

# Engage with JGI

USER  
OPPORTUNITIES  
AND EVENTS

## Meetings

**15th Annual Genomics of Energy & Environment Meeting**  
March 23–27, 2020, Oakland, CA

The Meeting will feature talks by leading researchers applying the latest omics, synthetic biology, and computational strategies to advance innovative energy and environmental science. The Meeting will also include the “VEGA 2020 Symposium: Viral EcoGenomics Applications” Workshops, including hands-on training to tap the tools and data of the DOE Systems Knowledgebase (KBase), will precede the main event. Meeting sponsorships are available.

For more information, contact David Gilbert: [degilbert@lbl.gov](mailto:degilbert@lbl.gov).  
<http://usermeeting.jgi.doe.gov/>

**Microbial Genomics & Metagenomics (MGM) Workshops**  
September 16–20, 2019, Berkeley, CA

Five-day workshops combining intensive seminars and hands-on tutorials for the IMG suite of tools for annotation and comparative analysis of prokaryotic and viral genomes and metagenomes.  
<http://mgm.jgi.doe.gov/>

## 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 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.

**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.

<http://jgi.doe.gov/user-program-info/>

18-JG-5000



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; as well as transcriptome, metatranscriptome, and methylome analysis.

[jgi.doe.gov](http://jgi.doe.gov)



DOE Joint Genome Institute  
Lawrence Berkeley National Laboratory

Questions? Contact [JGI-Brochure@lbl.gov](mailto:JGI-Brochure@lbl.gov)



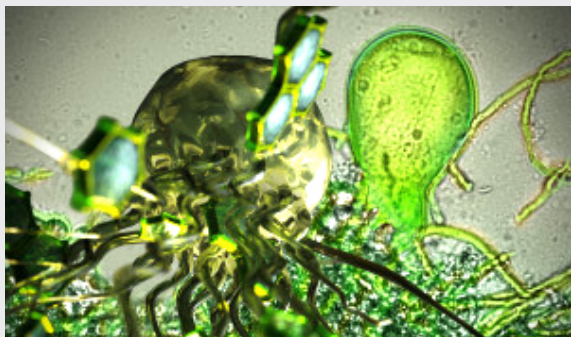
## Your Partner for Integrative Genome Science

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





## Sequenced-Based Science



**Early-branching gut fungi possess a large, comprehensive array of biomass-degrading enzymes.** This systems-level approach integrated transcriptomic sequencing, proteomics, phenotype and biochemical studies to identify a large array of novel biomass-degrading enzymes that synergistically degrade crude and untreated plant biomass.

Solomon, K. V. et al. (2016) *Science*. 10.1126/science.aad1431

**Lineage-specific chromatin signatures reveal a regulator of lipid metabolism in microalgae.** JGI

has published over 75 percent of all publicly available algal genomes including *Chlamydomonas reinhardtii* released in 2007. This study identified two transcription factors that play a pivotal role in lipid accumulation.

Ngan, C.Y. et al. (2015) *Nature Plants* 1(1). 10.1038/nplants.2015.107



**Comparative genomics of biotechnologically important yeasts.** JGI conducted a comparative genomic analysis of 29 yeasts, providing new

platforms for bioengineering cellulose degrading, lipid producing, acid tolerant yeasts that use a wide range of substrates.

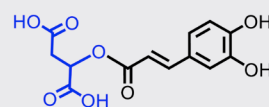
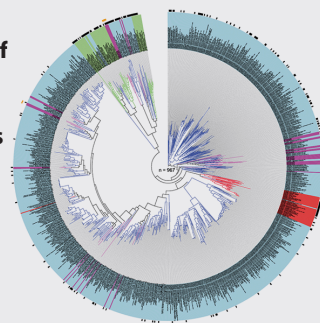
Riley, R. et al. (2016) *Proc Natl Acad Sci U S A*. 10.1073/pnas.1603941113

## DNA Synthesis/ Metabolomics

**Phylogenomically guided identification of industrially relevant GH1  $\beta$ -Glucosidases through DNA synthesis and nanostructure-initiator mass spectrometry.**

Developed a workflow combining DNA synthesis with high-throughput mass spectrometry to harness the biotechnological potential of the large number of proteins available in sequence databases.

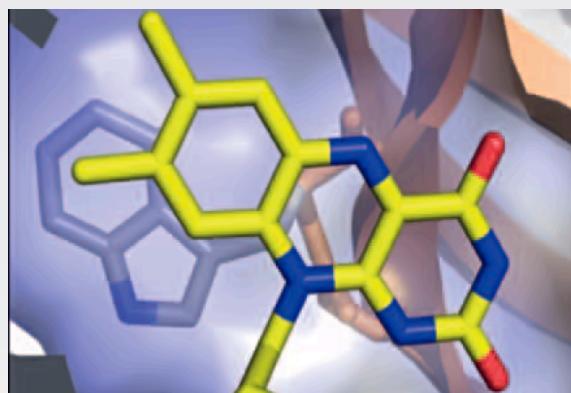
Heins, R. A. et al. (2014) *ACS Chemical Biology* 9(9), 2082-2091



**Exploiting plant enzymes to synthesize phenyl propanoids in yeast.**

Demonstrated the effectiveness of expressing members of the plant BAHD acyltransferase family in yeast for the synthesis of numerous valuable hydroxycinnamate and benzoate conjugates.

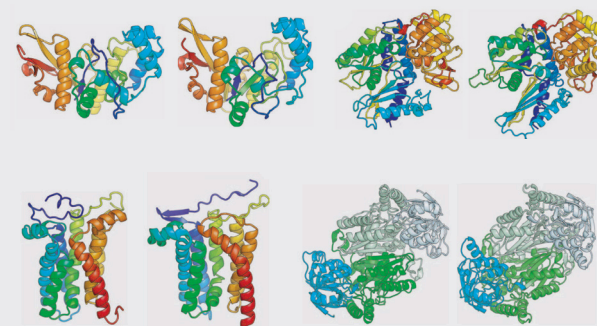
Eudes, A et al. *Microbial Cell Factory* (2016) 15:198



**A synthetic pathway for the fixation of carbon dioxide *in vitro*.** Described a synthetic cycle for the continuous fixation of CO<sub>2</sub> *in vitro* by metabolic retrosynthesis.

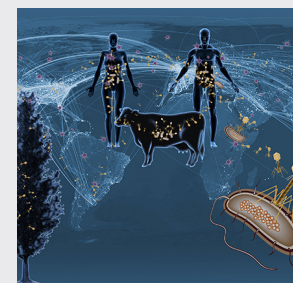
Schwander, T. et al. (2016) *Science* 354(6314), 900-904

## Big Data Science



**Protein structure determination using metagenome sequence data.** More than tripled the number of protein families with sufficient sequences for accurate modeling.

Ovchinnikov, S. et al. (2017) *Science* 355 (6322), 294-298.



**Uncovering Earth's virome.** Utilized the largest collection of assembled metagenomic datasets from around the world to uncover over 125,000 partial and complete viral genomes.

Paez-Espino, D. et al *Nature* (2016) Aug 25;536(7617):425-30.

**1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life.**

These phylogenetically diverse bacterial and archaeal reference genomes represent the single largest release to date.

Mukherjee, M. & Seshadri, R. et al, *Nature Biotechnology* 35, 676–683 (2017)

