JGI JOINT GENOME INSTITUTE
A DOE OFFICE OF SCIENCE USER FACILITY

2020
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**

It is safe to say that 2020 has been unlike any other year we have encountered in our lifetimes. The COVID-19 pandemic, racial inequity, the U.S. election, and more locally here in California, wildfires, placed burdens on all of us that we could not imagine a year ago. Through these challenging times, the JGI team has continued to deliver tremendous productivity to our users, develop and deploy state-of-the-science technologies, evolve our data pipelines and portals, and even conduct our successful move to the new Integrative Genomics Building (IGB). I couldn't be prouder of and more grateful to our entire team.

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

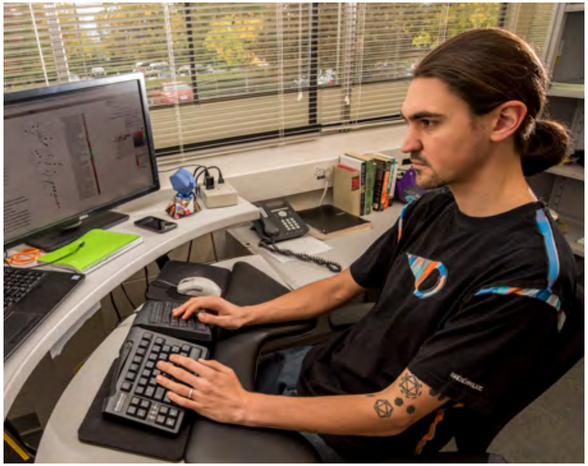
Nigel Mouncey, Director, DOE Joint Genome Institute

In December 2019, the JGI team, along with our colleagues from the DOE Systems Knowledgebase (KBase), the National Microbiome Data Collaborative, and Berkeley Lab's Environmental Genomics and Systems Biology (EGSB) Division, completed our successful move into the IGB.

The move was completed without incident and we were able to restart operations quicker than we anticipated. Essential to this success was the organizational mastery of our Deputy for Operations, Ray Turner, who took the helm for every aspect of building the IGB for our needs and orchestrating the complex move. It is then befitting that after this move and getting the occupants settled, Ray retired in the summer of 2020. We are eternally indebted to Ray and extend all of our thanks to him and congratulate him on his retirement.

Ray Turner at the staff orientation during the JGI's move into the IGB.

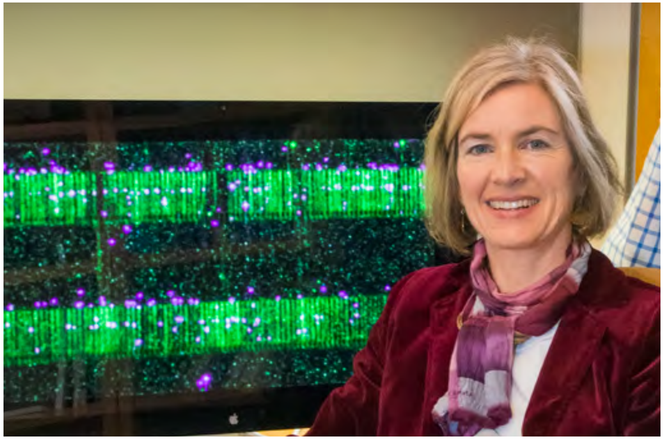
Despite the past year's challenges, the JGI continued to deliver remarkable support to our user community. In fiscal year 2020, the JGI's sequencing output exceeded 290 trillion bases, and DNA synthesis targets exceeded 7.6 million bases synthesized with over 5 million bases/constructs delivered to users. We have continued to meet or exceed the majority of our **Strategic Plan** implementation milestones with 85% completion of our two-year milestones. Our user base grew to 2,038 primary project users, with many tens of thousands of data users. Despite the cancellation of our 2020 Annual JGI User Meeting, we have sought new ways to engage with and reach out to our users, and conducted a series of **IMG Webinars** and **Engagement Webinars** to showcase core capabilities and hear from our users. We also successfully launched two new **podcasts**. "Genome Insider" covers JGI-wide topics from a user perspective, and "Natural Prodcast" focuses on natural products as part of our new scientific strategic thrust on secondary metabolites (more on page 26).



Left: Len Pennacchio with Nigel Mouncey at the 2019 Berkeley Lab Director's Awards. Right: Research Scientist Simon Roux received a DOE Early Career Research Award.

The JGI continues to deliver high-impact science by supporting user projects and through our internal **Science Program** projects, as evidenced by the 212 peer reviewed publications released over the past year. Some of these are featured in the highlights section that follow this message. Additionally, the caliber of the scientists supporting the JGI user community has been recognized by multiple organizations:

- A number of our scientists appear on an annual Clarivate Analytics list of **highly cited researchers**: Program Manager Kerrie Barry, Fungal and Algal Program Head Igor Grigoriev, Plant Program Library Construction Group Lead Jane Grimwood, Research Scientist Natalia Ivanova, Microbiome Data Science Lead Nikos Kyrpides, Computational Genomics Lead Dan Rokhsar, Staff Scientist Asaf Salamov, Plant Program Head Jeremy Schmutz, User Programs Deputy Susannah Tringe, and Microbial Program Head Tanja Woyke.
- Genomic Technologies Deputy Len Pennacchio received a **2019 Berkeley Lab Director's Award** for Exceptional Scientific Achievement.



Left: Tanja Woyke's van Niel Prize recognized her contributions in the field of microbial genomics, particularly the genomics of uncultivated microbes.
Right: JGI user Jennifer Doudna received the Nobel Prize in 2020.

- Research Scientist Simon Roux received a DOE Early Career Research Award.
- Interim User Programs Deputy and Microbial Program Head Tanja Woyke was elected an American Academy of Microbiology fellow and was awarded the van Niel International Prize for Studies in Bacterial Systematics for the triennium 2017–2020.
- And it goes without saying that we are thrilled long-time JGI user Jennifer Doudna received the Nobel Prize in 2020.

The COVID-19 pandemic brought challenges and constraints to the JGI: on-site lab operations were shut down for 10 weeks, and then resumed with limited staffing at the beginning of June. Since that time, we have gradually increased our on-site staffing to enable up to 80% of our targeted production capacity in December. As the pandemic continues, we will modify staffing in accordance with Berkeley Lab, local, and state guidance. Throughout this time, JGI staff have remained dedicated to our mission and have continued to their very best to meet the needs of our user community. The JGI team continues to operate with safety of each other as our top priority, and had no recordable injuries in 2020. We have continued to invest in state-of-the-science equipment (e.g., new Pacific Biosciences Sequel II instruments with increased capacity for long-read sequencing, new mass spectrometry equipment for metabolomics, and increased automated platforms for higher-throughput and increased capacity workflows). We are very grateful to the DOE for $3 million of Coronavirus Aid, Relief, and Economic Security (CARES) Act funding that was used to purchase some of this equipment. The JGI has also brought online new capabilities to support our users, such as host engineering, the JGI Analysis and Workflow System (JAWS), and Stable-Isotope Probing omics (SIP-omics).

The JGI has also been working on projects as part of the COVID-19 response. In three weeks, the Innovative Genomics Institute at the University of California (UC) Berkeley established a COVID-19 diagnostic testing lab in accordance with Clinical Laboratory Improvement Amendments (CLIA) regulations to meet the demand for fast-turnaround, high-quality testing for the UC and local communities. This was made possible with specialized teams focused on executing specific processes and a team of dedicated volunteers. Among the volunteers were the JGI's Kerrie Barry, L.T. Cornmesser, David Dilworth, and Christine

The JGI's Chief Informatics Officer Kjiersten Fagnan (right) with Dario Gil (leftmost), Director of IBM Research, and Shane Wall, Chief Technology Officer and Director, HP Labs, members of the President's Council of Advisors on Science and Technology (PCAST) visiting the IGB in January 2020.

