



**SEPTEMBER 22–23, 2026**

**Advances in Microbial Biodesign  
Using AI and Automation**

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## BRONZE

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# WELCOME

Dear Attendees,

Welcome to the **2026 Predictive Phenomics Conference: *Advances in Microbial Biodesign Using AI and Automation***. We are excited to gather the predictive phenomics community together for our second conference and continue building on the conversations and collaborations that began at our inaugural meeting last year.

Predictive phenomics combines expertise from molecular science, biotechnology, computation, and engineering to understand, and ultimately predict, how genomes interact with their environments to produce phenotypes. As the field advances, emerging capabilities in AI, automation, high-throughput experimentation, and synthetic biology are creating new opportunities to move from observing biological systems toward predicting and engineering their function faster than ever before. This year's conference focuses on these advances in the context of microbial phenotyping and biodesign, bringing together researchers developing state-of-the-art technologies with those applying them to challenging biological questions.

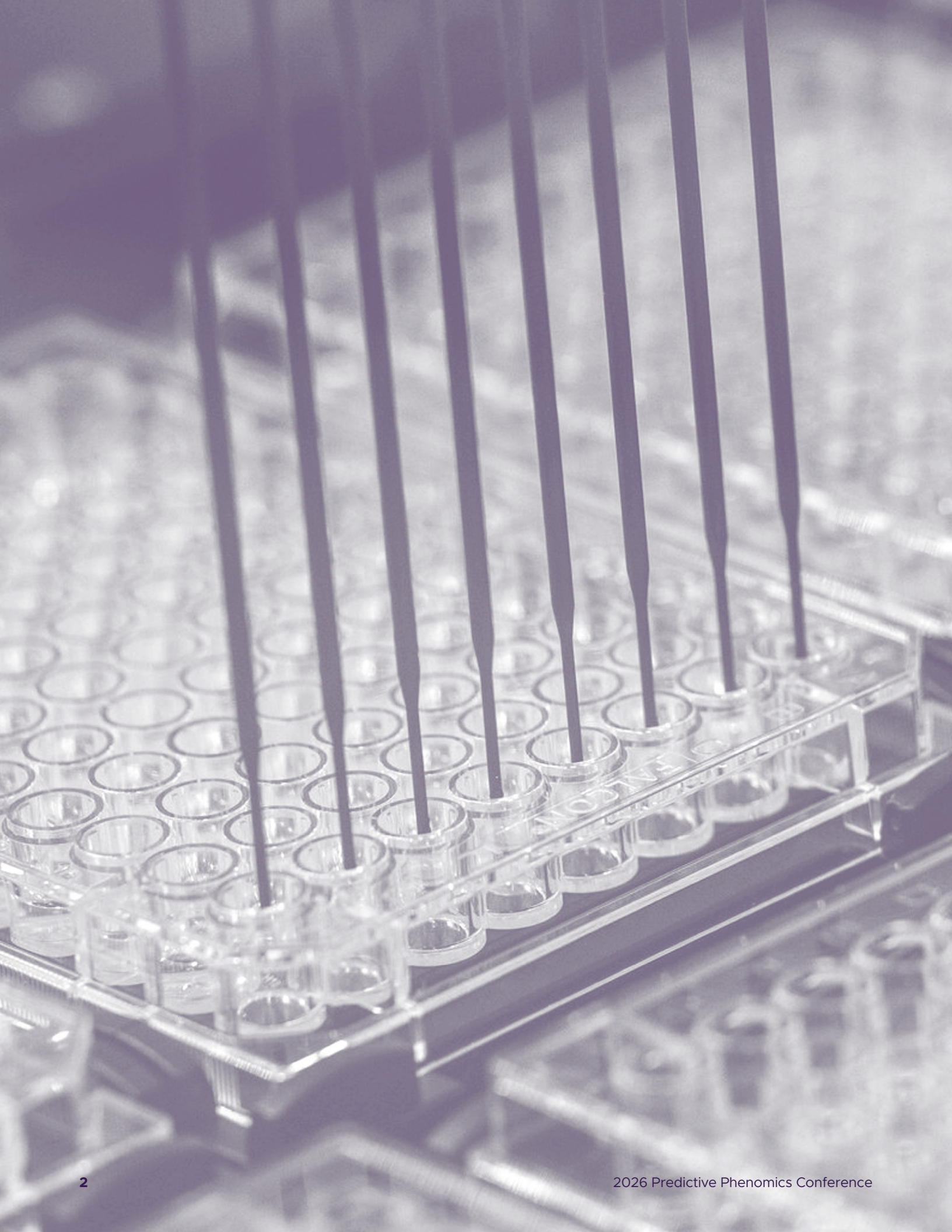
Over the next two days, we encourage you to connect with colleagues across institutions and disciplines, ask challenging questions, share new ideas, and identify opportunities to collaborate. Our goal for this conference is to continue growing a community where technology developers, computational scientists, and experimental biologists can collectively shape the future of predictive phenomics for the bioeconomy.

We extend our sincere thanks to our speakers and poster presenters for sharing their research and perspectives, and to our sponsors for helping make this event possible. Most importantly, thank you for being part of this community and contributing your expertise, ideas, and enthusiasm to the discussions ahead.

We look forward to an engaging and productive conference.

Sincerely,

The 2026 Predictive Phenomics Conference Organizing Committee



# AGENDA AT A GLANCE

## DAY 1 | TUESDAY, SEPTEMBER 22, 2026

| TIME                                                                                                   | TOPIC                                                                                                                                                                           |
|--------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 8:30 – 8:35 am                                                                                         | <b>Conference Logistics</b><br><i>Bobbie-Jo Webb-Robertson</i>                                                                                                                  |
| 8:35 – 8:45 am                                                                                         | <b>Conference Welcome</b><br><i>Douglas Mans</i>                                                                                                                                |
| 8:45 – 9:10 am                                                                                         | <b>Opening Remarks: Predictive Phenomics – Perspectives from DOE</b><br><i>Dorothy Koch, Associate Director for Biological and Environmental Research, Department of Energy</i> |
| 9:10 – 10:10 am                                                                                        | <b>Keynote – Accelerating Synthetic Biology Tools for Anaerobic Microbial Communities</b><br><i>Michelle A. O'Malley, University of California, Santa Barbara</i>               |
| 10:10 – 10:25 am                                                                                       | <b>Break</b>                                                                                                                                                                    |
| <b>SESSION 1 – High-throughput (HTP) Workflows for Microbial Phenotyping</b><br><i>Chair: Tom Metz</i> |                                                                                                                                                                                 |
| 10:25 – 11:10 am                                                                                       | <b>Invited Talk – Exploring Beyond the Literature with Automated Phenotyping</b><br><i>Paul Jensen, University of Michigan</i>                                                  |
| 11:10 – 11:35 am                                                                                       | <b>Closing the Gap: Enabling Predictive Phenomics for Faster Biomanufacturing Development</b><br><i>Christopher Petzold, Lawrence Berkeley National Laboratory</i>              |
| 11:35 am – 12:00 pm                                                                                    | <b>Scaling the Test Phase of Biodesign through Automated Phenotyping</b><br><i>Alex Beliaev, Pacific Northwest National Laboratory</i>                                          |
| 12:00 – 1:30 pm                                                                                        | <b>Lunch and Poster Flash Talks</b>                                                                                                                                             |

## SESSION 2 – Automating Platforms with AI

Chair: Dion Antonopoulos

1:30 –  
2:15 pm

### Invited Talk – Agentic AI for Autonomous Plant Phenotyping: From Foundation Models to Experimental Steering

*Dave Weston, Oak Ridge National Laboratory*

2:15 –  
2:40 pm

### Exploration of Growth Frontiers of Muconate Producing *Pseudomonas putida* using Reinforcement Learning

*Bram Stone, Pacific Northwest National Laboratory*

2:40 –  
3:05 pm

### Toward Autonomous Biosystems Engineering: Closed-loop AI Design and Robotic Adaptive Evolution in *Acinetobacter baylyi* ADP1

