



2022 Agenda

Genomic Science Program Annual PI Meeting

February 28–March 2

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Monday, February 28

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Poster Session
Breakout Sessions

NOTE: *All times EST*



U.S. DEPARTMENT OF
ENERGY

Office of
Science

Office of Biological and Environmental Research

NOTE: All times EST

MONDAY, FEBRUARY 28

Opening Session

- 10:00 a.m.** **Gather.town opens to meeting participants**
- 10:30 a.m.** **Sharlene Weatherwax, Associate Director, DOE Office of Biological and Environmental Research (BER)**
Opening Remarks
- 10:40 a.m.** **Todd Anderson, Director, Biological Systems Science Division (BSSD)**
Meeting Introduction

Keynote Presentation

- 11:00 a.m.** **Jennifer A. Doudna – Nobel Laureate in Chemistry**
Professor of Biochemistry, Biophysics, and Structural Biology
Department of Chemistry, Department of Molecular and Cell Biology
University of California, Berkeley

- 12:00 p.m.** **Break**

Note: After the shared opening keynote address, the Bioimaging Science Program (BSP) meeting will continue separately with a keynote presentation at 1:00 p.m. by Dr. Joachim Frank, Nobel Laureate in Chemistry, followed by plenary sessions. All are welcome to attend the presentation and sessions. The BSP meeting has a designated area in the shared Gather space. Please consult the meeting map and the [BSP agenda](#) for additional information.

Plenary Sessions

- 12:30 p.m.** **Bioenergy Research Center Technologies on the Pathway to Biofuels and Bioproducts**
Moderators: Kent Peters and Shing Kwok

Session Description: The Bioenergy Research Centers (BRCs) have been investigating and creating new technologies to make lignocellulose-derived biofuels and bioproducts a sustainable and commercially viable enterprise. Each Center will present an overview of their state-of-the-science technologies addressing sustainable production of biomass through biomass deconstruction and conversion to biofuels and bioproducts.

- 12:30 p.m.** **Great Lakes Bioenergy Research Center (GLBRC)**
Speaker: Trey Sato, University of Wisconsin, Madison
Presentation: A GLBRC pipeline for sustainable production of fuels and chemicals from lignocellulosic biomass

- 1:00 p.m.** **Center for Advanced Bioenergy and Bioproducts Innovation (CABBI)**
Speaker: Vijay Singh, University of Illinois at Urbana-Champaign
Presentation: CABBI feedstocks to products pipeline for biofuels and oleochemicals industries
- 1:30 p.m.** **Joint BioEnergy Institute (JBEI)**
Speaker: Blake Simmons, Lawrence Berkeley National Laboratory
Presentation: BRC technologies on the pathway to biofuels and bioproducts
- 2:00 p.m.** **Center for Bioenergy Innovation (CBI)**
Speaker: Gregg Beckham, National Renewable Energy Laboratory
Presentation: Holistic biomass valorization with consolidated bioprocessing and lignin refining
- 2:30 p.m.** **Break**
- 3:00 p.m.** **Early Career Research**
Moderator: Pablo Rabinowicz
- Session Description:** The 2021 DOE Office of Science Early Career Research Program awardees from BER's Biological Systems Science Division will present their projects to the Genomic Science Program community.
- 3:00–3:20 p.m.** **PI:** Melissa Cregger, Oak Ridge National Laboratory
Presentation: Understanding the effects of *Populus*-mycorrhizal associations on plant productivity and resistance to abiotic stress
- 3:20–3:40 p.m.** **PI:** Ruben Rellán-Alvarez, North Carolina State University
Presentation: Improving candidate gene discovery by combining multiple genetic mapping datasets
- 3:40–4:00 p.m.** **PI:** Benjamin Cole, Lawrence Berkeley National Laboratory
Presentation: Defining the influence of environmental stress on bioenergy feedstocks at single-cell resolution

Poster Session

4:30–5:45 p.m.