Naca, who implemented a robotic pipeline with automated liquid-handling robots to increase the lab's capacity to process samples and perform pooled surveillance testing. Using our expertise in viral genomics, JGI researchers have been exploring recombination, mutations, and viral variants, to better understand the evolution of the SARS-CoV-2 virus. These insights could be used to improve diagnostic testing and understand the disease's progression. The JGI also received additional funding from the DOE to explore viral-host relationships (watch "Deciphering the Virus-Bacterial Cell Network") using model rhizosphere systems to develop technology to explore genetic and evolutionary drivers for viral-host interactions.

Throughout 2020, JGI staff have demonstrated amazing resiliency, flexibility, and adaptability to the pandemic and with our move to the IGB. The JGI cares deeply about its users and each other, and our people have shown team support at its best. Additionally, over the summer, 11 JGI researchers virtually mentored a cohort of five graduate and five undergraduate student interns from our flagship education-workforce development partnership with UC Merced. Their experiences were captured in these videos.

We have continued to recruit and bring top talent into the JGI, with 35 positions successfully filled in 2020. Most notably, we recruited Nick Everson back to the JGI to serve as the JGI's Deputy for Operations. Tanja Woyke is currently serving as Interim Deputy for User Programs (while Susannah Tringe serves as Interim Director of EGSB). Tina Clarke, the JGI's Senior Human Resources Business Partner, has joined the JGI Senior Leadership Team, and we have conducted several reorganizations in parts of the JGI to strengthen alignment with our core mission.

While 2020 was an incredibly challenging year for everyone, the JGI team persevered, rising to the occasion to drive many successes. As we begin 2021, we can be filled with optimism and hope that COVID-19 can be controlled with vaccinations, and that hopefully later this year, we will be able to resume in-person interactions.

Please read on for vignettes describing the JGI's remarkable productivity in enabling groundbreaking user science achieved over a year that we will not soon forget.

Nigel J. Mouncey

Nigel Mouncey, DPhil
Director, DOE Joint Genome Institute

The Year at the JGI

In mid-March 2020, Berkeley Lab's research and operations went to stand-down status after six Bay Area, California counties announced "shelter-in-place" orders. Gradual return to work plans and policies were instituted three months later, and staff continue to navigate the changes and challenges brought on by the pandemic.


Top row (left to right): Suzie Kosina, Markus de Raad, Laura Sandor, and Hope Hundley at the Integrative Genomics Building (IGB). Bottom row: (left to right) DOE Office of Science Director Chris Fall, Berkeley Lab Director Mike Witherell and JGI Director Nigel Mouncey at the IGB. Scenes from Berkeley Lab while shelter-in-place orders were in effect.

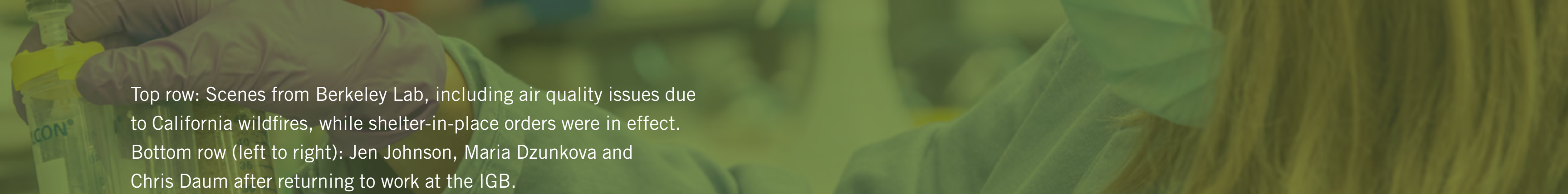
LBNL and COVID-19: Information and FAQ's

The health and safety of our employees and our workplace is our top priority.

COVID-19

status.lbl.gov

Get updates and Lab-specific information, and check out the extensive list of frequently asked questions.



Top row: Scenes from Berkeley Lab, including air quality issues due to California wildfires, while shelter-in-place orders were in effect. Bottom row (left to right): Jen Johnson, Maria Dzunkova and Chris Daum after returning to work at the IGB.

Science **Highlights**

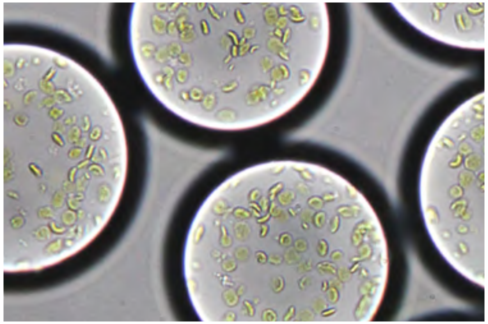
The sorghum “stay-green” variety BTx642 grown for 65 days without water. *(Jeffrey Dahlberg, UC ANR Agricultural Research and Extension Center)*

Sorghum’s Response to Drought Stress

(*PNAS*, December 2019)

The genes of sorghum plants are likely responsible for the crop’s ability to produce good yields under water-limiting conditions. Epigenetic Control of Drought Response in Sorghum (EPICON) is a five-year DOE project to determine what sorghum genes respond to drought conditions and how these conditions affect the crop and its microbiome. The field experiment was led by a consortium involving researchers from the UC Berkeley, UC Agriculture and Natural Resources (ANR), U.S. Department of Agriculture Plant Gene Expression Center, Pacific Northwest National Laboratory (PNNL), and the JGI. All EPICON data will be published on the JGI’s plant data portal, Phytozome.

Read more >



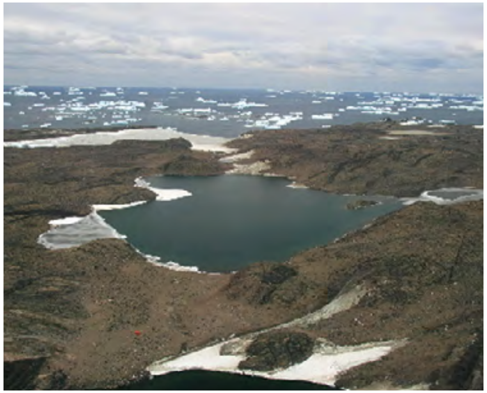
Artificial chloroplasts are photosynthetic membranes encapsulated within micro-droplets. *(Miller/Beneyton MPG)*

A Step toward Efficient Artificial Photosynthesis

(*Science*, May 2020)

A team led by Tobias Erb of the Max Planck Institute (MPI) for Terrestrial Microbiology successfully combined synthetic biology and microfluidics to develop a platform that mimics chloroplasts, a step toward making an artificial photosynthetic cell. The work is part of a long-term effort to capture and use the excess carbon from the atmosphere for producing high-value bioproducts. Supporting the Erb lab through the Community Science Program (CSP) Functional Genomics call, the JGI synthesized a library of genes that code for enoyl-CoA carboxylase/reductase (Ecr) enzyme variants. Ecr enzymes are capable of fixing CO_2 many times faster than RuBisCo, the most common CO_2-fixing enzyme in nature.

Read more >



Aerial view of Ace Lake in March, as ice begins to re-form on the surface. *(Courtesy of Anthony Hull)*

Boom or Bust Cycle for Antarctic Bacteria

(*Microbiome,* August 2020)

Working with the JGI, a team led by Rick Cavicchioli of the University of New South Wales in Australia found that microbial populations in Antarctica's Ace Lake do not shift from bacteria to archaea when sunlight becomes scant. The team conducted a decade-long, time-series study to understand the effect of the polar light cycle on microbial-driven nutrient cycles. They found that during the polar region's summer months, the lake's green sulfur bacteria population spiked to 83%, only to dramatically fall to 1% in early spring and rebound by the late spring.

Read more >

Watch the video: "How microbes of an Antarctic lake have adapted to the polar light cycle" produced for *Microbiome*.