*Christopher Henry, Argonne National Laboratory*

3:05 –  
3:20 pm

### Break

## SESSION 3 – Autonomous Experimentation Through Self-driving Labs

Chair: Bobbie-Jo Webb-Robertson

3:20 –  
4:05 pm

### Invited Talk – Using a GPT-5-driven Autonomous Lab to Optimize the Cost and Titer of Cell Free Protein Synthesis

*Reshma Shetty, Ginkgo Bioworks*

4:05 –  
4:30 pm

### A Proven Automated Experimentation Platform for High-throughput Evolutionary Engineering of Microbes

*Adam M. Feist, University of California San Diego*

4:30 –  
4:55 pm

### Agentic AI for Autonomous Science at Leadership-Class Facilities

*Rafael Ferreira da Silva, Oak Ridge National Laboratory*

4:55 –  
5:00 pm

### Evening Logistics

*Bobbie-Jo Webb-Robertson*

5:30 –  
7:30 pm

### Poster Session

## DAY 2 | WEDNESDAY, SEPTEMBER 23, 2026

| TIME                                                                                                 | TOPIC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 8:30 – 8:35 am                                                                                       | <b>Conference Welcome and Logistics</b><br><i>Bobbie-Jo Webb-Robertson</i>                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 8:35 – 8:55 am                                                                                       | <b>Securing America’s Scientific and Innovation Edge Against Emerging Threats</b><br><i>Scott Fagan, Director, Office of Threat Assessment, Bureau of Emerging Threats</i>                                                                                                                                                                                                                                                                                                                 |
| <b>SESSION 4 – AI-guided Protein and Pathway Engineering</b><br><i>Chair: Kristin Burnum-Johnson</i> |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| 8:55 – 9:40 am                                                                                       | <b>Invited Talk – Trifecta: Using AI Agents, High Performance Computing and Autonomous Labs for Biological Design</b><br><i>Arvind Ramanathan, Argonne National Laboratory</i>                                                                                                                                                                                                                                                                                                             |
| 9:40 – 10:05 am                                                                                      | <b>A Generalizable Biodesign-driven Framework for Tuning Metabolic Flux at the Protein Level</b><br><i>Elise Van Fossen, Pacific Northwest National Laboratory</i>                                                                                                                                                                                                                                                                                                                         |
| 10:05 – 10:20 am                                                                                     | <b>Break</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| 10:20 – 11:05 am                                                                                     | <b>Pathways in Context: Model-guided Engineering Across Genomes, Metabolism, and Engineered Environments</b><br><i>James Carothers, University of Washington</i>                                                                                                                                                                                                                                                                                                                           |
| 11:05 – 11:30 am                                                                                     | <b>OpenPhase: Condition-Aware Exploration of Multicomponent Biosystem Phase-Separating Behavior</b><br><i>Peiran Jian, Carnegie Mellon University</i>                                                                                                                                                                                                                                                                                                                                      |
| 11:30 am – 12:50 pm                                                                                  | <b>Lunch &amp; Panel: Future of Microbial Biodesign</b><br><i>Douglas Mans, Pacific Northwest National Laboratory,</i><br><i>Paul Adams, Lawrence Berkeley National Laboratory,</i><br><i>Dion Antonopoulos, Argonne National Laboratory,</i><br><i>Dave Weston, Oak Ridge National Laboratory,</i><br><i>Michelle A. O’Malley, University of California, San Diego,</i><br><i>Paul Jensen, University of Michigan</i><br><b>(Moderators: Kristin Burnum-Johnson &amp; Katrina Waters)</b> |

## SESSION 5 – Predictive Models for Microbial Engineering

Chair: Hector Garcia Martin

12:50 –  
1:15 pm | **Integrating Scale-down Bioreactors and Multi-Omic Machine Learning Analyses to Engineer Robust *Yarrowia lipolytica* Citrate Production**  
*Jeffrey Czajka, Pacific Northwest National Laboratory*

1:15 –  
1:40 pm | **ARThur: An Agentic Subsystem for Closing the Microbial Engineering DBTL Loop**  
*Satyarth Praveen, Lawrence Berkeley National Laboratory*

1:40 –  
2:05 pm | **CatPred 2.0: Extending Enzyme Kinetic Parameter Prediction for Enzyme Variants**  
*Somtirtha Santra, The Pennsylvania State University*

2:05 –  
2:15 pm | **Break**

2:15 –  
2:40 pm | **High-throughput Genetic Tools and Automation for Gene Discovery and Microbial Engineering**  
*Carrie Eckert, Oak Ridge National Laboratory*

2:40 –  
3:05 pm | **Universal Modular Cell Design for Scalable Biomanufacturing of Chemicals**  
*Cong Trinh, University of Tennessee*

3:05 –  
3:30 pm | **MAESTRO Identifies Dosage-Tunable Tandem Paralogues for Predictive Microbial Engineering**  
*Yasuo Yoshikuni, Lawrence Berkeley National Laboratory*

3:30 –  
3:35 pm | **Closing Remarks**

Learn about  
our speakers here



# AGENDA

## DAY 1 | TUESDAY, SEPTEMBER 22, 2026

| TIME            | TOPIC                                                                                                                                                                           |
|-----------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 8:30 – 8:35 am  | <b>Conference Logistics</b><br><i>Bobbie-Jo Webb-Robertson</i>                                                                                                                  |
| 8:35 – 8:45 am  | <b>Conference Welcome</b><br><i>Douglas Mans</i>                                                                                                                                |
| 8:45 – 9:10 am  | <b>Opening Remarks: Predictive Phenomics – Perspectives from DOE</b><br><i>Dorothy Koch, Associate Director for Biological and Environmental Research, Department of Energy</i> |
| 9:10 – 10:10 am | <b>Keynote – Accelerating Synthetic Biology Tools for Anaerobic Microbial Communities</b><br><i>Michelle A. O'Malley, University of California, Santa Barbara</i>               |

Anaerobic microbes work together in complex communities that decompose and recycle carbon biomass throughout the Earth—from our guts to landfills and compost piles. Despite their importance, little information exists to parse the role of anaerobes within their dynamic community because they are exceptionally difficult to culture and manipulate. Anaerobic communities are also not well suited for high-throughput screening and engineering platforms due to the need to maintain anoxic conditions. To address this need, we developed new experimental approaches and workflows within the NSF Biofoundry for Extreme & Exceptional Fungi, Archaea, and Bacteria (ExFAB) to grow anaerobic microbial communities, automate their disassembly and reassembly, and prototype synthetic microbial communities for an array of applications—from waste deconstruction and bioproduction to human health diagnostics and therapeutics. Using a community originally sourced from an anaerobic digester as a testbed, we quantified culture stability of a mixed community of biomass-degrading bacteria and anaerobic fungi and developed isolation approaches to reveal community members that target specific components of plant waste (e.g., lignin, hemicellulose, cellulose). Moreover, with ExFAB's advanced anaerobic colony-picking, phenotyping, and prototyping capacities, we developed an anaerobic agrobacterium mediated transformation method to genetically engineer anaerobic fungi to bolster medium chain fatty acid production in synthetic anaerobic communities. Currently we are adapting our anaerobic high-throughput cultivation platform to cultivate fecal-derived microbiomes from biobanked cohorts to determine how environmental pressures “sculpt” the trajectories of gut microbiomes in early life—specifically to identify mechanisms and critical windows that promote gut microbiome resilience. Overall, these approaches and the critical infrastructure of ExFAB serve to advance high-throughput screening, genetic engineering, and rapid phenotyping efforts in non-model anaerobes, as well as in custom-designed synthetic anaerobic communities for tailored application.

10:10 –  
10:25 am

## Break

10:25 am –  
12:00 pm

## SESSION 1 – High-throughput (HTP) Workflows for Microbial Phenotyping

*Chair: Tom Metz*

10:25 –  
11:10 am

### Invited Talk – Exploring Beyond the Literature with Automated Phenotyping

*Paul Jensen, University of Michigan*

Autonomous science agents optimize the ratio between an experiment's information gain and its cost. Often, engineers fix the costs of their experiments, allowing the agents to focus solely on maximizing information gain. This talk demonstrates how accounting for the costs (time, money, and resources) of an experiment can inform the design of optimal policies. We present new agentic frameworks that prioritize information reuse, efficient experimental execution, and the avoidance of rediscovery to scale up closed-loop phenotyping systems.

