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**2019**

# Progress Report

**U.S. Department of Energy  
Joint Genome Institute**



# Vision

The vision of the U.S. Department of Energy (DOE) Joint Genome Institute (JGI), a DOE Office of Science User Facility at Lawrence Berkeley National Laboratory (Berkeley Lab) is to become the leading integrative genome science user facility enabling researchers to solve the world's evolving energy and environmental challenges.

# Mission

The mission of the JGI is to provide the global research community with access to the most advanced integrative genome science capabilities in support of the DOE's research mission.





## Director's Perspective



The year 2019 has been pivotal in the continued evolution of the DOE Joint Genome Institute, most notably with our move from Walnut Creek, California, to the new Integrative Genomics Building (IGB) on the Berkeley Lab campus. With our ever-expanding set of capabilities, the JGI now serves a record number of primary users—those researchers who successfully apply for our resources—and data users, and we continue to enable a significant array of scientific outputs by our users, many in collaboration with internal Science Programs, several of which have been published in the highest impact journals. The JGI continues to operate efficiently, effectively, and above all, safely, with zero recordable injuries in 2019.

Samples used to demonstrate the efficacy of new technology developed through the JGI's Emerging Technologies Opportunity Program were taken from hot springs at Yellowstone National Park. *(Paul Blainey, Christina Mork and Geoffrey Schiebinger)*



Nigel Mouncey, Director, DOE Joint Genome Institute



In June, the IGB was dedicated with a DNA helix-ribbon cutting ceremony. Berkeley Lab's Director Mike Witherell noted that bringing JGI and KBase to the Lab's main campus immerses us in an ecosystem with other world-class facilities, including the Molecular Foundry, the National Energy Research Scientific Computing Center (NERSC), and the Advanced Light Source. Indeed, the move affords us new scientific synergies with our colleagues, and already our presence adjacent to University of California Berkeley is sparking new collaborative discussions. Our monumental move to the IGB was completed safely and smoothly in December. My gratitude goes out to Ray Turner, JGI Deputy of Operations, and his team for their diligent planning and coordination to make the move a success.



Catherine Adam (foreground) and Leo Baumgart (back) working with JGI's NextSeq sequencers.

Over the last year, it has been gratifying to see how, particularly as we began the transition to IGB, the engagement activities that we have advanced under the OurJGI initiative have begun to contribute to increasing inclusivity, skill and career development, teamwork, communication, respect, and scientific excellence.

As a DOE Office of Science User Facility, the JGI serves a diverse and global user community, and this year we have grown our active user base to over 1,900 and our registered data users to over 9,500. We have established the JGI User Executive Committee (UEC) to best represent our user needs and help position the JGI to meet them. View the UEC charter and membership at [bit.ly/JGI-UEC20](https://bit.ly/JGI-UEC20). We continue to actively seek new users through our New Investigator proposal calls and the efforts of our Partnerships Development Team. We expanded our outreach through meetings with dozens of companies and academic institutions to raise the visibility of and access to the JGI's resources and establish and formalize new collaborations. In one such partnership with Brightseed—a San Francisco-based biosciences company—the JGI's analysis enabled the company to identify and annotate secondary metabolites from plant extracts. You can read more about that productive interaction here: [bit.ly/JGI-Brightseed](https://bit.ly/JGI-Brightseed).

The JGI continues to deliver high-impact science by supporting user projects and through our internal Science Program projects, with over 200 publications in FY19. Several of our scientists have been recognized on a list of highly-cited researchers ([jgi.doe.gov/jgi-2018-highly-cited-researchers-list](https://jgi.doe.gov/jgi-2018-highly-cited-researchers-list)), and others have been sharing their expertise in environmental genomics by writing for the column Genome Watch in





Boca Raton Community High School students in Florida's Loxahatchee National Wildlife Preserve. (Alexander Klimczak)

*Nature Reviews Microbiology* ([jgi.doe.gov/jgi-scientists-pen-genome-watch-articles](https://jgi.doe.gov/jgi-scientists-pen-genome-watch-articles)). This recognition speaks to the caliber of the scientists supporting the JGI user community and enabling user research by accessing our resources.

As a vote of confidence for JGI's role in pioneering metagenome data science, Emiley Eloë-Fadrosch, JGI's Metagenome Program Head, was tapped to lead the National Microbiome Data Collaborative (NMDC), a new DOE Office of Science initiative launched to empower microbiome researchers to readily access and add value to microbiome data for applications in energy, environment, health, and agriculture. More: [newscenter.lbl.gov/2019/08/13/community-driven-data-science](https://newscenter.lbl.gov/2019/08/13/community-driven-data-science).

The JGI plays an important role in developing the next generation of the scientific workforce. Of note among these efforts are:

- **Early career researchers Emiley Eloë-Fadrosch and Simon Roux** offered perspectives on what the next five years of innovation could look like. More: [jgi.doe.gov/jgi-researchers-msystems-innovation-issue](https://jgi.doe.gov/jgi-researchers-msystems-innovation-issue).
- **Sabah Ul-Hasan, an alumnus of the JGI-UC Merced Genomics Internship Program**, described the microbial diversity patterns of Puerto Nuevo's coastal waters and sediment with collaborators at the Center for Scientific Research and Higher Education at Ensenada (CICESE) in her first microbial ecology paper, published in the journal *PLoS One*. More: [jgi.doe.gov/notes-microbial-diversity-puerto-nuevo-coastline](https://jgi.doe.gov/notes-microbial-diversity-puerto-nuevo-coastline).
- **The JGI pilot with Boca Raton Community High School students** resulted in a data report in the journal *Environmental Microbiome* on microbial communities in an untouched region of the Florida Everglades, the Loxahatchee National Wildlife Preserve. The collaboration is in its second year. More: [jgi.doe.gov/inspiring-stem-careers-hands-on-everglades-loxahatchee-microbiome](https://jgi.doe.gov/inspiring-stem-careers-hands-on-everglades-loxahatchee-microbiome).

