



# The Joint Genome Institute's User Programs

## USCCN Workshop: Genome Sequencing and Microbial Resources

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June 10, 2024



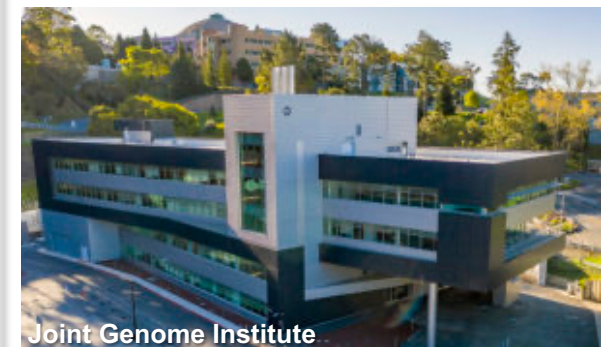
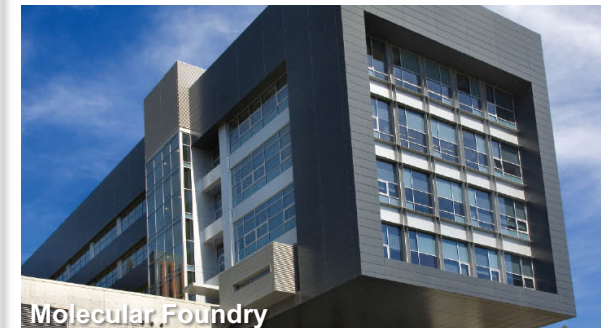
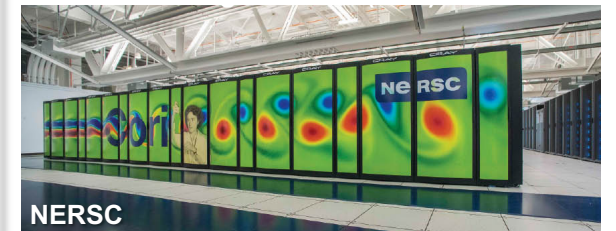
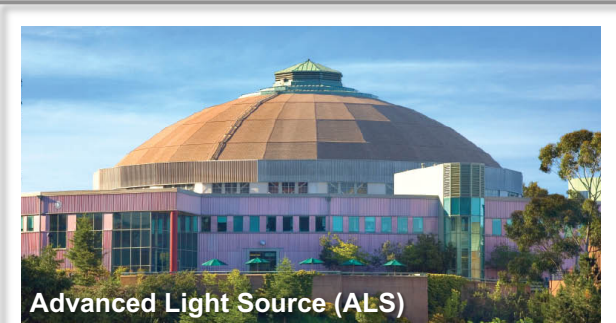
**Who are we?**

# DOE Office of Science User facilities

Associated with some of the National Laboratories, there are nearly 30 DOE Office of Science user facilities:

- accessed by >30,000 scientific users from universities, national laboratories, technology companies (free of charge)
- advancement of their research and development

The Office of Science national scientific user facilities provide researchers with the most advanced tools of modern science, including accelerators, colliders, supercomputers, light sources and neutron sources, as well as facilities for studying the nano world, the environment, and the atmosphere.



# The Joint Genome Institute is a DOE User Facility

We enable large-scale, multi-omic studies of plants, fungi, algae, bacteria, archaea & microbial communities relevant to the DOE goal of addressing energy & environmental challenges



# User Programs and Science Programs

JGI SCIENTIFIC PEER REVIEW

**40%**  
Community  
Science Program  
(CSP)

**10%**  
Facilities  
Integrating  
Collaborations for  
User Science  
(FICUS)



**30%**  
Bioenergy  
Research Centers  
(BRC)

**10%**  
Director's Science

**10%**  
Biological and  
Environmental Research  
Support Science (BERSS)

Plant



Fungal, Algal



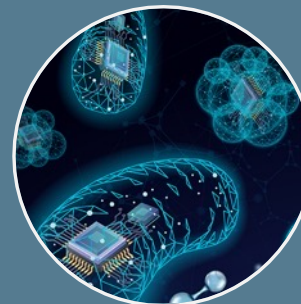
Metagenome



Microbial



DNA Synthesis



Metabolomics



2° Metabolites

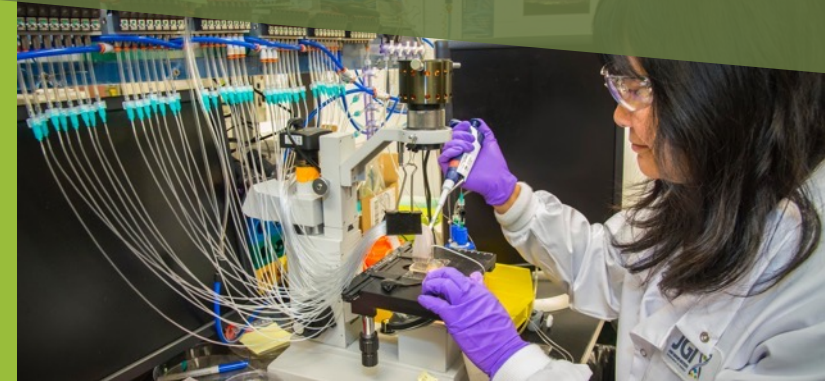
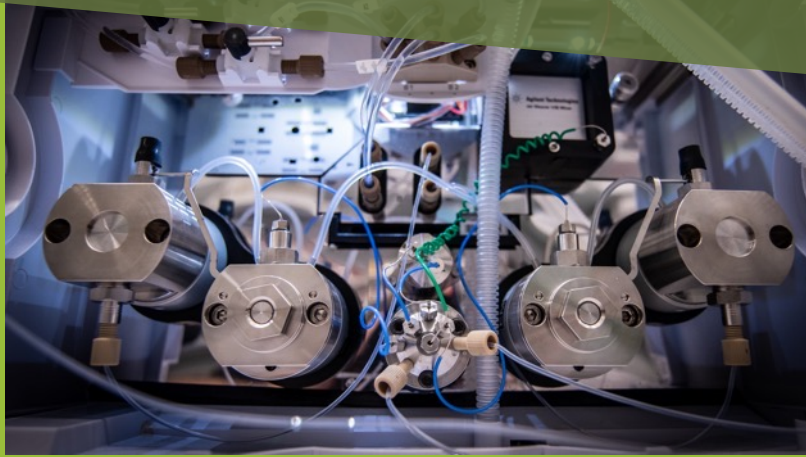
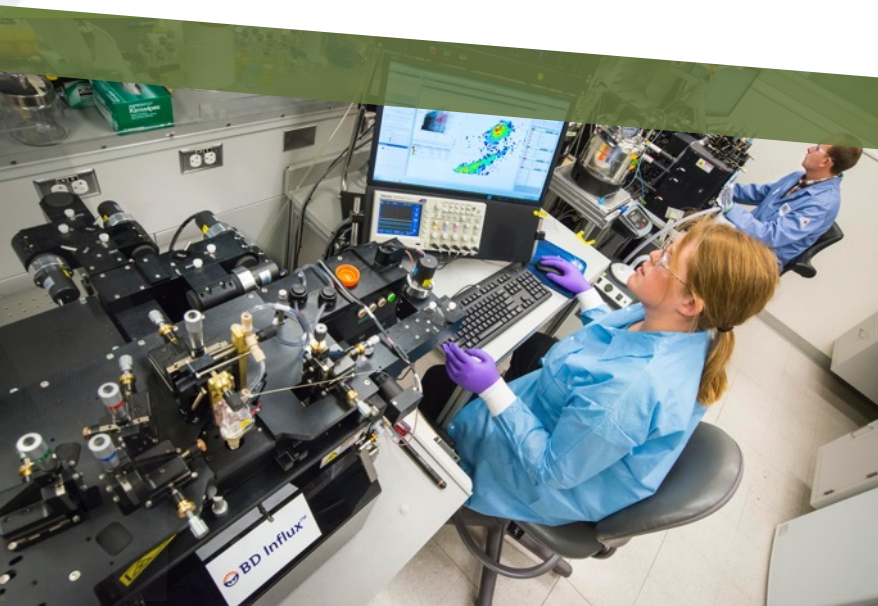
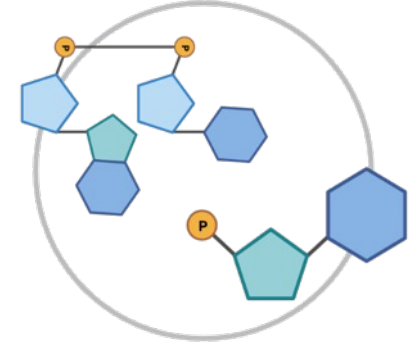
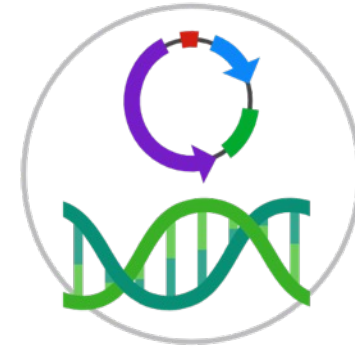
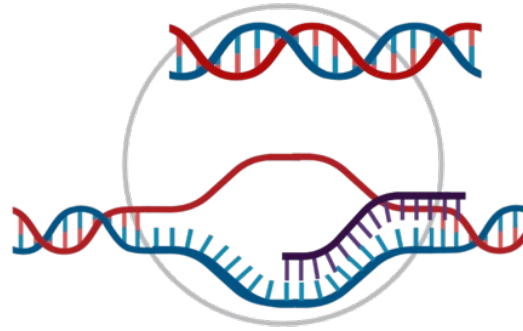