Brachypodium distachyon. (Pilar Catalán)

Brachypodium Model Traces Genome Evolution

(*Nature Communications,* July 2020)

Many plants, including agricultural staples and candidate bioenergy feedstock crops, are polyploids with multiple copies of their genome. Crop breeders have harnessed polyploidy to increase fruit and flower size and confer stress tolerance traits. A multi-institutional team led by Pilar Catalan at Spain's Universidad de Zaragoza and JGI researchers harnessed the model grass *Brachypodium hybridum*, a polyploid of *B. stacei* and the flagship plant *B. distachyon* to learn the origins, evolution, and development of plant polyploids. Reference *Brachypodium* genomes are available on **Phytozome.**

Read more >

Gossypium hirsutum, known as Upland cotton. *(Cotton Incorporated)*

Molecular Methods for Breeding Cotton

(*Nature Genetics*, April 2020)

In the United States, 95% of the cotton grown is known as upland cotton (*Gossypium hirsutum*), while the remaining 5% is called American Pima (*G. barbadense*). A multi-institutional team including researchers at the University of Texas at Austin, Cotton Incorporated, and the JGI has sequenced and assembled the genomes of the five cotton lineages. These genomes provide breeders with insights on crop improvements at a genetic level.

Additionally, cotton is almost entirely made up of cellulose and is a fiber model to understand the molecular development of cellulose. The genomes of all five cotton lineages are on **Phytozome.**

Read more >

Morel *(Hao Tan)*

Triggering Morel Fruiting

(*Environmental Microbiology*, December 2019)

Morels are economically, culturally, and ecologically important fungi. While prized as a culinary delicacy, they also influence geochemical cycling in forest ecosystems. A team led by Hao Tan from China's Sichuan Academy of Agricultural Sciences and involving Francis Martin from French National Institute for Agriculture, Food and Environment (INRAE) and the JGI's Igor Grigoriev determined the fruiting-related decomposition mechanisms of morels, as well as the gene-expression programs encoding the biochemical processes. The work is part of the JGI's **1000 Fungal Genomes Project**. The genome sequences and annotations are available on the JGI fungal portal **MycoCosm**.

Read more >

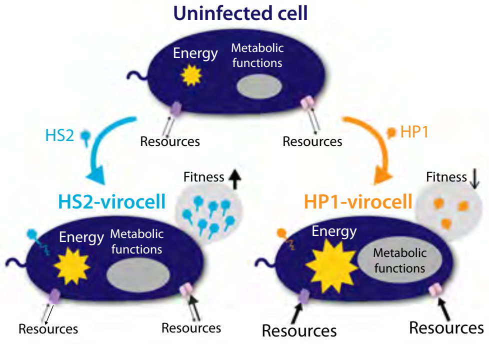
The filamentous fungus *Neurospora crassa* eating plant biomass. *(Vincent Wu)*

Tracing Fungal Gene Regulatory Networks

(*PNAS*, February 2020)

A team led by N. Louise Glass at UC Berkeley and her postdoctoral fellow Vincent Wu worked with JGI researchers to learn more about the regulatory networks in the model filamentous fungus *Neurospora crassa*. Filamentous fungi contain a wide array of plant cell-wall degrading enzymes. The team applied multiple omics techniques to reconstruct and model the gene regulatory networks as they responded to available carbon sources and determined which enzymes to deploy and in what order to break down plant cell-wall materials.

Read more >



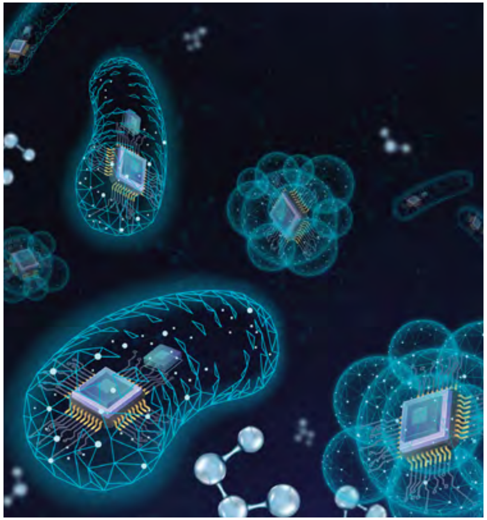
How a cell behaves as a virocell largely depends on the infecting virus and the genomic similarity between host and virus. *(Figure by Cristina Howard-Varona)*

Viruses Reprogram Cells into Different Virocells

(*The ISME Journal*, February 2020)

A team led by the University of Michigan's Melissa Duhaime, The Ohio State University's Matt Sullivan, and his postdoctoral researcher Cristina Howard-Varona reported that microbial cells infected by viruses undergo metabolic reprogramming and are functionally different from uninfected cells. Demonstrating that the costs of infecting microbes and their impacts on the ecosystems can vary is a step toward developing more efficient predictive ecosystems models. The team's research was enabled in part by the Facilities Integrating Collaborations for User Science (FICUS) collaborative science initiative between the JGI and the Environmental Molecular Sciences Laboratory (EMSL), a DOE Office of Science user facility located at PNNL.

Read more >



An illustration imagining the molecular machinery inside microbes as technology. *(Wayne Keefe/ Berkeley Lab)*

Enabling Biomanufacturing through Multiple Microbial Hosts

(*Nature Microbiology,* October 2019)

Led by JGI DNA Synthesis Science head Yasuo Yoshikuni and his group, a team including Goethe University Frankfurt and EMSL researchers has invented a genetic engineering tool that allows synthetic biologists to domesticate a broad range of bacterial hosts and successfully and efficiently insert functional genetic constructs in a single step. The chassis-independent recombinase-assisted genome engineering (CRAGE) tool was tested with multiple gammaproteobacterial species, uncovering novel secondary metabolites not normally produced by the hosts. It could be adapted to allow other organisms such as fungi, algae, and archaea to serve as novel hosts for biomanufacturing.

Read more >

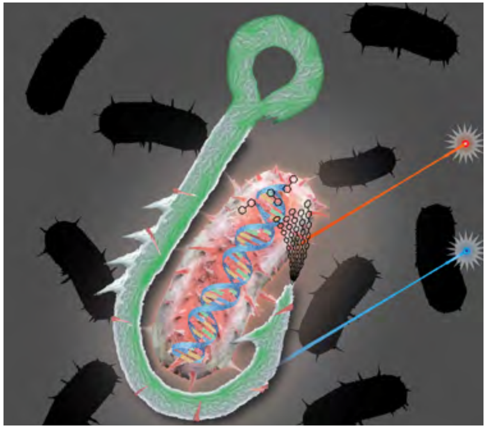
Gradient of the betaxanthins production in yeast across various cultures. (*Courtesy of Matthew Deaner)*

From On-Off Switch to Dial

(*PNAS*, July 2020)

A team led by Hal Alper of the University of Texas, Austin, and including JGI researchers has developed a more nuanced library approach to fine-tune gene expression in metabolic pathways. This capability allowed researchers to identify variations of essential genes in metabolic networks that were missed using traditional approaches. To demonstrate the versatility of this novel technique, the team applied this method to a production-based scenario and pinpointed multiple genes that were previously missed in knock-out screens. This new approach for fine-tuning gene expression in metabolic pathways could be used for biofuel optimization and other applications.

Read more >



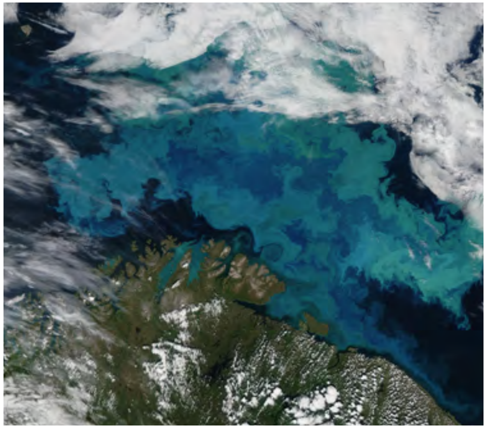
Graphical representation of the cellulose hook approach. *(Devin Doud)*

Fishing for Novel Cellulose Degraders

(*The ISME Journal*, November 2019)

The JGI Single Cell Genomics group developed a function-driven, single-cell screen described as a "bait and hook" approach to isolate cellulose-degrading microbes. They benchmarked the approach on model cellulose degraders and then applied it to environmental samples from the Great Boiling Spring in Nevada, where they uncovered a novel cellulose-degrading bacterium typically found in low abundances. Teaming up with the JGI's DNA synthesis and metabolomics teams, they were then able to show activity of its divergent cellulases. The approach can be further developed to "bait" for other specific functions and tease out uncultivated microbes of interest from complex environmental samples.