All in all, it's been yet another highly successful year for the JGI. I remain extremely proud of OurJGI team and enthusiastic about the prospects for the JGI further integrating with the Berkeley Lab research ecosystem.

A handwritten signature in blue ink that reads "Nigel J. Mouncey".

**Nigel Mouncey, DPhil**  
Director, DOE Joint Genome Institute





Clockwise (left to right): JGI and KBase residents at the IGB; IGB lobby (*Bruce Damonte Photography courtesy of SmithGroup*); Amber Golini.





One of the larger geothermal pools (temperature 65-70 °C, pH 6.4) located at Washburn Hot Springs. (Research Permit YELL-2012-SCI-05068. W. Inskeep)



*Blyttomyces helicus*, one of the fungi whose genomes were sequenced in this study, on spruce pollen grain. (Joyce Longcore)

## Diversity of Methane Metabolisms

(*Nature Microbiology*, April 2019)

Billions of years ago, methane-producing archaea likely played a key role in determining the composition of the Earth's atmosphere and regulating the global climate for life to flourish. Mining the JGI's Integrated Microbial Genomes & Microbiomes (IMG/M) database, Guillaume Borrel and Simonetta Gribaldo of the Institut Pasteur led a team that reconstructed 10 metagenome-assembled genomes (MAGs) representing new potential methanogenic, anaerobic methanotrophic and short-chain alkane-oxidizing archaea that suggest the diversity of methane metabolisms is "vastly underestimated."

[jgi.doe.gov/expanding-universe-methane-metabolisms-archaea](https://jgi.doe.gov/expanding-universe-methane-metabolisms-archaea)

## Single Cell Genomics for Fungal Genomic Diversity

(*Nature Microbiology*, October 2018)

JGI researchers partnered with Tim James of the University of Michigan to develop a pipeline to generate genomes from single cells of uncultivated fungi. The proof-of-principle work showed that the single-cell genomics approach can reconstruct near-complete fungal genomes and provide insights into phylogenetic position and metabolic capacities of diverse unculturable species from environmental samples.

[jgi.doe.gov/expanding-fungal-diversity-one-cell](https://jgi.doe.gov/expanding-fungal-diversity-one-cell)





Members of the winning ORNL-led team, including Fagnan (second from left). (SC18)

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## Achievements in High-Performance Computing

(November 2018)

Teams led by Berkeley Lab and Oak Ridge National Laboratory (ORNL) shared the 2018 Association for Computing Machinery's (ACM's) Gordon Bell Prize. JGI Chief Informatics Officer Kjersten Fagnan was part of the ORNL-led team that developed a genomics algorithm that was the first code in the world to break the exascale barrier.

[jgi.doe.gov/jgi-cio-kjersten-fagnan-on-winning-sc18-team](http://jgi.doe.gov/jgi-cio-kjersten-fagnan-on-winning-sc18-team)



*Panicum hallii* var. *filipes* and *P. hallii* var. *hallii* grown under controlled greenhouse conditions. (Amalia Díaz)

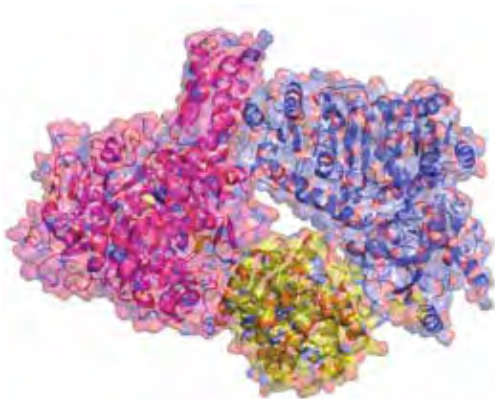
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## Drought Tolerance in Perennial Grasses

(*Nature Communications*, December 2018)

Near-complete genomes of *Panicum hallii* sequenced and assembled by the JGI allowed a team led by Tom Juenger at the University of Texas (UT) at Austin to identify and characterize the regulatory elements that influence adaptation and tolerance to stressors such as drought. The team aims to apply the resources developed for *P. hallii* towards stress tolerance improvement in its more complex relative, the candidate bioenergy crop switchgrass.

[jgi.doe.gov/hallii-model-system-for-perennial-grasses](http://jgi.doe.gov/hallii-model-system-for-perennial-grasses)



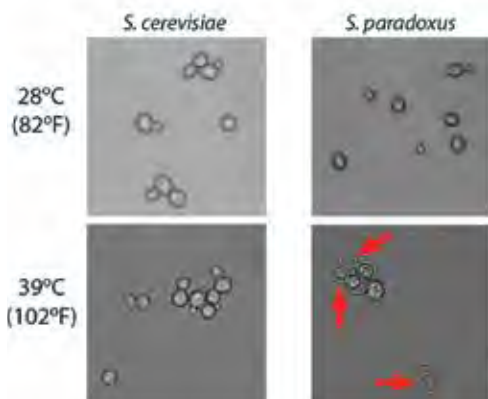
Atomic structure of propionyl-CoA synthase and its three domains. (Courtesy of MPI)

## Key Enzyme in CO<sub>2</sub>-fixation Cycle

(*Nature Chemical Biology*, December 2018)

Working with JGI's DNA Synthesis Science Program, Tobias Erb, Director at the Max Planck Institute for Terrestrial Microbiology in Germany, and his team reported the structure and function of propionyl-CoA synthase (PCS). The Erb lab focuses on identifying novel CO<sub>2</sub> converting enzymes and understanding the metabolic pathways involved. PCS is a key enzyme in a CO<sub>2</sub>-fixation bi-cycle, and one of the smallest multireaction chambers known to exist.

