**FY25 FICUS EMSL- or JGI-Based Research Proposal Template**

* *This template is provided for full proposal submission to the FY2025 FICUS EMSL- and JGI-based research proposal.*
* *Abstract needs to be submitted through the online portal. It is not required in the project description document below.*
* *Please refer to the* [*EMSL website*](https://www.emsl.pnnl.gov/proposals#types-of-proposals) *for full submission details, including formatting details (also provided below).*
* *Document formatting guidelines:*
* *Pagination is required. There is a 10-page limit to the Project Description. 1-inch margins necessary*
* *Additional 10 pages of supporting materials allowed, such as charts, graphs, and figures.*
* *11-point fonts (or larger for headings). Captions, symbols, special characters, can have a font of less than 11 points.*
* *No more than 5 lines of text within a vertical space of one inch and single-column format for text*
* *There are 7 appendices in this template. Appendices are not counted towards project description page-limit. Appendices 1-3 are compulsory. Appendix 4 is only relevant to proposals requesting JGI resources. Appendix 5 is only relevant to proposals requesting computing support. Appendix 6 is only relevant to proposals requesting Bio-SANS through CSMB resources. Appendix 7 is optional letter of support.*
* *Note that all required appendices must be combined with the Project Description in a single PDF file and uploaded to the* [*EMSL user portal*](https://nexus.emsl.pnnl.gov/portal)*.*
* *All italicized text should be deleted and replaced with proposal content.*

**Project Description (limit to 10 pages, excluding charts, graphs, and figures)**

1. **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.*
2. **Scientific Questions and Specific Objectives** *(~700 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.*
3. **Mission Relevance** *(~700 words).  Describe the relevance and impact of this project to DOE’s Office of Biological and Environmental Research* [*mission areas*](https://science.osti.gov/ber)*, as well as*[*EMSL*](https://www.emsl.pnnl.gov/about)*,*[*JGI*](https://jgi.doe.gov/user-programs/program-info/doe-mission-relevance/)*, and other partners’ missions (as relevant), and its economic or societal importance.*
4. **Background***(~400 words). Provide a concise discussion of previous work to make clear what the research problem is, why you want to do this study, exactly what has been accomplished, and demonstrate why the studies need to be continued.*
5. **Approach or Work Plan** *(~1200 to 1500 words). Describe the work to be conducted, along with any preliminary data, background measurements, or tests completed that validate the approach (include references where relevant and attach the full citations as an appendix). Address the strategy for preparing and delivering samples to relevant facilities, providing approximate shipping dates to each facility. Refer to the*[*JGI sample preparation requirements*](http://jgi.doe.gov/collaborate-with-jgi/pmo-overview/project-materials-submission-overview/)*for details on quantity and quality of material required for each product type.*
6. ***For JGI (if proposed) requests:***
   1. *For proposals including a sequencing component, specific technical details describing how the sequencing should be carried out are not necessary. If your proposal is accepted, JGI staff will work with you to define the sequencing scope in detail based on current capabilities and technologies, which are constantly changing. Include expectations from JGI beyond generating the raw sequencing reads and output from JGI's* [*standard analysis pipelines*](https://jgi.doe.gov/our-science/product-offerings/)*, along with justifications for the additional support.*
   2. *For proposals requesting metabolomics, please specify metabolic hypotheses that motivate the analyses, including target classes of metabolites, ideally specific target metabolites, and total number and types of samples (including replicates).*
   3. *All proposals including a synthetic biology component must describe the biosecurity, biosafety, biocontainment, and environmental aspects of the proposed research in Appendix 2 (resource request), including both the current aspects and the long-term implications of the work (desirable or otherwise). This information will be critically assessed during the* [*JGI's Synthetic Biology Internal Review*](https://jgi.doe.gov/our-science/science-programs/synthetic-biology/synthetic-biology-guidelines/) *process, and missing or incomplete information will jeopardize consideration of the proposal.*