**What do we offer?**

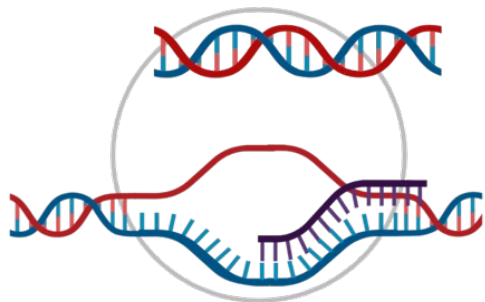
# What does JGI provide?

- DNA/RNA sequencing
- DNA synthesis
- Metabolomics



# Core sequencing capabilities

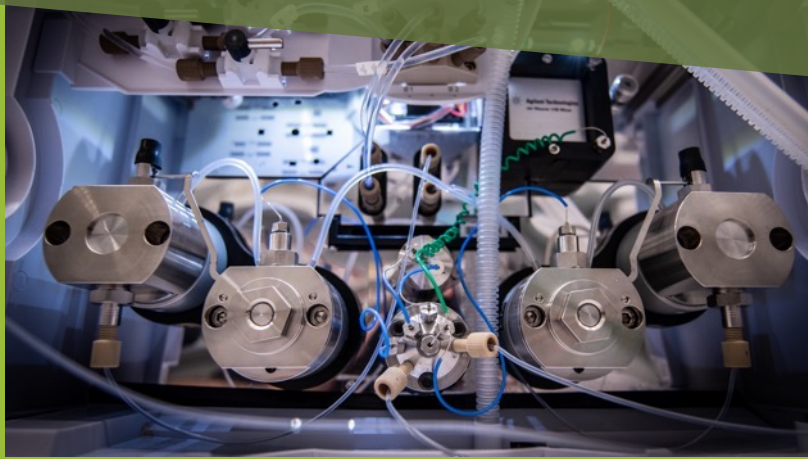
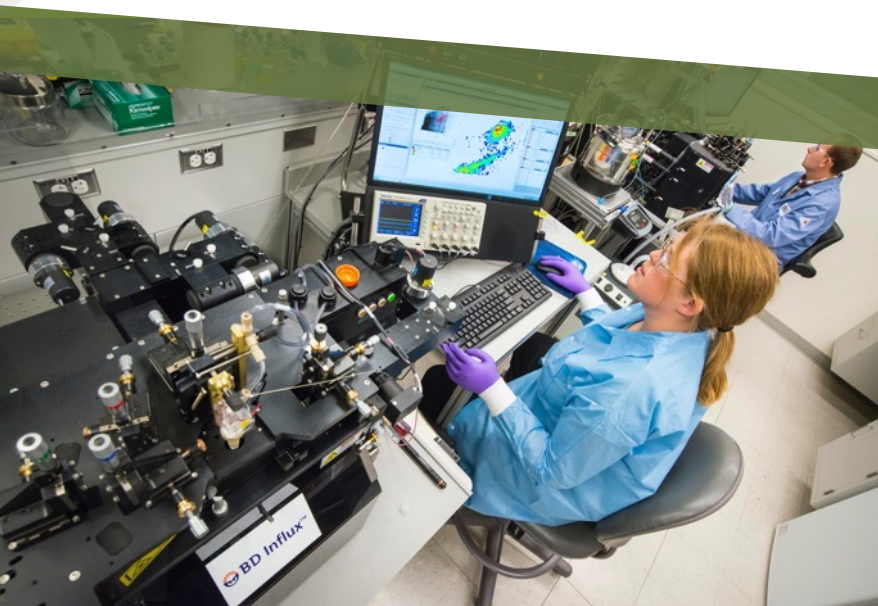
- De novo sequencing and annotation of plant, algal, fungal, bacterial, archaeal, and viral genomes
- Comprehensive transcriptome analysis
- Microbial community DNA/RNA sequencing and annotation
- Resequencing for variation detection
- Fluorescence activated cell sorting for mini-metagenomics and single-cell genomics
- Flow cytometric sorting and genomic analysis of active microbes labeled via Bio-Orthogonal Non-Canonical Amino acid Tagging (BONCAT)
- Stable isotope probing enabled metagenomics
- Whole genome DNA methylation analysis
- DAP-seq