11:10 –  
11:35 am

### Closing the Gap: Enabling Predictive Phenomics for Faster Biomanufacturing Development

*Christopher Petzold, Lawrence Berkeley National Laboratory*

Accelerating the U.S. bioeconomy requires biomanufacturing platforms that can reduce development timelines while improving the reproducibility and usefulness of phenotypic data. To address this need, we developed automated workflows, software and web-based AI/ML tools, and FAIR-compliant data capture and provenance into a platform for design-build-test-learn cycles. For this platform, strain construction is scaled using a novel 384-well high-throughput microfluidic electroporator (HTME) to perform transformations in <1 minute with >95% success. Subsequently, up to 5000 microbial strains are cultured in high-throughput at a time. Crucially, we implement high-throughput global proteomics to validate metabolic engineering efforts and CRISPR-mediated protein downregulation (CRISPRi), ensuring our active learning models (e.g., the Automated Recommendation Tool, ART) are trained exclusively on high-fidelity, accurate data. Another important component of this ecosystem is high-throughput screening using RapidFireQQ assays for quantitation of products from microbial fermentation cultures, chemical overlays, and intracellular lysates. These methods support screening at scales ranging from focused analytical studies to thousands of samples per day and provide reproducible, AI-ready phenotype data for iterative model-guided strain improvement. We have optimized sample preparation and data acquisition protocols for over 10 molecules, such as isoprenol, isoprenyl acetate, muconate, succinate, coumarate, and 3-hydroxypropionate (3-HP). In *Pseudomonas putida*, this broader capability has supported machine learning-guided optimization of isoprenol production across a large CRISPRi design space. This combined automation, analytics, and modeling strategy highlights how predictive phenomics can enable faster process development, lower cost of experimentation, and more agile production of multiple biomanufacturing target molecules. As an end-to-end platform for discovery and scale-up, this system offers a practical model for strengthening DOE's broader innovation ecosystem and supporting economically competitive, resilient supply chains.

11:35 am –  
12:00 pm

## Scaling the Test Phase of Biodesign through Automated Phenotyping

*Alex Beliaev, Pacific Northwest National Laboratory*

Luke A. Fisher<sup>1</sup>, R. Seth Wood<sup>1</sup>, Erin L. Bredeweg<sup>1</sup>, Allan V. Scott<sup>1</sup>, Clifford Morrison<sup>1</sup>, Jeffrey J. Czajika<sup>1</sup>, Joshua Elmore<sup>1</sup>, Alicia Cuevas<sup>1</sup>, Olga Shishkov<sup>1</sup>, Yejun Kim<sup>2</sup>, James Carothers<sup>2</sup>, Todd Edwards<sup>1</sup>, Scott E. Baker<sup>1</sup>, and Kristin Burnum-Johnson<sup>1</sup>

<sup>1</sup>Pacific Northwest National Laboratory, <sup>2</sup>University of Washington

Advances in DNA synthesis, genome engineering, and multi-omics have dramatically expanded the ability to construct microbial strains and interrogate their molecular and physiological states. Bioengineering approaches such as adaptive laboratory evolution, genetic circuit design, and targeted genetic and physicochemical perturbations generate large, complex sample sets spanning strains, conditions, and time points. Yet converting these samples into reproducible phenotypic and molecular measurements remains a major bottleneck, requiring extensive cultivation, sampling, processing, and analytical workflows. The Anaerobic Microbial Phenotyping Platform (AMP2) at Pacific Northwest National Laboratory provides a flexible, automated, high-throughput framework for reproducible microbial cultivation, phenotyping, and sample processing under both aerobic and strictly anaerobic conditions. Standardized cultivation and sampling regimes, combined with modular automated workflows, improve reproducibility while minimizing technical variability and human error, allowing the same infrastructure to be reconfigured across diverse biological questions. This presentation introduces the core capabilities and architecture of AMP2 and the classes of experiments it supports across the design-build-test-learn cycle: acceleration of the “test” phase through high-throughput growth, substrate-utilization, and product-formation phenotyping, including integrated targeted metabolite assays, to screen and prioritize mutant and CRISPR-based strain libraries; phenotypic characterization of environmentally relevant microbes; and condition-resolved characterization of engineered genetic circuits. Representative workflows, platform performance and reproducibility metrics, early results from ongoing efforts, and design principles emerging from the development of automated phenotyping pipelines will be presented. Collectively, AMP2 narrows the Build-Test gap, helping align the rate at which modern microbiology generates biological material with the capacity to extract meaningful insight from it.

12:00 –  
1:30 pm

## Lunch and Poster Flash Talks

1:30 –  
3:05 pm

## SESSION 2 – Automating Platforms with AI

Chair: Dion Antonopoulos

1:30 –  
2:15 pm

### Invited Talk – Agentic AI for Autonomous Plant Phenotyping: From Foundation Models to Experimental Steering

*Dave Weston, Oak Ridge National Laboratory*

John Lagergren<sup>1</sup>, Kelsey Carter<sup>1</sup>, Daniel Rosendo<sup>1</sup>, Renan Souza<sup>1</sup>, Shelaine L. Curd<sup>1</sup>, Rafael Ferreira da Silva<sup>1</sup>, Frédéric Suter<sup>1</sup>, Larry York<sup>1</sup>, Priya Ranjan<sup>1</sup>, Paul Adams<sup>2</sup>, Kristin Burnum-Johnson<sup>3</sup>, and Dionysios Antonopoulos<sup>4</sup>

<sup>1</sup>Oak Ridge National Laboratory, <sup>2</sup>Lawrence Berkeley National Laboratory,

<sup>3</sup>Pacific Northwest National Laboratory, <sup>4</sup>Argonne National Laboratory

Modern biology can generate data faster than scientists can analyze it. Across the DOE laboratories, high-throughput imaging, sequencing, and phenotyping systems produce large and complex datasets, but transforming those data into actionable scientific insight remains a major bottleneck. The Orchestrated Platform for Autonomous Laboratories (OPAL) was created to address this challenge. By combining artificial intelligence (AI), automated analysis, robotics, and experimentation across DOE laboratories, experimental results can quickly inform the next scientific decision. This talk focuses on OPAL at Oak Ridge National Laboratory's Advanced Plant Phenotyping Laboratory (APPL), which images hundreds to thousands of plants each day using up to 11 remote sensing modalities. A general-purpose AI foundation model, OPAL-ViT, is being trained across these modalities and will be fine-tuned to predict traits such as total leaf area, photosynthetic rate, and volatile emissions directly from images. An agentic co-scientist then empowers scientists to ask questions in natural language, automatically launches necessary analyses on the Frontier supercomputer, and returns traceable results. In one example, the system detected a sudden decline in plant water status, prompted an intervention, and confirmed plant recovery. These advancements reduce efforts that previously required hours of manual measurement and analysis each day to now returning answers and suggesting follow-up analyses in minutes.