***B. Appendices (Not counted under page limit. Appendices 1-3 are compulsory; Appendices 4-6 as relevant to resources requested in proposal. Appendix 7 is optional)***

**Appendix 1: List of References (required)**

*List all bibliographic citations following accepted scholarly practices in providing citations for source materials relied upon when preparing any section of the proposal. Each reference must include names of all authors (in the same sequence in which they appear in the publication), the article and journal title, book title, volume number, page numbers, and year of publication. If the document is available electronically, the website address should also be identified. In-text citations must use numbered formatting with brackets (i.e., [1] or [2-5]) corresponding to the full citation listed. This section does not have a page limit but must not be used to provide parenthetical information outside of the 10-page Project Description or 1-page Computing Approach.*

**Appendix 2: CVs (required)**

*Insert abbreviated CVs (2-page maximum each) for the PI and each of the co-PIs.*

**Appendix 3: Active Collaborators List (required)**

*Using the template below, 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 co-authors with whom you've actively interacted, co-editors, 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. Place an “X” in the appropriate column to indicate the type of conflict.*

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| --- | --- | --- | --- | --- |
| **PI name:** | | | | |
| **Last Name, First Name** | **Key Co-Author** | **Collaborator** | **Advisee / Advisor**  *(specify)* | **Other**  *(specify nature)* |
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| **Co-PI name:** | | | | |
| **Last Name, First Name** | **Key Co-Author** | **Collaborator** | **Advisee / Advisor**  *(specify)* | **Other**  *(specify nature)* |
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**Appendix 4: Joint Genome Institute Resources (if proposed)**

*Please indicate the capabilities that you are requesting from JGI. More information about these products, estimated sequence output, and analysis pipelines is available at* [*https://jgi.doe.gov/our-science/product-offerings/*](https://jgi.doe.gov/our-science/product-offerings/)*.*

*For questions about the JGI resource request form, please contact* [*jgi-jira+pmosupport@lbl.gov*](mailto:jgi-jira+pmosupport@lbl.gov)

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| **Cell sorting and SIP capabilities** | |  |
| ***Capability*** | ***# of Samples*** | ***Estimated date of sample shipment to JGI*** |
| Fluorescence-activated Cell Sorting (FACS) 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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| **Ecosystem Fabrication** | |
| ***Capability*** | ***Approx. # of Devices*** |
| EcoFAB (limit 50 devices) |  |

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

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| **Metabolomics** | |  |
| [*Capability*](https://jgi.doe.gov/user-programs/product-offerings/) | ***# of Samples*** | ***Estimated date of sample shipment to JGI*** |
| Non-polar 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** | |  |  |
| [*Capability*](https://jgi.doe.gov/user-programs/product-offerings/) | ***# of Samples*** | ***Estimated date of sample shipment to JGI*** | ***Analysis Support Requested beyond JGI’s*** [*standard pipelines*](https://jgi.doe.gov/user-program-info/product-offerings/) |
| Algal *de novo* genomes |  |  |  |
| Algal resequencing |  |  |  |
| Algal RNA-seq |  |  |  |
| Bacterial/archaeal/viral *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 |  |  |  |
| 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/)*.*

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| **Organism detail (add rows if needed)** | | |
| ***Kingdom*** | ***Genus, species*** | ***Genome size (Mb) – eukaryotes only*** |
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| **Environmental sample detail (add rows if needed)** | |
| ***General description of metagenome sample and source*** | ***Sequencing coverage requested (Gb)*** |
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| **DNA Synthesis (Biosafety certification required; see below)** | | |
| [*Capability*](https://jgi.doe.gov/user-programs/product-offerings/) | ***# of Constructs*** | ***Request (kb)*** |
| Constructs <5kb |  |  |
| Constructs 5-10kb |  |  |
| Constructs >10kb |  |  |
| Combinatorial library |  |  |
| Data mining |  |  |
| sgRNA library |  |  |
| Strain engineering/CRAGE |  |  |
| **TOTAL (request must be 100-500kb)** |  |  |

