

## **JGI Capabilities Available for the Call for FY2020 FICUS Research Proposals**

### **Core Capabilities Include:**

- *De novo* sequencing and annotation of plant, fungal, bacterial, and archaeal genomes
- Resequencing for variation detection
- Fluorescence activated cell sorting for targeted metagenomics and single-cell genomics
- Microbial community DNA/RNA sequencing and annotation
- Comprehensive transcriptome analysis including coding transcript annotation, non-coding RNA (both small and long ncRNA) characterization and expression profiling
- Target enriched re-sequencing
- Whole genome DNA methylation analysis
- Chromatin analysis including FAIRE and ChIP-seq
- DNA/gene synthesis
- Analysis pipelines for the datasets above
- High throughput metabolomics for functional genomics

### **JGI also has limited capacity for the following developing capabilities:**

- Flow cytometric sorting and genomic analysis of metabolically active microbes labeled via Bio-Orthogonal Non-Canonical Amino acid Tagging (BONCAT). Close consultation with JGI scientists regarding goals and experimental design is necessary.
- Custom genome analysis of generated datasets
- Access to high-performance computing at the National Energy Research Scientific Computing Center (NERSC)