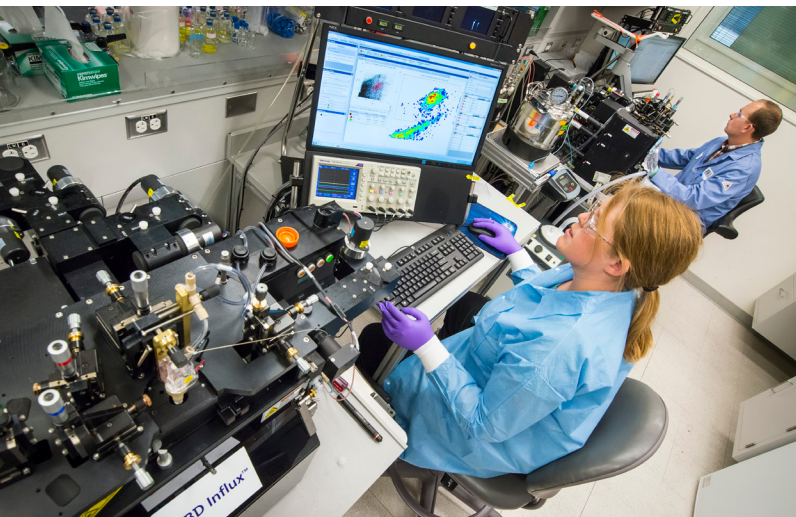
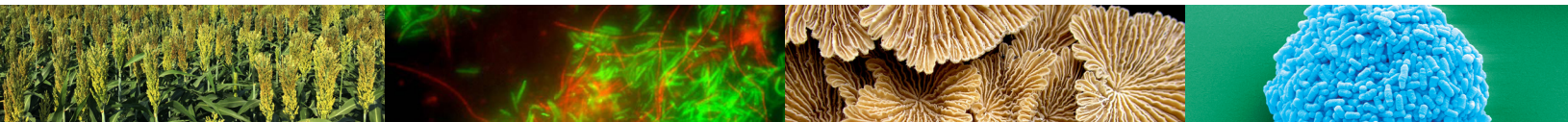


The DOE Joint Genome Institute Enabling Advances in Energy & Environmental Research



The U.S. Department of Energy (DOE) Joint Genome Institute (JGI) is the only federally-funded high-throughput genome sequencing and analysis facility dedicated to genomes of non-medical microbes, microbial communities, plants, fungi and other targets relevant to DOE missions in energy, climate, and environment. DOE JGI provides collaborators around the world with access to massive-scale DNA sequencing to underpin modern systems biology research and provide fundamental data on key genes that may link to biological functions, including microbial metabolic pathways and enzymes that are used to generate fuel molecules, affect plant biomass formation, degrade contaminants, or capture CO₂. The information can then be used to optimize organisms for biofuels production and other DOE missions.

Located in Walnut Creek, California, and supported by the DOE Office of Science, DOE JGI is managed by Lawrence Berkeley National Laboratory, drawing additional complementary capabilities from its partner laboratories: Lawrence Livermore National Laboratory, Los Alamos National Laboratory, Oak Ridge National Laboratory, Pacific Northwest National Laboratory, and the HudsonAlpha Institute for Biotechnology.

Among the DOE JGI's largest customers are the DOE Bioenergy Research Centers, which were established to accelerate basic research in the development of next-generation cellulosic and other biofuels through focused efforts on biomass improvement, biomass degradation, and strategies for fuels production.

Bioenergy

Projects focus on developing plants that can be used as feedstocks for biofuel production, identifying organisms (e.g. fungi and microbes) with enzymes and pathways that can break down the lignin and cellulose in plant cell walls, and characterizing enzymes and pathways that can ferment sugars into biofuels.

Carbon Cycle

As microbes make up the largest component of the Earth's biodiversity, understanding how they metabolize carbon, and how environmental changes affect these processes, is crucial for the development of better predictive models for reducing the effects of increasing carbon dioxide emissions on the global climate.

Biogeochemistry

The field of biogeochemistry explores the full spectrum of biological, physical, geological and chemical processes and reactions involved in sustaining life on Earth. One area of emphasis targets microbes and microbial communities (or metagenomes) that can degrade or otherwise transform environmental contaminants such as toxic chemicals or heavy metals.