Read more >



Algal blooms are abundant in the North Sea in late spring and early summer. *(NASA)*

Targeting a Microbial Needle within a Community Haystack

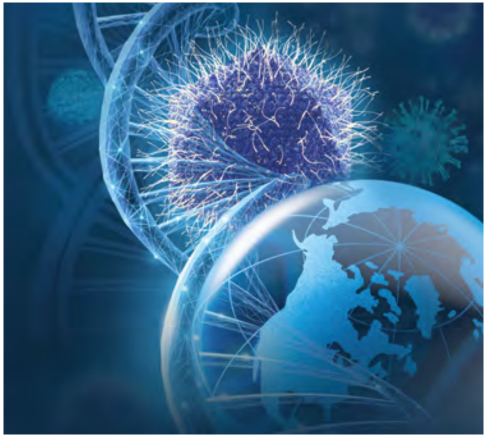
(*Microbiome*, February 2020)

Bernhard Fuchs and his postdoctoral researcher Anissa Grieb at the MPI for Marine Microbiology led a team that developed a workflow for capturing the genetic makeup of specific uncultivated microbes from complex environmental samples. The team's protocol combines multiple techniques and was demonstrated in a proof-of-principle study targeting a specific group of marine bacteria called "Vis6" that are found in North Sea algal blooms. The study demonstrated the workflow's viability for selectively enriching low abundance microbial groups from complex natural communities. The work was enabled by the JGI's Emerging Technologies Opportunity Program (ETOP).

Click to enlarge

Read more >

Watch the video: "Enriching target populations for genomic analyses using HCR-FISH" from the journal Microbiome describing the research.



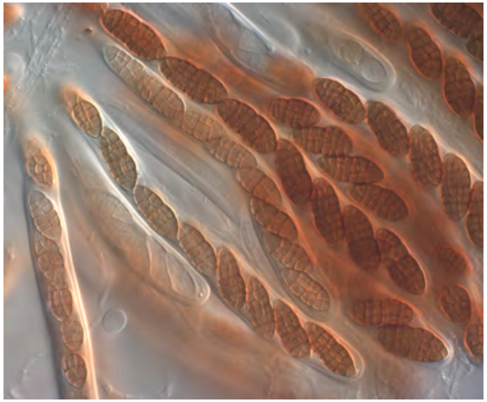
Art illustration capturing giant virus genomic diversity. *(Zosia Rostomian/Berkeley Lab)*

Large and Giant Viruses Abound Globally

(*Nature*, January 2020)

A team led by JGI researchers uncovered a broad diversity of large and giant viruses that belong to the nucleocytoplasmic large DNA viruses supergroup. For this first study taking a global look at giant viruses, they mined several thousand publicly available metagenome datasets in the **Integrated Microbial Genomes & Microbiomes (IMG/M)** system, generated from sampling sites around the world. The expansion of the diversity for large and giant viruses offered insights into how they might interact with their hosts, and how those interactions may in turn impact the host communities and their roles in carbon and other nutrient cycles.

Read more >



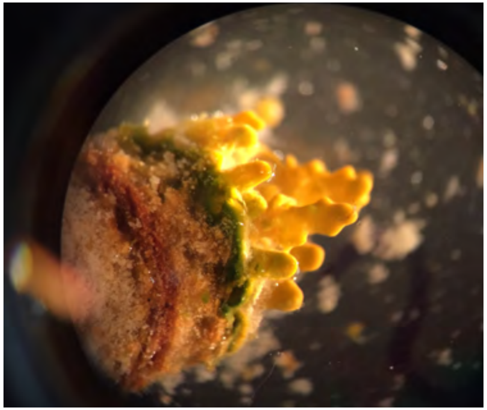
Aggregated cluster of ascomata in the saprobe *Cucurbita berberidis*, with cells arranged like a wall of bricks. *(Pedro Crous)*

Computationally Classifying Fungal Lifestyles

(*Studies in Mycology*, July 2020)

Dothideomycetes include fungi that obtain nutrients from decaying organic matter (saprobes) and many plant pathogens known to infect most major food crops and feedstocks for biomass and biofuel production. As a proof of concept, a team led by JGI researchers applied machine learning methods to classify 101 sequences of Dothideomycete genomes, the largest class of fungi, by lifestyles. They generated a more accurate phylogenetic tree tracking the evolution of these fungi. The team reported that the algorithm was over 95% successful at classifying the fungal genomes generated in part through the **1000 Fungal Genomes Project.**

Read more >



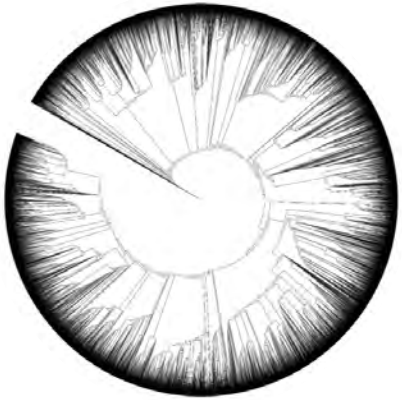
Microbial mat under the microscope. *(John Spear)*

Host-Virus Dynamics in a Microbial Mat

(*The ISME Journa*l, August 2020)

In microbial mats, communities of microbes live among viruses that infect them. A team co-led by JGI postdoctoral researchers Mária Džunková and Jessica Jarret in the Single Cell Genomics group applied single-cell and metagenomic sequencing to uncultured microbial populations to for the first time comprehensively characterize viral-host interactions in microbial mats. Their data suggest that, within these local populations, the viruses are not rapidly replicating, but instead may be abiding in or "piggybacking" on the host genomes to thrive.

Read more >



Phylogenetic tree of virophage diversity.
(David Paez-Espino)

Expanding Virophage Diversity

(*Microbiome,* December 2019)

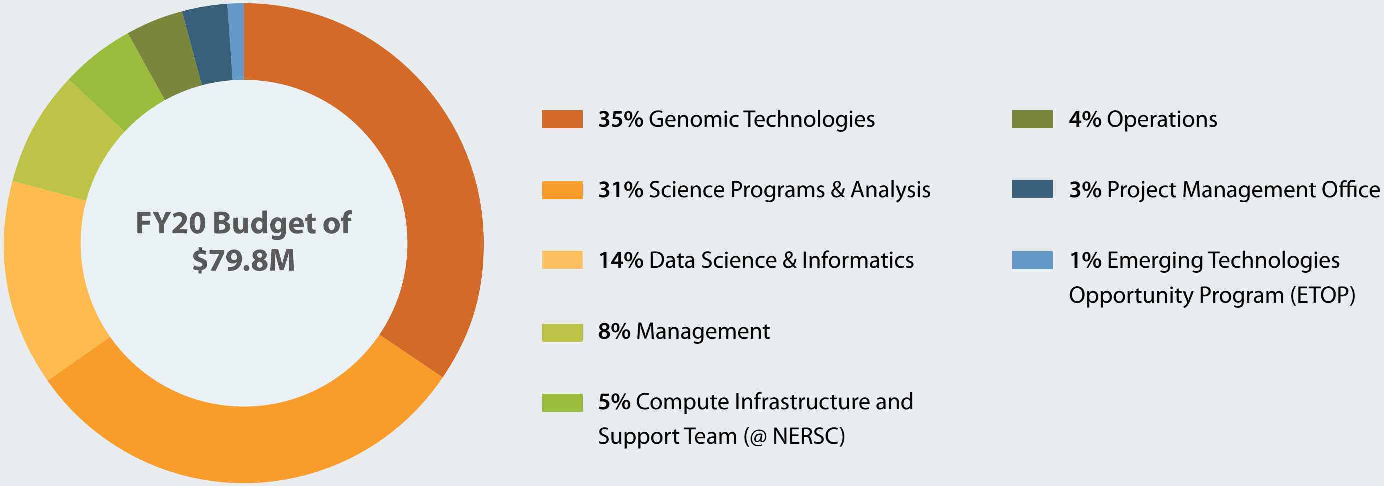
Virophages are small viruses with double-stranded DNA genomes that infect giant viruses. By mining more than 14,000 publicly available metagenomic datasets in the JGI's IMG/M data suite, which includes IMG/VR (for Virus), JGI researchers increased the number of known high-quality virophage genome sequences tenfold. Almost all known virophage genomes share only four genes in common: major and minor capsid proteins (MCP and mCP, respectively), ATPase involved in DNA packaging, and PRO, a cysteine protease involved in capsid maturation. Searching for the virophage marker gene MCP, the researchers were able to identify 44,221 total virophage partial sequences, including over 28,000 unique MCP sequences.