2:15 –  
2:40 pm

## Exploration of Growth Frontiers of Muconate Producing *Pseudomonas putida* using Reinforcement Learning

*Bram Stone, Pacific Northwest National Laboratory*

Joonhoon Kim, Andrew Frank, A. Victoria Reynolds, and Joshua Elmore

*Pacific Northwest National Laboratory*

The emerging need for AI-ready data in biology demands extensive exploration of large combinatorial parameter space. Automated design and exploration using reinforcement learning patterns offers a promising avenue to build such data. We used a modified version of BacterAI, to explore combinations of continuous variables that allow for the growth of *Pseudomonas putida* JE3959, which is engineered to produce muconate. We tested seven carbon compounds, two nitrogen sources, and sodium chloride to induce osmotic stress. Experiments were conducted in minimal media prepared to three pH values (5, 7, and 8.5). Experimental additions were made with a Tecan Fluent automatic liquid handler in 96-well plates and growth measured across three days via OD<sub>600</sub>. Consumable labware use in each run was minimized through the Gurobi optimizer. Across 10 rounds, we tested 2300 unique experimental conditions, during which the mean squared error of the central statistical model within BacterAI (a Gaussian Process Regressor, GPR) was reduced from 0.024 to 0.011 and accuracy increased from 0.66 to 0.92. We compared several different machine learning models on the final data, finding that random forest (RF) regression out-performed GPR models (RF  $R^2 = 0.78$ , GPR  $R^2 = 0.74$ ). However, when models were iteratively trained on previous rounds and tested on newly generated data, we observed similar performance of RF, GPR, bagged neural nets, and support vector machines. GPR and RF regressors were less robust to imbalanced growth outcomes in data than other models. GPR, RF, and bagged neural net regressors consistently identified pH, octanoate, and urea as the most important (in respective order) and all identified a negative association between growth and benzoate (a carbon source); however, importance rankings diverged after these three. Following high-throughput data generation, simple K-means clustering was sufficient to produce clusters whose centroids represented divergent growth outcomes and conditions, demonstrating the integration of this approach with down-selected and more intensive data gathering.

2:40 –  
3:05 pm

## **Toward Autonomous Biosystems Engineering: Closed-loop AI Design and Robotic Adaptive Evolution in *Acinetobacter baylyi* ADP1**

*Christopher Henry, Argonne National Laboratory*

Autonomous biosystems engineering requires closed-loop systems in which AI not only proposes biological designs but learns directly from high-throughput experimental outcomes. We are building such a platform in *Acinetobacter baylyi* ADP1—an ideal chassis for rapid genome rewriting via exceptionally efficient natural transformation with linear DNA—coupling lab automation, adaptive laboratory evolution (ALE), multi-omics, and genome sequencing with AI models that execute two reinforcement loops, for protein and strain design. In the protein-design loop, protein/DNA language models and agentic reasoning workflows generate candidate enzyme sequences, score them through an in-silico pipeline for foldability, activity and promiscuity, and bias generation toward improved designs. We apply it to two enzyme families: engineered aldolase variants (DgoA) that replace the canonical DAHP synthase step, and O-demethylases with specificity expanded to catabolize non-native lignin-derived aromatics.

In the strain-design loop, AI-driven experimental planning grounded in mechanistic and causal models of ADP1 metabolism selects interventions and ALE conditions. Robotics-enabled, plate-based ALE performs transformation, serial transfer, growth monitoring and competitive selection, while sequencing identifies designed and emergent mutations. The platform now delivers all of this end-to-end, discovering novel mutations in-plate, sustaining automated ALE over long timeframes, and resolving competing variants by amplicon sequencing. Applied to a combinatorial two-component demethylase library, it has surveyed 2,917 distinct enzyme-pair complexes—8% of a 35,000-member design space—and temporal barcode trajectories assign relative growth rates to 445 of them from a single substrate. Runs now underway extend this across all four methoxy-aromatic substrates. We will present the platform, ALE results for both enzyme families, and how temporal abundance turns automated evolution into quantitative training signal that in turn drives autonomous protein design. We will also present steps we have taken to translate this system into a full autonomous discovery and design platform.

3:05 –  
3:20 pm

## **Break**

3:20 –  
4:55 pm

### SESSION 3 – Autonomous Experimentation Through Self-driving Labs

Chair: *Bobbie-Jo Webb-Robertson*

3:20 –  
4:05 pm

#### **Invited Talk – Using a GPT-5-driven Autonomous Lab to Optimize the Cost and Titer of Cell Free Protein Synthesis**

*Reshma Shetty, Ginkgo Bioworks*

Ginkgo used an autonomous lab, comprising a large language model (LLM) and a fully automated cloud laboratory, to optimize the cost efficiency of cell-free protein synthesis (CFPS). By conducting iterative optimization, the LLM-driven autonomous lab was able to achieve a 40% reduction in the specific cost (\$/g protein) of CFPS relative to the state of the art (SOTA). This cost reduction was accompanied by a 27% increase in protein production titer (g/L). Iterative experimental design, experiment execution, data capture and analysis, data interpretation, and new hypothesis generation were all handled by the LLM-driven autonomous lab. The interface between OpenAI's GPT-5 LLM and Ginkgo Bioworks' cloud laboratory incorporated built-in validation checks via a Pydantic schema to ensure that AI-designed experiments were properly specified. Experimental designs were translated into programmatic specification of multi-instrument biological workflows by Ginkgo's Catalyst software and executed on Ginkgo's Reconfigurable Automation Cart (RAC) laboratory automation platform, with human intervention largely limited to reagent and consumables preparation, loading, and unloading. By integrating LLMs with programmatic control of a cloud lab, we demonstrate that an LLM-driven autonomous lab can successfully perform a real-world scientific task, highlighting the potential of AI-driven autonomous labs for scientific advancement.



4:05 –  
4:30 pm

## **A Proven Automated Experimentation Platform for High-throughput Evolutionary Engineering of Microbes**

*Adam M. Feist, University of California San Diego*

Developing high-performing, scalable microbial strains remains a central bottleneck across biomanufacturing and health, constrained less by biological ideas than by the throughput, reproducibility, and data quality of the experiments needed to test them. Over the past 15 years, our lab has built and refined an automated experimentation platform that integrates continuous cultivation, real-time data capture, automated analysis, and closed-loop process control to run cell phenotyping and adaptive laboratory evolution (ALE) at scale. The platform executes growth-coupled selection under precisely defined pressures, tracks every measurement with full data traceability, and pairs evolved phenotypes with whole-genome sequencing and mutational analysis pipelines to resolve the causal mutations behind them. Its strain-agnostic design makes it broadly deployable across organisms and objectives, and to date it has run more than 3,300 parallel evolution experiments across dozens of microbes spanning the phylogenetic tree, pursuing goals that range from improving tolerance to enhancing specific protein performance. As a recent example, the platform was used to evolve a *Pseudomonas putida* strain for stable, coordinated co-utilization of lignocellulosic hexose and pentose sugars under dynamic selection regimes, increasing total sugar consumption and improving production of the bioproduct indigoidine from mixed sugars. Crucially, the resulting genotype-phenotype datasets, among the largest of their kind, let us move beyond cataloguing individual mutations to resolving the higher-order interactions (epistasis) between them and treating those interactions as explicit design variables. This lays the groundwork for engineering cycles that integrate AI and laboratory information management toward self-driving experimentation. This is a mature, validated platform, not a prototype, and it already delivers industrially relevant strains while generating the structured, high-provenance data on which AI-guided microbial engineering depends. I will present the platform's capabilities, its proven industrial and biological applications, and its trajectory toward autonomous, predictive experimentation for the bioeconomy.

4:30 –  
4:55 pm

## **Agentic AI for Autonomous Science at Leadership-Class Facilities**

*Rafael Ferreira da Silva, Oak Ridge National Laboratory*

Renan Souza, Daniel Rosendo, Kelsey Carter, John Lagergren, Frédéric Suter,  
Shelaine L. Curd, and David Weston

*Oak Ridge National Laboratory*

Autonomous, self-driving laboratories promise to compress the discovery cycle, but bringing agentic AI to leadership-class science is less a modeling problem than an infrastructure one. The hard parts are federation across security domains, separation of control and data planes, and provenance rigorous enough to be reused as training data, none of which cloud-native agentic frameworks were designed to provide. We present an end-to-end agentic AI framework, built and deployed at Oak Ridge National Laboratory, that realizes this infrastructure for high-throughput plant phenotyping under the DOE Orchestrated Platform for Autonomous Laboratories (OPAL). The framework is organized as two execution domains that mirror the operational reality of a national laboratory. A cloud-hosted conversational plane exposes a co-scientist agent that translates natural-language scientific questions into structured analysis plans, and an HPC execution plane runs a headless compute agent that dispatches vision transformer inference across GPU nodes on the Frontier exascale supercomputer. The two agents, built on the Academy actor-model middleware, run in separate security and resource domains and communicate through a secure, token-authenticated streaming channel, while FlowCept captures end-to-end provenance, from natural-language prompt to returned result, for every interaction. This separation preserves the institutional security boundaries that real DOE deployments require while letting the conversational agent invoke remote HPC actions as if they were local. In early testing against APPL's live data lakehouse, a cold request that triggers computation on Frontier completes in about five minutes, semantically related follow-up questions return in under a minute, and provenance adds less than 1% execution overhead. We argue that this federation-, plane-, and provenance-aware pattern generalizes beyond one facility toward the interconnected autonomous-science network the DOE Genesis Mission envisions.