TUESDAY, MARCH 1

Plenary Session

- 10:00 a.m. User Facilities and Resources**
Moderator: Ramana Madupu
Session Description: Towards advancing its research goals, the Biological Systems Science Division supports national scientific user facilities, community resources, and computational resources. These world-class facilities and resources provide BER researchers and the broader user community access to a suite of enabling capabilities, technologies, and data. They also foster multidisciplinary research efforts through cross-facility integrative programs. In this session, speakers will provide an update on the latest capabilities and joint efforts among user facilities to advance Genomic Science research.
- 10:00–10:20 a.m. Joint Genome Institute (JGI)**
Lawrence Berkeley National Laboratory
Speaker: Nigel Mouncey, Director JGI
Presentation: Integrative and Collaborative Genome Science at JGI
- 10:20–10:40 a.m. Environmental Molecular Sciences Laboratory (EMSL)**
Pacific Northwest National Laboratory
Speaker: Douglas Mans
Presentation: Building a Digital Phenome: EMSL's roadmap and efforts to date
- 10:40–11:10 a.m. BER Beamline Resources**
Speaker: Hoi-Ying Holman, Director of Berkeley Synchrotron Infrared Structural Biology (BSISB) Program, MBIB, LBNL
Presentation: Shining Synchrotron infrared Light on the Microbial World
- 11:10–11:30 a.m. National Microbiome Data Collaborative (NMDC)**
Lawrence Berkeley National Laboratory
Speaker: Emiley Eloie-Fadrosch
Presentation: Advancing collaborative microbiome research with the National Microbiome Data Collaborative
- 11:30–11:50 a.m. DOE Systems Biology Knowledgebase (KBase)**
Lawrence Berkeley National Laboratory
Speaker: Adam Arkin
Presentation: Exploring mechanisms of environmental and biological interaction with multi-omic sample analysis in KBase
- 11:50-12:00 p.m. Q&A**

Poster Session

12:30–1:45 p.m.

Breakout Sessions — Tuesday

2:00 p.m. **SESSION A -- BREAKOUT ROOM A (ADENINE)**
Environmental Microbiology
Moderator: Boris Wawrik

Session Description: Environmental microbiomes are comprised of interconnected and dynamic populations of microbes with high phyletic and genomic diversity. Networks of microbial interactions shape and condition the environment in ways that profoundly affect the physical world. Increasingly sophisticated molecular tools coupled to computational techniques and high-resolution analytical technologies offer exciting and growing opportunities for investigating the functional properties of microbes in their natural context. This session highlights BER's support for studies that leverage integrated, multidisciplinary research to assess microbial cycling of elements in the environment and will seek to explore future trends and challenges in environmental microbiome research.

2:00–2:25 p.m. **Speaker/PI:** Ranjani Murali, California Institute of Technology
Project: Cell to ecosystem: Understanding methane and associated nutrient cycling by sediment-hosted syntrophic consortia and their viral predators
Presentation: Unpacking the pangenomes and hidden phenotypic heterogeneity among syntrophic methane-oxidizing consortia

2:25–2:50 p.m. **Speaker:** Pieter Candry, University of Washington
PI: Mari Winkler, University of Washington
Project: Integrating single-cell wetland microbiome structure, function, and activity to ecosystem-scale biogeochemical fluxes
Presentation: Experimental and mathematical models bridging single cell-to-ecosystem scales to evaluate climate-wetland feedback mechanisms

2:50–3:15 p.m. **Speaker:** Sophia Ewens, University of California, Berkeley
PI: John Coates, University of California, Berkeley
Project: Using a systems biology approach to describe the role of dissimilatory phosphite oxidation in the global phosphorus cycle
Presentation: The global prevalence and biogeochemical impact of ancient phosphorus-oxidizing bacteria

- 3:15–3:40 p.m.** **Speaker/PI:** Jennifer Bhatnagar, Boston University
Project: Molecular mechanisms of mycorrhizal-decomposer interactions and impacts on terrestrial biogeochemistry
Presentation: Ectomycorrhizal fungi regulate soil microbial function under varying resource availability
- 3:40–3:50 p.m.** **Break**
- 3:50–4:15 p.m.** **Speaker/PI:** Karen Lloyd, University of Tennessee
Project: Using culture-independent methods to link active compound-specific carbon degradation to greenhouse gas production and recycling in natural populations of permafrost microbes
Presentation: Complex microbial communities and mechanisms of carbon degradation in the arctic permafrost of Svalbard, Norway
- 4:15–4:40 p.m.** **Speaker:** Aaron Jon Robinson, Los Alamos National Laboratory
PI: Patrick Chain, Los Alamos National Laboratory
Project: National Lab Science Focus Area: Bacterial:Fungal Interactions and Their Role in Soil Functioning
Presentation: Multi-omics and image-based studies expand knowledge of bacterial-fungal interactions at variable scales
- 4:40–5:05 p.m.** **Speaker:** Mengting Yuan, University of California, Berkeley
PI: Mary Firestone, University of California, Berkeley
Project/Presentation: Cross-kingdom interactions: The foundation for nutrient cycling in grassland soils

2:00 p.m.