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| **Request for Data Mining** (**offered for proposals including a synthesis component)** |
| The JGI’s genome portals contain a wealth of genomic data from microbes, fungi, plants, microbiomes and viruses. Proposers may request assistance with database searches for the selection of target genes and pathways for synthesis. Note: JGI's overall capacity in data mining and analysis for synthesis projects is limited, and best used in constrained and well-defined searches. Users unsure about the scale of their proposed data mining tasks are encouraged to contact JGI in advance of submitting their project to discuss feasibility.  Are you requesting JGI support for data mining activities?  Yes  No  If yes, please describe in detail what data mining capabilities you are requesting from the JGI, including the types of sequences to be identified, the source data sets to be mined, and the search/identification/prioritization methods to be used: |

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| **Request for Strain Engineering/CRAGE (offered for proposals including a synthesis component)** |
| JGI is offering a limited capacity of Chassis-independent recombinase-assisted genome engineering ([CRAGE](https://jgi.doe.gov/an-age-of-crage-advances-in-rapidly-engineering-non-model-bacteria/)) to users. This technology enables integration of large, complex genetic constructs directly into the chromosomes of diverse gamma-proteobacteria with high accuracy and efficiency. Proposals may request up to 96 constructs to be cloned into a CRAGE compatible vector under the control of a T7 promoter and conjugated into a maximum of 5 Gamma-proteobacteria hosts.  **We currently do not offer domestication of new strains to users.**  Are you requesting JGI support for Strain Engineering?  Yes  No  If yes, how many constructs?  Choose up to 5 Gamma-proteobacteria strains:  *Pseudomonas putida KT2440*  *Pantoea agglomerans ATCC 13460 (Eh1087 (ICMP 13301))*  *Dickeya solani DSM 28711*  *Yersinia aldovae DSM 18303*  *Aeromonas piscicola LMG 24783*  *Photorhabdus luminescens laumondii TTO1*  *Shewanella oneidensis MR-1*  *Photobacterium halotolerans DSM 18316* |

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| **DNA Synthesis Biosafety Information (required for all proposals including a synthesis component)** |
| **Are any of the genes or fragments to be synthesized:**  1.Related to the pathogenicity of an organism?\*  Yes  No  2. Known to or has potential to encode any form of infectious agent or  viral life-cycle component?\*  Yes  No  3. Known to have any toxicity, or the likelihood that this project might  increase toxicity?\*  Yes  No  4. Intended for use in creating a vaccine?\*  Yes  No |
| **Comments (required if you answered Yes to any questions above):** |

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| **Biosecurity, Biosafety, Biocontainment, and Environmental screening (required for all proposals including a synthesis component)** |
| **For each required section listed below, describe aspects of your proposed research, including both the current aspects and the long-term implications of the work (desirable or otherwise). Describe what you will do to address any aspects of concern and how you will mitigate any undesirable outcomes. The information will be critically assessed during the JGI’s** [DNA Synthesis Internal Review process](https://jgi.doe.gov/our-science/science-programs/synthetic-biology/synthetic-biology-guidelines/)**, and your research may be delayed if modifications are needed due to insufficient consideration of these aspects.** |
| **Biosafety \*** - include measures to prevent large-scale loss of biological integrity, focusing both on ecology and human health. These measures may include but are not limited to conduction of regular reviews of the biosafety in laboratory settings, as well as strict guidelines to follow to protect from harmful incidents. |
| **Biosecurity/Biocontainment \*** - include measures aimed at preventing the introduction and/or spread of harmful organisms (e.g. viruses, bacteria, etc.) to animals and plants in the surrounding community or environment or to prevent potential bio-terrorism. |
| **Environmental Impact \*** - include your thoughts on the positive and/or negative impacts the results of your research may have on the environment in the near term or long term. |
| **Ethical, Legal, and Societal Issues \*** - discuss how your research may be viewed within the community as it relates to these issues and how you might mitigate concerns that citizens may have regarding the potential impacts. |

