



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 and environment. The 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, the JGI is managed by the University of California through Lawrence Berkeley National Laboratory, drawing additional staff from its partner laboratories—Lawrence Livermore National Laboratory and the HudsonAlpha Institute for Biotechnology.

Among the JGI's largest users 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.

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

- 1,598** FY2017 Users Worldwide—Individual Principal Investigators, Collaborators and Annotators (who conduct genome analysis) on active projects
- 1,113** FY2017 Users in the US (68%)
- 147** JGI-authored peer-reviewed scientific publications
- 1,702** scientific publications since FY2008
- 8,429** FY2017 projects completed
- 280** staff at Walnut Creek, California headquarters



Selected Recent JGI Publication Highlights



Toward More Effective Carbon Fixation

By tapping the DNA synthesis expertise of the JGI, a team from the Max Planck Institute (MPI) for Terrestrial Microbiology has reverse engineered a biosynthetic pathway for more effective carbon fixation. This novel pathway is based on a new CO₂-fixing enzyme that is nearly 20 times faster than the most prevalent enzyme in nature responsible for capturing CO₂ in plants by using sunlight as energy. Successfully reconstituting a synthetic enzymatic network in a test tube for the conversion of CO₂ into organic products could lead to potential future applications, such as artificial photosynthesis (*Science*, November 18, 2016).

Antarctic Adaptations in Diatoms

To learn more about how the Antarctic alga *Fragilariopsis cylindrus* adapted to its extremely cold environment, a team led by University of East Anglia (UEA) scientists conducted a comparative genomic analysis involving three diatoms by tapping the JGI's sequencing and annotation expertise. The paper was

named a Fast-Breaking Paper for Biology and Biochemistry by Clarivate Analytics (*Nature*, January 16, 2017).

***Aspergillus* Diversity for Industrial Applications**

An international team including JGI researchers reported sequencing the genomes of 10 novel *Aspergillus* species, more than doubling the number of *Aspergillus* species sequenced to date. Comparing the newly sequenced genomes with the eight other sequenced *Aspergillus* species provided the first ever genus-wide view. The consortium found that *Aspergillus* has a greater genomic and functional diversity than previously understood, broadening the range of potential applications for the fungi considered among the most important workhorses in biotechnology (*Genome Biology*, February 14, 2017).

Fungal Enzyme Complexes to Break Down Cellulose

A team led by researchers at the University of California (UC), Santa Barbara, has found for the first time that early lineages of fungi can form complexes of enzymes called "cellulosomes" capable of degrading plant biomass. Consolidating these enzymes, in effect into protein assembly lines, makes them team up to work more efficiently than they would as individuals. Through the "Facilities Integrating Collaborations for User Science" (FICUS) call between JGI and the Environmental Molecular Science Laboratory (EMSL), the team found cellulosomes in anaerobic gut fungi that attack plant biomass as a cluster of enzymes (*Nature Microbiology*, May 26, 2017).

IMG/M Helps Fill Previously Unknown Protein Structures

The Pfam database contains close to 15,000 protein families: groups of proteins that share an evolutionary origin.

A team led by the University of Washington's David Baker reported that structural models have been generated for 614 (12%) of the protein families that had previously had no structural information available. This accomplishment was made possible through a collaboration in which the Baker lab's protein structure prediction server, Rosetta, analyzed the publicly available metagenomic sequences on the JGI's Integrated Microbial Genomes and Microbiomes (IMG/M) system (*Science*, January 20, 2017).

1,003 Microbial Genomes Released

Culminating nearly a decade's worth of work, JGI's Prokaryotic Super Program head Nikos Kyrpides and his team reported the release of 1,003 phylogenetically diverse bacterial and archaeal reference genomes — the single largest release to date. With the release of this high-quality genomic information, the JGI provides a wealth of new sequences that will be invaluable to scientists interested in experiments such as characterizing biotechnologically relevant secondary metabolites or studying enzymes that work under specific conditions (*Nature Biotechnology*, June 12, 2017).

Novel Group of Giant Viruses Discovered

Giant viruses were first discovered in 2003, and a handful of other giant virus groups have been found since. JGI scientists' report of a novel group of giant viruses — dubbed "Klosneuviruses" — with a more complete set of translation machinery genes than any other virus known to date resolved the debate over viruses as a possible fourth domain of life by demonstrating that eukaryote translation-encoding genes had been taken up by and incorporated into the viral genomes (*Science*, April 7, 2017).