Read more >

Impact **2020**

Andrea Kuftin (foreground) and Amber Golini (back) in the metabolomics lab at the IGB.

Spending Profile **FY2020**



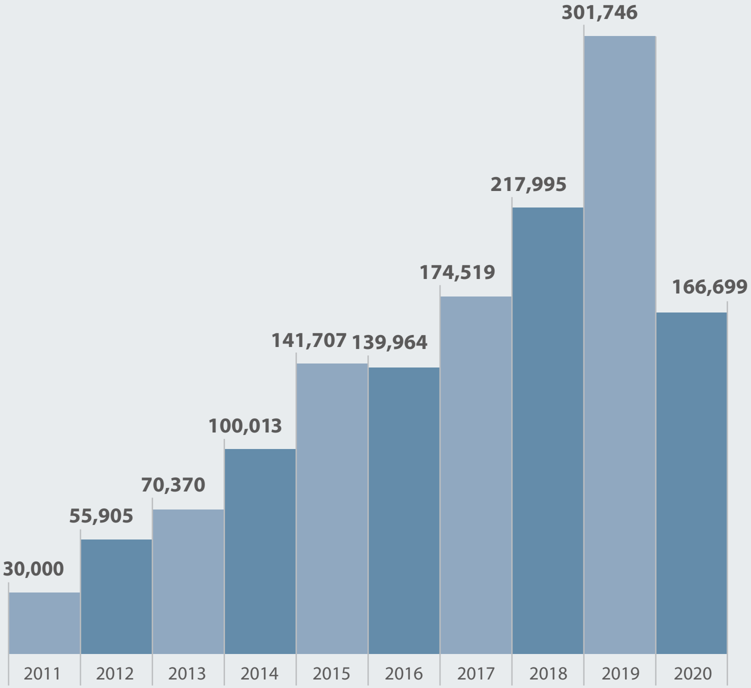
Sequence **Output**

(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 60,000–70,000 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 2020 was 290,492 GB.

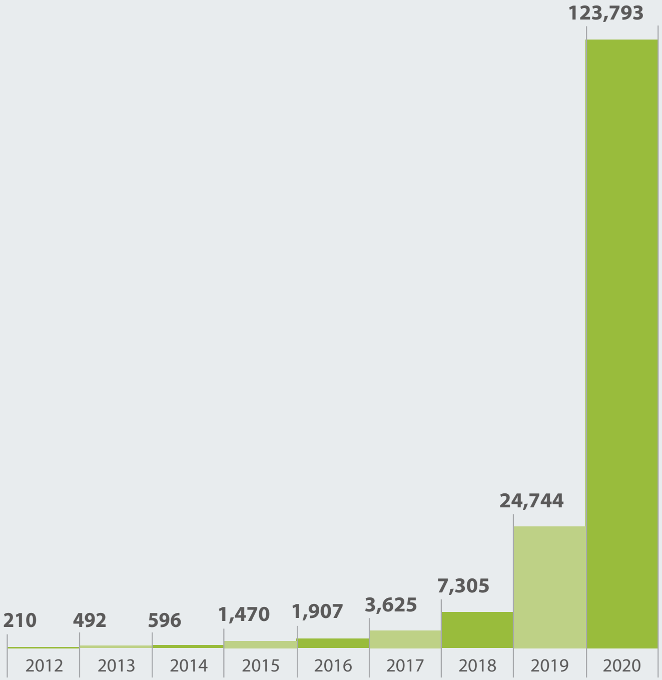
Massively Parallel **Short-Read Sequencing**

Basepairs (GB)



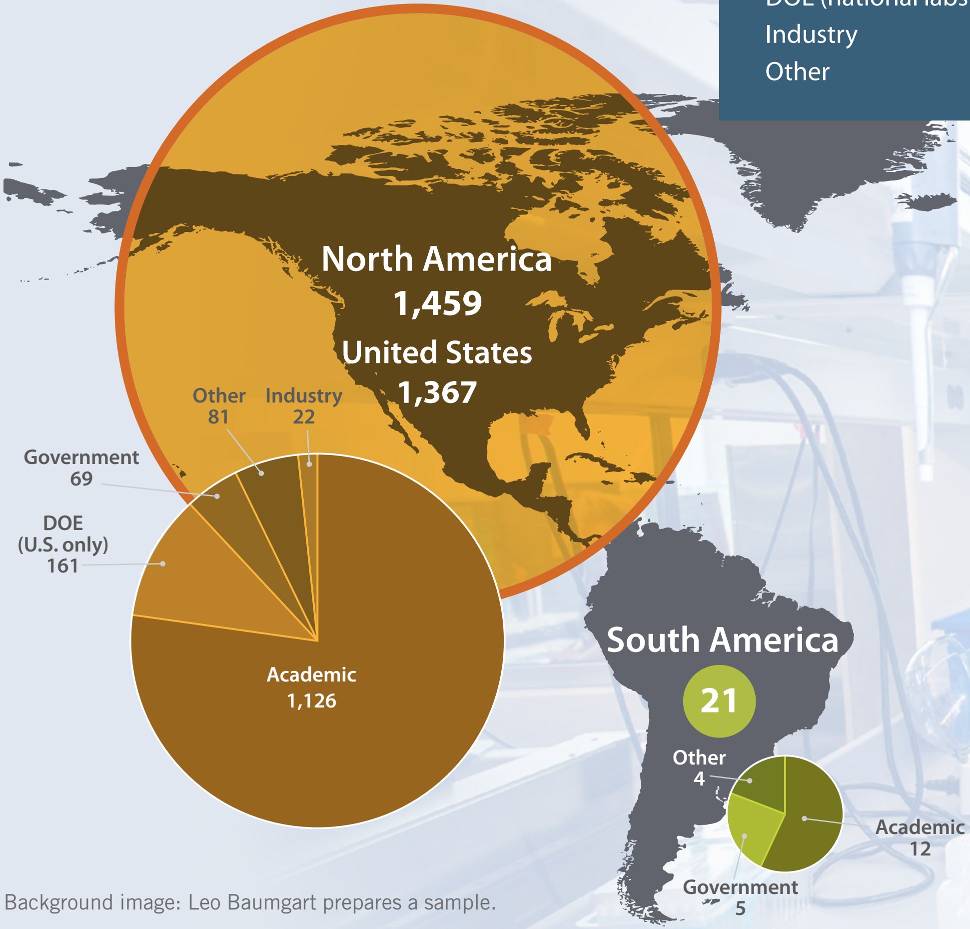
Single Molecule **Long-Read Sequencing**

