**Project Title:**

**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 DOE’s [mission](https://jgi.doe.gov/user-programs/program-info/doe-mission-relevance/), 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 tomography [ ]  8BM micro-XRF 2-D

[ ]  2ID-D nano-XRF and Ptychography under cryo temp

**X-ray Computed Tomography**

[ ]  2BM mono/pink-beam tomography [ ]  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

**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*

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| --- | --- | --- | --- |
| **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**

Additional information about these resources can be found on the [EMSL website](https://www.emsl.pnnl.gov/science/instruments-resources).

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| **Analytical**  |
| ***Capabilities Available*** | ***Approx. # of Samples*** | ***Optional Notes*** |
| [ ]  C, H, N, S Analyzer |  |  |
| [ ]  Confocal Raman Spectrometry |  |  |
| [ ]  Fluorescence Spectroscopy |  |  |
| [ ]  Inductively Coupled Plasma Mass Spectrometry (ICP-MS) |  |  |
| [ ]  Ion Chromatography |  |  |
| [ ]  Isotope Ratio Mass Spectrometry (IRMS) |  |  |
| [ ]  Mössbauer Spectrometry |  |  |
| [ ]  Pyrolysis Gas Chromatography/Mass Spectrometry (Pyrolysis GC/MS) |  |  |
| [ ]  Sum Frequency/Second Harmonic Generation (SFG/SHG) |  |  |
| [ ]  X-ray Diffraction (XRD) |  |  |

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| **Computational** |
| ***Capabilities Available*** | ***Approx. # of Samples*** | ***Optional Notes*** |
| [ ]  Data Analysis & Visualization |  |  |
| [ ]  Midrange Scientific Computing |  |  |

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| **Imaging** |
| ***Capabilities Available*** | ***Approx. # of Samples*** | ***Optional Notes*** |
| [ ]  Airyscan |  |  |
| [ ]  Atom Probe Tomography (APT) |  |  |
| [ ]  Atomic Force Microscopy |  |  |
| [ ]  Coherent Anti-Stokes Raman Scattering (CARS)/Stimulated Raman |  |  |
| [ ]  Confocal, FLIM & Multiphoton Fluorescence Microscopy |  |  |
| [ ]  Cryogenic Transmission Electron Microscopy (Environmental Microbiology, Structural Biology) |  |  |
| [ ]  Environmental Transmission Electron Microscopy (TEM) |  |  |
| [ ]  Fourier-Transform Infrared (FTIR) Microscopy |  |  |
| [ ]  Helium Ion Microscopy (HIM) |  |  |
| [ ]  Holographic 3-D Live Cell Imaging |  |  |
| [ ]  Lattice Light Sheet |  |  |
| [ ]  Mass Spectrometry Imaging |  |  |
| [ ]  Nanoscale Fourier-Transform Infrared(Nano FTIR) |  |  |
| [ ]  Nanoscale Secondary Ion Mass Spectrometry (NanoSIMS) |  |  |
| [ ]  Nanospray Desorption Electrospray Ionization Mass Spectrometry (NanoDESI) |  |  |
| [ ]  Optical Coherence Tomography |  |  |
| [ ]  Raman Atomic Force Microscopy (Raman AFM) |  |  |
| [ ]  Scanning Electron Microscopy |  |  |
| [ ]  Scanning Electron Microscopy–Energy-Dispersive X-ray (SEM-EDX) |  |  |
| [ ]  Single-Molecule Fluorescence Microscopy |  |  |
| [ ]  Structured Illumination Microscope & Confocal |  |  |
| [ ]  Super Resolution Fluorescence (STORM/PALM) |  |  |
| [ ]  Tender X-ray Nanotomography |  |  |
| [ ]  Time-of-Flight Secondary Ion Mass Spectrometry (ToF-SIMS) |  |  |
| [ ]  Transmission Electron Microscopy–Energy-Dispersive X-ray/Electron Energy-Loss Spectroscopy (TEM-EDX/EELS) |  |  |
| [ ]  X-ray Computed Tomography (XCT) |  |  |
| [ ]  X-ray Photoelectron Spectroscopy (XPS) |  |  |