# More custom capabilities

- EcoFAB projects studying plant-microbiome interactions
- Long-read (PacBio) metagenomes
- Custom analysis of JGI datasets



# Analysis tools and data portals

**Phytozome** 13

THE PLANT GENOMICS RESOURCE



**PhycoCosm**

THE ALGAL GENOMICS RESOURCE



**Mycocosm**

THE FUNGAL GENOMICS RESOURCE



**IMG/M**

INTEGRATED MICROBIAL GENOMES



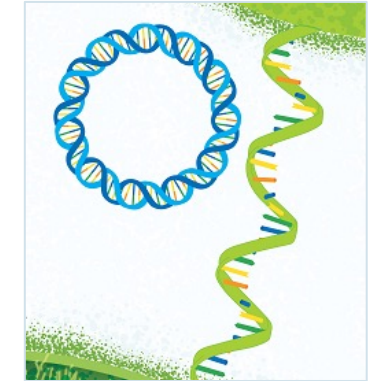
**IMG/VR**

INTEGRATED MICROBIAL GENOMES / VIRUS



**IMG/PR**

INTEGRATED MICROBIAL GENOMES / PLASMIDS

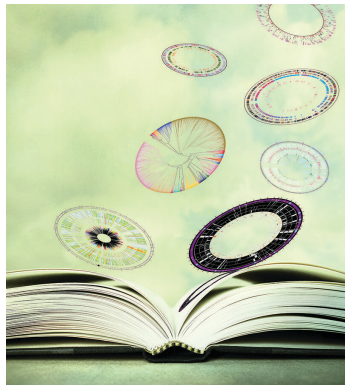


**GOLD**

GENOMES ONLINE DATABASE



**Genome Portal**



**Data Portal**



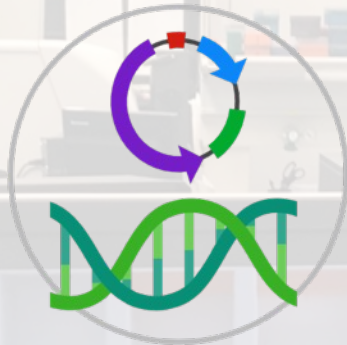
**SMC**

SECONDARY METABOLISM COLLABORATORY



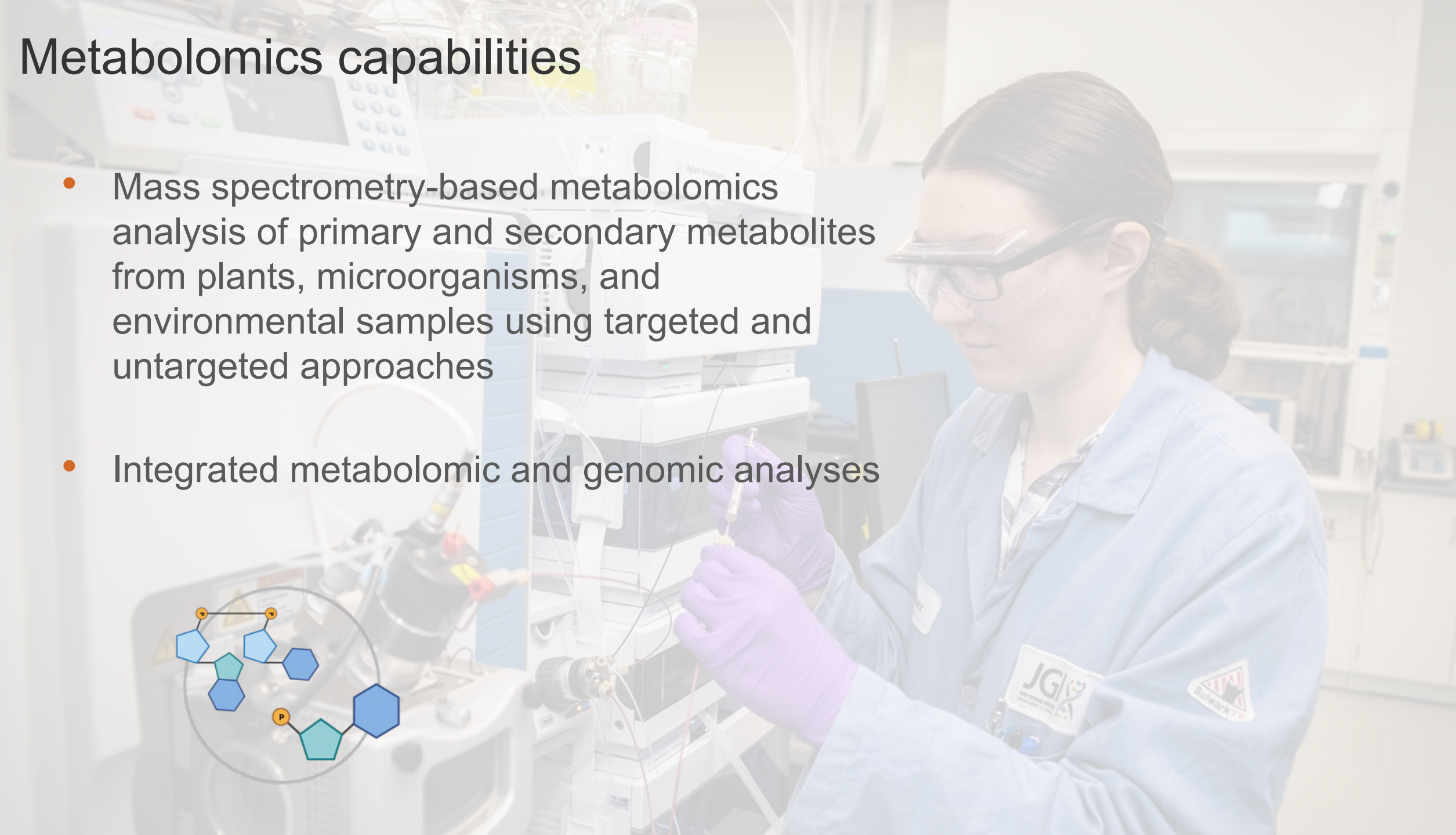
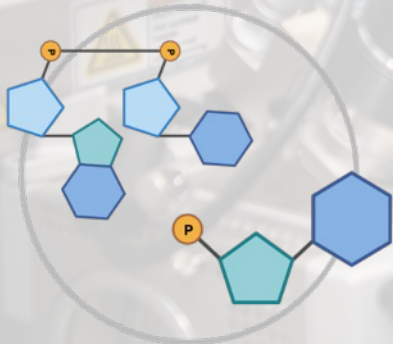
# DNA synthesis capabilities