[jgi.doe.gov/small-but-sophisticated-nanoreactor](https://jgi.doe.gov/small-but-sophisticated-nanoreactor)



At high temperature, *S. paradoxus* cells die in the act of cell division, with cell bodies shriveled away (highlighted by arrows) from the outer cell wall.

(Carly Weiss, courtesy of the Brem Lab)

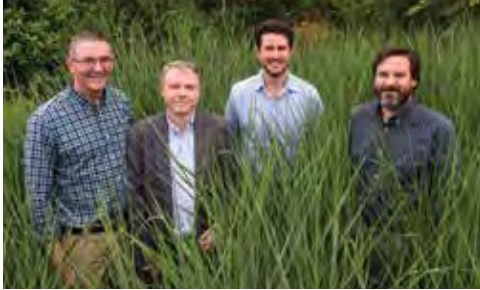
## Mapping Heat Resistance in Yeasts

(*Nature Genetics*, November 2018)

In a proof-of-concept study, researchers at the University of California, Berkeley and the Buck Institute for Research on Aging demonstrated that a new genetic mapping strategy called RH-Seq can identify genes that promote heat resistance in baker's yeast (*Saccharomyces cerevisiae*). The study highlights the genes that could be used to make other fungal species besides *S. cerevisiae* more thermotolerant, and paves the way for dissecting additional traits in fungi and beyond.

[jgi.doe.gov/rh-seq-mapping-heat-resistance-in-yeasts](https://jgi.doe.gov/rh-seq-mapping-heat-resistance-in-yeasts)





*PNAS* study authors (left to right): Jerry Jenkins; JGI Plant Program head Jeremy Schmutz; Adam Healey; and, study senior author Tom Juenger of UT-Austin. Jenkins and Healey are part of the JGI plant analysis team at the HudsonAlpha Institute for Biotechnology. (David Gilbert)

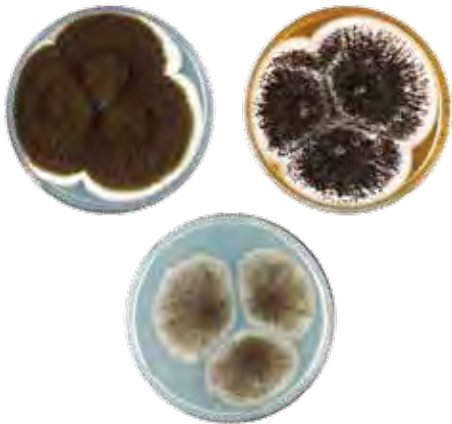
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## Community Gardens of Switchgrass

(*PNAS*, June 2019)

A multi-institution team led by Tom Juenger of UT-Austin and David Lowry of the Great Lakes Bioenergy Research Center conducted a large-scale field experiment spanning 10 field sites in the central United States. The community gardens allowed the team to uncover the genetic basis of local adaptation in switchgrass, and to consider how the plant's genes interact with the environment and look at the genes involved in specific fitness traits such as biomass production and flowering time. These results are helping them sort out the traits and underlying genes to develop a "generalist" switchgrass cultivar that would thrive and produce high levels of biomass in multiple planting zones.

[jgi.doe.gov/developing-switchgrass-for-biomass-production](https://jgi.doe.gov/developing-switchgrass-for-biomass-production)



*Aspergillus* section Nigri fungi sequenced and analyzed for this study (clockwise from top left): *A. heteromorphus*; *A. ibericus*; and *A. aculeatinus*. (Ellen Kirstine Lyhne, DTU)

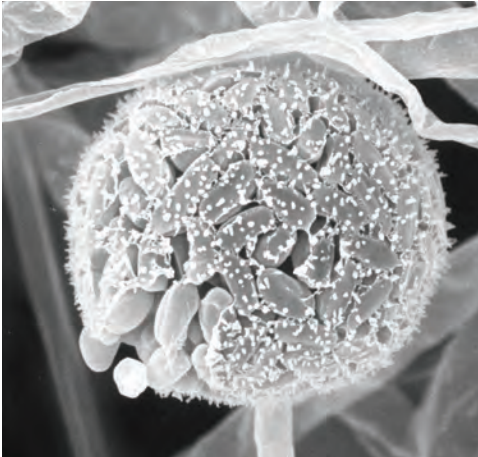
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## A Genetic Profile for a Section of *Aspergillus* Fungi

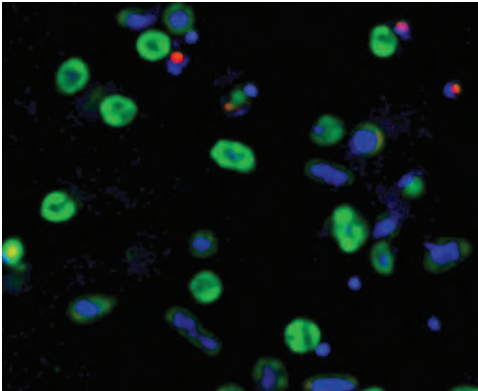
(*Nature Genetics*, October 2018)

As part of a long-term project to sequence, annotate, and analyze the genomes of more than 300 *Aspergillus* fungi, a team led by scientists at the Technical University of Denmark presented the first large analysis of an *Aspergillus* fungal subgroup, section Nigri. In choosing to focus on section Nigri, the researchers recognized the myriad of industrial applications for the fungi within this subgroup. They serve as production organisms for 20 percent of currently produced industrial enzymes and are also very efficient producers of secondary metabolites.

