

Engage with JGI

USER
OPPORTUNITIES
AND EVENTS

Meetings

2023 Annual Genomics of Energy & Environment Meeting usermeeting.jgi.doe.gov

August 21-23, 2023 | Berkeley, CA

The JGI Annual Meeting will be held in a hybrid mode at Lawrence Berkeley National Laboratory (Berkeley Lab) in Berkeley, Calif., and online.

The JGI Annual Meeting is the premier forum for convening members of the scientific community pursuing the frontiers of energy and environmental genomics, metabolomics, synthetic biology and secondary metabolites research; data science, and technology development. Workshops that complement the Annual Meeting will be held later in the same week.

Meeting sponsorships are available. For more information, contact Massie Ballon: mlballon@lbl.gov.

New Lineages of Life (NeLLi) Symposium jgi.doe.gov/events

August 24-25, 2023 | Berkeley, CA

Under the "sequence to function" umbrella, this symposium will focus on computational approaches to characterize novel microbial lineages and sequence novelty and experimental approaches to assign functional "read out" to sequence data.

Mechanisms to Tap JGI Resources jgi.doe.gov/user-programs

Community Science Program (CSP): Peer-reviewed selection process for massive-throughput sequencing and DNA synthesis for projects of relevance to sustainable energy production, global element cycling, and biogeochemistry.

Facilities Integrating Collaborations for User Science (FICUS): Enables researchers to tap genomics and molecular characterization in one research proposal in partnership with the Environmental Molecular Sciences Laboratory (EMSL). Areas include biofuels and bioproducts; plant-microbe interactions; and biogeochemistry of select inorganic elements.

Strategic Partnership Projects (SPPs): Enable research funded by an Industry partner to perform a defined scope of work using JGI's unique facilities, equipment, and personnel.

Cooperative Research and Development Agreements (CRADAs): Enable research jointly sponsored by the Berkeley Lab and one or more partners for shared benefit.

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 other 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; secondary metabolites; as well as transcriptome, metatranscriptome, and methylome analysis.

Your Partner for Integrative Genome Science

Venture inside for published examples of how the JGI has enabled advances in discoveries at the frontiers of energy and environmental research



Sequence-Based Science

A Team Effort Toward Targeted Crop Improvements

Combining field data with a JGI-generated reference switchgrass genome, researchers are associating climate adaptations with switchgrass biology, information relevant to the DOE's interest in harnessing the crop toward producing sustainable alternative fuels.



Lovell J. et al. Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. (2021) *Nature*. 10.1038/s41586-020-03127-1.

Bacteria Visible to the Naked Eye

JGI researchers described the biggest bacterium ever discovered - in Guadeloupe mangroves - and its unexpected genomic complexity. The team sequenced and assembled the bacterial genomes. Various imaging tools were harnessed to find novel membrane-bound compartments containing DNA clusters.



Volland J.M., Gonzalez-Rizzo S., Gros O. et al. "A centimeter-long bacterium with DNA contained in metabolically active membrane-bound organelles." (2022) *Science*. 10.1126/science.abb3634

Gut Fungi As A Source of Novel Chemicals

Herbivores like goats rely on anaerobic fungi in their guts to help them digest their leafy meals. By combing through the fungal genomes and conducting mass spectrometry analyses, researchers unexpectedly found that the fungi can make complex chemicals called natural products, a new source of novel compounds to help bolster the bioeconomy.



Swift C.L. et al. "Anaerobic gut fungi are an untapped reservoir of natural products." (2021) *PNAS*. 10.1073/pnas.2019855118

Big Data

Fast and Scalable Metagenome Assembly

A handful of soil or a drop of water can contain millions of genomes. Looking at this combined genome content in a sample makes metagenome assembly difficult; a tool called MetaHipMer can help. This publicly available metagenome assembler was recognized with a HPCwire Editors Choice Award for Best Use of HPC in Life Sciences. It is designed to run on high-performance supercomputers and can co-assemble multi-terabyte datasets, such as from multi-year experiments.



Hofmeyr, S. et al. "Terabase-scale metagenome coassembly with MetaHipMer." (2020) *Sci Rep*. 10.1038/s41598-020-67416-5

Bovine Bioinformatics for Biotechnology Education

In 2011, researchers used metagenomics to identify over 27,000 microbial genes in cow rumen that might help break down plant mass. Building off these gene predictions, in 2015 a course-based undergraduate research experience at a California State University campus began using the publicly-available data, along with the JGI's bioinformatics tools, for biotechnology education. The curriculum has expanded and faculty at multiple California State University campuses are now offering variations of the course.



Hess M., Sczyrba A. et al. "Metagenomic Discovery of Biomass-Degrading Genes and Genomes from Cow Rumen." (2011) *Science*. 10.1126/science.1200387

Tools and Technologies

Connecting Structure to Function in More Genes at Once

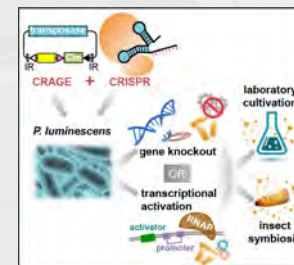
With decades of genomics expertise, JGI researchers are uniquely prepared to make connections between the structures and functions of genes. DAP-seq allows researchers to identify all the sites where transcription factors that control how genes are turned on bind quickly and efficiently in the genome. Two novel approaches innovate on DAP-seq: Biotin DAP-seq is a unique quick protein purification approach, while multiDAP allows researchers to conduct comparative analyses across the genomes of multiple species in a single experiment.



Baumgart L.A., Lee J.E. et al. "Persistence and plasticity in bacterial gene regulation." (2021) *Nat Methods*. 10.1038/s41592-021-01312-2.

CRAGE-CRISPR Combo Helps Extract Secrets of Secondary Metabolites

CRISPR technology can accurately edit genomes, but is limited to strains with robust tools for carrying CRISPR into microorganisms. CRAGE is a JGI-developed technology for inserting large DNA pieces directly into a microbial host.



Microbial secondary metabolites or natural products may now be easier to characterize, and the functions of biosynthetic gene clusters easier to identify and describe, following a proof-of-concept study combining these technologies.

Ke J et al. "CRAGE-CRISPR facilitates rapid activation of secondary metabolite biosynthetic gene clusters in bacteria." (2022) *Cell Chem Biol*. 10.1016/j.chembiol.2021.08.009