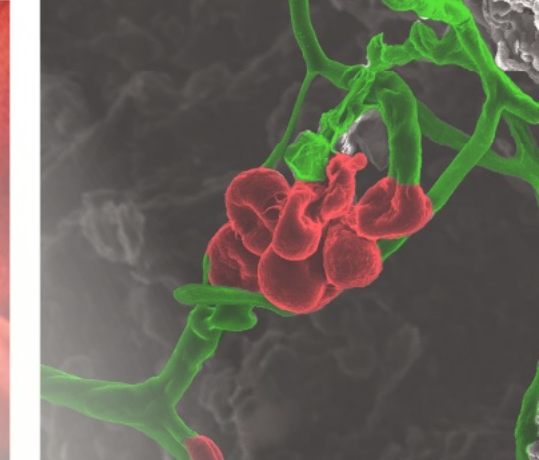
- Gene and pathway DNA synthesis, including codon optimization, refactoring, and assembly of biosynthetic pathways into appropriate vector systems for expression in heterologous hosts
- Whole-genome or partial-genome CRISPR-based gRNA library construction and QC



# Metabolomics capabilities

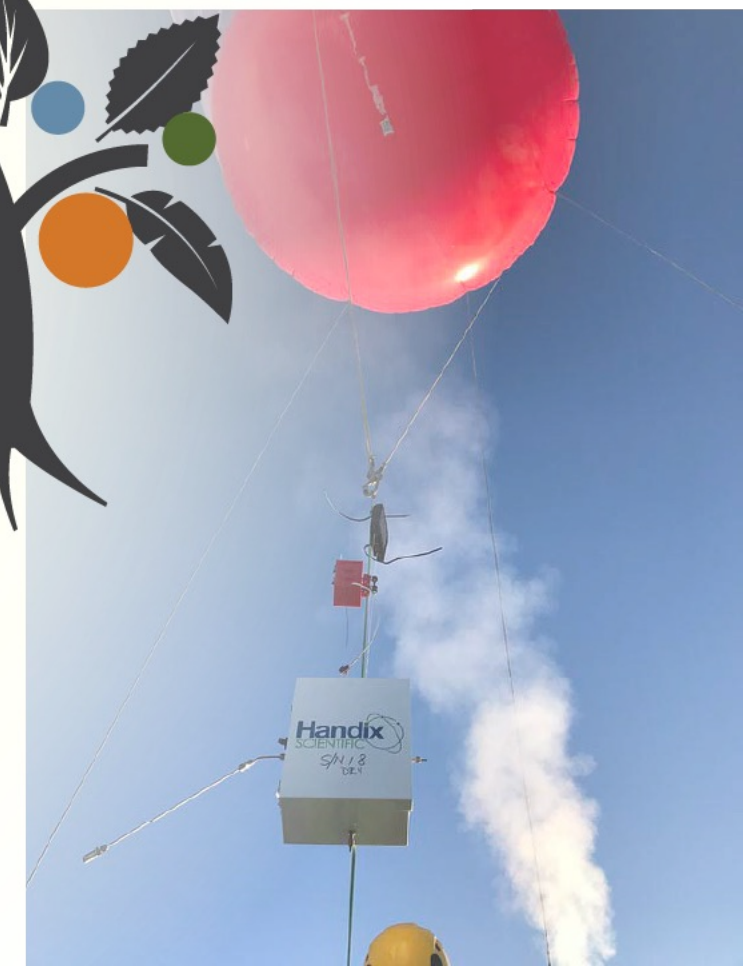
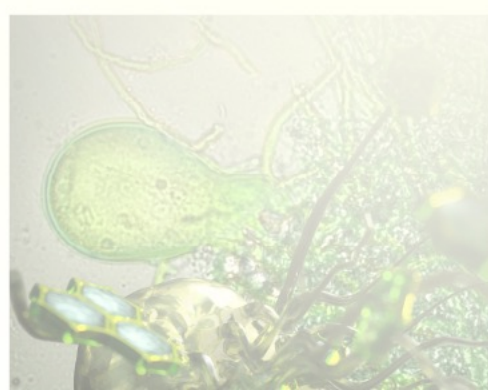
- Mass spectrometry-based metabolomics analysis of primary and secondary metabolites from plants, microorganisms, and environmental samples using targeted and untargeted approaches
- Integrated metabolomic and genomic analyses






# FICUS

Facilities Integrating  
Collaborations for User Science



# Access to additional capabilities through FICUS

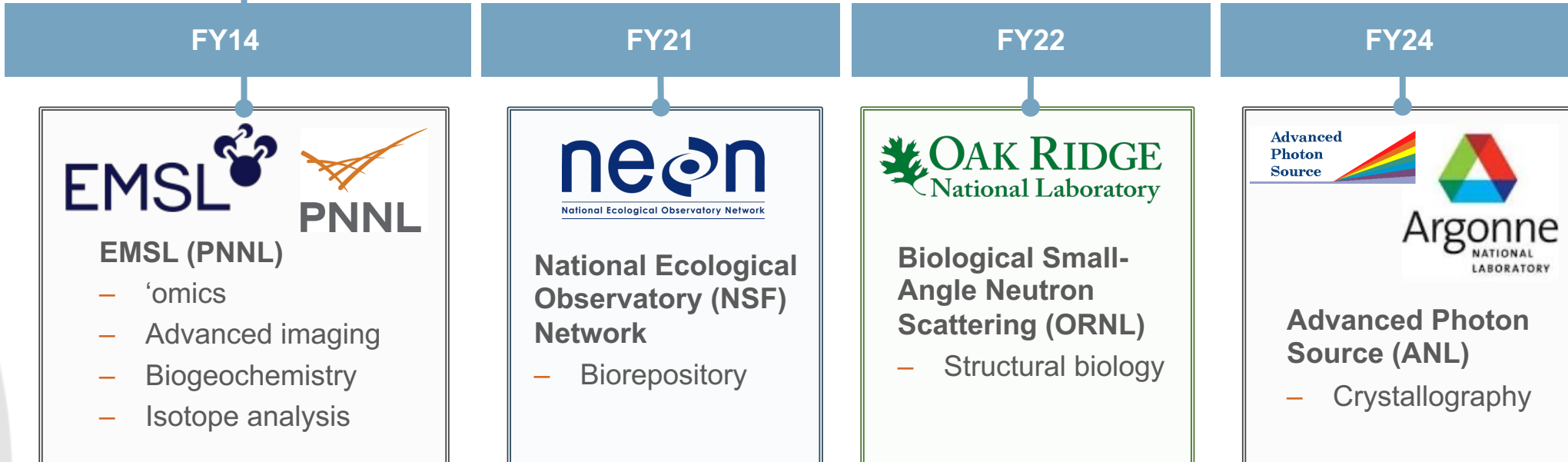


**JGI (LBNL)**

- DNA & RNA sequencing
- DNA synthesis
- Metabolomics

## Initiated in 2013 with FY14 call

through partnership with the Environmental Molecular Sciences Lab (EMSL) at Pacific Northwest National Laboratory (PNNL) to facilitate access to two DOE user facilities:



# Upcoming Resource Calls & Meetings

## Community Science Program (CSP)

**Large scale annual call deadline passed, check back early 2025**

[jointgeno.me/AnnualCSP](https://jointgeno.me/AnnualCSP)