Basepairs (GB)



Users **on the Map: 2,038**

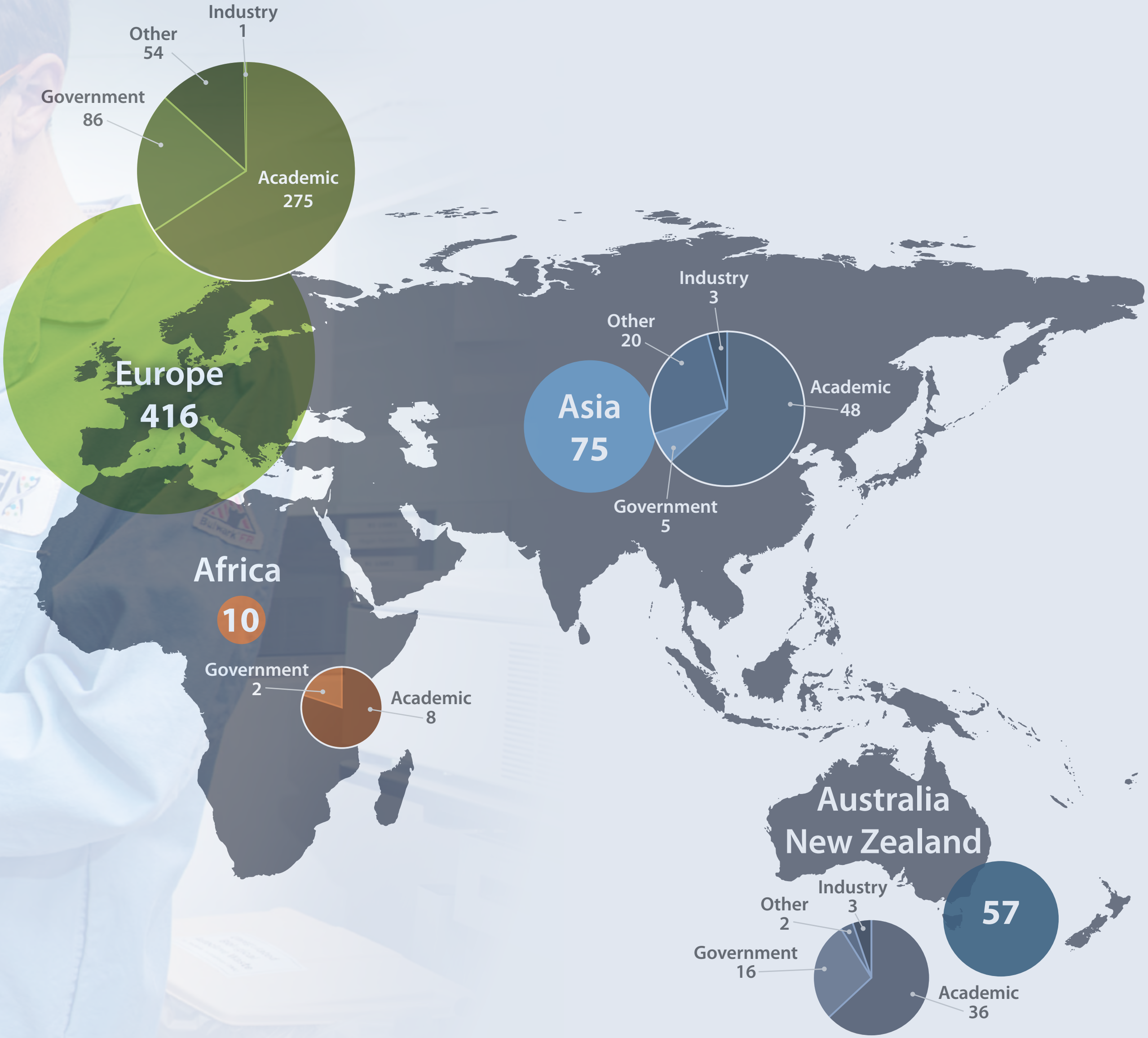
Academic	1,504
Government	183
DOE (national labs only)	161
Industry	29
Other	161



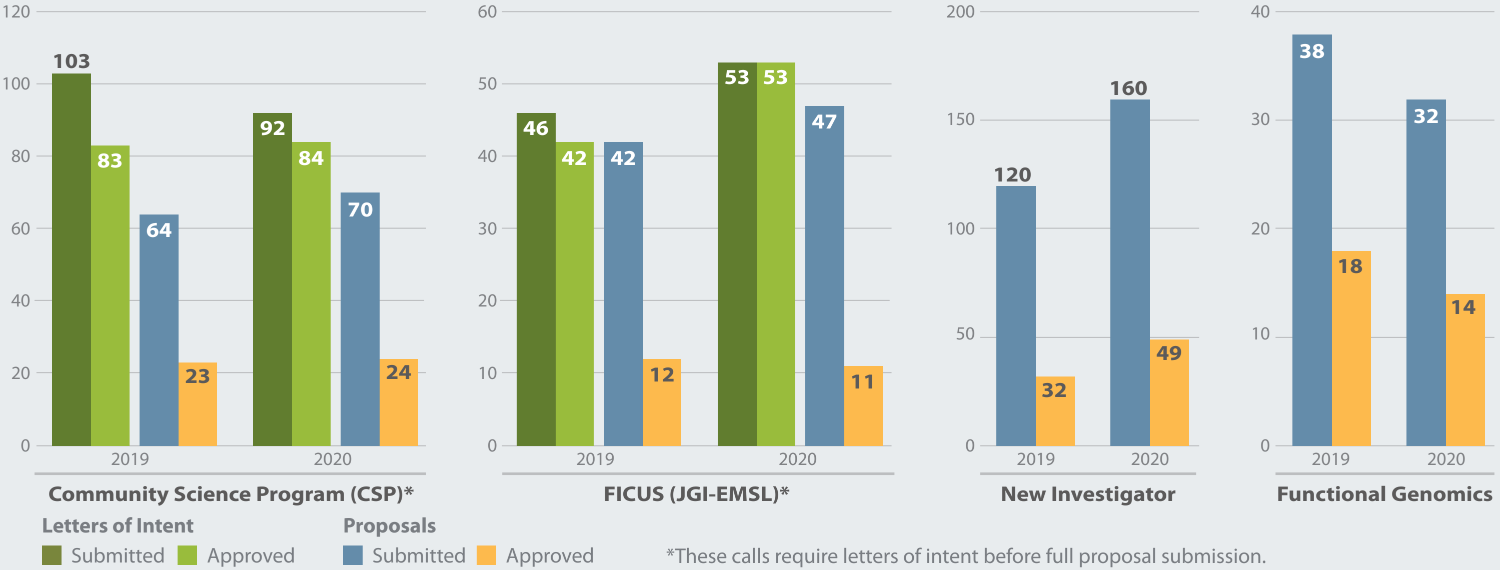
Background image: Leo Baumgart prepares a sample.