SESSION B -- BREAKOUT ROOM T (THYMINE)
Systems Biology of Bioenergy-Relevant Microbes

Moderator: Dawn Adin

Session Description: The Genomic Science program supports research aimed at understanding the fundamental properties of bioenergy-relevant organisms at the genomic scale and aims to have researchers translate that gained knowledge to enhance the production capabilities of microbes for sustainable bioenergy. The portfolio supports projects spanning a diverse range of organisms and approaches to understand and harness the biosynthetic processing power of the microbial world. This session will provide opportunities for different projects in the portfolio to share their current research.

- 2:00–2:25 p.m.** **Speaker/PI:** Jose Avalos, Princeton University
Presentation: Optogenetic control of microbial consortia populations for fuel and chemical production

- 2:25–2:50 p.m.** **Speaker/PI:** Danielle Tullman-Ercek, Northwestern University
Presentation: Exploring bacterial microcompartments to overcome bottlenecks in sustainable biochemical production
- 2:50–3:15 p.m.** **Speaker:** Ying Zhang, University of Rhode Island
PI: Michael Adams, University of Georgia
Presentation: Systems biology-based optimization of extremely thermophilic lignocellulose conversion to bioproducts
- 3:15–3:45 p.m.** **Break**
- 3:45–4:10 p.m.** **Speaker/PI:** Cong Trinh, University of Tennessee
Presentation: Discovery of novel genotypes and cellular processes underlying robustness in *Yarrowia lipolytica* for novel biotransformation
- 4:10–4:35 p.m.** **Speaker/PI:** Justin North, The Ohio State University
Presentation: Metabolic engineering and modeling of an anaerobic cycle for enhanced bacterial ethylene synthesis
- 4:35–5:00 p.m.** **Speaker/PI:** Michelle O'Malley, University of California, Santa Barbara
Presentation: Engineering synthetic anaerobic consortia inspired by the rumen for biomass breakdown and conversion

2:00 p.m.

SESSION C -- BREAKOUT ROOM C (CYTOSINE)

Breaking the Bottleneck of Genomes: Accelerating Functional Characterization of Regulatory Mechanisms and Multigene Traits in Bioenergy Crop Plants - I

Moderator: Cathy Ronning

Session Description: The rate of genome sequencing has greatly accelerated in recent years, outpacing the ability to determine function(s) of computationally discovered genes and resulting in thousands of genes annotated as “hypothetical” or “unknown.” Thus, characterization and validation of gene function are still major bottlenecks to fully understand and enable development of productive, sustainable bioenergy crops that are resilient and adaptable to changing environments. In 2019 a new effort in plant research was initiated for integrative genomics-based research and technology leading to transformative approaches to determine gene function in plants and plant processes of interest to BER. This is the first of two sessions featuring advances in defining the vast amounts of genomic information underlying bioenergy-relevant traits from the Genomic Science program’s Plant Gene Function portfolio.

- 2:00–2:25 p.m.** **Speaker/PI:** Ana Alonso, University of North Texas
Presentation: Functional analysis of candidate genes involved in oil storage and stability in pennycress

- 2:25–2:50 p.m.** **Speaker/PI:** José Dinneny, Stanford University
Project/Presentation: Discovering innovations in stress tolerance through comparative gene regulatory network analysis and cell-type specific expression maps
- 2:50–3:15 p.m.** **Speaker:** Lianyong Wang, Princeton University
PI: Martin Jonikas, Princeton University
Project/Presentation: Transforming our understanding of chloroplast-associated genes through comprehensive characterization of protein localizations and protein-protein interactions
- 3:15–3:45 p.m.** **Break**
- 3:45–4:10 p.m.** **Speaker/PI:** Kranthi Varala, Purdue University
Project: InferNet: Gene function inference by leveraging large, organ-specific expression datasets and validation of non-redundant regulators
Presentation: Learning novel regulators of seed lipid content and composition by inferring organ-specific transcriptional networks
- 4:10–4:35 p.m.** **Speaker/PI:** Brian Fox, University of Wisconsin, Madison
Project: Creation of an acyltransferase toolbox for plant biomass engineering
Presentation: Additions to the BAHD acyltransferase toolbox
- 4:35–5:00 p.m.** **Speaker/PI:** James Umen, Donald Danforth Plant Science Center
Project/Presentation: Deep Green: Structural and functional genomic characterization of conserved unannotated green lineage proteins

2:00 p.m.

