valuable insights into the local coordination environment, including the coordination number and the identity of nearest neighbors. It also reveals information about site symmetry, geometry, bond distances to neighboring atoms, and the electronic structure surrounding the absorber. This makes XAS uniquely suited for studying metal speciation and biogeochemical processes in soils, plants, and microorganisms, where trace elements play crucial roles in nutrient cycling, contaminant mobility, and enzymatic activity. (Contact: Debora Meira)

For general questions, contact Karolina Michalska.

National Ecological Observatory Network

NEON, a large facility project funded by the 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 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

For general questions, contact Michael SanClements.

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

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

The National Microbiome Data Collaborative (NMDC) is an integrated microbiome data ecosystem hosting high-quality, consistently processed multiomics 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 the sharing and publishing of datasets 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.

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 number 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 the capabilities requested from at least two 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)?

How to Apply

1) Get started – In order to submit a proposal, you will need to create a user account in the EMSL User Portal.

As part of the registration process, you will either need to register for an ORCID ID or enter your existing ORCID iD on your "User Info" page.

At this stage, you should familiarize yourself with the requirements and policies for users:

- EMSL User Agreement Requirements
- JGI's Data Management Policy
- EMSL's Data Management Policy
- Terms and Conditions of EMSL Use

For help at any point in the proposal submission process, please contact EMSL User Services.

2) Submit a Letter of Intent – Initiate a new Letter of Intent (LOI) by logging into the EMSL User Portal and clicking "Submit a Proposal/LOI" in the left-hand navigation of the home screen. The form will guide you to enter details about the proposal, the participants, funding, resources, and samples. Review the entire form well in advance of the submission deadline to make sure you have enough time to compile the required information.

The Proposed Research Project Description is uploaded into the form as a PDF. See the Letter of Intent Guidance for the FY27 FICUS Research program for formatting and content

requirements. Note that several required appendices must be included with the project description as a single PDF document.

Your LOI will be reviewed for responsiveness to the call and alignment to EMSL, partnering institutions, and DOE BER missions and feedback may be provided regarding the feasibility of the proposed research.

3) Submit a Full Proposal – If your Letter of Intent meets the stated criteria for responsiveness and mission alignment, you will be invited to submit a full proposal. Full proposals for this call may only be submitted by invitation.

Initiate a full proposal by logging into the EMSL User Portal. The form will be pre-populated with the details entered into your Letter of Intent but all content can be modified if needed.

The research project description is uploaded into the form as a PDF. See the Proposal Guidance for the FY27 FICUS Research Program for formatting and content requirements. Note that several required appendices must be included with the project description as a single PDF document.

Your proposal should incorporate or respond to any feedback provided following your Letter of Intent. You are strongly encouraged to contact facility staff to discuss your project prior to submitting the full proposal. Any discussions with staff should be initiated at least two weeks prior to the submission deadline.

Proposal Schedule

The full FY27 schedule is below:

Calls for proposals issued	January 6, 2026
Letters of intent received	February 19, 2026
Invitation of proposals	March 24, 2026
Proposals received	April 30, 2026
Technical and scientific review	June 2026

Approval and rejection notices sent	by July 30, 2026
Prepare user agreements	August – September 2026
Projects start	October 1, 2026 or as soon as user agreement is finalized