North America	**1,459**
United States	1,367
Canada	87
Mexico	5
South America	**21**
Argentina	1
Brazil	13
Chile	2
Colombia	1
Uruguay	4
Europe	**416**
Austria	17
Belgium	9
Czech Republic	7
Denmark	10
Estonia	2
Finland	16
France	57
Germany	84
Greece	3
Hungary	9
Iceland	1
Ireland	2
Italy	26
Netherlands	31
Norway	14
Poland	2
Portugal	6

Russia	4
Serbia	2
Slovenia	2
Spain	38
Sweden	22
Switzerland	11
United Kingdom	41
Africa	**10**
Egypt	1
Morocco	1
South Africa	7
Tunisia	1
Asia	**75**
China	25
Hong Kong	1
India	10
Israel	9
Japan	19
Malaysia	1
Oman	1
South Korea	5
Singapore	3
Taiwan	1
Australia & New Zealand	**57**
Australia	45
New Zealand	12

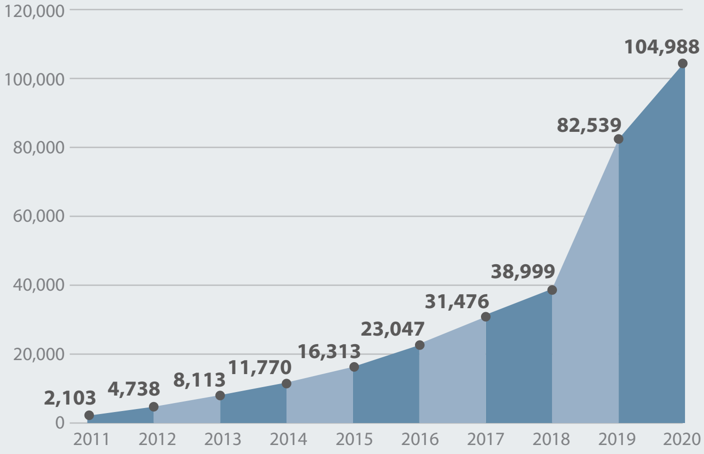


User Letters of Intent/Proposals **Submitted & Approved**

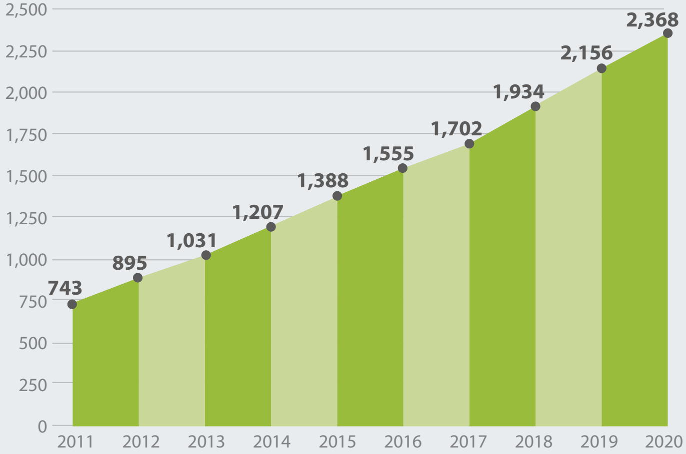


*These calls require letters of intent before full proposal submission.

Cumulative Number of **Projects Completed**



Cumulative Number of **Scientific Publications**



Computational **Infrastructure**

JGI Archive and Metadata Organizer (JAMO)

11.472 million files records

JAMO Archived Data Footprint

9.819 Petabytes

Data downloads in FY20

1,216 TB; 4.382 million files

Data transfer nodes 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)

Users of **JGI Tools & Data**

Number of Users **10,154**

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 upon user request, and this activity is logged. In 2020, JGI users downloaded 4.382 million files and a total of 1,216 terabytes (TB) of data.

Podcasts **2020**

The JGI launched two podcasts in March 2020, hosted by science communicator Alison Takemura and secondary metabolism researcher Dan Udwary. Check out these audio stories, complete with transcripts, at **jgi.doe.gov/category/podcasts**.

JGI podcast hosts Dan Udwary and Alison Takemura

"Natural Prodcast" is a "fireside chat"-style podcast about natural products and the science and scientists of secondary metabolism. Natural products, secondary metabolites, and specialized metabolites all refer to the chemicals that make species unique and different from one another. They are incredibly important to medicine, the environment, and human health. As the JGI acts on its goals in — and builds out its capabilities for — secondary metabolism research, "Natural Prodcast" serves as an important line of communication to the scientific community. Hosts Dan Udwary and Alison Takemura talk to luminaries in the field about current and future developments, and how the JGI can be part of that space.

Episode Highlights:

Episode 4:
Nancy Keller of the University of Wisconsin–Madison makes the case for studying fungal natural products in a field dominated by bacterial research. She talks about fungal toxins and why we want to understand their biosynthesis and her formative experience in the Peace Corps that led her into this field.

Listen here >

Episode 5:
Brad Moore, who has joint appointments at UC San Diego and Scripps Institution of Oceanography, talks about the reasoning behind studying marine natural products in the desert and expanding the toolbox of biocatalysts by studying red algae.

Listen here >

Episode 7:
Ben Shen of Scripps Research talks about enediynes and Scripps' acquisition of the Pfizer strain collection. He also discusses collaborating with the JGI to sequence that collection, mine genomes, and develop new technology to access natural products.

Listen here >

"Genome Insider" is a podcast that showcases the work of JGI collaborators in brief forays, connecting audiences with the people behind the science. Host Alison Takemura produces profiles of JGI-supported projects, delving into the researchers' motivations, the insights that amaze them, and how their work contributes to solving energy and environmental challenges.

Episode Highlights:

Episode 3: River Microbiomes around the World

Kelly Wrighton and her group at Colorado State University in Fort Collins have a massive undertaking: sequencing the world's river microbiomes. And they're using team science to do it. Listen here >

Episode 7: Decoding Yellowstone's Microbial Mats

Cyanobacteria began oxygenating Earth over two billion years ago. **Devaki Bhaya** of the Carnegie Institution for Science and her team report how these important bacteria live in densely populated microbial mats in Yellowstone National Park. Listen here >

Episode 5: Corals in Hot Water Get Help from Their Microbes

Mónica Medina at The Pennsylvania State University and her group are fascinated by corals. Corals comprise multiple organisms: a coral host, a photosynthetic microalgae, and a little-characterized microbiome. When warm waters stress corals — but before they bleach — a coral's microbes, including its photosynthetic partner, may be what helps corals take the heat. Listen here >

★★★★★

lynnie25, 06/28/2020

Actually talks the science!

This is a great podcast. Rather than just some random man reminiscing with another rando, the host talks actual science where I have to look things up and thereby actually learn something. I love it!

Very professional. No bragging, no insults. A real intellectual delight.

Thank you for sharing this work!!