SESSION D -- BREAKOUT ROOM G (GUANINE)
National Microbiome Data Collaborative Workshop

Session Description: The National Microbiome Data Collaborative (NMDC) team will host an interactive, two-hour workshop to showcase the features of the NMDC Data Portal and NMDC Metadata Submission System. During the first hour of the workshop, attendees will work in small breakout groups to search for specific pieces of data. During the second hour, attendees are invited to bring sample metadata from their own microbiome research studies to validate against existing data standards within the NMDC Metadata Submission System. Attendees will be encouraged to provide real-time user feedback to the NMDC team throughout the workshop.

Registration Link: <https://lbnl.zoom.us/meeting/register/tjUvfu2hrjksGt01Gs7VvFD-2jCsdXgvG15W7>

Contact: Pajau Vangay (pvangay@lbl.gov)

WEDNESDAY, MARCH 2

Plenary Session

10:00 a.m. **Functional Genomics: What's Structure Got to Do With It?**

Moderator: Amy Swain

Session Description: Gaining a predictive and functional understanding of complex biological systems is a fundamental goal of the Genomic Science program (GSP). Through the DOE Systems Biology Knowledgebase (KBase), GSP researchers have access to data and tools to analyze data and generate biological system models. Recent BER-supported collaboration between KBase and the Protein Data Bank (PDB) will enable bi-directional linkages and enhance integration and access to macromolecular structure information that can augment genomic studies. In addition to experimentally determined structures already available in PDB, highly accurate predicted protein structures are becoming available thanks to the advent of neural network-based protein structure prediction platforms. Through these platforms, structural models of plant and microbial proteomes can be generated on a timescale useful to BER's genomic studies, and this information can also be used to identify specific targets worth further exploration through experimental approaches. Speakers will discuss revolutionary new tools, their implications for genomics research, and their emerging accessibility to GSP scientists.

10:00–10:30 a.m. *Speaker:* David Baker, director, Institute for Protein Design; University of Washington

Presentation: Deep learning for protein structure modeling and design

10:30–10:50 a.m. *Speaker:* Christopher S. Henry, Argonne National Laboratory

Presentation: Integrating structure and omics data to understand protein function and organism phenotypes in KBase

10:50–11:10 a.m. *Speaker:* Stephen K. Burley, director, RCSB Protein Data Bank; Rutgers, The State University of New Jersey

Presentation: Digital data resources for understanding biomolecules in 3D at the atomic level

11:10–11:30 a.m. *Speaker:* Ada Sedova, Oak Ridge National Laboratory

Presentation: Breaking the genome annotation bottleneck with protein structure, deep learning, and high-performance computing

11:30–11:50 a.m. *Speaker:* Nikos C. Kyrpides, Lawrence Berkeley National Laboratory

Presentation: Uncovering the functional dark matter

11:50–12:00 p.m. **Q&A**

Poster Session

12:30–1:45 p.m.

Breakout Sessions — Wednesday

2:00 p.m.

SESSION E -- BREAKOUT ROOM A (ADENINE)

What We Learn by Designing, Building, and Testing Biosystems

Moderator: Pablo Rabinowicz

Session Description: Genome editing and other new synthetic biology technologies are enabling both precise and extensive modification of biological systems, resulting in the generation of organisms with functions not found in nature or previously thought unattainable. The iterative design, building, and testing of such engineered biosystems often uncovers unknown biological principles that not only allow improving the designs but also expand our knowledge of fundamental biology. This session will highlight what we have learned by engineering plants and microbes within the Genomic Science program's Biosystems Design portfolio.

2:00–2:05 p.m.

Introduction: Pablo Rabinowicz

2:05–2:30 p.m.

Speaker: Rob Martienssen, Cold Spring Harbor Laboratory

Presentation: Biological design of Lemnaceae aquatic plants for biodiesel production

2:30–2:55 p.m.

Speaker: Davinia Salvachua, National Renewable Energy Laboratory

Presentation: Systems biology in white-rot fungi: Lignin digestion and ingestion?

2:55–3:10 p.m.

Break

3:10–3:35 p.m.