[jgi.doe.gov/spotlighting-differences-closely-related-fungi-species](https://jgi.doe.gov/spotlighting-differences-closely-related-fungi-species)



*Parasitella parasitica*. (ZyGoLife Research Consortium on Flickr, CC BY-SA 2.0)



FISH of Nha-C enrichment with *Hrr. lacusprofundi* ACAM34-hmgA. (Josh Hamm, UNSW)

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## How a Fungal Gene Regulator Evolved

(*Nature Ecology & Evolution*, February 2019)

In many organisms, the modified base 5mC is an important piece of how they regulate their genomes. A team led by Robert Schmitz at the University of Georgia reported on the largest analysis of 5mC distribution across the fungal tree of life to date, involving more than 500 species of fungi. In fungi, 5mC is often found in transposable elements or transposons that can move to another location in the genome. Understanding the role of transposons and 5mC in fungi could help researchers find ways to protect potential bioenergy feedstocks from fungal pathogens.

[jgi.doe.gov/evolution-of-fungal-gene-expression-regulator-5m](https://jgi.doe.gov/evolution-of-fungal-gene-expression-regulator-5m)

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## Cultivating Symbiotic Antarctic Microbes

(*PNAS*, June 2019)

Using a combination of co-cultivation and multiple microscopy and omics techniques, a team led by Rick Cavicchioli at the University of New South Wales experimentally demonstrated that Nanohaloarchaeota are not free-living archaea but rather symbionts. In the composite image on the left, cells from Nanohaloarchaeota strain Nha-C are labelled with a Cy5 (red fluorescence) conjugated probe; *Hrr. lacusprofundi* cells are labelled with a Cy3 (yellow fluorescence, recolored to green to improve contrast) probe; all nucleic-acid containing cells stained with DAPI (blue fluorescence). The work sheds light on the range of archaeal symbiotic lifestyles found in Antarctic lakes.

[jgi.doe.gov/cultivating-symbiotic-antarctic-microbes](https://jgi.doe.gov/cultivating-symbiotic-antarctic-microbes)





Poplar cuttings inoculated with *M. elongata* strain PM193 (far right) grow larger in 30 percent forest soil and 70 percent sand than without PM193 (middle). On the left are controls grown in sterile sand. (Chih-Ming Hsu)

## How A Fungus Spurs Poplar Growth

(*Molecular Plant-Microbe Interactions*, July 2019)

The fungus *Mortierella elongata* is almost always found among and within poplar trees. In an effort to understand the fungus' influence on this plant, a team led by Hui-Ling (Sunny) Liao of the University of Florida collected forest samples of poplar and soil from Washington and Oregon. The cuttings included genotypes from the DOE BioEnergy Science Center (BESC), predecessor of DOE's Center for Bioenergy Innovation (CBI) at ORNL. Comparing poplar cuttings grown with and without an inoculation of the *M. elongata* strain PM193, the team found that adding PM193 caused poplar cuttings to grow about 30 percent larger by dry weight than without PM193.

[jgi.doe.gov/fungus-fuels-poplar-tree-growth](http://jgi.doe.gov/fungus-fuels-poplar-tree-growth)



Gray's Cup (*Cladonia grayi*) lichen. (Thomas Barlow)

## Symbiosis in the Lichen Superorganism

(*Molecular Plant-Microbe Interactions*, July 2019)

Lichens are a model for inter-kingdom communication and cooperation. Their partnership is widespread and cosmopolitan. However, despite 150 years of lichen research, many details of the symbiosis remain unclear. For the first time, an international team led by Daniele Armaleo, a biologist at Duke University, analyzed in parallel the genomes and transcriptomes of both partners to better understand lichen. Working with Gray's Cup lichen (*Cladonia grayi*), the analysis has opened the door for more incisive investigations into how lichens function.

[jgi.doe.gov/making-lichen-together](http://jgi.doe.gov/making-lichen-together)



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## Pioneering Science: Viral Genomics

Understanding how Earth's diverse microbes help regulate global nutrient cycles involves learning more about the viruses that infect the microbes and alter their functions and metabolic processes. The JGI continues to be a pioneer in viral genomics, revealing novel viral diversity, functions and host interactions.

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## Best Practices for Characterizing Uncultivated Viruses

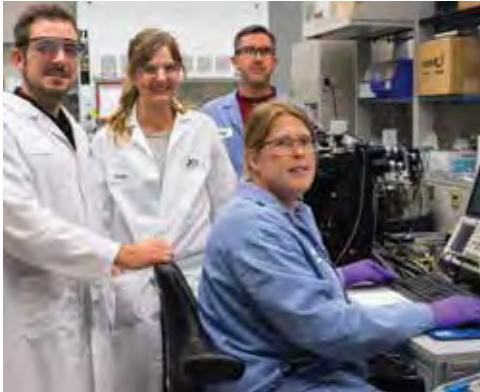
*(Nature Biotechnology, December 2018)*

As more and more researchers continue to assemble new genome sequences of uncultivated viruses, JGI researchers led a community effort to develop guidelines and best practices for defining virus data quality. In partnership with a number of virus experts, representatives from the Genomic Standards Consortium, an open-membership working body that engages the research community in the standards development process; and the International Committee on Taxonomy of Viruses, they outlined the minimum amount of information for an uncultivated virus genome, including the source, methods of identification of the virus genome, and data quality.

