

CSP FY2026 New Investigator Call (status: OPEN)

Bacterial, archaeal, and viral isolates and single cell draft genomes

The JGI will accept proposals for sequencing of collections of bacterial, archaeal, and viral genomes from cultivated isolates or physically isolated single cells. Proposed organisms should broaden phylogenetic representation among sequenced representatives or participate in processes directly relevant to [DOE missions](#). Type strains, including proposed strains prior to publication, are highly encouraged. Between 48 and 184 isolates may be proposed. For single-cell sequencing projects, JGI will sort up to 8 samples and sequence up to 384 single particle sorts (unverified by 16S) per proposal. For single virus sort sequencing projects, the amplified DNA needs to be provided by the PI, as JGI does not sort and genome amplify viral particles. Between 48 and 384 single virus sorts may be proposed for sequencing. For projects with larger numbers of genomes, please refer to the [CSP Annual Call](#).

Genome resequencing

The JGI seeks proposals centered on resequencing of bacterial, archaeal, fungal, algal and plant isolates for which a reference genome exists. Projects may focus on natural population structure, understanding gene function under selective pressure or in mutagenized strains, or developing pan and core genomes. We will also consider collections of highly related strains from nature that display differences in phenotypes related to DOE missions, e.g. lignocellulose decomposition, fermentation of sugar substrates or degradation of environmental toxins for bacteria and fungi or biomass composition for plants. Between 22 and 92 samples may be proposed for bacteria, fungi, plants, or algae. For projects with larger numbers of samples, please refer to the [CSP Annual Call](#).

Fungal draft genomes

Proposals will be considered for long-read sequencing of fungal genomes <60 Mb in size, including RNA for annotation. Between 1-6 genomes may be proposed. For larger numbers, please refer to the [CSP Annual Call](#).

Plant/algal genome size estimation

Proposals will be considered for low-pass short-read sequencing of plant and algal genomes to assess genome size and complexity in preparation for large-scale genome sequencing projects. PacBio may not be requested. Between 1-10 samples may be proposed. For larger number of samples, please refer to the [CSP Annual Call](#).

Plant/algal draft genomes

Proposals will be considered for long-read sequencing of plant and algal genomes, including RNA for annotation. Between 1-3 plant genomes may be proposed and are limited to genomes < 5Gb and 1-4n. Up to 2 cultured algal draft genomes may be proposed. For larger number of samples, please refer to the [CSP Annual Call](#).

RNA sequencing

The JGI solicits RNA sequencing projects for bacterial, archaeal, fungal, algal and plant genomes for which a reference genome is available. RNA-seq data may be used for improvement of genome annotation or for transcript counting applications (e.g. gene expression profiling of a bacterium during growth on an array of cellulosic substrates to decipher degradation pathways). Projects should be directly relevant to DOE missions; for plants, projects using the standard conditions defined by the Plant Gene Atlas are specifically encouraged. Between 22 and 92 samples (including replicates) may be proposed. For projects with >92 samples, please refer to the [CSP Annual Call](#).

Bacterial and archaeal epigenomes and high-quality draft genomes

Single molecule real time sequencing enables greater genome contiguity as well as assessment of DNA base modifications (6mA, 5mC, 4mC and others) of potential importance in host defense and gene regulation. The JGI will accept proposals including up to 12 samples for improved draft or epigenome sequencing. For projects with >12 samples, please refer to the [CSP Annual Call](#).

Metagenomes and metatranscriptomes

JGI is accepting proposals that include up to 184 metagenomes or metatranscriptomes (in any combination) from environmental samples, laboratory enrichments or synthetic communities. Up to 8 long-read metagenome samples may be also proposed, which will not count toward the 3 Tb cap. Projects examining sample series across time or space as well as those targeting viruses are particularly encouraged.

The JGI has limited capacity (≤ 16 biomass samples for sorting) for targeted sorting and metagenomic analysis of specific populations that can be fluorescently labeled, e.g.

naturally pigmented cells, cells labeled with Bio-Orthogonal Non-Canonical Amino acid Tagging (BONCAT), etc. This 'mini-metagenomic' approach does not require whole genome amplification assuming >10,000 target cells can be recovered, and target populations should be >1% of cells. Sequencing of up to 92 cell enrichments (mini-metagenomes), including viral enrichments, can be requested.

Samples for Stable Isotope Probing (SIP) fractionation may not be requested in the New Investigator call.

DNA synthesis for functional assays

DNA/gene synthesis linked to sequence data generation, including codon optimization, refactoring, and assembly of biosynthetic pathways into appropriate vector systems for expression in heterologous hosts. (Use of this capability is encouraged, but synthesis-only projects should be directed to the [Functional Genomics call](#)). JGI is accepting proposals for synthesis of up to 500 kb.

Metabolomics based functional analyses

Targeted and untargeted metabolomic technologies at JGI enable users to examine diverse polar and non-polar metabolites from plants, microbes, and environments. In addition, users may request targeted analysis of stable isotope labeling for specific metabolites. JGI is accepting proposals for up to 50 polar metabolite sample analyses and up to 150 non-polar metabolite sample analyses.

EcoFAB pilot projects

The JGI can provide up to 50 EcoFAB devices (<https://eco-fab.org/>) to study plant-microbiome interactions. These devices allow for non-destructive root imaging and sampling of the growth media while maintaining a sterile environment. In addition, the JGI can provide a standardized defined microbial community that colonizes plant roots and *Brachypodium* germplasm, if desired. Users would conduct experiments using these resources and return samples to the JGI for analysis by existing JGI capabilities e.g. metabolomics and transcriptomics.

Proposal Schedule

Proposals are accepted on a continuous basis and will be reviewed twice a year. Letters of intent are not required. Deadline for submission is 60 days prior to the review date. This call replaces the "Small Scale Microbial CSP call" which is no longer active.

Upcoming submission deadlines:

FY25: October 4, 2024 (review in December 2024)

FY26: September 9, 2025 (review in December 2025)