Speaker: Sabeeha Merchant, University of California, Berkeley

PI: Kris Noyogi, University of California, Berkeley

Presentation: Polycistronic mRNAs for synthetic gene expression

3:35–4:00 p.m.

Speaker: Ivan Baxter, Donald Danforth Plant Science Center

Presentation: Integrated understanding and engineering of whole plant water use efficiency in *Sorghum* and *Setaria*

4:00–4:25 p.m.

Speaker: Mike Jewett, Northwestern University

Presentation: Using cell-free systems to transform biosystems design for carbon-negative manufacturing

2:00 p.m.

SESSION F -- BREAKOUT ROOM T (THYMINE)
Enabling Capabilities for BSSD Science

Moderator: Ramana Madupu

Session Description: High-throughput, multi-omics techniques produce rich data layers of genomes, transcriptomes, proteomes, metabolomes, and other relevant data types. BSSD seeks to provide the scientific community and users access to open-source computational platforms and experimental capabilities for systems biology research. Integrative efforts within KBase, NMDC, and the Facilities Integrating Collaborations for User Science (FICUS) program at The Joint Genome Institute (JGI) and the Environmental Molecular Sciences Laboratory (EMSL) enable researchers to utilize a broad range of the experimental and data science capabilities for multidisciplinary science. This session will showcase projects that have leveraged BSSD user facilities and resources.

2:00–2:05 p.m.

Introduction: Ramana Madupu

2:05–2:30 p.m.

Speaker: Kevin Myers, Great Lakes Bioenergy Research Center, University of Wisconsin, Madison

Presentation: Leveraging genomic science facilities for bioenergy research and education

2:30–2:55 p.m.

Speaker: Jeff Blanchard, University of Massachusetts, Amherst

Presentation: Integration of mass spectroscopy and genetic results from DOE user facilities provides new insights on long-term warming at Harvard Forest

2:55–3:20 p.m.

Speaker: Mikayla Borton, Pacific Northwest National Laboratory

Presentation: Putting river microbiomes on the map: Continental-scale context for thousands of newly sampled microbial genomes from North America

3:20–3:40 p.m.

Break

3:40–4:30 p.m.

Panel Discussion: With speakers and representatives from JGI, NMDC, EMSL, and KBase

2:00 p.m.

SESSION G -- BREAKOUT ROOM G (GUANINE)

Synthetic Consortia and Microbiome Engineering

Moderators: Boris Wawrik and Dawn Adin

Session Description: Recent discoveries and technology developments in environmental microbiology has opened the door to new ways to study microbial populations in complex settings through the design and engineering of microbiomes and synthetic consortia. This session will address challenges related to establishing, modeling, and engineering microbiomes, as well as the tools necessary to make advances in this emerging field in microbial systems biology.

2:00–2:25 p.m.

Speaker: Trent Northen, Lawrence Berkeley National Laboratory

Project: National Lab Science Focus Area: m-CAFEs (Microbial Community Analysis & Functional Evaluation in Soils Scientific Focus Area)

Presentation: A standardized consortium and toolbox for deconstructing rhizosphere interactions

2:25–2:50 p.m.

Speaker: Oriane Moyne, University of California, San Diego

PI: Karsten Zengler, University of California, San Diego

Project Title: National Lab Science Focus Area: Trial Ecosystems for the Advancement of Microbiome Science (TEAMS)

Presentation: Functional niches enable the design of targeted interventions and predict outcomes in a microbial community

2:50–3:15 p.m.

Speaker: Nina Lin, University of Michigan

Project: Developing, understanding, and harnessing modular carbon/nitrogen-fixing tripartite microbial consortia for versatile production of biofuel and platform chemicals

Presentation: Towards highly efficient synthetic microbial consortia for converting unconventional feedstocks to advanced bioproducts: Opportunities and challenges

3:15–3:40 p.m.

Break

3:40–4:05 p.m.

Speaker: Ryan McClure, Pacific Northwest National Laboratory

Project: National Lab Science Focus Area: Phenotypic Response of the Soil Microbiome to Environmental Perturbations

Presentation: Defined microbial communities: Application of simplified systems to map complexities of soil microbiome interactions

4:05–4:30 p.m.

