***Instructions***

* *This template is provided for LOI submission to the FY 2026 EMSL-JGI FICUS Program.* ***All italicized text can be deleted.***
* *Please refer to the* [*EMSL website*](https://www.emsl.pnnl.gov/proposals#types-of-proposals) *for complete submission details, including formatting details (also provided below).*
* *Abstract (~400 words) will need to be submitted through the* [*EMSL User Portal*](https://nexus.emsl.pnnl.gov/Portal) *(NEXUS).*
  + *Note that all components below must be combined in a single PDF file and uploaded to the* [*EMSL User Portal*](https://nexus.emsl.pnnl.gov/Portal) *under Proposed Research.*

**Project Title.** *The project title must be brief, scientifically or technically valid, intelligible to a scientifically or technically literate reader, and suitable for use in the public press.*

**Scientific Questions and Specific Objectives (~250 words).** *Describe the scientific question(s) being addressed. State the specific objectives of the research proposed (e.g., to test a stated hypothesis, create a novel design, solve a specific problem, challenge an existing paradigm, address a critical barrier to progress in the field, or develop new technology), providing concise and unambiguous details.*

**Mission Relevance (~100 words).** *Clearly explain how your research addresses* *this call’s relevance to the listed call topics and describe the value/impact of its economic or societal importance.*

**Significance (~200 words).** *Describe (1) the anticipated importance or significance of the results to be obtained and (2) how the data will be used and by which scientific community(ies).*

**Approach or Work Plan (~500 words).** *Describe the work to be conducted, including estimated resource needs and how the data produced will be used. Include any preliminary data, background measurements, or tests completed that validate the approach. Address the strategy for preparing and delivering samples to the facilities, providing an approximate timeline. Refer to the* [*JGI sample preparation requirements*](http://jgi.doe.gov/collaborate-with-jgi/pmo-overview/project-materials-submission-overview/) *for details on the quantity and quality of the material required for each JGI product type.*

**Types of Resources Needed and Numbers of Samples Expected.** *Using the template provided, identify a high-level list of capabilities as relevant at eBERlight (APS), CSMB, EMSL, JGI, and NEON that you are considering for your research approach. At minimum, your proposal should request resources from two facilities and be inclusive of EMSL and/or JGI. Also include the numbers of samples being planned if applicable. This list allows management and scientific staff to get an idea of the information that would be needed for a full proposal. You will have the ability to add/remove resources during final proposal submission.*

**eBERlight Advanced Photon Source (APS) Resources**

**X-ray Fluorescence Imaging**

2ID-E nano-XRF mapping and tomography  8BM micro-XRF mapping

2ID-D nano-XRF mapping, tomography, and ptychography under cryo temp

**X-ray Computed Tomography**

2BM mono/pink-beam high-speed microtomography (phase/absorption contrast)

32ID nanotomography

7BM white-beam microtomography

**Macromolecular Crystallography (MX)**

21ID-D fully tunable (6.5–20 keV)  21ID-F fixed energy @12.7 keV

21ID-G fixed energy @12.7 keV

**Protein Production and MX Structure Determination by APS staff**

Gene cloning\*  Protein crystallization\*

Structure determination\*  Protein production\*

*\*These capabilities are also available to users who wish to come on site and do the work*

*themselves. Hands-on training provided.*

**Plant Growth**

Reach-in Plant Growth Chamber (only to be used in conjunction with APS data collection; basic controls are available)

**Center for Structural and Molecular Biology (CSMB) Resources**

**BIO-SANS**

Biological Small-Angle Neutron Scattering Instrument (BIO-SANS)

*If requesting HFIR Bio-SANS through CSMB, describe the groups of samples that share the same characteristics. Add more rows as needed for your samples.*

*Examples:*

*Information for a biological sample might be entered as*

*Sample Description: Protein in D2O.*

*Molecular Formula: C2399-H3803-N633-O730-S17 (0.5g) + D2-O (2g) + Na-Cl (1g)*

*Information for a thin film might be entered as*

*Sample Description: Bi-Se (50nm)/Gd-S (70nm)/Al2-O3.*

*Molecular Formula: Bi-Se (50nm)/Gd-S (70nm)/Al2-O3 on Si-O (2g) substrate*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Sample Name** | **Molecular Formula and Quantities** *(weight or thickness)* **of Each Component** | **Sample Description** | **Form** | |
|  |  |  | None  Polycrystal  Powder  Soil  Liquid | Nanomaterials  Polymer  Single Crystal  Thin Film  Gas |
|  |  |  | None  Polycrystal  Powder  Soil  Liquid | Nanomaterials  Polymer  Single Crystal  Thin Film  Gas |
|  |  |  | None  Polycrystal  Powder  Soil  Liquid | Nanomaterials  Polymer  Single Crystal  Thin Film  Gas |