4:55 –  
5:00 pm

## **Evening Logistics**

*Bobbie-Jo Webb-Robertson*

5:30 –  
7:30 pm

## **Poster Session**

## DAY 2 | WEDNESDAY, SEPTEMBER 23, 2026

| TIME            | TOPIC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|-----------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 8:30 – 8:35 am  | <b>Conference Welcome and Logistics</b><br><i>Bobbie-Jo Webb-Robertson</i>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| 8:35 – 8:55 am  | <b>Securing America’s Scientific and Innovation Edge Against Emerging Threats</b><br><i>Scott Fagan, Director, Office of Threat Assessment, Bureau of Emerging Threats</i>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| 8:55 – 11:30 am | <b>SESSION 4 – AI-guided Protein and Pathway Engineering</b><br><i>Chair: Kristin Burnum-Johnson</i>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 8:55 – 9:40 am  | <b>Invited Talk – Trifecta: Using AI Agents, High Performance Computing and Autonomous Labs for Biological Design</b><br><i>Arvind Ramanathan, Argonne National Laboratory</i> <p>Designing functional biomolecules such as enzymes, protein binders, and biotherapeutics has historically required years of iterative experimentation. We present a framework that compresses this cycle into an autonomous reasoning loop connecting three pillars: genome-scale foundation models, generative design engines, and robotic laboratory infrastructure. Genome-scale language models (GenSLM, HiGenLM) distill evolutionary sequence knowledge into rich biological representations that can be used to design enzymes such as tryptophan synthase B. We extend this to design therapeutic peptides through StructBioReasoner, a multi-agent system that navigates multi-objective fitness landscapes for disordered protein binder candidates against targets such as the NMNAT-2/p53 interface. Active experimental design feeds observations back into the generative cycle, iteratively refining structural hypotheses at scale. Together, this framework redefines biomolecular design as a continuously learning, machine-driven process accelerating discovery from genomes to therapeutic interventions.</p> |

9:40 –  
10:05 am

## **A Generalizable Biodesign-driven Framework for Tuning Metabolic Flux at the Protein Level**

*Elise Van Fossen, Pacific Northwest National Laboratory*

Chinemerem Ogbu, Oscar Rodriguez, Madelyn R. Berger, Rowan Wooldridge, Will Chrisler, Abdullah Shouaib, Samantha M. Powell

*Pacific Northwest National Laboratory*

Metabolic engineering has traditionally focused on genetically modifying gene expression or introducing heterologous enzymes to increase pathway flux. Here, we present two complementary strategies that instead act at the protein level; extrinsic activation via engineered protein binders and intrinsic activation via targeted post-translational modifications (PTMs). These strategies modulate key flux-controlling metabolic enzymes directly, while leaving native genetic machinery and regulation intact, with activation expressed under inducible control. We first present a selection workflow for identifying small protein binders capable of activating target enzymes via engineered protein-protein interactions. With this pipeline, we identify a nanobody that binds the metabolic enzyme isocitrate dehydrogenase (ICD) and increases its catalytic activity in living bacterial cells, leaving the native enzyme sequence unmodified. Second, using genetic code expansion, we generate pre-activated pyruvate kinase (PyK) bearing site-specific activating PTMs, which directly increase host growth rate in vivo. These orthogonal strategies represent a modular, biodesign-driven framework for tuning metabolic flux at the protein level, complementary to existing transcriptional and pathway engineering approaches, with broad applicability across high-value metabolic pathways and the potential to generate experimentally grounded datasets that inform future AI-guided protein and pathway engineering.

10:05 –  
10:20 am

## **Break**



10:20 –  
11:05 am

## **Pathways in Context: Model-guided Engineering Across Genomes, Metabolism, and Engineered Environments**

*James Carothers, University of Washington*

Biological pathways do not function in isolation. Their performance emerges from interactions with host genomes, endogenous metabolic networks, and the physical environments in which they operate. Predictive pathway engineering therefore requires approaches that treat these contexts as design variables and use complementary models to connect interventions with measurable phenotypes. This presentation will examine pathway engineering across three coupled contexts. First, we consider the host genome. Machine learning-guided design of multigene programs and CRISPR-enabled design-build-test-learn workflows enable systematic exploration of pathway and host-regulatory design space. Standardized genome integration allows identical genetic programs to be installed across diverse microbial hosts, revealing how strain-specific physiology shapes pathway performance. In one example, the same aromatic bioconversion pathway produced divergent outcomes in two closely related *Rhodopseudomonas palustris* strains. Pooled single-cell CRISPR transcriptomics provides a complementary approach for mapping genetic perturbations to regulatory states and identifying interactions relevant to pathway control. Second, we examine lysate-based cell-free systems. Carbon-conserving multienzyme pathways create opportunities to control carbon flux independently of cellular growth but remain coupled to endogenous lysate metabolism. Constraint-based and mechanistic kinetic models help explain these interactions and predict how enzyme levels, substrates, cofactors, lysate conditioning, and competing reactions shape pathway behavior. Automated model construction, high-performance parameter optimization, and code-enabled model interrogation expand the design spaces that can be evaluated while retaining mechanistic simulation and experiment as validation layers. Finally, we consider hydrogels as engineered pathway environments. Immobilizing multienzyme systems can improve catalyst retention and reuse, while encapsulating engineered cells can sustain responsive genetic programs and repeated bioproduction. Together, these examples establish a framework in which data-driven models, mechanistic models, and controlled experimentation are combined to design pathways across genomic, metabolic, and engineered environmental contexts.

11:05 –  
11:30 am

## **OpenPhase: Condition-Aware Exploration of Multicomponent Biosystem Phase-Separating Behavior**

*Peiran Jian, Carnegie Mellon University*

Adrita Das<sup>1</sup>, Weifeng Wu<sup>1</sup>, Dantong Zhu<sup>2</sup>, Huaiying Zhang<sup>1</sup>, and Jose Lugo-Martinez<sup>1</sup>

<sup>1</sup>Carnegie Mellon University, <sup>2</sup>Columbia University

Liquid-liquid phase separation (LLPS) organizes proteins, DNA, and RNA into biomolecular condensates, but its behavior depends strongly on molecular composition and experimental conditions. Current machine-learning approaches often treat these factors separately, limiting their ability to characterize multicomponent systems. We present OpenPhase, a condition-aware world model that jointly represents system components, experimental conditions, and phase outcomes. OpenPhase provides curated datasets of experimentally verified phase outcomes and formalizes three linked tasks: condition-aware phase-outcome prediction, condition inference and phase-diagram exploration, and conditional design of phase-separating systems. We instantiate these tasks with predictive and generative models and benchmark them against established approaches. OpenPhase supports forward prediction of phase outcomes, inverse exploration of conditions compatible with a target phase state, and generation of candidate components under specified conditions. The platform exposes these capabilities through a unified API for in silico model development and evaluation. OpenPhase provides a practical framework for connecting environmental context to multicomponent phase behavior and for generating experimentally testable hypotheses in biomolecular condensate research.