**Appendix 5: Computing Resources (if proposed)**

*Proposers need to complete two sections that include (i) a 1-page description (guidance provided below, and (ii) Computing Resource template provided below about the proposed computational method or approach, the software or code to be used, and details about the requested computing resources, file storage, and staff support needed.*

1. **Computing description guidance (1-page)** (Section 1 of 2)
   1. *Computing Resources*

*There is no upper limit on node-hours that can be requested, but the amount of time requested must be justified and tied to the scientific aims of the proposal. Tahoma allocations are awarded in units of wall-clock time expressed in node-hours, and there are a total of approximately 1,500,000 node-hours available per year. Tahoma's 160 CPU nodes each have 36 (3.1 GHz) Intel Xeon processor cores, so 10,000 Tahoma CPU node-hours are equal to 360,000 processor core-hours. The CPU nodes each have 384 GB of memory and 2 TB of on-node flash storage. Tahoma's 24 GPGPU nodes each have 36 processor cores and 2 Nvidia v100 GPGPUs, 1536 GB of memory, and 7 TB of on-node flash storage. Tahoma's 10 PB global file system is capable of 100 Gigabyte/sec bandwidth.*

*Upon successful review and approval of a proposal, computing resources will be allocated for analysis and archiving of experimental data generated at EMSL.* [*Additional details on Tahoma are available here.*](https://www.emsl.pnnl.gov/MSC/UserGuide/tahoma/tahoma_overview.html) *For questions regarding these requirements, please contact* [*Satish Karra*](https://www.emsl.pnnl.gov/staff/satish-karra)*.*

* 1. *Data Storage Resources*

*EMSL Computing Resources use large, shared file systems—as a result, it is important that project proposals provide a meaningful estimate of data storage needs. EMSL user projects are required to follow EMSL’s* [*Data Management Policy*](https://www.emsl.pnnl.gov/basic/data-management-policy/1243)*.*

1. **Computing Resource Template** (Section 2 of 2)

**Sensitive Data Restriction**

*The EMSL computing systems available to users are not approved for use with sensitive data. The processing, storage, or transmittal of sensitive data (e.g., Personally Identifiable Information, Official Use Only, etc.) are thus prohibited on Tahoma and Aurora. Due diligence must be used to prevent inadvertent disclosure of invention, patent, or other sensitive information.*

By checking this box, I confirm that participants on this proposal will NOT process, store, or transmit sensitive data on Tahoma or Aurora.

**Computing Resource Request**

*Using the form below, provide details regarding the amount of computer resources and support needed, as well as the amount of file storage you expect to need.*

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| **TOTAL RESOURCES REQUESTED** | | | | | |
| **CPU Hours** (total request for first year of project) | | |  | | |
| **GPGPU Hours** (total request for first year of project) | | |  | | |
| **Data Storage** (total request for first year of project) | | |  | | |
| **REQUEST DETAILS** | | | | | |
| **Software/Code** | **Node type** (CPU or GPU) | **Estimated number of jobs** | **Estimated total node-hours** | **Relevant expertise of team members** | **EMSL support requested** (E.g., compiling code, libraries needed, training, etc.) |
| *Example entry (can be deleted):*  *DataProcessTool 2.3* | *CPU* | *20* | *10,000* | *Expert at using. Minimal experience installing Windows version. No experience with Linux version, especially installation and using HPC (GPU and parallel versions of code; shared file system; job submission system).* | *Help installing on Tahoma. Tutorial and help logging in/running jobs. Guidance/training on managing archiving large output files to ensure compliance with EMSL data policies. Assistance to ensure reproducibility and sustainability of our workflows, e.g., using Docker or Singularity. Also, there is apparently a way to “program” the software to sweep and analyze many files using scripting; it would be helpful to learn to leverage this capability.* |
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**Appendix 6: Bio-SANS Resources (if proposed)**

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 |

**Appendix 7: Letter of Support (optional)**