Large scale genomics science questions, biofuels and bioproducts production, nutrient cycling, biogeochemistry

**New Investigator call deadline: October 4, 2024**

[jointgeno.me/CSPnewPI](https://jointgeno.me/CSPnewPI)

Bacterial, archaeal, viral isolates and single cell draft genomes; eukaryote draft genomes; metagenomes/metatranscriptomes; DNA synthesis; metabolomics-based functional analyses

**Functional Genomics call deadline: Jan. 30, 2025**

[jointgeno.me/CSPFunctionalGenomics](https://jointgeno.me/CSPFunctionalGenomics)

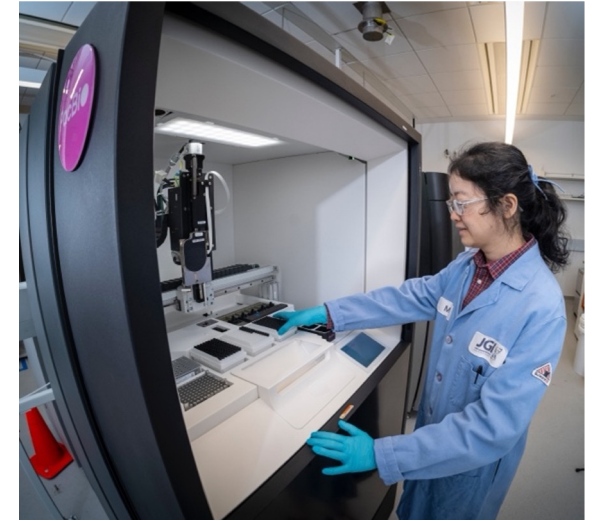
Genes/pathway synthesis, Strain engineering, Metabolomics/EcoFABs

## Facilities Integrating Collaborations for User Science

[jointgeno.me/FICUS-JGI-EMSL](https://jointgeno.me/FICUS-JGI-EMSL)

**Deadline passed, check back early 2025**

JGI Genomics and metabolomics, EcoFABs; proteomics, imaging via EMSL



[jointgeno.me/User Programs](https://jointgeno.me/UserPrograms)

# User Program calls: frequencies, scales and scopes

	Annual CSP	New Investigator CSP New PI!	Functional Genomics CSP	JGI-EMSL FICUS
FREQUENCY	Once per year	Once per year	Once per year	Once per year
SCALE	10 Tb Illumina, 1 Tb PacBio	3 Tb	54 RNAs	3 Tb
Sequencing				
Synthesis	500 kb (-1,500 kb) synthesized DNA	500 kb synthesized DNA	500 kb (-1,500 kb) synthesized DNA	500 kb synthesized DNA
Metabolomics	200 samples (polar), 500 samples (nonpolar)	50 samples (polar), 150 samples (nonpolar)	50 samples (polar), 150 samples (nonpolar)	200 samples (polar), 500 samples (nonpolar)
SCOPE	All JGI capabilities offered	Reference genomes, Resequencing, RNA-seq, Metagenomes & transcriptomes, DNA synthesis, Metabolomics	DNA synthesis, Reference genomes, RNA-seq, Metabolomics, Sequence data mining, Strain engineering, CRAGE and DAP-seq	All JGI capabilities offered



# Request size for microbial sequencing

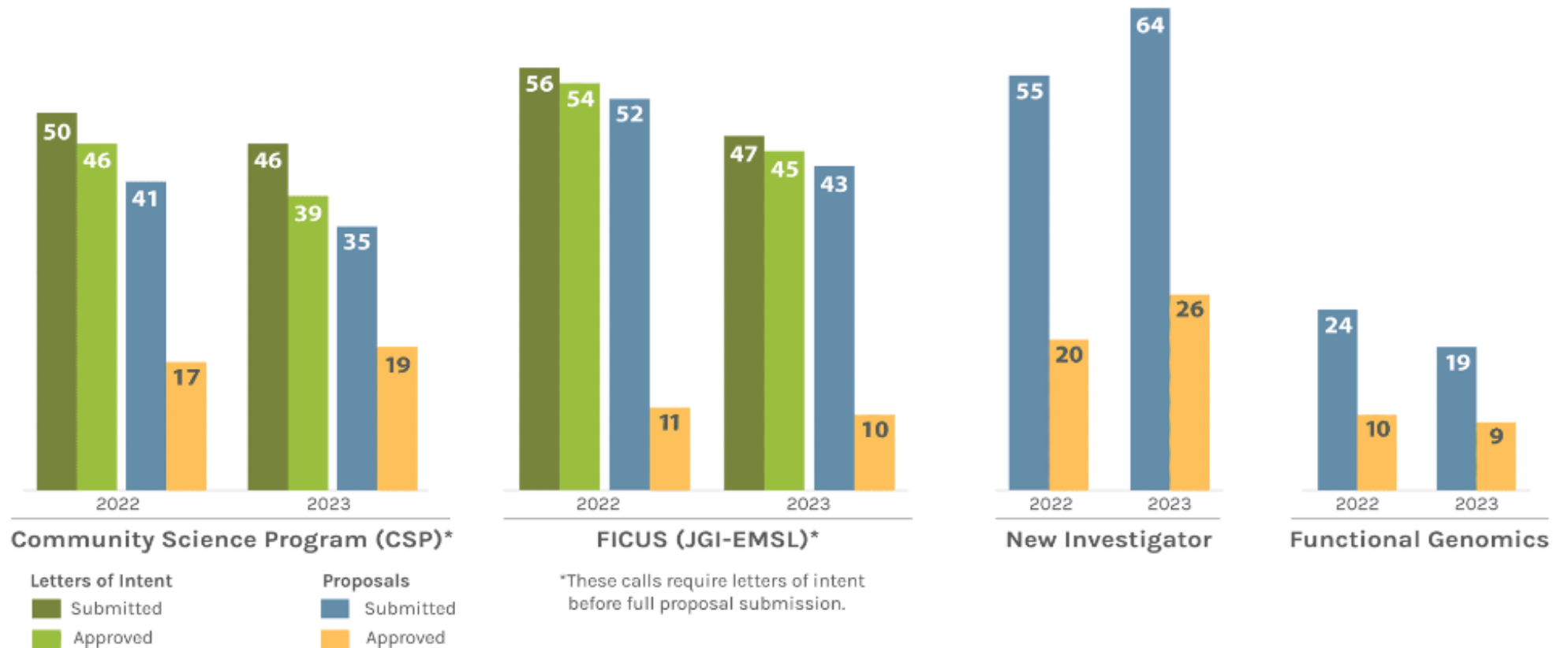
- **CSP Annual Call: 10Tb+ cap**
  - Microbial genomes requests in the range of many 100s is appropriate
  - Genome sequencing of collections of 1000s of isolate genomes is possible
- **FICUS JGI-EMSL: 3Tb cap**
  - Microbial genomes requests in the range of many 100s is appropriate
- **CSP New Investigator: 3Tb cap**
  - 48 to 184 isolates
  - up to 384 single particle sorts
  - 48 to 384 single virus sorts
  - 22 to 92 samples for resequencing
  - 22 to 92 samples for RNA-seq
- **CSP Functional Genomics**
  - 22 to 92 samples for RNA-seq