JGI Podcasts **Total Stats:**

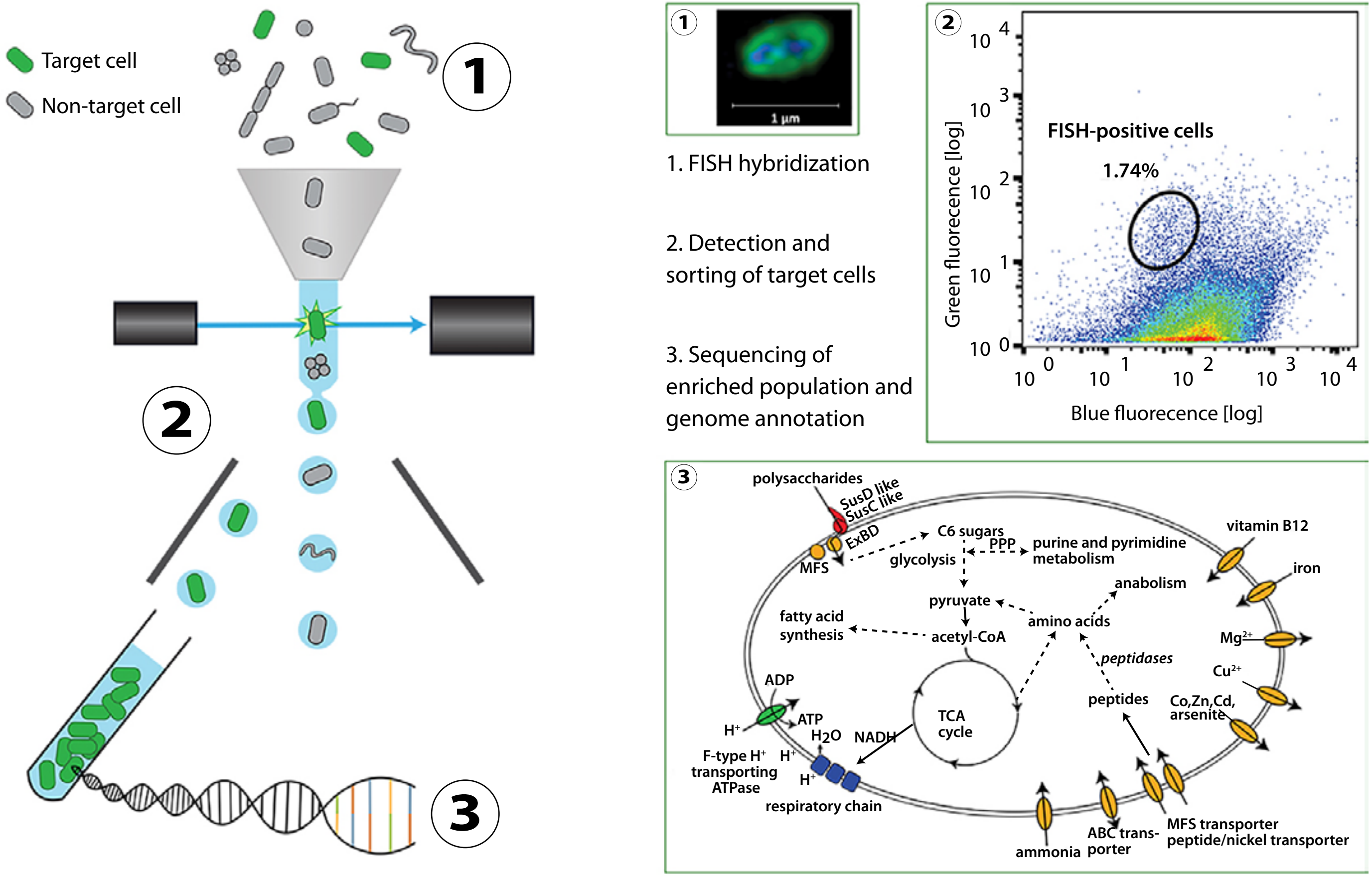
16 episodes

>7,000 downloads

Downloaded in 6 continents

Rated with 5 stars

Enlarged Figure 1: Targeting a Microbial Needle within a Community Haystack



1. FISH hybridization

2. Detection and sorting of target cells

3. Sequencing of enriched population and genome annotation

(Overview and Figure 1: Courtesy of Anissa Grieb. Figures 2 and 3: Grieb A et al. A pipeline for targeted metagenomics of environmental bacteria. *Microbiome.* 8:21;2020 Feb 17 CC-BY-4.0)

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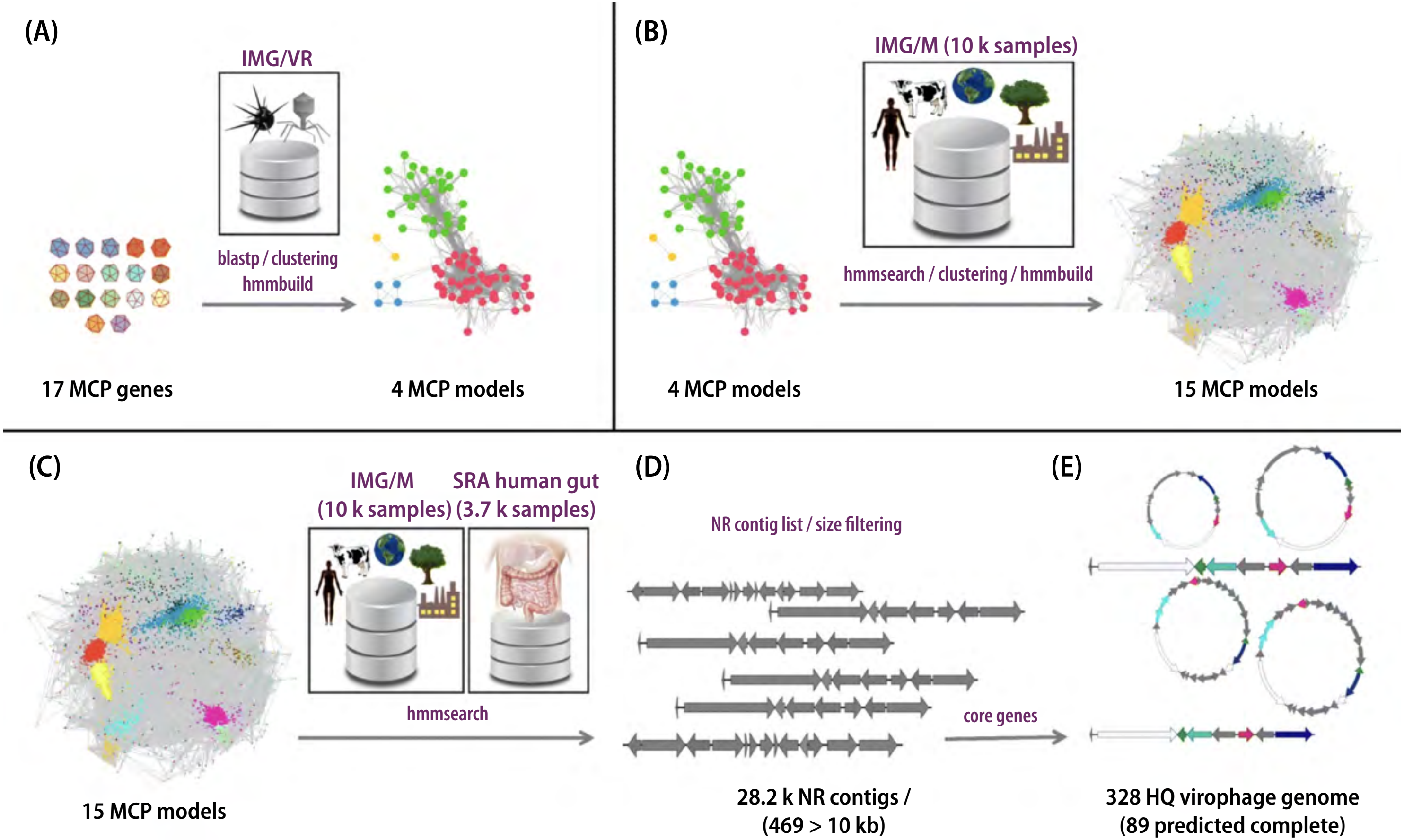
Enlarged Figure 2: Expanding Virophage Diversity



Virophage discovery pipeline. (Figure from Paez-Espino et al. *Microbiome* (2019) 7:157 https://doi.org/10.1186/s40168-019-0768-5)

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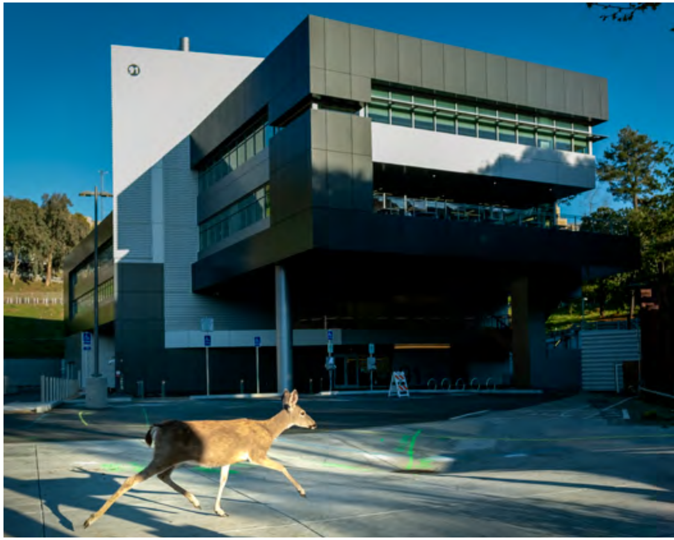

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Images by Thor Swift, Berkeley Lab Alison F. Takemura and Ashleigh Papp contributed to the highlights. Design by Creative Services, IT Division, Berkeley Lab

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