Engage with JGI

JGI Annual Genomics of Energy & Environment Meeting September 30-October 4, 2024 | Walnut Creek, CA usermeeting.jgi.doe.gov

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OPPORTUNITIES AND EVENTS

The 2024 JGI Annual Meeting will be held at the Walnut Creek Marriott. The Meeting highlights how researchers in diverse disciplines are addressing the most pressing energy and environmental challenges. Invited talks emphasize how the research infrastructure offered through the JGI's User Programs on a competitive, peer-reviewed basis to the worldwide scientific community can advance your research goals. Workshops complementing the Annual Meeting will also take place.

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

Microbial Genomics & Metagenomics (MGM) Workshop April 15-19, 2024 | Berkeley, CA mgm.jgi.doe.gov

The five-day workshop at Berkeley Lab combines intensive seminars and hands-on tutorials on how to use the IMG suite of tools for computational analysis and interpretation of sequence data.

Mechanisms to Tap JGI Resources

Community Science Program (CSP): Peer-reviewed selection process for massive-throughput sequencing and DNA synthesis for projects of relevance to issues in sustainable biofuel and bioproducts production, global carbon and nutrient cycling, and biogeochemistry.

Facilities Integrating Collaborations for User Science (FICUS): Enables researchers to tap genomics and molecular characterization through one research proposal with the Environmental Molecular Sciences Laboratory (EMSL) and other partners. Areas include biofuels and bioproducts, inter-organismal interactions, and novel applications of molecular techniques.

Emerging Technologies Opportunity Program (ETOP): Identifies and funds partnerships to develop new technical capabilities that could be provided to JGI users, including methods for rapid prototyping of gene and pathway function targeting organisms found in natural environments: high-throughput cell-based, cell-free and sensor-based technologies.

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.

24-JGI-23161

jgi.doe.gov/user-programs

The U.S. Department of Energy (DOE) Joint Genome Institute (JGI) is a DOE-supported genome science user facility. With the aim of leading genomic innovation for a sustainable bioeconomy, the JGI decodes the genetic information of plants, fungi, microbes, algae and other targets relevant to DOE missions. The JGI provides access to high-throughout genomics capabilities and data analysis, helping researchers find solutions to

energy and environmental challenges.

jgi.doe.gov

BERKELEY LAB



Your Partner for Integrative Genome Science

Venture inside for published examples of how JGI has enabled 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. The metagenome assembler was recognized with a HPCwire Editors Choice Award for Best Use of HPC in Life Sciences. MetaHipMer 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 California State University

course-based undergraduate research experience began using the publicly-available data, along with the JGI's bioinformatics tools, for biotechnology education. Faculty at multiple CSU 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

Identifying Mobile Genetic Elements in Massive Datasets

The geNomad tool can identify millions of new viruses and plasmids quickly. Those sequences and metadata are now available on the JGI's IMG Virus Resource (IMG/VR) and IMG Plasmid Resource (IMG/PR). geNomad is also



accessible through the National Microbiome Data Collaborative's EDGE platform.

Camargo, AP. et al. "Identification of mobile genetic elements with geNomad." (2023) Nat Biotechnology. 10.1038/s41587-023-01953-y

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 JGIdeveloped 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