[jgi.doe.gov/defining-quality-virus-datasets](https://jgi.doe.gov/defining-quality-virus-datasets)

*Virus illustration by Leah Pantea*





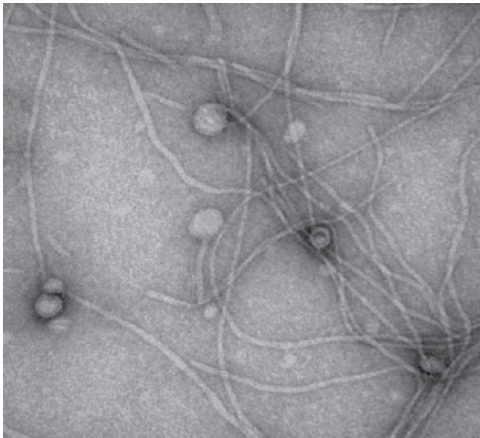
The JGI team involved in the study included (left to right): first author Frederik Schulz; senior author Tanja Woyke; Rex Malmstrom; and Danielle Goudeau (sitting). (*Janey Lee*)

## Novel Giant Viruses Found in a Soil Ecosystem

(*Nature Communications*, November 2018)

For the first time, giant virus genomes have been discovered in a forest soil ecosystem, the Harvard Forest in Massachusetts. Previous studies had focused on aquatic environments. The discovery was made by JGI and University of Massachusetts-Amherst researchers using a mini-metagenomics approach in which microbes from the samples were flow-sorted into several small pools of only 100 cells each and then each of the pools were sequenced separately.

[jgi.doe.gov/hidden-giant-virus-forest-soils](http://jgi.doe.gov/hidden-giant-virus-forest-soils)



EM image of *Pseudomonas* phage Pf. (*Courtesy of J. Driver and P. Secor, University of Montana*)

## Expanding Inovirus Diversity

(*Nature Microbiology*, July 2019)

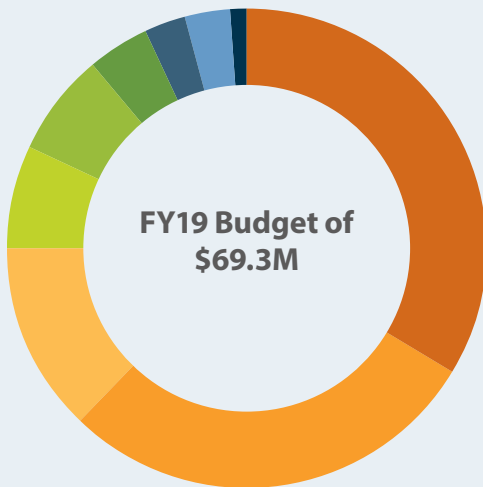
Inoviruses are filamentous viruses with small, single-stranded DNA genomes and a unique chronic infection cycle. A JGI-led team worked with Institut Pasteur researchers to develop a search tool that combed through more than 70,000 microbial and metagenome datasets, ultimately identifying more than 10,000 inovirus-like sequences compared to the 56 previously known inovirus genomes. The results revealed inoviruses are in every major microbial habitat—including soil, water, and humans—around the world.

[jgi.doe.gov/learning-to-look-inoviruses](http://jgi.doe.gov/learning-to-look-inoviruses)

# Impact 2019



## Spending Profile FY2019



33% Science Programs & Analysis

29% Genomic Technologies

13% Data Science & Informatics

7% Compute Infrastructure and Support Team (@ NERSC)

7% Management

Ph.D. student Albina Khasanova, seen preparing an EcoFab device, is a DOE Office of Science Graduate Student Research (SCGSR) intern visiting the Northern Lab in the IGB from the Juenger Lab, University of Texas at Austin.

4% Operations

3% Lease

3% Project Management Office

1% Emerging Technologies Opportunity Program (ETOP)



## Sequence Output

(in billions of bases or GB)

The JGI supports short and long read sequencers, where a read refers to a sequence of DNA bases. Short read sequencers produce billions of 300 base reads used for quantification such as in gene expression analysis. Long read sequencers currently average 50,000 basepair reads and are used for de novo genome assembly. Combined short read and long read totals per year give JGI's annual sequence output. The total sequence output in 2019 was 326,490 GB.

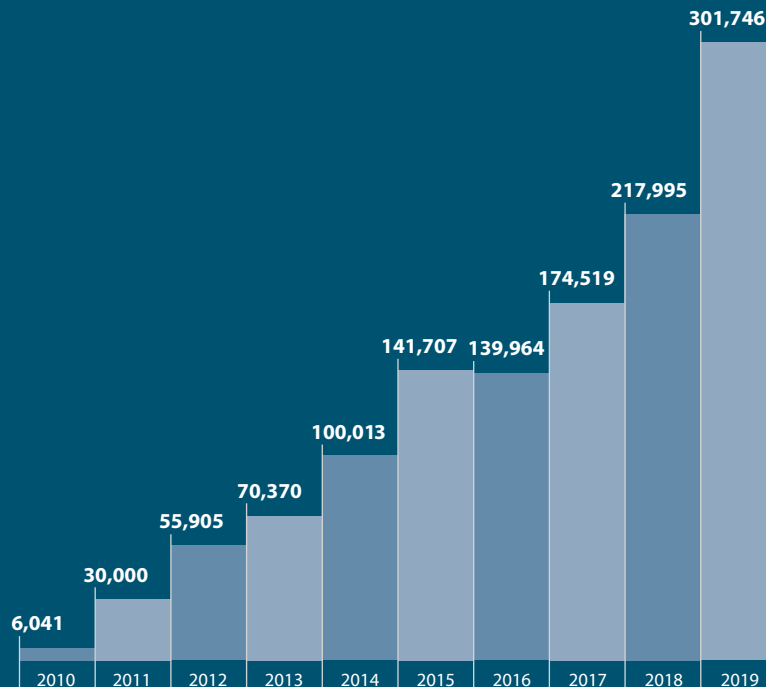
## User Demand: Synthetic Biology FY2019

Requested & Approved (MB)