**Mix & Match  
JGI products**

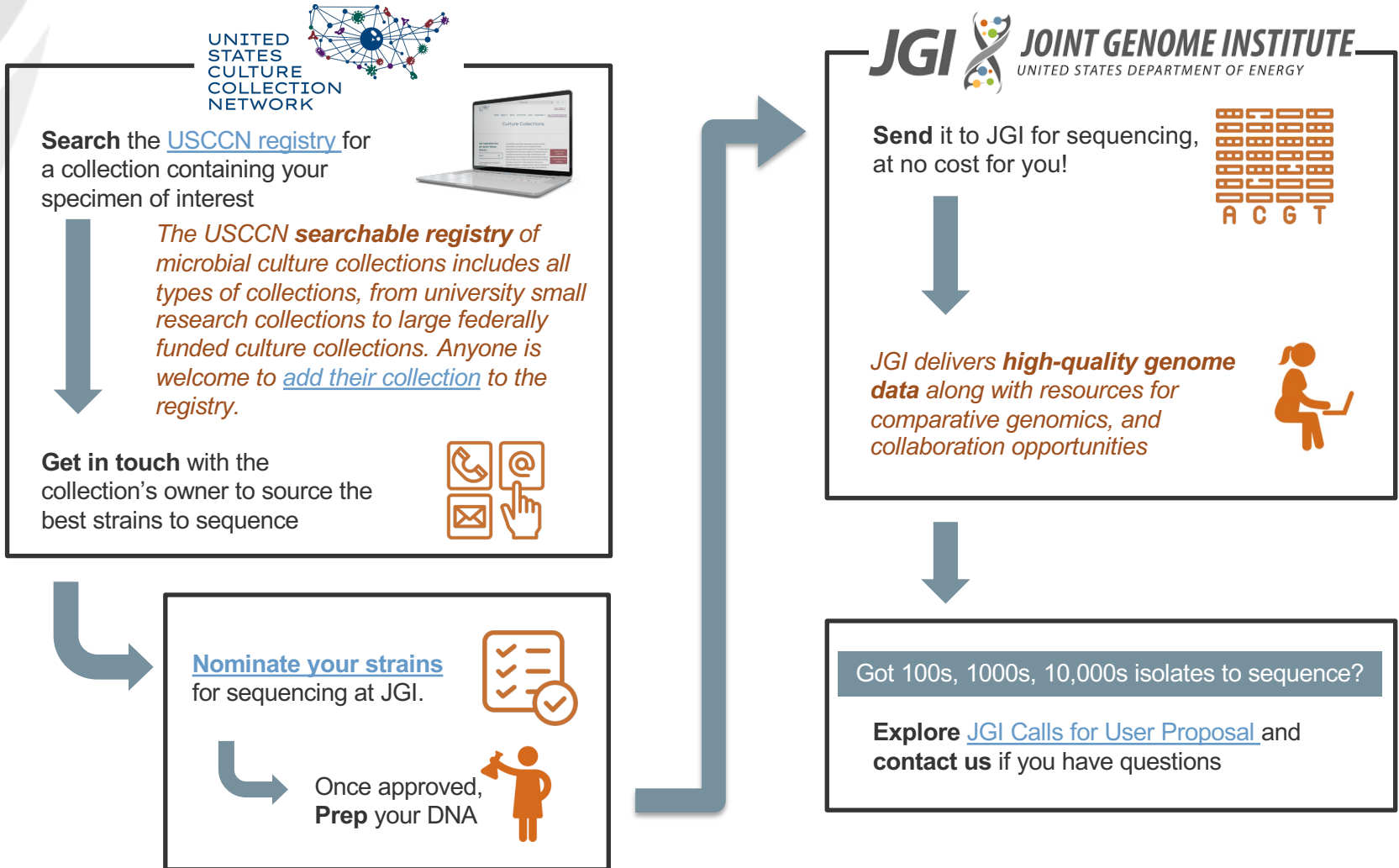
We accept between ~20-40% of proposals

## Users Letters of Intent/Proposals Submitted & Approved



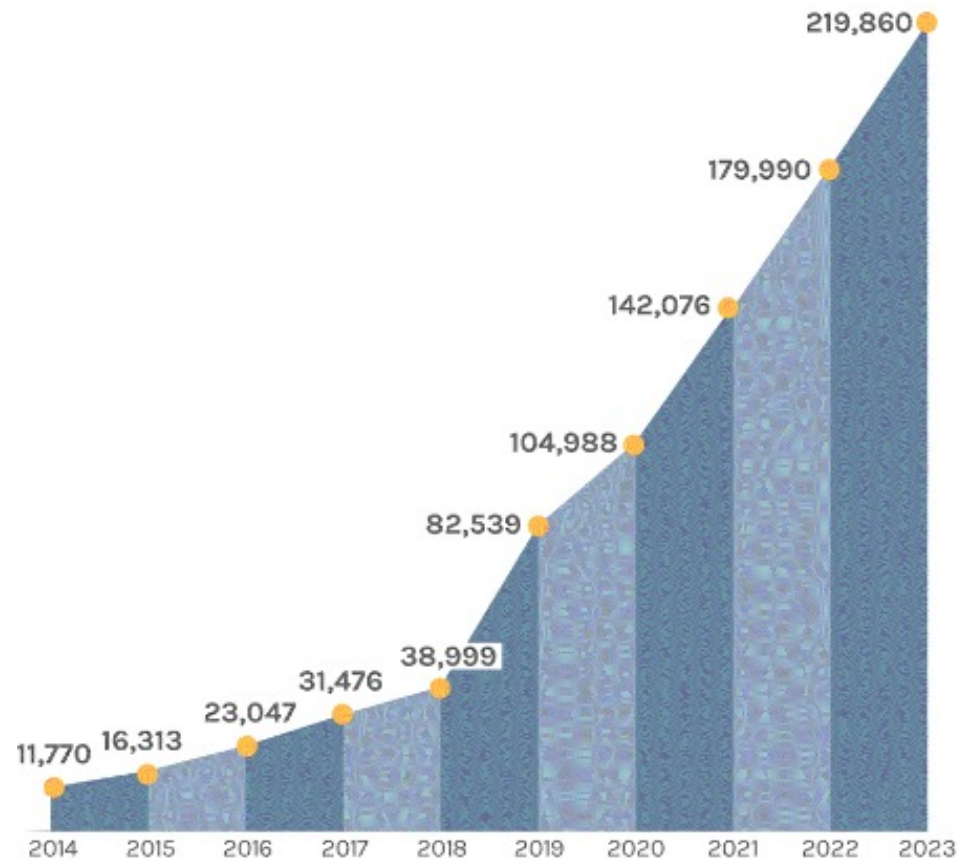
# Nominate your collections for sequencing @ the JGI