Speaker: Robert Egbert, Pacific Northwest National Laboratory

Project: National Lab Science Focus Area: Persistence Control of Engineered Functions in Complex Soil Microbiomes

Presentation: Biocontainment in the rhizosphere through persistence control engineering

4:30–4:55 p.m. **Speaker:** Jun Lee, Oak Ridge National Laboratory
PI: Mitch Doktycz, Oak Ridge National Laboratory
Project Title: National Lab Science Focus Area: Plant-Microbe Interfaces
Presentation Title: Plant-Microbe Interfaces: The use of synthetic communities and microbiome transfers to elucidate microbial-provided plant thermal benefits

2:00 p.m.

SESSION H -- BREAKOUT ROOM C (CYTOSINE)

Breaking the Bottleneck of Genomes: Accelerating Functional Characterization of Regulatory Mechanisms and Multigene Traits in Bioenergy Crop Plants – II

Moderator: Cathy Ronning

Session Description: The rate of genome sequencing has greatly accelerated in recent years, outpacing the ability to determine function(s) of computationally discovered genes and resulting in thousands of genes annotated as “hypothetical” or “unknown.” Thus, characterization and validation of gene function are still major bottlenecks to fully understand and enable development of productive, sustainable bioenergy crops that are resilient and adaptable to changing environments. In 2019 a new effort in plant research was initiated for integrative genomics-based research and technology leading to transformative approaches to determine gene function in plants and plant processes of interest to BER. This is the second of two sessions featuring advances in defining the vast amounts of genomic information underlying bioenergy-relevant traits from the Genomic Science program’s Plant Gene Function portfolio.

2:00–2:25 p.m. **Speaker:** Brian Dilkes, Purdue University
PI: Clint Chapple, Purdue University
Project/Presentation: Coupling metabolic source isotopic pair labeling and genome-wide association for metabolite and gene annotation in plants

2:25–2:50 p.m. **Speaker/PI:** Andrea Eveland, Donald Danforth Plant Science Center
Project: Elucidating the molecular mechanisms underlying drought resilience in *Sorghum*
Presentation: Using molecular genetics and precision phenotyping to elucidate gene function contributing to drought resilience in *Sorghum*

2:50–3:15 p.m. **Speaker/PI:** Hiroshi Maeda, University of Wisconsin, Madison
Project: Constructing the nitrogen flux maps (NFM) of plants
Presentation: Comprehensive characterization of aminotransferases (ATs) to construct nitrogen flux maps (NFM) of plants

3:15–3:45 p.m. **Break**

- 3:45–4:10 p.m.** **Speaker/PI:** Sue Rhee, Carnegie Institution of Washington
Project: High-throughput determination of a subcellular metabolic network map of plants
Presentation: A high-throughput determination of a subcellular metabolic network map of *Sorghum*
- 4:10–4:35 p.m.** **Speaker/PI:** James Schnable, University of Nebraska, Lincoln
Project/Presentation: TGCM: (T)rait, (G)ene, and (C)rop Growth (M)odel directed targeted gene characterization in *Sorghum*
- 4:35–5:00 p.m.** **Speaker/PI:** Gail Taylor, University of California, Davis
Project/Presentation: Combining genome-wide association studies and expression quantitative trait nucleotide mapping with molecular and genetic validations to identify transcriptional networks regulating drought tolerance

2:00–4:00 p.m. **KBase Training Session: Samples, Amplicons, and Chemical Abundance**

Session Description: This two-hour workshop will demonstrate KBase’s latest feature suite for analyzing environmental samples, amplicon, and omics data. Learn how to import your sampling and amplicon data into KBase. With amplicon data in KBase, you can link them with samples for analysis and build visualizations of community composition based on sample metadata. We’ll demonstrate how to compute and visualize abundances of OTUs across your samples. Our experts will walk through uploading sampling data, validating and verifying your data, and managing updates across your samples. We’ll also engage attendees to discuss their scientific problems and data analysis needs and coordinate extended support from the KBase team to the DOE research community. Read more about samples in KBase on our blog or check the recording of our recent introductory webinar.

Registration required: <https://lbl.zoom.us/meeting/register/tjEp dumopj0rHdl-YVuKHvKP-jLy9dP0Tn-u9>

KBase 1-on-1 Consultation and Help

KBase offers one-on-one consultation support throughout the GSP meeting as an opportunity to meet with KBase staff to discuss specific questions about using KBase in your research. Appointments are available 9:00 a.m.–4:30 p.m. Staff will be available for drop-in during the poster session.

Schedule time here: <https://calendly.com/kbase/gsp2022-consultation>