Requested	12.341
Approved	6.869

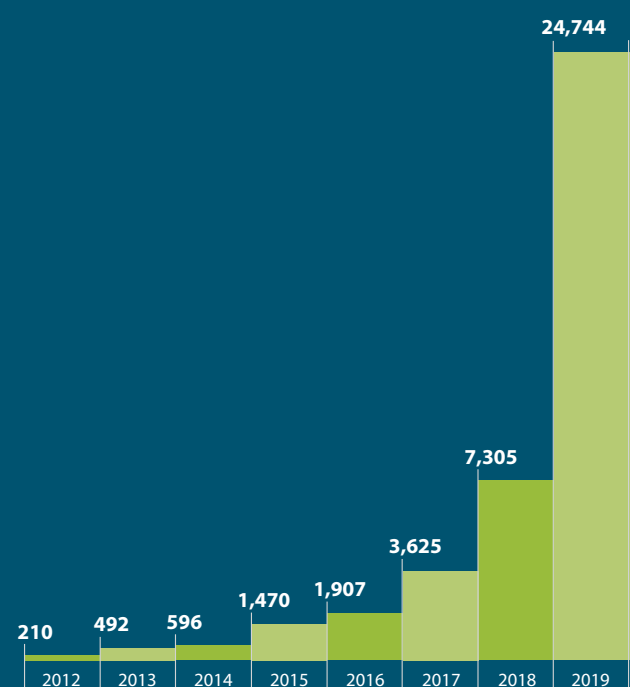
## Massively Parallel Short Read Sequencing

Basepairs (GB)



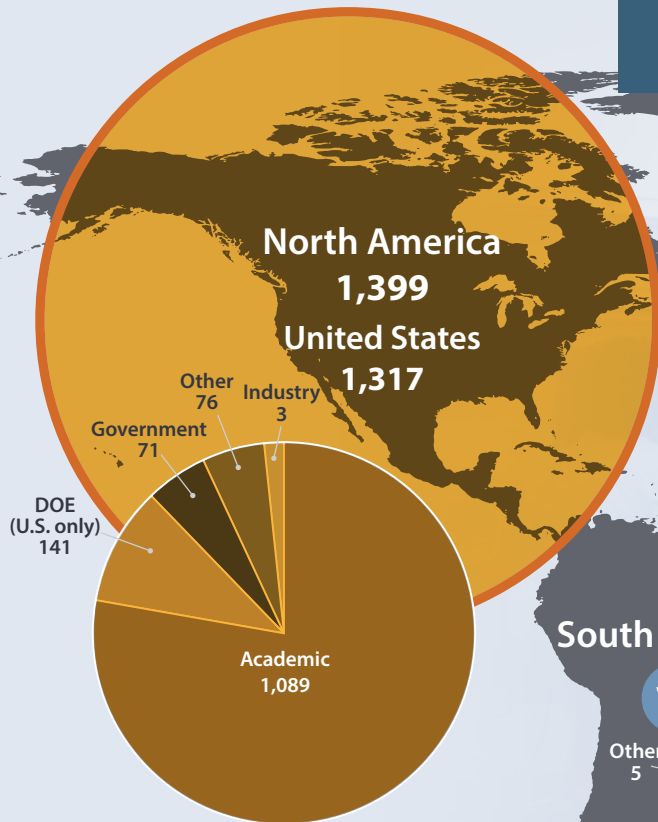
## Single Molecule Long Read Sequencing

Basepairs (GB)



## Users on the Map: 1,933

Academic	1,430
Government	154
DOE (national labs only)	141
Industry	29
Other	179



## North America 1,399

United States	1,317
Canada	77
Mexico	4
Panama	1

## South America 18

Brazil	9
Chile	2
Colombia	2
Peru	1
Uruguay	4

## Europe 377

Austria	16
Belgium	8
Czech Republic	6
Denmark	9
Estonia	1
Finland	16
France	59
Germany	74
Greece	3
Hungary	8
Iceland	1
Italy	23
Netherlands	30
Norway	9
Poland	2

Background image: Laura Sandor (left) and Jen Johnson (right foreground).

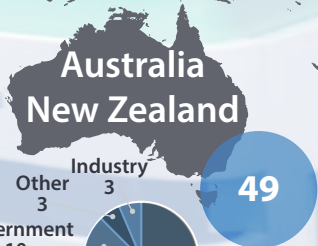
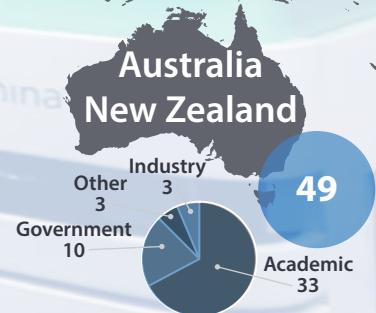
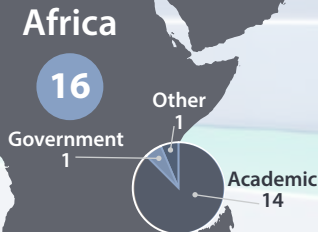
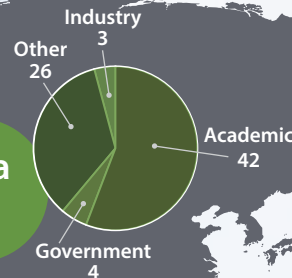
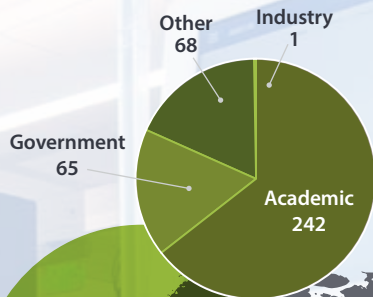


Portugal	6
Russian Federation	4
Slovenia	1
Spain	30
Sweden	20
Switzerland	14
Turkey	1
United Kingdom	36

<b>Africa</b>	<b>16</b>
Egypt	1
Morocco	1
South Africa	13
Tunisia	1

<b>Asia</b>	<b>74</b>
China	26
Hong Kong	1
India	9
Israel	10
Japan	22
Oman	1
Republic of Korea	4
Singapore	1