➔ Locate your strains of interest with the USCCN registry and sequence them at JGI

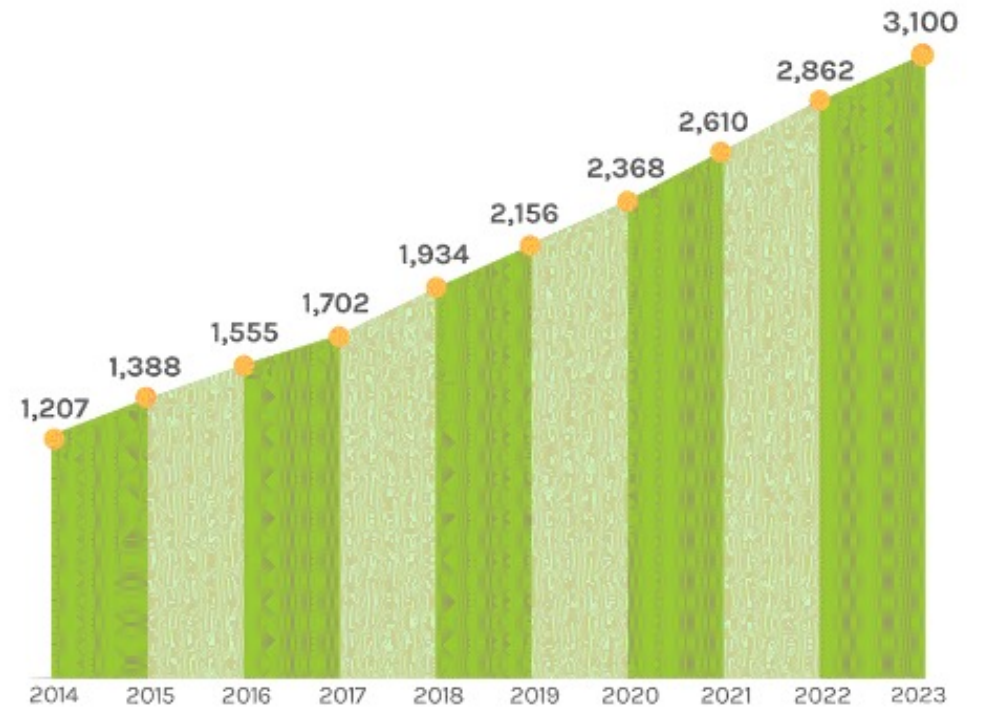


# Many JGI projects translate into many publications

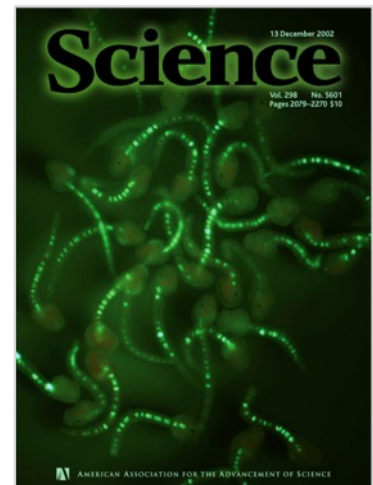
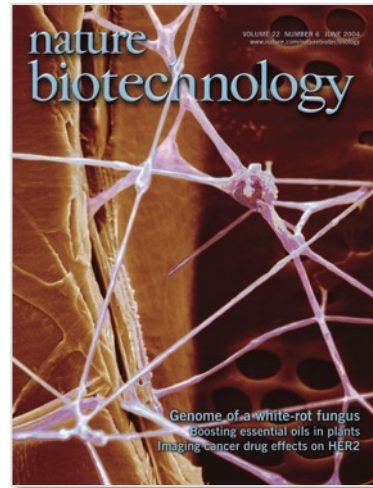
## Cumulative Number of Projects Completed