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| **Laboratory Preparations & Cell Separations** |
| ***Capabilities Available*** | ***Approx. # of Samples*** | ***Optional Notes*** |
| [ ]  Activity-Based Probes  |  |  |
| [ ]  Cell-Free Expression Pipeline |  |  |
| [ ]  Cryosectioning (Cryo-FIB/SEM) |  |  |
| [ ]  Fluorescence-Activated Cell Sorting (FACS) |  |  |
| [ ]  Focused Ion Beam–Scanning ElectronMicroscopy (FIB-SEM) |  |  |
| [ ]  Intermediate-Scale Flow Cells |  |  |
| [ ]  Laser Capture Dissection Microscope |  |  |
| [ ]  Mass Cytometer |  |  |
| [ ]  Pore Scale Micromodels |  |  |
| [ ]  Soil Hydraulic Property Measurement |  |  |
| [ ]  Soil Incubation |  |  |
| [ ]  Terraforms (synthetic habitats) |  |  |

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| **NMR & EPR** |
| ***Capabilities Available*** | ***Approx. # of Samples*** | ***Optional Notes*** |
| [ ]  Electron Paramagnetic Resonance (EPR) |  |  |
| [ ]  Liquid NMR - Organic Matter/Complex Mixtures (DOM/NOM and lignin)  |  |  |
| [ ]  Liquid NMR - Structural Biology (proteins, protein complexes) |  |  |
| [ ]  Liquid NMR for Metabolomics and Natural Products |  |  |
| [ ]  Solid-State NMR |  |  |

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| **Omics & Organic Matter Analysis** |
| ***Capabilities Available*** | ***Approx. # of Samples*** | ***Optional Notes*** |
| [ ]  Omics/Mass Spectrometry for Bottom-Up Proteomics |  |  |
| [ ]  Omics/Mass Spectrometry for Intact Proteins/Top-Down Proteomics |  |  |
| [ ]  Omics/Mass Spectrometry for Lipidomics |  |  |
| [ ]  Omics/Mass Spectrometry for Metabolomics |  |  |
| [ ]  Organic Matter Analysis (SOM/DOM): Fourier-Transform Ion Cyclotron Resonance (FTICR) |  |  |
| [ ]  Real-Time Mass Spectrometry |  |  |

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| **Plant Growth** |
| ***Capabilities Available*** | ***Approx. # of Samples*** | ***Optional Notes*** |
| [ ]  Portable Photosynthesis System (LI-COR) |  |  |
| [ ]  Growth Chambers (Walk-in, Reach-in, with add-on resources like Stable Isotope Probing, Fluorescence Labeling, and Imaging) |  |  |

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| **Single-Cell Transcriptomics** |
| ***Capabilities Available*** | ***Approx. # of Samples*** | ***Optional Notes*** |
| [ ]  Ion Proton B Sequencer |  |  |
| [ ]  Ion S5 Sequencer |  |  |
| [ ]  NextSeq550 Sequencer |  |  |

\*Optional notes may include sample considerations like agrochemical or isotope addition, media composition, salinity, pH, biomass yield, etc.

**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/>.

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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). |  |
| [ ]  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 (limit 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 (no iTags) - samples for SIP fractionation should be listed above in the “Cell Sorting and SIP Capabilities” section |  |
| [ ]  Metatranscriptomes |  |
| [ ]  Plant *de novo* genomes |  |
| [ ]  Plant resequencing |  |
| [ ]  Plant RNA-seq |  |
| [ ]  Other sequencing request |  |

*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**

If you are proposing to use soils from the NEON Biorepository, you must select the checkbox below 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. For more information about the available samples, visit <https://www.neonscience.org/samples/find-samples>.

**NEON Biorepository**

[ ]  Samples from the NEON Biorepository

**Active Collaborators List.** Provide a list of active collaborators and individuals who may represent a conflict of interest for the PI and co-PI(s) from the past 2 years. Conflicts of interest are not required for participants identified as “Team Members.” In addition to research project collaborators, the list must include coauthors with whom you’ve actively interacted, coeditors, advisors and advisees, and financial affiliations, all from the past 2 years. Participation in very large collaborative efforts with an individual does not necessarily constitute a conflict of interest. Identify those who would have a personal interest in this proposal or whose unbiased judgment would be questioned by a reasonable person familiar with your relationship. Lists of more than 100 collaborators (per investigator) should be shortened to include only the closest collaborators.

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| **PI name:** |
| **Last Name, First Name** | **Key Coauthor** | **Collaborator** | **Advisee / Advisor***(specify)* | **Other***(specify nature)* |
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| **Co-PI name:** |
| **Last Name, First Name** | **Key Coauthor** | **Collaborator** | **Advisee / Advisor***(specify)* | **Other***(specify nature)* |
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**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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| **Suggested Reviewers** |
| **Reviewer Name**  | **Institution** | **Email Address** |
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