# Community Sequencing Program: Project Proposal

Proposer’s Name:

**Project Title:**

**Proposal (WIP) ID**:

**General Guidelines**:

Please prepare your proposal in 12-point Times font using the guidelines and specific page limits for each section as given below. CVs/biosketches of lead participants should be appended to this document and are not counted in the page limits. A reference list and any letters of support or collaboration are also in addition to the page limits below.

Please write the proposal at a level appropriate for someone familiar with the general area of your research, but not necessarily having an exhaustive knowledge of the subject area. We suggest you read the [review criteria for JGI](http://www.jgi.doe.gov/CSP/user_guide/reviews.html) to help focus your proposal appropriately.

Please submit this and all other support documents in Microsoft Word (.DOC or .DOCX) or PDF format. The documents can be uploaded to the CSP proposal submission site at <http://proposals.jgi-psf.org/> after April 21, 2013.

NOTE: PLEASE USE THE [EMSL USER PORTAL](http://www.emsl.pnnl.gov/access/process.jsp) TO SUBMIT PROPOSALS FOR THE JOINT EMSL/JGI FOCUS AREA.

## Proposal Sections:

A) Brief description: (Limit 1 page)

*Abstract:*

Introduce the project, and briefly describe its scientific merits.

*Scope of Work:*

For proposals requesting sequencing, please state the organism(s) and/or environment(s) from which samples will be prepared and the general nature and amount of sequence requested. 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 this in detail based on current JGI capabilities, which are constantly changing. Include expectations from JGI beyond generating the raw sequencing reads, along with justifications, i.e., assembly, annotation, human validation, gene annotation jamborees, collaboration regarding interpretation, additional efforts at gap closure, etc.

For proposals requesting synthesis, please specify the number of constructs and the total amount of synthesis requested.

For all proposals, please describe why the present proposal requires the technical and/or computational resources and capabilities and/or the skills of JGI program staff to be successful.  Describe why the project could not be accomplished by using local core sequencing facilities or commercial sequencing services.

**B) Background information: (Limit 3 pages)**

*Technical Information:*

For genomes, include specific information on species, genome size, G+C content, polymorphism level, and repeat structure, with details about how these are known. **Proposals for eukaryotic genome sequencing must include high quality information about each of these factors or review cannot be completed.**

For metagenomes, provide as much detail as is known about the environment and its expected complexity.

For proposals requesting synthesis, please specify the average size and size range of the inserts, the total amount of synthesis requested and the average GC content. Additionally, please indicate the desired destination vector (including a vector map if not a commercial vector).

*Available Resources:*

For proposals requesting sequencing, specify genomic resources already in place to aid this project, e.g., physical maps, genetic maps, fingerprinted BAC libraries, reference genomes/transcriptomes.

*Technical Challenges:*

List any potential technical difficulties.

For single cell proposals, specifically discuss the likelihood that sorted cells will include the cells of interest.

*Starting Materials:*

For proposals requesting sequencing, specify availability of starting materials. The preparation of high quality DNA/RNA for sequencing is frequently a bottleneck for large projects. Please specifically address the community's strategy for preparing and delivering DNA/RNA to JGI in a timely fashion. Please refer to the JGI [Sample Preparation Requirements](http://my.jgi.doe.gov/general/gettingstarted.html#step2) for details on quantity and quality of material required for each project type.

For proposals requesting synthesis, please estimate when the list of sequences is expected to be available. Also please indicate whether any of the genes/fragments requested are related to the pathogenicity of any organism, encode any form of infectious agent or viral life-cycle component, or are known to have any toxicity.

C) Project Description: (Limit 10 pages)

Use this section to emphasize the scientific merits, feasibility and DOE relevance of your project. Your description should highlight:

i. the importance of the research,

ii. the scientific questions you expect to answer with the data in hand,

iii. preliminary data produced in support of the project,

iv. the size and nature of the larger community that will use the data,

v. the relevance of the project to the DOE mission and/or its economic or societal importance, and

vi. roles and responsibilities of the project team.

D) References: (No page limit)

[Bibliography that supports the proposal].

E) CV’s of lead investigators: (3 page limit for each investigator)

Use standard [NIH](http://grants.nih.gov/grants/funding/phs398/biosketchsample.doc) or [NSF](http://www.virginia.edu/opra/NSF/FastLane%20Instructions/Biographical%20Sketch.html) biosketch format or equivalent.

**F) Letters of support: (No limit)**