## Cumulative Number of Scientific Publications



# Enabling high quality User Science



# Enabling high quality User Science



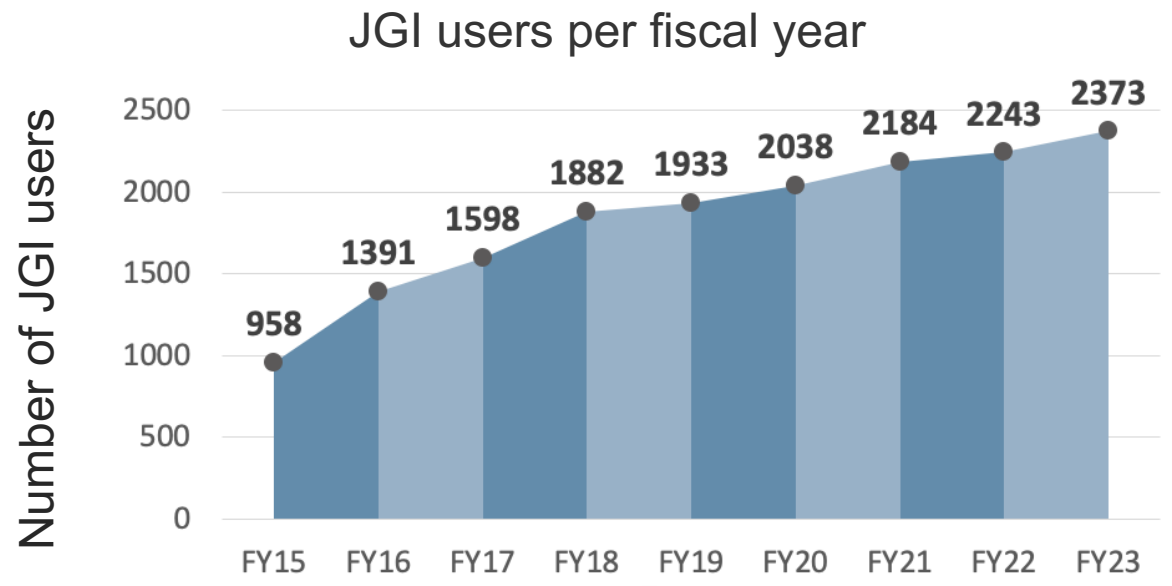


**Who do we serve?**

# JGI user engagements in the future?

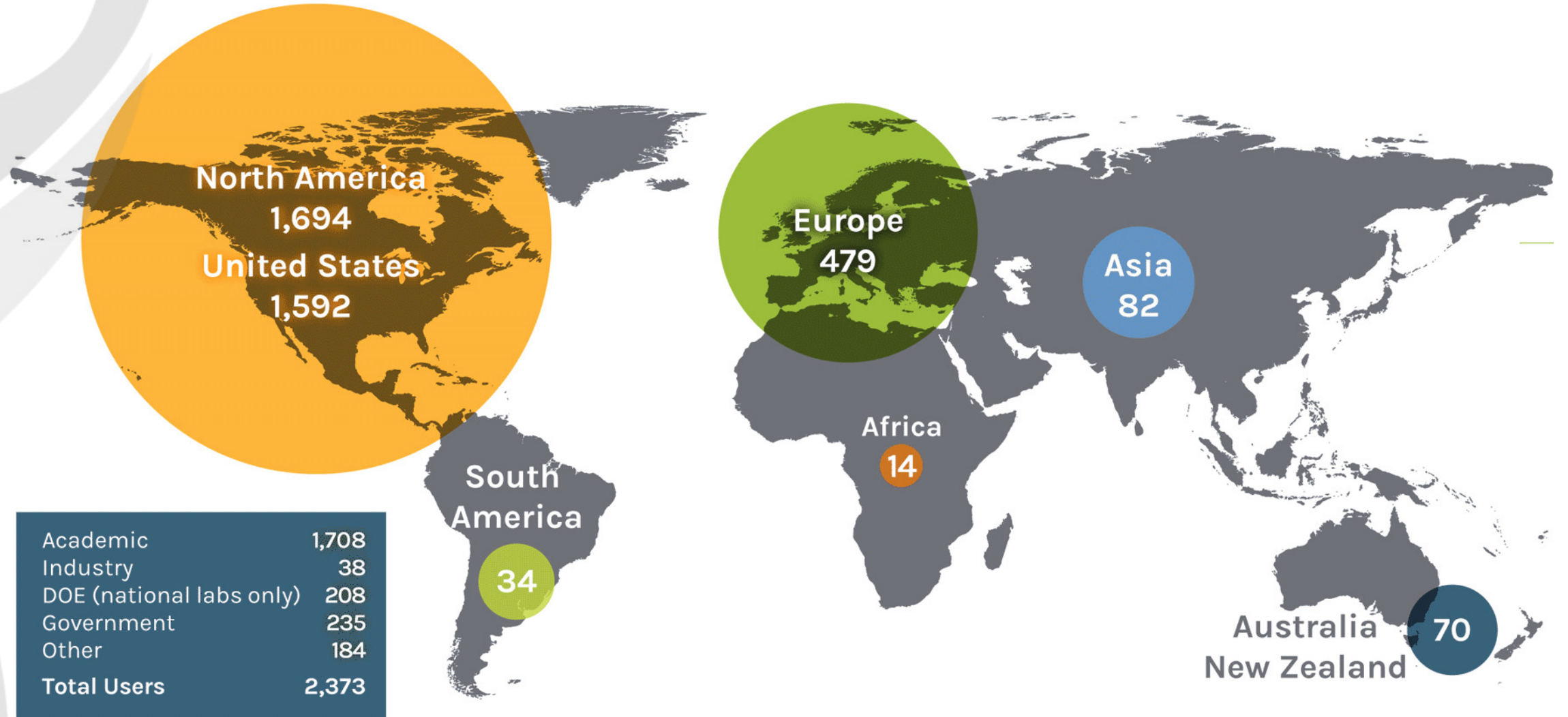
**Primary Users** collaborate closely with JGI personnel and are associated with one or more JGI User Program proposals, usually not on site

- JGI's user base grows each year
- Majority from academia, but growing number from government and DOE labs
- Broad geographic distribution with majority from the US

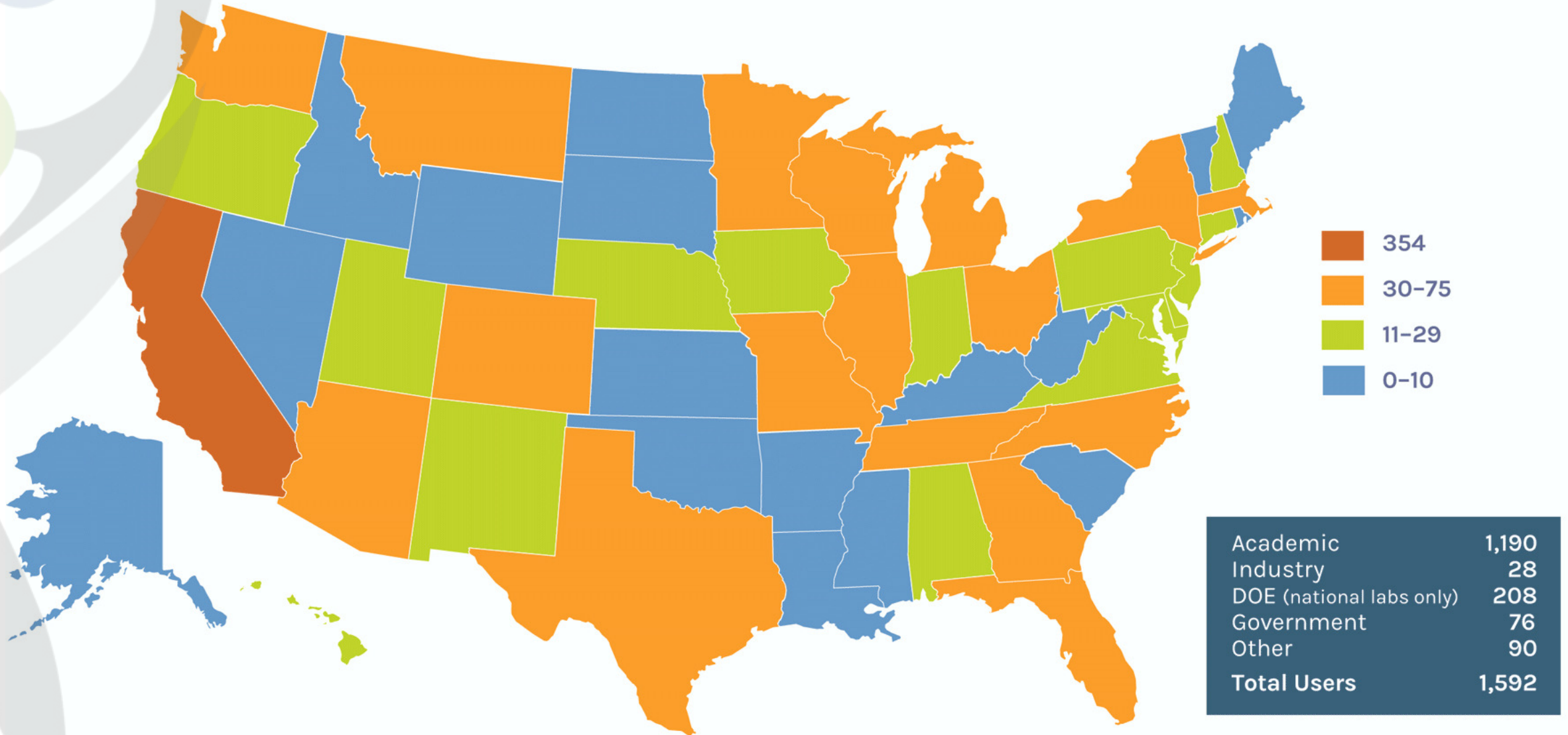




# JGI Worldwide users



# JGI U.S. users





**Thank you for your  
attention!**