

Lawrence Berkeley National Laboratory

Recent Work

Title

The Joint Genome Institute User Facility Sequencing Programs

Permalink

<https://escholarship.org/uc/item/3t50v7h4>

Authors

Richardson, Paul
Bruce, David
Lucas, Susan
[et al.](#)

Publication Date

2006-01-06

LBNL-59305 Abs

Title

The Joint Genome Institute User Facility Sequencing Programs

Authors

Paul Richardson, David Bruce, Susan Lucas, Thomas Brettin, Paul Gilna, Jim Bristow, Eddy Rubin and the JGI Sequencing Staff.

The Joint Genome Institute (JGI) is a high-throughput sequencing center and user facility funded primarily by the US Department of Energy (DOE). The JGI sequences genomes and environmental samples of interest to the scientific community in response to applications to several peer-review programs. The primary programs that review suggestions for sequencing from the research community are the DOE Microbial Genome Program (MGP) and the JGI Community Sequencing Program (CSP). The main goal of these programs is to utilize genomics to advance science related to DOE missions in bioenergy production, environmental remediation, and carbon management. Any research scientist may send in proposals to these programs to suggest targets for sequencing. Successful applicants do not receive monetary awards, but receive an allocation of JGI sequencing capacity and are expected to provide the DNA and other information to complete the project.

The JGI activities include DNA sequencing, assembling, and annotating genomes of prokaryotes, eukaryotes and environmental samples. The DNA sequences are made publicly available on the JGI website (www.jgi.doe.gov), and deposited in public databases such as GenBank. Virtually all genome projects are sequenced by the whole genome shotgun method. The process begins by shearing purified genomic DNA and ligating size selected fragments into different vector systems to produce multiple subclone libraries for sequencing. The libraries are sequenced by the production group to approximately 8.5X coverage. The resulting reads are trimmed for vector sequences and aligned with one another to produce a consensus draft genome assembly. There are various Quality Control checkpoints during the process to ensure the genome assembly accurately reflects the DNA sequence of the organism under study. Much of the sequencing capacity is devoted to microbial genomes and to date, the JGI has sequenced over 250 microbes and metagenomic samples to draft quality and completely finished over 70 microbial genomes. Genomes are annotated using automated pipelines that identify potential genes and these are assigned putative function based on similarity to known genes. Annotated genomes are uploaded to the JGI Integrated Microbial Genome database (IMG) tool for pathway analysis and comparative genomic approaches (<http://img.jgi.doe.gov>).

The JGI has sequenced a number of microbes relevant to DOE missions. These include organisms involved in Carbon production or sequestration including a variety of species of Chlorobia and Chloroflexi, marine organisms such as Prochlorococcus, Synechococcus Micromonas, and Tholassiosira pseudonana. The JGI sequences a large number of organisms that live in diverse environments and can process heavy metals or other toxic compounds. Examples include Burkholderia, Acidobacteria, Dehalococcoides, Deinococcus, Shewanella, and Geobacter. In addition, the JGI has sequenced organisms

that may be important in biofuel production. These include several Methanogens and Clostridia, Microbulbifer degradans, Phanerochaete chrysosporium, Postia placenta, and Pichia stipitis. A complete list of organisms, their sequence and annotations can be found at: <http://www.jgi.doe.gov/>. The JGI is made up of affiliates from a number of national laboratories including Lawrence Berkeley National Laboratory, Lawrence Livermore National Laboratory, Los Alamos National Laboratory, Oak Ridge National Laboratory, and Pacific Northwest National Laboratory.

This work was performed under the auspices of the US Department of Energy's Office of Science, Biological and Environmental Research Program, and by the University of California, Lawrence Livermore National Laboratory under Contract No. W-7405-Eng-48, Lawrence Berkeley National Laboratory under Contract No. DE-AC02-05CH11231 and Los Alamos National Laboratory under Contract No. W-7405-ENG-36.