JGI FACTS

- 958** FY2015 Users Worldwide—Individual Principal Investigators, Collaborators and Annotators (who conduct genome analysis) on active projects
- 652** FY2015 Users in the US (68%)
- 181** JGI-authored peer-reviewed scientific publications
- 5,070** FY2015 projects completed
- \$69 M** FY2015 budget from DOE Office of Science, Office of Biological and Environmental Research
- 280** staff at Walnut Creek
- 80,000** square foot headquarters

Selected Recent DOE JGI Publication Highlights



Seagrass Lends Insights to Salt Tolerance

A team that included DOE JGI researchers sequenced, analyzed and published the genome of the seagrass *Zostera marina*. To mitigate carbon emissions in the atmosphere, researchers have turned to sinks—reservoirs that accumulate and store carbon such as tropical rainforests. However, another lesser-known but very large carbon sink is located along shallow, soft-sediment shorelines. Seagrass ecosystems cover some 200,000 square kilometers. They account for an estimated 15 percent of carbon fixed in global ocean, and also impact sulfur and nitrogen cycles. Additionally, they act as nurseries for young fish and other organisms, protect the coastline from erosion, and help maintain water clarity (*Nature* February 18, 2016).

Biofuel Tech Straight from the Farm

The matrix of complex molecules found in plant cell walls—lignin, cellulose and hemicellulose—combine to create the biological equivalent of reinforced concrete.

When industry can't break down this biomass, they pretreat it with heat or chemicals. Or throw it away. Both options add to the cost of the finished product. Researchers from University of California, Santa Barbara found that anaerobic fungi found in the guts of goats, horses and sheep perform as well as the best fungi engineered by industry in their ability to convert plant material into sugars that are easily transformed into fuel and other products. These findings were enabled by tapping the capabilities of two DOE Office of Science user facilities: the DOE JGI and the Environmental Molecular Science Laboratory at Pacific Northwest National Laboratory through a program known as FICUS—Facilities Integrating Collaborations for User Science (*Science* February 18, 2016).

Functional Genomic Studies of Algae

Understanding the regulatory mechanisms that switch genes on and off (epigenomics) is critical to a better understanding of the meaning of genomic data. Some algae produce energy-dense oils or lipids that can be converted into fuels, but it can be challenging to produce them in adequate quantities for biofuel production. An in-depth epigenomic study of the green alga *Chlamydomonas reinhardtii* revealed key regulators in algal lipid production, opening the door to more effective use of algae as a biofuel feedstock. This study further solidified our position as a leader in algal genomics; DOE JGI has published over 75 percent of all publicly available algal genomes, including the *Chlamydomonas* reference genome that enabled this study (*Nature Plants*, July 27, 2015).

Understanding Permafrost Carbon Cycling

Vast areas of the planet are covered by permafrost soils, but they are highly

vulnerable to thawing as global temperatures continue to rise. Studies suggest such thawing could result in the largest contribution of carbon transferred to the atmosphere by a single terrestrial process, but the magnitude of this carbon output depends on the activities of microbes residing in the soil. With colleagues from several national laboratories, we applied multiple molecular technologies, collectively referred to as “omics,” to three types of Alaskan soils ranging from completely thawed to completely frozen, deepening our understanding of the role of microbial communities in degrading permafrost organic carbon and ultimately producing CO₂ and methane (*Nature*, March 4, 2015).

Finding Friends in the Root Microbiome

Understanding how microbial communities interact at the nexus of plant roots and soil is a key focus area for the DOE JGI, as cultivation of beneficial microbiomes will be critical to sustainable bioenergy crop production in the future. With colleagues, we used a combination of plant genetics, biochemistry and sequence-based community profiling to investigate the roles of three phytohormones in controlling the composition of the root microbiome in the model plant *Arabidopsis thaliana* (*Science*, August 21, 2015).

Mutualism for Beneficial Environmental Adaptations

Drawing on 49 fungal genomes, many sequenced at DOE JGI, we helped conduct the first broad, comparative phylogenomic analysis of mycorrhizal fungi. The results help explain how plants and fungi developed symbiotic relationships, and how this mutualistic association provides host plants with beneficial traits for environmental adaptation (*Nature Genetics*, February 23, 2015).