11:30 am –  
12:50 pm

## **Lunch Break**

*Douglas Mans, Pacific Northwest National Laboratory,  
Paul Adams, Lawrence Berkeley National Laboratory,  
Dion Antonopoulos, Argonne National Laboratory,  
Dave Weston, Oak Ridge National Laboratory,  
Michelle A. O'Malley, University of California, San Diego,  
Paul Jensen, University of Michigan*

**(Moderators: Kristin Burnum-Johnson & Katrina Waters)**

12:50 –  
3:30 pm

## SESSION 5 – Predictive Models for Microbial Engineering

Chair: Hector Garcia Martin

12:50 –  
1:15 pm

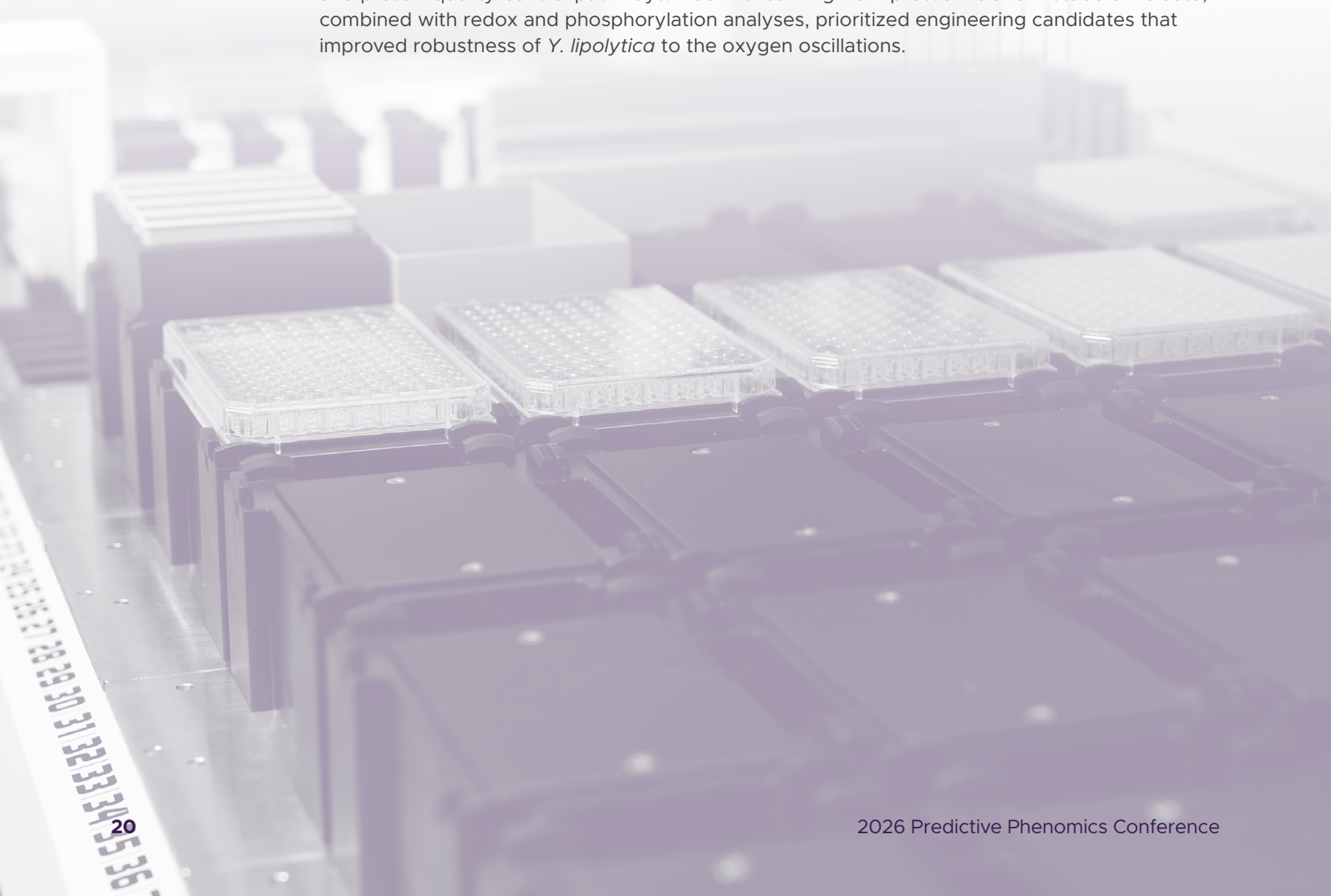
### **Integrating Scale-down Bioreactors and Multi-Omic Machine Learning Analyses to Engineer Robust *Yarrowia lipolytica* Citrate Production**

*Jeffrey Czajka, Pacific Northwest National Laboratory*

Shuang Deng<sup>1</sup>, Jasmin Alvarez<sup>1</sup>, Guoliang Yuan<sup>1</sup>, Yannick Mahlich<sup>1</sup>, Lummy M.O. Monteiro<sup>1</sup>, Xiaolu Li<sup>1</sup>, Song Feng<sup>1</sup>, Teresa Lemmon<sup>1</sup>, Marie Swita<sup>1</sup>, Heather Olson<sup>1</sup>, Josie G Eder<sup>1</sup>, Tong Zhang<sup>1</sup>, Sneha Couvillion<sup>1</sup>, Jason E. McDermott<sup>1,2</sup>, and Kyle R. Pomraning<sup>1</sup>

<sup>1</sup>Pacific Northwest National Laboratory, <sup>2</sup>Oregon Health & Science University

There is increasing demand for biotechnologies that support reliable domestic supply chains. Meeting this demand requires a deeper understanding of the fundamental challenges associated with microbial bioprocess scale-up. Here, the response of *Yarrowia lipolytica* to oxygen fluctuations encountered during bioprocess scale-up was characterized. The effects of 1-minute oscillations between low (5%) and sufficient (25–40%) dissolved oxygen on citric acid production were investigated using a scale-down bioreactor. Oscillations reduced citrate titer from  $30.8 \pm 1.8$  g/L to  $10.0 \pm 0.2$  g/L and decreased yield by 46% relative to a control (25% dissolved oxygen). Multi-omic profiling indicated that productivity loss under oscillations was not simply a chronic hypoxic response, as molecular signatures remained closer to the oxygen-sufficient control. Instead, oscillations selectively altered signaling, protein turnover, and protein quality-control pathways. Machine learning from proteomic and metabolomic data, combined with redox and phosphorylation analyses, prioritized engineering candidates that improved robustness of *Y. lipolytica* to the oxygen oscillations.



1:15 –  
1:40 pm

## **ARThur: An Agentic Subsystem for Closing the Microbial Engineering DBTL Loop**

*Satyarth Praveen, Lawrence Berkeley National Laboratory*

Apostolos Zournas, Jacob Rapp, Hector Garcia Martin

*Lawrence Berkeley National Laboratory*

High-throughput phenotyping demands rapid iteration through design-build-test-learn (DBTL) cycles, yet operating machine learning–powered optimization tools has traditionally required programming expertise. ARThur removes this prerequisite, making state-of-the-art experiment optimization accessible regardless of coding background. The core engine behind ARThur – Automated Recommendation Tool (ART) is a supervised learning algorithm combining machine learning, Bayesian inference, and Monte Carlo sampling to guide active learning cycles, particularly suited to the small-data, high-uncertainty conditions typical of biological experimentation. ARThur wraps around the ART engine to expose it through the Model Context Protocol (MCP), enabling AI coding assistants, like opencode or claude code, to act as intelligent intermediaries between scientists and the optimization framework. Scientists describe their experiment in natural language; the system handles generating recommendations, producing robotic instructions, and validating stock bounds. ARThur further simplifies this by introducing dedicated skills and sub-agents for navigating the experimentation process. The skill provides the domain-specific procedural workflow while complex sub-tasks within this workflow are delegated to the appropriate sub-agents. Together, this agentic sub-system mirrors how a well-run laboratory delegates work between a project manager and domain experts. This enables a modular, auditable, human-in-the-loop AI pipeline. Currently, ARThur ships with a media-optimization skill that guides scientists through the full DBTL workflow for microbial media composition, from feasibility bounds and ART recommendations to validated robotic liquid handling instructions. We are building this pipeline toward a fully autonomous DBTL cycle along with features for the user to easily investigate the intermediate data and scripts without any heavy programming intervention. ARThur taps into the realm of conversational AI as operational infrastructure for predictive phenomics, lowering the barrier to state-of-the-art experiment design and accelerating the rate at which genotype-phenotype space can be explored.



