

The U.S. Department of Energy Joint Genome Institute (JGI) is a large-scale genomic science user facility dedicated to aiding researchers in sequence-enabled science and genome analysis of microbes, microbial communities, plants, fungi, and other targets relevant to DOE missions in energy, environment and global carbon and nutrient cycling. The JGI provides users around the world with access, at no cost, to high-throughput genomic capabilities and data analysis. These include genome, metagenome, and single-cell sequencing; resequencing; DNA synthesis; metabolomics; as well as transcriptome, metatranscriptome, and methylome analysis.

<http://jgi.doe.gov/>



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Advancing your science  
with the

# DOE Joint Genome Institute

2017  
USER  
OPPORTUNITIES  
AND EVENTS

## Meetings

### 12th Annual Genomics of Energy and Environment Meeting

March 20–23, 2017, Walnut Creek, CA

The DOE JGI's annual User Meeting starts with two days of genome informatics tutorials and other workshops followed by two days of presentations and poster sessions on a diversity of topics connected to energy and environmental science, including: Microbial ecology and bioprospecting, genomic analysis of biofuel crops, single-cell genomics, systems biology, and synthetic biology.

<http://usermeeting.jgi.doe.gov/>

### NeLLi: From New Lineages of Life to New Functions

April 5–6, 2017, Walnut Creek, CA

This workshop will foster discussions on how to capture, define, quantify, and functionally characterize microbial and viral diversity. The workshop will focus on experimental innovations, computational advances, and other technological developments that will enable researchers to move from identification of microbial novelty to assigning metabolic and functional capabilities.

<http://jgi.doe.gov/events/nelli/>

### Microbial and Plant Systems Modulated by Secondary Metabolites Meeting

July 24–26 2017, Walnut Creek, CA

The aim of this meeting is to bring together a diverse group of investigators interested in the role of secondary metabolites in plant-microbe and microbe-microbe interactions. The meeting's goals include mediating an exchange of ideas and approaches for studying and manipulating the impact of secondary metabolites on environmental systems and to serve as an opportunity for the meeting participants to learn about JGI capabilities available to them.

<http://bit.ly/2017-JGI-Secondary-Metabolites>

### Microbial Genomics and Metagenomics (MGM) Workshops

February 27–March 3, 2017, Walnut Creek, CA

September 2017, Walnut Creek, CA

Five-day workshops combining intensive seminars and hands-on tutorials for the Integrated Microbial Genomes (IMG) suite of tools for comparative analysis and annotation of prokaryotic and eukaryotic genomes.

<http://mgm.jgi.doe.gov/>

## Resources

### Community Science Program (CSP)

Access to DNA Sequencing, Synthesis, and Analysis

Peer-reviewed selection process for massive-throughput sequencing and DNA synthesis for projects of relevance to sustainable energy production, global element cycling, and biogeochemistry.

#### Targeted Calls for Proposals

**Microbes/Metagenomes:** Proposals may include genome, metagenome, and single-cell sequencing or resequencing; transcriptome, metatranscriptome, and methylome analysis. Small-scale proposals (up to 48 prokaryotic isolate genomes or up to 24 microbial community samples) are accepted continuously and reviewed biannually. Priority is given to pilot projects for larger-scale CSP proposals.

**DNA Synthesis:** Proposals are encouraged that address the refactoring, screening, and functional characterization of multigene pathways in bacteria, archaea, or eukaryotes involved in DOE mission-relevant processes. Projects that involve functional prospecting of diverse species/metagenomes, require the construction of large DNA molecules (>10 kb), and exploit coupling to high-throughput screening technologies are encouraged.

Applications are being accepted until March 31, 2017.

<http://bit.ly/FY18-CSP>

### Facilities Integrating Collaborations for User Science (FICUS)

The FICUS initiative was established to enable researchers to more easily integrate the expertise and capabilities of multiple user facilities into their research.

#### JGI-EMSL Collaborative Science Call

The FICUS call between JGI and Environmental Molecular Science Laboratory (EMSL) represents a unique opportunity for researchers to combine the power of genomics and molecular characterization in one proposed research project. Both user facilities play critical roles in supporting DOE's energy, environment and basic research missions. Successful applications focus on high risk/high payoff projects in the areas of emphasis that can be completed on an accelerated timeline. In addition, they must utilize a broad range of the capabilities of each facility, and generate datasets beyond what each of these facilities could generate by itself. Applications are currently being accepted until April 3, 2017.

<http://bit.ly/FY18-FICUS>

#### JGI-NERSC Microbiome Data Science Call

Building upon the success of the JGI-EMSL collaborative science program, a second FICUS program has launched between the JGI and the National Energy Research Scientific Computing Center (NERSC), a user facility dedicated to accelerating scientific discovery at the DOE Office of Science through high performance computing (HPC) and data analysis. The JGI-NERSC Microbiome Data Science call will enable users to perform state-of-the-art computational genomics and metagenomics research and help them translate sequence information, generated by the JGI or elsewhere, into biological discovery. The call aims to help users perform large-scale computational analyses of sequence data to solve problems relevant to the DOE missions in bioenergy and the environment. Applications for JGI-NERSC collaborative science call are currently being accepted until March 1, 2017.

<http://bit.ly/FY18-JGI-NERSC>

### Data Management/Analysis

The JGI provides a suite of premier computational resources for the functional characterization, analysis, and improvement of a vast number of publicly available genomes and metagenomes. The JGI Genome Portal provides downloads of sequence data and annotations for all JGI genomes.

- **Integrated Microbial Genomes (IMG)**  
Comparative analysis and annotation of genomes from all domains of life as well as microbial communities. Paired with IMG Expert Review (IMG/ER) for functional annotation and curation.
- **Phytozome**  
Comparative analysis of plant genes, gene families, genomes and proteomes.
- **Mycocosm**  
Data access, visualization, and analysis tools for comparative genomics of fungi.

<http://bit.ly/JGI-Data-Tools>

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