**Environmental Molecular Sciences Laboratory (EMSL) Resources**

*Fill out the table below with a high-level overview of the samples you intend to analyze at EMSL throughout the duration of your project. For EMSL’s purposes, a sample is any material intended to be analyzed or used with EMSL resources. You will have the ability to add/remove resources during final proposal submission. Additional information about these resources can be found on the* [*EMSL website*](https://www.emsl.pnnl.gov/science/instruments-resources)*.*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| ***Goal of Analysis*** | ***Requested Resources*** | ***Sample Type*** | ***Estimated Number of Samples*** | ***Check If You Want Assistance with Statistical Design or Analysis*** |
| *Identification of 13C labeled metabolites* | *Liquid state NMR* | *soil* | *15* |  |
|  |  | Choose one.  If other: specify. |  |  |
|  |  | Choose one.  If other: specify. |  |  |
|  |  | Choose one.  If other: specify. |  |  |

**Joint Genome Institute (JGI) Resources**

*For each capability selected, please indicate the approximate number of samples being requested for each type. More information on the products listed can be found here:* [*https://jgi.doe.gov/our-science/product-offerings/*](https://jgi.doe.gov/our-science/product-offerings/)*.*

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| **Cell Sorting and SIP Capabilities** | |
| ***Capabilities Available*** | ***Approx. # of Samples*** |
| FACS sorting of bacterial/archaeal cells (limit: 8 environmental samples for standard single-cell whole genome amplification and 16 samples for mini-metagenomes of BONCAT-labeled cells). |  |
| Imaging/laser capture microdissection of microbial aggregates and particle-associated bacterial/archaeal cells (limit: 8 environmental samples, yielding up to 92 cell enrichments). Please discuss technical feasibility with [Rex Malmstrom](mailto:RRMalmstrom@lbl.gov) prior to LOI submission. |  |
| Stable isotope probing (SIP) fractionation (limit 36 samples, including all biological replicates and unlabeled controls; each sample is expected to yield 12–16 individual fractions for shotgun sequencing). |  |

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| **DNA Synthesis (must request 100–500 kb)** | |
| ***Capabilities Available*** | ***Approx. # of Constructs*** |
| Constructs <5 kb |  |
| Constructs 5–10 kb |  |
| Constructs >10 kb |  |
| Combinatorial libraries |  |
| sgRNA library |  |
| Data mining |  |
| Strain engineering/CRAGE |  |

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| --- | --- |
| **Ecosystem Fabrication (EcoFAB)** | |
| ***Capabilities Available*** | ***Approx. # of Devices*** |
| EcoFAB (limit 50 devices) |  |

*More information available at* [*https://eco-fab.org/*](https://eco-fab.org/).

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| **Metabolomics** | |
| ***Capabilities Available*** | ***Approx. # of Samples*** |
| Nonpolar metabolite analysis (LC/MS) (limit: 500 samples) |  |
| Polar metabolite analysis (LC/MS) (limit: 200 samples) |  |

*More information available at*

[*https://jgi.doe.gov/our-science/science-programs/metabolomics-technology/metabolite-analyses/*](https://jgi.doe.gov/our-science/science-programs/metabolomics-technology/metabolite-analyses/).

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| **Sequencing** | |
| ***Capabilities Available*** | ***Approx. # of Samples*** |
| Algal *de novo* genomes |  |
| Algal resequencing |  |
| Algal RNA-seq |  |
| Bacterial/archaeal *de novo* genomes |  |
| Bacterial/archaeal resequencing |  |
| Bacterial/archaeal RNA-seq |  |
| Bacterial/archaeal single cells |  |
| DAP-seq (minimum 92 TFs) |  |
| Fungal *de novo* genomes |  |
| Fungal resequencing |  |
| Fungal RNA-seq |  |
| Metagenomes (short read/Illumina) - samples for SIP fractionation should be listed above in the “Cell Sorting and SIP Capabilities” section |  |
| Metagenomes (long read/PacBio) - maximum 50 samples |  |
| Metatranscriptomes |  |
| Plant *de novo* genomes |  |
| Plant resequencing |  |
| Plant RNA-seq |  |
| Other sequencing request (must be approved by JGI staff prior to submission) |  |
| Other sequencing request details: | |

*NOTE: JGI has discontinued support for the following products; these should not be included in your request: iTags, smRNA, bisulfite sequencing, ChIP-seq, and ATAC-seq. More details here:* [*https://jgi.doe.gov/user-programs/phased-out-products/*](https://jgi.doe.gov/user-programs/phased-out-products/)*.*

**National Ecological Observatory Network (NEON) Resources**

For more information about the available samples, visit <https://www.neonscience.org/samples/find-samples>.

**NEON Biorepository**

Samples from the NEON Biorepository

**NEON Letter of Support (if requesting samples from NEON)**

*If you are proposing to use soils from the NEON Biorepository, you must select the checkbox above and also include a*[*letter of support from NEON*](https://www.neonscience.org/resources/research-support/letters-support) *for the specific samples in your Letter of Intent. The PDF version of the letter must be appended to your Project Description file by combining the two PDFs.*

**Suggested Reviewers (optional).** *Proposers may include a list of reviewers who they believe are especially well qualified to review the proposal and who are not recent collaborators/coauthors.*

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| **Reviewer Name** | **Institution** | **Email Address** |
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