1:40 –  
2:05 pm

## CatPred 2.0: Extending Enzyme Kinetic Parameter Prediction for Enzyme Variants

*Somtirtha Santra, The Pennsylvania State University*

Veda Sheersh Boorla, Haixing Piao, Noah Guyer, and Costas D. Maranas

*The Pennsylvania State University*

Enzyme engineering requires quantitative approaches that can predict how amino acid substitutions alter catalytic performance before experimental screening. We present CatPred 2.0, a machine learning framework for predicting absolute and mutation-induced changes in three kinetic parameters: turnover number ( $k_{cat}$ ), Michaelis constant ( $K_m$ ), and catalytic efficiency ( $k_{cat}/K_m$ ). CatPred 2.0 addresses key challenges in extending kinetic parameter prediction to enzyme variants, including the scarcity of paired wild-type and variant kinetic data. The framework combines protein language model embeddings, a message-passing substrate encoder, chemical language model representations, and a mutation-aware encoder capturing physicochemical property changes and evolutionary conservation. It is trained jointly on wild-type and variant enzyme data to model how individual mutations affect substrate binding and catalytic turnover within a single architecture. CatPred 2.0 improves on a retrained CatPred baseline across all three parameters and outperforms existing kinetic prediction methods, including DLKcat, UniKP, CataPro, and EITLEM-Kinetics. Generalization was assessed using sequence-similarity-based out-of-distribution splits and independent test sets spanning multiple enzyme families. Beyond predicting absolute kinetic parameters, modeling the differential effect of mutations enables direct prioritization of variants according to predicted changes in catalytic performance, extending kinetic parameter prediction toward mutation-aware enzyme design and providing a computational strategy for reducing the experimental search space in enzyme engineering.

2:05 –  
2:15 pm

## Break

2:15 –  
2:40 pm

## High-throughput Genetic Tools and Automation for Gene Discovery and Microbial Engineering

*Carrie Eckert, Oak Ridge National Laboratory*

Margaret Bales<sup>1,2</sup>, Jiwoo Kim<sup>1</sup>, Yasemin Kaygusuz<sup>1</sup>, Andrea Garza Elizando<sup>1</sup>, Rebecca Wilkes<sup>1</sup>, Ilene del Valle Kessra<sup>1</sup>, William Alexander<sup>1</sup>, Adam Guss<sup>1</sup>

<sup>1</sup>Oak Ridge National Laboratory, <sup>2</sup>University of Tennessee

The ability to effectively engineer microbes for the conversion of cheap feedstocks to a variety of performance-advantaged chemicals and products is key for achieving economically viable and scalable platforms for an emerging bio-based economy. Even the most studied chassis, *E. coli* and *S. cerevisiae*, remain limited in application due to a lack of functional understanding of all genes in their genomes and how to effectively engineer complex phenotypes (e.g., tolerance) and heterologous production pathways. There are many non-model microbes with natural capabilities for key bioconversion processes, but lagging genetic tool development slows engineering efforts. Approaches for accelerated microbial engineering rely on the development of enabling genetic toolsets across a broader range of microbial species and the deployment of these tools in a design-build-test-learn (DBTL) research cycle to expand generation of datasets, both global and targeted, to reveal underlying design principles to address engineering challenges. The application of CRISPR-Cas has enabled library based high-throughput and multiplexed experiments for genotype-phenotype mapping, protein engineering, strain engineering, and novel gene discovery in model microbial systems. Here I will discuss recent advances and future applications of genetic tool development and automation of microbial transformation towards engineering and high throughput functional genomics platforms for a broadening array of microbes.

2:40 –  
3:05 pm

## Universal Modular Cell Design for Scalable Biomanufacturing of Chemicals

*Cong Trinh, University of Tennessee*

Microbial metabolism provides a versatile platform for producing fuels, chemicals, and materials. However, conventional metabolic engineering optimizes strains one product at a time through multiple design-build-test-learn (DBTL) cycles, making strain development costly, labor intensive, and difficult to scale across broad chemical spaces. Modular cell (ModCell) design offers an alternative strategy in which a chassis strain is engineered for compatibility with multiple interchangeable production modules, enabling reuse of engineering efforts across many products and reducing the need for product-specific host development. Here, we present ModCell, a computational platform that systematically identifies chassis strains compatible with large libraries comprising hundreds of endogenous and heterologous production modules. ModCell integrates genome-scale metabolic modeling, mass balance, omics-based enzyme constraints, multi-objective evolutionary optimization, set combinatorics, and reinforcement learning to identify genetic designs that balance competing objectives across many products simultaneously. Unlike single-product approaches, ModCell maximizes compatibility while maintaining favorable production phenotypes across diverse target pathways. In addition, ModCell analyzes resource allocation tradeoffs using enzyme-constrained genome-scale models, evaluating proteome allocation, enzyme usage, and metabolic burden across chassis-module combinations. To support practical strain selection, ModCell incorporates a solution consolidation strategy based on the minimal set cover problem, identifying compact, high-coverage solution sets and deriving universal modular cell designs from Pareto-optimal outputs across hundreds of product modules. As an experimental testbed, we will demonstrate ModCell designs for the efficient, switchable biosynthesis of diverse alcohols and esters from cellulosic biomass, molecules with broad applications as fragrances, flavors, solvents, and fuels. We envision that ModCell will enable rapid strain development, shifting metabolic engineering from iterative DBTL cycles toward streamlined design-build (DB) processes, thereby supporting scalable and efficient biomanufacturing of chemicals.

3:05 –  
3:30 pm

## MAESTRO Identifies Dosage-Tunable Tandem Paralog for Predictive Microbial Engineering

*Yasuo Yoshikuni, Lawrence Berkeley National Laboratory*

Predicting microbial phenotypes from genomic variation remains difficult when strain cohorts are modest, variants are rare, and structurally complex features such as copy-number variation (CNV) are poorly captured by conventional genome-wide association approaches. We developed MAESTRO, a machine-learning framework that integrates quantitative CNV profiles with high-throughput phenotyping to prioritize genomic dosage features reproducibly associated with stress tolerance across repeated resampling. We applied MAESTRO to 170 natural isolates of the multi-stress-tolerant yeast *Pichia kudriavzevii*, an emerging industrial host for low-pH fermentation and biomanufacturing, phenotyped across diverse industrial and antifungal stresses. MAESTRO recovered established stress-response loci in *Saccharomyces cerevisiae* benchmarks and in *P. kudriavzevii* identified stress-associated CNVs strongly enriched at tandem paralogs (TPs) encoding transport and metabolic functions. These results show that MAESTRO can move beyond prediction to elucidate mechanisms underlying natural adaptive evolution by revealing interpretable routes through which stress tolerance emerges. To test whether these features remained accessible during ongoing adaptation, we independently applied MAESTRO to genome-wide CNV profiles from 168 isolates collected during time-resolved adaptive laboratory evolution under increasing chemical stress. Without prespecifying candidates from the natural population, MAESTRO again converged on TP dosage features. Evolutionary trajectories revealed both amplification and contraction of these loci, direction-specific perturbations reproduced the corresponding adaptive effects, and structural reconstruction showed that adaptive copy-number changes arose through local remodeling of pre-existing tandem arrays rather than duplication elsewhere in the genome. These findings support a “genomic equalizer” model in which tandem organization creates dosage-tunable loci that can be adjusted upward or downward as selective demands change. Because altered dosage states can persist across generations, TP arrays may also provide a heritable record of prior stress selection, linking environmental history to future adaptive potential. Together, MAESTRO provides an interpretable framework for uncovering mechanisms of natural adaptation while identifying actionable genomic features for engineering stress-robust industrial microbes.