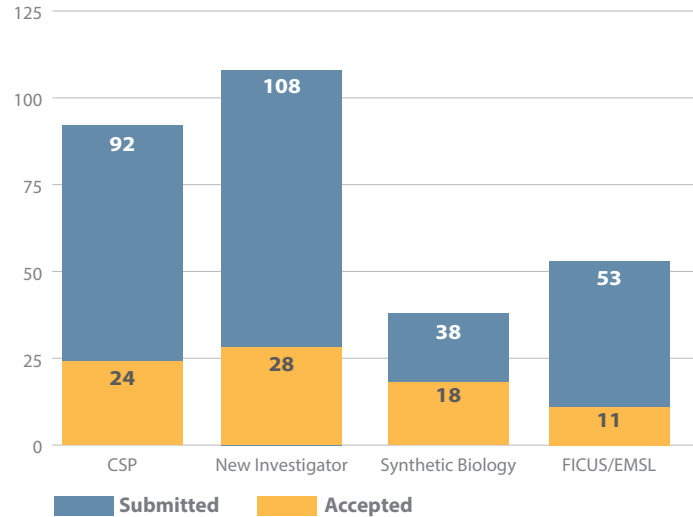
<b>Australia &amp; New Zealand</b>	<b>49</b>
Australia	39
New Zealand	10



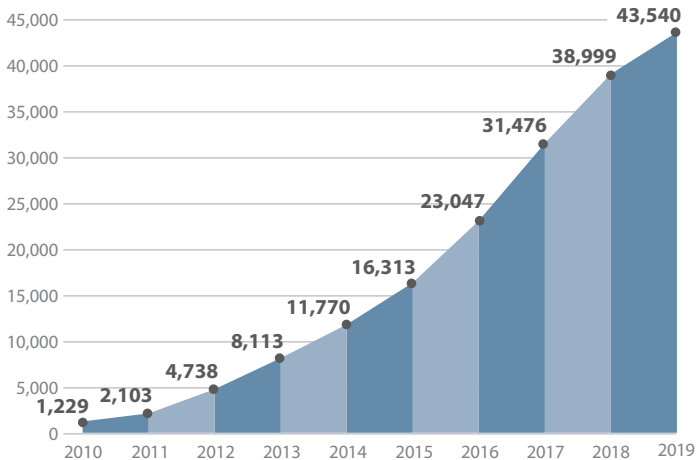
## Users of JGI Tools & Data

The JGI produces high-quality data that are made available to the community through our data portals. External Data Users are not included in the primary Data User count because their projects were not conducted as part of JGI's user programs. When Data Users log in to the systems and download data, this activity is tracked in order to help us understand which data sets are of greatest value to our Data Users. Additionally, the JGI's data management system is able to restore data from the High Performing Storage System (HPSS) upon user request and this activity is logged. In 2019, JGI users downloaded 2.16 million files and a total of 400 terabytes (TB) of data.

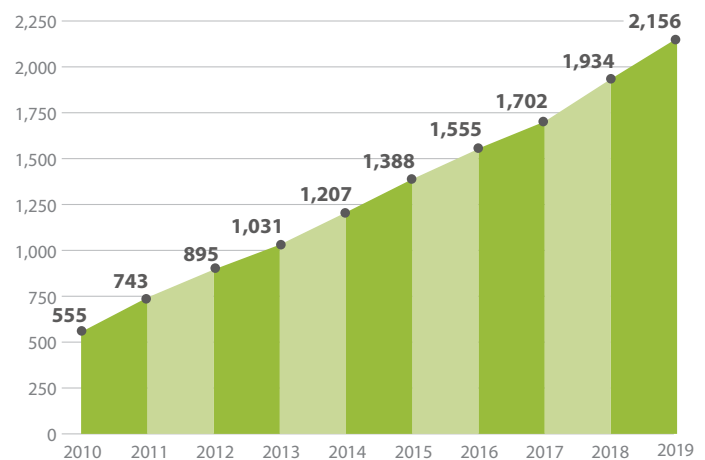
## User Proposals Submitted & Accepted FY2019