3:30 –  
3:40 pm

## Closing Remarks

# POSTER PRESENTATIONS

| POSTER<br>NUMBER | PRESENTER/TITLE                                                                                                                                                                                             | POSTER<br>NUMBER | PRESENTER/TITLE                                                                                                                                                                        |
|------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>1001</b>      | <b>Luke Fisher</b><br><i>Pacific Northwest National Laboratory</i><br>Accelerating Microbial Phenotyping through Automated, High-throughput Experimentation using the Anaerobic Phenotyping Platform (AMP2) | <b>2001</b>      | <b>Sutanay Choudhury</b><br><i>Pacific Northwest National Laboratory</i><br>Networked Human-AI Intelligence Accelerates Phenotype-Guided Experimental Design in a Multi-Omics Campaign |
| <b>1002</b>      | <b>Andrea Garza Elizondo</b><br><i>Oak Ridge National Laboratory</i><br>High-throughput Automated Genetic Transformation, Serial Dilution and Spot Plating of Bacteria                                      | <b>2002</b>      | <b>Archit Vasan</b><br><i>Argonne National Laboratory</i><br>RAGmosis: a Provenance-gated, Self-growing Knowledge-Graph with Diffusion Retrieval for Autonomous Scientific Agents      |
| <b>1003</b>      | <b>Cody Kamoku</b><br><i>Pacific Northwest National Laboratory</i><br>Whole Cell Biosensors for High-throughput Screening of Two Stage Bioprocesses                                                         | <b>2003</b>      | <b>Moses Obiri</b><br><i>Pacific Northwest National Laboratory</i><br>Transfer Learning Improves Proteomics-Based Infection Phenotyping                                                |
| <b>1004</b>      | <b>Sankar Krishnamoorthy</b><br><i>Pacific Northwest National Laboratory</i><br>Chemical Probes for Microbial Phenotyping and Mechanistic Investigation                                                     | <b>2004</b>      | <b>Jesus N. Pedroza-Montero</b><br><i>University of Texas at El Paso</i><br>GPU-Accelerated Molecular Phenomics for Screening PFAS Effects on Irregular and Chiral Biological Systems  |
| <b>1231</b>      | <b>Benjamin David</b><br><i>University of Michigan</i><br>From Designs to Data: The Logistics of Autonomous Microbial Growth Experiments                                                                    | <b>2005</b>      | <b>Kirsten Hofmockel</b><br><i>Pacific Northwest National Laboratory</i><br>AI-leveraged Workflows for Multi-Omics Integration                                                         |
| <b>1301</b>      | <b>R. Seth Wood</b><br><i>Pacific Northwest National Laboratory</i><br>Closing the Loop: Autonomous DBTL on a Dual-Atmosphere Phenotyping Platform                                                          | <b>2301</b>      | <b>Rob Egbert</b><br><i>Pacific Northwest National Laboratory</i><br>Autonomous Biodesign Platform Accelerates Bioproduction Discovery with Agentic AI                                 |
| <b>1302</b>      | <b>William Herbert</b><br><i>University of Michigan</i><br>Deriving the Value of Microbial Phenotyping Experiments through Prior Knowledge                                                                  | <b>2341</b>      | <b>Jacquelyn Martin</b><br><i>University of Arizona</i><br>The Raíces Project: A Framework for AI-Based Cancer Prediction in Genetically Admixed Populations                           |
| <b>1601</b>      | <b>Sina Barazandeh</b><br><i>Carnegie Mellon University</i><br>Agentic Fault Recovery for Autonomous Orchestration of Programmable Cloud Laboratories                                                       | <b>2401</b>      | <b>Costas Maranas</b><br><i>The Pennsylvania State University</i><br>PathLM: Balance-Constrained AI Design of Enzymatic Biosynthetic Pathways                                          |

POSTER  
NUMBER

PRESENTER/TITLE

**2402**

**Matthew Sinclair**

*Argonne National Laboratory*

Agentic Orchestration of Genomics-Informed Protein Language Models and Physics-Based Simulation for Glucose Dehydrogenase Engineering

**2403**

**Ben Drucker**

*Pacific Northwest National Laboratory*

Integrating Virus-Host Data and AI-Assisted Workflows to Illuminate Virome Dark Matter

**3001**

**Aivett Bilbao**

*Pacific Northwest National Laboratory*

AI-Assisted Mass Spectrometry Data Analysis with PeakDecoder: Towards Autonomous Predictive Phenomics for Microbial Systems

**3002**

**Noelle Toong**

*University of Michigan*

Adaptive screening designs for discovering minimal media with Bayesian optimization

**4001**

**Xinran Lian**

*Argonne National Laboratory*

Genomic Co-occurrence does not Predict the Best Enzyme Complex: AI-Driven Discovery, Characterization and Design of VerAB O-demethylases at Scale

POSTER  
NUMBER

PRESENTER/TITLE

**4002**

**Jason McDermott**

*Pacific Northwest National Laboratory*

PathwaySeeker: Evidence-Grounded AI Reasoning for AI-Guided Metabolic Pathway Engineering

**4003**

**Moeen Meigooni**

*Argonne National Laboratory*

Toward Autonomous Agentic Frameworks for Protein Binder Design Against Intrinsically Disordered Targets

**4004**

**Haixing Piao**

*The Pennsylvania State University*

Structure-Agnostic Prediction of Protein-Protein Binding Affinity from Sequence

**4005**

**Abdullah Shouaib**

*Pacific Northwest National Laboratory*

SynBinder: An AI-Driven Platform for End-to-End De Novo Protein Binder Design and Experimental Validation

**4006**

**Jina Son**

*Lawrence Berkeley National Laboratory*

AI-Guided Engineering of PHA Synthase for  $\alpha$ -Branched Monomer Polymerization

**4501**

**Yannick Mahlich**

*Pacific Northwest National Laboratory*

Leveraging Variation in Large-scale Omics Data with VaLPAS and VFM using AI to Enable Microbial Engineering

| POSTER<br>NUMBER | PRESENTER/TITLE                                                                                                                                                                                                       |
|------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>4502</b>      | <b>Xinran Lian</b><br><i>Argonne National Laboratory</i><br>High-throughput Screening and De novo<br>Design of Mevalonate 5-phosphate<br>decarboxylase for Enhanced isoprenol<br>Biosynthesis                         |
| <b>4503</b>      | <b>Dylan Ross</b><br><i>Pacific Northwest National Laboratory</i><br>Proteomics-guided Annotation of<br>Metabolomic Dark Matter Enables<br>Pathway-Resolved Phenotyping of<br>Engineered Microbes                     |
| <b>5001</b>      | <b>Margaret Cheung</b><br><i>Pacific Northwest National Laboratory</i><br>Stochastic 4D Whole-Cell Modeling<br>Reveals Redox-PTM Regulatory Networks<br>Driving Cyanobacterial Phenotypes under<br>Light Perturbation |
| <b>5002</b>      | <b>Vasumitra Rao</b><br><i>University of Michigan</i><br>ALERT: An Automated Discovery Pipeline<br>for Higher-order Interactions in Microbial<br>Growth Dynamics                                                      |

| POSTER<br>NUMBER | PRESENTER/TITLE                                                                                                                                                                                                                                      |
|------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>5003</b>      | <b>Winston Anthony</b><br><i>Pacific Northwest National Laboratory</i><br>GIMME: Warm-start Bayesian<br>Optimization using Pre-trained Neural<br>Network Embeddings meet or Exceed<br>Cold-start during in silico Autonomous<br>Laboratory Campaigns |
| <b>5004</b>      | <b>Kristofer Bouchard</b><br><i>Lawrence Berkeley National Laboratory</i><br>Massively Multimodal AI Foundation<br>Model for Protein Function Enhancement                                                                                            |
| <b>5005</b>      | <b>Amy Zimmerman</b><br><i>Pacific Northwest National Laboratory</i><br>Integrating Experiments and Genome-<br>scale Models to Understand Metabolic<br>Handoffs among Rhizobacteria and Drive<br>Autonomous Biodesign                                |

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## NOTES

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**2026 PREDICTIVE PHENOMICS  
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AI AND AUTOMATION