## Cumulative Number of Projects Completed



## Cumulative Number of Scientific Publications





# Computational Infrastructure



## **JGI Archived Metadata Organizer (JAMO)**

10.2 million files records

## **JAMO Archived Data Footprint**

8.3149 Petabytes

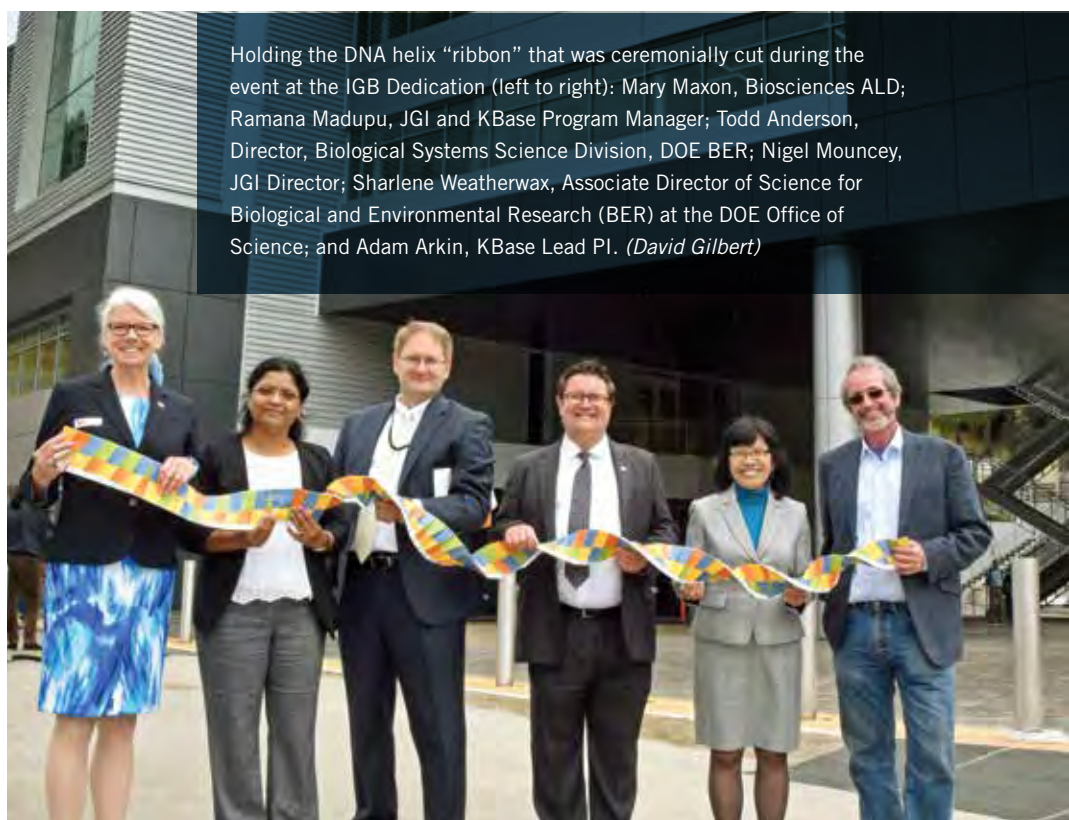
## **Data downloads in FY19**

400 TB; 2.16 million files

Data transfer nodes (shown here) in supercomputers like NERSC's Cori system perform transfers between storage resources at NERSC and other sites, facilitating high-speed data movement over ESnet's 100Gb wide-area network. A subset of nodes on Cori are reserved for exclusive use by JGI users. *(Marilyn Sargent, Berkeley Lab)*



Top right: Sunset at the IGB (Axel Visel). Bottom left: Movers bringing equipment into the IGB from Walnut Creek.



Holding the DNA helix “ribbon” that was ceremonially cut during the event at the IGB Dedication (left to right): Mary Maxon, Biosciences ALD; Ramana Madupu, JGI and KBase Program Manager; Todd Anderson, Director, Biological Systems Science Division, DOE BER; Nigel Mouncey, JGI Director; Sharlene Weatherwax, Associate Director of Science for Biological and Environmental Research (BER) at the DOE Office of Science; and Adam Arkin, KBase Lead PI. (David Gilbert)





# Integrative Genomics Building (IGB)

The IGB unites the combined staff and research assets of the JGI and KBase, two highly impactful programs supported by the BER, for catalyzing solutions to energy and environmental challenges. Together, the JGI and KBase have nearly 3,400 users of their DNA sequencing, synthesis, metabolomics and bioinformatics resources.

The JGI also supports Plant Program staff at the HudsonAlpha Institute for Biotechnology. The KBase partnership extends to ORNL, Argonne National Laboratory, Cold Spring Harbor Laboratory, and Brookhaven National Laboratory.

JGI and KBase are part of the Berkeley Lab's Biosciences Area, the largest biosciences program in the DOE's portfolio. Biosciences researchers at Berkeley Lab are dedicated to the discovery, understanding, and engineering of biology to solve energy, environmental, and health challenges. The IGB also houses scientists from the NMDC and from the Environmental Genomics and Systems Biology Division of the Biosciences Area.

The IGB was designed to conform with Berkeley Lab's policy on Sustainability Standards for New Construction.

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## IGB Facts:

- Funding ~\$108 M: \$91M from DOE Scientific Laboratory Infrastructure (SLI); \$17M from Berkeley Lab for Modular Utility Plant (MUP) and other non-construction costs
- Architect: SmithGroup
- Construction manager/general contractor: Rudolph & Sletten
- 80,880 gross square ft (comparable size to the JGI's previous Walnut Creek facility), 4 floors
- 60% offices & support spaces/40% laboratory space
- Floors 1 & 2: laboratory spaces; floors 3 & 4: office spaces; interactive space throughout
- ~300 staff (285 JGI, 20 KBase)

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## Features Include:

- Designed to use just 30% of the energy used by JGI at its previous Walnut Creek facility, saving up to \$500,000 in annual utility costs
- Designed to accommodate a solar photovoltaic array to offset over 10% of the building's energy use
- Designed to achieve LEED Gold certification under the green building certification system
- First Berkeley Lab building with all-LED lighting
- Electrified laboratory building, i.e., uses electric heat pumps and heat recovery to provide heat rather than relying on natural gas. This will allow the greenhouse gas footprint of the building to shrink over time as the state continues to shift towards a renewable electricity grid
- Abundance of interactive space to optimize scientific collaborations—a lobby with two-story atrium, a south-facing third floor patio area, a large lounge area, conference rooms, huddle rooms, etc.
- Optimum daylighting in lab spaces
- Horizontal transparency with office and lab workstations

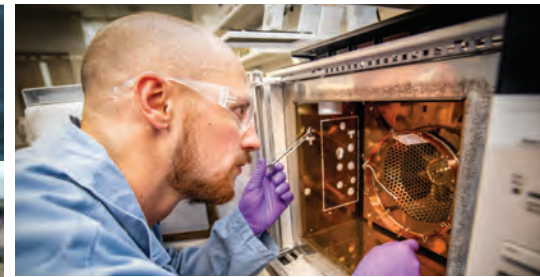


# IGB

Berkeley Lab Director Mike Witherell, Chief of Staff Margaret Dick, and Deputy Laboratory Director for Operations Michael Brandt bring donuts to the first wave of JGI staff moving into the IGB.



(Clockwise from top right): Hope Hundley; Nick Saichek; Zhiying "Jean" Zhao.



## CONTACT US

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*Images by Thor Swift, Berkeley Lab  
Alison F. Takemura contributed to the  
highlights. Design by Creative Services,  
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